Detailed Protein Report

Project Info

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

Note:

Sample Info & Protocols

Name: ID-M **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 22:06:28	/teeth-151208/ID-M/"Combined MS/MS spectra"	Mascot	refseq_human

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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: 1200.0

MW [kDa]: 69.3

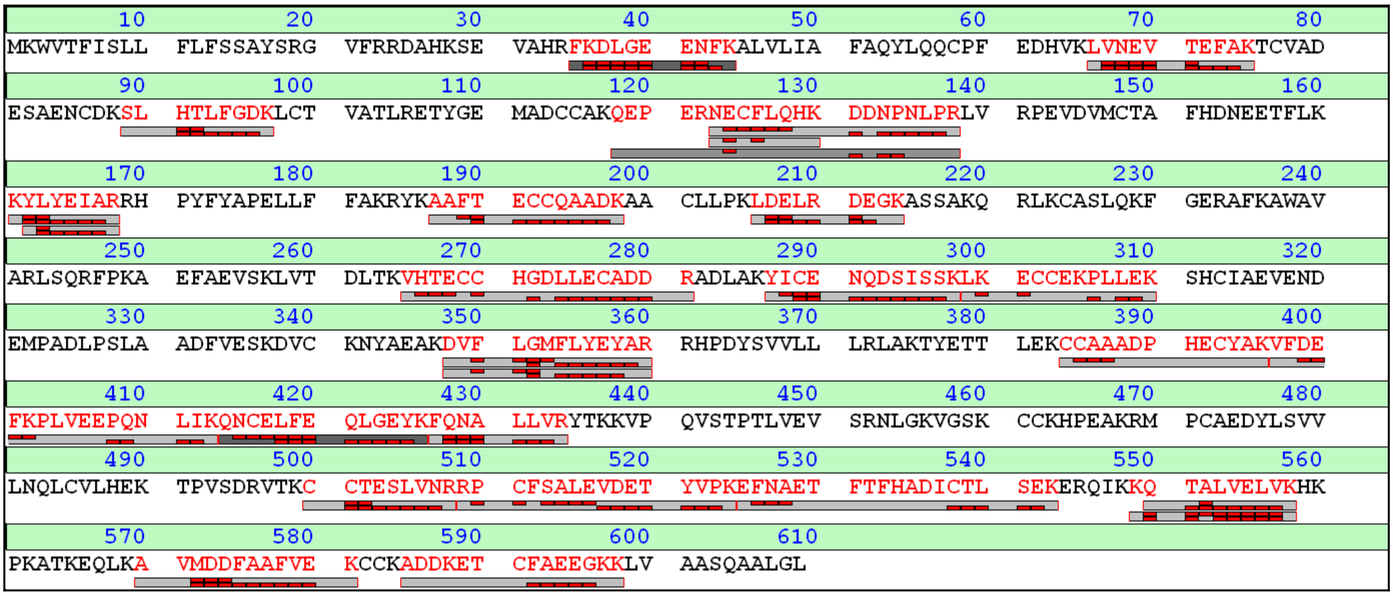
pI: 5.9

Sequence Coverage [%]: 43.3

No. of unique Peptides: 26

Quantitation

MD:MU **Median:** 0.95 **CV:** 48.22 % **No. of Peptides:** 11



Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
218	5	613.6618	-235.22	2	32.4	67.0	1	35-44	R.FKDLGEENFK.A		
581	11	575.1784	-230.65	2	36.9	63.0	0	66-75	K.LVNEVTEFAK.T		MD:MU 0.44
357	5	509.1363	-266.02	2	33.8	49.0	0	89-97	K.SLHTLFGDK.L		
166	2	879.4220	9.29	3	31.5	20.2	2	118-138	K.QEPERNECFLQHKDDNPNLPR.L	Carbamidomethyl: 8	MD:MU 1.14
328	1	509.7430	1.26	2	33.5	11.8	0	123-130	R.NECFLQHK.D		
213	1	666.3221	11.20	3	32.0	43.3	1	123-138	R.NECFLQHKDDNPNLPR.L	Carbamidomethyl: 3	MD:MU 0.65
258	1	528.1494	-281.00	2	32.9	20.3	1	161-168	K.KYLYEIAR.R		MD:MU 1.34
404	7	464.1276	-264.45	2	34.7	29.4	0	162-168	K.YLYEIAR.R		
41	2	686.2847	-3.37	2	30.2	57.0	0	187-198	K.AAFTECCQAADK.A	Carbamidomethyl: 6, 7	
											MD:MU 1.06

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
31	3	537.7767	3.24	2	30.1	45.4	1	206-214	K.LDELRDEGK.A		
143	2	696.2767	-10.48	3	31.5	53.1	0	265-281	K.VHTECCHGDLLECADDR.A	Carbamidomethyl: 5, 6, 13	MD:MU 0.47
43	6	722.3176	-9.77	2	29.9	70.8	0	287-298	K.YICENQDSISSK.L	Carbamidomethyl: 3	MD:MU 1.10
86	2	773.8871	-19.34	2	30.5	20.6	1	299-310	K.LKECCEKPLLEK.S	Carbamidomethyl: 4, 5	
2841	5	812.4044	8.52	2	65.9	42.2	0	348-360	K.DVFLGMFLYEYAR.R		
2327	7	820.2531	-172.78	2	59.0	52.7	0	348-360	K.DVFLGMFLYEYAR.R	Oxidation: 6	
4	7	776.8063	4.85	2	28.8	27.2	0	384-396	K.CCAAADPHECYAK.V	Carbamidomethyl: 1, 2, 10	
2151	19	1022.9578	-91.39	2	56.8	49.0	0	397-413	K.VFDEFKPLVEEPQNLIK.Q		
1272	10	829.3522	-33.47	2	45.5	60.5	0	414-426	K.QNCELFEQLGEYK.F	Carbamidomethyl: 3	MD:MU 0.70
645	6	480.6456	-289.76	2	37.6	42.7	0	427-434	K.FQNALLVR.Y		
78	3	569.7455	-12.45	2	30.7	62.5	0	500-508	K.CCTESLVNR.R	Carbamidomethyl: 1, 2	
1168	1	637.6405	-12.97	3	44.2	54.8	0	509-524	R.RPCFSALEVDETYVPK.E	Carbamidomethyl: 3	
2158	4	753.9220	-119.94	3	56.9	37.4	0	525-543	K.EFNAETFTFHADICTLSEK.E	Carbamidomethyl: 14	MD:MU 1.34
421	2	564.7074	-257.77	2	34.6	52.0	1	549-558	K.KQTALVELVK.H		MD:MU 1.95
804	9	500.6657	-279.19	2	39.5	47.2	0	550-558	K.QTALVELVK.H		MD:MU 1.38
1982	11	671.7238	-144.76	2	54.9	77.6	0	570-581	K.AVMDDFAAFVEK.C		
21	2	543.2367	-19.25	3	29.6	43.1	2	585-598	K.ADDKETCFAEEGKK.L	Carbamidomethyl: 7	

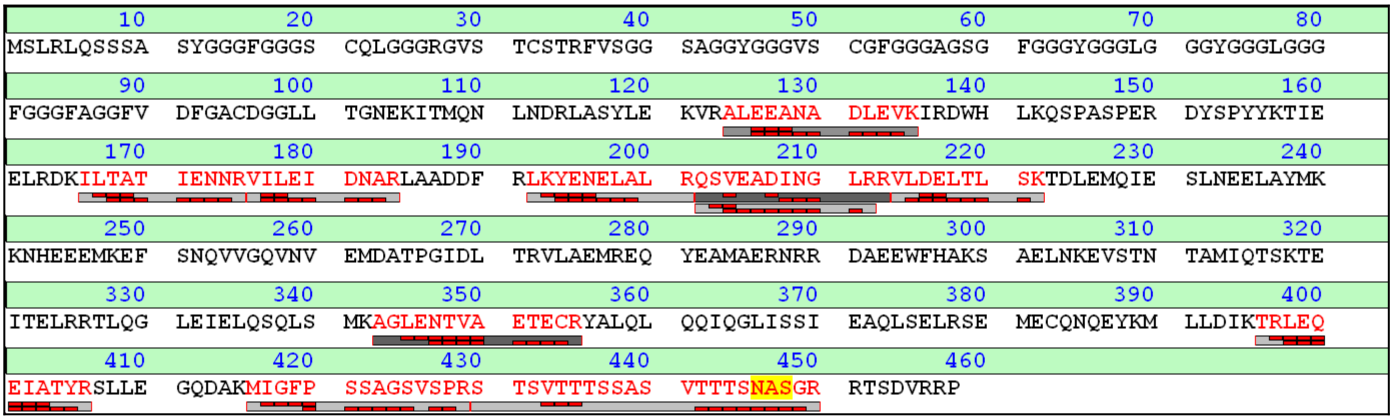
Detailed Protein Report

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

Accession:	gi|131412225	**Score:**	557.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	49.5
Database Date:	2015-11-30	**pI:**	4.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	26.4
		No. of unique Peptides:	11

Quantitation

MD:MU **Median:** 0.48 **CV:** 24.79 % **No. of Peptides:** 9



```
        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	
269	2	651.1939	-213.19	2	32.7	78.3	0	124-135	R.ALEEANADLEVK.I		MD:MU	0.38
211	1	572.8141	-9.69	2	32.3	55.6	0	166-175	K.ILTATIENNR.V		MD:MU	0.53
528	4	521.6763	-233.65	2	35.9	61.6	0	176-184	R.VILEIDNAR.L		MD:MU	0.37
395	1	624.8212	-47.61	2	34.3	26.0	1	192-201	R.LKYENELALR.Q		MD:MU	0.79
379	3	601.3190	11.24	2	34.1	54.4	0	202-212	R.QSVEADINGLR.R		MD:MU	0.36
235	1	679.3515	-16.64	2	32.3	26.4	1	202-213	R.QSVEADINGLRR.V		MD:MU	0.60
604	2	509.1500	-284.72	2	36.9	50.6	0	214-222	R.VLDELTLSK.T			
142	3	725.3217	-19.13	2	31.2	69.4	0	343-355	K.AGLENTVAETECR.Y	Carbamidomethyl: 12	MD:MU	0.44
269	3	690.3609	-9.58	2	33.1	55.3	1	396-406	K.TRLEQEIATYR.S		MD:MU	0.55
768	1	696.8079	-61.40	2	39.0	28.8	0	416-429	K.MIGFPSSAGSVSPR.S			
33	2	1001.9745	-5.27	2	29.8	50.9	0	430-450	R.STSVTTTSSASVTTTSNASGR.R		MD:MU	0.45

Detailed Protein Report

Protein 3: keratin, type II cytoskeletal 6A [Homo sapiens]

Accession:	gi|5031839	**Score:**	421.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	60.0
Database Date:	2015-11-30	**pI:**	8.9
		Sequence Coverage [%]:	18.1
		No. of unique Peptides:	9

Quantitation

MD:MU **Median:** 0.81 **CV:** 49.78 % **No. of Peptides:** 5

```
        10         20         30         40         50         60         70         80
MASTSTTIRS HSSSRRGFSA NSARLPGVSR SGFSSVSVSR SRGSGGLGGA CGGAGFGSRS LYGLGGSKRI SIGGGSCAIS

        90        100        110        120        130        140        150        160
GGYGSRAGGS YGFGGAGSGF GFGGGAGIGF GLGGGAGLAG GFGGPGFPVC PPGGIQEVTV NQSLLTPLNL QIDPTIQRVR

       170        180        190        200        210        220        230        240
AEEREQIKTL NNKFASFIDK VRFLEQQNKV LETKWTLLQE QGTKTVRQNL EPLFEQYINN LRRQLDSIVG ERGRLDSELR

       250        260        270        280        290        300        310        320
GMQDLVEDFK 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
QCANLQAAIA DAEQRGEMAL KDAKNKLEGL EDALQKAKQD LARLLKEYQE LMNVKLALDV EIATYRKLLE GEECRLNGEG

       490        500        510        520        530        540        550        560
VGQVNISVVQ STVSSGYGGA SGVGSGLGLG GGSSYSYGSG LGVGGGFSSS 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
646	5	602.1748	-244.40	2	37.4	36.8	0	195-204	K.WTLLQEQGTK.T		
2813	2	682.9825	-67.79	3	65.6	26.1	1	208-223	R.QNLEPLFEQYINNLRR.Q		
1215	2	591.1296	-252.65	2	44.9	47.4	0	241-250	R.GMQDLVEDFK.N		
212	1	675.8653	-2.24	2	32.0	57.5	1	261-272	R.TAAENEFVTLKK.D		MD:MU 0.49
1892	12	704.2620	-138.19	2	53.7	69.2	0	288-299	K.ADTLTDEINFLR.A		MD:MU 0.59
2394	1	665.3448	-32.87	2	59.8	62.6	0	327-338	R.NLDLDSIIAEVK.A		MD:MU 0.65
167	1	583.1671	-220.95	2	31.8	56.5	0	360-369	K.YEELQVTAGR.H		MD:MU 1.09
303	1	577.1338	-255.87	2	33.1	22.3	0	447-455	K.EYQELMNVK.L		
1633	5	632.2990	-81.98	2	50.2	43.1	0	456-466	K.LALDVEIATYR.K		MD:MU 1.76

Detailed Protein Report

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

Accession: gi|4557321
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

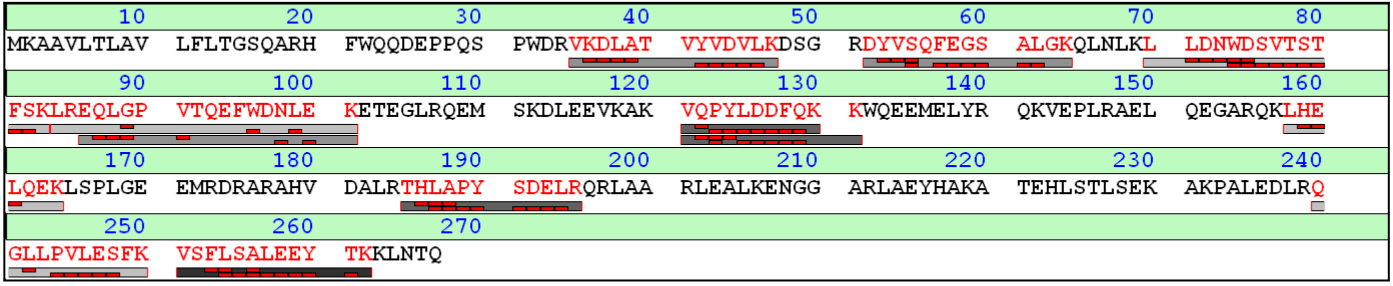
Score: 380.9
MW [kDa]: 30.8
pI: 5.5
Sequence Coverage [%]: 41.2
No. of unique Peptides: 11

Quantitation

MD:MU **Median:** 0.60 **CV:** 53.99 % **No. of Peptides:** 3

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
1864	3	731.8056	-169.23	2	53.2	27.6	1	35-47	R.VKDLATVYVDVLK.D		
879	1	700.6959	-203.14	2	40.4	28.4	0	52-64	R.DYVSQFEGSALGK.Q		MD:MU 1.22
1776	8	806.8793	-21.03	2	52.0	89.5	0	70-83	K.LLDNWDSVTSTFSK.L		
2784	1	734.7111	-0.04	3	66.2	16.8	1	84-101	K.LREQLGPVTQEFWDNLEK.E		
2222	1	966.8539	-120.62	2	57.6	15.7	0	86-101	R.EQLGPVTQEFWDNLEK.E		
556	4	626.8185	7.06	2	36.5	29.2	0	121-130	K.VQPYLDDFQK.K		MD:MU 0.48
345	1	690.7121	-216.32	2	34.0	32.1	1	121-131	K.VQPYLDDFQKK.W		
1373	1	896.6035	133.69	1	46.9	10.1	0	158-164	K.LHELQEK.L		
207	1	651.3188	-13.88	2	32.3	46.5	0	185-195	R.THLAPYSDELR.Q		MD:MU 0.38
1846	7	615.7644	-152.39	2	52.9	27.1	0	240-250	R.QGLLPVLESFK.V		
2827	19	693.8609	-0.42	2	65.8	57.9	0	251-262	K.VSFLSALEEYTK.K		

Detailed Protein Report

Protein 5: **keratin, type I cytoskeletal 15 [Homo sapiens]**

Accession:	gi|24430190	**Score:**	319.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	49.2
Database Date:	2015-11-30	**pI:**	4.6
		Sequence Coverage [%]:	14.0
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 0.55 **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	
811	4	515.1698	-253.80	2	39.5	44.9	0	215-223	R.VLDELTLAR.T		MD:MU	0.55

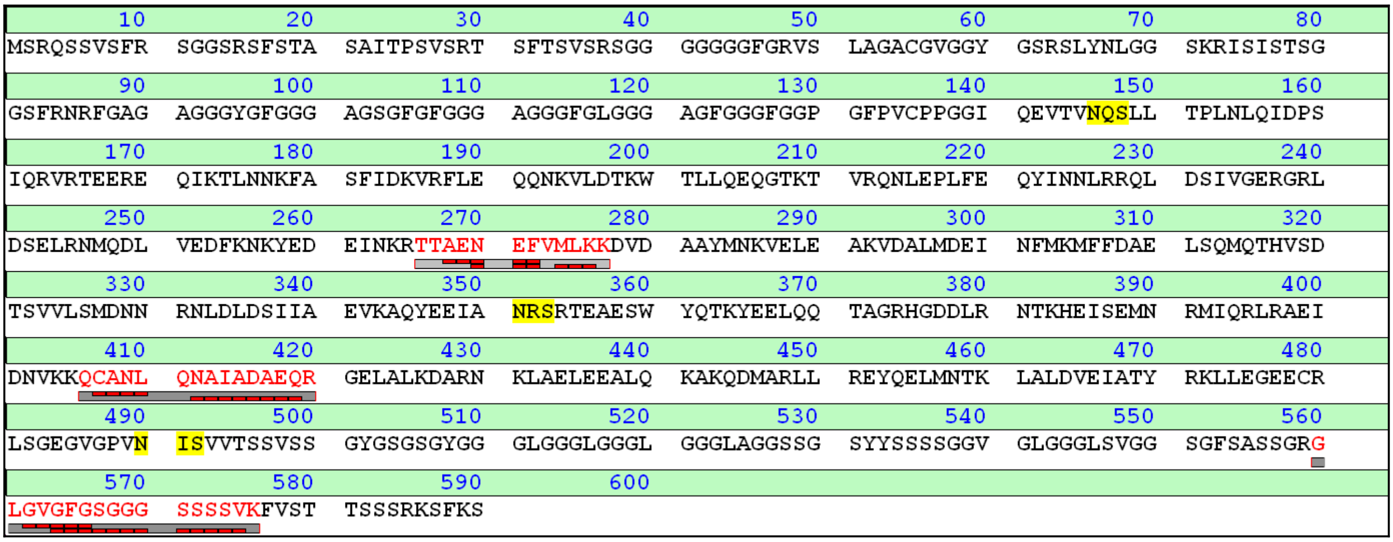
Detailed Protein Report

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

Accession:	gi|119395754	**Score:**	312.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	62.3
Database Date:	2015-11-30	**pI:**	8.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	15.8
		No. of unique Peptides:	3

Quantitation

MD:MU **Median:** 0.39 **CV:** 8.17 % **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
419	1	705.9605	130.39	2	34.6	27.4	1	266-277	R.TTAENEFVMLKK.D		MD:MU 0.42
553	2	851.4187	19.30	2	36.2	57.4	0	406-420	K.QCANLQNAIADAEQR.G	Carbamidomethyl: 2	MD:MU 0.36
334	2	720.3453	-20.22	2	33.5	59.4	0	560-576	R.GLGVGFGSGGGSSSSVK.F		

Detailed Protein Report

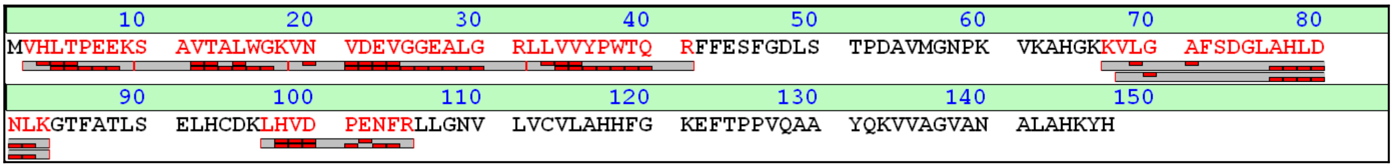
Protein 7: hemoglobin subunit beta [Homo sapiens]

Accession: gi|4504349
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 296.6
MW [kDa]: 16.0
pI: 6.9
Sequence Coverage [%]: 44.9
No. of unique Peptides: 7

Quantitation

MD:MU **Median:** 1.50 **CV:** 23.74 % **No. of Peptides:** 4



Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
63	1	476.7531	-11.35	2	30.5	38.7	0	2-9	M.VHLTPEEK.S		
718	2	466.6322	-281.50	2	38.5	27.6	0	10-18	K.SAVTALWGK.V		MD:MU 1.85
391	2	657.8281	-12.11	2	34.2	66.6	0	19-31	K.VNVDEVGGEALGR.L		MD:MU 1.10
2156	10	637.7714	-148.92	2	56.8	53.2	0	32-41	R.LLVVYPWTQR.F		MD:MU 1.30
2205	2	599.9528	-78.86	3	57.5	18.4	1	67-83	K.KVLGAFSDGLAHLDNLK.G		
2318	1	557.2358	-118.33	3	58.8	59.7	0	68-83	K.VLGAFSDGLAHLDNLK.G		
266	3	563.7687	-29.94	2	33.0	32.4	0	97-105	K.LHVDPENFR.L		MD:MU 1.93

Detailed Protein Report

Protein 8: PREDICTED: titin isoform X6 [Homo sapiens]

Accession:	gi|578804834	**Score:**	273.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	3773.1
Database Date:	2015-11-30	**pI:**	6.0
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	0.8
		No. of unique Peptides:	19

Quantitation

MD:MU	**Median:** 2.39	**CV:** 0.00 %	**No. of 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	QPAQEQQVRK	EAEKTAVTKV
490	500	510	520	530	540	550	560
VVAADKAKEQ	ELKSRTKEVI	TTKQEQMHVT	HEQIRKETEK	TFVPKVVISA	AKAKEQETRI	SEEITKKQKQ	VTQEAIRQET
570	580	590	600	610	620	630	640
EITAASMVVV	ATAKSTKLET	VPGAQEETTT	QQDQMHLSYE	KIMKETRKTV	VPKVIVATPK	VKEQDLVSRG	REGITTKREQ
650	660	670	680	690	700	710	720
VQITQEKMRK	EAEKTALSTI	AVATAKAKEQ	ETILRTRETM	ATRQEQIQVT	HGKVDVGKKA	EAVATVVAAV	DQARVREPRE
730	740	750	760	770	780	790	800
PGHLEESYAQ	QTTLEYGYKE	RISAAKVAEP	PQRPASEPHV	VPKAVKPRVI	QAPSETHIKT	TDQKGMHISS	QIKKTTDLTT
810	820	830	840	850	860	870	880
ERLVHVDKRP	RTASPHFTVS	KISVPKTEHG	YEASIAGSAI	ATLQKELSAT	SSAQKITKSV	KAPTVKPSET	RVRAEPTPLP
890	900	910	920	930	940	950	960
QFPFADTPDT	YKSEAGVEVK	KEVGVSITGT	TVREERFEVL	HGREAKVTET	ARVPAPVEIP	VTPPTLVSGL	KNVTVIEGES
970	980	990	1000	1010	1020	1030	1040
VTLECHISGY	PSPTVTWYRE	DYQIESSIDF	QITFQSGIAR	LMIREAFAED	SGRFTCSAVN	EAGTVSTSCY	LAVQVSEEFE
1050	1060	1070	1080	1090	1100	1110	1120
KETTAVTEKF	TTEEKRFVES	RDVVMTDTSL	TEEQAGPGEP	AAPYFITKPV	VQKLVEGGSV	VFGCQVGGNP	KPHVYWKKSG
1130	1140	1150	1160	1170	1180	1190	1200
VPLTTGYRYK	VSYNKQTGEC	KLVISMTFAD	DAGEYTIVVR	NKHGETSASA	SLLEEADYEL	LMKSQQEMLY	QTQVTAFVQE
1210	1220	1230	1240	1250	1260	1270	1280
PKVGETAPGF	VYSEYEKEYE	KEQALIRKKM	AKDTVVVRTY	VEDQEFHISS	FEERLIKEIE	YRIIKTTLEE	LLEEDGEEKM
1290	1300	1310	1320	1330	1340	1350	1360
AVDISESEAV	ESGFDSRIKN	YRILEGMGVT	FHCKMSGYPL	PKIAWYKDGK	RIKHGERYQM	DFLQDGRASL	RIPVVLPEDE
1370	1380	1390	1400	1410	1420	1430	1440
GIYTAFASNI	KGNAICSGKL	YVEPAAPLGA	PTYIPTLEPV	SRIRSLSPRS	VSRSPIRMSP	ARMSPARMSP	ARMSPARMSP
1450	1460	1470	1480	1490	1500	1510	1520
GRRLEETDES	QLERLYKPVF	VLKPVSFKCL	EGQTARFDLK	VVGRPMPETF	WFHDGQQIVN	DYTHKVVIKE	DGTQSLIIVP
1530	1540	1550	1560	1570	1580	1590	1600
ATPSDSGEWT	VVAQNRAGRS	SISVILTVEA	VEHQVKPMFV	EKLKNVNIKE	GSRLEMKVRA	TGNPNPDIVW	LKNSDIIVPH
1610	1620	1630	1640	1650	1660	1670	1680
KYPKIRIEGT	KGEAALKIDS	TVSQDSAWYT	ATAINKAGRD	TTRCKVNVEV	EFAEPEPERK	LIIPRGTYRA	KEIAAPELEP
1690	1700	1710	1720	1730	1740	1750	1760
LHLRYGQEQW	EEGDLYDKEK	QQKPFFKKKL	TSLRLKRFGP	AHFECRLTPI	GDPTMVVEWL	HDGKPLEAAN	RLRMINEFGY
1770	1780	1790	1800	1810	1820	1830	1840
CSLDYGVAYS	RDSGIITCRA	TNKYGTDHTS	ATLIVKDEKS	LVEESQLPEG	RKGLQRIEEL	ERMAHEGALT	GVTTDQKEKQ
1850	1860	1870	1880	1890	1900	1910	1920
KPDIVLYPEP	VRVLEGETAR	FRCRVTGYPQ	PKVNWYLNGQ	LIRKSKRFRV	RYDGIHYLDI	VDCKSYDTGE	VKVTAENPEG
1930	1940	1950	1960	1970	1980	1990	2000
VIEHKVKLEI	QQREDFRSVL	RRAPEPRPEF	HVHEPGKLQF	EVQKVDRPVD	TTETKEVVKL	KRAERITHEK	VPEESEELRS
2010	2020	2030	2040	2050	2060	2070	2080
KFKRRTEEGY	YEAITAVELK	SRKKDESYEE	LLRKTKDELL	HWTKELTEEE	KKALAEEGKI	TIPTFKPDKI	ELSPSMEAPK
2090	2100	2110	2120	2130	2140	2150	2160
IFERIQSQTV	GQGSDAHFRV	RVVGKPDPEC	EWYKNGVKIE	RSDRIYWYWP	EDNVCELVIR	DVTAEDSASI	MVKAINIAGE
2170	2180	2190	2200	2210	2220	2230	2240

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
619	1	690.3860	77.00	2	37.3	10.5	0	5395-5407	R.VTNEVGSSICSAR.V	Carbamidomethyl: 10	
2868	1	805.9212	74.64	2	66.3	17.2	0	6519-6533	K.AQNEVGSDTCVCTVK.L	Carbamidomethyl: 10	
1459	1	851.5485	120.85	2	48.0	14.8	0	7111-7125	K.DIEQTVGLPVTLTCR.L	Carbamidomethyl: 14	
2735	1	1045.0652	51.04	2	64.6	11.1	1	7556-7574	K.NDAGMRECSAVLTVLEPAR.I	Carbamidomethyl: 8	
1761	1	785.8716	-131.54	2	51.8	13.2	2	10202-10215	K.IHVAISKRVEPPPK.V		
1296	1	640.2561	-89.77	2	45.9	12.9	1	10647-10656	K.EVTIMEEKER.A	Oxidation: 5	
1495	1	620.4184	75.49	3	48.4	11.8	2	11427-11443	K.GPEISEKIIPPKKPPTK.V		
857	4	555.3421	99.88	2	40.3	14.9	0	11876-11886	K.GTAIFACDIAK.D		
2424	1	822.3339	-55.35	2	60.7	10.9	2	12942-12954	R.EKEMARFECELSR.E	Oxidation: 4	
2695	1	805.4194	19.35	2	64.9	15.3	2	12948-12960	R.FECELSRENAKVK.W	Carbamidomethyl: 3	
958	4	481.1097	-309.72	2	41.5	15.0	0	13690-13697	K.TWVLATDR.A		
2512	2	813.3358	-60.53	2	61.3	13.8	0	17628-17640	R.VPDLLEGCQYEFR.V	Carbamidomethyl: 8	
2371	2	805.2633	-115.33	2	60.0	12.7	0	26736-26748	R.EEEPLFDIDSEMR.K		
1812	1	658.3022	-97.61	2	52.7	11.3	0	27840-27851	K.AGEDVQVLIPFK.G		
2614	2	701.8585	19.90	2	62.7	22.1	1	28261-28272	K.MVCSSVARTTFK.V	Carbamidomethyl: 3; Oxidation: 1	
2485	1	862.3731	-106.42	2	61.5	10.8	0	29616-29633	R.AGSDLVLDAAVGGKPEPK.I		
496	1	677.6900	21.58	3	35.5	11.2	2	31650-31667	K.DAGFYVVCAKNRFGIDQK.T		
2811	1	1052.5183	-55.98	2	65.6	16.6	0	32829-32846	R.SLSPTYIELMRPVSELIR.S		
1561	1	745.7829	-73.36	2	49.4	15.1	0	33469-33482	K.TDTSDSGLYTCTVK.N		MD:MU 2.39

Detailed Protein Report

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

Accession: gi|15431310
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 194.1
MW [kDa]: 51.6
pI: 4.9
Sequence Coverage [%]: 10.0
No. of unique Peptides: 1

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
120	1	713.3140	-53.30	2	30.9	15.6	0	42-56	R.APSTYGGGLSVSSSR.F	

Detailed Protein Report

Protein 10: hemoglobin subunit alpha [Homo sapiens]

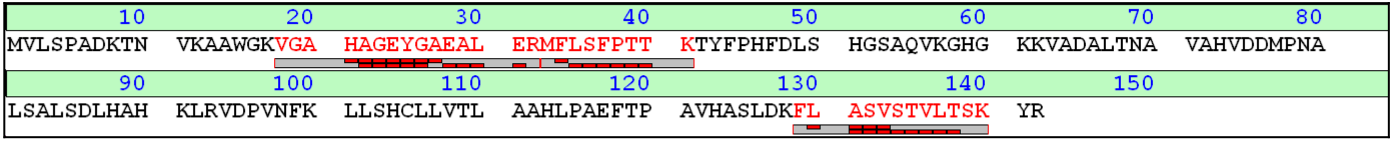
Accession:	gi|4504345	**Score:**	192.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	15.2
Database Date:	2015-11-30	**pI:**	9.4
		Sequence Coverage [%]:	25.4
		No. of unique Peptides:	3

Quantitation

MD:MU **Median:** 1.77 **CV:** 0.00 % **No. of Peptides:** 1

Alias proteins:

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



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         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
146	4	765.3477	-30.12	2	31.6	78.8	0	18-32	K.VGAHAGEYGAEALER.M		MD:MU 1.77
1666	2	536.1902	-168.98	2	50.7	47.8	0	33-41	R.MFLSFPTTK.T		
1467	1	626.8443	-26.58	2	48.0	65.8	0	129-140	K.FLASVSTVLTSK.Y		

Detailed Protein Report

Protein 11: keratin, type II cytoskeletal 2 epidermal [Homo sapiens]

Accession:	gi|47132620	**Score:**	151.0
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

MD:MU	**Median:** 0.69	**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
354	1	738.3735	-30.88	2	33.8	45.3	0	198-209	R.FLEQQNQVLQTK.W		MD:MU 0.69

Detailed Protein Report

Protein 12: **annexin A1 [Homo sapiens]**

Accession: gi|4502101

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Modification(s): Carbamidomethyl

Score: 148.6

MW [kDa]: 38.7

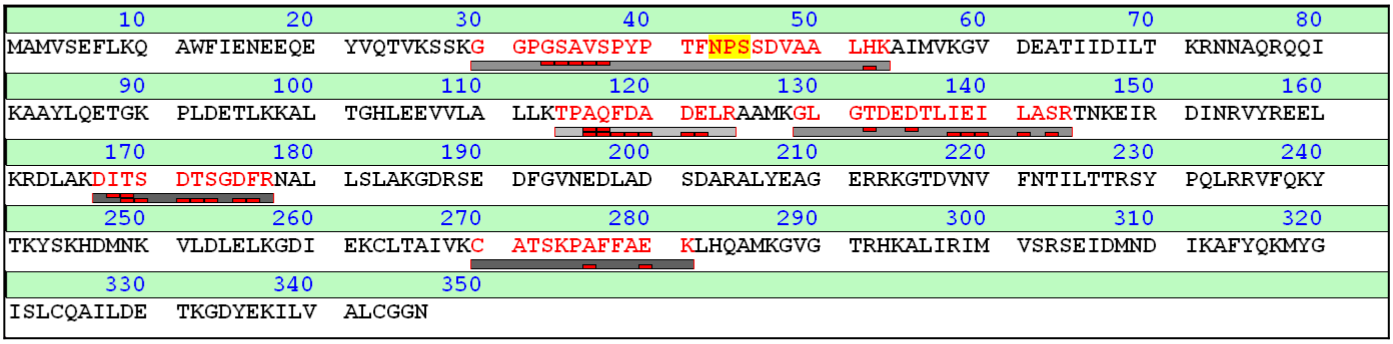
pI: 6.7

Sequence Coverage [%]: 21.4

No. of unique Peptides: 5

Quantitation

MD:MU **Median:** 0.80 **CV:** 13.75 % **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
1254	1	786.0316	-32.49	3	45.3	18.2	0	30-53	K.GGPGSAVSPYPTFNPSSDVAALHA		MD:MU 0.84
352	1	631.8010	-5.09	2	33.8	31.5	0	114-124	K.TPAQFDADELR.A		
2152	1	851.8249	-142.79	2	57.1	38.0	0	129-144	K.GLGTDEDTLIEILASR.T		
125	1	607.2634	-11.26	2	31.0	50.4	0	167-177	K.DITSDTSGDFR.N		MD:MU 0.91
2020	1	678.7710	-93.49	2	55.4	10.5	0	270-281	K.CATSKPAFFAEK.L	Carbamidomethyl: 1	MD:MU 0.66

Detailed Protein Report

Protein 13: **serotransferrin precursor [Homo sapiens]**

Accession: gi|4557871
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 131.2
MW [kDa]: 77.0
pI: 7.0
Sequence Coverage [%]: 5.0
No. of unique Peptides: 3

Quantitation

MD:MU **Median:** 1.14 **CV:** 68.81 % **No. of Peptides:** 3

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
431	2	637.3141	-25.64	2	35.0	51.8	0	226-236	K.HSTIFENLANK.A		MD:MU	0.72
678	1	638.8051	-22.74	2	38.0	31.2	0	300-310	K.EFQLFSSPHGK.D		MD:MU	2.74
229	1	761.3746	3.44	2	32.3	48.1	1	372-384	R.LKCDEWSVNSVGK.I	Carbamidomethyl: 3	MD:MU	0.75

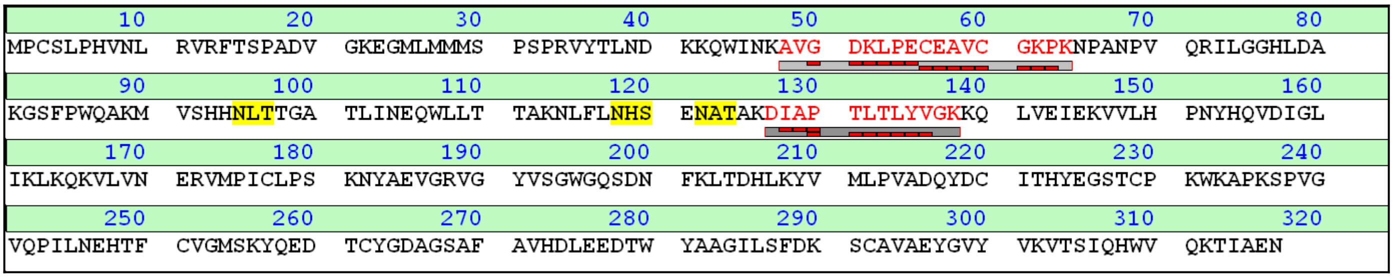
Detailed Protein Report

Protein 14: **PREDICTED: haptoglobin-related protein isoform X1 [Homo sapiens]**

Accession:	gi|578828965	**Score:**	110.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	35.3
Database Date:	2015-11-30	**pI:**	9.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	9.1
		No. of unique Peptides:	2

Quantitation

MD:MU **Median:** 1.36 **CV:** 0.00 % **No. of Peptides:** 1



10	20	30	40	50	60	70	80
MPCSLPHVNL	RVRFTSPADV	GKEGMLMMMS	PSPRVYTLND	KKQWINKAVG	DKLPECEAVC	GKPKNPANPV	QRILGGHLDA
90	100	110	120	130	140	150	160
KGSFPWQAKM	VSHHNLTTGA	TLINEQWLLT	TAKNLFLNHS	ENATAKDIAP	TLTLYVGKKQ	LVEIEKVVLH	PNYHQVDIGL
170	180	190	200	210	220	230	240
IKLKQKVLVN	ERVMPICLPS	KNYAEVGRVG	YVSGWGQSDN	FKLTDHLKYV	MLPVADQYDC	ITHYEGSTCP	KWKAPKSPVG
250	260	270	280	290	300	310	320
VQPILNEHTF	CVGMSKYQED	TCYGDAGSAF	AVHDLEEDTW	YAAGILSFDK	SCAVAEYGVY	VKVTSIQHWV	QKTIAEN

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
131	2	619.9592	-30.51	3	31.4	56.4	1	48-64	K.AVGDKLPECEAVCGKPK.N	Carbamidomethyl: 9, 13	MD:MU 1.36
1679	2	645.8477	-32.77	2	50.8	53.6	0	127-138	K.DIAPTLTLYVGK.K		

Detailed Protein Report

Protein 15: neutrophil defensin 1 preproprotein [Homo sapiens]

Accession: gi|4758146
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

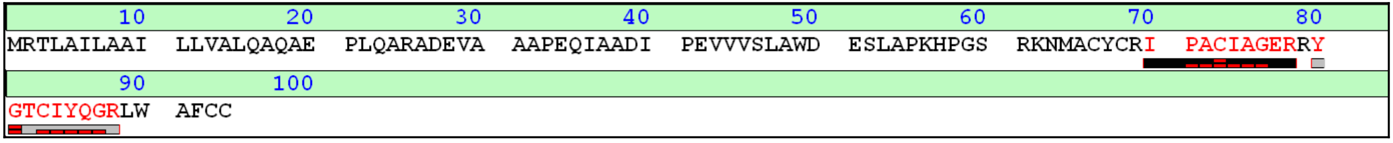
Score: 98.5
MW [kDa]: 10.2
pI: 7.6
Sequence Coverage [%]: 19.1
No. of unique Peptides: 2

Quantitation

MD:MU **Median:** 0.77 **CV:** 0.00 % **No. of Peptides:** 1

Alias proteins:

Accession	Name	Description
gi|124248516	refseq_huma (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
```

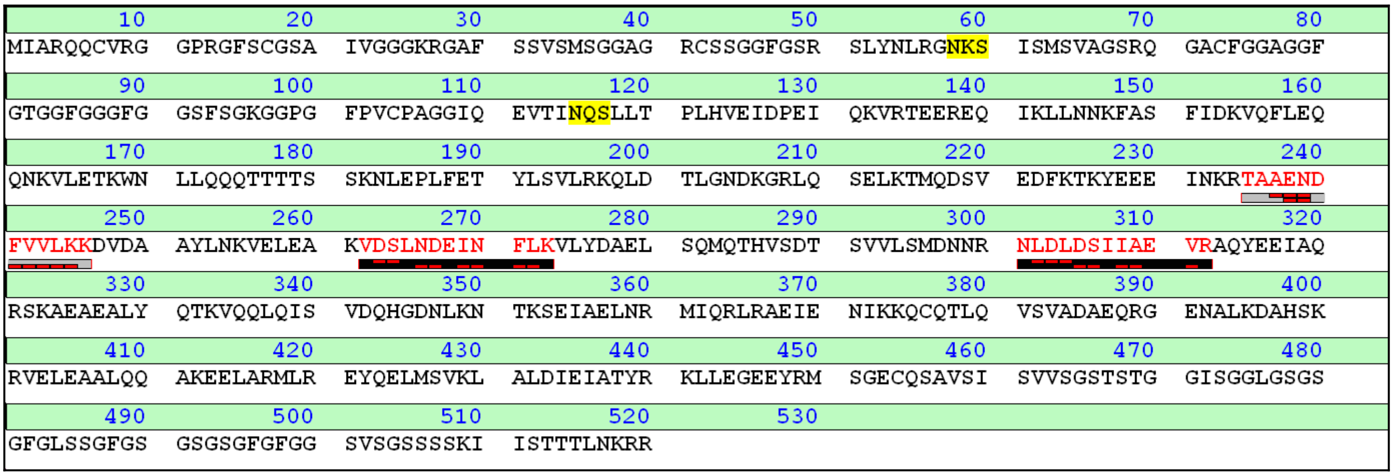
Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
108	1	493.6493	-220.14	2	30.7	45.9	0	70-78	R.IPACIAGER.R	Carbamidomethyl: 4	MD:MU	0.77
91	1	559.2458	-22.58	2	30.8	52.6	0	80-88	R.YGTCIYQGR.L	Carbamidomethyl: 4		

Protein 16: keratin, type II cytoskeletal 4 [Homo sapiens]

Accession:	gi|331999954	**Score:**	87.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	56.1
Database Date:	2015-11-30	**pI:**	6.2
		Sequence Coverage [%]:	6.9
		No. of unique Peptides:	3

Quantitation

MD:MU **Median:** 0.27 **CV:** 0.00 % **No. of Peptides:** 1



```
        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
326	1	667.8409	-42.57	2	33.4	33.2	1	235-246	R.TAAENDFVVLKK.D		
1586	1	703.8014	-85.66	2	49.7	20.9	0	262-273	K.VDSLNDEINFLK.V		
2400	1	679.3689	-1.20	2	60.3	33.7	0	301-312	R.NLDLDSIIAEVR.A		MD:MU 0.27

Protein 17: desmoplakin isoform I [Homo sapiens]

Accession:	gi|58530840	**Score:**	86.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	331.6
Database Date:	2015-11-30	**pI:**	6.4
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	3.4
		No. of unique Peptides:	5

Quantitation

MD:MU	**Median:**	1.47	**CV:**	0.00 %	**No. of Peptides:**	1	

Detailed Protein Report

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2092	1	1045.4569	7.22	2	56.0	12.2	0	46-64	R.GVITDQNSDGYCQTGTMSR.H	Carbamidomethyl: 12	
2088	1	596.7468	-112.69	2	56.0	10.2	1	1330-1339	R.LKAEFQEEAK.R		MD:MU 1.47
1858	1	616.2551	-101.28	2	53.1	10.2	1	1488-1497	K.QLIDKETNDR.K		
2423	1	837.8362	-126.41	2	60.6	16.4	2	1545-1558	R.VSQERTVKDQDITR.F		
2393	1	1176.1976	83.64	2	59.8	12.7	2	2465-2484	R.RVVIVDPETNKEMSVQEAYK.K	Oxidation: 13	

Detailed Protein Report

Protein 18: **PREDICTED: trinucleotide repeat-containing gene 18 protein isoform X2 [Homo sapiens]**

Accession:	gi|578813686	**Score:**	85.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	232.1
Database Date:	2015-11-30	**pI:**	9.7
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	3.7
		No. of unique Peptides:	5

Quantitation

MD:MU	**Median:** 2.72	**CV:** 127.82 %	**No. of Peptides:** 2

Detailed Protein Report

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1629	1	1052.2731	65.37	3	50.1	21.1	1	271-302	K. TKNAALQPSVLTMCNGGAGDVGL G	Carbamidomethyl: 14; Oxidation: 13	
1053	1	500.6425	-250.20	2	42.8	13.1	2	1545-1554	K.RGKSGHSSGK.L		MD:MU 7.28
307	1	846.3647	-83.38	2	33.2	17.3	2	1618-1632	K.KMASDQEQLASKLDK.A		
2682	1	734.8888	-6.21	2	63.7	11.3	2	1642-1655	K.LKSPFKFSDSAGGK.S		
177	1	613.7776	-171.05	2	31.9	22.8	1	1787-1797	R.TLKPKPATSRK.Q		MD:MU 1.02

Detailed Protein Report

Protein 19: heat shock protein beta-1 [Homo sapiens]

Accession:	gi|4504517	**Score:**	84.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	22.8
Database Date:	2015-11-30	**pI:**	6.0
		Sequence Coverage [%]:	13.2
		No. of unique Peptides:	2

Quantitation

MD:MU **Median:** 0.85 **CV:** 32.52 % **No. of Peptides:** 2

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
1713	7	582.2695	-76.42	2	51.2	61.7	0	28-37	R.LFDQAFGLPR.L		MD:MU	0.62
1635	1	953.4046	-99.49	2	50.2	22.4	0	172-188	K.LATQSNEITIPVTFESR.A		MD:MU	1.16

Protein 20: PREDICTED: DNA-directed RNA polymerase, mitochondrial isoform X1 [Homo sapiens]

Accession: gi|530425287

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Modification(s): Carbamidomethyl, Oxidation

Score: 84.0

MW [kDa]: 145.0

pI: 10.3

Sequence Coverage [%]: 5.0

No. of unique Peptides: 4

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2442	1	857.6864	-95.07	3	60.9	18.7	2	40-65	R.RGPVGWPGAACVMSALCWGRGAAGLK.R	
3	1	1244.4602	-117.14	2	28.9	10.3	1	41-65	R.GPVGWPGAACVMSALCWGRGAAGLK.R	Carbamidomethyl: 10; Oxidation: 12
2861	1	682.6750	3.46	3	66.2	16.6	0	584-601	K.YLCLLASDAEVPEPCLPR.Q	Carbamidomethyl: 3
2603	1	678.4838	186.95	1	63.1	15.6	0	1227-1231	R.EQFVR.L	

Detailed Protein Report

Protein 21: PREDICTED: nebulin isoform X22 [Homo sapiens]

Accession:	gi|530370465	**Score:**	82.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	961.5
Database Date:	2015-11-30	**pI:**	9.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.0
		No. of unique Peptides:	5

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2522	1	885.4523	-25.95	2	62.0	17.0	2	407-421	K.FKLDTVLQNFSSDKK.Y	
457	1	544.7651	77.28	2	35.3	13.1	0	646-654	K.SMNYCETPK.Y	Oxidation: 2
1248	1	796.3930	45.30	2	45.3	13.7	1	2813-2825	R.DDPKMMWSMHVAK.I	Oxidation: 5
2640	1	701.8709	47.97	2	63.1	10.8	0	6260-6270	R.CQYILSDLEYR.H	
2657	1	994.4910	10.30	2	63.3	10.6	1	8000-8015	K.LNQENFSSVLYKENMR.K	Oxidation: 15

Detailed Protein Report

Protein 22: dynein heavy chain 1, axonemal [Homo sapiens]

Accession:	gi|197927452	**Score:**	82.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	487.2
Database Date:	2015-11-30	**pI:**	5.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.9
		No. of unique Peptides:	6

Quantitation

MD:MU	**Median:**	1.02	**CV:**	0.00 %	**No. of Peptides:**	1	

Alias proteins:

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

```
        10         20         30         40         50         60         70         80
MEQPNSKGYS LGRTPQGPEC SSAPAVQVGT HRGLEYNPGK ILPGSDYGLG NPPALDPKLP HLPLPPAPPT LSDLGQPRKS

        90        100        110        120        130        140        150        160
PLTGTDKKYP LMKQRGFYSD ILSPGTLDQL GEVCRGPRMS QNLLRQADLD KFTPRVGSFE VPEDFQERME QQCIGSTTRL

       170        180        190        200        210        220        230        240
LAQTDFPLQA YEPKMQVPFQ VLPGQHPRKI EIERRKQQYL SLDIEQLLFS QGIDSNKLMP RHLDHQHPQT IEQGHDPIFP

       250        260        270        280        290        300        310        320
IYLPLKVFDN EDFDCRTPRE WINMGLEPGS LDRKPVPGKA LLPTDDFLGH EDPKSQKLKY KWCEVGVLDY DEEKKLYLVH

       330        340        350        360        370        380        390        400
KTDEKGLVRD EMGRPILNAG VTTEGRPPLQ VCQYWVPRIQ LLFCAEDPCM FAQRVVQANA LRKNTEALLL YNLYVDCMPS

       410        420        430        440        450        460        470        480
DGQHVISEQS LSKIKQWALS TPRMRKGPSV LEHLSSLARE VSLDYERSMN KINFDHVVSS KPETFSYVTL PKKEEEQVPE

       490        500        510        520        530        540        550        560
RGLVSVPKYH FWEQKEDFTF VSLLTRPEVI TALSKVRAEC NKVTAMSLFH SSLSKYSHLE EFEQIQSQTF SQVQMFLKDS

       570        580        590        600        610        620        630        640
WISSLKVAMR SSLRDMSKGW YNLYETNWEV YLMSKLRKLM ELVKYMLQDT LRFLVQDSLA SFSQFISDTC CSVLNCTDDM

       650        660        670        680        690        700        710        720
VWGDDLINSP YRPRKNPLFI MDLVLDSSGV HYSTPLEQFE ASLLNLFDKG ILATHAVPQL EKLVMEDIFI SGDPLLESVG

       730        740        750        760        770        780        790        800
LHEPLVEELR ATIASAVSKA MIPLQAYAKE YRKYLELNNN DIASFLKTYQ TQGLLAQEVR EVVLTHLREK EILDSSLPSS

       810        820        830        840        850        860        870        880
IIIGPFYINT DNVKQSLSKK RKALATSVLD ILAKNLHKEV DSICEEFRSI SRKIYEKPNS IEELAELREW MKGIPERLVG

       890        900        910        920        930        940        950        960
LEERIVKVMD DYQVMDEFLY NLSSDDFNDK WIASNWPSKI LGQIELVQQQ HVEDEEKFRK IQIMDQNNFQ EKLEGLQLVV

       970        980        990       1000       1010       1020       1030       1040
AGFSIHVEIS RAHEIANEVR RVKKQLKDCQ QLAMLYNNRE RIFSLPITNY DKLSRMVKEF QPYLDLWTTA SDWLRWSESW

      1050       1060       1070       1080       1090       1100       1110       1120
MNDPLSAIDA EQLEKNVVEA FKTMHKCVKQ FKDMPACQEV ALDIRARIEE FKPYIPLIQG LRNPGMRIRH WETLSNQINI

      1130       1140       1150       1160       1170       1180       1190       1200
NVRPKANLTF ARCLEMNLQD HIESISKVAE VAGKEYAIEQ ALDKMEKEWS TILFNVLPYK ATDTYILKSP DEASQLLDDH

      1210       1220       1230       1240       1250       1260       1270       1280
IVMTQNMSFS PYKKPFEQRI NSWENKLKLT QEVLEEWLNC QRSWLYLEPI FSSEDINQQL PVESKRYQTM ERIWKKIMKN

      1290       1300       1310       1320       1330       1340       1350       1360
AYENREVINV CSDLRMLDSL RDCNKILDLV QKGLSEYLET KRSAFPRFYF LSDDELLEIL SQTKDPTAVQ PHLRKCFENI

      1370       1380       1390       1400       1410       1420       1430       1440
ARLLFQEDLE ITHMYSAEGE EVQLCFSIYP SSNVEDWLRE VERSMKASVH DIIEKAIRAY PTMPRTQWVL NWPGQVTIAG

      1450       1460       1470       1480       1490       1500       1510       1520
CQTYWTMEVA EALEAGNLRS QLFPQLCQQL SDLVALVRGK LSRMQRAVLS ALIVIEVHAK DVVSKLIQEN VVSVNDFQWI

      1530       1540       1550       1560       1570       1580       1590       1600
SQLRYYWTNN DLYIRAVNAE FIYGYEYLGN SGRLVITPLT DRCYLTLTGA LHLKFGGAPA GPAGTGKTET TKDLGKALAI

      1610       1620       1630       1640       1650       1660       1670       1680
QTVVFNCSDQ LDFMAMGKFF KGLASAGAWA CFDEFNRIDI EVLSVVAQQI TTIQKAQQQR VERFMFEGVE IPLVPSCAVF

      1690       1700       1710       1720       1730       1740       1750       1760
ITMNPGYAGR TELPDNLKAL FRPVAMMVPD YAMITEISLY SFGFNEASVL AKKITTTFKL SSEQLSSQDH YDFGMRAVKT

      1770       1780       1790       1800       1810       1820       1830       1840
VISAAGNLKR ENPSMNEELI CLRAIRDVNV PKFLQEDLKL FSGIVSDLFP TIKEEDTDYG ILDEAIREAC RNSNLKDVEG

      1850       1860       1870       1880       1890       1900       1910       1920
FLTKCIQLYE TTVVRHGLML VGPTGSGKST CYRVLAAAMT SLKGQPSISG GMYEAVNYYV LNPKSITMGQ LYGEFDLLTH

      1930       1940       1950       1960       1970       1980       1990       2000
EWTDGIFSSF IRAGAITSDT NKKWYMFDGP VDAIWIENMN TVLDDNKKLC LSSGEIIKLT EAMTMMFEVQ DLAVASPATV

      2010       2020       2030       2040       2050       2060       2070       2080
SRCGMVYLEP SILGLMPFIE CWLRKLPPLL KPYEEHFKAL FVSFLEESIS FVRSSVKEVI ASTNCNLTMS LLKLLDCFFK

      2090       2100       2110       2120       2130       2140       2150       2160
PFLPREGLKK IPSEKLSRIV ELIEPWFIFS LIWSVGATGD SSGRTSFSHW LRLKMENEQL TLLFPEEGLV FDYRLEDAGI

      2170       2180       2190       2200       2210       2220       2230       2240
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1891	1	918.3580	-147.46	2	53.5	15.4	2	559-574	K.DSWISSLKVAMRSSLR.D		
449	1	565.3223	-66.47	2	35.3	17.9	2	596-604	K.LRKLMELVK.Y		
870	1	573.1350	-254.46	2	40.3	10.7	1	2478-2486	R.DRLVNEEDR.S		
178	1	715.8622	76.35	2	31.9	12.3	0	2496-2506	R.CMEQWEVTFNK.V	Oxidation: 2	MD:MU 1.02
2816	1	788.8905	-16.60	2	65.6	10.2	1	3081-3094	R.LREVEDGIATMQAK.Y	Oxidation: 11	
51	2	706.3163	-75.95	3	30.3	15.4	2	3699-3718	K.KLSAISLGQGQGPRAEAMMR.S	Oxidation: 18	

Detailed Protein Report

Protein 23: PREDICTED: histone-lysine N-methyltransferase 2A isoform X1 [Homo sapiens]

Accession:	gi|578822195	**Score:**	78.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	323.9
Database Date:	2015-11-30	**pI:**	9.2
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	2.7
		No. of unique Peptides:	5

```
        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
1751	1	1061.1573	33.03	3	51.7	15.9	2	144-170	R.SRRCGQCPGCQVPEDCGVCTNCLDKPK.F	Carbamidomethyl: 4, 10, 16, 19, 22
2129	11	682.2818	44.75	3	56.8	21.4	1	567-582	K.CYDDDDYESKMMQCGK.C	Carbamidomethyl: 1, 14
53	1	1096.9888	-34.10	2	30.4	17.5	1	1264-1284	R.TVVTVGNKNSHLDGSSSSEMK.Q	Oxidation: 20
11	1	820.3475	-49.73	1	29.3	12.9	1	2734-2739	K.HCRNYK.F	
395	1	625.3909	142.58	2	34.6	10.9	2	2950-2960	K.LPCNCGAKKCR.K	Carbamidomethyl: 5

Detailed Protein Report

Protein 24: collagen alpha-1(XIV) chain precursor [Homo sapiens]

Accession:	gi|55743096	**Score:**	77.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	193.4
Database Date:	2015-11-30	**pI:**	5.0
		Sequence Coverage [%]:	4.0
		No. of unique Peptides:	4

Quantitation

MD:MU	**Median:** 0.83	**CV:** 0.00 %	**No. of Peptides:** 1

Alias proteins:

Accession	Name	Description
gi|578816162	refseq_human (refseq_human_20140103.fasta)	PREDICTED: collagen alpha-1(XIV) chain isoform X2 [Homo sapiens]

Detailed Protein Report

```
        10         20         30         40         50         60         70         80
MKIFQRKMRY WLLPPFLAIV YFCTIVQGQV APPTRLRYNV ISHDSIQISW KAPRGKFGGY KLLVTPTSGG KTNQLNLQNT
        90        100        110        120        130        140        150        160
ATKAIIQGLM PDQNYTVQII AYNKDKESKP AQGQFRIKDL EKRKDPKPRV KVVDRGNGSR PSSPEEVKFV CQTPAIADIV
       170        180        190        200        210        220        230        240
ILVDGSWSIG RFNFRLVRHF LENLVTAFDV GSEKTRIGLA QYSGDPRIEW HLNAFSTKDE VIEAVRNLPY KGGNTLTGLA
       250        260        270        280        290        300        310        320
LNYIFENSFK PEAGSRTGVS KIGILITDGK SQDDIIPPSR NLRESGVELF AIGVKNADVN ELQEIASEPD STHVYNVAEF
       330        340        350        360        370        380        390        400
DLMHTVVESL TRTLCSRVEE QDREIKASAH AITGPPTELI TSEVTARSFM VNWTHAPGNV EKYRVVYYPT RGGKPDEVVV
       410        420        430        440        450        460        470        480
DGTVSSTVLK NLMSLTEYQI AVFAIYAHTA SEGLRGTETT LALPMASDLL LYDVTENSMR VKWDAVPGAS GYLILYAPLT
       490        500        510        520        530        540        550        560
EGLAGDEKEM KIGETHTDIE LSGLLPNTEY TVTVYAMFGE EASDPVTGQE TTLALSPPRN LRISNVGSNS ARLTWDPTSR
       570        580        590        600        610        620        630        640
QINGYRIVYN NADGTEINEV EVDPITTFPL KGLTPLTEYT IAIFSIYDEG QSEPLTGVFT TEEVPAQQYL EIDEVTTDSF
       650        660        670        680        690        700        710        720
RVTWHPLSAD EGLHKLMWIP VYGGKTEEVV LKEEQDSHVI EGLEPGTEYE VSLLAVLDDG SESEVVTAVG TTLDSFWTEP
       730        740        750        760        770        780        790        800
ATTIVPTTSV TSVFQTGIRN LVVGDETTSS LRVKWDISDS DVQQFRVTYM TAQGDPEEEV IGTVMVPGSQ NNLLLKPLLP
       810        820        830        840        850        860        870        880
DTEYKVTVTP IYTDGEGVSV SAPGKTLPSS GPQNLRVSEE WYNRLRITWD PPSSPVKGYR IVYKPVSVPG PTLETFVGAD
       890        900        910        920        930        940        950        960
INTILITNLL SGMDYNVKIF ASQASGFSDA LTGMVKTLFL GVTNLQAKHV EMTSLCAHWQ VHRHATAYRV VIESLQDRQK
       970        980        990       1000       1010       1020       1030       1040
QESTVGGGTT RHCFYGLQPD SEYKISVYTK LQEIEGPSVS IMEKTQSLPT RPPTFPPTIP PAKEVCKAAK ADLVFMVDGS
      1050       1060       1070       1080       1090       1100       1110       1120
WSIGDENFNK IISFLYSTVG ALNKIGTDGT QVAMVQFTDD PRTEFKLNAY KTKETLLDAI KHISYKGGNT KTGKAIKYVR
      1130       1140       1150       1160       1170       1180       1190       1200
DTLFTAESGT RRGIPKVIVV ITDGRSQDDV NKISREMQLD GYSIFAIGVA DADYSELVSI GSKPSARHVF FVDDFDAFKK
      1210       1220       1230       1240       1250       1260       1270       1280
IEDELITFVC ETASATCPVV HKDGIDLAGF KMMEMFGLVE KDFSSVEGVS MEPGTFNVFP CYQLHKDALV SQPTRYLHPE
      1290       1300       1310       1320       1330       1340       1350       1360
GLPSDYTISF LFRILPDTPQ EPFALWEILN KNSDPLVGVI LDNGGKTLTY FNYDQSGDFQ TVTFEGPEIR KIFYGSFHKL
      1370       1380       1390       1400       1410       1420       1430       1440
HIVVSETLVK VVIDCKQVGE KAMNASANIT SDGVEVLGKM VRSRGPGGNS APFQLQMFDI VCSTSWANTD KCCELPGLRD
      1450       1460       1470       1480       1490       1500       1510       1520
DESCPDLPHS CSCSETNEVA LGPAGPPGGP GLRGPKGQQG EPGPKGPDGP RGEIGLPGPQ GPPGPQGPSG LSIQGMPGMP
      1530       1540       1550       1560       1570       1580       1590       1600
GEKGEKGDTG LPGPQGIPGG VGSPGRDGSP GQRGLPGKDG SSGPPGPPGP IGIPGTPGVP GITGSMGPQG ALGPPGVPGA
      1610       1620       1630       1640       1650       1660       1670       1680
KGERGERGDL QSQAMVRSVA RQVCEQLIQS HMARYTAILN QIPSHSSSIR TVQGPPGEPG RPGSPGAPGE QGPPGTPGFP
      1690       1700       1710       1720       1730       1740       1750       1760
GNAGVPGTPG ERGLTGIKGE KGNPGVGTQG PRGPPGPAGP SGESRPGSPG PPGSPGPRGP PGHLGVPGPQ GPSGQPGYCD
      1770       1780       1790       1800
PSSCSAYGVR APHPDQPEFT PVQDELEAME LWGPGV
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2684	12	673.3700	31.83	2	63.7	19.1	0	208-218	R.IEWHLNAFSTK.D		
74	1	809.3972	-57.78	2	30.6	10.2	1	740-754	R.NLVVGDETTSSLRVK.W		MD:MU 0.83
2197	1	585.1748	-243.43	2	57.7	10.6	0	826-836	K.TLPSSGPQNLR.V		
834	1	683.9031	-31.20	2	40.0	13.1	1	1133-1145	R.GIPKVIVVITDGR.S		

Detailed Protein Report

Protein 25: keratin, type II cytoskeletal 1 [Homo sapiens]

Accession:	gi|119395750	**Score:**	77.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	66.0
Database Date:	2015-11-30	**pI:**	8.8
		Sequence Coverage [%]:	6.2
		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
1168	1	922.9918	16.42	2	44.2	12.8	1	417-432	K.KQISNLQQSISDAEQR.G	

Protein 26: actin, cytoplasmic 1 [Homo sapiens]

Accession:	gi|4501885	**Score:**	75.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	41.7
Database Date:	2015-11-30	**pI:**	5.2
		Sequence Coverage [%]:	8.3
		No. of unique Peptides:	2

Quantitation

MD:MU **Median:** 1.16 **CV:** 0.00 % **No. of Peptides:** 1

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1159	1	651.9980	-43.48	3	44.1	29.5	0	96-113	R.VAPEEHPVLLTEAPLNPK.A		
102	2	758.7219	-175.32	2	31.0	46.3	0	360-372	K.QEYDESGPSIVHR.K		MD:MU 1.16

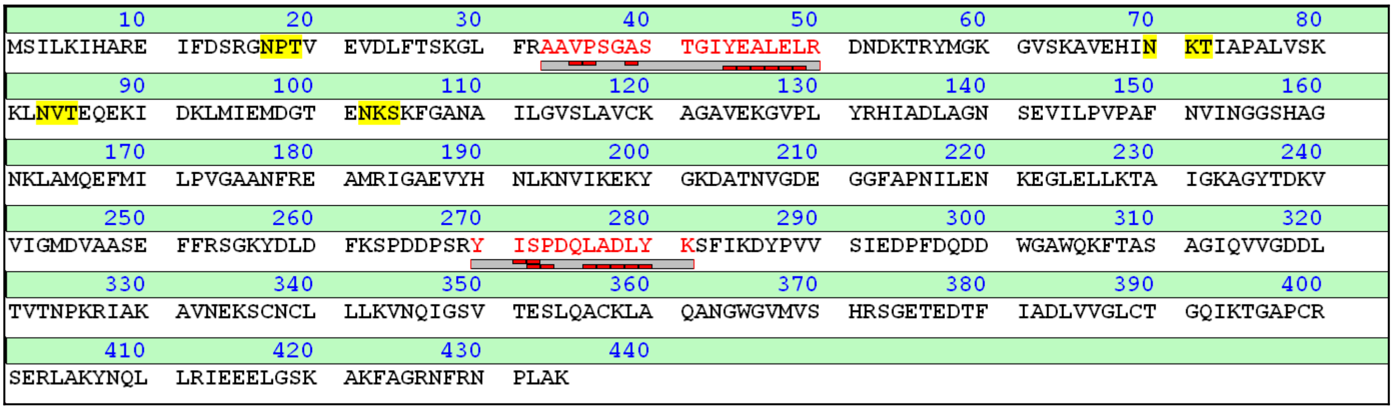
Detailed Protein Report

Protein 27: **alpha-enolase isoform 1 [Homo sapiens]**

Accession:	gi|4503571	**Score:**	75.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	47.1
Database Date:	2015-11-30	**pI:**	7.7
		Sequence Coverage [%]:	10.1
		No. of unique Peptides:	2

Quantitation

MD:MU **Median:** 0.96 **CV:** 9.80 % **No. of Peptides:** 2



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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
1942	2	902.8469	-142.55	2	54.2	18.2	0	33-50	R.AAVPSGASTGIYEALELR.D		MD:MU	1.06
1560	2	713.3678	1.67	2	49.2	40.1	0	270-281	R.YISPDQLADLYK.S		MD:MU	0.87

Detailed Protein Report

Protein 28: dynein heavy chain 2, axonemal [Homo sapiens]

Accession:	gi|75677365	**Score:**	75.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	507.4
Database Date:	2015-11-30	**pI:**	5.9
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	1.8
		No. of unique Peptides:	6

Quantitation

MD:MU	**Median:** 0.73	**CV:** 69.90 %	**No. of Peptides:** 3

Alias proteins:

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

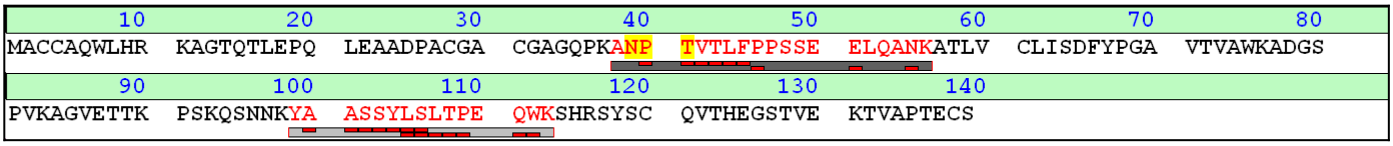
10	20	30	40	50	60	70	80
MSSKAEKKQR	LSGRGSSQAS	WSGRATRAAV	ATQEQGNAPA	VSEPELQAEL	PKEEPEPRLE	GPQAQSEESV	EPEADVKPLF
90	100	110	120	130	140	150	160
LSRAALTGLA	DAVWTQEHDA	ILEHFAQDPT	ESILTIFIDP	CFGLKLELGM	PVQTQNQLVY	FIRQAPVPIT	WENFEATVQF
170	180	190	200	210	220	230	240
GTVRGPYIPA	LLRLLGGVFA	PQIFANTGWP	ESIRNHFASH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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
58	1	827.0195	-82.92	3	30.1	13.2	1	1393-1414	R.LRGTEEVFQALEDNQVALSTMK.A			
271	1	701.3595	-80.46	2	33.1	11.1	2	1681-1692	K.VMKKNQVSILNK.Y		MD:MU	0.62
1377	1	976.4425	-17.17	2	46.8	10.3	1	2078-2095	R.HSTMIVGCTGSGKTASWR.I	Carbamidomethyl: 8; Oxidation: 4	MD:MU	1.69
312	1	712.8533	-32.33	2	33.2	10.2	2	3248-3258	K.LEMLKKQYDEK.L		MD:MU	0.37
2410	1	1023.8441	-100.67	2	60.0	14.9	2	4373-4389	K.KSAKGMYSCPCYYYPNR.A	Oxidation: 6		
2695	1	1044.5484	84.19	2	63.9	15.3	2	4373-4389	K.KSAKGMYSCPCYYYPNR.A	Carbamidomethyl: 9		

Detailed Protein Report

Protein 29: immunoglobulin lambda-like polypeptide 5 isoform 2 [Homo sapiens]

Accession:	gi|372466586	**Score:**	73.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	14.7
Database Date:	2015-11-30	**pI:**	7.7
		Sequence Coverage [%]:	24.5
		No. of unique Peptides:	2



```
        10         20         30         40         50         60         70         80
MACCAQWLHR KAGTQTLEPQ LEAADPACGA CGAGQPKANP TVTLFPPSSE ELQANKATLV CLISDFYPGA VTVAWKADGS
        90        100        110        120        130        140
PVKAGVETTK PSKQSNNKYA ASSYLSLTPE QWKSHRSYSC QVTHEGSTVE KTVAPTECS
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1468	1	1022.0062	-16.69	2	48.0	16.1	0	38-56	K.ANPTVTLFPPSSEELQANK.A	
1686	4	872.3793	-61.61	2	50.9	57.0	0	99-113	K.YAASSYLSLTPEQWK.S	

Detailed Protein Report

Protein 30: smoothelin isoform e [Homo sapiens]

Accession:	gi|333360860	**Score:**	72.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	104.8
Database Date:	2015-11-30	**pI:**	9.9
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	4.0
		No. of unique Peptides:	2

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1663	1	1044.8761	-92.00	2	50.6	17.6	1	1-20	-.MGGMGTPGDLHAACPSTTRR.D	Carbamidomethyl: 14; Oxidation: 1
1621	1	502.6927	-108.16	2	50.1	15.3	1	523-532	K.DGRGQASTGR.V	

Detailed Protein Report

Protein 31: glyceraldehyde-3-phosphate dehydrogenase isoform 2 [Homo sapiens]

Accession:	gi|378404908	**Score:**	69.2
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

MD:MU **Median:** 0.89 **CV:** 12.19 % **No. of Peptides:** 2

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
676	1	917.4657	2.44	2	38.0	53.0	0	104-120	K.IISNASCTTNCLAPLAK.V	Carbamidomethyl: 7, 11	MD:MU	0.79
1572	1	882.3573	-53.81	2	49.4	16.2	0	268-281	K.LISWYDNEFGYSNR.V		MD:MU	1.00

BRUKER

Detailed Protein Report

Protein 32: PREDICTED: ceruloplasmin isoform X3 [Homo sapiens]

Accession:	gi|578807065	**Score:**	67.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	122.1
Database Date:	2015-11-30	**pI:**	5.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.6
		No. of unique Peptides:	2

```
        10         20         30         40         50         60         70         80
MKILILGIFL FLCSTPAWAK EKHYYIGIIE TTWDYASDHG EKKLISVDTE HSNIYLQNGP DRIGRLYKKA LYLQYTDETF

        90        100        110        120        130        140        150        160
RTTIEKPVWL GFLGPIIKAE TGDKVYVHLK NLASRPYTFH SHGITYYKEH EGAIYPDNTT DFQRADDKVY PGEQYTYMLL

       170        180        190        200        210        220        230        240
ATEEQSPGEG DGNCVTRIYH SHIDAPKDIA SGLIGPLIIC KKDSLDKEKE KHIDREFVVM FSVVDENFSW YLEDNIKTYC

       250        260        270        280        290        300        310        320
SEPEKVDKDN EDFQESNRMY SVNGYTFGSL PGLSMCAEDR VKWYLFGMGN EVDVHAAFFH GQALTNKNYR IDTINLFPAT

       330        340        350        360        370        380        390        400
LFDAYMVAQN PGEWMLSCQN LNHLKAGLQA FFQVQECNKS SSKDNIRGKH VRHYYIAAEE IIWNYAPSGI DIFTKENLTA

       410        420        430        440        450        460        470        480
PGSDSAVFFE QGTTRIGGSY KKLVYREYTD ASFTNRKERG PEEEHLGILG PVIWAEVGDT IRVTFHNKGA YPLSIEPIGV

       490        500        510        520        530        540        550        560
RFNKNNEGTY YSPNYNPQSR SVPPSASHVA PTETFTYEWT VPKEVGPTNA DPVCLAKMYY SAVEPTKDIF TGLIGPMKIC

       570        580        590        600        610        620        630        640
KKGSLHANGR QKDVDKEFYL FPTVFDENES LLLEDNIRMF TTAPDQVDKE DEDFQESNKM HSMNGFMYGN QPGLTMCKGD

       650        660        670        680        690        700        710        720
SVVWYLFSAG NEADVHGIYF SGNTYLWRGE RRDTANLFPQ TSLTLHMWPD TEGTFNVECL TTDHYTGGMK QKYTVNQCRR

       730        740        750        760        770        780        790        800
QSEDSTFYLG ERTYYIAAVE VEWDYSPQRE WEKELHHLQE QNVSNAFLDK GEFYIGSKYK KVVYRQYTDS TFRVPVERKA

       810        820        830        840        850        860        870        880
EEEHLGILGP QLHADVGDKV KIIFKNMATR PYSIHAHGVQ TESSTVTPTL PGETLTYVWK IPERSGAGTE DSACIPWAYY

       890        900        910        920        930        940        950        960
STVDQVKDLY SGLIGPLIVC RRPYLKVFNP RRKLEFALLF LVFDENESWY LDDNIKTYSD HPEKVNKDDE EFIESNKMHA

       970        980        990       1000       1010       1020       1030       1040
INGRMFGNLQ GLTMHVGDEV NWYLMGMGNE IDLHTVHFHG HSFQYKHRGV YSSDVFDIFP GTYQTLEMFP RTPGIWLLHC

      1050       1060       1070
HVTDHIHAGM ETTYTVLQNE GGTSM
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2752	4	735.4129	-14.37	2	64.8	37.1	0	188-201	K.DIASGLIGPLIICK.K	Carbamidomethyl: 13
2789	2	788.4137	-22.96	2	65.3	30.2	0	888-901	K.DLYSGLIGPLIVCR.R	Carbamidomethyl: 13

Detailed Protein Report

Protein 33: **hemoglobin subunit gamma-2 [Homo sapiens]**

Accession:	gi|6715607	**Score:**	64.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	16.1
Database Date:	2015-11-30	**pI:**	6.8
		Sequence Coverage [%]:	15.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGHFTEEDKA	TITSLWGKVN	VEDAGGETLG	RLLVVYPWTQ	RFFDSFGNLS	SASAIMGNPK	VKAHGKKVLT	SLGDAIKHLD
90	**100**	**110**	**120**	**130**	**140**	**150**	
DLKGTFAQLS	ELHCDKLHVD	PENFKLLGNV	LVTVLAIHFG	KEFTPEVQAS	WQKMVTGVAS	ALSSRYH	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1800	1	658.7973	-43.08	2	52.5	11.5	0	19-31	K.VNVEDAGGETLGR.L	

Detailed Protein Report

Protein 34: lactotransferrin isoform 2 [Homo sapiens]

Accession:	gi|312433998	**Score:**	64.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	73.1
Database Date:	2015-11-30	**pI:**	9.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.5
		No. of unique Peptides:	2

Quantitation

MD:MU **Median:** 1.05 **CV:** 105.87 % **No. of Peptides:** 2

```
        10         20         30         40         50         60         70         80
MRKVRGPPVS CIKRDSPIQC IQAIAENRAD AVTLDGGFIY EAGLAPYKLR PVAAEVYGTE RQPRTHYYAV AVVKKGGSFQ

        90        100        110        120        130        140        150        160
LNELQGLKSC HTGLRRTAGW NVPIGTLRPF LNWTGPPEPI EAAVARFFSA SCVPGADKGQ FPNLCRLCAG TGENKCAFSS

       170        180        190        200        210        220        230        240
QEPYFSYSGA FKCLRDGAGD VAFIRESTVF EDLSDEAERD EYELLCPDNT RKPVDKFKDC HLARVPSHAV VARSVNGKED

       250        260        270        280        290        300        310        320
AIWNLLRQAQ EKFGKDKSPK FQLFGSPSGQ KDLLFKDSAI GFSRVPPRID SGLYLGSGYF TAIQNLRKSE EEVAARRARV

       330        340        350        360        370        380        390        400
VWCAVGEQEL RKCNQWSGLS EGSVTCSSAS TTEDCIALVL KGEADAMSLD GGYVYTAGKC GLVPVLAENY KSQQSSDPDP

       410        420        430        440        450        460        470        480
NCVDRPVEGY LAVAVVRRSD TSLTWNSVKG KKSCHTAVDR TAGWNIPMGL LFNQTGSCKF DEYFSQSCAP GSDPRSNLCA

       490        500        510        520        530        540        550        560
LCIGDEQGEN KCVPNSNERY YGYTGAFRCL AENAGDVAFV KDVTVLQNTD GNNNEAWAKD LKLADFALLC LDGKRKPVTE

       570        580        590        600        610        620        630        640
ARSCHLAMAP NHAVVSRMDK VERLKQVLLH QQAKFGRNGS DCPDKFCLFQ SETKNLLFND NTECLARLHG KTTYEKYLGP

       650        660        670
QYVAGITNLK KCSTSPLLEA CEFLRK
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
852	1	598.3199	18.32	2	40.1	36.0	0	261-271	K.FQLFGSPSGQK.D		MD:MU	0.44
2333	1	668.3646	18.05	2	59.0	28.6	0	543-554	K.LADFALLCLDGK.R	Carbamidomethyl: 8	MD:MU	2.50

Detailed Protein Report

Protein 35: alpha-2-macroglobulin precursor [Homo sapiens]

Accession:	gi|66932947	**Score:**	64.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	163.2
Database Date:	2015-11-30	**pI:**	6.0
		Sequence Coverage [%]:	2.6
		No. of unique Peptides:	3

Quantitation

MD:MU **Median:** 2.19 **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
1949	1	574.7312	-144.41	2	54.2	14.8	0	361-370	R.QGIPFFGQVR.L		
2267	1	942.4047	-130.24	2	58.2	14.1	0	824-841	R.VSVQLEASPAFLAVPVEK.E		
234	1	605.7801	-74.07	2	32.3	35.4	0	935-945	K.LPPNVVEESAR.A		MD:MU 2.19

Protein 36: PREDICTED: probable E3 ubiquitin-protein ligase MYCBP2 isoform X2 [Homo sapiens]

Accession:	gi|530402184	**Score:**	63.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	504.8
Database Date:	2015-11-30	**pI:**	6.6
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	2.0
		No. of unique Peptides:	3

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1222	1	927.2551	104.81	3	44.9	11.3	1	1184-1209	R.ALTTRSHAALHILGCLDTLAAMQDLK.M	Oxidation: 22
2398	1	1023.7079	112.56	2	59.9	13.0	2	2442-2460	K.VKDPPKGMIPPGTQLVKPK.S	Oxidation: 8
1461	1	799.6263	-94.96	3	48.0	13.1	1	4259-4279	K.AMVEFREHTGKPTTSSSEACR.F	Carbamidomethyl: 20; Oxidation: 2

Detailed Protein Report

Protein 37: **keratin, type II cytoskeletal 1b [Homo sapiens]**

Accession:	gi|194018511	**Score:**	62.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	61.9
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
MSHQFSSQSA	FSSMSRRVYS	TSSSAGSGGG	SPAVGSVCYA	RGRCGGGGYG	IHGRGFGSRS	LYNLGGSRSI	SINLMGRSTS
90	100	110	120	130	140	150	160
GFCQGGGVGG	FGGGRGFGVG	STGAGGFGGG	GFGGAGFGTS	NFGLGGFGPY	CPPGGIQEVT	INQSLLEPLH	LEVDPEIQRI
170	180	190	200	210	220	230	240
KTQEREQIMV	LNNKFASFID	KVRFLEQQNQ	VLQTKWELLQ	QVNTSTGTNN	LEPLLENYIG	DLRRQVDLLS	AEQMRQNAEV
250	260	270	280	290	300	310	320
RSMQDVVEDY	KSKYEDEINK	RTGSENDFVV	LKKDVDAAYV	SKVDLESRVD	TLTGEVNFLK	YLFLTELSQV	QTHISDTNVI
330	340	350	360	370	380	390	400
LSMDNNRSLD	LDSIIDAVRT	QYELIAQRSK	DEAEALYQTK	YQELQITAGR	HGDDLKNSKM	EIAELNRTVQ	RLQAEISNVK
410	420	430	440	450	460	470	480
KQIEQMQSLI	SDAEERGEQA	LQDAWQKLQD	LEEALQQSKE	ELARLLRDYQ	AMLGVKLSLD	VEIATYRQLL	EGEESRMSGE
490	500	510	520	530	540	550	560
LQSHVSISVQ	NSQVSVNGGA	GGGGSYGSGG	YGGGSGGGYG	GGRSYRGGGA	RGRSGGGYGS	GCGGGGGSYG	GSGRSGRGSS
570	580						
RVQIIQTSTN	TSHRRILE						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2780	1	922.4553	-14.26	2	66.1	16.9	1	361-376	K.YQELQITAGRHGDDLK.N	

Detailed Protein Report

Protein 38: nucleolar transcription factor 1 isoform b [Homo sapiens]

Accession:	gi|115529449	**Score:**	61.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	84.9
Database Date:	2015-11-30	**pI:**	5.3
Modification(s):	Oxidation	**Sequence Coverage [%]:**	5.2
		No. of unique Peptides:	4

Quantitation

MD:MU **Median:** 0.84 **CV:** 21.21 % **No. of Peptides:** 2

Alias proteins:

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

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1966	1	871.8504	-139.97	2	54.7	11.1	1	108-121	K.HPDFPKKPLTPYFR.F		MD:MU 0.68
2702	8	856.8935	-0.41	2	65.0	15.0	1	474-487	K.ALKAMEMTWNNMEK.K	Oxidation: 5	
2869	1	856.9447	59.29	2	66.4	17.0	1	474-487	K.ALKAMEMTWNNMEK.K	Oxidation: 7	
1591	1	472.2351	-22.65	2	49.6	18.5	0	513-522	R.APPAATNSSK.K		MD:MU 1.04

Detailed Protein Report

Protein 39: fibrillin-2 precursor [Homo sapiens]

Accession:	gi|66346695	**Score:**	60.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	314.6
Database Date:	2015-11-30	**pI:**	4.6
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	1.2
		No. of unique Peptides:	3

Quantitation

MD:MU	**Median:** 1.84	**CV:** 0.00 %	**No. of Peptides:** 1

10	20	30	40	50	60	70	80
MGRRRRLCLQ	LYFLWLGCVV	LWAQGTAGQP	QPPPPKPPRP	QPPPQQVRSA	TAGSEGGFLA	PEYREEGAAV	ASRVRRRGQQ
90	100	110	120	130	140	150	160
DVLRGPNVCG	SRFHSYCCPG	WKTLPGGNQC	IVPICRNSCG	DGFCSRPNMC	TCSSGQISST	CGSKSIQQCS	VRCMNGGTCA
170	180	190	200	210	220	230	240
DDHCQCQKGY	IGTYCGQPVC	ENGCQNGGRC	IGPNRCACVY	GFTGPQCERD	YRTGPCFTQV	NNQMCQGQLT	GIVCTKTLCC
250	260	270	280	290	300	310	320
ATIGRAWGHP	CEMCPAQPQP	CRRGFIPNIR	TGACQDVDEC	QAIPGICQGG	NCINTVGSFE	CRCPAGHKQS	ETTQKCEDID
330	340	350	360	370	380	390	400
ECSIIPGICE	TGECSNTVGS	YFCVCPRGYV	TSTDGSRCID	QRTGMCFSGL	VNGRCAQELP	GRMTKMQCCC	EPGRCWGIGT
410	420	430	440	450	460	470	480
IPEACPVRGS	EEYRRLCMDG	LPMGGIPGSA	GSRPGGTGGN	GFAPSGNGNG	YGPGGTGFIP	IPGGNGFSPG	VGGAGVGAGG
490	500	510	520	530	540	550	560
QGPIITGLTI	LNQTIDICKH	HANLCLNGRC	IPTVSSYRCE	CNMGYKQDAN	GDCIDVDECT	SNPCTNGDCV	NTPGSYYCKC
570	580	590	600	610	620	630	640
HAGFQRTPTK	QACIDIDECI	QNGVLCKNGR	CVNTDGSFQC	ICNAGFELTT	DGKNCVDHDE	CTTTNMCLNG	MCINEDGSFK
650	660	670	680	690	700	710	720
CICKPGFVLA	PNGRYCTDVD	ECQTPGICMN	GHCINSEGSF	RCDCPPGLAV	GMDGRVCVDT	HMRSTCYGGI	KKGVCVRPFP
730	740	750	760	770	780	790	800
GAVTKSECCC	ANPDYGFGEP	CQPCPAKNSA	EFHGLCSSGV	GITVDGRDIN	ECALDPDICA	NGICENLRGS	YRCNCNSGYE
810	820	830	840	850	860	870	880
PDASGRNCID	IDECLVNRLL	CDNGLCRNTP	GSYSCTCPPG	YVFRTETETC	EDINECESNP	CVNGACRNNL	GSFNCECSPG
890	900	910	920	930	940	950	960
SKLSSTGLIC	IDSLKGTCWL	NIQDSRCEVN	INGATLKSEC	CATLGAAWGS	PCERCELDTA	CPRGLARIKG	VTCEDVNECE
970	980	990	1000	1010	1020	1030	1040
VFPGVCPNGR	CVNSKGSFHC	ECPEGLTLDG	TGRVCLDIRM	EQCYLKWDED	ECIHPVPGKF	RMDACCCAVG	AAWGTECEEC
1050	1060	1070	1080	1090	1100	1110	1120
PKPGTKEYET	LCPRGAGFAN	RGDVLTGRPF	YKDINECKAF	PGMCTYGKCR	NTIGSFKCRC	NSGFALDMEE	RNCTDIDECR
1130	1140	1150	1160	1170	1180	1190	1200
ISPDLCGSGI	CVNTPGSFEC	ECFEGYESGF	MMMKNCMDID	ECERNPLLCR	GGTCVNTEGS	FQCDCPLGHE	LSPSREDCVD
1210	1220	1230	1240	1250	1260	1270	1280
INECSLSDNL	CRNGKCVNMI	GTYQCSCNPG	YQATPDRQGC	TDIDECMIMN	GGCDTQCTNS	EGSYECSCSE	GYALMPDGRS
1290	1300	1310	1320	1330	1340	1350	1360
CADIDECENN	PDICDGGQCT	NIPGEYRCLC	YDGFMASMDM	KTCIDVNECD	LNSNICMFGE	CENTKGSFIC	HCQLGYSVKK
1370	1380	1390	1400	1410	1420	1430	1440
GTTGCTDVDE	CEIGAHNCDM	HASCLNIPGS	FKCSCREGWI	GNGIKCIDLD	ECSNGTHQCS	INAQCVNTPG	SYRCACSEGF
1450	1460	1470	1480	1490	1500	1510	1520
TGDGFTCSDV	DECAENINLC	ENGQCLNVPG	AYRCECEMGF	TPASDSRSCQ	DIDECSFQNI	CVFGTCNNLP	GMFHCICDDG
1530	1540	1550	1560	1570	1580	1590	1600
YELDRTGGNC	TDIDECADPI	NCVNGLCVNT	PGRYECNCPP	DFQLNPTGVG	CVDNRVGNCY	LKFGPRGDGS	LSCNTEIGVG
1610	1620	1630	1640	1650	1660	1670	1680
VSRSSCCCSL	GKAWGNPCET	CPPVNSTEYY	TLCPGGEGFR	PNPITIILED	IDECQELPGL	CQGGNCINTF	GSFQCECPQG
1690	1700	1710	1720	1730	1740	1750	1760
YYLSEDTRIC	EDIDECFAHP	GVCGPGTCYN	TLGNYTCICP	PEYMQVNGGH	NCMDMRKSFC	YRSYNGTTCE	NELPFNVTKR
1770	1780	1790	1800	1810	1820	1830	1840
MCCCTYNVGK	AWNKPCEPCP	TPGTADFKTI	CGNIPGFTFD	IHTGKAVDID	ECKEIPGICA	NGVCINQIGS	FRCECPTGFS
1850	1860	1870	1880	1890	1900	1910	1920
YNDLLLVCED	IDECSNGDNL	CQRNADCINS	PGSYRCECAA	GFKLSPNGAC	VDRNECLEIP	NVCSHGLCVD	LQGSYQCICH
1930	1940	1950	1960	1970	1980	1990	2000
NGFKASQDQT	MCMDVDECER	HPCGNGTCKN	TVGSYNCLCY	PGFELTHNND	CLDIDECSSF	FGQVCRNGRC	FNEIGSFKCL
2010	2020	2030	2040	2050	2060	2070	2080
CNEGYELTPD	GKNCIDTNEC	VALPGSCSPG	TCQNLEGSFR	CICPPGYEVK	SENCIDINEC	DEDPNICLFG	SCTNTPGGFQ
2090	2100	2110	2120	2130	2140	2150	2160
CLCPPGFVLS	DNGRRCFDTR	QSFCFTNFEN	GKCSVPKAFN	TTKAKCCCSK	MPGEGWGDPC	ELCPKDDEVA	FQDLCPYGHG
2170	2180	2190	2200	2210	2220	2230	2240

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
534	2	730.1886	-131.49	2	36.0	10.1	1	383-394	R.MTKMQCCCEPGR.C	Carbamidomethyl: 6; Oxidation: 4	
522	1	730.1851	-136.21	2	35.9	15.8	1	383-394	R.MTKMQCCCEPGR.C	Carbamidomethyl: 8; Oxidation: 4	
304	5	642.1738	-171.43	2	33.2	24.4	1	2529-2539	K.TCKDLDECQTK.Q		MD:MU 1.84

Detailed Protein Report

Protein 40: laminin subunit alpha-2 isoform a precursor [Homo sapiens]

Accession:	gi|28559088	**Score:**	59.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	343.7
Database Date:	2015-11-30	**pI:**	6.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.8
		No. of unique Peptides:	5

Quantitation

MD:MU	**Median:**	0.58	**CV:**	0.00 %	**No. of Peptides:**	1

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Detailed Protein Report

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        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
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Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2021	1	665.3031	-44.41	2	55.2	14.0	1	295-306	R.ACPLDPATNKSR.C	Carbamidomethyl: 2	MD:MU 0.58
1220	1	1018.6209	-90.98	3	44.9	11.4	0	307-331	R.CECEHNTCGDSCDQCCPGFHQK.A	Carbamidomethyl: 12, 15, 16	
2360	1	1073.7380	-80.56	3	59.8	11.8	2	1380-1408	K.CDCPLGYSGLSCEACLPGFYRLR.T	Carbamidomethyl: 1, 12	
1065	1	836.1966	-317.81	1	42.9	11.8	1	1756-1762	K.KLFGESR.G		
1656	1	803.8745	-81.91	2	50.5	10.4	2	1969-1982	K.GCLQKSFRILNEAK.K		

Detailed Protein Report

Protein 41: macrophage mannose receptor 1 precursor [Homo sapiens]

Accession:	gi|4505245	**Score:**	59.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	165.9
Database Date:	2015-11-30	**pI:**	6.1
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	3.7
		No. of unique Peptides:	5

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
1884	1	621.2922	12.19	2	53.6	15.7	1	95-103	K.SEFQKWECK.N	Carbamidomethyl: 8
1876	1	914.3217	-127.99	2	53.5	10.7	2	477-491	R.GCEWPLGYICKMKSR.S	Carbamidomethyl: 10
2392	1	736.0727	87.47	3	60.2	10.6	1	586-604	R.FTHWNSDMPGRKPGCVAMR.T	Oxidation: 8
671	1	459.6231	-245.68	2	38.0	11.7	0	597-604	R.KPGCVAMR.T	Carbamidomethyl: 4
196	1	651.1714	-173.27	2	31.8	10.9	1	819-829	K.ETMDNARAFCK.R	Oxidation: 3

Detailed Protein Report

Protein 42: **androglobin [Homo sapiens]**

Accession:	gi|168823435	**Score:**	58.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	189.6
Database Date:	2015-11-30	**pI:**	9.1
		Sequence Coverage [%]:	3.2
		No. of unique Peptides:	3

10	20	30	40	50	60	70	80
MASKQTKKKE	VHRINSAHGS	DKSKDFYPFG	SNVQSGSTEQ	KKGKFPLWPE	WSEADINSEK	WDAGKGAKEK	DKTGKSPVFH
90	100	110	120	130	140	150	160
FFEDPEGKIE	LPPSLKIYSW	KRPQDILFSQ	TPVVVKNEIT	FDLFSANEHL	LCSELMRWII	SEIYAVWKIF	NGGILSNYFK
170	180	190	200	210	220	230	240
GTSGEPPLLP	WKPWEHIYSL	CKAVKGHMPL	FNSYGKYVVK	LYWMGCWRKI	TIDDFLPFDE	DNNLLLPATT	YEFELWPMLL
250	260	270	280	290	300	310	320
SKAIIKLANI	DIHVADRREL	GEFTVIHALT	GWLPEVISLH	PGYMDKVWEL	LKEILPEFKL	SDEASSESKI	AVLDSKLKEP
330	340	350	360	370	380	390	400
GKEGKEGKEI	KDGKEVKDVK	EFKPESSLTT	LKAPEKSDKV	PKEKADARDI	GKKRSKDGEK	EKFKFSLHGS	RPSSEVQYSV
410	420	430	440	450	460	470	480
QSLSDCSSAI	QTSHMVVYAT	FTPLYLFENK	IFSLEKMADS	AEKLREYGLS	HICSHPVLVT	RSRSCPLVAP	PKPPPLPPWK
490	500	510	520	530	540	550	560
LIRQKKETVI	TDEAQELIVK	KPERFLEISS	PFLNYRMTPF	TIPTEMHFVR	SLIKKGIPPG	SDLPSVSETD	ETATHSQTDL
570	580	590	600	610	620	630	640
SQITKATSQG	NTASQVILGK	GTDEQTDFGL	GDAHQSDGLN	LEREIVSQTT	ATQEKSQEEL	PTTNNSVSKE	IWLDFEDFCV
650	660	670	680	690	700	710	720
CFQNIYIFHK	PSSYCLNFQK	SEFKFSEERV	SYYLFVDSLK	PIELLVCFSA	LVRWGEYGAL	TKDSPPIEPG	LLTAETFSWK
730	740	750	760	770	780	790	800
SLKPGSLVLK	IHTYATKATV	VRLPVGRHML	LFNAYSPVGH	SIHICSMVSF	VIGDEHVVLP	NFEPESCRFT	EQSLLIMKAI
810	820	830	840	850	860	870	880
GNVIANFKDK	GKLSAALKDL	QTAHYPVPFH	DKELTAQHFR	VFHLSLWRLM	KKVQITKPPP	NFKFAFRAMV	LDLELLNSSL
890	900	910	920	930	940	950	960
EEVSLVEWLD	VKYCMPTSDK	EYSAEEVAAA	IKIQAMWRGT	YVRLLMKARI	PDTKENISVA	DTLQKVWAVL	EMNLEQYAVS
970	980	990	1000	1010	1020	1030	1040
LLRLMFKSKC	KSLESYPCYQ	DEETKIAFAD	YTVTYQEQPP	NSWFIVFRET	FLVHQDMILV	PKVYTTLPIC	ILHIVNNDTM
1050	1060	1070	1080	1090	1100	1110	1120
EQVPKVFQKV	VPYLYTKNKK	GYTFVAEAFT	GDTYVAASRW	KLRLIGSSAP	LPCLSRDSPC	NSFAIKEIRD	YYIPNDKKIL
1130	1140	1150	1160	1170	1180	1190	1200
FRYSVKVLTP	QPATIQVRTS	KPDAFIKLQV	LENEETMVSS	TGKGQAIIPA	FHFLKSEKGL	SSQSSKHILS	FHSASKKEQE
1210	1220	1230	1240	1250	1260	1270	1280
VYVKKKAAQG	IQKSPKGRAV	SAIQDIGLPL	VEEETTSTPT	REDSSSTPLQ	NYKYIIQCSV	LYNSWPLTES	QLTFVQALKD
1290	1300	1310	1320	1330	1340	1350	1360
LKKSNTKAYG	ERHEELINLG	SPDSHTISEG	QKSSVTSKTT	RKGKEKSSEK	EKTAKEKQAP	RFEPQISTVH	PQQEDPNKPY
1370	1380	1390	1400	1410	1420	1430	1440
WILRLVTEHN	ESELFEVKKD	TERADEIRAM	KQAWETTEPG	RAIKASQARL	HYLSGFIKKT	SDAESPPISE	SQTKPKEEVE
1450	1460	1470	1480	1490	1500	1510	1520
TAARGVKEPN	SKNSAGSESK	EMTQTGSGSA	VWKKWQLTKG	LRDVAKSTSS	ESGGVSSPGK	EEREQSTRKE	NIQTGPRTRS
1530	1540	1550	1560	1570	1580	1590	1600
PTILETSPRL	IRKALEFMDL	SQYVRKTDTD	PLLQTDELNQ	QQAMQKAEEI	HQFRQHRTRV	LSIRNIDQEE	RLKLKDEVLD
1610	1620	1630	1640	1650	1660	1670	
MYKEMQDSLD	EARQKIFDIR	EEYRNKLLEA	EHLKLETLAA	QEAAMKLETE	KMTPAPDTQK	KKKGKKK	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2723	1	921.1582	-5.50	3	65.3	17.8	1	138-160	R.WIISEIYAVWKIFNGGILSNYFK.G	
2431	1	590.4218	113.13	3	60.3	14.9	2	849-863	R.LMKKVQITKPPPNFK.F	
2707	2	933.4993	-17.55	2	65.1	26.2	2	913-927	K.IQAMWRGTYVRLLMK.A	

Detailed Protein Report

Protein 43: Alstrom syndrome protein 1 [Homo sapiens]

Accession:	gi|110349786	**Score:**	58.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	460.9
Database Date:	2015-11-30	**pI:**	5.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.1
		No. of unique Peptides:	2

Quantitation

MD:MU	**Median:**	3.08	**CV:**	0.00 %	**No. of Peptides:**	1

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

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
881	1	555.8212	17.82	2	40.6	26.2	0	1219-1229	K.VSPVLGPADQK.T		MD:MU 3.08
160	1	896.7503	-5.56	3	31.7	21.2	1	2566-2589	R.GMGCKPEAVCSHIIIESHEKGCFR.T	Carbamidomethyl: 4	

Detailed Protein Report

Protein 44: PREDICTED: rho GTPase-activating protein 26 isoform X6 [Homo sapiens]

Accession:	gi|530380462	**Score:**	58.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	69.9
Database Date:	2015-11-30	**pI:**	9.8
		Sequence Coverage [%]:	5.7
		No. of unique Peptides:	3

Quantitation

MD:MU **Median:** 0.47 **CV:** 0.00 % **No. of Peptides:** 1

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1954	10	710.2864	-113.94	2	54.5	21.4	1	35-48	R.ARHAGVPAVGPECR.A		MD:MU 0.47
286	1	716.6484	355.53	1	32.9	20.0	0	165-171	K.EQIGAAK.E		
42	2	768.2950	-133.93	2	29.9	16.8	1	340-353	K.QITMVPFDQKSGGK.G		

Detailed Protein Report

Protein 45:	**PREDICTED: neuroblast differentiation-associated protein AHNAK isoform X5 [Homo sapiens]**		
Accession:	gi|530397287	**Score:**	57.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	614.8
Database Date:	2015-11-30	**pI:**	5.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	0.9
		No. of unique Peptides:	4

Quantitation

MD:MU	**Median:**	1.04	**CV:**	0.00 %	**No. of Peptides:**	1

10	20	30	40	50	60	70	80
MEKEETTREL	LLPNWQGSGS	HGLTIAQRDD	GVFVQEVTQN	SPAARTGVVK	EGDQIVGATI	YFDNLQSGEV	TQLLNTMGHH
90	100	110	120	130	140	150	160
TVGLKLHRKG	DRSPEPGQTW	TREVFSSCSS	EVVLSGDDEE	YQRIYTTKIK	PRLKSEDGVE	GDLGETQSRT	ITVTRRVTAY
170	180	190	200	210	220	230	240
TVDVTGREGA	KDIDISSPEF	KIKIPRHELT	EISNVDVETQ	SGKTVIRLPS	GSGAASPTGS	AVDIRAGAIS	ASGPELQGAG
250	260	270	280	290	300	310	320
HSKLQVTMPG	IKVGGSGVNV	NAKGLDLGGR	GGVQVPAVDI	SSSLGGRAVE	VQGPSLESGD	HGKIKFPTMK	VPKFGVSTGR
330	340	350	360	370	380	390	400
EGQTPKAGLR	VSAPEVSVGH	KGGKPGLTIQ	APQLEVSVPS	ANIEGLEGKL	KGPQITGPSL	EGDLGLKGAK	PQGHIGVDAS
410	420	430	440	450	460	470	480
APQIGGSITG	PSVEVQAPDI	DVQGPGSKLN	VPKMKVPKFS	VSGAKGEETG	IDVTLPTGEV	TVPGVSGDVS	LPEIATGGLE
490	500	510	520	530	540	550	560
GKMKGTKVKT	PEMIIQKPKI	SMQDVDLSLG	SPKLKGDIKV	SAPGVQGDVK	GPQVALKGSR	VDIETPNLEG	TLTGPRLGSP
570	580	590	600	610	620	630	640
SGKTGTCRIS	MSEVDLNVAA	PKVKGGVDVT	LPRVEGKVKV	PEVDVRGPKV	DVSAPDVEAH	GPEWNLKMPK	MKMPTFSTPG
650	660	670	680	690	700	710	720
AKGEGPDVHM	TLPKGDISIS	GPKVNVEAPD	VNLEGLGGKL	KGPDVKLPDM	SVKTPKISMP	DVDLHVKGTK	VKGEYDVTVP
730	740	750	760	770	780	790	800
KLEGELKGPK	VDIDAPDVDV	HGPDWHLKMP	KMKMPKFSVP	GFKAEGPEVD	VNLPKADVDI	SGPKIDVTAP	DVSIEEPEGK
810	820	830	840	850	860	870	880
LKGPKFKMPE	MNIKVPKISM	PDVDLHLKGP	NVKGEYDVTM	PKVESEIKVP	DVELKSAKMD	IDVPDVEVQG	PDWHLKMPKM
890	900	910	920	930	940	950	960
KMPKFSMPGF	KAEGPEVDVN	LPKADVDISG	PKVGVEVPDV	NIEGPEGKLK	GPKFKMPEMN	IKAPKISMPD	VDLHMKGPKV
970	980	990	1000	1010	1020	1030	1040
KGEYDMTVPK	LEGDLKGPKV	DVSAPDVEMQ	GPDWNLKMPK	IKMPKFSMPS	LKGEGPEFDV	NLSKANVDIS	APKVDTNAPD
1050	1060	1070	1080	1090	1100	1110	1120
LSLEGPEGKL	KGPKFKMPEM	HFRAPKMSLP	DVDLDLKGPK	MKGNVDISAP	KIEGEMQVPD	VDIRGPKVDI	KAPDVEGQGL
1130	1140	1150	1160	1170	1180	1190	1200
DWSLKIPKMK	MPKFSMPSLK	GEGPEVDVNL	PKADVVVSGP	KVDIEAPDVS	LEGPEGKLKG	PKFKMPEMHF	KTPKISMPDV
1210	1220	1230	1240	1250	1260	1270	1280
DLHLKGPKVK	GDVDVSVPKV	EGEMKVPDVE	IKGPKMDIDA	PDVEVQGPDW	HLKMPKMKMP	KFSMPGFKGE	GREVDVNLPK
1290	1300	1310	1320	1330	1340	1350	1360
ADIDVSGPKV	DVEVPDVSLE	GPEGKLKGPK	FKMPEMHFKA	PKISMPDVDL	NLKGPKLKGD	VDVSLPEVEG	EMKVPDVDIK
1370	1380	1390	1400	1410	1420	1430	1440
GPKVDISAPD	VDVHGPDWHL	KMPKVKMPKF	SMPGFKGEGP	EVDVKLPKAD	VDVSGPKMDA	EVPDVNIEGP	DAKLKGPKFK
1450	1460	1470	1480	1490	1500	1510	1520
MPEMSIKPQK	ISIPDVGLHL	KGPKMKGDYD	VTVPKVEGEI	KAPDVDIKGP	KVDINAPDVE	VHGPDWHLKM	PKVKMPKFSM
1530	1540	1550	1560	1570	1580	1590	1600
PGFKGEGPEV	DMNLPKADLG	VSGPKVDIDV	PDVNLEAPEG	KLKGPKFKMP	SMNIQTHKIS	MPDVGLNLKA	PKLKTDVDVS
1610	1620	1630	1640	1650	1660	1670	1680
LPKVEGDLKG	PEIDVKAPKM	DVNVGDIDIE	GPEGKLKGPK	FKMPEMHFKA	PKISMPDVDL	HLKGPKVKGD	MDVSVPKVEG
1690	1700	1710	1720	1730	1740	1750	1760
EMKVPDVDIK	GPKVDIDAPD	VEVHDPDWHL	KMPKMKMPKF	SMPGFKAEGP	EVDVNLPKAD	IDVSGPSVDT	DAPDLDIEGP
1770	1780	1790	1800	1810	1820	1830	1840
EGKLKGSKFK	MPKLNIKAPK	VSMPDVDLNL	KGPKLKGEID	ASVPELEGDL	RGPQVDVKGP	FVEAEVPDVD	LECPDAKLKG
1850	1860	1870	1880	1890	1900	1910	1920
PKFKMPEMHF	KAPKISMPDV	DLHLKGPKVK	GDADVSVPKL	EGDLTGPSVG	VEVPDVELEC	PDAKLKGPKF	KMPDMHFKAP
1930	1940	1950	1960	1970	1980	1990	2000
KISMPDVDLH	LKGPKVKGDV	DVSVPKLEGD	LTGPSVGVEV	PDVELECPDA	KLKGPKFKMP	EMHFKTPKIS	MPDVDLHLKG
2010	2020	2030	2040	2050	2060	2070	2080
PKVKGDMDVS	VPKVEGEMKV	PDVDIKGPKM	DIDAPDVDVH	GPDWHLKMPK	MKMPKFSMPG	FKAEGPEVDV	NLPKADVVVS
2090	2100	2110	2120	2130	2140	2150	2160
GPKVDVEVPD	VSLEGPEGKL	KGPKLKMPEM	HFKAPKISMP	DVDLHLKGPK	VKGDVDVSLP	KLEGDLTGPS	VDVEVPDVEL
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
2716	1	849.3583	-170.01	2	65.2	15.5	2	485-499	K.GTKVKTPEMIIQKPK.I		
863	1	578.2806	-119.29	2	40.2	10.1	2	1771-1780	K.MPKLNIKAPK.V	Oxidation: 1	
1213	1	764.7682	-167.48	2	44.8	12.8	1	2851-2865	K.GDVDVTGPKVEGDLK.G		
1557	1	472.2329	-53.94	2	49.3	18.8	0	2979-2987	K.GDVDISLPK.V		MD:MU 1.04

Detailed Protein Report

Protein 46: phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 1 isoform b [Homo sapiens]

Accession:	gi|40254823	**Score:**	56.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	133.1
Database Date:	2015-11-30	**pI:**	7.9
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.6
		No. of unique Peptides:	3

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
499	2	584.8345	31.59	2	35.6	27.2	0	79-87	K.LDQLIEFYK.K	
234	1	850.8764	-41.35	2	32.6	12.8	0	167-181	R.LQSMDTSGLPEEHLK.A	Oxidation: 4
1543	1	1008.6543	64.47	2	49.1	16.6	1	1107-1125	K.TPVSSQAPVPAKRPIKPSR.S	

Detailed Protein Report

Protein 47: protocadherin Fat 2 precursor [Homo sapiens]

Accession:	gi|13787217	**Score:**	56.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	479.0
Database Date:	2015-11-30	**pI:**	4.9
		Sequence Coverage [%]:	1.5
		No. of unique Peptides:	3

Alias proteins:

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

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

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

Detailed Protein Report

Protein 48: pyruvate kinase PKM isoform a [Homo sapiens]

Accession:	gi|33286418	**Score:**	56.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	57.9
Database Date:	2015-11-30	**pI:**	9.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	5.5
		No. of unique Peptides:	2

Quantitation

MD:MU	**Median:** 0.57	**CV:** 0.00 %	**No. of Peptides:** 1

Alias proteins:

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

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
566	1	680.2094	-215.66	2	36.4	14.7	0	44-56	R.NTGIICTIGPASR.S	Carbamidomethyl: 6	
111	1	628.6466	11.60	3	30.8	41.8	0	74-89	R.LNFSHGTHEYHAETIK.N		MD:MU 0.57

Detailed Protein Report

Protein 49: PREDICTED: splicing factor, proline- and glutamine-rich isoform X5 [Homo sapiens]

Accession: gi|530363148
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 55.1
MW [kDa]: 72.2
pI: 9.7
Sequence Coverage [%]: 5.1
No. of unique Peptides: 3

Quantitation

MD:MU **Median:** 0.23 **CV:** 0.00 % **No. of Peptides:** 1

Alias proteins:

Accession	Name	Description
gi|530363150	refseq_human (refseq_human_20140103.fasta)	PREDICTED: splicing factor, proline- and glutamine-rich isoform X6 [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					
GYEANPGVPP	ATMSGSMMGS	DMVRMIDVG					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
376	4	678.1939	-185.67	2	34.0	29.1	1	268-279	R.SEEKISDSEGFK.A		MD:MU 0.23
14	1	1103.5206	70.68	2	29.5	14.3	1	609-630	R. DMRMGGGGAMNMGDPYGSGGQ F	Oxidation: 2, 12	
20	1	735.9950	41.81	3	29.6	11.7	1	609-630	R. DMRMGGGGAMNMGDPYGSGGQ F	Oxidation: 4, 10	

Detailed Protein Report

Protein 50: PREDICTED: MAX gene-associated protein isoform X6 [Homo sapiens]

Accession:	gi|530405566	**Score:**	55.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	341.2
Database Date:	2015-11-30	**pI:**	6.7
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	1.4
		No. of unique Peptides:	3

10	20	30	40	50	60	70	80
MEEKQQIILA	NQDGGTVAGA	APTFFVILKQ	PGNGKTDQGI	LVTNQDACAL	ASSVSSPVKS	KGKICLPADC	TVGGITVTLD
90	100	110	120	130	140	150	160
NNSMWNEFYH	RSTEMILTKQ	GRRMFPYCRY	WITGLDSNLK	YILVMDISPV	DNHRYKWNGR	WWEPSGKAEP	HVLGRVFIHP
170	180	190	200	210	220	230	240
ESPSTGHYWM	HQPVSFYKLK	LTNNTLDQEG	HIILHSMHRY	LPRLHLVPAE	KAVEVIQLNG	PGVHTFTFPQ	TEFFAVTAYQ
250	260	270	280	290	300	310	320
NIQITQLKID	YNPFAKGFRD	DGLNNKPQRD	GKQKNSSDQE	GNNISSSSGH	RVRLTEGQGS	EIQPGDLDPL	SRGHETSGKG
330	340	350	360	370	380	390	400
LEKTSLNIKR	DFLGFMDTDS	ALSEVPQLKQ	EISECLIASS	FEDDSRVASP	LDQNGSFNVV	IKEEPLDDYD	YELGECPEGV
410	420	430	440	450	460	470	480
TVKQEETDEE	TDVYSNSDDD	PILEKQLKRH	NKVDNPEADH	LSSKWLPSSP	SGVAKAKMFK	LDTGKMPVVY	LEPCAVTRST
490	500	510	520	530	540	550	560
VKISELPDNM	LSTSRKDKSS	MLAELEYLPT	YIENSNETAF	CLGKESENGL	RKHSPDLRVV	QKYPLLKEPQ	WKYPDISDSI
570	580	590	600	610	620	630	640
STERILDDSK	DSVGDSLSGK	EDLGRKRTTM	LKIATAAKVV	NANQNASPNV	PGKRGRPRKL	KLCKAGRPPK	NTGKSLISTK
650	660	670	680	690	700	710	720
NTPVSPGSTF	PDVKPDLEDV	DGVLFVSFES	KEALDIHAVD	GTTEESSSLQ	ASTTNDSGYR	ARISQLEKEL	IEDLKTLRHK
730	740	750	760	770	780	790	800
QVIHPGLQEV	GLKLNSVDPT	MSIDLKYLGV	QLPLAPATSF	PFWNLTGTNP	ASPDAGFPFV	SRTGKTNDFT	KIKGWRGKFH
810	820	830	840	850	860	870	880
SASASRNEGG	NSESSLKNRS	AFCSDKLDEY	LENEGKLMET	SMGFSSNAPT	SPVVYQLPTK	STSYVRTLDS	VLKKQSTISP
890	900	910	920	930	940	950	960
STSYSLKPHS	VPPVSRKAKS	QNRQATFSGR	TKSSYKSILP	YPVSPKQKYS	HVILGDKVTK	NSSGIISENQ	ANNFVVPTLD
970	980	990	1000	1010	1020	1030	1040
ENIFPKQISL	RQAQQQQQQQ	QGSRPPGLSK	SQVKLMDLED	CALWEGKPRT	YITEERADVS	LTTLLTAQAS	LKTKPIHTII
1050	1060	1070	1080	1090	1100	1110	1120
RKRAPPCNND	FCRLGCVCSS	LALEKRQPAH	CRRPDCMFGC	TCLKRKVVLV	KGGSKTKHFQ	RKAAHRDPVF	YDTLGEEARE
1130	1140	1150	1160	1170	1180	1190	1200
EEEGIREEEE	QLKEKKKRKK	LEYTICETEP	EQPVRHYPLW	VKVEGEVDPE	PVYIPTPSVI	EPMKPLLLPQ	PEVLSPTVKG
1210	1220	1230	1240	1250	1260	1270	1280
KLLTGIKSPR	SYTPKPNPVI	REEDKDPVYL	YFESMMTCAR	VRVYERKKED	QRQPSSSSSP	SPSFQQQTSC	HSSPENHNNA
1290	1300	1310	1320	1330	1340	1350	1360
KEPDSEQQPL	KQLTCDLEDD	SDKLQEKSWK	SSCNEGESSS	TSYMHQRSPG	GPTKLIEIIS	DCNWEEDRNK	ILSILSQHIN
1370	1380	1390	1400	1410	1420	1430	1440
SNMPQSLKVG	SFIIELASQR	KSRGEKNPPV	YSSRVKISMP	SCQDQDDMAE	KSGSETPDGP	LSPGKMEDIS	PVQTDALDSV
1450	1460	1470	1480	1490	1500	1510	1520
RERLHGGKGL	PFYAGLSPAG	KLVAYKRKPS	SSTSGLIQVN	GKSYPQAKLL	LGQMGALHPA	NRLAAYITGR	LRPSVLDLST
1530	1540	1550	1560	1570	1580	1590	1600
LSTVISKVAS	NAKVAASRKP	RTLLPSTSNS	KMASSSGTAT	NRPGKNLKAF	VPAKRPIAAR	PSPGGVFTQF	VMSKVGALQQ
1610	1620	1630	1640	1650	1660	1670	1680
KIPGVSTPQT	LAGTQKFSIR	PSPVMVVTPV	VSSEPVQVCS	PVTAAVTTTT	PQVFLENTTA	VTPMTAISDV	ETKETTYSSG
1690	1700	1710	1720	1730	1740	1750	1760
ATTTGVVEVS	ETNTSTSVTS	TQSTATVNLT	KTTGITTPVA	SVAFPKSLVA	SPSTITLPVA	STASTSLVVV	TAAASSSMVT
1770	1780	1790	1800	1810	1820	1830	1840
TPTSSLGSVP	IILSGINGSP	PVSQRPENAA	QIPVATPQVS	PNTVKRAGPR	LLLIPVQQGS	PTLRPVSNTQ	LQGHRMVLQP
1850	1860	1870	1880	1890	1900	1910	1920
VRSPSGMNLF	RHPNGQIVQL	LPLHQLRGSN	TQPNLQPVMF	RNPGSVMGIR	LPAPSKPSET	PPSSTSSSAF	SVMNPVIQAV
1930	1940	1950	1960	1970	1980	1990	2000
GSSSAVNVIT	QAPSLLSSGA	SFVSQAGTLT	LRISPPEPQS	FASKTGSETK	ITYSSGGQPV	GTASLIPLQS	GSFALLQLPG
2010	2020	2030	2040	2050	2060	2070	2080
QKPVPSSILQ	HVASLQMKRE	SQNPDQKDET	NSIKREQETK	KVLQSEGEAV	DPEANVIKQN	SGAATSEETL	NDSLEDRGDH
2090	2100	2110	2120	2130	2140	2150	2160
LDEECLPEEG	CATVKPSEHS	CITGSHTDQD	YKDVNEEYGA	RNRKSSKEKV	AVLEVRTISE	KASNKTVQNL	SKVQHQKLGD
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
1755	1	636.2889	-110.13	2	51.9	13.3	0	1211-1221	R.SYTPKPNPVIR.E	
2040	1	841.7905	46.48	3	55.6	10.9	2	2189-2210	K.FELSGSKVMEQQSNLQPEAKEK.E	Oxidation: 9
939	1	583.7035	-110.96	2	41.3	10.6	1	2234-2243	R.KCVGASQECK.K	Carbamidomethyl: 2, 9

Detailed Protein Report

Protein 51: small proline-rich protein 2A [Homo sapiens]

Accession:	gi|5174693	**Score:**	54.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	8.0
Database Date:	2015-11-30	**pI:**	10.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	36.1
		No. of unique Peptides:	2

Quantitation

MD:MU **Median:** 0.85 **CV:** 34.64 % **No. of Peptides:** 2

```
        10         20         30         40         50         60         70         80
MSYQQQQCKQ PCQPPPVCPT PKCPEPCPPP KCPEPCPPPK CPQPCPPQQC QQKYPPVTPS PPCQSKYPPK SK
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
85	4	753.3519	-18.26	2	30.5	41.0	0	10-22	K.QPCQPPPVCPTPK.C	Carbamidomethyl: 3, 9	MD:MU 1.19
171	1	729.5012	195.91	2	31.9	13.8	0	54-66	K.YPPVTPSPPCQSK.Y	Carbamidomethyl: 10	MD:MU 0.61

Detailed Protein Report

Protein 52: dynein heavy chain 11, axonemal [Homo sapiens]

Accession:	gi|459642365	**Score:**	54.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	520.0
Database Date:	2015-11-30	**pI:**	6.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.1
		No. of unique Peptides:	4

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1302	1	817.1657	-329.27	1	46.0	11.8	0	1-8	-.MAAQVAAR.E	
2700	1	920.8814	-102.30	2	65.0	16.0	2	857-872	R.REAAFTLEDKGDLFTK.K	
2478	1	589.2111	-228.33	2	60.9	14.1	0	2296-2304	R.LLFEIHHLR.S	
1863	1	965.8216	-153.66	2	53.3	12.4	2	4470-4484	R.QETKQTYECPVYRTK.L	Carbamidomethyl: 9

Detailed Protein Report

Protein 53: obscurin isoform a [Homo sapiens]

Accession:	gi|403501448	**Score:**	53.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	721.1
Database Date:	2015-11-30	**pI:**	5.4
		Sequence Coverage [%]:	0.5
		No. of unique Peptides:	3

Quantitation

MD:MU	**Median:**	0.66	**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
LRVSEPKVVF	AKEQLARRKL	QAEAGASATL	SCEVAQAQTE	VTWYKDGKKL	SSSSKVCMEA	TGCTRRLVVQ	QAGQADAGEY
970	980	990	1000	1010	1020	1030	1040
SCEAGGQRLS	FHLDVKEPKV	VFAKDQVAHS	EVQAEAGASA	TLSCEVAQAQ	TEVMWYKDGK	KLSSSLKVHV	EAKGCRRRLV
1050	1060	1070	1080	1090	1100	1110	1120
VQQAGKTDAG	DYSCEARGQR	VSFRLHITEP	KMMFAKEQSV	HNEVQAEAGA	SAMLSCEVAQ	AQTEVTWYKD	GKKLSSSSKV
1130	1140	1150	1160	1170	1180	1190	1200
GMEVKGCTRR	LVLPQAGKAD	AGEYSCEAGG	QRVSFHLHIT	EPKGVFAKEQ	SVHNEVQAEA	GTTAMLSCEV	AQPQTEVTWY
1210	1220	1230	1240	1250	1260	1270	1280
KDGKKLSSSS	KVRMEVKGCT	RRLVVQQVGK	ADAGEYSCEA	GGQRVSFQLH	ITEPKAVFAK	EQLVHNEVRT	EAGASATLSC
1290	1300	1310	1320	1330	1340	1350	1360
EVAQAQTEVT	WYKDGKKLSS	SSKVRIEAAG	CMRQLVVQQA	GQADAGEYTC	EAGGQRLSFH	LDVSEPKAVF	AKEQLAHRKV
1370	1380	1390	1400	1410	1420	1430	1440
QAEAGAIATL	SCEVAQAQTE	VTWYKDGKKL	SSSSKVRMEA	VGCTRRLVVQ	QACQADTGEY	SCEAGGQRLS	FSLDVAEPKV
1450	1460	1470	1480	1490	1500	1510	1520
VFAKEQPVHR	EVQAQAGAST	TLSCEVAQAQ	TEVMWYKDGK	KLSFSSKVRM	EAVGCTRRLV	VQQAGQAVAG	EYSCEAGSQR
1530	1540	1550	1560	1570	1580	1590	1600
LSFHLHVAEP	KAVFAKEQPA	SREVQAEAGT	SATLSCEVAQ	AQTEVTWYKD	GKKLSSSSKV	RMEAVGCTRR	LVVQEAGQAD
1610	1620	1630	1640	1650	1660	1670	1680
AGEYSCKAGD	QRLSFHLHVA	EPKVVFAKEQ	PAHREVQAEA	GASATLSCEV	AQAQTEVTWY	KDGKKLSSSS	KVRVEAVGCT
1690	1700	1710	1720	1730	1740	1750	1760
RRLVVQQAGQ	AEAGEYSCEA	GGQQLSFRLQ	VAELEPQISE	RPCRREPLVV	KEHEDIILTA	TLATPSAATV	TWLKDGVEIR
1770	1780	1790	1800	1810	1820	1830	1840
RSKRHETASQ	GDTHTLTVHG	AQVLDSAIYS	CRVGAEGQDF	PVQVEEVAAK	FCRLLEPVCG	ELGGTVTLAC	ELSPACAEVV
1850	1860	1870	1880	1890	1900	1910	1920
WRCGNTQLRV	GKRFQMVAEG	PVRSLTVLGL	RAEDAGEYVC	ESRDDHTSAQ	LTVSVPRVVK	FMSGLSTVVA	EEGGEATFQC
1930	1940	1950	1960	1970	1980	1990	2000
VVSPSDVAVV	WFRDGALLQP	SEKFAISQSG	ASHSLTISDL	VLEDAGQITV	EAEGASSSAA	LRVREAPVLF	KKKLEPQTVE
2010	2020	2030	2040	2050	2060	2070	2080
ERSSVTLEVE	LTRPWPELRW	TRNATALAPG	KNVEIHAEGA	RHRLVLHNVG	FADRGFFGCE	TPDDKTQAKL	TVEMRQVRLV
2090	2100	2110	2120	2130	2140	2150	2160
RGLQAVEARE	QGTATMEVQL	SHADVDGSWT	RDGLRFQQGP	TCHLAVRGPM	HTLTLSGLRP	EDSGLMVFKA	EGVHTSARLV
2170	2180	2190	2200	2210	2220	2230	2240
VTELPVSFSR	PLQDVVTTEK	EKVTLECELS	RPNVDVRWLK	DGVELRAGKT	MAIAAQGACR	SLTIYRCEFA	DQGVYVCDAH
2250	2260	2270	2280	2290	2300	2310	2320
DAQSSASVKV	QGRTYTLIYR	RVLAEDAGEI	QFVAENAESR	AQLRVKELPV	TLVRPLRDKI	AMEKHRGVLE	CQVSRASAQV
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
1991	2	643.3110	-83.65	2	54.8	19.9	2	338-347	K.RLQDLEVREK.E		MD:MU 0.66
2661	1	686.8980	-30.78	2	63.3	13.1	2	881-892	R.LRVSEPKVVFAK.E		
2091	1	709.3658	-116.08	2	56.0	20.8	2	5981-5992	R.KYLLQARTAIIK.S		

Detailed Protein Report

Protein 54:	**fibrillin-1 precursor [Homo sapiens]**		
Accession:	gi|281485550	**Score:**	53.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	312.1
Database Date:	2015-11-30	**pI:**	4.7
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	1.7
		No. of unique Peptides:	3

Quantitation

MD:MU	**Median:**	2.40	**CV:**	0.00 %	**No. of Peptides:**	1	

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1152	1	991.7003	-40.24	3	44.0	14.6	1	356-380	K. MQCCCDAGRCWSPGVTVAPEMC A	Carbamidomethyl: 3, 4, 5, 22; Oxidation: 1, 21	
821	5	635.1373	-218.44	2	39.8	23.3	1	2482-2492	R.SCKDLDECATK.Q	Carbamidomethyl: 8	MD:MU 2.40
2864	1	703.3686	82.89	2	66.3	15.8	0	2681-2694	R.IGQGHCVSGMGMGR.G	Oxidation: 12	

Detailed Protein Report

Protein 55: PREDICTED: uncharacterized protein LOC285556 isoform X2 [Homo sapiens]

Accession:	gi|578843586	**Score:**	53.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	190.0
Database Date:	2015-11-30	**pI:**	9.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.6
		No. of unique Peptides:	3

Alias proteins:

Accession	**Name**	**Description**
gi|578843588	refseq_human (refseq_human_20140103.fasta)	PREDICTED: uncharacterized protein LOC285556 isoform X3 [Homo sapiens]

10	20	30	40	50	60	70	80
MLSFHFWKSR	GQPTDAASSV	ADGIQTPRCC	RQCQANNWTG	QLSYRTLATV	SAGAAAPQPQ	TTSTASSRSL	PTSLRLAAAP
90	100	110	120	130	140	150	160
PQGLKNWEVV	AAVAAVPTAL	GPVQIRGTLL	RATLQPLRGQ	RRTQDFPSDH	HCLFLSLKPG	QGLIMEAAPP	ELNSKARQAE
170	180	190	200	210	220	230	240
VGDGVSSAQD	SQELKQQLWP	LPKPSASSQR	EAKYVDMCAS	AEVQRESPQT	MKLTLGHCPG	GQRASRSPKE	KAQDEPSSKT
250	260	270	280	290	300	310	320
PSPQNNPASS	QLSRSQHSAS	EEGGNFSSSS	SSSPMNKAEE	DGLSKMEDST	TSTGALATSS	SSLGFESESG	ESEGCQAVGG
330	340	350	360	370	380	390	400
EGEKISGGRG	GGKGGGGGGA	GDGTECRDII	AKSQGSRDPP	KVEEAHYITT	HEIQLSEVEQ	DMDFDVGLAS	RWDFEDNNVI
410	420	430	440	450	460	470	480
YSFVDYASFG	GSDETPGDIT	SLTEEDDDNS	CYLSTTPSTN	TTRTPSPTSS	DLARPNAGRS	GRDTSSTEVG	SGPSDSGPTP
490	500	510	520	530	540	550	560
PPTGPGTAPL	TEPLPETPEA	ASGAAAAAAS	SCGSAASQIL	LSIKPASRAI	NEPSNVRAKQ	NIIYAAKHEG	DMSLRVSTAA
570	580	590	600	610	620	630	640
EHNSSSLKQN	PAAAVAQDHA	KKFIAVPARL	QTRCGAIRAK	ELVDYSSGAS	SAVSELDDAD	KEVRNLTSRA	FRSLAYPYFE
650	660	670	680	690	700	710	720
ALNISSRESS	TTLSEVGFGR	WSTFLDLKCG	GVGARVEQSL	LRSSAASVAA	GLRKGSGARA	TADQLYIQSK	KSQTKALEFV
730	740	750	760	770	780	790	800
VSKVEGEIKH	VETPLCFQKQ	VQTGSRVVTL	LEPLNVRSES	KASSAPGPGR	ATKGPGKGPG	SAYTDDGSET	SEGSKPTSRA
810	820	830	840	850	860	870	880
DGPQKSKFAS	SLLKNVISKK	MQREHEFKME	RGEVMDTSHH	LSGTSKETEG	ARGSERQRER	GLQRQSSRHS	EAGSEYTVVS
890	900	910	920	930	940	950	960
MSDAGGEGSV	AGSKSPVFKA	STPRERNAGP	GRNFTDGHTE	VCEIKKSASE	TVKGIFLRSQ	NSAFRSWKEK	EAEKREEQAP
970	980	990	1000	1010	1020	1030	1040
IGKLKLPKGG	DWRADLGEIS	ASKNTIMSRL	FVPNIQQTPK	DKQPRKQATK	YPAAQATSTA	VIRPKAPEIK	IRLGSVQQPS
1050	1060	1070	1080	1090	1100	1110	1120
SDFNIAKLLT	PKLAGGSASN	LFKTIEDNSR	AQQKLFRGDN	LEKVPHFQVR	DIRDKSKAQG	PLHQVRDVRK	LIKGSGDSSD
1130	1140	1150	1160	1170	1180	1190	1200
KGSVTPEQGL	TGPKPRQLSA	AAGGSGSLSP	MVITCQAVVN	QREDSMDREP	RESMGKGGGS	RVLNSSSPEG	TVLVHRASGR
1210	1220	1230	1240	1250	1260	1270	1280
LPVATIAPNK	PEQGSYLPVL	KIVSKASTQK	TPEKLKEEEV	KEEGKATKPA	RNALEKLTAA	VRSMEELYSF	NRNEWKRKSD
1290	1300	1310	1320	1330	1340	1350	1360
PLPMMMDSHV	LSLIASEERE	GVVVADGDHD	KLSKRLGEVE	ERGTGNKAGV	VLRGAPIERL	QRRNSNPSAE	SVSARAAAFE
1370	1380	1390	1400	1410	1420	1430	1440
NLARERPRSL	YIPPVHKDVE	RTQPLQPLPP	LPSNRNVFTV	SASSIQKTGG	VAGKFPQGPS	PESPSAAKGI	KSQGLRSLKI
1450	1460	1470	1480	1490	1500	1510	1520
SPATRAPPDE	VTNRKSGSNL	EKSNSDCENY	LTIPLKGSSA	AGELLSRPGA	SREGPPNSSA	ATLCSLPPLS	ARSQVPSSSK
1530	1540	1550	1560	1570	1580	1590	1600
GSQVSGTSRP	AWRTKPDNPR	ETVAAPPGPQ	SPEHPPTTIY	HQPPLPFTLQ	GAQPQVLCFS	PPSMPAPAPA	ASAPVPTDPF
1610	1620	1630	1640	1650	1660	1670	1680
QQAQPQQTQR	KMLLDVTTGQ	YYLVDTPVQP	MTRRLFDPET	GQYVDVPMTS	QQQAVAPMSI	SVPPLALSPG	AYGPTYMIYP
1690	1700	1710	1720	1730	1740	1750	1760
GFLPTVLPTN	ALQPTPIARA	PRGSELSPLV	AEPSSKEAAA	TFTEAPYFMA	SGQSPASSTS	SAPAATSQLL	GAKAFAQLHG
1770	1780	1790	1800				
KPVISITSQP	LGPRIIAPPS	FDGTTMSFVV	EHR				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
886	1	575.7576	46.75	2	40.6	12.5	0	334-347	K.GGGGGGAGDGTECR.D	
1275	1	874.2865	-135.51	2	45.6	10.1	1	334-352	K.GGGGGGAGDGTECRDIIAK.S	Carbamidomethyl: 13
1984	1	634.7974	-113.89	2	54.7	11.7	2	955-965	K.REEQAPIGKLK.L	

Detailed Protein Report

Protein 56: dystonin isoform 1eA precursor [Homo sapiens]

Accession:	gi|34577049	**Score:**	51.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	590.7
Database Date:	2015-11-30	**pI:**	5.4
		Sequence Coverage [%]:	0.9
		No. of unique Peptides:	3

Quantitation

MD:MU	**Median:** 1.56	**CV:** 11.67 %	**No. of Peptides:** 2

10	20	30	40	50	60	70	80
MHSSSYSYRS	SDSVFSNTTS	TRTSLDSNEN	LLLVHCGPTL	INSCISFGSE	SFDGHRLEML	QQIANRVQRD	SVICEDKLIL
90	100	110	120	130	140	150	160
AGNALQSDSK	RLESGVQFQN	EAEIAGYILE	CENLLRQHVI	DVQILIDGKY	YQADQLVQRV	AKLRDEIMAL	RNECSSVYSK
170	180	190	200	210	220	230	240
GRILTTEQTK	LMISGITQSL	NSGFAQTLHP	SLTSGLTQSL	TPSLTSSSMT	SGLSSGMTSR	LTPSVTPAYT	PGFPSGLVPN
250	260	270	280	290	300	310	320
FSSGVEPNSL	QTLKLMQIRK	PLLKSSLLDQ	NLTEEEINMK	FVQDLLNWVD	EMQVQLDRTE	WGSDLPSVES	HLENHKNVHR
330	340	350	360	370	380	390	400
AIEEFESSLK	EAKISEIQMT	APLKLTYAEK	LHRLESQYAK	LLNTSRNQER	HLDTLHNFVS	RATNELIWLN	EKEEEEVAYD
410	420	430	440	450	460	470	480
WSERNTNIAR	KKDYHAELMR	ELDQKEENIK	SVQEIAEQLL	LENHPARLTI	EAYRAAMQTQ	WSWILQLCQC	VEQHIKENTA
490	500	510	520	530	540	550	560
YFEFFNDAKE	ATDYLRNLKD	AIQRKYSCDR	SSSIHKLEDL	VQESMEEKEE	LLQYKSTIAN	LMGKAKTIIQ	LKPRNSDCPL
570	580	590	600	610	620	630	640
KTSIPIKAIC	DYRQIEITIY	KDDECVLANN	SHRAKWKVIS	PTGNEAMVPS	VCFTVPPPNK	EAVDLANRIE	QQYQNVLTLW
650	660	670	680	690	700	710	720
HESHINMKSV	VSWHYLINEI	DRIRASNVAS	IKTMLPGEHQ	QVLSNLQSRF	EDFLEDSQES	QVFSGSDITQ	LEKEVNVCKQ
730	740	750	760	770	780	790	800
YYQELLKSAE	REEQEESVYN	LYISEVRNIR	LRLENCEDRL	IRQIRTPLER	DDLHESVFRI	TEQEKLKKEL	ERLKDDLGTI
810	820	830	840	850	860	870	880
TNKCEEFFSQ	AAASSSVPTL	RSELNVVLQN	MNQVYSMSST	YIDKLKTVNL	VLKNTQAAEA	LVKLYETKLC	EEEAVIADKN
890	900	910	920	930	940	950	960
NIENLISTLK	QWRSEVDEKR	QVFHALEDEL	QKAKAISDEM	FKTYKERDLD	FDWHKEKADQ	LVERWQNVHV	QIDNRLRDLE
970	980	990	1000	1010	1020	1030	1040
GIGKSLKYYR	DTYHPLDDWI	QQVETTQRKI	QENQPENSKT	LATQLNQQKM	LVSEIEMKQS	KMDECQKYAE	QYSATVKDYE
1050	1060	1070	1080	1090	1100	1110	1120
LQTMTYRAMV	DSQQKSPVKR	RRMQSSADLI	IQEFMDLRTR	YTALVTLMTQ	YIKFAGDSLK	RLEEEEKSLE	EEKKEHVEKA
1130	1140	1150	1160	1170	1180	1190	1200
KELQKWVSNI	SKTLKDAEKA	GKPPFSKQKI	SSEEISTKKE	QLSEALQTIQ	LFLAKHGDKM	TDEERNELEK	QVKTLQESYN
1210	1220	1230	1240	1250	1260	1270	1280
LLFSESLKQL	QESQTSGDVK	VEEKIVAERQ	QEYKEKLQGI	CDLLTQTENR	LIGHQEAFMI	GDGTVELKKY	QSKQEELQKD
1290	1300	1310	1320	1330	1340	1350	1360
MQGSAQALAE	VVKNTENFLK	ENGEKLSQED	KALIEQKLNE	AKIKCEQLNL	KAEQSKKELD	KVVTTAIKEE	TEKVAAVKQL
1370	1380	1390	1400	1410	1420	1430	1440
EESKTKIENL	LDWLSNVDKD	SERAGTKHKQ	VIEQNGTHFQ	EGDGKSAIGE	EDEVNGNLLE	TDVDGQVGTT	QENLNQQYQK
1450	1460	1470	1480	1490	1500	1510	1520
VKAQHEKIIS	QHQAVIIATQ	SAQVLLEKQG	QYLSPEEKEK	LQKNMKELKV	HYETALAESE	KKMKLTHSLQ	EELEKFDADY
1530	1540	1550	1560	1570	1580	1590	1600
TEFEHWLQQS	EQELENLEAG	ADDINGLMTK	LKRQKSFSED	VISHKGDLRY	ITISGNRVLE	AAKSCSKRDG	GKVDTSATHR
1610	1620	1630	1640	1650	1660	1670	1680
EVQRKLDHAT	DRFRSLYSKC	NVLGNNLKDL	VDKYQHYEDA	SCGLLAGLQA	CEATASKHLS	EPIAVDPKNL	QRQLEETKAL
1690	1700	1710	1720	1730	1740	1750	1760
QGQISSQQVA	VEKLKKTAEV	LLDARGSLLP	AKNDIQKTLD	DIVGRYEDLS	KSVNERNEKL	QITLTRSLSV	QDGLDEMLDW
1770	1780	1790	1800	1810	1820	1830	1840
MGNVESSLKE	QGQVPLNSTA	LQDIISKNIM	LEQDIAGRQS	SINAMNEKVK	KFMETTDPST	ASSLQAKMKD	LSARFSEASH
1850	1860	1870	1880	1890	1900	1910	1920
KHKETLAKME	ELKTKVELFE	NLSEKLQTFL	ETKTQALTEV	DVPGKDVTEL	SQYMQESTSE	FLEHKKHLEV	LHSLLKEISS
1930	1940	1950	1960	1970	1980	1990	2000
HGLPSDKALV	LEKTNNLSKK	FKEMEDTIKE	KKEAVTSCQE	QLDAFQVLVK	SLKSWIKETT	KKVPIVQPSF	GAEDLGKSLE
2010	2020	2030	2040	2050	2060	2070	2080
DTKKLQEKWS	LKTPEIQKVN	NSGISLCNLI	SAVTTPAKAI	AAVKSGGAVL	NGEGTATNTE	EFWANKGLTS	IKKDMTDISH
2090	2100	2110	2120	2130	2140	2150	2160
GYEDLGLLLK	DKIAELNTKL	SKLQKAQEES	SAMMQWLQKM	NKTATKWQQT	PAPTDTEAVK	TQVEQNKSFE	AELKQNVNKV
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	
585	1	558.7340	-142.02	2	36.6	17.2	1	143-151	K.LRDEIMALR.N		MD:MU	1.75
2450	1	684.2042	-212.00	2	61.0	10.9	1	2455-2466	K.EEQNKSHPISAK.L			
1580	3	781.3390	-110.38	2	49.5	12.4	2	4358-4371	R.SLKEKTSLADDNLK.L		MD:MU	1.39

Detailed Protein Report

Protein 57: coagulation factor VIII isoform a precursor [Homo sapiens]

Accession:	gi|4503647	**Score:**	51.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	266.8
Database Date:	2015-11-30	**pI:**	7.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.2
		No. of unique Peptides:	4

Quantitation

MD:MU	**Median:**	1.95	**CV:**	0.00 %	**No. of Peptides:**	1

Detailed Protein Report

```
        10         20         30         40         50         60         70         80
MQIELSTCFF LCLLRFCFSA TRRYYLGAVE LSWDYMQSDL GELPVDARFP PRVPKSFPFN TSVVYKKTLF VEFTDHLFNI
        90        100        110        120        130        140        150        160
AKPRPPWMGL LGPTIQAEVY DTVVITLKNM ASHPVSLHAV GVSYWKASEG AEYDDQTSQR EKEDDKVFPG GSHTYVWQVL
       170        180        190        200        210        220        230        240
KENGPMASDP LCLTYSYLSH VDLVKDLNSG LIGALLVCRE GSLAKEKTQT LHKFILLFAV FDEGKSWHSE TKNSLMQDRD
       250        260        270        280        290        300        310        320
AASARAWPKM HTVNGYVNRS LPGLIGCHRK SVYWHVIGMG TTPEVHSIFL EGHTFLVRNH RQASLEISPI TFLTAQTLLM
       330        340        350        360        370        380        390        400
DLGQFLLFCH ISSHQHDGME AYVKVDSCPE EPQLRMKNNE EAEDYDDDLT DSEMDVVRFD DDNSPSFIQI RSVAKKHPKT
       410        420        430        440        450        460        470        480
WVHYIAAEEE DWDYAPLVLA PDDRSYKSQY LNNGPQRIGR KYKKVRFMAY TDETFKTREA IQHESGILGP LLYGEVGDTL
       490        500        510        520        530        540        550        560
LIIFKNQASR PYNIYPHGIT DVRPLYSRRL PKGVKHLKDF PILPGEIFKY KWTVTVEDGP TKSDPRCLTR YYSSFVNMER
       570        580        590        600        610        620        630        640
DLASGLIGPL LICYKESVDQ RGNQIMSDKR NVILFSVFDE NRSWYLTENI QRFLPNPAGV QLEDPEFQAS NIMHSINGYV
       650        660        670        680        690        700        710        720
FDSLQLSVCL HEVAYWYILS IGAQTDFLSV FFSGYTFKHK MVYEDTLTLF PFSGETVFMS MENPGLWILG CHNSDFRNRG
       730        740        750        760        770        780        790        800
MTALLKVSSC DKNTGDYYED SYEDISAYLL SKNNAIEPRS FSQNSRHPST RQKQFNATTI PENDIEKTDP WFAHRTPMPK
       810        820        830        840        850        860        870        880
IQNVSSSDLL MLLRQSPTPH GLSLSDLQEA KYETFSDDPS PGAIDSNNSL SEMTHFRPQL HHSGDMVFTP ESGLQLRLNE
       890        900        910        920        930        940        950        960
KLGTTAATEL KKLDFKVSST SNNLISTIPS DNLAAGTDNT SSLGPPSMPV HYDSQLDTTL FGKKSSPLTE SGGPLSLSEE
       970        980        990       1000       1010       1020       1030       1040
NNDSKLLESG LMNSQESSWG KNVSSTESGR LFKGKRAHGP ALLTKDNALF KVSISLLKTN KTSNNSATNR KTHIDGPSLL
      1050       1060       1070       1080       1090       1100       1110       1120
IENSPSVWQN ILESDTEFKK VTPLIHDRML MDKNATALRL NHMSNKTTSS KNMEMVQQKK EGPIPPDAQN PDMSFFKMLF
      1130       1140       1150       1160       1170       1180       1190       1200
LPESARWIQR THGKNSLNSG QGPSPKQLVS LGPEKSVEGQ NFLSEKNKVV VGKGEFTKDV GLKEMVFPSS RNLFLTNLDN
      1210       1220       1230       1240       1250       1260       1270       1280
LHENNTHNQE KKIQEEIEKK ETLIQENVVL PQIHTVTGTK NFMKNLFLLS TRQNVEGSYD GAYAPVLQDF RSLNDSTNRT
      1290       1300       1310       1320       1330       1340       1350       1360
KKHTAHFSKK GEEENLEGLG NQTKQIVEKY ACTTRISPNT SQQNFVTQRS KRALKQFRLP LEETELEKRI IVDDTSTQWS
      1370       1380       1390       1400       1410       1420       1430       1440
KNMKHLTPST LTQIDYNEKE KGAITQSPLS DCLTRSHSIP QANRSPLPIA KVSSFPSIRP IYLTRVLFQD NSSHLPAASY
      1450       1460       1470       1480       1490       1500       1510       1520
RKKDSGVQES SHFLQGAKKN NLSLAILTLE MTGDQREVGS LGTSATNSVT YKKVENTVLP KPDLPKTSGK VELLPKVHIY
      1530       1540       1550       1560       1570       1580       1590       1600
QKDLFPTETS NGSPGHLDLV EGSLLQGTEG AIKWNEANRP GKVPFLRVAT ESSAKTPSKL LDPLAWDNHY GTQIPKEEWK
      1610       1620       1630       1640       1650       1660       1670       1680
SQEKSPEKTA FKKKDTILSL NACESNHAIA AINEGQNKPE IEVTWAKQGR TERLCSQNPP VLKRHQREIT RTTLQSDQEE
      1690       1700       1710       1720       1730       1740       1750       1760
IDYDDTISVE MKKEDFDIYD EDENQSPRSF QKKTRHYFIA AVERLWDYGM SSSPHVLRNR AQSGSVPQFK KVVFQEFTDG
      1770       1780       1790       1800       1810       1820       1830       1840
SFTQPLYRGE LNEHLGLLGP YIRAEVEDNI MVTFRNQASR PYSFYSSLIS YEEDQRQGAE PRKNFVKPNE TKTYFWKVQH
      1850       1860       1870       1880       1890       1900       1910       1920
HMAPTKDEFD CKAWAYFSDV DLEKDVHSGL IGPLLVCHTN TLNPAHGRQV TVQEFALFFT IFDETKSWYF TENMERNCRA
      1930       1940       1950       1960       1970       1980       1990       2000
PCNIQMEDPT FKENYRFHAI NGYIMDTLPG LVMAQDQRIR WYLLSMGSNE NIHSIHFSGH VFTVRKKEEY KMALYNLYPG
      2010       2020       2030       2040       2050       2060       2070       2080
VFETVEMLPS KAGIWRVECL IGEHLHAGMS TLFLVYSNKC QTPLGMASGH IRDFQITASG QYGQWAPKLA RLHYSGSINA
      2090       2100       2110       2120       2130       2140       2150       2160
WSTKEPFSWI KVDLLAPMII HGIKTQGARQ KFSSLYISQF IIMYSLDGKK WQTYRGNSTG TLMVFFGNVD SSGIKHNIFN
      2170       2180       2190       2200       2210       2220       2230       2240
```

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2041	1	856.8157	-171.77	2	55.6	11.8	2	1060-1073	K.KVTPLIHDRMLMDK.N	Oxidation: 12	
2156	1	953.3232	-120.41	2	57.2	11.3	0	1101-1117	K.EGPIPPDAQNPDMSFFK.M	Oxidation: 13	
2184	1	1061.5230	-9.68	3	57.5	13.4	0	1523-1553	K. DLFPTETSNGSPGHLDLVEGSLLQ W		
2720	1	710.3296	-131.82	2	65.3	14.5	0	2092-2104	K.VDLLAPMIIHGIK.T		MD:MU 1.95

Detailed Protein Report

Protein 58: PREDICTED: uncharacterized protein KIAA1551 isoform X1 [Homo sapiens]

Accession: gi|530399223

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Modification(s): Carbamidomethyl, Oxidation

Score: 51.0

MW [kDa]: 194.7

pI: 9.7

Sequence Coverage [%]: 2.1

No. of unique Peptides: 3

Quantitation

MD:MU **Median:** 0.59 **CV:** 0.00 % **No. of Peptides:** 1

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	

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2628	1	644.4984	138.82	1	63.6	19.8	1	391-395	K.EKLVR.D		MD:MU 0.59
2689	1	731.8632	-38.63	2	64.8	14.6	1	416-428	K.INKDLLMAAGCIK.M	Carbamidomethyl: 11; Oxidation: 7	
2006	1	1044.4022	-89.89	2	55.0	16.6	1	957-974	K.DKPVQCTDVSHKICDQSK.S	Carbamidomethyl: 6	

Detailed Protein Report

Protein 59: PREDICTED: Golgin subfamily A member 4 isoform X7 [Homo sapiens]

Accession:	gi|530372330	**Score:**	50.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	259.0
Database Date:	2015-11-30	**pI:**	5.2
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.4
		No. of unique Peptides:	4

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

Detailed Protein Report

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

Detailed Protein Report

Protein 60: **PREDICTED: striated muscle preferentially expressed protein kinase isoform X3 [Homo sapiens]**

Accession:	gi|530369683	**Score:**	50.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	345.1
Database Date:	2015-11-30	**pI:**	9.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.2
		No. of unique Peptides:	3

Quantitation

MD:MU	**Median:**	0.39	**CV:**	0.00 %	**No. of Peptides:**	1

Detailed Protein Report

```
        10         20         30         40         50         60         70         80
MKKLWVKKRF QKTGHSRRAF GRLTHVFRSC RKQSYDSETA EDDISDVQGT QRLELRDDGA FSTPTGGSDT LVGTSLDTPP
        90        100        110        120        130        140        150        160
TSVTGTSEEQ VSWWGSGQTV LEQEAGSGGG TRRLPGSPRQ AQATGAGPRH LGVEPLVRAS RANLVGASWG SEDSLSVASD
       170        180        190        200        210        220        230        240
LYGSAFSLYR GRALSIHVSV PQSGLRREEP DLQPQLASEA PRRPAQPPPS KSALLPPPSP RVGKRSPPGP PAQPAATPTS
       250        260        270        280        290        300        310        320
PHRRTQEPVL PEDTTTEEKR GKKSKSSGPS LAGTAESRPQ TPLSEASGRL SALGRSPRLV RAGSRILDKL QFFEERRRSL
       330        340        350        360        370        380        390        400
ERSDSPPAPL RPWVPLRKAR SLEQPKSERG APWGTPGASQ EELRAPGSVA ERRRLFQQKA ASLDERTRQR SPASDLELRF
       410        420        430        440        450        460        470        480
AQELGRIRRS TSREELVRSH ESLRATLQRA PSPREPGEPP LFSRPSTPKT SRAVSPAAAQ PPSPSSAEKP GDEPGRPRSR
       490        500        510        520        530        540        550        560
GPAGRTEPGE GPQQEVRRRD QFPLTRSRAI QECRSPVPPP AADPPEARTK APPGRKREPP AQAVRFLPWA TPGLEGAAVP
       570        580        590        600        610        620        630        640
QTLEKNRAGP EAEKRLRRGP EEDGPWGPWD RRGARSQGKG RRARPTSPEL ESSDDSYVSA GEEPLEAPVF EIPLQNVVVA
       650        660        670        680        690        700        710        720
PGADVLLKCI ITANPPPQVS WHKDGSALRS EGRLLLRAEG ERHTLLLREA RAADAGSYMA TATNELGQAT CAASLTVRPG
       730        740        750        760        770        780        790        800
GSTSPFSSPI TSDEEYLSPP EEFPEPGETW PRTPTMKPSP SQNRRSSDTG SKAPPTFKVS LMDQSVREGQ DVIMSIRVQG
       810        820        830        840        850        860        870        880
EPKPVVSWLR NRQPVRPDQR RFAEEAEGGL CRLRILAAER GDAGFYTCKA VNEYGARQCE ARLEVRAHPE SRSLAVLAPL
       890        900        910        920        930        940        950        960
QDVDVGAGEM ALFECLVAGP TDVEVDWLCR GRLLQPALLK CKMHFDGRKC KLLLTSVHED DSGVYTCKLS TAKDELTCSA
       970        980        990       1000       1010       1020       1030       1040
RLTVRPSLAP LFTRLLEDVE VLEGRAARFD CKISGTPPPV VTWTHFGCPM EESENLRLRQ DGGLHSLHIA HVGSEDEGLY
      1050       1060       1070       1080       1090       1100       1110       1120
AVSAVNTHGQ AHCSAQLYVE EPRTAASGPS SKLEKMPSIP EEPEQGELER LSIPDFLRPL QDLEVGLAKE AMLECQVTGL
      1130       1140       1150       1160       1170       1180       1190       1200
PYPTISWFHN GHRIQSSDDR RMTQYRDVHR LVFPAVGPQH AGVYKSVIAN KLGKAACYAH LYVTDVVPGP PDGAPQVVAV
      1210       1220       1230       1240       1250       1260       1270       1280
TGRMVTLTWN PPRSLDMAID PDSLTYTVQH QVLGSDQWTA LVTGLREPGW AATGLRKGVQ HIFRVLSTTV KSSSKPSPPS
      1290       1300       1310       1320       1330       1340       1350       1360
EPVQLLEHGP TLEEAPAMLD KPDIVYVVEG QPASVTVTFN HVEAQVVWRS CRGALLEARA GVYELSQPDD DQYCLRICRV
      1370       1380       1390       1400       1410       1420       1430       1440
SRRDMGALTC TARNRHGTQT CSVTLELAEA PRFESIMEDV EVGAGETARF AVVVEGKPLP DIMWYKDEVL LTESSHVSFV
      1450       1460       1470       1480       1490       1500       1510       1520
YEENECSLVV LSTGAQDGGV YTCTAQNLAG EVSCKAELAV HSAQTAMEVE GVGEDEDHRG RRLSDFYDIH QEIGRGAFSY
      1530       1540       1550       1560       1570       1580       1590       1600
LRRIVERSSG LEFAAKFIPS QAKPKASARR EARLLARLQH DCVLYFHEAF ERRRGLVIVT ELCTEELLER IARKPTVCES
      1610       1620       1630       1640       1650       1660       1670       1680
EIRAYMRQVL EGIHYLHQSH VLHLDVKPEN LLVWDGAAGE QQVRICDFGN AQELTPGEPQ YCQYGTPEFV APEIVNQSPV
      1690       1700       1710       1720       1730       1740       1750       1760
SGVTDIWPVG VVAFLCLTGI SPFVGENDRT TLMNIRNYNV AFEETTFLSL SREARGFLIK VLVQDRLRPT AEETLEHPWF
      1770       1780       1790       1800       1810       1820       1830       1840
KTQAKGAEVS TDHLKLFLSR RRWQRSQISY KCHLVLRPIP ELLRAPPERV WVTMPRRPPP SGGLSSSSDS EEEELEELPS
      1850       1860       1870       1880       1890       1900       1910       1920
VPRPLQPEFS GSRVSLTDIP TEDEALGTPE TGAATPMDWQ EQGRAPSQDQ EAPSPEALPS PGQEPAAGAS PRRGELRRGS
      1930       1940       1950       1960       1970       1980       1990       2000
SAESALPRAG PRELGRGLHK AASVELPQRR SPSPGATRLA RGGLGEGEYA QRLQALRQRL LRGGPEDGKV SGLRGPLLES
      2010       2020       2030       2040       2050       2060       2070       2080
LGGRARDPRM ARAASSEAAP HHQPPLENRG LQKSSSFSQG EAEPRGRHRR AGAPLEIPVA RLGARRLQES PSLSALSEAQ
      2090       2100       2110       2120       2130       2140       2150       2160
PSSPARPSAP KPSTPKSAEP SATTPSDAPQ PPAPQPAQDK APEPRPEPVR ASKPAPPPQA LQTLALPLTP YAQIIQSLQL
      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
661	1	480.6345	-248.82	2	37.8	10.5	1	10-17	R.FQKTGHSR.R		
92	1	531.9231	-79.62	3	30.5	25.4	2	1995-2009	R.GPLLESLGGRARDPR.M		MD:MU 0.39
43	1	796.8047	-128.81	2	30.2	14.7	2	2883-2896	R.FGVVRACRENATGR.T	Carbamidomethyl: 7	

Detailed Protein Report

Protein 61: semaphorin-5B isoform 3 precursor [Homo sapiens]

Accession: gi|373432662
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 50.6
MW [kDa]: 116.0
pI: 9.0
Sequence Coverage [%]: 4.7
No. of unique Peptides: 3

Quantitation

MD:MU **Median:** 2.06 **CV:** 0.00 % **No. of 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	Ratios
2274	5	682.6007	-55.67	3	58.3	18.2	2	113-129	R.SCQSKGKTEEECQNYVR.V	Carbamidomethyl: 2	
1589	1	648.3135	13.53	2	49.6	11.6	1	632-643	R.SCSNPAPRHGGR.I	Carbamidomethyl: 2	MD:MU 2.06
1478	1	1061.4566	-34.44	2	48.1	20.8	0	765-785	R. TCPADGSGSCDTDALVEVLLR.S		

Detailed Protein Report

Protein 62: PREDICTED: dynein heavy chain 3, axonemal isoform X1 [Homo sapiens]

Accession:	gi|578828592	**Score:**	50.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	466.0
Database Date:	2015-11-30	**pI:**	6.0
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	1.2
		No. of unique Peptides:	2

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	HHYDYGMRAV	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

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
301	1	874.1753	76.12	3	33.1	22.7	0	463-484	K.LEVSEPIIVFNPSFDGCWELIR.D	Carbamidomethyl: 17
2330	1	557.1827	-146.58	3	59.0	16.5	0	1935-1948	R.NLIMGMDDNHPRPK.S	Oxidation: 4, 6

Detailed Protein Report

Protein 63: neurogenic locus notch homolog protein 1 preproprotein [Homo sapiens]

Accession:	gi|148833508	**Score:**	50.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	272.3
Database Date:	2015-11-30	**pI:**	4.8
		Sequence Coverage [%]:	2.2
		No. of unique Peptides:	2

Quantitation

MD:MU	**Median:** 9.77	**CV:** 0.00 %	**No. of Peptides:**	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MPPLLAPLLC	LALLPALAAR	GPRCSQPGET	CLNGGKCEAA	NGTEACVCGG	AFVGPRCQDP	NPCLSTPCKN	AGTCHVVDRR
90	100	110	120	130	140	150	160
GVADYACSCA	LGFSGPLCLT	PLDNACLTNP	CRNGGTCDLL	TLTEYKCRCP	PGWSGKSCQQ	ADPCASNPCA	NGGQCLPFEA
170	180	190	200	210	220	230	240
SYICHCPPSF	HGPTCRQDVN	ECGQKPGLCR	HGGTCHNEVG	SYRCVCRATH	TGPNCERPYV	PCSPSPCQNG	GTCRPTGDVT
250	260	270	280	290	300	310	320
HECACLPGFT	GQNCEENIDD	CPGNNCKNGG	ACVDGVNTYN	CRCPPEWTGQ	YCTEDVDECQ	LMPNACQNGG	TCHNTHGGYN
330	340	350	360	370	380	390	400
CVCVNGWTGE	DCSENIDDCA	SAACFHGATC	HDRVASFYCE	CPHGRTGLLC	HLNDACISNP	CNEGSNCDTN	PVNGKAICTC
410	420	430	440	450	460	470	480
PSGYTGPACS	QDVDECSLGA	NPCEHAGKCI	NTLGSFECQC	LQGYTGPRCE	IDVNECVSNP	CQNDATCLDQ	IGEFQCICMP
490	500	510	520	530	540	550	560
GYEGVHCEVN	TDECASSPCL	HNGRCLDKIN	EFQCECPTGF	TGHLCQYDVD	ECASTPCKNG	AKCLDGPNTY	TCVCTEGYTG
570	580	590	600	610	620	630	640
THCEVDIDEC	DPDPCHYGSC	KDGVATFTCL	CRPGYTGHHC	ETNINECSSQ	PCRHGGTCQD	RDNAYLCFCL	KGTTGPNCEI
650	660	670	680	690	700	710	720
NLDDCASSPC	DSGTCLDKID	GYECACEPGY	TGSMCNINID	ECAGNPCHNG	GTCEDGINGF	TCRCPEGYHD	PTCLSEVNEC
730	740	750	760	770	780	790	800
NSNPCVHGAC	RDSLNGYKCD	CDPGWSGTNC	DINNNECESN	PCVNGGTCKD	MTSGYVCTCR	EGFSGPNCQT	NINECASNPC
810	820	830	840	850	860	870	880
LNQGTCIDDV	AGYKCNCLLP	YTGATCEVVL	APCAPSPCRN	GGECRQSEDY	ESFSCVCPTG	WQGQTCEVDI	NECVLSPCRH
890	900	910	920	930	940	950	960
GASCQNTHGG	YRCHCQAGYS	GRNCETDIDD	CRPNPCHNGG	SCTDGINTAF	CDCLPGFRGT	FCEEDINECA	SDPCRNGANC
970	980	990	1000	1010	1020	1030	1040
TDCVDSYTCT	CPAGFSGIHC	ENNTPDCTES	SCFNGGTCVD	GINSFTCLCP	PGFTGSYCQH	DVNECDSQPC	LHGGTCQDGC
1050	1060	1070	1080	1090	1100	1110	1120
GSYRCTCPQG	YTGPNCQNLV	HWCDSSPCKN	GGKCWQTHTQ	YRCECPSGWT	GLYCDVPSVS	CEVAAQRQGV	DVARLCQHGG
1130	1140	1150	1160	1170	1180	1190	1200
LCVDAGNTHH	CRCQAGYTGS	YCEDLVDECS	PSPCQNGATC	TDYLGGYSCK	CVAGYHGVNC	SEEIDECLSH	PCQNGGTCLD
1210	1220	1230	1240	1250	1260	1270	1280
LPNTYKCSCP	RGTQGVHCEI	NVDDCNPPVD	PVSRSPKCFN	NGTCVDQVGG	YSCTCPPGFV	GERCEGDVNE	CLSNPCDARG
1290	1300	1310	1320	1330	1340	1350	1360
TQNCVQRVND	FHCECRAGHT	GRRCESVING	CKGKPCKNGG	TCAVASNTAR	GFICKCPAGF	EGATCENDAR	TCGSLRCLNG
1370	1380	1390	1400	1410	1420	1430	1440
GTCISGPRSP	TCLCLGPFTG	PECQFPASSP	CLGGNPCYNQ	GTCEPTSESP	FYRCLCPAKF	NGLLCHILDY	SFGGGAGRDI
1450	1460	1470	1480	1490	1500	1510	1520
PPPLIEEACE	LPECQEDAGN	KVCSLQCNNH	ACGWDGGDCS	LNFNDPWKNC	TQSLQCWKYF	SDGHCDSQCN	SAGCLFDGFD
1530	1540	1550	1560	1570	1580	1590	1600
CQRAEGQCNP	LYDQYCKDHF	SDGHCDQGCN	SAECEWDGLD	CAEHVPERLA	AGTLVVVVLM	PPEQLRNSSF	HFLRELSRVL
1610	1620	1630	1640	1650	1660	1670	1680
HTNVVFKRDA	HGQQMIFPYY	GREEELRKHP	IKRAAEGWAA	PDALLGQVKA	SLLPGGSEGG	RRRRELDPMD	VRGSIVYLEI
1690	1700	1710	1720	1730	1740	1750	1760
DNRQCVQASS	QCFQSATDVA	AFLGALASLG	SLNIPYKIEA	VQSETVEPPP	PAQLHFMYVA	AAFVLLFFV	GCGVLLSRKR
1770	1780	1790	1800	1810	1820	1830	1840
RRQHGQLWFP	EGFKVSEASK	KKRREPLGED	SVGLKPLKNA	SDGALMDDNQ	NEWGDEDLET	KKFRFEEPVV	LPDLDDQTDH
1850	1860	1870	1880	1890	1900	1910	1920
RQWTQQHLDA	ADLRMSAMAP	TPPQGEVDAD	CMDVNVRGPD	GFTPLMIASC	SGGGLETGNS	EEEEDAPAVI	SDFIYQGASL
1930	1940	1950	1960	1970	1980	1990	2000
HNQTDRTGET	ALHLAARYSR	SDAAKRLLEA	SADANIQDNM	GRTPLHAAVS	ADAQGVFQIL	IRNRATDLDA	RMHDGTTPLI
2010	2020	2030	2040	2050	2060	2070	2080
LAARLAVEGM	LEDLINSHAD	VNAVDDLGKS	ALHWAAAVNN	VDAAVVLLKN	GANKDMQNNR	EETPLFLAAR	EGSYETAKVL
2090	2100	2110	2120	2130	2140	2150	2160
LDHFANRDIT	DHMDRLPRDI	AQERMHHDIV	RLLDEYNLVR	SPQLHGAPLG	GTPTLSPPLC	SPNGYLGSLK	PGVQGKKVRK
2170	2180	2190	2200	2210	2220	2230	2240

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1668	1	697.0259	81.08	3	50.6	14.2	1	1331-1350	R.GFICKCPAGFEGATCENDAR.T		
2073	4	698.2445	-185.84	2	55.8	21.5	0	1992-2004	R.MHDGTTPLILAAR.L		MD:MU 9.77

Detailed Protein Report

Protein 64: zinc finger protein 281 isoform 2 [Homo sapiens]

Accession:	gi|526253066	**Score:**	50.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	93.2
Database Date:	2015-11-30	**pI:**	9.3
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	4.4
		No. of unique Peptides:	3

10	20	30	40	50	60	70	80
MKIGSGFLSG	GGGTGSSGGS	GSGGGGSGGG	GGGGSSGRRA	EMEPTFPQAP	AAEPPPPPAP	DMTFKKEPAA	SAAAFPSQRT
90	100	110	120	130	140	150	160
SWGFLQSLVS	IKQEKPADPE	EQQSHHHHHH	HHYGGLFAGA	EERSPGLGGG	EGGSHGVIQD	LSILHQHVQQ	QPAQHHRDVL
170	180	190	200	210	220	230	240
LSSSSRTDDH	HGTEEPKQDT	NVKKAKRPKP	ESQGIKAKRK	PSASSKPSLV	GDGEGAILSP	SQKPHICDHC	SAAFRSSYHL
250	260	270	280	290	300	310	320
RRHVLIHTGE	RPFQCSQCSM	GFIQKYLLQR	HEKIHSREKP	FGCDQCSMKF	IQKYHMERHK	RTHSGEKPYK	CDTCQQYFSR
330	340	350	360	370	380	390	400
TDRLLKHRRT	CGEVIVKGAT	SAEPGSSNHT	NMGNLAVLSQ	GNTSSSRRKT	KSKSIAIENK	EQKTGKTNES	QISNNINMQS
410	420	430	440	450	460	470	480
YSVEMPTVSS	SGGIIGTGID	ELQKRVPKLI	FKKGSRKNTD	KNYLNFVSPL	PDIVGQKSLS	GKPSGSLGIV	SNNSVETIGL
490	500	510	520	530	540	550	560
LQSTSGKQGQ	ISSNYDDAMQ	FSKKRRYLPT	ASSNSAFSIN	VGHMVSQQSV	IQSAGVSVLD	NEAPLSLIDS	SALNAEIKSC
570	580	590	600	610	620	630	640
HDKSGIPDEV	LQSILDQYSN	KSESQKEDPF	NIAEPRVDLH	TSGEHSELVQ	EENLSPGTQT	PSNDKASMLQ	EYSKYLQQAF
650	660	670	680	690	700	710	720
EKSTNASFTL	GHGFQFVSLS	SPLHNHTLFP	EKQIYTTSPL	ECGFGQSVTS	VLPSSLPKPP	FGMLFGSQPG	LYLSALDATH
730	740	750	760	770	780	790	800
QQLTPSQELD	DLIDSQKNLE	TSSAFQSSSQ	KLTSQKEQKN	LESSTGFQIP	SQELASQIDP	QKDIEPRTTY	QIENFAQAFG
810	820	830	840	850	860		
SQFKSGSRVP	MTFITNSNGE	VDHRVRTSVS	DFSGYTNMMS	DVSEPCSTRV	KTPTSQSYR		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2793	1	840.4111	74.23	2	65.3	14.1	1	311-323	K.CDTCQQYFSRTDR.L	Carbamidomethyl: 4
2653	1	811.8976	73.50	2	64.2	24.6	1	311-323	K.CDTCQQYFSRTDR.L	
2862	1	693.8668	91.67	4	66.2	11.6	1	825-849	R.VRTSVSDFSGYTNMMSDVSEPCSTR.V	Oxidation: 14

Detailed Protein Report

Protein 65: ubiquitin carboxyl-terminal hydrolase 43 isoform 2 [Homo sapiens]

Accession:	gi|389616163	**Score:**	50.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	122.2
Database Date:	2015-11-30	**pI:**	10.2
		Sequence Coverage [%]:	3.5
		No. of unique Peptides:	2

Quantitation

MD:MU **Median:** 1.49 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MDLGPGDAAG	GGPLAPRPRR	RRSLRRLFSR	FLLALGSRSR	PGDSPPRPQP	GHCDGDGEGG	FACAPGPVPA	APGSPGEERP
90	100	110	120	130	140	150	160
PGPQPQLQLP	AGDGARPPGA	QGLKNHGNTC	FMNAVVQCLS	NTDLLAEFLA	LGRYRAAPGR	AEVTEQLAAL	VRALWTREYT
170	180	190	200	210	220	230	240
PQLSAEFKNA	VSKYGSQFQG	NSQHDALEFL	LWLLDRVHED	LEGSSRGPVS	EKLPPEATKT	SENCLSPSAQ	LPLGQSFVQS
250	260	270	280	290	300	310	320
HFQAQYRSSL	TCPHCLKQSN	TFDPFLCVSL	PIPLRQTRFL	SVTLVFPSKS	QRFLRVGLAV	PILSTVAALR	KMVAEEGGVP
330	340	350	360	370	380	390	400
ADEVILVELY	PSGFQRSFFD	EEDLNTIAEG	DNVYAFQVPP	SPSQGTLSAH	PLGLSASPRL	AAREGQRFSL	SLHSESKVLI
410	420	430	440	450	460	470	480
LFCNLVGSGQ	QASRFGPPFL	IREDRAVSWA	QLQQSILSKV	RHLMKSEAPV	QNLGSLFSIR	VVGLSVACSY	LSPKDSRPLC
490	500	510	520	530	540	550	560
HWAVDRVLHL	RRPGGPPHVK	LAVEWDSSVK	ERLFGSLQEE	RAQDADSVWQ	QQQAHQQHSC	TLDECFQFYT	KEEQLAQDDA
570	580	590	600	610	620	630	640
WKCPHCQVLQ	QGMVKLSLWT	LPDILIIHLK	RFCQVGERRN	KLSTLVKFPL	SGLNMAPHVA	QRSTSPEAGL	GPWPSWKQPD
650	660	670	680	690	700	710	720
CLPTSYPLDF	LYDLYAVCNH	HGNLQAYCRN	SLDGQWYSYD	DSTVEPLRED	EVNTRGAYIL	FYQKRNSIPP	WSASSSMRGS
730	740	750	760	770	780	790	800
TSSSLSDHWL	LRLGSHAGST	RGSLLSWSSA	PCPSLPQVPD	SPIFTNSLCN	QEKGGLEPRR	LVRGVKGRSI	SMKAPTTSRA
810	820	830	840	850	860	870	880
KQGPFKTMPL	RWSFGSKEKP	PGASVELVEY	LESRRRPRST	SQSIVSLLTG	TAGEDEKSAS	PRSNVALPAN	SEDGGRAIER
890	900	910	920	930	940	950	960
GPAGVPCPSA	QPNHCLAPGN	SDGPNTARKL	KENAGQDIKL	PRKFDLPLTV	MPSVEHEKPA	RPEGQKAMNW	KESFQMGSKS
970	980	990	1000	1010	1020	1030	1040
SPPSPYMGFS	GNSKDSRRGT	SELDRPLQGT	LTLLRSVFRK	KENRRNERAE	VSPQVPPVSL	VSGGLSPAMD	GQAPGSPPAL
1050	1060	1070	1080	1090	1100	1110	1120
RIPEGLARGL	GSRLERDVWS	APSSLRLPRK	ASRAPRGSAL	GMSQRTVPGE	QASYGTFQRV	KYHTLSLGRK	KTLPESSF

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2741	1	656.8579	50.64	2	64.6	11.9	0	158-168	R.EYTPQLSAEFK.N		
2554	5	812.4077	-74.32	2	62.4	18.3	2	1042-1056	R.IPEGLARGLGSRLER.D		MD:MU 1.49

Detailed Protein Report

Protein 66: leucine zipper protein 1 [Homo sapiens]

Accession: gi|216548085
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 50.0
MW [kDa]: 120.2
pI: 9.4
Sequence Coverage [%]: 5.4
No. of unique Peptides: 2

Alias proteins:

Accession	Name	Description
gi|216548091	refseq_human(refseq_human_20140103.fasta)	leucine zipper protein 1 [Homo sapiens]

10	20	30	40	50	60	70	80
MAEFTSYKET	ASSRHLRFKL	QSLSRRLDEL	EEATKNLQKA	EDELLDLQDK	VIQAEGSNSS	MLAEIEVLRQ	RVLRIEGKDE
90	100	110	120	130	140	150	160
EIKRAEDLCR	LMKEKLEEEE	NLTRELKSEI	ERLQKRMAEL	EKLEEAFSRS	KNDCTQLCLS	LNEERNLTKK	ISSELEMLRV
170	180	190	200	210	220	230	240
KVKELESSED	RLDKTEQSLA	SELEKLKSLT	LSFVSERKYL	NEKEKENEKL	IKELTQKLEQ	NKKMNRDYTR	NASNLERNDL
250	260	270	280	290	300	310	320
RIEDGISSTL	PSKESRRKGG	LDYLKQVENE	TRNKSENEKN	RNQEDNKVKD	LNQEIEKLKT	QIKHFESLEE	ELKKMKSKNN
330	340	350	360	370	380	390	400
DLQDNYLSEQ	NKNKLLASQL	EEIKLQIKKQ	KELENGEVEG	EDAFLSSKGR	HERTKFRGHG	SEASVSKHTA	RELSPQHKRE
410	420	430	440	450	460	470	480
RLRNREFALN	NENYSLSNRQ	VSSPSFTNRR	AAKASHMGVS	TDSGTQETKK	TEDRFVPGSS	QSEGKKSREQ	PSVLSRYPPA
490	500	510	520	530	540	550	560
AQEHSKAWKG	TSKPGTESGL	KGKVEKTTRT	FSDTTHGSVP	SDPLGRADKA	SDTSSETVFG	KRGHVLGNGS	QVTQAANSGC
570	580	590	600	610	620	630	640
SKAIGALASS	RRSSSEGLSK	GKKAANGLEA	DNSCPNSKAP	VLSKYPYSCR	SQENILQGFS	TSHKEGVNQP	AAVVMEDSSP
650	660	670	680	690	700	710	720
HEALRCRVIK	SSGREKPDSD	DDLDIASLVT	AKLVNTTITP	EPEPKPQPNS	REKAKTRGAP	RTSLFENDKD	AGMENESVKS
730	740	750	760	770	780	790	800
VRASTNTMEL	PDTNGAGVKS	QRPFSPREAL	RSRAIIKPVI	VDKDVKKIMG	GSGTETTLEK	QKPVSKPGPN	KVTSSITIYP
810	820	830	840	850	860	870	880
SDSSSPRAAP	GEALRERHTS	TSNIQVGLAE	LTSVSNHVSS	PFELSIHKHD	ITLQLAEAER	MADGPLKDRP	ETVVSRSSII
890	900	910	920	930	940	950	960
IKPSDPVERN	SHAPPAETIR	WKSHSAPSEV	GFSDARHVTV	RNAWKSRRDL	KSLEDPPTRI	GKNVESTNSN	AYTQRSSTDF
970	980	990	1000	1010	1020	1030	1040
SELEQPRSCL	FEQGTRRVGP	SSGDAPEPSS	RRTQSSLTVS	EVLTRRNRVG	DTITVAAWNH	SASMEEEGED	CTLSVYRQLH
1050	1060	1070	1080				
NSLDPSELPG	KQGLPESGRV	RAEERLRPTR	PCAEEN				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2080	1	1044.4112	-88.13	2	55.9	13.0	1	510-529	R.TFSDTTHGSVPSDPLGRADK.A	
2108	1	698.2650	-143.11	2	56.2	11.7	0	849-860	K.HDITLQLAEAER.M	

Detailed Protein Report

Protein 67: PREDICTED: protein AHNAK2 isoform X1 [Homo sapiens]

Accession:	gi|530403029	**Score:**	49.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	605.3
Database Date:	2015-11-30	**pI:**	5.1
		Sequence Coverage [%]:	0.8
		No. of unique Peptides:	3

Detailed Protein Report

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2566	1	913.4598	-15.26	2	62.5	16.5	1	369-385	R.DTTEGGTQIGPPEIRVR.V	
2037	1	596.7447	-195.99	2	55.6	14.7	2	384-393	R.VRVHDLKTPK.F	
597	1	1230.6275	14.93	2	36.8	18.6	1	685-707	K.AEVTAPDVKMSLSSMEVDVQAPR.A	

Protein 68: 14-3-3 protein zeta/delta [Homo sapiens]

Accession:	gi|4507953	**Score:**	49.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	27.7
Database Date:	2015-11-30	**pI:**	4.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	9.0
		No. of unique Peptides:	2

Alias proteins:

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

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2739	2	709.8489	-20.41	2	64.6	22.3	0	92-103	R.DICNDVLSLLEK.F	Carbamidomethyl: 3
2531	5	595.3252	-14.86	2	62.1	27.0	0	213-222	K.DSTLIMQLLR.D	

Detailed Protein Report

Protein 69: usherin isoform B [Homo sapiens]

Accession:	gi|219842266	**Score:**	49.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	575.2
Database Date:	2015-11-30	**pI:**	6.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.2
		No. of unique Peptides:	2

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2688	2	885.4613	98.77	2	63.8	13.3	0	838-851	R.QNNSFLCLPCNCDK.T	Carbamidomethyl: 7, 10, 12
206	1	898.4111	-54.24	3	32.3	10.4	2	5085-5108	K.RMSPLNVYPPGENHMGLADTKIPR.S	

Detailed Protein Report

Protein 70: **PREDICTED: microtubule-actin cross-linking factor 1 isoform X21 [Homo sapiens]**

Accession:	gi|578798822	**Score:**	49.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	853.1
Database Date:	2015-11-30	**pI:**	5.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	0.6
		No. of unique Peptides:	4

Quantitation

MD:MU	**Median:**	0.26	**CV:**	0.00 %	**No. of Peptides:**	1	

Detailed Protein Report

10	20	30	40	50	60	70	80
MPLLDSSYLP	PTIFILTHVL	GVAGVLYWKR	HARGRADERD	RVQKKTFTKW	VNKHLMKVRK	HINDLYEDLR	DGHNLISLLE
90	100	110	120	130	140	150	160
VLSGIKLPRE	KGRMRFHRLQ	NVQIALDFLK	QRQVKLVNIR	NDDITDGNPK	LTLGLIWTII	LHFQISDIYI	SGESGDMSAK
170	180	190	200	210	220	230	240
EKLLLWTQKV	TAGYTGIKCT	NFSSCWSDGK	MFNALIHRYR	PDLVDMERVQ	IQSNRENLEQ	AFEVAERLGV	TRLLDAEDVD
250	260	270	280	290	300	310	320
VPSPDEKSVI	TYVSSIYDAF	PKVPEGGEGI	SATEVDSRWQ	EYQSRVDSLI	PWIKQHTILM	SDKTFPQNPV	ELKALYNQYI
330	340	350	360	370	380	390	400
HFKETEILAK	EREKGRIEEL	YKLLEVWIEF	GRIKLPQGYH	PNDVEEEWGK	LIIEMLEREK	SLRPAVERLE	LLLQIANKIQ
410	420	430	440	450	460	470	480
NGALNCEEKL	TLAKNTLQAD	AAHLESGQPV	QCESDVIMYI	QECEGLIRQL	QVDLQILRDE	NYYQLEELAF	RVMRLQDELV
490	500	510	520	530	540	550	560
TLRLECTNLY	RKGHFTSLEL	VPPSTLTTTH	LKAEPLTKAT	HSSSTSWFRK	PMTRAELVAI	SSSEDEGNLR	FVYELLSWVE
570	580	590	600	610	620	630	640
EMQMKLERAE	WGNDLPSVEL	QLETQQHIHT	SVEELGSSVK	EARLYEGKMS	QNFHTSYAET	LGKLETQYCK	LKETSSFRMR
650	660	670	680	690	700	710	720
HLQSLHKFVS	RATAELIWLN	EKEEEELAYD	WSDNNSNISA	KRNYFSELTM	ELEEKQDVFR	SLQDTAELLS	LENHPAKQTV
730	740	750	760	770	780	790	800
EAYSAAVQSQ	LQWMKQLCLC	VEQHVKENTA	YFQFFSDARE	LESFLRNLQD	SIKRKYSCDH	NTSLSRLEDL	LQDSMDEKEQ
810	820	830	840	850	860	870	880
LIQSKSSVAS	LVGRSKTIVQ	LKPRSPDHVL	KNTISVKAVC	DYRQIEITIC	KNDECVLEDN	SQRTKWKVIS	PTGNEAMVPS
890	900	910	920	930	940	950	960
VCFLIPPPNK	DAIEMASRVE	QSYQKVMALW	HQLHVNTKSL	ISWNYLRKDL	DLVQTWNLEK	LRSSAPGECH	QIMKNLQAHY
970	980	990	1000	1010	1020	1030	1040
EDFLQDSRDS	VLFSVADRLR	LEEEVEACKA	RFQHLMKSME	NEDKEETVAK	MYISELKNIR	LRLEEYEQRV	VKRIQSLASS
1050	1060	1070	1080	1090	1100	1110	1120
RTDRDAWQDN	ALRIAEQEHT	QEDLQQLRSD	LDAVSMKCDS	FLHQSPSSSS	VPTLRSELNL	LVEKMDHVYG	LSTVYLNKLK
1130	1140	1150	1160	1170	1180	1190	1200
TVDVIVRSIQ	DAELLVKGYE	IKLSQEEVVL	ADLSALEAHW	STLRHWLSDV	KDKNSVFSVL	DEEIAKAKVV	AEQMSRLTPE
1210	1220	1230	1240	1250	1260	1270	1280
RNLDLERYQE	KGSQLQERWH	RVIAQLEIRQ	SELESIQEVL	GDYRACHGTL	IKWIEETTAQ	QEMMKPGQAE	DSRVLSEQLS
1290	1300	1310	1320	1330	1340	1350	1360
QQTALFAEIE	RNQTKLDQCQ	KFSQQYSTIV	KDYELQLMTY	KAFVESQQKS	PGKRRRMLSS	SDAITQEFMD	LRTRYTALVT
1370	1380	1390	1400	1410	1420	1430	1440
LTTQHVKYIS	DALRRLEEEE	KVVEEEKQEH	VEKVKELLGW	VSTLARNTQG	KATSSETKES	TDIEKAILEQ	QVLSEELTTK
1450	1460	1470	1480	1490	1500	1510	1520
KEQVSEAIKT	SQIFLAKHGH	KLSEKEKKQI	SEQLNALNKA	YHDLCDGSAN	QLQQLQSQLA	HQTEQKECRA	VAGVIDLGTV
1530	1540	1550	1560	1570	1580	1590	1600
EIFPIFKAMQ	KGLLDQDTGL	VLLESQVIMS	GLIAPETGEN	LSLEEGIARN	LINPQMYQQL	RELQDALALI	SRLTESRGPL
1610	1620	1630	1640	1650	1660	1670	1680
SVVEAIEKRI	ISETVGLKIL	EAHLATGGFS	LSPSENCINL	EEAFHQGLIS	AWLHSVLESY	LRTSKNLIDP	NTAEKIGLLD
1690	1700	1710	1720	1730	1740	1750	1760
LMQRCIVHQE	SGFKLLPVKQ	LAGGMVSLKS	GRKVSIFRAV	QEGLIDRQVT	VRLLEAQLFA	GGIVDPRTGH	RLTVEEAVRH
1770	1780	1790	1800	1810	1820	1830	1840
NLIDQDMACA	ILIRQLQTGG	IIDTVTGQRL	TIDEAVSNDL	VAAKIALVIL	ESLWSFMGLL	WPESGEILPI	TDALEQGIVS
1850	1860	1870	1880	1890	1900	1910	1920
TELAHKILSN	RQHIKALFLP	ATTEILSWKK	AIESGILDRD	LANNLKSICI	PDVMPHMQLA	DSAEQNINPG	AAVLPCSKSH
1930	1940	1950	1960	1970	1980	1990	2000
PKATASQSEN	LLFQLMTHSY	INVQNGQRLL	LLDKELMETL	TSRDEYQTSP	PKVVEIGHQR	QKTPEGLQES	ANVKISGTFS
2010	2020	2030	2040	2050	2060	2070	2080
SGWTVRLPEF	QFSSQNKEYP	DREDCTTEKG	KKTTVETEDS	SVENPEQDLF	VEQKERNPNI	DALKVINKVK	LEVQRQLIGT
2090	2100	2110	2120	2130	2140	2150	2160
QREDQTAVSV	RENASRGHLL	TIPPAEAEGV	PLVVDKDVFS	VETPKKEHQP	LRNTSFTCQN	EQAHTLETEY	IHDETGGSHI
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
324	1	755.2309	-145.08	2	33.4	13.7	1	998-1010	K.SMENEDKEETVAK.M		
371	1	625.3885	104.40	2	34.3	11.3	2	4866-4875	R.LKDCMQKAQK.Y	Carbamidomethyl: 4	
1272	1	673.3365	1.16	2	45.6	11.4	1	5890-5899	R.QQQEEMRQLR.E		
11	1	650.7452	-159.65	2	29.7	12.6	2	6624-6633	K.RAKQFHEAWK.K		MD:MU 0.26

Detailed Protein Report

Protein 71: **PREDICTED: arf-GAP with Rho-GAP domain, ANK repeat and PH domain-containing protein 3 isoform X7 [Homo sapiens]**

Accession: gi|578810904
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 48.8
MW [kDa]: 149.1
pI: 6.5
Sequence Coverage [%]: 1.7
No. of unique Peptides: 1

Quantitation

MD:MU **Median:** 1.02 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MDPGCLYYGV	QPVGTPGAPD	RRESRGVCQG	RAEHRLSRQD	LEAREDAGYA	SLELPGDSTL	LSPTLETEET	SDDLISPYAS
90	100	110	120	130	140	150	160
FSFTADRLTP	LLSGWLDKLS	PQGNYVFQRR	FVQFNGRSLM	YFGSDKDPFP	KGVIPLTAIE	MTRSSKDNKF	QVITGQRVFV
170	180	190	200	210	220	230	240
FRTESEAQRD	MWCSTLQSCL	KEQRLLGHPR	PPQPPRPLRT	GMLELRGHKA	KVFAALSPGE	LALYKSEQAF	SLGIGICFIE
250	260	270	280	290	300	310	320
LQGCSVRETK	SRSFDLLTPH	RCFSFTAESG	GARQSWAAAL	QEAVTETLSD	YEVAEKIWSN	RANRQCADCG	SSRPDWAAVN
330	340	350	360	370	380	390	400
LGVVICKQCA	GQHRALGSGI	SKVQSLKLDT	SVWSNEIVQL	FIVLGNDRAN	RFWAGTLPPG	EGLHPDATPG	PRGEFISRKY
410	420	430	440	450	460	470	480
RLGLFRKPHP	QYPDHSQLLQ	ALCAAVARPN	LLKNMTQLLC	VEAFEGEEPW	FPPAPDGSCP	GLLPSDPSPG	VYNEVVVRAT
490	500	510	520	530	540	550	560
YSGFLYCSPV	SNKAGPSPPR	RGRDAPPRLW	CVLGAALEMF	ASENSPEPLS	LIQPQDIVCL	GVSPPPTDPG	DRFPFSFELI
570	580	590	600	610	620	630	640
LAGGRIQHFG	TDGADSLEAW	TSAVGKWFSP	LSCHQLLGPG	LLRLGRLWLR	SPSHTAPAPG	LWLSGFGLLR	GDHLFLCSAP
650	660	670	680	690	700	710	720
GPGPPAPEDM	VHLRRLQEIS	VVSAADTPDK	KEHLVLVETG	RTLYLQGEGR	LDFTAWNAAI	GGAAGGGGTG	LQEQQMSRGD
730	740	750	760	770	780	790	800
IPIIVDACIS	FVTQHGLRLE	GVYRKGGARA	RSLRLLAEFR	RDARSVKLRP	GEHFVEDVTD	TLKRFFRELD	DPVTSARLLP
810	820	830	840	850	860	870	880
RWREAAELPQ	KNQRLEKYKD	VIGCLPRVNR	RTLATLIGHL	YRVQKCAALN	QMCTRNLALL	FAPSVFQTDG	RGEHEVRVLQ
890	900	910	920	930	940	950	960
ELIDGYISVF	DIDSDQVAQI	DLEVSLITTW	KDVQLSQAGD	LIMEVYIEQQ	LPDNCVTLKV	SPTLTAEELT	NQVLEMRGTA
970	980	990	1000	1010	1020	1030	1040
AGMDLWVTFE	IREHGELERP	LHPKEKVLEQ	ALQWCQLPEP	CSASLLLKKV	PLAQAGCLFT	GIRRESPRVG	LLRCREEPPR
1050	1060	1070	1080	1090	1100	1110	1120
LLGSRFQERF	FLLRGRCLLL	LKEKKSSKPE	REWPLEGAKV	YLGIRKKLKP	PTPWGFTLIL	EKMHLYLSCT	DEDEMWDWTT
1130	1140	1150	1160	1170	1180	1190	1200
SILKAQHDDQ	QPVVLRRHSS	SDLARQKFGT	MPLLPIRGDD	SGATLLSANQ	TLRRLHNRRT	LSMFFPMKSS	QGSVEEQEEL
1210	1220	1230	1240	1250	1260	1270	1280
EEPVYEEPVY	EEVGAFPELI	QDTSTSFSTT	REWTVKPENP	LTSQKSLDQP	FLSKSSTLGQ	EERPPEPPPG	PPSKSSPQAR
1290	1300	1310	1320	1330	1340	1350	
GSLEEQLLQE	LSSLILRKGE	TTAGLGSPSQ	PSSPQSPSPT	GLPTQTPGFP	TQPPCTSSPP	SSQPLT	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
164	1	715.8153	8.42	2	31.4	24.0	0	170-181	R.DMWCSTLQSCLK.E	Oxidation: 2	MD:MU 1.02

Detailed Protein Report

Protein 72: chromodomain-helicase-DNA-binding protein 2 isoform 1 [Homo sapiens]

Accession:	gi|118421089	**Score:**	48.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	211.2
Database Date:	2015-11-30	**pI:**	8.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.4
		No. of unique Peptides:	4

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]					
1421	1	846.6046	143.39	1	47.5	10.1	2	147-152	K.KQEKWK.Q	
2644	1	913.4624	-16.46	2	63.1	14.1	1	743-759	K.GTRGSTSGFLNIVMELK.K	Oxidation: 14
1792	1	898.7912	-12.20	3	52.2	11.6	1	1212-1234	K.ISGVQVNVKSIIQHEEEFEMLHK.S	
1619	1	1015.0002	-35.61	2	50.0	12.7	2	1531-1546	R.RNLWIFVSKFTEFDAR.K	

Detailed Protein Report

Protein 73: ATP-binding cassette sub-family A member 3 [Homo sapiens]

Accession: gi|116734710
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 48.1
MW [kDa]: 191.2
pI: 8.2
Sequence Coverage [%]: 1.4
No. of unique Peptides: 2

Quantitation

MD:MU **Median:** 1.13 **CV:** 0.00 % **No. of Peptides:** 1

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

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
198	1	424.2139	-143.01	3	32.2	15.7	1	672-684	R.KLSIGIALIAGSK.V		
448	2	607.1621	-217.19	2	34.9	32.4	0	988-998	K.DALQAEGQEPR.E		MD:MU 1.13

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

Accession: gi|114155133
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 47.9
MW [kDa]: 511.6
pI: 5.6
Sequence Coverage [%]: 0.8
No. of unique Peptides: 2

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
2873	2	731.8707	-28.75	2	66.4	25.7	1	1075-1086	R.LEPIKVFDGWMK.I	
54	1	796.7965	-120.13	2	30.4	11.9	0	3448-3461	R.MSVENATILINCER.W	

Detailed Protein Report

Protein 75: **PERQ amino acid-rich with GYF domain-containing protein 2 isoform c [Homo sapiens]**

Accession:	gi|156766047	**Score:**	47.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	149.4
Database Date:	2015-11-30	**pI:**	5.3
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.8
		No. of unique Peptides:	3

Quantitation

MD:MU **Median:** 0.58 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MAAETQTLNF	GPEWLRALSS	GGSITSPPLS	PALPKYKLAD	YRYGREEMLA	LFLKDNKIPS	DLLDKEFLPI	LQEEPLPPLA
90	100	110	120	130	140	150	160
LVPFTEEEQR	NFSMSVNSAA	VLRLTGRGGG	GTVVGAPRGR	SSSRGRGRGR	GECGFYQRSF	DEVEGVFGRG	GGREMHRSQS
170	180	190	200	210	220	230	240
WEERGDRRFE	KPGRKDVGRP	NFEEGGPTSV	GRKHEFIRSE	SENWRIFREE	QNGEDEDGGW	RLAGSRRDGE	RWRPHSPGWR
250	260	270	280	290	300	310	320
EHMERRRRFE	FDFRDRDDER	GYRRVRSGSG	SIDDDRDSLP	EWCLEDAEEE	MGTFDSSGAF	LSLKKVQKEP	IPEEQEMDFR
330	340	350	360	370	380	390	400
PVDEGEECSD	SEGSHNEEAK	EPDKTNKKEG	EKTDRVGVEA	SEETPQTSSS	SARPGTPSDH	QSQEASQFER	KDEPKTEQTE
410	420	430	440	450	460	470	480
KAEEETRMEN	SLPAKVPSRG	DEMVADVQQP	LSQIPSDTAS	PLLILPPPVP	NPSPTLRPVE	TPVVGAPGMG	SVSTEPDDEE
490	500	510	520	530	540	550	560
GLKHLEQQAE	KMVAYLQDSA	LDDERLASKL	QEHRAKGVSI	PLMHEAMQKW	YYKDPQGEIQ	GPFNNQEMAE	WFQAGYFTMS
570	580	590	600	610	620	630	640
LLVKRACDES	FQPLGDIMKM	WGRVPFSPGP	APPPHMGELD	QERLTRQQEL	TALYQMQHLQ	YQQFLIQQQY	AQVLAQQQKA
650	660	670	680	690	700	710	720
ALSSQQQQQL	ALLLQQFQTL	KMRISDQNII	PSVTRSVSVP	DTGSIWELQP	TASQPTVWEG	GSVWDLPLDT	TTPGPALEQL
730	740	750	760	770	780	790	800
QQLEKAKAAK	LEQERREAEM	RAKREEEERK	RQEELRRQQE	EILRRQQEEE	RKRREEEELA	RRKQEEALRR	QREQEIALRR
810	820	830	840	850	860	870	880
QREEEERQQQ	EEALRRLEER	RREEEERRKQ	EELLRKQEEE	AAKWAREEEE	AQRRLEENRL	RMEEEAARLR	HEEEERKRKE
890	900	910	920	930	940	950	960
LEVQRQKELM	RQRQQQEAL	RRLQQQQQQQ	QLAQMKLPSS	STWGQQSNTT	ACQSQATLSL	AEIQKLEEER	ERQLREEQRR
970	980	990	1000	1010	1020	1030	1040
QQRELMKALQ	QQQQQQQQKL	SGWGNVSKPS	GTTKSLLEIQ	QEEARQMQKQ	QQQQQQHQQP	NRARNNTHSN	LHTSIGNSVW
1050	1060	1070	1080	1090	1100	1110	1120
GSINTGPPNQ	WASDLVSSIW	SNADTKNSNM	GFWDDAVKEV	GPRNSTNKNK	NNASLSKSVG	VSNRQNKKVE	EEEKLLKLFQ
1130	1140	1150	1160	1170	1180	1190	1200
GVNKAQDGFT	QWCEQMLHAL	NTANNLDVPT	FVSFLKEVES	PYEVHDYIRA	YLGDTSEAKE	FAKQFLERRA	KQKANQQRQQ
1210	1220	1230	1240	1250	1260	1270	1280
QQLPQQQQQQ	PPQQPPQQPQ	QQDSVWGMNH	STLHSVFQTN	QSNNQQSNFE	AVQSGKKKKK	QKMVRADPSL	LGFSVNASSE
1290	1300						
RLNMGEIETL	DDY						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1750	1	863.3936	-7.87	2	51.7	13.5	1	565-579	K.RACDESFQPLGDIMK.M	Oxidation: 14	
1628	1	1071.6266	33.70	1	50.2	10.0	1	758-765	R.QQEEILRR.Q		
196	2	838.3951	-10.67	2	32.2	23.6	0	1010-1022	K.QQQQQQQHQQPNR.A		MD:MU 0.58

Protein 76: PREDICTED: dynein heavy chain 10, axonemal isoform X1 [Homo sapiens]

Accession:	gi|530401632	**Score:**	46.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	528.4
Database Date:	2015-11-30	**pI:**	5.5
		Sequence Coverage [%]:	0.9
		No. of unique Peptides:	2

Quantitation

MD:MU	**Median:** 0.86	**CV:** 0.00 %	**No. of Peptides:** 1

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1643	1	938.9588	-53.24	2	50.3	11.9	2	624-639	R.SAEAAFDMLLKFKHIR.S		
115	2	679.8485	-38.99	2	30.8	24.0	0	2780-2791	R.VFNGLVLTNPER.F		MD:MU 0.86

Detailed Protein Report

Protein 77: PREDICTED: G-protein coupled receptor 124 isoform X3 [Homo sapiens]

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

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2732	2	673.3595	29.93	2	64.5	15.8	1	33-45	R.GAPGCPLSIRSCK.C	Carbamidomethyl: 5
2870	14	673.3611	32.18	2	66.4	16.5	1	33-45	R.GAPGCPLSIRSCK.C	Carbamidomethyl: 12
1660	1	716.0007	12.17	3	50.5	14.1	1	1284-1304	K.GGKYDDVTLMGAEVASGGCMK.T	Carbamidomethyl: 19

Detailed Protein Report

Protein 78: insulin receptor-related protein precursor [Homo sapiens]

Accession:	gi|31657140	**Score:**	46.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	143.6
Database Date:	2015-11-30	**pI:**	6.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.0
		No. of unique Peptides:	2

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
561	1	730.2206	-117.87	2	36.3	16.7	0	213-225	R.VCPCPHGMACTAR.G	Carbamidomethyl: 2, 4
2751	1	922.4677	-48.57	2	65.7	17.3	2	499-512	R.ILLRWERYEPLEAR.D	

Detailed Protein Report

Protein 79: plastin-2 [Homo sapiens]

Accession:	gi|167614506	**Score:**	46.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	70.2
Database Date:	2015-11-30	**pI:**	5.2
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	8.0
		No. of unique Peptides:	4

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
545	1	652.1661	-227.16	2	36.1	14.5	0	402-412	R.NWMNSLGVNPR.V	Oxidation: 3
2352	1	836.1191	173.33	2	59.3	10.6	2	442-456	R.VNKPPYPKLGGNMKK.L	
1806	1	649.7882	-96.92	2	52.6	11.2	2	531-542	R.EAKKSSSISSFK.D	
2744	1	710.3515	31.99	2	65.6	10.2	0	611-622	K.MVMTVFACLMGK.G	Carbamidomethyl: 8; Oxidation: 1, 3

Detailed Protein Report

Protein 80: collagen alpha-3(VI) chain isoform 4 precursor [Homo sapiens]

Accession:	gi|240255535	**Score:**	46.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	278.0
Database Date:	2015-11-30	**pI:**	9.1
		Sequence Coverage [%]:	2.0
		No. of unique Peptides:	2

Detailed Protein Report

10	20	30	40	50	60	70	80
MRKHRHLPLV	AVFCLFLSGF	PTTHAQQQQA	VIEVNKRDIV	FLVDGSSALG	LANFNAIRDF	IAKVIQRLEI	GQDLIQVAVA
90	100	110	120	130	140	150	160
QYADTVRPEF	YFNTHPTKRE	VITAVRKMKP	LDGSALYTGS	ALDFVRNNLF	TSSAGYRAAE	GIPKLLVLIT	GGKSLDEISQ
170	180	190	200	210	220	230	240
PAQELKRSSI	MAFAIGNKGA	DQAELEEIAF	DSSLVFIPAE	FRAAPLQGML	PGLLAPLRTL	SGTPEESKRD	ILFLFDGSAN
250	260	270	280	290	300	310	320
LVGQFPVVRD	FLYKIIDELN	VKPEGTRIAV	AQYSDDVKVE	SRFDEHQSKP	EILNLVKRMK	IKTGKALNLG	YALDYAQRYI
330	340	350	360	370	380	390	400
FVKSAGSRIE	DGVLQFLVLL	VAGRSSDRVD	GPASNLKQSG	VVPFIFQAKN	ADPAELEQIV	LSPAFILAAE	SLPKIGDLHP
410	420	430	440	450	460	470	480
QIVNLLKSVH	NGAPAPVSGE	KDVVFLLDGS	EGVRSGFPLL	KEFVQRVVES	LDVGQDRVRV	AVVQYSDRTR	PEFYLNSYMN
490	500	510	520	530	540	550	560
KQDVVNAVRQ	LTLLGGPTPN	TGAALEFVLR	NILVSSAGSR	ITEGVPQLLI	VLTADRSGDD	VRNPSVVVKR	GGAVPIGIGI
570	580	590	600	610	620	630	640
GNADITEMQT	ISFIPDFAVA	IPTFRQLGTV	QQVISERVTQ	LTREELSRLQ	PVLQPLPSPG	VGGKRDVVFL	IDGSQSAGPE
650	660	670	680	690	700	710	720
FQYVRTLIER	LVDYLDVGFD	TTRVAVIQFS	DDPKVEFLLN	AHSSKDEVQN	AVQRLRPKGG	RQINVGNALE	YVSRNIFKRP
730	740	750	760	770	780	790	800
LGSRIEEGVP	QFLVLISSGK	SDDEVDDPAV	ELKQFGVAPF	TIARNADQEE	LVKISLSPEY	VFSVSTFREL	PSLEQKLLTP
810	820	830	840	850	860	870	880
ITTLTSEQIQ	KLLASTRYPP	PAVESDAADI	VFLIDSSEGV	RPDGFAHIRD	FVSRIVRRLN	IGPSKVRVGV	VQFSNDVFPE
890	900	910	920	930	940	950	960
FYLKTYRSQA	PVLDAIRRLR	LRGGSPLNTG	KALEFVARNL	FVKSAGSRIE	DGVPQHLVLV	LGGKSQDDVS	RFAQVIRSSG
970	980	990	1000	1010	1020	1030	1040
IVSLGVGDRN	IDRTELQTIT	NDPRLVFTVR	EFRELPNIEE	RIMNSFGPSA	ATPAPPGVDT	PPPSRPEKKK	ADIVFLLDGS
1050	1060	1070	1080	1090	1100	1110	1120
INFRRDSFQE	VLRFVSEIVD	TVYEDGDSIQ	VGLVQYNSDP	TDEFFLKDFS	TKRQIIDAIN	KVVYKGGRHA	NTKVGLEHLR
1130	1140	1150	1160	1170	1180	1190	1200
VNHFVPEAGS	RLDQRVPQIA	FVITGGKSVE	DAQDVSLALT	QRGVKVFAVG	VRNIDSEEVG	KIASNSATAF	RVGNVQELSE
1210	1220	1230	1240	1250	1260	1270	1280
LSEQVLETLH	DAMHETLCPG	VTDAAKACNL	DVILGFDGSR	DQNVFVAQKG	FESKVDAILN	RISQMHRVSC	SGGRSPTVRV
1290	1300	1310	1320	1330	1340	1350	1360
SVVANTPSGP	VEAFDFDEYQ	PEMLEKFRNM	RSQHPYVLTE	DTLKVYLNKF	RQSSPDSVKV	VIHFTDGADG	DLADLHRASE
1370	1380	1390	1400	1410	1420	1430	1440
NLRQEGVRAL	ILVGLERVVN	LERLMHLEFG	RGFMYDRPLR	LNLLDLDYEL	AEQLDNIAEK	ACCGVPCKCS	GQRGDRGPIG
1450	1460	1470	1480	1490	1500	1510	1520
SIGPKGIPGE	DGYRGYPGDE	GGPGERGPPG	VNGTQGFQGC	PGQRGVKGSR	GFPGEKGEVG	EIGLDGLDGE	DGDKGLPGSS
1530	1540	1550	1560	1570	1580	1590	1600
GEKGNPGRRG	DKGPRGEKGE	RGDVGIRGDP	GNPGQDSQER	GPKGETGDLG	PMGVPGRDGV	PGGPGETGKN	GGFGRRGPPG
1610	1620	1630	1640	1650	1660	1670	1680
AKGNKGGPGQ	PGFEGEQGTR	GAQGPAGPAG	PPGLIGEQGI	SGPRGSGGAA	GAPGERGRTG	PLGRKGEPGE	PGPKGGIGNR
1690	1700	1710	1720	1730	1740	1750	1760
GPRGETGDDG	RDGVGSEGRR	GKKGERGFPG	YPGPKGNPGE	PGLNGTTGPK	GIRGRRGNSG	PPGIVGQKGD	PGYPGPAGPK
1770	1780	1790	1800	1810	1820	1830	1840
GNRGDSIDQC	ALIQSIKDKC	PCCYGPLECP	VFPTELAFAL	DTSEGVNQDT	FGRMRDVVLS	IVNDLTIAES	NCPRGARVAV
1850	1860	1870	1880	1890	1900	1910	1920
VTYNNEVTTE	IRFADSKRKS	VLLDKIKNLQ	VALTSKQQSL	ETAMSFVARN	TFKRVRNGFL	MRKVAVFFSN	TPTRASPQLR
1930	1940	1950	1960	1970	1980	1990	2000
EAVLKLSDAG	ITPLFLTRQE	DRQLINALQI	NNTAVGHALV	LPAGRDLTDF	LENVLTCHVC	LDICNIDPSC	GFGSWRPSFR
2010	2020	2030	2040	2050	2060	2070	2080
DRRAAGSDVD	IDMAFILDSA	ETTTLFQFNE	MKKYIAYLVR	QLDMSPDPKA	SQHFARVAVV	QHAPSESVDN	ASMPPVKVEF
2090	2100	2110	2120	2130	2140	2150	2160
SLTDYGSKEK	LVDFLSRGMT	QLQGTRALGS	AIEYTIENVF	ESAPNPRDLK	IVVLMLTGEV	PEQQLEEAQR	VILQAKCKGY
2170	2180	2190	2200	2210	2220	2230	2240

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
605	1	472.1588	-273.18	2	37.1	12.8	1	99-106	K.REVITAVR.K	
1827	1	1056.0066	84.56	3	52.9	23.4	2	2131-2158	K.IVVLMLTGEVPEQQLEEAQRVILQAKCK.G	

Detailed Protein Report

Protein 81: protein kinase C-binding protein NELL2 isoform c precursor [Homo sapiens]

Accession: gi|223029474
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 46.3
MW [kDa]: 91.1
pI: 5.3
Sequence Coverage [%]: 6.0
No. of unique Peptides: 2

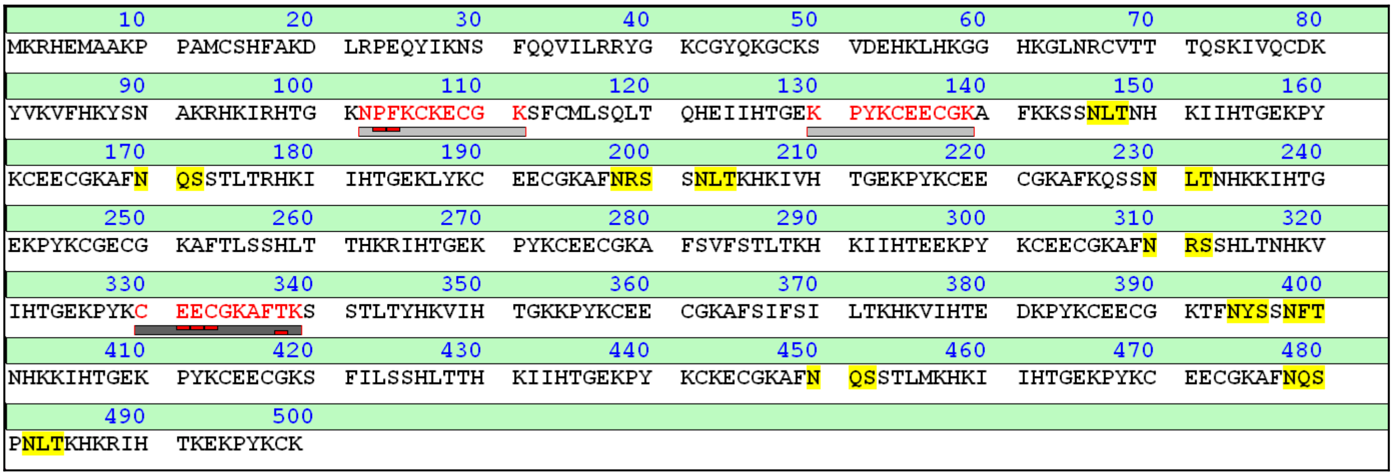
10	20	30	40	50	60	70	80
METGLGAPLF	KAWLLISVWG	LGVDPSLQID	VLTELELGES	TTGVRQVPGL	HNGTKAFLFQ	DTPRSIKAST	ATAEQFFQKL
90	100	110	120	130	140	150	160
RNKHEFTILV	TLKQTHLNSG	VILSIHHLDH	RYLELESSGH	RNEVRLHYRS	GSHRPHTEVF	PYILADDKWH	KLSLAISASH
170	180	190	200	210	220	230	240
LILHIDCNKI	YERVVEKPST	DLPLGTTFWL	GQRNNAHGYF	KGIMQDVQLL	VMPQGFIAQC	PDLNRTCPTC	NDFHGLVQKI
250	260	270	280	290	300	310	320
MELQDILAKT	SAKLSRAEQR	MNRLDQCYCE	RTCTMKGTTY	REFESWIDGC	KNCTCLNGTI	QCETLICPNP	DCPLKSALAY
330	340	350	360	370	380	390	400
VDGKCCKECK	SICQFQGRTY	FEGERNTVYS	SSGVCVLYEC	KDQTMKLVES	SGCPALDCPE	SHQITLSHSC	CKVCKGYDFC
410	420	430	440	450	460	470	480
SERHNCMENS	ICRNLNDRAV	CSCRDGFRAL	REDNAYCEDI	DECAEGRHYC	RENTMCVNTP	GSFMCICKTG	YIRIDDYSCT
490	500	510	520	530	540	550	560
EHDECITNQH	NCDENALCFN	TVGGHNCVCK	PGYTGNGTTC	KAFCKDGCRN	GGACIAANVC	ACPQGFTGPS	CETDIDECSD
570	580	590	600	610	620	630	640
GFVQCDSRAN	CINLPGWYHC	ECRDGYHDNG	MFSPSGESCE	DIDECGTGRH	SCANDTICFN	LDGGYDCRCP	HGKNCTGDCI
650	660	670	680	690	700	710	720
HDGKVKHNGQ	IWVLENDRCS	VCSCQNGFVM	CRRMVCDCEN	PTVDLFCCPE	CDPRLSSQCL	HQNGETLYNS	GDTWVQNCQQ
730	740	750	760	770	780	790	800
CRCLQGEVDC	WPLPCPDVEC	EFSILPENEC	CPRCVTDPCQ	ADTIRNDITK	TCLDEMNVVR	FTGSSWIKHG	TECTLCQCKN
810	820						
GHICCSVDPQ	CLQEL						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1492	1	450.0889	-239.47	2	48.4	12.4	1	522-529	K.AFCKDGCR.N	
1555	1	932.3749	-6.08	2	49.1	11.3	1	659-673	R.CSVCSCQNGFVMCRR.M	Carbamidomethyl: 1, 4, 6

Detailed Protein Report

Protein 82: PREDICTED: zinc finger protein 708 isoform X1 [Homo sapiens]

Accession:	gi|578833563	**Score:**	45.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	57.3
Database Date:	2015-11-30	**pI:**	10.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	6.0
		No. of unique Peptides:	3



```
        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
252	2	605.6643	-205.83	2	32.9	12.7	2	102-111	K.NPFKCKECGK.S	Carbamidomethyl: 8
1912	1	621.2738	-20.17	2	54.0	13.3	1	130-139	E.KPYKCEECGK.A	Carbamidomethyl: 5
1130	2	586.6095	-252.07	2	43.8	19.3	1	330-339	K.CEECGKAFTK.S	Carbamidomethyl: 4

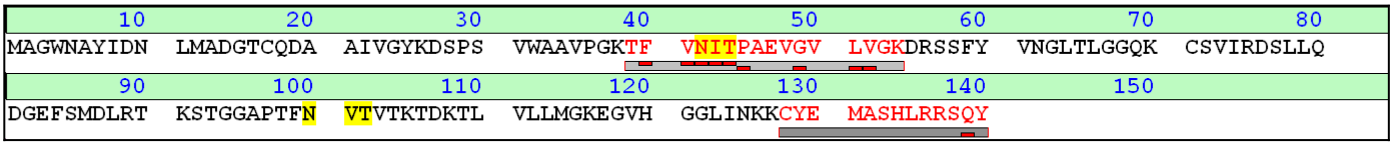
Detailed Protein Report

Protein 83: **profilin-1 [Homo sapiens]**

Accession:	gi|4826898	**Score:**	45.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	15.0
Database Date:	2015-11-30	**pI:**	9.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	20.7
		No. of unique Peptides:	2

Quantitation

MD:MU **Median:** 1.60 **CV:** 84.69 % **No. of Peptides:** 2



```
        10         20         30         40         50         60         70         80
MAGWNAYIDN LMADGTCQDA AIVGYKDSPS VWAAVPGKTF VNITPAEVGV LVGKDRSSFY VNGLTLGGQK CSVIRDSLLQ
        90        100        110        120        130        140        150
DGEFSMDLRT KSTGGAPTFN VTVTKTDKTL VLLMGKEGVH GGLINKKCYE MASHLRRSQY
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
2399	1	822.4646	-8.92	2	60.3	29.2	0	39-54	K.TFVNITPAEVGVLVGK.D		MD:MU	0.76
1495	1	850.7379	-173.16	2	48.5	15.9	2	128-140	K.CYEMASHLRRSQY.-	Carbamidomethyl: 1	MD:MU	3.33

Detailed Protein Report

Protein 84: zinc finger protein 492 [Homo sapiens]

Accession:	gi|148806865	**Score:**	44.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	61.1
Database Date:	2015-11-30	**pI:**	10.3
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	8.3
		No. of unique Peptides:	2

Quantitation

MD:MU	**Median:**	0.62	**CV:**	0.00 %	**No. of Peptides:**	1	

Alias proteins:

Accession	Name	Description
gi|578833408	refseq_human (refseq_human_20140103.fasta)	PREDICTED: zinc finger protein 492 isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MLENYRNLVF	VGIAASKPDL	ITCLEQGKEP	WNVKRHEMVA	EPPVVCSYFA	RDLWPKQGKK	NYFQKVILRR	YKKCGCENLQ
90	100	110	120	130	140	150	160
LRKYCKSMDE	CKVHKECYNG	LNQCLTTTQN	KIFQCDKYVK	VFHKFSNSNR	HTIRHTGKKS	FKCKECEKSF	CMLSHLAQHK
170	180	190	200	210	220	230	240
RIHSGEKPYK	CKECGKAYNE	TSNLSTHKRI	HTGKKPYKCE	ECGKAFNRLS	HLTTHKIIHT	GKKPYKCEEC	GKAFNQSANL
250	260	270	280	290	300	310	320
TTHKRIHTGE	KPYKCEECGR	AFSQSSTLTA	HKIIHAGEKP	YKCEECGKAF	SQSSTLTTHK	IIHTGEKFYK	CEECGKAFSQ
330	340	350	360	370	380	390	400
LSHLTTHKRI	HSGEKPYKCE	ECGKAFKQSS	TLTTHKRIHA	GEKFYKCEVC	SKAFSRFSHL	TTHKRIHTGE	KPYKCEECGK
410	420	430	440	450	460	470	480
AFNLSSQLTT	HKIIHTGEKP	YKCEECGKAF	NQSSTLSKHK	VIHTGEKPYK	YEECGKAFNQ	SSHLTTHKMI	HTGEKPYKCE
490	500	510	520	530	540		
ECGKAFNNSS	ILNRHKMIHT	GEKLYKPESC	NNACDNIAKI	SKYKRNCAGE	K		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1839	1	582.2374	12.53	2	53.0	13.4	1	84-92	K.YCKSMDECK.V	Carbamidomethyl: 8	MD:MU 0.62
2688	1	992.0980	-39.40	3	64.8	18.1	2	495-519	R. HKMIHTGEKLYKPESCNNACDNIA I	Carbamidomethyl: 16, 20; Oxidation: 3	

Detailed Protein Report

Protein 85: PREDICTED: plectin isoform X9 [Homo sapiens]

Accession:	gi|530389159	**Score:**	44.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	513.0
Database Date:	2015-11-30	**pI:**	5.5
		Sequence Coverage [%]:	0.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MKIVPDERDR	VQKKTFTKWV	NKHLIKHWRA	EAQRHISDLY	EDLRDGHNLI	SLLEVLSGDS	LPREKGRMRF	HKLQNVQIAL
90	100	110	120	130	140	150	160
DYLRHRQVKL	VNIRNDDIAD	GNPKLTLGLI	WTIILHFQIS	DIQVSGQSED	MTAKEKLLLW	SQRMVEGYQG	LRCDNFTSSW
170	180	190	200	210	220	230	240
RDGRLFNAII	HRHKPLLIDM	NKVYRQTNLE	NLDQAFSVAE	RDLGVTRLLD	PEDVDVPQPD	EKSIITYVSS	LYDAMPRVPD
250	260	270	280	290	300	310	320
VQDGVRANEL	QLRWQEYREL	VLLLLQWMRH	HTAAFEERRF	PSSFEEIEIL	WSQFLKFKEM	ELPAKEADKN	RSKGIYQSLE
330	340	350	360	370	380	390	400
GAVQAGQLKV	PPGYHPLDVE	KEWGKLHVAI	LEREKQLRSE	FERLECLQRI	VTKLQMEAGL	CEEQLNQADA	LLQSDVRLLA
410	420	430	440	450	460	470	480
AGKVPQRAGE	VERDLDKADS	MIRLLFNDVQ	TLKDGRHPQG	EQMYRRVYRL	HERLVAIRTE	YNLRLKAGVA	APATQVAQVT
490	500	510	520	530	540	550	560
LQSVQRRPEL	EDSTLRYLQD	LLAWVEENQH	RVDGAEWGVD	LPSVEAQLGS	HRGLHQSIEE	FRAKIERARS	DEGQLSPATR
570	580	590	600	610	620	630	640
GAYRDCLGRL	DLQYAKLLNS	SKARLRSLES	LHSFVAAATK	ELMWLNEKEE	EEVGFDWSDR	NTNMTAKKES	YSALMRELEL
650	660	670	680	690	700	710	720
KEKKIKELQN	AGDRLLREDH	PARPTVESFQ	AALQTQWSWM	LQLCCCIEAH	LKENAAYFQF	FSDVREAEGQ	LQKLQEALRR
730	740	750	760	770	780	790	800
KYSCDRSATV	TRLEDLLQDA	QDEKEQLNEY	KGHLSGLAKR	AKAVVQLKPR	HPAHPMRGRL	PLLAVCDYKQ	VEVTVHKGDE
810	820	830	840	850	860	870	880
CQLVGPAQPS	HWKVLSSSGS	EAAVPSVCFL	VPPPNQEAQE	AVTRLEAQHQ	ALVTLWHQLH	VDMKSLLAWQ	SLRRDVQLIR
890	900	910	920	930	940	950	960
SWSLATFRTL	KPEEQRQALH	SLELHYQAFL	RDSQDAGGFG	PEDRLMAERE	YGSCSHHYQQ	LLQSLEQGAQ	EESRCQRCIS
970	980	990	1000	1010	1020	1030	1040
ELKDIRLQLE	ACETRTVHRL	RLPLDKEPAR	ECAQRIAEQQ	KAQAEVEGLG	KGVARLSAEA	EKVLALPEPS	PAAPTLRSEL
1050	1060	1070	1080	1090	1100	1110	1120
ELTLGKLEQV	RSLSAIYLEK	LKTISLVIRG	TQGAEEVLRA	HEEQLKEAQA	VPATLPELEA	TKASLKKLRA	QAEAQQPTFD
1130	1140	1150	1160	1170	1180	1190	1200
ALRDELRGAQ	EVGERLQQRH	GERDVEVERW	RERVAQLLER	WQAVLAQTDV	RQRELEQLGR	QLRYYRESAD	PLGAWLQDAR
1210	1220	1230	1240	1250	1260	1270	1280
RRQEQIQAMP	LADSQAVREQ	LRQEQALLEE	IERHGEKVEE	CQRFAKQYIN	AIKDYELQLV	TYKAQLEPVA	SPAKKPKVQS
1290	1300	1310	1320	1330	1340	1350	1360
GSESVIQEYV	DLRTHYSELT	TLTSQYIKFI	SETLRRMEEE	ERLAEQQRAE	ERERLAEVEA	ALEKQRQLAE	AHAQAKAQAE
1370	1380	1390	1400	1410	1420	1430	1440
REAKELQQRM	QEEVVRREEA	AVDAQQQKRS	IQEELQQLRQ	SSEAEIQAKA	RQAEAAERSR	LRIEEEIRVV	RLQLEATERQ
1450	1460	1470	1480	1490	1500	1510	1520
RGGAEGELQA	LRARAEEAEA	QKRQAQEEAE	RLRRQVQDES	QRKRQAEVEL	ASRVKAEAEA	AREKQRALQA	LEELRLQAEE
1530	1540	1550	1560	1570	1580	1590	1600
AERRLRQAEV	ERARQVQVAL	ETAQRSAEAE	LQSKRASFAE	KTAQLERSLQ	EEHVAVAQLR	EEAERRAQQQ	AEAERAREEA
1610	1620	1630	1640	1650	1660	1670	1680
ERELERWQLK	ANEALRLRLQ	AEEVAQQKSL	AQAEAEKQKE	EAEREARRRG	KAEEQAVRQR	ELAEQELEKQ	RQLAEGTAQQ
1690	1700	1710	1720	1730	1740	1750	1760
RLAAEQELIR	LRAETEQGEQ	QRQLLEEELA	RLQREAAAAT	QKRQELEAEL	AKVRAEMEVL	LASKARAEEE	SRSTSEKSKQ
1770	1780	1790	1800	1810	1820	1830	1840
RLEAEAGRFR	ELAEEAARLR	ALAEEAKRQR	QLAEEDAARQ	RAEAERVLAE	KLAAIGEATR	LKTEAEIALK	EKEAENERLR
1850	1860	1870	1880	1890	1900	1910	1920
RLAEDEAFQR	RRLEEQAAQH	KADIEERLAQ	LRKASDSELE	RQKGLVEDTL	RQRRQVEEEI	LALKASFEKA	AAGKAELELE
1930	1940	1950	1960	1970	1980	1990	2000
LGRIRSNAED	TLRSKEQAEL	EAARQRQLAA	EEERRRREAE	ERVQKSLAAE	EEAARQRKAA	LEEVERLKAK	VEEARRLRER
2010	2020	2030	2040	2050	2060	2070	2080
AEQESARQLQ	LAQEAAQKRL	QAEEKAHAFA	VQQKEQELQQ	TLQQEQSVLD	QLRGEAEAAR	RAAEEAEEAR	VQAEREAAQS
2090	2100	2110	2120	2130	2140	2150	2160
RRQVEEAERL	KQSAEEQAQA	RAQAQAAAEK	LRKEAEQEAA	RRAQAEQAAL	RQKQAADAEM	EKHKKFAEQT	LRQKAQVEQE
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
1692	1	582.1401	-225.95	2	51.1	12.2	0	2348-2357	R.QLEMSAEAER.L	

Detailed Protein Report

Protein 86: PREDICTED: integrin beta-8 isoform X2 [Homo sapiens]

Accession:	gi|530384769	**Score:**	44.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	71.2
Database Date:	2015-11-30	**pI:**	9.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	7.4
		No. of unique Peptides:	2

Alias proteins:

Accession	Name	Description
gi|530384771	refseq_human (refseq_human_20140103.fasta)	PREDICTED: integrin beta-8 isoform X3 [Homo sapiens]

10	20	30	40	50	60	70	80
MLKVHPLKKY	PVDLYYLVDV	SASMHNNIEK	LNSVGNDLSR	KMAFFSRDFR	LGFGSYVDKT	VSPYISIHPE	RIHNQCSDYN
90	100	110	120	130	140	150	160
LDCMPPHGYI	HVLSLTENIT	EFEKAVHRQK	ISGNIDTPEG	GFDAMLQAAV	CESHIGWRKE	AKRLLLVMTD	QTSHLALDSK
170	180	190	200	210	220	230	240
LAGIVVPNDG	NCHLKNNVYV	KSTTMEHPSL	GQLSEKLIDN	NINVIFAVQG	KQFHWYKDLL	PLLPGTIAGE	IESKAANLNN
250	260	270	280	290	300	310	320
LVVEAYQKLI	SEVKVQVENQ	VQGIYFNITA	ICPDGSRKPG	MEGCRNVTSN	DEVLFNVTVT	MKKCDVTGGK	NYAIIKPIGF
330	340	350	360	370	380	390	400
NETAKIHIHR	NCSCQCEDNR	GPKGKCVDET	FLDSKCFQCD	ENKCHFDEDQ	FSSESCKSHK	DQPVCSGRGV	CVCGKCSCHK
410	420	430	440	450	460	470	480
IKLGKVYGKY	CEKDDFSCPY	HHGNLCAGHG	ECEAGRCQCF	SGWEGDRCQC	PSAAAQHCVN	SKGQVCSGRG	TCVCGRCECT
490	500	510	520	530	540	550	560
DPRSIGRFCE	HCPTCYTACK	ENWNCMQCLH	PHNLSQAILD	QCKTSCALME	QQHYVDQTSE	CFSSPSYLRI	FFIIFIVTFL
570	580	590	600	610	620	630	640
IGLLKVLIIR	QVILQWNSNK	IKSSSDYRVS	ASKKDKLILQ	SVCTRAVTYR	REKPEEIKMD	ISKLNAHETF	RCNF

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1358	1	955.9298	-52.51	2	46.6	10.6	0	286-302	R.NVTSNDEVLFNVTVTMK.K	
2775	1	746.3843	84.07	3	66.0	16.7	2	381-400	K.DQPVCSGRGVCVCGKCSCHK.I	Carbamidomethyl: 5, 11, 18

Detailed Protein Report

Protein 87: **PREDICTED: T-lymphoma invasion and metastasis-inducing protein 1 isoform X4 [Homo sapiens]**

Accession:	gi|530419050	**Score:**	44.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	161.7
Database Date:	2015-11-30	**pI:**	6.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.4
		No. of unique Peptides:	3

Quantitation

MD:MU **Median:** 3.23 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MGNAESQHVE HEFYGEKHAS LGRKHTSRSL RLSHKTRRTR HASSGKVIHR NSEVSTRSSS TPSIPQSLAE NGLEPFSQDG

        90        100        110        120        130        140        150        160
TLEDFGSPIW VDRVDMGLRP VSYTDSSVTP SVDSSIVLTA ASVQSMPDTE ESRLYGDDAT YLAEGGRRQH SYTSNGPTFM

       170        180        190        200        210        220        230        240
ETASFKKKRS KSADIWREDS LEFSLSDLSQ EHLTSNEEIL GSAEEKDCEE ARGMETRASP RQLSTCQRAN SLGDLYAQKN

       250        260        270        280        290        300        310        320
SGVTANGGPG SKFAGYCRNL VSDIPNLANH KMPPAAAEET PPYSNYNTLP CRKSHCLSEG ATNPQISHSN SMQGRRAKTT

       330        340        350        360        370        380        390        400
QDVNAGEGSE FADSGIEGAT TDTDLLSRRS NATNSSYSPT TGRAFVGSDS GSSSTGDAAR QGVYENFRRE LEMSTTNSES

       410        420        430        440        450        460        470        480
LEEAGSAHSD EQSSGTLSSP GQSDILLTAA QGTVRKAGAL AVKNFLVHKK NKKVESATRR KWKHYWVSLK GCTLFFYESD

       490        500        510        520        530        540        550        560
GRSGIDHNSI PKHAVWVENS IVQAVPEHPK KDFVFCLSNS LGDAFLFQTT SQTELENWIT AIHSACATAV ARHHHKEDTL

       570        580        590        600        610        620        630        640
RLLKSEIKKL EQKIDMDEKM KKMGEMQLSS VTDSKKKKTI LDQIFVWEQN LEQFQMDLFR FRCYLASLQG GELPNPKRLL

       650        660        670        680        690        700        710        720
AFASRPTKVA MGRLGIFSVS SFHALVAART GETGVRRRTQ AMSRSASKRR SRFSSLWGLD TTSKKKQGRP SINQVFGEGT

       730        740        750        760        770        780        790        800
EAVKKSLEGI FDDIVPDGKR EKEVVLPNVH QHNPDCDIWV HEYFTPSWFC LPNNQPALTV VRPGDTARDT LELICKTHQL

       810        820        830        840        850        860        870        880
DHSAHYLRLK FLIENKMQLY VPQPEEDIYE LLYKEIEICP KVTQSIHIEK SDTAADTYGF SLSSVEEDGI RRLYVNSVKE

       890        900        910        920        930        940        950        960
TGLASKKGLK AGDEILEINN RAADALNSSM LKDFLSQPSL GLLVRTYPEL EEGVELLESP PHRVDGPADL GESPLAFLTS

       970        980        990       1000       1010       1020       1030       1040
NPGHSLCSEQ GSSAETAPEE TEGPDLESSD ETDHSSKSTE QVAAFCRSLH EMNPSDQSPS PQDSTGPQLA TMRQLSDADK

      1050       1060       1070       1080       1090       1100       1110       1120
LRKVICELLE TERTYVKDLN CLMERYLKPL QKETFLTQDE LDVLFGNLTE MVEFQVEFLK TLEDGVRLVP DLEKLEKVDQ

      1130       1140       1150       1160       1170       1180       1190       1200
FKKVLFSLGG SFLYYADRFK LYSAFCASHT KVPKVLVKAK TDTAFKAFLD AQNPKQQHSS TLESYLIKPI QRILKYPLLL

      1210       1220       1230       1240       1250       1260       1270       1280
RELFALTDAE SEEHYHLDVA IKTMNKVASH INEMQKIHEE FGAVFDQLIA EQTGEKKEVA DLSMGDLLLH TTVIWLNPPA

      1290       1300       1310       1320       1330       1340       1350       1360
SLGKWKKEPE LAAFVFKTAV VLVYKDGSKQ KKKLVGSHRL SIYEDWDPFR FRHMIPTEAL QVRALASADA EANAVCEIVH

      1370       1380       1390       1400       1410       1420       1430       1440
VKSESEGRPE RVFHLCCSSP ESRKDFLKAV HSILRDKHRR QLLKTESLPS SQQYVPFGGK RLCALKGARP AMSRAGTVGI

      1450       1460
RTFKIPVTPT PQ
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
44	2	750.8174	-45.94	2	30.3	15.2	0	134-147	R.LYGDDATYLAEGGR.R		MD:MU 3.23
1584	1	1022.9716	-69.17	2	49.7	16.6	1	707-725	K.QGRPSINQVFGEGTEAVKK.S		
1360	1	942.5032	8.18	2	46.6	12.4	2	1139-1154	R.FKLYSAFCASHTKVPK.V	Carbamidomethyl: 8	

Detailed Protein Report

Protein 88: histone-lysine N-methyltransferase, H3 lysine-36 and H4 lysine-20 specific isoform a [Homo sapiens]

Accession:	gi|27477095	**Score:**	44.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	267.2
Database Date:	2015-11-30	**pI:**	9.9
		Sequence Coverage [%]:	0.9
		No. of unique Peptides:	1

Quantitation

MD:MU	**Median:**	0.98	**CV:**	0.00 %	**No. of Peptides:**	1

Alias proteins:

Accession	Name	Description
gi|578811200	refseq_human (refseq_human_20140103.fasta)	PREDICTED: histone-lysine N-methyltransferase, H3 lysine-36 and H4 lysine-20 specific isoform X6 [Homo sapiens]
gi|530381148	refseq_human (refseq_human_20140103.fasta)	PREDICTED: histone-lysine N-methyltransferase, H3 lysine-36 and H4 lysine-20 specific isoform X3 [Homo sapiens]
gi|530381146	refseq_human (refseq_human_20140103.fasta)	PREDICTED: histone-lysine N-methyltransferase, H3 lysine-36 and H4 lysine-20 specific isoform X2 [Homo sapiens]

Detailed Protein Report

10	20	30	40	50	60	70	80
MPLKTRTALS	DDPDSSTSTL	GNMLELPGTS	SSSTSQELPF	CQPKKKSTPL	KYEVGDLIWA	KFKRRPWWPC	RICSDPLINT
90	100	110	120	130	140	150	160
HSKMKVSNRR	PYRQYYVEAF	GDPSERAWVA	GKAIVMFEGR	HQFEELPVLR	RRGKQKEKGY	RHKVPQKILS	KWEASVGLAE
170	180	190	200	210	220	230	240
QYDVPKGSKN	RKCIPGSIKL	DSEEDMPFED	CTNDPESEHD	LLLNGCLKSL	AFDSEHSADE	KEKPCAKSRA	RKSSDNPKRT
250	260	270	280	290	300	310	320
SVKKGHIQFE	AHKDERRGKI	PENLGLNFIS	GDISDTQASN	ELSRIANSLT	GSNTAPGSFL	FSSCGKNTAK	KEFETSNGDS
330	340	350	360	370	380	390	400
LLGLPEGALI	SKCSREKNKP	QRSLVCGSKV	KLCYIGAGDE	EKRSDSISIC	TTSDDGSSDL	DPIEHSSESD	NSVLEIPDAF
410	420	430	440	450	460	470	480
DRTENMLSMQ	KNEKIKYSRF	AATNTRVKAK	QKPLISNSHT	DHLMGCTKSA	EPGTETSQVN	LSDLKASTLV	HKPQSDFTND
490	500	510	520	530	540	550	560
ALSPKFNLSS	SISSENSLIK	GGAANQALLH	SKSKQPKFRS	IKCKHKENPV	MAEPPVINEE	CSLKCCSSDT	KGSPLASISK
570	580	590	600	610	620	630	640
SGKVDGLKLL	NNMHEKTRDS	SDIETAVVKH	VLSELKELSY	RSLGEDVSDS	GTSKPSKPLL	FSSASSQNHI	PIEPDYKFST
650	660	670	680	690	700	710	720
LLMMLKDMHD	SKTKEQRLMT	AQNLVSYRSP	GRGDCSTNSP	VGVSKVLVSG	GSTHNSEKKG	DGTQNSANPS	PSGGDSALSG
730	740	750	760	770	780	790	800
ELSASLPGLL	SDKRDLPASG	KSRSDCVTRR	NCGRSKPSSK	LRDAFSAQMV	KNTVNRKALK	TERKRKLNQL	PSVTLDAVLQ
810	820	830	840	850	860	870	880
GDRERGGSLR	GGAEDPSKED	PLQIMGHLTS	EDGDHFSDVH	FDSKVKQSDP	GKISEKGLSF	ENGKGPELDS	VMNSENDELN
890	900	910	920	930	940	950	960
GVNQVVPKKR	WQRLNQRRTK	PRKRMNRFKE	KENSECAFRV	LLPSDPVQEG	RDEFPEHRTP	SASILEEPLT	EQNHADCLDS
970	980	990	1000	1010	1020	1030	1040
AGPRLNVCDK	SSASIGDMEK	EPGIPSLTPQ	AELPEPAVRS	EKKRLRKPSK	WLLEYTEEYD	QIFAPKKKQK	KVQEQVHKVS
1050	1060	1070	1080	1090	1100	1110	1120
SRCEEESLLA	RGRSSAQNKQ	VDENSLISTK	EEPPVLEREA	PFLEGPLAQS	ELGGGHAELP	QLTLSVPVAP	EVSPRPALES
1130	1140	1150	1160	1170	1180	1190	1200
EELLVKTPGN	YESKRQRKPT	KKLLESNDLD	PGFMPKKGDL	GLSKKCYEAG	HLENGITESC	ATSYSKDFGG	GTTKIFDKPR
1210	1220	1230	1240	1250	1260	1270	1280
KRKRQRHAAA	KMQCKKVKND	DSSKEIPGSE	GELMPHRTAT	SPKETVEEGV	EHDPGMPASK	KMQGERGGGA	ALKENVCQNC
1290	1300	1310	1320	1330	1340	1350	1360
EKLGELLLCE	AQCCGAFHLE	CLGLTEMPRG	KFICNECRTG	IHTCFVCKQS	GEDVKRCLLP	LCGKFYHEEC	VQKYPPTVMQ
1370	1380	1390	1400	1410	1420	1430	1440
NKGFRCSLHI	CITCHAANPA	NVSASKGRLM	RCVRCPVAYH	ANDFCLAAGS	KILASNSIIC	PNHFTPRRGC	RNHEHVNVSW
1450	1460	1470	1480	1490	1500	1510	1520
CFVCSEGGSL	LCCDSCPAAF	HRECLNIDIP	EGNWYCNDCK	AGKKPHYREI	VWVKVGRYRW	WPAEICHPRA	VPSNIDKMRH
1530	1540	1550	1560	1570	1580	1590	1600
DVGEFPVLFF	GSNDYLWTHQ	ARVFPYMEGD	VSSKDKMGKG	VDGTYKKALQ	EAAARFEELK	AQKELRQLQE	DRKNDKKPPP
1610	1620	1630	1640	1650	1660	1670	1680
YKHIKVNRPI	GRVQIFTADL	SEIPRCNCKA	TDENPCGIDS	ECINRMLLYE	CHPTVCPAGG	RCQNQCFSKR	QYPEVEIFRT
1690	1700	1710	1720	1730	1740	1750	1760
LQRGWGLRTK	TDIKKGEFVN	EYVGELIDEE	ECRARIRYAQ	EHDITNFYML	TLDKDRIIDA	GPKGNYARFM	NHCCQPNCET
1770	1780	1790	1800	1810	1820	1830	1840
QKWSVNGDTR	VGLFALSDIK	AGTELTFNYN	LECLGNGKTV	CKCGAPNCSG	FLGVRPKNQP	IATEEKSKKF	KKKQQGKRRT
1850	1860	1870	1880	1890	1900	1910	1920
QGEITKERED	ECFSCGDAGQ	LVSCKKPGCP	KVYHADCLNL	TKRPAGKWEC	PWHQCDICGK	EAASFCEMCP	SSFCKQHREG
1930	1940	1950	1960	1970	1980	1990	2000
MLFISKLDGR	LSCTEHDPCG	PNPLEPGEIR	EYVPPPVPLP	PGPSTHLAEQ	STGMAAQAPK	MSDKPPADTN	QMLSLSKKAL
2010	2020	2030	2040	2050	2060	2070	2080
AGTCQRPLLP	ERPLERTDSR	PQPLDKVRDL	AGSGTKSQSL	VSSQRPLDRP	PAVAGPRPQL	SDKPSPVTSP	SSSPSVRSQP
2090	2100	2110	2120	2130	2140	2150	2160
LERPLGTADP	RLDKSIGAAS	PRPQSLEKTS	VPTGLRLPPP	DRLLITSSPK	PQTSDRPTDK	PHASLSQRLP	PPEKVLSAVV
2170	2180	2190	2200	2210	2220	2230	2240
QTLVAKEKAL	RPVDQNTQSK	NRAALVMDLI	DLTPRQKERA	ASPHQVTPQA	DEKMPVLESS	SWPASKGLGH	MPRAVEKGCV
2250	2260	2270	2280	2290	2300	2310	2320
SDPLQTSGKA	AAPSEDPWQA	VKSLTQARLL	SQPPAKAFLY	EPTTQASGRA	SAGAEQTPGP	LSQSPGLVKQ	AKQMVGGQQL
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	
617	1	459.6161	-280.24	2	37.0	16.5	1	222-229	K.EKPCAKSR.A		MD:MU	0.98

Detailed Protein Report

Protein 89: **PREDICTED: low-density lipoprotein receptor-related protein 2 isoform X1 [Homo sapiens]**

Accession:	gi|578804333	**Score:**	44.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	522.2
Database Date:	2015-11-30	**pI:**	4.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	0.7
		No. of unique Peptides:	3

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	GTDESPLCNE	PQPDGNSCSD
1370	1380	1390	1400	1410	1420	1430	1440
FNGGCTHECV	QEPFGAKCLC	PLGFLLANDS	KTCEDIDECD	ILGSCSQHCY	NMRGSFRCSC	DTGYMLESDG	RTCKVTASES
1450	1460	1470	1480	1490	1500	1510	1520
LLLLVASQNK	IIADSVTSQV	HNIYSLVENG	SYIVAVDFDS	ISGRIFWSDA	TQGKTWSAFQ	NGTDRRVVFD	SSIILTETIA
1530	1540	1550	1560	1570	1580	1590	1600
IDWVGRNLYW	TDYALETIEV	SKIDGSHRTV	LISKNLTNPR	GLALDPRMNE	HLLFWSDWGH	HPRIERASMD	GSMRTVIVQD
1610	1620	1630	1640	1650	1660	1670	1680
KIFWPCGLTI	DYPNRLLYFM	DSYLDYMDFC	DYNGHHRRQV	IASDLIIRHP	YALTLFEDSV	YWTDRATRRV	MRANKWHGGN
1690	1700	1710	1720	1730	1740	1750	1760
QSVVMYNIQW	PLGIVAVHPS	KQPNSVNPCA	FSRCSHLCLL	SSQGPHFYSC	VCPSGWSLSP	DLLNCLRDDQ	PFLITVRQHI
1770	1780	1790	1800	1810	1820	1830	1840
IFGISLNPEV	KSNDAMVPIA	GIQNGLDVEF	DDAEQYIYWV	ENPGEIHRVK	TDGTNRTVFA	SISMVGPSMN	LALDWISRNL
1850	1860	1870	1880	1890	1900	1910	1920
YSTNPRTQSI	EVLTLHGDIR	YRKTLIANDG	TALGVGFPIG	ITVDPARGKL	YWSDQGTDSG	VPAKIASANM	DGTSVKTLFT
1930	1940	1950	1960	1970	1980	1990	2000
GNLEHLECVT	LDIEEQKLYW	AVTGRGVIER	GNVDGTDRMI	LVHQLSHPWG	IAVHDSFLYY	TDEQYEVIER	VDKATGANKI
2010	2020	2030	2040	2050	2060	2070	2080
VLRDNVPNLR	GLQVYHRRNA	AESSNGCSNN	MNACQQICLP	VPGGLFSCAC	ATGFKLNPDN	RSCSPYNSFI	VVSMLSAIRG
2090	2100	2110	2120	2130	2140	2150	2160
FSLELSDHSE	TMVPVAGQGR	NALHVDVDVS	SGFIYWCDFS	SSVASDNAIR	RIKPDGSSLM	NIVTHGIGEN	GVRGIAVDWV
2170	2180	2190	2200	2210	2220	2230	2240

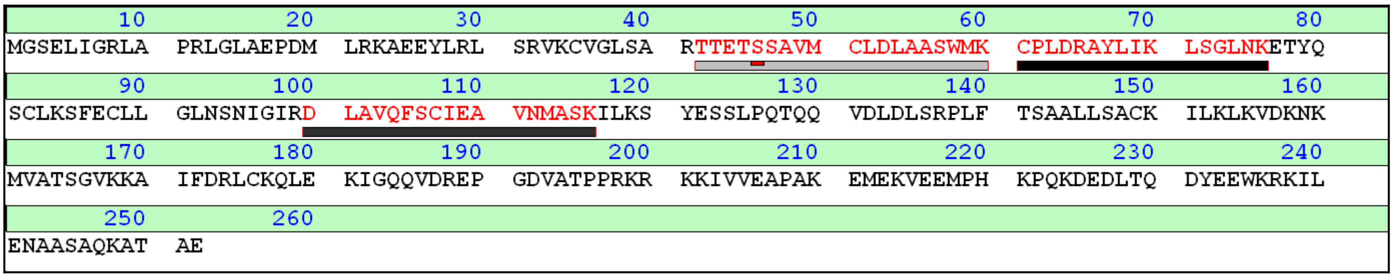
Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1173	1	786.4695	28.78	1	44.3	12.4	0	776-782	R.EILAANR.V	
23	1	788.3643	33.00	3	29.6	20.9	0	3802-3821	R.TCHPEYFQCTSGHCVHSELK.C	Carbamidomethyl: 2
1208	1	441.6040	-232.73	2	44.7	10.7	1	4264-4270	K.YDGTDRR.V	

Detailed Protein Report

Protein 90: **origin recognition complex subunit 6 [Homo sapiens]**

Accession:	gi|7657427	**Score:**	43.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	28.1
Database Date:	2015-11-30	**pI:**	9.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	20.6
		No. of unique Peptides:	3



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        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
2133	2	701.2686	-80.31	3	56.8	17.2	0	42-60	R.TTETSSAVMCLDLAASWMK.C	Carbamidomethyl: 10
55	1	930.9009	-129.85	2	30.4	14.2	2	61-76	K.CPLDRAYLIKLSGLNK.E	Carbamidomethyl: 1
2540	1	941.9343	-22.57	2	61.7	12.6	0	100-116	R.DLAVQFSCIEAVNMASK.I	Carbamidomethyl: 8

Detailed Protein Report

Protein 91: **coiled-coil domain-containing protein 168 [Homo sapiens]**

Accession:	gi|226246554	**Score:**	43.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	801.4
Database Date:	2015-11-30	**pI:**	9.6
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	0.9
		No. of unique Peptides:	4

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2490	1	610.2540	-89.47	2	61.1	10.6	2	3706-3716	K.QEGKMQEGKGK.S	
1634	1	803.8641	-92.41	2	50.2	10.9	0	5427-5440	K.MCILFSKPLPSNLK.L	Oxidation: 1
2403	2	974.2328	75.63	3	59.9	11.7	2	5658-5682	R.DEDIYFTGFGTIRSGKRPEWLFTGK.K	
1685	1	916.4063	-73.78	2	50.8	10.7	2	6846-6860	R.ECRKETLIITPPSCK.S	Carbamidomethyl: 2, 14

Detailed Protein Report

Protein 92: **PREDICTED: RING finger protein 17 isoform X10 [Homo sapiens]**

Accession:	gi|578824967	**Score:**	43.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	168.9
Database Date:	2015-11-30	**pI:**	5.0
		Sequence Coverage [%]:	2.6
		No. of unique Peptides:	1

Quantitation

MD:MU	**Median:** 0.99	**CV:** 0.00 %	**No. of Peptides:** 1

10	20	30	40	50	60	70	80
MLDTNTAEEI	DEALNTAHHS	FEQLSIAGKA	LEHMQKQTIE	ERERVIEVVE	KQFDQLLAFF	DSRKKNLCEE	FARTTDDYLS
90	100	110	120	130	140	150	160
NLIKAKSYIE	EKKNNLNAAM	NIARALQLSP	SLRTYCDLNQ	IIRTLQLTSD	SELAQVSSPQ	LRNPPRLSVN	CSEIICMFNN
170	180	190	200	210	220	230	240
MGKIEFRDST	KCYPQENEIR	QNVQKKYNNK	KELSCYDTYP	PLEKKKVDMS	VLTSEAPPPP	LQPETNDVHL	EAKNFQPQKD
250	260	270	280	290	300	310	320
VATASPKTIA	VLPQMGSSPD	VIIEEIIEDN	VESSAELVFV	SHVIDPCHFY	IRKYSQIKDA	KVLEKKVNEF	CNRSSHLDPS
330	340	350	360	370	380	390	400
DILELGARIF	VSSIKNGMWC	RGTITELIPI	EGRNTRKPCS	PTRLFVHEVA	LIQIFMVDFG	NSEVLIVTGV	VDTHVRPEHS
410	420	430	440	450	460	470	480
AKQHIALNDL	CLVLRKSEPY	TEGLLKDIQP	LAQPCSLKDI	VPQNSNEGWE	EEAKVEFLKM	VNNKAVSMKV	FREEDGVLIV
490	500	510	520	530	540	550	560
DLQKPPPNKI	SSDMPVSLRD	ALVFMELAKF	KSQSLRSHFE	KNTTLHYHPP	ILPKEMTDVS	VTVCHINSPG	DFYLQLIEGL
570	580	590	600	610	620	630	640
DILFLLKTIE	EFYKSEDGEN	LEILCPVQDQ	ACVAKFEDGI	WYRAKVIGLP	GHQEVEVKYV	DFGNTAKITI	KDVRKIKDEF
650	660	670	680	690	700	710	720
LNAPEKAIKC	KLAYIEPYKR	TMQWSKEAKE	KFEEKAQDKF	MTCSVIKILE	DNVLLVELFD	SLGAPEMTTT	SINDQLVKEG
730	740	750	760	770	780	790	800
LASYEIGYIL	KDNSQKHIEV	WDPSPEEIIS	NEVHNLNPVS	AKSLPNENFQ	SLYNKELPVH	ICNVISPEKI	YVQWLLTENL
810	820	830	840	850	860	870	880
LNSLEEKMIA	AYENSKWEPV	KWENDMHCAV	KIQDKNQWRR	GQIIRMVTDT	LVEVLLYDVG	VELVVNVDCL	RKLEENLKTM
890	900	910	920	930	940	950	960
GRLSLECSLV	DIRPAGGSDK	WTATACDCLS	LYLTGAVATI	ILQVDSEENN	TTWPLPVKIF	CRDEKGERVD	VSKYLIKKGL
970	980	990	1000	1010	1020	1030	1040
ALRERRINNL	DNSHSLSEKS	LEVPLEQEDS	VVTNCIKTNF	DPDKKTADII	SEQKVSEFQE	KILEPRTTRG	YKPPAIPNMN
1050	1060	1070	1080	1090	1100	1110	1120
VFEATVSCVG	DDGTIFVVPK	LSEFELIKMT	NEIQSNLKCL	GLLEPYFWKK	GEACAVRGSD	TLWYRGKVME	VVGGAVRVQY
1130	1140	1150	1160	1170	1180	1190	1200
LDHGFTEKIP	QCHLYPILLY	PDIPQFCIPC	QLHNTTPVGN	VWQPDAIEVL	QQLLSKRQVD	IHIMELPKNP	WEKLSIHLYF
1210	1220	1230	1240	1250	1260	1270	1280
DGMSLSYFMA	YYKYCTSEHT	EEMLKEKPRS	DHDKKYEEEQ	WEIRFEELLS	AETDTPLLPP	YLSSSLPSPG	ELYAVQVKHV
1290	1300	1310	1320	1330	1340	1350	1360
VSPNEVYICL	DSIETSNQSN	QHSDTDDSGV	SGESESESLD	EALQRVNKKV	EALPPLTDFR	TEMPCLAEYD	DGLWYRAKIV
1370	1380	1390	1400	1410	1420	1430	1440
AIKEFNPLSI	LVQFVDYGST	AKLTLNRLCQ	IPSHLMRYPA	RAIKVLLAGF	KPPLRDLGET	RIPYCPKWSM	EALWAMIDCL
1450	1460	1470	1480	1490			
QGKQLYAVSM	APAPEQIVTL	YDDEQHPVHM	PLVEMGLADK	DE			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
200	1	642.8816	92.45	2	32.2	16.1	1	596-605	K.FEDGIWYRAK.V		MD:MU 0.99

Detailed Protein Report

Protein 93:	**PREDICTED: centrosomal protein of 290 kDa isoform X4 [Homo sapiens]**		
Accession:	gi|530400856	**Score:**	43.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	234.7
Database Date:	2015-11-30	**pI:**	6.1
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.0
		No. of unique Peptides:	3

Quantitation

MD:MU	**Median:** 1.11	**CV:** 0.00 %	**No. of Peptides:** 1

Detailed Protein Report

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
1675	1	745.8585	-74.75	2	50.7	11.8	1	631-643	K.FAELTKINLDAQK.V		
1969	1	703.7594	-155.73	2	54.7	10.7	0	1496-1508	K.TTGMTVDQVLGIR.A	Oxidation: 4	
1615	1	494.1461	-276.33	2	50.1	10.7	2	1636-1643	K.EKAEVQRK.L		MD:MU 1.11

Detailed Protein Report

Protein 94: PREDICTED: tripartite motif-containing protein 2 isoform X2 [Homo sapiens]

Accession:	gi|578808962	**Score:**	43.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	84.7
Database Date:	2015-11-30	**pI:**	7.3
Modification(s):	Oxidation	**Sequence Coverage [%]:**	4.5
		No. of unique Peptides:	3

Quantitation

MD:MU **Median:** 9.77 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MHRSGRYGTQ	QRAGSKTAGP	PCQWSRMASE	GTNIPSPVVR	QIDKQFLICS	ICLERYKNPK	VLPCLHTFCE	RCLQNYIPAH
90	100	110	120	130	140	150	160
SLTLSCPVCR	QTSILPEKGV	AALQNNFFIT	NLMDVLQRTP	GSNAEESSIL	ETVTAVAAGK	PLSCPNHDGN	VMEFYCQSCE
170	180	190	200	210	220	230	240
TAMCRECTEG	EHAEHPTVPL	KDVVEQHKAS	LQVQLDAVNK	RLPEIDSALQ	FISEIIHQLT	NQKASIVDDI	HSTFDELQKT
250	260	270	280	290	300	310	320
LNVRKSVLLM	ELEVNYGLKH	KVLQSQLDTL	LQGQESIKSC	SNFTAQALNH	GTETEVLLVK	KQMSEKLNEL	ADQDFPLHPR
330	340	350	360	370	380	390	400
ENDQLDFIVE	TEGLKKSIHN	LGTILTTNAV	ASETVATGEG	LRQTIIGQPM	SVTITTKDKD	GELCKTGNAY	LTAELSTPDG
410	420	430	440	450	460	470	480
SVADGEILDN	KNGTYEFLYT	VQKEGDFTLS	LRLYDQHIRG	SPFKLKVIRS	ADVSPTTEGV	KRRVKSPGSG	HVKQKAVKRP
490	500	510	520	530	540	550	560
ASMYSTGKRK	ENPIEDDLIF	RVGTKGRNKG	EFTNLQGVAA	STNGKILIAD	SNNQCVQIFS	NDGQFKSRFG	IRGRSPGQLQ
570	580	590	600	610	620	630	640
RPTGVAVHPS	GDIIIADYDN	KWVSIFSSDG	KFKTKIGSGK	LMGPKGVSVD	RNGHIIVVDN	KACCVFIFQP	NGKIVTRFGS
650	660	670	680	690	700	710	720
RGNGDRQFAG	TLDGPHFAAV	NSNNEIIITD	FHNHSVKVFN	QEGEFMLKFG	SNGEGNGQFN	APTGVAVDSN	GNIIVADWGN
730	740	750	760	770	780		
SRIQVFDGSG	SFLSYINTSA	DPLYGPQGLA	LTSDGHVVVA	DSGNHCFKVY	RYLQ		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2668	1	673.3612	23.64	2	63.5	12.0	2	2-12	M.HRSGRYGTQQR.A		
2047	1	698.2586	-165.65	2	55.7	16.9	1	476-488	K.AVKRPASMYSTGK.R		MD:MU 9.77
428	2	587.8118	-7.20	2	34.7	14.2	1	601-611	K.LMGPKGVSVDR.N	Oxidation: 2	

Detailed Protein Report

Protein 95: RB1-inducible coiled-coil protein 1 isoform 2 [Homo sapiens]

Accession:	gi|134304846	**Score:**	43.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	182.7
Database Date:	2015-11-30	**pI:**	5.2
		Sequence Coverage [%]:	1.9
		No. of unique Peptides:	2

Alias proteins:

Accession	Name	Description
gi|578815756	refseq_human (refseq_human_20140103.fasta)	PREDICTED: RB1-inducible coiled-coil protein 1 isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MKLYVFLVNT	GTTLTFDTEL	TVQTVADLKH	AIQSKYKIAI	QHQVLVVNGG	ECMAADRRVC	TYSAGTDTNP	IFLFNKEMIL
90	100	110	120	130	140	150	160
CDRPPAIPKT	TFSTENDMEI	KVEESLMMPA	VFHTVASRTQ	LALEMYEVAK	KLCSFCEGLV	HDEHLQHQGW	AAIMANLEDC
170	180	190	200	210	220	230	240
SNSYQKLLFK	FESIYSNYLQ	SIEDIKLKLT	HLGTAVSVMA	KIPLLECLTR	HSYRECLGRL	DSLPEHEDSE	KAEMKRSTEL
250	260	270	280	290	300	310	320
VLSPDMPRTT	NESLLTSFPK	SVEHVSPDTA	DAESGKEIRE	SCQSTVHQQD	ETTIDTKDGD	LPFFNVSLLD	WINVQDRPND
330	340	350	360	370	380	390	400
VESLVRKCFD	SMSRLDPRII	RPFIAECRQT	IAKLDNQNMK	AIKGLEDRLY	ALDQMIASCG	RLVNEQKELA	QGFLANQKRA
410	420	430	440	450	460	470	480
ENLKDASVLP	DLCLSHANQL	MIMLQNHRKL	LDIKQKCTTA	KQELANNLHV	RLKWCCFVML	HADQDGEKLQ	ALLRLVIELL
490	500	510	520	530	540	550	560
ERVKIVEALS	TVPQMYCLAV	VEVVRRKMFI	KHYREWAGAL	VKDGKRLYEA	EKSKRESFGK	LFRKSFLRNR	LFRGLDSWPP
570	580	590	600	610	620	630	640
SFCTQKPRKF	DCELPDISLK	DLQFLQSFCP	SEVQPFLRVP	LLCDFEPLHQ	HVLALHNLVK	AAQSLDEMSQ	TITDLLSEQK
650	660	670	680	690	700	710	720
ASVSQTSPQS	ASSPRMESTA	GITTTTSPRT	PPPLTVQDPL	CPAVCPLEEL	SPDSIDAHTF	DFETIPHPNI	EQTIHQVSLD
730	740	750	760	770	780	790	800
LDSLAESPES	DFMSAVNEFV	IEENLSSPNP	ISDPQSPEMM	VESLYSSVIN	AIDSRRMQDT	NVCGKEDFGD	HTSLNVQLER
810	820	830	840	850	860	870	880
CRVVAQDSHF	SIQTIKEDLC	HFRTFVQKEQ	CDFSNSLKCT	AVEIRNIIEK	VKCSLEITLK	EKHQKELLSL	KNEYEGKLDG
890	900	910	920	930	940	950	960
LIKETEENEN	KIKKLKGELV	CLEEVLQNKD	NEFALVKHEK	EAVICLQNEK	DQKLLEMENI	MHSQNCEIKE	LKQSREIVLE
970	980	990	1000	1010	1020	1030	1040
DLKKLHVEND	EKLQLLRAEL	QSLEQSHLKE	LEDTLQVRHI	QEFEKVMTDH	RVSLEELKKE	NQQIINQIQE	SHAEIIQEKE
1050	1060	1070	1080	1090	1100	1110	1120
KQLQELKLKV	SDLSDTRCKL	EVELALKEAE	TDEIKILLEE	SRAQQKETLK	SLLEQETENL	RTEISKLNQK	IQDNNENYQV
1130	1140	1150	1160	1170	1180	1190	1200
GLAELRTLMT	IEKDQCISEL	ISRHEEESNI	LKAELNKVTS	LHNQAFEIEK	NLKEQIIELQ	SKLDSELSAL	ERQKDEKITQ
1210	1220	1230	1240	1250	1260	1270	1280
QEEKYEAIIQ	NLEKDRQKLV	SSQEQDREQL	IQKLNCEKDE	AIQTALKEFK	LEREVVEKEL	LEKVKHLENQ	IAKSPAIDST
1290	1300	1310	1320	1330	1340	1350	1360
RGDSSSLVAE	LQEKLQEEKA	KFLEQLEEQE	KRKNEEMQNV	RTSLIAEQQT	NFNTVLTREK	MRKENIINDL	SDKLKSTMQQ
1370	1380	1390	1400	1410	1420	1430	1440
QERDKDLIES	LSEDRARLLE	EKKKLEEEVS	KLRSSSFVPS	PYVATAPELY	GACAPELPGE	SDRSAVETAD	EGRVDSAMET
1450	1460	1470	1480	1490	1500	1510	1520
SMMSVQENIH	MLSEEKQRIM	LLERTLQLKE	EENKRLNQRL	MSQSMSSVSS	RHSEKIAIRD	FQVGDLVLII	LDERHDNYVL
1530	1540	1550	1560	1570	1580	1590	1600
FTVSPTLYFL	HSESLPALDL	KPASGASRRP	WVLGKVMEKE	YCQAKKAQNR	FKVPLGTKFY	RVKAVSWNKK	V

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2032	1	687.8227	-80.45	2	55.5	10.2	1	388-399	K.ELAQGFLANQKR.A	
1335	1	497.7323	-72.04	2	46.4	14.6	1	508-514	K.MFIKHYR.E	

Detailed Protein Report

Protein 96: **zinc finger protein 841 [Homo sapiens]**

Accession:	gi|211057416	**Score:**	43.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	106.0
Database Date:	2015-11-30	**pI:**	10.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	7.7
		No. of unique Peptides:	3

10	20	30	40	50	60	70	80
MALPQGSLTF	RDVAVEFSQE	EWKCLDPVQK	ALYRDVMLEN	YRNLGFLGLC	LPDLNIISML	EQGKEPWTVV	SQVKIARNPN
90	100	110	120	130	140	150	160
CGECMKGVIT	GISPKCVIKE	LPPIQNSNTG	EKFQAVMLEG	HESYDTENFY	FREIRKNLQE	VDFQWKDGEI	NYKEGPMTHK
170	180	190	200	210	220	230	240
NNLTGQRVRH	SQGDVENKHM	ENQLILRFQS	GLGELQKFQT	AEKIYGCNQI	ERTVNNCFLA	SPLQRIFPGV	QTNISRKYGN
250	260	270	280	290	300	310	320
DFLQLSLPTQ	DEKTHIREKP	YIGNECGKAF	RVSSSLINHQ	MIHTTEKPYR	CNESGKAFHR	GSLLTVHQIV	HTRGKPYQCD
330	340	350	360	370	380	390	400
VCGRIFRQNS	DLVNHRRSHT	GDKPYICNEC	GKSFSKSSHL	AVHQRIHTGE	KPYKCNRCGK	CFSQSSSLAT	HQTVHTGDKP
410	420	430	440	450	460	470	480
YKCNECGKTF	KRNSSLTAHH	IIHAGKKPYT	CDVCGKVFYQ	NSQLVRHQII	HTGETPYKCN	ECGKVFFQRS	RLAGHRRIHT
490	500	510	520	530	540	550	560
GEKPYKCNEC	GKVFSQHSHL	AVHQRVHTGE	KPYKCNECGK	AFNWGSLLTV	HQRIHTGEKP	YKCNVCGKVF	NYGGYLSVHM
570	580	590	600	610	620	630	640
RCHTGEKPLH	CNKCGMVFTY	YSCLARHQRM	HTGEKPYKCN	VCGKVFIDSG	NLSIHRRSHT	GEKPFQCNEC	GKVFSYYSCL
650	660	670	680	690	700	710	720
ARHRKIHTGE	KPYKCNDCGK	AYTQRSSLTK	HLVIHTGENP	YHCNEFGEAF	IQSSKLARYH	RNPTGEKPHK	CSECGRTFSH
730	740	750	760	770	780	790	800
KTSLVYHQRR	HTGEMPYKCI	ECGKVFNSTT	TLARHRRIHT	GEKPYKCNEC	GKVFRYRSGL	ARHWSIHTGE	KPYKCNECGK
810	820	830	840	850	860	870	880
AFRVRSILLN	HQMMHTGEKP	YKCNECGKAF	IERSNLVYHQ	RNHTGEKPYK	CMECGKAFGR	RSCLTKHQRI	HSSEKPYKCN
890	900	910	920	930			
ECGKSYISRS	GLTKHQIKHA	GENLTTKLNV	ERPLDVVLTS	GIPK			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1460	1	1011.7530	-79.39	3	48.0	16.8	2	590-616	R.MHTGEKPYKCNVCGKVFIDSGNLSIHR.R	
1732	1	1061.1490	-2.43	3	51.5	11.3	2	617-642	R.RSHTGEKPFQCNECGKVFSYYSCLAR.H	Carbamidomethyl: 11, 14, 23
1286	1	738.4255	114.34	3	45.7	15.0	2	699-716	R.YHRNPTGEKPHKCSECGR.T	Carbamidomethyl: 13, 16

Detailed Protein Report

Protein 97: PREDICTED: 14-3-3 protein epsilon isoform X1 [Homo sapiens]

Accession:	gi|530410617	**Score:**	43.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	27.4
Database Date:	2015-11-30	**pI:**	4.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	11.3
		No. of unique Peptides:	1

Alias proteins:

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

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

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

Detailed Protein Report

Protein 98: **PREDICTED: intraflagellar transport protein 88 homolog isoform X7 [Homo sapiens]**

Accession: gi|530402705

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Modification(s): Oxidation

Score: 42.9

MW [kDa]: 95.8

pI: 9.3

Sequence Coverage [%]: 4.4

No. of unique Peptides: 2

10	20	30	40	50	60	70	80
MKVESGMKIK	VHNNAESETA	VGFLEVDQGC	PIFGFPGPHR	KKNCLGPHMK	FTNTKVQMMQ	NVHLAPETDE	DDLYSGYNDY
90	100	110	120	130	140	150	160
NPIYDIEELE	NDAAFQQAVR	TSHGRRPPIT	AKISSTAVTR	PIATGYGSKT	SLASSIGRPM	TGAIQDGVTR	PMTAVRAAGF
170	180	190	200	210	220	230	240
TKAALRGSAF	DPLSQSRGPA	SPLEAKKKDS	PEEKIKQLEK	EVNELVEESC	IANSCGDLKL	ALEKAKDAGR	KERVLVRQRE
250	260	270	280	290	300	310	320
QVTTPENINL	DLTYSVLFNL	ASQYSVNEMY	AEALNTYQVI	VKNKMFSNAG	ILKMNMGNIY	LKQRNYSKAI	KFYRMALDQV
330	340	350	360	370	380	390	400
PSVNKQMRIK	IMQNIGVTFI	QAGQYSDAIN	SYEHIMSMAP	NLKAGYNLTI	CYFAIGDREK	MKKAFQKLIT	VPLEIDEDKY
410	420	430	440	450	460	470	480
ISPSDDPHTN	LVTEAIKNDH	LRQMERERKA	MAEKYIMTSA	KLIAPVIETS	FAAGYDWCVE	VVKASQYVEL	ANDLEINKAV
490	500	510	520	530	540	550	560
TYLRQKDYNQ	AVEILKVLEK	KDSRVKSAAA	TNLSALYYMG	KDFAQASSYA	DIAVNSDRYN	PAALTNKGNT	VFANGDYEKA
570	580	590	600	610	620	630	640
AEFYKEALRN	DSSCTEALYN	IGLTYEKLNR	LDEALDCFLK	LHAILRNSAE	VLYQIANIYE	LMENPSQAIE	WLMQVVSVIP
650	660	670	680	690	700	710	720
TDPQVLSKLG	ELYDREGDKS	QAFQYYYESY	RYFPCNIEVI	EWLGAYYIDT	QFWEKAIQYF	ERASLIQPTQ	VKWQLMVASC
730	740	750	760	770	780	790	800
FRRSGNYQKA	LDTYKDTHRK	FPENVECSGS	VRTGHMERDP	LNLLPRKSVL	PGPEIAKCNY	FSGEKYYLSA	FLSSSLHRSW
810	820	830	840	850			
IKRCSRICQK	TEEVGKNERN	KGTAHKVRQR	WQWGLPWQKR	RKC			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2105	1	937.3619	-150.42	2	56.5	15.6	2	315-330	R.MALDQVPSVNKQMRIK.I	Oxidation: 13
2734	1	772.4219	29.93	2	65.4	13.8	0	786-798	K.YYLSAFLSSSLHR.S	

Detailed Protein Report

Protein 99:	**spectrin beta chain, non-erythrocytic 1 isoform 2 [Homo sapiens]**		
Accession:	gi|112382252	**Score:**	42.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	251.2
Database Date:	2015-11-30	**pI:**	5.3
		Sequence Coverage [%]:	1.8
		No. of unique Peptides:	2

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
2681	1	1079.0243	7.01	2	64.7	12.9	1	627-642	R.LWKFFWEMAEEEGWIR.E	
452	4	607.8361	-46.62	2	35.3	12.6	2	820-829	K.EVAELTRLRK.Q	

Detailed Protein Report

Protein 100: dynein heavy chain 17, axonemal [Homo sapiens]

Accession:	gi|256542310	**Score:**	42.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	509.0
Database Date:	2015-11-30	**pI:**	5.4
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	0.9
		No. of unique Peptides:	2

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
AVTCDELFGI	INPVTREWKD	GLFSTIMRDL	ANITHDGPKW	IILDGDIDPM	WIESLNTVMD	DNKVLTLASN	ERIPLNRTMR
2250	2260	2270	2280	2290	2300	2310	2320
LVFEISHLRT	ATPATVSRAG	ILYINPADLG	WNPVVSSWIE	RRKVQSEKAN	LMILFDKYLP	TCLDKLRFGF	KKITPVPEIT
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
1870	1	704.2582	-146.54	2	53.4	13.7	0	1255-1267	K.SGGLFEVPVPDYK.Q	
1689	1	1051.5326	21.27	2	50.9	16.9	1	4025-4041	K.CMLFALCYFHAVVAERR.K	Carbamidomethyl: 1; Oxidation: 2

Detailed Protein Report

Protein 101: PREDICTED: protein ELYS isoform X2 [Homo sapiens]

Accession:	gi|578802192	**Score:**	42.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	252.3
Database Date:	2015-11-30	**pI:**	6.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.9
		No. of unique Peptides:	3

Quantitation

MD:MU	**Median:** 0.47	**CV:** 0.00 %	**No. of Peptides:** 1

Detailed Protein Report

```
        10         20         30         40         50         60         70         80
MRDLRAQVTS GLLPFPEVTL QALGEDEITL ESVLRGKFAA GKNGLACLAC GPQLEVVNSI TGERLSAYRF SGVNEQPPVV
        90        100        110        120        130        140        150        160
LAVKEFSWQK RTGLLIGLEE TEGSVLCLYD LGISKVVKAV VLPGRVTAIE PIINHGGASA STQHLHPSLR WLFGVAAVVT
       170        180        190        200        210        220        230        240
DVGQILLVDL CLDDLSCNQN EVEASDLEVL TGIPAEVPHI RESVMRQGRH LCFQLVSPTG TAVSTLSYIS RTNQLAVGFS
       250        260        270        280        290        300        310        320
DGYLALWNMK SMKREYYIQL ESGQVPVYAV TFQEPENDPR NCCYLWAVQS TQDSEGDVLS LHLLQLAFGN RKCLASGQIL
       330        340        350        360        370        380        390        400
YEGLEYCEER YTLDLTGGMF PLRGQTSNTK LLGCQSIEKF RSHGDREEGV NEALSPDTSV SVFTWQVNIY GQGKPSVYLG
       410        420        430        440        450        460        470        480
LFDINRWYHA QMPDSLRSGE YLHNCSYFAL WSLESVVSRT SPHGILDILV HERSLNRGVP PSYPPPEQFF NPSTYNFDAT
       490        500        510        520        530        540        550        560
CLLNSGVVHL TCTGFQKETL TFLKKSGPSL NELIPDGYNR CLVAGLLSPR FVDVQPSSLS QEEQLEAILS AAIQTSSLGL
       570        580        590        600        610        620        630        640
LTGYIRRWIT EEQPNSATNL RFVLEWTWNK VVLTKEEFDR LCVPLFDGSC HFMDPQTIQS IQQCYLLLSN LNIVLSCFAS
       650        660        670        680        690        700        710        720
EAREITERGL IDLSNKFVVS HLICQYAQVV LWFSHSGLLP EGIDDSVQLS RLCYNYPVIQ NYYTSRRQKF ERLSRGKWNP
       730        740        750        760        770        780        790        800
DCLMIDGLVS QLGERIEKLW KRDEGGTGKY PPASLHAVLD MYLLDGVTEA AKHSITIYLL LDIMYSFPNK TDTPIESFPT
       810        820        830        840        850        860        870        880
VFAISWGQVK LIQGFWLIDH NDYESGLDLL FHPATAKPLS WQHSKIIQAF MSQGEHRQAL RYIQTMKPTV SSGNDVILHL
       890        900        910        920        930        940        950        960
TVLLFNRCMV EAWNFLRQHC NRLNIEELLK HMYEVCQEMG LMEDLLKLPF TDTEQECLVK FLQSSASVQN HEFLLVHHLQ
       970        980        990       1000       1010       1020       1030       1040
RANYVPALKL NQTLKINVMN DRDPRLRERS LARNSILDQY GKILPRVHRK LAIERAKPYH LSTSSVFRLV SRPKPLSAVP
      1050       1060       1070       1080       1090       1100       1110       1120
KQVVTGTVLT RSVFINNVLS KIGEVWASKE PINSTTPFNS SKIEEPSPIV YSLPAPELPE AFFGTPISKA SQKISRLLDL
      1130       1140       1150       1160       1170       1180       1190       1200
VVQPVPRPSQ CSEFIQQSSM KSPLYLVSRS LPSSSQLKGS PQAISRASEL HLLETPLVVK KAKSLAMSVT TSGFSEFTPQ
      1210       1220       1230       1240       1250       1260       1270       1280
SILRSTLRST PLASPSPSPG RSPQRLKETR ISFVEEDVHP KWIPGAADDS KLEVFTTPKK CAVPVETEWL KSKDRTTSFF
      1290       1300       1310       1320       1330       1340       1350       1360
LNSPEKEHQE MDEGSQSLEK LDVSKGNSSV SITSDETTLE YQDAPSPEDL EETVFTASKP KSSSTALTTN VTEQTEKDGD
      1370       1380       1390       1400       1410       1420       1430       1440
KDVFASEVTP SDLQKQMGNL EDAETKDLLV AAEAFSELNH LSPVQGTEAS LCAPSVYEGK IFTQKSKVPV LDEGLTSVET
      1450       1460       1470       1480       1490       1500       1510       1520
YTPAIRANDN KSMADVLGDG GNSSLTISEG PIVSERRLNQ EVALNLKEDH EVEVGVLKES VDLPEEKLPI SDSPPDTQEI
      1530       1540       1550       1560       1570       1580       1590       1600
HVIEQEKLEA QDSGEEARNL SFNELYPSGT LKLQYNFDTI DQQFCDLADN KDTAECDIAE VDGELFVAQS NFTLILEGEE
      1610       1620       1630       1640       1650       1660       1670       1680
GEVEPGDFAS SDVLPKAANT ATEEKLVCSG ENDNHGQIAN LPSAVTSDQK SQKVDTLPYV PEPIKVAIAE NLLDVIKDTR
      1690       1700       1710       1720       1730       1740       1750       1760
SKEITSDTME QSIHETIPLV SQNIMCPTKL VKSAFKTAQE TSTMTMNVSQ VDDVVSSKTR TRGQRIQNVN VKSAQQEASA
      1770       1780       1790       1800       1810       1820       1830       1840
DVATPKMPGQ SVRKKTRKAK EISEASENIY SDVRGLSQNQ QIPQNSVTPR RGRRKKEVNQ DILENTSSVE QELQITTGRE
      1850       1860       1870       1880       1890       1900       1910       1920
SKRLKSSQLL EPAVEETTKK EVKVSSVTKR TPRRIKRSVE NQESVEIIND LKVSTVTSPS RMIRKLRSTN LDASENTGNK
      1930       1940       1950       1960       1970       1980       1990       2000
QDDKSSDKQL RIKHVRRVRG REVSPSDVRE DSNLESSQLT VQAEFDMSAI PRKRGRPRKI NPSEDVGSKA VKEERSPKKK
      2010       2020       2030       2040       2050       2060       2070       2080
EAPSIRRRST RNTPAKSENV DVGKPALGKS ILVPNEELSM VMSSKKKLTK KTESQSQKRS LHSVSEERTD EMTHKETNEQ
      2090       2100       2110       2120       2130       2140       2150       2160
EERLLATASF TKSSRSSRTR SSKAILLPDL SEPNNEPLFS PASEVPRKAK AKKIEVPAQL KELVSDLSSQ FVISPPALRS
      2170       2180       2190       2200       2210       2220       2230       2240
RQKNTSNKNK LEDELKDDAQ SVETLGKPKA KRIRTSKTKQ ASKNTEKESA WSPPPIEIRL ISPLASPADG VKSKPRKTTE
      2250       2260       2270
VTGTGLGRNR KKLSSYPKQI LRRKML
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2616	1	742.3664	-24.12	2	62.8	14.1	0	331-343	R.YTLDLTGGMFPLR.G		
2789	1	735.0657	-23.60	3	66.4	12.6	2	1010-1028	R.KLAIERAKPYHLSTSSVFR.L		
549	1	730.3654	-25.94	2	36.2	15.9	1	1260-1271	K.KCAVPVETEWLK.S	Carbamidomethyl: 2	MD:MU 0.47

Detailed Protein Report

Protein 102: PREDICTED: transcription termination factor 2 isoform X1 [Homo sapiens]

Accession:	gi|530363482	**Score:**	42.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	129.4
Database Date:	2015-11-30	**pI:**	9.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.4
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MEEVRCPEHG	TFCFLKTGVR	DGPNKGKSFY	VCRADTCSFV	RATDIPVSHC	LLHEDFVVEL	QGLLLPQDKK	EYRLFFRCIR
90	100	110	120	130	140	150	160
SKAEGKRWCG	SIPWQDPDSK	EHSVSNKSQH	ASETFHHSSN	WLRNPFKVLD	KNQEPALWKQ	LIKGEGEEKK	ADKKQREKGD
170	180	190	200	210	220	230	240
QLFDQKKEQK	PEMMEKDLSS	GLVPKKKQSV	VQEKKQEEGA	EIQCEAETGG	THKRDFSEIK	SQQCQGNELT	RPSASSQEKS
250	260	270	280	290	300	310	320
SGKSQDVQRE	SEPLREKVTQ	LLPQNVHSHN	SISKPQKGGP	LNKEYTNWEA	KETKAKDGPS	IQATQKSLPQ	GHFQERPETH
330	340	350	360	370	380	390	400
SVPAPGGPAA	QAAPAAPGLS	LGEGREAATS	SDDEEEDDVV	FVSSKPGSPL	LFDSTLDLET	KENLQFPDRS	VQRKVSPASG
410	420	430	440	450	460	470	480
VSKKVEPSDP	VARRVYLTTQ	LKQKKSTLAS	VNIQALPDKG	QKLIKQIQEL	EEVLSGLTLS	PEQGTNEKSN	SQVPQQSHFT
490	500	510	520	530	540	550	560
KTTTGPPHLV	PPQPLPRRGT	QPVGSLELKS	ACQVTAGGSS	QCYRGHTNQD	HVHAVWKITS	EAIGQLHRSL	ESCPGETVVA
570	580	590	600	610	620	630	640
EDPAGLKVPL	LLHQKQALAW	LLWRESQKPQ	GGILDDMGLG	KTLTMIALIL	TQKNQEKKEE	KEKSTALTWL	SKDDSCDFTS
650	660	670	680	690	700	710	720
HGTLIICPAS	LIHHWKNEVE	KRVNSNKLRV	YLYHGPNRDS	RARVLSTYDI	VITTYSLVAK	EIPTNKQEAE	IPGANLNVEG
730	740	750	760	770	780	790	800
TSTPLLRIAW	ARIILDEAHN	VKNPRVQTSI	AVCKLQACAR	WAVTGTPIQN	NLLDMYSLLK	FLRCSPFDEF	NLWRSQVDNG
810	820	830	840	850	860	870	880
SKKGGERLSI	LTKSLLLRRT	KDQLDSTGRP	LVILPQRKFQ	LHHLKLSEDE	ETVYNVFFAR	SRSALQSYLK	RHESRGNQSG
890	900	910	920	930	940	950	960
RSPNNPFSRV	ALEFGSEEPR	HSEAADSPRS	STVHILSQLL	RLRQCCCHLS	LLKSALDPME	LKGEGLVLSL	EEQLSALTLS
970	980	990	1000	1010	1020	1030	1040
ELRDSEPSST	VSLNGTFFKM	ELFEGMREST	KISSLLAELE	AIQRNSASQK	SVIVSQWTNM	LKVVALHLKK	HGLTYATIDG
1050	1060	1070	1080	1090	1100	1110	1120
SVNPKQRMDL	VEAFNHSRGP	QVMLISLLAG	GVGLNLTGGN	HLFLLDMHWN	PSLEDQACDR	IYRVGQQKDV	VIHRFVCEGT
1130	1140	1150	1160	1170			
VEEKILQLQE	KKKDLAKQVL	SGSGESVTKL	TLADLRVLFG	I			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2664	1	701.8434	-43.89	2	63.4	13.3	2	71-80	K.EYRLFFRCIR.S	
2866	1	655.3693	90.53	2	66.3	14.3	1	167-176	K.KEQKPEMMEK.D	Oxidation: 7, 8

Detailed Protein Report

Protein 103: GRIP and coiled-coil domain-containing protein 1 [Homo sapiens]

Accession:	gi|22208850	**Score:**	42.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	87.8
Database Date:	2015-11-30	**pI:**	5.2
		Sequence Coverage [%]:	5.0
		No. of unique Peptides:	2

Quantitation

MD:MU **Median:** 0.29 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MEKFGMNFGG	GPSKKDLLET	IETQKKQLLQ	YQARLKDVVR	AYKSLLKEKE	ALEASIKVLS	VSHEADVGLA	GVQLPGLTFP
90	100	110	120	130	140	150	160
DSVDDRCSTH	SEDSTGTATS	LDTAASLTST	KGEFGVEDDR	PARGPPPPKS	EEASWSESGV	SSSSGDGPFA	GGEVDKRLHQ
170	180	190	200	210	220	230	240
LKTQLATLTS	SLATVTQEKS	RMEASYLADK	KKMKQDLEDA	SNKAEEERAR	LEGELKGLQE	QIAETKARLI	TQQHDRAQEQ
250	260	270	280	290	300	310	320
SDHALMLREL	QKLLQEERTQ	RQDLELRLEE	TREALAGRAY	AAEQMEGFEL	QTKQLTREVE	ELKSELQAIR	DEKNQPDPRL
330	340	350	360	370	380	390	400
QELQEEAARL	KSHFQAQLQQ	EMRKTALAED	QLRQQSQVEE	QRVAALENQI	SEVSELLGTY	EKAKQKDQLA	IQKLKERILQ
410	420	430	440	450	460	470	480
LDLENKTLAL	AASSRSPLDS	HGEESSLDVN	VLKDKMEKLK	RLLQVAARKS	QVTLDVEKLC	DLEIMPSSEA	ADGEKATALY
490	500	510	520	530	540	550	560
YQQELKQLKE	EFERYKMRAQ	VVLKSKNTKD	GNLGKELEAA	QEQLAELKEK	YISLRLSCEE	LEHQHQEAD	DWKQELARLQ
570	580	590	600	610	620	630	640
QLHRQELERC	QLDFRDRTLK	LEEELHKQRD	RALAVLTEKD	LELEQLRSVA	LASGLPGRRS	PVGGGGPGDP	ADTSSSDSLT
650	660	670	680	690	700	710	720
QALQLAAANE	PTFFLYAEQL	ARKEVEITSL	RKQKHRLEVE	VHQLQDRLLE	EGERHREEVA	ALQSHIEKNI	RDQSREGANL
730	740	750	760	770	780		
EYLKNIIYRF	LTLPDSLGRQ	QTLTAILTIL	HFSPEEKQVI	MRLPTSASWW	PSGKR		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1918	2	572.7243	-166.46	2	54.0	17.8	1	344-353	R.KTALAEDQLR.Q		MD:MU 0.29
55	1	1096.9659	-93.00	2	30.1	11.7	0	363-382	R.VAALENQISEVSELLGTYEK.A		

Detailed Protein Report

Protein 104: **collagen alpha-2(XI) chain isoform 3 preproprotein [Homo sapiens]**

Accession:	gi|111118968	**Score:**	42.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	159.8
Database Date:	2015-11-30	**pI:**	9.5
		Sequence Coverage [%]:	2.6
		No. of unique Peptides:	3

10	20	30	40	50	60	70	80
MERCSRCHRL	LLLLPLVLGL	SAAPGWAGAP	PVDVLRALRF	PSLPDGVRRA	KGICPADVAY	RVARPAQLSA	PTRQLFPGGF
90	100	110	120	130	140	150	160
PKDFSLLTVV	RTRPGLQAPL	LTLYSAQGVR	QLGLELGRPV	RFLYEDQTGR	PQPPSQPVFR	GLSLADGKWH	RVAVAVKGQS
170	180	190	200	210	220	230	240
VTLIVDCKKR	VTRPLPRSAR	PVLDTHGVII	FGARILDEEV	FEGDVQELAI	VPGVQAAYES	CEQKELECEG	GQRERPQNQQ
250	260	270	280	290	300	310	320
PHRAQRSPQQ	QPSRLHRPQN	QEPQSQAAHG	PRGLKGEKGE	PAVLEPGMLV	EGPPGPEGPA	GLIGPPGIQG	NPGPVGDPGE
330	340	350	360	370	380	390	400
RGPPGRAGLP	GSDGAPGPPG	TSLMLPFRFG	SGGGDKGPVV	AAQEAQAQAI	LQQARLALRG	PPGPMGYTGR	PGPLGQPGSP
410	420	430	440	450	460	470	480
GLKGESGDLG	PQGPRGPQGL	TGPPGKAGRR	GRAGADGARG	MPGDPGVKGD	RGFDGLPGLP	GEKGHRGDTG	AQGLPGPPGE
490	500	510	520	530	540	550	560
DGERGDDGEI	GPRGLPGESG	PRGLLGPKGP	PGIPGPPGVR	GMDGPQGPKG	SLGPQGEPGP	PGQQGTPGTQ	GLPGPQGAIG
570	580	590	600	610	620	630	640
PHGEKGPQGK	PGLPGMPGSD	GPPGHPGKEG	PPGTKGNQGP	SGPQGPLGYP	GPRGVKGVDG	IRGLKGHKGE	KGEDGFPGFK
650	660	670	680	690	700	710	720
GDIGVKGDRG	EVGVPGSRGE	DGPEGPKGRT	GPTGDPGPPG	LMGEKGKLGV	PGLPGYPGRQ	GPKGSLGFPG	FPGASGEKGA
730	740	750	760	770	780	790	800
RGLSGKSGPR	GERGPTGPRG	QRGPRGATGK	SGAKGTSGGD	GPHGPPGERG	LPGPQGPNGF	PGPKGPPGPP	GKDGLPGHPG
810	820	830	840	850	860	870	880
QRGEVGFQGK	TGPPGPPGVV	GPQGAAGETG	PMGERGHPGP	PGPPGEQGLP	GTAGKEGTKG	DPGPPGAPGK	DGPAGLRGFP
890	900	910	920	930	940	950	960
GERGLPGTAG	GPGLKGNEGP	SGPPGPAGSP	GERGAAGSGG	PIGPPGRPGP	QGPPGAAGEK	GVPGEKGPIG	PTGRDGVQGP
970	980	990	1000	1010	1020	1030	1040
VGLPGPAGPP	GVAGEDGDKG	EVGDPGQKGT	KGNKGEHGPP	GPPGPIGPVG	QPGAAGADGE	PGARGPQGHF	GAKGDEGTRG
1050	1060	1070	1080	1090	1100	1110	1120
FNGPPGPIGL	QGLPGPSGEK	GETGDVGPMG	PPGPPGPRGP	AGPNGADGPQ	GPPGGVGNLG	PPGEKGEPGE	SGSPGIQGEP
1130	1140	1150	1160	1170	1180	1190	1200
GVKGPRGERG	EKGESGQPGE	PGPPGPKGPT	GDDGPKGNPG	PVGFPGDPGP	PGEGGPRGQD	GAKGDRGEDG	EPGQPGSPGP
1210	1220	1230	1240	1250	1260	1270	1280
TGENGPPGPL	GKRGPAGSPG	SEGRQGGKGA	KGDPGAIGAP	GKTGPVGPAG	PAGKPGPDGL	RGLPGSVGQQ	GRPGATGQAG
1290	1300	1310	1320	1330	1340	1350	1360
PPGPVGPPGL	PGLRGDAGAK	GEKGHPGLIG	LIGPPGEQGE	KGDRGLPGPQ	GSPGQKGEMG	IPGASGPIGP	GGPPGLPGPA
1370	1380	1390	1400	1410	1420	1430	1440
GPKGAKGATG	PGGPKGEKGV	QGPPGHPGPP	GEVIQPLPIQ	MPKKTRRSVD	GSRLMQEDEA	IPTGGAPGSP	GGLEEIFGSL
1450	1460	1470	1480	1490	1500	1510	1520
DSLREEIEQM	RRPTGTQDSP	ARTCQDLKLC	HPELPDGEYW	VDPNQGCARD	AFRVFCNFTA	GGETCVTPRD	DVTQFSYVDS
1530	1540	1550	1560	1570	1580	1590	1600
EGSPVGVVQL	TFLRLLSVSA	HQDVSYPCSG	AARDGPLRLR	GANEDELSPE	TSPYVKEFRD	GCQTQQGRTV	LEVRTPVLEQ
1610	1620	1630					
LPVLDASFSD	LGAPPRRGGV	LLGPVCFMG					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2716	2	645.8279	-46.54	2	64.3	18.2	1	158-169	K.GQSVTLIVDCKK.R	
2503	1	862.3584	-77.51	2	61.7	12.3	1	668-685	K.GRTGPTGDPGPPGLMGEK.G	
230	2	575.1791	-198.73	2	32.6	11.4	0	1618-1629	R.GGVLLGPVCFMG.-	

Detailed Protein Report

Protein 105: **PREDICTED: chromodomain-helicase-DNA-binding protein 4 isoform X6 [Homo sapiens]**

Accession:	gi|578822562	**Score:**	41.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	216.7
Database Date:	2015-11-30	**pI:**	5.7
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	2.5
		No. of unique Peptides:	2

Detailed Protein Report

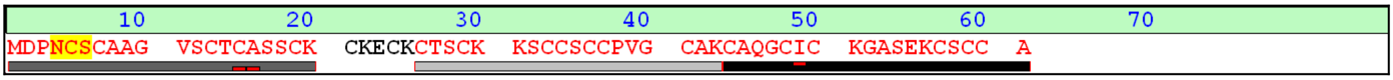
10	20	30	40	50	60	70	80
MASGLGSPSP	CSAGSEEEDM	DALLNNSLPP	PHPENEEDPE	EDLSETETPK	LKKKKKPKKP	RDPKIPKSKR	QKKERMLLCR
90	100	110	120	130	140	150	160
QLGDSSGEGP	EFVEEEEEVA	LRSDSEGSDY	TPGKKKKKKL	GPKKEKKSKS	KRKEEEEEED	DDDDSKEPKS	SAQLLEDWGM
170	180	190	200	210	220	230	240
EDIDHVFSEE	DYRTLTNYKA	FSQFVRPLIA	AKNPKIAVSK	MMMVLGAKWR	EFSTNNPFKG	SSGASVAAAA	AAAVAVVESM
250	260	270	280	290	300	310	320
VTATEVAPPP	PPVEVPIRKA	KTKEGKGPNA	RRKPKGSPRV	PDAKKPKPKK	VAPLKIKLGG	FGSKRKRSSS	EDDDLDVESD
330	340	350	360	370	380	390	400
FDDASINSYS	VSDGSTSRSS	RSRKKLRTTK	KKKKDHQDYC	EVCQQGGEII	LCDTCPRAYH	MVCLDPDMEK	APEGKWSCPH
410	420	430	440	450	460	470	480
CEKEGIQWEA	KEDNSEGEEI	LEEVGGDLEE	EDDHHMEFCR	VCKDGGELLC	CDTCPSSYHI	HCLNPPLPEI	PNGEWLCPRC
490	500	510	520	530	540	550	560
TCPALKGKVQ	KILIWKWGQP	PSPTPVPRPP	DADPNTPSPK	PLEGRPERQF	FVKWQGMSYW	HCSWVSELQL	ELHCQVMFRN
570	580	590	600	610	620	630	640
YQRKNDMDEP	PSGDFGGDEE	KSRKRKNKDP	KFAEMEERFY	RYGIKPEWMM	IHRILNHSVD	KKGHVHYLIK	WRDLPYDQAS
650	660	670	680	690	700	710	720
WESEDVEIQD	YDLFKQSYWN	HRELMRGEEG	RPGKKLKKVK	LRKLERPPET	PTVDPTVKYE	RQPEYLDATG	GTLHPYQMEG
730	740	750	760	770	780	790	800
LNWLRFSWAQ	GTDTILADEM	GLGKTVQTAV	FLYSLYKEGH	SKGPFLVSAP	LSTIINWERE	FEMWAPDMYV	VTYVGDKDSR
810	820	830	840	850	860	870	880
AIIRENEFSF	EDNAIRGGKK	ASRMKKEASV	KFHVLLTSYE	LITIDMAILG	SIDWACLIVD	EAHRLKNNQS	KFFRVLNGYS
890	900	910	920	930	940	950	960
LQHKLLLTGT	PLQNNLEELF	HLLNFLTPER	FHNLEGFLEE	FADIAKEDQI	KKLHDMLGPH	MLRRLKADVF	KNMPSKTELI
970	980	990	1000	1010	1020	1030	1040
VRVELSPMQK	KYYKYILTRN	FEALNARGGG	NQVSLLNVVM	DLKKCCNHPY	LFPVAAMEAP	KMPNGMYDGS	ALIRASGKLL
1050	1060	1070	1080	1090	1100	1110	1120
LLQKMLKNLK	EGGHRVLIFS	QMTKMLDLLE	DFLEHEGYKY	ERIDGGITGN	MRQEAIDRFN	APGAQQFCFL	LSTRAGGLGI
1130	1140	1150	1160	1170	1180	1190	1200
NLATADTVII	YDSDWNPHND	IQAFSRAHRI	GQNKKVMIYR	FVTRASVEER	ITQVAKKKMM	LTHLVVRPGL	GSKTGSMSKQ
1210	1220	1230	1240	1250	1260	1270	1280
ELDDILKFGT	EELFKDEATD	GGGDNKEGED	SSVIHYDDKA	IERLLDRNQD	ETEDTELQGM	NEYLSSFKVA	QYVVREEEMG
1290	1300	1310	1320	1330	1340	1350	1360
EEEEVEREII	KQEESVDPDY	WEKLLRHHYE	QQQEDLARNL	GKGKRIRKQV	NYNDGSQEDR	DWQDDQSDNQ	SDYSVASEEG
1370	1380	1390	1400	1410	1420	1430	1440
DEDFDERSEA	PRRPSRKGLR	NDKDKPLPPL	LARVGGNIEV	LGFNARQRKA	FLNAIMRYGM	PPQDAFTTQW	LVRDLRGKSE
1450	1460	1470	1480	1490	1500	1510	1520
KEFKAYVSLF	MRHLCEPGAD	GAETFADGVP	REGLSRQHVL	TRIGVMSLIR	KKVQEFEHVN	GRWSMPELAE	VEENKKMSQP
1530	1540	1550	1560	1570	1580	1590	1600
GSPSPKTPTP	STPGDTQPNT	PAPVPPAEDG	IKIEENSLKE	EESIEGEKEV	KSTAPETAIE	CTQAPAPASE	DEKVVVEPPE
1610	1620	1630	1640	1650	1660	1670	1680
GEEKVEKAEV	KERTEEPMET	EPKGKGAADV	EKVEEKSAID	LTPIVVEDKE	EKKEEEEKKE	VMLQNGETPK	DLNDEKQKKN
1690	1700	1710	1720	1730	1740	1750	1760
IKQRFMFNIA	DGGFTELHSL	WQNEERAATV	TKKTYEIWHR	RHDYWLLAGI	INHGYARWQD	IQNDPRYAIL	NEPFKGEMNR
1770	1780	1790	1800	1810	1820	1830	1840
GNFLEIKNKF	LARRFKLLEQ	ALVIEEQLRR	AAYLNMSEDP	SHPSMALNTR	FAEVECLAES	HQHLSKESMA	GNKPANAVLH
1850	1860	1870	1880	1890	1900	1910	
KGILKQLEEL	LSDMKADVTR	LPATIARIPP	VAVRLQMSER	NILSRLANRA	PEPTPQQVAQ	QQ	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2366	1	649.8737	-146.01	3	59.4	13.6	0	1005-1021	K.CCNHPYLFPVAAMEAPK.M	Carbamidomethyl: 1
505	1	699.1373	103.36	3	35.9	10.8	2	1868-1885	R.IPPVAVRLQMSERNILSR.L	Oxidation: 10

Detailed Protein Report

Protein 106: **metallothionein-1G [Homo sapiens]**

Accession:	gi|10835230	**Score:**	41.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	6.1
Database Date:	2015-11-30	**pI:**	10.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	91.8
		No. of unique Peptides:	3



```
          10        20        30        40        50        60        70
MDPNCSCAAG VSCTCASSCK CKECKCTSCK KSCCSCCPVG CAKCAQGCIC KGASEKCSCC A
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
834	1	703.6768	119.69	3	39.8	13.8	0	1-20	-.MDPNCSCAAGVSCTCASSCK.C	Carbamidomethyl: 5, 15, 19
2136	1	1019.7667	-122.67	2	56.9	14.5	2	26-43	K.CTSCKKSCCSCCPVGCAK.C	Carbamidomethyl: 1, 11, 12, 16
1283	1	882.7587	-88.50	2	45.6	13.5	2	44-61	K.CAQGCICKGASEKCSCCA.-	

Detailed Protein Report

Protein 107: ectonucleoside triphosphate diphosphohydrolase 4 isoform b [Homo sapiens]

Accession:	gi|193083168	**Score:**	41.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	69.4
Database Date:	2015-11-30	**pI:**	9.3
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	7.2
		No. of unique Peptides:	3

```
        10         20         30         40         50         60         70         80
MGRIGISCLF PASWHFSISP VGCPRILNTN LRQIMVISVL AAAVSLLYFS VVIIRNKYGR LTRDKKFQRY LARVTDIEAT
        90        100        110        120        130        140        150        160
DTNNPNVNYG IVVDCGSSGS RVFVYCWPRH NGNPHDLLDI RQMRDKNRKP VVMKIKPGIS EFATSPEKVS DYISPLLNFA
       170        180        190        200        210        220        230        240
AEHVPRAKHK ETPLYILCTA GMRILPESQQ KAILEDLLTD IPVHFDFLFS DSHAEVISGK QEGVYAWIGI NFVLGRFEHI
       250        260        270        280        290        300        310        320
EDDDEAVVEV NIPGSESSEA IVRKRTAGIL DMGGVSTQIA YEVPKTEEVA KNLLAEFNLG CDVHQTEHVY RVYVATFLGF
       330        340        350        360        370        380        390        400
GGNAARQRYE DRIFANTIQK NRLLGKQTGL TPDMPYLDPC LPLDIKDEIQ QNGQTIYLRG TGDFDLCRET IQPFMNKTNE
       410        420        430        440        450        460        470        480
TQTSLNGVYQ PPIHFQNSEF YGFSEFYYCT EDVLRMGGDY NAAKFTKAAK DYCATKWSIL RERFDRGLYA SHADLHRLKY
       490        500        510        520        530        540        550        560
QCFKSAWMFE VFHRGFSFPV NYKSLKTALQ VYDKEVQWTL GAILYRTRFL PLRDIQQEAF RASHTHWRGV SFVYNHYLFS
       570        580        590        600        610
GCFLVVLLAI LLYLLRLRRI HRRTPRSSSA AALWMEEGLP AQNAPGTL
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2648	1	994.9726	-51.73	2	63.2	14.2	2	167-183	R.AKHKETPLYILCTAGMR.I	Carbamidomethyl: 12
2772	1	696.6903	49.74	3	65.0	14.8	1	380-397	R.GTGDFDLCRETIQPFMNK.T	Oxidation: 16
1075	1	463.6184	-187.66	2	43.0	12.9	0	436-444	R.MGGDYNAAK.F	

Detailed Protein Report

Protein 108: dedicator of cytokinesis protein 6 [Homo sapiens]

Accession:	gi|157426887	**Score:**	41.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	229.4
Database Date:	2015-11-30	**pI:**	6.3
		Sequence Coverage [%]:	1.4
		No. of unique Peptides:	2

Quantitation

MD:MU	**Median:** 0.36	**CV:** 0.00 %	**No. of Peptides:** 1

Detailed Protein Report

10	20	30	40	50	60	70	80
MAASERRAFA	HKINRTVAAE	VRKQVSRERS	GSPHSSRRCS	SSLGVPLTEV	VEPLDFEDVL	LSRPPDAEPG	PLRDLVEFPA
90	100	110	120	130	140	150	160
DDLELLLQPR	ECRTTEPGIP	KDEKLDAQVR	AAVEMYIEDW	VIVHRRYQYL	SAAYSPVTTD	TQRERQKGLP	RQVFEQDASG
170	180	190	200	210	220	230	240
DERSGPEDSN	DSRRGSGSPE	DTPRSSGASS	IFDLRNLAAD	SLLPSLLERA	APEDVDRRNE	TLRRQHRPPA	LLTLYPAPDE
250	260	270	280	290	300	310	320
DEAVERCSRP	EPPREHFGQR	ILVKCLSLKF	EIEIEPIFGI	LALYDVREKK	KISENFYFDL	NSDSMKGLLR	AHGTHPAIST
330	340	350	360	370	380	390	400
LARSAIFSVT	YPSPDIFLVI	KLEKVLQQGD	ISECCEPYMV	LKEVDTAKNK	EKLEKLRLAA	EQFCTRLGRY	RMPFAWTAVH
410	420	430	440	450	460	470	480
LANIVSSAGQ	LDRDSDSEGE	RRPAWTDRRR	RGPQDRASSG	DDACSFSGFR	PATLTVTNFF	KQEAERLSDE	DLFKFLADMR
490	500	510	520	530	540	550	560
RPSSLLRRLR	PVTAQLKIDI	SPAPENPHFC	LSPELLHIKP	YPDPRGRPTK	EILEFPAREV	YAPHTSYRNL	LYVYPHSLNF
570	580	590	600	610	620	630	640
SSRQGSVRNL	AVRVQYMTGE	DPSQALPVIF	GKSSCSEFTR	EAFTPVVYHN	KSPEFYEEFK	LHLPACVTEN	HHLLFTFYHV
650	660	670	680	690	700	710	720
SCQPRPGTAL	ETPVGFTWIP	LLQHGRLRTG	PFCLPVSVDQ	PPPSYSVLTP	DVALPGMRWV	DGHKGVFSVE	LTAVSSVHPQ
730	740	750	760	770	780	790	800
DPYLDKFFTL	VHVLEEGAFP	FRLKDTVLSE	GNVEQELRAS	LAALRLASPE	PLVAFSHHVL	DKLVRLVIRP	PIISGQIVNL
810	820	830	840	850	860	870	880
GRGAFEAMAH	VVSLVHRSLE	AAQDARGHCP	QLAAYVHYAF	RLPGTEPSLP	DGAPPVTVQA	ATLARGSGRP	ASLYLARSKS
890	900	910	920	930	940	950	960
ISSSNPDLAV	APGSVDDEVS	RILASKLLHE	ELALQWVVSS	SAVREAILQH	AWFFFQLMVK	SMALHLLLGQ	RLDTPRKLRF
970	980	990	1000	1010	1020	1030	1040
PGRFLDDITA	LVGSVGLEVI	TRVHKDVELA	EHLNASLAFF	LSDLLSLVDR	GFVFSLVRAH	YKQVATRLQS	SPNPAALLTL
1050	1060	1070	1080	1090	1100	1110	1120
RMEFTRILCS	HEHYVTLNLP	CCPLSPPASP	SPSVSSTTSQ	SSTFSSQAPD	PKVTSMFELS	GPFRQQHFLA	GLLLTELALA
1130	1140	1150	1160	1170	1180	1190	1200
LEPEAEGAFL	LHKKAISAVH	SLLCGHDTDP	RYAEATVKAR	VAELYLPLLS	IARDTLPRLH	DFAEGPGQRS	RLASMLDSDT
1210	1220	1230	1240	1250	1260	1270	1280
EGEGDIAGTI	NPSVAMAIAG	GPLAPGSRAS	ISQGPPTASR	AGCALSAESS	RTLLACVLWV	LKNTEPALLQ	RWATDLTLPQ
1290	1300	1310	1320	1330	1340	1350	1360
LGRLLDLLYL	CLAAFEYKGK	KAFERINSLT	FKKSLDMKAR	LEEAILGTIG	ARQEMVRRSR	ERSPFGNPEN	VRWRKSVTHW
1370	1380	1390	1400	1410	1420	1430	1440
KQTSDRVDKT	KDEMEHEALV	EGNLATEASL	VVLDTLEIIV	QTVMLSEARE	SVLGAVLKVV	LYSLGSAQSA	LFLQHGLATQ
1450	1460	1470	1480	1490	1500	1510	1520
RALVSKFPEL	LFEEDTELCA	DLCLRLLRHC	GSRISTIRTH	ASASLYLLMR	QNFEIGHNFA	RVKMQVTMSL	SSLVGTTQNF
1530	1540	1550	1560	1570	1580	1590	1600
SEEHLRRSLK	TILTYAEEDM	GLRDSTFAEQ	VQDLMFNLHM	ILTDTVKMKE	HQEDPEMLID	LMYRIARGYQ	GSPDLRLTWL
1610	1620	1630	1640	1650	1660	1670	1680
QNMAGKHAEL	GNHAEAAQCM	VHAAALVAEY	LALLEDHRHL	PVGCVSFQNI	SSNVLEESAI	SDDILSPDEE	GFCSGKHFTE
1690	1700	1710	1720	1730	1740	1750	1760
LGLVGLLEQA	AGYFTMGGLY	EAVNEVYKNL	IPILEAHRDY	KKLAAVHGKL	QEAFTKIMHQ	SSGWERVFGT	YFRVGFYGAH
1770	1780	1790	1800	1810	1820	1830	1840
FGDLDEQEFV	YKEPSITKLA	EISHRLEEFY	TERFGDDVVE	IIKDSNPVDK	SKLDSQKAYI	QITYVEPYFD	TYELKDRVTY
1850	1860	1870	1880	1890	1900	1910	1920
FDRNYGLRTF	LFCTPFTPDG	RAHGELPEQH	KRKTLLSTDH	AFPYIKTRIR	VCHREETVLT	PVEVAIEDMQ	KKTRELAFAT
1930	1940	1950	1960	1970	1980	1990	2000
EQDPPDAKML	QMVLQGSVGP	TVNQGPLEVA	QVFLAEIPED	PKLFRHHNKL	RLCFKDFCKK	CEDALRKNKA	LIGPDQKEYH
2010	2020	2030	2040	2050			
RELERNYCRL	REALQPLLTQ	RLPQLMAPTP	PGLRNSLNRA	SFRKADL			

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
1750	1	628.2499	-105.50	2	51.8	11.8	2	28-38	R.ERSGSPHSSRR.C		
1355	1	695.8559	-59.65	2	46.5	14.1	0	2022-2034	R.LPQLMAPTPPGLR.N		MD:MU 0.36

Detailed Protein Report

Protein 109: transcription initiation factor TFIID subunit 4 [Homo sapiens]

Accession:	gi|110832843	**Score:**	41.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	110.0
Database Date:	2015-11-30	**pI:**	10.6
		Sequence Coverage [%]:	2.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAAGSDLLDE	VFFNSEVDEK	VVSDLVGSLE	SQLAASAAHH	HHLAPRTPEV	RAAAAGALGN	HVVSGSPAGA	AGAGPAAPAE
90	100	110	120	130	140	150	160
GAPGAAPEPP	PAGRARPGGG	GPQRPGPPSP	RRPLVPAGPA	PPAAKLRPPP	EGSAGSCAPV	PAAAAVAAGP	EPAPAGPAKP
170	180	190	200	210	220	230	240
AGPAALAARA	GPGPGPGPGP	GPGPGPGKPA	GPGAAQTLNG	SAALLNSHHA	AAPAVSLVNN	GPAALLPLPK	PAAPGTVIQT
250	260	270	280	290	300	310	320
PPFVGAAAPP	APAAPSPPAA	PAPAAPAAAP	PPPPPAPATL	ARPPGHPAGP	PTAAPAVPPP	AAAQNGGSAG	AAPAPAPAAG
330	340	350	360	370	380	390	400
GPAGVSGQPG	PGAAAAAPAP	GVKAESPKRV	VQAAPPAAQT	LAASGPASTA	ASMVIGPTMQ	GALPSPAAVP	PPAPGTPTGL
410	420	430	440	450	460	470	480
PKGAAGAVTQ	SLSRTPTATT	SGIRATLTPT	VLAPRLPQPP	QNPTNIQNFQ	LPPGMVLVRS	ENGQLLMIPQ	QALAQMQAQA
490	500	510	520	530	540	550	560
HAQPQTTMAP	RPATPTSAPP	VQISTVQAPG	TPIIARQVTP	TTIIKQVSQA	QTTVQPSATL	QRSPGVQPQL	VLGGAAQTAS
570	580	590	600	610	620	630	640
LGTATAVQTG	TPQRTVPGAT	TTSSAATETM	ENVKKCKNFL	STLIKLASSG	KQSTETAANV	KELVQNLLDG	KIEAEDFTSR
650	660	670	680	690	700	710	720
LYRELNSSPQ	PYLVPFLKRS	LPALRQLTPD	SAAFIQQSQQ	QPPPPTSQAT	TALTAVVLSS	SVQRTAGKTA	ATVTSALQPP
730	740	750	760	770	780	790	800
VLSLTQPTQV	GVGKQGQPTP	LVIQQPPKPG	ALIRPPQVTL	TQTPMVALRQ	PHNRIMLTTP	QQIQLNPLQP	VPVVKPAVLP
810	820	830	840	850	860	870	880
GTKALSAVSA	QAAAAQKNKL	KEPGGGSFRD	DDDINDVASM	AGVNLSEESA	RILATNSELV	GTLTRSCKDE	TFLLQAPLQR
890	900	910	920	930	940	950	960
RILEIGKKHG	ITELHPDVVS	YVSHATQQRL	QNLVEKISET	AQQKNFSYKD	DDRYEQASDV	RAQLKFFEQL	DQIEKQRKDE
970	980	990	1000	1010	1020	1030	1040
QEREILMRAA	KSRSRQEDPE	QLRLKQKAKE	MQQQELAQMR	QRDANLTALA	AIGPRKKRKV	DCPGPGSGAE	GSGPGSVVPG
1050	1060	1070	1080	1090			
SSGVGTPRQF	TRQRITRVNL	RDLIFCLENE	RETSHSLLLY	KAFLK			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1978	1	643.7875	-107.62	2	54.6	19.5	0	804-817	K.ALSAVSAQAAAAQK.N	

Detailed Protein Report

Protein 110: probable ATP-dependent RNA helicase DDX58 [Homo sapiens]

Accession: gi|27881482
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 41.4
MW [kDa]: 106.5
pI: 6.0
Sequence Coverage [%]: 3.8
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MTTEQRRSLQ	AFQDYIRKTL	DPTYILSYMA	PWFREEEVQY	IQAEKNNKGP	MEAATLFLKF	LLELQEEGWF	RGFLDALDHA
90	100	110	120	130	140	150	160
GYSGLYEAIE	SWDFKKIEKL	EEYRLLLKRL	QPEFKTRIIP	TDIISDLSEC	LINQECEEIL	QICSTKGMMA	GAEKLVECLL
170	180	190	200	210	220	230	240
RSDKENWPKT	LKLALEKERN	KFSELWIVEK	GIKDVETEDL	EDKMETSDIQ	IFYQEDPECQ	NLSENSCPPS	EVSDTNLYSP
250	260	270	280	290	300	310	320
FKPRNYQLEL	ALPAMKGKNT	IICAPTGCGK	TFVSLLICEH	HLKKFPQGQK	GKVVFFANQI	PVYEQQKSVF	SKYFERHGYR
330	340	350	360	370	380	390	400
VTGISGATAE	NVPVEQIVEN	NDIIILTPQI	LVNNLKKGTI	PSLSIFTLMI	FDECHNTSKQ	HPYNMIMFNY	LDQKLGGSSG
410	420	430	440	450	460	470	480
PLPQVIGLTA	SVGVGDAKNT	DEALDYICKL	CASLDASVIA	TVKHNLEELE	QVVYKPQKFF	RKVESRISDK	FKYIIAQLMR
490	500	510	520	530	540	550	560
DTESLAKRIC	KDLENLSQIQ	NREFGTQKYE	QWIVTVQKAC	MVFQMPDKDE	ESRICKALFL	YTSHLRKYND	ALIISEHARM
570	580	590	600	610	620	630	640
KDALDYLKDF	FSNVRAAGFD	EIEQDLTQRF	EEKLQELESV	SRDPSNENPK	LEDLCFILQE	EYHLNPETIT	ILFVKTRALV
650	660	670	680	690	700	710	720
DALKNWIEGN	PKLSFLKPGI	LTGRGKTNQN	TGMTLPAQKC	ILDAFKASGD	HNILIATSVA	DEGIDIAQCN	LVILYEYVGN
730	740	750	760	770	780	790	800
VIKMIQTRGR	GRARGSKCFL	LTSNAGVIEK	EQINMYKEKM	MNDSILRLQT	WDEAVFREKI	LHIQTHEKFI	RDSQEKPKPV
810	820	830	840	850	860	870	880
PDKENKKLLC	RKCKALACYT	ADVRVIEECH	YTVLGDAFKE	CFVSRPHPKP	KQFSSFEKRA	KIFCARQNCS	HDWGIHVKYK
890	900	910	920	930			
TFEIPVIKIE	SFVVEDIATG	VQTLYSKWKD	FHFEKIPFDP	AEMSK			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1833	1	599.7809	-18.91	2	52.9	13.8	1	751-759	K.EQINMYKEK.M	Oxidation: 5

Detailed Protein Report

Protein 111: hemopexin precursor [Homo sapiens]

Accession:	gi|11321561	**Score:**	41.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	51.6
Database Date:	2015-11-30	**pI:**	6.6
		Sequence Coverage [%]:	9.5
		No. of unique Peptides:	1

Quantitation

MD:MU	**Median:**	1.18	**CV:**	0.00 %	**No. of Peptides:**	1

Alias proteins:

Accession	Name	Description
gi|530395269	refseq_human (refseq_human_20140103.fasta)	PREDICTED: hemopexin isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MARVLGAPVA	LGLWSLCWSL	AIATPLPPTS	AHGNVAEGET	KPDPDVTERC	SDGWSFDATT	LDDNGTMLFF	KGEFVWKSHK
90	100	110	120	130	140	150	160
WDRELISERW	KNFPSPVDAA	FRQGHNSVFL	IKGDKVWVYP	PEKKEKGYPK	LLQDEFPGIP	SPLDAAVECH	RGECQAEGVL
170	180	190	200	210	220	230	240
FFQGDREWFW	DLATGTMKER	SWPAVGNCSS	ALRWLGRYYC	FQGNQFLRFD	PVRGEVPPRY	PRDVRDYFMP	CPGRGHGHRN
250	260	270	280	290	300	310	320
GTGHGNSTHH	GPEYMRCSPH	LVLSALTSDN	HGATYAFSGT	HYWRLDTSRD	GWHSWPIAHQ	WPQGPSAVDA	AFSWEEKLYL
330	340	350	360	370	380	390	400
VQGTQVYVFL	TKGGYTLVSG	YPKRLEKEVG	TPHGIILDSV	DAAFICPGSS	RLHIMAGRRL	WWLDLKSGAQ	ATWTELPWPH
410	420	430	440	450	460	470	
EKVDGALCME	KSLGPNSCSA	NGPGLYLIHG	PNLYCYSDVE	KLNAAKALPQ	PQNVTSLLGC	TH	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
1637	2	919.3696	-84.22	2	50.2	24.4	0	387-402	K.SGAQATWTELPWPHEK.V		MD:MU	1.18

Detailed Protein Report

Protein 112: complement receptor type 1 isoform F precursor [Homo sapiens]

Accession:	gi|86793036	**Score:**	41.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	223.5
Database Date:	2015-11-30	**pI:**	6.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.8
		No. of unique Peptides:	1

Quantitation

MD:MU	**Median:**	0.35	**CV:**	0.00 %	**No. of Peptides:**	1

10	20	30	40	50	60	70	80
MGASSPRSPE	PVGPPAPGLP	FCCGGSLLAV	VVLLALPVAW	GQCNAPEWLP	FARPTNLTDE	FEFPIGTYLN	YECRPGYSGR
90	100	110	120	130	140	150	160
PFSIICLKNS	VWTGAKDRCR	RKSCRNPPDP	VNGMVHVIKG	IQFGSQIKYS	CTKGYRLIGS	SSATCIISGD	TVIWDNETPI
170	180	190	200	210	220	230	240
CDRIPCGLPP	TITNGDFIST	NRENFHYGSV	VTYRCNPGSG	GRKVFELVGE	PSIYCTSNDD	QVGIWSGPAP	QCIIPNKCTP
250	260	270	280	290	300	310	320
PNVENGILVS	DNRSLFSLNE	VVEFRCQPGF	VMKGPRRVKC	QALNKWEPEL	PSCSRVCQPP	PDVLHAERTQ	RDKDNFSPGQ
330	340	350	360	370	380	390	400
EVFYSCEPGY	DLRGAASMRC	TPQGDWSPAA	PTCEVKSCDD	FMGQLLNGRV	LFPVNLQLGA	KVDFVCDEGF	QLKGSSASYC
410	420	430	440	450	460	470	480
VLAGMESLWN	SSVPVCEQIF	CPSPPVIPNG	RHTGKPLEVF	PFGKTVNYTC	DPHPDRGTSF	DLIGESTIRC	TSDPQGNGVW
490	500	510	520	530	540	550	560
SSPAPRCGIL	GHCQAPDHFL	FAKLKTQTNA	SDFPIGTSLK	YECRPEYYGR	PFSITCLDNL	VWSSPKDVCK	RKSCKTPPDP
570	580	590	600	610	620	630	640
VNGMVHVITD	IQVGSRINYS	CTTGHRLIGH	SSAECILSGN	AAHWSTKPPI	CQRIPCGLPP	TIANGDFIST	NRENFHYGSV
650	660	670	680	690	700	710	720
VTYRCNPGSG	GRKVFELVGE	PSIYCTSNDD	QVGIWSGPAP	QCIIPNKCTP	PNVENGILVS	DNRSLFSLNE	VVEFRCQPGF
730	740	750	760	770	780	790	800
VMKGPRRVKC	QALNKWEPEL	PSCSRVCQPP	PDVLHAERTQ	RDKDNFSPGQ	EVFYSCEPGY	DLRGAASMRC	TPQGDWSPAA
810	820	830	840	850	860	870	880
PTCEVKSCDD	FMGQLLNGRV	LFPVNLQLGA	KVDFVCDEGF	QLKGSSASYC	VLAGMESLWN	SSVPVCEQIF	CPSPPVIPNG
890	900	910	920	930	940	950	960
RHTGKPLEVF	PFGKAVNYTC	DPHPDRGTSF	DLIGESTIRC	TSDPQGNGVW	SSPAPRCGIL	GHCQAPDHFL	FAKLKTQTNA
970	980	990	1000	1010	1020	1030	1040
SDFPIGTSLK	YECRPEYYGR	PFSITCLDNL	VWSSPKDVCK	RKSCKTPPDP	VNGMVHVITD	IQVGSRINYS	CTTGHRLIGH
1050	1060	1070	1080	1090	1100	1110	1120
SSAECILSGN	TAHWSTKPPI	CQRIPCGLPP	TIANGDFIST	NRENFHYGSV	VTYRCNLGSR	GRKVFELVGE	PSIYCTSNDD
1130	1140	1150	1160	1170	1180	1190	1200
QVGIWSGPAP	QCIIPNKCTP	PNVENGILVS	DNRSLFSLNE	VVEFRCQPGF	VMKGPRRVKC	QALNKWEPEL	PSCSRVCQPP
1210	1220	1230	1240	1250	1260	1270	1280
PEILHGEHTP	SHQDNFSPGQ	EVFYSCEPGY	DLRGAASLHC	TPQGDWSPEA	PRCAVKSCDD	FLGQLPHGRV	LFPLNLQLGA
1290	1300	1310	1320	1330	1340	1350	1360
KVSFVCDEGF	RLKGSSVSHC	VLVGMRSLWN	NSVPVCEHIF	CPNPPAILNG	RHTGTPSGDI	PYGKEISYTC	DPHPDRGMTF
1370	1380	1390	1400	1410	1420	1430	1440
NLIGESTIRC	TSDPHGNGVW	SSPAPRCELS	VRAGHCKTPE	QFPFASPTIP	INDFEFPVGT	SLNYECRPGY	FGKMFSISCL
1450	1460	1470	1480	1490	1500	1510	1520
ENLVWSSVED	NCRRKSCGPP	PEPFNGMVHI	NTDTQFGSTV	NYSCNEGFRL	IGSPSTTCLV	SGNNVTWDKK	APICEIISCE
1530	1540	1550	1560	1570	1580	1590	1600
PPPTISNGDF	YSNNRTSFHN	GTVVTYQCHT	GPDGEQLFEL	VGERSIYCTS	KDDQVGVWSS	PPPRCISTNK	CTAPEVENAI
1610	1620	1630	1640	1650	1660	1670	1680
RVPGNRSFFT	LTEIIRFRCQ	PGFVMVGSHT	VQCQTNGRWG	PKLPHCSRVC	QPPPEILHGE	HTLSHQDNFS	PGQEVFYSCE
1690	1700	1710	1720	1730	1740	1750	1760
PSYDLRGAAS	LHCTPQGDWS	PEAPRCTVKS	CDDFLGQLPH	GRVLLPLNLQ	LGAKVSFVCD	EGFRLKGRSA	SHCVLAGMKA
1770	1780	1790	1800	1810	1820	1830	1840
LWNSSVPVCE	QIFCPNPPAI	LNGRHTGTPF	GDIPYGKEIS	YACDTHPDRG	MTFNLIGESS	IRCTSDPQGN	GVWSSPAPRC
1850	1860	1870	1880	1890	1900	1910	1920
ELSVPAACPH	PPKIQNGHYI	GGHVSLYLPG	MTISYICDPG	YLLVGKGFIF	CTDQGIWSQL	DHYCKEVNCS	FPLFMNGISK
1930	1940	1950	1960	1970	1980	1990	2000
ELEMKKVYHY	GDYVTLKCED	GYTLEGSPWS	QCQADDRWDP	PLAKCTSRTH	DALIVGTLSG	TIFFILLIIF	LSWIILKHRK
2010	2020	2030	2040				
GNNAHENPKE	VAIHLHSQGG	SSVHPRTLQT	NEENSRVLP				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
73	1	826.3528	-22.94	3	30.6	30.9	1	334-356	R.GAASMRCTPQGDWSPAAPTCEVS	Carbamidomethyl: 7, 20	MD:MU 0.35

Detailed Protein Report

Protein 113: **PREDICTED: cleavage and polyadenylation specificity factor subunit 1 isoform X2 [Homo sapiens]**

Accession:	gi|578815945	**Score:**	41.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	151.9
Database Date:	2015-11-30	**pI:**	5.9
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	3.2
		No. of unique Peptides:	3

10	20	30	40	50	60	70	80
MSMASVQLAG	AKRDALLLSF	KDAKLSVVEY	DPGTHDLKTL	SLHYFEEPEL	RDGFVQNVHT	PRVRVDPDGR	CAAMLVYGTR
90	100	110	120	130	140	150	160
LVVLPFRRES	LAEEHEGLVG	EGQRSSFLPS	YIIDVRALDE	KLLNIIDLQF	LHGYYEPTLL	ILFEPNQTWP	GRVAVRQDTC
170	180	190	200	210	220	230	240
SIVAISLNIT	QKVHPVIWSL	TSLPFDCTQA	LAVPKPIGGV	VVFAVNSLLY	LNQSVPPYGV	ALNSLTTGTT	AFPLRTQEGV
250	260	270	280	290	300	310	320
RITLDCAQAT	FISYDKMVIS	LKGGEIYVLT	LITDGMRSVR	AFHFDKAAAS	VLTTSMVTME	PGYLFLGSRL	GNSLLLKYTE
330	340	350	360	370	380	390	400
KLQEPPASAV	REAADKEEPP	SKKKRVDATA	GWSAAGKSVP	QDEVDEIEVY	GSEAQSGTQL	ATYSFEVCDS	ILNIGPCANA
410	420	430	440	450	460	470	480
AVGEPAFLSE	EFQNSPEPDL	EIVVCSGHGK	NGALSVLQKS	IRPQVVTTFE	LPGCYDMWTV	IAPVRKEEED	NPKGEGTEQE
490	500	510	520	530	540	550	560
PSTTPEADDD	GRRHGFLILS	REDSTMILQT	GQEIMELDTS	GFATQGPTVF	AGNIGDNRYI	VQVSPLGIRL	LEGVNQLHFI
570	580	590	600	610	620	630	640
PVDLGAPIVQ	CAVADPYVVI	MSAEGHVTMF	LLKSDSYGGR	HHRLALHKPP	LHHQSKVITL	CLYRDLSGMF	TTESRLGGAR
650	660	670	680	690	700	710	720
DELGGRSGPE	AEGLGSETSP	TVDDEEEMLY	GDSGSLFSPS	KEEARRSSQP	PADRDPAPFR	AEPTHWCLLV	RENGTMEIYQ
730	740	750	760	770	780	790	800
LPDWRLVFLV	KNFPVGQRVL	VDSSFGQPTT	QGEARREEAT	RQGELPLVKE	VLLVALGSRQ	SRPYLLVHVD	QELLIYEAFP
810	820	830	840	850	860	870	880
HDSQLGQGNL	KVRFKKVPHN	INFREKKPKP	SKKKAEGGGA	EEGAGARGRV	ARFRYFEDIY	GYSGVFICGP	SPHWLLVTGR
890	900	910	920	930	940	950	960
GALRLHPMAI	DGPVDSFAPF	HNVNCPRGFL	YFNRQGELRI	SVLPAYLSYD	APWPVRKIPL	RCTAHYVAYH	VESKVYAVAT
970	980	990	1000	1010	1020	1030	1040
STNTPCARIP	RMTGEEKEFE	TIERDERYIH	PQQEAFSIQL	ISPVSWEAIP	NARIELQEWE	HVTCMKTVSL	RSEETVSGLK
1050	1060	1070	1080	1090	1100	1110	1120
GYVAAGTCLM	QGEEVTCRGR	ILIMDVIEVV	PEPGQPLTKN	KFKVLYEKEQ	KGPVTALCHC	NGHLVSAIGQ	KIFLWSLRAS
1130	1140	1150	1160	1170	1180	1190	1200
ELTGMAFIDT	QLYIHQMISV	KNFILAADVM	KSISLLRYQE	ESKTLSLVSR	DAKPLEVYSV	DFMVDNAQLG	FLVSDRDRNL
1210	1220	1230	1240	1250	1260	1270	1280
MVYMYLPEAK	ESFGGMRLLR	RADFHVGAHV	NTFWRTPCRG	ATEGLSKKSV	VWENKHITWF	ATLDGGIGLL	LPMQEKTYRR
1290	1300	1310	1320	1330	1340	1350	1360
LLMLQNALTT	MLPHHAGLNP	RAFRMLHVDR	RTLQNAVRNV	LDGELLNRYL	YLSTMERSEL	AKKIGTTPDI	ILDDLLETDR
1370							
VTAHF							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2669	1	948.3641	-105.24	2	64.6	16.7	1	88-104	R.RESLAEEHEGLVGEGQR.S	
297	1	626.2973	-49.17	3	33.4	14.0	1	955-971	K.VYAVATSTNTPCARIPR.M	Carbamidomethyl: 12
2457	1	596.2158	-123.37	2	61.1	10.4	0	1329-1337	R.YLYLSTMER.S	Oxidation: 7

Detailed Protein Report

Protein 114: histone H4 [Homo sapiens]

Accession:	gi|4504301	**Score:**	41.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	11.4
Database Date:	2015-11-30	**pI:**	11.8
		Sequence Coverage [%]:	7.8
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 0.60 **CV:** 0.00 % **No. of Peptides:** 1

Alias proteins:

Accession	Name	Description
gi|77539758	refseq_human (refseq_human_20140103.fasta)	histone H4 [Homo sapiens]
gi|28173560	refseq_human (refseq_human_20140103.fasta)	histone H4 [Homo sapiens]
gi|11415030	refseq_human (refseq_human_20140103.fasta)	histone H4 [Homo sapiens]
gi|4504323	refseq_human (refseq_human_20140103.fasta)	histone H4 [Homo sapiens]
gi|4504321	refseq_human (refseq_human_20140103.fasta)	histone H4 [Homo sapiens]
gi|4504317	refseq_human (refseq_human_20140103.fasta)	histone H4 [Homo sapiens]
gi|4504315	refseq_human (refseq_human_20140103.fasta)	histone H4 [Homo sapiens]
gi|4504313	refseq_human (refseq_human_20140103.fasta)	histone H4 [Homo sapiens]
gi|4504311	refseq_human (refseq_human_20140103.fasta)	histone H4 [Homo sapiens]
gi|4504309	refseq_human (refseq_human_20140103.fasta)	histone H4 [Homo sapiens]
gi|4504307	refseq_human (refseq_human_20140103.fasta)	histone H4 [Homo sapiens]
gi|4504305	refseq_human (refseq_human_20140103.fasta)	histone H4 [Homo sapiens]
gi|4504303	refseq_human (refseq_human_20140103.fasta)	histone H4 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MSGRGKGGKG LGKGGAKRHR KVLRDNIQGI TKPAIRRLAR RGGVKRISGL IYEETRGVLK VFLENVIRDA VTYTEHAKRK
        90        100        110
TVTAMDVVYA LKRQGRTLYG FGG
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1293	7	495.1457	-296.53	2	45.8	41.1	0	61-68	K.VFLENVIR.D		MD:MU 0.60

Detailed Protein Report

Protein 115: PREDICTED: muskelin isoform X4 [Homo sapiens]

Accession: gi|578814266
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 40.9
MW [kDa]: 80.3
pI: 6.1
Sequence Coverage [%]: 3.7
No. of unique Peptides: 2

10	20	30	40	50	60	70	80
MAAGGAVAAA	PECRLLPYAL	HKWSSFSSTY	LPENILVDKP	NDQSSRWSSE	SNYPPQYLIL	KLERPAIVQN	ITFGKYEKTH
90	100	110	120	130	140	150	160
VCNLKKFKVF	GGMNEENMTE	LLSSGLKNDY	NKETFTLKHK	IDEQMFPCRF	IKIVPLLSWG	PSFNFSIWYV	ELSGIDDPDI
170	180	190	200	210	220	230	240
VQPCLNWYSK	YREQEAIRLC	LKHFRQHNYT	EAFESLQKKT	KIALEHPMLT	DIHDKLVLKG	DFDACEELIE	KAVNDGLFNQ
250	260	270	280	290	300	310	320
YISQQEYKPR	WSQIIPKSTK	GDGEDNRPGM	RGGHQMVIDV	QTETVYLFGG	WDGTQDLADF	WAYSVKENQW	TCISRDTEKE
330	340	350	360	370	380	390	400
NGPSARSCHK	MCIDIQRRQI	YTLGRYLDSS	VRNSKSLKSD	FYRYDIDTNT	WMLLSEDTAA	DGGPKLVFDH	QMCMDSEKHM
410	420	430	440	450	460	470	480
IYTFGGRILT	CNGSVDDSRA	SEPQFSGLFA	FNCQCQTWKL	LREDSCNAGP	EDIQSRIGHC	MLFHSKNRCL	YVFGGQRSKT
490	500	510	520	530	540	550	560
YLNDFFSYDV	DSDHVDIISD	GTKKDSGMVP	MTGFTQRATI	DPELNEIHVL	SGLSKDKEKR	EENVRNSFWI	YDIVRNSWSC
570	580	590	600	610	620	630	640
VYKNDQAAKD	NPTKSLQEEE	PCPRFAHQLV	YDELHKVHYL	FGGNPGKSCS	PKMRLDDFWS	LKLCRPSKDY	LLRHCKYLIR
650	660	670	680	690	700		
KHRFEEKAQV	DPLSALKYLQ	NDLYITVDHS	DPEETKEFQL	LASALFKSGS	DFTALA		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1158	1	477.6545	-288.11	2	44.1	17.4	0	15-22	R.LLPYALHK.W	
2161	2	1051.4053	-78.68	2	56.9	11.4	2	320-337	K.ENGPSARSCHKMCIDIQR.R	Carbamidomethyl: 9

Detailed Protein Report

Protein 116: PREDICTED: tetratricopeptide repeat protein 13 isoform X7 [Homo sapiens]

Accession:	gi|578802328	**Score:**	40.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	57.4
Database Date:	2015-11-30	**pI:**	9.3
		Sequence Coverage [%]:	7.0
		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
1611	1	820.8315	-147.56	2	49.9	12.3	1	234-247	R.SLSRGFNNHINLIR.G	

Detailed Protein Report

Protein 117: zinc finger protein 646 [Homo sapiens]

Accession:	gi|215820619	**Score:**	40.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	200.7
Database Date:	2015-11-30	**pI:**	6.8
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	2.1
		No. of unique Peptides:	3

Alias proteins:

Accession	Name	Description
gi|530409437	refseq_human (refseq_human_20140103.fasta)	PREDICTED: zinc finger protein 646 isoform X2 [Homo sapiens]
gi|530409435	refseq_human (refseq_human_20140103.fasta)	PREDICTED: zinc finger protein 646 isoform X1 [Homo sapiens]

Detailed Protein Report

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	1820	1830	1840
FTCPHCPRHF	RRRISFVQHQ	QQHQEEWTVA	GSGAPVAPVT	GRGDLPLPPP	PTPTTPLLDP	SPQWPADLSF	SL

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2169	1	701.2467	-130.95	3	57.3	10.5	1	308-324	R.ELLEHQQSHEGERQEPR.W	
1307	1	1023.7335	252.51	1	46.0	17.9	0	1557-1564	R.HYCLLCSK.E	Carbamidomethyl: 3
1325	1	640.6479	-226.44	2	46.2	12.3	0	1661-1673	R.GGQAVTSMAAEDK.E	Oxidation: 8

Detailed Protein Report

Protein 118: **PREDICTED: zinc finger protein 510 isoform X3 [Homo sapiens]**

Accession:	gi|530390743	**Score:**	40.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	72.1
Database Date:	2015-11-30	**pI:**	10.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	6.6
		No. of unique Peptides:	1

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

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

Detailed Protein Report

Protein 119: PREDICTED: diacylglycerol kinase alpha isoform X2 [Homo sapiens]

Accession:	gi|530399854	**Score:**	40.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	69.9
Database Date:	2015-11-30	**pI:**	9.3
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	3.9
		No. of unique Peptides:	2

Alias proteins:

Accession	Name	Description
gi|530399856	refseq_human (refseq_human_20140103.fasta)	PREDICTED: diacylglycerol kinase alpha isoform X3 [Homo sapiens]

10	20	30	40	50	60	70	80
MVLRNRRGWG	ERLSPLGLNL	KEVDKIILQM	MRVAEYLDWD	VSELRPILQE	MMKEIDYDGS	GSVSQAEWVR	AGATTVPLLV
90	100	110	120	130	140	150	160
LLGLEMTLKD	DGQHMWRPKR	FPRPVYCNLC	ESSIGLGKQG	LSCNLCKYTV	HDQCAMKALP	CEVSTYAKSR	KDIGVQSHVW
170	180	190	200	210	220	230	240
VRGGCESGRC	DRCQKKIRIY	HSLTGLHCVW	CHLEIHDDCL	QAVGHECDCG	LLRDHILPPS	SIYPSVLASG	PDRKNSKTSQ
250	260	270	280	290	300	310	320
KTMDDLNLST	SEALRIDPVP	NTHPLLVFVN	PKSGGKQGQR	VLWKFQYILN	PRQVFNLLKD	GPEIGLRLFK	DVPDSRILVC
330	340	350	360	370	380	390	400
GGDGTVGWIL	ETIDKANLPV	LPPVAVLPLG	TGNDLARCLR	WGGGYEGQNL	AKILKDLEMS	KVVHMDRWSV	EVIPQQTEEK
410	420	430	440	450	460	470	480
SDPVPFQIIN	NYFSIGVDAS	IAHRFHIMRE	KYPEKFNSRM	KNKLWYFEFA	TSESIFSTCK	KLEESLTVEI	CGKPLDLSNL
490	500	510	520	530	540	550	560
SLEGIAVLNI	PSMHGGSNLW	GDTRRPHGDI	YGINQALGAT	AKVITDPDIL	KTCVPDLSDK	RLEVVGLEGA	IEMGQIYTKL
570	580	590	600	610	620	630	
KNAGRRLAKC	SEITFHTTKT	LPMQIDGEPW	MQTPCTIKIT	HKNQMPMLMG	PPPRSTNFFG	FLS	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1596	1	480.7905	22.53	2	49.7	13.2	2	1-7	-.MVLRNRR.G	Oxidation: 1
1847	1	577.2815	93.89	2	52.9	16.5	1	163-172	R.GGCESGRCDR.C	Carbamidomethyl: 3, 8

Detailed Protein Report

Protein 120: PREDICTED: ubiquitin-protein ligase E3C isoform X3 [Homo sapiens]

Accession:	gi|530387311	**Score:**	40.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	116.7
Database Date:	2015-11-30	**pI:**	6.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.3
		No. of unique Peptides:	3

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
2476	4	817.2871	-207.41	1	61.3	12.6	0	124-130	K.HSSLFVK.Q	
259	1	862.8548	57.47	3	32.6	16.7	2	689-712	K.RIRVHLLNAHGLDEAGIDGGGIFR.E	
2651	1	856.4088	-69.02	2	64.2	10.9	2	866-878	R.LNRQIRQHCLAFR.Q	Carbamidomethyl: 9

Detailed Protein Report

Protein 121: PREDICTED: nipped-B-like protein isoform X4 [Homo sapiens]

Accession:	gi|530378766	**Score:**	40.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	257.1
Database Date:	2015-11-30	**pI:**	9.1
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.0
		No. of unique Peptides:	3

Detailed Protein Report

10	20	30	40	50	60	70	80
MVSIDLHQAG	RVDSQASITQ	DSDSIKKPEE	IKQCNDAPVS	VLQEDIVGSL	KSTPENHPET	PKKKSDPELS	KSEMKQSESR
90	100	110	120	130	140	150	160
LAESKPNENR	LVETKSSENK	LETKVETQTE	ELKQNESRTT	ECKQNESTIV	EPKQNENRLS	DTKPNDNKQN	NGRSETTKSR
170	180	190	200	210	220	230	240
PETPKQKGES	RPETPKQKSD	GHPETPKQKG	DGRPETPKQK	GESRPETPKQ	KNEGRPETPK	HRHDNRRDSG	KPSTEKKPEV
250	260	270	280	290	300	310	320
SKHKQDTKSD	SPRLKSERAE	ALKQRPDGRS	VSESLRRDHD	NKQKSDDRGE	SERHRGDQSR	VRRPETLRSS	SRNEHGIKSD
330	340	350	360	370	380	390	400
SSKTDKLERK	HRHESGDSRE	RPSSGEQKSR	PDSPRVKQGD	SNKSRSDKLG	FKSPTSKDDK	RTEGNKSKVD	TNKAHPDNKA
410	420	430	440	450	460	470	480
EFPSYLLGGR	SGALKNFVIP	KIKRDKDGNV	TQETKKMEMK	GEPKDKVEKI	GLVEDLNKGA	KPVVVLQKLS	LDDVQKLIKD
490	500	510	520	530	540	550	560
REDKSRSSLK	PIKNKPSKSN	KGSIDQSVLK	ELPPELLAEI	ESTMPLCERV	KMNKRKRSTV	NEKPKYAEIS	SDEDNDSDEA
570	580	590	600	610	620	630	640
FESSRKRHKK	DDDKAWEYEE	RDRRSSGDHR	RSGHSHEGRR	SSGGGRYRNR	SPSDSDMEDY	SPPPSLSEVA	RKMKKKEKQK
650	660	670	680	690	700	710	720
KRKAYEPKLT	PEEMMDSSTF	KRFTASIENI	LDNLEDMDFT	AFGDDDEIPQ	ELLLGKHQLN	ELGSESAKIK	AMGIMDKLST
730	740	750	760	770	780	790	800
DKTVKVLNIL	EKNIQDGSKL	STLLNHNNDT	EEEERLWRDL	IMERVTKSAD	ACLTTINIMT	SPNMPKAVYI	EDVIERVIQY
810	820	830	840	850	860	870	880
TKFHLQNTLY	PQYDPVYRLD	PHGGGLLSSK	AKRAKCSTHK	QRVIVMLYNK	VCDIVSSLSE	LLEIQLLTDT	TILQVSSMGI
890	900	910	920	930	940	950	960
TPFFVENVSE	LQLCAIKLVT	AVFSRYEKHR	QLILEEIFTS	LARLPTSKRS	LRNFRLNSSD	MDGEPMYIQM	VTALVLQLIQ
970	980	990	1000	1010	1020	1030	1040
CVVHLPSSEK	DSNAEEDSNK	KIDQDVVITN	SYETAMRTAQ	NFLSIFLKKC	GSKQGEEDYR	PLFENFVQDL	LSTVNKPEWP
1050	1060	1070	1080	1090	1100	1110	1120
AAELLLSLLG	RLLVHQFSNK	STEMALRVAS	LDYLGTVAAR	LRKDAVTSKM	DQGSIERILK	QVSGGEDEIQ	QLQKALLDYL
1130	1140	1150	1160	1170	1180	1190	1200
DENTETDPSL	VFSRKFYIAQ	WFRDTTLETE	KAMKSQKDEE	SSEGTHHAKE	IETTGQIMHR	AENRKKFLRS	IIKTTPSQFS
1210	1220	1230	1240	1250	1260	1270	1280
TLKMNSDTVD	YDDACLIVRY	LASMRPFAQS	FDIYLTQILR	VLGENAIAVR	TKAMKCLSEV	VAVDPSILAR	LDMQRGVHGR
1290	1300	1310	1320	1330	1340	1350	1360
LMDNSTSVRE	AAVELLGRFV	LCRPQLAEQY	YDMLIERILD	TGISVRKRVI	KILRDICIEQ	PTFPKITEMC	VKMIRRVNDE
1370	1380	1390	1400	1410	1420	1430	1440
EGIKKLVNET	FQKLWFTPTP	HNDKEAMTRK	ILNITDVVAA	CRDTGYDWFE	QLLQNLLKSE	EDSSYKPVKK	ACTQLVDNLV
1450	1460	1470	1480	1490	1500	1510	1520
EHILKYEESL	ADSDNKGVNS	GRLVACITTL	FLFSKIRPQL	MVKHAMTMQP	YLTTKCSTQN	DFMVICNVAK	ILELVVPLME
1530	1540	1550	1560	1570	1580	1590	1600
HPSETFLATI	EEDLMKLIIK	YGMTVVQHCV	SCLGAVVNKV	TQNFKFVWAC	FNRYYGAISK	LKSQHQEDPN	NTSLLTNKPA
1610	1620	1630	1640	1650	1660	1670	1680
LLRSLFTVGA	LCRHFDFDLE	DFKGNSKVNI	KDKVLELLMY	FTKHSDEEVQ	TKAIIGLGFA	FIQHPSLMFE	QEVKNLYNNI
1690	1700	1710	1720	1730	1740	1750	1760
LSDKNSSVNL	KIQVLKNLQT	YLQEEDTRMQ	QADRDWKKVA	KQEDLKEMGD	VSSGMSSSIM	QLYLKQVLEA	FFHTQSSVRH
1770	1780	1790	1800	1810	1820	1830	1840
FALNVIALTL	NQGLIHPVQC	VPYLIAMGTD	PEPAMRNKAD	QQLVEIDKKY	AGFIHMKAVA	GMKMSYQVQQ	AINTCLKDPV
1850	1860	1870	1880	1890	1900	1910	1920
RGFRQDESSS	ALCSHLYSMI	RGNRQHRRAF	LISLLNLFDD	TAKTDVTMLL	YIADNLACFP	YQTQEEPLFI	MHHIDITLSV
1930	1940	1950	1960	1970	1980	1990	2000
SGSNLLQSFK	ESMVKDKRKE	RKSSPSKENE	SSDSEEEVSR	PRKSRKRVDS	DSDSDSEDDI	NSVMKCLPEN	SAPLIEFANV
2010	2020	2030	2040	2050	2060	2070	2080
SQGILLLLML	KQHLKNLCGF	SDSKIQKYSP	SESAKVYDKA	INRKTGVHFH	PKQTLDFLRS	DMANSKITEE	VKRSIVKQYL
2090	2100	2110	2120	2130	2140	2150	2160
DFKLLMEHLD	PDEEEEEGEV	SASTNARNKA	ITSLLGGGSP	KNNTAAETED	DESDGEDRGG	GTSGSLRRSK	RNSDSTELAA
2170	2180	2190	2200	2210	2220	2230	2240
QMNESVDVMD	VIAICCPKYK	DRPQIARVVQ	KTSSGFSVQW	MAGSYSGSWT	EAKRRDGRKL	VPWVDTIKES	DIIYKKIALT
2250	2260	2270					
SANKLTNKVV	QTLRSLYAAK	DGTSS					

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
887	1	491.6754	-84.38	2	40.6	13.5	0	575-581	K.AWEYEER.D	
2607	1	913.4633	-59.64	2	62.6	12.0	1	909-923	K.HRQLILEEIFTSLAR.L	
425	1	946.2023	58.66	3	35.0	14.6	2	1692-1714	K.IQVLKNLQTYLQEEDTRMQQADR.D	Oxidation: 18

Detailed Protein Report

Protein 122: PDZ domain-containing protein MAGIX isoform d [Homo sapiens]

Accession:	gi|532164745	**Score:**	40.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	26.7
Database Date:	2015-11-30	**pI:**	11.6
		Sequence Coverage [%]:	11.9
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MEPRTGDAAD	PRGSRGGRGP	SPLAGPSARQ	LLARLDARPL	AARAAVDVAA	LVRRAGATLR	LRRKEAVSVL	DSADIEVTDS
90	100	110	120	130	140	150	160
RLPHATIVDH	RPQVGDLVLH	INGESTQGLT	HAQAVERIRA	GGPQLHLVIR	RPLETHPGKP	RGVGEPRKGV	DRSPDPGGPE
170	180	190	200	210	220	230	240
VTGSRSSSTS	LVQHPPSRTT	LKKTRGSPEP	SPEAAADGPT	VSPPERRAED	PNDQIPGSPG	PWLVPSEERL	SRALGVRGAA
250	260						
QLAQEMAAGR	RRH						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1080	1	841.9573	58.27	2	43.1	19.2	1	149-165	K.GVDRSPDPGGPEVTGSR.S	
1710	2	1273.4767	-121.71	1	51.3	20.9	0	238-250	R.GAAQLAQEMAAGR.R	

Detailed Protein Report

Protein 123: ubiquitin carboxyl-terminal hydrolase 17 [Homo sapiens]

Accession:	gi|153792150	**Score:**	40.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	59.6
Database Date:	2015-11-30	**pI:**	9.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	8.5
		No. of unique Peptides:	2

```
        10         20         30         40         50         60         70         80
MEDDSLYLGG EWQFNHFSKL TSSRPDAAFA EIQRTSLPEK SPLSSEARVD LCDDLAPVAR QLAPRKKLPL SSRRPAAVGA
        90        100        110        120        130        140        150        160
GLQNMGNTCY ENASLQCLTY TPPLANYMLS REHSQTCQRP KCCMLCTMQA HITWALHSPG HVIQPSQALA AGFHRGKQED
       170        180        190        200        210        220        230        240
AHEFLMFTVD AMKKACLPGH KQVDHHSKDT TLIHQIFGGC WRSQIKCLHC HGISDTFDPY LDIALDIQAA QSVKQALEQL
       250        260        270        280        290        300        310        320
VKPEELNGEN AYHCGLCLQR APASKTLTLH TSAKVLILVL KRFSDVTGNK LAKNVQYPEC LDMQPYMSQQ NTGPLVYVLY
       330        340        350        360        370        380        390        400
AVLVHAGWSC HDGHYFSYVK AQEGQWYKMD DAKVTACSIT SVLSQQAYVL FYIQKSEWER HSESVSRGRE PRALGAEDTD
       410        420        430        440        450        460        470        480
RRATQGELKR DHPCLQAPEL DERLVERATQ ESTLDHWKFP QEQNKTKPEF NVRKVEGTLP PNVLVIHQSK YKCGMKNHHP
       490        500        510        520        530        540
EQQSSLLNLS STTRTDQESV NTGTLASLQG RTRRSKGKNK HSKRALLVCQ
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1128	1	1019.1809	129.35	2	43.7	15.4	2	49-66	R.VDLCDDLAPVARQLAPRK.K	Carbamidomethyl: 4
184	1	424.2193	37.35	3	32.0	12.9	0	112-121	R.EHSQTCQRPK.C	Carbamidomethyl: 6

Detailed Protein Report

Protein 124: **uncharacterized protein C9orf172 [Homo sapiens]**

Accession:	gi|148762978	**Score:**	40.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	106.6
Database Date:	2015-11-30	**pI:**	10.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.9
		No. of unique Peptides:	3

```
        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
46	1	731.3139	-91.02	3	30.3	16.4	1	1-19	-.MTRTDPPDLLVSTVYQDIK.V	
2506	1	741.8376	-49.69	2	61.8	10.3	2	708-720	K.ARCVYGRVGSVCR.H	Carbamidomethyl: 3
1901	1	599.9186	-47.48	3	53.6	13.3	0	946-961	R.TGRPFMCMIMAASEPR.A	

Detailed Protein Report

Protein 125: **basement membrane-specific heparan sulfate proteoglycan core protein precursor [Homo sapiens]**

Accession:	gi|126012571	**Score:**	39.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	468.5
Database Date:	2015-11-30	**pI:**	6.1
		Sequence Coverage [%]:	0.9
		No. of unique Peptides:	2

Detailed Protein Report

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	TVPQFPRACT	EAEFACHSYN	ECVALEYRCD	RRPDCRDMSD	ELNCEEPVLG
250	260	270	280	290	300	310	320
ISPTFSLLVE	TTSLPPRPET	TIMRQPPVTH	APQPLLPGSV	RPLPCGPQEA	ACRNGHCIPR	DYLCDGQEDC	EDGSDELDCG
330	340	350	360	370	380	390	400
PPPPCEPNEF	PCGNGHCALK	LWRCDGDFDC	EDRTDEANCP	TKRPEEVCGP	TQFRCVSTNM	CIPASFHCDE	ESDCPDRSDE
410	420	430	440	450	460	470	480
FGCMPPQVVT	PPRESIQASR	GQTVTFTCVA	IGVPTPIINW	RLNWGHIPSH	PRVTVTSEGG	RGTLIIRDVK	ESDQGAYTCE
490	500	510	520	530	540	550	560
AMNARGMVFG	IPDGVLELVP	QRGPCPDGHF	YLEHSAACLP	CFCFGITSVC	QSTRRFRDQI	RLRFDQPDDF	KGVNVTMPAQ
570	580	590	600	610	620	630	640
PGTPPLSSTQ	LQIDPSLHEF	QLVDLSRRFL	VHDSFWALPE	QFLGNKVDSY	GGSLRYNVRY	ELARGMLEPV	QRPDVVLMGA
650	660	670	680	690	700	710	720
GYRLLSRGHT	PTQPGALNQR	QVQFSEEHWV	HESGRPVQRA	ELLQVLQSLE	AVLIQTVYNT	KMASVGLSDI	AMDTTVTHAT
730	740	750	760	770	780	790	800
SHGRAHSVEE	CRCPIGYSGL	SCESCDAHFT	RVPGGPYLGT	CSGCNCNGHA	SSCDPVYGHC	LNCQHNTEGP	QCNKCKAGFF
810	820	830	840	850	860	870	880
GDAMKATATS	CRPCPCPYID	ASRRFSDTCF	LDTDGQATCD	ACAPGYTGRR	CESCAPGYEG	NPIQPGGKCR	PVNQEIVRCD
890	900	910	920	930	940	950	960
ERGSMGTSGE	ACRCKNNVVG	RLCNECADGS	FHLSTRNPDG	CLKCFCMGVS	RHCTSSSWSR	AQLHGASEEP	GHFSLTNAAS
970	980	990	1000	1010	1020	1030	1040
THTTNEGIFS	PTPGELGFSS	FHRLLSGPYF	WSLPSRFLGD	KVTSYGGELR	FTVTQRSQPG	STPLHGQPLV	VLQGNNIILE
1050	1060	1070	1080	1090	1100	1110	1120
HHVAQEPSPG	QPSTFIVPFR	EQAWQRPDGQ	PATREHLLMA	LAGIDTLLIR	ASYAQQPAES	RVSGISMDVA	VPEETGQDPA
1130	1140	1150	1160	1170	1180	1190	1200
LEVEQCSCPP	GYRGPSCQDC	DTGYTRTPSG	LYLGTCERCS	CHGHSEACEP	ETGACQGCQH	HTEGPRCEQC	QPGYYGDAQR
1210	1220	1230	1240	1250	1260	1270	1280
GTPQDCQLCP	CYGDPAAGQA	AHTCFLDTDG	HPTCDACSPG	HSGRHCERCA	PGYYGNPSQG	QPCQRDSQVP	GPIGCNCDPQ
1290	1300	1310	1320	1330	1340	1350	1360
GSVSSQCDAA	GQCQCKAQVE	GLTCSHCRPH	HFHLSASNPD	GCLPCFCMGI	TQQCASSAYT	RHLISTHFAP	GDFQGFALVN
1370	1380	1390	1400	1410	1420	1430	1440
PQRNSRLTGE	FTVEPVPEGA	QLSFGNFAQL	GHESFYWQLP	ETYQGDKVAA	YGGKLRYTLS	YTAGPQGSPL	SDPDVQITGN
1450	1460	1470	1480	1490	1500	1510	1520
NIMLVASQPA	LQGPERRSYE	IMFREEFWRR	PDGQPATREH	LLMALADLDE	LLIRATFSSV	PLAASISAVS	LEVAQPGPSN
1530	1540	1550	1560	1570	1580	1590	1600
RPRALEVEEC	RCPPGYIGLS	CQDCAPGYTR	TGSGLYLGHC	ELCECNGHSD	LCHPETGACS	QCQHNAAGEF	CELCAPGYYG
1610	1620	1630	1640	1650	1660	1670	1680
DATAGTPEDC	QPCACPLTNP	ENMFSRTCES	LGAGGYRCTA	CEPGYTGQYC	EQCGPGYVGN	PSVQGGQCLP	ETNQAPLVVE
1690	1700	1710	1720	1730	1740	1750	1760
VHPARSIVPQ	GGSHSLRCQV	SGSPPHYFYW	SREDGRPVPS	GTQQRHQGSE	LHFPSVQPSD	AGVYICTCRN	LHQSNTSRAE
1770	1780	1790	1800	1810	1820	1830	1840
LLVTEAPSKP	ITVTVEEQRS	QSVRPGADVT	FICTAKSKSP	AYTLVWTRLH	NGKLPTRAMD	FNGILTIRNV	QLSDAGTYVC
1850	1860	1870	1880	1890	1900	1910	1920
TGSNMFAMDQ	GTATLHVQAS	GTLSAPVVSI	HPPQLTVQPG	QLAEFRCSAT	GSPTPTLEWT	GGPGGQLPAK	AQIHGGILRL
1930	1940	1950	1960	1970	1980	1990	2000
PAVEPTDQAQ	YLCRAHSSAG	QQVARAVLHV	HGGGGPRVQV	SPERTQVHAG	RTVRLYCRAA	GVPSATITWR	KEGGSLPPQA
2010	2020	2030	2040	2050	2060	2070	2080
RSERTDIATL	LIPAITTADA	GFYLCVATSP	AGTAQARIQV	VVLSASDASP	PPVKIESSSP	SVTEGQTLDL	NCVVAGSAHA
2090	2100	2110	2120	2130	2140	2150	2160
QVTWYRRGGS	LPPHTQVHGS	RLRLPQVSPA	DSGEYVCRVE	NGSGPKEASI	TVSVLHGTHS	GPSYTPVPGS	TRPIRIEPSS
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2417	1	1175.2100	-20.32	2	60.1	10.2	1	5-27	R.AAGALLLALLLHGRLLAVTHGLR.A	
362	1	457.1238	-295.03	2	33.9	17.6	0	4004-4012	R.SAEPLALGR.W	

Detailed Protein Report

Protein 126: PREDICTED: centlein isoform X2 [Homo sapiens]

Accession:	gi|578816553	**Score:**	39.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	155.6
Database Date:	2015-11-30	**pI:**	9.1
		Sequence Coverage [%]:	2.5
		No. of unique Peptides:	2

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
1953	1	643.3047	-169.45	1	54.5	11.9	0	1136-1141	R.LNVAVK.E	
2736	1	683.3656	57.65	3	65.5	15.2	2	1144-1159	K.SQYEQMYQKSKEELEK.K	

Detailed Protein Report

Protein 127: protein piccolo isoform 2 [Homo sapiens]

Accession:	gi|150170670	**Score:**	39.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	537.6
Database Date:	2015-11-30	**pI:**	5.9
		Sequence Coverage [%]:	1.0
		No. of unique Peptides:	2

Quantitation

MD:MU	**Median:** 1.06	**CV:** 0.00 %	**No. of Peptides:** 1

10	20	30	40	50	60	70	80
MGNEASLEGE	GLPEGLAAAA	AAGGGASGAG	SPSHTAIPAG	MEADLSQLSE	EERRQIAAVM	SRAQGLPKGS	VPPAAAESPS
90	100	110	120	130	140	150	160
MHRKQELDSS	HPPKQSGRPP	DPGRPAQPGL	SKSRTTDTFR	SEQKLPGRSP	STISLKESKS	RTDLKEEHKS	SMMPGFLSEV
170	180	190	200	210	220	230	240
NALSAVSSVV	NKFNPFDLIS	DSEASQEETT	KKQKVVQKEQ	GKPEGIIKPP	LQQQPPKPIP	KQQGPGRDPL	QQDGTPKSIS
250	260	270	280	290	300	310	320
SQQPEKIKSQ	PPGTGKPIQG	PTQTPQTDHA	KLPLQRDASR	PQTKQADIVR	GESVKPSLPS	PSKPPIQQPT	PGKPPAQQPG
330	340	350	360	370	380	390	400
HEKSQPGPAK	PPAQPSGLTK	PLAQQPGTVK	PPVQPPGTTK	PPAQPLGPAK	PPAQQTGSEK	PSSEQPGPKA	LAQPPGVGKT
410	420	430	440	450	460	470	480
PAQQPGPAKP	PTQQVGTPKP	LAQQPGLQSP	AKAPGPTKTP	VQQPGPGKIP	AQQAGPGKTS	AQQTGPTKPP	SQLPGPAKPP
490	500	510	520	530	540	550	560
PQQPGPAKPP	PQQPGSAKPP	SQQPGSTKPP	PQQPGPAKPS	PQQPGSTKPP	SQQPGSAKPS	AQQPSPAKPS	AQQSTKPVSQ
570	580	590	600	610	620	630	640
TGSGKPLQPP	TVSPSAKQPP	SQGLPKTICP	LCNTTELLLH	VPEKANFNTC	TECQTTVCSL	CGFNPNPHLT	EVKEWLCLNC
650	660	670	680	690	700	710	720
QMKRALGGDL	APVPSSPQPK	LKTAPVTTTS	AVSKSSPQPQ	QTSPKKDAAP	KQDLSKAPEP	KKPPPLVKQP	TLHGSPSAKA
730	740	750	760	770	780	790	800
KQPPEADSLS	KPAPPKEPSV	PSEQDKAPVA	DDKPKQPKMV	KPTTDLVSSS	SATTKPDIPS	SKVQSQAEEK	TTPPLKTDSA
810	820	830	840	850	860	870	880
KPSQSFPPTG	EKVSPFDSKA	IPRPASDSKI	ISHPGPSSES	KGQKQVDPVQ	KKEEPKKAQT	KMSPKPDAKP	MPKGSPTPPG
890	900	910	920	930	940	950	960
PRPTAGQTVP	TPQQSPKPQE	QSRRFSLNLG	SITDAPKSQP	TTPQETVTGK	LFGFGASIFS	QASNLISTAG	QPGPHSQSGP
970	980	990	1000	1010	1020	1030	1040
GAPMKQAPAP	SQPPTSQGPP	KSTGQAPPAP	AKSIPVKKET	KAPAAEKLEP	KAEQAPTVKR	TETEKKPPPI	KDSKSLTAEP
1050	1060	1070	1080	1090	1100	1110	1120
QKAVLPTKLE	KSPKPESTCP	LCKTELNIGS	KDPPNFNTCT	ECKNQVCNLC	GFNPTPHLTE	IQEWLCLNCQ	TQRAISGQLG
1130	1140	1150	1160	1170	1180	1190	1200
DIRKMPPAPS	GPKASPMPVP	TESSSQKTAV	PPQVKLVKKQ	EQEVKTEAEK	VILEKVKETL	SMEKIPPMVT	TDQKQEESKL
1210	1220	1230	1240	1250	1260	1270	1280
EKDKASALQE	KKPLPEEKKL	IPEEEKIRSE	EKKPLLEEKK	PTPEDKKLLP	EAKTSAPEEQ	KHDLLKSQVQ	IAEEKLEGRV
1290	1300	1310	1320	1330	1340	1350	1360
APKTVQEGKQ	PQTKMEGLPS	GTPQSLPKED	DKTTKTIKEQ	PQPPCTAKPD	QVEPGKEKTE	KEDDKSDTSS	SQQPKSPQGL
1370	1380	1390	1400	1410	1420	1430	1440
SDTGYSSDGI	SSSLGEIPSL	IPTDEKDILK	GLKKDSFSQE	SSPSSPSDLA	KLESTVLSIL	EAQASTLADE	KSEKKTQPHE
1450	1460	1470	1480	1490	1500	1510	1520
VSPEQPKDQE	KTQSLSETLE	ITISEEEIKE	SQEERKDTFK	KDSQQDIPSS	KDHKEKSEFV	DDITTRREPY	DSVEESSESE
1530	1540	1550	1560	1570	1580	1590	1600
NSPVPQRKRR	TSVGSSSSDE	YKQEDSQGSG	EEEDFIRKQI	IEMSADEDAS	GSEDDEFIRN	QLKEISSSTE	SQKKEETKGK
1610	1620	1630	1640	1650	1660	1670	1680
GKITAGKHRR	LTRKSSTSID	EDAGRRHSWH	DEDDEAFDES	PELKYRETKS	QESEELVVTG	GGGLRRFKTI	ELNSTIADKY
1690	1700	1710	1720	1730	1740	1750	1760
SAESSQKKTS	LYFDEEPELE	MESLTDSPED	RSRGEGSSSL	HASSFTPGTS	PTSVSSLDED	SDSSPSHKKG	ESKQQRKARH
1770	1780	1790	1800	1810	1820	1830	1840
RPHGPLLPTI	EDSSEEEELR	EEEELLKEQE	KQREIEQQQR	KSSSKKSKKD	KDELRAQRRR	ERPKTPPSNL	SPIEDASPTE
1850	1860	1870	1880	1890	1900	1910	1920
ELRQAAEMEE	LHRSSCSEYS	PSIESDPEGF	EISPEKIIEV	QKVYKLPTAV	SLYSPTDEQS	IMQKEGSQKA	LKSAEEMYEE
1930	1940	1950	1960	1970	1980	1990	2000
MMHKTHKYKA	FPAANERDEV	FEKEPLYGGM	LIEDYIYESL	VEDTYNGSVD	GSLLTRQEEE	NGFMQQKGRE	QKIRLSEQIY
2010	2020	2030	2040	2050	2060	2070	2080
EDPMQKITDL	QKEFYELESL	HSVVPQEDIV	SSSFIIPESH	EIVDLGTMVT	STEEERKLLD	ADAAYEELMK	RQQMQLTPGS
2090	2100	2110	2120	2130	2140	2150	2160
SPTQAPIGED	MTESTMDFDR	MPDASLTSSV	LSGASLTDST	SSATLSIPDV	KITQHFSTEE	IEDEYVTDYT	REIQEIIAHE
2170	2180	2190	2200	2210	2220	2230	2240
SLILTYSEPS	ESATSVPPSD	TPSLTSSVSS	VCTTDSSSPI	TTLDSITTVY	TEPVDMITKF	EDSEEISSST	YFPGSIIDYP
2250	2260	2270	2280	2290	2300	2310	2320
EEISVSLDRT	APPDGRASAD	HIVISLSDMA	SSIIESVVPK	PEGPVADTVS	TDLLISEKDP	VKKAKKETGN	GIILEVLEAY
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
2516	1	941.4560	-98.82	2	61.9	13.1	1	702-719	K.KPPPLVKQPTLHGSPSAK.A		
1917	1	902.8454	-85.60	2	54.0	12.9	0	3678-3694	R.SMSDPKPLSPTADESSR.A		MD:MU 1.06

Detailed Protein Report

Protein 128: PREDICTED: nesprin-2 isoform X8 [Homo sapiens]

Accession:	gi|578825626	**Score:**	39.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	553.3
Database Date:	2015-11-30	**pI:**	5.1
		Sequence Coverage [%]:	0.8
		No. of unique Peptides:	2

Quantitation

MD:MU	**Median:**	1.00	**CV:**	0.00 %		**No. of Peptides:**	1

Detailed Protein Report

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

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2639	1	686.8883	34.43	2	63.0	14.6	0	451-462	K.DENHLPLVPPNK.L		
1518	1	882.6077	144.13	2	48.8	11.3	2	3618-3632	K.SEQFEELQSILKKGK.L		MD:MU 1.00

Detailed Protein Report

Protein 129: **coiled-coil domain-containing protein 178 isoform 2 [Homo sapiens]**

Accession:	gi|157671917	**Score:**	39.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	97.5
Database Date:	2015-11-30	**pI:**	5.9
		Sequence Coverage [%]:	3.4
		No. of unique Peptides:	3

10	20	30	40	50	60	70	80
MTENKTVSSS	STRDDQTNIG	LTCQEVKALR	EKAWSRTNEG	NAMSQSLVLY	GASKENSEGF	HESKMTNTEG	VNKGIYFSYP
90	100	110	120	130	140	150	160
CRRHSCAVVN	IPAPCVNKMI	SHIQDVESKI	QEHLKRFETS	FEEWSRTSST	KDLKEDWSVT	TPVKEVKPGE	KRDEKCPELK
170	180	190	200	210	220	230	240
QEMETLLSEA	IRLIKSLETD	RADAEEALKQ	QRSRKNMINM	KIDSWSVWKL	QELPLAVQKE	HEAYLSDVIE	LQWHLEDKAN
250	260	270	280	290	300	310	320
QLQHFEKQKT	ELEEANAKIQ	ADIDYMNEHG	PLLDSKQNQE	LQDLKNHYKK	KMEVMDLHRK	VNEELEEALE	ACENARLKAQ
330	340	350	360	370	380	390	400
QIKEEIDKDI	YQDEKTIEAY	KREIYQLNSL	FDHYSSSVIN	VNTNIEEKEE	EVTEAIRETK	SSKNELHSLS	KMLEDLRRVY
410	420	430	440	450	460	470	480
DQLTWKQKSH	ENQYLEAVND	FYAAKKTWDI	ELSDVAKDFS	AISLACTKLT	EDNKKLEIDI	NKITVKTNES	IRKKSKYESE
490	500	510	520	530	540	550	560
IKYLTIMKLK	NDKHLKNIYK	EAYRIGTLFH	LTKHKTDEME	DKIAEVRRKF	KGREEFLKKL	TQGEVAAGMV	LQKKLYSIYE
570	580	590	600	610	620	630	640
VQALERKELI	KNRAICAMSL	AELQEPLLQL	EDEAERIRSL	DKEHSVSKRS	AIFKDLEATK	SKTMIFYAKI	NELNEELKAK
650	660	670	680	690	700	710	720
EEEKKSFDQT	LEILKNKFIT	MRFKREHAQT	VFDHYMQEKK	DCEERIFEED	QRFRVLLAVR	QKTLQDTQKI	IADSLEENLR
730	740	750	760	770	780	790	800
LAQEYQQLQI	TFLKEKDNYF	NIYDKQLSLD	TSIRDKKQLC	QLQRRMHTLW	QEHFKLVVLF	SQMRLANFQT	DSQESIQKIL
810	820	830					
AVQEESSNLM	QHILGFFQTL	TDGTCENDG					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1067	1	942.2514	-302.71	1	42.9	13.2	1	145-152	K.EVKPGEKR.D	
299	1	559.1629	-222.10	2	33.4	13.3	2	152-160	K.RDEKCPELK.Q	
2736	2	694.8753	-15.16	2	64.6	13.1	2	603-614	K.EHSVSKRSAIFK.D	

Detailed Protein Report

Protein 130: replication factor C subunit 1 isoform 1 [Homo sapiens]

Accession:	gi|32528306	**Score:**	39.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	128.1
Database Date:	2015-11-30	**pI:**	9.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.1
		No. of unique Peptides:	2

Quantitation

MD:MU **Median:** 1.04 **CV:** 0.00 % **No. of Peptides:** 1

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1265	1	990.4490	-59.66	2	45.4	11.3	2	745-760	K.IPIICMCNDRNHPKIR.S	Carbamidomethyl: 5	
6	1	776.7890	-162.05	2	28.8	17.4	1	776-789	R.VEQIKGAMMSIAFK.E		MD:MU 1.04

Detailed Protein Report

Protein 131: protein unc-13 homolog A [Homo sapiens]

Accession:	gi|283837842	**Score:**	39.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	192.9
Database Date:	2015-11-30	**pI:**	5.1
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	2.5
		No. of unique Peptides:	3

```
        10         20         30         40         50         60         70         80
MSLLCVGVKK AKFDGAQEKF NTYVTLKVQN VKSTTIAVRG SQPSWEQDFM FEINRLDLGL TVEVWNKGLI WDTMVGTVWI
        90        100        110        120        130        140        150        160
PLRTIRQSNE EGPGEWLTLD SQVIMADSEI CGTKDPTFHR ILLDTRFELP LDIPEEEARY WAKKLEQLNA MRDQDEYSFQ
       170        180        190        200        210        220        230        240
DEQDKPLPVP SNQCCNWNYF GWGEQHNDDP DSAVDDRDSD YRSETSNSIP PPYYTTSQPN ASVHQYSVRP PPLGSRESYS
       250        260        270        280        290        300        310        320
DSMHSYEEFS EPQALSPTGS SRYASSGELS QGSSQLSEDF DPDEHSLQGS DMEDERDRDS YHSCHSSVSY HKDSPRWDQD
       330        340        350        360        370        380        390        400
EEELEEDLED FLEEEELPED EEELEEEEEE VPDDLGSYAQ REDVAVAEPK DFKRISLPPA APGKEDKAPV APTEAPDMAK
       410        420        430        440        450        460        470        480
VAPKPATPDK VPAAEQIPEA EPPKDEESFR PREDEEGQEG QDSMSRAKAN WLRAFNKVRM QLQEARGEGE MSKSLWFKGG
       490        500        510        520        530        540        550        560
PGGGLIIIDS MPDIRKRKPI PLVSDLAMSL VQSRKAGITS ALASSTLNNE ELKNHVYKKT LQALIYPISC TTPHNFEVWT
       570        580        590        600        610        620        630        640
ATTPTYCYEC EGLLWGIARQ GMRCTECGVK CHEKCQDLLN ADCLQRAAEK SSKHGAEDRT QNIIMVLKDR MKIRERNKPE
       650        660        670        680        690        700        710        720
IFELIQEIFA VTKTAHTQQM KAVKQSVLDG TSKWSAKISI TVVCAQGLQA KDKTGSSDPY VTVQVGKTKK RTKTIYGNLN
       730        740        750        760        770        780        790        800
PVWEENFHFE CHNSSDRIKV RVWDEDDDIK SRVKQRFKRE SDDFLGQTII EVRTLSGEMD VWYNLDKRTD KSAVSGAIRL
       810        820        830        840        850        860        870        880
HISVEIKGEE KVAPYHVQYT CLHENLFHFV TDVQNNGVVK IPDAKGDDAW KVYYDETAQE IVDEFAMRYG VESIYQAMTH
       890        900        910        920        930        940        950        960
FACLSSKYMC PGVPAVMSTL LANINAYYAH TTASTNVSAS DRFAASNFGK ERFVKLLDQL HNSLRIDLSM YRNNFPASSP
       970        980        990       1000       1010       1020       1030       1040
ERLQDLKSTV DLLTSITFFR MKVQELQSPP RASQVVKDCV KACLNSTYEY IFNNCHELYS REYQTDPAKK GEVLPEEQGP
      1050       1060       1070       1080       1090       1100       1110       1120
SIKNLDFWSK LITLIVSIIE EDKNSYTPCL NQFPQELNVG KISAEVMWNL FAQDMKYAME EHDKHRLCKS ADYMNLHFKV
      1130       1140       1150       1160       1170       1180       1190       1200
KWLYNEYVTE LPAFKDRVPE YPAWFEPFVI QWLDENEEVS RDFLHGALER DKKDGFQQTS EHALFSCSVV DVFSQLNQSF
      1210       1220       1230       1240       1250       1260       1270       1280
EIIKKLECPD PQIVGHYMRR FAKTISNVLL QYADIISKDF ASYCSKEKEK VPCILMNNTQ QLRVQLEKMF EAMGGKELDA
      1290       1300       1310       1320       1330       1340       1350       1360
EASDILKELQ VKLNNVLDEL SRVFATSFQP HIEECVKQMG DILSQVKGTG NVPASACSSV AQDADNVLQP IMDLLDSNLT
      1370       1380       1390       1400       1410       1420       1430       1440
LFAKICEKTV LKRVLKELWK LVMNTMEKTI VLPPLTDQTM IGNLLRKHGK GLEKGRVKLP SHSDGTQMIF NAAKELGQLS
      1450       1460       1470       1480       1490       1500       1510       1520
KLKDHMVREE AKSLTPKQCA VVELALDTIK QYFHAGGVGL KKTFLEKSPD LQSLRYALSL YTQATDLLIK TFVQTQSAQG
      1530       1540       1550       1560       1570       1580       1590       1600
LGVEDPVGEV SVHVELFTHP GTGEHKVTVK VVAANDLKWQ TSGIFRPFIE VNIIGPQLSD KKRKFATKSK NNSWAPKYNE
      1610       1620       1630       1640       1650       1660       1670       1680
SFQFTLSADA GPECYELQVC VKDYCFARED RTVGLAVLQL RELAQRGSAA CWLPLGRRIH MDDTGLTVLR ILSQRSNDEV
      1690       1700       1710
AKEFVKLKSD TRSAEEGGAA PAP
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2705	1	805.4372	84.57	2	65.1	14.8	1	460-473	R.MQLQEARGEGEMSK.S	Oxidation: 1
2064	1	753.2991	-61.50	2	55.9	14.2	0	595-606	K.CQDLLNADCLQR.A	Carbamidomethyl: 1, 9

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2215	1	682.1038	136.60	3	57.9	10.1	1	1122-1137	K.WLYNEYVTELPAFKDR.V	

Detailed Protein Report

Protein 132: PREDICTED: RAS guanyl-releasing protein 2 isoform X1 [Homo sapiens]

Accession:	gi|578821076	**Score:**	39.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	75.4
Database Date:	2015-11-30	**pI:**	10.1
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	8.4
		No. of unique Peptides:	3

10	20	30	40	50	60	70	80
MGVCACVWEC	TCVERHCLAC	VHTCEDVSAC	VAAGLKAGLA	QVNSTSRRRP	RPRVCILGWT	SWGFGPSPVG	GSRSAAWAQP
90	100	110	120	130	140	150	160
TPRRRPWQAP	WTWTRAARWR	SCSAGASKPS	LAAKLLHIYQ	QSRKDNSNSL	QVKTCHLVRY	WISAFPAEFD	LNPELAEQIK
170	180	190	200	210	220	230	240
ELKALLDQEG	NRRHSSLIDI	DSVPTYKWKR	QVTQRNPVGQ	KKRKMSLLFD	HLEPMELAEH	LTYLEYRSFC	KILFQDYHSF
250	260	270	280	290	300	310	320
VTHGCTVDNP	VLERFISLFN	SVSQWVQLMI	LSKPTAPQRA	LVITHFVHVA	EKLLQLQNFN	TLMAVVGGLS	HSSISRLKET
330	340	350	360	370	380	390	400
HSHVSPETIK	LWEGLTELVT	ATGNYGNYRR	RLAACVGFRF	PILGVHLKDL	VALQLALPDW	LDPARTRLNG	AKMKQLFSIL
410	420	430	440	450	460	470	480
EELAMVTSLR	PPVQANPDLL	SLLTVSLDQY	QTEDELYQLS	LQREPRSKSS	PTSPTSCTPP	PRPPVLEEWT	SAAKPKLDQA
490	500	510	520	530	540	550	560
LVVEHIEKMV	ESVFRNFDVD	GDGHISQEEF	QIIRGNFPYL	SAFGDLDQNQ	DGCISREEMV	SYFLRSSSVL	GGRMGFVHNF
570	580	590	600	610	620	630	640
QESNSLRPVA	CRHCKALILG	IYKQGLKCRA	CGVNCHKQCK	DRLSVECRRR	AQSVSLEGSA	PSPSPMHSHH	HRAFSFSLPR
650	660	670					
PGRRGSRPPE	IREEEVQTVE	DGVFDIHL					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2165	1	938.2937	-80.66	2	56.9	12.3	0	1-15	-.MGVCACVWECTCVER.H	Carbamidomethyl: 4, 6, 10; Oxidation: 1
1804	1	1056.6673	56.24	3	52.5	10.2	2	360-387	R.FPILGVHLKDLVALQLALPDWLDPARTR.L	
2600	1	731.3793	68.68	2	63.1	16.6	2	590-602	R.ACGVNCHKQCKDR.L	

Detailed Protein Report

Protein 133: 14-3-3 protein sigma [Homo sapiens]

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

Score: 38.9
MW [kDa]: 27.8
pI: 4.5
Sequence Coverage [%]: 11.3
No. of unique Peptides: 1

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2105	1	1051.3989	-101.77	2	56.2	11.9	2	10-27	K.AKLAEQAERYEDMAAFMK.G	

Detailed Protein Report

Protein 134: centromere protein F [Homo sapiens]

Accession:	gi|55770834	**Score:**	38.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	357.3
Database Date:	2015-11-30	**pI:**	4.9
Modification(s):	Oxidation	**Sequence Coverage [%]:**	0.9
		No. of unique Peptides:	1

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
2707	1	821.4735	62.12	2	64.1	11.9	2	301-314	R.LQGHEKEMKGQVNK.F	Oxidation: 8

Detailed Protein Report

Protein 135: **PREDICTED: zinc finger protein 737 isoform X4 [Homo sapiens]**

Accession:	gi|530414419	**Score:**	38.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	60.3
Database Date:	2015-11-30	**pI:**	10.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	6.5
		No. of unique Peptides:	2

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	NLTTHKIIHT	GEKPYKCEEC	GKAFKRSSIL	TAHKIIHSGE	KPYKCEECGK
330	340	350	360	370	380	390	400
AFKHPSVLTT	HKRIHTGEKP	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
1955	1	1022.8979	-86.37	2	54.5	10.5	2	399-416	K.CEECGKAFKCFSILTTHK.R	
2857	1	1051.5637	63.44	2	66.2	11.3	2	399-416	K.CEECGKAFKCFSILTTHK.R	Carbamidomethyl: 1

Detailed Protein Report

Protein 136: **PREDICTED: caspase-10 isoform X3 [Homo sapiens]**

Accession:	gi|530371073	**Score:**	38.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	34.9
Database Date:	2015-11-30	**pI:**	6.5
		Sequence Coverage [%]:	10.1
		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	
GNRATNGAPS	LVSRGMQGAS	ANTLNSETST	KRAAVYRMNR	NHRGLCVIVN	NHSFTSLKDR	QGTHKDAG	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1677	1	933.3261	-154.07	2	50.9	26.9	1	236-254	K.HAGSNGNRATNGAPSLVSR.G	

Detailed Protein Report

Protein 137: zinc finger protein 610 isoform a [Homo sapiens]

Accession:	gi|239787098	**Score:**	38.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	53.5
Database Date:	2015-11-30	**pI:**	10.3
		Sequence Coverage [%]:	10.6
		No. of unique Peptides:	2

Alias proteins:

Accession	**Name**	**Description**
gi|239787104	refseq_human (refseq_human_20140103.fasta)	zinc finger protein 610 isoform a [Homo sapiens]
gi|239787101	refseq_human (refseq_human_20140103.fasta)	zinc finger protein 610 isoform a [Homo sapiens]

10	20	30	40	50	60	70	80
MLCDEEAQKR	KAKESGMALP	QGRLTFMDVA	IEFSQEEWKS	LDPGQRALYR	DVMLENYRNL	VFLGICLPDL	SIISMLKQRR
90	100	110	120	130	140	150	160
EPLILQSQVK	IVKNTDGREC	VRSVNTGRSC	VLGSNAENKP	IKNQLGLTLE	AHLSELQLFQ	AGRKIYRSNQ	VEKFTNHRSS
170	180	190	200	210	220	230	240
VSPLQKISSS	FTTHIFNKYR	NDLIDFPLLP	QEEKAYIRGK	SYEYECSEDG	EVFRVRASLT	NHQVIHTAEK	PYKCTECGKV
250	260	270	280	290	300	310	320
FSRNSHLVEH	WRIHTGQKPY	KCSECDKVFN	RNSNLARHQR	IHTGEKPHKC	NECGKAFREC	SGLTTHLVIH	TGEKPYKCNE
330	340	350	360	370	380	390	400
CGKNFRHKFS	LTNHQRSHTA	EKPYKCNECG	KVFSLLSYLA	RHQIIHSTEK	PYKCNECGRA	FHKRPGLMAH	LLIHTGEKPY
410	420	430	440	450	460	470	
KCNECDKVFG	RKLYLTNHQR	IHTGERPYKC	NACGKVFNQN	PHLSRHRKIH	AGENSLRTLQ	ME	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2725	2	1045.0312	-59.71	2	64.4	11.5	0	59-77	R.NLVFLGICLPDLSIISMLK.Q	
1493	1	949.3248	-78.23	2	48.5	12.6	1	199-214	R.GKSYEYECSEDGEVFR.V	

Detailed Protein Report

Protein 138: **syntaxin-binding protein 5 isoform b [Homo sapiens]**

Accession:	gi|189217915	**Score:**	38.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	127.5
Database Date:	2015-11-30	**pI:**	7.1
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.5
		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
1682	1	796.3351	-89.13	2	50.8	10.5	1	143-155	R.ERVTFCHLPFQSK.W	
2747	1	807.3929	-21.85	2	65.6	15.2	2	743-756	K.FSKMVANDIAKMSR.K	Oxidation: 4

Detailed Protein Report

Protein 139: **PREDICTED: UDP-glucose:glycoprotein glucosyltransferase 1 isoform X3 [Homo sapiens]**

Accession:	gi|578804605	**Score:**	38.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	176.2
Database Date:	2015-11-30	**pI:**	5.3
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	3.6
		No. of unique Peptides:	3

```
        10         20         30         40         50         60         70         80
MGCKGDASGV CYKMGVLVVL TVLWLFSSVK ADSKAITTSL TTKWFSTPLL LEASEFLAED SQEKFWNFVE ASQNIGSSDH
        90        100        110        120        130        140        150        160
DGTDYSYYHA ILEAAFQFLS PLQQNLFKFC LSLRSYSATI QAFQQIAADE PPPEGCNSFF SVHGKKTCES DTLEALLLTA
       170        180        190        200        210        220        230        240
SERPKPLLFK GDHRYPSSNP ESPVVIFYSE IGSEEFSNFH RQLISKSNAG KINYVFRHYI FNPRKEPVYL SGYGVELAIK
       250        260        270        280        290        300        310        320
STEYKAKDDT QVKGTEVNTT VIGENDPIDE VQGFLFGKLR DLHPDLEGQL KELRKHLVES TNEMAPLKVW QLQDLSFQTA
       330        340        350        360        370        380        390        400
ARILASPVEL ALVVMKDLSQ NFPTKARAIT KTAVSSELRT EVEENQKYFK GTLGLQPGDS ALFINGLHMD LDTQDIFSLF
       410        420        430        440        450        460        470        480
DVLRNEARVM EGLHRLGIEG LSLHNVLKLN IQPSEADYAV DIRSPAISWV NNLEVDSRYN SWPSSLQELL RPTFPGVIRQ
       490        500        510        520        530        540        550        560
IRKNLHNMVF IVDPAHETTA ELMNTAEMFL SNHIPLRIGF IFVVNDSEDV DGMQDAGVAV LRAYNYVAQE VDDYHAFQTL
       570        580        590        600        610        620        630        640
THIYNKVRTG EKVKVEHVVS VLEKKYPYVE VNSILGIDSA YDRNRKEARG YYEQTGVGPL PVVLFNGMPF EREQLDPDEL
       650        660        670        680        690        700        710        720
ETITMHKILE TTTFFQRAVY LGELPHDQDV VEYIMNQPNV VPRINSRILT AERDYLDLTA SNNFFVDDYA RFTILDSQGK
       730        740        750        760        770        780        790        800
TAAVANSMNY LTKKGMSSKE IYDDSFIRPV TFWIVGDFDS PSGRQLLYDA IKHQKSSNNV RISMINNPAK EISYENTQIS
       810        820        830        840        850        860        870        880
RAIWAALQTQ TSNAAKNFIT KMAKEGAAEA LAAGADIAEF SVGGMDFSLF KEVFESSKMD FILSHAVYCR DVLKLKKGQR
       890        900        910        920        930        940        950        960
AVISNGRIIG PLEDSELFNQ DDFHLLENII LKTSGQKIKS HIQQLRVEED VASDLVMKVD ALLSAQPKGD PRIEYQFFED
       970        980        990       1000       1010       1020       1030       1040
RHSAIKLRPK EGETYFDVVA VVDPVTREAQ RLAPLLLVLA QLINMNLRVF MNCQSKLSDM PLKSFYRYVL EPEISFTSDN
      1050       1060       1070       1080       1090       1100       1110       1120
SFAKGPIAKF LDMPQSPLFT LNLNTPESWM VESVRTPYDL DNIYLEEVDS VVAAEYELEY LLLEGHCYDI TTGQPPRGLQ
      1130       1140       1150       1160       1170       1180       1190       1200
FTLGTSANPV IVDTIVMANL GYFQLKANPG AWILRLRKGR SEDIYRIYSH DGTDSPPDAD EVVIVLNNFK SKIIKVKVQK
      1210       1220       1230       1240       1250       1260       1270       1280
KADMVNEDLL SDGTSENESG FWDSFKWGFT GQKTEEVKQD KDDIINIFSV ASGHLYERFL RIMMLSVLKN TKTPVKFWFL
      1290       1300       1310       1320       1330       1340       1350       1360
KNYLSPTFKE FIPYMANEYN FQYELVQYKW PRWLHQQTEK QRIIWGYKIL FLDVLFPLVV DKFLFVDADQ IVRTDLKELR
      1370       1380       1390       1400       1410       1420       1430       1440
DFNLDGAPYG YTPFCDSRRE MDGYRFWKSG YWASHLAGRK YHISALYVVD LKKFRKIAAG DRLRGQYQGL SQDPNSLSNL
      1450       1460       1470       1480       1490       1500       1510       1520
DQDLPNNMIH QVPIKSLPQE WLWCETWCDD ASKKRAKTID LCNNPMTKEP KLEAAVRIVP EWQDYDQEIK QLQIRFQKEK
      1530       1540       1550
ETGALYKEKT KEPSREGPQK REEL
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1963	1	696.2530	-54.87	2	54.6	12.7	1	1-13	-.MGCKGDASGVCYK.M	Carbamidomethyl: 11; Oxidation: 1
1565	1	1018.8365	-18.21	3	49.3	12.6	2	606-632	R.KEARGYYEQTGVGPLPVVLFNGMPFER.E	
1888	1	600.2525	-61.03	3	53.5	13.2	0	633-647	R.EQLDPDELETITMHK.I	

Protein 140: numb-like protein [Homo sapiens]

Accession:	gi|10863899	**Score:**	38.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	64.9
Database Date:	2015-11-30	**pI:**	10.1
		Sequence Coverage [%]:	8.7
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MSRSAAASGG	PRRPERHLPP	APCGAPGPPE	TCRTEPDGAG	TMNKLRQSLR	RRKPAYVPEA	SRPHQWQADE	DAVRKGTCSF
90	100	110	120	130	140	150	160
PVRYLGHVEV	EESRGMHVCE	DAVKKLKAMG	RKSVKSVLWV	SADGLRVVDD	KTKDLLVDQT	IEKVSFCAPD	RNLDKAFSYI
170	180	190	200	210	220	230	240
CRDGTTRRWI	CHCFLALKDS	GERLSHAVGC	AFAACLERKQ	RREKECGVTA	AFDASRTSFA	REGSFRLSGG	GRPAEREAPD
250	260	270	280	290	300	310	320
KKKAEAAAAP	TVAPGPAQPG	HVSPTPATTS	PGEKGEAGTP	VAAGTTAAAI	PRRHAPLEQL	VRQGSFRGFP	ALSQKNSPFK
330	340	350	360	370	380	390	400
RQLSLRLNEL	PSTLQRRTDF	QVKGTVPEME	PPGAGDSDSI	NALCTQISSS	FASAGAPAPG	PPPATTGTSA	WGEPSVPPAA
410	420	430	440	450	460	470	480
AFQPGHKRTP	SEAERWLEEV	SQVAKAQQQQ	QQQQQQQQQQ	QQQQQQAASV	APVPTMPPAL	QPFPAPVGPF	DAAPAQVAVF
490	500	510	520	530	540	550	560
LPPPHMQPPF	VPAYPGLGYP	PMPRVPVVGI	TPSQMVANAF	CSAAQLQPQP	ATLLGKAGAF	PPPAIPSAPG	SQARPRPNGA
570	580	590	600	610			
PWPPEPAPAP	APELDPFEAQ	WAALEGKATV	EKPSNPFSGD	LQKTFEIEL			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2693	1	1023.5273	37.29	2	64.9	10.3	2	203-221	R.EKECGVTAAFDASRTSFAR.E	
2525	1	834.4332	-13.93	2	62.0	11.3	2	227-242	R.LSGGGRPAEREAPDKK.K	

Detailed Protein Report

Protein 141: ubiquilin-like protein [Homo sapiens]

Accession:	gi|145580580	**Score:**	38.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	52.9
Database Date:	2015-11-30	**pI:**	5.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	8.8
		No. of unique Peptides:	2

Quantitation

MD:MU **Median:** 3.04 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MWHAISRTSR	MSQSGCPSGL	LADKNISSSA	TRVIVKTAGN	QKDFMVADDI	SVRQFKEMLL	AHFQCQMDQL	VLVFMGCLLK
90	100	110	120	130	140	150	160
DHDTLSQRGI	MDGHTIYLVI	KSKQGSRSLA	HSFRDLPTND	PCHRDRNTKG	NSSRVHQPTG	MNQAPVELAH	FVGSDAPKVH
170	180	190	200	210	220	230	240
TQNLEVSHPE	CKAQMLENPS	IQRLLSNMEF	MWQFISEHLD	TQQLMQQNPE	VSRLLLDNSE	ILLQTLELAR	NLAMIQEIMQ
250	260	270	280	290	300	310	320
IQQPSQNLEY	PLNPQPYLGL	ETMPGGNNAL	GQNYADINDQ	MLNSMQDPFG	GNPFTALLAG	QVLEQVQSSP	PPPPPSQEQQ
330	340	350	360	370	380	390	400
DQLTQHPATR	VIYNSSGGFS	SNTSANDTLN	KVNHTSKANT	AMISTKGQSH	ICATRQPAWI	PALPSIELTQ	QLQEEYKDAT
410	420	430	440	450	460	470	480
VSLSSSRQTL	KGDLQLSDEQ	SSSQITGGMM	QLLMNNPYLA	AQIMLFTSMP	QLSEQWRQQL	PTFLQQTQIS	DLLSA

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
177	1	642.3095	14.02	2	31.6	11.3	0	43-53	K.DFMVADDISVR.Q	Oxidation: 3	MD:MU 3.04
2144	1	953.3984	-72.07	2	57.0	10.6	1	358-375	K.ANTAMISTKGQSHICATR.Q	Oxidation: 5	

Detailed Protein Report

Protein 142: PREDICTED: zinc finger protein 675 isoform X3 [Homo sapiens]

Accession:	gi|530414622	**Score:**	38.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	58.2
Database Date:	2015-11-30	**pI:**	10.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	5.6
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MVNEPPVMCS	HFAQEFWPEQ	NIKDSFEKVT	LRRYEKCGND	NFQLKGCKSV	DECKLHKGGY	NGLNQCLPTM	QSKMFQCDKY
90	100	110	120	130	140	150	160
VKVFNKFSHS	DRHKIKHMEN	KPFKCKECGR	SFCMLSHLTR	HERNYTKVNF	CKCEECEKAV	NQSSKLTKHK	RIYTCEKLYK
170	180	190	200	210	220	230	240
CQECDRTFNQ	FSNLTEYKKD	YAREKPYKCE	ECGKAFNQSS	HLTTHKIIHT	GEKPYKCEEC	GKAFNQFSNL	TTHKKIHTGE
250	260	270	280	290	300	310	320
QPYICEECGK	AFTQSSTLTT	HKRIHTGEKP	YKCEECGKAF	NRSSKLTEHK	NIHTGEQPYK	CEECGKAFNR	SSNLTEHRKI
330	340	350	360	370	380	390	400
HTEEKPYKCK	ECGKAFKHSS	ALTTHKRIHT	GEKPYKCEEC	GKAFNRSSKL	TEHKKLHTGK	KPYKCEECGK	AFIQSSKLTE
410	420	430	440	450	460	470	480
HKKIHSGEIP	YKCEECGKAF	KHSSSLTTHK	RIHTGEKPYK	CEECGKAFSR	SSKLTEHKII	HTGEKPYKCE	RCDKAFNQSA
490	500						
NLTKHKKIHT	GEKLQNWNV						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1793	1	682.2364	-94.72	3	52.4	10.6	2	37-54	K.CGNDNFQLKGCKSVDECK.L	Carbamidomethyl: 17
2097	2	701.2282	-113.98	3	56.4	14.4	2	37-54	K.CGNDNFQLKGCKSVDECK.L	Carbamidomethyl: 1, 17

Detailed Protein Report

Protein 143: PREDICTED: histone-lysine N-methyltransferase setd3 isoform X3 [Homo sapiens]

Accession:	gi|530404751	**Score:**	38.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	56.3
Database Date:	2015-11-30	**pI:**	5.7
		Sequence Coverage [%]:	3.4
		No. of unique Peptides:	2

Quantitation

MD:MU **Median:** 1.36 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MCRSGLWLRK	YGKSKKAEEL	FLWVPRKLLM	TVESAKNSVL	GPLYSQDRIL	QAMGNIALAF	HLLCERASPN	SFWQPYIQTL
90	100	110	120	130	140	150	160
PSEYDTPLYF	EEDEVRYLQS	TQAIHDVFSQ	YKNTARQYAY	FYKVIQTHPH	ANKLPLKDSF	TYEDYRWAVS	SVMTRQNQIP
170	180	190	200	210	220	230	240
TEDGSRVTLA	LIPLWDMCNH	TNGLITTGYN	LEDDRCECVA	LQDFRAGEQI	YIFYGTRSNA	EFVIHSGFFF	DNNSHDRVKI
250	260	270	280	290	300	310	320
KLGVSKSDRL	YAMKAEVLAR	AGIPTSSVFA	LHFTEPPISA	QLLAFLRVFC	MTEEELKEHL	LGDSAIDRIF	TLGNSEFPVS
330	340	350	360	370	380	390	400
WDNEVKLWTF	LEDRASLLLK	TYKTTIEEDK	SVLKNHDLSV	RAKMAIKLRL	GEKEILEKAV	KSAAVNREYY	RQQMEEKAPL
410	420	430	440	450	460	470	480
PKYEESNLGL	LESSVGDSRL	PLVLRNLEEE	AGVQDALNIR	EAISKAKATE	NGLVNGENSI	PNGTRSENES	LNQESKRAVE
490	500						
DAKGSSSDST	AGVKE						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
832	1	491.6524	-172.14	2	39.8	26.5	0	117-123	R.QYAYFYK.V		
263	1	592.1181	-248.62	2	33.0	11.7	0	196-205	R.CECVALQDFR.A		MD:MU 1.36

Detailed Protein Report

Protein 144: PREDICTED: protein unc-45 homolog A isoform X3 [Homo sapiens]

Accession:	gi|530407244	**Score:**	38.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	87.2
Database Date:	2015-11-30	**pI:**	5.6
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	3.4
		No. of unique Peptides:	3

```
        10         20         30         40         50         60         70         80
MSSTDAKVEQ MFQILLDPEE KGTEKKQKAS QNLVVLARED AGAEKIFRSN GVQLLQRLLD MGETDLMLAA LRTLVGICSE
        90        100        110        120        130        140        150        160
HQSRTVATLS ILGTRRVVSI LGVESQAVSL AACHLLQVMF DALKEGVKKG FRGKEGAIIV DPARELKVLI SNLLDLLTEV
       170        180        190        200        210        220        230        240
GVSGQGRDNA LTLLIKAVPR KSLKDPNNSL TLWVIDQGLK KILEVGGSLQ DPPGELAVTA NSRMSASILL SKLFDDLKCD
       250        260        270        280        290        300        310        320
AERENFHRLC ENYIKSWFEG QGLAGKLRAI QTVSCLLQGP CDAGNRALEL SGVMESVIAL CASEQEEEQL VAVEALIHAA
       330        340        350        360        370        380        390        400
GKAKRASFIT ANGVSLLKDL YKCSEKDSIR IRALVGLCKL GSAGGTDFSM KQFAEGSTLK LAKQCRKWLC NDQIDAGTRR
       410        420        430        440        450        460        470        480
WAVEGLAYLT FDADVKEEFV EDAAALKALF QLSRLEERSV LFAVASALVN CTNSYDYEEP DPKMVELAKY AKQHVPEQHP
       490        500        510        520        530        540        550        560
KDKPSFVRAR VKKLLAAGVV SAMVCMVKTE SPVLTSSCRE LLSRVFLALV EEVEDRGTVV AQGGGRALIP LALEGTDVGQ
       570        580        590        600        610        620        630        640
TKAAQALAKL TITSNPEMTF PGERIYEVVR PLVSLLHLNC SGLQNFEALM ALTNLAGISE RLRQKILKEK AVPMIEGYMF
       650        660        670        680        690        700        710        720
EEHEMIRRAA TECMCNLAMS KEVQDLFEAQ GNDRLKLLVL YSGEDDELLQ RAAAGGLAML TSMRPTLCSR IPQVTTHWLE
       730        740        750        760        770        780        790        800
ILQALLLSSN QELQHRGAVV VLNMVEASRE IASTLMESEM MEILSVLAKG DHSPVTRAAA ACLDKAVEYG LIQPNQDGE
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1687	1	793.3789	34.81	2	51.0	14.1	1	648-661	R.RAATECMCNLAMSK.E	Carbamidomethyl: 6
2677	1	731.3736	106.62	2	64.7	11.8	0	649-661	R.AATECMCNLAMSK.E	Carbamidomethyl: 5; Oxidation: 6, 11
150	1	977.7995	37.53	3	31.3	12.2	1	649-674	R.AATECMCNLAMSKEVQDLFEAQGNDR.L	Carbamidomethyl: 5

Detailed Protein Report

Protein 145: **PREDICTED: nuclear receptor subfamily 1 group D member 2 isoform X2 [Homo sapiens]**

Accession:	gi|578806859	**Score:**	38.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	49.9
Database Date:	2015-11-30	**pI:**	9.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	12.1
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MEVNAGGVIA	YISSSSSASS	PASCHSEGSE	NSFQSSSSSV	PSSPNSSNSD	TNGNPKNGDL	ANIEGILKND	RIDCSMKTSK
90	100	110	120	130	140	150	160
SSAPGMTKSH	SGVTKFSGMV	LLCKVCGDVA	SGFHYGVHAC	EGCKGFFRRS	IQQNIQYKKC	LKNENCSIMR	MNRNRCQQCR
170	180	190	200	210	220	230	240
FKKCLSVGMS	RDAVRFGRIP	KREKQRMLIE	MQSAMKTMMN	SQFSGHLQND	TLVEHHEQTA	LPAQEQLRPK	PQLEQENIKS
250	260	270	280	290	300	310	320
SSPPSSDFAK	EEVIGMVTRA	HKDTFMYNQE	QQENSAESMQ	PQRGERIPKN	MEQYNLNHDH	CGNGLSSHFP	CSESQQHLNG
330	340	350	360	370	380	390	400
QFKGRNIMHY	PNGHAICIAN	GHCMNFSNAY	TQRVCDRVPI	DGFSQNENKN	SYLCNTGGRM	HLVCPMSKSP	YVDPHKSGHE
410	420	430	440	450			
IWEEFSMSFT	PAVKEVVEFA	KRIPGFRDLS	QHDQVNLLKA	GTFEIDLE			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1576	1	1011.7169	-72.08	3	49.6	10.7	1	96-124	K.FSGMVLLCKVCGDVASGFHYGVHACEGCK.G	Oxidation: 4
80	1	877.8666	-76.26	2	30.7	12.1	2	183-196	R.EKQRMLIEMQSAMK.T	Oxidation: 9, 13

Detailed Protein Report

Protein 146: PREDICTED: UPF0505 protein C16orf62 isoform X2 [Homo sapiens]

Accession:	gi|530408446	**Score:**	38.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	107.9
Database Date:	2015-11-30	**pI:**	8.9
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	5.7
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MAPAGVVTRA	VRSGELPLTS	MASAENEACA	VRSVACPSQA	WRLQKVLCGR	CGAASCPSQT	WRPRGAGSGG	VRMGSRADGP
90	100	110	120	130	140	150	160
RTSGHVTGKM	AVFPWHSRNR	NYKAEFASCR	LEAVPLEFGD	YHPLKPITVT	ESKTKKVNRK	GSTSSTSSSS	SSSVVDPLSS
170	180	190	200	210	220	230	240
VLDGTDPLSM	FAATADPAAL	AAAMDSSRRK	RDRDDNSVVG	SDFEPWTNKR	GEILARYTTT	EKLSINLFMG	SEKGKAGTAT
250	260	270	280	290	300	310	320
LAMSEKVRTR	LEELDDFEEG	SQKELLNLTQ	QDYVNRIEEL	NQSLKDAWAS	DQKVKALKIV	IQCSKLLSDT	SVIQFYPSKF
330	340	350	360	370	380	390	400
VLITDILDTF	GKLVYERIFS	MCVDSRSVLP	DHFSPENAND	TAKETCLNWF	FKIASIRELI	PRFYVEASIL	KCNKFLSKTG
410	420	430	440	450	460	470	480
ISECLPRLTC	MIRGIGDPLV	SVYARAYLCR	ALLTEMMERC	KKLGNNALLL	NSVMSAFRAE	FIATRSMDFI	GMIKECDESG
490	500	510	520	530	540	550	560
FPKHLLFRSL	GLNLALADPP	ESDRLQILNE	AWKVITKLKN	PQDYINCAEV	WVEYTCKHFT	KREVNTVLAD	VIKHMTPDRA
570	580	590	600	610	620	630	640
FEDSYPQLQL	IIKKVIAHFH	DFSVLFSVEK	FLPFLDMFQK	ESVRVEVCKC	IMDAFIKHQQ	EPTKDPVILN	ALLHVCKTMH
650	660	670	680	690	700	710	720
DSVNALTLED	EKRMLSYLIN	GFIKMVSFGR	DFEQQLSFYV	ESRSMFCNLE	PVLVQLIHAC	VAYCFITIPS	LAGIFTRLNL
730	740	750	760	770	780	790	800
YLHSGQVALA	NQCLSQADAF	FKAAISLVPE	VPKMINIDGK	MRPSESFLLE	FLCNFFSTLL	IVPDHPEHGV	LFLVRELLNV
810	820	830	840	850	860	870	880
IQDYTWEDNS	DEKIRIYTCV	LHLLSAMSQE	TYLYHIDKVD	SNDSLYGGDS	KFLAENNKLC	ETVMAQILEH	LKTLAKDEAL
890	900	910	920	930	940	950	960
KRQSSLGLSF	FNSILAHGDL	RNNKLNQLSV	NLWHLAQRHG	CADTRTMVKT	LEYIKKQSKQ	PDMTHLTELA	LRLPLQTRT

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1659	1	1273.7346	60.72	2	50.7	10.5	2	554-574	K.HMTPDRAFEDSYPQLQLIIKK.V	Oxidation: 2
1481	2	949.1566	5.84	3	48.3	12.1	2	902-925	R.NNKLNQLSVNLWHLAQRHGCADTR.T	Carbamidomethyl: 20

Detailed Protein Report

Protein 147: PREDICTED: uncharacterized protein LOC102723569 isoform X1 [Homo sapiens]

Accession:	gi|578835246	**Score:**	38.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	28.7
Database Date:	2015-11-30	**pI:**	10.2
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	15.3
		No. of unique Peptides:	1

Quantitation

MD:MU	**Median:** 1.33	**CV:** 0.00 %	**No. of Peptides:** 1

10	20	30	40	50	60	70	80
MCMASNAVCS	APETLAGYRI	IKMLPGSLKR	EDTRKQVKII	LLLFCIQQAS	YYGTAVMGQA	YLPELGTQWG	PPWLSLTGVT
90	100	110	120	130	140	150	160
TGCRQTPVLS	ILLARPAESS	ESRVGYWMPR	REEGAREVSP	KVLQGPQQAW	TEEVWTAWPC	PEPLCIITAV	PNLHPTLSLP
170	180	190	200	210	220	230	240
IPGPGALLLC	SRDSWSSLRQ	HTVLLWRRPS	PTHAGMLQPV	PEQVVAGGCW	QRRDNGPAPG	GKCWLQGTES	SPCHSPCYPL
250	260	270					
GNLKGISKNS	GSATLLSFLW	NM					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2778	2	958.9830	67.11	2	66.1	25.9	0	2-19	M.CMASNAVCSAPETLAGYR.I	Carbamidomethyl: 1; Oxidation: 2	MD:MU 1.33

Detailed Protein Report

Protein 148: **PREDICTED: vacuolar protein sorting-associated protein 8 homolog isoform X4 [Homo sapiens]**

Accession:	gi|530374200	**Score:**	37.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	117.1
Database Date:	2015-11-30	**pI:**	5.3
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MENEPDHENV	EQSLCAKTSE	EELNKSFNLE	ASLSKFSYID	MDKELEFKND	LIDDKEFDIP	QVDTPPTLES	ILNETDDEDE
90	100	110	120	130	140	150	160
SFILEDPTLL	NIDTIDSHSY	DTSSVASSDS	GDRTNLKRKK	KLPDSFSLHG	SVMRHSLLKG	ISAQIVSAAD	KVDAGLPTAI
170	180	190	200	210	220	230	240
AVSSLIAVGT	SHGLALIFGK	DQNQALRLCL	GSTSVGGQYG	AISALSINND	CSRLLCGFAK	GQITMWDLAS	GKLLRSITDA
250	260	270	280	290	300	310	320
HPPGTAILHI	KFTDDPTLAI	CNDSGGSVFE	LTFKRVMGVR	TCESRCLFSG	SKGEVCCIEP	LHSKPELKDH	PITQFSLLAM
330	340	350	360	370	380	390	400
ASLTKILVIG	LKPSLKVWMT	FPYGRMDPSS	VPLLAWHFVA	VQNYVNPMLA	FCRGDVVHFL	LVKRDESGAI	HVTKQKHLHL
410	420	430	440	450	460	470	480
YYDLINFTWI	NSRTVVLLDS	VEKLHVIDRQ	TQEELETVEI	SEVQLVYNSS	HFKSLATGGN	VSQALALVGE	KACYQSISSY
490	500	510	520	530	540	550	560
GGQIFYLGTK	SVYVMMLRSW	RERVDHLLKQ	DCLTEALALA	WSFHEGKAKA	VVGLSGDASK	RKAIVADRMV	EILFHYADRA
570	580	590	600	610	620	630	640
LKKCPDQGKI	QVMEQHFQDM	VPVIVDYCLL	LQRKDLLFSQ	MYDKLSENSV	AKGVFLECLE	PYILSDKLVG	ITPQVMKDLI
650	660	670	680	690	700	710	720
VHFQDKKLME	NVEALIVHMD	ITSLDIQQVV	LMCWENRLYD	AMIYVYNRGM	NEFISPMEKL	FRVIAPPLNA	GKTLTDEQVV
730	740	750	760	770	780	790	800
MGNKLLVYIS	CCLAGRAYPL	GDIPEDLVPL	VKNQVFEFLI	RLHSAEASPE	EEIYPYIRTL	LHFDTREFLN	VLALTFEDFK
810	820	830	840	850	860	870	880
NDKQAVEYQQ	RIVDILLKVM	VENSDFTPSQ	VGCLFTFLAR	QLAKPDNTLF	VNRTLFDQVL	EFLCSPDDDS	RHSERQQVLL
890	900	910	920	930	940	950	960
ELLQAGGIVQ	FEESRLIRMA	EKAEFYQICE	FMYEREHQYD	KIIDCYLRDP	LREEEVFNYI	HNILSIPGHS	AEEKQSVWQK
970	980	990	1000	1010	1020	1030	1040
AMDHIEELVS	LKPCKAAELV	ATHFSGHIET	VIKKLQNQVL	LFKFLRSLLD	PSCRFLMQWG	CLKDNTKGHV	FFVRP

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1784	1	840.7706	-147.85	2	52.3	10.4	1	36-48	K.FSYIDMDKELEFK.N	Oxidation: 6

Detailed Protein Report

Protein 149: mucin-2 precursor [Homo sapiens]

Accession:	gi|557129045	**Score:**	37.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	539.8
Database Date:	2015-11-30	**pI:**	5.4
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	1.1
		No. of unique Peptides:	2

Quantitation

MD:MU	**Median:**	1.17	**CV:**	0.00 %	**No. of Peptides:**	1	

10	20	30	40	50	60	70	80
MGLPLARLAA	VCLALSLAGG	SELQTEGRTR	NHGHNVCSTW	GNFHYKTFDG	DVFRFPGPCD	YNFASDCRGS	YKEFAVHLKR
90	100	110	120	130	140	150	160
GPGQAEAPAG	VESILLTIKD	DTIYLTRHLA	VLNGAVVSTP	HYSPGLLIEK	SDAYTKVYSR	AGLTLMWNRE	DALMLELDTK
170	180	190	200	210	220	230	240
FRNHTCGLCG	DYNGLQSYSE	FLSDGVLFSP	LEFGNMQKIN	QPDVVCEDPE	EEVAPASCSE	HRAECERLLT	AEAFADCQDL
250	260	270	280	290	300	310	320
VPLEPYLRAC	QQDRCRCPGG	DTCVCSTVAE	FSRQCSHAGG	RPGNWRTATL	CPKTCPGNLV	YLESGSPCMD	TCSHLEVSSL
330	340	350	360	370	380	390	400
CEEHRMDGCF	CPEGTVYDDI	GDSGCVPVSQ	CHCRLHGHLY	TPGQEITNDC	EQCVCNAGRW	VCKDLPCPGT	CALEGGSHIT
410	420	430	440	450	460	470	480
TFDGKTYTFH	GDCYYVLAKG	DHNDSYALLG	ELAPCGSTDK	QTCLKTVVLL	ADKKKNVVVF	KSDGSVLLNE	LQVNLPHVTA
490	500	510	520	530	540	550	560
SFSVFRPSSY	HIMVSMAIGV	RLQVQLAPVM	QLFVTLDQAS	QGQVQGLCGN	FNGLEGDDFK	TASGLVEATG	AGFANTWKAQ
570	580	590	600	610	620	630	640
STCHDKLDWL	DDPCSLNIES	ANYAEHWCSL	LKKTETPFGR	CHSAVDPAEY	YKRCKYDTCN	CQNNEDCLCA	ALSSYARACT
650	660	670	680	690	700	710	720
AKGVMLWGWR	EHVCNKDVGS	CPNSQVFLYN	LTTCQQTCRS	LSEADSHCLE	GFAPVDGCGC	PDHTFLDEKG	RCVPLAKCSC
730	740	750	760	770	780	790	800
YHRGLYLEAG	DVVVRQEERC	VCRDGRLHCR	QIRLIGQSCT	APKIHMDCSN	LTALATSKPR	ALSCQTLAAG	YYHTECVSGC
810	820	830	840	850	860	870	880
VCPDGLMDDG	RGGCVVEKEC	PCVHNNDLYS	SGAKIKVDCN	TCTCKRGRWV	CTQAVCHGTC	SIYGSGHYIT	FDGKYYDFDG
890	900	910	920	930	940	950	960
HCSYVAVQDY	CGQNSSLGSF	SIITENVPCG	TTGVTCSKAI	KIFMGRTELK	LEDKHRVVIQ	RDEGHHVAYT	TREVGQYLVV
970	980	990	1000	1010	1020	1030	1040
ESSTGIIVIW	DKRTTVFIKL	APSYKGTVCG	LCGNFDHRSN	NDFTTRDHMV	VSSELDFGNS	WKEAPTCPDV	STNPEPCSLN
1050	1060	1070	1080	1090	1100	1110	1120
PHRRSWAEKQ	CSILKSSVFS	ICHSKVDPKP	FYEACVHDSC	SCDTGGDCEC	FCSAVASYAQ	ECTKEGACVF	WRTPDLCPIF
1130	1140	1150	1160	1170	1180	1190	1200
CDYYNPPHEC	EWHYEPCGNR	SFETCRTING	IHSNISVSYL	EGCYPRCPKD	RPIYEEDLKK	CVTADKCGCY	VEDTHYPPGA
1210	1220	1230	1240	1250	1260	1270	1280
SVPTEETCKS	CVCTNSSQVV	CRPEEGKILN	QTQDGAFCYW	EICGPNGTVE	KHFNICSITT	RPSTLTTFTT	ITLPTTPTTF
1290	1300	1310	1320	1330	1340	1350	1360
TTTTTTTTPT	SSTVLSTTPK	LCCLWSDWIN	EDHPSSGSDD	GDRETFDGVC	GAPEDIECRS	VKDPHLSLEQ	LGQKVQCDVS
1370	1380	1390	1400	1410	1420	1430	1440
VGFICKNEDQ	FGNGPFGLCY	DYKIRVNCCW	PMDKCITTPS	PPTTTPSPPP	TSTTTLPPTT	TPSPPTTTTT	TPPPTTTPSP
1450	1460	1470	1480	1490	1500	1510	1520
PITTTTTPPP	TTTPSPPIST	TTTPPPTTTP	SPPTTTPSPP	TTTPSPPTTT	TTTPPPTTTP	SPPTTTPITP	PASTTTLPPT
1530	1540	1550	1560	1570	1580	1590	1600
TTPSPPTTTT	TTPPPTTTPS	PPTTTPITPP	TSTTTLPPTT	TPSPPPTTTT	TPPPTTTPSP	PTTTTPSPPT	ITTTTPPPTT
1610	1620	1630	1640	1650	1660	1670	1680
TPSPPTTTTT	TPPPTTTPSP	PTTTPITPPT	STTTLPPTTT	PSPPPTTTTT	PPPTTTPSPP	TTTTPSPPIT	TTTTPPPTTT
1690	1700	1710	1720	1730	1740	1750	1760
PSSPITTTPS	PPTTTMTTPS	PTTTPSSPIT	TTTTPSSTTT	PSPPPTTMTT	PSPTTTPSPP	TTTMTTLPPT	TTSSPLTTTP
1770	1780	1790	1800	1810	1820	1830	1840
LPPSITPPTF	SPFSTTTPTT	PCVPLCNWTG	WLDSGKPNFH	KPGGDTELIG	DVCGPGWAAN	ISCRATMYPD	VPIGQLGQTV
1850	1860	1870	1880	1890	1900	1910	1920
VCDVSVGLIC	KNEDQKPGGV	IPMAFCLNYE	INVQCCECVT	QPTTMTTTTT	ENPTPPTTTP	ITTTTTVTPT	PTPTGTQTPT
1930	1940	1950	1960	1970	1980	1990	2000
TTPITTTTTV	TPTPTPTGTQ	TPTTTPITTT	TTVTPTPTPT	GTQTPTTTPI	TTTTTVTPTP	TPTGTQTPTT	TPITTTTTVT
2010	2020	2030	2040	2050	2060	2070	2080
PTPTPTGTQT	PTTTPITTTT	TVTPTPTPTG	TQTPTTTPIT	TTTTVTPTPT	PTGTQTPTTT	PITTTTTVTP	TPTPTGTQTP
2090	2100	2110	2120	2130	2140	2150	2160
TTTPITTTTT	VTPTPTPTGT	QTPTTTPITT	TTTVTPTPTP	TGTQTPTTTP	ITTTTTVTPT	PTPTGTQTPT	TTPITTTTTV
2170	2180	2190	2200	2210	2220	2230	2240
TPTPTPTGTQ	TPTTTPITTT	TTVTPTPTPT	GTQTPTTTPI	TTTTTVTPTP	TPTGTQTPTT	TPITTTTTVT	PTPTPTGTQT
2250	2260	2270	2280	2290	2300	2310	2320
PTTTPITTTT	TVTPTPTPTG	TQTPTTTPIT	TTTTVTPTPT	PTGTQTPTTT	PITTTTTVTP	TPTPTGTQTP	TTTPITTTTT
2330	2340	2350	2360	2370	2380	2390	2400

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2678	1	857.6944	26.58	3	64.7	10.2	0	616-637	K.YDTCNCQNNEDCLCAALSSYAR.A	Carbamidomethyl: 4, 12	
2127	2	937.3845	-87.61	2	56.5	16.1	0	764-780	K.IHMDCSNLTALATSKPR.A	Oxidation: 3	MD:MU 1.17

Detailed Protein Report

Protein 150: PREDICTED: uncharacterized protein C22orf15 isoform X12 [Homo sapiens]

Accession:	gi|578836949	**Score:**	37.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	22.9
Database Date:	2015-11-30	**pI:**	11.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	14.6
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MFIKVMFGAG	CSVLVNTSCR	LVNLTAHLRQ	KAGLPPDATI	ALLAEDGNLV	SLEEDLKEGA	SRAQTMGNSL	LKERAIYVLV
90	100	110	120	130	140	150	160
RIIKGEDMAS	TRYESLLENL	DDHYPELAEE	LRRLSGLSSV	GHNWRKRMGT	RRGRHEQSPT	SRPRKVQTDN	NPAGLLLQNL
170	180	190	200	210			
ELLRSCISKR	GKVRQDLRPP	GAPKLWVQRM	GCRGRDKKGR	GGRYP			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1676	1	1045.0153	-7.55	2	50.7	23.1	1	2-20	M.FIKVMFGAGCSVLVNTSCR.L	Carbamidomethyl: 18
2567	1	709.8660	-0.61	2	62.5	14.7	2	185-195	K.LWVQRMGCRGR.D	Carbamidomethyl: 8

Detailed Protein Report

Protein 151: zinc finger CCCH domain-containing protein 13 [Homo sapiens]

Accession:	gi|116008442	**Score:**	37.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	184.8
Database Date:	2015-11-30	**pI:**	10.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.9
		No. of unique Peptides:	3

Alias proteins:

Accession	Name	Description
gi|530402208	refseq_human (refseq_human_20140103.fasta)	PREDICTED: zinc finger CCCH domain-containing protein 13 isoform X12 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MSKIRRKVTV ENTKTISDST SRRPSVFERL GPSTGSTAET QCRNWLKTGN CLYGNTCRFV HGPSPRGKGY SSNYRRSPER
        90        100        110        120        130        140        150        160
PTGDLRERMK NKRQDVDTEP QKRNTEESSS PVRKESSRGR HREKEDIKIT KERTPESEEE NVEWETNRDD SDNGDINYDY
       170        180        190        200        210        220        230        240
VHELSLEMKR QKIQRELMKL EQENMEKREE IIIKKEVSPE VVRSKLSPSP SLRKSSKSPK RKSSPKSSSA SKKDRKTSAV
       250        260        270        280        290        300        310        320
SSPLLDQQRN SKTNQSKKKG PRTPSPPPPI PEDIALGKKY KEKYKVKDRI EEKTRDGKDR GRDFERQREK RDKPRSTSPA
       330        340        350        360        370        380        390        400
GQHHSPISSR HHSSSSQSGS SIQRHSPSPR RKRTPSPSYQ RTLTPPLRRS ASPYPSHSLS SPQRKQSPPR HRSPMREKGR
       410        420        430        440        450        460        470        480
HDHERTSQSH DRRHERREDT RGKRDREKDS REEREYEQDQ SSSRDHRDDR EPRDGRDRRD ARDTRDRREL RDSRDMRDSR
       490        500        510        520        530        540        550        560
EMRDYSRDTK ESRDPRDSRS TRDAHDYRDR EGRDTHRKED TYPEESRSYG RNHLREESSR TEIRNESRNE SRSEIRNDRM
       570        580        590        600        610        620        630        640
GRSRGRVPEL PEKGSRGSRG SQIDSHSSNS NYHDSWETRS SYPERDRYPE RDNRDQARDS SFERRHGERD RRDNRERDQR
       650        660        670        680        690        700        710        720
PSSPIRHQGR NDELERDERR EERRVDRVDD RRDERARERD RERERDRERE RERERERDRE REKERELERE RARERERERE
       730        740        750        760        770        780        790        800
KERDRERDRD RDHDRERERE RERDREKERE REREERERER ERERERERER ERERERARER DKERERQRDW EDKDKGRDDR
       810        820        830        840        850        860        870        880
REKREEIRED RNPRDGHDER KSKKRYRNEG SPSPRQSPKR RREHSPDSDA YNSGDDKNEK HRLLSQVVRP QESRSLSPSH
       890        900        910        920        930        940        950        960
LTEDRQGRWK EEDRKPERKE SSRRYEEQEL KEKVSSVDKQ REQTEILESS RMRAQDIIGH HQSEDRETSD RAHDENKKKA
       970        980        990       1000       1010       1020       1030       1040
KIQKKPIKKK KEDDVGIERG NIETTSEDGQ VFSPKKGQKK KSIEKKRKKS KGDSDISDEE AAQQSKKKRG PRTPPITTKE
      1050       1060       1070       1080       1090       1100       1110       1120
ELVEMCNGKN GILEDSQKKE DTAFSDWSDE DVPDRTEVTE AEHTATATTP GSTPSPLSSL LPPPPPVATA TATTVPATLA
      1130       1140       1150       1160       1170       1180       1190       1200
ATTAAAATSF STSAITISTS ATPTNTTNNT FANEDSHRKC HRTRVEKVET PHVTIEDAQH RKPMDQKRSS SLGSNRSNRS
      1210       1220       1230       1240       1250       1260       1270       1280
HTSGRLRSPS NDSAHRSGDD QSGRKRVLHS GSRDREKTKS LEITGERKSR IDQLKRGEPS RSTSSDRQDS RSHSSRRSSP
      1290       1300       1310       1320       1330       1340       1350       1360
ESDRQVHSRS GSFDSRDRLQ ERDRYEHDRE RERERRDTRQ REWDRDADKD WPRNRDRDRL RERERERERD KRRDLDRERE
      1370       1380       1390       1400       1410       1420       1430       1440
RLISDSVERD RDRDRDRTFE SSQIESVKRC EAKLEGEHER DLESTSRDSL ALDKERMDKD LGSVQGFEET NKSERTESLE
      1450       1460       1470       1480       1490       1500       1510       1520
AGDDESKLDD AHSLGSGAGE GYEPISDDEL DEILAGDAEK REDQQDEEKM PDPLDVIDVD WSGLMPKHPK EPREPGAALL
      1530       1540       1550       1560       1570
KFTPGAVMLR VGISKKLAGS ELFAKVKETC QRLLEKPKGS FILL
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
760	1	856.2336	-297.82	1	38.9	11.7	0	206-213	K.LSPSPSLR.K	
1864	1	606.2622	-6.93	2	53.3	12.3	2	475-483	R.DMRDSREMR.D	Oxidation: 8

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1287	1	795.9839	117.71	2	45.8	13.8	2	528-540	R.SYGRNHLREESSR.T	

Detailed Protein Report

Protein 152: **PREDICTED: 1-acyl-sn-glycerol-3-phosphate acyltransferase gamma isoform X1 [Homo sapiens]**

Accession:	gi|530419317	**Score:**	37.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	52.2
Database Date:	2015-11-30	**pI:**	9.9
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	6.0
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MCITALSVAP	KGWVPAACRQ	GAYHRGTSMP	WGSLSSHGCA	LGAVPGPSQK	HRAGPAGPDA	MGFCVCEPLE	KDGCPQRGAV
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
HPLLSSAMGL	LAFLKTQFVL	HLLVGFVFVV	SGLVINFVQL	CTLALWPVSK	QLYRRLNCRL	AYSLWSQLVM	LLEWWSCTEC
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
TLFTDQATVE	RFGKEHAVII	LNHNFEIDFL	CGWTMCERFG	VLGSSKVLAK	KELLYVPLIG	WTWYFLEIVF	CKRKWEEDRD
250	**260**	**270**	**280**	**290**	**300**	**310**	**320**
TVVEGLRRLS	DYPEYMWFLL	YCEGTRFTET	KHRVSMEVAA	AKGLPVLKYH	LLPRTKGFTT	AVKCLRGTVA	AVYDVTLNFR
330	**340**	**350**	**360**	**370**	**380**	**390**	**400**
GNKNPSLLGI	LYGKKYEADM	CVRRFPLEDI	PLDEKEAAQW	LHKLYQEKDA	LQEIYNQKGM	FPGEQFKPAR	RPWTLLNFLS
410	**420**	**430**	**440**	**450**	**460**	**470**	
WATILLSPLF	SFVLGVFASG	SPLLILTFLG	FVGAASFGVR	RLIGVTEIEK	GSSYGNQEFK	KKE	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2765	2	702.0547	47.21	3	65.9	20.2	1	1-19	-.MCITALSVAPKGWVPAACR.Q	Carbamidomethyl: 2, 18; Oxidation: 1
2735	1	905.4845	9.33	1	65.5	17.5	0	274-282	R.VSMEVAAAK.G	

Detailed Protein Report

Protein 153: **PREDICTED: probable ATP-dependent RNA helicase DDX60-like isoform X6 [Homo sapiens]**

Accession:	gi|578809622	**Score:**	37.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	193.4
Database Date:	2015-11-30	**pI:**	9.2
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	2.2
		No. of unique Peptides:	3

Quantitation

MD:MU **Median:** 1.16 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MGSKDHAVFF	REMTQLILNE	MPKAGYSSIL	NDFVESNFFV	IDGDSLLVTC	LGVKSFKWGQ	NLHFFYLVEC	YLVDLLSNGG
90	100	110	120	130	140	150	160
QFTIVFFKDA	EYAYFDFPEL	LSLRTALILH	LQHNTNIDVQ	TEFSGCLSQD	WKLFLEQHYP	YFLIVSEEGL	SDLQTYLFNF
170	180	190	200	210	220	230	240
LIIHSWGMKV	NVVLSSGHES	DTLRFYAYTM	ESTDRNQTFS	KENETVIQSA	YKSLIQHLEE	IRVLVLATHF	EHLKWNDMME
250	260	270	280	290	300	310	320
EAYQTLFLLQ	HLWSEGSDIQ	RVLCVTSCSL	SLRMYHRVLV	HSNCLSLQEV	EDFCRLRCLC	VAFQLHLPLS	QRACSRVITC
330	340	350	360	370	380	390	400
SWIRNSDSFL	KMNKWCEYFI	LSNLNVFGCW	NLNLNHVSDL	YDEQLLKNIA	FYYEFESTQE	PHLNLGDSIR	RDYEDLWNVV
410	420	430	440	450	460	470	480
SHLVKEFNVG	KSFPLRTTRR	HFLRQEKSVI	QEISLEKMPS	VGFIPMTSAV	IDEFVGDMMK	DLPILKSDDP	VVPSLFKQKT
490	500	510	520	530	540	550	560
SDELLHWHAQ	RLLSDDYDRI	KCHVDEQSRD	PHVLDFLKKI	QDYQQFYGKS	LESISTKVIV	TQTTRPKEDS	SGASGEILQN
570	580	590	600	610	620	630	640
TKPHQITKKS	KKKSFLKEDQ	NKAQQNDDLL	FSIEEEMKNN	LHSGIRKLED	YLTSCASNSV	KFGVEMLGLI	ACFKAWKKHC
650	660	670	680	690	700	710	720
RGEGKISKDL	SIAVQMMKRI	HSLLERYPEI	LEAEHHQYIA	KCLKYLGFND	LANSLDPTLI	GDDKNKKKYS	IDIGPARFQL
730	740	750	760	770	780	790	800
QYMGHYLIRD	ERKDRDPRVQ	DFIPNAWQQE	LLDVVDKNES	AVIVAPTSSG	KTYASYYCME	KVLRESDVGV	VVYVAPAKSL
810	820	830	840	850	860	870	880
VGQVAATVEN	RFTKTLPAGR	TLCGAFTRDY	CHNVLNCQVL	ITVPECFEIL	LLAPHRQKWV	ERIRYVIFDE	VHYLGREVGA
890	900	910	920	930	940	950	960
KFWELLLVII	RCPFLVLSAT	INNPNLLTKW	LQSVKQYWKQ	ADKIMEEKCI	SEKQADKCLN	FLQDHSYKNQ	SYEVRLVLCG
970	980	990	1000	1010	1020	1030	1040
ERYNDLEKHI	CSVKHDDVYF	DHFHPCAALT	TDIIEKYGFP	PDLTLTPQES	IQLYDTMAQV	WETWPRAQEL	CPEEFILFKN
1050	1060	1070	1080	1090	1100	1110	1120
KIVIKKLDAR	KYEENLKAEL	TNWIKNGQVK	KVKRVLKNLS	PDSLSSSKDM	VKMFPLLVEK	LRQMDKLPAI	FFLFKNDDVG
1130	1140	1150	1160	1170	1180	1190	1200
KRAGSVCTFL	EKTETKSHPH	TECHSYVFAI	DEVLEKVRKT	QKRISTKKNP	KKAEKLERKK	VYRAEYINFL	ENLKILEISE
1210	1220	1230	1240	1250	1260	1270	1280
DCTYADVKAL	HTEITRNKDS	TLERVLPRVR	FTRHGKELKA	LAQRGIGYHH	SSMYFKEKEF	VEILFVKGLI	RVVTATETLA
1290	1300	1310	1320	1330	1340	1350	1360
LGIHMPCKSV	VFAQDSVYLD	ALNYRQMSGR	AGRRGQDLLG	NVYFFDIPLP	KIKRLLASSV	PELRGQFPLS	ITLVLRLMLL
1370	1380	1390	1400	1410	1420	1430	1440
ASKGDDPEDA	KAKDYLNKKG	NPKKFAGLAS	YLHGHEPSNL	VFVNFLKRGL	FHNLCKPAWK	GSQQFSQDVM	EKLVLVLANL
1450	1460	1470	1480	1490	1500	1510	1520
FGRKYIPAKF	QNANLSFSQS	KVILAELPED	FKAALYEYNL	AVMKDFASFL	LIASKSVNMK	KEHQLPLSRI	KFTGKECEDS
1530	1540	1550	1560	1570	1580	1590	1600
QLVSHLMSCK	KGRVAISPFV	CLSGNTDNDL	LRPETINQVI	LRTVGVSGTQ	APLLWPWKLD	NRGRRMPLNA	YVLNFYKHNC
1610	1620	1630	1640	1650	1660	1670	1680
LTRLDQKNGM	RMGQLLKCLK	DFAFNIQAIS	DSLSELCENK	RDNVVLAFKQ	LSQTFYEKLQ	EMQIQMSQNH	LE

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

			[ppm]								
1058	1	586.1731	-222.69	2	42.8	12.2	2	639-648	K.HCRGEGKISK.D	Carbamidomethyl: 2	
225	1	641.7812	-36.28	2	32.5	12.3	1	924-933	K.IMEEKCISEK.Q	Carbamidomethyl: 6; Oxidation: 2	
1639	1	926.8312	-90.99	2	50.2	13.2	1	1516-1531	K.ECEDSQLVSHLMSCKK.G	Oxidation: 12	MD:MU 1.16

Detailed Protein Report

Protein 154: PREDICTED: cytoplasmic tyrosine-protein kinase BMX isoform X1 [Homo sapiens]

Accession:	gi|578837945	**Score:**	37.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	77.9
Database Date:	2015-11-30	**pI:**	9.3
Modification(s):	Oxidation	**Sequence Coverage [%]:**	5.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDTKSILEEL	LLKRSQQKKK	MSPNNYKERL	FVLTKTNLSY	YEYDKMKRGS	RKGSIEIKKI	RCVEKVNLEE	QTPVERQYPF
90	100	110	120	130	140	150	160
QIVYKDGLLY	VYASNEESRS	QWLKALQKEI	RGNPHLLVKY	HSGFFVDGKF	LCCQQSCKAA	PGCTLWEAYA	NLHTAVNEEK
170	180	190	200	210	220	230	240
HRVPTFPDRV	LKIPRAVPVL	KMDAPSSSTT	LAQYDNESKK	NYGSQPPSSS	TSLAQYDSNS	KKIYGSQPNF	NMQYIPREDF
250	260	270	280	290	300	310	320
PDWWQVRKLK	SSSSEDVASS	NQKERNVNHT	TSKISWEFPE	SSSSEEEENL	DDYDWFAGNI	SRSQSEQLLR	QKGKEGAFMV
330	340	350	360	370	380	390	400
RNSSQVGMYT	VSLFSKAVND	KKGTVKHYHV	HTNAENKLYL	AENYCFDSIP	KLIHYHQHNS	AGMITRLRHP	VSTKANKVPD
410	420	430	440	450	460	470	480
SVSLGNGIWE	LKREEITLLK	ELGSGQFGVV	QLGKWKGQYD	VAVKMIKEGS	MSEDEFFQEA	QTMMKLSHPK	LVKFYGVCSK
490	500	510	520	530	540	550	560
EYPIYIVTEY	ISNGCLLNYL	RSHGKGLEPS	QLLEMCYDVC	EGMAFLESHQ	FIHRDLAARN	CLVDRDLCVK	VSDFGMTRYV
570	580	590	600	610	620	630	640
LDDQYVSSVG	TKFPVKWSAP	EVFHYFKYSS	KSDVWAFGIL	MWEVFSLGKQ	PYDLYDNSQV	VLKVSQGHRL	YRPHLASDTI
650	660	670	680				
YQIMYSCWHE	LPEKRPTFQQ	LLSSIEPLRE	KDKH				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2282	1	701.1125	131.58	3	58.4	20.9	0	592-609	K.SDVWAFGILMWEVFSLGK.Q	Oxidation: 10

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Detailed Protein Report

Protein 155: PREDICTED: tudor domain-containing protein 7 isoform X2 [Homo sapiens]

Accession:	gi|578817240	**Score:**	37.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	74.0
Database Date:	2015-11-30	**pI:**	6.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	6.6
		No. of unique Peptides:	2

Quantitation

MD:MU **Median:** 0.75 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MAFGYLSFHI	FTKSYIKKTL	IKEFYNSLNT	GLIFARYVGK	DYSAAQELME	DEMKEYYSKN	PKITPVQAVN	VGQLLAVNAE
90	100	110	120	130	140	150	160
EDAWLRAQVI	STEENKIKVC	YVDYGFSENV	EKSKAYKLNP	KFCSLSFQAT	KCKLAGLEVL	SDDPDLVKVV	ESLTCGKIFA
170	180	190	200	210	220	230	240
VEILDKADIP	LVVLYDTSGE	DDININATCL	KAICDKSLEV	HLQVDAMYTN	VKVTNICSDG	TLYCQVPCKG	LNKLSDLLRK
250	260	270	280	290	300	310	320
IEDYFHCKHM	TSECFVSLPF	CGKICLFHCK	GKWLRVEITN	VHSSRALDVQ	FLDSGTVTSV	KVSELREIPP	RFLQEMIAIP
330	340	350	360	370	380	390	400
PQAIKCCLAD	LPQSIGMWTP	DAVLWLRDSV	LNCSDCSIKV	TKVDETRGIA	HVYLFTPKNF	PDPHRSINRQ	ITNADLWKHQ
410	420	430	440	450	460	470	480
KDVFLSAISS	GADSPNSKNG	NMPMSGNTGE	NFRKNLTDVI	KKSMVDHTSA	FSTEELPPPV	HLSKPGEHMD	VYVPVACHPG
490	500	510	520	530	540	550	560
YFVIQPWQEI	HKLEVLMEEM	ILYYSVSEER	HIAVEKDQVY	AAKVENKWHR	VLLKGILTNG	LVSVYELDYG	KHELVNIRKV
570	580	590	600	610	620	630	640
QPLVDMFRKL	PFQAVTAQLA	GVKCNQWSEE	ASMVFRNHVE	KKPLVALVQT	VIENANPWDR	KVVVYLVDTS	LPDTDTWIHD
650	660						
FMSEYLIELS	KVN						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1797	1	851.2615	-133.71	2	52.3	11.4	0	249-263	K.HMTSECFVSLPFCGK.I	Oxidation: 2	MD:MU 0.75
2544	1	885.4222	38.31	2	61.8	14.1	1	419-434	K.NGNMPMSGNTGENFRK.N	Oxidation: 4	

Detailed Protein Report

Protein 156: PREDICTED: utrophin isoform X8 [Homo sapiens]

Accession:	gi|578812959	**Score:**	37.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	287.1
Database Date:	2015-11-30	**pI:**	5.2
Modification(s):	Oxidation	**Sequence Coverage [%]:**	0.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSLMILPRWR	RPCKKKKTLD	EILENQKPAL	HKLAEETKAL	EKNVHPDVEK	LYKQEFDDVQ	GKWNKLKVLV	SKDLHLLEEI
90	100	110	120	130	140	150	160
ALTLRAFEAD	STVIEKWMDG	VKDFLMKQQA	AQGDDAGLQR	QLDQCSAFVN	EIETIESSLK	NMKEIETNLR	SGPVAGIKTW
170	180	190	200	210	220	230	240
VQTRLGDYQT	QLEKLSKEIA	TQKSRLSESQ	EKAANLKKDL	AEMQEWMTQA	EEEYLERDFE	YKSPEELESA	VEEMKRAKED
250	260	270	280	290	300	310	320
VLQKEVRVKI	LKDNIKLLAA	KVPSGGQELT	SELNVVLENY	QLLCNRIRGK	CHTLEEVWSC	WIELLHYLDL	ETTWLNTLEE
330	340	350	360	370	380	390	400
RMKSTEVLPE	KTDAVNEALE	SLESVLRHPA	DNRTQIRELG	QTLIDGGILD	DIISEKLEAF	NSRYEDLSHL	AESKQISLEK
410	420	430	440	450	460	470	480
QLQVLRETDQ	MLQVLQESLG	ELDKQLTTYL	TDRIDAFQVP	QEAQKIQAEI	SAHELTLEEL	RRNMRSQPLT	SPESRTARGG
490	500	510	520	530	540	550	560
SQMDVLQRKL	REVSTKFQLF	QKPANFEQRM	LDCKRVLDGV	KAELHVLDVK	DVDPDVIQTH	LDKCMKLYKT	LSEVKLEVET
570	580	590	600	610	620	630	640
VIKTGRHIVQ	KQQTDNPKGM	DEQLTSLKVL	YNDLGAQVTE	GKQDLERASQ	LARKMKKEAA	SLSEWLSATE	TELVQKSTSE
650	660	670	680	690	700	710	720
GLLGDLDTEI	SWAKNVLKDL	EKRKADLNTI	TESSAALQNL	IEGSEPILEE	RLCVLNAGWS	RVRTWTEDWC	NTLMNHQNQL
730	740	750	760	770	780	790	800
EIFDGNVAHI	STWLYQAEAL	LDEIEKKPTS	KQEEIVKRLV	SELDDANLQV	ENVRDQALIL	MNARGSSSRE	LVEPKLAELN
810	820	830	840	850	860	870	880
RNFEKVSQHI	KSAKLLIAQE	PLYQCLVTTE	TFETGVPFSD	LEKLENDIEN	MLKFVEKHLE	SSDEDEKMDE	ESAQIEEVLQ
890	900	910	920	930	940	950	960
RGEEMLHQPM	EDNKKEKIRL	QLLLLHTRYN	KIKAIPIQQR	KMGQLASGIR	SSLLPTDYLV	EINKILLCMD	DVELSLNVPE
970	980	990	1000	1010	1020	1030	1040
LNTAIYEDFS	FQEDSLKNIK	DQLDKLGEQI	AVIHEKQPDV	ILEASGPEAI	QIRDTLTQLN	AKWDRINRMY	SDRKGCFDRA
1050	1060	1070	1080	1090	1100	1110	1120
MEEWRQFHCD	LNDLTQWITE	AEELLVDTCA	PGGSLDLEKA	RIHQQELEVG	ISSHQPSFAA	LNRTGDGIVQ	KLSQADGSFL
1130	1140	1150	1160	1170	1180	1190	1200
KEKLAGLNQR	WDAIVAEVKD	RQPRLKGESK	QVMKYRHQLD	EIICWLTKAE	HAMQKRSTTE	LGENLQELRD	LTQEMEVHAE
1210	1220	1230	1240	1250	1260	1270	1280
KLKWLNRTEL	EMLSDKSLSL	PERDKISESL	RTVNMTWNKI	CREVPTTLKE	CIQEPSSVSQ	TRIAAHPNVQ	KVVLVSSASD
1290	1300	1310	1320	1330	1340	1350	1360
IPVQSHRTSE	ISIPADLDKT	ITELADWLVL	IDQMLKSNIV	TVGDVEEINK	TVSRMKITKA	DLEQRHPQLD	YVFTLAQNLK
1370	1380	1390	1400	1410	1420	1430	1440
NKASSSDMRT	AITEKLERVK	NQWDGTQHGV	ELRQQQLEDM	IIDSLQWDDH	REETEELMRK	YEARLYILQQ	ARRDPLTKQI
1450	1460	1470	1480	1490	1500	1510	1520
SDNQILLQEL	GPGDGIVMAF	DNVLQKLLEE	YGSDDTRNVK	ETTEYLKTSW	INLKQSIADR	QNALEAEWRT	VQASRRDLEN
1530	1540	1550	1560	1570	1580	1590	1600
FLKWIQEAET	TVNVLVDASH	RENALQDSIL	ARELKQQMQD	IQAEIDAHND	IFKSIDGNRQ	KMVKALGNSE	EATMLQHRLD
1610	1620	1630	1640	1650	1660	1670	1680
DMNQRWNDLK	AKSASIRAHL	EASAEKWNRL	LMSLEELIKW	LNMKDEELKK	QMPIGGDVPA	LQLQYDHCKA	LRRELKEKEY
1690	1700	1710	1720	1730	1740	1750	1760
SVLNAVDQAR	VFLADQPIEA	PEEPRRNLQS	KTELTPEERA	QKIAKAMRKQ	SSEVKEKWES	LNAVTSNWQK	QVDKALEKLR
1770	1780	1790	1800	1810	1820	1830	1840
DLQGAMDDLD	ADMKEAESVR	NGWKPVGDLL	IDSLQDHIEK	IMAFREEIAP	INFKVKTVND	LSSQLSPLDL	HPSLKMSRQL
1850	1860	1870	1880	1890	1900	1910	1920
DDLNMRWKLL	QVSVDDRLKQ	LQEAHRDFGP	SSQHFLSTSV	QLPWQRSISH	NKVPYYINHQ	TQTTCWDHPK	MTELFQSLAD
1930	1940	1950	1960	1970	1980	1990	2000
LNNVRFSAYR	TAIKIRRLQK	ALCLDLLELS	TTNEIFKQHK	LNQNDQLLSV	PDVINCLTTT	YDGLEQMHKD	LVNVPLCVDM
2010	2020	2030	2040	2050	2060	2070	2080
CLNWLLNVYD	TGRTGKIRVQ	SLKIGLMSLS	KGLLEEKYRY	LFKEVAGPTE	MCDQRQLGLL	LHDAIQIPRQ	LGEVAAFGGS
2090	2100	2110	2120	2130	2140	2150	2160
NIEPSVRSCF	QQNNNKPEIS	VKEFIDWMHL	EPQSMVWLPV	LHRVAAAETA	KHQAKCNICK	ECPIVGFRYR	SLKHFNYDVC
2170	2180	2190	2200	2210	2220	2230	2240
QSCFFSGRTA	KGHKLHYPMV	EYCIPTTSGE	DVRDFTKVLK	NKFRSKKYFA	KHPRLGYLPV	QTVLEGDNLE	TPITLISMWP
2250	2260	2270	2280	2290	2300	2310	2320
EHYDPSQSPQ	LFHDDTHSRI	EQYATRLAQM	ERTNGSFLTD	SSSTTGSVED	EHALIQQYCQ	TLGGESPVSQ	PQSPAQILKS
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
1249	1	764.3778	23.73	2	45.3	11.3	2	1023-1033	K.WDRINRMYSDR.K	Oxidation: 7

Detailed Protein Report

Protein 157: peptidyl-prolyl cis-trans isomerase A [Homo sapiens]

Accession:	gi|10863927	**Score:**	37.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	18.0
Database Date:	2015-11-30	**pI:**	9.0
		Sequence Coverage [%]:	27.3
		No. of unique Peptides:	2

```
         10         20         30         40         50         60         70         80
MVNPTVFFDI AVDGEPLGRV SFELFADKVP KTAENFRALS TGEKGFGYKG SCFHRIIPGF MCQGGDFTRH NGTGGKSIYG
         90        100        110        120        130        140        150        160
EKFEDENFIL KHTGPGILSM ANAGPNTNGS QFFICTAKTE WLDGKHVVFG KVKEGMNIVE AMERFGSRNG KTSKKITIAD
        170
CGQLE
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2768	1	973.5119	7.60	2	65.0	13.8	0	2-19	M.VNPTVFFDIAVDGEPLGR.V	
2048	2	753.7914	-137.80	2	55.7	13.1	2	152-165	K.TSKKITIADCGQLE.-	

Detailed Protein Report

Protein 158:	**polycystic kidney disease and receptor for egg jelly-related protein precursor [Homo sapiens]**		
Accession:	gi|5174633	**Score:**	37.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	255.3
Database Date:	2015-11-30	**pI:**	10.0
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	1.5
		No. of unique Peptides:	3

10	20	30	40	50	60	70	80
MRPGPALLLL	GVGLSLSVGR	LPLPPVPRGA	QAAVSGAPGG	LLRGAPGLGV	RGGRALLSLR	PSAVRAGGAV	LSGRGSLCFP
90	100	110	120	130	140	150	160
HGGTGRRWYC	LDLRVLLSAQ	RLPWPAAPAL	ALVDLQLSAR	GGRLSLTWSV	RLPRSPGRLA	WAFRLRLLGP	GAARPASPAA
170	180	190	200	210	220	230	240
RVSPRSAAPG	PRPQQGFVAR	TECPTDGPAR	VMLQAVNSSS	HRAVESSVSC	QINACVIQRV	RINTDQKGAP	VRLSMQAEAT
250	260	270	280	290	300	310	320
INASVQLDCP	AARAIAQYWQ	VFSVPAVGQA	PDWTQPLDLP	QLEIRNSPLF	IHIPNNSLQW	GVYVFNFTVS	ITTGNPKMPE
330	340	350	360	370	380	390	400
VKDSDAVYVW	IVRSSLQAVM	LGDANITANF	TEQLILDGST	SSDPDADSPL	QGLQFFWYCT	TDPRNYGGDR	IILGSKEVCH
410	420	430	440	450	460	470	480
PEQANLKWPW	ASGPVLTLLP	ETLKGDHVYF	FRMVIRKDSR	TAFSDKRVHV	LQGPKAIAHI	TCIENCERNF	IVSDRFSLFL
490	500	510	520	530	540	550	560
NCTNCASRDF	YKWSILSSSG	GEMLFDWMGE	TVTGRNGAYL	SIKAFAFRHF	LEAEFSISLY	LACWSGVTSV	FRHSFIINHG
570	580	590	600	610	620	630	640
PQIGECKINP	AKGIALITKF	VVQCSNFRDK	HVPLTYKIIV	SDLHSVGEIS	SVKENTLGTI	LYLGPQSTVP	PSFLPVGMLA
650	660	670	680	690	700	710	720
SQYGLKIYAQ	VYDSLGAFSQ	VTLHATAQAP	TDKNSSKTVL	NQLLSFTVGP	SSLLSTLIQK	KDFLPAGYLL	YIVASVLNNM
730	740	750	760	770	780	790	800
KTELPLRDDR	VNLRKHLIDQ	SFLLPVSTLV	EIGQVVMTIT	KLTQKPSEFT	WDAQKRATMR	VWQANQALQE	YQQKDKRFRS
810	820	830	840	850	860	870	880
EQIEIVSTGI	LMSLSNILKM	TSPHQVVKDP	FYVIESLSDT	ILANKVPGNK	TTSMRTPNFN	MYVKKVEKWG	INQLFRNEKH
890	900	910	920	930	940	950	960
CRNCFYPTLN	VSSVPGLSAN	GPISTMFCDF	TNDLFPWLND	QENTSVEVSG	FRMTGVADNG	SVLEITPDVA	EVYLVRKNLT
970	980	990	1000	1010	1020	1030	1040
FAAFNLTVGP	NSEVDGSLKK	TTGGFSFQVD	STVLREVLVH	IVTEVMVLFT	VLVYTGSQIT	PTALVATFLV	PHDIPPFASQ
1050	1060	1070	1080	1090	1100	1110	1120
SALFDPACTV	KKARVVCLPV	SLLQLIAQHS	HSPHCTVSIV	LQAPRFVMKL	NDKLVRISIF	SVQCLDMYGI	QSEWREGYCI
1130	1140	1150	1160	1170	1180	1190	1200
LGEKTSWYEV	HCICKNVVRA	RRQLGTIGLT	GIHLHTHYVM	AKVIVIPNPV	DLRLNIIKSL	HQNPVTLFTV	LFIILLYVGL
1210	1220	1230	1240	1250	1260	1270	1280
AFWALYRDEM	DQHLRGHVIV	LPDNDPYDNL	CYLVTIFTGS	RWGSGTRANV	FVQLRGTVST	SDVHCLSHPH	FTTLYRGSIN
1290	1300	1310	1320	1330	1340	1350	1360
TFLLTTKSDL	GDIHSIRVWH	NNEGRSPSWY	LSRIKVENLF	SRHIWLFICQ	KWLSVDTTLD	RTFHVTHPDE	RLTRKDFFFI
1370	1380	1390	1400	1410	1420	1430	1440
DVSSNLRKNH	MWFSIFASVV	AKTFNRLQRL	SCCLAMLLSS	LLCNIMFFNL	NRQEQTESRE	RKYMRSMMIG	IESVLITIPV
1450	1460	1470	1480	1490	1500	1510	1520
QLLITFLFTC	SQRKPQADLK	EVSPQKHPLM	SEASEHWEEY	LRKWHAYETA	KVHPREVAKP	ASKGKPRLPK	ASPKATSKPK
1530	1540	1550	1560	1570	1580	1590	1600
HRHRKAQIKT	PETLGPNTNS	NNNIEDDQDV	HSEQHPSQKD	LQQLKKKPRI	VLPWWCVYVA	WFLVFATSSI	SSFFIVFYGL
1610	1620	1630	1640	1650	1660	1670	1680
TYGYDKSIEW	LFASFCSFCQ	SVLLVQPSKI	ILLSGFRTNK	PKYCKNLSWS	TKYKYTEIRL	DGMRMHPEEM	QRIHDQIVRI
1690	1700	1710	1720	1730	1740	1750	1760
RGTRMYQPLT	EDEIRIFKRK	KRIKRRALLF	LSYILTHFIF	LALLLILIVL	LRHTDCFYYN	QFIRDRFSMD	LATVTKLEDI
1770	1780	1790	1800	1810	1820	1830	1840
YRWLNSVLLP	LLHNDLNPTF	LPESSSKILG	LPLMRQVRAK	SSEKMCLPAE	KFVQNSIRRE	IHCHPKYGID	PEDTKNYSGF
1850	1860	1870	1880	1890	1900	1910	1920
WNEVDKQAID	ESTNGFTYKP	QGTQWLYYSY	GLLHTYGSGG	YALYFFPEQQ	RFNSTLRLKE	LQESNWLDEK	TWAVVLELTT
1930	1940	1950	1960	1970	1980	1990	2000
FNPDINLFCS	ISVIFEVSQL	GVVNTSISLH	SFSLADFDRK	ASAEIYLYVA	ILIFFLAYVV	DEGCIIMQER	ASYVRSVYNL
2010	2020	2030	2040	2050	2060	2070	2080
LNFALKCIFT	VLIVLFLRKH	FLATGIIRFY	LSNPEDFIPF	HAVSQVDHIM	RIILGFLLFL	TILKTLRYSR	FFYDVRLAQR
2090	2100	2110	2120	2130	2140	2150	2160
AIQAALPGIC	HMAFVVSVYF	FVYMAFGYLV	FGQHEWNYSN	LIHSTQTVFS	YCVSAFQNTE	FSNNRILGVL	FLSSFMLVMI
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2763	1	741.8475	25.09	2	64.9	12.5	0	1125-1135	K.TSWYEVHCICK.N	Carbamidomethyl: 8, 10
2608	1	648.3616	-63.29	2	62.6	12.8	1	1788-1798	K.ILGLPLMRQVR.A	
2593	3	648.3609	90.56	2	62.4	11.8	1	1801-1811	K.SSEKMCLPAEK.F	Carbamidomethyl: 6; Oxidation: 5

Detailed Protein Report

Protein 159: sacsin isoform 1 [Homo sapiens]

Accession:	gi|163659918	**Score:**	36.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	520.8
Database Date:	2015-11-30	**pI:**	6.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.1
		No. of unique Peptides:	3

10	20	30	40	50	60	70	80
METKENRWVP	VTVLPGCVGC	RTVAALASWT	VRDVKERIFA	ETGFPVSEQR	LWRGGRELSD	WIKIGDLTSK	NCHLFVNLQS
90	100	110	120	130	140	150	160
KGLKGGGRFG	QTTPPLVDFL	KDILRRYPEG	GQILKELIQN	AEDAGATEVK	FLYDETQYGT	ETLWSKDMAP	YQGPALYVYN
170	180	190	200	210	220	230	240
NAVFTPEDWH	GIQEIARSRK	KDDPLKVGRF	GIGFNSVYHI	TDVPCIFSGD	QIGMLDPHQT	LFGPHESGQC	WNLKDDSKEI
250	260	270	280	290	300	310	320
SELSDQFAPF	VGIFGSTKET	FINGNFPGTF	FRFPLRLQPS	QLSSNLYNKQ	KVLELFESFR	ADADTVLLFL	KSVQDVSLYV
330	340	350	360	370	380	390	400
READGTEKLV	FRVTSSESKA	LKHERPNSIK	ILGTAISNYC	KKTPSNNITC	VTYHVNIVLE	EESTKDAQKT	SWLVCNSVGG
410	420	430	440	450	460	470	480
RGISSKLDSL	ADELKFVPII	GIAMPLSSRD	DEAKGATSDF	SGKAFCFLPL	PPGEESSTGL	PVHISGFFGL	TDNRRSIKWR
490	500	510	520	530	540	550	560
ELDQWRDPAA	LWNEFLVMNV	VPKAYATLIL	DSIKRLEMEK	SSDFPLSVDV	IYKLWPEASK	VKVHWQPVLE	PLFSELLQNA
570	580	590	600	610	620	630	640
VIYSISCDWV	RLEQVYFSEL	DENLEYTKTV	LNYLQSSGKQ	IAKVPGNVDA	AVQLTAASGT	TPVRKVTPAW	VRQVLRKCAH
650	660	670	680	690	700	710	720
LGCAEEKLHL	LEFVLSDQAY	SELLGLELLP	LQNGNFVPFS	SSVSDQDVIY	ITSAEYPRSL	FPSLEGRFIL	DNLKPHLVAA
730	740	750	760	770	780	790	800
LKEAAQTRGR	PCTQLQLLNP	ERFARLIKEV	MNTFWPGREL	IVQWYPFDEN	RNHPSVSWLK	MVWKNLYIHF	SEDLTLFDEM
810	820	830	840	850	860	870	880
PLIPRTILEE	GQTCVELIRL	RIPSLVILDD	ESEAQLPEFL	ADIVQKLGGF	VLKKLDASIQ	HPLIKKYIHS	PLPSAVLQIM
890	900	910	920	930	940	950	960
EKMPLQKLCN	QITSLLPTHK	DALRKFLASL	TDSSEKEKRI	IQELAIFKRI	NHSSDQGISS	YTKLKGCKVL	HHTAKLPADL
970	980	990	1000	1010	1020	1030	1040
RLSISVIDSS	DEATIRLANM	LKIEQLKTTS	CLKLVLKDIE	NAFYSHEEVT	QLMLWVLENL	SSLKNENPNV	LEWLTPLKFI
1050	1060	1070	1080	1090	1100	1110	1120
QISQEQMVSA	GELFDPDIEV	LKDLFCNEEG	TYFPPSVFTS	PDILHSLRQI	GLKNEASLKE	KDVVQVAKKI	EALQVGACPD
1130	1140	1150	1160	1170	1180	1190	1200
QDVLLKKAKT	LLLVLNKNHT	LLQSSEGKMT	LKKIKWVPAC	KERPPNYPGS	LVWKGDLCNL	CAPPDMCDVG	HAILIGSSLP
1210	1220	1230	1240	1250	1260	1270	1280
LVESIHVNLE	KALGIFTKPS	LSAVLKHFKI	VVDWYSSKTF	SDEDYYQFQH	ILLEIYGFMH	DHLNEGKDSF	RALKFPWVWT
1290	1300	1310	1320	1330	1340	1350	1360
GKKFCPLAQA	VIKPIHDLDL	QPYLHNVPKT	MAKFHQLFKV	CGSIEELTSD	HISMVIQKIY	LKSDQDLSEQ	ESKQNLHLML
1370	1380	1390	1400	1410	1420	1430	1440
NIIRWLYSNQ	IPASPNTPVP	IHHSKNPSKL	IMKPIHECCY	CDIKVDDLND	LLEDSVEPII	LVHEDIPMKT	AEWLKVPCLS
1450	1460	1470	1480	1490	1500	1510	1520
TRLINPENMG	FEQSGQREPL	TVRIKNILEE	YPSVSDIFKE	LLQNADDANA	TECSFLIDMR	RNMDIRENLL	DPGMAACHGP
1530	1540	1550	1560	1570	1580	1590	1600
ALWSFNNSQF	SDSDFVNITR	LGESLKRGEV	DKVGKFGLGF	NSVYHITDIP	IIMSREFMIM	FDPNINHISK	HIKDKSNPGI
1610	1620	1630	1640	1650	1660	1670	1680
KINWSKQQKR	LRKFPNQFKP	FIDVFGCQLP	LTVEAPYSYN	GTLFRLSFRT	QQEAKVSEVS	STCYNTADIY	SLVDEFSLCG
1690	1700	1710	1720	1730	1740	1750	1760
HRLIIFTQSV	KSMYLKYLKI	EETNPSLAQD	TVIIKKKSCS	SKALNTPVLS	VLKEAAKLMK	TCSSSNKKLP	SDEPKSSCIL
1770	1780	1790	1800	1810	1820	1830	1840
QITVEEFHHV	FRRIADLQSP	LFRGPDDDPA	ALFEMAKSGQ	SKKPSDELSQ	KTVECTTWLL	CTCMDTGEAL	KFSLSESGRR
1850	1860	1870	1880	1890	1900	1910	1920
LGLVPCGAVG	VQLSEIQDQK	WTVKPHIGEV	FCYLPLRIKT	GLPVHINGCF	AVTSNRKEIW	KTDTKGRWNT	TFMRHVIVKA
1930	1940	1950	1960	1970	1980	1990	2000
YLQVLSVLRD	LATSGELMDY	TYYAVWPDPD	LVHDDFSVIC	QGFYEDIAHG	KGKELTKVFS	DGSTWVSMKN	VRFLDDSILK
2010	2020	2030	2040	2050	2060	2070	2080
RRDVGSAAFK	IFLKYLKKTG	SKNLCAVELP	SSVKLGFEEA	GCKQILLENT	FSEKQFFSEV	FFPNIQEIEA	ELRDPLMIFV
2090	2100	2110	2120	2130	2140	2150	2160
LNEKVDEFSG	VLRVTPCIPC	SLEGHPLVLP	SRLIHPEGRV	AKLFDIKDGR	FPYGSTQDYL	NPIILIKLVQ	LGMAKDDILW
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
2078	1	1029.6855	128.38	2	56.1	10.5	0	1861-1877	K.WTVKPHIGEVFCYLPLR.I	
71	1	845.3572	-104.63	2	30.3	12.1	1	2019-2034	K.TGSKNLCAVELPSSVK.L	Carbamidomethyl: 7
2171	1	1022.8841	-140.49	2	57.3	14.3	2	2478-2495	K.DTTVKYCHADIPREVAVK.L	

Detailed Protein Report

Protein 160: PREDICTED: mucin-5AC [Homo sapiens]

Accession:	gi|578821001	**Score:**	36.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	520.3
Database Date:	2015-11-30	**pI:**	6.6
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	0.9
		No. of unique Peptides:	3

Detailed Protein Report

10	20	30	40	50	60	70	80
MSVGRRKLAL	LWALALALAC	TRHTGHAQDG	SSESSYKHHP	ALSPIARGPS	GVPLRGATVF	PSLRTIPVVR	ASNPAHNGRV
90	100	110	120	130	140	150	160
CSTWGSFHYK	TFDGDVFRFP	GLCNYVFSEH	CGAAYEDFNI	QLRRSQESAA	PTLSRVLMKV	DGVVIQLTKG	SVLVNGHPVL
170	180	190	200	210	220	230	240
LPFSQSGVLI	QQSSSYTKVE	ARLGLVLMWN	HDDSLLLELD	TKYANKTCGL	CGDFNGMPVV	SELLSHNTKL	TPMEFGNLQK
250	260	270	280	290	300	310	320
MDDPTDQCQD	PVPEPPRNCS	TGFGICEELL	HGQLFSGCVA	LVDVGSYLEA	CRQDLCFCED	TDLLSCVCHT	LAEYSRQCTH
330	340	350	360	370	380	390	400
AGGLPQDWRG	PDFCPQKCPN	NMQYHECRSP	CADTCSNQEH	SRACEDHCVA	GCFCPEGTVL	DDIGQTGCVP	VSKCACVYNG
410	420	430	440	450	460	470	480
AAYAPGATYS	TDCTNCTCSG	GRWSCQEVPC	PGTCSVLGGA	HFSTFDGKQY	TVHGDCSYVL	TKPCDSSAFT	VLAELRRCGL
490	500	510	520	530	540	550	560
TDSETCLKSV	TLSLDGAQTV	VVIKASGEVF	LNQIYTQLPI	SAANVTIFRP	STFFIIAQTS	LGLQLNLQLV	PTMQLFMQLA
570	580	590	600	610	620	630	640
PKLRGQTCGL	CGNFNSIQAD	DFRTLSGVVE	ATAAAFFNTF	KTQAACPNIR	NSFEDPCSLS	VENEKYAQHW	CSQLTDADGP
650	660	670	680	690	700	710	720
FGRCHAAVKP	GTYYSNCMFD	TCNCERSEDC	LCAALSSYVH	ACAAKGVQLG	GWRDGVCTKP	MTTCPKSMTY	HYHVSTCQPT
730	740	750	760	770	780	790	800
CRSLSEGDIT	CSVGFIPVDG	CICPKGTFLD	DTGKCVQASN	CPCYHRGSMI	PNGESVHDSG	AICTCTHGKL	SCIGGQAPAP
810	820	830	840	850	860	870	880
VCAAPMVFFD	CRNATPGDTG	AGCQKSCHTL	DMTCYSPQCV	PGCVCPDGLV	ADGEGGCITA	EDCPCVHNEA	SYRAGQTIRV
890	900	910	920	930	940	950	960
GCNTCTCDSR	MWRCTDDPCL	ATCAVYGDGH	YLTFDGQSYS	FNGDCEYTLV	QNHCGGKDST	QDSFRVVTEN	VPCGTTGTTC
970	980	990	1000	1010	1020	1030	1040
SKAIKIFLGG	FELKLSHGKV	EVIGTDESQE	VPYTIRQMGI	YLVVDTDIGL	VLLWDKKTSI	FINLSPEFKG	RVCGLCGNFD
1050	1060	1070	1080	1090	1100	1110	1120
DIAVNDFATR	SRSVVGDVLE	FGNSWKLSPS	CPDALAPKDP	CTANPFRKSW	AQKQCSILHG	PTFAACHAHV	EPARYYEACV
1130	1140	1150	1160	1170	1180	1190	1200
NDACACDSGG	DCECFCTAVA	AYAQACHEVG	LCVSWRTPSI	CPLFCDYYNP	EGQCEWHYQP	CGVPCLRTCR	NPRGDCLRDV
1210	1220	1230	1240	1250	1260	1270	1280
RGLEGCYPKC	PPEAPIFDED	KMQCVATCPT	PPLPPRCHVH	GKSYRPGAVV	PSDKNCQSCL	CTERGVECTY	KAEACVCTYN
1290	1300	1310	1320	1330	1340	1350	1360
GQRFHPGDVI	YHTTDGTGGC	ISARCGANGT	IERRVYPCSP	TTPVPPTTFS	FSTPPLVVSS	THTPSNGPSS	AHTGPPSSAW
1370	1380	1390	1400	1410	1420	1430	1440
PTTAGTSPRT	RLPTASASLP	PVCGEKCLWS	PWMDVSRPGR	GTDSGDFDTL	ENLRAHGYRV	CESPRSVECR	AEDAPGVPLR
1450	1460	1470	1480	1490	1500	1510	1520
ALGQRVQCSP	DVGLTCRNRE	QASGLCYNYQ	IRVQCCTPLP	CSTSSSPAQT	TPPTTSKTTE	TRASGSSAPS	STPGTVSLST
1530	1540	1550	1560	1570	1580	1590	1600
ARTTPAPGTA	TSVKKTFSTP	SPPPVPATST	SSMSTTAPGT	SVVSSKPTPT	EPSTSSCLQE	LCTWTEWIDG	SYPAPGINGG
1610	1620	1630	1640	1650	1660	1670	1680
DFDTFQNLRD	EGYTFCESPR	SVQCRAESFP	NTPLADLGQD	VICSHTEGLI	CLNKNQLPPI	CYNYEIRIQC	CETVNVCRDI
1690	1700	1710	1720	1730	1740	1750	1760
TRLPKTVATT	RPTPHPTGAQ	TQTTFTTHMP	SASTEQPTAT	SRGGPTATSV	TQGTHTTLVT	RNCHPRCTWT	KWFDVDFPSP
1770	1780	1790	1800	1810	1820	1830	1840
GPHGGDKETY	NNIIRSGEKI	CRRPEEITRL	QCRAKSHPEV	SIEHLGQVVQ	CSREEGLVCR	NQDQQGPFKM	CLNYEVRVLC
1850	1860	1870	1880	1890	1900	1910	1920
CETPRGCHMT	STPGSTSSSP	AQTTPSTTSK	TTETQASGSS	APSSTPGTVS	LSTARTTPAP	GTATSVKKTF	STPSPPPVPA
1930	1940	1950	1960	1970	1980	1990	2000
TSTSSMSTTA	PGTSVVSSKP	TPTEPSTSSC	LQELCTWTEW	IDGSYPAPGI	NGGDFDTFQN	LRDEGYTFCE	SPRSVQCRAE
2010	2020	2030	2040	2050	2060	2070	2080
SFPNTPLADL	GQDVICSHTE	GLICLNKNQL	PPICYNYEIR	IQCCETVNVC	RDITRPPKTV	ATTRPTPHPT	GAQTQTTFTT
2090	2100	2110	2120	2130	2140	2150	2160
HMPSASTEQP	TATSRGGPTA	TSVTQGTHTT	PVTRNCHPRC	TWTTWFDVDF	PSPGPHGGDK	ETYNNIIRSG	EKICRRPEEI
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1356	1	863.9173	-123.12	2	46.6	12.1	1	7-22	R.KLALLWALALALACTR.H	
2649	1	734.8562	20.51	2	63.2	12.1	0	317-329	R.QCTHAGGLPQDWR.G	
2548	1	1044.5297	54.57	2	61.8	12.6	1	2203-2218	K.MCLNYEVRVLCCETPK.G	Carbamidomethyl: 2, 11, 12; Oxidation: 1

Detailed Protein Report

Protein 161: podocan isoform 2 [Homo sapiens]

Accession:	gi|312283621	**Score:**	36.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	72.1
Database Date:	2015-11-30	**pI:**	6.3
		Sequence Coverage [%]:	6.2
		No. of unique Peptides:	3

Alias proteins:

Accession	Name	Description
gi|312283625	refseq_huma (refseq_human_20140103.fasta)	podocan isoform 2 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MEGEEAEQPA WFRQPWRPGA SDSAPPAGTM AQSRVLLLLL LLPPQLHLGP VLAVRAPGFG RSGGHSLSPE ENEFAEEEPV
        90        100        110        120        130        140        150        160
LVLSPEEPGP GPAAVSCPRD CACSQEGVVD CGGIDLREFP GDLPEHTNHL SLQNNQLEKI YPEELSRLHR LETLNLQNNR
       170        180        190        200        210        220        230        240
LTSRGLPEKA FEHLTNLNYL YLANNKLTLA PRFLPNALIS VDFAANYLTK IYGLTFGQKP NLRSVYLHNN KLADAGLPDN
       250        260        270        280        290        300        310        320
MFNGSSNVEV LILSSNFLRH VPKHLPPALY KLHLKNNKLE KIPPGAFSEL SSLRELYLQN NYLTDEGLDN ETFWKLSSLE
       330        340        350        360        370        380        390        400
YLDLSSNNLS RVPAGLPRSL VLLHLEKNAI RSVDANVLTP IRSLEYLLLH SNQLREQGIH PLAFQGLKRL HTVHLYNNAL
       410        420        430        440        450        460        470        480
ERVPSGLPRR VRTLMILHNQ ITGIGREDFA TTYFLEELNL SYNRITSPQV HRDAFRKLRL LRSLDLSGNR LHTLPPGLPR
       490        500        510        520        530        540        550        560
NVHVLKVKRN ELAALARGAL VGMAQLRELY LTSNRLRSRA LGPRAWVDLA HLQLLDIAGN QLTEIPEGLP ESLEYLYLQN
       570        580        590        600        610        620        630        640
NKISAVPANA FDSTPNLKGI FLRFNKLAVG SVVDSAFRRL KHLQVLDIEG NLEFGDISKD RGRLGKEKEE EEEEEEEEEE
       650
TR
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
127	1	724.8357	13.78	2	31.3	12.7	0	2-13	M.EGEEAEQPAWFR.Q	
1952	1	753.7987	-167.47	2	54.5	11.4	0	211-223	K.IYGLTFGQKPNLR.S	
16	1	819.8519	-141.56	2	29.5	12.6	1	348-362	K.NAIRSVDANVLTPIR.S	

Detailed Protein Report

Protein 162: myeloperoxidase precursor [Homo sapiens]

Accession:	gi|4557759	**Score:**	36.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	83.8
Database Date:	2015-11-30	**pI:**	10.1
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.0
		No. of unique Peptides:	2

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
873	1	575.3008	19.33	2	40.5	19.5	0	396-405	R.IPCFLAGDTR.S	Carbamidomethyl: 3
1741	1	640.7565	-196.31	2	51.7	17.2	0	537-548	R.VVLEGGIDPILR.G	

Detailed Protein Report

Protein 163: PREDICTED: guanine nucleotide exchange factor VAV3 isoform X4 [Homo sapiens]

Accession:	gi|530361574	**Score:**	36.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	72.1
Database Date:	2015-11-30	**pI:**	6.9
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	4.8
		No. of unique Peptides:	2

Quantitation

MD:MU **Median:** 1.43 **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
154	1	968.4666	19.86	2	31.6	10.4	1	74-89	K.NIRTFLTACCETFGMR.K	Carbamidomethyl: 10; Oxidation: 15	MD:MU 1.43
103	1	807.7358	-182.29	2	31.0	26.3	2	551-564	R.AHKECLGRVDNCGR.V	Carbamidomethyl: 12	

Detailed Protein Report

Protein 164: PREDICTED: testis-expressed sequence 2 protein isoform X4 [Homo sapiens]

Accession:	gi|530412523	**Score:**	36.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	125.0
Database Date:	2015-11-30	**pI:**	5.6
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	3.0
		No. of unique Peptides:	2

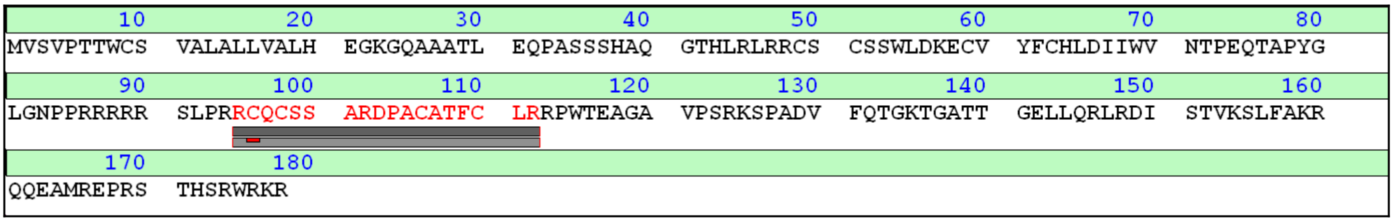
10	20	30	40	50	60	70	80
MTSLYGRHAE	KTTDMPKPSA	PKVHVQRSVS	RDTIAIHFSA	SGEEEEEEEE	EFREYFEEGL	DDQSIVTGLE	AKEDLYLEPQ
90	100	110	120	130	140	150	160
VGHDPAGPAA	SPVLADGLSV	SQAPAILPVS	KNTVKLLESP	VPAAQVLSTV	PLAVSPGSSS	SGPLASSPSV	SSLSEQKTSS
170	180	190	200	210	220	230	240
SSPLSSPSKS	PILSSSASTS	TLSSAKPFMS	LVKSLSTEVE	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
2499	1	1044.5086	15.43	2	61.7	15.0	1	632-648	K.KYPICIELGQQDDFMSK.A	Carbamidomethyl: 5; Oxidation: 15
2481	1	449.6389	-282.20	2	61.0	10.9	0	920-927	K.EPLVEALK.V	

Detailed Protein Report

Protein 165: endothelin-2 preproprotein [Homo sapiens]

Accession:	gi|4503463	**Score:**	36.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	19.9
Database Date:	2015-11-30	**pI:**	12.1
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	14.0
		No. of unique Peptides:	2



```
        10         20         30         40         50         60         70         80
MVSVPTTWCS VALALLVALH EGKGQAAATL EQPASSSHAQ GTHLRLRRCS CSSWLDKECV YFCHLDIIWV NTPEQTAPYG
        90        100        110        120        130        140        150        160
LGNPPRRRRR SLPRRCQCSS ARDPACATFC LRRPWTEAGA VPSRKSPADV FQTGKTGATT GELLQRLRDI STVKSLFAKR
       170        180
QQEAMREPRS THSRWRKR
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2021	1	682.2548	-70.07	3	55.4	12.1	2	95-112	R.RCQCSSARDPACATFCLR.R	Carbamidomethyl: 16
1575	1	682.3132	15.52	3	49.5	12.7	2	95-112	R.RCQCSSARDPACATFCLR.R	Carbamidomethyl: 2

Detailed Protein Report

Protein 166: centrosome-associated protein 350 [Homo sapiens]

Accession:	gi|171184451	**Score:**	36.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	350.7
Database Date:	2015-11-30	**pI:**	5.9
		Sequence Coverage [%]:	1.5
		No. of unique Peptides:	1

Quantitation

MD:MU	**Median:** 1.23	**CV:** 0.00 %	**No. of Peptides:** 1

Detailed Protein Report

10	20	30	40	50	60	70	80
MRSSKSKEVP	LPNPRNSQSK	DTVQADITTS	WDALSQTKAA	LRHIENKLEV	APTSTAVCDS	VMDTKKSSTS	ATRKISRKDG
90	100	110	120	130	140	150	160
RYLDDSWVNA	PISKSTKSRK	EKSRSPLRAT	TLESNVKKNN	RVEFREPLVS	YREIHGAPSN	FSSSHLESKH	VYCVDVNEEK
170	180	190	200	210	220	230	240
TESGNWMIGS	REERNIRSCD	FESSQSSVIN	DTVVRFLNDR	PAIDALQNSE	CLIRMGASMR	TEEEMPNRTK	GSENNLKLSV
250	260	270	280	290	300	310	320
NNMAHDTDPK	ALRLTDSSPS	STSTSNSQRL	DILKRRQHDV	KLEKLKERIR	KQWEHSEETN	GRGQKLGHID	HPVMVVNVDN
330	340	350	360	370	380	390	400
SVTAKVRKVA	TAPPAPAYKG	FNPSETKIRT	PDGKVWQEAE	FQNMSRELYR	DLALHFADDI	SIKEKPAEKS	KEKKVVKPVR
410	420	430	440	450	460	470	480
KVQKVAQLSS	TECRTGSSHL	ISTSSWRDGQ	KLVKKILGPA	PRMEPKEQRT	ASSDRGGRER	TAKSGGHIGR	AESDPRLDVL
490	500	510	520	530	540	550	560
HRHLQRNSER	SRSKSRSENN	IKKLASSLPD	NKQEENTALN	KDFLPIEIRG	ILDDLQLDST	AHTAKQDTVE	LQNQKSSAPV
570	580	590	600	610	620	630	640
HAPRSHSPVK	RKPDKITANE	DPPVISKRRH	YDTDEVRQYI	VRQQEERKRK	QNEEKKAQKE	ATEQKNKRLQ	ELYRKQKEAF
650	660	670	680	690	700	710	720
TKVKNVPPSE	PSATRRLQET	YSKLLLEKTL	LEEPSHQHVT	QETQAKPGYQ	PSGESDKENK	VQERPPSASS	SSDMSLSEPP
730	740	750	760	770	780	790	800
QPLARKDLME	STWMQPERLS	PQVHHSQPQP	FAGTAGSLLS	HLLSLEHVGI	LHKDFESILP	TRKNHNMASR	PLTFTPQPYV
810	820	830	840	850	860	870	880
TSPAAYTDAL	LKPSASQYKS	KLDRIEALKA	TAASLSSRIE	SEAKKLAGAS	INYGSAWNTE	YDVQQAPQED	GPWTKAVTPP
890	900	910	920	930	940	950	960
VKDDNEDVFS	ARIQKMLGSC	VSHATFDDDL	PGVGNLSEFK	KLPEMIRPQS	AISSFRVRSP	GPKPEGLLAQ	LCKRQTDSSS
970	980	990	1000	1010	1020	1030	1040
SDMQACSQDK	AKISLGSSID	SVSEGPLLSE	GSLSEEEGDQ	DGQPLLKVAE	ILKEKEFCPG	ERNSYEPIKE	FQKEAEKFLP
1050	1060	1070	1080	1090	1100	1110	1120
LFGHIGGTQS	KGPWEELAKG	SPHSVINIFT	KSYQLYGKGF	EDKLDRGTST	SRPLNATATP	LSGVSYEDDF	VSSPGTGTST
1130	1140	1150	1160	1170	1180	1190	1200
EKKSTLEPHS	TLSPQEDHSN	RKSAYDPSSV	DVTSQHSSGA	QSAASSRSST	SSKGKKGKKE	KTEWLDSFTG	NVQNSLLDEE
1210	1220	1230	1240	1250	1260	1270	1280
KAERGSHQGK	KSGTSSKLSV	KDFEQTLDTD	STLEDLSGHS	VSVSSDKGRS	QKTPTSPLSP	SSQKSLQFDV	AGTSSERSKS
1290	1300	1310	1320	1330	1340	1350	1360
SVMPPTITGF	KPNAPLTDLN	PAASRTTTEN	MAPIPGSKRF	SPAGLHHRMA	AELSYLNAIE	ESVRQLSDVE	RVRGISLAQQ
1370	1380	1390	1400	1410	1420	1430	1440
ESVSLAQIIK	AQQQRHERDL	ALLKLKAEQE	ALESQRQLEE	TRNKAAQVHA	ESLQQVVQSQ	REVTEVLQEA	TCKIAAQQSE
1450	1460	1470	1480	1490	1500	1510	1520
TARLTTDAAR	QICEMAELTR	THISDAVVAS	GAPLAILYDH	QRQHLPDFVK	QLRTRTETDR	KSPSVSLSQS	KEGTLDSKHQ
1530	1540	1550	1560	1570	1580	1590	1600
KYSASYDSYS	ESSGYKNHDR	RSSSGSSRQE	SPSVPSCKEN	EKKLNGEKIE	SSIDEQVQTA	ADDSLRSDSV	PSLPDEKDST
1610	1620	1630	1640	1650	1660	1670	1680
SIATEYSLKF	DESMTEDEIE	EQSFRSLLPS	ESHRRFNMEK	RRGHHDDSDE	EASPEKTTLS	TAKELNMPFS	GGQDSFSKFT
1690	1700	1710	1720	1730	1740	1750	1760
MEMVRQYMKE	EEMRAAHQSS	LLRLREKALK	EKTKAELAWL	EHQKKHLRDK	GEDDKMPPLR	KKQRGLLLRL	QQEKAEIKRL
1770	1780	1790	1800	1810	1820	1830	1840
QEANKAARKE	RQLILKQQEE	IEKIRQTTIK	LQEKLKSAGE	SKLDSHSDDD	TKDNKATSPG	PTDLETRSPS	PISISSSETS
1850	1860	1870	1880	1890	1900	1910	1920
SIMQKLKKMR	SRMDEKFLTK	REQKLMQRRQ	HAEELLEWKR	RLDAEEAEIR	QMEKQALAAW	DKELIKPKTP	KKELEDQRTE
1930	1940	1950	1960	1970	1980	1990	2000
QKEIASEEES	PVPLYSHLNS	ESSIPEELGS	PAVEYVPSES	IGQEQPGSPD	HSILTEEMIC	SQELESSTSP	SKHSLPKSCT
2010	2020	2030	2040	2050	2060	2070	2080
SVSKQESSKG	SHRTGGQCHL	PIKSHQHCYS	WSDESLSMTQ	SETTSDQSDI	EGRIRALKDE	LRKRKSVVNQ	LKKEQKKRQK
2090	2100	2110	2120	2130	2140	2150	2160
ERLKAQEASL	IKQLESYDEF	IKKTEAELSQ	DLETSPTAKP	QIKTLSSASE	KPKIKPLTPL	HRSETAKNWK	SLTESERSRG
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
316	1	966.9340	-27.85	2	33.3	11.1	2	1795-1812	K.LKSAGESKLDSHSDDDTK.D		MD:MU 1.23

Detailed Protein Report

Protein 167: staphylococcal nuclease domain-containing protein 1 [Homo sapiens]

Accession: gi|77404397
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 36.4
MW [kDa]: 101.9
pI: 6.8
Sequence Coverage [%]: 4.7
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
2148	1	966.3470	-130.61	2	56.7	12.8	2	161-177	K.KGMWSEGNGSHTIRDLK.Y	Oxidation: 3

Detailed Protein Report

Protein 168: ATP-binding cassette sub-family B member 5 isoform 2 [Homo sapiens]

Accession:	gi|148612844	**Score:**	36.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	89.8
Database Date:	2015-11-30	**pI:**	8.7
		Sequence Coverage [%]:	6.8
		No. of unique Peptides:	3

10	20	30	40	50	60	70	80
MVDENDIRAL	NVRHYRDHIG	VVSQEPVLFG	TTISNNIKYG	RDDVTDEEME	RAAREANAYD	FIMEFPNKFN	TLVGEKGAQM
90	100	110	120	130	140	150	160
SGGQKQRIAI	ARALVRNPKI	LILDEATSAL	DSESKSAVQA	ALEKASKGRT	TIVVAHRLST	IRSADLIVTL	KDGMLAEKGA
170	180	190	200	210	220	230	240
HAELMAKRGL	YYSLVMSQDI	KKADEQMESM	TYSTERKTNS	LPLHSVKSIK	SDFIDKAEES	TQSKEISLPE	VSLLKILKLN
250	260	270	280	290	300	310	320
KPEWPFVVLG	TLASVLNGTV	HPVFSIIFAK	IITMFGNNDK	TTLKHDAEIY	SMIFVILGVI	CFVSYFMQGL	FYGRAGEILT
330	340	350	360	370	380	390	400
MRLRHLAFKA	MLYQDIAWFD	EKENSTGGLT	TILAIDIAQI	QGATGSRIGV	LTQNATNMGL	SVIISFIYGW	EMTFLILSIA
410	420	430	440	450	460	470	480
PVLAVTGMIE	TAAMTGFANK	DKQELKHAGK	IATEALENIR	TIVSLTREKA	FEQMYEEMLQ	TQHRNTSKKA	QIIGSCYAFS
490	500	510	520	530	540	550	560
HAFIYFAYAA	GFRFGAYLIQ	AGRMTPEGMF	IVFTAIAYGA	MAIGETLVLA	PEYSKAKSGA	AHLFALLEKK	PNIDSRSQEG
570	580	590	600	610	620	630	640
KKPDTCEGNL	EFREVSFFYP	CRPDVFILRG	LSLSIERGKT	VAFVGSSGCG	KSTSVQLLQR	LYDPVQGQVL	FDGVDAKELN
650	660	670	680	690	700	710	720
VQWLRSQIAI	VPQEPVLFNC	SIAENIAYGD	NSRVVPLDEI	KEAANAANIH	SFIEGLPEKY	NTQVGLKGAQ	LSGGQKQRLA
730	740	750	760	770	780	790	800
IARALLQKPK	ILLLDEATSA	LDNDSEKVVQ	HALDKARTGR	TCLVVTHRLS	AIQNADLIVV	LHNGKIKEQG	THQELLRNRD
810	820						
IYFKLVNAQS	VQ						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1505	1	1022.6536	107.11	2	48.5	10.6	1	97-115	R.NPKILILDEATSALDSESK.S	
439	1	565.3076	0.55	2	35.1	13.4	1	708-718	K.GAQLSGGQKQR.L	
2759	1	905.4805	-31.89	3	65.8	12.2	1	761-785	R.TCLVVTHRLSAIQNADLIVVLHNGK.I	

Detailed Protein Report

Protein 169: **T-complex protein 11 homolog isoform 3 [Homo sapiens]**

Accession: gi|387849264
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 36.3
MW [kDa]: 56.8
pI: 5.0
Sequence Coverage [%]: 5.7
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MTRGGGGDT	ISKMPDVKES	VPPKYPGDSE	GRSCKPETSG	PPQEDKSGSE	DPPPCLTETV	NEVSKLSNKI	GMNCDYYMEE
90	100	110	120	130	140	150	160
KVLPPSSLEG	KVKETVHNAF	WDHLKEQLSA	TPPDFSCALE	LLKEIKEILL	SLLLPRQNRL	RIEIEEALDM	DLLKQEAEHG
170	180	190	200	210	220	230	240
ALKVLYLSKY	VLNMMALLCA	PVRDEAVQKL	ENITDPVWLL	RGIFQVLGRM	KMDMVNYTIQ	SLQPHLQEHS	IQYERAKFQE
250	260	270	280	290	300	310	320
LLNKQPSLLN	HTTKWLTQAA	GDLTMSPPTC	PDTSDSSSVA	GPSPNEAANN	PEPLSPTMVL	CQGFLNLLLW	DLENEEFPET
330	340	350	360	370	380	390	400
LLMDRTRLQE	LKSQLHQLTV	MASVLLVASS	FSGSVLFGSP	QFVDKLKRIT	KSLLEDFHSR	PEEAILTVSE	QVSQEIHQSL
410	420	430	440	450	460	470	480
KNMGLVALSS	DNTASLMGQL	QNIAKKENCV	CSVIDQRIHL	FLKCCLVLGV	QRSLLDLPGG	LTLIEAELAE	LGQKFVNLTH
490	500	510	520				
HNQQVFGPYY	TEILKTLISP	AQALETKVES	V				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2154	1	1052.4435	-57.89	2	57.1	16.6	2	14-32	K.MPDVKESVPPKYPGDSEGR.S	Oxidation: 1

Detailed Protein Report

Protein 170: exportin-5 [Homo sapiens]

Accession:	gi|22748937	**Score:**	36.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	136.2
Database Date:	2015-11-30	**pI:**	5.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.7
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MAMDQVNALC	EQLVKAVTVM	MDPNSTQRYR	LEALKFCEEF	KEKCPICVPC	GLRLAEKTQV	AIVRHFGLQI	LEHVVKFRWN
90	100	110	120	130	140	150	160
GMSRLEKVYL	KNSVMELIAN	GTLNILEEEN	HIKDALSRIV	VEMIKREWPQ	HWPDMLIELD	TLSKQGETQT	ELVMFILLRL
170	180	190	200	210	220	230	240
AEDVVTFQTL	PPQRRRDIQQ	TLTQNMERIF	SFLLNTLQEN	VNKYQQVKTD	TSQESKAQAN	CRVGVAALNT	LAGYIDWVSM
250	260	270	280	290	300	310	320
SHITAENCKL	LEILCLLLNE	QELQLGAAEC	LLIAVSRKGK	LEDRKPLMVL	FGDVAMHYIL	SAAQTADGGG	LVEKHYVFLK
330	340	350	360	370	380	390	400
RLCQVLCALG	NQLCALLGAD	SDVETPSNFG	KYLESFLAFT	THPSQFLRSS	TQMTWGALFR	HEILSRDPLL	LAIIPKYLRA
410	420	430	440	450	460	470	480
SMTNLVKMGF	PSKTDSPSCE	YSRFDFDSDE	DFNAFFNSSR	AQQGEVMRLA	CRLDPKTSFQ	MAGEWLKYQL	STFLDAGSVN
490	500	510	520	530	540	550	560
SCSAVGTGEG	SLCSVFSPSF	VQWEAMTLFL	ESVITQMFRT	LNREEIPVND	GIELLQMVLN	FDTKDPLILS	CVLTNVSALF
570	580	590	600	610	620	630	640
PFVTYRPEFL	PQVFSKLFSS	VTFETVEESK	APRTRAVRNV	RRHACSSIIK	MCRDYPQLVL	PNFDMLYNHV	KQLLSNELLL
650	660	670	680	690	700	710	720
TQMEKCALME	ALVLISNQFK	NYERQKVFLE	ELMAPVASIW	LSQDMHRVLS	DVDAFIAYVG	TDQKSCDPGL	EDPCGLNRAR
730	740	750	760	770	780	790	800
MSFCVYSILG	VVKRTCWPTD	LEEAKAGGFV	VGYTSSGNPI	FRNPCTEQIL	KLLDNLLALI	RTHNTLYAPE	MLAKMAEPFT
810	820	830	840	850	860	870	880
KALDMLDAEK	SAILGLPQPL	LELNDSPVFK	TVLERMQRFF	STLYENCFHI	LGKAGPSMQQ	DFYTVEDLAT	QLLSSAFVNL
890	900	910	920	930	940	950	960
NNIPDYRLRP	MLRVFVKPLV	LFCPPEHYEA	LVSPILGPLF	TYLHMRLSQK	WQVINQRSLL	CGEDEAADEN	PESQEMLEEQ
970	980	990	1000	1010	1020	1030	1040
LVRMLTREVM	DLITVCCVSK	KGADHSSAPP	ADGDDEEMMA	TEVTPSAMAE	LTDLGKCLMK	HEDVCTALLI	TAFNSLAWKD
1050	1060	1070	1080	1090	1100	1110	1120
TLSCQRTTSQ	LCWPLLKQVL	SGTLLADAVT	WLFTSVLKGL	QMHGQHDGCM	ASLVHLAFQI	YEALRPRYLE	IRAVMEQIPE
1130	1140	1150	1160	1170	1180	1190	1200
IQKDSLDQFD	CKLLNPSLQK	VADKRRKDQF	KRLIAGCIGK	PLGEQFRKEV	HIKNLPSLFK	KTKPMLETEV	LDNDGGGLAT
1210							
IFEP							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
629	1	459.6075	-259.30	2	37.2	12.3	0	441-448	R.AQQGEVMR.L	
1960	1	731.2880	-122.56	2	54.6	12.4	0	721-733	R.MSFCVYSILGVVK.R	Oxidation: 1

Detailed Protein Report

Protein 171: **PREDICTED: Fanconi anemia-associated protein of 100 kDa isoform X2 [Homo sapiens]**

Accession: gi|578831470
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 35.9
MW [kDa]: 77.0
pI: 5.0
Sequence Coverage [%]: 3.3
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MQLFEQPCPG	EDPRPGGQIG	EVELSSYTPP	AGVPGKPAAP	HFLPVLCSVS	PSGSRVPHDL	LGGSGGFTLE	DALFGLLFGA
90	100	110	120	130	140	150	160
DATLLQSPVV	LCGLPDGQLC	CVILKALVTS	RSAPGDPNAL	VKILHHLEEP	VIFIGALKTE	PQAAEAAENF	LPDEDVHCDC
170	180	190	200	210	220	230	240
LVAFGHHGRM	LAIKASWDES	GKLVPELREY	CLPGPVLCAA	CGGGGRVYHS	TPSDLCVVDL	SRGSTPLGPE	QPEEGPGGLP
250	260	270	280	290	300	310	320
PMLCPASLNI	CSVVSLSASP	RTHEGGTKLL	ALSAKGRLMT	CSLDLDSEMP	GPARMTTESA	GQKIKELLSG	IGNISERVSF
330	340	350	360	370	380	390	400
LKKAVDQRNK	ALTSLNEAMN	VSCALLSSGT	GPRPISCTTS	TTWSRLQTQD	VLMATCVLEN	SSSFSLDQGW	TLCIQVLTSS
410	420	430	440	450	460	470	480
CALDLDSACS	AITYTIPVDQ	LGPGARREVT	LPLGPGENGG	LDLPVTVSCT	LFYSLREVVG	GALAPSDSED	PFLDECPSDV
490	500	510	520	530	540	550	560
LPEQEGVCLP	LSRHTVDMLQ	CLRFPGLAPP	HTRAPSPLGP	TRDPVATFLE	TCREPGSQPA	GPASLRAEYL	PPSVASIKVS
570	580	590	600	610	620	630	640
AELLRAALKD	GHSGVPLCCA	TLQWLLAENA	AVDVVRARAL	SSIQGVAPDG	ANVHLIVREV	AMTDLCPAGP	IQAVEIQVES
650	660	670	680	690	700	710	720
SSLADICRAH	HAVVGRMQTM	VTEQATQGSS	APDLRVQYLR	QIHANHETLL	REVQTLRDRL	CTEDEASSCA	TAQRLLQVYR
730	740						
QLRHPSLILL							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1236	1	765.0123	96.72	2	45.1	17.1	1	304-317	K.IKELLSGIGNISER.V	

Detailed Protein Report

Protein 172: PREDICTED: diphthine synthase isoform X1 [Homo sapiens]

Accession:	gi|530362777	**Score:**	35.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	27.1
Database Date:	2015-11-30	**pI:**	9.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	7.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLYLIGLGLG	DAKDITVKGL	EVVRRCSRVY	LEAYTSVLTV	GKEALEEFYG	RKLVVADREE	VEQEADNILK	DADISDVAFL
90	100	110	120	130	140	150	160
VVGDPFGATT	HSDLVLRATK	LGIPYRVIHN	ASIMNAVGCC	GLQLYKFGET	VSIVFWTDTW	RPESFFDKVK	KNRQNGMHTL
170	180	190	200	210	220	230	240
CLLDIKVKEQ	SLENLINSYR	GDTLCWLSQG	WSRRPENCSR	HFKANVHCGL	GRTIAFLDHH	RRQHTSNGDG	DAKSVFHTRK
250							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1993	1	698.2622	-135.48	2	55.0	20.1	1	201-212	R.HFKANVHCGLGR.T	Carbamidomethyl: 8

Detailed Protein Report

Protein 173: PREDICTED: coiled-coil domain-containing protein 146 isoform X3 [Homo sapiens]

Accession:	gi|530386260	**Score:**	35.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	97.2
Database Date:	2015-11-30	**pI:**	9.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.2
		No. of unique Peptides:	3

Quantitation

MD:MU **Median:** 0.66 **CV:** 25.52 % **No. of Peptides:** 2

```
        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	Ratios	
1670	1	524.8066	68.22	2	50.8	14.1	0	33-41	K.ITKPGEMEK.K	Oxidation: 7	MD:MU	0.85
1783	1	870.2900	-263.69	1	52.3	10.4	0	396-402	K.FVNLLHK.A			
595	1	572.7739	-48.16	2	36.8	11.3	0	506-515	R.NESGVQLIER.E		MD:MU	0.51

Detailed Protein Report

Protein 174: **testis-specific serine/threonine-protein kinase 2 [Homo sapiens]**

Accession:	gi|194294513	**Score:**	35.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	40.9
Database Date:	2015-11-30	**pI:**	9.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.8
		No. of unique Peptides:	1

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
185	1	642.3289	7.21	2	32.0	16.0	2	293-302	K.YRAECKLDTK.T	Carbamidomethyl: 5

Detailed Protein Report

Protein 175: **PREDICTED: LOW QUALITY PROTEIN: double homeobox protein 4-like protein 4 [Homo sapiens]**

Accession:	gi|578798033	**Score:**	35.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	45.9
Database Date:	2015-11-30	**pI:**	10.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	5.0
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MTLPTPSEST	LPAEARGWGQ	RRRLVWTPRQ	REALXACFYR	NPYMGIATRV	QLAQSIGIPE	TRVXIYFQNE	RSRQLRQHRR
90	100	110	120	130	140	150	160
ESRPWPVRRG	PQEGRTAVIG	SQTALLLRAF	EKDRLPGIEA	REELARERGL	LESRIQIWFQ	IRRARHQGQA	GRAPAQAGGR
170	180	190	200	210	220	230	240
SNAAPAXCHP	ARSWVAFAHT	GRWGRVFPHP	XVPCAPGALP	QGAFVNQGAR	AFLVFQHSQA	APVEGISQPA	LGRGDFSYTA
250	260	270	280	290	300	310	320
PAPLEGALSH	PQSPPXPPHT	GKSRENRDPQ	RDGLLGTCVV	GQPGPAQAGP	QGQGVLAPPA	SQGIPWWGWA	WGPQASGAAW
330	340	350	360	370	380	390	400
EPQARAASPR	QPMPPEDSAR	QGQMQGMPAP	SQALQELGRS	SALPSGLLLD	KFLASLVFLQ	QVQSFLETET	PGELEALEEA
410	420						
VSLEEPLSEQ	EYRALLEEI						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2748	1	826.4475	66.34	3	65.6	12.9	2	0-0	.QREALCACFYRNPYMGIATR.	Carbamidomethyl: 6, 8
2114	1	1131.4444	-110.45	1	56.6	10.9	0	173-182	R.SWVAFAHTGR.W	

Detailed Protein Report

Protein 176: 60 kDa heat shock protein, mitochondrial [Homo sapiens]

Accession:	gi|31542947	**Score:**	35.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	61.0
Database Date:	2015-11-30	**pI:**	5.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	4.4
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530370277	refseq_human (refseq_human_20140103.fasta)	PREDICTED: 60 kDa heat shock protein, mitochondrial isoform X1 [Homo sapiens]
gi|41399285	refseq_human (refseq_human_20140103.fasta)	60 kDa heat shock protein, mitochondrial [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MLRLPTVFRQ MRPVSRVLAP HLTRAYAKDV KFGADARALM LQGVDLLADA VAVTMGPKGR TVIIEQSWGS PKVTKDGVTV
        90        100        110        120        130        140        150        160
AKSIDLKDKY KNIGAKLVQD VANNTNEEAG DGTTTATVLA RSIAKEGFEK ISKGANPVEI RRGVMLAVDA VIAELKKQSK
       170        180        190        200        210        220        230        240
PVTTPEEIAQ VATISANGDK EIGNIISDAM KKVGRKGVIT VKDGKTLNDE LEIIEGMKFD RGYISPYFIN TSKGQKCEFQ
       250        260        270        280        290        300        310        320
DAYVLLSEKK ISSIQSIVPA LEIANAHRKP LVIIAEDVDG EALSTLVLNR LKVGLQVVAV KAPGFGDNRK NQLKDMAIAT
       330        340        350        360        370        380        390        400
GGAVFGEEGL TLNLEDVQPH DLGKVGEVIV TKDDAMLLKG KGDKAQIEKR IQEIIEQLDV TTSEYEKEKL NERLAKLSDG
       410        420        430        440        450        460        470        480
VAVLKVGGTS DVEVNEKKDR VTDALNATRA AVEEGIVLGG GCALLRCIPA LDSLTPANED QKIGIEIIKR TLKIPAMTIA
       490        500        510        520        530        540        550        560
KNAGVEGSLI VEKIMQSSSE VGYDAMAGDF VNMVEKGIID PTKVVRTALL DAAGVASLLT TAEVVVTEIP KEEKDPGMGA
       570        580
MGGMGGGMGG GMF
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
29	1	1001.9624	-98.76	2	30.0	16.6	2	1-16	-.MLRLPTVFRQMRPVSR.V	Oxidation: 11

Detailed Protein Report

Protein 177: PREDICTED: RANBP2-like and GRIP domain-containing protein 5/6 isoform X5 [Homo sapiens]

Accession:	gi|530369376	**Score:**	35.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	165.9
Database Date:	2015-11-30	**pI:**	6.1
		Sequence Coverage [%]:	2.9
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|530369509	refseq_human (refseq_human_20140103.fasta)	PREDICTED: RANBP2-like and GRIP domain-containing protein 5/6 isoform X5 [Homo sapiens]

10	20	30	40	50	60	70	80
MKGHFYMYAG	SLLLKMGQHG	NNVQWRALSE	LAALCYLIAF	QVPRPKIKLR	EGKAGQNLLE	MMACDRLSQS	GHMLLSLSRG
90	100	110	120	130	140	150	160
KQDFLKEVVE	TFANKIGQSA	LYDALFSSQS	PKDTSFLGSD	DIGKIDVQEP	ELEDLARYDV	GAIRAHNGSL	QHLTWLGLQW
170	180	190	200	210	220	230	240
NSLPALPGIR	KWLKQLFHRL	PHETSRLETN	APESICILDL	EVFLLGVVYT	SHLQLKEKCN	SHHSSYQPLC	LPFPVCKQLC
250	260	270	280	290	300	310	320
TERQKSWWDA	VCTLIHRKAV	PGNLAKLRLL	VQHEINTLRA	QEKHGLQPAL	LVHWAKYLQK	TGSGLNSFYG	QLEYIGRSVH
330	340	350	360	370	380	390	400
YWKKVLPLLK	IIKKNSIPEP	IDPLFKHFHS	VDIQASEIVE	YEEDAHITFA	MLDAVNGNIE	DAVTAFESIK	SVVSYWNLAL
410	420	430	440	450	460	470	480
IFHRKAEDIE	NDALSPEEQE	ECRNYLTKTR	DYLIKIIDDG	DSNLSVVKKL	PVPLESVKQM	LNSVMQELED	YSEGGPLYKN
490	500	510	520	530	540	550	560
GSLRNADSEI	KHSTPSPTKY	SLSPSKSYKY	SPETPPRWTE	DRNSLLNMIC	QQVEAIKKEM	QELKLNSSKS	ASRHRWPTEN
570	580	590	600	610	620	630	640
YGPDSVPDGY	QGSQTFHGAP	LTVATTGPSV	YYSQSPAYNS	QYLLRPAANV	TPTKGSSNTE	FKSTKEGFSI	PVSADGFKFG
650	660	670	680	690	700	710	720
ISEPGNQEKK	REKPLENDTG	FQAQDISGRK	KGRGVIFGQT	SSTFTFADVA	KSTSGEGFQF	GKKDLNFKGF	SGAGEKLFSS
730	740	750	760	770	780	790	800
RYGKMANKAN	TSGDFEKDDD	AYKTEDSDDI	HFEPVVQMPE	KVELVTGEEG	EKVLYSQGVK	LFRFDAEVRQ	WKERGLGNLK
810	820	830	840	850	860	870	880
ILKNEVNGKL	RMLMRREQVL	KVCANHWITT	TMNLKPLSGS	DRAWMWSASD	FSDGDAKLER	LAAKFKTPEL	AEEFKQKFEE
890	900	910	920	930	940	950	960
CQRLLLDIPL	QTPHKLVDTG	RAAKLIQRAE	EMKSGLKDFK	TFLTNDQTKV	TEEENKGSGT	GAAGASDTTI	KPNAENTGPT
970	980	990	1000	1010	1020	1030	1040
LEWDNYDLRE	DALDDSVSSS	SVHASPLASS	PVRKNLFRFD	ESTTGSNFSF	KSALSLSKSP	AKLNQSGTSV	GTDEESVVTQ
1050	1060	1070	1080	1090	1100	1110	1120
EEERDGQYFE	PVVPLPDLVE	VSSGEENEQV	VFSHRAEIYR	YDKDVGQWKE	RGIGDIKILQ	NYDNKQVRIV	MRRDQVLKLC
1130	1140	1150	1160	1170	1180	1190	1200
ANHRITPDMS	LQNMKGTERV	WVWTACDFAD	GERKVEHLAV	RFKLQDVADS	FKKIFDEAKT	AQEKDSLITP	HVSRSSTPRE
1210	1220	1230	1240	1250	1260	1270	1280
SPCGKIAVAI	LEETTRERTD	VIQGDDVADA	ASEVEVSSTS	ETTTKAVVSP	PKFVFVSESV	KRIFSSEKSK	PFVFGNSSAT
1290	1300	1310	1320	1330	1340	1350	1360
GSLFGFSFNA	PLKSNNSETS	SVAQSGSESK	VEPKKCELSK	NSDIEQSSDS	KVKNLSASFP	TEESSINYTF	KTPEKEPPLW
1370	1380	1390	1400	1410	1420	1430	1440
HAEFTKEELV	QKLRSTTKSA	DHLNGLLREI	EATNAVLMEQ	IKLLKSEIRR	LERNQEREKS	AANLEYLKNV	LLQFIFLKPG
1450	1460	1470	1480	1490			
SERERLLPVI	NTMLQLSPEE	KGKLAAVAQD	EEENASRSSG				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1535	1	1023.6824	101.59	2	49.0	12.2	1	1429-1445	K.NVLLQFIFLKPGSERER.L	

Detailed Protein Report

Protein 178: PREDICTED: probable tubulin polyglutamylase TTLL2 isoform X1 [Homo sapiens]

Accession:	gi|578812991	**Score:**	35.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	59.5
Database Date:	2015-11-30	**pI:**	9.4
		Sequence Coverage [%]:	5.2
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MAEDEPSGAL	LKPLVFRVDE	TTPAVVQSVL	LERGWNKFDK	QEQNAEDWNL	YWRTSSFRMT	EHNSVKPWQQ	LNHHPGTTKL
90	100	110	120	130	140	150	160
TRKDCLAKHL	KHMRRMYGTS	LYQFIPLTFV	MPNDYTKFVA	EYFQERQMLG	TKHSYWICKP	AELSRGRGIL	IFSDFKDFIF
170	180	190	200	210	220	230	240
DDMYIVQKYI	SNPLLIGRYK	CDLRIYVCVT	GFKPLTIYVY	QEGLVRFATE	KFDLSNLQNN	YAHLTNSSIN	KSGASYEKIK
250	260	270	280	290	300	310	320
EVIGHGCKWT	LSRFFSYLRS	WDVDDLLLWK	KIHRMVILTI	LAIAPSVPFA	ANCFELFGFD	ILIDDNLKPW	LLEVNYSPAL
330	340	350	360	370	380	390	400
TLDCSTDVLV	KRKLVHDIID	LIYLNGLRNE	GREASNATHG	NSNIDAAKSD	RGGLDAPDCL	PYDSLSFTSR	MYNEDDSVVE
410	420	430	440	450	460	470	480
KAVSVRPEAA	PASQLEGEMS	GQDFHLSTRE	MPQSKPKLRS	RHTPHKTLMP	YASLFQSHSC	KTKTSPCVLS	DRGKAPDPQA
490	500	510	520				
GNFVLVFPFN	EATLGASRNG	LNVKRIIQEL	QKLMNKQHS				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
429	1	542.2853	-31.85	2	35.0	16.8	1	239-248	K.IKEVIGHGCK.W	
89	1	647.9192	-109.54	3	30.5	18.2	1	447-463	K.TLMPYASLFQSHSCKTK.T	

Detailed Protein Report

Protein 179: leucine-rich repeat and calponin homology domain-containing protein 1 isoform 3 [Homo sapiens]

Accession:	gi|256017180	**Score:**	35.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	77.2
Database Date:	2015-11-30	**pI:**	5.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MATPGSEPQP	FVPALSVATL	HPLHHPHHHH	HHHQHHGGTG	APGGAGGGGG	GSGGFNLPLN	RGLERALEEA	ANSGGLNLSA
90	100	110	120	130	140	150	160
RKLKEFPRTA	APGHDLSDTV	QADLSKNRLV	EVPMELCHFV	SLEILNLYHN	CIRVIPEAIV	NLQMLTYLNL	SRNQLSALPA
170	180	190	200	210	220	230	240
CLCGLPLKVL	IASNNKLGSL	PEEIGQLKQL	MELDVSCNEI	TALPQQIGQL	KSLRELNVRR	NYLKVLPQEL	VDLPLVKFDF
250	260	270	280	290	300	310	320
SCNKVLVIPI	CFREMKQLQV	LLLENNPLQS	PPAQICTKGK	VHIFKYLSIQ	ACQIKTADSL	YLHTMERPHL	HQHVEDGKKD
330	340	350	360	370	380	390	400
SDSGVGSDNG	DKRLSATEPS	DEDTVSLNVP	MSNIMEEEQI	IKEDSCHRLS	PVKGEFHQEF	QPEPSLLGDS	TNSGEERDQF
410	420	430	440	450	460	470	480
TDRADGLHSE	FMNYKARAED	CEELLRIEED	VHWQTEGIIS	SSKDQDMDIA	MIEQLREAVD	LLQDPNGLST	DITERSVLNL
490	500	510	520	530	540	550	560
YPMGSAEALE	LQDSALNGQI	QLETSPVCEV	QSDLTLQSNG	SQYSPNEIRE	NSPAVSPTTN	STAPFGLKPR	SVFLRPQRNL
570	580	590	600	610	620	630	640
ESIDPQFTIR	RKMEQMREEK	ELVEQLRESI	EMRLKVSLHE	DLGAALMDGV	VLCHLVNHIR	PRSVASIHVP	SPAVPKLSMA
650	660	670	680	690	700		
KCRRNVENFL	EACRKLGVPE	EKLCLPHHIL	EEKGLVKVGI	TIQALLDITV	TKALFT		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
599	1	690.3992	85.05	2	36.8	23.5	1	645-655	R.NVENFLEACRK.L	Carbamidomethyl: 9

Detailed Protein Report

Protein 180: G-protein coupled receptor 98 precursor [Homo sapiens]

Accession:	gi|113722120	**Score:**	34.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	692.6
Database Date:	2015-11-30	**pI:**	4.4
Modification(s):	Oxidation	**Sequence Coverage [%]:**	0.7
		No. of unique Peptides:	2

Detailed Protein Report

10	20	30	40	50	60	70	80
MSVFLGPGMP	SASLLVNLLS	ALLILFVFGE	TEIRFTGQTE	FVVNETSTTV	IRLIIERIGE	PANVTAIVSL	YGEDAGDFFD
90	100	110	120	130	140	150	160
TYAAAFIPAG	ETNRTVYIAV	CDDDLPEPDE	TFIFHLTLQK	PSANVKLGWP	RTVTVTILSN	DNAFGIISFN	MLPSIAVSEP
170	180	190	200	210	220	230	240
KGRNESMPLT	LIREKGTYGM	VMVTFEVEGG	PNPPDEDLSP	VKGNITFPPG	RATVIYNLTV	LDDEVPENDE	IFLIQLKSVE
250	260	270	280	290	300	310	320
GGAEINTSRN	SIEIIIKKND	SPVRFLQSIY	LVPEEDHILI	IPVVRGKDNN	GNLIGSDEYE	VSISYAVTTG	NSTAHAQQNL
330	340	350	360	370	380	390	400
DFIDLQPNTT	VVFPPFIHES	HLKFQIVDDT	IPEIAESFHI	MLLKDTLQGD	AVLISPSVVQ	VTIKPNDKPY	GVLSFNSVLF
410	420	430	440	450	460	470	480
ERTVIIDEDR	ISRYEEITVV	RNGGTHGNVS	ANWVLTRNST	DPSPVTADIR	PSSGVLHFAQ	GQMLATIPLT	VVDDDLPEEA
490	500	510	520	530	540	550	560
EAYLLQILPH	TIRGGAEVSE	PAELLFYIQD	SDDVYGLITF	FPMENQKIES	SPGERYLSLS	FTRLGGTKGD	VRLLYSVLYI
570	580	590	600	610	620	630	640
PAGAVDPLQA	KEGILNISRR	NDLIFPEQKT	QVTTKLPIRN	DAFLQNGAHF	LVQLETVELL	NIIPLIPPIS	PRFGEICNIS
650	660	670	680	690	700	710	720
LLVTPAIANG	EIGFLSNLPI	ILHEPEDFAA	EVVYIPLHRD	GTDGQATVYW	SLKPSGFNSK	AVTPDDIGPF	NGSVLFLSGQ
730	740	750	760	770	780	790	800
SDTTINITIK	GDDIPEMNET	VTLSLDRVNV	ENQVLKSGYT	SRDLIILEND	DPGGVFEFSP	ASRGPYVIKE	GESVELHIIR
810	820	830	840	850	860	870	880
SRGSLVKQFL	HYRVEPRDSN	EFYGNTGVLE	FKPGEREIVI	TLLARLDGIP	ELDEHYWVVL	SSHGERESKL	GSATIVNITI
890	900	910	920	930	940	950	960
LKNDDPHGII	EFVSDGLIVM	INESKGDAIY	SAVYDVVRNR	GNFGDVSVSW	VVSPDFTQDV	FPVQGTVVFG	DQEFSKNITI
970	980	990	1000	1010	1020	1030	1040
YSLPDEIPEE	MEEFTVILLN	GTGGAKVGNR	TTATLRIRRN	DDPIYFAEPR	VVRVQEGETA	NFTVLRNGSV	DVTCMVQYAT
1050	1060	1070	1080	1090	1100	1110	1120
KDGKATARER	DFIPVEKGET	LIFEVGSRQQ	SISIFVNEDG	IPETDEPFYI	ILLNSTGDTV	VYQYGVATVI	IEANDDPNGI
1130	1140	1150	1160	1170	1180	1190	1200
FSLEPIDKAV	EEGKTNAFWI	LRHRGYFGSV	SVSWQLFQND	SALQPGQEFY	ETSGTVNFMD	GEEAKPIILH	AFPDKIPEFN
1210	1220	1230	1240	1250	1260	1270	1280
EFYFLKLVNI	SGGSPGPGGQ	LAETNLQVTV	MVPFNDDPFG	VFILDPECLE	REVAEDVLSE	DDMSYITNFT	ILRQQGVFGD
1290	1300	1310	1320	1330	1340	1350	1360
VQLGWEILSS	EFPAGLPPMI	DFLLVGIFPT	TVHLQQHMRR	HHSGTDALYF	TGLEGAFGTV	NPKYHPSRNN	TIANFTFSAW
1370	1380	1390	1400	1410	1420	1430	1440
VMPNANTNGF	IIAKDDGNGS	IYYGVKIQTN	ESHVTLSLHY	KTLGSNATYI	AKTTVMKYLE	ESVWLHLLII	LEDGIIEFYL
1450	1460	1470	1480	1490	1500	1510	1520
DGNAMPRGIK	SLKGEAITDG	PGILRIGAGI	NGNDRFTGLM	QDVRSYERKL	TLEEIYELHA	MPAKSDLHPI	SGYLEFRQGE
1530	1540	1550	1560	1570	1580	1590	1600
TNKSFIISAR	DDNDEEGEEL	FILKLVSVYG	GARISEENTT	ARLTIQKSDN	ANGLFGFTGA	CIPEIAEEGS	TISCVVERTR
1610	1620	1630	1640	1650	1660	1670	1680
GALDYVHVFY	TISQIETDGI	NYLVDDFANA	SGTITFLPWQ	RSEVLNIYVL	DDDIPELNEY	FRVTLVSAIP	GDGKLGSTPT
1690	1700	1710	1720	1730	1740	1750	1760
SGASIDPEKE	TTDITIKASD	HPYGLLQFST	GLPPQPKDAM	TLPASSVPHI	TVEEEDGEIR	LLVIRAQGLL	GRVTAEFRTV
1770	1780	1790	1800	1810	1820	1830	1840
SLTAFSPEDY	QNVAGTLEFQ	PGERYKYIFI	NITDNSIPEL	EKSFKVELLN	LEGGVAELFR	VDGSGSGDGD	MEFFLPTIHK
1850	1860	1870	1880	1890	1900	1910	1920
RASLGVASQI	LVTIAASDHA	HGVFEFSPES	LFVSGTEPED	GYSTVTLNVI	RHHGTLSPVT	LHWNIDSDPD	GDLAFTSGNI
1930	1940	1950	1960	1970	1980	1990	2000
TFEIGQTSAN	ITVEILPDED	PELDKAFSVS	VLSVSSGSLG	AHINATLTVL	ASDDPYGIFI	FSEKNRPVKV	EEATQNITLS
2010	2020	2030	2040	2050	2060	2070	2080
IIRLKGLMGK	VLVSYATLDD	MEKPPYFPPN	LARATQGRDY	IPASGFALFG	ANQSEATIAI	SILDDDEPER	SESVFIELLN
2090	2100	2110	2120	2130	2140	2150	2160
STLVAKVQSR	SIPNSPRLGP	KVETIAQLII	IANDDAFGTL	QLSAPIVRVA	ENHVGPIINV	TRTGGAFADV	SVKFKAVPIT
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
137	1	793.8712	-87.93	2	31.4	10.7	0	1990-2003	K.VEEATQNITLSIIR.L	
780	1	696.6836	-200.93	2	39.1	12.4	0	5266-5277	R.CAQMEPNALPFR.G	Oxidation: 4

Detailed Protein Report

Protein 181: sodium-driven chloride bicarbonate exchanger isoform 1 [Homo sapiens]

Accession:	gi|295821221	**Score:**	34.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	125.9
Database Date:	2015-11-30	**pI:**	6.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.5
		No. of unique Peptides:	2

Quantitation

MD:MU	**Median:** 1.37	**CV:** 0.00 %	**No. of Peptides:** 1

10	20	30	40	50	60	70	80
MEIKDQGAQM	EPLLPTRNDE	EAVVDRGGTR	SILKTHFEKE	DLEGHRTLFI	GVHVPLGGRK	SHRRHRHRGH	KHRKRDRERD
90	100	110	120	130	140	150	160
SGLEDGRESP	SFDTPSQRVQ	FILGTEDDDE	EHIPHDLFTE	LDEICWREGE	DAEWRETARW	LKFEEDVEDG	GERWSKPYVA
170	180	190	200	210	220	230	240
TLSLHSLFEL	RSCILNGTVL	LDMHANTLEE	IADMVLDQQV	SSGQLNEDVR	HRVHEALMKQ	HHHQNQKKLT	NRIPIVRSFA
250	260	270	280	290	300	310	320
DIGKKQSEPN	SMDKNAGQVV	SPQSAPACVE	NKNDVSRENS	TVDFSKGLGG	QQKGHTSPCG	MKQRHEKGPP	HQQEREVDLH
330	340	350	360	370	380	390	400
FMKKIPPGAE	ASNILVGELE	FLDRTVVAFV	RLSPAVLLQG	LAEVPIPTRF	LFILLGPLGK	GQQYHEIGRS	IATLMTDEVF
410	420	430	440	450	460	470	480
HDVAYKAKDR	NDLVSGIDEF	LDQVTVLPPG	EWDPSIRIEP	PKNVPSQEKR	KIPAVPNGTA	AHGEAEPHGG	HSGPELQRTG
490	500	510	520	530	540	550	560
RIFGGLILDI	KRKAPYFWSD	FRDAFSLQCL	ASFLFLYCAC	MSPVITFGGL	LGEATEGRIS	AIESLFGASM	TGIAYSLFGG
570	580	590	600	610	620	630	640
QPLTILGSTG	PVLVFEKILF	KFCKEYGLSY	LSLRASIGLW	TATLCIILVA	TDASSLVCYI	TRFTEEAFAS	LICIIFIYEA
650	660	670	680	690	700	710	720
LEKLFELSEA	YPINMHNDLE	LLTQYSCNCV	EPHNPSNGTL	KEWRESNISA	SDIIWENLTV	SECKSLHGEY	VGRACGHDHP
730	740	750	760	770	780	790	800
YVPDVLFWSV	ILFFSTVTLS	ATLKQFKTSR	YFPTKVRSIV	SDFAVFLTIL	CMVLIDYAIG	IPSPKLQVPS	VFKPTRDDRG
810	820	830	840	850	860	870	880
WFVTPLGPNP	WWTVIAAIIP	ALLCTILIFM	DQQITAVIIN	RKEHKLKKGC	GYHLDLLMVA	VMLGVCSIMG	LPWFVAATVL
890	900	910	920	930	940	950	960
SITHVNSLKL	ESECSAPGEQ	PKFLGIREQR	VTGLMIFILM	GSSVFMTSIL	KFIPMPVLYG	VFLYMGASSL	KGIQFFDRIK
970	980	990	1000	1010	1020	1030	1040
LFWMPAKHQP	DFIYLRHVPL	RKVHLFTIIQ	MSCLGLLWII	KVSRAAIVFP	MMVLALVFVR	KLMDLLFTKR	ELSWLDDLMP
1050	1060	1070	1080	1090	1100	1110	1120
ESKKKKLEDA	EKEEEQSMLA	MEDEGTVQLP	LEGHYRDDPS	VINISDEMSK	TALWRNLLIT	ADNSKDKESS	FPSKSSPS

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1817	1	847.8355	-100.68	2	52.5	10.3	1	278-293	R.ENSTVDFSKGLGGQQK.G		
1399	1	783.2967	-72.60	2	47.2	11.8	0	1077-1090	R.DDPSVINISDEMSK.T	Oxidation: 12	MD:MU 1.37

Detailed Protein Report

Protein 182: transcription regulator protein BACH1 [Homo sapiens]

Accession: gi|4502353
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 34.6
MW [kDa]: 81.9
pI: 4.8
Sequence Coverage [%]: 3.7
No. of unique Peptides: 2

Alias proteins:

Accession	Name	Description
gi|530418993	refseq_human (refseq_human_20140103.fasta)	PREDICTED: transcription regulator protein BACH1 isoform X3 [Homo sapiens]
gi|530418991	refseq_human (refseq_human_20140103.fasta)	PREDICTED: transcription regulator protein BACH1 isoform X2 [Homo sapiens]
gi|530418989	refseq_human (refseq_human_20140103.fasta)	PREDICTED: transcription regulator protein BACH1 isoform X1 [Homo sapiens]
gi|45827690	refseq_human (refseq_human_20140103.fasta)	transcription regulator protein BACH1 [Homo sapiens]

```
        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        640
IRRRSKNRIA AQRCRKRKLD CIQNLESEIE KLQSEKESLL KERDHILSTL GETKQNLTGL CQKVCKEAAL SQEQIQILAK
       650        660        670        680        690        700        710        720
YSAADCPLSF LISEKDKSTP DGELALPSIF SLSDRPPAVL PPCARGNSEP GYARGQESQQ MSTATSEQAG PAEQCRQSGG
       730        740
ISDFCQQMTD KCTTDE
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
504	1	667.7055	-215.81	2	35.6	22.1	1	615-626	K.QNLTGLCQKVCK.E	
1770	1	851.2192	-170.05	2	52.1	12.5	0	717-731	R.QSGGISDFCQQMTDK.C	Carbamidomethyl: 9

Detailed Protein Report

Protein 183: myosin-9 [Homo sapiens]

Accession:	gi|12667788	**Score:**	34.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	226.4
Database Date:	2015-11-30	**pI:**	5.4
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.2
		No. of unique Peptides:	2

Quantitation

MD:MU	**Median:**	1.09	**CV:**	0.00 %	**No. of Peptides:**	1	

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	Ratios
1950	1	856.8003	-136.41	2	54.5	12.5	1	910-923	K.KQELEEICHDLEAR.V		
502	2	567.1670	-259.21	2	35.6	22.1	2	1604-1613	K.QRSMAVAARK.K	Oxidation: 4	MD:MU 1.09

Detailed Protein Report

Protein 184: neuron navigator 2 isoform 3 [Homo sapiens]

Accession: gi|161169015
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl, Oxidation

Score: 34.5
MW [kDa]: 254.8
pI: 9.7
Sequence Coverage [%]: 1.3
No. of unique Peptides: 2

```
        10         20         30         40         50         60         70         80
MESVSESSQQ QKRKPVIHGL EDQKRIYTDW ANHYLAKSGH KRLIRDLQQD VTDGVLLAQI IQVVANEKIE DINGCPKNRS
        90        100        110        120        130        140        150        160
QMIENIDACL NFLAAKGINI QGLSAEEIRN GNLKAILGLF FSLSRYKQQQ QQPQKQHLSS PLPPAVSQVA GAPSQCQAGT
       170        180        190        200        210        220        230        240
PQQQVPVTPQ APCQPHQPAP HQQSKAQAEM QSRLPGPTAR VSAAGSEAKT RGGSTTANNR RSQSFNNYDK SKPVTSPPPP
       250        260        270        280        290        300        310        320
PSSHEKEPLA SSASSHPGMS DNAPASLESG SSSTPTNCST SSAIPQPGAA TKPWRSKSLS VKHSATVSML SVKPPGPEAP
       330        340        350        360        370        380        390        400
RPTPEAMKPA PNNQKSMLEK LKLFNSKGGS KAGEGPGSRD TSCERLETLP SFEESEELEA ASRMLTTVGP ASSSPKIALK
       410        420        430        440        450        460        470        480
GIAQRTFSRA LTNKKSSLKG NEKEKEKQQR EKDKEKSKDL AKRASVTERL DLKEEPKEDP SGAAVPEMPK KSSKIASFIP
       490        500        510        520        530        540        550        560
KGGKLNSAKK EPMAPSHSGI PKPGMKSMPG KSPSAPAPSK EGERSRSGKL SSGLPQQKPQ LDGRHSSSSS SLASSEGKGP
       570        580        590        600        610        620        630        640
GGTTLNHSIS SQTVSGSVGT TQTTGSNTVS VQLPQPQQQY NHPNTATVAP FLYRSQTDTE GNVTAESSST GVSVEPSHFT
       650        660        670        680        690        700        710        720
KTGQPALEEL TGEDPEARRL RTVKNIADLR QNLEETMSSL RGTQVTHSTL ETTFDTNVTT EMSGRSILSL TGRPTPLSWR
       730        740        750        760        770        780        790        800
LGQSSPRLQA GDAPSMGNGY PPRANASRFI NTESGRYVYS APLRRQLASR GSSVCHVDVS DKAGDEMDLE GISMDAPGYM
       810        820        830        840        850        860        870        880
SDGDVLSKNI RTDDITSGYM TDGGLGLYTR RLNRLPDGMA VVRETLQRNT SLGLGDADSW DDSSSVSSGI SDTIDNLSTD
       890        900        910        920        930        940        950        960
DINTSSSISS YANTPASSRK NLDVQTDAEK HSQVERNSLW SGDDVKKSDG GSDSGIKMEP GSKWRRNPSD VSDESDKSTS
       970        980        990       1000       1010       1020       1030       1040
GKKNPVISQT GSWRRGMTAQ VGITMPRTKP SAPAGALKTP GTGKTDDAKV SEKGRLSPKA SQVKRSPSDA GRSSGDESKK
      1050       1060       1070       1080       1090       1100       1110       1120
PLPSSSRTPT ANANSFGFKK QSGSAAGLAM ITASGVTVTS RSATLGKIPK SSALVSRSAG RKSSMDGAQN QDDGYLALSS
      1130       1140       1150       1160       1170       1180       1190       1200
RTNLQYRSLP RPSKSNSRNG AGNRSSTSSI DSNISSKSAG LPVPKLREPS KTALGSSLPG LVNQTDKEKG ISSDNESVAS
      1210       1220       1230       1240       1250       1260       1270       1280
CNSVKVNPAA QPVSSPAQTS LQPGAKYPDV ASPTLRRLFG GKPTKQVPIA TAENMKNSVV ISNPHATMTQ QGNLDSPSGS
      1290       1300       1310       1320       1330       1340       1350       1360
GVLSSGSSSP LYSKNVDLNQ SPLASSPSSA HSAPSNSLTW GTNASSSSAV SKDGLGFQSV SSLHTSCESI DISLSSGGVP
      1370       1380       1390       1400       1410       1420       1430       1440
SHNSSTGLIA SSKDDSLTPF VRTNSVKTTL SESPLSSPAA SPKFCRSTLP RKQDSDPHLD RNTLPKKGLR YTPTSQLRTQ
      1450       1460       1470       1480       1490       1500       1510       1520
EDAKEWLRSH SAGGLQDTAA NSPFSSGSSV TSPSGTRFNF SQLASPTTVT QMSLSNPTML RTHSLSNADG QYDPYTDSRF
      1530       1540       1550       1560       1570       1580       1590       1600
RNSSMSLDEK SRTMSRSGSF RDGFEEVHGS SLSLVSSTSS VYSTPEEKCQ SEIRKLRREL DASQEKVSAL TTQLTANAHL
      1610       1620       1630       1640       1650       1660       1670       1680
VAAFEQSLGN MTIRLQSLTM TAEQKDSELN ELRKTIELLK KQNAAAQAAI NGVINTPELN CKGNGTAQSA DLRIRRQHSS
      1690       1700       1710       1720       1730       1740       1750       1760
DSVSSINSAT SHSSVGSNIE SDSKKKKRKN WLRSSFKQAF GKKKSPKSAS SHSDIEEMTD SSLPSSPKLP HNGSTGSTPL
      1770       1780       1790       1800       1810       1820       1830       1840
LRNSHSNSLI SECMDSEAET VMQLRNELRD KEMKLTDIRL EALSSAHQLD QLREAMNRMQ SEIEKLKAEN DRLKSESQGS
      1850       1860       1870       1880       1890       1900       1910       1920
GCSRAPSQVS ISASPRQSMG LSQHSLNLTE STSLDMLLDD TGECSARKEG GRHVKIVVSF QEEMKWKEDS RPHLFLIGCI
      1930       1940       1950       1960       1970       1980       1990       2000
GVSGKTKWDV LDGVVRRLFK EYIIHVDPVS QLGLNSDSVL GYSIGEIKRS NTSETPELLP CGYLVGENTT ISVTVKGLAE
      2010       2020       2030       2040       2050       2060       2070       2080
NSLDSLVFES LIPKPILQRY VSLLIEHRRI ILSGPSGTGK TYLANRLSEY IVLREGRELT DGVIATFNVD HKSSKELRQY
      2090       2100       2110       2120       2130       2140       2150       2160
LSNLADQCNS ENNAVDMPLV IILDNLHHVS SLGEIFNGLL NCKYHKCPYI IGTMNQATSS TPNLQLHHNF RWVLCANHTE
      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
183	1	904.3719	-34.40	2	31.7	10.6	2	348-365	K.GGSKAGEGPGSRDTSCER.L	Carbamidomethyl: 16
2463	1	647.1849	-205.84	2	61.2	24.0	0	976-987	R.GMTAQVGITMPR.T	Oxidation: 2, 10

Detailed Protein Report

Protein 185: PREDICTED: DNA polymerase kappa isoform X3 [Homo sapiens]

Accession: gi|530379363
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 34.5
MW [kDa]: 57.6
pI: 9.2
Sequence Coverage [%]: 10.1
No. of unique Peptides: 2

10	20	30	40	50	60	70	80
MDSTKEKCDS	YKDDLLLRMG	LNDNKAGMEG	LDKEKINKII	MEATKGSRFY	GNELKKEKQV	NQRIENMMQQ	KAQITSQQLR
90	100	110	120	130	140	150	160
KAQLQVDRFA	MELEQSRNLS	NTIVHIDMDA	FYAAVEMRDN	PELKDKPIAV	GSMSMLSTSN	YHARRFGVRA	AMPGFIAKRL
170	180	190	200	210	220	230	240
CPQLIIVPPN	FDKYRAVSKE	VKEILADYDP	NFMAMSLDEA	YLNITKHLEE	RQNWPEDKRR	YFIKMGSSVE	NDLQNLYIQR
250	260	270	280	290	300	310	320
SITFTDNPGK	EVNKLSEHER	SISPLLFEES	PSDVQPPGDP	FQVNFEEQNN	PQILQNSVVF	GTSAQEVVKE	IRFRIEQKTT
330	340	350	360	370	380	390	400
LTASAGIAPN	TMLAKVCSDK	NKPNGQYQIL	PNRQAVMDFI	KDLPIRKVSG	IGKVTEKMLK	ALGIITCTEL	YQQRALLSLL
410	420	430	440	450	460	470	480
FSETSWHYFL	HISLGLGSTH	LTRDGERKSM	SVERTFSEIN	KAEEQYSLCQ	ELCSELAQDL	QKERLKVFGY	LVFPMKRTGN
490	500	510					
TNKGALLAFY	RLETKPCQPL	SVH					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2396	1	1045.2249	47.66	3	60.3	12.4	1	180-206	K.EVKEILADYDPNFMAMSLDEAYLNITK.H	
1772	1	807.4927	33.69	2	52.1	10.9	2	465-477	R.LKVFGYLVFPMKR.T	Oxidation: 11

Detailed Protein Report

Protein 186: PREDICTED: methylcytosine dioxygenase TET3 isoform X1 [Homo sapiens]

Accession:	gi|530367326	**Score:**	34.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	193.6
Database Date:	2015-11-30	**pI:**	9.0
		Sequence Coverage [%]:	0.8
		No. of unique Peptides:	1

Alias proteins:

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

Detailed Protein Report

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
806	1	546.9707	-505.05	1	39.6	11.3	0	1562-1566	K.GEEGR.I	

Detailed Protein Report

Protein 187: scm-like with four MBT domains protein 1 [Homo sapiens]

Accession:	gi|53692193	**Score:**	34.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	98.1
Database Date:	2015-11-30	**pI:**	5.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	4.5
		No. of unique Peptides:	2

Alias proteins:

Accession	**Name**	**Description**
gi|578806223	refseq_human (refseq_human_20140103.fasta)	PREDICTED: scm-like with four MBT domains protein 1 isoform X4 [Homo sapiens]
gi|578806221	refseq_human (refseq_human_20140103.fasta)	PREDICTED: scm-like with four MBT domains protein 1 isoform X3 [Homo sapiens]
gi|530372640	refseq_human (refseq_human_20140103.fasta)	PREDICTED: scm-like with four MBT domains protein 1 isoform X2 [Homo sapiens]

10	20	30	40	50	60	70	80
MNGEQQLDAD	AGSGMEEVEL	SWEDYLEETG	STAVPYGSFK	HVDTRLQNGF	APGMKLEVAV	RTDPETYWVA	TVITTCEQLL
90	100	110	120	130	140	150	160
LLRYDGYGED	RRADFWCDIR	KADLYPIGWC	EQNKKTLEAP	EGIRDKVSDW	DEFLRQTLIG	ACSPPVPLLE	GLRNGRNPLD
170	180	190	200	210	220	230	240
LIAPGSRLEC	QAFQDSLSTW	IVTVVENIGG	RLKLRYEGLE	SSDNYEHWLY	YLDPFLHHVG	WAAQQGYELQ	PPSAIRHLKN
250	260	270	280	290	300	310	320
EAEWQEILAK	VKEEEEEPLP	SYLFKDKQVI	GIHTFSVNMK	LEAVDPWSPF	GISPATVVKV	FDEKYFLVEM	DDLRPENHAR
330	340	350	360	370	380	390	400
RSFVCHADSP	GIFPVQWSLK	NGLHISPPPG	YPSQDFDWAD	YLKQCGAEAA	PQRCFPPLIS	EHEFKENMKL	EAVNPILPEE
410	420	430	440	450	460	470	480
VCVATITAVR	GSYLWLQLEG	SKKPIPECIV	SVESMDIFPL	GWCETNGHPL	STPRRARVYK	QRKIAVVQPE	KQVPSSRTVH
490	500	510	520	530	540	550	560
EGLRNQELNS	TESVMINGKY	CCPKIYFNHR	CFSGPYLNKG	RIAELPQCVG	PGNCVLVLRE	VLTLLINAAY	KPSRVLRELQ
570	580	590	600	610	620	630	640
LDKDSVWHGC	GEVLKAKYKG	KSYRATVEIV	KTADRVTEFC	RQTCIKLECC	PNLFGPRMVL	DKCSENCSVL	TKTKYTHYYG
650	660	670	680	690	700	710	720
KKKNKRIGRP	PGGHSNLACA	LKKASKRRKR	RKNVFVHKKK	RSSASVDNTP	AGSPQGSGGE	DEDDPDEGDD	DSLSEGSTSE
730	740	750	760	770	780	790	800
QQDELQEESE	MSEKKSCSSS	PTQSEISTSL	PPDRQRRKRE	LRTFSFSDDE	NKPPSPKEIR	IEVAERLHLD	SNPLKWSVAD
810	820	830	840	850	860	870	
VVRFIRSTDC	APLARIFLDQ	EIDGQALLLL	TLPTVQECMD	LKLGPAIKLC	HHIERIKFAF	YEQFAN	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2196	1	873.3355	-156.25	2	57.3	10.7	1	46-61	R.LQNGFAPGMKLEVAVR.T	Oxidation: 9
1978	2	656.8089	-9.85	2	54.8	12.3	1	623-634	K.CSENCSVLTKTK.Y	

Detailed Protein Report

Protein 188: proteoglycan 4 isoform D precursor [Homo sapiens]

Accession:	gi|189181724	**Score:**	34.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	136.5
Database Date:	2015-11-30	**pI:**	10.1
		Sequence Coverage [%]:	1.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAWKTLPIYL	LLLLSVFVIQ	QVSSQELSCK	GRCFESFERG	RECDCDAQCK	KYDKCCPDYE	SFCAEVKDNK	KNRTKKKPTP
90	100	110	120	130	140	150	160
KPPVVDEAGS	GLDNGDFKVT	TPDTSTTQHN	KVSTSPKITT	AKPINPRPSL	PPNSDTSKET	SLTVNKETTV	ETKETTTTNK
170	180	190	200	210	220	230	240
QTSTDGKEKT	TSAKETQSIE	KTSAKDLAPT	SKVLAKPTPK	AETTTKGPAL	TTPKEPTPTT	PKEPASTTPK	EPTPTTIKSA
250	260	270	280	290	300	310	320
PTTPKEPAPT	TTKSAPTTPK	EPAPTTTKEP	APTTPKEPAP	TTTKEPAPTT	TKSAPTTPKE	PAPTTPKKPA	PTTPKEPAPT
330	340	350	360	370	380	390	400
TPKEPTPTTP	KEPAPTTKEP	APTTPKEPAP	TAPKKPAPTT	PKEPAPTTPK	EPAPTTTKEP	SPTTPKEPAP	TTTKSAPTTT
410	420	430	440	450	460	470	480
KEPAPTTTKS	APTTPKEPSP	TTTKEPAPTT	PKEPAPTTPK	KPAPTTPKEP	APTTPKEPAP	TTTKKPAPTT	PKEPAPTTPK
490	500	510	520	530	540	550	560
ETAPTTPKKL	TPTTPEKLAP	TTPEKPAPTT	PEELAPTTPE	EPTPTTPEEP	APTTPKAAAP	NTPKEPAPTT	PKEPAPTTPK
570	580	590	600	610	620	630	640
EPAPTTPKET	APTTPKGTAP	TTLKEPAPTT	PKKPAPKELA	PTTTKEPTST	TCDKPAPTTP	KGTAPTTPKE	PAPTTPKEPA
650	660	670	680	690	700	710	720
PTTPKGTAPT	TLKEPAPTTP	KKPAPKELAP	TTTKGPTSTT	SDKPAPTTPK	ETAPTTPKEP	APTTPKKPAP	TTPETPPPTT
730	740	750	760	770	780	790	800
SEVSTPTTTK	EPTTIHKSPD	ESTPELSAEP	TPKALENSPK	EPGVPTTKTP	AATKPEMTTT	AKDKTTERDL	RTTPETTTAA
810	820	830	840	850	860	870	880
PKMTKETATT	TEKTTESKIT	ATTTQVTSTT	TQDTTPFKIT	TLKTTTLAPK	VTTTKKTITT	TEIMNKPEET	AKPKDRATNS
890	900	910	920	930	940	950	960
KATTPKPQKP	TKAPKKPTST	KKPKTMPRVR	KPKTTPTPRK	MTSTMPELNP	TSRIAEAMLQ	TTTRPNQTPN	SKLVEVNPKS
970	980	990	1000	1010	1020	1030	1040
EDAGGAEGET	PHMLLRPHVF	MPEVTPDMDY	LPRVPNQGII	INPMLSDETN	ICNGKPVDGL	TTLRNGTLVA	FRGHYFWMLS
1050	1060	1070	1080	1090	1100	1110	1120
PFSPPSPARR	ITEVWGIPSP	IDTVFTRCNC	EGKTFFFKDS	QYWRFTNDIK	DAGYPKPIFK	GFGGLTGQIV	AALSTAKYKN
1130	1140	1150	1160	1170	1180	1190	1200
WPESVYFFKR	GGSIQQYIYK	QEPVQKCPGR	RPALNYPVYG	ETTQVRRRRF	ERAIGPSQTH	TIRIQYSPAR	LAYQDKGVLH
1210	1220	1230	1240	1250	1260	1270	1280
NEVKVSILWR	GLPNVVTSAI	SLPNIRKPDG	YDYYAFSKDQ	YYNIDVPSRT	ARAITTRSGQ	TLSKVWYNCP	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2237	1	994.8741	-142.64	2	57.8	23.9	2	785-802	K.TTERDLRTTPETTTAAPK.M	

Detailed Protein Report

Protein 189: DNA-directed RNA polymerase II subunit RPB1 [Homo sapiens]

Accession:	gi|4505939	**Score:**	34.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	217.1
Database Date:	2015-11-30	**pI:**	7.1
		Sequence Coverage [%]:	2.2
		No. of unique Peptides:	1

Detailed Protein Report

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        10         20         30         40         50         60         70         80
MHGGGPPSGD SACPLRTIKR VQFGVLSPDE LKRMSVTEGG IKYPETTEGG RPKLGGLMDP RQGVIERTGR CQTCAGNMTE
        90        100        110        120        130        140        150        160
CPGHFGHIEL AKPVFHVGFL VKTMKVLRCV CFFCSKLLVD SNNPKIKDIL AKSKGQPKKR LTHVYDLCKG KNICEGGEEM
       170        180        190        200        210        220        230        240
DNKFGVEQPE GDEDLTKEKG HGGCGRYQPR IRRSGLELYA EWKHVNEDSQ EKKILLSPER VHEIFKRISD EECFVLGMEP
       250        260        270        280        290        300        310        320
RYARPEWMIV TVLPVPPLSV RPAVVMQGSA RNQDDLTHKL ADIVKINNQL RRNEQNGAAA HVIAEDVKLL QFHVATMVDN
       330        340        350        360        370        380        390        400
ELPGLPRAMQ KSGRPLKSLK QRLKGKEGRV RGNLMGKRVD FSARTVITPD PNLSIDQVGV PRSIAANMTF AEIVTPFNID
       410        420        430        440        450        460        470        480
RLQELVRRGN SQYPGAKYII RDNGDRIDLR FHPKPSDLHL QTGYKVERHM CDGDIVIFNR QPTLHKMSMM GHRVRILPWS
       490        500        510        520        530        540        550        560
TFRLNLSVTT PYNADFDGDE MNLHLPQSLE TRAEIQELAM VPRMIVTPQS NRPVMGIVQD TLTAVRKFTK RDVFLERGEV
       570        580        590        600        610        620        630        640
MNLLMFLSTW DGKVPQPAIL KPRPLWTGKQ IFSLIIPGHI NCIRTHSTHP DDEDSGPYKH ISPGDTKVVV ENGELIMGIL
       650        660        670        680        690        700        710        720
CKKSLGTSAG SLVHISYLEM GHDITRLFYS NIQTVINNWL LIEGHTIGIG DSIADSKTYQ DIQNTIKKAK QDVIEVIEKA
       730        740        750        760        770        780        790        800
HNNELEPTPG NTLRQTFENQ VNRILNDARD KTGSSAQKSL SEYNNFKSMV VSGAKGSKIN ISQVIAVVGQ QNVEGKRIPF
       810        820        830        840        850        860        870        880
GFKHRTLPHF IKDDYGPESR GFVENSYLAG LTPTEFFFHA MGGREGLIDT AVKTAETGYI QRRLIKSMES VMVKYDATVR
       890        900        910        920        930        940        950        960
NSINQVVQLR YGEDGLAGES VEFQNLATLK PSNKAFEKKF RFDYTNERAL RRTLQEDLVK DVLSNAHIQN ELEREFERMR
       970        980        990       1000       1010       1020       1030       1040
EDREVLRVIF PTGDSKVVLP CNLLRMIWNA QKIFHINPRL PSDLHPIKVV EGVKELSKKL VIVNGDDPLS RQAQENATLL
      1050       1060       1070       1080       1090       1100       1110       1120
FNIHLRSTLC SRRMAEEFRL SGEAFDWLLG EIESKFNQAI AHPGEMVGAL AAQSLGEPAT QMTLNTFHYA GVSAKNVTLG
      1130       1140       1150       1160       1170       1180       1190       1200
VPRLKELINI SKKPKTPSLT VFLLGQSARD AERAKDILCR LEHTTLRKVT ANTAIYYDPN PQSTVVAEDQ EWVNVYYEMP
      1210       1220       1230       1240       1250       1260       1270       1280
DFDVARISPW LLRVELDRKH MTDRKLTMEQ IAEKINAGFG DDLNCIFNDD NAEKLVLRIR IMNSDENKMQ EEEEVVDKMD
      1290       1300       1310       1320       1330       1340       1350       1360
DDVFLRCIES NMLTDMTLQG IEQISKVYMH LPQTDNKKKI IITEDGEFKA LQEWILETDG VSLMRVLSEK DVDPVRTTSN
      1370       1380       1390       1400       1410       1420       1430       1440
DIVEIFTVLG IEAVRKALER ELYHVISFDG SYVNYRHLAL LCDTMTCRGH LMAITRHGVN RQDTGPLMKC SFEETVDVLM
      1450       1460       1470       1480       1490       1500       1510       1520
EAAAHGESDP MKGVSENIML GQLAPAGTGC FDLLLDAEKC KYGMEIPTNI PGLGAAGPTG MFFGSAPSPM GGISPAMTPW
      1530       1540       1550       1560       1570       1580       1590       1600
NQGATPAYGA WSPSVGSGMT PGAAGFSPSA ASDASGFSPG YSPAWSPTPG SPGSPGPSSP YIPSPGGAMS PSYSPTSPAY
      1610       1620       1630       1640       1650       1660       1670       1680
EPRSPGGYTP QSPSYSPTSP SYSPTSPSYS PTSPNYSPTS PSYSPTSPSY SPTSPSYSPT SPSYSPTSPS YSPTSPSYSP
      1690       1700       1710       1720       1730       1740       1750       1760
TSPSYSPTSP SYSPTSPSYS PTSPSYSPTS PSYSPTSPSY SPTSPSYSPT SPSYSPTSPS YSPTSPNYSP TSPNYTPTSP
      1770       1780       1790       1800       1810       1820       1830       1840
SYSPTSPSYS PTSPNYTPTS PNYSPTSPSY SPTSPSYSPT SPSYSPSSPR YTPQSPTYTP SSPSYSPSSP SYSPTSPKYT
      1850       1860       1870       1880       1890       1900       1910       1920
PTSPSYSPSS PEYTPTSPKY SPTSPKYSPT SPKYSPTSPT YSPTTPKYSP TSPTYSPTSP VYTPTSPKYS PTSPTYSPTS
      1930       1940       1950       1960       1970       1980
PKYSPTSPTY SPTSPKGSTY SPTSPGYSPT SPTYSLTSPA ISPDDSDEEN
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
652	1	918.1693	7.00	3	37.5	17.7	2	358-382	K.RVDFSARTVITPDPNLSIDQVGVPR.S	

Detailed Protein Report

Protein 190: **monofunctional C1-tetrahydrofolate synthase, mitochondrial isoform 3 [Homo sapiens]**

Accession:	gi|337756507	**Score:**	34.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	99.2
Database Date:	2015-11-30	**pI:**	7.0
		Sequence Coverage [%]:	3.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MQSRRARPRR	EVIQNSKEVL	SLLQEKNPAF	KPVLAIIQAG	DDNLMQEINQ	NLAEEAGLNI	THICLPPDSS	EAEIIDEILK
90	100	110	120	130	140	150	160
INEDTRVHGL	ALQISENLFS	NKVLNALKPE	KDVDGVTDIN	LGKLVRGDAH	ECFVSPVAKA	VIELLEKSVG	VNLDGKKILV
170	180	190	200	210	220	230	240
VGAHGSLEAA	LQCLFQRKGS	MTMSIQWKTR	QLQSKLHEAD	IVVLGSPKPE	EIPLTWIQPG	TTVLNCSHDF	LSGKVGCGSP
250	260	270	280	290	300	310	320
RIHFGGLIEE	DDVILLAAAL	RIQNMVSSGR	RWLREQQHRR	WRLHCLKLQP	LSPVPSDIEI	SRGQTPKAVD	VLAKEIGLLA
330	340	350	360	370	380	390	400
DEIEIYGKSK	AKVRLSVLER	LKDQADGKYV	LVAGITPTPL	GEGKSTVTIG	LVQALTAHLN	VNSFACLRQP	SQGPTFGVKG
410	420	430	440	450	460	470	480
GAAGGGYAQV	IPMEEFNLHL	TGDIHAITAA	NNLLAAAIDT	RILHENTQTD	KALYNRLVPL	VNGVREFSEI	QLARLKKLGI
490	500	510	520	530	540	550	560
NKTDPSTLTE	EEVSKFARLD	IDPSTITWQR	VLDTNDRFLR	KITIGQGNTE	KGHYRQAQFD	IAVASEIMAV	LALTDSLADM
570	580	590	600	610	620	630	640
KARLGRMVVA	SDKSGQPVTA	DDLGVTGALT	VLMKDAIKPN	LMQTLEGTPV	FVHAGPFANI	AHGNSSVLAD	KIALKLVGEE
650	660	670	680	690	700	710	720
GFVVTEAGFG	ADIGMEKFFN	IKCRASGLVP	NVVVLVATVR	ALKMHGGGPS	VTAGVPLKKE	YTEENIQLVA	DGCCNLQKQI
730	740	750	760	770	780	790	800
QITQLFGVPV	VVALNVFKTD	TRAEIDLVCE	LAKRAGAFDA	VPCYHWSVGG	KGSVDLARAV	REAASKRSRF	QFLYDVQVPI
810	820	830	840	850	860	870	880
VDKIRTIAQA	VYGAKDIELS	PEAQAKIDRY	TQQGFGNLPI	CMAKTHLSLS	HQPDKKGVPR	DFILPISDVR	ASIGAGFIYP
890	900	910	920				
LVGTMSTMPG	LPTRPCFYDI	DLDTETEQVK	GLF				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
228	1	801.7963	-174.05	2	32.6	23.3	2	262-274	R.IQNMVSSGRRWLR.E	

Detailed Protein Report

Protein 191: phospholipase B1, membrane-associated isoform 2 precursor [Homo sapiens]

Accession:	gi|283436114	**Score:**	34.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	161.6
Database Date:	2015-11-30	**pI:**	5.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.5
		No. of unique Peptides:	2

```
        10         20         30         40         50         60         70         80
MGLRPGIFLL ELLLLLGQGT PQIHTSPRKS TLEGQLWPET LKNSPFPCNP NKLGVNMPSK SVHSLKPSDI KFVAAIGNLE
        90        100        110        120        130        140        150        160
IPPDPGTGDL EKQDWTERPQ QVCMGVMTVL SDIIRYFSPS VPMPVCHTGK RVIPHDGAED LWIQAQELVR NMKENLQLDF
       170        180        190        200        210        220        230        240
QFDWKLINVF FSNASQCYLC PSAQQAPSLS TVLLSQNGLA AGGVDELMGV LDYLQQEVPR AFVNLVDLSE VAEVSRQYHG
       250        260        270        280        290        300        310        320
TWLSPAPEPC NCSEETTRLA KVVMQWSYQE AWNSLLASSR YSEQESFTVV FQPFFYETTP SLHSEDPRLQ DSTTLAWHLW
       330        340        350        360        370        380        390        400
NRMMEPAGEK DEPLSVKHGR PMKCPSQESP YLFSYRNSNY LTRLQKPQDK LEVREGAEIR CPDKDPSDTV PTSVHRLKPA
       410        420        430        440        450        460        470        480
DINVIGALGD SLTAGNGAGS TPGNVLDVLT QYRGLSWSVG GDENIGTVTT LANILREFNP SLKGFSVGTG KETSPNAFLN
       490        500        510        520        530        540        550        560
QAVAGGRAED LPVQARRLVD LMKNDTRIHF QEDWKIITLF IGGNDLCDFC NDLVPRAFVN LVTVLEIVNL RELYQEKKVY
       570        580        590        600        610        620        630        640
CPRMILRSLC PCVLKFDDNS TELATLIEFN KKFQEKTHQL IESGRYDTRE DFTVVVQPFF ENVDMPKTSE GLPDNSFFAP
       650        660        670        680        690        700        710        720
DCFHFSSKSH SRAASALWNN MLEPVGQKTT RHKFENKINI TCPNQVQPFL RTYKNSMQGH GTWLPCRDRA PSALHPTSVH
       730        740        750        760        770        780        790        800
ALRPADIQVV AALGDSLTAG NGIGSKPDDL PDVTTQYRGL SYSAGGDGSL ENVTTLPNIL REFNRNLTGY AVGTGDANDT
       810        820        830        840        850        860        870        880
NAFLNQAVPG AKAEDLMSQV QTLMQKMKDD HRVNFHEDWK VITVLIGGSD LCDYCTDSNL YSAANFVHHL RNALDVLHRE
       890        900        910        920        930        940        950        960
VPRVLVNLVD FLNPTIMRQV FLGNPDKCPV QQASVLCNCV LTLRENSQEL ARLEAFSRAY RSSMRELVGS GRYDTQEDFS
       970        980        990       1000       1010       1020       1030       1040
VVLQPFFQNI QLPVLADGLP DTSFFAPDCI HPNQKFHSQL ARALWTNMLE PLGSKTETLD LRAEMPITCP TQNEPFLRTP
      1050       1060       1070       1080       1090       1100       1110       1120
RNSNYTYPIK PAIENWGSDF LCTEWKASNS VPTSVHQLRP ADIKVVAALG DSLTTAVGAR PNNSSDLPTS WRGLSWSIGG
      1130       1140       1150       1160       1170       1180       1190       1200
DGNLETHTTL PNILKKFNPY LLGFSTSTWE GTAGLNVAAE GARARDMPAQ AWDLVERMKN SPDINLEKDW KLVTLFIGVN
      1210       1220       1230       1240       1250       1260       1270       1280
DLCHYCENPE AHLATEYVQH IQQALDILSE ELPRAFVNVV EVMELASLYQ GQGGKCAMLA AQNNCTCLRH SQSSLEKQEL
      1290       1300       1310       1320       1330       1340       1350       1360
KKVNWNLQHG ISSFSYWHQY TQREDFAVVV QPFFQNTLTP LNERGDTDLT FFSEDCFHFS DRGHAEMAIA LWNNMLEPVG
      1370       1380       1390       1400       1410       1420       1430       1440
RKTTSNNFTH SRAKLKCPSP ESPYLYTLRN SRLLPDQAEE APEVLYWAVP VAAGVGLVVG IIGTVVWRCR RGGRREDPPM
      1450
SLRTVAL
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
413	1	587.7939	24.16	2	34.5	11.6	1	375-384	R.EGAEIRCPDK.D	Carbamidomethyl: 7
2292	1	816.2731	-168.26	2	58.9	11.1	0	472-487	K.ETSPNAFLNQAVAGGR.A	

Detailed Protein Report

Protein 192:	**PREDICTED: transforming acidic coiled-coil-containing protein 2 isoform X20 [Homo sapiens]**		
Accession:	gi|578818751	**Score:**	34.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	296.6
Database Date:	2015-11-30	**pI:**	4.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.6
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MGNENSTSDN	QRTLSAQTPR	SAQPPGNSQN	IKRKQQDTPG	SPDHRDASSI	GSVGLGGFCT	ASESSASLDP	CLVSPEVTEP
90	100	110	120	130	140	150	160
RKDPQGARGP	EGSLLPSPPP	SQEREHPSSS	MPFAECPPEG	CLASPAAAPE	DGPQTQSPRR	EPAPNAPGDI	AAAFPAERDS
170	180	190	200	210	220	230	240
STPYQEIAAV	PSAGRERQPK	EEGQKSSFSF	SSGIDQSPGM	SPVPLREPMK	APLCGEGDQP	GGFESQEKEA	AGGFPPAESR
250	260	270	280	290	300	310	320
QGVASVQVTP	EAPAAAQQGT	ESSAVLEKSP	LKPMAPIPQD	PAPRASDRER	GQGEAPPQYL	TDDLEFLRAC	HLPRSNSGAA
330	340	350	360	370	380	390	400
PEAEVNAASQ	ESCQQPVGAY	LPHAELPWGL	PSPALVPEAG	GSGKEALDTI	DVQGHPQTGM	RGTKPNQVVC	VAAGGQPEGG
410	420	430	440	450	460	470	480
LPVSPEPSLL	TPTEEAHPAS	SLASFPAAQI	PIAVEEPGSS	SRESVSKAGM	PVSADAAKEV	VDAGLVGLER	QVSDLGSKGE
490	500	510	520	530	540	550	560
HPEGDPGEVP	APSPQERGEH	LNTEQSHEVQ	PGVPPPPLPK	EQSHEVQPGA	PPPPLPKAPS	ESARGPPGPT	DGAKVHEDST
570	580	590	600	610	620	630	640
SPAVAKEGSR	SPGDSPGGKE	EAPEPPDGGD	PGNLQGEDSQ	AFSSKRDPEV	GKDELSKPSS	DAESRDHPSS	HSAQPPRKGG
650	660	670	680	690	700	710	720
AGHTDGPHSQ	TAEADASGLP	HKLGEEDPVL	PPVPDGAGEP	TVPEGAIWEG	SGLQPKCPDT	LQSREGLGRM	ESFLTLESEK
730	740	750	760	770	780	790	800
SDFPPTPVAE	VAPKAQEGES	TLEIRKMGSC	DGEGLLTSPD	QPRGPACDAS	RQEFHAGVPH	PPQGENLAAD	LGLTALILDQ
810	820	830	840	850	860	870	880
DQQGIPSCPG	EGWIRGAASE	WPLLSSEKHL	QPSQAQPETS	IFDVLKEQAQ	PPENGKETSP	SHPGFKDQGA	DSSQIHVPVE
890	900	910	920	930	940	950	960
PQEDNNLPTH	GGQEQALGSE	LQSQLPKGTL	SDTPTSSPTD	MVWESSLTEE	SELSAPTRQK	LPALGEKRPE	GACGDGQSSR
970	980	990	1000	1010	1020	1030	1040
VSPPAADVLK	DFSLAGNFSR	KETCCTGQGP	NKSQQALADA	LEEGSQHEEA	CQRHPGASEA	ADGCSPLWGL	SKREMASGNT
1050	1060	1070	1080	1090	1100	1110	1120
GEAPPCQPDS	VALLDAVPCL	PALAPASPGV	TPTQDAPETE	ACDETQEGRQ	QPVPAPQQKM	ECWATSDAES	PKLLASFPSA
1130	1140	1150	1160	1170	1180	1190	1200
GEQGGEAGAA	ETGGSAGAGD	PGKQQAPEKP	GEATLSCGLL	QTEHCLTSGE	EASTSALRES	CQAEHPMASC	QDALLPAREL
1210	1220	1230	1240	1250	1260	1270	1280
GGIPRSTMDF	STHQAVPDPK	ELLLSGPPEV	AAPDTPYLHV	DSAAQRGAED	SGVKAVSSAD	PRAPGESPCP	VGEPPLALEN
1290	1300	1310	1320	1330	1340	1350	1360
AASLKLFAGS	LAPLLQPGAA	GGEIPAVQAS	SGSPKARTTE	GPVDSMPCLD	RMPLLAKGKQ	ATGEEKAATA	PGAGAKASGE
1370	1380	1390	1400	1410	1420	1430	1440
GMAGDAAGET	EGSMERMGEP	SQDPKQGTSG	GVDTSSEQIA	TLTGFPDFRE	HIAKIFEKPV	LGALATPGEK	AGAGRSAVGK
1450	1460	1470	1480	1490	1500	1510	1520
DLTRPLGPEK	LLDGPPGVDV	TLLPAPPARL	QVEKKQQLAG	EAEISHLALQ	DPASDKLLGP	AGLTWERNLP	GAGVGKEMAG
1530	1540	1550	1560	1570	1580	1590	1600
VPPTLREDER	PEGPGAAWPG	LEGQAYSQLE	RSRQELASGL	PSPAATQELP	VERAAAFQVA	PHSHGEEAVA	QDRIPSGKQH
1610	1620	1630	1640	1650	1660	1670	1680
QETSACDSPH	GEDGPGDFAH	TGVPGHVPRS	TCAPSPQREV	LTVPEANSEP	WTLDTLGGER	RPGVTAGILE	MRNALGNQST
1690	1700	1710	1720	1730	1740	1750	1760
PAPPTGEVAD	TPLEPGKVAG	AAGEAEGDIT	LSTAETQACA	SGDLPEAGTT	RTFSVVAGDL	VLPGSCQDPA	CSDKAPGMEG
1770	1780	1790	1800	1810	1820	1830	1840
TAALHGDSPA	RPQQAKEQPG	PERPIPAGDG	KVCVSSPPEP	DETHDPKLQH	LAPEELHTDR	ESPRPGPSML	PSVPKKDAPR
1850	1860	1870	1880	1890	1900	1910	1920
VMDKVTSDET	RGAEGTESSP	VADDIIQPAA	PADLESPTLA	ASSYHGDVVG	QVSTDLIAQR	SSDSEEAFET	PESTTPVKAP
1930	1940	1950	1960	1970	1980	1990	2000
PAPPPPPPEV	IPEPEVSTQP	PPEEPGCGSE	TVPVPDGPRS	DSVEGSPFRP	PSHSFSAVFD	EDKPIASSGT	YNLDFDNIEL
2010	2020	2030	2040	2050	2060	2070	2080
VDTFQTLEPR	ASDAKNQEGK	VNTRRKSTDS	VPISKSTLSR	SLSLQASDFD	GASSSGNPEA	VALAPDAYST	GSSSASSTLK
2090	2100	2110	2120	2130	2140	2150	2160
RTKKPRPPSL	KKKQTTKKPT	ETPPVKETQQ	EPDEESLVPS	GENLASETKT	ESAKTEGPSP	ALLEETPLEP	AVGPKAACPL
2170	2180	2190	2200	2210	2220	2230	2240
DSESAEGVVP	PASGGGRVQN	SPPVGRKTLP	LTTAPEAGEV	TPSDSGGQED	SPAKGLSVRL	EFDYSEDKSS	WDNQQENPPP
2250	2260	2270	2280	2290	2300	2310	2320
TKKIGKKPVA	KMPLRRPKMK	KTPEKLDNTP	ASPPRSPAEP	NDIPIAKGTY	TFDIDKWDDP	NFNPFSSTSK	MQESPKLPQQ
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
858	1	474.1144	-271.75	2	40.2	10.8	1	1338-1346	K.GKQATGEEK.A	
1463	1	1023.6735	127.47	2	48.1	13.1	2	2806-2822	K.NKEIEELTKICDELIAK.M	Carbamidomethyl: 11

Detailed Protein Report

Protein 193: PREDICTED: uncharacterized protein C1orf159 isoform X8 [Homo sapiens]

Accession:	gi|578799328	**Score:**	33.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	30.9
Database Date:	2015-11-30	**pI:**	11.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	8.9
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MSVVPILEGQ	PHSISLAPHA	PPCGRLCASA	PGMALRHLAL	LAGLLVGVAS	KSMENTAQLP	ECCVDVVGVN	ASCPGASLCG
90	100	110	120	130	140	150	160
PGCYRRWNAD	GSASCVRCGN	GTLPAYNGSE	CRSFAGPGAP	FPMNRSSGTP	GRPHPGAPRV	AASLFLGTFF	ISSGLILSVA
170	180	190	200	210	220	230	240
GFFYLKRSSK	LPRACYRRNK	APALQPGEAA	AMIPPPQSSG	PTLTSPVSDP	FQYGSRATSG	GSGPWTGPRI	PLPSRGRPVS
250	260	270	280	290	300	310	
AMSDLEAETT	PRTWRQGPGG	RPLGGNQHKV	LASPGARDSP	GHSLGSESLR	LPATDAKGSR	AA	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2311	2	682.9198	139.69	2	58.8	23.8	0	113-125	R.SFAGPGAPFPMNR.S	Oxidation: 11
2555	1	701.8644	-5.90	2	61.9	10.1	0	256-269	R.QGPGGRPLGGNQHK.V	

Detailed Protein Report

Protein 194:	**voltage-dependent P/Q-type calcium channel subunit alpha-1A isoform 4 [Homo sapiens]**		
Accession:	gi|187828892	**Score:**	33.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	282.4
Database Date:	2015-11-30	**pI:**	9.6
		Sequence Coverage [%]:	1.8
		No. of unique Peptides:	2

Detailed Protein Report

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

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
66	1	796.7909	-127.42	2	30.5	10.0	0	12-31	R.YGGGGSGAAAGVVVGSGGGR.G	
2706	1	741.8621	-28.64	2	64.1	11.6	2	2371-2384	R.VPGPARSESPRACR.H	

Detailed Protein Report

Protein 195: zinc finger protein 177 isoform b [Homo sapiens]

Accession:	gi|289547607	**Score:**	33.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	36.4
Database Date:	2015-11-30	**pI:**	9.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	8.1
		No. of unique Peptides:	2

Alias proteins:

Accession	Name	Description
gi|289547609	refseq_human(refseq_human_20140103.fasta)	zinc finger protein 177 isoform b [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MAAGWLTTWS QNSVTFQEVA VDFSQEEWAL LDPAQKNLYK DVMLENFRNL ASVGYQLCRH SLISKVDQEQ LKTDERGILQ
        90        100        110        120        130        140        150        160
GDCADWETQL KPKDTIAMQN IPGGKTSNGI NTNCVRTHSG EMPYECSDCG KAFIFQSSLK KHMRSHTGEK PYECDHCGKS
       170        180        190        200        210        220        230        240
FSQSSHLNVH KRTHTGEKPY DCKECGKAFT VPSSLQKHVR THTGEKPYEC SDCGKAFIDQ SSLKKHTRSH TGEKPYECNQ
       250        260        270        280        290        300        310        320
CGKSFSTGSY LIVHKRTHTG EKTYECKECG KAFRNSSCLR VHVRTHTGEK PYKCIQCEKA FSTSTNLIMH KRIHNGQKLH
       330
E
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2666	3	973.5093	-8.38	2	63.4	16.7	1	49-65	R.NLASVGYQLCRHSLISK.V	Carbamidomethyl: 10
1517	1	1008.6274	90.62	1	48.8	16.8	0	216-224	K.AFIDQSSLK.K	

Detailed Protein Report

Protein 196: **PREDICTED: ras-specific guanine nucleotide-releasing factor 2 isoform X1 [Homo sapiens]**

Accession:	gi|530379425	**Score:**	33.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	133.5
Database Date:	2015-11-30	**pI:**	8.3
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MQKSVRYNEG	HALYLAFLAR	KEGTKRGFLS	KKTAEASRWH	EKWFALYQNV	LFYFEGEQSC	RPAGMYLLEG	CSCERTPAPP
90	100	110	120	130	140	150	160
RAGAGQGGVR	DALDKQYYFT	VLFGHEGQKP	LELRCEEEQD	GKEWMEAIHQ	ASYADILIER	EVLMQKYIHL	VQIVETEKIA
170	180	190	200	210	220	230	240
ANQLRHQLED	QDTEIERLKS	EIIALNKTKE	RMRPYQSNQE	DEDPDIKKIK	KVQSFMRGWL	CRRKWKTIVQ	DYICSPHAES
250	260	270	280	290	300	310	320
MRKRNQIVFT	MVEAESEYVH	QLYILVNGFL	RPLRMAASSK	KPPISHDDVS	SIFLNSETIM	FLHEIFHQGL	KARIANWPTL
330	340	350	360	370	380	390	400
ILADLFDILL	PMLNIYQEFV	RNHQYSLQVL	ANCKQNRDFD	KLLKQYEANP	ACEGRMLETF	LTYPMFQIPR	YIITLHELLA
410	420	430	440	450	460	470	480
HTPHEHVERK	SLEFAKSKLE	ELSRVMHDEV	SDTENIRKNL	AIERMIVEGC	DILLDTSQTF	IRQGSLIQVP	SVERGKLSKV
490	500	510	520	530	540	550	560
RLGSLSLKKE	GERQCFLFTK	HFLICTRSSG	GKLHLLKTGG	VLSLIDCTLI	EEPDASDDDS	KGSGQVFGHL	DFKIVVEPPD
570	580	590	600	610	620	630	640
AAAFTVVLLA	PSRQEKAAWM	SDISQCVDNI	RCNGLMTIVF	EENSKVTVPH	MIKSDARLHK	DDTDICFSKT	LNSCKVPQIR
650	660	670	680	690	700	710	720
YASVERLLER	LTDLRFLSID	FLNTFLHTYR	IFTTAAVVLG	KLSDIYKRPF	TSIPVRSLEL	FFATSQNNRG	EHLVDGKSPR
730	740	750	760	770	780	790	800
LCRKFSSPPP	LAVSRTSSPV	RARKLSLTSP	LNSKIGALDL	TTSSSPTTTT	QSPAASPPPH	TGQIPLDLSR	GLSSPEQSPG
810	820	830	840	850	860	870	880
TVEENVDNPR	VDLCNKLKRS	IQKGFNNTER	TCDKEFIIRR	TATNRVLNVL	RHWVSKHAQD	FELNNELKMN	VLNLLEEVLR
890	900	910	920	930	940	950	960
DPDLLPQERK	AAANILRALS	QDDQDDIHLK	LEDIIQMTDC	MKAECFESLS	AMELAEQITL	LDHVIFRSIP	YEEFLGQGWM
970	980	990	1000	1010	1020	1030	1040
KLDKNERTPY	IMKTSQHFND	MSNLVASQIM	NYADVSSRAN	AIEKWVAVAD	ICRCLHNYNG	VLEITSALNR	SAIYRLKKTW
1050	1060	1070	1080	1090	1100	1110	1120
AKVSKQTKAL	MDKLQKTVSS	EGRFKNLRET	LKNCNPPAVP	YLGMYLTDLA	FIEEGTPNFT	EEGLVNFSKM	RMISHIIREI
1130	1140	1150	1160	1170			
RQFQQTSYRI	DHQPKVAQYL	LDKDLIIDED	TLYELSLKIE	PRLPA			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1027	1	984.1548	34.58	3	42.4	33.5	1	898-922	R.ALSQDDQDDIHLKLEDIIQMTDCMK.A	Oxidation: 20, 24

Detailed Protein Report

Protein 197: PREDICTED: probable E3 ubiquitin-protein ligase HERC1 isoform X6 [Homo sapiens]

Accession:	gi|530406610	**Score:**	33.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	524.9
Database Date:	2015-11-30	**pI:**	5.7
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	1.1
		No. of unique Peptides:	3

10	20	30	40	50	60	70	80
MATMIPPVKL	KWLEHLNSSW	ITEDSESIAT	REGVAVLYSK	LVSNKEVVPL	PQQVLCLKGP	QLPDFERESL	SSDEQDHYLD
90	100	110	120	130	140	150	160
ALLSSQLALA	KMVCSDSPFA	GALRKRLLVL	QRVFYALSNK	YHDKGKVKQQ	QHSPESSSGS	ADVHSVSERP	RSSTDALIEM
170	180	190	200	210	220	230	240
GVRTGLSLLF	ALLRQSWMMP	VSGPGLSLCN	DVIHTAIEVV	SSLPPLSLAN	ESKIPPMGLD	CLSQVTTFLK	GVTIPNSGAD
250	260	270	280	290	300	310	320
TLGRRLASEL	LLGLAAQRGS	LRYLLEWIEM	ALGASAVVHT	MEKGKLLSSQ	EGMISFDCFM	TILMQMRRSL	GSSADRSQWR
330	340	350	360	370	380	390	400
EPTRTSDGLC	SLYEAALCLF	EEIEAGQYCT	FVISTDGSVR	ACGKGSYGRL	GLGDSNNQST	LKKLTFEPHR	SIKKVSSSKG
410	420	430	440	450	460	470	480
SDGHTLAFTT	EGEVFSWGDG	DYGKLGHGNS	STQKYPKLIQ	GPLQGKVVVC	VSAGYRHSAA	VTEDGELYTW	GEGDFGRLGH
490	500	510	520	530	540	550	560
GDSNSRNIPT	LVKDISNVGE	VSCGSSHTIA	LSKDGRTVWS	FGGGDNGKLG	HGDTNRVYKP	KVIEALQGMF	IRKVCAGSQS
570	580	590	600	610	620	630	640
SLALTSTGQV	YAWGCGACLG	CGSSEATALR	PKLIEELAAT	RIVDVSIGDS	HCLALSHDNE	VYAWGNNSMG	QCGQGNSTGP
650	660	670	680	690	700	710	720
ITKPKKVSGL	DGIAIQQISA	GTSHSLAWTA	LPRDRQVVAW	HRPYCVDLEE	STFSHLRSFL	ERYCDKINSE	IPPLPFPSSR
730	740	750	760	770	780	790	800
EHHSFLKLCL	KLLSNHLALA	LAGGVATSIL	GRQAGPLRNL	LFRLMDSTVP	DEIQEVVIET	LSVGATMLLP	PLRERMELLH
810	820	830	840	850	860	870	880
SLLPQGPDRW	ESLSKGQRMQ	LDIILTSLQD	HTHVASLLGY	SSPSDAADLS	SVCTGYGNLS	DQPYGTQSCH	PDTHLAEILM
890	900	910	920	930	940	950	960
KTLLRNLGFY	TDQAFGELEK	NSDKFLLGTS	SSENSQPAHL	HELLCSLQKQ	LLAFCHINNI	SENSSSVALL	HKHLQLLLPH
970	980	990	1000	1010	1020	1030	1040
ATDIYSRSAN	LLKESPWNGS	VGEKLRDVIY	VSAAGSMLCQ	IVNSLLLLPV	SVARPLLSYL	LDLLPPLDCL	NRLLPAADLL
1050	1060	1070	1080	1090	1100	1110	1120
EDQELQWPLH	GGPELIDPAG	LPLPQPAQSW	VWLVDLERTI	ALLIGRCLGG	MLQGSPVSPE	EQDTAYWMKT	PLFSDGVEMD
1130	1140	1150	1160	1170	1180	1190	1200
TPQLDKCMSC	LLEVALSGNE	EQKPFDYKLR	PEIAVYVDLA	LGCSKEPARS	LWISMQDYAV	SKDWDSATLS	NESLLDTVSR
1210	1220	1230	1240	1250	1260	1270	1280
FVLAALLKHT	NLLSQACGES	RYQPGKHLSE	VYRCVYKVRS	RLLACKNLEL	IQTRSSSRDR	WISENQDSAD	VDPQEHSFTR
1290	1300	1310	1320	1330	1340	1350	1360
TIDEEAEMEE	QAERDREEGH	PEPEDEEEER	EHEVMTAGKI	FQCFLSAREV	ARSRDRDRMN	SGAGSGARAD	DPPPQSQQER
1370	1380	1390	1400	1410	1420	1430	1440
RVSTDLPEGQ	DVYTAACNSV	IHRCALLILG	VSPVIDELQK	RREEGQLQQP	STSASEGGGL	MTRSESLTAE	SRLVHTSPNY
1450	1460	1470	1480	1490	1500	1510	1520
RLIKSRSESD	LSQPESDEEG	YALSGRRNVD	LDLAASHRKR	GPMHSQLESL	SDSWARLKHS	RDWLCNSSYS	FESDFDLTKS
1530	1540	1550	1560	1570	1580	1590	1600
LGVHTLIENV	VSFVSGDVGN	APGFKEPEES	MSTSPQASII	AMEQQQLRAE	LRLEALHQIL	VLLSGMEEKG	SISLAGSRLS
1610	1620	1630	1640	1650	1660	1670	1680
SGFQSSTLLT	SVRLQFLAGC	FGLGTVGHTG	GKGESGRLHH	YQDGIRAAKR	NIQIEIQVAV	HKIYQQLSAT	LERALQANKH
1690	1700	1710	1720	1730	1740	1750	1760
HIEAQQRLLL	VTVFALSVHY	QPVDVSLAIS	TGLLNVLSQL	CGTDTMLGQP	LQLLPKTGVS	QLSTALKVAS	TRLLQILAIT
1770	1780	1790	1800	1810	1820	1830	1840
TGTYADKLSP	KVVQSLLDLL	CSQLKNLLSQ	TGVLHMASFG	EGEQEDGEEE	EKKVDSSGET	EKKDFRAALR	KQHAAELHLG
1850	1860	1870	1880	1890	1900	1910	1920
DFLVFLRRVV	SSKAIQSKMA	SPKWTEVLLN	IASQKCSSGI	PLVGNLRTRL	LALHVLEAVL	PACESGVEDD	QMAQIVERLF
1930	1940	1950	1960	1970	1980	1990	2000
SLLSDCMWET	PIAQAKHAIQ	IKEKEQEIKL	QKQGELEEED	ENLPIQEVSF	DPEKAQCCLV	ENGQILTHGS	GGKGYGLAST
2010	2020	2030	2040	2050	2060	2070	2080
GVTSGCYQWK	FYIVKENRGN	EGTCVGVSRW	PVHDFNHRTT	SDMWLYRAYS	GNLYHNGEQT	LTLSSFTQGD	FITCVLDMEA
2090	2100	2110	2120	2130	2140	2150	2160
RTISFGKNGE	EPKLAFEDVD	AAELYPCVMF	YSSNPGEKVK	ICDMQMRGTP	RDLLPGDPIC	SPVAAVLAEA	TIQLIRILHR
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1613	1	954.4635	-82.64	2	49.9	11.5	1	537-552	R.VYKPKVIEALQGMFIR.K	Oxidation: 13
1890	1	1023.4178	-75.16	2	53.5	10.4	1	1209-1226	K.HTNLLSQACGESRYQPGK.H	Carbamidomethyl: 9
2149	1	701.2767	-121.55	3	57.0	11.4	1	4282-4301	R.QISAGRCHSAAWTAPPVPPR.A	

BRUKER

Detailed Protein Report

Protein 198: mitochondrial intermediate peptidase [Homo sapiens]

Accession:	gi|156105687	**Score:**	33.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	80.6
Database Date:	2015-11-30	**pI:**	6.6
		Sequence Coverage [%]:	2.9
		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
2877	3	703.3682	28.70	2	66.7	15.9	0	675-686	R.EPMLMVEGMLQK.C	

Detailed Protein Report

Protein 199: histone acetyltransferase KAT6B isoform 1 [Homo sapiens]

Accession:	gi|100816397	**Score:**	33.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	231.2
Database Date:	2015-11-30	**pI:**	5.6
		Sequence Coverage [%]:	1.9
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|530393350	refseq_human (refseq_human_20140103.fasta)	PREDICTED: histone acetyltransferase KAT6B isoform X1 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MVKLANPLYT EWILEAIQKI KKQKQRPSEE RICHAVSTSH GLDKKTVSEQ LELSVQDGSV LKVTNKGLAS YKDPDNPGRF
        90        100        110        120        130        140        150        160
SSVKPGTFPK SAKGSRGSCN DLRNVDWNKL LRRAIEGLEE PNGSSLKNIE KYLRSQSDLT STTNNPAFQQ RLRLGAKRAV
       170        180        190        200        210        220        230        240
NNGRLLKDGP QYRVNYGSLD GKGAPQYPSA FPSSLPPVSL LPHEKDQPRA DPIPICSFCL GTKESNREKK PEELLSCADC
       250        260        270        280        290        300        310        320
GSSGHPSCLK FCPELTTNVK ALRWQCIECK TCSACRVQGR NADNMLFCDS CDRGFHMECC DPPLSRMPKG MWICQVCRPK
       330        340        350        360        370        380        390        400
KKGRKLLHEK AAQIKRRYAK PIGRPKNKLK QRLLSVTSDE GSMNAFTGRG SPGRGQKTKV CTTPSSGHAA SGKDSSSRLA
       410        420        430        440        450        460        470        480
VTDPTRPGAT TKITTTSTYI SASTLKVNKK TKGLIDGLTK FFTPSPDGRR SRGEIIDFSK HYRPRKKVSQ KQSCTSHVLA
       490        500        510        520        530        540        550        560
TGTTQKLKPP PSSLPPPTPI SGQSPSSQKS STATSSPSPQ SSSSQCSVPS LSSLTTNSQL KALFDGLSHI YTTQGQSRKK
       570        580        590        600        610        620        630        640
GHPSYAPPKR MRRKTELSST AKSKAHFFGK RDIRSRFISH SSSSSWGMAR GSIFKAIAHF KRTTFLKKHR MLGRLKYKVT
       650        660        670        680        690        700        710        720
PQMGTPSPGK GSLTDGRIKP DQDDDTEIKI NIKQESADVN VIGNKDVVTE EDLDVFKQAQ ELSWEKIECE SGVEDCGRYP
       730        740        750        760        770        780        790        800
SVIEFGKYEI QTWYSSPYPQ EYARLPKLYL CEFCLKYMKS KNILLRHSKK CGWFHPPANE IYRRKDLSVF EVDGNMSKIY
       810        820        830        840        850        860        870        880
CQNLCLLAKL FLDHKTLYYD VEPFLFYVLT KNDEKGCHLV GYFSKEKLCQ QKYNVSCIMI MPQHQRQGFG RFLIDFSYLL
       890        900        910        920        930        940        950        960
SRREGQAGSP EKPLSDLGRL SYLAYWKSVI LEYLYHHHER HISIKAISRA TGMCPHDIAT TLQHLHMIDK RDGRFVIIRR
       970        980        990       1000       1010       1020       1030       1040
EKLILSHMEK LKTCSRANEL DPDSLRWTPI LISNAAVSEE EREAEKEAER LMEQASCWEK EEQEILSTRA NSRQSPAKVQ
      1050       1060       1070       1080       1090       1100       1110       1120
SKNKYLHSPE SRPVTGERGQ LLELSKESSE EEEEEEDEEE EEEEEEEEED EEEEEEEEEE EEEENIQSSP PRLTKPQSVA
      1130       1140       1150       1160       1170       1180       1190       1200
IKRKRPFVLK KKRGRKRRRI NSSVTTETIS ETTEVLNEPF DNSDEERPMP QLEPTCEIEV EEDGRKPVLR KAFQHQPGKK
      1210       1220       1230       1240       1250       1260       1270       1280
RQTEEEEGKD NHCFKNADPC RNNMNDDSSN LKEGSKDNPE PLKCKQVWPK GTKRGLSKWR QNKERKTGFK LNLYTPPETP
      1290       1300       1310       1320       1330       1340       1350       1360
MEPDEQVTVE EQKETSEGKT SPSPIRIEEE VKETGEALLP QEENRREETC APVSPNTSPG EKPEDDLIKP EEEEEEEEEE
      1370       1380       1390       1400       1410       1420       1430       1440
EEEEEEEEGE EEEGGGNVEK DPDGAKSQEK EEPEISTEKE DSARLDDHEE EEEEDEEPSH NEDHDADDED DSHMESAEVE
      1450       1460       1470       1480       1490       1500       1510       1520
KEELPRESFK EVLENQETFL DLNVQPGHSN PEVLMDCGVD LTASCNSEPK ELAGDPEAVP ESDEEPPPGE QAQKQDQKNS
      1530       1540       1550       1560       1570       1580       1590       1600
KEVDTEFKEG NPATMEIDSE TVQAVQSLTQ ESSEQDDTFQ DCAETQEACR SLQNYTRADQ SPQIATTLDD CQQSDHSSPV
      1610       1620       1630       1640       1650       1660       1670       1680
SSVHSHPGQS VRSVNSPSVP ALENSYAQIS PDQSAISVPS LQNMETSPMM DVPSVSDHSQ QVVDSGFSDL GSIESTTENY
      1690       1700       1710       1720       1730       1740       1750       1760
ENPSSYDSTM GGSICGNGSS QNSCSYSNLT SSSLTQSSCA VTQQMSNISG SCSMLQQTSI SSPPTCSVKS PQGCVVERPP
      1770       1780       1790       1800       1810       1820       1830       1840
SSSQQLAQCS MAANFTPPMQ LAEIPETSNA NIGLYERMGQ SDFGAGHYPQ PSATFSLAKL QQLTNTLIDH SLPYSHSAAV
      1850       1860       1870       1880       1890       1900       1910       1920
TSYANSASLS TPLSNTGLVQ LSQSPHSVPG GPQAQATMTP PPNLTPPPMN LPPPLLQRNM AASNIGISHS QRLQTQIASK
      1930       1940       1950       1960       1970       1980       1990       2000
GHISMRTKSA SLSPAAATHQ SQIYGRSQTV AMQGPARTLT MQRGMNMSVN LMPAPAYNVN SVNMNMNTLN AMNGYSMSQP
      2010       2020       2030       2040       2050       2060       2070       2080
MMNSGYHSNH GYMNQTPQYP MQMQMGMMGT QPYAQQPMQT PPHGNMMYTA PGHHGYMNTG MSKQSLNGSY MRR
```

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
1354	1	684.3815	59.97	2	46.5	10.7	0	32-44	R.ICHAVSTSHGLDK.K	

Detailed Protein Report

Protein 200: **A disintegrin and metalloproteinase with thrombospondin motifs 19 preproprotein [Homo sapiens]**

Accession:	gi|112789555	**Score:**	33.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	134.0
Database Date:	2015-11-30	**pI:**	9.1
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.4
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MRLTHICCCC LLYQLGFLSN GIVSELQFAP DREEWEVVFP ALWRREPVDP AGGSGGSADP GWVRGVGGGG SARAQAAGSS
        90        100        110        120        130        140        150        160
REVRSVAPVP LEEPVEGRSE SRLRPPPPSE GEEDEELESQ ELPRGSSGAA ALSPGAPASW QPPPPPQPPP SPPPAQHAEP
       170        180        190        200        210        220        230        240
DGDEVLLRIP AFSRDLYLLL RRDGRFLAPR FAVEQRPNPG PGPTGAASAP QPPAPPDAGC FYTGAVLRHP GSLASFSTCG
       250        260        270        280        290        300        310        320
GGLMGFIQLN EDFIFIEPLN DTMAITGHPH RVYRQKRSME EKVTEKSALH SHYCGIISDK GRPRSRKIAE SGRGKRYSYK
       330        340        350        360        370        380        390        400
LPQEYNIETV VVADPAMVSY HGADAARRFI LTILNMVFNL FQHKSLSVQV NLRVIKLILL HETPPELYIG HHGEKMLESF
       410        420        430        440        450        460        470        480
CKWQHEEFGK KNDIHLEMST NWGEDMTSVD AAILITRKDF CVHKDEPCDT VGIAYLSGMC SEKRKCIIAE DNGLNLAFTI
       490        500        510        520        530        540        550        560
AHEMGHNMGI NHDNDHPSCA DGLHIMSGEW IKGQNLGDVS WSRCSKEDLE RFLRSKASNC LLQTNPQSVN SVMVPSKLPG
       570        580        590        600        610        620        630        640
MTYTADEQCQ ILFGPLASFC QEMQHVICTG LWCKVEGEKE CRTKLDPPMD GTDCDLGKWC KAGECTSRTS APEHLAGEWS
       650        660        670        680        690        700        710        720
LWSPCSRTCS AGISSRERKC PGLDSEARDC NGPRKQYRIC ENPPCPAGLP GFRDWQCQAY SVRTSSPKHI LQWQAVLDEE
       730        740        750        760        770        780        790        800
KPCALFCSPV GKEQPILLSE KVMDGTSCGY QGLDICANGR CQKVGCDGLL GSLAREDHCG VCNGNGKSCK IIKGDFNHTR
       810        820        830        840        850        860        870        880
GAGYVEVLVI PAGARRIKVV EEKPAHSYLA LRDAGKQSIN SDWKIEHSGA FNLAGTTVHY VRRGLWEKIS AKGPTTAPLH
       890        900        910        920        930        940        950        960
LLVLLFQDQN YGLHYEYTIP SDPLPENQSS KAPEPLFMWT HTSWEDCDAT CGGGERKTTV SCTKIMSKNI SIVDNEKCKY
       970        980        990       1000       1010       1020       1030       1040
LTKPEPQIRK CNEQPCQTRW MMTEWTPCSR TCGKGMQSRQ VACTQQLSNG TLIRARERDC IGPKPASAQR CEGQDCMTVW
      1050       1060       1070       1080       1090       1100       1110       1120
EAGVWSECSV KCGKGIRHRT VRCTNPRKKC VLSTRPREAE DCEDYSKCYV WRMGDWSKCS ITCGKGMQSR VIQCMHKITG
      1130       1140       1150       1160       1170       1180       1190       1200
RHGNECFSSE KPAAYRPCHL QPCNEKINVN TITSPRLAAL TFKCLGDQWP VYCRVIREKN LCQDMRWYQR CCETCRDFYA
      1210
QKLQQKS
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
109	1	1098.0910	-64.88	3	31.1	12.4	2	619-647	K.WCKAGECTSRTSAPEHLAGEWSLWSPCSR.T	Carbamidomethyl: 2

Protein 201: PREDICTED: serine/threonine-protein kinase 31 isoform X3 [Homo sapiens]

Accession:	gi|578813577	**Score:**	33.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	95.7
Database Date:	2015-11-30	**pI:**	4.8
		Sequence Coverage [%]:	3.1
		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
277	3	592.1990	-132.59	2	33.2	18.2	0	581-591	K.GYSVDVDTEAK.V	

Detailed Protein Report

Protein 202: spectrin beta chain, non-erythrocytic 5 [Homo sapiens]

Accession:	gi|485837026	**Score:**	33.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	416.5
Database Date:	2015-11-30	**pI:**	6.2
		Sequence Coverage [%]:	0.9
		No. of unique Peptides:	2

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
1932	1	724.3207	-73.16	2	54.2	11.4	1	962-973	R.QRYPGNSTQIQR.Q	
2799	2	665.3651	-30.72	2	65.4	11.8	0	3278-3291	R.LGQLHPAAPGGLAK.V	

Detailed Protein Report

Protein 203: serine/threonine-protein kinase 3 isoform 2 [Homo sapiens]

Accession:	gi|372622373	**Score:**	33.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	59.4
Database Date:	2015-11-30	**pI:**	5.0
		Sequence Coverage [%]:	5.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLQLMDSGIT	ICLRNGAASV	FKKKEWSTQG	EENKQDSKLK	KLSEDSLTKQ	PEEVFDVLEK	LGEGSYGSVF	KAIHKESGQV
90	100	110	120	130	140	150	160
VAIKQVPVES	DLQEIIKEIS	IMQQCDSPYV	VKYYGSYFKN	TDLWIVMEYC	GAGSVSDIIR	LRNKTLIEDE	IATILKSTLK
170	180	190	200	210	220	230	240
GLEYLHFMRK	IHRDIKAGNI	LLNTEGHAKL	ADFGVAGQLT	DTMAKRNTVI	GTPFWMAPEV	IQEIGYNCVA	DIWSLGITSI
250	260	270	280	290	300	310	320
EMAEGKPPYA	DIHPMRAIFM	IPTNPPPTFR	KPELWSDDFT	DFVKKCLVKN	PEQRATATQL	LQHPFIKNAK	PVSILRDLIT
330	340	350	360	370	380	390	400
EAMEIKAKRH	EEQQRELEEE	EENSDEDELD	SHTMVKTSVE	SVGTMRATST	MSEGAQTMIE	HNSTMLESDL	GTMVINSEDE
410	420	430	440	450	460	470	480
EEEDGTMKRN	ATSPQVQRPS	FMDYFDKQDF	KNKSHENCNQ	NMHEPFPMSK	NVFPDNWKVP	QDGDFDFLKN	LSLEELQMRL
490	500	510	520				
KALDPMMERE	IEELRQRYTA	KRQPILDAMD	AKKRRQQNF				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2001	2	731.8177	-100.79	2	55.1	18.2	0	2-14	M.LQLMDSGITICLR.N	

Detailed Protein Report

Protein 204: **PREDICTED: LIM and senescent cell antigen-like-containing domain protein 1 isoform X7 [Homo sapiens]**

Accession: gi|578804328
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 33.0
MW [kDa]: 39.4
pI: 9.8
Sequence Coverage [%]: 16.0
No. of unique Peptides: 2

10	20	30	40	50	60	70	80
MPSQSSNMAN	ALASATCERC	KGGFAPAEKI	VNSNGELYHE	QCFVCAQCFQ	QFPEGLFYEF	EGRKYCEHDF	QMLFAPCCHQ
90	100	110	120	130	140	150	160
CGEFIIGRVI	KAMNNSWHPE	CFRCDLCQEV	LADIGFVKNA	GRHLCRPCHN	REKARGLGKY	ICQKCHAIID	EQPLIFKNDP
170	180	190	200	210	220	230	240
YHPDHFNCAN	CGKELTADAR	ELKGELYCLP	CHDKMGVPIC	GACRRPIEGR	VVNAMGKQWH	VEHFVCAKCE	KPFLGHRHYE
250	260	270	280	290	300	310	320
RKGLAYCETH	YNQLFGDVCF	HCNRVIEGDV	VSALNKAWCV	NCFACSTCNT	KLTLKDKFVE	IDLKPVCKHC	YEKMPEEFKR
330	340	350					
RLAKREREAK	DKDKQKKKKP	VCL					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1893	1	573.2288	-144.49	2	53.7	11.3	1	174-183	K.ELTADARELK.G	
1542	1	978.1217	1.51	3	49.0	11.6	1	265-291	R.VIEGDVVSALNKAWCVNCFACSTCNTK.L	Carbamidomethyl: 21

Detailed Protein Report

Protein 205: rapamycin-insensitive companion of mTOR isoform 3 [Homo sapiens]

Accession:	gi|550544215	**Score:**	33.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	155.8
Database Date:	2015-11-30	**pI:**	6.8
		Sequence Coverage [%]:	1.9
		No. of unique Peptides:	2

Quantitation

MD:MU **Median:** 1.85 **CV:** 0.00 % **No. of Peptides:** 1

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	Ratios
2600	6	741.8765	-155.82	2	62.5	20.5	1	516-528	K.GLLLLLRFLSIPK.G		
275	1	795.2750	-158.71	2	33.1	12.4	1	916-929	R.ERLVVESSTSSHMK.I		MD:MU 1.85

Detailed Protein Report

Protein 206: PREDICTED: NEDD8 ultimate buster 1 isoform X3 [Homo sapiens]

Accession:	gi|530387034	**Score:**	32.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	67.7
Database Date:	2015-11-30	**pI:**	5.7
		Sequence Coverage [%]:	5.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MKTNGGRCRI	RALCWSRREW	RGAGMAQKKY	LQAKLTQFLR	EDRIQLWKPP	YTDENKKVGL	ALKDLAKQYS	DRLECCENEV
90	100	110	120	130	140	150	160
EKVIEEIRCK	AIERGTGNDN	YRTTGIATIE	VFLPPRLKKD	RKNLLETRLH	ITGRELRSKI	AETFGLQENY	IKIVINKKQL
170	180	190	200	210	220	230	240
QLGKTLEEQG	VAHNVKAMVL	ELKQSEEDAR	KNFQLEEEEQ	NEAKLKEKQI	QRTKRGLEIL	AKRAAETVVD	PEMTPYLDIA
250	260	270	280	290	300	310	320
NQTGRSIRIP	PSERKALMLA	MGYHEKGRAF	LKRKEYGIAL	PCLLDADKYF	CECCRELLDT	VDNYAVLQLD	IVWCYFRLEQ
330	340	350	360	370	380	390	400
LECLDDAEKK	LNLAQKCFKN	CYGENHQRLV	HIKGNCGKEK	VLFLRLYLLQ	GIRNYHSGND	VEAYEYLNKA	RQLFKELYID
410	420	430	440	450	460	470	480
PSKVDNLLQL	GFTAQEARLG	LRACDGNVDH	AATHITNRRE	ILLSNPQMWW	LNDSNPETDN	RQESPSQENI	DRLVYMGFDA
490	500	510	520	530	540	550	560
LVAEAALRVF	RGNVQLAAQT	LAHNGGSLPP	ELPLSPEDSL	SPPATSPSDS	AGTSSASTDE	DMETEAVNEI	LEDIPEHEED
570	580	590	600				
YLDSTLEDEE	IIIAEYLSYV	ENRKSATKKN					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2129	1	596.7885	-98.31	2	56.5	10.5	2	330-339	K.KLNLAQKCFK.N	

Detailed Protein Report

Protein 207: **E3 ubiquitin-protein ligase RNF213 isoform 3 [Homo sapiens]**

Accession:	gi|366039979	**Score:**	32.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	591.0
Database Date:	2015-11-30	**pI:**	6.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	0.5
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MECPSCQHVS	KEETPKFCSQ	CGERLPPAAP	IADSENNNST	MASASEGEME	CGQELKEEGG	PCLFPGSDSW	QENPEEPCSK
90	100	110	120	130	140	150	160
ASWTVQESKK	KKRKKKKKGN	KSASSELASL	PLSPASPCHL	TLLSNPWPQD	TALPHSQAQQ	SGPTGQPSQP	PGTATTPLEG
170	180	190	200	210	220	230	240
DGLSAPTEVG	DSPLQAQALG	EAGVATGSEA	QSSPQFQDHT	EGEDQDASIP	SGGRGLSQEG	TGPPTSAGEG	HSRTEDAAQE
250	260	270	280	290	300	310	320
LLLPESKGGS	SEPGTELQTT	EQQAGASASM	AVDAVAEPAN	AVKGAGKEMK	EKTQRMKQPP	ATTPPFKTHC	QEAETKTKDE
330	340	350	360	370	380	390	400
MAAAEEKVGK	NEQGEPEDLK	KPEGKNRSAA	AVKNEKEQKN	QEADVQEVKA	STLSPGGGVT	VFFHAIISLH	FPFNPDLHKV
410	420	430	440	450	460	470	480
FIRGGEEFGE	SKWDSNICEL	HYTRDLGHDR	VLVEGIVCIS	KKHLDKYIPY	KYVIYNGESF	EYEFIYKHQQ	KKGEYVNRCL
490	500	510	520	530	540	550	560
FIKSSLLGSG	DWHQYYDIVY	MKPHGRLQKV	MNHITDGPRK	DLVKGKQIAA	ALMLDSTFSI	LQTWDTINLN	SFFTQFEQFC
570	580	590	600	610	620	630	640
FVLQQPMIYE	GQAQLWTDLQ	YREKEVKRYL	WQHLKKHVVP	LPDGKSTDFL	PVDCPVRSKL	KTGLIVLFVV	EKIELLLEGS
650	660	670	680	690	700	710	720
LDWLCHLLTS	DASSPDEFHR	DLSHILGIPQ	SWRLYLVNLC	QRCMDTRTYT	WLGALPVLHC	CMELAPRHKD	AWRQPEDTWA
730	740	750	760	770	780	790	800
ALEGLSFSPF	REQMLDTSSL	LQFMREKQHL	LSIDEPLFRS	WFSLLPLSHL	VMYMENFIEH	LGRFPAHILD	CLSGIYYRLP
810	820	830	840	850	860	870	880
GLEQVLNTQD	VQDVQNVQNI	LEMLLRLLDT	YRDKIPEEAL	SPSYLTVCLK	LHEAICSSTK	LLKFYELPAL	SAEIVCRMIR
890	900	910	920	930	940	950	960
LLSLVDSAGQ	RDETGNNSVQ	TVFQGTLAAT	KRWLREVFTK	NMLTSSGASF	TYVKEIEVWR	RLVEIQFPAE	HGWKESLLGD
970	980	990	1000	1010	1020	1030	1040
MEWRLTKEEP	LSQITAYCNS	CWDTKGLEDS	VAKTFEKCII	EAVSSACQSQ	TSILQGFSYS	DLRKFGIVLS	AVITKSWPRT
1050	1060	1070	1080	1090	1100	1110	1120
ADNFNDILKH	LLTLADVKHV	FRLCGTDEKI	LANVTEDAKR	LIAVADSVLT	KVVGDLLSGT	ILVGQLELII	KHKNQFLDIW
1130	1140	1150	1160	1170	1180	1190	1200
QLREKSLSPQ	DEQCAVEEAL	DWRREELLLL	KKEKRCVDSL	LKMCGNVKHL	IQVDFGVLAV	RHSQDLSSKR	LNDTVTVRLS
1210	1220	1230	1240	1250	1260	1270	1280
TSSNSQRATH	YHLSSQVQEM	AGKIDLLRDS	HIFQLFWREA	AEPLSEPKED	QEAAELLSEP	EEESERHILE	LEEVYDYLYQ
1290	1300	1310	1320	1330	1340	1350	1360
PSYRKFIKLH	QDLKSGEVTL	AEIDVIFKDF	VNKYTDLDSE	LKIMCTVDHQ	DQRDWIKDRV	EQIKEYHHLH	QAVHAAKVIL
1370	1380	1390	1400	1410	1420	1430	1440
QVKESLGLNG	DFSVLNTLLN	FTDNFDDFRR	ETLDQINQEL	IQAKKLLQDI	SEARCKGLQA	LSLRKEFICW	VREALGGINE
1450	1460	1470	1480	1490	1500	1510	1520
LKVFVDLASI	SAGENDIDVD	RVACFHDAVQ	GYASLLFKLD	PSVDFSAFMK	HLKKLWKALD	KDQYLPRKLC	DSARNLEWLK
1530	1540	1550	1560	1570	1580	1590	1600
TVNESHGSVE	RSSLTLATAI	NQRGIYVIQA	PKGGQKISPD	TVLHLILPES	PGSHEESREY	SLEEVKELLN	KLMLMSGKKD
1610	1620	1630	1640	1650	1660	1670	1680
RNNTEVERFS	EVFCSVQRLS	QAFIDLHSAG	NMLFRTWIAM	AYCSPKQGVS	LQMDFGLDLV	TELKEGGDVT	ELLAALCRQM
1690	1700	1710	1720	1730	1740	1750	1760
EHFLDSWKRF	VTQKRMEHFY	LNFYTAEQLV	YLSTELRKQP	PSDAALTMLS	FIKSNCTLRD	VLRASVGCGS	EAARYRMRRV
1770	1780	1790	1800	1810	1820	1830	1840
MEELPLMLLS	EFSLVDKLRI	IMEQSMRCLP	AFLPDCLDLE	TLGHCLAHLA	GMGGSPVERC	LPRGLQVGQP	NLVVCGHSEV
1850	1860	1870	1880	1890	1900	1910	1920
LPAALAVYMQ	TPSQPLPTYD	EVLLCTPATT	FEEVALLLRR	CLTLGSLGHK	VYSLLFADQL	SYEVARQAEE	LFHNLCTQQH
1930	1940	1950	1960	1970	1980	1990	2000
REDYQLVMVC	DGDWEHCYLP	SAFSQHKVFV	TPQAPLEAIQ	AYLAGHYRVP	KQTLSAAAVF	NDRLCVGIVA	SERAGVGKSL
2010	2020	2030	2040	2050	2060	2070	2080
YVKRLHDKMK	MQLNVKNVPL	KTIRLIDPQV	DESRVLGALL	PFLDAQYQKV	PVLFHLDVTS	SVQTGIWVFL	FKLLILQYLM
2090	2100	2110	2120	2130	2140	2150	2160
DINGKMWLRN	PCHLYIVEIL	ERRTSVPSRS	SSALRTRVPQ	FSFLDIFPKV	TCRPPKEVID	MELSALRSDT	EPGMDLWEFC
2170	2180	2190	2200	2210	2220	2230	2240

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1737	1	863.0655	110.54	2	51.5	19.4	1	746-759	R.EKQHLLSIDEPLFR.S	
2481	1	856.9085	-24.89	2	61.4	13.6	1	4661-4674	R.LLNFDTELSTKEMR.N	Oxidation: 13

Detailed Protein Report

Protein 208: PREDICTED: agrin isoform X5 [Homo sapiens]

Accession:	gi|578799096	**Score:**	32.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	200.0
Database Date:	2015-11-30	**pI:**	6.0
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	3.5
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MAGRSHPGPL	RPLLPLLVVA	ACVLPGAGGT	CPERALERRE	EEANVVLTGT	VEEILNVDPV	QHTYSCKVRV	WRYLKGKDLV
90	100	110	120	130	140	150	160
ARESLLDGGN	KVVISGFGDP	LICDNQVSTG	DTRIFFVNPA	PPYLWPAHKN	ELMLNSSLMR	ITLRNLEEVE	FCVEDKPGTH
170	180	190	200	210	220	230	240
FTPVPPTPPD	ACRGMLCGFG	AVCEPNAEGP	GRASCVCKKS	PCPSVVAPVC	GSDASTYSNE	CELQRAQCSQ	QRRIRLLSRG
250	260	270	280	290	300	310	320
PCGSRDPCSN	VTCSFGSTCA	RSADGLTASC	LCPATCRGAP	EGTVCGSDGA	DYPGECQLLR	RACARQENVF	KKFDGPCDPC
330	340	350	360	370	380	390	400
QGALPDPSRS	CRVNPRTRRP	EMLLRPESCP	ARQAPVCGDD	GVTYENDCVM	GRSGAARGLL	LQKVRSGQCQ	GRDQCPEPCR
410	420	430	440	450	460	470	480
FNAVCLSRRG	RPRCSCDRVT	CDGAYRPVCA	QDGRTYDSDC	WRQQAECRQQ	RAIPSKHQGP	CDQAPSPCLG	VQCAFGATCA
490	500	510	520	530	540	550	560
VKNGQAACEC	LQACSSLYDP	VCGSDGVTYG	SACELEATAC	TLGREIQVAR	KGPCDRCGQC	RFGALCEAET	GRCVCPSECV
570	580	590	600	610	620	630	640
ALAQPVCGSD	GHTYPSECML	HVHACTHQIS	LHVASAGPCE	TCGDAVCAFG	AVCSAGQCVC	PRCEHPPPGP	VCGSDGVTYG
650	660	670	680	690	700	710	720
SACELREAAC	LQQTQIEEAR	AGPCEQAECG	SGGSGSGEDG	DCEQELCRQR	GGIWDEDSED	GPCVCDFSCQ	SVPGSPVCGS
730	740	750	760	770	780	790	800
DGVTYSTECE	LKKARCESQR	GLYVAAQGAC	RGPTFAPLPP	VAPLHCAQTP	YGCCQDNITA	ARGVGLAGCP	SACQCNPHGS
810	820	830	840	850	860	870	880
YGGTCDPATG	QCSCRPGVGG	LRCDRCEPGF	WNFRGIVTDG	RSGCTPCSCD	PQGAVRDDCE	QMTGLCSCKP	GVAGPKCGQC
890	900	910	920	930	940	950	960
PDGRALGPAG	CEADASAPAT	CAEMRCEFGA	RCVEESGSAH	CVCPMLTCPE	ANATKVCGSD	GVTYGNECQL	KTIACRQGLQ
970	980	990	1000	1010	1020	1030	1040
ISIQSLGPCQ	EAVAPSTHPT	SASVTVTTPG	LLLSQALPAP	PGALPLAPSS	TAHSQTTPPP	SSRPRTTASV	PRTTVWPVLT
1050	1060	1070	1080	1090	1100	1110	1120
VPPTAPSPAP	SLVASAFGES	GSTDGSSDEE	LSGDQEASGG	GSGGLEPLEG	SSVATPGPPV	ERASCYNSAL	GCCSDGKTPS
1130	1140	1150	1160	1170	1180	1190	1200
LDAEGSNCPA	TKVFQGVLEL	EGVEGQELFY	TPEMADPKSE	LFGETARSIE	STLDDLFRNS	DVKKDFRSVR	LRDLGPGKSV
1210	1220	1230	1240	1250	1260	1270	1280
RAIVDVHFDP	TTAFRAPDVA	RALLRQIQVS	RRRSLGVRRP	LQEHVRFMDF	DWFPAFITGA	TSGAIAAGAT	ARATTASRLP
1290	1300	1310	1320	1330	1340	1350	1360
SSAVTPRAPH	PSHTSQPVAK	TTAAPTTRRP	PTTAPSRVPG	RRPPAPQQPP	KPCDSQPCFH	GGTCQDWALG	GGFTCSCPAG
1370	1380	1390	1400	1410	1420	1430	1440
RGGAVCEKVL	GAPVPAFEGR	SFLAFPTLRA	YHTLRLALEF	RALEPQGLLL	YNGNARGKDF	LALALLDGRV	QLRFDTGSGP
1450	1460	1470	1480	1490	1500	1510	1520
AVLTSAVPVE	PGQWHRLELS	RHWRRGTLSV	DGETPVLGES	PSGTDGLNLD	TDLFVGGVPE	DQAAVALERT	FVGAGLRGCI
1530	1540	1550	1560	1570	1580	1590	1600
RLLDVNNQRL	ELGIGPGAAT	RGSGVGECGD	HPCLPNPCHG	GAPCQNLEAG	RFHCQCPPGR	VGPTCADEKS	PCQPNPCHGA
1610	1620	1630	1640	1650	1660	1670	1680
APCRVLPEGG	AQCECPLGRE	GTFCQTASGQ	DGSGPFLADF	NGFSHLELRG	LHTFARDLGE	KMALEVVFLA	RGPSGLLLYN
1690	1700	1710	1720	1730	1740	1750	1760
GQKTDGKGDF	VSLALRDRRL	EFRYDLGKGA	AVIRSREPVT	LGAWTRVSLE	RNGRKGALRV	GDGPRVLGES	PKSRKVPHTV
1770	1780	1790	1800	1810	1820	1830	1840
LNLKEPLYVG	GAPDFSKLAR	AAAVSSGFDG	AIQLVSLGGR	QLLTPEHVLR	QVDVTSFAGH	PCTRASGHPC	LNGASCVPRE
1850	1860	1870	1880	1890	1900	1910	
AAYVCLCPGG	FSGPHCEKGL	VEKSAGDVDT	LAFDGRTFVE	YLNAVTESEL	ANEIPVPETL	DSGALHR	

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1808	1	774.2788	-97.08	2	52.4	10.1	0	1118-1132	K.TPSLDAEGSNCPATK.V	Carbamidomethyl: 11
2489	1	981.1592	15.45	3	61.0	10.5	0	1133-1158	K.VFQGVLELEGVEGQELFYTPEMADPK.S	Oxidation: 22

Detailed Protein Report

Protein 209: endonuclease 8-like 3 [Homo sapiens]

Accession:	gi|157388969	**Score:**	32.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	67.8
Database Date:	2015-11-30	**pI:**	10.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	5.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MVEGPGCTLN	GEKIRARVLP	GQAVTGVRGS	ALRSLQGRAL	RLAASTVVVS	PQAAALNNDS	SQNVLSLFNG	YVYSGVETLG
90	100	110	120	130	140	150	160
KELFMYFGPK	ALRIHFGMKG	FIMINPLEYK	YKNGASPVLE	VQLTKDLICF	FDSSVELRNS	MESQQRIRMM	KELDVCSPEF
170	180	190	200	210	220	230	240
SFLRAESEVK	KQKGRMLGDV	LMDQNVLPGV	GNIIKNEALF	DSGLHPAVKV	CQLTDEQIHH	LMKMIRDFSI	LFYRCRKAGL
250	260	270	280	290	300	310	320
ALSKHYKVYK	RPNCGQCHCR	ITVCRFGDNN	RMTYFCPHCQ	KENPQHVDIC	KLPTRNTIIS	WTSSRVDHVM	DSVARKSEEH
330	340	350	360	370	380	390	400
WTCVVCTLIN	KPSSKACDAC	LTSRPIDSVL	KSEENSTVFS	HLMKYPCNTF	GKPHTEVKIN	RKTAFGTTTL	VLTDFSNKSS
410	420	430	440	450	460	470	480
TLERKTKQNQ	ILDEEFQNSP	PASVCLNDIQ	HPSKKTTNDI	TQPSSKVNIS	PTISSESKLF	SPAHKKPKTA	QYSSPELKSC
490	500	510	520	530	540	550	560
NPGYSNSELQ	INMTDGPRTL	NPDSPRCSKH	NRLCILRVVR	KDGENKGRQF	YACPLPREAQ	CGFFEWADLS	FPFCNHGKRS
570	580	590	600	610			
TMKTVLKIGP	NNGKNFFVCP	LGKEKQCNFF	QWAENGPGIK	IIPGC			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1708	1	735.0267	-63.51	3	51.1	14.2	2	564-583	K.TVLKIGPNNGKNFFVCPLGK.E	Carbamidomethyl: 16

Detailed Protein Report

Protein 210: **PREDICTED: latent-transforming growth factor beta-binding protein 1 isoform X5 [Homo sapiens]**

Accession: gi|530367595
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl, Oxidation

Score: 32.8
MW [kDa]: 134.0
pI: 9.1
Sequence Coverage [%]: 2.8
No. of unique Peptides: 1

```
        10         20         30         40         50         60         70         80
MAGAWLRWGL LLWAGLLASS AHGRLRRITY VVHPGPGLAA GALPLSGPPR SRTFNVALNA RYSRSSAAAG APSRASPGVP
        90        100        110        120        130        140        150        160
SERTRRTSKP GGAALQGLRP PPPPPPEPAR PAVPGGQLHP NPGGHPAAAP FTKQGRQVVR SKVPQETQSG GGSRLQVHQK
       170        180        190        200        210        220        230        240
QQLQGVNVCG GRCCHGWSKA PGSQRCTKPS CVPPCQNGGM CLRPQLCVCK PGTKGKACET IAAQDTSSPV FGGQSPGAAS
       250        260        270        280        290        300        310        320
SWGPPEQAAK HTSSKKADTL PRVSPVAQMT LTLKPKPSVG LPQQIHSQVT PLSSQSVVIH HGQTQEYVLK PKYFPAQKGI
       330        340        350        360        370        380        390        400
SGEQSTEGSF PLRYVQDQVA APFQLSNHTG RIKVVFTPSI CKVTCTKGSC QNSCEKGNTT TLISENGHAA DTLTATNFRV
       410        420        430        440        450        460        470        480
VICHLPCMNG GQCSSRDKCQ CPPNFTGKLC QIPVHGASVP KLYQHSQQPG KALGTHVIHS THTLPLTVTS QQGVKVKFPP
       490        500        510        520        530        540        550        560
NIVNIHVKHP PEASVQIHQV SRIDGPTGQK TKEAQPGQSQ VSYQGLPVQK TQTIHSTYSH QQVIPHVYPV AAKTQLGRCF
       570        580        590        600        610        620        630        640
QETIGSQCGK ALPGLSKQED CCGTVGTSWG FNKCQKCPKK PSYHGYNQMM ECLPGYKRVN NTFCQDINEC QLQGVCPNGE
       650        660        670        680        690        700        710        720
CLNTMGSYRC TCKIGFGPDP TFSSCVPDPP VISEEKGPCY RLVSSGRQCM HPLSVHLTKQ LCCCSVGKAW GPHCEKCPLP
       730        740        750        760        770        780        790        800
GTAAFKEICP GGMGYTVSGV HRRRPIHHHV GKGPVFVKPK NTQPVAKSTH PPPLPAKEEP VEALTFSREH GPGVAEPEVA
       810        820        830        840        850        860        870        880
TAPPEKEIPS LDQEKTKLEP GQPQLSPGIS TIHLHPQFPV VIEKTSPPVP VEVAPEASTS SASQVIAPTQ VTEINECTVN
       890        900        910        920        930        940        950        960
PDICGAGHCI NLPVRYTCIC YEGYRFSEQQ RKCVDIDECT QVQHLCSQGR CENTEGSFLC ICPAGFMASE EGTNCIDVDE
       970        980        990       1000       1010       1020       1030       1040
CLRPDVCGEG HCVNTVGAFR CEYCDSGYRM TQRGRCEDID ECLNPSTCPD EQCVNSPGSY QCVPCTEGFR GWNGQCLDVD
      1050       1060       1070       1080       1090       1100       1110       1120
ECLEPNVCAN GDCSNLEGSY MCSCHKGYTR TPDHKHCRDI DECQQGNLCV NGQCKNTEGS FRCTCGQGYQ LSAAKDQCED
      1130       1140       1150       1160       1170       1180       1190       1200
IDECQHRHLC AHGQCRNTEG SFQCVCDQGY RASGLGDHCE DINECLEDKS VCQRGDCINT AGSYDCTCPD GFQLDDNKTC
      1210       1220       1230       1240       1250
QDINECEHPG LCGPQGECLN TEGSFHCVCQ QGFSISADGR TCEDVNE
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
65	1	1240.0095	73.75	3	30.2	22.4	1	180-214	K.APGSQRCTKPSCVPPCQNGGMCLRPQLCVCKPGTK.G	Carbamidomethyl: 7; Oxidation: 21

Detailed Protein Report

Protein 211: putative ribosomal RNA methyltransferase NOP2 isoform 4 [Homo sapiens]

Accession:	gi|385198063	**Score:**	32.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	69.6
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
MGRKLDPTKE	KRGPGRKARK	QKGAETELVR	FLPAVSDENS	KRLSSRARKR	AAKRRLGSVE	APKTNKSPEA	KPLPGKLPKG
90	100	110	120	130	140	150	160
AVQTAGKKGP	QSLFNAPRGK	KRPAPGSDEE	EEEEDSEEDG	MVNHGDLWGS	EDDADTVDDY	GADSNSEDEE	EGEALLPIER
170	180	190	200	210	220	230	240
AARKQKAREA	AAGIQWSEEE	TEDEEEEKEV	TPESGPPKVE	EADGGLQINV	DEEPFVLPPA	GEMEQDAQAP	DLQRVHKRIQ
250	260	270	280	290	300	310	320
DIVGILRDFG	AQREEGRSRS	EYLNRLKKDL	AIYYSYGDFL	LGKLMDLFPL	SELVEFLEAN	EVPRPVTLRT	NTLKTRRRDL
330	340	350	360	370	380	390	400
AQALINRGVN	LDPLGKWSKT	GLVVYDSSVP	IGATPEYLAG	HYMLQGASSM	LPVMALAPQE	HERILDMCCA	PGGKTSYMAQ
410	420	430	440	450	460	470	480
LMKNTGVILA	NDANAERLKS	VVGNLHRLGV	TNTIISHYDG	RQFPKVVGGF	DRVLLDAPCS	GTGVISKDPA	VKTNKDEKDI
490	500	510	520	530	540	550	560
LRCAHLQKEL	LLSAIDSVNA	TSKTGGYLVY	CTCSITVEEN	EWVVDYALKK	RNVRLVPTGL	DFGQEGFTRF	RERRFHPSLR
570	580	590	600	610	620	630	
STRRFYPHTH	NMDGFFIAKF	KKFSNSIPQS	QTDGVLLCRS	GWTAVVQSQL	IATSTFQVQA	ILVPQTPK	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2674	1	933.1060	151.43	2	64.6	13.8	0	583-599	K.FSNSIPQSQTDGVLLCR.S	

Protein 212: BPI fold-containing family B member 6 precursor [Homo sapiens]

Accession:	gi|28372525	**Score:**	32.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	49.7
Database Date:	2015-11-30	**pI:**	9.6
		Sequence Coverage [%]:	9.9
		No. of unique Peptides:	2

```
        10         20         30         40         50         60         70         80
MLRILCLALC SLLTGTRADP GALLRLGMDI MNQVQSAMDE SHILEKMAAE AGKKQPGMKP IKGITNLKVK DVQLPVITLN
        90        100        110        120        130        140        150        160
FVPGVGIFQC VSTGMTVTGK SFMGGNMEII VALNITATNR LLRDEETGLP VFKSEGCEVI LVNVKTNLPS NMLPKMVNKF
       170        180        190        200        210        220        230        240
LDSTLHKVLP GLMCPAIDAV LVYVNRKWTN LSDPMPVGQM GTVKYVLMSA PATTASYIQL DFSPVVQQQK GKTIKLADAG
       250        260        270        280        290        300        310        320
EALTFPEGYA KGSSQLLLPA TFLSAELALL QKSFHVNIQD TMIGELPPQT TKTLARFIPE VAVAYPKSKP LTTQIKIKKP
       330        340        350        360        370        380        390        400
PKVTMKTGKS LLHLHSTLEM FAARWRSKAP MSLFLLEVHF NLKVQYSVHE NQLQMATSLD RLLSLSRKSS SIGNFNEREL
       410        420        430        440        450        460
TGFITSYLEE AYIPVVNDVL QVGLPLPDFL AMNYNLAELD IVENALMLDL KLG
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1223	1	873.6526	163.19	2	45.0	15.9	1	2-17	M.LRILCLALCSLLTGTR.A	
1632	1	1061.4621	-60.44	3	50.1	16.5	1	18-46	R.ADPGALLRLGMDIMNQVQSAMDESHILEK.M	

Detailed Protein Report

Protein 213: **PREDICTED: serine/threonine-protein kinase B-raf isoform X2 [Homo sapiens]**

Accession:	gi|530387108	**Score:**	32.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	83.9
Database Date:	2015-11-30	**pI:**	7.9
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.1
		No. of unique Peptides:	2

Quantitation

MD:MU **Median:** 1.36 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MAALSGGGGG GAEPGQALFN GDMEPEAGAG AGAAASSAAD PAIPEEVWNI KQMIKLTQEH IEALLDKFGG EHNPPSIYLE

        90        100        110        120        130        140        150        160
AYEEYTSKLD ALQQREQQLL ESLGNGTDFS VSSSASMDTV TSSSSSSLSV LPSSLSVFQN PTDVARSNPK SPQKPIVRVF

       170        180        190        200        210        220        230        240
LPNKQRTVVP ARCGVTVRDS LKKALMMRGL IPECCAVYRI QDGEKKPIGW DTDISWLTGE ELHVEVLENV PLTTHNFVRK

       250        260        270        280        290        300        310        320
TFFTLAFCDF CRKLLFQGFR CQTCGYKFHQ RCSTEVPLMC VNYDQLDLLF VSKFFEHHPI PQEEASLAET ALTSGSSPSA

       330        340        350        360        370        380        390        400
PASDSIGPQI LTSPSPSKSI PIPQPFRPAD EDHRNQFGQR DRSSSAPNVH INTIEPVNID DLIRDQGFRG DGGSTTGLSA

       410        420        430        440        450        460        470        480
TPPASLPGSL TNVKALQKSP GPQRERKSSS SSEDRNRMKT LGRRDSSDDW EIPDGQITVG QRIGSGSFGT VYKGKWHGDV

       490        500        510        520        530        540        550        560
AVKMLNVTAP TPQQLQAFKN EVGVLRKTRH VNILLFMGYS TKPQLAIVTQ WCEGSSLYHH LHIIETKFEM IKLIDIARQT

       570        580        590        600        610        620        630        640
AQGMDYLHAK SIIHRDLKSN NIFLHEDLTV KIGDFGLATV KSRWSGSHQF EQLSGSILWM APEVIRMQDK NPYSFQSDVY

       650        660        670        680        690        700        710        720
AFGIVLYELM TGQLPYSNIN NRDQIIFMVG RGYLSPDLSK VRSNCPKAMK RLMAECLKKK RDERPLFPQE NLQPSSSHHH

       730        740        750        760
GSICSYFLSL VFVQFVNIKT QFCSSNLFLK IQNFCQCIS
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
116	1	929.4622	17.68	2	30.9	16.0	1	184-199	K.ALMMRGLIPECCAVYR.I	Oxidation: 3, 4	MD:MU 1.36
2507	1	913.4337	-18.76	2	61.8	16.4	1	184-199	K.ALMMRGLIPECCAVYR.I		

Detailed Protein Report

Protein 214: PREDICTED: angiopoietin-1 receptor isoform X3 [Homo sapiens]

Accession: gi|530390111
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 32.3
MW [kDa]: 120.9
pI: 6.5
Sequence Coverage [%]: 2.4
No. of unique Peptides: 2

10	20	30	40	50	60	70	80
MDSLASLVLC	GVSLLLSGTV	EGAMDLILIN	SLPLVSDAET	SLTCIASGWR	PHEPITIGRD	FEALMNQHQD	PLEVTQDVTR
90	100	110	120	130	140	150	160
EWAKKVVWKR	EKASKINGAY	FCEGRVRGEA	IRIRTMKMRQ	QASFLPATLT	MTVDKGDNVN	ISFKKVLIKE	EDAVIYKNGS
170	180	190	200	210	220	230	240
FIHSVPRHEV	PDILEVHLPH	AQPQDAGVYS	ARYIGGNLFT	SAFTRLIVRR	CEAQKWGPEC	NHLCTACMNN	GVCHEDTGEC
250	260	270	280	290	300	310	320
ICPPGFMGRT	CEKACELHTF	GRTCKERCSG	QEGCKSYVFC	LPDPYGCSCA	TGWKGLQCNE	GIQRMTPKIV	DLPDHIEVNS
330	340	350	360	370	380	390	400
GKFNPICKAS	GWPLPTNEEM	TLVKPDGTVL	HPKDFNHTDH	FSVAIFTIHR	ILPPDSGVWV	CSVNTVAGMV	EKPFNISVKV
410	420	430	440	450	460	470	480
LPKPLNAPNV	IDTGHNFAVI	NISSEPYFGD	GPIKSKKLLY	KPVNHYEAWQ	HIQVTNEIVT	LNYLEPRTEY	ELCVQLVRRG
490	500	510	520	530	540	550	560
EGGEGHPGPV	RRFTTASIGL	PPPRGLNLLP	KSQTTLNLTW	QPIFPSSEDD	FYVEVERRSV	QKSDQQNIKV	PGNLTSVLLN
570	580	590	600	610	620	630	640
NLHPREQYVV	RARVNTKAQG	EWSEDLTAWT	LSDILPPQPE	NIKISNITHS	SAVISWTILD	GYSISSITIR	YKVQGKNEDQ
650	660	670	680	690	700	710	720
HVDVKIKNAT	ITQYQLKGLE	PETAYQVDIF	AENNIGSSNP	AFSHELVTLP	ESQAPADLGG	GKMLLIAILG	SAGMTCLTVL
730	740	750	760	770	780	790	800
LAFLIILQLK	RANVQRRMAQ	AFQNREEPAV	QFNSGTLALN	RKVKNNPDPT	IYPVLDWNDI	KFQDVIGEGN	FGQVLKARIK
810	820	830	840	850	860	870	880
KDGLRMDAAI	KRMKEYASKD	DHRDFAGELE	VLCKLGHHPN	IINLLGACEH	RGYLYLAIEY	APHGNLLDFL	RKSRVLETDP
890	900	910	920	930	940	950	960
AFAIANSTAS	TLSSQQLLHF	AADVARGMDY	LSQKQFIHRD	LAARNILVGE	NYVAKIADFG	LSRGQEVYVK	KTMGRLPVRW
970	980	990	1000	1010	1020	1030	1040
MAIESLNYSV	YTTNSDVWSY	GVLLWEIVSL	GGTPYCGMTC	AELYEKLPQG	YRLEKPLNCD	DEVYDLMRQC	WREKPYERPS
1050	1060	1070	1080	1090			
FAQILVSLNR	MLEERKTYVN	TTLYEKFTYA	GIDCSAEEAA				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
710	1	676.9374	132.70	2	38.2	12.4	0	468-478	R.TEYELCVQLVR.R	
2675	1	841.3883	-72.13	2	63.6	20.0	1	936-950	K.IADFGLSRGQEVYVK.K	

Detailed Protein Report

Protein 215: stAR-related lipid transfer protein 8 isoform a [Homo sapiens]

Accession:	gi|215820650	**Score:**	32.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	121.7
Database Date:	2015-11-30	**pI:**	5.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.4
		No. of unique Peptides:	2

Quantitation

MD:MU **Median:** 0.67 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MPLLDVFWSC FRKVKCFPLL QVKKNAEAEA KRACEWLQAT GFPQYVQLFE EGSFPLDIGS VKKNHGFLDE DSLGALCRRL
        90        100        110        120        130        140        150        160
MTLNNCASMK LEVHFQSKQN EDSEEEEQCT ISSHWAFQQE SKCWSPMGSS DLLAPPSPGL PATSSCESVL TELSATSLPV
       170        180        190        200        210        220        230        240
ITVSLPPEPA DLPLPGRAPS SSDRPLLSPT QGQEGPQDKA KKRHRNRSFL KHLESLRRKE KSGSQQAEPK HSPATSEKVS
       250        260        270        280        290        300        310        320
KASSFRSCRG FLSAGFYRAK NWAATSAGGS GANTRKAWEA WPVASFRHPQ WTHRGDCLVH VPGDHKPGTF PRSLSIESLC
       330        340        350        360        370        380        390        400
PEDGHRLADW QPGRRWGCEG RRGSCGSTGS HASTYDNLPE LYPAEPVMVG AEAEDEDDEE SGGSYAHLDD ILQHVWGLQQ
       410        420        430        440        450        460        470        480
RVELWSRAMY PDLGPGDEEE EEATSSVEIA TVEVKCQAEA LSQMEVPAHG ESPAWAQAEV QPAVLAPAQA PAEAEPVAQE
       490        500        510        520        530        540        550        560
EAEAPAPAPA PAPAQDSEQE AHSGGEPTFA SSLSVEEGHS ISDTVASSSE LDSSGNSMNE AEAAGPLAGL QASMPRERRD
       570        580        590        600        610        620        630        640
SGVGASLTRP CRKLRWHSFQ NSHRPSLNSE SLEINRQFAG QINLLHKGSL LRLTAFMEKY TVPHKQGWVW SMPKFMRRNK
       650        660        670        680        690        700        710        720
TPDYRGQHVF GVPPLIHVQR TGQPLPQSIQ QAMRYLRSQC LDQVGIFRKS GVKSRIQNLR QMNETSPDNV CYEGQSAYDV
       730        740        750        760        770        780        790        800
ADLLKQYFRD LPEPIFTSKL TTTFLQIYQL LPKDQWLAAA QAATLLLPDE NREVLQTLLY FLSDIASAEE NQMTAGNLAV
       810        820        830        840        850        860        870        880
CLAPSIFHLN VSKKDSPSPR IKSKRSLIGR PGPRDLSDNM AATQGLSHMI SDCKKLFQVP QDMVLQLCSS YSAAELSPPG
       890        900        910        920        930        940        950        960
PALAELRQAQ AAGVSLSLYM EENIQDLLRD AAERFKGWMS VPGPQHTELA CRKAPDGHPL RLWKASTEVA APPAVVLHRV
       970        980        990       1000       1010       1020       1030       1040
LRERALWDED LLRAQVLEAL MPGVELYHYV TDSMAPHPCR DFVVLRMWRS DLPRGGCLLV SQSLDPEQPV PESGVRALML
      1050       1060       1070       1080       1090       1100       1110
TSQYLMEPCG LGRSRLTHIC RADLRGRSPD WYNKVFGHLC AMEVAKIRDS FPTLQAAGPE TKL
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1731	1	916.4065	-38.11	2	51.4	19.9	1	63-78	K.KNHGFLDEDSLGALCR.R	Carbamidomethyl: 15	MD:MU 0.67
1810	1	641.7727	-44.44	2	52.6	12.4	0	80-90	R.LMTLNNCASMK.L	Carbamidomethyl: 7	

Detailed Protein Report

Protein 216: **PREDICTED: tenomodulin isoform X1 [Homo sapiens]**

Accession:	gi|530422140	**Score:**	32.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	30.0
Database Date:	2015-11-30	**pI:**	4.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	11.4
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MEHTFYSNGE	KKKIYMEIDP	VTRTEIFRSG	NGTDETLEVH	DFKNGYTGIY	FVGLQKCFIK	TQIKVIPEFS	EPEEEIDENE
90	100	110	120	130	140	150	160
EITTTFFEQS	VIWVPAEKPI	ENRDFLKNSK	ILEICDNVTM	YWINPTLISV	SELQDFEEEG	EDLHFPANEK	KGIEQNEQWV
170	180	190	200	210	220	230	240
VPQVKVEKTR	HARQASEEEL	PINDYTENGI	EFDPMLDERG	YCCIYCRRGN	RYCRRVCEPL	LGYYPYPYCY	QGGRVICRVI
250	260						
MPCNWWVARM	LGRV						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1182	1	679.6416	-214.99	2	44.4	15.1	0	1-11	-.MEHTFYSNGEK.K	Oxidation: 1
72	1	1069.4912	-86.67	2	30.6	17.2	2	151-168	K.KGIEQNEQWVVPQVKVEK.T	

Detailed Protein Report

Protein 217: PHD and RING finger domain-containing protein 1 isoform 4 [Homo sapiens]

Accession:	gi|557440810	**Score:**	32.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	178.1
Database Date:	2015-11-30	**pI:**	10.1
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.3
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MDDDSLDELV	ARSPGPDGHP	QVGPADPAES	SVGSSGDSGD	DSDSEHGDGT	DGEDEGASEE	EDLEDRSGSE	DSEDDGETLL
90	100	110	120	130	140	150	160
EVAGTQGKLE	AAGSFNSDDD	AESCPICLNA	FRDQAVGTPE	NCAHYFCLDC	IVEWSKNANS	CPVDRTLFKC	ICIRAQFGGK
170	180	190	200	210	220	230	240
ILRKIPVENT	KASEEEEDPT	FCEVCGRSDR	EDRLLLCDGC	DAGYHMECLD	PPLQEVPVDE	WFCPECAAPG	VVLAADAGPV
250	260	270	280	290	300	310	320
SEEEVSLLLA	DVVPTTSRLR	PRAGRTRAIA	RTRQSERVRA	TVNRNRISTA	RRVQHTPGRL	GSSLLDEAIE	AVATGLSTAV
330	340	350	360	370	380	390	400
YQRPLTPRTP	ARRKRKTRRR	KKVPGRKKTP	SGPSAKSKSS	ATRSKKRQHR	VKKRRGKKVK	SEATTRSRIA	RTLGLRRPVH
410	420	430	440	450	460	470	480
SSCIPSVLKP	VEPSLGLLRA	DIGAASLSLF	GDPYELDPFD	SSEELSANPL	SPLSAKRRAL	SRSALQSHQP	VARPVSVGLS
490	500	510	520	530	540	550	560
RRRLPAAVPE	PDLEEEPVPD	LLGSILSGQS	LLMLGSSDVI	IHRDGSLSAK	RAAPVSFQRN	SGSLSRGEEG	FKGCLQPRAL
570	580	590	600	610	620	630	640
PSGSPAQGPS	GNRPQSTGLS	CQGRSRTPAR	TAGAPVRLDL	PAAPGAVQAR	NLSNGSVPGF	RQSHSPWFNG	TNKHTLPLAS
650	660	670	680	690	700	710	720
AASKISSRDS	KPPCRSVVPG	PPLKPAPRRT	DISELPRIPK	IRRDDGGGRR	DAAPAHGQSI	EIPSACISRL	TGREGTGQPG
730	740	750	760	770	780	790	800
RGTRAESEAS	SRVPREPGVH	TGSSRPPAPS	SHGSLAPLGP	SRGKGVGSTF	ESFRINIPGN	MAHSSQLSSP	GFCNTFRPVD
810	820	830	840	850	860	870	880
DKEQRKENPS	PLFSIKKTKQ	LRSEVYDPSD	PTGSDSSAPG	SSPERSGPGL	LPSEITRTIS	INSPKAQTVQ	AVRCVTSYTV
890	900	910	920	930	940	950	960
ESIFGTEPEP	PLGPSSAMSK	LRGAVAAEGA	SDTEREEPTE	SQGLAARLRR	PSPPEPWDEE	DGASCSTFFG	SEERTVTCVT
970	980	990	1000	1010	1020	1030	1040
VVEPEAPPSP	DVLQAATHRV	VELRPPSRSR	STSSSRSRKK	AKRKRVSREH	GRTRSGTRSE	SRDRSSRSAS	PSVGEERPRR
1050	1060	1070	1080	1090	1100	1110	1120
QRSKAKSRRS	SSDRSSSRER	AKRKKAKDKS	REHRRGPWGH	SRRTSRSRSG	SPGSSSYEHY	ESRKKKKRRS	ASRPRGRECS
1130	1140	1150	1160	1170	1180	1190	1200
PTSSLERLCR	HKHQRERSHE	RPDRKESVAW	PRDRRKRRSR	SPSSEHRARE	HRRPRSREKW	PQTRSHSPER	KGAVREASPA
1210	1220	1230	1240	1250	1260	1270	1280
PLAQGEPGRE	DLPTRLPALG	EAHVSPEVAT	ADKAPLQAPP	VLEVAAECEP	DDLDLDYGDS	VEAGHVFDDF	SSDAVFIQLD
1290	1300	1310	1320	1330	1340	1350	1360
DMSSPPSPES	TDSSPERDFP	LKPALPPASL	AVAAIQREVS	LMHDEDPSQP	PPLPEGTQEP	HLLRPDAAEK	AEAPSSPDVA
1370	1380	1390	1400	1410	1420	1430	1440
PAGKEDSPSA	SGRVQEAARP	EEVVSQTPLL	RSRALVKRVT	WNLQESESSA	PAEDRAPRAP	LHRPQKPREG	AWDMEDVAPT
1450	1460	1470	1480	1490	1500	1510	1520
GVRQVFSELP	FPSHVLPEPG	FPDTDPSQVY	SPGLPPAPAQ	PSSIPPCALV	SQPTVQFILQ	GSLPLVGCGA	AQTLAPVPAA
1530	1540	1550	1560	1570	1580	1590	1600
LTPASEPASQ	ATAASNSEEK	TPAPRLAAEK	TKKEEYMKKL	HMQERAVEEV	KLAIKPFYQK	REVTKEEYKD	ILRKAVQKIC
1610	1620	1630	1640	1650			
HSKSGEINPV	KVANLVKAYV	DKYRHMRRHK	KPEAGEEPPT	QGAEG			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1686	1	697.6744	-192.66	2	51.0	20.4	0	1-12	-.MDDDSLDELVAR.S	Oxidation: 1
1064	1	500.6481	-289.29	2	42.9	11.8	2	347-356	R.KKTPSGPSAK.S	

Detailed Protein Report

Protein 218: keratin, type II cuticular Hb4 [Homo sapiens]

Accession: gi|15431316

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Modification(s): Carbamidomethyl, Oxidation

Score: 32.2

MW [kDa]: 64.8

pI: 9.0

Sequence Coverage [%]: 4.0

No. of unique Peptides: 1

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
603	1	652.6252	-207.98	2	36.9	13.1	0	79-91	R.FGAGCGMGFGDGR.G	Carbamidomethyl: 5; Oxidation: 7

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Detailed Protein Report

Protein 219: fibulin-1 isoform D precursor [Homo sapiens]

Accession:	gi|34734066	**Score:**	32.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	77.2
Database Date:	2015-11-30	**pI:**	5.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MERAAPSRRV	PLPLLLLGGL	ALLAAGVDAD	VLLEACCADG	HRMATHQKDC	SLPYATESKE	CRMVQEQCCH	SQLEELHCAT
90	100	110	120	130	140	150	160
GISLANEQDR	CATPHGDNAS	LEATFVKRCC	HCCLLGRAAQ	AQGQSCEYSL	MVGYQCGQVF	RACCVKSQET	GDLDVGGLQE
170	180	190	200	210	220	230	240
TDKIIEVEEE	QEDPYLNDRC	RGGGPCKQQC	RDTGDEVVCS	CFVGYQLLSD	GVSCEDVNEC	ITGSHSCRLG	ESCINTVGSF
250	260	270	280	290	300	310	320
RCQRDSSCGT	GYELTEDNSC	KDIDECESGI	HNCLPDFICQ	NTLGSFRCRP	KLQCKSGFIQ	DALGNCIDIN	ECLSISAPCP
330	340	350	360	370	380	390	400
IGHTCINTEG	SYTCQKNVPN	CGRGYHLNEE	GTRCVDVDEC	APPAEPCGKG	HRCVNSPGSF	RCECKTGYYF	DGISRMCVDV
410	420	430	440	450	460	470	480
NECQRYPGRL	CGHKCENTLG	SYLCSCSVGF	RLSVDGRSCE	DINECSSSPC	SQECANVYGS	YQCYCRRGYQ	LSDVDGVTCE
490	500	510	520	530	540	550	560
DIDECALPTG	GHICSYRCIN	IPGSFQCSCP	SSGYRLAPNG	RNCQDIDECV	TGIHNCSINE	TCFNIQGGFR	CLAFECPENY
570	580	590	600	610	620	630	640
RRSAATLQQE	KTDTVRCIKS	CRPNDVTCVF	DPVHTISHTV	ISLPTFREFT	RPEEIIFLRA	ITPPHPASQA	NIIFDITEGN
650	660	670	680	690	700	710	
LRDSFDIIKR	YMDGMTVGVV	RQVRPIVGPF	HAVLKLEMNY	VVGGVVSHRN	VVNVHIFVSE	YWF	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2101	2	788.3311	-88.71	2	56.1	18.9	0	676-689	K.LEMNYVVGGVVSHR.N	Oxidation: 3

Detailed Protein Report

Protein 220: E3 ubiquitin-protein ligase RNF213 isoform 2 [Homo sapiens]

Accession:	gi|66529203	**Score:**	32.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	118.4
Database Date:	2015-11-30	**pI:**	5.4
		Sequence Coverage [%]:	3.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MECPSCQHVS	KEETPKFCSQ	CGERLPPAAP	IADSENNNST	MASASEGEME	CGQELKEEGG	PCLFPGSDSW	QENPEEPCSK
90	100	110	120	130	140	150	160
ASWTVQESKK	KKRKKKKKGN	KSASSELASL	PLSPASPCHL	TLLSNPWPQD	TALPHSQAQQ	SGPTGQPSQP	PGTATTPLEG
170	180	190	200	210	220	230	240
DGLSAPTEVG	DSPLQAQALG	EAGVATGSEA	QSSPQFQDHT	EGEDQDASIP	SGGRGLSQEG	TGPPTSAGEG	HSRTEDAAQE
250	260	270	280	290	300	310	320
LLLPESKGGS	SEPGTELQTT	EQQAGASASM	AVDAVAEPAN	AVKGAGKEMK	EKTQRMKQPP	ATTPPFKTHC	QEAETKTKDE
330	340	350	360	370	380	390	400
MAAAEEKVGK	NEQGEPEDLK	KPEGKNRSAA	AVKNEKEQKN	QEADVQEVKA	STLSPGGGVT	VFFHAIISLH	FPFNPDLHKV
410	420	430	440	450	460	470	480
FIRGGEEFGE	SKWDSNICEL	HYTRDLGHDR	VLVEGIVCIS	KKHLDKYIPY	KYVIYNGESF	EYEFIYKHQQ	KKGEYVNRCL
490	500	510	520	530	540	550	560
FIKSSLLGSG	DWHQYYDIVY	MKPHGRLQKV	MNHITDGPRK	DLVKGKQIAA	ALMLDSTFSI	LQTWDTINLN	SFFTQFEQFC
570	580	590	600	610	620	630	640
FVLQQPMIYE	GQAQLWTDLQ	YREKEVKRYL	WQHLKKHVVP	LPDGKSTDFL	PVDCPVRSKL	KTGLIVLFVV	EKIELLLEGS
650	660	670	680	690	700	710	720
LDWLCHLLTS	DASSPDEFHR	DLSHILGIPQ	SWRLYLVNLC	QRCMDTRTYT	WLGALPVLHC	CMELAPRHKD	AWRQPEDTWA
730	740	750	760	770	780	790	800
ALEGLSFSPF	REQMLDTSSL	LQFMREKQHL	LSIDEPLFRS	WFSLLPLSHL	VMYMENFIEH	LGRFPAHILD	CLSGIYYRLP
810	820	830	840	850	860	870	880
GLEQVLNTQD	VQDVQNVQNI	LEMLLRLLDT	YRDKIPEEAL	SPSYLTVCLK	LHEAICSSTK	LLKFYELPAL	SAEIVCRMIR
890	900	910	920	930	940	950	960
LLSLVDSAGQ	RDETGNNSVQ	TVFQGTLAAT	KRWLREVFTK	NMLTSSGASF	TYVKEIEVWR	RLVEIQFPAE	HGWKESLLGD
970	980	990	1000	1010	1020	1030	1040
MEWRLTKEEP	LSQITAYCNS	CWDTKGLEDS	VAKTFEKCII	EAVSSACQVN	NLSSWETDSG	SQLCSAMTQL	RAMKHPLGLS
1050	1060	1070					
SSANSEIGKW	APSSLAKGNG	AEI					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2673	1	913.9847	10.52	2	63.5	12.7	1	1032-1049	R.AMKHPLGLSSSANSEIGK.W	

Detailed Protein Report

Protein 221: **PREDICTED: histone-lysine N-methyltransferase ASH1L isoform X3 [Homo sapiens]**

Accession:	gi|530365072	**Score:**	32.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	191.3
Database Date:	2015-11-30	**pI:**	10.4
		Sequence Coverage [%]:	1.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDPRNTAMLG	LGSDSEGFSR	KSPSAISTGT	LVSKREVELE	KNTKEEEDLR	KRNRERNIEA	GKDDGLTDAQ	QQFSVKETNF
90	100	110	120	130	140	150	160
SEGNLKLKIG	LQAKRTKKPP	KNLENYVCRP	AIKTTIKHPR	KALKSGKMTD	EKNEHCPSKR	DPSKLYKKAD	DVAAIECQSE
170	180	190	200	210	220	230	240
EVIRLHSQGE	NNPLSKKLSP	VHSEMADYIN	ATPSTLLGSR	DPDLKDRALL	NGGTSVTEKL	AQLIATCPPS	KSSKTKPKKL
250	260	270	280	290	300	310	320
GTGTTAGLVS	KDLIRKAGVG	SVAGIIHKDL	IKKPTISTAV	GLVTKDPGKK	PVFNAAVGLV	NKDSVKKLGT	GTTAVFINKN
330	340	350	360	370	380	390	400
LGKKPGTITT	VGLLSKDSGK	KLGIGIVPGL	VHKESGKKLG	LGTVVGLVNK	DLGKKLGSTV	GLVAKDCAKK	IVASSAMGLV
410	420	430	440	450	460	470	480
NKDIGKKLMS	CPLAGLISKD	AINLKAEALL	PTQEPLKASC	STNINNQESQ	ELSESLKDSA	TSKTFEKNVV	RQNKESILEK
490	500	510	520	530	540	550	560
FSVRKEIINL	EKEMFNEGTC	IQQDSFSSSE	KGSYETSKHE	KQPPVYCTSP	DFKMGGASDV	STAKSPFSAV	GESNLPSPSP
570	580	590	600	610	620	630	640
TVSVNPLTRS	PPETSSQLAP	NPLLLSSTTE	LIEEISESVG	KNQFTSESTH	LNVGHRSVGH	SISIECKGID	KEVNDSKTTH
650	660	670	680	690	700	710	720
IDIPRISSSL	GKKPSLTSES	SIHTITPSVV	NFTSLFSNKP	FLKLGAVSAS	DKHCQVAESL	STSLQSKPLK	KRKGRKPRWT
730	740	750	760	770	780	790	800
KVVARSTCRS	PKGLELERSE	LFKNVSCSSL	SNSNSEPAKF	MKNIGPPSFV	DHDFLKRRLP	KLSKSTAPSL	ALLADSEKPS
810	820	830	840	850	860	870	880
HKSFATHKLS	SSMCVSSDLL	SDIYKPKRGR	PKSKEMPQLE	GPPKRTLKIP	ASKVFSLQSK	EEQEPPILQP	EIEIPSFKQG
890	900	910	920	930	940	950	960
LSVSPFPKKR	GRPKRQMRSP	VKMKPPVLSV	APFVATESPS	KLESESDNHR	SSSDFFESED	QLQDPDDLDD	SHRPSVCSMS
970	980	990	1000	1010	1020	1030	1040
DLEMEPDKKI	TKRNNGQLMK	TIIRKINKMK	TLKRKKLLNQ	ILSSSVESSN	KGKVQSKLHN	TVSSLAATFG	SKLGQQINVS
1050	1060	1070	1080	1090	1100	1110	1120
KKGTIYIGKR	RGRKPKTVLN	GILSGSPTSL	AVLEQTAQQA	AGSALGQILP	PLLPSSASSS	EILPSPICSQ	SSGTSGGQSP
1130	1140	1150	1160	1170	1180	1190	1200
VSSDAGFVEP	SSVPYLHLHS	RQGSMIQTLA	MKKASKGRRR	LSPPTLLPNS	PSHLSELTSL	KEATPSPISE	SHSDETIPSD
1210	1220	1230	1240	1250	1260	1270	1280
SGIGTDNNST	SDRAEKFCGQ	KKRRHSFEHV	SLIPPETSTV	LSSLKEKHKH	KCKRRNHDYL	SYDKMKRQKR	KRKKKYPQLR
1290	1300	1310	1320	1330	1340	1350	1360
NRQDPDFIAE	LEELISRLSE	IRITHRSHHF	IPRDLLPTIF	RINFNSFYTH	PSFPLDPLHY	IRKPDLKKKR	GRPPKMREAM
1370	1380	1390	1400	1410	1420	1430	1440
AEMPFMHSLS	FPLSSTGFYP	SYGMPYSPSP	LTAAPIGLGY	YGRYPPTLYP	PPPSPSFTTP	LPPPSYMHAG	HLLLNPAKYH
1450	1460	1470	1480	1490	1500	1510	1520
KKKHKLLRQE	AFLTTSRTPL	LSMSTYPSVP	PEMAYGWMVE	HKHRHRHKHR	EHRSSEQPQV	SMDTGSSRSV	LESLKRYRFG
1530	1540	1550	1560	1570	1580	1590	1600
KDAVGERYKH	KEKHRCHMSC	PHLSPSKSLI	NREEQWVHRE	PSESSPLALG	LQTPLQIDCS	ESSPSLSLGG	FTPNSEPASS
1610	1620	1630	1640	1650	1660	1670	1680
DEHTNLFTSA	IGSCRVSNPN	SSGRKKLTDS	PGLFSAQDTS	LNRLHRKESL	PSNERAVQTL	AGSQPTSDKP	SQRPSESTNC
1690	1700	1710	1720	1730	1740	1750	
SPTRKRSSSE	STSSTDKTED	WYEYLEVTYI	LMIIETMRIN	MFPVGNKRSS	LSKSKISCFW	G	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2429	1	856.6272	147.06	2	60.7	15.4	1	273-289	K.KPTISTAVGLVTKDPGK.K	

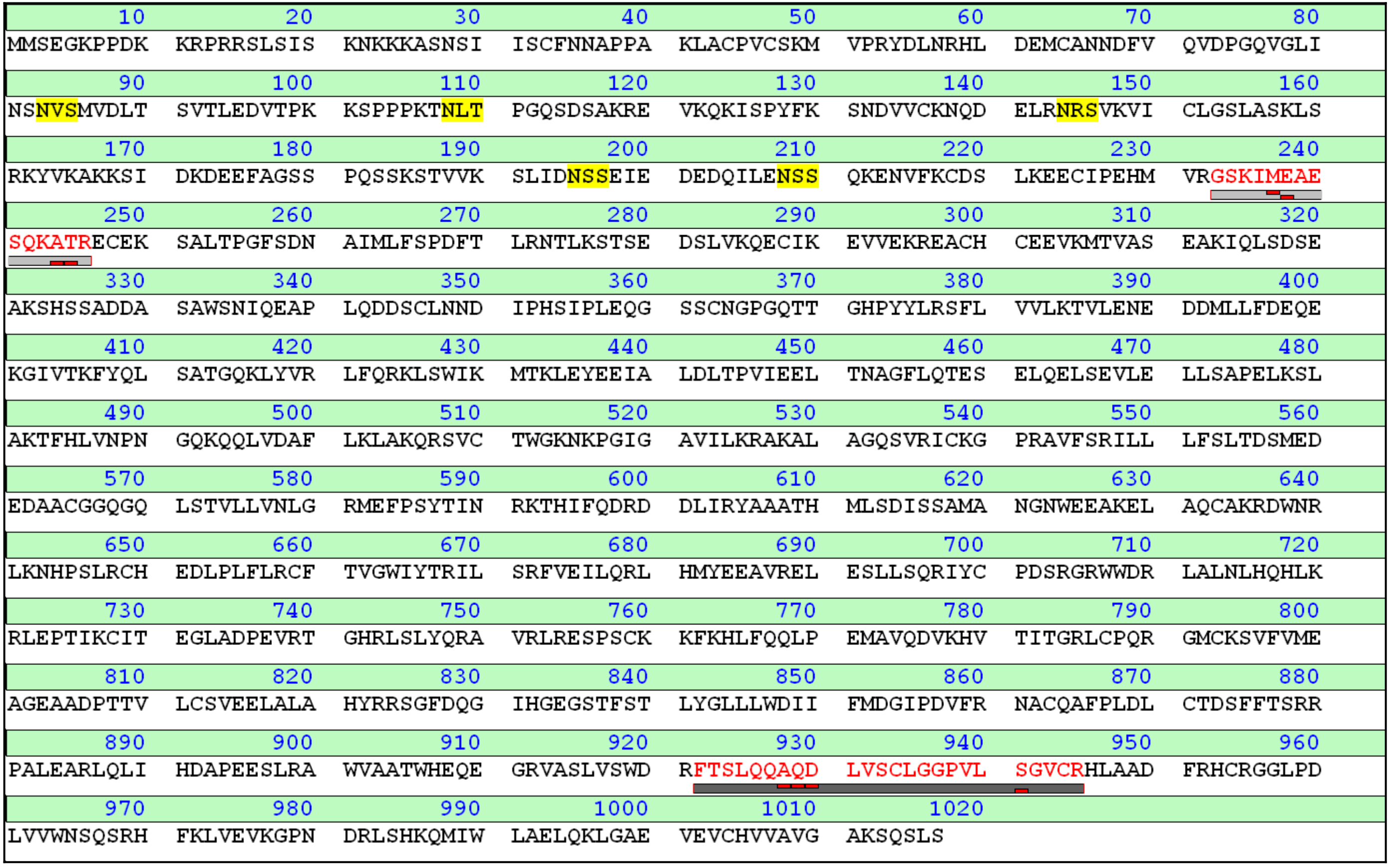
Detailed Protein Report

Protein 222: fanconi-associated nuclease 1 isoform a [Homo sapiens]

Accession:	gi|226246523	**Score:**	32.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	114.2
Database Date:	2015-11-30	**pI:**	7.4
		Sequence Coverage [%]:	3.7
		No. of unique Peptides:	2

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
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
60	3	768.2851	-144.27	2	30.4	19.5	2	233-246	R.GSKIMEAESQKATR.E	

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
83	1	826.6984	-67.49	3	30.8	12.5	0	922-945	R.FTSLQQAQDLVSCLGGPVLSGVCR.H	

Detailed Protein Report

Protein 223: zinc finger protein 518A isoform a [Homo sapiens]

Accession:	gi|57242807	**Score:**	32.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	166.7
Database Date:	2015-11-30	**pI:**	10.2
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	2.8
		No. of unique Peptides:	2

Alias proteins:

Accession	Name	Description
gi|512388675	refseq_human (refseq_human_20140103.fasta)	zinc finger protein 518A isoform a [Homo sapiens]
gi|512388673	refseq_human (refseq_human_20140103.fasta)	zinc finger protein 518A isoform a [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MPSEQKQLFC DEKQTTLKKD YDVKNEIVDR SAPKPKISGS IHYALKNVKI DLPKINIPNE VLLKHEVDKY RKLFQSKQQT
        90        100        110        120        130        140        150        160
ARKSISIKTV SCVEECTLLH KSERAEEEGV KMSAKILNFS CLKCRDNTRY SPNDLQKHFQ MWHHGELPSY PCEMCNFSAN
       170        180        190        200        210        220        230        240
DFQVFKQHRR THRSTLVKCD ICNNESVYTL LNLTKHFTST HCVNGNFQCE KCKFSTQDVG TFVQHIHRHN EIHYKCGKCH
       250        260        270        280        290        300        310        320
HVCFTKGELQ KHLHIHSGTF PFTCQYCSYG ATRREHLVRH VITLHKEHLY AKEKLEKDKY EKRMAKTSAG LKLILKRYKI
       330        340        350        360        370        380        390        400
GASRKTFWKR KKINSGSDRS IEKNTQVLKK MNKTQTKSED QSHVVQEHLS EEKDERLHCE NNDKAPESES EKPTPLSTGQ
       410        420        430        440        450        460        470        480
GNRAEEGPNA SSGFMKTAVL GPTLKNVMMK NNKLAVSPNY NATFMGFKMM DGKQHIVLKL VPIKQNVCSP GSQSGAAKDG
       490        500        510        520        530        540        550        560
TANLQPQTLD TNGFLTGVTT ELNDTVYMKA ATPFSCSSSI LSGKASSEKE MTLISQRNNM LQTMDYEKSV SSLSATSELV
       570        580        590        600        610        620        630        640
TASVNLTTKF ETRDNVDFWG NHLTQSHPEV LGTTIKSPDK VNCVAKPNAY NSGDMHNYCI NYGNCELPVE SSNQGSLPFH
       650        660        670        680        690        700        710        720
NYSKVNNSNK RRRFSGTAVY ENPQRESSSS KTVVQQPISE SFLSLVRQES SKPDSLLASI SLLNDKDGTL KAKSEIEEQY
       730        740        750        760        770        780        790        800
VLEKGQNIDG QNLYSNENQN LECATEKSKW EDFSNVDSPM MPRITSVFSL QSQQASEFLP PEVNQLLQDV LKIKPDVKQD
       810        820        830        840        850        860        870        880
SSNTPNKGLP LHCDQSFQKH EREGKIVESS KDFKVQGIFP VPPGSVGINV PTNDLNLKFG KEKQVSSIPQ DVRDSEKMPR
       890        900        910        920        930        940        950        960
ISGFGTLLKT QSDAIITQQL VKDKLRATTQ NLGSFYMQSP LLNSEQKKTI IVQTSKGFLI PLNITNKPGL PVIPGNALPL
       970        980        990       1000       1010       1020       1030       1040
VNSQGIPASL FVNKKPGMVL TLNNGKLEGV SAVKTEGAPA RGTVTKEPCK TPILKVEPNN NCLTPGLCSS IGSCLSMKSS
      1050       1060       1070       1080       1090       1100       1110       1120
SENTLPLKGP YILKPTSSVK AVLIPNMLSE QQSTKLNISD SVKQQNEIFP KPPLYTFLPD GKQAVFLKCV MPNKTELLKP
      1130       1140       1150       1160       1170       1180       1190       1200
KLVQNSTYQN IQPKKPEGTP QRILLKIFNP VLNVTAANNL SVSNSASSLQ KDNVPSNQII GGEQKEPESR DALPFLLDDL
      1210       1220       1230       1240       1250       1260       1270       1280
MPANEIVITS TATCPESSEE PICVSDCSES RVLRCKTNCR IERNFNRKKT SKKIFSKTKT HGSKDSETAF VSRNRNCKRK
      1290       1300       1310       1320       1330       1340       1350       1360
CRDSYQEPPR RKATLHRKCK EKAKPEDVRE TFGFSRPRLS KDSIRTLRLF PFSSKQLVKC PRRNQPVVVL NHPDADAPEV
      1370       1380       1390       1400       1410       1420       1430       1440
VSVMKTIAKF NGHVLKVSLS KRTINALLKP VCYNPPKTTY DDFSKRHKTF KPVSSVKERF VLKLTLKKTS KNNYQIVKTT
      1450       1460       1470       1480       1490
SENILKAKFN CWFCGRVFDN QDTWAGHGQR HLMEATRDWN MLE
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1117	1	1019.4619	-129.58	2	43.5	17.7	2	31-49	R.SAPKPKISGSIHYALKNVK.I	
63	1	814.0267	-13.11	3	30.1	14.3	0	1016-	K.VEPNNNCLTPGLCSSIGSCLSMK.S	Carbamidomethyl: 7;

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
								1038		Oxidation: 22

Detailed Protein Report

Protein 224: PREDICTED: SH3 domain-containing protein 21 isoform X4 [Homo sapiens]

Accession:	gi|578799774	**Score:**	32.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	84.7
Database Date:	2015-11-30	**pI:**	5.6
		Sequence Coverage [%]:	2.7
		No. of unique Peptides:	2

Quantitation

MD:MU **Median:** 0.32 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MEVLVLAGYR	AQKEDELSLA	PGDVVRQVRW	VPARGWLRGE	FGGRYGLFPE	RLVQEIPETL	RGSGEARRPR	CARRRGHPAK
90	100	110	120	130	140	150	160
HPRPQRWCKV	NFSYSPEQAD	ELKLQAGEIV	EMIKEIEDGW	WLGKKNGQLG	AFPSNFVELL	DSGPPSLGNP	DMPSVSPGPQ
170	180	190	200	210	220	230	240
RPPKLSSLAY	DSPPDYLQTV	SHPEVYRVLF	DYQPEAPDEL	ALRRGDVVKV	LSKTTEDKGW	WEGECQGRRG	VFPDNFVLPP
250	260	270	280	290	300	310	320
PPIKKLVPRK	VVSRESAPIK	EPKKLMPKTS	LPTVKKLATA	TTGPSKAKTS	RTPSRDSQKL	TSRDSGPNGG	FQSGGSYHPG
330	340	350	360	370	380	390	400
RKRSKTQTPQ	QRSVSSQEEE	HSSPVKAPSV	KRTPMPDKTA	TPERPPAPEN	APSSKKIPAP	DKVPSPEKTL	TLGDKASIPG
410	420	430	440	450	460	470	480
NSTSGKIPAP	DKVPTPEKMV	TPEDKASIPE	NSIIPEETLT	VDKPSTPERV	FSVEESPALE	APPMDKVPNP	KMAPLGDEAP
490	500	510	520	530	540	550	560
TLEKVLTPEL	SEEEVSTRDD	IQFHHFSSEE	ALQKVKYFVA	KEDPSSQEEA	HTPEAPPPQP	PSSERCLGEM	KCTLVRGDSS
570	580	590	600	610	620	630	640
PRQAELKSGP	ASRPALEKPH	PHEEATTLPE	EAPSNDERTP	EEEAPPNEQR	PLREEVLPKE	GVASKEEVTL	KEELPPKEEV
650	660	670	680	690	700	710	720
APKEEVPPIE	RAFAQKTRPI	KPPPDSQETL	ALPSLVPQNY	TENKNEGVDV	TSLRGEVESL	RRALELMEEE	ADRHLGGAEE
730	740	750	760	770	780		
REGAAPAAGG	PVYEPRALWG	QGDVCPGVCR	GLPWPSQARW	EKRQPCPGGF			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
949	1	473.1120	-311.20	2	41.4	19.1	1	695-702	R.GEVESLRR.A		MD:MU 0.32
2858	1	805.9291	-2.54	2	66.2	12.9	2	751-763	R.GLPWPSQARWEKR.Q		

Detailed Protein Report

Protein 225: **polycystic kidney disease protein 1-like 3 precursor [Homo sapiens]**

Accession:	gi|31559825	**Score:**	32.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	195.8
Database Date:	2015-11-30	**pI:**	9.6
		Sequence Coverage [%]:	2.1
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MFFKGGSWLW LYIRTSIILG SELNSPAPHG QNNCYQLNRF QCSFEEAQHY CHVQRGFLAH IWNKEVQDLI RDYLEEGKKW
        90        100        110        120        130        140        150        160
WIGQNVMPLK KHQDNKYPAD VAANGPPKPL SCTYLSRNFI RISSKGDKCL LKYYFICQTG DFLDGDAHYE RNGNNSHLYQ
       170        180        190        200        210        220        230        240
RHKKTKRGVA IARDKMPPGP GHLPTTCHYP LPAHLSKTLC HPISQFPSVL SSITSQVTSA ASEPSSQPLP VITQLTMPVS
       250        260        270        280        290        300        310        320
VTHAGQSLAE TTSSPKEEGH PNTFTSYLQV SLQKASGQVI DEIAGNFSRA VHGLQALNKL QEACEFLQKL TALTPRFSKP
       330        340        350        360        370        380        390        400
AQVNLINSLI YLSEELLRIP FQNNNSLGFK VPPTVCPFHS LNNVTKAGEG SWLESKRHTE PVEDILEMSL VEFGNIGEAF
       410        420        430        440        450        460        470        480
LEQNQSPESS VTLTSANATL LLSRQNISTL PLSSYTLGHP APVRLGFPSA LALKELLNKH PGVNVQITGL AFNPFKDLDN
       490        500        510        520        530        540        550        560
RNIVGSIGSV LLSANRKLLQ VHDLMEDIEI MLWRNVSLET HPTSLNMSTH QLTITVNVTS LEKSLIVSID PDSPLLMTLY
       570        580        590        600        610        620        630        640
LGFQYQPNCT HFHLNITLPK DKVWQKDEEY TWVLNPEHLQ HGIGTYYITA VLSERQEGAQ QTPSLVSVIT AVTQCYYWEI
       650        660        670        680        690        700        710        720
HNQTWSSAGC QVGPQSTILR TQCLCNHLTF FASDFFVVPR TVNVEDTIKL FLRVTNNPVG VSLLASLLGF YVITVVWARK
       730        740        750        760        770        780        790        800
KDQADMQKVK VTVLADNDPS AQFHYLIQVY TGYRRSAATT AKVVITLYGS EGRSEPHHLC DPQKTVFERG GLDVFLLTTW
       810        820        830        840        850        860        870        880
TSLGNLHSLR LWHDNSGVSP SWYVSQVIVC DMAVKRKWHF LCNCWLAVDL GDCELDRVFI PVSKRELFSF RHLFSSMIVE
       890        900        910        920        930        940        950        960
KFTQDYLWLS IATRHPWNQF TRVQRLSCCM TLLLCNMVIN VMFWKINSTT AKRDEQMRPF AVAWSELLVS IHTAVILFPI
       970        980        990       1000       1010       1020       1030       1040
NLVIGRLFPL IEPQETLPLF PPIQASCLSD ASVEPLSATM VVEELKETVR FLLRRNTYLL SKCEQPPWSS WDITKLVKLL
      1050       1060       1070       1080       1090       1100       1110       1120
SSLVSSHLEG QGCHQQGERH WARVVPENHH HFCCYLHRVL QRLKSHLGTL GLTQGHQSCD FLDAASQLQK LQELLETHIL
      1130       1140       1150       1160       1170       1180       1190       1200
PTEQEPSREV TSFAILSSEE GKKPISNGLS KWLTSVCWLL LGFTSLASAF FTALYSLELS KDQATSWMIS IILSVLQNIF
      1210       1220       1230       1240       1250       1260       1270       1280
ISQPVKVVFF TFLYSLMMSR MPRLNKENEQ QTKRILALLA KCSSSVPGSR DKNNPVYVAP AINSPTKHPE RTLKKKKLFK
      1290       1300       1310       1320       1330       1340       1350       1360
LTGDILVQIL FLTLLMTAIY SAKNSNRFYL HQAIWKTFSH QFSEIKLLQD FYPWANHILL PSLYGDYRGK NAVLEPSHCK
      1370       1380       1390       1400       1410       1420       1430       1440
CGVQLIFQIP RTKTYEKVDE GQLAFCDNGH TCGRPKSLFP GLHLRRFSYI CSPRPMVLIP TDELHERLTS KNENGFSYIM
      1450       1460       1470       1480       1490       1500       1510       1520
RGAFFTSLRL ESFTSLQMSK KGCVWSIISQ VIYYLLVCYY AFIQGCQLKQ QKWRFFTGKR NILDTSIILI SFILLGLDMK
      1530       1540       1550       1560       1570       1580       1590       1600
SISLHKKNMA RYRDDQDRFI SFYEAVKVNS AATHLVGFPV LLATVQLWNL LRHSPRLRVI SRTLSRAWDE VVGFLLIILI
      1610       1620       1630       1640       1650       1660       1670       1680
LLTGYAIAFN LLFGCSISDY RTFFSSAVTV VGLLMGISHQ EEVFALDPVL GTFLILTSVI LMVLVVINLF VSAILMAFGK
      1690       1700       1710       1720       1730       1740
ERKSLKKEAA LIDTLLQKLS NLLGISWPQK TSSEQAATTA VGSDTEVLDE LP
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
146	1	896.8772	102.59	3	31.2	18.7	2	1242-1267	K.CSSSVPGSRDKNNPVYVAPAINSPTK.H	

Detailed Protein Report

Protein 226: sorting nexin-8 [Homo sapiens]

Accession:	gi|23943858	**Score:**	31.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	52.5
Database Date:	2015-11-30	**pI:**	7.2
Modification(s):	Oxidation	**Sequence Coverage [%]:**	5.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MTGRAMDPLP	AAAVGAAAEA	EADEEADPPA	SDLPTPQAIE	PQAIVQQVPA	PSRMQMPQGN	PLLLSHTLQE	LLARDTVQVE
90	100	110	120	130	140	150	160
LIPEKKGLFL	KHVEYEVSSQ	RFKSSVYRRY	NDFVVFQEML	LHKFPYRMVP	ALPPKRMLGA	DREFIEARRR	ALKRFVNLVA
170	180	190	200	210	220	230	240
RHPLFSEDVV	LKLFLSFSGS	DVQNKLKESA	QCVGDEFLNC	KLATRAKDFL	PADIQAQFAI	SRELIRNIYN	SFHKLRDRAE
250	260	270	280	290	300	310	320
RIASRAIDNA	ADLLIFGKEL	SAIGSDTTPL	PSWAALNSST	WGSLKQALKG	LSVEFALLAD	KAAQQGKQEE	NDVVEKLNLF
330	340	350	360	370	380	390	400
LDLLQSYKDL	CERHEKGVLH	KHQRALHKYS	LMKRQMMSAT	AQNREPESVE	QLESRIVEQE	NAIQTMELRN	YFSLYCLHQE
410	420	430	440	450	460	470	
TQLIHVYLPL	TSHILRAFVN	SQIQGHKEMS	KVWNDLRPKL	SCLFAGPHST	LTPPCSPPED	GLCPH	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1502	1	978.1127	119.49	2	48.6	18.2	1	109-123	R.RYNDFVVFQEMLLHK.F	Oxidation: 11

Detailed Protein Report

Protein 227: peroxisome biogenesis factor 1 isoform 3 [Homo sapiens]

Accession:	gi|544186104	**Score:**	31.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	119.5
Database Date:	2015-11-30	**pI:**	5.7
		Sequence Coverage [%]:	0.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MMKELQTKQL	QSNTVGITES	NENESEIPVD	SSSVASLWTM	IGSIFSFQSE	KKQETSWGLT	EINAFKNMQS	KVVPLDNIFR
90	100	110	120	130	140	150	160
VCKSQPPSIY	NASATSVFHK	HCAIHVFPWD	QEYFDVEPSF	TVTYGKLVKL	LSPKQQQSKT	KQNVLSPEKE	KQMSEPLDQK
170	180	190	200	210	220	230	240
KIRSDHNEED	EKACVLQVVW	NGLEELNNAI	KYTKNVEVLH	LGKVWIPDDL	RKRLNIEMHA	VVRITPVEVT	PKIPRSLKLQ
250	260	270	280	290	300	310	320
PRENLPKDIS	EEDIKTVFYS	WLQQSTTTML	PLVISEEEFI	KLETKDGLKE	FSLSIVHSWE	KEKDKNIFLL	SPNLLQKTTI
330	340	350	360	370	380	390	400
QVLLDPMVKE	ENSEEIDFIL	PFLKLSSLGG	VNSLGVSSLE	HITHSLLGRP	LSRQLMSLVA	GLRNGALLLT	GGKGSGKSTL
410	420	430	440	450	460	470	480
AKAICKEAFD	KLDAHVERVD	CKALRGKRLE	NIQKTLEVAF	SEAVWMQPSV	VLLDDLDLIA	GLPAVPEHEH	SPDAVQSQRL
490	500	510	520	530	540	550	560
AHALNDMIKE	FISMGSLVAL	IATSQSQQSL	HPLLVSAQGV	HIFQCVQHIQ	PPNQEQRCEI	LCNVIKNKLD	CDINKFTDLD
570	580	590	600	610	620	630	640
LQHVAKETGG	FVARDFTVLV	DRAIHSRLSR	QSISTREKLV	LTTLDFQKAL	RGFLPASLRS	VNLHKPRDLG	WDKIGGLHEV
650	660	670	680	690	700	710	720
RQILMDTIQL	PAKYPELFAN	LPIRQRTGIL	LYGPPGTGKT	LLAGVIARES	RMNFISVKGP	ELLSKYIGAS	EQAVRDIFIR
730	740	750	760	770	780	790	800
AQAAKPCILF	FDEFESIAPR	RGHDNTGVTD	RVVNQLLTQL	DGVEGLQGVY	VLAATSRPDL	IDPALLRPGR	LDKCVYCPPP
810	820	830	840	850	860	870	880
DQVSRLEILN	VLSDSLPLAD	DVDLQHVASV	TDSFTGADLK	ALLYNAQLEA	LHGMLLSSGL	QDGSSSSDSD	LSLSSMVFLN
890	900	910	920	930	940	950	960
HSSGSDDSAG	DGECGLDQSL	VSLEMSEILP	DESKFNMYRL	YFGSSYESEL	GNGTSSDLSS	QCLSAPSSMT	QDLPGVPGKD
970	980	990	1000	1010	1020	1030	1040
QLFSQPPVLR	TASQEGCQEL	TQEQRDQLRA	DISIIKGRYR	SQSGEDESMN	QPGPIKTRLA	ISQSHLMTAL	GHTRPSISED
1050	1060	1070	1080				
DWKNFAELYE	SFQNPKRRKN	QSGTMFRPGQ	KVTLA				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1073	5	1207.9210	130.55	1	43.0	31.9	2	233-242	K.IPRSLKLQPR.E	

Detailed Protein Report

Protein 228: fibronectin isoform 6 preproprotein [Homo sapiens]

Accession:	gi|47132549	**Score:**	31.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	239.5
Database Date:	2015-11-30	**pI:**	5.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.5
		No. of unique Peptides:	2

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

Detailed Protein Report

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

Detailed Protein Report

Protein 229: **PREDICTED: zinc finger protein 554 isoform X2 [Homo sapiens]**

Accession:	gi|578832959	**Score:**	31.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	43.7
Database Date:	2015-11-30	**pI:**	9.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	7.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MTVLRNQDST	YKKVALQEEP	ASGINMIKLI	REDGGWKQLE	DSHEDPQGLL	SQKASLHVVA	VPQEKATAWH	GFGENGNLSP
90	100	110	120	130	140	150	160
ALVLSQGSSK	GNHLCGSELD	ITSLASDSVL	NHHQLGYADR	RPCESNECGN	AIRQNSHFIQ	HGGKMFVYLE	NGQSLNHGMA
170	180	190	200	210	220	230	240
LTIHNKINTA	EKPFECHQCG	KVFNRRHSLS	EHQRIHTGEK	PYECQECGRA	FTHSSTLTRH	LRTHTGEKPY	GCGECGKAFN
250	260	270	280	290	300	310	320
RISSLTQHQR	IHTGEKPYKC	EDCGKSFCQS	SYLILHKRTH	TGEKPYECSE	CGKAFSDRSS	LNQHERTHTG	ENPYECKQCG
330	340	350	360	370	380	390	
RAFSQRSSLV	RHERTHTGEK	PYRCQECGKA	FSQSSSLVTH	QKTHSSQKTY	KIIDCGKAFY	QNRHLIGY	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2623	1	812.4211	89.86	2	63.6	11.3	0	223-237	R.THTGEKPYGCGECGK.A	Carbamidomethyl: 13

Detailed Protein Report

Protein 230: **PREDICTED: unhealthy ribosome biogenesis protein 2 homolog isoform X1 [Homo sapiens]**

Accession:	gi|530366678	**Score:**	31.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	166.5
Database Date:	2015-11-30	**pI:**	6.9
		Sequence Coverage [%]:	1.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAAVYSGISL	KLKSKTTSWE	DKLKLAHFAW	ISHQCFLPNK	EQVLLDWARQ	SLVAFYKKKL	ELKEDIVERL	WIYIDNILHS
90	100	110	120	130	140	150	160
RKLQNLLKNG	KTINLQISLV	KIINERVAEF	SLSGSQRNIC	AVLRCCQGIL	STPALAVIYT	AKQELMVALL	SQLCWSACRQ
170	180	190	200	210	220	230	240
PEGAVVAQLF	EVIHLALGHY	LLILQQQVNP	RRAFGDVTAH	LLQPCLVLRH	LLSGGTWTQA	GQGQLRQVLS	RDIRSQIEAM
250	260	270	280	290	300	310	320
FRGGIFQPEL	LSSYKEGLLD	QQQGDVKTGA	MKNLLAPMDT	VLNRLVDAGY	CAASLHTSVV	ANSVALLYKL	FLDSYFKEGN
330	340	350	360	370	380	390	400
QLLCFQVLPR	LFGCLKISHL	QEEQSKALST	SDWTTELLVV	EQLLNSVANN	NIYNIAADRI	RHEEAQFRFY	RHVAELLINH
410	420	430	440	450	460	470	480
AQAPIPAWFR	CLKTLISLNH	LILEPDLDDL	LASAWIDAEV	TEFRTKKAQE	ALIRTVFQTY	AKLRQVPRLF	EEVLGVICRP
490	500	510	520	530	540	550	560
AAEALRQPVL	ASGPSTVLSA	CLLELPPSQI	LDTWSLVLEK	FQSLVLPYLQ	SDADMALKSL	SLSLLLHCIM	FNMRSLDSST
570	580	590	600	610	620	630	640
PLPIVRRTQC	MMERMMRELV	QPLLALLPDT	PGPEPELWLQ	KVSDSVLLLS	YTWAQVDAMF	SLNCSQYHSM	SGPLIGVALE
650	660	670	680	690	700	710	720
ISNLPSLLPG	VKTQHWKKIE	KFTAQFSSLG	TYCLEQLYLQ	KMKRTLMQTS	FRSEGAIQSL	RCDAAFIIGS	GRKSLNQRTT
730	740	750	760	770	780	790	800
ASWDGQVGMV	SGLTYPVAHW	HLIVSNLTIL	ISYLCPDDVG	YLASVLLRTL	PMGKAQEVSI	DEEAYITLEK	ISKAFLHSPL
810	820	830	840	850	860	870	880
FPEMQSLHSA	FLTCVTTSCS	SILCSGAQRD	SGLVSQQLPW	LFEKDHMVVG	HWENRFAKAG	PEGIEPRGEI	AQNLLSLVKS
890	900	910	920	930	940	950	960
DFPIQLEGEQ	LESILGLLEV	ISALQLDSLL	PPYHVHYFLV	LLSMAVTKLG	CSCSSSLALK	FLTTCYQLLG	YLQKGKSARS
970	980	990	1000	1010	1020	1030	1040
VFKIMYGSDI	FEVVLTSLFR	ASSRFLIEMD	DPAWLEFLQV	IGTFLEELMQ	MLIQMKLSLV	LNFRKITAFL	SSSKPYTEAA
1050	1060	1070	1080	1090	1100	1110	1120
SSKQLENQNP	QGRQLLLVSL	TRLCHVLGPF	LKEQKLGQEA	PAALSELLQQ	VVLQTGAVLQ	LCSVPGARGW	RLPSVLISSV
1130	1140	1150	1160	1170	1180	1190	1200
STLLEADLGQ	HCRDGGADIS	QGSDRTLLSH	VALYQGVYSQ	ILLELPALAG	HDQSFQAALQ	FLTLFFLAPE	LHPKKDSVFT
1210	1220	1230	1240	1250	1260	1270	1280
SMFHSVRRVL	ADPEIPVQVT	QDIEPHLGAL	FTQMLEVGTT	EDLRLVMQCI	LQGLDVSNMW	KADVQLLNRE	ASQEQPVSLT
1290	1300	1310	1320	1330	1340	1350	1360
VVGPVLDVLA	ALLRQGEEAI	GNPHHVSLAF	SILLTVPLDH	LKPLEYGSVF	PRLHNVLFSI	LQCHPKVMLK	AIPSFLNSFN
1370	1380	1390	1400	1410	1420	1430	1440
RLVFSVMREG	RQKDKGSIDD	LPTVLKCARL	VERMYSHIAA	RAEEFAVFSP	FMVAQYVLEV	QKVTLYPAVK	SLLQEGIYLI
1450	1460	1470	1480	1490			
LDLCIEPDVQ	FLRASLQPGM	RDIFKELYND	YLKYHKAKHE	GEKRYTA			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
598	1	661.8686	26.39	2	36.8	13.9	2	12-22	K.LKSKTTSWEDK.L	

Detailed Protein Report

Protein 231: **PREDICTED: cortactin-binding protein 2 isoform X2 [Homo sapiens]**

Accession:	gi|530386510	**Score:**	31.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	106.1
Database Date:	2015-11-30	**pI:**	9.1
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.0
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MSGGPAPLAG RPTLLQQAAA QGNVTLLSML LNEEGLDINY SCEDGHSALY SAAKNGHTDC VRLLLSAEAQ VNAADKNGFT
        90        100        110        120        130        140        150        160
PLCAAAAQGH FECVELLISY DANINHAADG GQTPLYLACK NGNKECIKLL LEAGTNRSVK TTDGWTPVHA AVDTGNVDSL
       170        180        190        200        210        220        230        240
KLLMYHRIPA HGNSFNEEES ESSVFDLDGG EESPEGISKP VVPADLINHA NREGWTAAHI AASKGFKNCL EILCRHGGLE
       250        260        270        280        290        300        310        320
PERRDKCNRT VHDVATDDCK HLLENLNALK IPLRISVGEI EPSNYGSDDL ECENTICALN IRKQTSWDDF SKAVSQALTN
       330        340        350        360        370        380        390        400
HFQAISSDGW WSLEDVTCNN TTDSNIGLSA RSIRSITLGN VPWSVGQSFA QSPWDFMRKN KAEHITVLLS GPQEGCLSSV
       410        420        430        440        450        460        470        480
TYASMIPLQM MQNYLRLVEQ YHNVIFHGPE GSLQDYIVHQ LALCLKHRQM AAGFSCEIVR AEVDAGFSKE QLLDLFISSA
       490        500        510        520        530        540        550        560
CLIPVKQSPS KKKIIIILEN LEKSSLSELL RDFLAPLENR STESPCTFQK GNGLSECYYF HENCFLMGTI AKACLQGSDL
       570        580        590        600        610        620        630        640
LVQQHFRWVQ LRWDGEPMQG LLQRFLRRKV VNKFKGQAPS PCDPVCKIVD WALSVWRQLN SCLARLGTPE ALLGPKYFLS
       650        660        670        680        690        700        710        720
CPVVPGHAQV TVKWMSKLWN GVIAPRVQEA ILSRASVKRQ PGFGQTTAKR HPSQGQQAVV KAALSILLNK AVLHGCPLPR
       730        740        750        760        770        780        790        800
AELDQHTADF KGGSFPLSIV SSYNTCNKKK GESGAWRKVN TSPRRKSGRF SLPTWNKPDL STEGMKNKTI SQLNCNRNAS
       810        820        830        840        850        860        870        880
LSKQKSLEND LSLTLNLDQR LSLGSDDEAD LVKELQSMCS SKSESDISKI ADSRDDLRMF DSSGNNPVLS ATINNLRMPV
       890        900        910        920        930        940        950        960
SQKEVSPLSS HQTTECSNSK SKTELGVSRV KSFLPVPRSK VTQCSQNTKR SSSSSNTRQI EINNNSKEVN WNLHKNEHLE
       970
KPNK
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2703	2	973.4604	-78.66	2	65.0	13.9	0	470-486	K.EQLLDLFISSACLIPVK.Q	Carbamidomethyl: 12

Detailed Protein Report

Protein 232: **rho GTPase-activating protein 42 [Homo sapiens]**

Accession:	gi|221307575	**Score:**	31.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	98.5
Database Date:	2015-11-30	**pI:**	8.9
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.5
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MGLPTLEFSD SYLDSPDFRE RLQCHEIELE RTNKFIKELI KDGSLLIGAL RNLSMAVQKF SQSLQDFQFE CIGDAETDDE
        90        100        110        120        130        140        150        160
ISIAQSLKEF ARLLIAVEEE RRRLIQNAND VLIAPLEKFR KEQIGAAKDG KKKFDKESEK YYSILEKHLN LSAKKKESHL
       170        180        190        200        210        220        230        240
QEADTQIDRE HQNFYEASLE YVFKIQEVQE KKKFEFVEPL LSFLQGLFTF YHEGYELAQE FAPYKQQLQF NLQNTRNNFE
       250        260        270        280        290        300        310        320
STRQEVERLM QRMKSANQDY RPPSQWTMEG YLYVQEKRPL GFTWIKHYCT YDKGSKTFTM SVSEMKSSGK MNGLVTSSPE
       330        340        350        360        370        380        390        400
MFKLKSCIRR KTDSIDKRFC FDIEVVERHG IITLQAFSEA NRKLWLEAMD GKEPIYTLPA IISKKEEMYL NEAGFNFVRK
       410        420        430        440        450        460        470        480
CIQAVETRGI TILGLYRIGG VNSKVQKLMN TTFSPKSPPD IDIDIELWDN KTITSGLKNY LRCLAEPLMT YKLHKDFIIA
       490        500        510        520        530        540        550        560
VKSDDQNYRV EAVHALVHKL PEKNREMLDI LIKHLVKVSL HSQQNLMTVS NLGVIFGPTL MRAQEETVAA MMNIKFQNIV
       570        580        590        600        610        620        630        640
VEILIEHYEK IFHTAPDPSI PLPQPQSRSG SRRTRAICLS TGSRKPRGRY TPCLAEPDSD SYSSSPDSTP MGSIESLSSH
       650        660        670        680        690        700        710        720
SSEQNSTTKS ASCQPREKSG GIPWIATPSS SNGQKSLGLW TTSPESSSRE DATKTDAESD CQSVASVTSP GDVSPPIDLV
       730        740        750        760        770        780        790        800
KKEPYGLSGL KRASASSLRS ISAAEGNKSY SGSIQSLTSV GSKETPKASP NPDLPPKMCR RLRLDTASSN GYQRPGSVVA
       810        820        830        840        850        860        870        880
AKAQLFENVG SPKPVSSGRQ AKAMYSCKAE HSHELSFPQG AIFSNVYPSV EPGWLKATYE GKTGLVPENY VVFL
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
150	1	849.3532	-94.77	2	31.6	11.8	1	311-325	K.MNGLVTSSPEMFKLK.S	Oxidation: 11

Detailed Protein Report

Protein 233: **serine/threonine-protein kinase Nek8 [Homo sapiens]**

Accession:	gi|30039692	**Score:**	31.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	74.8
Database Date:	2015-11-30	**pI:**	9.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.9
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MEKYERIRVV GRGAFGIVHL CLRKADQKLV IIKQIPVEQM TKEERQAAQN ECQVLKLLNH PNVIEYYENF LEDKALMIAM
        90        100        110        120        130        140        150        160
EYAPGGTLAE FIQKRCNSLL EEETILHFFV QILLALHHVH THLILHRDLK TQNILLDKHR MVVKIGDFGI SKILSSKSKA
       170        180        190        200        210        220        230        240
YTVVGTPCYI SPELCEGKPY NQKSDIWALG CVLYELASLK RAFEAANLPA LVLKIMSGTF APISDRYSPE LRQLVLSLLS
       250        260        270        280        290        300        310        320
LEPAQRPPLS HIMAQPLCIR ALLNLHTDVG SVRMRRAEKS VAPSNTGSRT TSVRCRGIPR GPVRPAIPPP LSSVYAWGGG
       330        340        350        360        370        380        390        400
LGTPLRLPML NTEVVQVAAG RTQKAGVTRS GRLILWEAPP LGAGGGSLLP GAVEQPQPQF ISRFLEGQSG VTIKHVACGD
       410        420        430        440        450        460        470        480
FFTACLTDRG IIMTFGSGSN GCLGHGSLTD ISQPTIVEAL LGYEMVQVAC GASHVLALST ERELFAWGRG DSGRLGLGTR
       490        500        510        520        530        540        550        560
ESHSCPQQVP MPPGQEAQRV VCGIDSSMIL TVPGQALACG SNRFNKLGLD HLSLGEEPVP HQQVEEALSF TLLGSAPLDQ
       570        580        590        600        610        620        630        640
EPLLSIDLGT AHSAAVTASG DCYTFGSNQH GQLGTNTRRG SRAPCKVQGL EGIKMAMVAC GDAFTVAIGA ESEVYSWGKG
       650        660        670        680        690        700
ARGRLGRRDE DAGLPRPVQL DETHPYTVTS VSCCHGNTLL AVRSVTDEPV PP
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1879	2	918.3405	-130.83	2	53.4	19.3	2	280-296	K.SVAPSNTGSRTTSVRCR.G	Carbamidomethyl: 16

Detailed Protein Report

Protein 234: transient receptor potential cation channel subfamily M member 8 [Homo sapiens]

Accession:	gi|109689695	**Score:**	31.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	127.6
Database Date:	2015-11-30	**pI:**	7.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSFRAARLSM	RNRRNDTLDS	TRTLYSSASR	STDLSYSESD	LVNFIQANFK	KRECVFFTKD	SKATENVCKC	GYAQSQHMEG
90	100	110	120	130	140	150	160
TQINQSEKWN	YKKHTKEFPT	DAFGDIQFET	LGKKGKYIRL	SCDTDAEILY	ELLTQHWHLK	TPNLVISVTG	GAKNFALKPR
170	180	190	200	210	220	230	240
MRKIFSRLIY	IAQSKGAWIL	TGGTHYGLMK	YIGEVVRDNT	ISRSSEENIV	AIGIAAWGMV	SNRDTLIRNC	DAEGYFLAQY
250	260	270	280	290	300	310	320
LMDDFTRDPL	YILDNNHTHL	LLVDNGCHGH	PTVEAKLRNQ	LEKYISERTI	QDSNYGGKIP	IVCFAQGGGK	ETLKAINTSI
330	340	350	360	370	380	390	400
KNKIPCVVVE	GSGQIADVIA	SLVEVEDALT	SSAVKEKLVR	FLPRTVSRLP	EEETESWIKW	LKEILECSHL	LTVIKMEEAG
410	420	430	440	450	460	470	480
DEIVSNAISY	ALYKAFSTSE	QDKDNWNGQL	KLLLEWNQLD	LANDEIFTND	RRWESADLQE	VMFTALIKDR	PKFVRLFLEN
490	500	510	520	530	540	550	560
GLNLRKFLTH	DVLTELFSNH	FSTLVYRNLQ	IAKNSYNDAL	LTFVWKLVAN	FRRGFRKEDR	NGRDEMDIEL	HDVSPITRHP
570	580	590	600	610	620	630	640
LQALFIWAIL	QNKKELSKVI	WEQTRGCTLA	ALGASKLLKT	LAKVKNDINA	AGESEELANE	YETRAVELFT	ECYSSDEDLA
650	660	670	680	690	700	710	720
EQLLVYSCEA	WGGSNCLELA	VEATDQHFIA	QPGVQNFLSK	QWYGEISRDT	KNWKIILCLF	IIPLVGCGFV	SFRKKPVDKH
730	740	750	760	770	780	790	800
KKLLWYYVAF	FTSPFVVFSW	NVVFYIAFLL	LFAYVLLMDF	HSVPHPPELV	LYSLVFVLFC	DEVRQWYVNG	VNYFTDLWNV
810	820	830	840	850	860	870	880
MDTLGLFYFI	AGIVFRLHSS	NKSSLYSGRV	IFCLDYIIFT	LRLIHIFTVS	RNLGPKIIML	QRMLIDVFFF	LFLFAVWMVA
890	900	910	920	930	940	950	960
FGVARQGILR	QNEQRWRWIF	RSVIYEPYLA	MFGQVPSDVD	GTTYDFAHCT	FTGNESKPLC	VELDEHNLPR	FPEWITIPLV
970	980	990	1000	1010	1020	1030	1040
CIYMLSTNIL	LVNLLVAMFG	YTVGTVQENN	DQVWKFQRYF	LVQEYCSRLN	IPFPFIVFAY	FYMVVKKCFK	CCCKEKNMES
1050	1060	1070	1080	1090	1100	1110	
SVCCFKNEDN	ETLAWEGVMK	ENYLVKINTK	ANDTSEEMRH	RFRQLDTKLN	DLKGLLKEIA	NKIK	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2072	1	731.2846	-37.73	2	56.1	12.0	1	1035-1046	K.EKNMESSVCCFK.N	Carbamidomethyl: 9

Detailed Protein Report

Protein 235: receptor-type tyrosine-protein phosphatase O isoform b precursor [Homo sapiens]

Accession: gi|4506323
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 31.6
MW [kDa]: 134.9
pI: 5.6
Sequence Coverage [%]: 2.4
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MGHLPTGIHG	ARRLLPLLWL	FVLFKNATAF	HVTVQDDNNI	VVSLEASDVI	SPASVYVVKI	TGESKNYFFE	FEEFNSTLPP
90	100	110	120	130	140	150	160
PVIFKASYHG	LYYIITLVVV	NGNVVTKPSR	SITVLTKPLP	VTSVSIYDYK	PSPETGVLFE	IHYPEKYNVF	TRVNISYWEG
170	180	190	200	210	220	230	240
KDFRTMLYKD	FFKGKTVFNH	WLPGMCYSNI	TFQLVSEATF	NKSTLVEYSG	VSHEPKQHRT	APYPPQNISV	RIVNLNKNNW
250	260	270	280	290	300	310	320
EEQSGNFPEE	SFMRSQDTIG	KEKLFHFTEE	TPEIPSGNIS	SGWPDFNSSD	YETTSQPYWW	DSASAAPESE	DEFVSVLPME
330	340	350	360	370	380	390	400
YENNSTLSET	EKSTSGSFSF	FPVQMILTWL	PPKPPTAFDG	FHIHIEREEN	FTEYLMVDEE	AHEFVAELKE	PGKYKLSVTT
410	420	430	440	450	460	470	480
FSSSGSCETR	KSQSAKSLSF	YISPSGEWIE	ELTEKPQHVS	VHVLSSTTAL	MSWTSSQENY	NSTIVSVVSL	TCQKQKESQR
490	500	510	520	530	540	550	560
LEKQYCTQVN	SSKPIIENLV	PGAQYQVVIY	LRKGPLIGPP	SDPVTFAIVP	TGIKDLMLYP	LGPTAVVLSW	TRPYLGVFRK
570	580	590	600	610	620	630	640
YVVEMFYFNP	ATMTSEWTTY	YEIAATVSLT	ASVRIANLLP	AWYYNFRVTM	VTWGDPELSC	CDSSTISFIT	APVAPEITSV
650	660	670	680	690	700	710	720
EYFNSLLYIS	WTYGDDTTDL	SHSRMLHWMV	VAEGKKKIKK	SVTRNVMTAI	LSLPPGDIYN	LSVTACTERG	SNTSMLRLVK
730	740	750	760	770	780	790	800
LEPAPPKSLF	AVNKTQTSVT	LLWVEEGVAD	FFEVFCQQVG	SSQKTKLQEP	VAVSSHVVTI	SSLLPATAYN	CSVTSFSHDS
810	820	830	840	850	860	870	880
PSVPTFIAVS	TMVTEMNPNV	VVISVLAILS	TLLIGLLLVT	LIILRKKHLQ	MARECGAGTF	VNFASLERDG	KLPYNWSKNG
890	900	910	920	930	940	950	960
LKKRKLTNPV	QLDDFDAYIK	DMAKDSDYKF	SLQFEELKLI	GLDIPHFAAD	LPLNRCKNRY	TNILPYDFSR	VRLVSMNEEE
970	980	990	1000	1010	1020	1030	1040
GADYINANYI	PGYNSPQEYI	ATQGPLPETR	NDFWKMVLQQ	KSQIIVMLTQ	CNEKRRVKCD	HYWPFTEEPI	AYGDITVEMI
1050	1060	1070	1080	1090	1100	1110	1120
SEEEQDDWAC	RHFRINYADE	MQDVMHFNYT	AWPDHGVPTA	NAAESILQFV	HMVRQQATKS	KGPMIIHCSA	GVGRTGTFIA
1130	1140	1150	1160	1170	1180	1190	
LDRLLQHIRD	HEFVDILGLV	SEMRSYRMSM	VQTEEQYIFI	HQCVQLMWMK	KKQQFCISDV	IYENVSKS	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1528	1	977.3724	-122.90	2	48.9	18.9	1	203-219	K.STLVEYSGVSHEPKQHR.T	

Detailed Protein Report

Protein 236: **zinc finger protein 585B [Homo sapiens]**

Accession:	gi|289547716	**Score:**	31.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	88.0
Database Date:	2015-11-30	**pI:**	10.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.6
		No. of unique Peptides:	2

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
2053	1	575.2161	-125.57	3	55.6	15.5	1	151-165	K.VPTGEKLYVCIECGR.A	Carbamidomethyl: 10
1964	3	753.7894	-100.09	2	54.7	16.1	0	222-234	K.GFPYNSDLSIHEK.I	

Detailed Protein Report

Protein 237: centromere-associated protein E isoform 2 [Homo sapiens]

Accession:	gi|557878612	**Score:**	31.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	301.6
Database Date:	2015-11-30	**pI:**	5.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAEEGAVAVC	VRVRPLNSRE	ESLGETAQVY	WKTDNNVIYQ	VDGSKSFNFD	RVFHGNETTK	NVYEEIAAPI	IDSAIQGYNG
90	100	110	120	130	140	150	160
TIFAYGQTAS	GKTYTMMGSE	DHLGVIPRAI	HDIFQKIKKF	PDREFLLRVS	YMEIYNETIT	DLLCGTQKMK	PLIIREDVNR
170	180	190	200	210	220	230	240
NVYVADLTEE	VVYTSEMALK	WITKGEKSRH	YGETKMNQRS	SRSHTIFRMI	LESREKGEPS	NCEGSVKVSH	LNLVDLAGSE
250	260	270	280	290	300	310	320
RAAQTGAAGV	RLKEGCNINR	SLFILGQVIK	KLSDGQVGGF	INYRDSKLTR	ILQNSLGGNA	KTRIICTITP	VSFDETLTAL
330	340	350	360	370	380	390	400
QFASTAKYMK	NTPYVNEVST	DEALLKRYRK	EIMDLKKQLE	EVSLETRAQA	MEKDQLAQLL	EEKDLLQKVQ	NEKIENLTRM
410	420	430	440	450	460	470	480
LVTSSSLTLQ	QELKAKRKRR	VTWCLGKINK	MKNSNYADQF	NIPTNITTKT	HKLSINLLRE	IDESVCSESD	VFSNTLDTLS
490	500	510	520	530	540	550	560
EIEWNPATKL	LNQENIESEL	NSLRADYDNL	VLDYEQLRTE	KEEMELKLKE	KNDLDEFEAL	ERKTKKDQEN	ELSSKVELLR
570	580	590	600	610	620	630	640
EKEDQIKKLQ	EYIDSQKLEN	IKMDLSYSLE	SIEDPKQMKQ	TLFDAETVAL	DAKRESAFLR	SENLELKEKM	KELATTYKQM
650	660	670	680	690	700	710	720
ENDIQLYQSQ	LEAKKKMQVD	LEKELQSAFN	EITKLTSLID	GKVPKDLLCN	LELEGKITDL	QKELNKEVEE	NEALREEVIL
730	740	750	760	770	780	790	800
LSELKSLPSE	VERLRKEIQD	KSEELHIITS	EKDKLFSEVV	HKESRVQGLL	EEIGKTKDDL	ATTQSNYKST	DQEFQNFKTL
810	820	830	840	850	860	870	880
HMDFEQKYKM	VLEENERMNQ	EIVNLSKEAQ	KFDSSLGALK	TELSYKTQEL	QEKTREVQER	LNEMEQLKEQ	LENRDSTLQT
890	900	910	920	930	940	950	960
VEREKTLITE	KLQQTLEEVK	TLTQEKDDLK	QLQESLQIER	DQLKSDIHDT	VNMNIDTQEQ	LRNALESLKQ	HQETINTLKS
970	980	990	1000	1010	1020	1030	1040
KISEEVSRNL	HMEENTGETK	DEFQQKMVGI	DKKQDLEAKN	TQTLTADVKD	NEIIEQQRKI	FSLIQEKNEL	QQMLESVIAE
1050	1060	1070	1080	1090	1100	1110	1120
KEQLKTDLKE	NIEMTIENQE	ELRLLGDELK	KQQEIVAQEK	NHAIKKEGEL	SRTCDRLAEV	EEKLKEKSQQ	LQEKQQQLLN
1130	1140	1150	1160	1170	1180	1190	1200
VQEEMSEMQK	KINEIENLKN	ELKNKELTLE	HMETERLELA	QKLNENYEEV	KSITKERKVL	KELQKSFETE	RDHLRGYIRE
1210	1220	1230	1240	1250	1260	1270	1280
IEATGLQTKE	ELKIAHIHLK	EHQETIDELR	RSVSEKTAQI	INTQDLEKSH	TKLQEEIPVL	HEEQELLPNV	KEVSETQETM
1290	1300	1310	1320	1330	1340	1350	1360
NELELLTEQS	TTKDSTTLAR	IEMERLRLNE	KFQESQEEIK	SLTKERDNLK	TIKEALEVKH	DQLKEHIRET	LAKIQESQSK
1370	1380	1390	1400	1410	1420	1430	1440
QEQSLNMKEK	DNETTKIVSE	MEQFKPKDSA	LLRIEIEMLG	LSKRLQESHD	EMKSVAKEKD	DLQRLQEVLQ	SESDQLKENI
1450	1460	1470	1480	1490	1500	1510	1520
KEIVAKHLET	EEELKVAHCC	LKEQEETINE	LRVNLSEKET	EISTIQKQLE	AINDKLQNKI	QEIYEKEEQF	NIKQISEVQE
1530	1540	1550	1560	1570	1580	1590	1600
KVNELKQFKE	HRKAKDSALQ	SIESKMLELT	NRLQESQEEI	QIMIKEKEEM	KRVQEALQIE	RDQLKENTKE	IVAKMKESQE
1610	1620	1630	1640	1650	1660	1670	1680
KEYQFLKMTA	VNETQEKMCE	IEHLKEQFET	QKLNLENIET	ENIRLTQILH	ENLEEMRSVT	KERDDLRSVE	ETLKVERDQL
1690	1700	1710	1720	1730	1740	1750	1760
KENLRETITR	DLEKQEELKI	VHMHLKEHQE	TIDKLRGIVS	EKTNEISNMQ	KDLEHSNDAL	KAQDLKIQEE	LRIAHMHLKE
1770	1780	1790	1800	1810	1820	1830	1840
QQETIDKLRG	IVSEKTDKLS	NMQKDLENSN	AKLQEKIQEL	KANEHQLITL	KKDVNETQKK	VSEMEQLKKQ	IKDQSLTLSK
1850	1860	1870	1880	1890	1900	1910	1920
LEIENLNLAQ	KLHENLEEMK	SVMKERDNLR	RVEETLKLER	DQLKESLQET	KARDLEIQQE	LKTARMLSKE	HKETVDKLRE
1930	1940	1950	1960	1970	1980	1990	2000
KISEKTIQIS	DIQKDLDKSK	DELQKKQDRQ	NHQVKPEKRL	LSDGQQHLTE	SLREKCSRIK	ELLKRYSEMD	DHYECLNRLS
2010	2020	2030	2040	2050	2060	2070	2080
LDLEKEIEFQ	KELSMRVKAN	LSLPYLQTKH	IEKLFTANQR	CSMEFHRIMK	KLKYVLSYVT	KIKEEQHESI	NKFEMDFIDE
2090	2100	2110	2120	2130	2140	2150	2160
VEKQKELLIK	IQHLQQDCDV	PSRELRDLKL	NQNMDLHIEE	ILKDFSESEF	PSIKTEFQQV	LSNRKEMTQF	LEEWLNTRFD
2170	2180	2190	2200	2210	2220	2230	2240
IEKLKNGIQK	ENDRICQVNN	FFNNRIIAIM	NESTEFEERS	ATISKEWEQD	LKSLKEKNEK	LFKNYQTLKT	SLASGAQVNP
2250	2260	2270	2280	2290	2300	2310	2320
TTQDNKNPHV	TSRATQLTTE	KIRELENSLH	EAKESAMHKE	SKIIKMQKEL	EVTNDIIAKL	QAKVHESNKC	LEKTKETIQV
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
1821	1	920.3533	-110.00	2	52.8	20.0	2	2474-2489	R.EAHKQVTCENSPKSPK.V	Carbamidomethyl: 8

Detailed Protein Report

Protein 238: ubiquitin-conjugating enzyme E2 J2 isoform 3 [Homo sapiens]

Accession:	gi|37577130	**Score:**	31.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	22.9
Database Date:	2015-11-30	**pI:**	7.8
		Sequence Coverage [%]:	5.8
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|37577132	refseq_human (refseq_human_20140103.fasta)	ubiquitin-conjugating enzyme E2 J2 isoform 3 [Homo sapiens]

```
         10         20         30         40         50         60         70         80
MTPYEGGYYH GKLIFPREFP FKPPSIYMIT PNGRFKCNTR LCLSITDFHP DTWNPAWSVS TILTGLLSFM VEKGPTLGSI
         90        100        110        120        130        140        150        160
ETSDFTKRQL AVQSLAFNLK DKVFCELFPE VVEEIKQKQK AQDELSSRPQ TLPLPDVVPD GETHLVQNGI QLLNGHAPGA
        170        180        190        200        210
VPNLAGLQQA NRHHGLLGGA LANLFVIVGF AAFAYTVKYV LRSIAQE
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
188	1	636.3948	167.51	2	32.1	12.9	0	2-12	M.TPYEGGYYHGK.L	

Detailed Protein Report

Protein 239: prosaposin receptor GPR37 precursor [Homo sapiens]

Accession:	gi|4885323	**Score:**	31.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	67.1
Database Date:	2015-11-30	**pI:**	9.9
Modification(s):	Oxidation	**Sequence Coverage [%]:**	4.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MRAPGALLAR	MSRLLLLLLL	KVSASSALGV	APASRNETCL	GESCAPTVIQ	RRGRDAWGPG	NSARDVLRAR	APREEQGAAF
90	100	110	120	130	140	150	160
LAGPSWDLPA	APGRDPAAGR	GAEASAAGPP	GPPTRPPGPW	RWKGARGQEP	SETLGRGNPT	ALQLFLQISE	EEEKGPRGAG
170	180	190	200	210	220	230	240
ISGRSQEQSV	KTVPGASDLF	YWPRRAGKLQ	GSHHKPLSKT	ANGLAGHEGW	TIALPGRALA	QNGSLGEGIH	EPGGPRRGNS
250	260	270	280	290	300	310	320
TNRRVRLKNP	FYPLTQESYG	AYAVMCLSVV	IFGTGIIGNL	AVMCIVCHNY	YMRSISNSLL	ANLAFWDFLI	IFFCLPLVIF
330	340	350	360	370	380	390	400
HELTKKWLLE	DFSCKIVPYI	EVASLGVTTF	TLCALCIDRF	RAATNVQMYY	EMIENCSSTT	AKLAVIWVGA	LLLALPEVVL
410	420	430	440	450	460	470	480
RQLSKEDLGF	SGRAPAERCI	IKISPDLPDT	IYVLALTYDS	ARLWWYFGCY	FCLPTLFTIT	CSLVTARKIR	KAEKACTRGN
490	500	510	520	530	540	550	560
KRQIQLESQM	NCTVVALTIL	YGFCIIPENI	CNIVTAYMAT	GVSQQTMDLL	NIISQFLLFF	KSCVTPVLLF	CLCKPFSRAF
570	580	590	600	610	620		
MECCCCCCEE	CIQKSSTVTS	DDNDNEYTTE	LELSPFSTIR	REMSTFASVG	THC		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2128	2	721.2347	-109.30	2	56.8	13.5	1	601-613	R.REMSTFASVGTHC.-	Oxidation: 3

Detailed Protein Report

Protein 240: PREDICTED: thyroglobulin isoform X9 [Homo sapiens]

Accession:	gi|530389281	**Score:**	31.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	232.1
Database Date:	2015-11-30	**pI:**	5.1
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.2
		No. of unique Peptides:	1

Quantitation

MD:MU	**Median:** 0.53	**CV:** 0.00 %	**No. of Peptides:** 1

Detailed Protein Report

```
        10         20         30         40         50         60         70         80
MALVLEIFTL LASICWVSAN IFEYQVDAQP LRPCELQRET AFLKQADYVP QCAEDGSFQT VQCQNDGRSC WCVGANGSEV
        90        100        110        120        130        140        150        160
LGSRQPGRPV ACLSFCQLQK QQILLSGYIN STDTSYLPQC QDSGDYAPVQ CDVQQVQCWC VDAEGMEVYG TRQLGRPKRC
       170        180        190        200        210        220        230        240
PRSCEIRNRR LLHGVGDKSP PQCSAEGEFM PVQCKFVNTT DMMIFDLVHS YNRFPDAFVT FSSFQRRFPE VSGYCHCADS
       250        260        270        280        290        300        310        320
QGRELAETGL ELLLDEIYDT IFAGLDLPST FTETTLYRIL QRRFLAVQSV ISGRFCRPTK 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
865	1	623.9049	-34.22	3	40.3	10.8	0	228-243	R.FPEVSGYCHCADSQGR.E	Carbamidomethyl: 8, 10	MD:MU 0.53

Protein 241: complement C4-A isoform 2 preproprotein [Homo sapiens]

Accession: gi|356582273
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 31.1
MW [kDa]: 187.6
pI: 6.7
Sequence Coverage [%]: 1.8
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MRLLWGLIWA	SSFFTLSLQK	PRLLLFSPSV	VHLGVPLSVG	VQLQDVPRGQ	VVKGSVFLRN	PSRNNVPCSP	KVDFTLSSER
90	100	110	120	130	140	150	160
DFALLSLQVP	LKDAKSCGLH	QLLRGPEVQL	VAHSPWLKDS	LSRTTNIQGI	NLLFSSRRGH	LFLQTDQPIY	NPGQRVRYRV
170	180	190	200	210	220	230	240
FALDQKMRPS	TDTITVMVEN	SHGLRVRKKE	VYMPSSIFQD	DFVIPDISEP	GTWKISARFS	DGLESNSSTQ	FEVKKYVLPN
250	260	270	280	290	300	310	320
FEVKITPGKP	YILTVPGHLD	EMQLDIQARY	IYGKPVQGVA	YVRFGLLDED	GKKTFFRGLE	SQTKLVNGQS	HISLSKAEFQ
330	340	350	360	370	380	390	400
DALEKLNMGI	TDLQGLRLYV	AAAIIESPGG	EMEEAELTSW	YFVSSPFSLD	LSKTKRHLVP	GAPFLLQALV	REMSGSPASG
410	420	430	440	450	460	470	480
IPVKVSATVS	SPGSVPEVQD	IQQNTDGSGQ	VSIPIIIPQT	ISELQLSVSA	GSPHPAIARL	TVAAPPSGGP	GFLSIERPDS
490	500	510	520	530	540	550	560
RPPRVGDTLN	LNLRAVGSGA	TFSHYYYMIL	SRGQIVFMNR	EPKRTLTSVS	VFVDHHLAPS	FYFVAFYYHG	DHPVANSLRV
570	580	590	600	610	620	630	640
DVQAGACEGK	LELSVDGAKQ	YRNGESVKLH	LETDSLALVA	LGALDTALYA	AGSKSHKPLN	MGKVFEAMNS	YDLGCGPGGG
650	660	670	680	690	700	710	720
DSALQVFQAA	GLAFSDGDQW	TLSRKRLSCP	KEKTTRKKRN	VNFQKAINEK	LGQYASPTAK	RCCQDGVTRL	PMMRSCEQRA
730	740	750	760	770	780	790	800
ARVQQPDCRE	PFLSCCQFAE	SLRKKSRDKG	QAGLQRALEI	LQEEDLIDED	DIPVRSFFPE	NWLWRVETVD	RFQILTLWLP
810	820	830	840	850	860	870	880
DSLTTWEIHG	LSLSKTKGLC	VATPVQLRVF	REFHLHLRLP	MSVRRFEQLE	LRPVLYNYLD	KNLTVSVHVS	PVEGLCLAGG
890	900	910	920	930	940	950	960
GGLAQQVLVP	AGSARPVAFS	VVPTAAAAVS	LKVVARGSFE	FPVGDAVSKV	LQIEKEGAIH	REELVYELNP	LDHRGRTLEI
970	980	990	1000	1010	1020	1030	1040
PGNSDPNMIP	DGDFNSYVRV	TASDPLDTLG	SEGALSPGGV	ASLLRLPRGC	GEQTMIYLAP	TLAASRYLDK	TEQWSTLPPE
1050	1060	1070	1080	1090	1100	1110	1120
TKDHAVDLIQ	KGYMRIQQFR	KADGSYAAWL	SRDSSTWLTA	FVLKVLSLAQ	EQVGGSPEKL	QETSNWLLSQ	QQADGSFQDP
1130	1140	1150	1160	1170	1180	1190	1200
CPVLDRSMQG	GLVGNDETVA	LTAFVTIALH	HGLAVFQDEG	AEPLKQRVEA	SISKANSFLG	EKASAGLLGA	HAAAITAYAL
1210	1220	1230	1240	1250	1260	1270	1280
TLTKAPVDLL	GVAHNNLMAM	AQETGDNLYW	GSVTGSQSNA	VSPTPAPRNP	SDPMPQAPAL	WIETTAYALL	HLLLHEGKAE
1290	1300	1310	1320	1330	1340	1350	1360
MADQASAWLT	RQGSFQGGFR	STQDTVIALD	ALSAYWIASH	TTEERGLNVT	LSSTGRNGFK	SHALQLNNRQ	IRGLEEELQF
1370	1380	1390	1400	1410	1420	1430	1440
SLGSKINVKV	GGNSKGTLKV	LRTYNVLDMK	NTTCQDLQIE	VTVKGHVEYT	MEANEDYEDY	EYDELPAKDD	PDAPLQPVTP
1450	1460	1470	1480	1490	1500	1510	1520
LQLFEGRRNR	RRREAPKLTS	LSDRYVSHFE	TEGPHVLLYF	DSVPTSRECV	GFEAVQEVPV	GLVQPASATL	YDYYNPERRC
1530	1540	1550	1560	1570	1580	1590	1600
SVFYGAPSKS	RLLATLCSAE	VCQCAEGKCP	RQRRALERGL	QDEDGYRMKF	ACYYPRVEYG	FQVKVLREDS	RAAFRLFETK
1610	1620	1630	1640	1650	1660	1670	1680
ITQVLHFTKD	VKAAANQMRN	FLVRASCRLR	LEPGKEYLIM	GLDGATYDLE	GHPQYLLDSN	SWIEEMPSER	LCRSTRQRAA
1690	1700						
CAQLNDFLQE	YGTQGCQV						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1442	2	1061.4940	-67.98	2	47.8	19.8	1	119-137	K.DSLSRTTNIQGINLLFSSR.R	

Detailed Protein Report

Protein 242: PREDICTED: zinc finger protein 468 isoform X2 [Homo sapiens]

Accession:	gi|578835091	**Score:**	31.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	54.3
Database Date:	2015-11-30	**pI:**	10.3
		Sequence Coverage [%]:	4.5
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MLKTLSSTGQ	GNTEVIHTGT	LHRQASHHIG	EFCFHEIEKD	IHGFEFQWKE	DETNGHAAPM	TEIKELAGST	GQHDQRHAGN
90	100	110	120	130	140	150	160
KRIKDQLGSS	FHLHLPEPHI	FQSEGKIGNQ	VEKSINNASS	VSTSQRICCR	PKTHISNKYG	NNSLHSSLLT	QKWEVHMREK
170	180	190	200	210	220	230	240
SFECIQSFKS	FNCSSLLKKH	QIIHLEEKQC	KCDVCGKVFN	QKRYLACHRR	CHTGEKPYKC	NECGKTFGHN	SSLFIHKALH
250	260	270	280	290	300	310	320
TGEKPYECEE	CDKVFSRKSH	LERHKRIHTG	EKPYKCKVCD	EAFAYNSYLA	KHTILHTGEK	PYTCNECGKV	FNRLSTLARH
330	340	350	360	370	380	390	400
HRLHTGEKPY	KCEECDKVFS	RKSHLERHRR	IHSGEKPYKC	EECCKVFSRK	SNLERHRRIH	TGEKPYKCKV	CDKAFQRDSH
410	420	430	440	450	460	470	
LAQHQRVHTG	EKPYKCNECG	KTFGQTSSLI	IHRRLHTGEK	PYKCNECGKT	FSQMSSLVYH	HRLHSGEKP	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1828	7	673.2559	-104.81	2	52.9	19.8	1	159-169	R.EKSFECIQSFK.S	
232	1	563.7487	-90.74	2	32.3	11.2	1	170-179	K.SFNCSSLLKK.H	

Detailed Protein Report

Protein 243: PREDICTED: pericentrin isoform X7 [Homo sapiens]

Accession:	gi|530419256	**Score:**	31.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	305.6
Database Date:	2015-11-30	**pI:**	4.9
		Sequence Coverage [%]:	1.1
		No. of unique Peptides:	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MEVEQEQRRR	KVEAGRTKLA	HFRQRKTKGD	SSHSEKKTAK	RKGSAVDASV	QEESPVTKED	SALCGGGDIC	KSTSCDDTPD
90	100	110	120	130	140	150	160
GAGGAFAAQP	EDCDGEKRED	LEQLQQKQVN	DHPPEQCGMF	TVSDHPPEQH	GMFTVGDHPP	EQRGMFTVSD	HPPEQHGMFT
170	180	190	200	210	220	230	240
VSDHPPEQRG	MFTISDHQPE	QRGMFTVSDH	TPEQRGIFTI	SDHPAEQRGM	FTKECEQECE	LAITDLESGR	EDEAGLHQSQ
250	260	270	280	290	300	310	320
AVHGLELEAL	RLSLSNMHTA	QLELTQANLQ	KEKETALTEL	REMLNSRRAQ	ELALLQSRQQ	HELELLREQH	AREKEEVVLR
330	340	350	360	370	380	390	400
CGQEAAELKE	KLQSEMEKNA	QIVKTLKEDW	ESEKDLCLEN	LRKELSAKHQ	SEMEDLQNQF	QKELAEQRAE	LEKIFQDKNQ
410	420	430	440	450	460	470	480
AERALRNLES	HHQAAIEKLR	EDLQSEHGRC	LEDLEFKFKE	SEKEKQLELE	NLQASYEDLK	AQSQEEIRRL	WSQLDSARTS
490	500	510	520	530	540	550	560
RQELSELHEQ	LLARTSRVED	LEQLKQREKT	QHESELEQLR	IYFEKKLRDA	EKTYQEDLTL	LQQRLQGARE	DALLDSVEVG
570	580	590	600	610	620	630	640
LSCVGLEEKP	EKGRKDHVDE	LEPERHKESL	PRFQAELEES	HRHQLEALES	PLCIQHEGHV	SDRCCVETSA	LGHEWRLEPS
650	660	670	680	690	700	710	720
EGHSQELPWV	HLQGVQDGDL	EADTERAARV	LGLETEHKVQ	LSLLQTELKE	EIELLKIENR	NLYGKLQHET	RLKDDLEKVK
730	740	750	760	770	780	790	800
HNLIEDHQKE	LNNAKQKTEL	MKQEFQRKET	DWKVMKEELQ	REAEEKLTLM	LLELREKAES	EKQTIINKFE	LREAEMRQLQ
810	820	830	840	850	860	870	880
DQQAAQILDL	ERSLTEQQGR	LQQLEQDLTS	DDALHCSQCG	REPPTAQDGE	LAALHVKEDC	ALQLMLARSR	FLEERKEITE
890	900	910	920	930	940	950	960
KFSAEQDAFL	QEAQEQHARE	LQLLQERHQQ	QLLSVTAELE	ARHQAALGEL	TASLESKQGA	LLAARVAELQ	TKHAADLGAL
970	980	990	1000	1010	1020	1030	1040
ETRHLSSLDS	LESCYLSEFQ	TIREEHRQAL	ELLRADFEEQ	LWKKDSLHQT	ILTQELEKLK	RKHEGELQSV	RDHLRTEVST
1050	1060	1070	1080	1090	1100	1110	1120
ELAGTVAHEL	QGVHQGEFGS	EKKTALHEKE	ETLRLQSAQA	QPFHQEEKES	LSLQLQKKNH	QVQQLKDQVL	SLSHEIEECR
1130	1140	1150	1160	1170	1180	1190	1200
SELEVLQQRR	ERENREGANL	LSMLKADVNL	SHSERGALQD	ALRRLLGLFG	ETLRAAVTLR	SRIGERVGLC	LDDAGAGLAL
1210	1220	1230	1240	1250	1260	1270	1280
STAPALEETW	SDVALPELDR	TLSECAEMSS	VAEISSHMRE	SFLMSPESVR	ECEQPIRRVF	QSLSLAVDGL	MEMALDSSRQ
1290	1300	1310	1320	1330	1340	1350	1360
LEEARQIHSR	FEKEFSFKNE	ETAQVVRKHQ	ELLECLKEES	AAKAELALEL	HKTQGTLEGF	KVETADLKEV	LAGKEDSEHR
1370	1380	1390	1400	1410	1420	1430	1440
LVLELESLRR	QLQQAAQEQA	ALREECTRLW	SRGEATATDA	EAREAGTAVT	AAHKDSALRK	EVEDLTKEQS	ETRKQAEKDR
1450	1460	1470	1480	1490	1500	1510	1520
SALLSQMKIL	ESELEEQLSQ	HRGCAKQAEA	VTALEQQVAS	LDKHLRNQRQ	FMDEQAAERE	HEREEFQQEI	QRLEGQLRQA
1530	1540	1550	1560	1570	1580	1590	1600
AKPQPWGPRD	SQQAPLDGEV	ELLQQKLREK	LDEFNELAIQ	KESADRQVLM	QEEEIKRLEE	MNINIRKKVA	QLQEEVEKQK
1610	1620	1630	1640	1650	1660	1670	1680
NIVKGLEQDK	EVLKKQQMSS	LLLASTLQST	LDAGRCPEPP	SGSPPEGPEI	QLEVTQRALL	RRESEVLDLK	EQLEKMKGDL
1690	1700	1710	1720	1730	1740	1750	1760
ESKNEEILHL	NLKLDMQNSQ	TAVSLRELEE	ENTSLKVIYT	RSSEIEELKA	TIENLQENQK	RLQKEKAEEI	EQLHEVIEKL
1770	1780	1790	1800	1810	1820	1830	1840
QHELSLMGPV	VHEVSDSQAG	SLQSELLCSQ	AGGPRGQALQ	GELEAALEAK	EALSRLLADQ	ERRHSQALEA	LQQRLQGAEE
1850	1860	1870	1880	1890	1900	1910	1920
AAELQLAELE	RNVALREAEV	EDMASRIQEF	EAALKAKEAT	IAERNLEIDA	LNQRKAAHSA	ELEAVLLALA	RIRRALEQQP
1930	1940	1950	1960	1970	1980	1990	2000
LAAGAAPPEL	QWLRAQCARL	SRQLQVLHQR	FLRCQVELDR	RQARRATAHT	RVPGAHPQPR	MDGGAKAQVT	GDVEASHDAA
2010	2020	2030	2040	2050	2060	2070	2080
LEPVVPDPQG	DLQPVLVTLK	DAPLCKQEGV	MSVLTVCQRQ	LQSELLLVKN	EMRLSLEDGG	KGKEKVLEDC	QLPKVDLVAQ
2090	2100	2110	2120	2130	2140	2150	2160
VKQLQEKLNR	LLYSMTFQNV	DAADTKSLWP	MASAHLLESS	WSDDSCDGEE	PDISPHIDTC	DANTATGGVT	DVIKNQAIDA
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
2759	2	1044.5699	44.47	2	64.9	15.2	2	1291-1307	R.FEKEFSFKNEETAQVVR.K	

Detailed Protein Report

Protein 244: PREDICTED: tubulin polyglutamylase TTLL4 isoform X5 [Homo sapiens]

Accession:	gi|578805262	**Score:**	31.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	127.2
Database Date:	2015-11-30	**pI:**	9.9
		Sequence Coverage [%]:	1.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MASAGTQHYS	IGLRQKNSFK	QSGPSGTVPA	TPPEKPSEGR	VWPQAHQQVK	PIWKLEKKQV	ETLSAGLGPG	LLGVPPQPAY
90	100	110	120	130	140	150	160
FFCPSTLCSS	GTTAVIAGHS	SSCYLHSLPD	LFNSTLLYRR	SSYRQKPYQQ	LESFCLRSSP	SEKSPFSLPQ	KSLPVSLTAN
170	180	190	200	210	220	230	240
KATSSMVFSM	AQPMASSSTE	PYLCLAAAGE	NPSGKSLASA	ISGKIPSPLS	SSYKPMLNNN	SFMWPNSTPV	PLLQTTQGLK
250	260	270	280	290	300	310	320
PVSPPKIQPV	SWHHSGGTGD	CAPQPVDHKV	PKSIGTVPAD	ASAHIALSTA	SSHDTSTTSV	ASSWYNRNNL	AMRAEPLSCA
330	340	350	360	370	380	390	400
LDDSSDSQDP	TKEIRFTEAV	RKLTARGFEK	MPRQGCQLEQ	SSFLNPSFQW	NVLNRSRRWK	PPAVNQQFPQ	EDAGSVRRVL
410	420	430	440	450	460	470	480
PGASDTLGLD	NTVFCTKRIS	IHLLASHASG	LNHNPACESV	IDSSAFGEGK	APGPPFPQTL	GIANVATRLS	SIQLGQSEKE
490	500	510	520	530	540	550	560
RPEEARELDS	SDRDISSATD	LQPDQAETED	TEEELVDGLE	DCCSRDENEE	EEGDSECSSL	SAVSPSESVA	MISRSCMEIL
570	580	590	600	610	620	630	640
TKPLSNHEKV	VRPALIYSLF	PNVPPTIYFG	TRDERVEKLP	WEQRKLLRWK	MSTVTPNIVK	QTIGRSHFKI	SKRNDDWLGC
650	660	670	680	690	700	710	720
WGHHMKSPSF	RSIREHQKLN	HFPGSFQIGR	KDRLWRNLSR	MQSRFGKKEF	SFFPQSFILP	QDAKLLRKAW	ESSSRQKWIV
730	740	750	760	770	780	790	800
KPPASARGIG	IQVIHKWSQL	PKRRPLLVQR	YLHKPYLISG	SKFDLRIYVY	VTSYDPLRIY	LFSDGLVRFA	SCKYSPSMKS
810	820	830	840	850	860	870	880
LGNKFMHLTN	YSVNKKNAEY	QANADEMACQ	GHKWALKALW	NYLSQKGVNS	DAIWEKIKDV	VVKTIISSEP	YVTSLLKMYV
890	900	910	920	930	940	950	960
RRPYSCHELF	GFDIMLDENL	KPWVLEVNIS	PSLHSSSPLD	ISIKGQMIRD	LLNLAGFVLP	NAEDIISSPS	SCSSSTTSLP
970	980	990	1000	1010	1020	1030	1040
TSPGDKCRMA	PEHVTAQKMK	KAYYLTQKIP	DQDFYASVLD	VLTPDDVRIL	VEMEDEFSRR	GQFERIFPSH	ISSRYLRFFE
1050	1060	1070	1080	1090	1100	1110	1120
QPRYFNILTT	QWEQKYHGNK	LKGVDLLRSW	CYKGFHMGVV	SDSAPVWSLP	TSLLTISKDD	VILNAFSKSE	TSKLGNPVPQ
1130	1140						
RTVRTPAKSP	AFLPRRYL						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
445	1	592.8266	3.11	2	34.9	13.4	1	596-604	R.VEKLPWEQR.K	

Detailed Protein Report

Protein 245: dystrophin Dp260-2 isoform [Homo sapiens]

Accession:	gi|5032291	**Score:**	30.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	270.9
Database Date:	2015-11-30	**pI:**	5.9
		Sequence Coverage [%]:	0.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSARKLRNLS	YKKAVRRQKL	LEQSIQSAQE	TEKSLHLIQE	SLTFIDKQLA	AYIADKVDAA	QMPQEAQKIQ	SDLTSHEISL
90	100	110	120	130	140	150	160
EEMKKHNQGK	EAAQRVLSQI	DVAQKKLQDV	SMKFRLFQKP	ANFEQRLQES	KMILDEVKMH	LPALETKSVE	QEVVQSQLNH
170	180	190	200	210	220	230	240
CVNLYKSLSE	VKSEVEMVIK	TGRQIVQKKQ	TENPKELDER	VTALKLHYNE	LGAKVTERKQ	QLEKCLKLSR	KMRKEMNVLT
250	260	270	280	290	300	310	320
EWLAATDMEL	TKRSAVEGMP	SNLDSEVAWG	KATQKEIEKQ	KVHLKSITEV	GEALKTVLGK	KETLVEDKLS	LLNSNWIAVT
330	340	350	360	370	380	390	400
SRAEEWLNLL	LEYQKHMETF	DQNVDHITKW	IIQADTLLDE	SEKKKPQQKE	DVLKRLKAEL	NDIRPKVDST	RDQAANLMAN
410	420	430	440	450	460	470	480
RGDHCRKLVE	PQISELNHRF	AAISHRIKTG	KASIPLKELE	QFNSDIQKLL	EPLEAEIQQG	VNLKEEDFNK	DMNEDNEGTV
490	500	510	520	530	540	550	560
KELLQRGDNL	QQRITDERKR	EEIKIKQQLL	QTKHNALKDL	RSQRRKKALE	ISHQWYQYKR	QADDLLKCLD	DIEKKLASLP
570	580	590	600	610	620	630	640
EPRDERKIKE	IDRELQKKKE	ELNAVRRQAE	GLSEDGAAMA	VEPTQIQLSK	RWREIESKFA	QFRRLNFAQI	HTVREETMMV
650	660	670	680	690	700	710	720
MTEDMPLEIS	YVPSTYLTEI	THVSQALLEV	EQLLNAPDLC	AKDFEDLFKQ	EESLKNIKDS	LQQSSGRIDI	IHSKKTAALQ
730	740	750	760	770	780	790	800
SATPVERVKL	QEALSQLDFQ	WEKVNKMYKD	RQGRFDRSVE	KWRRFHYDIK	IFNQWLTEAE	QFLRKTQIPE	NWEHAKYKWY
810	820	830	840	850	860	870	880
LKELQDGIGQ	RQTVVRTLNA	TGEEIIQQSS	KTDASILQEK	LGSLNLRWQE	VCKQLSDRKK	RLEEQKNILS	EFQRDLNEFV
890	900	910	920	930	940	950	960
LWLEEADNIA	SIPLEPGKEQ	QLKEKLEQVK	LLVEELPLRQ	GILKQLNETG	GPVLVSAPIS	PEEQDKLENK	LKQTNLQWIK
970	980	990	1000	1010	1020	1030	1040
VSRALPEKQG	EIEAQIKDLG	QLEKKLEDLE	EQLNHLLLWL	SPIRNQLEIY	NQPNQEGPFD	VQETEIAVQA	KQPDVEEILS
1050	1060	1070	1080	1090	1100	1110	1120
KGQHLYKEKP	ATQPVKRKLE	DLSSEWKAVN	RLLQELRAKQ	PDLAPGLTTI	GASPTQTVTL	VTQPVVTKET	AISKLEMPSS
1130	1140	1150	1160	1170	1180	1190	1200
LMLEVPALAD	FNRAWTELTD	WLSLLDQVIK	SQRVMVGDLE	DINEMIIKQK	ATMQDLEQRR	PQLEELITAA	QNLKNKTSNQ
1210	1220	1230	1240	1250	1260	1270	1280
EARTIITDRI	ERIQNQWDEV	QEHLQNRRQQ	LNEMLKDSTQ	WLEAKEEAEQ	VLGQARAKLE	SWKEGPYTVD	AIQKKITETK
1290	1300	1310	1320	1330	1340	1350	1360
QLAKDLRQWQ	TNVDVANDLA	LKLLRDYSAD	DTRKVHMITE	NINASWRSIH	KRVSEREAAL	EETHRLLQQF	PLDLEKFLAW
1370	1380	1390	1400	1410	1420	1430	1440
LTEAETTANV	LQDATRKERL	LEDSKGVKEL	MKQWQDLQGE	IEAHTDVYHN	LDENSQKILR	SLEGSDDAVL	LQRRLDNMNF
1450	1460	1470	1480	1490	1500	1510	1520
KWSELRKKSL	NIRSHLEASS	DQWKRLHLSL	QELLVWLQLK	DDELSRQAPI	GGDFPAVQKQ	NDVHRAFKRE	LKTKEPVIMS
1530	1540	1550	1560	1570	1580	1590	1600
TLETVRIFLT	EQPLEGLEKL	YQEPRELPPE	ERAQNVTRLL	RKQAEEVNTE	WEKLNLHSAD	WQRKIDETLE	RLQELQEATD
1610	1620	1630	1640	1650	1660	1670	1680
ELDLKLRQAE	VIKGSWQPVG	DLLIDSLQDH	LEKVKALRGE	IAPLKENVSH	VNDLARQLTT	LGIQLSPYNL	STLEDLNTRW
1690	1700	1710	1720	1730	1740	1750	1760
KLLQVAVEDR	VRQLHEAHRD	FGPASQHFLS	TSVQGPWERA	ISPNKVPYYI	NHETQTTCWD	HPKMTELYQS	LADLNNVRFS
1770	1780	1790	1800	1810	1820	1830	1840
AYRTAMKLRR	LQKALCLDLL	SLSAACDALD	QHNLKQNDQP	MDILQIINCL	TTIYDRLEQE	HNNLVNVPLC	VDMCLNWLLN
1850	1860	1870	1880	1890	1900	1910	1920
VYDTGRTGRI	RVLSFKTGII	SLCKAHLEDK	YRYLFKQVAS	STGFCDQRRL	GLLLHDSIQI	PRQLGEVASF	GGSNIEPSVR
1930	1940	1950	1960	1970	1980	1990	2000
SCFQFANNKP	EIEAALFLDW	MRLEPQSMVW	LPVLHRVAAA	ETAKHQAKCN	ICKECPIIGF	RYRSLKHFNY	DICQSCFFSG
2010	2020	2030	2040	2050	2060	2070	2080
RVAKGHKMHY	PMVEYCTPTT	SGEDVRDFAK	VLKNKFRTKR	YFAKHPRMGY	LPVQTVLEGD	NMETPVTLIN	FWPVDSAPAS
2090	2100	2110	2120	2130	2140	2150	2160
SPQLSHDDTH	SRIEHYASRL	AEMENSNGSY	LNDSISPNES	IDDEHLLIQH	YCQSLNQDSP	LSQPRSPAQI	LISLESEERG
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
982	1	712.1299	-301.49	1	41.8	17.8	1	747-751	K.MYKDR.Q	

Detailed Protein Report

Protein 246: PREDICTED: SH2 domain-containing adapter protein E isoform X1 [Homo sapiens]

Accession:	gi|530364158	**Score:**	30.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	47.7
Database Date:	2015-11-30	**pI:**	9.9
		Sequence Coverage [%]:	5.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MQWSPTPGAS	ACLGWASSLA	CSTAPTLLGR	AGRGPLMAAK	WFKEFPLNLK	TVSERAKPGG	GGGKLRKNSE	AGGAGPGPGK
90	100	110	120	130	140	150	160
GRKNSAAELG	SGRAGVGPKD	SRLSRDSLQG	LIQAAAGKGR	KNSRATEEEP	HRGATKSSGC	STYINRLIKV	DTQEKNGKSN
170	180	190	200	210	220	230	240
YPSSSSSSSS	SSSSASSSPS	SLGPELDKGK	IIKQQETVII	LEDYADPYDA	KRTKGQRDAE	RVGENDGYME	PYDAQQMITE
250	260	270	280	290	300	310	320
IRRRGSKDPL	VKALQLLDSP	CEPADGGLKS	ETLAKRRSSK	DLLGKPPQLY	DTPYEPAEGG	PRAEGKARPP	DSRLPENDER
330	340	350	360	370	380	390	400
PAAEYEQPWE	WKKEQIVRAL	SVQFEGAERP	SFREETVRQH	HRQKSWTQKI	LKPALSDHSE	GEKVDPGLPL	EKQPWYHGAI
410	420	430	440	450			
SRAEAESRLQ	PCKEAGYLVR	NSESGNSRYS	IALKNHHLLS				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2769	1	863.9639	30.41	2	65.0	11.1	0	253-269	K.ALQLLDSPCEPADGGLK.S	

Detailed Protein Report

Protein 247: PREDICTED: short transient receptor potential channel 7 isoform X1 [Homo sapiens]

Accession:	gi|530380051	**Score:**	30.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	55.5
Database Date:	2015-11-30	**pI:**	9.0
		Sequence Coverage [%]:	4.8
		No. of unique Peptides:	2

```
        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
965	1	607.1283	-333.12	1	41.6	14.2	0	342-346	K.MCLIK.L	
1931	1	1022.8987	-78.15	2	54.2	16.6	2	352-369	K.AKSCENDLEMGMLNSKFK.K	

Detailed Protein Report

Protein 248: **PREDICTED: PR domain zinc finger protein 1 isoform X1 [Homo sapiens]**

Accession:	gi|530383954	**Score:**	30.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	73.8
Database Date:	2015-11-30	**pI:**	9.9
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.6
		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
1164	3	598.6419	-220.44	2	44.1	12.0	0	129-138	R.GSPEMPFYPR.V	Oxidation: 5

Detailed Protein Report

Protein 249: **MAP7 domain-containing protein 2 isoform 4 [Homo sapiens]**

Accession:	gi|270483747	**Score:**	30.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	76.6
Database Date:	2015-11-30	**pI:**	9.4
		Sequence Coverage [%]:	3.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEGFLKSDER	QRLAKERREE	REKCLAAREQ	QILEKQKRAR	LQYEKQMEER	WRKLEEQRQR	EDQKRAAVEE	KRKQKLREEE
90	100	110	120	130	140	150	160
ERLEAMMRRS	LERTQQLELK	KKYSWGAPLA	IGPGGHDACD	KLSTSTMSLP	KPTEPPMNKR	LSSSTVAISY	SPDRAPLGPL
170	180	190	200	210	220	230	240
NPSYKSSPTR	NIEKKKATST	STSGAGDVGK	EALSGGEASL	VEKVKRGQRT	ATSLPVVNFG	SPLRRCEFSG	GIPKRPSSPV
250	260	270	280	290	300	310	320
ISKTATKAYP	QSPKTTKPPY	PGSPVKYRLP	ALSGQDMPKR	KAEKEKSNKE	REGTLAQQAA	GPQGEEALEK	HVVDKHASEK
330	340	350	360	370	380	390	400
HAAAAGGKAE	NSAALGKPTA	GTTDAGEAAK	ILAEKRRQAR	LQKEQEEQER	LEKEEQDRLE	REELKRKAEE	ERLRLEEEAR
410	420	430	440	450	460	470	480
KQEEERKRQE	EEKKKQEGEE	KRKAGEEAKR	KAEEELLLKE	KQEQEKQEKA	MIEKQKEAAE	TKAREVAEQM	RLEREQIMLQ
490	500	510	520	530	540	550	560
IEQERLERKK	RIDEIMKRTR	KSDVSPQVKK	EDPKVGVQPA	VCVEKKTKLV	VPNKMEINGL	NTCQEVNGVD	HAAPETYPQD
570	580	590	600	610	620	630	640
IFSNGLKPAG	GLIHLDALDG	KSNSLDDSTE	EVQSMDVSPV	SKEELISIPE	FSPVSEMIPG	VSLDQNGTGN	ARALQDLLDF
650	660	670	680	690			
TGPPTFPKRS	SENLSLDDCN	KNLIEGFNSP	GQETPLNTFC				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1648	1	575.1737	-226.87	2	50.5	13.4	1	311-320	K.HVVDKHASEK.H	

Detailed Protein Report

Protein 250: chromodomain-helicase-DNA-binding protein 8 isoform 2 [Homo sapiens]

Accession:	gi|114326455	**Score:**	30.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	262.2
Database Date:	2015-11-30	**pI:**	6.2
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MKGESKRITL	VLQQPQSGGP	QGHRHVVLGS	LPGKIVLQGN	QLAALTQAKN	AQGQPAKVVT	IQLQVQQPQQ	KIQIVPQPPS
90	100	110	120	130	140	150	160
SQPQPQQPPS	TQPVTLSSVQ	QAQIMGPGQS	PGQRLSVPVK	VVLQPQAGSS	QGASSGLSVV	KVLSASEVAA	LSSPASSAPH
170	180	190	200	210	220	230	240
SGGKTGMEEN	RRLEHQKKQE	KANRIVAEAI	ARARARGEQN	IPRVLNEDEL	PSVRPEEEGE	KKRRKKSAGE	RLKEEKPKKS
250	260	270	280	290	300	310	320
KTSGASKTKG	KSKLNTITPV	VGKKRKRNTS	SDNSDVEVMP	AQSPREDEES	SIQKRRSNRQ	VKRKKYTEDL	DIKITDDEEE
330	340	350	360	370	380	390	400
EEVDVTGPIK	PEPILPEPVQ	EPDGETLPSM	QFFVENPSEE	DAAIVDKVLS	MRIVKKELPS	GQYTEAEEFF	VKYKNYSYLH
410	420	430	440	450	460	470	480
CEWATISQLE	KDKRIHQKLK	RFKTKMAQMR	HFFHEDEEPF	NPDYVEVDRI	LDESHSIDKD	NGEPVIYYLV	KWCSLPYEDS
490	500	510	520	530	540	550	560
TWELKEDVDE	GKIREFKRIQ	SRHPELKRVN	RPQASAWKKL	ELSHEYKNRN	QLREYQLEGV	NWLLFNWYNR	QNCILADEMG
570	580	590	600	610	620	630	640
LGKTIQSIAF	LQEVYNVGIH	GPFLVIAPLS	TITNWEREFN	TWTEMNTIVY	HGSLASRQMI	QQYEMYCKDS	RGRLIPGAYK
650	660	670	680	690	700	710	720
FDALITTFEM	ILSDCPELRE	IEWRCVIIDE	AHRLKNRNCK	LLDSLKHMDL	EHKVLLTGTP	LQNTVEELFS	LLHFLEPSQF
730	740	750	760	770	780	790	800
PSESEFLKDF	GDLKTEEQVQ	KLQAILKPMM	LRRLKEDVEK	NLAPKQETII	EVELTNIQKK	YYRAILEKNF	SFLSKGAGHT
810	820	830	840	850	860	870	880
NMPNLLNTMM	ELRKCCNHPY	LINGAEEKIL	TEFREACHII	PHDFHLQAMV	RSAGKLVLID	KLLPKLKAGG	HKVLIFSQMV
890	900	910	920	930	940	950	960
RCLDILEDYL	IQRRYLYERI	DGRVRGNLRQ	AAIDRFSKPD	SDRFVFLLCT	RAGGLGINLT	AADTCIIFDS	DWNPQNDLQA
970	980	990	1000	1010	1020	1030	1040
QARCHRIGQS	KAVKVYRLIT	RNSYEREMFD	KASLKLGLDK	AVLQSMSGRD	GNITGIQQFS	KKEIEDLLRK	GAYAAIMEED
1050	1060	1070	1080	1090	1100	1110	1120
DEGSKFCEED	IDQILLRRTT	TITIESEGKG	STFAKASFVA	SENRTDISLD	DPNFWQKWAK	KADLDMDLLN	SKNNLVIDTP
1130	1140	1150	1160	1170	1180	1190	1200
RVRKQTRHFS	TLKDDDLVEF	SDLESEDDER	PRSRRHDRHH	AYGRTDCFRV	EKHLLVYGWG	RWRDILSHGR	FKRRMTERDV
1210	1220	1230	1240	1250	1260	1270	1280
ETICRAILVY	CLLHYRGDEN	IKGFIWDLIS	PAENGKTKEL	QNHSGLSIPV	PRGRKGKKVK	SQSTFDIHKA	DWIRKYNPDT
1290	1300	1310	1320	1330	1340	1350	1360
LFQDESYKKH	LKHQCNKVLL	RVRMLYYLRQ	EVIGDQAEKV	LGGAIASEID	IWFPVVDQLE	VPTTWWDSEA	DKSLLIGVFK
1370	1380	1390	1400	1410	1420	1430	1440
HGYEKYNTMR	ADPALCFLEK	AGRPDDKAIA	AEHRVLDNFS	DIVEGVDFDK	DCEDPEYKPL	QGPPKDQDDE	GDPLMMMDEE
1450	1460	1470	1480	1490	1500	1510	1520
ISVIDGDEAQ	VTQQPGHLFW	PPGSALTARL	RRLVTAYQRS	YKREQMKIEA	AERGDRRRRR	CEAAFKLKEI	ARREKQQRWT
1530	1540	1550	1560	1570	1580	1590	1600
RREQTDFYRV	VSTFGVEYDP	DTMQFHWDRF	RTFARLDKKT	DESLTKYFHG	FVAMCRQVCR	LPPAAGDEPP	DPNLFIEPIT
1610	1620	1630	1640	1650	1660	1670	1680
EERASRTLYR	IELLRRLREQ	VLCHPLLEDR	LALCQPPGPE	LPKWWEPVRH	DGELLRGAAR	HGVSQTDCNI	MQDPDFSFLA
1690	1700	1710	1720	1730	1740	1750	1760
ARMNYMQNHQ	AGAPAPSLSR	CSTPLLHQQY	TSRTASPLPL	RPDAPVEKSP	EETATQVPSL	ESLTLKLEHE	VVARSRPTPQ
1770	1780	1790	1800	1810	1820	1830	1840
DYEMRVSPSD	TTPLVSRSVP	PVKLEDEDDS	DSELDLSKLS	PSSSSSSSSS	SSSSSTDESE	DEKEEKLTDQ	SRSKLYDEES
1850	1860	1870	1880	1890	1900	1910	1920
LLSLTMSQDG	FPNEDGEQMT	PELLLLQERQ	RASEWPKDRV	LINRIDLVCQ	AVLSGKWPSS	RRSQEMVTGG	ILGPGNHLLD
1930	1940	1950	1960	1970	1980	1990	2000
SPSLTPGEYG	DSPVPTPRSS	SAASMAEEEA	SAVSTAAAQF	TKLRRGMDEK	EFTVQIKDEE	GLKLTFQKHK	LMANGVMGDG
2010	2020	2030	2040	2050	2060	2070	2080
HPLFHKKKGN	RKKLVELEVE	CMEEPNHLDV	DLETRIPVIN	KVDGTLLVGE	DAPRRAELEM	WLQGHPEFAV	DPRFLAYMED
2090	2100	2110	2120	2130	2140	2150	2160
RRKQKWQRCK	KNNKAELNCL	GMEPVQTANS	RNGKKGHHTE	TVFNRVLPGP	IAPESSKKRA	RRMRPDLSKM	MALMQGGSTG
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
1309	1	863.9074	-143.00	2	46.0	10.4	2	742-755	K.LQAILKPMMLRRLK.E	Oxidation: 8

Detailed Protein Report

Protein 251: **PREDICTED: ras-GEF domain-containing family member 1B isoform X2 [Homo sapiens]**

Accession:	gi|530377246	**Score:**	30.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	50.3
Database Date:	2015-11-30	**pI:**	9.0
		Sequence Coverage [%]:	6.3
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 3.28 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MPQTPPFSAM	FDSSGYNRNL	YQSAEDSCGG	LYYHDNNLLS	GSLEALIQHL	VPNVDYYPDN	QMRKIAPKIL	QLLTEWTETF
90	100	110	120	130	140	150	160
PYDFRDERMM	RNLKDLAHRI	ASGEETYRKN	VQQMMQCLIR	KLAALSQYEE	VLAKISSTST	DRLTVLKTKP	QSIQRDIITV
170	180	190	200	210	220	230	240
CNDPYTLAQQ	LTHIELERLN	YIGPEEFVQA	FVQKDPLDND	KSCYSERKKT	RNLEAYVEWF	NRLSYLVATE	ICMPVKKKHR
250	260	270	280	290	300	310	320
ARMIEYFIDV	ARECFNIGNF	NSLMAIISGM	NMSPVSRLKK	TWAKVKTAKF	DILEHQMDPS	SNFYNYRTAL	RGAAQRSLTA
330	340	350	360	370	380	390	400
HSSREKIVIP	FFSLLIKDIY	FLNEGCANRL	PNGHVNFEKF	WELAKQVSEF	MTWKQVECPF	ERDRKILQYL	LTVPVFSEDA
410	420	430	440				
LYLASYESEG	PENHIEKDRW	KSLRSSLLGR	V				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
2529	1	913.4616	-10.11	2	62.1	13.5	2	209-222	K.KTRNLEAYVEWFNR.L		MD:MU	3.28

Detailed Protein Report

Protein 252: PREDICTED: collagen alpha-2(I) chain-like [Homo sapiens]

Accession:	gi|530375734	**Score:**	30.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	28.8
Database Date:	2015-11-30	**pI:**	12.9
		Sequence Coverage [%]:	5.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAPFHLSHAP	AGARKVKLRH	PRKWSPSGSP	QPPAQLQPLE	APRLPGEVRT	SGRLATWFCR	LLARRSAAQR	KSKSRKDLNR
90	100	110	120	130	140	150	160
RVQSPLTPHS	FHYFSSQGIG	GGGGGRDKFA	GRLAWSNPRG	WDRPRGSGGA	LPRPEGDCGG	ARPPAGGAGR	WASPGAAGRW
170	180	190	200	210	220	230	240
SLPGRVCGAF	AQPAPCPHLT	SSPPRPLGGP	LRCAAQARSV	AARAVRPRSL	GQGPGAQGVG	RAGRERGRPS	TASGSARAGA
250	260	270	280				
ALPAAVRPRE	GPRGPSACAL	GRRRLCVGRP	GGPRGTD				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2843	4	731.8776	7.32	2	66.0	30.6	0	1-14	-.MAPFHLSHAPAGAR.K	

Detailed Protein Report

Protein 253: PREDICTED: serine/arginine repetitive matrix protein 1-like [Homo sapiens]

Accession:	gi|578794871	**Score:**	30.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	45.0
Database Date:	2015-11-30	**pI:**	12.4
		Sequence Coverage [%]:	7.5
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 3.28 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MTVATKSQRS	LSARCGTELA	QQGKPGPRAL	SFSLAQPQCS	AGYGLRKPQL	PYVKNGGQEI	HGLLRARVHP	CMAVNAPPQV
90	100	110	120	130	140	150	160
MTKSTTSFPF	LAMENKSALL	QGSFWGAPPK	PREEAGEPSL	QPRAAQRRHR	TCESLCAPLR	APATRRRDSE	PAPAATPHPP
170	180	190	200	210	220	230	240
ARQPARPVRP	PAQASQPRVA	RSLVGPRPLV	LPLAYSPPAR	EKPGRSEARR	PGPGCYIGRR	PNPAWTRQRP	PAPPLGSPPP
250	260	270	280	290	300	310	320
RAAQHPGGPP	NCRRGSASFF	RVGKAVPRSW	EINHLQKAEG	ARPARTRVET	TEDQKGSRKD	GCSGSRCHQY	RPPPQNQKKN
330	340	350	360	370	380	390	400
LKGCPPHRKR	MATLARGYKG	SRAICRDVSL	NLWQSRRSTE	SCIGHRINYR	NPLQWSHAEG	VRRSSGPGVI	SKAVGAEMWR
410	420						
TGAHHFLGSS	AVL						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2683	1	913.4777	3.59	2	63.7	10.3	2	146-162	R.RRDSEPAPAATPHPPAR.Q		MD:MU 3.28

Detailed Protein Report

Protein 254: F-box only protein 41 [Homo sapiens]

Accession:	gi|289803020	**Score:**	30.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	94.4
Database Date:	2015-11-30	**pI:**	9.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.4
		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
2595	2	813.9315	23.86	2	62.4	14.8	1	568-580	R.TLLHAAEVCRDWR.F	Carbamidomethyl: 9

Detailed Protein Report

Protein 255: solute carrier organic anion transporter family member 1B1 [Homo sapiens]

Accession:	gi|225543525	**Score:**	30.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	76.4
Database Date:	2015-11-30	**pI:**	9.7
		Sequence Coverage [%]:	3.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDQNQHLNKT	AEAQPSENKK	TRYCNGLKMF	LAALSLSFIA	KTLGAIIMKS	SIIHIERRFE	ISSSLVGFID	GSFEIGNLLV
90	100	110	120	130	140	150	160
IVFVSYFGSK	LHRPKLIGIG	CFIMGIGGVL	TALPHFFMGY	YRYSKETNIN	SSENSTSTLS	TCLINQILSL	NRASPEIVGK
170	180	190	200	210	220	230	240
GCLKESGSYM	WIYVFMGNML	RGIGETPIVP	LGLSYIDDFA	KEGHSSLYLG	ILNAIAMIGP	IIGFTLGSLF	SKMYVDIGYV
250	260	270	280	290	300	310	320
DLSTIRITPT	DSRWVGAWWL	NFLVSGLFSI	ISSIPFFFLP	QTPNKPQKER	KASLSLHVLE	TNDEKDQTAN	LTNQGKNITK
330	340	350	360	370	380	390	400
NVTGFFQSFK	SILTNPLYVM	FVLLTLLQVS	SYIGAFTYVF	KYVEQQYGQP	SSKANILLGV	ITIPIFASGM	FLGGYIIKKF
410	420	430	440	450	460	470	480
KLNTVGIAKF	SCFTAVMSLS	FYLLYFFILC	ENKSVAGLTM	TYDGNNPVTS	HRDVPLSYCN	SDCNCDESQW	EPVCGNNGIT
490	500	510	520	530	540	550	560
YISPCLAGCK	SSSGNKKPIV	FYNCSCLEVT	GLQNRNYSAH	LGECPRDDAC	TRKFYFFVAI	QVLNLFFSAL	GGTSHVMLIV
570	580	590	600	610	620	630	640
KIVQPELKSL	ALGFHSMVIR	ALGGILAPIY	FGALIDTTCI	KWSTNNCGTR	GSCRTYNSTS	FSRVYLGLSS	MLRVSSLVLY
650	660	670	680	690	700		
IILIYAMKKK	YQEKDINASE	NGSVMDEANL	ESLNKNKHFV	PSAGADSETH	C		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
216	1	487.1727	-168.54	3	32.4	17.4	2	10-22	K.TAEAQPSENKKTR.Y	

Detailed Protein Report

Protein 256: **PREDICTED: bifunctional heparan sulfate N-deacetylase/N-sulfotransferase 2 isoform X2 [Homo sapiens]**

Accession:	gi|530394565	**Score:**	30.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	59.2
Database Date:	2015-11-30	**pI:**	9.8
		Sequence Coverage [%]:	6.3
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MLLKHRKEFW	WFPHMWSHMQ	PHLFHNRSVL	ADQMRLNKQF	ALEHGIPTDL	GYAVAPHHSG	VYPIHTQLYE	AWKSVWGIQV
90	100	110	120	130	140	150	160
TSTEEYPHLR	PARYRRGFIH	NGIMVLPRQT	CGLFTHTIFY	NEYPGGSREL	DRSIRGGELF	LTVLLNPISI	FMTHLSNYGN
170	180	190	200	210	220	230	240
DRLGLYTFES	LVRFLQCWTR	LRLQTLPPVP	LAQKYFELFP	QERSPLWQNP	CDDKRHKDIW	SKEKTCDRLP	KFLIVGPQKT
250	260	270	280	290	300	310	320
GTTAIHFFLS	LHPAVTSSFP	SPSTFEEIQF	FNSPNYHKGI	DWYMDFFPVP	SNASTDFLFE	KSATYFDSEV	VPRRGAALLP
330	340	350	360	370	380	390	400
RAKIITVLTN	PADRAYSWYQ	HQRAHGDPVA	LNYTFYQVIS	ASSQTPLALR	SLQNRCLVPG	YYSTHLQRWL	TYYPSGQLLI
410	420	430	440	450	460	470	480
VDGQELRTNP	AASMESIQKF	LGITPFLNYT	RTLRFDDDKG	FWCQGLEGGK	TRCLGRSKGR	RYPDMDTESR	LFLTDFFRNH
490	500	510					
NLELSKLLSR	LGQPVPSWLR	EELQHSSLG					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
618	1	677.3937	25.26	2	37.3	10.3	0	97-108	R.GFIHNGIMVLPR.Q	
1699	1	1045.7064	77.05	2	51.0	20.0	2	315-334	R.GAALLPRAKIITVLTNPADR.A	

Protein 257: E3 ubiquitin-protein ligase listerin [Homo sapiens]

Accession:	gi|231573214	**Score:**	30.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	205.0
Database Date:	2015-11-30	**pI:**	6.1
		Sequence Coverage [%]:	1.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDRVGGGKGP	GGSYYRVSSS	AARSRKLCPG	RVNRGLSAQS	TAATATMGGK	NKQRTKGNLR	PSNSGRAAEL	LAKEQGTVPG
90	100	110	120	130	140	150	160
FIGFGTSQSD	LGYVPAIQGA	EEIDSLVDSD	FRMVLRKLSK	KDVTTKLKAM	QEFGTMCTER	DTETVKGVLP	YWPRIFCKIS
170	180	190	200	210	220	230	240
LDHDRRVREA	TQQAFEKLIL	KVKKQLAPYL	KSLMGYWLMA	QCDTYTPAAF	AAKDAFEAAF	PPSKQPEAIA	FCKDEITSVL
250	260	270	280	290	300	310	320
QDHLIKETPD	TLSDPQTVPE	EEREAKFYRV	VTCSLLALKR	LLCLLPDNEL	DSLEEKFKSL	LSQNKFWKYG	KHSVPQIRSA
330	340	350	360	370	380	390	400
YFELVSALCQ	RIPQLMKEEA	SKVSPSVLLS	IDDSDPIVCP	ALWEAVLYTL	TTIEDCWLHV	NAKKSVFPKL	STVIREGGRG
410	420	430	440	450	460	470	480
LATVIYPYLL	PFISKLPQSI	TNPKLDFFKN	FLTSLVAGLS	TERTKTSSLE	SSAVISAFFE	CLRFIMQQNL	GEEEIEQMLV
490	500	510	520	530	540	550	560
NDQLIPFIDA	VLKDPGLQHG	QLFNHLAETL	SSWEAKADTE	KDEKTAHNLE	NVLIHFWERL	SEICVAKISE	PEADVESVLG
570	580	590	600	610	620	630	640
VSNLLQVLQK	PKSSLKSSKK	KNGKVRFADE	ILESNKENEK	CVSSEGEKIE	GWELTTEPSL	THNSSGLLSP	LRKKPLEDLV
650	660	670	680	690	700	710	720
CKLADISINY	VNERKSEQHL	RFLSTLLDSF	SSSRVFKMLL	GDEKQSIVQA	KPLEIAKLVQ	KNPAVQFLYQ	KLIGWLNEDQ
730	740	750	760	770	780	790	800
RKDFGFLVDI	LYSALRCCDN	DMERKKVLDD	LTKVDLKWNS	LLKIIEKACP	SSDKHALVTP	WLKGDILGEK	LVNLADCLCN
810	820	830	840	850	860	870	880
EDLESRVSSE	SHFSERWTLL	SLVLSQHVKN	DYLIGDVYVE	RIIVRLHETL	FKTKKLSEAE	SSDSSVSFIC	DVAYNYFSSA
890	900	910	920	930	940	950	960
KGCLLMPSSE	DLLLTLFQLC	AQSKEKTHLP	DFLICKLKNT	WLSGVNLLVH	QTDSSYKEST	FLHLSALWLK	NQVQASSLDI
970	980	990	1000	1010	1020	1030	1040
NSLQVLLSAV	DDLLNTLLES	EDSYLMGVYI	GSVMPNDSEW	EKMRQSLPMQ	WLHRPLLEGR	LSLNYECFKT	DFKEQDIKTL
1050	1060	1070	1080	1090	1100	1110	1120
PSHLCTSALL	SKMVLIALRK	ETVLENNELE	KIIAELLYSL	QWCEELDNPP	IFLIGFCEIL	QKMNITYDNL	RVLGNTSGLL
1130	1140	1150	1160	1170	1180	1190	1200
QLLFNRSREH	GTLWSLIIAK	LILSRSISSD	EVKPHYKRKE	SFFPLTEGNL	HTIQSLCPFL	SKEEKKEFSA	QCIPALLGWT
1210	1220	1230	1240	1250	1260	1270	1280
KKDLCSTNGG	FGHLAIFNSC	LQTKSIDDGE	LLHGILKIII	SWKKEHEDIF	LFSCNLSEAS	PEVLGVNIEI	IRFLSLFLKY
1290	1300	1310	1320	1330	1340	1350	1360
CSSPLAESEW	DFIMCSMLAW	LETTSENQAL	YSIPLVQLFA	CVSCDLACDL	SAFFDSTTLD	TIGNLPVNLI	SEWKEFFSQG
1370	1380	1390	1400	1410	1420	1430	1440
IHSLLLPILV	TVTGENKDVS	ETSFQNAMLK	PMCETLTYIS	KEQLLSHKLP	ARLVADQKTN	LPEYLQTLLN	TLAPLLLFRA
1450	1460	1470	1480	1490	1500	1510	1520
RPVQIAVYHM	LYKLMPELPQ	YDQDNLKSYG	DEEEEPALSP	PAALMSLLSI	QEDLLENVLG	CIPVGQIVTI	KPLSEDFCYV
1530	1540	1550	1560	1570	1580	1590	1600
LGYLLTWKLI	LTFFKAASSQ	LRALYSMYLR	KTKSLNKLLY	HLFRLMPENP	TYAETAVEVP	NKDPKTFFTE	ELQLSIRETT
1610	1620	1630	1640	1650	1660	1670	1680
MLPYHIPHLA	CSVYHMTLKD	LPAMVRLWWN	SSEKRVFNIV	DRFTSKYVSS	VLSFQEISSV	QTSTQLFNGM	TVKARATTRE
1690	1700	1710	1720	1730	1740	1750	1760
VMATYTIEDI	VIELIIQLPS	NYPLGSIIVE	SGKRVGVAVQ	QWRNWMLQLS	TYLTHQNGSI	MEGLALWKNN	VDKRFEGVED
1770	1780	1790	1800	1810	1820		
CMICFSVIHG	FNYSLPKKAC	RTCKKKFHSA	CLYKWFTSSN	KSTCPLCRET	FF		

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

	Cmpds.		[ppm]		[min]					
57	1	731.6721	-129.70	3	30.4	30.4	2	1127-1145	R.SREHGTLWSLIIAKLILSR.S	

Detailed Protein Report

Protein 258: contactin-2 precursor [Homo sapiens]

Accession:	gi|4827022	**Score:**	30.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	113.3
Database Date:	2015-11-30	**pI:**	8.9
		Sequence Coverage [%]:	3.6
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MGTATRRKPH	LLLVAAVALV	SSSAWSSALG	SQTTFGPVFE	DQPLSVLFPE	ESTEEQVLLA	CRARASPPAT	YRWKMNGTEM
90	100	110	120	130	140	150	160
KLEPGSRHQL	VGGNLVIMNP	TKAQDAGVYQ	CLASNPVGTV	VSREAILRFG	FLQEFSKEER	DPVKAHEGWG	VMLPCNPPAH
170	180	190	200	210	220	230	240
YPGLSYRWLL	NEFPNFIPTD	GRHFVSQTTG	NLYIARTNAS	DLGNYSCLAT	SHMDFSTKSV	FSKFAQLNLA	AEDTRLFAPS
250	260	270	280	290	300	310	320
IKARFPAETY	ALVGQQVTLE	CFAFGNPVPR	IKWRKVDGSL	SPQWTTAEPT	LQIPSVSFED	EGTYECEAEN	SKGRDTVQGR
330	340	350	360	370	380	390	400
IIVQAQPEWL	KVISDTEADI	GSNLRWGCAA	AGKPRPTVRW	LRNGEPLASQ	NRVEVLAGDL	RFSKLSLEDS	GMYQCVAENK
410	420	430	440	450	460	470	480
HGTIYASAEL	AVQALAPDFR	LNPVRRLIPA	ARGGEILIPC	QPRAAPKAVV	LWSKGTEILV	NSSRVTVTPD	GTLIIRNISR
490	500	510	520	530	540	550	560
SDEGKYTCFA	ENFMGKANST	GILSVRDATK	ITLAPSSADI	NLGDNLTLQC	HASHDPTMDL	TFTWTLDDFP	IDFDKPGGHY
570	580	590	600	610	620	630	640
RRTNVKETIG	DLTILNAQLR	HGGKYTCMAQ	TVVDSASKEA	TVLVRGPPGP	PGGVVVRDIG	DTTIQLSWSR	GFDNHSPIAK
650	660	670	680	690	700	710	720
YTLQARTPPA	GKWKQVRTNP	ANIEGNAETA	QVLGLTPWMD	YEFRVIASNI	LGTGEPSGPS	SKIRTREAAP	SVAPSGLSGG
730	740	750	760	770	780	790	800
GGAPGELIVN	WTPMSREYQN	GDGFGYLLSF	RRQGSTHWQT	ARVPGADAQY	FVYSNESVRP	YTPFEVKIRS	YNRRGDGPES
810	820	830	840	850	860	870	880
LTALVYSAEE	EPRVAPTKVW	AKGVSSSEMN	VTWEPVQQDM	NGILLGYEIR	YWKAGDKEAA	ADRVRTAGLD	TSARVSGLHP
890	900	910	920	930	940	950	960
NTKYHVTVRA	YNRAGTGPAS	PSANATTMKP	PPRRPPGNIS	WTFSSSSLSI	KWDPVVPFRN	ESAVTGYKML	YQNDLHLTPT
970	980	990	1000	1010	1020	1030	1040
LHLTGKNWIE	IPVPEDIGHA	LVQIRTTGPG	GDGIPAEVHI	VRNGGTSMMV	ENMAVRPAPH	PGTVISHSVA	MLILIGSLEL
1050							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
159	1	619.6506	-71.74	3	31.7	14.0	1	599-617	K.EATVLVRGPPGPPGGVVVR.D	
1718	1	857.4054	-57.25	2	51.4	16.3	0	685-702	R.VIASNILGTGEPSGPSSK.I	

Detailed Protein Report

Protein 259: spindle assembly abnormal protein 6 homolog [Homo sapiens]

Accession:	gi|35038601	**Score:**	30.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	74.4
Database Date:	2015-11-30	**pI:**	7.9
		Sequence Coverage [%]:	4.4
		No. of unique Peptides:	2

```
        10         20         30         40         50         60         70         80
MSQVLFHQLV PLQVKCKDCE ERRVSIRMSI ELQSVSNPVH RKDLVIRLTD DTDPFFLYNL VISEEDFQSL KFQQGLLVDF
        90        100        110        120        130        140        150        160
LAFPQKFIDL LQQCTQEHAK EIPRFLLQLV SPAAILDNSP AFLNVVETNP FKHLTHLSLK LLPGNDVEIK KFLAGCLKCS
       170        180        190        200        210        220        230        240
KEEKLSLMQS LDDATKQLDF TRKTLAEKKQ ELDKLRNEWA SHTAALTNKH SQELTNEKEK ALQAQVQYQQ QHEQQKKDLE
       250        260        270        280        290        300        310        320
ILHQQNIHQL QNRLSELEAA NKDLTERKYK GDSTIRELKA KLSGVEEELQ RTKQEVLSLR RENSTLDVEC HEKEKHVNQL
       330        340        350        360        370        380        390        400
QTKVAVLEQE IKDKDQLVLR TKEAFDTIQE QKVVLEENGE KNQVQLGKLE ATIKSLSAEL LKANEIIKKL QGDLKTLMGK
       410        420        430        440        450        460        470        480
LKLKNTVTIQ QEKLLAEKEE KLQKEQKELQ DVGQSLRIKE QEVCKLQEQL EATVKKLEES KQLLKNNEKL ITWLNKELNE
       490        500        510        520        530        540        550        560
NQLVRKQDVL GPSTTPPAHS SSNTIRSGIS PNLNVVDGRL TYPTCGIGYP VSSAFAFQNT FPHSISAKNT SHPGSGTKVQ
       570        580        590        600        610        620        630        640
FNLQFTKPNA SLGDVQSGAT ISMPCSTDKE NGENVGLESK YLKKREDSIP LRGLSQNLFS NSDHQRDGTL GALHTSSKPT
       650        660
ALPSASSAYF PGQLPNS
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1496	1	829.1351	164.97	2	48.5	18.4	2	375-389	K.SLSAELLKANEIIKK.L	
239	1	801.7845	-124.85	2	32.7	11.9	0	613-626	R.GLSQNLFSNSDHQR.D	

Detailed Protein Report

Protein 260: neuroblastoma-amplified sequence [Homo sapiens]

Accession:	gi|41393547	**Score:**	30.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	268.4
Database Date:	2015-11-30	**pI:**	5.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.4
		No. of unique Peptides:	2

Quantitation

MD:MU	**Median:**	1.95	**CV:**	0.00 %	**No. of Peptides:**	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MAAPESGPAL	SPGTAEGEEE	TILYDLLVNT	EWPPETEVQP	RGNQKHGASF	IITKAIRDRL	LFLRQYIWYS	PAPFLLPDGL
90	100	110	120	130	140	150	160
VRLVNKQINW	HLVLASNGKL	LAAVQDQCVE	IRSAKDDFTS	IIGKCQVPKD	PKPQWRRVAW	SYDCTLLAYA	ESTGTVRVFD
170	180	190	200	210	220	230	240
LMGSELFVIS	PASSFIGDLS	YAIAGLIFLE	YKASAQWSAE	LLVINYRGEL	RSYLVSVGTN	QSYQESHCFS	FSSHYPHGIN
250	260	270	280	290	300	310	320
TAIYHPGHRL	LLVGGCETAE	VGMSKASSCG	LSAWRVLSGS	PYYKQVTNGG	DGVTAVPKTL	GLLRMLSVKF	YSRQGQEQDG
330	340	350	360	370	380	390	400
IFKMSLSPDG	MLLAAIHFSG	KLSIWAIPSL	KQQGEWGQNE	QPGYDDLNPD	WRLSTEKRKK	IKDKESFYPL	IDVNWWADSA
410	420	430	440	450	460	470	480
VTLARCSGAL	TVSSVKTLKN	LLGKSCEWFE	PSPQVTATHD	GGFLSLECEI	KLAPKRSRLE	TRAGEEDEGE	EDSDSDYEIS
490	500	510	520	530	540	550	560
AKARYFGYIK	QGLYLVTEME	RFAPPRKRPR	TITKNYRLVS	LRSTTPEELY	QRKIESEEYE	EALSLAHTYG	LDTDLVYQRQ
570	580	590	600	610	620	630	640
WRKSAVNVAS	IQNYLSKIKK	RSWVLHECLE	RVPENVDAAK	ELLQYGLKGT	DLEALLAIGK	GADDGRFTLP	GEIDIDSISY
650	660	670	680	690	700	710	720
EELSPPDEEP	AKNKKEKELK	KRQELLKLVN	FSKLTLEQKE	LCRCRRKLLT	YLDRLATYEE	ILGVPHASEQ	RYDAEFFKKF
730	740	750	760	770	780	790	800
RNQNIVLSAR	TYAQESNVQA	LEILFTYHGS	DLLPHRLAIL	SNFPETTSPH	EYSVLLPEAC	FNGDSLMIIP	WHEHKHRAKD
810	820	830	840	850	860	870	880
WCEELACRMV	VEPNLQDESE	FLYAAQPELL	RFRMTQLTVE	KVMDWYQTRA	EEIEHYARQV	DCALSLIRLG	MERNIPGLLV
890	900	910	920	930	940	950	960
LCDNLVTLET	LVYEARCDVT	LTLKELQQMK	DIEKLRLLMN	SCSEDKYVTS	AYQWMVPFLH	RCEKQSPGVA	NELLKEYLVT
970	980	990	1000	1010	1020	1030	1040
LAKGDLKFPL	KIFQHSKPDL	QQKIIPDQDQ	LMAIALECIY	TCERNDQLCL	CYDLLECLPE	RGYGDKTEAT	TKLHDMVDQL
1050	1060	1070	1080	1090	1100	1110	1120
EQILSVSELL	EKHGLEKPIS	FVKNTQSSSE	EARKLMVRLT	RHTGRKQPPV	SESHWRTLLQ	DMLTMQQNVY	TCLDSDACYE
1130	1140	1150	1160	1170	1180	1190	1200
IFTESLLCSS	RLENIHLAGQ	MMHCSACSEN	PPAGIAHKGK	PHYRVSYEKS	IDLVLAASRE	YFNSSTNLTD	SCMDLARCCL
1210	1220	1230	1240	1250	1260	1270	1280
QLITDRPPAI	QEELDLIQAV	GCLEEFGVKI	LPLQVRLCPD	RISLIKECIS	QSPTCYKQST	KLLGLAELLR	VAGENPEERR
1290	1300	1310	1320	1330	1340	1350	1360
GQVLILLVEQ	ALRFHDYKAA	SMHCQELMAT	GYPKSWDVCS	QLGQSEGYQD	LATRQELMAF	ALTHCPPSSI	ELLLAASSSL
1370	1380	1390	1400	1410	1420	1430	1440
QTEILYQRVN	FQIHHEGGEN	ISASPLTSKA	VQEDEVGVPG	SNSADLLRWT	TATTMKVLSN	TTTTTKAVLQ	AVSDGQWWKK
1450	1460	1470	1480	1490	1500	1510	1520
SLTYLRPLQG	QKCGGAYQIG	TTANEDLEKQ	GCHPFYESVI	SNPFVAESEG	TYDTYQHVPV	ESFAEVLLRT	GKLAEAKNKG
1530	1540	1550	1560	1570	1580	1590	1600
EVFPTTEVLL	QLASEALPND	MTLALAYLLA	LPQVLDANRC	FEKQSPSALS	LQLAAYYYSL	QIYARLAPCF	RDKCHPLYRA
1610	1620	1630	1640	1650	1660	1670	1680
DPKELIKMVT	RHVTRHEHEA	WPEDLISLTK	QLHCYNERLL	DFTQAQILQG	LRKGVDVQRF	TADDQYKRET	ILGLAETLEE
1690	1700	1710	1720	1730	1740	1750	1760
SVYSIAISLA	QRYSVSRWEV	FMTHLEFLFT	DSGLSTLEIE	NRAQDLHLFE	TLKTDPEAFH	QHMVKYIYPT	IGGFDHERLQ
1770	1780	1790	1800	1810	1820	1830	1840
YYFTLLENCG	CADLGNCAIK	PETHIRLLKK	FKVVASGLNY	KKLTDENMSP	LEALEPVLSS	QNILSISKLV	PKIPEKDGQM
1850	1860	1870	1880	1890	1900	1910	1920
LSPSSLYTIW	LQKLFWTGDP	HLIKQVPGSS	PEWLHAYDVC	MKYFDRLHPG	DLITVVDAVT	FSPKAVTKLS	VEARKEMTRK
1930	1940	1950	1960	1970	1980	1990	2000
AIKTVKHFIE	KPRKRNSEDE	AQEAKDSKVT	YADTLNHLEK	SLAHLETLSH	SFILSLKNSE	QETLQKYSHL	YDLSRSEKEK
2010	2020	2030	2040	2050	2060	2070	2080
LHDEAVAICL	DGQPLAMIQQ	LLEVAVGPLD	ISPKDIVQSA	IMKIISALSG	GSADLGGPRD	PLKVLEGVVA	AVHASVDKGE
2090	2100	2110	2120	2130	2140	2150	2160
ELVSPEDLLE	WLRPFCADDA	WPVRPRIHVL	QILGQSFHLT	EEDSKLLVFF	RTEAILKASW	PQRQVDIADI	ENEENRYCLF
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
2612	1	1045.0458	32.19	2	62.7	16.8	1	266-284	K.ASSCGLSAWRVLSGSPYYK.Q	Carbamidomethyl: 4	
70	1	877.8816	-65.42	2	30.6	13.5	2	1987-2000	K.YSHLYDLSRSEKEK.L		MD:MU 1.95

Detailed Protein Report

Protein 261: zinc finger protein 761 [Homo sapiens]

Accession:	gi|209954795	**Score:**	30.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	87.7
Database Date:	2015-11-30	**pI:**	10.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAFSQGLLTF	RDVAIEFSQE	EWKCLDPAQR	TLYRDVMLEN	YRNLVSLDIS	SKCTMKEFLS	TAQGNREVFH	AGTLQIHESH
90	100	110	120	130	140	150	160
HNGDFCYQDV	DKDIHDYEFQ	WQEDERNGHE	APMTKIKKLT	GITERYDQSH	ARNKPIKDQL	GSSFHSHLPE	MHIFQTEEKI
170	180	190	200	210	220	230	240
DNQVVKSVHD	ASLVSTAQRI	SCRPKTHISN	NHGNNFWNSS	LLTQKQEVHM	REKSFQCNES	GKAFNYSSLL	RKHQIIHLAD
250	260	270	280	290	300	310	320
KYKCDVCGKL	FNQKRNLACH	RRCHTGENPY	KCNECGKTFS	QTSSLTCHRR	LHTGEKPYKC	EECDKAFHFK	SILERHRIIH
330	340	350	360	370	380	390	400
TEEKPYKCNE	CGKTFRQKSI	LTRHHRLHTG	EKPYKCNECG	KTFSHKSSLT	CHHRLHTGEK	PYKCNECGKT	FSHKSSLTCH
410	420	430	440	450	460	470	480
RRLHTGEKPY	KCEECDKAYS	FRSNFEIHRK	IHTEDNAYKC	NECGKTFSRT	SSLTCHRRRH	TGEQPYKCEE	CDKAFRFKSN
490	500	510	520	530	540	550	560
LERHRRIHTG	EKPYKCNECG	KTFSRKSYLT	CHHRLHTGEK	AYKCNECGKT	FSWKSSLTCH	RRLHSGEKPY	KCKECGKTFN
570	580	590	600	610	620	630	640
QQLTLKRHRR	LHSGENPYKC	EDSDKAYSFK	SNLEIHQKIH	TEENPYKCNE	CGKTFSRTSS	LTCHRRLHTG	EKPYKCEECD
650	660	670	680	690	700	710	720
KAFRVKSNLE	GHRRIHTGEK	PYKCNECGKT	FSRKSYFICH	HRLHTGEKPY	KCNECGKNFS	QKSSLICHHR	LHTGEKPYKC
730	740	750					
NECGKTFSQK	SNLTCHRRLH	TGEKQV					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1972	1	665.2897	-23.77	2	54.8	11.9	2	496-506	K.CNECGKTFSRK.S	Carbamidomethyl: 4

Detailed Protein Report

Protein 262: **PREDICTED: calcium-dependent secretion activator 2 isoform X14 [Homo sapiens]**

Accession:	gi|530386656	**Score:**	30.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	142.8
Database Date:	2015-11-30	**pI:**	5.7
		Sequence Coverage [%]:	2.6
		No. of unique Peptides:	2

Quantitation

MD:MU **Median:** 3.60 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MLDPSSSEEE	SDEGLEEESR	DVLVAAGSSQ	RAPPAPTREG	RRDAPGRAGG	GGAARSVSPS	PSVLSEGRDE	PQRQLDDEQE
90	100	110	120	130	140	150	160
RRIRLQLYVF	VVRCIAYPFN	AKQPTDMARR	QQKLNKQQLQ	LLKERFQAFL	NGETQIVADE	AFCNAVRSYY	EVFLKSDRVA
170	180	190	200	210	220	230	240
RMVQSGGCSA	NDFREVFKKN	IEKRVRSLPE	IDGLSKETVL	SSWIAKYDAI	YRGEEDLCKQ	PNRMALSAVS	ELILSKEQLY
250	260	270	280	290	300	310	320
EMFQQILGIK	KLEHQLLYNA	CQLDNADEQA	AQIRRELDGR	LQLADKMAKE	RKFPKFIAKD	MENMYIEELR	SSVNLLMANL
330	340	350	360	370	380	390	400
ESLPVSKGGP	EFKLQKLKRS	QNSAFLDIGD	ENEIQLSKSD	VVLSFTLEIV	IMEVQGLKSV	APNRIVYCTM	EVEGEKLQTD
410	420	430	440	450	460	470	480
QAEASRPQWG	TQGDFTTTHP	RPVVKVKLFT	ESTGVLALED	KELGRVILYP	TSNSSKSAEL	HRMVVPKNSQ	DSDLKIKLAV
490	500	510	520	530	540	550	560
RMDKPAHMKH	SGYLYALGQK	VWKRWKKRYF	VLVQVSQYTF	AMCSYREKKS	EPQELMQLEG	YTVDYTDPHP	GLQGGCMFFN
570	580	590	600	610	620	630	640
AVKEGDTVIF	ASDDEQDRIL	WVQAMYRATG	QSYKPVPAIQ	TQKLNPKGGT	LHADAQLYAD	RFQKHGMDEF	ISANPCKLDH
650	660	670	680	690	700	710	720
AFLFRILQRQ	TLDHRLNDSY	SCLGWFSPGQ	VFVLDEYCAR	YGVRGCHRHL	CYLAELMEHS	ENGAVIDPTL	LHYSFAFCAS
730	740	750	760	770	780	790	800
HVHGNRPDGI	GTVSVEEKER	FEEIKERLSS	LLENQISHFR	YCFPFGRPEG	ALKATLSLLE	RVLMKDIATP	IPAEEVKKVV
810	820	830	840	850	860	870	880
RKCLEKAALI	NYTRLTEYAK	IEETMNQASP	ARKLEEILHL	AELCIEVLQQ	NEEHHAEAFA	WWPDLLAEHA	EKFWALFTVD
890	900	910	920	930	940	950	960
MDTALEAQPQ	DSWDSFPLFQ	LLNNFLRNDT	LLCNGKFHKH	LQEIFVPLVV	RYVDLMESSI	AQSIHRGFEQ	ETWQPVNNGS
970	980	990	1000	1010	1020	1030	1040
ATSEDLFWKL	DALQMFVFDL	HWPEQEFAHH	LEQRLKLMAS	DMLEACVKRT	RTAFELKLQK	ASKTTDLRIP	ASVCTMFNVL
1050	1060	1070	1080	1090	1100	1110	1120
VDAKKQSTKL	CALDGGQEQQ	YHSKIDDLID	NSVKEIISLL	VSKFVSVLEG	VLSKLSRYDE	GTFFSSILSF	TVKAAAKYVD
1130	1140	1150	1160	1170	1180	1190	1200
VPKPGMDLAD	TYIMFVRQNQ	DILREKVNEE	MYIEKLFDQW	YSSSMKVICV	WLTDRLDLQL	HIYQLKTLIK	IVKKTYRDFR
1210	1220	1230	1240	1250	1260		
LQGVLEGTLN	SKTYDTVHRR	LTVEEATASV	SEGGGLQGIT	MKDSDEEEEG			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2170	1	951.3588	-156.41	2	57.0	13.7	1	446-462	R.VILYPTSNSSKSAELHR.M		MD:MU 3.60
1840	1	920.8515	-111.10	2	53.0	16.5	0	1098-1113	R.YDEGTFFSSILSFTVK.A		

Detailed Protein Report

Protein 263: **PREDICTED: glutamine-rich protein 2 isoform X2 [Homo sapiens]**

Accession:	gi|578831523	**Score:**	30.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	72.2
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
MRSRPAKPTW	RRSSSCWHRW	VERLQRILEG	EGNQEAGKEL	KAGELRLQLG	VLRVTVADIE	KELAELRESQ	DRGKAAMENS
90	100	110	120	130	140	150	160
VSEASLYLQD	QLDKLRMIIE	SMLTSSSTLL	SMSMAPHKAH	TLAPGQIDPE	ATCPACSLDV	SHQVSTLVRR	YEQLQDMVNS
170	180	190	200	210	220	230	240
LAVSRPSKKA	KLQRQDEELL	GRVQSAILQV	QGDCEKLNIT	TSNLIEDHRQ	KQKDIAMLYQ	GLEKLEKEKA	NREHLEMEID
250	260	270	280	290	300	310	320
VKADKSALAT	KVSRVQFDAT	TEQLNHMMQE	LVAKMSGQEQ	DWQKMLDRLL	TEMDNKLDRL	ELDPVKQLLE	DRWKSLRQQL
330	340	350	360	370	380	390	400
RERPPLYQAD	EAAAMRRQLL	AHFHCLSCDR	PLETPVTGHA	IPVTPAGPGL	PGHHSIRPYT	VFELEQVRQH	SRNLKLGSAF
410	420	430	440	450	460	470	480
PRGDLAQMEQ	SVGRLRSMHS	KMLMNIEKVQ	IHFGGSTKAS	SQIIRELLHA	QCLGSPCYKR	VTDMADYTYS	TVPRRCGGSH
490	500	510	520	530	540	550	560
TLTYPYHRSR	PQHLPRGLYP	TEEIQIAMKH	DEVDILGLDG	HIYKGRMDTR	LPGILRKDSS	GTSKRKSQQP	RPHVHRPPSL
570	580	590	600	610	620	630	640
SSNGQLPSRP	QSAQISAGNT	SVSSRQQKDR	PSSEGRLSQP	NTAHPPSSAA	VANRGLERHV	DMPPGEGLEE	PTRGPRSSTA
650							
Q							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2513	1	410.0863	-280.49	2	61.4	19.3	1	68-74	R.ESQDRGK.A	
2139	1	937.3370	-142.40	2	56.6	10.9	1	322-337	R.ERPPLYQADEAAAMRR.Q	

Detailed Protein Report

Protein 264: PREDICTED: ubiquitin carboxyl-terminal hydrolase 40 isoform X4 [Homo sapiens]

Accession:	gi|530371419	**Score:**	30.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	125.8
Database Date:	2015-11-30	**pI:**	5.5
		Sequence Coverage [%]:	1.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MRQHDVQELN	RILFSALETS	LVGTSGHDLI	YRLYHGTIVN	QIVCKECKNV	SERQEDFLDL	TVAVKNVSGL	EDALWNMYVE
90	100	110	120	130	140	150	160
EEVFDCDNLY	HCGTCDRLVK	AAKSAKLRKL	PPFLTVSLLR	FNFDFVKCER	YKETSCYTFP	LRINLKPFCE	QSELDDLEYI
170	180	190	200	210	220	230	240
YDLFSVIIHK	GGCYGGHYHV	YIKDVDHLGN	WQFQEEKSKP	DVNLKDLQSE	EEIDHPLMIL	KAILLEEENN	LIPVDQLGQK
250	260	270	280	290	300	310	320
LLKKIGISWN	KKYRKQHGPL	RKFLQLHSQI	FLLSSDESTV	RLLKNSSLQA	ESDFQRNDQQ	IFKMLPPESP	GLNNSISCPH
330	340	350	360	370	380	390	400
WFDINDSKVQ	PIREKDIEQQ	FQGKESAYML	FYRKSQLQRP	PEARANPRYG	VPCHLLNEMD	AANIELQTKR	AECDSANNTF
410	420	430	440	450	460	470	480
ELHLHLGPQY	HFFNGALHPV	VSQTESVWDL	TFDKRKTLGD	LRQSIFQLLE	FWEGDMVLSV	AKLVPAGLHI	YQSLGGDELT
490	500	510	520	530	540	550	560
LCETEIADGE	DIFVWNGVEV	GGVHIQTGID	CEPLLLNVLH	LDTSSDGEKC	CQVIESPHVF	PANAEVGTVL	TALAIPAGVI
570	580	590	600	610	620	630	640
FINSAGCPGG	EGWTAIPKED	MRKTFREQGL	RNGSSILIQD	SHDDNSLLTK	EEKWVTSMNE	IDWLHVKNLC	QLESEEKQVK
650	660	670	680	690	700	710	720
ISATVNTMVF	DIRIKAIKEL	KLMKELADNS	CLRPIDRNGK	LLCPVPDSYT	LKEAELKMGS	SLGLCLGKAP	SSSQLFLFFA
730	740	750	760	770	780	790	800
MGSDVQPGTE	MEIVVEETIS	VRDCLKLMLK	KSGLQGDAWH	LRKMDWCYEA	GEPLCEEDAT	LKELLICSGD	TLLLIEGQLP
810	820	830	840	850	860	870	880
PLGFLKVPIW	WYQLQGPSGH	WESHQDQTNC	TSSWGRVWRA	TSSQGASGNE	PAQVSLLYLG	DIEISEDATL	AELKSQAMTL
890	900	910	920	930	940	950	960
PPFLEFGVPS	PAHLRAWTVE	RKRPGRLLRT	DRQPLREYKL	GRRIEICLEP	LQKGENLGPQ	DVLLRTQVRI	PGERTYAPAL
970	980	990	1000	1010	1020	1030	1040
DLVWNAAQGG	TAGSLRQRVA	DFYRLPVEKI	EIAKYFPEKF	EWLPISSWNQ	QITKRKKKKK	QDYLQGAPYY	LKDGDTIGVK
1050	1060	1070	1080	1090	1100	1110	
NLLIDDDDDF	STIRDDTGKE	KQKQRALGRR	KSQEALHEQS	SYILSSAETP	ARPRAPETSL	SIHVGSFR	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2823	1	826.4280	41.02	2	65.7	30.1	0	1041- 1054	K.NLLIDDDDDFSTIR.D	

Detailed Protein Report

Protein 265: PREDICTED: pericentriolar material 1 protein isoform X28 [Homo sapiens]

Accession:	gi|578815347	**Score:**	30.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	180.4
Database Date:	2015-11-30	**pI:**	5.3
		Sequence Coverage [%]:	2.1
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MATGGGPFED	GMNDQDLPNW	SNENVDDRLN	NMDWGAQQKK	ANRSSEKNKK	KFGVESDKRV	TNDISPESSP	GVGRRRTKTP
90	100	110	120	130	140	150	160
HTFPHSRYMS	QMSVPEQAEL	EKLKQRINFS	DLDQRSIGSD	SQGRATAANN	KRQLSENRKP	FNFLPMQINT	NKSKDASTNP
170	180	190	200	210	220	230	240
PNRETIGSAQ	CKELFASALS	NDLLQNCQVS	EEDGRGEPAM	ESSQIVSRLV	QIRDYITKAS	SMREDLVEKN	ERSANVERLT
250	260	270	280	290	300	310	320
HLIDHLKEQE	KSYMKFLKKI	LARENEEEDV	RTIDSAVGSG	SVAESTSLNI	DVQSEASDTT	EEASFSLRIR	PCIEDKLGNS
330	340	350	360	370	380	390	400
ASQEQVSDID	VTTSPKGKGD	RPQNDRELRP	NRKYSQKRGF	PSKARDPQQE	PMEEIENLKK	QHDLLKRMLQ	QQEQLRALQG
410	420	430	440	450	460	470	480
RQAALLALQH	KAEQAIAVMD	DSVVAETAGS	LSGVSITSEL	NEELNDLIQR	FHNQLRDSQP	PAVPDNRRQA	ESLSLTREVS
490	500	510	520	530	540	550	560
QSRKPSASER	LPDEKVELFS	KMRVLQEKKQ	KMDKLLGELH	TLRDQHLNNS	SSSPQRSVDQ	RSTSAPSASV	GLAPVVNGES
570	580	590	600	610	620	630	640
NSLTSSVPYP	TASLVSQNES	ENEGHLNPSE	KLQKLNEVRK	RLNELRELVH	YYEQTSDMMT	DAVNENRKDE	ETEESEYDSE
650	660	670	680	690	700	710	720
HENSEPVTNI	RNPQVASTWN	EVNSHSNAQC	VSNNRDGRTV	NSNCEINNRS	AANIRALNMP	PSLADCRYNR	EGEQEIHVAQ
730	740	750	760	770	780	790	800
GEDDEEEEEE	AEEEGVSGAS	LSSHRSSLVD	EHPEDAEFEQ	KINRLMAAKQ	KLRQLQDLVA	MVQDDDAAQG	VISASASNLD
810	820	830	840	850	860	870	880
DFYPAEEDTK	QNSNNTRGNA	NKTQKDTGVN	EKAREKFYEA	KLQQQQRELK	QLQEERKKLI	DIQEKIQALQ	TACPDLQLSA
890	900	910	920	930	940	950	960
ASVGNCPTKK	YMPAVTSTPT	VNQHETSTSK	SVFEPEDSSI	VDNELWSEMR	RHEMLREELR	QRRKQLEALM	AEHQRRQGLA
970	980	990	1000	1010	1020	1030	1040
ETASPVAVSL	RSDGSENLCT	PQQSRTEKTM	ATWGGSTQCA	LDEEGDEDGY	LSEGIVRTDE	EEEEEQDASS	NDNFSVCPSN
1050	1060	1070	1080	1090	1100	1110	1120
SVNHNSYNGK	ETKNRWKNNC	PFSADENYRP	LAKTRQQNIS	MQRQENLRWV	SELSYVEEKE	QWQEQINQLK	KQLDFSVSIC
1130	1140	1150	1160	1170	1180	1190	1200
QTLMQDQQTL	SCLLQTLLTG	PYSVMPSNVA	SPQVHFIMHQ	LNQCYTQLTW	QQNNVQRLKQ	MLNELMRQQN	QHPEKPGGKE
1210	1220	1230	1240	1250	1260	1270	1280
RGSSASHPPS	PSLFCPFSFP	TQPVNLFNIP	GFTNFSSFAP	GMNFSPLFPS	NFGDFSQNIS	TPSEQQQPLA	QNSSGKTEYM
1290	1300	1310	1320	1330	1340	1350	1360
AFPKPFESSS	SIGAEKPRNK	KLPEEEVESS	RTPWLYEQEG	EVEKPFIKTG	FSVSVEKSTS	SNRKNQLDTN	GRRRQFDEES
1370	1380	1390	1400	1410	1420	1430	1440
LESFSSMPDP	VDPTTVTKTF	KTRKASAQAS	LASKDKTPKS	KSKKRNSTQL	KSRVKNIRYE	SASMSSTCEP	CKSRNRHSAQ
1450	1460	1470	1480	1490	1500	1510	1520
TEEPVQAKVF	SRKNHEQLEK	IIKCNRSTEI	SSAHARRILQ	QSNRNACNEA	PETGSDFSMF	EALRDTIYSE	VATLISQNES
1530	1540	1550	1560	1570	1580	1590	1600
RPHFLIELFH	ELQLLNTDYL	RQRALYALQD	IVSRHISESH	EKGENVKSVN	SGTWIASNSE	LTPSESLATT	DDVFIQEK

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
86	2	809.3666	-141.33	2	30.8	12.3	1	397-411	R.ALQGRQAALLALQHK.A	
1791	1	732.8049	117.99	3	52.4	17.8	1	1544-1562	R.ALYALQDIVSRHISESHEK.G	

Detailed Protein Report

Protein 266: **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: 30.0
MW [kDa]: 210.6
pI: 5.7
Sequence Coverage [%]: 2.1
No. of unique Peptides: 2

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				

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1746	3	1023.9594	-58.70	2	51.6	16.7	1	433-448	K.WILQDKPVFMEEPDRK.D	Oxidation: 10
1736	2	1273.5367	-62.63	2	51.5	13.3	0	1341-1363	K.SSEPVQYHSSAELGNLLTVEEEK.K	

Detailed Protein Report

Protein 267: polypeptide N-acetylgalactosaminyltransferase 14 isoform 3 [Homo sapiens]

Accession:	gi|359465585	**Score:**	29.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	61.5
Database Date:	2015-11-30	**pI:**	6.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSFPMSLARS	SVPFADSGLS	SSQPSDADWD	DLWDQFDERR	YLNAKKWRVG	DDPYKLYAFN	QRESERISSN	RAIPDTRHLR
90	100	110	120	130	140	150	160
CTLLVYCTDL	PPTSIIITFH	NEARSTLLRT	IRSVLNRTPT	HLIREIILVD	DFSNDPDDCK	QLIKLPKVKC	LRNNERQGLV
170	180	190	200	210	220	230	240
RSRIRGADIA	QGTTLTFLDS	HCEVNRDWLQ	PLLHRVKEDY	TRVVCPVIDI	INLDTFTYIE	SASELRGGFD	WSLHFQWEQL
250	260	270	280	290	300	310	320
SPEQKARRLD	PTEPIRTPII	AGGLFVIDKA	WFDYLGKYDM	DMDIWGGENF	EISFRVWMCG	GSLEIVPCSR	VGHVFRKKHP
330	340	350	360	370	380	390	400
YVFPDGNANT	YIKNTKRTAE	VWMDEYKQYY	YAARPFALER	PFGNVESRLD	LRKNLRCQSF	KWYLENIYPE	LSIPKESSIQ
410	420	430	440	450	460	470	480
KGNIRQRQKC	LESQRQNNQE	TPNLKLSPCA	KVKGEDAKSQ	VWAFTYTQQI	LQEELCLSVI	TLFPGAPVVL	VLCKNGDDRQ
490	500	510	520	530	540		
QWTKTGSHIE	HIASHLCLDT	DMFGDGTENG	KEIVVNPCES	SLMSQHWDMV	SS		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
14	1	847.2854	-131.18	2	29.8	15.5	0	296-310	R.VWMCGGSLEIVPCSR.V	Carbamidomethyl: 13

Detailed Protein Report

Protein 268: thrombospondin type-1 domain-containing protein 7B [Homo sapiens]

Accession:	gi|122937257	**Score:**	29.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	175.5
Database Date:	2015-11-30	**pI:**	9.1
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MHNTADEVVL	YHKLAGPWGR	CTGDCGPGGV	QSRAVWCFHV	DGWTSHLSNC	GESNRPPKER	SCFRVCDWHS	DLFQWEVSDW
90	100	110	120	130	140	150	160
HHCVLVPYAR	GEVKPRTAEC	VTAQHGLQHR	MVRCIQKLNR	TVVANEICEH	FALQPPTEQA	CLIPCPRDCV	VSEFLPWSNC
170	180	190	200	210	220	230	240
SKGCGKKLQH	RTRAVIAPPL	FGGLQCPNLT	ESRACDAPIS	CPLGEEEYTF	SLKVGPWSKC	RLPHLKEINP	SGRTVLDFNS
250	260	270	280	290	300	310	320
DSNERVTFKH	QSYKAHHHSK	SWAIEIGYQT	RQVSCTRSDG	QNAMLSLCLQ	DSFPLTVQSC	IMPKDCETSQ	WSSWSPCSKT
330	340	350	360	370	380	390	400
CRSGSLLPGF	RSRSRNVKHM	AIGGGKECPE	LLEKEACIVE	GELLQQCPRY	SWRTSEWKEC	QVSLLLEQQD	PHWHVTGPVC
410	420	430	440	450	460	470	480
GGGIQTREVY	CAQSVPAAAA	LRAKEVSRPV	EKALCVGPAP	LPSQLCNIPC	STDCIVSSWS	AWGLCIHENC	HDPQGKKGFR
490	500	510	520	530	540	550	560
TRQRHVLMES	TGPAGHCPHL	VESVPCEDPM	CYRWLASEGI	CFPDHGKCGL	GHRILKAVCQ	NDRGEDVSGS	LCPVPPPPER
570	580	590	600	610	620	630	640
KSCEIPCRMD	CVLSEWTEWS	SCSQSCSNKN	SDGKQTRSRT	ILALAGEGGK	PCPPSQALQE	HRLCNDHSCM	QLHWETSPWG
650	660	670	680	690	700	710	720
PCSEDTLVTA	LNATIGWNGE	ATCGVGIQTR	RVFCVKSHVG	QVMTKRCPDS	TRPETVRPCF	LPCKKDCIVT	AFSEWTPCPR
730	740	750	760	770	780	790	800
MCQAGNATVK	QSRYRIIIQE	AANGGQECPD	TLYEERECED	VSLCPVYRWK	PQKWSPCILV	PESVWQGITG	SSEACGKGLQ
810	820	830	840	850	860	870	880
TRAVSCISDD	NRSAEMMECL	KQTNGMPLLV	QECTVPCRED	CTFTAWSKFT	PCSTNCEATK	SRRRQLTGKS	RKKEKCQDSD
890	900	910	920	930	940	950	960
LYPLVETELC	PCDEFISQPY	GNWSDCILPE	GRREPHRGLR	VQADSKECGE	GLRFRAVACS	DKNGRPVDPS	FCSSSGYIQE
970	980	990	1000	1010	1020	1030	1040
KCVIPCPFDC	KLSDWSSWGS	CSSSCGIGVR	IRSKWLKEKP	YNGGRPCPKL	DLKNQAQVHE	AVPCYSECNQ	YSWVVEHWSS
1050	1060	1070	1080	1090	1100	1110	1120
CKINNELRSL	RCGGGTQSRK	IRCVNTADGE	GGAVDSNLCN	QDEIPPETQS	CSLMCPNECV	MSEWGLWSKC	PQSCDPHTMQ
1130	1140	1150	1160	1170	1180	1190	1200
RRTRHLLRPS	LNSRTCAEDS	QVQPCLLNEN	CFQFQYNLTE	WSTCQLSENA	PCGQGVRTRL	LSCVCSDGKP	VSMDQCEQHN
1210	1220	1230	1240	1250	1260	1270	1280
LEKPQRMSIP	CLVECVVNCQ	LSGWTAWTEC	SQTCGHGGRM	SRTRFIIMPT	QGEGRPCPTE	LTQEKTCPVT	PCYSWVLGNW
1290	1300	1310	1320	1330	1340	1350	1360
SACKLEGGDC	GEGVQIRSLS	CMVHSGSISH	AAGRVEDALC	GEMPFQDSIL	KQLCSVPCPG	DCHLTEWSEW	STCELTCIDG
1370	1380	1390	1400	1410	1420	1430	1440
RSFETVGRQS	RSRTFIIQSF	ENQDSCPQQV	LETRPCTGGK	CYHYTWKASL	WNNNERTVWC	QRSDGVNVTG	GCSPQARPAA
1450	1460	1470	1480	1490	1500	1510	1520
IRQCIPACRK	PFSYCTQGGV	CGCEKGYTEI	MKSNGFLDYC	MKVPGSEDKK	ADVKNLSGKN	RPVNSKIHDI	FKGWSLQPLD
1530	1540	1550	1560	1570	1580		
PDGRVKIWVY	GVSGGAFLIM	IFLIFTSYLV	CKKPKPHQST	PPQQKPLTLA	YDGDLDM		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1180	1	883.7188	-3.03	3	44.4	19.1	1	1443-1465	R.QCIPACRKPFSYCTQGGVCGCEK.G	Carbamidomethyl: 2, 6, 13

Detailed Protein Report

Protein 269: FCH domain only protein 1 isoform a [Homo sapiens]

Accession:	gi|239049440	**Score:**	29.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	97.0
Database Date:	2015-11-30	**pI:**	6.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.7
		No. of unique Peptides:	2

```
        10         20         30         40         50         60         70         80
MSYFGEHFWG EKNHGFEVLY HSVKQGPIST KELADFIRER ATIEETYSKA MAKLSKLASN GTPMGTFAPL WEVFRVSSDK
        90        100        110        120        130        140        150        160
LALCHLELTR KLQDLIKDVL RYGEEQLKTH KKCKEEVVST LDAVQVLSGV SQLLPKSREN YLNRCMDQER LRRESTSQKE
       170        180        190        200        210        220        230        240
MDKAETKTKK AAESLRRSVE KYNSARADFE QKMLDSALRF QAMEETHLRH MKALLGSYAH SVEDTHVQIG QVHEEFKQNI
       250        260        270        280        290        300        310        320
ENVSVEMLLR KFAESKGTGR EKPGPLDFEA YSAAALQEAM KRLRGAKAFR LPGLSRRERE PEPPAAVDFL EPDSGTCPEV
       330        340        350        360        370        380        390        400
DEEGFTVRPD VTQNSTAEPS RFSSSDSDFD DEEPRKFYVH IKPAPARAPA CSPEAAAAQL RATAGSLILP PGPGGTMKRH
       410        420        430        440        450        460        470        480
SSRDAAGKPQ RPRSAPRTSS CAERLQSEEQ VSKNLFGPPL ESAFDHEDFT GSSSLGFTSS PSPFSSSSPE NVEDSGLDSP
       490        500        510        520        530        540        550        560
SHAAPGPSPD SWVPRPGTPQ SPPSCRAPPP EARGIRAPPL PDSPQPLASS PGPWGLEALA GGDLMPAPAD PTAREGLAAP
       570        580        590        600        610        620        630        640
PRRLRSRKVS CPLTRSNGDL SRSLSPSPLG SSAASTALER PSFLSQTGHG VSRGPSPVVL GSQDALPIAT AFTEYVHAYF
       650        660        670        680        690        700        710        720
RGHSPSCLAR VTGELTMTFP AGIVRVFSGT PPPPVLSFRL VHTTAIEHFQ PNADLLFSDP SQSDPETKDF WLNMAALTEA
       730        740        750        760        770        780        790        800
LQRQAEQNPT ASYYNVVLLR YQFSRPGPQS VPLQLSAHWQ CGATLTQVSV EYGYRPGATA VPTPLTNVQI LLPVGEPVTN
       810        820        830        840        850        860        870        880
VRLQPAATWN LEEKRLTWRL PDVSEAGGSG RLSASWEPLS GPSTPSPVAA QFTSEGTTLS GVDLELVGSG YRMSLVKRRF
       890        900
ATAAPPQGCT W
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1900	1	693.7929	-23.70	2	53.8	12.5	0	2-12	M.SYFGEHFWGEK.N	
2590	1	731.8881	54.25	2	62.9	17.4	1	879-891	R.RFATAAPPQGCTW.-	Carbamidomethyl: 11

Detailed Protein Report

Protein 270: probable G-protein coupled receptor 27 [Homo sapiens]

Accession: gi|9506747
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 29.9
MW [kDa]: 39.8
pI: 10.7
Sequence Coverage [%]: 12.0
No. of unique Peptides: 2

```
        10         20         30         40         50         60         70         80
MANASEPGGS GGGEAAALGL KLATLSLLLC VSLAGNVLFA LLIVRERSLH RAPYYLLLDL CLADGLRALA CLPAVMLAAR
        90        100        110        120        130        140        150        160
RAAAAAGAPP GALGCKLLAF LAALFCFHAA FLLLGVGVTR YLAIAHHRFY AERLAGWPCA AMLVCAAWAL ALAAAFPPVL
       170        180        190        200        210        220        230        240
DGGGDDEDAP CALEQRPDGA PGALGFLLLL AVVVGATHLV YLRLLFFIHD RRKMRPARLV PAVSHDWTFH GPGATGQAAA
       250        260        270        280        290        300        310        320
NWTAGFGRGP TPPALVGIRP AGPGRGARRL LVLEEFKTEK RLCKMFYAVT LLFLLLWGPY VVASYLRVLV RPGAVPQAYL
       330        340        350        360        370        380
TASVWLTFAQ AGINPVVCFL FNRELRDCFR AQFPCCQSPR TTQATHPCDL KGIGL
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1926	1	857.3073	-135.85	2	54.2	12.0	0	2-21	M.ANASEPGGSGGGEAAALGLK.L	
250	1	910.4923	61.03	3	32.8	17.9	2	351-375	R.AQFPCCQSPRTTQATHPCDLKGIGL.-	Carbamidomethyl: 6

Detailed Protein Report

Protein 271: **PREDICTED: transforming acidic coiled-coil-containing protein 3 isoform X2 [Homo sapiens]**

Accession:	gi|530375987	**Score:**	29.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	53.9
Database Date:	2015-11-30	**pI:**	5.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	5.2
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MSLQVLNDKN VSNEKNTENC DFLFSPPEVT GRSSVLRVSQ KENVPPKNLA KAMKVTFQTP LRDPQTHRIL SPSMASKLEA
        90        100        110        120        130        140        150        160
PFTQDDTLGL ENSHPVWTQK EKQLHSASAE DTPVVQLAAE TPTAESKERA LNSASTSLPT SCPGSEPVPT HQQGQPALEL
       170        180        190        200        210        220        230        240
KEESFRDPAE VLGTGAEVDY LEQFGTSSFK ESALRKQSLY LKFDPLLRDS PGRPVPVATE TSSMHGANET PSGRPREAKL
       250        260        270        280        290        300        310        320
VEFDFLGALD IPVPGPPPGV PAPGGPPLST GPIVDLLQYS QKDLDAVVRT QVKATQEENR ELRSRCEELH GKNLELGKIM
       330        340        350        360        370        380        390        400
DRFEEVVYQA MEEVQKQKEL SKAEIQKVLK EKDQLTTDLN SMEKSFSDLF KRFEKQKEVI EGYRKNEESL KKCVEDYLAR
       410        420        430        440        450        460        470        480
ITQEGQRYQA LKAHAEEKLQ LANEEIAQVR SKAQAEALAL QASLRKEQMR IQSLEKTVEQ KTKENEELTR ICDDLISKME
       490
KI
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1875	1	917.8351	-120.99	2	53.5	12.8	1	464-478	K.ENEELTRICDDLISK.M	Carbamidomethyl: 9

Detailed Protein Report

Protein 272: ATP-binding cassette sub-family A member 12 isoform b [Homo sapiens]

Accession:	gi|27881501	**Score:**	29.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	256.8
Database Date:	2015-11-30	**pI:**	7.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.1
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MFTYIKIITS	GDSDNITHVW	NEDDGQTLSP	SSLAAQLLIL	ENFEDALLNI	SANSPYIPYL	ACVRNVTDSL	ARGSPENLRL
90	100	110	120	130	140	150	160
LQSTIRFKKS	FLRNGSYEDY	FPPVPEVLKS	KLSQLRNLTE	LLCESETFSL	IEKSCQLSDM	SFGSLCEESE	FDLQLLEAAE
170	180	190	200	210	220	230	240
LGTEIAASLL	YHDNVISKKV	RDLLTGDPSK	INLNMDQFLE	QALQMNYLEN	ITQLIPIIEA	MLHVNNSADA	SEKPGQLLEM
250	260	270	280	290	300	310	320
FKNVEELKED	LRRTTGMSNR	TIDKLLAIPI	PDNRAEIISQ	VFWLHSCDTN	ITTPKLEDAM	KEFCNLSLSE	RSRQSYLIGL
330	340	350	360	370	380	390	400
TLLHYLNIYN	FTYKVFFPRK	DQKPVEKMME	LFIRLKEILN	QMASGTHPLL	DKMRSLKQMH	LPRSVPLTQA	MYRSNRMNTP
410	420	430	440	450	460	470	480
QGSFSTISQA	LCSQGITTEY	LTAMLPSSQR	PKGNHTKDFL	TYKLTKEQIA	SKYGIPINST	PFCFSLYKDI	INMPAGPVIW
490	500	510	520	530	540	550	560
AFLKPMLLGR	ILYAPYNPVT	KAIMEKSNVT	LRQLAELREK	SQEWMDKSPL	FMNSFHLLNQ	AIPMLQNTLR	NPFVQVFVKF
570	580	590	600	610	620	630	640
SVGLDAVELL	KQIDELDILR	LKLENNIDII	DQLNTLSSLT	VNISSCVLYD	RIQAAKTIDE	MEREAKRLYK	SNELFGSVIF
650	660	670	680	690	700	710	720
KLPSNRSWHR	GYDSGNVFLP	PVIKYTIRMS	LKTAQTTRSL	RTKIWAPGPH	NSPSHNQIYG	RAFIYLQDSI	ERAIIELQTG
730	740	750	760	770	780	790	800
RNSQEIAVQV	QAIPYPCFMK	DNFLTSVSYS	LPIVLMVAWV	VFIAAFVKKL	VYEKDLRLHE	YMKMMGVNSC	SHFFAWLIES
810	820	830	840	850	860	870	880
VGFLLVTIVI	LIIILKFGNI	LPKTNGFILF	LYFSDYSFSV	IAMSYLISVF	FNNTNIAALI	GSLIYIIAFF	PFIVLVTVEN
890	900	910	920	930	940	950	960
ELSYVLKVFM	SLLSPTAFSY	ASQYIARYEE	QGIGLQWENM	YTSPVQDDTT	SFGWLCCLIL	ADSFIYFLIA	WYVRNVFPGT
970	980	990	1000	1010	1020	1030	1040
YGMAAPWYFP	ILPSYWKERF	GCAEVKPEKS	NGLMFTNIMM	QNTNPSASPE	YMFSSNIEPE	PKDLTVGVAL	HGVTKIYGSK
1050	1060	1070	1080	1090	1100	1110	1120
VAVDNLNLNF	YEGHITSLLG	PNGAGKTTTI	SMLTGLFGAS	AGTIFVYGKD	IKTDLHTVRK	NMGVCMQHDV	LFSYLTTKEH
1130	1140	1150	1160	1170	1180	1190	1200
LLLYGSIKVP	HWTKKQLHEE	VKRTLKDTGL	YSHRHKRVGT	LSGGMKRKLS	ISIALIGGSR	VVILDEPSTG	VDPCSRRSIW
1210	1220	1230	1240	1250	1260	1270	1280
DVISKNKTAR	TIILSTHHLD	EAEVLSDRIA	FLEQGGLRCC	GSPFYLKEAF	GDGYHLTLTK	KKSPNLNANA	VCDTMAVTAM
1290	1300	1310	1320	1330	1340	1350	1360
IQSHLPEAYL	KEDIGGELVY	VLPPFSTKVS	GAYLSLLRAL	DNGMGDLNIG	CYGISDTTVE	EVFLNLTKES	QKNSAMSLEH
1370	1380	1390	1400	1410	1420	1430	1440
LTQKKIGNSN	ANGISTPDDL	SVSSSNFTDR	DDKILTRGER	LDGFGLLLKK	IMAILIKRFH	HTRRNWKGLI	AQVILPIVFV
1450	1460	1470	1480	1490	1500	1510	1520
TTAMGLGTLR	NSSNSYPEIQ	ISPSLYGTSE	QTAFYANYHP	STEALVSAMW	DFPGIDNMCL	NTSDLQCLNK	DSLEKWNTSG
1530	1540	1550	1560	1570	1580	1590	1600
EPITNFGVCS	CSENVQECPK	FNYSPPHRRT	YSSQVIYNLT	GQRVENYLIS	TANEFVQKRY	GGWSFGLPLT	KDLRFDITGV
1610	1620	1630	1640	1650	1660	1670	1680
PANRTLAKVW	YDPEGYHSLP	AYLNSLNNFL	LRVNMSKYDA	ARHGIIMYSH	PYPGVQDQEQ	ATISSLIDIL	VALSILMGYS
1690	1700	1710	1720	1730	1740	1750	1760
VTTASFVTYV	VREHQTKAKQ	LQHISGIGVT	CYWVTNFIYD	MVFYLVPVAF	SIGIIAIFKL	PAFYSENNLG	AVSLLLLLFG
1770	1780	1790	1800	1810	1820	1830	1840
YATFSWMYLL	AGLFHETGMA	FITYVCVNLF	FGINSIVSLS	VVYFLSKEKP	NDPTLELISE	TLKRIFLIFP	QFCFGYGLIE
1850	1860	1870	1880	1890	1900	1910	1920
LSQQQSVLDF	LKAYGVEYPN	ETFEMNKLGA	MFVALVSQGT	MFFSLRLLIN	ESLIKKLRLF	FRKFNSSHVR	ETIDEDEDVR
1930	1940	1950	1960	1970	1980	1990	2000
AERLRVESGA	AEFDLVQLYC	LTKTYQLIHK	KIIAVNNISI	GIPAGECFGL	LGVNGAGKTT	IFKMLTGDII	PSSGNILIRN
2010	2020	2030	2040	2050	2060	2070	2080
KTGSLGHVDS	HSSLVGYCPQ	EDALDDLVTV	EEHLYFYARV	HGIPEKDIKE	TVHKLLRRLH	LMPFKDRATS	MCSYGTKRKL
2090	2100	2110	2120	2130	2140	2150	2160
STALALIGKP	SILLLDEPSS	GMDPKSKRHL	WKIISEEVQN	KCSVILTSHS	MEECEALCTR	LAIMVNGKFQ	CIGSLQHIKS
2170	2180	2190	2200	2210	2220	2230	2240
RFGRGFTVKV	HLKNNKVTME	TLTKFMQLHF	PKTYLKDQHL	SMLEYHVPVT	AGGVANIFDL	LETNKTALNI	TNFLVSQTTL
2250	2260	2270	2280				
EEVFINFAKD	QKSYETADTS	SQGSTISVDS	QDDQMES				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1898	1	890.3676	-104.02	2	53.6	10.7	1	341-354	K.DQKPVEKMMELFIR.L	Oxidation: 8
2766	1	702.8107	-71.83	2	65.0	19.2	1	612-623	R.IQAAKTIDEMER.E	

Detailed Protein Report

Protein 273: zinc finger C4H2 domain-containing protein isoform 2 [Homo sapiens]

Accession:	gi|295842335	**Score:**	29.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	23.5
Database Date:	2015-11-30	**pI:**	7.9
		Sequence Coverage [%]:	13.9
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|345091006	refseq_human (refseq_human_20140103.fasta)	zinc finger C4H2 domain-containing protein isoform 2 [Homo sapiens]

10	20	30	40	50	60	70	80
MEKIKARLKA	EFEALESEER	HLKEYKQEMD	LLLQEKMAHV	EELRLIHADI	NVMENTIKQS	ENDLNKLLES	TRRLHDEYKP
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
LKEHVDALRM	TLGLQRLPDL	CEEEEKLSLD	YFEKQKAEWQ	TEPQEPPIPE	SLAAAAAAAQ	QLQVARKQDT	RQTATFRQQP
170	**180**	**190**	**200**	**210**			
PPMKACLSCH	QQIHRNAPIC	PLCKAKSRSR	NPKKPKRKQD	E			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2312	1	1051.3738	-133.19	2	58.8	13.3	1	158-175	R.QQPPPMKACLSCHQQIHR.N	

Detailed Protein Report

Protein 274: PREDICTED: uncharacterized protein LOC102724905 [Homo sapiens]

Accession:	gi|578835678	**Score:**	29.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	22.0
Database Date:	2015-11-30	**pI:**	10.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	8.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MKCSTSNCII	SIKDYTSIRI	NVAEVDKVTS	RFNGQFKTYA	FGGSPGTGVT	GGKGREGGRS	FCAGEGNERN	GKGTAGCEAR
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
DVPGSAAGPA	RGRAAPLHPA	PGPPLRGAIL	QAAVAGTGGG	GCSGHCGAEA	RRQDGNHASC	SQLGLDSTNG	DFSYGFELGP
170	**180**	**190**	**200**	**210**	**220**		
WCISKCNSAN	CNGKHMDRST	PHHLGAKRCR	LQASSLLENR	GLQALEEPAD	PGLLA		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2384	1	1045.1618	131.45	2	60.1	16.4	2	2-19	M.KCSTSNCIISIKDYTSIR.I	Carbamidomethyl: 7

Detailed Protein Report

Protein 275: structural maintenance of chromosomes protein 4 isoform 2 [Homo sapiens]

Accession:	gi|570700827	**Score:**	29.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	144.4
Database Date:	2015-11-30	**pI:**	6.7
		Sequence Coverage [%]:	2.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
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
289	4	862.8586	-89.06	2	33.0	18.8	2	457-471	R.EKELMGFSKSVNEAR.S	

Detailed Protein Report

Protein 276: PREDICTED: integrin beta-4 isoform X9 [Homo sapiens]

Accession: gi|578830859

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Modification(s): Carbamidomethyl

Score: 29.7

MW [kDa]: 198.8

pI: 5.8

Sequence Coverage [%]: 1.2

No. of unique Peptides: 1

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

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

Detailed Protein Report

	Cmpds.		[ppm]		[min]					
2157	1	841.3003	-27.93	2	57.2	16.5	1	82-94	K.DCAYCTDEMFRDR.R	Carbamidomethyl: 2

Detailed Protein Report

Protein 277: **zinc-binding alcohol dehydrogenase domain-containing protein 2 [Homo sapiens]**

Accession:	gi|28557745	**Score:**	29.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	40.1
Database Date:	2015-11-30	**pI:**	9.2
Modification(s):	Oxidation	**Sequence Coverage [%]:**	9.0
		No. of unique Peptides:	2

Quantitation

MD:MU **Median:** 0.80 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MLRLVPTGAR	AIVDMSYARH	FLDFQGSAIP	QAMQKLVVTR	LSPNFREAVT	LSRDCPVPLP	GDGDLLVRNR	FVGVNASDIN
90	100	110	120	130	140	150	160
YSAGRYDPSV	KPPFDIGFEG	IGEVVALGLS	ASARYTVGQA	VAYMAPGSFA	EYTVVPASIA	TPVPSVKPEY	LTLLVSGTTA
170	180	190	200	210	220	230	240
YISLKELGGL	SEGKKVLVTA	AAGGTGQFAM	QLSKKAKCHV	IGTCSSDEKS	AFLKSLGCDR	PINYKTEPVG	TVLKQEYPEG
250	260	270	280	290	300	310	320
VDVVYESVGG	AMFDLAVDAL	ATKGRLIVIG	FISGYQTPTG	LSPVKAGTLP	AKLLKKSASV	QGFFLNHYLS	KYQAAMSHLL
330	340	350	360	370	380		
EMCVSGDLVC	EVDLGDLSPE	GRFTGLESIF	RAVNYMYMGK	NTGKIVVELP	HSVNSKL		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
40	4	1068.4865	-82.29	2	29.9	13.9	2	1-19	-.MLRLVPTGARAIVDMSYAR.H	Oxidation: 1	
117	1	849.3965	-46.47	2	30.9	15.8	0	297-311	K.SASVQGFFLNHYLSK.Y		MD:MU 0.80

Detailed Protein Report

Protein 278: cyclic nucleotide-gated cation channel beta-1 isoform c [Homo sapiens]

Accession:	gi|554790418	**Score:**	29.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	139.1
Database Date:	2015-11-30	**pI:**	4.6
		Sequence Coverage [%]:	1.9
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MLGWVQRVLP QPPGTPRKTK MQEEEEVEPE PEMEAEVEPE PNPEEAETES ESMPPEESFK EEEVAVADPS PQETKEAALT
        90        100        110        120        130        140        150        160
STISLRAQGA EISEMNSPSR RVLTWLMKGV EKVIPQPVHS ITEDPAQILG HGSTGDTGCT DEPNEALEAQ DTRPGLRLLL
       170        180        190        200        210        220        230        240
WLEQNLERVL PQPPKSSEVW RDEPAVATAP PGRPQEMGPK LQARETPSLP TPIPLQPKEE PKEAPAPEPQ PGSQAQTSSL
       250        260        270        280        290        300        310        320
PPTRDPARLV AWVLHRLEMA LPQPVLHGKI GEQEPDSPGI CDVQTISILP GGQVEPDLVL EEVEPPWEDA HQDVSTSPQG
       330        340        350        360        370        380        390        400
TEVVPAYEEE NKAVEKMPRE LSRIEEEKED EEEEEEEEEE EEEEEVTEVL LDSCVVSQVG VGQSEEDGTR PQSTSDQKLW
       410        420        430        440        450        460        470        480
EEVGEEAKKE AEEKAKEEAE EVAEEEAEKE PQDWAETKEE PEAEAEAASS GVPATKQHPE VQVEDTDADS CPLMAEENPP
       490        500        510        520        530        540        550        560
STVLPPPSPA KSDTLIVPSS ASGTHRKKLP SEDDEAEELK ALSPAESPVV AWSDPTTPKD TDGQDRAAST ASTNSAIIND
       570        580        590        600        610        620        630        640
RLQELVKLFK ERTEKVKEKL IDPDVTSDEE SPKPSPAKKA PEPAPDTKPA EAEPVEEEHY CDMLCCKFKH RPWKKYQFPQ
       650        660        670        680        690        700        710        720
SIDPLTNLMY VLWLFFVVMA WNWNCWLIPV RWAFPYQTPD NIHHWLLMDY LCDLIYFLDI TVFQTRLQFV RGGDIITDKK
       730        740        750        760        770        780        790        800
DMRNNYLKSR RFKMDLLSLL PLDFLYLKVG VNPLLRLPRC LKYMAFFEFN SRLESILSKA YVYRVIRTTA YLLYSLHLNS
       810        820        830        840        850        860        870        880
CLYYWASAYQ GLGSTHWVYD GVGNSYIRCY YFAVKTLITI GGLPDPKTLF EIVFQLLNYF TGVFAFSVMI GQMRDVVGAA
       890        900        910        920        930        940        950        960
TAGQTYYRSC MDSTVKYMNF YKIPKSVQNR VKTWYEYTWH SQGMLDESEL MVQLPDKMRL DLAIDVNYNI VSKVALFQGC
       970        980        990       1000       1010       1020       1030       1040
DRQMIFDMLK RLRSVVYLPN DYVCKKGEIG REMYIIQAGQ VQVLGGPDGK SVLVTLKAGS VFGEISLLAV GGGNRRTANV
      1050       1060       1070       1080       1090       1100       1110       1120
VAHGFTNLFI LDKKDLNEIL VHYPESQKLL RKKARRMLRS NNKPKEEKSV LILPPRAGTP KLFNAALAMT GKMGGKGAKG
      1130       1140       1150       1160       1170       1180       1190       1200
GKLAHLRARL KELAALEAAA KQQELVEQAK SSQDVKGEEG SAAPDQHTHP KEAATDPPAP RTPPEPPGSP PSSPPPASLG
      1210       1220       1230       1240       1250
RPEGEEEGPA EPEEHSVRIC MSPGPEPGEQ ILSVKMPEER EEKAE
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1512	1	851.5801	69.44	1	48.6	11.1	1	1120-1127	K.GGKLAHLR.A	

Detailed Protein Report

Protein 279: transient receptor potential cation channel subfamily V member 5 [Homo sapiens]

Accession: gi|17505200
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 29.6
MW [kDa]: 82.5
pI: 6.0
Sequence Coverage [%]: 3.0
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MGGFLPKAEG	PGSQLQKLLP	SFLVREQDWD	QHLDKLHMLQ	QKRILESPLL	RASKENDLSV	LRQLLLDCTC	DVRQRGALGE
90	100	110	120	130	140	150	160
TALHIAALYD	NLEAALVLME	AAPELVFEPT	TCEAFAGQTA	LHIAVVNQNV	NLVRALLTRR	ASVSARATGT	AFRRSPRNLI
170	180	190	200	210	220	230	240
YFGEHPLSFA	ACVNSEEIVR	LLIEHGADIR	AQDSLGNTVL	HILILQPNKT	FACQMYNLLL	SYDGHGDHLQ	PLDLVPNHQG
250	260	270	280	290	300	310	320
LTPFKLAGVE	GNTVMFQHLM	QKRRHIQWTY	GPLTSILYDL	TEIDSWGEEL	SFLELVVSSD	KREARQILEQ	TPVKELVSFK
330	340	350	360	370	380	390	400
WNKYGRPYFC	ILAALYLLYM	ICFTTCCVYR	PLKFRGGNRT	HSRDITILQQ	KLLQEAYETR	EDIIRLVGEL	VSIVGAVIIL
410	420	430	440	450	460	470	480
LLEIPDIFRV	GASRYFGKTI	LGGPFHVIII	TYASLVLVTM	VMRLTNTNGE	VVPMSFALVL	GWCSVMYFTR	GFQMLGPFTI
490	500	510	520	530	540	550	560
MIQKMIFGDL	MRFCWLMAVV	ILGFASAFYI	IFQTEDPTSL	GQFYDYPMAL	FTTFELFLTV	IDAPANYDVD	LPFMFSIVNF
570	580	590	600	610	620	630	640
AFAIIATLLM	LNLFIAMMGD	THWRVAQERD	ELWRAQVVAT	TVMLERKLPR	CLWPRSGICG	CEFGLGDRWF	LRVENHNDQN
650	660	670	680	690	700	710	720
PLRVLRYVEV	FKNSDKEDDQ	EHPSEKQPSG	AESGTLARAS	LALPTSSLSR	TASQSSSHRG	WEILRQNTLG	HLNLGLNLSE
730							
GDGEEVYHF							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
87	1	829.3594	10.76	2	30.8	10.5	1	653-666	K.NSDKEDDQEHPSEK.Q	

Detailed Protein Report

Protein 280: spindle and kinetochore-associated protein 1 [Homo sapiens]

Accession:	gi|21450832	**Score:**	29.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	29.5
Database Date:	2015-11-30	**pI:**	6.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	12.5
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|88014625	refseq_human (refseq_human_20140103.fasta)	spindle and kinetochore-associated protein 1 [Homo sapiens]

10	20	30	40	50	60	70	80
MASSDLEQLC	SHVNEKIGNI	KKTLSLRNCG	QEPTLKTVLN	KIGDEIIVIN	ELLNKLELEI	QYQEQTNNSL	KELCESLEED
90	100	110	120	130	140	150	160
YKDIEHLKEN	VPSHLPQVTV	TQSCVKGSDL	DPEEPIKVEE	PEPVKKPPKE	QRSIKEMPFI	TCDEFNGVPS	YMKSRLTYNQ
170	180	190	200	210	220	230	240
INDVIKEINK	AVISKYKILH	QPKKSMNSVT	RNLYHRFIDE	ETKDTKGRYF	IVEADIKEFT	TLKADKKFHV	LLNILRHCRR
250	260						
LSEVRGGGLT	RYVIT						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1627	1	853.3841	-128.05	2	50.1	16.5	2	227-239	K.KFHVLLNILRHCR.R	Carbamidomethyl: 12

Detailed Protein Report

Protein 281: probable ATP-dependent RNA helicase DDX46 [Homo sapiens]

Accession:	gi|41327773	**Score:**	29.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	117.3
Database Date:	2015-11-30	**pI:**	9.9
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	3.0
		No. of unique Peptides:	2

```
        10         20         30         40         50         60         70         80
MGRESRHYRK RSASRGRSGS RSRSRSPSDK RSKRGDDRRS RSRDRDRRRE RSRSRDKRRS RSRDRKRLRR SRSRERDRSR
        90        100        110        120        130        140        150        160
ERRRSRSRDR RRSRSRSRGR RSRSSSPGNK SKKTENRSRS KEKTDGGESS KEKKKDKDDK EDEKEKDAGN FDQNKLEEEM
       170        180        190        200        210        220        230        240
RKRKERVEKW REEQRKKAME NIGELKKEIE EMKQGKKWSL EDDDDDEDDP AEAEKEGNEM EGEELDPLDA YMEEVKEEVK
       250        260        270        280        290        300        310        320
KFNMRSVKGG GGNEKKSGPT VTKVVTVVTT KKAVVDSDKK KGELMENDQD AMEYSSEEEE VDLQTALTGY QTKQRKLLEP
       330        340        350        360        370        380        390        400
VDHGKIEYEP FRKNFYVEVP ELAKMSQEEV NVFRLEMEGI TVKGKGCPKP IKSWVQCGIS MKILNSLKKH GYEKPTPIQT
       410        420        430        440        450        460        470        480
QAIPAIMSGR DLIGIAKTGS GKTIAFLLPM FRHIMDQRSL EEGEGPIAVI MTPTRELALQ ITKECKKFSK TLGLRVVCVY
       490        500        510        520        530        540        550        560
GGTGISEQIA ELKRGAEIIV CTPGRMIDML AANSGRVTNL RRVTYVVLDE ADRMFDMGFE PQVMRIVDNV RPDRQTVMFS
       570        580        590        600        610        620        630        640
ATFPRAMEAL ARRILSKPIE VQVGGRSVVC SDVEQQVIVI EEEKKFLKLL ELLGHYQESG SVIIFVDKQE HADGLLKDLM
       650        660        670        680        690        700        710        720
RASYPCMSLH GGIDQYDRDS IINDFKNGTC KLLVATSVAA RGLDVKHLIL VVNYSCPNHY EDYVHRAGRT GRAGNKGYAY
       730        740        750        760        770        780        790        800
TFITEDQARY AGDIIKALEL SGTAVPPDLE KLWSDFKDQQ KAEGKIIKKS SGFSGKGFKF DETEQALANE RKKLQKAALG
       810        820        830        840        850        860        870        880
LQDSDDEDAA VDIDEQIESM FNSKKRVKDM AAPGTSSVPA PTAGNAEKLE IAKRLALRIN AQKNLGIESQ DVMQQATNAI
       890        900        910        920        930        940        950        960
LRGGTILAPT VSAKTIAEQL AEKINAKLNY VPLEKQEEER QDGGQNESFK RYEEELEIND FPQTARWKVT SKEALQRISE
       970        980        990       1000       1010       1020       1030       1040
YSEAAITIRG TYFPPGKEPK EGERKIYLAI ESANELAVQK AKAEITRLIK EELIRLQNSY QPTNKGRYKV L
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1641	1	1052.5617	14.08	2	50.3	18.9	2	364-382	K.GKGCPKPIKSWVQCGISMK.I	Carbamidomethyl: 4
1054	1	752.4550	172.69	2	42.8	10.7	0	534-545	R.MFDMGFEPQVMR.I	Oxidation: 1

Detailed Protein Report

Protein 282: ATP-binding cassette sub-family A member 13 [Homo sapiens]

Accession:	gi|31657092	**Score:**	29.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	575.8
Database Date:	2015-11-30	**pI:**	6.0
		Sequence Coverage [%]:	0.5
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MGHAGCQFKA LLWKNWLCRL RNPVLFLAEF FWPCILFVIL TVLRFQEPPR YRDICYLQPR DLPSCGVIPF VQSLLCNTGS
        90        100        110        120        130        140        150        160
RCRNFSYEGS MEHHFRLSRF QTAADPKKVN NLAFLKEIQD LAEEIHGMMD KAKNLKRLWV ERSNTPDSSY GSSFFTMDLN
       170        180        190        200        210        220        230        240
KTEEVILKLE SLHQQPHIWD FLLLLPRLHT SHDHVEDGMD VAVNLLQTIL NSLISLEDLD WLPLNQTFSQ VSELVLNVTI
       250        260        270        280        290        300        310        320
STLTFLQQHG VAVTEPVYHL SMQNIVWDPQ KVQYDLKSQF GFDDLHTEQI LNSSAELKEI PTDTSLEKMV CSVLSSTSED
       330        340        350        360        370        380        390        400
EAEKWGHVGG CHPKWSEAKN YLVHAVSWLR VYQQVFVQWQ QGSLLQKTLT GMGHSLEALR NQFEEESKPW KVVEALHTAL
       410        420        430        440        450        460        470        480
LLLNDSLSAD GPKDNHTFPK ILQHLWKLQS LLQNLPQWPA LKRFLQLDGA LRNAIAQNLH FVQEVLICLE TSANDFKWFE
       490        500        510        520        530        540        550        560
LNQLKLEKDV FFWELKQMLA KNAVCPNGRF SEKEVFLPPG NSSIWGGLQG LLCYCNSSET SVLNKLLGSV EDADRILQEV
       570        580        590        600        610        620        630        640
ITWHKNMSVL IPEEYLDWQE LEMQLSEASL SCTRLFLLLG ADPSPENDVF SSDCKHQLVS TVIFHTLEKT QFFLEQAYYW
       650        660        670        680        690        700        710        720
KAFKKFIRKT CEVAQYVNMQ ESFQNRLLAF PEESPCFEEN MDWKMISDNY FQFLNNLLKS PTASISRALN FTKHLLMMEK
       730        740        750        760        770        780        790        800
KLHTLEDEQM NFLLSFVEFF EKLLLPNLFD SSIVPSFHSL PSLTEDILNI SSLWTNHLKS LKRDPSATDA QKLLEFGNEV
       810        820        830        840        850        860        870        880
IWKMQTLGSH WIRKEPKNLL RFIELILFEI NPKLLELWAY GISKGKRAKL ENFFTLLNFS VPENEILSTS FNFSQLFHSD
       890        900        910        920        930        940        950        960
WPKSPAMNID FVRLSEAIIT SLHEFGFLEQ EQISEALNTV YAIRNASDLF SALSEPQKQE VDKILTHIHL NVFQDKDSAL
       970        980        990       1000       1010       1020       1030       1040
LLQIYSSFYR YIYELLNIQS RGSSLTFLTQ ISKHILDIIK QFNFQNISKA FAFLFKTAEV LGGISNVSYC QQLLSIFNFL
      1050       1060       1070       1080       1090       1100       1110       1120
ELQAQSFMST EGQELEVIHT TLTGLKQLLI IDEDFRISLF QYMSQFFNSS VEDLLDNKCL ISDNKHISSV NYSTSEESSF
      1130       1140       1150       1160       1170       1180       1190       1200
VFPLAQIFSN LSANVSVFNK FMSIHCTVSW LQMWTEIWET ISQLFKFDMN VFTSLHHGFT QLLDELEDDV KVSKSCQGIL
      1210       1220       1230       1240       1250       1260       1270       1280
PTHNVARLIL NLFKNVTQAN DFHNWEDFLD LRDFLVALGN ALVSVKKLNL EQVEKSLFTM EAALHQLKTF PFNESTSREF
      1290       1300       1310       1320       1330       1340       1350       1360
LNSLLEVFIE FSSTSEYIVR NLDSINDFLS NNLTNYGEKF ENIITELREA IVFLRNVSHD RDLFSCADIF QNVTECILED
      1370       1380       1390       1400       1410       1420       1430       1440
GFLYVNTSQR MLRILDTLNS TFSSENTISS LKGCIVWLDV INHLYLLSNS SFSQGHLQNI LGNFRDIENK MNSILKIVTW
      1450       1460       1470       1480       1490       1500       1510       1520
VLNIKKPLCS SNGSHINCVN IYLKDVTDFL NIVLTTVFEK EKKPKFEILL ALLNDSTKQV RMSINNLTTD FDFASQSNWR
      1530       1540       1550       1560       1570       1580       1590       1600
YFTELILRPI EMSDEIPNQF QNIWLHLITL GKEFQKLVKG IYFNILENNS SSKTENLLNI FATSPKEKDV NSVGNSIYHL
      1610       1620       1630       1640       1650       1660       1670       1680
ASYLAFSLSH DLQNSPKIII SPEIMKATGL GIQLIRDVFN SLMPVVHHTS PQNAGYMQAL KKVTSVMRTL KKADIDLLVD
      1690       1700       1710       1720       1730       1740       1750       1760
QLEQVSVNLM DFFKNISSVG TGNLVVNLLV GLMEKFADSS HSWNVNHLLQ LSRLFPKDVV DAVIDVYYVL PHAVRLLQGV
      1770       1780       1790       1800       1810       1820       1830       1840
PGKNITEGLK DVYSFTLLHG ITISNITKED FAIVIKILLD TIELVSDKPD IISEALACFP VVWCWNHTNS GFRQNSKIDP
      1850       1860       1870       1880       1890       1900       1910       1920
CNVHGLMSSS FYGKVASILD HFHLSPQGED SPCSNESSRM EITRKVVCII HELVDWNSIL LELSEVFHVN ISLVKTVQKF
      1930       1940       1950       1960       1970       1980       1990       2000
WHKILPFVPP SINQTRDSIS ELCPSGSIKQ VALQIIEKLK NVNFTKVTSG ENILDKLSSL NKILNINEDT ETSVQNIISS
      2010       2020       2030       2040       2050       2060       2070       2080
NLERTVQLIS EDWSLEKSTH NLLSLFMMLQ NANVTGSSLE ALSSFIEKSE TPYNFEELWP KFQQIMKDLT QDFRIRHLLS
      2090       2100       2110       2120       2130       2140       2150       2160
EMNKGIKSIN SMALQKITLQ FAHFLEILDS PSLKTLEIIE DFLLVTKNWL QEYANEDYSR MIETLFIPVT NESSTEDIAL
      2170       2180       2190       2200       2210       2220       2230       2240
LAKAIATFWG SLKNISRAGN FDVAFLTHLL NQEQLTNFSV VQLLFENILI NLINNLAGNS QEAAWNLNDT DLQIMNFINL
      2250       2260       2270       2280       2290       2300       2310       2320
ILNHMQSETS RKTVLSLRSI VDFTEQFLKT FFSLFLKEDS ENKISLLLKY FHKDVIAEMS FVPKDKILEI LKLDQFLTLM
      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
2092	1	1030.3822	-211.70	1	56.3	15.0	1	3972-3981	K.QTRALSGGLK.R	

Detailed Protein Report

Protein 283: PREDICTED: uncharacterized protein KIAA1109 isoform X13 [Homo sapiens]

Accession:	gi|578809469	**Score:**	29.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	409.1
Database Date:	2015-11-30	**pI:**	6.0
		Sequence Coverage [%]:	0.9
		No. of unique Peptides:	2

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Detailed Protein Report

10	20	30	40	50	60	70	80
MDQRKNESIV	PSITQLEDFL	TEHNSNVVWL	LVATILSCGW	IIYLTYYNSR	NVGLILTLVL	NRLYKHGYIH	IGSFSFSVLS
90	100	110	120	130	140	150	160
GKVMVREIYY	ITEDMSIRIQ	DGFIIFRWWK	MYNPKQKQHD	PKAETRLYIT	VNDFEFHVYN	RSDLYGRLQE	LFGLEPTIIP
170	180	190	200	210	220	230	240
PKKDDDKTRE	IGRTRTQSKI	ERVKVKTESQ	DPTSSWRSLI	PVIKVNVSTG	RLAFGNHYQP	QTLCINFDDA	FLTYTTKPPS
250	260	270	280	290	300	310	320
SHLDQFMHIV	KGKLENVRVM	LVPSPRYVGL	QNDEPPRLMG	EGFVVMQSND	VDIYYYMDEP	GLVPEETEEN	IEGEMSSEDC
330	340	350	360	370	380	390	400
KLQDLPPCWG	LDIVCGKGTD	FNYGPWADRQ	RDCLWKFFFP	PDYQVLKVSE	IAQPGRPRQI	LAFELRMNII	ADATIDLLFT
410	420	430	440	450	460	470	480
KNRETNAVHV	NVGAGSYLEI	NIPMTVEENG	YTPAIKGQLL	HVDATTSMQY	RTLLEAEMLA	FHINASYPRI	WNMPQTWQCE
490	500	510	520	530	540	550	560
LEVYKATYHF	IFAQKNFFTD	LIQDWSSDSP	PDIFSFVPYT	WNFKIMFHQF	EMIWAANQHN	WIDCSTKQQE	NVYLAACGET
570	580	590	600	610	620	630	640
LNIDFSLPFT	DFVPATCNTK	FSLRGEDVDL	HLFLPDCHPS	KYSLFMLVKN	CHPNKMIHDT	GIPAECQSGQ	KTVKPKWRNV
650	660	670	680	690	700	710	720
TQEKSGWVEC	WTVPSVMLTI	DYTWHPIYPQ	KADEQLKQSL	SEMEETMLSV	LRPSQKTSDR	VVSSPSTSSR	PPIDPSELPP
730	740	750	760	770	780	790	800
DKLHVEMELS	PDSQITLYGP	LLNAFLCIKE	NYFGEDDMYM	DFEEVISSPV	LSLSTSSSSG	WTAVGMENDK	KENEGSAKSI
810	820	830	840	850	860	870	880
HPLALRPWDI	TVLVNLYKVH	GRLPVHGTTD	GPECPTAFLE	RLCFEMKKGF	RETMLQLILS	PLNVFVSDNY	QQRPPVDEVL
890	900	910	920	930	940	950	960
REGHINLSGL	QLRAHAMFSA	EGLPLGSDSL	EYAWLIDVQA	GSLTAKVTAP	QLACLLEWGQ	TFVFHVVCRE	YELERPKSVI
970	980	990	1000	1010	1020	1030	1040
ICQHGIDRRF	CESKLSCIPG	PCPTSDDLKY	TMIRLAVDGA	DIYIVEHGCA	TNIKMGAIRV	ANCNLHNQSV	GEGISAAIQD
1050	1060	1070	1080	1090	1100	1110	1120
FQVRQYIEQL	NNCRIGLQPA	VLRRAYWLEA	GSANLGLITV	DIALAADHHS	KHEAQRHFLE	THDARTKRLW	FLWPDDILKN
1130	1140	1150	1160	1170	1180	1190	1200
KRCRNKCGCL	GGCRFFGGTV	TGLDFFKLEE	LTPSSSSAFS	STSAESDMYY	GQSLLQPGEW	IITKEIPKII	DGNVNGMKRK
1210	1220	1230	1240	1250	1260	1270	1280
EWENKSVGIE	VERKTQHLSL	QVPLRSHSSS	SSSEENSSSS	AAQPLLAGEK	ESPSSVADDH	LVQKEFLHGT	KRDDGQASIP
1290	1300	1310	1320	1330	1340	1350	1360
TEISGNSPVS	PNTQDKSVGQ	SPLRSPLKRQ	ASVCSTRLGS	TKSLTAAFYG	DKQPVTVGVQ	FSSDVSRSDE	NVLDSPKQRR
1370	1380	1390	1400	1410	1420	1430	1440
SFGSFPYTPS	ADSNSFHQYR	SMDSSMSMAD	SEAYFSAAEE	FEPISSDEGP	GTYPGRKKKK	KQTQQIDYSR	GSIYHSVEGP
1450	1460	1470	1480	1490	1500	1510	1520
LTGHGESIQD	SRTLPFKTHP	SQASFVSALG	GEDDVIEHLY	IVEGEKTVES	EQITPQQPVM	NCYQTYLTQF	QVINWSVKHP
1530	1540	1550	1560	1570	1580	1590	1600
TNKRTSKSSL	HRPLDLDTPT	SEESSSSFEQ	LSVPTFKVIK	QGLTANSLLD	RGMQLSGSTS	NTPYTPLEKK	LADNTDDETL
1610	1620	1630	1640	1650	1660	1670	1680
TEEWTLDQPV	SQTRTTAIVE	VKGTVDIVLT	PLVAEALDRY	IEAMVHCAST	RHPAAIVDDL	HAKVLREAVQ	NSKTTFSENL
1690	1700	1710	1720	1730	1740	1750	1760
SSKQDIRGTK	TEQSTIGTTN	QGQAQTNLTM	KQDNVTIKGL	QTNVSIPKVN	LCLLQASVEE	SPTTAPSRSV	THVSLVALCF
1770	1780	1790	1800	1810	1820	1830	1840
DRIATQVRMN	RGVVEETSNN	AEPGRTSNFD	RYVHATKMQP	QSSGSLRSNA	GAEKGKEIAA	KLNIHRVHGQ	LRGLDTTDIG
1850	1860	1870	1880	1890	1900	1910	1920
TCAITAIPFE	KSKVLFTLEE	LDEFTFVDET	DQQAVPDVTR	IGPSQEKWGW	IMFECGLENL	TIKGGRQSGA	VLYNSFGIMG
1930	1940	1950	1960	1970	1980	1990	2000
KASDTERGGV	LTSNNSSDSP	TGSGYNTDVS	DDNLPCDRTS	PSSDLNGNSV	SDEQDEGVES	DDLKKDLPLM	PPPPDSCSMK
2010	2020	2030	2040	2050	2060	2070	2080
LTIKEIWFSF	AAPTNVRSHT	HAFSRQLNLL	STATPAVGAW	LVPIDQLKSS	LNKLETEGTL	RICAVMGCIM	TEALENKSVH
2090	2100	2110	2120	2130	2140	2150	2160
FPLRSKYNRL	TKVARFLQEN	PSCLLCNILH	HYLHQANYSI	IDDATMSDGL	PALVTLKKGL	VALARQWMKF	IVVTPAFKGV
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
117	1	774.3916	-26.77	3	31.2	15.7	1	66-86	K.HGYIHIGSFSFSVLSGKVMVR.E	
1348	1	669.3232	-39.50	2	46.5	13.8	2	116-126	K.QKQHDPKAETR.L	

Detailed Protein Report

Protein 284: caspase recruitment domain-containing protein 9 isoform 2 [Homo sapiens]

Accession:	gi|16554562	**Score:**	29.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	56.6
Database Date:	2015-11-30	**pI:**	5.5
		Sequence Coverage [%]:	3.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSDYENDDEC	WSVLEGFRVT	LTSVIDPSRI	TPYLRQCKVL	NPDDEEQVLS	DPNLVIRKRK	VGVLLDILQR	TGHKGYVAFL
90	100	110	120	130	140	150	160
ESLELYYPQL	YKKVTGKEPA	RVFSMIIDAS	GESGLTQLLM	TEVMKLQKKV	QDLTALLSSK	DDFIKELRVK	DSLLRKHQER
170	180	190	200	210	220	230	240
VQRLKEECEA	GSRELKRCKE	ENYDLAMRLA	HQSEEKGAAL	MRNRDLQLEI	DQLKHSLMKA	EDDCKVERKH	TLKLRHAMEQ
250	260	270	280	290	300	310	320
RPSQELLWEL	QQEKALLQAR	VQELEASVQE	GKLDRSSPYI	QVLEEDWRQA	LRDHQEQANT	IFSLRKDLRQ	GEARRLRCME
330	340	350	360	370	380	390	400
EKEMFELQCL	ALRKDSKMYK	DRIEAILLQM	EEVAIERDQA	IATREELHAQ	HARGLQEKDA	LRKQVRELGE	KADELQLQVF
410	420	430	440	450	460	470	480
QCEAQLLAVE	GRLRRQQLET	LVLSSDLEDG	SPRRSQELSL	PQDLEDTQLS	DKGCLAGGGS	PKQPFAALHQ	EQVLRNPHDA
490	500						
GPAGLPGIGA	VC						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1435	1	627.2993	-161.59	2	47.6	11.8	1	60-70	R.KVGVLLDILQR.T	

Detailed Protein Report

Protein 285: **transformation/transcription domain-associated protein isoform 2 [Homo sapiens]**

Accession:	gi|4507691	**Score:**	29.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	434.1
Database Date:	2015-11-30	**pI:**	9.3
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAFVATQGAT	VVDQTTLMKK	YLQFVAALTD	VNTPDETKLK	MMQEVSENFE	NVTSSPQYST	FLEHIIPRFL	TFLQDGEVQF
90	100	110	120	130	140	150	160
LQEKPAQQLR	KLVLEIIHRI	PTNEHLRPHT	KNVLSVMFRF	LETENEENVL	ICLRIIIELH	KQFRPPITQE	IHHFLDFVKQ
170	180	190	200	210	220	230	240
IYKELPKVVN	RYFENPQVIP	ENTVPPPEMV	GMITTIAVKV	NPEREDSETR	THSIIPRGSL	SLKVLAELPI	IVVLMYQLYK
250	260	270	280	290	300	310	320
LNIHNVVAEF	VPLIMNTIAI	QVSAQARQHK	LYNKELYADF	IAAQIKTLSF	LAYIIRIYQE	LVTKYSQQMV	KGMLQLLSNC
330	340	350	360	370	380	390	400
PAETAHLRKE	LLIAAKHILT	TELRNQFIPC	MDKLFDESIL	IGSGYTARET	LRPLAYSTLA	DLVHHVRQHL	PLSDLSLAVQ
410	420	430	440	450	460	470	480
LFAKNIDDES	LPSSIQTMSC	KLLLNLVDCI	RSKSEQESGN	GRDVLMRMLE	VFVLKFHTIA	RYQLSAIFKK	CKPQSELGAV
490	500	510	520	530	540	550	560
EAALPGVPTA	PAAPGPAPSP	APVPAPPPPP	PPPPPATPVT	PAPVPPFEKQ	GEKDKEDKQT	FQVTDCRSLV	KTLVCGVKTI
570	580	590	600	610	620	630	640
TWGITSCKAP	GEAQFIPNKQ	LQPKETQIYI	KLVKYAMQAL	DIYQVQIAGN	GQTYIRVANC	QTVRMKEEKE	VLEHFAGVFT
650	660	670	680	690	700	710	720
MMNPLTFKEI	FQTTVPYMVE	RISKNYALQI	VANSFLANPT	TSALFATILV	EYLLDRLPEM	GSNVELSNLY	LKLFKLVFGS
730	740	750	760	770	780	790	800
VSLFAAENEQ	MLKPHLHKIV	NSSMELAQTA	KEPYNYFLLL	RALFRSIGGG	SHDLLYQEFL	PLLPNLLQGL	NMLQSGLHKQ
810	820	830	840	850	860	870	880
HMKDLFVELC	LTVPVRLSSL	LPYLPMLMDP	LVSALNGSQT	LVSQGLRTLE	LCVDNLQPDF	LYDHIQPVRA	ELMQALWRTL
890	900	910	920	930	940	950	960
RNPADSISHV	AYRVLGKFGG	SNRKMLKESQ	KLHYVVTEVQ	GPSITVEFSD	CKASLQLPME	KAIETALDCL	KSANTEPYYR
970	980	990	1000	1010	1020	1030	1040
RQAWEVIKCF	LVAMMSLEDN	KHALYQLLAH	PNFTEKTIPN	VIISHRYKAQ	DTPARKTFEQ	ALTGAFMSAV	IKDLRPSALP
1050	1060	1070	1080	1090	1100	1110	1120
FVASLIRHYT	MVAVAQQCGP	FLLPCYQVGS	QPSTAMFHSE	ENGSKGMDPL	VLIDAIAICM	AYEEKELCKI	GEVALAVIFD
1130	1140	1150	1160	1170	1180	1190	1200
VASIILGSKE	RACQLPLFSY	IVERLCACCY	EQAWYAKLGG	VVSIKFLMER	LPLTWVLQNQ	QTFLKALLFV	MMDLTGEVSN
1210	1220	1230	1240	1250	1260	1270	1280
GAVAMAKTTL	EQLLMRCATP	LKDEERAEEI	VAAQEKSFHH	VTHDLVREVT	SPNSTVRKQA	MHSLQVLAQV	TGKSVTVIME
1290	1300	1310	1320	1330	1340	1350	1360
PHKEVLQDMV	PPKKHLLRHQ	PANAQIGLME	GNTFCTTLQP	RLFTMDLNVV	EHKVFYTELL	NLCEAEDSAL	TKLPCYKSLP
1370	1380	1390	1400	1410	1420	1430	1440
SLVPLRIAAL	NALAACNYLP	QSREKIIAAL	FKALNSTNSE	LQEAGEACMR	KFLEGATIEV	DQIHTHMRPL	LMMLGDYRSL
1450	1460	1470	1480	1490	1500	1510	1520
TLNVVNRLTS	VTRLFPNSFN	DKFCDQMMQH	LRKWMEVVVI	THKGGQRSDG	NEMKICSAII	NLFHLIPAAP	QTLVKPLLEV
1530	1540	1550	1560	1570	1580	1590	1600
VMKTERAMLI	EAGSPFREPL	IKFLTRHPSQ	TVELFMMEAT	LNDPQWSRMF	MSFLKHKDAR	PLRDVLAANP	NRFITLLLPG
1610	1620	1630	1640	1650	1660	1670	1680
GAQTAVRPGS	PSTSTMRLDL	QFQAIKIISI	IVKNDDSWLA	SQHSLVSQLR	RVWVSENFQE	RHRKENMAAT	NWKEPKLLAY
1690	1700	1710	1720	1730	1740	1750	1760
CLLNYCKRNY	GDIELLFQLL	RAFTGRFLCN	MTFLKEYMEE	EIPKNYSIAQ	KRALFFRFVD	FNDPNFGDEL	KAKVLQHILN
1770	1780	1790	1800	1810	1820	1830	1840
PAFLYSFEKG	EGEQLLGPPN	PEGDNPESIT	SVFITKVLDP	EKQADMLDSL	RIYLLQYATL	LVEHAPHHIH	DNNKNRNSKL
1850	1860	1870	1880	1890	1900	1910	1920
RRLMTFAWPC	LLSKACVDPA	CKYSGHLLLA	HIIAKFAIHK	KIVLQVFHSL	LKAHAMEARA	IVRQAMAILT	PAVPARMEDG
1930	1940	1950	1960	1970	1980	1990	2000
HQMLTHWTRK	IIVEEGHTVP	QLVHILHLIV	QHFKVYYPVR	HHLVQHMVSA	MQRLGFTPSV	TIEQRRLAVD	LSEVVIKWEL
2010	2020	2030	2040	2050	2060	2070	2080
QRIKDQQPDS	DMDPNSSGEG	VNSVSSSIKR	GLSVDSAQEV	KRFRTATGAI	SAVFGRSQSL	PGADSLLAKP	IDKQHTDTVV
2090	2100	2110	2120	2130	2140	2150	2160
NFLIRVACQV	NDNTNTAGSP	GEVLSRRCVN	LLKTALRPDM	WPKSELKLQW	FDKLLMTVEQ	PNQVNYGNIC	TGLEVLSFLL
2170	2180	2190	2200	2210	2220	2230	2240
TVLQSPAILS	SFKPLQRGIA	ACMTCGNTKV	LRAVHSLLSR	LMSIFPTEPS	TSSVASKYEE	LECLYAAVGK	VIYEGLTNYE
2250	2260	2270	2280	2290	2300	2310	2320
KATNANPSQL	FGTLMILKSA	CSNNPSYIDR	LISVFMRSLQ	KMVREHLNPQ	AASGSTEATS	GTSELVMLSL	ELVKTRLAVM
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
873	1	946.4119	-18.65	3	40.4	15.0	1	2003-2029	R.IKDQQPDSDMDPNSSGEGVNSVSSSIK.R	Oxidation: 10

Detailed Protein Report

Protein 286: **PREDICTED: MAP kinase-activating death domain protein isoform X20 [Homo sapiens]**

Accession:	gi|530395950	**Score:**	29.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	136.1
Database Date:	2015-11-30	**pI:**	5.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MVQKKKFCPR	LLDYLVIVGA	RHPSSDSVAQ	TPELLRRYPL	EDHTEFPLPP	DVVFFCQPEG	CLSVRQRRMS	LRDDTSFVFT
90	100	110	120	130	140	150	160
LTDKDTGVTR	YGICVNFYRS	FQKRISKEKG	EGGAGSRGKE	GTHATCASEE	GGTESSESGS	SLQPLSADST	PDVNQSPRGK
170	180	190	200	210	220	230	240
RRAKAGSRSR	NSTLTSLCVL	SHYPFFSTFR	ECLYTLKRLV	DCCSERLLGK	KLGIPRGVQR	DTMWRIFTGS	LLVEEKSSAL
250	260	270	280	290	300	310	320
LHDLREIEAW	IYRLLRSPVP	VSGQKRVDIE	VLPQELQPAL	TFALPDPSRF	TLVDFPLHLP	LELLGVDACL	QVLTCILLEH
330	340	350	360	370	380	390	400
KVVLQSRDYN	ALSMSVMAFV	AMIYPLEYMF	PVIPLLPTCM	ASAEQLLLAP	TPYIIGVPAS	FFLYKLDFKM	PDDVWLVDLD
410	420	430	440	450	460	470	480
SNRVIAPTNA	EVLPILPEPE	SLELKKHLKQ	ALASMSLNTQ	PILNLEKFHE	GQEIPLLLGR	PSNDLQSTPS	TEFNPLIYGN
490	500	510	520	530	540	550	560
DVDSVDVATR	VAMVRFFNSA	NVLQGFQMHT	RTLRLFPRPV	VAFQAGSFLA	SRPRQTPFAE	KLARTQAVEY	FGEWILNPTN
570	580	590	600	610	620	630	640
YAFQRIHNNM	FDPALIGDKP	KWYAHQLQPI	HYRVYDSNSQ	LAEALSVPPE	RDSDSEPTDD	SGSDSMDYDD	SSSSYSSLGD
650	660	670	680	690	700	710	720
FVSEMMKCDI	NGDTPNVDPL	THAALGDASE	VEIDELQNQK	EAEEPGPDSE	NSQENPPLRS	SSSTTASSSP	STVIHGANSE
730	740	750	760	770	780	790	800
PADSTEMDDK	AAVGVSKPLP	SVPPSIGKSN	VDRRQAEIGE	GSVRRRIYDN	PYFEPQYGFP	PEEDEDEQGE	SYTPRFSQHV
810	820	830	840	850	860	870	880
SGNRAQKLLR	PNSLRLASDS	DAESDSRASS	PNSTVSNTST	EGFGGIMSFA	SSLYRNHSTS	FSLSNLTLPT	KGAREKATPF
890	900	910	920	930	940	950	960
PSLKVFGLNT	LMEIVTEAGP	GSGEGNRRAL	VDQKSSVIKH	SPTVKREPPS	PQGRSSNSSE	NQQFLKEVVH	SVLDGQGVGW
970	980	990	1000	1010	1020	1030	1040
LNMKKVRRLL	ESEQLRVFVL	SKLNRMVQSE	DDARQDIIPD	VEISRKVYKG	MLDLLKCTVL	SLEQSYAHAG	LGGMASIFGL
1050	1060	1070	1080	1090	1100	1110	1120
LEIAQTHYYS	KEPDKRKRSP	TESVNTPVGK	DPGLAGRGDP	KAMAQLRVPQ	LGPRAPSATG	KGPKELDTRS	LKEENFIASI
1130	1140	1150	1160	1170	1180	1190	1200
ELWNKHQEVK	KQKALEKQRP	EVIKPVFDLG	ETEEKKSQIS	ADSGVSLTSS	SQRTDQDSVI	GVSPAVMIRS	SSQDSEVSTV
1210	1220	1230	1240				
VGEHHTGILV	CVYEISPRAS	HLIKKVLPEA	I				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1913	1	682.2568	-100.43	3	54.0	15.5	2	191-206	R.ECLYTLKRLVDCCSER.L	Carbamidomethyl: 12, 13

Detailed Protein Report

Protein 287: PREDICTED: telomerase-binding protein EST1A isoform X2 [Homo sapiens]

Accession:	gi|530410168	**Score:**	29.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	101.9
Database Date:	2015-11-30	**pI:**	9.8
		Sequence Coverage [%]:	3.6
		No. of unique Peptides:	1

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        10         20         30         40         50         60         70         80
MAEGLERVRI SASELRGILA TLAPQAGSRE NMKELKEARP RKDNRRPDLE IYKPGLSRLR NKPKIKEPPG SEEFKDEIVN
        90        100        110        120        130        140        150        160
DRDCSAVENG TQPVKDVCKE LNNQEQNGPI DPENNRGQES FPRTAGQEDR SLKIIKRTKK PDLQIYQPGR RLQTVSKESA
       170        180        190        200        210        220        230        240
SRVEEEEVLN QVEQLRVEED ECRGNVAKEE VANKPDRAEI EKSPGGGRVG AAKGEKGKRM GKGEGVRETH DDPARGRPGS
       250        260        270        280        290        300        310        320
AKRYSRSDKR RNRYRTRSTS SAGSNNSAEG AGLTDNGCRR RRQDRTKERP RLKKQVSVSS TDSLDEDRID EPDGLGPRRS
       330        340        350        360        370        380        390        400
SERKRHLERN WSGRGEGEQK NSAKEYRGTL RVTFDAEAMN KESPMVRSAR DDMDRGKPDK GLSSGGKGSE KQESKNPKQE
       410        420        430        440        450        460        470        480
LRGRGRGILI LPAHTTLSVN SAGSPESAPL GPRLLFGSGS KGSRSWGRGG TTRRLWDPNN PDQKPALKTQ TPQLHFLDTD
       490        500        510        520        530        540        550        560
DEVSPTSWGD SRQAQASYYK FQNSDNPYYY PRTPGPASQY PYTGYNPLQY PVGPTNGVYP GPYYPGYPTP SGQYVCSPLP
       570        580        590        600        610        620        630        640
TSTMSPEEVE QHMRNLQQQE LHRLLRVADN QELQLSNLLS RDRISPEGLE KMAQLRAELL QLYERCILLD IEFSDNQNVD
       650        660        670        680        690        700        710        720
QILWKNAFYQ VIEKFRQLVK DPNVENPEQI RNRLLELLDE GSDFFDSLLQ KLQVTYKFKL EDYMDGLAIR SKPLRKTVKY
       730        740        750        760        770        780        790        800
ALISAQRCMI CQGDIARYRE QASDTANYGK ARSWYLKAQH IAPKNGRPYN QLALLAVYTR RKLDAVYYYM RSLAASNPIL
       810        820        830        840        850        860        870        880
TAKESLMSLF EETKRKAEQM EKKQHEEFDL SPDQWRKGKK STFRHVGDDT TRLEIWIHPS HPRSSQGTES GKDSEQENGL
       890        900
GSLSPSDATS PRRNLQFLA
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1729	1	1051.5453	20.59	2	51.4	14.5	2	65-82	K.IKEPPGSEEFKDEIVNDR.D	

Detailed Protein Report

Protein 288: DNA repair and recombination protein RAD54-like [Homo sapiens]

Accession:	gi|216548186	**Score:**	29.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	84.3
Database Date:	2015-11-30	**pI:**	9.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.7
		No. of unique Peptides:	2

Alias proteins:

Accession	**Name**	**Description**
gi|216548193	refseq_human (refseq_human_20140103.fasta)	DNA repair and recombination protein RAD54-like [Homo sapiens]

10	20	30	40	50	60	70	80
MRRSLAPSQL	AKRKPEGRSC	DDEDWQPGLV	TPRKRKSSSE	TQIQECFLSP	FRKPLSQLTN	QPPCLDSSQH	EAFIRSILSK
90	100	110	120	130	140	150	160
PFKVPIPNYQ	GPLGSRALGL	KRAGVRRALH	DPLEKDALVL	YEPPPLSAHD	QLKLDKEKLP	VHVVVDPILS	KVLRPHQREG
170	180	190	200	210	220	230	240
VKFLWECVTS	RRIPGSHGCI	MADEMGLGKT	LQCITLMWTL	LRQSPECKPE	IDKAVVVSPS	SLVKNWYNEV	GKWLGGRIQP
250	260	270	280	290	300	310	320
LAIDGGSKDE	IDQKLEGFMN	QRGARVSSPI	LIISYETFRL	HVGVLQKGSV	GLVICDEGHR	LKNSENQTYQ	ALDSLNTSRR
330	340	350	360	370	380	390	400
VLISGTPIQN	DLLEYFSLVH	FVNSGILGTA	HEFKKHFELP	ILKGRDAAAS	EADRQLGEER	LRELTSIVNR	CLIRRTSDIL
410	420	430	440	450	460	470	480
SKYLPVKIEQ	VVCCRLTPLQ	TELYKRFLRQ	AKPAEELLEG	KMSVSSLSSI	TSLKKLCNHP	ALIYDKCVEE	EDGFVGALDL
490	500	510	520	530	540	550	560
FPPGYSSKAL	EPQLSGKMLV	LDYILAVTRS	RSSDKVVLVS	NYTQTLDLFE	KLCRARRYLY	VRLDGTMSIK	KRAKVVERFN
570	580	590	600	610	620	630	640
SPSSPDFVFM	LSSKAGGCGL	NLIGANRLVM	FDPDWNPAND	EQAMARVWRD	GQKKTCYIYR	LLSAGTIEEK	IFQRQSHKKA
650	660	670	680	690	700	710	720
LSSCVVDEEQ	DVERHFSLGE	LKELFILDEA	SLSDTHDRLH	CRRCVNSRQI	RPPPDGSDCT	SDLAGWNHCT	DKWGLRDEVL
730	740	750					
QAAWDAASTA	ITFVFHQRSH	EEQRGLR					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
656	1	677.1638	133.53	3	37.8	16.7	2	134-151	K.LDKEKLPVHVVVDPILSK.V	
1883	2	1022.8975	-139.69	2	53.6	12.7	2	614-630	K.KTCYIYRLLSAGTIEEK.I	Carbamidomethyl: 3

Detailed Protein Report

Protein 289: PREDICTED: integrin beta-7 isoform X3 [Homo sapiens]

Accession:	gi|578823673	**Score:**	29.4
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:	1

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
2663	2	731.3721	63.85	2	64.5	13.4	0	54-65	K.CILSHPSCAWCK.Q	Carbamidomethyl: 1, 11

Detailed Protein Report

Protein 290: palladin isoform 2 [Homo sapiens]

Accession:	gi|93102361	**Score:**	29.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	122.0
Database Date:	2015-11-30	**pI:**	6.5
		Sequence Coverage [%]:	2.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSGTSSHESF	YDSLSDMQEE	SKNTDFFPGL	SAFLSQEEIN	KSLDLARRAI	ADSETEDFDS	EKEISQIFST	SPASLCEHPS
90	100	110	120	130	140	150	160
HKETKLGEHA	SRRPQDNRST	PVQPLAEKQT	KSISSPVSKR	KPAMSPLLTR	PSYIRSLRKA	EKRGAKTPST	NVKPKTPHQR
170	180	190	200	210	220	230	240
KGGPQSQLCD	KAANLIEELT	SIFKAAKPRN	RSPNGESSSP	DSGYLSPKNQ	PSALLSASAS	QSPMEDQGEM	EREVKSPGAR
250	260	270	280	290	300	310	320
HCYQDNQDLA	VPHNRKSHPQ	PHSALHFPAA	PRFIQKLRSQ	EVAEGSRVYL	ECRVTGNPTP	RVRWFCEGKE	LHNTPDIQIH
330	340	350	360	370	380	390	400
CEGGDLHTLI	IAEAFEDDTG	RYTCLATNPS	GSDTTSAEVF	IEGASSTDSD	SESLAFKSRA	GAMPQAQKKT	TSVSLTIGSS
410	420	430	440	450	460	470	480
SPKTGVTTAV	IQPLSVPVQQ	VHSPTSYLCR	PDGTTTAYFP	PVFTKELQNT	AVAEGQVVVL	ECRVRGAPPL	QVQWFRQGSE
490	500	510	520	530	540	550	560
IQDSPDFRIL	QKKPRSTAEP	EEICTLVIAE	TFPEDAGIFT	CSARNDYGSA	TSTAQLVVTS	ANTENCSYES	MGESNNDHFQ
570	580	590	600	610	620	630	640
HFPPPPPILE	TSSLELASKK	PSEIQQVNNP	ELGLSRAALQ	MQFNAAERET	NGVHPSRGVN	GLINGKANSN	KSLPTPAVLL
650	660	670	680	690	700	710	720
SPTKEPPPLL	AKPKLGFPKK	ASRTARIASD	EEIQGTKDAV	IQDLERKLRF	KEDLLNNGQP	RLTYEERMAR	RLLGADSATV
730	740	750	760	770	780	790	800
FNIQEPEEET	ANQEYKVSSC	EQRLISEIEY	RLERSPVDES	GDEVQYGDVP	VENGMAPFFE	MKLKHYKIFE	GMPVTFTCRV
810	820	830	840	850	860	870	880
AGNPKPKIYW	FKDGKQISPK	SDHYTIQRDL	DGTCSLHTTA	STLDDDGNYT	IMAANPQGRI	SCTGRLMVQA	VNQRGRSPRS
890	900	910	920	930	940	950	960
PSGHPHVRRP	RSRSRDSGDE	NEPIQERFFR	PHFLQAPGDL	TVQEGKLCRM	DCKVSGLPTP	DLSWQLDGKP	VRPDSAHKML
970	980	990	1000	1010	1020	1030	1040
VRENGVHSLI	IEPVTSRDAG	IYTCIATNRA	GQNSFSLELV	VAAKEAHKPP	VFIEKLQNTG	VADGYPVRLE	CRVLGVPPPQ
1050	1060	1070	1080	1090	1100	1110	
IFWKKENESL	THSTDRVSMH	QDNHGYICLL	IQGATKEDAG	WYTVSAKNEA	GIVSCTARLD	VYISRH	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2009	2	945.8529	-132.43	2	55.0	12.3	1	1016- 1032	K.LQNTGVADGYPVRLECR.V	

Detailed Protein Report

Protein 291:	**PREDICTED: myosin phosphatase Rho-interacting protein isoform X6 [Homo sapiens]**		
Accession:	gi|578829807	**Score:**	29.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	258.7
Database Date:	2015-11-30	**pI:**	5.3
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.6
		No. of unique Peptides:	2

Detailed Protein Report

10	20	30	40	50	60	70	80
MRRGRAEPLA	RRERQAGQAC	AAAAAAVAAA	PTMSAAKENP	CRKFQANIFN	KSKCQNCFKP	RESHLLNDED	LTQAKPIYGG
90	100	110	120	130	140	150	160
WLLLAPDGTD	FDNPVHRSRK	WQRRFFILYE	HGLLRYALDE	MPTTLPQGTI	NMNQCTDVVD	GEGRTGQKFS	LCILTPEKEH
170	180	190	200	210	220	230	240
FIRAETKEIV	SGWLEMLMVY	PRTNKQNQKK	KRKVEPPTPQ	EPGPAKVAVT	SSSSSSSSSS	SIPSAEKVPT	TKSTLWQEEM
250	260	270	280	290	300	310	320
RTKDQPDGSS	LSPAQSPSQS	QPPAASSLRE	PGLESKEEES	AMSSDRMDCG	RKVRVESGYF	SLEKTKQDLK	AEEQQLPPPL
330	340	350	360	370	380	390	400
SPPSPSTPNH	RRSQVIEKFE	ALDIEKAEHM	ETNAVGPSPS	SDTRQGRSEK	RAFPRKRDFT	NEAPPAPLPD	ASASPLSPHR
410	420	430	440	450	460	470	480
RAKSLDRRST	EPSVTPDLLN	FKKGWLTKQY	EDGQWKKHWF	VLADQSLRYY	RDSVAEEAAD	LDGEIDLSAC	YDVTEYPVQR
490	500	510	520	530	540	550	560
NYGFQIHTKE	GEFTLSAMTS	GIRRNWIQTI	MKHVHPTTAP	DVTSSLPEEK	NKSSCSFETC	PRPTEKQEAE	LGEPDPEQKR
570	580	590	600	610	620	630	640
SRARERRREG	RSKTFDWAEF	RPIQQALAQE	RVGGVGPADT	HEPLRPEAEP	GELERERARR	REERRKRFGM	LDATDGPGTE
650	660	670	680	690	700	710	720
DAALRMEVDR	SPGLPMSDLK	THNVHVEIEQ	RWHQVETTPL	REEKQVPIAP	VHLSSEDGGD	RLSTHELTSL	LEKELEQSQK
730	740	750	760	770	780	790	800
EASDLLEQNR	LLQDQLRVAL	GREQSAREGY	VLQTEVAASP	SGAWQRLHRV	NQDLQSELEA	QCQRQELITH	QIQTLKRSYG
810	820	830	840	850	860	870	880
EAKDTIRHHE	AEIRSLQARL	SNAAAELAIK	EQALAKLKGD	LKREQGRVRE	QLEERQHSEA	ALSSQLRASE	QKLKSAEALL
890	900	910	920	930	940	950	960
LEKTQELRGL	ETQQALQRDR	QKEVQRLQER	IADLSQQLGA	SEQAQRLMEE	KLQRNYELLL	ESCEKEKQAL	LQNLKEVEDK
970	980	990	1000	1010	1020	1030	1040
ASAYEDQLQG	QAQQVETLQK	EKLSATFEGS	EQVHQLEEQL	EAREASVRRL	AEHVQSLCDE	RDLLRQRFQE	LTERVATSDE
1050	1060	1070	1080	1090	1100	1110	1120
DVAELREKLR	RREADNQSLE	HSYQRVSSQL	QSMHTLLREK	EEELERIKEA	HEKVLEKKEQ	DLNEALVKMV	ALGSSLEETE
1130	1140	1150	1160	1170	1180	1190	1200
IKLQAKEEIL	RKFASESPKD	MEEPRSTPEE	TERDGTLLPG	QPVQATRAPL	GLPHTRLEDE	DEDLGAPPGE	EYGDGSPSRE
1210	1220	1230	1240	1250	1260	1270	1280
DSMVPPKSVE	VLDREGHQQG	TAKLDQGAPG	VKRQRIRFST	IQCQRYIHPE	GSEKTWTSST	SSDTSQDRSP	SEESMSSEPA
1290	1300	1310	1320	1330	1340	1350	1360
PSVLPATGDS	DTYLSIIHSL	ETKLYVTEEK	LKDVTVRLES	QQGQSREALL	ALHHQWAGTE	AQLREQLRAS	LLQVGALASQ
1370	1380	1390	1400	1410	1420	1430	1440
LEQERQERAR	RVEGHVGELG	DFQVKNSQAL	MCLENCREQL	RSLPRASQED	EQDARAASLA	SVESALVSAI	QALQHWPAPA
1450	1460	1470	1480	1490	1500	1510	1520
HGGARAQLET	GGTEENGKPA	SLQQCSQSEL	TEQEQVRLLS	DQIALEASLI	SQIADSLKNT	TSDVSRMLHE	ISWSGQPPME
1530	1540	1550	1560	1570	1580	1590	1600
SAGAPVDTWA	RKVLVDGEFW	SQVESLRKHL	GTLGGEAVGA	SGDGQQSIPQ	GLAPILANAT	WVRAELSFAT	QSVRESFHRR
1610	1620	1630	1640	1650	1660	1670	1680
LQSIQETLRG	TQTALRQHKC	LLREILGAYQ	TPDFERVMQQ	VLEALRLPAG	HEDGVQLSWD	LSPLGEVLGR	DSDSSQEPFD
1690	1700	1710	1720	1730	1740	1750	1760
VSDQSPGAFV	AIQEELAQQL	KEKASLLEEI	AAALPSLPPV	ESLRDCQKLL	QVSQSLSYNT	CLGGLGQYSS	LLVQDAIIQA
1770	1780	1790	1800	1810	1820	1830	1840
QVCYASCRIR	LEYEKELQLC	KESWQTREPS	CSEQAQAARA	LREEYEELLR	KQKSEYLDVI	AIVERENAEL	KAKAAQLDHQ
1850	1860	1870	1880	1890	1900	1910	1920
QQCLEDAESK	HSMSMFTLRG	RYEEEIRCVV	EQLTRTESTL	QAERSRVLSQ	LDASVRDRQD	MERHHGEQIQ	TLEDRFQLKV
1930	1940	1950	1960	1970	1980	1990	2000
RELQTIHEEE	LRTLQEHYSQ	SLRCLQDTLC	LHQGPHPKAL	PAPAPNWQAT	QGEADSMTGL	RERIQELEAQ	MDVMREELGH
2010	2020	2030	2040	2050	2060	2070	2080
KDLEGDAATL	REKYQRDLES	LKATCERGFA	AMEETHQKKI	EDLQRQHQRE	LEKLREEKDR	LLAEETAATI	SAIEAMKNAH
2090	2100	2110	2120	2130	2140	2150	2160
REEMERELEK	SQRSQISSVN	SDVEALRRQY	LEELQSVQRE	LEVLSEQYSQ	KCLENAHLAQ	ALEAERQALR	QCQRENQELN
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
1449	1	1011.7606	-72.73	3	47.9	13.8	2	646-671	R.MEVDRSPGLPMSDLKTHNVHVEIEQR.W	Oxidation: 11
448	1	593.8428	14.41	2	35.2	15.6	0	1637-1646	R.VMQQVLEALR.L	

Detailed Protein Report

Protein 292: probable G-protein coupled receptor 179 precursor [Homo sapiens]

Accession:	gi|93352554	**Score:**	29.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	257.2
Database Date:	2015-11-30	**pI:**	5.4
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	0.7
		No. of unique Peptides:	2

Quantitation

MD:MU	**Median:**	0.63	**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

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
479	1	475.6002	-274.91	2	35.6	13.9	0	1164-1170	R.MLQVCQR.E	Carbamidomethyl: 5; Oxidation: 1	MD:MU 0.63
799	1	509.1480	-293.13	2	39.5	15.4	1	1195-1204	R.AGKTGLAMLR.Q		

Protein 293: PREDICTED: receptor-type tyrosine-protein phosphatase F isoform X12 [Homo sapiens]

Accession: gi|578799535
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 29.2
MW [kDa]: 192.7
pI: 5.8
Sequence Coverage [%]: 1.6
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MAPEPAPGRT	MVPLVPALVM	LGLVAGAHGD	SKPVFIKVPE	DQTGLSGGVA	SFVCQATGEP	KPRITWMKKG	KKVSSQRFEV
90	100	110	120	130	140	150	160
IEFDDGAGSV	LRIQPLRVQR	DEAIYECTAT	NSLGEINTSA	KLSVLEEEQL	PPGFPSIDMG	PQLKVVEKAR	TATMLCAAGG
170	180	190	200	210	220	230	240
NPDPEISWFK	DFLPVDPATS	NGRIKQLRSG	ALQIESSEES	DQGKYECVAT	NSAGTRYSAP	ANLYVRDQRE	VRRVAPRFSI
250	260	270	280	290	300	310	320
PPSSQEVMPG	GSVNLTCVAV	GAPMPYVKWM	MGAEELTKED	EMPVGRNVLE	LSNVVRSANY	TCVAISSLGM	IEATAQVTVK
330	340	350	360	370	380	390	400
ALPKPPIDLV	VTETTATSVT	LTWDSGNSEP	VTYYGIQYRA	AGTEGPFQEV	DGVATTRYSI	GGLSPFSEYA	FRVLAVNSIG
410	420	430	440	450	460	470	480
RGPPSEAVRA	RTGEQAPSSP	PRRVQARMLS	ASTMLVQWEP	PEEPNGLVRG	YRVYYTPDSR	RPPNAWHKHN	TDAGLLTTVG
490	500	510	520	530	540	550	560
SLLPGITYSL	RVLAFTAVGD	GPPSPTIQVK	TQQGVPAQPA	DFQAEVESDT	RIQLSWLLPP	QERIIMYELV	YWAAEDEDQQ
570	580	590	600	610	620	630	640
HKVTFDPTSS	YTLEDLKPDT	LYRFQLAARS	DMGVGVFTPT	IEARTAQSTP	SAPPQKVMCV	SMGSTTVRVS	WVPPPADSRN
650	660	670	680	690	700	710	720
GVITQYSVAY	EAVDGEDRGR	HVVDGISREH	SSWDLVGLEK	WTEYRVWVRA	HTDVGPGPES	SPVLVRTDED	VPSGPPRKVE
730	740	750	760	770	780	790	800
VEPLNSTAVH	VYWKLPVPSK	QHGQIRGYQV	TYVRLENGEP	RGLPIIQDVM	LAEAQWRPEE	SEDYETTISG	LTPETTYSVT
810	820	830	840	850	860	870	880
VAAYTTKGDG	ARSKPKIVTT	TGAVFAKNFR	VAAAMKTSVL	LSWEVPDSYK	SAVPFKILYN	GQSVEVDGHS	MRKLIADLQP
890	900	910	920	930	940	950	960
NTEYSFVLMN	RGSSAGGLQH	LVSIRTAPDL	LPHKPLPASA	YIEDGRFDLS	MPHVQDPSLV	RWFYIVVVPI	DRVGGSMLTP
970	980	990	1000	1010	1020	1030	1040
RWSTPEELEL	DELLEAIEQG	GEEQRRRRRQ	AERLKPYVAA	QLDVLPETFT	LGDKKNYRGF	YNRPLSPDLS	YQCFVLASLK
1050	1060	1070	1080	1090	1100	1110	1120
EPMDQKRYAS	SPYSDEIVVQ	VTPAQQQEEP	EMLWVTGPVL	AVILIILIVI	AILLFKRKRT	HSPSSKDEQS	IGLKDSLLAH
1130	1140	1150	1160	1170	1180	1190	1200
SSDPVEMRRL	NYQTPGSSVP	SCPNTSSMRD	HPPIPITDLA	DNIERLKAND	GLKFSQEYES	IDPGQQFTWE	NSNLEVNKPK
1210	1220	1230	1240	1250	1260	1270	1280
NRYANVIAYD	HSRVILTSID	GVPGSDYINA	NYIDGYRKQN	AYIATQGPLP	ETMGDFWRMV	WEQRTATVVM	MTRLEEKSRV
1290	1300	1310	1320	1330	1340	1350	1360
KCDQYWPARG	TETCGLIQVT	LLDTVELATY	TVRTFALHKS	GSSEKRELRQ	FQFMAWPDHG	VPEYPTPILA	FLRRVKACNP
1370	1380	1390	1400	1410	1420	1430	1440
LDAGPMVVHC	SAGVGRTGCF	IVIDAMLERM	KHEKTVDIYG	HVTCMRSQRN	YMVQTEDQYV	FIHEALLEAA	TCGHTEVPAR
1450	1460	1470	1480	1490	1500	1510	1520
NLYAHIQKLG	QVPPGESVTA	MELEFKLLAS	SKAHTSRFIS	ANLPCNKFKN	RLVNIMPYEL	TRVCLQPIRG	VEGSDYINAS
1530	1540	1550	1560	1570	1580	1590	1600
FLDGYRQQKA	YIATQGPLAE	STEDFWRMLW	EHNSTIIVML	TKLREMGREK	CHQYWPAERS	ARYQYFVVDP	MAEYNMPQYI
1610	1620	1630	1640	1650	1660	1670	1680
LREFKVTDAR	DGQSRTIRQF	QFTDWPEQGV	PKTGEGFIDF	IGQVHKTKEQ	FGQDGPITVH	CSAGVGRTGV	FITLSIVLER
1690	1700	1710	1720	1730			
MRYEGVVDMF	QTVKTLRTQR	PAMVQTEDQY	QLCYRAALEY	LGSFDHYAT			

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

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2797	1	1024.5150	17.18	2	65.4	15.2	2	1390-1406	R.MKHEKTVDIYGHVTCMR.S	

Detailed Protein Report

Protein 294: **PREDICTED: probable JmjC domain-containing histone demethylation protein 2C isoform X6 [Homo sapiens]**

Accession:	gi|530393271	**Score:**	29.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	250.9
Database Date:	2015-11-30	**pI:**	9.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	0.7
		No. of unique Peptides:	2

Detailed Protein Report

10	20	30	40	50	60	70	80
MNSQAAVPKQ	NTHQQQQQRS	IRPNKRKGSD	SSIPDEEKMK	EEKYDYISRG	ENPKGKNKHL	MNKRRKPEED	EKKLNMKRLR
90	100	110	120	130	140	150	160
TDNVSDFSES	SDSENSNKRI	IDNSSEQKPE	NELKNKNTSK	INGEEGKPHN	NEKAGEETLK	NSQPPWDQIQ	EDKKHEEAEK
170	180	190	200	210	220	230	240
RKSVDTQLQE	DMIIHSSEQS	TVSDHNSNDL	LPQECNMDKT	HTMELLPKEK	FVSRPPTPKC	VIDITNDTNL	EKVAQENSST
250	260	270	280	290	300	310	320
FGLQTLQKMD	PNVSDSKHSI	ANAKFLETAK	KDSDQSWVSD	VVKVDLTQSS	VTNASSGNDH	LNMEKEKYVS	YISPLSAVSV
330	340	350	360	370	380	390	400
MEDKLHKRSP	PPETIKSKLN	TSVDTHKIKS	SPSPEVVKPK	ITHSPDSVKS	KATYVNSQAT	GERRLANKIE	HELSRCSFHP
410	420	430	440	450	460	470	480
IPTRSSTLET	TKSPLIIDKN	EHFTVYRDPA	LIGSETGANH	ISPFLSQHPF	PLHSSSHRTC	LNPGTHHPAL	TPAPHLLAGS
490	500	510	520	530	540	550	560
SSQTPLPTIN	THPLTSGPHH	AVHHPHLLPT	VLPGVPTASL	LGGHPRLESA	HASSLSHLAL	AHQQQQQLLQ	HQSPHLLGQA
570	580	590	600	610	620	630	640
HPSASYNQLG	LYPIIWQYPN	GTHAYSGLGL	PSSKWVHPEN	AVNAEASLRR	NSPSPWLHQP	TPVTSADGIG	LLSHIPVRPS
650	660	670	680	690	700	710	720
SAEPHRPLKI	TAHSSPPLTK	TLVDHHKEEL	ERKAFMEPLR	SVASTSAKND	LDLNRSQTGK	DCHLHRHFVD	PVLNQLQRPP
730	740	750	760	770	780	790	800
QETGERLNKY	KEEHRRILQE	SIDVAPFTTK	IKGLEGEREN	YSRVASSSSS	PKSHIIKQDM	DVERSVSDLY	KMKHSVPQSL
810	820	830	840	850	860	870	880
PQSNYFTTLS	NSVVNEPPRS	YPSKEVSNIY	GDKQSNALAA	AAANPQTLTS	FITSLSKPPP	LIKHQPESEG	LVGKIPEHLP
890	900	910	920	930	940	950	960
HQIASHSVTT	FRNDCRSPTH	LTVSSTNTLR	SMPALHRAPV	FHPPIHHSLE	RKEGSYSSLS	PPTLTPVMPV	NAGGKVQESQ
970	980	990	1000	1010	1020	1030	1040
KPPTLIPEPK	DSQANFKSSS	EQSLTEMWRP	NNNLSKEKTE	WHVEKSSGKL	QAAMASVIVR	PSSSTKTDSM	PAMQLASKDR
1050	1060	1070	1080	1090	1100	1110	1120
VSERSSAGAH	KTDCLKLAEA	GETGRIILPN	VNSDSVHTKS	EKNFQAVSQG	SVPSSVMSAV	NTMCNTKTDV	ITSAADTTSV
1130	1140	1150	1160	1170	1180	1190	1200
SSWGGSEVIS	SLSNTILAST	SSECVSSKSV	SQPVAQKQEC	KVSTTAPVTL	ASSKTGSVVQ	PSSGFSGTTD	FIHLKKHKAA
1210	1220	1230	1240	1250	1260	1270	1280
LAAAQYKSSN	ASETEPNAIK	NQTLSASLPL	DSTVICSTIN	KANSVGNGQA	SQTSQPNYHT	KLKKAWLTRH	SEEDKNTNKM
1290	1300	1310	1320	1330	1340	1350	1360
ENSGNSVSEI	IKPCSVNLIA	STSSDIQNSV	DSKIIVDKYV	KDDKVNRRKA	KRTYESGSES	GDSDESESKS	EQRTKRQPKP
1370	1380	1390	1400	1410	1420	1430	1440
TYKKKQNDLQ	KRKGEIEEDL	KPNGVLSRSA	KERSKLKLQS	NSNTGIPRSV	LKDWRKVKKL	KQTGESFLQD	DSCCEIGPNL
1450	1460	1470	1480	1490	1500	1510	1520
QKCRECRLIR	SKKGEEPAHS	PVFCRFYYFR	RLSFSKNGVV	RIDGFSSPDQ	YDDEAMSLWT	HENFEDDELD	IETSKYILDI
1530	1540	1550	1560	1570	1580	1590	1600
IGDKFCQLVT	SEKTALSWVK	KDAKIAWKRA	VRGVREMCDA	CEATLFNIHW	VCQKCGFVVC	LDCYKAKERK	SSRDKELYAW
1610	1620	1630	1640	1650	1660	1670	1680
MKCVKGQPHD	HKHLMPTQII	PGSVLTDLLD	AMHTLREKYG	IKSHCHCTNK	QNLQVGNFPT	MNGVSQVLQN	VLNHSNKISL
1690	1700	1710	1720	1730	1740	1750	1760
CMPESQQQNT	PPKSEKNGGS	SPESDVGTDN	KLTPPESQSP	LHWLADLAEQ	KAREEKKENK	ELTLENQIKE	EREQDNSESP
1770	1780	1790	1800	1810	1820	1830	1840
NGRTSPLVSQ	NNEQGSTLRD	LLTTTAGKLR	VGSTDAGIAF	APVYSMGAPS	SKSGRTMPNI	LDDIIASVVE	NKIPPSKTSK
1850	1860	1870	1880	1890	1900	1910	1920
INVKPELKEE	PEESIISAVD	ENNKLYSDIP	HSWICEKHIL	WLKDYKNSSN	WKLFKECWKQ	GQPAVVSGVH	KKMNISLWKA
1930	1940	1950	1960	1970	1980	1990	2000
ESISLDFGDH	QADLLNCKDS	IISNANVKEF	WDGFEEVSKR	QKNKSGETVV	LKLKDWPSGE	DFKTMMPARY	EDLLKSLPLP
2010	2020	2030	2040	2050	2060	2070	2080
EYCNPEGKFN	LASHLPGFFV	RPDLGPRLCS	AYGVVAAKDH	DIGTTNLHIE	VSDVVNILVY	VGIAKGNGIL	SKAGILKKFE
2090	2100	2110	2120	2130	2140	2150	2160
EEDLDDILRK	RLKDSSEIPG	ALWHIYAGKD	VDKIREFLQK	ISKEQGLEVL	PEHDPIRDQS	WYVNKKLRQR	LLEEYGVRTC
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
343	1	528.7540	-68.44	2	33.9	11.7	2	57-64	K.NKHLMNKR.R	Oxidation: 5
1263	1	1019.5782	7.40	1	45.5	17.4	1	1912-1919	K.KMNISLWK.A	

Detailed Protein Report

Protein 295: PREDICTED: contactin-associated protein-like 3 isoform X8 [Homo sapiens]

Accession:	gi|578816738	**Score:**	29.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	126.5
Database Date:	2015-11-30	**pI:**	9.6
		Sequence Coverage [%]:	3.2
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 1.18 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MASVAWAVLK	VLLLLPTQTW	SPVGAGNPPD	CDAPLASALP	RSSFSSSSEL	SSSHGPGFSR	LNRRDGAGGW	TPLVSNKYQW
90	100	110	120	130	140	150	160
LQIDLGERME	VTAVATQGGY	GSSDWVTSYL	LMFSDGGRNW	KQYRREESIW	GFPGNTNADS	VVHYRLQPPF	EARFLRFLPL
170	180	190	200	210	220	230	240
AWNPRGRIGM	RIEVYGCAYK	SEVVYFDGQS	ALLYRLDKKP	LKPIRDVISL	KFKAMQSNGI	LLHREGQHGN	HITLELIKGK
250	260	270	280	290	300	310	320
LVFFLNSGNA	KLPSTIAPVT	LTLGSLLDDQ	HWHSVLIELL	DTQVNFTVDK	HTHHFQAKGD	SSYLDLNFEI	SFGGIPTPGR
330	340	350	360	370	380	390	400
SRAFRRKSFH	GCLENLYYNG	VDVTELAKKH	KPQILMMGNV	SFSCPQPQTV	PVTFLSSRSY	LALPGNSGED	KVSVTFQFRT
410	420	430	440	450	460	470	480
WNRAGHLLFG	ELRRGSGSFV	LFLKDGKLKL	SLFQPGQSPR	NVTAGAGLND	GQWHSVSFSA	KWSHMNVVVD	DDTAVQPLVA
490	500	510	520	530	540	550	560
VLIDSGDTYY	FGDAAWTVVQ	HGGPDAVTLR	GAPSGHPRSA	VSFAYAAGAG	QLRSAVNLAE	RCEQRLALRC	GTARRPDSRD
570	580	590	600	610	620	630	640
GTPLSWWVGR	TNETHTSWGG	SLPDAQKCTC	GLEGNCIDSQ	YYCNCDAGRN	EWTSDTIVLS	QKEHLPVTQI	VMTDAGRPHS
650	660	670	680	690	700	710	720
EAAYTLGPLL	CRGDQSFWNS	ASFNTETSYL	HFPAFHGELT	ADVCFFFKTT	VSSGVFMENL	GITDFIRIEL	RAPTEVTFSF
730	740	750	760	770	780	790	800
DVGNGPCEVT	VQSPTPFNDN	QWHHVRAERN	VKGASLQVDQ	LPQKMQPAPA	DGHVRLQLNS	QLFIGGTATR	QRGFLGCIRS
810	820	830	840	850	860	870	880
LQLNGVALDL	EERATVTPGV	EPGCAGHCST	YGHLCRNGGR	CREKRRGVTC	DCAFSAYDGP	FCSNEISAYF	ATGSSMTYHF
890	900	910	920	930	940	950	960
QEHYTLSENS	SSLVSSLHRD	VTLTREMITL	SFRTTRTPSL	LLYVSSFYEE	YLSVILANNG	SLQIRYKLDR	HQNPDAFTFD
970	980	990	1000	1010	1020	1030	1040
FKNMADGQLH	QVKINREEAV	VMVEVNQSTK	KQVILSSGTE	FNAVKSLILG	KVLEAAGADP	DTRRAATSGF	TGCLSAVRFG
1050	1060	1070	1080	1090	1100	1110	1120
RAAPLKAALR	PSGPSRVTVR	GHVAPMARCA	AGAASGSPAR	ELAPRLAGGA	GRSGPADEGE	PLVNADRRDS	AVIGGVIAVV
1130	1140	1150	1160				
IFILLCITAI	AIRIYQQRKL	RKENESKVSK	KEEC				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1567	1	919.5953	159.08	2	49.4	13.7	1	1061-1080	R.GHVAPMARCAAGAASGSPAR.E		MD:MU 1.18

Detailed Protein Report

Protein 296: interferon regulatory factor 2-binding protein 2 isoform B [Homo sapiens]

Accession:	gi|116734706	**Score:**	29.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	59.4
Database Date:	2015-11-30	**pI:**	10.1
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.4
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MAAAVAVAAA	SRRQSCYLCD	LPRMPWAMIW	DFTEPVCRGC	VNYEGADRVE	FVIETARQLK	RAHGCFPEGR	SPPGAAASAA
90	100	110	120	130	140	150	160
AKPPPLSAKD	ILLQQQQQLG	HGGPEAAPRA	PQALERYPLA	AAAERPPRLG	SDFGSSRPAA	SLAQPPTPQP	PPVNGILVPN
170	180	190	200	210	220	230	240
GFSKLEEPPE	LNRQSPNPRR	GHAVPPTLVP	LMNGSATPLP	TALGLGGRAA	ASLAAVSGTA	AASLGSAQPT	DLGAHKRPAS
250	260	270	280	290	300	310	320
VSSSAAVEHE	QREAAAKEKQ	PPPPAHRGPA	DSLSTAAGAA	ELSAEGAGKS	RGSGEQDWVN	RPKTVRDTLL	ALHQHGHSGP
330	340	350	360	370	380	390	400
FESKFKKEPA	LTAVARTARK	RKPSPEPEGE	VGPPKINGEA	QPWLSTSTEG	LKIPMTPTSS	FVSPPPPTAS	PHSNRTTPPE
410	420	430	440	450	460	470	480
AAQNGQSPMA	ALILVADNAG	GSHASKDANQ	VHSTTRRNSN	SPPSPSSMNQ	RRLGPREVGG	QGAGNTGGLE	PVHPASLPDS
490	500	510	520	530	540	550	560
SLATSAPLCC	TLCHERLEDT	HFVQCPSVPS	HKFCFPCSRQ	SIKQQGASGE	VYCPSGEKCP	LVGSNVPWAF	MQGEIATILA
570	580						
GDVKVKKERD	S						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1850	1	724.2703	-144.49	2	53.0	18.8	0	342-355	R.KPSPEPEGEVGPPK.I	
2516	1	715.2357	-144.98	2	61.4	10.3	1	513-523	K.FCFPCSRQSIK.Q	Carbamidomethyl: 2, 5

Detailed Protein Report

Protein 297: PREDICTED: TGF-beta-activated kinase 1 and MAP3K7-binding protein 3 isoform X3 [Homo sapiens]

Accession:	gi|578837866	**Score:**	29.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	75.0
Database Date:	2015-11-30	**pI:**	9.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	5.9
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MAQSSPQLDI	QVLHDLRQRF	PEIPEGVVSQ	CMLQNNNNLE	ACCRALSQES	SKYLYMEYHS	PDDNRMNRNR	LLHINLGIHS
90	100	110	120	130	140	150	160
PSSYHPGDGA	QLNGGRTLVH	SSSDGHIDPQ	HAAGKQLICL	VQEPHSAPAV	VAATPNYNPF	FMNEQNRSAA	TPPSQPPQQP
170	180	190	200	210	220	230	240
SSMQTGMNPS	AMQGPSPPPP	PPSYMHIPRY	STNPITVTVS	QNLPSGQTVP	RALQILPQIP	SNLYGSPGSI	YIRQTSQSSS
250	260	270	280	290	300	310	320
GRQTPQSTPW	QSSPQGPVPH	YSQRPLPVYP	HQQNYQPSQY	SPKQQQIPQS	AYHSPPPSQC	PSPFSSPQHQ	VQPSQLGHIF
330	340	350	360	370	380	390	400
MPPSPSTTPP	HPYQQGPPSY	QKQGSHSVAY	LPYTASSLSK	GSMKKIEITV	EPSQRPGTAI	NRSPSPISNQ	PSPRNQHSLY
410	420	430	440	450	460	470	480
TATTPPSSSP	SRGISSQPKP	PFSVNPVYIT	YTQPTGPSCT	PSPSPRVIPN	PTTVFKITVG	RATTENLLNL	VDQEERSAAP
490	500	510	520	530	540	550	560
EPIQPISVIP	GSGGEKGSHK	YQRSSSSGSD	DYAYTQALLL	HQRARMERLA	KQLKLEKEEL	ERLKSEVNGM	EHDLMQRRLR
570	580	590	600	610	620	630	640
RVSCTTAIPT	PEEMTRLRSM	NRQLQINVDC	TLKEVDLLQS	RGNFDPKAMN	NFYDNIEPGP	VVPPKPSKKE	HRTGSTQSPR
650	660	670	680				
TQPRDEDYEG	APWNCDSCTF	LNHPALNRCE	QCEMPRYT				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1041	1	955.6888	-79.15	3	42.6	18.2	0	20-44	R.FPEIPEGVVSQCMLQNNNNLEACCR.A	Carbamidomethyl: 23
2667	1	821.4359	-63.35	2	63.5	10.8	1	447-461	R.VIPNPTTVFKITVGR.A	

Detailed Protein Report

Protein 298: **ADP/ATP translocase 1 [Homo sapiens]**

Accession:	gi|55749577	**Score:**	29.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	33.0
Database Date:	2015-11-30	**pI:**	10.3
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	11.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGDHAWSFLK	DFLAGGVAAA	VSKTAVAPIE	RVKLLLQVQH	ASKQISAEKQ	YKGIIDCVVR	IPKEQGFLSF	WRGNLANVIR
90	100	110	120	130	140	150	160
YFPTQALNFA	FKDKYKQLFL	GGVDRHKQFW	RYFAGNLASG	GAAGATSLCF	VYPLDFARTR	LAADVGKGAA	QREFHGLGDC
170	180	190	200	210	220	230	240
IIKIFKSDGL	RGLYQGFNVS	VQGIIIYRAA	YFGVYDTAKG	MLPDPKNVHI	FVSWMIAQSV	TAVAGLVSYP	FDTVRRRMMM
250	260	270	280	290	300		
QSGRKGADIM	YTGTVDCWRK	IAKDEGAKAF	FKGAWSNVLR	GMGGAFVLVL	YDEIKKYV		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2202	1	1051.1584	137.54	2	57.7	12.3	2	246-263	K.GADIMYTGTVDCWRKIAK.D	Carbamidomethyl: 12; Oxidation: 5

Detailed Protein Report

Protein 299: xylosyltransferase 1 precursor [Homo sapiens]

Accession:	gi|28269693	**Score:**	29.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	107.5
Database Date:	2015-11-30	**pI:**	10.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.8
		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
1789	1	916.3008	-236.11	1	52.4	13.7	0	289-296	K.LGLLMPEK.V	Oxidation: 5
2109	1	701.2880	-90.93	3	56.5	15.4	0	388-406	R.MATIWGGASLLSTYLQSMR.D	Oxidation: 18

Detailed Protein Report

Protein 300: ATP-dependent DNA helicase Q1 [Homo sapiens]

Accession:	gi|14591902	**Score:**	29.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	73.4
Database Date:	2015-11-30	**pI:**	9.0
		Sequence Coverage [%]:	4.3
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578823000	refseq_human (refseq_human_20140103.fasta)	PREDICTED: ATP-dependent DNA helicase Q1 isoform X5 [Homo sapiens]
gi|530399347	refseq_human (refseq_human_20140103.fasta)	PREDICTED: ATP-dependent DNA helicase Q1 isoform X4 [Homo sapiens]
gi|530399345	refseq_human (refseq_human_20140103.fasta)	PREDICTED: ATP-dependent DNA helicase Q1 isoform X3 [Homo sapiens]
gi|530399343	refseq_human (refseq_human_20140103.fasta)	PREDICTED: ATP-dependent DNA helicase Q1 isoform X2 [Homo sapiens]
gi|530399341	refseq_human (refseq_human_20140103.fasta)	PREDICTED: ATP-dependent DNA helicase Q1 isoform X1 [Homo sapiens]
gi|14591904	refseq_human (refseq_human_20140103.fasta)	ATP-dependent DNA helicase Q1 [Homo sapiens]

10	20	30	40	50	60	70	80
MASVSALTEE	LDSITSELHA	VEIQIQELTE	RQQELIQKKK	VLTKKIKQCL	EDSDAGASNE	YDSSPAAWNK	EDFPWSGKVK
90	100	110	120	130	140	150	160
DILQNVFKLE	KFRPLQLETI	NVTMAGKEVF	LVMPTGGGKS	LCYQLPALCS	DGFTLVICPL	ISLMEDQLMV	LKQLGISATM
170	180	190	200	210	220	230	240
LNASSSKEHV	KWVHAEMVNK	NSELKLIYVT	PEKIAKSKMF	MSRLEKAYEA	RRFTRIAVDE	VHCCSQWGHD	FRPDYKALGI
250	260	270	280	290	300	310	320
LKRQFPNASL	IGLTATATNH	VLTDAQKILC	IEKCFTFTAS	FNRPNLYYEV	RQKPSNTEDF	IEDIVKLING	RYKGQSGIIY
330	340	350	360	370	380	390	400
CFSQKDSEQV	TVSLQNLGIH	AGAYHANLEP	EDKTTVHRKW	SANEIQVVVA	TVAFGMGIDK	PDVRFVIHHS	MSKSMENYYQ
410	420	430	440	450	460	470	480
ESGRAGRDDM	KADCILYYGF	GDIFRISSMV	VMENVGQQKL	YEMVSYCQNI	SKCRRVLMAQ	HFDEVWNSEA	CNKMCDNCCK
490	500	510	520	530	540	550	560
DSAFERKNIT	EYCRDLIKIL	KQAEELNEKL	TPLKLIDSWM	GKGAAKLRVA	GVVAPTLPRE	DLEKIIAHFL	IQQYLKEDYS
570	580	590	600	610	620	630	640
FTAYATISYL	KIGPKANLLN	NEAHAITMQV	TKSTQNSFRA	ESSQTCHSEQ	GDKKMEEKNS	GNFQKKAANM	LQQSGSKNTG
650							
AKKRKIDDA							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2269	1	701.1276	94.64	3	58.2	13.1	1	540-556	R.EDLEKIIAHFLIQQYLK.E	

Detailed Protein Report

Protein 301: ectodysplasin-A isoform 2 [Homo sapiens]

Accession:	gi|54112101		**Score:**	28.9
Database:	refseq_human(refseq_human_20140103.fasta)		**MW [kDa]:**	41.0
Database Date:	2015-11-30		**pI:**	9.6
			Sequence Coverage [%]:	8.7
			No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGYPEVERRE	LLPAAAPRER	GSQGCGCGGA	PARAGEGNSC	LLFLGFFGLS	LALHLLTLCC	YLELRSELRR	ERGAESRLGG
90	100	110	120	130	140	150	160
SGTPGTSGTL	SSLGGLDPDS	PITSHLGQPS	PKQQPLEPGE	AALHSDSQDG	HQMALLNFFF	PDEKPYSEEE	SRRVRRNKRS
170	180	190	200	210	220	230	240
KSNEGADGPV	KNKKKGKKAG	PPGPNGPPGP	PGPPGPQGPP	GIPGIPGIPG	TTVMGPPGPP	GPPGPQGPPG	LQGPSGAADK
250	260	270	280	290	300	310	320
AGTRENQPAV	VHLQGQGSAI	QVKNDLSGGV	LNDWSRITMN	PKVFKLHPRS	GELEVLVDGT	YFIYSQVYYI	NFTDFASYEV
330	340	350	360	370	380	390	
VVDEKPFLQC	TRSIETGKTN	YNTCYTAGVC	LLKARQKIAV	KMVHADISIN	MSKHTTFFGA	IRLGEAPAS	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1518	1	1059.0796	50.76	2	48.7	16.6	1	264-282	K.NDLSGGVLNDWSRITMNPK.V	

Detailed Protein Report

Protein 302: PREDICTED: MDS1 and EVI1 complex locus protein EVI1 isoform X16 [Homo sapiens]

Accession:	gi|578807160	**Score:**	28.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	93.9
Database Date:	2015-11-30	**pI:**	6.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.2
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MRSKGRARKL	ATNNECVYGN	YPEIPLEEMP	DADGVASTPS	LNIQEPCSPA	TSSEAFTPKE	GSPYKAPIYI	PDDIPIPAEF
90	100	110	120	130	140	150	160
ELRESNMPGA	GLGIWTKRKI	EVGEKFGPYV	GEQRSNLKDP	SYGWEILDEF	YNVKFCIDAS	QPDVGSWLKY	IRFAGCYDQH
170	180	190	200	210	220	230	240
NLVACQINDQ	IFYRVVADIA	PGEELLLFMK	SEDYPHETMA	PDIHEERQYR	CEDCDQLFES	KAELADHQKF	PCSTPHSAFS
250	260	270	280	290	300	310	320
MVEEDFQQKL	ESENDLQEIH	TIQECKECDQ	VFPDLQSLEK	HMLSHTEERE	YKCDQCPKAF	NWKSNLIRHQ	MSHDSGKHYE
330	340	350	360	370	380	390	400
CENCAKQVFT	DPSNLQRHIR	SQHVGARAHA	CPECGKTFAT	SSGLKQHKHI	HSSVKPFICE	VCHKSYTQFS	NLCRHKRMHA
410	420	430	440	450	460	470	480
DCRTQIKCKD	CGQMFSTTSS	LNKHRRFCEG	KNHFAAGGFF	GQGISLPGTP	AMDKTSMVNM	SHANPGLADY	FGANRHPAGL
490	500	510	520	530	540	550	560
TFPTAPGFSF	SFPGLFPSGL	YHRPPLIPAS	SPVKGLSSTE	QTNKSQSPLM	THPQILPATQ	DILKALSKHP	SVGDNKPVEL
570	580	590	600	610	620	630	640
QPERSSEERP	FEKISDQSES	SDLDDVSTPS	GSDLETTSGS	DLESDIESDK	EKFKENGKMF	KDKVSPLQNL	ASINNKKEYS
650	660	670	680	690	700	710	720
NHSIFSPSLE	EQTAVSGAVN	DSIKAIASIA	EKYFGSTGLV	GLQDKKVGAL	PYPSMFPLPF	FPAFSQSMYP	FPDRDLRSLP
730	740	750	760	770	780	790	800
LKMEPQSPGE	VKKLQKGSSE	SPFDLTTKRK	DEKPLTPVPS	KPPVTPATSQ	DQPLDLSMGS	RSRASGTKLT	EPRKNHVFGG
810	820	830	840	850			
KKGSNVESRP	ASDGSLQHAR	PTPFFMDPIY	RCQLLKTWQK	S			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2185	2	1052.4145	-10.10	2	57.2	11.8	1	309-326	R.HQMSHDSGKHYECENCAK.Q	
668	1	602.8050	-39.80	2	37.9	17.1	1	832-840	R.CQLLKTWQK.S	Carbamidomethyl: 1

Detailed Protein Report

Protein 303: **PREDICTED: bromodomain adjacent to zinc finger domain protein 2A isoform X11 [Homo sapiens]**

Accession:	gi|578823227	**Score:**	28.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	170.8
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
MEVACILHTR GGVQKTGERR EMEANDHFNF TGLPPAPAAS GLKPSPSSGE GLYTNGSPMN FPQQGKSLNG DVNVNGLSTV
        90        100        110        120        130        140        150        160
SHTTTSGILN SAPHSSSTSH LHHPSVAYDC LWNYSQYPSA NPGSNLKDPP LLSQFSGGQY PLNGILGGSR QPSSPSHNTN
       170        180        190        200        210        220        230        240
LRAGSQEFWA NGTQSPMGLN FDSQELYDSF PDQNFEVMPN GPPSFFTSPQ TSPMLGSSIQ TFAPSQEVGS GIHPDEAAEK
       250        260        270        280        290        300        310        320
EMTSVVAENG TGLVGSLELE EEQPELKMCG YNGSVPSVES LHQEVSVLVP DPTVSCLDDP SHLPDQLEDT PILSEDSLEP
       330        340        350        360        370        380        390        400
FNSLAPEPVS GGLYGIDDTE LMGAEDKLPL EDSPVISALD CPSLNNATAF SLLADDSQTS TSIFASPTSP PVLGESVLQD
       410        420        430        440        450        460        470        480
NSFDLNNGSD AEQEEMETQS SDFPPSLTQP APDQSSTIQL HPATSPAVSP TTSPAVSLVV SPAASPEISP EVCPAASTVV
       490        500        510        520        530        540        550        560
SPAVFSVVSP ASSAVLPAVS LEVPLTASVT SPKASPVTSP AAAFPTASPA NKDVSSFLET TADVEEITGE GLTASGSGDV
       570        580        590        600        610        620        630        640
MRRRIATPEE VRLPLQHGWR REVRIKKGSH RWQGETWYYG PCGKRMKQFP EVIKYLSRNV VHSVRREHFS FSPRMPVGDF
       650        660        670        680        690        700        710        720
FEERDTPEGL QWVQLSAEEI PSRIQAITGK RGRPRNTEKA KTKEVPKVKR GRGRPPKVKI TELLNKTDNR PLKKLEAQET
       730        740        750        760        770        780        790        800
LNEEDKAKIA KSKKKMRQKV QRGECQTTIQ GQARNKRKQE TKSLKQKEAK KKSKAEKEKG KTKQEKLKEK VKREKKEKVK
       810        820        830        840        850        860        870        880
MKEKEEVTKA KPACKADKTL ATQRRLEERQ RQQMILEEMK KPTEDMCLTD HQPLPDFSRV PGLTLPSGAF SDCLTIVEFL
       890        900        910        920        930        940        950        960
HSFGKVLGFD PAKDVPSLGV LQEGLLCQGD SLGEVQDLLV RLLKAALHDP GFPSYCQSLK ILGEKVSEIP LTRDNVSEIL
       970        980        990       1000       1010       1020       1030       1040
RCFLMAYGVE PALCDRLRTQ PFQAQPPQQK AAVLAFLVHE LNGSTLIINE IDKTLESMSS YRKNKWIVEG RLRRLKTVLA
      1050       1060       1070       1080       1090       1100       1110       1120
KRTGRSEVEM EGPEECLGRR RSSRIMEETS GMEEEEEEES IAAVPGRRGR RDGEVDATAS SIPELERQIE KLSKRQLFFR
      1130       1140       1150       1160       1170       1180       1190       1200
KKLLHSSQML RAVSLGQDRY RRRYWVLPYL AGIFVEGTEG NLVPEEVIKK ETDSLKVAAH ASLNPALFSM KMELAGSNTT
      1210       1220       1230       1240       1250       1260       1270       1280
ASSPARARGR PRKTKPGSMQ PRHLKSPVRG QDSEQPQAQL QPEAQLHAPA QPQPQLQLQL QSHKGFLEQE GSPLSLGQSQ
      1290       1300       1310       1320       1330       1340       1350       1360
HDLSQSAFLS WLSQTQSHSS LLSSSVLTPD SSPGKLDPAP SQPPEEPEPD EAESSPDPQA LWFNISAQMP CNAAPTPPPA
      1370       1380       1390       1400       1410       1420       1430       1440
VSEDQPTPSP QQLASSKPMN RPSAANPCSP VQFSSTPLAG LAPKRRAGDP GEMPQSPTGL GQPKRRGRPP SKFFKQMEQR
      1450       1460       1470       1480       1490       1500       1510       1520
YLTQLTAQPV PPEMCSGWWW IRDPEMLDAM LKALHPRGIR EKALHKHLNK HRDFLQEVCL RPSADPIFEP RQLPAFQEGI
      1530       1540       1550       1560
MSWSPKEKTY ETDLAVLQWV EELEQRVIMS DLQIR
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2577	1	941.5794	21.02	2	62.2	13.8	2	698-713	K.VKITELLNKTDNRPLK.K	

Detailed Protein Report

Protein 304: **latent-transforming growth factor beta-binding protein 4 isoform c precursor [Homo sapiens]**

Accession:	gi|110347437	**Score:**	28.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	165.6
Database Date:	2015-11-30	**pI:**	4.8
		Sequence Coverage [%]:	1.7
		No. of unique Peptides:	2

```
        10         20         30         40         50         60         70         80
MAGGVRLLWV SLLVLLAQLG PQPGLGRLGE RLRVRFTPVV CGLRCVHGPT GSRCTPTCAP RNATSVDSGA PGGAAPGGPG
        90        100        110        120        130        140        150        160
FRAFLCPLIC HNGGVCVKPD RCLCPPDFAG KFCQLHSSGA RPPAPAVPGL TRSVYTMPLA NHRDDEHGVA SMVSVHVEHP
       170        180        190        200        210        220        230        240
QEASVVVHQV ERVSGPWEEA DAEAVARAEA AARAEAAAPY TVLAQSAPRE DGYSDASGFG YCFRELRGGE CASPLPGLRT
       250        260        270        280        290        300        310        320
QEVCCRGAGL AWGVHDCQLC SERLGNSERV SAPDGPCPTG FERVNGSCED VDECATGGRC QHGECANTRG GYTCVCPDGF
       330        340        350        360        370        380        390        400
LLDSSRSSCI SQHVISEAKG PCFRVLRDGG CSLPILRNIT KQICCCSRVG KAWGRGCQLC PPFGSEGFRE ICPAGPGYHY
       410        420        430        440        450        460        470        480
SASDLRYNTR PLGQEPPRVS LSQPRTLPAT SRPSAGFLPT HRLEPRPEPR PDPRPGPELP LPSIPAWTGP EIPESGPSSG
       490        500        510        520        530        540        550        560
MCQRNPQVCG PGRCISRPSG YTCACDSGFR LSPQGTRCID VDECRRVPPP CAPGRCENSP GSFRCVCGPG FRAGPRAAEC
       570        580        590        600        610        620        630        640
LDVDECHRVP PPCDLGRCEN TPGSFLCVCP AGYQAAPHGA SCQDVDECTQ SPGLCGRGAC KNLPGSFRCV CPAGFRGSAC
       650        660        670        680        690        700        710        720
EEDVDECAQE PPPCGPGRCD NTAGSFHCAC PAGFRSRGPG APCQDVDECA RSPPPCTYGR CENTEGSFQC VCPMGFQPNT
       730        740        750        760        770        780        790        800
AGSECEDVDE CENHLACPGQ ECVNSPGSFQ CRTCPSGHHL HRGRCTDVDE CSSGAPPCGP HGHCTNTEGS FRCSCAPGYR
       810        820        830        840        850        860        870        880
APSGRPGPCA DVNECLEGDF CFPHGECLNT DGSFACTCAP GYRPGPRGAS CLDVDECSEE DLCQSGICTN TDGSFECICP
       890        900        910        920        930        940        950        960
PGHRAGPDLA SCLDVDECRE RGPALCGSQR CENSPGSYRC VRDCDPGYHA GPEGTCDDVD ECQEYGPEIC GAQRCENTPG
       970        980        990       1000       1010       1020       1030       1040
SYRCTPACDP GYQPTPGGGC QDVDECRNRS FCGAHAVCQN LPGSFQCLCD QGYEGARDGR HCVDVNECET LQGVCGAALC
      1050       1060       1070       1080       1090       1100       1110       1120
ENVEGSFLCV CPNSPEEFDP MTGRCVPPRT SAGTFPGSQP QAPASPVLPA RPPPPPLPRR PSTPRQGPVG SGRRECYFDT
      1130       1140       1150       1160       1170       1180       1190       1200
AAPDACDNIL ARNVTWQECC CTVGEGWGSG CRIQQCPGTE TAEYQSLCPH GRGYLAPSGD LSLRRDVDEC QLFRDQVCKS
      1210       1220       1230       1240       1250       1260       1270       1280
GVCVNTAPGY SCYCSNGYYY HTQRLECIDN DECADEEPAC EGGRCVNTVG SYHCTCEPPL VLDGSQRRCV SNESQSLDDN
      1290       1300       1310       1320       1330       1340       1350       1360
LGVCWQEVGA DLVCSHPRLD RQATYTECCC LYGEAWGMDC ALCPAQDSDD FEALCNVLRP PAYSPPRPGG FGLPYEYGPD
      1370       1380       1390       1400       1410       1420       1430       1440
LGPPYQGLPY GPELYPPPAL PYDPYPPPPG PFARREAPYG APRFDMPDFE DDGGPYGESE APAPPGPGTR WPYRSRDTRR
      1450       1460       1470       1480       1490       1500       1510       1520
SFPEPEEPPE GGSYAGSLAE PYEELEAEEC GILDGCTNGR CVRVPEGFTC RCFDGYRLDM TRMACVDINE CDEAEAASPL
      1530       1540       1550       1560
CVNARCLNTD GSFRCICRPG FAPTHQPHHC APARPRA
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1055	1	941.2810	-147.80	2	42.8	15.8	1	902-919	R.GPALCGSQRCENSPGSYR.C	
373	1	457.1205	-287.06	2	34.0	13.0	1	1106-1114	R.QGPVGSGRR.E	

Detailed Protein Report

Protein 305: relA-associated inhibitor [Homo sapiens]

Accession: gi|63003907
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 28.7
MW [kDa]: 89.0
pI: 6.4
Sequence Coverage [%]: 4.1
No. of unique Peptides: 1

Alias proteins:

Accession	Name	Description
gi|215820635	refseq_human (refseq_human_20140103.fasta)	relA-associated inhibitor [Homo sapiens]

10	20	30	40	50	60	70	80
MDSEAFQSAR	DFLDMNFQSL	AMKHMDLKQM	ELDTAAAKVD	ELTKQLESLW	SDSPAPPGPQ	AGPPSRPPRY	SSSSIPEPFG
90	100	110	120	130	140	150	160
SRGSPRKAAT	DGADTPFGRS	ESAPTLHPYS	PLSPKGRPSS	PRTPLYLQPD	AYGSLDRATS	PRPRAFDGAG	SSLGRAPSPR
170	180	190	200	210	220	230	240
PGPGPLRQQG	PPTPFDFLGR	AGSPRGSPLA	EGPQAFFPER	GPSPRPPATA	YDAPASAFGS	SLLGSGGSAF	APPLRAQDDL
250	260	270	280	290	300	310	320
TLRRRPPKAW	NESDLDVAYE	KKPSQTASYE	RLDVFARPAS	PSLQLLPWRE	SSLDGLGGTG	KDNLTSATLP	RNYKVSPLAS
330	340	350	360	370	380	390	400
DRRSDAGSYR	RSLGSAGPSG	TLPRSWQPVS	RIPMPPSSPQ	PRGAPRQRPI	PLSMIFKLQN	AFWEHGASRA	MLPGSPLFTR
410	420	430	440	450	460	470	480
APPPKLQPQP	QPQPQPQSQP	QPQLPPQPQT	QPQTPTPAPQ	HPQQTWPPVN	EGPPKPPTEL	EPEPEIEGLL	TPVLEAGDVD
490	500	510	520	530	540	550	560
EGPVARPLSP	TRLQPALPPE	AQSVPELEEV	ARVLAEIPRP	LKRRGSMEQA	PAVALPPTHK	KQYQQIISRL	FHRHGGPGPG
570	580	590	600	610	620	630	640
GPEPELSPIT	EGSEARAGPP	APAPPAPIPP	PAPSQSSPPE	QPQSMEMRSV	LRKAGSPRKA	RRARLNPLVL	LLDAALTGEL
650	660	670	680	690	700	710	720
EVVQQAVKEM	NDPSQPNEEG	ITALHNAICG	ANYSIVDFLI	TAGANVNSPD	SHGWTPLHCA	ASCNDTVICM	ALVQHGAAIF
730	740	750	760	770	780	790	800
ATTLSDGATA	FEKCDPYREG	YADCATYLAD	VEQSMGLMNS	GAVYALWDYS	AEFGDELSFR	EGESVTVLRR	DGPEETDWWW
810	820	830					
AALHGQEGYV	PRNYFGLFPR	VKPQRSKV					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
100	1	1301.5284	-95.57	2	31.0	12.3	1	378-400	K.LQNAFWEHGASRAMLPGSPLFTR.A	Oxidation: 14

Detailed Protein Report

Protein 306: zinc finger and SCAN domain-containing protein 1 [Homo sapiens]

Accession:	gi|110431336	**Score:**	28.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	45.3
Database Date:	2015-11-30	**pI:**	10.0
		Sequence Coverage [%]:	10.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLPRPKAPAS	PRRPQTPTPS	EQDADPGPAS	PRDTEAQRLR	FRQFQYHVAS	GPHLALGQLW	TLCRQWLRPE	ARSKEQMLEL
90	100	110	120	130	140	150	160
LVLEQFLGAL	PSKMRTWVQS	QGPRSCREAA	SLVEDLTQMC	QQEVLVSLDS	VEPQDWSFGE	EEDGKSPRSQ	KEPSQASELI
170	180	190	200	210	220	230	240
LDAVAAAPAL	PEESEWLETT	QLQQSLHTRA	EAEAPRAPGL	LGSRARLPLK	PSIWDEPEDL	LAGPSSDLRA	EGTVISSPKG
250	260	270	280	290	300	310	320
PSAQRISPRR	RNRNTDQSGR	HQPSLKHTKG	GTQEAVAGIS	VVPRGPRGGR	PFQCADCGMV	FTWVTHFIEH	QKTHREEGPF
330	340	350	360	370	380	390	400
PCPECGKVFL	HNSVLTEHGK	IHLLEPPRKK	APRSKGPRES	VPPRDGAQGP	VAPRSPKRPF	QCSVCGKAFP	WMVHLIDHQK
410							
LHTAHGHM							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2130	2	1052.4295	-73.05	2	56.8	17.6	0	13-32	R.RPQTPTPSEQDADPGPASPR.D	

Detailed Protein Report

Protein 307: protein MROH8 isoform 1 [Homo sapiens]

Accession:	gi|194595501	**Score:**	28.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	119.2
Database Date:	2015-11-30	**pI:**	9.5
		Sequence Coverage [%]:	2.7
		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	IIKHLVPWLQ	SVKDHERERA	TASMAQVLKC	LSKHLNLKLP	LRFQRLGHLV	ALMALLCGDP	QEKVAEEAAE
410	420	430	440	450	460	470	480
GIHSLLHITL	RLKYITHDKK	DQQNLKRALT	KCREFLELHS	SAAKCFYNCP	FRIAQVFEGF	LDSNELCQFI	MTTFDTLKTL
490	500	510	520	530	540	550	560
KHPCIQRSAG	ELLLTLAKNT	ESQFEKVPEI	MGVICAQLSI	ISQPRVRQQI	INTVSLFISR	PKYTDIVLSF	LLCHPVPYNR
570	580	590	600	610	620	630	640
HLAEVWRMLS	VELPSTTWIL	WRLLRKLQKC	HNEPAQEKMA	YVAVAATDAL	YEVFLGNRLR	AATFRLFPQL	LMTLLIQIHH
650	660	670	680	690	700	710	720
SIGLTMSDVD	IPSGLYTEQE	VPSEVTPLCF	AMQATKTLLL	RTCCLQEFNI	MEKNKGWALL	GGKDGHLQGL	FLLANALLER
730	740	750	760	770	780	790	800
NQLLAQKVMY	LLVPLLNRGN	DKHKLTSAGF	FVELLRSPVA	KRLPSIYSVA	RFKDWLQDGN	HLFRILGLRG	LYNLVGHQEM
810	820	830	840	850	860	870	880
REDIKSLLPY	IVDSLRETDE	KIVLSAIQIL	LQLVRTMDFT	TLAAMMRTLF	SLFGDVRSDV	HRFSVTLFGA	AIKSVKNPDK
890	900	910	920	930	940	950	960
KSIENQVLDS	LVPLLLYSQD	ENDAVAEESR	QVLTICAQFL	KWKLPQEVYS	KDPWHIKPTE	AGTICRFFEK	KCKGKINILE
970	980	990	1000	1010	1020	1030	1040
QTLMYSKNPK	LPIRRSAVLF	VGLLSKYMDH	NELRRMGTDW	IEDDLRDLLC	DPEPSLCIIA	SQTLLLVQMA	RAEPKPKQRV
1050	1060						
NWLQKLMGRS	SA						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1490	1	977.1102	85.91	2	48.4	10.9	1	774-789	K.DWLQDGNHLFRILGLR.G	

Detailed Protein Report

Protein 308: **hydrocephalus-inducing protein homolog isoform a [Homo sapiens]**

Accession:	gi|401664560	**Score:**	28.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	575.5
Database Date:	2015-11-30	**pI:**	5.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	0.8
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MTSRRLEESM	GAVQMGLVNM	FKGFQSKVLP	PLSPKVVTEE	EVNRMLTPSE	FLKEMSLTTE	QRLAKTRLMC	RPQIIELLDM
90	100	110	120	130	140	150	160
GETTHQKFSG	IDLDQALFQP	FPSEIIFQNY	TPCEVYEVPL	ILRNNDKIPR	LVKVVEESSP	YFKVISPKDI	GHKVAPGVPS
170	180	190	200	210	220	230	240
IFRILFTPEE	NKDYAHTLTC	VTEREKFIVP	IKARGARAIL	DFPDKLNFST	CPVKYSTQKI	LLVRNIGNKN	AVFHIKTCRP
250	260	270	280	290	300	310	320
FSIEPAIGTL	NVGESMQLEV	EFEPQSVGDH	SGRLIVCYDT	GEKVFVSLYG	AAIDMNIRLD	KNSLTIEKTY	ISLANQRTIT
330	340	350	360	370	380	390	400
IHNRSNIIAH	FLWKVFATQQ	EEDREKYRAC	DDLIKEEKDE	TDEFFEECIT	DPLLREHLSV	LSRTFANQRR	LVQGDSKLFF
410	420	430	440	450	460	470	480
NNVFTVEPLE	GDVWPNSSAE	ITVYFNPLEA	KLYQQTIYCD	ILGREIRLPL	RIKGEGMGPK	IHFNFELLDI	GKVFTGSAHC
490	500	510	520	530	540	550	560
YEAILYNKGS	IDALFNMTPP	TSALGACFVF	SPKEGIIEPS	GVQAIQISFS	STILGNFEEE	FLVNVNGSPE	PVKLTIRGCV
570	580	590	600	610	620	630	640
IGPTFHFNVP	ALHFGDVSFG	FPHTLICSLN	NTSLIPMTYK	LRIPGDGLGH	KSISYCEQHV	DYKRPSWTKE	EISSMKPKEF
650	660	670	680	690	700	710	720
TISPDCGTIR	PQGFAAIRVT	LCSNTVQKYE	LALVVDVEGI	GEEVLALLIT	ARCVVPALHL	VNTEVDFGHC	FLKYPYEKTL
730	740	750	760	770	780	790	800
QLANQDDLPG	FYEVQPQVCE	EVPTVLFSSP	TPSGVISPSS	TIHIPLVLET	QVTGEHRSTV	YISIFGSQDP	PLVCHLKSAG
810	820	830	840	850	860	870	880
EGPVIYVHPN	QVDFGNIYVL	KDSSRILNLC	NQSFIPAFFQ	AHMAHKKSLW	TIEPNEGMVP	PETDVQLALT	ANLNDTLTFK
890	900	910	920	930	940	950	960
DCVILDIENS	STYRIPVQAS	GTGSTIVSDK	PFAPELNLGA	HFSLDTHYYH	FKLINKGRRI	QQLFWMNDSF	RPQAKLSKKG
970	980	990	1000	1010	1020	1030	1040
RVKKGHAHVQ	PQPSGSQEPR	DPQSPVFHLH	PASMELYPGQ	AIDVILEGYS	ATPRIVKEKL	VCHAIIGAQK	GKSLVMAVNI
1050	1060	1070	1080	1090	1100	1110	1120
TCEFVAPLIQ	LSTKQLIYRL	EKKPNSILKP	DYQPLAIKNI	STLPVNLLLS	TSGPFFICET	DKSLLPATPE	PIKLEIDEEK
1130	1140	1150	1160	1170	1180	1190	1200
NLLIKFDPSY	RNDLNNWVAE	EILAIKYVEH	PQIDSLDLRG	EVHYPNLSFE	TKELDFGCIL	NDTELIRYVT	ITNCSPLVVK
1210	1220	1230	1240	1250	1260	1270	1280
FRWFFLVNDE	ENQIRFVTLP	KKPYSAPVSQ	MESIPATSEA	ASPPAILVTV	ESPEMDLNDF	VKTVLVDEDA	RPEEKELRKT
1290	1300	1310	1320	1330	1340	1350	1360
KASSVISDEI	KISSTEIERI	YSSQSQVEDQ	ESLQTCEQNE	MLSIGIEEVF	DILPLFGVLQ	PHSSHQISFT	FYGHANIIAQ
1370	1380	1390	1400	1410	1420	1430	1440
AKALCEVEEG	PTYEITLKGE	ASLVNYSFDT	KDIHYGLQLF	DHVTEREITL	TNMGKVGFEF	KVLTDHQSSP	DNLLPGVPLI
1450	1460	1470	1480	1490	1500	1510	1520
LPVSGFISSH	QEQVLKVYYL	PGVPEVFKRS	FQIQIAHLDP	ENITLSGEGI	FPQICLDLPR	NLTANEKYEM	FLNQARKNTD
1530	1540	1550	1560	1570	1580	1590	1600
KEYNKCEMLD	HFDIITEEVP	EDEPAEVSAH	LQMEVERLIV	QSYVLEHQKT	TTPDPMDDPC	FSHRSRRKLA	KIQLPEYILD
1610	1620	1630	1640	1650	1660	1670	1680
FGYIILGEVR	THIIKIINTS	HFPVSFHADK	RVLHETGFST	ELDRVKNLPH	CETEIFEVRF	DPQGANLPVG	SKEVILPIKV
1690	1700	1710	1720	1730	1740	1750	1760
VGGPTVHICL	QAKVTIPTMT	LSRGKVDFAT	IQCGQCLVET	IQLSNHLQVP	CEWFVQSQKP	VDKLEKHMPK	YLRQKLRAEL
1770	1780	1790	1800	1810	1820	1830	1840
KPKTRIFEIQ	PISGVLDPGE	KSNVQVKFMP	KEEKFYSQTL	VFQIAQSAQK	LTLLARGQGL	EPRLEFSPSV	LDLGPLLLCA
1850	1860	1870	1880	1890	1900	1910	1920
PGDEAEVIVK	NPCNFPIEFY	SLEFDQQYLI	EEKILRKLKG	YDSYNTLLLP	PRNPGEKLPP	ELYEYFKEIK	KSKEEQMRAK
1930	1940	1950	1960	1970	1980	1990	2000
YLENLAQENE	EEDITSSDQG	TSNSTKRTSL	SRGISVTSNL	EEWHALLVES	KTYLEEEEDE	ESLEKIIFQT	DKLQSIDSHS
2010	2020	2030	2040	2050	2060	2070	2080
MEEVGEVENN	PVSKAIARHL	GIDISAEGRL	AKNRKGIAII	IHGTPLSGKS	ANAVSVAKYY	NAACLSIDSI	VLEAVANSNN
2090	2100	2110	2120	2130	2140	2150	2160
IPGIRARELC	IRAAIEQSVK	EGEEAAQEAA	VGQNVIGQGR	LSTDTLGKLA	SEMTLVAPEI	KPGKSVRGSV	VITKSKADSH
2170	2180	2190	2200	2210	2220	2230	2240
GSGSQKQHHS	HQSETPQISS	SPLPPGPIHR	WLSVSPSVGG	ETGLMSCVLP	DELLVQILAE	RIQLSDCYRG	VVFDGLDTLF
2250	2260	2270	2280	2290	2300	2310	2320
AQNAAAALLC	LLKAIGSREH	IYILNMAQDY	AAMKAQEKAK	KEQEERKHKG	ALEKEKERLQ	NMDEEEYDAL	TEEEKLTFDR
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
1684	1	1273.9976	-90.58	2	50.8	13.8	2	1-22	-.MTSRRLEESMGAVQMGLVNMFK.G	Oxidation: 1, 10
1422	1	982.5936	82.29	2	47.5	14.9	1	1282-1299	K.ASSVISDEIKISSTEIER.I	

Detailed Protein Report

Protein 309: WASH complex subunit FAM21B [Homo sapiens]

Accession:	gi|154090959	**Score:**	28.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	136.9
Database Date:	2015-11-30	**pI:**	4.5
		Sequence Coverage [%]:	1.8
		No. of unique Peptides:	2

Quantitation

MD:MU	**Median:** 3.67	**CV:** 0.00 %	**No. of Peptides:** 1

10	20	30	40	50	60	70	80
MPRLSGKSVR	VYDEEVEEPV	LKAEAEKTEQ	EKTREQKEVD	LIPKVQEAVN	YGLQVLDSAF	EQLDIKAGNS	DSEEDDANGR
90	100	110	120	130	140	150	160
VELILEPKDL	YIDRPLPYLI	GSKLFMEQED	VGLGELSSEE	GSVGSDRGSI	VDTEEEKEEE	ESDEDFAHHS	DNEQNRHTTQ
170	180	190	200	210	220	230	240
MSDEEEDDDG	CDLFADSEKE	EEDIEDIEEN	TRPKRSRPTS	FADELAARIK	GDAVGRVDEE	PTTLPSGEAK	PRKTLKEKKE
250	260	270	280	290	300	310	320
RRTPSDDEED	NLFTPPKLTD	EDFSPFGSGG	GLFSGGKGLF	DDEDEESDLF	TEAPQDRQAG	ASVKEESSSS	KPGKKIPAGA
330	340	350	360	370	380	390	400
VSVFLGDTDV	FGAASVPSMK	EPQKPEQPTP	RKSPYGPPPT	GLFDDDDGDD	DDDFFSAPHS	KPSKTGKVQS	TADIFGDEEG
410	420	430	440	450	460	470	480
DLFKEKAVAS	PEATVSQTDE	NKARAEKKVT	LSSSKNLKPS	SETKTQKGLF	SDEEDSEDLF	SSQSASKLKG	ASLLPGKLPT
490	500	510	520	530	540	550	560
SVSLFDDEDE	EDNLFGGTAA	KKQTLCLQAQ	REEKAKASEL	SKKKASALLF	SSDEEDQWNI	PASQTHLASD	SRSKGEPRDS
570	580	590	600	610	620	630	640
GTLQSQEAKA	VKKTSLFEED	EEDDLFAIAK	DSQKKTQRVS	LLFEDDVDSR	GSLFGSPPTS	VPPATKKKET	VSEAPPLLFS
650	660	670	680	690	700	710	720
DEEEKEAQLG	VKSVDKKVES	AKESLKFGRT	DVAESEKEGL	LTRSAQETVK	HSDLFSSSSP	WDKGTKPRTK	TVLSLFDEEE
730	740	750	760	770	780	790	800
DKMEDQNIIQ	APQKEVGKGR	DPDAHPKSTG	VFQDEELLFS	HKLQKDNDPD	VDLFAGTKKT	KLLEPSVGSL	FGDDEDDDLF
810	820	830	840	850	860	870	880
SSAKSQPLVQ	EKKRVVKKDH	SVDSFKNQKH	PESIQGSKEK	GIWKPETPQD	SSGLAPFKTK	EPSTRIGKIQ	ANLAINPAAL
890	900	910	920	930	940	950	960
LPTAASQISE	VKPVLPELAF	PSSEHRRSHG	LESVPVLPGS	GEAGVSFDLP	AQADTLHSAN	KSRVKMRGKR	RPQTRAARRL
970	980	990	1000	1010	1020	1030	1040
AAQESSETED	MSVPRGPIAQ	WADGAISPNG	HRPQLRAASG	EDSTEEALAA	AAAPWEGGPV	PGVDRSPFAK	SLGHSRGEAD
1050	1060	1070	1080	1090	1100	1110	1120
LFDSGDIFST	GTGSQSVERT	KPKAKIAENP	ANPPVGGKAK	SPMFPALGEA	SSDDDLFQSA	KPKPAKKTNT	FPLLEDEDDL
1130	1140	1150	1160	1170	1180	1190	1200
FTDQKVKKNE	TKSNSQQDVI	LTTQDIFEDD	IFATEAIKPS	QKTREKEKTL	ESNLFDDNID	IFADLTVKPK	EKSKKKVEAK
1210	1220	1230	1240	1250	1260		
SIFDDDMDDI	FSSGIQAKTT	KPKSRSAQAA	PEPRFEHKVS	NIFDDPLNAF	GGQ		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
500	1	599.8540	27.43	2	35.6	16.5	1	35-44	R.EQKEVDLIPK.V		
2876	2	703.3637	1.39	2	66.6	12.1	2	735-747	K.EVGKGRDPDAHPK.S		MD:MU 3.67

Detailed Protein Report

Protein 310: **probable exonuclease mut-7 homolog isoform a [Homo sapiens]**

Accession:	gi|145279204	**Score:**	28.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	96.5
Database Date:	2015-11-30	**pI:**	9.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDPGDPAGDP	AAGERHRMGR	DPLLLLQALQ	TLWSTRERKQ	LREEAWRGFA	ALDDPLAGLL	DMLESCRGQR	GEGPSLAAWI
90	100	110	120	130	140	150	160
SHQLQCWLQA	QPCPSLAQHS	LRLKQLQARA	VKVLTESPPS	LAAPLASIFQ	LQDADRSCLL	AHVHRLHHEG	RFREAATLGA
170	180	190	200	210	220	230	240
TLKLQSELGV	EKMSIPLLLQ	DKVALVERYV	AGFPDLQRRL	LVLMDSWCQP	GFDIKDVARR	YPEVTSLSLE	KLSPKALSRQ
250	260	270	280	290	300	310	320
VLRLQERYGV	APALCPNAAI	QQRLAALRHL	CHKRFVEKSL	SQENWTDHVQ	GLVGQSPWLQ	EQLSQLLVSH	SDPVTAAQCA
330	340	350	360	370	380	390	400
MELLLPEERL	PAAVAVELRR	FRLQGRATEA	DSRLEVKDMK	DRYYQLPIPR	ENVHLLASWE	DLTRHEGALL	QCHQVVGVDV
410	420	430	440	450	460	470	480
EWTPVFVAGG	RPRPSLLQVA	VEGHVFLLDV	LALSQPPTGQ	GAQAFSRLVA	QLLSDPSITK	LGYGMVGDLQ	KLGTSCPALA
490	500	510	520	530	540	550	560
HVEKQILGGM	DLLLVHRQMR	VASVPAPAVD	RARELRGLSL	LVQQVLGTAL	DKTQQLSNWD	RRPLCEEQVI	YAAADAYCLL
570	580	590	600	610	620	630	640
EVHQALCREP	ARFHLSEDLA	GSRRPRHRER	PGARKPPGLQ	KASAPAAPRQ	VPVAVAVSEG	AAPQIPARAF	RVVCDNMLQG
650	660	670	680	690	700	710	720
LARSLRCLGV	DARMLGNGED	HRRAAEVARQ	EGRIILTSGQ	PFHKLRAQVG	AGRCLSVDCS	LKAQQQAKAV	LKHFNVRVTH
730	740	750	760	770	780	790	800
ADIFSRCQAC	NCDQYLKVSR	DMMKQLMWLS	SHQEGPRSSG	DEATQSQAVQ	EPGPAPDAAP	EGCTYDRPCR	WLQMADLRAE
810	820	830	840	850	860	870	880
TPDMLADGTR	LQLAGVPVGV	LRTPGLRCFY	CCTGCGKVFW	DGSHLGRVAT	HFRDMLESAP	SPCEPSPAPS	PASSPF

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1319	1	571.1608	-69.20	2	46.1	14.7	0	828-837	R.CFYCCTGCGK.V	Carbamidomethyl: 5

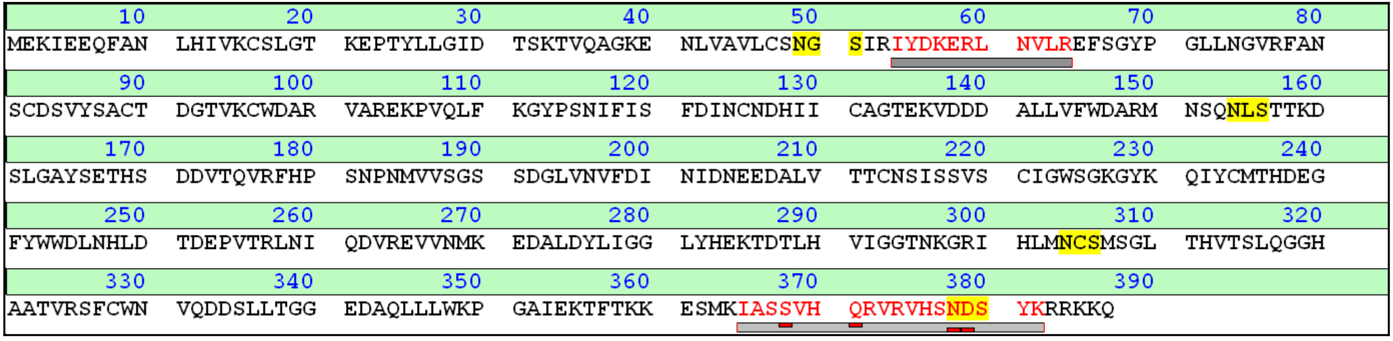
Detailed Protein Report

Protein 311: WD repeat-containing protein 89 [Homo sapiens]

Accession:	gi|18087841	**Score:**	28.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	43.2
Database Date:	2015-11-30	**pI:**	5.7
		Sequence Coverage [%]:	7.5
		No. of unique Peptides:	2

Alias proteins:

Accession	Name	Description
gi|384871679	refseq_human (refseq_human_20140103.fasta)	WD repeat-containing protein 89 [Homo sapiens]
gi|57165359	refseq_human (refseq_human_20140103.fasta)	WD repeat-containing protein 89 [Homo sapiens]



```
        10         20         30         40         50         60         70         80
MEKIEEQFAN LHIVKCSLGT KEPTYLLGID TSKTVQAGKE NLVAVLCSNG SIRIYDKERL NVLREFSGYP GLLNGVRFAN
        90        100        110        120        130        140        150        160
SCDSVYSACT DGTVKCWDAR VAREKPVQLF KGYPSNIFIS FDINCNDHII CAGTEKVDDD ALLVFWDARM NSQNLSTTKD
       170        180        190        200        210        220        230        240
SLGAYSETHS DDVTQVRFHP SNPNMVVSGS SDGLVNVFDI NIDNEEDALV TTCNSISSVS CIGWSGKGYK QIYCMTHDEG
       250        260        270        280        290        300        310        320
FYWWDLNHLD TDEPVTRLNI QDVREVVNMK EDALDYLIGG LYHEKTDTLH VIGGTNKGRI HLMNCSMSGL THVTSLQGGH
       330        340        350        360        370        380        390
AATVRSFCWN VQDDSLLTGG EDAQLLLWKP GAIEKTFTKK ESMKIASSVH QRVRVHSNDS YKRRKKQ
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2497	1	709.8401	-97.59	2	61.6	14.1	2	54-64	R.IYDKERLNVLR.E	
633	1	1042.1848	135.88	2	37.2	14.5	2	365-382	K.IASSVHQRVRVHSNDSYK.R	

Detailed Protein Report

Protein 312: **PREDICTED: coiled-coil domain-containing protein 38 isoform X2 [Homo sapiens]**

Accession:	gi|578823287	**Score:**	28.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	42.7
Database Date:	2015-11-30	**pI:**	9.1
		Sequence Coverage [%]:	9.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSSNLLPTLN	SGGKVKDGST	KEDRPYKIFF	RDLFLVKENE	MAAKETEKFM	NRNMKVYQKT	TFSSRMKSHS	YLSQLAFYPK
90	100	110	120	130	140	150	160
RSGRSFEKFG	PGPAPIPRLI	EGSDTKRTVH	EFINDQRDRF	LLEYALSTKR	NTIKKFEKDI	AMRERQLKKA	EKKLQDDALA
170	180	190	200	210	220	230	240
FEEFLRENDQ	RSVDALKMAA	QETINKLQMT	AELKKASMEV	QAVKSEIAKT	EFLLREYMKY	GFFLLQMSPK	HWQIQQALKR
250	260	270	280	290	300	310	320
AQASKSKANI	ILPKILAKLS	LHSSNKEGIL	EESGRTAVLS	EDASQGRDSQ	GKPSRSLTRT	PEKKKSNLAE	SFGSEDSLEF
330	340	350	360	370	380		
LLDDEMDVDL	EPALYFKEPE	ELLQVLRELE	EQNLTLFQYS	QDVDENLEEK			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
39	1	750.3346	-92.35	2	29.8	15.7	1	85-98	R.SFEKFGPGPAPIPR.L	

Detailed Protein Report

Protein 313: laminin subunit gamma-1 precursor [Homo sapiens]

Accession:	gi|145309326	**Score:**	28.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	177.5
Database Date:	2015-11-30	**pI:**	4.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.6
		No. of unique Peptides:	2

Quantitation

MD:MU **Median:** 1.91 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MRGSHRAAPA	LRPRGRLWPV	LAVLAAAAAA	GCAQAAMDEC	TDEGGRPQRC	MPEFVNAAFN	VTVVATNTCG	TPPEEYCVQT
90	100	110	120	130	140	150	160
GVTGVTKSCH	LCDAGQPHLQ	HGAAFLTDYN	NQADTTWWQS	QTMLAGVQYP	SSINLTLHLG	KAFDITYVRL	KFHTSRPESF
170	180	190	200	210	220	230	240
AIYKRTREDG	PWIPYQYYSG	SCENTYSKAN	RGFIRTGGDE	QQALCTDEFS	DISPLTGGNV	AFSTLEGRPS	AYNFDNSPVL
250	260	270	280	290	300	310	320
QEWVTATDIR	VTLNRLNTFG	DEVFNDPKVL	KSYYYAISDF	AVGGRCKCNG	HASECMKNEF	DKLVCNCKHN	TYGVDCEKCL
330	340	350	360	370	380	390	400
PFFNDRPWRR	ATAESASECL	PCDCNGRSQE	CYFDPELYRS	TGHGGHCTNC	QDNTDGAHCE	RCRENFFRLG	NNEACSSCHC
410	420	430	440	450	460	470	480
SPVGSLSTQC	DSYGRCSCKP	GVMGDKCDRC	QPGFHSLTEA	GCRPCSCDPS	GSIDECNIET	GRCVCKDNVE	GFNCERCKPG
490	500	510	520	530	540	550	560
FFNLESSNPR	GCTPCFCFGH	SSVCTNAVGY	SVYSISSTFQ	IDEDGWRAEQ	RDGSEASLEW	SSERQDIAVI	SDSYFPRYFI
570	580	590	600	610	620	630	640
APAKFLGKQV	LSYGQNLSFS	FRVDRRDTRL	SAEDLVLEGA	GLRVSVPLIA	QGNSYPSETT	VKYVFRLHEA	TDYPWRPALT
650	660	670	680	690	700	710	720
PFEFQKLLNN	LTSIKIRGTY	SERSAGYLDD	VTLASARPGP	GVPATWVESC	TCPVGYGGQF	CEMCLSGYRR	ETPNLGPYSP
730	740	750	760	770	780	790	800
CVLCACNGHS	ETCDPETGVC	NCRDNTAGPH	CEKCSDGYYG	DSTAGTSSDC	QPCPCPGGSS	CAVVPKTKEV	VCTNCPTGTT
810	820	830	840	850	860	870	880
GKRCELCDDG	YFGDPLGRNG	PVRLCRLCQC	SDNIDPNAVG	NCNRLTGECL	KCIYNTAGFY	CDRCKDGFFG	NPLAPNPADK
890	900	910	920	930	940	950	960
CKACNCNLYG	TMKQQSSCNP	VTGQCECLPH	VTGQDCGACD	PGFYNLQSGQ	GCERCDCHAL	GSTNGQCDIR	TGQCECQPGI
970	980	990	1000	1010	1020	1030	1040
TGQHCERCEV	NHFGFGPEGC	KPCDCHPEGS	LSLQCKDDGR	CECREGFVGN	RCDQCEENYF	YNRSWPGCQE	CPACYRLVKD
1050	1060	1070	1080	1090	1100	1110	1120
KVADHRVKLQ	ELESLIANLG	TGDEMVTDQA	FEDRLKEAER	EVMDLLREAQ	DVKDVDQNLM	DRLQRVNNTL	SSQISRLQNI
1130	1140	1150	1160	1170	1180	1190	1200
RNTIEETGNL	AEQARAHVEN	TERLIEIASR	ELEKAKVAAA	NVSVTQPEST	GDPNNMTLLA	EEARKLAERH	KQEADDIVRV
1210	1220	1230	1240	1250	1260	1270	1280
AKTANDTSTE	AYNLLLRTLA	GENQTAFEIE	ELNRKYEQAK	NISQDLEKQA	ARVHEEAKRA	GDKAVEIYAS	VAQLSPLDSE
1290	1300	1310	1320	1330	1340	1350	1360
TLENEANNIK	MEAENLEQLI	DQKLKDYEDL	REDMRGKELE	VKNLLEKGKT	EQQTADQLLA	RADAAKALAE	EAAKKGRDTL
1370	1380	1390	1400	1410	1420	1430	1440
QEANDILNNL	KDFDRRVNDN	KTAAEEALRK	IPAINQTITE	ANEKTREAQQ	ALGSAAADAT	EAKNKAHEAE	RIASAVQKNA
1450	1460	1470	1480	1490	1500	1510	1520
TSTKAEAERT	FAEVTDLDNE	VNNMLKQLQE	AEKELKRKQD	DADQDMMMAG	MASQAAQEAE	INARKAKNSV	TSLLSIINDL
1530	1540	1550	1560	1570	1580	1590	1600
LEQLGQLDTV	DLNKLNEIEG	TLNKAKDEMK	VSDLDRKVSD	LENEAKKQEA	AIMDYNRDIE	EIMKDIRNLE	DIRKTLPSGC
1610							
FNTPSIEKP							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2564	2	941.9632	50.20	2	62.0	15.2	1	303-318	K.LVCNCKHNTYGVDCEK.C	Carbamidomethyl: 14	

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1858	1	590.7710	-122.60	2	53.3	13.3	2	1037-1046	R.LVKDKVADHR.V		MD:MU 1.91

Detailed Protein Report

Protein 314: **testis-specific serine kinase substrate [Homo sapiens]**

Accession:	gi|11119430	**Score:**	28.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	65.0
Database Date:	2015-11-30	**pI:**	5.6
		Sequence Coverage [%]:	5.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MASVVVKTIW	QSKEIHEAGD	TPTGVESCSQ	LVPEAPRRVT	SRAKGIPKKK	KAVSFHGVEP	QMSHQPMHWC	LNLKRSSACT
90	100	110	120	130	140	150	160
NVSLLNLAAM	EPTDSTGTDS	TVEDLSGQLT	LAGPPASPTL	PWDPDDADIT	EILSGVNSGL	VRAKDSITSL	KEKTNRVNQH
170	180	190	200	210	220	230	240
VQSLQSECSV	LSENLERRRQ	EAEELEGYCI	QLKENCWKVT	RSVEDAEIKT	NVLKQNSALL	EEKLRYLQQQ	LQDETPRRQE
250	260	270	280	290	300	310	320
AELQEPEEKQ	EPEEKQEPEE	KQKPEAGLSW	NSLGPAATSQ	GCPGPPGSPD	KPSRPHGLVP	AGWGMGPRAG	EGPYVSEQEL
330	340	350	360	370	380	390	400
QKLFTGIEEL	RREVSSLTAR	WHQEEGAVQE	ALRLLGGLGG	RVDGFLGQWE	RAQREQAQTA	RDLQELRGRA	DELCTMVERS
410	420	430	440	450	460	470	480
AVSVASLRSE	LEGLGPLKPI	LEEFGRQFQN	SRRGPDLSMN	LDRSHQGNCA	RCASQGSQLS	TESLQQLLDR	ALTSLVDEVK
490	500	510	520	530	540	550	560
QRGLTPACPS	CQRLHKKILE	LERQALAKHV	RAEALSSTLR	LAQDEALRAK	NLLLTDKMKP	EEKMATLDHL	HLKMCSLHDH
570	580	590	600				
LSNLPLEGST	GTMGGGSSAG	TPPKQGGSAP	EQ				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
24	1	819.8334	-120.26	2	29.6	15.2	2	483-497	R.GLTPACPSCQRLHKK.I	

Detailed Protein Report

Protein 315: caseinolytic peptidase B protein homolog isoform 3 [Homo sapiens]

Accession:	gi|385719196	**Score:**	28.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	72.2
Database Date:	2015-11-30	**pI:**	9.7
		Sequence Coverage [%]:	3.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLGSLVLRRK	ALAPRLLLRL	LRSPTLRGHG	GASGRNVTTG	SLGEPQWLRV	ATGGRPGTSP	ALFSGRGAAT	GGRQGGRFDT
90	100	110	120	130	140	150	160
KCLAAATWGR	LPGPEETLPG	QDSWNGVPSR	AGLGMCALAA	ALVVHCYSKS	PSNKDAALLE	AARANNMQEV	SSVVQVLLAA
170	180	190	200	210	220	230	240
GADPNLGDDF	SSVYKTAKEQ	GIHSLEVLIT	REDDFNNRLN	NRASFKGCTA	LHYAVLADDY	RTVKELLDGG	ANPLQRNEMG
250	260	270	280	290	300	310	320
HTPLDYAREG	EVMKLLRTSE	AKYQEKQRKR	EAEERRRFPL	EQRLKEHIIG	QESAIATVGA	AIRRKENGWY	DEEHPLVFLF
330	340	350	360	370	380	390	400
LGSSGIGKTE	LAKQTAKYMH	KDAKKGFIRL	DMSEFQERHE	VAKFIGSPPG	YVGHEEGGQL	TKKLKQCPNA	VVLFDEVDKA
410	420	430	440	450	460	470	480
HPDVLTIMLQ	LFDEGRLTDG	KGKTIDCKDA	IFIMTSNVAS	DEIAQHALQL	RQEALEMSRN	RIAENLGDVQ	ISDKITISKN
490	500	510	520	530	540	550	560
FKENVIRPIL	KAHFRRDEFL	GRINEIVYFL	PFCHSELIQL	VNKELNFWAK	RAKQRHNITL	LWDREVADVL	VDGYNVHYGA
570	580	590	600	610	620	630	640
RSIKHEVERR	VVNQLAAAYE	QDLLPGGCTL	RITVEDSDKQ	LLKSPELPSP	QAEKRLPKLR	LEIIDKDSKT	RRLDIRAPLH
650							
PEKVCNTI							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1569	1	788.7801	-136.01	2	49.5	16.8	0	386-399	K.QCPNAVVLFDEVDK.A	

Detailed Protein Report

Protein 316: sortilin-related receptor preproprotein [Homo sapiens]

Accession:	gi|4507157	**Score:**	28.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	248.3
Database Date:	2015-11-30	**pI:**	5.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	0.7
		No. of unique Peptides:	2

Quantitation

MD:MU	**Median:** 1.16	**CV:** 0.00 %	**No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MATRSSRRES RLPFLFTLVA LLPPGALCEV WTQRLHGGSA PLPQDRGFLV VQGDPRELRL WARGDARGAS RADEKPLRRK
        90        100        110        120        130        140        150        160
RSAALQPEPI KVYGQVSLND SHNQMVVHWA GEKSNVIVAL ARDSLALARP KSSDVYVSYD YGKSFKKISD KLNFGLGNRS
       170        180        190        200        210        220        230        240
EAVIAQFYHS PADNKRYIFA DAYAQYLWIT FDFCNTLQGF SIPFRAADLL LHSKASNLLL GFDRSHPNKQ LWKSDDFGQT
       250        260        270        280        290        300        310        320
WIMIQEHVKS FSWGIDPYDK PNTIYIERHE PSGYSTVFRS TDFFQSRENQ EVILEEVRDF QLRDKYMFAT KVVHLLGSEQ
       330        340        350        360        370        380        390        400
QSSVQLWVSF GRKPMRAAQF VTRHPINEYY IADASEDQVF VCVSHSNNRT NLYISEAEGL KFSLSLENVL YYSPGGAGSD
       410        420        430        440        450        460        470        480
TLVRYFANEP FADFHRVEGL QGVYIATLIN GSMNEENMRS VITFDKGGTW EFLQAPAFTG YGEKINCELS QGCSLHLAQR
       490        500        510        520        530        540        550        560
LSQLLNLQLR RMPILSKESA PGLIIATGSV GKNLASKTNV YISSSAGARW REALPGPHYY TWGDHGGIIT AIAQGMETNE
       570        580        590        600        610        620        630        640
LKYSTNEGET WKTFIFSEKP VFVYGLLTEP GEKSTVFTIF GSNKENVHSW LILQVNATDA LGVPCTENDY KLWSPSDERG
       650        660        670        680        690        700        710        720
NECLLGHKTV FKRRTPHATC FNGEDFDRPV VVSNCSCTRE DYECDFGFKM SEDLSLEVCV PDPEFSGKSY SPPVPCPVGS
       730        740        750        760        770        780        790        800
TYRRTRGYRK ISGDTCSGGD VEARLEGELV PCPLAEENEF ILYAVRKSIY RYDLASGATE QLPLTGLRAA VALDFDYEHN
       810        820        830        840        850        860        870        880
CLYWSDLALD VIQRLCLNGS TGQEVIINSG LETVEALAFE PLSQLLYWVD AGFKKIEVAN PDGDFRLTIV NSSVLDRPRA
       890        900        910        920        930        940        950        960
LVLVPQEGVM FWTDWGDLKP GIYRSNMDGS AAYHLVSEDV KWPNGISVDD QWIYWTDAYL ECIERITFSG QQRSVILDNL
       970        980        990       1000       1010       1020       1030       1040
PHPYAIAVFK NEIYWDDWSQ LSIFRASKYS GSQMEILANQ LTGLMDMKIF YKGKNTGSNA CVPRPCSLLC LPKANNSRSC
      1050       1060       1070       1080       1090       1100       1110       1120
RCPEDVSSSV LPSGDLMCDC PQGYQLKNNT CVKEENTCLR NQYRCSNGNC INSIWWCDFD NDCGDMSDER NCPTTICDLD
      1130       1140       1150       1160       1170       1180       1190       1200
TQFRCQESGT CIPLSYKCDL EDDCGDNSDE SHCEMHQCRS DEYNCSSGMC IRSSWVCDGD NDCRDWSDEA NCTAIYHTCE
      1210       1220       1230       1240       1250       1260       1270       1280
ASNFQCRNGH CIPQRWACDG DTDCQDGSDE DPVNCEKKCN GFRCPNGTCI PSSKHCDGLR DCSDGSDEQH CEPLCTHFMD
      1290       1300       1310       1320       1330       1340       1350       1360
FVCKNRQQCL FHSMVCDGII QCRDGSDEDA AFAGCSQDPE FHKVCDEFGF QCQNGVCISL IWKCDGMDDC GDYSDEANCE
      1370       1380       1390       1400       1410       1420       1430       1440
NPTEAPNCSR YFQFRCENGH CIPNRWKCDR ENDCGDWSDE KDCGDSHILP FSTPGPSTCL PNYYRCSSGT CVMDTWVCDG
      1450       1460       1470       1480       1490       1500       1510       1520
YRDCADGSDE EACPLLANVT AASTPTQLGR CDRFEFECHQ PKTCIPNWKR CDGHQDCQDG RDEANCPTHS TLTCMSREFQ
      1530       1540       1550       1560       1570       1580       1590       1600
CEDGEACIVL SERCDGFLDC SDESDEKACS DELTVYKVQN LQWTADFSGD VTLTWMRPKK MPSASCVYNV YYRVVGESIW
      1610       1620       1630       1640       1650       1660       1670       1680
KTLETHSNKT NTVLKVLKPD TTYQVKVQVQ CLSKAHNTND FVTLRTPEGL PDAPRNLQLS LPREAEGVIV GHWAPPIHTH
      1690       1700       1710       1720       1730       1740       1750       1760
GLIREYIVEY SRSGSKMWAS QRAASNFTEI KNLLVNTLYT VRVAAVTSRG IGNWSDSKSI TTIKGKVIPP PDIHIDSYGE
      1770       1780       1790       1800       1810       1820       1830       1840
NYLSFTLTME SDIKVNGYVV NLFWAFDTHK QERRTLNFRG SILSHKVGNL TAHTSYEISA WAKTDLGDSP LAFEHVMTRG
      1850       1860       1870       1880       1890       1900       1910       1920
VRPPAPSLKA KAINQTAVEC TWTGPRNVVY GIFYATSFLD LYRNPKSLTT SLHNKTVIVS KDEQYLFLVR VVVPYQGPSS
      1930       1940       1950       1960       1970       1980       1990       2000
DYVVVKMIPD SRLPPRHLHV VHTGKTSVVI KWESPYDSPD QDLLYAIAVK DLIRKTDRSY KVKSRNSTVE YTLNKLEPGG
      2010       2020       2030       2040       2050       2060       2070       2080
KYHIIVQLGN MSKDSSIKIT TVSLSAPDAL KIITENDHVL LFWKSLALKE KHFNESRGYE IHMFDSAMNI TAYLGNTTDN
      2090       2100       2110       2120       2130       2140       2150       2160
FFKISNLKMG HNYTFTVQAR CLFGNQICGE PAILLYDELG SGADASATQA ARSTDVAAVV VPILFLILLS LGVGFAILYT
      2170       2180       2190       2200       2210       2220
```

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2231	1	599.9323	-0.25	3	57.8	14.4	1	1239-1254	K.CNGFRCPNGTCIPSSK.H	Carbamidomethyl: 1, 11	
1162	1	610.6492	-203.57	2	44.2	14.0	0	1244-1254	R.CPNGTCIPSSK.H	Carbamidomethyl: 1, 6	MD:MU 1.16

Detailed Protein Report

Protein 317: 60 kDa SS-A/Ro ribonucleoprotein isoform 4 [Homo sapiens]

Accession:	gi|291084635	**Score:**	28.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	58.4
Database Date:	2015-11-30	**pI:**	9.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.9
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MEESVNQMQP	LNEKQIANSQ	DGYVWQVTDM	NRLHRFLCFG	SEGGTYYIKE	QKLGLENAEA	LIRLIEDGRG	CEVIQEIKSF
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
SQEGRTTKQE	PMLFALAICS	QCSDISTKQA	AFKAVSEVCR	IPTHLFTFIQ	FKKDLKESMK	CGMWGRALRK	AIADWYNEKG
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
GMALALAVTK	YKQRNGWSHK	DLLRLSHLKP	SSEGLAIVTK	YITKGWKEVH	ELYKEKALSV	ETEKLLKYLE	AVEKVKRTRD
250	**260**	**270**	**280**	**290**	**300**	**310**	**320**
ELEVIHLIEE	HRLVREHLLT	NHLKSKEVWK	ALLQEMPLTA	LLRNLGKMTA	NSVLEPGNSE	VSLVCEKLCN	EKLLKKARIH
330	**340**	**350**	**360**	**370**	**380**	**390**	**400**
PFHILIALET	YKTGHGLRGK	LKWRPDEEIL	KALDAAFYKT	FKTVEPTGKR	FLLAVDVSAS	MNQRVLGSIL	NASTVAAAMC
410	**420**	**430**	**440**	**450**	**460**	**470**	**480**
MVVTRTEKDS	YVVAFSDEMV	PCPVTTDMTL	QQVLMAMSQI	PAGGTDCSLP	MIWAQKTNTP	ADVFIVFTDN	ETFAGGVHPA
490	**500**	**510**	**520**				
IALREYRKKM	DIPAKLIVCG	MTSNGFTIAD	PDDRDTVK				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1633	1	821.2438	-171.33	2	50.3	12.3	0	36-49	R.FLCFGSEGGTYYIK.E	Carbamidomethyl: 3
2854	2	702.3710	-10.04	1	66.1	16.1	0	64-69	R.LIEDGR.G	

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Detailed Protein Report

Protein 318: PREDICTED: latrophilin-1 isoform X5 [Homo sapiens]

Accession:	gi|578833089	**Score:**	28.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	96.9
Database Date:	2015-11-30	**pI:**	6.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MARLAAVLWN	LCVTAVLVTS	ATQGLSRAGL	PFGLMRRELA	CEGYPIELRC	PGSDVIMVEN	ANYGRTDDKI	CDADPFQMEN
90	100	110	120	130	140	150	160
VQCYLPDAFK	IMSQRCNNRT	QCVVVAGSDA	FPDPCPGTYK	YLEVQYDCVP	YKVEQKVFVC	PGTLQKVLEP	TSTHESEHQS
170	180	190	200	210	220	230	240
GAWCKDPLQA	GDRIYVMPWI	PYRTDTLTEY	ASWEDYVAAR	HTTTYRLPNR	VDGTGFVVYD	GAVFYNKERT	RNIVKYDLRT
250	260	270	280	290	300	310	320
RIKSGETVIN	TANYHDTSPY	RWGGKTDIDL	AVDENGLWVI	YATEGNNGRL	VVSQLNPYTL	RFEGTWETGY	DKRSASNAFM
330	340	350	360	370	380	390	400
VCGVLYVLRS	VYVDDDSEAA	GNRVDYAFNT	NANREEPVSL	TFPNPYQFIS	SVDYNPRDNQ	LYVWNNYFVV	RYSLEFGPPD
410	420	430	440	450	460	470	480
PSAGPATSPP	LSTTTTARPT	PLTSTASPAA	TTPLRRAPLT	THPVGAINQL	GPDLPPATAP	VPSTRRPPAP	NLHVSPELFC
490	500	510	520	530	540	550	560
EPREVRRVQW	PATQQGMLVE	RPCPKGTRGI	ASFQCLPALG	LWNPRGPDLS	NCTSPWVNQV	AQKIKSGENA	ANIASELARH
570	580	590	600	610	620	630	640
TRGSIYAGDV	SSSVKLMEQL	LDILDAQLQA	LRPIERESAG	KNYNKMHKRE	RTCKDYIKAV	VETVDNLLRP	EALESWKDMN
650	660	670	680	690	700	710	720
ATEQVHTATM	LLDVLEEGAF	LLADNVREPA	RFLAAKENVV	LEVTVLNTEG	QVQELVFPQE	EYPRKNSIQL	SAKTIKQNSR
730	740	750	760	770	780	790	800
NGVVKVVFIL	YNNLGLFLST	ENATVKLAGE	AGPGGPGGAS	LVVNSQVIAA	SINKESSRVF	LMDPVIFTVA	HLEDKNHFNA
810	820	830	840	850	860	870	880
NCSFWNYSER	SMLGYWSTQG	CRLVESNKTH	TTCACSHLTN	FAVLMAHREI	ALWRSKLVLR	WSSLHKPSRA	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2050	1	900.3480	-63.50	3	55.8	14.3	1	96-120	R.CNNRTQCVVVAGSDAFPDPCPGTYK.Y	Carbamidomethyl: 7

Detailed Protein Report

Protein 319: **RNA polymerase II subunit A C-terminal domain phosphatase isoform 3 [Homo sapiens]**

Accession:	gi|321267522	**Score:**	28.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	92.3
Database Date:	2015-11-30	**pI:**	4.9
		Sequence Coverage [%]:	4.5
		No. of unique Peptides:	1

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1973	1	899.3577	-124.16	2	54.6	12.7	2	779-797	R.TLGAPASSERSAAGGRGPR.G	

Detailed Protein Report

Protein 320: PREDICTED: RING finger protein 112 isoform X3 [Homo sapiens]

Accession: gi|578830030
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 28.2
MW [kDa]: 66.2
pI: 9.8
Sequence Coverage [%]: 3.4
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MGNSGNSWSH	TPFPKLELGL	GPQPMAPREL	PTCSICLERL	RDPISLDCGH	DFCIRCFSTH	RLPGCEPPCC	PECRKICKQK
90	100	110	120	130	140	150	160
RGLRSLGEKM	KLLPQRPLPP	ALQETCPVRA	EPLLLVRINA	SGGLILRMGA	INRCLKHPLA	RDTPVCLLAV	LGEQHSGKSF
170	180	190	200	210	220	230	240
LLNHLLQGLP	GLESGEGGRP	RGGEASLQGC	RWGANGLARG	IWMWSHPFLL	GKEGKKVAVF	LVDTGDAMSP	ELSRETRIKL
250	260	270	280	290	300	310	320
CALTTMLSSY	QILSTSQELK	DTDLDYLEMF	VHVAEVMGKH	YGMVPIQHLD	LLVRDSSHPN	KAGQGHVGNI	FQSTPLAASQ
330	340	350	360	370	380	390	400
RLSGRYPKVQ	ELLQGKRARC	CLLPAPGRRR	MNQGHASPGD	TDDDFRHLLG	AYVSDVLSAA	PQHAKSRCQG	YWNEGRAVAR
410	420	430	440	450	460	470	480
GDRRLLTGQQ	LAQEIKNLSG	WMGRTGPGFT	SPDEMAAQLH	DLRKVEAAKR	EFEEYVRQQD	VATKRIFSAL	RVLPDTMRNL
490	500	510	520	530	540	550	560
LSTQKDAILA	RHGVALLCKG	RDQTLEALEA	ELQATAKAFM	DSYTMRFCGH	LAAVGGAVGA	GLMGLAGGVV	GAGMAAAALA
570	580	590	600	610	620		
AEAGMVAAGA	AVGATGAAVV	GGGVGAGLAA	TVGCMEKEED	ERLLEGDREP	LLQEE		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2148	1	1062.3966	-148.73	1	57.0	17.9	1	128-136	R.MGAINRCLK.H	Carbamidomethyl: 7

Detailed Protein Report

Protein 321: prolactin-inducible protein precursor [Homo sapiens]

Accession: gi|4505821
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 28.1
MW [kDa]: 16.6
pI: 9.3
Sequence Coverage [%]: 8.2
No. of unique Peptides: 1

Quantitation

MD:MU **Median:** 0.27 **CV:** 0.00 % **No. of 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	Ratios
2176	2	642.3028	-132.15	2	57.4	28.1	0	107-118	R.TVQIAAVVDVIR.E		MD:MU 0.27

Detailed Protein Report

Protein 322: PREDICTED: uncharacterized protein LOC101928409 [Homo sapiens]

Accession:	gi|530358441	**Score:**	28.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	60.4
Database Date:	2015-11-30	**pI:**	11.3
		Sequence Coverage [%]:	3.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLGTVASPRP	GSLFSPPLAV	IKPGYEQGFK	SSLPHPQVYR	AAPELSDMLR	CGGQRRGGGI	ALCSLGVKSN	MNVKYCGKTE
90	100	110	120	130	140	150	160
SFQSRQRGPS	AGGPGRPESL	LPRVRLPEAL	LLAEDCRGNV	GEGEMDGGSR	AYKSDKYAHT	LTVTASHHAP	PPPTHMEGFE
170	180	190	200	210	220	230	240
LFHLPELCSP	SQDAQTTGRT	QMKPDHSPRP	SHRGRWVPKR	LLRLHPSSRV	VVRLVAEGAD	GARFGNTPHC	ILFHFTSTKE
250	260	270	280	290	300	310	320
ESRIGGRPPS	CFLMQITQHS	NRKSKLQGLL	LRGALEKEER	VVRARAGASE	AKSHSRGGWD	AWGLKANARG	RDGVGSGGRS
330	340	350	360	370	380	390	400
ALQSRPLPPA	SLEGGSGTCA	RSLSPGLCAS	AWRLPGKNLI	YFLPSRVSSL	PPRAAPFRRP	EPAPGPRGCS	GERGLGMSGG
410	420	430	440	450	460	470	480
VRAPPHPRAL	LGGDIQELKE	IPQEEVETSE	RRGNRLFCKK	TERRLEGLRK	AADGSQDNSV	RPVLQGNFNP	TRTQAKTIYI
490	500	510	520	530	540	550	560
YIYELTQNRA	TLVPTPPQVG	RHIQVALSED	GTWRLAGVAL	WRSRSPVSSY	EVSLLLQSSL	QRGDLATSLP	LGFPVNPL

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2625	1	885.4475	-93.73	1	62.9	13.6	0	515-522	R.LAGVALWR.S	

Detailed Protein Report

Protein 323: contactin-associated protein-like 4 isoform 2 [Homo sapiens]

Accession:	gi|148664242	**Score:**	28.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	137.4
Database Date:	2015-11-30	**pI:**	6.1
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.1
		No. of unique Peptides:	2

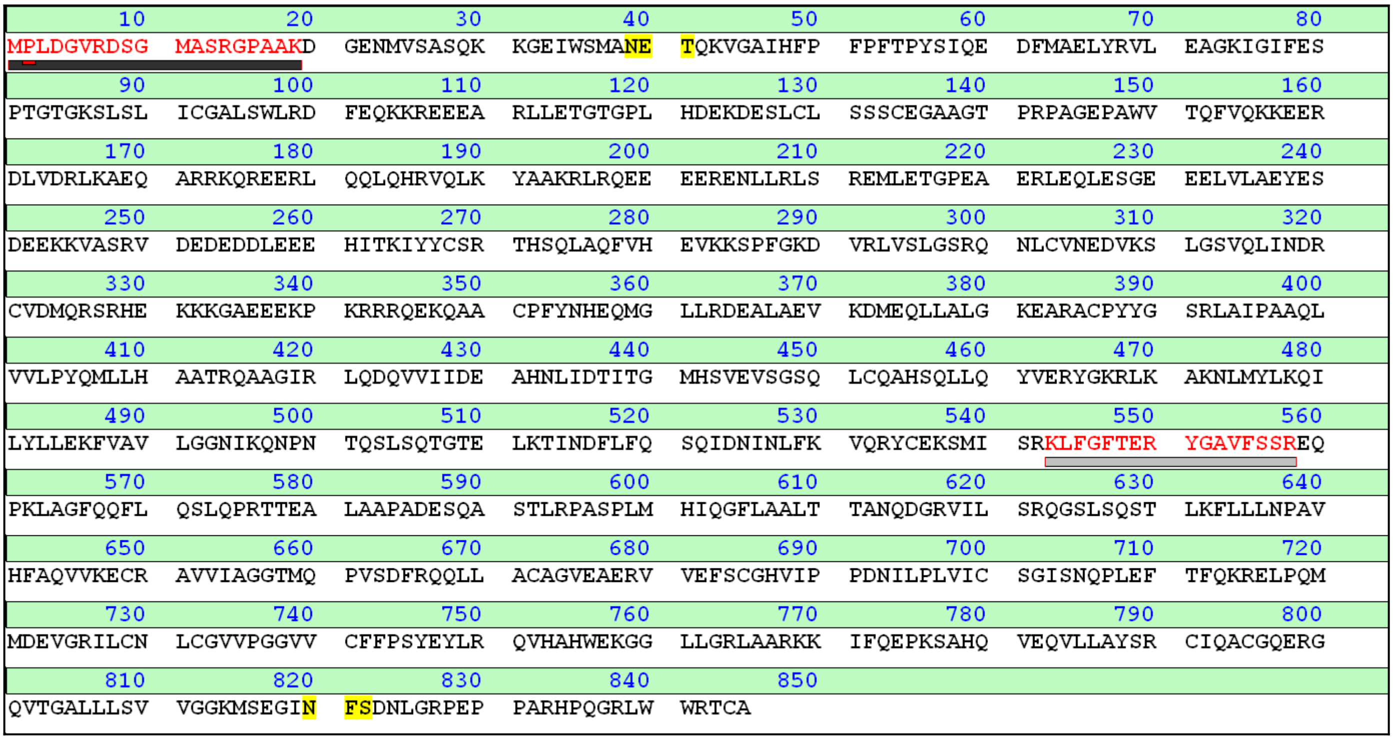
10	20	30	40	50	60	70	80
MWNYDCDDPL	VSALPQASFS	SSSELSSSHG	PGFARLNRRD	GAGGWSPLVS	NKYQWLQIDL	GERMEVTAVA	TQGGYGSSNW
90	100	110	120	130	140	150	160
VTSYLLMFSD	SGWNWKQYRQ	EDSIWGFSGN	ANADSVVYYR	LQPSIKARFL	RFIPLEWNPK	GRIGMRIEVF	GCAYRSEVVD
170	180	190	200	210	220	230	240
LDGKSSLLYR	FDQKSLSPIK	DIISLKFKTM	QSDGILLHRE	GPNGDHITLQ	LRRARLFLLI	NSGEAKLPST	STLVNLTLGS
250	260	270	280	290	300	310	320
LLDDQHWHSV	LIQRLGKQVN	FTVDEHRHHF	HARGEFNLMN	LDYEGNVSFS	CSQPQSMPVT	FLSSRSYLAL	PDFSGEEEVS
330	340	350	360	370	380	390	400
ATFQFRTWNK	AGLLLFSELQ	LISGGILLFL	SDGKLKSNLY	QPGKLPSDIT	AGVELNDGQW	HSVSLSAKKN	HLSVAVDGQM
410	420	430	440	450	460	470	480
ASAAPLLGPE	QIYSGGTYYF	GGCPDKSFGS	KCKSPLGGFQ	GCMRLISISG	KVVDLISVQQ	GSLGNFSDLQ	IDSCGISDRC
490	500	510	520	530	540	550	560
LPNYCEHGGE	CSQSWSTFHC	NCTNTGYRGA	TCHNSIYEQS	CEAYKHRGNT	SGFYYIDSDG	SGPLEPFLLY	CNMTETAWTI
570	580	590	600	610	620	630	640
IQHNGSDLTR	VRNTNPENPY	AGFFEYVASM	EQLQATINRA	EHCEQEFTYY	CKKSRLVNKQ	DGTPLSWWVG	RTNETQTYWG
650	660	670	680	690	700	710	720
GSSPDLQKCT	CGLEGNCIDS	QYYCNCDADR	NEWTNDTGLL	AYKEHLPVTK	IVITDTGRLH	SEAAYKLGPL	LCQGDRSFWN
730	740	750	760	770	780	790	800
SASFDTEASY	LHFPTFHGEL	SADVSFFFKT	TASSGVFLEN	LGIADFIRIE	LRSPTVVTFS	FDVGNGPFEI	SVQSPTHFND
810	820	830	840	850	860	870	880
NQWHHVRVER	NMKEASLQVD	QLTPKTQPAP	ADGHVLLQLN	SQLFVGGTAT	RQRGFLGCIR	SLQLNGMTLD	LEERAQVTPE
890	900	910	920	930	940	950	960
VQPGCRGHCS	SYGKLCRNGG	KCRERPIGFF	CDCTFSAYTG	PFCSNEISAY	FGSGSSVIYN	FQENYLLSKN	SSSHAASFHG
970	980	990	1000	1010	1020	1030	1040
DMKLSREMIK	FSFRTTRTPS	LLLFVSSFYK	EYLSVIIAKN	GSLQIRYKLN	KYQEPDVVNF	DFKNMADGQL	HHIMINREEG
1050	1060	1070	1080	1090	1100	1110	1120
VVFIEIDDNR	RRQVHLSSGT	EFSAVKSLVL	GRILEHSDVD	QDTALAGAQG	FTGCLSAVQL	SHVAPLKAAL	HPSHPDPVTV
1130	1140	1150	1160	1170	1180	1190	1200
TGHVTESSCM	AQPGTDATSR	ERTHSFADHS	GTIDDREPLA	NAIKSDSAVI	GGLIAVVIFI	LLCITAIAVR	IYQQKRLYKR
1210	1220	1230	1240				
SEAKRSENVD	SAEAVLKSEL	NIQNAVNENQ	KEYFF				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2542	1	715.3361	-67.84	2	61.7	15.1	2	964-974	K.LSREMIKFSFR.T	Oxidation: 5
1571	1	1061.1650	-10.98	3	49.3	12.9	1	1024-1050	K.NMADGQLHHIMINREEGVVFIEIDDNR.R	Oxidation: 2

Detailed Protein Report

Protein 324: **PREDICTED: probable ATP-dependent RNA helicase DDX11 isoform X15 [Homo sapiens]**

Accession:	gi|578822806	**Score:**	28.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	94.9
Database Date:	2015-11-30	**pI:**	6.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	4.1
		No. of unique Peptides:	2



```
        10         20         30         40         50         60         70         80
MPLDGVRDSG MASRGPAAKD GENMVSASQK KGEIWSMANE TQKVGAIHFP FPFTPYSIQE DFMAELYRVL EAGKIGIFES
        90        100        110        120        130        140        150        160
PTGTGKSLSL ICGALSWLRD FEQKKREEEA RLLETGTGPL HDEKDESLCL SSSCEGAAGT PRPAGEPAWV TQFVQKKEER
       170        180        190        200        210        220        230        240
DLVDRLKAEQ ARRKQREERL QQLQHRVQLK YAAKRLRQEE EERENLLRLS REMLETGPEA ERLEQLESGE EELVLAEYES
       250        260        270        280        290        300        310        320
DEEKKVASRV DEDEDDLEEE HITKIYYCSR THSQLAQFVH EVKKSPFGKD VRLVSLGSRQ NLCVNEDVKS LGSVQLINDR
       330        340        350        360        370        380        390        400
CVDMQRSRHE KKKGAEEEKP KRRRQEKQAA CPFYNHEQMG LLRDEALAEV KDMEQLLALG KEARACPYYG SRLAIPAAQL
       410        420        430        440        450        460        470        480
VVLPYQMLLH AATRQAAGIR LQDQVVIIDE AHNLIDTITG MHSVEVSGSQ LCQAHSQLLQ YVERYGKRLK AKNLMYLKQI
       490        500        510        520        530        540        550        560
LYLLEKFVAV LGGNIKQNPN TQSLSQTGTE LKTINDFLFQ SQIDNINLFK VQRYCEKSMI SRKLFGFTER YGAVFSSREQ
       570        580        590        600        610        620        630        640
PKLAGFQQFL QSLQPRTTEA LAAPADESQA STLRPASPLM HIQGFLAALT TANQDGRVIL SRQGSLSQST LKFLLLNPAV
       650        660        670        680        690        700        710        720
HFAQVVKECR AVVIAGGTMQ PVSDFRQQLL ACAGVEAERV VEFSCGHVIP PDNILPLVIC SGISNQPLEF TFQKRELPQM
       730        740        750        760        770        780        790        800
MDEVGRILCN LCGVVPGGVV CFFPSYEYLR QVHAHWEKGG LLGRLAARKK IFQEPKSAHQ VEQVLLAYSR CIQACGQERG
       810        820        830        840        850
QVTGALLLSV VGGKMSEGIN FSDNLGRPEP PARHPQGRLW WRTCA
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2190	1	966.3871	-90.93	2	57.6	10.3	2	1-19	-.MPLDGVRDSGMASRGPAAK.D	Oxidation: 11
1689	1	932.9135	-80.83	2	51.0	17.7	2	543-558	R.KLFGFTERYGAVFSSR.E	

Detailed Protein Report

Protein 325: PREDICTED: inactive ribonuclease-like protein 10 isoform X1 [Homo sapiens]

Accession:	gi|530403621	**Score:**	27.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	27.0
Database Date:	2015-11-30	**pI:**	5.0
		Sequence Coverage [%]:	3.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MWGAPLPRRP	VWDVRSASAG	PQPCLGGKMK	LNLVQIFFML	LMLLLGLGMG	LGLGLHMATA	VLEESDQPLN	EFWSSDSQDK
90	100	110	120	130	140	150	160
AEATEEGDGT	QTTETLVLSN	KEVVQPGWPE	DPILGEDEVG	GNKMLRASAL	FQSNKDYLRL	DQTDRECNDM	MAHKMKEPSQ
170	180	190	200	210	220	230	240
SCIAQYAFIH	EDLNTVKAVC	NSPVIACELK	GGKCHKSSRP	FDLTLCELSQ	PDQVTPNCNY	LTSVIKKHII	ITCNDMKRQL
250							
PTGQ							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1593	1	927.7563	290.39	1	49.8	27.9	0	1-8	-.MWGAPLPR.R	

Detailed Protein Report

Protein 326: lysine-specific demethylase 3A [Homo sapiens]

Accession:	gi|20357522	**Score:**	27.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	147.2
Database Date:	2015-11-30	**pI:**	9.4
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	2.4
		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
81	1	821.0339	-27.87	3	30.4	17.2	2	457-480	K.AGVNSDSPNNCSGKKVEPSALACR.S	Carbamidomethyl: 23
624	1	472.1185	-315.94	2	37.4	10.7	0	840-847	K.QPTMPILK.N	Oxidation: 4

Detailed Protein Report

Protein 327: PREDICTED: regulator of G-protein signaling 22 isoform X8 [Homo sapiens]

Accession:	gi|578815920	**Score:**	27.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	121.2
Database Date:	2015-11-30	**pI:**	6.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPEKRLTAEP	PTITEEEFED	SLATDDFLVD	YFNEFLSLPT	FSEAIRFNAD	YGVFEVANDA	PQFLEKQLKK	ILQNQQPRNP
90	100	110	120	130	140	150	160
IYDVVRKGKN	EVKPVQMNAP	DEDETINVNY	NIMCLSREEG	IKWIKKERLP	AFLESDCYFE	YRLAKLVSQV	RWSKSGMNFT
170	180	190	200	210	220	230	240
VGSNFSPWIV	KKPPSLPPPA	TEEDNLVIMK	KFYVSLGEAS	YTQTKDWFAL	AKQSQQTVST	FSLPCCVPYN	KLKSPAISSV
250	260	270	280	290	300	310	320
SENFIFDDGV	HPRTKKDPSK	TNKLISEFEE	EEGEEEEVSV	SLQDTPSQAL	LRVYLEKKQD	VDESLTMHFS	TCEEFLSSYI
330	340	350	360	370	380	390	400
YFILRGAIQQ	IVGKPVGETP	DYINFNNITK	VSFDDCFESI	HGKNFLSELV	QTTKERSEEI	EQTSLSSKNE	SAGPESRADW
410	420	430	440	450	460	470	480
CISHRTYDIG	NRKEFERFKK	FIKGTLGERY	WWLWMDIERL	KVLKDPGRHQ	RHLEKMKKCY	LVSNGDYYLS	AEILSKFKLL
490	500	510	520	530	540	550	560
DGSQWNEEHL	RNIQSEVLKP	LLLYWAPRFC	VTHSASTKYA	SAELKFWHLR	QAKPRKDIDP	FPQMATLLPL	RPKSCIPQIP
570	580	590	600	610	620	630	640
EIQKEEFSLS	QPPKSPNKSP	EVKTATQKPW	KRELLYPGSS	KDDVIEKGSK	YMSESSKVIH	LTSFTDISEC	LKPQLDRRYA
650	660	670	680	690	700	710	720
YTEEPRVKTV	SDVGALGGSD	MENLLQSLYV	ENRAGFFFTK	FCEHSGNKLW	KNSVYFWFDL	QAYHQLFYQE	TLQPFKVCKQ
730	740	750	760	770	780	790	800
AQYLFATYVA	PSATLDIGLQ	QEKKKEIYMK	IQPPFEDLFD	TAEEYILLLL	LEPWTKMVKS	DQIAYKKVEL	VEETRQLDST
810	820	830	840	850	860	870	880
YFRKLQALHK	ETFSKKAEVQ	MKDIAEELLL	QKAEKKIGVW	KDLCHSHCDE	SVIQKKITTI	INCFINSSIP	PALQIDIPVE
890	900	910	920	930	940	950	960
QAQKIIEHRK	ELGPYVFREA	QMTIFGVLFK	FWPQFCEFRK	NLTDENIMSV	LERRQEYNKQ	KKKLAVLEDE	KSGKDGIKQY
970	980	990	1000	1010	1020	1030	1040
ANTSVPAIKT	ALLSDSFLGL	QPYGRQPTWC	YSKYIEALEQ	ERILLKIQEE	LEKKLFAGLQ	PLTNFKASSS	TMSLKKNMSA
1050							
HSSQK							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2278	1	557.5521	-50.47	3	58.7	12.0	0	842-855	K.DLCHSHCDESVIQK.K	Carbamidomethyl: 7

Detailed Protein Report

Protein 328: **PREDICTED: leukocyte immunoglobulin-like receptor subfamily B member 3-like isoform X4 [Homo sapiens]**

Accession:	gi|578842508	**Score:**	27.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	69.3
Database Date:	2015-11-30	**pI:**	6.2
		Sequence Coverage [%]:	5.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MTPALTALLC	LGLSLGPRTR	VQAGPFPKPT	LWAEPGSVIS	WGSPVTIWCQ	GSLEAQEYRL	DKEGSPEPLD	RNNPLEPKNK
90	100	110	120	130	140	150	160
ARFSIPSMTE	HHAGRYRCHY	YSSAGWSEPS	DPLELVMTGF	YNKPTLSALP	SPVVASGGNM	TLRCGSQKGY	HHFVLMKEGE
170	180	190	200	210	220	230	240
HQLPRTLDSQ	QLHSGGFQAL	FPVGPVNPSH	RWRFTCYYYY	MNTPQVWSHP	SDPLEILPSG	VSRKPSLLTL	QGPVLAPGQS
250	260	270	280	290	300	310	320
LTLQCGSDVG	YDRFVLYKEG	ERDFLQRPGQ	QPQAGLSQAN	FTLGPVSPSH	GGQYRCYGAH	NLSSEWSAPS	DPLNILMAGQ
330	340	350	360	370	380	390	400
IYDTVSLSAQ	PGPTVASGEN	VTLLCQSWWQ	FDTFLLTKEG	AAHPPLRLRS	MYGAHKYQAE	FPMSPVTSAH	AGTYRCYGSY
410	420	430	440	450	460	470	480
SSNPHLLSFP	SEPLELMVSG	HSGGSSLPPT	GPPSTPGLGR	YLEVLIGVSV	AFVLLLFLLL	FLLLRRQRHS	KHRTSDQRKT
490	500	510	520	530	540	550	560
DFQRPAGAAE	TEPKDRGLLR	RSSPAADVQE	ENLYAAVKDT	QSEDRVELDS	QSPHDEDPQA	VTYAPVKHSS	PRREMASPPS
570	580	590	600	610	620	630	640
SLSGEFLDTK	DRQVEEDRQM	DTEAAASEAS	QDVTYAQLHS	LTLRRKATEP	PPSQEGEPPA	EPSIYATLAI	H

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1409	1	927.1324	25.05	3	47.2	16.3	2	501-525	R.RSSPAADVQEENLYAAVKDTQSEDR.V	

Detailed Protein Report

Protein 329: **leucine-rich repeats and immunoglobulin-like domains protein 1 precursor [Homo sapiens]**

Accession:	gi|54607118	**Score:**	27.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	119.0
Database Date:	2015-11-30	**pI:**	6.7
		Sequence Coverage [%]:	2.9
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 1.61 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MARPVRGGLG	APRRSPCLLL	LWLLLLRLEP	VTAAAGPRAP	CAAACTCAGD	SLDCGGRGLA	ALPGDLPSWT	RSLNLSYNKL
90	100	110	120	130	140	150	160
SEIDPAGFED	LPNLQEVYLN	NNELTAVPSL	GAASSHVVSL	FLQHNKIRSV	EGSQLKAYLS	LEVLDLSLNN	ITEVRNTCFP
170	180	190	200	210	220	230	240
HGPPIKELNL	AGNRIGTLEL	GAFDGLSRSL	LTLRLSKNRI	TQLPVRAFKL	PRLTQLDLNR	NRIRLIEGLT	FQGLNSLEVL
250	260	270	280	290	300	310	320
KLQRNNISKL	TDGAFWGLSK	MHVLHLEYNS	LVEVNSGSLY	GLTALHQLHL	SNNSIARIHR	KGWSFCQKLH	ELVLSFNNLT
330	340	350	360	370	380	390	400
RLDEESLAEL	SSLSVLRLSH	NSISHIAEGA	FKGLRSLRVL	DLDHNEISGT	IEDTSGAFSG	LDSLSKLTLF	GNKIKSVAKR
410	420	430	440	450	460	470	480
AFSGLEGLEH	LNLGGNAIRS	VQFDAFVKMK	NLKELHISSD	SFLCDCQLKW	LPPWLIGRML	QAFVTATCAH	PESLKGQSIF
490	500	510	520	530	540	550	560
SVPPESFVCD	DFLKPQIITQ	PETTMAMVGK	DIRFTCSAAS	SSSSPMTFAW	KKDNEVLTNA	DMENFVHVHA	QDGEVMEYTT
570	580	590	600	610	620	630	640
ILHLRQVTFG	HEGRYQCVIT	NHFGSTYSHK	ARLTVNVLPS	FTKTPHDITI	RTTTMARLEC	AATGHPNPQI	AWQKDGGTDF
650	660	670	680	690	700	710	720
PAARERRMHV	MPDDDVFFIT	DVKIDDAGVY	SCTAQNSAGS	ISANATLTVL	ETPSLVVPLE	DRVVSVGETV	ALQCKATGNP
730	740	750	760	770	780	790	800
PPRITWFKGD	RPLSLTERHH	LTPDNQLLVV	QNVVAEDAGR	YTCEMSNTLG	TERAHSQLSV	LPAAGCRKDG	TTVGIFTIAV
810	820	830	840	850	860	870	880
VSSIVLTSLV	WVCIIYQTRK	KSEEYSVTNT	DETVVPPDVP	SYLSSQGTLS	DRQETVVRTE	GGPQANGHIE	SNGVCPRDAS
890	900	910	920	930	940	950	960
HFPEPDTHSV	ACRQPKLCAG	SAYHKEPWKA	MEKAEGTPGP	HKMEHGGRVV	CSDCNTEVDC	YSRGQAFHPQ	PVSRDSAQPS
970	980	990	1000	1010	1020	1030	1040
APNGPEPGGS	DQEHSPHHQC	SRTAAGSCPE	CQGSLYPSNH	DRMLTAVKKK	PMASLDGKGD	SSWTLARLYH	PDSTELQPAS
1050	1060	1070	1080	1090	1100		
SLTSGSPERA	EAQYLLVSNG	HLPKACDASP	ESTPLTGQLP	GKQRVPLLLA	PKS		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
45	1	1096.9782	-54.15	2	29.9	16.3	1	431-449	K.NLKELHISSDSFLCDCQLK.W		MD:MU 1.61

Detailed Protein Report

Protein 330: coiled-coil domain-containing protein 80 precursor [Homo sapiens]

Accession:	gi|41152074	**Score:**	27.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	108.1
Database Date:	2015-11-30	**pI:**	10.2
Modification(s):	Oxidation	**Sequence Coverage [%]:**	4.2
		No. of unique Peptides:	2

Quantitation

MD:MU	**Median:** 3.85	**CV:** 0.00 %	**No. of Peptides:** 1

Alias proteins:

Accession	Name	Description
gi|41152076	refseq_huma (refseq_human_20140103.fasta)	coiled-coil domain-containing protein 80 precursor [Homo sapiens]

10	20	30	40	50	60	70	80
MTWRMGPRFT	MLLAMWLVCG	SEPHPHATIR	GSHGGRKVPL	VSPDSSRPAR	FLRHTGRSRG	IERSTLEEPN	LQPLQRRRSV
90	100	110	120	130	140	150	160
PVLRLARPTE	PPARSDINGA	AVRPEQRPAA	RGSPREMIRD	EGSSARSRML	RFPSGSSSPN	ILASFAGKNR	VWVISAPHAS
170	180	190	200	210	220	230	240
EGYYRLMMSL	LKDDVYCELA	ERHIQQIVLF	HQAGEEGGKV	RRITSEGQIL	EQPLDPSLIP	KLMSFLKLEK	GKFGMVLLKK
250	260	270	280	290	300	310	320
TLQVEERYPY	PVRLEAMYEV	IDQGPIRRIE	KIRQKGFVQK	CKASGVEGQV	VAEGNDGGGG	AGRPSLGSEK	KKEDPRRAQV
330	340	350	360	370	380	390	400
PPTRESRVKV	LRKLAATAPA	LPQPPSTPRA	TTLPPAPATT	VTRSTSRAVT	VAARPMTTTA	FPTTQRPWTP	SPSHRPPTTT
410	420	430	440	450	460	470	480
EVITARRPSV	SENLYPPSRK	DQHRERPQTT	RRPSKATSLE	SFTNAPPTTI	SEPSTRAAGP	GRFRDNRMDR	REHGHRDPNV
490	500	510	520	530	540	550	560
VPGPPKPAKE	KPPKKKAQDK	ILSNEYEEKY	DLSRPTASQL	EDELQVGNVP	LKKAKESKKH	EKLEKPEKEK	KKKMKNENAD
570	580	590	600	610	620	630	640
KLLKSEKQMK	KSEKKSKQEK	EKSKKKKGGK	TEQDGYQKPT	NKHFTQSPKK	SVADLLGSFE	GKRRLLLITA	PKAENNMYVQ
650	660	670	680	690	700	710	720
QRDEYLESFC	KMATRKISVI	TIFGPVNNST	MKIDHFQLDN	EKPMRVVDDE	DLVDQRLISE	LRKEYGMTYN	DFFMVLTDVD
730	740	750	760	770	780	790	800
LRVKQYYEVP	ITMKSVFDLI	DTFQSRIKDM	EKQKKEGIVC	KEDKKQSLEN	FLSRFRWRRR	LLVISAPNDE	DWAYSQQLSA
810	820	830	840	850	860	870	880
LSGQACNFGL	RHITILKLLG	VGEEVGGVLE	LFPINGSSVV	EREDVPAHLV	KDIRNYFQVS	PEYFSMLLVG	KDGNVKSWYP
890	900	910	920	930	940	950	960
SPMWSMVIVY	DLIDSMQLRR	QEMAIQQSLG	MRCPEDEYAG	YGYHSYHQGY	QDGYQDDYRH	HESYHHGYPY	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1256	5	698.8457	-68.14	2	45.4	14.9	0	350-363	R.ATTLPPAPATTVTR.S		MD:MU 3.85
1645	1	1062.1080	-81.53	3	50.3	12.9	2	697-722	R. LISELRKEYGMTYNDFFMVLTDVD V	Oxidation: 18	

Detailed Protein Report

Protein 331: **PREDICTED: E3 ubiquitin-protein ligase HERC2 isoform X5 [Homo sapiens]**

Accession:	gi|578827509	**Score:**	27.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	517.6
Database Date:	2015-11-30	**pI:**	5.9
		Sequence Coverage [%]:	0.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPSESFCLAA	QARLDSKWLK	TDIQLAFTRD	GLCGLWNEMV	KDGEIVYTGT	ESTQNGELPP	RKDDSVEPSG	TKKEDLNDKE
90	100	110	120	130	140	150	160
KKDEEETPAP	IYRAKSILDS	WVWGKQPDVN	ELKECLSVLV	KEQQALAVQS	ATTTLSALRL	KQRLVILERY	FIALNRTVFQ
170	180	190	200	210	220	230	240
ENVKVKWKSS	GISLPPVDKK	RDVHGTPATK	GPGSIPLQDQ	HLALAILLEL	AVQRGTLSQM	LSAILLLLQL	WDSGAQETDN
250	260	270	280	290	300	310	320
ERSAQGTSAP	LLPLLQRFQS	IICRKDAPHS	EGDMHLLSGP	LSPNESFLRY	LTLPQDNELA	IDLRQTAVVV	MAHLDRLATP
330	340	350	360	370	380	390	400
CMPPLCSSPT	SHKGSLQEVI	GWGLIGWKYY	ANVIGPIQCE	GLANLGVTQI	ACAEKRFLIL	SRNGRVYTQA	YNSDTLAPQL
410	420	430	440	450	460	470	480
VQGLASRNIV	KIAAHSDGHH	YLALAATGEV	YSWGCGDGGR	LGHGDTVPLE	EPKVISAFSG	KQAGKHVVHI	ACGSTYSAAI
490	500	510	520	530	540	550	560
TAEGELYTWG	RGNYGRLGHG	SSEDEAIPML	VAGLKGLKVI	DVACGSGDAQ	TLAVTENGQV	WSWGDGDYGK	LGRGGSDGCK
570	580	590	600	610	620	630	640
TPKLIEKLQD	LDVVKVRCGS	QFSIALTKDG	QVYSWGKGDN	QRLGHGTEEH	VRYPKLLEGL	QGKKVIDVAA	GSTHCLALTE
650	660	670	680	690	700	710	720
DSEVHSWGSN	DQCQHFDTLR	VTKPEPAALP	GLDTKHIVGI	ACGPAQSFAW	SSCSEWSIGL	RVPFVVDICS	MTFEQLDLLL
730	740	750	760	770	780	790	800
RQVSEGMDGS	ADWPPPQEKE	CVAVATLNLL	RLQLHAAISH	QVDPEFLGLG	LGSILLNSLK	QTVVTLASSA	GVLSTVQSAA
810	820	830	840	850	860	870	880
QAVLQSGWSV	LLPTAEERAR	ALSALLPCAV	SGNEVNISPG	RRFMIDLLVG	SLMADGGLES	ALHAAITAEI	QDIEAKKEAQ
890	900	910	920	930	940	950	960
KEKEIDEQEA	NASTFHRSRT	PLDKDLINTG	ICESSGKQCL	PLVQLIQQLL	RNIASQTVAR	LKDVARRISS	CLDFEQHSRE
970	980	990	1000	1010	1020	1030	1040
RSASLDLLLR	FQRLLISKLY	PGESIGQTSD	ISSPELMGVG	SLLKKYTALL	CTHIGDILPV	AASIASTSWR	HFAEVAYIVE
1050	1060	1070	1080	1090	1100	1110	1120
GDFTGVLLPE	LVVSIVLLLS	KNAGLMQEAG	AVPLLGGLLE	HLDRFNHLAP	GKERDDHEEL	AWPGIMESFF	TGQNCRNNEE
1130	1140	1150	1160	1170	1180	1190	1200
VTLIRKADLE	NHNKDGGFWT	VIDGKVYDIK	DFQTQSLTGN	SILAQFAGED	PVVALEAALQ	FEDTRESMHA	FCVGQYLEPD
1210	1220	1230	1240	1250	1260	1270	1280
QEIVTIPDLG	SLSSPLIDTE	RNLGLLLGLH	ASYLAMSTPL	SPVEIECAKW	LQSSIFSGGL	QTSQIHYSYN	EEKDEDHCSS
1290	1300	1310	1320	1330	1340	1350	1360
PGGTPASKSR	LCSHRRALGD	HSQAFLQAIA	DNNIQDHNVK	DFLCQIERYC	RQCHLTTPIM	FPPEHPVEEV	GRLLLCCLLK
1370	1380	1390	1400	1410	1420	1430	1440
HEDLGHVALS	LVHAGALGIE	QVKHRTLPKS	VVDVCRVVYQ	AKCSLIKTHQ	EQGRSYKEVC	APVIERLRFL	FNELRPAVCN
1450	1460	1470	1480	1490	1500	1510	1520
DLSIMSKFKL	LSSLPRWRRI	AQKIIRERRK	KRVPKKPEST	DDEEKIGNEE	SDLEEACILP	HSPINVDKRP	IAIKSPKDKW
1530	1540	1550	1560	1570	1580	1590	1600
QPLLSTVTGV	HKYKWLKQNV	QGLYPQSPLL	STIAEFALKE	EPVDVEKMRK	CLLKQLERAE	VRLEGIDTIL	KLASKNFLLP
1610	1620	1630	1640	1650	1660	1670	1680
SVQYAMFCGW	QRLIPEGIDI	GEPLTDCLKD	VDLIPPFNRM	LLEVTFGKLY	AWAVQNIRNV	LMDASAKFKE	LGIQPVPLQT
1690	1700	1710	1720	1730	1740	1750	1760
ITNENPSGPS	LGTIPQARFL	LVMLSMLTLQ	HGANNLDLLL	NSGMLALTQT	ALRLIGPSCD	NVEEDMNASA	QGASATVLEE
1770	1780	1790	1800	1810	1820	1830	1840
TRKETAPVQL	PVSGPELAAM	MKIGTRVMRG	VDWKWGDQDG	PPPGLGRVIG	ELGEDGWIRV	QWDTGSTNSY	RMGKEGKYDL
1850	1860	1870	1880	1890	1900	1910	1920
KLAELPAAAQ	PSAEDSDTED	DSEAEQTERN	IHPTAMMFTS	TINLLQTLCL	SAGVHAEIMQ	SEATKTLCGL	LRMLVESGTT
1930	1940	1950	1960	1970	1980	1990	2000
DKTSSPNRLV	YREQHRSWCT	LGFVRSIALT	PQVCGALSSP	QWITLLMKVV	EGHAPFTATS	LQRQILAVHL	LQAVLPSWDK
2010	2020	2030	2040	2050	2060	2070	2080
TERARDMKCL	VEKLFDFLGS	LLTTCSSDVP	LLRESTLRRR	RVRPQASLTA	THSSTLAEEV	VALLRTLHSL	TQWNGLINKY
2090	2100	2110	2120	2130	2140	2150	2160
INSQLRSITH	SFVGRPSEGA	QLEDYFPDSE	NPEVGGLMAV	LAVIGGIDGR	LRLGGQVMHD	EFGEGTVTRI	TPKGKITVQF
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
360	1	543.1311	-259.95	2	33.8	14.2	0	3920-3930	K.LYATGYGAGGR.L	

Detailed Protein Report

Protein 332: PREDICTED: coiled-coil domain-containing protein 91 isoform X6 [Homo sapiens]

Accession: gi|578822930
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 27.8
MW [kDa]: 51.6
pI: 5.4
Sequence Coverage [%]: 5.8
No. of unique Peptides: 1

Quantitation

MD:MU **Median:** 0.58 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MWVQQHRPEN	TFGDQRETCN	FHCELPSRVY	GRTSLKLLMP	MWNKVSGVHL	SPSSPEIVLD	RDHSSSIGCL	SSDAIISSPE
90	100	110	120	130	140	150	160
NTHAANSIVS	QTIPKAQIQQ	STHTHLDISL	FPLGLTDEKS	NGTIALVDDS	EDPGANVSNI	QLQQKISSLE	IKLKVSEEEK
170	180	190	200	210	220	230	240
QRIKQDVESL	MEKHNVLEKG	FLKEKEQEAI	SFQDRYKELQ	EKHKQELEDM	RKAGHEALSI	IVDEYKALLQ	SSVKQQVEAI
250	260	270	280	290	300	310	320
EKQYISAIEK	QAHKCEELLN	AQHQRLLEML	DTEKELLKEK	IKEALIQQSQ	EQKEILEKCL	EEERQRNKEA	LVSAAKLEKE
330	340	350	360	370	380	390	400
AVKDAVLKVV	EEERKNLEKA	HAEERELWKT	EHAKDQEKVS	QEIQKAIQEQ	RKISQETVKA	AIIEEQKRSE	KAVEEAVKRT
410	420	430	440	450			
RDELIEYIKE	QKRLDQVIRQ	RSLSSLELFL	SCAQKQLSAL	IATEPVDIE			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1996	1	665.3129	-29.71	2	55.1	11.2	2	203-212	K.HKQELEDMRK.A	Oxidation: 8	MD:MU 0.58

Detailed Protein Report

Protein 333: engulfment and cell motility protein 1 isoform 2 [Homo sapiens]

Accession:	gi|18765702	**Score:**	27.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	28.7
Database Date:	2015-11-30	**pI:**	6.0
		Sequence Coverage [%]:	10.1
		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
1550	1	1011.5446	-2.78	2	49.2	15.4	2	128-146	K.LPVADIKAVVTGKDCPHMK.E	

Detailed Protein Report

Protein 334: glutathione S-transferase P [Homo sapiens]

Accession:	gi|4504183	**Score:**	27.7
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
1594	1	942.4301	-51.36	2	49.6	27.7	0	56-71	K.FQDGDLTLYQSNTILR.H	

Detailed Protein Report

Protein 335: pleckstrin homology domain-containing family A member 7 [Homo sapiens]

Accession: gi|239047795
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 27.6
MW [kDa]: 127.1
pI: 9.9
Sequence Coverage [%]: 2.7
No. of unique Peptides: 1

```
        10          20          30          40          50          60          70          80
MAAATVGRDT  LPEHWSYGVC  RDGRVFFIND  QLRCTTWLHP  RTGEPVNSGH  MIRSDLPRGW  EEGFTEEGAS  YFIDHNQQTT
        90         100         110         120         130         140         150         160
AFRHPVTGQF  SPENSEFILQ  EEPNPHMSKQ  DRNQRPSSMV  SETSTAGTAS  TLEAKPGPKI  IKSSSKVHSF  GKRDQAIRRN
       170         180         190         200         210         220         230         240
PNVPVVVRGW  LHKQDSSGMR  LWKRRWFVLA  DYCLFYYKDS  REEAVLGSIP  LPSYVISPVA  PEDRISRKYS  FKAVHTGMRA
       250         260         270         280         290         300         310         320
LIYNSSTAGS  QAEQSGMRTY  YFSADTQEDM  NAWVRAMNQA  AQVLSRSSLK  RDMEKVERQA  VPQANHTESC  HECGRVGPGH
       330         340         350         360         370         380         390         400
TRDCPHRGHD  DIVNFERQEQ  EGEQYRSQRD  PLEGKRDRSK  ARSPYSPAEE  DALFMDLPTG  PRGQQAQPQR  AEKNGMLPAS
       410         420         430         440         450         460         470         480
YGPGEQNGTG  GYQRAFPPRT  NPEKHSQRKS  NLAQVEHWAR  AQKGDSRSLP  LDQTLPRQGP  GQSLSFPENY  QTLPKSTRHP
       490         500         510         520         530         540         550         560
SGGSSPPPRN  LPSDYKYAQD  RASHLKMSSE  ERRAHRDGTV  WQLYEWQQRQ  QFRHGSPTAP  ICLGSPEFTD  QGRSRSMLEV
       570         580         590         600         610         620         630         640
PRSISVPPSP  SDIPPPGPPR  VFPPRRPHTP  AERVTVKPPD  QRRSVDISLG  DSPRRARGHA  VKNSSHVDRR  SMPSMGYMTH
       650         660         670         680         690         700         710         720
TVSAPSLHGK  SADDTYLQLK  KDLEYLDLKM  TGRDLLKDRS  LKPVKIAESD  TDVKLSIFCE  QDRVLQDLED  KIRALKENKD
       730         740         750         760         770         780         790         800
QLESVLEVLH  RQMEQYRDQP  QHLEKIAYQQ  KLLQEDLVHI  RAELSRESTE  MENAWNEYLK  LENDVEQLKQ  TLQEQHRRAF
       810         820         830         840         850         860         870         880
FFQEKSQIQK  DLWRIEDVTA  GLSANKENFR  ILVESVKNPE  RKTVPLFPHP  PVPSLSTSES  KPPPQPSPPT  SPVRTPLEVR
       890         900         910         920         930         940         950         960
LFPQLQTYVP  YRPHPPQLRK  VTSPLQSPTK  AKPKVEDEAP  PRPPLPELYS  PEDQPPAVPP  LPREATIIRH  TSVRGLKRQS
       970         980         990        1000        1010        1020        1030        1040
DERKRDRELG  QCVNGDSRVE  LRSYVSEPEL  ATLSGDMAQP  SLGLVGPESR  YQTLPGRGLS  GSTSRLQQSS  TIAPYVTLRR
      1050        1060        1070        1080        1090        1100        1110        1120
GLNAESSKAT  FPRPKSALER  LYSGDHQRGK  MSAEEQLERM  KRHQKALVRE  RKRTLGQGER  TGLPSSRYLS  RPLPGDLGSV
      1130
C
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2724	1	973.5090	30.70	2	64.4	12.7	2	966-982	R.DRELGQCVNGDSRVELR.S	

Detailed Protein Report

Protein 336: PREDICTED: rap guanine nucleotide exchange factor 3 isoform X4 [Homo sapiens]

Accession: gi|530399604
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl, Oxidation

Score: 27.6
MW [kDa]: 55.9
pI: 9.9
Sequence Coverage [%]: 5.1
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MPSAQLCAAL	LHHFHVEPAG	GSEQERSTYV	CNKRQQILRL	VSQWVALYGS	MLHTDPVATS	FLQKLSDLVG	RDTRLSNLLR
90	100	110	120	130	140	150	160
EQWPERRRCH	RLENGCGNAS	PQMKARNLPV	WLPNQDEPLP	GSSCAIQVGD	KVPYDICRPD	HSVLTLQLPV	TASVREVMAA
170	180	190	200	210	220	230	240
LAQEDGWTKG	QVLVKVNSAG	DAIGLQPDAR	GVATSLGLNE	RLFVVNPQEV	HELIPHPDQL	GPTVGSAEGL	DLVSAKDLAG
250	260	270	280	290	300	310	320
QLTDHDWSLF	NSIHQVELIH	YVLGPQHLRD	VTTANLERFM	RRFNELQYWV	ATELCLCPVP	GPRAQLLRKF	IKLAAHLKEQ
330	340	350	360	370	380	390	400
KNLNSFFAVM	FGLSNSAISR	LAHTWERLPH	KVRKLYSALE	RLLDPSWNHR	VYRLALAKLS	PPVIPFMPLL	LKDMTFIHEG
410	420	430	440	450	460	470	480
NHTLVENLIN	FEKMRMMARA	ARMLHHCRSH	NPVPLSPLRS	RVSHLHEDSQ	VARISTCSEQ	SLSTRSPAST	WAYVQQLKVI
490	500						
DNQRELSRLS	RELEP						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1805	1	937.7928	-121.06	2	52.4	13.0	1	89-104	R.CHRLENGCGNASPQMK.A	Carbamidomethyl: 1, 8; Oxidation: 15

Detailed Protein Report

Protein 337: **PREDICTED: DNA (cytosine-5)-methyltransferase 1 isoform X1 [Homo sapiens]**

Accession:	gi|578833065	**Score:**	27.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	169.3
Database Date:	2015-11-30	**pI:**	8.8
		Sequence Coverage [%]:	1.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MADANSPPKP	LSKPRTPRRS	KSDGEAKPEP	SPSPRITRKS	TRQTTITSHF	AKGPAKRKPQ	EESERAKSDE	SIKEEDKDQD
90	100	110	120	130	140	150	160
EKRRRVTSRE	RVARPLPAEE	PERAKSGTRT	EKEEERDEKE	EKRLRSQTKE	PTPKQKLKEE	PDREARAGVQ	ADEDEDGDEK
170	180	190	200	210	220	230	240
DEKKHRSQPK	DLAAKRRPEE	KEPEKVNPQI	SDEKDEDEKE	EKRRKTTPKE	PTEKKMARAK	TVMNSKTHPP	KCIQCGQYLD
250	260	270	280	290	300	310	320
DPDLKYGQHP	PDAVDEPQML	TNEKLSIFDA	NESGFESYEA	LPQHKLTCFS	VYCKHGHLCP	IDTGLIEKNI	ELFFSGSAKP
330	340	350	360	370	380	390	400
IYDDDPSLEG	GVNGKNLGPI	NEWWITGFDG	GEKALIGFST	SFAEYILMDP	SPEYAPIFGL	MQEKIYISKI	VVEFLQSNSD
410	420	430	440	450	460	470	480
STYEDLINKI	ETTVPPSGLN	LNRFTEDSLL	RHAQFVVEQV	ESYDEAGDSD	EQPIFLTPCM	RDLIKLAGVT	LGQRRAQARR
490	500	510	520	530	540	550	560
QTIRHSTREK	DRGPTKATTT	KLVYQIFDTF	FAEQIEKDDR	EDKENAFKRR	RCGVCEVCQQ	PECGKCKACK	DMVKFGGSGR
570	580	590	600	610	620	630	640
SKQACQERRC	PNMAMKEADD	DEEVDDNIPE	MPSPKKMHQG	KKKKQNKNRI	SWVGEAVKTD	GKKSYYKKVC	IDAETLEVGD
650	660	670	680	690	700	710	720
CVSVIPDDSS	KPLYLARVTA	LWEDSSNGQM	FHAHWFCAGT	DTVLGATSDP	LELFLVDECE	DMQLSYIHSK	VKVIYKAPSE
730	740	750	760	770	780	790	800
NWAMEGGMDP	ESLLEGDDGK	TYFYQLWYDQ	DYARFESPPK	TQPTEDNKFK	FCVSCARLAE	MRQKEIPRVL	EQLEDLDSRV
810	820	830	840	850	860	870	880
LYYSATKNGI	LYRVGDGVYL	PPEAFTFNIK	LSSPVKRPRK	EPVDEDLYPE	HYRKYSDYIK	GSNLDAPEPY	RIGRIKEIFC
890	900	910	920	930	940	950	960
PKKSNGRPNE	TDIKIRVNKF	YRPENTHKST	PASYHADINL	LYWSDEEAVV	DFKAVQGRCT	VEYGEDLPEC	VQVYSMGGPN
970	980	990	1000	1010	1020	1030	1040
RFYFLEAYNA	KSKSFEDPPN	HARSPGNKGK	GKGKGKGKPK	SQACEPSEPE	IEIKLPKLRT	LDVFSGCGGL	SEGFHQAGIS
1050	1060	1070	1080	1090	1100	1110	1120
DTLWAIEMWD	PAAQAFRLNN	PGSTVFTEDC	NILLKLVMAG	ETTNSRGQRL	PQKGDVEMLC	GGPPCQGFSG	MNRFNSRTYS
1130	1140	1150	1160	1170	1180	1190	1200
KFKNSLVVSF	LSYCDYYRPR	FFLLENVRNF	VSFKRSMVLK	LTLRCLVRMG	YQCTFGVLQA	GQYGVAQTRR	RAIILAAAPG
1210	1220	1230	1240	1250	1260	1270	1280
EKLPLFPEPL	HVFAPRACQL	SVVVDDKKFV	SNITRLSSGP	FRTITVRDTM	SDLPEVRNGA	SALEISYNGE	PQSWFQRQLR
1290	1300	1310	1320	1330	1340	1350	1360
GAQYQPILRD	HICKDMSALV	AARMRHIPLA	PGSDWRDLPN	IEVRLSDGTM	ARKLRYTHHD	RKNGRSSSGA	LRGVCSCVEA
1370	1380	1390	1400	1410	1420	1430	1440
GKACDPAARQ	FNTLIPWCLP	HTGNRHNHWA	GLYGRLEWDG	FFSTTVTNPE	PMGKQGRVLH	PEQHRVVSVR	ECARSQGFPD
1450	1460	1470	1480	1490	1500		
TYRLFGNILD	KHRQVGNAVP	PPLAKAIGLE	IKLCMLAKAR	ESASAKIKEE	EAAKD		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
273	1	685.7423	-204.14	2	32.8	12.1	2	778-788	R.LAEMRQKEIPR.V	

Detailed Protein Report

Protein 338: partitioning defective 3 homolog isoform 8 [Homo sapiens]

Accession:	gi|296278200	**Score:**	27.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	138.2
Database Date:	2015-11-30	**pI:**	8.4
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MKVTVCFGRT	RVVVPCGDGH	MKVFSLIQQA	VTRYRKAIAK	DPNYWIQVHR	LEHGDGGILD	LDDILCDVAD	DKDRLVAVFD
90	100	110	120	130	140	150	160
EQDPHHGGDG	TSASSTGTQS	PEIFGSELGT	NNVSAFQPYQ	ATSEIEVTPS	VLRANMPLHV	RRSSDPALIG	LSTSVSDSNF
170	180	190	200	210	220	230	240
SSEEPSRKNP	TRWSTTAGFL	KQNTAGSPKT	CDRKDEDGTE	EDNSRVEPVG	HADTGLEHIP	NFSLDDMVKL	VEVPNDGGPL
250	260	270	280	290	300	310	320
GIHVVPFSAR	GGRTLGLLVK	RLEKGGKAEH	ENLFRENDCI	VRINDGDLRN	RRFEQAQHMF	RQAMRTPIIW	FHVVPAANKE
330	340	350	360	370	380	390	400
QYEQLSQSEK	NNYYSSRFSP	DSQYIDNRSV	NSAGLHTVQR	APRLNHPPEQ	IDSHSRLPHS	AHPSGKPPSA	PASAPQNVFS
410	420	430	440	450	460	470	480
TTVSSGYNTK	KIGKRLNIQL	KKGTEGLGFS	ITSRDVTIGG	SAPIYVKNIL	PRGAAIQDGR	LKAGDRLIEV	NGVDLVGKSQ
490	500	510	520	530	540	550	560
EEVVSLLRST	KMEGTVSLLV	FRQEDAFHPR	ELKAEDEDIV	LTPDGTREFL	TFEVPLNDSG	SAGLGVSVKG	NRSKENHADL
570	580	590	600	610	620	630	640
GIFVKSIING	GAASKDGRLR	VNDQLIAVNG	ESLLGKTNQD	AMETLRRSMS	TEGNKRGMIQ	LIVARRISKC	NELKSPGSPP
650	660	670	680	690	700	710	720
GPELPIETAL	DDRERRISHS	LYSGIEGLDE	SPSRNAALSR	IMGKYQLSPT	VNMPQDDTVI	IEDDRLPVLP	PHLSDQSSSS
730	740	750	760	770	780	790	800
SHDDVGFVTA	DAGTWAKAAI	SDSADCSLSP	DVDPVLAFQR	EGFGRQSMSE	KRTKQFSDAS	QLDFVKTRKS	KSMDLGSSPS
810	820	830	840	850	860	870	880
RDVGPSLGLK	KSSSLESLQT	AVAEVTLNGD	IPFHRPRPRI	IRGRGCNESF	RAAIDKSYDK	PAVDDDDEGM	ETLEEDTEES
890	900	910	920	930	940	950	960
SRSGRESVST	ASDQPSHSLE	RQMNGNQEKG	DKTDRKKDKT	GKEKKKDRDK	EKDKMKAKKG	MLKGLGDMFR	IQAKTREFRE
970	980	990	1000	1010	1020	1030	1040
RQARERDYAE	IQDFHRTFGC	DDELMYGGVS	SYEGSMALNA	RPQSPREGHM	MDALYAQVKK	PRNSKPSPVD	SNRSTPSNHD
1050	1060	1070	1080	1090	1100	1110	1120
RIQRLRQEFQ	QAKQDEDVED	RRRTYSFEQP	WPNARPATQS	GRHSVSVEVQ	MQRQRQEERE	SSQQAQRQYS	SLPRQSRKNA
1130	1140	1150	1160	1170	1180	1190	1200
SSVSQDSWEQ	NYSPGEGFQS	AKENPRYSSY	QGSRNGYLGG	HGFNARVMLE	TQELLRQEQR	RKEQQMKKQP	PSEGPSNYDS
1210	1220	1230	1240	1250			
YKKVQDPSYA	PPKGPFRQDV	PPSPSQVARL	NRLQTPEKGR	PFYS			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2354	1	711.9476	-118.31	3	59.3	10.7	2	790-810	K.SKSMDLGSSPSRDVGPSLGLK.K	Oxidation: 4

Detailed Protein Report

Protein 339: metastasis-associated in colon cancer protein 1 [Homo sapiens]

Accession:	gi|157502191	**Score:**	27.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	96.6
Database Date:	2015-11-30	**pI:**	6.5
		Sequence Coverage [%]:	3.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLITERKHFR	SGRIAQSMSE	ANLIDMEAGK	LSKSCNITEC	QDPDLLHNWP	DAFTLRGNNA	SKVANPFWNQ	LSASNPFLDD
90	100	110	120	130	140	150	160
ITQLRNNRKR	NNISILKEDP	FLFCREIENG	NSFDSSGDEL	DVHQLLRQTS	SRNSGRSKSV	SELLDILDDT	AHAHQSIHNS
170	180	190	200	210	220	230	240
DQILLHDLEW	LKNDREAYKM	AWLSQRQLAR	SCLDLNTISQ	SPGWAQTQLA	EVTIACKVNH	QGGSVQLPES	DITVHVPQGH
250	260	270	280	290	300	310	320
VAVGEFQEVS	LRAFLDPPHM	LNHDLSCTVS	PLLEIMLGNL	NTMEALLLEM	KIGAEVRKDP	FSQVMTEMVC	LHSLGKEGPF
330	340	350	360	370	380	390	400
KVLSNCYIYK	DTIQVKLIDL	SQVMYLVVAA	QAKALPSPAA	TIWDYIHKTT	SIGIYGPKYI	HPSFTVVLTV	CGHNYMPGQL
410	420	430	440	450	460	470	480
TISDIKKGGK	NISPVVFQLW	GKQSFLLDKP	QDLSISIFSC	DPDFEVKTEG	ERKEIKQKQL	EAGEVVHQQF	LFSLVEHREM
490	500	510	520	530	540	550	560
HLFDFCVQVE	PPNGEPVAQF	SITTPDPTPN	LKRLSNLPGY	LQKKEEIKSA	PLSPKILVKY	PTFQDKTLNF	SNYGVTLKAV
570	580	590	600	610	620	630	640
LRQSKIDYFL	EYFKGDTIAL	LGEGKVKAIG	QSKVKEWYVG	VLRGKIGLVH	CKNVKVISKE	QVMFMSDSVF	TTRNLLEQIV
650	660	670	680	690	700	710	720
LPLKKLTYIY	SVVLTLVSEK	VYDWKVLADV	LGYSHLSLED	FDQIQADKES	EKVSYVIKKL	KEDCHTERNT	RKFLYELIVA
730	740	750	760	770	780	790	800
LLKMDCQELV	ARLIQEAAVL	TSAVKLGKGW	RELAEKLVRL	TKQQMEAYEI	PHRGNTGDVA	VEMMWKPAYD	FLYTWSAHYG
810	820	830	840	850	860		
NNYRDVLQDL	QSALDRMKNP	VTKHWRELTG	VLILVNSLEV	LRVTAFSTSE	EV		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2511	1	841.8162	-157.28	2	61.3	16.7	0	354-368	K.ALPSPAATIWDYIHK.T	

Detailed Protein Report

Protein 340: **kinesin-like protein KIF20B isoform 2 [Homo sapiens]**

Accession:	gi|46049114	**Score:**	27.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	206.0
Database Date:	2015-11-30	**pI:**	5.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.7
		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]					
20	1	1103.5042	-42.73	2	29.9	14.1	2	93-112	K.EPQCILGRLSEKSSGQMAQK.F	Oxidation: 17

Detailed Protein Report

Protein 341: unconventional myosin-XV [Homo sapiens]

Accession:	gi|118402590	**Score:**	27.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	395.0
Database Date:	2015-11-30	**pI:**	9.8
		Sequence Coverage [%]:	0.7
		No. of unique Peptides:	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MAKEEDEEKK	AKKGKKGKKA	PEPEKPKRSL	KGTSRLFMGF	RDRTPKISKK	GQFRSASAFF	WGLHTGPQKT	KRKRKARTVL
90	100	110	120	130	140	150	160
KSTSKLMTQM	RMGKKKRAMK	GKKPSFMVIR	FPGRRGYGRL	RPRARSLSKA	STAINWLTKK	FLLKKAEESG	SEQATVDAWL
170	180	190	200	210	220	230	240
QRSSSRMGSR	KLPFPSGAEI	LRPGGRLRRF	PRSRSIYASG	EPLGFLPFED	EAPFHHSGSR	KSLYGLEGFQ	DLGEYYDYHR
250	260	270	280	290	300	310	320
DGDDYYDRQS	LHRYEEQEPY	LAGLGPYSPA	WPPYGDHYYG	YPPEDPYDYY	HPDYYGGPFD	PGYTYGYGYD	DYEPPYAPPS
330	340	350	360	370	380	390	400
GYSSPYSYHD	GYEGEAHPYG	YYLDPYAPYD	APYPPYDLPY	HTPYDVPYFD	PYGVHYTVPY	AEGVYGGGDE	AIYPPEVPYF
410	420	430	440	450	460	470	480
YPEESASAFV	YPWVPPPIPS	PHNPYAHAMD	DIAELEEPED	AGVERQGTSF	RLPSAAFFEQ	QGMDKPARSK	LSLIRKFRLF
490	500	510	520	530	540	550	560
PRPQVKLFGK	EKLEVPLPPS	LDIPLPLGDA	DEEEDEEELP	PVSAVPYGHP	FWGFLTPRQR	NLQRALSAFG	AHRGLGFGPE
570	580	590	600	610	620	630	640
FGRPVPRPAT	SLARFLKKTL	SEKKPIARLR	GSQKARAGGP	AVREAAYKRF	GYKLAGMDPE	KPGTPIVLRR	AQPRARSSND
650	660	670	680	690	700	710	720
ARRPPAPQPA	PRTLSHWSAL	LSPPVPPRPP	SSGPPPAPPL	SPALSGLPRP	ASPYGSLRRH	PPPWAAPAHV	PPAPQASWWA
730	740	750	760	770	780	790	800
FVEPPAVSPE	VPPDLLAFPG	PRPSFRGSRR	RGAAFGFPGA	SPRASRRRAW	SPLASPQPSL	RSSPGLGYCS	PLAPPSPQLS
810	820	830	840	850	860	870	880
LRTGPFQPPF	LPPARRPRSL	QESPAPRRAA	GRLGPPGSPL	PGSPRPPSPP	LGLCHSPRRS	SLNLPSRLPH	TWRRLSEPPT
890	900	910	920	930	940	950	960
RAVKPQVRLP	FHRPPRAGAW	RAPLEHRESP	REPEDSETPW	TVPPLAPSWD	VDMPPTQRPP	SPWPGGAGSR	RGFSRPPPVP
970	980	990	1000	1010	1020	1030	1040
ENPFLQLLGP	VPSPTLQPED	PAADMTRVFL	GRHHEPGPGQ	LTKSAGPTPE	KPEEEATLGD	PQLPAETKPP	TPAPPKDVTP
1050	1060	1070	1080	1090	1100	1110	1120
PKDITPPKDV	LPEQKTLRPS	LSYPLAACDQ	TRATWPPWHR	WGTLPQAAAP	LAPIRAPEPL	PKGGERRQAA	PGRFAVVMPR
1130	1140	1150	1160	1170	1180	1190	1200
VQKLSSFQRV	GPATLKPQVQ	PIQDPKPRAC	SLRWSCLWLR	ADAYGPWPRV	HTHPQSCHLG	PGAACLSLRG	SWEEVGPPSW
1210	1220	1230	1240	1250	1260	1270	1280
RNKMHSIRNL	PSMRFREQHG	EDGVEDMTQL	EDLQETTVLS	NLKIRFERNL	IYTYIGSILV	SVNPYQMFGI	YGPEQVQQYN
1290	1300	1310	1320	1330	1340	1350	1360
GRALGENPPH	LFAVANLAFA	KMLDAKQNQC	IIISGESGSG	KTEATKLILR	YLAAMNQKRE	VMQQIKILEA	TPLLESFGNA
1370	1380	1390	1400	1410	1420	1430	1440
KTVRNDNSSR	FGKFVEIFLE	GGVISGAITS	QYLLEKSRIV	FQAKNERNYH	IFYELLAGLP	AQLRQAFSLQ	EAETYYYLNQ
1450	1460	1470	1480	1490	1500	1510	1520
GGNCEIAGKS	DADDFRRLLA	AMEVLGFSSE	DQDSIFRILA	SILHLGNVYF	EKYETDAQEV	ASVVSAREIQ	AVAELLQISP
1530	1540	1550	1560	1570	1580	1590	1600
EGLQKAITFK	VTETMREKIF	TPLTVESAVD	ARDAIAKVLY	ALLFSWLITR	VNALVSPRQD	TLSIAILDIY	GFEDLSFNSF
1610	1620	1630	1640	1650	1660	1670	1680
EQLCINYANE	NLQYLFNKIV	FQEEQEEYIR	EQIDWQEITF	ADNQPCINLI	SLKPYGILRI	LDDQCCFPQA	TDHTFLQKCH
1690	1700	1710	1720	1730	1740	1750	1760
YHHGANPLYS	KPKMPLPEFT	IKHYAGKVTY	QVHKFLDKNH	DQVRQDVLDL	FVRSRTRVVA	HLFSSHAPQA	APQRLGKSSS
1770	1780	1790	1800	1810	1820	1830	1840
VTRLYKAHTV	AAKFQQSLLD	LVEKMERCNP	LFMRCLKPNH	KKEPGLFEPD	VVMAQLRYSG	VLETVRIRKE	GFPVRLPFQG
1850	1860	1870	1880	1890	1900	1910	1920
FIDRYCCLVA	LKHDLPANGD	MCVSVLSRLC	KVMPNMYRVG	VSKLFLKEHL	YQLLESMREH	VLNLAALTLQ	RCLRGFFIKR
1930	1940	1950	1960	1970	1980	1990	2000
RFRSLRHKII	LLQSRARGYL	ARQRYQQMRR	SLVKFRSLVH	AYVSRRRYLK	LRAEWRCQVE	GALLWEQEEL	SKREVVAVGH
2010	2020	2030	2040	2050	2060	2070	2080
LEVPAELAGL	LQAVAGLGLA	QVPQVAPVRT	PRLQAEPRVT	LPLDINNYPM	AKFVQCHFKE	PAFGMLTVPL	RTPLTQLPAE
2090	2100	2110	2120	2130	2140	2150	2160
HHAEAVSIFK	LILRFMGDPH	LHGARENIFG	NYIVQKGLAV	PELRDEILAQ	LANQVWHNHN	AHNAERGWLL	LAACLSGFAP
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
2655	1	673.3551	-22.70	2	64.3	13.5	2	597-609	R.AGGPAVREAAYKR.F	

Detailed Protein Report

Protein 342: kinesin heavy chain isoform 5A [Homo sapiens]

Accession:	gi|45446749	**Score:**	27.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	117.3
Database Date:	2015-11-30	**pI:**	5.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.6
		No. of unique Peptides:	2

Quantitation

MD:MU **Median:** 0.75 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MAETNNECSI	KVLCRFRPLN	QAEILRGDKF	IPIFQGDDSV	VIGGKPYVFD	RVFPPNTTQE	QVYHACAMQI	VKDVLAGYNG
90	100	110	120	130	140	150	160
TIFAYGQTSS	GKTHTMEGKL	HDPQLMGIIP	RIARDIFNHI	YSMDENLEFH	IKVSYFEIYL	DKIRDLLDVT	KTNLSVHEDK
170	180	190	200	210	220	230	240
NRVPFVKGCT	ERFVSSPEEI	LDVIDEGKSN	RHVAVTNMNE	HSSRSHSIFL	INIKQENMET	EQKLSGKLYL	VDLAGSEKVS
250	260	270	280	290	300	310	320
KTGAEGAVLD	EAKNINKSLS	ALGNVISALA	EGTKSYVPYR	DSKMTRILQD	SLGGNCRTTM	FICCSPSSYN	DAETKSTLMF
330	340	350	360	370	380	390	400
GQRAKTIKNT	ASVNLELTAE	QWKKKYEKEK	EKTKAQKETI	AKLEAELSRW	RNGENVPETE	RLAGEEAALG	AELCEETPVN
410	420	430	440	450	460	470	480
DNSSIVVRIA	PEERQKYEEE	IRRLYKQLDD	KDDEINQQSQ	LIEKLKQQML	DQEELLVSTR	GDNEKVQREL	SHLQSENDAA
490	500	510	520	530	540	550	560
KDEVKEVLQA	LEELAVNYDQ	KSQEVEEKSQ	QNQLLVDELS	QKVATMLSLE	SELQRLQEVS	GHQRKRIAEV	LNGLMKDLSE
570	580	590	600	610	620	630	640
FSVIVGNGEI	KLPVEISGAI	EEEFTVARLY	ISKIKSEVKS	VVKRCRQLEN	LQVECHRKME	VTGRELSSCQ	LLISQHEAKI
650	660	670	680	690	700	710	720
RSLTEYMQSV	ELKKRHLEES	YDSLSDELAK	LQAQETVHEV	ALKDKEPDTQ	DADEVKKALE	LQMESHREAH	HRQLARLRDE
730	740	750	760	770	780	790	800
INEKQKTIDE	LKDLNQKLQL	ELEKLQADYE	KLKSEEHEKS	TKLQELTFLY	ERHEQSKQDL	KGLEETVARE	LQTLHNLRKL
810	820	830	840	850	860	870	880
FVQDVTTRVK	KSAEMEPEDS	GGIHSQKQKI	SFLENNLEQL	TKVHKQLVRD	NADLRCELPK	LEKRLRATAE	RVKALEGALK
890	900	910	920	930	940	950	960
EAKEGAMKDK	RRYQQEVDRI	KEAVRYKSSG	KRGHSAQIAK	PVRPGHYPAS	SPTNPYGTRS	PECISYTNSL	FQNYQNLYLQ
970	980	990	1000	1010	1020	1030	1040
ATPSSTSDMY	FANSCTSSGA	TSSGGPLASY	QKANMDNGNA	TDINDNRSDL	PCGYEAEDQA	KLFPLHQETA	AS

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2155	1	713.2696	-111.00	2	57.1	15.2	0	607-617	R.QLENLQVECHR.K	Carbamidomethyl: 9	
1747	1	851.2332	-164.00	2	51.8	12.2	0	812-827	K.SAEMEPEDSGGIHSQK.Q		MD:MU 0.75

Detailed Protein Report

Protein 343: transmembrane protease serine 12 precursor [Homo sapiens]

Accession:	gi|32698940	**Score:**	27.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	38.6
Database Date:	2015-11-30	**pI:**	10.0
		Sequence Coverage [%]:	8.6
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MRLGLLSVAL	LFVGSSHLYS	DHYSPSGRHR	LGPSPEPAAS	SQQAEAVRKR	LRRRREGGAH	AKDCGTAPLK	DVLQGSRIIG
90	100	110	120	130	140	150	160
GTEAQAGAWP	WVVSLQIKYG	RVLVHVCGGT	LVRERWVLTA	AHCTKDASDP	LMWTAVIGTN	NIHGRYPHTK	KIKIKAIIIH
170	180	190	200	210	220	230	240
PNFILESYVN	DIALFHLKKA	VRYNDYIQPI	CLPFDVFQIL	DGNTKCFISG	WGRTKEEGNA	TNILQDAEVH	YISREMCNSE
250	260	270	280	290	300	310	320
RSYGGIIPNT	SFCAGDEDGA	FDTCRGDSGG	PLMCYLPEYK	RFFVMGITSY	GHGCGRRGFP	GVYIGPSFYQ	KWLTEHFFHA
330	340	350					
STQGILTINI	LRGQILIALC	FVILLATT					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1840	3	897.8543	-109.51	2	52.9	14.9	0	31-48	R.LGPSPEPAASSQQAEAVR.K	
2601	1	626.8465	-26.97	2	63.1	12.5	0	102-113	R.VLVHVCGGTLVR.E	

Detailed Protein Report

Protein 344: PREDICTED: rab11 family-interacting protein 4 isoform X1 [Homo sapiens]

Accession: gi|530411171
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 27.4
MW [kDa]: 67.7
pI: 4.8
Sequence Coverage [%]: 5.1
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MSPQLDTKSP	SAHAGLPATG	GGGAAPSTGA	QKCERQRRGR	DCSCASGLPA	ASPRAADPRP	LASAPLPGSG	PRMRTPPALG
90	100	110	120	130	140	150	160
SQGSEVTGPT	FADGELIPRE	PGFFPEDEEE	AMTLAPPEGP	QELYTDSPME	STQSLEGSVG	SPAEKDGGLG	GLFLPEDKSL
170	180	190	200	210	220	230	240
VHTPSMTTSD	LSTHSTTSLI	SNEEQFEDYG	EGDDVDCAPS	SPCPDDETRT	NVYSDLGSSV	SSSAGQTPRK	MRHVYNSELL
250	260	270	280	290	300	310	320
DVYCSQCCKK	INLLNDLEAR	LKNLKANSPN	RKISSTAFGR	QLMHSSNFSS	SNGSTEDLFR	DSIDSCDNDI	TEKVSFLEKK
330	340	350	360	370	380	390	400
VTELENDSLT	NGDLKSKLKQ	ENTQLVHRVH	ELEEMVKDQE	TTAEQALEEE	ARRHREAYGK	LEREKATEVE	LLNARVQQLE
410	420	430	440	450	460	470	480
EENTELRTTV	TRLKSQTEKL	DEERQRMSDR	LEDTSLRLKD	EMDLYKRMMD	KLRQNRLEFQ	KEREATQELI	EDLRKELEHL
490	500	510	520	530	540	550	560
QMYKLDCERP	GRGRSASSGL	GEFNARAREV	ELEHEVKRLK	QENYKLRDQN	DDLNGQILSL	SLYEAKNLFA	AQTKAQSLAA
570	580	590	600	610			
EIDTASRDEL	MEALKEQEEI	NFRLRQYMDK	IILAILDHNP	SILEIKH			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1981	1	696.2626	-62.02	2	54.7	16.3	0	41-54	R.DCSCASGLPAASPR.A	Carbamidomethyl: 2

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Detailed Protein Report

Protein 345: PREDICTED: suppressor of tumorigenicity 7 protein-like isoform X10 [Homo sapiens]

Accession:	gi|530362849	**Score:**	27.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	35.9
Database Date:	2015-11-30	**pI:**	9.9
Modification(s):	Oxidation	**Sequence Coverage [%]:**	5.6
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MADRGGVGEA	AAVGASPASV	PGLNPTLGWR	ERLRAGLAGT	GASLWFVAGL	GLLYALRIPL	RLCENLAAVT	VFLNSLTPKF
90	100	110	120	130	140	150	160
YVALTGTSSL	ISGLIFIFEW	WYFHKHGTSF	IEQVSVSHLQ	PLMGGTESSI	SEPGSPSRNR	ENETSRQNLS	ECKVWRNPLN
170	180	190	200	210	220	230	240
LFRGAEYRRY	TWVTGKEPLT	YYDMNLSAQD	HQTFFTCDTD	FLRPSDTVMQ	KAWRERNPPA	RIKAAYQALE	LNNDCATAYV
250	260	270	280	290	300	310	320
LLAEEEATTI	VDAERLFKQA	LKAGETIYRQ	SQQCQHQSPQ	HEAQLRRDTN	VLVYIKRRLA	MCARKLGRIR	EAVKIMRDI

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2033	1	625.2626	-137.48	2	55.3	14.2	1	259-269	K.QALKAGETIYR.Q	
2273	2	836.1691	-303.52	1	58.7	13.2	1	298-304	R.RLAMCAR.K	Oxidation: 4

Detailed Protein Report

Protein 346: PREDICTED: homeobox protein Hox-A6 isoform X1 [Homo sapiens]

Accession:	gi|578813472	**Score:**	27.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	23.6
Database Date:	2015-11-30	**pI:**	12.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	13.7
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MWMRTVNMNF	FIISLARIEP	HSFAPLRPAC	FGALPSSRAR	LCFVRRWRAK	GSPGQARPGG	SRWRLGALRS	RRRGSSFATR
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
NLANFLRPLA	PGKRTILLSG	CPSDSCQRGR	SFWEPPSEGA	VYGSHGRRGR	QTYTRYQTLE	LEKEFHFNRY	LTRRRRIEIA
170	**180**	**190**	**200**	**210**			
NALCLTERQI	KIWFQNRRMK	WKKENKLINS	TQPSGEDSEA	KAGE			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2501	1	834.4079	-45.05	2	61.7	10.3	2	47-62	R.WRAKGSPGQARPGGSR.W	
2519	1	701.8340	-53.57	2	61.5	17.0	0	157-168	R.IEIANALCLTER.Q	Carbamidomethyl: 8

Detailed Protein Report

Protein 347: **PREDICTED: phosphoenolpyruvate carboxykinase [GTP], mitochondrial isoform X2 [Homo sapiens]**

Accession:	gi|578825848	**Score:**	27.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	55.9
Database Date:	2015-11-30	**pI:**	6.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	7.5
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MSPADFQRAV	DERFPGCMQG	RTMYVLPFSM	GPVGSPLSRI	GVQLTDSAYV	VASMRIMTRL	GTPVLQALGD	GDFVKCLHSV
90	100	110	120	130	140	150	160
GQPLTGQGEP	VSQWPCNPEK	TLIGHVPDQR	EIISFGSGYG	GNSLLGKKCF	ALRIASRLAR	DEGWLAEHML	ILGITSPAGK
170	180	190	200	210	220	230	240
KRYVAAAFPS	ACGKTNLAMM	RPALPGWKVE	CVGDDIAWMR	FDSEGRLRAI	NPENGFFGVA	PGTSATTNPN	AMATIQSNTI
250	260	270	280	290	300	310	320
FTNVAETSDG	GVYWEGIDQP	LPPGVTVTSW	LGKPWKPGDK	EPCAHPNSRF	CAPARQCPIM	DPAWEAPEGV	PIDAIIFGGR
330	340	350	360	370	380	390	400
RPKGVPLVYE	AFNWRHGVFV	GSAMRSESTA	AAEHKGKIIM	HDPFAMRPFF	GYNFGHYLEH	WLSMEGRKGA	QLPRIFHVNW
410	420	430	440	450	460	470	480
FRRDEAGHFL	WPGFGENARV	LDWICRRLEG	EDSARETPIG	LVPKEGALDL	SGLRAIDTTQ	LFSLPKDFWE	QEVRDIRSYL
490	500	510					
TEQVNQDLPK	EVLAELEALE	RRVHKM					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2104	1	1044.4007	-95.08	2	56.2	12.0	1	336-355	R.HGVFVGSAMRSESTAAAEHK.G	Oxidation: 9
972	1	984.1646	135.28	2	41.7	15.3	2	427-444	R.RLEGEDSARETPIGLVPK.E	

Protein 348: DNA damage-inducible transcript 4-like protein [Homo sapiens]

Accession:	gi|21687001	**Score:**	27.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	21.7
Database Date:	2015-11-30	**pI:**	9.0
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	13.0
		No. of unique Peptides:	2

Alias proteins:

Accession	Name	Description
gi|530377132	refseq_human (refseq_human_20140103.fasta)	PREDICTED: DNA damage-inducible transcript 4-like protein isoform X1 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MVATGSLSSK NPASISELLD CGYHPESLLS DFDYWDYVVP EPNLNEVIFE ESTCQNLVKM LENCLSKSKQ TKLGCSKVLV
        90        100        110        120        130        140        150        160
PEKLTQRIAQ DVLRLSSTEP CGLRGCVMHV NLEIENVCKK LDRIVCDSSV VPTFELTLVF KQENCSWTSF RDFFFSRGRF
       170        180        190        200
SSGFRRTLIL SSGFRLVKKK LYSLIGTTVI EGS
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1701	1	606.5258	-149.20	3	51.2	15.7	0	105-119	R.GCVMHVNLEIENVCK.K	Carbamidomethyl: 2, 14; Oxidation: 4
2065	1	575.2075	-231.33	2	55.7	11.6	1	166-175	R.RTLILSSGFR.L	

Detailed Protein Report

Protein 349:	**A disintegrin and metalloproteinase with thrombospondin motifs 20 preproprotein [Homo sapiens]**		
Accession:	gi|124430557	**Score:**	27.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	214.6
Database Date:	2015-11-30	**pI:**	7.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.2
		No. of unique Peptides:	1

Quantitation

MD:MU	**Median:**	0.59	**CV:**	0.00 %	**No. of 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	Ratios
1189	1	599.1520	-198.95	2	44.5	12.7	1	1541-1550	R.LNCSTSCERK.D	Carbamidomethyl: 7	MD:MU 0.59

Detailed Protein Report

Protein 350: PREDICTED: uncharacterized protein LOC101930265 [Homo sapiens]

Accession:	gi|530355909	**Score:**	27.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	38.6
Database Date:	2015-11-30	**pI:**	10.5
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	7.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGAQVRTWKP	RCLHGNPGAC	METRVRAWKP	GCVHGNPGVC	METQECAWKL	RCVHGSPGAW	METQMCAWEP	RCVDGNPGVC
90	100	110	120	130	140	150	160
METQVCAWEP	RCVRGNSGAC	MEPRCVDGNP	GVCMGAQVCG	RKPRCVHGSP	GVCMETRVCA	WEPGCVHGSP	GVCIKTQVCA
170	180	190	200	210	220	230	240
WEPRCVHGSP	GVCMETQVCA	WEPRCVHGSP	GVCMETQVCA	WEPRCVHGSP	GVCMETQVCA	WEPRCVHGNP	GVCMGAQVCV
250	260	270	280	290	300	310	320
WKTSCVHGNP	GVCMGAQVCV	WKTSCVHGNP	GVCMEAQVCA	WKTRCVHGSP	VCAWEPRRVH	GKPGVCIGAQ	VCAWEPRCVD
330	340	350	360	370			
GNPGVCTGAQ	VCAWEPGCVH	ESLGVCMGTR	VCAWKPVAAL	L			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
883	1	759.6775	-182.21	2	40.5	10.1	0	12-24	R.CLHGNPGACMETR.V	Carbamidomethyl: 1, 9; Oxidation: 10

Detailed Protein Report

Protein 351: **PREDICTED: coiled-coil domain-containing protein 108 isoform X2 [Homo sapiens]**

Accession:	gi|578804012	**Score:**	27.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	87.3
Database Date:	2015-11-30	**pI:**	9.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDSLCVSSAY	ISLISSERPV	HNWRGKSVQK	KQAESKSQIK	LHTQSAPFGL	CPKDMMLTQA	PSSVVRSRNS	RNHTVNSGGS
90	100	110	120	130	140	150	160
CLSASTVAIP	AINDSSAAMS	ACSTISAQPA	SSMDTQMHSP	KKQERVNKRV	IWGIEVAEEL	HWKGWELGKE	TTRNLVLKNR
170	180	190	200	210	220	230	240
SLKLQKMKYR	PPKTKFFFTV	IPQPIFLSPG	ITLTLPIVFR	PLEAKEYMDQ	LWFEKAEGMF	CVGLRATLPC	HRLICRPPSL
250	260	270	280	290	300	310	320
QLPMCAVGDT	TEAFFCLDNV	GDLPTFFTWE	FSSPFQMLPA	TGLLEPGQAS	QIKVTFQPLT	AVIYEVQATC	WYGAGSRQRS
330	340	350	360	370	380	390	400
SIQLQAVAKC	AQLLVSIKHK	CPEDQDAEGF	QKLLYFGSVA	VGCTSERQIR	LHNPSAVNAP	FRIEISPDEL	AEDQAFSCPT
410	420	430	440	450	460	470	480
AHGIVLPGEK	KCVSVFFHPK	TLDTRTVDYC	SIMPSGCASK	TLLKVVGFCR	GPAVSLQHYC	VNFSWVNLGE	RSEQPLWIEN
490	500	510	520	530	540	550	560
QSDCTAHFQF	AIDCLESVFT	IRPAFGTLVG	KARMTLHCAF	QPTHPIICFR	RVACLIHHQD	PLFLDLMGTC	HSDSTKPAIL
570	580	590	600	610	620	630	640
KPQHLTWYRT	HLARGLTLYP	PDILDAMLKE	KKLAQDQNGA	LMIPIQDLED	MPAPQYPYIP	PMTEFFFDGT	SDITIFPPPI
650	660	670	680	690	700	710	720
SVEPVEVDFG	ACPGPEAPNP	VPLCLMNHTK	GKIMVVWTRR	SDCPFWVTPE	SCDVPPLKSM	AMRLHFQPPH	PNCLYTVELE
730	740	750	760	770	780	790	
AFAIYKVCAR	NEREECGVSA	RSLSGLVGWQ	EVTEGSFRLH	PLRARLSLGW	TVTPMSLSPP	KLLA	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
640	1	712.1825	-155.63	2	37.3	10.0	0	341-352	K.CPEDQDAEGFQK.L	Carbamidomethyl: 1

Detailed Protein Report

Protein 352: **ankyrin repeat and BTB/POZ domain-containing protein BTBD11 isoform a [Homo sapiens]**

Accession:	gi|65786661	**Score:**	27.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	120.8
Database Date:	2015-11-30	**pI:**	6.4
		Sequence Coverage [%]:	0.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MARRGKKPVV	RTLEDLTLDS	GYGGAADSVR	SSNLSLCCSD	SHPASPYGGS	CWPPLADSMH	SRHNSFDTVN	TALVEDSEGL
90	100	110	120	130	140	150	160
DCAGQHCSRL	LPDLDEVPWT	LQELEALLLR	SRDPRAGPAV	PGGLPKDALA	KLSTLVSRAL	VRIAKEAQRL	SLRFAKCTKY
170	180	190	200	210	220	230	240
EIQSAMEIVL	SWGLAAHCTA	AALAALSLYN	MSSAGGDRLG	RGKSARCGLT	FSVGRVYRWM	VDSRVALRIH	EHAAIYLTAC
250	260	270	280	290	300	310	320
MESLFRDIYS	RVVASGVPRS	CSGPGSGSGS	GPGPSSGPGA	APAADKEREA	PGGGAASGGA	CSAASSASGG	SSCCAPPAAA
330	340	350	360	370	380	390	400
AAAVPPAAAA	NHHHHHHHAL	HEAPKFTVET	LEHTVNNDSE	IWGLLQPYQH	LICGKNASGV	LCLPDSLNLH	RDPQRSNKPG
410	420	430	440	450	460	470	480
ELPMFSQSEL	RTIEQSLLAT	RVGSIAELSD	LVSRAMHHLQ	PLNAKHHGNG	TPLHHKQGAL	YWEPEALYTL	CYFMHCPQME
490	500	510	520	530	540	550	560
WENPNVEPSK	VNLQVERPFL	VLPPLMEWIR	VAVAHAGHRR	SFSMDSDDVR	QAARLLLPGV	DCEPRQLRAD	DCFCASRKLD
570	580	590	600	610	620	630	640
AVAIEAKFKQ	DLGFRMLNCG	RTDLVKQAVS	LLGPDGINTM	SEQGMTPLMY	ACVRGDEAMV	QMLLDAGADL	NVEVVSTPHK
650	660	670	680	690	700	710	720
YPSVHPETRH	WTALTFAVLH	GHIPVVQLLL	DAGAKVEGSV	EHGEENYSET	PLQLAAAVGN	FELVSLLLER	GADPLIGTMY
730	740	750	760	770	780	790	800
RNGISTTPQG	DMNSFSQAAA	HGHRNVFRKL	LAQPEKEKSD	ILSLEEILAE	GTDLAETAPP	PLCASRNSKA	KLRALREAMY
810	820	830	840	850	860	870	880
HSAEHGYVDV	TIDIRSIGVP	WTLHTWLESL	RIAFQQHRRP	LIQCLLKEFK	TIQEEEYTEE	LVTQGLPLMF	EILKASKNEV
890	900	910	920	930	940	950	960
ISQQLCVIFT	HCYGPYPIPK	LTEIKRKQTS	RLDPHFLNNK	EMSDVTFLVE	GRPFYAHKVL	LFTASPRFKA	LLSSKPTNDG
970	980	990	1000	1010	1020	1030	1040
TCIEIGYVKY	SIFQLVMQYL	YYGGPESLLI	KNNEIMELLS	AAKFFQLEAL	QRHCEIICAK	SINTDNCVDI	YNHAKFLGVT
1050	1060	1070	1080	1090	1100	1110	
ELSAYCEGYF	LKNMMVLIEN	EAFKQLLYDK	NGEGTGQDVL	QDLQRTLAIR	IQSIHLSSSK	GSVV	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1645	1	583.7942	-77.28	2	50.5	27.0	2	150-159	R.LSLRFAKCTK.Y	

Detailed Protein Report

Protein 353: ankyrin repeat and SOCS box protein 16 [Homo sapiens]

Accession:	gi|24586688	**Score:**	27.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	49.6
Database Date:	2015-11-30	**pI:**	9.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.6
		No. of unique Peptides:	2

Quantitation

MD:MU **Median:** 0.98 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MARETFPFTS	SMLRSLRLQQ	EWLEWEDRRR	AAAQQCRSRR	CPSSPRARLT	RPHRSCRDPA	VHQALFSGNL	QQVQALFQDE
90	100	110	120	130	140	150	160
EAANMIVETV	SNQLAWSAEQ	GFWVLTPKTK	QTAPLAIATA	RGYTDCARHL	IRQGAELDAR	VGGRAALHEA	CARAQFDCVR
170	180	190	200	210	220	230	240
LLLTFGAKAN	VLTEEGTTPL	HLCTIPESLQ	CAKLLLEAGA	TVNLAAGESQ	ETPLHVAAAR	GLEQHVALYL	EHGADVGLRT
250	260	270	280	290	300	310	320
SQGETALNTA	CAGAEGPGSC	RRHQAAARRL	LEAGADARAA	GRKRHTPLHN	ACANGCGGLA	ELLLRYGARA	EVPNGAGHTP
330	340	350	360	370	380	390	400
MDCALQAVQD	SPNWEPEVLF	AALLDYGAQP	VRPEMLKHCA	NFPRALEVLL	NAYPCVPSCE	TWVEAVLPEL	WKEHEAFYSS
410	420	430	440	450	460		
ALCMVNQPRQ	LQHLARLAVR	ARLGSRCRQG	ATRLPLPPLL	RDYLLLRVEG	CIQ		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
660	1	459.6081	-321.96	2	37.8	16.3	2	421-428	R.ARLGSRCR.Q		MD:MU 0.98
1199	1	874.6540	165.48	2	44.7	10.7	2	427-441	R.CRQGATRLPLPPLLR.D	Carbamidomethyl: 1	

Detailed Protein Report

Protein 354: **PREDICTED: ranBP2-like and GRIP domain-containing protein 4 isoform X1 [Homo sapiens]**

Accession:	gi|578804143	**Score:**	27.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	197.0
Database Date:	2015-11-30	**pI:**	5.9
		Sequence Coverage [%]:	1.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSCSKAYGER	YVASVQGSAP	SPRKKSTRGF	YFAKLYYEAK	EYDLAKKYIC	TYINVREMDP	RAHRFLGLLY	ELEENTEKAV
90	100	110	120	130	140	150	160
ECYRRSVELN	PTQKDLVLKI	AELLCKNDVT	DGRAKYWVER	AAKLFPGSPA	IYKLKEQLLD	CEGEDGWNKL	FDLIQSELYV
170	180	190	200	210	220	230	240
RPDDVHVNIR	LVELYRSTKR	LKDAVARCHE	AERNIALRSS	LEWNSCVVQT	LKEYLESLQC	LESDKSDWRA	TNTDLLLAYA
250	260	270	280	290	300	310	320
NLMLLTLSTR	DVQESRELLE	SFDSALQSAK	SSLGGNDELS	ATFLEMKGHF	YMHAGSLLLK	MGQHGNNVQW	RALSELAALC
330	340	350	360	370	380	390	400
YLIAFQVPRP	KIKLIKGEAG	QNLLEMMACD	RLSQSGHMLL	NLSRGKQDFL	KVVVETFANK	SGQSALYDAL	FSSQSPKDTS
410	420	430	440	450	460	470	480
FLGSDDIGNI	DVQEPELEDL	ARYDVGAIRA	HNGSLQHLTW	LGLQWNSLPA	LPGIRKWLKQ	LFHHLPQETS	RLETNAPESI
490	500	510	520	530	540	550	560
CILDLEVFLL	GVVYTSHLQL	KEKCNSHHSS	YQPLCLPLPV	CKQLCTERQK	SWWDAVCTLI	HRKAVPGNSA	KLRLLVQHEI
570	580	590	600	610	620	630	640
NTLRAQEKHG	LQPALLVHWA	KCLQKMGSGL	NSFYDQREYI	GRSVHYWKKV	LPLLKIIKKK	NSIPEPIDPL	FKHFHSVDIQ
650	660	670	680	690	700	710	720
ASEIVEYEED	AHVTFAILDA	VNGNIEDAMT	AFESIKSVVS	YWNLALIFHR	KAEDIANDAL	SPEEQEECKN	YLRKTRGYLI
730	740	750	760	770	780	790	800
KILDDSDSNL	SVVKKLPVPL	ESVKEMLKSV	MQELENYSEG	DPLYKNGSLR	NADSEIKHST	PSPTKYSLSP	SKSYKYSPKT
810	820	830	840	850	860	870	880
PPRWAEDQNS	LLKMIRQEVK	AIKEEMQELK	LNSSKSASHH	RWPTENYGPD	SVPDGYQGSQ	TFHGAPLTVA	TTGPSVYYSQ
890	900	910	920	930	940	950	960
SPAYNSQYLL	RPAANVTPTK	GSSNTEFKST	KEGFSIPVSA	DGFKFGISEP	GNQEKESEKP	LENDTGFQAQ	DISGQKNGRG
970	980	990	1000	1010	1020	1030	1040
VIFGQTSSTF	TFADVAKSTS	GEGFQFGKKD	PNFKGFSGAG	EKLFSSQCGK	MANKANTSGD	FEKDDDAYKT	EDSDDIHFEP
1050	1060	1070	1080	1090	1100	1110	1120
VVQMPEKVEL	VIGEEGEKVL	YSQGVKLFRF	DAEVRQWKER	GLGNLKILKN	EVNGKPRMLM	RREQVLKVCA	NHWITTTMNL
1130	1140	1150	1160	1170	1180	1190	1200
KPLSGSDRAW	MWSASDFSDG	DAKLERLAAK	FKTPELAEEF	KQKFEECQQL	LLDIPLQTPH	KLVDTGRAAK	LIQRAEEMKS
1210	1220	1230	1240	1250	1260	1270	1280
GLKDFKTFLT	NDQTKVTEEE	NKGSGTGAAG	ASDTTIKPNP	ENTGPTLEWD	NCDLREDALD	DSVSSSSVHA	SPLASSPVRK
1290	1300	1310	1320	1330	1340	1350	1360
NLFHFGESTT	GSNFSFKSAL	SPSKSPAKLN	QSGTSVGTDE	ESDVTQEEER	DGQYFEPVVP	LPDLVEVSSG	EENEKVVFSH
1370	1380	1390	1400	1410	1420	1430	1440
RAELYRYDKD	VGQWKERGIG	DIKILQNYDN	KQVRIVMRRD	QVLKLCANHT	ITPDMSLQNM	KGTERVWVWT	ACDFADGERK
1450	1460	1470	1480	1490	1500	1510	1520
VEHLAVRFKL	QDVADSFKKI	FDEAKTAQEK	DSLITPHVSR	SSTPRESPCG	KIAVAVLEET	TRERTDVIQG	DDVADAASEV
1530	1540	1550	1560	1570	1580	1590	1600
EVSSTSETTT	KAVVSPPKFV	FGSESVKRIF	SSEKSKPFAF	GNSSATGSLF	GFSFNASLKS	NNSETSSVAQ	SGSESKVEPK
1610	1620	1630	1640	1650	1660	1670	1680
KCELSKNSDI	EQSSDSKVKN	LSASFPMEES	SINYTFKTPE	KEPPLWHAEF	TKEELVQKLS	STTKSADHLN	GLLREAEATS
1690	1700	1710	1720	1730	1740	1750	1760
AVLMEQIKLL	KSEIRRLERN	QEQEESAANV	EHLKNVLLQF	IFLKPGSERE	RLLPVINTML	QLSPEEKGKL	AAVAQGG

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
2527	1	863.4144	10.20	2	62.0	14.8	0	1700-1714	R.NQEQEESAANVEHLK.N	

Detailed Protein Report

Protein 355: **PREDICTED: ryanodine receptor 2 isoform X7 [Homo sapiens]**

Accession:	gi|578802309	**Score:**	27.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	557.1
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
MADGGEGEDE	IQFLRTDDEV	VLQCTATIHK	EQQKLCLAAE	GFGNRLCFLE	STSNSKNVPP	DLSICTFVLE	QSLSVRALQE
90	100	110	120	130	140	150	160
MLANTVEKSE	GQVDVEKWKF	MMKTAQGGGH	RTLLYGHAIL	LRHSYSGMYL	CCLSTSRSST	DKLAFDVGLQ	EDTTGEACWW
170	180	190	200	210	220	230	240
TIHPASKQRS	EGEKVRVGDD	LILVSVSSER	YLHLSYGNGS	LHVDAAFQQT	LWSVAPISSG	SEAAQGYLIG	GDVLRLLHGH
250	260	270	280	290	300	310	320
MDECLTVPSG	EHGEEQRRTV	HYEGGAVSVH	ARSLWRLETL	RVAWSGSHIR	WGQPFRLRHV	TTGKYLSLME	DKNLLLMDKE
330	340	350	360	370	380	390	400
KADVKSTAFT	FRSSKEKLDV	GVRKEVDGMG	TSEIKYGDSV	CYIQHVDTGL	WLTYQSVDVK	SVRMGSIQRK	AIMHHEGHMD
410	420	430	440	450	460	470	480
DGISLSRSQH	EESRTARVIR	STVFLFNRFI	RGLDALSKKA	KASTVDLPIE	SVSLSLQDLI	GYFHPPDEHL	EHEDKQNRLR
490	500	510	520	530	540	550	560
ALKNRQNLFQ	EEGMINLVLE	CIDRLHVYSS	AAHFADVAGR	EAGESWKSIL	NSLYELLAAL	IRGNRKNCAQ	FSGSLDWLIS
570	580	590	600	610	620	630	640
RLERLEASSG	ILEVLHCVLV	ESPEALNIIK	EGHIKSIISL	LDKHGRNHKV	LDVLCSLCVC	HGVAVRSNQH	LICDNLLPGR
650	660	670	680	690	700	710	720
DLLLQTRLVN	HVSSMRPNIF	LGVSEGSAQY	KKWYYELMVD	HTEPFVTAEA	THLRVGWAST	EGYSPYPGGG	EEWGGNGVGD
730	740	750	760	770	780	790	800
DLFSYGFDGL	HLWSGCIART	VSSPNQHLLR	TDDVISCCLD	LSAPSISFRI	NGQPVQGMFE	NFNIDGLFFP	VVSFSAGIKV
810	820	830	840	850	860	870	880
RFLLGGRHGE	FKFLPPPGYA	PCYEAVLPKE	KLKVEHSREY	KQERTYTRDL	LGPTVSLTQA	AFTPIPVDTS	QIVLPPHLER
890	900	910	920	930	940	950	960
IREKLAENIH	ELWVMNKIEL	GWQYGPVRDD	NKRQHPCLVE	FSKLPEQERN	YNLQMSLETL	KTLLALGCHV	GISDEHAEDK
970	980	990	1000	1010	1020	1030	1040
VKKMKLPKNY	QLTSGYKPAP	MDLSFIKLTP	SQEAMVDKLA	ENAHNVWARD	RIRQGWTYGI	QQDVKNRRNP	RLVPYTLLDD
1050	1060	1070	1080	1090	1100	1110	1120
RTKKSNKDSL	REAVRTLLGY	GYNLEAPDQD	HAARAEVCSG	TGERFRIFRA	EKTYAVKAGR	WYFEFETVTA	GDMRVGWSRP
1130	1140	1150	1160	1170	1180	1190	1200
GCQPDQELGS	DERAFAFDGF	KAQRWHQGNE	HYGRSWQAGD	VVGCMVDMNE	HTMMFTLNGE	ILLDDSGSEL	AFKDFDVGDG
1210	1220	1230	1240	1250	1260	1270	1280
FIPVCSLGVA	QVGRMNFGKD	VSTLKYFTIC	GLQEGYEPFA	VNTNRDITMW	LSKRLPQFLQ	VPSNHEHIEV	TRIDGTIDSS
1290	1300	1310	1320	1330	1340	1350	1360
PCLKVTQKSF	GSQNSNTDIM	FYRLSMPIEC	AEVFSKTVAG	GLPGAGLFGP	KNDLEDYDAD	SDFEVLMKTA	HGHLVPDRVD
1370	1380	1390	1400	1410	1420	1430	1440
KDKEATKPEF	NNHKDYAQEK	PSRLKQRFLL	RRTKPDYSTS	HSARLTEDVL	ADDRDDYDFL	MQTSTYYYSV	RIFPGQEPAN
1450	1460	1470	1480	1490	1500	1510	1520
VWVGWITSDF	HQYDTGFDLD	RVRTVTVTLG	DEKGKVHESF	AIDSLCGFGI	KRSNCYMVCA	GESMSPGQGR	NNNGLEIGCV
1530	1540	1550	1560	1570	1580	1590	1600
VDAASGLLTF	IANGKELSTY	YQVEPSTKLF	PAVFAQATSP	NVFQFELGRI	KNVMPLSAGL	FKSEHKNPVP	QCPPRLHVQF
1610	1620	1630	1640	1650	1660	1670	1680
LSHVLWSRMP	NQFLKVDVSR	ISERQGWLVQ	CLDPLQFMSL	HIPEENRSVD	ILELTEQEEL	LKFHYHTLRL	YSAVCALGNH
1690	1700	1710	1720	1730	1740	1750	1760
RVAHALCSHV	DEPQLLYAIE	NKYMPGLLRA	GYYDLLIDIH	LSSYATARLM	MNNEYIVPMT	EETKSITLFP	DENKKHGLPG
1770	1780	1790	1800	1810	1820	1830	1840
IGLSTSLRPR	MQFSSPSFVS	ISNECYQYSP	EFPLDILKSK	TIQMLTEAVK	EGSLHARDPV	GGTTEFLFVP	LIKLFYTLLI
1850	1860	1870	1880	1890	1900	1910	1920
MGIFHNEDLK	HILQLIEPSV	FKEAATPEEE	SDTLEKELSV	DDAKLQGAGE	EEAKGGKRPK	EGLLQMKLPE	PVKLQMCLLL
1930	1940	1950	1960	1970	1980	1990	2000
QYLCDCQVRH	RIEAIVAFSD	DFVAKLQDNQ	RFRYNEVMQA	LNMSAALTAR	KTKEFRSPPQ	EQINMLLNFK	DDKSECPCPE
2010	2020	2030	2040	2050	2060	2070	2080
EIRDQLLDFH	EDLMTHCGIE	LDEDGSLDGN	SDLTIRGRLL	SLVEKVTYLK	KKQAEKPVES	DSKKSSTLQQ	LISETMVRWA
2090	2100	2110	2120	2130	2140	2150	2160
QESVIEDPEL	VRAMFVLLHR	QYDGIGGLVR	ALPKTYTING	VSVEDTINLL	ASLGQIRSLL	SVRMGKEEEK	LMIRGLGDIM
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
2416	1	447.0974	-322.64	2	60.5	12.0	1	3605-3612	R.TALTEKCK.L	

Detailed Protein Report

Protein 356: LIM/homeobox protein Lhx5 [Homo sapiens]

Accession:	gi|11641283	**Score:**	27.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	44.4
Database Date:	2015-11-30	**pI:**	9.1
		Sequence Coverage [%]:	8.5
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 0.86 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MMVHCAGCER	PILDRFLLNV	LDRAWHIKCV	QCCECKTNLS	EKCFSREGKL	YCKNDFFRRF	GTKCAGCAQG	ISPSDLVRKA
90	100	110	120	130	140	150	160
RSKVFHLNCF	TCMVCNKQLS	TGEELYVIDE	NKFVCKDDYL	SSSSLKEGSL	NSVSSCTDRS	LSPDLQDALQ	DDPKETDNST
170	180	190	200	210	220	230	240
SSDKETANNE	NEEQNSGTKR	RGPRTTIKAK	QLETLKAAFA	ATPKPTRHIR	EQLAQETGLN	MRVIQVWFQN	RRSKERRMKQ
250	260	270	280	290	300	310	320
LSALGARRHA	FFRSPRRMRP	LGGRLDESEM	LGSTPYTYYG	DYQGDYYAPG	SNYDFFAHGP	PSQAQSPADS	SFLAASGPGS
330	340	350	360	370	380	390	400
TPLGALEPPL	AGPHAADNPR	FTDMISHPDT	PSPEPGLPGT	LHPMPGEVFS	GGPSPPFPMS	GTSGYSGPLS	HPNPELNEAA
410							
VW							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
1688	1	916.3971	-76.21	2	51.0	10.9	2	64-81	K.CAGCAQGISPSDLVRKAR.S		MD:MU	0.86

Detailed Protein Report

Protein 357: **chordin-like protein 1 isoform 4 precursor [Homo sapiens]**

Accession:	gi|291084494	**Score:**	26.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	43.5
Database Date:	2015-11-30	**pI:**	9.9
		Sequence Coverage [%]:	8.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MRKKWKMGGM	KYIFSLLFFL	LLEGGKTEQV	KHSETYCMFQ	DKKYRVGERW	HPYLEPYGLV	YCVNCICSEN	GNVLCSRVRC
90	100	110	120	130	140	150	160
PNVHCLSPVH	IPHLCCPRCP	GDGELSWEHS	DGDIFRQPAN	REARHSYHRS	HYDPPPSRQA	GGLSRFPGAR	SHRGALMDSQ
170	180	190	200	210	220	230	240
QASGTIVQIV	INNKHKHGQV	CVSNGKTYSH	GESWHPNLRA	FGIVECVLCT	CNVTKQECKK	IHCPNRYPCK	YPQKIDGKCC
250	260	270	280	290	300	310	320
KVCPGKKAKE	ELPGQSFDNK	GYFCGEETMP	VYESVFMEDG	ETTRKIALET	ERPPQVEVHV	WTIRKGILQH	FHIEKISKRM
330	340	350	360	370	380		
FEELPHFKLV	TRTTLSQWKI	FTEGEAQISQ	MCSSRVCRTE	LEDLVKVLYL	ERSEKGHC		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1642	1	701.3735	65.53	3	50.3	10.1	2	27-43	K.TEQVKHSETYCMFQDKK.Y	

Detailed Protein Report

Protein 358: polyadenylate-binding protein 4 isoform 3 [Homo sapiens]

Accession: gi|208431836
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 26.9
MW [kDa]: 69.5
pI: 10.0
Sequence Coverage [%]: 3.0
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MNAAASSYPM	ASLYVGDLHS	DVTEAMLYEK	FSPAGPVLSI	RVCRDMITRR	SLGYAYVNFQ	QPADAERALD	TMNFDVIKGK
90	100	110	120	130	140	150	160
PIRIMWSQRD	PSLRKSGVGN	VFIKNLDKSI	DNKALYDTFS	AFGNILSCKV	VCDENGSKGY	AFVHFETQEA	ADKAIEKMNG
170	180	190	200	210	220	230	240
MLLNDRKVFV	GRFKSRKERE	AELGAKAKEF	TNVYIKNFGE	EVDDESLKEL	FSQFGKTLSV	KVMRDPNGKS	KGFGFVSYEK
250	260	270	280	290	300	310	320
HEDANKAVEE	MNGKEISGKI	IFVGRAQKKV	ERQAELKRKF	EQLKQERISR	YQGVNLYIKN	LDDTIDDEKL	RKEFSPFGSI
330	340	350	360	370	380	390	400
TSAKVMLEDG	RSKGFGFVCF	SSPEEATKAV	TEMNGRIVGS	KPLYVALAQR	KEERKAHLTN	QYMQRVAGMR	ALPANAILNQ
410	420	430	440	450	460	470	480
FQPAAGGYFV	PAVPQAQGRP	PYYTPNQLAQ	MRPNPRWQQG	GRPQGFQGMP	SAIRQSGPRP	TLRHLAPTGN	APASRGLPTT
490	500	510	520	530	540	550	560
TQRVGVPTAV	QNLAPRAAVA	AAAPRAVAPY	KYASSVRSPH	PAIQPLQAPQ	PAVHVQGQEP	LTASMLAAAP	PQEQKQMLGE
570	580	590	600	610	620	630	640
RLFPLIQTMH	SNLAGKITGM	LLEIDNSELL	HMLESPESLR	SKVDEAVAVL	QAHHAKKEAA	QKVGAVAAAT	S

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2821	1	1051.5459	48.78	2	65.7	12.8	2	241-259	K.HEDANKAVEEMNGKEISGK.I	Oxidation: 11

Detailed Protein Report

Protein 359: **PREDICTED: core histone macro-H2A.1 isoform X3 [Homo sapiens]**

Accession:	gi|530380257	**Score:**	26.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	39.0
Database Date:	2015-11-30	**pI:**	10.3
		Sequence Coverage [%]:	9.0
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MSSRGGKKKS	TKTSRSAKAG	VIFPVGRMLR	YIKKGHPKYR	IGVGAPVYMA	AVLEYLTAEI	LELAGNAARD	NKKGRVTPRH
90	100	110	120	130	140	150	160
ILLAVANDEE	LNQLLKGVTI	ASGGVLPNIH	PELLAKKRGS	KGKLEAIITP	PPAKKAKSPS	QKKPVSKKAG	GKKGARKSKK
170	180	190	200	210	220	230	240
QGEVSKAASA	DSTTEGTPAD	GFTVLSTKSL	FLGQKLQVVQ	ADIASIDSDA	VVHPTNTDFY	IGGEVGNTLE	KKGGKEFVEA
250	260	270	280	290	300	310	320
VLELRKKNGP	LEVAGAAVSA	GHGLPAKFVI	HCNSPVWGAD	KCEELLEKTV	KNCLALADDK	KLKSIAFPSI	GSGRNGFPKQ
330	340	350	360	370			
TAAQLILKAI	SSYFVSTMSS	SIKTVYFVLF	DSESIGIYVQ	EMAKLDAN			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2553	1	639.3415	-83.77	2	61.9	15.2	1	124-135	K.LEAIITPPPAKK.A	
2834	1	806.4289	45.18	3	65.9	11.7	1	268-288	K.FVIHCNSPVWGADKCEELLEK.T	

Detailed Protein Report

Protein 360: transmembrane protein 151A [Homo sapiens]

Accession:	gi|23397566	**Score:**	26.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	51.2
Database Date:	2015-11-30	**pI:**	9.3
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	9.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPEDGAGDGG	EVPALIPDGE	PLREEQRPLK	QSLGSSLCRE	SHWKCLLLTL	LIHACGAVVA	WCRLATVPRL	VLGPEAALAR
90	100	110	120	130	140	150	160
GAGGPPPTYP	ASPCSDGYLY	IPLAFVSLLY	LLYLAECWHC	HVRSCQAPRT	DAHTVLALIR	RLQQAPPCVW	WKATSYHYVR
170	180	190	200	210	220	230	240
RTRQITRYRN	GDAYTTTQVY	HERADSRTAR	GEFDYSAHGV	RDVSKELVGL	AEHAATRLRF	TKCFSFGSAE	AEASYLTQRA
250	260	270	280	290	300	310	320
RFFSANEGLD	DYLEAREGMH	LKDVDFRESL	MVFADPRSPP	WYARAWVFWL	VSAATLSWPL	RVVAAYGTAH	VHYQVEKLFG
330	340	350	360	370	380	390	400
ASSPPPGAVP	SGPPLSRVAT	VDFTELEWHI	CSNRQLVPSY	SEAVVMGAGS	GAYLRGCQRC	RRSVSSNSLP	PARPSGPRLP
410	420	430	440	450	460	470	
FSRSRLSLGA	GGRATPGVFR	SLSGGPLGRR	GEDTEPLESP	PCYEDALYFP	VLIVHGDSGC	QGDGQGAL	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
136	1	977.7569	-49.80	3	31.1	10.2	2	355-381	R.QLVPSYSEAVVMGAGSGAYLRGCQRCR.R	Carbamidomethyl: 23; Oxidation: 12

Detailed Protein Report

Protein 361: PREDICTED: RAD51-associated protein 2 isoform X1 [Homo sapiens]

Accession:	gi|530367071	**Score:**	26.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	132.8
Database Date:	2015-11-30	**pI:**	7.1
		Sequence Coverage [%]:	2.7
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 1.32 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MAELRKPTSS LTPPEDPDSQ PPSSKRLCLE EPGGVFKAGW RLPLVPRLSE AEKVWELSPR PFKGLLVSTN AIFDNSTDSC

        90        100        110        120        130        140        150        160
VEKSVSGKQI CNLKCSNLKF QMSSCLQSPP SQSPDSDLRA SGRSEAGLHD REAFSVHRSN SSKAGVSQLL PSTSIHDIHG

       170        180        190        200        210        220        230        240
IRNENRKQQF VQGRDNVHKE NPFLDVTFYK ETKSPFHEIK NRCKANSVVP SNKRENNISS SVLKISKSQN QPSLEIAKPS

       250        260        270        280        290        300        310        320
YFRDSGTISV PQFPMDLNSK MSSVYLKEIA KKKNDKKEAY VRDFTNIYWS QNRPDVKKQK LQNDKKTVEA ENIFSKCYEN

       330        340        350        360        370        380        390        400
DYPSLSSQNT CKRKDLISSN YCNCSSIQCN VRDSRKNFAI LENANWEEAE CLDSYVLTRL EKSQNWDCNV RHILRRNRGN

       410        420        430        440        450        460        470        480
CWIINNCKTK CENMKKTEEK WNWLLLLEID LLSKEDYHCA KVINAYEEQS KLLVREILGS QTALITTVWL NGKGENDNTL

       490        500        510        520        530        540        550        560
QLRYNTTQKV FHVNNPFESF IIEIFYFHKS ISGNKKDNSI LTCCNILKCK KQIGIIGIQN LITRNMNTNI KNGILSIYLQ

       570        580        590        600        610        620        630        640
DSVSEPLDIL LKTNIAFLLN NFDSLTRIEN DFELEEECIF KCMLYLKYPK NIVENHTAYL VKILTSSRLL EDNMKPMLKK

       650        660        670        680        690        700        710        720
RKLFRTEQVF EKSKKKLINS FSMTTQNTGF PIFETYEKIP LLMDFDDMDE ISLIREITCQ NMSCPQQVVN VENWAHYNSS

       730        740        750        760        770        780        790        800
TVKAHGNSCP QFIQNNRGYI NENFYEVNMH SQDLNMERKQ GHNKISNFDC EHIFEDLCNV RQQAIPASHN IIHNEETHTT

       810        820        830        840        850        860        870        880
SITQVLNFWN LLSEIEEKKY DLILKEEVKV TAESLTNSCQ VHKDTKIEKE EKDSFFPMDD MFSVQSVSLI SKEVNVEENK

       890        900        910        920        930        940        950        960
YVNQNYVTNT NEYESILPER EIANSKDFHR KNDSALYINH QFETGLSEGN DECFQDLAAK YLSTEALTIV KDFEMKRKFD

       970        980        990       1000       1010       1020       1030       1040
LVLEELRMFH EISRENELLS TVETNNGQEN YFGENDAEKV KMEIEKDLKM VVVNKIRASS SFHDTIAGPN MGKSHQSLFK

      1050       1060       1070       1080       1090       1100       1110       1120
WKTVPNNGEQ EVPNESCYPS RSEEELLYST SEKDCETPLP KRPAFLPDEC KEEFNYLLRG GSHFPHGISR VRPLKTCSRP

      1130       1140       1150       1160
IRIGLSRKAR IKQLHPYLKQ MCYGNLKENF
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1446	1	698.8871	-14.31	2	47.7	15.2	2	261-272	K.MSSVYLKEIAKK.K		MD:MU 1.32

Detailed Protein Report

Protein 362: PREDICTED: uncharacterized protein LOC100996701 [Homo sapiens]

Accession:	gi|397139476	**Score:**	26.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	22.6
Database Date:	2015-11-30	**pI:**	12.1
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	15.0
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 0.67 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MAALCLRKGP	LPLCPRPSHG	LKAMGGEGSC	QDDTESGALI	FLPSDDAQPG	KALRPQRSGP	GGSERRGRGW	GRAGALEEQV
90	100	110	120	130	140	150	160
RQGPSAQRHP	RTQACSRPCS	PSPHCSCGKG	KHGALPQGQC	SAWLELTMVT	VPCCHHCSHC	PGGQPGPQLH	CAWTVWSWAV
170	180	190	200	210	220		
PSSASRACGD	GHRRSTCQAQ	GSCTGLPPLR	GCLSRLVPGC	PCPHLRQQDK	GKWN		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1676	1	916.3092	-152.23	2	50.9	15.0	1	174-190	R.RSTCQAQGSCTGLPPLR.G	Carbamidomethyl: 10	MD:MU 0.67

Detailed Protein Report

Protein 363: PREDICTED: double zinc ribbon and ankyrin repeat-containing protein 1 isoform X3 [Homo sapiens]

Accession:	gi|530425777	**Score:**	26.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	63.6
Database Date:	2015-11-30	**pI:**	9.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	6.5
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MLTLESFQSP	GFAHVSGQKC	LTSTEIMRIQ	RETDFLKCAH	CLAPRPSDPF	ARFCQECGSP	VPPIFGCRLP	PPEGAQMGLC
90	100	110	120	130	140	150	160
AECRSLVPMN	TPICVVCEAP	LALQLQPQAS	LHLKEKVICR	ACGTGNPAHL	RYCVTCEGAL	PSSQESMCSG	DKAPPPPTQK
170	180	190	200	210	220	230	240
GGTISCYRCG	RWNLWEASFC	GWCGAMLGIP	AGCSVCPKCG	ASNHLSARFC	GSCGICVKSL	VKLSLDRSLA	LAAEEPRPFS
250	260	270	280	290	300	310	320
EPRCAWQSLN	IPLPRSDVGT	KRDIGTQTVG	LFYPSGKLLA	KKEQELASQK	QRQEKMSDHK	PLLTAISPGR	GYWRRQLDHI
330	340	350	360	370	380	390	400
SAHLRCYAQN	NPEFRALIAE	PRMGKLISAT	VHEDGCEVSI	RLNYSQVSNK	NLYLNKAVNF	SDHLLSSAAE	GDGGLCGSRS
410	420	430	440	450	460	470	480
SWVSDYSQST	SDTIEKIKRI	KNFKTKTFQE	KKEQLIPENR	LLLKEVGPTG	EGRVSVIEQL	LDEGADPNCC	DEDNRPVITV
490	500	510	520	530	540	550	560
AVMNKHHEAI	PVLVQRGADI	DQQWGPLRNT	ALHEATLLGL	AGRESTATLL	GCNASIQKKN	AGGQTAYDLA	LNTGDDLVTS
570	580	590					
LFAAKFGQGL	EDQLAQTRSL	SLDDC					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2106	1	1052.4447	-67.35	3	56.5	13.1	1	1-28	-.MLTLESFQSPGFAHVSGQKCLTSTEIMR.I	Carbamidomethyl: 20
1819	1	649.7840	1.98	2	52.7	13.7	0	326-335	R.CYAQNNPEFR.A	Carbamidomethyl: 1

Detailed Protein Report

Protein 364: PREDICTED: phenylalanine--tRNA ligase beta subunit isoform X1 [Homo sapiens]

Accession:	gi|578803432	**Score:**	26.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	54.8
Database Date:	2015-11-30	**pI:**	7.8
		Sequence Coverage [%]:	3.5
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578803436	refseq_human (refseq_human_20140103.fasta)	PREDICTED: phenylalanine--tRNA ligase beta subunit isoform X3 [Homo sapiens]
gi|578803434	refseq_human (refseq_human_20140103.fasta)	PREDICTED: phenylalanine--tRNA ligase beta subunit isoform X2 [Homo sapiens]

10	20	30	40	50	60	70	80
MPDGKIQKLI	ITEETAKIRP	FAVAAVLRNI	KFTKDRYDSF	IELQEKLHQN	ICRKRALVAI	GTHDLDTLSG	PFTYTAKRPS
90	100	110	120	130	140	150	160
DIKFKPLNKT	KEYTACELMN	IYKTDNHLKH	YLHIIENKPL	YPVIYDSNGV	VLSMPPIING	DHSRITVNTR	NIFIECTGTD
170	180	190	200	210	220	230	240
FTKAKIVLDI	IVTMFSEYCE	NQFTVEAAEV	VFPNGKSHTF	PELAYRKEMV	RADLINKKVG	IRETPENLAK	LLTRMYLKSE
250	260	270	280	290	300	310	320
VIGDGNQIEI	EIPPTRADII	HACDIVEDAA	IAYGYNNIQM	TLPKTYTIAN	QFPLNKLTEL	LRHDMAAAGF	TEALTFALCS
330	340	350	360	370	380	390	400
QEDIADKLGV	DISATKAVHI	SNPKTAEFQV	ARTTLLPGLL	KTIAANRKMP	LPLKLFEISD	IVIKDSNTDV	GAKNYRHLCA
410	420	430	440	450	460	470	480
VYYNKNPGFE	IIHGLLDRIM	QLLDVPPGED	KGGYVIKASE	GPAFFPGRCA	EIFARGQSVG	KLGVLHPDVI	TKFELTMPCS
490	500						
SLEINVGPFL							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1331	1	721.8048	-169.98	2	46.2	11.2	1	78-89	K.RPSDIKFKPLNK.T	

Detailed Protein Report

Protein 365: complexin-3 precursor [Homo sapiens]

Accession:	gi|71725345	**Score:**	26.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	17.5
Database Date:	2015-11-30	**pI:**	4.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	19.6
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MAFMVKTMVG GQLKNLTGSL GGGEDKGDGD KSAAEAQGMS REEYEEYQKQ LVEEKMERDA QFTQRKAERA TLRSHFRDKY
        90        100        110        120        130        140        150        160
RLPKNETDES QIQMAGGDVE LPRELAKMIE EDTEEEEEKA SVLGQLASLP GLNLGSLKDK AQATLGDLKQ SAEKCHVM
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1306	1	721.2739	-148.07	2	45.9	11.1	1	2-14	M.AFMVKTMVGGQLK.N	Oxidation: 3, 7

Detailed Protein Report

Protein 366: **partitioning defective 3 homolog B isoform a [Homo sapiens]**

Accession:	gi|119120907	**Score:**	26.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	121.1
Database Date:	2015-11-30	**pI:**	9.4
		Sequence Coverage [%]:	2.8
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 2.39 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MKVTVCFGRT	GIVVPCKEGQ	LRVGELTQQA	LQRYLKTREK	GPGYWVKIHH	LEYTDGGILD	PDDVLADVVE	DKDKLIAVFE
90	100	110	120	130	140	150	160
EQEPLHKIES	PSGNPADRQS	PDAFETEVAA	QLAAFKPIGG	EIEVTPSALK	LGTPLLVRRS	SDPVPGPPAD	TQPSASHPGG
170	180	190	200	210	220	230	240
QSLKLVVPDS	TQNLEDREVL	NGVQTELLTS	PRTKDTLSDM	TRTVEISGEG	GPLGIHVVPF	FSSLSGRILG	LFIRGIEDNS
250	260	270	280	290	300	310	320
RSKREGLFHE	NECIVKINNV	DLVDKTFAQA	QDVFRQAMKS	PSVLLHVLPP	QNREQYEKSV	IGSLNIFGNN	DGVLKTKVPP
330	340	350	360	370	380	390	400
PVHGKSGLKT	ANLTGTDSPE	TDASASLQQN	KSPRVPRLGG	KPSSPSLSPL	MGFGSNKNAK	KIKIDLKKGP	EGLGFTVVTR
410	420	430	440	450	460	470	480
DSSIHGPGPI	FVKNILPKGA	AIKDGRLQSG	DRILEVNGRD	VTGRTQEELV	AMLRSTKQGE	TASLVIARQE	GHFLPRELKG
490	500	510	520	530	540	550	560
EPDCCALSLE	TSEQLTFEIP	LNDSGSAGLG	VSLKGNKSRE	TGTDLGIFIK	SIIHGGAAFK	DGRLRMNDQL	IAVNGESLLG
570	580	590	600	610	620	630	640
KSNHEAMETL	RRSMSMEGNI	RGMIQLVILR	RPERPMEDPA	ECGAFSKPCF	ENCQNAVTTS	RRNDNSILHP	LGTCSPQDKQ
650	660	670	680	690	700	710	720
KGLLLPNDGW	AESEVPPSPT	PHSALGLGLE	DYSHSSGVDS	AVYFPDQHIN	FRSVTPARQP	ESINLKASKS	MDLVPDESKV
730	740	750	760	770	780	790	800
HSLAGQKSES	PSKDFGPTLG	LKKSSSLESL	QTAVAEVRKN	DLPFHRPRPH	MVRGRGCNES	FRAAIDKSYD	GPEEIEADGL
810	820	830	840	850	860	870	880
SDKSSHSGQG	ALNCESAPQG	NSELEDMENK	ARKVKKTKEK	EKKKEKGKLK	VKEKKRKEEN	EDPERKIKKK	GFGAMLRFGK
890	900	910	920	930	940	950	960
KKEDKGGKAE	QKGTLKHGGL	REEELEKMKE	ERESGRPTGG	STDRIQKLRK	EYYQARREGF	PLYEDDEGRA	RPSEYDLLWV
970	980	990	1000	1010	1020	1030	1040
PGRGPDGNAH	NLRFEGMERQ	YASLPRGGPA	DPVDYLPAAP	RGLYKERELP	YYPGAHPMHP	PKGSYPRPTE	LRVADLRYPQ
1050	1060	1070	1080	1090	1100	1110	
HYPPPPAPQH	KGPFRQDVPP	SPPQHQRMPA	YQETGRPGPR	GGSPDQYPYR	TQDSRQKNPM	TAAV	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
268	1	549.5949	-92.30	3	33.0	10.2	1	23-36	R.VGELTQQALQRYLK.T		MD:MU	2.39

Detailed Protein Report

Protein 367: PREDICTED: neuroligin-2 isoform X1 [Homo sapiens]

Accession:	gi|530410532	**Score:**	26.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	88.9
Database Date:	2015-11-30	**pI:**	5.7
		Sequence Coverage [%]:	4.5
		No. of unique Peptides:	2

Quantitation

MD:MU **Median:** 2.27 **CV:** 59.28 % **No. of Peptides:** 2

10	20	30	40	50	60	70	80
MWLLALCLVG	LAGAQRGGGG	PGGGAPGGPG	LGLGSLGEER	FPVVNTAYGR	VRGVRRELNN	EILGPVVQFL	GVPYATPPLG
90	100	110	120	130	140	150	160
ARRFQPPEAP	ASWPGVRNAT	TLPPACPQNL	HGALPAIMLP	VWFTDNLEAA	ATYVQNQSED	CLYLNLYVPT	EDDIRDPGKK
170	180	190	200	210	220	230	240
PVMLFLHGGS	YMEGTGNMFD	GSVLAAYGNV	IVATLNYRLG	VLGFLSTGDQ	AAKGNYGLLD	QIQALRWLSE	NIAHFGGDPE
250	260	270	280	290	300	310	320
RITIFGSGAG	ASCVNLLILS	HHSEGLFQKA	IAQSGTAISS	WSVNYQPLKY	TRLLAAKVGC	DREDSAEAVE	CLRRKPSREL
330	340	350	360	370	380	390	400
VDQDVQPARY	HIAFGPVVDG	DVVPDDPEIL	MQQGEFLNYD	MLIGVNQGEG	LKFVEDSAES	EDGVSASAFD	FTVSNFVDNL
410	420	430	440	450	460	470	480
YGYPEGKDVL	RETIKFMYTD	WADRDNGEMR	RKTLLALFTD	HQWVAPAVAT	AKLHADYQSP	VYFYTFYHHC	QAEGRPEWAD
490	500	510	520	530	540	550	560
AAHGDELPYV	FGVPMVGATD	LFPCNFSKND	VMLSAVVMTY	WTNFAKTGDP	NQPVPQDTKF	IHTKPNRFEE	VVWSKFNSKE
570	580	590	600	610	620	630	640
KQYLHIGLKP	RVRDNYRANK	VAFWLELVPH	LHNLHTELFT	TTTRLPPYAT	RWPPRPPAGA	PGTRRPPPPA	TLPPEPEPEP
650	660	670	680	690	700	710	720
GPRAYDRFPG	DSRDYSTELS	VTVAVGASLL	FLNILAFAAL	YYKRDRRQEL	RCRRLSPPGG	SGSGVPGGGP	LLPAAGRELP
730	740	750	760	770	780	790	800
PEEELVSLQL	KRGGGVGADP	AEALRPACPP	DYTLALRRAP	DDVPLLAPGA	LTLLPSGLGP	PPPPPPPSLH	PFGPFPPPPP
810	820						
TATSHNNTLP	HPHSTTRV						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1419	1	981.9479	-37.80	2	47.5	11.8	0	17-40	R. GGGGPGGGAPGGPGLGLGSLGE F		MD:MU 3.94
1556	1	698.7932	-65.19	2	49.1	14.9	0	527-539	K.TGDPNQPVPQDTK.F		MD:MU 1.31

Detailed Protein Report

Protein 368: prolow-density lipoprotein receptor-related protein 1 precursor [Homo sapiens]

Accession:	gi|126012562	**Score:**	26.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	504.3
Database Date:	2015-11-30	**pI:**	5.0
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	0.6
		No. of unique Peptides:	2

Quantitation

MD:MU **Median:** 0.80 **CV:** 0.00 % **No. of Peptides:** 1

Detailed Protein Report

10	20	30	40	50	60	70	80
MLTPPLLLLL	PLLSALVAAA	IDAPKTCSPK	QFACRDQITC	ISKGWRCDGE	RDCPDGSDEA	PEICPQSKAQ	RCQPNEHNCL
90	100	110	120	130	140	150	160
GTELCVPMSR	LCNGVQDCMD	GSDEGPHCRE	LQGNCSRLGC	QHHCVPTLDG	PTCYCNSSFQ	LQADGKTCKD	FDECSVYGTC
170	180	190	200	210	220	230	240
SQLCTNTDGS	FICGCVEGYL	LQPDNRSCKA	KNEPVDRPPV	LLIANSQNIL	ATYLSGAQVS	TITPTSTRQT	TAMDFSYANE
250	260	270	280	290	300	310	320
TVCWVHVGDS	AAQTQLKCAR	MPGLKGFVDE	HTINISLSLH	HVEQMAIDWL	TGNFYFVDDI	DDRIFVCNRN	GDTCVTLLDL
330	340	350	360	370	380	390	400
ELYNPKGIAL	DPAMGKVFFT	DYGQIPKVER	CDMDGQNRTK	LVDSKIVFPH	GITLDLVSRL	VYWADAYLDY	IEVVDYEGKG
410	420	430	440	450	460	470	480
RQTIIQGILI	EHLYGLTVFE	NYLYATNSDN	ANAQQKTSVI	RVNRFNSTEY	QVVTRVDKGG	ALHIYHQRRQ	PRVRSHACEN
490	500	510	520	530	540	550	560
DQYGKPGGCS	DICLLANSHK	ARTCRCRSGF	SLGSDGKSCK	KPEHELFLVY	GKGRPGIIRG	MDMGAKVPDE	HMIPIENLMN
570	580	590	600	610	620	630	640
PRALDFHAET	GFIYFADTTS	YLIGRQKIDG	TERETILKDG	IHNVEGVAVD	WMGDNLYWTD	DGPKKTISVA	RLEKAAQTRK
650	660	670	680	690	700	710	720
TLIEGKMTHP	RAIVVDPLNG	WMYWTDWEED	PKDSRRGRLE	RAWMDGSHRD	IFVTSKTVLW	PNGLSLDIPA	GRLYWVDAFY
730	740	750	760	770	780	790	800
DRIETILLNG	TDRKIVYEGP	ELNHAFGLCH	HGNYLFWTEY	RSGSVYRLER	GVGGAPPTVT	LLRSERPPIF	EIRMYDAQQQ
810	820	830	840	850	860	870	880
QVGTNKCRVN	NGGCSSLCLA	TPGSRQCACA	EDQVLDADGV	TCLANPSYVP	PPQCQPGEFA	CANSRCIQER	WKCDGDNDCL
890	900	910	920	930	940	950	960
DNSDEAPALC	HQHTCPSDRF	KCENNRCIPN	RWLCDGDNDC	GNSEDESNAT	CSARTCPPNQ	FSCASGRCIP	ISWTCDLDDD
970	980	990	1000	1010	1020	1030	1040
CGDRSDESAS	CAYPTCFPLT	QFTCNNGRCI	NINWRCDNDN	DCGDNSDEAG	CSHSCSSTQF	KCNSGRCIPE	HWTCDGDNDC
1050	1060	1070	1080	1090	1100	1110	1120
GDYSDETHAN	CTNQATRPPG	GCHTDEFQCR	LDGLCIPLRW	RCDGDTDCMD	SSDEKSCEGV	THVCDPSVKF	GCKDSARCIS
1130	1140	1150	1160	1170	1180	1190	1200
KAWVCDGDND	CEDNSDEENC	ESLACRPPSH	PCANNTSVCL	PPDKLCDGND	DCGDGSDEGE	LCDQCSLNNG	GCSHNCSVAP
1210	1220	1230	1240	1250	1260	1270	1280
GEGIVCSCPL	GMELGPDNHT	CQIQSYCAKH	LKCSQKCDQN	KFSVKCSCYE	GWVLEPDGES	CRSLDPFKPF	IIFSNRHEIR
1290	1300	1310	1320	1330	1340	1350	1360
RIDLHKGDYS	VLVPGLRNTI	ALDFHLSQSA	LYWTDVVEDK	IYRGKLLDNG	ALTSFEVVIQ	YGLATPEGLA	VDWIAGNIYW
1370	1380	1390	1400	1410	1420	1430	1440
VESNLDQIEV	AKLDGTLRTT	LLAGDIEHPR	AIALDPRDGI	LFWTDWDASL	PRIEAASMSG	AGRRTVHRET	GSGGWPNGLT
1450	1460	1470	1480	1490	1500	1510	1520
VDYLEKRILW	IDARSDAIYS	ARYDGSGHME	VLRGHEFLSH	PFAVTLYGGE	VYWTDWRTNT	LAKANKWTGH	NVTVVQRTNT
1530	1540	1550	1560	1570	1580	1590	1600
QPFDLQVYHP	SRQPMAPNPC	EANGGQGPCS	HLCLINYNRT	VSCACPHLMK	LHKDNTTCYE	FKKFLLYARQ	MEIRGVDLDA
1610	1620	1630	1640	1650	1660	1670	1680
PYYNYIISFT	VPDIDNVTVL	DYDAREQRVY	WSDVRTQAIK	RAFINGTGVE	TVVSADLPNA	HGLAVDWVSR	NLFWTSYDTN
1690	1700	1710	1720	1730	1740	1750	1760
KKQINVARLD	GSFKNAVVQG	LEQPHGLVVH	PLRGKLYWTD	GDNISMANMD	GSNRTLLFSG	QKGPVGLAID	FPESKLYWIS
1770	1780	1790	1800	1810	1820	1830	1840
SGNHTINRCN	LDGSGLEVID	AMRSQLGKAT	ALAIMGDKLW	WADQVSEKMG	TCSKADGSGS	VVLRNSTTLV	MHMKVYDESI
1850	1860	1870	1880	1890	1900	1910	1920
QLDHKGTNPC	SVNNGDCSQL	CLPTSETTRS	CMCTAGYSLR	SGQQACEGVG	SFLLYSVHEG	IRGIPLDPND	KSDALVPVSG
1930	1940	1950	1960	1970	1980	1990	2000
TSLAVGIDFH	AENDTIYWVD	MGLSTISRAK	RDQTWREDVV	TNGIGRVEGI	AVDWIAGNIY	WTDQGFDVIE	VARLNGSFRY
2010	2020	2030	2040	2050	2060	2070	2080
VVISQGLDKP	RAITVHPEKG	YLFWTEWGQY	PRIERSRLDG	TERVVLVNVS	ISWPNGISVD	YQDGKLYWCD	ARTDKIERID
2090	2100	2110	2120	2130	2140	2150	2160
LETGENREVV	LSSNNMDMFS	VSVFEDFIYW	SDRTHANGSI	KRGSKDNATD	SVPLRTGIGV	QLKDIKVFNR	DRQKGTNVCA
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
138	1	849.3804	-44.02	2	31.5	11.0	1	1560-1573	R.TVSCACPHLMKLHK.D	Carbamidomethyl: 4, 6; Oxidation: 10	MD:MU 0.80
2236	2	873.3305	-116.11	2	57.8	15.6	1	1952-1966	R.DQTWREDVVTNGIGR.V		

Detailed Protein Report

Protein 369: PRAME family member 1 [Homo sapiens]

Accession:	gi|12738831	**Score:**	26.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	55.1
Database Date:	2015-11-30	**pI:**	9.9
		Sequence Coverage [%]:	3.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSIQAPPRLL	ELAGQSLLRD	QALSISAMEE	LPRVLYLPLF	MEAFSRRHFQ	TLTVMVQAWP	FTCLPLGSLM	KTLHLETLKA
90	100	110	120	130	140	150	160
LLEGLHMLLT	QKDRPRRWKL	QVLDLRDVDE	NFWARWPGAW	ALSCFPETTS	KRQTAEDCPR	MGEHQPLKVF	IDICLKEIPQ
170	180	190	200	210	220	230	240
DECLRYLFQW	VYQRRGLVHL	CCSKLVNYLT	PIKYLRKSLK	IIYLNSIQEL	EIRNMSWPRL	IRKLRCYLKE	MKNLRKLVFS
250	260	270	280	290	300	310	320
RCHHYTSDNE	LQGRLVAKFS	SVFLRLEHLQ	LLKIKLITFF	SGHLEQLIRC	LQNPLENLEL	TYGYLLEEDM	KCLSQYPSLG
330	340	350	360	370	380	390	400
YLKHLNLSYV	LLFRISLEPL	GALLEKIAAS	LKTLILEGCQ	IHYSQLSAIL	PALSRCSQLT	TFYFGRNCMS	IDALKDLLRH
410	420	430	440	450	460	470	480
TSGLSKLSLE	TYPAPEESLN	SLVRVNWEIF	TPLRAELMCT	LREVRQPKRI	FIGPTPCPSC	GSSPSEELEL	HLCC

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1448	1	428.2129	-107.14	3	47.7	10.6	0	335-346	R.ISLEPLGALLEK.I	

Detailed Protein Report

Protein 370: PREDICTED: protein CASP isoform X6 [Homo sapiens]

Accession:	gi|578813926	**Score:**	26.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	172.0
Database Date:	2015-11-30	**pI:**	5.9
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	1.5
		No. of unique Peptides:	2

Quantitation

MD:MU **Median:** 9.99 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MERAAGALGD AFSGRVLESR APGARWDRGM PGGGPRAESP APRGDRAGAP RPAPESPPCP RGECLPATPR PEERRTLRVR
        90        100        110        120        130        140        150        160
PARASSAPAA PGQPRDSARW MLCVAGARLK RELDATATVL ANRQDESEQS RKRLIEQSRE FKKNTPEDLR KQVAPLLKSF
       170        180        190        200        210        220        230        240
QGEIDALSKR SKEAEAAFLN VYKRLIDVPD PVPALDLGQQ LQLKVQRLHD IETENQKLRE TLEEYNKEFA EVKNQEVTIK
       250        260        270        280        290        300        310        320
ALKEKIREYE QTLKNQAETI ALEKEQKLQN DFAEKERKLQ ETQMSTTSKL EEAEHKVQSL QTALEKTRTE LFDLKTKYDE
       330        340        350        360        370        380        390        400
ETTAKADEIE MIMTDLERAN QRAEVAQREA ETLREQLSSA NHSLQLASQI QKAPDVEQAI EVLTRSSLEV ELAAKEREIA
       410        420        430        440        450        460        470        480
QLVEDVQRLQ ASLTKLRENS ASQISQLEQQ LSAKNSTLKQ LEEKLKGQAD YEEVKKELNI LKSMEFAPSE GAGTQDAAKP
       490        500        510        520        530        540        550        560
LEVLLLEKNR SLQSENAALR ISNSDLSGSA RRKGKDQPES RRPGSLPAPP PSQLPRNPGE QASNTNGTHQ FSPAGLSQDF
       570        580        590        600        610        620        630        640
FSSSLASPSL PLASTGKFAL NSLLQRQLMQ SFYSKAMQEA GSTSMIFSTG PYSTNSISSQ SPLQQSPDVN GMAPSPSQSE
       650        660        670        680        690        700        710        720
SAGSVSEGEE MDTAEIARQV KEQLIKHNIG QRIFGHYVLG LSQGSVSEIL ARPKPWNKLT VRGKEPFHKM KQFLSDEQNI
       730        740        750        760        770        780        790        800
LALRSIQGRQ RGNITTRIRA SETGSDEAIK SILEQAKREL QVQKTAEPAQ PSSASGSGNS DDAIRSILQQ ARREMEAQQA
       810        820        830        840        850        860        870        880
ALDPALKQAP LSQSDITILT PKLLSTSPMP TVSSYPPLAI SLKKPSAAPE AGASALPNPP ALKKEAQDAP GLDPQGAADC
       890        900        910        920        930        940        950        960
AQGVLRQVKN EVGRSGAWKD HWWSAVQPER RNAASSEEAK AEETGGGKEK GSGGSGGGSQ PRAERSQLQG PSSSEYWKEW
       970        980        990       1000       1010       1020       1030       1040
PSAESPYSQS SELSLTGASR SETPQNSPLP SSPIVPMSKP TKPSVPPLTP EQYEVYMYQE VDTIELTRQV KEKLAKNGIC
      1050       1060       1070       1080       1090       1100       1110       1120
QRIFGEKVLG LSQGSVSDML SRPKPWSKLT QKGREPFIRM QLWLNGELGQ GVLPVQGQQQ GPVLHSVTSL QDPLQQGCVS
      1130       1140       1150       1160       1170       1180       1190       1200
SESTPKTSAS CSPAPESPMS SSESVKSLTE LVQQPCPPIE ASKDSKPPEP SDPPASDSQP TTPLPLSGHS ALSIQELVAM
      1210       1220       1230       1240       1250       1260       1270       1280
SPELDTYGIT KRVKEVLTDN NLGQRLFGET ILGLTQGSVS DLLARPKPWH KLSLKGREPF VRMQLWLNDP NNVEKLMDMK
      1290       1300       1310       1320       1330       1340       1350       1360
RMEKKAYMKR RHSSVSDSQP CEPPSVGTEY SQGASPQPQH QLKKPRVVLA PEEKEALKRA YQQKPYPSPK TIEDLATQLN
      1370       1380       1390       1400       1410       1420       1430       1440
LKTSTVINWF HNYRSRIRRE LFIEEIQAGS QGQAGASDSP SARSGRAAPS SEGDSCDGVE ATEGPGSADT EEPKSQGEAE
      1450       1460       1470       1480       1490       1500       1510       1520
REEVPRPAEQ TEPPPSGTPG PDDARDDDHE GGPVEGPGPL PSPASATATA APAAPEDAAT SAAAAPGEGP AAPSSAPPPS
      1530       1540       1550       1560       1570       1580       1590
NSSSSSAPRR PSSLQSLFGL PEAAGARDSR DNPLRKKKAA NLNSIIHRLE KAASREEPIE WEF
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1855	1	738.7765	-167.06	2	53.2	12.2	2	100-111	R.WMLCVAGARLKR.E	Carbamidomethyl: 4; Oxidation: 2	
597	3	661.1918	-220.59	2	37.0	14.5	1	1037-1047	K.NGICQRIFGEK.V	Carbamidomethyl: 4	MD:MU 9.99

Detailed Protein Report

Protein 371: PREDICTED: coiled-coil domain-containing protein 111 isoform X3 [Homo sapiens]

Accession:	gi|578808887	**Score:**	26.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	58.1
Database Date:	2015-11-30	**pI:**	8.8
		Sequence Coverage [%]:	2.2
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 5.03 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MNRKWEAKLK	QIEERASHYE	RKPLSSVYRP	RLSKPEEPPS	IWRLFHRQAQ	AFNFVKSCKE	DVHVFALECK	VGDGQRIYLV
90	100	110	120	130	140	150	160
TTYAEFWFYY	KSRKNLLHCY	EVIPENAVCK	LYFDLEFNKP	ANPGADGKKM	VALLIEYVCK	ALQELYGVNC	SAEDVLNLDS
170	180	190	200	210	220	230	240
STDEKFSRHL	IFQLHDVAFK	DNIHVGNFLR	KILQPALDLL	GSEDDDSAPE	TTGHGFPHFS	EAPARQGFSF	NKMFTEKATE
250	260	270	280	290	300	310	320
ESWTSNSKKL	ERLGSAEQSS	PDLSFLVVKN	NMGEKHLFVD	LGVYTRNRNF	RLYKSSKIGK	RVALEVTEDN	KFFPIQSKDV
330	340	350	360	370	380	390	400
SDEYQYFLSS	LVSNVRFSDT	LRILTCEPSQ	NKQKGVGYFN	SIGTSVETIE	GFQCSPYPEV	DHFVLSLVNK	DGIKGGIRRW
410	420	430	440	450	460	470	480
NYFFPEELLV	YDICKYRWCE	NIGRAHKSNN	IMILVDLKNE	VWYQKCHDPV	CKAENFKSDC	FPLPAEVCLL	FLFKELDCPL
490	500	510					
VKKLNPPLLF	RRGVLKSMCT	EL					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1088	1	540.6458	-238.97	2	43.2	12.3	1	493-502	R.GVLKSMCTEL.-		MD:MU 5.03

Detailed Protein Report

Protein 372: spectrin beta chain, non-erythrocytic 4 isoform sigma1 [Homo sapiens]

Accession:	gi|115430237	**Score:**	26.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	288.8
Database Date:	2015-11-30	**pI:**	5.7
		Sequence Coverage [%]:	1.1
		No. of unique Peptides:	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MAQVPGEVDN	MEGLPAPNNN	PAARWESPDR	GWEREQPAAS	TAAASLFECS	RIKALADERE	AVQKKTFTKW	VNSHLARVGC
90	100	110	120	130	140	150	160
HIGDLYVDLR	DGFVLTRLLE	VLSGEQLPRP	TRGRMRIHSL	ENVDKALQFL	KEQRVHLENV	GSHDIVDGNH	RLTLGLVWTI
170	180	190	200	210	220	230	240
ILRFQIQVIK	IETEDNRETR	SAKDALLLWC	QMKTAGYPEV	NIQNFTTSWR	DGLAFNALIH	RHRPDLVDFS	KLTKSNANYN
250	260	270	280	290	300	310	320
LQRAFRTAEQ	HLGLARLLDP	EDVNMEAPDE	KSIITYVVSF	YHYFSKMKAL	AVEGKRIGKV	LDQVLEVGKI	IERYEELAAE
330	340	350	360	370	380	390	400
LLAWIHRTVG	LISNQKFANS	LSGVQQQLQA	FTAYCTLEKP	VKFQEKGNLE	VLLFSIQSKL	RACNRRLFVP	REGCGIWDID
410	420	430	440	450	460	470	480
KAWGELEKAE	HEREAALRAE	LIRQEKLELL	AQRFDHKVAM	RESWLNENQR	LVSQDNFGYE	LPAVEAAMKK	HEAIEADIAA
490	500	510	520	530	540	550	560
YEERVQGVAE	LAQALAAEGY	YDIRRVAAQR	DSVLRQWALL	TGLVGARRTR	LEQNLALQKV	FQEMVYMVDW	MEEMQAQLLS
570	580	590	600	610	620	630	640
RECGQHLVEA	DDLLQKHGLL	EGDIAAQSER	VEALNAAALR	FSQLQGYQPC	DPQVICNRVN	HVHGCLAELQ	EQAARRRAEL
650	660	670	680	690	700	710	720
EASRSLWALL	QELEEAESWA	RDKERLLEAA	GGGGAAGAAG	AAGTAGGAHD	LSSTARLLAQ	HKILQGELGG	RRALLQQALR
730	740	750	760	770	780	790	800
CGEELVAAGG	AVGPGADTVH	LVGLAERAAS	ARRRWQRLEE	AAARRERRLQ	EARALHQFGA	DLDGLLDWLR	DAYRLAAAGD
810	820	830	840	850	860	870	880
FGHDEASSRR	LARQHRALTG	EVEAHRGPVS	GLRRQLATLG	GASGAGPLVV	ALQVRVVEAE	QLFAEVTEVA	ALRRQWLRDA
890	900	910	920	930	940	950	960
LAVYRMFGEV	HACELWIGEK	EQWLLSMRVP	DSLDDVEVVQ	HRFESLDQEM	NSLMGRVLDV	NHTVQELVEG	GHPSSDEVRS
970	980	990	1000	1010	1020	1030	1040
CQDHLNSRWN	RIVELVEQRK	EEMSAVLLVE	NHVLEVAEVR	AQVREKRRAV	ESAPRAGGAL	QWRLSGLEAA	LQALEPRQAA
1050	1060	1070	1080	1090	1100	1110	1120
LLEEAALLAE	RFPAQAARLH	QGAEELGAEW	GALASAAQAC	GEAVAAAGRL	QRFLHDLDAF	LDWLVRAQEA	AGGSEGPLPN
1130	1140	1150	1160	1170	1180	1190	1200
SLEEADALLA	RHAALKEEVD	QREEDYARIV	AASEALLAAD	GAELGPGLAL	DEWLPHLELG	WHKLLGLWEA	RREALVQAHI
1210	1220	1230	1240	1250	1260	1270	1280
YQLFLRDLRQ	ALVVLRNQEM	ALSGAELPGT	VESVEEALKQ	HRDFLTTMEL	SQQKMQVAVQ	AAEGLLRQGN	IYGEQAQEAV
1290	1300	1310	1320	1330	1340	1350	1360
TRLLEKNQEN	QLRAQQWMQK	LHDQLELQHF	LRDCHELDGW	IHEKMLMARD	GTREDNHKLH	KRWLRHQAFM	AELAQNKEWL
1370	1380	1390	1400	1410	1420	1430	1440
EKIEREGQQL	MQEKPELAAS	VRKKLGEIRQ	CWAELESTTQ	AKARQLFEAS	KADQLVQSFA	ELDKKLLHME	SQLQDVDPGG
1450	1460	1470	1480	1490	1500	1510	1520
DLATVNSQLK	KLQSMESQVE	EWYREVGELQ	AQTAALPLEP	ASKELVGERQ	NAVGERLVRL	LEPLQERRRL	LLASKELHQV
1530	1540	1550	1560	1570	1580	1590	1600
AHDLDDELAW	VQERLPLAMQ	TERGNGLQAV	QQHIKKNQGL	RREIQAHGPR	LEEVLERAGA	LASLRSPEAE	AVRRGLEQLQ
1610	1620	1630	1640	1650	1660	1670	1680
SAWAGLREAA	ERRQQVLDAA	FQVEQYYFDV	AEVEAWLGEQ	ELLMMSEDKG	KDEQSTLQLL	KKHLQLEQGV	ENYEESIAQL
1690	1700	1710	1720	1730	1740	1750	1760
SRQCRALLEM	GHPDSEQISR	RQSQVDRLYV	ALKELGEERR	VALEQQYWLY	QLSRQVSELE	HWIAEKEVVA	GSPELGQDFE
1770	1780	1790	1800	1810	1820	1830	1840
HVSVLQEKFS	EFASETGMAG	RERLAAVNQM	VDELIECGHT	AAATMAEWKD	GLNEAWAELL	ELMGTRAQLL	AASRELHKFF
1850	1860	1870	1880	1890	1900	1910	1920
SDARELQGQI	EEKRRRLPRL	TTPPEPRPSA	SSMQRTLRAF	EHDLQLLVSQ	VRQLQEGAAQ	LRTVYAGEHA	EAIASREQEV
1930	1940	1950	1960	1970	1980	1990	2000
LQGWKELLSA	CEDARLHVSS	TADALRFHSQ	VRDLLSWMDG	IASQIGAADK	PRDVSSVEVL	MNYHQGLKTE	LEARVPELTT
2010	2020	2030	2040	2050	2060	2070	2080
CQELGRSLLL	NKSAMADEIQ	AQLDKLGTRK	EEVSEKWDRH	WEWLQQMLEV	HQFAQEAVVA	DAWLTAQEPL	LQSRELGSSV
2090	2100	2110	2120	2130	2140	2150	2160
DEVEQLIRRH	EAFRKAAAAW	EERFSSLRRL	TTIEKIKAEQ	SKQPPTPLLG	RKFFGDPTEL	AAKAAPLLRP	GGYERGLEPL
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1079	4	530.6190	-276.49	2	43.1	12.2	2	2553-2562	R.EGGDRRASGR.R	

Detailed Protein Report

Protein 373: spectrin beta chain, erythrocytic isoform b [Homo sapiens]

Accession:	gi|67782319	**Score:**	26.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	246.3
Database Date:	2015-11-30	**pI:**	5.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.0
		No. of unique Peptides:	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MTSATEFENV	GNQPPYSRIN	ARWDAPDDEL	DNDNSSARLF	ERSRIKALAD	EREVVQKKTF	TKWVNSHLAR	VSCRITDLYK
90	100	110	120	130	140	150	160
DLRDGRMLIK	LLEVLSGEML	PKPTKGKMRI	HCLENVDKAL	QFLKEQRVHL	ENMGSHDIVD	GNHRLVLGLI	WTIILRFQIQ
170	180	190	200	210	220	230	240
DIVVQTQEGR	ETRSAKDALL	LWCQMKTAGY	PHVNVTNFTS	SWKDGLAFNA	LIHKHRPDLI	DFDKLKDSNA	RHNLEHAFNV
250	260	270	280	290	300	310	320
AERQLGIIPL	LDPEDVFTEN	PDEKSIITYV	VAFYHYFSKM	KVLAVEGKRV	GKVIDHAIET	EKMIEKYSGL	ASDLLTWIEQ
330	340	350	360	370	380	390	400
TITVLNSRKF	ANSLTGVQQQ	LQAFSTYRTV	EKPPKFQEKG	NLEVLLFTIQ	SRMRANNQKV	YTPHDGKLVS	DINRAWESLE
410	420	430	440	450	460	470	480
EAEYRRELAL	RNELIRQEKL	EQLARRFDRK	AAMRETWLSE	NQRLVAQDNF	GYDLAAVEAA	KKKHEAIETD	TAAYEERVRA
490	500	510	520	530	540	550	560
LEDLAQELEK	ENYHDQKRIT	ARKDNILRLW	SYLQELLQSR	RQRLETTLAL	QKLFQDMLHS	IDWMDEIKAH	LLSAEFGKHL
570	580	590	600	610	620	630	640
LEVEDLLQKH	KLMEADIAIQ	GDKVKAITAA	TLKFTEGKGY	QPCDPQVIQD	RISHLEQCFE	ELSNMAAGRK	AQLEQSKRLW
650	660	670	680	690	700	710	720
KFFWEMDEAE	SWIKEKEQIY	SSLDYGKDLT	SVLILQRKHK	AFEDELRGLD	AHLEQIFQEA	HGMVARKQFG	HPQIEARIKE
730	740	750	760	770	780	790	800
VSAQWDQLKD	LAAFCKKNLQ	DAENFFQFQG	DADDLKAWLQ	DAHRLLSGED	VGQDEGATRA	LGKKHKDFLE	ELEESRGVME
810	820	830	840	850	860	870	880
HLEQQAQGFP	EEFRDSPDVT	HRLQALRELY	QQVVAQADLR	QQRLQEALDL	YTVFGETDAC	ELWMGEKEKW	LAEMEMPDTL
890	900	910	920	930	940	950	960
EDLEVVQHRF	DILDQEMKTL	MTQIDGVNLA	ANSLVESGHP	RSREVKQYQD	HLNTRWQAFQ	TLVSERREAV	DSALRVHNYC
970	980	990	1000	1010	1020	1030	1040
VDCEETSKWI	TDKTKVVEST	KDLGRDLAGI	IAIQRKLSGL	ERDVAAIQAR	VDALERESQQ	LMDSHPEQKE	DIGQRQKHLE
1050	1060	1070	1080	1090	1100	1110	1120
ELWQGLQQSL	QGQEDLLGEV	SQLQAFLQDL	DDFQAWLSIT	QKAVASEDMP	ESLPEAEQLL	QQHAGIKDEI	DGHQDSYQRV
1130	1140	1150	1160	1170	1180	1190	1200
KESGEKVIQG	QTDPEYLLLG	QRLEGLDTGW	NALGRMWESR	SHTLAQCLGF	QEFQKDAKQA	EAILSNQEYT	LAHLEPPDSL
1210	1220	1230	1240	1250	1260	1270	1280
EAAEAGIRKF	EDFLGSMENN	RDKVLSPVDS	GNKLVAEGNL	YSDKIKEKVQ	LIEDRHRKNN	EKAQEASVLL	RDNLELQNFL
1290	1300	1310	1320	1330	1340	1350	1360
QNCQELTLWI	NDKLLTSQDV	SYDEARNLHN	KWLKHQAFVA	ELASHEGWLE	NIDAEGKQLM	DEKPQFTALV	SQKLEALHRL
1370	1380	1390	1400	1410	1420	1430	1440
WDELQATTKE	KTQHLSAARS	SDLRLQTHAD	LNKWISAMED	QLRSDDPGKD	LTSVNRMLAK	LKRVEDQVNV	RKEELGELFA
1450	1460	1470	1480	1490	1500	1510	1520
QVPSMGEEGG	DADLSIEKRF	LDLLEPLGRR	KKQLESSRAK	LQISRDLEDE	TLWVEERLPL	AQSADYGTNL	QTVQLFMKKN
1530	1540	1550	1560	1570	1580	1590	1600
QTLQNEILGH	TPRVEDVLQR	GQQLVEAAEI	DCQDLEERLG	HLQSSWDRLR	EAAAGRLQRL	RDANEAQQYY	LDADEAEAWI
1610	1620	1630	1640	1650	1660	1670	1680
GEQELYVISD	EIPKDEEGAI	VMLKRHLRQQ	RAVEDYGRNI	KQLASRAQGL	LSAGHPEGEQ	IIRLQGQVDK	HYAGLKDVAE
1690	1700	1710	1720	1730	1740	1750	1760
ERKRKLENMY	HLFQLKRETD	DLEQWISEKE	LVASSPEMGQ	DFDHVTLLRD	KFRDFARETG	AIGQERVDNV	NAFIERLIDA
1770	1780	1790	1800	1810	1820	1830	1840
GHSEAATIAE	WKDGLNEMWA	DLLELIDTRM	QLLAASYDLH	RYFYTGAEIL	GLIDEKHREL	PEDVGLDAST	AESFHRVHTA
1850	1860	1870	1880	1890	1900	1910	1920
FERELHLLGV	QVQQFQDVAT	RLQTAYAGEK	AEAIQNKEQE	VSAAWQALLD	ACAGRRTQLV	DTADKFRFFS	MARDLLSWME
1930	1940	1950	1960	1970	1980	1990	2000
SIIRQIETQE	RPRDVSSVEL	LMKYHQGINA	EIETRSKNFS	ACLELGESLL	QRQHQASEEI	REKLQQVMSR	RKEMNEKWEA
2010	2020	2030	2040	2050	2060	2070	2080
RWERLRMLLE	VCQFSRDASV	AEAWLIAQEP	YLASGDFGHT	VDSVEKLIKR	HEAFEKSTAS	WAERFAALEK	PTTLELKERQ
2090	2100	2110	2120	2130	2140		
IAERPAEETG	PQEEEGETAG	EAPVSHHAAT	ERTSPVSLWS	RLSSSWESLQ	PEPSHPY		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2770	1	905.4785	51.90	3	66.0	26.5	1	868-889	K.EKWLAEMEMPDTLEDLEVVQHR.F	Oxidation: 9

Detailed Protein Report

Protein 374: tumor necrosis factor alpha-induced protein 3 [Homo sapiens]

Accession:	gi|5454132	**Score:**	26.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	89.6
Database Date:	2015-11-30	**pI:**	9.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.7
		No. of unique Peptides:	1

Quantitation

MD:MU	**Median:**	1.10	**CV:**	0.00 %	**No. of Peptides:**	1

Alias proteins:

Accession	**Name**	**Description**
gi|530384006	refseq_human (refseq_human_20140103.fasta)	PREDICTED: tumor necrosis factor alpha-induced protein 3 isoform X1 [Homo sapiens]
gi|395393997	refseq_human (refseq_human_20140103.fasta)	tumor necrosis factor alpha-induced protein 3 [Homo sapiens]
gi|395393995	refseq_human (refseq_human_20140103.fasta)	tumor necrosis factor alpha-induced protein 3 [Homo sapiens]

10	20	30	40	50	60	70	80
MAEQVLPQAL	YLSNMRKAVK	IRERTPEDIF	KPTNGIIHHF	KTMHRYTLEM	FRTCQFCPQF	REIIHKALID	RNIQATLESQ
90	100	110	120	130	140	150	160
KKLNWCREVR	KLVALKTNGD	GNCLMHATSQ	YMWGVQDTDL	VLRKALFSTL	KETDTRNFKF	RWQLESLKSQ	EFVETGLCYD
170	180	190	200	210	220	230	240
TRNWNDEWDN	LIKMASTDTP	MARSGLQYNS	LEEIHIFVLC	NILRRPIIVI	SDKMLRSLES	GSNFAPLKVG	GIYLPLHWPA
250	260	270	280	290	300	310	320
QECYRYPIVL	GYDSHHFVPL	VTLKDSGPEI	RAVPLVNRDR	GRFEDLKVHF	LTDPENEMKE	KLLKEYLMVI	EIPVQGWDHG
330	340	350	360	370	380	390	400
TTHLINAAKL	DEANLPKEIN	LVDDYFELVQ	HEYKKWQENS	EQGRREGHAQ	NPMEPSVPQL	SLMDVKCETP	NCPFFMSVNT
410	420	430	440	450	460	470	480
QPLCHECSER	RQKNQNKLPK	LNSKPGPEGL	PGMALGASRG	EAYEPLAWNP	EESTGGPHSA	PPTAPSPFLF	SETTAMKCRS
490	500	510	520	530	540	550	560
PGCPFTLNVQ	HNGFCERCHN	ARQLHASHAP	DHTRHLDPGK	CQACLQDVTR	TFNGICSTCF	KRTTAEASSS	LSTSLPPSCH
570	580	590	600	610	620	630	640
QRSKSDPSRL	VRSPSPHSCH	RAGNDAPAGC	LSQAARTPGD	RTGTSKCRKA	GCVYFGTPEN	KGFCTLCFIE	YRENKHFAAA
650	660	670	680	690	700	710	720
SGKVSPTASR	FQNTIPCLGR	ECGTLGSTMF	EGYCQKCFIE	AQNQRFHEAK	RTEEQLRSSQ	RRDVPRTTQS	TSRPKCARAS
730	740	750	760	770	780	790	800
CKNILACRSE	ELCMECQHPN	QRMGPGAHRG	EPAPEDPPKQ	RCRAPACDHF	GNAKCNGYCN	ECFQFKQMYG	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1527	1	932.4083	-48.26	2	48.9	13.5	1	53-66	R.TCQFCPQFREIIHK.A	Carbamidomethyl: 2, 5	MD:MU 1.10

Detailed Protein Report

Protein 375: **PREDICTED: serine/threonine-protein phosphatase with EF-hands 2 isoform X1 [Homo sapiens]**

Accession:	gi|578809184	**Score:**	26.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	69.0
Database Date:	2015-11-30	**pI:**	9.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGSGTSTQHH	FAFQNAERAF	KAAALIQRWY	RRYVARLEMR	RRCTWSIFQS	IEYAGQQDQV	KLHDFFSYLM	DHFIPSSHND
90	100	110	120	130	140	150	160
RDFLTRIFTE	DRFAQDSEMK	KCSDYESIEV	PDSYTGPRLS	FPLLPDHATA	LVEAFRLKQQ	LHARYVLNLL	YETKKHLVQL
170	180	190	200	210	220	230	240
PNINRVSTCY	SEEITVCGDL	HGQLDDLIFI	FYKNGLPSPE	RSYVFNGDFV	DRGKDSVEIL	MILFAFMLVY	PKEFHLNRGN
250	260	270	280	290	300	310	320
HEDHMVNLRY	GFTKEVMNKY	KVHGKEILRT	LQDVFCWLPL	ATLIDEKVLI	LHGGVSDITD	LELLDKIERS	KIVSTMRCKT
330	340	350	360	370	380	390	400
RQKSEKQMEE	KRRANQKSSA	QGPIPWFLPE	SRSLPSSPLR	LGSYKAQKTS	RSSSIPCSGS	LDGRELSRQV	RSSVELELER
410	420	430	440	450	460	470	480
CRQQAGLLVT	GEKEEPSRSA	SEADSEAGEL	RKPTQEEWRQ	VVDILWSDPM	AQEGCKANTI	RGGGCYFGPD	VTQQLLQKYN
490	500	510	520	530	540	550	560
MQFLIRSHEC	KPEGYEFCHN	RKVLTIFSAS	NYYEVGSNRG	AYVKLGPALT	PHIVQYQANK	VTHTLTMRQR	ISRVEESALR
570	580	590	600				
ALREKLFAHS	SDLLSEFKKH	DADKVGLASS	QLCYYQQK				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2068	1	946.8198	-78.17	2	55.7	14.8	0	487-501	R.SHECKPEGYEFCHNR.K	Carbamidomethyl: 4

Detailed Protein Report

Protein 376: zinc finger protein 483 isoform a [Homo sapiens]

Accession:	gi|190014620	**Score:**	26.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	85.0
Database Date:	2015-11-30	**pI:**	9.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MQAVVPLNKM	TAISPEPQTL	ASTEQNEVPR	VVTSGEQEAI	LRGNAADAES	FRQRFRWFCY	SEVAGPRKAL	SQLWELCNQW
90	100	110	120	130	140	150	160
LRPDIHTKEQ	ILELLVFEQF	LTILPGEIRI	WVKSQHPESS	EEVVTLIEDL	TQMLEEKDPV	SQDSTVSQEE	NSKEDKMVTV
170	180	190	200	210	220	230	240
CPNTESCESI	TLKDVAVNFS	RGEWKKLEPF	QKELYKEVLL	ENLRNLEFLD	FPVSKLELIS	QLKWVELPWL	LEEVSKSSRL
250	260	270	280	290	300	310	320
DESALDKIIE	RCLRDDDHGL	MEESQQYCGS	SEEDHGNQGN	SKGRVAQNKT	LGSGSRGKKF	DPDKSPFGHN	FKETSDLIKH
330	340	350	360	370	380	390	400
LRVYLRKKSR	RYNESKKPFS	FHSDLVLNRK	EKTAGEKSRK	SNDGGKVLSH	SSALTEHQKR	QKIHLGDRSQ	KCSKCGIIFI
410	420	430	440	450	460	470	480
RRSTLSRRKT	PMCEKCRKDS	CQEAALNKDE	GNESGEKTHK	CSKCGKAFGY	SASLTKHRRI	HTGEKPYMCN	ECGKAFSDSS
490	500	510	520	530	540	550	560
SLTPHHRTHS	GEKPFKCDDC	GKGFTLSAHL	IKHQRIHTGE	KPYKCKDCGR	PFSDSSSLIQ	HQRIHTGEKP	YTCSNCGKSF
570	580	590	600	610	620	630	640
SHSSSLSKHQ	RIHTGEKPYK	CGECGKAFRQ	NSCLTRHQRI	HTGEKPYLCN	DCGMTFSHFT	SVIYHQRLHS	GEKPYKCNQC
650	660	670	680	690	700	710	720
EKAFPTHSLL	SRHQRIHTGV	KPYKCKECGK	SFSQSSSLNE	HHRIHTGEKP	YECNYCGATF	SRSSILVEHL	KIHTGRREYE
730	740	750					
CNECEKTFKS	NSGLIRHRGF	HSAE					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
173	1	1318.5770	-87.18	2	31.6	12.9	1	68-88	R.KALSQLWELCNQWLRPDIHTK.E	Carbamidomethyl: 10

Detailed Protein Report

Protein 377: PREDICTED: zinc finger protein 41 isoform X5 [Homo sapiens]

Accession:	gi|530421580	**Score:**	26.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	79.5
Database Date:	2015-11-30	**pI:**	10.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.5
		No. of unique Peptides:	2

Alias proteins:

Accession	Name	Description
gi|578838101	refseq_human (refseq_human_20140103.fasta)	PREDICTED: zinc finger protein 41 isoform X15 [Homo sapiens]
gi|530421582	refseq_human (refseq_human_20140103.fasta)	PREDICTED: zinc finger protein 41 isoform X6 [Homo sapiens]

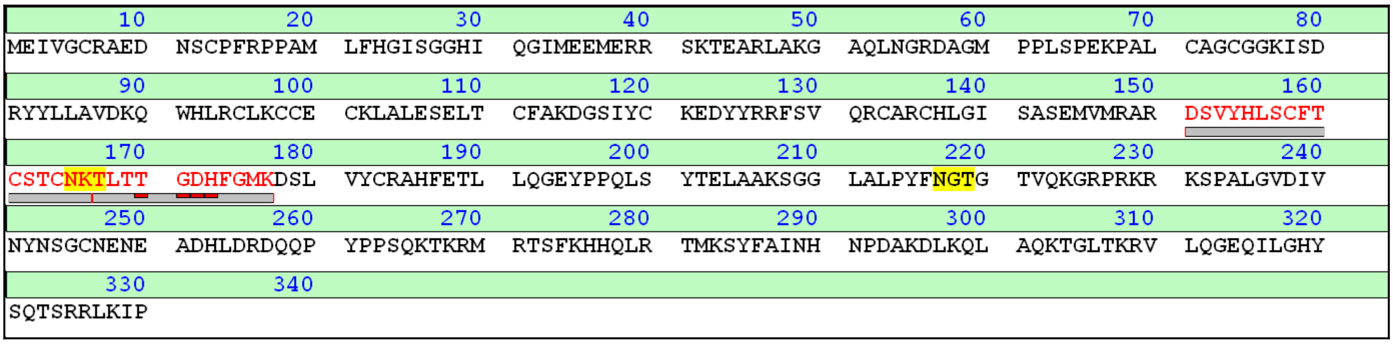
10	20	30	40	50	60	70	80
MLEGEAPHQS	CSGEAIGKMQ	QQGIPGGIFF	HCERFDQPIG	EDSLCSILEE	LWQDNDQLEQ	RQENQNNLLS	HVKVLIKERG
90	100	110	120	130	140	150	160
YEHKNIEKII	HVTTKLVPSI	KRLHNCDTIL	KHTLNSHNHN	RNSATKNLGK	IFGNGNNFPH	SPSSTKNENA	KTGANSCEHD
170	180	190	200	210	220	230	240
HYEKHLSHKQ	APTHHQKIHP	EEKLYVCTEC	VMGFTQKSHL	FEHQRIHAGE	KSRECDKSNK	VFPQKPQVDV	HPSVYTGEKP
250	260	270	280	290	300	310	320
YLCTQCGKVF	TLKSNLITHQ	KIHTGQKPYK	CSECGKAFFQ	RSDLFRHLRI	HTGEKPYECS	ECGKGFSQNS	DLSIHQKTHT
330	340	350	360	370	380	390	400
GEKHYECNEC	GKAFTRKSAL	RMHQRIHTGE	KPYVCADCGK	AFIQKSHFNT	HQRIHTGEKP	YECSDCGKSF	TKKSQLHVHQ
410	420	430	440	450	460	470	480
RIHTGEKPYI	CTECGKVFTH	RTNLTTHQKT	HTGEKPYMCA	ECGKAFTDQS	NLIKHQKTHT	GEKPYKCNGC	GKAFIWKSRL
490	500	510	520	530	540	550	560
KIHQKSHIGE	RHYECKDCGK	AFIQKSTLSV	HQRIHTGEKP	YVCPECGKAF	IQKSHFIAHH	RIHTGEKPYE	CSDCGKCFTK
570	580	590	600	610	620	630	640
KSQLRVHQKI	HTGEKPNICA	ECGKAFTDRS	NLITHQKIHT	REKPYECGDC	GKTFTWKSRL	NIHQKSHTGE	RHYECSKCGK
650	660	670	680	690	700		
AFIQKATLSM	HQIIHTGKKP	YACTECQKAF	TDRSNLIKHQ	KMHSGEKRYK	ASD		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1222	1	955.6757	154.26	2	44.9	10.3	2	80-95	R.GYEHKNIEKIIHVTTK.L	
2726	1	884.9432	75.73	2	64.4	16.1	0	430-444	K.THTGEKPYMCAECGK.A	Carbamidomethyl: 10, 13

Detailed Protein Report

Protein 378: PREDICTED: LIM/homeobox protein Lhx9 isoform X2 [Homo sapiens]

Accession:	gi|530365098	**Score:**	26.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	37.1
Database Date:	2015-11-30	**pI:**	10.2
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	8.2
		No. of unique Peptides:	2



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
2658	1	932.9537	71.73	2	64.4	15.8	0	151-166	R.DSVYHLSCFTCSTCNK.T	Carbamidomethyl: 11
929	1	612.4347	236.48	2	41.1	10.6	0	167-177	K.TLTTGDHFGMK.D	Oxidation: 10

Detailed Protein Report

Protein 379: **proline-rich protein 18 [Homo sapiens]**

Accession:	gi|58331144	**Score:**	26.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	30.9
Database Date:	2015-11-30	**pI:**	12.1
		Sequence Coverage [%]:	5.1
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MPFPPMPPPP	APAPGAQAAR	QLPRRPCAAG	DKKKRPPQRP	EGLLSSSWPS	ATLKRPPARR	GPGLDRTQPP	APPGVSPQAL
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
PSRARAPATC	APPRPAGSGH	SPARTTYAAT	SAGTGTTAAG	TSSGAGPCPD	SAARFCLNLT	PEAVLVIQKR	HLEKQLLARP
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
RRPFPSPSAE	PRRLLAPCLP	ARAAGPRRGG	PASDPDAPPT	AGQGRRAPPP	GAQLLHGGLQ	VPQLSPRPGA	LRPMLKVSLL
250	**260**	**270**	**280**	**290**	**300**		
NERHRYDDVE	YEEEPEAVDE	GLVRKCTEWL	RGVESAAAAR	GRAGALDSRR	HLSTL		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1740	1	555.2376	-174.09	2	51.7	12.3	1	173-182	R.RLLAPCLPAR.A	
2875	2	703.3735	-49.65	2	66.6	14.1	1	174-187	R.LLAPCLPARAAGPR.R	

Protein 380: **spermatogenesis-associated protein 31E1 [Homo sapiens]**

Accession:	gi|155029550	**Score:**	26.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	157.0
Database Date:	2015-11-30	**pI:**	10.3
		Sequence Coverage [%]:	1.8
		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
1848	1	805.3101	-128.16	2	53.1	14.3	2	1394-1407	R.GIRDRDSSWAPPPR.E	

Detailed Protein Report

Protein 381: probable global transcription activator SNF2L2 isoform c [Homo sapiens]

Accession:	gi|574957245	**Score:**	26.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	172.5
Database Date:	2015-11-30	**pI:**	6.7
		Sequence Coverage [%]:	1.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSTPTDPGAM	PHPGPSPGPG	PSPGPILGPS	PGPGPSPGSV	HSMMGPSPGP	PSVSHPMPTM	GSTDFPQEGM	HQMHKPIDGI
90	100	110	120	130	140	150	160
HDKGIVEDIH	CGSMKGTGMR	PPHPGMGPPQ	SPMDQHSQGY	MSPHPSPLGA	PEHVSSPMSG	GGPTPPQMPP	SQPGALIPGD
170	180	190	200	210	220	230	240
PQAMSQPNRG	PSPFSPVQLH	QLRAQILAYK	MLARGQPLPE	TLQLAVQGKR	TLPGLQQQQQ	QQQQQQQQQQ	QQQQQQQQPQ
250	260	270	280	290	300	310	320
QQPPQPQTQQ	QQQPALVNYN	RPSGPGPELS	GPSTPQKLPV	PAPGGRPSPA	PPAAAQPPAA	AVPGPSVPQP	APGQPSPVLQ
330	340	350	360	370	380	390	400
LQQKQSRISP	IQKPQGLDPV	EILQEREYRL	QARIAHRIQE	LENLPGSLPP	DLRTKATVEL	KALRLLNFQR	QLRQEVVACM
410	420	430	440	450	460	470	480
RRDTTLETAL	NSKAYKRSKR	QTLREARMTE	KLEKQQKIEQ	ERKRRQKHQE	YLNSILQHAK	DFKEYHRSVA	GKIQKLSKAV
490	500	510	520	530	540	550	560
ATWHANTERE	QKKETERIEK	ERMRRLMAED	EEGYRKLIDQ	KKDRRLAYLL	QQTDEYVANL	TNLVWEHKQA	QAAKEKKKRR
570	580	590	600	610	620	630	640
RRKKKAEENA	EGGESALGPD	GEPIDESSQM	SDLPVKVTHT	ETGKVLFGPE	APKASQLDAW	LEMNPGYEVA	PRSDSEESDS
650	660	670	680	690	700	710	720
DYEEEDEEEE	SSRQETEEKI	LLDPNSEEVS	EKDAKQIIET	AKQDVDDEYS	MQYSARGSQS	YYTVAHAISE	RVEKQSALLI
730	740	750	760	770	780	790	800
NGTLKHYQLQ	GLEWMVSLYN	NNLNGILADE	MGLGKTIQTI	ALITYLMEHK	RLNGPYLIIV	PLSTLSNWTY	EFDKWAPSVV
810	820	830	840	850	860	870	880
KISYKGTPAM	RRSLVPQLRS	GKFNVLLTTY	EYIIKDKHIL	AKIRWKYMIV	DEGHRMKNHH	CKLTQVDLNE	EETILIIRRL
890	900	910	920	930	940	950	960
HKVLRPFLLR	RLKKEVESQL	PEKVEYVIKC	DMSALQKILY	RHMQAKGILL	TDGSEKDKKG	KGGAKTLMNT	IMQLRKICNH
970	980	990	1000	1010	1020	1030	1040
PYMFQHIEES	FAEHLGYSNG	VINGAELYRA	SGKFELLDRI	LPKLRATNHR	VLLFCQMTSL	MTIMEDYFAF	RNFLYLRLDG
1050	1060	1070	1080	1090	1100	1110	1120
TTKSEDRAAL	LKKFNEPGSQ	YFIFLLSTRA	GGLGLNLQAA	DTVVIFDSDW	NPHQDLQAQD	RAHRIGQQNE	VRVLRLCTVN
1130	1140	1150	1160	1170	1180	1190	1200
SVEEKILAAA	KYKLNVDQKV	IQAGMFDQKS	SSHERRAFLQ	AILEHEEENE	EEDEVPDDET	LNQMIARREE	EFDLFMRMDM
1210	1220	1230	1240	1250	1260	1270	1280
DRRREDARNP	KRKPRLMEED	ELPSWIIKDD	AEVERLTCEE	EEEKIFGRGS	RQRRDVDYSD	ALTEKQWLRA	IEDGNLEEME
1290	1300	1310	1320	1330	1340	1350	1360
EEVRLKKRKR	RRNVDKDPAK	EDVEKAKKRR	GRPPAEKLSP	NPPKLTKQMN	AIIDTVINYK	DSSGRQLSEV	FIQLPSRKEL
1370	1380	1390	1400	1410	1420	1430	1440
PEYYELIRKP	VDFKKIKERI	RNHKYRSLGD	LEKDVMLLCH	NAQTFNLEGS	QIYEDSIVLQ	SVFKSARQKI	AKEEESEDES
1450	1460	1470	1480	1490	1500	1510	1520
NEEEEEEDEE	ESESEAKSVK	VKIKLNKKDD	KGRDKGKGKK	RPNRGKAKPV	VSDFDSDEEQ	DEREQSEGSG	TDDE

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2825	2	1024.0347	-1.30	2	65.7	15.7	1	1053-1069	K.KFNEPGSQYFIFLLSTR.A	

Detailed Protein Report

Protein 382: zinc finger protein 275 [Homo sapiens]

Accession:	gi|298231195	**Score:**	26.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	37.0
Database Date:	2015-11-30	**pI:**	10.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	6.7
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MMSHPCVSLL	GVPVLNPALV	PHLAQGQVLL	VSDPSPNTDP	AKYSESTSAT	RHQMKGEDAQ	PQEMASTSFP	RASGPSPEFR
90	100	110	120	130	140	150	160
QHGDSDGKRG	SPQNLPIEHH	FACKECGDTF	RLKVLLVQHQ	RVHSEEKGWE	CGDCGKVFRG	VAEFNEHRKS	HVAAEPQPGP
170	180	190	200	210	220	230	240
SRALENAAEK	REQMEREAKP	FECEECGKRF	KKNAGLSQHL	RVHSREKPFD	CEECGRSFKV	NTHLFRHQKL	HTSEKPFACK
250	260	270	280	290	300	310	320
ACSRDFLDRQ	ELLKHQRMHT	GHLPFDCDDC	GKSFRGVNGL	AEHQRIHSGA	KPYGCPHCGK	LFRRSSELTK	HRRIHTGEKP
330							
YACGLPWAL							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2741	1	806.4367	70.79	2	65.5	13.9	0	286-300	R.IHSGAKPYGCPHCGK.L	Carbamidomethyl: 13
803	1	820.2164	-287.56	1	39.4	12.4	1	304-310	R.RSSELTK.H	

Detailed Protein Report

Protein 383: SH3 and multiple ankyrin repeat domains protein 3 [Homo sapiens]

Accession:	gi|380748963	**Score:**	26.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	184.6
Database Date:	2015-11-30	**pI:**	9.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.8
		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
1868	1	840.7873	-166.49	2	53.4	13.8	1	693-707	R.SKSMTAELEELASIR.R	Oxidation: 4

Detailed Protein Report

Protein 384: **PREDICTED: polyribonucleotide nucleotidyltransferase 1, mitochondrial isoform X1 [Homo sapiens]**

Accession:	gi|530368250	**Score:**	26.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	77.3
Database Date:	2015-11-30	**pI:**	6.2
		Sequence Coverage [%]:	4.7
		No. of unique Peptides:	2

```
        10         20         30         40         50         60         70         80
MVTAVSKTKP SPSQFMPLVV DYRQKAAAAG RIPTNYLRRE IGTSDKEILT SRIIDRSIRP LFPAGYFDYT 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
2331	1	973.5348	3.64	2	59.0	11.2	2	40-56	R.EIGTSDKEILTSRIIDR.S	
2737	1	885.4690	-31.70	2	64.6	15.2	1	671-686	K.VLQSPATTVVRTLNDR.S	

Detailed Protein Report

Protein 385: mitochondrial inner membrane protein OXA1L [Homo sapiens]

Accession: gi|223718097
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 26.3
MW [kDa]: 55.2
pI: 10.6
Sequence Coverage [%]: 3.2
No. of unique Peptides: 1

Quantitation

MD:MU **Median:** 1.09 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MVTWLYRFLP	TSNMAAKLRS	LLPPDLRLQF	WLHARLQKCF	LSRGCGSYCA	GAKASPLPGK	MAMGLMCGRR	ELLRLLQSGR
90	100	110	120	130	140	150	160
RVHSVAGPSQ	WLGKPLTTRL	LFPAAPCCCR	PHYLFLAASG	PRSLSTSAIS	FAEVQVQAPP	VVAATPSPTA	VPEVASGETA
170	180	190	200	210	220	230	240
DVVQTAAEQS	FAELGLGSYT	PVGLIQNLLE	FMHVDLGLPW	WGAIAACTVF	ARCLIFPLIV	TGQREAARIH	NHLPEIQKFS
250	260	270	280	290	300	310	320
SRIREAKLAG	DHIEYYKASS	EMALYQKKHG	IKLYKPLILP	VTQAPIFISF	FIALREMANL	PVPSLQTGGL	WWFQDLTVSD
330	340	350	360	370	380	390	400
PIYILPLAVT	ATMWAVLELG	AETGVQSSDL	QWMRNVIRMM	PLITLPITMH	FPTAVFMYWL	SSNLFSLVQV	SCLRIPAVRT
410	420	430	440	450	460	470	480
VLKIPQRVVH	DLDKLPPREG	FLESFKKGWK	NAEMTRQLRE	REQRMRNQLE	LAARGPLRQT	FTHNPLLQPG	KDNPPNIPSS
490	500						
SSKPKSKYPW	HDTLG						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1726	1	546.7057	-111.00	2	51.5	15.2	1	428-436	K.GWKNAEMTR.Q		MD:MU 1.09

Detailed Protein Report

Protein 386: **PREDICTED: E3 ubiquitin-protein ligase UBR4 isoform X13 [Homo sapiens]**

Accession:	gi|578798776	**Score:**	26.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	573.4
Database Date:	2015-11-30	**pI:**	5.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	0.6
		No. of unique Peptides:	2

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
270	1	530.5999	-29.12	3	33.1	13.6	2	1777-1790	K.VADEEKPKKSSLCR.T	
1759	2	920.8290	-80.75	2	52.0	12.7	0	4469-4485	K.MAGVMAQCGGLECMLNR.L	Carbamidomethyl: 13

Detailed Protein Report

Protein 387: eukaryotic translation initiation factor 3 subunit B [Homo sapiens]

Accession:	gi|33239445	**Score:**	26.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	92.4
Database Date:	2015-11-30	**pI:**	4.7
		Sequence Coverage [%]:	2.8
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 0.46 **CV:** 0.00 % **No. of Peptides:** 1

Alias proteins:

Accession	Name	Description
gi|83367072	refseq_human (refseq_human_20140103.fasta)	eukaryotic translation initiation factor 3 subunit B [Homo sapiens]

10	20	30	40	50	60	70	80
MQDAENVAVP	EAAEERAEPG	QQQPAAEPPP	AEGLLRPAGP	GAPEAAGTEA	SSEEVGIAEA	GPESEVRTEP	AAEAEAASGP
90	100	110	120	130	140	150	160
SESPSPPAAE	ELPGSHAEPP	VPAQGEAPGE	QARDERSDSR	AQAVSEDAGG	NEGRAAEAEP	RALENGDADE	PSFSDPEDFV
170	180	190	200	210	220	230	240
DDVSEEELLG	DVLKDRPQEA	DGIDSVIVVD	NVPQVGPDRL	EKLKNVIHKI	FSKFGKITND	FYPEEDGKTK	GYIFLEYASP
250	260	270	280	290	300	310	320
AHAVDAVKNA	DGYKLDKQHT	FRVNLFTDFD	KYMTISDEWD	IPEKQPFKDL	GNLRYWLEEA	ECRDQYSVIF	ESGDRTSIFW
330	340	350	360	370	380	390	400
NDVKDPVSIE	ERARWTETYV	RWSPKGTYLA	TFHQRGIALW	GGEKFKQIQR	FSHQGVQLID	FSPCERYLVT	FSPLMDTQDD
410	420	430	440	450	460	470	480
PQAIIIWDIL	TGHKKRGFHC	ESSAHWPIFK	WSHDGKFFAR	MTLDTLSIYE	TPSMGLLDKK	SLKISGIKDF	SWSPGGNIIA
490	500	510	520	530	540	550	560
FWVPEDKDIP	ARVTLMQLPT	RQEIRVRNLF	NVVDCKLHWQ	KNGDYLCVKV	DRTPKGTQGV	VTNFEIFRMR	EKQVPVDVVE
570	580	590	600	610	620	630	640
MKETIIAFAW	EPNGSKFAVL	HGEAPRISVS	FYHVKNNGKI	ELIKMFDKQQ	ANTIFWSPQG	QFVVLAGLRS	MNGALAFVDT
650	660	670	680	690	700	710	720
SDCTVMNIAE	HYMASDVEWD	PTGRYVVTSV	SWWSHKVDNA	YWLWTFQGRL	LQKNNKDRFC	QLLWRPRPPT	LLSQEQIKQI
730	740	750	760	770	780	790	800
KKDLKKYSKI	FEQKDRLSQS	KASKELVERR	RTMMEDFRKY	RKMAQELYME	QKNERLELRG	GVDTDELDSN	VDDWEEETIE
810	820						
FFVTEEIIPL	GNQE						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
450	1	680.6717	-200.25	2	34.9	12.9	0	121-134	R.AQAVSEDAGGNEGR.A		MD:MU 0.46

Detailed Protein Report

Protein 388: metabotropic glutamate receptor 4 isoform 5 [Homo sapiens]

Accession:	gi|378548216	**Score:**	26.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	83.5
Database Date:	2015-11-30	**pI:**	9.9
		Sequence Coverage [%]:	3.2
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MSCKIPQISY	ASTAPDLSDN	SRYDFFSRVV	PSDTYQAQAM	VDIVRALKWN	YVSTVASEGS	YGESGVEAFI	QKSREDGGVC
90	100	110	120	130	140	150	160
IAQSVKIPRE	PKAGEFDKII	RRLLETSNAR	AVIIFANEDD	IRRVLEAARR	ANQTGHFFWM	GSDSWGSKIA	PVLHLEEVAE
170	180	190	200	210	220	230	240
GAVTILPKRM	SVRGFDRYFS	SRTLDNNRRN	IWFAEFWEDN	FHCKLSRHAL	KKGSHVKKCT	NRERIGQDSA	YEQEGKVQFV
250	260	270	280	290	300	310	320
IDAVYAMGHA	LHAMHRDLCP	GRVGLCPRMD	PVDGTQLLKY	IRNVNFSGIA	GNPVTFNENG	DAPGRYDIYQ	YQLRNDSAEY
330	340	350	360	370	380	390	400
KVIGSWTDHL	HLRIERMHWP	GSGQQLPRSI	CSLPCQPGER	KKTVKGMPCC	WHCEPCTGYQ	YQVDRYTCKT	CPYDMRPTEN
410	420	430	440	450	460	470	480
RTGCRPIPII	KLEWGSPWAV	LPLFLAVVGI	AATLFVVITF	VRYNDTPIVK	ASGRELSYVL	LAGIFLCYAT	TFLMIAEPDL
490	500	510	520	530	540	550	560
GTCSLRRIFL	GLGMSISYAA	LLTKTNRIYR	IFEQGKRSVS	APRFISPASQ	LAITFSLISL	QLLGICVWFV	VDPSHSVVDF
570	580	590	600	610	620	630	640
QDQRTLDPRF	ARGVLKCDIS	DLSLICLLGY	SMLLMVTCTV	YAIKTRGVPE	TFNEAKPIGF	TMYTTCIVWL	AFIPIFFGTS
650	660	670	680	690	700	710	720
QSADKLYIQT	TTLTVSVSLS	ASVSLGMLYM	PKVYIILFHP	EQNVPKRKRS	LKAVVTAATM	SNKFTQKGNF	RPNGEAKSEL
730	740	750					
CENLEAPALA	TKQTYVTYTN	HAI					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2591	1	701.8584	-42.25	2	62.4	10.3	2	90-101	R.EPKAGEFDKIIR.R	
2594	1	741.8530	35.29	2	63.0	15.9	0	390-401	K.TCPYDMRPTENR.T	

Detailed Protein Report

Protein 389: NF-X1-type zinc finger protein NFXL1 [Homo sapiens]

Accession:	gi|89363020	**Score:**	26.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	101.3
Database Date:	2015-11-30	**pI:**	10.5
		Sequence Coverage [%]:	2.9
		No. of unique Peptides:	1

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
490	1	587.1540	-200.57	2	35.5	10.2	2	475-483	R.DCQKHQCRR.K	

Detailed Protein Report

Protein 390: **tubulin--tyrosine ligase-like protein 12 [Homo sapiens]**

Accession:	gi|11056036	**Score:**	26.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	74.4
Database Date:	2015-11-30	**pI:**	5.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.7
		No. of unique Peptides:	1

```
        10          20          30          40          50          60          70          80
MEAERGPERR  PAERSSPGQT  PEEGAQALAE  FAALHGPALR  ASGVPERYWG  RLLHKLEHEV  FDAGEVFGIM  QVEEVEEEED

        90         100         110         120         130         140         150         160
EAAREVRKQQ  PNPGNELCYK  VIVTRESGLQ  AAHPNSIFLI  DHAWTCRVEH  ARQQLQQVPG  LLHRMANLMG  IEFHGELPST

       170         180         190         200         210         220         230         240
EAVALVLEEM  WKFNQTYQLA  HGTAEEKMPV  WYIMDEFGSR  IQHADVPSFA  TAPFFYMPQQ  VAYTLLWPLR  DLDTGEEVTR

       250         260         270         280         290         300         310         320
DFAYGETDPL  IRKCMLLPWA  PTDMLDLSSC  TPEPPAEHYQ  AILEENKEKL  PLDINPVVHP  HGHIFKVYTD  VQQVASSLTH

       330         340         350         360         370         380         390         400
PRFTLTQSEA  DADILFNFSH  FKDYRKLSQE  RPGVLLNQFP  CENLLTVKDC  LASIARRAGG  PEGPPWLPRT  FNLRTELPQF

       410         420         430         440         450         460         470         480
VSYFQQRERW  GEDNHWICKP  WNLARSLDTH  VTKSLHSIIR  HRESTPKVVS  KYIESPVLFL  REDVGKVKFD  IRYIVLLRSV

       490         500         510         520         530         540         550         560
RPLRLFVYDV  FWLRFSNRAF  ALNDLDDYEK  HFTVMNYDPD  VVLKQVHCEE  FIPEFEKQYP  EFPWTDVQAE  IFRAFTELFQ

       570         580         590         600         610         620         630         640
VACAKPPPLG  LCDYPSSRAM  YAVDLMLKWD  NGPDGRRVMQ  PQILEVNFNP  DCERACRYHP  TFFNDVFSTL  FLDQPGGCHV

       650
TCLV
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1692	1	696.9748	-35.52	3	50.9	10.5	0	598-614	R.VMQPQILEVNFNPDCER.A	Carbamidomethyl: 15

Detailed Protein Report

Protein 391: **multiple epidermal growth factor-like domains protein 8 isoform 2 precursor [Homo sapiens]**

Accession:	gi|145701025	**Score:**	26.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	295.7
Database Date:	2015-11-30	**pI:**	6.5
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	1.8
		No. of unique Peptides:	2

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
1619	1	1023.8271	-75.44	3	50.1	15.1	2	1-31	-.MALGKVLAMALVLALAVLGSLSPGARAGDCK.G	Carbamidomethyl: 30; Oxidation: 1
112	1	668.6652	6.60	3	31.1	11.1	0	608-626	R.LLGDCQACLAFSSPTAPPR.G	Carbamidomethyl: 8

Detailed Protein Report

Protein 392: PREDICTED: dynamin-binding protein isoform X1 [Homo sapiens]

Accession:	gi|578819186	**Score:**	26.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	172.2
Database Date:	2015-11-30	**pI:**	5.1
		Sequence Coverage [%]:	2.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEAGSVVRAI	FDFCPSVSEE	LPLFVGDIIE	VLAVVDEFWL	LGKKEDVTGQ	FPSSFVEIVT	IPSLKEGERL	FVCICEFTSQ
90	100	110	120	130	140	150	160
ELDNLPLHRG	DLVILDGIPT	AGWLQGRSCW	GARGFFPSSC	VRELCLSSQS	RQWHSQSALF	QIPEYSMGQA	RALMGLSAQL
170	180	190	200	210	220	230	240
DEELDFREGD	VITIIGVPEP	GWFEGELEGR	RGIFPEGFVE	LLGPLRTVDE	SVSSGNQDDC	IVNGEVDTPV	GEEEIGPDED
250	260	270	280	290	300	310	320
EEEPGTYGVA	LYRFQALEPN	ELDFEVGDKI	RILATLEDGW	LEGSLKGRTG	IFPYRFVKLC	PDTRVEETMA	LPQEGSLARI
330	340	350	360	370	380	390	400
PETSLDCLEN	TLGVEEQRHE	TSDHEAEEPD	CIISEAPTSP	LGHLTSEYDT	DRNSYQDEDT	AGGPPRSPGV	EWEMPLATDS
410	420	430	440	450	460	470	480
PTSDPTEVVN	GISSQPQVPF	HPNLQKSQYY	STVGGSHPHS	EQYPDLLPLE	ARTRDYASLP	PKRMYSQLKT	LQKPVLPLYR
490	500	510	520	530	540	550	560
GSSVSASRVV	KPRQSSPQLH	NLASYTKKHH	TSSVYSISER	LEMKPGPQAQ	GLVMEAATHS	QGDGSTDLDS	KLTQQLIEFE
570	580	590	600	610	620	630	640
KSLAGPGTEP	DKILRHFSIM	DFNSEKDIVR	GSSKLITEQE	LPERRKALRP	PPPRPCTPVS	TSPHLLVDQN	LKPAPPLVVR
650	660	670	680	690	700	710	720
PSRPAPLPPS	AQQRTNAVSP	KLLSRHRPTC	ETLEKEGPGH	MGRSLDQTSP	CPLVLVRIEE	MERDLDMYSR	AQEELNLMLE
730	740	750	760	770	780	790	800
EKQDESSRAE	TLEDLKFCES	NIESLNMELQ	QLREMTLLSS	QSSSLVAPSG	SVSAENPEQR	MLEKRAKVIE	ELLQTERDYI
810	820	830	840	850	860	870	880
RDLEMCIERI	MVPMQQAQVP	NIDFEGLFGN	MQMVIKVSKQ	LLAALEISDA	VGPVFLGHRD	ELEGTYKIYC	QNHDEAIALL
890	900	910	920	930	940	950	960
EIYEKDEKIQ	KHLQDSLADL	KSLYNEWGCT	NYINLGSFLI	KPVQRVMRYP	LLLMELLNST	PESHPDKVPL	TNAVLAVKEI
970	980	990	1000	1010	1020	1030	1040
NVNINEYKRR	KDLVLKYRKG	DEDSLMEKIS	KLNIHSIIKK	SNRVSSHLKH	LTGFAPQIKD	EVFEETEKNF	RMQERLIKSF
1050	1060	1070	1080	1090	1100	1110	1120
IRDLSLYLQH	IRKERTERLV	ISPLNQLLSM	FTGPHKLVQK	RFDKLLDFYN	CTERAEKLKD	KKTLEELQSA	RNNYEALNAQ
1130	1140	1150	1160	1170	1180	1190	1200
LLDELPKFHQ	YAQGLFTNCV	HGYAEAHCDF	VHQALEQLKP	LLSLLKVAGR	EGNLIAIFHE	EHSRVLQQLQ	VFTFFPESLP
1210	1220	1230	1240	1250	1260	1270	1280
ATKKPFERKT	IDRQSARKPL	LGLPSYMLQS	EELRASLLAR	YPPEKLFQAE	RNFNAAQDLD	VSLLEGDLVG	VIKKKDPMGS
1290	1300	1310	1320	1330	1340	1350	1360
QNRWLIDNGV	TKGFVYSSFL	KPYNPRRSHS	DASVGSHSST	ESEHGSSSPR	FPRQNSGSTL	TFNPSSMAVS	FTSGSCQKQP
1370	1380	1390	1400	1410	1420	1430	1440
QDASPPPKEC	DQGTLSASLN	PSNSESSPSR	CPSDPDSTSQ	PRSGDSADVA	RDVKQPTATP	RSYRNFRHPE	IVGYSVPGRN
1450	1460	1470	1480	1490	1500	1510	1520
GQSQDLVKGC	ARTAQAPEDR	STEPDGSEAE	GNQVYFAVYT	FKARNPNELS	VSANQKLKIL	EFKDVTGNTE	WWLAEVNGKK
1530	1540						
GYVPSNYIRK	TEYT						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2669	1	995.0095	-40.18	2	63.5	15.5	2	1235- 1251	R.ASLLARYPPEKLFQAER.N	

Detailed Protein Report

Protein 393: **PREDICTED: rootletin isoform X5 [Homo sapiens]**

Accession:	gi|578800146	**Score:**	26.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	196.6
Database Date:	2015-11-30	**pI:**	5.4
		Sequence Coverage [%]:	1.3
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MVFLPSLLGG	GCPTGPRSQP	CAHCPLPVLL	PATEMASLLS	LQEENQLLQQ	ELSRVEDLLA	QSRAERDELA	IKYNAVSERL
90	100	110	120	130	140	150	160
EQALRLEPGE	LETQEPRGLV	RQSVELRRQL	QEEQASYRRK	LQAYQEGQQR	QAQLVQRLQG	KILQYKKRCS	ELEQQLLERS
170	180	190	200	210	220	230	240
GELEQQRLRD	TEHSQDLESA	LIRLEEEQQR	SASLAQVNAM	LREQLDQAGS	ANQALSEDIR	KVTNDWTRCR	KELEHREAAW
250	260	270	280	290	300	310	320
RREEESFNAY	FSNEHSRLLL	LWRQVVGFRR	LVSEVKMFTE	RDLLQLGGEL	ARTSRAVQEA	GLGLSTGLRL	AESRAEAALE
330	340	350	360	370	380	390	400
KQALLQAQLE	EQLRDKVLRE	KDLAQQQMQS	DLDKADLSAR	VTELGLAVKR	LEKQNLEKDQ	VNKDLTEKLE	ALESLRLQEQ
410	420	430	440	450	460	470	480
AALETEDGEG	LQQTLRDLAQ	AVLSDSESGV	QLSGSERTAD	ASNGSLRGLS	GQRTPSPPRR	SSPGRGRSPR	RGPSPACSDS
490	500	510	520	530	540	550	560
STLALIHSAL	HKRQLQVQDM	RGRYEASQDL	LGTLRKQLSD	SESERRALEE	QLQRLRDKTD	GAMQAHEDAQ	REVQRLRSAN
570	580	590	600	610	620	630	640
ELLSREKSNL	AHSLQVAQQQ	AEELRQEREK	LQAAQEELRR	QRDRLEEEQE	DAVQDGARVR	RELERSHRQL	EQLEGKRSVL
650	660	670	680	690	700	710	720
AKELVEVREA	LSRATLQRDM	LQAEKAEVAE	ALTKAEAGRV	ELELSMTKLR	AEEASLQDSL	SKLSALNESL	AQDKLDLNRL
730	740	750	760	770	780	790	800
VAQLEEEKSA	LQGRQRQAEQ	EATVAREEQE	RLEELRLEQE	VARQGLEGSL	RVAEQAQEAL	EQQLPTLRHE	RSQLQEQLAQ
810	820	830	840	850	860	870	880
LSRQLSGREQ	ELEQARREAQ	RQVEALERAA	REKEALAKEH	AGLAVQLVAA	EREGRTLSEE	ATRLRLEKEA	LEGSLFEVQR
890	900	910	920	930	940	950	960
QLAQLEARRE	QLEAEGQALL	LAKETLTGEL	AGLRQQIIAT	QEKASLDKEL	MAQKLVQAER	EAQASLREQR	AAHEEDLQRL
970	980	990	1000	1010	1020	1030	1040
QREKEAAWRE	LEAERAQLQS	QLQREQEELL	ARLEAEKEEL	SEEIAALQQE	RDEGLLLAES	EKQQALSLKE	SEKTALSEKL
1050	1060	1070	1080	1090	1100	1110	1120
MGTRHSLATI	SLEMERQKRD	AQSRQEQDRS	TVNALTSELR	DLRAQREEAA	AAHAQEVRRL	QEQARDLGKQ	RDSCLREAEE
1130	1140	1150	1160	1170	1180	1190	1200
LRTQLRLLED	ARDGLRRELL	EAQRKLRESQ	EGREVQRQEA	GELRRSLGEG	AKEREALRRS	NEELRSAVKK	AESERISLKL
1210	1220	1230	1240	1250	1260	1270	1280
ANEDKEQKLA	LLEEARTAVG	KEAGELRTGL	QEVERSRLEA	RRELQELRRQ	MKMLDSENTR	LGRELAELQG	RLALGERAEK
1290	1300	1310	1320	1330	1340	1350	1360
ESRRETLGLR	QRLLKGEASL	EVMRQELQVA	QRKLQEQEGE	FRTRERRLLG	SLEEARGTEK	QQLDHARGLE	LKLEAARAEA
1370	1380	1390	1400	1410	1420	1430	1440
AELGLRLSAA	EGRAQGLEAE	LARVEVQRRA	AEAQLGGLRS	ALRRGLGLGR	APSPAPRPVP	GSPARDAPAE	GSGEGLNSPS
1450	1460	1470	1480	1490	1500	1510	1520
TLECSPGSQP	PSPGPATSPA	SPDLDPEAVR	GALREFLQEL	RSAQRERDEL	RTQTSALNRQ	LAEMEAERDS	ATSRARQLQK
1530	1540	1550	1560	1570	1580	1590	1600
AVAESEEARR	SVDGRLSGVQ	AELALQEESV	RRSERERRAT	LDQVATLERS	LQATESELRA	SQEKISKMKA	NETKLEGDKR
1610	1620	1630	1640	1650	1660	1670	1680
RLKEVLDASE	SRTVKLELQR	RSLEGELQRS	RLGLSDREAQ	AQALQDRVDS	LQRQVADSEV	KAGTLQLTVE	RLNGALAKVE
1690	1700	1710	1720	1730	1740		
ESEGALRDKV	RGLTEALAQS	SASLNSTRDK	NLHLQKALTA	CEHDRQVLQR	YRIERTP		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
427	1	457.6259	-312.42	2	34.7	12.4	0	1209-1216	K.LALLEEAR.T	

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2749	1	863.9191	-72.24	2	64.7	13.7	2	1616-1629	K.LELQRRSLEGELQR.S	

BRUKER

Detailed Protein Report

Protein 394: nitric oxide synthase, inducible [Homo sapiens]

Accession:	gi|24041029	**Score:**	26.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	131.0
Database Date:	2015-11-30	**pI:**	9.1
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	2.3
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MACPWKFLFK	TKFHQYAMNG	EKDINNNVEK	APCATSSPVT	QDDLQYHNLS	KQQNESPQPL	VETGKKSPES	LVKLDATPLS
90	100	110	120	130	140	150	160
SPRHVRIKNW	GSGMTFQDTL	HHKAKGILTC	RSKSCLGSIM	TPKSLTRGPR	DKPTPPDELL	PQAIEFVNQY	YGSFKEAKIE
170	180	190	200	210	220	230	240
EHLARVEAVT	KEIETTGTYQ	LTGDELIFAT	KQAWRNAPRC	IGRIQWSNLQ	VFDARSCSTA	REMFEHICRH	VRYSTNNGNI
250	260	270	280	290	300	310	320
RSAITVFPQR	SDGKHDFRVW	NAQLIRYAGY	QMPDGSIRGD	PANVEFTQLC	IDLGWKPKYG	RFDVVPLVLQ	ANGRDPELFE
330	340	350	360	370	380	390	400
IPPDLVLEVA	MEHPKYEWFR	ELELKWYALP	AVANMLLEVG	GLEFPGCPFN	GWYMGTEIGV	RDFCDVQRYN	ILEEVGRRMG
410	420	430	440	450	460	470	480
LETHKLASLW	KDQAVVEINI	AVLHSFQKQN	VTIMDHHSAA	ESFMKYMQNE	YRSRGGCPAD	WIWLVPPMSG	SITPVFHQEM
490	500	510	520	530	540	550	560
LNYVLSPFYY	YQVEAWKTHV	WQDEKRRPKR	REIPLKVLVK	AVLFACMLMR	KTMASRVRVT	ILFATETGKS	EALAWDLGAL
570	580	590	600	610	620	630	640
FSCAFNPKVV	CMDKYRLSCL	EEERLLLVVT	STFGNGDCPG	NGEKLKKSLF	MLKELNNKFR	YAVFGLGSSM	YPRFCAFAHD
650	660	670	680	690	700	710	720
IDQKLSHLGA	SQLTPMGEGD	ELSGQEDAFR	SWAVQTFKAA	CETFDVRGKQ	HIQIPKLYTS	NVTWDPHHYR	LVQDSQPLDL
730	740	750	760	770	780	790	800
SKALSSMHAK	NVFTMRLKSR	QNLQSPTSSR	ATILVELSCE	DGQGLNYLPG	EHLGVCPGNQ	PALVQGILER	VVDGPTPHQT
810	820	830	840	850	860	870	880
VRLEALDESG	SYWVSDKRLP	PCSLSQALTY	FLDITTPPTQ	LLLQKLAQVA	TEEPERQRLE	ALCQPSEYSK	WKFTNSPTFL
890	900	910	920	930	940	950	960
EVLEEFPSLR	VSAGFLLSQL	PILKPRFYSI	SSSRDHTPTE	IHLTVAVVTY	HTRDGQGPLH	HGVCSTWLNS	LKPQDPVPCF
970	980	990	1000	1010	1020	1030	1040
VRNASGFHLP	EDPSHPCILI	GPGTGIAPFR	SFWQQRLHDS	QHKGVRGGRM	TLVFGCRRPD	EDHIYQEEML	EMAQKGVLHA
1050	1060	1070	1080	1090	1100	1110	1120
VHTAYSRLPG	KPKVYVQDIL	RQQLASEVLR	VLHKEPGHLY	VCGDVRMARD	VAHTLKQLVA	AKLKLNEEQV	EDYFFQLKSQ
1130	1140	1150	1160				
KRYHEDIFGA	VFPYEAKKDR	VAVQPSSLEM	SAL				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2024	1	687.3070	-6.35	2	55.4	12.0	0	267-278	R.YAGYQMPDGSIR.G	Oxidation: 6
2767	1	841.9071	-64.44	2	65.0	14.1	1	517-530	K.VLVKAVLFACMLMR.K	Carbamidomethyl: 10; Oxidation: 11, 13

Detailed Protein Report

Protein 395: PREDICTED: ankyrin repeat domain-containing protein 11 isoform X4 [Homo sapiens]

Accession:	gi|578828959	**Score:**	26.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	286.8
Database Date:	2015-11-30	**pI:**	6.4
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.1
		No. of unique Peptides:	1

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

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1507	1	619.9684	9.93	3	48.5	11.3	1	1471-1486	R.EKLLGDGDLMMTSFER.M	Oxidation: 11

Detailed Protein Report

Protein 396: glutamate decarboxylase 2 [Homo sapiens]

Accession:	gi|4503875	**Score:**	26.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	65.4
Database Date:	2015-11-30	**pI:**	6.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	4.1
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|197276620	refseq_human (refseq_human_20140103.fasta)	glutamate decarboxylase 2 [Homo sapiens]

10	20	30	40	50	60	70	80
MASPGSGFWS	FGSEDGSGDS	ENPGTARAWC	QVAQKFTGGI	GNKLCALLYG	DAEKPAESGG	SQPPRAAARK	AACACDQKPC
90	100	110	120	130	140	150	160
SCSKVDVNYA	FLHATDLLPA	CDGERPTLAF	LQDVMNILLQ	YVVKSFDRST	KVIDFHYPNE	LLQEYNWELA	DQPQNLEEIL
170	180	190	200	210	220	230	240
MHCQTTLKYA	IKTGHPRYFN	QLSTGLDMVG	LAADWLTSTA	NTNMFTYEIA	PVFVLLEYVT	LKKMREIIGW	PGGSGDGIFS
250	260	270	280	290	300	310	320
PGGAISNMYA	MMIARFKMFP	EVKEKGMAAL	PRLIAFTSEH	SHFSLKKGAA	ALGIGTDSVI	LIKCDERGKM	IPSDLERRIL
330	340	350	360	370	380	390	400
EAKQKGFVPF	LVSATAGTTV	YGAFDPLLAV	ADICKKYKIW	MHVDAAWGGG	LLMSRKHKWK	LSGVERANSV	TWNPHKMMGV
410	420	430	440	450	460	470	480
PLQCSALLVR	EEGLMQNCNQ	MHASYLFQQD	KHYDLSYDTG	DKALQCGRHV	DVFKLWLMWR	AKGTTGFEAH	VDKCLELAEY
490	500	510	520	530	540	550	560
LYNIIKNREG	YEMVFDGKPQ	HTNVCFWYIP	PSLRTLEDNE	ERMSRLSKVA	PVIKARMMEY	GTTMVSYQPL	GDKVNFFRMV
570	580	590					
ISNPAATHQD	IDFLIEEIER	LGQDL					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2204	1	767.2614	-182.11	2	57.4	12.9	0	397-410	K.MMGVPLQCSALLVR.E	Oxidation: 2

Detailed Protein Report

Protein 397: PREDICTED: L-fucose kinase isoform X3 [Homo sapiens]

Accession:	gi|578828897	**Score:**	26.1
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
2085	1	698.2938	-34.34	2	56.0	13.4	0	744-756	K.LLGTEASTCCPFP.-	Carbamidomethyl: 9

Detailed Protein Report

Protein 398: nuclear receptor corepressor 1 isoform 1 [Homo sapiens]

Accession:	gi|22538461	**Score:**	26.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	270.0
Database Date:	2015-11-30	**pI:**	6.7
		Sequence Coverage [%]:	1.2
		No. of unique Peptides:	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MSSSGYPPNQ	GAFSTEQSRY	PPHSVQYTFP	NTRHQQEFAV	PDYRSSHLEV	SQASQLLQQQ	QQQQLRRRPS	LLSEFHPGSD
90	100	110	120	130	140	150	160
RPQERRTSYE	PFHPGPSPVD	HDSLESKRPR	LEQVSDSHFQ	RVSAAVLPLV	HPLPEGLRAS	ADAKKDPAFG	GKHEAPSSPI
170	180	190	200	210	220	230	240
SGQPCGDDQN	ASPSKLSKEE	LIQSMDRVDR	EIAKVEQQIL	KLKKKQQQLE	EEAAKPPEPE	KPVSPPPVEQ	KHRSIVQIIY
250	260	270	280	290	300	310	320
DENRKKAEEA	HKIFEGLGPK	VELPLYNQPS	DTKVYHENIK	TNQVMRKKLI	LFFKRRNHAR	KQREQKICQR	YDQLMEAWEK
330	340	350	360	370	380	390	400
KVDRIENNPR	RKAKESKTRE	YYEKQFPEIR	KQREQQERFQ	RVGQRGAGLS	ATIARSEHEI	SEIIDGLSEQ	ENNEKQMRQL
410	420	430	440	450	460	470	480
SVIPPMMFDA	EQRRVKFINM	NGLMEDPMKV	YKDRQFMNVW	TDHEKEIFKD	KFIQHPKNFG	LIASYLERKS	VPDCVLYYYL
490	500	510	520	530	540	550	560
TKKNENYKAL	VRRNYGKRRG	RNQQIARPSQ	EEKVEEKEED	KAEKTEKKEE	EKKDEEEKDE	KEDSKENTKE	KDKIDGTAEE
570	580	590	600	610	620	630	640
TEEREQATPR	GRKTANSQGR	RKGRITRSMT	NEAAAASAAA	AAATEEPPPP	LPPPPEPIST	EPVETSRWTE	EEMEVAKKGL
650	660	670	680	690	700	710	720
VEHGRNWAAI	AKMVGTKSEA	QCKNFYFNYK	RRHNLDNLLQ	QHKQKTSRKP	REERDVSQCE	SVASTVSAQE	DEDIEASNEE
730	740	750	760	770	780	790	800
ENPEDSEVEA	VKPSEDSPEN	ATSRGNTEPA	VELEPTTETA	PSTSPSLAVP	STKPAEDESV	ETQVNDSISA	ETAEQMDVDQ
810	820	830	840	850	860	870	880
QEHSAEEGSV	CDPPPATKAD	SVDVEVRVPE	NHASKVEGDN	TKERDLDRAS	EKVEPRDEDL	VVAQQINAQR	PEPQSDNDSS
890	900	910	920	930	940	950	960
ATCSADEDVD	GEPERQRMFP	MDSKPSLLNP	TGSILVSSPL	KPNPLDLPQL	QHRAAVIPPM	VSCTPCNIPI	GTPVSGYALY
970	980	990	1000	1010	1020	1030	1040
QRHIKAMHES	ALLEEQRQRQ	EQIDLECRSS	TSPCGTSKSP	NREWEVLQPA	PHQVITNLPE	GVRLPTTRPT	RPPPPLIPSS
1050	1060	1070	1080	1090	1100	1110	1120
KTTVASEKPS	FIMGGSISQG	TPGTYLTSHN	QASYTQETPK	PSVGSISLGL	PRQQESAKSA	TLPYIKQEEF	SPRSQNSQPE
1130	1140	1150	1160	1170	1180	1190	1200
GLLVRAQHEG	VVRGTAGAIQ	EGSITRGTPT	SKISVESIPS	LRGSITQGTP	ALPQTGIPTE	ALVKGSISRM	PIEDSSPEKG
1210	1220	1230	1240	1250	1260	1270	1280
REEAASKGHV	IYEGKSGHIL	SYDNIKNARE	GTRSPRTAHE	ISLKRSYESV	EGNIKQGMSM	RESPVSAPLE	GLICRALPRG
1290	1300	1310	1320	1330	1340	1350	1360
SPHSDLKERT	VLSGSIMQGT	PRATTESFED	GLKYPKQIKR	ESPPIRAFEG	AITKGKPYDG	ITTIKEMGRS	IHEIPRQDIL
1370	1380	1390	1400	1410	1420	1430	1440
TQESRKTPEV	VQSTRPIIEG	SISQGTPIKF	DNNSGQSAIK	HNVKSLITGP	SKLSRGMPPL	EIVPENIKVV	ERGKYEDVKA
1450	1460	1470	1480	1490	1500	1510	1520
GETVRSRHTS	VVSSGPSVLR	STLHEAPKAQ	LSPGIYDDTS	ARRTPVSYQN	TMSRGSPMMN	RTSDVTISSN	KSTNHERKST
1530	1540	1550	1560	1570	1580	1590	1600
LTPTQRESIP	AKSPVPGVDP	VVSHSPFDPH	HRGSTAGEVY	RSHLPTHLDP	AMPFHRALDP	AAAAYLFQRQ	LSPTPGYPSQ
1610	1620	1630	1640	1650	1660	1670	1680
YQLYAMENTR	QTILNDYITS	QQMQVNLRPD	VARGLSPREQ	PLGLPYPATR	GIIDLTNMPP	TILVPHPGGT	STPPMDRITY
1690	1700	1710	1720	1730	1740	1750	1760
IPGTQITFPP	RPYNSASMSP	GHPTHLAAAA	SAERERERER	EKERERERIA	AASSDLYLRP	GSEQPGRPGS	HGYVRSPSPS
1770	1780	1790	1800	1810	1820	1830	1840
VRTQETMLQQ	RPSVFQGTNG	TSVITPLDPT	AQLRIMPLPA	GGPSISQGLP	ASRYNTAADA	LAALVDAAAS	APQMDVSKTK
1850	1860	1870	1880	1890	1900	1910	1920
ESKHEAARLE	ENLRSRSAAV	SEQQQLEQKT	LEVEKRSVQC	LYTSSAFPSG	KPQPHSSVVY	SEAGKDKGPP	PKSRYEEELR
1930	1940	1950	1960	1970	1980	1990	2000
TRGKTTITAA	NFIDVIITRQ	IASDKDARER	GSQSSDSSSS	LSSHRYETPS	DAIEVISPAS	SPAPPQEKLQ	TYQPEVVKAN
2010	2020	2030	2040	2050	2060	2070	2080
QAENDPTRQY	EGPLHHYRPQ	QESPSPQQQL	PPSSQAEGMG	QVPRTHRLIT	LADHICQIIT	QDFARNQVSS	QTPQQPPTST
2090	2100	2110	2120	2130	2140	2150	2160
FQNSPSALVS	TPVRTKTSNR	YSPESQAQSV	HHQRPGSRVS	PENLVDKSRG	SRPGKSPERS	HVSSEPYEPI	SPPQVPVVHE
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
911	1	492.2027	-52.98	2	40.9	10.7	0	2270-2278	K.ALMGSFDDK.V	

Detailed Protein Report

Protein 399: PREDICTED: phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic subunit beta isoform isoform X3 [Homo sapiens]

Accession:	gi|530374778	**Score:**	26.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	121.0
Database Date:	2015-11-30	**pI:**	7.1
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MCFSFIMPPA	MADILDIWAV	DSQIASDGSI	PVDFLLPTGI	YIQLEVPREA	TISYIKQMLW	KQVHNYPMFN	LLMDIDSYMF
90	100	110	120	130	140	150	160
ACVNQTAVYE	ELEDETRRLC	DVRPFLPVLK	LVTRSCDPGE	KLDSKIGVLI	GKGLHEFDSL	KDPEVNEFRR	KMRKFSEEKI
170	180	190	200	210	220	230	240
LSLVGLSWMD	WLKQTYPPEH	EPSIPENLED	KLYGGKLIVA	VHFENCQDVF	SFQVSPNMNP	IKVNELAIQK	RLTIHGKEDE
250	260	270	280	290	300	310	320
VSPYDYVLQV	SGRVEYVFGD	HPLIQFQYIR	NCVMNRALPH	FILVECCKIK	KMYEQEMIAI	EAAINRNSSN	LPLPLPPKKT
330	340	350	360	370	380	390	400
RIISHVWENN	NPFQIVLVKG	NKLNTEETVK	VHVRAGLFHG	TELLCKTIVS	SEVSGKNDHI	WNEPLEFDIN	ICDLPRMARL
410	420	430	440	450	460	470	480
CFAVYAVLDK	VKTKKSTKTI	NPSKYQTIRK	AGKVHYPVAW	VNTMVFDFKG	QLRTGDIILH	SWSSFPDELE	EMLNPMGTVQ
490	500	510	520	530	540	550	560
TNPYTENATA	LHVKFPENKK	QPYYYPPFDK	SRGGKKFLPV	LKEILDRDPL	SQLCENEMDL	IWTLRQDCRE	IFPQSLPKLL
570	580	590	600	610	620	630	640
LSIKWNKLED	VAQLQALLQI	WPKLPPREAL	ELLDFNYPDQ	YVREYAVGCL	RQMSDEELSQ	YLLQLVQVLK	YEPFLDCALS
650	660	670	680	690	700	710	720
RFLLERALGN	RRIGQFLFWH	LRSEVHIPAV	SVQFGVILEA	YCRGSVGHMK	VLSKQVEALN	KLKTLNSLIK	LNAVKLNRAK
730	740	750	760	770	780	790	800
GKEAMHTCLK	QSAYREALSD	LQSPLNPCVI	LSELYVEKCK	YMDSKMKPLW	LVYNNKVFGE	DSVGVIFKNG	DDLRQDMLTL
810	820	830	840	850	860	870	880
QMLRLMDLLW	KEAGLDLRML	PYGCLATGDR	SGLIEVVSTS	ETIADIQLNS	SNVAAAAAFN	KDALLNWLKE	YNSGDDLDRA
890	900	910	920	930	940	950	960
IEEFTLSCAG	YCVASYVLGI	GDRHSDNIMV	KKTGQLFHID	FGHILGNFKS	KFGIKRERVP	FILTYDFIHV	IQQGKTGNTE
970	980	990	1000	1010	1020	1030	1040
KFGRFRQCCE	DAYLILRRHG	NLFITLFALM	LTAGLPELTS	VKDIQYLKDS	LALGKSEEEA	LKQFKQKFDE	ALRESWTTKV
1050	1060						
NWMAHTVRKD	YRS						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2763	1	959.4928	32.66	1	65.8	10.7	0	904-911	R.HSDNIMVK.K	Oxidation: 6

Detailed Protein Report

Protein 400: FERM domain-containing protein 6 isoform 1 [Homo sapiens]

Accession:	gi|22748721	**Score:**	25.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	70.9
Database Date:	2015-11-30	**pI:**	7.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.4
		No. of unique Peptides:	2

Alias proteins:

Accession	Name	Description
gi|578825482	refseq_human(refseq_human_20140103.fasta)	PREDICTED: FERM domain-containing protein 6 isoform X2 [Homo sapiens]
gi|109715866	refseq_human(refseq_human_20140103.fasta)	FERM domain-containing protein 6 isoform 1 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MNKLNFHNNR VMQDRRSVCI FLPNDESLNI IINVKILCHQ LLVQVCDLLR LKDCHLFGLS VIQNNEHVYM ELSQKLYKYC
        90        100        110        120        130        140        150        160
PKEWKKEASK GIDQFGPPMI IHFRVQYYVE NGRLISDRAA RYYYYWHLRK QVLHSQCVLR EEAYFLLAAF ALQADLGNFK
       170        180        190        200        210        220        230        240
RNKHYGKYFE PEAYFPSWVV SKRGKDYILK HIPNMHKDQF ALTASEAHLK YIKEAVRLDD VAVHYYRLYK DKREIEASLT
       250        260        270        280        290        300        310        320
LGLTMRGIQI FQNLDEEKQL LYDFPWTNVG KLVFVGKKFE ILPDGLPSAR KLIYYTGCPM RSRHLLQLLS NSHRLYMNLQ
       330        340        350        360        370        380        390        400
PVLRHIRKLE ENEEKKQYRE SYISDNLDLD MDQLEKRSRA SGSSAGSMKH KRLSRHSTAS HSSSHTSGIE ADTKPRDTGP
       410        420        430        440        450        460        470        480
EDSYSSSAIH RKLKTCSSMT SHGSSHTSGV ESGGKDRLEE DLQDDEIEML VDDPRDLEQM NEESLEVSPD MCIYITEDML
       490        500        510        520        530        540        550        560
MSRKLNGHSG LIVKEIGSST SSSSETVVKL RGQSTDSLPQ TICRKPKTST DRHSLSLDDI RLYQKDFLRI AGLCQDTAQS
       570        580        590        600        610        620
YTFGCGHELD EEGLYCNSCL AQQCINIQDA FPVKRTSKYF SLDLTHDEVP EFVV
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
237	1	795.3910	-58.65	2	32.3	12.8	1	233-246	K.REIEASLTLGLTMR.G	
1818	1	731.8030	-66.05	2	52.7	13.2	0	512-524	R.GQSTDSLPQTICR.K	Carbamidomethyl: 12

Detailed Protein Report

Protein 401: PREDICTED: chromodomain-helicase-DNA-binding protein 7 isoform X4 [Homo sapiens]

Accession:	gi|578815680	**Score:**	25.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	214.1
Database Date:	2015-11-30	**pI:**	5.2
		Sequence Coverage [%]:	1.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MILTDCPELR	NIPWRCVVID	EAHRLKNRNC	KLLEGLKMMD	LEHKVLLTGT	PLQNTVEELF	SLLHFLEPSR	FPSETTFMQE
90	100	110	120	130	140	150	160
FGDLKTEEQV	QKLQAILKPM	MLRRLKEDVE	KNLAPKEETI	IEVELTNIQK	KYYRAILEKN	FTFLSKGGGQ	ANVPNLLNTM
170	180	190	200	210	220	230	240
MELRKCCNHP	YLINGAEEKI	LEEFKETHNA	ESPDFQLQAM	IQAAGKLVLI	DKLLPKLKAG	GHRVLIFSQM	VRCLDILEDY
250	260	270	280	290	300	310	320
LIQRRYPYER	IDGRVRGNLR	QAAIDRFSKP	DSDRFVFLLC	TRAGGLGINL	TAADTCIIFD	SDWNPQNDLQ	AQARCHRIGQ
330	340	350	360	370	380	390	400
SKSVKIYRLI	TRNSYEREMF	DKASLKLGLD	KAVLQSMSGR	ENATNGVQQL	SKKEIEDLLR	KGAYGALMDE	EDEGSKFCEE
410	420	430	440	450	460	470	480
DIDQILLRRT	HTITIESEGK	GSTFAKASFV	ASGNRTDISL	DDPNFWQKWA	KKAELDIDAL	NGRNNLVIDT	PRVRKQTRLY
490	500	510	520	530	540	550	560
SAVKEDELME	FSDLESDSEE	KPCAKPRRPQ	DKSQGYARSE	CFRVEKNLLV	YGWGRWTDIL	SHGRYKRQLT	EQDVETICRT
570	580	590	600	610	620	630	640
ILVYCLNHYK	GDENIKSFIW	DLITPTADGQ	TRALVNHSGL	SAPVPRGRKG	KKVKAQSTQP	VVQDADWLAS	CNPDALFQED
650	660	670	680	690	700	710	720
SYKKHLKHHC	NKVLLRVRML	YYLRQEVIGD	QADKILEGAD	SSEADVWIPE	PFHAEVPADW	WDKEADKSLL	IGVFKHGYEK
730	740	750	760	770	780	790	800
YNSMRADPAL	CFLERVGMPD	AKAIAAEQRG	TDMLADGGDG	GEFDREDEDP	EYKPTRTPFK	DEIDEFANSP	SEDKEESMEI
810	820	830	840	850	860	870	880
HATGKHSESN	AELGQLYWPN	TSTLTTRLRR	LITAYQRSYK	RQQMRQEALM	KTDRRRRRPR	EEVRALEAER	EAIISEKRQK
890	900	910	920	930	940	950	960
WTRREEADFY	RVVSTFGVIF	DPVKQQFDWN	QFRAFARLDK	KSDESLEKYF	SCFVAMCRRV	CRMPVKPDDE	PPDLSSIIEP
970	980	990	1000	1010	1020	1030	1040
ITEERASRTL	YRIELLRKIR	EQVLHHPQLG	ERLKLCQPSL	DLPEWWECGR	HDRDLLVGAA	KHGVSRTDYH	ILNDPELSFL
1050	1060	1070	1080	1090	1100	1110	1120
DAHKNFAQNR	GAGNTSSLNP	LAVGFVQTPP	VISSAHIQDE	RVLEQAEGKV	EEPENPAAKE	KCEGKEEEEE	TDGSGKESKQ
1130	1140	1150	1160	1170	1180	1190	1200
ECEAEASSVK	NELKGVEVGA	DTGSKSISEK	GSEEDEEEKL	EDDDKSEESS	QPEAGAVSRG	KNFDEESNAS	MSTARDETRD
1210	1220	1230	1240	1250	1260	1270	1280
GFYMEDGDPS	VAQLLHERTF	AFSFWPKDRV	MINRLDNICE	AVLKGKWPVN	RRQMFDFQGL	IPGYTPTTVD	SPLQKRSFAE
1290	1300	1310	1320	1330	1340	1350	1360
LSMVGQASIS	GSEDITTSPQ	LSKEDALNLS	VPRQRRRRRR	KIEIEAERAA	KRRNLMEMVA	QLRESQVVSE	NGQEKVVDLS
1370	1380	1390	1400	1410	1420	1430	1440
KASREATSST	SNFSSLSSKF	ILPNVSTPVS	DAFKTQMELL	QAGLSRTPTR	HLLNGSLVDG	EPPMKRRRGR	RKNVEGLDLL
1450	1460	1470	1480	1490	1500	1510	1520
FMSHKRTSLS	AEDAEVTKAF	EEDIETPPTR	NIPSPGQLDP	DTRIPVINLE	DGTRLVGEDA	PKNKDLVEWL	KLHPTYTVDM
1530	1540	1550	1560	1570	1580	1590	1600
PSYVPKNADV	LFSSFQKPKQ	KRHRCRNPNK	LDINTLTGEE	RVPVVNKRNG	KKMGGAMAPP	MKDLPRWLEE	NPEFAVAPDW
1610	1620	1630	1640	1650	1660	1670	1680
TDIVKQSGFV	PESMFDRLLT	GPVVRGEGAS	RRGRRPKSEI	ARAAAAAAAV	ASTSGINPLL	VNSLFAGMDL	TSLQNLQNLQ
1690	1700	1710	1720	1730	1740	1750	1760
SLQLAGLMGF	PPGLATAATA	GGDAKNPAAV	LPLMLPGMAG	LPNVFGLGGL	LNNPLSAATG	NTTTASSQGE	PEDSTSKGEE
1770	1780	1790	1800	1810	1820	1830	1840
KGNENEDENK	DSEKSTDAVS	AADSANGSVG	AATAPAGLPS	NPLAFNPFLL	STMAPGLFYP	SMFLPPGLGG	LTLPGFPALA
1850	1860	1870	1880	1890	1900	1910	1920
GLQNAVGSSE	EKAADKAEGG	PFKDGETLEG	SDAEESLDKT	AESSLLEDEI	AQGEELDSLD	GGDEIENNEN	DE

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

Detailed Protein Report

	Cmpds.		Δ m/z [ppm]		[min]					
1713	1	806.6994	-162.85	2	51.4	15.5	0	750-765	R.GTDMLADGGDGGEFDR.E	

Detailed Protein Report

Protein 402: **PREDICTED: U3 small nucleolar RNA-associated protein 6 homolog isoform X1 [Homo sapiens]**

Accession:	gi|530411102	**Score:**	25.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	55.6
Database Date:	2015-11-30	**pI:**	6.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	8.4
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MRLRILLYTG	YKVFSSVPQQ	NGKTMFNFGS	PMWLFVRSGL	LKLDLARYSL	PCWRFIPTNQ	YFRMELMHAE	KLRKEKEEFE
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
KASMDVENPD	YSEEILKGEL	AWIIYKNSVS	IIKGAEFHVS	LLSIAQLFDF	AKDLQKEIYD	DLQALHTDDP	LTWDYVARRE
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
LEIESQTEEQ	PTTKQAKAVE	VGRKEERCCA	VYEEAVKTLP	TEAMWKCYIT	FCLERFTKKS	NSGFLRGKRL	ERTMTVFRKA
250	**260**	**270**	**280**	**290**	**300**	**310**	**320**
HELKLLSECQ	YKQLSVSLLC	YNFLREALEV	AVAGTELFRD	SGTMWQLKLQ	VLIESKSPDI	AMLFEEAFVH	LKPQVCLPLW
330	**340**	**350**	**360**	**370**	**380**	**390**	**400**
ISWAEWSEGA	KSQEDTEAVF	KKALLAVIGA	DSVTLKNKYL	DWAYRSGGYK	KARAVFKSLQ	ESRPFSVDFF	RKMIQFEKEQ
410	**420**	**430**	**440**	**450**	**460**	**470**	**480**
ESCNMANIRE	YYERALREFG	SADSDLWMDY	MKEELNHPLG	RPENCGQIYW	RAMKMLQGES	AEAFVAKHAM	HQTGHL

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2485	1	1045.1567	132.37	2	61.0	12.6	1	160-177	R.ELEIESQTEEQPTTKQAK.A	
15	1	803.7134	-7.51	3	29.5	13.3	1	455-476	K.MLQGESAEAFVAKHAMHQTGHL.-	Oxidation: 1

Detailed Protein Report

Protein 403: **toll-like receptor 9 precursor [Homo sapiens]**

Accession:	gi|8394456	**Score:**	25.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	115.8
Database Date:	2015-11-30	**pI:**	9.7
		Sequence Coverage [%]:	1.9
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MGFCRSALHP	LSLLVQAIML	AMTLALGTLP	AFLPCELQPH	GLVNCNWLFL	KSVPHFSMAA	PRGNVTSLSL	SSNRIHHLHD
90	100	110	120	130	140	150	160
SDFAHLPSLR	HLNLKWNCPP	VGLSPMHFPC	HMTIEPSTFL	AVPTLEELNL	SYNNIMTVPA	LPKSLISLSL	SHTNILMLDS
170	180	190	200	210	220	230	240
ASLAGLHALR	FLFMDGNCYY	KNPCRQALEV	APGALLGLGN	LTHLSLKYNN	LTVVPRNLPS	SLEYLLLSYN	RIVKLAPEDL
250	260	270	280	290	300	310	320
ANLTALRVLD	VGGNCRRCDH	APNPCMECPR	HFPQLHPDTF	SHLSRLEGLV	LKDSSLSWLN	ASWFRGLGNL	RVLDLSENFL
330	340	350	360	370	380	390	400
YKCITKTKAF	QGLTQLRKLN	LSFNYQKRVS	FAHLSLAPSF	GSLVALKELD	MHGIFFRSLD	ETTLRPLARL	PMLQTLRLQM
410	420	430	440	450	460	470	480
NFINQAQLGI	FRAFPGLRYV	DLSDNRISGA	SELTATMGEA	DGGEKVWLQP	GDLAPAPVDT	PSSEDFRPNC	STLNFTLDLS
490	500	510	520	530	540	550	560
RNNLVTVQPE	MFAQLSHLQC	LRLSHNCISQ	AVNGSQFLPL	TGLQVLDLSH	NKLDLYHEHS	FTELPRLEAL	DLSYNSQPFG
570	580	590	600	610	620	630	640
MQGVGHNFSF	VAHLRTLRHL	SLAHNNIHSQ	VSQQLCSTSL	RALDFSGNAL	GHMWAEGDLY	LHFFQGLSGL	IWLDLSQNRL
650	660	670	680	690	700	710	720
HTLLPQTLRN	LPKSLQVLRL	RDNYLAFFKW	WSLHFLPKLE	VLDLAGNQLK	ALTNGSLPAG	TRLRRLDVSC	NSISFVAPGF
730	740	750	760	770	780	790	800
FSKAKELREL	NLSANALKTV	DHSWFGPLAS	ALQILDVSAN	PLHCACGAAF	MDFLLEVQAA	VPGLPSRVKC	GSPGQLQGLS
810	820	830	840	850	860	870	880
IFAQDLRLCL	DEALSWDCFA	LSLLAVALGL	GVPMLHHLCG	WDLWYCFHLC	LAWLPWRGRQ	SGRDEDALPY	DAFVVFDKTQ
890	900	910	920	930	940	950	960
SAVADWVYNE	LRGQLEECRG	RWALRLCLEE	RDWLPGKTLF	ENLWASVYGS	RKTLFVLAHT	DRVSGLLRAS	FLLAQQRLLE
970	980	990	1000	1010	1020	1030	1040
DRKDVVVLVI	LSPDGRRSRY	VRLRQRLCRQ	SVLLWPHQPS	GQRSFWAQLG	MALTRDNHHF	YNRNFCQGPT	AE

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1454	1	1059.0764	13.42	2	48.0	15.1	1	788-807	R.VKCGSPGQLQGLSIFAQDLR.L	
399	1	945.4882	8.09	2	34.3	10.8	0	790-807	K.CGSPGQLQGLSIFAQDLR.L	

Detailed Protein Report

Protein 404: endoplasmic reticulum-Golgi intermediate compartment protein 2 [Homo sapiens]

Accession:	gi|50959176	**Score:**	25.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	42.5
Database Date:	2015-11-30	**pI:**	6.3
Modification(s):	Oxidation	**Sequence Coverage [%]:**	5.6
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MRRLNRKKTL	SLVKELDAFP	KVPESYVETS	ASGGTVSLIA	FTTMALLTIM	EFSVYQDTWM	KYEYEVDKDF	SSKLRINIDI
90	100	110	120	130	140	150	160
TVAMKCQYVG	ADVLDLAETM	VASADGLVYE	PTVFDLSPQQ	KEWQRMLQLI	QSRLQEEHSL	QDVIFKSAFK	STSTALPPRE
170	180	190	200	210	220	230	240
DDSSQSPNAC	RIHGHLYVNK	VAGNFHITVG	KAIPHPRGHA	HLAALVNHES	YNFSHRIDHL	SFGELVPAII	NPLDGTEKIA
250	260	270	280	290	300	310	320
IDHNQMFQYF	ITVVPTKLHT	YKISADTHQF	SVTERERIIN	HAAGSHGVSG	IFMKYDLSSL	MVTVTEEHMP	FWQFFVRLCG
330	340	350	360	370	380		
IVGGIFSTTG	MLHGIGKFIV	EIICCRFRLG	SYKPVNSVPF	EDGHTDNHLP	LLENNTH		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2603	1	701.8580	-71.21	2	62.6	14.2	1	74-85	K.LRINIDITVAMK.C	Oxidation: 11
1411	1	1095.6964	116.34	1	47.3	11.8	0	338-346	K.FIVEIICCR.F	

Detailed Protein Report

Protein 405: **protein TALPID3 isoform 3 [Homo sapiens]**

Accession:	gi|346644665	**Score:**	25.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	161.7
Database Date:	2015-11-30	**pI:**	5.2
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.1
		No. of unique Peptides:	2

Quantitation

MD:MU **Median:** 1.29 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MVSESDFSKD	VAVQVLPLDK	IEENNKQKAN	DIFISQYTMG	QKDALRTVLK	QKAQSMPVFK	EVKVHLLEDA	GIEKDAVTQE
90	100	110	120	130	140	150	160
TRISPSGIDS	ATTVAAATAA	AIATAAPLIK	VQSDLEAKVN	SVTELLSKLQ	ETDKHLQRVT	EQQTSIQRKQ	EKLHCHDHEK
170	180	190	200	210	220	230	240
QMNVFMEQHI	RHLEKLQQQQ	IDIQTHFISA	ALKTSSFQPV	SMPSSRAVEK	YSVKPEHPNL	GSCNPSLYNT	FASKQAPLKE
250	260	270	280	290	300	310	320
VEDTSFDKQK	SPLETPAPRR	FAPVPVSRDD	ELSKRENLLE	EKENMEVSCH	RGNVRLLEQI	LNNNDSLTRK	SESSNTTSLT
330	340	350	360	370	380	390	400
RSKIGWTPEK	TNRFPSCEEL	ETTKVTMQKS	DDVLHDLGQK	EKETNSMVQP	KESLSMLKLP	DLPQNSVKLQ	TTNTTRSVLK
410	420	430	440	450	460	470	480
DAEKILRGVQ	NNKKVLEENL	EAIIRAKDGA	AMYSLINALS	TNREMSEKIR	IRKTVDEWIK	TISAEIQDEL	SRTDYEQKRF
490	500	510	520	530	540	550	560
DQKNQRTKKG	QNMTKDIRTN	TQDKTVNKSV	IPRKHSQKQI	EEHFRNLPMR	GMPASSLQKE	RKEGLLKATT	VIQDEDYMLQ
570	580	590	600	610	620	630	640
VYGKPVYQGH	RSTLKKGPYL	RFNSPSPKSR	PQRPKVIERV	KGTKVKSIRT	QTDFYATKPK	KMDSKMKHSV	PVLPHGDQQY
650	660	670	680	690	700	710	720
LFSPSREMPT	FSGTLEGHLI	PMAILLGQTQ	SNSDTMPPAG	VIVSKPHPVT	VTTSIPPSSR	KVETGVKKPN	IAIVEMKSEK
730	740	750	760	770	780	790	800
KDPPQLTVQV	LPSVDIDSIS	NSSADVLSPL	SSPKEASLPP	VQTWIKTPEI	MKVDEEEVKF	PGTNFDEIID	VIQEEEKCDE
810	820	830	840	850	860	870	880
IPDSEPILEF	NRSVKADSTK	YNGPPFPPVA	STFQPTADIL	DKVIERKETL	ENSLIQWVEQ	EIMSRIISGL	FPVQQQIAPS
890	900	910	920	930	940	950	960
ISVSVSETSE	PLTSDIVEGT	SSGALQLFVD	AGVPVNSNVI	KHFVNEALAE	TIAVMLGDRE	AKKQGPVATG	VSGDASTNET
970	980	990	1000	1010	1020	1030	1040
YLPARVCTPL	PTPQPTPPCS	PSSPAKECVL	VKTPDSSPCD	SDHDMAFPVK	EICAEKGDDM	PAIMLVNTPT	VTPTTTPPPA
1050	1060	1070	1080	1090	1100	1110	1120
AAVFTPTLSD	ISIDKLKVSS	PELPKPWGDG	DLPLEEENPN	SPQEELHPRA	IVMSVAKDEE	PESMDFPAQP	PPPEPVPFMP
1130	1140	1150	1160	1170	1180	1190	1200
FPAGTKAPSP	SQMPGSDSST	LESTLSVTVT	ETETLDKPIS	EGEILFSCGQ	KLAPKILEDI	GLYLTNLNDS	LSSTLHDAVE
1210	1220	1230	1240	1250	1260	1270	1280
MEDDPPSEGQ	VIRMSHKKFH	ADAILSFAKQ	NQESAVSQQA	VYHSEDLENS	VGELSEGQRP	QLTAAAENIL	MGHSLYMQPP
1290	1300	1310	1320	1330	1340	1350	1360
VTNTQSLDQQ	CDPKPLSRQF	DTVSGSIYED	SCASHGPMSL	GELELEPNSK	LVLPTTLLTA	QENDVNLPVA	AEDFSQYQLK
1370	1380	1390	1400	1410	1420	1430	1440
QNQDVKQVEH	KPSQSYLRVR	NKSDIAPSQQ	QVSPGDMDRT	QIELNPYLTC	VFSGGKAVPL	SASQMPPAKM	SVMLPSVNLE
1450	1460	1470					
DCSQSLSLST	MQEDMESSGA	DTF					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2296	1	653.8345	23.68	2	58.6	11.0	1	361-371	K.EKETNSMVQPK.E	Oxidation: 7	MD:MU 1.29
1681	1	1044.8573	-121.61	2	50.9	14.9	1	1381-1399	R.NKSDIAPSQQQVSPGDMDR.T	Oxidation: 17	

Detailed Protein Report

Protein 406: PREDICTED: serine/arginine repetitive matrix protein 1 isoform X6 [Homo sapiens]

Accession: gi|530360793
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 25.9
MW [kDa]: 100.2
pI: 12.3
Sequence Coverage [%]: 2.6
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MDAGFFRGTS	AEQDNRFSNK	QKKLLKQLKF	AECLEKKVDM	SKVNLEVIKP	WITKRVTEIL	GFEDDVVIEF	IFNQLEVKNP
90	100	110	120	130	140	150	160
DSKMMQINLT	GFLNGKNARE	FMGELWPLLL	SAQENIAGIP	SAFLELKKEE	IKQRQIEQEK	LASMKKQDED	KDKRDKEEKE
170	180	190	200	210	220	230	240
SSREKRERSR	SPRRTKSRSP	SPAPEKKEKT	PELPEPSVKV	KEPSVQEATS	TSDILKVPKP	EPIPEPKEPS	PEKNSKKEKE
250	260	270	280	290	300	310	320
KEKTRPRSRS	RSKSRSRTRS	RSPSHTRPRR	RHRSRSRSYS	PRRRPSPRRR	PSPRRRTPPR	RMPPPPRHRR	SRSPVRRRRR
330	340	350	360	370	380	390	400
SSASLSGSSS	SSSSSRSRSP	PKKPPKRTSS	PPRKTRRLSP	SASPPRRRHR	PSPPATPPPK	TRHSPTPQQS	NRTRKSRVSV
410	420	430	440	450	460	470	480
SPGRTSGKVT	KHKGTEKRES	PSPAPKPRKV	ELSESEEDKG	GKMAAADSVQ	QRRQYRRQNQ	QSSSDSGSSS	SSEDERPKRS
490	500	510	520	530	540	550	560
HVKNGEVGRR	RRHSPSRSAS	PSPRKRQKET	SPRMQMGKRW	QSPVTKSGRR	RRSPSPPPTR	RRRSPSPAPP	PRRRRTPTPP
570	580	590	600	610	620	630	640
PRRRTPSPPP	RRRSPSPRRY	SPPIQRRYSP	SPPPKRRTAS	PPPPPKRRAS	PSPPPKRRVS	HSPPPKQRSS	PVTKRRSPSL
650	660	670	680	690	700	710	720
SSKHRKGSSP	SRSTREARSP	QPNKRHSPSP	RPRAPQTSSS	PPPVRRGASS	SPQRRQSPSP	STRPIRRVSR	TPEPKKIKKA
730	740	750	760	770	780	790	800
ASPSPQSVRR	VSSSRSVSGS	PEPAAKKPPA	PPSPVQSQSP	STNWSPAVPV	KKAKSPTPSP	SPPRNSDQEG	GGKKKKKKKD
810	820	830	840	850	860	870	880
KKHKKDKKHK	KHKKHKKEKA	VAAAAAAAVT	PAAIAAATTT	LAQEEPVAAP	EPKKETESEA	EDNLDDLEKH	LREKALRSMR
890							
KAQVSPQS							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1844	1	590.7772	1.91	2	53.1	11.4	1	509-518	K.ETSPRMQMGK.R	Oxidation: 6

Detailed Protein Report

Protein 407: condensin complex subunit 1 [Homo sapiens]

Accession:	gi|178056552	**Score:**	25.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	157.1
Database Date:	2015-11-30	**pI:**	6.2
		Sequence Coverage [%]:	1.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAPQMYEFHL	PLSPEELLKS	GGVNQYVVQE	VLSIKHLPPQ	LRAFQAAFRA	QGPLAMLQHF	DTIYSILHHF	RSIDPGLKED
90	100	110	120	130	140	150	160
TLQFLIKVVS	RHSQELPAIL	DDTTLSGSDR	NAHLNALKMN	CYALIRLLES	FETMASQTNL	VDLDLGGKGK	KARTKAAHGF
170	180	190	200	210	220	230	240
DWEEERQPIL	QLLTQLLQLD	IRHLWNHSII	EEEFVSLVTG	CCYRLLENPT	INHQKNRPTR	EAITHLLGVA	LTRYNHMLSA
250	260	270	280	290	300	310	320
TVKIIQMLQH	FEHLAPVLVA	AVSLWATDYG	MKSIVGEIVR	EIGQKCPQEL	SRDPSGTKGF	AAFLTELAER	VPAILMSSMC
330	340	350	360	370	380	390	400
ILLDHLDGEN	YMMRNAVLAA	MAEMVLQVLS	GDQLEAAARD	TRDQFLDTLQ	AHGHDVNSFV	RSRVLQLFTR	IVQQKALPLT
410	420	430	440	450	460	470	480
RFQAVVALAV	GRLADKSVLV	CKNAIQLLAS	FLANNPFSCK	LSDADLAGPL	QKETQKLQEM	RAQRRTAAAS	AVLDPEEEWE
490	500	510	520	530	540	550	560
AMLPELKSTL	QQLLQLPQGE	EEIPEQIANT	ETTEDVKGRI	YQLLAKASYK	KAIILTREAT	GHFQESEPFS	HIDPEESEET
570	580	590	600	610	620	630	640
RLLNILGLIF	KGPAASTQEK	NPRESTGNMV	TGQTVCKNKP	NMSDPEESRG	NDELVKQEML	VQYLQDAYSF	SRKITEAIGI
650	660	670	680	690	700	710	720
ISKMMYENTT	TVVQEVIEFF	VMVFQFGVPQ	ALFGVRRMLP	LIWSKEPGVR	EAVLNAYRQL	YLNPKGDSAR	AKAQALIQNL
730	740	750	760	770	780	790	800
SLLLVDASVG	TIQCLEEILC	EFVQKDELKP	AVTQLLWERA	TEKVACCPLE	RCSSVMLLGM	MARGKPEIVG	SNLDTLVSIG
810	820	830	840	850	860	870	880
LDEKFPQDYR	LAQQVCHAIA	NISDRRKPSL	GKRHPPFRLP	QEHRLFERLR	ETVTKGFVHP	DPLWIPFKEV	AVTLIYQLAE
890	900	910	920	930	940	950	960
GPEVICAQIL	QGCAKQALEK	LEEKRTSQED	PKESPAMLPT	FLLMNLLSLA	GDVALQQLVH	LEQAVSGELC	RRRVLREEQE
970	980	990	1000	1010	1020	1030	1040
HKTKDPKEKN	TSSETTMEEE	LGLVGATADD	TEAELIRGIC	EMELLDGKQT	LAAFVPLLLK	VCNNPGLYSN	PDLSAAASLA
1050	1060	1070	1080	1090	1100	1110	1120
LGKFCMISAT	FCDSQLRLLF	TMLEKSPLPI	VRSNLMVATG	DLAIRFPNLV	DPWTPHLYAR	LRDPAQQVRK	TAGLVMTHLI
1130	1140	1150	1160	1170	1180	1190	1200
LKDMVKVKGQ	VSEMAVLLID	PEPQIAALAK	NFFNELSHKG	NAIYNLLPDI	ISRLSDPELG	VEEEPFHTIM	KQLLSYITKD
1210	1220	1230	1240	1250	1260	1270	1280
KQTESLVEKL	CQRFRTSRTE	RQQRDLAYCV	SQLPLTERGL	RKMLDNFDCF	GDKLSDESIF	SAFLSVVGKL	RRGAKPEGKA
1290	1300	1310	1320	1330	1340	1350	1360
IIDEFEQKLR	ACHTRGLDGI	KELEIGQAGS	QRAPSAKKPS	TGSRYQPLAS	TASDNDFVTP	EPRRTTRRHP	NTQQRASKKK
1370	1380	1390	1400	1410			
PKVVFSSDES	SEEDLSAEMT	EDETPKKTTP	ILRASARRHR	S			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1765	1	788.2766	-109.58	2	52.0	10.1	1	154-166	R.TKAAHGFDWEEER.Q	

Detailed Protein Report

Protein 408: PREDICTED: LIM/homeobox protein Lhx3 isoform X1 [Homo sapiens]

Accession:	gi|530426634	**Score:**	25.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	42.3
Database Date:	2015-11-30	**pI:**	9.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	8.5
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MTLNMKETRW	GAPAPEIPLC	AGCDQHILDR	FILKALDRHW	HSKCLKCSDC	HTPLAERCFS	RGESVYCKDD	FFKRFGTKCA
90	100	110	120	130	140	150	160
ACQLGIPPTQ	VVRRAQDFVY	HLHCFACVVC	KRQLATGDEF	YLMEDSRLVC	KADYETAKQR	EAEATAKRPR	TTITAKQLET
170	180	190	200	210	220	230	240
LKSAYNTSPK	PARHVREQLS	SETGLDMRVV	QVWFQNRRAK	EKRLKKDAGR	QRWGQYFRNM	KRSRGGSKSD	KDSVQEGQDS
250	260	270	280	290	300	310	320
DAEVSFPDEP	SLAEMGPANG	LYGSLGEPTQ	ALGRPSGALG	NFSLEHGGLA	GPEQYRELRP	GSPYGVPPSP	AAPQSLPGPQ
330	340	350	360	370	380	390	
PLLSSLVYPD	TSLGLVPSGA	PGGPPPMRVL	AGNGPSSDLS	TGSSGGYPDF	PASPASWLDE	VDHAQF	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2005	1	788.2933	-81.32	2	55.0	10.3	1	44-57	K.CLKCSDCHTPLAER.C	
2172	1	1051.9909	-51.91	2	57.0	15.5	1	75-93	R.FGTKCAACQLGIPPTQVVR.R	Carbamidomethyl: 5, 8

Detailed Protein Report

Protein 409: **protein-glutamine gamma-glutamyltransferase 5 isoform 2 [Homo sapiens]**

Accession:	gi|4759230	**Score:**	25.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	71.9
Database Date:	2015-11-30	**pI:**	5.9
		Sequence Coverage [%]:	6.0
		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
1787	1	1023.8570	-1.46	3	52.3	10.0	1	429-455	K.FKLLDPPNMGQDICFVLLALNMSSQFK.D	

Detailed Protein Report

Protein 410: cytochrome P450 3A43 isoform 4 [Homo sapiens]

Accession:	gi|525458843	**Score:**	25.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	44.8
Database Date:	2015-11-30	**pI:**	9.8
		Sequence Coverage [%]:	4.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDLIPNFAME	TWVLVATSLV	LLYIYGTHSH	KLFKKLGIPG	PTPLPFLGTI	LFYLRRSLNK	IPSWAWWLTP	VIPALWEAEA
90	100	110	120	130	140	150	160
GGSPKVRSSR	PALPTWVFGI	LTENVMKNTE	KCGALFPFLT	PVFEALNIGL	FPKDVTHFLK	NSIERMKESR	LKDKQKHRVD
170	180	190	200	210	220	230	240
FFQQMIDSQN	SKETKSHKAL	SDLELVAQSI	IIIFAAYDTT	STTLPFIMYE	LATHPDVQQK	LQEEIDAVLP	NKAPVTYDAL
250	260	270	280	290	300	310	320
VQMEYLDMVV	NETLRLFPVV	SRVTRVCKKD	IEINGVFIPK	GLAVMVPIYA	LHHDPKYWTE	PEKFCPERFS	KKNKDSIDLY
330	340	350	360	370	380	390	400
RYIPFGAGPR	NCIGMRFALT	NIKLAVIRAL	QNFSFKPCKE	TQIPLKLDNL	PILQPEKPIV	LKVHLRDGIT	SGP

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
398	1	587.3194	-67.09	2	34.3	11.8	1	256-265	R.LFPVVSRVTR.V	

Detailed Protein Report

Protein 411: NMDA receptor-regulated protein 2 isoform c [Homo sapiens]

Accession:	gi|446713799	**Score:**	25.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	43.8
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
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	
VIYINSPLPQ	KKMTMRERNQ	IFHEVPLKFM	MSKNTSVPVS	AVFMDKPEEF	ISEMDVCNAF	FFP	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
9	1	650.7714	-185.46	2	29.3	12.0	2	178-188	K.ILRACIEQVKK.Y	

Detailed Protein Report

Protein 412: PREDICTED: diphosphomevalonate decarboxylase isoform X2 [Homo sapiens]

Accession:	gi|578828983	**Score:**	25.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	24.8
Database Date:	2015-11-30	**pI:**	6.1
		Sequence Coverage [%]:	16.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGEQADGKDS	IARQVAPESH	WPELRVLILV	VSAEKKLTGS	TVGMRASVET	SPLLRFRAES	VVPARMAEMA	RCIRERDFPS
90	100	110	120	130	140	150	160
FAQLTMKDSN	QFHATCLDTF	PPISYLNAIS	WRIIHLVHRF	NAHHGDTKVA	YTFDAGPNAV	IFTLDDTVAE	FVAAVWHGFP
170	180	190	200	210	220	230	
PGSNGDTFLK	GLQVRPAPLS	AELQAALAME	PTPGGVKYII	VTQVGPGPQI	LDDPCAHLLG	PDGLPKPAA	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1514	1	1052.1817	93.63	2	48.6	11.8	2	36-55	K.KLTGSTVGMRASVETSPLLR.F	

Detailed Protein Report

Protein 413: PREDICTED: protein unc-13 homolog B isoform X1 [Homo sapiens]

Accession:	gi|578816361	**Score:**	25.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	268.9
Database Date:	2015-11-30	**pI:**	5.4
		Sequence Coverage [%]:	1.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSLLCVRVKR	AKFQGSPDKF	NTYVTLKVQN	VKSTTVAVRG	DQPSWEQDFM	FEISRLDLGL	SVEVWNKGLI	WDTMVGTVWI
90	100	110	120	130	140	150	160
ALKTIRQSDE	EGPGEWSTLE	AETLMKDDEI	CGTRNPTPHK	ILLDTRFELP	FDIPEEEARY	WTYKWEQINA	LGADNEYSSQ
170	180	190	200	210	220	230	240
EESQRKPLPT	AAAQCCHWTY	LGWGEQQTFE	DPDSAVDDRD	SDYRSETSNS	FPPPYHTASQ	PNASVHQFPV	PVRSPQQLLL
250	260	270	280	290	300	310	320
QGSSRDSCND	SMQSYDLDYP	ERRAISPTSS	SRYGSSCNVS	QGSSQLSELD	QYHEQDDDHR	ETDSIHSCHS	SHSLSRDGQA
330	340	350	360	370	380	390	400
GFGEQEKPLE	VTGQAEKEAA	CEPKEMKEDA	TTHPPPDLVL	QKDHFLGPQE	SFPEENASSP	FTQARAHWIR	AVTKVRLQLQ
410	420	430	440	450	460	470	480
EVGNLFYILT	RNKRKKQRTP	QTLREKMKRL	LQESEEEIMV	TLGPSSRLSP	DKAKAETMCG	TKSKSSGPAG	SLPEDNSLPP
490	500	510	520	530	540	550	560
CCGSAALAIG	GDRDGDLAQL	CSFGQQNNSQ	LPLGSTAYVS	GSGSQDPSSV	SITTSCQEPS	ERNQTKTLLS	RGHGQGCSRE
570	580	590	600	610	620	630	640
QREPLGDVVE	YIIRELQGIS	RLQTEIAELQ	QHLSQVQGSV	DEVSSCVDSV	LSEIEGLQVS	TCSLAKVCEG	EKAQEPHVDR
650	660	670	680	690	700	710	720
PSEEAILYLY	GLPEQDGENT	MELVESFLAK	HLCVNGMQCN	RYIKKAYRAG	TSPSPRPTVV	KLAHLEHRDF	ILQKSILLQN
730	740	750	760	770	780	790	800
VGVRIATREE	PSCPQGNKNP	QKESISFFQQ	QHQDYSQTSL	NQDEPVLQME	TGDRGPITGT	YQMKAQDQQR	EHQAPEQQGP
810	820	830	840	850	860	870	880
CFLLKNNLSK	ESDVPKLGDE	IKGASRTSQV	ISGSCDELSE	KKASLSTPHQ	FEEPALVLIS	KEEASGKSQF	FKQYSQKHEA
890	900	910	920	930	940	950	960
CKVGKPENDC	HDKSEASSCL	SLSGLLKTER	INAEDKLLGC	EAGLDILSSK	ELEDLLADKS	RRLAALSCDS	MMEEIIIGPE
970	980	990	1000	1010	1020	1030	1040
TFSDMVHIDL	NEEEECAAHV	LKDVFDKSSC	VLGGSQEDED	VEIKFYTSKL	GRAIHHFRSA	LQGVFQKLEN	SGSISPEDLE
1050	1060	1070	1080	1090	1100	1110	1120
SNESGSQSEN	SDRLLGTVSS	GGAQDCSLES	PGSQGSESLL	SVVSGGVGVS	TQGEQTPQDP	STFSLASNNS	LPSVALAPCL
1130	1140	1150	1160	1170	1180	1190	1200
GSETCSRPGS	PKQGRLSLEQ	VCTETVYLNK	CINNFKNVLR	EKRLRQKKLL	HELVQKANRL	SVEDIHSEEK	RGALQIPDDG
1210	1220	1230	1240	1250	1260	1270	1280
DPSLPQWLPE	GPAGGLYGID	SMPDLRRKKP	LPLVSDLAMS	LVQSRKAGIT	SAMATRTSLK	DEELKSHVYK	KTLQALIYPI
1290	1300	1310	1320	1330	1340	1350	1360
SCTTPHNFEV	WTATTPTYCY	ECEGLLWGIA	RQGMRCSECG	VKCHEKCQDL	LNADCLQRAA	EKSCKHGAED	RTQNIIMAMK
1370	1380	1390	1400	1410	1420	1430	1440
DRMKIRERNK	PEIFEVIRDV	FTVNKAAHVQ	QMKTVKQSVL	DGTSKWSAKI	TITVVCAQGL	QAKDKTGSSD	PYVTVQVSKT
1450	1460	1470	1480	1490	1500	1510	1520
KKRTKTIFGN	LNPVWEEKFH	FECHNSSDRI	KVRVWDEDDD	IKSRVKQRLK	RESDDFLGQT	IIEVRTLSGE	MDVWYNLEKR
1530	1540	1550	1560	1570	1580	1590	1600
TDKSAVSGAI	RLQISVEIKG	EEKVAPYHVQ	YTCLHENLFH	YLTDIQGSGG	VRIPEARGDD	AWKVYFDETA	QEIVDEFAMR
1610	1620	1630	1640	1650	1660	1670	1680
YGIESIYQAM	THFACLSSKY	MCPGVPAVMS	TLLANINAYY	AHTTASTNVS	ASDRFAASNF	GKERFVKLLD	QLHNSLRIDL
1690	1700	1710	1720	1730	1740	1750	1760
STYRNNFPAG	SPERLQDLKS	TVDLLTSITF	FRMKVQELQS	PPRASQVVKD	CVKACLNSTY	EYIFNNCHDL	YSRQYQLKQE
1770	1780	1790	1800	1810	1820	1830	1840
LPPEEQGPSI	RNLDFWPKLI	TLIVSIIEED	KNSYTPVLNQ	FPQELNVGKV	SAEVMWHLFA	QDMKYALEEH	EKDHLCKSAD
1850	1860	1870	1880	1890	1900	1910	1920
YMNLHFKVKW	LHNEYVRDLP	VLQGQVPEYP	AWFEQFVLQW	LDENEDVSLE	FLRGALERDK	KDGFQQTSEH	ALFSCSVVDV
1930	1940	1950	1960	1970	1980	1990	2000
FTQLNQSFEI	IRKLECPDPS	ILAHYMRRFA	KTIGKVLMQY	ADILSKDFPA	YCTKEKLPCI	LMNNVQQLRV	QLEKMFEAMG
2010	2020	2030	2040	2050	2060	2070	2080
GKELDLEAAD	SLKELQVKLN	TVLDELSMVF	GNSFQVRIDE	CVRQMADILG	QVRGTGNASP	DARASAAQDA	DSVLRPLMDF
2090	2100	2110	2120	2130	2140	2150	2160
LDGNLTLFAT	VCEKTVLKRV	LKELWRVVMN	TMERMIVLPP	LTDQTGTQLI	FTAAKELSHL	SKLKDHMVRE	ETRNLTPKQC
2170	2180	2190	2200	2210	2220	2230	2240
AVLDLALDTI	KQYFHAGGNG	LKKTFLEKSP	DLQSLRYALS	LYTQTTDTLI	KTFVRSQTTQ	GSGVDDPVGE	VSIQVDLFTH
2250	2260	2270	2280	2290	2300	2310	2320
PGTGEHKVTV	KVVAANDLKW	QTAGMFRPFV	EVTMVGPHQS	DKKRKFTTKS	KSNNWAPKYN	ETFHFLLGNE	EGPESYELQI
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
2611	1	709.8596	-31.02	2	63.3	11.5	0	917-930	K.LLGCEAGLDILSSK.E	

Detailed Protein Report

Protein 414: integrin beta-like protein 1 isoform 3 [Homo sapiens]

Accession:	gi|418203907	**Score:**	25.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	43.9
Database Date:	2015-11-30	**pI:**	5.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	10.0
		No. of unique 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
2134	1	1062.3814	-60.33	2	56.8	10.7	1	52-70	K.NSQDIICSNAGTCHCGRCK.C	Carbamidomethyl: 13, 15

Detailed Protein Report

Protein 415: PREDICTED: GRAM domain-containing protein 1C isoform X2 [Homo sapiens]

Accession:	gi|530374810	**Score:**	25.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	69.6
Database Date:	2015-11-30	**pI:**	6.9
		Sequence Coverage [%]:	3.8
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MEGAPTVRQV	MNEGDSSLAT	DLQEDVEENP	SPTVEENNVV	VKKQGPNLHN	WSGDWSFWIS	SSTYKDRNEE	YRRQFTHLPD
90	100	110	120	130	140	150	160
TERLIADYAC	ALQRDILLQG	RLYLSENWLC	FYSNIFRWET	TISIALKNIT	FMTKEKTARL	IPNAIQIVTE	SEKFFFTSFG
170	180	190	200	210	220	230	240
ARDRSYLSIF	RLWQNVLLDK	SLTRQEFWQL	LQQNYGTELG	LNAEEMENLS	LSIEDVQPRS	PGRSSLDDSG	ERDEKLSKSI
250	260	270	280	290	300	310	320
SFTSESISRV	SETESFDGNS	SKGGLGKEES	QNEKQTKKSL	LPTLEKKLTR	VPSKSLDLNK	NEYLSLDKSS	TSDSVDEENV
330	340	350	360	370	380	390	400
PEKDLHGRLF	INRIFHISAD	RMFELLFTSS	RFMQKFASSR	NIIDVVSTPW	TAELGGDQLR	TMTYTIVLNS	PLTGKCTAAT
410	420	430	440	450	460	470	480
EKQTLYKESR	EARFYLVDSE	VLTHDVPYHD	YFYTVNRYCI	IRSSKQKCRL	RVSTDLKYRK	QPWGLVKSLI	EKNSWSSLED
490	500	510	520	530	540	550	560
YFKQLGKKKE	MENYNVTLIV	VMSIFVLLLV	LLNVTLFLKL	SKIEHAAQSF	YRLRLQEEKS	LNLASDMVSR	AETIQKNKDQ
570	580	590	600	610			
AHRLKGVLRD	SIVMLEQLKS	SLIMLQKTFD	LLNKNKTGMA	VES			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1154	1	981.6192	184.16	1	44.1	11.5	1	66-72	K.DRNEEYR.R	
2537	1	884.5766	142.07	2	62.2	14.2	2	588-603	K.TFDLLNKNKTGMAVES.-	

Detailed Protein Report

Protein 416: PREDICTED: acetyl-CoA acetyltransferase, cytosolic isoform X1 [Homo sapiens]

Accession:	gi|530383698	**Score:**	25.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	44.6
Database Date:	2015-11-30	**pI:**	9.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	9.4
		No. of unique Peptides:	2

Quantitation

MD:MU	**Median:** 1.10	**CV:** 0.00 %	**No. of Peptides:** 1

10	20	30	40	50	60	70	80
MGSHPVLRIW	GNRRATAASL	GRSGGRLSSP	RLLRVVAPTL	TFAQTSRCSF	NGALAAVPVQ	DLGSTVIKEV	LKRATVAPED
90	100	110	120	130	140	150	160
VSEVIFGHVL	AAGCGQNPVR	QASVGAGIPY	SVPAWSCQMI	CGSGLKAVCL	AVQSIGIGDS	SIVVAGGMEN	MSKAPHLAYL
170	180	190	200	210	220	230	240
RTGVKIGEMP	LTDSILCDGL	TDAFHNCHMG	ITAENVAKKW	QVSREDQDKV	AVLSQNRTEN	AQKAGHFDKE	IVPVLVSTRK
250	260	270	280	290	300	310	320
GLIEVKTDEF	PRHGSNIEAM	SKLKPYFLTD	GTGTVTPANA	SGINDGAAAV	VLMKKSEADK	RGLTPLARIV	SWSQVGVEPS
330	340	350	360	370	380	390	400
IMGIGPIPAI	KQAVTKAGWS	LEDVDIFEIN	EAFAAVSAAI	VKELGLNPEK	VNIEGGAIAL	GHPLGASGCR	ILVTLLHTLE
410	420	430					
RMGRSRGVAA	LCIGGGMGIA	MCVQRE					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2173	1	1045.4885	-59.90	2	57.0	15.6	0	48-68	R.CSFNGALAAVPVQDLGSTVIK.E		
1603	1	932.4687	12.96	2	49.8	10.1	0	407-425	R.GVAALCIGGGMGIAMCVQR.E	Carbamidomethyl: 16	MD:MU 1.10

Detailed Protein Report

Protein 417: tubulin beta-4B chain [Homo sapiens]

Accession:	gi|5174735	**Score:**	25.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	49.8
Database Date:	2015-11-30	**pI:**	4.6
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	9.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MREIVHLQAG	QCGNQIGAKF	WEVISDEHGI	DPTGTYHGDS	DLQLERINVY	YNEATGGKYV	PRAVLVDLEP	GTMDSVRSGP
90	100	110	120	130	140	150	160
FGQIFRPDNF	VFGQSGAGNN	WAKGHYTEGA	ELVDSVLDVV	RKEAESCDCL	QGFQLTHSLG	GGTGSGMGTL	LISKIREEYP
170	180	190	200	210	220	230	240
DRIMNTFSVV	PSPKVSDTVV	EPYNATLSVH	QLVENTDETY	CIDNEALYDI	CFRTLKLTTP	TYGDLNHLVS	ATMSGVTTCL
250	260	270	280	290	300	310	320
RFPGQLNADL	RKLAVNMVPF	PRLHFFMPGF	APLTSRGSQQ	YRALTVPELT	QQMFDAKNMM	AACDPRHGRY	LTVAAVFRGR
330	340	350	360	370	380	390	400
MSMKEVDEQM	LNVQNKNSSY	FVEWIPNNVK	TAVCDIPPRG	LKMSATFIGN	STAIQELFKR	ISEQFTAMFR	RKAFLHWYTG
410	420	430	440	450			
EGMDEMEFTE	AESNMNDLVS	EYQQYQDATA	EEEGEFEEEA	EEVA			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1621	1	1061.1775	-37.83	3	50.0	12.9	2	351-379	K.TAVCDIPPRGLKMSATFIGNSTAIQELFK.R	Carbamidomethyl: 4; Oxidation: 13

Detailed Protein Report

Protein 418: methyl-CpG-binding domain protein 5 [Homo sapiens]

Accession:	gi|38202209	**Score:**	25.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	159.8
Database Date:	2015-11-30	**pI:**	10.0
		Sequence Coverage [%]:	1.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MNGGKECDGG	DKEGGLPAIQ	VPVGWQRRVD	QNGVLYVSPS	GSLLSCLEQV	KTYLLTDGTC	KCGLECPLIL	PKVFNFDPGA
90	100	110	120	130	140	150	160
AVKQRTAEDV	KADEDVTKLC	IHKRKIIAVA	TLHKSMEAPH	PSLVLTSPGG	GTNATPVVPS	RAATPRSVRN	KSHEGITNSV
170	180	190	200	210	220	230	240
MPECKNPFKL	MIGSSNAMGR	LYVQELPGSQ	QQELHPVYPR	QRLGSSEHGQ	KSPFRGSHGG	LPSPASSGSQ	IYGDGSISPR
250	260	270	280	290	300	310	320
TDPLGSPDVF	TRSNPGFHGA	PNSSPIHLNR	TPLSPPSVML	HGSPVQSSCA	MAGRTNIPLS	PTLTTKSPVM	KKPMCNFSTN
330	340	350	360	370	380	390	400
MEIPRAMFHH	KPPQGPPPPP	PPSCALQKKP	LTSEKDPLGI	LDPIPSKPVN	QNPVIINPTS	FHSNVHSQVP	MMNVSMPPAV
410	420	430	440	450	460	470	480
VPLPSNLPLP	TVKPGHMNHG	SHVQRVQHSA	STSLSPSPVT	SPVHMMGTGI	GRIEASPQRS	RSSSTSSDHG	NFMMPPVGPQ
490	500	510	520	530	540	550	560
ATSSGIKVPP	RSPRSTIGSP	RPSMPSSPST	KSDGHHQYKD	IPNPLIAGIS	NVLNTPSSAA	FPTASAGSSS	VKSQPGLLGM
570	580	590	600	610	620	630	640
PLNQILNQHN	AASFPASSLL	SAAAKAQLAN	QNKLAGNNSS	SSSNSGAVAG	SGNTEGHSTL	NTMFPPTANM	LLPTGEGQSG
650	660	670	680	690	700	710	720
RAALRDKLMS	QQKDALRKRK	QPPTTVLSLL	RQSQMDSSAV	PKPGPDLLRK	QGQGSFPISS	MSQLLQSMSC	QSSHLSSNST
730	740	750	760	770	780	790	800
PGCGASNTAL	PCSANQLHFT	DPSMNSSVLQ	NIPLRGEAVH	CHNANTNFVH	SNSPVPNHHL	AGLINQIQAS	GNCGMLSQSG
810	820	830	840	850	860	870	880
MALGNSLHPN	PPQSRISTSS	TPVIPNSIVS	SYNQTSSEAG	GSGPSSSIAI	AGTNHPAITK	TTSVLQDGVI	VTTAAGNPLQ
890	900	910	920	930	940	950	960
SQLPIGSDFP	FVGQEHALHF	PSNSTSNNHL	PHPLNPSLLS	SLPISLPVNQ	QHLLNQNLLN	ILQPSAGEGD	MSSINNTLSN
970	980	990	1000	1010	1020	1030	1040
HQLTHLQSLL	NNNQMFPPNQ	QQQQLLQGYQ	NLQAFQGQST	IPCPANNNPM	ACLFQNFQVR	MQEDAALLNK	RISTQPGLTA
1050	1060	1070	1080	1090	1100	1110	1120
LPENPNTTLP	PFQDTPCELQ	PRIDPSLGQQ	VKDGLVVGGP	GDASVDAIYK	AVVDAASKGM	QVVITTAVNS	TTQISPIPAL
1130	1140	1150	1160	1170	1180	1190	1200
SAMSAFTASI	GDPLNLSSAV	SAVIHGRNMG	GVDHDGRLRN	SRGARLPKNL	DHGKNVNEGD	GFEYFKSASC	HTSKKQWDGE
1210	1220	1230	1240	1250	1260	1270	1280
QSPRGERNRW	KYEEFLDHPG	HIHSSPCHER	PNNVSTLPFL	PGEQHPILLP	PRNCPGDKIL	EENFRYNNYK	RTMMSFKERL
1290	1300	1310	1320	1330	1340	1350	1360
ENTVERCAHI	NGNRPRQSRG	FGELLSTAKQ	DLVLEEQSPS	SSNSLENSLV	KDYIHYNGDF	NAKSVNGCVP	SPSDAKSISS
1370	1380	1390	1400	1410	1420	1430	1440
EDDLRNPDSP	SSNELIHYRP	RTFNVGDLVW	GQIKGLTSWP	GKLVREDDVH	NSCQQSPEEG	KVEPEKLKTL	TEGLEAYSRV
1450	1460	1470	1480	1490	1500		
RKRNRKSGKL	NNHLEAAIHE	AMSELDKMSG	TVHQIPQGDR	QMRPPKPKRR	KISR		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2584	1	834.4230	41.03	2	62.8	12.5	0	312-325	K.KPMCNFSTNMEIPR.A	

Detailed Protein Report

Protein 419: PREDICTED: sterol regulatory element-binding protein 1 isoform X2 [Homo sapiens]

Accession:	gi|578830023	**Score:**	25.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	119.1
Database Date:	2015-11-30	**pI:**	9.9
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.4
		No. of unique 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
1578	1	798.3570	-33.20	2	49.4	11.7	0	85-99	K.MYPSMPAFSPGPGIK.E	Oxidation: 5

Detailed Protein Report

Protein 420: **insulin-like peptide INSL6 precursor [Homo sapiens]**

Accession:	gi|38569396	**Score:**	25.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	24.8
Database Date:	2015-11-30	**pI:**	10.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	12.7
		No. of unique Peptides:	2

```
        10         20         30         40         50         60         70         80
MPRLLRLSLL WLGLLLVRFS RELSDISSAR KLCGRYLVKE IEKLCGHANW SQFRFEEETP FSRLIAQASE KVEAYSPYQF
        90        100        110        120        130        140        150        160
ESPQTASPAR GRGTNPVSTS WEEAVNSWEM QSLPEYKDKK GYSPLGKTRE FSSSHNINVY IHENAKFQKK RRNKIKTLSN
       170        180        190        200        210        220
LFWGHHPQRK RRGYSEKCCL TGCTKEELSI ACLPYIDFKR LKEKRSSLVT KIY
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1976	1	753.7938	-38.59	2	54.8	12.2	1	173-185	R.GYSEKCCLTGCTK.E	Carbamidomethyl: 7, 11
2810	1	1024.4996	19.87	3	65.5	13.4	2	173-199	R.GYSEKCCLTGCTKEELSIACLPYIDFK.R	Carbamidomethyl: 11

Detailed Protein Report

Protein 421: PREDICTED: kinesin-like protein KIF13A isoform X8 [Homo sapiens]

Accession: gi|578811856
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 25.6
MW [kDa]: 194.6
pI: 5.3
Sequence Coverage [%]: 1.2
No. of unique Peptides: 2

10	20	30	40	50	60	70	80
MMGHAEQLGL	IPRLCCALFK	RISLEQNESQ	TFKVEVSYME	IYNEKVRDLL	DPKGSRQSLK	VREHKVLGPY	VDGLSQLAVT
90	100	110	120	130	140	150	160
SFEDIESLMS	EGNKSRTVAA	TNMNEESSRS	HAVFNIIITQ	TLYDLQSGNS	GEKVSKVSLV	DLAGSERVSK	TGAAGERLKE
170	180	190	200	210	220	230	240
GSNINKSLTT	LGLVISSLAD	QAAGKGKSKF	VPYRDSVLTW	LLKDNLGGNS	QTSMIATISP	AADNYEETLS	TLRYADRAKR
250	260	270	280	290	300	310	320
IVNHAVVNED	PNAKVIRELR	EEVEKLREQL	SQAEAMKAPE	LKEKLEESEK	LIKELTVTWE	EKLRKTEEIA	QERQRQLESM
330	340	350	360	370	380	390	400
GISLEMSGIK	VGDDKCYLVN	LNADPALNEL	LVYYLKDHTR	VGADTSQDIQ	LFGIGIQPQH	CEIDIASDGD	VTLTPKENAR
410	420	430	440	450	460	470	480
SCVNGTLVCS	TTQLWHGDRI	LWGNNHFFRI	NLPKRKRRDW	LKDFEKETGP	PEHDLDAASE	ASSEPDYNYE	FAQMEVIMKT
490	500	510	520	530	540	550	560
LNSNGGFPII	SLSAWWSSPW	WSYLKILFPL	MWFQTKLLHK	HWDKDPVQNV	VQVLEKQYLE	EKRSALEEQR	LMYERELEQL
570	580	590	600	610	620	630	640
RQQLSPDRQP	QSSGPDRLAY	SSQTAQQKVT	QWAEERDELF	RQSLAKLREQ	LVKANTLVRE	ANFLAEEMSK	LTDYQVTLQI
650	660	670	680	690	700	710	720
PAANLSANRK	RGAIVSEPAI	QVRRKGKSTQ	VWTIEKLENK	LIDMRDLYQE	WKEKVPEAKR	LYGKRGDPFY	EAQENHNLIG
730	740	750	760	770	780	790	800
VANVFLECLF	CDVKLQYAVP	IISQQGEVAG	RLHVEVMRVT	GAVPERVVED	DSSENSSESG	SLEVVDSSGE	IIHRVKKLTC
810	820	830	840	850	860	870	880
RVKIKEATGL	PLNLSNFVFC	QYTFWDQCES	TVAAPVVDPE	VPSPQSKDAQ	YTVTFSHCKD	YVVNVTEEFL	EFISDGALAI
890	900	910	920	930	940	950	960
EVWGHRCAGN	GSSIWEVDSL	HAKTRTLHDR	WNEVTRRIEM	WISILELNEL	GEYAAVELHQ	AKDVNTGGIF	QLRQGHSRRV
970	980	990	1000	1010	1020	1030	1040
QVTVKPVQHS	GTLPLMVEAI	LSVSIGCVTA	RSTKLQRGLD	SYQRDDEDGD	DMDSYQEEDL	NCVRERWSDA	LIKRREYLDE
1050	1060	1070	1080	1090	1100	1110	1120
QIKKVSNKTE	KTEDDVEREA	QLVEQWVGLT	EERNAVLVPA	PGSGIPGAPA	DWIPPPGMET	HIPVLFLDLN	ADDLSANEQL
1130	1140	1150	1160	1170	1180	1190	1200
VGPHASGVNS	ILPKEHGSQF	FYLPIIKHSD	DEVSATASWD	SSVHDSVHLN	RVTPQNERIY	LIVKTTVQLS	HPAAMELVLR
1210	1220	1230	1240	1250	1260	1270	1280
KRIAANIYNK	QSFTQSLKRR	ISLKNIFYSC	GVTYEIVSNI	PKATEEIEDR	ETLALLAARS	ENEGTSDGET	YIEKYTRGVL
1290	1300	1310	1320	1330	1340	1350	1360
QVENILSLER	LRQAVTVKEA	LSTKARHIRR	SLSTPNVHNV	SSSRPDLSGF	DEDDKGWPEN	QLDMSDYSSS	YQDVACYGTL
1370	1380	1390	1400	1410	1420	1430	1440
PRDSPRRNKE	GCTSETPHAL	TVSPFKAFSP	QPPKFFKPLM	PVKEEHKKRI	ALEARPLLSQ	ESMPPPQAHN	PGCIVPSGSN
1450	1460	1470	1480	1490	1500	1510	1520
GSSMPVEHNS	KREKKIDSEE	EENELEAINR	KLISSQPYVP	VEFADFSVYN	ASLENREWFS	SKVDLSNSRV	LEKEVSRSPT
1530	1540	1550	1560	1570	1580	1590	1600
TSSITSGYFS	HSASNATLSD	MVVPSSDSSD	QLAIQTKDAD	STEHSTPSLV	HDFRPSSNKE	LTEVEKGLVK	DKIIVVPLKE
1610	1620	1630	1640	1650	1660	1670	1680
NSALAKGSPS	SQSIPEKNSK	SLCRTGSCSE	LDACPSKISQ	PARGFCPREV	TVEHTTNILE	DHSFTEFMGV	SEGKDFDGLT
1690	1700	1710	1720	1730	1740		
DSSAGELSSR	RSLPNKTGGK	TVSDGLHHPS	QLHSKLENDQ	VIIPEAAFWV	LCCQ		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
978	1	955.6278	74.00	1	41.8	12.8	1	46-53	K.VRDLLDPK.G	
2115	1	840.8591	-81.82	2	56.6	12.8	2	543-555	K.RSALEEQRLMYER.E	

Detailed Protein Report

Protein 422: abnormal spindle-like microcephaly-associated protein isoform 1 [Homo sapiens]

Accession:	gi|126116596	**Score:**	25.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	409.5
Database Date:	2015-11-30	**pI:**	11.2
		Sequence Coverage [%]:	0.7
		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	ASLIQGYWRR
1370	1380	1390	1400	1410	1420	1430	1440
YSTRQRFLKL	KYYSIILQSR	IRMIIAVTSY	KRYLWATVTI	QRHWRAYLRR	KQDQQRYEML	KSSTLIIQSM	FRKWKQRKMQ
1450	1460	1470	1480	1490	1500	1510	1520
SQVKATVILQ	RAFREWHLRK	QAKEENSAII	IQSWYRMHKE	LRKYIYIRSC	VVIIQKRFRC	FQAQKLYKRR	KESILTIQKY
1530	1540	1550	1560	1570	1580	1590	1600
YKAYLKGKIE	RTNYLQKRAA	AIQLQAAFRR	LKAHNLCRQI	RAACVIQSYW	RMRQDRVRFL	NLKKTIIKFQ	AHVRKHQQRQ
1610	1620	1630	1640	1650	1660	1670	1680
KYKKMKKAAV	IIQTHFRAYI	FAMKVLASYQ	KTRSAVIVLQ	SAYRGMQARK	MYIHILTSVI	KIQSYYRAYV	SKKEFLSLKN
1690	1700	1710	1720	1730	1740	1750	1760
ATIKLQSTVK	MKQTRKQYLH	LRAAALFIQQ	CYRSKKIAAQ	KREEYMQMRE	SCIKLQAFVR	GYLVRKQMRL	QRKAVISLQS
1770	1780	1790	1800	1810	1820	1830	1840
YFRMRKARQY	YLKMYKAIIV	IQNYYHAYKA	QVNQRKNFLQ	VKKAATCLQA	AYRGYKVRQL	IKQQSIAALK	IQSAFRGYNK
1850	1860	1870	1880	1890	1900	1910	1920
RVKYQSVLQS	IIKIQRWYRA	YKTLHDTRTH	FLKTKAAVIS	LQSAYRGWKV	RKQIRREHQA	ALKIQSAFRM	AKAQKQFRLF
1930	1940	1950	1960	1970	1980	1990	2000
KTAALVIQQN	FRAWTAGRKQ	CMEYIELRHA	VLVLQSMWKG	KTLRRQLQRQ	HKCAIIIQSY	YRMHVQQKKW	KIMKKAALLI
2010	2020	2030	2040	2050	2060	2070	2080
QKYYRAYSIG	REQNHLYLKT	KAAVVTLQSA	YRGMKVRKRI	KDCNKAAVTI	QSKYRAYKTK	KKYATYRASA	IIIQRWYRGI
2090	2100	2110	2120	2130	2140	2150	2160
KITNHQHKEY	LNLKKTAIKI	QSVYRGIRVR	RHIQHMHRAA	TFIKAMFKMH	QSRISYHTMR	KAAIVIQVRC	RAYYQGKMQR
2170	2180	2190	2200	2210	2220	2230	2240
EKYLTILKAV	KVLQASFRGV	RVRRTLRKMQ	TAATLIQSNY	RRYRQQTYFN	KLKKITKTVQ	QRYWAMKERN	IQFQRYNKLR
2250	2260	2270	2280	2290	2300	2310	2320
HSVIYIQAIF	RGKKARRHLK	MMHIAATLIQ	RRFRTLMMRR	RFLSLKKTAI	LIQRKYRAHL	CTKHHLQFLQ	VQNAVIKIQS
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
402	1	711.3339	-88.13	2	34.3	14.6	2	178-189	K.TFSVSQKVDRVR.S	

Detailed Protein Report

Protein 423: PREDICTED: leucine-rich repeat and coiled-coil domain-containing protein 1 isoform X6 [Homo sapiens]

Accession: gi|530388606
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 25.6
MW [kDa]: 77.0
pI: 6.0
Sequence Coverage [%]: 3.2
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MKPPYLKELY	VSSSLANCPM	LQESEKPKTE	IIKVDQSHSE	DNTYQSLVEQ	LDQEREKRWR	AEQAENKLMD	YIDELHKHAN
90	100	110	120	130	140	150	160
EKEDIHSLAL	LTTDRLKEII	FRERNSKGQL	EVMVHKLQNE	IKKLTVELMK	AKDQQEDHLK	HLRTLEKTLE	KMERQKRQQQ
170	180	190	200	210	220	230	240
AAQIRLIQEV	ELKASAADRE	IYLLRTSLHR	EREQAQQLHQ	LLALKEQEHR	KELETREFFT	DADFQDALAK	EIAKEEKKHE
250	260	270	280	290	300	310	320
QMIKEYQEKI	DVLSQQYMDL	ENEFRIALTV	EARRFQDVKD	GFENVATELA	KSKHALIWAQ	RKENESSSLI	KDLTCMVKEQ
330	340	350	360	370	380	390	400
KTKLAEVSKL	KQETAANLQN	QINTLEILIE	DDKQKSIQIE	LLKHEKVQLI	SELAAKESLI	FGLRTERKVW	GHELAQQGSS
410	420	430	440	450	460	470	480
LAQNRGKLEA	QIESLSRENE	CLRKTNESDS	DALRIKCKII	DDQTETIRKL	KDCLQEKDEH	IKRLQEKITE	IEKCTQEQLD
490	500	510	520	530	540	550	560
EKSSQLDEVL	EKLERHNERK	EKLKQQLKGK	EVELEEIRKA	YSTLNRKWHD	KGELLCHLET	QVKEVKEKFE	NKEKKLKAER
570	580	590	600	610	620	630	640
DKSIELQKNA	MEKLHSMDDA	FKRQVDAIVE	AHQAEIAQLA	NEKQKCIDSA	NLKVHQIEKE	MRELLEETCK	NKKTMEAKIK
650	660						
QLAFALNEIQ	QDM						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2425	1	679.2638	-89.31	2	60.7	11.3	1	452-462	K.DCLQEKDEHIK.R	

Detailed Protein Report

Protein 424: pro-MCH preproprotein [Homo sapiens]

Accession:	gi|71361684	**Score:**	25.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	18.7
Database Date:	2015-11-30	**pI:**	7.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	15.8
		No. of unique Peptides:	1

```
         10         20         30         40         50         60         70         80
MAKMNLSSYI LILTFSLFSQ GILLSASKSI RNLDDDMVFN TFRLGKGFQK EDTAEKSVIA PSLEQYKNDE SSFMNEEENK
         90        100        110        120        130        140        150        160
VSKNTGSKHN FLNHGLPLNL AIKPYLALKG SVAFPAENGV QNTESTQEKR EIGDEENSAK FPIGRRDFDM LRCMLGRVYR
        170
PCWQV
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
118	1	929.9543	13.99	2	31.2	15.3	1	29-43	K.SIRNLDDDMVFNTFR.L	Oxidation: 9

Detailed Protein Report

Protein 425:	**phosphatidylinositol 3,4,5-trisphosphate-dependent Rac exchanger 1 protein [Homo sapiens]**

Accession:	gi|34452732	**Score:**	25.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	186.1
Database Date:	2015-11-30	**pI:**	6.0
		Sequence Coverage [%]:	2.0
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MEAPSGSEPG	GDGAGDCAHP	DPRAPGAAAP	SSGPGPCAAA	RESERQLRLR	LCVLNEILGT	ERDYVGTLRF	LQSAFLHRIR
90	100	110	120	130	140	150	160
QNVADSVEKG	LTEENVKVLF	SNIEDILEVH	KDFLAALEYC	LHPEPQSQHE	LGNVFLKFKD	KFCVYEEYCS	NHEKALRLLV
170	180	190	200	210	220	230	240
ELNKIPTVRA	FFLLSCMLLGG	RKTTDIPLEG	YLLSPIQRIC	KYPLLLKELA	KRTPGKHPDH	PAVQSALQAM	KTVCSNINET
250	260	270	280	290	300	310	320
KRQMEKLEAL	EQLQSHIEGW	EGSNLTDICT	QLLLQGTLLK	ISAGNIQERA	FFLFDNLLVY	CKRKSRVTGS	KKSTKRTKSI
330	340	350	360	370	380	390	400
NGSLYIFRGR	INTEVMEVEN	VEDGTADYHS	NGYTVTNGWK	IHNTAKNKWF	VCMAKTAEEK	QKWLDAIIRE	REQRESLKLG
410	420	430	440	450	460	470	480
MERDAYVMIA	EKGEKLYHMM	MNKKVNLIKD	RRRKLSTVPK	CFLGNEFVAW	LLEIGEISKT	EEGVNLGQAL	LENGIIHHVS
490	500	510	520	530	540	550	560
DKHQFKNEQV	MYRFRYDDGT	YKARSELEDI	MSKGVRLYCR	LHSLYTPVIK	DRDYHLKTYK	SVLPGSKLVD	WLLAQGDCQT
570	580	590	600	610	620	630	640
REEAVALGVG	LCNNGFMHHV	LEKSEFRDES	QYFRFHADEE	MEGTSSKNKQ	LRNDFKLVEN	ILAKRLLILP	QEEDYGFDIE
650	660	670	680	690	700	710	720
EKNKAVVVKS	VQRGSLAEVA	GLQVGRKIYS	INEDLVFLRP	FSEVESILNQ	SFCSRRPLRL	LVATKAKEII	KIPDQPDTLC
730	740	750	760	770	780	790	800
FQIRGAAPPY	VYAVGRGSEA	MAAGLCAGQC	ILKVNGSNVM	NDGAPEVLEH	FQAFRSRREE	ALGLYQWIYH	THEDAQEARA
810	820	830	840	850	860	870	880
SQEASTEDPS	GEQAQEEDQA	DSAFPLLSLG	PRLSLCEDSP	MVTLTVDNVH	LEHGVVYEYV	STAGVRCHVL	EKIVEPRGCF
890	900	910	920	930	940	950	960
GLTAKILEAF	AANDSVFVEN	CRRLMALSSA	IVTMPHFEFR	NICDTKLESI	GQRIACYQEF	AAQLKSRVSP	PFKQAPLEPH
970	980	990	1000	1010	1020	1030	1040
PLCGLDFCPT	NCHINLMEVS	YPKTTPSVGR	SFSIRFGRKP	SLIGLDPEQG	HLNPMSYTQH	CITTMAAPSW	KCLPAAEGDP
1050	1060	1070	1080	1090	1100	1110	1120
QGQGLHDGSF	GPASGTLGQE	DRGLSFLLKQ	EDREIQDAYL	QLFTKLDVAL	KEMKQYVTQI	NRLLSTITEP	TSGGSCDASL
1130	1140	1150	1160	1170	1180	1190	1200
AEEASSLPLV	SEESEMDRSD	HGGIKKVCFK	VAEEDQEDSG	HDTMSYRDSY	SECNSNRDSV	LSYTSVRSNS	SYLGSDEMGS
1210	1220	1230	1240	1250	1260	1270	1280
GDELPCDMRI	PSDKQDKLHG	CLEHLFNQVD	SINALLKGPV	MSRAFEETKH	FPMNHSLQEF	KQKEECTIRG	RSLIQISIQE
1290	1300	1310	1320	1330	1340	1350	1360
DPWNLPNSIK	TLVDNIQRYV	EDGKNQLLLA	LLKCTDTELQ	LRRDAIFCQA	LVAAVCTFSE	QLLAALGYRY	NNNGEYEESS
1370	1380	1390	1400	1410	1420	1430	1440
RDASRKWLEQ	VAATGVLLHC	QSLLSPATVK	EERTMLEDIW	VTLSELDNVT	FSFKQLDENY	VANTNVFYHI	EGSRQALKVI
1450	1460	1470	1480	1490	1500	1510	1520
FYLDSYHFSK	LPSRLEGGAS	LRLHTALFTK	VLENVEGLPS	PGSQAAEDLQ	QDINAQSLEK	VQQYYRKLRA	FYLERSNLPT
1530	1540	1550	1560	1570	1580	1590	1600
DASTTAVKID	QLIRPINALD	ELCRLMKSFV	HPKPGAAGSV	GAGLIPISSE	LCYRLGACQM	VMCGTGMQRS	TLSVSLEQAA
1610	1620	1630	1640	1650	1660		
ILARSHGLLP	KCIMQATDIM	RKQGPRVEIL	AKNLRVKDQM	PQGAPRLYRL	CQPPVDGDL		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1541	1	789.6495	-94.76	3	49.1	12.7	0	562-583	R.EEAVALGVGLCNNGFMHHVLEK.S	
2660	1	734.8652	-30.72	2	63.3	12.9	0	1074-1085	R.EIQDAYLQLFTK.L	

Detailed Protein Report

Protein 426: tRNA selenocysteine 1-associated protein 1 [Homo sapiens]

Accession: gi|8923460
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 25.6
MW [kDa]: 32.5
pI: 4.5
Sequence Coverage [%]: 9.1
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MAASLWMGDL	EPYMDENFIS	RAFATMGETV	MSVKIIRNRL	TGIPAGYCFV	EFADLATAEK	CLHKINGKPL	PGATPAKRFK
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
LNYATYGKQP	DNSPEYSLFV	GDLTPDVDDG	MLYEFFVKVY	PSCRGGKVVL	DQTGVSKGYG	FVKFTDELEQ	KRALTECQGA
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
VGLGSKPVRL	SVAIPKASRV	KPVEYSQMYS	YSYNQYYQQY	QNYYAQWGYD	QNTGSYSYSY	PQYGYTQSTM	QTYEEVGDDA
250	**260**	**270**	**280**	**290**			
LEDPMPQLDV	TEANKEFMEQ	SEELYDALMD	CHWQPLDTVS	SEIPAMM			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1961	1	686.2209	-167.75	2	54.6	10.7	0	22-34	R.AFATMGETVMSVK.I	

Detailed Protein Report

Protein 427: plexin-A1 precursor [Homo sapiens]

Accession:	gi|262118282	**Score:**	25.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	210.9
Database Date:	2015-11-30	**pI:**	6.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.7
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MPLPPRSLQV	LLLLLLLLLL	LPGMWAEAGL	PRAGGGSQPP	FRTFSASDWG	LTHLVVHEQT	GEVYVGAVNR	IYKLSGNLTL
90	100	110	120	130	140	150	160
LRAHVTGPVE	DNEKCYPPPS	VQSCPHGLGS	TDNVNKLLLL	DYAANRLLAC	GSASQGICQF	LRLDDLFKLG	EPHHRKEHYL
170	180	190	200	210	220	230	240
SSVQEAGSMA	GVLIAGPPGQ	GQAKLFVGTP	IDGKSEYFPT	LSSRRLMANE	EDADMFGFVY	QDEFVSSQLK	IPSDTLSKFP
250	260	270	280	290	300	310	320
AFDIYYVYSF	RSEQFVYYLT	LQLDTQLTSP	DAAGEHFFTS	KIVRLCVDDP	KFYSYVEFPI	GCEQAGVEYR	LVQDAYLSRP
330	340	350	360	370	380	390	400
GRALAHQLGL	AEDEDVLFTV	FAQGQKNRVK	PPKESALCLF	TLRAIKEKIK	ERIQSCYRGE	GKLSLPWLLN	KELGCINSPL
410	420	430	440	450	460	470	480
QIDDDFCGQD	FNQPLGGTVT	IEGTPLFVDK	DDGLTAVAAY	DYRGRTVVFA	GTRSGRIRKI	LVDLSNPGGR	PALAYESVVA
490	500	510	520	530	540	550	560
QEGSPILRDL	VLSPNHQYLY	AMTEKQVTRV	PVESCVQYTS	CELCLGSRDP	HCGWCVLHSI	CSRRDACERA	DEPQRFAADL
570	580	590	600	610	620	630	640
LQCVQLTVQP	RNVSVTMSQV	PLVLQAWNVP	DLSAGVNCSF	EDFTESESVL	EDGRIHCRSP	SAREVAPITR	GQGDQRVVKL
650	660	670	680	690	700	710	720
YLKSKETGKK	FASVDFVFYN	CSVHQSCLSC	VNGSFPCHWC	KYRHVCTHNV	ADCAFLEGRV	NVSEDCPQIL	PSTQIYVPVG
730	740	750	760	770	780	790	800
VVKPITLAAR	NLPQPQSGQR	GYECLFHIPG	SPARVTALRF	NSSSLQCQNS	SYSYEGNDVS	DLPVNLSVVW	NGNFVIDNPQ
810	820	830	840	850	860	870	880
NIQAHLYKCP	ALRESCGLCL	KADPRFECGW	CVAERRCSLR	HHCAADTPAS	WMHARHGSSR	CTDPKILKLS	PETGPRQGGT
890	900	910	920	930	940	950	960
RLTITGENLG	LRFEDVRLGV	RVGKVLCSPV	ESEYISAEQI	VCEIGDASSV	RAHDALVEVC	VRDCSPHYRA	LSPKRFTFVT
970	980	990	1000	1010	1020	1030	1040
PTFYRVSPSR	GPLSGGTWIG	IEGSHLNAGS	DVAVSVGGRP	CSFSWRNSRE	IRCLTPPGQS	PGSAPIIINI	NRAQLTNPEV
1050	1060	1070	1080	1090	1100	1110	1120
KYNYTEDPTI	LRIDPEWSIN	SGGTLLTVTG	TNLATVREPR	IRAKYGGIER	ENGCLVYNDT	TMVCRAPSVA	NPVRSPPELG
1130	1140	1150	1160	1170	1180	1190	1200
ERPDELGFVM	DNVRSLLVLN	STSFLYYPDP	VLEPLSPTGL	LELKPSSPLI	LKGRNLLPPA	PGNSRLNYTV	LIGSTPCTLT
1210	1220	1230	1240	1250	1260	1270	1280
VSETQLLCEA	PNLTGQHKVT	VRAGGFEFSP	GTLQVYSDSL	LTLPAIVGIG	GGGGLLLLVI	VAVLIAYKRK	SRDADRTLKR
1290	1300	1310	1320	1330	1340	1350	1360
LQLQMDNLES	RVALECKEAF	AELQTDIHEL	TNDLDGAGIP	FLDYRTYAMR	VLFPGIEDHP	VLKEMEVQAN	VEKSLTLFGQ
1370	1380	1390	1400	1410	1420	1430	1440
LLTKKHFLLT	FIRTLEAQRS	FSMRDRGNVA	SLIMTALQGE	MEYATGVLKQ	LLSDLIEKNL	ESKNHPKLLL	RRTESVAEKM
1450	1460	1470	1480	1490	1500	1510	1520
LTNWFTFLLY	KFLKECAGEP	LFMLYCAIKQ	QMEKGPIDAI	TGEARYSLSE	DKLIRQQIDY	KTLTLNCVNP	ENENAPEVPV
1530	1540	1550	1560	1570	1580	1590	1600
KGLDCDTVTQ	AKEKLLDAAY	KGVPYSQRPK	AADMDLEWRQ	GRMARIILQD	EDVTTKIDND	WKRLNTLAHY	QVTDGSSVAL
1610	1620	1630	1640	1650	1660	1670	1680
VPKQTSAYNI	SNSSTFTKSL	SRYESMLRTA	SSPDSLRSRT	PMITPDLESG	TKLWHLVKNH	DHLDQREGDR	GSKMVSEIYL
1690	1700	1710	1720	1730	1740	1750	1760
TRLLATKGTL	QKFVDDLFET	IFSTAHRGSA	LPLAIKYMFD	FLDEQADKHQ	IHDADVRHTW	KSNCLPLRFW	VNVIKNPQFV
1770	1780	1790	1800	1810	1820	1830	1840
FDIHKNSITD	ACLSVVAQTF	MDSCSTSEHK	LGKDSPSNKL	LYAKDIPNYK	SWVERYYADI	AKMPAISDQD	MSAYLAEQSR
1850	1860	1870	1880	1890	1900		
LHLSQFNSMS	ALHEIYSYIT	KYKDEILAAL	EKDEQARRQR	LRSKLEQVVD	TMALSS		

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
2833	1	1051.5514	-6.99	2	65.8	13.1	1	1326-1343	R.TYAMRVLFPGIEDHPVLK.E	Oxidation: 4
1277	1	990.9708	-66.25	2	45.6	12.4	1	1440-1454	K.MLTNWFTFLLYKFLK.E	Oxidation: 1

Detailed Protein Report

Protein 428: chromosome-associated kinesin KIF4A [Homo sapiens]

Accession:	gi|116686122	**Score:**	25.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	139.8
Database Date:	2015-11-30	**pI:**	5.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.9
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MKEEVKGIPV	RVALRCRPLV	PKEISEGCQM	CLSFVPGEPQ	VVVGTDKSFT	YDFVFDPSTE	QEEVFNTAVA	PLIKGVFKGY
90	100	110	120	130	140	150	160
NATVLAYGQT	GSGKTYSMGG	AYTAEQENEP	TVGVIPRVIQ	LLFKEIDKKS	DFEFTLKVSY	LEIYNEEILD	LLCPSREKAQ
170	180	190	200	210	220	230	240
INIREDPKEG	IKIVGLTEKT	VLVALDTVSC	LEQGNNSRTV	ASTAMNSQSS	RSHAIFTISL	EQRKKSDKNS	SFRSKLHLVD
250	260	270	280	290	300	310	320
LAGSERQKKT	KAEGDRLKEG	ININRGLLCL	GNVISALGDD	KKGGFVPYRD	SKLTRLLQDS	LGGNSHTLMI	ACVSPADSNL
330	340	350	360	370	380	390	400
EETLNTLRYA	DRARKIKNKP	IVNIDPQTAE	LNHLKQQVQQ	LQVLLLQAHG	GTLPGSITVE	PSENLQSLME	KNQSLVEENE
410	420	430	440	450	460	470	480
KLSRGLSEAA	GQTAQMLERI	ILTEQANEKM	NAKLEELRQH	AACKLDLQKL	VETLEDQELK	ENVEIICNLQ	QLITQLSDET
490	500	510	520	530	540	550	560
VACMAAAIDT	AVEQEAQVET	SPETSRSSDA	FTTQHALRQA	QMSKELVELN	KALALKEALA	RKMTQNDSQL	QPIQYQYQDN
570	580	590	600	610	620	630	640
IKELELEVIN	LQKEKEELVL	ELQTAKKDAN	QAKLSERRRK	RLQELEGQIA	DLKKKLNEQS	KLLKLKESTE	RTVSKLNQEI
650	660	670	680	690	700	710	720
RMMKNQRVQL	MRQMKEDAEK	FRQWKQKKDK	EVIQLKERDR	KRQYELLKLE	RNFQKQSNVL	RRKTEEAAAA	NKRLKDALQK
730	740	750	760	770	780	790	800
QREVADKRKE	TQSRGMEGTA	ARVKNWLGNE	IEVMVSTEEA	KRHLNDLLED	RKILAQDVAQ	LKEKKESGEN	PPPKLRRRTF
810	820	830	840	850	860	870	880
SLTEVRGQVS	ESEDSITKQI	ESLETEMEFR	SAQIADLQQK	LLDAESEDRP	KQRWENIATI	LEAKCALKYL	IGELVSSKIQ
890	900	910	920	930	940	950	960
VSKLESSLKQ	SKTSCADMQK	MLFEERNHFA	EIETELQAEL	VRMEQQHQEK	VLYLLSQLQQ	SQMAEKQLEE	SVSEKEQQLL
970	980	990	1000	1010	1020	1030	1040
STLKCQDEEL	EKMREVCEQN	QQLLRENEII	KQKLTLLQVA	SRQKHLPKDT	LLSPDSSFEY	VPPKPKPSRV	KEKFLEQSMD
1050	1060	1070	1080	1090	1100	1110	1120
IEDLKYCSEH	SVNEHEDGDG	DDDEGDDEEW	KPTKLVKVSR	KNIQGCSCKG	WCGNKQCGCR	KQKSDCGVDC	CCDPTKCRNR
1130	1140	1150	1160	1170	1180	1190	1200
QQGKDSLGTV	ERTQDSEGSF	KLEDPTEVTP	GLSFFNPVCA	TPNSKILKEM	CDVEQVLSKK	TPPAPSPFDL	PELKHVATEY
1210	1220	1230	1240				
QENKAPGKKK	KRALASNTSF	FSGCSPIEEE	AH				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2074	1	701.2275	-91.47	3	56.1	10.6	2	1082-1100	K.NIQGCSCKGWCGNKQCGCR.K	Carbamidomethyl: 18
1950	2	1023.4041	14.44	2	54.3	14.9	2	1104-1120	K.SDCGVDCCCDPTKCRNR.Q	Carbamidomethyl: 3, 7, 8

Detailed Protein Report

Protein 429: vacuolar protein sorting-associated protein 13B isoform 1 [Homo sapiens]

Accession:	gi|35493701	**Score:**	25.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	445.7
Database Date:	2015-11-30	**pI:**	6.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	0.9
		No. of unique Peptides:	2

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        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
LSINDFLLKT SLKERSRILI GPCCATANLE AKWCKHSGNP GPEQSIPKIS IDLRGGLLQV FWGQEHLNCL VLLHELLNGY
      2250       2260       2270       2280       2290       2300       2310       2320
LNEEGNFEVQ VSEPVPQMSS PVEKNQTFKS EQSSDDLRTG LFQYVQDAES LKLPGVYEVL FYNETEDCPG MMLWRYPEPR
      2330       2340       2350       2360       2370       2380       2390       2400
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Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1794	2	1023.9088	-120.39	2	52.3	12.4	1	385-402	K.DPIVSIGFYCTKATVTFK.L	Carbamidomethyl: 10
1721	1	682.3288	-51.59	3	51.5	13.2	1	2196-2214	K.HSGNPGPEQSIPKISIDLR.G	

Detailed Protein Report

Protein 430: vascular endothelial growth factor receptor 3 isoform 2 precursor [Homo sapiens]

Accession:	gi|103472027	**Score:**	25.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	145.5
Database Date:	2015-11-30	**pI:**	5.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.1
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MQRGAALCLR	LWLCLGLLDG	LVSGYSMTPP	TLNITEESHV	IDTGDSLSIS	CRGQHPLEWA	WPGAQEAPAT	GDKDSEDTGV
90	100	110	120	130	140	150	160
VRDCEGTDAR	PYCKVLLLHE	VHANDTGSYV	CYYKYIKARI	EGTTAASSYV	FVRDFEQPFI	NKPDTLLVNR	KDAMWVPCLV
170	180	190	200	210	220	230	240
SIPGLNVTLR	SQSSVLWPDG	QEVVWDDRRG	MLVSTPLLHD	ALYLQCETTW	GDQDFLSNPF	LVHITGNELY	DIQLLPRKSL
250	260	270	280	290	300	310	320
ELLVGEKLVL	NCTVWAEFNS	GVTFDWDYPG	KQAERGKWVP	ERRSQQTHTE	LSSILTIHNV	SQHDLGSYVC	KANNGIQRFR
330	340	350	360	370	380	390	400
ESTEVIVHEN	PFISVEWLKG	PILEATAGDE	LVKLPVKLAA	YPPPEFQWYK	DGKALSGRHS	PHALVLKEVT	EASTGTYTLA
410	420	430	440	450	460	470	480
LWNSAAGLRR	NISLELVVNV	PPQIHEKEAS	SPSIYSRHSR	QALTCTAYGV	PLPLSIQWHW	RPWTPCKMFA	QRSLRRRQQQ
490	500	510	520	530	540	550	560
DLMPQCRDWR	AVTTQDAVNP	IESLDTWTEF	VEGKNKTVSK	LVIQNANVSA	MYKCVVSNKV	GQDERLIYFY	VTTIPDGFTI
570	580	590	600	610	620	630	640
ESKPSEELLE	GQPVLLSCQA	DSYKYEHLRW	YRLNLSTLHD	AHGNPLLLDC	KNVHLFATPL	AASLEEVAPG	ARHATLSLSI
650	660	670	680	690	700	710	720
PRVAPEHEGH	YVCEVQDRRS	HDKHCHKKYL	SVQALEAPRL	TQNLTDLLVN	VSDSLEMQCL	VAGAHAPSIV	WYKDERLLEE
730	740	750	760	770	780	790	800
KSGVDLADSN	QKLSIQRVRE	EDAGRYLCSV	CNAKGCVNSS	ASVAVEGSED	KGSMEIVILV	GTGVIAVFFW	VLLLLIFCNM
810	820	830	840	850	860	870	880
RRPAHADIKT	GYLSIIMDPG	EVPLEEQCEY	LSYDASQWEF	PRERLHLGRV	LGYGAFGKVV	EASAFGIHKG	SSCDTVAVKM
890	900	910	920	930	940	950	960
LKEGATASEH	RALMSELKIL	IHIGNHLNVV	NLLGACTKPQ	GPLMVIVEFC	KYGNLSNFLR	AKRDAFSPCA	EKSPEQRGRF
970	980	990	1000	1010	1020	1030	1040
RAMVELARLD	RRRPGSSDRV	LFARFSKTEG	GARRASPDQE	AEDLWLSPLT	MEDLVCYSFQ	VARGMEFLAS	RKCIHRDLAA
1050	1060	1070	1080	1090	1100	1110	1120
RNILLSESDV	VKICDFGLAR	DIYKDPDYVR	KGSARLPLKW	MAPESIFDKV	YTTQSDVWSF	GVLLWEIFSL	GASPYPGVQI
1130	1140	1150	1160	1170	1180	1190	1200
NEEFCQRLRD	GTRMRAPELA	TPAIRRIMLN	CWSGDPKARP	AFSELVEILG	DLLQGRGLQE	EEEVCMAPRS	SQSSEEGSFS
1210	1220	1230	1240	1250	1260	1270	1280
QVSTMALHIA	QADAEDSPPS	LQRHSLAARY	YNWVSFPGCL	ARGAETRGSS	RMKTFEEFPM	TPTTYKGSVD	NQTDSGMVLA
1290	1300						
SEEFEQIESR	HRQESGFR						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2767	1	683.0222	-25.88	3	65.9	12.6	1	354-370	K.LPVKLAAYPPPEFQWYK.D	
1787	2	620.2385	-164.56	2	52.2	12.8	2	1032-1041	R.KCIHRDLAAR.N	Carbamidomethyl: 2

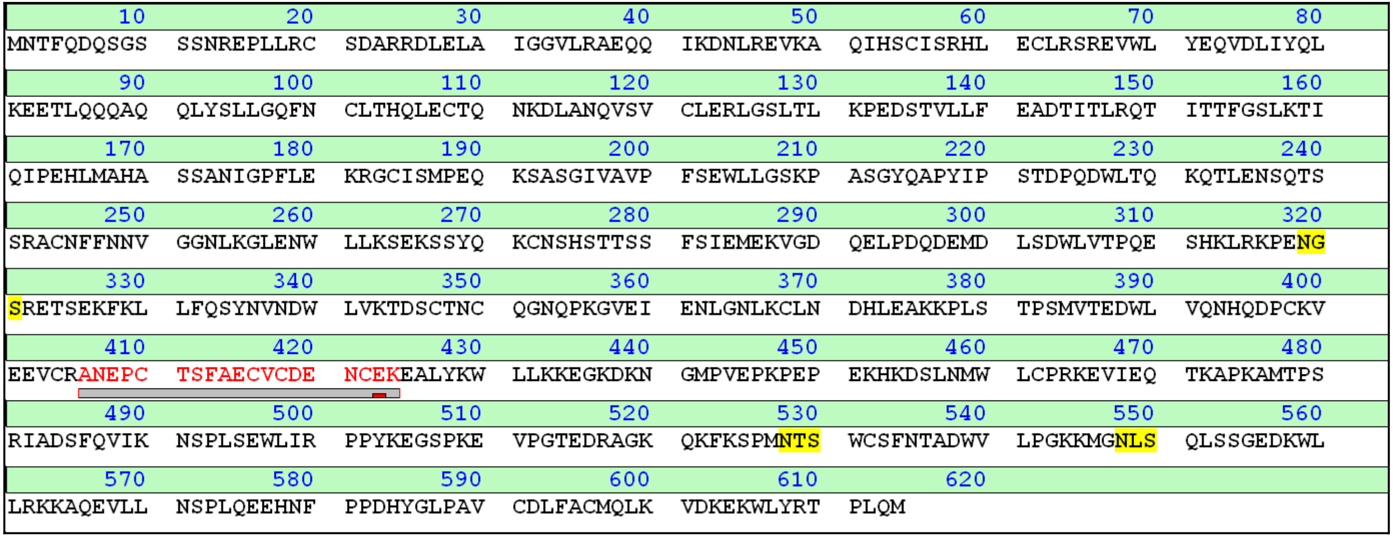
Detailed Protein Report

Protein 431: nuclear receptor coactivator 4 isoform 3 [Homo sapiens]

Accession:	gi|14149617	**Score:**	25.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	69.7
Database Date:	2015-11-30	**pI:**	5.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.1
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|223890287	refseq_human (refseq_human_20140103.fasta)	nuclear receptor coactivator 4 isoform 3 [Homo sapiens]
gi|223890284	refseq_human (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
39	1	1103.4999	78.53	2	30.2	25.4	0	406-424	R.ANEPCTSFAECVCDENCEK.E	Carbamidomethyl: 5, 17

Detailed Protein Report

Protein 432: WD repeat and FYVE domain-containing protein 1 [Homo sapiens]

Accession:	gi|18482373	**Score:**	25.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	46.3
Database Date:	2015-11-30	**pI:**	7.2
		Sequence Coverage [%]:	6.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAAEIHSRPQ	SSRPVLLSKI	EGHQDAVTAA	LLIPKEDGVI	TASEDRTIRV	WLKRDSGQYW	PSIYHTMASP	CSAMAYHHDS
90	100	110	120	130	140	150	160
RRIFVGQDNG	AVMEFHVSED	FNKMNFIKTY	PAHQNRVSAI	IFSLATEWVI	STGHDKCVSW	MCTRSGNMLG	RHFFTSWASC
170	180	190	200	210	220	230	240
LQYDFDTQYA	FVGDYSGQIT	LLKLEQNTCS	VITTLKGHEG	SVACLWWDPI	QRLLFSGASD	NSIIMWDIGG	RKGRTLLLQG
250	260	270	280	290	300	310	320
HHDKVQSLCY	LQLTRQLVSC	SSDGGIAVWN	MDVSREEAPQ	WLESDSCQKC	EQPFFWNIKQ	MWDTKTLGLR	QHHCRKCGQA
330	340	350	360	370	380	390	400
VCGKCSSKRS	SYPVMGFEFQ	VRVCDSCYDS	IKDEDRTSLA	TFHEGKHNIS	HMSMDIARGL	MVTCGTDRIV	KIWDMTPVVG
410	420						
CSLATGFSPH							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2193	1	1009.4117	-66.86	2	57.6	13.1	0	392-410	K.IWDMTPVVGCSLATGFSPH.-	

Detailed Protein Report

Protein 433: **PREDICTED: leucine-rich repeat serine/threonine-protein kinase 2 isoform X1 [Homo sapiens]**

Accession:	gi|530399725	**Score:**	25.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	285.2
Database Date:	2015-11-30	**pI:**	6.3
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.5
		No. of unique 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
NSRNASIWLG	CGHTDRGQLS	FLDLNTEGYT	SEEVADSRIL	CLALVHLPVE	KESWIVSGTQ	SGTLLVINTE	DGKKRHTLEK
2250	2260	2270	2280	2290	2300	2310	2320
MTDSVTCLYC	NSFSKQSKQK	NFLLVGTADG	KLAIFEDKTV	KLKGAAPLKI	LNIGNVSTPL	MCLSESTNST	ERNVMWGGCG
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
1730	1	796.0646	-20.88	3	51.4	11.0	1	2457-2477	R.VMMTAQLGSLKNVMLVLGYNR.K	Oxidation: 2, 3, 14

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Detailed Protein Report

Protein 434: **PREDICTED: zinc finger protein 33B isoform X3 [Homo sapiens]**

Accession:	gi|578819760	**Score:**	25.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	92.3
Database Date:	2015-11-30	**pI:**	9.9
		Sequence Coverage [%]:	4.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPHPLATSAF	LRFRLSFCLS	HVLRGRRSRD	FRGLPALLWR	MQPEERVSCI	FRVVSVFPRT	EQNEQGYCAH	KPEVIFRLEQ
90	100	110	120	130	140	150	160
GEEPWRLEEE	FPSQSFPVWT	ADHLKERSQE	NQSKHLWEVV	FINNEMLTKE	QGNVIGIPFN	MDVSSFPSRK	MFCQYDSRGM
170	180	190	200	210	220	230	240
SFNTVSELVI	SKINYLGKKS	DEFNACGKLL	LNIKHDETHT	REKNEVLKNR	NTLSHRENTL	QHEKIQTLDH	NFEYSICQET
250	260	270	280	290	300	310	320
LLEKAVFNTR	KRENAEENNC	DYNEFGRTFC	DSSSLLFHQI	PPSKDSHYEF	SDCEKFLCVK	STLSKHDGVP	VKHYDCGESG
330	340	350	360	370	380	390	400
NNFRRKLCLS	QLQKGDKGEK	HFECNECGKA	FWEKSHLTRH	QRVHTGEKHF	QCNQCGKTFW	EKSNLTKHQR	SHTGEKPFEC
410	420	430	440	450	460	470	480
NECGKAFSHK	SALTLHQRTH	TGEKPYQCNA	CGKTFYQKSD	LTKHQRTHTG	QKPYECYECG	KSFCMNSHLT	VHQRTHTGEK
490	500	510	520	530	540	550	560
PFECLECGKS	FCQKSHLTQH	QRTHIGDKPY	ECNACGKTFY	HKSVLTRHQI	IHTGLKPYEC	YECGKTFCLK	SDLTIHQRTH
570	580	590	600	610	620	630	640
TGEKPFACPE	CGKFFSHKST	LSQHYRTHTG	EKPYECHECG	KIFYNKSYLT	KHNRTHTGEK	PYECNECGKT	FCQKSQLTQH
650	660	670	680	690	700	710	720
QRIHIGEKPY	ECNECGKAFC	HKSALIVHQR	THTQEKPYKC	NECGKSFCVK	SGLILHERKH	TGEKPYECNE	CGKSFSHKSS
730	740	750	760	770	780	790	800
LTVHHRAHTG	EKSCQCNECG	KIFYRKSDLA	KHQRSHTGEK	PYECNTCRKT	FSQKSNLIVH	QRTHIGEKPY	E

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2070	1	682.5545	-123.95	3	56.0	12.2	1	752-768	K.HQRSHTGEKPYECNTCR.K	

Detailed Protein Report

Protein 435: **tristetraprolin [Homo sapiens]**

Accession:	gi|393539038	**Score:**	25.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	34.7
Database Date:	2015-11-30	**pI:**	10.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	6.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MANRYTMDLT	AIYESLLSLS	PDVPVPSDHG	GTESSPGWGS	SGPWSLSPSD	SSPSGVTSRL	PGRSTSLVEG	RSCGWVPPPP
90	100	110	120	130	140	150	160
GFAPLAPRLG	PELSPSPTSP	TATSTTPSRY	KTELCRTFSE	SGRCRYGAKC	QFAHGLGELR	QANRHPKYKT	ELCHKFYLQG
170	180	190	200	210	220	230	240
RCPYGSRCHF	IHNPSEDLAA	PGHPPVLRQS	ISFSGLPSGR	RTSPPPPGLA	GPSLSSSSFS	PSSSPPPPGD	LPLSPSAFSA
250	260	270	280	290	300	310	320
APGTPLARRD	PTPVCCPSCR	RATPISVWGP	LGGLVRTPSV	QSLGSDPDEY	ASSGSSLGGS	DSPVFEAGVF	APPQPVAAPR
330	340						
RLPIFNRISV	SE						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
373	1	644.3883	111.01	2	34.3	10.7	0	130-140	K.CQFAHGLGELR.Q	Carbamidomethyl: 1

Detailed Protein Report

Protein 436: PREDICTED: adenomatous polyposis coli protein 2 isoform X5 [Homo sapiens]

Accession:	gi|578832904	**Score:**	25.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	243.7
Database Date:	2015-11-30	**pI:**	10.0
		Sequence Coverage [%]:	1.4
		No. of unique Peptides:	1

Quantitation

MD:MU	**Median:** 0.58	**CV:** 0.00 %	**No. of Peptides:** 1

10	20	30	40	50	60	70	80
MASSVAPYEQ	LVRQVEALKA	ENSHLRQELR	DNSSHLSKLE	TETSGMKEVL	KHLQGKLEQE	ARVLVSSGQT	EVLEQLKALQ
90	100	110	120	130	140	150	160
MDITSLYNLK	FQPPTLGPEP	AARTPEGSPV	HGSGPSKDSF	GELSRATIRL	LEELDRERCF	LLNEIEKEEK	EKLWYYSQLQ
170	180	190	200	210	220	230	240
GLSKRLDELP	HVETFSMQMD	LIRQQLEFEA	QHIRSLMEER	FGTSDEMVQR	AQIRASRLEQ	IDKELLEAQD	RVQQTEPQAL
250	260	270	280	290	300	310	320
LAVKSVPVDE	DPETEVPTHP	EDGTPQPGNS	KVEVVFWLLS	MLATRDQEDT	ARTLLAMSSS	PESCVAMRRS	GCLPLLLQIL
330	340	350	360	370	380	390	400
HGTEAAAGGR	AGAPGAPGAK	DARMRANAAL	HNIVFSQPDQ	GLARKEMRVL	HVLEQIRAYC	ETCWDWLQAR	DGGPEGGGAG
410	420	430	440	450	460	470	480
SAPIPIEPQI	CQATCAVMKL	SFDEEYRRAM	NELGGLQAVA	ELLQVDYEMH	KMTRDPLNLA	LRRYAGMTLT	NLTFGDVANK
490	500	510	520	530	540	550	560
ATLCARRGCM	EAIVAQLASD	SEELHQVVSS	ILRNLSWRAD	INSKKVLREA	GSVTALVQCV	LRATKESTLK	SVLSALWNLS
570	580	590	600	610	620	630	640
AHSTENKAAI	CQVDGALGFL	VSTLTYKCQS	NSLAIIESGG	GILRNVSSLV	ATREDYRQVL	RDHNCLQTLL	QHLTSHSLTI
650	660	670	680	690	700	710	720
VSNACGTLWN	LSARSARDQE	LLWDLGAVGM	LRNLVHSKHK	MIAMGSAAAL	RNLLAHRPAK	HQAAATAVSP	GSCVPSLYVR
730	740	750	760	770	780	790	800
KQRALEAELD	ARHLAQALEH	LEKQGPPAAE	AATKKPLPPL	RHLDGLAQDY	ASDSGCFDDD	DAPSSLAAAA	ATGEPASPAA
810	820	830	840	850	860	870	880
LSLFLGSPFL	QGQALARTPP	TRRGGKEAEK	DTSGEAAVAA	KAKAKLALAV	ARIDQLVEDI	SALHTSSDDS	FSLSSGDPGQ
890	900	910	920	930	940	950	960
EAPREGRAQS	CSPCRGPEGG	RREAGSRAHP	LLRLKAAHAS	LSNDSLNSGS	ASDGYCPREH	MLPCPLAALA	SRREDPRCGQ
970	980	990	1000	1010	1020	1030	1040
PRPSRLDLDL	PGCQAEPPAR	EATSADARVR	TIKLSPTYQH	VPLLEGASRA	GAEPLAGPGI	SPGARKQAWL	PADHLSKVPE
1050	1060	1070	1080	1090	1100	1110	1120
KLAAAPLSVA	SKALQKLAAQ	EGPLSLSRCS	SLSSLSSAGR	PGPSEGGDLD	DSDSSLEGLE	EAGPSEAELD	STWRAPGATS
1130	1140	1150	1160	1170	1180	1190	1200
LPVAIPAPRR	NRGRGLGVED	ATPSSSSENY	VQETPLVLSR	CSSVSSLGSF	ESPSIASSIP	SEPCSGQGSG	TISPSELPDS
1210	1220	1230	1240	1250	1260	1270	1280
PGQTMPPSRS	KTPPLAPAPQ	GPPEATQFSL	QWESYVKRFL	DIADCRERCR	LPSELDAGSV	RFTVEKPDEN	FSCASSLSAL
1290	1300	1310	1320	1330	1340	1350	1360
ALHEHYVQQD	VELRLLPSAC	PERGGGAGGA	GLHFAGHRRR	EEGPAPTGSR	PRGAADQELE	LLRECLGAAV	PARLRKVASA
1370	1380	1390	1400	1410	1420	1430	1440
LVPGRRALPV	PVYMLVPAPA	PAQEDDSCTD	SAEGTPVNFS	SAASLSDETL	QGPPRDQPGG	PAGRQRPTGR	PTSARQAMGH
1450	1460	1470	1480	1490	1500	1510	1520
RHKAGGAGRS	AEQSRGAGKN	RAGLELPLGR	PPSAPADKDG	SKPGRTRGDG	ALQSLCLTTP	TEEAVYCFYG	NDSDEEPPAA
1530	1540	1550	1560	1570	1580	1590	1600
APTPTHRRTS	AIPRAFTRER	PQGRKEAPAP	SKAAPAAPPP	ARTQPSLIAD	ETPPCYSLSS	SASSLSEPEP	SEPPAVHPRG
1610	1620	1630	1640	1650	1660	1670	1680
REPAVTKDPG	PGGGRDSSPS	PRAAEELLQR	CISSALPRRR	PPVSGLRRRK	PRATRLDERP	AEGSRERGEE	AAGSDRASDL
1690	1700	1710	1720	1730	1740	1750	1760
DSVEWRAIQE	GANSIVTWLH	QAAAATREAS	SESDSILSFV	SGLSVGSTLQ	PPKHRKGRQA	EGEMGSARRP	EKRGAASVKT
1770	1780	1790	1800	1810	1820	1830	1840
SGSPRSPAGP	EKPRGTQKTT	PGVPAVLRGR	TVIYVPSPAP	RAQPKGTPGP	RATPRKVAPP	CLAQPAAPAK	VPSPGQQRSR
1850	1860	1870	1880	1890	1900	1910	1920
SLHRPAKTSE	LATLSQPPRS	ATPPARLAKT	PSSSSSQTSP	ASQPLPRKRP	PVTQAAGALP	GPGASPVPKT	PARTLLAKQH
1930	1940	1950	1960	1970	1980	1990	2000
KTQRSPVRIP	FMQRPARRGP	PPLARAVPEP	GPRGRAGTEA	GPGARGGRLG	LVRVASALSS	GSESSDRSGF	RRQLTFIKES
2010	2020	2030	2040	2050	2060	2070	2080
PGLRRRRSEL	SSAESAASAP	QGASPRRGRP	ALPAVFLCSS	RCEELRAAPR	QGPAPARQRP	PAARPSPGER	PARRTTSESP
2090	2100	2110	2120	2130	2140	2150	2160
SRLPVRAPAA	RPETVKRYAS	LPHISVARRP	DGAVPAAPAS	ADAARRSSDG	EPRPLPRVAA	PGTTWRRIRD	EDVPHILRST
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1997	1	731.3112	-143.18	2	54.9	10.6	1	1816-1830	R.KVAPPCLAQPAAPAK.V		MD:MU 0.58

Detailed Protein Report

Protein 437: chitotriosidase-1 isoform 2 precursor [Homo sapiens]

Accession:	gi|388890228	**Score:**	25.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	49.6
Database Date:	2015-11-30	**pI:**	5.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	5.8
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MVRSVAWAGF	MVLLMIPWGS	AAKLVCYFTN	WAQYRQGEAR	FLPKDLDPSL	CTHLIYAFAG	MTNHQLSTTE	WNDETLYQEF
90	100	110	120	130	140	150	160
NGLKKMFTDM	VATANNRQTF	VNSAIRFLRK	YSFDGLDLDW	EYPGSQGSPA	VDKERFTTLV	QDLANAFQQE	AQTSGKERLL
170	180	190	200	210	220	230	240
LSAAVPAGQT	YVDAGYEVDK	IAQNLDFVNL	MAYDFHGSWE	KVTGHNSPLY	KRQEESGAAA	SLNVDAAVQQ	WLQKGTPASK
250	260	270	280	290	300	310	320
LILGMPTYGR	SFTLASSSDT	RVGAPATGSG	TPGPFTKEGG	MLAYYEVCSW	KGATKQRIQD	QKVPYIFRDN	QWVGFDDVES
330	340	350	360	370	380	390	400
FKTKVSYLKQ	KGLGGAMVWA	LDLDDFAGFS	CNQGRYPLIQ	TLRQELSLPY	LPSGTPELEV	PKPGQPSEPE	HGPSPGQDTF
410	420	430	440	450			
CQGKADGLYP	NPRERSSFYS	CAAGRLFQQS	CPTGLVFSNS	CKCCTWN			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2531	1	701.8609	75.18	2	61.6	11.3	0	86-97	K.MFTDMVATANNR.Q	Oxidation: 1, 5
2659	1	826.4139	65.06	2	64.4	13.9	0	278-291	K.EGGMLAYYEVCSWK.G	Oxidation: 4

Detailed Protein Report

Protein 438: leucine-rich repeat-containing protein 14B [Homo sapiens]

Accession:	gi|122937351	**Score:**	25.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	56.7
Database Date:	2015-11-30	**pI:**	6.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	5.4
		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
1949	1	682.2553	-54.37	3	54.5	10.3	0	428-445	K.DCYPEGAAYPQDELAMSK.F	Carbamidomethyl: 2

Detailed Protein Report

Protein 439: C-type mannose receptor 2 precursor [Homo sapiens]

Accession:	gi|110624774	**Score:**	25.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	166.6
Database Date:	2015-11-30	**pI:**	5.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.4
		No. of unique Peptides:	2

Quantitation

MD:MU	**Median:** 2.82	**CV:** 120.49 %	**No. of Peptides:** 2

10	20	30	40	50	60	70	80
MGPGRPAPAP	WPRHLLRCVL	LLGCLHLGRP	GAPGDAALPE	PNVFLIFSHG	LQGCLEAQGG	QVRVTPACNT	SLPAQRWKWV
90	100	110	120	130	140	150	160
SRNRLFNLGT	MQCLGTGWPG	TNTTASLGMY	ECDREALNLR	WHCRTLGDQL	SLLLGARTSN	ISKPGTLERG	DQTRSGQWRI
170	180	190	200	210	220	230	240
YGSEEDLCAL	PYHEVYTIQG	NSHGKPCTIP	FKYDNQWFHG	CTSTGREDGH	LWCATTQDYG	KDERWGFCPI	KSNDCETFWD
250	260	270	280	290	300	310	320
KDQLTDSCYQ	FNFQSTLSWR	EAWASCEQQG	ADLLSITEIH	EQTYINGLLT	GYSSTLWIGL	NDLDTSGGWQ	WSDNSPLKYL
330	340	350	360	370	380	390	400
NWESDQPDNP	SEENCGVIRT	ESSGGWQNRD	CSIALPYVCK	KKPNATAEPT	PPDRWANVKV	ECEPSWQPFQ	GHCYRLQAEK
410	420	430	440	450	460	470	480
RSWQESKKAC	LRGGGDLVSI	HSMAELEFIT	KQIKQEVEEL	WIGLNDLKLQ	MNFEWSDGSL	VSFTHWHPFE	PNNFRDSLED
490	500	510	520	530	540	550	560
CVTIWGPEGR	WNDSPCNQSL	PSICKKAGQL	SQGAAEEDHG	CRKGWTWHSP	SCYWLGEDQV	TYSEARRLCT	DHGSQLVTIT
570	580	590	600	610	620	630	640
NRFEQAFVSS	LIYNWEGEYF	WTALQDLNST	GSFFWLSGDE	VMYTHWNRDQ	PGYSRGGCVA	LATGSAMGLW	EVKNCTSFRA
650	660	670	680	690	700	710	720
RYICRQSLGT	PVTPELPGPD	PTPSLTGSCP	QGWASDTKLR	YCYKVFSSER	LQDKKSWVQA	QGACQELGAQ	LLSLASYEEE
730	740	750	760	770	780	790	800
HFVANMLNKI	FGESEPEIHE	QHWFWIGLNR	RDPRGGQSWR	WSDGVGFSYH	NFDRSRHDDD	DIRGCAVLDL	ASLQWVAMQC
810	820	830	840	850	860	870	880
DTQLDWICKI	PRGTDVREPD	DSPQGRREWL	RFQEAEYKFF	EHHSTWAQAQ	RICTWFQAEL	TSVHSQAELD	FLSHNLQKFS
890	900	910	920	930	940	950	960
RAQEQHWWIG	LHTSESDGRF	RWTDGSIINF	ISWAPGKPRP	VGKDKKCVYM	TASREDWGDQ	RCLTALPYIC	KRSNVTKETQ
970	980	990	1000	1010	1020	1030	1040
PPDLPTTALG	GCPSDWIQFL	NKCFQVQGQE	PQSRVKWSEA	QFSCEQQEAQ	LVTITNPLEQ	AFITASLPNV	TFDLWIGLHA
1050	1060	1070	1080	1090	1100	1110	1120
SQRDFQWVEQ	EPLMYANWAP	GEPSGPSPAP	SGNKPTSCAV	VLHSPSAHFT	GRWDDRSCTE	ETHGFICQKG	TDPSLSPSPA
1130	1140	1150	1160	1170	1180	1190	1200
ALPPAPGTEL	SYLNGTFRLL	QKPLRWHDAL	LLCESRNASL	AYVPDPYTQA	FLTQAARGLR	TPLWIGLAGE	EGSRRYSWVS
1210	1220	1230	1240	1250	1260	1270	1280
EEPLNYVGWQ	DGEPQQPGGC	TYVDVDGAWR	TTSCDTKLQG	AVCGVSSGPP	PPRRISYHGS	CPQGLADSAW	IPFREHCYSF
1290	1300	1310	1320	1330	1340	1350	1360
HMELLLGHKE	ARQRCQRAGG	AVLSILDEME	NVFVWEHLQS	YEGQSRGAWL	GMNFNPKGGT	LVWQDNTAVN	YSNWGPPGLG
1370	1380	1390	1400	1410	1420	1430	1440
PSMLSHNSCY	WIQSNSGLWR	PGACTNITMG	VVCKLPRAEQ	SSFSPSALPE	NPAALVVVLM	AVLLLLALLT	AALILYRRRQ
1450	1460	1470	1480				
SIERGAFEGA	RYSRSSSSPT	EATEKNILVS	DMEMNEQQE				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1293	1	727.3351	-37.75	2	45.8	10.7	1	350-361	R.DCSIALPYVCKK.K	Carbamidomethyl: 2, 10	MD:MU 1.10
1150	3	500.6507	-138.75	2	44.0	14.5	0	818-826	R.EPDDSPQGR.R		MD:MU 7.28

Detailed Protein Report

Protein 440: PREDICTED: PDZ domain-containing protein 2 isoform X9 [Homo sapiens]

Accession:	gi|578809883	**Score:**	25.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	269.5
Database Date:	2015-11-30	**pI:**	9.0
		Sequence Coverage [%]:	1.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MTNAASQKVG	RRTSNRVTAW	HGRKLAEYGR	WSCSKNRMGW	EFRDGRLSLG	DELLVINGHL	LVGLSHEEAV	AILRSATGMV
90	100	110	120	130	140	150	160
QLVVASKENS	AEDLLRLTSK	SLPDLTSSVE	DVSSWTDNED	QEADGEEDEG	TSSSVQRAMP	GTDEPQDVCG	AEESKGNLES
170	180	190	200	210	220	230	240
PKQGSNKIKL	KSRLSGGVHR	LESVEEYNEL	MVRNGDPRIR	MLEVSRDGRK	HSLPQLLDSS	SASQEYHIVK	KSTRSLSTTQ
250	260	270	280	290	300	310	320
VESPWRLIRP	SVISIIGLYK	EKGKGLGFSI	AGGRDCIRGQ	MGIFVKTIFP	NGSAAEDGRL	KEGDEILDVN	GIPIKGLTFQ
330	340	350	360	370	380	390	400
EAIHTFKQIR	SGLFVLTVRT	KLVSPSLTPC	STPTHMSRSA	SPNFNTSGGA	SAGGSDEGSS	SSLGRKTPGP	KDRIVMEVTL
410	420	430	440	450	460	470	480
NKEPRVGLGI	GACCLALENS	PPGIYIHSLA	PGSVAKMESN	LSRGDQILEV	NSVNVRHAAL	SKVHAILSKC	PPGPVRLVIG
490	500	510	520	530	540	550	560
RHPNPKVSEQ	EMDEVIARST	YQESKEANSS	PGLGTPLKSP	SLAKKDSLIS	ESELSQYFAH	DVPGPLSDFM	VAGSEDEDHP
570	580	590	600	610	620	630	640
GSGCSTSEEG	SLPPSTSTHK	EPGKPRANSL	VTLGSHRASG	LFHKQVTVAR	QASLPGSPQA	LRNPLLRQRK	VGCYDANDAS
650	660	670	680	690	700	710	720
DEEEFDREGD	CISLPGALPG	PIRPLSEDDP	RRVSISSSKG	MDVHNQEERP	RKTLVSKAIS	APLLGSSVDL	EESIPEGMVD
730	740	750	760	770	780	790	800
AASYAANLTD	SAEAPKGSPG	SWWKKELSGS	SSAPKLEYTV	RTDTQSPTNT	GSPSSPQQKS	EGLGSRHRPV	ARVSPHCKRS
810	820	830	840	850	860	870	880
EAEAKPSGSQ	TVNLTGRAND	PCDLDSRVQA	TSVKVTVAGF	QPGGAVEKES	LGKLTTGDAC	VSTSCELASA	LSHLDASHLT
890	900	910	920	930	940	950	960
ENLPKAASEL	GQQPMTELDS	SSDLISSPGK	KGAAHPDPSK	TSVDTGQVSR	PENPSQPASP	RVTKCKARSP	VRLPHEGSPS
970	980	990	1000	1010	1020	1030	1040
PGEKAAAPPD	YSKTRSASET	STPHNTRRVA	ALRGAGPGAE	GMTPAGAVLP	GDPLTSQEQR	QGAPGNHSKA	LEMTGIHAPE
1050	1060	1070	1080	1090	1100	1110	1120
SSQEPSLLEG	ADSVSSRAPQ	ASLSMLPSTD	NTKEACGHVS	GHCCPGGSRE	SPVTDIDSFI	KELDASAARS	PSSQTGDSGS
1130	1140	1150	1160	1170	1180	1190	1200
QEGSAQGHPP	AGAGGGSSCR	AEPVPGGQTS	SPRRAWAAGA	PAYPQWASQP	SVLDSINPDK	HFTVNKNFLS	NYSRNFSSFH
1210	1220	1230	1240	1250	1260	1270	1280
EDSTSLSGLG	DSTEPSLSSM	YGDAEDSSSD	PESLTEAPRA	SARDGWSPPR	SRVSLHKEDP	SESEEEQIEI	CSTRGCPNPP
1290	1300	1310	1320	1330	1340	1350	1360
SSPAHLPTQA	AICPASAKVL	SLKYSTPRES	VASPREKAAC	LPGSYTSGPD	SSQPSSLLEM	SSQEHETHAD	ISTSQNHRPS
1370	1380	1390	1400	1410	1420	1430	1440
CAEETTEVTS	ASSAMENSPL	SKVARHFHSP	PIILSSPNMV	NGLEHDLLDD	ETLNQYETSI	NAAASLSSFS	VDVPKNGESV
1450	1460	1470	1480	1490	1500	1510	1520
LENLHISESQ	DLDDLLQKPK	MIARRPIMAW	FKEINKHNQG	THLRSKTEKE	QPLMPARSPD	SKIQMVSSSQ	KKGVTVPHSP
1530	1540	1550	1560	1570	1580	1590	1600
PQPKTNLENK	DLSKKSPAEM	LLTNGQKAKC	GPKLKRLSLK	GKAKVNSEAP	AANAVKAGGT	DHRKPLISPQ	TSHKTLSKAV
1610	1620	1630	1640	1650	1660	1670	1680
SQRLHVADHE	DPDRNTTAAP	RSPQCVLESK	PPLATSGPLK	PSVSDTSIRT	FVSPLTSPKP	VPEQGMWSRF	HMAVLSEPDR
1690	1700	1710	1720	1730	1740	1750	1760
GCPTTPKSPK	CRAEGRAPRA	DSGPVSPAAS	RNGMSVAGNR	QSEPRLASHV	AADTAQPRPT	GEKGGNIMAS	DRLERTNQLK
1770	1780	1790	1800	1810	1820	1830	1840
IVEISAEAVS	ETVCGNKPAE	SDRRGGCLAQ	GNCQEKSEIR	LYRQVAESST	SHPSSLPSHA	SQAEQEMSRS	FSMAKLASSS
1850	1860	1870	1880	1890	1900	1910	1920
SSLQTAIRKA	EYSQGKSSLM	SDSRGVPRNS	IPGGPSGEDH	LYFTPRPATR	TYSMPAQFSS	HFGREGHPPH	SLGRSRDSQV
1930	1940	1950	1960	1970	1980	1990	2000
PVTSSVVPEA	KASRGGLPSL	ANGQGIYSVK	PLLDTSRNLP	ATDEGDIISV	QETSCLVTDK	IKVTRRHYCY	EQNWPHESTS
2010	2020	2030	2040	2050	2060	2070	2080
FFSVKQRIKS	FENLANADRP	VAKSGASPFL	SVSSKPPIGR	RSSGSIVSGS	LGHPGDAAAR	LLRRSLSSCS	ENQSEAGTLL
2090	2100	2110	2120	2130	2140	2150	2160
PQMAKSPSIM	TLTISRQNPP	ETSSKGSDSE	LKKSLGPLGI	PTPTMTLASP	VKRNKSSVRH	TQPSPVSRSK	LQELRALSMP
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
444	1	848.1390	136.74	2	35.2	10.0	1	2429-2444	R.IGRPTVLLGSSAVIRR.S	

Detailed Protein Report

Protein 441: PREDICTED: laminin subunit alpha-5 isoform X3 [Homo sapiens]

Accession:	gi|578836003	**Score:**	25.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	248.1
Database Date:	2015-11-30	**pI:**	6.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.8
		No. of unique Peptides:	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MAKRLCAGSA	LCVRGPRGPA	PLLLVGLALL	GAARAREEAG	GGFSLHPPYF	NLAEGARIAA	SATCGEEAPA	RGSPRPTEDL
90	100	110	120	130	140	150	160
YCKLVGGPVA	GGDPNQTIRG	QYCDICTAAN	SNKAHPASNA	IDGTERWWQS	PPLSRGLEYN	EVNVTLDLGQ	VFHVAYVLIK
170	180	190	200	210	220	230	240
FANSPRPDLW	VLERSMDFGR	TYQPWQFFAS	SKRDCLERFG	PQTLERITRD	DAAICTTEYS	RIVPLENGEI	VVSLVNGRPG
250	260	270	280	290	300	310	320
AMNFSYSPLL	REFTKATNVR	LRFLRTNTLL	GHLMGKALRD	PTVTRRYYYS	IKDISIGGRC	VCHGHADACD	AKDPTDPFRL
330	340	350	360	370	380	390	400
QCTCQHNTCG	GTCDRCCPGF	NQQPWKPATA	NSANECQSCN	CYGHATDCYY	DPEVDRRRAS	QSLDGTYQGG	GVCIDCQHHT
410	420	430	440	450	460	470	480
TGVNCERCLP	GFYRSPNHPL	DSPHVCRRCN	CESDFTDGTC	EDLTGRCYCR	PNFSGERCDV	CAEGFTGFPS	CYPTPSSSND
490	500	510	520	530	540	550	560
TREQVLPAGQ	IVNCDCSAAG	TQGNACRKDP	RVGRCLCKPN	FQGTHCELCA	PGFYGPGCQP	CQCSSPGVAD	DRCDPDTGQC
570	580	590	600	610	620	630	640
RCRVGFEGAT	CDRCAPGYFH	FPLCQLCGCS	PAGTLPEGCD	EAGRCLCQPE	FAGPHCDRCR	PGYHGFPNCQ	ACTCDPRGAL
650	660	670	680	690	700	710	720
DQLCGAGGLC	RCRPGYTGTA	CQECSPGFHG	FPSCVPCHCS	AEGSLHAACD	PRSGQCSCRP	RVTGLRCDTC	VPGAYNFPYC
730	740	750	760	770	780	790	800
EAGSCHPAGL	APVDPALPEA	QVPCMCRAHV	EGPSCDRCKP	GFWGLSPSNP	EGCTRCSCDL	RGTLGGVAEC	QPGTGQCFCK
810	820	830	840	850	860	870	880
PHVCGQACAS	CKDGFFGLDQ	ADYFGCRSCR	CDIGGALGQS	CEPRTGVCRC	RPNTQGPTCS	EPARDHYLPD	LHHLRLELEE
890	900	910	920	930	940	950	960
AATPEGHAVR	FGFNPLEFEN	FSWRGYAQMA	PVQPRIVARL	NLTSPDLFWL	VFRYVNRGAM	SVSGRVSVRE	EGRSATCANC
970	980	990	1000	1010	1020	1030	1040
TAQSQPVAFP	PSTEPAFITV	PQRGFGEPFV	LNPGTWALRV	EAEGVLLDYV	VLLPSAYYEA	ALLQLRVTEA	CTYRPSAQQS
1050	1060	1070	1080	1090	1100	1110	1120
GDNCLLYTHL	PLDGFPSAAG	LEALCRQDNS	LPRPCPTEQL	SPSHPPLITC	TGSDVDVQLQ	VAVPQPGRYA	LVVEYANEDA
1130	1140	1150	1160	1170	1180	1190	1200
RQEVGVAVHT	PQRAPQQGLL	SLHPCLYSTL	CRGTARDTQD	HLAVFHLDSE	ASVRLTAEQA	RFFLHGVTLV	PIEEFSPEFV
1210	1220	1230	1240	1250	1260	1270	1280
EPRVSCISSH	GAFGPNSAAC	LPSRFPKPPQ	PIILRDCQVI	PLPPGLPLTH	AQDLTPAMSP	AGPRPRPPTA	VDPDAEPTLL
1290	1300	1310	1320	1330	1340	1350	1360
REPQATVVFT	THVPTLGRYA	FLLHGYQPAH	PTFPVEVLIN	AGRVWQGHAN	ASFCPHGYGC	RTLVVCEGQA	LLDVTHSELT
1370	1380	1390	1400	1410	1420	1430	1440
VTVRVPKGRW	LWLDYVLVVP	ENVYSFGYLR	EEPLDKSYDF	ISHCAAQGYH	ISPSSSSLFC	RNAAASLSLF	YNNGARPCGC
1450	1460	1470	1480	1490	1500	1510	1520
HEVGATGPTC	EPFGGQCPCH	AHVIGRDCSR	CATGYWGFPN	CRPCDCGARL	CDELTGQCIC	PPRTIPPDCL	LCQPQTFGCH
1530	1540	1550	1560	1570	1580	1590	1600
PLVGCEECNC	SGPGIQELTD	PTCDTDSGQC	KCRPNVTGRR	CDTCSPGFHG	YPRCRPCDCH	EAGTAPGVCD	PLTGQCYCKE
1610	1620	1630	1640	1650	1660	1670	1680
NVQGPKCDQC	SLGTFSLDAA	NPKGCTRCFC	FGATERCRSS	SYTRQEFVDM	EGWVLLSTDR	QVVPHERQPG	TEMLRADLRH
1690	1700	1710	1720	1730	1740	1750	1760
VPEAVPEAFP	ELYWQAPPSY	LGDRVSSYGG	TLRYELHSET	QRGDVFVPME	SRPDVVLQGN	QMSITFLEPA	YPTPGHVHRG
1770	1780	1790	1800	1810	1820	1830	1840
QLQLVEGNFR	HTETRNTVSR	EELMMVLASL	EQLQIRALFS	QISSAVFLRR	VALEVASPAG	QGALASNVEL	CLCPASYRGD
1850	1860	1870	1880	1890	1900	1910	1920
SCQECAPGFY	RDVKGLFLGR	CVPCQCHGHS	DRCLPGSGVC	VDCQHNTEGA	HCERCQAGFV	SSRDDPSAPC	VSCPCPLSVP
1930	1940	1950	1960	1970	1980	1990	2000
SNNFAEGCVL	RGGRTQCLCK	PGYAGASCER	CAPGFFGNPL	VLGSSCQPCD	CSGNGDPNLL	FSDCDPLTGA	CRGCLRHTTG
2010	2020	2030	2040	2050	2060	2070	2080
PRCEICAPGF	YGNALLPGNC	TRCDCTPCGT	EACDPHSGHC	LCKAGVTGRR	CDRCQEGHFG	FDGCGGCRPC	ACGPAAEGSE
2090	2100	2110	2120	2130	2140	2150	2160
CHPQSGQCHC	RPGTMGPQCR	ECAPGYWGLP	EQGCRRCQCP	GGRCDPHTGR	CNCPPGLSGE	RCDTCSQQHQ	VPVPGGPVGH
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1502	1	1052.1977	73.86	3	48.4	12.0	0	782-812	R.GTLGGVAECQPGTGQCFCKPHVCGQACASCK.D	Carbamidomethyl: 16, 18

Detailed Protein Report

Protein 442: vitamin D3 receptor isoform VDRA [Homo sapiens]

Accession:	gi|4507883	**Score:**	25.2
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:	1

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
2538	1	673.3328	74.17	2	61.7	14.1	0	403-413	R.CLSFQPECSMK.L	Carbamidomethyl: 8; Oxidation: 10

Detailed Protein Report

Protein 443: zinc finger protein 567 [Homo sapiens]

Accession: gi|34303941
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl, Oxidation

Score: 25.1
MW [kDa]: 71.5
pI: 10.3
Sequence Coverage [%]: 4.5
No. of unique Peptides: 2

10	20	30	40	50	60	70	80
MDVMLENYCH	LISVGCHMTK	PDVILKLERG	EEPWTSFAGH	TCLEENWKAE	DFLVKFKEHQ	EKYSRSVVSI	NHKKLVKEKS
90	100	110	120	130	140	150	160
KIYEKTFTLG	KNPVNSKNLP	PEYDTHGRIL	KNVSELIISN	LNPARKRLSE	YNGYGKSLLS	TKQETTHPEV	KSHNQSARAF
170	180	190	200	210	220	230	240
SHNEVLMQYQ	KTETPAQSFG	YNDCEKSFLQ	RGGLITHSRP	YKGENPSVYN	KKRRATNIEK	KHTCNECGKS	FCRKSVLILH
250	260	270	280	290	300	310	320
QGIHSEEKPY	QCHQCGNAFR	RKSYLIDHQR	THTGEKPFVC	NECGKSFRLK	TALTDHQRTH	TGEKSYECLQ	CRNAFRLKSH
330	340	350	360	370	380	390	400
LIRHQRTHTG	EKPYECNDCG	KSFRQKTTLS	LHQRIHTGEK	PYICKECGKS	FHQKANLTVH	QRTHTGEKPY	ICNECGKSFS
410	420	430	440	450	460	470	480
QKTTLALHEK	THNEEKPYIC	SECGKSFRQK	TTLVAHQRTH	TGEKSYECPH	CGKAFRMKSY	LIDHHRTHTG	EKPYECNECG
490	500	510	520	530	540	550	560
KSFSQKTNLN	LHQRIHTGEK	PYVCNECGKS	FRQKATLTVH	QKIHTGQKSY	ECPQCGKAFS	RKSYLIHHQR	THTGEKPYKC
570	580	590	600	610	620		
SECGKCFRQK	TNLIVHQRTH	TGEKPYVCNE	CGKSFSYKRN	LIVHQRTHKG	ENIEMQ		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1824	1	805.8049	-99.60	2	52.8	12.3	0	159-171	R.AFSHNEVLMQYQK.T	Oxidation: 9
1247	1	873.9372	79.81	2	45.3	12.8	0	172-186	K.TETPAQSFGYNDCEK.S	Carbamidomethyl: 13

Detailed Protein Report

Protein 444: non-receptor tyrosine-protein kinase TYK2 [Homo sapiens]

Accession:	gi|187608615	**Score:**	25.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	133.6
Database Date:	2015-11-30	**pI:**	6.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.9
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MPLRHWGMAR	GSKPVGDGAQ	PMAAMGGLKV	LLHWAGPGGG	EPWVTFSESS	LTAEEVCIHI	AHKVGITPPC	FNLFALFDAQ
90	100	110	120	130	140	150	160
AQVWLPPNHI	LEIPRDASLM	LYFRIRFYFR	NWHGMNPREP	AVYRCGPPGT	EASSDQTAQG	MQLLDPASFE	YLFEQGKHEF
170	180	190	200	210	220	230	240
VNDVASLWEL	STEEEIHHFK	NESLGMAFLH	LCHLALRHGI	PLEEVAKKTS	FKDCIPRSFR	RHIRQHSALT	RLRLRNVFRR
250	260	270	280	290	300	310	320
FLRDFQPGRL	SQQMVMVKYL	ATLERLAPRF	GTERVPVCHL	RLLAQAEGEP	CYIRDSGVAP	TDPGPESAAG	PPTHEVLVTG
330	340	350	360	370	380	390	400
TGGIQWWPVE	EEVNKEEGSS	GSSGRNPQAS	LFGKKAKAHK	AVGQPADRPR	EPLWAYFCDF	RDITHVVLKE	HCVSIHRQDN
410	420	430	440	450	460	470	480
KCLELSLPSR	AAALSFVSLV	DGYFRLTADS	SHYLCHEVAP	PRLVMSIRDG	IHGPLLEPFV	QAKLRPEDGL	YLIHWSTSHP
490	500	510	520	530	540	550	560
YRLILTVAQR	SQAPDGMQSL	RLRKFPIEQQ	DGAFVLEGWG	RSFPSVRELG	AALQGCLLRA	GDDCFSLRRC	CLPQPGETSN
570	580	590	600	610	620	630	640
LIIMRGARAS	PRTLNLSQLS	FHRVDQKEIT	QLSHLGQGTR	TNVYEGRLRV	EGSGDPEEGK	MDDEDPLVPG	RDRGQELRVV
650	660	670	680	690	700	710	720
LKVLDPSHHD	IALAFYETAS	LMSQVSHTHL	AFVHGVCVRG	PENIMVTEYV	EHGPLDVWLR	RERGHVPMAW	KMVVAQQLAS
730	740	750	760	770	780	790	800
ALSYLENKNL	VHGNVCGRNI	LLARLGLAEG	TSPFIKLSDP	GVGLGALSRE	ERVERIPWLA	PECLPGGANS	LSTAMDKWGF
810	820	830	840	850	860	870	880
GATLLEICFD	GEAPLQSRSP	SEKEHFYQRQ	HRLPEPSCPQ	LATLTSQCLT	YEPTQRPSFR	TILRDLTRLQ	PHNLADVLTV
890	900	910	920	930	940	950	960
NPDSPASDPT	VFHKRYLKKI	RDLGEGHFGK	VSLYCYDPTN	DGTGEMVAVK	ALKADCGPQH	RSGWKQEIDI	LRTLYHEHII
970	980	990	1000	1010	1020	1030	1040
KYKGCCEDQG	EKSLQLVMEY	VPLGSLRDYL	PRHSIGLAQL	LLFAQQICEG	MAYLHAQHYI	HRDLAARNVL	LDNDRLVKIG
1050	1060	1070	1080	1090	1100	1110	1120
DFGLAKAVPE	GHEYYRVRED	GDSPVFWYAP	ECLKEYKFYY	ASDVWSFGVT	LYELLTHCDS	SQSPPTKFLE	LIGIAQGQMT
1130	1140	1150	1160	1170	1180	1190	
VLRLTELLER	GERLPRPDKC	PCEVYHLMKN	CWETEASFRP	TFENLIPILK	TVHEKYQGQA	PSVFSVC	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2015	1	731.8181	-73.05	2	55.1	13.5	0	282-294	R.LLAQAEGEPCYIR.D	
623	1	824.1088	42.34	3	37.4	11.6	0	680-700	R.GPENIMVTEYVEHGPLDVWLR.R	Oxidation: 6

Detailed Protein Report

Protein 445: PREDICTED: tubulin-specific chaperone D isoform X12 [Homo sapiens]

Accession:	gi|578832042	**Score:**	25.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	129.5
Database Date:	2015-11-30	**pI:**	5.8
		Sequence Coverage [%]:	2.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MALSDEPAAG	GPEEEAEDET	LAFGAALEAF	GESAETRALL	GRLREVHGGG	AEREVALERF	RVIMDKYQEQ	PHLLDPHLEW
90	100	110	120	130	140	150	160
MMNLLLDIVQ	DQTSPASLVH	LAFKFLYIIT	KVRGYKTFLR	LFPHEVADVE	PVLDLVTIQN	PKDHEAWETR	YMLLLWLSVT
170	180	190	200	210	220	230	240
CLIPFDFSRL	DGNLLTQPGQ	ARMSIMDRIL	QIAESYLIVS	DKARDAAAVL	VSRFITRPDV	KQSKMAEFLD	WSLCNLARSS
250	260	270	280	290	300	310	320
FQTMQGVITM	DGTLQALAQI	FKHGKREDCL	PYAATVLRCL	DGCRLPESNQ	TLLRKLGVKL	VQRLGLTFLK	PKVAAWRYQR
330	340	350	360	370	380	390	400
GCRSLAANLQ	LLTQGQSEQK	PLILTEDDDE	DDDVPEGVER	VIEQLLVGLK	DKDTVVRWSA	AKGIGRMAGR	LPRALADDVV
410	420	430	440	450	460	470	480
GSVLDCFSFQ	ETDKAWHGGC	LALAELGRRG	LLLPSRLVDV	VAVILKALTY	DEKRGACSVG	TNVRDAACYV	CWAFARAYEP
490	500	510	520	530	540	550	560
QELKPFVTAI	SSALVIAAVF	DRDINCRRAA	SAAFQENVGR	QGTFPHGIDI	LTTADYFAVG	NRSNCFLVIR	VIRELAARAL
570	580	590	600	610	620	630	640
HNLAQQAPEF	SATQVFPRLL	SMTLSPDLHM	RHGSILACAE	VAYALYKLAA	QENRPVTDHL	DEQAVQGLKQ	IHQQLYDRQL
650	660	670	680	690	700	710	720
YRGLGGQLMR	QAVCVLIEKL	SLSKMPFRGD	TVIDGWQWLI	NDTLRHLHLI	SSHSRQQMKD	AAVSALAALC	SEYYMKEPGE
730	740	750	760	770	780	790	800
ADPAIQEELI	TQYLAELRNP	EEMTRCGFSL	ALGALPGFLL	KGRLQQVLTG	LRAVTHTSPE	DVSFAESRRD	GLKAIARICQ
810	820	830	840	850	860	870	880
TVGVKAGAPD	EAVCGENVSQ	IYCALLGCMD	DYTTDSRGDV	GTWVRKAAMT	SLMDLTLLLA	RSQPELIEAH	TCERIMCCVA
890	900	910	920	930	940	950	960
QQASEKIDRF	RAHAASVFLT	LLHFDSPPIP	HVPHRGELEK	LFPRSDVASV	NWSAPSQAFP	RITQLLGLPT	YRYHVLLGLV
970	980	990	1000	1010	1020	1030	1040
VSLGGLTEST	IRHSTQSLFE	YMKGIQSDPQ	ALGSFSGTLL	QIFEDNLLNE	RVSVPLLKTL	DHVLTHGCFD	IFTTEEDHPF
1050	1060	1070	1080	1090	1100	1110	1120
AVKLLALCKK	EIKNSKDIQK	LLSGIAVFCE	MVQFPGDVRR	QALLQLCLLL	CHRFPLIRKT	TASQVYETLL	TYSDVVGADV
1130	1140	1150	1160	1170			
LDEVVTVLSD	TAWDAELAVV	REQRNRLCDL	LGVPRPQLVP	QPGAC			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1258	2	727.3443	-38.23	2	45.4	13.9	0	415-428	K.AWHGGCLALAELGR.R	

Detailed Protein Report

Protein 446: structural maintenance of chromosomes protein 2 [Homo sapiens]

Accession:	gi|110347418	**Score:**	25.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	135.6
Database Date:	2015-11-30	**pI:**	9.1
		Sequence Coverage [%]:	2.6
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578816998	refseq_human (refseq_human_20140103.fasta)	PREDICTED: structural maintenance of chromosomes protein 2 isoform X1 [Homo sapiens]
gi|388240808	refseq_human (refseq_human_20140103.fasta)	structural maintenance of chromosomes protein 2 [Homo sapiens]
gi|110347425	refseq_human (refseq_human_20140103.fasta)	structural maintenance of chromosomes protein 2 [Homo sapiens]
gi|110347420	refseq_human (refseq_human_20140103.fasta)	structural maintenance of chromosomes protein 2 [Homo sapiens]

10	20	30	40	50	60	70	80
MHIKSIILEG	FKSYAQRTEV	NGFDPLFNAI	TGLNGSGKSN	ILDSICFLLG	ISNLSQVRAS	NLQDLVYKNG	QAGITKASVS
90	100	110	120	130	140	150	160
ITFDNSDKKQ	SPLGFEVHDE	ITVTRQVVIG	GRNKYLINGV	NANNTRVQDL	FCSVGLNVNN	PHFLIMQGRI	TKVLNMKPPE
170	180	190	200	210	220	230	240
ILSMIEEAAG	TRMYEYKKIA	AQKTIEKKEA	KLKEIKTILE	EEITPTIQKL	KEERSSYLEY	QKVMREIEHL	SRLYIAYQFL
250	260	270	280	290	300	310	320
LAEDTKVRSA	EELKEMQDKV	IKLQEELSEN	DKKIKALNHE	IEELEKRKDK	ETGGILRSLE	DALAEAQRVN	TKSQSAFDLK
330	340	350	360	370	380	390	400
KKNLACEESK	RKELEKNMVE	DSKTLAAKEK	EVKKITDGLH	ALQEASNKDA	EALAAAQQHF	NAVSAGLSSN	EDGAEATLAG
410	420	430	440	450	460	470	480
QMMACKNDIS	KAQTEAKQAQ	MKLKHAQQEL	KNKQAEVKKM	DSGYRKDQEA	LEAVKRLKEK	LEAEMKKLNY	EENKEESLLE
490	500	510	520	530	540	550	560
KRRQLSRDIG	RLKETYEALL	ARFPNLRFAY	KDPEKNWNRN	CVKGLVASLI	SVKDTSATTA	LELVAGERLY	NVVVDTEVTG
570	580	590	600	610	620	630	640
KKLLERGELK	RRYTIIPLNK	ISARCIAPET	LRVAQNLVGP	DNVHVALSLV	EYKPELQKAM	EFVFGTTFVC	DNMDNAKKVA
650	660	670	680	690	700	710	720
FDKRIMTRTV	TLGGDVFDPH	GTLSGGARSQ	AASILTKFQE	LKDVQDELRI	KENELRALEE	ELAGLKNTAE	KYRQLKQQWE
730	740	750	760	770	780	790	800
MKTEEADLLQ	TKLQQSSYHK	QQEELDALKK	TIEESEETLK	NTKEIQRKAE	EKYEVLENKM	KNAEAERERE	LKDAQKKLDC
810	820	830	840	850	860	870	880
AKTKADASSK	KMKEKQQEVE	AITLELEELK	REHTSYKQQL	EAVNEAIKSY	ESQIEVMAAE	VAKNKESVNK	AQEEVTKQKE
890	900	910	920	930	940	950	960
VITAQDTVIK	AKYAEVAKHK	EQNNDSQLKI	KELDHNISKH	KREAEDGAAK	VSKMLKDYDW	INAERHLFGQ	PNSAYDFKTN
970	980	990	1000	1010	1020	1030	1040
NPKEAGQRLQ	KLQEMKEKLG	RNVNMRAMNV	LTEAEERYND	LMKKKRIVEN	DKSKILTTIE	DLDQKKNQAL	NIAWQKVNKD
1050	1060	1070	1080	1090	1100	1110	1120
FGSIFSTLLP	GANAMLAPPE	GQTVLDGLEF	KVALGNTWKE	NLTELSGGQR	SLVALSLILS	MLLFKPAPIY	ILDEVDAALD
1130	1140	1150	1160	1170	1180	1190	1200
LSHTQNIGQM	LRTHFTHSQF	IVVSLKEGMF	NNANVLFKTK	FVDGVSTVAR	FTQCQNGKIS	KEAKSKAKPP	KGAHVEV

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2304	1	1022.8910	-124.62	2	59.1	14.3	1	733-749	K.LQQSSYHKQQEELDALK.K	

Detailed Protein Report

Protein 447: **putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16 isoform 2 [Homo sapiens]**

Accession:	gi|256000749	**Score:**	25.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	112.4
Database Date:	2015-11-30	**pI:**	6.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSEDPRGPKV	PRKAVVEKPA	RAAEREARAL	LEKNRSYRLL	EDSEESSEET	VSRAGSSLQK	KRKKRKHLRK	KREEEEEEEA
90	100	110	120	130	140	150	160
SEKGKKKTGG	SKQQTEKPES	EDEWERTERE	RLQDLEERDA	FAERVRQRDK	DRTRNVLERS	DKKAYEEAQK	RLKMAEEDRK
170	180	190	200	210	220	230	240
AMVPELRKKS	RREYLAKRER	EKLEDLEAEL	ADEEFLFGDV	ELSRHERQEL	KYKRRVRDLA	REYRAAGEQE	KLEATNRYHM
250	260	270	280	290	300	310	320
PKETRGQPAR	AVDLVEEESG	APGEEQRRWE	EARLGAASLK	FGARDAASQE	PKYQLVLEEE	ETIEFVRATQ	LQGDEEPSAP
330	340	350	360	370	380	390	400
PTSTQAQQKE	SIQAVRRSLP	VFPFREELLA	AIANHQVLII	EGETGSGKTT	QIPQYLFEEG	YTNKGMKIAC	TQPRRVAAMS
410	420	430	440	450	460	470	480
VAARVAREMG	VKLGNEVGYS	IRFEDCTSER	TVLRYMTDGM	LLREFLSEPD	LASYSVVMVD	EAHERTLHTD	ILFGLIKDVA
490	500	510	520	530	540	550	560
RFRPELKVLV	ASATMDTARF	STFFDDAPVF	RIPGRRFPVD	IFYTKAPEAD	YLEACVVSVL	QIHVTQPPGD	ILVFLTGQEE
570	580	590	600	610	620	630	640
IEAACEMLQD	RCRRLGSKIR	ELLVLPIYAN	LPSDMQARIF	QPTPPGARKV	VVATNIAETS	LTIEGIIYVL	DPGFCKQKSY
650	660	670	680	690	700	710	720
NPRTGMESLT	VTPCSKASAN	QRAGRAGRVA	AGKCFRLYTA	WAYQHELEET	TVPEIQRTSL	GNVVLLLKSL	GIHDLMHFDF
730	740	750	760	770	780	790	800
LDPPPYETLL	LALEQLYALG	ALNHLGELTT	SGRKMAELPV	DPMLSKMILA	SEKYSCSEEI	LTVAAMLSVN	NSIFYRPKDK
810	820	830	840	850	860	870	880
VVHADNARVN	FFLPGGDHLV	LLNVYTQWAE	SGYSSQWCYE	NFVQFRSMRR	ARDVREQLEG	LLERVEVGLS	SCQGDYIRVR
890	900	910	920	930	940	950	960
KAITAGYFYH	TARLTRSGYR	TVKQQQTVFI	HPNSSLFEQQ	PRWLLYHELV	LTTKEFMRQV	LEIESSWLLE	VAPHYYKAKE
970	980	990					
LEDPHAKKMP	KKIGKTREEL	G					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1748	1	1044.9652	-43.04	2	51.7	25.1	2	225-242	R.AAGEQEKLEATNRYHMPK.E	Oxidation: 16

Detailed Protein Report

Protein 448: neuroblastoma breakpoint family member 3 isoform 3 [Homo sapiens]

Accession:	gi|374088176	**Score:**	25.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	65.1
Database Date:	2015-11-30	**pI:**	4.2
Modification(s):	Oxidation	**Sequence Coverage [%]:**	4.1
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 1.18 **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	
1974	2	696.2762	-133.49	2	54.8	13.9	2	51-61	K.DLIKSMLRDER.L	Oxidation: 6	MD:MU	1.18

Detailed Protein Report

Protein 449: **zinc finger protein 30 isoform b [Homo sapiens]**

Accession:	gi|152963633	**Score:**	25.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	71.4
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
MAHKYVGLQY	HGSVTFEDVA	IAFSQQEWES	LDSSQRGLYR	DVMLENYRNL	VSMGHSRSKP	HVIALLEQWK	EPEVTVRKDG
90	100	110	120	130	140	150	160
RRWCTDLQLE	DDTIGCKEMP	TSENCPSFAL	HQKISRQKPR	ECQEYGKTLC	QDSKPVQHER	IHSSEKPNRC	KECGKNFSNG
170	180	190	200	210	220	230	240
HQLTIHQRLH	VGEKPYKYEK	CGKAFISGSA	FVKHGRIHTG	EKPLKCKQCG	KTISGSYQLT	VHKSIHTGKK	PYECGECGKA
250	260	270	280	290	300	310	320
FLVYGKLTRH	QSTHTGEKPF	GCEECGKAFS	TFSYLVQHQR	IHTSEKPYEC	KECGKAFSTS	SPLAKHQRIH	TGEKPYECKE
330	340	350	360	370	380	390	400
CGKSFTVYGQ	LTRHQSIHTG	EKPFECKECG	KAFRLSSFLH	AHQRIHAEIK	PYGCKECGRT	FSRASYLVQH	GRLHTGEKPY
410	420	430	440	450	460	470	480
ECKECGKAFS	TGSYLVQHQR	IHTGEKPYEC	KECGKAFISR	HQLTVHQRVH	TGEKPYECKE	CGKAFRVHVH	LTQHRKIHTD
490	500	510	520	530	540	550	560
VKPYECKECG	KTFSRASYLV	QHSRIHTGKK	PYECKECGKA	FSSGSYLVQH	QRIHTGEKPY	ECNKCGKAFT	VYGQLIGHQS
570	580	590	600	610	620	630	
VHTGEKPFEC	KECGKAFRLN	SFLTEHQRVH	TGEKPFKCKK	CGKTFRYSSA	LKVHLRKHMS	VIP	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1857	1	939.3363	-138.12	2	53.1	11.7	2	476-491	R.KIHTDVKPYECKECGK.T	

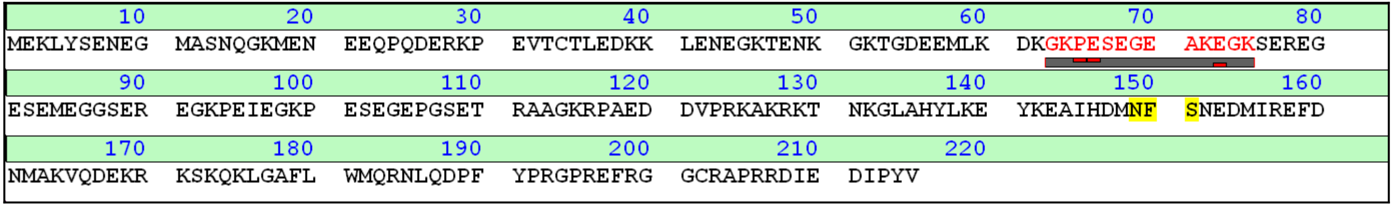
Detailed Protein Report

Protein 450: transcription elongation factor A protein-like 4 [Homo sapiens]

Accession:	gi|55749442	**Score:**	25.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	24.6
Database Date:	2015-11-30	**pI:**	5.0
		Sequence Coverage [%]:	10.2
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530422178	refseq_human (refseq_human_20140103.fasta)	PREDICTED: transcription elongation factor A protein-like 4 isoform X3 [Homo sapiens]
gi|530422176	refseq_human (refseq_human_20140103.fasta)	PREDICTED: transcription elongation factor A protein-like 4 isoform X2 [Homo sapiens]
gi|65505873	refseq_human (refseq_human_20140103.fasta)	transcription elongation factor A protein-like 4 [Homo sapiens]
gi|55749459	refseq_human (refseq_human_20140103.fasta)	transcription elongation factor A protein-like 4 [Homo sapiens]



```
        10         20         30         40         50         60         70         80
MEKLYSENEG MASNQGKMEN EEQPQDERKP EVTCTLEDKK LENEGKTENK GKTGDEEMLK DKGKPESEGE AKEGKSEREG
        90        100        110        120        130        140        150        160
ESEMEGGSER EGKPEIEGKP ESEGEPGSET RAAGKRPAED DVPRKAKRKT NKGLAHYLKE YKEAIHDMNF SNEDMIREFD
       170        180        190        200        210        220
NMAKVQDEKR KSKQKLGAFL WMQRNLQDPF YPRGPREFRG GCRAPRRDIE DIPYV
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1816	1	673.2645	-102.29	2	52.7	13.7	1	63-75	K.GKPESEGEAKEGK.S	

Detailed Protein Report

Protein 451: PREDICTED: cytosolic carboxypeptidase 2 isoform X4 [Homo sapiens]

Accession:	gi|530395811	**Score:**	25.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	90.6
Database Date:	2015-11-30	**pI:**	9.4
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.7
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MFPALETHLK	QTIPDPYEDF	MYRHLQYYGY	FKAQRGSLPN	SATHQHVRKN	NPQCLLNGSL	GEKDDLIPDT	LQKEKLLWPI
90	100	110	120	130	140	150	160
SLSSAVHRQI	EAINRDSHML	SLPHLRSRQL	LYDELDEVNP	RLREPQELFS	ILSTKRPLQA	PRWPIECEVI	KENIHHIEWA
170	180	190	200	210	220	230	240
PPQPEYFYQP	KGNEKVPEIV	GEKKGTVVYQ	LDSVPIEGSY	FTSSRVGGKR	GIVKELAVTL	QGPEDNTLLF	ESRFESGNLQ
250	260	270	280	290	300	310	320
KAVRVDTYEY	ELTLRTDLYT	NKHTQWFYFR	VQNTRKDATY	RFTIVNLLKP	KSLYTVGMKP	LLYSQLDANT	RNIGWRREGN
330	340	350	360	370	380	390	400
EIKYYKNNTD	DGQQPFYCLT	WTIQFPYDQD	TCFFAHFYPY	TYTDLQCYLL	SVANNPIQSQ	FCKLQTLCRS	LAGNTVYLLT
410	420	430	440	450	460	470	480
ITNPSQTPQE	AAAKKAVVLS	ARVHPGESNG	SWVMKGFLDF	ILSNSPDAQL	LRDIFVFKVL	PMLNPDGVIV	GNYRCSLAGR
490	500	510	520	530	540	550	560
DLNRHYKTIL	KESFPCIWYT	RNMIKRLLEE	REVLLYCDFH	GHSRKNNIFL	YGCNNNNRKY	WLHERVFPLM	LCKNAPDKFS
570	580	590	600	610	620	630	640
FHSCNFKVQK	CKEGTGRVVM	WRMGILNSYT	MESTFGGSTL	GNKRDTHFTI	EDLKSLGYHV	CDTLLDFCDP	DQMKFTQCLA
650	660	670	680	690	700	710	720
ELKELLRQEI	HKKFHELGQD	VDLEGSWSDI	SLSDIESSTS	GSDSSLSDGL	PVHLANIADE	TNLNRRDKDT	PLDPSMATLI
730	740	750	760	770	780	790	
LPKNKGRMQN	KKPGFTVSCS	PKRTINSSQE	PAPGMKPNWP	RSRYPATKRG	CAAMAAYPSL	HIYTYP	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
179	1	879.8295	-147.14	2	31.6	13.6	1	33-48	K.AQRGSLPNSATHQHVR.K	
1977	1	746.3572	-41.97	2	54.8	11.3	1	546-558	R.VFPLMLCKNAPDK.F	Oxidation: 5

Detailed Protein Report

Protein 452: ran GTPase-activating protein 1 [Homo sapiens]

Accession:	gi|4506411	**Score:**	24.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	63.5
Database Date:	2015-11-30	**pI:**	4.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	4.3
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578837322	refseq_human (refseq_human_20140103.fasta)	PREDICTED: ran GTPase-activating protein 1 isoform X3 [Homo sapiens]
gi|520975387	refseq_human (refseq_human_20140103.fasta)	ran GTPase-activating protein 1 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MASEDIAKLA ETLAKTQVAG GQLSFKGKSL KLNTAEDAKD VIKEIEDFDS LEALRLEGNT VGVEAARVIA KALEKKSELK
        90        100        110        120        130        140        150        160
RCHWSDMFTG RLRTEIPPAL ISLGEGLITA GAQLVELDLS DNAFGPDGVQ GFEALLKSSA CFTLQELKLN NCGMGIGGGK
       170        180        190        200        210        220        230        240
ILAAALTECH RKSSAQGKPL ALKVFVAGRN RLENDGATAL AEAFRVIGTL EEVHMPQNGI NHPGITALAQ AFAVNPLLRV
       250        260        270        280        290        300        310        320
INLNDNTFTE KGAVAMAETL KTLRQVEVIN FGDCLVRSKG AVAIADAIRG GLPKLKELNL SFCEIKRDAA LAVAEAMADK
       330        340        350        360        370        380        390        400
AELEKLDLNG NTLGEEGCEQ LQEVLEGFNM AKVLASLSDD EDEEEEEEGE EEEEEAEEEE EEDEEEEEEE EEEEEEEPQQ
       410        420        430        440        450        460        470        480
RGQGEKSATP SRKILDPNTG EPAPVLSSPP PADVSTFLAF PSPEKLLRLG PKSSVLIAQQ TDTSDPEKVV SAFLKVSSVF
       490        500        510        520        530        540        550        560
KDEATVRMAV QDAVDALMQK AFNSSSFNSN TFLTRLLVHM GLLKSEDKVK AIANLYGPLM ALNHMVQQDY FPKALAPLLL
       570        580        590
AFVTKPNSAL ESCSFARHSL LQTLYKV
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1782	1	568.7446	-32.25	2	52.3	12.8	0	149-160	K.LNNCGMGIGGGK.I	Oxidation: 6

Detailed Protein Report

Protein 453: centrosomal protein of 63 kDa isoform c [Homo sapiens]

Accession:	gi|109255226	**Score:**	24.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	57.9
Database Date:	2015-11-30	**pI:**	5.9
		Sequence Coverage [%]:	8.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEALLEGIQN	RGHGGGFLTS	CEAELQELMK	QIDIMVAHKK	SEWEGRTHAL	ETCLKIREQE	LKSLRSQLDV	THKEVGMLHQ
90	100	110	120	130	140	150	160
QVEEHEKIKQ	EMTMEYKQEL	KKLHEELCIL	KRSYEKLQKK	QMREFRGNTK	NHREDRSEIE	RLTAKIEEFR	QKSLDWEKQR
170	180	190	200	210	220	230	240
LIYQQQVSSL	EAQRKALAEQ	SEIIQAQLVN	RKQKLESVEL	SSQSEIQHLS	SKLERANDTI	CANELEIERL	TMRVNDLVGT
250	260	270	280	290	300	310	320
SMTVLQEQQQ	KEEKLRESEK	LLEALQEEKR	ELKAALQSQE	NLIHEARIQK	EKLQEKVKAT	NTQHAVEAIS	LESVSATCKQ
330	340	350	360	370	380	390	400
LSQELMEKYE	ELKRMEAHNN	EYKAEIKKLK	EQILQGEQSY	SSALEGMKME	ISHLTQELHQ	RDITIASTKG	SSSDMEKRLR
410	420	430	440	450	460	470	480
AEMQKAEDKA	VEHKEILDQL	ESLKLENRHL	SEMVMKLELG	LHECSLPVSP	LGSIATRFLE	EEELRSHHIL	ERLDAHIEEL
490	500						
KRESEKTVRQ	FTALK						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2671	1	1079.8373	-57.12	3	64.6	12.7	1	437-465	K.LELGLHECSLPVSPLGSIATRFLEEEELR.S	

Detailed Protein Report

Protein 454: myomesin-1 isoform b [Homo sapiens]

Accession:	gi|140560917	**Score:**	24.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	177.6
Database Date:	2015-11-30	**pI:**	6.4
		Sequence Coverage [%]:	1.5
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 3.08 **CV:** 0.00 % **No. of Peptides:** 1

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
764	1	555.8059	19.32	2	38.9	10.8	0	697-706	R.FALFDLAEGK.S		MD:MU 3.08

Detailed Protein Report

Protein 455: NTPase KAP family P-loop domain-containing protein 1 [Homo sapiens]

Accession:	gi|254553319	**Score:**	24.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	91.8
Database Date:	2015-11-30	**pI:**	10.3
		Sequence Coverage [%]:	2.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MHKHYKVHFA	KDAQSPNGHY	FWDPELGHRK	GCCHQWRQDS	AALRAHGPCR	PSPQSHWQLA	YHSHQVGGSG	WRRGLLPSVL
90	100	110	120	130	140	150	160
QQQRQPQSQP	SPPSPLRQRL	CPIHEAQKGL	PATSTVPKEP	ASAPQAPTLP	TTAPAMARSG	PALPSAAGVL	LKPSEPTDAR
170	180	190	200	210	220	230	240
PLPAPAACGS	FTAYSSDILT	EDDVYCSCLA	KTLCHVPVPV	TVGFYAPFGC	RLHMMLDKIT	ALMQQEAAQR	ESEELQHVQW
250	260	270	280	290	300	310	320
RPRAVSGWGV	PQLLWYLVFL	QPIITEVHLR	RRNVQFLFIR	FSAWQYAGTD	KLWAGLVTTL	CEGIRRHYGA	LPFSVYSVLG
330	340	350	360	370	380	390	400
NKPATRQDCC	QSEWHCRRRV	CLGLLALLAA	LGLGVGLLYL	SLGGHALGHG	SPSGSLLKVF	GGAATTLSGS	GLLMAVYSVG
410	420	430	440	450	460	470	480
KHLFVSQRKK	IERLVSREKF	GSQLGFMCEV	KKEVELLTDF	LCFLEIYQRR	RLRVVLEVTG	LDTCYPERVV	GVLNAINTLL
490	500	510	520	530	540	550	560
SDSHAPFIFI	LVVDPSILAA	CLESAGNMKG	TADNGYLFLN	RTVTLPFSVP	IMGRRTKLQF	LHDAVQSRDD	LLYREMTRKP
570	580	590	600	610	620	630	640
WLPGDAGGES	AQLLAVQAQA	GTERGQGRID	DEAARRIQEA	LFCLHDERDC	LYEYVPDNVV	SMRRIVNTVP	ITVRLLQQQQ
650	660	670	680	690	700	710	720
QQGDFGGPTP	RQAVAWVVLA	NQWPCRLSWA	LQCLEDRQQT	GGAPEGRARL	WDVFRDNSRE	LHTMTKALQN	VLDLDGDPEL
730	740	750	760	770	780	790	800
FERFLGADFP	FTVAEAQSLL	RCTVNLDHSI	RRRMGLIRAV	SALKPPSPPK	SPTRDTPHAA	HRANSASRAP	PSGRASGQAG
810	820	830	840				
EGHHTGDLAH	RGKLWPVACA	LFRPGQSSPG	GP				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1838	1	673.2555	-124.96	2	53.0	13.9	1	771-782	K.SPTRDTPHAAHR.A	

Detailed Protein Report

Protein 456: **PREDICTED: myotubularin-related protein 5 isoform X5 [Homo sapiens]**

Accession: gi|530420851
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 24.8
MW [kDa]: 208.2
pI: 6.5
Sequence Coverage [%]: 1.2
No. of unique Peptides: 2

```
        10         20         30         40         50         60         70         80
MARLADYFVL VAFGPHPRGS GEGQGQILQR FPEKDWEDNP FPQGIELFCQ PSGWQLCPER NPPTFFVAVL TDINSERHYC
        90        100        110        120        130        140        150        160
ACLTFWEPAE PSQETTRVED ATEREEEGDE GGQTHLSPTA PAPSAQLFAP KTLVLVSRLD HTEVFRNSLG LIYAIHVEGL
       170        180        190        200        210        220        230        240
NVCLENVIGN LLTCTVPLAG GSQRTISLGA GDRQVIQTPL ADSLPVSRCS VALLFRQLGI TNVLSLFCAA LTEHKVLFLS
       250        260        270        280        290        300        310        320
RSYQRLADAC RGLLALLFPL RYSFTYVPIL PAQLLEVLST PTPFIIGVNA AFQAETQELL DVIVADLDGG TVTIPECVHI
       330        340        350        360        370        380        390        400
PPLPEPLQSQ THSVLSMVLD PELELADLAF PPPTTSTSSL KMQDKELRAV FLRLFAQLLQ GYRWCLHVVR IHPEPVIRFH
       410        420        430        440        450        460        470        480
KAAFLGQRGL VEDDFLMKVL EGMAFAGFVS ERGVPYRPTD LFDELVAHEV ARMRADENHP QRVLRHVQEL AEQLYKNENP
       490        500        510        520        530        540        550        560
YPAVAMHKVQ RPGESSHLRR VPRPFPRLDE GTVQWIVDQA AAKMQGAPPA VKAERRTTVP SGPPMTAILE RCSGLHVNSA
       570        580        590        600        610        620        630        640
RRLEVVRNCI SYVFEGKMLE AKKLLPAVLR ALKGRAARRC LAQELHLHVQ QNRAVLDHQQ FDFVVRMMNC CLQDCTSLDE
       650        660        670        680        690        700        710        720
HGIAAALLPL VTAFCRKLSP GVTQFAYSCV QEHVVWSTPQ FWEAMFYGDV QTHIRALYLE PTEDLAPAQE VGEAPSQEDE
       730        740        750        760        770        780        790        800
RSALDVASEQ RRLWPTLSRE KQQELVQKEE STVFSQAIHY ANRMSYLLLP LDSSKSRLLR ERAGLGDLES ASNSLVTNSM
       810        820        830        840        850        860        870        880
AGSVAESYDT ESGFEDAETC DVAGAVVRFI NRFVDKVCTE SGVTSDHLKG LHVMVPDIVQ MHIETLEAVQ RESRRLPPIQ
       890        900        910        920        930        940        950        960
KPKLLRPRLL PGEECVLDGL RVYLLPDGRE EGAGGSAGGP ALLPAEGAVF LTTYRVIFTG MPTDPLVGEQ VVVRSFPVAA
       970        980        990       1000       1010       1020       1030       1040
LTKEKRISVQ TPVDQLLQDG LQLRSCTFQL LKMAFDEEVG SDSAELFRKQ LHKLRYPPDI RATFAFTLGS AHTPGRPPRV
      1050       1060       1070       1080       1090       1100       1110       1120
TKDKGPSLRT LSRNLVKNAK KTIGRQHVTR KKYNPPSWEH RGQPPPEDQE DEISVSEELE PSTLTPSSAL KPSDRMTMSS
      1130       1140       1150       1160       1170       1180       1190       1200
LVERACCRDY QRLGLGTLSS SLSRAKSEPF RISPVNRMYA ICRSYPGLLI VPQSVQDNAL QRVSRCYRQN RFPVVCWRSG
      1210       1220       1230       1240       1250       1260       1270       1280
RSKAVLLRSG GLHGKGVVGL FKAQNAPSPG QSQADSSSLE QEKYLQAVVS SMPRYADASG RNTLSGFSSA HMGSHGKWGS
      1290       1300       1310       1320       1330       1340       1350       1360
VRTSGRSSGL GTDVGSRLAG RDALAPPQAN GGPPDPGFLR PQRAALYILG DKAQLKGVRS DPLQQWELVP IEVFEARQVK
      1370       1380       1390       1400       1410       1420       1430       1440
ASFKKLLKAC VPGCPAAEPS PASFLRSLED SEWLIQIHKL LQVSVLVVEL LDSGSSVLVG LEDGWDITTQ VVSLVQLLSD
      1450       1460       1470       1480       1490       1500       1510       1520
PFYRTLEGFR LLVEKEWLSF GHRFSHRGAH TLAGQSSGFT PVFLQFLDCV HQVHLQFPME FEFSQFYLKF LGYHHVSRRF
      1530       1540       1550       1560       1570       1580       1590       1600
RTFLLDSDYE RIELGLLYEE KGERRGQVPC RSVWEYVDRL SKRTPVFHNY MYAPEDAEVL RPYSNVSNLK VWDFYTEETL
      1610       1620       1630       1640       1650       1660       1670       1680
AEGPPYDWEL AQGPPEPPEE ERSDGGAPQS RRRVVWPCYD SCPRAQPDAI SRLLEELQRL ETELGQPAER WKDTWDRVKA
      1690       1700       1710       1720       1730       1740       1750       1760
AQRLEGRPDG RGTPSSLLVS TAPHHRRSLG VYLQEGPVGS TLSLSLDSDQ SSGSTTSGSR QAARRSTSTL YSQFQTAESE
      1770       1780       1790       1800       1810       1820       1830       1840
NRSYEGTLYK KGAFMKPWKA RWFVLDKTKH QLRYYDHRVD TECKGVIDLA EVEAVAPGTP TMGAPKTVDE KAFFDVKTTR
      1850       1860       1870
RVYNFCAQDV PSAQQWVDRI QSCLSDA
```

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
292	1	591.6596	-216.66	2	33.3	11.6	1	242-251	R.SYQRLADACR.G	
348	1	800.7371	-149.37	2	33.7	13.1	1	1116-1128	R.MTMSSLVERACCR.D	Carbamidomethyl: 11, 12

Detailed Protein Report

Protein 457: ankyrin repeat domain-containing protein 62 [Homo sapiens]

Accession:	gi|472339087	**Score:**	24.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	106.4
Database Date:	2015-11-30	**pI:**	6.2
		Sequence Coverage [%]:	2.7
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MEVRGSFLAA	CRRRMATWRK	NRDKDGFSNP	GYRVRQKDLG	MIHKAAIAGD	VNKVMESILL	RLNDLNDRDK	KNRTALLLAC
90	100	110	120	130	140	150	160
AHGRPGVVAD	LVARKCQLNL	TDSENRTALI	KAVQCQEEVC	ASILLEHGAN	PNVRDMYGNT	ALHYAIDNEN	ISMARKLLAY
170	180	190	200	210	220	230	240
GADIEARSQD	GHTSLLLAVN	RKKEQMVAFL	LKKKPDLTAI	DNFGRTALIL	AARNGSTSVV	YQLLQHNIDV	FCQDISGWTA
250	260	270	280	290	300	310	320
EDYAVASKFQ	AIRGMISEYK	ANKRCKSLQN	SNSEQDLEMT	SEGEQERLEG	CESSQPQVEE	KMKKCRNKKM	EVSRNVHADD
330	340	350	360	370	380	390	400
SDNYNDDVDE	LIHKIKNRKP	DNHQSPGKEN	GEFDRLARKT	SNEKSKVKSQ	IYFTDDLNDI	SGSSEKTSED	DELPYSDDEN
410	420	430	440	450	460	470	480
FMLLIEQSGM	ECKDFVSLSK	SKNATAACGR	SIEDQKCYCE	RLKVKFQKMK	NNISVLQKVL	SETDKTKSQS	EHQNLQGKKK
490	500	510	520	530	540	550	560
LCNLRFILQQ	QEEERIKAEE	LYEKDIEELK	IMEEQYRTQT	EVKKQSKLTL	KSLEVELKTV	RSNSNQNFHT	HERERDLWQE
570	580	590	600	610	620	630	640
NHLMRDEIAR	LRLEIDTIKH	QNQETENKYF	KDIEIIKENN	EDLEKTLKRN	EEALTKTITR	YSKELNVLMD	ENTMLNSELQ
650	660	670	680	690	700	710	720
KEKQSMSRLE	TEMESYRCRL	AAALCDHDQR	QSSKRDLQLA	FQSTVNEWCH	LQEDTNSHIQ	ILSQQLSKAE	STSSGLETEL
730	740	750	760	770	780	790	800
HYEREALKEK	TLHIEHMQGV	LSRTQRRLED	IEHMYQNDQP	ILEKYVRKQQ	SVEDGLFQLQ	SQNLLYQQQC	NDARKKADNQ
810	820	830	840	850	860	870	880
EKTIINIQVK	CEDTVEKLQA	ECRKLEENNK	GLMKECTLLK	ERQCQYEKEK	EEREVVRRQL	QREVDDALNK	QLLLEAMLEI
890	900	910	920				
SSERRINLED	EAQSLKKKLG	QMRSQVCMKL	SMSTVTL				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2195	1	900.3616	-160.41	2	57.3	12.4	1	45-61	K.AAIAGDVNKVMESILLR.L	
1860	1	915.3255	-218.76	1	53.3	12.3	0	451-458	K.NNISVLQK.V	

Detailed Protein Report

Protein 458: protein FAM117B [Homo sapiens]

Accession:	gi|254910983	**Score:**	24.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	61.9
Database Date:	2015-11-30	**pI:**	10.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	5.1
		No. of unique Peptides:	2

Quantitation

MD:MU **Median:** 1.70 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MSQRVRRNGS	PTPAGSLGGG	AVATAGGPGS	RLQPMRATVP	FQLKQQQQQQ	HGSPTRSGGG	GGGNNNGGCC	GGASGPAGGG
90	100	110	120	130	140	150	160
GGGGPRTASR	STSPTRGGGN	AAARTSPTVA	TQTGASATST	RGTSPTRSAA	PGARGSPPRP	PPPPPLLGTV	SSPSSSPTHL
170	180	190	200	210	220	230	240
WTGEVSAAPP	PARVRHRRRS	PEQSRSSPEK	RSPSAPVCKA	GDKTRQPSSS	PSSIIRRTSS	LDTLAAPYLA	GHWPRDSHGQ
250	260	270	280	290	300	310	320
AAPCMRDKAT	QTESAWAEEY	SEKKKGSHKR	SASWGSTDQL	KEIAKLRQQL	QRSKHSSRHH	RDKERQSPFH	GNHAAINQCQ
330	340	350	360	370	380	390	400
APVPKSALIP	VIPITKSTGS	RFRNSVEGLN	QEIEIIIKET	GEKEEQLIPQ	DIPDGHRAPP	PLVQRSSSTR	SIDTQTPGGA
410	420	430	440	450	460	470	480
DRGSNNSSRS	QSVSPTSFLT	ISNEGSEESP	CSADDLLVDP	RDKENGNNSP	LPKYATSPKP	NNSYMFKREP	PEGCERVKVF
490	500	510	520	530	540	550	560
EECSPKQLHE	IPAFYCPDKN	KVNFIPKSGS	AFCLVSILKP	LLPTPDLTLK	GSGHSLTVTT	GMTTTLLQPI	AVASLSTNTE
570	580	590					
QDRVSRGTST	VMPSASLLPP	PEPIEEAEG					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2120	1	753.8961	-98.38	3	56.7	11.3	0	57-86	R. SGGGGGGNNNGGCCGGASGPA T		MD:MU 1.70
2079	1	772.9176	-77.41	3	55.9	13.4	0	57-86	R. SGGGGGGNNNGGCCGGASGPA T	Carbamidomethyl: 14	

Detailed Protein Report

Protein 459: PREDICTED: beclin-1 isoform X2 [Homo sapiens]

Accession:	gi|530413037	**Score:**	24.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	43.8
Database Date:	2015-11-30	**pI:**	4.6
		Sequence Coverage [%]:	6.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEGSKTSNNS	TMQVSFVCQR	CSQPLKLDTS	FKILDRVTIQ	ELTAPLLTTA	QAKPGETQEE	ETNSGEEPFI	ETPRQDGVSR
90	100	110	120	130	140	150	160
RFIPPARMMS	TESANSFTLI	GEASDGGTME	NLSRRLKVTG	DLFDIMSGQT	DVDHPLCEEC	TDTLLDQLDT	QLNVTENECQ
170	180	190	200	210	220	230	240
NYKRCLEILE	QMNEDDSEQL	QMELKELALE	EERLIQELED	VEKNRKIVAE	NLEKVQAEAE	RLDQEEAQYQ	REYSEFKRQQ
250	260	270	280	290	300	310	320
LELDDELKSV	ENQMRYAQTQ	LDKLKKTNVF	NATFHIWHSG	QFGTINNFRL	GRLPSVPVEW	NEINAAWGQT	VLLLHALANK
330	340	350	360	370	380	390	
MGLKFQRMDV	EKGKIEDTGG	SGGSYSIKTQ	FNSEEQWTKA	LKFMLTNLKW	GLAWVSSQFY	NK	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1558	1	685.6866	-202.29	2	49.2	11.8	0	335-348	K.IEDTGGSGGSYSIK.T	

Detailed Protein Report

Protein 460: serine/threonine-protein kinase mTOR [Homo sapiens]

Accession:	gi|4826730	**Score:**	24.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	288.7
Database Date:	2015-11-30	**pI:**	6.8
		Sequence Coverage [%]:	0.8
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|530360517	refseq_human (refseq_human_20140103.fasta)	PREDICTED: serine/threonine-protein kinase mTOR isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MLGTGPAAAT	TAATTSSNVS	VLQQFASGLK	SRNEETRAKA	AKELQHYVTM	ELREMSQEES	TRFYDQLNHH	IFELVSSSDA
90	100	110	120	130	140	150	160
NERKGGILAI	ASLIGVEGGN	ATRIGRFANY	LRNLLPSNDP	VVMEMASKAI	GRLAMAGDTF	TAEYVEFEVK	RALEWLGADR
170	180	190	200	210	220	230	240
NEGRRHAAVL	VLRELAISVP	TFFFQQVQPF	FDNIFVAVWD	PKQAIREGAV	AALRACLILT	TQREPKEMQK	PQWYRHTFEE
250	260	270	280	290	300	310	320
AEKGFDETLA	KEKGMNRDDR	IHGALLILNE	LVRISSMEGE	RLREEMEEIT	QQQLVHDKYC	KDLMGFGTKP	RHITPFTSFQ
330	340	350	360	370	380	390	400
AVQPQQSNAL	VGLLGYSSHQ	GLMGFGTSPS	PAKSTLVESR	CCRDLMEEKF	DQVCQWVLKC	RNSKNSLIQM	TILNLLPRLA
410	420	430	440	450	460	470	480
AFRPSAFTDT	QYLQDTMNHV	LSCVKKEKER	TAAFQALGLL	SVAVRSEFKV	YLPRVLDIIR	AALPPKDFAH	KRQKAMQVDA
490	500	510	520	530	540	550	560
TVFTCISMLA	RAMGPGIQQD	IKELLEPMLA	VGLSPALTAV	LYDLSRQIPQ	LKKDIQDGLL	KMLSLVLMHK	PLRHPGMPKG
570	580	590	600	610	620	630	640
LAHQLASPGL	TTLPEASDVG	SITLALRTLG	SFEFEGHSLT	QFVRHCADHF	LNSEHKEIRM	EAARTCSRLL	TPSIHLISGH
650	660	670	680	690	700	710	720
AHVVSQTAVQ	VVADVLSKLL	VVGITDPDPD	IRYCVLASLD	ERFDAHLAQA	ENLQALFVAL	NDQVFEIREL	AICTVGRLSS
730	740	750	760	770	780	790	800
MNPAFVMPFL	RKMLIQILTE	LEHSGIGRIK	EQSARMLGHL	VSNAPRLIRP	YMEPILKALI	LKLKDPDPDP	NPGVINNVLA
810	820	830	840	850	860	870	880
TIGELAQVSG	LEMRKWVDEL	FIIIMDMLQD	SSLLAKRQVA	LWTLGQLVAS	TGYVVEPYRK	YPTLLEVLLN	FLKTEQNQGT
890	900	910	920	930	940	950	960
RREAIRVLGL	LGALDPYKHK	VNIGMIDQSR	DASAVSLSES	KSSQDSSDYS	TSEMLVNMGN	LPLDEFYPAV	SMVALMRIFR
970	980	990	1000	1010	1020	1030	1040
DQSLSHHHTM	VVQAITFIFK	SLGLKCVQFL	PQVMPTFLNV	IRVCDGAIRE	FLFQQLGMLV	SFVKSHIRPY	MDEIVTLMRE
1050	1060	1070	1080	1090	1100	1110	1120
FWVMNTSIQS	TIILLIEQIV	VALGGEFKLY	LPQLIPHMLR	VFMHDNSPGR	IVSIKLLAAI	QLFGANLDDY	LHLLLPPIVK
1130	1140	1150	1160	1170	1180	1190	1200
LFDAPEAPLP	SRKAALETVD	RLTESLDFTD	YASRIIHPIV	RTLDQSPELR	STAMDTLSSL	VFQLGKKYQI	FIPMVNKVLV
1210	1220	1230	1240	1250	1260	1270	1280
RHRINHQRYD	VLICRIVKGY	TLADEEEDPL	IYQHRMLRSG	QGDALASGPV	ETGPMKKLHV	STINLQKAWG	AARRVSKDDW
1290	1300	1310	1320	1330	1340	1350	1360
LEWLRRLSLE	LLKDSSSPSL	RSCWALAQAY	NPMARDLFNA	AFVSCWSELN	EDQQDELIRS	IELALTSQDI	AEVTQTLLNL
1370	1380	1390	1400	1410	1420	1430	1440
AEFMEHSDKG	PLPLRDDNGI	VLLGERAAKC	RAYAKALHYK	ELEFQKGPTP	AILESLISIN	NKLQQPEAAA	GVLEYAMKHF
1450	1460	1470	1480	1490	1500	1510	1520
GELEIQATWY	EKLHEWEDAL	VAYDKKMDTN	KDDPELMLGR	MRCLEALGEW	GQLHQQCCEK	WTLVNDETQA	KMARMAAAAA
1530	1540	1550	1560	1570	1580	1590	1600
WGLGQWDSME	EYTCMIPRDT	HDGAFYRAVL	ALHQDLFSLA	QQCIDKARDL	LDAELTAMAG	ESYSRAYGAM	VSCHMLSELE
1610	1620	1630	1640	1650	1660	1670	1680
EVIQYKLVPE	RREIIRQIWW	ERLQGCQRIV	EDWQKILMVR	SLVVSPHEDM	RTWLKYASLC	GKSGRLALAH	KTLVLLLGVD
1690	1700	1710	1720	1730	1740	1750	1760
PSRQLDHPLP	TVHPQVTYAY	MKNMWKSARK	IDAFQHMQHF	VQTMQQQAQH	AIATEDQQHK	QELHKLMARC	FLKLGEWQLN
1770	1780	1790	1800	1810	1820	1830	1840
LQGINESTIP	KVLQYYSAAT	EHDRSWYKAW	HAWAVMNFEA	VLHYKHQNQA	RDEKKKLRHA	SGANITNATT	AATTAATATT
1850	1860	1870	1880	1890	1900	1910	1920
TASTEGSNSE	SEAESTENSP	TPSPLQKKVT	EDLSKTLLMY	TVPAVQGFFR	SISLSRGNNL	QDTLRVLTLW	FDYGHWPDVN
1930	1940	1950	1960	1970	1980	1990	2000
EALVEGVKAI	QIDTWLQVIP	QLIARIDTPR	PLVGRLIHQL	LTDIGRYHPQ	ALIYPLTVAS	KSTTTARHNA	ANKILKNMCE
2010	2020	2030	2040	2050	2060	2070	2080
HSNTLVQQAM	MVSEELIRVA	ILWHEMWHEG	LEEASRLYFG	ERNVKGMFEV	LEPLHAMMER	GPQTLKETSF	NQAYGRDLME
2090	2100	2110	2120	2130	2140	2150	2160
AQEWCRKYMK	SGNVKDLTQA	WDLYYHVFRR	ISKQLPQLTS	LELQYVSPKL	LMCRDLELAV	PGTYDPNQPI	IRIQSIAPSL
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
1142	1	586.6322	-235.21	2	43.9	12.9	0	2067-2076	K.ETSFNQAYGR.D	

Detailed Protein Report

Protein 461: **PREDICTED: leucine-rich repeat and IQ domain-containing protein 3 isoform X3 [Homo sapiens]**

Accession:	gi|530361769	**Score:**	24.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	39.2
Database Date:	2015-11-30	**pI:**	10.2
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	9.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MFHGTVTEEL	TSHEEWSHYN	ENIREGQKDF	VFVKFNGLHL	KSMENLQSCI	SLRVCIFSNN	FITDIHPLQS	CIKLIKLDLH
90	100	110	120	130	140	150	160
GNQIKSLPNT	KFWNGLKNLK	LLYLHDNGFA	KLKNICVLSA	CPTLIALTMF	DCPVSLKKGY	RHVLVNSIWP	LKALDHHVIS
170	180	190	200	210	220	230	240
DEEIIQNWHL	PERFKACNHR	LFFNFCPALR	KGTTYEEEIN	NIKHITSKIN	AILAHNSPVL	IVQRWIRGFL	VRKNLSPVFF
250	260	270	280	290	300	310	320
HKKKQQEKII	RGYEAKWIYI	TKGYEDKLLK	DLFFKPETNI	KGKLAYWKHN	IYYPVDLKNS	SEHRKHVSSI	LCELKPKDLG
330	340						
MKSKTSRHLI	QKDGS						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1395	1	727.3741	43.73	2	47.1	12.0	0	42-53	K.SMENLQSCISLR.V	Carbamidomethyl: 8; Oxidation: 2

Detailed Protein Report

Protein 462: zinc finger protein 622 [Homo sapiens]

Accession:	gi|15529978	**Score:**	24.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	54.2
Database Date:	2015-11-30	**pI:**	5.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	5.7
		No. of unique Peptides:	2

Quantitation

MD:MU	**Median:** 0.79	**CV:** 0.00 %	**No. of Peptides:** 1

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2592	1	822.7237	16.97	3	62.4	10.6	2	1-20	-.MATYTCITCRVAFRDADMQR.A	Carbamidomethyl: 6, 9	
1586	1	480.6461	-220.76	2	49.5	14.0	1	395-401	R.SLMRYYK.Q		MD:MU 0.79

Detailed Protein Report

Protein 463: ras GTPase-activating protein 1 isoform 2 [Homo sapiens]

Accession:	gi|12545406	**Score:**	24.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	100.3
Database Date:	2015-11-30	**pI:**	7.9
Modification(s):	Oxidation	**Sequence Coverage [%]:**	4.5
		No. of unique Peptides:	2

Quantitation

MD:MU	**Median:** 0.27	**CV:** 0.00 %	**No. of Peptides:** 1

10	20	30	40	50	60	70	80
MKGWYHGKLD	RTIAEERLRQ	AGKSGSYLIR	ESDRRPGSFV	LSFLSQMNVV	NHFRIIAMCG	DYYIGGRRFS	SLSDLIGYYS
90	100	110	120	130	140	150	160
HVSCLLKGEK	LLYPVAPPEP	VEDRRRVRAI	LPYTKVPDTD	EISFLKGDMF	IVHNELEDGW	MWVTNLRTDE	QGLIVEDLVE
170	180	190	200	210	220	230	240
EVGREEDPHE	GKIWFHGKIS	KQEAYNLLMT	VGQVCSFLVR	PSDNTPGDYS	LYFRTNENIQ	RFKICPTPNN	QFMMGGRYYN
250	260	270	280	290	300	310	320
SIGDIIDHYR	KEQIVEGYYL	KEPVPMQDQE	QVLNDTVDGK	EIYNTIRRKT	KDAFYKNIVK	KGYLLKKGKG	KRWKNLYFIL
330	340	350	360	370	380	390	400
EGSDAQLIYF	ESEKRATKPK	GLIDLSVCSV	YVVHDSLFGR	PNCFQIVVQH	FSEEHYIFYF	AGETPEQAED	WMKGLQAFCN
410	420	430	440	450	460	470	480
LRKSSPGTSN	KRLRQVSSLV	LHIEEAHKLP	VKHFTNPYCN	IYLNSVQVAK	THAREGQNPV	WSEEFVFDDL	PPDINRFEIT
490	500	510	520	530	540	550	560
LSNKTKKSKD	PDILFMRCQL	SRLQKGHATD	EWFLLSSHIP	LKGIEPGSLR	VRARYSMEKI	MPEEEYSEFK	ELILQKELHV
570	580	590	600	610	620	630	640
VYALSHVCGQ	DRTLLASILL	RIFLHEKLES	LLLCTLNDRE	ISMEDEATTL	FRATTLASTL	MEQYMKATAT	QFVHHALKDS
650	660	670	680	690	700	710	720
ILKIMESKQS	CELSPSKLEK	NEDVNTNLTH	LLNILSELVE	KIFMASEILP	PTLRYIYGCL	QKSVQHKWPT	NTTMRTRVVS
730	740	750	760	770	780	790	800
GFVFLRLICP	AILNPRMFNI	ISDSPSPIAA	RTLILVAKSV	QNLANLVEFG	AKEPYMEGVN	PFIKSNKHRM	IMFLDELGNV
810	820	830	840	850	860	870	880
PELPDTTEHS	RTDLSRDLAA	LHEICVAHSD	ELRTLSNERG	AQQHVLKKLL	AITELLQQKQ	NQYTKTNDVR	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1295	1	1023.3898	-122.23	2	45.9	11.7	2	773-789	K.EPYMEGVNPFIKSNKHR.M		
82	1	951.7644	-30.51	3	30.7	12.9	1	788-811	K. HRMIMFLDELGNVPELPDTTEHS T	Oxidation: 5	MD:MU 0.27

Detailed Protein Report

Protein 464: protein shisa-9 isoform 2 precursor [Homo sapiens]

Accession:	gi|291463301	**Score:**	24.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	24.4
Database Date:	2015-11-30	**pI:**	9.1
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	19.9
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MRRVLRLLLG CFLTELCARV CRAQERAGHG QLAQLGGVLL LAGGNRSGAA SGEASEGAEA SDAPPTRAPT PDFCRGYFDV
        90        100        110        120        130        140        150        160
MGQWDPPFNC SSGDFIFCCG TCGFRFCCTF KKRRLNQSTC TNYDTPLWLN TGKPPARKDD PLHDPTKDKT NLIVYIICGV
       170        180        190        200        210        220        230
VAVMVLVGIF TKLGLEKAHR PQREHMSRLY DNLLFMEAQI SFQEDEPAPG EWSVGLQTWT V
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2323	1	1175.1820	36.25	2	59.3	14.4	2	4-22	R.VLRLLLGCFLTELCARVCR.A	Carbamidomethyl: 8, 14, 18

Detailed Protein Report

Protein 465: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform a [Homo sapiens]

Accession:	gi|4502285	**Score:**	24.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	109.6
Database Date:	2015-11-30	**pI:**	5.1
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	1.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MENAHTKTVE	EVLGHFGVNE	STGLSLEQVK	KLKERWGSNE	LPAEEGKTLL	ELVIEQFEDL	LVRILLLAAC	ISFVLAWFEE
90	100	110	120	130	140	150	160
GEETITAFVE	PFVILLILVA	NAIVGVWQER	NAENAIEALK	EYEPEMGKVY	RQDRKSVQRI	KAKDIVPGDI	VEIAVGDKVP
170	180	190	200	210	220	230	240
ADIRLTSIKS	TTLRVDQSIL	TGESVSVIKH	TDPVPDPRAV	NQDKKNMLFS	GTNIAAGKAM	GVVVATGVNT	EIGKIRDEMV
250	260	270	280	290	300	310	320
ATEQERTPLQ	QKLDEFGEQL	SKVISLICIA	VWIINIGHFN	DPVHGGSWIR	GAIYYFKIAV	ALAVAAIPEG	LPAVITTCLA
330	340	350	360	370	380	390	400
LGTRRMAKKN	AIVRSLPSVE	TLGCTSVICS	DKTGTLTTNQ	MSVCRMFILD	RVEGDTCSLN	EFTITGSTYA	PIGEVHKDDK
410	420	430	440	450	460	470	480
PVNCHQYDGL	VELATICALC	NDSALDYNEA	KGVYEKVGEA	TETALTCLVE	KMNVFDTELK	GLSKIERANA	CNSVIKQLMK
490	500	510	520	530	540	550	560
KEFTLEFSRD	RKSMSVYCTP	NKPSRTSMSK	MFVKGAPEGV	IDRCTHIRVG	STKVPMTSGV	KQKIMSVIRE	WGSGSDTLRC
570	580	590	600	610	620	630	640
LALATHDNPL	RREEMHLEDS	ANFIKYETNL	TFVGCVGMLD	PPRIEVASSV	KLCRQAGIRV	IMITGDNKGT	AVAICRRIGI
650	660	670	680	690	700	710	720
FGQDEDVTSK	AFTGREFDEL	NPSAQRDACL	NARCFARVEP	SHKSKIVEFL	QSFDEITAMT	GDGVNDAPAL	KKAEIGIAMG
730	740	750	760	770	780	790	800
SGTAVAKTAS	EMVLADDNFS	TIVAAVEEGR	AIYNNMKQFI	RYLISSNVGE	VVCIFLTAAL	GFPEALIPVQ	LLWVNLVTDG
810	820	830	840	850	860	870	880
LPATALGFNP	PDLDIMNKPP	RNPKEPLISG	WLFFRYLAIG	CYVGAATVGA	AAWWFIAADG	GPRVSFYQLS	HFLQCKEDNP
890	900	910	920	930	940	950	960
DFEGVDCAIF	ESPYPMTMAL	SVLVTIEMCN	ALNSLSENQS	LLRMPPWENI	WLVGSICLSM	SLHFLILYVE	PLPLIFQITP
970	980	990	1000				
LNVTQWLMVL	KISLPVILMD	ETLKFVARNY	LEPAILE				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2121	1	701.2646	-134.99	3	56.7	14.0	2	511-528	K.MFVKGAPEGVIDRCTHIR.V	Carbamidomethyl: 14; Oxidation: 1

Detailed Protein Report

Protein 466: CCR4-NOT transcription complex subunit 1 isoform c [Homo sapiens]

Accession:	gi|388454220	**Score:**	24.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	266.2
Database Date:	2015-11-30	**pI:**	6.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MNLDSLSLAL	SQISYLVDNL	TKKNYRASQQ	EIQHIVNRHG	PEADRHLLRC	LFSHVDFSGD	GKSSGKDFHQ	TQFLIQECAL
90	100	110	120	130	140	150	160
LITKPNFIST	LSYAIDNPLH	YQKSLKPAPH	LFAQLSKVLK	LSKVQEVIFG	LALLNSSSSD	LRGFAAQFIK	QKLPDLLRSY
170	180	190	200	210	220	230	240
IDADVSGNQE	GGFQDIAIEV	LHLLLSHLLF	GQKGAFGVGQ	EQIDAFLKTL	RRDFPQERCP	VVLAPLLYPE	KRDILMDRIL
250	260	270	280	290	300	310	320
PDSGGVAKTM	MESSLADFMQ	EVGYGFCASI	EECRNIIVQF	GVREVTAAQV	ARVLGMMART	HSGLTDGIPL	QSISAPGSGI
330	340	350	360	370	380	390	400
WSDGKDKSDG	AQAHTWNVEV	LIDVLKELNP	SLNFKEVTYE	LDHPGFQIRD	SKGLHNVVYG	IQRGLGMEVF	PVDLIYRPWK
410	420	430	440	450	460	470	480
HAEGQLSFIQ	HSLINPEIFC	FADYPCHTVA	TDILKAPPED	DNREIATWKS	LDLIESLLRL	AEVGQYEQVK	QLFSFPIKHC
490	500	510	520	530	540	550	560
PDMLVLALLQ	INTSWHTLRH	ELISTLMPIF	LGNHPNSAII	LHYAWHGQGQ	SPSIRQLIMH	AMAEWYMRGE	QYDQAKLSRI
570	580	590	600	610	620	630	640
LDVAQDLKAL	SMLLNGTPFA	FVIDLAALAS	RREYLKLDKW	LTDKIREHGE	PFIQACMTFL	KRRCPSILGG	LAPEKDQPKS
650	660	670	680	690	700	710	720
AQLPPETLAT	MLACLQACAG	SVSQELSETI	LTMVANCSNV	MNKARQPPPG	VMPKGRPPSA	SSLDAISPVQ	IDPLAGMTSL
730	740	750	760	770	780	790	800
SIGGSAAPHT	QSMQGFPPNL	GSAFSTPQSP	AKAFPPLSTP	NQTTAFSGIG	GLSSQLPVGG	LGTGSLTGIG	TGALGLPAVN
810	820	830	840	850	860	870	880
NDPFVQRKLG	TSGLNQPTFQ	QTDLSQVWPE	ANQHFSKEID	DEANSYFQRI	YNHPPHPTMS	VDEVLEMLQR	FKDSTIKRER
890	900	910	920	930	940	950	960
EVFNCMLRNL	FEEYRFFPQY	PDKELHITAC	LFGGIIEKGL	VTYMALGLAL	RYVLEALRKP	FGSKMYYFGI	AALDRFKNRL
970	980	990	1000	1010	1020	1030	1040
KDYPQYCQHL	ASISHFMQFP	HHLQEYIEYG	QQSRDPPVKM	QGSITTPGSI	ALAQAQAQAQ	VPAKAPLAGQ	VSTMVTTSTT
1050	1060	1070	1080	1090	1100	1110	1120
TTVAKTVTVT	RPTGVSFKKD	VPPSINTTNI	DTLLVATDQT	ERIVEPPENI	QEKIAFIFNN	LSQSNMTQKV	EELKETVKEE
1130	1140	1150	1160	1170	1180	1190	1200
FMPWVSQYLV	MKRVSIEPNF	HSLYSNFLDT	LKNPEFNKMV	LNETYRNIKV	LLTSDKAAAN	FSDRSLLKNL	GHWLGMITLA
1210	1220	1230	1240	1250	1260	1270	1280
KNKPILHTDL	DVKSLLLEAY	VKGQQELLYV	VPFVAKVLES	SIRSVVFRPP	NPWTMAIMNV	LAELHQEHDL	KLNLKFEIEV
1290	1300	1310	1320	1330	1340	1350	1360
LCKNLALDIN	ELKPGNLLKD	KDRLKNLDEQ	LSAPKKDVKQ	PEELPPITTT	TTSTTPATNT	TCTATVPPQP	QYSYHDINVY
1370	1380	1390	1400	1410	1420	1430	1440
SLAGLAPHIT	LNPTIPLFQA	HPQLKQCVRQ	AIERAVQELV	HPVVDRSIKI	AMTTCEQIVR	KDFALDSEES	RMRIAAHHMM
1450	1460	1470	1480	1490	1500	1510	1520
RNLTAGMAMI	TCREPLLMSI	STNLKNSFAS	ALRTASPQQR	EMMDQAAAQL	AQDNCELACC	FIQKTAVEKA	GPEMDKRLAT
1530	1540	1550	1560	1570	1580	1590	1600
EFELRKHARQ	EGRRYCDPVV	LTYQAERMPE	QIRLKVGGVD	PKQLAVYEEF	ARNVPGFLPT	NDLSQPTGFL	AQPMKQAWAT
1610	1620	1630	1640	1650	1660	1670	1680
DDVAQIYDKC	ITELEQHLHA	IPPTLAMNPQ	AQALRSLLEV	VVLSRNSRDA	IAALGLLQKA	VEGLLDATSG	ADADLLLRYR
1690	1700	1710	1720	1730	1740	1750	1760
ECHLLVLKAL	QDGRAYGSPW	CNKQITRCLI	ECRDEYKYNV	EAVELLIRNH	LVNMQQYDLH	LAQSMENGLN	YMAVAFAMQL
1770	1780	1790	1800	1810	1820	1830	1840
VKILLVDERS	VAHVTEADLF	HTIETLMRIN	AHSRGNAPEG	LPQLMEVVRS	NYEAMIDRAH	GGPNFMMHSG	ISQASEYDDP
1850	1860	1870	1880	1890	1900	1910	1920
PGLREKAEYL	LREWVNLYHS	AAAGRDSTKA	FSAFVGQMHQ	QGILKTDDLI	TRFFRLCTEM	CVEISYRAQA	EQQHNPAANP
1930	1940	1950	1960	1970	1980	1990	2000
TMIRAKCYHN	LDAFVRLIAL	LVKHSGEATN	TVTKINLLNK	VLGIVVGVLL	QDHDVRQSEF	QQLPYHRIFI	MLLLELNAPE
2010	2020	2030	2040	2050	2060	2070	2080
HVLETINFQT	LTAFCNTFHI	LRPTKAPGFV	YAWLELISHR	IFIARMLAHT	PQQKGWPMYA	QLLIDLFKYL	APFLRNVELT
2090	2100	2110	2120	2130	2140	2150	2160
KPMQILYKGT	LRVLLVLLHD	FPEFLCDYHY	GFCDVIPPNC	IQLRNLILSA	FPRNMRLPDP	FTPNLKVDML	SEINIAPRIL
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1883	1	946.8565	-104.22	2	53.4	12.0	0	1908-1924	R.AQAEQQHNPAANPTMIR.A	Oxidation: 15

Detailed Protein Report

Protein 467: keratin, type I cuticular Ha2 [Homo sapiens]

Accession:	gi|116488398	**Score:**	24.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	50.3
Database Date:	2015-11-30	**pI:**	4.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.2
		No. of unique Peptides:	2

```
        10         20         30         40         50         60         70         80
MTSSCCVTNN LQASLKSCPR PASVCSSGVN CRPELCLGYV CQPMACLPSV CLPTTFRPAS CLSKTYLSSS CQAASGISGS
        90        100        110        120        130        140        150        160
MGPGSWYSEG AFNGNEKETM QFLNDRLASY LTRVRQLEQE NAELESRIQE ASHSQVLTMT PDYQSHFRTI EELQQKILCT
       170        180        190        200        210        220        230        240
KAENARMVVN IDNAKLAADD FRAKYEAELA MRQLVEADIN GLRRILDDLT LCKADLEAQV ESLKEELMCL KKNHEEEVGS
       250        260        270        280        290        300        310        320
LRCQLGDRLN IEVDAAPPVD LTRVLEEMRC QYEAMVEANR RDVEEWFNMQ MEELNQQVAT SSEQLQNYQS DIIDLRRTVN
       330        340        350        360        370        380        390        400
TLEIELQAQH SLRDSLENTL TESEARYSSQ LAQMQCMITN VEAQLAEIRA DLERQNQEYQ VLLDVRARLE GEINTYRSLL
       410        420        430        440        450
ENEDCKLPCN PCSTPSCTTC VPSPCVPRTV CVPRTVGMPC SPCPQGRY
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2706	1	1051.5703	74.71	2	65.1	11.7	1	429-447	R.TVCVPRTVGMPCSPCPQGR.Y	Carbamidomethyl: 12, 15
2221	1	1051.4304	-58.38	2	57.6	12.8	1	429-447	R.TVCVPRTVGMPCSPCPQGR.Y	Carbamidomethyl: 3, 15

Detailed Protein Report

Protein 468: EPM2A-interacting protein 1 [Homo sapiens]

Accession:	gi|7662294	**Score:**	24.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	70.3
Database Date:	2015-11-30	**pI:**	5.7
		Sequence Coverage [%]:	6.4
		No. of unique Peptides:	1

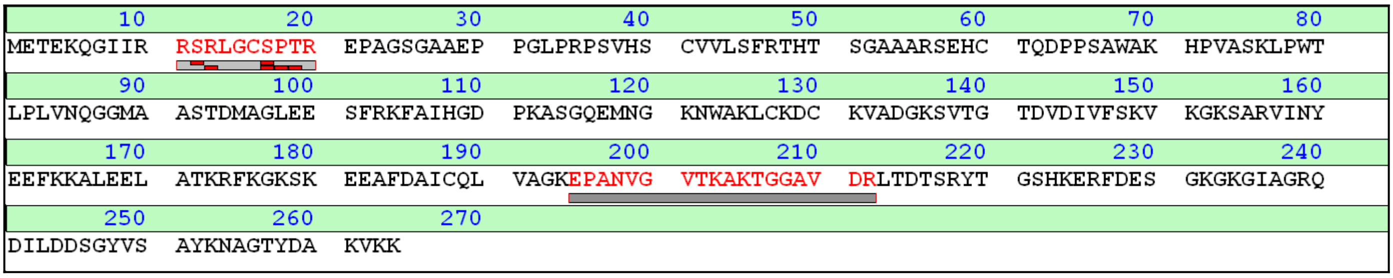
10	20	30	40	50	60	70	80
MWMTPKRSKM	EVDEALVFRP	EWTQRYLVVE	PPEGDGALCL	VCRRLIVATR	ERDVRRHYEA	EHEYYERYVA	DGERAALVER
90	100	110	120	130	140	150	160
LRQGDLPVAS	FTPEERAARA	GLGLCRLLAL	KGRGWGEGDF	VYQCMEVLLR	EVLPEHVSVL	QGVDLSPDIT	RQRILSIDRN
170	180	190	200	210	220	230	240
LRNQLFNRAR	DFKAYSLALD	DQAFVAYENY	LLVFIRGVGP	ELEVQEDLLT	IINLTHHFSV	GALMSAILES	LQTAGLSLQR
250	260	270	280	290	300	310	320
MVGLTTTHTL	RMIGENSGLV	SYMREKAVSP	NCWNVIHYSG	FLHLELLSSY	DVDVNQIINT	ISEWIVLIKT	RGVRRPEFQT
330	340	350	360	370	380	390	400
LLTESESEHG	ERVNGRCLNN	WLRRGKTLKL	IFSLRKEMEA	FLVSVGATTV	HFSDKQWLCD	FGFLVDIMEH	LRELSEELRV
410	420	430	440	450	460	470	480
SKVFAAAAFD	HICTFEVKLN	LFQRHIEEKN	LTDFPALREV	VDELKQQNKE	DEKIFDPDRY	QMVICRLQKE	FERHFKDLRF
490	500	510	520	530	540	550	560
IKKDLELFSN	PFNFKPEYAP	ISVRVELTKL	QANTNLWNEY	RIKDLGQFYA	GLSAESYPII	KGVACKVASL	FDSNQICEKA
570	580	590	600	610			
FSYLTRNQHT	LSQPLTDEHL	QALFRVATTE	MEPGWDDLVR	ERNESNP			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
829	1	859.6189	172.24	2	39.9	10.2	2	68-82	R.YVADGERAALVERLR.Q	

Detailed Protein Report

Protein 469: PREDICTED: tubulin polymerization-promoting protein family member 3 isoform X1 [Homo sapiens]

Accession:	gi|530423965	**Score:**	24.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	28.3
Database Date:	2015-11-30	**pI:**	10.1
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	10.6
		No. of unique Peptides:	2



```
        10         20         30         40         50         60         70         80
METEKQGIIR RSRLGCSPTR EPAGSGAAEP PGLPRPSVHS CVVLSFRTHT SGAAARSEHC TQDPPSAWAK HPVASKLPWT
        90        100        110        120        130        140        150        160
LPLVNQGGMA ASTDMAGLEE SFRKFAIHGD PKASGQEMNG KNWAKLCKDC KVADGKSVTG TDVDIVFSKV KGKSARVINY
       170        180        190        200        210        220        230        240
EEFKKALEEL ATKRFKGKSK EEAFDAICQL VAGKEPANVG VTKAKTGGAV DRLTDTSRYT GSHKERFDES GKGKGIAGRQ
       250        260        270
DILDDSGYVS AYKNAGTYDA KVKK
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
396	1	595.2630	-86.70	2	34.3	12.8	2	11-20	R.RSRLGCSPTR.E	Carbamidomethyl: 6
2670	1	885.4398	-44.05	2	63.5	11.8	2	195-212	K.EPANVGVTKAKTGGAVDR.L	

Detailed Protein Report

Protein 470: PREDICTED: WD repeat-containing protein 87 isoform X3 [Homo sapiens]

Accession:	gi|578834971	**Score:**	24.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	316.9
Database Date:	2015-11-30	**pI:**	6.9
		Sequence Coverage [%]:	0.8
		No. of unique Peptides:	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MSSPRLIPLW	KDLKLLLNDT	INKSKQPSED	PKNCLIVLSD	RSQVLFKESR	YPQNMPCVCY	YFSDAHFFAS	LSWVTSNTKE
90	100	110	120	130	140	150	160
IQAVAWMKSK	TEDMVEKRTF	SMTERLPPIQ	SMVHAGSFHI	LVVYCGDLIL	RLFGDHFRAF	KPLGKVPCRF	NISCLCYDPE
170	180	190	200	210	220	230	240
MKMLLSGILG	AVVTWVIELG	GTGLQIAHMV	SMPGDELVQD	IVLNGPSGSL	LALCETVVRV	LMHQGKGQLG	EVKRFTSTSS
250	260	270	280	290	300	310	320
GSSITCCFTC	FDQGFLYAGN	QAGEIQVWSL	QQGHPLHSFQ	AHQSGVICIR	SRPEAHTLLT	AGSDSLIKEW	NLTSGSLLRR
330	340	350	360	370	380	390	400
LELGEELYRL	QFIDSITFFC	QTAHSFSLHR	LPCFYSLFNV	CGSAPQQLRR	VCCGNNWFRI	LCTTEDGLLR	FVSPVTGDLL
410	420	430	440	450	460	470	480
VITWPFSILD	QAVDWAYDPG	KEELFVATGS	SEVLVFDTTR	CPCPAKYLLG	TSPNSQDFVQ	CLAYGHFNLG	RGLEGLIFSG
490	500	510	520	530	540	550	560
HQSGVIRVLS	QHSCARLEKF	MHFGAVLALS	TLSGGIFGGQ	GNSLLCSYGM	DDYVHLSEAV	LDGVKVQLRP	LASILSSCHL
570	580	590	600	610	620	630	640
THLILLPKSV	GAITETNCLR	LWKFHDFLSS	GSQNGLKFIE	TLPLHLCAIT	SFDVCLSLSL	FVTGSADGSV	RIWDFHGRLI
650	660	670	680	690	700	710	720
GILDSSLHFG	PVCFANDRGD	LLVTFNQSLY	LVSCLKLLPP	ALLTRLSFMS	ISDEVLEVPK	PFIPSFFFSF	ETMFVPKYIY
730	740	750	760	770	780	790	800
PGQAQQKLVG	LEKLVNNRAI	AFDHSVPHVI	EEDEEGSPVL	LRSSMHYSLQ	DMEDWMQVSP	ALRSETARRL	LNDTTNSNPL
810	820	830	840	850	860	870	880
IRELAWEGLK	RLGMITHLFA	MPLAQGLMDK	DERVRIKTLS	LMAEIGIHSR	TSLLQLTQKQ	ETFREMQQQM	IGEEPLDHLL
890	900	910	920	930	940	950	960
GMRATDLQIL	STQVEQRLNE	NLTLSHRDEK	PAFSLDVSMP	SELKSSLKPP	TVSEESEVAI	KPSKGQRRGQ	AGVKKHSQKW
970	980	990	1000	1010	1020	1030	1040
LRGLKKTKER	DSKQMSTEPG	LLEDESGTEA	APIEMEEASV	YSQWSSSTSV	IKLSKDVDSQ	EKDISKDHIA	LTLKRLQKIR
1050	1060	1070	1080	1090	1100	1110	1120
DKRDKKATAQ	KLKKKHKKKG	KEAKVINEET	TPPVMEQPVT	KKVKIQGRGA	SGISGRRSTA	GDGSSWRDDL	CRLMALRISG
1130	1140	1150	1160	1170	1180	1190	1200
SQTKMSENLN	AELVTFAQEM	LVDRHPSWEL	FQEICPLLKK	ESKVLLEDLD	WDVVPPEKKP	IFIQEGAIRE	DMIQGVTQEV
1210	1220	1230	1240	1250	1260	1270	1280
IRHKEVMPRE	EEQAQKKARD	MLGLEETQVI	LKKGKKVIFL	EPGNVTMGKE	ISKKEEKKTF	QKSPKQGRKA	VQKERKVGKI
1290	1300	1310	1320	1330	1340	1350	1360
KREMTKEERD	MSEEVEEMAT	LEEKVVKQEG	KLVMIERTPS	WQDWKKAWDE	WKQVHGETRK	SWKAWKEEWE	KRLLQEEEKL
1370	1380	1390	1400	1410	1420	1430	1440
HQAGEKLSPE	EEMLQEDKKL	KWEEWKQVWE	NMLSSKSKEQ	QYKDEEEVTL	EEEVSREGEE	KEQQVTEEQR	HIQEEHKWAR
1450	1460	1470	1480	1490	1500	1510	1520
IHRKRARAEK	KRAQEERKLA	QEEEKLAQEE	RQLAQEERKL	AQAYVKITQD	DREMAQAEGK	FAQKEETLAQ	RGEKLSQEAE
1530	1540	1550	1560	1570	1580	1590	1600
KLAQKRKKLA	KKWEKVAREE	EKLAKKGGKL	AEVKNILAQK	VEELPQREQN	LDWQEKELAQ	ELEELEWDME	ELSWKEEELN
1610	1620	1630	1640	1650	1660	1670	1680
QEEGKLVEEK	KKLAEEEEAL	AWQREKLSEE	ETKLAQEEEL	LIQEKEKLAQ	HKEKMPEEEE	RLGRKREQLI	EKKMKLAQKR
1690	1700	1710	1720	1730	1740	1750	1760
ERWINSMEEL	TKNKMILYQK	KNLAQEKKNL	AQEKEKLAQR	KENLLYNKER	LTHSKKQLVQ	VKNKLGMFNK	ILAQVEEKLT
1770	1780	1790	1800	1810	1820	1830	1840
QEKETVIKKK	EKLAETEKKL	VQVEDSLAKK	QEKLAQEKMK	LALEKAMVQG	KKRLRGELDI	AKEEKALNLE	MKRLAEEKMR
1850	1860	1870	1880	1890	1900	1910	1920
LVEGKETLSK	GETPETSRQR	KMTQVEQELF	ERKLSLEEKI	LLHEDRILAM	EESEIAKGKL	EFTRGQRIFV	QGQRKLAKAS
1930	1940	1950	1960	1970	1980	1990	2000
RKLIKKRESL	SKEPAKLNKI	LKALQKLTRD	ERKLTQEEIK	MTKMKRALFV	KERRLSIEQS	KLDIKEWDFS	EKRSELTKDE
2010	2020	2030	2040	2050	2060	2070	2080
KKLARKQRKL	ANKMRRMINK	EEKMTEEESK	LARKHSEVIL	DDEEEGGIEE	EEVIPFLKRR	WRKRKEAKRG	DKPKEKFSSQ
2090	2100	2110	2120	2130	2140	2150	2160
VDEVESEEHF	SEEMESLLDE	LEKQESLSSE	EEEEREEEEE	REEEEEREEE	EERKEEEEGE	EKQVEKEEEE	KKKKKKEKKK
2170	2180	2190	2200	2210	2220	2230	2240
EEVQEKEEVF	EEKEEIMSEE	ETESLSDEEE	EEESCSLEEE	VDREKEILKK	EKQFKLQEQR	RKSLRGRERV	LSILRGVPHG
2250	2260	2270	2280	2290	2300	2310	2320
KGRAIRLGVL	KSPLKKLMST	ALEMKEKTPV	PVPEKQISWE	DKKATVVEIP	RKFLGTMDKE	REVMGKYEPI	PPHVLGTVLE
2330	2340	2350	2360	2370	2380	2390	2400

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
698	1	512.1244	-202.48	2	38.3	13.5	0	1098-1107	R.STAGDGSSWR.D	

Detailed Protein Report

Protein 471: PREDICTED: E3 ubiquitin-protein ligase SHPRH isoform X8 [Homo sapiens]

Accession:	gi|578812645	**Score:**	24.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	173.4
Database Date:	2015-11-30	**pI:**	7.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSSRRKRAPP	VRVDEEKRQQ	LHWNMHEDRR	NEPIIISDDD	EQPCPGSDTS	SAHYIILSDS	LKEEVAHRDK	KRCSKVVSFS
90	100	110	120	130	140	150	160
KPIEKEETVG	IFSPLSVKLN	IVISPYHFDN	SWKAFLGELT	LQLLPAQSLI	ENFSERSITL	MSSESSNQFL	IYVHSKGEDV
170	180	190	200	210	220	230	240
EKQKKEPMSI	CDKGILVESS	FSGEMLEDLG	WLQKKRRIKL	YQKPEGNHII	KVGIYLLEAG	LAKLDFLSDA	NSRMKKFNQL
250	260	270	280	290	300	310	320
MKKVMEKLHN	SIIPDVLEED	EDDPESEPEG	QDIDELYHFV	KQTHQQETQS	IQVDVQHPAL	IPVLRPYQRE	AVNWMLQQEC
330	340	350	360	370	380	390	400
FRSSPATESA	LHFLWREIVT	SEGLKLYYNP	YTGCIIREYP	NSGPQLLGGI	LADEMGLGKT	VEVLALILTH	TRQDVKQDAL
410	420	430	440	450	460	470	480
TLPEGKVVNY	FIPSHYFGGK	LKKTEIQNIE	FEPKEKVQCP	PTRVMILTAV	KEMNGKKGVS	ILSIYKYVSS	IYRYDVQRNR
490	500	510	520	530	540	550	560
SLLKRMLKCL	IFEGLVKQIK	GHGFSGTFTL	GKNYKEEDIC	DKTKKQAVGS	PRKIQKETRK	SGNKDTDSEY	LPSDTSDDDD
570	580	590	600	610	620	630	640
DPYYYYYKSR	RNRSKLRKKL	VPSTKKGKSQ	PFINPDSQGH	CPATSDSGIT	DVAMSKSTCI	SEFNQEHETE	DCAESLNHAD
650	660	670	680	690	700	710	720
SDVPPSNTMS	PFNTSDYRFE	CICGELDQID	RKPRVQCLKC	HLWQHAKCVN	YDEKNLKIKP	FYCPHCLVAM	EPVSTRATLI
730	740	750	760	770	780	790	800
ISPSSICHQW	VDEINRHVRS	SSLRVLVYQG	VKKDGFLQPH	FLAEQDIVII	TYDVLRSELN	YVDIPHSNSE	DGRRLRNQKR
810	820	830	840	850	860	870	880
YMAIPSPLVA	VEWWRICLDE	AQMVECPTVK	AAEMAQRLSG	INRWCISGTP	VQRGLEDLFG	LVVFLGIEPY	CVKHWWVRLL
890	900	910	920	930	940	950	960
YRPYCKKNPQ	HLYSFIAKIL	WRSAKKDVID	QIQIPPQTEE	IHWLHFSPVE	RHFYHRQHEV	CCQDVVVKLR	KISDWALKLS
970	980	990	1000	1010	1020	1030	1040
SLDRRTVTSI	LYPLLRLRQA	CCHPQAVRGE	FLPLQKSTMT	MEELLTSLQK	KCGTECEEAH	RQLVCALNGL	AGIHIIKGEY
1050	1060	1070	1080	1090	1100	1110	1120
ALAAELYREV	LRSSEEHKGK	LKTDSLQRLH	ATHNLMELLI	ARHPGIPPTL	RDGRLEEEAK	QLREHYMSKC	NTEVAEAQQA
1130	1140	1150	1160	1170	1180	1190	1200
LYPVQQTIHE	LQRKIHSNSP	WWLNVIHRAI	EFTIDEELVQ	RVRNEITSNY	KQQTGKLSMS	EKFRDCRGLQ	FLLTTQMEEL
1210	1220	1230	1240	1250	1260	1270	1280
NKCQKLVREA	VKNLEGPPSR	NVIESATVCH	LRPARLPLNC	CVFCKADELF	TEYESKLFSN	TVKGQTAIFE	EMIEDEEGLV
1290	1300	1310	1320	1330	1340	1350	1360
DDRAPTTTRG	LWAISETERS	MKAILSFAKS	HRFDVEFVDE	GSTSMDLFEA	WKKEYKLLHE	YWMALRNRVS	AVDELAMATE
1370	1380	1390	1400	1410	1420	1430	1440
RLRVRDPREP	KPNPPVLHII	EPHEVEQNRI	KLLNDKAVAT	SQLQKKLGQL	LYLTNLEKSQ	DKTSGGVNPE	PCPICARQLG
1450	1460	1470	1480	1490	1500	1510	
KQWAVLTCGH	CFCNECISII	IEQYSVGSHR	SSIKCAICRQ	TTSHKEISYV	FTSEKANQEE	DIPVKVF	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1767	1	856.7921	-163.45	2	52.1	10.0	1	937-950	R.QHEVCCQDVVVKLR.K	Carbamidomethyl: 5

Detailed Protein Report

Protein 472: uncharacterized protein KIAA0513 isoform b [Homo sapiens]

Accession:	gi|557440789	**Score:**	24.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	45.5
Database Date:	2015-11-30	**pI:**	4.9
		Sequence Coverage [%]:	7.0
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
METPEVPVGS LIDFGPEAPT SSPLEAPPPV LQDGDGSLGD GASESETTES ADSENDMGES PSHPSWDQDR RSSSNESFSS
        90        100        110        120        130        140        150        160
NQSTESTQDE ETLALRDFMR GYVEKIFSGG EDLDQEEKAK FGEYCSSENG KGREWFARYV SAQRCNSKCV SEATFYRLVQ
       170        180        190        200        210        220        230        240
SFAVVLFECH QMDDFGPAKN LMTMCFTYYH IGKPQLLPPE SREKPAGSID SYLKSANSWL AEKKDIAERL LKNTSARTEN
       250        260        270        280        290        300        310        320
VKGFFGGLET KLKGPLARRN EEDENKPQEK RPRAVTAYSP EDEKKGEKIY LYTHLKQQPI WHTLRFWNAA FFDAVHCERT
       330        340        350        360        370        380        390        400
KRSPTTREKW CHMTQEERDD SLRFNENITF GQLGTFTHNM LAFGLNKKLC NDFLKKQAVI GNLDEEQYKL LSDHIEQMAT
       410
E
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
470	1	564.2533	-129.11	3	35.5	14.4	2	243-258	K.GFFGGLETKLKGPLAR.R	

BRUKER

Detailed Protein Report

Protein 473: serine/threonine-protein kinase PINK1, mitochondrial precursor [Homo sapiens]

Accession:	gi|14165272	**Score:**	24.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	62.7
Database Date:	2015-11-30	**pI:**	10.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.6
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MAVRQALGRG	LQLGRALLLR	FTGKPGRAYG	LGRPGPAAGC	VRGERPGWAA	GPGAEPRRVG	LGLPNRLRFF	RQSVAGLAAR
90	100	110	120	130	140	150	160
LQRQFVVRAW	GCAGPCGRAV	FLAFGLGLGL	IEEKQAESRR	AVSACQEIQA	IFTQKSKPGP	DPLDTRRLQG	FRLEEYLIGQ
170	180	190	200	210	220	230	240
SIGKGCSAAV	YEATMPTLPQ	NLEVTKSTGL	LPGRGPGTSA	PGEGQERAPG	APAFPLAIKM	MWNISAGSSS	EAILNTMSQE
250	260	270	280	290	300	310	320
LVPASRVALA	GEYGAVTYRK	SKRGPKQLAP	HPNIIRVLRA	FTSSVPLLPG	ALVDYPDVLP	SRLHPEGLGH	GRTLFLVMKN
330	340	350	360	370	380	390	400
YPCTLRQYLC	VNTPSPRLAA	MMLLQLLEGV	DHLVQQGIAH	RDLKSDNILV	ELDPDGCPWL	VIADFGCCLA	DESIGLQLPF
410	420	430	440	450	460	470	480
SSWYVDRGGN	GCLMAPEVST	ARPGPRAVID	YSKADAWAVG	AIAYEIFGLV	NPFYGQGKAH	LESRSYQEAQ	LPALPESVPP
490	500	510	520	530	540	550	560
DVRQLVRALL	QREASKRPSA	RVAANVLHLS	LWGEHILALK	NLKLDKMVGW	LLQQSAATLL	ANRLTEKCCV	ETKMKMLFLA
570	580	590					
NLECETLCQA	ALLLCSWRAA	L					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2329	1	1002.8159	-41.27	3	59.0	13.9	2	527-553	K.MVGWLLQQSAATLLANRLTEKCCVETK.M	
274	1	605.6515	-235.18	2	33.1	10.5	1	544-553	R.LTEKCCVETK.M	Carbamidomethyl: 6

Detailed Protein Report

Protein 474: **mitogen-activated protein kinase kinase kinase kinase 5 [Homo sapiens]**

Accession:	gi|14589909	**Score:**	24.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	95.0
Database Date:	2015-11-30	**pI:**	8.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.5
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578825438	refseq_human (refseq_human_20140103.fasta)	PREDICTED: mitogen-activated protein kinase kinase kinase kinase 5 isoform X1 [Homo sapiens]
gi|38570135	refseq_human (refseq_human_20140103.fasta)	mitogen-activated protein kinase kinase kinase kinase 5 [Homo sapiens]

10	20	30	40	50	60	70	80
MEAPLRPAAD	ILRRNPQQDY	ELVQRVGSGT	YGDVYKARNV	HTGELAAVKI	IKLEPGDDFS	LIQQEIFMVK	ECKHCNIVAY
90	100	110	120	130	140	150	160
FGSYLSREKL	WICMEYCGGG	SLQDIYHVTG	PLSELQIAYV	CRETLQGLAY	LHTKGKMHRD	IKGANILLTD	HGDVKLADFG
170	180	190	200	210	220	230	240
VAAKITATIA	KRKSFIGTPY	WMAPEVAAVE	KNGGYNQLCD	IWAVGITAIE	LGELQPPMFD	LHPMRALFLM	SKSNFQPPKL
250	260	270	280	290	300	310	320
KDKTKWSSTF	HNFVKIALTK	NPKKRPTAER	LLTHTFVAQP	GLSRALAVEL	LDKVNNPDNH	AHYTEADDDD	FEPHAIIRHT
330	340	350	360	370	380	390	400
IRSTNRNARA	ERTASEINFD	KLQFEPPLRK	ETEARDEMGL	SSDPNFMLQW	NPFVDGANTG	KSTSKRAIPP	PLPPKPRISS
410	420	430	440	450	460	470	480
YPEDNFPDEE	KASTIKHCPD	SESRAPQILR	RQSSPSCGPV	AETSSIGNGD	GISKLMSENT	EGSAQAPQLP	RKKDKRDFPK
490	500	510	520	530	540	550	560
PAINGLPPTP	KVLMGACFSK	VFDGCPLKIN	CATSWIHPDT	KDQYIIFGTE	DGIYTLNLNE	LHEATMEQLF	PRKCTWLYVI
570	580	590	600	610	620	630	640
NNTLMSLSEG	KTFQLYSHNL	IALFEHAKKP	GLAAHIQTHR	FPDRILPRKF	ALTTKIPDTK	GCHKCCIVRN	PYTGHKYLCG
650	660	670	680	690	700	710	720
ALQSGIVLLQ	WYEPMQKFML	IKHFDFPLPS	PLNVFEMLVI	PEQEYPMVCV	AISKGTESNQ	VVQFETINLN	SASSWFTEIG
730	740	750	760	770	780	790	800
AGSQQLDSIH	VTQLERDTVL	VCLDKFVKIV	NLQGKLKSSK	KLASELSFDF	RIESVVCLQD	SVLAFWKHGM	QGKSFKSDEV
810	820	830	840	850			
TQEISDETRV	FRLLGSDRVV	VLESRPTENP	TAHSNLYILA	GHENSY			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1739	2	1023.8681	-109.14	2	51.7	12.0	1	71-87	K.ECKHCNIVAYFGSYLSR.E	Carbamidomethyl: 2

Detailed Protein Report

Protein 475: actin-binding Rho-activating protein [Homo sapiens]

Accession:	gi|21040251	**Score:**	24.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	43.1
Database Date:	2015-11-30	**pI:**	9.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	7.9
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MAPGEKESGE	GPAKSALRKI	RTATLVISLA	RGWQQWANEN	SIRQAQEPTG	WLPGGTQDSP	QAPKPITPPT	SHQKAQSAPK
90	100	110	120	130	140	150	160
SPPRLPEGHG	DGQSSEKAPE	VSHIKKKEVS	KTVVSKTYER	GGDVSHLSHR	YERDAGVLEP	GQPENDIDRI	LHSHGSPTRR
170	180	190	200	210	220	230	240
RKCANLVSEL	TKGWRVMEQE	EPTWRSDSVD	TEDSGYGGEA	EERPEQDGVQ	VAVVRIKRPL	PSQVNRFTEK	LNCKAQQKYS
250	260	270	280	290	300	310	320
PVGNLKGRWQ	QWADEHIQSQ	KLNPFSEEFD	YELAMSTRLH	KGDEGYGRPK	EGTKTAERAK	RAEEHIYREM	MDMCFIICTM
330	340	350	360	370	380	390	
ARHRRDGKIQ	VTFGDLFDRY	VRISDKVVGI	LMRARKHGLV	DFEGEMLWQG	RDDHVVITLL	K	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1991	1	1022.8793	-58.83	2	55.0	10.7	1	309-324	R.EMMDMCFIICTMARHR.R	Carbamidomethyl: 6
1836	1	805.7966	-143.60	2	53.0	13.7	1	326-339	R.DGKIQVTFGDLFDR.Y	

Detailed Protein Report

Protein 476: alpha-1-antitrypsin precursor [Homo sapiens]

Accession:	gi|50363217	**Score:**	24.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	46.7
Database Date:	2015-11-30	**pI:**	5.3
		Sequence Coverage [%]:	3.3
		No. of unique Peptides:	1

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
2521	1	821.3964	-47.50	2	61.5	24.3	0	50-63	K.ITPNLAEFAFSLYR.Q	

Detailed Protein Report

Protein 477: DIS3-like exonuclease 1 isoform 2 [Homo sapiens]

Accession:	gi|19115966	**Score:**	24.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	111.0
Database Date:	2015-11-30	**pI:**	5.9
		Sequence Coverage [%]:	2.5
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530405359	refseq_human (refseq_human_20140103.fasta)	PREDICTED: DIS3-like exonuclease 1 isoform X4 [Homo sapiens]
gi|530405355	refseq_human (refseq_human_20140103.fasta)	PREDICTED: DIS3-like exonuclease 1 isoform X2 [Homo sapiens]

10	20	30	40	50	60	70	80
MQTACQAVQH	QRGRRQYNKL	RNLLKDARHD	CILFANEFQQ	CCYLPRERGE	SMEKWQTRSI	YNAAVWYYHH	CQDRMPIVMV
90	100	110	120	130	140	150	160
TEDEEAIQQY	GSETEGVFVI	TFKNYLDNFW	PDLKAAHELC	DSILQSRRER	ENESQESHGK	EYPEHLPLEV	LEAGIKSGRY
170	180	190	200	210	220	230	240
IQGILNVNKH	RAQIEAFVRL	QGASSKDSDL	VSDILIHGMK	ARNRSIHGDV	VVVELLPKNE	WKGRTVALCE	NDCDDKASGE
250	260	270	280	290	300	310	320
SPSEPMPTGR	VVGILQKNWR	DYVVTFPSKE	EVQSQGKNAQ	KILVTPWDYR	IPKIRISTQQ	AETLQDFRVV	VRIDSWESTS
330	340	350	360	370	380	390	400
VYPNGHFVRV	LGRIGDLEGE	IATILVENSI	SVIPFSEAQM	CEMPVNTPES	PWKVSPEEEQ	KRKDLRKSHL	VFSIDPKGCE
410	420	430	440	450	460	470	480
DVDDTLSVRT	LNNGNLELGV	HIADVTHFVA	PNSYIDIEAR	TRATTYYLAD	RRYDMLPSVL	SADLCSLLGG	VDRYAVSIMW
490	500	510	520	530	540	550	560
ELDKASYEIK	KVWYGRTIIR	SAYKLFYEAA	QELLDGNLSV	VDDIPEFKDL	DEKSRQAKLE	ELVWAIGKLT	DIARHVRAKR
570	580	590	600	610	620	630	640
DGCGALELEG	VEVCVQLDDK	KNIHDLIPKQ	PLEVHETVAE	CMILANHWVA	KKIWESFPHQ	ALLRQHPPPH	QEFFSELREC
650	660	670	680	690	700	710	720
AKAKGFFIDT	RSNKTLADSL	DNANDPHDPI	VNRLLRSMAT	QAMSNALYFS	TGSCAEEEFH	HYGLALDKYT	HFTSPIRRYS
730	740	750	760	770	780	790	800
DIVVHRLLMA	AISKDKKMEI	KGNLFSNKDL	EELCRHINNR	NQAAQHSQKQ	STELFQCMYF	KDKDPATEER	CISDGVIYSI
810	820	830	840	850	860	870	880
RTNGVLLFIP	RFGIKGAAYL	KNKDGLVISC	GPDSCSEWKP	GSLQRFQNKI	TSTTTDGESV	TFHLFDHVTV	RISIQASRCH
890	900	910	920	930	940	950	960
SDTIRLEIIS	NKPYKIPNTE	LIHQSSPLLK	SELVKEVTKS	VEEAQLAQEV	KVNIIQEEYQ	EYRQTKGRSL	YTLLEEIRDL
970	980						
ALLDVSNNYG	I						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1844	1	655.2608	-189.42	2	52.9	10.1	2	812-823	R.FGIKGAAYLKNK.D	

Detailed Protein Report

Protein 478: **gametogenetin-binding protein 2 [Homo sapiens]**

Accession:	gi|13376245	**Score:**	24.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	79.0
Database Date:	2015-11-30	**pI:**	6.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MARLVAVCRD	GEEEFPFERR	QIPLYIDDTL	TMVMEFPDNV	LNLDGHQNNG	AQLKQFIQRH	GMLKQQDLSI	AMVVTSREVL
90	100	110	120	130	140	150	160
SALSQLVPCV	GCRRSVERLF	SQLVESGNPA	LEPLTVGPKG	VLSVTRSCMT	DAKKLYTLFY	VHGSKLNDMI	DAIPKSKKNK
170	180	190	200	210	220	230	240
RCQLHSLDTH	KPKPLGGCWM	DVWELMSQEC	RDEVVLIDSS	CLLETLETYL	RKHRFCTDCK	NKVLRAYNIL	IGELDCSKEK
250	260	270	280	290	300	310	320
GYCAALYEGL	RCCPHERHIH	VCCETDFIAH	LLGRAEPEFA	GGRRERHAKT	IDIAQEEVLT	CLGIHLYERL	HRIWQKLRAE
330	340	350	360	370	380	390	400
EQTWQMLFYL	GVDALRKSFE	MTVEKVQGIS	RLEQLCEEFS	EEERVRELKQ	EKKRQKRKNR	RKNKCVCDIP	TPLQTADEKE
410	420	430	440	450	460	470	480
VSQEKETDFI	ENSSCKACGS	TEDGNTCVEV	IVTNENTSCT	CPSSGNLLGS	PKIKKGLSPH	CNGSDCGYSS	SMEGSETGSR
490	500	510	520	530	540	550	560
EGSDVACTEG	ICNHDEHGDD	SCVHHCEDKE	DDGDSCVECW	ANSEENDTKG	KNKKKKKKSK	ILKCDEHIQK	LGSCITDPGN
570	580	590	600	610	620	630	640
RETSGNTMHT	VFHRDKTKDT	HPESCCSSEK	GGQPLPWFEH	RKNVPQFAEP	TETLFGPDSG	KGAKSLVELL	DESECTSDEE
650	660	670	680	690	700		
IFISQDEIQS	FMANNQSFYS	NREQYRQHLK	EKFNKYCRLN	DHKRPICSGW	LTTAGAN		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
124	1	896.3913	-30.48	3	30.9	13.9	1	551-574	K.LGSCITDPGNRETSGNTMHTVFHR.D	Carbamidomethyl: 4

Detailed Protein Report

Protein 479: **PREDICTED: nucleolar GTP-binding protein 1-like [Homo sapiens]**

Accession:	gi|578839277	**Score:**	24.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	66.4
Database Date:	2015-11-30	**pI:**	9.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	4.9
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 6.95 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MRKVKFTQQN YHDRLSQILT DFPKLDDIHP FYADLMNILY DKDHYKLALG QINIAKNLVD NVAKDYVRLM KYGDSLYRCK
        90        100        110        120        130        140        150        160
QLKRAALGRM CTIIKRQKQS LEYLEQVRQH LSRLPTIDPN TRTLLLCGYP NVGKSSFINK VTRADVDVQP YAFTTKSLFV
       170        180        190        200        210        220        230        240
GHMDYKYLRW QVVDTPGILD HPLEDRNTIE MQAITALAHL RAAVLYVMDL SEQCGHGLKE QLELFQNIRP LFINKPLIVV
       250        260        270        280        290        300        310        320
ANKCDVKRIT ELSEEDQKIF TDLQAEGFPV IETSTLTEEG VIQVKTEACD RLLAHRVETK MKGNKVNEVL NRLHLAVPNK
       330        340        350        360        370        380        390        400
RDDKERPPFI PEGVVARRKR MEIVEPRKKR ERDLELEMGD DYILDLQKYW DLMNSSEKYD KIPEIWEGHN VADYIDPAIM
       410        420        430        440        450        460        470        480
KKLEELEKEE ELRTAAGEYD SDSESEDEEM MEIRQLAKQI REKKKLKILQ SKEKNTQGPR MPRTAKKVQR ADLENEMRSL
       490        500        510        520        530        540        550        560
GVDMDDKDNA HYAVQARRSR SVTRKRKREE SVPPSSIARS RSCSRTPRDV SGLRDVKVSF LDREQKKGAF RVFIVQNLQQ
       570        580
TVVQRSTVVE
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2112	1	596.7627	-113.88	2	56.3	12.1	1	85-95	R.AALGRMCTIIK.R	Oxidation: 6	MD:MU 6.95

Detailed Protein Report

Protein 480: PREDICTED: multiple PDZ domain protein isoform X3 [Homo sapiens]

Accession:	gi|530390235	**Score:**	24.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	213.7
Database Date:	2015-11-30	**pI:**	4.8
		Sequence Coverage [%]:	1.4
		No. of unique Peptides:	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MLEAIDKNRA	LHAAERLQTK	LRERGDVANE	DKLSLLKSVL	QSPLFSQILS	LQTSVQQLKD	QVNIATSATS	NIEYAHVPHL
90	100	110	120	130	140	150	160
SPAVIPTLQN	ESFLLSPNNG	NLEALTGPGI	PHINGKPACD	EFDQLIKNMA	QGRHVEVFEL	LKPPSGGLGF	SVVGLRSENR
170	180	190	200	210	220	230	240
GELGIFVQEI	QEGSVAHRDG	RLKETDQILA	INGQALDQTI	THQQAISILQ	KAKDTVQLVI	ARGSLPQLVS	PIVSRSPSAA
250	260	270	280	290	300	310	320
STISAHSNPV	HWQHMETIEL	VNDGSGLGFG	IIGGKATGVI	VKTILPGGVA	DQHGRLCSGD	HILKIGDTDL	AGMSSEQVAQ
330	340	350	360	370	380	390	400
VLRQCGNRVK	LMIARGAIEE	RTAPTALGIT	LSSSPTSTPE	LRVDASTQKG	EESETFDVEL	TKNVQGLGIT	IAGYIGDKKL
410	420	430	440	450	460	470	480
EPSGIFVKSI	TKSSAVEHDG	RIQIGDQIIA	VDGTNLQGFT	NQQAVEVLRH	TGQTVLLTLM	RRGMKQEAEL	MSREDVTKDA
490	500	510	520	530	540	550	560
DLSPVNASII	KENYEKDEDF	LSSTRNTNIL	PTEEEGYPLL	SAEIEEIEDA	QKQEAALLTK	WQRIMGINYE	IVVAHVSKFS
570	580	590	600	610	620	630	640
ENSGLGISLE	ATVGHHFIRS	VLPEGPVGHS	GKLFSGDELL	EVNGITLLGE	NHQDVVNILK	ELPIEVTMVC	CRRTVPPTTQ
650	660	670	680	690	700	710	720
SELDSLDLCD	IELTEKPHVD	LGEFIGSSET	EDPVLAMTDA	GQSTEEVQAP	LAMWEAGIQH	IELEKGSKGL	GFSILDYQDP
730	740	750	760	770	780	790	800
IDPASTVIII	RSLVPGGIAE	KDGRLLPGDR	LMFVNDVNLE	NSSLEEAVEA	LKGAPSGTVR	IGVAKPLPLS	PEEGYVSAKE
810	820	830	840	850	860	870	880
DSFLYPPHSC	EEAGLADKPL	FRADLALVGT	NDADLVDEST	FESPYSPEND	SIYSTQASIL	SLHGSSCGDG	LNYGSSLPSS
890	900	910	920	930	940	950	960
PPKDVIENSC	DPVLDLHMSL	EELYTQNLLQ	RQDENTPSVD	ISMGPASGFT	INDYTPANAI	EQQYECENTI	VWTESHLPSE
970	980	990	1000	1010	1020	1030	1040
VISSAELPSV	LPDSAGKGSE	YLLEQSSLAC	NAECVMLQNV	SKESFERTIN	IAKGNSSLGM	TVSANKDGLG	MIVRSIIHGG
1050	1060	1070	1080	1090	1100	1110	1120
AISRDGRIAI	GDCILSINEE	STISVTNAQA	RAMLRRHSLI	GPDIKITYVP	AEHLEEFKIS	LGQQSGRVMA	LDIFSSYTGR
1130	1140	1150	1160	1170	1180	1190	1200
DIPELPEREE	GEGEESELQN	TAYSNWNQPR	RVELWREPSK	SLGISIVGGR	GMGSRLSNGE	VMRGIFIKHV	LEDSPAGKNG
1210	1220	1230	1240	1250	1260	1270	1280
TLKPGDRIVE	APSQSESEPE	KAPLCSVPPP	PPSAFAEMGS	DHTQSSASKI	SQDVDKEDEF	GYSWKNIRER	YGTLTGELHM
1290	1300	1310	1320	1330	1340	1350	1360
IELEKGHSGL	GLSLAGNKDR	SRMSVFIVGI	DPNGAAGKDG	RLQIADELLE	INGQILYGRS	HQNASSIIKC	APSKVKIIFI
1370	1380	1390	1400	1410	1420	1430	1440
RNKDAVNQMA	VCPGNAVEPL	PSNSENLQNK	ETEPTVTTSD	AAVDLSSFKN	VQHLELPKDQ	GGLGIAISEE	DTLSGVIIKS
1450	1460	1470	1480	1490	1500	1510	1520
LTEHGVAATD	GRLKVGDQIL	AVDDEIVVGY	PIEKFISLLK	TAKMTVKLTI	HAENPDSQAV	PSAAGAASGE	KKNSSQSLMV
1530	1540	1550	1560	1570	1580	1590	1600
PQSGSPEPES	IRNTSRSSTP	AIFASDPATC	PIIPGCETTI	EISKGRTGLG	LSIVGGSDTL	LGAIIIHEVY	EEGAACKDGR
1610	1620	1630	1640	1650	1660	1670	1680
LWAGDQILEV	NGIDLRKATH	DEAINVLRQT	PQRVRLTLYR	DEAPYKEEEV	CDTLTIELQK	KPGKGLGLSI	VGKRNDTGVF
1690	1700	1710	1720	1730	1740	1750	1760
VSDIVKGGIA	DADGRLMQGD	QILMVNGEDV	RNATQEAVAA	LLKCSLGTVT	LEVGRIKAGP	FHSERRPSQS	SQVSEGSLSS
1770	1780	1790	1800	1810	1820	1830	1840
FTFPLSGSST	SESLESSSKK	NALASEIQGL	RTVEMKKGPT	DSLGISIAGG	VGSPLGDVPI	FIAMMHPTGV	AAQTQKLRVG
1850	1860	1870	1880	1890	1900	1910	1920
DRIVTICGTS	TEGMTHTQAV	NLLKNASGSI	EMQVVAGGDV	SVVTGHQQEP	ASSSLSFTGL	TSSSIFQDDL	GPPQCKSITL
1930	1940	1950	1960	1970	1980	1990	2000
ERGPDGLGFS	IVGGYGSPHG	DLPIYVKTVF	AKGAASEDGR	LKRGDQIIAV	NGQSLEGVTH	EEAVAILKRT	KGTVTLMVLS
2010							

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

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2017	1	788.3019	-141.73	2	55.1	14.1	0	1303-1318	R.MSVFIVGIDPNGAAGK.D	

Detailed Protein Report

Protein 481: serine/threonine-protein kinase TNNI3K [Homo sapiens]

Accession:	gi|7705748	**Score:**	24.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	92.8
Database Date:	2015-11-30	**pI:**	6.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGNYKSRPTQ	TCTDEWKKKV	SESYVITIER	LEDDLQIKEK	ELTELRNIFG	SDEAFSKVNL	NYRTENGLSL	LHLCCICGGK
90	100	110	120	130	140	150	160
KSHIRTLMLK	GLRPSRLTRN	GFTALHLAVY	KDNAELITSL	LHSGADIQQV	GYGGLTALHI	ATIAGHLEAA	DVLLQHGANV
170	180	190	200	210	220	230	240
NIQDAVFFTP	LHIAAYYGHE	QVTRLLLKFG	ADVNVSGEVG	DRPLHLASAK	GFLNIAKLLM	EEGSKADVNA	QDNEDHVPLH
250	260	270	280	290	300	310	320
FCSRFGHHDI	VKYLLQSDLE	VQPHVVNIYG	DTPLHLACYN	GKFEVAKEII	QISGTESLTK	ENIFSETAFH	SACTYGKSID
330	340	350	360	370	380	390	400
LVKFLLDQNV	ININHQGRDG	HTGLHSACYH	GHIRLVQFLL	DNGADMNLVA	CDPSRSSGEK	DEQTCLMWAY	EKGHDAIVTL
410	420	430	440	450	460	470	480
LKHYKRPQDE	LPCNEYSQPG	GDGSYVSVPS	PLGKIKSMTK	EKADILLLRA	GLPSHFHLQL	SEIEFHEIIG	SGSFGKVYKG
490	500	510	520	530	540	550	560
RCRNKIVAIK	RYRANTYCSK	SDVDMFCREV	SILCQLNHPC	VIQFVGACLN	DPSQFAIVTQ	YISGGSLFSL	LHEQKRILDL
570	580	590	600	610	620	630	640
QSKLIIAVDV	AKGMEYLHNL	TQPIIHRDLN	SHNILLYEDG	HAVVADFGES	RFLQSLDEDN	MTKQPGNLRW	MAPEVFTQCT
650	660	670	680	690	700	710	720
RYTIKADVFS	YALCLWEILT	GEIPFAHLKP	AAAAADMAYH	HIRPPIGYSI	PKPISSLLIR	GWNACPEGRP	EFSEVVMKLE
730	740	750	760	770	780	790	800
ECLCNIELMS	PASSNSSGSL	SPSSSSDCLV	NRGGPGRSHV	AALRSRFELE	YALNARSYAA	LSQSAGQYSS	QGLSLEEMKR
810	820	830	840				
SLQYTPIDKY	GYVSDPMSSM	HFHSCRNSSS	FEDSS				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2206	1	701.3221	4.21	3	57.5	10.6	1	1-17	-.MGNYKSRPTQTCTDEWK.K	Carbamidomethyl: 12

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Detailed Protein Report

Protein 482: PREDICTED: protein sel-1 homolog 2 isoform X5 [Homo sapiens]

Accession:	gi|578835602	**Score:**	24.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	66.4
Database Date:	2015-11-30	**pI:**	9.7
		Sequence Coverage [%]:	4.4
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578835604	refseq_human (refseq_human_20140103.fasta)	PREDICTED: protein sel-1 homolog 2 isoform X6 [Homo sapiens]

10	20	30	40	50	60	70	80
MKPLSLLIEI	LIILGVTIKT	IKAEEHNKRQ	KERNVTTQVS	VNEIKQYLSH	ILEQRTSSNV	INKRENLLEK	KKNQRKIRIK
90	100	110	120	130	140	150	160
GIQNKDILKR	NKNHLQKQAE	KNFTDEGDQL	FKMGIKVLQQ	SKSQKQKEEA	YLLFAKAADM	GNLKAMEKMA	DALLFGNFGV
170	180	190	200	210	220	230	240
QNITAAIQLY	ESLAKEGSCK	AQNALGFLSS	YGIGMEYDQA	KALIYYTFGS	AGGNMMSQMI	LGYRYLSGIN	VLQNCEVALS
250	260	270	280	290	300	310	320
YYKKVADYIA	DTFEKSEGVP	VEKVRLTERP	ENLSSNSEIL	DWDIYQYYKF	LAERGDVQIQ	VSLGQLHLIG	RKGLDQDYYK
330	340	350	360	370	380	390	400
ALHYFLKAAK	AGSANAMAFI	GKMYLEGNAA	VPQNNATAFK	YFSMAASKGN	AIGLHGLGLL	YFHGKGVPLN	YAEALKYFQK
410	420	430	440	450	460	470	480
AAEKGWPDAQ	FQLGFMYYSG	SGIWKDYKLA	FKYFYLASQS	GQPLAIYYLA	KMYATGTGVV	RSCRTAVELY	KGVCELGHWA
490	500	510	520	530	540	550	560
EKFLTAYFAY	KDGDIDSSLV	QYALLAEMGY	EVAQSNSAFI	LESKKANILE	KEKMYPMALL	LWNRAAIQGH	SLGQKIVRHG
570	580	590	600				
CSNESRCPHT	CALCRHETGN	YAFAPGYPVF					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
629	1	509.6880	-191.47	2	37.4	10.0	1	56-64	R.TSSNVINKR.E	

Detailed Protein Report

Protein 483: serine/threonine-protein kinase Nek11 isoform 2 [Homo sapiens]

Accession:	gi|41281753	**Score:**	24.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	54.0
Database Date:	2015-11-30	**pI:**	5.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.0
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MLKFQEAAKC VSGSTAISTY PKTLIARRYV LQQKLGSGSF GTVYLVSDKK AKRGEELKVL KEISVGELNP NETVQANLEA
        90        100        110        120        130        140        150        160
QLLSKLDHPA IVKFHASFVE QDNFCIITEY CEGRDLDDKI QEYKQAGKIF PENQIIEWFI QLLLGVDYMH ERRILHRDLK
       170        180        190        200        210        220        230        240
SKNVFLKNNL LKIGDFGVSR LLMGSCDLAT TLTGTPHYMS PEALKHQGYD TKSDIWSLAC ILYEMCCMNH AFAGSNFLSI
       250        260        270        280        290        300        310        320
VLKIVEGDTP SLPERYPKEL NAIMESMLNK NPSLRPSAIE ILKIPYLDEQ LQNLMCRYSE MTLEDKNLDC QKEAAHIINA
       330        340        350        360        370        380        390        400
MQKRIHLQTL RALSEVQKMT PRERMRLRKL QAADEKARKL KKIVEEKYEE NSKRMQELRS RNFQQLSVDV LHEKTHLKGM
       410        420        430        440        450        460        470        480
EEKEEQPEGR LSCSPQDEDE ERWQGREEES DEPTLENLPE SQPIPSMDLH ELESIVEDAT SDLGYHATHS
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1841	1	682.2595	-115.74	3	53.0	24.3	1	4-22	K.FQEAAKCVSGSTAISTYPK.T	Carbamidomethyl: 7

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Detailed Protein Report

Protein 484: **cartilage intermediate layer protein 1 preproprotein [Homo sapiens]**

Accession:	gi|192449445	**Score:**	24.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	132.5
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
MVGTKAWVFS	FLVLEVTSVL	GRQTMLTQSV	RRVQPGKKNP	SIFAKPADTL	ESPGEWTTWF	NIDYPGGKGD	YERLDAIRFY
90	100	110	120	130	140	150	160
YGDRVCARPL	RLEARTTDWT	PAGSTGQVVH	GSPREGFWCL	NREQRPGQNC	SNYTVRFLCP	PGSLRRDTER	IWSPWSPWSK
170	180	190	200	210	220	230	240
CSAACGQTGV	QTRTRICLAE	MVSLCSEASE	EGQHCMGQDC	TACDLTCPMG	QVNADCDACM	CQDFMLHGAV	SLPGGAPASG
250	260	270	280	290	300	310	320
AAIYLLTKTP	KLLTQTDSDG	RFRIPGLCPD	GKSILKITKV	KFAPIVLTMP	KTSLKAATIK	AEFVRAETPY	MVMNPETKAR
330	340	350	360	370	380	390	400
RAGQSVSLCC	KATGKPRPDK	YFWYHNDTLL	DPSLYKHESK	LVLRKLQQHQ	AGEYFCKAQS	DAGAVKSKVA	QLIVIASDET
410	420	430	440	450	460	470	480
PCNPVPESYL	IRLPHDCFQN	ATNSFYYDVG	RCPVKTCAGQ	QDNGIRCRDA	VQNCCGISKT	EEREIQCSGY	TLPTKVAKEC
490	500	510	520	530	540	550	560
SCQRCTETRS	IVRGRVSAAD	NGEPMRFGHV	YMGNSRVSMT	GYKGTFTLHV	PQDTERLVLT	FVDRLQKFVN	TTKVLPFNKK
570	580	590	600	610	620	630	640
GSAVFHEIKM	LRRKEPITLE	AMETNIIPLG	EVVGEDPMAE	LEIPSRSFYR	QNGEPYIGKV	KASVTFLDPR	NISTATAAQT
650	660	670	680	690	700	710	720
DLNFINDEGD	TFPLRTYGMF	SVDFRDEVTS	EPLNAGKVKV	HLDSTQVKMP	EHISTVKLWS	LNPDTGLWEE	EGDFKFENQR
730	740	750	760	770	780	790	800
RNKREDRTFL	VGNLEIRERR	LFNLDVPESR	RCFVKVRAYR	SERFLPSEQI	QGVVISVINL	EPRTGFLSNP	RAWGRFDSVI
810	820	830	840	850	860	870	880
TGPNGACVPA	FCDDQSPDAY	SAYVLASLAG	EELQAVESSP	KFNPNAIGVP	QPYLNKLNYR	RTDHEDPRVK	KTAFQISMAK
890	900	910	920	930	940	950	960
PRPNSAEESN	GPIYAFENLR	ACEEAPPSAA	HFRFYQIEGD	RYDYNTVPFN	EDDPMSWTED	YLAWWPKPME	FRACYIKVKI
970	980	990	1000	1010	1020	1030	1040
VGPLEVNVRS	RNMGGTHRQT	VGKLYGIRDV	RSTRDRDQPN	VSAACLEFKC	SGMLYDQDRV	DRTLVKVIPQ	GSCRRASVNP
1050	1060	1070	1080	1090	1100	1110	1120
MLHEYLVNHL	PLAVNNDTSE	YTMLAPLDPL	GHNYGIYTVT	DQDPRTAKEI	ALGRCFDGTS	DGSSRIMKSN	VGVALTFNCV
1130	1140	1150	1160	1170	1180	1190	
ERQVGRQSAF	QYLQSTPAQS	PAAGTVQGRV	PSRRQQRASR	GGQRQGGVVA	SLRFPRVAQQ	PLIN	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1333	1	1061.5792	19.46	1	46.4	13.3	1	378-388	K.AQSDAGAVKSK.V	

Detailed Protein Report

Protein 485: PREDICTED: serine/threonine-protein phosphatase 4 regulatory subunit 4 isoform X1 [Homo sapiens]

Accession:	gi|530404339	**Score:**	24.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	87.3
Database Date:	2015-11-30	**pI:**	9.4
		Sequence Coverage [%]:	4.7
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|578839938	refseq_human (refseq_human_20140103.fasta)	PREDICTED: serine/threonine-protein phosphatase 4 regulatory subunit 4 isoform X3 [Homo sapiens]
gi|578839936	refseq_human (refseq_human_20140103.fasta)	PREDICTED: serine/threonine-protein phosphatase 4 regulatory subunit 4 isoform X2 [Homo sapiens]
gi|578839934	refseq_human (refseq_human_20140103.fasta)	PREDICTED: serine/threonine-protein phosphatase 4 regulatory subunit 4 isoform X1 [Homo sapiens]
gi|578826014	refseq_human (refseq_human_20140103.fasta)	PREDICTED: serine/threonine-protein phosphatase 4 regulatory subunit 4 isoform X3 [Homo sapiens]
gi|530404341	refseq_human (refseq_human_20140103.fasta)	PREDICTED: serine/threonine-protein phosphatase 4 regulatory subunit 4 isoform X2 [Homo sapiens]

10	20	30	40	50	60	70	80
MQLTAAMSFL	TILQDESVSI	HAYTHSFLQV	ILLHLEHRDT	GVSNAWLETL	LSVIEVLPKE	TLRHEILNPL	VSKAQLSQTV
90	100	110	120	130	140	150	160
QSRLVSCKIL	GKLTNKFDAH	TIKREILPLV	KSLCQDVEYE	VRSCMCRQLE	NIAQGIGTEL	TKSVVLPELI	ELSRDEGSSV
170	180	190	200	210	220	230	240
RLAAFETLVN	LLDIFDTDDR	SQTILPLVKS	FCEKSFKADE	SILISLSFHL	GKLCHGLYGI	FTPDQHLRFL	EFYKKLCTLG
250	260	270	280	290	300	310	320
LQQENGHNEN	QIPPQILEQE	KKYISVRKNC	AYNFPAMIVF	VDPKNFHMEL	YSTFFCLCHD	PEVPVRYTIA	ICFYEVSKLL
330	340	350	360	370	380	390	400
NSGVYLIHKE	LITLLQDESL	EVLDALIDHL	PEILELMSTG	GESSVQENKL	SSLPDLIPAL	TAAEQRAAAS	LKWRTHEKLL
410	420	430	440	450	460	470	480
QKYACLPHVI	SSDQIYYRFL	QRMFTIMMTN	NVLPVQKAAS	RTLCIFLRYN	RKQEQRHEVI	QKLIEQLGQG	KSYWNRLRFL
490	500	510	520	530	540	550	560
DTCEFIIEIF	SKSFFCKYFF	LPAIELTHDP	VANVRMKLCY	LLPKVKSTLK	IPADKHLLQQ	LEMCVRKLLC	QEKDKDVLAI
570	580	590	600	610	620	630	640
VKRTVLELDR	MEMSMDAFQK	KFYEKDLLDQ	EKEREELLLL	EMEQLEKEKQ	QNDGRPMSDK	MFEKKRRDTK	TPTQSLPKNI
650	660	670	680	690	700	710	720
PISVPGPSSV	TPSTSKEIKK	SKLIRSQSFN	NQAFHAKYGN	LEKCASKSST	TGYTTSVSGL	GKTSVLSLAD	DSFRTRNASS
730	740	750	760	770			
VPSSFSPNTP	LPSTSRGTGN	SVDPKSSGSK	DTQPRKATLK	SRKSNP			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
119	1	566.9137	-154.93	3	30.9	13.4	2	89-103	K.ILGKLTNKFDAHTIK.R	

Detailed Protein Report

Protein 486: **protein SMG8 [Homo sapiens]**

Accession:	gi|47777319	**Score:**	24.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	109.6
Database Date:	2015-11-30	**pI:**	8.7
		Sequence Coverage [%]:	3.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAGPVSLRDL	LMGASAWMGS	ESPGGSPTEG	GGSAAGGPEP	PWREDEICVV	GIFGKTALRL	NSEKFSLVNT	VCDRQVFPLF
90	100	110	120	130	140	150	160
RHQDPGDPGP	GIRTEAGAVG	EAGGAEDPGA	AAGGSVRGSG	AVAEGNRTEA	GSQDYSLLQA	YYSQESKVLY	LLLTSICDNS
170	180	190	200	210	220	230	240
QLLRACRALQ	SGEAGGGLSL	PHAEAHEFWK	HQEKLQCLSL	LYLFSVCHIL	LLVHPTCSFD	ITYDRVFRAL	DGLRQKVLPL
250	260	270	280	290	300	310	320
LKTAIKDCPV	GKDWKLNCRP	CPPRLLFLFQ	LNGALKVEPP	RNQDPAHPDK	PKKHSPKRRL	QHALEDQIYR	IFRKSRVLTN
330	340	350	360	370	380	390	400
QSINCLFTVP	ANQAFVYIVP	GSQEEDPVGM	LLDQLRSHCT	VKDPESLLVP	APLSGPRRYQ	VMRQHSRQQL	SFHIDSSSSS
410	420	430	440	450	460	470	480
SSGQLVDFTL	REFLWQHVEL	VLSKKGFDDS	VGRNPQPSHF	ELPTYQKWIS	AASKLYEVAI	DGKEEDLGSP	TGELTSKILS
490	500	510	520	530	540	550	560
SIKVLEGFLD	IDTKFSENRC	QKALPMAHSA	YQSNLPHNYT	MTVHKNQLAQ	ALRVYSQHAR	GPAFHKYAMQ	LHEDCYKFWS
570	580	590	600	610	620	630	640
NGHQLCEERS	LTDQHCVHKF	HSLPKSGEKP	EADRNPPVLY	HNSRARSTGA	CNCGRKQAPR	DDPFDIKAAN	YDFYQLLEEK
650	660	670	680	690	700	710	720
CCGKLDHINF	PVFEPSTPDP	APAKNESSPA	PPDSDADKLK	EKEPQTQGES	TSLSLALSLG	QSTDSLGTYP	ADPQAGGDNP
730	740	750	760	770	780	790	800
EVHGQVEVKT	EKRPNFVDRQ	ASTVEYLPGM	LHSNCPKGLL	PKFSSWSLVK	LGPAKSYNFH	TGLDQQGFIP	GTNYLMPWDI
810	820	830	840	850	860	870	880
VIRTRAEDEG	DLDTNSWPAP	NKAIPGKRSA	VVMGRGRRRD	DIARAFVGFE	YEDSRGRRFM	CSGPDKVMKV	MGSGPKESAL
890	900	910	920	930	940	950	960
KALNSDMPLY	ILSSSQGRGL	KPHYAQLMRL	FVVVPDAPLQ	IILMPQVQPG	PPPCPVFYPE	KQEITLPPDG	LWVLRFPYAY
970	980	990	1000				
VTERGPCFPP	KENVQLMSYK	VLRGVLKAVT	Q				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2766	1	735.0575	1.78	3	65.9	14.0	1	357-377	R.SHCTVKDPESLLVPAPLSGPR.R	

Detailed Protein Report

Protein 487: mastermind-like protein 2 [Homo sapiens]

Accession:	gi|33286444		**Score:**	24.2
Database:	refseq_human(refseq_human_20140103.fasta)		**MW [kDa]:**	125.1
Database Date:	2015-11-30		**pI:**	10.0
Modification(s):	Carbamidomethyl		**Sequence Coverage [%]:**	1.5
			No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGDTAPPQAP	AGGLGGASGA	GLLGGGSVTP	RVHSAIVERL	RARIAVCRQH	HLSCEGRYER	GRAESSDRER	ESTLQLLSLV
90	100	110	120	130	140	150	160
QHGQGARKAG	KHTKATATAA	TTTAPPPPPA	APPAASQAAA	TAAPPPPPDY	HHHHQQHLLN	SSNNGGSGGI	NGEQQPPAST
170	180	190	200	210	220	230	240
PGDQRNSALI	ALQGSLKRKQ	VVNLSPANSK	RPNGFVDNSF	LDIKRIRVGE	NLSAGQGGLQ	INNGQSQIMS	GTLPMSQAPL
250	260	270	280	290	300	310	320
RKTNTLPSHT	HSPGNGLFNM	GLKEVKKEPG	ETLSCSKHMD	GQMTQENIFP	NRYGDDPGEQ	LMDPELQELF	NELTNISVPP
330	340	350	360	370	380	390	400
MSDLELENMI	NATIKQDDPF	NIDLGQQSQR	STPRPSLPME	KIVIKSEYSP	GLTQGPSGSP	QLRPPSAGPA	FSMANSALST
410	420	430	440	450	460	470	480
SSPIPSVPQS	QAQPQTGSGA	SRALPSWQEV	SHAQQLKQIA	ANRQQHARMQ	QHQQQHQPTN	WSALPSSAGP	SPGPFGQEKI
490	500	510	520	530	540	550	560
PSPSFGQQTF	SPQSSPMPGV	AGGSGQSKVM	ANYMYKAGPS	AQGGHLDVLM	QQKPQDLSRS	FINNPHPAME	PRQGNTKPLF
570	580	590	600	610	620	630	640
HFNSDQANQQ	MPSVLPSQNK	PSLLHYTQQQ	QQQQQQQQQQ	QQQQQQQQQQ	QQQQQQQQQQ	QSSISAQQQQ	QQQSSISAQQ
650	660	670	680	690	700	710	720
QQQQQQQQQQ	QQQQQQQQQQ	QQQQQPSSQP	AQSLPSQPLL	RSPLPLQQKL	LLQQMQNQPI	AGMGYQVSQQ	QRQDQHSVVG
730	740	750	760	770	780	790	800
QNTGPSPSPN	PCSNPNTGSG	YMNSQQSLLN	QQLMGKKQTL	QRQIMEQKQQ	LLLQQQMLAD	AEKIAPQDQI	NRHLSRPPPD
810	820	830	840	850	860	870	880
YKDQRRNVGN	MQPTAQYSGG	SSTISLNSNQ	ALANPVSTHT	ILTPNSSLLS	TSHGTRMPSL	STAVQNMGMY	GNLPCNQPNT
890	900	910	920	930	940	950	960
YSVTSGMNQL	TQQRNPKQLL	ANQNNPMMPR	PPTLGPSNNN	NVATFGAGSV	GNSQQLRPNL	THSMASMPPQ	RTSNVMITSN
970	980	990	1000	1010	1020	1030	1040
TTAPNWASQE	GTSKQQEALT	SAGVRFPTGT	PAAYTPNQSL	QQAVGSQQFS	QRAVAPPNQL	TPAVQMRPMN	QMSQTLNGQT
1050	1060	1070	1080	1090	1100	1110	1120
MGPLRGLNLR	PNQLSTQILP	NLNQSGTGLN	QSRTGINQPP	SLTPSNFPSP	NQSSRAFQGT	DHSSDLAFDF	LSQQNDNMGP
1130	1140	1150	1160				
ALNSDADFID	SLLKTEPGND	DWMKDINLDE	ILGNNS				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1771	1	1057.5151	4.71	2	52.0	24.2	2	44-60	R.IAVCRQHHLSCEGRYER.G	Carbamidomethyl: 11

Detailed Protein Report

Protein 488: connective tissue growth factor precursor [Homo sapiens]

Accession:	gi|4503123	**Score:**	24.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	38.0
Database Date:	2015-11-30	**pI:**	9.9
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	9.2
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MTAASMGPVR VAFVVLLALC SRPAVGQNCS GPCRCPDEPA PRCPAGVSLV LDGCGCCRVC AKQLGELCTE RDPCDPHKGL
        90        100        110        120        130        140        150        160
FCDFGSPANR KIGVCTAKDG APCIFGGTVY RSGESFQSSC KYQCTCLDGA VGCMPLCSMD VRLPSPDCPF PRRVKLPGKC
       170        180        190        200        210        220        230        240
CEEWVCDEPK DQTVVGPALA AYRLEDTFGP DPTMIRANCL VQTTEWSACS KTCGMGISTR VTNDNASCRL EKQSRLCMVR
       250        260        270        280        290        300        310        320
PCEADLEENI KKGKKCIRTP KISKPIKFEL SGCTSMKTYR AKFCGVCTDG RCCTPHRTTT LPVEFKCPDG EVMKKNMMFI
       330        340        350
KTCACHYNCP GDNDIFESLY YRKMYGDMA
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1888	1	921.3555	-133.61	2	53.7	12.6	1	262-277	K.ISKPIKFELSGCTSMK.T	Carbamidomethyl: 12; Oxidation: 15

Detailed Protein Report

Protein 489: **secreted frizzled-related protein 4 precursor [Homo sapiens]**

Accession:	gi|170784838	**Score:**	24.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	39.8
Database Date:	2015-11-30	**pI:**	10.3
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	11.3
		No. of unique Peptides:	1

```
         10         20         30         40         50         60         70         80
MFLSILVALC LWLHLALGVR GAPCEAVRIP MCRHMPWNIT RMPNHLHHST QENAILAIEQ YEELVDVNCS AVLRFFLCAM
         90        100        110        120        130        140        150        160
YAPICTLEFL HDPIKPCKSV CQRARDDCEP LMKMYNHSWP ESLACDELPV YDRGVCISPE AIVTDLPEDV KWIDITPDMM
        170        180        190        200        210        220        230        240
VQERPLDVDC KRLSPDRCKC KKVKPTLATY LSKNYSYVIH AKIKAVQRSG CNEVTTVVDV KEIFKSSSPI PRTQVPLITN
        250        260        270        280        290        300        310        320
SSCQCPHILP HQDVLIMCYE WRSRMMLLEN CLVEKWRDQL SKRSIQWEER LQEQRRTVQD KKKTAGRTSR SNPPKPKGKP
        330        340        350
PAPKPASPKK NIKTRSAQKR TNPKRV
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
768	1	698.4267	127.49	2	39.2	13.0	0	265-275	R.MMLLENCLVEK.W	Carbamidomethyl: 7; Oxidation: 1

Detailed Protein Report

Protein 490: PREDICTED: SCL-interrupting locus protein isoform X2 [Homo sapiens]

Accession:	gi|578799618	**Score:**	24.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	92.6
Database Date:	2015-11-30	**pI:**	5.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MVNNENPPLI	NHLEHLKPLQ	PQLYDEKHSP	EVEAGEPSLR	GIPNQLNQDK	PALLRHCKVR	QPPAYKKGNP	HTRNSIKPSS
90	100	110	120	130	140	150	160
HNGPSHDIFE	KLQTVSAGNV	QNEEYPIRPS	TLNSRQSSLA	PQSQPHDFVF	SPHNSGRPME	LQIPTPPLPS	YCSTNVCRCC
170	180	190	200	210	220	230	240
QHHSHIQYSP	LNSWQGANTV	GSIQDVQSEA	LQKHSLFHPS	GCPALYCNAF	CSSSSPIALR	PQGDMGSCSP	HSNIEPSPVA
250	260	270	280	290	300	310	320
RPPSHMDLCN	PQPCTVCMHT	PKTESDNGMM	GLSPDAYRFL	TEQDRQLRLL	QAQIQRLLEA	QSLMPCSPKT	TAVEDTVQAG
330	340	350	360	370	380	390	400
RQMELVSVEA	QSSPGLHMRK	GVSIAVSTGA	SLFWNAAGED	QEPDSQMKQD	DTKISSEDMN	FSVDINNEVT	SLPGSASSLK
410	420	430	440	450	460	470	480
AVDIPSFEES	NIAVEEEFNQ	PLSVSNSSSL	VVRKEPDVPV	FFPSGQLAES	VSMCLQTGPT	GGASNNSETS	EEPKIEHVMQ
490	500	510	520	530	540	550	560
PLLHQPSDNQ	KIYQDLLGQV	NHLLNSSSKE	TEQPSTKAVI	ISHECTRTQN	VYHTKKKTHH	SRLVDKDCVL	NATLKQLRSL
570	580	590	600	610	620	630	640
GVKIDSPTKV	KKNAHNVDHA	SVLACISPEA	VISGLNCMSF	ANVGMSGLSP	NGVDLSMEAN	AIALKYLNEN	QLSQLSVTRS
650	660	670	680	690	700	710	720
NQNNCDPFSL	LHINTDRSTV	GLSLISPNNM	SFATKKYMKR	YGLLQSSDNS	EDEEEPPDNA	DSKSEYLLNQ	NLRSIPEQLG
730	740	750	760	770	780	790	800
GQKEPSKNDH	EIINCSNCES	VGTNADTPVL	RNITNEVLQT	KAKQQLTEKP	AFLVKNLKPS	PAVNLRTGKA	EFTQHPEKEN
810	820	830	840	850			
EGDITIFPES	LQPSETLKQM	NSMNSVGTFL	DVKRLRQLPK	LF			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2867	3	1051.5491	-17.97	2	66.3	24.2	1	41-58	R.GIPNQLNQDKPALLRHCK.V	Carbamidomethyl: 17

Detailed Protein Report

Protein 491: PREDICTED: BRCA1-A complex subunit Abraxas isoform X1 [Homo sapiens]

Accession:	gi|530378285	**Score:**	24.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	41.6
Database Date:	2015-11-30	**pI:**	9.2
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDDVEVVYTI	DIQKYIPCYQ	LFSFYNSSGE	VNEQALKKIL	SNVKKNVVGW	YKFRRHSDQI	MTFRERLLHK	NLQEHFSNQD
90	100	110	120	130	140	150	160
LVFLLLTPSI	ITESCSTHRL	EHSLYKPQKG	LFHRVPLVVA	NLGMSEQLGY	KTVSGSCMST	GFSRAVQTHS	SKFFEEDGSL
170	180	190	200	210	220	230	240
KEVHKINEMY	ASLQEELKSI	CKKVEDSEQA	VDKLVKDVNR	LKREIEKRRG	AQIQAAREKN	IQKDPQENIF	LCQALRTFFP
250	260	270	280	290	300	310	320
NSEFLHSCVM	SLKNRHVSKS	SCNYNHHLDV	VDNLTLMVEH	TDIPEASPAS	TPQIIKHKAL	DLDDRWQFKR	SRLLDTQDKR
330	340	350	360	370			
SKADTGSSNQ	DKASKMSSPE	TDEEIEKMKG	FGEYSRSPTF				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1271	1	796.3744	-21.47	2	45.6	24.2	2	55-66	R.RHSDQIMTFRER.L	Oxidation: 7

Detailed Protein Report

Protein 492: PREDICTED: unconventional myosin-X isoform X3 [Homo sapiens]

Accession:	gi|578809923	**Score:**	24.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	234.6
Database Date:	2015-11-30	**pI:**	5.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.1
		No. of unique Peptides:	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MDNFFTEGTR	VWLRENGQHF	PSTVNSCAEG	IVVFRTDYGQ	VFTYKQSTIT	HQKVTAMHPT	NEEGVDDMAS	LTELHGGSIM
90	100	110	120	130	140	150	160
YNLFQRYKRN	QIYTYIGSIL	ASVNPYQPIA	GLYEPATMEQ	YSRRHLGELP	PHIFAIANEC	YRCLWKRHDN	QCILISGESG
170	180	190	200	210	220	230	240
AGKTESTKLI	LKFLSVISQQ	SLELSLKEKT	SCVERAILES	SPIMEAFGNA	KTVYNNNSSR	FGKFVQLNIC	QKGNIQGGRI
250	260	270	280	290	300	310	320
VDYLLEKNRV	VRQNPGERNY	HIFYALLAGL	EHEEREEFYL	STPENYHYLN	QSGCVEDKTI	SDQESFREVI	TAMDVMQFSK
330	340	350	360	370	380	390	400
EEVREVSRLL	AGILHLGNIE	FITAGGAQVS	FKTALGRSAE	LLGLDPTQLT	DALTQRSMFL	RGEEILTPLN	VQQAVDSRDS
410	420	430	440	450	460	470	480
LAMALYACCF	EWVIKKINSR	IKGNEDFKSI	GILDIFGFEN	FEVNHFEQFN	INYANEKLQE	YFNKHIFSLE	QLEYSREGLV
490	500	510	520	530	540	550	560
WEDIDWIDNG	ECLDLIEKKL	GLLALINEES	HFPQATDSTL	LEKLHSQHAV	QYDVRGILEK	NRDTFRDDLL	NLLRESRFDF
570	580	590	600	610	620	630	640
IYDLFEHVSS	RNNQDTLKCG	SKHRRPTVSS	QFKDSLHSLM	ATLSSSNPFF	VRCIKPNMQK	MPDQFDQAVV	LNQLRYSGML
650	660	670	680	690	700	710	720
ETVRIRKAGY	AVRRPFQDFY	KRYKVLMRNL	ALPEDVRGKC	TSLLQLYDAS	NSEWQLGKTK	VFLRESLEQK	LEKRREEEVS
730	740	750	760	770	780	790	800
HAAMVIRAHV	LGFLARKQYR	KVLYCVVIIQ	KNYRAFLLRR	RFLHLKKAAI	VFQKQLRGQI	ARRVYRQLLA	EKREQEEKKK
810	820	830	840	850	860	870	880
QEEEEKKKRE	EEERERERER	REAELRAQQE	EETRKQQELE	ALQKSQKEAE	LTRELEKQKE	NKQVEEILRL	EKEIEDLQRM
890	900	910	920	930	940	950	960
KEQQELSLTE	ASLQKLQERR	DQELRRLEEE	ACRAAQEFLE	SLNFDEIDEC	VRNIERSLSV	GSEFSSELAE	SACEEKPNFN
970	980	990	1000	1010	1020	1030	1040
FSQPYPEEEV	DEGFEADDDA	FKDSPNPSEH	GHSDQRTSGI	RTSDDSSEED	PYMNDTVVPT	SPSADSTVLL	APSVQDSGSL
1050	1060	1070	1080	1090	1100	1110	1120
HNSSSGESTY	CMPQNAGDLP	SPDGDYDYDQ	DDYEDGAITS	GSSVTFSNSY	GSQWSPDYRC	SVGTYNSSGA	YRFSSEGAQS
1130	1140	1150	1160	1170	1180	1190	1200
SFEDSEEDFD	SRFDTDDELS	YRRDSVYSCV	TLPYFHSFLY	MKGGLMNSWK	RRWCVLKDET	FLWFRSKQEA	LKQGWLHKKG
1210	1220	1230	1240	1250	1260	1270	1280
GGSSTLSRRN	WKKRWFVLRQ	SKLMYFENDS	EEKLKGTVEV	RTAKEIIDNT	TKENGIDIIM	ADRTFHLIAE	SPEDASQWFS
1290	1300	1310	1320	1330	1340	1350	1360
VLSQVHASTD	QEIQEMHDEQ	ANPQNAVGTL	DVGLIDSVCA	SDSPDRPNSF	VIITANRVLH	CNADTPEEMH	HWITLLQRSK
1370	1380	1390	1400	1410	1420	1430	1440
GDTRVEGQEF	IVRGWLHKEV	KNSPKMSSLK	LKKRWFVLTH	NSLDYYKSSE	KNALKLGTLV	LNSLCSVVPP	DEKIFKETGY
1450	1460	1470	1480	1490	1500	1510	1520
WNVTVYGRKH	CYRLYTKLLN	EATRWSSAIQ	NVTDTKAPID	TPTQQLIQDI	KENCLNSDVV	EQIYKRNPIL	RYTHHPLHSP
1530	1540	1550	1560	1570	1580	1590	1600
LLPLPYGDIN	LNLLKDKGYT	TLQDEAIKIF	NSLQQLESMS	DPIPIIQGIL	QTGHDLRPLR	DELYCQLIKQ	TNKVPHPGSV
1610	1620	1630	1640	1650	1660	1670	1680
GNLYSWQILT	CLSCTFLPSR	GILKYLKFHL	KRIREQFPGS	EMEKYALFTY	ESLKKTKCRE	FVPSRDEIEA	LIHRQEMTST
1690	1700	1710	1720	1730	1740	1750	1760
VYCHGGGSCK	ITINSHTTAG	EVVEKLIRGL	AMEDSRNMFA	LFEYNGHVDK	AIESRTVVAD	VLAKFEKLAA	TSEVGDLPWK
1770	1780	1790	1800	1810	1820	1830	1840
FYFKLYCFLD	TDNVPKDSVE	FAFMFEQAHE	AVIHGHHPAP	EENLQVLAAL	RLQYLQGDYT	LHAAIPPLEE	VYSLQRLKAR
1850	1860	1870	1880	1890	1900	1910	1920
ISQSTKTFTP	CERLEKRRTS	FLEGTLRRSF	RTGSVVRQKV	EEEQMLDMWI	KEEVSSARAS	IIDKWRKFQG	MNQEQAMAKY
1930	1940	1950	1960	1970	1980	1990	2000
MALIKEWPGY	GSTLFDVECK	EGGFPQELWL	GVSADAVSVY	KRGEGRPLEV	FQYEHILSFG	APLANTYKIV	VDERELLFET
2010	2020	2030	2040				
SEVVDVAKLM	KAYISMIVKK	RYSTTRSASS	QGSSR				

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
1694	1	1108.8433	-4.24	3	51.1	11.2	1	1675-1705	R.QEMTSTVYCHGGGSCKITINSHTTAGEVVEK.L	Carbamidomethyl: 15

Detailed Protein Report

Protein 493: PREDICTED: uncharacterized protein LOC102724413 [Homo sapiens]

Accession:	gi|578838161	**Score:**	24.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	27.4
Database Date:	2015-11-30	**pI:**	12.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	13.1
		No. of unique Peptides:	2

Quantitation

MD:MU	**Median:**	1.98	**CV:**	0.00 %	**No. of Peptides:**	1

Alias proteins:

Accession	Name	Description
gi|578847088	refseq_human (refseq_human_20140103.fasta)	PREDICTED: uncharacterized protein LOC102724413 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MWPASGPGTR PAIRQPCTSF TPVPWLPTRP RASPAELARC PAAAPKLRAP RRLSRQPEAW SPTAQDWRAQ FVSPGWDCWF
        90        100        110        120        130        140        150        160
RVAHDHSPLN TRPARARAQT HKHTRLPSAQ PASRASAFPS SSPLGRFGSP WRLCAAPGKS PGRGDRAALF PPKVCAHASI
       170        180        190        200        210        220        230        240
LRKHSQACGF PSSREMTAAG EDLFAPCFAM ARGSEERTGR WGLRVDEGGA RETPWIRGWA GQRRRPAALA NPRPRGGQAG
       250        260
LGAGRPGCTC RR
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2132	1	899.3904	-102.48	2	56.5	14.0	1	82-97	R.VAHDHSPLNTRPARAR.A		MD:MU 1.98
2739	1	922.4796	7.26	2	65.5	10.1	2	127-143	R.FGSPWRLCAAPGKSPGR.G	Carbamidomethyl: 8	

Detailed Protein Report

Protein 494: **PREDICTED: zinc finger protein 813 isoform X1 [Homo sapiens]**

Accession:	gi|578833930	**Score:**	24.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	62.1
Database Date:	2015-11-30	**pI:**	10.5
		Sequence Coverage [%]:	3.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MALPQGLLTF	RDVAIEFSQE	EWKCLDPAQR	TLYRDVMLEN	YRNLVSLDIS	SKCMMKEFSS	TAQGNREVIH	TGTLQRHESH
90	100	110	120	130	140	150	160
HTGDFRFQEI	DKDIHNLEFQ	WQEDERNSHE	APMTEIKKLT	GSADRYDQRH	AGNKPIKDQL	GSSFHSHLPE	LHMFQTQGKI
170	180	190	200	210	220	230	240
GNQVEKSIND	ASSISTSQRI	SCRPKTHISN	NYGNNFRNSS	LLTQKQEVHM	REKSFQCNES	GKAFNYSSLL	RKHQIIHLGE
250	260	270	280	290	300	310	320
KQYKCDVCGK	VFNRKRNLVC	HRRCHTGEKP	YRCNECGKTF	SQTYSLTCHR	RLHTGEKPYK	CEECDKAFSF	KSNLKRHRRI
330	340	350	360	370	380	390	400
HAGEKPYKCN	ECGKTFSQTS	SLTCHRRLHT	GEKPFKCNEC	GKTFSRKSSL	TCHHRLHTGE	KPYKCNECGK	TFSQELTLKC
410	420	430	440	450	460	470	480
HRRLHTGEKP	YKCNECGKGF	NRKTHLACHH	RLHTGEKPYK	CNECGKVFNR	KTHLAHHHRL	HTGDKPYKCN	ECGKVFNQKA
490	500	510	520	530	540		
HLARHHRLHT	GEKPYKCNEC	GKVFNQKANL	ARHHRLHTGE	KPYKFNECGK	AFN		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2454	1	611.6737	-159.08	2	61.0	12.2	0	77-86	R.HESHHTGDFR.F	

Detailed Protein Report

Protein 495: uncharacterized protein LOC100144595 [Homo sapiens]

Accession: gi|373838702
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 24.1
MW [kDa]: 11.6
pI: 11.4
Sequence Coverage [%]: 13.7
No. of unique Peptides: 1

```
        10         20         30         40         50         60         70         80
MATYILKLRA CPWETLNGVL LCRQAGVHWR NLGLLQPPPP GFKRFSCLSL PSGWDYRHAP PCRPNVLYFS RDGVSLCWPG
        90        100        110
WSQSPDLMIH LPRPPKVLGL QV
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2266	1	787.7912	-131.21	2	58.2	24.1	0	10-23	R.ACPWETLNGVLLCR.Q	

Detailed Protein Report

Protein 496: exocyst complex component 2 [Homo sapiens]

Accession:	gi|21361625	**Score:**	24.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	104.0
Database Date:	2015-11-30	**pI:**	6.5
		Sequence Coverage [%]:	4.0
		No. of unique Peptides:	2

Alias proteins:

Accession	**Name**	**Description**
gi|578811797	refseq_human (refseq_human_20140103.fasta)	PREDICTED: exocyst complex component 2 isoform X2 [Homo sapiens]
gi|578811795	refseq_human (refseq_human_20140103.fasta)	PREDICTED: exocyst complex component 2 isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MSRSRQPPLV	TGISPNEGIP	WTKVTIRGEN	LGTGPTDLIG	LTICGHNCLL	TAEWMSASKI	VCRVGQAKND	KGDIIVTTKS
90	100	110	120	130	140	150	160
GGRGTSTVSF	KLLKPEKIGI	LDQSAVWVDE	MNYYDMRTDR	NKGIPPLSLR	PANPLGIEIE	KSKFSQKDLE	MLFHGMSADF
170	180	190	200	210	220	230	240
TSENFSAAWY	LIENHSNTSF	EQLKMAVTNL	KRQANKKSEG	SLAYVKGGLS	TFFEAQDALS	AIHQKLEADG	TEKVEGSMTQ
250	260	270	280	290	300	310	320
KLENVLNRAS	NTADTLFQEV	LGRKDKADST	RNALNVLQRF	KFLFNLPLNI	ERNIQKGDYD	VVINDYEKAK	SLFGKTEVQV
330	340	350	360	370	380	390	400
FKKYYAEVET	RIEALRELLL	DKLLETPSTL	HDQKRYIRYL	SDLHASGDPA	WQCIGAQHKW	ILQLMHSCKE	GYVKDLKGNP
410	420	430	440	450	460	470	480
GLHSPMLDLD	NDTRPSVLGH	LSQTASLKRG	SSFQSGRDDT	WRYKTPHRVA	FVEKLTKLVL	SQLPNFWKLW	ISYVNGSLFS
490	500	510	520	530	540	550	560
ETAEKSGQIE	RSKNVRQRQN	DFKKMIQEVM	HSLVKLTRGA	LLPLSIRDGE	AKQYGGWEVK	CELSGQWLAH	AIQTVRLTHE
570	580	590	600	610	620	630	640
SLTALEIPND	LLQTIQDLIL	DLRVRCVMAT	LQHTAEEIKR	LAEKEDWIVD	NEGLTSLPCQ	FEQCIVCSLQ	SLKGVLECKP
650	660	670	680	690	700	710	720
GEASVFQQPK	TQEEVCQLSI	NIMQVFIYCL	EQLSTKPDAD	IDTTHLSVDV	SSPDLFGSIH	EDFSLTSEQR	LLIVLSNCCY
730	740	750	760	770	780	790	800
LERHTFLNIA	EHFEKHNFQG	IEKITQVSMA	SLKELDQRLF	ENYIELKADP	IVGSLEPGIY	AGYFDWKDCL	PPTGVRNYLK
810	820	830	840	850	860	870	880
EALVNIIAVH	AEVFTISKEL	VPRVLSKVIE	AVSEELSRLM	QCVSSFSKNG	ALQARLEICA	LRDTVAVYLT	PESKSSFKQA
890	900	910	920	930			
LEALPQLSSG	ADKKLLEELL	NKFKSSMHLQ	LTCFQAASST	MMKT			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1723	1	1011.4144	-64.38	3	51.5	12.9	2	98-122	K.IGILDQSAVWVDEMNYYDMRTDRNK.G	
2856	1	655.3750	-67.75	2	66.1	11.1	1	516-527	K.LTRGALLPLSIR.D	

Detailed Protein Report

Protein 497: biorientation of chromosomes in cell division protein 1-like 1 [Homo sapiens]

Accession:	gi|87299628	**Score:**	23.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	330.3
Database Date:	2015-11-30	**pI:**	4.9
		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

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
582	1	848.5905	146.58	2	36.6	10.8	2	853-867	K.DSLGSKQHGITLQRR.S	

Detailed Protein Report

Protein 498: PREDICTED: protein SZT2 isoform X3 [Homo sapiens]

Accession:	gi|578798759	**Score:**	23.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	345.4
Database Date:	2015-11-30	**pI:**	6.0
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	1.0
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MVGGVYSYDC	SFGHVPNVEL	MKFIAMATFG	SYLSTCPEPE	PGNLGLTVYH	RAFLLYSFLR	SGEALNPEYY	CGSQHRLFNE
90	100	110	120	130	140	150	160
HLVSASSNPA	LALRRKKHTE	KEVPADLVST	VSVRLREGYS	VREVTLAKGG	SQLEVKLVLL	WKHNMRIEYV	AMAPWPLEPE
170	180	190	200	210	220	230	240
GPRVTRVEVT	MEGGYDILHD	VSCALRQPIR	SLYRTHVIRR	FWNTLQSINQ	TDQMLAHLQS	FSSVPEHFTL	PDSTKSGVPL
250	260	270	280	290	300	310	320
FYIPPGSTTP	VLSLQPSGSD	SSHAQFAAYW	KPVLSMDANS	WQRWLHMHRL	VLILEHDTPI	PKHLHTPGSN	GRYSTIQCRI
330	340	350	360	370	380	390	400
SHSSLTSLLR	DWSSFVLVEG	YSYVKLLSSA	PDQPPNSFYM	VRIISKAPCM	VLRLGFPIGT	PAPARHKIVS	GLREEILRLR
410	420	430	440	450	460	470	480
FPHRVQSKEP	TPKVKRKGLG	GAGGGSSPSK	SPPVLGPQQA	LSDRPCLVVL	HKPLDKLLIR	YEKLPLDYRA	PFLLTLEPPG
490	500	510	520	530	540	550	560
PLPLVSGRSA	SSSLASLSRY	LYHQRWLWSV	PSGLAPALPL	SAIAQLLSIL	TEVRLSEGFH	FACSGEGIIN	MVLELPIQNE
570	580	590	600	610	620	630	640
PPGQAAAEEK	HTCVVQYILF	PPHSTSTKDS	FSTDDDNDVE	VEALEGDSEL	NLVTEVWVEP	QYGRVGPGPG	IWKHLQDLTY
650	660	670	680	690	700	710	720
SEIPQALHPR	DAACIGSMLS	FEYLIQLCQS	KEWGPLPPEP	RVSDGLDQGG	DTCVHEIPFH	FDLMGLLPQC	QQLQMFFLLL
730	740	750	760	770	780	790	800
AREPEGVPFA	EGSCPANDMV	LCLLHSCLGQ	ELSDREIPLT	PVDQAAFLSE	VLRRTCHVPG	AEGPLLGVHG	IPKEQAVGST
810	820	830	840	850	860	870	880
QATGDSAFTS	LSVGLPETLK	PLISAQPPQW	RCYARLVNPQ	HVFLTFLPAT	FSDVQRLAAC	GLEGPPQEET	KPKFGDWSGA
890	900	910	920	930	940	950	960
PSLKDLGGTG	IKATKSHVPV	LSVTLASDNA	QNQGELSPPF	RRDLQAYAGR	QASQTESADG	PRTRCPVYIY	SCSLEALREQ
970	980	990	1000	1010	1020	1030	1040
MVGMQPPQAP	RDLIFRTQFL	DHPSPSSAWM	EPRYKEAANH	CALLQEHAQR	CYVRGLFRSL	QQAQSVTSQD	LLTAVDACEE
1050	1060	1070	1080	1090	1100	1110	1120
LLQEIDITPF	LLALCGHTWG	LPHAPPSPGP	LSPGPFSSSM	EEGAEPRERA	ILASESSIET	EDLSEPEFQS	TRVPGIPDPG
1130	1140	1150	1160	1170	1180	1190	1200
PEISLTDVCQ	LRGEAHGALH	SVIQEKFLEI	SRLHFRTVPS	NPHYFFYCPP	SSRREDEGPR	DTVDRKISDL	EFSEAELMGE
1210	1220	1230	1240	1250	1260	1270	1280
EGDTSACCVV	TESDPELEVE	YRESRESDLG	PAGLDSASLS	DVDTVNPDED	SFSILGGDSP	TGPESFLHDL	PPLFLHLTCS
1290	1300	1310	1320	1330	1340	1350	1360
VRLRGQHSSV	PVCSLPTCLG	QVLSSLEGPP	VGGRVPLRDL	SVTLDVFMLT	LPLEVELPTA	SDPQHHRSTS	ESSASFPRSP
1370	1380	1390	1400	1410	1420	1430	1440
GQPSSLRSDD	GLGPPLPPPE	EERHPGLSNL	ATPHRLAIET	TMNEIRWLLE	DEMVGALRRG	GIPQSPALHR	AAAHIHSSPG
1450	1460	1470	1480	1490	1500	1510	1520
RSTCLRQTLP	LSFVFGPERS	LTQFKEEFRR	LHLPGHVLLE	DPDSGFFFVA	AGQQPGGSHG	EPSSAAWAWH	SHEDRAEGIE
1530	1540	1550	1560	1570	1580	1590	1600
GETLTASPQA	PGSPEDSEGV	PLISLPRVPQ	GGSQPGPSRG	LSLMSSQGSV	DSDHLGYDGG	SSGSDSEGPN	DTLGEKAPFT
1610	1620	1630	1640	1650	1660	1670	1680
LRTPPGPAPP	QPSLSGLPGP	CLPDFWLIVR	VLQDRVEVYA	HARSLIREDG	GPGTECRHLQ	QLLVRRVGEI	CREVNQRLLL
1690	1700	1710	1720	1730	1740	1750	1760
QDLHDSHVCN	SLLVAESEED	LWRSETPFHS	RQRAPLPSDD	YAADESCAPR	GYLAATMQFV	PGHFSCDVVW	GTVIRVHSRL
1770	1780	1790	1800	1810	1820	1830	1840
KMGPSMGVSR	AIQALRSVLN	AFSVVNRKNM	FVYQERATKA	VYYLRLLETS	CSDRPWKGDA	LPPSLALSRS	QEPIYSEEAS
1850	1860	1870	1880	1890	1900	1910	1920
GPRSPLDMVS	SRSSDAARPV	GQVDRHIQLL	VHGVGQAGPE	ITDELVRVLC	RRLDEATLDV	ITVMLVRNCK	LTPADVEFIQ
1930	1940	1950	1960	1970	1980	1990	2000
PPGSLPSEVL	HLALPTSCRP	WLPALAWYLR	QNLLIFLHSP	KYTDSNSRNH	FQHPLPPQGG	LPDLDIYLYN	KPGGQGTGGK
2010	2020	2030	2040	2050	2060	2070	2080
GVACITLAFV	DEGGAPLSLA	LWPPSSPGPP	DPLREEEFEQ	LTQVIRCPVV	VDSSSAQNGA	PRLRLDVWEK	GNISIVQLEE
2090	2100	2110	2120	2130	2140	2150	2160
KLRGAARQAL	ADAIIELQLL	PASLCTEDTP	TGSLRNGSLE	TKSSAGRAST	FPPAPVPGEP	VTPPSKAGRR	SFWDMLSKTE
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2101	1	599.9147	-73.79	3	56.4	12.3	1	2656-2672	R.AMAILGTEGRGSFSCPK.T	Carbamidomethyl: 15; Oxidation: 2
2181	1	952.3242	-131.11	2	57.1	11.6	0	2746-2760	R.DLMHVHSFSYDFHLR.L	

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Detailed Protein Report

Protein 499: PREDICTED: terminal uridylyltransferase 4 isoform X5 [Homo sapiens]

Accession:	gi|530362240	**Score:**	23.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	184.6
Database Date:	2015-11-30	**pI:**	9.3
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEESKTLKSE	NHEPKKNVIC	EESKAVQVIG	NQTLKARNDK	SVKEIENSSP	NRNSSKKNKQ	NDICIEKTEV	KSCKVNAANL
90	100	110	120	130	140	150	160
PGPKDLGLVL	RDQSHCKAKK	FPNSPVKAEK	ATISQAKSEK	ATSLQAKAEK	SPKSPNSVKA	EKASSYQMKS	EKVPSSPAEA
170	180	190	200	210	220	230	240
EKGPSLLLKD	MRQKTELQQI	GKKIPSSFTS	VDKVNIEAVG	GEKCALQNSP	RSQKQQTCTD	NTGDSDDSAS	GIEDVSDDLS
250	260	270	280	290	300	310	320
KMKNDESNKE	NSSEMDYLEN	ATVIDESALT	PEQRLGLKQA	EERLERDHIF	RLEKRSPEYT	NCRYLCKLCL	IHIENIQGAH
330	340	350	360	370	380	390	400
KHIKEKRHKK	NILEKQEESE	LRSLPPPSPA	HLAALSVAVI	ELAKEHGITD	DDLRVRQEIV	EEMSKVITTF	LPECSLRLYG
410	420	430	440	450	460	470	480
SSLTRFALKS	SDVNIDIKFP	PKMNHPDLLI	KVLGILKKNV	LYVDVESDFH	AKVPVVVCRD	RKSGLLCRVS	AGNDMACLTT
490	500	510	520	530	540	550	560
DLLTALGKIE	PVFIPLVLAF	RYWAKLCYID	SQTDGGIPSY	CFALMVMFFL	QQRKPPLLPC	LLGSWIEGFD	PKRMDDFQLK
570	580	590	600	610	620	630	640
GIVEEKFVKW	ECNSSSATEK	NSIAEENKAK	ADQPKDDTKK	TETDNQSNAM	KEKHGKSPLA	LETPNRVSLG	QLWLELLKFY
650	660	670	680	690	700	710	720
TLDFALEEYV	ICVRIQDILT	RENKNWPKRR	IAIEDPFSVK	RNVARSLNSQ	LVYEYVVERF	RAAYRYFACP	QTKGGNKSTV
730	740	750	760	770	780	790	800
DFKKREKGKI	SNKKPVKSNN	MATNGCILLG	ETTEKINAER	EQPVQCDEMD	CTSQRCIIDN	NNLLVNELDF	ADHGQDSSSL
810	820	830	840	850	860	870	880
STSKSSEIEP	KLDKKQDDLA	PSETCLKKEL	SQCNCIDLSK	SPDPDKSTGT	DCRSNLETES	SHQSVCTDTS	ATSCNCKATE
890	900	910	920	930	940	950	960
DASDLNDDDN	LPTQELYYVF	DKFILTSGKP	PTIVCSICKK	DGHSKNDCPE	DFRKIDLKPL	PPMTNRFREI	LDLVCKRCFD
970	980	990	1000	1010	1020	1030	1040
ELSPPCSEQH	NREQILIGLE	KFIQKEYDEK	ARLCLFGSSK	NGFGFRDSDL	DICMTLEGHE	NAEKLNCKEI	IENLAKILKR
1050	1060	1070	1080	1090	1100	1110	1120
HPGLRNILPI	TTAKVPIVKF	EHRRSGLEGD	ISLYNTLAQH	NTRMLATYAA	IDPRVQYLGY	TMKVFAKRCD	IGDASRGSLS
1130	1140	1150	1160	1170	1180	1190	1200
SYAYILMVLY	FLQQRKPPVI	PVLQEIFDGK	QIPQRMVDGW	NAFFFDKTEE	LKKRLPSLGK	NTESLGELWL	GLLRFYTEEF
1210	1220	1230	1240	1250	1260	1270	1280
DFKEYVISIR	QKKLLTTFEK	QWTSKCIAIE	DPFDLNHNLG	AGVSRKMTNF	IMKAFINGRK	LFGTPFYPLI	GREAEYFFDS
1290	1300	1310	1320	1330	1340	1350	1360
RVLTDGELAP	NDRCCRVCGK	IGHYMKDCPK	RKRLKKKDSE	EEKEGNEEEK	DSRDVLDPRD	LHDTRDFRDP	RDLRCFICGD
1370	1380	1390	1400	1410	1420	1430	1440
AGHVRRECPE	VKLARQRNSS	VAAAQLVRNL	VNAQQVAGSA	QQQGDQSIRT	RQSSECSESP	SYSPQPQPFP	QNSSQSAAIT
1450	1460	1470	1480	1490	1500	1510	1520
QPSSQPGSQP	KLGPPQQGAQ	PPHQVQMPLY	NFPQSPPAQY	SPMHNMGLLP	MHPLQIPAPS	WPIHGPVIHS	APGSAPSNIG
1530	1540	1550	1560	1570	1580	1590	1600
LNDPSIIFAQ	PAARPVAIPN	TSHDGHWPRT	VAPNSLVNSG	AVGNSEPGFR	GLTPPIPWEH	APRPHFPLVP	ASWPYGLHQN
1610	1620	1630	1640	1650			
FMHQGNARFQ	PNKPFYTQDR	CATRRCRERC	PHPPRGNVSE				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1985	4	862.2984	-161.67	2	54.7	12.6	2	553-566	K.RMDDFQLKGIVEEK.F	Oxidation: 2

Detailed Protein Report

Protein 500: **PREDICTED: uncharacterized protein C3orf17 isoform X4 [Homo sapiens]**

Accession:	gi|530374250	**Score:**	23.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	49.6
Database Date:	2015-11-30	**pI:**	10.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MKVLGACKLL	LRLLDCCCKT	FLLTVKHLGL	QEFIILNLVM	VGLVSRLWVL	YKGVLKRLIL	LYEPLFGLLQ	EVARIQPMPY
90	100	110	120	130	140	150	160
FKDFTFPSDI	TEFLGQPYFE	AFKKKMPIAF	AAKGINKLLN	KLFLINEQSP	RASEETLLGI	SKKAKQMKIN	VQNNVDLGQP
170	180	190	200	210	220	230	240
VKNKRVFKEE	SSEFDVRAFC	NQLKHKATQE	TSFDFKCSQS	RLKTTKYSSQ	KVIGTPHAKS	FVQRFREAES	FTQLSEEIQM
250	260	270	280	290	300	310	320
AVVWCRSKKL	KAQAIFLGNK	LLKSNRLKHL	EAQGTSLPKK	LECIKTSICN	HLLRGSGIKT	SKHHLRQRRS	QNKFLRRQRK
330	340	350	360	370	380	390	400
PQRKLQSTLL	REIQQFSQGT	RKSATDTSAK	WRLSHCTVHR	TDLYPNSKQL	LNSGVSMPVI	QTKEKMIHEN	LRGIHENETD
410	420	430	440				
SWTVMQINKN	STSGTIKETD	DIDDIFALMG	V				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2818	1	732.4805	137.02	2	65.7	10.2	1	9-19	K.LLLRLLDCCCK.T	Carbamidomethyl: 8, 9, 10

Detailed Protein Report

Protein 501: **cullin-7 isoform 2 [Homo sapiens]**

Accession:	gi|41872646	**Score:**	23.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	191.0
Database Date:	2015-11-30	**pI:**	5.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.6
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MVGELRYREF RVPLGPGLHA YPDELIRQRV GHDGHPEYQI RWLILRRGDE GDGGSGQVDC KAEHILLWMS KDEIYANCHK
        90        100        110        120        130        140        150        160
MLGEDGQVIG PSQESAGEVG ALDKSVLEEM ETDVKSLIQR ALRQLEECVG TIPPAPLLHT VHVLSAYASI EPLTGVFKDP
       170        180        190        200        210        220        230        240
RVLDLLMHML SSPDYQIRWS AGRMIQALSS HDAGTRTQIL LSLSQQEAIE KHLDFDSRCA LLALFAQATL SEHPMSFEGI
       250        260        270        280        290        300        310        320
QLPQVPGRVL FSLVKRYLHV TSLLDQLNDS AAEPGAQNTS APEELSGERG QLELEFSMAM GTLISELVQA MRWDQASDRP
       330        340        350        360        370        380        390        400
RSSARSPGSI FQPQLADVSP GLPAAQAQPS FRRSRRFRPR SEFASGNTYA LYVRDTLQPG MRVRMLDDYE EISAGDEGEF
       410        420        430        440        450        460        470        480
RQSNNGVPPV QVFWESTGRT YWVHWHMLEI LGFEEDIEDM VEADEYQGAV ASRVLGRALP AWRWRPMTEL YAVPYVLPED
       490        500        510        520        530        540        550        560
EDTEECEHLT LAEWWELLFF IKKLDGPDHQ EVLQILQENL DGEILDDEIL AELAVPIELA QDLLLTLPQR LNDSALRDLI
       570        580        590        600        610        620        630        640
NCHVYKKYGP EALAGNQAYP SLLEAQEDVL LLDAQAQAKD SEDAAKVEAK EPPSQSPNTP LQRLVEGYGP AGKILLDLEQ
       650        660        670        680        690        700        710        720
ALSSEGTQEN KVKPLLLQLQ RQPQPFLALM QSLDTPETNR TLHLTVLRIL KQLVDFPEAL LLPWHEAVDA CMACLRSPNT
       730        740        750        760        770        780        790        800
DREVLQELIF FLHRLTSVSR DYAVVLNQLG ARDAISKALE KHLGKLELAQ ELRDMVFKCE KHAHLYRKLI TNILGGCIQM
       810        820        830        840        850        860        870        880
VLGQIEDHRR THQPINIPFF DVFLRYLCQG SSVEVKEDKC WEKVEVSSNP HRASKLTDHN PKTYWESNGS AGSHYITLHM
       890        900        910        920        930        940        950        960
RRGILIRQLT LLVASEDSSY MPARVVVCGG DSTSSLHTEL NSVNVMPSAS RVILLENLTR FWPIIQIRIK RCQQGGIDTR
       970        980        990       1000       1010       1020       1030       1040
IRGLEILGPK PTFWPVFREQ LCRHTRLFYM VRAQAWSQDM AEDRRSLLHL SSRLNGALRQ EQNFADRFLP DDEAAQALGK
      1050       1060       1070       1080       1090       1100       1110       1120
TCWEALVSPV VQNITSPDED GISPLGWLLD QYLECQEAVF NPQSRGPAFF SRVRRLTHLL VHVEPCEAPP PVVATPRPKG
      1130       1140       1150       1160       1170       1180       1190       1200
RNRSHDWSSL ATRGLPSSIM RNLTRCWRAV VEKQVNNFLT SSWRDDDFVP RYCEHFNILQ NSSSELFGPR AAFLLALQNG
      1210       1220       1230       1240       1250       1260       1270       1280
CAGALLKLPF LKAAHVSEQF ARHIDQQIQG SRIGGAQEME RLAQLQQCLQ AVLIFSGLEI ATTFEHYYQH YMADRLLGVV
      1290       1300       1310       1320       1330       1340       1350       1360
SSWLEGAVLE QIGPCFPNRL PQQMLQSLST SKELQRQFHV YQLQQLDQEL LKLEDTEKKI QVGLGASGKE HKSEKEEEAG
      1370       1380       1390       1400       1410       1420       1430       1440
AAAVVDVAEG EEEEEENEDL YYEGAMPEVS VLVLSRHSWP VASICHTLNP RTCLPSYLRG TLNRYSNFYN KSQSHPALER
      1450       1460       1470       1480       1490       1500       1510       1520
GSQRRLQWTW LGWAELQFGN QTLHVSTVQM WLLLYLNDLK AVSVESLLAF SGLSADMLNQ AIGPLTSSRG PLDLHEQKDI
      1530       1540       1550       1560       1570       1580       1590       1600
PGGVLKIRDG SKEPRSRWDI VRLIPPQTYL QAEGEDGQNL EKRRNLLNCL IVRILKAHGD EGLHIDQLVC LVLEAWQKGP
      1610       1620       1630       1640       1650       1660       1670       1680
CPPRGLVSSL GKGSACSSTD VLSCILHLLG KGTLRRHDDR PQVLSYAVPV TVMEPHTESL NPGSSGPNPP LTFHTLQIRS
      1690       1700
RGVPYASCTA TQSFSTFR
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1825	1	768.7766	-57.45	2	52.8	12.4	1	47-61	R.RGDEGDGGSGQVDCK.A	Carbamidomethyl: 14

Detailed Protein Report

Protein 502: pleckstrin homology domain-containing family A member 4 isoform 2 [Homo sapiens]

Accession:	gi|238859653	**Score:**	23.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	64.2
Database Date:	2015-11-30	**pI:**	10.7
		Sequence Coverage [%]:	3.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEGSRPRSSL	SLASSASTIS	SLSSLSPKKP	TRAVNKIHAF	GKRGNALRRD	PNLPVHIRGW	LHKQDSSGLR	LWKRRWFVLS
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
GHCLFYYKDS	REESVLGSVL	LPSYNIRPDG	PGAPRGRRFT	FTAEHPGMRT	YVLAADTLED	LRGWLRALGR	ASRAEGDDYG
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
QPRSPARPQP	GEGPGGPGGP	PEVSRGEEGR	ISESPEVTRL	SRGRGRPRLL	TPSPTTDLHS	GLQMRRARSP	DLFTPLSRPP
250	**260**	**270**	**280**	**290**	**300**	**310**	**320**
SPLSLPRPRS	APARRPPAPS	GDTAPPARPH	TPLSRIDVRP	PLDWGPQRQT	LSRPPTPRRG	PPSEAGGGKP	PRSPQHWSQE
330	**340**	**350**	**360**	**370**	**380**	**390**	**400**
PRTQPGPPLE	STFHQSLETD	TLLTKLCGQD	RLLRRLQEEI	DQKQEEKEQL	EAALELTRQQ	LGQATREAGA	PGRAWGRQRL
410	**420**	**430**	**440**	**450**	**460**	**470**	**480**
LQDRLVSVRA	TLCHLTQERE	RVWDTYSGLE	QELGTLRETL	EYLLHLGSPQ	DRVSAQQQLW	MVEDTLAGLG	GPQKPPPHTE
490	**500**	**510**	**520**	**530**	**540**	**550**	**560**
PDSPSPVLQG	EESSERESLP	ESLELSSPRS	PETDWGRPPG	GDKDLASPHL	GLGSPRVSRA	SSPEGRHLPS	PQLGTKSKEH
570	**580**	**590**					
HPLLADFRRS	PGAGSQPLPS	PGY					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
411	1	603.6782	-226.42	2	34.8	12.5	0	300-312	R.GPPSEAGGGKPPR.S	

Detailed Protein Report

Protein 503: **FYVE, RhoGEF and PH domain-containing protein 4 [Homo sapiens]**

Accession: gi|198041928
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 23.8
MW [kDa]: 86.6
pI: 5.7
Sequence Coverage [%]: 2.7
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MEEIKPASAS	CVSKEKPSKV	SDLISRFEGG	SSLSNYSDLK	KESAVNLNAP	RTPGRHGLTT	TPQQKLLSQH	LPQRQGNDTD
90	100	110	120	130	140	150	160
KTQGAQTCVA	NGVMAAQNQM	ECEEEKAATL	SSDTSIQASE	PLLDTHIVNG	ERDETATAPA	SPTTDSCDGN	ASDSSYRTPG
170	180	190	200	210	220	230	240
IGPVLPLEER	GAETETKVQE	RENGESPLEL	EQLDQHHEMK	ETNEQKLHKI	ANELLLTERA	YVNRLDLLDQ	VFYCKLLEEA
250	260	270	280	290	300	310	320
NRGSFPAEMV	NKIFSNISSI	NAFHSKFLLP	ELEKRMQEWE	TTPRIGDILQ	KLAPFLKMYG	EYVKGFDNAM	ELVKNMTERI
330	340	350	360	370	380	390	400
PQFKSVVEEI	QKQKICGSLT	LQHHMLEPVQ	RIPRYEMLLK	DYLRKLPPDS	LDWNDAKKSL	EIISTAASHS	NSAIRKMENL
410	420	430	440	450	460	470	480
KKLLEIYEML	GEEEDIVNPS	NELIKEGQIL	KLAARNTSAQ	ERYLFLFNNM	LLYCVPKFSL	VGSKFTVRTR	VGIDGMKIVE
490	500	510	520	530	540	550	560
TQNEEYPHTF	QVSGKERTLE	LQASSAQDKE	EWIKALQETI	DAFHQRHETF	RNAIAKDNDI	HSEVSTAELG	KRAPRWIRDN
570	580	590	600	610	620	630	640
EVTMCMKCKE	PFNALTRRRH	HCRACGYVVC	WKCSDYKAQL	EYDGGKLSKV	CKDCYQIISG	FTDSEEKKRK	GILEIESAEV
650	660	670	680	690	700	710	720
SGNSVVCSFL	QYMEKSKPWQ	KAWCVIPKQD	PLVLYMYGAP	QDVRAQATIP	LLGYVVDEMP	RSADLPHSFK	LTQSKSVHSF
730	740	750	760	770			
AADSEELKQK	WLKVILLAVT	GETPGGPNEH	PATLDDHPEP	KKKSEC			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
889	1	540.2259	-68.97	2	40.6	13.0	0	243-252	R.GSFPAEMVNK.I	

Detailed Protein Report

Protein 504: alpha-amylase 1 precursor [Homo sapiens]

Accession:	gi|40254482	**Score:**	23.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	57.7
Database Date:	2015-11-30	**pI:**	6.5
		Sequence Coverage [%]:	6.8
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578798954	refseq_human (refseq_human_20140103.fasta)	PREDICTED: alpha-amylase 1 isoform X3 [Homo sapiens]
gi|578798952	refseq_human (refseq_human_20140103.fasta)	PREDICTED: alpha-amylase 1 isoform X3 [Homo sapiens]
gi|578798950	refseq_human (refseq_human_20140103.fasta)	PREDICTED: alpha-amylase 1 isoform X2 [Homo sapiens]
gi|530362403	refseq_human (refseq_human_20140103.fasta)	PREDICTED: alpha-amylase 1 isoform X2 [Homo sapiens]
gi|530362397	refseq_human (refseq_human_20140103.fasta)	PREDICTED: alpha-amylase 1 isoform X2 [Homo sapiens]
gi|530362391	refseq_human (refseq_human_20140103.fasta)	PREDICTED: alpha-amylase 1 isoform X1 [Homo sapiens]
gi|56549664	refseq_human (refseq_human_20140103.fasta)	alpha-amylase 1 precursor [Homo sapiens]
gi|56549662	refseq_human (refseq_human_20140103.fasta)	alpha-amylase 1 precursor [Homo sapiens]
gi|56549660	refseq_human (refseq_human_20140103.fasta)	alpha-amylase 1 precursor [Homo sapiens]

10	20	30	40	50	60	70	80
MKLFWLLFTI	GFCWAQYSSN	TQQGRTSIVH	LFEWRWVDIA	LECERYLAPK	GFGGVQVSPP	NENVAIHNPF	RPWWERYQPV
90	100	110	120	130	140	150	160
SYKLCTRSGN	EDEFRNMVTR	CNNVGVRIYV	DAVINHMCGN	AVSAGTSSTC	GSYFNPGSRD	FPAVPYSGWD	FNDGKCKTGS
170	180	190	200	210	220	230	240
GDIENYNDAT	QVRDCRLSGL	LDLALGKDYV	RSKIAEYMNH	LIDIGVAGFR	IDASKHMWPG	DIKAILDKLH	NLNSNWFPEG
250	260	270	280	290	300	310	320
SKPFIYQEVI	DLGGEPIKSS	DYFGNGRVTE	FKYGAKLGTV	IRKWNGEKMS	YLKNWGEGWG	FMPSDRALVF	VDNHDNQRGH
330	340	350	360	370	380	390	400
GAGGASILTF	WDARLYKMAV	GFMLAHPYGF	TRVMSSYRWP	RYFENGKDVN	DWVGPPNDNG	VTKEVTINPD	TTCGNDWVCE
410	420	430	440	450	460	470	480
HRWRQIRNMV	NFRNVVDGQP	FTNWYDNGSN	QVAFGRGNRG	FIVFNNDDWT	FSLTLQTGLP	AGTYCDVISG	DKINGNCTGI
490	500	510	520				
KIYVSDDGKA	HFSISNSAED	PFIAIHAESK	L				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1297	1	863.8565	-56.34	2	45.8	11.6	0	368-383	K.DVNDWVGPPNDNGVTK.E	

Detailed Protein Report

Protein 505: ataxin-1 [Homo sapiens]

Accession:	gi|51479158	**Score:**	23.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	86.9
Database Date:	2015-11-30	**pI:**	9.2
		Sequence Coverage [%]:	3.1
		No. of unique Peptides:	2

Quantitation

MD:MU	**Median:**	1.18	**CV:**	0.00 %	**No. of 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	Ratios
1037	3	612.4575	170.02	2	42.5	13.3	0	698-709	K.GQPVDPASVLLK.H		
1970	1	696.2657	-144.31	2	54.5	10.5	2	710-722	K.HSKADGLAGSRHR.Y		MD:MU 1.18

Detailed Protein Report

Protein 506: PREDICTED: histone acetyltransferase KAT6A isoform X1 [Homo sapiens]

Accession: gi|530388073
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 23.7
MW [kDa]: 224.1
pI: 5.4
Sequence Coverage [%]: 0.9
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MVKLANPLYT	EWILEAIKKV	KKQKQRPSEE	RICNAVSSSH	GLDRKTVLEQ	LELSVKDGTI	LKVSNKGLNS	YKDPDNPGRI
90	100	110	120	130	140	150	160
ALPKPRNHGK	LDNKQNVDWN	KLIKRAVEGL	AESGGSTLKS	IERFLKGQKD	VSALFGGSAA	SGFHQQLRLA	IKRAIGHGRL
170	180	190	200	210	220	230	240
LKDGPLYRLN	TKATNVDGKE	SCESLSCLPP	VSLLPHEKDK	PVAEPIPICS	FCLGTKEQNR	EKKPEELISC	ADCGNSGHPS
250	260	270	280	290	300	310	320
CLKFSPELTV	RVKALRWQCI	ECKTCSSCRD	QGKNADNMLF	CDSCDRGFHM	ECCDPPLTRM	PKGMWICQIC	RPRKKGRKLL
330	340	350	360	370	380	390	400
QKKAAQIKRR	YTNPIGRPKN	RSKGPFSKVR	TGPGRGRKRK	ITLSSQSASS	SSEEGYLERI	DGLDFCRDSN	VSLKFNKKTK
410	420	430	440	450	460	470	480
GLIDGLTKFF	TPSPDGRKAR	GEVVDYSEQY	RIRKRGNRKS	STSDWPTDNQ	DGWDGKQENE	ERLFGSQEIM	TEKDMELFRD
490	500	510	520	530	540	550	560
IQEQALQKVG	VTGPPDPQVR	CPSVIEFGKY	EIHTWYSSPY	PQEYSRLPKL	YLCEFCLKYM	KSRTILQQHM	KKCGWFHPPA
570	580	590	600	610	620	630	640
NEIYRKNNIS	VFEVDGNVST	IYCQNLCLLA	KLFLDHKTLY	YDVEPFLFYV	LTQNDVKGCH	LVGYFSKEKH	CQQKYNVSCI
650	660	670	680	690	700	710	720
MILPQYQRKG	YGRFLIDFSY	LLSKREGQAG	SPEKPLSDLG	RLSYMAYWKS	VILECLYHQN	DKQISIKKLS	KLTGICPQDI
730	740	750	760	770	780	790	800
TSTLHHLRML	DFRSDQFVII	RREKLIQDHM	AKLQLNLRPV	DVDPECLRWT	PVIVSNSVVS	EEEEEEAEEG	ENEEPQCQER
810	820	830	840	850	860	870	880
ELEISVGKSV	SHENKEQDSY	SVESEKKPEV	MAPVSSTRLS	KQVLPHDSLP	ANSQPSRRGR	WGRKNRKTQE	RFGDKDSKLL
890	900	910	920	930	940	950	960
LEETSSAPQE	QYGECGEKSE	ATQEQYTESE	EQLVASEEQP	SQDGKPDLPK	RRLSEGVEPW	RGQLKKSPEA	LKCRLTEGSE
970	980	990	1000	1010	1020	1030	1040
RLPRRYSEGD	RAVLRGFSES	SEEEEEPESP	RSSSPPILTK	PTLKRKKPFL	HRRRRVRKRK	HHNSSVVTET	ISETTEVLDE
1050	1060	1070	1080	1090	1100	1110	1120
PFEDSDSERP	MPRLEPTFEI	DEEEEEEDEN	ELFPREYFRR	LSSQDVLRCQ	SSSKRKSKDE	EEDEESDDAD	DTPILKPVSL
1130	1140	1150	1160	1170	1180	1190	1200
LRKRDVKNSP	LEPDTSTPLK	KKKGWPKGKS	RKPIHWKKRP	GRKPGFKLSR	EIMPVSTQAC	VIEPIVSIPK	AGRKPKIQES
1210	1220	1230	1240	1250	1260	1270	1280
EETVEPKEDM	PLPEERKEEE	EMQAEAEEAE	EGEEEDAASS	EVPAASPADS	SNSPETETKE	PEVEEEEEKP	RVSEEQRQSE
1290	1300	1310	1320	1330	1340	1350	1360
EEQQELEEPE	PEEEEDAAAE	TAQNDDHDAD	DEDDGHLEST	KKKELEEQPT	REDVKEEPGV	QESFLDANMQ	KSREKIKDKE
1370	1380	1390	1400	1410	1420	1430	1440
ETELDSEEEQ	PSHDTSVVSE	QMAGSEDDHE	EDSHTKEELI	ELKEEEEIPH	SELDLETVQA	VQSLTQEESS	EHEGAYQDCE
1450	1460	1470	1480	1490	1500	1510	1520
ETLAACQTLQ	SYTQADEDPQ	MSMVEDCHAS	EHNSPISSVQ	SHPSQSVRSV	SSPNVPALES	GYTQISPEQG	SLSAPSMQNM
1530	1540	1550	1560	1570	1580	1590	1600
ETSPMMDVPS	VSDHSQQVVD	SGFSDLGSIE	STTENYENPS	SYDSTMGGSI	CGNSSSQSSC	SYGGLSSSSS	LTQSSCVVTQ
1610	1620	1630	1640	1650	1660	1670	1680
QMASMGSSCS	MMQQSSVQPA	ANCSIKSPQS	CVVERPPSNQ	QQQPPPPPPQ	QPQPPPPQPQ	PAPQPPPPQQ	QPQQQPQPQP
1690	1700	1710	1720	1730	1740	1750	1760
QQPPPPPPPQ	QQPPLSQCSM	NNSFTPAPMI	MEIPESGSTG	NISIYERIPG	DFGAGSYSQP	SATFSLAKLQ	QLTNTIMDPH
1770	1780	1790	1800	1810	1820	1830	1840
AMPYSHSPAV	TSYATSVSLS	NTGLAQLAPS	HPLAGTPQAQ	ATMTPPPNLA	STTMNLTSPL	LQCNMSATNI	GIPHTQRLQG
1850	1860	1870	1880	1890	1900	1910	1920
QMPVKGHISI	RSKSAPLPSA	AAHQQQLYGR	SPSAVAMQAG	PRALAVQRGM	NMGVNLMPTP	AYNVNSMNMN	TLNAMNSYRM
1930	1940	1950	1960	1970	1980	1990	2000
TQPMMNSSYH	SNPAYMNQTA	QYPMQMQMGM	MGSQAYTQQP	MQPNPHGNMM	YTGPSHHSYM	NAAGVPKQSL	NGPYMRR

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1722	1	1044.9651	24.46	2	51.3	23.7	2	257-273	R.WQCIECKTCSSCRDQGK.N	Carbamidomethyl: 3, 6

Detailed Protein Report

Protein 507: PREDICTED: sperm-associated antigen 17 isoform X5 [Homo sapiens]

Accession:	gi|578798575	**Score:**	23.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	149.1
Database Date:	2015-11-30	**pI:**	5.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAPKKEKGGT	VNTSSKIWEP	SLIAAQFNQN	DWQASIAFVV	GNQIEDDLLI	QALTVAVQVP	QRKLFSMVSW	QDILQQINEI
90	100	110	120	130	140	150	160
NTLVGSASSK	KAKKPVGGNA	PLYYEVLTAA	KAIMDSGEKL	TLPLIGKLLK	FQLLQIKFKD	QQRRENEKKV	IEDKPKLEKD
170	180	190	200	210	220	230	240
KGKAKSPKEK	KAPSAKPAKG	KGKDQPEANA	PVKKTTQLKR	RGEDDHTNRY	IDDEPDDGAQ	HYIIVVGFNN	PQLLAIMAEL
250	260	270	280	290	300	310	320
GIPITSVIKI	SSENYEPLQT	HLAAVNQQQE	VLLQSEDLEA	EKLKKENAIK	ELKTFWKYLE	PVLNNEKPET	NLFDVARLEY
330	340	350	360	370	380	390	400
MVKAADFPSD	WSDGEMMLKL	GTDIFENIAC	LMYDILDWKR	QHQHYLESMQ	LINVPQVVNE	KPVLEAMPTS	EAPQPAVPAP
410	420	430	440	450	460	470	480
GKKKAQYEEP	QAPPPVTSVI	TTEVDMRYYN	YLLNPIREEF	ISVPLILHCM	LEQVVATEED	LVPPSLREPS	PRADGLDHRI
490	500	510	520	530	540	550	560
AAHIVSLLPS	LCLSEREKKN	LHDIFLSEEE	NESKAVPKGP	LLLNYHDAHA	HKKYALQDQK	NFDPVQIEQE	MQSKLPLWEF
570	580	590	600	610	620	630	640
LQFPLPPPWN	NTKRLATIHE	LMHFCTSDVL	SWNEVERAFK	VFTFESLKLS	EVDEKGKLKP	SGMMCGSDSE	MFNIPWDNPA
650	660	670	680	690	700	710	720
RFAKQIRQQY	VMKMNTQEAK	QKADIKIKDR	TLFVDQNLSM	SVQDNESNRE	PSDPSQCDAN	NMKHSDLNNL	KLSVPDNRQL
730	740	750	760	770	780	790	800
LEQESIMKAQ	PQHESLEQTT	NNEIKDDAVT	KADSHEKKPK	KMMVEADLED	IKKTQQRSLM	DWSFTEHFKP	KVLLQVLQEA
810	820	830	840	850	860	870	880
HKQYRCVDSY	YHTQDNSLLL	VFHNPMNRQR	LHCEYWNIAL	HSNVGFRNYL	ELVAKSIQDW	ITKEEAIYQE	SKMNEKIIRT
890	900	910	920	930	940	950	960
RAELELKSSA	NAKLTSASKI	FSIKESKSNK	GISKTEISDQ	EKEKEKEKIP	FILEGSLKAW	KEEQHRLAEE	ERLREEKKAE
970	980	990	1000	1010	1020	1030	1040
KKGKEAGKKK	GKDNAEKEDS	RSLKKKSPYK	EKSKEEQVKI	QEVTEESPHQ	PEPKITYPFH	GYNMGNIPTQ	ISGSNYYLYP
1050	1060	1070	1080	1090	1100	1110	1120
SDGGQIEVEK	TMFEKGPTFI	KVRVVKDNHN	FMIHLNDPKE	IVKKEEKGDY	YLEEEEEGDE	EQSLETEVSD	AKNKAFSKFG
1130	1140	1150	1160	1170	1180	1190	1200
SFSATLENGI	CLSISYYGSN	GMAPEDKDPD	LETILNIPSA	LTPTVVPVIV	TVPQSKAKGK	IKGKEKPKES	LKEEEHPKEE
1210	1220	1230	1240	1250	1260	1270	1280
EKKEEEVEPE	PVLQETLDVP	TFQSLNVSCP	SGLLLTFIGQ	ESTGQYVIDE	EPTWDIMVRQ	SYPQRVKHYE	FYKTVMPPAE
1290	1300	1310					
QEASRVITSQ	GTVVKYMLDG	STQIR					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2219	1	900.3315	-71.18	3	57.6	13.7	0	618-641	K.LKPSGMMCGSDSEMFNIPWDNPAR.F	Oxidation: 6

Detailed Protein Report

Protein 508: protein FAM160A1 [Homo sapiens]

Accession:	gi|158341646	**Score:**	23.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	116.5
Database Date:	2015-11-30	**pI:**	4.6
		Sequence Coverage [%]:	2.2
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530378111	refseq_human (refseq_human_20140103.fasta)	PREDICTED: protein FAM160A1 isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MMSSVSTESK	LQQAVSLQGV	DPETCMIVFK	NHWAQVVKIL	EKHDPLKNTQ	AKYGSIPPDE	ASAVQNYVEH	MLFLLIEEQA
90	100	110	120	130	140	150	160
KDAAMGPILE	FVVSENIMEK	LFLWSLRREF	TDETKIEQLK	MYEMLVTQSH	QPLLHHKPIL	KPLMMLLSSC	SGTTTPTVEE
170	180	190	200	210	220	230	240
KLVVLLNQLC	SILAKDPSIL	ELFFHTSEDQ	GAANFLIFSL	LIPFIHREGS	VGQQARDALL	FIMSLSAENT	MVAHHIVENT
250	260	270	280	290	300	310	320
YFCPVLATGL	SGLYSSLPTK	LEEKGEEWHC	LLKDDWLLLP	SLVQFMNSLE	FCNAVIQVAH	PLIRNQLVNY	IYNGFLVPVL
330	340	350	360	370	380	390	400
APALHKVTVE	EVMTTTAYLD	LFLRSISEPA	LLEIFLRFIL	LHQHENVHIL	DTLTSRINTP	FRLCVVSLAL	FRTLIGLHCE
410	420	430	440	450	460	470	480
DVMLQLVLRY	LIPCNHMMLS	QRWAVKERDC	YSVSAAKLLA	LTPVCCSSGI	TLTLGNQERD	YILWSKCMHD	TSGPVERPFP
490	500	510	520	530	540	550	560
EAFSESACIV	EYGKALDISY	LQYLWEAHTN	ILRCMRDCRV	WSALYDGDSP	DPEMFLQSLT	EEGSVSSACP	VFGLPQQLPR
570	580	590	600	610	620	630	640
KTGPQLAPRK	DKSQTELEWD	DSYDTGISSG	ADVGSPGPYD	DLEVSGPPAP	IDPPKHIQEM	KKNALLLFKG	SYIEESDFQD
650	660	670	680	690	700	710	720
DVMVYRLCAE	KDSEDMKDSQ	EEAARPPAEA	QAEVQSVPIN	NGPLLSTQPE	TDSEEEWNRD	NSDPFHSEPK	EPKQEREPEA
730	740	750	760	770	780	790	800
APESNSELAS	PAPEAEHSSN	LTAAHPESEE	LIAQYDQIIK	ELDSGAEGLM	EQNYPTPDPL	LLTKEEEGKE	ESKGEKEKEG
810	820	830	840	850	860	870	880
KKELEDEEDD	FDSFIAEMPA	VETVPSPFVG	RDEAAFASRH	PVRTQSTPFT	GPFISVVLSK	LENMLENSLH	VNLLLIGIIT
890	900	910	920	930	940	950	960
QLASYPQPLL	RSFLLNTNMV	FQPSVRSLYQ	VLASVKNKIE	QFASVERDFP	GLLIQAQQYL	LFRVDMSDMT	PAALTKDPIQ
970	980	990	1000	1010	1020	1030	1040
EASRTGSGKN	LLDGPPRVLQ	PFLTHRTKVA	EAPPNLPLPV	RNPMLAAALF	PEFLKELAAL	AQEHSILCYK	ILGDFEDSCC
1050							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
468	1	686.9223	31.03	2	35.5	11.6	0	989-1001	K.VAEAPPNLPLPVR.N	

Detailed Protein Report

Protein 509: brain-derived neurotrophic factor isoform a preproprotein [Homo sapiens]

Accession:	gi|25306253	**Score:**	23.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	27.8
Database Date:	2015-11-30	**pI:**	9.8
		Sequence Coverage [%]:	7.7
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|219842314	refseq_human (refseq_human_20140103.fasta)	brain-derived neurotrophic factor isoform a preproprotein [Homo sapiens]
gi|219842309	refseq_human (refseq_human_20140103.fasta)	brain-derived neurotrophic factor isoform a preproprotein [Homo sapiens]
gi|219842306	refseq_human (refseq_human_20140103.fasta)	brain-derived neurotrophic factor isoform a preproprotein [Homo sapiens]
gi|219842303	refseq_human (refseq_human_20140103.fasta)	brain-derived neurotrophic factor isoform a preproprotein [Homo sapiens]
gi|219842300	refseq_human (refseq_human_20140103.fasta)	brain-derived neurotrophic factor isoform a preproprotein [Homo sapiens]
gi|219842294	refseq_human (refseq_human_20140103.fasta)	brain-derived neurotrophic factor isoform a preproprotein [Homo sapiens]
gi|219842292	refseq_human (refseq_human_20140103.fasta)	brain-derived neurotrophic factor isoform a preproprotein [Homo sapiens]
gi|219842290	refseq_human (refseq_human_20140103.fasta)	brain-derived neurotrophic factor isoform a preproprotein [Homo sapiens]
gi|219842288	refseq_human (refseq_human_20140103.fasta)	brain-derived neurotrophic factor isoform a preproprotein [Homo sapiens]
gi|25306267	refseq_human (refseq_human_20140103.fasta)	brain-derived neurotrophic factor isoform a preproprotein [Homo sapiens]
gi|25306264	refseq_human (refseq_human_20140103.fasta)	brain-derived neurotrophic factor isoform a preproprotein [Homo sapiens]
gi|25306257	refseq_human (refseq_human_20140103.fasta)	brain-derived neurotrophic factor isoform a preproprotein [Homo sapiens]

10	20	30	40	50	60	70	80
MTILFLTMVI	SYFGCMKAAP	MKEANIRGQG	GLAYPGVRTH	GTLESVNGPK	AGSRGLTSLA	DTFEHVIEEL	LDEDQKVRPN
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
EENNKDADLY	TSRVMLSSQV	PLEPPLLFLL	EEYKNYLDAA	NMSMRVRRHS	DPARRGELSV	CDSISEWVTA	ADKKTAVDMS
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
GGTVTVLEKV	PVSKGQLKQY	FYETKCNPMG	YTKEGCRGID	KRHWNSQCRT	TQSYVRALTM	DSKKRIGWRF	IRIDTSCVCT
250							
LTIKRGR							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2135	1	1149.9035	-125.59	2	56.6	23.7	2	175-193	K.GQLKQYFYETKCNPMGYTK.E	

Detailed Protein Report

Protein 510: PREDICTED: protein dopey-1 isoform X9 [Homo sapiens]

Accession:	gi|578812549	**Score:**	23.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	226.8
Database Date:	2015-11-30	**pI:**	5.7
		Sequence Coverage [%]:	1.7
		No. of unique Peptides:	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MNTEELELLS	DSKYRNYVAA	IDKALKNFEY	SSEWADLISA	LGKLNKVLQN	NAKYQVVPKK	LTIGKRLAQC	LHPALPGGVH
90	100	110	120	130	140	150	160
RKALETYEII	FKIIGPKRLA	KDLFLYSSGL	FPLLANAAMS	VKPTLLSLYE	IYYLPLGKTL	KPGLQGLLTG	ILPGLEEGSE
170	180	190	200	210	220	230	240
YYERTNMLLE	KVAAAVDQSA	FYSALWGSLL	TSPAVRLPGI	TYVLAHLNRK	LSMEDQLYII	GSDIELMVEA	VSTSVQDSSV
250	260	270	280	290	300	310	320
LVQRSTLDLI	LFCFPFHMSQ	ATRPDMIRIL	SAALHVVLRR	DMSLNRRLYA	WLLGFDNNGA	IIGPRSTRHS	NPEEHATYYF
330	340	350	360	370	380	390	400
TTFSKELLVQ	AMVGILQVNG	FGEENTLMQD	LKPFRILISL	LDKPELGPVI	LEDVLIEVFR	TLYSQCKAEL	DLQTEPPFSK
410	420	430	440	450	460	470	480
DHAQLSSKLR	ENKKTAELIK	TANLLFNSFE	PYYMWDYVAR	WFEECCRRTL	HVRLQIGPGD	SNDSSELQLT	NFCLLVDFLL
490	500	510	520	530	540	550	560
DIVSLPTRSM	RVLCQETYIE	IQTEHLPQLL	LRMISALTSH	LQTLHLSELT	DSLRLCSKIL	SKVQPPLLSA	STGGVLQFPS
570	580	590	600	610	620	630	640
GQNNSVKEWE	DKKVSSVSHE	NPTEVFEDGE	NPPSSRSSES	GFTEFIQYQA	DRTDDIDREL	SEGQGAAAIP	IGSTSSETET
650	660	670	680	690	700	710	720
ASTVGSEETI	IQTPSVVTQG	TATRSRKTAQ	KTAMQCCLEY	VQQFLTRLIN	LYIIQNNSFS	QSLATEHQGD	LGREQGETSK
730	740	750	760	770	780	790	800
WDRNSQGDVK	EKNISKQKTS	KEYLSAFLAA	CQLFLECSSF	PVYIAEGNHT	SELRSEKLET	DCEHVQPPQW	LQTLMNACSQ
810	820	830	840	850	860	870	880
ASDFSVQSVA	ISLVMDLVGL	TQSVAMVTGE	NINSVEPAQP	LSPNQGRVAV	VIRPPLTQGN	LRYIAEKTEF	FKHVALTLWD
890	900	910	920	930	940	950	960
QLGDGTPQHH	QKSVELFYQL	HNLVPSSSIC	EDVISQQLTH	KDKKIRMEAH	AKFAVLWHLT	RDLHINKSSS	FVRSFDRSLF
970	980	990	1000	1010	1020	1030	1040
IMLDSLNSLD	GSTSSVGQAW	LNQVLQRHDI	ARVLEPLLLL	LLHPKTQRVS	VQRVQAERYW	NKSPCYPGEE	SDKHFMQNFA
1050	1060	1070	1080	1090	1100	1110	1120
CSNVSQVQLI	TSKGNGEKPL	TMDEIENFSL	TVNPLSDRLS	LLSTSSETIP	MVVSDFDLPD	QQIEILQSSD	SGCSQSSAGD
1130	1140	1150	1160	1170	1180	1190	1200
NLSYEVDPET	VNAQEDSQMP	KESSPDDDVQ	QVVFDLICKV	VSGLEVESAS	VTSQLEIEAM	PPKCSDIDPD	EETIKIEDDS
1210	1220	1230	1240	1250	1260	1270	1280
IQQSQNALLS	NESSQFLSVS	AEGGHECVAN	GISRNSSSPC	ISGTTHTLHD	SSVASIETKS	RQRSHSSIQF	SFKEKLSEKV
1290	1300	1310	1320	1330	1340	1350	1360
SEKETIVKES	GKQPGAKPKV	KLARKKDDDK	KKSSNEKLKQ	TSVFFSDGLD	LENWYSCGEG	DISEIESDMG	SPGSRKSPNF
1370	1380	1390	1400	1410	1420	1430	1440
NIHPLYQHVL	LYLQLYDSSR	TLYAFSAIKA	ILKTNPIAFV	NAISTTSVNN	AYTPQLSLLQ	NLLARHRISV	MGKDFYSHIP
1450	1460	1470	1480	1490	1500	1510	1520
VDSNHNFRSS	MYIEILISLC	LYYMRSHYPT	HVKVTAQDLI	GNRNMQMMSI	EILTLLFTEL	AKVIESSAKG	FPSFISDMLS
1530	1540	1550	1560	1570	1580	1590	1600
KCKVQKVILH	CLLSSIFSAQ	KWHSEKMAGK	NLVAVEEGFS	EDSLINFSED	EFDNGSTLQS	QLLKVLQRLI	VLEHRVMTIP
1610	1620	1630	1640	1650	1660	1670	1680
EENETGFDFV	VSDLEHISPH	QPMTSLQYLH	AQPITCQGMF	LCAVIRALHQ	HCACKMHPQW	IGLITSTLPY	MGKVLQRVVV
1690	1700	1710	1720	1730	1740	1750	1760
SVTLQLCRNL	DNLIQQYKYE	TGLSDSRPLW	MASIIPPDMI	LTLLEGITAI	IHYCLLDPTT	QYHQLLVSVD	QKHLFEARSG
1770	1780	1790	1800	1810	1820	1830	1840
ILSILHMIMS	SVTLLWSILH	QADSSEKMTI	AASASLTTIN	LGATKNLRQQ	ILELLGPISM	NHGVHFMAAI	AFVWNERRQN
1850	1860	1870	1880	1890	1900	1910	1920
KTTTRTKVIP	AASEEQLLLV	ELVRSISVMR	AETVIQTVKE	VLKQPPAIAK	DKKHLSLEVC	MLQFFYAYIQ	RIPVPNLVDS
1930	1940	1950	1960	1970	1980	1990	2000
WASLLILLKD	SIQLSLPAPG	QFLILGVLNE	FIMKNPSLEN	KKDQRDLQDV	THKIVDAIGA	IAGSSLEQTT	WLRRNLEVKP
2010	2020	2030					
SPKIMVDGTN	LESDVEGFGS	SFGYGFL					

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
2760	1	848.9242	-69.58	2	64.9	12.9	2	1284-1299	K.ETIVKESGKQPGAKPK.V	

Detailed Protein Report

Protein 511: CUB and sushi domain-containing protein 1 precursor [Homo sapiens]

Accession:	gi|259013213	**Score:**	23.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	388.5
Database Date:	2015-11-30	**pI:**	5.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.0
		No. of unique Peptides:	2

Detailed Protein Report

10	20	30	40	50	60	70	80
MTAWRRFQSL	LLLLGLLVLC	ARLLTAAKGQ	NCGGLVQGPN	GTIESPGFPH	GYPNYANCTW	IIITGERNRI	QLSFHTFALE
90	100	110	120	130	140	150	160
EDFDILSVYD	GQPQQGNLKV	RLSGFQLPSS	IVSTGSILTL	WFTTDFAVSA	QGFKALYEVL	PSHTCGNPGE	ILKGVLHGTR
170	180	190	200	210	220	230	240
FNIGDKIRYS	CLPGYILEGH	AILTCIVSPG	NGASWDFPAP	FCRAEGACGG	TLRGTSSSIS	SPHFPSEYEN	NADCTWTILA
250	260	270	280	290	300	310	320
EPGDTIALVF	TDFQLEEGYD	FLEISGTEAP	SIWLTGMNLP	SPVISSKNWL	RLHFTSDSNH	RRKGFNAQFQ	VKKAIELKSR
330	340	350	360	370	380	390	400
GVKMLPSKDG	SHKNSVLSQG	GVALVSDMCP	DPGIPENGRR	AGSDFRVGAN	VQFSCEDNYV	LQGSKSITCQ	RVTETLAAWS
410	420	430	440	450	460	470	480
DHRPICRART	CGSNLRGPSG	VITSPNYPVQ	YEDNAHCVWV	ITTTDPDKVI	KLAFEEFELE	RGYDTLTVGD	AGKVGDTRSV
490	500	510	520	530	540	550	560
LYVLTGSSVP	DLIVSMSNQM	WLHLQSDDSI	GSPGFKAVYQ	EIEKGGCGDP	GIPAYGKRTG	SSFLHGDTLT	FECPAAFELV
570	580	590	600	610	620	630	640
GERVITCQQN	NQWSGNKPSC	VFSCFFNFTA	SSGIILSPNY	PEEYGNNMNC	VWLIISEPGS	RIHLIFNDFD	VEPQFDFLAV
650	660	670	680	690	700	710	720
KDDGISDITV	LGTFSGNEVP	SQLASSGHIV	RLEFQSDHST	TGRGFNITYT	TFGQNECHDP	GIPINGRRFG	DRFLLGSSVS
730	740	750	760	770	780	790	800
FHCDDGFVKT	QGSESITCIL	QDGNVVWSST	VPRCEAPCGG	HLTASSGVIL	PPGWPGYYKD	SLHCEWIIEA	KPGHSIKITF
810	820	830	840	850	860	870	880
DRFQTEVNYD	TLEVRDGPAS	SSPLIGEYHG	TQAPQFLIST	GNFMYLLFTT	DNSRSSIGFL	IHYESVTLES	DSCLDPGIPV
890	900	910	920	930	940	950	960
NGHRHGGDFG	IRSTVTFSCD	PGYTLSDDEP	LVCERNHQWN	HALPSCDALC	GGYIQGKSGT	VLSPGFPDFY	PNSLNCTWTI
970	980	990	1000	1010	1020	1030	1040
EVSHGKGVQM	IFHTFHLESS	HDYLLITEDG	SFSEPVARLT	GSVLPHTIKA	GLFGNFTAQL	RFISDFSISY	EGFNITFSEY
1050	1060	1070	1080	1090	1100	1110	1120
DLEPCDDPGV	PAFSRRIGFH	FGVGDSLTFS	CFLGYRLEGA	TKLTCLGGGR	RVWSAPLPRC	VAECGASVKG	NEGTLLSPNF
1130	1140	1150	1160	1170	1180	1190	1200
PSNYDNNHEC	IYKIETEAGK	GIHLRTRSFQ	LFEGDTLKVY	DGKDSSSRPL	GTFTKNELLG	LILNSTSNHL	WLEFNTNGSD
1210	1220	1230	1240	1250	1260	1270	1280
TDQGFQLTYT	SFDLVKCEDP	GIPNYGYRIR	DEGHFTDTVV	LYSCNPGYAM	HGSNTLTCLS	GDRRVWDKPL	PSCIAECGGQ
1290	1300	1310	1320	1330	1340	1350	1360
IHAATSGRIL	SPGYPAPYDN	NLHCTWIIEA	DPGKTISLHF	IVFDTEMAHD	ILKVWDGPVD	SDILLKEWSG	SALPEDIHST
1370	1380	1390	1400	1410	1420	1430	1440
FNSLTLQFDS	DFFISKSGFS	IQFSTSIAAT	CNDPGMPQNG	TRYGDSREAG	DTVTFQCDPG	YQLQGQAKIT	CVQLNNRFFW
1450	1460	1470	1480	1490	1500	1510	1520
QPDPPTCIAA	CGGNLTGPAG	VILSPNYPQP	YPPGKECDWR	VKVNPDFVIA	LIFKSFNMEP	SYDFLHIYEG	EDSNSPLIGS
1530	1540	1550	1560	1570	1580	1590	1600
YQGSQAPERI	ESSGNSLFLA	FRSDASVGLS	GFAIEFKEKP	REACFDPGNI	MNGTRVGTDF	KLGSTITYQC	DSGYKILDPS
1610	1620	1630	1640	1650	1660	1670	1680
SITCVIGADG	KPSWDQVLPS	CNAPCGGQYT	GSEGVVLSPN	YPHNYTAGQI	CLYSITVPKE	FVVFGQFAYF	QTALNDLAEL
1690	1700	1710	1720	1730	1740	1750	1760
FDGTHAQARL	LSSLSGSHSG	ETLPLATSNQ	ILLRFSAKSG	ASARGFHFVY	QAVPRTSDTQ	CSSVPEPRYG	RRIGSEFSAG
1770	1780	1790	1800	1810	1820	1830	1840
SIVRFECNPG	YLLQGSTALH	CQSVPNALAQ	WNDTIPSCVV	PCSGNFTQRR	GTILSPGYPE	PYGNNLNCIW	KIIVTEGSGI
1850	1860	1870	1880	1890	1900	1910	1920
QIQVISFATE	QNWDSLEIHD	GGDVTAPRLG	SFSGTTVPAL	LNSTSNQLYL	HFQSDISVAA	AGFHLEYKTV	GLAACQEPAL
1930	1940	1950	1960	1970	1980	1990	2000
PSNSIKIGDR	YMVNDVLSFQ	CEPGYTLQGR	SHISCMPGTV	RRWNYPSPLC	IATCGGTLST	LGGVILSPGF	PGSYPNNLDC
2010	2020	2030	2040	2050	2060	2070	2080
TWRISLPIGY	GAHIQFLNFS	TEANHDFLEI	QNGPYHTSPM	IGQFSGTDLP	AALLSTTHET	LIHFYSDHSQ	NRQGFKLAYQ
2090	2100	2110	2120	2130	2140	2150	2160
AYELQNCPDP	PPFQNGYMIN	SDYSVGQSVS	FECYPGYILI	GHPVLTCQHG	INRNWNYPFP	RCDAPCGYNV	TSQNGTIYSP
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
77	1	845.3458	-32.83	3	30.7	11.7	0	893-915	R.STVTFSCDPGYTLSDDEPLVCER.N	
570	1	720.8066	-10.56	2	36.7	12.0	0	1217-1228	K.CEDPGIPNYGYR.I	Carbamidomethyl: 1

Detailed Protein Report

Protein 512: **ubiquitin carboxyl-terminal hydrolase 34 [Homo sapiens]**

Accession:	gi|110347427	**Score:**	23.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	404.0
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
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
DGGHYYSFIR	DIVNPHAYKN	NKWYLFNDAE	VKPFDSAQLA	SECFGGEMTT	KTYDSVTDKF	MDFSFEKTHS	AYMLFYKRME
2250	2260	2270	2280	2290	2300	2310	2320
PEEENGREYK	FDVSSELLEW	IWHDNMQFLQ	DKNIFEHTYF	GFMWQLCSCI	PSTLPDPKAV	SLMTAKLSTS	FVLETFIHSK
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
2144	1	899.3487	-134.27	2	56.7	10.7	0	404-419	R.LSTQHIDCIWAAAQLK.H	

Detailed Protein Report

Protein 513: ryanodine receptor 3 isoform 2 [Homo sapiens]

Accession:	gi|345842488	**Score:**	23.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	551.1
Database Date:	2015-11-30	**pI:**	5.4
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	0.6
		No. of unique Peptides:	2

Detailed Protein Report

10	20	30	40	50	60	70	80
MAEGGEGGED	EIQFLRTEDE	VVLQCIATIH	KEQRKFCLAA	EGLGNRLCFL	EPTSEAKYIP	PDLCVCNFVL	EQSLSVRALQ
90	100	110	120	130	140	150	160
EMLANTGENG	GEGAAQGGGH	RTLLYGHAVL	LRHSFSGMYL	TCLTTSRSQT	DKLAFDVGLR	EHATGEACWW	TIHPASKQRS
170	180	190	200	210	220	230	240
EGEKVRIGDD	LILVSVSSER	YLHLSVSNGN	IQVDASFMQT	LWNVHPTCSG	SSIEEGYLLG	GHVVRLFHGH	DECLTIPSTD
250	260	270	280	290	300	310	320
QNDSQHRRIF	YEAGGAGTRA	RSLWRVEPLR	ISWSGSNIRW	GQAFRLRHLT	TGHYLALTED	QGLILQDRAK	SDTKSTAFSF
330	340	350	360	370	380	390	400
RASKELKEKL	DSSHKRDIEG	MGVPEIKYGD	SVCFVQHIAS	GLWVTYKAQD	AKTSRLGPLK	RKVILHQEGH	MDDGLTLQRC
410	420	430	440	450	460	470	480
QREESQAARI	IRNTTALFSQ	FVSGNNRTAA	PITLPIEEVL	QTLQDLIAYF	QPPEEEMRHE	DKQNKLRSLK	NRQNLFKEEG
490	500	510	520	530	540	550	560
MLALVLNCID	RLNVYNSVAH	FAGIAREESG	MAWKEILNLL	YKLLAALIRG	NRNNCAQFSN	NLDWLISKLD	RLESSSGILE
570	580	590	600	610	620	630	640
VLHCILTESP	EALNLIAEGH	IKSIISLLDK	HGRNHKVLDI	LCSLCLCNGV	AVRANQNLIC	DNLLPRRNLL	LQTRLINDVT
650	660	670	680	690	700	710	720
SIRPNIFLGV	AEGSAQYKKW	YFELIIDQVD	PFLTAEPTHL	RVGWASSSGY	APYPGGGEGW	GGNGVGDDLY	SYGFDGLHLW
730	740	750	760	770	780	790	800
SGRIPRAVAS	INQHLLRSDD	VVSCCLDLGV	PSISFRINGQ	PVQGMFENFN	TDGLFFPVMS	FSAGVKVRFL	MGGRHGEFKF
810	820	830	840	850	860	870	880
LPPSGYAPCY	EALLPKEKMR	LEPVKEYKRD	ADGIRDLLGT	TQFLSQASFI	PCPVDTSQVI	LPPHLEKIRD	RLAENIHELW
890	900	910	920	930	940	950	960
GMNKIELGWT	FGKIRDDNKR	QHPCLVEFSK	LPETEKNYNL	QMSTETLKTL	LALGCHIAHV	NPAAEEDLKK	VKLPKNYMMS
970	980	990	1000	1010	1020	1030	1040
NGYKPAPLDL	SDVKLLPPQE	ILVDKLAENA	HNVWAKDRIK	QGWTYGIQQD	LKNKRNPRLV	PYALLDERTK	KSNRDSLREA
1050	1060	1070	1080	1090	1100	1110	1120
VRTFVGYGYN	IEPSDQELAD	SAVEKVSIDK	IRFFRVERSY	AVRSGKWYFE	FEVVTGGDMR	VGWARPGCRP	DVELGADDQA
1130	1140	1150	1160	1170	1180	1190	1200
FVFEGNRGQR	WHQGSGYFGR	TWQPGDVVGC	MINLDDASMI	FTLNGELLIT	NKGSELAFAD	YEIENGFVPI	CCLGLSQIGR
1210	1220	1230	1240	1250	1260	1270	1280
MNLGTDASTF	KFYTMCGLQE	GFEPFAVNMN	RDVAMWFSKR	LPTFVNVPKD	HPHIEVMRID	GTMDSPPCLK	VTHKTFGTQN
1290	1300	1310	1320	1330	1340	1350	1360
SNADMIYCRL	SMPVECHSSF	SHSPCLDSEA	FQKRKQMQEI	LSHTTTQCYY	AIRIFAGQDP	SCVWVGWVTP	DYHLYSEKFD
1370	1380	1390	1400	1410	1420	1430	1440
LNKNCTVTVT	LGDERGRVHE	SVKRSNCYMV	WGGDIVASSQ	RSNRSNVDLE	IGCLVDLAMG	MLSFSANGKE	LGTCYQVEPN
1450	1460	1470	1480	1490	1500	1510	1520
TKVFPAVFLQ	PTSTSLFQFE	LGKLKNAMPL	SAAIFRSEEK	NPVPQCPPRL	DVQTIQPVLW	SRMPNSFLKV	ETERVSERHG
1530	1540	1550	1560	1570	1580	1590	1600
WVVQCLEPLQ	MMALHIPEEN	RCVDILELCE	QEDLMRFHYH	TLRLYSAVCA	LGNSRVAYAL	CSHVDLSQLF	YAIDNKYLPG
1610	1620	1630	1640	1650	1660	1670	1680
LLRSGFYDLL	ISIHLASAKE	RKLMMKNEYI	IPITSTTRNI	RLFPDESKRH	GLPGVGLRTC	LKPGFRFSTP	CFVVTGEDHQ
1690	1700	1710	1720	1730	1740	1750	1760
KQSPEIPLES	LRTKALSMLT	EAVQCSGAHI	RDPVGGSVEF	QFVPVLKLIG	TLLVMGVFDD	DDVRQILLLI	DPSVFGEHSA
1770	1780	1790	1800	1810	1820	1830	1840
GTEEGAEKEE	VTQVEEKAVE	AGEKAGKEAP	VKGLLQTRLP	ESVKLQMCEL	LSYLCDCELQ	HRVEAIVAFG	DIYVSKLQAN
1850	1860	1870	1880	1890	1900	1910	1920
QKFRYNELMQ	ALNMSAALTA	RKTKEFRSPP	QEQINMLLNF	QLGENCPCPE	EIREELYDFH	EDLLLHCGVP	LEEEEEEEED
1930	1940	1950	1960	1970	1980	1990	2000
TSWTGKLCAL	VYKIKGPPKP	EKEQPTEEEE	RCPTTLKELI	SQTMICWAQE	DQIQDSELVR	MMFNLLRRQY	DSIGELLQAL
2010	2020	2030	2040	2050	2060	2070	2080
RKTYTISHTS	VSDTINLLAA	LGQIRSLLSV	RMGKEEELLM	INGLGDIMNN	KVFYQHPNLM	RVLGMHETVM	EVMVNVLGTE
2090	2100	2110	2120	2130	2140	2150	2160
KSQIAFPKMV	ASCCRFLCYF	CRISRQNQKA	MFEHLSYLLE	NSSVGLASPS	MRGSTPLDVA	ASSVMDNNEL	ALSLEEPDLE
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
833	1	575.1451	-229.53	2	39.8	12.5	0	1250-1258	K.DHPHIEVMR.I	Oxidation: 8
2682	1	1051.5508	66.61	2	64.7	11.2	1	1384-1401	K.RSNCYMVWGGDIVASSQR.S	Carbamidomethyl: 4; Oxidation: 6

Detailed Protein Report

Protein 514: **PREDICTED: receptor-type tyrosine-protein phosphatase delta isoform X16 [Homo sapiens]**

Accession:	gi|578816637	**Score:**	23.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	211.2
Database Date:	2015-11-30	**pI:**	6.2
Modification(s):	Oxidation	**Sequence Coverage [%]:**	0.9
		No. of unique Peptides:	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MVHVARLLLL	LLTFFLRTDA	ETPPRFTRTP	VDQTGVSGGV	ASFICQATGD	PRPKIVWNKK	GKKVSNQRFE	VIEFDDGSGS
90	100	110	120	130	140	150	160
VLRIQPLRTP	RDEAIYECVA	SNNVGEISVS	TRLTVLREDQ	IPRGFPTIDM	GPQLKVVERT	RTATMLCAAS	GNPDPEITWF
170	180	190	200	210	220	230	240
KDFLPVDTSN	NNGRIKQLRS	VRRVPPRFSI	PPTNHEIMPG	GSVNITCVAV	GSPMPYVKWM	LGAEDLTPED	DMPIGRNVLE
250	260	270	280	290	300	310	320
LNDVRQSANY	TCVAMSTLGV	IEAIAQITVK	ALPKPPGTPV	VTESTATSIT	LTWDSGNPEP	VSYYIIQHKP	KNSEELYKEI
330	340	350	360	370	380	390	400
DGVATTRYSV	AGLSPYSDYE	FRVVAVNNIG	RGPPSEPVLT	QTSEQAPSSA	PRDVQARMLS	STTILVQWKE	PEEPNGQIQG
410	420	430	440	450	460	470	480
YRVYYTMDPT	QHVNNWMKHN	VADSQITTIG	NLVPQKTYSV	KVLAFTSIGD	GPLSSDIQVI	TQTGVPGQPL	NFKAEPESET
490	500	510	520	530	540	550	560
SILLSWTPPR	SDTIANYELV	YKDGEHGEEQ	RITIEPGTSY	RLQGLKPNSL	YYFRLAARSP	QGLGASTAEI	SARTMQSKPS
570	580	590	600	610	620	630	640
APPQDISCTS	PSSTSILVSW	QPPPVEKQNG	IITEYSIKYT	AVDGEDDKPH	EILGIPSDTT	KYLLEQLEKW	TEYRITVTAH
650	660	670	680	690	700	710	720
TDVGPGPESL	SVLIRTNEDV	PSGPPRKVEV	EAVNSTSVKV	SWRSPVPNKQ	HGQIRGYQVH	YVRMENGEPK	GQPMLKDVML
730	740	750	760	770	780	790	800
ADAQWEFDDT	TEHDMIISGL	QPETSYSLTV	TAYTTKGDGA	RSKPKLVSTT	GAVPGKPRLV	INHTQMNTAL	IQWHPPVDTF
810	820	830	840	850	860	870	880
GPLQGYRLKF	GRKDMEPLTT	LEFSEKEDHF	TATDIHKGAS	YVFRLSARNK	VGFGEEMVKE	ISIPEEVPTG	FPQNLHSEGT
890	900	910	920	930	940	950	960
TSTSVQLSWQ	PPVLAERNGI	ITKYTLLYRD	INIPLLPMEQ	LIVPADTTMT	LTGLKPDTTY	DVKVRAHTSK	GPGPYSPSVQ
970	980	990	1000	1010	1020	1030	1040
FRTLPVDQAV	FAKNFHVKAV	MKTSVLLSWE	IPENYNSAMP	FKILYDDGKM	VEEVDGRATQ	KLIVNLKPEK	SYSFVLTNRG
1050	1060	1070	1080	1090	1100	1110	1120
NSAGGLQHRV	TAKTAPDVLR	TKPAFIGKTN	LDGMITVQLP	EVPANENIKG	YYIIIVPLKK	SRGKFIKPWE	SPDEMELDEL
1130	1140	1150	1160	1170	1180	1190	1200
LKEISRKRRS	IRYGREVELK	PYIAAHFDVL	PTEFTLGDDK	HYGGFTNKQL	QSGQEYVFFV	LAVMEHAESK	MYATSPYSDP
1210	1220	1230	1240	1250	1260	1270	1280
VVSMDLDPQP	ITDEEEGLIW	VVGPVLAVVF	IICIVIAILL	YKSSKPDRKR	AESDSRKSSI	PNNKEIPSHH	PTDPVELRRL
1290	1300	1310	1320	1330	1340	1350	1360
NFQTPGSDDS	GYPGNLHSSS	MASHPPIPIL	ELADHIERLK	ANDNLKFSQE	YESIDPGQQF	TWEHSNLEVN	KPKNRYANVI
1370	1380	1390	1400	1410	1420	1430	1440
AYDHSRVLLS	AIEGIPGSDY	VNANYIDGYR	KQNAYIATQG	SLPETFGDFW	RMIWEQRSAT	VVMMTKLEER	SRVKCDQYWP
1450	1460	1470	1480	1490	1500	1510	1520
SRGTETHGLV	QVTLLDTVEL	ATYCVRTFAL	YKNGSSEKRE	VRQFQFTAWP	DHGVPEHPTP	FLAFLRRVKT	CNPPDAGPMV
1530	1540	1550	1560	1570	1580	1590	1600
VHCSAGVGRT	GCFIVIDAML	ERIKHEKTVD	IYGHVTLMRA	QRNYMVQTED	QYIFIHDALL	EAVTCGNTEV	PARNLYAYIQ
1610	1620	1630	1640	1650	1660	1670	1680
KLTQIETGEN	VTGMELEFKR	LASSKAHTSR	FISANLPCNK	FKNRLVNIMP	YESTRVCLQP	IRGVEGSDYI	NASFIDGYRQ
1690	1700	1710	1720	1730	1740	1750	1760
QKAYIATQGP	LAETTEDFWR	MLWEHNSTIV	VMLTKLREMG	REKCHQYWPA	ERSARYQYFV	VDPMAEYNMP	QYILREFKVT
1770	1780	1790	1800	1810	1820	1830	1840
DARDGQSRTV	RQFQFTDWPE	QGVPKSGEGF	IDFIGQVHKT	KEQFGQDGPI	SVHCSAGVGR	TGVFITLSIV	LERMRYEGVV
1850	1860	1870	1880	1890			
DIFQTVKMLR	TQRPAMVQTE	DQYQFSYRAA	LEYLGSFDHY	AT			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1512	1	682.1037	142.22	3	48.7	23.6	2	810-826	K.FGRKDMEPLTTLEFSEK.E	Oxidation: 6

Detailed Protein Report

Protein 515: leukocyte receptor cluster member 1 [Homo sapiens]

Accession: gi|24308289
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 23.6
MW [kDa]: 30.5
pI: 10.1
Sequence Coverage [%]: 4.2
No. of unique Peptides: 1

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        10         20         30         40         50         60         70         80
MNILPKKSWH VRNKDNVARV RRDEAQAREE EKERERRVLL AQQEARTEFL RKKARHQNSL PELEAAEAGA PGSGPVDLFR
        90        100        110        120        130        140        150        160
ELLEEGKGVI RGNKEYEEEK RQEKERQEKA LGILTYLGQS AAEAQTQPPW YQLPPGRGGP PPGPAPDEKI KSRLDPLREM
       170        180        190        200        210        220        230        240
QKHLGKKRQH GGDEGSRSRK EKEGSEKQRP KEPPSLDQLR AERLRREAAE RSRAEALLAR VQGRALQEGQ PEEDETDDRR
       250        260        270
RRYNSQFNPQ LARRPRQQDP HLTH
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
575	1	565.3015	-6.83	2	36.5	11.1	1	154-162	R.LDPLREMQK.H	

Detailed Protein Report

Protein 516: **PREDICTED: calcyphosin-like protein isoform X2 [Homo sapiens]**

Accession:	gi|578809847	**Score:**	23.5
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
19	3	1205.0501	-38.96	2	29.8	23.5	0	107-127	K.DGNGTIDFNEFLLTLRPPMSR.A	Oxidation: 19

Detailed Protein Report

Protein 517: E3 ubiquitin-protein ligase BRE1A [Homo sapiens]

Accession:	gi|34878777	**Score:**	23.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	113.6
Database Date:	2015-11-30	**pI:**	5.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.5
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 0.63 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MSGIGNKRAA	GEPGTSMPPE	KKAAVEDSGT	TVETIKLGGV	SSTEELDIRT	LQTKNRKLAE	MLDQRQAIED	ELREHIEKLE
90	100	110	120	130	140	150	160
RRQATDDASL	LIVNRYWSQF	DENIRIILKR	YDLEQGLGDL	LTERKALVVP	EPEPDSDSNQ	ERKDDRERGE	GQEPAFSFLA
170	180	190	200	210	220	230	240
TLASSSSEEM	ESQLQERVES	SRRAVSQIVT	VYDKLQEKVE	LLSRKLNSGD	NLIVEEAVQE	LNSFLAQENM	RLQELTDLLQ
250	260	270	280	290	300	310	320
EKHRTMSQEF	SKLQSKVETA	ESRVSVLESM	IDDLQWDIDK	IRKREQRLNR	HLAEVLERVN	SKGYKVYGAG	SSLYGGTITI
330	340	350	360	370	380	390	400
NARKFEEMNA	ELEENKELAQ	NRLCELEKLR	QDFEEVTTQN	EKLKVELRSA	VEQVVKETPE	YRCMQSQFSV	LYNESLQLKA
410	420	430	440	450	460	470	480
HLDEARTLLH	GTRGTHQHQV	ELIERDEVSL	HKKLRTEVIQ	LEDTLAQVRK	EYEMLRIEFE	QTLAANEQAG	PINREMRHLI
490	500	510	520	530	540	550	560
SSLQNHNHQL	KGEVLRYKRK	LREAQSDLNK	TRLRSGSALL	QSQSSTEDPK	DEPAELKPDS	EDLSSQSSAS	KASQEDANEI
570	580	590	600	610	620	630	640
KSKRDEEERE	RERREKERER	EREREKEKER	EREKQKLKES	EKERDSAKDK	EKGKHDDGRK	KEAEIIKQLK	IELKKAQESQ
650	660	670	680	690	700	710	720
KEMKLLLDMY	RSAPKEQRDK	VQLMAAEKKS	KAELEDLRQR	LKDLEDKEKK	ENKKMADEDA	LRKIRAVEEQ	IEYLQKKLAM
730	740	750	760	770	780	790	800
AKQEEEALLS	EMDVTGQAFE	DMQEQNIRLM	QQLREKDDAN	FKLMSERIKS	NQIHKLLKEE	KEELADQVLT	LKTQVDAQLQ
810	820	830	840	850	860	870	880
VVRKLEEKEH	LLQSNIGTGE	KELGLRTQAL	EMNKRKAMEA	AQLADDLKAQ	LELAQKKLHD	FQDEIVENSV	TKEKDMFNFK
890	900	910	920	930	940	950	960
RAQEDISRLR	RKLETTKKPD	NVPKCDEILM	EEIKDYKARL	TCPCCNMRKK	DAVLTKCFHV	FCFECVKTRY	DTRQRKCPKC
970	980						
NAAFGANDFH	RIYIG						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
463	1	475.6020	-277.84	2	35.1	11.6	0	827-834	R.TQALEMNK.R	Oxidation: 6	MD:MU 0.63

Detailed Protein Report

Protein 518: PREDICTED: complement C1q tumor necrosis factor-related protein 1 isoform X4 [Homo sapiens]

Accession: gi|578830336
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 23.5
MW [kDa]: 32.7
pI: 7.0
Sequence Coverage [%]: 4.8
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MMSATGPGRK	MGSRGQGLLL	AYCLLLAFAS	GLVLSRVPHV	QGEQQEWEGT	EELPSPPDHA	ERAEEQHEKY	RPSQDQGLPA
90	100	110	120	130	140	150	160
SRCLRCCDPG	TSMYPATAVP	QINITILKGE	KGDRGDRGLQ	GKYGKTGSAG	ARGHTGPKGQ	KGSMGAPGER	CKSHYAAFSV
170	180	190	200	210	220	230	240
GRKKPMHSNH	YYQTVIFDTE	FVNLYDHFNM	FTGKFYCYVP	GLYFFSLNVH	TWNQKETYLH	IMKNEEEVVI	LFAQVGDRSI
250	260	270	280	290	300		
MQSQSLMLEL	REQDQVWVRL	YKGERENAIF	SEELDTYITF	SGYLVKHATE	P		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2717	1	741.8557	4.52	2	64.3	11.4	2	1-14	-.MMSATGPGRKMGSR.G	Oxidation: 11

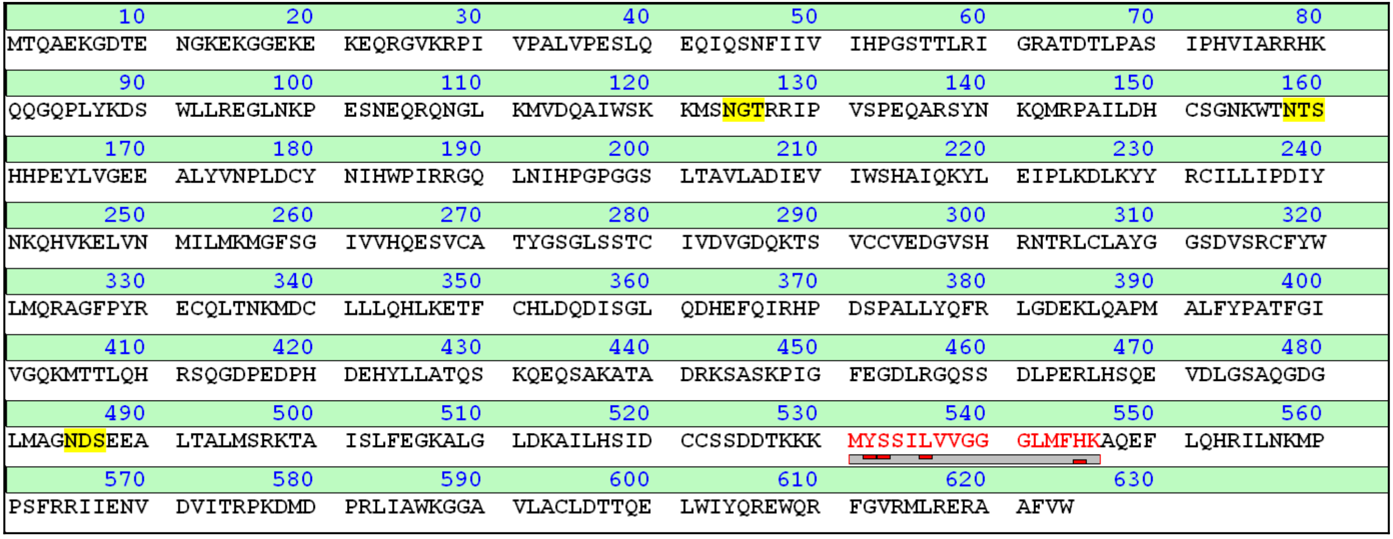
Detailed Protein Report

Protein 519: actin-related protein 8 [Homo sapiens]

Accession:	gi|39812115	**Score:**	23.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	70.4
Database Date:	2015-11-30	**pI:**	8.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.6
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578806774	refseq_human (refseq_human_20140103.fasta)	PREDICTED: actin-related protein 8 isoform X2 [Homo sapiens]
gi|530373398	refseq_human (refseq_human_20140103.fasta)	PREDICTED: actin-related protein 8 isoform X1 [Homo sapiens]



10	20	30	40	50	60	70	80
MTQAEKGDTE	NGKEKGGEKE	KEQRGVKRPI	VPALVPESLQ	EQIQSNFIIV	IHPGSTTLRI	GRATDTLPAS	IPHVIARRHK
90	100	110	120	130	140	150	160
QQGQPLYKDS	WLLREGLNKP	ESNEQRQNGL	KMVDQAIWSK	KMSNGTRRIP	VSPEQARSYN	KQMRPAILDH	CSGNKWTNTS
170	180	190	200	210	220	230	240
HHPEYLVGEE	ALYVNPLDCY	NIHWPIRRGQ	LNIHPGPGGS	LTAVLADIEV	IWSHAIQKYL	EIPLKDLKYY	RCILLIPDIY
250	260	270	280	290	300	310	320
NKQHVKELVN	MILMKMGFSG	IVVHQESVCA	TYGSGLSSTC	IVDVGDQKTS	VCCVEDGVSH	RNTRLCLAYG	GSDVSRCFYW
330	340	350	360	370	380	390	400
LMQRAGFPYR	ECQLTNKMDC	LLLQHLKETF	CHLDQDISGL	QDHEFQIRHP	DSPALLYQFR	LGDEKLQAPM	ALFYPATFGI
410	420	430	440	450	460	470	480
VGQKMTTLQH	RSQGDPEDPH	DEHYLLATQS	KQEQSAKATA	DRKSASKPIG	FEGDLRGQSS	DLPERLHSQE	VDLGSAQGDG
490	500	510	520	530	540	550	560
LMAGNDSEEA	LTALMSRKTA	ISLFEGKALG	LDKAILHSID	CCSSDDTKKK	MYSSILVVGG	GLMFHKAQEF	LQHRILNKMP
570	580	590	600	610	620	630	
PSFRRIIENV	DVITRPKDMD	PRLIAWKGGA	VLACLDTTQE	LWIYQREWQR	FGVRMLRERA	AFVW	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
775	1	585.7012	109.37	3	39.1	11.6	0	531-546	K.MYSSILVVGGGLMFHK.A	Oxidation: 1

Detailed Protein Report

Protein 520: myocyte-specific enhancer factor 2C isoform 3 [Homo sapiens]

Accession:	gi|301069380	**Score:**	23.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	52.3
Database Date:	2015-11-30	**pI:**	9.5
		Sequence Coverage [%]:	6.4
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 0.93 **CV:** 0.00 % **No. of Peptides:** 1

Alias proteins:

Accession	**Name**	**Description**
gi|578810376	refseq_human (refseq_human_20140103.fasta)	PREDICTED: myocyte-specific enhancer factor 2C isoform X12 [Homo sapiens]

10	20	30	40	50	60	70	80
MGRKKIQITR	IMDERNRQVT	FTKRKFGLMK	KAYELSVLCD	CEIALIIFNS	TNKLFQYAST	DMDKVLLKYT	EYNEPHESRT
90	100	110	120	130	140	150	160
NSDIVETLRK	KGLNGCDSPD	PDADDSALNK	KENKGCESPD	PDSSYALTPR	TEEKYKKINE	EFDNMIKSHK	IPAVPPPNFE
170	180	190	200	210	220	230	240
MPVSIPVSSH	NSLVYSNPVS	SLGNPNLLPL	AHPSLQRNSM	SPGVTHRPPS	AGNTGGLMGG	DLTSGAGTSA	GNGYGNPRNS
250	260	270	280	290	300	310	320
PGLLVSPGNL	NKNMQAKSPP	PMNLGMNNRK	PDLRVLIPPG	SKNTMPSVNQ	RINNSQSAQS	LATPVVSVAT	PTLPGQGMGG
330	340	350	360	370	380	390	400
YPSAISTTYG	TEYSLSSADL	SSLSGFNTAS	ALHLGSVTGW	QQQHLHNMPP	SALSQLGACT	STHLSQSSNL	SLPSTQSLNI
410	420	430	440	450	460	470	480
KSEPVSPPRD	RTTTPSRYPQ	HTRHEAGRSP	VDSLSSCSSS	YDGSDREDHR	NEFHSPIGLT	RPSPDERESP	SVKRMRLSEG
490							
WAT							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
672	1	676.1898	-213.65	2	37.7	11.3	1	418-428	R.YPQHTRHEAGR.S		MD:MU 0.93

Detailed Protein Report

Protein 521: melanoma-associated antigen 8 [Homo sapiens]

Accession:	gi|19923308	**Score:**	23.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	35.2
Database Date:	2015-11-30	**pI:**	4.6
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	4.4
		No. of unique Peptides:	1

Quantitation

MD:MU	**Median:** 1.68	**CV:** 0.00 %	**No. of Peptides:** 1

Alias proteins:

Accession	Name	Description
gi|261878490	refseq_huma (refseq_human_20140103.fasta)	melanoma-associated antigen 8 [Homo sapiens]
gi|261878488	refseq_huma (refseq_human_20140103.fasta)	melanoma-associated antigen 8 [Homo sapiens]

10	20	30	40	50	60	70	80
MLLGQKSQRY	KAEEGLQAQG	EAPGLMDVQI	PTAEEQKAAS	SSSTLIMGTL	EEVTDSGSPS	PPQSPEGASS	SLTVTDSTLW
90	100	110	120	130	140	150	160
SQSDEGSSSN	EEEGPSTSPD	PAHLESLFRE	ALDEKVAELV	RFLLRKYQIK	EPVTKAEMLE	SVIKNYKNHF	PDIFSKASEC
170	180	190	200	210	220	230	240
MQVIFGIDVK	EVDPAGHSYI	LVTCLGLSYD	GLLGDDQSTP	KTGLLIIVLG	MILMEGSRAP	EEAIWEALSV	MGLYDGREHS
250	260	270	280	290	300	310	320
VYWKLRKLLT	QEWVQENYLE	YRQAPGSDPV	RYEFLWGPRA	LAETSYVKVL	EHVVRVNARV	RISYPSLHEE	ALGEEKGV

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1776	1	806.7498	-172.60	2	52.2	23.4	0	157-170	K.ASECMQVIFGIDVK.E	Carbamidomethyl: 4; Oxidation: 5	MD:MU 1.68

Detailed Protein Report

Protein 522: gastric inhibitory polypeptide receptor precursor [Homo sapiens]

Accession:	gi|4503999	**Score:**	23.4
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
1715	6	1023.7648	265.10	1	51.4	23.4	2	327-333	R.TRQMRCR.D	Carbamidomethyl: 6; Oxidation: 4

Detailed Protein Report

Protein 523: PREDICTED: collagen alpha-1(III) chain-like [Homo sapiens]

Accession:	gi|530433770	**Score:**	23.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	26.9
Database Date:	2015-11-30	**pI:**	12.5
		Sequence Coverage [%]:	14.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MIPAVSSAER	PGPVFVFSPP	PTPPRGREGA	GGGGPGTGGL	EGARQQPGRR	EPESERGPSP	APCLPSPAAA	WVEAAARQRA
90	100	110	120	130	140	150	160
GEQAVGRTER	LERPTLLRVP	LTPTRGSALP	FYPAPSRPPG	KPGVESGAGA	GRGTDSLPSL	HKGGGERTSR	GGGRPSAAFA
170	180	190	200	210	220	230	240
RQRRRRRLRR	KPGPEPAHLW	SLRRLPPGVP	IQVCPLPAVP	RGAGSVNFTR	GCKIGQSLRP	RPPRPSPDPL	AAGPVRWLLL
250	260						
STSTALFVFK	AFYGPR						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
953	1	637.0944	77.56	3	41.4	11.8	1	184-201	R.RLPPGVPIQVCPLPAVPR.G	

Detailed Protein Report

Protein 524: 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase epsilon-1 isoform 2 [Homo sapiens]

Accession:	gi|260166694	**Score:**	23.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	223.7
Database Date:	2015-11-30	**pI:**	6.2
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.1
		No. of unique Peptides:	1

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
2703	1	673.3636	55.13	2	64.1	13.1	1	1065-1075	R.FLMDKENFASK.N	Oxidation: 3

Detailed Protein Report

Protein 525: **methyltransferase-like protein 17, mitochondrial isoform 1 precursor [Homo sapiens]**

Accession:	gi|71999135	**Score:**	23.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	53.0
Database Date:	2015-11-30	**pI:**	10.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	6.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAAALKCLLT	LGRWCPGLGV	APQARALAAL	VPGVTQVDNK	SGFLQKRPHR	QHPGILKLPH	VRLPQALANG	AQLLLLGSAG
90	100	110	120	130	140	150	160
PTMENQVQTL	TSYLWSRHLP	VEPEELQRRA	RHLEKKFLEN	PDLSQTEEKL	RGAVLHALRK	TTYHWQELSY	TEGLSLVYMA
170	180	190	200	210	220	230	240
ARLDGGFAAV	SRAFHEIRAR	NPAFQPQTLM	DFGSGTGSVT	WAAHSIWGQS	LREYMCVDRS	AAMLVLAEKL	LKGGSESGEP
250	260	270	280	290	300	310	320
YIPGVFFRQF	LPVSPKVQFD	VVVSAFSLSE	LPSKADRTEV	VQTLWRKTGH	FLVLVENGTK	AGHSLLMDAR	DLVLKGKEKS
330	340	350	360	370	380	390	400
PLDPRPGFVF	APCPHELPCP	QLTNLACSFS	QAYHPIPFSW	NKKPKEEKFS	MVILARGSPE	EAHRWPRITQ	PVLKRPRHVH
410	420	430	440	450	460	470	480
CHLCCPDGHM	QHAVLTARRH	GRYGGCDQNQ	WDVAGSCSPR	QHLFPQGFVS	LCPCQLLGRS	FTCAYSVCVS	SIYGSGSL

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2043	1	709.3053	-139.87	2	55.7	12.2	1	1-13	-.MAAALKCLLTLGR.W	Carbamidomethyl: 7

Detailed Protein Report

Protein 526: PREDICTED: ankyrin-2 isoform X16 [Homo sapiens]

Accession:	gi|578809070	**Score:**	23.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	454.5
Database Date:	2015-11-30	**pI:**	4.9
		Sequence Coverage [%]:	0.5
		No. of unique Peptides:	2

Quantitation

MD:MU **Median:** 1.07 **CV:** 0.00 % **No. of Peptides:** 1

Detailed Protein Report

10	20	30	40	50	60	70	80
MGNAALCSSC	HADKSIRAQG	NMQELDKTPD	YYGCNSEDVK	EPGVWVTCPQ	MKPEAANIEK	SDSNASFLRA	ARAGNLDKVV
90	100	110	120	130	140	150	160
EYLKGGIDIN	TCNQNGLNAL	HLAAKEGHVG	LVQELLGRGS	SVDSATKKGN	TALHIASLAG	QAEVVKVLVK	EGANINAQSQ
170	180	190	200	210	220	230	240
NGFTPLYMAA	QENHIDVVKY	LLENGANQST	ATEDGFTPLA	VALQQGHNQA	VAILLENDTK	GKVRLPALHI	AARKDDTKSA
250	260	270	280	290	300	310	320
ALLLQNDHNA	DVQSKSGFTP	LHIAAHYGNV	NVATLLLNRG	AAVDFTARNG	ITPLHVASKR	GNTNMVKLLL	DRGGQIDAKT
330	340	350	360	370	380	390	400
RDGLTPLHCA	ARSGHDQVVE	LLLERGAPLL	ARTKNGLSPL	HMAAQGDHVE	CVKHLLQHKA	PVDDVTLDYL	TALHVAAHCG
410	420	430	440	450	460	470	480
HYRVTKLLLD	KRANPNARAL	NGFTPLHIAC	KKNRIKVMEL	LVKYGASIQA	ITESGLTPIH	VAAFMGHLNI	VLLLLQNGAS
490	500	510	520	530	540	550	560
PDVTNIRGET	ALHMAARAGQ	VEVVRCLLRN	GALVDARARE	EQTPLHIASR	LGKTEIVQLL	LQHMAHPDAA	TTNGYTPLHI
570	580	590	600	610	620	630	640
SAREGQVDVA	SVLLEAGAAH	SLATKKGFTP	LHVAAKYGSL	DVAKLLLQRR	AAADSAGKNG	LTPLHVAAHY	DNQKVALLLL
650	660	670	680	690	700	710	720
EKGASPHATA	KNGYTPLHIA	AKKNQMQIAS	TLLNYGAETN	IVTKQGVTPL	HLASQEGHTD	MVTLLLDKGA	NIHMSTKSGL
730	740	750	760	770	780	790	800
TSLHLAAQED	KVNVADILTK	HGADQDAHTK	LGYTPLIVAC	HYGNVKMVNF	LLKQGANVNA	KTKNGYTPLH	QAAQQGHTHI
810	820	830	840	850	860	870	880
INVLLQHGAK	PNATTANGNT	ALAIAKRLGY	ISVVDTLKVV	TEEVTTTTTT	ITEKHKLNVP	ETMTEVLDVS	DEEALKQFGD
890	900	910	920	930	940	950	960
HFIDGEALSD	SGDDTMTGDG	GEYLRPEDLK	ELGDDSLPSS	QFLDGMNYLR	YSLEGGRSDS	LRSFSSDRSH	TLSHASYLRD
970	980	990	1000	1010	1020	1030	1040
SAVMDDSVVI	PSHQVSTLAK	EAERNSYRLS	WGTENLDNVA	LSSSPIHSGF	LVSFMVDARG	GAMRGCRHNG	LRIIIPPRKC
1050	1060	1070	1080	1090	1100	1110	1120
TAPTRVTCRL	VKRHRLATMP	PMVEGEGLAS	RLIEVGPSGA	QFLGPVIVEI	PHFAALRGKE	RELVVLRSEN	GDSWKEHFCD
1130	1140	1150	1160	1170	1180	1190	1200
YTEDELNEIL	NGMDEVLDSP	EDLEKKRICR	IITRDFPQYF	AVVSRIKQDS	NLIGPEGGVL	SSTVVPQVQA	VFPEGALTKR
1210	1220	1230	1240	1250	1260	1270	1280
IRVGLQAQPM	HSELVKKILG	NKATFSPIVT	LEPRRRKFHK	PITMTIPVPK	ASSDVMLNGF	GGDAPTLRLL	CSITGGTTPA
1290	1300	1310	1320	1330	1340	1350	1360
QWEDITGTTP	LTFVNECVSF	TTNVSARFWL	IDCRQIQESV	TFASQVYREI	ICVPYMAKFV	VFAKSHDPIE	ARLRCFCMTD
1370	1380	1390	1400	1410	1420	1430	1440
DKVDKTLEQQ	ENFAEVARSR	DVEVLEGKPI	YVDCFGNLVP	LTKSGQHHIF	SFFAFKENRL	PLFVKVRDTT	QEPCGRLSFM
1450	1460	1470	1480	1490	1500	1510	1520
KEPKSTRGLV	HQAICNLNIT	LPIYTKESES	DQEQEEEIDM	TSEKNDETES	TETSVLKSHL	VNEVPVLASP	DLLSEVSEMK
1530	1540	1550	1560	1570	1580	1590	1600
QDLIKMTAIL	TTDVSDKAGS	IKVKELVKAA	EEEPGEPFEI	VERVKEDLEK	VNEILRSGTC	TRDESSVQSS	RSERGLVEEE
1610	1620	1630	1640	1650	1660	1670	1680
WVIVSDEEIE	EARQKAPLEI	TEYPCVEVRI	DKEIKGKVEK	DSTGLVNYLT	DDLNTCVPLP	KEQLQTVQDK	AGKKCEALAV
1690	1700	1710	1720	1730	1740	1750	1760
GRSSEKEGKD	IPPDETQSTQ	KQHKPSLGIK	KPVRRKLKEK	QKQKEEGLQA	SAEKAELKKG	SSEESLGEDP	GLAPEPLPTV
1770	1780	1790	1800	1810	1820	1830	1840
KATSPLIEET	PIGSIKDKVK	ALQKRVEDEQ	KGRSKLPIRV	KGKEDVPKKT	THRPHPAASP	SLKSERHAPG	SPSPKTERHS
1850	1860	1870	1880	1890	1900	1910	1920
TLSSSAKTER	HPPVSPSSKT	EKHSPVSPSA	KTERHSPASS	SSKTEKHSPV	SPSTKTERHS	PVSSTKTERH	PPVSPSGKTD
1930	1940	1950	1960	1970	1980	1990	2000
KRPPVSPSGR	TEKHPPVSPG	RTEKRLPVSP	SGRTDKHQPV	STAGKTEKHL	PVSPSGKTEK	QPPVSPTSKT	ERIEETMSVR
2010	2020	2030	2040	2050	2060	2070	2080
ELMKAFQSGQ	DPSKHKTGLF	EHKSAKQKQP	QEKGKVRVEK	EKGPILTQRE	AQKTENQTIK	RGQRLPVTGT	AESKRGVRVS
2090	2100	2110	2120	2130	2140	2150	2160
SIGVKKEDAA	GGKEKVLSHK	IPEPVQSVPE	EESHRESEVP	KEKMADEQGD	MDLQISPDRK	TSTDFSEVIK	QELEDNDKYQ
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
182	1	745.2293	-195.45	2	31.7	10.9	1	15-27	K.SIRAQGNMQELDK.T		MD:MU 1.07
298	1	535.7922	-16.95	2	33.1	12.4	2	2027-2035	K.QKQPQEKGK.V		

Detailed Protein Report

Protein 527: transcription factor HIVEP3 isoform b [Homo sapiens]

Accession:	gi|189181750	**Score:**	23.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	259.2
Database Date:	2015-11-30	**pI:**	8.6
		Sequence Coverage [%]:	1.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDPEQSVKGT	KKAEGSPRKR	LTKGEAIQTS	VSSSVPYPGS	GTAATQESPA	QELLAPQPFP	GPSSVLREGS	QEKTGQQQKP
90	100	110	120	130	140	150	160
PKRPPIEASV	HISQLPQHPL	TPAFMSPGKP	EHLLEGSTWQ	LVDPMRPGPS	GSFVAPGLHP	QSQLLPSHAS	IIPPEDLPGV
170	180	190	200	210	220	230	240
PKVFVPRPSQ	VSLKPTEEAH	KKERKPQKPG	KYICQYCSRP	CAKPSVLQKH	IRSHTGERPY	PCGPCGFSFK	TKSNLYKHRK
250	260	270	280	290	300	310	320
SHAHRIKAGL	ASGMGGEMYP	HGLEMERIPG	EEFEEPTEGE	STDSEEETSA	TSGHPAELSP	RPKQPLLSSG	LYSSGSHSSS
330	340	350	360	370	380	390	400
HERCSLSQSS	TAQSLEDPPP	FVEPSSEHPL	SHKPEDTHTI	KQKLALRLSE	RKKVIDEQAF	LSPGSKGSTE	SGYFSRSESA
410	420	430	440	450	460	470	480
EQQVSPPNTN	AKSYAEIIFG	KCGRIGQRTA	MLTATSTQPL	LPLSTEDKPS	LVPLSVPRTQ	VIEHITKLIT	INEAVVDTSE
490	500	510	520	530	540	550	560
IDSVKPRRSS	LSRRSSMESP	KSSLYREPLS	SHSEKTKPEQ	SLLSLQHPPS	TAPPVPLLRS	HSMPSAACTI	STPHHPFRGS
570	580	590	600	610	620	630	640
YSFDDHITDS	EALSHSSHVF	TSHPRMLKRQ	PAIELPLGGE	YSSEEPGPSS	KDTASKPSDE	VEPKESELTK	KTKKGLKTKG
650	660	670	680	690	700	710	720
VIYECNICGA	RYKKRDNYEA	HKKYYCSELQ	IAKPISAGTH	TSPEAEKSQI	EHEPWSQMMH	YKLGTTLELT	PLRKRRKEKS
730	740	750	760	770	780	790	800
LGDEEEPPAF	ESTKSQFGSP	GPSDAARNLP	LESTKSPAEP	SKSVPSLEGP	TGFQPRTPKP	GSGSESGKER	RTTSKEISVI
810	820	830	840	850	860	870	880
QHTSSFEKSD	SLEQPSGLEG	EDKPLAQFPS	PPPAPHGRSA	HSLQPKLVRQ	PNIQVPEILV	TEEPDRPDTE	PEPPPKEPEK
890	900	910	920	930	940	950	960
TEEFQWPQRS	QTLAQLPAEK	LPPKKKRLRL	AEMAQSSGES	SFESSVPLSR	SPSQESNVSL	SGSSRSASFE	RDDHGKAEAP
970	980	990	1000	1010	1020	1030	1040
SPSSDMRPKP	LGTHMLTVPS	HHPHAREMRR	SASEQSPNVS	HSAHMTETRS	KSFDYGSLSL	TGPSAPAPVA	PPARVAPPER
1050	1060	1070	1080	1090	1100	1110	1120
RKCFLVRQAS	LSRPPESELE	VAPKGRQESE	EPQPSSSKPS	AKSSLSQISS	AATSHGGPPG	GKGPGQDRPP	LGPTVPYTEA
1130	1140	1150	1160	1170	1180	1190	1200
LQVFHHPVAQ	TPLHEKPYLP	PPVSLFSFQH	LVQHEPGQSP	EFFSTQAMSS	LLSSPYSMPP	LPPSLFQAPP	LPLQPTVLHP
1210	1220	1230	1240	1250	1260	1270	1280
GQLHLPQLMP	HPANIPFRQP	PSFLPMPYPT	SSALSSGFFL	PLQSQFALQL	PGDVESHLPQ	IKTSLAPLAT	GSAGLSPSTE
1290	1300	1310	1320	1330	1340	1350	1360
YSSDIRLPPV	APPASSSAPT	SAPPLALPAC	PDTMVSLVVP	VRVQTNMPSY	GSAMYTTLSQ	ILVTQSQGSS	ATVALPKFEE
1370	1380	1390	1400	1410	1420	1430	1440
PPSKGTTVCG	ADVHEVGPGP	SGLSEEQSRA	FPTPYLRVPV	TLPERKGTSL	SSESILSLEG	SSSTAGGSKR	VLSPAGSLEL
1450	1460	1470	1480	1490	1500	1510	1520
TMETQQQKRV	KEEEASKADE	KLELVKPCSV	VLTSTEDGKR	PEKSHLGNQG	QGRRELEMLS	SLSSDPSDTK	EIPPLPHPAL
1530	1540	1550	1560	1570	1580	1590	1600
SHGTAPGSEA	LKEYPQPSGK	PHRRGLTPLS	VKKEDSKEQP	DLPSLAPPSS	LPLSETSSRP	AKSQEGTDSK	KVLQFPSLHT
1610	1620	1630	1640	1650	1660	1670	1680
TTNVSWCYLN	YIKPNHIQHA	DRRSSVYAGW	CISLYNPNLP	GVSTKAALSL	LRSKQKVSKE	TYTMATAPHP	EAGRLVPSSS
1690	1700	1710	1720	1730	1740	1750	1760
RKPRMTEVHL	PSLVSPEGQK	DLARVEKEEE	RRGEPEEDAP	ASQRGEPARI	KIFEGGYKSN	EEYVYVRGRG	RGKYVCEECG
1770	1780	1790	1800	1810	1820	1830	1840
IRCKKPSMLK	KHIRTHTDVR	PYVCKHCHFA	FKTKGNLTKH	MKSKAHSKKC	QETGVLEELE	AEEGTSDDLF	QDSEGREGSE
1850	1860	1870	1880	1890	1900	1910	1920
AVEEHQFSDL	EDSDSDSDLD	EDEDEDEEES	QDELSRPSSE	APPPGPPHAL	RADSSPILGP	QPPDAPASGT	EATRGSSVSE
1930	1940	1950	1960	1970	1980	1990	2000
AERLTASSCS	MSSQSMPGLP	WLGPAPLGSV	EKDTGSALSY	KPVSPRRPWS	PSKEAGSRPP	LARKHSLTKN	DSSPQRCSPA
2010	2020	2030	2040	2050	2060	2070	2080
REPQASAPSP	PGLHVDPGRG	MGALPCGSPR	LQLSPLTLCP	LGRELAPRAH	VLSKLEGTTD	PGLPRYSPTR	RWSPGQAESP
2090	2100	2110	2120	2130	2140	2150	2160
PRSAPPGKWA	LAGPGSPSAG	EHGPGLGLDP	RVLFPPAPLP	HKLLSRSPET	CASPWKAESR	SPSCSPGPAH	PLSSRPFSAL
2170	2180	2190	2200	2210	2220	2230	2240
HDFHGHILAR	TEENIFSHLP	LHSQHLTRAP	CPLIPIGGIQ	MVQARPGAHP	TLLPGPTAAW	VSGFSGGGSD	LTGAREAQER
2250	2260	2270	2280	2290	2300	2310	2320
GRWSPTESSS	ASVSPVAKVS	KFTLSSELEG	GDYPKERERT	GGGPGRPPDW	TPHGTGAPAE	PTPTHSPCTP	PDTLPRPPQG
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
1349	1	942.4987	40.33	2	46.5	10.1	2	1985-2001	K.HSLTKNDSSPQRCSPAR.E	

Detailed Protein Report

Protein 528: **PREDICTED: zinc finger protein 823 isoform X1 [Homo sapiens]**

Accession: gi|530415003
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 23.3
MW [kDa]: 49.6
pI: 10.4
Sequence Coverage [%]: 6.5
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MAAHHGDGPY	KCKLCGKAFV	WPSLFHLHER	THTGEKPYEC	KQCSKAFPFY	SSYLRHERIH	TGEKAYECKQ	CSKAFPDYST
90	100	110	120	130	140	150	160
YLRHERTHTG	EKPYKCTQCG	KAFSCYYYTR	LHERTHTGEQ	PYACKQCGKT	FYHHTSFRRH	MIRHTGDGPH	KCKICGKGFD
170	180	190	200	210	220	230	240
CPSSVRNHET	THTGEKPYEC	KQCGKVLSHS	SSFRSHMITH	TGDGPQKCKI	CGKAFGCPSL	FQRHERTHTG	EKPYQCKQCG
250	260	270	280	290	300	310	320
KAFSLAGSLR	RHEATHTGVK	PYKCQCGKAF	SDLSSFQNHE	TTHTGEKPYE	CKECGKAFSC	FKYLSQHKRT	HTVEKPYECK
330	340	350	360	370	380	390	400
TCRKAFSHFS	NLKVHERIHS	GEKPYECKEC	GKAFSWLTCL	LRHERIHTGE	KPYECLQCGK	AFTRSRFLRG	HEKTHTGEKL
410	420	430					
YECKECGKAL	SSLRSLHRHK	RTHWKDTL					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
739	1	512.6267	-200.37	2	38.8	10.6	0	158-166	K.GFDCPSSVR.N	Carbamidomethyl: 4

Detailed Protein Report

Protein 529: dynein heavy chain 12, axonemal isoform 1 [Homo sapiens]

Accession:	gi|194440727	**Score:**	23.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	356.7
Database Date:	2015-11-30	**pI:**	5.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.6
		No. of unique Peptides:	2

Detailed Protein Report

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
HSIFSHLRKQ	NAPVTEEDLR	NLMFGDYMNP	DLEGDDRVYI	EIPNIHHFSD	VVDQCLDEYN	QTHKTRMNLV	IFRYVLEHLS
2250	2260	2270	2280	2290	2300	2310	2320
RICRVLKQSG	GNALLVGLGG	SGRQSLTRLA	TSMAKMHIFQ	PEISKSYGMN	EWREDMKSFI	AVPVTNRIVD	NKSKILEKRL
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
47	1	1103.4984	-39.62	2	29.9	12.9	1	73-91	R.TPLLPPPDYPQTMTSEMKK.K	Oxidation: 13, 17
2090	1	1159.8674	-54.47	3	56.0	10.4	2	1512-1540	K.FFLEKIIQTYEMMIVRHGFMLVGEPFAAK.T	Oxidation: 12, 20

Protein 530: granulysin isoform 519 [Homo sapiens]

Accession: gi|157502222
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 23.3
MW [kDa]: 14.8
pI: 10.5
Sequence Coverage [%]: 10.8
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
74	1	767.7586	-180.19	2	30.3	23.3	2	72-85	R.SVSNAATRVCRTGR.S	Carbamidomethyl: 10

Detailed Protein Report

Protein 531: **PREDICTED: zinc finger protein 728 isoform X1 [Homo sapiens]**

Accession:	gi|578833255	**Score:**	23.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	68.5
Database Date:	2015-11-30	**pI:**	10.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGSLTFRDVA	IQFSLEEWQC	LDTAQQNLYR	NVMLENYRNL	VFLGIAAPKP	DLIIFLEQGK	EPWNMKRHEL	VKEPPVICSH
90	100	110	120	130	140	150	160
FAQDLWPEQG	REDSFQKVIL	RRYEKCGHEN	LQLKIGCTNV	DECKVHKKGY	NKLNQSLTTT	QSKVFQCGKY	ANIFHKCSNS
170	180	190	200	210	220	230	240
KRHKIRHTGK	KLLKCKEYVR	SFCMLSHLSQ	HKRIYTRENS	YKSEEHGKAF	NWSSALTYKR	IHTGEKPCKC	EECGKAFSKF
250	260	270	280	290	300	310	320
SILTKHKVIH	TGEKHYKCEE	CGKAFTRSSS	LIEHKRSHAG	EKPYKCEECG	KAFSKASTLT	AHKTIHAGEK	PYKCEECGKA
330	340	350	360	370	380	390	400
FNRSSNLMEH	KRIHTGEKPC	KCEECGKAFG	NFSTLTKHKV	IHTGEKPYKC	EECGKAFSWP	SSLTEHKRIH	AGDKPYKCEE
410	420	430	440	450	460	470	480
CGKTFKWSST	LTKHKIIHTG	EKPYKCEECG	KAFTTFSSLT	KHKVIHTGEK	HYKCEECGKV	FSWSSSLTTH	KRIHTGEKPY
490	500	510	520	530	540	550	560
KCEECGKAFS	KVANLTKHKV	IHTGEKQYKC	EECGKAFIWS	SRLSEHKRIH	TGEKPYKCEE	CGKAFSWVSV	LNKHKKIHAG
570	580	590	600				
KKFYKCEECG	KDFNQSSHLT	THKRIHTGGK	TLQM				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2120	1	924.3321	-133.13	2	56.4	11.9	2	230-245	K.CEECGKAFSKFSILTK.H	Carbamidomethyl: 1

Detailed Protein Report

Protein 532: mucin-19 precursor [Homo sapiens]

Accession:	gi|533112494	**Score:**	23.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	804.8
Database Date:	2015-11-30	**pI:**	4.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	0.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MKLILWYLVV	ALWCFFKDVE	ALLYRQKSDG	KIAASRSGGF	SYGSSSSGDL	DRKKPLFSLE	FGSPGETEDK	SRQRQDAGSP
90	100	110	120	130	140	150	160
KSEDTPAGGF	FNSSSSSGDS	DRTKPFFSLG	LGAPGKAEDK	SGDSQDAGGS	KSEDTPPGGF	FYGSSSSGDS	DKKKPLFSFE
170	180	190	200	210	220	230	240
FGATGEDEDK	SRERWDAGNS	RSEDSPADST	NTRYGAGFSS	SGASLDVGFG	WGISDEKGLE	VSKADGRETR	GSGSAGGETI
250	260	270	280	290	300	310	320
VFGPDAGSSV	GTGSSGLKLG	AGKGDAAFGF	EVSDSNSFGD	TGISSKTVEG	NQTSSSGGSV	SIDLGDTSFR	SENQFVGGGS
330	340	350	360	370	380	390	400
LNSISNLWDS	GQEGFGINEI	GGNGMSGSVS	AEAGFKGFGS	DSSSSGDSSA	RNGFENSSGI	SEDSGVILGS	SDQHEVELSR
410	420	430	440	450	460	470	480
TGGNRKRSSD	PDEAGNLSPG	SDVSDSGGNT	WSSDSGSGGG	GVTSSSEYST	SGPLNTPEKG	SHIPEATPKY	SETNAIIGEI
490	500	510	520	530	540	550	560
STWSKGAYKS	FNGRIFFFES	SCPYTFCRHC	IESGGDFNIE	IKRNNDSEIE	KITVLIDNND	VSIFGDTILV	NGESVQIPYN
570	580	590	600	610	620	630	640
NKLIHIKKYG	EHNVLNSRRG	ILTLMWDKNN	KLSLTLHKQY	PTCGLCGNFN	STPGQDINEH	IANSKIPGDC	PNAVGKSYEV
650	660	670	680	690	700	710	720
CEDGIQHCNK	IIGTYFEKCG	KVAALSNDYK	MICIDEYCQT	RDKTSTCDTY	SELSRLCASD	GPGTFESWRS	DSDVVCGTQR
730	740	750	760	770	780	790	800
CPEQHIYKEC	GPSNPATCSN	VAPFQDSECV	SGCTCPEGYL	LDDIGEKGKC	VLKAECPCES	SGTVYQPGEV	REGPCGSQCT
810	820	830	840	850	860	870	880
CQDAKWSCTE	ALCPGRCKVE	GSSLTTFDGV	KYNFPGNCHF	LAVHNEDWSI	SVELRPCPSG	QTGTCLNSVT	LLLNSSVPVD
890	900	910	920	930	940	950	960
KYVFNSDGTV	TNDKIRNQGY	YYSDKIQIFN	ASSSYLQVET	YFHVKLQIQI	VPVMQLYVSM	PPNQFTDTVG	LCGSYNNKAE
970	980	990	1000	1010	1020	1030	1040
DDFMSSQNIL	EKTSQAFANS	WEMMSCPKGN	PSSCISIEKE	KFAERHCGIL	LDSSGPLASC	HPIVNPKPYH	EECKKYTCTC
1050	1060	1070	1080	1090	1100	1110	1120
ENSQDCLCTI	LGNYVKACAE	KETYIVGWRT	GLCEHSCPSG	LVFKYNVKAC	NSSCRSLSER	DRSCDVEDVP	VDGCTCPDAM
1130	1140	1150	1160	1170	1180	1190	1200
YQNNEGNCVL	KSQCDCYIND	EVMQPGKLIH	IDDNKCVCRD	GILLCQIPID	LTLQNCSGGA	EYVDCSDPKA	QRRTNRTCST
1210	1220	1230	1240	1250	1260	1270	1280
RNIPVFDENL	PCKRGCFCPE	GMVRNSKGIC	VFPNDCPCSF	GGREYDEGSV	TSVGCNECTC	IKGSWSCTQN	ECQTICHIYG
1290	1300	1310	1320	1330	1340	1350	1360
EGHVRTFDGK	SYSFDGLCQY	SFLEDYCGHE	NGTFRILTES	VPCCEDGLTC	SRKIIVAFQD	QNIVLQDGKV	TAVKSTESKK
1370	1380	1390	1400	1410	1420	1430	1440
CELNANAYSI	HTVGLYLILK	FQNGIIVIWD	KNTRLSVILD	PNWNGKVCGL	CGNNNGDLKD	DFTTRYSSVA	SGALEFGNSW
1450	1460	1470	1480	1490	1500	1510	1520
KTSQECSDTV	AQTFPCDSNP	YCKAWAVRKC	EILRDSTFRD	CHNKVDPSAY	HDACIEEACA	CDMEGKYLGF	CTAVAMYAEA
1530	1540	1550	1560	1570	1580	1590	1600
CSAVGVCVSW	RKPNLCPVYC	DYYNAPGECR	WHYEPCGTVT	AKTCKDQLVG	QKFSSLLEGC	YAKCPDSAPY	LDENTMKCVS
1610	1620	1630	1640	1650	1660	1670	1680
LSECSCFYND	VIPAGGVIED	NCGRTCYCIA	GQLECSETAP	TNSTFAVSTT	TATTILSTGA	AITLVTGGPS	TAASIPAITT
1690	1700	1710	1720	1730	1740	1750	1760
SSSETTGTTL	GPLTEPFTTG	ITETSVPIIS	TSGNAGMTGV	VSPTVTGASG	MAGTTGGVDA	ATTGAASENT	SERAGTPRVS
1770	1780	1790	1800	1810	1820	1830	1840
GETPAVGGGS	TPGEAGPGAT	VSGSTGVSAG	SITASPGASA	TSSESSKSGT	TGPSVGGKTG	ATSSEATSSE	GMSGVTGQSL
1850	1860	1870	1880	1890	1900	1910	1920
GSTAGSDSEI	TAKTSFTGSS	PPGKLTRPSP	GSPGHFSGGT	TEWGNVATTG	AAGENTSGAL	GSTEGSVEAT	TSAGSGNTAG
1930	1940	1950	1960	1970	1980	1990	2000
TSGTGDTGPG	NTAVSGTPVV	SPGATPGAPG	SSTPGEADIG	NTSFGKSGTP	TVSAASTTSS	PVSKHTDAAS	ATAVTISGSK
2010	2020	2030	2040	2050	2060	2070	2080
PGTPGTPGGA	TSGGKITSGW	SSSGTSTGAS	NTPGATGSST	GQTDTSGPSA	KVTGNYGQSS	EIPGTIKSSS	DVSGTMGQSD
2090	2100	2110	2120	2130	2140	2150	2160
TTSGPSVAVT	RTSEQSSGVT	VASEPSVGVS	GTTGPLAEIS	GTTRPLVSGL	RTTGSSAEGS	GTTGPSSRES	VTTRPLAEGS
2170	2180	2190	2200	2210	2220	2230	2240
GTSGQSVTGS	RATGLSATEL	GTTVSFTGGL	GTSRSSARET	RTTGPSADGS	GTTGPSVVRS	GTTRLSVGVT	RATESSPGVT
2250	2260	2270	2280	2290	2300	2310	2320
GTTTPSAEES	RTTGPSVLVT	GTTGQSGQGS	GTTGKSFIES	GPSVVGSGTT	GPTSAGLGTT	APSTRRSSTT	KPSVGRTGTT
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
2090	1	1131.3695	-118.05	2	56.3	11.2	1	8209-8227	K.LVKFQSNDTCCEIGYCEPR.T	Carbamidomethyl: 10

Detailed Protein Report

Protein 533: PREDICTED: radial spoke head 10 homolog B isoform X5 [Homo sapiens]

Accession:	gi|530384952	**Score:**	23.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	59.8
Database Date:	2015-11-30	**pI:**	6.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MVKEKKKADK	KGEKSARSPS	SLSDNLDFSK	QDGNTTRQEM	SPAGVPLLGM	QLNEVKPKKD	RQNVQQNEDA	SQYEESILTK
90	100	110	120	130	140	150	160
LIVESYEGEK	VRGLYEGEGF	AAFQGGCTYR	GMFSEGLMHG	QGTYIWADGL	KYEGDFVKNV	PMNHGVYTWP	DGSMYEGEVV
170	180	190	200	210	220	230	240
NGMRNGFGMF	KCSTQPVSYI	GHWCNGKRHG	KGSIYYNQEG	TCWYEGDWVQ	NIKKGWGIRC	YKSGNIYEGQ	WEDNMRHGEG
250	260	270	280	290	300	310	320
RMRWLTTNEE	YTGRWERGIQ	NGFGTHTWFL	KRIRSSQYPL	RNEYIGEFVN	GYRHGRGKFY	YASGAMYDGE	WVSNKKHGMF
330	340	350	360	370	380	390	400
FCLQGRLTFK	NGRVYEGAFS	NDHIAGFPDL	EVEFISCLDL	SSGVAPRLSR	SAELIRKLDG	SESHSVLGSS	IELDLNLLLD
410	420	430	440	450	460	470	480
MYPETVQPEE	KKQVEYAVLR	NITELRRIYS	FYSSLGCGHS	LDNTFLMTKL	HFWRFLKDCK	FHHHKLTLAD	MDRILSANND
490	500	510	520				
IPVEEIHSPF	TTILLRTFLN	YLLHLAYHIY	HEEFQQFIP				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2029	1	857.8121	-55.71	2	55.5	23.2	0	223-236	K.SGNIYEGQWEDNMR.H	Oxidation: 13

Protein 534: PREDICTED: F-box/LRR-repeat protein 17 isoform X3 [Homo sapiens]

Accession: gi|530380083
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 23.2
MW [kDa]: 53.6
pI: 10.2
Sequence Coverage [%]: 7.1
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MGHLLSKEPR	NRPSQKRPRC	CSWCRRRRPL	LRLPRRTPAK	VPPQPAAPRS	RDCFFRGPCM	LCFIVHSPGA	PAPAGPEEEP
90	100	110	120	130	140	150	160
PLSPPPRDGA	YAAASSSQHL	ARRYAALAAE	DCAAAARRFL	LSSAAAAAAA	AASASSPASC	CKELGLAAAA	AWEQQGRSLF
170	180	190	200	210	220	230	240
LASLGPVRFL	GPPAAVQLFR	GPTPSPAELP	TPPEMVCKRK	GAGVPACTPC	KQPRCGGGGC	GGGGGGGGGG	GPAGGGASPP
250	260	270	280	290	300	310	320
RPPDAGCCQA	PEQPPQPLCP	PPSSPTSEGA	PTEAGGDAVR	AGGTAPLSAQ	QQHECGDADC	RESPENPCDC	HREPPPETPD
330	340	350	360	370	380	390	400
INQLPPSILL	KIFSNLSLDE	RCLSASLVCK	YWRDLCLDFQ	FWKQLDLSSR	QQVTDELLEK	IASRSQNIIE	INISDCRSMS
410	420	430	440	450	460	470	480
DNGVCVLAFK	CPGLLRYTAY	RCKQLSDTSI	IAVASHCPLL	QKVHVGNQDK	LTDEGLKQLG	SKCRELKDIH	FGQCYKISDE
490	500	510					
GMIVIAKGCL	KLQRIYMQEN	KLILD					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
191	1	879.7026	-94.05	3	32.1	12.5	2	465-487	R.ELKDIHFGQCYKISDEGMIVIAK.G	

Detailed Protein Report

Protein 535: nitric oxide-inducible gene protein [Homo sapiens]

Accession: gi|194239694
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 23.1
MW [kDa]: 111.5
pI: 6.9
Sequence Coverage [%]: 2.9
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MNRRRKFLLA	SVLALQNSSF	IYPSCQKCFS	RIILVSKRSN	CPKCGSTGES	GNANYRYKLS	LKVAESNKLF	VITVFGSCLD
90	100	110	120	130	140	150	160
TFFGLTATGL	HRYIQDPNKI	PETLDNDTTQ	NLLTKAVETC	FVGQSFIFGV	TNFENQPGQG	SDASNFLQQC	SDHKRKAKAL
170	180	190	200	210	220	230	240
VACQIVLPDP	GIAGFTVIDY	FHQLLQTFNF	RKLQCDSQAP	NNHLLALDHS	NSDLSSIYTS	DSTSDFFKSC	SKDTFSKFWQ
250	260	270	280	290	300	310	320
PSLEFTCIVS	QLTDNDDFSA	SEQSKAFGTL	QQNRKSISIA	EATGSSSCHD	PIQDSWSLVS	YMDKKSTAEK	LGKELGLQAK
330	340	350	360	370	380	390	400
ELSAVHSSHH	EIGVNDSNLF	SLEMREPLES	SNTKSFHSAV	EIKNRSQHEL	PCFQHHGIDT	PTSLQKRSAC	CPPSLLRLEE
410	420	430	440	450	460	470	480
TASSSQDGDP	QIWDDLPFSE	SLNKFLAVLE	SEIAVTQADV	SSRKHHVDND	IDKFHADHSR	LSVTPQRTTG	ALHTPPIALR
490	500	510	520	530	540	550	560
SSQVIVKANC	SKDDFLFNCK	GNLSPSVEKE	SQPDNKVEAV	SVNHNGRDMS	EYFLPNPYLS	ALSSSSKDLE	TIVTLKKTIR
570	580	590	600	610	620	630	640
ISPHRESDHS	SLNNKYLNGC	GEISVSEMNE	KLTTLCYRKY	NDVSDLCKLE	NKQYCRWSKN	QDDSFTICRK	LTYPLETLCN
650	660	670	680	690	700	710	720
SPNRSTNTLK	EMPWGHINNN	VTQSYSIGYE	GSYDASADLF	DDIAKEMDIA	TEITKKSQDI	LLKWGTSLAE	SHPSESDFSL
730	740	750	760	770	780	790	800
RSLSEDFIQP	SQKLSLQSLS	DSRHSRTCSP	TPHFQSDSEY	NFENSQDFVP	CSQSTPISGF	HQTRIHGINR	AFKKPVFYSD
810	820	830	840	850	860	870	880
LDGNYEKIRI	FPENDKQQAS	PSCPKNIKTP	SQKIRSPIVS	GVSQPDVFNH	YPFAECHETD	SDEWVPPTTQ	KIFPSDMLGF
890	900	910	920	930	940	950	960
QGIGLGKCLA	AYHFPDQQEL	PRKKLKHIRQ	GTNKGLIKKK	LKNMLAAVVT	KKKTHKYNCK	SSGWISKCPD	IQVLAAPQLH
970	980	990	1000				
PILGPDSCSE	VKCCLPFSEK	GPPSVCETRS	AWSPELFS				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2056	1	1029.5727	121.71	2	55.8	10.9	2	38-56	K.RSNCPKCGSTGESGNANYR.Y	Carbamidomethyl: 4

Detailed Protein Report

Protein 536: DENN domain-containing protein 1B isoform 4 [Homo sapiens]

Accession:	gi|304571967	**Score:**	23.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	8.3
Database Date:	2015-11-30	**pI:**	9.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	21.1
		No. of unique Peptides:	1

```
         10         20         30         40         50         60         70         80
MDCRTKANPD RTFDLVLKVK CHASENEEDS PAYLPRIPPG KVRRFAFCIK KLENFPVGPG VAPPVSGVDL VPAETA
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2093	2	937.8811	-22.59	2	56.3	23.1	0	21-36	K.CHASENEEDSPAYLPR.I	Carbamidomethyl: 1

Detailed Protein Report

Protein 537: PREDICTED: diacylglycerol kinase iota isoform X2 [Homo sapiens]

Accession:	gi|578814735	**Score:**	23.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	113.9
Database Date:	2015-11-30	**pI:**	9.1
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.9
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MNPSSSAGEE	KGATGGSSSS	GSGAGSCCLG	AEGGADPRGA	GSAAAAGAAA	LDEPAAAGQK	EKDEALEEKL	RNLTFRKQVS
90	100	110	120	130	140	150	160
YRKAISRAGL	QHLAPAHPLS	LPVANGPAKE	PRATLDWSEN	AVNGEHLWLE	TNVSGDLCYL	GEENCQVRFA	KSALRRKCAV
170	180	190	200	210	220	230	240
CKIVVHTACI	EQLEKINFRC	KPTFREGGSR	SPRENFVRHH	WVHRRRQEGK	CKQCGKGFQQ	KFSFHSKEIV	AISCSWCKQA
250	260	270	280	290	300	310	320
FHNKVTCFML	HHIEEPCSLG	AHAAVIVPPT	WIIKVKKPQN	SLKASNRKKK	RTSFKRKASK	RGMEQENKGR	PFVIKPISSP
330	340	350	360	370	380	390	400
LMKPLLVFVN	PKSGGNQGTK	VLQMFMWYLN	PRQVFDLSQE	GPKDALELYR	KVPNLRILAC	GGDGTVGWIL	SILDELQLSP
410	420	430	440	450	460	470	480
QPPVGVLPLG	TGNDLARTLN	WGGGYTDEPV	SKILCQVEDG	TVVQLDRWNL	HVERNPDLPP	EELEDGVCKK	LDRKQLKYKE
490	500	510	520	530	540	550	560
EYHMDILPLN	VFNNYFSLGF	DAHVTLEFHE	SREANPEKFN	SRFRNKMFYA	GAAFSDFLQR	SSRDLSKHVK	VVCDGTDLTP
570	580	590	600	610	620	630	640
KIQELKFQCI	VFLNIPRYCA	GTMPWGNPGD	HHDFEPQRHD	DGYIEVIGFT	MASLAALQVG	GHGERLHQCR	EVMLLTYKSI
650	660	670	680	690	700	710	720
PMQVDGEPCR	LAPAMIRISL	RNQANMVQKS	KRRTSMPLLN	DPQSVPDRLR	IRVNKISLQD	YEGFHYDKEK	LREASIPLGI
730	740	750	760	770	780	790	800
LVVRGDCDLE	TCRMYIDRLQ	EDLQSVSSGS	QRVHYQDHET	SFPRALSAQR	LSPRWCFLDA	TSADRFYRID	RSQEHLHFVM
810	820	830	840	850	860	870	880
EISQDEIFIL	DPDMVVSQPA	GTPPGMPDLV	VEQASGISDW	WNPALRKRML	SDSGLGMIAP	YYEDSDLKDL	SHSRVLQSPV
890	900	910	920	930	940	950	960
SSEDHAILQA	VIAGDLMKLI	ESYKNGGSLL	IQGPDHCSLL	HYAAKTGNGE	IVKYILDHGP	SELLDMADSE	TGETALHKAA
970	980	990	1000	1010	1020	1030	
CQRNRAVCQL	LVDAGASLRK	TDSKGKTPQE	RAQQAGDPDL	AAYLESRQNY	KVIGHEDLET	AV	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1635	1	1100.4411	-20.69	3	50.3	12.6	1	2-38	M.NPSSSAGEEKGATGGSSSSGSGAGSCCLGAEGGADPR.G	Carbamidomethyl: 26
2495	1	735.4148	-22.06	2	61.6	10.5	2	275-287	K.VKKPQNSLKASNR.K	

Detailed Protein Report

Protein 538: **UPF0598 protein C8orf82 [Homo sapiens]**

Accession:	gi|49169841	**Score:**	23.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	23.9
Database Date:	2015-11-30	**pI:**	10.4
		Sequence Coverage [%]:	14.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MWPPCGTLRT	LALARSRGAR	ACSGDGGVSY	TQGQSPEPRT	REYFYYVDHQ	GQLFLDDSKM	KNFITCFKDP	QFLVTFFSRL
90	100	110	120	130	140	150	160
RPNRSGRYEA	AFPFLSPCGR	ERNFLRCEDR	PVVFTHLLTA	DHGPPRLSYC	GGGEALAVPF	EPARLLPLAA	NGRLYHPAPE
170	180	190	200	210	220		
RAGGVGLVRS	ALAFELSACF	EYGPGAPALP	SHVRWQGRRL	ALTMDLAPLL	LAARSP		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
367	1	846.3873	-98.49	2	34.2	12.6	1	154-169	R.LYHPAPERAGGVGLVR.S	

Detailed Protein Report

Protein 539: **PREDICTED: zinc finger protein 236 isoform X1 [Homo sapiens]**

Accession:	gi|530414335	**Score:**	23.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	197.2
Database Date:	2015-11-30	**pI:**	9.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.7
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MRDHERNDKP	HRCDQCPQTF	NVEFNLTLHK	CTHSGEDPTC	PVCNKKFSRV	ASLKAHIMLH	EKEENLICSE	CGDEFTLQSQ
90	100	110	120	130	140	150	160
LAVHMEEHRQ	ELAGTRQHAC	KACKKEFETS	SELKEHMKTH	YKIRVSSTRS	YNRNIDRSGF	TYSCPHCGKT	FQKPSQLTRH
170	180	190	200	210	220	230	240
IRIHTGERPF	KCSECGKAFN	QKGALQTHMI	KHTGEKPHAC	AFCPAAFSQK	GNLQSHVQRV	HSEVKNGPTY	NCTECSCVFK
250	260	270	280	290	300	310	320
SLGSLNTHIS	KMHMGGPQNS	TSSTETAHVL	TATLFQTLPL	QQTEAQATSA	SSQPSSQAVS	DVIQQLLELS	EPAPVESGQS
330	340	350	360	370	380	390	400
PQPGQQLSIT	VGINQDILQQ	ALENSGLSSI	PAAAHPNDSC	HAKTSAPHAQ	NPDVSSVSNE	QTDPTDAEQE	KEQESPEKLD
410	420	430	440	450	460	470	480
KKEKKMIKKK	SPFLPGSIRE	ENGVRWHVCP	YCAKEFRKPS	DLVRHIRIHT	HEKPFKCPQC	FRAFAVKSTL	TAHIKTHTGI
490	500	510	520	530	540	550	560
KAFKCQYCMK	SFSTSGSLKV	HIRLHTGVRP	FACPHCDKKF	RTSGHRKTHI	ASHFKHTELR	KMRHQRKPAK	VRVGKTNIPV
570	580	590	600	610	620	630	640
PDIPLQEPIL	ITDLGLIQPI	PKNQFFQSYF	NNNFVNEADR	PYKCFYCHRA	YKKSCHLKQH	IRSHTGEKPF	KCSQCGRGFV
650	660	670	680	690	700	710	720
SAGVLKAHIR	THTGLKSFKC	LICNGAFTTG	GSLRRHMGIH	NDLRPYMCPY	CQKTFKTSLN	CKKHMKTHRY	ELAQQLQQHQ
730	740	750	760	770	780	790	800
QAASIDDSTV	DQQSMQASTQ	MQVEIESDEL	PQTAEVVAAN	PEAMLDLEPQ	HVVGTEEAGL	GQQLADQPLE	ADEDGFVAPQ
810	820	830	840	850	860	870	880
DPLRGHVDQF	EEQSPAQQSF	EPAGLPQGFT	VTDTYHQQPQ	FPPVQQLQDS	STLESQALST	SFHQQSLLQA	PSSDGMNVTT
890	900	910	920	930	940	950	960
RLIQESSQEE	LDLQAQGSQF	LEDNEDQSRR	SYRCDYCNKG	FKKSSHLKQH	VRSHTGEKPY	KCKLCGRGFV	SSGVLKSHEK
970	980	990	1000	1010	1020	1030	1040
THTGVKAFSC	SVCNASFTTN	GSLTRHMATH	MSMKPYKCPF	CEEGFRTTVH	CKKHMKRHQT	VPSAVSATGE	TEGGDICMEE
1050	1060	1070	1080	1090	1100	1110	1120
EEEHSDRNAS	RKSRPEVITF	TEEETAQLAK	IRPQESATVS	EKVLVQSAAE	KDRISELRDK	QAELQDEPKH	ANCCTYCPKS
1130	1140	1150	1160	1170	1180	1190	1200
FKKPSDLVRH	VRIHTGEKPY	KCDECGKSFT	VKSTLDCHVK	THTGQKLFSC	HVCSNAFSTK	GSLKVHMRLH	TGAKPFKCPH
1210	1220	1230	1240	1250	1260	1270	1280
CELRFRTSGR	RKTHMQFHYK	PDPKKARKPM	TRSSSEGLQP	VNLLNSSSTD	PNVFIMNNSV	LTGQFDQNLL	QPGLVGQAIL
1290	1300	1310	1320	1330	1340	1350	1360
PASVSAGGDL	TVSLTDGSLA	TLEGIQLQLA	ANLVGPNVQI	SGIDAASINN	ITLQIDPSIL	QQTLQQGNLL	AQQLTGEPGL
1370	1380	1390	1400	1410	1420	1430	1440
APQNSSLQTS	DSTVPASVVI	QPISGLSLQP	TVTSANLTIG	PLSEQDSVLT	TNSSGTQDLT	QVMTSQGLVS	PSGGPHEITL
1450	1460	1470	1480	1490	1500	1510	1520
TINNSSLSQV	LAQAAGPTAT	SSSGSPQEIT	LTISELNTTS	GSLPSTTPMS	PSAISTQNLV	MSSSGVGGDA	SVTLTLADTQ
1530	1540	1550	1560	1570	1580	1590	1600
GMLSGGLDTV	TLNITSQGQQ	FPALLTDPSL	SGQGGAGSPQ	VILVSHTPQS	ASAACEEIAY	QVAGVSGNLA	PGNQPEKEGR
1610	1620	1630	1640	1650	1660	1670	1680
AHQCLECDRA	FSSAAVLMHH	SKEVHGRERI	HGCPVCRKAF	KRATHLKEHM	QTHQAGPSLS	SQKPRVFKCD	TCEKAFAKPS
1690	1700	1710	1720	1730	1740	1750	1760
QLERHSRIHT	GERPFHCTLC	EKAFNQKSAL	QVHMKKHTGE	RPYKCAYCVM	GFTQKSNMKL	HMKRAHSYAG	ALQESAGHPE
1770	1780	1790	1800				
QDGEELSRTL	HLEEVVQEAA	GEWQALTHVF					

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

	Cmpds.		[ppm]		[min]					
2391	1	862.0720	174.01	2	60.2	10.8	2	105-118	K.KEFETSSELKEHMK.T	
1447	1	947.6235	148.95	2	47.9	12.3	1	1189-1204	R.LHTGAKPFKCPHCELR.F	Carbamidomethyl: 10

Detailed Protein Report

Protein 540: PREDICTED: midasin isoform X3 [Homo sapiens]

Accession:	gi|578812559	**Score:**	23.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	627.0
Database Date:	2015-11-30	**pI:**	5.4
		Sequence Coverage [%]:	0.6
		No. of unique Peptides:	1

Detailed Protein Report

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

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1915	1	918.3456	-31.31	2	53.8	12.2	1	4832-4848	K.EEKEEAEADDGGQGEDK.I	

Detailed Protein Report

Protein 541: integrin alpha-IIb preproprotein [Homo sapiens]

Accession:	gi|88758615	**Score:**	23.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	113.3
Database Date:	2015-11-30	**pI:**	5.1
		Sequence Coverage [%]:	1.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MARALCPLQA	LWLLEWVLLL	LGPCAAPPAW	ALNLDPVQLT	FYAGPNGSQF	GFSLDFHKDS	HGRVAIVVGA	PRTLGPSQEE
90	100	110	120	130	140	150	160
TGGVFLCPWR	AEGGQCPSLL	FDLRDETRNV	GSQTLQTFKA	RQGLGASVVS	WSDVIVACAP	WQHWNVLEKT	EEAEKTPVGS
170	180	190	200	210	220	230	240
CFLAQPESGR	RAEYSPCRGN	TLSRIYVEND	FSWDKRYCEA	GFSSVVTQAG	ELVLGAPGGY	YFLGLLAQAP	VADIFSSYRP
250	260	270	280	290	300	310	320
GILLWHVSSQ	SLSFDSSNPE	YFDGYWGYSV	AVGEFDGDLN	TTEYVVGAPT	WSWTLGAVEI	LDSYYQRLHR	LRGEQMASYF
330	340	350	360	370	380	390	400
GHSVAVTDVN	GDGRHDLLVG	APLYMESRAD	RKLAEVGRVY	LFLQPRGPHA	LGAPSLLLTG	TQLYGRFGSA	IAPLGDLDRD
410	420	430	440	450	460	470	480
GYNDIAVAAP	YGGPSGRGQV	LVFLGQSEGL	RSRPSQVLDS	PFPTGSAFGF	SLRGAVDIDD	NGYPDLIVGA	YGANQVAVYR
490	500	510	520	530	540	550	560
AQPVVKASVQ	LLVQDSLNPA	VKSCVLPQTK	TPVSCFNIQM	CVGATGHNIP	QKLSLNAELQ	LDRQKPRQGR	RVLLLGSQQA
570	580	590	600	610	620	630	640
GTTLNLDLGG	KHSPICHTTM	AFLRDEADFR	DKLSPIVLSL	NVSLPPTEAG	MAPAVVLHGD	THVQEQTRIV	LDCGEDDVCV
650	660	670	680	690	700	710	720
PQLQLTASVT	GSPLLVGADN	VLELQMDAAN	EGEGAYEAEL	AVHLPQGAHY	MRALSNVEGF	ERLICNQKKE	NETRVVLCEL
730	740	750	760	770	780	790	800
GNPMKKNAQI	GIAMLVSVGN	LEEAGESVSF	QLQIRSKNSQ	NPNSKIVLLD	VPVRAEAQVE	LRGNSFPASL	VVAAEEGERE
810	820	830	840	850	860	870	880
QNSLDSWGPK	VEHTYELHNN	GPGTVNGLHL	SIHLPGQSQP	SDLLYILDIQ	PQGGLQCFPQ	PPVNPLKVDW	GLPIPSPSPI
890	900	910	920	930	940	950	960
HPAHHKRDRR	QIFLPEPEQP	SRLQDPVLVS	CDSAPCTVVQ	CDLQEMARGQ	RAMVTVLAFL	WLPSLYQRPL	DQFVLQSHAW
970	980	990	1000	1010	1020	1030	1040
FNVSSLPYAV	PPLSLPRGEA	QVWTQLLRAL	EERAIPIWWV	LVGVLGGLLL	LTILVLAMWK	VGFFKRNRPP	LEEDDEEGE

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
183	1	862.4693	40.75	2	32.0	23.0	1	105-119	R.DETRNVGSQTLQTFK.A	

Detailed Protein Report

Protein 542: PREDICTED: PR domain zinc finger protein 15 isoform X1 [Homo sapiens]

Accession:	gi|578836643	**Score:**	23.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	130.3
Database Date:	2015-11-30	**pI:**	9.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.1
		No. of unique Peptides:	2

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        10         20         30         40         50         60         70         80
MPRRRPPASG AAQFPERIAT RSPDPIPLCT FQRQVSEMAE DGSEEIMFIW CEDCSQYHDS ECPELGPVVM VKDSFVLSRA
        90        100        110        120        130        140        150        160
RSSLPPNLEI RRLEDGAEGV FAITQLVKRT QFGPFESRRV AKWEKESAFP LKVFQKDGHP VCFDTSNEDD CNWMMLVRPA
       170        180        190        200        210        220        230        240
AEAEHQNLTA YQHGSDVYFT TSRDIPPGTE LRVWYAAFYA KKMDKPMLKQ AGSGVHAAGT PENSAPVESE PSQWACKVCS
       250        260        270        280        290        300        310        320
ATFLELQLLN EHLLGHLEQA KSLPPGSQSE AAAPEKEQDT PRGEPPAVPE SENVATKEQK KKPRRGRKPK VSKAEQPLVI
       330        340        350        360        370        380        390        400
VEDKEPTEQV AEIITEVPPD EPVSATPDER IMELVLGKLA TTTTDTSSVP KFTHHQNNTI TLKRSLILSS RHGIRRKLIK
       410        420        430        440        450        460        470        480
QLGEHKRVYQ CNICSKIFQN SSNLSRHVRS HGDKLFKCEE CAKLFSRKES LKQHVSYKHS RNEVDGEYRY RCGTCEKTFR
       490        500        510        520        530        540        550        560
IESALEFHNC RTGLIAHPGE GGPGGSRLRD LPDDKTFQCE MCFRFFSTNS NLSKHKKKHG DKKFACEVCS KMFYRKDVML
       570        580        590        600        610        620        630        640
DHQRRHLEGV RRVKREDLEA GGENLVRYKK EPSGCPVCGK DIALMDDHQR EEFIGKIGIS SEENDDNSDE SADSEPHKYS
       650        660        670        680        690        700        710        720
CKRCQLTFGR GKEYLKHIME VHKEKGYGCS ICNRRFALKA TYHAHMVIHR ENLPDPNVQK YIHPCEICGR IFNSIGNLER
       730        740        750        760        770        780        790        800
HKLIHTGVKS HACEQCGKSF ARKDMLKEHM RVHDNVREYL CAECGKGMKT KHALRHHMKL HKGIKEYECK ECHRRFAQKV
       810        820        830        840        850        860        870        880
NMLKHCKRHT GIKDFMCELC GKTFSERNTM ETHKLIHTVG KQWTCSVCDK KYVTEYMLQK HVQLTHDKVE AQSCQLCGTK
       890        900        910        920        930        940        950        960
VSTRASMSRH MRRKHPEVLA VRIDDLDHLP ETTTIDASSI GIVQPELTLE QEDLAEGKHG KAAKRSHKRK QKPEEEAGAP
       970        980        990       1000       1010       1020       1030       1040
VPEDATFSEY SEKETEFTGS VGDETNSAVQ SIQQVVVTLG DPNVTTPSSS VGLTNITVTP ITTAAATQFT NLQPVAVGHL
      1050       1060       1070       1080       1090       1100       1110       1120
TTPERQLQLD NSILTVTFDT VSGSAMLHNR QNDVQIHPQP EASNPQSVAH FINLTTLVNS ITPLGSQLSD QHPLTWRAVP
      1130       1140       1150       1160
QTDVLPPSQP QAPPQQAAQP QVQAEQQQQQ MYSY
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1448	1	699.6392	-84.48	3	47.9	11.3	1	184-201	R.DIPPGTELRVWYAAFYAK.K	
1744	1	1030.2489	59.15	3	51.6	11.7	2	481-509	R.IESALEFHNCRTGLIAHPGEGGPGGSRLR.D	Carbamidomethyl: 10

Detailed Protein Report

Protein 543: PREDICTED: insulin-like growth factor 1 receptor isoform X2 [Homo sapiens]

Accession:	gi|530407102	**Score:**	23.0
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 [%]:**	1.4
		No. of unique Peptides:	1

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
1628	1	716.0279	112.96	3	50.1	12.0	0	56-73	K.ECGDLCPGTMEEKPMCEK.T	Carbamidomethyl: 2, 16; Oxidation: 10, 15

Detailed Protein Report

Protein 544: **PREDICTED: rho guanine nucleotide exchange factor 12 isoform X3 [Homo sapiens]**

Accession:	gi|530397943	**Score:**	22.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	161.8
Database Date:	2015-11-30	**pI:**	5.3
		Sequence Coverage [%]:	1.5
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MRAGVQTGDR	IIKVNGTLVT	HSNHLEVVKL	IKSGSYVALT	VQGRPPGSPQ	IPLADSEVEP	SVIGHMSPIM	TSPHSPGASG
90	100	110	120	130	140	150	160
NMERITSPVL	MGEENNVVHN	QKVEILRKML	QKEQERLQLL	QEDYNRTPAQ	RLLKEIQEAK	KHIPQLQEQL	SKATGSAQDG
170	180	190	200	210	220	230	240
AVVTPSRPLG	DTLTVSEAET	DPGDVLGRTD	CSSGDASRPS	SDNADSPKSG	PKERIYLEEN	PEKSETIQDT	DTQSLVGSPS
250	260	270	280	290	300	310	320
TRIAPHIIGA	EDDDFGTEHE	QINGQCSCFQ	SIELLKSRPA	HLAVFLHHVV	SQFDPATLLC	YLYSDLYKHT	NSKETRRIFL
330	340	350	360	370	380	390	400
EFHQFFLDRS	AHLKVSVPDE	MSADLEKRRP	ELIPEDLHRH	YIQTMQERVH	PEVQRHLEDF	RQKRSMGLTL	AESELTKLDA
410	420	430	440	450	460	470	480
ERDKDRLTLE	KERTCAEQIV	AKIEEVLMTA	QAVEEDKSST	MQYVILMYMK	HLGVKVKEPR	NLEHKRGRIG	FLPKIKQSMK
490	500	510	520	530	540	550	560
KDKEGEEKGK	RRGFPSILGP	PRRPSRHDNS	AIGRAMELQK	ARHPKHLSTP	SSVSPEPQDS	AKLRQSGLAN	EGTDAGYLPA
570	580	590	600	610	620	630	640
NSMSSVASGA	SFSQEGGKEN	DTGSKQVGET	SAPGDTLDGT	PRTLNTVFDF	PPPPLDQVQE	EECEVERVTE	HGTPKPFRKF
650	660	670	680	690	700	710	720
DSVAFGESQS	EDEQFENDLE	TDPPNWQQLV	SREVLLGLKP	CEIKRQEVIN	ELFYTERAHV	RTLKVLDQVF	YQRVSREGIL
730	740	750	760	770	780	790	800
SPSELRKIFS	NLEDILQLHI	GLNEQMKAVR	KRNETSVIDQ	IGEDLLTWFS	GPGEEKLKHA	AATFCSNQPF	ALEMIKSRQK
810	820	830	840	850	860	870	880
KDSRFQTFVQ	DAESNPLCRR	LQLKDIIPTQ	MQRLTKYPLL	LDNIAKYTEW	PTEREKVKKA	ADHCRQILNY	VNQAVKEAEN
890	900	910	920	930	940	950	960
KQRLEDYQRR	LDTSSLKLSE	YPNVEELRNL	DLTKRKMIHE	GPLVWKVNRD	KTIDLYTLLL	EDILVLLQKQ	DDRLVLRCHS
970	980	990	1000	1010	1020	1030	1040
KILASTADSK	HTFSPVIKLS	TVLVRQVATD	NKALFVISMS	DNGAQIYELV	AQTVSEKTVW	QDLICRMAAS	VKEQSTKPIP
1050	1060	1070	1080	1090	1100	1110	1120
LPQSTPGEGD	NDEEDPSKLK	EEQHGISVTG	LQSPDRDLGL	ESTLISSKPQ	SHSLSTSGKS	EVRDLFVAER	QFAKEQHTDG
1130	1140	1150	1160	1170	1180	1190	1200
TLKEVGEDYQ	IAIPDSHLPV	SEERWALDAL	RNLGLLKQLL	VQQLGLTEKS	VQEDWQHFPR	YRTASQGPQT	DSVIQNSENI
1210	1220	1230	1240	1250	1260	1270	1280
KAYHSGEGHM	PFRTGTGDIA	TCYSPRTSTE	SFAPRDSVGL	APQDSQASNI	LVMDHMIMTP	EMPTMEPEGG	LDDSGEHFFD
1290	1300	1310	1320	1330	1340	1350	1360
AREAHSDENP	SEGDGAVNKE	EKDVNLRISG	NYLILDGYDP	VQESSTDEEV	ASSLTLQPMT	GIPAVESTHQ	QQHSPQNTHS
1370	1380	1390	1400	1410	1420	1430	1440
DGAISPFTPE	FLVQQRWGAM	EYSCFEIQSP	SSCADSQSQI	MEYIHKIEAD	LEHLKKVEES	YTILCQRLAG	SALTDKHSDK
1450							
S							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
85	1	710.2749	-87.79	2	30.8	12.0	0	335-347	K.VSVPDEMSADLEK.R	
1443	1	1022.6499	109.61	1	47.7	10.9	1	458-465	K.EPRNLEHK.R	

Detailed Protein Report

Protein 545: **complement component 1 Q subcomponent-binding protein, mitochondrial precursor [Homo sapiens]**

Accession:	gi|4502491	**Score:**	22.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	31.3
Database Date:	2015-11-30	**pI:**	4.6
		Sequence Coverage [%]:	10.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLPLLRCVPR	VLGSSVAGLR	AAAPASPFRQ	LLQPAPRLCT	RPFGLLSVRA	GSERRPGLLR	PRGPCACGCG	CGSLHTDGDK
90	100	110	120	130	140	150	160
AFVDFLSDEI	KEERKIQKHK	TLPKMSGGWE	LELNGTEAKL	VRKVAGEKIT	VTFNINNSIP	PTFDGEEEPS	QGQKVEEQEP
170	180	190	200	210	220	230	240
ELTSTPNFVV	EVIKNDDGKK	ALVLDCHYPE	DEVGQEDEAE	SDIFSIREVS	FQSTGESEWK	DTNYTLNTDS	LDWALYDHLM
250	260	270	280	290			
DFLADRGVDN	TFADELVELS	TALEHQEYIT	FLEDLKSFVK	SQ			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1934	1	840.8059	-11.17	2	54.3	12.6	0	63-80	R.GPCACGCGCGSLHTDGDK.A	

Detailed Protein Report

Protein 546: histone-lysine N-methyltransferase SETD1B [Homo sapiens]

Accession:	gi|210032580	**Score:**	22.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	208.6
Database Date:	2015-11-30	**pI:**	4.7
		Sequence Coverage [%]:	0.8
		No. of unique Peptides:	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MENSHPPHHH	HQQPPPQPGP	SGERRNHHWR	SYKLMIDPAL	KKGHHKLYRY	DGQHFSLAMS	SNRPVEIVED	PRVVGIWTKN
90	100	110	120	130	140	150	160
KELELSVPKF	KIDEFYVGPV	PPKQVTFAKL	NDNIRENFLR	DMCKKYGEVE	EVEILYNPKT	KKHLGIAKVV	FATVRGAKDA
170	180	190	200	210	220	230	240
VQHLHSTSVM	GNIIHVELDT	KGETRMRFYE	LLVTGRYTPQ	TLPVGELDAV	SPIVNETLQL	SDALKRLKDG	GLSAGCGSGS
250	260	270	280	290	300	310	320
SSVTPNSGGT	PFSQDTAYSS	CRLDTPNSYG	QGTPLTPRLG	TPFSQDSSYS	SRQPTPSYLF	SQDPAVTFKA	RRHESKFTDA
330	340	350	360	370	380	390	400
YNRRHEHHYV	HNSPAVTAVA	GATAAFRGSS	DLPFGAVGGT	GGSSGPPFKA	QPQDSATFAH	TPPPAQATPA	PGFKSAFSPY
410	420	430	440	450	460	470	480
QTPVAHFPPP	PEEPTATAAF	GARDSGEFRR	APAPPPLPPA	EPLAKEKPGT	PPGPPPPDTN	SMELGGRPTF	GWSPEPCDSP
490	500	510	520	530	540	550	560
GTPTLESSPA	GPEKPHDSLD	SRIEMLLKEQ	RTKLLFLREP	DSDTELQMEG	SPISSSSSQL	SPLAPFGTNS	QPGFRGPTPP
570	580	590	600	610	620	630	640
SSRPSSTGLE	DISPTPLPDS	DEDEELDLGL	GPRPPPEPGP	PDPAGLLSQT	AEVALDLVGD	RTPTSEKMDE	GQQSSGEDME
650	660	670	680	690	700	710	720
ISDDEMPSAP	ITSADCPKPM	VVTPGAAAVA	APSVLAPTLP	LPPPPGFPPL	PPPPPPPPPQ	PGFPMPPPLP	PPPPPPPPAH
730	740	750	760	770	780	790	800
PAVTVPPPPL	PAPPGVPPPP	ILPPLPPFPP	GLFPVMQVDM	SHVLGGQWGG	MPMSFQMQTQ	VLSRLMTGQG	ACPYPPFMAA
810	820	830	840	850	860	870	880
AAAAASAGLQ	FVNLPPYRGP	FSLSNSGPGR	GQHWPPLPKF	DPSVPPPGYM	PRQEDPHKAT	VDGVLLVVLK	ELKAIMKRDL
890	900	910	920	930	940	950	960
NRKMVEVVAF	RAFDEWWDKK	ERMAKASLTP	VKSGEHKDED	RPKPKDRIAS	CLLESWGKGE	GLGYEGLGLG	IGLRGAIRLP
970	980	990	1000	1010	1020	1030	1040
SFKVKRKEPP	DTTSSGDQKR	LRPSTSVDEE	DEESERERDR	DMADTPCELA	KRDPKGVGVR	RRPARPLELD	SGGEEDEKES
1050	1060	1070	1080	1090	1100	1110	1120
LSEEQESTEE	EEEAEEEEEE	EDDDDDDSDD	RDESENDDED	TALSEASEKD	EGDSDEEETV	SIVTSKAEAT	SSSESSESSE
1130	1140	1150	1160	1170	1180	1190	1200
FESSSESSPS	SSEDEEEVVA	REEEEEEEEE	EMVAEESMAS	AGPEDFEQDG	EEAALAPGAP	AVDSLGMEEE	VDIETEAVAP
1210	1220	1230	1240	1250	1260	1270	1280
EERPSMLDEP	PLPVGVEEPA	DSREPPEEPG	LSQEGAMLLS	PEPPAKEVEA	RPPLSPERAP	EHDLEVEPEP	PMMLPLPLQP
1290	1300	1310	1320	1330	1340	1350	1360
PLPPPRPPRP	PSPPPEPETT	DASHPSVPPE	PLAEDHPPHT	PGLCGSLAKS	QSTETVPATP	GGEPPLSGGS	SGLSLSSPQV
1370	1380	1390	1400	1410	1420	1430	1440
PGSPFSYPAP	SPSLSSGGLP	RTPGRDFSFT	PTFSEPSGPL	LLPVCPLPTG	RRDERSGPLA	SPVLLETGLP	LPLPLPLPLP
1450	1460	1470	1480	1490	1500	1510	1520
LALPAVLRAQ	ARAPTPLPPL	LPAPLASCPP	PMKRKPGRPR	RSPPSMLSLD	GPLVRPPAGA	ALGRELLLLP	GQPQTPVFPS
1530	1540	1550	1560	1570	1580	1590	1600
THDPRTVTLD	FRNAGIPAPP	PPLPPQPPPP	PPPPPVEPTK	LPFKELDNQW	PSEAIPPGPR	GRDEVTEEYM	ELAKSRGPWR
1610	1620	1630	1640	1650	1660	1670	1680
RPPKKRHEDL	VPPAGSPELS	PPQPLFRPRS	EFEEMTILYD	IWNGGIDEED	IRFLCVTYER	LLQQDNGMDW	LNDTLWVYHP
1690	1700	1710	1720	1730	1740	1750	1760
STSLSSAKKK	KRDDGIREHV	TGCARSEGFY	TIDKKDKLRY	LNSSRASTDE	PPADTQGMSI	PAQPHASTRA	GSERRSEQRR
1770	1780	1790	1800	1810	1820	1830	1840
LLSSFTGSCD	SDLLKFNQLK	FRKKKLKFCK	SHIHDWGLFA	MEPIAADEMV	IEYVGQNIRQ	VIADMREKRY	EDEGIGSSYM
1850	1860	1870	1880	1890	1900	1910	1920
FRVDHDTIID	ATKCGNFARF	INHSCNPNCY	AKVITVESQK	KIVIYSKQHI	NVNEEITYDY	KFPIEDVKIP	CLCGSENCRG
1930							
TLN							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
837	1	801.1846	-354.77	1	40.0	10.6	2	878-883	K.RDLNRK.M	

Detailed Protein Report

Protein 547: **hepatoma-derived growth factor isoform a [Homo sapiens]**

Accession:	gi|4758516	**Score:**	22.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	26.8
Database Date:	2015-11-30	**pI:**	4.6
		Sequence Coverage [%]:	12.9
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MSRSNRQKEY KCGDLVFAKM KGYPHWPARI DEMPEAAVKS TANKYQVFFF GTHETAFLGP KDLFPYEESK EKFGKPNKRK
        90        100        110        120        130        140        150        160
GFSEGLWEIE NNPTVKASGY QSSQKKSCVE EPEPEPEAAE GDGDKKGNAE GSSDEEGKLV IDEPAKEKNE KGALKRRAGD
       170        180        190        200        210        220        230        240
LLEDSPKRPK EAENPEGEEK EAATLEVERP LPMEVEKNST PSEPGSGRGP PQEEEEEEDE EEEATKEDAE APGIRDHESL
       250
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1973	1	682.2866	-59.46	3	54.8	11.7	1	127-146	K.GNAEGSSDEEGKLVIDEPAK.E	

Detailed Protein Report

Protein 548: leucine-rich repeat and transmembrane domain-containing protein 2 precursor [Homo sapiens]

Accession:	gi|84781739	**Score:**	22.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	41.1
Database Date:	2015-11-30	**pI:**	9.5
		Sequence Coverage [%]:	6.5
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|578822678	refseq_human (refseq_human_20140103.fasta)	PREDICTED: leucine-rich repeat and transmembrane domain-containing protein 2 isoform X1 [Homo sapiens]
gi|255652964	refseq_human (refseq_human_20140103.fasta)	leucine-rich repeat and transmembrane domain-containing protein 2 precursor [Homo sapiens]
gi|255652962	refseq_human (refseq_human_20140103.fasta)	leucine-rich repeat and transmembrane domain-containing protein 2 precursor [Homo sapiens]

10	20	30	40	50	60	70	80
MLAPGSSPGQ	RGRLALQWRQ	VSWITCWIAL	YAVEALPTCP	FSCKCDSRSL	EVDCSGLGLT	TVPPDVPAAT	RTLLLLNNKL
90	100	110	120	130	140	150	160
SALPSWAFAN	LSSLQRLDLS	NNFLDRLPRS	IFGDLTNLTE	LQLRNNSIRT	LDRDLLRHSP	LLRHLDLSIN	GLAQLPPGLF
170	180	190	200	210	220	230	240
DGLLALRSLS	LRSNRLQNLD	RLTFEPLANL	QLLQVGDNPW	ECDCNLREFK	HWMEWFSYRG	GRLDQLACTL	PKELRGKDMR
250	260	270	280	290	300	310	320
MVPMEMFNYC	SQLEDENSSA	GLDIPGPPCT	KASPEPAKPK	PGAEPEPEPS	TACPQKQRHR	PASVRRAMGT	VIIAGVVCGV
330	340	350	360	370	380		
VCIMMVVAAA	YGCIYASLMA	KYHRELKKRQ	PLMGDPEGEH	EDQKQISSVA			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1746	1	1272.3522	103.26	2	51.8	22.8	0	144-167	R.HLDLSINGLAQLPPGLFDGLLALR.S	

Protein 549: zinc finger protein 674 isoform 2 [Homo sapiens]

Accession: gi|226371655
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 22.8
MW [kDa]: 66.5
pI: 10.3
Sequence Coverage [%]: 6.1
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MAMSQESLTF	KDVFVDFTLE	EWQQLDSAQK	NLYRDVMLEN	YSHLVSVGHL	VGKPDVIFRL	GPGDESWMAD	GGTPVRTCAV
90	100	110	120	130	140	150	160
WEVDEQIDHY	KESQDKFLWQ	AAFIGKETLK	DESGQECKIC	RKIIYLNTDF	VSVKQRLPKY	YSWERCSKHH	LNFLGQNRSY
170	180	190	200	210	220	230	240
VRKKDDGCKA	YWKVCLHYNL	HKAQPAERFF	DPNQRGKALH	QKQALRKSQR	SQTGEKLYKC	TECGKVFIQK	ANLVVHQRTH
250	260	270	280	290	300	310	320
TGEKPYECCE	CAKAFSQKST	LIAHQRTHTG	EKPYECSECG	KTFIQKSTLI	KHQRTHTGEK	PFVCDKCPKA	FKSSYHLIRH
330	340	350	360	370	380	390	400
EKTHIRQAFY	KGIKCTTSSL	IYQRIHTSEK	PQCSEHGKAS	DEKPSPTKHW	RTHTKENIYE	CSKCGKSFRG	KSHLSVHQRI
410	420	430	440	450	460	470	480
HTGEKPYECS	ICGKTFSGKS	HLSVHHRTHT	GEKPYECRRC	GKAFGEKSTL	IVHQRMHTGE	KPYKCNECGK	AFSEKSPLIK
490	500	510	520	530	540	550	560
HQRIHTGERP	YECTDCKKAF	SRKSTLIKHQ	RIHTGEKPYK	CSECGKAFSV	KSTLIVHHRT	HTGEKPYECR	DCGKAFSGKS
570	580						
TLIKHQRSHT	GDKNL						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1639	1	1136.1099	81.18	2	50.4	11.8	2	540-559	R.THTGEKPYECRDCGKAFSGK.S	Carbamidomethyl: 13

Protein 550: fibrinogen-like protein 1 precursor [Homo sapiens]

Accession:	gi|42544189	**Score:**	22.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	36.4
Database Date:	2015-11-30	**pI:**	5.5
		Sequence Coverage [%]:	2.9
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|42544202	refseq_huma (refseq_human_20140103.fasta)	fibrinogen-like protein 1 precursor [Homo sapiens]
gi|42544200	refseq_huma (refseq_human_20140103.fasta)	fibrinogen-like protein 1 precursor [Homo sapiens]
gi|42544198	refseq_huma (refseq_human_20140103.fasta)	fibrinogen-like protein 1 precursor [Homo sapiens]

10	20	30	40	50	60	70	80
MAKVFSFILV	TTALTMGREI	SALEDCAQEQ	MRLRAQVRLL	ETRVKQQQVK	IKQLLQENEV	QFLDKGDENT	VIDLGSKRQY
90	100	110	120	130	140	150	160
ADCSEIFNDG	YKLSGFYKIK	PLQSPAEFSV	YCDMSDGGGW	TVIQRRSDGS	ENFNRGWKDY	ENGFGNFVQK	HGEYWLGNKN
170	180	190	200	210	220	230	240
LHFLTTQEDY	TLKIDLADFE	KNSRYAQYKN	FKVGDEKNFY	ELNIGEYSGT	AGDSLAGNFH	PEVQWWASHQ	RMKFSTWDRD
250	260	270	280	290	300	310	320
HDNYEGNCAE	EDQSGWWFNR	CHSANLNGVY	YSGPYTAKTD	NGIVWYTWHG	WWYSLKSVVM	KIRPNDFIPN	VI

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1516	1	513.1182	-194.06	2	48.6	22.8	0	127-135	R.SDGSENFNR.G	

Detailed Protein Report

Protein 551: nucleolar protein 11 [Homo sapiens]

Accession:	gi|21361468	**Score:**	22.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	81.1
Database Date:	2015-11-30	**pI:**	5.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAALEEEFTL	SSVVLSAGPE	GLLGVEQSDK	TDQFLVTDSG	RTVILYKVSD	QKPLGSWSVK	QGQIITCPAV	CNFQTGEYVV
90	100	110	120	130	140	150	160
VHDNKVLRIW	NNEDVNLDKV	FKATLSAEVY	RILSVQGTEP	LVLFKEGAVR	GLEALLADPQ	QKIETVISDE	EVIKWTKFFV
170	180	190	200	210	220	230	240
VFRHPVLIFI	TEKHGNYFAY	VQMFNSRILT	KYTLLLGQDE	NSVIKSFTAS	VDRKFISLMS	LSSDGCIYET	LIPIRPADPE
250	260	270	280	290	300	310	320
KNQSLVKSLL	LKAVVSGNAR	NGVALTALDQ	DHVAVLGSPL	AASKECLSVW	NIKFQTLQTS	KELPQGTSGQ	LWYYGEHLFM
330	340	350	360	370	380	390	400
LHGKSLTVIP	YKCEVSSLAG	ALGKLKHSQD	PGTHVVSHFV	NWETPQGCGL	GFQNSEQSRR	ILRRRKIEVS	LQPEVPPSKQ
410	420	430	440	450	460	470	480
LLSTIMKDSE	KHIEVEVRKF	LALKQTPDFH	TVIGDTVTGL	LERCKAEPSF	YPRNCLMQLI	QTHVLSYSLC	PDLMEIALKK
490	500	510	520	530	540	550	560
KDVQLLQLCL	QQFPDIPESV	TCACLKIFLS	IGDDSLQETD	VNMESVFDYS	INSVHDEKME	EQTEILQNGF	NPEEDKCNNC
570	580	590	600	610	620	630	640
DQELNKKPQD	ETKESTSCPV	VQKRAALLNA	ILHSAYSETF	LLPHLKDIPA	QHITLFLKYL	YFLYLKCSEN	ATMTLPGIHP
650	660	670	680	690	700	710	720
PTLNQIMDWI	CLLLDANFTV	VVMMPEAKRL	LINLYKLVKS	QISVYSELNK	IEVSFRELQK	LNQEKNNRGL	YSIEVLELF

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
913	1	645.6782	-230.66	2	40.9	11.4	1	574-584	K.ESTSCPVVQKR.A	Carbamidomethyl: 5

Detailed Protein Report

Protein 552: PREDICTED: mitochondrial Rho GTPase 2 isoform X9 [Homo sapiens]

Accession:	gi|578828338	**Score:**	22.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	52.3
Database Date:	2015-11-30	**pI:**	6.7
		Sequence Coverage [%]:	5.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGGPRRGPVG	NKSDLRSGSS	MEAVLPIMSQ	FPEIETCVEC	SAKNLRNISE	LFYYAQKAVL	HPTAPLYDPE	AKQKSCFGHP
90	100	110	120	130	140	150	160
LAPQALEDVK	TVVCRNVAGG	VREDRLTLDG	FLFLNTLFIQ	RGRHETTWTI	LRRFGYSDAL	ELTADYLSPL	IHVPPGCSTE
170	180	190	200	210	220	230	240
LNHLGYQFVQ	RVFEKHDQDR	DGALSPVELQ	SLFSVFPAAP	WGPELPRTVR	TEAGRLPLHG	YLCQWTLVTY	LDVRSCLGHL
250	260	270	280	290	300	310	320
GYLGYPTLCE	QDQAHAITVT	REKRLDQEKG	QTQRSVLLCK	VVGARGVGKS	AFLQAFLGRG	LGHQDTREQP	PGYAIDTVQV
330	340	350	360	370	380	390	400
NGQEKYLILC	EVGTDGLLAT	SLDATCDVAC	LMFDGSDPKS	FAHCASVYKH	HYMDGQTPCL	FVSSKADLPE	GVAVSGPSPA
410	420	430	440	450	460	470	480
EFCRKHRLPA	PVPFSCAGPA	EPSTTIFTQL	ATMAAFPHLV	HAELHPSSFW	LRGLLGVVGA	AVAAVLSFSL	YRVLVKSQ

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2627	2	727.3858	-48.33	1	63.6	12.4	1	6-12	R.RGPVGNK.S	

Detailed Protein Report

Protein 553: gamma-tubulin complex component 6 [Homo sapiens]

Accession:	gi|56788364	**Score:**	22.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	200.4
Database Date:	2015-11-30	**pI:**	5.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MASITQLFDD	LCEALLPAAK	THLGQRSVNR	KRAKRSLKKV	AYNALFTNLF	QDETQQLQPD	MSKLPARNKI	LMLSFDLRVG
90	100	110	120	130	140	150	160
GLGPKADRLE	ELVEELEAAP	CCPLLEVGSV	LDLLVQLAGS	GPPQVLPRKR	DYFLNNKHVG	RNVPYSGYDC	DDLSVFEMDV
170	180	190	200	210	220	230	240
QSLISREECL	CHSMIQETLQ	VMEAAPGTGL	PTVGLFSFGD	PCGDRFERDT	RVSLFGALVH	SRTYDMDVRL	GLPPVPDNAD
250	260	270	280	290	300	310	320
LSGLAIKVPP	SVDQWEDEGF	QSASNLTPDS	QSEPSVTPDV	DLWEAALTYE	ASKRRCWERV	GCPPGHREEP	YLTEAGRDAF
330	340	350	360	370	380	390	400
DKFCRLHQGE	LQLLAGGVLQ	APQPVLVKEC	ELVKDVLNVL	IGVVSATFSL	CQPAQAFVVK	RGVHVSGASP	ESISSLLSEV
410	420	430	440	450	460	470	480
AEYGTCYTRL	SHFSLQPVLD	SLYSKGLVFQ	AFTSGLRRYL	QYYRACVLST	PPTLSLLTIG	FLFKKLGRQL	RYLAELCGVG
490	500	510	520	530	540	550	560
AVLPGTCGGG	PRAAFPTGVK	LLSYLYQEAL	HNCSNEHYPV	LLSLLKTSCE	PYTRFIHDWV	YSGVFRDAYG	EFMIQVNHEY
570	580	590	600	610	620	630	640
LSFRDKLYWT	HGYVLISKEV	EDCVPVFLKH	IAHDIYVCGK	TINLLKLCCP	RHYLCWSDVP	VPRISVIFSL	EELKEIEKDC
650	660	670	680	690	700	710	720
AVYVGRMERV	ARHSSVSKEE	KELRMEIAKQ	ELIAHAREAA	SRVLSALSDR	QMSERMALDA	RKREQFQRLK	EQFVKDQERR
730	740	750	760	770	780	790	800
QAARQEELDD	DFSYARELRD	RERRLKSLEE	ELERKARQAL	VDHYSKLSAE	AARREQKALW	RIQRHRLESA	RLRFLLEDEK
810	820	830	840	850	860	870	880
HIQEMLKAVS	EAHQPQEPPD	VLLSVHPQVT	SPGPEHPEGG	QGCDSGSAEQ	HSPAWDGWNR	PGLLTPQPLK	PLAVGAGGRG
890	900	910	920	930	940	950	960
LQQAEGARPF	SDSLSIGDFL	PVGPGAEPSV	QTGMVPLLEV	ALQTINLDLP	PSAPGEAPAA	ASTQPSRPQE	YDFSTVLRPA
970	980	990	1000	1010	1020	1030	1040
VATSPAPGPL	QAAECSLGSS	GLQLWEDSCG	KMDACGSASR	ETLLPSHPPR	RAALEEGSSQ	PTERLFGQVS	GGGLPTGDYA
1050	1060	1070	1080	1090	1100	1110	1120
SEIAPTRPRW	NTHGHVSDAS	IRVGENVSDV	APTQPRWNTH	GHVSNASISL	GESVSDVAPT	RPRWNIHGHV	SNASIRVGEN
1130	1140	1150	1160	1170	1180	1190	1200
VSDVAPTRPR	WNTHGHVSNA	SIRVGENVSD	VAPTRPRWNT	HGHVSDASIS	LGESVSDMAP	ARPRWNTHGH	VSDASISLGE
1210	1220	1230	1240	1250	1260	1270	1280
SVSDMAPTRP	RWNTHGHVSD	TSIRVGENVS	DVAPIRSRCN	THGHVSDASI	SLGEPVSDVV	STRPRWNTHV	PIPPPHMVLG
1290	1300	1310	1320	1330	1340	1350	1360
ALSPEAEPNT	PRPQQSPPGH	TSQSALSLGA	QSTVLDCGPR	LPVEVGPSLS	SPSSGCGEGS	ISVGENVSDV	APTQPWWPNT
1370	1380	1390	1400	1410	1420	1430	1440
PGDSVSEELG	PGRSGDTEDL	SPNWPLNSQE	DTAAQSSPGR	GEEAEASAAE	AQGGEQAYLA	GLAGQYHLER	YPDSYESMSE
1450	1460	1470	1480	1490	1500	1510	1520
PPIAHLLRPV	LPRAFAFPVD	PQVQSAADET	AVQLSELLTL	PVLMKRSITA	PLAAHISLVN	KAAVDYFFVE	LHLEAHYEAL
1530	1540	1550	1560	1570	1580	1590	1600
RHFLLMEDGE	FAQSLSDLLF	EKLGAGQTPG	ELLNPLVLNS	VLSKALQCSL	HGDTPHASNL	SLALKYLPEV	FAPNAPDVLS
1610	1620	1630	1640	1650	1660	1670	1680
CLELRYKVDW	PLNIVITEGC	LSKYSGVFSF	LLQLKLMMWA	LKDVCFHLKR	TALLSHMAGS	VQFRQLQLFK	HEMQHFVKVI
1690	1700	1710	1720	1730	1740	1750	1760
QGYIANQILH	VTWCEFRARL	ATVGDLEEIQ	RAHAEYLHKA	VFRGLLTEKA	APVMNVIHSI	FSLVLKFRSQ	LISQAWGPPG
1770	1780	1790	1800	1810	1820		
GPRGAEHPNF	ALMQQSYNTF	KYYSHFLFKV	VTKLVNRGYQ	PHLEDFLLRI	NFNNYYQDA		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2334	1	1023.8623	-142.84	2	59.1	12.7	0	472-492	R.YLAELCGVGAVLPGTCGGGPR.A	Carbamidomethyl: 6

Detailed Protein Report

Protein 554: **PREDICTED: receptor-type tyrosine-protein phosphatase mu isoform X4 [Homo sapiens]**

Accession:	gi|578832170	**Score:**	22.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	161.1
Database Date:	2015-11-30	**pI:**	6.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPSGSFMLVN	ASGRPEGQRA	HLLLPQLKEN	DTHCIDFHYF	VSSKSNSPPG	LLNVYVKVNN	GPLGNPIWNI	SGDPTRTWNR
90	100	110	120	130	140	150	160
AELAISTFWP	NFYQVIFEVI	TSGHQGYLAI	DEVKVLGHPC	TRTPHFLRIQ	NVEVNAGQFA	TFQCSAIGRT	VAGDRLWLQG
170	180	190	200	210	220	230	240
IDVRDAPLKE	IKVTSSRRFI	ASFNVVNTTK	RDAGKYRCMI	RTEGGVGISN	YAELVVKEPP	VPIAPPQLAS	VGATYLWIQL
250	260	270	280	290	300	310	320
NANSINGDGP	IVAREVEYCT	ASGSWNDRQP	VDSTSYKIGH	LDPDTEYEIS	VLLTRPGEGG	TGSPGPALRT	RTKCADPMRG
330	340	350	360	370	380	390	400
PRKLEVVEVK	SRQITIRWEP	FGYNVTRCHS	YNLTVHYCYQ	VGGQEQVREE	VSWDTENSHP	QHTITNLSPY	TNVSVKLILM
410	420	430	440	450	460	470	480
NPEGRKESQE	LIVQTDEDLP	GAVPTESIQG	STFEEKIFLQ	WREPTQTYGV	ITLYEITYKA	VSSFDPEIDL	SNQSGRVSKL
490	500	510	520	530	540	550	560
GNETHFLFFG	LYPGTTYSFT	IRASTAKGFG	PPATNQFTTK	ISAPSMPAYE	LETPLNQTDN	TVTVMLKPAH	SRGAPVSVYQ
570	580	590	600	610	620	630	640
IVVEEERPRR	TKKTTEILKC	YPVPIHFQNA	SLLNSQYYFA	AEFPADSLQA	AQPFTIGDNK	TYNGYWNTPL	LPYKSYRIYF
650	660	670	680	690	700	710	720
QAASRANGET	KIDCVQVATK	AAIIVTQLTT	PYIRIAPAAG	DGQLTGAATP	KPVPEPEKQT	DHTVKIAGVI	AGILLFVIIF
730	740	750	760	770	780	790	800
LGVVLVMKKR	KLAKKRKETM	SSTRQEMTVM	VNSMDKSYAE	QGTNCDEAFS	FMDTHNLNGR	SVSSPSSFTM	KTNTLSTSVP
810	820	830	840	850	860	870	880
NSYYPDETHT	MASDTSSLVQ	SHTYKKREPA	DVPYQTGQLH	PAIRVADLLQ	HITQMKCAEG	YGFKEEYESF	FEGQSAPWDS
890	900	910	920	930	940	950	960
AKKDENRMKN	RYGNIIAYDH	SRVRLQTIEG	DTNSDYINGN	YIDGYHRPNH	YIATQGPMQE	TIYDFWRMVW	HENTASIIMV
970	980	990	1000	1010	1020	1030	1040
TNLVEVGRVK	CCKYWPDDTE	IYKDIKVTLI	ETELLAEYVI	RTFAVEKGGA	GGEANCSPSR	EVSQRGVHEI	REIRQFHFTG
1050	1060	1070	1080	1090	1100	1110	1120
WPDHGVPYHA	TGLLGFVRQV	KSKSPPSAGP	LVVHCSAGAG	RTGCFIVIDI	MLDMAEREGV	VDIYNCVREL	RSRRVNMVQT
1130	1140	1150	1160	1170	1180	1190	1200
EEQYVFIHDA	ILEACLCGDT	SVPASQVRSL	YYDMNKLDPQ	TNSSQIKEEF	RTLNMVTPTL	RVEDCSIALL	PRNHEKNRCM
1210	1220	1230	1240	1250	1260	1270	1280
DILPPDRCLP	FLITIDGESS	NYINAALMDS	YKQPSAFIVT	QHPLPNTVKD	FWRLVLDYHC	TSVVMLNDVD	PAQLCPQYWP
1290	1300	1310	1320	1330	1340	1350	1360
ENGVHRHGPI	QVEFVSADLE	EDIISRIFRI	YNAARPQDGY	RMVQQFQFLG	WPMYRDTPVS	KRSFLKLIRQ	VDKWQEEYNG
1370	1380	1390	1400	1410	1420	1430	1440
GEGRTVVHCL	NGGGRSGTFC	AISIVCEMLR	HQRTVDVFHA	VKTLRNNKPN	MVDLLDQYKF	CYEVALEYLN	SG

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1436	1	927.4440	-10.35	3	47.6	22.6	1	1365-1390	R.TVVHCLNGGGRSGTFCAISIVCEMLR.H	Carbamidomethyl: 22

Detailed Protein Report

Protein 555: PREDICTED: exophilin-5 isoform X3 [Homo sapiens]

Accession:	gi|578822067	**Score:**	22.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	201.0
Database Date:	2015-11-30	**pI:**	6.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.0
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MREESGMPPP	WDASLLENEF	FQVLDDLDSK	LAQEQSASSV	NTRTPLNYGS	RTQFGHFYSS	GNRHGNITER	HKKHYNETSN
90	100	110	120	130	140	150	160
MSIYDILRPG	TPREGFKTFS	PRTSTIYDMY	RTREPRVFKE	DYVQKNTFGS	TSLCFDSRQR	SALPATGHFT	ARSLHFPATT
170	180	190	200	210	220	230	240
QSKSGFIPPR	HQQSPKRTPL	SSIIWNRSDS	SRDRENQEEF	LRAPSPMEID	PADKYVYPRG	FQENKRYESY	HSQNVYQRVS
250	260	270	280	290	300	310	320
LNAPMENAMS	PDTFENSENM	PFYHQSNTFT	RSFFSNTFGR	SGEQRRFGQG	PFWGQEKGHS	FWSDFHRSRK	SFSSSDRDFE
330	340	350	360	370	380	390	400
MISMEANSVS	AIHGHNVSSE	HWESFSSGYG	TDVSRGQEEP	HPWQFDFQRS	TLDSMVVSHG	NETQLTPHFG	TPNVCSMTGS
410	420	430	440	450	460	470	480
SYHVKSSELV	SQQDSSPVEV	HINKEASSFG	IAQTLASSFK	TSFSQISDDR	RNPQSPNLQN	PTVTLQKIFP	NKPASHPMRS
490	500	510	520	530	540	550	560
HTEVTVTSSN	SVDSLPLAKS	QPNILVTEVN	NEKDLNESIS	EEDKQLSKMD	QTNKAGEIPQ	PVSQTGISNS	LPDFQNPLSQ
570	580	590	600	610	620	630	640
DSAKSNGFGF	NASTIISSKK	SPRVFSRKDT	SKMYIPHTDK	SNDIKQDKRF	TENRKLGSTA	SLPFIQEHRT	PPSFPRTDQG
650	660	670	680	690	700	710	720
CHQELTVNNE	DISRIITNNH	WSSALTDTQN	AQYSKCKLTP	GHKTSCDSLD	LSSAALPDSS	PSKNSSLDAP	VVPSTTVFSR
730	740	750	760	770	780	790	800
RSPSDKDPSL	GEREEKDNAG	KNQKNQFIVS	HSENQERNDS	PVPTHDEVVD	VKCHSHSPFR	NERGKGKIRH	HISCIEKLSK
810	820	830	840	850	860	870	880
TESISVPTSD	HRSLIEANQS	NSKVSELDTI	YCTLPRKSSS	FLIHGRQSGS	KIMAASLRNG	PPPFQIKNNV	EDAMGNYMLN
890	900	910	920	930	940	950	960
KFSPSSPESA	NECSKVLSDS	ALEAPEATER	MTNVKSSGST	SVRKGPLPFL	INRAMSCPSG	EPHASTGREG	RKKPLTSGMD
970	980	990	1000	1010	1020	1030	1040
ASELTPRAWE	RIISPVESDS	SVRDCSLTKR	QHQKENFQEY	TEKEGKMAAS	RRSVFALSNE	DPLPFCSDLS	GKERGKTLHK
1050	1060	1070	1080	1090	1100	1110	1120
VKTTSTFSVS	GDEDNVKCLE	VVSIYYTLPR	KPSKKFCNLL	QQYTQNTNLL	IESPQVETET	FPNALEKDKQ	NYSTREQSGT
1130	1140	1150	1160	1170	1180	1190	1200
PSCENLKMSV	NSDQTLTTEN	MTAFRLSNRG	PLAPTLQEMA	SVEAAVSLPE	EESKAREIFS	DNLAKTPLGD	SENKKERGKK
1210	1220	1230	1240	1250	1260	1270	1280
LQSETLHTSL	MLQRKNVSEE	KSENCQQSIN	SSNSGPSSLP	ALSEVNIGNS	QTRRSSWECT	GSGRAIPFTG	SGKCPQKDHT
1290	1300	1310	1320	1330	1340	1350	1360
STAVGDGSSG	SQPREGRGDI	GTNCQKMTNK	TLSHSESQVF	ALTPALHKLQ	LGEETQSDEP	NLESLQSEPR	ELPQRSQEAN
1370	1380	1390	1400	1410	1420	1430	1440
MTESRKAEDE	MQKSAWDQPS	LPEGNKNKTN	LDDLVKGENR	SSVKHRLAAM	SKASRKFPAK	DVSPRRHVAT	IFPQSGSRSG
1450	1460	1470	1480	1490	1500	1510	1520
FDHLSLGTVE	CNPLFPEPTP	KSAESIGESR	LSENGKHVKK	SENLLPITVL	PNREPSTHVS	NQKSNSISQR	HQNEFKNVSE
1530	1540	1550	1560	1570	1580	1590	1600
SPSKHENSKD	VTAAQNLVRE	SGAPSPITFT	SLREAEFSDN	QRRLSPPFPL	EPAQKSRVSS	PLASFLQQQR	SASSLEWEPE
1610	1620	1630	1640	1650	1660	1670	1680
PHLYRSKSLK	SINVHGDLLR	KSHPPKVRER	HFSESTSIDN	ALSRLTLGNE	FSVNNGYSRR	FRSFSELPSC	DGNESWAYRS
1690	1700	1710	1720	1730	1740	1750	1760
GTKTGPRSAI	SIYRPIDYGI	FGKEQQLAFL	ENVKRSLTQG	RLWKPSFLKN	PGFLKDDLRN	PPNPSESLSS	NSPSSQVPED
1770	1780	1790	1800	1810			
GLSPSEPLNI	YEDDPVDSDC	DTDTTTDDEY	YLDENDKESE	L			

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

	Cmpds.		[ppm]		[min]					
309	1	558.5767	-48.96	3	33.2	12.3	2	722-736	R.SPSDKDPSLGEREEK.D	
2720	1	1086.5521	56.79	2	64.3	10.3	1	1274-1294	K.CPQKDHTSTAVGDGSSGSQPR.E	Carbamidomethyl: 1

Detailed Protein Report

Protein 556: uncharacterized protein KIAA0408 [Homo sapiens]

Accession:	gi|59806363	**Score:**	22.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	79.1
Database Date:	2015-11-30	**pI:**	9.6
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	3.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDLHKQWENT	ETNWHKEKME	LLDQFDNERK	EWESQWKIMQ	KKIEELCREV	KLWRKININE	SAKIIDLYHE	KTIPEKVIES
90	100	110	120	130	140	150	160
SPNYPDLGQS	EFIRTNHKDG	LRKENKREQS	LVSGGNQMCK	EQKATKKSKV	GFLDPLATDN	QKECEAWPDL	RTSEEDSKSC
170	180	190	200	210	220	230	240
SGALSTALEE	LAKVSEELCS	FQEEIRKRSN	HRRMKSDSFL	QEMPNVTNIP	HGDPMINNDQ	CILPISLEKE	KQKNRKNLSC
250	260	270	280	290	300	310	320
TNVLQSNSTK	KCGIDTIDLK	RNETPPVPPP	RSTSRNFPSS	DSEQAYERWK	ERLDHNSWVP	HEGRSKRNYN	PHFPLRQQEM
330	340	350	360	370	380	390	400
SMLYPNEGKT	SKDGIIFSSL	VPEVKIDSKP	PSNEDVGLSM	WSCDIGIGAK	RSPSTSWFQK	TCSTPSNPKY	EMVIPDHPAK
410	420	430	440	450	460	470	480
SHPDLHVSND	CSSSVAESSS	PLRNFSCGFE	RTTRNEKLAA	KTDEFNRTVF	RTDRNCQAIQ	QNHSCSKSSE	DLKPCDTSST
490	500	510	520	530	540	550	560
HTGSISQSND	VSGIWKTNAH	MPVPMENVPD	NPTKKSTTGL	VRQMQGHLSP	RSYRNMLHEH	DWRPSNLSGR	PRSADPRSNY
570	580	590	600	610	620	630	640
GVVEKLLKTY	ETATESALQN	SKCFQDNWTK	CNSDVSGGAT	LSQHLEMLQM	EQQFQQKTAV	WGGQEVKQGI	DPKKITEESM
650	660	670	680	690	700		
SVNASHGKGF	SRPARPANRR	LPSRWASRSP	SAPPALRRTT	HNYTISLRSE	ALMV		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1324	1	727.1757	-204.08	2	46.2	10.1	0	108-120	R.EQSLVSGGNQMCK.E	Carbamidomethyl: 12; Oxidation: 11

Detailed Protein Report

Protein 557: **regulator of G-protein signaling 3 isoform 3 [Homo sapiens]**

Accession:	gi|62865654	**Score:**	22.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	67.2
Database Date:	2015-11-30	**pI:**	9.9
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	4.3
		No. of unique Peptides:	1

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			
ASPPDSKKLH	PFGSLQQEMG	PVNSTNATQD	RSFTSPGQTL	IG			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1945	1	700.2356	-147.65	2	54.4	10.8	0	119-131	R.QSGLIGCMSFGVK.S	Carbamidomethyl: 7; Oxidation: 8

Detailed Protein Report

Protein 558: PREDICTED: PAX3- and PAX7-binding protein 1 isoform X2 [Homo sapiens]

Accession:	gi|578836733	**Score:**	22.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	86.2
Database Date:	2015-11-30	**pI:**	5.1
		Sequence Coverage [%]:	4.0
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MFRKARRVNV	RKRNDSEEEE	RERDEEQEPP	PLLPPPGTGE	EAGPGGGDRA	PGGESLLGPG	PSPPSALTPG	LGAEAGGGFP
90	100	110	120	130	140	150	160
GGAEPGNGLK	PRKRPRENKE	VPRASLLSFQ	DEEEENEEVF	KVKKSSYSKK	IVKLLKKEYK	EDLEKSKIKT	ELNSSAESEQ
170	180	190	200	210	220	230	240
PLDKTGHVKD	TNQEDGVIIS	EHGEDEMDME	SEKEEEKPKT	GGAFSNALSS	LNVLRPGEIP	DAAFIHAARK	KRQMARELGD
250	260	270	280	290	300	310	320
FTPHDNEPGK	GRLVREDEND	ASDDEDDDEK	RRIVFSVKEK	SQRQKIAEEI	GIEGSDDDAL	VTGEQDEELS	RWEQEQIRKG
330	340	350	360	370	380	390	400
INIPQVQASQ	PAEVNMYYQN	TYQTMPYGSS	YGIPYSYTAY	GSSDAKSQKT	DNTVPFKTPS	NEMTPVTIDL	VKKQLKDRLD
410	420	430	440	450	460	470	480
SMKELHKTNR	QQHEKHLQSR	VDSTRAIERL	EGSSGGIGER	YKFLQEMRGY	VQDLLECFSE	KVPLINELES	AIHQLYKQRA
490	500	510	520	530	540	550	560
SRLVQRRQDD	IKDESSEFSS	HSNKALMAPN	LDSFGRDRAL	YQEHAKRRIA	EREARRTRRR	QAREQTGKMA	DHLEGLSSDD
570	580	590	600	610	620	630	640
EETSTDITNF	NLEKDRISKE	SGKVFEDVLE	SFYSIDCIKS	QFEAWRSKYY	TSYKDAYIGL	CLPKLFNPLI	RLQLLTWTPL
650	660	670	680	690	700	710	720
EAKCRDFENM	LWFESLLFYG	CEEREQEKDD	VDVALLPTIV	EKVILPKLTV	IAENMWDPFS	TTQTSRMVGI	TLKLINGYPS
730	740	750	760				
VVNAENKNTQ	VYLKALLLRM	RRTLDDDVFM	PLYPKNC				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
584	1	824.2497	-169.01	2	36.9	10.9	0	150-164	K.TELNSSAESEQPLDK.T	
156	1	822.7809	-180.37	2	31.7	11.6	0	378-392	K.TPSNEMTPVTIDLVK.K	

Detailed Protein Report

Protein 559: tyrosine-protein kinase Lck precursor [Homo sapiens]

Accession:	gi|112789546	**Score:**	22.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	58.0
Database Date:	2015-11-30	**pI:**	5.1
		Sequence Coverage [%]:	2.9
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|112789548	refseq_human (refseq_human_20140103.fasta)	tyrosine-protein kinase Lck precursor [Homo sapiens]

10	20	30	40	50	60	70	80
MGCGCSSHPE	DDWMENIDVC	ENCHYPIVPL	DGKGTLLIRN	GSEVRDPLVT	YEGSNPPASP	LQDNLVIALH	SYEPSHDGDL
90	100	110	120	130	140	150	160
GFEKGEQLRI	LEQSGEWWKA	QSLTTGQEGF	IPFNFVAKAN	SLEPEPWFFK	NLSRKDAERQ	LLAPGNTHGS	FLIRESESTA
170	180	190	200	210	220	230	240
GSFSLSVRDF	DQNQGEVVKH	YKIRNLDNGG	FYISPRITFP	GLHELVRHYT	NASDGLCTRL	SRPCQTQKPQ	KPWWEDEWEV
250	260	270	280	290	300	310	320
PRETLKLVER	LGAGQFGEVW	MGYYNGHTKV	AVKSLKQGSM	SPDAFLAEAN	LMKQLQHQRL	VRLYAVVTQE	PIYIITEYME
330	340	350	360	370	380	390	400
NGSLVDFLKT	PSGIKLTINK	LLDMAAQIAE	GMAFIEERNY	IHRDLRAANI	LVSDTLSCKI	ADFGLARLIE	DNEYTAREGA
410	420	430	440	450	460	470	480
KFPIKWTAPE	AINYGTFTIK	SDVWSFGILL	TEIVTHGRIP	YPGMTNPEVI	QNLERGYRMV	RPDNCPEELY	QLMRLCWKER
490	500	510					
PEDRPTFDYL	RSVLEDFFTA	TEGQYQPQP					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2661	1	812.3984	-65.88	2	64.5	22.4	0	140-154	R.QLLAPGNTHGSFLIR.E	

Detailed Protein Report

Protein 560: PREDICTED: formin-binding protein 1 isoform X20 [Homo sapiens]

Accession:	gi|530390795	**Score:**	22.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	64.0
Database Date:	2015-11-30	**pI:**	5.0
		Sequence Coverage [%]:	3.4
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 0.61 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MSWGTELWDQ	FDNLEKHTQW	GIDILEKYIK	FVKERTEIEL	SYAKQLRNLS	KKYQPKKNSK	EEEEYKYTSC	KAFISNLNEM
90	100	110	120	130	140	150	160
NDYAGQHEVI	SENMASQIIV	DLARYVQELK	QERKSNFHDG	RKAQQHIETC	WKQLESSKRR	FERDCKEADR	AQQYFEKMDA
170	180	190	200	210	220	230	240
DINVTKADVE	KARQQAQIRH	QMAEDSKADY	SSILQKFNHE	QHEYYHTHIP	NIFQKIQEME	ERRIVRMGES	MKTYAEVDRQ
250	260	270	280	290	300	310	320
VIPIIGKCLD	GIVKAAESID	QKNDSQLVIE	AYKSGFEPPG	DIEFEDYTQP	MKRTVSDNSL	SNSRGEGKPD	LKFGGKSKGK
330	340	350	360	370	380	390	400
LWPFIKKNKG	ATPEDFSNLP	PEQRRKKLQQ	KVDELNKEIQ	KEMDQRDAIT	KMKDVYLKNP	QMGDPASLDH	KLAEVSQNIE
410	420	430	440	450	460	470	480
KLRVETQKFE	AWLAEVEGRL	PARSEQARRQ	SGLYDSQNPP	TVNNCAQDRE	SPDGSYTEEQ	SQESEMKVLA	TDFDDEFDDE
490	500	510	520	530	540	550	560
EPLPAIGTCK	ALYTFEGQNE	GTISVVEGET	LYVIEEDKGD	GWTRIRRNED	EEGYVPTSYV	EVCLDKNAKD	S

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
812	1	603.7427	-137.75	2	39.7	11.4	2	223-232	R.RIVRMGESMK.T		MD:MU 0.61

Detailed Protein Report

Protein 561: PREDICTED: cyclin-dependent kinase-like 5 isoform X2 [Homo sapiens]

Accession:	gi|530421243	**Score:**	22.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	110.0
Database Date:	2015-11-30	**pI:**	10.1
		Sequence Coverage [%]:	3.0
		No. of unique Peptides:	1

Quantitation

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

10	20	30	40	50	60	70	80
MKIPNIGNVM	NKFEILGVVG	EGAYGVVLKC	RHKETHEIVA	IKKFKDSEEN	EEVKETTLRE	LKMLRTLKQE	NIVELKEAFR
90	100	110	120	130	140	150	160
RRGKLYLVFE	YVEKNMLELL	EEMPNGVPPE	KVKSYIYQLI	KAIHWCHKND	IVHRDIKPEN	LLISHNDVLK	LCDFGFARNL
170	180	190	200	210	220	230	240
SEGNNANYTE	YVATRWYRSP	ELLLGAPYGK	SVDMWSVGCI	LGELSDGQPL	FPGESEIDQL	FTIQKVLGPL	PSEQMKLFYS
250	260	270	280	290	300	310	320
NPRFHGLRFP	AVNHPQSLER	RYLGILNSVL	LDLMKNLLKL	DPADRYLTEQ	CLNHPTFQTQ	RLLDRSPSRN	QAGKSTALQS
330	340	350	360	370	380	390	400
HHRSNSKDIQ	NLSVGLPRAD	EGLPANESFL	NGNLAGASLS	PLHTKTYQAS	SQPGSTSKDL	TNNNIPHLLS	PKEAKSKTEF
410	420	430	440	450	460	470	480
DFNIDPKPSE	GPGTKYLKSN	SRSQQNRHSF	MESSQSKAGT	LQPNEKQSRH	SYIDTIPQSS	RSPSYRTKAK	SHGALSDSKS
490	500	510	520	530	540	550	560
VSNLSEARAQ	IAEPSTSRYF	PSSCLDLNSP	TSPTPTRHSD	TRTLLSPSGR	NNRNEGTLDS	RRTTTRHSKT	MEELKLPEHM
570	580	590	600	610	620	630	640
DSSHSHSLSA	PHESFSYGLG	YTSPFSSQQR	PHRHSMYVTR	DKVRAKGLDG	SLSIGQGMAA	RANSLQLLSP	QPGEQLPPEM
650	660	670	680	690	700	710	720
TVARSSVKET	SREGTSSFHT	RQKSEGGVYH	DPHSDDGTAP	KENRHLYNDP	VPRRVGSFYR	VPSPRPDNSF	HENNVSTRVS
730	740	750	760	770	780	790	800
SLPSESSSGT	NHSKRQPAFD	PWKSPENISH	SEQLKEKEKQ	GFFRSMKKKK	KKSQTTDSTN	GENPSIKKSL	FPLFNSKNHL
810	820	830	840	850	860	870	880
KHSSSLKKLP	VVTPPMVPNS	DSPDLLTLQK	SIHSASTPSS	RPKEWRPEKI	SDLQTQSQPL	KSLRKLLHLS	SASNHPASSD
890	900	910	920	930	940	950	960
PRFQPLTAQQ	TKNSFSEIRI	HPLSQASGGS	SNIRQEPAPK	GRPALQLPGQ	MDPGWHVSSV	TRSATEGPSY	SEQLGAKSGP
970	980	990					
NGHPYNRTNR	SRMPNLNDLK	ETAL					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
198	1	671.1826	-201.27	2	31.9	11.2	0	366-378	K.TYQASSQPGSTSK.D		MD:MU 0.94

Detailed Protein Report

Protein 562: disrupted in schizophrenia 1 protein isoform f [Homo sapiens]

Accession:	gi|257153469	**Score:**	22.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	74.3
Database Date:	2015-11-30	**pI:**	6.9
		Sequence Coverage [%]:	4.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPGGGPQGAP	AAAGGGGVSH	RAGSRDCLPP	AACFRRRRLA	RRPGYMRSST	GPGIGFLSPA	VGTLFRFPGG	VSGEESHHSE
90	100	110	120	130	140	150	160
SRARQCGLDS	RGLLVRSPVS	KSAAAPTVTS	VRGTSAHFGI	QLRGGTRLPD	RLSWPCGPGS	AGWQQEFAAM	DSSETLDASW
170	180	190	200	210	220	230	240
EAACSDGARR	VRAAGSLPSA	ELSSNSCSPG	CGPEVPPTPP	GSHSAFTSSF	SFIRLSLGSA	GERGEAEGCP	PSREAESHCQ
250	260	270	280	290	300	310	320
SPQEMGAKAA	SLDGPHEDPR	CLSRPFSLLA	TRVSADLAQA	ARNSSRPERD	MHSLPDMDPG	SSSSLDPSLA	GCGGDGSSGS
330	340	350	360	370	380	390	400
GDAHSWDTLL	RKWEPVLRDC	LLRNRRQMEV	ISLRLKLQKL	QEDAVENDDY	DKAETLQQRL	EDLEQEKISL	HFQLPSRQPA
410	420	430	440	450	460	470	480
LSSFLGHLAA	QVQAALRRGA	TQQASGDDTH	TPLRMEPRLL	EPTAQDSLHV	SITRRDWLLQ	EKQQLQKEIE	ALQARMFVLE
490	500	510	520	530	540	550	560
AKDQQLRREI	EEQEQQLQWQ	GCDLTPLVGQ	LSLGQLQEVS	KALQDTLASA	GQIPFHAEPP	ETIRSLQERI	KSLNLSLKEI
570	580	590	600	610	620	630	640
TTKVCMSEKF	CSTLRKKVND	IETQLPALLE	AKMHAISGNH	FWTAKDLTEE	IRSLTSEREG	LEGLLSKLLV	LSSRNVKKLG
650	660	670	680	690			
SVKEDYNRLR	REVEHQETAY	ETSVKENTMK	YMETLKNKLC	R			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
12	1	803.7126	-4.89	3	29.3	12.4	2	651-670	R.REVEHQETAYETSVKENTMK.Y	

Detailed Protein Report

Protein 563: tigger transposable element-derived protein 7 [Homo sapiens]

Accession:	gi|22325392	**Score:**	22.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	63.2
Database Date:	2015-11-30	**pI:**	9.6
		Sequence Coverage [%]:	4.2
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 3.93 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MNKRGKYTTL	NLEEKMKVLS	RIEAGRSLKS	VMDEFGISKS	TFYDIKKNKK	LILDFVLKQD	MPLVGAEKRK	RTTGAKYGDV
90	100	110	120	130	140	150	160
DDAVYMWYQQ	KRSAGVPVRG	VELQAAAERF	ARCFGRTDFK	ASTGWLFRFR	NRHAIGNRKG	CGEQVLSSVS	ENVEPFRQKL
170	180	190	200	210	220	230	240
SMIIKEEKLC	LAQLYSGDET	DLFWKSMPEN	SQASRKDICL	PGKKINKERL	SAFLCANADG	THKLKSIIIG	KSKLPKSVKE
250	260	270	280	290	300	310	320
DTSTLPVIYK	PSKDVWFTRE	LFSEWFFQNF	VPEVRHFQLN	VLRFHDEDVR	ALLLLDSCPA	HPSSESLTSE	DGRIKCMFFP
330	340	350	360	370	380	390	400
HNTSTLIQPM	NQGVILSCKR	LYRWKQLEES	LVIFEESDDE	QEKGDKGVSK	IKIYNIKSAI	FNWAKSWEEV	KQITIANAWE
410	420	430	440	450	460	470	480
NLLYKKEPEY	DFQGLEHGDY	REILEKCGEL	ETKLDDDRVW	LNGDEEKGCL	LKTKGGITKE	VVQKGGEAEK	QTAEFKLSAV
490	500	510	520	530	540	550	
RESLDYLLDF	VDATPEFQRF	HFTLKEMQQE	IVKKQFQSKI	HSRIGSFLKP	RPHNIKDSFS	GPSTSGSNH	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2435	1	648.2013	-222.78	2	60.8	10.6	1	5-15	R.GKYTTLNLEEK.M		MD:MU 3.93

Detailed Protein Report

Protein 564: PREDICTED: G patch domain-containing protein 8 isoform X1 [Homo sapiens]

Accession:	gi|578830624	**Score:**	22.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	155.1
Database Date:	2015-11-30	**pI:**	9.6
		Sequence Coverage [%]:	1.8
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578830628	refseq_human (refseq_human_20140103.fasta)	PREDICTED: G patch domain-containing protein 8 isoform X3 [Homo sapiens]
gi|578830626	refseq_human (refseq_human_20140103.fasta)	PREDICTED: G patch domain-containing protein 8 isoform X2 [Homo sapiens]

10	20	30	40	50	60	70	80
MGMGRMEMEL	DYAEDATERR	RVLEVEKEDT	EELRQKYKDY	VDKEKAIAKA	LEDLRANFYC	ELCDKQYQKH	QEFDNHINSY
90	100	110	120	130	140	150	160
DHAHKQRLKD	LKQREFARNV	SSRSRKDEKK	QEKALRRLHE	LAEQRKQAEC	APGSGPMFKP	TTVAVDEEGG	EDDKDESATN
170	180	190	200	210	220	230	240
SGTGATASCG	LGSEFSTDKG	GPFTAVQITN	TTGLAQAPGL	ASQGISFGIK	NNLGTPLQKL	GVSFSFAKKA	PVKLESIASV
250	260	270	280	290	300	310	320
FKDHAEEGTS	EDGTKPDEKS	SDQGLQKVGD	SDGSSNLDGK	KEDEDPQDGG	SLASTLSKLK	RMKREEGAGA	TEPEYYHYIP
330	340	350	360	370	380	390	400
PAHCKVKPNF	PFLLFMRASE	QMDGDNTTHP	KNAPESKKGS	SPKPKSCIKA	AASQGAEKTV	SEVSEQPKET	SMTEPSEPGS
410	420	430	440	450	460	470	480
KAEAKKALGG	DVSDQSLESH	SQKVSETQMC	ESNSSKETSL	ATPAGKESQE	GPKHPTGPFF	PVLSKDESTA	LQWPSELLIF
490	500	510	520	530	540	550	560
TKAEPSISYS	CNPLYFDFKL	SRNKDARTKG	TEKPKDIGSS	SKDHLQGLDP	GEPNKSKEVG	GEKIVRSSGG	RMDAPASGSA
570	580	590	600	610	620	630	640
CSGLNKQEPG	GSHGSETEDT	GRSLPSKKER	SGKSHRHKKK	KKHKKSSKHK	RKHKADTEEK	SSKAESGEKS	KKRKKRKRKK
650	660	670	680	690	700	710	720
NKSSAPADSE	RGPKPEPPGS	GSPAPPRRRR	RAQDDSQRRS	LPAEEGSSGK	KDEGGGGSSS	QDHGGRKHKG	ELPPSSCQRR
730	740	750	760	770	780	790	800
AGTKRSSRSS	HRSQPSSGDE	DSDDASSHRL	HQKSPSQYSE	EEEEEDSGSE	HSRSRSRSGR	RHSSHRSSRR	SYSSSSDASS
810	820	830	840	850	860	870	880
DQSCYSRQRS	YSDDSYSDYS	DRSRRHSKRS	HDSDDSDYAS	SKHRSKRHKY	SSSDDDYSLS	CSQSRSRSRS	HTRERSRSRG
890	900	910	920	930	940	950	960
RSRSSSCSRS	RSKRRSRSTT	AHSWQRSRSY	SRDRSRSTRS	PSQRSGSRKR	SWGHESPEER	HSGRRDFIRS	KIYRSQSPHY
970	980	990	1000	1010	1020	1030	1040
FRSGRGEGPG	KKDDGRGDDS	KATGPPSQNS	NIGTGRGSEG	DCSPEDKNSV	TAKLLLEKIQ	SRKVERKPSV	SEEVQATPNK
1050	1060	1070	1080	1090	1100	1110	1120
AGPKLKDPPQ	GYFGPKLPPS	LGNKPVLPLI	GKLPATRKPN	KKCEESGLER	GEEQEQSETE	EGPPGSSDAL	FGHQFPSEET
1130	1140	1150	1160	1170	1180	1190	1200
TGPLLDPPPE	ESKSGEATAD	HPVAPLGTPA	HSDCYPGDPT	ISHNYLPDPS	DGDTLESLDS	SSQPGPVESS	LLPIAPDLEH
1210	1220	1230	1240	1250	1260	1270	1280
FPSYAPPSGD	PSIESTDGAE	DASLAPLESQ	PITFTPEEME	KYSKLQQAAQ	QHIQQQLLAK	QVKAFPASAA	LAPATPALQP
1290	1300	1310	1320	1330	1340	1350	1360
IHIQQPATAS	ATSITTVQHA	ILQHHAAAAA	AAIGIHPHPH	PQPLAQVHHI	PQPHLTPISL	SHLTHSIIPG	HPATFLASHP
1370	1380	1390	1400	1410	1420	1430	
IHIIPASAIH	PGPFTFHPVP	HAALYPTLLA	PRPAAAAATA	LHLHPLLHPI	FSGQDLQHPP	SHGT	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2163	1	1131.2917	-238.27	1	57.2	12.1	2	671-679	R.RAQDDSQRR.S	

Detailed Protein Report

Protein 565: RNA-binding protein MEX3A [Homo sapiens]

Accession:	gi|147902746	**Score:**	22.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	54.1
Database Date:	2015-11-30	**pI:**	7.8
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	6.7
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MPSLVVSGIM ERNGGFGELG CFGGSAKDRG LLEDERALQL ALDQLCLLGL GEPPAPTAGE DGGGGGGGAP AQPAAPPQPA
        90        100        110        120        130        140        150        160
PPPPPAAPPA APTAAPAAQT PQPPTAPKGA SDAKLCALYK EAELRLKGSS NTTECVPVPT SEHVAEIVGR QGCKIKALRA
       170        180        190        200        210        220        230        240
KTNTYIKTPV RGEEPVFMVT GRREDVATAR REIISAAEHF SMIRASRNKS GAAFGVAPAL PGQVTIRVRV PYRVVGLVVG
       250        260        270        280        290        300        310        320
PKGATIKRIQ QQTNTYIITP SRDRDPVFEI TGAPGNVERA REEIETHIAV RTGKILEYNN ENDFLAGSPD AAIDSRYSDA
       330        340        350        360        370        380        390        400
WRVHQPGCKP LSTFRQNSLG CIGECGVDSG FEAPRLGEQG GDFGYGGYLF PGYGVGKQDV YYGVAETSPP LWAGQENATP
       410        420        430        440        450        460        470        480
TSVLFSSASS SSSSSAKARA GPPGAHRSPA TSAGPELAGL PRRPPGEPLQ GFSKLGGGGL RSPGGGRDCM VCFESEVTAA
       490        500        510        520        530
LVPCGHNLFC MECAVRICER TDPECPVCHI TATQAIRIFS
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1760	1	1273.5603	8.38	3	51.8	22.3	1	462-496	R.SPGGGRDCMVCFESEVTAALVPCGHNLFCMECAVR.I	Carbamidomethyl: 8, 11; Oxidation: 9

Detailed Protein Report

Protein 566: PREDICTED: pecanex-like protein 3 isoform X4 [Homo sapiens]

Accession:	gi|530396772	**Score:**	22.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	115.4
Database Date:	2015-11-30	**pI:**	6.0
		Sequence Coverage [%]:	3.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGSQVLQILR	QGVWASLTGG	WFFDPHQSTF	SNCFHLYVWI	FLLIFPFLLY	MVLPPSLMVA	GVYCLVVAVI	FATIKTVNYR
90	100	110	120	130	140	150	160
LHAMFDQGEI	VEKRSSTMGE	LEEEPAQGDS	NPPRDPGVEM	TVFRKVSSTP	PVRCSSQHSV	FGFNQVSELL	PRMEDSGPLR
170	180	190	200	210	220	230	240
DIKELVREQG	SNNVIVTSAD	REMLKLSSQE	KLIGDLPQTP	PGAVPDPSLA	STDSSEPSPL	AGDGAPWSGS	SMADTPMSPL
250	260	270	280	290	300	310	320
LKGSLSQELS	KSFLTLTQPD	RALVRTSSRR	EQRRGAGGYQ	PLDRRGSGEP	TPQKAGSSDS	CFSGTDRETL	SSFKSEKTNS
330	340	350	360	370	380	390	400
THLDSPPGGP	APEGSDTDPP	SEAELPASPD	AGVPSDDTLR	SFDTVIGAGT	PPGLAEPLLV	VRPKDLALLR	PSKRQPPLRR
410	420	430	440	450	460	470	480
HSPPGRAPRR	PLLEGGGFFE	DEDTSEGSEL	SPASSLRSQR	RYSTDSSSST	SCYSPESSRG	AAGGPRKRRA	PHGAEEGTAV
490	500	510	520	530	540	550	560
PPKRPYGTQR	TPSTASAKTH	ARVLSMDGAG	GDVLRPPLAG	CKAELEAQVG	VEQAASEPVV	LPAEARRGPA	ANQPGWRGEL
570	580	590	600	610	620	630	640
QEEGAVGGAA	EETGRRDRSS	SVRRTQAIRR	RHNAGSNPTP	PASVMGSPPS	SLQEAQRGRA	ASHSRALTLP	SALHFASSLL
650	660	670	680	690	700	710	720
LTRAGANVHE	ACTFDDTSEG	AVHYFYDESG	VRRSYTFGLA	GGGYENPVGQ	QGEQTANGAW	DRHSHSSSFH	SADVPEATGG
730	740	750	760	770	780	790	800
LNLLQPRPVV	LQGMQVRRVP	LEIPEFDLLD	QDSLHESQEQ	TLMEEAPPRA	QHSYKYWLLP	GRWTSVRYER	LALLALLDRT
810	820	830	840	850	860	870	880
RGVLENIFGV	GLSSLVAFLG	YLLLLKGFFT	DIWVFQFCLV	IASCQYSLLK	SVQPDAASPM	HGHNWVIAYS	RPVYFCICCL
890	900	910	920	930	940	950	960
LIWLLDALGS	AQPFPPVSLY	GLTLFSASFF	FCARDVATVF	TLCFPFVFLL	GLLPQVNTCL	MYLLEQIDMH	GFGGTAATSP
970	980	990	1000	1010	1020	1030	1040
LTAVFSLSRS	LLAAALLYGF	CLGAIKTPWP	EQHVPVLFSV	FCGLLVALSY	HLSRQSSDPT	VLWSLIRSKL	FPELEERSLE
1050	1060	1070					
TARAEPPDPL	PDKMRQSVLN	VSPGPAA					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2754	1	1086.0034	31.79	2	64.8	11.5	1	286-307	R.GSGEPTPQKAGSSDSCFSGTDR.E	

Detailed Protein Report

Protein 567: PREDICTED: uncharacterized protein LOC101929845 [Homo sapiens]

Accession:	gi|578845877	**Score:**	22.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	90.2
Database Date:	2015-11-30	**pI:**	12.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEESAEQAPR	CDETRVGRRR	HSWRNTCGGV	GRAGTAVRRD	AASQSCCPTC	TGVATRRHSW	RRRQSRQTKE	FIFSELLSNL
90	100	110	120	130	140	150	160
YSRGNEQTLV	EALAEQADQG	VHLLRAAVQP	ALAWEREDTR	GGVGRAGRPR	SSSSQSCCPN	CTRVGTRRHS	WRSRQSRHRG
170	180	190	200	210	220	230	240
VTRLAWEEED	TPGGVGRAGR	PRSSSSRSCC	PTCTRVGTCR	HSWRRRQSRQ	TKEFIFSELL	SNLYSRGNEK	TLVEASAEQA
250	260	270	280	290	300	310	320
DQGVHLLRAA	VQPVLAWERE	DTRGGVGRAG	RPRSSSSQSC	CPTCTRVGTR	RHSWRSRPSR	HSGVTRLAWE	EEDTPGGVGR
330	340	350	360	370	380	390	400
AGRPRSSSSR	SCCPTCTRVG	TCRHLWRSRQ	SRHSGATRCC	FSELLSNLHW	RGNEKTLVEA	LAEQADQGVH	LLRAAVQPVL
410	420	430	440	450	460	470	480
AWERADTRGG	VGRAGRPRSS	SSQSCCPTCT	RVGTRRHSWR	RRQSRQTKEF	IFSELLSKLH	SRGNEKTLME	ESAEQAQRCD
490	500	510	520	530	540	550	560
ETRVGRRRHS	WRSRQSRQTK	KFIFSELLSN	LYSRRNLQTL	VEASAEQADQ	GVHLLRAAVQ	PVLAWEREDT	RGGVGRAGRP
570	580	590	600	610	620	630	640
RSSSSQSCCP	TCTRVGTRRH	SWRRRQSRQT	KEFIFSELLS	NLHSRGNEKT	LMEESAEQAQ	RRDETRVGRR	RHSWRSRQSR
650	660	670	680	690	700	710	720
QTKEFIFSEL	LSNLYSRRNL	QTLVEESAEQ	AQRCDKMLLL	RAAVQPALAW	EREDTRGGVG	RAGRPRSSSS	QSCCPTCPRV
730	740	750	760	770	780	790	800
GTRRHSWRRR	QSRQTKEFIF	SELLSNLHSR	GNEKTLVEAS	AEQADQGVHL	LRAAVQTALA	WEREDTHGGV	GRAGTEV

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
48	1	1220.0219	-37.76	2	30.0	11.4	2	33-56	R.AGTAVRRDAASQSCCPTCTGVATR.R	Carbamidomethyl: 14

Detailed Protein Report

Protein 568: PREDICTED: protein FAM188A isoform X3 [Homo sapiens]

Accession:	gi|530392461	**Score:**	22.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	30.5
Database Date:	2015-11-30	**pI:**	4.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	14.3
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530392465	refseq_human (refseq_human_20140103.fasta)	PREDICTED: protein FAM188A isoform X5 [Homo sapiens]
gi|530392463	refseq_human (refseq_human_20140103.fasta)	PREDICTED: protein FAM188A isoform X4 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MWGNKFGVLL FLYSVLLTKG IENIKNEIED ASEPLIDPVY GHGSQSLINL LLTGHAVSNV WDGDRECSGM KLLGIHEQAA
        90        100        110        120        130        140        150        160
VGFLTLMEAL RYCKVGSYLK SPKFPIWIVG SETHLTVFFA KDMALVAPEA PSEQARRVFQ TYDPEDNGFI PDSLLEDVMK
       170        180        190        200        210        220        230        240
ALDLVSDPEY INLMKNKLDP EGLGIILLGP FLQEFFPDQG SSGPESFTVY HYNGLKQSNY NEKVMYVEGT AVVMGFEDPM
       250        260        270        280
LQTDDTPIKR CLQTKWPYIE LLWTTDRSPS LN
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1733	1	1030.7459	-72.31	3	51.5	11.5	1	224-250	K.VMYVEGTAVVMGFEDPMLQTDDTPIKR.C	Oxidation: 2, 11, 17

Detailed Protein Report

Protein 569: PREDICTED: disks large-associated protein 1 isoform X7 [Homo sapiens]

Accession:	gi|578832238	**Score:**	22.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	81.4
Database Date:	2015-11-30	**pI:**	6.6
		Sequence Coverage [%]:	2.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MIDLFKAEWV	SSVCVQVSRN	GRTDQSKLKR	LKGHLSQVAF	VKVKAVWSRK	AVLPAAKKMQ	RNRVPQDEWT	GYTPRGKDDE
90	100	110	120	130	140	150	160
IPCRRMRSGS	YIKAMGDEDS	GDSDTSPKPS	PKVAARRESY	LKATQPSLTE	LTTLKISNEH	SPKLQIRSHS	YLRAVSEVSI
170	180	190	200	210	220	230	240
NRSLDSLDPA	GLLTSPKFRS	RNESYMRAMS	TISQVSEMEV	NGQFESVCES	VFSELESQAV	EALDLPMPGC	FRMRSHSYVR
250	260	270	280	290	300	310	320
AIEKGCSQDD	ECVSLRSSSP	PRTTTTVRTI	QSSTGVIKLS	SAVEVSSCIT	TYKKTPPPVP	PRTTTKPFIS	ITAQSSTESA
330	340	350	360	370	380	390	400
QDAYMDGQGQ	RGDIISQSGL	SNSTESLDSM	KALTAAIEAA	NAQIHGPASQ	HMGNNTATVT	TTTTIATVTT	EDRKKDHFKK
410	420	430	440	450	460	470	480
NRCLSIGIQV	DDAEEPDKTG	ENKAPSKFQS	VGVQVEEEKC	FRRFTRSNSV	TTAVQADLDF	HDNLENSLES	IEDNSCPGPM
490	500	510	520	530	540	550	560
ARQFSRDAST	STVSIQGSGN	HYHACAADDD	FDTDFDPSIL	PPPDPWIDSI	TEDPLEAVQR	SVCHRDGHWF	LKLLQAERDR
570	580	590	600	610	620	630	640
MEGWCQQMER	EERENNLPED	ILGKIRTAVG	SAQLLMAQKF	YQFRELCEEN	LNPNAHPRPT	SQDLAGFWDM	LQLSIENISM
650	660	670	680	690	700	710	720
KFDELHQLKA	NNWKQMDPLD	KKERRAPPPV	PKKPAKGPAP	LIRERSLESS	QRQEARKRLM	AAKRAASVRQ	NSATESAESI
730	740						
EIYIPEAQTR	L						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1338	1	845.6519	163.33	1	46.4	12.0	2	698-704	K.RLMAAKR.A	

Detailed Protein Report

Protein 570: PREDICTED: tau-tubulin kinase 1 isoform X1 [Homo sapiens]

Accession:	gi|578812010	**Score:**	22.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	84.4
Database Date:	2015-11-30	**pI:**	8.9
		Sequence Coverage [%]:	4.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSGGGEQADI	LPANYVVKDR	WKVLKKIGGG	GFGEIYEAMD	LLTRENVALK	VESAQQPKQV	LKMEVAVLKK	LQGKDHVCRF
90	100	110	120	130	140	150	160
IGCGRNEKFN	YVVMQLQGRN	LADLRRSQPR	GTFTLSTTLR	LGKQILESIE	AIHSVGFLHR	DIKPSNFAMG	RLPSTYRKCY
170	180	190	200	210	220	230	240
MLDFGLARQY	TNTTGDVRPP	RNVAGFRGTV	RYASVNAHKN	REMGRHDDLW	SLFYMLVEFA	VGQLPWRKIK	DKEQVGMIKE
250	260	270	280	290	300	310	320
KYEHRMLLKH	MPSEFHLFLD	HIASLDYFTK	PDYQLIMSVF	ENSMKERGIA	ENEAFDWEKA	GTDALLSTST	STPPQQNTRQ
330	340	350	360	370	380	390	400
TAAMFGVVNV	TPVPGDLLRE	NTEDVLQGEH	LSDQENAPPI	LPGRPSEGLG	PSPHLVPHPG	GPEAEVWEET	DVNRNKLRIN
410	420	430	440	450	460	470	480
IGKVTAARAK	GSPCVEEEQS	RGMGVPSSPV	RAPPDSPTTP	VRSLRYRRVN	SPESERLSTA	DGRVELPERR	SRMDLPGSPS
490	500	510	520	530	540	550	560
RQACSSQPAQ	MLSVDTGHAD	RQASGRMDVS	ASVEQEALSN	AFRSVPLAEE	EDFDSKEWVI	IDKETELKDF	PPGAEPSTSG
570	580	590	600	610	620	630	640
TTDEEPEELR	PLPEEGEERR	RLGAEPTVRP	RGRSMQALAE	EDLQHLPPQP	LPPQLSQGDG	RSETSQPPTP	GSPSHSPLHS
650	660	670	680	690	700	710	720
GPRPRRRESD	PTGPQRQLEE	DRLSGHSLPR	YSPLRRLASS	VFSSSTLETE	HYPHPGGGGS	SGSSGSLIQR	SRSAESSPVR
730	740	750	760				
APHRRHAPLA	AGNHRLMPSV	LRISRSQLQQ	VWARFTHKT				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1658	1	697.8038	-143.18	2	50.5	11.5	1	111-123	R.GTFTLSTTLRLGK.Q	

Detailed Protein Report

Protein 571: conserved oligomeric Golgi complex subunit 5 isoform 2 [Homo sapiens]

Accession:	gi|240849537	**Score:**	22.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	92.7
Database Date:	2015-11-30	**pI:**	6.1
		Sequence Coverage [%]:	4.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGWVGGRRRD	SASPPGRSRS	AADDINPAPA	NMEGGGGSVA	VAGLGARGSG	AAAATVRELL	QDGCYSDFLN	EDFDVKTYTS
90	100	110	120	130	140	150	160
QSIHQAVIAE	QLAKLAQGIS	QLDRELHLQV	VARHEDLLAQ	ATGIESLEGV	LQMMQTRIGA	LQGAVDRIKA	KIVEPYNKIV
170	180	190	200	210	220	230	240
ARTAQLARLQ	VACDLLRRII	RILNLSKRLQ	GQLQGGSREI	TKAAQSLNEL	DYLSQGIDLS	GIEVIENDLL	FIARARLEVE
250	260	270	280	290	300	310	320
NQAKRLLEQG	LETQNPTQVG	TALQVFYNLG	TLKDTITSVV	DGYCATLEEN	INSALDIKVL	TQPSQSAVRG	GPGRSTMPTP
330	340	350	360	370	380	390	400
GNTAALRASF	WTNMEKLMDH	IYAVCGQVQH	LQKVLAKKRD	PVSHICFIEE	IVKDGQPEIF	YTFWNSVTQA	LSSQFHMATN
410	420	430	440	450	460	470	480
SSMFLKQAFE	GEYPKLLRLY	NDLWKRLQQY	SQHIQGNFNA	SGTTDLYVDL	QHMEDDAQDI	FIPKKPDYDP	EKALKDSLQP
490	500	510	520	530	540	550	560
YEAAYLSKSL	SRLFDPINLV	FPPGGRNPPS	SDELDGIIKT	IASELNVAAV	DTNLTLAVSK	NVAKTIQLYS	VKSEQLLSTQ
570	580	590	600	610	620	630	640
GDASQVIGPL	TEGQRRNVAV	VNSLYKLHQS	VTKAIHALME	NAVQPLLTSV	GDAIEAIIIT	MHQEDFSGSL	SSSGKPDVPC
650	660	670	680	690	700	710	720
SLYMKELQGF	IARVMSDYFK	HFECLDFVFD	NTEAIAQRAV	ELFIRHASLI	RPLGEGGKMR	LAADFAQMEL	AVGPFCRRVS
730	740	750	760	770	780	790	800
DLGKSYRMLR	SFRPLLFQAS	EHVASSPALG	DVIPFSIIIQ	FLFTRAPAEL	KSPFQRAEWS	HTRFSQWLDD	HPSEKDRLLL
810	820	830	840				
IRGALEAYVQ	SVRSREGKEF	APVYPIMVQL	LQKAMSALQ				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2238	1	682.1284	82.08	3	58.2	10.8	2	798-815	R.LLLIRGALEAYVQSVRSR.E	

Detailed Protein Report

Protein 572: guanine nucleotide-binding protein-like 3 isoform 2 [Homo sapiens]

Accession:	gi|45643127	**Score:**	22.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	60.5
Database Date:	2015-11-30	**pI:**	9.6
		Sequence Coverage [%]:	5.0
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 1.31 **CV:** 0.00 % **No. of Peptides:** 1

Alias proteins:

Accession	Name	Description
gi|45643129	refseq_human (refseq_human_20140103.fasta)	guanine nucleotide-binding protein-like 3 isoform 2 [Homo sapiens]

10	20	30	40	50	60	70	80
MTCHKRYKIQ	KKVREHHRKL	RKEAKKRGHK	KPRKDPGVPN	SAPFKEALLR	EAELRKQRLE	ELKQQQKLDR	QKELEKKRKL
90	100	110	120	130	140	150	160
ETNPDIKPSN	VEPMEKEFGL	CKTENKAKSG	KQNSKKLYCQ	ELKKVIEASD	VVLEVLDARD	PLGCRCPQVE	EAIVQSGQKK
170	180	190	200	210	220	230	240
LVLILNKSDL	VPKENLESWL	NYLKKELPTV	VFRASTKPKD	KGKITKRVKA	KKNAAPFRSE	VCFGKEGLWK	LLGGFQETCS
250	260	270	280	290	300	310	320
KAIRVGVIGF	PNVGKSSIIN	SLKQEQMCNV	GVSMGLTRSM	QVVPLDKQIT	IIDSPSFIVS	PLNSSSALAL	RSPASIEVVK
330	340	350	360	370	380	390	400
PMEAASAILS	QADARQVVLK	YTVPGYRNSL	EFFTVLAQRR	GMHQKGGIPN	VEGAAKLLWS	EWTGASLAYY	CHPPTSWTPP
410	420	430	440	450	460	470	480
PYFNESIVVD	MKSGFNLEEL	EKNNAQSIRA	IKGPHLANSI	LFQSSGLTNG	IIEEKDIHEE	LPKRKERKQE	EREDDKDSDQ
490	500	510	520	530	540		
ETVDEEVDEN	SSGMFAAEET	GEALSEETTA	GEQSTRSFIL	DKIIEEDDAY	DFSTDYV		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
107	1	591.7687	-44.15	2	31.1	10.4	0	231-241	K.LLGGFQETCSK.A		MD:MU 1.31

Detailed Protein Report

Protein 573: **TFIIH basal transcription factor complex helicase XPD subunit isoform 2 [Homo sapiens]**

Accession:	gi|195947407	**Score:**	22.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	46.2
Database Date:	2015-11-30	**pI:**	9.7
		Sequence Coverage [%]:	2.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MRELKRTLDA	KGHGVLEMPS	GTGKTVSLLA	LIMAYQRAYP	LEVTKLIYCS	RTVPEIEKVI	EELRKLLNFY	EKQEGEKLPF
90	100	110	120	130	140	150	160
LGLALSSRKN	LCIHPEVTPL	RFGKDVDGKC	HSLTASYVRA	QYQHDTSLPH	CRFYEEFDAH	GREVPLPAGI	YNLDDLKALG
170	180	190	200	210	220	230	240
RRQGWCPYFL	ARYSILHANV	VVYSYHYLLD	PKIADLVSKE	LARKAVVVFD	EAHNIDNVCI	DSMSVNLTRR	TLDRCQGNLE
250	260	270	280	290	300	310	320
TLQKTVLRIK	ETDEQRLRDE	YRRLVEGLRE	ASAARETDAH	LANPVLPDEV	LQEAVPGSIR	TAEHFLGFLR	RLLEYVKWRL
330	340	350	360	370	380	390	400
RVQHVVQESP	PAFLSGLAQR	VCIQRKPLRF	CAERLRSLLH	TLEITDLADF	SPLTLLANFA	TLVSTYAKGQ	AQHCGSSRNQ
410							
KRSHP							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1794	1	568.7414	-67.06	2	52.4	22.1	0	110-119	K.CHSLTASYVR.A	

Detailed Protein Report

Protein 574: **breast cancer anti-estrogen resistance protein 3 isoform 2 [Homo sapiens]**

Accession:	gi|387157911	**Score:**	22.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	82.3
Database Date:	2015-11-30	**pI:**	9.4
		Sequence Coverage [%]:	4.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPKECSAFHA	LSAALCCFYH	RKSFIGVKFS	KERHIMDRTP	EKLKKELEEE	LLLSSEDLRS	HAWYHGRIPR	QVSENLVQRD
90	100	110	120	130	140	150	160
GDFLVRDSLS	SPGNFVLTCQ	WKNLAQHFKI	NRTVLRLSEA	YSRVQYQFEM	ESFDSIPGLV	RCYVGNRRPI	SQQSGAIIFQ
170	180	190	200	210	220	230	240
PINRTVPLRC	LEEHYGTSPG	QAREGSLTKG	RPDVAKRLSL	TMGGVQAREQ	NLPRGNLLRN	KEKSGSQPAC	LDHMQDRRAL
250	260	270	280	290	300	310	320
SLKAHQSESY	LPIGCKLPPQ	SSGVDTSPCP	NSPVFRTGSE	PALSPAVVRR	VSSDARAGEA	LRGSDSQLCP	KPPPKPCKVP
330	340	350	360	370	380	390	400
FLKVPSSPSA	WLNSEANYCE	LNPAFATGCG	RGAKLPSCAQ	GSHTELLTAK	QNEAPGPRNS	GVNYLILDDD	DRERPWEPAA
410	420	430	440	450	460	470	480
AQMEKGQWDK	GEFVTPLLET	VSSFRPNEFE	SKFLPPENKP	LETAMLKRAK	ELFTNNDPKV	IAQHVLSMDC	RVARILGVSE
490	500	510	520	530	540	550	560
EMRRNMGVSS	GLELITLPHG	HQLRLDIIER	HNTMAIGIAV	DILGCTGTLE	DRAATLSKII	QVAVELKDSM	GDLYSFSALM
570	580	590	600	610	620	630	640
KALEMPQITR	LEKTWTALRH	QYTQTAILYE	KQLKPFSKLL	HEGRESTCVP	PNNVSVPLLM	PLVTLMERQA	VTFEGTDMWE
650	660	670	680	690	700	710	720
KNDQSCEIML	NHLATARFMA	EAADSYRMNA	ERILAGFQPD	EEMNEICKTE	FQMRLLWGSK	GAQVNQTERY	EKFNQILTAL
730	740						
SRKLEPPPVK	QAEL						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
127	1	849.3900	-71.21	2	31.0	11.9	1	460-474	K.VIAQHVLSMDCRVAR.I	

Detailed Protein Report

Protein 575: PREDICTED: diacylglycerol kinase iota isoform X1 [Homo sapiens]

Accession:	gi|578814733	**Score:**	22.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	116.2
Database Date:	2015-11-30	**pI:**	9.2
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	3.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDAAGRGCHL	LPLPAARGPA	RAPAAAAAAA	ASPPGPCSGA	ACAPSAAAGA	GAMNPSSSAG	EEKGATGGSS	SSGSGAGSCC
90	100	110	120	130	140	150	160
LGAEGGADPR	GAGSAAAAGA	AALDEPAAAG	QKEKDEALEE	KLRNLTFRKQ	VSYRKAISRA	GLQHLAPAHP	LSLPVANGPA
170	180	190	200	210	220	230	240
KEPRATLDWS	ENAVNGEHLW	LETNVSGDLC	YLGEENCQVR	FAKSALRRKC	AVCKIVVHTA	CIEQLEKINF	RCKPTFREGG
250	260	270	280	290	300	310	320
SRSPRENFVR	HHWVHRRRQE	GKCKQCGKGF	QQKFSFHSKE	IVAISCSWCK	QAFHNKVTCF	MLHHIEEPCS	LGAHAAVIVP
330	340	350	360	370	380	390	400
PTWIIKVKKP	QNSLKASNRK	KKRTSFKRKA	SKRGMEQENK	GRPFVIKPIS	SPLMKPLLVF	VNPKSGGNQG	TKVLQMFMWY
410	420	430	440	450	460	470	480
LNPRQVFDLS	QEGPKDALEL	YRKVPNLRIL	ACGGDGTVGW	ILSILDELQL	SPQPPVGVLP	LGTGNDLART	LNWGGGYTDE
490	500	510	520	530	540	550	560
PVSKILCQVE	DGTVVQLDRW	NLHVERNPDL	PPEELEDGVC	KLPLNVFNNY	FSLGFDAHVT	LEFHESREAN	PEKFNSRFRN
570	580	590	600	610	620	630	640
KMFYAGAAFS	DFLQRSSRDL	SKHVKVVCDG	TDLTPKIQEL	KFQCIVFLNI	PRYCAGTMPW	GNPGDHHDFE	PQRHDDGYIE
650	660	670	680	690	700	710	720
VIGFTMASLA	ALQVGGHGER	LHQCREVMLL	TYKSIPMQVD	GEPCRLAPAM	IRISLRNQAN	MVQKSKRRTS	MPLLNDPQSV
730	740	750	760	770	780	790	800
PDRLRIRVNK	ISLQDYEGFH	YDKEKLREAS	IPLGILVVRG	DCDLETCRMY	IDRLQEDLQS	VSSGSQRVHY	QDHETSFPRA
810	820	830	840	850	860	870	880
LSAQRLSPRW	CFLDATSADR	FYRIDRSQEH	LHFVMEISQD	EIFILDPDMV	VSQPAGTPPG	MPDLVVEQAS	GISDWWNPAL
890	900	910	920	930	940	950	960
RKRMLSDSGL	GMIAPYYEDS	DLKDLSHSRV	LQSPVSSEDH	AILQAVIAGD	LMKLIESYKN	GGSLLIQGPD	HCSLLHYAAK
970	980	990	1000	1010	1020	1030	1040
TGNGEIVKYI	LDHGPSELLD	MADSETGETA	LHKAACQRNR	AVCQLLVDAG	ASLRKTDSKG	KTPQERAQQA	GDPDLAAYLE
1050	1060						
SRQNYKVIGH	EDLETAV						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1696	1	1102.1837	102.80	2	51.0	11.5	2	1-21	-.MDAAGRGCHLLPLPAARGPAR.A	Carbamidomethyl: 8; Oxidation: 1

Detailed Protein Report

Protein 576: PREDICTED: zinc finger MYM-type protein 2 isoform X7 [Homo sapiens]

Accession:	gi|578824999	**Score:**	22.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	129.3
Database Date:	2015-11-30	**pI:**	6.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.8
		No. of unique Peptides:	2

Quantitation

MD:MU **Median:** 0.48 **CV:** 27.16 % **No. of Peptides:** 2

10	20	30	40	50	60	70	80
MDTSSVGGLE	LTDQTPVLLG	STAMATSLTN	VGNSFSGPAN	PLVSRSNKFQ	NSSVEDDDDV	VFIEPVQPPP	PSVPVVADQR
90	100	110	120	130	140	150	160
TITFTSSKNE	ELQGNDSKIT	PSSKELASQK	GSVSETIVID	DEEDMETNQG	QEKNSSNFIE	RRPPETKNRT	NDVDFSTSSF
170	180	190	200	210	220	230	240
SRSKVNAGMG	NSGITTEPDS	EIQIANVTTL	ETGVSSVNDG	QLENTDGRDM	NLMITHVTSL	QNTNLGDVSN	GLQSSNFGVN
250	260	270	280	290	300	310	320
IQTYTPSLTS	QTKTGVGPFN	PGRMNVAGDV	FQNGESATHH	NPDSWISQSA	SFPRNQKQPG	VDSLSPVASL	PKQIFQPSVQ
330	340	350	360	370	380	390	400
QQPTKPVKVT	CANCKKPLQK	GQTAYQRKGS	AHLFCSTTCL	SSFSHKPAPK	KLCVMCKKDI	TTMKGTIVAQ	VDSSESFQEF
410	420	430	440	450	460	470	480
CSTSCLSLYE	DKQNPTKGAL	NKSRCTICGK	LTEIRHEVSF	KNMTHKLCSD	HCFNRYRMAN	GLIMNCCEQC	GEYLPSKGAG
490	500	510	520	530	540	550	560
NNVLVIDGQQ	KRFCCQSCVS	EYKQVGSHPS	FLKEVRDHMQ	DSFLMQPEKY	GKLTTCTGCR	TQCRFFDMTQ	CIGPNGYMEP
570	580	590	600	610	620	630	640
YCSTACMNSH	KTKYAKSQSL	GIICHFCKRN	SLPQYQATMP	DGKLYNFCNS	SCVAKFQALS	MQSSPNGQFV	APSDIQLKCN
650	660	670	680	690	700	710	720
YCKNSFCSKP	EILEWENKVH	QFCSKTCSDD	YKKLHCIVTY	CEYCQEEKTL	HETVNFSGVK	RPFCSEGCKL	LYKQDFARRL
730	740	750	760	770	780	790	800
GLRCVTCNYC	SQLCKKGATK	ELDGVVRDFC	SEDCCKKFQD	WYYKAARCDC	CKSQGTLKER	VQWRGEMKHF	CDQHCLLRFY
810	820	830	840	850	860	870	880
CQQNEPNMTT	QKGPENLHYD	QGCQTSRTKM	TGSAPPPSPT	PNKEMKNKAV	LCKPLTMTKA	TYCKPHMQTK	SCQTDDTWRT
890	900	910	920	930	940	950	960
EYVPVPIPVP	VYIPVPMHMY	SQNIPVPTTV	PVPVPVPVFL	PAPLDSSEKI	PAAIEELKSK	VSSDALDTEL	LTMTDMMSED
970	980	990	1000	1010	1020	1030	1040
EGKTETTNIN	SVIIETDIIG	SDLLKNSDPE	TQSSMPDVPY	EPDLDIEIDF	PRAAEELDME	NEFLLPPVFG	EEYEEQPRPR
1050	1060	1070	1080	1090	1100	1110	1120
SKKKGAKRKA	VSGYQSHDDS	SDNSECSFPF	KYTYGVNAWK	HWVKTRQLDE	DLLVLDELKS	SKSVKLKEDL	LSHTTAELNY
1130	1140	1150	1160				
GLAHFVNEIR	RPNGENYAPD	SIYYLCLGIQ	EDRNLLKIL				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
1160	1	713.6536	1.59	3	44.1	11.9	2	442-457	K.NMTHKLCSDHCFNRYR.M	Carbamidomethyl: 7, 11	MD:MU	0.37
2179	1	966.3391	-135.18	2	57.4	10.1	2	720-736	R.LGLRCVTCNYCSQLCKK.G		MD:MU	0.63

Detailed Protein Report

Protein 577: PREDICTED: microtubule-associated protein 1B isoform X1 [Homo sapiens]

Accession:	gi|530379305	**Score:**	22.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	256.6
Database Date:	2015-11-30	**pI:**	4.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	0.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MITDAARHKL	LVLTGQCFEN	TGELILQSGS	FSFQNFIEIF	TDQEIGELLS	TTHPANKASL	TLFCPEEGDW	KNSNLDRHNL
90	100	110	120	130	140	150	160
QDFINIKLNS	ASILPEMEGL	SEFTEYLSES	VEVPSPFDIL	EPPTSGGFLK	LSKPCCYIFP	GGRGDSALFA	VNGFNMLING
170	180	190	200	210	220	230	240
GSERKSCFWK	LIRHLDRVDS	ILLTHIGDDN	LPGINSMLQR	KIAELEEEQS	QGSTTNSDWM	KNLISPDLGV	VFLNVPENLK
250	260	270	280	290	300	310	320
NPEPNIKMKR	SIEEACFTLQ	YLNKLSMKPE	PLFRSVGNTI	DPVILFQKMG	VGKLEMYVLN	PVKSSKEMQY	FMQQWTGTNK
330	340	350	360	370	380	390	400
DKAEFILPNG	QEVDLPISYL	TSVSSLIVWH	PANPAEKIIR	VLFPGNSTQY	NILEGLEKLK	HLDFLKQPLA	TQKDLTGQVP
410	420	430	440	450	460	470	480
TPVVKQTKLK	QRADSRESLK	PAAKPLPSKS	VRKESKEETP	EVTKVNHVEK	PPKVESKEKV	MVKKDKPIKT	ETKPSVTEKE
490	500	510	520	530	540	550	560
VPSKEEPSPV	KAEVAEKQAT	DVKPKAAKEK	TVKKETKVKP	EDKKEEKEKP	KKEVAKKEDK	TPIKKEEKPK	KEEVKKEVKK
570	580	590	600	610	620	630	640
EIKKEEKKEP	KKEVKKETPP	KEVKKEVKKE	EKKEVKKEEK	EPKKEIKKLP	KDAKKSSTPL	SEAKKPAALK	PKVPKKEESV
650	660	670	680	690	700	710	720
KKDSVAAGKP	KEKGKIKVIK	KEGKAAEAVA	AAVGTGATTA	AVMAAAGIAA	IGPAKELEAE	RSLMSSPEDL	TKDFEELKAE
730	740	750	760	770	780	790	800
EVDVTKDIKP	QLELIEDEEK	LKETEPVEAY	VIQKEREVTK	GPAESPDEGI	TTTEGEGECE	QTPEELEPVE	KQGVDDIEKF
810	820	830	840	850	860	870	880
EDEGAGFEES	SETGDYEEKA	ETEEAEEPEE	DGEEHVCVSA	SKHSPTEDEE	SAKAEADAYI	REKRESVASG	DDRAEEDMDE
890	900	910	920	930	940	950	960
AIEKGEAEQS	EEEADEEDKA	EDAREEEYEP	EKMEAEDYVM	AVVDKAAEAG	GAEEQYGFLT	TPTKQLGAQS	PGREPASSIH
970	980	990	1000	1010	1020	1030	1040
DETLPGGSES	EATASDEENR	EDQPEEFTAT	SGYTQSTIEI	SSEPTPMDEM	STPRDVMSDE	TNNEETESPS	QEFVNITKYE
1050	1060	1070	1080	1090	1100	1110	1120
SSLYSQEYSK	PADVTPLNGF	SEGSKTDATD	GKDYNASAST	ISPPSSMEED	KFSRSALRDA	YCSEVKASTT	LDIKDSISAV
1130	1140	1150	1160	1170	1180	1190	1200
SSEKVSPSKS	PSLSPSPPSP	LEKTPLGERS	VNFSLTPNEI	KVSAEAEVAP	VSPEVTQEVV	EEHCASPEDK	TLEVVSPSQS
1210	1220	1230	1240	1250	1260	1270	1280
VTGSAGHTPY	YQSPTDEKSS	HLPTEVIEKP	PAVPVSFEFS	DAKDENERAS	VSPMDEPVPD	SESPIEKVLS	PLRSPPLIGS
1290	1300	1310	1320	1330	1340	1350	1360
ESAYESFLSA	DDKASGRGAE	SPFEEKSGKQ	GSPDQVSPVS	EMTSTSLYQD	KQEGKSTDFA	PIKEDFGQEK	KTDDVEAMSS
1370	1380	1390	1400	1410	1420	1430	1440
QPALALDERK	LGDVSPTQID	VSQFGSFKED	TKMSISEGTV	SDKSATPVDE	GVAEDTYSHM	EGVASVSTAS	VATSSFPEPT
1450	1460	1470	1480	1490	1500	1510	1520
TDDVSPSLHA	EVGSPHSTEV	DDSLSVSVVQ	TPTTFQETEM	SPSKEECPRP	MSISPPDFSP	KTAKSRTPVQ	DHRSEQSSMS
1530	1540	1550	1560	1570	1580	1590	1600
IEFGQESPEQ	SLAMDFSRQS	PDHPTVGAGV	LHITENGPTE	VDYSPSDMQD	SSLSHKIPPM	EEPSYTQDND	LSELISVSQV
1610	1620	1630	1640	1650	1660	1670	1680
EASPSTSSAH	TPSQIASPLQ	EDTLSDVAPP	RDMSLYASLT	SEKVQSLEGE	KLSPKSDISP	LTPRESSPLY	SPTFSDSTSA
1690	1700	1710	1720	1730	1740	1750	1760
VKEKTATCHS	SSSPPIDAAS	AEPYGFRASV	LFDTMQHHLA	LNRDLSTPGL	EKDSGGKTPG	DFSYAYQKPE	ETTRSPDEED
1770	1780	1790	1800	1810	1820	1830	1840
YDYESYEKTT	RTSDVGGYYY	EKIERTTKSP	SDSGYSYETI	GKTTKTPEDG	DYSYEIIEKT	TRTPEEGGYS	YDISEKTTSP
1850	1860	1870	1880	1890	1900	1910	1920
PEVSGYSYEK	TERSRRLLDD	ISNGYDDSED	GGHTLGDPSY	SYETTEKITS	FPESEGYSYE	TSTKTTRTPD	TSTYCYETAE
1930	1940	1950	1960	1970	1980	1990	2000
KITRTPQAST	YSYETSDLCY	TAEKKSPSEA	RQDVDLCLVS	SCEYKHPKTE	LSPSFINPNP	LEWFASEEPT	EESEKPLTQS
2010	2020	2030	2040	2050	2060	2070	2080
GGAPPPPGGK	QQGRQCDETP	PTSVSESAPS	QTDSDVPPET	EECPSITADA	NIDSEDESET	IPTDKTVTYK	HMDPPPAPVQ
2090	2100	2110	2120	2130	2140	2150	2160
DRSPSPRHPD	VSMVDPEALA	IEQNLGKALK	KDLKEKTKTK	KPGTKTKSSS	PVKKSDGKSK	PLAASPKPAG	LKESSDKVSR
2170	2180	2190	2200	2210	2220	2230	2240
VASPKKKESV	EKAAKPTTTP	EVKAARGEEK	DKETKNAANA	SASKSAKTAT	AGPGTTKTTK	SSAVPPGLPV	YLDLCYIPNH
2250	2260	2270	2280	2290	2300	2310	2320
SNSKNVDVEF	FKRVRSSYYV	VSGNDPAAEE	PSRAVLDALL	EGKAQWGSNM	QVTLIPTHDS	EVMREWYQET	HEKQQDLNIM
2330	2340	2350					

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1859	1	1022.9020	-33.49	2	53.3	22.0	0	1073-1091	K.DYNASASTISPPSSMEEDK.F	Oxidation: 15

Detailed Protein Report

Protein 578: leucine-rich repeat-containing protein 8B [Homo sapiens]

Accession:	gi|21245134	**Score:**	22.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	92.3
Database Date:	2015-11-30	**pI:**	6.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.5
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578798841	refseq_human (refseq_human_20140103.fasta)	PREDICTED: leucine-rich repeat-containing protein 8B isoform X5 [Homo sapiens]
gi|530362288	refseq_human (refseq_human_20140103.fasta)	PREDICTED: leucine-rich repeat-containing protein 8B isoform X4 [Homo sapiens]
gi|530362286	refseq_human (refseq_human_20140103.fasta)	PREDICTED: leucine-rich repeat-containing protein 8B isoform X3 [Homo sapiens]
gi|530362284	refseq_human (refseq_human_20140103.fasta)	PREDICTED: leucine-rich repeat-containing protein 8B isoform X2 [Homo sapiens]
gi|530362282	refseq_human (refseq_human_20140103.fasta)	PREDICTED: leucine-rich repeat-containing protein 8B isoform X1 [Homo sapiens]
gi|197333692	refseq_human (refseq_human_20140103.fasta)	leucine-rich repeat-containing protein 8B [Homo sapiens]

10	20	30	40	50	60	70	80
MITLTELKCL	ADAQSSYHIL	KPWWDVFWYY	ITLIMLLVAV	LAGALQLTQS	RVLCCLPCKV	EFDNHCAVPW	DILKASMNTS
90	100	110	120	130	140	150	160
SNPGTPLPLP	LRIQNDLHRQ	QYSYIDAVCY	EKQLHWFAKF	FPYLVLLHTL	IFAACSNFWL	HYPSTSSRLE	HFVAILHKCF
170	180	190	200	210	220	230	240
DSPWTTRALS	ETVAEQSVRP	LKLSKSKILL	SSSGCSADID	SGKQSLPYPQ	PGLESAGIES	PTSSVLDKKE	GEQAKAIFEK
250	260	270	280	290	300	310	320
VKRFRMHVEQ	KDIIYRVYLK	QIIVKVILFV	LIITYVPYFL	THITLEIDCS	VDVQAFTGYK	RYQCVYSLAE	IFKVLASFYV
330	340	350	360	370	380	390	400
ILVILYGLTS	SYSLWWMLRS	SLKQYSFEAL	REKSNYSDIP	DVKNDFAFIL	HLADQYDPLY	SKRFSIFLSE	VSENKLKQIN
410	420	430	440	450	460	470	480
LNNEWTVEKL	KSKLVKNAQD	KIELHLFMLN	GLPDNVFELT	EMEVLSLELI	PEVKLPSAVS	QLVNLKELRV	YHSSLVVDHP
490	500	510	520	530	540	550	560
ALAFLEENLK	ILRLKFTEMG	KIPRWVFHLK	NLKELYLSGC	VLPEQLSTMQ	LEGFQDLKNL	RTLYLKSSLS	RIPQVVTDLL
570	580	590	600	610	620	630	640
PSLQKLSLDN	EGSKLVVLNN	LKKMVNLKSL	ELISCDLERI	PHSIFSLNNL	HELDLRENNL	KTVEEIISFQ	HLQNLSCLKL
650	660	670	680	690	700	710	720
WHNNIAYIPA	QIGALSNLEQ	LSLDHNNIEN	LPLQLFLCTK	LHYLDLSYNH	LTFIPEEIQY	LSNLQYFAVT	NNNIEMLPDG
730	740	750	760	770	780	790	800
LFQCKKLQCL	LLGKNSLMNL	SPHVGELSNL	THLELIGNYL	ETLPPELEGC	QSLKRNCLIV	EENLLNTLPL	PVTERLQTCL
810							
DKC							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1622	1	1100.2202	-11.62	3	50.2	22.0	2	776-803	R.NCLIVEENLLNTLPLPVTERLQTCLDKC.-	Carbamidomethyl: 24, 28

Detailed Protein Report

Protein 579: PREDICTED: collagen alpha-4(IV) chain isoform X9 [Homo sapiens]

Accession:	gi|578803629	**Score:**	22.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	135.0
Database Date:	2015-11-30	**pI:**	10.1
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.5
		No. of unique Peptides:	2

Quantitation

MD:MU	**Median:** 3.74	**CV:** 0.00 %	**No. of Peptides:** 1

10	20	30	40	50	60	70	80
MWSLHIVLMR	CSFRLTKSLA	TGPWSLILIL	FSVQYVYGSG	KKYIGPCGGR	DCSVCHCVPE	KGSRGPPGPP	GPQGPIGPLG
90	100	110	120	130	140	150	160
APGPIGLSGE	KGMRGDRGPP	GAAGDKGDKG	PTGVPGFPGL	DGIPGHPGPP	GPRGKPGMSG	HNGSRGDPGF	PGGRGALGPG
170	180	190	200	210	220	230	240
GPLGHPGEKG	EKGNSVFILG	AVKGIQGDRG	DPGLPGLPGS	WGAGGPAGPT	GYPGEPGLVG	PPGQPGRPGL	KGNPGVGVKG
250	260	270	280	290	300	310	320
QMGDPGEVGQ	QGSPGPTLLV	EPPDFCLYKG	EKGIKGIPGM	VGLPGPPGRK	GESGIGAKGE	KGIPGFPGPR	GDPGSYGSPG
330	340	350	360	370	380	390	400
FPGLKGELGL	VGDPGLFGLI	GPKGDPGNRG	HPGPPGVLVT	PPLPLKGPPG	DPGFPGRYGE	TGDVGPPGPP	GLLGRPGEAC
410	420	430	440	450	460	470	480
AGMIGPPGPQ	GFPGLPGLPG	EAGIPGRPDS	APGKPGKPGS	PGLPGAPGLQ	GLPGSSVIYC	SVGNPGPQGI	KGKVGPPGGR
490	500	510	520	530	540	550	560
GPKGEKGNEG	LCACEPGPMG	PPGPPGLPGR	QGSKGDLGLP	GWLGTKGDPG	PPGAEGPPGL	PGKHGASGPP	GNKGAKGDMV
570	580	590	600	610	620	630	640
VSRVKGHKGE	RGPDGPPGFP	GQPGSHGRDG	HAGEKGDPGP	PGDHEDATPG	GKGFPGPLGP	PGKAGPVGPP	GLGFPGPPGE
650	660	670	680	690	700	710	720
RGHPGVPGHP	GVRGPDGLKG	QKGDTISCNV	TYPGRHGPPG	FDGPPGPKGF	PGPQGAPGLS	GSDGHKGRPG	TPGTAEIPGP
730	740	750	760	770	780	790	800
PGFRGDMGDP	GFGGEKGSSP	VGPPGPPGSP	GVNGQKGIPG	DPAFGHLGPP	GKRGLSGVPG	IKGPRGDPGC	PGAEGPAGIP
810	820	830	840	850	860	870	880
GFLGLKGPKG	REGHAGFPGV	PGPPGHSCER	GAPGIPGQPG	LPGYPGSPGA	PGGKGQPGDV	GPPGPAGMKG	LPGLPGRPGA
890	900	910	920	930	940	950	960
HGPPGLPGIP	GPFGDDGLPG	PPGPKGPRGL	PGFPGFPGER	GKPGAEGCPG	AKGEPGEKGM	SGLPGDRGLR	GAKGAIGPPG
970	980	990	1000	1010	1020	1030	1040
DEGEMAIISQ	KGTPGEPGPP	GDDGFPGERG	DKGTPGMQGR	RGEPGRYGPP	GFHRGEPGEK	GQPGPPGPPG	PPGSTGLRGF
1050	1060	1070	1080	1090	1100	1110	1120
IGFPGLPGDQ	GEPGSPGPPG	FSGIDGARGP	KGNKGDPASH	FGPPGPKGEP	GSPGCPGHFG	ASGEQGLPGI	QGPRGSPGRP
1130	1140	1150	1160	1170	1180	1190	1200
GPPGSSGPPG	CPGDHGMPGL	RGQPGEMGDP	GPRGLQGDPG	IPGPPGIKGP	SGSPGLNGLH	GLKGQKGTKG	ASGLHDVGPP
1210	1220	1230	1240	1250	1260	1270	1280
GPVGIPGLKG	ERGDPGSPGI	SPPGPRGKKG	PPGPPGSSGP	PGPAGATGRA	PKDIPDPGPP	GDQGPPGPDG	PRGAPGPPGL
1290	1300	1310	1320	1330	1340	1350	1360
PGSVDLLRGE	PGDCGLPGPP	GPPGPPGPPG	YKGFPGCDGK	DGQKGPVGFP	GPQGPHGFPG	PPGEKGLPGP	PGRKGPTGLP
1370	1380	1390	1400	1410	1420	1430	
GPRGEPGPPA	DVDDCPRIPG	LPGAPGMRGP	EGAMGLPGMR	GPSGPGGTRG	RQTALRKTCN		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
474	1	607.1354	-216.53	2	35.2	11.4	0	1142- 1153	R.GQPGEMGDPGPR.G	Oxidation: 6	MD:MU 3.74
950	1	984.1390	132.77	2	41.4	10.5	1	1230- 1252	K. GPPGPPGSSGPPGPAGATGRAP D		

Detailed Protein Report

Protein 580: PREDICTED: A-kinase anchor protein 10, mitochondrial isoform X4 [Homo sapiens]

Accession:	gi|578829668	**Score:**	22.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	65.4
Database Date:	2015-11-30	**pI:**	5.2
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDSFSSSRTA	TLKKQPSHME	AAHFGDLGRS	CLDYQTQETK	SSLSKTLEQV	LHDTIVLPYF	IQFMELRRME	HLVKFWLEAE
90	100	110	120	130	140	150	160
SFHSTTWSRI	RAHSLNTVKQ	SSLAEPVSPS	KKHETTASFL	TDSLDKRLED	SGSAQLFMTH	SEGIDLNNRT	NSTQNHLLLS
170	180	190	200	210	220	230	240
QECDSAHSLR	LEMARAGTHQ	VSMETQESSS	TLTVASRNSP	ASPLKELSGK	LMKSIEQDAV	NTFTKYISPD	AAKPIPITEA
250	260	270	280	290	300	310	320
MRNDIIARIC	GEDGQVDPNC	FVLAQSIVFS	AMEQEHFSEF	LRSHHFCKYQ	IEVLTSGTVY	LADILFCESA	LFYFSEYMEK
330	340	350	360	370	380	390	400
EDAVNILQFW	LAADNFQSQL	AAKKGQYDGQ	EAQNDAMILY	DKYFSLQATH	PLGFDDVVRL	EIESNICREG	GPLPNCFTTP
410	420	430	440	450	460	470	480
LRQAWTTMEK	VFLPGFLSSN	LYYKYLNDLI	HSVRGDEFLG	GNVSLTAPGS	VGPPDESHPG	SSDSSASQSS	VKKASIKILK
490	500	510	520	530	540	550	560
NFDEAIIVDA	ASLDPESLYQ	RTYAGKMTFG	RVSDLGQFIR	ESEPEPDVRK	SKGSMFSQAM	KKWVQGNTDE	AQEELAWKIA
570	580	590					
KMIVSDIMQQ	AQYDQPLEKS	TKL					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1254	1	673.3228	-16.24	2	45.3	22.0	2	531-542	K.SKGSMFSQAMKK.W	Oxidation: 10

Detailed Protein Report

Protein 581: PREDICTED: myomegalin isoform X1 [Homo sapiens]

Accession:	gi|530432185	**Score:**	22.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	287.2
Database Date:	2015-11-30	**pI:**	5.4
		Sequence Coverage [%]:	1.2
		No. of unique Peptides:	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MKEICRICAR	ELCGNQRRWI	FHTASKLNLQ	VLLSHVLGKD	VPRDGKAEFA	CSKCAFMLDR	IYRFDTVIAR	IEALSIERLQ
90	100	110	120	130	140	150	160
KLLLEKDRLK	FCIASMYRKN	NDDSGAEIKA	GNGTVDMSVL	PDARYSALLQ	EDFAYSGFEC	WVENEDQIQE	PHSCHGSEGP
170	180	190	200	210	220	230	240
GNRPRRCRGC	AALRVADSDY	EAICKVPRKV	ARSISCGPSS	RWSTSICTEE	PALSEVGPPD	LASTKVPPDG	ESMEEETPGS
250	260	270	280	290	300	310	320
SVESLDASVQ	ASPPQQKDEE	TERSAKELGK	CDCCSDDQAP	QHGCNHKLEL	ALSMIKGLDY	KPIQSPRGSR	LPIPVKSSLP
330	340	350	360	370	380	390	400
GAKPGPSMTD	GVSSGFLNRS	LKPLYKTPVS	YPLELSDLQE	LWDDLCEDYL	PLRVQPMTEE	LLKQQKLNSH	ETTITQQSVS
410	420	430	440	450	460	470	480
DSHLAELQEK	IQQTEATNKI	LQEKLNEMSY	ELKCAQESSQ	KQDGTIQNLK	ETLKSRERET	EELYQVIEGQ	NDTMAKLREM
490	500	510	520	530	540	550	560
LHQSQLGQLH	SSEGTSPAQQ	QVALLDLQSA	LFCSQLEIQK	LQRVVRQKER	QLADAKQCVQ	FVEAAAHESE	QQKEASWKHN
570	580	590	600	610	620	630	640
QELRKALQQL	QEELQNKSQQ	LRAWEAEKYN	EIRTQEQNIQ	HLNHSLSHKE	QLLQEFRELL	QYRDNSDKTL	EANEMLLEKL
650	660	670	680	690	700	710	720
RQRIHDKAVA	LERAIDEKFS	ALEEKEKELR	QLRLAVRERD	HDLERLRDVL	SSNEATMQSM	ESLLRAKGLE	VEQLSTTCQN
730	740	750	760	770	780	790	800
LQWLKEEMET	KFSRWQKEQE	SIIQQLQTSL	HDRNKEVEDL	SATLLCKLGP	GQSEIAEELC	QRLQRKERML	QDLLSDRNKQ
810	820	830	840	850	860	870	880
VLEHEMEIQG	LLQSVSTREQ	ESQAAAEKLV	QALMERNSEL	QALRQYLGGR	DSLMSQAPIS	NQQAEVTPTG	RLGKQTDQGS
890	900	910	920	930	940	950	960
MQIPSRDDST	SLTAKEDVSI	PRSTLGDLDT	VAGLEKELSN	AKEELELMAK	KERESQMELS	ALQSMMAVQE	EELQVQAADM
970	980	990	1000	1010	1020	1030	1040
ESLTRNIQIK	EDLIKDLQMQ	LVDPEDIPAM	ERLTQEVLLL	REKVASVESQ	GQEISGNRRQ	QLLLMLEGLV	DERSRLNEAL
1050	1060	1070	1080	1090	1100	1110	1120
QAERQLYSSL	VKFHAHPESS	ERDRTLQVEL	EGAQVLRSRL	EEVLGRSLER	LNRLETLAAI	GGAAAGDDTE	DTSTEFTDSI
1130	1140	1150	1160	1170	1180	1190	1200
EEEAAHHSHQ	QLVKVALEKS	LATVETQNPS	FSPPSPMGGD	SNRCLQEEML	HLRAEFHQHL	EEKRKAEEEL	KELKAQIEEA
1210	1220	1230	1240	1250	1260	1270	1280
GFSSVSHIRN	TMLSLCLENA	ELKEQMGEAM	SDGWEIEEDK	EKGEVMVETV	VTKEGLSESS	LQAEFRKLQG	KLKNAHNIIN
1290	1300	1310	1320	1330	1340	1350	1360
LLKEQLVLSS	KEGNSKLTPE	LLVHLTSTIE	RINTELVGSP	GKHQHQEEGN	VTVRPFPRPQ	SLDLGATFTV	DAHQLDNQSQ
1370	1380	1390	1400	1410	1420	1430	1440
PRDPGPQSAF	SLPGSTQHLR	SQLSQCKQRY	QDLQEKLLLS	EATVFAQANE	LEKYRVMLTG	ESLVKQDSKQ	IQVDLQDLGY
1450	1460	1470	1480	1490	1500	1510	1520
ETCGRSENEA	EREETTSPEC	EEHNSLKEMV	LMEGLCSEQG	RRGSTLASSS	ERKPLENQLG	KQEEFRVYGK	SENILVLRKD
1530	1540	1550	1560	1570	1580	1590	1600
IKDLKAQLQN	ANKVIQNLKS	RVRSLSVTSD	YSSSLERPRK	LRAVGTLEGS	SPHSVPDEDE	GWLSDGTGAF	YSPGLQAKKD
1610	1620	1630	1640	1650	1660	1670	1680
LESLIQRVSQ	LEAQLPKNGL	EEKLAEELRS	ASWPGKYDSL	IQDQARELSY	LRQKIREGRG	ICYLITRHAK	DTVKSFEDLL
1690	1700	1710	1720	1730	1740	1750	1760
RSNDIDYYLG	QSFREQLAQG	SQLTERLTSK	LSTKDHKSEK	DQAGLEPLAL	RLSRELQEKE	KVIEVLQAKL	DARSLTPSSS
1770	1780	1790	1800	1810	1820	1830	1840
HALSDSHRSP	SSTSFLSDEL	EACSDMDIVS	EYTHYEEKKA	SPSHSDSIHH	SSHSAVLSSK	PSSTSASQGA	KAESNSNPIS
1850	1860	1870	1880	1890	1900	1910	1920
LPTPQNTPKE	ANQAHSGFHF	HSIPKLASLP	QAPLPSAPSS	FLPFSPTGPL	LLGCCETPVV	SLAEAQQELQ	MLQKQLGESA
1930	1940	1950	1960	1970	1980	1990	2000
STVPPASTAT	LLSNDLEADS	SYYLNSAQPH	SPPRGTIELG	RILEPGYLGS	SGKWDVMRPQ	KGSVSGDLSS	GSSVYQLNSK
2010	2020	2030	2040	2050	2060	2070	2080
PTGADLLEEH	LGEIRNLRQR	LEESICINDR	LREQLEHRLT	STARGRGSTS	NFYSQGLESI	PQLCNENRVL	REDNRRLQAQ
2090	2100	2110	2120	2130	2140	2150	2160
LSHVSREHSQ	ETESLREALL	SSRSHLQELE	KELEHQKVER	QQLLEDLREK	QQEVLHFREE	RLSLQENDSR	LQHKLVLLQQ
2170	2180	2190	2200	2210	2220	2230	2240
QCEEKQQLFE	SLQSELQIYE	ALYGNSKKGL	KAYSLDACHQ	IPLSSDLSHL	VAEVRALRGQ	LEQSIQGNNC	LRLQLQQQLE
2250	2260	2270	2280	2290	2300	2310	2320
SGAGKASLSP	SSINQNFPAS	TDPGNKQLLL	QDSAVSPPVR	DVGMNSPALV	FPSSASSTPG	SETPIINRAN	GLGLDTSPVM
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
569	1	671.4345	38.57	2	36.4	10.8	1	993-1003	R.LTQEVLLLREK.V	

Detailed Protein Report

Protein 582: NACHT, LRR and PYD domains-containing protein 2 isoform 3 [Homo sapiens]

Accession:	gi|291463280	**Score:**	21.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	117.8
Database Date:	2015-11-30	**pI:**	5.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.6
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MVSSAQMGFN	LQALLEQLSQ	DELSKFKYLI	TTFSLAHELQ	KIPHKEMASL	QVFEKMHRMD	LSERAKDEVR	EAALKSFNKR
90	100	110	120	130	140	150	160
KPLSLGITRK	ERPPLDVDEM	LERFKTEAQA	FTETKGNVIC	LGKEVFKGKK	PDKDNRCRYI	LKTKFREMWK	SWPGDSKEVQ
170	180	190	200	210	220	230	240
VMAERYKMLI	PFSNPRVLPG	PFSYTVVLYG	PAGLGKTTLA	QKLMLDWAED	NLIHKFKYAF	YLSCRELSRL	GPCSFAELVF
250	260	270	280	290	300	310	320
RDWPELQDDI	PHILAQARKI	LFVIDGFDEL	GAAPGALIED	ICGDWEKKKP	VPVLLGSLLN	RVMLPKAALL	VTTRPRALRD
330	340	350	360	370	380	390	400
LRILAEEPIY	IRVEGFLEED	RRAYFLRHFG	DEDQAMRAFE	LMRSNAALFQ	LGSAPAVCWI	VCTTLKLQME	KGEDPVPTCL
410	420	430	440	450	460	470	480
TRTGLFLRFL	CSRFPQGAQL	RGALRTLSLL	AAQGLWAQTS	VLHREDLERL	GVQESDLRLF	LDGDILRQDR	VSKGCYSFIH
490	500	510	520	530	540	550	560
LSFQQFLTAL	FYTLEKEEEE	DRDGHTWDIG	DVQKLLSGVE	RLRNPDLIQA	GYYSFGLANE	KRAKELEATF	GCRMSPDIKQ
570	580	590	600	610	620	630	640
ELLRCDISCK	GGHSTVTDLQ	ELLGCLYESQ	EEELVKEVMA	QFKEISLHLN	AVDVVPSSFC	VKHCRNLQKM	SLQVIKENLP
650	660	670	680	690	700	710	720
ENVTASESDA	EVERSQDDQH	MLPFWTDLCS	IFGSNKDLMG	LAINDSFLSA	SLVRILCEQI	ASDTCHLQRV	VFKNISPADA
730	740	750	760	770	780	790	800
HRNLCLALRG	HKTVTYLTLQ	GNDQDDMFPA	LCEVLRHPEC	NLRYLGLVSC	SATTQQWADL	SLALEVNQSL	TCVNLSDNEL
810	820	830	840	850	860	870	880
LDEGAKLLYT	TLRHPKCFLQ	RLSLENCHLT	EANCKDLAAV	LVVSRELTHL	CLAKNPIGNT	GVKFLCEGLR	YPECKLQTLV
890	900	910	920	930	940	950	960
LWNCDITSDG	CCDLTKLLQE	KSSLLCLDLG	LNHIGVKGMK	FLCEALRKPL	CNLRCLWLWG	CSIPPFSCED	LCSALSCNQS
970	980	990	1000	1010	1020	1030	1040
LVTLDLGQNP	LGSSGVKMLF	ETLTCSSGTL	RTLRLKIDDF	NDELNKLLEE	IEEKNPQLII	DTEKHHPWAE	RPSSHDFMI

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1922	1	893.8122	-134.43	2	53.9	11.2	0	695-709	R.ILCEQIASDTCHLQR.V	Carbamidomethyl: 3
1197	1	786.4909	152.63	2	44.6	10.8	1	864-875	K.FLCEGLRYPECK.L	Carbamidomethyl: 3, 11

Detailed Protein Report

Protein 583: E3 ubiquitin-protein ligase HECW1 isoform b [Homo sapiens]

Accession:	gi|559098413	**Score:**	21.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	175.6
Database Date:	2015-11-30	**pI:**	5.2
		Sequence Coverage [%]:	2.0
		No. of unique Peptides:	2

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
405	1	631.2089	-107.18	3	34.4	10.9	0	505-521	K.EQEEEGDVSTLEQGEGR.L	
1838	1	731.2905	-123.49	2	52.8	11.1	1	1387-1400	R.ELKSGGANTQVTEK.N	

Detailed Protein Report

Protein 584: rho guanine nucleotide exchange factor 33 [Homo sapiens]

Accession:	gi|290463441	**Score:**	21.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	97.5
Database Date:	2015-11-30	**pI:**	6.4
		Sequence Coverage [%]:	3.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEKTKTKQGE	NEHMPVNNPS	TQIYQLQALA	SELKTGFTEA	MQELSRIQHG	EYALEEKVKS	CRCSMEEKVT	EMKNSLNYFK
90	100	110	120	130	140	150	160
EELSNAMSMI	QAITSKQEEM	QQKIEQLQQE	KRRESRKVKA	KKTQKEEHSS	QAGPAQAQGS	PFRSINIPEP	VLPSEDFTNL
170	180	190	200	210	220	230	240
LPSQAYEKAQ	ESRSVHVGDS	NVKGMMGPGV	NPTTPEAEEN	LKSCLSADIQ	SKGHLPSGMW	RQPKDGKEWG	EEYVTKDHPD
250	260	270	280	290	300	310	320
KLKEAGQGRH	SSLENVLCET	SLAAKRQTVA	LELLESERKY	VINISLILKI	KATFQGSDGK	RNSKERSLFP	GSLRYLVQQH
330	340	350	360	370	380	390	400
LDLLHALQER	VLKWPRQGVL	GDLFLKLTND	ENNFLDYYVA	YLRDLPECIS	LVHVVVLKEG	DEEIKSDIYT	LFFHIVQRIP
410	420	430	440	450	460	470	480
EYLIHLQNVL	KFTEQEHPDY	YLLLVCVQRL	RVFISHYTLL	FQCNEDLLIQ	KRKKLKKSSM	AKLYKGLASQ	CANAGQDASP
490	500	510	520	530	540	550	560
TAGPEAVRDT	GIHSEELLQP	YPSAPSSGPA	ITHLMPPVKK	SQQQQSLMES	MQPGKPSDWE	LEGRKHERPE	SLLAPTQFCA
570	580	590	600	610	620	630	640
AEQDVKALAG	PLQAIPEMDF	ESSPAEPLGN	VERSLRAPAE	LLPDARGFVP	AAYEEFEYGG	EIFALPAPYD	EEPFQAPALF
650	660	670	680	690	700	710	720
ENCSPASSES	SLDICFLRPV	SFAMEAERPE	HPLQPLPKSA	TSPAGSSSAY	KLEAAAQAHG	KAKPLSRSLK	EFPRAPPADG
730	740	750	760	770	780	790	800
VAPRLYSTRS	SSGGRAPIKA	ERAAQAHGPA	AAAVAARGAS	RTFFPQQRSQ	SEKQTYLEVR	REMHLEDTTR	FCPKEERESE
810	820	830	840	850	860	870	880
QTSFSDQNPR	QDQKGGFRSS	FRKLFKKKSS	GSEYREKTNE	NPSMDPSPTK	QDFFRNRLAL	ANDLDQGTAV	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1626	2	745.8661	-55.26	2	50.1	11.4	2	302-314	R.NSKERSLFPGSLR.Y	

Detailed Protein Report

Protein 585: PREDICTED: nuclear body protein SP140 isoform X7 [Homo sapiens]

Accession:	gi|530369725	**Score:**	21.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	77.3
Database Date:	2015-11-30	**pI:**	7.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	5.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAQQGQQGQM	ASGDSNLNFR	MVAEIQNVEG	QNLQEQVCPE	PIFRFFRENK	VEIASAITRP	FPFLMGLRDR	SFISEQMYEH
90	100	110	120	130	140	150	160
FQEAFRNLVP	VTRVMYCVLS	ELEKTFGWSH	LEALFSRINL	MAYPDLNEIY	RSFQNVCYEH	SPLQMNNVND	LEDRPRLLPY
170	180	190	200	210	220	230	240
GKQENSNACH	EMDDIAVPQE	ALSSSPRCEP	GFSSESCEQL	ALPKAGGGDA	EDAPSLLPGG	GVSSELENHP	MNEEGESEEL
250	260	270	280	290	300	310	320
ASSLLYDNVP	GAEQSAYENE	KCSCVMCFSE	EVPGSPEART	ESDQACGTMD	TVDIANNSTL	GKPKRKRRKK	RGHGWSRMRM
330	340	350	360	370	380	390	400
RRQENSQQND	NSKADGQVVS	SEKKANVNLK	DLSKIRGRKR	GKPGTRFTQS	DRAAQKRVRS	RASRKHKDET	VDFKAPLLPV
410	420	430	440	450	460	470	480
TCGGVKGILH	KKKLQQGILV	KCIQTEDGKW	FTPTEFEIKG	GHARSKNWRL	SVRCGGWPLR	WLMENGFLPD	PPRIRYRKKK
490	500	510	520	530	540	550	560
RILKSQNNSS	VDPCMRNLDE	CEVCRDGGEL	FCCDTCSRVF	HEDCHIPPVE	AERTPWNCIF	CRMKESPGSQ	QCCQESEVLE
570	580	590	600	610	620	630	640
RQMCPEEQLK	CEFLLLKVYC	CSESSFFAKI	PYYYYIREAC	QGLKEPMWLD	KIKKRLNEHG	YPQVEGFVQD	MRLIFQNHRA
650	660	670	680				
SYKYKDFGQM	GFRLEAEFEK	NFKEVFAIQE	TNGNN				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2587	1	941.5681	155.71	2	62.4	10.3	0	188-204	R.CEPGFSSESCEQLALPK.A	Carbamidomethyl: 1

Detailed Protein Report

Protein 586: inactive serine protease 35 precursor [Homo sapiens]

Accession:	gi|281427284	**Score:**	21.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	47.1
Database Date:	2015-11-30	**pI:**	10.3
Modification(s):	Oxidation	**Sequence Coverage [%]:**	10.2
		No. of unique Peptides:	2

Alias proteins:

Accession	Name	Description
gi|281427286	refseq_human (refseq_human_20140103.fasta)	inactive serine protease 35 precursor [Homo sapiens]

```
         10         20         30         40         50         60         70         80
MENMLLWLIF FTPGWTLIDG SEMEWDFMWH LRKVPRIVSE RTFHLTSPAF EADAKMMVNT VCGIECQKEL PTPSLSELED
         90        100        110        120        130        140        150        160
YLSYETVFEN GTRTLTRVKV QDLVLEPTQN ITTKGVSVRR KRQVYGTDSR FSILDKRFLT NFPFSTAVKL STGCSGILIS
        170        180        190        200        210        220        230        240
PQHVLTAAHC VHDGKDYVKG SKKLRVGLLK MRNKSGGKKR RGSKRSRREA SGGDQREGTR EHLRERAKGG RRRKKSGRGQ
        250        260        270        280        290        300        310        320
RIAEGRPSFQ WTRVKNTHIP KGWARGGMGD ATLDYDYALL ELKRAHKKKY MELGISPTIK KMPGGMIHFS GFDNDRADQL
        330        340        350        360        370        380        390        400
VYRFCSVSDE SNDLLYQYCD AESGSTGSGV YLRLKDPDKK NWKRKIIAVY SGHQWVDVHG VQKDYNVAVR ITPLKYAQIC
        410        420
LWIHGNDANC AYG
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2001	1	698.2933	-125.88	2	54.9	10.1	1	289-300	K.KYMELGISPTIK.K	Oxidation: 3
1626	1	1135.9599	6.52	3	50.2	11.8	2	366-395	K.IIAVYSGHQWVDVHGVQKDYNVAVRITPLK.Y	

Detailed Protein Report

Protein 587: cleavage and polyadenylation specificity factor subunit 2 [Homo sapiens]

Accession:	gi|34101288	**Score:**	21.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	88.4
Database Date:	2015-11-30	**pI:**	4.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.4
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|530403998	refseq_human (refseq_human_20140103.fasta)	PREDICTED: cleavage and polyadenylation specificity factor subunit 2 isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MTSIIKLTTL	SGVQEESALC	YLLQVDEFRF	LLDCGWDEHF	SMDIIDSLRK	HVHQIDAVLL	SHPDPLHLGA	LPYAVGKLGL
90	100	110	120	130	140	150	160
NCAIYATIPV	YKMGQMFMYD	LYQSRHNTED	FTLFTLDDVD	AAFDKIQQLK	FSQIVNLKGK	GHGLSITPLP	AGHMIGGTIW
170	180	190	200	210	220	230	240
KIVKDGEEEI	VYAVDFNHKR	EIHLNGCSLE	MLSRPSLLIT	DSFNATYVQP	RRKQRDEQLL	TNVLETLRGD	GNVLIAVDTA
250	260	270	280	290	300	310	320
GRVLELAQLL	DQIWRTKDAG	LGVYSLALLN	NVSYNVVEFS	KSQVEWMSDK	LMRCFEDKRN	NPFQFRHLSL	CHGLSDLARV
330	340	350	360	370	380	390	400
PSPKVVLASQ	PDLECGFSRD	LFIQWCQDPK	NSIILTYRTT	PGTLARFLID	NPSEKITEIE	LRKRVKLEGK	ELEEYLEKEK
410	420	430	440	450	460	470	480
LKKEAAKKLE	QSKEADIDSS	DESDIEEDID	QPSAHKTKHD	LMMKGEGSRK	GSFFKQAKKS	YPMFPAPEER	IKWDEYGEII
490	500	510	520	530	540	550	560
KPEDFLVPEL	QATEEEKSKL	ESGLTNGDEP	MDQDLSDVPT	KCISTTESIE	IKARVTYIDY	EGRSDGDSIK	KIINQMKPRQ
570	580	590	600	610	620	630	640
LIIVHGPPEA	SQDLAECCRA	FGGKDIKVYM	PKLHETVDAT	SETHIYQVRL	KDSLVSSLQF	CKAKDAELAW	IDGVLDMRVS
650	660	670	680	690	700	710	720
KVDTGVILEE	GELKDDGEDS	EMQVEAPSDS	SVIAQQKAMK	SLFGDDEKET	GEESEIIPTL	EPLPPHEVPG	HQSVFMNEPR
730	740	750	760	770	780	790	
LSDFKQVLLR	EGIQAEFVGG	VLVCNNQVAV	RRTETGRIGL	EGCLCQDFYR	IRDLLYEQYA	IV	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
303	1	1292.7280	120.56	1	33.5	21.9	1	439-449	K.HDLMMKGEGSR.K	Oxidation: 4, 5

Detailed Protein Report

Protein 588: **52 kDa repressor of the inhibitor of the protein kinase [Homo sapiens]**

Accession:	gi|19923268	**Score:**	21.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	87.6
Database Date:	2015-11-30	**pI:**	5.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.5
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 0.58 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MPNFCAAPNC	TRKSTQSDLA	FFRFPRDPAR	CQKWVENCRR	ADLEDKTPDQ	LNKHYRLCAK	HFETSMICRT	SPYRTVLRDN
90	100	110	120	130	140	150	160
AIPTIFDLTS	HLNNPHSRHR	KRIKELSEDE	IRTLKQKKID	ETSEQEQKHK	ETNNSNAQNP	SEEEGEGQDE	DILPLTLEEK
170	180	190	200	210	220	230	240
ENKEYLKSLF	EILILMGKQN	IPLDGHEADE	IPEGLFTPDN	FQALLECRIN	SGEEVLRKRF	ETTAVNTLFC	SKTQQRQMLE
250	260	270	280	290	300	310	320
ICESCIREET	LREVRDSHFF	SIITDDVVDI	AGEEHLPVLV	RFVDESHNLR	EEFIGFLPYE	ADAEILAVKF	HTMITEKWGL
330	340	350	360	370	380	390	400
NMEYCRGQAY	IVSSGFSSKM	KVVASRLLEK	YPQAIYTLCS	SCALNMWLAK	SVPVMGVSVA	LGTIEEVCSF	FHRSPQLLLE
410	420	430	440	450	460	470	480
LDNVISVLFQ	NSKERGKELK	EICHSQWTGR	HDAFEILVEL	LQALVLCLDG	INSDTNIRWN	NYIAGRAFVL	CSAVSDFDFI
490	500	510	520	530	540	550	560
VTIVVLKNVL	SFTRAFGKNL	QGQTSDVFFA	AGSLTAVLHS	LNEVMENIEV	YHEFWFEEAT	NLATKLDIQM	KLPGKFRRAH
570	580	590	600	610	620	630	640
QGNLESQLTS	ESYYKETLSV	PTVEHIIQEL	KDIFSEQHLK	ALKCLSLVPS	VMGQLKFNTS	EEHHADMYRS	DLPNPDTLSA
650	660	670	680	690	700	710	720
ELHCWRIKWK	HRGKDIELPS	TIYEALHLPD	IKFFPNVYAL	LKVLCILPVM	KVENERYENG	RKRLKAYLRN	TLTDQRSSNL
730	740	750	760	770			
ALLNINFDIK	HDLDLMVDTY	IKLYTSKSEL	PTDNSETVEN	T			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2085	1	731.3255	-123.74	2	56.2	10.1	2	546-557	K.LDIQMKLPGKFR.R	Oxidation: 5	MD:MU 0.58

Detailed Protein Report

Protein 589: PREDICTED: glycylpeptide N-tetradecanoyltransferase 1 isoform X1 [Homo sapiens]

Accession:	gi|530412338	**Score:**	21.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	61.3
Database Date:	2015-11-30	**pI:**	9.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.5
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MPGGRPVPKG	TPHVVGRGAL	LSQLKMADES	ETAVKPPAPP	LPQMMEGNGN	GHEHCSDCEN	EEDNSYNRGG	LSPANDTGAK
90	100	110	120	130	140	150	160
KKKKKQKKKK	EKGSETDSAQ	DQPVKMNSLP	AERIQEIQKA	IELFSVGQGP	AKTMEEASKR	SYQFWDTQPV	PKLGEVVNTH
170	180	190	200	210	220	230	240
GPVEPDKDNI	RQEPYTLPQG	FTWDALDLGD	RGVLKELYTL	LNENYVEDDD	NMFRFDYSPE	FLLWALRPPG	WLPQWHCGVR
250	260	270	280	290	300	310	320
VVSSRKLVGF	ISAIPANIHI	YDTEKKMVEI	NFLCVHKKLR	SKRVAPVLIR	EITRRVHLEG	IFQAVYTAGV	VLPKPVGTCR
330	340	350	360	370	380	390	400
YWHRSLNPRK	LIEVKFSHLS	RNMTMQRTMK	LYRLPETPKT	AGLRPMETKD	IPVVHQLLTR	YLKQFHLTPV	MSQEEVEHWF
410	420	430	440	450	460	470	480
YPQENIIDTF	VVENANGEVT	DFLSFYTLPS	TIMNHPTHKS	LKAAYSFYNV	HTQTPLLDLM	SDALVLAKMV	RSRRGGLWRC
490	500	510	520	530	540	550	
AGKRQWSHGE	HSSRDAASHG	LEALSPPHLF	CLGRVPAVFR	QKLKTWREQG	ASEVKALNSS		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
653	1	820.5245	82.19	1	37.7	10.3	2	469-474	K.MVRSRR.G	Oxidation: 1
2042	1	766.2799	-176.23	2	55.4	11.5	2	523-535	K.LKTWREQGASEVK.A	

Detailed Protein Report

Protein 590: PREDICTED: PR domain zinc finger protein 15 isoform X2 [Homo sapiens]

Accession:	gi|578836645	**Score:**	21.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	128.4
Database Date:	2015-11-30	**pI:**	9.2
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	3.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPRRRPPASG	AAQFPERIAT	RSPDPIPLCT	FQRQVSEMAE	DGSEEIMFIW	CEDCSQYHDS	ECPELGPVVM	VKDSFVLSRA
90	100	110	120	130	140	150	160
RSSLPPNLEI	RRLEDGAEGV	FAITQLVKRT	QFGPFESRRV	AKWEKESAFP	LKVFQKDGHP	VCFDTSNEDD	CNWMMLVRPA
170	180	190	200	210	220	230	240
AEAEHQNLTA	YQHGSDVYFT	TSRDIPPGTE	LRVWYAAFYA	KKMDKPMLKQ	AGSGVHAAGT	PENSAPVESE	PSQWACKVCS
250	260	270	280	290	300	310	320
ATFLELQLLN	EHLLGHLEQA	KSLPPGSQSE	AAAPEKEQDT	PRGEPPAVPE	SENVATKEQK	KKPRRGRKPK	VSKAEQPLVI
330	340	350	360	370	380	390	400
VEDKEPTEQV	AEIITEVPPD	EPVSATPDER	IMELVLGKLA	TTTTDTSSVP	KFTHHQNNTI	TLKRSLILSS	RHGIRRKLIK
410	420	430	440	450	460	470	480
QLGEHKRVYQ	CNICSKIFQN	SSNLSRHVRS	HGDKLFKCEE	CAKLFSRKES	LKQHVSYKHS	RNEVDGEYRY	RCGTCEKTFR
490	500	510	520	530	540	550	560
IESALEFHNC	RTDDKTFQCE	MCFRFFSTNS	NLSKHKKKHG	DKKFACEVCS	KMFYRKDVML	DHQRRHLEGV	RRVKREDLEA
570	580	590	600	610	620	630	640
GGENLVRYKK	EPSGCPVCGK	DIALMDDHQR	EEFIGKIGIS	SEENDDNSDE	SADSEPHKYS	CKRCQLTFGR	GKEYLKHIME
650	660	670	680	690	700	710	720
VHKEKGYGCS	ICNRRFALKA	TYHAHMVIHR	ENLPDPNVQK	YIHPCEICGR	IFNSIGNLER	HKLIHTGVKS	HACEQCGKSF
730	740	750	760	770	780	790	800
ARKDMLKEHM	RVHDNVREYL	CAECGKGMKT	KHALRHHMKL	HKGIKEYECK	ECHRRFAQKV	NMLKHCKRHT	GIKDFMCELC
810	820	830	840	850	860	870	880
GKTFSERNTM	ETHKLIHTVG	KQWTCSVCDK	KYVTEYMLQK	HVQLTHDKVE	AQSCQLCGTK	VSTRASMSRH	MRRKHPEVLA
890	900	910	920	930	940	950	960
VRIDDLDHLP	ETTTIDASSI	GIVQPELTLE	QEDLAEGKHG	KAAKRSHKRK	QKPEEEAGAP	VPEDATFSEY	SEKETEFTGS
970	980	990	1000	1010	1020	1030	1040
VGDETNSAVQ	SIQQVVVTLG	DPNVTTPSSS	VGLTNITVTP	ITTAAATQFT	NLQPVAVGHL	TTPERQLQLD	NSILTVTFDT
1050	1060	1070	1080	1090	1100	1110	1120
VSGSAMLHNR	QNDVQIHPQP	EASNPQSVAH	FINLTTLVNS	ITPLGSQLSD	QHPLTWRAVP	QTDVLPPSQP	QAPPQQAAQP
1130	1140						
QVQAEQQQQQ	MYSY						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1553	1	1018.4978	58.27	3	49.1	10.5	2	481-504	R.IESALEFHNCRTDDKTFQCEMCFR.F	Carbamidomethyl: 19, 22; Oxidation: 21

Detailed Protein Report

Protein 591: PREDICTED: growth/differentiation factor 9 isoform X1 [Homo sapiens]

Accession:	gi|530379837	**Score:**	21.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	41.8
Database Date:	2015-11-30	**pI:**	10.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.1
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578810283	refseq_human (refseq_human_20140103.fasta)	PREDICTED: growth/differentiation factor 9 isoform X2 [Homo sapiens]
gi|572153064	refseq_human (refseq_human_20140103.fasta)	growth/differentiation factor 9 isoform 2 [Homo sapiens]
gi|572153044	refseq_human (refseq_human_20140103.fasta)	growth/differentiation factor 9 isoform 2 [Homo sapiens]
gi|572152931	refseq_human (refseq_human_20140103.fasta)	growth/differentiation factor 9 isoform 2 [Homo sapiens]
gi|572152923	refseq_human (refseq_human_20140103.fasta)	growth/differentiation factor 9 isoform 2 [Homo sapiens]
gi|572152852	refseq_human (refseq_human_20140103.fasta)	growth/differentiation factor 9 isoform 2 [Homo sapiens]

10	20	30	40	50	60	70	80
MKKLYKTYAT	KEGIPKSNRS	HLYNTVRLFT	PCTRHKQAPG	DQVTGILPSV	ELLFNLDRIT	TVEHLLKSVL	LYNINNSVSF
90	100	110	120	130	140	150	160
SSAVKCVCNL	MIKEPKSSSR	TLGRAPYSFT	FNSQFEFGKK	HKWIQIDVTS	LLQPLVASNK	RSIHMSINFT	CMKDQLEHPS
170	180	190	200	210	220	230	240
AQNGLFNMTL	VSPSLILYLN	DTSAQAYHSW	YSLHYKRRPS	QGPDQERSLS	AYPVGEEAAE	DGRSSHHRHR	RGQETVSSEL
250	260	270	280	290	300	310	320
KKPLGPASFN	LSEYFRQFLL	PQNECELHDF	RLSFSQLKWD	NWIVAPHRYN	PRYCKGDCPR	AVGHRYGSPV	HTMVQNIIYE
330	340	350	360	370			
KLDSSVPRPS	CVPAKYSPLS	VLTIEPDGSI	AYKEYEDMIA	TKCTCR			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1385	1	905.0891	159.82	2	46.9	10.8	2	86-100	K.CVCNLMIKEPKSSSR.T	Carbamidomethyl: 1, 3

Detailed Protein Report

Protein 592: kinesin-like protein KIF1B isoform alpha [Homo sapiens]

Accession:	gi|41393559	**Score:**	21.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	130.3
Database Date:	2015-11-30	**pI:**	9.4
		Sequence Coverage [%]:	2.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSGASVKVAV	RVRPFNSRET	SKESKCIIQM	QGNSTSIINP	KNPKEAPKSF	SFDYSYWSHT	SPEDPCFASQ	NRVYNDIGKE
90	100	110	120	130	140	150	160
MLLHAFEGYN	VCIFAYGQTG	AGKSYTMMGK	QEESQAGIIP	QLCEELFEKI	NDNCNEEMSY	SVEVSYMEIY	CERVRDLLNP
170	180	190	200	210	220	230	240
KNKGNLRVRE	HPLLGPYVED	LSKLAVTSYT	DIADLMDAGN	KARTVAATNM	NETSSRSHAV	FTIVFTQKKH	DNETNLSTEK
250	260	270	280	290	300	310	320
VSKISLVDLA	GSERADSTGA	KGTRLKEGAN	INKSLTTLGK	VISALAEVSK	KKKKTDFIPY	RDSVLTWLLR	ENLGGNSRTA
330	340	350	360	370	380	390	400
MVAALSPADI	NYDETLSTLR	YADRAKQIKC	NAVINEDPNA	KLVRELKEEV	TRLKDLLRAQ	GLGDIIDTSM	GSLTSSPSSC
410	420	430	440	450	460	470	480
SLSSQVGLTS	VTSIQERIMS	TPGGEEAIER	LKESEKIIAE	LNETWEEKLR	KTEAIRMERE	ALLAEMGVAI	REDGGTLGVF
490	500	510	520	530	540	550	560
SPKKTPHLVN	LNEDPLMSEC	LLYYIKDGIT	RVGQADAERR	QDIVLSGAHI	KEEHCIFRSE	RSNSGEVIVT	LEPCERSETY
570	580	590	600	610	620	630	640
VNGKRVSQPV	QLRSGNRIIM	GKNHVFRFNH	PEQARAEREK	TPSAETPSEP	VDWTFAQREL	LEKQGIDMKQ	EMEKRLQEME
650	660	670	680	690	700	710	720
ILYKKEKEEA	DLLLEQQRLD	ADSDSGDDSD	KRSCEESWKL	ITSLREKLPP	SKLQTIVKKC	GLPSSGKKRE	PIKMYQIPQR
730	740	750	760	770	780	790	800
RRLSKDSKWV	TISDLKIQAV	KEICYEVALN	DFRHSRQEIE	ALAIVKMKEL	CAMYGKKDPN	ERDSWRAVAR	DVWDTVGVGD
810	820	830	840	850	860	870	880
EKIEDVMATG	KGSTDVDDLK	VHIDKLEDIL	QEVKKQNNMK	DEEIKVLRNK	MLKMEKVLPL	IGSQEQKSPG	SHKAKEPVGA
890	900	910	920	930	940	950	960
GVSSTSENNV	SKGDNGELAK	EERVSQLMNG	DPAFRRGRLR	WMRQEQIRFK	NLQQQEITKQ	LRRQNVPHRF	IPPENRKPRF
970	980	990	1000	1010	1020	1030	1040
PFKSNPKHRN	SWSPGTHIII	TEDEVIELRI	PKDDEARKGN	KEESQEKGGK	GAFKDPQFPW	GSQGMRSQDH	IQVSKQHINN
1050	1060	1070	1080	1090	1100	1110	1120
QQQPPQLRWR	SNSLNNGQPK	STRCQASASA	ESLNSHSGHP	TADVQTFQAK	RHIHQHRQSY	CNYNTGGQLE	GNAATSYQKQ
1130	1140	1150	1160				
TDKPSHCSQF	VTPPRMRRQF	SAPNLKAGRE	TTV				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1501	1	671.0963	120.59	3	48.4	10.5	1	737-753	K.IQAVKEICYEVALNDFR.H	

Detailed Protein Report

Protein 593: pantetheinase precursor [Homo sapiens]

Accession:	gi|223633991	**Score:**	21.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	57.0
Database Date:	2015-11-30	**pI:**	5.2
		Sequence Coverage [%]:	3.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MTTQLPAYVA	ILLFYVSRAS	CQDTFTAAVY	EHAAILPNAT	LTPVSREEAL	ALMNRNLDIL	EGAITSAADQ	GAHIIVTPED
90	100	110	120	130	140	150	160
AIYGWNFNRD	SLYPYLEDIP	DPEVNWIPCN	NRNRFGQTPV	QERLSCLAKN	NSIYVVANIG	DKKPCDTSDP	QCPPDGRYQY
170	180	190	200	210	220	230	240
NTDVVFDSQG	KLVARYHKQN	LFMGENQFNV	PKEPEIVTFN	TTFGSFGIFT	CFDILFHDPA	VTLVKDFHVD	TIVFPTAWMN
250	260	270	280	290	300	310	320
VLPHLSAVEF	HSAWAMGMRV	NFLASNIHYP	SKKMTGSGIY	APNSSRAFHY	DMKTEEGKLL	LSQLDSHPSH	SAVVNWTSYA
330	340	350	360	370	380	390	400
SSIEALSSGN	KEFKGTVFFD	EFTFVKLTGV	AGNYTVCQKD	LCCHLSYKMS	ENIPNEVYAL	GAFDGLHTVE	GRYYLQICTL
410	420	430	440	450	460	470	480
LKCKTTNLNT	CGDSAETAST	RFEMFSLSGT	FGTQYVFPEV	LLSENQLAPG	EFQVSTDGRL	FSLKPTSGPV	LTVTLFGRLY
490	500	510	520				
EKDWASNASS	GLTAQARIIM	LIVIAPIVCS	LSW				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2233	1	1043.7218	141.72	2	57.8	21.6	0	1-18	-.MTTQLPAYVAILLFYVSR.A	

Detailed Protein Report

Protein 594: complement C3 precursor [Homo sapiens]

Accession:	gi|115298678	**Score:**	21.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	187.0
Database Date:	2015-11-30	**pI:**	6.0
		Sequence Coverage [%]:	0.8
		No. of unique Peptides:	1

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2396	1	701.3860	-50.24	2	59.8	21.6	0	892-904	K.SSLSVPYVIVPLK.T	

Detailed Protein Report

Protein 595: PREDICTED: neurobeachin-like protein 1 isoform X8 [Homo sapiens]

Accession:	gi|578804777	**Score:**	21.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	305.4
Database Date:	2015-11-30	**pI:**	6.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	0.7
		No. of unique Peptides:	2

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

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2277	1	816.2926	-155.86	2	58.7	11.5	1	7-18	R.LFELWMLYCTKK.D	Carbamidomethyl: 9
2089	1	925.3261	-72.47	1	56.3	10.1	0	1269-1276	K.NMSTEDTK.K	

Detailed Protein Report

Protein 596: **nuclear RNA export factor 5 [Homo sapiens]**

Accession:	gi|254039592	**Score:**	21.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	42.1
Database Date:	2015-11-30	**pI:**	9.9
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	7.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MRRNTQDENM	RKWFKVTIPY	GIKYDKAWLM	NSIQSNCSVP	FTPVDFHYIR	NRACFFVQVA	SAASALKDVS	YKIYDDENQK
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
ICIFVSHFTA	PYSVKNKLKP	GQMEMLKLTM	NKRYNVSQQA	LDLQNLRFDP	DLMGRDIDII	LNRRNCMAAT	LKITERNFPE
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
LLSLNLCNNK	LYQLDGLSDI	TEKAPKVKTL	NLSKNKLESA	WELGKVKGLK	LEELWLEGNP	LCSTFSDQSA	YVSAIRDCFP
250	**260**	**270**	**280**	**290**	**300**	**310**	**320**
KLLRLDGREL	SAPVIVDIDS	SETMKPCKEN	FTGSETLKHL	VLQFLQQSNL	CKYFKDSRNI	KILKDPYLQR	KLLKHTKCPR
330	**340**	**350**	**360**	**370**			
NVDSLSALPE	TQHDFTSILV	DMWYQTVNTC	FLPRAGPESQ	SLRPL			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2208	1	1061.5011	-52.58	3	57.8	21.5	2	81-107	K.ICIFVSHFTAPYSVKNKLKPGQMEMLK.L	Carbamidomethyl: 2; Oxidation: 23

Detailed Protein Report

Protein 597: forkhead box protein D3 [Homo sapiens]

Accession:	gi|6912372	**Score:**	21.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	47.6
Database Date:	2015-11-30	**pI:**	6.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	7.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MTLSGGGSAS	DMSGQTVLTA	EDVDIDVVGE	GDDGLEEKDS	DAGCDSPAGP	PELRLDEADE	VPPAAPHHGQ	PQPPHQQPLT
90	100	110	120	130	140	150	160
LPKEAAGAGA	GPGGDVGAPE	ADGCKGGVGG	EEGGASGGGP	GAGSGSAGGL	APSKPKNSLV	KPPYSYIALI	TMAILQSPQK
170	180	190	200	210	220	230	240
KLTLSGICEF	ISNRFPYYRE	KFPAWQNSIR	HNLSLNDCFV	KIPREPGNPG	KGNYWTLDPQ	SEDMFDNGSF	LRRRKRFKRH
250	260	270	280	290	300	310	320
QQEHLREQTA	LMMQSFGAYS	LAAAAGAAGP	YGRPYGLHPA	AAAGAYSHPA	AAAAAAAAAA	LQYPYALPPV	APVLPPAVPL
330	340	350	360	370	380	390	400
LPSGELGRKA	AAFGSQLGPG	LQLQLNSLGA	AAAAAGTAGA	AGTTASLIKS	EPSARPSFSI	ENIIGGGPAA	PGGSAVGAGV
410	420	430	440	450	460	470	480
AGGTGGSGGG	STAQSFLRPP	GTVQSAALMA	THQPLSLSRT	TATIAPILSV	PLSGQFLQPA	ASAAAAAAAA	AQAKWPAQ

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1915	1	856.8032	-169.79	2	54.0	10.8	1	191-204	R.HNLSLNDCFVKIPR.E	Carbamidomethyl: 8

Detailed Protein Report

Protein 598: **MAM and LDL-receptor class A domain-containing protein C10orf112 precursor [Homo sapiens]**

Accession:	gi|565671710	**Score:**	21.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	240.9
Database Date:	2015-11-30	**pI:**	4.9
		Sequence Coverage [%]:	1.4
		No. of unique Peptides:	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MLFFLDRMLA	FPMNETFCCL	WIACVFNSTL	AQQGTESFQC	DNGVSLPPDS	ICDFTDQCGD	SSDERHCLNY	ERCDFEDGLC
90	100	110	120	130	140	150	160
HMTQDQSLQP	SWTKRSGMIG	LSPPFYDHNG	DVSAHFLSLV	SRVDSISSSL	RSRVFLPTND	QHDCQITFYY	FSCQVSGKLM
170	180	190	200	210	220	230	240
VGLQTACGGP	IQHLWQNTAA	LPNQWERNVI	KIQSSQRFQV	VFEGQMASTY	EQDEVIAIDD	ISFSSGCLPA	NDGILLCQEA
250	260	270	280	290	300	310	320
LNAERELCHP	DTDLCRFDAT	DEELRLCQAC	GFEFDMCEWT	SEASAGQISW	MRTKAREIPA	FESTPQQDQG	GDDEGYYVWV
330	340	350	360	370	380	390	400
GAKHGFTLNH	LDSRAYLNSS	VCHCLGKSCH	LQFYYAMESS	VLRVRLYNNK	EEEIFWTYNI	STHSQWVKAD	VLIPEDLKTF
410	420	430	440	450	460	470	480
KIIFEGTLLS	QRSFIALDHL	WVYACGQTQS	RKLCSADEFP	CTSGQCIAKE	SVCDSRQDCS	DESDEDPATC	SKHLTCDFES
490	500	510	520	530	540	550	560
GFCGWEPFLT	EDSHWKLMKG	LNNGEHHFPA	ADHTANINHG	SFIYLEAQRS	PGVAKLGSPV	LTKLLTASTP	CQVQFWYHLS
570	580	590	600	610	620	630	640
QHSNLSVFTR	TSLDGNLQKQ	GKIIRFSESQ	WSHAKIDLIA	EAGESTLPFQ	LILEATVLSS	NATVALDDIS	VSQECEISYK
650	660	670	680	690	700	710	720
SLPRTSTQSK	FSKCDFEANS	CDWFEAISGD	HFDWIRSSQS	ELSADFEHQA	PPRDHSLNAS	QGHFMFILKK	SSSLWQVAKL
730	740	750	760	770	780	790	800
QSPTFSQTGP	GCILSFWFYN	YGLSVGAAEL	QLHMENSHDS	TVIWRVLYNQ	GKQWLEATIQ	LGRLSQPFHL	SLDKVSLGIY
810	820	830	840	850	860	870	880
DGVSAIDDIR	FENCTLPLPA	ESCEGLDHFW	CRHTRACIEK	LRLCDLVDDC	GDRTDEVNCA	PELQCNFETG	ICNWEQDAKD
890	900	910	920	930	940	950	960
DFDWTRSQGP	TPTLNTGPMK	DNTLGTAKGH	YLYIESSEPQ	AFQDSAALLS	PILNATDTKG	CTFRFYYHMF	GKRIYRLAIY
970	980	990	1000	1010	1020	1030	1040
QRIWSDSRGQ	LLWQIFGNQG	NRWIRKHLNI	SSRQPFQILV	EASVGDGFTG	DIAIDDLSFM	DCTLYPGNLP	ADLPTPPETS
1050	1060	1070	1080	1090	1100	1110	1120
VPVTLPPHNC	TDNEFICRSD	GHCIEKMQKC	DFKYDCPDKS	DEASCVMEVC	SFEKRSLCKW	YQPIPVHLLQ	DSNTFRWGLG
1130	1140	1150	1160	1170	1180	1190	1200
NGISIHHGEE	NHRPSVDHTQ	NTTDGWYLYA	DSSNGKFGDT	ADILTPIISL	TGPKCTLVFW	THMNGATVGS	LQVLIKKDNV
1210	1220	1230	1240	1250	1260	1270	1280
TSKLWAQTGQ	QGAQWKRAEV	FLGIRSHTQI	VFRAKRGISY	IGDVAVDDIS	FQDCSPLLSP	ERKCTDHEFM	CANKHCIAKD
1290	1300	1310	1320	1330	1340	1350	1360
KLCDFVNDCA	DNSDETTFIC	RTSSGRCDFE	FDLCSWKQEK	DEDFDWNLKA	SSIPAAGTEP	AADHTLGNSS	GHYIFIKSLF
1370	1380	1390	1400	1410	1420	1430	1440
PQQPMRAARI	SSPVISKRSK	NCKIIFHYHM	YGNGIGALTL	MQVSVTNQTK	VLLNLTVEQG	NFWRREELSL	FGDEDFQLKF
1450	1460	1470	1480	1490	1500	1510	1520
EGRVGKGQRG	DIALDDIVLT	ENCLSLHDSV	QEELAVPLPT	GFCPLGYREC	HNGKCYRLEQ	SCNFVDNCGD	NTDENECGSS
1530	1540	1550	1560	1570	1580	1590	1600
CTFEKGWCGW	QNSQADNFDW	VLGVGSHQSL	RPPKDHTLGN	ENGHFMYLEA	TAVGLRGDKA	HFRSTMWRES	SAACTMSFWY
1610	1620	1630	1640	1650	1660	1670	1680
FVSAKATGSI	QILIKTEKGL	SKVWQESKQN	PGNHWQKADI	LLGKLRNFEV	IFQGIRTRDL	GGGAAIDDIE	FKNCTTVGEI
1690	1700	1710	1720	1730	1740	1750	1760
SELCPEITDF	LCRDKKCIAS	HLLCDYKPDC	SDRSDEAHCA	HYTSTTGSCN	FETSSGNWTT	ACSLTQDSED	DLDWAIGSRI
1770	1780	1790	1800	1810	1820	1830	1840
PAKALIPDSD	HTPGSGQHFL	YVNSSGSKEG	SVARITTSKS	FPASLGMCTV	RFWFYMIDPR	SMGILKVYTI	EESGLNILVW
1850	1860	1870	1880	1890	1900	1910	1920
SVIGNKRTGW	TYGSVPLSSN	SPFKVAFEAD	LDGNEDIFIA	LDDISFTPEC	VTGGPVPVQP	SPCEADQFSC	IYTLQCVPLS
1930	1940	1950	1960	1970	1980	1990	2000
GKCDGHEDCI	DGSDEMDCPL	SPTPPLCSNM	EFPCSTDECI	PSLLLCDGVP	DCHFNEDELI	CSNKSCSNGA	LVCASSNSCI
2010	2020	2030	2040	2050	2060	2070	2080
PAHQRCDGFA	DCMDFQLDES	SCSECPLNYC	RNGGTCVVEK	NGPMCRCRQG	WKGNRCHIKF	NPPATDFTYA	QNNTWTLLGI
2090	2100	2110	2120	2130	2140	2150	2160
GLAFLMTHIT	VAVLCFLANR	KVPIRKTEGS	GNCAFVNPVY	GNWSNPEKTE	SSVYSFSNPL	YGTTSGSLET	LSHHLK

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2517	1	913.4615	10.45	2	61.9	10.8	1	1425-1439	R.REELSLFGDEDFQLK.F	

Detailed Protein Report

Protein 599: **astrotactin-1 isoform 2 precursor [Homo sapiens]**

Accession:	gi|46488921	**Score:**	21.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	135.0
Database Date:	2015-11-30	**pI:**	4.9
		Sequence Coverage [%]:	3.2
		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
2260	1	1061.4977	-63.82	3	58.5	11.2	2	185-214	R.RVPQPQKSASAEAANEIHYIPSVLIGGHGR.E	

Detailed Protein Report

Protein 600: PREDICTED: CAS1 domain-containing protein 1 isoform X2 [Homo sapiens]

Accession:	gi|578814529	**Score:**	21.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	72.0
Database Date:	2015-11-30	**pI:**	9.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.2
		No. of unique Peptides:	2

Quantitation

MD:MU	**Median:**	1.76	**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
161	1	793.8859	18.63	2	31.7	10.1	1	160-173	R.RQPQCCPCAAPLSR.S	Carbamidomethyl: 8	
149	1	793.8480	-29.08	2	31.6	11.2	1	160-173	R.RQPQCCPCAAPLSR.S	Carbamidomethyl: 6	MD:MU 1.76

Detailed Protein Report

Protein 601: BRCA1-associated protein [Homo sapiens]

Accession:	gi|188497705	**Score:**	21.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	67.3
Database Date:	2015-11-30	**pI:**	5.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.5
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 0.20 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MSVSLVVIRL	ELAEHSPVPA	GFGFSAAAGE	MSDEEIKKTT	LASAVACLEG	KSPGEKVAII	HQHLGRREMT	DVIIETMKSN
90	100	110	120	130	140	150	160
PDELKTTVEE	RKSSEASPTA	QRSKDHSKEC	INAAPDSPSK	QLPDQISFFS	GNPSVEIVHG	IMHLYKTNKM	TSLKEDVRRS
170	180	190	200	210	220	230	240
AMLCILTVPA	AMTSHDLMKF	VAPFNEVIEQ	MKIIRDSTPN	QYMVLIKFRA	QADADSFYMT	CNGRQFNSIE	DDVCQLVYVE
250	260	270	280	290	300	310	320
RAEVLKSEDG	ASLPVMDLTE	LPKCTVCLER	MDESVNGILT	TLCNHSFHSQ	CLQRWDDTTC	PVCRYCQTPE	PVEENKCFEC
330	340	350	360	370	380	390	400
GVQENLWICL	ICGHIGCGRY	VSRHAYKHFE	ETQHTYAMQL	TNHRVWDYAG	DNYVHRLVAS	KTDGKIVQYE	CEGDTCQEEK
410	420	430	440	450	460	470	480
IDALQLEYSY	LLTSQLESQR	IYWENKIVRI	EKDTAEEINN	MKTKFKETIE	KCDNLEHKLN	DLLKEKQSVE	RKCTQLNTKV
490	500	510	520	530	540	550	560
AKLTNELKEE	QEMNKCLRAN	QVLLQNKLKE	EERVLKETCD	QKDLQITEIQ	EQLRDVMFYL	ETQQKINHLP	AETRQEIQEG
570	580	590	600				
QINIAMASAS	SPASSGGSGK	LPSRKGRSKR	GK				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
257	1	569.4703	-171.75	3	32.6	21.3	0	210-224	R.AQADADSFYMTCNGR.Q	Carbamidomethyl: 12	MD:MU 0.20

Detailed Protein Report

Protein 602: spermatogenesis-associated serine-rich protein 2 [Homo sapiens]

Accession: gi|148746220

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Score: 21.3

MW [kDa]: 59.5

pI: 9.7

Sequence Coverage [%]: 4.0

No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MSRKQNQKDS	SGFIFDLQSN	TVLAQGGAFE	NMKEKINAVR	AIVPNKSNNE	IILVLQHFDN	CVDKTVQAFM	EGSASEVLKE
90	100	110	120	130	140	150	160
WTVTGKKKNK	KKKNKPKPAA	EPSNGIPDSS	KSVSIQEEQS	APSSEKGGMN	GYHVNGAIND	TESVDSLSEG	LETLSIDARE
170	180	190	200	210	220	230	240
LEDPESAMLD	TLDRTGSMLQ	NGVSDFETKS	LTMHSIHNSQ	QPRNAAKSLS	RPTTETQFSN	MGMEDVPLAT	SKKLSSNIEK
250	260	270	280	290	300	310	320
SVKDLQRCTV	SLARYRVVVK	EEMDASIKKM	KQAFAELESC	LMDREVALLA	EMDKVKAEAM	EILLSRQKKA	ELLKKMTHVA
330	340	350	360	370	380	390	400
VQMSEQQLVE	LRADIKHFVS	ERKYDEDLGR	VARFTCDVET	LKKSIDSFGQ	VSHPKNSYST	RSRCSSVTSV	SLSSPSDASA
410	420	430	440	450	460	470	480
ASSSTCASPP	SLTSANKKNF	APGETPAAIA	NSSGQPYQPL	REVLPGNRRG	GQGYRPQGQK	SNDPMNQGRH	DSMGRYRNSS
490	500	510	520	530	540	550	
WYSSGSRYQS	APSQAPGNTI	ERGQTHSAGT	NGTGVSMEPS	PPTPSFKKGL	PQRKPRTSQT	EAVNS	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1227	1	565.6011	-257.29	2	45.0	10.2	0	478-487	R.NSSWYSSGSR.Y	

Detailed Protein Report

Protein 603:	**disintegrin and metalloproteinase domain-containing protein 20 preproprotein [Homo sapiens]**

Accession:	gi|50845382	**Score:**	21.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	87.0
Database Date:	2015-11-30	**pI:**	6.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.8
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|530404802	refseq_human (refseq_human_20140103.fasta)	PREDICTED: disintegrin and metalloproteinase domain-containing protein 20 isoform X2 [Homo sapiens]
gi|530404800	refseq_human (refseq_human_20140103.fasta)	PREDICTED: disintegrin and metalloproteinase domain-containing protein 20 isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MVQLHQDTDP	QIPKGQPCTL	NSSEGGARPA	VPHTLFSSAL	DRWLHNDSFI	MAVGEPLVHI	RVTLLLLWFG	MFLSISGHSQ
90	100	110	120	130	140	150	160
ARPSQYFTSP	EVVIPLKVIS	RGRGAKAPGW	LSYSLRFGGQ	RYIVHMRVNK	LLFAAHLPVF	TYTEQHALLQ	DQPFIQDDCY
170	180	190	200	210	220	230	240
YHGYVEGVPE	SLVALSTCSG	GFLGMLQIND	LVYEIKPISV	SATFEHLVYK	IDSDDTQFPP	MRCGLTEEKI	AHQMELQLSY
250	260	270	280	290	300	310	320
NFTLKQSSFV	GWWTHQRFVE	LVVVVDNIRY	LFSQSNATTV	QHEVFNVVNI	VDSFYHPLEV	DVILTGIDIW	TASNPLPTSG
330	340	350	360	370	380	390	400
DLDNVLEDFS	IWKNYNLNNR	LQHDVAHLFI	KDTQGMKLGV	AYVKGICQNP	FNTGVDVFED	NRLVVFAITL	GHELGHNLGM
410	420	430	440	450	460	470	480
QHDTQWCVCE	LQWCIMHAYR	KVTTKFSNCS	YAQYWDSTIS	SGLCIQPPPY	PGNIFRLKYC	GNLVVEEGEE	CDCGTIRQCA
490	500	510	520	530	540	550	560
KDPCCLLNCT	LHPGAACAFG	ICCKDCKFLP	SGTLCRQQVG	ECDLPEWCNG	TSHQCPDDVY	VQDGISCNVN	AFCYEKTCNN
570	580	590	600	610	620	630	640
HDIQCKEIFG	QDARSASQSC	YQEINTQGNR	FGHCGIVGTT	YVKCWTPDIM	CGRVQCENVG	VIPNLIEHST	VQQFHLNDTT
650	660	670	680	690	700	710	720
CWGTDYHLGM	AIPDIGEVKD	GTVCGPEKIC	IRKKCASMVH	LSQACQPKTC	NMRGICNNKQ	HCHCNHEWAP	PYCKDKGYGG
730	740	750	760	770	780		
SADSGPPPKN	NMEGLNVMGK	LRYLSLLCLL	PLVAFLLFCL	HVLFKKRTKS	KEDEEG		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1299	1	727.3560	8.30	2	45.9	10.7	1	505-516	K.DCKFLPSGTLCR.Q	Carbamidomethyl: 2, 11

Detailed Protein Report

Protein 604: PREDICTED: probable cation-transporting ATPase 13A3 isoform X4 [Homo sapiens]

Accession:	gi|530375932	**Score:**	21.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	123.9
Database Date:	2015-11-30	**pI:**	6.1
		Sequence Coverage [%]:	3.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDREERKTIN	QGQEDEMEIY	GYNLSRWKLA	IVSLGVICSG	GFLLLLLYWM	PEWRVKATCV	RAAIKDCEVV	LLRTTDEFKM
90	100	110	120	130	140	150	160
WFCAKIRVLS	LETYPVSSPK	SMSNKLSNGH	AVCLIENPTE	ENRHRISKYS	QTESQQIRYF	THHSVKYFWN	DTIHNFDFLK
170	180	190	200	210	220	230	240
GLDEGVSCTS	IYEKHSAGLT	KGMHAYRKLL	YGVNEIAVKV	PSVFKLLIKE	VLNPFYIFQL	FSVILWSTDE	YYYYALAIVV
250	260	270	280	290	300	310	320
MSIVSIVSSL	YSIRKQYVML	HDMVATHSTV	RVSVCRVNEE	IEEIFSTDLV	PGDVMVIPLN	GTIMPCDAVL	INGTCIVNES
330	340	350	360	370	380	390	400
MLTGESVPVT	KTNLPNPSVD	VKGIGDELYN	PETHKRHTLF	CGTTVIQTRF	YTGELVKAIV	VRTGFSTSKG	QLVRSILYPK
410	420	430	440	450	460	470	480
PTDFKLYRDA	YLFLLCLVAV	AGIGFIYTII	NSILNEVQVG	VIIIESLDII	TITVPPALPA	AMTAGIVYAQ	RRLKKIGIFC
490	500	510	520	530	540	550	560
ISPQRINICG	QLNLVCFDKT	GTLTEDGLDL	WGIQRVENAR	FLSPEENVCN	EMLVKSQFVA	CMATCHSLTK	IEGVLSGDPL
570	580	590	600	610	620	630	640
DLKMFEAIGW	ILEEATEEET	ALHNRIMPTV	VRPPKQLLPE	STPAGNQEME	LFELPATYEI	GIVRQFPFSS	ALQRMSVVAR
650	660	670	680	690	700	710	720
VLGDRKMDAY	MKGAPEAIAG	LCKPETVPVD	FQNVLEDFTK	QGFRVIALAH	RKLESKLTWH	KVQNISRDAI	ENNMDFMGLI
730	740	750	760	770	780	790	800
IMQNKLKQET	PAVLEDLHKA	NIRTVMVTGD	SMLTAVSVAR	DCGMILPQDK	VIIAEALPPK	DGKVAKINWH	YADSLTQCSH
810	820	830	840	850	860	870	880
PSAIDPEAIP	VKLVHDSLED	LQMTRYHFAM	NGKSFSVILE	HFQDLVPKLM	LHGTVFARMA	PDQKTQLIEA	LQNVDYFVGM
890	900	910	920	930	940	950	960
CGDGANDCGA	LKRAHGGISL	SELEASVASP	FTSKTPSISC	VPNLIREGRA	ALITSFCVFK	FMALYSIIQY	FSVTLLYSIL
970	980	990	1000	1010	1020	1030	1040
SNLGDFQFLF	IDLAIILVVV	FTMSLNPAWK	ELVAQRPPSG	LISGALLFSV	LSQIIICIGF	QSLGFFWVKQ	QPWYEVWHPK
1050	1060	1070	1080	1090	1100	1110	
SDACNTTGSG	FWNSSHVDNE	TELDEHNIQN	YENTTVFFIS	SFQYLIVAIA	FSKGKPFRQP	CYKN	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2025	1	1044.3877	-140.05	2	55.2	10.4	0	894-914	R.AHGGISLSELEASVASPFTSK.T	

Detailed Protein Report

Protein 605: membrane-bound transcription factor site-1 protease preproprotein [Homo sapiens]

Accession:	gi|4506775	**Score:**	21.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	117.7
Database Date:	2015-11-30	**pI:**	9.5
Modification(s):	Oxidation	**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
1464	1	742.6304	-61.81	3	48.1	21.1	1	645-662	R.MKNDPLDWNGDHIHTNFR.D	Oxidation: 1

Detailed Protein Report

Protein 606: **suppressor of IKBKE 1 isoform 2 [Homo sapiens]**

Accession:	gi|156151377	**Score:**	21.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	23.7
Database Date:	2015-11-30	**pI:**	5.0
		Sequence Coverage [%]:	11.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSCTIEKILT	DAKTLLERLR	EHDAAAESLV	DQSAALHRRV	AAMREAGTAL	PDQYQEDASD	MKDMSKYKPH	ILLSQENTQI
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
RDLQQENREL	WISLEEHQDA	LELIMSKYRK	QMLQLMVAKK	AVDAEPVLKA	HQSHSAEIES	QIDRICEMGE	VMRKAVQVDD
170	**180**	**190**	**200**	**210**			
DQFCKIQEKL	AQLELENKEL	RELLSISSES	LQARKENSMD	TASQAIK			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1321	1	781.0677	172.15	2	46.2	10.9	1	182-195	R.ELLSISSESLQARK.E	

Detailed Protein Report

Protein 607: late cornified envelope protein 3E [Homo sapiens]

Accession:	gi|30410033	**Score:**	21.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	9.5
Database Date:	2015-11-30	**pI:**	12.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	30.4
		No. of unique Peptides:	2

```
        10         20         30         40         50         60         70         80
MSCQQNQKQC QPPPKCPSPK CPPKNPVQCL PPASSGCAPS SGGCGPSSEG GCFLNHHRRH HRCRRQRSNS CDRGSGQQGG
        90        100
GSGCCHGSGG CC
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1406	1	956.6395	178.07	1	47.2	10.6	1	16-24	K.CPSPKCPPK.N	
2462	1	885.2390	-64.11	2	60.7	10.5	0	74-92	R.GSGQQGGGSGCCHGSGGCC.-	Carbamidomethyl: 12, 18, 19

Detailed Protein Report

Protein 608: PREDICTED: xylulose kinase isoform X4 [Homo sapiens]

Accession:	gi|578806855	**Score:**	21.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	51.1
Database Date:	2015-11-30	**pI:**	5.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	7.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAEHAPRRCC	LGWDFSTQQV	KVVAVDAELN	VFYEESVHFD	RDLPEFGTQG	GVHVHKDGLT	VTSPVLMWVQ	ALDIILEKMK
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
ASGFDFSQVL	ALSGAGQQHG	SIYWKAGAQQ	ALTSLSPDLR	LHQQLQDCFS	ISDCPVWMDS	STTAQCRQLE	AAVGGAQALS
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
CLTGSRAYER	FTGNQIAKIY	QQNPEAYSHT	ERISLVSSFA	ASLFLGSYSP	IDYSDGSGMN	LLQIQDKVWS	QACLGACAPH
250	**260**	**270**	**280**	**290**	**300**	**310**	**320**
LEEKLSPPVP	SCSVVGAISS	YYVQRYGFPP	GCKVVAFTGD	NPASLAGMRL	EEGDIAVSLG	TSDTLFLWLQ	EPMPALEGHI
330	**340**	**350**	**360**	**370**	**380**	**390**	**400**
FCNPVDSQHY	MALLCFKNGS	LMREKIRNES	VSRSWSDFSK	ALQSTEMGNG	GNLGFYFDVM	EITPEIIGRH	RFNTENHKVA
410	**420**	**430**	**440**	**450**	**460**	**470**	
AFPGDVEVRA	LIEGQFMAKR	IHAEGLGYRC	PRQRFWPQEE	HLTIEKSYRC	LQMCLMPRCM	L	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
766	1	859.6992	-41.80	3	39.0	10.2	2	1-21	-.MAEHAPRRCCLGWDFSTQQVK.V	Carbamidomethyl: 9, 10

Detailed Protein Report

Protein 609: PREDICTED: 5'-3' exoribonuclease 1 isoform X6 [Homo sapiens]

Accession:	gi|578807507	**Score:**	20.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	108.1
Database Date:	2015-11-30	**pI:**	6.1
		Sequence Coverage [%]:	2.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGVPKFYRWI	SERYPCLSEV	VKEHQIPEFD	NLYLDMNGII	HQCSHPNDDD	VHFRISDDKI	FTDIFHYLEV	LFRIIKPRKV
90	100	110	120	130	140	150	160
FFMAVDGVAP	RAKMNQQRGR	RFRSAKEAED	KIKKAIEKGE	TLPTEARFDS	NCITPGTEFM	ARLHEHLKYF	VNMKISTDKS
170	180	190	200	210	220	230	240
WQGVTIYFSG	HETPGEGEHK	IMEFIRSEKA	KPDHDPNTRH	CLYGLDADLI	MLGLTSHEAH	FSLLREEVRF	GGKKTQRVCA
250	260	270	280	290	300	310	320
PEETTFHLLH	LSLMREYIDY	EFSVLKEKIT	FKYDIERIID	DWILMGFLVG	NDFIPHLPHL	HINHDALPLL	YGTYVTILPE
330	340	350	360	370	380	390	400
LGGYINESGH	LNLPRFEKYL	VKLSDFDREH	FSEVFVDLKW	FESKVGNKYL	NEAAGVAAEE	ARNYKEKKKL	KGQENSLCWT
410	420	430	440	450	460	470	480
ALDKNEGEMI	TSKDNLEDET	EDDDLFETEF	RQYKRTYYMT	KMGVDVVSDD	FLADQAACYV	QAIQWILHYY	YHGVQSWSWY
490	500	510	520	530	540	550	560
YPYHYAPFLS	DIHNISTLKI	HFELGKPFKP	FEQLLAVLPA	ASKNLLPACY	QHLMTNEDSP	IIEYYPPDFK	TDLNGKQQEW
570	580	590	600	610	620	630	640
EAVVLIPFID	EKRLLEAMET	CNHSLKKEER	KRNQHSECLM	CWYDRDTEFI	YPSPWPEKFP	AIERCCTRYK	IISLDAWRVD
650	660	670	680	690	700	710	720
INKNKITRID	QKALYFCGFP	TLKHIRHKFF	LKKSGVQVFQ	QSSRGENMML	EILVDAESDE	LTVENVASSV	LGKSVFVNWP
730	740	750	760	770	780	790	800
HLEEARVVAV	SDGETKFYLE	EPPGTQKLYS	GRTAPPSKVV	HLGDKEQSNW	AKEVQGISEH	YLRRKGIIIN	ETSAVVYAQL
810	820	830	840	850	860	870	880
LTGRKYQINQ	NGEVRLEKQW	SKQVVPFVYQ	TIVKDIRAFD	SRFSNIKTLD	DLFPLRSMVF	MLGTPYYGCT	GEVQDSGDVI
890	900	910	920	930			
TEGRIRVIFS	IPCEPNLDAL	IQNQHEKERG	AEKFCLQILS	KKRGNGSK			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
263	1	795.8251	-113.37	2	32.7	10.2	1	806-818	K.YQINQNGEVRLEK.Q	

Detailed Protein Report

Protein 610: zinc finger protein 467 [Homo sapiens]

Accession:	gi|46409310	**Score:**	20.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	65.1
Database Date:	2015-11-30	**pI:**	11.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	5.4
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578813959	refseq_human (refseq_human_20140103.fasta)	PREDICTED: zinc finger protein 467 isoform X6 [Homo sapiens]
gi|530386928	refseq_human (refseq_human_20140103.fasta)	PREDICTED: zinc finger protein 467 isoform X3 [Homo sapiens]
gi|530386926	refseq_human (refseq_human_20140103.fasta)	PREDICTED: zinc finger protein 467 isoform X2 [Homo sapiens]
gi|530386924	refseq_human (refseq_human_20140103.fasta)	PREDICTED: zinc finger protein 467 isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MRETLEALSS	LGFSVGQPEM	APQSEPREGS	HNAQEQMSSS	REERALGVCS	GHEAPTPEEG	AHTEQAEAPC	RGQACSAQKA
90	100	110	120	130	140	150	160
QPVGTCPGEE	WMIRKVKVED	EDQEAEEEVE	WPQHLSLLPS	PFPAPDLGHL	AAAYKLEPGA	PGALSGLALS	GWGPMPEKPY
170	180	190	200	210	220	230	240
GCGECERRFR	DQLTLRLHQR	LHRGEGPCAC	PDCGRSFTQR	AHMLLHQRSH	RGERPFPCSE	CDKRFSKKAH	LTRHLRTHTG
250	260	270	280	290	300	310	320
ERPYPCAECG	KRFSQKIHLG	SHQKTHTGER	PFPCTECEKR	FRKKTHLIRH	QRIHTGERPY	QCAQCARSFT	HKQHLVRHQR
330	340	350	360	370	380	390	400
VHQTAGPARP	SPDSSASPHS	TAPSPTPSFP	GPKPFACSDC	GLSFGWKKNL	ATHQCLHRSE	GRPFGCDECA	LGATVDAPAA
410	420	430	440	450	460	470	480
KPLASAPGGP	GCGPGSDPVV	PQRAPSGERS	FFCPDCGRGF	SHGQHLARHP	RVHTGERPFA	CTQCDRRFGS	RPNLVAHSRA
490	500	510	520	530	540	550	560
HSGARPFACA	QCGRRFSRKS	HLGRHQAVHT	GSRPHACAVC	ARSFSSKTNL	VRHQAIHTGS	RPFSCPQCGK	SFSRKTHLVR
570	580	590	600				
HQLIHGEAAH	AAPDAALAAP	AWSAPPEVAP	PPLFF				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2174	1	849.0086	-71.63	3	57.0	10.8	1	533-554	R.HQAIHTGSRPFSCPQCGKSFSR.K	Carbamidomethyl: 13, 16

Detailed Protein Report

Protein 611: **PREDICTED: EGF-containing fibulin-like extracellular matrix protein 1 isoform X2 [Homo sapiens]**

Accession:	gi|530367362	**Score:**	20.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	59.3
Database Date:	2015-11-30	**pI:**	9.5
		Sequence Coverage [%]:	5.5
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 4.40 **CV:** 0.00 % **No. of 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	Ratios
555	1	676.8735	43.07	2	36.3	10.5	0	110-122	R.SAAAQVFLLCCAR.N		MD:MU 4.40

Detailed Protein Report

Protein 612: protein-methionine sulfoxide oxidase MICAL3 isoform 1 [Homo sapiens]

Accession:	gi|209862789	**Score:**	20.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	224.2
Database Date:	2015-11-30	**pI:**	5.3
		Sequence Coverage [%]:	1.3
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|530426255	refseq_human (refseq_human_20140103.fasta)	PREDICTED: protein-methionine sulfoxide oxidase MICAL3 isoform X6 [Homo sapiens]

Detailed Protein Report

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        10          20          30          40          50          60          70          80
MEERKHETMN  PAHVLFDRFV  QATTCKGTLK  AFQELCDHLE  LKPKDYRSFY  HKLKSKLNYW  KAKALWAKLD  KRGSHKDYKK
        90         100         110         120         130         140         150         160
GKACTNTKCL  IIGAGPCGLR  TAIDLSLLGA  KVVVIEKRDA  FSRNNVLHLW  PFTIHDLRGL  GAKKFYGKFC  AGAIDHISIR
       170         180         190         200         210         220         230         240
QLQLILLKVA  LILGIEIHVN  VEFQGLIQPP  EDQENERIGW  RALVHPKTHP  VSEYEFEVII  GGDGRRNTLE  GFRRKEFRGK
       250         260         270         280         290         300         310         320
LAIAITANFI  NRNTTAEAKV  EEISGVAFIF  NQKFFQELRE  ATGIDLENIV  YYKDDTHYFV  MTAKKQSLLD  KGVILHDYAD
       330         340         350         360         370         380         390         400
TELLLSRENV  DQEALLSYAR  EAADFSTQQQ  LPSLDFAINH  YGQPDVAMFD  FTCMYASENA  ALVREQNGHQ  LLVALVGDSL
       410         420         430         440         450         460         470         480
LEPFWPMGTG  IARGFLAAMD  SAWMVRSWSL  GTSPLEVLAE  RESIYRLLPQ  TTPENVSKNF  SQYSIDPVTR  YPNINVNFLR
       490         500         510         520         530         540         550         560
PSQVRHLYDT  GETKDIHLEM  ESLVNSRTTP  KLTRNESVAR  SSKLLGWCQR  QTDGYAGVNV  TDLTMSWKSG  LALCAIIHRY
       570         580         590         600         610         620         630         640
RPDLIDFDSL  DEQNVEKNNQ  LAFDIAEKEL  GISPIMTGKE  MASVGEPDKL  SMVMYLTQFY  EMFKDSLPSS  DTLDLNAEEK
       650         660         670         680         690         700         710         720
AVLIASTRSP  ISFLSKLGQT  ISRKRSPKDK  KEKDLDGAGK  RRKTSQSEEE  EAPRGHRGER  PTLVSTLTDR  RMDVAVGNQN
       730         740         750         760         770         780         790         800
KVKYMATQLL  AKFEENAPAQ  SIGIRRQGSM  KKEFPQNLGG  SDTCYFCQKR  VYVMERLSAE  GKFFHRSCFK  CEYCATTLRL
       810         820         830         840         850         860         870         880
SAYAYDIEDG  KFYCKPHYCY  RLSGYAQRKR  PAVAPLSGKE  AKGPLQDGAT  TDANGRANAV  ASSTERTPGS  GVNGLEEPSI
       890         900         910         920         930         940         950         960
AKRLRGTPER  IELENYRLSL  RQAEALQEVP  EETQAEHNLS  SVLDTGAEED  VASSSSESEM  EEEGEEEEEE  PRLPPSDLGG
       970         980         990        1000        1010        1020        1030        1040
VPWKEAVRIH  ALLKGKSEEE  LEASKSFGPG  NEEEEEEEEE  YEEEEEEDYD  EEEEESSEAG  NQRLQQVMHA  ADPLEIQADV
      1050        1060        1070        1080        1090        1100        1110        1120
HWTHIREREE  EERMAPASES  SASGAPLDEN  DLEEDVDSEP  AEIEGEAAED  GDPGDTGAEL  DDDQHWSDSP  SDADRELRLP
      1130        1140        1150        1160        1170        1180        1190        1200
CPAEGEAELE  LRVSEDEEKL  PASPKHQERG  PSQATSPIRS  PQESALLFIP  VHSPSTEGPQ  LPPVPAATQE  KSPEERLFPE
      1210        1220        1230        1240        1250        1260        1270        1280
PLLPKEKPKA  DAPSDLKAVH  SPIRSQPVTL  PEARTPVSPG  SPQPQPPVAA  STPPPSPLPI  CSQPQPSTEA  TVPSPTQSPI
      1290        1300        1310        1320        1330        1340        1350        1360
RFQPAPAKTS  TPLAPLPVQS  QSDTKDRLGS  PLAVDEALRR  SDLVEEFWMK  SAEIRRSLGL  TPVDRSKGPE  PSFPTPAFRP
      1370        1380        1390        1400        1410        1420        1430        1440
VSLKSYSVEK  SPQDEGLHLL  KPLSIPKRLG  LPKPEGEPLS  LPTPRSPSDR  ELRSAQEERR  ELSSSSGLGL  HGSSSNMKTL
      1450        1460        1470        1480        1490        1500        1510        1520
GSQSFNTSDS  AMLTPPSSPP  PPPPPGEEPA  TLRRKLREAE  PNASVVPPPL  PATWMRPPRE  PAQPPREEVR  KSFVESVEEI
      1530        1540        1550        1560        1570        1580        1590        1600
PFADDVEDTY  DDKTEDSSLQ  EKFFTPPSCW  PRPEKPRHPP  LAKENGRLPA  LEGTLQPQKR  GLPLVSAEAK  ELAEERMRAR
      1610        1620        1630        1640        1650        1660        1670        1680
EKSVKSQALR  DAMARQLSRM  QQMELASGAP  RPRKASSAPS  QGKERRPDSP  TRPTLRGSEE  PTLKHEATSE  EVLSPPSDSG
      1690        1700        1710        1720        1730        1740        1750        1760
GPDGSFTSSE  GSSGKSKKRS  SLFSPRRNKK  EKKSKGEGRP  PEKPSSNLLE  EAAAKPKSLW  KSVFSGYKKD  KKKKADDKSC
      1770        1780        1790        1800        1810        1820        1830        1840
PSTPSSGATV  DSGKHRVLPV  VRAELQLRRQ  LSFSEDSDLS  SDDVLEKSSQ  KSRREPRTYT  EEELNAKLTR  RVQKAARRQA
      1850        1860        1870        1880        1890        1900        1910        1920
KQEELKRLHR  AQIIQRQLQQ  VEERQRRLEE  RGVAVEKALR  GEAGMGKKDD  PKLMQEWFKL  VQEKNAMVRY  ESELMIFARE
      1930        1940        1950        1960        1970        1980        1990        2000
LELEDRQSRL  QQELRERMAV  EDHLKTEEEL  SEEKQILNEM  LEVVEQRDSL  VALLEEQRLR  EREEDKDLEA  AMLSKGFSLN
      2010
WS
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2512	1	834.4289	-40.88	2	61.8	10.6	2	1306-1320	K.DRLGSPLAVDEALRR.S	

Detailed Protein Report

Protein 613: **mitogen-activated protein kinase kinase kinase 15 [Homo sapiens]**

Accession:	gi|282847398	**Score:**	20.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	147.3
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
MESGGGNAPA	GALGAASESP	QCPPPPGVEG	AAGPAEPDGA	AEGAAGGSGE	GESGGGPRRA	LRAVYVRSES	SQGGAAGGPE
90	100	110	120	130	140	150	160
AGARQCLLRA	CEAEGAHLTS	VPFGELDFGE	TAVLDAFYDA	DVAVVDMSDV	SRQPSLFYHL	GVRESFDMAN	NVILYHDTDA
170	180	190	200	210	220	230	240
DTALSLKDMV	TQKNTASSGN	YYFIPYIVTP	CADYFCCESD	AQRRASEYMQ	PNWDNILGPL	CMPLVDRFIS	LLKDIHVTSC
250	260	270	280	290	300	310	320
VYYKETLLND	IRKAREKYQG	EELAKELARI	KLRMDNTEVL	TSDIIINLLL	SYRDIQDYDA	MVKLVETLEM	LPTCDLADQH
330	340	350	360	370	380	390	400
NIKFHYAFAL	NRRNSTGDRE	KALQIMLQVL	QSCDHPGPDM	FCLCGRIYKD	IFLDSDCKDD	TSRDSAIEWY	RKGFELQSSL
410	420	430	440	450	460	470	480
YSGINLAVLL	IVAGQQFETS	LELRKIGVRL	NSLLGRKGSL	EKMNNYWDVG	QFFSVSMLAH	DVGKAVQAAE	RLFKLKPPVW
490	500	510	520	530	540	550	560
YLRSLVQNLL	LIRRFKKTII	EHSPRQERLN	FWLDIIFEAT	NEVTNGLRFP	VLVIEPTKVY	QPSYVSINNE	AEERTVSLWH
570	580	590	600	610	620	630	640
VSPTEMKQMH	EWNFTASSIK	GISLSKFDER	CCFLYVHDNS	DDFQIYFSTE	EQCSRFFSLV	KEMITNTAGS	TVELEGETDG
650	660	670	680	690	700	710	720
DTLEYEYDHD	ANGERVVLGK	GTYGIVYAGR	DLSNQVRIAI	KEIPERDSRY	SQPLHEEIAL	HKYLKHRNIV	QYLGSVSENG
730	740	750	760	770	780	790	800
YIKIFMEQVP	GGSLSALLRS	KWGPMKEPTI	KFYTKQILEG	LKYLHENQIV	HRDIKGDNVL	VNTYSGVVKI	SDFGTSKRLA
810	820	830	840	850	860	870	880
GVNPCTETFT	GTLQYMAPEI	IDQGPRGYGA	PADIWSLGCT	IIEMATSKPP	FHELGEPQAA	MFKVGMFKIH	PEIPEALSAE
890	900	910	920	930	940	950	960
ARAFILSCFE	PDPHKRATTA	ELLREGFLRQ	VNKGKKNRIA	FKPSEGPRGV	VLALPTQGEP	MATSSSEHGS	VSPDSDAQPD
970	980	990	1000	1010	1020	1030	1040
ALFERTRAPR	HHLGHLLSVP	DESSALEDRG	LASSPEDRDQ	GLFLLRKDSE	RRAILYKILW	EEQNQVASNL	QECVAQSSEE
1050	1060	1070	1080	1090	1100	1110	1120
LHLSVGHIKQ	IIGILRDFIR	SPEHRVMATT	ISKLKVDLDF	DSSSISQIHL	VLFGFQDAVN	KILRNHLIRP	HWMFAMDNII
1130	1140	1150	1160	1170	1180	1190	1200
RRAVQAAVTI	LIPELRAHFE	PTCETEGVDK	DMDEAEEGYP	PATGPGQEAQ	PHQQHLSLQL	GELRQETNRL	LEHLVEKERE
1210	1220	1230	1240	1250	1260	1270	1280
YQNLLRQTLE	QKTQELYHLQ	LKLKSNCITE	NPAGPYGQRT	DKELIDWLRL	QGADAKTIEK	IVEEGYTLSD	ILNEITKEDL
1290	1300	1310	1320				
RYLRLRGGLL	CRLWSAVSQY	RRAQEASETK	DKA				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1857	1	599.2758	-1.14	2	53.3	10.5	0	294-303	R.DIQDYDAMVK.L	
1128	1	874.6829	210.03	1	43.7	10.1	0	897-904	R.ATTAELLR.E	

Detailed Protein Report

Protein 614: **PREDICTED: arf-GAP domain and FG repeat-containing protein 2 isoform X2 [Homo sapiens]**

Accession:	gi|578814185	**Score:**	20.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	47.4
Database Date:	2015-11-30	**pI:**	10.2
		Sequence Coverage [%]:	3.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MVMAAKKGPG	PGGGVSGGKA	EAEAASEVWC	RRVRELGGCS	QAGNRHCFEC	AQRGVTYVDI	TVGSFVCTTC	SGLLRGLNPP
90	100	110	120	130	140	150	160
HRVKSISMTT	FTEPEVVFLQ	SRGNEVCRKI	WLGLFDARTS	LVPDSRDPQK	VKEFLQEKYE	KKRWYVPPDQ	VKGPTYTKGS
170	180	190	200	210	220	230	240
ASTPVQGSIP	EGKPLRTLLG	DPAPSLSVAA	STSSQPVSQS	HARTSQARST	QPPPHSSVKK	ASTDLLADIG	GDPFAAPQMA
250	260	270	280	290	300	310	320
PAFAAFPAFG	GQTPSQGGFA	NFDAFSSGPS	SSVFGSLPPA	GQASFQAQPT	PAASRMLTES	YSFGSSQGTP	FGATPLAPAS
330	340	350	360	370	380	390	400
QPNSLADVGS	FLGPGVPAAG	VPSSLFGMAG	QVPPLQSVTM	GGGGGSSTGL	AFGGPGFGMS	SAGPGFPQAV	PPTGAFASSF
410	420	430	440	450	460	470	
PAPLFPPQTP	LVQQQNGSSF	GDLGSAKLGQ	RPLSQPAGIS	TNPFMTGPSS	SPFASKPPTT	NPFL	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2745	1	973.4995	-29.64	2	64.7	20.5	1	110-126	K.IWLGLFDARTSLVPDSR.D	

Detailed Protein Report

Protein 615: **PREDICTED: ankyrin repeat and protein kinase domain-containing protein 1 isoform X1 [Homo sapiens]**

Accession:	gi|578822107	**Score:**	20.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	79.1
Database Date:	2015-11-30	**pI:**	6.7
		Sequence Coverage [%]:	1.7
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 1.26 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MGHPLPYLAP	PLHSSDVNYL	IEEAAKMKKI	KFQHIVSIYG	VCKQPLGIVM	EFMANGSLEK	VLSTHSLCWK	LRFRIIHETS
90	100	110	120	130	140	150	160
LAMNFLHSIK	PPLLHLDLKP	GNILLDSNMH	VKISDFGLSK	WMEQSTRMQY	IERSALRGML	SYIPPEMFLE	SNKAPGPKYD
170	180	190	200	210	220	230	240
VYSFAIVIWE	LLTQKKPYSG	FNMMMIIIRV	AAGMRPSLQP	VSDQWPSEAQ	QMVDLMKRCW	DQDPKKRPCF	LDITIETDIL
250	260	270	280	290	300	310	320
LSLLQSRVAV	PESKALARKV	SCKLSLRQPG	EVNEDISQEL	MDSDSGNYLK	RALQLSDRKN	LVPRDEELCI	YENKVTPLHF
330	340	350	360	370	380	390	400
LVAQGSVEQV	RLLLAHEVDV	DCQTASGYTP	LLIAAQDQQP	DLCALLLAHG	ADANRVDEDG	WAPLHFAAQN	GDDGTARLLL
410	420	430	440	450	460	470	480
DHGACVDAQE	REGWTPLHLA	AQNNFENVAR	LLVSRQADPN	LHEAEGKTPL	HVAAYFGHVS	LVKLLTSQGA	ELDAQQRNLR
490	500	510	520	530	540	550	560
TPLHLAVERG	KVRAIQHLLK	SGAVPDALDQ	SGYGPLHTAA	ARGKYLICKM	LLRYGASLEL	PTHQGWTPLH	LAAYKGHLEI
570	580	590	600	610	620	630	640
IHLLAESHAN	MGALGAVNWT	PLHLAARHGE	EAVVSALLQC	GADPNAAEQS	GWTPLHLAVQ	RSTFLSVINL	LEHHANVHAR
650	660	670	680	690	700	710	720
NKVGWTPAHL	AALKGNTAIL	KVLVEAGAQL	DVQDGVSCTP	LQLALRSRKQ	GIMSFLEGKE	PSVATLGGSK	PGAEMEI

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2290	1	697.2835	-121.83	2	58.5	20.5	0	32-43	K.FQHIVSIYGVCK.Q		MD:MU 1.26

Detailed Protein Report

Protein 616: coiled-coil domain-containing protein 181 [Homo sapiens]

Accession:	gi|10880975	**Score:**	20.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	59.9
Database Date:	2015-11-30	**pI:**	5.6
		Sequence Coverage [%]:	3.9
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|530365168	refseq_human (refseq_human_20140103.fasta)	PREDICTED: coiled-coil domain-containing protein 181 isoform X4 [Homo sapiens]

10	20	30	40	50	60	70	80
MNENKDTDSK	KSEEYEDDFE	KDLEWLINEN	EKSDASIIEM	ACEKEENINQ	DLKENETVME	HTKRHSDPDK	SLQDEVSPRR
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
NDIISVPGIQ	PLDPISDSDS	ENSFQESKLE	SQKDLEEEED	EEVRRYIMEK	IVQANKLLQN	QEPVNDKRER	KLKFKDQLVD
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
LEVPPLEDTT	TFKNYFENER	NMFGKLSQLC	ISNDFGQEDV	LLSLTNGSCE	ENKDRTILVE	RDGKFELLNL	QDIASQGFLP
250	**260**	**270**	**280**	**290**	**300**	**310**	**320**
PINNANSTEN	DPQQLLPRSS	NSSVSGTKKE	DSTAKIHAVT	HSSTGEPLAY	IAQPPLNRKT	CPSSAVNSDR	SKGNGKSNHR
330	**340**	**350**	**360**	**370**	**380**	**390**	**400**
TQSAHISPVT	STYCLSPRQK	ELQKQLEEKR	EKLKREEERR	KIEEEKEKKR	ENDIVFKAWL	QKKREQVLEM	RRIQRAKEIE
410	**420**	**430**	**440**	**450**	**460**	**470**	**480**
DMNSRENRDP	QQAFRLWLKK	KHEEQMKERQ	TEELRKQEEC	LFFLKGTEGR	ERAFKQWLRR	KRMEKMAEQQ	AVRERTRQLR
490	**500**	**510**					
LEAKRSKQLQ	HHLYMSEAKP	FRFTDHYN					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2777	1	735.3766	1.06	3	66.0	20.4	1	321-340	R.TQSAHISPVTSTYCLSPRQK.E	

Detailed Protein Report

Protein 617: notch homolog 2 N-terminal-like protein [Homo sapiens]

Accession:	gi|46397353	**Score:**	20.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	25.8
Database Date:	2015-11-30	**pI:**	5.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	11.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MCVTYHNGTG	YCKCPEGFLG	EYCQHRDPCE	KNRCQNGGTC	VAQAMLGKAT	CRCASGFTGE	DCQYSTSHPC	FVSRPCLNGG
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
TCHMLSRDTY	ECTCQVGFTG	KECQWTDACL	SHPCANGSTC	TTVANQFSCK	CLTGFTGQKC	ETDVNECDIP	GHCQHGGTCL
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
NLPGSYQCQC	LQGFTGQYCD	SLYVPCAPSP	CVNGGTCRQT	GDFTFECNCL	PETVRRGTEL	WERDREVWNG	KEHDEN

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1871	2	1037.3636	-66.59	3	53.2	20.4	1	1-26	-.MCVTYHNGTGYCKCPEGFLGEYCQHR.D	Carbamidomethyl: 2, 23

Protein 618: sodium channel protein type 3 subunit alpha isoform 3 [Homo sapiens]

Accession: gi|126362955
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 20.3
MW [kDa]: 221.3
pI: 5.5
Sequence Coverage [%]: 2.3
No. of unique Peptides: 2

10	20	30	40	50	60	70	80
MAQALLVPPG	PESFRLFTRE	SLAAIEKRAA	EEKAKKPKKE	QDNDDENKPK	PNSDLEAGKN	LPFIYGDIPP	EMVSEPLEDL
90	100	110	120	130	140	150	160
DPYYINKKTF	IVMNKGKAIF	RFSATSALYI	LTPLNPVRKI	AIKILVHSLF	SMLIMCTILT	NCVFMTLSNP	PDWTKNVEYT
170	180	190	200	210	220	230	240
FTGIYTFESL	IKILARGFCL	EDFTFLRDPW	NWLDFSVIVM	AYVTEFVSLG	NVSALRTFRV	LRALKTISVI	PGLKTIVGAL
250	260	270	280	290	300	310	320
IQSVKKLSDV	MILTVFCLSV	FALIGLQLFM	GNLRNKCLQW	PPSDSAFETN	TTSYFNGTMD	SNGTFVNVTM	STFNWKDYIG
330	340	350	360	370	380	390	400
DDSHFYVLDG	QKDPLLCGNG	SDAGQCPEGY	ICVKAGRNPN	YGYTSFDTFS	WAFLSLFRLM	TQDYWENLYQ	LTLRAAGKTY
410	420	430	440	450	460	470	480
MIFFVLVIFL	GSFYLVNLIL	AVVAMAYEEQ	NQATLEEAEQ	KEAEFQQMLE	QLKKQQEEAQ	AVAAASAASR	DFSGIGGLGE
490	500	510	520	530	540	550	560
LLESSSEASK	LSSKSAKEWR	NRRKKRRQRE	HLEGNNKGER	DSFPKSESED	SVKRSSFLFS	MDGNRLTSDK	KFCSPHQSLL
570	580	590	600	610	620	630	640
SIRGSLFSPR	RNSKTSIFSF	RGRAKDVGSE	NDFADDEHST	FEDSESRRDS	LFVPHRHGER	RNSNGTTTET	EVRKRRLSSY
650	660	670	680	690	700	710	720
QISMEMLEDS	SGRQRAVSIA	SILTNTMEEL	EESRQKCPPC	WYRFANVFLI	WDCCDAWLKV	KHLVNLIVMD	PFVDLAITIC
730	740	750	760	770	780	790	800
IVLNTLFMAM	EHYPMTEQFS	SVLTVGNLVF	TGIFTAEMVL	KIIAMDPYYY	FQEGWNIFDG	IIVSLSLMEL	GLSNVEGLSV
810	820	830	840	850	860	870	880
LRSFRLLRVF	KLAKSWPTLN	MLIKIIGNSV	GALGNLTLVL	AIIVFIFAVV	GMQLFGKSYK	ECVCKINDDC	TLPRWHMNDF
890	900	910	920	930	940	950	960
FHSFLIVFRV	LCGEWIETMW	DCMEVAGQTM	CLIVFMLVMV	IGNLVVLNLF	LALLLSSFSS	DNLAATDDDN	EMNNLQIAVG
970	980	990	1000	1010	1020	1030	1040
RMQKGIDYVK	NKMRECFQKA	FFRKPKVIEI	HEGNKIDSCM	SNNTGIEISK	ELNYLRDGNG	TTSGVGTGSS	VEKYVIDEND
1050	1060	1070	1080	1090	1100	1110	1120
YMSFINNPSL	TVTVPIAVGE	SDFENLNTEE	FSSESELEES	KEKLNATSSS	EGSTVDVVLP	REGEQAETEP	EEDLKPEACF
1130	1140	1150	1160	1170	1180	1190	1200
TEGCIKKFPF	CQVSTEEGKG	KIWWNLRKTC	YSIVEHNWFE	TFIVFMILLS	SGALAFEDIY	IEQRKTIKTM	LEYADKVFTY
1210	1220	1230	1240	1250	1260	1270	1280
IFILEMLLKW	VAYGFQTYFT	NAWCWLDFLI	VDVSLVSLVA	NALGYSELGA	IKSLRTLRAL	RPLRALSRFE	GMRVVVNALV
1290	1300	1310	1320	1330	1340	1350	1360
GAIPSIMNVL	LVCLIFWLIF	SIMGVNLFAG	KFYHCVNMTT	GNMFDISDVN	NLSDCQALGK	QARWKNVKVN	FDNVGAGYLA
1370	1380	1390	1400	1410	1420	1430	1440
LLQVATFKGW	MDIMYAAVDS	RDVKLQPVYE	ENLYMYLYFV	IFIIFGSFFT	LNLFIGVIID	NFNQQKKKFG	GQDIFMTEEQ
1450	1460	1470	1480	1490	1500	1510	1520
KKYYNAMKKL	GSKKPQKPIP	RPANKFQGMV	FDFVTRQVFD	ISIMILICLN	MVTMMVETDD	QGKYMTLVLS	RINLVFIVLF
1530	1540	1550	1560	1570	1580	1590	1600
TGEFVLKLVS	LRHYYFTIGW	NIFDFVVVIL	SIVGMFLAEM	IEKYFVSPTL	FRVIRLARIG	RILRLIKGAK	GIRTLLFALM
1610	1620	1630	1640	1650	1660	1670	1680
MSLPALFNIG	LLLFLVMFIY	AIFGMSNFAY	VKKEAGIDDM	FNFETFGNSM	ICLFQITTSA	GWDGLLAPIL	NSAPPDCDPD
1690	1700	1710	1720	1730	1740	1750	1760
TIHPGSSVKG	DCGNPSVGIF	FFVSYIIISF	LVVVNMYIAV	ILENFSVATE	ESAEPLSEDD	FEMFYEVWEK	FDPDATQFIE
1770	1780	1790	1800	1810	1820	1830	1840
FSKLSDFAAA	LDPPLLIAKP	NKVQLIAMDL	PMVSGDRIHC	LDILFAFTKR	VLGESGEMDA	LRIQMEDRFM	ASNPSKVSYE
1850	1860	1870	1880	1890	1900	1910	1920
PITTTLKRKQ	EEVSAAIIQR	NFRCYLLKQR	LKNISSNYNK	EAIKGRIDLP	IKQDMIIDKL	NGNSTPEKTD	GSSSTTSPPS
1930	1940	1950	1960				
YDSVTKPDKE	KFEKDKPEKE	SKGKEVRENQ	K				

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2349	1	1073.7513	-75.47	3	59.7	10.2	2	675-699	R.QKCPPCWYRFANVFLIWDCCDAWLK.V	Carbamidomethyl: 6, 19
2533	1	1045.0400	-2.11	2	61.6	10.0	1	1082-1101	K.EKLNATSSSEGSTVDVVLPR.E	

Protein 619: mothers against decapentaplegic homolog 3 isoform 1 [Homo sapiens]

Accession: gi|5174513
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 20.3
MW [kDa]: 48.0
pI: 6.8
Sequence Coverage [%]: 4.5
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MSSILPFTPP	IVKRLLGWKK	GEQNGQEEKW	CEKAVKSLVK	KLKKTGQLDE	LEKAITTQNV	NTKCITIPRS	LDGRLQVSHR
90	100	110	120	130	140	150	160
KGLPHVIYCR	LWRWPDLHSH	HELRAMELCE	FAFNMKKDEV	CVNPYHYQRV	ETPVLPPVLV	PRHTEIPAEF	PPLDDYSHSI
170	180	190	200	210	220	230	240
PENTNFPAGI	EPQSNIPETP	PPGYLSEDGE	TSDHQMNHSM	DAGSPNLSPN	PMSPAHNNLD	LQPVTYCEPA	FWCSISYYEL
250	260	270	280	290	300	310	320
NQRVGETFHA	SQPSMTVDGF	TDPSNSERFC	LGLLSNVNRN	AAVELTRRHI	GRGVRLYYIG	GEVFAECLSD	SAIFVQSPNC
330	340	350	360	370	380	390	400
NQRYGWHPAT	VCKIPPGCNL	KIFNNQEFAA	LLAQSVNQGF	EAVYQLTRMC	TIRMSFVKGW	GAEYRRQTVT	STPCWIELHL
410	420	430					
NGPLQWLDKV	LTQMGSPSIR	CSSVS					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1610	1	1100.1365	-2.93	2	50.0	20.3	2	1-19	-.MSSILPFTPPIVKRLLGWK.K	Oxidation: 1

Detailed Protein Report

Protein 620: uncharacterized protein C6orf203 isoform a [Homo sapiens]

Accession:	gi|7706029	**Score:**	20.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	27.9
Database Date:	2015-11-30	**pI:**	9.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	10.8
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|215599508	refseq_human (refseq_human_20140103.fasta)	uncharacterized protein C6orf203 isoform a [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MAMASVKLLA GVLRKPDAWI GLWGVLRGTP SSYKLCTSWN RYLYFSSTKL RAPNYKTLFY NIFSLRLPGL LLSPECIFPF
        90        100        110        120        130        140        150        160
SVRLKSNIRS TKSTKKSLQK VDEEDSDEES HHDEMSEQEE ELEDDPTVVK NYKDLEKAVQ SFRYDVVLKT GLDIGRNKVE
       170        180        190        200        210        220        230        240
DAFYKGELRL NEEKLWKKSR TVKVGDTLDL LIGEDKEAGT ETVMRILLKK VFEEKTESEK YRVVLRRWKS LKLPKKRMSK
       250
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1123	1	946.1417	-80.24	3	43.7	20.1	2	2-27	M.AMASVKLLAGVLRKPDAWIGLWGVLR.G	Oxidation: 2

Detailed Protein Report

Protein 621: glycine receptor subunit alpha-4 isoform 2 precursor [Homo sapiens]

Accession:	gi|288683407	**Score:**	19.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	39.0
Database Date:	2015-11-30	**pI:**	9.3
Modification(s):	Oxidation	**Sequence Coverage [%]:**	5.0
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 1.98 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MTTLVPATLS	FLLLWTLPGQ	VLLRVALAKE	EVKSGTKGSQ	PMSPSDFLDK	LMGRTSGYDA	RIRPNFKGPP	VNVTCNIFIN
90	100	110	120	130	140	150	160
SFSSITKTTM	DYRVNVFLRQ	QWNDPRLSYR	EYPDDSLDLD	PSMLDSIWKP	DLFFANEKGA	NFHEVTTDNK	LLRIFKNGNV
170	180	190	200	210	220	230	240
LYSIRLTLIL	SCLMDLKNFP	MDIQTCTMQL	ESFGYTMKDL	VFEWLEDAPA	VQVAEGLTLP	QFILRDEKDL	GCCTKHYNTG
250	260	270	280	290	300	310	320
KFTCIEVKFH	LERQMGYYLI	QMYIPSLLIV	ILSWVSFWIN	MDAAPARVGL	GITTVLTMTT	QSSGSRASLP	KVKRHARELA
330	340	350					
CHRVPHFPFI	PMCPPAHHLP	WI					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2077	1	599.9042	-74.64	3	56.1	19.8	1	34-50	K.SGTKGSQPMSPSDFLDK.L	Oxidation: 9	MD:MU 1.98

Detailed Protein Report

Protein 622: tubulin polyglutamylase TTLL6 isoform 2 [Homo sapiens]

Accession:	gi|195963416	**Score:**	19.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	65.9
Database Date:	2015-11-30	**pI:**	9.7
		Sequence Coverage [%]:	3.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MRIGTPTAGP	GPSAVMEGCL	GVAELRKLST	FSAYLEDHSY	NVEQIWRDIE	DVIIKTLISA	HPIIRHNYHT	CFPNHTLNSA
90	100	110	120	130	140	150	160
CFEILGFDIL	LDHKLKPWLL	EVNHSPSFST	DSRLDKEVKD	GLLYDTLVLI	NLESCDKKKV	LEEERQRGQF	LQQCCSREMR
170	180	190	200	210	220	230	240
IEEAKGFRAV	QLKKTETYEK	ENCGGFRLIY	PSLNSEKYEK	FFQDNNSLFQ	NTVASRAREE	YARQLIQELR	LKREKKPFQM
250	260	270	280	290	300	310	320
KKKVEMQGES	AGEQVRKKGM	RGWQQKQQQK	DKAATQASKQ	YIQPLTLVSY	TPDLLLSVRG	ERKNETDSSL	NQEAPTEEAS
330	340	350	360	370	380	390	400
SVFPKLTSAK	PFSSLPDLRN	INLSSSKLEP	SKPNFSIKEA	KSASAVNVFT	GTVHLTSVET	TPESTTQLSI	SPKSPPTLAV
410	420	430	440	450	460	470	480
TASSEYSGPE	TDRVVSFKCK	KQQTPPHLTQ	KKMLKSFLPT	KSKSFWESPN	TNWTLLKSDM	NKPHLISELL	TKLQLSGKLS
490	500	510	520	530	540	550	560
FFPAHYNPKL	GMNNLSQNPS	LPGECHSRSD	SSGEKRQLDV	SSLLLQSPQS	YNVTLRDLLV	IATPAQLDPR	PCRSHASAMR
570	580	590					
DPCMQDQEAY	SHCLISGQKG	CERS					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
271	1	1293.7773	110.12	2	32.8	19.7	1	27-47	R.KLSTFSAYLEDHSYNVEQIWR.D	

Detailed Protein Report

Protein 623: **CMP-N-acetylneuraminate-beta-1,4-galactoside alpha-2,3-sialyltransferase isoform n [Homo sapiens]**

Accession:	gi|394953753	**Score:**	19.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	26.7
Database Date:	2015-11-30	**pI:**	10.2
		Sequence Coverage [%]:	4.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGLLVFVRNL	LLALCLFLVL	GFLYYSAWKL	HLLQWEEDSK	YDRLGFLLNL	DSKLFSKPAP	MFLDDSFRKW	ARIREFVPPF
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
GIKGQDNLIK	AILSVTKEYR	LTPALDSLRC	RRCIIVGNGG	VLANKSLGSR	IDDYDIVVRL	NSAPVKGFEK	DVGSKTTLRI
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
TYPEGAMQRP	EQYERDSLFV	LAGFKWQDFK	WLKYIVYKER	VSWTHNIQRE	KEFLRKLVKA	RVITDLSSGI	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2153	1	1131.4149	-196.06	1	56.8	19.7	1	220-230	K.ARVITDLSSGI.-	

Detailed Protein Report

Protein 624: eukaryotic translation initiation factor 4 gamma 3 isoform 1 [Homo sapiens]

Accession:	gi|311771714	**Score:**	19.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	180.4
Database Date:	2015-11-30	**pI:**	5.2
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	0.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MNSQPQTRSP	FFQRPQIQPP	RATIPNSSPS	IRPGAQTPTA	VYQANQHIMM	VNHLPMPYPV	PQGPQYCIPQ	YRHSGPPYVG
90	100	110	120	130	140	150	160
PPQQYPVQPP	GPGPFYPGPG	PGDFPNAYGT	PFYPSQPVYQ	SAPIIVPTQQ	QPPPAKREKK	TIRIRDPNQG	GKDITEEIMS
170	180	190	200	210	220	230	240
GGGSRNPTPP	IGRPTSTPTP	PQLPSQVPEH	SPVVYGTVES	AHLAASTPVT	AASDQKQEEK	PKPDPVLKSP	SPVLRLVLSG
250	260	270	280	290	300	310	320
EKKEQEGQTS	ETTAIVSIAE	LPLPPSPTTV	SSVARSTIAA	PTSSALSSQP	IFTTAIDDRC	ELSSPREDTI	PIPSLTSCTE
330	340	350	360	370	380	390	400
TSDPLPTNEN	DDDICKKPCS	VAPNDIPLVS	STNLINEING	VSEKLSATES	IVEIVKQEVL	PLTLELEILE	NPPEEMKLEC
410	420	430	440	450	460	470	480
IPAPITPSTV	PSFPPTPPTP	PASPPHTPVI	VPAAATTVSS	PSAAITVQRV	LEEDESIRTC	LSEDAKEIQN	KIEVEADGQT
490	500	510	520	530	540	550	560
EEILDSQNLN	SRRSPVPAQI	AITVPKTWKK	PKDRTRTTEE	MLEAELELKA	EEELSIDKVL	ESEQDKMSQG	FHPERDPSDL
570	580	590	600	610	620	630	640
KKVKAVEENG	EEAEPVRNGA	ESVSEGEGID	ANSGSTDSSG	DGVTFPFKPE	SWKPTDTEGK	KQYDREFLLD	FQFMPACIQK
650	660	670	680	690	700	710	720
PEGLPPISDV	VLDKINQPKL	PMRTLDPRIL	PRGPDFTPAF	ADFGRQTPGG	RGVPICKVQS	RHGLPILEQS	KAPTCPPLVM
730	740	750	760	770	780	790	800
SHPPMKSLPL	GLLNVGSRRS	QPGQRREPRK	IITVSVKEDV	HLKKAENAWK	PSQKRDSQAD	DPENIKTQEL	FRKVRSILNK
810	820	830	840	850	860	870	880
LTPQMFNQLM	KQVSGLTVDT	EERLKGVIDL	VFEKAIDEPS	FSVAYANMCR	CLVTLKVPMA	DKPGNTVNFR	KLLLNRCQKE
890	900	910	920	930	940	950	960
FEKDKADDDV	FEKKQKELEA	ASAPEERTRL	HDELEEAKDK	ARRRSIGNIK	FIGELFKLKM	LTEAIMHDCV	VKLLKNHDEE
970	980	990	1000	1010	1020	1030	1040
SLECLCRLLT	TIGKDLDFEK	AKPRMDQYFN	QMEKIVKERK	TSSRIRFMLQ	DVIDLRLCNW	VSRRADQGPK	TIEQIHKEAK
1050	1060	1070	1080	1090	1100	1110	1120
IEEQEEQRKV	QQLMTKEKRR	PGVQRVDEGG	WNTVQGAKNS	RVLDPSKFLK	ITKPTIDEKI	QLVPKAQLGS	WGKGSSGGAK
1130	1140	1150	1160	1170	1180	1190	1200
ASETDALRSS	ASSLNRFSAL	QPPAPSGSTP	STPVEFDSRR	TLTSRGSMGR	EKNDKPLPSA	TARPNTFMRG	GSSKDLLDNQ
1210	1220	1230	1240	1250	1260	1270	1280
SQEEQRREML	ETVKQLTGGV	DVERNSTEAE	RNKTRESAKP	EISAMSAHDK	AALSEEELER	KSKSIIDEFL	HINDFKEAMQ
1290	1300	1310	1320	1330	1340	1350	1360
CVEELNAQGL	LHVFVRVGVE	STLERSQITR	DHMGQLLYQL	VQSEKLSKQD	FFKGFSETLE	LADDMAIDIP	HIWLYLAELV
1370	1380	1390	1400	1410	1420	1430	1440
TPMLKEGGIS	MRELTIEFSK	PLLPVGRAGV	LLSEILHLLC	KQMSHKKVGA	LWREADLSWK	DFLPEGEDVH	NFLLEQKLDF
1450	1460	1470	1480	1490	1500	1510	1520
IESDSPCSSE	ALSKKELSAE	ELYKRLEKLI	IEDKANDEQI	FDWVEANLDE	IQMSSPTFLR	ALMTAVCKAA	IIADSSTFRV
1530	1540	1550	1560	1570	1580	1590	1600
DTAVIKQRVP	ILLKYLDSDT	EKELQALYAL	QASIVKLDQP	ANLLRMFFDC	LYDEEVISED	AFYKWESSKD	PAEQNGKGVA
1610	1620	1630					
LKSVTAFFTW	LREAEEESED	N					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2704	1	847.8687	-44.85	2	65.0	19.4	0	712-726	K.APTCPPLVMSHPPMK.S	Carbamidomethyl: 4; Oxidation: 9, 14

Detailed Protein Report

Protein 625: PREDICTED: protein spire homolog 1 isoform X1 [Homo sapiens]

Accession:	gi|530424894	**Score:**	19.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	79.4
Database Date:	2015-11-30	**pI:**	9.8
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	3.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MMDDGKLGYS	QCMETEVIES	LGIIIYKALD	YGLKENEERE	LSPPLEQLID	HMANTVEADG	SNDEGYEAAE	EGLGDEDEKR
90	100	110	120	130	140	150	160
KISAIRSYRD	VMKLCAAHLP	TESDAPNHYQ	AVCRALFAET	MELHTFLTKI	KSAKENLKKI	QEMEKSDESS	TDLEELKNAD
170	180	190	200	210	220	230	240
WARFWVQVMR	DLRNGVKLKK	VQERQYNPLP	IEYQLTPYEM	LMDDIRCKRY	TLRKVMVNGD	IPPRLKKSAH	EIILDFIRSR
250	260	270	280	290	300	310	320
PPLNPVSARK	LKPTPPRPRS	LHERILEEIK	AERKLRPVSP	EEIRRSRLDV	TTPESTKNLV	ESSMVNGGLT	SQTKENGLST
330	340	350	360	370	380	390	400
SQQVPAQRKK	LLRAPTLAEL	DSSESEEETL	HKSTSSSSVS	PSFPEEPVLE	AVSTRKKPPK	FLPISSTPQP	ERRQPPQRRH
410	420	430	440	450	460	470	480
SIEKETPTNV	RQFLPPSRQS	SRSLVPRITS	VWPRTPFRPL	FSTIQTASLL	SSHPFEAAMF	GVAGAMYYLC	ERAFTSRWKS
490	500	510	520	530	540	550	560
SKEEFCYPVE	CLALTVEEVM	HIRQVLVKAE	LEKYQQYKDI	YTALKKGKLC	FCCRTRRFSF	FTWSYTCQFC	KRPVCSQCCK
570	580	590	600	610	620	630	640
KMRLPSKPYS	TLPIFSLGPS	ALQRGESSMR	SEKPSTAHHR	PLRSIARFSS	KSKSMDKSDE	ELQFPKELME	DWSTMEVCVD
650	660	670	680	690	700		
CKKFISEIIS	SSRRSLVLAN	KRARLKRKTQ	SFYMSSPGPS	EYCPSERTIS	EI		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2094	1	1052.4646	-27.32	3	56.3	19.4	1	1-27	-.MMDDGKLGYSQCMETEVIESLGIIIYK.A	Carbamidomethyl: 12; Oxidation: 1, 2

Detailed Protein Report

Protein 626: **prostaglandin E2 receptor EP3 subtype isoform 8 [Homo sapiens]**

Accession:	gi|38505186	**Score:**	19.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	46.7
Database Date:	2015-11-30	**pI:**	11.4
		Sequence Coverage [%]:	6.2
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MKETRGYGGD APFCTRLNHS YTGMWAPERS AEARGNLTRP PGSGEDCGSV SVAFPITMLL TGFVGNALAM LLVSRSYRRR
        90        100        110        120        130        140        150        160
ESKRKKSFLL CIGWLALTDL VGQLLTTPVV IVVYLSKQRW EHIDPSGRLC TFFGLTMTVF GLSSLFIASA MAVERALAIR
       170        180        190        200        210        220        230        240
APHWYASHMK TRATRAVLLG VWLAVLAFAL LPVLGVGQYT VQWPGTWCFI STGRGGNGTS SSHNWGNLFF ASAFAFLGLL
       250        260        270        280        290        300        310        320
ALTVTFSCNL ATIKALVSRC RAKATASQSS AQWGRITTET AIQLMGIMCV LSVCWSPLLI MMLKMIFNQT SVEHCKTHTE
       330        340        350        360        370        380        390        400
KQKECNFFLI AVRLASLNQI LDPWVYLLLR KILLRKFCQM RKRRLREQLI CSLQNSQIQR ATAHCGQVQT YRVLNREEME
       410        420
VLVSSINVYT RISTVKTE
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2724	1	992.4655	-25.39	3	65.3	19.4	1	367-392	R.EQLICSLQNSQIQRATAHCGQVQTYR.V	

Detailed Protein Report

Protein 627: **PREDICTED: mothers against decapentaplegic homolog 9 isoform X5 [Homo sapiens]**

Accession:	gi|530402395	**Score:**	19.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	40.6
Database Date:	2015-11-30	**pI:**	10.0
		Sequence Coverage [%]:	5.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MHSTTPISSL	FSFTSPAVKR	LLGWKQGDEE	EKWAEKAVDS	LVKKLKKKKG	AMDELERALS	CPGQPSKCVT	IPRSLDGRLQ
90	100	110	120	130	140	150	160
VSHRKGLPHV	IYCRVWRWPD	LQSHHELKPL	ECCEFPFGSK	QKEVCINPYH	YRRVETPDFR	PVCYEEPQHW	CSVAYYELNN
170	180	190	200	210	220	230	240
RVGETFQASS	RSVLIDGFTD	PSNNRNRFCL	GLLSNVNRNS	TIENTRRHIG	KGVHLYYVGG	EVYAECVSDS	SIFVQSRNCN
250	260	270	280	290	300	310	320
YQHGFHPATV	CKIPSGCSLK	VFNNQLFAQL	LAQSVHHGFE	VVYELTKMCT	IRMSFVKVAM	KAGEPRKFLS	GKERQLGLYM
330	340	350	360				
EVKAFSFITC	YFVCCKVLAN	ESSISKYGLI	KVSGYV				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1665	1	944.8090	-147.29	2	50.7	19.3	1	50-67	K.GAMDELERALSCPGQPSK.C	

Detailed Protein Report

Protein 628: PREDICTED: cleavage and polyadenylation specificity factor subunit 7 isoform X5 [Homo sapiens]

Accession:	gi|530397403	**Score:**	19.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	41.9
Database Date:	2015-11-30	**pI:**	10.1
		Sequence Coverage [%]:	3.9
		No. of unique Peptides:	1

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
2002	2	794.7799	-153.57	2	54.9	19.3	0	36-50	K.GYAEVVVASENSVHK.L	

Detailed Protein Report

Protein 629: PREDICTED: exosome complex exonuclease RRP44 isoform X1 [Homo sapiens]

Accession: gi|530402172
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 19.3
MW [kDa]: 90.5
pI: 6.5
Sequence Coverage [%]: 2.0
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MSADNQLQVI	FITNDRRNKE	KAIEEGIPAF	TCEEYVKSLT	ANPELIDRLA	CLSEEGNEIE	SGKIIFSEHL	PLSKLQQGIK
90	100	110	120	130	140	150	160
SGTYLQGTFR	ASRENYLEAT	VWIHGDNEEN	KEIILQGLKH	LNRAVHEDIV	AVELLPKSQW	VAPSSVVLHD	EGQNEEDVEK
170	180	190	200	210	220	230	240
EEETERMLKT	AVSEKMLKPT	GRVVGIIKRN	WRPYCGMLSK	SDIKESRRHL	FTPADKRIPR	IRIETRQAST	LEGRRIIVAI
250	260	270	280	290	300	310	320
DGWPRNSRYP	NGHFVRNLGD	VGEKETETEV	LLLEHDVPHQ	PFSQAVLSFL	PKMPWSITEK	DMKNREDLRH	LCICSVDPPG
330	340	350	360	370	380	390	400
CTDIDDALHC	RELENGNLEV	GVHIADVSHF	IRPGNALDQE	SARRGTTVYL	CEKRIDMVPE	LLSSNLCSLK	CDVDRLAFSC
410	420	430	440	450	460	470	480
IWEMNHNAEI	LKTKFTKSVI	NSKASLTYAE	AQLRIDSANM	NDDITTSLRG	LNKLAKILKK	RRIEKGALTL	SSPEVRFHMD
490	500	510	520	530	540	550	560
SETHDPIDLQ	TKELRETNSM	VEEFMLLANI	SVAKKIHEEF	SEHALLRKHP	APPPSNYEIL	VKAARSRNLE	IKTDTAKSLA
570	580	590	600	610	620	630	640
ESLDQAESPT	FPYLNTLLRI	LATRCMMQAV	YFCSGMDNDF	HHYGLASPIY	THFTSPIRRY	ADVIVHRLLA	VAIGADCTYP
650	660	670	680	690	700	710	720
ELTDKHKLAD	ICKNLNFRHK	MAQYAQRASV	AFHTQLFFKS	KGIVSEEAYI	LFVRKNAIVV	LIPKYGLEGT	VFFEEKDKPN
730	740	750	760	770	780	790	800
PQLIYDDEIP	SLKIEDTVFH	VFDKVKVKIM	LDSSNLQHQK	IRMSLVEPQI	PGISIPTDTS	NMDLNGPKKK	KMKLGK

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1167	1	977.5217	29.45	2	44.2	19.3	2	189-204	K.RNWRPYCGMLSKSDIK.E	

Detailed Protein Report

Protein 630: protein Tob2 [Homo sapiens]

Accession:	gi|7706739	**Score:**	19.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	36.6
Database Date:	2015-11-30	**pI:**	6.6
		Sequence Coverage [%]:	8.1
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578836864	refseq_human (refseq_human_20140103.fasta)	PREDICTED: protein Tob2 isoform X2 [Homo sapiens]
gi|530419484	refseq_human (refseq_human_20140103.fasta)	PREDICTED: protein Tob2 isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MQLEIKVALN	FIISYLYNKL	PRRRADLFGE	ELERLLKKKY	EGHWYPEKPL	KGSGFRCVHI	GEMVDPVVEL	AAKRSGLAVE
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
DVRANVPEEL	SVWIDPFEVS	YQIGEKGAVK	VLYLDDSEGC	GAPELDKEIK	SSFNPDAQVF	VPIGSQDSSL	SNSPSPSFGQ
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
SPSPTFIPRS	AQPITFTTAS	FAATKFGSTK	MKKGGGAASG	GGVASSGAGG	QQPPQQPRMA	RSPTNSLLKH	KSLSLSMHSL
250	**260**	**270**	**280**	**290**	**300**	**310**	**320**
NFITANPAPQ	SQLSPNAKEF	VYNGGGSPSL	FFDAADGQGS	GTPGPFGGSG	AGTCNSSSFD	MAQVFGGGAN	SLFLEKTPFV
330	**340**	**350**					
EGLSYNLNTM	QYPSQQFQPV	VLAN					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2780	1	841.6618	-109.74	3	65.2	19.2	2	191-218	K.MKKGGGAASGGGVASSGAGGQQPPQQPR.M	

Protein 631: PREDICTED: mucin-6 isoform X1 [Homo sapiens]

Accession: gi|578840955
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 19.2
MW [kDa]: 141.7
pI: 5.7
Sequence Coverage [%]: 1.1
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
1896	1	840.7895	-54.74	2	53.8	19.2	0	168-182	K.YMGQMCGLCGNFDGK.V	Carbamidomethyl: 9

Detailed Protein Report

Protein 632: probable G-protein coupled receptor 141 [Homo sapiens]

Accession: gi|32401435
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 19.1
MW [kDa]: 35.4
pI: 10.1
Sequence Coverage [%]: 5.6
No. of unique Peptides: 1

```
        10         20         30         40         50         60         70         80
MPGHNTSRNS SCDPIVTPHL ISLYFIVLIG GLVGVISILF LLVKMNTRSV TTMAVINLVV VHSVFLLTVP FRLTYLIKKT
        90        100        110        120        130        140        150        160
WMFGLPFCKF VSAMLHIHMY LTFLFYVVIL VTRYLIFFKC KDKVEFYRKL HAVAASAGMW TLVIVIVVPL VVSRYGIHEE
       170        180        190        200        210        220        230        240
YNEEHCFKFH KELAYTYVKI INYMIVIFVI AVAVILLVFQ VFIIMLMVQK LRHSLLSHQE FWAQLKNLFF IGVILVCFLP
       250        260        270        280        290        300        310
YQFFRIYYLN VVTHSNACNS KVAFYNEIFL SVTAISCYDL LLFVFGGSHW FKQKIIGLWN CVLCR
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1711	1	1044.9814	-87.18	2	51.2	19.1	2	73-89	R.LTYLIKKTWMFGLPFCK.F	

Detailed Protein Report

Protein 633: **protein FAM83G [Homo sapiens]**

Accession:	gi|115392150	**Score:**	19.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	90.8
Database Date:	2015-11-30	**pI:**	5.9
		Sequence Coverage [%]:	1.0
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 0.74 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MAFSQVQCLD	DNHVNWRSSE	SKPEFFYSEE	QRLALEALVA	RGRDAFYEVL	KRENIRDFLS	ELELKRILET	IEVYDPGSED
90	100	110	120	130	140	150	160
PRGTGPSQGP	EDNGVGDGEE	ASGADGVPIE	AEPLPSLEYW	PQKSDRSIPQ	LDLGWPDTIA	YRGVTRASVY	MQPPIDGQAH
170	180	190	200	210	220	230	240
IKEVVRKMIS	QAQKVIAVVM	DMFTDVDIFK	DLLDAGFKRK	VAVYIIVDES	NVKYFLHMCE	RACMHLGHLK	NLRVRSSGGT
250	260	270	280	290	300	310	320
EFFTRSATKF	KGALAQKFMF	VDGDRAVCGS	YSFTWSAART	DRNVISVLSG	QVVEMFDRQF	QELYLMSHSV	SLKGIPMEKE
330	340	350	360	370	380	390	400
PEPEPIVLPS	VVPLVPAGTV	AKKLVNPKYA	LVKAKSVDEI	AKISSEKQEA	KKPLGLKGPA	LAEHPGELPE	LLPPIHPGLL
410	420	430	440	450	460	470	480
HLERANMFEY	LPTWVEPDPE	PGSDILGYIN	IIDPNIWNPQ	PSQMNRIKIR	DTSQASAQHQ	LWKQSQDSRP	RPEPCPPPEP
490	500	510	520	530	540	550	560
SAPQDGVPAE	NGLPQGDPEP	LPPVPKPRTV	PVADVLARDS	SDIGWVLELP	KEEAPQNGTD	HRLPRMAGPG	HAPLQRQLSV
570	580	590	600	610	620	630	640
TQDDPESLGV	GLPNGLDGVE	EEDDDDYVTL	SDQDSHSGSS	GRGPGPRRPS	VASSVSEEYF	EVREHSVPLR	RRHSEQVANG
650	660	670	680	690	700	710	720
PTPPPRRQLS	APHITRGTFV	GPQGGSPWAQ	SRGREEADAL	KRMQAQRSTD	KEAQGQQFHH	HRVPASGTRD	KDGFPGPPRY
730	740	750	760	770	780	790	800
RSAADSVQSS	TRNAGPAMAG	PHHWQAKGGQ	VPRLLPDPGS	PRLAQNARPM	TDGRATEEHP	SPFGIPYSKL	SQSKHLKART
810	820	830					
GGSQWASSDS	KRRAQAPRDR	KDP					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
546	4	492.6414	-231.48	2	36.4	19.0	0	44-51	R.DAFYEVLK.R		MD:MU 0.74

Detailed Protein Report

Protein 634: PREDICTED: zinc finger protein 606 isoform X2 [Homo sapiens]

Accession:	gi|530417293	**Score:**	18.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	81.7
Database Date:	2015-11-30	**pI:**	9.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLETYGHLLS	VGNQIAKPEV	ISLLEQGEEP	WSVEQACPQR	TCPEWVRNLE	SKALIPAQSI	FEEEQSHGMK	LERYIWDDPW
90	100	110	120	130	140	150	160
FSRLEVLGCK	DQLEMYHMNQ	STAMRQMVFM	QKQVLSQRSS	EFCGLGAEFS	QNLNFVPSQR	VSQIEHFYKP	DTHAQSWRCD
170	180	190	200	210	220	230	240
SAIMYADKVT	CENNDYDKTV	YQSIQPIYPA	RIQTGDNLFK	CTDAVKSFNH	IIHFGDHKGI	HTGEKLYEYK	ECHQIFNQSP
250	260	270	280	290	300	310	320
SFNEHPRLHV	GENQYNYKEY	ENIFYFSSFM	EHQKIGTVEK	AYKYNEWEKV	FGYDSFLTQH	TSTYTAEKPY	DYNECGTSFI
330	340	350	360	370	380	390	400
WSSYLIQHKK	THTGEKPYEC	DKCGKVFRNR	SALTKHERTH	TGIKPYECNK	CGKAFSWNSH	LIVHKRIHTG	EKPYVCNECG
410	420	430	440	450	460	470	480
KSFNWNSHLI	GHQRTHTGEK	PFECTECGKS	FSWSSHLIAH	MRMHTGEKPF	KCDECEKAFR	DYSALSKHER	THSGAKPYKC
490	500	510	520	530	540	550	560
TECGKSFSWS	SHLIAHQRTH	TGEKPYNCQE	CGKAFRERSA	LTKHEIIHSG	IKPYECNKCG	KSCSQMAHLV	RHQRTHTGEK
570	580	590	600	610	620	630	640
PYECNKCGKS	FSQSCHLVAH	RRIHTGEKPY	KCNQCERSFN	CSSHLIAHRR	THTGEKPYRC	NECGKAFNES	SSLIVHLRNH
650	660	670	680	690	700	710	
TGEKPYKCNH	CEKAFCKNSS	LIIHQRMHSG	EKRFICSECG	KAFSGHSALL	QHQRNHSEEK	LN	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1657	1	1044.8456	-136.96	2	50.6	18.9	2	468-485	K.HERTHSGAKPYKCTECGK.S	Carbamidomethyl: 13

Detailed Protein Report

Protein 635: something about silencing protein 10 [Homo sapiens]

Accession:	gi|9966799	**Score:**	18.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	54.5
Database Date:	2015-11-30	**pI:**	5.4
		Sequence Coverage [%]:	4.0
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 1.07 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MVGRSRRRGA	AKWAAVRAKA	GPTLTDENGD	DLGLPPSPGD	TSYYQDQVDD	FHEARSRAAL	AKGWNEVQSG	DEEDGEEEEE
90	100	110	120	130	140	150	160
EVLALDMDDE	DDEDGGNAGE	EEEEENADDD	GGSSVQSEAE	ASVDPSLSWG	QRKKLYYDTD	YGSKSRGRQS	QQEAEEEERE
170	180	190	200	210	220	230	240
EEEEAQIIQR	RLAQALQEDD	FGVAWVEAFA	KPVPQVDEAE	TRVVKDLAKV	SVKEKLKMLR	KESPELLELI	EDLKVKLTEV
250	260	270	280	290	300	310	320
KDELEPLLEL	VEQGIIPPGK	GSQYLRTKYN	LYLNYCSNIS	FYLILKARRV	PAHGHPVIER	LVTYRNLINK	LSVVDQKLSS
330	340	350	360	370	380	390	400
EIRHLLTLKD	DAVKKELIPK	AKSTKPKPKS	VSKTSAAACA	VTDLSDDSDF	DEKAKLKYYK	EIEDRQKLKR	KKEENSTEEQ
410	420	430	440	450	460	470	480
ALEDQNAKRA	ITYQIAKNRG	LTPRRKKIDR	NPRVKHREKF	RRAKIRRRGQ	VREVRKEEQR	YSGELSGIRA	GVKKSIKLK

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1704	1	697.0043	-68.98	3	51.1	18.9	0	242-260	K.DELEPLLELVEQGIIPPGK.G		MD:MU 1.07

Detailed Protein Report

Protein 636: PREDICTED: rho GTPase-activating protein 18 isoform X2 [Homo sapiens]

Accession: gi|530384204
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 18.8
MW [kDa]: 66.4
pI: 6.5
Sequence Coverage [%]: 1.5
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MSWLSSSQGV	VLTAYHPSGK	DQTVGNSHAK	AGEEATSSRR	YGQYTMNQES	TTIKVMEKPP	FDRSISQDSL	DELSMEDYWI
90	100	110	120	130	140	150	160
ELENIKKSSE	NSQEDQEVVV	VKEPDEGELE	EEWLKEAGLS	NLFGESAGDP	QESIVFLSTL	TRTQAAAVQK	RVETVSQTLR
170	180	190	200	210	220	230	240
KKNKQYQIPD	VRDIFAQQRE	SKETAPGGTE	SQSLRTNENK	YQGRDDEASN	LVGEEKLIPP	EETPAPETDI	NLEVSFAEQA
250	260	270	280	290	300	310	320
LNQKESSKEK	IQKSKGDDAT	LPSFRLPKDK	TGTTRIGDLA	PQDMKKVCHL	ALIELTALYD	VLGIELKQQK	AVKIKTKDSG
330	340	350	360	370	380	390	400
LFCVPLTALL	EQDQRKVPGM	RIPLIFQKLI	SRIEERGLET	EGLLRIPGAA	IRIKNLCQEL	EAKFYEGTFN	WESVKQHDAA
410	420	430	440	450	460	470	480
SLLKLFIREL	PQPLLSVEYL	KAFQAVQNLP	TKKQQLQALN	LLVILLPDAN	RDTLKALLEF	LQRVIDNKEK	NKMTVMNVAM
490	500	510	520	530	540	550	560
VMAPNLFMCH	ALGLKSSEQR	EFVMAAGTAN	TMHLLIKYQK	LLWTIPKFIV	NQVRKQNTEN	HKKDKRAMKK	LLKKMAYDRE
570	580	590					
KYEKQDKSTN	DWGCPDSQER	RSFFV					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
875	1	491.6668	-208.81	2	40.5	18.8	0	396-404	K.QHDAASLLK.L	

Detailed Protein Report

Protein 637: N-acylglucosamine 2-epimerase [Homo sapiens]

Accession:	gi|213417820	**Score:**	18.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	48.8
Database Date:	2015-11-30	**pI:**	5.9
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSKGLPARQD	MEKERETLQA	WKERVGQELD	RVVAFWMEHS	HDQEHGGFFT	CLGREGRVYD	DLKYVWLQGR	QVWMYCRLYR
90	100	110	120	130	140	150	160
TFERFRHAQL	LDAAKAGGEF	LLRYARVAPP	GKKCAFVLTR	DGRPVKVQRT	IFSECFYTMA	MNELWRATGE	VRYQTEAVEM
170	180	190	200	210	220	230	240
MDQIVHWVQE	DASGLGRPQL	QGAPAAEPMA	VPMMLLNLVE	QLGEADEELA	GKYAELGDWC	ARRILQHVQR	DGQAVLENVS
250	260	270	280	290	300	310	320
EGGKELPGCL	GRQQNPGHTL	EAGWFLLRHC	IRKGDPELRA	HVIDKFLLLP	FHSGWDPDHG	GLFYFQDADN	FCPTQLEWAM
330	340	350	360	370	380	390	400
KLWWPHSEAM	IAFLMGYSDS	GDPVLLRLFY	QVAEYTFRQF	RDPEYGEWFG	YLSREGKVAL	SIKGGPFKGC	FHVPRCLAMC
410	420	430					
EEMLGALLSR	PAPAPSPAPT	PACRGAE					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2036	1	753.8094	-85.39	2	55.6	18.8	2	1-13	-.MSKGLPARQDMEK.E	Oxidation: 11

Protein 638: protein dispatched homolog 2 [Homo sapiens]

Accession: gi|25121980

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Score: 18.7

MW [kDa]: 151.9

pI: 9.3

Sequence Coverage [%]: 0.6

No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MDGDSSSSSG	GSGPAPGPGP	EGEQRPEGEP	LAPDGGSPDS	TQTKAVPPEA	SPERSCSLHS	CPLEDPSSSS	GPPPTTSTLQ
90	100	110	120	130	140	150	160
PVGPSSPLAP	AHFTYPRALQ	EYQGGSSLPG	LGDRAALCSH	GSSLSPSPAP	SQRDGTWKPP	AVQHHVVSVR	QERAFQMPKS
170	180	190	200	210	220	230	240
YSQLIAEWPV	AVLMLCLAVI	FLCTLAGLLG	ARLPDFSKPL	LGFEPRDTDI	GSKLVVWRAL	QALTGPRKLL	FLSPDLELNS
250	260	270	280	290	300	310	320
SSSHNTLRPA	PRGSAQESAV	RPRRMVEPLE	DRRQENFFCG	PPEKSYAKLV	FMSTSSGSLW	NLHAIHSMCR	MEQDQIRSHT
330	340	350	360	370	380	390	400
SFGALCQRTA	ANQCCPSWSL	GNYLAVLSNR	SSCLDTTQAD	AARTLALLRT	CALYYHSGAL	VPSCLGPGQN	KSPRCAQVPT
410	420	430	440	450	460	470	480
KCSQSSAIYQ	LLHFLLDRDF	LSPQTTDYQV	PSLKYSLLFL	PTPKGASLMD	IYLDRLATPW	GLADNYTSVT	GMDLGLKQEL
490	500	510	520	530	540	550	560
LRHFLVQDTV	YPLLALVAIF	FGMALYLRSL	FLTLMVLLGV	LGSLLVAFFL	YQVAFRMAYF	PFVNLAALLL	LSSVCANHTL
570	580	590	600	610	620	630	640
IFFDLWRLSK	SQLPSGGLAQ	RVGRTMHHFG	YLLLVSGLTT	SAAFYASYLS	RLPAVRCLAL	FMGTAVLVHL	ALTLVWLPAS
650	660	670	680	690	700	710	720
AVLHERYLAR	GCARRARGRW	EGSAPRRLLL	ALHRRLRGLR	RAAAGTSRLL	FQRLLPCGVI	KFRYIWICWF	AALAAGGAYI
730	740	750	760	770	780	790	800
AGVSPRLRLP	TLPPPGGQVF	RPSHPFERFD	AEYRQLFLFE	QLPQGEGGHM	PVVLVWGVLP	VDTGDPLDPR	SNSSLVRDPA
810	820	830	840	850	860	870	880
FSASGPEAQR	WLLALCHRAR	NQSFFDTLQE	GWPTLCFVET	LQRWMESPSC	ARLGPDLCCG	HSDFPWAPQF	FLHCLKMMAL
890	900	910	920	930	940	950	960
EQGPDGTQDL	GLRFDAHGSL	AALVLQFQTN	FRNSPDYNQT	QLFYNEVSHW	LAAELGMAPP	GLRRGWFTSR	LELYSLQHSL
970	980	990	1000	1010	1020	1030	1040
STEPAVVLGL	ALALAFATLL	LGTWNVPLSL	FSVAAVAGTV	LLTVGLLVLL	EWQLNTAEAL	FLSASVGLSV	DFTVNYCISY
1050	1060	1070	1080	1090	1100	1110	1120
HLCPHPDRLS	RVAFSLRQTS	CATAVGAAAL	FAAGVLMLPA	TVLLYRKLGI	ILMMVKCVSC	GFASFFFQSL	CCFFGPEKNC
1130	1140	1150	1160	1170	1180	1190	1200
GQILWPCAHL	PWDAGTGDPG	GEKAGRPRPG	SVGGMPGSCS	EQYELQPLAR	RRSPSFDTST	ATSKLSHRPS	VLSEDLQLHD
1210	1220	1230	1240	1250	1260	1270	1280
GPCCSRPPPA	PASPRELLLD	HQAVFSQCPA	LQTSSPYKQA	GPSPKTRARQ	DSQGEEAEPL	PASPEAPAHS	PKAKAADPPD
1290	1300	1310	1320	1330	1340	1350	1360
GFCSSASTLE	GLSVSDETCL	STSEPSARVP	DSVGVSPDDL	DDTGQPVLER	GQLNGKRDTL	WLALRETVYD	PSLPASHHSS
1370	1380	1390	1400	1410			
LSWKGRGGPG	DGSPVVLPNS	QPDLPDVWLR	RPSTHTSGYS	S			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1767	2	1011.7857	227.39	1	51.9	18.7	0	811-818	R.WLLALCHR.A	

Detailed Protein Report

Protein 639: PREDICTED: leucine-rich repeat-containing protein 16A isoform X6 [Homo sapiens]

Accession:	gi|578811792	**Score:**	18.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	105.2
Database Date:	2015-11-30	**pI:**	6.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MTEESSDVPR	ELIESIKDVI	GRKIKISVKK	KVKLEVKGDK	VENKVLVLTS	CRAFLVTARI	PTKLELTFSY	LEIHGVVCSK
90	100	110	120	130	140	150	160
SAQMIVETEK	CSISMKMASP	EDVSEVLAHI	GTCLRKIFPG	LSPVRIMKKV	SMEPSERLAS	LQALWDSQTV	AEQGPCGGFS
170	180	190	200	210	220	230	240
QMYACVCDWL	GFSYREEVQW	DVDTIYLTQD	TRELNLQDFS	HLDHRDLIPI	IAALEYNQWF	TKLSSKDLKL	STDVCEQILR
250	260	270	280	290	300	310	320
VVSRSNRLEE	LVLENAGLRT	DFAQKLASAL	AHNPNSGLHT	INLAGNPLED	RGVSSLSIQF	AKLPKGLKHL	NLSKTSLSPK
330	340	350	360	370	380	390	400
GVNSLSQSLS	ANPLTASTLV	HLDLSGNVLR	GDDLSHMYNF	LAQPNAIVHL	DLSNTECSLD	MVCGALLRGC	LQYLAVLNLS
410	420	430	440	450	460	470	480
RTVFSHRKGK	EVPPSFKQFF	SSSLALMHIN	LSGTKLSPEP	LKALLLGLAC	NHNLKGVSLD	LSNCELGHCL	RSGGAQVLEG
490	500	510	520	530	540	550	560
CIAEIHNITS	LDISDNGLES	DLSTLIVWLS	KNRSIQHLAL	GKNFNNMKSK	NLTPVLDNLV	QMIQDEESPL	QSLSLADSKL
570	580	590	600	610	620	630	640
KTEVTIIINA	LGSNTSLTKV	DISGNGMGDM	GAKMLAKALQ	INTKLRTVIW	DKNNITAQGF	QDIAVAMEKN	YTLRFMPIPM
650	660	670	680	690	700	710	720
YDASQALKTN	PEKTEDALQK	IENYLLRNHE	TRKYLQEQAY	RLQQGIVTST	TQQMIDRICV	KVQDHLNSLR	NCGGDAIQED
730	740	750	760	770	780	790	800
LKSAERLMRD	AKNSKTLLPN	LYHVGGASWA	GASGLLSSPI	QETLESMAGE	VTRVVDEQLK	ALLESMVDAA	ENLCPNVMKK
810	820	830	840	850	860	870	880
AHIRQDLIHA	STEKISIPRT	FVKNVLLEQS	GIDILNKISE	VKLTVASFLS	DRIVDEILDA	LSHCHHKLAD	HFSRRGKTLP
890	900	910	920	930	940	950	
QQESLEIELA	EEKPVKRSII	TVEELTEIER	LEDLDTCMKP	HAFQHAMMTF	ASTTFRLCQK	SSKLSLLSS	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
843	1	946.5224	65.61	3	40.1	18.7	2	91-116	K.CSISMKMASPEDVSEVLAHIGTCLRK.I	Oxidation: 5, 7

Detailed Protein Report

Protein 640: **myosin-binding protein C, slow-type isoform 9 [Homo sapiens]**

Accession:	gi|360039225	**Score:**	18.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	126.3
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
MPEPTKKEDW	TLVETPPGEE	QAKQNANSQL	SILFIEKPQG	GTVKVGEDIT	FIAKVKAEDL	LRKPTIKWFK	GKWMDLASKA
90	100	110	120	130	140	150	160
GKHLQLKETF	ERHSRVYTFE	MQIIKAKDNF	AGNYRCEVTY	KDKFDSCSFD	LEVHESTGTT	PNIDIRSAFK	RSGEGQEDAG
170	180	190	200	210	220	230	240
ELDFSGLLKR	REVKQQEEEP	QVDVWELLKN	AKPSEYEKIA	FQYGITDLRG	MLKRLKRMRR	EEKKSAAFAK	ILDPAYQVDK
250	260	270	280	290	300	310	320
GGRVRFVVEL	ADPKLEVKWY	KNGQEIRPST	KYIFEHKGCQ	RILFINNCQM	TDDSEYYVTA	GDEKCSTELF	VREPPIMVTK
330	340	350	360	370	380	390	400
QLEDTTAYCG	ERVELECEVS	EDDANVKWFK	NGEEIIPGPK	SRYRIRVEGK	KHILIIEGAT	KADAAEYSVM	TTGGQSSAKL
410	420	430	440	450	460	470	480
SVDLKPLKIL	TPLTDQTVNL	GKEICLKCEI	SENIPGKWTK	NGLPVQESDR	LKVVHKGRIH	KLVIANALTE	DEGDYVFAPD
490	500	510	520	530	540	550	560
AYNVTLPAKV	HVIDPPKIIL	DGLDADNTVT	VIAGNKLRLE	IPISGEPPPK	AMWSRGDKAI	MEGSGRIRTE	SYPDSSTLVI
570	580	590	600	610	620	630	640
DIAERDDSGV	YHINLKNEAG	EAHASIKVKV	VDFPDPPVAP	TVTEVGDDWC	IMNWEPPAYD	GGSPILGYFI	ERKKKQSSRW
650	660	670	680	690	700	710	720
MRLNFDLCKE	TTFEPKKMIE	GVAYEVRIFA	VNAIGISKPS	MPSRPFVPLA	VTSPPTLLTV	DSVTDTTVTM	RWRPPDHIGA
730	740	750	760	770	780	790	800
AGLDGYVLEY	CFEGTEDWIV	ANKDLIDKTK	FTITGLPTDA	KIFVRVKAVN	AAGASEPKYY	SQPILVKEII	EPPKIRIPRH
810	820	830	840	850	860	870	880
LKQTYIRRVG	EAVNLVIPFQ	GKPRPELTWK	KDGAEIDKNQ	INIRNSETDT	IIFIRKAERS	HSGKYDLQVK	VDKFVETASI
890	900	910	920	930	940	950	960
DIQIIDRPGP	PQIVKIEDVW	GENVALTWTP	PKDDGNAAIT	GYTIQKADKK	SMEWFTVIEH	YHRTSATITE	LVIGNEYYFR
970	980	990	1000	1010	1020	1030	1040
VFSENMCGLS	EDATMTKESA	VIARDGKIYK	NPVYEDFDFS	EAPMFTQPLV	NTYAIAGYNA	TLNCSVRGNP	KPKITWMKNK
1050	1060	1070	1080	1090	1100	1110	1120
VAIVDDPRYR	MFSNQGVCTL	EIRKPSPYDG	GTYCCKAVND	LGTVEIECKL	EVKVIYQGVN	TPGQPVFLEG	QQQSLHNKDF
1130							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1458	1	982.5602	12.16	2	48.0	18.6	2	246-261	R.FVVELADPKLEVKWYK.N	

Detailed Protein Report

Protein 641: DAN domain family member 5 precursor [Homo sapiens]

Accession:	gi|22749329	**Score:**	18.6
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
1379	1	1023.1562	107.05	2	47.0	18.6	2	155-172	R.WAPVVLWCLTGSSASRRR.V	

Detailed Protein Report

Protein 642: **PREDICTED: dyslexia-associated protein KIAA0319-like protein isoform X6 [Homo sapiens]**

Accession:	gi|578799795	**Score:**	18.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	76.2
Database Date:	2015-11-30	**pI:**	5.4
		Sequence Coverage [%]:	2.2
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|578799797	refseq_human (refseq_human_20140103.fasta)	PREDICTED: dyslexia-associated protein KIAA0319-like protein isoform X7 [Homo sapiens]

10	20	30	40	50	60	70	80
MEGKHSQILK	LSKLTPGLYE	FKVIVEGQNA	HGEGYVNVTV	KPEPRKNRPP	IAIVSPQFQE	ISLPTTSTVI	DGSQSTDDDK
90	100	110	120	130	140	150	160
IVQYHWEELK	GPLREEKISE	DTAILKLSKL	VPGNYTFSLT	VVDSDGATNS	TTANLTVNKA	VDYPPVANAG	PNQVITLPQN
170	180	190	200	210	220	230	240
SITLFGNQST	DDHGITSYEW	SLSPSSKGKV	VEMQGVRTPT	LQLSAMQEGD	YTYQLTVTDT	IGQQATAQVT	VIVQPENNKP
250	260	270	280	290	300	310	320
PQADAGPDKE	LTLPVDSTTL	DGSKSSDDQK	IISYLWEKTQ	GPDGVQLENA	NSSVATVTGL	QVGTYVFTLT	VKDERNLQSQ
330	340	350	360	370	380	390	400
SSVNVIVKEE	INKPPIAKIT	GNVVITLPTS	TAELDGSKSS	DDKGIVSYLW	TRDEGSPAAG	EVLNHSDHHP	ILFLSNLVEG
410	420	430	440	450	460	470	480
TYTFHLKVTD	AKGESDTDRT	TVEVKPDPRK	NNLVEIILDI	NVSQLTERLK	GMFIRQIGVL	LGVLDSDIIV	QKIQPYTEQS
490	500	510	520	530	540	550	560
TKMVFFVQNE	PPHQIFKGHE	VAAMLKSELR	KQKADFLIFR	ALEVNTVTCQ	LNCSDHGHCD	SFTKRCICDP	FWMENFIKVQ
570	580	590	600	610	620	630	640
LRDGDSNCEW	SVLYVIIATF	VIVVALGILS	WTVICCCKRQ	KGKPKRKSKY	KILDATDQES	LELKPTSRAG	IKQKGLLLSS
650	660	670	680	690	700		
SLMHSESELD	SDDAIFTWPD	REKGKLLHGQ	NGSVPNGQTP	LKARSPREEI	L		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2117	1	788.3020	-135.99	2	56.3	18.5	0	250-264	K.ELTLPVDSTTLDGSK.S	

Detailed Protein Report

Protein 643: **PREDICTED: E3 ubiquitin-protein ligase pellino homolog 3 isoform X2 [Homo sapiens]**

Accession: gi|578821247
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 18.5
MW [kDa]: 27.9
pI: 9.1
Sequence Coverage [%]: 11.7
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MADPRWPDGW	TDHQWSPGDA	PGRRLLRGLS	PGCLAGDLGL	WECVHIAGQP	LSPAAGQAVR	PFYCLWQVEN	ESNVLQDGSL
90	100	110	120	130	140	150	160
IDLCGATLLW	RTPAGLLRAP	TLKQLEAQRQ	EANAARPQCP	VGLSTLAFPS	PARGRTAPDK	QQPWVYVRCG	HVHGYHGWGC
170	180	190	200	210	220	230	240
RRERGPQERE	CPLCRLVGPY	VPLWLGQEAG	LCLDPGPPSH	AFAPCGHVCS	EKTARYWAQT	PLPHGTHAFH	AACPFCGAWL
250	260						
TGEHGCVRLI	FQGPLD						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
36	1	1069.4752	-74.05	3	30.1	18.5	1	104-133	K.QLEAQRQEANAARPQCPVGLSTLAFPSPAR.G	

Detailed Protein Report

Protein 644: alpha-tocopherol transfer protein-like isoform 1 [Homo sapiens]

Accession:	gi|85861243	**Score:**	18.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	38.5
Database Date:	2015-11-30	**pI:**	6.0
		Sequence Coverage [%]:	2.9
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530418391	refseq_human (refseq_human_20140103.fasta)	PREDICTED: alpha-tocopherol transfer protein-like isoform X1 [Homo sapiens]
gi|85861250	refseq_human (refseq_human_20140103.fasta)	alpha-tocopherol transfer protein-like isoform 1 [Homo sapiens]

10	20	30	40	50	60	70	80
MSEESDSLRT	SPSVASLSEN	ELPPPPEPPG	YVCSLTEDLV	TKAREELQEK	PEWRLRDVQA	LRDMVRKEYP	NLSTSLDDAF
90	100	110	120	130	140	150	160
LLRFLRARKF	DYDRALQLLV	NYHSCRRSWP	EVFNNLKPSA	LKDVLASGFL	TVLPHTDPRG	CHVVCIRPDR	WIPSNYPITE
170	180	190	200	210	220	230	240
NIRAIYLTLE	KLIQSEETQV	NGIVILADYK	GVSLSKASHF	GPFIAKKVIG	ILQDGFPIRI	KAVHVVNEPR	IFKGIFAIIK
250	260	270	280	290	300	310	320
PFLKEKIANR	FFLHGSDLNS	LHTNLPRSIL	PKEYGGTAGE	LDTATWNAVL	LASEDDFVKE	FCQPVPACDS	ILGQTLLPEG
330	340	350					
LTSDAQCDDS	LRAVKSQLYS	CY					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
22	1	537.7431	-87.57	2	29.9	18.5	0	197-206	K.ASHFGPFIAK.K	

Detailed Protein Report

Protein 645: putative ATP-dependent RNA helicase DHX57 [Homo sapiens]

Accession: gi|39777586
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 18.4
MW [kDa]: 155.5
pI: 8.7
Sequence Coverage [%]: 1.4
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MSSSVRRKGK	PGKGGGKGSS	RGGRGGRSHA	SKSHGSGGGG	GGGGGGGGGN	RKASSRIWDD	GDDFCIFSES	RRPSRPSNSN
90	100	110	120	130	140	150	160
ISKGESRPKW	KPKAKVPLQT	LHMTSENQEK	VKALLRDLQE	QDADAGSERG	LSGEEEDDEP	DCCNDERYWP	AGQEPSLVPD
170	180	190	200	210	220	230	240
LDPLEYAGLA	SVEPYVPEFT	VSPFAVQKLS	RYGFNTERCQ	AVLRMCDGDV	GASLEHLLTQ	CFSETFGERM	KISEAVNQIS
250	260	270	280	290	300	310	320
LDECMEQRQE	EAFALKSICG	EKFIERIQNR	VWTIGLELEY	LTSRFRKSKP	KESTKNVQEN	SLEICKFYLK	GNCKFGSKCR
330	340	350	360	370	380	390	400
FKHEVPPNQI	VGRIERSVDD	SHLNAIEDAS	FLYELEIRFS	KDHKYPYQAP	LVAFYSTNEN	LPLACRLHIS	EFLYDKALTF
410	420	430	440	450	460	470	480
AETSEPVVYS	LITLLEEESE	IVKLLTNTHH	KYSDPPVNFL	PVPSRTRINN	PACHKTVIPN	NSFVSNQIPE	VEKASESEES
490	500	510	520	530	540	550	560
DEDDGPAPVI	VENESYVNLK	KKISKRYDWQ	AKSVHAENGK	ICKQFRMKQA	SRQFQSILQE	RQSLPAWEER	ETILNLLRKH
570	580	590	600	610	620	630	640
QVVVISGMTG	CGKTTQIPQF	ILDDSLNGPP	EKVANIICTQ	PRRISAISVA	ERVAKERAER	VGLTVGYQIR	LESVKSSATR
650	660	670	680	690	700	710	720
LLYCTTGVLL	RRLEGDTALQ	GVSHIIVDEV	HERTEESDFL	LLVLKDIVSQ	RPGLQVILMS	ATLNAELFSD	YFNSCPVITI
730	740	750	760	770	780	790	800
PGRTFPVDQF	FLEDAIAVTR	YVLQDGSPYM	RSMKQISKEK	LKARRNRTAF	EEVEEDLRLS	LHLQDQDSVK	DAVPDQQLDF
810	820	830	840	850	860	870	880
KQLLARYKGV	SKSVIKTMSI	MDFEKVNLEL	IEALLEWIVD	GKHSYPPGAI	LVFLPGLAEI	KMLYEQLQSN	SLFNNRRSNR
890	900	910	920	930	940	950	960
CVIHPLHSSL	SSEEQQAVFV	KPPAGVTKII	ISTNIAETSI	TIDDVVYVID	SGKMKEKRYD	ASKGMESLED	TFVSQANALQ
970	980	990	1000	1010	1020	1030	1040
RKGRAGRVAS	GVCFHLFTSH	HYNHQLLKQQ	LPEIQRVPLE	QLCLRIKILE	MFSAHNLQSV	FSRLIEPPHT	DSLRASKIRL
1050	1060	1070	1080	1090	1100	1110	1120
RDLGALTPDE	RLTPLGYHLA	SLPVDVRIGK	LMLFGSIFRC	LDPALTIAAS	LAFKSPFVSP	WDKKEEANQK	KLEFAFANSD
1130	1140	1150	1160	1170	1180	1190	1200
YLALLQAYKG	WQLSTKEGVR	ASYNYCRQNF	LSGRVLQEMA	SLKRQFTELL	SDIGFAREGL	RAREIEKRAQ	GGDGVLDATG
1210	1220	1230	1240	1250	1260	1270	1280
EEANSNAENP	KLISAMLCAA	LYPNVVQVKS	PEGKFQKTST	GAVRMQPKSA	ELKFVTKNDG	YVHIHPSSVN	YQVRHFDSPY
1290	1300	1310	1320	1330	1340	1350	1360
LLYHEKIKTS	RVFIRDCSMV	SVYPLVLFGG	GQVNVQLQRG	EFVVSLDDGW	IRFVAASHQV	AELVKELRCE	LDQLLQDKIK
1370	1380	1390					
NPSIDLCTCP	RGSRIISTIV	KLVTTQ					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1483	2	699.6611	-193.23	2	48.2	18.4	0	33-51	K.SHGSGGGGGGGGGGGGGNR.K	

Detailed Protein Report

Protein 646: storkhead-box protein 1 isoform c [Homo sapiens]

Accession:	gi|194328689	**Score:**	18.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	19.0
Database Date:	2015-11-30	**pI:**	12.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	9.5
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MARPVQLAPG SLALVLCRLE AQKAAGAAEE PGGRAVFRAF RRANARCFWN ARLARAASRL AFQGWLRRGV LLVRAPPACL
        90        100        110        120        130        140        150        160
QVLRDAWRRR ALRPPRGFRI RAVGDVFPVQ MNPITQSQFV PLGEVLCCAI SDMNTAQIVV TQESLLERLM KHYPGHRVWD
       170
LIIQSFWMD
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1506	1	881.6342	118.58	2	48.6	18.4	1	69-84	R.GVLLVRAPPACLQVLR.D	Carbamidomethyl: 11

Detailed Protein Report

Protein 647: homeobox protein Nkx-2.4 [Homo sapiens]

Accession:	gi|157426823	**Score:**	18.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	36.2
Database Date:	2015-11-30	**pI:**	10.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	6.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSLSPKHTTP	FSVSDILSPI	EETYKKFSGA	MDGAPPGLGA	PLGAAAAYRA	PPPGPSSQAA	TVAGMQPSHA	MAGHNAAAAA
90	100	110	120	130	140	150	160
AAAAAAAAAA	ATYHMPPGVS	QFPHGAMGSY	CNGGLGNMGE	LPAYTDGMRG	GAATGWYGAN	PDPRYSSISR	FMGPSAGVNV
170	180	190	200	210	220	230	240
AGMGSLTGIA	DAAKSLGPLH	AAAAAAAPRR	KRRVLFSQAQ	VYELERRFKQ	QKYLSAPERE	HLASMIHLTP	TQVKIWFQNH
250	260	270	280	290	300	310	320
RYKMKRQAKD	KAAQQLQQEG	GLGPPPPPPP	SPRRVAVPVL	VKDGKPCQNG	ASTPTPGQAG	PQPPAPTPAP	ELEELSPSPP
330	340	350	360				
ALHGPGGGLA	ALDAAAGEYS	GGVLGANLLY	GRTW				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2128	1	1131.4206	-132.38	2	56.5	18.4	1	26-49	K.KFSGAMDGAPPGLGAPLGAAAAYR.A	Oxidation: 6

Detailed Protein Report

Protein 648: **PREDICTED: janus kinase and microtubule-interacting protein 3 isoform X5 [Homo sapiens]**

Accession: gi|530394820
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl, Oxidation

Score: 18.3
MW [kDa]: 105.7
pI: 6.1
Sequence Coverage [%]: 2.2
No. of unique Peptides: 1

Quantitation

MD:MU **Median:** 1.07 **CV:** 0.00 % **No. of Peptides:** 1

```
        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 LQLDEKDARR FQLKIAELSA IIRKLEDRNA
       250        260        270        280        290        300        310        320
LLSEERNELL KRVREAESQY KPLLDKNKRL SRKNEDLSHA LRRMENKLKF VTQENIEMRQ RAGIIRRPSS LNDLDQSQDE
       330        340        350        360        370        380        390        400
REVDFLKLQI VEQQNLIDEL SKTLETAGYV KSVLERDKLL RFRKQRKKMA KLPKPVVVET FFGYDEEASL ESDGSSVSYQ
       410        420        430        440        450        460        470        480
TDRTDQTPCT PDDDLEEGMA KEETELRFRQ LTMEYQALQR AYALLQEQVG GTLDAEREVK TREQLQAEVQ RAQARIEDLE
       490        500        510        520        530        540        550        560
KALAEQGQDM KWIEEKQALY RRNQELVEKI KQMETEEARL RHEVQDARDQ NELLEFRILE LEERERKSPA ISFHHTPFVD
       570        580        590        600        610        620        630        640
GKSPLQVYCE AEGVTDIVVA ELMKKLDILG DNAVSNLTNE EQVVVIQART VLTLAEKWLQ QIEETEAALQ RKMVDLESEK
       650        660        670        680        690        700        710        720
ELFSKQKGYL DEELDYRKQA LDQANKHILE LEAMLYDALQ QEAGAKVAEL LSEEEREKLK VAVEQWKRQV MSELRERDAQ
       730        740        750        760        770        780        790        800
ILRERMELLQ LAQQRIKELE ERIEAQKRQI KELEEKLSFS GHSPSWHPDV PHIESDPFPP VGPESRDKMG RRVSILKTQG
       810        820        830        840        850        860        870        880
DLVSARPSRG GRVRRGSVWG VELPSTWDVP ELELALPTSR GLLRDGPGLG CWTLGPFSRT AAPIPFPGMC SIPCQAGVRT
       890        900        910        920
ASVQKHQPRV PSSLLVLTVA ATGVWRKIFR NNRGLA
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1669	1	1045.0250	19.09	2	50.8	18.3	0	860-879	R.TAAPIPFPGMCSIPCQAGVR.T	Carbamidomethyl: 15; Oxidation: 10	MD:MU 1.07

Detailed Protein Report

Protein 649: PREDICTED: zinc finger protein 831 isoform X4 [Homo sapiens]

Accession:	gi|530417824	**Score:**	18.3
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
2187	6	1023.8998	-84.84	2	57.2	18.3	1	258-276	K.NLDVRTEAAPCPGSAFADR.E	Carbamidomethyl: 11

Detailed Protein Report

Protein 650: prominin-2 precursor [Homo sapiens]

Accession:	gi|260764009	**Score:**	18.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	91.8
Database Date:	2015-11-30	**pI:**	5.8
		Sequence Coverage [%]:	1.8
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530368507	refseq_human(refseq_human_20140103.fasta)	PREDICTED: prominin-2 isoform X1 [Homo sapiens]
gi|260764013	refseq_human(refseq_human_20140103.fasta)	prominin-2 precursor [Homo sapiens]
gi|260764011	refseq_human(refseq_human_20140103.fasta)	prominin-2 precursor [Homo sapiens]

10	20	30	40	50	60	70	80
MKHTLALLAP	LLGLGLGLAL	SQLAAGATDC	KFLGPAEHLT	FTPAARARWL	APRVRAPGLL	DSLYGTVRRF	LSVVQLNPFP
90	100	110	120	130	140	150	160
SELVKALLNE	LASVKVNEVV	RYEAGYVVCA	VIAGLYLLLV	PTAGLCFCCC	RCHRRCGGRV	KTEHKALACE	RAALMVFLLL
170	180	190	200	210	220	230	240
TTLLLLIGVV	CAFVTNQRTH	EQMGPSIEAM	PETLLSLWGL	VSDVPQELQA	VAQQFSLPQE	QVSEELDGVG	VSIGSAIHTQ
250	260	270	280	290	300	310	320
LRSSVYPLLA	AVGSLGQVLQ	VSVHHLQTLN	ATVVELQAGQ	QDLEPAIREH	RDRLLELLQE	ARCQGDCAGA	LSWARTLELG
330	340	350	360	370	380	390	400
ADFSQVPSVD	HVLHQLKGVP	EANFSSMVQE	ENSTFNALPA	LAAMQTSSVV	QELKKAVAQQ	PEGVRTLAEG	FPGLEAASRW
410	420	430	440	450	460	470	480
AQALQEVEES	SRPYLQEVQR	YETYRWIVGC	VLCSVVLFVV	LCNLLGLNLG	IWGLSARDDP	SHPEAKGEAG	ARFLMAGVGL
490	500	510	520	530	540	550	560
SFLFAAPLIL	LVFATFLVGG	NVQTLVCQSW	ENGELFEFAD	TPGNLPPSMN	LSQLLGLRKN	ISIHQAYQQC	KEGAALWTVL
570	580	590	600	610	620	630	640
QLNDSYDLEE	HLDINQYTNK	LRQELQSLKV	DTQSLDLLSS	AARRDLEALQ	SSGLQRIHYP	DFLVQIQRPV	VKTSMEQLAQ
650	660	670	680	690	700	710	720
ELQGLAQAQD	NSVLGQRLQE	EAQGLRNLHQ	EKVVPQQSLV	AKLNLSVRAL	ESSAPNLQLE	TSDVLANVTY	LKGELPAWAA
730	740	750	760	770	780	790	800
RILRNVSECF	LAREMGYFSQ	YVAWVREEVT	QRIATCQPLS	GALDNSRVIL	CDMMADPWNA	FWFCLAWCTF	FLIPSIIFAV
810	820	830	840				
KTSKYFRPIR	KRLSSTSSEE	TQLFHIPRVT	SLKL				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
17	1	814.3561	-94.62	2	29.5	18.2	0	32-46	K.FLGPAEHLTFTPAAR.A	

Detailed Protein Report

Protein 651: coiled-coil domain-containing protein 120 isoform 4 [Homo sapiens]

Accession: gi|254039614
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 18.2
MW [kDa]: 66.3
pI: 10.5
Sequence Coverage [%]: 2.6
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MEVKAALFGE	AAPQVKSERL	RGLLDRQRTL	QEALSLKLQE	LRKVCLQEAE	LTGQLPPECP	LEPGERPQLV	RRRPPTARAY
90	100	110	120	130	140	150	160
PPPHPNQAHH	SLCPAEELAL	EALEREVSVQ	QQIAAAARRL	ALAPDLSTEQ	RRRRRQVQAD	ALRRLHELEE	QLRDVRARLG
170	180	190	200	210	220	230	240
LPVLPLPQPL	PLSTGSVITT	QGVCLGMRLA	QLSQEDVVLH	SESSSLSESG	ASHDNEEPHG	CFSLAERPSP	PKAWDQLRAV
250	260	270	280	290	300	310	320
SGGSPERRTP	WKPPPSDLYG	DLKSRRNSVA	SPTSPTRSLP	RSASSFEGRS	VPATPVLTRG	AGPQLCKPEG	LHSRQWSGSQ
330	340	350	360	370	380	390	400
DSQMGFPRAD	PASDRASLFV	ARTRRSNSSE	ALLVDRAAGG	GAGSPPAPLA	PSASGPPVCK	SSEVLYERPQ	PTPAFSSRTA
410	420	430	440	450	460	470	480
GPPDPPRAAR	PSSAAPASRG	APRLPPVCGD	FLLDYSLDRG	LPRSGGGTGW	GELPPAAEVP	GPLSRRDGLL	TMLPGPPPVY
490	500	510	520	530	540	550	560
AADSNSPLLR	TKDPHTRATR	TKPCGLPPEA	AEGPEVHPNP	LLWMPPPTRI	PSAGERSGHK	NLALEGLRDW	YIRNSGLAAG
570	580	590	600	610	620		
PQRRPVLPSV	GPPHPPFLHA	RCYEVGQALY	GAPSQAPLPH	SRSFTAPPVS	GRYGGCFY		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
500	1	642.6194	-139.68	3	35.9	18.2	2	27-42	R.QRTLQEALSLKLQELR.K	

Detailed Protein Report

Protein 652: PREDICTED: retinoid isomerohydrolase isoform X1 [Homo sapiens]

Accession:	gi|578799557	**Score:**	18.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	65.6
Database Date:	2015-11-30	**pI:**	8.4
		Sequence Coverage [%]:	1.9
		No. of unique Peptides:	1

Quantitation

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

10	20	30	40	50	60	70	80
MQKVLKPVAV	LKQCGYSPRT	PKAAQGYLRK	ALGADTGTSK	TGFSSPRRVE	HPAGGYKKLF	ETVEELSSPL	TAHVTGRIPL
90	100	110	120	130	140	150	160
WLTGSLLRCG	PGLFEVGSEP	FYHLFDGQAL	LHKFDFKEGH	VTYHRRFIRT	DAYVRAMTEK	RIVITEFGTC	AFPDPCKNIF
170	180	190	200	210	220	230	240
SRFFSYFRGV	EVTDNALVNV	YPVGEDYYAC	TETNFITKIN	PETLETIKQV	DLCNYVSVNG	ATAHPHIEND	GTVYNIGNCF
250	260	270	280	290	300	310	320
GKNFSIAYNI	VKIPPLQADK	EDPISKSEIV	VQFPCSDRFK	PSYVHSFGLT	PNYIVFVETP	VKINLFKFLS	SWSLWGANYM
330	340	350	360	370	380	390	400
DCFESNETMG	VWLHIADKKR	KKYLNNKYRT	SPFNLFHHIN	TYEDNGFLIV	DLCCWKGFEF	VYNYLYLANL	RENWEEVKKN
410	420	430	440	450	460	470	480
ARKAPQPEVR	RYVLPLNIDK	ADTGKNLVTL	PNTTATAILC	SDETIWLEPE	VLFSGPRQAF	EFPQINYQKY	CGKPYTYAYG
490	500	510	520	530	540	550	560
LGLNHFVPDR	LCKLNVKTKE	TWVWQEPDSY	PSEPIFVSHP	DALEEDDGVV	LSVVVSPGAG	QKPAYLLILN	AKDLSEVARA
570	580						
EVEINIPVTF	HGLFKKS						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1724	1	524.7781	-13.64	2	51.3	18.1	1	30-40	R.KALGADTGTSK.T		MD:MU 0.85

Detailed Protein Report

Protein 653: PREDICTED: parkin coregulated gene protein isoform X3 [Homo sapiens]

Accession:	gi|530383379	**Score:**	18.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	24.0
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
MVAEKETLSL	NKCPDKMPKR	TKLLAQQPLP	VHQPHSLVSE	GFTVKAMMKN	SVVRGPPAAG	AFKERPTKPT	AFRKFYERGD
90	100	110	120	130	140	150	160
FPIALEHDSK	GNKIAWKVEI	EKLDYHHYLP	LFFDGLCEMT	FPYEFFARQG	IHDMLEHGGN	KILPVLPQLI	IPIKNALNLR
170	180	190	200	210	220		
NRQVICVTLK	VLQHLVVSAE	MVGKALVPYY	RQILPVLNIF	KNMNGDTVPN	Y		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1618	1	804.1891	-319.55	1	50.1	18.1	0	6-12	K.ETLSLNK.C	

Detailed Protein Report

Protein 654: PREDICTED: RING finger protein 10 isoform X5 [Homo sapiens]

Accession:	gi|530401582	**Score:**	18.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	85.1
Database Date:	2015-11-30	**pI:**	7.0
		Sequence Coverage [%]:	2.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPLSSPNAAA	TASDMDKNSG	SNSSSASSGS	SKGQQPPRSA	SAGPAGESKP	KSDGKNSSGS	KRYNRKRELS	YPKNESFNNQ
90	100	110	120	130	140	150	160
SRRSSSQKSK	TFNKMPPQRG	GGSSKLFSSS	FNGGRRDEVA	EAQRAEFSPA	QFSGPKKINL	NHLLNFTFEP	RGQTGHFEGS
170	180	190	200	210	220	230	240
GHGSWGKRNK	WGHKPFNKEL	FLQANCQFVV	SEDQDYTAHF	ADPDTLVNWD	FVEQVRICSH	EVPSCPICLY	PPTAAKITRC
250	260	270	280	290	300	310	320
GHIFCWACIL	HYLSLSEKTW	SKCPICYSSV	HKKDLKSVVA	TESHQYVVGD	TITMQLMKRE	KGVLVALPKS	KWMNVDHPIH
330	340	350	360	370	380	390	400
LGDEQHSQYS	KLLLASKEQV	LHRVVLEEKV	ALEQQLAEEK	HTPESCFIEA	AIQELKTREE	ALSGLAGSRR	EVTGVVAALE
410	420	430	440	450	460	470	480
QLVLMAPLAK	ESVFQPRKSL	LQQGVLEYLS	AFDEETTEVC	SLDTPSRPLA	LPLVEEEEAV	SEPEPEGLPE	ACDDLELADD
490	500	510	520	530	540	550	560
NLKEGTICTE	SSQQEPITKS	GFTRLSSSPC	YYFYQAEDGQ	HMFLHPVNVR	CLVREYGSLE	RSPEKISATV	VEIAGYSMSE
570	580	590	600	610	620	630	640
DVRQRHRYLS	HLPLTCEFSI	CELALQPPVV	SKETLEMFSD	DIEKRKRQRQ	KKAREERRRE	RRIEIEENKK	QGKYFLLTPL
650	660	670	680	690	700	710	720
SPTASQGSPS	FCVGSLEEDS	PFPSFAQMLR	VGKAKADVWP	KTAPKKDENS	LVPPAPVDSD	GESDNSDRVP	VPSFQNSFSQ
730	740	750	760	770			
AIEAAFMKLD	TPATSDPLSE	EKGGKKRKKQ	KQKLLFSTSV	VHTK			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2030	1	788.2772	-117.15	2	55.3	18.0	0	2-17	M.PLSSPNAAATASDMDK.N	

Detailed Protein Report

Protein 655: PREDICTED: zinc finger protein 337 isoform X1 [Homo sapiens]

Accession: gi|530425693
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 18.0
MW [kDa]: 83.1
pI: 10.9
Sequence Coverage [%]: 1.9
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MGPQGARRQA	FLAFGDVTVD	FTQKEWRLLS	PAQRALYREV	TLENYSHLVS	LGIYAEHVLR	PKNLGLAHQR	QQQLQFSDQS
90	100	110	120	130	140	150	160
FQSDTAEGQE	KEKSTKPMAF	SSPPLRHAVS	SRRRNSVVEI	ESSQGQRENP	TEIDKVLKGI	ENSRWGAFKC	AERGQDFSRK
170	180	190	200	210	220	230	240
MMVIIHKKAH	SRQKLFTCRE	CHQGFRDESA	LLLHQNTHTG	EKSYVCSVCG	RGFSLKANLL	RHQRTHSGEK	PFLCKVCGRG
250	260	270	280	290	300	310	320
YTSKSYLTVH	ERTHTGEKPY	ECQECGRRFN	DKSSYNKHLK	AHSGEKPFVC	KECGRGYTNK	SYFVVHKRIH	SGEKPYRCQE
330	340	350	360	370	380	390	400
CGRGFSNKSH	LITHQRTHSG	EKPFACRQCK	QSFSVKGSLL	RHQRTHSGEK	PFVCKDCERS	FSQKSTLVYH	QRTHSGEKPF
410	420	430	440	450	460	470	480
VCRECGQGFI	QKSTLVKHQI	THSEEKPFVC	KDCGRGFIQK	STFTLHQRTH	SEEKPYGCRE	CGRRFRDKSS	YNKHLRAHLG
490	500	510	520	530	540	550	560
EKRFFCRDCG	RGFTLKPNLT	IHQRTHSGEK	PFMCKQCEKS	FSLKANLLRH	QWTHSGERPF	NCKDCGRGFI	LKSTLLFHQK
570	580	590	600	610	620	630	640
THSGEKPFIC	SECGQGFIWK	SNLVKHQLAH	SGKQPFVCKE	CGRGFNWKGN	LLTHQRTHSG	EKPFVCNVCG	QGFSWKRSLT
650	660	670	680	690	700	710	720
RHHWRIHSKE	KPFVCQECKR	GYTSKSDLTV	HERIHTGERP	YECQECGRKF	SNKSYYSKHL	KRHLREKRFC	TGSVGEASS

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2755	2	821.9192	-50.21	2	64.8	18.0	2	351-364	K.QSFSVKGSLLRHQR.T	

Detailed Protein Report

Protein 656: **PREDICTED: myotubularin-related protein 1 isoform X9 [Homo sapiens]**

Accession: gi|578838954
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 17.9
MW [kDa]: 65.3
pI: 6.5
Sequence Coverage [%]: 3.2
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MEEAPLFPGE	SIKAIVKDVM	YICPFMGAVS	GTLTVTDFKL	YFKNVERDPH	FILDVPLGVI	SRVEKIGAQS	HGDNSCGIEI
90	100	110	120	130	140	150	160
VCKDMRNLRL	AYKQEEQSKL	GIFENLNKHA	FPLSNGQALF	AFSYKEKFPI	NGWKVYDPVS	EYKRQGLPNE	SWKISKINSN
170	180	190	200	210	220	230	240
YEFCDTYPAI	IVVPTSVKDD	DLSKVAAFRA	KGRVPVLSWI	HPESQATITR	CSQPLVGPND	KRCKEDEKYL	QTIMDANAQS
250	260	270	280	290	300	310	320
HKLIIFDARQ	NSVADTNKTK	GGGYESESAY	PNAELVFLEI	HNIHVMRESL	RKLKEIVYPS	IDEARWLSNV	DGTHWLEYIR
330	340	350	360	370	380	390	400
MLLAGAVRIA	DKIESGKTSV	VVHCSDGWDR	TAQLTSLAML	MLDSYYRTIK	GFETLVEKEW	ISFGHRFALR	VGHGNDNHAD
410	420	430	440	450	460	470	480
ADRSPIFLQF	VDCVWQMTRQ	FPSAFEFNEL	FLITILDHLY	SCLFGTFLCN	CEQQRFKEDV	YTKTISLWSY	INSQLDEFSN
490	500	510	520	530	540	550	560
PFFVNYENHV	LYPVASLSHL	ELWVNYYVRW	NPRMRPQMPI	HQNLKELLAV	RAELQKRVEG	LQREVATRAV	SSSSERGSSP
570	580						
SHSATSVHTS	V						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2379	1	736.0972	37.32	3	60.1	17.9	1	514-531	R.MRPQMPIHQNLKELLAVR.A	Oxidation: 1, 5

Detailed Protein Report

Protein 657: uncharacterized protein C20orf144 [Homo sapiens]

Accession:	gi|18250302	**Score:**	17.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	17.2
Database Date:	2015-11-30	**pI:**	12.1
		Sequence Coverage [%]:	12.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGNYSSHKRT	KAPKQARKER	PADMDKAWWK	SFLNHLTRKK	PATRIVLILP	LDKRQPLANA	GQRIDYASGA	GLGSPAAPRL
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
RGAGEGSERE	PRMPVLLLLR	RQEARRPEEG	GARAALSWPR	LLSRFRSPGK	APREAGPAEE	QPRKRCRCPR	PQL

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
50	1	712.9918	-65.56	3	30.3	17.9	2	102-120	R.QEARRPEEGGARAALSWPR.L	

Detailed Protein Report

Protein 658: PREDICTED: protein CEI isoform X1 [Homo sapiens]

Accession:	gi|530378712	**Score:**	17.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	24.4
Database Date:	2015-11-30	**pI:**	12.7
		Sequence Coverage [%]:	7.1
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 0.28 **CV:** 0.00 % **No. of Peptides:** 1

```
         10         20         30         40         50         60         70         80
MVAPAARVFL RAVRAALTST VPDLLCLLAR GSPRGLASGR LPLAVHSAQH GPGSGAPWLR IARRALRFVL SKHWGDDCYL
         90        100        110        120        130        140        150        160
TNRLWQDLKP PSHVENGQEL RLAPPVQWAL QPKNLERVYV DTQVSASGDF LRGRARGTAG PGGSGSGSPR GRGRLRRPGR
        170        180        190        200        210        220        230
SPGAAPSSVS RGRKEATQAR SRARGRRGGA VARVCRPESR QRWARPTSSP GGLIRGRRKN GIEAFQ
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
550	1	679.2027	-190.28	2	36.2	17.9	1	137-152	R.GTAGPGGSGSGSPRGR.G		MD:MU 0.28

Detailed Protein Report

Protein 659: phosphatase and actin regulator 2 isoform 2 [Homo sapiens]

Accession:	gi|154354970	**Score:**	17.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	62.4
Database Date:	2015-11-30	**pI:**	5.8
		Sequence Coverage [%]:	3.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGQTSVSTLS	PQPGSVDGLD	KASIANSDGP	TAGSQTPPFK	RKGKLSTIGK	IFKPWKWRKK	KTSDKFRETS	AVLERKISTR
90	100	110	120	130	140	150	160
QSREELIRRG	VLKELPDQDG	DVTVNFENSN	GHMIPIGEES	TREENVVKSE	EGNGSVSEKT	PPLEEQAEDK	KAGSSHSKKT
170	180	190	200	210	220	230	240
TGSKASASPS	TSSTSSRPKA	SKETVSSKAG	TVGTTKGKRK	TDKQPITSHL	SSDTTTSGTS	DLKGEPAETR	VESFKLEQTV
250	260	270	280	290	300	310	320
PGAEEQNTGK	FKSMVPPPPV	APAPSPLAPP	LPLEDQCITA	SDTPVVLVSV	GADLPVSALD	PSQLLWAEEP	TNRTTLYSGT
330	340	350	360	370	380	390	400
GLSVNRENAK	CFTTKEELGK	TVPQLLTPGL	MGESSESFSA	SEDEGHREYQ	ANDSDSDGPI	LYTDDEDEDE	DEDGSGESAL
410	420	430	440	450	460	470	480
ASKIRRRDTL	AIKLGNRPSK	KELEDKNILQ	RTSEEERQEI	RQQIGTKLVR	RLSQRPTTEE	LEQRNILKQK	NEEEEQEAKM
490	500	510	520	530	540	550	560
ELKRRLSRKL	SLRPTVAELQ	ARRILRFNEY	VEVTDSPDYD	RRADKPWARL	TPADKAAIRK	ELNEFKSTEM	EVHEESRQFT
570							
RFHRP							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2694	1	1052.5494	32.68	2	64.9	17.9	0	1-21	-.MGQTSVSTLSPQPGSVDGLDK.A	

Detailed Protein Report

Protein 660: sodium/hydrogen exchanger 9B1 isoform 2 [Homo sapiens]

Accession:	gi|154937338	**Score:**	17.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	52.2
Database Date:	2015-11-30	**pI:**	9.5
		Sequence Coverage [%]:	4.4
		No. of unique Peptides:	1

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
2262	1	682.1402	136.94	3	58.5	17.9	0	337-357	R.IGLHGSGGLCTLVLSFIAGTK.W	

Detailed Protein Report

Protein 661: **immunoglobulin-like domain-containing receptor 1 isoform 3 precursor [Homo sapiens]**

Accession:	gi|315259080	**Score:**	17.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	52.7
Database Date:	2015-11-30	**pI:**	10.8
		Sequence Coverage [%]:	2.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAWPKLPAPW	LLLCTWLPAG	CLSLLVTVQH	TERYVTLFAS	IILKCDYTTS	AQLQDVVVTW	RFKSFCKDPI	FDYYSASYQA
90	100	110	120	130	140	150	160
ALSLGQDPSN	DCNDNQREVR	IVAQRRGQNE	PVLGVDYRQR	KITIQNPLAR	HRYMKQAQAL	GPQMMGKPLY	WGADRSSQVS
170	180	190	200	210	220	230	240
SYPMHPLLQR	DLSLPSSLPQ	MPMTQTTNQP	PIANGVLEYL	EKELRNLNLA	QPLPPDLKGR	FGHPCSMLSS	LGSEVVERRI
250	260	270	280	290	300	310	320
IHLPPLIRDL	SSSRRTSDSL	HQQWLTPIPS	RPWDLREGRS	HHHYPDFHQE	LQDRGPKSWA	LERRELDPSW	SGRHRSSRLN
330	340	350	360	370	380	390	400
GSPIHWSDRD	SLSDVPSSSE	ARWRPSHPPF	RSRCQERPRR	PSPRESTQRH	GRRRRHRSYS	PPLPSGLSSW	SSEEDKERQP
410	420	430	440	450	460		
QSWRAHRRGS	HSPHWPEEKP	PSYRSLDITP	GKNSRKKGSV	ERRSEKDSSH	SGRSVVI		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2765	1	673.8074	-46.32	2	65.0	17.9	0	107-118	R.GQNEPVLGVDYR.Q	

Detailed Protein Report

Protein 662: **PREDICTED: keratin-associated protein 9-8 [Homo sapiens]**

Accession:	gi|578846434	**Score:**	17.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	16.8
Database Date:	2015-11-30	**pI:**	11.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	11.3
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MTHCCSPCCQ PTCCRTTCWK PTTVTTCSST PCCQPSCCVS SCCQPCCRPT CCQNTCCQPI CVTSCCQPSC CSTPCCQPTC
        90        100        110        120        130        140        150        160
CGQTSCGSSC GQSSSCAPVY CRRTCYHPTT VCLPGCLNQS CGSSCCQPCC RPACCETTCC RTTCFQPTCV YSCCQPSCC
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2119	1	1044.4110	33.02	2	56.4	17.8	0	142-159	R.TTCFQPTCVYSCCQPSCC.-	Carbamidomethyl: 3, 8

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Detailed Protein Report

Protein 663: PREDICTED: another transcription unit protein-like [Homo sapiens]

Accession:	gi|410170274	**Score:**	17.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	33.9
Database Date:	2015-11-30	**pI:**	12.6
		Sequence Coverage [%]:	3.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSSPVLEPSP	GPQSPYLHGL	YLLLGEVLGH	SALGAQHAQP	ANGDADELLE	LPALLQHLAG	CDPCASLRDS	CVTPATALLL
90	100	110	120	130	140	150	160
LSHRGQVQRR	SMQAAAAQEQ	SLGRGCLGKE	PPKWESSTRS	GPRRCLSQDA	SRSGSRVCRS	RPQTRGGGGK	KPRRGQKAAT
170	180	190	200	210	220	230	240
AGAKSRGGGV	RSRGGKKIRR	RGQKAAAAGA	KSCGGGGKKP	QKARAVGARR	RGWKKLRRRG	KKAAAAGGEK	AGKKLRQQGE
250	260	270	280	290	300	310	320
KGRKKPRRRG	QKAAAAGGER	CKKPRRQKAA	AVSAKSPKKP	RRRVLNSARL	GAESRKNPQR	RGQKSMAAKS	RVGSGKIVEM
330							
G							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
928	1	573.2590	-111.53	2	41.2	17.7	2	155-166	R.GQKAATAGAKSR.G	

Detailed Protein Report

Protein 664: PREDICTED: kin of IRRE-like protein 3 isoform X1 [Homo sapiens]

Accession:	gi|530398440	**Score:**	17.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	84.1
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
MKPFQLDLLF	VCFFLFSQEL	GLQKRGCCLV	LGYMAKDKFR	RMNEGQVYSF	SQQPQDQVVV	SGQPVTLLCA	IPEYDGFVLW
90	100	110	120	130	140	150	160
IKDGLALGVG	RDLSSYPQYL	VVGNHLSGEH	HLKILRAELQ	DDAVYECQAI	QAAIRSRPAR	LTVLVPPDDP	VILGGPVISL
170	180	190	200	210	220	230	240
RAGDPLNLTC	HADNAKPAAS	IIWLRKGEVI	NGATYSKTLL	RDGKRESIVS	TLFISPGDVE	NGQSIVCRAT	NKAIPGGKET
250	260	270	280	290	300	310	320
SVTIDIQHPP	LVNLSVEPQP	VLEDNVVTFH	CSAKANPAVT	QYRWAKRGQI	IKEASGEVYR	TTVDYTYFSE	PVSCEVTNAL
330	340	350	360	370	380	390	400
GSTNLSRTVD	VYFGPRMTTE	PQSLLVDLGS	DAIFSCAWTG	NPSLTIVWMK	RGSGVVLSNE	KTLTLKSVRQ	EDAGKYVCRA
410	420	430	440	450	460	470	480
VVPRVGAGER	EVTLTVNGPP	IISSTQTQHA	LHGEKGQIKC	FIRSTPPPDR	IAWSWKENVL	ESGTSGRYTV	ETISTEEGVI
490	500	510	520	530	540	550	560
STLTISNIVR	ADFQTIYNCT	AWNSFGSDTE	IIRLKEQESV	PMAVIIGVAV	GAGVAFLVLM	ATIVAFCCAR	SQRNLKGVVS
570	580	590	600	610	620	630	640
AKNDIRVEIV	HKEPASGREG	EEHSTIKQLM	MDRGEFQQDS	VLKQLEVLKE	EEKEFQNLKD	PTNGYYSVNT	FKEHHSTPTI
650	660	670	680	690	700	710	720
SLSSCQPDLR	PAGKQRVPTG	MSFTNIYSTL	SGQGRLYDYG	QRFVLGMGSS	SIELCEREFQ	RGSLSDSSSF	LDTQCDSSVS
730	740	750	760	770			
SSGKQDGYVQ	FDKASKASAS	SSHHSQSSSQ	NSDPSRPLQR	RMQTHV			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1604	1	910.4351	-62.80	2	49.8	17.6	2	563-578	K.NDIRVEIVHKEPASGR.E	

Detailed Protein Report

Protein 665: PREDICTED: dedicator of cytokinesis protein 11 isoform X2 [Homo sapiens]

Accession:	gi|530422336	**Score:**	17.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	235.7
Database Date:	2015-11-30	**pI:**	8.1
Modification(s):	Oxidation	**Sequence Coverage [%]:**	0.5
		No. of unique Peptides:	1

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 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
2214	2	682.8959	102.27	2	57.6	17.6	1	279-289	R.SMHPELMKYGR.E	Oxidation: 7

Detailed Protein Report

Protein 666: PREDICTED: armadillo repeat-containing protein 3 isoform X3 [Homo sapiens]

Accession: gi|530392014
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 17.6
MW [kDa]: 86.5
pI: 5.8
Sequence Coverage [%]: 1.7
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MIFGILASNN	DVKKLLRELD	VMNSVIAQLA	PEEEVVIHEF	ASLCLANMSA	EYTSKVQIFE	HGGLEPLIRL	LSSPDPDVKK
90	100	110	120	130	140	150	160
NSMECIYNLV	QDFQCRAKLQ	ELNAIPPILD	LLKSEYPVIQ	LLALKTLGVI	ANDKESRTML	RDNQGLDHLI	KILETKELND
170	180	190	200	210	220	230	240
LHIEALAVIA	NCLEDMDTMV	QIQQTGGLKK	LLSFAENSTI	PDIQKNAAKA	ITKAAYDPEN	RKLFHEQEVE	KCLVALLGSE
250	260	270	280	290	300	310	320
NDGTKIAASQ	AISAMCENSG	SKDFFNNQGI	PQLIQLLKSD	NEEVREAAAL	ALANLTTCNP	ANANAAAEAD	GIDPLINLLS
330	340	350	360	370	380	390	400
SKRDGAIANA	ATVLTNMAMQ	EPLRLNIQNH	DIMHAIISPL	RSANTVVQSK	AALAVTATAC	DVEARTELRN	SGGLEPLVEL
410	420	430	440	450	460	470	480
LRSKNDEVRK	HASWAVMVCA	GDELTANELC	RLGALDILEE	VNVSGTRKNK	FSEAAYNKLL	NNNLSLKYSQ	TGYLSSSNII
490	500	510	520	530	540	550	560
NDGFYDYGRI	NPGTKLLPLK	ELCLQEPSDL	RAVLLINSKS	YVSPPSSMED	KSDVGYGRSI	SSSSSLRRSS	KEKNKKNSYH
570	580	590	600	610	620	630	640
FSAGFGSPIE	DKSEPASGRN	TVLSKSATKE	KGWRKSKGKK	EEEKVKEEEE	VMVVPKFVGE	GSSDKEWCPP	SDPDFSMYVY
650	660	670	680	690	700	710	720
EVTKSILPIT	NIKEQIEDLA	KYVAEKMGGK	IPKEKLPDFS	WELHISELKF	QLKSNVIPIG	HVKKGIFYHR	ALLFKALADR
730	740	750	760	770	780	790	
IGIGCSLVRG	EYGRAWNEVM	LQNDSRKGVI	GGLPAPEMYV	IDLMFHPGGL	MKLRSREADL	YRFI	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2698	1	709.8343	-97.82	2	64.9	17.6	1	2-14	M.IFGILASNNDVKK.L	

Detailed Protein Report

Protein 667: GS homeobox 1 [Homo sapiens]

Accession:	gi|33457326	**Score:**	17.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	27.9
Database Date:	2015-11-30	**pI:**	10.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	9.8
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 1.61 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MPRSFLVDSL	VLREAGEKKA	PEGSPPPLFP	YAVPPPHALH	GLSPGACHAR	KAGLLCVCPL	CVTASQLHGP	PGPPALPLLK
90	100	110	120	130	140	150	160
ASFPPFGSQY	CHAPLGRQHS	AVSPGVAHGP	AAAAAAAALY	QTSYPLPDPR	QFHCISVDSS	SNQLPSSKRM	RTAFTSTQLL
170	180	190	200	210	220	230	240
ELEREFASNM	YLSRLRRIEI	ATYLNLSEKQ	VKIWFQNRRV	KHKKEGKGSN	HRGGGGGGAG	GGGSAPQGCK	CASLSSAKCS
250	260	270					
EDDDELPMSP	SSSGKDDRDL	TVTP					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
42	1	1096.9830	-8.41	2	30.2	17.6	1	213-238	R. GGGGGGAGGGGSAPQGCKCASI C	Carbamidomethyl: 17, 19	MD:MU 1.61

Detailed Protein Report

Protein 668: protein XRP2 [Homo sapiens]

Accession:	gi|170016081	**Score:**	17.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	39.6
Database Date:	2015-11-30	**pI:**	4.9
		Sequence Coverage [%]:	3.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGCFFSKRRK	ADKESRPENE	EERPKQYSWD	QREKVDPKDY	MFSGLKDETV	GRLPGTVAGQ	QFLIQDCENC	NIYIFDHSAT
90	100	110	120	130	140	150	160
VTIDDCTNCI	IFLGPVKGSV	FFRNCRDCKC	TLACQQFRVR	DCRKLEVFLC	CATQPIIESS	SNIKFGCFQW	YYPELAFQFK
170	180	190	200	210	220	230	240
DAGLSIFNNT	WSNIHDFTPV	SGELNWSLLP	EDAVVQDYVP	IPTTEELKAV	RVSTEANRSI	VPISRGQRQK	SSDESCLVVL
250	260	270	280	290	300	310	320
FAGDYTIANA	RKLIDEMVGK	GFFLVQTKEV	SMKAEDAQRV	FREKAPDFLP	LLNKGPVIAL	EFNGDGAVEV	CQLIVNEIFN
330	340	350	360				
GTKMFVSESK	ETASGDVDSF	YNFADIQMGI					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1957	1	700.2365	-161.94	2	54.6	17.6	1	35-46	K.VDPKDYMFSGLK.D	

Detailed Protein Report

Protein 669: PREDICTED: unconventional myosin-VI isoform X8 [Homo sapiens]

Accession:	gi|530383156	**Score:**	17.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	144.9
Database Date:	2015-11-30	**pI:**	9.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEDGKPVWAP	HPTDGFQMGN	IVDIGPDSLT	IEPLNQKGKT	FLALINQVFP	AEEDSKKDVE	DNCSLMYLNE	ATLLHNIKVR
90	100	110	120	130	140	150	160
YSKDRIYTYV	ANILIAVNPY	FDIPKIYSSE	AIKSYQGKSL	GTRPPHVFAI	ADKAFRDMKV	LKMSQSIIVS	GESGAGKTEN
170	180	190	200	210	220	230	240
TKFVLRYLTE	SYGTGQDIDD	RIVEANPLLE	AFGNAKTVRN	NNSSRFGKFV	EIHFNEKSSV	VGGFVSHYLL	EKSRICVQGK
250	260	270	280	290	300	310	320
EERNYHIFYR	LCAGASEDIR	EKLHLSSPDN	FRYLNRGCTR	YFANKETDKQ	ILQNRKSPEY	LKAGSMKDPL	LDDHGDFIRM
330	340	350	360	370	380	390	400
CTAMKKIGLD	DEEKLDLFRV	VAGVLHLGNI	DFEEAGSTSG	GCNLKNKSAQ	SLEYCAELLG	LDQDDLRVSL	TTRVMLTTAG
410	420	430	440	450	460	470	480
GTKGTVIKVP	LKVEQANNAR	DALAKTVYSH	LFDHVVNRVN	QCFPFETSSY	FIGVLDIAGF	EYFEHNSFEQ	FCINYCNEKL
490	500	510	520	530	540	550	560
QQFFNERILK	EEQELYQKEG	LGVNEVHYVD	NQDCIDLIEA	KLVGILDILD	EENRLPQPSD	QHFTSAVHQK	HKDHFRLTIP
570	580	590	600	610	620	630	640
RKSKLAVHRN	IRDDEGFIIR	HFAGAVCYET	TQFVEKNNDA	LHMSLESLIC	ESRDKFIREL	FESSTNNNKD	TKQKAGKLSF
650	660	670	680	690	700	710	720
ISVGNKFKTQ	LNLLLDKLRS	TGASFIRCIK	PNLKMTSHHF	EGAQILSQLQ	CSGMVSVLDL	MQGGYPSRAS	FHELYNMYKK
730	740	750	760	770	780	790	800
YMPDKLARLD	PRLFCKALFK	ALGLNENDYK	FGLTKVFFRP	GKFAEFDQIM	KSDPDHLAEL	VKRVNHWLTC	SRWKKVQWCS
810	820	830	840	850	860	870	880
LSVIKLKNKI	KYRAEACIKM	QKTIRMWLCK	RRHKPRIDGL	VKVGTLKKRL	DKFNEVVSVL	KDGKPEMNKQ	IKNLEISIDT
890	900	910	920	930	940	950	960
LMAKIKSTMM	TQEQIQKEYD	ALVKSSEELL	SALQKKKQQE	EEAERLRRIQ	EEMEKERKRR	EEDEKRRRKE	EEERRMKLEM
970	980	990	1000	1010	1020	1030	1040
EAKRKQEEEE	RKKREDDEKR	IQAEVEAQLA	RQKEEESQQQ	AVLEQERRDR	ELALRIAQSE	AELISDEAQA	DLALRRGPAV
1050	1060	1070	1080	1090	1100	1110	1120
LATKAAAGTK	KYDLSKWKYA	ELRDTINTSC	DIELLAACRE	EFHRRLKVYH	AWKSKNKKRN	TETEQRAPKS	VTDYAQQNPA
1130	1140	1150	1160	1170	1180	1190	1200
AQIPARQREI	EMNRQQRFFR	IPFIRPADQY	KDPQSKKKGW	WYAHFDGPWI	ARQMELHPDK	PPILLVAGKD	DMEMCELNLE
1210	1220	1230	1240	1250	1260		
ETGLTRKRGA	EILPRQFEEI	WERCGGIQYL	QNAIESRQAR	PTYATAMLQS	LLK		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1221	1	985.1783	21.41	3	44.9	17.5	1	368-393	K.SAQSLEYCAELLGLDQDDLRVSLTTR.V	Carbamidomethyl: 8

Detailed Protein Report

Protein 670: carbohydrate sulfotransferase 4 [Homo sapiens]

Accession:	gi|5031735	**Score:**	17.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	45.1
Database Date:	2015-11-30	**pI:**	9.9
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.9
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 0.41 **CV:** 0.00 % **No. of Peptides:** 1

Alias proteins:

Accession	Name	Description
gi|262205558	refseq_human (refseq_human_20140103.fasta)	carbohydrate sulfotransferase 4 [Homo sapiens]

10	20	30	40	50	60	70	80
MLLPKKMKLL	LFLVSQMAIL	ALFFHMYSHN	ISSLSMKAQP	ERMHVLVLSS	WRSGSSFVGQ	LFGQHPDVFY	LMEPAWHVWM
90	100	110	120	130	140	150	160
TFKQSTAWML	HMAVRDLIRA	VFLCDMSVFD	AYMEPGPRRQ	SSLFQWENSR	ALCSAPACDI	IPQDEIIPRA	HCRLLCSQQP
170	180	190	200	210	220	230	240
FEVVEKACRS	YSHVVLKEVR	FFNLQSLYPL	LKDPSLNLHI	VHLVRDPRAV	FRSRERTKGD	LMIDSRIVMG	QHEQKLKKED
250	260	270	280	290	300	310	320
QPYYVMQVIC	QSQLEIYKTI	QSLPKALQER	YLLVRYEDLA	RAPVAQTSRM	YEFVGLEFLP	HLQTWVHNIT	RGKGMGDHAF
330	340	350	360	370	380	390	
HTNARDALNV	SQAWRWSLPY	EKVSRLQKAC	GDAMNLLGYR	HVRSEQEQRN	LLLDLLSTWT	VPEQIH	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
94	1	846.3548	-63.91	2	30.6	17.4	1	349-363	K.ACGDAMNLLGYRHVR.S	Oxidation: 6	MD:MU 0.41

Detailed Protein Report

Protein 671: PREDICTED: lysine-specific demethylase 5D isoform X4 [Homo sapiens]

Accession:	gi|530423193	**Score:**	17.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	90.3
Database Date:	2015-11-30	**pI:**	6.0
		Sequence Coverage [%]:	1.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEPGCDEFLP	PPECPVFEPS	WAEFQDPLGY	IAKIRPIAEK	SGICKIRPPA	DWQPPFAVEV	DNFRFTPRVQ	RLNELEAQTR
90	100	110	120	130	140	150	160
VKLNYLDQIA	KFWEIQGSSL	KIPNVERKIL	DLYSLSKIVI	EEGGYEAICK	DRRWARVAQR	LHYPPGKNIG	SLLRSHYERI
170	180	190	200	210	220	230	240
IYPYEMFQSG	ANHVQCNTHP	FDNEVKDKEY	KPHSIPLRQS	VQPSKFSSYS	RRAKRLQPDP	EPTEEDIEKH	PELKKLQIYG
250	260	270	280	290	300	310	320
PGPKMMGLGL	MAKDKDKTVH	KKVTCPPTVT	VKDEQSGGGN	VSSTLLKQHL	SLEPCTKTTM	QLRKNHSSAQ	FIDSYICQVC
330	340	350	360	370	380	390	400
SRGDEDDKLL	FCDGCDDNYH	IFCLLPPLPE	IPRGIWRCPK	CILAECKQPP	EAFGFEQATQ	EYSLQSFGEM	ADSFKSDYFN
410	420	430	440	450	460	470	480
MPVHMVPTEL	VEKEFWRLVS	SIEEDVTVEY	GADIHSKEFG	SGFPVSNSKQ	NLSPEEKEYA	TSGWNLNVMP	VLDQSVLCHI
490	500	510	520	530	540	550	560
NADISGMKVP	WLYVGMVFSA	FCWHIEDHWS	YSINYLHWGE	PKTWYGVPSL	AAEHLEEVMK	MLTPELFDSQ	PDLLHQLVTL
570	580	590	600	610	620	630	640
MNPNTLMSHG	VPVVRTNQCA	GEFVITFPRA	YHSGFNQGYN	FAEAVNFCTA	DWLPAGRQCI	EHYRRLRRYC	VFSHEELICK
650	660	670	680	690	700	710	720
MAAFPETLDL	NLAVAVHKEM	FIMVQEERRL	RKALLEKGVT	EAEREAFELL	PDDERQCIKC	KTTCFLSALA	CYDCPDGLVC
730	740	750	760	770	780	790	
LSHINDLCKC	SSSRQYLRYR	YTLDELPTML	HKLKIRAESF	DTWANKVRVA	LEVEDGRKRR	WTLHS	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1861	1	890.3640	-106.19	2	53.3	17.4	1	739-752	R.YRYTLDELPTMLHK.L	

Detailed Protein Report

Protein 672: **arf-GAP with Rho-GAP domain, ANK repeat and PH domain-containing protein 1 isoform d [Homo sapiens]**

Accession:	gi|206597515	**Score:**	17.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	127.6
Database Date:	2015-11-30	**pI:**	5.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.2
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MTKKEEPPPS RVPRAVRVAS LLSEGEELSG DDQGDEEEDD HAYEGVPNGG WHTSSLSLSL PSTIAAPHPM DGPPGGSTPV
        90        100        110        120        130        140        150        160
TPVIKAGWLD KNPPQGSYIY QKRWVRLDTD HLRYFDSNKD AYSKRFISVA CISHVAAIGD QKFEVITNNR TFAFRAESDV
       170        180        190        200        210        220        230        240
ERKEWMQALQ QAMAEQRARA RLSSAYLLGV PGSEQPDRAG SLELRGFKNK LYVAVVGDKV QLYKNLEEYH LGIGITFIDM
       250        260        270        280        290        300        310        320
SVGNVKEVDR RSFDLTTPYR IFSFSADSEL EKEQWLEAMQ GAIAEALSTS EVAERIWAAA PNRFCADCGA PQPDWASINL
       330        340        350        360        370        380        390        400
CVVICKRCAG EHRGLGAGVS KVRSLKMDRK VWTETLIEAL CAAVTTTDLA ETQALLGCGA GINCFSGDPE APTPLALAEQ
       410        420        430        440        450        460        470        480
AGQTLQMEFL RNNRTTEVPR LDSMKPLEKH YSVVLPTVSH SGFLYKTASA GKLLQDRRAR EEFSRRWCVL GDGVLSYFEN
       490        500        510        520        530        540        550        560
ERAVTPNGEI RASEIVCLAV PPPDTHGFEH TFEVYTEGER LYLFGLESAE QAHEWVKCIA KAFVPPLAED LLARDFERLG
       570        580        590        600        610        620        630        640
RLPYKAGLSL QRAQEGWFSL SGSELRAVFP EGPCEEPLQL RKLQELSIQG DSENQVLVLV ERRRTLYIQG ERRLDFMGWL
       650        660        670        680        690        700        710        720
GAIQKAAASM GDTLSEQQLG DSDIPVIVYR CVDYITQCGL TSEGIYRKCG QTSKTQRLLE SLRQDARSVH LKEGEQHVDD
       730        740        750        760        770        780        790        800
VSSALKRFLR DLPDGLFTRA QRLTWLEASE IEDEEEKVSR YRELLVRLPP VNRATVKALI SHLYCVQCFS DTNQMNVHNL
       810        820        830        840        850        860        870        880
AIVFGPTLFQ TDGQDYKAGR VVEDLINHYV VVFSVDEEEL RKQREEITAI VKMRVAGTAS GTQHAGDFIC TVYLEEKKAE
       890        900        910        920        930        940        950        960
TEQHIKVPAS MTAEELTLEI LDRRNVGIRE KDYWTCFEVN EREEAERPLH FAEKVLPILH GLGTDSHLVV KKHQAMEAML
       970        980        990       1000       1010       1020       1030       1040
LYLASRVGDT KHGMMKFRED RSLLGLGLPS GGFHDRYFIL NSSCLRLYKE VRSHRPEKEW PIKSLKVYLG VKKKLRPPTC
      1050       1060       1070       1080       1090       1100       1110       1120
WGFTVVHETE KHEKQQWYLC CDTQMELREW FATFLFVQHD GLVWPSEPSR VSRAVPEVRL GSVSLIPLRG SENEMRRSVA
      1130       1140
AFTADPLSLL RNV
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2177	1	937.2849	-128.31	2	57.1	17.3	0	1055-1068	K.QQWYLCCDTQMELR.E	Carbamidomethyl: 7

Detailed Protein Report

Protein 673: uncharacterized protein C2orf53 [Homo sapiens]

Accession:	gi|148236531	**Score:**	17.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	44.7
Database Date:	2015-11-30	**pI:**	11.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.7
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 0.97 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MLPQNKDQVL PQTSVLPGRP TWGFSQLVDS SPHNLQPLSP HQGLPPSQPP FSSTQSRRPS SPPPASPSPG FQFGSCDSNS

        90        100        110        120        130        140        150        160
DFAPHPYSPS LPSSPTFFHQ NYLSLPRPRA SSPSNHWLYP SPPLTPSFSP SQPQNSSLPH SPCQSPSHPE ELHSSTLTSP

       170        180        190        200        210        220        230        240
GPSPPSHRLH SNRQTWRWHQ YRDTGSGSPG VVERCVPSEK DPAQFRDPGA LAQALVVQLG HRRIAHDLRL LLLQHLWLGR

       250        260        270        280        290        300        310        320
TGQAPVVEYP ICLVCLRPRS PSCPLPRYRT GPRLLAFPQL LPCVQGQESG PLRIGIGFGL RLPQGQARAL HLLPEKRPKE

       330        340        350        360        370        380        390        400
AGPQGKATQA CGHQLPASQP PAAQARADPV PGTPSQTRSF RSAGLQSPNS PRCFSGPPPR APKQVTTSLK PRPCPGPKRP

       410        420
VSLELILQKS SV
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
2480	3	607.3093	-2.65	2	61.4	17.3	1	373-383	R.CFSGPPPRAPK.Q	Carbamidomethyl: 1	MD:MU	0.97

Detailed Protein Report

Protein 674: **PREDICTED: membrane-associated guanylate kinase, WW and PDZ domain-containing protein 2 isoform X1 [Homo sapiens]**

Accession:	gi|530386693	**Score:**	17.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	157.1
Database Date:	2015-11-30	**pI:**	5.9
		Sequence Coverage [%]:	0.8
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 0.66 **CV:** 0.00 % **No. of 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	Ratios
1930	1	643.2948	-156.54	2	54.2	17.3	1	980-991	K.LIKDAGLSVTLR.I		MD:MU 0.66

Detailed Protein Report

Protein 675: PREDICTED: complement factor H-related protein 2 isoform X1 [Homo sapiens]

Accession:	gi|530364612	**Score:**	17.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	22.9
Database Date:	2015-11-30	**pI:**	6.1
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	13.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MWLLVSVILI	SRISSVGGEG	LCFFPFVENG	HSESSGQTHL	EGDTVQIICN	TGYRLQNNEN	NISCVERGWS	TPPKCRSTIS
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
AEKCGPPPPI	DNGDITSFLL	SVYAPGSSVE	YQCQNLYQLE	GNNQITCRNG	QWSEPPKCLD	PCVISQEIME	KYNIKLKWTN
170	**180**	**190**	**200**	**210**			
QQKLYSRTGD	IVEFVCKSGY	HPTKSHSFRA	MCQNGKLVYP	SCEEK			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
32	1	1069.4360	-74.28	3	29.7	17.3	2	129-155	R.NGQWSEPPKCLDPCVISQEIMEKYNIK.L	Carbamidomethyl: 10

Detailed Protein Report

Protein 676: PREDICTED: coiled-coil domain-containing protein 144A isoform X3 [Homo sapiens]

Accession: gi|578830130
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 17.3
MW [kDa]: 71.9
pI: 4.6
Sequence Coverage [%]: 3.0
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MASWGGEKRG	GAEGSPKPAV	YATRKTPSVG	SQGDQWYLGY	PGDQWSSGFP	YSWWKNSVGS	ESKHGEGALD	QPQHDVRLED
90	100	110	120	130	140	150	160
LGELHRAARS	GDVPGVEHIL	APGDTGVDKR	DRKKSIQQLV	PEYKEKQTPE	SLPQNNNPDW	HPTNLTLSDE	TCQRSKNLKV
170	180	190	200	210	220	230	240
DDKCPSVSPS	MPENQSATKE	LGQMNLTERE	KMDTGVVLLS	GNDTLHDLCQ	SQLPENKESK	EAEQDSELTS	EEEQERLKGC
250	260	270	280	290	300	310	320
ENKQPQKTSQ	EPEMAKDCDR	EDIPIYPVLP	HVQKSEEMWI	EQGKLEWKNQ	LKLVINELKQ	RFGEIYEKYK	IPACPEEEPL
330	340	350	360	370	380	390	400
LDNSTRGTDV	KDIPFNLTNN	IPGCEEEDAS	EISVSVVFET	FPEQKEPSLK	NIIHPYYHPY	SGSQEHVCQS	SSKFHLHENK
410	420	430	440	450	460	470	480
LDCDNDNKPG	IGHIFSTDKN	FHNDASTKKA	RNPEVVMVEM	KEDQEFDLQM	TKNMNQNSDS	GSTNNYKSLK	PKLENLSSLP
490	500	510	520	530	540	550	560
PDSDRTSEVY	LHEELQQDMQ	KFKNEVNTLE	EEFLALKKED	VQLHKDVEEE	MEKHRSNSTE	LSGTLTDGTT	VGNDDDGLNQ
570	580	590	600	610	620	630	640
QIPRKENGEH	DRPADKTSNE	KNEVKNQIYP	EADFADSMEP	SEIASEDCEL	SHSVYENFML	LIEQLRMEYK	DLP

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1687	1	1044.9895	2.94	2	50.9	17.3	0	401-419	K.LDCDNDNKPGIGHIFSTDK.N	

Detailed Protein Report

Protein 677: arachidonate 15-lipoxygenase [Homo sapiens]

Accession: gi|40316937
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 17.2
MW [kDa]: 74.8
pI: 6.1
Sequence Coverage [%]: 4.2
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MGLYRIRVST	GASLYAGSNN	QVQLWLVGQH	GEAALGKRLW	PARGKETELK	VEVPEYLGPL	LFVKLRKRHL	LKDDAWFCNW
90	100	110	120	130	140	150	160
ISVQGPGAGD	EVRFPCYRWV	EGNGVLSLPE	GTGRTVGEDP	QGLFQKHREE	ELEERRKLYR	WGNWKDGLIL	NMAGAKLYDL
170	180	190	200	210	220	230	240
PVDERFLEDK	RVDFEVSLAK	GLADLAIKDS	LNVLTCWKDL	DDFNRIFWCG	QSKLAERVRD	SWKEDALFGY	QFLNGANPVV
250	260	270	280	290	300	310	320
LRRSAHLPAR	LVFPPGMEEL	QAQLEKELEG	GTLFEADFSL	LDGIKANVIL	CSQQHLAAPL	VMLKLQPDGK	LLPMVIQLQL
330	340	350	360	370	380	390	400
PRTGSPPPPL	FLPTDPPMAW	LLAKCWVRSS	DFQLHELQSH	LLRGHLMAEV	IVVATMRCLP	SIHPIFKLII	PHLRYTLEIN
410	420	430	440	450	460	470	480
VRARTGLVSD	MGIFDQIMST	GGGGHVQLLK	QAGAFLTYSS	FCPPDDLADR	GLLGVKSSFY	AQDALRLWEI	IYRYVEGIVS
490	500	510	520	530	540	550	560
LHYKTDVAVK	DDPELQTWCR	EITEIGLQGA	QDRGFPVSLQ	ARDQVCHFVT	MCIFTCTGQH	ASVHLGQLDW	YSWVPNAPCT
570	580	590	600	610	620	630	640
MRLPPPTTKD	ATLETVMATL	PNFHQASLQM	SITWQLGRRQ	PVMVAVGQHE	EEYFSGPEPK	AVLKKFREEL	AALDKEIEIR
650	660	670					
NAKLDMPYEY	LRPSVVENSV	AI					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2691	1	974.1911	31.88	3	64.9	17.2	1	403-430	R.ARTGLVSDMGIFDQIMSTGGGGHVQLLK.Q	Oxidation: 9, 16

Detailed Protein Report

Protein 678: PREDICTED: nef-associated protein 1 isoform X2 [Homo sapiens]

Accession:	gi|530391237	**Score:**	17.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	32.6
Database Date:	2015-11-30	**pI:**	5.3
		Sequence Coverage [%]:	4.7
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530391241	refseq_human (refseq_human_20140103.fasta)	PREDICTED: nef-associated protein 1 isoform X4 [Homo sapiens]
gi|530391239	refseq_human (refseq_human_20140103.fasta)	PREDICTED: nef-associated protein 1 isoform X3 [Homo sapiens]

10	20	30	40	50	60	70	80
MIHGTPVLDI	KPYIAEYDSP	QNVMEPLADF	NLQNNQHTPN	TVSQSDSKTD	SCDQRQLSGC	DEPQPHHSTK	RKPKCPEDRT
90	100	110	120	130	140	150	160
SEENYLTHSD	TARIQQAFPM	HREIAVDFGL	ESRRDQSSSV	AEEQIGPYCP	EKSFSEKGTD	KKLERVEGAA	VLQGSRAETQ
170	180	190	200	210	220	230	240
PMAPHCPAGR	ADGAPRSVVP	AWVTEAPVAT	LEVRFTPHAE	MDLGQLSSQD	VGQASFKYFQ	SAEEAKRAIE	AVLSADPRSV
250	260	270	280	290	300		
YRRKLCQDRL	FYFTVDIAHV	TCWFGDGFAE	VLRIKPASEP	VHMTGPVGSL	VSLGS		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2863	1	812.4116	56.30	2	66.2	17.2	0	80-93	R.TSEENYLTHSDTAR.I	

Detailed Protein Report

Protein 679: vacuolar protein sorting-associated protein 26A isoform 1 [Homo sapiens]

Accession:	gi|17978519	**Score:**	17.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	38.1
Database Date:	2015-11-30	**pI:**	6.1
		Sequence Coverage [%]:	3.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSFLGGFFGP	ICEIDIVLND	GETRKMAEMK	TEDGKVEKHY	LFYDGESVSG	KVNLAFKQPG	KRLEHQGIRI	EFVGQIELFN
90	100	110	120	130	140	150	160
DKSNTHEFVN	LVKELALPGE	LTQSRSYDFE	FMQVEKPYES	YIGANVRLRY	FLKVTIVRRL	TDLVKEYDLI	VHQLATYPDV
170	180	190	200	210	220	230	240
NNSIKMEVGI	EDCLHIEFEY	NKSKYHLKDV	IVGKIYFLLV	RIKIQHMELQ	LIKKEITGIG	PSTTTETETI	AKYEIMDGAP
250	260	270	280	290	300	310	320
VKGESIPIRL	FLAGYDPTPT	MRDVNKKFSV	RYFLNLVLVD	EEDRRYFKQQ	EIILWRKAPE	KLRKQRTNFH	QRFESPESQA
330							
SAEQPEM							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2850	1	826.4426	-32.68	2	66.0	17.2	2	286-297	R.YFKQQEIILWRK.A	

Detailed Protein Report

Protein 680: gamma-tubulin complex component 4 isoform b [Homo sapiens]

Accession:	gi|38454194	**Score:**	17.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	76.0
Database Date:	2015-11-30	**pI:**	6.2
		Sequence Coverage [%]:	2.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MIHELLLALS	GYPGSIFTWN	KRSGLQVSQD	FPFLHPSETS	VLNRLCRLGT	DYIRFTEFIE	QYTGHVQQQD	HHPSQQGQGG
90	100	110	120	130	140	150	160
LHGIYLRAFC	TGLDSVLQPY	RQALLDLEQE	FLGDPHLSIS	HVNYFLDQFQ	LLFPSVMVVV	EQIKSQKIHG	CQILETVYKH
170	180	190	200	210	220	230	240
SCGGLPPVRS	ALEKILAVCH	GVMYKQLSAW	MLHGLLLDQH	EEFFIKQGPS	SGNVSAQPEE	DEEDLGIGGL	TGKQLRELQD
250	260	270	280	290	300	310	320
LRLIEEENML	APSLKQFSLR	VEILPSYIPV	RVAEKILFVG	ESVQMFENQN	VNLTRKGSIL	KNQEDTFAAE	LHRLKQQPLF
330	340	350	360	370	380	390	400
SLVDFEQVVD	RIRSTVAEHL	WKLMVEESDL	LGQLKIIKDF	YLLGRGELFQ	AFIDTAQHML	KTPPTAVTEH	DVNVAFQQSA
410	420	430	440	450	460	470	480
HKVLLDDDNL	LPLLHLTIEY	HGKEHKDATQ	AREGPSRETS	PREAPASGWA	ALGLSYKVQW	PLHILFTPAV	LEKYNVVFKY
490	500	510	520	530	540	550	560
LLSVRRVQAE	LQHCWALQMQ	RKHLKSNQTD	AIKWRLRNHM	AFLVDNLQYY	LQVDVLESQF	SQLLHQINST	RDFESIRLAH
570	580	590	600	610	620	630	640
DHFLSNLLAQ	SFILLKPVFH	CLNEILDLCH	SFCSLVSQNL	GPLDERGAAQ	LSILVKGFSR	QSSLLFKILS	SVRNHQINSD
650	660	670					
LAQLLLRLDY	NKYYTQAGGT	LGSFGM					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1982	4	726.7832	-60.06	2	54.7	17.2	0	653-666	K.YYTQAGGTLGSFGM.-	

Detailed Protein Report

Protein 681: **PREDICTED: SLIT-ROBO Rho GTPase-activating protein 2 isoform X7 [Homo sapiens]**

Accession:	gi|578800751	**Score:**	17.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	110.6
Database Date:	2015-11-30	**pI:**	6.4
		Sequence Coverage [%]:	2.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MTSPAKFKKD	KEIIAEYDTQ	VKEIRAQLTE	QMKCLDQQCE	LRVQLLQDLQ	DFFRKKAEIE	MDYSRNLEKL	AERFLAKTRS
90	100	110	120	130	140	150	160
TKDQQFKKDQ	NVLSPVNCWN	LLLNQVKRES	RDHTTLSDIY	LNNIIPRFVQ	VSEDSGRLFK	KSKEVGQQLQ	DDLMKVLNEL
170	180	190	200	210	220	230	240
YSVMKTYHMY	NADSISAQSK	LKEAEKQEEK	QIGKSVKQED	RQTPRSPDST	ANVRIEEKHV	RRSSVKKIEK	MKEKRQAKYT
250	260	270	280	290	300	310	320
ENKLKAIKAR	NEYLLALEAT	NASVFKYYIH	DLSDLIDQCC	DLGYHASLNR	ALRTFLSAEL	NLEQSKHEGL	DAIENAVENL
330	340	350	360	370	380	390	400
DATSDKQRLM	EMYNNVFCPP	MKFEFQPHMG	DMASQLCAQQ	PVQSELVQRC	QQLQSRLSTL	KIENEEVKKT	MEATLQTIQD
410	420	430	440	450	460	470	480
IVTVEDFDVS	DCFQYSNSME	SVKSTVSETF	MSKPSIAKRR	ANQQETEQFY	FTKMKEYLEG	RNLITKLQAK	HDLLQKTLGE
490	500	510	520	530	540	550	560
SQRTDCSLAR	RSSTVRKQDS	SQAIPLVVES	CIRFISRHGL	QHEGIFRVSG	SQVEVNDIKN	AFERGEDPLA	GDQNDHDMDS
570	580	590	600	610	620	630	640
IAGVLKLYFR	GLEHPLFPKD	IFHDLMACVT	MDNLQERALH	IRKVLLVLPK	TTLIIMRYLF	AFLNHLSQFS	EENMMDPYNL
650	660	670	680	690	700	710	720
AICFGPSLMS	VPEGHDQVSC	QAHVNELIKT	IIIQHENIFP	SPRELEGPVY	SRGGSMEDYC	DSPHGETTSV	EDSTQDVTAE
730	740	750	760	770	780	790	800
HHTSDDECEP	IEAIAKFDYV	GRTARELSFK	KGASLLLYQR	ASDDWWEGRH	NGIDGLIPHQ	YIVVQDTEDG	VVERSSPKSE
810	820	830	840	850	860	870	880
IEVISEPPEE	KVTARAGASC	PSGGHVADIY	LANINKQRKR	PESGSIRKTF	RSDSHGLSSS	LTDSSSPGVG	ASCRPSSQPI
890	900	910	920	930	940	950	960
MSQSLPKEGP	DKCSISGHGS	LNSISRHSSL	KNRLDSPQIR	KTATAGRSKS	FNNHRPMDPE	VIAQRSNPTS	KNPTTGATPS
970	980						
SSLRRLSQLY	NFH						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2584	2	914.0716	-57.66	3	62.3	17.1	2	928-951	R.SKSFNNHRPMDPEVIAQRSNPTSK.N	

Detailed Protein Report

Protein 682: pyrroline-5-carboxylate reductase 2 isoform 2 [Homo sapiens]

Accession:	gi|410991931	**Score:**	17.1
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
290	1	1074.7498	98.90	2	33.0	17.1	2	121-141	K.MGLPRRLAIQLGAQALLGAAK.M	

Detailed Protein Report

Protein 683: angiopoietin-related protein 1 precursor [Homo sapiens]

Accession:	gi|4757752	**Score:**	17.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	56.7
Database Date:	2015-11-30	**pI:**	9.1
		Sequence Coverage [%]:	5.3
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|530365564	refseq_human (refseq_human_20140103.fasta)	PREDICTED: angiopoietin-related protein 1 isoform X1 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MKTFTWTLGV LFFLLVDTGH CRGGQFKIKK INQRRYPRAT DGKEEAKKCA YTFLVPEQRI TGPICVNTKG QDASTIKDMI
        90        100        110        120        130        140        150        160
TRMDLENLKD VLSRQKREID VLQLVVDVDG NIVNEVKLLR KESRNMNSRV TQLYMQLLHE IIRKRDNSLE LSQLENKILN
       170        180        190        200        210        220        230        240
VTTEMLKMAT RYRELEVKYA SLTDLVNNQS VMITLLEEQC LRIFSRQDTH VSPPLVQVVP QHIPNSQQYT PGLLGGNEIQ
       250        260        270        280        290        300        310        320
RDPGYPRDLM PPPDLATSPT KSPFKIPPVT FINEGPFKDC QQAKEAGHSV SGIYMIKPEN SNGPMQLWCE NSLDPGGWTV
       330        340        350        360        370        380        390        400
IQKRTDGSVN FFRNWENYKK GFGNIDGEYW LGLENIYMLS NQDNYKLLIE LEDWSDKKVY AEYSSFRLEP ESEFYRLRLG
       410        420        430        440        450        460        470        480
TYQGNAGDSM MWHNGKQFTT LDRDKDMYAG NCAHFHKGGW WYNACAHSNL NGVWYRGGHY RSKHQDGIFW AEYRGGSYSL
       490        500
RAVQMMIKPI D
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2041	1	1018.3938	-75.83	3	55.4	17.0	0	341-366	K.GFGNIDGEYWLGLENIYMLSNQDNYK.L	

Detailed Protein Report

Protein 684: PREDICTED: amphiphysin isoform X1 [Homo sapiens]

Accession: gi|578813410
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 17.0
MW [kDa]: 134.8
pI: 4.3
Sequence Coverage [%]: 0.8
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MADIKTGIFA	KNVQKRLNRA	QEKVLQKLGK	ADETKDEQFE	EYVQNFKRQE	AEGTRLQREL	RGYLAAIKGM	QEASMKLTES
90	100	110	120	130	140	150	160
LHEVYEPDWY	GREDVKMVGE	KCDVLWEDFH	QKLVDGSLLT	LDTYLGQFPD	IKNRIAKRSR	KLVDYDSARH	HLEALQSSKR
170	180	190	200	210	220	230	240
KDESRISKAE	EEFQKAQKVF	EEFNVDLQEE	LPSLWSRRVG	FYVNTFKNVS	SLEAKFHKEI	AVLCHKLYEV	MTKLGDQHAD
250	260	270	280	290	300	310	320
KAFTIQGAPS	DSGPLRIAKT	PSPPEEPSPL	PSPTASPNHT	LAPASPAPAR	PRSPSQTRKG	PPVPPLPKVT	PTKELQQENI
330	340	350	360	370	380	390	400
ISFFEDNFVP	EISVTTPSQN	EVPEVKKEET	LLDLDFDPFK	PEVTPAGSAG	VTHSPMSQTL	PWDLWTTDSS	ESLSLCNLIM
410	420	430	440	450	460	470	480
EETPDSGLAE	EIQRSQNDIG	AFTWGPDAST	DRVSQEVTSG	GFGEDSACPS	ETEQDIRLST	SLLSSADWPT	VAEESEHAPG
490	500	510	520	530	540	550	560
PAFPGGNEQL	PPKPAPEAGV	AIAACVEMEQ	LYDPLDSDMP	AMDTAGLFKE	SHEDMKKSDE	EEEKQKMEDS	LWAGVEACQK
570	580	590	600	610	620	630	640
VDTGAIDIKT	LEGTEEFEEK	ACERTGNRVV	ELLNTIGKED	HKTLKINEVE	TRKDLRAGYK	ESTNANENYF	EKTDLLEKDM
650	660	670	680	690	700	710	720
EGGDMAKELS	DRDQGLHDGI	QKVINNCGMI	EGFGAKPANH	PDILNPSLQT	YSVSNIEDGS	PEGWDLTRKD	IKKNAIDTPN
730	740	750	760	770	780	790	800
HDMIFYPAQD	STDAEEIQCE	TVLNALVGDR	DKNQAVLSIK	LEVEAQSRTD	LNYSLGRDAN	RRDLCSCKAE	SSLIEGSERT
810	820	830	840	850	860	870	880
VTENRSHTVN	LPRIAEIDSW	GTDPGQIWQP	SLDSAMNNLD	ITGFSGIPDG	QASGFASCLD	SINHWPIRDT	EGLDNSWTHS
890	900	910	920	930	940	950	960
DVVEHKEELK	VDLLAGDCRE	QAIASCWEQS	QEIARPLILG	TSWNASTESS	ASSRDQDINN	SDLSEDEIAN	QRYGLLYQEI
970	980	990	1000	1010	1020	1030	1040
EADKDEASGG	SFNGFTQPQD	TSLFTMQTDQ	SMICNLIIPG	ADADAAVGTL	VSAAEGAPGE	EAEAEKATVP	AGEGVSLEEA
1050	1060	1070	1080	1090	1100	1110	1120
KIGTETTEGA	ESAQPEAEEL	EATVPQEKVI	PSVVIEPASN	HEEEGENEIT	IGAEPKETTE	DAAPPGPTSE	TPELATEQKP
1130	1140	1150	1160	1170	1180	1190	1200
IQDPQPTPSA	PAMGAADQLA	SAREASQELP	PGFLYKVETL	HDFEAANSDE	LTLQRGDVVL	VVPSDSEADQ	DAGWLVGVKE
1210	1220	1230					
SDWLQYRDLA	TYKGLFPENF	TRRLD					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1311	1	1115.7434	90.99	1	46.1	17.0	1	751-760	R.DKNQAVLSIK.L	

Detailed Protein Report

Protein 685: **neugrin precursor [Homo sapiens]**

Accession: gi|75677385
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 17.0
MW [kDa]: 32.4
pI: 9.8
Sequence Coverage [%]: 5.2
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MAVTLSLLLG	GRVCAAVTRC	GFATRGVAGP	GPIGREPDPD	SDWEPEEREL	QEVESTLKRQ	KQAIRFQKIR	RQMEAPGAPP
90	100	110	120	130	140	150	160
RTLTWEAMEQ	IRYLHEEFPE	SWSVPRLAEG	FDVSTDVIRR	VLKSKFLPTL	EQKLKQDQKV	LKKAGLAHSL	QHLRGSGNTS
170	180	190	200	210	220	230	240
KLLPAGHSVS	GSLLMPGHEA	SSKDPNHSTA	LKVIESDTHR	TNTPRRRKGR	NKEIQDLEES	FVPVAAPLGH	PRELQKYSSD
250	260	270	280	290	300		
SESPRGTGSG	ALPSGQKLEE	LKAEEPDNFS	SKVVQRGREF	FDSNGNFLYR	I		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
912	1	836.1322	143.24	2	41.0	17.0	2	140-154	K.VLKKAGLAHSLQHLR.G	

Detailed Protein Report

Protein 686: proto-oncogene tyrosine-protein kinase Src [Homo sapiens]

Accession: gi|4885609
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl, Oxidation

Score: 16.9
MW [kDa]: 59.8
pI: 7.7
Sequence Coverage [%]: 5.0
No. of unique Peptides: 1

Alias proteins:

Accession	Name	Description
gi|38202217	refseq_human (refseq_human_20140103.fasta)	proto-oncogene tyrosine-protein kinase Src [Homo sapiens]

10	20	30	40	50	60	70	80
MGSNKSKPKD	ASQRRRSLEP	AENVHGAGGG	AFPASQTPSK	PASADGHRGP	SAAFAPAAAE	PKLFGGFNSS	DTVTSPQRAG
90	100	110	120	130	140	150	160
PLAGGVTTFV	ALYDYESRTE	TDLSFKKGER	LQIVNNTEGD	WWLAHSLSTG	QTGYIPSNYV	APSDSIQAEE	WYFGKITRRE
170	180	190	200	210	220	230	240
SERLLLNAEN	PRGTFLVRES	ETTKGAYCLS	VSDFDNAKGL	NVKHYKIRKL	DSGGFYITSR	TQFNSLQQLV	AYYSKHADGL
250	260	270	280	290	300	310	320
CHRLTTVCPT	SKPQTQGLAK	DAWEIPRESL	RLEVKLGQGC	FGEVWMGTWN	GTTRVAIKTL	KPGTMSPEAF	LQEAQVMKKL
330	340	350	360	370	380	390	400
RHEKLVQLYA	VVSEEPIYIV	TEYMSKGSLL	DFLKGETGKY	LRLPQLVDMA	AQIASGMAYV	ERMNYVHRDL	RAANILVGEN
410	420	430	440	450	460	470	480
LVCKVADFGL	ARLIEDNEYT	ARQGAKFPIK	WTAPEAALYG	RFTIKSDVWS	FGILLTELTT	KGRVPYPGMV	NREVLDQVER
490	500	510	520	530	540		
GYRMPCPPEC	PESLHDLMCQ	CWRKEPEERP	TFEYLQAFLE	DYFTSTEPQY	QPGENL		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1597	1	1018.4971	-18.56	3	49.7	16.9	2	272-298	R.LEVKLGQGCFGEVWMGTWNGTTRVAIK.T	Carbamidomethyl: 9; Oxidation: 15

Detailed Protein Report

Protein 687: PREDICTED: matrix extracellular phosphoglycoprotein isoform X1 [Homo sapiens]

Accession:	gi|578809281	**Score:**	16.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	62.1
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
MRVFCVGLLL	FSVTWAAPTF	QPQTEKTKQS	CVEEQRITYK	GHYEKHGHYV	FKCVYMSPEK	KNQTDVKQEE	KNKDNIGFHH
90	100	110	120	130	140	150	160
LGKRINQELS	SKENIVQERK	KDLSLSEASE	NKGSSKSQNY	FTNRQRLNKE	YSISNKENTH	NGLRMSIYPK	STGNKGFEDG
170	180	190	200	210	220	230	240
DDAISKLHDQ	EEYGAALIRN	NMQHIMGPVT	AIKLLGEENK	ENTPRNVLNI	IPASMNYAKA	HSKDKKKPQR	DSQAQKSPVK
250	260	270	280	290	300	310	320
SKSTHRIQHN	IDYLKHLSKV	KKIPSDFEGS	GYTDLQERGD	NDISPFSGDG	QPFKDIPGKG	EATGPDLEGK	DIQTGFAGPS
330	340	350	360	370	380	390	400
EAESTHLDTK	KPGYNEIPER	EENGGNTIGT	RDETAKEADA	VDVSLVEGSN	DIMGSTNFKE	LPGREGNRVD	AGSQNAHQGK
410	420	430	440	450	460	470	480
VEFHYPPAPS	KEKRKEGSSD	AAESTNYNEI	PKNGKGSTRK	GVDHSNRNQA	TLNEKQRFPS	KGKSQGLPIP	SRGLDNEIKN
490	500	510	520	530	540	550	560
EMDSFNGPSH	ENIITHGRKY	HYVPHRQNNS	TRNKGMPQGK	GSWGRQPHSN	RRFSSRRRDD	SSESSDSGSS	SESDGD

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2687	1	920.7982	-142.16	2	64.8	16.9	1	46-60	K.HGHYVFKCVYMSPEK.K	Oxidation: 11

Detailed Protein Report

Protein 688: PREDICTED: dedicator of cytokinesis protein 3 isoform X8 [Homo sapiens]

Accession: gi|578805738
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 16.9
MW [kDa]: 215.9
pI: 7.2
Sequence Coverage [%]: 0.9
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MWTPTEEEKY	GVVICSFRGS	VPQGLVLEIG	ETVQILEKCE	GWYRGVSTKK	PNVKGIFPAN	YIHLKKAIVS	NRGQYETVVP
90	100	110	120	130	140	150	160
LEDSIVTEVT	ATLQEWASLW	KQLYVKHKVD	LFYKLRHVMN	ELIDLRRQLL	SGHLTQDQVR	EVKRHITVRL	DWGNEHLGLD
170	180	190	200	210	220	230	240
LVPRKDFEVV	DSDQISVSDL	YKMHLSSRQS	VQQSTSQVDT	MRPRHGETCR	MPVPHHFFLS	LKSFTYNTIG	EDTDVFFSLY
250	260	270	280	290	300	310	320
DMREGKQISE	RFLVRLNKNG	GPRNPEKIER	MCALFTDLSS	KDMKRDLYIV	AHVIRIGRML	LNDSKKGPPH	LHYRRPYGCA
330	340	350	360	370	380	390	400
VLSILDVLQS	LTEVKEEKDF	VLKVYTCNNE	SEWSQIHENI	IRKSSAKYSA	PSASHGLIIS	LQLLRGDMEQ	IRRENPMIFN
410	420	430	440	450	460	470	480
RGLAITRKLG	FPDVIMPGDI	RNDLYLTLEK	GDFERGGKSV	QKNIEVTMYV	LYADGEILKD	CISLGSGEPN	RSSYHSFVLY
490	500	510	520	530	540	550	560
HSNSPRWGEI	IKLPIPIDRF	RGSHLRFEFR	HCSTKDKGEK	KLFGFAFSTL	MRDDGTTLSD	DIHELYVYKC	DENSTFNNHA
570	580	590	600	610	620	630	640
LYLGLPCCKE	DYNGCPNIPS	SLIFQRSTKE	SFFISTQLSS	TKLTQNVDLL	ALLKWKAFPD	RIMDVLGRLR	HVSGEEIVKF
650	660	670	680	690	700	710	720
LQDILDTLFV	ILDDNTEKYG	LLVFQSLVFI	INLLRDIKYF	HFRPVMDTYI	QKHFAGALAY	KELIRCLKWY	MDCSAELIRQ
730	740	750	760	770	780	790	800
DHIQEAMRAL	EYLFKFIVQS	RILYSRATCG	MEEEQFRSSI	QELFQSIRFV	LSLDSRNSET	LLFTQAALLN	SFPTIFDELL
810	820	830	840	850	860	870	880
QMFTVQEVAE	FVRGTLGSMP	STVHIGQSMD	VVKLQSIART	VDSRLFSFSE	SRRILLPVVL	HHIHLHLRQQ	KELLICSGIL
890	900	910	920	930	940	950	960
GSIFSIVKTS	SLEADVMEEV	EMMVESLLDV	LLQTLLTIMS	KSHAQEAVRG	QRCPQCTAEI	TGEYVSCLLS	LLRQMCDTHF
970	980	990	1000	1010	1020	1030	1040
QHLLDNFQSK	DELKEFLLKI	FCVFRNLMKM	SVFPRDWMVM	RLLTSNIIVT	TVQYLSSALH	KNFTETDFDF	KVWNSYFSLA
1050	1060	1070	1080	1090	1100	1110	1120
VLFINQPSLQ	LEIITSAKRK	KILDKYGDMR	VMMAYELFSM	WQNLGEHKIH	FIPGMIGPFL	GVTLVPQPEV	RNIMIPIFHD
1130	1140	1150	1160	1170	1180	1190	1200
MMDWEQRKNG	NFKQVEAELI	DKLDSMVSEG	KGDESYRELF	SLLTQLFGPY	PSLLEKVEQE	TWRETGISFV	TSVTRLMERL
1210	1220	1230	1240	1250	1260	1270	1280
LDYRDCMKGE	ETENKKIGCT	VNLMNFYKSE	INKEEMYIRY	IHKLCDMHLQ	AENYTEAAFT	LLLYCELLQW	EDRPLREFLH
1290	1300	1310	1320	1330	1340	1350	1360
YPSQTEWQRK	EGLCRKIIHY	FNKGKSWEFG	IPLCRELACQ	YESLYDYQSL	SWIRKMEASY	YDNIMEQQRL	EPEFFRVGFY
1370	1380	1390	1400	1410	1420	1430	1440
GRKFPFFLRN	KEYVCRGHDY	ERLEAFQQRM	LSEFPQAVAM	QHPNHPDDAI	LQCDAQYLQI	YAVTPIPDYV	DVLQMDRVPD
1450	1460	1470	1480	1490	1500	1510	1520
RVKSFYRVNN	VRKFRYDRPF	HKGPKDKENE	FKSLWIERTT	LTLTHSLPGI	SRWFEVERRE	LVEVSPLENA	IQVVENKNQE
1530	1540	1550	1560	1570	1580	1590	1600
LRSLISQYQH	KQVHGNINLL	SMCLNGVIDA	AVNGGIARYQ	EAFFDKDYIN	KHPGDAEKIT	QLKELMQEQV	HVLGVGLAVH
1610	1620	1630	1640	1650	1660	1670	1680
EKFVHPEMRP	LHKKLIDQFQ	MMRASLYHEF	PGLDKLSPAC	SGTSTPRGNV	LASHSPMSPE	SIKMTHRHSP	MNLMGTGRHS
1690	1700	1710	1720	1730	1740	1750	1760
SSSLSSHASS	EAGNMVMLGD	GSMGDAPEDL	YHHMQLAYPN	PRYQGSVTNV	SVLSSSQASP	SSSSLSSTHS	APSQMITSAP
1770	1780	1790	1800	1810	1820	1830	1840
SSARGSPSLP	DKYRHAREMM	LLLPTYRDRP	SSAMYPAAIL	ENGQPPNFQR	ALFQQVVGAC	KPCSDPNLSV	AEKVSSPPYP
1850	1860	1870					
SLPHKPPVRS	GRQQLYAVRQ	CQQRRVLLE					

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1591	1	920.1649	140.51	2	49.7	16.9	1	50-65	K.KPNVKGIFPANYIHLK.K	

Detailed Protein Report

Protein 689: transmembrane protein 110 [Homo sapiens]

Accession:	gi|38348402	**Score:**	16.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	33.2
Database Date:	2015-11-30	**pI:**	9.2
		Sequence Coverage [%]:	3.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MQGPAGNASR	GLPGGPPSTV	ASGAGRCESG	ALMHSFGIFL	QGLLGVVAFS	TLMLKRFREP	KHERRPWRIW	FLDTSKQAIG
90	100	110	120	130	140	150	160
MLFIHFANVY	LADLTEEDPC	SLYLINFLLD	ATVGMLLIYV	GVRAVSVLVE	WQQWESLRFG	EYGDPLQCGA	WVGQCALYIV
170	180	190	200	210	220	230	240
IMIFEKSVVF	IVLLILQWKK	VALLNPIENP	DLKLAIVMLI	VPFFVNALMF	WVVDNFLMRK	GKTKAKLEER	GANQDSRNGS
250	260	270	280	290	300		
KVRYRRAASH	EESESEILIS	ADDEMEESDV	EEDLRRLTPL	KPVKKKKHRF	GLPV		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1547	1	1023.7372	43.65	1	49.2	16.9	1	277-285	R.LTPLKPVKK.K	

Detailed Protein Report

Protein 690: PREDICTED: serine protease hepsin isoform X3 [Homo sapiens]

Accession:	gi|578834381	**Score:**	16.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	42.9
Database Date:	2015-11-30	**pI:**	9.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MCKMRTREDM	QLGNEGPGTA	LRLIHLQVSS	ADARLMVFDK	TEGTWRLLCS	SRSNARVAGL	SCEEMGFLRA	LTHSELDVRT
90	100	110	120	130	140	150	160
AGANGTSGFF	CVDEGRLPHT	QRLLEVISVC	DCPRGRFLAA	ICQDCGRRKL	PVDRIVGGRD	TSLGRWPWQV	SLRYDGAHLC
170	180	190	200	210	220	230	240
GGSLLSGDWV	LTAAHCFPER	NRVLSRWRVF	AGAVAQASPH	GLQLGVQAVV	YHGGYLPFRD	PNSEENSNDI	ALVHLSSPLP
250	260	270	280	290	300	310	320
LTEYIQPVCL	PAAGQALVDG	KICTVTGWGN	TQYYGQQAGV	LQEARVPIIS	NDVCNGADFY	GNQIKPKMFC	AGYPEGGIDA
330	340	350	360	370	380	390	400
CQGDSGGPFV	CEDSISRTPR	WRLCGIVSWG	TGCALAQKPG	VYTKVSDFRE	WIFQAIKVKV	GSRWEPGWGR	LGV

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
54	1	731.6654	-66.09	3	30.0	16.8	1	97-114	R.LPHTQRLLEVISVCDCPR.G	Carbamidomethyl: 14, 16

Detailed Protein Report

Protein 691: integrin alpha-D precursor [Homo sapiens]

Accession:	gi|62548866	**Score:**	16.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	126.7
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
MTFGTVLLLS	VLASYHGFNL	DVEEPTIFQE	DAGGFGQSVV	QFGGSRLVVG	APLEVVAANQ	TGRLYDCAAA	TGMCQPIPLH
90	100	110	120	130	140	150	160
IRPEAVNMSL	GLTLAASTNG	SRLLACGPTL	HRVCGENSYS	KGSCLLLGSR	WEIIQTVPDA	TPECPHQEMD	IVFLIDGSGS
170	180	190	200	210	220	230	240
IDQNDFNQMK	GFVQAVMGQF	EGTDTLFALM	QYSNLLKIHF	TFTQFRTSPS	QQSLVDPIVQ	LKGLTFTATG	ILTVVTQLFH
250	260	270	280	290	300	310	320
HKNGARKSAK	KILIVITDGQ	KYKDPLEYSD	VIPQAEKAGI	IRYAIGVGHA	FQGPTARQEL	NTISSAPPQD	HVFKVDNFAA
330	340	350	360	370	380	390	400
LGSIQKQLQE	KIYAVEGTQS	RASSSFQHEM	SQEGFSTALT	MDGLFLGAVG	SFSWSGGAFL	YPPNMSPTFI	NMSQENVDMR
410	420	430	440	450	460	470	480
DSYLGYSTEL	ALWKGVQNLV	LGAPRYQHTG	KAVIFTQVSR	QWRKKAEVTG	TQIGSYFGAS	LCSVDVDSDG	STDLILIGAP
490	500	510	520	530	540	550	560
HYYEQTRGGQ	VSVCPLPRGR	VQWQCDAVLR	GEQGHPWGRF	GAALTVLGDV	NEDKLIDVAI	GAPGEQENRG	AVYLFHGASE
570	580	590	600	610	620	630	640
SGISPSHSQR	IASSQLSPRL	QYFGQALSGG	QDLTQDGLMD	LAVGARGQVL	LLRSLPVLKV	GVAMRFSPVE	VAKAVYRCWE
650	660	670	680	690	700	710	720
EKPSALEAGD	ATVCLTIQKS	SLDQLGDIQS	SVRFDLALDP	GRLTSRAIFN	ETKNPTLTRR	KTLGLGIHCE	TLKLLLPDCV
730	740	750	760	770	780	790	800
EDVVSPIILH	LNFSLVREPI	PSPQNLRPVL	AVGSQDLFTA	SLPFEKNCGQ	DGLCEGDLGV	TLSFSGLQTL	TVGSSLELNV
810	820	830	840	850	860	870	880
IVTVWNAGED	SYGTVVSLYY	PAGLSHRRVS	GAQKQPHQSA	LRLACETVPT	EDEGLRSSRC	SVNHPIFHEG	SNGTFIVTFD
890	900	910	920	930	940	950	960
VSYKATLGDR	MLMRASASSE	NNKASSSKAT	FQLELPVKYA	VYTMISRQEE	STKYFNFATS	DEKKMKEAEH	RYRVNNLSQR
970	980	990	1000	1010	1020	1030	1040
DLAISINFWV	PVLLNGVAVW	DVVMEAPSQS	LPCVSERKPP	QHSDFLTQIS	RSPMLDCSIA	DCLQFRCDVP	SFSVQEELDF
1050	1060	1070	1080	1090	1100	1110	1120
TLKGNLSFGW	VRETLQKKVL	VVSVAEITFD	TSVYSQLPGQ	EAFMRAQMEM	VLEEDEVYNA	IPIIMGSSVG	ALLLLALITA
1130	1140	1150	1160	1170			
TLYKLGFFKR	HYKEMLEDKP	EDTATFSGDD	FSCVAPNVPL	S			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
987	1	798.0925	46.27	3	41.9	16.8	0	638-659	R.CWEEKPSALEAGDATVCLTIQK.S	

Detailed Protein Report

Protein 692: **PREDICTED: pre-mRNA-splicing factor ATP-dependent RNA helicase PRP16 isoform X2 [Homo sapiens]**

Accession:	gi|530424571	**Score:**	16.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	136.2
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
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
145	1	896.4035	-68.20	3	31.5	16.8	2	800-824	R.IGMDALQIYPISQANANQRSGRAGR.T	

Detailed Protein Report

Protein 693: unconventional myosin-Ih [Homo sapiens]

Accession:	gi|254028267	**Score:**	16.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	117.9
Database Date:	2015-11-30	**pI:**	9.8
		Sequence Coverage [%]:	1.5
		No. of unique Peptides:	1

Quantitation

MD:MU	**Median:** 1.51	**CV:** 0.00 %	**No. of Peptides:** 1

10	20	30	40	50	60	70	80
MEGALTARDK	VGVQDFVLLD	AYTSESAFVD	NLRKRFSENL	IYTYIGTLLV	SVNPYQELGI	YTVSQMELYQ	GVNFFELPPH
90	100	110	120	130	140	150	160
VYAIADNAYR	MMCAELNNHF	ILISGESGAG	KTEASKKILE	YFAVTCPMTQ	SLQIARDRLL	FSNPVLEAFG	NARTLRNDNS
170	180	190	200	210	220	230	240
SRFGKYMDIQ	FDFQGIPVGG	HIISYLIEKS	RVVYQNEGER	NFHIFYQLLA	GGEEERLSYL	GLERDPQLYK	YLSQGHCAKE
250	260	270	280	290	300	310	320
SSISDKNDWK	TVSNAFSVID	FTEADLENLF	GIIASVLHLG	NIGFEEDDQG	CATIPDTHEI	KWIAKLLGVH	PSVLLEALTH
330	340	350	360	370	380	390	400
RKIEAKTEEV	ICPLTLELSV	YARDAMAKAV	YGRTFTWLVN	KINSSLVNKD	FTRKTVIGLL	DIYGFEVFDK	NGFEQFCINY
410	420	430	440	450	460	470	480
CNEKLQQLLI	ERTLKAEQAE	YEMEGIEWEP	IKYFNNKIIC	DLVEERHKGI	ISILDEECIR	PGPATDLSFL	EKLEEKVGKH
490	500	510	520	530	540	550	560
AHFETRKLAG	PKGRKRIGWM	EFRLLHYAGE	VTYCTKGFLE	KNNDLLYRHL	KEVLCKSKNI	ILRECFLLAE	LENRRRPPTV
570	580	590	600	610	620	630	640
GTQFKNSLSS	LLETLISKEP	SYIRCIKPND	RKEPSKFDDF	LIRHQIKYLG	LMEHLRVRRA	GFAYRRKYEH	FLQRYKSLCP
650	660	670	680	690	700	710	720
DTWPHWHGPP	AEGVERLIKY	IGYKPEEYKL	GKTKIFIRFP	RTLFATEDAF	EFSKHQLVAR	IQATYKRCLG	RREYVKKRQA
730	740	750	760	770	780	790	800
AIKLEAHWRG	ALARKAIQRR	KWAVRIIRKF	IKGFISRNKP	LCPDNEEFIV	FVRKNYILNL	RYHLPKTVLD	KSWLRPPGIL
810	820	830	840	850	860	870	880
ENASDLLRKM	CVRNLVQKYC	RGITAERKAM	MQQKVVTSEI	FRGRKDGYTE	SLNQPFVNSR	IDEGDINPKV	LQLISHEKIQ
890	900	910	920	930	940	950	960
YGVPVIKYDR	KGFKARQRQL	ILTQKAAYVV	ELAKIKQKIE	YSALKGVSTS	NLSDGILVIH	VSPEDSKQKG	DAVLQCGHVF
970	980	990	1000	1010	1020	1030	
EAVTKLVMLV	KKENIVNVVQ	GSLQFFISPG	KEGTIVFDTG	LEEQVYKNKN	GQLTVVSVRR	KS	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1186	1	863.9897	97.78	2	44.4	16.8	0	846-860	K.DGYTESLNQPFVNSR.I		MD:MU 1.51

Detailed Protein Report

Protein 694: PREDICTED: uncharacterized protein C11orf63 isoform X3 [Homo sapiens]

Accession:	gi|530398394	**Score:**	16.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	81.3
Database Date:	2015-11-30	**pI:**	9.8
		Sequence Coverage [%]:	2.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSKRKLIPKL	SIQSPVLHTN	LNVQSTHPPL	KKEDLHRISK	DSLESDSESL	TQEIMCHSEF	DDRIRGNGME	PDSLDEEESP
90	100	110	120	130	140	150	160
RWGSLHEMEE	EASGKAAQMA	REQNHHTWDQ	GANNRQQPIE	DKYSDLRYDP	NWKSKKEEGQ	LLSVEALPES	TDSSLENLPL
170	180	190	200	210	220	230	240
APLYPSQETS	MELSGGKGEQ	KESPQSAASL	LGSEFLSPNY	EHGARRSKPF	SELSDSDLEE	KSSSLSPYVK	SSSSHNEVFL
250	260	270	280	290	300	310	320
PGSRGPRRRK	SKQHFVEKNK	LTLGLPTPKT	DSYLQLHNKK	RGESHPEQIS	YPVRVTDKTS	IQNAKEMENA	AIDPEDKWHQ
330	340	350	360	370	380	390	400
RAQQLKNYQE	HWSQYESTKS	SNVPRGQPSD	MVNDHQPSRR	PAKLKIRKQC	KHQNGLKSST	TEEVTASQGN	QNNPPRQQQN
410	420	430	440	450	460	470	480
QNKPLDTSTK	PESIVIMHAS	NNDVQASRAL	RSHNLKETSN	TFAPPKQAFD	KVLSKNSTGC	DSGLNVNKER	GHKDQEEKRF
490	500	510	520	530	540	550	560
SYQQLHTLSD	MDLNNLNELS	KRHVLLSQKG	SQFVYHINTH	GSTKNKKQLK	QPYTETKYRN	LEMLWKFHSS	SDSQTVRASP
570	580	590	600	610	620	630	640
DSWLTQIMEQ	HQQALVQLTD	VQPSEGALSS	VTLPPILSRV	ESESQLSSER	SQRNQVKISR	SNSEGYLFQL	EKGKKHKKRS
650	660	670	680	690	700	710	720
SSKNTKLKGY	QKRDVKLGGL	GPDFESIRDK	TQKLIQQKEY	AKQVKEYNMK	TLSILSKPQT	EKTQKKSAIP	RQKN

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2757	1	840.9032	-14.10	2	64.8	16.8	1	437-451	K.ETSNTFAPPKQAFDK.V	

Detailed Protein Report

Protein 695: **PREDICTED: PHD finger protein 11 isoform X1 [Homo sapiens]**

Accession:	gi|530402423	**Score:**	16.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	19.5
Database Date:	2015-11-30	**pI:**	7.8
		Sequence Coverage [%]:	10.1
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MPTAFYAKFS GVKRKRGRKK PLSGNHVQPP ETMKCNTFIR QVKEEHGRHT DATVKVPFLK KCKEAGLLNY LLEEILDKVH
        90        100        110        120        130        140        150        160
SIPEKLMDET TSESDYEEIG SALFDCRLFE DTFVNFQAAI EKKIHASQQR WQQLKEEIEL LQDLKQTLCS FQENRDLMSS
       170
STSISSLSY
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1408	1	982.6133	90.85	2	47.3	16.7	1	62-78	K.CKEAGLLNYLLEEILDK.V	

Detailed Protein Report

Protein 696: **myotubularin-related protein 8 [Homo sapiens]**

Accession:	gi|21361759	**Score:**	16.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	78.9
Database Date:	2015-11-30	**pI:**	6.2
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDHITVPKVE	NVKLVDRYVS	KKPANGILYL	TATHLIYVEA	SGAARKETWI	ALHHIATVEK	LPITSLGCPL	TLRCKNFRVA
90	100	110	120	130	140	150	160
HFVLDSDLVC	HEVYISLLKL	SQPALPEDLY	AFSYNPKSSK	EMRESGWKLI	DPISDFGRMG	IPNRNWTITD	ANRNYEICST
170	180	190	200	210	220	230	240
YPPEIVVPKS	VTLGTVVGSS	KFRSKERVPV	LSYLYKENNA	AICRCSQPLS	GFYTRCVDDE	LLLEAISQTN	PGSQFMYVVD
250	260	270	280	290	300	310	320
TRPKLNAMAN	RAAGKGYENE	DNYANIRFRF	MGIENIHVMR	SSLQKLLEVC	ELKTPTMSEF	LSGLESSGWL	RHIKAIMDAG
330	340	350	360	370	380	390	400
IFITKAVKVE	KASVLVHCSD	GWDRTAQVCS	VASILLDPFY	RTFKGLMILI	EKEWISMGHK	FSQRCGHLDG	DSKEVSPIFT
410	420	430	440	450	460	470	480
QFLDCIWQLM	EQFPCAFEFN	ENFLLEIHDH	VFSCQFGNFL	GNCQKDREDL	RVYEKTHSVW	PFLVQRKPDF	RNPLYKGFTM
490	500	510	520	530	540	550	560
YGVLNPSTVP	YNIQFWCGMY	NRFDKGLQPK	QSMLESLLEI	KKQRAMLETD	VHELEKKLKV	RDEPPEEICT	CSQLGNILSQ
570	580	590	600	610	620	630	640
HLGSPLTNPL	GFMGINGDLN	TLMENGTLSR	EGGLRAQMDQ	VKSQGADLHH	NCCEIVGSLR	AINISGDVGI	SEAMGISGDM
650	660	670	680	690	700	710	
CTFEATGFSK	DLGICGAMDI	SEATGISGNL	GISEARGFSG	DMGILGDTGI	SKASTKEADY	SKHQ	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1182	5	956.7083	231.35	1	44.4	16.6	0	1-8	-.MDHITVPK.V	Oxidation: 1

Detailed Protein Report

Protein 697: FERM, RhoGEF and pleckstrin domain-containing protein 2 isoform c [Homo sapiens]

Accession:	gi|545478189	**Score:**	16.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	72.2
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
MGEIEGTYRV	LQTAGMRLGA	QTPVGVSTLE	PGQTLLPRMQ	EKHLHLRVKL	LDNTMEIFDI	EPKCDGQVLL	TQVWKRLNLV
90	100	110	120	130	140	150	160
ECDYFGMEFQ	NTQSYWIWLE	PMKPIIRQIR	RPKNVVLRLA	VKFFPPDPGQ	LQEEYTRYLF	ALQLKRDLLE	ERLTCADTTA
170	180	190	200	210	220	230	240
ALLTSHLLQS	EIGDYDETLD	REHLKVNEYL	PGQQHCLEKI	LEFHQKHVGQ	TPAESDFQVL	EIARKLEMYG	IRFHMASDRE
250	260	270	280	290	300	310	320
GTKIQLAVSH	MGVLVFQGTT	KINTFNWSKV	RKLSFKRKRF	LIKLHPEVHG	PYQDTLEFLL	GSRDECKNFW	KICVEYHTFF
330	340	350	360	370	380	390	400
RLLDQPKPKA	KAVFFSRGSS	FRYSGRTQKQ	LVDYFKDSGM	KRIPYERRHS	KTHTSVRALT	ADLPKQSISF	PEGLRTPASP
410	420	430	440	450	460	470	480
SSANAFYSLS	PSTLVPSGLP	EFKDSSSSLT	DPQVSYVKSP	AAERRSGAVA	GGPDTPSAQP	LGPPALQPGP	GLSTKSPQPS
490	500	510	520	530	540	550	560
PSSRKSPLSL	SPAFQVPLGP	AEQGSSPLLS	PVLSDAGGAG	MDCEEPRHKR	VPADEAYFIV	KEILATERTY	LKDLEVITVW
570	580	590	600	610	620	630	640
FRSAVVKEDA	MPATLMTLLF	SNIDPIYEFH	RGFLREVEQR	LALWEGPSKA	HTKGSHQRIG	DILLRNMRQL	KAAHEFTT

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
22	1	1001.9616	-70.42	2	29.6	16.6	2	601-618	R.LALWEGPSKAHTKGSHQR.I	

Detailed Protein Report

Protein 698: pleckstrin homology domain-containing family S member 1 isoform 3 [Homo sapiens]

Accession:	gi|46391075	**Score:**	16.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	41.0
Database Date:	2015-11-30	**pI:**	4.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	4.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEPKPQKSPG	KQFTFSYENE	VCKQDYFIKS	PPSQLFSSVT	SWKKRFFILS	KAGEKSFSLS	YYKDHHHRGS	IEIDQNSSVE
90	100	110	120	130	140	150	160
VGISSQEKMQ	SVQKMFKCHP	DEVMSIRTTN	REYFLIGHDR	EKIKDWVSFM	SSFRQDIKAT	QQNTEEELSL	GNKRTLFYSS
170	180	190	200	210	220	230	240
PLLGPSSTSE	AVGSSSPRNG	LQDKHLMEQS	SPGFRQTHLQ	DLSEATQDVK	EENHYLTPRS	VLLELDNIIA	SSDSGESIET
250	260	270	280	290	300	310	320
DGPDQVSGRI	ECHYEPMESY	FFKETSHESV	DSSKEEPQTL	PETQDGDLHL	QEQGSGIDWC	LSPADVEAQT	TNDQKGSASL
330	340	350	360	370			
TVVQLSILIN	NIPDESQVEK	LNVFLSPPDV	INYLALTEAT	GRI			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
44	1	1001.9591	-47.22	2	29.9	16.6	2	123-138	K.IKDWVSFMSSFRQDIK.A	Oxidation: 8

Detailed Protein Report

Protein 699: heterogeneous nuclear ribonucleoproteins C1/C2 isoform b [Homo sapiens]

Accession:	gi|117190174	**Score:**	16.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	32.3
Database Date:	2015-11-30	**pI:**	4.8
		Sequence Coverage [%]:	6.1
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578825754	refseq_human (refseq_human_20140103.fasta)	PREDICTED: heterogeneous nuclear ribonucleoproteins C1/C2 isoform X3 [Homo sapiens]
gi|578825752	refseq_human (refseq_human_20140103.fasta)	PREDICTED: heterogeneous nuclear ribonucleoproteins C1/C2 isoform X2 [Homo sapiens]
gi|117190254	refseq_human (refseq_human_20140103.fasta)	heterogeneous nuclear ribonucleoproteins C1/C2 isoform b [Homo sapiens]

10	20	30	40	50	60	70	80
MASNVTNKTD	PRSMNSRVFI	GNLNTLVVKK	SDVEAIFSKY	GKIVGCSVHK	GFAFVQYVNE	RNARAAVAGE	DGRMIAGQVL
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
DINLAAEPKV	NRGKAGVKRS	AAEMYGSSFD	LDYDFQRDYY	DRMYSYPARV	PPPPPIARAV	VPSKRQRVSG	NTSRRGKSGF
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
NSKSGQRGSS	KSGKLKGDDL	QAIKKELTQI	KQKVDSLLEN	LEKIEKEQSK	QAVEMKNDKS	EEEQSSSSVK	KDETNVKMES
250	**260**	**270**	**280**	**290**	**300**		
EGGADDSAEE	GDLLDDDDNE	DRGDDQLELI	KDDEKEAEEG	EDDRDSANGE	DDS		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2178	1	1051.4078	-34.41	2	57.4	16.6	0	100-117	R.SAAEMYGSSFDLDYDFQR.D	

Detailed Protein Report

Protein 700: PREDICTED: syntaxin-2 isoform X3 [Homo sapiens]

Accession:	gi|578823407	**Score:**	16.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	30.1
Database Date:	2015-11-30	**pI:**	6.1
		Sequence Coverage [%]:	6.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDDFFHQVEE	IRNSIDKITQ	YVEEVKKNHS	IILSAPNPEG	KIKEELEDLN	KEIKKTANKI	RAKLKAIEQS	FDQDESGNRT
90	100	110	120	130	140	150	160
SVDLRIRRTQ	HSVLSRKFVE	AMAEYNEAQT	LFRERSKGRI	QRQLEITGRT	TTDDELEEML	ESGKPSIFTS	DIISDSQITR
170	180	190	200	210	220	230	240
QALNEIESRH	KDIMKLETSI	RELHEMFMDM	AMFVETQGEM	INNIERNVMN	ATDYVEHAKE	ETKKAIKYQS	KARRKKWIII
250	260	270					
AVSVVLVAII	ALIIGLSVGK						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2713	1	1024.0489	46.45	2	65.1	16.6	1	97-113	R.KFVEAMAEYNEAQTLFR.E	

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Detailed Protein Report

Protein 701: **PREDICTED: peptide chain release factor 1-like, mitochondrial isoform X3 [Homo sapiens]**

Accession:	gi|530383836	**Score:**	16.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	26.4
Database Date:	2015-11-30	**pI:**	10.0
		Sequence Coverage [%]:	7.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MRSRVLWGAA	RWLWPRRAVG	PARRPLSSGS	PPLEELFTRG	GPLRTFLERQ	AGSEAHLKVR	RPELLAVIKL	LNEKERELRE
90	100	110	120	130	140	150	160
TEHLLHDENE	DLRKLAENEI	TLCQKEITQL	KHQIILLLVP	SEETDENDLI	LEVTAGVGGG	LRHASASIGG	SEAYRHMKFE
170	180	190	200	210	220	230	240
GGVHRVQRVP	KTEKQGRVHT	STMTVAILPQ	PTEINLVINP	KDLRIDTKRA	SGAGGQHVNT	TDSAVRIVHL	PTDWK

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1562	1	1051.5516	-26.89	2	49.2	16.6	2	94-111	R.KLAENEITLCQKEITQLK.H	

Detailed Protein Report

Protein 702: homeobox protein unc-4 homolog [Homo sapiens]

Accession:	gi|122937321	**Score:**	16.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	53.7
Database Date:	2015-11-30	**pI:**	6.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	4.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MMDGRLLEHP	HAQFGGSLGG	VVGFPYPLGH	HHVYELAGHQ	LQSAAAAASV	PFSIDGLLGG	SCAAAASVVN	PTPLLPAACG
90	100	110	120	130	140	150	160
VGGDGQPFKL	SDSGDPDKES	PGCKRRRTRT	NFTGWQLEEL	EKAFNESHYP	DVFMREALAL	RLDLVESRVQ	VWFQNRRAKW
170	180	190	200	210	220	230	240
RKKENTKKGP	GRPAHNSHPT	TCSGEPMDPE	EIARKELEKM	EKKKRKHEKK	LLKSQGRHLH	SPGGLSLHSA	PSSDSDSGGG
250	260	270	280	290	300	310	320
GLSPEPPEPP	PPAAKGPGAH	ASGAAGTAPA	PPGEPPAPGT	CDPAFYPSQR	SGAGPQPRPG	RPADKDAASC	GPGAAVAAVE
330	340	350	360	370	380	390	400
RGAAGLPKAS	PFSVESLLSD	SPPRRKAASN	AAAAAAAGLD	FAPGLPCAPR	TLIGKGHFLL	YPITQPLGFL	VPQAALKGGA
410	420	430	440	450	460	470	480
GLEPAPKDAP	PAPAVPPAPP	AQASFGAFSG	PGGAPDSAFA	RRSPDAVASP	GAPAPAPAPF	RDLASAAATE	GGGGDCADAG
490	500	510	520	530	540		
TAGPAPPPPA	PSPRPGPRPP	SPAEEPATCG	VPEPGAAAGP	SPPEGEELDM	D		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2711	1	920.4891	82.07	3	65.1	16.6	0	169-194	K.GPGRPAHNSHPTTCSGEPMDPEEIAR.K	Oxidation: 19

Detailed Protein Report

Protein 703: dnaJ homolog subfamily C member 4 [Homo sapiens]

Accession:	gi|157671935	**Score:**	16.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	27.6
Database Date:	2015-11-30	**pI:**	11.2
Modification(s):	Oxidation	**Sequence Coverage [%]:**	5.0
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 0.89 **CV:** 0.00 % **No. of Peptides:** 1

```
         10         20         30         40         50         60         70         80
MPPLLPLRLC RLWPRNPPSR LLGAAAGQRS RPSTYYELLG VHPGASTEEV KRAFFSKSKE LHPDRDPGNP SLHSRFVELS
         90        100        110        120        130        140        150        160
EAYRVLSREQ SRRSYDDQLR SGSPPKSPRT TVHDKSAHQT HSSWTPPNAQ YWSQFHSVRP QGPQLRQQQH KQNKQVLGYC
        170        180        190        200        210        220        230        240
LLLMLAGMGL HYIAFRKVKQ MHLNFMDEKD RIITAFYNEA RARARANRGI LQQERQRLGQ RQPPPSEPTQ GPEIVPRGAG
        250
P
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
52	1	776.2895	-101.58	2	30.3	16.6	1	178-189	K.VKQMHLNFMDEK.D	Oxidation: 4, 9	MD:MU	0.89

Detailed Protein Report

Protein 704: **PREDICTED: mitogen-activated protein kinase kinase kinase 12 isoform X5 [Homo sapiens]**

Accession:	gi|578824204	**Score:**	16.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	82.6
Database Date:	2015-11-30	**pI:**	6.2
		Sequence Coverage [%]:	2.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MIGKAYSTEH	KQQQEDLWEV	PFEEILDLQW	VGSGAQGAVF	LGRFHGEEVA	VKKVRDLKET	DIKHLRKLKH	PNIITFKGVC
90	100	110	120	130	140	150	160
TQAPCYCILM	EFCAQGQLYE	VLRAGRPVTP	SLLVDWSMGI	AGGMNYLHLH	KIIHRDLKSP	NMLITYDDVV	KISDFGTSKE
170	180	190	200	210	220	230	240
LSDKSTKMSF	AGTVAWMAPE	VIRNEPVSEK	VDIWSFGVVL	WELLTGEIPY	KDVDSSAIIW	GVGSNSLHLP	VPSSCPDGFK
250	260	270	280	290	300	310	320
ILLRQCWNSK	PRNRPSFRQI	LLHLDIASAD	VLSTPQETYF	KSQAEWREEV	KLHFEKIKSE	GTCLHRLEEE	LVMRRREELR
330	340	350	360	370	380	390	400
HALDIREHYE	RKLERANNLY	MELNALMLQL	ELKERELLRR	EQALERRCPG	LLKPHPSRGL	LHGNTMEKLI	KKRNVPQKLS
410	420	430	440	450	460	470	480
PHSKRPDILK	TESLLPKLDA	ALSGVGLPGC	PKGPPSPGRS	RRGKTRHRKA	SAKGSCGDLP	GLRTAVPPHE	PGGPGSPGGL
490	500	510	520	530	540	550	560
GGGPSAWEAC	PPALRGLHHD	LLLRKMSSSS	PDLLSAALGS	RGRGATGGAG	DPGSPPPARG	DTPPSEGSAP	GSTSPDSPGG
570	580	590	600	610	620	630	640
AKGEPPPPVG	PGEGVGLLGT	GREGTSGRGG	SRAGSQHLTP	AALLYRAAVT	RSQKRGISSE	EEEGEVDSEV	ELTSSQRWPQ
650	660	670	680	690	700	710	720
SLNMRQSLST	FSSENPSDGE	EGTASEPSPS	GTPEVGSTNT	DERPDERSDD	MCSQGSEIPL	DPPPSEVIPG	PEPSSLPIPH
730	740	750	760				
QELLRERGPP	NSEDSDCDST	ELDNSNSVDA	LRPPASLPP				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1424	1	699.3669	-13.78	2	47.6	16.5	0	418-432	K.LDAALSGVGLPGCPK.G	

Detailed Protein Report

Protein 705: ephrin type-A receptor 6 isoform b [Homo sapiens]

Accession:	gi|27734955	**Score:**	16.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	37.3
Database Date:	2015-11-30	**pI:**	9.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	4.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MKDSPFQVTK	LYWLNEKWDF	IASASDMAAE	QGQILVIATA	AVGGFTLLVI	LTLFFLITGR	CQWYIKAKMK	SEEKRRNHLQ
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
NGHLRFPGIK	TYIDPDTYED	PSLAVHEFAK	EIDPSRIRIE	RVIGAGEFGE	VCSGRLKTPG	KREIPVAIKT	LKGGHMDRQR
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
RDFLREASIM	GQFDHPNIIR	LEGVVTKRSF	PAIGVEAFCP	SFLRAGFLNS	IQAPHPVPGG	GSLPPRIPAG	RPVMIVVEYM
250	**260**	**270**	**280**	**290**	**300**	**310**	**320**
ENGSLDSFLR	KHDGHFTVIQ	LVGMLRGIAS	GMKYLSDMGY	VHRDLAARNI	LVNSNLVCKV	SDFGLSRVLE	DDPEAAYTTT
330	**340**						
DLFQTLTLNL	CYSA						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2662	1	933.9882	-16.89	2	64.5	16.5	1	251-266	R.KHDGHFTVIQLVGMLR.G	Oxidation: 14

Detailed Protein Report

Protein 706: MYCBP-associated protein [Homo sapiens]

Accession:	gi|203098334	**Score:**	16.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	111.9
Database Date:	2015-11-30	**pI:**	9.1
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MRAPARGTGC	CGRSGGRWLA	GAAQPRCLWA	GGAGQRFMVP	GGTMKSLKKD	SRLRITPTRL	LEASENVKEK	KRAKGPEQPT
90	100	110	120	130	140	150	160
PTIQEEPEPV	SNVLQGDDIL	ALAIKKEDLK	EQHIPRLTEK	EDKRVITQKF	IIRKLKPMDP	RRKVCHLVAR	PANPDEATKP
170	180	190	200	210	220	230	240
LDYSGPGDSF	DGSDQILPHH	ILGSLQDFKR	IALARGNTQL	AERIPTSPCL	MTLISAEGES	KQKAPKEEKR	PPWAPPPQHN
250	260	270	280	290	300	310	320
FLKNWQRNTA	LRKKQQEALS	EHLKKPVSEL	LMHTGETYRR	IQEERELIDC	TLPTRRDRKS	WENSGFWSRL	EYLGDEMTGL
330	340	350	360	370	380	390	400
VMTKTKTQRG	LMEPITHIRK	PHSIRVETGL	PAQRDASYRY	TWDRSLFLIY	RRKELQRIME	ELDFSQQDID	GLEVVGKGWP
410	420	430	440	450	460	470	480
FSAVTVEDYT	VFERSQGSSS	EDTAYLGTLA	SSSDVSMPIL	GPSLLFCGKP	ACWIRGSNPQ	DKRQVGIAAH	LTFETLEGEK
490	500	510	520	530	540	550	560
TSSELTVVNN	GTVAIWYDWR	RQHQPDTFQD	LKKNRMQRFY	FDNREGVILP	GEIKTFTFFF	KSLTAGVFRE	FWEFRTHPTL
570	580	590	600	610	620	630	640
LGGAILQVNL	HAVSLTQDVF	EDERKVLESK	LTAHEAVTVV	REVLQELLMG	VLTPERTPSP	VDAYLTEEDL	FRHRNPPLHY
650	660	670	680	690	700	710	720
EHQVVQSLHQ	LWRQYMTLPA	KAEEARPGDK	EHVSPIATEK	ASVNAELLPR	FRSPISETQV	PRPENEALRE	SGSQKARVGT
730	740	750	760	770	780	790	800
KSPQRKSIME	EILVEESPDV	DSTKSPWEPD	GLPLLEWNLC	LEDFRKAVMV	LPDENHREDA	LMRLNKAALE	LCQKPRPLQS
810	820	830	840	850	860	870	880
NLLHQMCLQL	WRDVIDSLVG	HSMWLRSVLG	LPEKETIYLN	VPEEQDQKSP	PIMEVKVPVG	KAGKEERKGA	AQEKKQLGIK
890	900	910	920	930	940	950	960
DKEDKKGAKL	LGKEDRPNSK	KHKAKDDKKV	IKSASQDRFS	LEDPTPDIIL	SSQEPIDPLV	MGKYTQSLHS	EVRGLLDTLV
970	980	990					
TDLMVLADEL	SPIKNVEEAL	RLCR					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1353	2	676.3577	69.54	2	46.5	16.4	2	1-13	-.MRAPARGTGCCGR.S	Oxidation: 1

Detailed Protein Report

Protein 707: **PREDICTED: peroxisome proliferator-activated receptor alpha isoform X8 [Homo sapiens]**

Accession:	gi|578837284	**Score:**	16.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	28.2
Database Date:	2015-11-30	**pI:**	6.1
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	5.8
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 1.18 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MVDTESPLCP LSPLEAGDLE SPLSEEFLQE MGNIQEISQS IGEDSSGSFG FTEYQYLGSC PGSDGSVITD TLSPASSPSS
        90        100        110        120        130        140        150        160
VTYPVVPGSV DESPSGALNI ECRICGDKAS GYHYGVHACE GCKGFFRRTI RLKLVYDKCD RSCKIQKKNR NKCQYCRFHK
       170        180        190        200        210        220        230        240
CLSVGMSHNA IRFGRMPRSE KAKLKAEILT CEHDIEDSET ADLKSLAKRI YEAYLKNFNM NKVKARVILS GKASNNPVGV
       250        260
CGCSGFSWQH GTSVVEDD
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
10	1	819.8432	0.15	2	29.6	16.4	0	109-123	K.ASGYHYGVHACEGCK.G	Carbamidomethyl: 11	MD:MU 1.18

Detailed Protein Report

Protein 708: glycine N-methyltransferase [Homo sapiens]

Accession:	gi|9506741	**Score:**	16.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	32.7
Database Date:	2015-11-30	**pI:**	6.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	8.1
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MVDSVYRTRS LGVAAEGLPD QYADGEAARV WQLYIGDTRS RTAEYKAWLL GLLRQHGCQR VLDVACGTGV DSIMLVEEGF
        90        100        110        120        130        140        150        160
SVTSVDASDK MLKYALKERW NRRHEPAFDK WVIEEANWMT LDKDVPQSAE GGFDAVICLG NSFAHLPDCK GDQSEHRLAL
       170        180        190        200        210        220        230        240
KNIASMVRAG GLLVIDHRNY DHILSTGCAP PGKNIYYKSD LTKDVTTSVL IVNNKAHMVT LDYTVQVPGA GQDGSPGLSK
       250        260        270        280        290        300
FRLSYYPHCL ASFTELLQAA FGGKCQHSVL GDFKPYKPGQ TYIPCYFIHV LKRTD
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1352	1	926.2202	91.62	3	46.5	16.4	1	241-264	K.FRLSYYPHCLASFTELLQAAFGGK.C	Carbamidomethyl: 9

Detailed Protein Report

Protein 709: caytaxin [Homo sapiens]

Accession:	gi|29336043	**Score:**	16.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	42.1
Database Date:	2015-11-30	**pI:**	4.4
		Sequence Coverage [%]:	2.7
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 1.44 **CV:** 0.00 % **No. of Peptides:** 1

```
         10         20         30         40         50         60         70         80
MGTTEATLRM ENVDVKEEWQ DEDLPRPLPE ETGVELLGSP VEDTSSPPNT LNFNGAHRKR KTLVAPEINI SLDQSEGSLL
         90        100        110        120        130        140        150        160
SDDFLDTPDD LDINVDDIET PDETDSLEFL GNGNELEWED DTPVATAKNM PGDSADLFGD GTTEDGSAAN GRLWRTVIIG
        170        180        190        200        210        220        230        240
EQEHRIDLHM IRPYMKVVTH GGYYGEGLNA IIVFAACFLP DSSLPDYHYI MENLFLYVIS SLELLVAEDY MIVYLNGATP
        250        260        270        280        290        300        310        320
RRRMPGIGWL KKCYQMIDRR LRKNLKSLII VHPSWFIRTV LAISRPFISV KFINKIQYVH SLEDLEQLIP MEHVQIPDCV
        330        340        350        360        370        380
LQYEEERLKA RRESARPQPE FVLPRSEEKP EVAPVENRSA LVSEDQETSM S
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
518	1	593.2066	-241.45	2	36.1	16.4	2	243-252	R.RMPGIGWLKK.C		MD:MU 1.44

Detailed Protein Report

Protein 710: voltage-dependent R-type calcium channel subunit alpha-1E isoform 2 [Homo sapiens]

Accession:	gi|329663531	**Score:**	16.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	254.4
Database Date:	2015-11-30	**pI:**	9.3
Modification(s):	Oxidation	**Sequence Coverage [%]:**	0.8
		No. of unique 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
2194	1	973.4542	-4.91	2	57.6	16.3	1	734-750	K.EVSPMSAPNMPSIERER.R	Oxidation: 10

Detailed Protein Report

Protein 711: PREDICTED: collagen alpha-2(IX) chain isoform X1 [Homo sapiens]

Accession:	gi|530361823	**Score:**	16.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	56.3
Database Date:	2015-11-30	**pI:**	10.0
		Sequence Coverage [%]:	3.5
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 3.30 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MGIPGVKGQP	GLPGPPGLPG	PGFAGPPGPP	GPVGLPGEIG	IRGPKGDPGP	DGPSGPPGPP	GKPGRPGTIQ	GLEGSADFLC
90	100	110	120	130	140	150	160
PTNCPPGMKG	PPGLQGVKGH	AGKRGILGDP	GHQGKPGPKG	DVGASGEQGI	PGPPGPQGIR	GYPGMAGPKG	ETGPHGYKGM
170	180	190	200	210	220	230	240
VGAIGATGPP	GEEGPRGPPG	RAGEKGDEGS	PGIRGPQGIT	GPKGATGPPG	INGKDGTPGT	PGMKGSAGQA	GQPGSPGHQG
250	260	270	280	290	300	310	320
LAGVPGQPGT	KGGPGDQGEP	GPQGLPGFSG	PPGKEGEPGP	RGEIGPQGIM	GQKGDQGERG	PVGQPGPQGR	QGPKGEQGPP
330	340	350	360	370	380	390	400
GIPGPQGLPG	VKGDKGSPGK	TGPRGKVGDP	GVAGLPGEKG	EKGESGEPGP	KGQQGVRGEP	GYPGPSGDAG	APGVQGYPGP
410	420	430	440	450	460	470	480
PGPRGLAGNR	GVPGQPGRQG	VEGRDATDQH	IVDVALKMLQ	EQLAEVAVSA	KREALGAVGM	MGPPGPPGPP	GYPGKQGPHG
490	500	510	520	530	540	550	560
HPGPRGVPGI	VGAVGQIGNT	GPKGKRGEKG	DPGEVGRGHP	GMPGPPGIPG	LPGRPGQAIN	GKDGDRGSPG	APGEAGRPGL
570	580	590	600				
PGPVGLPGFC	EPAACLGASA	YASARLTEPG	SIKGP				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2440	1	973.3563	-137.30	2	60.4	16.3	0	120-140	K. GDVGASGEQGIPGPPGPQGIR. G		MD:MU 3.30

Detailed Protein Report

Protein 712: UPF0711 protein C18orf21 isoform b [Homo sapiens]

Accession:	gi|319918862	**Score:**	16.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	14.5
Database Date:	2015-11-30	**pI:**	11.8
		Sequence Coverage [%]:	9.8
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578832731	refseq_human (refseq_human_20140103.fasta)	PREDICTED: UPF0711 protein C18orf21 isoform X2 [Homo sapiens]
gi|319918866	refseq_human (refseq_human_20140103.fasta)	UPF0711 protein C18orf21 isoform b [Homo sapiens]

10	20	30	40	50	60	70	80
MVKKFKDSKS	VLLITCKTCN	RTVKHHGKSR	SFVSTLKSNP	ATPTSKLSLK	TPERRTANPN	HDMSGSKGKS	PASVFRTPTS
90	100	110	120	130	140		
GQSVSTCSSK	NTSKTKKHFS	QLKMLLSQNE	SQKIPKVDFR	NFLSSLKGGL	LK		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2557	1	741.5671	193.81	2	62.4	16.3	2	5-17	K.FKDSKSVLLITCK.T	

Detailed Protein Report

Protein 713: zinc finger protein 502 [Homo sapiens]

Accession:	gi|21361857	**Score:**	16.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	62.9
Database Date:	2015-11-30	**pI:**	10.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.5
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578806699	refseq_human (refseq_human_20140103.fasta)	PREDICTED: zinc finger protein 502 isoform X1 [Homo sapiens]
gi|544583446	refseq_human (refseq_human_20140103.fasta)	zinc finger protein 502 [Homo sapiens]
gi|197313746	refseq_human (refseq_human_20140103.fasta)	zinc finger protein 502 [Homo sapiens]
gi|197313744	refseq_human (refseq_human_20140103.fasta)	zinc finger protein 502 [Homo sapiens]
gi|197313742	refseq_human (refseq_human_20140103.fasta)	zinc finger protein 502 [Homo sapiens]

10	20	30	40	50	60	70	80
MLNMQGAEER	DIRRETCPGW	VNKNKPALEQ	DVCKIDSSGI	VVKRFQEDEY	QDSTFEEKYA	CEGMKENSPR	EIAESCLFQE
90	100	110	120	130	140	150	160
GGFGRITFIH	KEAPPEIISQ	GYNFEKSLLL	TSSLVTRLRV	STEESLHQWE	TSNIQTNDIS	DQSKCPTLCT	QKKSWKCNEC
170	180	190	200	210	220	230	240
GKTFTQSSSL	TQHQRTHTGE	RPYTCEECGK	AFSRSSFLVQ	HQRIHTGVKP	YGCEQCGKTF	RCRSFLTQHQ	RIHTGEKPYK
250	260	270	280	290	300	310	320
CNECGNSFRN	HSHLTEHQRI	HTGEKPYKCN	RCGKAFNQNT	HLIHHQRIHT	GEKPYICSEC	GSSFRKHSNL	TQHQRIHTGE
330	340	350	360	370	380	390	400
KPHKCDECGK	TFQTKANLSQ	HQRIHSGEKP	YKCKECGKAF	CQSPSLIKHQ	RIHTGEKPYK	CKECGKAFTQ	STPLTKHQRI
410	420	430	440	450	460	470	480
HTGERPYKCS	ECGKAFIQSI	CLIRHQRSHT	GEKPYKCNEC	GKGFNQNTCL	TQHMRIHTGE	KPYKCKECGK	AFAHSSSLTE
490	500	510	520	530	540	550	
HHRTHTGEKL	YKCSECEKTF	RKYAHLSEHY	RIHTGEKPYE	CIECGKFFRH	SSVLFRHQKL	HSGD	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2143	1	797.8056	108.87	3	57.0	16.3	2	269-287	K.CNRCGKAFNQNTHLIHHQR.I	Carbamidomethyl: 1, 4

Detailed Protein Report

Protein 714: inositol hexakisphosphate kinase 1 isoform 2 [Homo sapiens]

Accession:	gi|55769518	**Score:**	16.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	31.5
Database Date:	2015-11-30	**pI:**	9.7
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	8.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLDGNSGLSS	EKISHNPWSL	RCHKQQLSRM	RSESKDRKLY	KFLLLENVVH	HFKYPCVLDL	KMGTRQHGDD	ASAEKAARQM
90	100	110	120	130	140	150	160
RKCEQSTSAT	LGVRVCGMQV	YQLDTGHYLC	RNKYYGRGLS	IEGFRNALYQ	YLHNGLDLRR	DLFEPILSKL	RGLKAVLERQ
170	180	190	200	210	220	230	240
ASYRFYSSSL	LVIYDGKECR	AESCLDRRSE	MRLKHLDMVL	PEVASSCGPS	TSPSNTSPEA	GPSSQPKVDV	RMIDFAHSTF
250	260	270	280				
KGFRDDPTVH	DGPDRGYVFG	LENLISIMEQ	MRDENQ				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1510	1	982.5936	72.36	3	48.6	16.3	2	42-65	K.FLLLENVVHHFKYPCVLDLKMGTR.Q	Carbamidomethyl: 15; Oxidation: 21

Detailed Protein Report

Protein 715: **apoptosis regulatory protein Siva isoform 2 [Homo sapiens]**

Accession:	gi|11277470	**Score:**	16.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	11.8
Database Date:	2015-11-30	**pI:**	9.3
		Sequence Coverage [%]:	14.5
		No. of unique Peptides:	1

```
         10         20         30         40         50         60         70         80
MPKRSCPFAD VAPLQLKVRV SQRELSRGVC AERYSQEVFD PSGVASIACS SCVRAVDGKA VCGQCERALC GQCVRTCWGC
         90        100        110        120
GSVACTLCGL VDCSDMYEKV LCTSCAMFET
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2602	1	885.4491	-46.37	2	62.6	16.2	2	2-17	M.PKRSCPFADVAPLQLK.V	

Detailed Protein Report

Protein 716: apolipoprotein B-100 precursor [Homo sapiens]

Accession:	gi|105990532	**Score:**	16.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	515.2
Database Date:	2015-11-30	**pI:**	6.6
		Sequence Coverage [%]:	0.2
		No. of unique Peptides:	1

Quantitation

MD:MU	**Median:** 2.69	**CV:** 0.00 %	**No. of Peptides:** 1

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

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
353	1	559.1708	-266.41	2	34.1	16.2	1	3690-3699	K.LDVTTSIGRR.Q		MD:MU 2.69

Detailed Protein Report

Protein 717: pre-mRNA-splicing factor CWC22 homolog [Homo sapiens]

Accession:	gi|55749769	**Score:**	16.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	105.4
Database Date:	2015-11-30	**pI:**	6.6
		Sequence Coverage [%]:	1.5
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530370697	refseq_human (refseq_human_20140103.fasta)	PREDICTED: pre-mRNA-splicing factor CWC22 homolog isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MKSSVAQIKP	SSGHDRRENL	NSYQRNSSPE	DRYEEQERSP	RDRDYFDYSR	SDYEHSRRGR	SYDSSMESRN	RDREKRRERE
90	100	110	120	130	140	150	160
RDTDRKRSRK	SPSPGRRNPE	TSVTQSSSAQ	DEPATKKKKD	ELDPLLTRTG	GAYIPPAKLR	MMQEQITDKN	SLAYQRMSWE
170	180	190	200	210	220	230	240
ALKKSINGLI	NKVNISNISI	IIQELLQENI	VRGRGLLSRS	VLQAQSASPI	FTHVYAALVA	IINSKFPQIG	ELILKRLILN
250	260	270	280	290	300	310	320
FRKGYRRNDK	QLCLTASKFV	AHLINQNVAH	EVLCLEMLTL	LLERPTDDSV	EVAIGFLKEC	GLKLTQVSPR	GINAIFERLR
330	340	350	360	370	380	390	400
NILHESEIDK	RVQYMIEVMF	AVRKDGFKDH	PIILEGLDLV	EEDDQFTHML	PLEDDYNPED	VLNVFKMDPN	FMENEEKYKA
410	420	430	440	450	460	470	480
IKKEILDEGD	TDSNTDQDAG	SSEEDEEEEE	EEGEEDEEGQ	KVTIHDKTEI	NLVSFRRTIY	LAIQSSLDFE	ECAHKLLKME
490	500	510	520	530	540	550	560
FPESQTKELC	NMILDCCAQQ	RTYEKFFGLL	AGRFCMLKKE	YMESFEGIFK	EQYDTIHRLE	TNKLRNVAKM	FAHLLYTDSL
570	580	590	600	610	620	630	640
PWSVLECIKL	SEETTTSSSR	IFVKIFFQEL	CEYMGLPKLN	ARLKDETLQP	FFEGLLPRDN	PRNTRFAINF	FTSIGLGGLT
650	660	670	680	690	700	710	720
DELREHLKNT	PKVIVAQKPD	VEQNKSSPSS	SSSASSSSES	DSSDSDSDSS	DSSSESSSEE	SDSSSISSHS	SASANDVRKK
730	740	750	760	770	780	790	800
GHGKTRSKEV	DKLIRNQQTN	DRKQKERRQE	HGHQETRTER	ERRSEKHRDQ	NSSGSNWRDP	ITKYTSDKDV	PSERNNYSRV
810	820	830	840	850	860	870	880
ANDRDQEMHI	DLENKHGDPK	KKRGERRNSF	SENEKHTHRI	KDSENFRRKD	RSKSKEMNRK	HSGSRSDEDR	YQNGAERRWE
890	900	910					
KSSRYSEQSR	ESKKNQDRRR	EKSPAKQK					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
844	1	820.2213	-164.89	2	40.1	16.2	0	488-501	K.ELCNMILDCCAQQR.T	

Detailed Protein Report

Protein 718: **PREDICTED: probable global transcription activator SNF2L1 isoform X5 [Homo sapiens]**

Accession:	gi|578838748	**Score:**	16.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	121.1
Database Date:	2015-11-30	**pI:**	9.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEQDTAAVAA	TVAAADATAT	IVVIEDEQPG	PSTSQEEGAA	AAATEATAAT	EKGEKKKEKN	VSSFQLKLAA	KAPKSEKEMD
90	100	110	120	130	140	150	160
PEYEEKMKAD	RAKRFEFLLK	QTELFAHFIQ	PSAQKSPTSP	LNMKLGRPRI	KKDEKQSLIS	AGDYRHRRTE	QEEDEELLSE
170	180	190	200	210	220	230	240
SRKTSNVCIR	FEVSPSYVKG	GPLRDYQIRG	LNWLISLYEN	GVNGILADEM	GLGKTLQTIA	LLGYLKHYRN	IPGPHMVLVP
250	260	270	280	290	300	310	320
KSTLHNWMNE	FKRWVPSLRV	ICFVGDKDAR	AAFIRDEMMP	GEWDVCVTSY	EMVIKEKSVF	KKFHWRYLVI	DEAHRIKNEK
330	340	350	360	370	380	390	400
SKLSEIVREF	KSTNRLLLTG	TPLQNNLHEL	WALLNFLLPD	VFNSADDFDS	WFDTKNCLGD	QKLVERLHAV	LKPFLLRRIK
410	420	430	440	450	460	470	480
TDVEKSLPPK	KEIKIYLGLS	KMQREWYTKI	LMKDIDVLNS	SGKMDKMRLL	NILMQLRKCC	NHPYLFDGAE	PGPPYTTDEH
490	500	510	520	530	540	550	560
IVSNSGKMVV	LDKLLAKLKE	QGSRVLIFSQ	MTRLLDILED	YCMWRGYEYC	RLDGQTPHEE	REEAIEAFNA	PNSSKFIFML
570	580	590	600	610	620	630	640
STRAGGLGIN	LASADVVILY	DSDWNPQVDL	QAMDRAHRIG	QKKPVRVFRL	ITDNTVEERI	VERAEIKLRL	DSIVIQQGRL
650	660	670	680	690	700	710	720
IDQQSNKLAK	EEMLQMIRHG	ATHVFASKES	ELTDEDITTI	LERGEKKTAE	MNERLQKMGE	SSLRNFRMDI	EQSLYKFEGE
730	740	750	760	770	780	790	800
DYREKQKLGM	VEWIEPPKRE	RKANYAVDAY	FREALRVSEP	KIPKAPRPPK	QPNVQDFQFF	PPRLFELLEK	EILYYRKTIG
810	820	830	840	850	860	870	880
YKVPRNPDIP	NPALAQREEQ	KKIDGAEPLT	PEETEEKEKL	LTQGFTNWTK	RDFNQFIKAN	EKYGRDDIDN	IAREVEGKSP
890	900	910	920	930	940	950	960
EEVMEYSAVF	WERCNELQDI	EKIMAQIERG	EARIQRRISI	KKALDAKIAR	YKAPFHQLRI	QYGTSKGKNY	TEEEDRFLIC
970	980	990	1000	1010	1020	1030	1040
MLHKMGFDRE	NVYEELRQCV	RNAPQFRFDW	FIKSRTAMEF	QRRCNTLISL	IEKENMEIEE	RERAEKKKRA	TKTPMVKFSA
1050							
FS							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1545	1	765.2820	-48.68	2	49.2	16.1	1	75-86	K.SEKEMDPEYEEK.M	Oxidation: 5

Detailed Protein Report

Protein 719: **PREDICTED: exonuclease 3'-5' domain-containing protein 2 isoform X4 [Homo sapiens]**

Accession:	gi|530404104	**Score:**	16.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	42.3
Database Date:	2015-11-30	**pI:**	9.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLRLSQRTRN	SPGEKNDDHS	SWRKVLEKCQ	GVVDIPFRSK	GMSRLGEEVN	GEATESQQKP	RNKKSKMDGM	VPGNHQGRDP
90	100	110	120	130	140	150	160
RKHKRKPLGV	GYSARKSPLY	DNCFLHAPDG	QPLCTCDRRK	AQWYLDKGIG	ELVSEEPFVV	KLRFEPAGRP	ESPGDYYLMV
170	180	190	200	210	220	230	240
KENLCVVCGK	RDSYIRKNVI	PHEYRKHFPI	EMKDHNSHDV	LLLCTSCHAI	SNYYDNHLKQ	QLAKEFQAPI	GSEEGLRLLE
250	260	270	280	290	300	310	320
DPERRQVRSG	ARALLNAESL	PTQRKEELLQ	ALREFYNTDV	VTEEMLQEAA	SLETRISNEN	YVPHGLKVVQ	CHSQGGLRSL
330	340	350	360	370			
MQLESRWRQH	FLDSMQPKHL	PQQWSVDHNH	QKLLRKFGED	LPIQLS			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1568	1	917.7517	323.46	1	49.3	16.1	0	187-193	K.HFPIEMK.D	Oxidation: 6

Detailed Protein Report

Protein 720: PREDICTED: keratin, type I cuticular Ha4-like [Homo sapiens]

Accession: gi|341916344
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 16.1
MW [kDa]: 49.4
pI: 4.9
Sequence Coverage [%]: 6.4
No. of unique Peptides: 1

```
        10         20         30         40         50         60         70         80
MLYAKPPPTI NGIKGLQRKE RLKPAHIHLQ QLTCFSITCS STMSYSCCLP SLGCRTSCSS RPCVPPSCHG YTLPGACNIP
        90        100        110        120        130        140        150        160
ANVSNCNWFC EGSFNGSEKE TMQFLNDRLA SYLEKVRQLE RDNAELEKLI QERSQQQEPL LCPSYQSYFK TIEELQQKIL
       170        180        190        200        210        220        230        240
CAKAENARLV VNIDNAKLAS DDFRSKYQTE QSLRLLVESD INSIRRILDE LTLCKSDLES QVESLREELI CLKKNHEEEV
       250        260        270        280        290        300        310        320
NTLRSQLGDR LNVEVDTAPT VDLNQVLNET RSQYEALVET NRREVEQWFA TQTEELNKQV VSSSEQLQSC QAEIIELRRT
       330        340        350        360        370        380        390        400
VNALEIELQA QHNLRDSLEN TLTESEAHYS SQLSQVQSLI TNVESQLAEI RCDLERQNQE YQVLLDVRAR LECEINTYRS
       410        420        430        440
LLESEDCKLP CNPCATTNAS GNSCGPCGTS QKGCCN
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1092	2	991.6375	-83.74	3	43.3	16.1	1	409-436	K.LPCNPCATTNASGNSCGPCGTSQKGCCN.-	Carbamidomethyl: 3, 6, 16, 19, 27

Detailed Protein Report

Protein 721: **PREDICTED: WD repeat-containing protein 70 isoform X2 [Homo sapiens]**

Accession:	gi|578809933	**Score:**	16.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	43.2
Database Date:	2015-11-30	**pI:**	4.8
		Sequence Coverage [%]:	6.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MERSGPSEVT	GSDASGPDPQ	LAVTMGFTGF	GKKARTFDLE	AMFEQTRRTA	VERSRKTLEA	REKEEEMNRE	KELRRQNEDI
90	100	110	120	130	140	150	160
EPTSSRSNVV	RDCSKSSSRD	TSSSESEQSS	DSSDDELIGP	PLPPKMVGKP	VNFMEEDILG	PLPPPLNEEE	EEAEEEEEEE
170	180	190	200	210	220	230	240
EEEENPVHKI	PDSHEITLKH	GTKTVSALGL	DPSGARLVTG	GYDYDVKFWD	FAGMDASFKA	FRSLQPCECH	QIKSLQYSNT
250	260	270	280	290	300	310	320
GDMILVVSGS	SQAKVIDRDG	FEVMECIKGD	QYIVDMANTK	GHTAMLHTGS	WHPKIKGEFM	TCSNDATVRT	WEVENPKKQK
330	340	350	360	370	380	390	
SVFKPRTMQG	KKVIPTTCTY	SRDGNLIAAA	CQNGSIQIWD	RNLTSNKLRL	SYGTVCMLWA	HTEVCVM	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1703	1	901.3942	-60.47	3	51.1	16.1	1	343-367	R.DGNLIAAACQNGSIQIWDRNLTSNK.L	

Detailed Protein Report

Protein 722: BRCA1-associated RING domain protein 1 isoform 2 [Homo sapiens]

Accession:	gi|543583787	**Score:**	16.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	84.5
Database Date:	2015-11-30	**pI:**	9.9
		Sequence Coverage [%]:	2.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPDNRQPRNR	QPRIRSGNEP	RSAPAMEPDG	RGAWAHSRAA	LDRLEKLLRC	SRCNCVSDCI	GTGCPVCYTP	AWIQDLKINR
90	100	110	120	130	140	150	160
QLDSMIQLCS	KLRNLLHDNE	LSDLKEDKPR	KSLFNDAGNK	KNSIKMWFSP	RSKKVRYVVS	KASVQTQPAI	KKDASAQQDS
170	180	190	200	210	220	230	240
YEFVSPSPPA	DVSERAKKAS	ARSGKKQKKK	TLAEINQKWN	LEAEKEDGEF	DSKEESKQKL	VSFCSQPSVI	SSPQINGEID
250	260	270	280	290	300	310	320
LLASGSLTES	ECFGSLTEVS	LPLAEQIESP	DTKSRNEVVT	PEKVCKNYLT	SKKSLPLENN	GKRGHHNRLS	SPISKRCRTS
330	340	350	360	370	380	390	400
ILSTSGDFVK	QTVPSENIPL	PECSSPPSCK	RKVGGTSGRK	NSNMSDEFIS	LSPGTPPSTL	SSSSYRRVMS	SPSAMKLLPN
410	420	430	440	450	460	470	480
MAVKRNHRGE	TLLHIASIKG	DIPSVEYLLQ	NGSDPNVKDH	AGWTPLHEAC	NHGHLKVVEL	LLQHKALVNT	TGYQNDSPLH
490	500	510	520	530	540	550	560
DAAKNGHVDI	VKLLLSYGAS	RNAVNIFGLR	PVDYTDDESM	KSLLLLPEKN	ESSSASHCSV	MNTGQRRDGP	LVLIGSGLSS
570	580	590	600	610	620	630	640
EQQKMLSELA	VILKAKKYTE	FDSTVTHVVV	PGDAVQSTLK	CMLGILNGCW	ILKFEWVKAC	LRRKVCEQEE	KYEIPEGPRR
650	660	670	680	690	700	710	720
SRLNREQLLP	KLFDGCYFYL	WGTFKHHPKD	NLIKLVTAGG	GQILSRKPKP	DSDVTQTINT	VAYHARPDSD	QRFCTQYIIY
730	740	750	760				
EDLCNYHPER	VRQGKVWKAP	SSWFIDCVMS	FELLPLDS				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2243	1	1022.9437	-67.63	2	58.3	16.1	0	420-438	K.GDIPSVEYLLQNGSDPNVK.D	

Detailed Protein Report

Protein 723: PREDICTED: putative zinc finger protein 66-like [Homo sapiens]

Accession:	gi|578846704	**Score:**	16.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	32.7
Database Date:	2015-11-30	**pI:**	10.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	6.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSRNPKNVKN	VAKPLSTPVP	LLHTTHKIIH	TGEKSHKCEE	CGKAFNWSSQ	LAIHKITHTG	EQPYKRKECS	KAFNHPTTPS
90	100	110	120	130	140	150	160
SHKKTHTGEK	PCKCDKCGKA	FIFSSTLSKH	EKIHTGEKPY	KCEECGKAFR	WSSHLTTHKI	THTGEKPYKC	EECGNGFKYS
170	180	190	200	210	220	230	240
STLTEHKIIH	TGEKSYKCEE	CGKAFNWPSQ	LAIHKVTHTG	EQPYKCKECG	KAFKHPATLS	SHNKTHTGEK	PYKCDKCGKA
250	260	270	280	290			
FISSSTLSKH	EKIHTGEKPY	KCEECGKAFN	WSSDFNKHKR	IHSGQKPIL			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2133	1	1045.4499	-1.32	2	56.6	16.1	1	150-167	K.CEECGNGFKYSSTLTEHK.I	Carbamidomethyl: 1

Detailed Protein Report

Protein 724: Krueppel-like factor 12 [Homo sapiens]

Accession:	gi|21071074	**Score:**	16.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	44.2
Database Date:	2015-11-30	**pI:**	10.6
		Sequence Coverage [%]:	5.5
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578824739	refseq_human (refseq_human_20140103.fasta)	PREDICTED: Krueppel-like factor 12 isoform X3 [Homo sapiens]
gi|530402087	refseq_human (refseq_human_20140103.fasta)	PREDICTED: Krueppel-like factor 12 isoform X2 [Homo sapiens]
gi|530402085	refseq_human (refseq_human_20140103.fasta)	PREDICTED: Krueppel-like factor 12 isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MNIHMKRKTI	KNINTFENRM	LMLDGMPAVR	VKTELLESEQ	GSPNVHNYPD	MEAVPLLLNN	VKGEPPEDSL	SVDHFQTQTE
90	100	110	120	130	140	150	160
PVDLSINKAR	TSPTAVSSSP	VSMTASASSP	SSTSTSSSSS	SRLASSPTVI	TSVSSASSSS	TVLTPGPLVA	SASGVGGQQF
170	180	190	200	210	220	230	240
LHIIHPVPPS	SPMNLQSNKL	SHVHRIPVVV	QSVPVVYTAV	RSPGNVNNTI	VVPLLEDGRG	HGKAQMDPRG	LSPRQSKSDS
250	260	270	280	290	300	310	320
DDDDLPNVTL	DSVNETGSTA	LSIARAVQEV	HPSPVSRVRG	NRMNNQKFPC	SISPFSIEST	RRQRRSESPD	SRKRRIHRCD
330	340	350	360	370	380	390	400
FEGCNKVYTK	SSHLKAHRRT	HTGEKPYKCT	WEGCTWKFAR	SDELTRHYRK	HTGVKPFKCA	DCDRSFSRSD	HLALHRRRHM
410							
LV							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1218	1	758.4479	56.96	3	44.8	16.1	1	202-223	R.SPGNVNNTIVVPLLEDGRGHGK.A	

Detailed Protein Report

Protein 725: protein scribble homolog isoform b [Homo sapiens]

Accession:	gi|355390315	**Score:**	16.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	174.8
Database Date:	2015-11-30	**pI:**	4.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLKCIPLWRC	NRHVESVDKR	HCSLQAVPEE	IYRYSRSLEE	LLLDANQLRE	LPKPFFRLLN	LRKLGLSDNE	IQRLPPEVAN
90	100	110	120	130	140	150	160
FMQLVELDVS	RNDIPEIPES	IKFCKALEIA	DFSGNPLSRL	PDGFTQLRSL	AHLALNDVSL	QALPGDVGNL	ANLVTLELRE
170	180	190	200	210	220	230	240
NLLKSLPASL	SFLVKLEQLD	LGGNDLEVLP	DTLGALPNLR	ELWLDRNQLS	ALPPELGNLR	RLVCLDVSEN	RLEELPAELG
250	260	270	280	290	300	310	320
GLVLLTDLLL	SQNLLRRLPD	GIGQLKQLSI	LKVDQNRLCE	VTEAIGDCEN	LSELILTENL	LMALPRSLGK	LTKLTNLNVD
330	340	350	360	370	380	390	400
RNHLEALPPE	IGGCVALSVL	SLRDNRLAVL	PPELAHTTEL	HVLDVAGNRL	QSLPFALTHL	NLKALWLAEN	QAQPMLRFQT
410	420	430	440	450	460	470	480
EDDARTGEKV	LTCYLLPQQP	PPSLEDAGQQ	GSLSETWSDA	PPSRVSVIQF	LEAPIGDEDA	EEAAAEKRGL	QRRATPHPSE
490	500	510	520	530	540	550	560
LKVMKRSIEG	RRSEACPCQP	DSGSPLPAEE	EKRLSAESGL	SEDSRPSAST	VSEAEPEGPS	AEAQGGSQQE	ATTAGGEEDA
570	580	590	600	610	620	630	640
EEDYQEPTVH	FAEDALLPGD	DREIEEGQPE	APWTLPGGRQ	RLIRKDTPHY	KKHFKISKLP	QPEAVVALLQ	GMQPDGEGPV
650	660	670	680	690	700	710	720
APGGWHNGPH	APWAPRAQKE	EEEEEEGSPQ	EEEEEEEEEN	RAEEEEASTE	EEDKEGAVVS	APSVKGVSFD	QANNLLIEPA
730	740	750	760	770	780	790	800
RIEEEELTLT	ILRQTGGLGI	SIAGGKGSTP	YKGDDEGIFI	SRVSEEGPAA	RAGVRVGDKL	LEVNGVALQG	AEHHEAVEAL
810	820	830	840	850	860	870	880
RGAGTAVQMR	VWRERMVEPE	NAVTITPLRP	EDDYSPRERR	GGGLRLPLLP	PESPGPLRQR	HVACLARSER	GLGFSIAGGK
890	900	910	920	930	940	950	960
GSTPYRAGDA	GIFVSRIAEG	GAAHRAGTLQ	VGDRVLSING	VDVTEARHDH	AVSLLTAASP	TIALLLEREA	GGPLPPSPLP
970	980	990	1000	1010	1020	1030	1040
HSSPPTAAVA	TTSITTATPG	VPGLPSLAPS	LLAAALEGPY	PVEEIRLPRA	GGPLGLSIVG	GSDHSSHPFG	VQEPGVFISK
1050	1060	1070	1080	1090	1100	1110	1120
VLPRGLAARS	GLRVGDRILA	VNGQDVRDAT	HQEAVSALLR	PCLELSLLVR	RDPAPPGLRE	LCIQKAPGER	LGISIRGGAR
1130	1140	1150	1160	1170	1180	1190	1200
GHAGNPRDPT	DEGIFISKVS	PTGAAGRDGR	LRVGLRLLEV	NQQSLLGLTH	GEAVQLLRSV	GDTLTVLVCD	GFEASTDAAL
1210	1220	1230	1240	1250	1260	1270	1280
EVSPGVIANP	FAAGIGHRNS	LESISSIDRE	LSPEGPGKEK	ELPGQTLHWG	PEATEAAGRG	LQPLKLDYRA	LAAVPSAGSV
1290	1300	1310	1320	1330	1340	1350	1360
QRVPSGAAGG	KMAESPCSPS	GQQPPSPPSP	DELPANVKQA	YRAFAAVPTS	HPPEDAPAQP	PTPGPAASPE	QLSFRERQKY
1370	1380	1390	1400	1410	1420	1430	1440
FELEVRVPQA	EGPPKRVSLV	GADDLRKMQE	EEARKLQQKR	AQMLREAAEA	GAEARLALDG	ETLGEEEQED	EQPPWASPSP
1450	1460	1470	1480	1490	1500	1510	1520
TSRQSPASPP	PLGGGAPVRT	AKAERRHQER	LRVQSPEPPA	PERALSPAEL	RALEAEKRAL	WRAARMKSLE	QDALRAQMVL
1530	1540	1550	1560	1570	1580	1590	1600
SRSQEGRGTR	GPLERLAEAP	SPAPTPSPTP	VEDLGPQTST	SPGRLSPDFA	EELRSLEPSP	SPGPQEEDGE	VALVLLGRPS
1610	1620	1630	1640				
PGAVGPEDVA	LCSSRRPVRP	GRRGLGPVPS					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
129	1	696.1281	130.45	3	31.3	16.1	2	861-880	R.HVACLARSERGLGFSIAGGK.G	Carbamidomethyl: 4

Detailed Protein Report

Protein 726: **PREDICTED: myosin-7B isoform X1 [Homo sapiens]**

Accession:	gi|578836098	**Score:**	16.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	203.5
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
MAPSLYGLRS GCLQGKAPLR FPAPYICGGG QRLQRHAAQP RQPVHADHQF LATKTGGTLE DQIIEANPAM EAFGNAKTLR
        90        100        110        120        130        140        150        160
NDNSSRFGKF IRIHFGPSGK LASADIDSYL LEKSRVIFQL PGERSYHVYY QILSGRKPEL QDMLLLSMNP YDYHFCSQGV
       170        180        190        200        210        220        230        240
ITVDNMNDGE ELIATDHAMD ILGFSVDEKC ACYKIVGALL HFGNMKFKQK QREEQAEADG TESADKAAYL MGVSSGDLLK
       250        260        270        280        290        300        310        320
GLLHPRVRVG NEYVTKGQSV EQVVFAVGAL AKATYDRLFR WLVSRINQTL DTKLPRQFFI GVLDIAGFEI FEFNSFEQLC
       330        340        350        360        370        380        390        400
INFTNEKLQQ FFNQHMFVLE QEEYKREGID WVFIDFGLDL QPCIDLIEKP LGILSILEEE CMFPKASDAS FRAKLYDNHA
       410        420        430        440        450        460        470        480
GKSPNFQQPR PDKKRKYQAH FEVVHYAGVV PYSIVGWLEK NKDPLNETVV PIFQKSQNRL LATLYENYAG SCSTEPPKSG
       490        500        510        520        530        540        550        560
VKEKRKKAAS FQTVSQLHKE NLNKLMTNLR ATQPHFVRCI VPNENKTPGV MDAFLVLHQL RCNGVLEGIR ICRQGFPNRL
       570        580        590        600        610        620        630        640
LYTDFRQRYR ILNPSAIPDD TFMDSRKATE KLLGSLDLDH TQYQFGHTKV FFKAGLLGVL EELRDQRLAK VLTLLQARSR
       650        660        670        680        690        700        710        720
GRLMRLEYQR LLGGRDALFT IQWNIRAFNA VKNWSWMKLF FKMKPLLRSA QAEEELAALR AELRGLRGAL AAAEAKRQEL
       730        740        750        760        770        780        790        800
EETHVSITQE KNDLALQLQA EQDNLADAEE RCHLLIKSKV QLEGKVKELS ERLEDEEEVN ADLAARRRKL EDECTELKKD
       810        820        830        840        850        860        870        880
IDDLELTLAK AEKEKQATEN KVKNLTEEMA ALDESVARLT KEKKALQEAH QQALGDLQAE EDRVSALTKA KLRLEQQVED
       890        900        910        920        930        940        950        960
LECSLEQEKK LRMDTERAKR KLEGDLKLTQ ESVADAAQDK QQLEEKLKKK DSELSQLSLR VEDEQLLGAQ MQKKIKELQA
       970        980        990       1000       1010       1020       1030       1040
RAEELEEELE AERAARARVE KQRAEAAREL EELSERLEEA GGASAGQREG CRKREAELGR LRRELEEAAL RHEATVAALR
      1050       1060       1070       1080       1090       1100       1110       1120
RKQAEGAAEL GEQVDSLQRV RQKLEKEKSE LRMEVDDLAA NVETLTRAKA SAEKLCRTYE DQLSEAKIKV EELQRQLADA
      1130       1140       1150       1160       1170       1180       1190       1200
STQRGRLQTE SGELSRLLEE KECLISQLSR GKALAAQSLE ELRRQLEEES KAKSALAHAV QALRHDCDLL REQHEEEAEA
      1210       1220       1230       1240       1250       1260       1270       1280
QAELQRLLSK ANAEVAQWRS KYEADAIQRT EELEEAKKKL ALRLQEAEEG VEAANAKCSS LEKAKLRLQT ESEDVTLELE
      1290       1300       1310       1320       1330       1340       1350       1360
RATSAAAALD KKQRHLERAL EERRRQEEEM QRELEAAQRE SRGLGTELFR LRHGHEEALE ALETLKRENK NLQEEISDLT
      1370       1380       1390       1400       1410       1420       1430       1440
DQVSLSGKSI QELEKTKKAL EGEKSEIQAA LEEAEGALEL EETKTLRIQL ELSQVKAEVD RKLAEKDEEC ANLRRNHQRA
      1450       1460       1470       1480       1490       1500       1510       1520
VESLQASLDA ETRARNEALR LKKKMEGDLN DLELQLGHAT RQATEAQAAT RLMQAQLKEE QAGRDEEQRL AAELHEQAQA
      1530       1540       1550       1560       1570       1580       1590       1600
LERRASLLAA ELEELRAALE QGERSRRLAE QELLEATERL NLLHSQNTGL LNQKKKLEAD LAQLSGEVEE AAQERREAEE
      1610       1620       1630       1640       1650       1660       1670       1680
KAKKAITDAA MMAEELKKEQ DTSAHLERMK KTLEQTVREL QARLEEAEQA ALRGGKKQVQ KLEAKVRELE AELDAEQKKH
      1690       1700       1710       1720       1730       1740       1750       1760
AEALKGVRKH ERRVKELAYQ AEEDRKNLAR MQDLVDKLQS KVKSYKRQFE EAEQQANTNL AKYRKAQHEL DDAEERADMA
      1770       1780       1790
ETQANKLRAR TRDALGPKLS LSPQHKE
```

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

	Cmpds.		[ppm]		[min]					
1310	1	939.8664	-147.69	2	46.0	16.1	1	1024-1040	R.ELEEAALRHEATVAALR.R	

Detailed Protein Report

Protein 727: PREDICTED: gem-associated protein 4 isoform X4 [Homo sapiens]

Accession:	gi|530410380	**Score:**	16.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	118.7
Database Date:	2015-11-30	**pI:**	5.8
		Sequence Coverage [%]:	1.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MTILHGGFLL	AEQLFHPKAL	AELTKSDWER	VGRPIVEALR	EISSAAAHSQ	PFAWKKKALI	IIWAKVLQPH	PVTPSDTETR
90	100	110	120	130	140	150	160
WQEDLFFSVG	NMIPTINHTI	LFELLKSLEA	SGLFIQLLMA	LPTTICHAEL	ERFLEHVTVD	TSAEDVAFFL	DVWWEVMKHK
170	180	190	200	210	220	230	240
GHPQDPLLSQ	FSAMAHKYLP	ALDEFPHPPK	RLRSDPDACP	TMPLLAMLLR	GLTQIQSRIL	GPGRKCCALA	NLADMLTVFA
250	260	270	280	290	300	310	320
LTEDDPQEVS	ATVYLDKLAT	VISVWNSDTQ	NPYHQQALAE	KVKEAERDVS	LTSLAKLPSE	TIFVGCEFLH	HLLREWGEEL
330	340	350	360	370	380	390	400
QAVLRSSQGT	SYDSYRLCDS	LTSFSQNATL	YLNRTSLSKE	DRQVVSELAE	CVRDFLRKTS	TVLKNRALED	ITASIAMAVI
410	420	430	440	450	460	470	480
QQKMDRHMEV	CYIFASEKKW	AFSDEWVACL	GSNRALFRQP	DLVLRLLETV	IDVSTADRAI	PESQIRQVIH	LILECYADLS
490	500	510	520	530	540	550	560
LPGKNKVLAG	ILRSWGRKGL	SEKLLAYVEG	FQEDLNTTFN	QLTQSASEQG	LAKAVASVAR	LVIVHPEVTV	KKMCSLAVVN
570	580	590	600	610	620	630	640
LGTHKFLAQI	LTAFPALRFV	EEQGPNSSAT	FMVSCLKETV	WMKFSTPKEE	KQFLELLNCL	MSPVKPQGIP	VAALLEPDEV
650	660	670	680	690	700	710	720
LKEFVLPFLR	LDVEEVDLSL	RIFIQTLEAN	ACREEYWLQT	CSPFPLLFSL	CQLLDRFSKY	WQLPKEKRCL	SLDRKDLAIH
730	740	750	760	770	780	790	800
ILELLCEIVS	ANAETFSPDV	WIKSLSWLHR	KLEQLDWTVG	LRLKSFFEGH	FKCEVPATLF	EICKLSEDEW	TSQAHPGYGA
810	820	830	840	850	860	870	880
GTGLLAWMEC	CCVSSGISER	MLSLLVVDVG	NPEEVRLFSK	GFLVALVQVM	PWCSPQEWQR	LHQLTRRLLE	KQLLHVPYSL
890	900	910	920	930	940	950	960
EYIQFVPLLN	LKPFAQELQL	SVLFLRTFQF	LCSHSCRDWL	PLEGWNHVVK	LLCGSLTRLL	DSVRAIQAAG	PWVQGPEQDL
970	980	990	1000	1010	1020	1030	1040
TQEALFVYTQ	VFCHALHIMA	MLHPEVCEPL	YVLALETLTC	YETLSKTNPS	VSSLLQRAHE	QRFLKSIAEG	IGPEERRQTL
1050							
LQKMSSF							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
553	1	731.0325	133.55	2	36.5	16.0	0	566-578	K.FLAQILTAFPALR.F	

Detailed Protein Report

Protein 728: **PREDICTED: serine/threonine-protein kinase MRCK beta isoform X4 [Homo sapiens]**

Accession:	gi|530404963	**Score:**	16.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	169.5
Database Date:	2015-11-30	**pI:**	5.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSAKVRLKKL	EQLLLDGPWR	NESALSVETL	LDVLVCLYTE	CSHSALRRDK	YVAEFLEWAK	PFTQLVKEMQ	LHREDFEIIK
90	100	110	120	130	140	150	160
VIGRGAFGEV	AVVKMKNTER	IYAMKILNKW	EMLKRAETAC	FREERDVLVN	GDCQWITALH	YAFQDENHLY	LVMDYYVGGD
170	180	190	200	210	220	230	240
LLTLLSKFED	KLPEDMARFY	IGEMVLAIDS	IHQLHYVHRD	IKPDNVLLDV	NGHIRLADFG	SCLKMNDDGT	VQSSVAVGTP
250	260	270	280	290	300	310	320
DYISPEILQA	MEDGMGKYGP	ECDWWSLGVC	MYEMLYGETP	FYAESLVETY	GKIMNHEERF	QFPSHVTDVS	EEAKDLIQRL
330	340	350	360	370	380	390	400
ICSRERRLGQ	NGIEDFKKHA	FFEGLNWENI	RNLEAPYIPD	VSSPSDTSNF	DVDDDVLRNT	EILPPGSHTG	FSGLHLPFIG
410	420	430	440	450	460	470	480
FTFTTESCFS	DRGSLKSIMQ	SNTLTKDEDV	QRDLEHSLQM	EAYERRIRRL	EQEKLELSRK	LQESTQTVQS	LHGSSRALSN
490	500	510	520	530	540	550	560
SNRDKEIKKL	NEEIERLKNK	IADSNRLERQ	LEDTVALRQE	REDSTQRLRG	LEKQHRVVRQ	EKEELHKQLV	EASERLKSQA
570	580	590	600	610	620	630	640
KELKDAHQQR	KLALQEFSEL	NERMAELRAQ	KQKVSRQLRD	KEEEMEVATQ	KVDAMRQEMR	RAEKLRKELE	AQLDDAVAEA
650	660	670	680	690	700	710	720
SKERKLREHS	ENFCKQMESE	LEALKVKQGG	RGAGATLEHQ	QEISKIKSEL	EKKVLFYEEE	LVRREASHVL	EVKNVKKEVH
730	740	750	760	770	780	790	800
DSESHQLALQ	KEILMLKDKL	EKSKRERHNE	MEEAVGTIKD	KYERERAMLF	DENKKLTAEN	EKLCSFVDKL	TAQNRQLEDE
810	820	830	840	850	860	870	880
LQDLAAKKES	VAHWEAQIAE	IIQWVSDEKD	ARGYLQALAS	KMTEELEALR	SSSLGSRTLD	PLWKVRRSQK	LDMSARLELQ
890	900	910	920	930	940	950	960
SALEAEIRAK	QLVQEELRKV	KDANLTLESK	LKDSEAKNRE	LLEEMEILKK	KMEEKFRADT	GLKLPDFQDS	IFEYFNTAPL
970	980	990	1000	1010	1020	1030	1040
AHDLTFRDSL	SSSSASSLLA	FWEETSSASE	QETQAPKPEA	SPSMSVAASE	QQEDMARPPQ	RPSAVPLPTT	QALALAGPKP
1050	1060	1070	1080	1090	1100	1110	1120
KAHQFSIKSF	SSPTQCSHCT	SLMVGLIRQG	YACEVCSFAC	HVSCKDGAPQ	VCPIPPEQSK	RPLGVDVQRG	IGTAYKGHVK
1130	1140	1150	1160	1170	1180	1190	1200
VPKPTGVKKG	WQRAYAVVCD	CKLFLYDLPE	GKSTQPGVIA	SQVLDLRDDE	FSVSSVLASD	VIHATRRDIP	CIFRVTASLL
1210	1220	1230	1240	1250	1260	1270	1280
GAPSKTSSLL	ILTENENEKR	KWVGILEGLQ	SILHKNRLRN	QVVHVPLEAY	DSSLPLIKAI	LTAAIVDADR	IAVGLEEGLY
1290	1300	1310	1320	1330	1340	1350	1360
VIEVTRDVIV	RAADCKKVHQ	IELAPREKIV	ILLCGRNHHV	HLYPWSSLDG	AEGSFDIKLP	ETKGCQLMAT	ATLKRNSGTC
1370	1380	1390	1400	1410	1420	1430	1440
LFVAVKRLIL	CYEIQRTKPF	HRKFNEIVAP	GSVQCLAVLR	DRLCVGYPSG	FCLLSIQGDG	QPLNLVNPND	PSLAFLSQQS
1450	1460	1470	1480	1490	1500		
FDALCAVELE	SEEYLLCFSH	MGLYVDPQGR	RARAQELMWP	AAPVACKEKS			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
413	1	946.2338	-157.99	2	34.8	16.0	0	1069-1085	R.QGYACEVCSFACHVSCK.D	Carbamidomethyl: 16

Detailed Protein Report

Protein 729: thioredoxin reductase 1, cytoplasmic isoform 5 [Homo sapiens]

Accession:	gi|387598071	**Score:**	16.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	50.9
Database Date:	2015-11-30	**pI:**	6.2
		Sequence Coverage [%]:	2.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MVLDFVTPTP	LGTRWGLGGT	CVNVGCIPKK	LMHQAALLGQ	ALQDSRNYGW	KVEETVKHDW	DRMIEAVQNH	IGSLNWGYRV
90	100	110	120	130	140	150	160
ALREKKVVYE	NAYGQFIGPH	RIKATNNKGK	EKIYSAERFL	IATGERPRYL	GIPGDKEYCI	SSDDLFSLPY	CPGKTLVVGA
170	180	190	200	210	220	230	240
SYVALECAGF	LAGIGLDVTV	MVRSILLRGF	DQDMANKIGE	HMEEHGIKFI	RQFVPIKVEQ	IEAGTPGRLR	VVAQSTNSEE
250	260	270	280	290	300	310	320
IIEGEYNTVM	LAIGRDACTR	KIGLETVGVK	INEKTGKIPV	TDEEQTNVPY	IYAIGDILED	KVELTPVAIQ	AGRLLAQRLY
330	340	350	360	370	380	390	400
AGSTVKCDYE	NVPTTVFTPL	EYGACGLSEE	KAVEKFGEEN	IEVYHSYFWP	LEWTIPSRDN	NKCYAKIICN	TKDNERVVGF
410	420	430	440	450	460	470	
HVLGPNAGEV	TQGFAAALKC	GLTKKQLDST	IGIHPVCAEV	FTTLSVTKRS	GASILQAGCU	G	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1255	2	640.3104	2.78	2	45.4	16.0	0	198-208	K.IGEHMEEHGIK.F	

Detailed Protein Report

Protein 730: collagen triple helix repeat-containing protein 1 isoform 2 [Homo sapiens]

Accession:	gi|368711292	**Score:**	15.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	24.8
Database Date:	2015-11-30	**pI:**	9.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	7.0
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MWPPGRSITV KLREKTVSRK LEMNGPSAFQ GLICGKYNGM CLQGPAGVPG RDGSPGANGI PGTPGIPGRD GFKGEKGECL
        90        100        110        120        130        140        150        160
RESFEESWTP NYKQCSWSSL NYGIDLGKIA ECTFTKMRSN SALRVLFSGS LRLKCRNACC QRWYFTFNGA ECSGPLPIEA
       170        180        190        200        210        220        230
IIYLDQGSPE MNSTINIHRT SSVEGLCEGI GAGLVDVAIW VGTCSDYPKG DASTGWNSVS RIIIEELPK
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1796	3	840.7691	-164.92	2	52.5	15.9	0	21-36	K.LEMNGPSAFQGLICGK.Y	Oxidation: 3

Detailed Protein Report

Protein 731: ovochymase-2 precursor [Homo sapiens]

Accession:	gi|373838920	**Score:**	15.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	62.6
Database Date:	2015-11-30	**pI:**	6.2
		Sequence Coverage [%]:	2.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLISRNKLIL	LLGIVFFERG	KSATLSLPKA	PSCGQSLVKV	QPWNYFNIFS	RILGGSQVEK	GSYPWQVSLK	QRQKHICGGS
90	100	110	120	130	140	150	160
IVSPQWVITA	AHCIANRNIV	STLNVTAGEY	DLSQTDPGEQ	TLTIETVIIH	PHFSTKKPMD	YDIALLKMAG	AFQFGHFVGP
170	180	190	200	210	220	230	240
ICLPELREQF	EAGFICTTAG	WGRLTEGGVL	SQVLQEVNLP	ILTWEECVAA	LLTLKRPISG	KTFLCTGFPD	GGRDACQGDS
250	260	270	280	290	300	310	320
GGSLMCRNKK	GAWTLAGVTS	WGLGCGRGWR	NNVRKSDQGS	PGIFTDISKV	LPWIHEHIQT	GNRRKSSRAW	CSEQDVIVSG
330	340	350	360	370	380	390	400
AEGKLHFPES	LHLYYESKQR	CVWTLLVPEE	MHVLLSFSHL	DVESCHHSYL	SMYSLEDRPI	GKFCGESLPS	SILIGSNSLR
410	420	430	440	450	460	470	480
LKFVSDATDN	AAGFNLTYKA	LKPNYIPDSG	CSYLTVLFEE	GLIQSLNYPE	NYSDKANCDW	IFQASKHHLI	KLSFQSLEIE
490	500	510	520	530	540	550	560
ESGDCTSDYV	TVHSDVERKK	EIARLCGYDV	PTPVLSPSSI	MLISFQSDEN	GTCRGFQATV	SFIPKAVYPD	LNISISEDES
570							
MFLET							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1500	3	850.5937	163.04	2	48.4	15.9	0	290-303	K.VLPWIHEHIQTGNR.R	

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Detailed Protein Report

Protein 732: UPF0705 protein C11orf49 isoform 1 [Homo sapiens]

Accession:	gi|51558745	**Score:**	15.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	31.3
Database Date:	2015-11-30	**pI:**	5.2
		Sequence Coverage [%]:	6.6
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 0.33 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MLSPERLALP DYEYLAQRHV LTYMEDAVCQ LLENREDISQ YGIARFFTEY FNSVCQGTHI LFREFSFVQA TPHNRVSFLR
        90        100        110        120        130        140        150        160
AFWRCFRTVG KNGDLLTMKE YHCLLQLLCP DFPLELTQKA ARIVLMDDAM DCLMSFSDFL FAFQIQFYYS EFLDSVAAIY
       170        180        190        200        210        220        230        240
EDLLSGKNPN TVIVPTSSSG QHRQRPALGG AGTLEGVEAS LFYQCLENLC DRHKYSCPPP ALVKEALSNV QRLTFYGFLM
       250        260        270        280
ALSKHRGINQ ALGALPDKGD LMHDPAMDEE LERL
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2174	1	986.3858	-135.71	2	57.4	15.9	1	215-232	K.YSCPPPALVKEALSNVQR.L		MD:MU 0.33

Detailed Protein Report

Protein 733: absent in melanoma 1 protein [Homo sapiens]

Accession:	gi|62988361	**Score:**	15.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	188.5
Database Date:	2015-11-30	**pI:**	5.6
		Sequence Coverage [%]:	0.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEKRSSGRRS	GRRRGSQKST	DSPGADAELP	ESAARDDAVF	DDEVAPNAAS	DNASAEKKVK	SPRAALDGGV	ASAASPESKP
90	100	110	120	130	140	150	160
SPGTKGQLRG	ESDRSKQPPP	ASSPTKRKGR	SRALEAVPAP	PASGPRAPAK	ESPPKRVPDP	SPVTKGTAAE	SGEEAARAIP
170	180	190	200	210	220	230	240
RELPVKSSSL	LPEIKPEHKR	GPLPNHFNGR	AEGGRSRELG	RAAGAPGASD	ADGLKPRNHF	GVGRSTVTTK	VTLPAKPKHV
250	260	270	280	290	300	310	320
ELNLKTPKNL	DSLGNEHNPF	SQPVHKGNTA	TKISLFENKR	TNSSPRHTDI	RGQRNTPASS	KTFVGRAKLN	LAKKAKEMEQ
330	340	350	360	370	380	390	400
PEKKVMPNSP	QNGVLVKETA	IETKVTVSEE	EILPATRGMN	GDSSENQALG	PQPNQDDKAD	VQTDAGCLSE	PVASALIPVK
410	420	430	440	450	460	470	480
DHKLLEKEDS	EAADSKSLVL	ENVTDTAQDI	PTTVDTKDLP	PTAMPKPQHT	FSDSQSPAES	SPGPSLSLSA	PAPGDVPKDT
490	500	510	520	530	540	550	560
CVQSPISSFP	CTDLKVSENH	KGCVLPVSRQ	NNEKMPLLEL	GGETTPPLST	ERSPEAVGSE	CPSRVLVQVR	SFVLPVESTQ
570	580	590	600	610	620	630	640
DVSSQVIPES	SEVREVQLPT	CHSNEPEVVS	VASCAPPQEE	VLGNEHSHCT	AELAAKSGPQ	VIPPASEKTL	PIQAQSQGSR
650	660	670	680	690	700	710	720
TPLMAESSPT	NSPSSGNHLA	TPQRPDQTVT	NGQDSPASLL	NISAGSDDSV	FDSSSDMEKF	TEIIKQMDSA	VCMPMKRKKA
730	740	750	760	770	780	790	800
RMPNSPAPHF	AMPPIHEDHL	EKVFDPKVFT	FGLGKKKESQ	PEMSPALHLM	QNLDTKSKLR	PKRASAEQSV	LFKSLHTNTN
810	820	830	840	850	860	870	880
GNSEPLVMPE	INDKENRDVT	NGGIKRSRLE	KSALFSSLLS	SLPQDKIFSP	SVTSVNTMTT	AFSTSQNGSL	SQSSVSQPTT
890	900	910	920	930	940	950	960
EGAPPCGLNK	EQSNLLPDNS	LKVFNFNSSS	TSHSSLKSPS	HMEKYPQKEK	TKEDLDSRSN	LHLPETKFSE	LSKLKNDDME
970	980	990	1000	1010	1020	1030	1040
KANHIESVIK	SNLPNCANSD	TDFMGLFKSS	RYDPSISFSG	MSLSDTMTLR	GSVQNKLNPR	PGKVVIYSEP	DVSEKCIEVF
1050	1060	1070	1080	1090	1100	1110	1120
SDIQDCSSWS	LSPVILIKVV	RGCWILYEQP	NFEGHSIPLE	EGELELSGLW	GIEDILERHE	EAESDKPVVI	GSIRHVVQDY
1130	1140	1150	1160	1170	1180	1190	1200
RVSHIDLFTE	PEGLGILSSY	FDDTEEMQGF	GVMQKTCSMK	VHWGTWLIYE	EPGFQGVPFI	LEPGEYPDLS	FWDTEAAYIG
1210	1220	1230	1240	1250	1260	1270	1280
SMRPLKMGGR	KVEFPTDPKV	VVYEKPFFEG	KCVELETGMC	SFVMEGGETE	EATGDDHLPF	TSVGSMKVLR	GIWVAYEKPG
1290	1300	1310	1320	1330	1340	1350	1360
FTGHQYLLEE	GEYRDWKAWG	GYNGELQSLR	PILGDFSNAH	MIMYSEKNFG	SKGSSIDVLG	IVANLKETGY	GVKTQSINVL
1370	1380	1390	1400	1410	1420	1430	1440
SGVWVAYENP	DFTGEQYILD	KGFYTSFEDW	GGKNCKISSV	QPICLDSFTG	PRRRNQIHLF	SEPQFQGHSQ	SFEETTSQID
1450	1460	1470	1480	1490	1500	1510	1520
DSFSTKSCRV	SGGSWVVYDG	ENFTGNQYVL	EEGHYPCLSA	MGCPPGATFK	SLRFIDVEFS	EPTIILFERE	DFKGKKIELN
1530	1540	1550	1560	1570	1580	1590	1600
AETVNLRSLG	FNTQIRSVQV	IGGIWVTYEY	GSYRGRQFLL	SPAEVPNWYE	FSGCRQIGSL	RPFVQKRIYF	RLRNKATGLF
1610	1620	1630	1640	1650	1660	1670	1680
MSTNGNLEDL	KLLRIQVMED	VGADDQIWIY	QEGCIKCRIA	EDCCLTIVGS	LVTSGSKLGL	ALDQNADSQF	WSLKSDGRIY
1690	1700	1710	1720	1730			
SKLKPNLVLD	IKGGTQYDQN	HIILNTVSKE	KFTQVWEAMV	LYT			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
284	1	939.2416	-290.57	1	33.2	15.9	0	137-145	R.VPDPSPVTK.G	

Detailed Protein Report

Protein 734: C2 calcium-dependent domain-containing protein 4A [Homo sapiens]

Accession:	gi|147903292	**Score:**	15.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	39.7
Database Date:	2015-11-30	**pI:**	12.2
		Sequence Coverage [%]:	3.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MWCLERLRLG	PECLRRSGDW	LLPGRARGAK	SRTTAACANV	LTPDRIPEFC	IPPRLMPRLA	LAALRNSWVE	EAGMDEGAGR
90	100	110	120	130	140	150	160
TDWDPRSQAA	LSLPHLPRVR	TAYGFCALLE	SPHTRRKESL	LLGGPPAPRP	RAHTYGGGGG	PDALLGTLRV	PRAPGPATPA
170	180	190	200	210	220	230	240
APGCPRPPQD	ALARRPRGCR	LLRVPDGLLS	RALRAGRSRR	LTRVRSVSSG	NEDKERRAGS	QSPARAPSTS	PPSSRVPFPE
250	260	270	280	290	300	310	320
RLEAEGTVAL	GRAGDALRLA	AEYCPGTGRL	RLRLLRAESP	AGGAPGPRAV	SCRLSLVLRP	PGTALRQCST	VVGRSRKASF
330	340	350	360	370			
DQDFCFDGLS	EDEVRRLAVR	VKARDEGRGR	ERGRLLGQGE	LSLGALLLL			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
88	1	516.5686	-78.89	3	30.5	15.8	2	201-214	R.LTRVRSVSSGNEDK.E	

Detailed Protein Report

Protein 735: PREDICTED: prothymosin alpha-like [Homo sapiens]

Accession:	gi|530355638	**Score:**	15.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	13.0
Database Date:	2015-11-30	**pI:**	3.6
		Sequence Coverage [%]:	14.4
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530436984	refseq_human (refseq_human_20140103.fasta)	PREDICTED: prothymosin alpha-like [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MSDAAVDTSS EITTEDLKEK KEVVEEAENG RDAPANRNAN EENGEPEADN EVDEEEEEGG EEEEEEEGDG EEEDGDEDEG
        90        100        110        120
AESATGKRAA EDDEDDDVDT QKQKTDEDDQ TAKKEKLN
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1558	1	942.3938	-74.41	2	49.3	15.7	2	21-37	K.KEVVEEAENGRDAPANR.N	

Detailed Protein Report

Protein 736: PREDICTED: telomeric repeat-binding factor 2 isoform X4 [Homo sapiens]

Accession:	gi|530424267	**Score:**	15.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	50.4
Database Date:	2015-11-30	**pI:**	9.9
		Sequence Coverage [%]:	2.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAAGAGTAGP	ASGPGVVRDP	AASQPRKRPG	REGGEGARRS	DTMAGGGGSS	DGSGRAAGRR	ASRSSGRARR	GRHEPGLGGP
90	100	110	120	130	140	150	160
AERGAGEARL	EEAVNRWVLK	FYFHEALRAF	RGSRYGDFRQ	IRDIMQALLV	RPLGKEHTVS	RLLRVMQCLS	RIEEGENLDC
170	180	190	200	210	220	230	240
SFDMEAELTP	LESAINVLEM	IKTEFTLTEA	VVESSRKLVK	EAMAKKALKS	ESAASSTGKE	DKQPAPGPVE	KPPREPARQL
250	260	270	280	290	300	310	320
RNPPTTIGMM	TLKAAFKTLS	GAQDSEAAFA	KLDQKDLVLP	TQALPASPAL	KNKRPRKDEN	ESSAPADGEG	GSELQPKNKR
330	340	350	360	370	380	390	400
MTISRLVLEE	DSQSTEPSAG	LNSSQEAASA	PPSKPTVLNQ	PLPGEKNPKV	PKGKWNSSNG	VEEKETWVEE	DELFQVQAAP
410	420	430	440	450	460	470	
DEDSTTNITK	KQKWTVEESE	WVKAGVQKYG	EGNWAAISKN	YPFVNRTAVM	IKDRWRTMKR	LGMN	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
455	1	666.9184	114.60	2	35.3	15.7	1	71-83	R.GRHEPGLGGPAER.G	

Detailed Protein Report

Protein 737: tetratricopeptide repeat protein 40 [Homo sapiens]

Accession:	gi|359385708	**Score:**	15.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	303.3
Database Date:	2015-11-30	**pI:**	7.2
Modification(s):	Oxidation	**Sequence Coverage [%]:**	0.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDLVITQELA	RAESQQDAAS	LKKAYELIKS	ANLGKSEFDP	SESFSPDLFV	LCAEQALKMR	QPEVSEDCIQ	MYFKVKAPIT
90	100	110	120	130	140	150	160
QFLGRAHLCR	AQMCAPKSAE	NLEEFENCVT	EYMKAINFAK	GEPRYYFLVY	NASVLYWQMV	RPFLKPGYRH	HLIPSLSQII
170	180	190	200	210	220	230	240
NVLSQTEEED	KEWRAELMLE	LLECYLQAGR	KEEAARFCST	AAPFIKSHVP	QKYRQIFSVM	VRHELMDELQ	LKEEKKNSIS
250	260	270	280	290	300	310	320
LSVTFYINML	KAKAEQNDLP	GDISVILRKA	YRHLGHYNHQ	RFPSISEEKM	LLLFELARFS	LTLKCMEISS	ACLSDLKKME
330	340	350	360	370	380	390	400
SKDPGKLIEM	ECLECESEAL	RLESKMKVYN	RAAVEAQLDI	IQRLDVALQR	AVRLGDPRVI	HVVCATQWNT	CLPLLQHNLR
410	420	430	440	450	460	470	480
HHLRKPLAGV	ADVLEKLDSL	MTLLRCQVHM	EMAQIEEDED	RLEPATEHLR	KAARLDSLGL	YRDRIQMAST	RLRLCTTLYQ
490	500	510	520	530	540	550	560
APERAEDKAI	MAVEQAKKAT	PKDSVRKKRA	LLVNAGLALA	PDAFQIVLDS	ENEAKVSTGK	NRGRFTYLCA	KAWHHTVSVD
570	580	590	600	610	620	630	640
KAAGHLRRLG	NENDKERIQI	WAELAKVARK	QGVWDVCRTA	SRFCLLYDNV	KVKKLRLRRG	KKKRGRDGSV	QDTWSQPEVV
650	660	670	680	690	700	710	720
LQRQVCPDLL	RKFAEVGFIH	AEATVHLLRS	EGVELNDRAI	PPEDLSQHPA	GYVPEPPEVN	AEWITYRTWI	ESLSRCAMNN
730	740	750	760	770	780	790	800
WLRSAEIGQE	IQEAWIVQNA	VVYVLNHNHH	LILAGRQKEL	VDALYHLLSI	VKATGHSGDP	VMLVTLCNTL	ARGLIISWIP
810	820	830	840	850	860	870	880
VQAAEKSRKF	MRPNAFHSPL	DAGATSEIKT	AVEVCEFALN	LTNGSAPEET	VPTGTRQQLI	ATWVKAKQLL	QQQIGPRLGT
890	900	910	920	930	940	950	960
EEQGTNEDVS	SVTRVLVALE	MYSCNGLGLM	DFTVPSLAQL	VKMASECNWS	DPLVELQTLT	RLTHFAHAAR	DHETTMACAH
970	980	990	1000	1010	1020	1030	1040
RALEMGIKYL	KKFGPEESRL	VAEMLCTATA	IQGRSIMENL	KGRKQLRLVA	AKAFTESARF	GGIAGSSALV	MLAARHYWNA
1050	1060	1070	1080	1090	1100	1110	1120
WLPLLSSAVY	RKKAKGALKR	LIGIINKTEA	RKQEKGKTLL	LHQWPTADFQ	GGGTTEGYFL	PGAEDDLALR	AALYGLLFHS
1130	1140	1150	1160	1170	1180	1190	1200
HADQDDWEGG	LKVLDEAVQV	LPRTAHRLLI	FKHMVIVKAK	LGQNFSMEIQ	KFKAESEDYL	ARMWHRLALN	SPSVSGELAC
1210	1220	1230	1240	1250	1260	1270	1280
YNNAIQALQK	PEMEWQKVEY	LMEFGQWLHH	RHFPLEDVVF	HLRWAVEILL	AMKPPGDVPE	PQPTPDGEYV	AVEMPPRSPV
1290	1300	1310	1320	1330	1340	1350	1360
SEAEEAVSLE	QLRSVRQLEA	LARVHILLAL	VLSPGAEGYE	DCCLAAYAFF	RHIWQVSLMT	AGKSVLENRP	LAATSSHLLL
1370	1380	1390	1400	1410	1420	1430	1440
PKKEKENERS	KEKEKERSKE	KENERSKEKD	KEKGKEEKVK	EPKQSQSPAP	IKQLEDLPMS	IEEWASYSCP	EEVLSVLKQD
1450	1460	1470	1480	1490	1500	1510	1520
RSDSTVNPSS	IQKPTYSLYF	LDHLVKALQK	MCLHELTVPV	LQLGVLISDS	VVGSKGLSDL	YHLRLAHACS	ELKLREAAAR
1530	1540	1550	1560	1570	1580	1590	1600
HEEAVGQVCV	SELEQASCRK	EIALKKEKNK	EPLLEESLPA	LNEQTLPVQP	GEIKPLDAKD	KILKMNGETG	RDLDGTSFPH
1610	1620	1630	1640	1650	1660	1670	1680
LWMLKAEVLL	EMNLYQPARL	LLSEAYLAFQ	ELDEPCAEAQ	CLLLLAQLAN	KEKNYGQAKK	MIAQAQHLGG	SEEFWYNSTL
1690	1700	1710	1720	1730	1740	1750	1760
TLAEALLSME	HSGREATVCH	IFQKLINAFK	ILKKERPNRL	PLLEFMITDL	EARCLSLRVR	VAQHSAVTEP	TECSLLLKEM
1770	1780	1790	1800	1810	1820	1830	1840
DDGLLEIERK	FIDCGCKENC	VDVKLERAKI	KRLRAQNEKD	EEQKTAYYLE	AYGLAQGAVA	EEEGRLHSIQ	GLYGLAQGAM
1850	1860	1870	1880	1890	1900	1910	1920
AEEEGRLHSV	QGLLSLQDLQ	NVNTPLMRKL	ARLKLGLVEM	ALDMLQFIWE	EAHGQQSEQG	SLEKLLADYL	QNTSDYTSVG
1930	1940	1950	1960	1970	1980	1990	2000
LQWFTLKRTL	AHGALAQLGS	LQPLSVGCVE	IRARLLGLAG	RALHLLAMQA	DPVHPTCYWE	AGPSVGAKLS	GLKSLELEVE
2010	2020	2030	2040	2050	2060	2070	2080
EEGATKSSRD	PPASRAAPEE	HCRRGEDLKR	RMVLAQQYLA	QASEVLLQCL	QVALGSGLLD	VAAAASLEMV	ECVGTLDPAT
2090	2100	2110	2120	2130	2140	2150	2160
TCQFLALSQS	CSASETMRDV	LLAATANTSS	SQLAALLQLQ	HQLRCQDRTT	TSLGARVEQR	LAAVSKAWQN	LCVTEQHFNL
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
114	1	793.3810	-31.26	2	30.8	15.7	1	1161-1173	K.LGQNFSMEIQKFK.A	Oxidation: 7

Detailed Protein Report

Protein 738: visinin-like protein 1 [Homo sapiens]

Accession: gi|21361559
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 15.7
MW [kDa]: 22.1
pI: 4.9
Sequence Coverage [%]: 7.3
No. of unique Peptides: 1

Quantitation

MD:MU **Median:** 0.91 **CV:** 0.00 % **No. of Peptides:** 1

```
         10         20         30         40         50         60         70         80
MGKQNSKLAP EVMEDLVKST EFNEHELKQW YKGFLKDCPS GRLNLEEFQQ LYVKFFPYGD ASKFAQHAFR TFDKNGDGTI
         90        100        110        120        130        140        150        160
DFREFICALS ITSRGSFEQK LNWAFNMYDL DGDGKITRVE MLEIIEAIYK MVGTVIMMKM NEDGLTPEQR VDKIFSKMDK
        170        180        190        200
NKDDQITLDE FKEAAKSDPS IVLLLQCDIQ K
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1378	1	816.3763	-14.76	2	46.8	15.7	1	140-153	K.MNEDGLTPEQRVDK.I		MD:MU 0.91

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Detailed Protein Report

Protein 739: guanine nucleotide-binding protein subunit alpha-15 [Homo sapiens]

Accession:	gi|156104883	**Score:**	15.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	43.5
Database Date:	2015-11-30	**pI:**	9.5
		Sequence Coverage [%]:	4.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MARSLTWRCC	PWCLTEDEKA	AARVDQEINR	ILLEQKKQDR	GELKLLLLGP	GESGKSTFIK	QMRIIHGAGY	SEEERKGFRP
90	100	110	120	130	140	150	160
LVYQNIFVSM	RAMIEAMERL	QIPFSRPESK	HHASLVMSQD	PYKVTTFEKR	YAAAMQWLWR	DAGIRAYYER	RREFHLLDSA
170	180	190	200	210	220	230	240
VYYLSHLERI	TEEGYVPTAQ	DVLRSRMPTT	GINEYCFSVQ	KTNLRIVDVG	GQKSERKKWI	HCFENVIALI	YLASLSEYDQ
250	260	270	280	290	300	310	320
CLEENNQENR	MKESLALFGT	ILELPWFKST	SVILFLNKTD	ILEEKIPTSH	LATYFPSFQG	PKQDAEAAKR	FILDMYTRMY
330	340	350	360	370	380		
TGCVDGPEGS	KKGARSRRLF	SHYTCATDTQ	NIRKVFKDVR	DSVLARYLDE	INLL		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1346	1	955.6732	140.57	2	46.4	15.7	2	38-55	K.QDRGELKLLLLGPGESGK.S	

Detailed Protein Report

Protein 740: **mas-related G-protein coupled receptor member X1 [Homo sapiens]**

Accession:	gi|125660451	**Score:**	15.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	36.2
Database Date:	2015-11-30	**pI:**	9.0
		Sequence Coverage [%]:	8.1
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MDPTISTLDT ELTPINGTEE TLCYKQTLSL TVLTCIVSLV GLTGNAVVLW LLGCRMRRNA FSIYILNLAA ADFLFLSGRL
        90        100        110        120        130        140        150        160
IYSLLSFISI PHTISKILYP VMMFSYFAGL SFLSAVSTER CLSVLWPIWY RCHRPTHLSA VVCVLLWALS LLRSILEWML
       170        180        190        200        210        220        230        240
CGFLFSGADS AWCQTSDFIT VAWLIFLCVV LCGSSLVLLI RILCGSRKIP LTRLYVTILL TVLVFLLCGL PFGIQFFLFL
       250        260        270        280        290        300        310        320
WIHVDREVLF CHVHLVSIFL SALNSSANPI IYFFVGSFRQ RQNRQNLKLV LQRALQDASE VDEGGGQLPE EILELSGSRL
       330
EQ
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2182	1	900.3512	-96.83	3	57.2	15.7	0	294-319	R.ALQDASEVDEGGGQLPEEILELSGSR.L	

Detailed Protein Report

Protein 741: PREDICTED: zinc finger protein 654 isoform X3 [Homo sapiens]

Accession:	gi|578806340	**Score:**	15.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	117.3
Database Date:	2015-11-30	**pI:**	5.0
		Sequence Coverage [%]:	1.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAEEESDQEA	ERLGEELVAI	VESPLGPVGL	RAAGDGRGGA	GSGNCGGGVG	ISSRDYCRRF	CQVVEDYAGR	WQVPLPQLQV
90	100	110	120	130	140	150	160
LQTALCCFTT	ASASFPDECE	HVQYVLSSLA	VSFFELLLFF	GRDEFYEEPL	KDILGSFQHL	LKTDCKSGID	IICNAEKEGK
170	180	190	200	210	220	230	240
TMLALQLCES	FLIPQLQNGD	MYCIWELIFI	WSKLQLKSNP	SKQVFVDQCY	QLLRTATNVR	VIFPFMKIIK	DEVEEEGLQI
250	260	270	280	290	300	310	320
CVEICGCALQ	LDLHDDPKTK	CLIYKTIAHF	LPNDLEILRI	CALSIFFLER	SLEAYRTVEE	LYKRPDEEYN	EGTSSVQNRV
330	340	350	360	370	380	390	400
RFELLPILKK	GLFFDPEFWN	FVMIKKNCVA	LLSDKSAVRF	LNESTLENNA	GNLKRTEEQQ	GLDEGFDSLT	DQSTGETDPD
410	420	430	440	450	460	470	480
DVSGVQPKGH	INTKKNLTAL	STSKVDHNVP	RHRCMLCNKE	FLGGHIVRHA	QAHQKKGSFA	CVICGRKFRN	RGLMQKHLKN
490	500	510	520	530	540	550	560
HVKKIQRQQI	AAAQQDDQEV	TALEEINCSS	SSISFENGNS	DSKDLEVETL	TASSEGNKEV	IPEHVAEFIE	IPISVPEDVI
570	580	590	600	610	620	630	640
ENVIENGSPN	NSLNNVFKPL	TECGDDYEEE	EDEEGDYEED	DYDLNQETSV	IHKINGTVCH	PKDIYATDQE	GNFKCPALGC
650	660	670	680	690	700	710	720
VRIFKRIGFL	NKHAMTVHPT	DLNVRQTVMK	WSKGKCKFCQ	RQFEDSQHFI	DHLNRHSYPN	VYFCLHFNCN	ESFKLPFQLA
730	740	750	760	770	780	790	800
QHTKSHRIFQ	AQCSFPECHE	LFEDLPLLYE	HEAQHYLSKT	PESSAQPSET	ILWDVQTDSN	PNQEKDSSSN	EKQTISLPVS
810	820	830	840	850	860	870	880
TSKSRKESTE	PKTCIESMEK	KTDSLVQNGN	ERSDDTVSNI	SLIDQKMPDI	EPNSENNCSS	SDIVNGHSEI	EQTPLVSSDP
890	900	910	920	930	940	950	960
ALKIDTNRIR	TENGSILPSV	VPQEHNTLPV	SQAPSKPNLT	SEHTSYGLIL	TKPYVRPLPP	SYLDERYLSM	PKRRKFLTDR
970	980	990	1000	1010	1020	1030	1040
VDACSDQDNV	YKKSVKRLRC	GKCLTTYCNA	EALEAHLAQK	KCQTLFGFDS	DDESKSSVFL	VEVSVERENG	INKTIIDL

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2796	1	974.5012	-59.59	2	65.4	15.6	0	13-31	R.LGEELVAIVESPLGPVGLR.A	

Detailed Protein Report

Protein 742: PREDICTED: cadherin-11 isoform X6 [Homo sapiens]

Accession:	gi|530423519	**Score:**	15.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	62.7
Database Date:	2015-11-30	**pI:**	5.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MKENYCLQAA	LVCLGMLCHS	HAFAPERRGH	LRPSFHGHHE	KGKEGQVLQR	SKRGWVWNQF	FVIEEYTGPD	PVLVGRLHSD
90	100	110	120	130	140	150	160
IDSGDGNIKY	ILSGEGAGTI	FVIDDKSGNI	HATKTLDREE	RAQYTLMAQA	VDRDTNRPLE	PPSEFIVKVQ	DINDNPPEFL
170	180	190	200	210	220	230	240
HETYHANVPE	RSNVGTSVIQ	VTASDADDPT	YGNSAKLVYS	ILEGQPYFSV	EAQTGIIRTA	LPNMDREAKE	EYHVVIQAKD
250	260	270	280	290	300	310	320
MGGHMGGLSG	TTKVTITLTD	VNDNPPKFPQ	SVYQMSVSEA	AVPGEEVGRV	KAKDPDIGEN	GLVTYNIVDG	DGMESFEITT
330	340	350	360	370	380	390	400
DYETQEGVIK	LKKPVDFETK	RAYSLKVEAA	NVHIDPKFIS	NGPFKDTVTV	KISVEDADEP	PMFLAPSYIH	EVQENAAAGT
410	420	430	440	450	460	470	480
VVGRVHAKDP	DAANSPIRYS	IDRHTDLDRF	FTINPEDGFI	KTTKPLDREE	TAWLNITVFA	AEIHNRHQEA	KVPVAIRVLD
490	500	510	520	530	540	550	560
VNDNAPKFAA	PYEGFICESD	QTKPLSNQPI	VTISADDKDD	TANGPRFIFS	LPPEIIHNPN	FTVRDNRDAV	EPHGHNHIIM
570							
VLKEF							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2302	1	701.2728	-116.45	3	58.7	15.6	1	548-565	R.DAVEPHGHNHIIMVLKEF.-	Oxidation: 13

Detailed Protein Report

Protein 743: PREDICTED: histone acetyltransferase KAT2A isoform X2 [Homo sapiens]

Accession:	gi|578830713	**Score:**	15.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	54.1
Database Date:	2015-11-30	**pI:**	9.6
		Sequence Coverage [%]:	1.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLEEEIYGAN	SPIWESGFTM	PPSEGTQLVP	RPASVSAAVV	PSTPIFSPSM	GGGSNSSLSL	DSAGAEPMPG	EKRTLPENLT
90	100	110	120	130	140	150	160
LEDAKRLRVM	GDIPMELVNE	VMLTITDPAA	MLGPETSLLS	ANAARDETAR	LEERRGIIEF	HVIGNSLTPK	ANRRVLLWLV
170	180	190	200	210	220	230	240
GLQNVFSHQL	PRMPKEYIAR	LVFDPKHKTL	ALIKDGRVIG	GICFRMFPTQ	GFTEIVFCAV	TSNEQVKGYG	THLMNHLKEY
250	260	270	280	290	300	310	320
HIKHNILYFL	TYADEYAIGY	FKKQGFSKDI	KVPKSRYLGY	IKDYEGATLM	ECELNPRIPY	TELSHIIKKQ	KEVIIKKLIE
330	340	350	360	370	380	390	400
RKQAQIRKVY	PGLSCFKEGV	RQIPVESVPG	IRETGWKPLG	KEKGKELKDP	DQLYTTLKNL	LAQIKSHPSA	WPFMEPVKKS
410	420	430	440	450	460	470	480
EAPDYYEVIR	FPIDLKTMTE	RLRSRYYVTR	KLFVADLQRV	IANCREYNPP	DSEYCRCASA	LEKFFYFKLK	EGGLIDK

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1555	1	699.2025	-339.50	1	49.3	15.6	1	269-274	K.DIKVPK.S	

Detailed Protein Report

Protein 744: O(6)-methylguanine-induced apoptosis 2 isoform 2 [Homo sapiens]

Accession:	gi|30794260	**Score:**	15.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	31.5
Database Date:	2015-11-30	**pI:**	10.3
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	6.3
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530361426	refseq_human (refseq_human_20140103.fasta)	PREDICTED: O(6)-methylguanine-induced apoptosis 2 isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MNALANIPDV	PVKYRKNDIP	GPGFYNVIHQ	SPVSNSVSLS	KKGTCMFPSM	CARLDTIISK	YPAANAYTIP	SDFISKRDFS
90	100	110	120	130	140	150	160
NSCSSMFQLP	SFMKALKFET	PAPNYYNASV	SCCKQRNNVC	TRAGFMSKTQ	RGSFAFADKG	PPPGHYDINE	SLVKQSPNTL
170	180	190	200	210	220	230	240
MSCFKSKTNR	GLKLTSTGPG	PGYYNPSDCT	KVPKKTLFPK	NPILNFSAQP	SPLPPKPPFP	GPGQYEIVDY	LGPRKHFISS
250	260	270	280	290			
ASFVSNTSRW	TAAPPQPGLP	GPATYKPELP	GKQSFLYNED	KKWIPVL			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2746	1	683.0052	25.96	3	65.6	15.5	1	43-60	K.GTCMFPSMCARLDTIISK.Y	Carbamidomethyl: 9; Oxidation: 8

Detailed Protein Report

Protein 745: PREDICTED: AP-4 complex subunit beta-1 isoform X2 [Homo sapiens]

Accession:	gi|530361620	**Score:**	15.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	45.7
Database Date:	2015-11-30	**pI:**	6.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	4.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPYLGSEDVV	KELKKALCNP	HIQADRLRYR	NVIQRVIRYM	TQGLDMSGVF	MEMVKASATV	DIVQKKLVYL	YMCTYAPLKP
90	100	110	120	130	140	150	160
DLALLAINTL	CKDCSDPNPM	VRGLALRSMC	SLRMPGVQEY	IQQPILNGLR	DKASYVRRVA	VLGCAKMHNL	HGDSEVDGAL
170	180	190	200	210	220	230	240
VNELYSLLRD	QDPIVVVNCL	RSLEEILKQE	GGVVINKPIA	HHLLNRMSKL	DQWGQAEVLN	FLLRYQPRSE	EELFDILNLL
250	260	270	280	290	300	310	320
DSFLKSSSPG	VVMGATKLFL	ILAKMFPHVQ	TDVLVRVKGP	LLAACSSESR	ELCFVALCHV	RQILHSLPGH	FSSHYKKFFC
330	340	350	360	370	380	390	400
SYSEPHYIKL	QKVEVLCELV	NDENVQQVLE	ELRGYCTDVS	ADFAQAAIFA	IGGIARTYTD	QCVQILTELL	GLRQEHITTE
410							
IQPES							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2122	1	672.2261	-98.76	3	56.7	15.5	0	39-55	R.YMTQGLDMSGVFMEMVK.A	Oxidation: 2, 13, 15

Detailed Protein Report

Protein 746: **synaptophysin [Homo sapiens]**

Accession: gi|27764867

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Modification(s): Oxidation

Score: 15.5

MW [kDa]: 33.8

pI: 4.5

Sequence Coverage [%]: 4.2

No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MLLLADMDVV	NQLVAGGQFR	VVKEPLGFVK	VLQWVFAIFA	FATCGSYSGE	LQLSVDCANK	TESDLSIEVE	FEYPFRLHQV
90	100	110	120	130	140	150	160
YFDAPTCRGG	TTKVFLVGDY	SSSAEFFVTV	AVFAFLYSMG	ALATYIFLQN	KYRENNKGPM	LDFLATAVFA	FMWLVSSSAW
170	180	190	200	210	220	230	240
AKGLSDVKMA	TDPENIIKEM	PVCRQTGNTC	KELRDPVTSG	LNTSVVFGFL	NLVLWVGNLW	FVFKETGWAA	PFLRAPPGAP
250	260	270	280	290	300	310	320
EKQPAPGDAY	GDAGYGQGPG	GYGPQDSYGP	QGGYQPDYGQ	PAGSGGSGYG	PQGDYGQQGY	GPQGAPTSFS	NQM

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2580	1	741.8624	45.69	2	62.8	15.5	1	179-191	K.EMPVCRQTGNTCK.E	Oxidation: 2

Detailed Protein Report

Protein 747: PREDICTED: synaptotagmin-7 isoform X8 [Homo sapiens]

Accession:	gi|530397583	**Score:**	15.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	28.7
Database Date:	2015-11-30	**pI:**	10.1
		Sequence Coverage [%]:	4.0
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MKAQELPAKD FSGTSDPFVK IYLLPDKKHK LETKVKRKNL NPHWNETFLF EGFPYEKVVQ RILYLQVLDY DRFSRNDPIG

        90        100        110        120        130        140        150        160
EVSIPLNKVD LTQMQTFWKD LKPCSDGSGS RGELLLSLCY NPSANSIIVN IIKARNLKAM DIGGTSDPYV KVWLMYKDKR

       170        180        190        200        210        220        230        240
VEKKKTVTMK RNLNPIFNES FAFDIPTEKL RETTIIITVM DKDKLSRNDV IGKIYLSWKS GPGEVKHWKD MIARPRQPVA

       250
QWHQLKA
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2844	1	655.3688	27.19	2	66.0	15.5	1	227-236	K.HWKDMIARPR.Q	

Detailed Protein Report

Protein 748: **WD repeat and SOCS box-containing protein 2 isoform 3 [Homo sapiens]**

Accession:	gi|514052675	**Score:**	15.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	21.8
Database Date:	2015-11-30	**pI:**	9.6
		Sequence Coverage [%]:	11.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLCSAAGEKS	VFLWSMRSYT	LIRKLEGHQS	SVVSCDFSPD	SALLVTASYD	TNVIMWDPYT	GERLRSLHHT	QVDPAMDDSD
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
VHISSLRSVC	FSPEGLYLAT	VADDRLLRIW	ALELKTPIAF	APMTNGLCCT	FFPHGGVIAT	GTRDGHVQFW	TAPRVLSSLK
170	**180**	**190**	**200**				
HLCRKALRSF	LTTYQVLALP	IPKKMKEFLT	YRTF				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
642	1	820.7414	21.33	3	37.6	15.5	0	66-87	R.SLHHTQVDPAMDDSDVHISSLR.S	

Detailed Protein Report

Protein 749: PREDICTED: zinc finger protein 347 isoform X2 [Homo sapiens]

Accession:	gi|530417417	**Score:**	15.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	89.1
Database Date:	2015-11-30	**pI:**	10.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLEQGKEPFT	LESQVQIAGN	PDGWEWIKAV	ITALSSEFVM	KDLLHKGKSN	TGEVFQTVML	ERQESQDIEG	CSFREVQKNT
90	100	110	120	130	140	150	160
HGLEYQCRDA	EGNYKGVLLT	QEGNLTHGRD	EHDKRDARNK	LIKNQLGLSL	QSHLPELQLF	QYEGKIYECN	QVEKSFNNNS
170	180	190	200	210	220	230	240
SVSPPQQMPY	NVKTHISKKY	LKDFISSLLL	TQGQKANNWG	SPYKSNGCGM	VFPQNSHLAS	HQRSHTKEKP	YKCYECGKAF
250	260	270	280	290	300	310	320
RTRSNLTTHQ	VIHTGEKRYK	CNECGKVFSR	NSQLSQHQKI	HTGEKPYKCN	ECGKVFTQNS	HLVRHRGIHT	GEKPYKCNEC
330	340	350	360	370	380	390	400
GKAFRARSSL	AIHQATHSGE	KPYKCNECGK	VFTQNSHLTN	HWRIHTGEKP	YKCNECGKAF	GVRSSLAIHL	VIHTGEKPYK
410	420	430	440	450	460	470	480
CHECGKVFRR	NSHLARHQLI	HTGEKPYKCN	ECGKAFRAHS	NLTTHQVIHT	GEKPYKCNEC	GKVFTQNSHL	ANHQRIHTGV
490	500	510	520	530	540	550	560
KPYMCNECGK	AFSVYSSLTT	HQVIHTGEKP	YKCNECGKVF	TQNSHLARHR	GIHTGEKPYK	CNECGKVFRH	NSYLSRHQRI
570	580	590	600	610	620	630	640
HTGEKPYKYN	EYGKAFSEHS	NLTTHQVIHT	GEKPYKCNEC	GKVFTQNSHL	ARHRRVHTGG	KPYQCNECGK	AFSQTSKLAR
650	660	670	680	690	700	710	720
HQRVHTGEKP	YECNQCGKAF	SVRSSLTTHQ	AIHTGKKPYK	CNECGKVFTQ	NSHLARHRGI	HTGEKPYKCN	ECGKAFSQTS
730	740	750	760	770	780	790	
KLARHQRIHT	GEKPYECGKP	FSICSSLTTH	QTIHTGGKPY	KCNVWKVLKS	EFKPCKPSQN	S	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2362	1	1133.2721	-189.27	1	59.8	15.5	1	233-241	K.CYECGKAFR.T	Carbamidomethyl: 1

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Detailed Protein Report

Protein 750: serine protease inhibitor Kazal-type 9 precursor [Homo sapiens]

Accession:	gi|94536774	**Score:**	15.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	9.7
Database Date:	2015-11-30	**pI:**	10.3
		Sequence Coverage [%]:	20.9
		No. of unique Peptides:	1

```
         10         20         30         40         50         60         70         80
MRATAIVLLL ALTLATMFSI ECAKQTKQMV DCSHYKKLPP GQQRFCHHMY DPICGSDGKT YKNDCFFCSK VKKTDGTLKF
         90
VHFGKC
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1574	1	1051.4917	39.60	2	49.4	15.4	1	45-62	R.FCHHMYDPICGSDGKTYK.N	

Detailed Protein Report

Protein 751: **mesencephalic astrocyte-derived neurotrophic factor precursor [Homo sapiens]**

Accession:	gi|299523086	**Score:**	15.4
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
1716	1	697.0204	21.45	3	51.3	15.4	2	69-87	R.GKENRLCYYIGATDDAATK.I	

Detailed Protein Report

Protein 752: phosphatidylinositol 3-kinase regulatory subunit gamma [Homo sapiens]

Accession:	gi|166795245	**Score:**	15.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	54.4
Database Date:	2015-11-30	**pI:**	5.6
		Sequence Coverage [%]:	3.9
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|166795247	refseq_human(refseq_human_20140103.fasta)	phosphatidylinositol 3-kinase regulatory subunit gamma [Homo sapiens]

10	20	30	40	50	60	70	80
MYNTVWSMDR	DDADWREVMM	PYSTELIFYI	EMDPPALPPK	PPKPMTSAVP	NGMKDSSVSL	QDAEWYWGDI	SREEVNDKLR
90	100	110	120	130	140	150	160
DMPDGTFLVR	DASTKMQGDY	TLTLRKGGNN	KLIKIYHRDG	KYGFSDPLTF	NSVVELINHY	HHESLAQYNP	KLDVKLMYPV
170	180	190	200	210	220	230	240
SRYQQDQLVK	EDNIDAVGKK	LQEYHSQYQE	KSKEYDRLYE	EYTRTSQEIQ	MKRTAIEAFN	ETIKIFEEQC	HTQEQHSKEY
250	260	270	280	290	300	310	320
IERFRREGNE	KEIERIMMNY	DKLKSRLGEI	HDSKMRLEQD	LKNQALDNRE	IDKKMNSIKP	DLIQLRKIRD	QHLVWLNHKG
330	340	350	360	370	380	390	400
VRQKRLNVWL	GIKNEDADEN	YFINEEDENL	PHYDEKTWFV	EDINRVQAED	LLYGKPDGAF	LIRESSKKGC	YACSVVADGE
410	420	430	440	450	460	470	
VKHCVIYSTA	RGYGFAEPYN	LYSSLKELVL	HYQQTSLVQH	NDSLNVRLAY	PVHAQMPSLC	R	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2317	1	1002.9127	-128.18	2	58.8	15.4	0	366-383	R.VQAEDLLYGKPDGAFLIR.E	

Detailed Protein Report

Protein 753: PREDICTED: talin-2 isoform X15 [Homo sapiens]

Accession:	gi|578827491	**Score:**	15.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	267.3
Database Date:	2015-11-30	**pI:**	5.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	0.7
		No. of unique Peptides:	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MVALSLKICV	RHCNVVKTMQ	FEPSTAVYDA	CRVIRERVPE	AQTGQASDYG	LFLSDEDPRK	GIWLEAGRTL	DYYMLRNGDI
90	100	110	120	130	140	150	160
LEYKKKQRPQ	KIRMLDGSVK	TVMVDDSKTV	GELLVTICSR	IGITNYEEYS	LIQETIEEKK	EEGTGTLKKD	RTLLRDERKM
170	180	190	200	210	220	230	240
EKLKAKLHTD	DDLNWLDHSR	TFREQGVDEN	ETLLLRRKFF	YSDQNVDSRD	PVQLNLLYVQ	ARDDILNGSH	PVSFEKACEF
250	260	270	280	290	300	310	320
GGFQAQIQFG	PHVEHKHKPG	FLDLKEFLPK	EYIKQRGAEK	RIFQEHKNCG	EMSEIEAKVK	YVKLARSLRT	YGVSFFLVKE
330	340	350	360	370	380	390	400
KMKGKNKLVP	RLLGITKDSV	MRVDEKTKEV	LQEWPLTTVK	RWAASPKSFT	LDFGEYQESY	YSVQTTEGEQ	ISQLIAGYID
410	420	430	440	450	460	470	480
IILKKKQSKD	RFGLEGDEES	TMLEESVSPK	KSTILQQQFN	RTGKAEHGSV	ALPAVMRSGS	SGPETFNVGS	MPSPQQQVMV
490	500	510	520	530	540	550	560
GQMHRGHMPP	LTSAQQALMG	TINTSMHAVQ	QAQDDLSELD	SLPPLGQDMA	SRVWVQNKVD	ESKHEIHSQV	DAITAGTASV
570	580	590	600	610	620	630	640
VNLTAGDPAD	TDYTAVGCAI	TTISSNLTEM	SKGVKLLAAL	MDDEVGSGED	LLRAARTLAG	AVSDLLKAVQ	PTSGEPRQTV
650	660	670	680	690	700	710	720
LTAAGSIGQA	SGDLLRQIGE	NETDERFQDV	LMSLAKAVAN	AAAMLVLKAK	NVAQVAEDTV	LQNRVIAAAT	QCALSTSQLV
730	740	750	760	770	780	790	800
ACAKVVSPTI	SSPVCQEQLI	EAGKLVDRSV	ENCVRACQAA	TTDSELLKQV	SAAASVVSQA	LHDLLQHVRQ	FASRGEPIGR
810	820	830	840	850	860	870	880
YDQATDTIMC	VTESIFSSMG	DAGEMVRQAR	VLAQATSDLV	NAMRSDAEAE	IDMENSKKLL	AAAKLLADST	ARMVEAAKGA
890	900	910	920	930	940	950	960
AANPENEDQQ	QRLREAAEGL	RVATNAAAQN	AIKKKIVNRL	EVAAKQAAAA	ATQTIAASQN	AAVSNKNPAA	QQQLVQSCKA
970	980	990	1000	1010	1020	1030	1040
VADHIPQLVQ	GVRGSQAQAE	DLSAQLALII	SSQNFLQPGS	KMVSSAKAAV	PTVSDQAAAM	QLSQCAKNLA	TSLAELRTAS
1050	1060	1070	1080	1090	1100	1110	1120
QKAHEACGPM	EIDSALNTVQ	TLKNELQDAK	MAAVESQLKP	LPGETLEKCA	QDLGSTSKAV	GSSMAQLLTC	AAQGNEHYTG
1130	1140	1150	1160	1170	1180	1190	1200
VAARETAQAL	KTLAQAARGV	AASTTDPAAA	HAMLDSARDV	MEGSAMLIQE	AKQALIAPGD	AERQQRLAQV	AKAVSHSLNN
1210	1220	1230	1240	1250	1260	1270	1280
CVNCLPGQKD	VDVALKSIGE	SSKKLLVDSL	PPSTKPFQEA	QSELNQAAAD	LNQSAGEVVH	ATRGQSGELA	AASGKFSDDF
1290	1300	1310	1320	1330	1340	1350	1360
DEFLDAGIEM	AGQAQTKEDQ	IQVIGNLKNI	SMASSKLLLA	AKSLSVDPGA	PNAKNLLAAA	ARAVTESINQ	LITLCTQQAP
1370	1380	1390	1400	1410	1420	1430	1440
GQKECDNALR	ELETVKGMLD	NPNEPVSDLS	YFDCIESVME	NSKVLGESMA	GISQNAKTGD	LPAFGECVGI	ASKALCGLTE
1450	1460	1470	1480	1490	1500	1510	1520
AAAQAAYLVG	ISDPNSQAGH	QGLVDPIQFA	RANQAIQMAC	QNLVDPGSSP	SQVLSAATIV	AKHTSALCNA	CRIASSKTAN
1530	1540	1550	1560	1570	1580	1590	1600
PVAKRHFVQS	AKEVANSTAN	LVKTIKALDG	DFSEDNRNKC	RIATAPLIEA	VENLTAFASN	PEFVSIPAQI	SSEGSQAQEP
1610	1620	1630	1640	1650	1660	1670	1680
ILVSAKTMLE	SSSYLIRTAR	SLAINPKDPP	TWSVLAGHSH	TVSDSIKSLI	TSIRDKAPGQ	RECDYSIDGI	NRCIRDIEQA
1690	1700	1710	1720	1730	1740	1750	1760
SLAAVSQSLA	TRDDISVEAL	QEQLTSVVQE	IGHLIDPIAT	AARGEAAQLG	HKVTQLASYF	EPLILAAVGV	ASKILDHQQQ
1770	1780	1790	1800	1810	1820	1830	1840
MTVLDQTKTL	AESALQMLYA	AKEGGGNPKA	QHTHDAITEA	AQLMKEAVDD	IMVTLNEAAS	EVGLVGGMVD	AIAEAMSKLD
1850	1860	1870	1880	1890	1900	1910	1920
EGTPPEPKGT	FVDYQTTVVK	YSKAIAVTAQ	EMIGFQIRTR	VQDLGHGCIF	LVQKAGALQV	CPTDSYTKRE	LIECARAVTE
1930	1940	1950	1960	1970	1980	1990	2000
KVSLVLSALQ	AGNKGTQACI	TAATAVSGII	ADLDTTIMFA	TAGTLNAENS	ETFADHRENI	LKTAKALVED	TKLLVSGAAS
2010	2020	2030	2040	2050	2060	2070	2080
TPDKLAQAAQ	SSAATITQLA	EVVKLGAASL	GSDDPETQVV	LINAIKDVAK	ALSDLISATK	GAASKPVDDP	SMYQLKGAAK
2090	2100	2110	2120	2130	2140	2150	2160
VMVTNVTSLL	KTVKAVEDEA	TRGTRALEAT	IECIKQELTV	FQSKDVPEKT	SSPEESIRMT	KGITMATAKA	VAAGNSCRQE
2170	2180	2190	2200	2210	2220	2230	2240
DVIATANLSR	KAVSDMLTAC	KQASFHPDVS	DEVRTRALRF	GTECTLGYLD	LLEHVLVILQ	KPTPEFKQQL	AAFSKRVAGA
2250	2260	2270	2280	2290	2300	2310	2320
VTELIQAAEA	MKGTEWVDPE	DPTVIAETEL	LGAAASIEAA	AKKLEQLKPR	AKPKQADETL	DFEEQILEAA	KSIAAATSAL
2330	2340	2350	2360	2370	2380	2390	2400

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1771	1	920.8147	-139.56	2	52.1	15.4	0	1193-1209	K.AVSHSLNNCVNCLPGQK.D	Carbamidomethyl: 9

Detailed Protein Report

Protein 754: phosphatidylcholine:ceramide cholinephosphotransferase 1 [Homo sapiens]

Accession: gi|29789379
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 15.4
MW [kDa]: 48.6
pI: 9.4
Sequence Coverage [%]: 4.4
No. of unique Peptides: 1

Alias proteins:

Accession	Name	Description
gi|530393372	refseq_human (refseq_human_20140103.fasta)	PREDICTED: phosphatidylcholine:ceramide cholinephosphotransferase 1 isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MKEVVYWSPK	KVADWLLENA	MPEYCEPLEH	FTGQDLINLT	QEDFKKPPLC	RVSSDNGQRL	LDMIETLKME	HHLEAHKNGH
90	100	110	120	130	140	150	160
ANGHLNIGVD	IPTPDGSFSI	KIKPNGMPNG	YRKEMIKIPM	PELERSQYPM	EWGKTFLAFL	YALSCFVLTT	VMISVVHERV
170	180	190	200	210	220	230	240
PPKEVQPPLP	DTFFDHFNRV	QWAFSICEIN	GMILVGLWLI	QWLLLKYKSI	ISRRFFCIVG	TLYLYRCITM	YVTTLPVPGM
250	260	270	280	290	300	310	320
HFNCSPKLFG	DWEAQLRRIM	KLIAGGGLSI	TGSHNMCGDY	LYSGHTVMLT	LTYLFIKEYS	PRRLWWYHWI	CWLLSVVGIF
330	340	350	360	370	380	390	400
CILLAHDHYT	VDVVVAYYIT	TRLFWWYHTM	ANQQVLKEAS	QMNLLARVWW	YRPFQYFEKN	VQGIVPRSYH	WPFPWPVVHL
410	420						
SRQVKYSRLV	NDT						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
25	1	1132.0072	-81.78	2	30.0	15.4	1	388-405	R.SYHWPFPWPVVHLSRQVK.Y	

Detailed Protein Report

Protein 755: PREDICTED: Golgin subfamily A member 8A isoform X1 [Homo sapiens]

Accession:	gi|578826741	**Score:**	15.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	67.1
Database Date:	2015-11-30	**pI:**	6.4
		Sequence Coverage [%]:	1.7
		No. of unique Peptides:	1

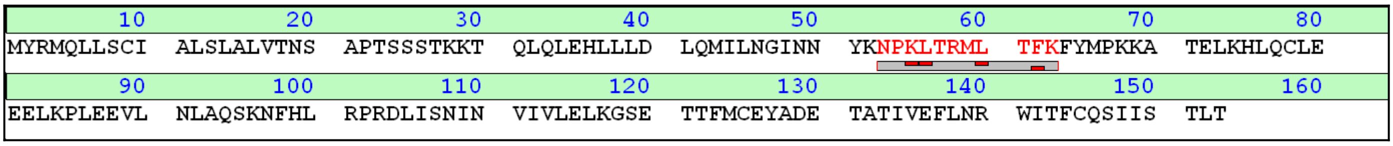
10	20	30	40	50	60	70	80
MAEETGQSKL	AAAKKKFKEY	WQRNRPGVPA	AAKRNTKANG	SSPETAASGG	CHSSEASSSA	SSSLHARQSP	CQEQAAVLNS
90	100	110	120	130	140	150	160
RSIKISRLND	TIKSLKQQKK	QVEHQLEEEK	KANNEKQKAE	RELEGQIQRL	NTEKKKLNTD	LYHMKHSLRY	FEEESKDLAG
170	180	190	200	210	220	230	240
RLQRSSQRIG	ELEWSLCAVA	ATQKKKPDGF	SSRSKALLKR	QLEQSIREQI	LLKGHVTQLK	ESLKEVQLER	DQYAEQIKGE
250	260	270	280	290	300	310	320
RAQWQQRMRK	MSQEVCTLKE	EKKHDTHRVE	ELERSLSRLK	NQMAEPLPPD	APAVSSEVEL	QDLRKELERV	AGELQAQVEN
330	340	350	360	370	380	390	400
NQCISLLNRG	QKERLREQEE	RLQEQQERLR	EREKRLQQLA	EPQSDLEELH	ENKSALQLEQ	QVKELQEKLG	QVMETLTSAE
410	420	430	440	450	460	470	480
KEPEAAVPAS	GTGGESSGLM	DLLEEKADLR	EHVEKLELGF	IQYRRERCHQ	KVHRLLTEPG	DSAKDASPGG	GHHQAGPGQG
490	500	510	520	530	540	550	560
GEEGEAAGAA	GDGVAACGSY	SEGHGKFLAA	ARNPAAEPSP	GAPAPQELGA	ADKHGDLCEA	SLTNSVEPAQ	GEAREGSSQD
570	580	590	600	610			
NPTAQPVVQL	LGEMQDHQEH	PGLGSNCCVP	CFCWAWLPRR	RR			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
865	1	647.7984	-105.89	2	40.3	15.4	1	436-445	K.LELGFIQYRR.E	

Detailed Protein Report

Protein 756: interleukin-2 precursor [Homo sapiens]

Accession:	gi|28178861	**Score:**	15.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	17.6
Database Date:	2015-11-30	**pI:**	9.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	7.2
		No. of unique Peptides:	1



```
        10         20         30         40         50         60         70         80
MYRMQLLSCI ALSLALVTNS APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE
        90        100        110        120        130        140        150        160
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR WITFCQSIIS TLT
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2286	1	682.7901	-145.71	2	58.5	15.4	2	53-63	K.NPKLTRMLTFK.F	Oxidation: 7

Detailed Protein Report

Protein 757: zinc finger protein 667 [Homo sapiens]

Accession:	gi|268607677	**Score:**	15.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	70.1
Database Date:	2015-11-30	**pI:**	10.9
		Sequence Coverage [%]:	2.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPSARGKSKS	KAPITFGDLA	IYFSQEEWEW	LSPIQKDLYE	DVMLENYRNL	VSLGLSFRRP	NVITLLEKGK	APWMVEPVRR
90	100	110	120	130	140	150	160
RRAPDSGSKC	ETKKLPPNQC	NKSGQSICQK	LVSAQQKAPT	RKSGCNKNSV	LVKPKKGHSG	KKPLKCNDCG	KTFSRSFSLK
170	180	190	200	210	220	230	240
LHQNIHTGEK	PFECSNCRKA	FRQISSILLH	QRIHSGKKSH	ECNKCGESFN	QRTTLILHMR	IHDGKEILDC	GKALSQCQSF
250	260	270	280	290	300	310	320
NIHQKIHVVG	NVCQCRKCGK	AFNQMSSLLL	HKKIHNGKKT	HKYNKCGRGF	KKKSVFVVHK	RIHAGEKIPE	NAKALSQSLQ
330	340	350	360	370	380	390	400
QRSHHLENPF	KCRKCGKLFN	RISPLMLHQR	IHTSEKPYKC	DKCDKFFRRL	STLILHLRIH	NGEKLYRCNK	CEKVCNRHSS
410	420	430	440	450	460	470	480
LIQHQKVHTK	KKKLFECKEC	GKMFSGTANL	KIHQNIHSEE	KPFKCNKCSK	VFGRQSFLIE	HQRIHTGEKP	YQCEECGKAF
490	500	510	520	530	540	550	560
SHRISLTRHK	RIHTEDRPYE	CDQCGKAFSQ	SAHLAQHERI	HTGEKPYTCK	TCGKAFSQRT	SLILHERSHT	GEKPYECNEC
570	580	590	600	610	620		
GKAFSSGSDL	IRHQRSHSSE	KPYECSKCGK	AYSRSSSLIR	HQNTHSEEKA			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
58	2	779.3515	-98.67	2	30.4	15.4	1	535-547	K.AFSQRTSLILHER.S	

Detailed Protein Report

Protein 758: zinc finger C2HC domain-containing protein 1C isoform a [Homo sapiens]

Accession:	gi|109452611	**Score:**	15.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	51.6
Database Date:	2015-11-30	**pI:**	10.2
		Sequence Coverage [%]:	3.5
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530404614	refseq_human (refseq_human_20140103.fasta)	PREDICTED: zinc finger C2HC domain-containing protein 1C isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MAGLQRLASH	LPVGVMLPHN	TTEAPGPHSA	KQDSYEQGDS	SQQSLKGHLR	NNFQKQLLSN	KELILDKVYT	HPKWNTQTKA
90	100	110	120	130	140	150	160
RSYSYPHCTG	ISQQDPESDS	QGQGNGLFYS	SGPQSWYPKA	NNQDFIPFTK	KRVGVDRAFP	LKPMVHRKSC	STGEAGTDGD
170	180	190	200	210	220	230	240
HNVYPRPPEP	REFSSRNFGV	RNQGNFSVVG	TVLAATQAEK	AVANFDRTEW	VQIRRLEAAG	ESLEEEIRRK	QILLRGKLKK
250	260	270	280	290	300	310	320
TEEELRRIQT	QKEQAKENEN	GELQKIILPR	SRVKGNKSNT	MYKPIFSPEF	EFEEEFSRDR	REDETWGRSQ	QNSGPFQFSD
330	340	350	360	370	380	390	400
YRIQRLKRER	LVASNNKIRD	PVSEPSVEKF	SPPSETPVGA	LQGSARNSSL	SMAPDSSGSS	GSIEEPQLGE	CSHCGRKFLS
410	420	430	440	450	460		
FRLERHSNIC	SRMRGSKRKV	FDSSRARAKG	TELEQYLNWK	GPASAKAEPP	QKSNWR		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2078	1	862.3310	-134.98	2	55.9	15.3	2	441-456	K.GPASAKAEPPQKSNWR.-	

Detailed Protein Report

Protein 759: **PREDICTED: N-acetyllactosaminide beta-1,6-N-acetylglucosaminyl-transferase isoform X7 [Homo sapiens]**

Accession:	gi|578811583	**Score:**	15.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	35.7
Database Date:	2015-11-30	**pI:**	9.4
		Sequence Coverage [%]:	8.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPLSMRYLFI	ISVSSVIIFI	VFSVFNFGGD	PSFQRLNISD	PLRLTQVCTS	FINGKTRFLW	KNKLMIHEKS	SCKEYLTQSH
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
YITAPLSKEE	ADFPLAYIMV	IHHHFDTFAR	LFRAIYMPQN	IYCVHVDEKA	TTEFKDAVEQ	LLSCFPNAFL	ASKMEPVVYG
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
GISRLQADLN	CIRDLSAFEV	SWKYVINTCG	QDFPLKTNKE	IVQYLKGFKG	KNITPGVLPP	AHAIGRTKYV	HQEHLGKELS
250	**260**	**270**	**280**	**290**	**300**	**310**	**320**
YVIRTTALKP	PPPHNLTIYF	GSAYVALSRE	FANFVLHDPR	AVDLLQWSKD	TFSPDEHFWV	TLNRIPVIQN	E

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1363	1	945.2770	90.99	3	46.7	15.3	2	212-237	K.NITPGVLPPAHAIGRTKYVHQEHLGK.E	

Detailed Protein Report

Protein 760: **PREDICTED: nck-associated protein 1 isoform X2 [Homo sapiens]**

Accession:	gi|578803513	**Score:**	15.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	128.5
Database Date:	2015-11-30	**pI:**	6.2
		Sequence Coverage [%]:	1.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSRSVLQPSQ	QKLAEKLTIL	NDRGVGMLTR	LYNIKKACGD	PKAKPSYLID	KNLESAVKFI	VRKFPAVETR	NNNLAQLQKE
90	100	110	120	130	140	150	160
KSEILKNLAL	YYFTFVDVME	FKDHVCELLN	TIDVCQVFFD	ITVNFDLTKN	YLDLIITYTT	LMILLSRIEE	RKAIIGLYNY
170	180	190	200	210	220	230	240
AHEMTHGASD	REYPRLGQMI	VDYENPLKKM	MEEFVPHSKS	LSDALISLQM	VYPRRNLSAD	QWRNAQLLSL	ISAPSTMLNP
250	260	270	280	290	300	310	320
AQSDTMPCEY	LSLDAMEKWI	IFGFILCHGI	LNTDATALNL	WKLALQSSSC	LSLFRDEVFH	IHKAAEDLFV	NIRGYNKRIN
330	340	350	360	370	380	390	400
DIRECKEAAV	SHAGSMHRER	RKFLRSALKE	LATVLSDQPG	LLGPKALFVF	MALSFARDEI	IWLLRHADNM	PKKSADDFID
410	420	430	440	450	460	470	480
KHIAELIFYM	EELRAHVRKY	GPVMQRYYVQ	YLSGFDAVVL	NELVQNLSVC	PEDESIIMSS	FVNTMTSLSV	KQVEDGEVFD
490	500	510	520	530	540	550	560
FRGMRLDWFR	LQAYTSVSKA	SLGLADHREL	GKMMNTIIFH	TKMVDSLVEM	LVETSDLSIF	CFYSRAFEKM	FQQCLELPSQ
570	580	590	600	610	620	630	640
SRYSIAFPLL	CTHFMSCTHE	LCPEERHHIG	DRSLSLCNMF	LDEMAKQARN	LITDICTEQC	TLSDQLLPKH	CAKTISQAVN
650	660	670	680	690	700	710	720
KKSKKQTGKK	GEPEREKPGV	ESMRKNRLVV	TNLDKLHTAL	SELCFSINYV	PNMVVWEHTF	TPREYLTSHL	EIRFTKSIVG
730	740	750	760	770	780	790	800
MTMYNQATQE	IAKPSELLTS	VRAYMTVLQS	IENYVQIDIT	RVFNNVLLQQ	TQHLDSHGEP	TITSLYTNWY	LETLLRQVSN
810	820	830	840	850	860	870	880
GHIAYFPAMK	AFVNLPTENE	LTFNAEEYSD	ISEMRSLSEL	LGPYGMKFLS	ESLMWHISSQ	VAELKKLVVE	NVDVLTQMRT
890	900	910	920	930	940	950	960
SFDKPDQMAA	LFKRLSSVDS	VLKRMTIIGV	ILSFRSLAQE	ALRDVLSYHI	PFLVSSIEDF	KDHIPRETDM	KVAMNVYELS
970	980	990	1000	1010	1020	1030	1040
SAAGLPCEID	PALVVALSSQ	KSENISPEEE	YKIACLLMVF	VAVSLPTLAS	NVMSQYSPAI	EGHCNNIHCL	AKAINQIAAA
1050	1060	1070	1080	1090	1100	1110	1120
LFTIHKGSIE	DRLKEFLALA	SSSLLKIGQE	TDKTTTRNRE	SVYLLLDMIV	QESPFLTMDL	LESCFPYVLL	RNAYHAVYKQ
1130							
SVTSSA							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2717	1	805.4289	10.68	2	65.2	15.3	1	304-317	K.AAEDLFVNIRGYNK.R	

Detailed Protein Report

Protein 761: PREDICTED: ras association domain-containing protein 3 isoform X1 [Homo sapiens]

Accession:	gi|578823589	**Score:**	15.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	26.3
Database Date:	2015-11-30	**pI:**	8.8
		Sequence Coverage [%]:	4.8
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MSHCAWPAIW IFKSTLASSA YSLPTLQDVE KEKETHSYLS KEEIKEKVHK YNLAVTDKLK MTLNSNGIYT GFIKVQMELC
        90        100        110        120        130        140        150        160
KPPQTSPNSG KLSPSSNGCM NTLHISSTNT VGEVIEALLK KFLVTESPAK FALYKRCHRE DQVYACKLSD REHPLYLRLV
       170        180        190        200        210        220        230
AGPRTDTLSF VLREHEIGEW EAFSLPELQN FLRILDKEED EQLQNLKRRY TAYRQKLEEA LREVWKPD
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
684	3	676.1721	-185.76	2	37.9	15.3	1	137-147	R.CHREDQVYACK.L	

Detailed Protein Report

Protein 762: **protein KIAA1045 [Homo sapiens]**

Accession:	gi|149944593	**Score:**	15.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	45.2
Database Date:	2015-11-30	**pI:**	5.4
		Sequence Coverage [%]:	4.8
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530389814	refseq_human (refseq_human_20140103.fasta)	PREDICTED: protein KIAA1045 isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MGVLMSKRQT	VEQVQKVSLA	VSAFKDGLRD	RPSIRRTGEL	PGSRRGTVEG	SVQEVQEEKE	AEAGTSVVQE	ESSAGRAAWE
90	100	110	120	130	140	150	160
RLRDGRGVEP	EEFDRTSRFT	PPAFIRPTRK	LDDDKPPEIC	LEPREPVVND	EMCDVCEVWT	AESLFPCRVC	TRVFHDGCLR
170	180	190	200	210	220	230	240
RMGYIQGDSA	AEVTEMAHTE	TGWSCHYCDN	INLLLTEEEM	YSLTETFQRC	KVIPDCSLTL	EDFLRYRHQA	AKRGDRDRAL
250	260	270	280	290	300	310	320
SEEQEEQAAR	QFAALDPEHR	GHIEWPDFLS	HESLLLLQQL	RPQNSLLRLL	TVKERERARA	AFLARGSGST	VSEAECRRAQ
330	340	350	360	370	380	390	400
HSWFCKRFPE	APSCSVSISH	VGPIADSSPA	SSSSKSQDKT	LLPTEQESRF	VDWPTFLQEN	VLYILAARPN	SAAIHLKPPG
410							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2572	1	1044.0320	-55.24	2	62.1	15.3	2	17-35	K.VSLAVSAFKDGLRDRPSIR.R	

Detailed Protein Report

Protein 763: **protein lin-37 homolog [Homo sapiens]**

Accession:	gi|28144916	**Score:**	15.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	28.4
Database Date:	2015-11-30	**pI:**	9.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	8.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MFPVKVKVEK	SELEMAKARN	QLDAVLQCLL	EKSHMDRERL	DEEAGKTPSD	THNKDCSIAA	TGKRPSARFP	HQRRKKRREM
90	100	110	120	130	140	150	160
DDGLAEGGPQ	RSNTYVIKLF	DRSVDLAQFS	ENTPLYPICR	AWMRNSPSVR	ERECSPSSPL	PPLPEDEEGS	EVTNSKSRDV
170	180	190	200	210	220	230	240
YKLPPPTPPG	PPGDACRSRI	PSPLQPEMQG	TPDDEPSEPE	PSPSTLIYRN	MQRWKRIRQR	WKEASHRNQL	RYSESMKILR
250							
EMYERQ							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
260	1	881.1909	94.66	3	32.6	15.3	1	99-120	K.LFDRSVDLAQFSENTPLYPICR.A	Carbamidomethyl: 21

Detailed Protein Report

Protein 764: FERM and PDZ domain-containing protein 1 [Homo sapiens]

Accession:	gi|239582741	**Score:**	15.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	173.3
Database Date:	2015-11-30	**pI:**	5.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEELETSLFQ	TRKAHRIEQM	VARWLRRSRD	SSARAKVAAA	DGPARNPTQT	LIPVRHTVKI	DKDTLLQDYG	FHISESLPLT
90	100	110	120	130	140	150	160
VVAVTAGGSA	HGKLFPGDQI	LQMNNEPAED	LSWERAVDIL	REAEDSLSIT	VVRCTSGVPK	SSFLTEEKRA	RLKTNPVKVH
170	180	190	200	210	220	230	240
FAEEVLISGH	SQGNSLLCMP	NVLKLYLENG	QTKAFKFEAN	TTVKDIILTV	KEKLSIRSIE	YFALALEEQY	SISRLHLLHE
250	260	270	280	290	300	310	320
EELIQQVVER	EESHDYRCLF	RVCFVPKDPL	DLLKEDPVAF	EYLYLQSCSD	VLQERFAVEM	KCSSALRLAA	LHIQERIYAC
330	340	350	360	370	380	390	400
AQPQKISLKY	IEKDWGIENF	ISPTLLRNMK	GKDIKKAISF	HMKRNQNLLE	PRQKQLISAA	QLRLNYLQIL	GELKTYGGRI
410	420	430	440	450	460	470	480
FNATLMLQDR	ESYIALLVGA	KYGISQVINS	KLNIMSTLAE	FANISRVELT	EESEKVSVVK	VYLQDVKVLT	LLLESNSAKD
490	500	510	520	530	540	550	560
LACLIAGYYR	LLVDPVTSIF	LWPGNKQQAH	RVSAEEGYES	RACSDSEESS	EVDCVLEPLS	DRRLVKLAPC	RSLIKEEQPP
570	580	590	600	610	620	630	640
GNSPTPEVAR	RGPSTCGASS	TTDSAESEAS	DSANTESRGY	RTSGSSESMD	ALEEDDLDTC	SSSRSTFFHF	GSPGLAESID
650	660	670	680	690	700	710	720
SDSQEERSGI	ETSGFLCLLD	LAQRANPQCQ	KTEFSESAAL	ETFGWAPELS	TVRLDPRLYE	GSHADYYSLC	SSVSPASYLS
730	740	750	760	770	780	790	800
DSSESTASRQ	GGAPPAWGQQ	GWTEAQPSSM	LEPLALHPPL	AFEDGSSDEE	YYDAADKLTP	PGPPSGPRDV	STAEPSATSL
810	820	830	840	850	860	870	880
QNKASTSSPE	NSLPCGPDGR	QPSRRGGVKK	YAKTLRKRRS	FLQTDYTSQV	SFPLVPSASL	ESVDDVCYYD	REPYLALGAP
890	900	910	920	930	940	950	960
SPTVSSLQDM	QGEPGLLETK	ALGLLAPLRE	TKSTNPASRV	MEMEPETMET	KSVIDSRVSS	ISAIRFRIDP	NNKENSGVVP
970	980	990	1000	1010	1020	1030	1040
AASSSASTPH	CSNPGSSGPD	TAQARPSQIL	PLSQDLDGIA	PKEPTIEHGD	SSFSLSSGDP	NPDRACLASN	PGLNNVSQGD
1050	1060	1070	1080	1090	1100	1110	1120
TLELQLEPHV	QLEMGLESFC	TNHIQETAPK	YTEPLLSPRD	EPRSDECGIN	PGEKIASIPT	KEEPQGQLSL	ERDREVTNKN
1130	1140	1150	1160	1170	1180	1190	1200
GTNVFQEESR	KDSGDSPGDV	SNNVSQTLDI	SSPAGKIVTS	LSLDAPVTGT	EQIPPHPPRD	PQGQSREPPG	QGCQAQEQKL
1210	1220	1230	1240	1250	1260	1270	1280
FVELDLDPDF	FLGKQTVSPA	VPPEGIKAEA	PNHVTGQDIA	PRDSPEWVCF	NPEPSLPEPL	PCPQEDPHLE	TSNHCLLSEG
1290	1300	1310	1320	1330	1340	1350	1360
KSDSSSICLS	AEKSFLCFAP	ESHPEVSASL	RVATSLGFAG	MNEMVAPRIG	MDQCSCQFSY	ATCFRGPQPE	TEEEDRDLEA
1370	1380	1390	1400	1410	1420	1430	1440
HPMAPLTSPP	SAGSPVVLPW	RPARAHSCTT	APLSRKSHIW	PEYCSRALRQ	LKATPASTPE	GFIQLMESLL	ELQDILETSW
1450	1460	1470	1480	1490	1500	1510	1520
GVGNKHPPEK	CTWHFTESRS	RLCMGSQKLL	SSCRHVIRMD	QSPEEMQGAV	RDTFQHLVQL	AGLCFQFTDC	SRCSARHREA
1530	1540	1550	1560	1570	1580		
AGNLRDVVYT	YHQFIEAAKS	TCERGYHDLS	VKLLARQCTA	LTAAVFCLTQ	KFRASTAL		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2077	1	1158.9066	-123.27	2	55.9	15.3	1	1526-1544	R.DVVYTYHQFIEAAKSTCER.G	Carbamidomethyl: 17

Detailed Protein Report

Protein 765: olfactory receptor 52B6 [Homo sapiens]

Accession:	gi|148229439	**Score:**	15.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	36.9
Database Date:	2015-11-30	**pI:**	9.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	5.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAQVRALHKI	MALFSANSIG	AMNNSDTRIA	GCFLTGIPGL	EQLHIWLSIP	FCIMYITALE	GNGILICVIL	SQAILHEPMY
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
IFLSMLASAD	VLLSTTTMPK	ALANLWLGYS	LISFDGCLTQ	MFFIHFLFIH	SAVLLAMAFD	RYVAICSPLR	YVTILTSKVI
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
GKIVTAALSH	SFIIMFPSIF	LLEHLHYCQI	NIIAHTFCEH	MGIAHLSCSD	ISINVWYGLA	AALLSTGLDI	MLITVSYIHI
250	**260**	**270**	**280**	**290**	**300**	**310**	**320**
LQAVFRLLSQ	DARSKALSTC	GSHICVILLF	YVPALFSVFA	YRFGGRSVPC	YVHILLASLY	VVIPPMLNPV	IYGVRTKPIL
330	**340**						
EGAKQMFSNL	AKGSK						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1979	1	1022.8769	-95.89	2	54.9	15.2	0	10-28	K.IMALFSANSIGAMNNSDTR.I	Oxidation: 2, 13

Detailed Protein Report

Protein 766: **undifferentiated embryonic cell transcription factor 1 [Homo sapiens]**

Accession:	gi|71043876	**Score:**	15.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	36.4
Database Date:	2015-11-30	**pI:**	11.8
		Sequence Coverage [%]:	6.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLLRPRRPPP	LAPPAPPSPA	SPDPEPRTPG	DAPGTPPRRP	ASPSALGELG	LPVSPGSAQR	TPWSARETEL	LLGTLLQPAV
90	100	110	120	130	140	150	160
WRALLLDRRQ	ALPTYRRVSA	ALAQQQVRRT	PAQCRRRYKF	LKDKFREAHG	QPPGPFDEQI	RKLMGLLGDN	GRKRPRRRSP
170	180	190	200	210	220	230	240
GSGRPQRARR	PVPNAHAPAP	SEPDATPLPT	ARDRDADPTW	TLRFSPSPPK	SADASPAPGS	PPAPAPTALA	TCIPEDRAPV
250	260	270	280	290	300	310	320
RGPGSPPPPP	AREDPDSPPG	RPEDCAPPPA	APPSLNTALL	QTLGHLGDIA	NILGPLRDQL	LTLNQHVEQL	RGAFDQTVSL
330	340	350					
AVGFILGSAA	AERGVLRDPC	Q					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2319	1	788.1227	53.82	3	59.3	15.2	0	170-192	R.RPVPNAHAPAPSEPDATPLPTAR.D	

Detailed Protein Report

Protein 767: olfactory receptor 2T10 [Homo sapiens]

Accession: gi|52317215
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 15.2
MW [kDa]: 35.4
pI: 9.7
Sequence Coverage [%]: 5.4
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MRLANQTLGG	DFFLLGIFSQ	ISHPGRLCLL	IFSIFLMAVS	WNITLILLIH	IDSSLHTPMY	FFINQLSLID	LTYISVTVPK
90	100	110	120	130	140	150	160
MLVNQLAKDK	TISVLGCGTQ	MYFYLQLGGA	ECCLLAAMAY	DRYVAICHPL	RYSVLMSHRV	CLLLASGCWF	VGSVDGFMLT
170	180	190	200	210	220	230	240
PIAMSFPFCR	SHEIQHFFCE	VPAVLKLSCS	DTSLYKIFMY	LCCVIMLLIP	VTVISVSYYY	IILTIHKMNS	VEGRKKAFTT
250	260	270	280	290	300	310	320
CSSHITVVSL	FYGAAIYNYM	LPSSYQTPEK	DMMSSFFYTI	LTPVLNPIIY	SFRNKDVTRA	LKKMLSVQKP	PY

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2039	1	1022.8938	-135.34	2	55.6	15.2	1	123-139	R.YVAICHPLRYSVLMSHR.V	

Detailed Protein Report

Protein 768: PREDICTED: peroxidasin homolog isoform X2 [Homo sapiens]

Accession:	gi|578802575	**Score:**	15.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	155.5
Database Date:	2015-11-30	**pI:**	7.1
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	0.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAKRSRGPGR	RCLLALVLFC	AWGTLAVVAQ	KPGAGCPSRC	LCFRTTVRCM	HLLLEAVPAV	APQTSILDLR	FNRIREIQPG
90	100	110	120	130	140	150	160
AFRRLRNLNT	LLLNNNQIKR	IPSGAFEDLE	NLKYLYLYKN	EIQSIDRQAF	KGLASLEQLY	LHFNQIETLD	PDSFQHLPKL
170	180	190	200	210	220	230	240
ERLFLHNNRI	THLVPGTFNH	LESMKRLRLD	SNTLHCDCEI	LWLADLLKTY	AESGNAQAAA	ICEYPRRIQG	RSVATITPEE
250	260	270	280	290	300	310	320
LNCERPRITS	EPQDADVTSG	NTVYFTCRAE	GNPKPEIIWL	RNNNELSMKT	DSRLNLLDDG	TLMIQNTQET	DQGIYQCMAK
330	340	350	360	370	380	390	400
NVAGEVKTQE	VTLRYFGSPA	LPQFTVTPQD	RVVIEGQTVD	FQCEAKGNPP	PVIAWTKGGS	QLSVDRRHLV	LSSGTLRISG
410	420	430	440	450	460	470	480
VALHDQGQYE	CQAVNIIGSQ	KVVAHLTVQP	RVTPVFASIP	SDTTVEVGAN	VQLPCSSQGE	PEPAITWNKD	GVQVTESGKF
490	500	510	520	530	540	550	560
HISPEGFLTI	NDVGPADAGR	YECVARNTIG	SASVSMVLSV	NVPDVSRNGD	PFVATSIVEA	IATVDRAINS	TRTHLFDSRP
570	580	590	600	610	620	630	640
RSPNDLLALF	RYPRDPYTVE	QARAGEIFER	TLQLIQEHVQ	HGLMVDLNGT	SYHYNDLVSP	QYLNLIANLS	GCTAHRRVNN
650	660	670	680	690	700	710	720
CSDMCFHQKY	RTHDGTCNNL	QHPMWGASLT	AFERLLKSVY	ENGFNTPRGI	NPHRLYNGHA	LPMPRLVSTT	LIGTETVTPD
730	740	750	760	770	780	790	800
EQFTHMLMQW	GQFLDHDLDS	TVVALSQARF	SDGQHCSNVC	SNDPPCFSVM	IPPNDSRARS	GARCMFFVRS	SPVCGSGMTS
810	820	830	840	850	860	870	880
LLMNSVYPRE	QINQLTSYID	ASNVYGSTEH	EARSIRDLAS	HRGLLRQGIV	QRSGKPLLPF	ATGPPTECMR	DENESPIPCF
890	900	910	920	930	940	950	960
LAGDHRANEQ	LGLTSMHTLW	FREHNRIATE	LLKLNPHWDG	DTIYYETRKI	VGAEIQHITY	QHWLPKILGE	VGMRTLGEYH
970	980	990	1000	1010	1020	1030	1040
GYDPGINAGI	FNAFATAAFR	FGHTLVNPLL	YRLDENFQPI	AQDHLPLHKA	FFSPFRIVNE	GGIDPLLRGL	FGVAGKMRVP
1050	1060	1070	1080	1090	1100	1110	1120
SQLLNTELTE	RLFSMAHTVA	LDLAAINIQR	GRDHGIPPYH	DYRVYCNLSA	AHTFEDLKNE	IKNPEIREKL	KRLYGSTLNI
1130	1140	1150	1160	1170	1180	1190	1200
DLFPALVVED	LVPGSRLGPT	LMCLLSTQFK	RLRDGDRLWY	ENPGVFSPAQ	LTQIKQTSLA	RILCDNADNI	TRVQSDVFRV
1210	1220	1230	1240	1250	1260	1270	1280
AEFPHGYGSC	DEIPRVDLRV	WQDCCEDCRT	RGQFNAFSYH	FRGRRSLEFS	YQEDKPTKKT	RPRKIPSVGR	QGEHLSNSTS
1290	1300	1310	1320	1330	1340	1350	1360
AFSTRSDASG	TNDFREFVLE	MQKTITDLRT	QIKKLESRLS	TTECVDAGGE	SHANNTKWKK	DACTICECKD	GQVTCFVEAC
1370	1380	1390					
PPATCAVPVN	IPGACCPVCL	QKRAEEKP					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2617	1	741.8602	81.44	2	63.4	15.2	0	638-649	R.VNNCSDMCFHQK.Y	Carbamidomethyl: 4

Detailed Protein Report

Protein 769: tissue factor pathway inhibitor 2 isoform 3 precursor [Homo sapiens]

Accession:	gi|401871061	**Score:**	15.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	20.9
Database Date:	2015-11-30	**pI:**	5.1
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	9.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDPARPLGLS	ILLLFLTEAA	LGDAAQEPTG	NNAEICLLPL	DYGPCRALLL	RYYYDRYTQS	CRQFLYGGCE	GNANNFYTWE
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
ACDDACWRIE	KVPKVCRLQV	SVDDQCEGST	EKYFFNLSSM	TCEKFFSGGC	HRNRIENRFP	DEATCMGFCA	PKKNTEPVML
170	**180**	**190**					
SPILAVEGMT	ITLLAGRIAN	VHVQKL					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1701	1	1051.4907	28.58	2	51.1	15.2	1	135-152	R.IENRFPDEATCMGFCAPK.K	Carbamidomethyl: 15; Oxidation: 12

Detailed Protein Report

Protein 770: **small ubiquitin-related modifier 2 isoform a precursor [Homo sapiens]**

Accession:	gi|54792069	**Score:**	15.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	10.9
Database Date:	2015-11-30	**pI:**	5.2
Modification(s):	Oxidation	**Sequence Coverage [%]:**	14.7
		No. of unique Peptides:	1

```
         10         20         30         40         50         60         70         80
MADEKPKEGV KTENNDHINL KVAGQDGSVV QFKIKRHTPL SKLMKAYCER QGLSMRQIRF RFDGQPINET DTPAQLEMED
         90        100
EDTIDVFQQQ TGGVY
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1786	1	851.2906	-146.43	2	52.2	15.2	2	43-56	K.LMKAYCERQGLSMR.Q	Oxidation: 13

Detailed Protein Report

Protein 771: **FXYD6-FXYD2 read-through protein isoform 2 precursor [Homo sapiens]**

Accession:	gi|343790943	**Score:**	15.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	12.8
Database Date:	2015-11-30	**pI:**	11.0
		Sequence Coverage [%]:	10.7
		No. of unique Peptides:	1

```
         10         20         30         40         50         60         70         80
MELVLVFLCS LLAPMVLASA AEKEKEMDPF HYDYQTLRIG GLVFAVVLFS VGILLILRPQ EMRKPRWRTS SPPMQQSPRK
         90        100        110        120
QRTEVQPSGG RRQPQGGRGP VLLWQKIPLW GQ
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
426	1	672.4157	111.99	2	34.6	15.2	1	69-80	R.TSSPPMQQSPRK.Q	

Detailed Protein Report

Protein 772: PREDICTED: DNA mismatch repair protein Msh2 isoform X1 [Homo sapiens]

Accession: gi|530367623
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 15.2
MW [kDa]: 103.1
pI: 5.7
Sequence Coverage [%]: 2.0
No. of unique Peptides: 1

```
        10         20         30         40         50         60         70         80
MAVQPKETLQ LESAAEVGFV RFFQGMPEKP TTTVRLFDRG DFYTAHGEDA LLAAREVFKT QGVIKYMGPA GAKNLQSVVL

        90        100        110        120        130        140        150        160
SKMNFESFVK DLLLVRQYRV EVYKNRAGNK ASKENDWYLA YKASPGNLSQ FEDILFGNND MSASIGVVGV KMSAVDGQRQ

       170        180        190        200        210        220        230        240
VGVGYVDSIQ RKLGLCEFPD NDQFSNLEAL LIQIGPKECV LPGGETAGDM GKLRQIIQRG GILITERKKA DFSTKDIYQD

       250        260        270        280        290        300        310        320
LNRLLKGKKG EQMNSAVLPE MENQVAVSSL SAVIKFLELL SDDSNFGQFE LTTFDFSQYM KLDIAAVRAL NLFQGSVEDT

       330        340        350        360        370        380        390        400
TGSQSLAALL NKCKTPQGQR LVNQWIKQPL MDKNRIEERL NLVEAFVEDA ELRQTLQEDL LRRFPDLNRL AKKFQRQAAN

       410        420        430        440        450        460        470        480
LQDCYRLYQG INQLPNVIQA LEKHEGKHQK LLLAVFVTPL TDLRSDFSKF QEMIETTLDM DQVENHEFLV KPSFDPNLSE

       490        500        510        520        530        540        550        560
LREIMNDLEK KMQSTLISAA RDLGLDPGKQ IKLDSSAQFG YYFRVTCKEE KVLRNNKNFS TVDIQKNGVK FTNSKLTSLN

       570        580        590        600        610        620        630        640
EEYTKNKTEY EEAQDAIVKE IVNISSGYVE PMQTLNDVLA QLDAVVSFAH VSNGAPVPYV RPAILEKGQG RIILKASRHA

       650        660        670        680        690        700        710        720
CVEVQDEIAF IPNDVYFEKD KQMFHIITGP NMGGKSTYIR QTGVIVLMAQ IGCFVPCESA EVSIVDCILA RVGAGDSQLK

       730        740        750        760        770        780        790        800
GVSTFMAEML ETASILRSAT KDSLIIIDEL GRGTSTYDGF GLAWAISEYI ATKIGAFCMF ATHFHELTAL ANQIPTVNNL

       810        820        830        840        850        860        870        880
HVTALTTEET LTMLYQVKKG VCDQSFGIHV AELANFPKHV IECAKQKALE LEEFQYIGES QGYDIMEPAA KKCYLERENL

       890        900        910        920        930
RVTEPKDQCL ILLTWKRKLR GGKRSACSRP ERQNQGSGEL S
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
151	1	981.4369	-27.53	2	31.6	15.2	2	904-921	K.RSACSRPERQNQGSGELS.-	

Detailed Protein Report

Protein 773: zinc finger and SCAN domain-containing protein 32 isoform c [Homo sapiens]

Accession:	gi|548960717	**Score:**	15.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	46.2
Database Date:	2015-11-30	**pI:**	10.0
		Sequence Coverage [%]:	2.7
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 1.06 **CV:** 0.00 % **No. of Peptides:** 1

Alias proteins:

Accession	Name	Description
gi|548961843	refseq_human (refseq_human_20140103.fasta)	zinc finger and SCAN domain-containing protein 32 isoform c [Homo sapiens]

10	20	30	40	50	60	70	80
MAEGLWEQGF	LRTPEQCRTK	FKSLQLSYRK	VRRGRVPEPC	IFYEEMNALS	GSWASAPPMA	SDAVPGQEGS	DIEAGELNHQ
90	100	110	120	130	140	150	160
NGEPTEVEDG	TVDGADRDEK	DFRNPGQEVR	KLDLPVLFPN	RLGFEFKNEI	KKENLKWDDS	EEVEINKALQ	RKSRGVYWHS
170	180	190	200	210	220	230	240
ELQKGLESEP	TSRRQCRNSP	GESEEKTPSQ	EKMSHQSFCA	RDKACTHILC	GKNCSQSVHS	PHKPALKLEK	VSQCPECGKT
250	260	270	280	290	300	310	320
FSRSSYLVRH	QRIHTGEKPH	KCSECGKGFS	ERSNLTAHLR	THTGERPYQC	GQCGKSFNQS	SSLIVHQRTH	TGEKPYQCIV
330	340	350	360	370	380	390	400
CGKRFNNSSQ	FSAHRRIHTG	ESPYKCAVCG	KIFNNSSHFS	AHRKTHTGEK	PYRCSHCERG	FTKNSALTRH	QTVHMKAVLS
410							
SQEGRDAL							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
707	1	647.6537	-225.58	2	38.4	15.1	0	325-335	R.FNNSSQFSAHR.R		MD:MU 1.06

Detailed Protein Report

Protein 774: PREDICTED: FH1/FH2 domain-containing protein 3 isoform X6 [Homo sapiens]

Accession:	gi|530413959	**Score:**	15.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	170.6
Database Date:	2015-11-30	**pI:**	5.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MATLACRVQF	LDDTDPFNST	NFPEPSRPPL	FTFREDLALG	TQLAGVHRLL	QAPHKLDDCT	LQLSHNGAYL	DLEATLAEQR
90	100	110	120	130	140	150	160
DELEGFQDDA	GRGKKHSIIL	RTQLSVRVHA	CIEKLYNSSG	RDLRRALFSL	KQIFQDDKDL	VHEFVVAEGL	TCLIKVGAEA
170	180	190	200	210	220	230	240
DQNYQNYILR	ALGQIMLYVD	GMNGVINRNE	TIQWLYTLIG	SKFRLVVKTA	LKLLLVFVEY	SESNAPLLIQ	AVTAVDTKRG
250	260	270	280	290	300	310	320
VKPWSNIMEI	LEEKDGVDTE	LLVYAMTLVN	KTLSGLPDQD	TFYDVVDCLE	ELGIAAVSQR	HLNKKGTDLD	LVEQLNIYEV
330	340	350	360	370	380	390	400
ALRHEDGDET	TEPPPSGCRD	RRRASVCSSG	GGEHRGLDRR	RSRRHSVQSI	KSTLSAPTSP	CSQSAPSFKP	NQVRDLREKE
410	420	430	440	450	460	470	480
EEEEEEQPIT	EPSSEEERED	DASCQGKDSK	VGAASGQSPT	GRDAAPKSSA	LPAVSNASSQ	GKPLLVGTAG	GTTWHSGSSG
490	500	510	520	530	540	550	560
SEATPSALLS	PPASAARPSS	ATPGSLKVSP	TIDKLPYVPH	SPFHLFSYDF	EDSSLSTKEK	EAESQKENSS	SDSFSLSTYS
570	580	590	600	610	620	630	640
ASEPYHFRSF	SSNRYSNFGN	NSYHSSRPSS	GSSVPTTPTS	SVSPPQEARL	ERSSPSGLLT	SSFRQHQESL	AAERERRRQE
650	660	670	680	690	700	710	720
REERLQRIER	EERNKFSRDY	LDKREEQRQA	REERYKYLEQ	LAAEEHEKEL	RSRSVSRGRA	DLSLDLTSPA	APACLAPLSH
730	740	750	760	770	780	790	800
SPSSSDSQEA	LTVSASSPGT	PHHPQASAGD	PEPESEAEPE	AEAGAGQVAD	EAGQDIASAH	EGAETEVEQA	LEQEPEERAS
810	820	830	840	850	860	870	880
LSEKERQNEG	VNERDNCSAS	SVSSSSSTLE	REEKEDKLSR	DRTTGLWPAG	VQDAGVNGQC	GDILTNKRFM	LDMLYAHNRK
890	900	910	920	930	940	950	960
SPDDEEKGDG	EAGRTQQEAE	AVASLATRIS	TLQANSQTQD	ESVRRVDVGC	LDNRGSVKAF	AEKFNSGDLG	RGSISPDAEP
970	980	990	1000	1010	1020	1030	1040
NDKVPETAPV	QPKTESDYIW	DQLMANPREL	RIQDMDFTDL	GEEDDIDVLD	VDLGHREAPG	PPPPPPPTFL	GLPPPPPPPL
1050	1060	1070	1080	1090	1100	1110	1120
LDSIPPPPVP	GNLLVPPPPV	FNAPQGLGWS	QVPRGQPTFT	KKKKTIRLFW	NEVRPFDWPC	KNNRRCREFL	WSKLEPIKVD
1130	1140	1150	1160	1170	1180	1190	1200
TSRLEHLFES	KSKELSVSKK	TAADGKRQEI	IVLDSKRSNA	INIGLTVLPP	PRTIKIAILN	FDEYALNKEG	IEKILTMIPT
1210	1220	1230	1240	1250	1260	1270	1280
DEEKQKIQEA	QLANPEIPLG	SAEQFLLTLS	SISELSARLH	LWAFKMDYET	TEKEVAEPLL	DLKEGIDQLE	NNKTLGFILS
1290	1300	1310	1320	1330	1340	1350	1360
TLLAIGNFLN	GTNAKAFELS	YLEKVPEVKD	TVHKQSLLHH	VCTMVVENFP	DSSDLYSEIG	AITRSAKVDF	DQLQDNLCQM
1370	1380	1390	1400	1410	1420	1430	1440
ERRCKASWDH	LKAIAKHEMK	PVLKQRMSEF	LKDCAERIII	LKIVHRRIIN	RFHSFLLFMG	HPPYAIREVN	INKFCRIISE
1450	1460	1470	1480	1490	1500	1510	1520
FALEYRTTRE	RVLQQKQKRA	NHRERNKTRG	KMITDDPLVP	GLWELMTRPM	SQMMQLMRSW	TASSSQPPKC	PVSEWCRGRG
1530	1540						
NDPGPTGNLC	EEP						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
876	1	835.2166	-178.08	2	40.5	15.1	1	1518-1533	R.GRGNDPGPTGNLCEEP.-	Carbamidomethyl: 13

Detailed Protein Report

Protein 775: zinc finger protein 441 [Homo sapiens]

Accession:	gi|193083160	**Score:**	15.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	80.1
Database Date:	2015-11-30	**pI:**	9.9
		Sequence Coverage [%]:	2.2
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 1.16 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MDSVAFEDVA	INFTCEEWAL	LGPSQKSLYR	DVMQETIRNL	DCIGMIWQNH	DIEEDQYKDL	RRNLRCHMVE	RACEIKDNSQ
90	100	110	120	130	140	150	160
CGGPFTQTQD	SIVNEKIPGV	DPWESSECTD	VLMGRSSLNC	YVRVDSEHKP	CEYQEYGEKP	YTHTQCGTAF	SYQPCFQIHE
170	180	190	200	210	220	230	240
RPQHGKKLYD	CKECASFSSL	ENLQRHMAAH	HGDGPRICKL	CGNAFIWPSL	FHMLRRTHTE	EKPYEYEQCS	TAFPAYSSTL
250	260	270	280	290	300	310	320
RHERTHSGEK	PYQCKQCGKA	FSCSCYTQLY	ERTHTGEQSY	ECKQCGKAFY	HLGSFQRHMI	VHTGDGPHKC	KICGKGFLSP
330	340	350	360	370	380	390	400
SSVRRHKRTH	TGEKPYECKY	CGKAFSDCTG	FRRHMITHTG	DGPHKCKVCG	KAFDSPSLCR	RHETTHTGEK	PYKCECGKAF
410	420	430	440	450	460	470	480
SDFYYFRNHE	TTHTGEKPYK	CKQCGKAFIC	CTYLQIHERI	HTGERPYKCK	QCGKAFRSSN	YIRVHEKTHT	GEKPYECKQC
490	500	510	520	530	540	550	560
GKALSHLKSF	QRHMIMHTGD	GPHKCKICGK	SFDSPSSFRR	HERIHTGERP	YKCKLCGKGF	RSSSYIQLHE	RTHTGEKPYG
570	580	590	600	610	620	630	640
CQQCGKALSD	LSSFRRHMIT	HTGNGPHKCK	ICGKGFDYPS	SVQRHERTHT	GEKPYECKEC	GKAFSHSSYL	RIHERVHTGE
650	660	670	680	690	700		
KPYKCKECGK	PFHCPSAFHK	HERTHSMEKP	YKCKECGEAF	HCISSFHKHE	MTH		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
864	1	893.3321	-112.97	2	40.2	15.1	1	464-478	R.VHEKTHTGEKPYECK.Q		MD:MU 1.16

Detailed Protein Report

Protein 776: **E3 ubiquitin-protein ligase RNF103 isoform 2 [Homo sapiens]**

Accession:	gi|312147324	**Score:**	15.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	78.6
Database Date:	2015-11-30	**pI:**	5.5
		Sequence Coverage [%]:	2.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSRLRPRPPL	IHGCGGFFEA	IVWYETGIFA	TQLVDPVALS	FKKLKTILEC	RGLGYSGLPE	KKDVRELVEK	SGDLMEGELY
90	100	110	120	130	140	150	160
SALKEEEASE	SVSSTNFSGE	MHFYELVEDT	KDGIWLVQVI	ANDRSPLVGK	IHWEKMVKKV	SRFGIRTGTF	NCSSDPRYCR
170	180	190	200	210	220	230	240
RRGWVRSTLI	MSVPQTSTSK	GKVMLKEYSG	RKIEVEHIFK	WITAHAASRI	KTIYNAEHLK	EEWNKSDQYW	LKIYLFANLD
250	260	270	280	290	300	310	320
QPPAFFSALS	IKFTGRVEFI	FVNVENWDNK	SYMTDIGIYN	MPSYILRTPE	GIYRYGNHTG	EFISLQAMDS	FLRSLQPEVN
330	340	350	360	370	380	390	400
DLFVLSLVLV	NLMAWMDLFI	TQGATIKRFV	VLISTLGTYN	SLLIISWLPV	LGFLQLPYLD	SFYEYSLKLL	RYSNTTTLAS
410	420	430	440	450	460	470	480
WVRADWMFYS	SHPALFLSTY	LGHGLLIDYF	EKKRRRNNNN	DEVNANNLEW	LSSLWDWYTS	YLFHPIASFQ	NFPVESDWDE
490	500	510	520	530	540	550	560
DPDLFLERLA	FPDLWLHPLI	PTDYIKNLPM	WRFKCLGVQS	EEEMSEGSQD	TENDSESENT	DTLSSEKEVF	EDKQSVLHNS
570	580	590	600	610	620	630	640
PGTASHCDAE	ACSCANKYCQ	TSPCERKGRS	YGSYNTNEDM	EPDWLTWPAD	MLHCTECVVC	LENFENGCLL	MGLPCGHVFH
650	660	670	680	690			
QNCIVMWLAG	GRHCCPVCRW	PSYKKKQPYA	QHQPLSNDVP	S			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1808	1	840.7848	-139.97	2	52.6	15.1	0	667-681	K.QPYAQHQPLSNDVPS.-	

Detailed Protein Report

Protein 777: **zinc finger protein 786 [Homo sapiens]**

Accession:	gi|170932473	**Score:**	15.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	89.8
Database Date:	2015-11-30	**pI:**	10.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAEPPRLPLT	FEDVAIYFSE	QEWQDLEAWQ	KELYKHVMRS	NYETLVSLDD	GLPKPELISW	IEHGGEPFRK	WRESQKSGNI
90	100	110	120	130	140	150	160
ICSSVDMHFD	PGFEEQLFWG	SQQAMNSGKT	KSHFQLDPES	QCSFGSFVSF	RPDQGITLGS	PQRHDARAPP	PLACGPSEST
170	180	190	200	210	220	230	240
LKEGIPGPRN	LDLPGLWDVP	AWESTQHPWP	VCGESCWENN	HLVMHQRGHS	KDRTRRAWEK	FNKRAETQMP	WSSPRVQRHF
250	260	270	280	290	300	310	320
RCGVCGKSFR	RKLCLLRHLA	AHTGRGPFRN	ADGEMCFRHE	LTHPSHRLPQ	QGEKPAQCTP	CGKRSLPVDS	TQARRCQHSR
330	340	350	360	370	380	390	400
EGPASWREGR	GASSSVHSGQ	KPGSRLPQEG	NSHQEGDTEA	LQHGAEGPCS	CSECGERSPM	SARLASPCRA	HTGEKPFQCA
410	420	430	440	450	460	470	480
HCTKRFRLRR	LLQVHQHAHG	GERPFSCRKC	GKGFAKQCKL	TEHIRVHSGE	KPFRCAKCGR	NFRQRGQLLR	HQRLHTDEKP
490	500	510	520	530	540	550	560
FQCPECGLSF	RLESMLRAHR	LRHGGERPFS	CSECGRGFTH	QCKLREHLRV	HSGERPFQCL	KCDKRFRLKG	ILKAHQHTHS
570	580	590	600	610	620	630	640
KERPFSCGEC	GKGFTRQSKL	TEHLRVHSGE	RPFQCPECNR	SFRLKGQLLS	HQRLHTGERP	FQCPECDKRY	RVKADMKAHQ
650	660	670	680	690	700	710	720
LLHSGEMPFS	CECGKGFVKH	SKLIEHIRTH	TGEKPFQCPK	CDKSFRLKAQ	LLSHQGLHTG	ERPFHCPECD	KNFRERGHML
730	740	750	760	770	780	790	
RHQRIHRPER	PFACGDCGKG	FIYKSKLAEH	IRVHTKSCPA	PNELDIKKRL	SQLFAMIEAD	WS	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1191	1	883.7560	20.93	3	44.5	15.0	2	501-523	R.LRHGGERPFSCSECGRGFTHQCK.L	Carbamidomethyl: 11

Protein 778: GEM-interacting protein isoform 2 [Homo sapiens]

Accession:	gi|573014822	**Score:**	15.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	103.6
Database Date:	2015-11-30	**pI:**	5.5
		Sequence Coverage [%]:	1.6
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 2.39 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MDAAEPGLPP	GPEGRKRYSD	IFRSLDNLEI	SLGNVTLEML	AGDPLLSEDP	EPDKTPTATV	TNEASCWSGP	SPEGPVPLTG
90	100	110	120	130	140	150	160
EELDLRLIRT	KGGVDAALEY	AKTWSRYAKE	LLAWTEKRAS	YELEFAKSTM	KIAEAGKVSI	QQQSHMPLQY	IYTLFLEHDL
170	180	190	200	210	220	230	240
SLGTLAMETV	AQQKRDYYQP	LAAKRTEIEK	WRKEFKEQWM	KEQKRMNEAV	QALRRAQLQY	VQRSEDLRAR	SQGSPEDSAP
250	260	270	280	290	300	310	320
QASPGPSKQQ	ERRRRSREEA	QAKAQEAEAL	YQACVREANA	RQQDLEIAKQ	RIVSHVRKLV	FQGDEVLRRV	TLSLFGLRGA
330	340	350	360	370	380	390	400
QAERGPRAFA	ALAECCAPFE	PGQRYQEFVR	ALRPEAPPPP	PPAFSFQEFL	PSLNSSPLDI	RKKLSGPLPP	RLDENSAEPG
410	420	430	440	450	460	470	480
PWEDPGTGWR	WQGPTPGSDV	DSVGGGSESR	SLDSPTSSPD	LGDGLENGLG	SPFGKWTLSS	AAQTHQLRRL	RGPAKCRECE
490	500	510	520	530	540	550	560
AFMVSGTECE	ECFLTCHKRC	LETLLILCGH	RRLPARTPLF	GVDFLQLPRD	FPEEVPFVVT	KCTAEIEHRA	LDVQGIYRVS
570	580	590	600	610	620	630	640
GSRVRVERLC	QAFENGRALV	ELSGNSPHDV	SSVLKRFLQE	LTEPVIPFHL	YDAFISLAKT	LHADPGDDPG	TPSPSPEVIR
650	660	670	680	690	700	710	720
SLKTLLVQLP	DSNYNTLRHL	VAHLFRVAAR	FMENKMSANN	LGIVFGPTLL	RPPDGPRAAS	AIPVTCLLDS	GHQAQLVEFL
730	740	750	760	770	780	790	800
IVHYEQIFGM	DELPQATEPP	PQDSSPAPGP	LTTSSQPPPP	HLDPDSQPPV	LASDPGPDPQ	HHSTLEQHPT	ATPTEIPTPQ
810	820	830	840	850	860	870	880
SDQREDVAED	TKDGGGEVSS	QGPEDSLLGT	QSRGHFSRQP	VKYPRGGVRP	VTHQLSSLAL	VASKLCEETP	ITSVPRGSLR
890	900	910	920	930	940	950	
GRGPSPAAAS	PEGSPLRRTP	LPKHFEITQE	TARLLSKLDS	EAVPRATCCP	DVQPEEAEDH	L	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1688	1	745.8381	-60.85	2	50.9	15.0	1	2-16	M.DAAEPGLPPGPEGRK.R		MD:MU 2.39

Detailed Protein Report

Protein 779: PREDICTED: NCK-interacting protein with SH3 domain isoform X2 [Homo sapiens]

Accession:	gi|530372644	**Score:**	14.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	70.2
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
MRDGGKYSLE	QRGVLQKLIH	HRKETLSRRG	PSASSVAVMT	SSTSDHHLDA	AAARQPNGVC	RAGFERQHSL	PSSEHLGADG
90	100	110	120	130	140	150	160
GLYQIPLPSS	QIPPQPRRAA	PTTPPPPVKR	RDREALMASG	SGGHNTMPSG	GNSVSSGSSV	SSTSLDTLYT	SSSPSEPGSS
170	180	190	200	210	220	230	240
CSPTPPPVPR	RGTHTTVSQV	QPPPSKASAP	EPPAEEEVAT	GTTSASDDLE	ALGTLSLGTT	EEKAAAEAAV	PRTIGAELME
250	260	270	280	290	300	310	320
LVRRNTGLSH	ELCRVAIGII	VGHIQASVPA	SSPVMEQVLL	SLVEGKDLSM	ALPSGQVCHD	QQRLEVIFAD	LARRKDDAQQ
330	340	350	360	370	380	390	400
RSWALYEDEG	VIRCYLEELL	HILTDADPEV	CKKMCKRNEF	ESVLALVAYY	QMEHRASLRL	LLLKCFGAMC	SLDAAIISTL
410	420	430	440	450	460	470	480
VSSVLPVELA	RDMQTDTQDH	QKLCYSALIL	AMVFSMGEAV	PYAHYEHLGT	PFAQFLLNIV	EDGLPLDTTE	QLPDLCVNLL
490	500	510	520	530	540	550	560
LALNLHLPAA	DQNVIMAALS	KHANVKIFSE	KLLLLLNRGD	DPVRIFKHEP	QPPHSVLKFL	QDVFGSPATA	AIFYHTDMMA
570	580	590	600	610	620	630	640
LIDITVRHIA	DLSPGDKLRM	EYLSLMHAIV	RTTPYLQHRH	RLPDLQAILR	RILNEEETSP	QCQMDRMIVR	EMCKEFLVLG
650							
EAPS							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1879	1	719.2624	-127.38	2	53.5	14.9	0	322-333	R.SWALYEDEGVIR.C	

Detailed Protein Report

Protein 780: **PREDICTED: integrin alpha-11 isoform X2 [Homo sapiens]**

Accession:	gi|530405525	**Score:**	14.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	122.0
Database Date:	2015-11-30	**pI:**	6.0
		Sequence Coverage [%]:	1.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MRLGLSLATN	PKDNSFLACS	PLWSHECGSS	YYTTGMCSRV	NSNFRFSKTV	APALQRCQTY	MDIVIVLDGS	NSIYPWVEVQ
90	100	110	120	130	140	150	160
HFLINILKKF	YIGPGQIQVG	VVQYGEDVVH	EFHLNDYRSV	KDVVEAASHI	EQRGGTETRT	AFGIEFARSE	AFQKGGRKGA
170	180	190	200	210	220	230	240
KKVMIVITDG	ESHDSPDLEK	VIQQSERDNV	TRYAVAVLGY	YNRRGINPET	FLNEIKYIAS	DPDDKHFFNV	TDEAALKDIV
250	260	270	280	290	300	310	320
DALGDRIFSL	EGTNKNETSF	GLEMSQTGFS	SHVVEDGVLL	GAVGAYDWNG	AVLKETSAGK	VIPLRESYLK	EFPEELKNHG
330	340	350	360	370	380	390	400
AYLGYTVTSV	VSSRQGRVYV	AGAPRFNHTG	KVILFTMHNN	RSLTIHQAMR	GQQIGSYFGS	EITSVDIDGD	GVTDVLLVGA
410	420	430	440	450	460	470	480
PMYFNEGRER	GKVYVYELRQ	NLFVYNGTLK	DSHSYQNARF	GSSIASVRDL	NQDSYNDVVV	GAPLEDNHAG	AIYIFHGFRG
490	500	510	520	530	540	550	560
SILKTPKQRI	TASELATGLQ	YFGCSIHGQL	DLNEDGLIDL	AVGALGNAVI	LWSRPVVQIN	ASLHFEPSKI	NIFHRDCKRS
570	580	590	600	610	620	630	640
GRDATCLAAF	LCFTPIFLAP	HFQTTTVGIR	YNATMDERRY	TPRAHLDEGG	DRFTNRAVLL	SSGQELCERI	NFHVLDTADY
650	660	670	680	690	700	710	720
VKPVTFSVEY	SLEDPDHGPM	LDDGWPTTLR	VSVPFWNGCN	EDEHCVPDLV	LDARSDLPTA	MEYCQRVLRK	PAQDCSAYTL
730	740	750	760	770	780	790	800
SFDTTVFIIE	STRQRVAVEA	TLENRGENAY	STVLNISQSA	NLQFASLIQK	EDSDGSIECV	NEERRLQKQV	CNVSYPFFRA
810	820	830	840	850	860	870	880
KAKVAFRLDF	EFSKSIFLHH	LEIELAAGSD	SNERDSTKED	NVAPLRFHLK	YEADVLFTRS	SSLSHYEVKP	NSSLERYDGI
890	900	910	920	930	940	950	960
GPPFSCIFRI	QNLGLFPIHG	MMMKITIPIA	TRSGNRLLKL	RDFLTDEANT	SCNIWGNSTE	YRPTPVEEDL	RRAPQLNHSN
970	980	990	1000	1010	1020	1030	1040
SDVVSINCNI	RLVPNQEINF	HLLGNLWLRS	LKALKYKSMK	IMVNAALQRQ	FHSPFIFREE	DPSRQIVFEI	SKQEDWQVPI
1050	1060	1070	1080	1090			
WIIVGSTLGG	LLLLALLVLA	LWKLGFFRSA	RRRREPGLDP	TPKVLE			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
294	1	680.1976	-193.61	2	33.0	14.9	0	789-799	K.QVCNVSYPFFR.A	

Detailed Protein Report

Protein 781: **PREDICTED: coiled-coil domain-containing protein 141 isoform X1 [Homo sapiens]**

Accession:	gi|578804115	**Score:**	14.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	167.8
Database Date:	2015-11-30	**pI:**	5.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSSQGSPSVA	LSTTTVSSVA	VQAGDSKIVI	AVIKCGKWVQ	LQLAESQPNL	LEIGSSQDET	KKLLHDHELL	LAKLKALEDR
90	100	110	120	130	140	150	160
VWELLQEADK	TAEENKDQSQ	VYDAMAETLG	EAWAALVSML	ERRTELLRLT	SEFFENALEF	AIKIDQAEDF	LQNTHEFESA
170	180	190	200	210	220	230	240
ESLKSLLQLH	EHHTKELLER	SLALLNKSQQ	LTDFIEKFKC	EGPNVNPELT	QGAHSSCLKV	DRLLELLQDR	RRQLDKYLKQ
250	260	270	280	290	300	310	320
QWQELSQVLQ	ICQWDQQENQ	VTCWFQKTIR	NLQEQSLGSS	LSDNEDRIHK	QEELIIKAKE	WNSAVEKLKS	EALRILLSKD
330	340	350	360	370	380	390	400
YVEKEHLQLS	HQKLSQLQEE	FGQLMVERNT	WLKKANEFFN	SANKAFDVLG	RVEAYLKLLK	SEGLSLAVLA	VRHEELHRKI
410	420	430	440	450	460	470	480
KDCTTDALQK	GQTLISQVDS	CSSQVSGIHE	MMGCIKRRVD	HLTEQCSAHK	EYALKKQQLT	ASVEGYLRKV	EMSIQKISPV
490	500	510	520	530	540	550	560
LSNAMDVGST	RSESEKILNK	YLELDIQAKE	TSHELEAAAK	TMMEKNEFVS	DEMVSLSSKA	RWLAEELNLF	GQSIDYRSQV
570	580	590	600	610	620	630	640
LQTYVAFLKS	SEEAKENEIL	DVKNEVYLMK	NTMENQKAER	EELSLLRLAW	QLKATESKPG	KQQWAAFKEQ	LKKTSHNLKL
650	660	670	680	690	700	710	720
LQEALMPVSA	LDLGGSLQFI	LDLRQKWNDM	KPQFQQLNDE	VQYIMKESEE	LTGRGAPVKE	KSQQLKDLIH	FHQKQKERIQ
730	740	750	760	770	780	790	800
DYEDILYKVV	QFHQVKEELG	RLIKSRELEF	VEQPKELGDA	HDVQIHLRCS	QEKQARVDHL	HRLALSLGVD	IISSVQRPHC
810	820	830	840	850	860	870	880
SNVSAKNLQQ	QLELLEEDSM	KWRAKAEEYG	RTLSRSVEYC	AMRDEINELK	DSFKDIKKKF	NNLKFNYTKK	NEKSRNLKAL
890	900	910	920	930	940	950	960
KYQIQQVDMY	AEKMQALKRK	MEKVSNKTSD	SFLNYPSDKV	NVLLEVMKDL	QKHVDDFDKV	VTDYKKNLDL	TEHFQEVIEE
970	980	990	1000	1010	1020	1030	1040
CHFWYEDASA	TVVRVGKYST	ECKTKEAVKI	LHQQFNKFIA	PSVPQQEERI	QEATDLAQHL	YGLEEGQKYI	EKIVTKHKEV
1050	1060	1070	1080	1090	1100	1110	1120
LESVTELCES	LTELEEKLKQ	GDVLKMNPNL	EDFHYDYIDL	LKEPAKNKQT	IFNEERNKGQ	VQVADLLGIN	GTGEERLPQD
1130	1140	1150	1160	1170	1180	1190	1200
LKVSTDKEGG	VQDLLLPEDM	LSGEEYECVS	PDDISLPPLP	GSPESPLAPS	DMEVEEPVSS	SLSLHISSYG	VQAGTSSPGD
1210	1220	1230	1240	1250	1260	1270	1280
AQESVLPPPV	AFADACNDKR	ETFSSHFERP	YLQFKAEPPL	TSRGFVEKST	ALHRISAEHP	ESMMSEVHER	ALQQHPQAQG
1290	1300	1310	1320	1330	1340	1350	1360
GLLETREKMH	ADNNFTKTQD	RLHASSDAFS	GLRFQSGTSR	GYQRQMVPRE	EIKSTSAKSS	VVSLADQAPN	FSRLLSNVTV
1370	1380	1390	1400	1410	1420	1430	1440
MEGSPVTLEV	EVTGFPEPTL	TWYKKGQKLS	ADGHLQVLHK	ETRHSVFIPK	VCKADAGLYV	ARAQNSSGAL	SSNVILHVTG
1450	1460	1470	1480				
NCRLPITRVN	WITLCVVYVS	VSLMYWLLTQ					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1525	1	1052.1493	126.64	2	48.7	14.9	1	882-898	K.YQIQQVDMYAEKMQALK.R	Oxidation: 8

Detailed Protein Report

Protein 782: prolyl 3-hydroxylase 3 precursor [Homo sapiens]

Accession:	gi|28466983	**Score:**	14.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	81.8
Database Date:	2015-11-30	**pI:**	5.9
		Sequence Coverage [%]:	1.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLRLLRPLLL	LLLLPPPGSP	EPPGLTQLSP	GAPPQAPDLL	YADGLRAYAA	GAWAPAVALL	REALRSQAAL	GRVRLDCGAS
90	100	110	120	130	140	150	160
CAADPGAALP	AVLLGAPEPD	SGPGPTQGSW	ERQLLRAALR	RADCLTQCAA	RRLGPGGAAR	LRVGSALRDA	FRRREPYNYL
170	180	190	200	210	220	230	240
QRAYYQLKKL	DLAAAAAHTF	FVANPMHLQM	REDMAKYRRM	SGVRPQSFRD	LETPPHWAAY	DTGLELLGRQ	EAGLALPRLE
250	260	270	280	290	300	310	320
EALQGSLAQM	ESCRADCEGP	EEQQGAEEEE	DGAASQGGLY	EAIAGHWIQV	LQCRQRCVGE	TATRPGRSFP	VPDFLPNQLR
330	340	350	360	370	380	390	400
RLHEAHAQVG	NLSQAIENVL	SVLLFYPEDE	AAKRALNQYQ	AQLGEPRPGL	GPREDIQRFI	LRSLGEKRQL	YYAMEHLGTS
410	420	430	440	450	460	470	480
FKDPDPWTPA	ALIPEALREK	LREDQEKRPW	DHEPVKPKPL	TYWKDVLLLE	GVTLTQDSRQ	LNGSERAVLD	GLLTPAECGV
490	500	510	520	530	540	550	560
LLQLAKDAAG	AGARSGYRGR	RSPHTPHERF	EGLTVLKAAQ	LARAGTVGSQ	GAKLLLEVSE	RVRTLTQAYF	SPERPLHLSF
570	580	590	600	610	620	630	640
THLVCRSAIE	GEQEQRMDLS	HPVHADNCVL	DPDTGECWRE	PPAYTYRDYS	GLLYLNDDFQ	GGDLFFTEPN	ALTVTARVRP
650	660	670	680	690	700	710	720
RCGRLVAFSS	GVENPHGVWA	VTRGRRCALA	LWHTWAPEHR	EQEWIEAKEL	LQESQEEEEE	EEEEMPSKDP	SPEPPSRRHQ
730	740						
RVQDKTGRAP	RVREEL						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1015	1	967.4606	-122.98	1	42.3	14.9	1	133-142	R.LGPGGAARLR.V	

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Detailed Protein Report

Protein 783: **nuclear body protein SP140 isoform 2 [Homo sapiens]**

Accession:	gi|52487277	**Score:**	14.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	20.0
Database Date:	2015-11-30	**pI:**	5.5
		Sequence Coverage [%]:	7.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAQQGQQGQM	ASGDSNLNFR	MVAEIQNVEG	QNLQEQVCPE	PIFRFFRENK	VEIASAITRP	FPFLMGLRDR	SFISEQMYEH
90	100	110	120	130	140	150	160
FQEAFRNLVP	VTRVMYCVLS	ELEKTFGWSH	LEALFSRINL	MAYPDLNEIY	RSFQNENLSS	SAVLCQLVSP	NKDWRSHEES
170	180						
LAHTGTLRRS	CM						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1971	1	719.2914	-92.19	2	54.5	14.9	0	156-168	R.SHEESLAHTGTLR.R	

Detailed Protein Report

Protein 784: caspase-14 precursor [Homo sapiens]

Accession:	gi|6912286	**Score:**	14.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	27.7
Database Date:	2015-11-30	**pI:**	5.3
		Sequence Coverage [%]:	6.6
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MSNPRSLEEE KYDMSGARLA LILCVTKARE GSEEDLDALE HMFRQLRFES TMKRDPTAEQ FQEELEKFQQ AIDSREDPVS
        90        100        110        120        130        140        150        160
CAFVVLMAHG REGFLKGEDG EMVKLENLFE ALNNKNCQAL RAKPKVYIIQ ACRGEQRDPG ETVGGDEIVM VIKDSPQTIP
       170        180        190        200        210        220        230        240
TYTDALHVYS TVEGYIAYRH DQKGSCFIQT LVDVFTKRKG HILELLTEVT RRMAEAELVQ EGKARKTNPE IQSTLRKRLY
       250
LQ
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1910	2	865.8067	-132.27	2	54.0	14.9	0	76-91	R.EDPVSCAFVVLMAHGR.E	

Detailed Protein Report

Protein 785: melanoma-associated antigen B6 [Homo sapiens]

Accession:	gi|29337290	**Score:**	14.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	44.0
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
MPRGHKSKLR	TCEKRQETNG	QPQGLTGPQA	TAEKQEESHS	SSSSSRACLG	DCRRSSDASI	PQESQGVSPT	GSPDAVVSYS
90	100	110	120	130	140	150	160
KSDVAANGQD	EKSPSTSRDA	SVPQESQGAS	PTGSPDAGVS	GSKYDVAANG	QDEKSPSTSH	DVSVPQESQG	ASPTGSPDAG
170	180	190	200	210	220	230	240
VSGSKYDVAA	EGEDEESVSA	SQKAIIFKRL	SKDAVKKKAC	TLAQFLQKKF	EKKESILKAD	MLKCVRREYK	PYFPQILNRT
250	260	270	280	290	300	310	320
SQHLVVAFGV	ELKEMDSSGE	SYTLVSKLGL	PSEGILSGDN	ALPKSGLLMS	LLVVIFMNGN	CATEEEVWEF	LGLLGIYDGI
330	340	350	360	370	380	390	400
LHSIYGDARK	IITEDLVQDK	YVVYRQVCNS	DPPCYEFLWG	PRAYAETTKM	RVLRVLADSS	NTSPGLYPHL	YEDALIDEVE
410							
RALRLRA							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2515	1	862.3895	-90.54	2	61.9	14.9	1	227-239	R.REYKPYFPQILNR.T	

Detailed Protein Report

Protein 786: **cbp/p300-interacting transactivator 4 [Homo sapiens]**

Accession:	gi|19263349	**Score:**	14.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	18.6
Database Date:	2015-11-30	**pI:**	5.3
		Sequence Coverage [%]:	6.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MADHLMLAEG	YRLVQRPPSA	AAAHGPHALR	TLPPYAGPGL	DSGLRPRGAP	LGPPPPRQPG	ALAYGAFGPP	SSFQPFPAVP
90	100	110	120	130	140	150	160
PPAAGIAHLQ	PVATPYPGRA	AAPPNAPGGP	PGPQPAPSAA	APPPPAHALG	GMDAELIDEE	ALTSLELELG	LHRVRELPEL
170	180	190					
FLGQSEFDCF	SDLGSAPPAG	SVSC					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1602	1	703.7006	-185.91	2	49.9	14.9	0	1-12	-.MADHLMLAEGYR.L	

Detailed Protein Report

Protein 787: kinase D-interacting substrate of 220 kDa [Homo sapiens]

Accession:	gi|55741641	**Score:**	14.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	196.4
Database Date:	2015-11-30	**pI:**	6.2
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.2
		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

Detailed Protein Report

	Cmpds.		[ppm]		[min]					
1150	1	1137.7077	130.83	2	44.0	14.9	0	35-55	R.NECGQTPLMIAAEQGNLEIVK.E	Oxidation: 9

Detailed Protein Report

Protein 788: **olfactory receptor 56A1 [Homo sapiens]**

Accession:	gi|284172508	**Score:**	14.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	35.8
Database Date:	2015-11-30	**pI:**	10.1
		Sequence Coverage [%]:	9.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MIQPMASPSN	SSTVPVSEFL	LICFPNFQSW	QHWLSLPLSL	LFLLAMGANT	TLLITIQLEA	SLHQPLYYLL	SLLSLLDIVL
90	100	110	120	130	140	150	160
CLTVIPKVLA	IFWYDLRSIS	FPACFLQMFI	MNSFLPMESC	TFMVMAYDRY	VAICHPLRYP	SIITNQFVAK	ASVFIVVRNA
170	180	190	200	210	220	230	240
LLTAPIPILT	SLLHYCGENV	IENCICANLS	VSRLSCDNFT	LNRIYQFVAG	WTLLGSDLFL	IFLSYTFILR	AVLRFKAEGA
250	260	270	280	290	300	310	320
AVKALSTCGS	HFILILFFST	ILLVVVLTNV	ARKKVPMDIL	ILLNVLHHLI	PPALNPIVYG	VRTKEIKQGI	QKLLQRGR

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2787	1	1086.6653	15.08	3	65.2	14.8	1	274-302	K.KVPMDILILLNVLHHLIPPALNPIVYGVR.T	

Detailed Protein Report

Protein 789: PREDICTED: death ligand signal enhancer isoform X6 [Homo sapiens]

Accession:	gi|530380768	**Score:**	14.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	42.7
Database Date:	2015-11-30	**pI:**	10.1
		Sequence Coverage [%]:	3.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MWRLPGLLGR	ALPRTLGPSL	WRVTPKSTSP	DGPQTTSSTL	LVPVPNLDRS	GPHGPGTSGG	PRSHGWKDAF	QWMSSRVSPN
90	100	110	120	130	140	150	160
TLWDAISWGT	LAVLALQLAR	QIHFQASLPA	GPQRVEHCSW	HSPLDRFFSS	PLWHPCSSLR	QHILPSPDGP	APRHTGLREP
170	180	190	200	210	220	230	240
RLGQEEASAQ	PRNFSHNSLR	GARPQDPSEE	GPGDFGFLHA	SSSIESEAKP	AQPQPTGEKE	QDKSKTLSLE	EAVTSIQQLF
250	260	270	280	290	300	310	320
QLSVSIAFNF	LGTENMKSGD	HTAAFSYFQK	AAARGYSKAQ	YNAGLCHEHG	RGTPRDISKA	VLYYQLAASQ	GHSLAQYRYA
330	340	350	360	370	380	390	
RCLLRDPASS	WNPERQRAVS	LLKQAADSGL	REAQAFLGVL	FTKEPYLDEQ	RAVKYLWLAA	NNGPRGPAT	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2125	1	775.3350	-103.58	2	56.7	14.8	0	101-114	R.QIHFQASLPAGPQR.V	

Detailed Protein Report

Protein 790: **PREDICTED: choline transporter-like protein 3 isoform X4 [Homo sapiens]**

Accession:	gi|530361747	**Score:**	14.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	64.8
Database Date:	2015-11-30	**pI:**	9.7
		Sequence Coverage [%]:	3.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MHCLGAEYLV	SAEGAPRQRE	WRPQIYRKCT	DTAWLFLFFL	FWTGLVFIMG	YSVVAGAAGR	LLFGYDSFGN	MCGKKNSPVE
90	100	110	120	130	140	150	160
GAPLSGQDMT	LKKHVFFMNS	CNLEVKGTQL	NRMALCVSNC	PEEQLDSLEE	VQFFANTSGS	FLCVYSLNSF	NYTHSPKADS
170	180	190	200	210	220	230	240
LCPRLPVPPS	KSFPLFNRCV	PQTPECYSLF	ASVLINDVDT	LHRILSGIMS	GRDTILGLCI	LALALSLAMM	FTFRFITTLL
250	260	270	280	290	300	310	320
VHIFISLVIL	GLLFVCGVLW	WLYYDYTNDL	SIELDTEREN	MKCVLGFAIV	STGITAVLLV	LIFVLRKRIK	LTVELFQITN
330	340	350	360	370	380	390	400
KAISSAPFLL	FQPLWTFAIL	IFFWVLWVAV	LLSLGTAGAA	QVMEGGQVEY	KPLSGIRYMW	SYHLIGLIWT	SEFILACQQM
410	420	430	440	450	460	470	480
TIAGAVVTCY	FNRSKNDPPD	HPILSSLSIL	FFYHQGTVVK	GSFLISVVRI	PRIIVMYMQN	ALKEQQHGAL	SRYLFRCCYC
490	500	510	520	530	540	550	560
CFWCLDKYLL	HLNQNAYTTT	AINGTDFCTS	AKDAFKILSK	NSSHFTSINC	FGDFIIFLGK	SFVKRSNKLN	NARAQQDKHS
570	580						
LRNEEGTELQ	AIVR						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2747	1	1044.5342	23.81	2	64.7	14.8	1	1-19	-.MHCLGAEYLVSAEGAPRQR.E	

Detailed Protein Report

Protein 791: claudin-3 [Homo sapiens]

Accession:	gi|4502875	**Score:**	14.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	23.3
Database Date:	2015-11-30	**pI:**	9.3
		Sequence Coverage [%]:	15.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSMGLEITGT	ALAVLGWLGT	IVCCALPMWR	VSAFIGSNII	TSQNIWEGLW	MNCVVQSTGQ	MQCKVYDSLL	ALPQDLQAAR
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
ALIVVAILLA	AFGLLVALVG	AQCTNCVQDD	TAKAKITIVA	GVLFLLAALL	TLVPVSWSAN	TIIRDFYNPV	VPEAQKREMG
170	**180**	**190**	**200**	**210**	**220**	**230**	
AGLYVGWAAA	ALQLLGGALL	CCSCPPREKK	YTATKVVYSA	PRSTGPGASL	GTGYDRKDYV		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1768	1	1105.3391	53.26	3	52.1	14.8	0	81-113	R.ALIVVAILLAAFGLLVALVGAQCTNCVQDDTAK.A	

Protein 792: uncharacterized protein C11orf94 precursor [Homo sapiens]

Accession:	gi|148229481	**Score:**	14.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	10.9
Database Date:	2015-11-30	**pI:**	10.2
		Sequence Coverage [%]:	15.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MVLAMLGALH	PRAGLSLFLH	LILAVALLRS	QPLRSQRSVP	EAFSAPLELS	QPLSGLVDDY	GILPKHPRPR	GPRPLLSRAQ
90	100						
QRKRDGPDLA	EYYYDAHL						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2213	1	899.3247	-92.16	2	57.5	14.8	1	84-98	K.RDGPDLAEYYYDAHL.-	

Detailed Protein Report

Protein 793: **glycolipid transfer protein [Homo sapiens]**

Accession:	gi|7705987	**Score:**	14.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	23.8
Database Date:	2015-11-30	**pI:**	7.7
		Sequence Coverage [%]:	7.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MALLAEHLLK	PLPADKQIET	GPFLEAVSHL	PPFFDCLGSP	VFTPIKADIS	GNITKIKAVY	DTNPAKFRTL	QNILEVEKEM
90	100	110	120	130	140	150	160
YGAEWPKVGA	TLALMWLKRG	LRFIQVFLQS	ICDGERDENH	PNLIRVNATK	AYEMALKKYH	GWIVQKIFQA	ALYAAPYKSD
170	180	190	200	210			
FLKALSKGQN	VTEEECLEKI	RLFLVNYTAT	IDVIYEMYTQ	MNAELNYKV			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1016	1	983.1678	145.88	2	42.3	14.8	2	131-146	K.AYEMALKKYHGWIVQK.I	

Detailed Protein Report

Protein 794: mediator of RNA polymerase II transcription subunit 6 isoform 2 [Homo sapiens]

Accession:	gi|42544155	**Score:**	14.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	28.4
Database Date:	2015-11-30	**pI:**	9.3
		Sequence Coverage [%]:	6.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAAVDIRDNL	LGISWVDSSW	IPILNSGSVL	DYFSERSNPF	YDRTCNNEVV	KMQRLTLEHL	NQMVGIEYIL	LHAQEPILFI
90	100	110	120	130	140	150	160
IRKQQRQSPA	QVIPLADYYI	IAGVIYQAPD	LGSVINSRVL	TAVHGIQSAF	DEAMSYCRYH	PSKGYWWHFK	DHEEQDKVRP
170	180	190	200	210	220	230	240
KAKRKEEPSS	IFQRQRVDAL	LLDLRQKFPP	KFVQLKPGEK	PVPVDQTKKE	AEPIPETVKP	EEKETTKNVQ	QTVSAKGPPE
250							
KRMRLQ							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1210	1	955.6887	154.62	2	44.7	14.8	0	192-208	K.FVQLKPGEKPVPVDQTK.K	

Detailed Protein Report

Protein 795: potassium channel subfamily K member 10 isoform 1 precursor [Homo sapiens]

Accession:	gi|10863961	**Score:**	14.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	59.7
Database Date:	2015-11-30	**pI:**	9.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MFFLYTDFFL	SLVAVPAAAP	VCQPKSATNG	QPPAPAPTPT	PRLSISSRAT	VVARMEGTSQ	GGLQTVMKWK	TVVAIFVVVV
90	100	110	120	130	140	150	160
VYLVTGGLVF	RALEQPFESS	QKNTIALEKA	EFLRDHVCVS	PQELETLIQH	ALDADNAGVS	PIGNSSNNSS	HWDLGSAFFF
170	180	190	200	210	220	230	240
AGTVITTIGY	GNIAPSTEGG	KIFCILYAIF	GIPLFGFLLA	GIGDQLGTIF	GKSIARVEKV	FRKKQVSQTK	IRVISTILFI
250	260	270	280	290	300	310	320
LAGCIVFVTI	PAVIFKYIEG	WTALESIYFV	VVTLTTVGFG	DFVAGGNAGI	NYREWYKPLV	WFWILVGLAY	FAAVLSMIGD
330	340	350	360	370	380	390	400
WLRVLSKKTK	EEVGEIKAHA	AEWKANVTAE	FRETRRRLSV	EIHDKLQRAA	TIRSMERRRL	GLDQRAHSLD	MLSPEKRSVF
410	420	430	440	450	460	470	480
AALDTGRFKA	SSQESINNRP	NNLRLKGPEQ	LNKHGQGASE	DNIINKFGST	SRLTKRKNKD	LKKTLPEDVQ	KIYKTFRNYS
490	500	510	520	530	540		
LDEEKKEEET	EKMCNSDNSS	TAMLTDCIQQ	HAELENGMIP	TDTKDREPEN	NSLLEDRN		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2750	1	741.8557	7.67	2	64.8	14.8	0	55-68	R.MEGTSQGGLQTVMK.W	Oxidation: 13

Detailed Protein Report

Protein 796: uncharacterized protein LOC100132994 [Homo sapiens]

Accession:	gi|223468690	**Score:**	14.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	54.4
Database Date:	2015-11-30	**pI:**	10.1
		Sequence Coverage [%]:	3.1
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|223468693	refseq_human (refseq_human_20140103.fasta)	putative uncharacterized protein CXorf49 [Homo sapiens]

10	20	30	40	50	60	70	80
MSSPDKVSVC	GAGFDLEGGK	KAGSRTASPG	APGAHSHGLD	LGVPGSGDGK	SESGFTDPEG	FSFESESELI	EQGRVVLWGR
90	100	110	120	130	140	150	160
EGRPGTPVDD	QGDVVDYSFY	LADEPAAIVP	PPSVQGHPFP	EGAAAEGSAE	NWADAEVGPS	GRDVLGHSPG	KWQQASAGRL
170	180	190	200	210	220	230	240
HLCGPGPVRA	WKNPERGSKS	RWSLRVDPQQ	PSAKGPTRLP	THDSDSADES	SDLPLMKVGI	CRNEGSQAKP	GSPKKRADTS
250	260	270	280	290	300	310	320
RQASFHCKES	YLPVPGRFLT	SAPRGLTPVA	ERPAVGELED	SPQKKMQSRA	WGKVEVRPSC	SGAAAAGALP	QGLSRRKMAG
330	340	350	360	370	380	390	400
GKKSLGGASQ	LALGRGFPAC	GERLSAAPPE	PATFPPFSGV	RPQGMSKKPQ	KPKHSSPGKK	PAGRKTRESQ	AAAREDNDPN
410	420	430	440	450	460	470	480
RDEVPRAQLP	THRPGLPRLS	VRRGEFSSSD	PNIRAPQLPG	TSEPSAYSPG	GLVPRRHAPS	GNQQPPVHPP	RPERQQQPPG
490	500	510	520				
AQGCPRCIWL	QREIEDLTQQ	LAAMQFLTDK	FQDL				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1392	1	895.6264	159.72	2	47.0	14.8	1	249-264	K.ESYLPVPGRFLTSAPR.G	

Detailed Protein Report

Protein 797: basic helix-loop-helix domain-containing protein KIAA2018 [Homo sapiens]

Accession:	gi|114431248	**Score:**	14.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	241.5
Database Date:	2015-11-30	**pI:**	7.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	0.5
		No. of unique Peptides:	1

Quantitation

MD:MU	**Median:** 3.84	**CV:** 0.00 %	**No. of Peptides:** 1

Detailed Protein Report

10	20	30	40	50	60	70	80
MPEMTENETP	TKKQHRKKNR	ETHNAVERHR	KKKINAGINR	IGELIPCSPA	LKQSKNMILD	QAFKYITELK	RQNDELLLNG
90	100	110	120	130	140	150	160
GNNEQAEEIK	KLRKQLEEIQ	KENGRYIELL	KANDICLYDD	PTIHWKGNLK	NSKVSVVIPS	DQVQKKIIVY	SNGNQPGGNS
170	180	190	200	210	220	230	240
QGTAVQGITF	NVSHNLQKQT	ANVVPVQRTC	NLVTPVSISG	VYPSENKPWH	QTTVPALATN	QPVPLCLPAA	ISAQSILELP
250	260	270	280	290	300	310	320
TSESESNVLG	ATSGSLIAVS	IESEPHQHHS	LHTCLNDQNS	SENKNGQENP	KVLKKMTPCV	TNIPHSSSAT	ATKVHHGNKS
330	340	350	360	370	380	390	400
CLSIQDFRGD	FQNTFVVSVT	TTVCSQPPRT	AGDSSPMSIS	KSADLTSTAT	VVASSAPGVG	KATIPISTLS	GNPLDNGWTL
410	420	430	440	450	460	470	480
SCSLPSSSVS	TSDLKNINSL	TRISSAGNTQ	TTWTTLQLAG	NTIQPLSQTP	SSAVTPVLNE	SGTSPTTSNH	SRYVATDINL
490	500	510	520	530	540	550	560
NNSFPADGQP	VEQVVVTLPS	CPSLPMQPLI	AQPQVKSQPP	KNILPLNSAM	QVIQMAQPVG	SAVNSAPTNQ	NVIILQPPST
570	580	590	600	610	620	630	640
TPCPTVMRAE	VSNQTVGQQI	VIIQAANQNP	LPLLPAPPPG	SVRLPINGAN	TVIGSNNSVQ	NVPTPQTFGG	KHLVHILPRP
650	660	670	680	690	700	710	720
SSLSASNSTQ	TFSVTMSNQQ	PQTISLNGQL	FALQPVMSSS	GTTNQTPMQI	IQPTTSEDPN	TNVALNTFGA	LASLNQSISQ
730	740	750	760	770	780	790	800
MAGQSCVQLS	ISQPANSQTA	ANSQTTTANC	VSLTTTAAPP	VTTDSSATLA	STYNLVSTSS	MNTVACLPNM	KSKRLNKKPG
810	820	830	840	850	860	870	880
GRKHLAANKS	ACPLNSVRDV	SKLDCPNTEG	SAEPPCNDGL	LESFPAVLPS	VSVSQANSVS	VSASHSLGVL	SSESLIPESV
890	900	910	920	930	940	950	960
SKSKSAEKSS	PPSQESVTSE	HFAMAAAKSK	DSTPNLQQET	SQDKPPSSLA	LSDAAKPCAS	ANVLIPSPSD	PHILVSQVPG
970	980	990	1000	1010	1020	1030	1040
LSSTTSTTST	DCVSEVEIIA	EPCRVEQDSS	DTMQTTGLLK	GQGLTTLLSD	LAKKKNPQKS	SLSDQMDHPD	FSSENPKIVD
1050	1060	1070	1080	1090	1100	1110	1120
SSVNLHPKQE	LLLMNNDDRD	PPQHHSCLPD	QEVINGSLIN	GRQADSPMST	SSGSSRSFSV	ASMLPETTRE	DVTSNATTNT
1130	1140	1150	1160	1170	1180	1190	1200
CDSCTFVEQT	DIVALAARAI	FDQENLEKGR	VGLQADIREV	ASKPSEASLL	EGDPPFKSQI	PKESGTGQAE	ATPNEFNSQG
1210	1220	1230	1240	1250	1260	1270	1280
SIEATMERPL	EKPSCSLGIK	TSNASLQDST	SQPPSITSLS	VNNLIHQSSI	SHPLASCAGL	SPTSEQTTVP	ATVNLTVSSS
1290	1300	1310	1320	1330	1340	1350	1360
SYGSQPPGPS	LMTEYSQEQL	NTMTSTIPNS	QIQEPLLKPS	HESRKDSAKR	AVQDDLLLSS	AKRQKHCQPA	PLRLESMSLM
1370	1380	1390	1400	1410	1420	1430	1440
SRTPDTISDQ	TQMMVSQIPP	NSSNSVVPVS	NPAHGDGLTR	LFPPSNNFVT	PALRQTEVQC	GSQPSVAEQQ	QTQASQHLQA
1450	1460	1470	1480	1490	1500	1510	1520
LQQHVPAQGV	SHLHSNHLYI	KQQQQQQQQQ	QQQQQQQQAG	QLRERHHLYQ	MQHHVPHAES	SVHSQPHNVH	QQRTLQQEVQ
1530	1540	1550	1560	1570	1580	1590	1600
MQKKRNLVQG	TQTSQLSLQP	KHHGTDQSRS	KTGQPHPHHQ	QMQQQMQQHF	GSSQTEKSCE	NPSTSRNHHN	HPQNHLNQDI
1610	1620	1630	1640	1650	1660	1670	1680
MHQQQDVGSR	QQGSGVSSEH	VSGHNPMQRL	LTSRGLEQQM	VSQPSIVTRS	SDMTCTPHRP	ERNRVSSYSA	EALIGKTSSN
1690	1700	1710	1720	1730	1740	1750	1760
SEQRMGISIQ	GSRVSDQLEM	RSYLDVPRNK	SLAIHNMQGR	VDHTVASDIR	LSDCQTFKPS	GASQQPQSNF	EVQSSRNNEI
1770	1780	1790	1800	1810	1820	1830	1840
GNPVSSLRSM	QSQAFRISQN	TGPPPIDRQK	RLSYPPVQSI	PTGNGIPSRD	SENTCHQSFM	QSLLAPHLSD	QVIGSQRSLS
1850	1860	1870	1880	1890	1900	1910	1920
EHQRNTQCGP	SSAIEYNCPP	THENVHIRRE	SESQNRESCD	MSLGAINTRN	STLNIPFSSS	SSSGDIQGRN	TSPNVSVQKS
1930	1940	1950	1960	1970	1980	1990	2000
NPMRITESHA	TKGHMNPPVT	TNMHGVARPA	LPHPSVSHGN	GDQGPAVRQA	NSSVPQRSRH	PLQDSSGSKI	RQPERNRSGN
2010	2020	2030	2040	2050	2060	2070	2080
QRQSTVFDPS	LPHLPLSTGG	SMILGRQQPA	TEKRGSIVRF	MPDSPQVPND	NSGPDQHTLS	QNFGFSFIPE	GGMNPPINAN
2090	2100	2110	2120	2130	2140	2150	2160
ASFIPQVTQP	SATRTPALIP	VDPQNTLPSF	YPPYSPAHPT	LSNDISIPYF	PNQMFSNPST	EKVNSGSLNN	RFGSILSPPR
2170	2180	2190	2200	2210	2220	2230	2240
PVGFAQPSFP	LLPDMPPMHM	TNSHLSNFNM	TSLFPEIATV	LPDGSAMSPL	LTIANSSASD	SSKQSSNRPA	HNISHILGHD
2250							
CSSAV							

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
1909	1	719.7917	-110.90	2	53.9	14.7	1	53-64	K.QSKNMILDQAFK.Y	Oxidation: 5	MD:MU	3.84

Detailed Protein Report

Protein 798: PREDICTED: gametocyte-specific factor 1 isoform X1 [Homo sapiens]

Accession:	gi|578823302	**Score:**	14.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	20.3
Database Date:	2015-11-30	**pI:**	5.7
		Sequence Coverage [%]:	8.5
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578823304	refseq_human (refseq_human_20140103.fasta)	PREDICTED: gametocyte-specific factor 1 isoform X2 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MEETYTDSLD PEKLLQCPYD KNHQIRACRF PYHLIKCRKN HPDVASKLAT CPFNARHQVP RAEISHHISS CDDRSCIEQD
        90        100        110        120        130        140        150        160
VVNQTRSLRQ ETLAESTWQC PPCDEDWDKD LWEQTSTPFV WGTTHYSDNN SPASNIVTEH KNNLASGMRV PKSLPYVLPW
       170        180
KNNSDSLDFS LCYCLS
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1702	2	840.7508	-115.12	2	51.2	14.7	0	162-176	K.NNSDSLDFSLCYCLS.-	

Detailed Protein Report

Protein 799: TNF receptor-associated factor 6 [Homo sapiens]

Accession:	gi|4759254	**Score:**	14.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	59.5
Database Date:	2015-11-30	**pI:**	6.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.7
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|22027630	refseq_human (refseq_human_20140103.fasta)	TNF receptor-associated factor 6 [Homo sapiens]

10	20	30	40	50	60	70	80
MSLLNCENSC	GSSQSESDCC	VAMASSCSAV	TKDDSVGGTA	STGNLSSSFM	EEIQGYDVEF	DPPLESKYEC	PICLMALREA
90	100	110	120	130	140	150	160
VQTPCGHRFC	KACIIKSIRD	AGHKCPVDNE	ILLENQLFPD	NFAKREILSL	MVKCPNEGCL	HKMELRHLED	HQAHCEFALM
170	180	190	200	210	220	230	240
DCPQCQRPFQ	KFHINIHILK	DCPRRQVSCD	NCAASMAFED	KEIHDQNCPL	ANVICEYCNT	ILIREQMPNH	YDLDCPTAPI
250	260	270	280	290	300	310	320
PCTFSTFGCH	EKMQRNHLAR	HLQENTQSHM	RMLAQAVHSL	SVIPDSGYIS	EVRNFQETIH	QLEGRLVRQD	HQIRELTAKM
330	340	350	360	370	380	390	400
ETQSMYVSEL	KRTIRTLEDK	VAEIEAQQCN	GIYIWKIGNF	GMHLKCQEEE	KPVVIHSPGF	YTGKPGYKLC	MRLHLQLPTA
410	420	430	440	450	460	470	480
QRCANYISLF	VHTMQGEYDS	HLPWPFQGTI	RLTILDQSEA	PVRQNHEEIM	DAKPELLAFQ	RPTIPRNPKG	FGYVTFMHLE
490	500	510	520	530			
ALRQRTFIKD	DTLLVRCEVS	TRFDMGSLRR	EGFQPRSTDA	GV			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1778	5	1057.3158	-132.00	1	52.2	14.7	0	134-142	K.CPNEGCLHK.M	Carbamidomethyl: 1

Detailed Protein Report

Protein 800: deleted in autism protein 1 isoform a precursor [Homo sapiens]

Accession:	gi|27734895	**Score:**	14.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	49.5
Database Date:	2015-11-30	**pI:**	9.8
		Sequence Coverage [%]:	3.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MWRLVPPKLG	RLSRSLKLAA	LGSLLVLMVL	HSPSLLASWQ	RNELTDRRFL	QLNKCPACFG	TSWCRRFLNG	QVVFEAWGRL
90	100	110	120	130	140	150	160
RLLDFLNVKN	VYFAQYGEPR	EGGRRRVVLK	RLGSQRELAQ	LDQSICKRAT	GRPRCDLLQA	MPRTEFARLN	GDVRLLTPEA
170	180	190	200	210	220	230	240
VEGWSDLVHC	PSQRLLDRLV	RRYAETKDSG	SFLLRNLKDS	ERMQLLLTLA	FNPEPLVLQS	FPSDEGWPFA	KYLGACGRMV
250	260	270	280	290	300	310	320
AVNYVGEELW	SYFNAPWEKR	VDLAWQLMEI	AEQLTNNDFE	FALYLLDVSF	DNFAVGPRDG	KVIIVDAENV	LVADKRLIRQ
330	340	350	360	370	380	390	400
NKPENWDVWY	ESKFDDCDKE	ACLSFSKEIL	CARATVDHNY	YAVCQNLLSR	HATWRGTSGG	LLHDPPSEIA	KDGRLEALLD
410	420	430	440				
ECANPKKRYG	RFQAAKELRE	YLAQLSNNVR					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1386	1	896.6123	140.58	2	47.1	14.7	1	67-81	R.FLNGQVVFEAWGRLR.L	

Detailed Protein Report

Protein 801: PREDICTED: DENN domain-containing protein 2D isoform X2 [Homo sapiens]

Accession:	gi|578799819	**Score:**	14.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	45.8
Database Date:	2015-11-30	**pI:**	9.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.6
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578799823	refseq_human (refseq_human_20140103.fasta)	PREDICTED: DENN domain-containing protein 2D isoform X4 [Homo sapiens]
gi|578799821	refseq_human (refseq_human_20140103.fasta)	PREDICTED: DENN domain-containing protein 2D isoform X3 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MWMGAERLDT AGASWSVQLR TAPSFLQSAQ LHGWACSSLS CKTPGLLAAL VVEKAQPRTC CHASAPSAAP QARGPDAPSP
        90        100        110        120        130        140        150        160
AAGQALPAGP GPRLPKVYCI ISCIGCFGLF SKILDEVEKR HQISMAVIYP FMQGLREAAF PAPGKTVTLK SFIPDSGTEF
       170        180        190        200        210        220        230        240
ISLTRPLDSH LEHVDFSSLL HCLSFEQILQ IFASAVLERK IIFLAEGLST LSQCIHAAAA LLYPFSWAHT YIPVVPESLL
       250        260        270        280        290        300        310        320
ATVCCPTPFM VGVQMRFQQE VMDSPMEEVL LVNLCEGTFL MSVGDEKDIL PPKLQDDILD SLGQGINELK TAEQINEHVS
       330        340        350        360        370        380        390        400
GPFVQFFVKI VGHYASYIKR EANGQGHFQE RSFCKALTSK TNRRFVKKFV KTQLFSLFIQ EAEKSKNPPA GYFQQKILEY
       410        420
EEQKKQKKPR EKTVK
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1183	1	1018.8946	-82.56	2	44.4	14.7	1	55-73	K.AQPRTCCHASAPSAAPQAR.G	Carbamidomethyl: 6, 7

Detailed Protein Report

Protein 802: PREDICTED: solute carrier family 40 member 1 isoform X2 [Homo sapiens]

Accession:	gi|530370249	**Score:**	14.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	58.1
Database Date:	2015-11-30	**pI:**	5.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MWHFAVSVFL	VELYGNSLLL	TAVYGLVVAG	SVLVLGAIIG	DWVDKNARLK	VAQTSLVVQN	VSVILCGIIL	MMVFLHKHEL
90	100	110	120	130	140	150	160
LTMYHGWVLT	SCYILIITIA	NIANLASTAT	AITIQRDWIV	VVAGEDRSKL	ANMNATIRRI	DQLTNILAPM	AVGQIMTFGS
170	180	190	200	210	220	230	240
PVIGCGFISG	WNLVSMCVEY	VLLWKVYQKT	PALAVKAGLK	EEETELKQLN	LHKDTEPKPL	EGTHLMGVKD	SNIHELEHEQ
250	260	270	280	290	300	310	320
EPTCASQMAE	PFRTFRDGWV	SYYNQPVFLA	GMGLAFLYMT	VLGFDCITTG	YAYTQGLSGS	ILSILMGASA	ITGIMGTVAF
330	340	350	360	370	380	390	400
TWLRRKCGLV	RTGLISGLAQ	LSCLILCVIS	VFMPGSPLDL	SVSPFEDIRS	RFIQGESITP	TKIPEITTEI	YMSNGSNSAN
410	420	430	440	450	460	470	480
IVPETSPESV	PIISVSLLFA	GVIAARIGLW	SFDLTVTQLL	QENVIESERG	IINGVQNSMN	YLLDLLHFIM	VILAPNPEAF
490	500	510	520	530	540		
GLLVLISVSF	VAMGHIMYFR	FAQNTLGNKL	FACGPDAKEV	RKENQANTSV	V		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2620	1	732.5473	175.86	1	63.5	14.7	1	326-331	R.KCGLVR.T	Carbamidomethyl: 2

Detailed Protein Report

Protein 803: BTB/POZ domain-containing protein 9 isoform b [Homo sapiens]

Accession:	gi|151108435	**Score:**	14.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	61.5
Database Date:	2015-11-30	**pI:**	5.1
		Sequence Coverage [%]:	4.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MRESQPEAEI	PLQDTTAEAF	TMLLKYIYTG	RATLTDEKEE	VLLDFLSLAH	KYGFPELEDS	TSEYLCTILN	IQNVCMTFDV
90	100	110	120	130	140	150	160
ASLYSLPKLT	CMCCMFMDRN	AQEVLSSEGF	LSLSKTALLN	IVLRDSFAAP	EKDIFLALLN	WCKHNSKENH	AEIMQAVRLP
170	180	190	200	210	220	230	240
LMSLTELLNV	VRPSGLLSPD	AILDAIKVRS	ESRDMDLNYR	GMLIPEENIA	TMKYGAQVVK	GELKSALLDG	DTQNYDLDHG
250	260	270	280	290	300	310	320
FSRHPIDDDC	RSGIEIKLGQ	PSIINHIRIL	LWDRDSRSYS	YFIEVSMDEL	DWVRVIDHSQ	YLCRSWQKLY	FPARVCRYIR
330	340	350	360	370	380	390	400
IVGTHNTVNK	IFHIVAFECM	FTNKTFTLEK	GLIVPMENVA	TIADCASVIE	GVSRSRNALL	NGDTKNYDWD	SGYTCHQLGS
410	420	430	440	450	460	470	480
GAIVVQLAQP	YMIGSIRLLL	WDCDDRSYSY	YVEVSTNQQQ	WTMVADRTKV	SCKSWQSVTF	ERQPASFIRI	VGTHNTANEV
490	500	510	520	530	540	550	
FHCVHFECPE	QQSSQKEENS	EESGTGDTSL	AGQQLDSHAL	RAPSGSSLPS	SPGSNSRSPN	RQHQ	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2400	1	938.4644	18.43	3	59.9	14.7	2	190-213	R.SESRDMDLNYRGMLIPEENIATMK.Y	

Detailed Protein Report

Protein 804: RNA 3'-terminal phosphate cyclase isoform a [Homo sapiens]

Accession:	gi|195927044	**Score:**	14.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	40.7
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
MAGPRVEVDG	SIMEGGGQIL	RVSTALSCLL	GLPLRVQKIR	AGRSTPGLSS	GGWKSKIKVL	TRPQHLSGLE	MIRDLCDGQL
90	100	110	120	130	140	150	160
EGAEIGSTEI	TFTPEKIKGG	IHTADTKTAG	SVCLLMQVSM	PCVLFAASPS	ELHLKGGTNA	EMAPQIDYTV	MVFKPIVEKF
170	180	190	200	210	220	230	240
GFIFNCDIKT	RGYYPKGGGE	VIVRMSPVKQ	LNPINLTERG	CVTKIYGRAF	VAGVLPFKVA	KDMAAAAVRC	IRKEIRDLYV
250	260	270	280	290	300	310	320
NIQPVQEPKD	QAFGNGNGII	IIAETSTGCL	FAGSSLGKRG	VNADKVGIEA	AEMLLANLRH	GGTVDEYLQD	QLIVFMALAN
330	340	350	360	370	380		
GVSRIKTGPV	TLHTQTAIHF	AEQIAKAKFI	VKKSEDEEDA	AKDTYIIECQ	GIGMTNPNL		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2147	1	788.3156	-126.72	2	56.7	14.6	2	41-56	R.AGRSTPGLSSGGWKSK.I	

Detailed Protein Report

Protein 805: **zinc finger protein 182 isoform 2 [Homo sapiens]**

Accession:	gi|55769561	**Score:**	14.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	71.5
Database Date:	2015-11-30	**pI:**	10.0
		Sequence Coverage [%]:	2.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAKPQGLVTF	EDVAVDFTQE	EWQYLNPPQR	TLYRDVMLET	YSNLVFVGQQ	VTKPNLILKL	EVEECPAEGK	IPFWNFPEVC
90	100	110	120	130	140	150	160
QVDEQIERQH	QDDQDKCLLM	QVGFSDKKTI	ITKSARDCHE	FGNILHLSTN	LVASIQRPDK	HESFGNNMVD	NLDLFSRSSA
170	180	190	200	210	220	230	240
ENKYDNGCAK	LFFHTEYEKT	NPGMKPYGYK	ECGKGLRRKK	GLSLHQRIKN	GEKPFECTAC	RKTFSKKSHL	IVHWRTHTGE
250	260	270	280	290	300	310	320
KPFGCTECGK	AFSQKSQLII	HLRTHTGERP	FECPECGKAF	REKSTVIIHY	RTHTGEKPYE	CNECGKAFTQ	KSNLIVHQKT
330	340	350	360	370	380	390	400
HTGEKTYECT	KCGESFIQKL	DLIIHHSTHT	GKKPHECNEC	KKTFSDKSTL	IIHQRTHTGE	KPHKCTECGK	SFNEKSTLIV
410	420	430	440	450	460	470	480
HQRTHTGEKP	YECDVCGKTF	TQKSNLGVHQ	RTHSGEKPFE	CNECEKAFSQ	KSYLMLHQRG	HTGEKPYECN	ECEKAFSQKS
490	500	510	520	530	540	550	560
YLIIHQRTHT	EEKPYKCNEC	GKAFREKSKL	IIHQRIHTGE	KPYECPVCWK	AFSQKSQLII	HQRTHTGEKP	YACTECGKAF
570	580	590	600	610	620	630	
REKSTFTVHQ	RTHTGEKPYK	CTECGKAFTQ	KSNLIVHQRT	HAGKKAHGRG	HTRKSKFMAH		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2247	3	820.1114	178.53	2	58.3	14.6	2	223-235	K.TFSKKSHLIVHWR.T	

Detailed Protein Report

Protein 806: mucin-5B precursor [Homo sapiens]

Accession:	gi|301172750	**Score:**	14.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	596.0
Database Date:	2015-11-30	**pI:**	6.2
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	0.3
		No. of unique Peptides:	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MGAPSACRTL	VLALAAMLVV	PQAETQGPVE	PSWENAGHTM	DGGAPTSSPT	RRVSFVPPVT	VFPSLSPLNP	AHNGRVCSTW
90	100	110	120	130	140	150	160
GDFHYKTFDG	DVFRFPGLCN	YVFSEHCRAA	YEDFNVQLRR	GLVGSRPVVT	RVVIKAQGLV	LEASNGSVLI	NGQREELPYS
170	180	190	200	210	220	230	240
RTGLLVEQSG	DYIKVSIRLV	LTFLWNGEDS	ALLELDPKYA	NQTCGLCGDF	NGLPAFNEFY	AHNARLTPLQ	FGNLQKLDGP
250	260	270	280	290	300	310	320
TEQCPDPLPL	PAGNCTDEEG	ICHRTLLGPA	FAECHALVDS	TAYLAACAQD	LCRCPTCPCA	TFVEYSRQCA	HAGGQPRNWR
330	340	350	360	370	380	390	400
CPELCPRTCP	LNMQHQECGS	PCTDTCSNPQ	RAQLCEDHCV	DGCFCPPGTV	LDDITHSGCL	PLGQCPCTHG	GRTYSPGTSF
410	420	430	440	450	460	470	480
NTTCSSCTCS	GGLWQCQDLP	CPGTCSVQGG	AHISTYDEKL	YDLHGDCSYV	LSKKCADSSF	TVLAELRKCG	LTDNENCLKA
490	500	510	520	530	540	550	560
VTLSLDGGDT	AIRVQADGGV	FLNSIYTQLP	LSAANITLFT	PSSFFIVVQT	GLGLQLLVQL	VPLMQVFVRL	DPAHQGQMCG
570	580	590	600	610	620	630	640
LCGNFNQNQA	DDFTALSGVV	EATGAAFANT	WKAQAACANA	RNSFEDPCSL	SVENENYARH	WCSRLTDPNS	AFSRCHSIIN
650	660	670	680	690	700	710	720
PKPFHSNCMF	DTCNCERSED	CLCAALSSYV	HACAAKGVQL	SDWRDGVCTK	YMQNCPKSQR	YAYVVDACQP	TCRGLSEADV
730	740	750	760	770	780	790	800
TCSVSFVPVD	GCTCPAGTFL	NDAGACVPAQ	ECPCYAHGTV	LAPGEVVHDE	GAVCSCTGGK	LSCLGASLQK	STGCAAPMVY
810	820	830	840	850	860	870	880
LDCSNSSAGT	PGAECLRSCH	TLDVGCFSTH	CVSGCVCPPG	LVSDGSGGCI	AEEDCPCVHN	EATYKPGETI	RVDCNTCTCR
890	900	910	920	930	940	950	960
NRRWECSHRL	CLGTCVAYGD	GHFITFDGDR	YSFEGSCEYI	LAQDYCGDNT	THGTFRIVTE	NIPCGTTGTT	CSKAIKLFVE
970	980	990	1000	1010	1020	1030	1040
SYELILQEGT	FKAVARGPGG	DPPYKIRYMG	IFLVIETHGM	AVSWDRKTSV	FIRLHQDYKG	RVCGLCGNFD	DNAINDFATR
1050	1060	1070	1080	1090	1100	1110	1120
SRSVVGDALE	FGNSWKLSPS	CPDALAPKDP	CTANPFRKSW	AQKQCSILHG	PTFAACRSQV	DSTKYYEACV	NDACACDSGG
1130	1140	1150	1160	1170	1180	1190	1200
DCECFCTAVA	AYAQACHDAG	LCVSWRTPDT	CPLFCDFYNP	HGGCEWHYQP	CGAPCLKTCR	NPSGHCLVDL	PGLEGCYPKC
1210	1220	1230	1240	1250	1260	1270	1280
PPSQPFFNED	QMKCVAQCGC	YDKDGNYYDV	GARVPTAENC	QSCNCTPSGI	QCAHSLEACT	CTYEDRTYSY	QDVIYNTTDG
1290	1300	1310	1320	1330	1340	1350	1360
LGACLIAICG	SNGTIIRKAV	ACPGTPATTP	FTFTTAWVPH	STTSPALPVS	TVCVREVCRW	SSWYNGHRPE	PGLGGGDFET
1370	1380	1390	1400	1410	1420	1430	1440
FENLRQRGYQ	VCPVLADIEC	RAAQLPDMPL	EELGQQVDCD	RMRGLMCANS	QQSPPLCHDY	ELRVLCCEYV	PCGPSPAPGT
1450	1460	1470	1480	1490	1500	1510	1520
SPQPSLSAST	EPAVPTPTQT	TATEKTTLWV	TPSIRSTAAL	TSQTGSSSGP	VTVTPSAPGT	TTCQPRCQWT	EWFDEDYPKS
1530	1540	1550	1560	1570	1580	1590	1600
EQLGGDVESY	DKIRAAGGHL	CQQPKDIECQ	AESFPNWTLA	QVGQKVHCDV	HFGLVCRNWE	QEGVFKMCYN	YRIRVLCCSD
1610	1620	1630	1640	1650	1660	1670	1680
DHCRGRATTP	PPTTELETAT	TTTTQALFST	PQPTSSPGLT	RAPPASTTAV	PTLSEGLTSP	RYTSTLGTAT	TGGPTTPAGS
1690	1700	1710	1720	1730	1740	1750	1760
TEPTVPGVAT	STLPTRSALP	GTTGSLGTWR	PSQPPTLAPT	TMATSRARPT	GTASTASKEP	LTTSLAPTLT	SELSTSQAET
1770	1780	1790	1800	1810	1820	1830	1840
STPRTETTMS	PLTNTTTSQG	TTRCQPKCEW	TEWFDVDFPT	SGVAGGDMET	FENIRAAGGK	MCWAPKSIEC	RAENYPEVSI
1850	1860	1870	1880	1890	1900	1910	1920
DQVGQVLTCS	LETGLTCKNE	DQTGRFNMCF	NYNVRVLCCD	DYSHCPSTPA	TSSTATPSST	PGTTWILTKP	TTTATTTAST
1930	1940	1950	1960	1970	1980	1990	2000
GSTATPTSTL	RTAPPPKVLT	TTATTPTVTS	SKATPSSSPG	TATALPALRS	TATTPTATSV	TPIPSSSLGT	TWTRLSQTTT
2010	2020	2030	2040	2050	2060	2070	2080
PTATMSTATP	SSTPETAHTS	TVLTATATTT	GATGSVATPS	STPGTAHTTK	VPTTTTTGFT	ATPSSSPGTA	LTPPVWISTT
2090	2100	2110	2120	2130	2140	2150	2160
TTPTTRGSTV	TPSSIPGTTH	TATVLTTTTT	TVATGSMATP	SSSTQTSGTP	PSLTTTATTI	TATGSTTNPS	STPGTTPIPP
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
1998	1	1051.3664	-80.43	2	55.1	14.5	2	5230-5248	R.DDCLQRDGTTAASCKDMAK.T	Carbamidomethyl: 3; Oxidation: 17

Detailed Protein Report

Protein 807: desmoglein-2 preproprotein [Homo sapiens]

Accession:	gi|116534898	**Score:**	14.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	122.2
Database Date:	2015-11-30	**pI:**	5.0
		Sequence Coverage [%]:	0.7
		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
911	1	955.7392	190.53	1	40.9	14.5	1	33-40	R.NENKLLPK.H	

Detailed Protein Report

Protein 808: protein EURL homolog isoform 3 [Homo sapiens]

Accession:	gi|154426270	**Score:**	14.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	25.3
Database Date:	2015-11-30	**pI:**	6.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	10.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MNEEEQFVNI	DLNDDNICSV	CKLGTDKETL	SFCHICFELN	IEGVPKSDLL	HTKSLRGHKD	CFEKYHLIAN	QGCPRSKLSK
90	100	110	120	130	140	150	160
STYEEVKTIL	SKKINWIVQY	AQNKDLDSDS	ECSKNPQHHL	FNFRHKPEEK	LLPQFDSQVP	KYSAKWIDGS	AGGISNCTQR
170	180	190	200	210	220	230	
ILEQRENTDF	GLSMLQDSGA	TLCRNSVLWP	HSHNQAQKKE	ETISSPEANV	QTQHPHYSRE	E	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
175	1	877.0244	-23.87	3	31.9	14.5	0	1-22	-.MNEEEQFVNIDLNDDNICSVCK.L	Carbamidomethyl: 18

Detailed Protein Report

Protein 809: PREDICTED: target of Nesh-SH3 isoform X33 [Homo sapiens]

Accession:	gi|530374326	**Score:**	14.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	148.7
Database Date:	2015-11-30	**pI:**	10.3
		Sequence Coverage [%]:	0.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MRGGKCNMLS	SLGCLLLCGS	ITLALGNAQK	LPKGKRPNLK	VHINTTSDSI	LLKFLRPSPN	VKLEGLLLGY	GSNVSPNQYF
90	100	110	120	130	140	150	160
PLPAEGKFTE	AIVDAEPKYL	IVVRPAPPPS	QKKSCSGKTR	SRKPLQLVVG	TLTPSSVFLS	WGFLINPHHD	WTLPSHCPND
170	180	190	200	210	220	230	240
RFYTIRYREK	DKEKKWIFQI	CPATETIVEN	LKPNTVYEFG	VKDNVEGGIW	SKIFNHKTVV	GSKKVNGKIQ	STYDQDHTVP
250	260	270	280	290	300	310	320
AYVPRKLIPI	TIIKQVIQNV	THKDSAKSPE	KAPLGGVILV	HLIIPGLNET	TVKLPASLMF	EISDALKTQL	AKNETLALPA
330	340	350	360	370	380	390	400
ESKTPEVEKI	SARPTTVTPE	TVPRSTKPTT	SSALDVSETT	LVLSKRTPET	LQTILIPQFE	LPLSTLAPKS	LPEFPEAKTP
410	420	430	440	450	460	470	480
FPFEKPRGTL	ASSEKPWIVP	TAKISEDSKV	LQPQTATYDV	FSSPTTSDEP	EISDSYTATS	DRILDSIPPK	TSRTLEQPRA
490	500	510	520	530	540	550	560
TLAPSETPFV	PQKLEIFTSP	EMQPTTPAPQ	QTTSIPSTPK	RRPRPKPPRT	KPERTTSAGT	ITPKISKSPE	PTWTTPAPGK
570	580	590	600	610	620	630	640
TQFISLKPKI	PLSPEVTHTK	PAPEPQTLLP	SQSTIGPETP	GTKPSTTLAP	RKTKRPGRRP	RPRPRPKTTP	SPEVPKSKPA
650	660	670	680	690	700	710	720
LEPATIQPEP	LVPTTASKPS	ERPKTTHRPD	APQIQPGSKP	PKQLLPKPQT	TAEPDMPPTK	SVSEPVPFET	EAPSMTIVPT
730	740	750	760	770	780	790	800
TDIEPVTVRT	EATVTTLAPK	TSQRTRTRRP	RPKHKTTPRP	ETLQTKLDFG	PITPGTSSAP	TTTTKRTRRP	HPKPKTTPHP
810	820	830	840	850	860	870	880
EVPQTKLAPK	QTPRAPPKPK	TSPRPRIPQT	QPVPKVPQRV	TAKPKTSPSP	EVSYTTPAPK	DVLLPHKPYP	EVSQSEPAPL
890	900	910	920	930	940	950	960
ETRGIPFIPM	ISPSPSQEEL	QTTLEETDQS	TQEPFTTKIP	RTTELAKTTQ	APHRFYTTVR	PRTSDKPHIR	PGVKQAPRPS
970	980	990	1000	1010	1020	1030	1040
GADRNVSVDS	THPTKKPGTR	RPPLPPRPTH	PRRKPLPPNN	VTGKPGSAGI	ISSGPITTPP	LRSTPRPTGT	PLERIETDIK
1050	1060	1070	1080	1090	1100	1110	1120
QPTVPASGEE	LENITDFSSS	PTRETDPLGK	PRFKGPHVRY	IQKPDNSPCS	ITDSVKRFPK	EEATEGNATS	PPQNPPTNLT
1130	1140	1150	1160	1170	1180	1190	1200
VVTVEGCPSF	VILDWEKPLN	DTVTEYEVIS	RENGSFSGKN	KSIQMTNQTF	STVENLKPNT	SYEFQVKPKN	PLGEGPVSNT
1210	1220	1230	1240	1250	1260	1270	1280
VAFSTESADP	RVSEPVSAGR	DAIWTERPFN	SDSYSECKGK	QYVKRTWYKK	FVGVQLCNSL	RYKIYLSDSL	TGKFYNIGDQ
1290	1300	1310	1320	1330	1340	1350	1360
RGHGEDHCQF	VDSFLDGRTG	QQLTSDQLPI	KEGYFRAVRQ	EPVQFGEIGG	HTQINYVQWY	ECGTTIPGKW	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
986	2	955.6747	172.89	1	41.9	14.5	0	628-636	K.TTPSPEVPK.S	

Detailed Protein Report

Protein 810: PREDICTED: 6-phosphofructokinase, liver type isoform X4 [Homo sapiens]

Accession:	gi|530419271	**Score:**	14.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	82.2
Database Date:	2015-11-30	**pI:**	7.9
		Sequence Coverage [%]:	1.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MNAAVRAVTR	MGIYVGAKVF	LIYEGYEGLV	EGGENIKQAN	WLSVSNIIQL	GGTIIGSARC	KAFTTREGRR	AAAYNLVQHG
90	100	110	120	130	140	150	160
ITNLCVIGGD	GSLTGANIFR	SEWGSLLEEL	VAEGKISETT	ARTYSHLNIA	GLVGSIDNDF	CGTDMTIGTD	SALHRIMEVI
170	180	190	200	210	220	230	240
DAITTTAQSH	QRTFVLEVMG	RHCGYLALVS	ALASGADWLF	IPEAPPEDGW	ENFMCERLGE	TRSRGSRLNI	IIIAEGAIDR
250	260	270	280	290	300	310	320
NGKPISSSYV	KDLVVQRLGF	DTRVTVLGHV	QRGGTPSAFD	RILSSKMGME	AVMALLEATP	DTPACVVTLS	GNQSVRLPLM
330	340	350	360	370	380	390	400
ECVQMTKEVQ	KAMDDKRFDE	ATQLRGGSFE	NNWNIYKLLA	HQKPPKEKSN	FSLAILNVGA	PAAGMNAAVR	SAVRTGISHG
410	420	430	440	450	460	470	480
HTVYVVHDGF	EGLAKGQVQE	VGWHDVAGWL	GRGGSMLGTK	RTLPKGQLES	IVENIRIYGI	HALLVVGGFE	AYEGVLQLVE
490	500	510	520	530	540	550	560
ARGRYEELCI	VMCVIPATIS	NNVPGTDFSL	GSDTAVNAAM	ESCDRIKQSA	SGTKRRVFIV	ETMGGYCGYL	ATVTGIAVGA
570	580	590	600	610	620	630	640
DAAYVFEDPF	NIHDLKVNVE	HMTEKMKTDI	QRGLVLRNEK	CHDYYTTEFL	YNLYSSEGKG	VFDCRTNVLG	HLQQGGAPTP
650	660	670	680	690	700	710	720
FDRNYGTKLG	VKAMLWLSEK	LREVYRKGRV	FANAPDSACV	IGLKKKAVAF	SPVTELKKDT	DFEHRMPREQ	WWLSLRLMLK
730	740	750	760				
MLAQYRISMA	AYVSGELEHV	TRRTLSMDKG	F				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
156	1	584.6910	-183.35	2	31.3	14.4	2	60-69	R.CKAFTTREGR.R	

Detailed Protein Report

Protein 811: PREDICTED: nephronectin isoform X3 [Homo sapiens]

Accession:	gi|530377475	**Score:**	14.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	50.2
Database Date:	2015-11-30	**pI:**	9.8
		Sequence Coverage [%]:	4.3
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|578808996	refseq_human (refseq_human_20140103.fasta)	PREDICTED: nephronectin isoform X4 [Homo sapiens]

10	20	30	40	50	60	70	80
MNTYGSYKCY	CLNGYMLMPD	GSCSSALTCS	MANCQYGCDV	VKGQIRCQCP	SPGLQLAPDG	RTCVDVDECA	TGRASCPRFR
90	100	110	120	130	140	150	160
QCVNTFGSYI	CKCHKGFDLM	YIGGKYQCHD	IDECSLGQYQ	CSSFARCYNI	RGSYKCKCKE	GYQGDGLTCV	YIPKVMIEPS
170	180	190	200	210	220	230	240
GPIHVPKGNG	TILKGDTGNN	NWIPDVGSTW	WPPKTPYIPP	IITNRPTSKP	TTRPTPKPTP	IPTPPPPPPL	PTELRTPLPP
250	260	270	280	290	300	310	320
TTPERPTTGL	TTIAPAASTP	PGGITVDNRV	QTDPQKPRGD	VFIPRQPSND	LFEIFEIERG	VSADDEAKDD	PGVLVHSCNF
330	340	350	360	370	380	390	400
DHGLCGWIRE	KDNDLHWEPI	RDPAGGQYLT	VSAAKAPGGK	AARLVLPLGR	LMHSGDLCLS	FRHKVTGLHS	GTLQVFVRKH
410	420	430	440	450	460	470	
GAHGAALWGR	NGGHGWRQTQ	ITLRGADIKS	VVFKGEKRRG	HTGEIGLDDV	SLKKGHCSEE	R	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2444	1	1044.1842	92.38	2	60.9	14.4	1	155-174	K.VMIEPSGPIHVPKGNGTILK.G	

Detailed Protein Report

Protein 812: PREDICTED: zinc finger CCHC domain-containing protein 10 isoform X4 [Homo sapiens]

Accession:	gi|530380033	**Score:**	14.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	13.8
Database Date:	2015-11-30	**pI:**	11.3
		Sequence Coverage [%]:	6.1
		No. of unique Peptides:	1

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
380	1	464.6667	-199.17	2	34.4	14.4	0	64-70	K.YLHRPSR.T	

Detailed Protein Report

Protein 813: 3-hydroxyacyl-CoA dehydrogenase type-2 isoform 2 [Homo sapiens]

Accession:	gi|83715985	**Score:**	14.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	26.0
Database Date:	2015-11-30	**pI:**	7.7
		Sequence Coverage [%]:	9.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAAACRSVKG	LVAVITGGAS	GLGLATAERL	VGQGASAVLL	DLPNSGGEAQ	AKKLGNNCVF	APADVTSEKD	VQTALALAKG
90	100	110	120	130	140	150	160
KFGRVDVAVN	CAGIAVASKT	YNLKKGQTHT	LEDFQRVLDV	NLMGTFNVIR	LVAGEMGQNE	PDQGGQRGVI	INTASVAAFE
170	180	190	200	210	220	230	240
GQVGQAAYSA	SKGGIVGMTL	PIARDLAPIG	LFGTPLLTSL	PEKVCNFLAS	QVPFPSRLGD	PAEYAHLVQA	IIENPFLNGE
250	260						
VIRLDGAIRM	QP						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
50	1	813.6863	-84.85	3	30.0	14.4	0	148-172	R.GVIINTASVAAFEGQVGQAAYSASK.G	

Detailed Protein Report

Protein 814: serpin H1 precursor [Homo sapiens]

Accession:	gi|32454741	**Score:**	14.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	46.4
Database Date:	2015-11-30	**pI:**	9.3
		Sequence Coverage [%]:	4.1
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578821832	refseq_human (refseq_human_20140103.fasta)	PREDICTED: serpin H1 isoform X3 [Homo sapiens]
gi|578821830	refseq_human (refseq_human_20140103.fasta)	PREDICTED: serpin H1 isoform X2 [Homo sapiens]
gi|578821828	refseq_human (refseq_human_20140103.fasta)	PREDICTED: serpin H1 isoform X1 [Homo sapiens]
gi|333360851	refseq_human (refseq_human_20140103.fasta)	serpin H1 precursor [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MRSLLLLSAF CLLEAALAAE VKKPAAAAAP GTAEKLSPKA ATLAERSAGL AFSLYQAMAK DQAVENILVS PVVVASSLGL
        90        100        110        120        130        140        150        160
VSLGGKATTA SQAKAVLSAE QLRDEEVHAG LGELLRSLSN STARNVTWKL GSRLYGPSSV SFADDFVRSS KQHYNCEHSK
       170        180        190        200        210        220        230        240
INFRDKRSAL QSINEWAAQT TDGKLPEVTK DVERTDGALL VNAMFFKPHW DEKFHHKMVD NRGFMVTRSY TVGVMMMHRT
       250        260        270        280        290        300        310        320
GLYNYYDDEK EKLQIVEMPL AHKLSSLIIL MPHHVEPLER LEKLLTKEQL KIWMGKMQKK AVAISLPKGV VEVTHDLQKH
       330        340        350        360        370        380        390        400
LAGLGLTEAI DKNKADLSRM SGKKDLYLAS VFHATAFELD TDGNPFDQDI YGREELRSPK LFYADHPFIF LVRDTQSGSL
       410        420
LFIGRLVRPK GDKMRDEL
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1592	1	910.3836	-67.04	2	49.6	14.4	0	168-184	R.SALQSINEWAAQTTDGK.L	

Detailed Protein Report

Protein 815: UPF0609 protein C4orf27 [Homo sapiens]

Accession:	gi|157388914	**Score:**	14.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	39.4
Database Date:	2015-11-30	**pI:**	6.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MVGGGGKRRP	GGEGPQCEKT	TDVKKSKFCE	ADVSSDLRKE	VENHYKLSLP	EDFYHFWKFC	EELDPEKPSD	SLSASLGLQL
90	100	110	120	130	140	150	160
VGPYDILAGK	HKTKKKSTGL	NFNLHWRFYY	DPPEFQTIII	GDNKTQYHMG	YFRDSPDEFP	VYVGINEAKK	NCIIVPNGDN
170	180	190	200	210	220	230	240
VFAAVKLFLT	KKLREITDKK	KINLLKNIDE	KLTEAARELG	YSLEQRTVKM	KQRDKKVVTK	TFHGAGLVVP	VDKNDVGYRE
250	260	270	280	290	300	310	320
LPETDADLKR	ICKTIVEAAS	DEERLKAFAP	IQEMMTFVQF	ANDECDYGMG	LELGMDLFCY	GSHYFHKVAG	QLLPLAYNLL
330	340	350					
KRNLFAEIIE	EHLANRSQEN	IDQLAA					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1471	1	620.4233	145.55	3	48.1	14.4	1	150-166	K.KNCIIVPNGDNVFAAVK.L	Carbamidomethyl: 3

Detailed Protein Report

Protein 816: nucleoporin NDC1 isoform 2 [Homo sapiens]

Accession:	gi|271398379	**Score:**	14.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	71.9
Database Date:	2015-11-30	**pI:**	9.8
		Sequence Coverage [%]:	3.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MATAVSRPCA	GRSRDILWRV	LGWRIVASIV	WSVLFLPICT	TVFIIFSRID	LFHPIQWLSD	SFSDLYSSYV	IFYFLLLSVV
90	100	110	120	130	140	150	160
IIIISIFNVE	FYAVITQGQY	SFLVVPCTGT	NSFGSPAAQT	CLNEYHLFFL	LTGAFMGYSY	SLLYFVNNMN	YLPFPIIQQY
170	180	190	200	210	220	230	240
KFLRFRRSLL	LLVKHSCVES	LFLVRNFCIL	YYFLGYIPKA	WISTAMNLHI	DEQVHRPLDT	VSGLLNLSLL	YHVWLCGVFL
250	260	270	280	290	300	310	320
LTTWYVSWIL	FKIYATEAHV	FPVQPPFAEG	SDECLPKVLN	SNPPPIIKYL	ALQDLMLLSQ	YSPSRRQEVF	SLSQPGGHPH
330	340	350	360	370	380	390	400
NWTAISRECL	NLLNGMTQKL	ILYQEAAATN	GRVSSSYPVE	PKKLNSPEET	AFQTPKSSQM	PRPSVPPLVK	TSLFSSKLST
410	420	430	440	450	460	470	480
PDVVSPFGTP	FGSSVMNRMA	GIFDVNTCYG	SPQSPQLIRR	GPRLWTSASD	QQMTEFSNPS	PSTSISAEGK	TMRQPSVIYS
490	500	510	520	530	540	550	560
WIQNKREQIK	NFLSKRVLIM	YFFSKHPEAS	IQAVFSDAQM	HIWALEGLSH	LVAASFTEDR	FGVVQTTLPA	ILNTLLTLQE
570	580	590	600	610	620	630	640
AVDKYFKLPH	ASSKPPRISG	SLVDTSYKTL	RFAFRASLKT	AIYRITTTFG	EHLNAVQASA	EHQKRLQQFL	EFKE

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2487	1	1073.4872	-67.54	2	61.5	14.4	2	1-19	-.MATAVSRPCAGRSRDILWR.V	

Detailed Protein Report

Protein 817: E3 ubiquitin-protein ligase DTX3L [Homo sapiens]

Accession: gi|19923717
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 14.4
MW [kDa]: 83.5
pI: 9.2
Sequence Coverage [%]: 2.3
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MASHLRPPSP	LLVRVYKSGP	RVRRKLESYF	QSSKSSGGGE	CTVSTQEHEA	PGTFRVEFSE	RAAKERVLKK	GEHQILVDEK
90	100	110	120	130	140	150	160
PVPIFLVPTE	NSIKKNTRPQ	ISSLTQSQAE	TPSGDMHQHE	GHIPNAVDSC	LQKIFLTVTA	DLNCNLFSKE	QRAYITTLCP
170	180	190	200	210	220	230	240
SIRKMEGHDG	IEKVCGDFQD	IERIHQFLSE	QFLESEQKQQ	FSPSMTERKP	LSQQERDSCI	SPSEPETKAE	QKSNYFEVPL
250	260	270	280	290	300	310	320
PYFEYFKYIC	PDKINSIEKR	FGVNIEIQES	SPNMVCLDFT	SSRSGDLEAA	RESFASEFQK	NTEPLKQECV	SLADSKQANK
330	340	350	360	370	380	390	400
FKQELNHQFT	KLLIKEKGGE	LTLLGTQDDI	SAAKQKISEA	FVKIPVKLFA	ANYMMNVIEV	DSAHYKLLET	ELLQEISEIE
410	420	430	440	450	460	470	480
KRYDICSKVS	EKGQKTCILF	ESKDRQVDLS	VHAYASFIDA	FQHASCQLMR	EVLLLKSLGK	ERKHLHQTKF	ADDFRKRHPN
490	500	510	520	530	540	550	560
VHFVLNQESM	TLTGLPNHLA	KAKQYVLKGG	GMSSLAGKKL	KEGHETPMDI	DSDDSKAASP	PLKGSVSSEA	SELDKKEKGI
570	580	590	600	610	620	630	640
CVICMDTISN	KKVLPKCKHE	FCAPCINKAM	SYKPICPTCQ	TSYGIQKGNQ	PEGSMVFTVS	RDSLPGYESF	GTIVITYSMK
650	660	670	680	690	700	710	720
AGIQTEEHPN	PGKRYPGIQR	TAYLPDNKEG	RKVLKLLYRA	FDQKLIFTVG	YSRVLGVSDV	ITWNDIHHKT	SRFGGPEMYG
730	740	750					
YPDPSYLKRV	KEELKAKGIE						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1498	1	982.5825	15.99	2	48.4	14.4	1	1-17	-.MASHLRPPSPLLVRVYK.S	

Detailed Protein Report

Protein 818: **transcription factor 25 [Homo sapiens]**

Accession:	gi|14149657	**Score:**	14.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	76.6
Database Date:	2015-11-30	**pI:**	5.9
		Sequence Coverage [%]:	2.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSRRALRRLR	GEQRGQEPLG	PGALHFDLRD	DDDAEEEGPK	RELGVRRPGG	AGKEGVRVNN	RFELINIDDL	EDDPVVNGER
90	100	110	120	130	140	150	160
SGCALTDAVA	PGNKGRGQRG	NTESKTDGDD	TETVPSEQSH	ASGKLRKKKK	KQKNKKSSTG	EASENGLEDI	DRILERIEDS
170	180	190	200	210	220	230	240
TGLNRPGPAP	LSSRKHVLYV	EHRHLNPDTE	LKRYFGARAI	LGEQRPRQRQ	RVYPKCTWLT	TPKSTWPRYS	KPGLSMRLLE
250	260	270	280	290	300	310	320
SKKGLSFFAF	EHSEEYQQAQ	HKFLVAVESM	EPNNIVVLLQ	TSPYHVDSLL	QLSDACRFQE	DQEMARDLVE	RALYSMECAF
330	340	350	360	370	380	390	400
HPLFSLTSGA	CRLDYRRPEN	RSFYLALYKQ	MSFLEKRGCP	RTALEYCKLI	LSLEPDEDPL	CMLLLIDHLA	LRARNYEYLI
410	420	430	440	450	460	470	480
RLFQEWEAHR	NLSQLPNFAF	SVPLAYFLLS	QQTDLPECEQ	SSARQKASLL	IQQALTMFPG	VLLPLLESCS	VRPDASVSSH
490	500	510	520	530	540	550	560
RFFGPNAEIS	QPPALSQLVN	LYLGRSHFLW	KEPATMSWLE	ENVHEVLQAV	DAGDPAVEAC	ENRRKVLYQR	APRNIHRHVI
570	580	590	600	610	620	630	640
LSEIKEAVAA	LPPDVTTQSV	MGFDPLPPSD	TIYSYVRPER	LSPISHGNTI	ALFFRSLLPN	YTMEGERPEE	GVAGGLNRNQ
650	660	670	680				
GLNRLMLAVR	DMMANFHLND	LEAPHEDDAE	GEGEWD				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2737	1	959.5194	-10.55	2	65.5	14.4	2	194-209	R.YFGARAILGEQRPRQR.Q	

Detailed Protein Report

Protein 819: lymphoid-specific helicase isoform 7 [Homo sapiens]

Accession:	gi|574275777	**Score:**	14.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	81.6
Database Date:	2015-11-30	**pI:**	8.8
		Sequence Coverage [%]:	1.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPAERPAGSG	GSEAPAMVEQ	LDTAVITPAM	LEEEEQLEAA	GLERERKMLE	KARMSWDRES	TEIRYRRLQH	LLEKSNIYSK
90	100	110	120	130	140	150	160
FLLTKMEQQQ	LEEQKKKEKL	ERKKESLKVK	KGKNSIDASE	EKPVMRKKRG	REDESYNISE	VMSKEEILSV	AKKNKKENED
170	180	190	200	210	220	230	240
ENSSSTNLCV	EDLQKNKDSN	SIIKDRLSET	VRQNTKFFFD	PVRKCNGQPV	PFQQPKHFTG	GVMRWYQVEG	MEWLRMLWEN
250	260	270	280	290	300	310	320
GINGILADEM	GLGKTVQCIA	TIALMIQRGV	PGPFLVCGPL	STLPNWMAEF	KRFTPDIPTM	LYHGTQEERQ	KLILTPFLLR
330	340	350	360	370	380	390	400
RLKSDVALEV	PPKREVVVYA	PLSKKQEIFY	TAIVNRTIAN	MFGSSEKETI	ELSPTGRPKR	RTRKSINYSK	IDDFPNELEK
410	420	430	440	450	460	470	480
LISQIQPEVD	RERAVVEVNI	PVESEVNLKL	QNIMMLLRKC	CNHPYLIEYP	IDPVTQEFKI	DEELVTNSGK	FLILDRMLPE
490	500	510	520	530	540	550	560
LKKRGHKVLL	FSQMTSMLDI	LMDYCHLRDF	NFSRLDGSMS	YSEREKNMHS	FNTDPEVFIF	LVSTRAGGLG	INLTAADTVI
570	580	590	600	610	620	630	640
IYDSDWNPQS	DLQAQDRCHR	IGQTKPVVVY	RLVTANTIDQ	KIVERAAAKR	KLEKLIIHKN	HFKGGQSGLN	LSKNFLDPKE
650	660	670	680	690	700	710	
LMELLKSRDY	EREIKGSREK	VISDKDLELL	LDRSDLIDQM	NASGPIKEKM	GIFKILENSE	DSSPECLF	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1513	1	671.4128	-32.26	2	48.6	14.4	1	310-320	R.QKLILTPFLLR.R	

Detailed Protein Report

Protein 820: A-kinase anchor protein 2 isoform 2 [Homo sapiens]

Accession:	gi|211971074	**Score:**	14.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	94.6
Database Date:	2015-11-30	**pI:**	4.9
		Sequence Coverage [%]:	1.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEIEVSVAEC	KSVPGITSTP	HPMDHPSAFY	SPPHNGLLTD	HHESLDNDVA	REIRYLDEVL	EANCCDSAVD	GTYNGTSSPE
90	100	110	120	130	140	150	160
PGAVVLVGGL	SPPVHEATQP	EPTERTASRQ	APPHIELSNS	SPDPMAEAER	TNGHSPSQPR	DALGDSLQVP	VSPSSTTSSR
170	180	190	200	210	220	230	240
CSSRDGEFTL	TTLKKEAKFE	LRAFHEDKKP	SKLFEDDEHE	KEQYCIRKVR	PSEEMLELEK	ERRELIRSQA	VKKNPGIAAK
250	260	270	280	290	300	310	320
WWNPPQEKTI	EEQLDEEHLE	SHKKYKERKE	RRAQQEQLLL	QKQLQQQQQQ	PPSQLCTAPA	SSHERASMID	KAKEDIVTEQ
330	340	350	360	370	380	390	400
IDFSAARKQF	QLMENSRQAV	AKGQSTPRLF	SIKPFYRPLG	SVNSDKPLTN	PRPPSVGGPP	EDSGASAAKG	QKSPGALETP
410	420	430	440	450	460	470	480
SAAGSQGNTA	SQGKEGPYSE	PSKRGPLSKL	WAEDGEFTSA	RAVLTVVKDD	DHGILDQFSR	SVNVSLTQEE	LDSGLDELSV
490	500	510	520	530	540	550	560
RSQDTTVLET	LSNDFSMDNI	SDSGASNETT	NALQENSLAD	FSLPQTPQTD	NPSEGRGEGV	SKSFSDHGFY	SPSSTLGDSP
570	580	590	600	610	620	630	640
LVDDPLEYQA	GLLVQNAIQQ	AIAEQVDKAV	SKTSRDGAEQ	QGPEATVEEA	EAAAFGSEKP	QSMFEPPQVS	SPVQEKRDVL
650	660	670	680	690	700	710	720
PKILPAEDRA	LRERGPPQPL	PAVQPSGPIN	MEETRPEGSY	FSKYSEAAEL	RSTASLLATQ	ESDVMVGPFK	LRSRKQRTLS
730	740	750	760	770	780	790	800
MIEEEIRAAQ	EREEELKRQR	QVLQSTQSPR	TKNAPSLPSR	TCYKTAPGKI	EKVKPPPSPT	TEGPSLQPDL	APEEAAGTQR
810	820	830	840	850	860		
PKNLMQTLME	DYETHKSKRR	ERMDDSSVLE	ATRVNRRKSA	LALRWEAGIY	ANQEEEDNE		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2188	1	796.7740	-143.67	2	57.6	14.4	1	823-836	R.MDDSSVLEATRVNR.R	

Detailed Protein Report

Protein 821: PREDICTED: SEC14-like protein 4 isoform X6 [Homo sapiens]

Accession:	gi|578837189	**Score:**	14.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	40.2
Database Date:	2015-11-30	**pI:**	6.8
		Sequence Coverage [%]:	4.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLRRHMEFRK	QQDLDNIVTW	QPPEVIQLYD	SGGLCGYDYE	GCPVYFNIIG	SLDPKGLLLS	ASKQDMIRKR	IKVCELLLHE
90	100	110	120	130	140	150	160
CELQTQKLGR	KIEMALMVFD	MEGLSLKHLW	KPAVEVYQQF	FSILEANYPE	TLKNLIVIRA	PKLFPVAFNL	VKSFMSEETR
170	180	190	200	210	220	230	240
RKIVILGDNW	KQELTKFISP	DQLPVEFGGT	MTDPDGNPKC	LTKINYGGEV	PKSYYLCEQV	RLQYEHTRSV	GRGSSLQVEN
250	260	270	280	290	300	310	320
EILFPGCVLR	WQFASDGGDI	GFGVFLKTKM	GEQQSAREMT	EVLPSQRYNA	HMVPEDGSLT	CLQAGVYVLR	FDNTYSRMHA
330	340	350	360				
KKLSYTVEVL	LPDKASEETL	QSLKAMRPSP	TQ				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1473	1	829.0747	126.77	2	48.2	14.3	1	163-176	K.IVILGDNWKQELTK.F	

Detailed Protein Report

Protein 822: G protein-activated inward rectifier potassium channel 3 [Homo sapiens]

Accession:	gi|25121970	**Score:**	14.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	44.0
Database Date:	2015-11-30	**pI:**	4.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	4.3
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578800900	refseq_human (refseq_human_20140103.fasta)	PREDICTED: G protein-activated inward rectifier potassium channel 3 isoform X2 [Homo sapiens]

10	20	30	40	50	60	70	80
MAQENAAFSP	GQEEPPRRRG	RQRYVEKDGR	CNVQQGNVRE	TYRYLTDLFT	TLVDLQWRLS	LLFFVLAYAL	TWLFFGAIWW
90	100	110	120	130	140	150	160
LIAYGRGDLE	HLEDTAWTPC	VNNLNGFVAA	FLFSIETETT	IGYGHRVITD	QCPEGIVLLL	LQAILGSMVN	AFMVGCMFVK
170	180	190	200	210	220	230	240
ISQPNKRAAT	LVFSSHAVVS	LRDGRLCLMF	RVGDLRSSHI	VEASIRAKLI	RSRQTLEGEF	IPLHQTDLSV	GFDTGDDRLF
250	260	270	280	290	300	310	320
LVSPLVISHE	IDAASPFWEA	SRRALERDDF	EIVVILEGMV	EATGMTCQAR	SSYLVDEVLW	GHRFTSVLTL	EDGFYEVDYA
330	340	350	360	370	380	390	400
SFHETFEVPT	PSCSARELAE	AAARLDAHLY	WSIPSRLDEK	VEEEGAGEGA	GGEAGADKEQ	NGCLPPPESE	SKV

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1255	1	937.9577	39.66	2	45.3	14.3	0	1-17	-.MAQENAAFSPGQEEPPR.R	Oxidation: 1

Detailed Protein Report

Protein 823: anaphase-promoting complex subunit 11 isoform 4 [Homo sapiens]

Accession:	gi|574956971	**Score:**	14.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	14.9
Database Date:	2015-11-30	**pI:**	12.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	21.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MKVKIKCWNG	VATWLWVAND	ENCGICRMAF	NGCCPDCPLH	GESISRCLGW	CPQPVPVLGG	RAHPQARCPA	TTARWCGASA
90	**100**	**110**	**120**	**130**	**140**	**150**	
PTASTCIASS	SGCTHSRCSS	TAPCAARNGS	SRSEARPGSR	WRGILRLLPH	AGADGCWGQR	P	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1140	1	1019.2076	93.06	3	43.8	14.3	1	68-97	R.CPATTARWCGASAPTASTCIASSSGCTHSR.C	Carbamidomethyl: 9, 19

Detailed Protein Report

Protein 824: upstream stimulatory factor 2 isoform 2 [Homo sapiens]

Accession:	gi|46877105	**Score:**	14.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	30.6
Database Date:	2015-11-30	**pI:**	5.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	6.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDMLDPGLDP	AASATAAAAA	SHDKGPEAEE	GVELQEGGDG	PGAEEQTAVA	ITSVQQAAFG	DHNIQYQFRT	ETNGGQAVIQ
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
NPFSNGGSPA	AEAVSGEARF	AYFPASSVGD	TTAVSVQTTD	QSLQAGGQFY	VMMTPQDVLQ	TGTQRTIAPR	THPYSPKIDG
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
TRTPRDERRR	AQHNEVERRR	RDKINNWIVQ	LSKIIPDCNA	DNSKTGASKG	GILSKACDYI	RELRQTNQRM	QETFKEAERL
250	**260**	**270**	**280**				
QMDNELLRQQ	IEELKNENAL	LRAQLQQHNL	EMVGEGTRQ				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1816	2	898.8604	-121.72	2	52.5	14.3	2	205-221	K.TGASKGGILSKACDYIR.E	Carbamidomethyl: 13

Detailed Protein Report

Protein 825: PREDICTED: cyclin-dependent kinase inhibitor 2A isoform X3 [Homo sapiens]

Accession:	gi|530389655	**Score:**	14.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	11.2
Database Date:	2015-11-30	**pI:**	5.6
		Sequence Coverage [%]:	11.4
		No. of unique Peptides:	1

```
         10         20         30         40         50         60         70         80
MMMGSARVAE LLLLHGAEPN CADPATLTRP VHDAAREGFL DTLVVLHRAG ARLDVRDAWG RLPVDLAEEL GHRDVARYLR
         90        100        110
AAAGGTRGSN HARIDAAEGP SDIPD
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
704	1	600.1941	-134.67	2	38.4	14.3	0	94-105	R.IDAAEGPSDIPD.-	

Detailed Protein Report

Protein 826: PREDICTED: uncharacterized protein LOC646670 [Homo sapiens]

Accession:	gi|578797043	**Score:**	14.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	34.5
Database Date:	2015-11-30	**pI:**	10.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGLWRVWGRQ	CFCGSLREGS	SLESTRVSWY	PQLLRGVYLE	SLVYTRCSAT	PHGLAMTSLP	PEQPWPREEA	VSASNDRWKM
90	100	110	120	130	140	150	160
EVGMIALKRS	QGGGQDSGRR	RSRRQHFAPG	TSSGLRSAPG	LTRAGPAPPE	AVSPSHVIVD	SADLAGPEKE	IPGPWLPRAM
170	180	190	200	210	220	230	240
YEAPGVKRAW	AAGAGMRGRQ	WLRKRVEVVC	TGRSANTVCA	GVRAAGLSSV	KLQLLCSQVL	KELLGQGIDV	KDQKLTADAK
250	260	270	280	290	300	310	320
FESGDVKATV	AVLSFILSGA	AKHSVDGKSL	ASELQQLGLP	KEHAASPCCC	YEEKQSPLQK	HLRVCSLRSK	YEASQGPGSS
330							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
963	1	560.4165	248.16	2	41.5	14.3	1	169-179	R.AWAAGAGMRGR.Q	Oxidation: 8

Detailed Protein Report

Protein 827: developmental pluripotency-associated 5 protein [Homo sapiens]

Accession:	gi|70608179	**Score:**	14.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	13.5
Database Date:	2015-11-30	**pI:**	9.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	9.5
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MGTLPARRHI PPWVKVPEDL KDPEVFQVQT RLLKAIFGPD GSRIPYIEQV SKAMLELKAL ESSDLTEVVV YGSYLYKLRT
        90        100        110        120
KWMLQSMAEW HRQRQERGML KLAEAMNALE LGPWMK
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2012	1	753.7422	-122.39	2	55.3	14.2	0	82-92	K.WMLQSMAEWHR.Q	Oxidation: 2, 6

Detailed Protein Report

Protein 828: LON peptidase N-terminal domain and RING finger protein 2 [Homo sapiens]

Accession:	gi|148528975	**Score:**	14.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	83.6
Database Date:	2015-11-30	**pI:**	5.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.1
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 1.55 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MSPEPVPPPP	PPQCPGCDRA	EPIAQRLEEG	DEAFRAGDYE	MAAELFRSML	AGLAQPDRGL	CLRLGDALAR	AGRLPEALGA
90	100	110	120	130	140	150	160
FRGAARLGAL	RPEELEELAG	GLVRAVGLRD	RPLSAENPGG	EPEAPGEGGP	APEPRAPRDL	LGCPRCRRLL	HKPVTLPCGL
170	180	190	200	210	220	230	240
TVCKRCVEPG	PARPQVRRVN	VVLSGLLEKC	FPAECRLRRL	AGQARSLQRQ	QQPEAALLRC	DQALELAPDD	NSLLLLRAEL
250	260	270	280	290	300	310	320
YLTMKNYEQA	LQDASAACQN	EPLLIKGHQV	KAQALSGLGR	SKEVLKEFLY	CLALNPECNS	VKKEAQKVMC	EVLFSATANV
330	340	350	360	370	380	390	400
HENLTSSIQS	RLKAQGHSHM	NAQALLEEGD	AGSSENSSEK	SDMLGNTNSS	VLYFILGLHF	EEDKKALESI	LPTAPSAGLK
410	420	430	440	450	460	470	480
RQFPDDVEDA	PDLNAPGKIP	KKDLSLQRSP	NSETEESQGL	SLDVTDFECA	LCMRLLFEPV	TTPCGHTFCL	KCLERCLDHA
490	500	510	520	530	540	550	560
PHCPLCKDKL	SELLASRNFN	ITVLAEELIF	RYLPDELSDR	KRIYDEEMSE	LSNLTRDVPI	FVCAMAFPTV	PCPLHVFEPR
570	580	590	600	610	620	630	640
YRLMIRRCME	TGTKRFGMCL	SAEHAGLSEY	GCMLEIKDVR	TFPDGSSVVD	AIGISRFRVL	SHRHRDGYNT	ADIEYLEDEK
650	660	670	680	690	700	710	720
VEGPEYEELA	ALHDSVHQQS	VSWFASLQDR	MKEQILSHFG	VMPDREPEPQ	SNPSGPAWSW	WILAVLPLER	KAQLAILGMT
730	740	750	760				
SLKERLLAIR	RILVIITRKM	NSRQELANAR	ERNN				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
899	1	491.6498	-154.78	2	40.8	14.2	1	568-575	R.CMETGTKR.F	Carbamidomethyl: 1	MD:MU 1.55

Detailed Protein Report

Protein 829: TRAF-type zinc finger domain-containing protein 1 [Homo sapiens]

Accession:	gi|5729828	**Score:**	14.2
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
2118	1	1052.3339	-103.36	2	56.6	14.2	1	1-17	-.MAEFLDDQETRLCDNCK.K	Carbamidomethyl: 13; Oxidation: 1

Detailed Protein Report

Protein 830: leucine-rich repeat-containing protein 10 [Homo sapiens]

Accession: gi|63003903
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 14.2
MW [kDa]: 31.6
pI: 9.9
Sequence Coverage [%]: 3.6
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MGNTIRALVA	FIPADRCQNY	VVRDLREMPL	DKMVDLSGSQ	LRRFPLHVCS	FRELVKLYLS	DNHLNSLPPE	LGQLQNLQIL
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
ALDFNNFKAL	PQVVCTLKQL	CILYLGNNKL	CDLPSELSLL	QNLRTLWIEA	NCLTQLPDVV	CELSLLKTLH	AGSNALRLLP
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
GQLRRLQELR	TIWLSGNRLT	DFPTVLLHMP	FLEVIDVDWN	SIRYFPSLAH	LSSLKLVIYD	HNPCRNAPKV	AKGVRRVGRW
250	**260**	**270**	**280**				
AEETPEPDPR	KARRYALVRE	ESQELQAPVP	LLPPTNS				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
611	1	536.1729	-265.36	2	37.2	14.2	0	89-98	K.ALPQVVCTLK.Q	

Detailed Protein Report

Protein 831: 60S acidic ribosomal protein P0 [Homo sapiens]

Accession:	gi|4506667	**Score:**	14.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	34.3
Database Date:	2015-11-30	**pI:**	5.6
		Sequence Coverage [%]:	5.0
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|16933546	refseq_human(refseq_human_20140103.fasta)	60S acidic ribosomal protein P0 [Homo sapiens]

10	20	30	40	50	60	70	80
MPREDRATWK	SNYFLKIIQL	LDDYPKCFIV	GADNVGSKQM	QQIRMSLRGK	AVVLMGKNTM	MRKAIRGHLE	NNPALEKLLP
90	100	110	120	130	140	150	160
HIRGNVGFVF	TKEDLTEIRD	MLLANKVPAA	ARAGAIAPCE	VTVPAQNTGL	GPEKTSFFQA	LGITTKISRG	TIEILSDVQL
170	180	190	200	210	220	230	240
IKTGDKVGAS	EATLLNMLNI	SPFSFGLVIQ	QVFDNGSIYN	PEVLDITEET	LHSRFLEGVR	NVASVCLQIG	YPTVASVPHS
250	260	270	280	290	300	310	320
IINGYKRVLA	LSVETDYTFP	LAEKVKAFLA	DPSAFVAAAP	VAAATTAAPA	AAAAPAKVEA	KEESEESDED	MGFGLFD

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1927	1	918.3436	-0.04	2	54.0	14.2	0	302-317	K.EESEESDEDMGFGLFD.-	

Protein 832: **PREDICTED: nuclear receptor subfamily 4 group A member 1 isoform X2 [Homo sapiens]**

Accession:	gi|530400145	**Score:**	14.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	70.4
Database Date:	2015-11-30	**pI:**	8.9
		Sequence Coverage [%]:	2.8
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MTSAQYKIKI LIEGLHHGQR PGPAPPRQPG SFCWALKADG IMWLAKACWS IQSEMPCIQA QYGTPAPSPG PRDHLASDPL
        90        100        110        120        130        140        150        160
TPEFIKPTMD LASPEAAPAA PTALPSFSTF MDGYTGEFDT FLYQLPGTVQ PCSSASSSAS STSSSSATSP ASASFKFEDF
       170        180        190        200        210        220        230        240
QVYGCYPGPL SGPVDEALSS SGSDYYGSPC SAPSPSTPSF QPPQLSPWDG SFGHFSPSQT YEGLRAWTEQ LPKASGPPQP
       250        260        270        280        290        300        310        320
PAFFSFSPPT GPSPSLAQSP LKLFPSQATH QLGEGESYSM PTAFPGLAPT SPHLEGSGIL DTPVTSTKAR SGAPGGSEGR
       330        340        350        360        370        380        390        400
CAVCGDNASC QHYGVRTCEG CKGFFKRTVQ KNAKYICLAN KDCPVDKRRR NRCQFCRFQK CLAVGMVKEV VRTDSLKGRR
       410        420        430        440        450        460        470        480
GRLPSKPKQP PDASPANLLT SLVRAHLDSG PSTAKLDYSK FQELVLPHFG KEDAGDVQQF YDLLSGSLEV IRKWAEKIPG
       490        500        510        520        530        540        550        560
FAELSPADQD LLLESAFLEL FILRLAYRSK PGEGKLIFCS GLVLHRLQCA RGFGDWIDSI LAFSRSLHSL LVDVPAFACL
       570        580        590        600        610        620        630        640
SALVLITDRH GLQEPRRVEE LQNRIASCLK EHVAAVAGEP QPASCLSRLL GKLPELRTLC TQGLQRIFYL KLEDLVPPPP
       650        660
IIDKIFMDTL PF
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2308	1	973.1508	106.11	2	58.7	14.2	0	10-27	K.ILIEGLHHGQRPGPAPPR.Q	

Detailed Protein Report

Protein 833: PREDICTED: coiled-coil domain-containing protein 60 isoform X1 [Homo sapiens]

Accession:	gi|530401235	**Score:**	14.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	47.8
Database Date:	2015-11-30	**pI:**	10.4
		Sequence Coverage [%]:	4.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MTKVPATKKL	QSSPNSGAVR	PFYASENLRQ	VPDKPMKSIK	YMDKEIINLK	KDLIRSRFLI	QSVKIGRGYF	AILREETAKK
90	100	110	120	130	140	150	160
KKQQQLQKLK	EEERNKFQPA	EKISEIHYGD	TLLSTYDDEK	LKTLGARVTR	RPFTPIHSCI	ISPSLTEAHV	EPLFRQLCAL
170	180	190	200	210	220	230	240
HWLLEALTID	HTHHTMKPVI	TCWNPKDPGG	SKSTIKKINK	DKSMGQKWEH	FITAPKTKKF	KIPTMRVTNR	KPSRRGSTLS
250	260	270	280	290	300	310	320
LSRASGGSSP	QSSMISVNPG	SDEPPSVNTQ	VTSSKDIEDN	ESSSTKPDEE	PLYMNLQKLL	EMVREDARRT	VTIENGMQRK
330	340	350	360	370	380	390	400
APSILSVLKQ	NKSNSAYKEM	QTTLKSSERS	SSTSAESHIQ	PVQKKSKNRT	NCDINIHYKS	GVCNTMRAKF	YSVAQEAGFC
410	420	430					
LQDKMEILMN	LLLDSRDHPS	R					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2374	1	1022.9281	-68.61	2	59.6	14.2	1	346-364	K.SSERSSSTSAESHIQPVQK.K	

Detailed Protein Report

Protein 834: **PREDICTED: glycine, alanine and asparagine-rich protein-like [Homo sapiens]**

Accession:	gi|578802104	**Score:**	14.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	24.0
Database Date:	2015-11-30	**pI:**	12.2
		Sequence Coverage [%]:	9.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MVRGIDKELL	ECLQIKAIVP	RGEVRTGEGG	LREPVPGQAT	HRAAKLHREG	RNPSRPGRKA	GRDVGGAAGG	AGLRVGSLWS
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
SPVICRWIRD	GSGLGGVGGG	SARGDVRGGA	ARAVGGGGGS	VSRSRVEVGR	SELLGAVSPP	AASARLYRRA	SEFPRVLGGA
170	**180**	**190**	**200**	**210**	**220**	**230**	
PPSFQSPRTG	PSSFYLTAPV	FRRLLALSVG	PIPARFLLLP	IEALEMNVSI	SSEMNQIMMH	HYHRRNSCL	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2459	1	1014.8801	-137.62	2	60.6	14.2	2	87-107	R.WIRDGSGLGGVGGGSARGDVR.G	

Detailed Protein Report

Protein 835: PREDICTED: zinc finger protein 440 isoform X2 [Homo sapiens]

Accession:	gi|578832975		**Score:**	14.1
Database:	refseq_human(refseq_human_20140103.fasta)		**MW [kDa]:**	54.8
Database Date:	2015-11-30		**pI:**	10.5
			Sequence Coverage [%]:	5.1
			No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MNIRGDIGHK	AYEYQEYGPK	PCKCQQPKKA	FRYRPSFRTQ	ERDHTGEKPN	ACKVCGKTFI	SHSSVRRHMV	MHSGDGPYKC
90	100	110	120	130	140	150	160
KFCGKAFHCL	RLYLIHERIH	TGEKPCECKQ	CGKSFSYSAT	HRIHKRTHTG	EKPYEYQECG	KAFHSPRSYR	RHERIHMGEK
170	180	190	200	210	220	230	240
AYQCKECGKA	FTCPRYVRIH	ERTHSRKNLY	ECKQCGKALS	SLTSFQTHVR	LHSGERPYEC	KICGKDFCSV	NSFQRHEKIH
250	260	270	280	290	300	310	320
SGEKPYKCKQ	CGKAFPHSSS	LRYHERTHTG	EKPYECKQCG	KAFRSASHLR	VHGRTHTGEK	PYECKECGKA	FRYVNNLQSH
330	340	350	360	370	380	390	400
ERTQTHIRIH	SGERRYKCKI	CGKGFYCPKS	FQRHEKTHTG	EKLYECKQRS	VVPSVVPVPF	DIMKGLTLER	SPINASNVGK
410	420	430	440	450	460	470	480
PSELCQSFEC	MVGLTLKRNP	MSVSNDGKPS	DLPHTFEYVV	GHTMERSPMH	VRNVGNPSDL	PRTFEFMKGH	KHT

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1614	1	954.2238	104.31	3	50.1	14.1	2	254-277	K.AFPHSSSLRYHERTHTGEKPYECK.Q	

Detailed Protein Report

Protein 836: heterogeneous nuclear ribonucleoprotein U isoform b [Homo sapiens]

Accession:	gi|14141161	**Score:**	14.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	88.9
Database Date:	2015-11-30	**pI:**	5.5
		Sequence Coverage [%]:	1.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSSSPVNVKK	LKVSELKEEL	KKRRLSDKGL	KAELMERLQA	ALDDEEAGGR	PAMEPGNGSL	DLGGDSAGRS	GAGLEQEAAA
90	100	110	120	130	140	150	160
GGDEEEEEEE	EEEEGISALD	GDQMELGEEN	GAAGAADSGP	MEEEEAASED	ENGDDQGFQE	GEDELGDEEE	GAGDENGHGE
170	180	190	200	210	220	230	240
QQPQPPATQQ	QQPQQQRGAA	KEAAGKSSGP	TSLFAVTVAP	PGARQGQQQA	GGDGKTEQKG	GDKKRGVKRP	REDHGRGYFE
250	260	270	280	290	300	310	320
YIEENKYSRA	KSPQPPVEEE	DEHFDDTVVC	LDTYNCDLHF	KISRDRLSAS	SLTMESFAFL	WAGGRASYGV	SKGKVCFEMK
330	340	350	360	370	380	390	400
VTEKIPVRHL	YTKDIDIHEV	RIGWSLTTSG	MLLGEEEFSY	GYSLKGIKTC	NCETEDYGEK	FDENDVITCF	ANFESDEVEL
410	420	430	440	450	460	470	480
SYAKNGQDLG	VAFKISKEVL	AGRPLFPHVL	CHNCAVEFNF	GQKEKPYFPI	PEEYTFIQNV	PLEDRVRGPK	GPEEKKDCEV
490	500	510	520	530	540	550	560
VMMIGLPGAG	KTTWVTKHAA	ENPGKYNILG	TNTIMDKMMV	AGFKKQMADT	GKLNTLLQRA	PQCLGKFIEI	AARKKRNFIL
570	580	590	600	610	620	630	640
DQTNVSAAAQ	RRKMCLFAGF	QRKAVVVCPK	DEDYKQRTQK	KAEVEGKDLP	EHAVLKMKGN	FTLPEVAECF	DEITYVELQK
650	660	670	680	690	700	710	720
EEAQKLLEQY	KEESKKALPP	EKKQNTGSKK	SNKNKSGKNQ	FNRGGGHRGR	GGFNMRGGNF	RGGAPGNRGG	YNRRGNMPQR
730	740	750	760	770	780	790	800
GGGGGGSGGI	GYPYPRAPVF	PGRGSYSNRG	NYNRGGMPNR	GNYNQNFRGR	GNNRGYKNQS	QGYNQWQQGQ	FWGQKPWSQH
810							
YHQGYY							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
437	1	658.3928	-3.68	2	35.1	14.1	2	11-21	K.LKVSELKEELK.K	

Detailed Protein Report

Protein 837: beta-Ala-His dipeptidase precursor [Homo sapiens]

Accession:	gi|21071039	**Score:**	14.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	56.7
Database Date:	2015-11-30	**pI:**	5.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	6.7
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MDPKLGRMAA SLLAVLLLLL ERGMFSSPSP PPALLEKVFQ YIDLHQDEFV QTLKEWVAIE SDSVQPVPRF RQELFRMMAV
        90        100        110        120        130        140        150        160
AADTLQRLGA RVASVDMGPQ QLPDGQSLPI PPVILAELGS DPTKGTVCFY GHLDVQPADR GDGWLTDPYV LTEVDGKLYG
       170        180        190        200        210        220        230        240
RGATDNKGPV LAWINAVSAF RALEQDLPVN IKFIIEGMEE AGSVALEELV EKEKDRFFSG VDYIVISDNL WISQRKPAIT
       250        260        270        280        290        300        310        320
YGTRGNSYFM VEVKCRDQDF HSGTFGGILH EPMADLVALL GSLVDSSGHI LVPGIYDEVV PLTEEEINTY KAIHLDLEEY
       330        340        350        360        370        380        390        400
RNSSRVEKFL FDTKEEILMH LWRYPSLSIH GIEGAFDEPG TKTVIPGRVI GKFSIRLVPH MNVSAVEKQV TRHLEDVFSK
       410        420        430        440        450        460        470        480
RNSSNKMVVS MTLGLHPWIA NIDDTQYLAA KRAIRTVFGT EPDMIRDGST IPIAKMFQEI VHKSVVLIPL GAVDDGEHSQ
       490        500        510
NEKINRWNYI EGTKLFAAFF LEMAQLH
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2217	1	1288.9464	-38.66	3	57.6	14.1	2	335-368	K.EEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGR.V	Oxidation: 5

Detailed Protein Report

Protein 838: **PREDICTED: leucine-rich repeat flightless-interacting protein 2 isoform X39 [Homo sapiens]**

Accession:	gi|578806740	**Score:**	14.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	52.2
Database Date:	2015-11-30	**pI:**	8.5
		Sequence Coverage [%]:	2.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGTPASGRKR	TPVKDRFSAE	DEALSNIARE	AEARLAAKRA	ARAEARDIRM	RELERQQKEY	SLHSFDRKWG	QIQKWLEDSE
90	100	110	120	130	140	150	160
RARYSHRSSH	HRPYLGVEDA	LSIRSVGSHR	YDMFKDRSSR	LSSLNHSYSH	SHGMKKRSSD	SHKDLLSGLY	FDQRNYSSLR
170	180	190	200	210	220	230	240
HSKPTSAYYT	RQSSSLYSDP	LATYKSDRAS	PTANSGLLRS	ASLASLYNGG	LYNPYGPRTP	SECSYYSSRI	SSARSSPGFT
250	260	270	280	290	300	310	320
NDDTASIVSS	DRASRGRRES	VVSAADYFSR	SNRRGSVVSE	VDDISIPDLS	SLDEKSDKQY	AENYTRPSSR	NSASATTPLS
330	340	350	360	370	380	390	400
GNSSRRGSGD	TSSLIDPDTS	LSELRDIYDL	KDQIQDVEGR	YMQGLKELKE	SLSEVEEKYK	KAMVSNAQLD	NEKNNLIYQV
410	420	430	440	450	460		
DTLKDVIEEQ	EEQMAEFYRE	NEEKSKELER	QKHMCSVLQH	KMEELKEGLR	QRDELIEM		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1798	1	577.2449	-38.82	2	52.5	14.1	0	59-67	K.EYSLHSFDR.K	

Detailed Protein Report

Protein 839: arachidonate 12-lipoxygenase, 12S-type [Homo sapiens]

Accession:	gi|154426292	**Score:**	14.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	75.6
Database Date:	2015-11-30	**pI:**	5.8
		Sequence Coverage [%]:	2.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGRYRIRVAT	GAWLFSGSYN	RVQLWLVGTR	GEAELELQLR	PARGEEEEFD	HDVAEDLGLL	QFVRLRKHHW	LVDDAWFCDR
90	100	110	120	130	140	150	160
ITVQGPGACA	EVAFPCYRWV	QGEDILSLPE	GTARLPGDNA	LDMFQKHREK	ELKDRQQIYC	WATWKEGLPL	TIAADRKDDL
170	180	190	200	210	220	230	240
PPNMRFHEEK	RLDFEWTLKA	GALEMALKRV	YTLLSSWNCL	EDFDQIFWGQ	KSALAEKVRQ	CWQDDELFSY	QFLNGANPML
250	260	270	280	290	300	310	320
LRRSTSLPSR	LVLPSGMEEL	QAQLEKELQN	GSLFEADFIL	LDGIPANVIR	GEKQYLAAPL	VMLKMEPNGK	LQPMVIQIQP
330	340	350	360	370	380	390	400
PNPSSPTPTL	FLPSDPPLAW	LLAKSWVRNS	DFQLHEIQYH	LLNTHLVAEV	IAVATMRCLP	GLHPIFKFLI	PHIRYTMEIN
410	420	430	440	450	460	470	480
TRARTQLISD	GGIFDKAVST	GGGGHVQLLR	RAAAQLTYCS	LCPPDDLADR	GLLGLPGALY	AHDALRLWEI	IARYVEGIVH
490	500	510	520	530	540	550	560
LFYQRDDIVK	GDPELQAWCR	EITEVGLCQA	QDRGFPVSFQ	SQSQLCHFLT	MCVFTCTAQH	AAINQGQLDW	YAWVPNAPCT
570	580	590	600	610	620	630	640
MRMPPPTTKE	DVTMATVMGS	LPDVRQACLQ	MAISWHLSRR	QPDMVPLGHH	KEKYFSGPKP	KAVLNQFRTD	LEKLEKEITA
650	660	670					
RNEQLDWPYE	YLKPSCIENS	VTI					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2554	1	821.4177	7.06	2	61.9	14.1	1	115-128	R.LPGDNALDMFQKHR.E	

Detailed Protein Report

Protein 840: PREDICTED: FERM and PDZ domain-containing protein 4 isoform X2 [Homo sapiens]

Accession: gi|578837988

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Modification(s): Carbamidomethyl

Score: 14.1

MW [kDa]: 189.7

pI: 5.2

Sequence Coverage [%]: 0.5

No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MDTVHPGSHS	WDFCHRTKSS	GWPPPSGTWG	LSQVPPYGWE	MTANRDGRDY	FINHMTQAIP	FDDPRLESCQ	IIPPAPRKVE
90	100	110	120	130	140	150	160
MRRDPVLGFG	FVAGSEKPVV	VRSVTPGGPS	EGKLIPGDQI	VMINDEPVSA	APRERVIDLV	RSCKESILLT	VIQPYPSPKS
170	180	190	200	210	220	230	240
AFISAAKKAR	LKSNPVKVRF	SEEVIINGQV	SETVKDNSLL	FMPNVLKVYL	ENGQTKSFRF	DCSTSIKDVI	LTLQEKLSIK
250	260	270	280	290	300	310	320
GIEHFSLMLE	QRTEGAGTKL	LLLHEQETLT	QVTQRPSSHK	MRCLFRISFV	PKDPIDLLRR	DPVAFEYLYV	QSCNDVVQER
330	340	350	360	370	380	390	400
FGPELKYDIA	LRLAALQMYI	ATVTTKQTQK	ISLKYIEKEW	GLETFLPSAV	LQSMKEKNIK	KALSHLVKAN	QNLVPPGKKQ
410	420	430	440	450	460	470	480
AEKRSEVTLL	VGPRYGISHV	INTKTNLVAL	LADFSHVNRI	EMFSEEESLV	RVELHVLDVK	PITLLMESSD	AMNLACLTAG
490	500	510	520	530	540	550	560
YYRLLVDSRR	SIFNMANKKN	TATQETGPEN	KGKHNLLGPD	WNCIPQMTTF	IGEGEQEAQI	TYIDSKQKTV	EITDSTMCPK
570	580	590	600	610	620	630	640
EHRHLYIDNA	YSSDGLNQQL	SQPGEAPCEA	DYRSLAQRSL	LTLSGPETLK	KAQESPRGAK	VSFIFGDFAL	DDGISPPTLG
650	660	670	680	690	700	710	720
YETLLDEGPE	MLEKQRNLYI	GSANDMKGLD	LTPEAEGIQF	VENSVYANIG	DVKSFQAAEG	IEEPLLHDIC	YAENTDDAED
730	740	750	760	770	780	790	800
EDEVSCEEDL	VVGEMNQPAI	LNLSGSSDDI	IDLTSLPPPE	GDDNEDDFLL	RSLNMAIAAP	PPGFRDSSDE	EDSQSQAASF
810	820	830	840	850	860	870	880
PEDKEKGSSL	QNDEIPVSLI	DAVPTSAEGK	CEKGLDNAVV	STLGALEALS	VSEEQQTSDN	SGVAILRAYS	PESSSDSGNE
890	900	910	920	930	940	950	960
TNSSEMTESS	ELATAQKQSE	NLSRMFLATH	EGYHPLAEEQ	TEFPASKTPA	GGLPPKSSHA	LAARPATDLP	PKVVPSKQLL
970	980	990	1000	1010	1020	1030	1040
HSDHMEMEPE	TMETKSVTDY	FSKLHMGSVA	YSCTSKRKSK	LADGEGKAPP	NGNTTGKKQQ	GTKTAEMEEE	ASGKFGTVSS
1050	1060	1070	1080	1090	1100	1110	1120
RDSQHLSTFN	LERTAFRKDS	QRWYVATEGG	MAEKSGLEAA	TGKTFPRASG	LGAREAEGKE	EGAPDGETSD	GSGLGQGDRF
1130	1140	1150	1160	1170	1180	1190	1200
LTDVTCASSA	KDLDNPEDAD	SSTCDHPSKL	PEADESVARL	CDYHLAKRMS	SLQSEGHFSL	QSSQGSSVDA	GCGTGSSGSA
1210	1220	1230	1240	1250	1260	1270	1280
CATPVESPLC	PSLGKHLIPD	ASGKGVNYIP	SEERAPGLPN	HGATFKELHP	QTEGMCPRMT	VPALHTAINT	EPLFGTLRDG
1290	1300	1310	1320	1330	1340	1350	1360
CHRLPKIKET	TALTEPGKER	RGGMPSAWSQ	HPEADPILLP	SNIHSESKVP	IPNQDPNDFS	QANQAYGEAV	SWRPPDLRGG
1370	1380	1390	1400	1410	1420	1430	1440
SLRTPPSQKA	LRHSSSILSG	SVDLETFRER	TKGAVSLKCP	GITEAQEASS	ERRAELPLGR	KLTKSFSQSS	MHLSSEGRFH
1450	1460	1470	1480	1490	1500	1510	1520
KRSPVAHKDS	KLYRTLPLRK	LEGSNWRCRG	PFSYCFLNRG	QDEDGEEEEE	RGEATVQVSC	LYRPQMTQAM	PEPSSPCLAV
1530	1540	1550	1560	1570	1580	1590	1600
AIQKQRGELS	RGSVLKVWAE	DLRDPDDLDF	SNLAFDARIA	RINALKESTY	AMPDGFLAAQ	NDANELLCLV	RATKEKREES
1610	1620	1630	1640	1650	1660	1670	1680
RPEAYDLTLS	QYKQLLSIES	RQLGSACRKM	AMAEKSPEEM	LLAMTSSFQV	LCCLTEACMR	LVKVVNSETQ	RQEIVGKIDE
1690	1700	1710	1720	1730	1740		
VVINYICLLK	AAEAATGKNP	GDPNVGLSAR	HSTTMAALVS	TLTRSLKRLL	NK		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
684	1	460.1264	-252.38	2	38.1	14.1	1	1622-1629	R.QLGSACRK.M	Carbamidomethyl: 6

Detailed Protein Report

Protein 841: abhydrolase domain-containing protein 16A isoform b [Homo sapiens]

Accession:	gi|294660765	**Score:**	14.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	59.3
Database Date:	2015-11-30	**pI:**	9.0
		Sequence Coverage [%]:	4.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPPPALFLSS	LYPRLEFQND	FYRSCIRRSS	PQPPPNLAWR	PESLYSGELA	GGGYLSLSKV	VPFSHYAGTL	LLLLAGVACL
90	100	110	120	130	140	150	160
RGIGRWTNPQ	YRQFITILEA	THRNQSSENK	RQLANYNFDF	RSWPVDFHWE	EPSSRKESRG	GPSRRGVALL	RPEPLHRGTA
170	180	190	200	210	220	230	240
DTLLNRVKKL	PCQITSYLVA	HTLGRRMLYP	GSVYLLQKAL	MPVLLQGQAR	LVEECNGRRA	KLLACDGNEI	DTMFVDRRGT
250	260	270	280	290	300	310	320
AEPQGQKLVI	CCEGNAGFYE	VGCVSTPLEA	GYSVLGWNHP	GFAGSTGVPF	PQNEANAMDV	VVQFAIHRLG	FQPQDIIIYA
330	340	350	360	370	380	390	400
WSIGGFTATW	AAMSYPDVSA	MILDASFDDL	VPLALKVMPD	SWRGLVTRTV	RQHLNLNNAE	QLCRYQGPVL	LIRRTKDEII
410	420	430	440	450	460	470	480
TTTVPEDIMS	NRGNDLLLKL	LQHRYPRVMA	EEGLRVVRQW	LEASSQLEEA	SIYSRWEVEE	DWCLSVLRSY	QAEHGPDFPW
490	500	510	520	530			
SVGEDMSADG	RRQLALFLAR	KHLHNFEATH	CTPLPAQNFQ	MPWHL			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1466	1	846.6175	-88.48	3	48.0	14.1	0	469-491	R.SYQAEHGPDFPWSVGEDMSADGR.R	

Detailed Protein Report

Protein 842: zinc transporter SLC39A7 isoform 2 [Homo sapiens]

Accession:	gi|571026676	**Score:**	14.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	36.3
Database Date:	2015-11-30	**pI:**	8.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MTTCTTICKR	TSMATATVLI	SAAPFFVLFL	IPVESNSPRH	RSLLQILLSF	ASGGLLGDAF	LHLIPHALEP	HSHHTLEQPG
90	100	110	120	130	140	150	160
HGHSHSGQGP	ILSVGLWVLS	GIVAFLVVEK	FVRHVKGGHG	HSHGHGHAHS	HTRGSHGHGR	QERSTKEKQS	SEEEEKETRG
170	180	190	200	210	220	230	240
VQKRRGGSTV	PKDGPVRPQN	AEEEKRGLDL	RVSGYLNLAA	DLAHNFTDGL	AIGASFRGGR	GLGILTTMTV	LLHEVPHEVG
250	260	270	280	290	300	310	320
DFAILVQSGC	SKKQAMRLQL	LTAVGALAGT	ACALLTEGGA	VGSEIAGGAG	PGWVLPFTAG	GFIYVATVSV	LPELLREASP
330	340	350					
LQSLLEVLGL	LGGVIMMVLI	AHLE					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
675	1	529.7280	-18.04	2	37.8	14.1	0	1-9	-.MTTCTTICK.R	Carbamidomethyl: 4

Detailed Protein Report

Protein 843: T-complex protein 11 homolog isoform 5 [Homo sapiens]

Accession: gi|387849269
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 14.0
MW [kDa]: 51.9
pI: 5.2
Sequence Coverage [%]: 3.9
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MTRGGGGGGL	TETVNEVSKL	SNKIGMNCDY	YMEEKVLPPS	SLEGKVKETV	HNAFWDHLKE	QLSATPPDFS	CALELLKEIK
90	100	110	120	130	140	150	160
EILLSLLLPR	QNRLRIEIEE	ALDMDLLKQE	AEHGALKVLY	LSKYVLNMMA	LLCAPVRDEA	VQKLENITDP	VWLLRGIFQV
170	180	190	200	210	220	230	240
LGRMKMDMVN	YTIQSLQPHL	QEHSIQYERA	KFQELLNKQP	SLLNHTTKWL	TQAAGDLTMS	PPTCPDTSDS	SSVAGPSPNE
250	260	270	280	290	300	310	320
AANNPEPLSP	TMVLCQGFLN	LLLWDLENEE	FPETLLMDRT	RLQELKSQLH	QLTVMASVLL	VASSFSGSVL	FGSPQFVDKL
330	340	350	360	370	380	390	400
KRITKSLLED	FHSRPEEAIL	TVSEQVSQEI	HQSLKNMGLV	ALSSDNTASL	MGQLQNIAKK	ENCVCSVIDQ	RIHLFLKCCL
410	420	430	440	450	460	470	
VLGVQRSLLD	LPGGLTLIEA	ELAELGQKFV	NLTHHNQQVF	GPYYTEILKT	LISPAQALET	KVESV	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
770	1	573.6008	-45.89	3	39.0	14.0	1	2-19	M.TRGGGGGGLTETVNEVSK.L	

Detailed Protein Report

Protein 844: PREDICTED: peptidase M20 domain-containing protein 2 isoform X3 [Homo sapiens]

Accession:	gi|578812421	**Score:**	14.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	27.6
Database Date:	2015-11-30	**pI:**	5.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	6.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MRPGGERPVE	GGACNGRSEL	ELLKLRSAEC	IDEAAERLGA	LSRAIWSQPE	LAYEEHHAHR	VLTHFFEREP	PAASWAVQPH
90	100	110	120	130	140	150	160
YQLPTAFRAE	WEPPEARAPS	ATPRPLHLGF	LCEYDALPGI	GHACGHNLIA	EVGAAAALGV	RGALEGLPRP	PPPVKVVVLG
170	180	190	200	210	220	230	240
TPAEEDGGGK	IDLIEAGAFT	NLDVVFMAHP	SQENAAYLPD	MAEHDVTVKY	YGKASHSASY	PWEGLNALDA	AVLAYNNLSV
250	260						
FRQQMKPTWR	VHGGN						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2068	1	900.3125	-122.80	2	56.0	14.0	0	1-17	-.MRPGGERPVEGGACNGR.S	Carbamidomethyl: 14

Detailed Protein Report

Protein 845: protein limb expression 1 homolog [Homo sapiens]

Accession:	gi|167466286	**Score:**	14.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	31.9
Database Date:	2015-11-30	**pI:**	5.3
		Sequence Coverage [%]:	5.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDRTLESLRH	IIAQVLPHRD	PALVFKDLNV	VSMLQEFWES	KQQQKAAFPS	EGVVVYESLP	APGPPFVSYV	TLPGGSCFGN
90	100	110	120	130	140	150	160
FQCCLSRAEA	RRDAAKVALI	NSLFNELPSR	RITKEFIMES	VQEAVASTSG	TLDDADDPST	SVGAYHYMLE	SNMGKTMLEF
170	180	190	200	210	220	230	240
QELMTIFQLL	HWNGSLKALR	ETKCSRQEVI	SYYSQYSLDE	KMRSHMALDW	IMKERDSPGI	VSQELRMALR	QLEEARKAGQ
250	260	270	280	290			
ELRFYKEKKE	ILSLALTQIC	SDPDTSSPSD	DQLSLTALCG	YH			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2110	1	902.3468	-108.11	2	56.5	14.0	2	202-215	K.MRSHMALDWIMKER.D	

Detailed Protein Report

Protein 846: histone H1x [Homo sapiens]

Accession:	gi|5174449	**Score:**	13.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	22.5
Database Date:	2015-11-30	**pI:**	11.2
Modification(s):	Oxidation	**Sequence Coverage [%]:**	10.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSVELEEALP	VTTAEGMAKK	VTKAGGSAAL	SPSKKRKNSK	KKNQPGKYSQ	LVVETIRRLG	ERNGSSLAKI	YTEAKKVPWF
90	100	110	120	130	140	150	160
DQQNGRTYLK	YSIKALVQND	TLLQVKGTGA	NGSFKLNRKK	LEGGGERRGA	PAAATAPAPT	AHKAKKAAPG	AAGSRRADKK
170	180	190	200	210	220		
PARGQKPEQR	SHKKGAGAKK	DKGGKAKKTA	AAGGKKVKKA	AKPSVPKVPK	GRK		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
70	1	826.6853	-97.38	3	30.3	13.9	2	1-23	-.MSVELEEALPVTTAEGMAKKVTK.A	Oxidation: 1

Detailed Protein Report

Protein 847: putative phospholipase B-like 2 isoform 1 precursor [Homo sapiens]

Accession:	gi|229093316	**Score:**	13.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	65.4
Database Date:	2015-11-30	**pI:**	6.4
		Sequence Coverage [%]:	4.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MVGQMYCYPG	SHLARALTRA	LALALVLALL	VGPFLSGLAG	AIPAPGGRWA	RDGQVPPASR	SRSVLLDVSA	GQLLMVDGRH
90	100	110	120	130	140	150	160
PDAVAWANLT	NAIRETGWAF	LELGTSGQYN	DSLQAYAAGV	VEAAVSEELI	YMHWMNTVVN	YCGPFEYEVG	YCERLKSFLE
170	180	190	200	210	220	230	240
ANLEWMQEEM	ESNPDSPYWH	QVRLTLLQLK	GLEDSYEGRV	SFPAGKFTIK	PLGFLLLQLS	GDLEDLELAL	NKTKIKPSLG
250	260	270	280	290	300	310	320
SGSCSALIKL	LPGQSDLLVA	HNTWNNYQHM	LRVIKKYWLQ	FREGPWGDYP	LVPGNKLVFS	SYPGTIFSCD	DFYILGSGLV
330	340	350	360	370	380	390	400
TLETTIGNKN	PALWKYVRPR	GCVLEWVRNI	VANRLASDGA	TWADIFKRFN	SGTYNNQWMI	VDYKAFIPGG	PSPGSRVLTI
410	420	430	440	450	460	470	480
LEQIPGMVVV	ADKTSELYQK	TYWASYNIPS	FETVFNASGL	QALVAQYGDW	FSYDGSPRAQ	IFRRNQSLVQ	DMDSMVRLMR
490	500	510	520	530	540	550	560
YNDFLHDPLS	LCKACNPQPN	GENAISARSD	LNPANGSYPF	QALRQRSHGG	IDVKVTSMSL	ARILSLLAAS	GPTWDQVPPF
570	580	590					
QWSTSPFSGL	LHMGQPDLWK	FAPVKVSWD					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1000	1	983.6289	82.86	3	42.1	13.9	1	385-413	K.AFIPGGPSPGSRVLTILEQIPGMVVVADK.T	

Detailed Protein Report

Protein 848: F-box only protein 31 isoform 1 [Homo sapiens]

Accession:	gi|83035136	**Score:**	13.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	60.6
Database Date:	2015-11-30	**pI:**	6.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAVCARLCGV	GPSRGCRRRQ	QRRGPAETAA	ADSEPDTDPE	EERIEASAGV	GGGLCAGPSP	PPPRCSLLEL	PPELLVEIFA
90	100	110	120	130	140	150	160
SLPGTDLPSL	AQVCTKFRRI	LHTDTIWRRR	CREEYGVCEN	LRKLEITGVS	CRDVYAKLLH	RYRHILGLWQ	PDIGPYGGLL
170	180	190	200	210	220	230	240
NVVVDGLFII	GWMYLPPHDP	HVDDPMRFKP	LFRIHLMERK	AATVECMYGH	KGPHHGHIQI	VKKDEFSTKC	NQTDHHRMSG
250	260	270	280	290	300	310	320
GRQEEFRTWL	REEWGRTLED	IFHEHMQELI	LMKFIYTSQY	DNCLTYRRIY	LPPSRPDDLI	KPGLFKGTYG	SHGLEIVMLS
330	340	350	360	370	380	390	400
FHGRRARGTK	ITGDPNIPAG	QQTVEIDLRH	RIQLPDLENQ	RNFNELSRIV	LEVRERVRQE	QQEGGHEAGE	GRGRQGPRES
410	420	430	440	450	460	470	480
QPSPAQPRAE	APSKGPDGTP	GEDGGEPGDA	VAAAEQPAQC	GQGQPFVLPV	GVSSRNEDYP	RTCRMCFYGT	GLIAGHGFTS
490	500	510	520	530	540		
PERTPGVFIL	FDEDRFGFVW	LELKSFSLYS	RVQATFRNAD	APSPQAFDEM	LKNIQSLTS		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2106	1	925.3145	-137.61	2	56.2	13.9	2	1-17	-.MAVCARLCGVGPSRGCR.R	Carbamidomethyl: 4, 8

Detailed Protein Report

Protein 849: collagen alpha-1(IV) chain preproprotein [Homo sapiens]

Accession:	gi|148536825	**Score:**	13.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	160.5
Database Date:	2015-11-30	**pI:**	9.4
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.3
		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
62	1	713.3305	-7.33	3	30.5	13.9	1	927-947	K.GDVGLPGKPGSMDKVDMGSMK.G	Oxidation: 12, 17

Detailed Protein Report

Protein 850: **leucine-rich repeat-containing protein 23 isoform b [Homo sapiens]**

Accession:	gi|5901898	**Score:**	13.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	36.1
Database Date:	2015-11-30	**pI:**	4.9
Modification(s):	Oxidation	**Sequence Coverage [%]:**	6.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSDEDDLEDS	EPDQDDSEKE	EDEKETEEGE	DYRKEGEEFP	EEWLPTPLTE	DMMKEGLSLL	CKTGNGLAHA	YVKLEVKERD
90	100	110	120	130	140	150	160
LTDIYLLRSY	IHLRYVDISE	NHLTDLSPLN	YLTHLLWLKA	DGNRLRSAQM	NELPYLQIAS	FAYNQITDTE	GISHPRLETL
170	180	190	200	210	220	230	240
NLKGNSIHMV	TGLDPEKLIS	LHTVELRGNQ	LESTLGINLP	KLKNLYLAQN	MLKKVEGLED	LSNLTTLHLR	DNQIDTLSGF
250	260	270	280	290	300	310	320
SREMKSLQYL	NLRRSKTLAF	RPDQTPRGSH	HMYDREQRMP	VFAPKLEIHH	NLRPRICSVP	VLWAVWGAEW	GA

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1720	1	1107.9876	76.40	2	51.4	13.9	0	1-19	-.MSDEDDLEDSEPDQDDSEK.E	Oxidation: 1

Detailed Protein Report

Protein 851: dynein assembly factor 3, axonemal isoform 2 [Homo sapiens]

Accession:	gi|73476319	**Score:**	13.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	64.4
Database Date:	2015-11-30	**pI:**	6.0
		Sequence Coverage [%]:	3.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLPLLDSSKR	AGTLGSGCGV	PRVHSAALSR	EEGASRDIWR	IKVWARVMTT	PAGSGSGFGS	VSWWGLSPAL	DLQAESPPVD
90	100	110	120	130	140	150	160
PDSQADTVHS	NPELDVLLLG	SVDGRHLLRT	LSRAKFWPRR	RFNFFVLENN	LEAVARHMLI	FSLALEEPEK	MGLQERSETF
170	180	190	200	210	220	230	240
LEVWGNALLR	PPVAAFVRAQ	ADLLAHLVPE	PDRLEEQLPW	LSLRALKFRE	RDALEAVFRF	WAGGEKGPQA	FPMSRLWDSR
250	260	270	280	290	300	310	320
LRHYLGSRYD	ARRGVSDWDL	RMKLHDRGAQ	VIHPQEFRRW	RDTGVAFELR	DSSAYHVPNR	TLASGRLLSY	RGERVAARGY
330	340	350	360	370	380	390	400
WGDIATGPFV	AFGIEADDES	LLRTSNGQPV	KTAGEITQHN	VTELLRDVAA	WGRARATGGD	LEEQQHAEGS	PEPGTPAAPT
410	420	430	440	450	460	470	480
PESFTVHFLP	LNSAQTLHHK	SCYNGRFQLL	YVACGMVHLL	IPELGACVAP	GGNLIVELAR	YLVDVRQEQL	QGFNTRVREL
490	500	510	520	530	540	550	560
AQAAGFAPQT	GARPSETFAR	FCKSQESALG	NTVPAVEPGT	PPLDILAQPL	EASNPALEGL	TQPLQGGTPH	CEPCQLPSES
570	580	590					
PGSLSEVLAQ	PQGALAPPNC	ESDSKTGV					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
436	1	738.9740	-117.81	3	35.1	13.9	2	1-22	-.MLPLLDSSKRAGTLGSGCGVPR.V	

Protein 852: sterile alpha motif domain-containing protein 9 [Homo sapiens]

Accession:	gi|38201706	**Score:**	13.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	184.2
Database Date:	2015-11-30	**pI:**	8.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.0
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|300863105	refseq_human (refseq_human_20140103.fasta)	sterile alpha motif domain-containing protein 9 [Homo sapiens]

10	20	30	40	50	60	70	80
MAKQLNLPEN	TDDWTKEDVN	QWLESHKIDQ	KHREILTEQD	VNGAVLKWLK	KEHLVDMGIT	HGPAIQIEEL	FKELRKTAIE
90	100	110	120	130	140	150	160
DSIQTSKMGK	PSKNAPKDQT	VSQKERRETS	KQKQKGKENP	DMANPSAMST	TAKGSKSLKV	ELIEDKIDYT	KERQPSIDLT
170	180	190	200	210	220	230	240
CVSYPFDEFS	NPYRYKLDFS	LQPETGPGNL	IDPIHEFKAF	TNTATATEED	VKMKFSNEVF	RFASACMNSR	TNGTIHFGVK
250	260	270	280	290	300	310	320
DKPHGKIVGI	KVTNDTKEAL	INHFNLMINK	YFEDHQVQQA	KKCIREPRFV	EVLLPNSTLS	DRFVIEVDII	PQFSECQYDY
330	340	350	360	370	380	390	400
FQIKMQNYNN	KIWEQSKKFS	LFVRDGTSSK	DITKNKVDFR	AFKADFKTLA	ESRKAAEEKF	RAKTNKKERE	GPKLVKLLTG
410	420	430	440	450	460	470	480
NQDLLDNSYY	EQYILVTNKC	HPDQTKHLDF	LKEIKWFAVL	EFDPESNING	VVKAYKESRV	ANLHFPSVYV	EQKTTPNETI
490	500	510	520	530	540	550	560
STLNLYHQPS	WIFCNGRLDL	DSEKYKPFDP	SSWQRERASD	VRKLISFLTH	EDIMPRGKFL	VVFLLLSSVD	DPRDPLIETF
570	580	590	600	610	620	630	640
CAFYQDLKGM	ENILCICVHP	HIFQGWKDLL	EARLIKHQDE	ISSQCISALS	LEEINGTILK	LKSVTQSSKR	LLPSIGLSTV
650	660	670	680	690	700	710	720
LLKKEEDIMT	ALEIICENEC	EGTLLEKDKN	KFLEFKASKE	EDFYRGGKVS	WWNFYFSSES	YSSPFVKRDK	YERLEAMIQN
730	740	750	760	770	780	790	800
CADSSKPTST	KIIHLYHHPG	CGGTTLAMHI	LWELRKKFRC	AVLKNKTVDF	SEIGEQVTSL	ITYGAMNRQE	YVPVLLLVDD
810	820	830	840	850	860	870	880
FEEQDNVYLL	QYSIQTAIAK	KYIRYEKPLV	IILNCMRSQN	PEKSARIPDS	IAVIQQLSPK	EQRAFELKLK	EIKEQHKNFE
890	900	910	920	930	940	950	960
DFYSFMIMKT	NFNKEYIENV	VRNILKGQNI	FTKEAKLFSF	LALLNSYVPD	TTISLSQCEK	FLGIGNKKAF	WGTEKFEDKM
970	980	990	1000	1010	1020	1030	1040
GTYSTILIKT	EVIECGNYCG	VRIIHSLIAE	FSLEELKKSY	HLNKSQIMLD	MLTENLFFDT	GMGKSKFLQD	MHTLLLTRHR
1050	1060	1070	1080	1090	1100	1110	1120
DEHEGETGNW	FSPFIEALHK	DEGNEAVEAV	LLESIHRFNP	NAFICQALAR	HFYIKKKDFG	NALNWAKQAK	IIEPDNSYIS
1130	1140	1150	1160	1170	1180	1190	1200
DTLGQVYKSK	IRWWIEENGG	NGNISVDDLI	ALLDLAEHAS	SAFKESQQQS	EDREYEVKER	LYPKSKRRYD	TYNIAGYQGE
1210	1220	1230	1240	1250	1260	1270	1280
IEVGLYTIQI	LQLIPFFDNK	NELSKRYMVN	FVSGSSDIPG	DPNNEYKLAL	KNYIPYLTKL	KFSLKKSFDF	FDEYFVLLKP
1290	1300	1310	1320	1330	1340	1350	1360
RNNIKQNEEA	KTRRKVAGYF	KKYVDIFCLL	EESQNNTGLG	SKFSEPLQVE	RCRRNLVALK	ADKFSGLLEY	LIKSQEDAIS
1370	1380	1390	1400	1410	1420	1430	1440
TMKCIVNEYT	FLLEQCTVKI	QSKEKLNFIL	ANIILSCIQP	TSRLVKPVEK	LKDQLREVLQ	PIGLTYQFSE	PYFLASLLFW
1450	1460	1470	1480	1490	1500	1510	1520
PENQQLDQHS	EQMKEYAQAL	KNSFKGQYKH	MHRTKQPIAY	FFLGKGKRLE	RLVHKGKIDQ	CFKKTPDINS	LWQSGDVWKE
1530	1540	1550	1560	1570	1580	1590	
EKVQELLLRL	QGRAENNCLY	IEYGINEKIT	IPITPAFLGQ	LRSGRSIEKV	SFYLGFSIGG	PLAYDIEIV	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2028	2	840.7762	-104.20	2	55.5	13.9	0	118-133	K.ENPDMANPSAMSTTAK.G	Oxidation: 5

Detailed Protein Report

Protein 853: PREDICTED: SH2 domain-containing protein 3A isoform X9 [Homo sapiens]

Accession:	gi|530425071	**Score:**	13.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	44.1
Database Date:	2015-11-30	**pI:**	9.2
Modification(s):	Oxidation	**Sequence Coverage [%]:**	4.8
		No. of unique Peptides:	1

Quantitation

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

10	20	30	40	50	60	70	80
MQVPQDGEDL	AGQPWYHGLL	SRQKAEALLQ	QNGDFLVRAS	GSRGGNPVIS	CRWRGSALHF	EVFRVALRPR	PGRPTALFQL
90	100	110	120	130	140	150	160
EDEQFPSIPA	LVHSYMTGRR	PLSQATGAVV	SRPVTWQGPL	RRSFSEDTLM	DGPARIEPLR	ARKWSNSQPA	DLAHMGRSRE
170	180	190	200	210	220	230	240
DPAGMEASTM	PISALPRTSS	DPVLLKAPAP	LGTVADSLRA	SDGQLQAKAP	TKPPRTPSFE	LPDASERPPT	YCELVPRVPS
250	260	270	280	290	300	310	320
VQGTSPSQSC	PEPEAPWWEA	EEDEEEENRC	FTRPQAEISF	CPHDAPSCLL	GPQNRPLEPQ	VLHTLRGLFL	EHHPGSTALH
330	340	350	360	370	380	390	400
LLLVDCQATG	LLGVTRDQRG	NMGVSSGLEL	LTLPHGHHLR	LELLERPLPS	TSAGIRHWRW	PGRWRCWAAR	GRWRSAQPH

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
31	1	735.9836	-70.52	3	29.7	13.9	2	122-140	R.RSFSEDTLMDGPARIEPLR.A	Oxidation: 9	MD:MU 0.55

Detailed Protein Report

Protein 854: protocadherin beta-1 precursor [Homo sapiens]

Accession: gi|14195607
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 13.8
MW [kDa]: 90.4
pI: 5.1
Sequence Coverage [%]: 2.4
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MAGTRRKSLQ	NRQVGSLLIF	LCISVGDATT	IRYSVAEEME	SGSFVANVAK	DLGLEVGKLA	ARGARLVSEG	NKMHFRLHRK
90	100	110	120	130	140	150	160
TGDLFVKEKL	DRESLCGKAD	PCVLHFEVVL	VEPLQSFRAE	VRVFDINDNA	PVFLNKEPLL	KIPESTPLGS	RFPLQSAQDL
170	180	190	200	210	220	230	240
DVGLNGLQNY	TLSANGYFHL	HTRFCSHGPK	YAELVLNKPL	DREEQPEVNL	TITAVDGGSP	PKSGTAHIHV	VVLDVNDHVP
250	260	270	280	290	300	310	320
QFSRLVYRAQ	VSENSPNGSL	VATVTAVDLD	EGTNKAITYS	LAQNPEAILK	TFQIDPQNGE	VRLRGPLDFE	AIETYDIDIQ
330	340	350	360	370	380	390	400
ATDGGGLSAH	SKVLVEVVDV	NDNPPEVMVS	SVSSPLPEDS	PPQTVVALFT	IRDRDIRVGG	KVTCFLREDL	PFVIKPTFGN
410	420	430	440	450	460	470	480
SYSLVTDRSL	DREEVSGYNI	TIVAMDTGPP	SLSAETMIEV	LISDVNDNPP	IFREDSYILT	VRENNSPAVF	IGKVHAEDLD
490	500	510	520	530	540	550	560
LGENAQITYS	LLPPKNGDLS	VFAYISINSG	NGKLYALRTM	DYEAIQDFQF	VVKATDGGFL	SLSSQVTVRV	VVLDDNDNRP
570	580	590	600	610	620	630	640
MILYPLQNGT	LPCNDLVPRS	AEAGYLVTKV	VAVDGDSGQN	SWLSYHLLKA	TDLGLFSVQR	QNGEIHTLRQ	ISERDPMMQK
650	660	670	680	690	700	710	720
LIILVQDHGQ	PALSTTVSLN	ILLVDGFSEP	YLQFQDPTKH	SRKVNPSTKY	LVISLVILSF	LFLLSVIVIF	IIHVYQKIKY
730	740	750	760	770	780	790	800
REKFTIQEHF	YDDCNFSNNL	VQGQGNGSLS	RPCPYEMCSA	TGTGNSEFRF	LKRFMPNFPF	PHATGEIKME	AGSSLPPNSD
810	820						
RNKSQRLEGH	DQVSDDYM						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
283	1	815.0883	28.08	3	33.2	13.8	2	621-640	R.QNGEIHTLRQISERDPMMQK.L	Oxidation: 17, 18

Detailed Protein Report

Protein 855: **PREDICTED: lysine-specific demethylase 6A isoform X7 [Homo sapiens]**

Accession:	gi|530421565	**Score:**	13.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	145.1
Database Date:	2015-11-30	**pI:**	7.4
		Sequence Coverage [%]:	0.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MKSCGVSLAT	AAAAAAAFGD	EEKKMAAGKA	SGESEEASPS	LTAEEREALG	GLDSRLFGFV	RFHEDGARTK	ALLGKAVRCY
90	100	110	120	130	140	150	160
ESLILKAEGK	VESDFFCQLG	HFNLLLEDYP	KALSAYQRYY	SLQSDYWKNA	AFLYGLGLVY	FHYNAFQWAI	KAFQEVLYVD
170	180	190	200	210	220	230	240
PSFCRAKEIH	LRLGLMFKVN	TDYESSLKHF	QLALVDCNPC	TLSNAEIQFH	IAHLYETQRK	YHSAKEAYEQ	LLQTENLSAQ
250	260	270	280	290	300	310	320
VKATVLQQLG	WMHHTVDLLG	DKATKESYAI	QYLQKSLEAD	PNSGQSWYFL	GRCYSSIGKV	QDAFISYRQS	IDKSEASADT
330	340	350	360	370	380	390	400
WCSIGVLYQQ	QNQPMDALQA	YICAVQLDHG	HAAAWMDLGT	LYESCNQPQD	AIKCYLNATR	SKSCSNTSAL	AARIKYLQNT
410	420	430	440	450	460	470	480
SDNWSGGHAV	SHPPVQQQAH	SWCLTPQKLQ	MRPTGVAQVR	STGIPNGPTA	DSSLPTNSVS	GQQPQLALTR	VPSVSQPGVR
490	500	510	520	530	540	550	560
PACPGQPLAN	GPFSAGHVPC	STSRTLGSTD	TILIGNNHIT	GSGSNGNVPY	LQRNALTLPH	NRTNLTSSAE	EPWKNQLSNS
570	580	590	600	610	620	630	640
TQGLHKGQSS	HSAGPNGERP	LSSTGPSQHL	QAAGSGIQNQ	NGHPTLPSNS	VTQGAALNHL	SSHTATSGGQ	QGITLTKESK
650	660	670	680	690	700	710	720
PSGNILTVPE	TSRHTGETPN	STASVEGLPN	HVHQMTADAV	CSPSHGDSKS	PGLLSSDNPQ	LSALLMGKAN	NNVGTGTCDK
730	740	750	760	770	780	790	800
VNNIHPAVHT	KTDNSVASSP	SSAISTATPS	PKSTEQTTTN	SVTSLNSPHS	GLHTINGEGM	EESQSPMKTD	LLLVNHKPSP
810	820	830	840	850	860	870	880
QIIPSMSVSI	YPSSAEVLKA	CRNLGKNGLS	NSSILLDKCP	PPRPPSSPYP	PLPKDKLNPP	TPSIYLENKR	DAFFPPLHQF
890	900	910	920	930	940	950	960
CTNPNNPVTV	IRGLAGALKL	DLGLFSTKTL	VEANNEHMVE	VRTQLLQPAD	ENWDPTGTKK	IWHCESNRSH	TTIAKYAQYQ
970	980	990	1000	1010	1020	1030	1040
ASSFQESLRE	ENEKRSHHKD	HSDSESTSSD	NSGRRRKGPF	KTIKFGTNID	LSDDKKWKLQ	LHELTKLPAF	VRVVSAGNLL
1050	1060	1070	1080	1090	1100	1110	1120
SHVGHTILGM	NTVQLYMKVP	GSRTPGHQEN	NNFCSVNINI	GPGDCEWFVV	PEGYWGVLND	FCEKNNLNFL	MGSWWPNLED
1130	1140	1150	1160	1170	1180	1190	1200
LYEANVPVYR	FIQRPGDLVW	INAGTVHWVQ	AIGWCNNIAW	NVGPLTACQY	KLAVERYEWN	KLQSVKSIVP	MVHLSWNMAR
1210	1220	1230	1240	1250	1260	1270	1280
NIKVSDPKLF	EMIKYCLLRT	LKQCQTLREA	LIAAGKEIIW	HGRTKEEPAH	YCSICEVEVF	DLLFVTNESN	SRKTYIVHCQ
1290	1300	1310	1320	1330			
DCARKTSGNL	ENFVVLEQYK	MEDLMQVYDQ	FTLAPPLPSA	SS			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
642	1	917.2547	-233.20	1	37.4	13.8	0	47-55	R.EALGGLDSR.L	

Detailed Protein Report

Protein 856: PREDICTED: xaa-Pro aminopeptidase 1 isoform X4 [Homo sapiens]

Accession:	gi|578819756	**Score:**	13.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	62.1
Database Date:	2015-11-30	**pI:**	5.4
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	4.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MWTDGRYFLQ	AAKQMDSNWT	LMKMGLKDTP	TQEDWLVSVL	PEGSRVGVDP	LIIPTDYWKK	MAKVLRSAGH	HLIPVKENLV
90	100	110	120	130	140	150	160
DKIWTDRPER	PCKPLLTLGL	DYTGISWKDK	VADLRLKMAE	RNVMWFVVTA	LDEIAWLFNL	RGSDVEHNPV	FFSYAIIGLE
170	180	190	200	210	220	230	240
TIMLFIDGDR	IDAPSVKEHL	LLDLGLEAEY	RIQVHPYKSI	LSELKALCAD	LSPREKVWVS	DKASYAVSET	IPKDHRCCMP
250	260	270	280	290	300	310	320
YTPICIAKAV	KNSAESEGMR	RAHIKDAVAL	CELFNWLEKE	VPKGGVTEIS	AADKAEEFRR	QQADFVDLSF	PTISSTGPNG
330	340	350	360	370	380	390	400
AIIHYAPVPE	TNRTLSLDEV	YLIDSGAQYK	DGTTDVTRTM	HFGTPTAYEK	ECFTYVLKGH	IAVSAAVFPT	GTKGHLLDSF
410	420	430	440	450	460	470	480
ARSALWDSGL	DYLHGTGHGV	GSFLNVHEGP	CGISYKTFSD	EPLEAGMIVT	DEPGYYEDGA	FGIRIENVVL	VVPVKTKYNF
490	500	510	520	530	540	550	560
NNRGSLTFEP	LTLVPIQTKM	IDVDSLTDKE	CDWLNNYHLT	CRDVIGKELQ	KQGRQEALEW	LIRETQPISK	QH

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
172	1	897.7312	-10.27	3	31.5	13.8	2	237-260	R.CCMPYTPICIAKAVKNSAESEGMR.R	Carbamidomethyl: 9; Oxidation: 3, 23

Detailed Protein Report

Protein 857: **PREDICTED: mitogen-activated protein kinase kinase kinase 8 isoform X4 [Homo sapiens]**

Accession:	gi|578818254	**Score:**	13.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	44.9
Database Date:	2015-11-30	**pI:**	6.3
		Sequence Coverage [%]:	3.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEYMSTGSDN	KEEIDLLIKH	LNVSDVIDIM	ENLYASEEPA	VYEPSLMTMC	QDSNQNDERS	KSLLLSGQEV	PWLSSVRYGT
90	100	110	120	130	140	150	160
VEDLLAFANH	ISNTAKHFYG	QRPQESGILL	NMVITPQNGR	YQIDSDVLLI	PWKLTYRNIG	SDFIPRGAFG	KVYLAQDIKT
170	180	190	200	210	220	230	240
KKRMACKLIP	VDQFKPSDVE	IQACFRHENI	AELYGAVLWG	ETVHLFMEAG	EGGSVLEKLE	SCGPMREFEI	IWVTKHVLKG
250	260	270	280	290	300	310	320
LDFLHSKKVI	HHDIKPSNIV	FMSTKAVLVD	FGLSVQMTED	VYFPKDLRGT	EIYMSPEVIL	CRGHSTKADI	YSLGATLIHM
330	340	350	360	370	380	390	400
QTGTPPWVKR	YPRSAYPSYL	YIILRAQEAP	RNLRCSRGNA	LSTSTSALWL	ATSILFGDHQ	RLNMAEGCHV	CSKLRQH

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
949	1	646.1628	-186.29	2	41.4	13.8	0	382-393	R.LNMAEGCHVCSK.L	

Detailed Protein Report

Protein 858: cohesin subunit SA-3 isoform 3 [Homo sapiens]

Accession:	gi|544186091	**Score:**	13.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	132.2
Database Date:	2015-11-30	**pI:**	5.2
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSSPLQRAVG	DTKRALSASS	SSSASLPFDD	RDSNHTSEGN	GDSLLADEDT	DFEDSLNRNV	KKRAAKRPPK	TTPVAKHPKK
90	100	110	120	130	140	150	160
GSRVVHRHSR	KQSEPPANDL	FNAVKAAKSD	MQDSGDYPLI	APGPSWKKFQ	GSFCEFVRTL	VCQCQYSLLY	DGFPMDDLIS
170	180	190	200	210	220	230	240
LLTGLSDSQV	RAFRHTSTLA	AMKLMTSLVK	VALQLSVHQD	NNQRQYEAER	NKGPGQRAPE	RLESLLEKRK	ELQEHQEEIE
250	260	270	280	290	300	310	320
GMMNALFRGV	FVHRYRDVLP	EIRAICIEEI	GCWMQSYSTS	FLTDSYLKYI	GWTLHDKHRE	VRLKCVKALK	GLYGNRDLTT
330	340	350	360	370	380	390	400
RLELFTSRFK	DRMVSMVMDR	EYDVAVEAVR	LLILILKNME	GVLTDADCES	VYPVVYASHR	GLASAAGEFL	YWKLFYPECE
410	420	430	440	450	460	470	480
IRMMGGREQR	QSPGAQRTFF	QLLLSFFVES	ELHDHAAYLV	DSLWDCAGAR	LKDWEGLTSL	LLEKDQNLGD	VQESTLIEIL
490	500	510	520	530	540	550	560
VSSARQASEG	HPPVGRVTGR	KGLTSKERKT	QADDRVKLTE	HLIPLLPQLL	AKFSADAEKV	TPLLQLLSCF	DLHIYCTGRL
570	580	590	600	610	620	630	640
EKHLELFLQQ	LQEVVVKHAE	PAVLEAGAHA	LYLLCNPEFT	FFSRADFARS	QLVDLLTDRF	QQELEELLQS	SFLDEDEVYN
650	660	670	680	690	700	710	720
LAATLKRLSA	FYNTHDLTRW	ELYEPCCQLL	QKAVDTGEVP	HQVILPALTL	VYFSILWTLT	HISKSDASQK	QLSSLRDRMV
730	740	750	760	770	780	790	800
AFCELCQSCL	SDVDTEIQEQ	AFVLLSDLLL	IFSPQMIVGG	RDFLRPLVFF	PEATLQSELA	SFLMDHVFIQ	PGDLGSGDSQ
810	820	830	840	850	860	870	880
EDHLQIERLH	QRRRLLAGFC	KLLLYGVLEM	DAASDVFKHY	NKFYNDYGDI	IKETLTRARQ	IDRSHCSRIL	LLSLKQLYTE
890	900	910	920	930	940	950	960
LLQEHGPQGL	NELPAFIEMR	DLARRFALSF	GPQQLQNRDL	VVMLHKEGIQ	FSLSELPPAG	SSNQPPNLAF	LELLSEFSPR
970	980	990	1000	1010	1020	1030	1040
LFHQDKQLLL	SYLEKCLQHV	SQAPGHPWGP	VTTYCHSLSP	VENTAETSPQ	VLPSSKRRRV	EGPAKPNRED	VSSSQEESLQ
1050	1060	1070	1080	1090	1100	1110	1120
LNSIPPTPTL	TSTAVKSRQP	LWGLKEMEEE	DGSELDFAQG	QPVAGTERSR	FLGPQYFQTP	HNPSGPGLGN	QLMRLSLMEE
1130	1140	1150	1160	1170			
DEEEELEIQD	ESNEERQDTD	MQASSYSSTS	ERGLDLLDST	ELDIEDF			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1226	1	1061.4989	-75.63	2	45.0	13.8	2	172-190	R.AFRHTSTLAAMKLMTSLVK.V	Oxidation: 11

Detailed Protein Report

Protein 859: CD97 antigen isoform 2 preproprotein [Homo sapiens]

Accession: gi|17978489
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 13.8
MW [kDa]: 81.7
pI: 6.8
Sequence Coverage [%]: 2.0
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MGGRVFLAFC	VWLTLPGAET	QDSRGCARWC	PQNSSCVNAT	ACRCNPGFSS	FSEIITTPTE	TCDDINECAT	PSKVSCGKFS
90	100	110	120	130	140	150	160
DCWNTEGSYD	CVCSPGYEPV	SGAKTFKNES	ENTCQDVDEC	SSGQHQCDSS	TVCFNTVGSY	SCRCRPGWKP	RHGIPNNQKD
170	180	190	200	210	220	230	240
TVCEDMTFST	WTPPPGVHSQ	TLSRFFDKVQ	DLGRDSKTSS	AEVTIQNVIK	LVDELMEAPG	DVEALAPPVR	HLIATQLLSN
250	260	270	280	290	300	310	320
LEDIMRILAK	SLPKGPFTYI	SPSNTELTLM	IQERGDKNVT	MGQSSARMKL	NWAVAAGAED	PGPAVAGILS	IQNMTTLLAN
330	340	350	360	370	380	390	400
ASLNLHSKKQ	AELEEIYESS	IRGVQLRRLS	AVNSIFLSHN	NTKELNSPIL	FAFSHLESSD	GEAGRDPPAK	DVMPGPRQEL
410	420	430	440	450	460	470	480
LCAFWKSDSD	RGGHWATEGC	QVLGSKNGST	TCQCSHLSSF	AILMAHYDVE	DWKLTLITRV	GLALSLFCLL	LCILTFLLVR
490	500	510	520	530	540	550	560
PIQGSRTTIH	LHLCICLFVG	STIFLAGIEN	EGGQVGLRCR	LVAGLLHYCF	LAAFCWMSLE	GLELYFLVVR	VFQGQGLSTR
570	580	590	600	610	620	630	640
WLCLIGYGVP	LLIVGVSAAI	YSKGYGRPRY	CWLDFEQGFL	WSFLGPVTFI	ILCNAVIFVT	TVWKLTQKFS	EINPDMKKLK
650	660	670	680	690	700	710	720
KARALTITAI	AQLFLLGCTW	VFGLFIFDDR	SLVLTYVFTI	LNCLQGAFLY	LLHCLLNKKV	REEYRKWACL	VAGGSKYSEF
730	740	750					
TSTTSGTGHN	QTRALRASES	GI					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2771	1	848.8935	47.67	2	65.0	13.8	0	29-43	R.WCPQNSSCVNATACR.C	Carbamidomethyl: 2

Detailed Protein Report

Protein 860: growth factor receptor-bound protein 14 [Homo sapiens]

Accession:	gi|71979663	**Score:**	13.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	60.9
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
MTTSLQDGQS	AASRAAARDS	PLAAQVCGAA	QGRGDAHDLA	PAPWLHARAL	LPLPDGTRGC	AADRRKKKDL	DVPEMPSIPN
90	100	110	120	130	140	150	160
PFPELCCSPF	TSVLSADLFP	KANSRKKQVI	KVYSEDETSR	ALDVPSDITA	RDVCQLLILK	NHYIDDHSWT	LFEHLPHIGV
170	180	190	200	210	220	230	240
ERTIEDHELV	IEVLSNWGIE	EENKLYFRKN	YAKYEFFKNP	MYFFPEHMVS	FATETNGEIS	PTQILQMFLS	SSTYPEIHGF
250	260	270	280	290	300	310	320
LHAKEQGKKS	WKKIYFFLRR	SGLYFSTKGT	SKEPRHLQFF	SEFGNSDIYV	SLAGKKKHGA	PTNYGFCFKP	NKAGGPRDLK
330	340	350	360	370	380	390	400
MLCAEEEQSR	TCWVTAIRLL	KYGMQLYQNY	MHPYQGRSGC	SSQSISPMRS	ISENSLVAMD	FSGQKSRVIE	NPTEALSVAV
410	420	430	440	450	460	470	480
EEGLAWRKKG	CLRLGTHGSP	TASSQSSATN	MAIHRSQPWF	HHKISRDEAQ	RLIIQQGLVD	GVFLVRDSQS	NPKTFVLSMS
490	500	510	520	530	540	550	
HGQKIKHFQI	IPVEDDGEMF	HTLDDGHTRF	TDLIQLVEFY	QLNKGVLPCK	LKHYCARIAL		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2069	1	1052.3235	-272.07	1	56.0	13.8	0	49-58	R.ALLPLPDGTR.G	

Detailed Protein Report

Protein 861: PREDICTED: DDB1- and CUL4-associated factor 12 isoform X1 [Homo sapiens]

Accession:	gi|578816454	**Score:**	13.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	48.4
Database Date:	2015-11-30	**pI:**	9.7
		Sequence Coverage [%]:	3.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MQPMSFGWDH	SLHKRKRLPP	VKRSLVYYLK	NREVRLQNET	SYSRVLHGYA	AQQLPSLLKE	REFHLGTLNK	VFASQWLNHR
90	100	110	120	130	140	150	160
QVVCGTKCNT	LFVVDVQTSQ	ITKIPILKDR	EPGGVTQQGC	GIHAIELNPS	RTLLATGGDN	PNSLAIYRLP	TLDPVCVGDD
170	180	190	200	210	220	230	240
GHKDWIFSIA	WISDTMAVSG	SRDGSMGLWE	VTDDVLTKSD	ARHNVSRVPV	YAHITHKALK	DIPKEDTNPD	NCKVRALAFN
250	260	270	280	290	300	310	320
NKNKELGAVS	LDGYFHLWKA	ENTLSKLLST	KLPYCRENVC	LAYGSEWSVY	AVGSQAHVSF	LDPRQPSYNV	KSVCSRERGS
330	340	350	360	370	380	390	400
GIRSVSFYEH	IITVGTGQGS	LLFYDIRAQR	FLEERLSACY	GSKPRLAGEN	LKLTTGKGWL	NHDETWRNYF	SDIDFFPNAV
410	420	430	440				
YTHCYDSSGT	KLFVAGGPLP	SGLHGNYAGL	WS				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1429	1	783.3597	-32.33	2	47.6	13.7	0	149-163	R.LPTLDPVCVGDDGHK.D	

Detailed Protein Report

Protein 862: ATP-dependent RNA helicase DQX1 [Homo sapiens]

Accession:	gi|163914394	**Score:**	13.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	79.4
Database Date:	2015-11-30	**pI:**	4.8
		Sequence Coverage [%]:	2.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MTSQPLRLAE	EYGPSPGESE	LAVNPFDGLP	FSSRYYELLK	QRQALPIWAA	RFTFLEQLES	NPTGVVLVSG	EPGSGKSTQI
90	100	110	120	130	140	150	160
PQWCAEFALA	RGFQKGQVTV	TQPYPLAARS	LALRVADEMD	LTLGHEVGYS	IPQEDCTGPN	TLLRFCWDRL	LLQEVASTRG
170	180	190	200	210	220	230	240
TGAWGVLVLD	EAQERSVASD	SLQGLLQDAR	LEKLPGDLRV	VVVTDPALEP	KLRAFWGNPP	IVHIPREPGE	RPSPIYWDTI
250	260	270	280	290	300	310	320
PPDRVEAACQ	AVLELCRKEL	PGDVLVFLPS	EEEISLCCES	LSREVESLLL	QGLPPRVLPL	HPDCGRAVQA	VYEDMDARKV
330	340	350	360	370	380	390	400
VVTHWLADFS	FSLPSIQHVI	DSGLELRSVY	NPRIRAEFQV	LRPISKCQAE	ARRLRARGFP	PGSCLCLYPK	SFLELEAPPL
410	420	430	440	450	460	470	480
PQPRVCEENL	SSLVLLLKRR	QIAEPGECHF	LDQPAPEALM	QALEDLDYLA	ALDDDGDLSD	LGVILSEFPL	APELAKALLA
490	500	510	520	530	540	550	560
SCEFDCVDEM	LTLAAMLTAA	PGFTRPPLSA	EEAALRRALE	HTDGDHSSLI	QVYEAFIQSG	ADEAWCQARG	LNWAALCQAH
570	580	590	600	610	620	630	640
KLRGELLELM	QRIELPLSLP	AFGSEQNRRD	LQKALVSGYF	LKVARDTDGT	GNYLLLTHKH	VAQLSSYCCY	RSRRAPARPP
650	660	670	680	690	700	710	720
PWVLYHNFTI	SKDNCLSIVS	EIQPQMLVEL	APPYFLSNLP	PSESRDLLNQ	LREGMADSTA	GSKSSSAQEF	RDPCVLQ

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1652	1	626.6317	-57.06	3	50.4	13.7	2	374-390	R.LRARGFPPGSCLCLYPK.S	

Detailed Protein Report

Protein 863: inactive hydroxysteroid dehydrogenase-like protein 1 isoform b [Homo sapiens]

Accession:	gi|226371733	**Score:**	13.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	30.8
Database Date:	2015-11-30	**pI:**	10.0
		Sequence Coverage [%]:	5.1
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 0.70 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MAAVDSFYLL	YREIARSCNC	YMEALALVGA	WYTARKSITV	ICDFYSLIRL	HFIPRLGSRA	DLIKQYGRWA	VVSGATDGIG
90	100	110	120	130	140	150	160
KAYAEELASR	GLNIILISRN	EEKLQYFTQL	SEDKLWDIIN	VNIAAASLMV	HVVLPGMVER	KKGAIVTISS	GSCCKPTPQL
170	180	190	200	210	220	230	240
AAFSASKAYL	DHFSRALQYE	YASKGIFVQS	LIPFYVATSM	TAPSNFLHRC	SWLVPSPKVY	AHHAVSTLGI	SKRTTGYWSH
250	260	270	280				
SIQFLFAQYM	PEWLWVWGAN	ILNRSLRKEA	LSCTA				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1441	1	829.5817	155.48	2	47.8	13.7	1	36-49	R.KSITVICDFYSLIR.L		MD:MU 0.70

Detailed Protein Report

Protein 864: interphotoreceptor matrix proteoglycan 2 precursor [Homo sapiens]

Accession:	gi|57242793	**Score:**	13.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	138.5
Database Date:	2015-11-30	**pI:**	4.4
		Sequence Coverage [%]:	1.1
		No. of unique Peptides:	1

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
1944	1	766.2461	-123.88	2	54.4	13.7	1	1067-1080	K.CDIMPGHGAICRCR.V	

Detailed Protein Report

Protein 865: glucose-dependent insulinotropic receptor [Homo sapiens]

Accession:	gi|30425400	**Score:**	13.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	36.9
Database Date:	2015-11-30	**pI:**	10.1
Modification(s):	Oxidation	**Sequence Coverage [%]:**	6.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MESSFSFGVI	LAVLASLIIA	TNTLVAVAVL	LLIHKNDGVS	LCFTLNLAVA	DTLIGVAISG	LLTDQLSSPS	RPTQKTLCSL
90	100	110	120	130	140	150	160
RMAFVTSSAA	ASVLTVMLIT	FDRYLAIKQP	FRYLKIMSGF	VAGACIAGLW	LVSYLIGFLP	LGIPMFQQTA	YKGQCSFFAV
170	180	190	200	210	220	230	240
FHPHFVLTLS	CVGFFPAMLL	FVFFYCDMLK	IASMHSQQIR	KMEHAGAMAG	GYRSPRTPSD	FKALRTVSVL	IGSFALSWTP
250	260	270	280	290	300	310	320
FLITGIVQVA	CQECHLYLVL	ERYLWLLGVG	NSLLNPLIYA	YWQKEVRLQL	YHMALGVKKV	LTSFLLFLSA	RNCGPERPRE
330	340						
SSCHIVTISS	SEFDG						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1747	1	1273.4623	-117.75	2	51.6	13.7	2	191-213	K.IASMHSQQIRKMEHAGAMAGGYR.S	Oxidation: 12

Detailed Protein Report

Protein 866: **branched-chain-amino-acid aminotransferase, mitochondrial isoform b [Homo sapiens]**

Accession:	gi|258614015	**Score:**	13.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	33.8
Database Date:	2015-11-30	**pI:**	8.9
		Sequence Coverage [%]:	4.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAAAALGQLF	EGMKAFKGKD	QQVRLFRPWL	NMDRMLRSAM	RLCLPSFDKL	ELLECIRRLI	EVDKDWVPDA	AGTSLYVRPV
90	100	110	120	130	140	150	160
LIGNEPSLGV	SQPTRALLFV	ILCPVGAYFP	GGSVTPVSLL	ADPAFIRAWV	GGVGNYKLGG	NYGPTVLVQQ	EALKRGCEQV
170	180	190	200	210	220	230	240
LWLYGPDHQL	TEVGTMNIFV	YWTHEDGVLE	LVTPPLNGVI	LPGVVRQSLL	DMAQTWGEFR	VVERTITMKQ	LLRALEEGRV
250	260	270	280	290	300	310	
REVFGSGTAC	QVCPVHRILY	KDRNLHIPTM	ENGPELILRF	QKELKEIQYG	IRAHEWMFPV		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2104	1	841.3395	-76.37	2	56.5	13.7	0	207-220	R.QSLLDMAQTWGEFR.V	

Detailed Protein Report

Protein 867: ret finger protein-like 3 isoform 2 [Homo sapiens]

Accession: gi|5730013
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 13.7
MW [kDa]: 32.1
pI: 6.7
Sequence Coverage [%]: 6.3
No. of unique Peptides: 1

```
        10         20         30         40         50         60         70         80
MAALFQEASS CPVCSDYLEK PMSLECGCTV CLKCINSLQK EPHGEDLLCC CCSMVSQRNK IRPNRQLERL VSHIKELEPK
        90        100        110        120        130        140        150        160
LKKILQMNPR MRKFQVDMTL DADTANNFLL ISDDLRSVRS GLITQNRQDL AERFDVSVCI LGSPRFTCGR HYWEVDVGTS
       170        180        190        200        210        220        230        240
TEWDLGVCRE SVHCKGKIQL TTELGFWTVS LRDGSRLSAS TVPLTFLLVD RKLQRVGIFL DMGMQNVSFF DAESGSHVYT
       250        260        270        280        290
FRSVSAEEPL RPFLAPSIPP NGDQGVLSIC PLMNSGTTDA PVRPGEAK
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2145	2	1013.3708	-30.21	2	56.7	13.7	0	41-58	K.EPHGEDLLCCCCSMVSQR.N	Oxidation: 14

Detailed Protein Report

Protein 868: PREDICTED: tyrosine-protein phosphatase non-receptor type 23 isoform X3 [Homo sapiens]

Accession:	gi|530372237	**Score:**	13.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	164.5
Database Date:	2015-11-30	**pI:**	6.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	0.5
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 16.67 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MLGAMDKRVS	EEGMKVSCTH	FQCAAGAFAY	LREHFPQAYS	VDMSRQILTL	NVNLMLGQAQ	ECLLEKSMLD	NRKSFLVARI
90	100	110	120	130	140	150	160
SAQVVDYYKE	ACRALENPDT	ASLLGRIQKD	WKKLVQMKIY	YFAAVAHLHM	GKQAEEQQKF	GERVAYFQSA	LDKLNEAIKL
170	180	190	200	210	220	230	240
AKGQPDTVQD	ALRFTMDVIG	GKYNSAKKDN	DFIYHEAVPA	LDTLQPVKGA	PLVKPLPVNP	TDPAVTGPDI	FAKLVPMAAH
250	260	270	280	290	300	310	320
EASSLYSEEK	AKLLREMMAK	IEDKNEVLDQ	FMDSMQLDPE	TVDNLDAYSH	IPPQLMEKCA	ALSVRPDTVR	NLVQSMQVLS
330	340	350	360	370	380	390	400
GVFTDVEASL	KDIRDLLEED	ELLEQKFQEA	VGQAGAISIT	SKAELAEVRR	EWAKYMEVHE	KASFTNSELH	RAMNLHVGNL
410	420	430	440	450	460	470	480
RLLSGPLDQV	RAALPTPALS	PEDKAVLQNL	KRILAKVQEM	RDQRVSLEQQ	LRELIQKDDI	TASLVTTDHS	EMKKLFEEQL
490	500	510	520	530	540	550	560
KKYDQLKVYL	EQNLAAQDRV	LCALTEANVQ	YAAVRRVLSD	LDQKWNSTLQ	TLVASYEAYE	DLMKKSQEGR	DFYADLESKV
570	580	590	600	610	620	630	640
AALLERTQST	CQAREAARQQ	LLDRELKKKP	PPRPTAPKPL	LPRREESEAV	EAGDPPEELR	SLPPDMVAGP	RLPDTFLGSA
650	660	670	680	690	700	710	720
TPLHFPPSPF	PSSTGPGPHY	LSGPLPPGTY	SGPTQLIQPR	APGPHAMPVA	PGPALYPAPA	YTPELGLVPR	SSPQHGVVSS
730	740	750	760	770	780	790	800
PYVGVGPAPP	VAGLPSAPPP	QFSGPELAMA	VRPATTTVDS	IQAPIPSHTA	PRPNPTPAPP	PPCFPVPPPQ	PLPTPYTYPA
810	820	830	840	850	860	870	880
GAKQPIPAQH	HFSSGIPAGF	PAPRIGPQPQ	PHPQPHPSQA	FGPQPPQQPL	PLQHPHLFPP	QAPGLLPPQS	PYPYAPQPGV
890	900	910	920	930	940	950	960
LGQPPPPLHT	QLYPGPAQDP	LPAHSGALPF	PSPGPPQPPH	PPLAYGPAPS	TRPMGPQAAP	LTIRGPSSAG	QSTPSPHLVP
970	980	990	1000	1010	1020	1030	1040
SPAPSPGPGP	VPPRPPAAEP	PPCLRRGAAA	ADLLSSSPES	QHGGTQSPGG	GQPLLQPTKV	DAAEGRRPQA	LRLIERDPYE
1050	1060	1070	1080	1090	1100	1110	1120
HPERLRQLQQ	ELEAFRGQLG	DVGALDTVWR	ELQDAQEHDA	RGRSIAIARC	YSLKNRHQDV	MPYDSNRVVL	RSGKDDYINA
1130	1140	1150	1160	1170	1180	1190	1200
SCVEGLSPYC	PPLVATQAPL	PGTAADFWLM	VHEQKVSVIV	MLVSEAEMEK	QKVARYFPTE	RGQPMVHGAL	SLALSSVRST
1210	1220	1230	1240	1250	1260	1270	1280
ETHVERVLSL	QFRDQSLKRS	LVHLHFPTWP	ELGLPDSPSN	LLRFIQEVHA	HYLHQRPLHT	PIIVHCSSGV	GRTGAFALLY
1290	1300	1310	1320	1330	1340	1350	1360
AAVQEVEAGN	GIPELPQLVR	RMRQQRKHML	QEKLHLRFCY	EAVVRHVEQV	LQRHGVPPPC	KPLASASISQ	KNHLPQDSQD
1370	1380	1390	1400	1410	1420	1430	1440
LVLGGDVPIS	SIQATIAKLS	IRPPGGLESP	VASLPGPAEP	PGLPPASLPE	STPIPSSSPP	PLSSPLPEAP	QPKEEPPVPE
1450	1460	1470	1480	1490	1500	1510	1520
APSSGPPSSS	LELLASLTPE	AFSLDSSLRG	KQRMSKHNFL	QAHNGQGLRA	TRPSDDPLSL	LDPLWTLNKT	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
674	1	512.2810	21.70	2	38.0	13.7	1	253-260	K.LLREMMAK.I	Oxidation: 5, 6	MD:MU 16.67

Detailed Protein Report

Protein 869: PREDICTED: PITH domain-containing protein 1 isoform X1 [Homo sapiens]

Accession:	gi|530361255	**Score:**	13.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	21.6
Database Date:	2015-11-30	**pI:**	5.0
		Sequence Coverage [%]:	6.9
		No. of unique 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
2456	1	640.2291	-51.38	2	61.1	13.6	0	1-13	-.MSHGHSHGGGGCR.C	

Detailed Protein Report

Protein 870: PREDICTED: urea transporter 1 isoform X6 [Homo sapiens]

Accession: gi|578832648
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 13.6
MW [kDa]: 46.4
pI: 5.2
Sequence Coverage [%]: 5.7
No. of unique Peptides: 1

```
        10         20         30         40         50         60         70         80
MFVGPDTAPY EIKDQNILMV ALQTLMAKEP EEEIAMEDSP TMVRVDSPTM VRGENQVSPC QGRRCFPKAL GYVTGDMKEL
        90        100        110        120        130        140        150        160
ANQLKDKPVV LQFIDWILRG ISQVVFVNNP VSGILILVGL LVQNPWWALT GWLGTVVSTL MALLLSQDRS LIASGLYGYN
       170        180        190        200        210        220        230        240
ATLVGVLMAV FSDKGDYFWW LLLPVCAMSM TCPIFSSALN SMLSKWDLPV FTLPFNMALS MYLSATGHYN PFFPAKLVIP
       250        260        270        280        290        300        310        320
ITTAPNISWS DLSALELLKS IPVGVGQIYG CDNPWTGGIF LGAILLSSPL MCLHAAIGSL LGIAAGLSLS APFEDIYFGL
       330        340        350        360        370        380        390        400
WGFNSSLACI AMGGMFMALT WQTHLLALGC ALFTAYLGVG MANFMAEVGL PACTWPFCLA TLLFLIMTTK NSNIYKMPLS
       410        420        430
KVTYPEENRI FYLQAKKRMV ESPL
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1598	1	927.4639	48.47	3	49.7	13.6	1	29-52	K.EPEEEIAMEDSPTMVRVDSPTMVR.G	Oxidation: 14, 22

Detailed Protein Report

Protein 871: **tumor necrosis factor receptor superfamily member 21 precursor [Homo sapiens]**

Accession:	gi|7657039	**Score:**	13.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	71.8
Database Date:	2015-11-30	**pI:**	9.3
		Sequence Coverage [%]:	1.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGTSPSSSTA	LASCSRIARR	ATATMIAGSL	LLLGFLSTTT	AQPEQKASNL	IGTYRHVDRA	TGQVLTCDKC	PAGTYVSEHC
90	100	110	120	130	140	150	160
TNTSLRVCSS	CPVGTFTRHE	NGIEKCHDCS	QPCPWPMIEK	LPCAALTDRE	CTCPPGMFQS	NATCAPHTVC	PVGWGVRKKG
170	180	190	200	210	220	230	240
TETEDVRCKQ	CARGTFSDVP	SSVMKCKAYT	DCLSQNLVVI	KPGTKETDNV	CGTLPSFSSS	TSPSPGTAIF	PRPEHMETHE
250	260	270	280	290	300	310	320
VPSSTYVPKG	MNSTESNSSA	SVRPKVLSSI	QEGTVPDNTS	SARGKEDVNK	TLPNLQVVNH	QQGPHHRHIL	KLLPSMEATG
330	340	350	360	370	380	390	400
GEKSSTPIKG	PKRGHPRQNL	HKHFDINEHL	PWMIVLFLLL	VLVVIVVCSI	RKSSRTLKKG	PRQDPSAIVE	KAGLKKSMTP
410	420	430	440	450	460	470	480
TQNREKWIYY	CNGHGIDILK	LVAAQVGSQW	KDIYQFLCNA	SEREVAAFSN	GYTADHERAY	AALQHWTIRG	PEASLAQLIS
490	500	510	520	530	540	550	560
ALRQHRRNDV	VEKIRGLMED	TTQLETDKLA	LPMSPSPLSP	SPIPSPNAKL	ENSALLTVEP	SPQDKNKGFF	VDESEPLLRC
570	580	590	600	610	620	630	640
DSTSSGSSAL	SRNGSFITKE	KKDTVLRQVR	LDPCDLQPIF	DDMLHFLNPE	ELRVIEEIPQ	AEDKLDRLFE	IIGVKSQEAS
650	660						
QTLLDSVYSH	LPDLL						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
163	1	635.7783	-81.22	2	31.4	13.6	0	614-624	R.VIEEIPQAEDK.L	

Detailed Protein Report

Protein 872: testis- and ovary-specific PAZ domain-containing protein 1 [Homo sapiens]

Accession:	gi|222537754	**Score:**	13.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	190.8
Database Date:	2015-11-30	**pI:**	9.1
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.1
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 1.06 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MRRPPPLGPT	TASGPEGNVR	NLQKRQAPGP	GAAGGCGPEA	GGCRENKQKR	RMVARATPGR	GEVESDKSVA	ASGAGKAARR
90	100	110	120	130	140	150	160
QVEGRRGPVS	PSDSSDPRGL	EAAKEAELPL	QTERHTKEKR	KVTEASSDDP	QPGLDLVRKE	SLTSSESFQT	VECLQSLGKE
170	180	190	200	210	220	230	240
SIIEGIKRRI	RNKKLKSLEN	PPLKITENEA	TQNIKVEFQD	ELYKNTPKYS	CNILSPEVEN	NSVLKLRDCN	CFPHSKGCND
250	260	270	280	290	300	310	320
ENNLPYKPDG	GCMHVAENFS	KKENLRSLAE	KSDTNSIPQL	LQTEENVMGV	NKLLPEESDL	YQSKTNGLLS	CLQHEKNKYS
330	340	350	360	370	380	390	400
IEESSVGRKP	RKRMKLSEKA	DETVTEMNFS	NEYNKSELML	QENQMIADGK	EAETKSPLNV	LRKVSHNTVS	LMDHLLSVPE
410	420	430	440	450	460	470	480
TVEKETSSEH	HVNAVFQKTI	EPLLKEETEN	ASEPLGYESM	ASKEDFKSMK	SFIGKSPNEY	HIERRSSRED	LRSASEELKL
490	500	510	520	530	540	550	560
SCQRTIPMTG	KRTWPYYSCA	RISAWCWKKA	SLPESSYFLR	GSQESCRQVD	VPKHQTNQTH	LTDSKLLLQS	SLTETNTESS
570	580	590	600	610	620	630	640
SKEKLDSNSN	CLSSVSAVEP	TLMVIKEPII	KDDKKIKSEE	LSRRGSEVIS	NTTEDTQLTS	ETQSLTGNKK	KARGNLTKLN
650	660	670	680	690	700	710	720
LTATSKDGQE	ANNSAGKTIH	RKACIAQQTF	IVPDLVKILN	TGRLTNFKIP	LLKNKSEKRK	EVNAKSSERE	AYSPLELLDN
730	740	750	760	770	780	790	800
LSGADVRQNR	SKENVSMMML	GPQTLSIRNS	VTPVQASSDS	FYNKKSYSIS	PSFTKQGNNS	KPSNHVSEPG	NIVSNKEVAS
810	820	830	840	850	860	870	880
LTVENNAFSC	DPGYVEKSPS	FCCNEQETFR	PVSSEVRGRK	ITKNFSEVGF	PDILKAYEDD	VLLIDVIQDD	PDLFGVSNEG
890	900	910	920	930	940	950	960
ELSFTSEVPK	ISQEPNVAGE	HQSTDSKYME	TPVKKEPSDD	LRELPVLDCG	WIKPDICASN	SAESEIKRDP	KDVNTSLGEV
970	980	990	1000	1010	1020	1030	1040
ANETSENETL	GDFSEQIKGS	DLDEKHRFTD	KVITKEEKEN	IYEVCKSKDS	RNADFMVGEC	QFAVPVPKPL	CLLVPPLNLS
1050	1060	1070	1080	1090	1100	1110	1120
GRQEDTILNT	WMNDFRFLGK	HSVLKLQNPE	TCEIFKREKN	VGVFQKSLGL	MIPYKYCKFH	FNTLRGCERP	LCKFAHVPEQ
1130	1140	1150	1160	1170	1180	1190	1200
GDEKVCMDVF	KKYININELC	LLQRAVNIFM	EYYRKFPPGV	YFDLQVLNDL	LNSLLKHCLL	KEVFQIVNLS	IMVKMLPSLK
1210	1220	1230	1240	1250	1260	1270	1280
ILLNIFEYVA	TMKLRNAVPA	LIDIFCKLVE	AGMVLDPEHF	NYIVKLLYQV	QASKQEITAV	LEMKSRLQMR	RFKKNWKCDL
1290	1300	1310	1320	1330	1340	1350	1360
DSALNKLEHC	KEKGDWTKLG	KLYINVKMGC	EKFADFQTFC	ACIAETLTKN	YEDERPDIPF	CEFAETVSKD	PQNSKVDKGV
1370	1380	1390	1400	1410	1420	1430	1440
LGRIGISAMY	FYHKLLQWSK	GRKVLEKLYE	LKIHFTSLKG	LIGPEKLASR	CQIVNVAAEI	FLKSGSLDGA	IWVMRESEWI
1450	1460	1470	1480	1490	1500	1510	1520
INTPLWPCDR	LDVLNRHNLL	CTIAHEILAK	SLYRQTFEVL	QNLPGFQNSQ	ETVEVSQYSL	LFNKLLGSCI	ESSSLGMSSS
1530	1540	1550	1560	1570	1580	1590	1600
VAEFMISKSI	PIDFSFLRRL	ITSLGRSRLW	LKARAHYKSA	LSLGCYPPLE	GNLYRKLLLI	PSYLSEIEML	LAIEIFMVSN
1610	1620	1630	1640	1650	1660	1670	1680
ASSIQSPGTS	TQILQIVLKR	CEDNQSRSND	DYQAAVERLI	MAARISDPKL	FVKHMTVNVN	KEQVYSLEHC	SALKWLKENM
1690	1700						
KWAGKVWLFS	NH						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
64	1	1068.4736	-22.86	2	30.2	13.6	1	1114-1131	K.FAHVPEQGDEKVCMDVFK.K	Carbamidomethyl: 13	MD:MU 1.06

Detailed Protein Report

Protein 873: **PREDICTED: inositol polyphosphate 5-phosphatase OCRL-1 isoform X2 [Homo sapiens]**

Accession:	gi|530422443	**Score:**	13.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	86.4
Database Date:	2015-11-30	**pI:**	6.9
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MNLDKKINSQ	NQPTGIHREP	PPPPFSVNKM	LPREKEASNK	EQPKVTNTMR	KLFVPNTQSG	QREGLIKHIL	AKREKEYVNI
90	100	110	120	130	140	150	160
QTFRFFVGTW	NVNGQSPDSG	LEPWLNCDPN	PPDIYCIGFQ	ELDLSTEAFF	YFESVKEQEW	SMAVERGLHS	KAKYKKVQLV
170	180	190	200	210	220	230	240
RLVGMMLLIF	ARKDQCRYIR	DIATETVGTG	IMGKMGNKGG	VAVRFVFHNT	TFCIVNSHLA	AHVEDFERRN	QDYKDICARM
250	260	270	280	290	300	310	320
SFVVPNQTLP	QLNIMKHEVV	IWLGDLNYRL	CMPDANEVKS	LINKKDLQRL	LKFDQLNIQR	TQKKAFVDFN	EGEIKFIPTY
330	340	350	360	370	380	390	400
KYDSKTDRWD	SSGKCRVPAW	CDRILWRGTN	VNQLNYRSHM	ELKTSDHKPV	SALFHIGVKV	VDERRYRKVF	EDSVRIMDRM
410	420	430	440	450	460	470	480
ENDFLPSLEL	SRREFVFENV	KFRQLQKEKF	QISNNGQVPC	HFSFIPKLND	SQYCKPWLRA	EPFEGYLEPN	ETVDISLDVY
490	500	510	520	530	540	550	560
VSKDSVTILN	SGEDKIEDIL	VLHLDRGKDY	FLTISGNYLP	SCFGTSLEAL	CRMKRPIREV	PVTKLIDLEE	DSFLEKEKSL
570	580	590	600	610	620	630	640
LQMVPLDEGA	SERPLQVPKE	IWLLVDHLFK	YACHQEDLFQ	TPGMQEELQQ	IIDCLDTSIP	ETIPGSNHSV	AEALLIFLEA
650	660	670	680	690	700	710	720
LPEPVICYEL	YQRCLDSAYD	PRICRQVISQ	LPRCHRNVFR	YLMAFLRELL	KFSEYNSVNA	NMIATLFTSL	LLRPPPNLMA
730	740	750					
RQTPSDRQRA	IQFLLGFLLG	SEED					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
746	1	648.4767	173.28	2	38.7	13.6	0	162-172	R.LVGMMLLIFAR.K	Oxidation: 4, 5

Detailed Protein Report

Protein 874: low-density lipoprotein receptor-related protein 8 isoform 4 precursor [Homo sapiens]

Accession:	gi|65301119	**Score:**	13.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	99.0
Database Date:	2015-11-30	**pI:**	4.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGLPEPGPLR	LLALLLLLLL	LLLLQLQHLA	AAAADPLLGG	QGPAKDCEKD	QFQCRNERCI	PSVWRCDEDD	DCLDHSDEDD
90	100	110	120	130	140	150	160
CPKKTCADSD	FTCDNGHCIH	ERWKCDGEEE	CPDGSDESEA	TCTKQVCPAE	KLSCGPTSHK	CVPASWRCDG	EKDCEGGADE
170	180	190	200	210	220	230	240
AGCATLCAPH	EFQCGNRSCL	AAVFVCDGDD	DCGDGSDERG	CADPACGPRE	FRCGGDGGGA	CIPERWVCDR	QFDCEDRSDE
250	260	270	280	290	300	310	320
AAELCGRPGP	GATSAPAACA	TASQFACRSG	ECVHLGWRCD	GDRDCKDKSD	EADCPLGTCR	GDEFQCGDGT	CVLAIKHCNQ
330	340	350	360	370	380	390	400
EQDCPDGSDE	AGCLQGLNEC	LHNNGGCSHI	CTDLKIGFEC	TCPAGFQLLD	QKTCGDIDEC	KDPDACSQIC	VNYKGYFKCE
410	420	430	440	450	460	470	480
CYPGYEMDLL	TKNCKAAAGK	SPSLIFTNRH	EVRRIDLVKR	NYSRLIPMLK	NVVALDVEVA	TNRIYWCDLS	YRKIYSAYMD
490	500	510	520	530	540	550	560
KASDPKEQEV	LIDEQLHSPE	GLAVDWVHKH	IYWTDSGNKT	ISVATVDGGR	RRTLFSRNLS	EPRAIAVDPL	RGFMYWSDWG
570	580	590	600	610	620	630	640
DQAKIEKSGL	NGVDRQTLVS	DNIEWPNGIT	LDLLSQRLYW	VDSKLHQLSS	IDFSGGNRKT	LISSTDFLSH	PFGIAVFEDK
650	660	670	680	690	700	710	720
VFWTDLENEA	IFSANRLNGL	EISILAENLN	NPHDIVIFHE	LKQPRAPDAC	ELSVQPNGGC	EYLCLPAPQI	SSHSPKYTCA
730	740	750	760	770	780	790	800
CPDTMWLGPD	MKRCYRAPQS	TSTTTLASTM	TRTVPATTRA	PGTTVHRSTY	QNHSTETPSL	TAAVPSSVSV	PRAPSISPST
810	820	830	840	850	860	870	880
LSPATSNHSQ	HYANEDSKMG	STVTAAVIGI	IVPIVVIALL	CMSGYLIWRN	WKRKNTKSMN	FDNPVYRKTT	EEEDEDELHI
890	900	910					
GRTAQIGHVY	PARVALSLED	DGLP					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1832	1	840.7988	-78.14	2	52.9	13.5	1	210-225	R.EFRCGGDGGGACIPER.W	Carbamidomethyl: 4

Protein 875: **V-type proton ATPase subunit G 2 isoform c [Homo sapiens]**

Accession: gi|323276655
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 13.5
MW [kDa]: 8.9
pI: 12.4
Sequence Coverage [%]: 15.4
No. of unique Peptides: 1

```
        10         20         30         40         50         60         70         80
MASQSQGIQQ LLQAEKRAAE KVADARKRKA RRLKQATRRQ VQGMQSSQQR NRERVLAQLL GMVCDVRPQV HPNYRISA
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1822	1	724.7658	-122.70	2	52.8	13.5	1	39-50	R.RQVQGMQSSQQR.N	Oxidation: 6

Detailed Protein Report

Protein 876: **PREDICTED: receptor-type tyrosine-protein phosphatase zeta isoform X2 [Homo sapiens]**

Accession:	gi|578814473	**Score:**	13.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	207.2
Database Date:	2015-11-30	**pI:**	4.7
		Sequence Coverage [%]:	1.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MRILKRFLAC	IQLLCVCRLD	WANGYYRQQR	KLVEEIGWSY	TGALNQKNWG	KKYPTCNSPK	QSPINIDEDL	TQVNVNLKKL
90	100	110	120	130	140	150	160
KFQGWDKTSL	ENTFIHNTGK	TVEINLTNDY	RVSGGVSEMV	FKASKITFHW	GKCNMSSDGS	EHSLEGQKFP	LEMQIYCFDA
170	180	190	200	210	220	230	240
DRFSSFEEAV	KGKGKLRALS	ILFEVGTEEN	LDFKAIIDGV	ESVSRFGKQA	ALDPFILLNL	LPNSTDKYYI	YNGSLTSPPC
250	260	270	280	290	300	310	320
TDTVDWIVFK	DTVSISESQL	AVFCEVLTMQ	QSGYVMLMDY	LQNNFREQQY	KFSRQVFSSY	TGKEEIHEAV	CSSEPENVQA
330	340	350	360	370	380	390	400
DPENYTSLLV	TWERPRVVYD	TMIEKFAVLY	QQLDGEDQTK	HEFLTDGYQD	LGAILNNLLP	NMSYVLQIVA	ICTNGLYGKY
410	420	430	440	450	460	470	480
SDQLIVDMPT	DNPELDLFPE	LIGTEEIIKE	EEEGKDIEEG	AIVNPGRDSA	TNQIRKKEPQ	ISTTTHYNRI	GTKYNEAKTN
490	500	510	520	530	540	550	560
RSPTRGSEFS	GKGDVPNTSL	NSTSQPVTKL	ATEKDISLTS	QTVTELPPHT	VEGTSASLND	GSKTVLRSPH	MNLSGTAESL
570	580	590	600	610	620	630	640
NTVSITEYEE	ESLLTSFKLD	TGAEDSSGSS	PATSAIPFIS	ENISQGYIFS	SENPETITYD	VLIPESARNA	SEDSTSSGSE
650	660	670	680	690	700	710	720
ESLKDPSMEG	NVWFPSSTDI	TAQPDVGSGR	ESFLQTNYTE	IRVDESEKTT	KSFSAGPVMS	QGPSVTDLEM	PHYSTFAYFP
730	740	750	760	770	780	790	800
TEVTPHAFTP	SSRQQDLVST	VNVVYSQTTQ	PVYNAVPSDP	ILVETPKVDK	ISSTMLHLIV	SNSASSENML	HSTSVPVFDV
810	820	830	840	850	860	870	880
SPTSHMHSAS	LQGLTISYAS	EKYEPVLLKS	ESSHQVVPSL	YSNDELFQTA	NLEINQAHPP	KGRHVFATPV	LSIDEPLNTL
890	900	910	920	930	940	950	960
INKLIHSDEI	LTSTKSSVTG	KVFAGIPTVA	SDTFVSTDHS	VPIGNGHVAI	TAVSPHRDGS	VTSTKLLFPS	KATSELSHSA
970	980	990	1000	1010	1020	1030	1040
KSDAGLVGGG	EDGDTDDDGD	DDDDDRGSDG	LSIHKCMSCS	SYRESQEKVM	NDSDTHENSL	MDQNNPISYS	LSENSEEDNR
1050	1060	1070	1080	1090	1100	1110	1120
VTSVSSDSQT	GMDRSPGKSP	SANGLSQKHN	DGKEENDIQT	GSALLPLSPE	SKAWAVLTSD	EESGSGQGTS	DSLNENETST
1130	1140	1150	1160	1170	1180	1190	1200
DFSFADTNEK	DADGILAAGD	SEITPGFPQS	PTSSVTSENS	EVFHVSEAEA	SNSSHESRIG	LAEGLESEKK	AVIPLVIVSA
1210	1220	1230	1240	1250	1260	1270	1280
LTFICLVVLV	GILIYWRKCF	QTAHFYLEDS	TSPRVISTPP	TPIFPISDDV	GAIPIKHFPK	HVADLHASSG	FTEEFETLKE
1290	1300	1310	1320	1330	1340	1350	1360
FYQEVQSCTV	DLGITADSSN	HPDNKHKNRY	INIVAYDHSR	VKLAQLAEKD	GKLTDYINAN	YVDGYNRPKA	YIAAQGPLKS
1370	1380	1390	1400	1410	1420	1430	1440
TAEDFWRMIW	EHNVEVIVMI	TNLVEKGRRK	CDQYWPADGS	EEYGNFLVTQ	KSVQVLAYYT	VRNFTLRNTK	IKKGSQKGRP
1450	1460	1470	1480	1490	1500	1510	1520
SGRVVTQYHY	TQWPDMGVPE	YSLPVLTFVR	KAAYAKRHAV	GPVVVHCSAG	VGRTGTYIVL	DSMLQQIQHE	GTVNIFGFLK
1530	1540	1550	1560	1570	1580	1590	1600
HIRSQRNYLV	QTEEQYVFIH	DTLVEAILSK	ETEVLDSHIH	AYVNALLIPG	PAGKTKLEKQ	FQLLSQSNIQ	QSDYSAALKQ
1610	1620	1630	1640	1650	1660	1670	1680
CNREKNRTSS	IIPVERSRVG	ISSLSGEGTD	YINASYIMGY	YQSNEFIITQ	HPLLHTIKDF	WRMIWDHNAQ	LVVMIPDGQN
1690	1700	1710	1720	1730	1740	1750	1760
MAEDEFVYWP	NKDEPINCES	FKVTLMAEEH	KCLSNEEKLI	IQDFILEATQ	DDYVLEVRHF	QCPKWPNPDS	PISKTFELIS
1770	1780	1790	1800	1810	1820	1830	1840
VIKEEAANRD	GPMIVHDEHG	GVTAGTFCAL	TTLMHQLEKE	NSVDVYQVAK	MINLMRPGVF	ADIEQYQFLY	KVILSLVSTR
1850	1860	1870					
QEENPSTSLD	SNGAALPDGN	IAESLESLV					

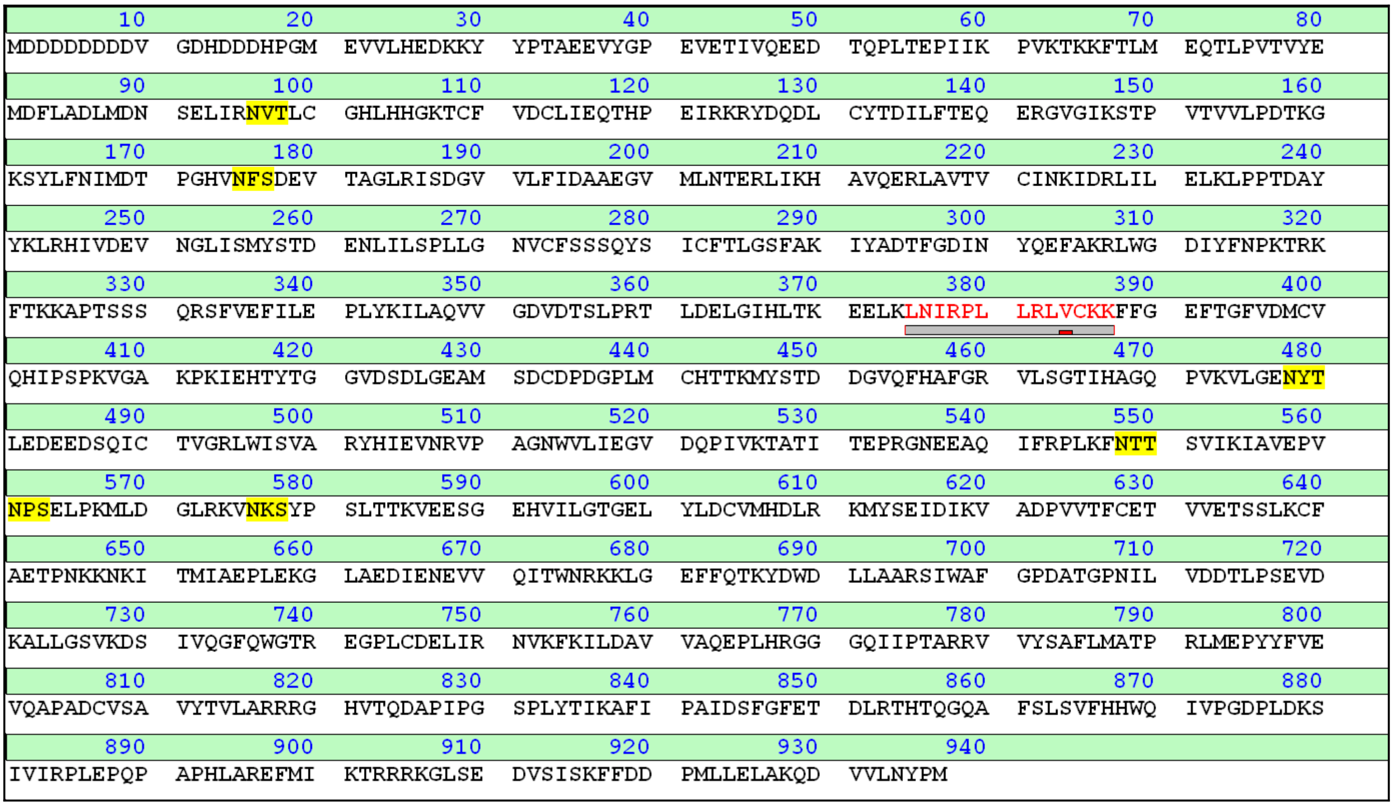
Cmpd.	No. of	m/z meas.		z	Rt	Score	P	Range	Sequence	Modification

	Cmpds.		Δ m/z [ppm]		[min]					
2103	1	1131.3567	-83.48	3	56.2	13.5	1	962-995	K.SDAGLVGGGEDGDTDDDGDDDDDDRGSDGLSIHK.C	

Detailed Protein Report

Protein 877: **116 kDa U5 small nuclear ribonucleoprotein component isoform b [Homo sapiens]**

Accession:	gi|217272894	**Score:**	13.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	105.3
Database Date:	2015-11-30	**pI:**	4.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.4
		No. of unique Peptides:	1



10	20	30	40	50	60	70	80
MDDDDDDDDV	GDHDDDHPGM	EVVLHEDKKY	YPTAEEVYGP	EVETIVQEED	TQPLTEPIIK	PVKTKKFTLM	EQTLPVTVYE
90	100	110	120	130	140	150	160
MDFLADLMDN	SELIRNVTLC	GHLHHGKTCF	VDCLIEQTHP	EIRKRYDQDL	CYTDILFTEQ	ERGVGIKSTP	VTVVLPDTKG
170	180	190	200	210	220	230	240
KSYLFNIMDT	PGHVNFSDEV	TAGLRISDGV	VLFIDAAEGV	MLNTERLIKH	AVQERLAVTV	CINKIDRLIL	ELKLPPTDAY
250	260	270	280	290	300	310	320
YKLRHIVDEV	NGLISMYSTD	ENLILSPLLG	NVCFSSSQYS	ICFTLGSFAK	IYADTFGDIN	YQEFAKRLWG	DIYFNPKTRK
330	340	350	360	370	380	390	400
FTKKAPTSSS	QRSFVEFILE	PLYKILAQVV	GDVDTSLPRT	LDELGIHLTK	EELKLNIRPL	LRLVCKKFFG	EFTGFVDMCV
410	420	430	440	450	460	470	480
QHIPSPKVGA	KPKIEHTYTG	GVDSDLGEAM	SDCDPDGPLM	CHTTKMYSTD	DGVQFHAFGR	VLSGTIHAGQ	PVKVLGENYT
490	500	510	520	530	540	550	560
LEDEEDSQIC	TVGRLWISVA	RYHIEVNRVP	AGNWVLIEGV	DQPIVKTATI	TEPRGNEEAQ	IFRPLKFNTT	SVIKIAVEPV
570	580	590	600	610	620	630	640
NPSELPKMLD	GLRKVNKSYP	SLTTKVEESG	EHVILGTGEL	YLDCVMHDLR	KMYSEIDIKV	ADPVVTFCET	VVETSSLKCF
650	660	670	680	690	700	710	720
AETPNKKNKI	TMIAEPLEKG	LAEDIENEVV	QITWNRKKLG	EFFQTKYDWD	LLAARSIWAF	GPDATGPNIL	VDDTLPSEVD
730	740	750	760	770	780	790	800
KALLGSVKDS	IVQGFQWGTR	EGPLCDELIR	NVKFKILDAV	VAQEPLHRGG	GQIIPTARRV	VYSAFLMATP	RLMEPYYFVE
810	820	830	840	850	860	870	880
VQAPADCVSA	VYTVLARRRG	HVTQDAPIPG	SPLYTIKAFI	PAIDSFGFET	DLRTHTQGQA	FSLSVFHHWQ	IVPGDPLDKS
890	900	910	920	930	940		
IVIRPLEPQP	APHLAREFMI	KTRRRKGLSE	DVSISKFFDD	PMLLELAKQD	VVLNYPM		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2465	2	812.1395	151.93	2	61.2	13.5	2	375-387	K.LNIRPLLRLVCKK.F	Carbamidomethyl: 11

Detailed Protein Report

Protein 878: RAS guanyl-releasing protein 4 isoform f [Homo sapiens]

Accession:	gi|226246584	**Score:**	13.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	53.9
Database Date:	2015-11-30	**pI:**	8.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	5.4
		No. of unique Peptides:	1

```
         10         20         30         40         50         60         70         80
MNRKDSKRKS HQECTGKIGG RGRPRQVRRH KTCPSPREIS KVMASMNLGL LSEGGCSEDE LLEKCIQSFD SAGSLCHEDH
         90        100        110        120        130        140        150        160
MLNMVLAMHS WVLPSADLAA RLLTSYQKAT GDTQELRRLQ ICHLVRYWLM RHPEVMHQDP QLEEVIGRFW ATVAREGNSA
        170        180        190        200        210        220        230        240
QRRLGDSSDL LSPGGPGPPL PMSSPGLGKK RKVSLLFDHL ETGELAQHLT YLEFRSFQAI TLSLDLFYTE DEIYELSYAR
        250        260        270        280        290        300        310        320
EPRCPKSLPP SPFNAPLVVE WAPGVTPKPD RVTLGRHVEQ LVESVFKNYD PEGRGTISQE DFERLSGNFP FACHGLHPPP
        330        340        350        360        370        380        390        400
RQGRGSFSRE ELTGYLLRAS AICSKLGLAF LHTFHEVTFR KPTFCDSCSG FLWGVTKQGY RCRECGLCCH KHCRDQVKVE
        410        420        430        440        450        460        470        480
CKKRPGAKGD AGPPGAPVPS TPAPHASCGS EENHSYTLSL EPETGCQLRH AWTQTESPHP SWETDTVPCP VMDPPSTASS
        490
KLDS
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1426	1	817.1045	28.93	3	47.5	13.5	0	164-189	R.LGDSSDLLSPGGPGPPLPMSSPGLGK.K	Oxidation: 19

Detailed Protein Report

Protein 879: cyclic AMP-responsive element-binding protein 3-like protein 4 isoform 2 [Homo sapiens]

Accession:	gi|364023829	**Score:**	13.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	41.2
Database Date:	2015-11-30	**pI:**	5.1
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	6.7
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578800562	refseq_human (refseq_human_20140103.fasta)	PREDICTED: cyclic AMP-responsive element-binding protein 3-like protein 4 isoform X1 [Homo sapiens]
gi|364023831	refseq_human (refseq_human_20140103.fasta)	cyclic AMP-responsive element-binding protein 3-like protein 4 isoform 2 [Homo sapiens]

10	20	30	40	50	60	70	80
MDLGIPDLLD	AWLEPPEDIF	STGSVLELGL	HCPPPEVPGL	QESEPEDFLK	LFIDPNEVYC	SEASPGSDSG	ISEDPCHPDS
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
PPAPRATSSP	MLYEVVYEAG	ALERMQGETG	PNVGLISIQL	DQWSPAFMVP	DSCMVSELPF	DAHAHILPRA	GTVAPVPCTT
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
LLPCQTLFLT	DEEKRLLGQE	GVSLPSHLPL	TKAEERVLKK	VRRKIRNKQS	AQDSRRRKKE	YIDGLESRVA	ACSAQNQELQ
250	**260**	**270**	**280**	**290**	**300**	**310**	**320**
KKVQELERHN	ISLVAQLRQL	QTLIAQTSNK	AAQTSTCVLI	LLFSLALIIL	PSFSPFQSRP	EAGSEDYQPH	GVTSRNILTH
330	**340**	**350**	**360**	**370**	**380**		
KDVTENLETQ	VVESRLREPP	GAKDANGSTR	TLLEKMGGKP	RPSGRIRSVL	HADEM		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
634	1	676.8750	44.62	4	37.5	13.5	0	150-174	R.AGTVAPVPCTTLLPCQTLFLTDEEK.R	Carbamidomethyl: 9

Detailed Protein Report

Protein 880: caspase recruitment domain-containing protein 16 isoform 2 [Homo sapiens]

Accession: gi|16751833
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 13.5
MW [kDa]: 10.7
pI: 5.0
Sequence Coverage [%]: 19.6
No. of unique Peptides: 1

```
         10         20         30         40         50         60         70         80
MADKVLKEKR KLFIHSMGEG TINGLLDELL QTRVLNQEEM EKVKRENATV MDKTRALIDS VIPKGAQACQ ICITYICEED
         90        100
SYLAETLGLS AGPIPGN
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1484	1	1059.1226	52.34	2	48.2	13.5	2	46-64	R.ENATVMDKTRALIDSVIPK.G	Oxidation: 6

Detailed Protein Report

Protein 881: A disintegrin and metalloproteinase with thrombospondin motifs 16 preproprotein [Homo sapiens]

Accession:	gi|110735441	**Score:**	13.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	136.1
Database Date:	2015-11-30	**pI:**	10.2
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	2.0
		No. of unique Peptides:	1

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
2449	1	1025.1077	-9.04	3	60.5	13.5	2	1186-1209	K.KDAFCKDYFHWCYLVPQHGMCSHK.F	Carbamidomethyl: 5, 12; Oxidation: 20

Detailed Protein Report

Protein 882: tubulointerstitial nephritis antigen-like isoform 3 [Homo sapiens]

Accession:	gi|324713036	**Score:**	13.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	40.8
Database Date:	2015-11-30	**pI:**	6.5
		Sequence Coverage [%]:	5.0
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|530363132	refseq_human (refseq_human_20140103.fasta)	PREDICTED: tubulointerstitial nephritis antigen-like isoform X2 [Homo sapiens]

10	20	30	40	50	60	70	80
MHGGRIYPVL	GTYWDNCNRC	TCQENRQWQC	DQEPCLVDPD	MIKAINQGNY	GWQAGNHSAF	WGMTLDEGIR	YRLGTIRPSS
90	100	110	120	130	140	150	160
SVMNMHEIYT	VLNPGEVLPT	AFEASEKWPN	LIHEPLDQGN	CAGSWAFSTA	AVASDRVSIH	SLGHMTPVLS	PQNLLSCDTH
170	180	190	200	210	220	230	240
QQQGCRGGRL	DGAWWFLRRR	GVVSDHCYPF	SGRERDEAGP	APPCMMHSRA	MGRGKRQATA	HCPNSYVNNN	DIYQVTPVYR
250	260	270	280	290	300	310	320
LGSNDKEIMK	ELMENGPVQA	LMEVHEDFFL	YKGGIYSHTP	VSLGRPERYR	RHGTHSVKIT	GWGEETLPDG	RTLKYWTAAN
330	340	350	360	370			
SWGPAWGERG	HFRIVRGVNE	CDIESFVLGV	WGRVGMEDMG	HH			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1925	1	682.2617	-145.05	3	54.1	13.5	1	273-290	K.GGIYSHTPVSLGRPERYR.R	

Detailed Protein Report

Protein 883: low molecular weight phosphotyrosine protein phosphatase isoform d [Homo sapiens]

Accession:	gi|96304457	**Score:**	13.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	12.2
Database Date:	2015-11-30	**pI:**	9.3
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	25.0
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MAEQATKSVL FVCLGNICRS PIAEAVFRKL VTDQNISENW RVDSAATSGY EIGNPPDYRG QSCMKRHGIP MSHVARQVPS
        90        100        110        120
LDLKLCVLCF SGSLTAVLFL TGTWAGPQTQ EL
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1657	1	1061.8014	-69.49	3	50.5	13.5	2	1-28	-.MAEQATKSVLFVCLGNICRSPIAEAVFR.K	Carbamidomethyl: 13, 18; Oxidation: 1

Detailed Protein Report

Protein 884: 28S ribosomal protein S18c, mitochondrial [Homo sapiens]

Accession:	gi|7705630	**Score:**	13.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	15.8
Database Date:	2015-11-30	**pI:**	10.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	7.7
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MAAVVAVCGG LGRKKLTHLV TAAVSLTHPG THTVLWRRGC SQQVSSNEDL PISMENPYKE PLKKCILCGK HVDYKNVQLL
        90        100        110        120        130        140        150
SQFVSPFTGC IYGRHITGLC GKKQKEITKA IKRAQIMGFM PVTYKDPAYL KDPKVCNIRY RE
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2756	1	673.3574	-18.95	2	64.8	13.5	2	60-70	K.EPLKKCILCGK.H	Carbamidomethyl: 6, 9

Detailed Protein Report

Protein 885: PREDICTED: gamma-glutamyltranspeptidase 2-like isoform X10 [Homo sapiens]

Accession:	gi|578839185	**Score:**	13.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	53.8
Database Date:	2015-11-30	**pI:**	6.4
		Sequence Coverage [%]:	2.6
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 1.26 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MPGNMNATHP	APRSNTLGVN	SAKMNLVGGL	SVAVPGEIRG	YELAHQRHGR	LPWARLFQPS	IQLARQGFPV	GKGLAAVLEN
90	100	110	120	130	140	150	160
KRTVIEQQPV	LCEVFCRDRK	VLWEGERLTL	PRLADTYEML	AIEGAQAFYN	GSLMAQIVKD	IQAAGGIVTA	EDLNNYCAEL
170	180	190	200	210	220	230	240
IEHPLNISLG	DAVLYMPSAR	LSGPVLALIL	NILKGYNFSR	ESVETPEQKG	LTYYRIVEAF	RFAYAKRTLL	GDPKFVDVTE
250	260	270	280	290	300	310	320
VVRNMTSEFF	TAQLRSQISD	HTTHPISYYK	PEFYTPDDGG	TAHLSVVAED	GSAVSATSTI	NLYFGSKVCS	PVSGILFNNE
330	340	350	360	370	380	390	400
WTTSALPAFT	NEFGAPPSPA	NFIQPGKQPL	LSMCPTIMVG	QDGQVRMVVG	AAGGTQITTD	TALVCVTPFL	PGPAHSAQPP
410	420	430	440	450	460	470	480
SHADHTPMPQ	AIIYNLWFGY	DVKRAVEEPR	LHNKLLPNVT	TVERNIDQAV	TAALETRHHH	TQIASTFIAV	VQAIVRTAGG
490	500						
WAAASDSRKG	GEPAGY						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2245	1	697.3039	-32.93	2	58.3	13.5	0	1-13	-.MPGNMNATHPAPR.S		MD:MU 1.26

Detailed Protein Report

Protein 886: uncharacterized membrane protein C3orf80 precursor [Homo sapiens]

Accession:	gi|270265902	**Score:**	13.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	25.7
Database Date:	2015-11-30	**pI:**	5.4
		Sequence Coverage [%]:	7.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MWGPGVTAEG	LSVAPAPPPL	LPLLLLLALA	LVAPSRGGGG	CAELACGERE	RCCDATNATA	VRCCKLPLHA	FLDNVGWFVR
90	100	110	120	130	140	150	160
KLSGLLILLV	LFAIGYFLQR	IICPSPRRYP	RGQARPGQRP	GPPGGAGPLG	GAGPPDDDDD	SPALLRDEAA	AGSQDSLLDS
170	180	190	200	210	220	230	240
GGGGRGRGGG	GRSDPSCASE	HEMRVVSPVF	LQLPSYEEVK	YLPTYEESMR	LQQLSPGEVV	LPVSVLGRPR	GGVAAEPDGG
250							
EGRYPLI							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2758	1	973.5021	83.13	2	64.9	13.5	2	166-184	R.GRGGGGRSDPSCASEHEMR.V	

Detailed Protein Report

Protein 887: PREDICTED: zona pellucida-like domain-containing protein 1 isoform X1 [Homo sapiens]

Accession:	gi|530373904	**Score:**	13.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	45.5
Database Date:	2015-11-30	**pI:**	9.1
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEQIWLLLLL	TIRVLPGSAQ	FNGYNCDANL	HSRFPAERDI	SVYCGVQAIT	MKINFCTVLF	SGYSETDLAL	NGRHGDSHCR
90	100	110	120	130	140	150	160
GFINNNTFPA	VVIFIINLST	LEGCGNNLVV	STIPGVSAYG	NATSVQVGNI	SGYIDTPDPP	TIISYLPGLL	YKFSCSYPLE
170	180	190	200	210	220	230	240
YLVNNTQLAS	SSAAISVREN	NGTFVSTLNL	LLYNDSTYNQ	QLIIPSIGLP	LKTKVFAAVQ	ATNLDGRWNV	LMDYCYTTPS
250	260	270	280	290	300	310	320
GNPNDDIRYD	LFLSCDKDPQ	TTVIENGRSQ	RGRFSFEVFR	FVKHKNQKMS	TVFLHCVTKL	CRADDCPFLM	PICSHRERRD
330	340	350	360	370	380	390	400
AGRRTTWSPQ	SSSGSAVLSA	GPIITRSDET	PTNNSQLGSP	SMPPFQLNAI	TSALISGMVI	LGVTSFSLLL	CSLALLHRKG
410	420						
PTSLVLNGIR	NPVFD						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2168	1	953.2792	-151.74	2	57.3	13.4	1	303-318	R.ADDCPFLMPICSHRER.R	Oxidation: 8

Detailed Protein Report

Protein 888: mRNA cap guanine-N7 methyltransferase [Homo sapiens]

Accession:	gi|4506567	**Score:**	13.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	54.8
Database Date:	2015-11-30	**pI:**	6.3
		Sequence Coverage [%]:	3.4
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530424977	refseq_human (refseq_human_20140103.fasta)	PREDICTED: mRNA cap guanine-N7 methyltransferase isoform X3 [Homo sapiens]

10	20	30	40	50	60	70	80
MANSAKAEEY	EKMSLEQAKA	SVNSETESSF	NINENTTASG	TGLSEKTSVC	RQVDIARKRK	EFEDDLVKES	SSCGKDTPSK
90	100	110	120	130	140	150	160
KRKLDPEIVP	EEKDCGDAEG	NSKKRKRETE	DVPKDKSSTG	DGTQNKRKIA	LEDVPEKQKN	LEEGHSSTVA	AHYNELQEVG
170	180	190	200	210	220	230	240
LEKRSQSRIF	YLRNFNNWMK	SVLIGEFLEK	VRQKKKRDIT	VLDLGCGKGG	DLLKWKKGRI	NKLVCTDIAD	VSVKQCQQRY
250	260	270	280	290	300	310	320
EDMKNRRDSE	YIFSAEFITA	DSSKELLIDK	FRDPQMCFDI	CSCQFVCHYS	FESYEQADMM	LRNACERLSP	GGYFIGTTPN
330	340	350	360	370	380	390	400
SFELIRRLEA	SETESFGNEI	YTVKFQKKGD	YPLFGCKYDF	NLEGVVDVPE	FLVYFPLLNE	MAKKYNMKLV	YKKTFLEFYE
410	420	430	440	450	460	470	480
EKIKNNENKM	LLKRMQALEP	YPANESSKLV	SEKVDDYEHA	AKYMKNSQVR	LPLGTLSKSE	WEATSIYLVF	AFEKQQ

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1511	1	1023.6607	144.77	2	48.7	13.4	2	394-409	K.TFLEFYEEKIKNNENK.M	

Detailed Protein Report

Protein 889: complement component C9 precursor [Homo sapiens]

Accession:	gi|4502511	**Score:**	13.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	63.1
Database Date:	2015-11-30	**pI:**	5.3
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	3.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSACRSFAVA	ICILEISILT	AQYTTSYDPE	LTESSGSASH	IDCRMSPWSE	WSQCDPCLRQ	MFRSRSIEVF	GQFNGKRCTD
90	100	110	120	130	140	150	160
AVGDRRQCVP	TEPCEDAEDD	CGNDFQCSTG	RCIKMRLRCN	GDNDCGDFSD	EDDCESEPRP	PCRDRVVEES	ELARTAGYGI
170	180	190	200	210	220	230	240
NILGMDPLST	PFDNEFYNGL	CNRDRDGNTL	TYYRRPWNVA	SLIYETKGEK	NFRTEHYEEQ	IEAFKSIIQE	KTSNFNAAIS
250	260	270	280	290	300	310	320
LKFTPTETNK	AEQCCEETAS	SISLHGKGSF	RFSYSKNETY	QLFLSYSSKK	EKMFLHVKGE	IHLGRFVMRN	RDVVLTTTFV
330	340	350	360	370	380	390	400
DDIKALPTTY	EKGEYFAFLE	TYGTHYSSSG	SLGGLYELIY	VLDKASMKRK	GVELKDIKRC	LGYHLDVSLA	FSEISVGAEF
410	420	430	440	450	460	470	480
NKDDCVKRGE	GRAVNITSEN	LIDDVVSLIR	GGTRKYAFEL	KEKLLRGTVI	DVTDFVNWAS	SINDAPVLIS	QKLSPIYNLV
490	500	510	520	530	540	550	560
PVKMKNAHLK	KQNLERAIED	YINEFSVRKC	HTCQNGGTVI	LMDGKCLCAC	PFKFEGIACE	ISKQKISEGL	PALEFPNEK

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1664	1	626.5306	-153.93	3	50.6	13.4	1	509-525	R.KCHTCQNGGTVILMDGK.C	Carbamidomethyl: 2; Oxidation: 14

Detailed Protein Report

Protein 890: neuroepithelial cell-transforming gene 1 protein isoform 2 [Homo sapiens]

Accession:	gi|19923327	**Score:**	13.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	61.8
Database Date:	2015-11-30	**pI:**	9.7
		Sequence Coverage [%]:	2.4
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 0.83 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MVAHDETGGL	LPIKRTIRVL	DVNNQSFREQ	EEPSNKRVRP	LARVTSLANL	ISPVRNGAVR	RFGQTIQSFT	LRGDHRSPAS
90	100	110	120	130	140	150	160
AQKFSSRSTV	PTPAKRRSSA	LWSEMLDITM	KESLTTREIR	RQEAIYEMSR	GEQDLIEDLK	LARKAYHDPM	LKLSIMSEEE
170	180	190	200	210	220	230	240
LTHIFGDLDS	YIPLHEDLLT	RIGEATKPDG	TVEQIGHILV	SWLPRLNAYR	GYCSNQLAAK	ALLDQKKQDP	RVQDFLQRCL
250	260	270	280	290	300	310	320
ESPFSRKLDL	WSFLDIPRSR	LVKYPLLLKE	ILKHTPKEHP	DVQLLEDAIL	IIQGVLSDIN	LKKGESECQY	YIDKLEYLDE
330	340	350	360	370	380	390	400
KQRDPRIEAS	KVLLCHGELR	SKSGHKLYIF	LFQDILVLTR	PVTRNERHSY	QVYRQPIPVQ	ELVLEDLQDG	DVRMGGSFRG
410	420	430	440	450	460	470	480
AFSNSEKAKN	IFRIRFHDPS	PAQSHTLQAN	DVFHKQQWFN	CIRAAIAPFQ	SAGSPPELQG	LPELHEECEG	NHPSARKLTA
490	500	510	520	530	540	550	
QRRASTVSSV	TQVEVDENAY	RCGSGMQMAE	DSKSLKTHQT	QPGIRRARDK	ALSGGKRKET	LV	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
68	1	809.3763	-79.90	2	30.2	13.4	1	248-260	K.LDLWSFLDIPRSR.L		MD:MU 0.83

Detailed Protein Report

Protein 891: PREDICTED: 28S ribosomal protein S10, mitochondrial isoform X1 [Homo sapiens]

Accession:	gi|530382202	**Score:**	13.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	22.9
Database Date:	2015-11-30	**pI:**	8.8
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	6.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAARTAFGAV	CRRLWQGLGN	FSVNTSKGNT	AKNGGLLLTN	MKWVQFSNLH	VDVPKDLTKP	VVTISDEPDI	LYKRLSVLVK
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
GHDKAVLDSY	EYFAVLAAKE	LGISIKVHEP	PRKIERFTLL	QSVHIYKKHR	VQYEMRTLYR	CLELEHLTGS	TADVYLEYIQ
170	**180**	**190**	**200**	**210**			
RNLPEGVAME	VTKTQLEQLP	EHIKEPIWET	LSEEKEESKS				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2635	1	741.8693	-6.93	2	63.8	13.4	2	1-13	-.MAARTAFGAVCRR.L	Carbamidomethyl: 11; Oxidation: 1

Detailed Protein Report

Protein 892: **PREDICTED: probable G-protein coupled receptor 157 isoform X2 [Homo sapiens]**

Accession:	gi|530360643	**Score:**	13.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	29.3
Database Date:	2015-11-30	**pI:**	10.1
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	6.7
		No. of unique Peptides:	1

```
        10          20          30          40          50          60          70          80
MQPSPPPTEL  VPSERAVVLL  SCALSALGSG  LLVATHALWP  DLRSRARRLL  LFLSLADLLS  AASYFYGVLQ  NFAGPSWDCV
        90         100         110         120         130         140         150         160
LQGALSTFAN  TSSFFWTVAI  ALYLYLSIVR  AARGPRTDRL  LWAFHVVSWG  VPLVITVAAV  ALKKIGYDAS  DVSVGWCWID
       170         180         190         200         210         220         230         240
LEAKDHVLWM  LLTGKLWEML  AYVLLPLLYL  LVRKHINRAG  IGNTFQGGAN  CIMFVLCTRA  VRTRLFSLCC  CCCSSQPPTK
       250         260         270         280
SPAGTPKAPA  PSKPGESQES  QGTPGELPST
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1650	1	697.5485	-126.05	3	50.5	13.4	1	223-240	R.TRLFSLCCCCCSSQPPTK.S	Carbamidomethyl: 7, 11

Detailed Protein Report

Protein 893: **UDP-glucuronosyltransferase 1-6 isoform 2 [Homo sapiens]**

Accession: gi|45827767

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Modification(s): Oxidation

Score: 13.4

MW [kDa]: 29.6

pI: 10.0

Sequence Coverage [%]: 4.9

No. of unique Peptides: 1

```
        10          20          30          40          50          60          70          80
MPNMVFIGGI  NCKKRKDLSQ  EFEAYINASG  EHGIVVFSLG  SMVSEIPEKK  AMAIADALGK  IPQTVLWRYT  GTRPSNLANN
        90         100         110         120         130         140         150         160
TILVKWLPQN  DLLGHPMTRA  FITHAGSHGV  YESICNGVPM  VMMPLFGDQM  DNAKRMETKG  AGVTLNVLEM  TSEDLENALK
       170         180         190         200         210         220         230         240
AVINDKSYKE  NIMRLSSLHK  DRPVEPLDLA  VFWVEFVMRH  KGAPHLRPAA  HDLTWYQYHS  LDVIGFLLAV  VLTVAFITFK
       250         260         270
CCAYGYRKCL  GKKGRVKKAH  KSKTH
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1581	1	720.3513	7.56	2	49.5	13.4	0	1-13	-.MPNMVFIGGINCK.K	Oxidation: 4

Detailed Protein Report

Protein 894: PREDICTED: ubiquitin carboxyl-terminal hydrolase 21 isoform X1 [Homo sapiens]

Accession:	gi|578800816	**Score:**	13.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	42.5
Database Date:	2015-11-30	**pI:**	11.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	8.0
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 1.00 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MPQASEHRLG	RTREPPVNIQ	PRVGSKLPFA	PRARSKERRN	PASGPNPMLR	PLPPRPGLPD	ERLKKLELGR	GRTSGPRPRG
90	100	110	120	130	140	150	160
PLRADHGVPL	PGSPPPTVAL	PLPSRTNLAR	SKSVSSGDLR	PMGIALGGHR	GTGELGAALS	RLALRPEPPT	LRRSTSLRRL
170	180	190	200	210	220	230	240
GGFPGPPTLF	SIRTEPPASH	GSFHMISARS	SEPFYSDDKM	AHHTLLLGSG	HVGLRNLGNT	CFLNAVLQCL	SSTRPLRDFC
250	260	270	280	290	300	310	320
LRRDFRQEVP	GGGRAQELTE	AFADVIGALW	HPDSCEAVNP	TRFRAVFQKY	VPSFSGYSQQ	DAQEFLKLLM	ERLHLEINRR
330	340	350	360	370	380	390	
GRRAPPILAN	GPVPSPPRRG	GALLEEPELS	DDDRANLMWK	RYLEREDSKI	VDLFVGQLKS	CLKCQA	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1329	1	1018.4526	-81.05	3	46.2	13.4	2	111-141	R.SKSVSSGDLRPMGIALGGHRGTGL	Oxidation: 12	MD:MU 1.00

Detailed Protein Report

Protein 895: **SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1-related [Homo sapiens]**

Accession:	gi|83715964	**Score:**	13.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	35.8
Database Date:	2015-11-30	**pI:**	9.9
		Sequence Coverage [%]:	4.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSHGPKQPGA	AAAPAGGKAP	GQHGGFVVTV	KQERGEGPRA	GEKGSHEEEP	VKKRGWPKGK	KRKKILPNGP	KAPVTGYVRF
90	100	110	120	130	140	150	160
LNERREQIRT	RHPDLPFPEI	TKMLGAEWSK	LQPTEKQRYL	DEAEREKQQY	MKELRAYQQS	EAYKMCTEKI	QEKKIKKEDS
170	180	190	200	210	220	230	240
SSGLMNTLLN	GHKGGDCDGF	STFDVPIFTE	EFLDQNKARE	AELRRLRKMN	VAFEEQNAVL	QRHTQSMSSA	RERLEQELAL
250	260	270	280	290	300	310	320
EERRTLALQQ	QLQAVRQALT	ASFASLPVPG	TGETPTLGTL	DFYMARLHGA	IERDPAQHEK	LIVRIKEILA	QVASEHL

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
132	1	725.9894	99.94	2	31.0	13.4	1	305-317	R.IKEILAQVASEHL.-	

Detailed Protein Report

Protein 896: **PREDICTED: C-type lectin domain family 18 member C isoform X3 [Homo sapiens]**

Accession:	gi|530423816	**Score:**	13.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	45.5
Database Date:	2015-11-30	**pI:**	10.0
		Sequence Coverage [%]:	4.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLHPETSPGR	GHLLAVLLAL	LGTAWAEVWP	PQLQEQAPMA	GALNRKESFL	LLSLHNRLRS	WVQPPAADMR	RLDWSDSLAQ
90	100	110	120	130	140	150	160
LAQARAALCG	IPTPSLASGL	WRTLQVGWNM	QLLPAGLASF	VEVVSLWFAE	GQRYSHAAGE	CARNATCTHY	TQVSVLQLVW
170	180	190	200	210	220	230	240
ATSSQLGCGR	HLCSAGQAAI	EAFVCAYSPR	GNWEVNGKTI	VPYKKGAWCS	LCTASVSGCF	KAWDHAGGLC	EVPRNPCRMS
250	260	270	280	290	300	310	320
CQNHGRLNIS	TCHCHCPPGY	TGRYCQVRCS	LQCVHGRFRE	EECSCVCDIG	YGGAQCATKV	HFPFHTCDLR	IDGDCFMVSS
330	340	350	360	370	380	390	400
EADTYYRARM	KCQRKGGVLA	QIKSQKVQDI	LAFYLGRLET	TNEVIDSDFE	TRNFWIAQGS	PTRPPRTPSA	GPQGSTRPSP
410	420						
VLPLGSLTTT	DPPAIL						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2848	3	856.9527	-9.97	2	66.0	13.4	0	86-102	R.AALCGIPTPSLASGLWR.T	

Detailed Protein Report

Protein 897: **PREDICTED: nuclear factor erythroid 2-related factor 1 isoform X6 [Homo sapiens]**

Accession:	gi|530412326	**Score:**	13.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	80.1
Database Date:	2015-11-30	**pI:**	4.4
		Sequence Coverage [%]:	2.1
		No. of unique Peptides:	1

Quantitation

MD:MU	**Median:**	0.83	**CV:**	0.00 %	**No. of 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	Ratios
179	1	879.5102	25.46	2	32.0	13.4	0	589-603	K.IINLPVEEFNELLSK.Y		MD:MU 0.83

Detailed Protein Report

Protein 898: zinc finger protein 317 isoform 2 [Homo sapiens]

Accession:	gi|299782608	**Score:**	13.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	64.4
Database Date:	2015-11-30	**pI:**	10.4
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.7
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 0.91 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MAALSPTFAT	STQDSTCLQD	SEFPVSSKDH	SCPQNLDLFV	CSGLEPHTPS	VGSQESVTFQ	DVAVDFTEKE	WPLLDSSQRK
90	100	110	120	130	140	150	160
LYKDVMLENY	SNLTSLDWET	PSKTKWSLLM	EDIFGKETPS	GVTMERAGLG	EKSTEYAHLF	EVFGMDPHLT	QPMGRHAGKR
170	180	190	200	210	220	230	240
PYHRRDYGVA	FKGRPHLTQH	MSMYDGRKMH	ECHQCQKAFT	TSASLTRHRR	IHTGEKPYEC	SDCGKAFNDP	SALRSHARTH
250	260	270	280	290	300	310	320
LKEKPFDCSQ	CGNAFRTLSA	LKIHMRVHTG	ERPYKCDQCG	KAYGRSCHLI	AHKRTHTGER	PYECHDCGKA	FQHPSHLKEH
330	340	350	360	370	380	390	400
VRNHTGEKPY	ACTQCGKAFR	WKSNFNLHKK	NHMVEKTYEC	KECGKSFGDL	VSRRKHMRIH	IVKKPVECRQ	CGKTFRNQSI
410	420	430	440	450	460	470	480
LKTHMNSHTG	EKPYGCDLCG	KAFSASSNLT	AHRKIHTQER	RYECAACGKV	FGDYLSRRRH	MSVHLVKKRV	ECRQCGKAFR
490	500	510	520	530	540	550	560
NQSTLKTHMR	SHTGEKPYEC	DHCGKAFSIG	SNLNVHRRIH	TGEKPYECLV	CGKAFSDHSS	LRSHVKTHRG	EKLFVSSVWK
570							
RLQ							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
459	1	820.1336	90.77	3	35.1	13.3	1	106-126	K. WSLLMEDIFGKETPSGVTMER.A	Oxidation: 5, 19	MD:MU 0.91

Detailed Protein Report

Protein 899: PREDICTED: semaphorin-3E isoform X1 [Homo sapiens]

Accession:	gi|578814789	**Score:**	13.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	66.2
Database Date:	2015-11-30	**pI:**	6.5
		Sequence Coverage [%]:	2.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MASAGHIITL	LLWGYLLELW	TGGHTADTTH	PRLRLSHKEL	LNLNRTSIFH	SPFGFLDLHT	MLLDEYQERL	FVGGRDLVYS
90	100	110	120	130	140	150	160
LSLERISDGY	KEIHWPSTAL	KMEECIMKGK	DAGECANYVR	VLHHYNRTHL	LTCGTGAFDP	VCAFIRVGYH	LEDPLFHLES
170	180	190	200	210	220	230	240
PRSERGRGRC	PFDPSSSFIS	TLIGSELFAG	LYSDYWSRDA	AIFRSMGRLA	HIRTEHDDER	LLKEPKFVGS	YMIPDNEDRD
250	260	270	280	290	300	310	320
DNKVYFFFTE	KALEAENNAH	AIYTRVGRLC	VNDVGGQRIL	VNKWSTFLKA	RLVCSVPGMN	GIDTYFDELE	DVFLLPTRDH
330	340	350	360	370	380	390	400
KNPVIFGLFN	TTSNIFRGHA	ICVYHMSSIR	AAFNGPYAHK	EGPEYHWSVY	EGKVPYPRPG	SCASKVNGGR	YGTTKDYPDD
410	420	430	440	450	460	470	480
AIRFARSHPL	MYQAIKPAHK	KPILVKTDGK	YNLKQIAVDR	VEAEDGQYDV	LFIGTDNGIV	LKVITIYNQE	MESMEEVILE
490	500	510	520	530	540	550	560
ELQIFKDPVP	IISMEISSKR	QQLYIGSASA	VAQVRFHHCD	MYGSACADCC	LARDPYCAWD	GISCSRYYPT	GTHAKKAFPE
570	580	590					
TRCSTWKCSS	AVLWTTVCWG	CFG					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1096	1	737.2178	-190.33	2	43.3	13.3	0	338-350	R.GHAICVYHMSSIR.A	

Detailed Protein Report

Protein 900: **protein PRRC2B [Homo sapiens]**

Accession:	gi|149192855	**Score:**	13.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	242.8
Database Date:	2015-11-30	**pI:**	9.2
Modification(s):	Oxidation	**Sequence Coverage [%]:**	0.7
		No. of unique Peptides:	1

```
        10          20          30          40          50          60          70          80
MSDRLGQITK  GKDGKSKYST  LSLFDKYKGK  SVDAIRSSVI  PRHGLQSLGK  VAAARRMPPP  ANLPSLKSEN  KGNDPNIVIV
        90         100         110         120         130         140         150         160
PKDGTGWANK  QDQQDPKSSS  ATASQPPESL  PQPGLQKSVS  NLQKPTQSIS  QENTNSVPGG  PKSWAQLNGK  PVGHEGGLRG
       170         180         190         200         210         220         230         240
SSRLLSFSPE  EFPTLKAAGG  QDKAGKEKGV  LDLSYGPGPS  LRPQNVTSWR  EGGGRHIISA  TSLSTSPTEL  GSRNSSTGDG
       250         260         270         280         290         300         310         320
APSSACTSDS  KDPSLRPAQP  VRKGASQFMG  NVYHPPTYHD  MLPAFMCSPK  SSENQGTVER  GSFPLPQLRL  EPRVPFRQFQ
       330         340         350         360         370         380         390         400
MNDQDGKENR  LGLSRPLRPL  RQLVERAPRP  TIINAENLKG  LDDLDADADD  GWAGLHEEVD  YSEKLKFSDD  EEEEEVVKDG
       410         420         430         440         450         460         470         480
RPKWNSWDPR  RQRQLSMSSA  DSADAKRTRE  EGKDWAEAVG  ASRVVRKAPD  PQPPPRKLHG  WAPGPDYQKS  SMGSMFRQQS
       490         500         510         520         530         540         550         560
IEDKEDKPPP  RQKFIQSEMS  EAVERARKRR  EEEERRAREE  RLAACAAKLK  QLDQKCKQAR  KAGEARKQAE  KEVPWSPSAE
       570         580         590         600         610         620         630         640
KASPQENGPA  VHKGSPEFPA  QETPTTFPEE  APTVSPAVAQ  SNSSEEEARE  AGSPAQEFKY  QKSLPPRFQR  QQQQQQQEQL
       650         660         670         680         690         700         710         720
YKMQHWQPVY  PPPSHPQRTF  YPHHPQMLGF  DPRWMMMPSY  MDPRITPTRT  PVDFYPSALH  PSGLMKPMMP  QESLNGTGCR
       730         740         750         760         770         780         790         800
SEDQNCVPPL  QERKVTPIDS  PPVWSPEGYM  ALQSKGYPLP  HPKSSDTLAM  DMRVRNESSF  SASLGRAGGV  SAQRDLFEER
       810         820         830         840         850         860         870         880
GEEYLSAFDK  KAQADFDSCI  SSQRIGQELL  FPPQENVQDA  GAPGGHTQNL  RCSPLEPDFV  PDEKKPECGS  WDVSHQPETA
       890         900         910         920         930         940         950         960
DTAHGVERET  PREGTAFNIS  SWDKNGSPNK  QPSSEPEWTP  EPRSSSSQHP  EQTGRTRRSG  PIKKPVLKAL  KVEDKEKELE
       970         980         990        1000        1010        1020        1030        1040
KIKQELGEES  TRLAKEKEQS  PTAEKDEDEE  NDASLANSST  TTLEDKGPGH  ATFGREATKF  EEEEKPDKAW  EARPPRESSD
      1050        1060        1070        1080        1090        1100        1110        1120
VPPMKRNNWI  FIDEEQAFGV  RGQARGRGRG  FREFTFRGRP  AGGNGSGLCG  GGVLGARSIY  CSSQRSGRGR  GLREFARPED
      1130        1140        1150        1160        1170        1180        1190        1200
CPRAKPRRRV  ASETHSEGSE  YEELPKRRRQ  RGSENGNEGS  LLEREESTLK  KGDCRDSWRS  NKGCSEDHSG  LDAKSRGPRA
      1210        1220        1230        1240        1250        1260        1270        1280
FGRALPPRLS  NCGYGRRTFV  SKESPHWQSK  SPGSSWQEYG  PSDTCGSRRP  TDRDYVPDSY  RHPDAFGGRG  FEDSRAEDKR
      1290        1300        1310        1320        1330        1340        1350        1360
SFFQDEHVAD  SENAENRPFR  RRRPPRQDKP  PRFRRLRQER  ESLGLWGPEE  EPHLLAGQWP  GRPKLCSGDK  SGTVGRRSPE
      1370        1380        1390        1400        1410        1420        1430        1440
LSYQNSSDHA  NEEWETASES  SDFSERRERR  EGPGSEPDSQ  VDGGLSGASL  GEKKELAKRS  FSSQRPVVDR  QSRKLEPGGF
      1450        1460        1470        1480        1490        1500        1510        1520
GEKPVRPGGG  DTSPRYESQQ  NGTPLKVKRS  PDEALPGGLS  GCSSGSGHSP  YALERAAHAS  ADLPEASSKK  AEKEAKLAAP
      1530        1540        1550        1560        1570        1580        1590        1600
RAGEQGEAMK  QFDLNYGSAI  IENCGSSPGE  ESEVGSMVGE  GFIEVLTKKQ  RRLLEEERRK  KEQAVQVPVK  GRGLSSRIPP
      1610        1620        1630        1640        1650        1660        1670        1680
RFAKKQNNLC  LEQGDVTVPG  SSLGTEIWES  SSQALPVQAP  ANDSWRKAVT  AFSSTETGSA  EQGFKSSQGD  SGVDLSAESR
      1690        1700        1710        1720        1730        1740        1750        1760
ESSATSSQRS  SPYGTLKPEE  MSGPGLAEPK  ADSHKEQAPK  PSEQKDSEQG  SGQSKEHRPG  PIGNERSLKN  RKGSEGAERL
      1770        1780        1790        1800        1810        1820        1830        1840
QGAVVPPVNG  VEIHVDSVLP  VPPIEFGVSP  KDSDFSLPPG  SASGPTGSPV  VKLQDALASN  AGLTQSIPIL  RRDHHIQRAI
      1850        1860        1870        1880        1890        1900        1910        1920
GLSPMSFPTA  DLTLKMESAR  KAWENSPSLP  EQSSPGGAGS  GIQPPSSVGA  SSGVNYSSFG  GVSMPPMPVA  SVAPSASMPG
      1930        1940        1950        1960        1970        1980        1990        2000
SHLPPLYLDG  HVFASQPRLV  PQTIPQQQSY  QQAAAAQQIP  ISLHTSLQAQ  AQLGLRGGLP  VSQSQEIFSS  LQPFRSQVYM
      2010        2020        2030        2040        2050        2060        2070        2080
HPSLSPPSTM  ILSGGTALKP  PYSAFPGMQP  LEMVKPQSGS  PYQPMSGNQA  LVYEGQLSQA  AGLGASQMLD  SQLPQLTMPL
      2090        2100        2110        2120        2130        2140        2150        2160
PRYGSGQQPL  ILPQSIQLPP  GQSLSVGAPR  RIPPPGSQPP  VLNTSREPSQ  MEMKGFHFAD  SKQNVPSGGP  VPSPQTYRPS
      2170        2180        2190        2200        2210        2220        2230
```

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1757	1	897.9578	-24.93	2	51.8	13.3	2	56-71	R.RMPPPANLPSLKSENK.G	Oxidation: 2

Detailed Protein Report

Protein 901: inactive ribonuclease-like protein 9 isoform 1 precursor [Homo sapiens]

Accession:	gi|160333409	**Score:**	13.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	24.8
Database Date:	2015-11-30	**pI:**	6.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.8
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|160333428	refseq_huma (refseq_human_20140103.fasta)	inactive ribonuclease-like protein 9 isoform 1 precursor [Homo sapiens]
gi|160333420	refseq_huma (refseq_human_20140103.fasta)	inactive ribonuclease-like protein 9 isoform 1 precursor [Homo sapiens]
gi|160333415	refseq_huma (refseq_human_20140103.fasta)	inactive ribonuclease-like protein 9 isoform 1 precursor [Homo sapiens]

10	20	30	40	50	60	70	80
MSAGKMMRTL	ITTHPLPLLL	LPQQLLQLVQ	FQEVDTDFDF	PEEDKKEEFE	ECLEKFFSTG	PARPPTKEKV	KRRVLIEPGM
90	100	110	120	130	140	150	160
PLNHIEYCNH	EIMGKNVYYK	HRWVAEHYFL	LMQYDELQKI	CYNRFVPCKN	GIRKCNRSKG	LVEGVYCNLT	EAFEIPACKY
170	180	190	200	210	220		
ESLYRKGYVL	ITCSWQNEMQ	KRIPHTINDL	VEPPEHRSFL	SEDGVFVISP			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1624	1	927.6889	288.96	1	50.2	13.3	1	1-8	-.MSAGKMMR.T	Oxidation: 6

Detailed Protein Report

Protein 902: PREDICTED: group IIF secretory phospholipase A2 isoform X1 [Homo sapiens]

Accession:	gi|578799581	**Score:**	13.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	12.9
Database Date:	2015-11-30	**pI:**	10.9
Modification(s):	Oxidation	**Sequence Coverage [%]:**	8.2
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MADGAKANPK GFKKKVLDRC FSGWRGPRFG ASCPSRTSRS SLGMKKFFTV AILAGSVLST AHGSLLNLKA MVEAVTGRSA
        90        100        110        120        130
ILSFVGYGCY CGLGGRGQPK DEVDWKGPLT CSKTHMGEQS HS
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1142	1	509.6230	-255.01	2	43.9	13.3	1	1-10	-.MADGAKANPK.G	Oxidation: 1

Detailed Protein Report

Protein 903: PREDICTED: uncharacterized protein LOC102725509 [Homo sapiens]

Accession:	gi|578796799	**Score:**	13.3
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
991	4	955.6427	92.95	2	41.9	13.3	1	149-169	R.INMVGLGLVGGAGAGLVRGAK.W	

Detailed Protein Report

Protein 904: **PREDICTED: ankyrin repeat domain-containing protein SOWAHC-like [Homo sapiens]**

Accession:	gi|341914886	**Score:**	13.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	25.7
Database Date:	2015-11-30	**pI:**	12.2
		Sequence Coverage [%]:	4.9
		No. of unique Peptides:	1

```
        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
1952	1	661.2554	-170.97	2	54.3	13.3	1	1-12	-.MRSAAFTIPSLK.Q	

Detailed Protein Report

Protein 905: sex-determining region Y protein [Homo sapiens]

Accession:	gi|4507225	**Score:**	13.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	23.9
Database Date:	2015-11-30	**pI:**	10.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	13.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MQSYASAMLS	VFNSDDYSPA	VQENIPALRR	SSSFLCTESC	NSKYQCETGE	NSKGNVQDRV	KRPMNAFIVW	SRDQRRKMAL
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
ENPRMRNSEI	SKQLGYQWKM	LTEAEKWPFF	QEAQKLQAMH	REKYPNYKYR	PRRKAKMLPK	NCSLLPADPA	SVLCSEVQLD
170	**180**	**190**	**200**	**210**			
NRLYRDDCTK	ATHSRMEHQL	GHLPPINAAS	SPQQRDRYSH	WTKL			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1830	2	1023.8975	40.66	3	52.7	13.2	2	135-162	K.AKMLPKNCSLLPADPASVLCSEVQLDNR.L	Carbamidomethyl: 8

Detailed Protein Report

Protein 906: nuclear pore-associated protein 1 [Homo sapiens]

Accession:	gi|112421134	**Score:**	13.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	120.9
Database Date:	2015-11-30	**pI:**	9.8
		Sequence Coverage [%]:	0.9
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MGNLLSKFRP GCRRRPLPGP GRGAPAPLSR DASPPGRAHS VPTPRPFRGL FRRNARRRPS AASIFVAPKR PCPLPRAAAA

        90        100        110        120        130        140        150        160
PLGVLPAVGW GLAIRKTPML PARNPPRFGH PSSVRIPPPS RMFTLLLPSP REPAVKARKP IPATLLEETE VWAQEGPRRV

       170        180        190        200        210        220        230        240
KKDEDPVQIE GEDDEKRTPL SSGEASSTSR SQGTQGDVAS FRCSPGPLEG NVYHKFSENS MSEKAQASPA SSCLEGPAMP

       250        260        270        280        290        300        310        320
STHSQAGCAR HLGKPDPDAT APPEPAVGCS LLQQKLAAEV LNEEPPPSSL GLPIPLMSGK RMPDEKPFCI PPRSAAPPRA

       330        340        350        360        370        380        390        400
ARNRPCKRKM SIPLLLPLPP SLPLLWDRGE LPPPAKLPCL SVEGDLHTLE KSPEYKRNSR ILEDKTETMT NSSITQPAPS

       410        420        430        440        450        460        470        480
FSQPVQTTDS LPLTTYTSQV SAPLPIPDLA DLATGPLILP IPPLSTTPKM DEKIAFTIPN SPLALPADLV PILGDQSNEK

       490        500        510        520        530        540        550        560
GGSYNSVVGA APLTSDPPTP PSSTPSFKPP VTRESPISMC VDSPPPLSFL TLLPVPSTGT SVITSKPMNS TSVISTVTTN

       570        580        590        600        610        620        630        640
ASAHLTSQTA VDPEVVNMDT TAPSQVVIFT SSLSSRVSSL PNSQIHCSAE QRHPGKTSVY TSPLPFIFHN TTPSFNQLFG

       650        660        670        680        690        700        710        720
KEATPQPKFE APDGQPQKAS LPSACVFLSL PIIPPPDTST LVNSASTASS SKPPIETNAM HTTPPSKAVI LQSASVSKKY

       730        740        750        760        770        780        790        800
LPFYLGLPGS GNTQPSGNTA SVQGSTSLPA QSVRAPATAS NHPLNPGATP QPKFGAPDGP QQKTSLPSAH DFLSLPIMVP

       810        820        830        840        850        860        870        880
PDTSTLVSSA SAASLSKPAI DTSDMNTTPP SKTVILQSTF VSRKEEYIRF YMGLPGSGNT LHSDSIASAQ VSTSFPAQAD

       890        900        910        920        930        940        950        960
RRPTTTSSHP LNTGSISHST LGATDGQQKS DSSFILGNPA TPAPVIGLTS PSVQPLSGSI IPPGFAELTS PYTALGTPVN

       970        980        990       1000       1010       1020       1030       1040
AEPVEGHNAS AFPNGTAKTS GFRIATGMPG TGDSTLLVGN TIPGPQVIMG PGTPMDGGSI GFSMSAPGPS STSGELNIGQ

      1050       1060       1070       1080       1090       1100       1110       1120
GQSGTPSTTS VFPFGQAAWD PTGHSMAAAP QGASNIPVFG YTSAAAYIPG LDPPTQNSCS GMGGDGTRSI VGGPCVPAFQ

      1130       1140       1150       1160
QCILQHTWTE RKFYTSSTHY YGQETYVRRH VCFQLP
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1640	1	1044.2554	-244.56	1	50.4	13.2	0	774-783	K.FGAPDGPQQK.T	

Detailed Protein Report

Protein 907: GDNF family receptor alpha-2 isoform c precursor [Homo sapiens]

Accession:	gi|259089453	**Score:**	13.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	36.4
Database Date:	2015-11-30	**pI:**	9.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	5.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MILANVFCLF	FFLGTGADPV	VSAKSNHCLD	AAKACNLNDN	CKKLRSSYIS	ICNREISPTE	RCNRRKCHKA	LRQFFDRVPS
90	100	110	120	130	140	150	160
EYTYRMLFCS	CQDQACAERR	RQTILPSCSY	EDKEKPNCLD	LRGVCRTDHL	CRSRLADFHA	NCRASYQTVT	SCPADNYQAC
170	180	190	200	210	220	230	240
LGSYAGMIGF	DMTPNYVDSS	PTGIVVSPWC	SCRGSGNMEE	ECEKFLRDFT	ENPCLRNAIQ	AFGNGTDVNV	SPKGPSFQAT
250	260	270	280	290	300	310	320
QAPRVEKTPS	LPDDLSDSTS	LGTSVITTCT	SVQEQGLKAN	NSKELSMCFT	ELTTNIIPGS	NKVIKPNSGP	SRARPSAALT
330	340						
VLSVLMLKLA	L						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2756	1	683.3062	14.56	3	65.8	13.2	1	25-42	K.SNHCLDAAKACNLNDNCK.K	Carbamidomethyl: 11, 17

Detailed Protein Report

Protein 908: absent in melanoma 1-like protein [Homo sapiens]

Accession:	gi|301069394	**Score:**	13.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	177.8
Database Date:	2015-11-30	**pI:**	5.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	0.8
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|530361198	refseq_human (refseq_human_20140103.fasta)	PREDICTED: absent in melanoma 1-like protein isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MEEAGGPMAR	AKARVVSATL	TWRQRPPTQE	EIKHGFHKVS	LVSGAQMEAP	QKEMFEFSRR	EEVEVNGFAT	QEEETVNCQG
90	100	110	120	130	140	150	160
PRDTAGSKNF	QSHGPIFSKK	YIPPPKEKRP	EGRLKEAVDQ	SDGSRQAPRT	EPPCVGAMAR	TELLVPLPGP	REPSPHPGVG
170	180	190	200	210	220	230	240
LTSGSSRSLE	EYRVTRTVRT	TTVVGGHVDR	RMSSSVTVRP	VSSGEALPRG	RQVSRMVPPV	VVGSPPGSPS	RSQAVKVLSN
250	260	270	280	290	300	310	320
LVPAGHSPPA	SHLPRPTAGG	PRSTGLGSTV	GAALRQLPET	GTAELKDSSA	LASTGIPASA	HLPKNQDAPA	ACPDRDQGRA
330	340	350	360	370	380	390	400
PDARACELWQ	VLGAPSSTEL	PLQTSQGQAS	VPSSPRLETH	VPSPGLTHPA	KQPVVPTHPG	ARLTPLVLPP	KKKDGPVDPP
410	420	430	440	450	460	470	480
AATVLPMVRS	EHVTVPGQPP	APSTTRRKDV	PSPGGLSAPS	SPRNKFVQNS	ENVPVLPFTQ	REVVKGPGAP	AASSPTRKEV
490	500	510	520	530	540	550	560
VQGSSASAAS	SPTWKEVVKG	PGAPAASSPT	QKEVVQGSSA	PAALFPTWKE	VVKGPGAPDA	SFPTWKEVVK	GPGAPAASSP
570	580	590	600	610	620	630	640
TQKEVVQGSG	APAALSTTPK	EVVKGPGAPA	ASSPTQKEVV	KGPCAPAASS	PTQKEVVQGS	GAPAALSPKS	TEVVQGPKGS
650	660	670	680	690	700	710	720
SSIQKEAVQG	IAGSLAPPLT	KEETVQGPIA	PATSLPKQDK	GVQDSEGSPI	SSLTQKEVVQ	DPDALPAPSS	SVDRVSPSPG
730	740	750	760	770	780	790	800
GTPAPVPTGA	EASTESQLVS	DPTEGKTCTE	TSREEDEVAL	AADLEIFLDT	LRSMEPPEIL	RTHRLPRAPR	SSYLSMYATL
810	820	830	840	850	860	870	880
PAIEEDQLGP	WVLGPGPQEV	PSLEEKEEEE	EEEPENPYLS	DDEKLQRRQE	KAGPSPSRDL	HPARPTQVSC	SPLEMMKKHV
890	900	910	920	930	940	950	960
AGTKGPHSEL	GLELQGGSRP	TSRLGGSLLF	GSLVPTAKEA	STPEPLGTKL	SALLPHGAPG	LRKVPGQLPL	LCSERSSPTE
970	980	990	1000	1010	1020	1030	1040
KLACSLPLEG	WSPALKTQGK	LNTRPGKVIF	FSESGCQGSG	REVWGDIVDA	SGWAPVASIR	VVRGCWVLYE	EPEFRGQKLV
1050	1060	1070	1080	1090	1100	1110	1120
LPEGDMELRT	PGTKWSPQGI	GSLRRVVWDY	STPEISLFSE	EGLKGEQVKL	TEALKNSQGL	EKPLQVASAT	VSAGLWLLYP
1130	1140	1150	1160	1170	1180	1190	1200
KPLFEDTPYI	LEPGEYPTSE	AWGTSDPSVG	SLKPMRLGCP	SVEKPGEPRA	VVYEAPGFQG	RSWEVSRDIY	NLQQPEDSQS
1210	1220	1230	1240	1250	1260	1270	1280
PHLASVGSLR	VLGGCWVGYE	KEGFRGHQYL	LEEGEYPDWS	HWGGYDELLT	SLRVIRTDFG	DPAVVLFEAM	DFEGHGVEVS
1290	1300	1310	1320	1330	1340	1350	1360
KALPDVELVQ	HGPSTQAIHV	LSGVWVAYQE	VGFSGEQYVL	EKGVYRNCED	WGAGNSTLAS	LQPVLQVGEH	DLHFVSKIQL
1370	1380	1390	1400	1410	1420	1430	1440
FSRPDFLGDH	FSFEDDQAAL	PASFRPQSCR	VHGGSWILFD	ETNFEGDQHI	LSEGEFPTLT	AMGCLASTVL	GSLQKVSLHF
1450	1460	1470	1480	1490	1500	1510	1520
SEPSIFLYGL	ECFEGKEIEL	SREVRSLQAE	GFNNHVLSVR	IKGGIWVLCE	HSDFRGRQWL	VGSCEITNWL	TYSGTQRVGS
1530	1540	1550	1560	1570	1580	1590	1600
LYPIKQRRVY	FRLWNAALGG	FLAVPDHVED	MKAGRVVVAD	PQAGGSCIWY	YEDGLLKNQM	APTMSLQVIG	PPSPGSKVVL
1610	1620	1630	1640	1650	1660	1670	
WAESRLPRQT	WSISESGHIC	SQMFEGQILD	VKGGRGYDRD	HVVLWEPDED	RASQIWTIHV	L	

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

Detailed Protein Report

	Cmpds.		[ppm]		[min]					
1638	1	745.8087	-73.79	2	50.2	13.2	2	1-14	-.MEEAGGPMARAKAR.V	Oxidation: 1

Detailed Protein Report

Protein 909: PREDICTED: PR domain zinc finger protein 5 isoform X3 [Homo sapiens]

Accession:	gi|530377106	**Score:**	13.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	39.6
Database Date:	2015-11-30	**pI:**	7.9
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLGMYVPDRF	SLKSSRVQDG	MGLYTARRVR	KGEKFGPFAG	EKRMPEDLDE	NMDYRLMWEV	RGSKGEVLYI	LDATNPRHSN
90	100	110	120	130	140	150	160
WLRFVHEAPS	QEQKNLAAIQ	EGENIFYLAV	EDIETDTELL	IGYLDSDMEA	EEEEQQIMTV	IKEGEVENSR	RQSTAGRKDR
170	180	190	200	210	220	230	240
LGCKEDYACP	QCESSFTSED	ILAEHLQTLH	QKPTEEKEFK	CKNCGKKFPV	KQALQRHVLQ	CTAKSSLKES	SRSFQCSVCN
250	260	270	280	290	300	310	320
SSFSSASSFE	QHQETCRGDA	RFVCKADSCG	KRLKSKDALK	RHQENVHTGD	PKKKLICSVC	NKKCSSASSL	QEHRKIHEIF
330	340	350					
DCQECMKKFI	SANQLKRHMI	THSDPL					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1184	1	533.6372	-216.94	2	44.4	13.2	0	338-346	R.HMITHSDPL.-	Oxidation: 2

Detailed Protein Report

Protein 910: PREDICTED: enhancer of polycomb homolog 2 isoform X1 [Homo sapiens]

Accession:	gi|578804049	**Score:**	13.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	77.3
Database Date:	2015-11-30	**pI:**	9.9
		Sequence Coverage [%]:	2.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDSEDETLLN	RLNRKMEIKP	LQFEIMIDRL	EKASSNQLVT	LQEAKLLLNE	DDYLIKAVYD	YWVRKRKNCR	GPSLIPQIKQ
90	100	110	120	130	140	150	160
EKRDGSTNND	PYVAFRRRTE	KMQTRKNRKN	DEASYEKMLK	LRREFSRAIT	ILEMIKRREK	TKRELLHLTL	EVVEKRYHLG
170	180	190	200	210	220	230	240
DYGGEILNEV	KISRSEKELY	ATPATLHNGN	HHKVQECKTK	HPHHLSLKEE	ASDVVRQKKK	YPKKPKAEAL	ITSQQPTPET
250	260	270	280	290	300	310	320
LPVINKSDIK	QYDFHSSDED	EFPQVLSPVS	EPEEENDPDG	PCAFRRRAGC	QYYAPRLDQA	NHSCENSELA	DLDKLRYRHC
330	340	350	360	370	380	390	400
LTTLTVPRRC	IGFARRRIGR	GGRVIMDRIS	TEHDPVLKQI	DPEMLNSFSS	SSQTIDFSSN	FSRTNASSKH	CENRLSLSEI
410	420	430	440	450	460	470	480
LSNIRSCRLQ	CFQPRLLNLQ	DSDSEECTSR	KPGQTVNNKR	VSAASVALLN	TSKNGISGGI	TEEQFQTHQQ	QLVQMQRQQL
490	500	510	520	530	540	550	560
AQLQQKQQSQ	HSSQQTHPKA	QGSSTSDCMS	KTLDSASAHF	AASAVVSAPV	PSRSEVAKEQ	NTGHNNINGV	VQPSGTSKTL
570	580	590	600	610	620	630	640
YSTNMALSSS	PGISAVQLVR	TVGHTTTNHL	IPALCTSSPQ	TLPMNNSCLT	NAVHLNNVSV	VSPVNVHINT	RTSAPSPTAL
650	660	670	680	690			
KLATVAASMD	RVPKVTPSSA	ISSIARENHE	PERLGLNGIA	ETTVAMEVT			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2296	1	1001.3292	-115.17	2	59.0	13.2	0	297-314	R.LDQANHSCENSELADLDK.L	

Detailed Protein Report

Protein 911:	**PREDICTED: transmembrane and TPR repeat-containing protein 4 isoform X5 [Homo sapiens]**

Accession:	gi|578825275	**Score:**	13.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	58.0
Database Date:	2015-11-30	**pI:**	10.1
		Sequence Coverage [%]:	3.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGLNAVFDIL	VIGKFNVLEI	VQKVLHKDKS	LENLGMLRNG	GLLFRMTLLT	SGGAGMLYVR	WRIMGTGPPA	FTEVDNPASF
90	100	110	120	130	140	150	160
ADSMLVRAVN	YNYYYSLNAW	LLLCPWWLCF	DWSMGCIPLI	KSISDWRVIA	LAALWFCLIG	LICQALCSED	GHKRRILTLG
170	180	190	200	210	220	230	240
LGFLVIPFLP	ASNLFFRVGF	VVAERVLYLP	SVGYCVLLTF	GFGALSKHTK	KKKLIAAVVL	GILFINTLRC	VLRSGEWRSE
250	260	270	280	290	300	310	320
EQLFRSALSV	CPLNAKVHYN	IGKNLADKGN	QTAAIRYYRE	AVRLNPKYVH	AMNNLGNILK	ERNELQEAEE	LLSLAVQIQP
330	340	350	360	370	380	390	400
DFAAAWMNLG	IVQNSLKRFE	AAEQSYRTAI	KHRRKYPDCY	YNLGRLYADL	NRHVDALNAW	RNATVLKPEH	SLAWNNMIIL
410	420	430	440	450	460	470	480
LDNTGNLAQA	EAVGREALEL	IPNDHSLMFS	LANVLGKSQK	YKESEALFLK	AIKANPNAAS	YHGNLAVLYH	RWGHLDLAKK
490	500	510	520				
HYEISLQLDP	TASGTKENYG	LLRRKLELMQ	KKAV				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2358	1	863.6875	155.63	2	59.8	13.2	0	214-229	K.LIAAVVLGILFINTLR.C	

Detailed Protein Report

Protein 912: **thrombospondin-1 precursor [Homo sapiens]**

Accession:	gi|40317626	**Score:**	13.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	129.3
Database Date:	2015-11-30	**pI:**	4.6
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	1.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGLAWGLGVL	FLMHVCGTNR	IPESGGDNSV	FDIFELTGAA	RKGSGRRLVK	GPDPSSPAFR	IEDANLIPPV	PDDKFQDLVD
90	100	110	120	130	140	150	160
AVRAEKGFLL	LASLRQMKKT	RGTLLALERK	DHSGQVFSVV	SNGKAGTLDL	SLTVQGKQHV	VSVEEALLAT	GQWKSITLFV
170	180	190	200	210	220	230	240
QEDRAQLYID	CEKMENAELD	VPIQSVFTRD	LASIARLRIA	KGGVNDNFQG	VLQNVRFVFG	TTPEDILRNK	GCSSSTSVLL
250	260	270	280	290	300	310	320
TLDNNVVNGS	SPAIRTNYIG	HKTKDLQAIC	GISCDELSSM	VLELRGLRTI	VTTLQDSIRK	VTEENKELAN	ELRRPPLCYH
330	340	350	360	370	380	390	400
NGVQYRNNEE	WTVDSCTECH	CQNSVTICKK	VSCPIMPCSN	ATVPDGECCP	RCWPSDSADD	GWSPWSEWTS	CSTSCGNGIQ
410	420	430	440	450	460	470	480
QRGRSCDSLN	NRCEGSSVQT	RTCHIQECDK	RFKQDGGWSH	WSPWSSCSVT	CGDGVITRIR	LCNSPSPQMN	GKPCEGEARE
490	500	510	520	530	540	550	560
TKACKKDACP	INGGWGPWSP	WDICSVTCGG	GVQKRSRLCN	NPTPQFGGKD	CVGDVTENQI	CNKQDCPIDG	CLSNPCFAGV
570	580	590	600	610	620	630	640
KCTSYPDGSW	KCGACPPGYS	GNGIQCTDVD	ECKEVPDACF	NHNGEHRCEN	TDPGYNCLPC	PPRFTGSQPF	GQGVEHATAN
650	660	670	680	690	700	710	720
KQVCKPRNPC	TDGTHDCNKN	AKCNYLGHYS	DPMYRCECKP	GYAGNGIICG	EDTDLDGWPN	ENLVCVANAT	YHCKKDNCPN
730	740	750	760	770	780	790	800
LPNSGQEDYD	KDGIGDACDD	DDDNDKIPDD	RDNCPFHYNP	AQYDYDRDDV	GDRCDNCPYN	HNPDQADTDN	NGEGDACAAD
810	820	830	840	850	860	870	880
IDGDGILNER	DNCQYVYNVD	QRDTDMDGVG	DQCDNCPLEH	NPDQLDSDSD	RIGDTCDNNQ	DIDEDGHQNN	LDNCPYVPNA
890	900	910	920	930	940	950	960
NQADHDKDGK	GDACDHDDDN	DGIPDDKDNC	RLVPNPDQKD	SDGDGRGDAC	KDDFDHDSVP	DIDDICPENV	DISETDFRRF
970	980	990	1000	1010	1020	1030	1040
QMIPLDPKGT	SQNDPNWVVR	HQGKELVQTV	NCDPGLAVGY	DEFNAVDFSG	TFFINTERDD	DYAGFVFGYQ	SSSRFYVVMW
1050	1060	1070	1080	1090	1100	1110	1120
KQVTQSYWDT	NPTRAQGYSG	LSVKVVNSTT	GPGEHLRNAL	WHTGNTPGQV	RTLWHDPRHI	GWKDFTAYRW	RLSHRPKTGF
1130	1140	1150	1160	1170	1180		
IRVVMYEGKK	IMADSGPIYD	KTYAGGRLGL	FVFSQEMVFF	SDLKYECRDP			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1365	1	817.1004	80.07	3	46.8	13.2	1	461-482	R.LCNSPSPQMNGKPCEGEARETK.A	Carbamidomethyl: 2; Oxidation: 9

Detailed Protein Report

Protein 913: coxsackievirus and adenovirus receptor isoform 1 precursor [Homo sapiens]

Accession:	gi|4503173	**Score:**	13.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	40.0
Database Date:	2015-11-30	**pI:**	8.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MALLLCFVLL	CGVVDFARSL	SITTPEEMIE	KAKGETAYLP	CKFTLSPEDQ	GPLDIEWLIS	PADNQKVDQV	IILYSGDKIY
90	100	110	120	130	140	150	160
DDYYPDLKGR	VHFTSNDLKS	GDASINVTNL	QLSDIGTYQC	KVKKAPGVAN	KKIHLVVLVK	PSGARCYVDG	SEEIGSDFKI
170	180	190	200	210	220	230	240
KCEPKEGSLP	LQYEWQKLSD	SQKMPTSWLA	EMTSSVISVK	NASSEYSGTY	SCTVRNRVGS	DQCLLRLNVV	PPSNKAGLIA
250	260	270	280	290	300	310	320
GAIIGTLLAL	ALIGLIIFCC	RKKRREEKYE	KEVHHDIRED	VPPPKSRTST	ARSYIGSNHS	SLGSMSPSNM	EGYSKTQYNQ
330	340	350	360	370			
VPSEDFERTP	QSPTLPPAKV	AAPNLSRMGA	IPVMIPAQSK	DGSIV			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2013	1	687.7835	-110.67	2	55.3	13.2	0	348-360	R.MGAIPVMIPAQSK.D	Oxidation: 1, 7

Detailed Protein Report

Protein 914: GTP-binding protein 10 isoform 1 [Homo sapiens]

Accession:	gi|111955063	**Score:**	13.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	34.6
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
MVHCSCVLFR	KYGNFIDKLR	LFTRGGSGGM	GYPRLGGEGG	KGGDVWVVAQ	NRMTLKQLKD	RYPRKRFVAG	VGANSKFPNA
90	100	110	120	130	140	150	160
GKSSLLSCVS	HAKPAIADYA	FTTLKPELGK	IMYSDFKQIS	VADLPGLIEG	AHMNKGMGHK	FLKHIERTRQ	LLFVVDISGF
170	180	190	200	210	220	230	240
QLSSHTQYRT	AFETIILLTK	ELELYKEELQ	TKPALLAVNK	MDLPDAQDKF	HELMSQLQNP	KDFLHLFEKN	MIPERTVEFQ
250	260	270	280	290	300	310	
HIIPISAVTG	EGIEELKNCI	RKSLDEQANQ	ENDALHKKQL	LNLWISDTMS	STEPPSKHAV	TTSKMDII	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
861	1	736.2893	-94.91	2	40.2	13.2	1	21-34	R.LFTRGGSGGMGYPR.L	Oxidation: 10

Detailed Protein Report

Protein 915: testis-expressed sequence 35 protein isoform 4 [Homo sapiens]

Accession:	gi|282398137	**Score:**	13.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	24.0
Database Date:	2015-11-30	**pI:**	10.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	6.3
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MSAKRAELKK THLSKNYKAV CLELKPEPTK TFDYKAVKQE GRFTKAGVTQ DLKNELREVR EELKEKMEEI KQIKDLMDKD
        90        100        110        120        130        140        150        160
FDKLHEFVEI MKEMQKDMDE KMDILINTQK NYKLPLRRAP KEQQELRLMG KTHREPQLRP KKMDGASGVN GAPCALHKKT
       170        180        190        200        210
MAPQKTKQGS LDPLHHCGTC CEKCLLCALK NNYNRGIYAA VGLLDLW
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1608	1	821.4460	21.75	2	50.0	13.2	2	122-134	K.EQQELRLMGKTHR.E	Oxidation: 8

Detailed Protein Report

Protein 916: adenosine 3'-phospho 5'-phosphosulfate transporter 1 isoform f [Homo sapiens]

Accession:	gi|557357687	**Score:**	13.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	32.6
Database Date:	2015-11-30	**pI:**	10.4
		Sequence Coverage [%]:	4.7
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|557357693	refseq_human (refseq_human_20140103.fasta)	adenosine 3'-phospho 5'-phosphosulfate transporter 1 isoform f [Homo sapiens]

10	20	30	40	50	60	70	80
MTRSYGATAT	SPGERFTDSQ	FLVLMNRVLA	LIVAGLSCVL	CKQPRHGAPM	YRYSFASLSN	VLSSWCQYEA	LKFVSFPTQV
90	100	110	120	130	140	150	160
LAKASKVIPV	MLMGKLVSRR	SYEHWEYLTA	TLISIGVSMF	LLSSGPEPRS	SPATTLSGLI	LLAGYIAFDS	FTSNWQDALF
170	180	190	200	210	220	230	240
AYKMSSVQMM	FGVNFFSCLF	TVGSLLEQGA	LLEGTRFMGR	HSEFAAHALL	LSICSACGQL	FIFYTIGQFG	AAVFTIIMTL
250	260	270	280	290	300		
RQAFAILLSC	LLYGHTVTVV	GGLGVAVVFA	ALLLRVYARG	RLKQRGKKAV	PVESPVQKV		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1312	1	727.2069	-203.76	2	46.0	13.2	1	2-15	M.TRSYGATATSPGER.F	

Detailed Protein Report

Protein 917: PREDICTED: sal-like protein 4 isoform X1 [Homo sapiens]

Accession:	gi|530418220	**Score:**	13.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	100.9
Database Date:	2015-11-30	**pI:**	9.3
		Sequence Coverage [%]:	1.8
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578836089	refseq_human (refseq_human_20140103.fasta)	PREDICTED: sal-like protein 4 isoform X3 [Homo sapiens]
gi|578836087	refseq_human (refseq_human_20140103.fasta)	PREDICTED: sal-like protein 4 isoform X2 [Homo sapiens]

10	20	30	40	50	60	70	80
MNDSEGPVPS	EDFSGAVLSH	QPTSPGSKDC	HRENGGSSED	MKEKPDAESV	VYLKTETALP	PTPQDISYLA	KGKVANTNVT
90	100	110	120	130	140	150	160
LQALRGTKVA	VNQRSADALP	APVPGANSIP	WVLEQILCLQ	QQQLQQIQLT	EQIRIQVNMW	ASHALHSSGA	GADTLKTLGS
170	180	190	200	210	220	230	240
HMSQQVSAAV	ALLSQKAGSQ	GLSLDALKQA	KLPHANIPSA	TSSLSPGLAP	FTLKPDGTRV	LPNVMSRLPS	ALLPQAPGSV
250	260	270	280	290	300	310	320
LFQSPFSTVA	LDTSKKGKGK	PPNISAVDVK	PKDEAALYKH	KCKYCSKVFG	TDSSLQIHLR	SHTGERPFVC	SVCGHRFTTK
330	340	350	360	370	380	390	400
GNLKVHFHRH	PQVKANPQLF	AEFQDKVAAG	NGIPYALSVP	DPIDEPSLSL	DSKPVLVTTS	VGLPQNLSSG	TNPKDLTGGS
410	420	430	440	450	460	470	480
LPGDLQPGPS	PESEGGPTLP	GVGPNYNSPR	AGGFQGSGTP	EPGSETLKLQ	QLVENIDKAT	TDPNECLICH	RVLSCQSSLK
490	500	510	520	530	540	550	560
MHYRTHTGER	PFQCKICGRA	FSTKGNLKTH	LGVHRTNTSI	KTQHSCPICQ	KKFTNAVMLQ	QHIRMHMGGQ	IPNTPLPENP
570	580	590	600	610	620	630	640
CDFTGSEPMT	VGENGSTGAI	CHDDVIESID	VEEVSSQEAP	SSSSKVPTPL	PSIHSASPTL	GFAMMASLDA	PGKVGPAPFN
650	660	670	680	690	700	710	720
LQRQGSRENG	SVESDGLTND	SSSLMGDQEY	QSRSPDILET	TSFQALSPAN	SQAESIKSKS	PDAGSKAESS	ENSRTEMEGR
730	740	750	760	770	780	790	800
SSLPSTFIRA	PPTYVKVEVP	GTFVGPSTLS	PGMTPLLAAQ	PRRQAKQHGC	TRCGKNFSSA	SALQIHERTH	TGEKPFVCNI
810	820	830	840	850	860	870	880
CGRAFTTKGN	LKVHYMTHGA	NNNSARRGRK	LAIENTMALL	GTDGKRVSEI	FPKEILAPSV	NVDPVVWNQY	TSMLNGGLAV
890	900	910	920	930	940	950	960
KTNEISVIQS	GGVPTLPVSL	GATSVVNNAT	VSKMDGSQSG	ISADVEKPSA	TDGVPKHQFP	HFLEENKIAV	S

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1542	1	882.1342	117.56	2	49.1	13.2	2	256-272	K.KGKGKPPNISAVDVKPK.D	

Detailed Protein Report

Protein 918: vitronectin precursor [Homo sapiens]

Accession:	gi|88853069	**Score:**	13.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	54.3
Database Date:	2015-11-30	**pI:**	5.5
		Sequence Coverage [%]:	3.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAPLRPLLIL	ALLAWVALAD	QESCKGRCTE	GFNVDKKCQC	DELCSYYQSC	CTDYTAECKP	QVTRGDVFTM	PEDEYTVYDD
90	100	110	120	130	140	150	160
GEEKNNATVH	EQVGGPSLTS	DLQAQSKGNP	EQTPVLKPEE	EAPAPEVGAS	KPEGIDSRPE	TLHPGRPQPP	AEEELCSGKP
170	180	190	200	210	220	230	240
FDAFTDLKNG	SLFAFRGQYC	YELDEKAVRP	GYPKLIRDVW	GIEGPIDAAF	TRINCQGKTY	LFKGSQYWRF	EDGVLDPDYP
250	260	270	280	290	300	310	320
RNISDGFDGI	PDNVDAALAL	PAHSYSGRER	VYFFKGKQYW	EYQFQHQPSQ	EECEGSSLSA	VFEHFAMMQR	DSWEDIFELL
330	340	350	360	370	380	390	400
FWGRTSAGTR	QPQFISRDWH	GVPGQVDAAM	AGRIYISGMA	PRPSLAKKQR	FRHRNRKGYR	SQRGHSRGRN	QNSRRPSRAT
410	420	430	440	450	460	470	480
WLSLFSSEES	NLGANNYDDY	RMDWLVPATC	EPIQSVFFFS	GDKYYRVNLR	TRRVDTVDPP	YPRSIAQYWL	GCPAPGHL

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
267	1	823.8888	-28.56	2	33.0	13.2	0	198-212	R.DVWGIEGPIDAAFTR.I	

Detailed Protein Report

Protein 919: transcriptional adapter 3 isoform b [Homo sapiens]

Accession: gi|19743894
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 13.1
MW [kDa]: 41.4
pI: 5.2
Sequence Coverage [%]: 4.6
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MSELKDCPLQ	FHDFKSVDHL	KVCPRYTAVL	ARSEDDGIGI	EELDTLQLEL	ETLLSSASRR	LRVLEAETQI	LTDWQDKKGD
90	100	110	120	130	140	150	160
RRFLKLGRDH	ELGAPPKHGK	PKKQKLEGKA	GHGPGPGPGR	PKSKNLQPKI	QEYEFTDDPI	DVPRIPKNDA	PNRFWASVEP
170	180	190	200	210	220	230	240
YCADITSEEV	RTLEELLKPP	EDEAEHYKIP	PLGKHYSQRW	AQEDLLEEQK	DGARAAAVAD	KKKGLMGPLT	ELDTKDVDAL
250	260	270	280	290	300	310	320
LKKSEAQHEQ	PEDGCPFGAL	TQRLLQALVE	ENIISPMEDS	PIPDMSGKES	GADGASTSPR	NQNKPFSVPH	TKSLESRIKE
330	340	350	360	370			
ELIAQGLLES	EDRPAEDSED	EVLAELRKRQ	AELKALSAHN	RTKKHDLLR			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2846	1	806.4262	-16.33	2	66.0	13.1	1	106-122	K.LEGKAGHGPGPGPGRPK.S	

Detailed Protein Report

Protein 920: histone deacetylase 9 isoform 1 [Homo sapiens]

Accession: gi|17158039
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 13.1
MW [kDa]: 111.2
pI: 6.4
Sequence Coverage [%]: 1.2
No. of unique Peptides: 1

```
        10         20         30         40         50         60         70         80
MHSMISSVDV KSEVPVGLEP ISPLDLRTDL RMMMPVVDPV VREKQLQQEL LLIQQQQQIQ KQLLIAEFQK QHENLTRQHQ

        90        100        110        120        130        140        150        160
AQLQEHIKEL LAIKQQQELL EKEQKLEQQR QEQEVERHRR EQQLPPLRGK DRGRERAVAS TEVKQKLQEF LLSKSATKDT

       170        180        190        200        210        220        230        240
PTNGKNHSVS RHPKLWYTAA HHTSLDQSSP PLSGTSPSYK YTLPGAQDAK DDFPLRKTAS EPNLKVRSRL KQKVAERRSS

       250        260        270        280        290        300        310        320
PLLRRKDGNV VTSFKKRMFE VTESSVSSSS PGSGPSSPNN GPTGSVTENE TSVLPPTPHA EQMVSQQRIL IHEDSMNLLS

       330        340        350        360        370        380        390        400
LYTSPSLPNI TLGLPAVPSQ LNASNSLKEK QKCETQTLRQ GVPLPGQYGG SIPASSSHPH VTLEGKPPNS SHQALLQHLL

       410        420        430        440        450        460        470        480
LKEQMRQQKL LVAGGVPLHP QSPLATKERI SPGIRGTHKL PRHRPLNRTQ SAPLPQSTLA QLVIQQQHQQ FLEKQKQYQQ

       490        500        510        520        530        540        550        560
QIHMNKLLSK SIEQLKQPGS HLEEAEEELQ GDQAMQEDRA PSSGNSTRSD SSACVDDTLG QVGAVKVKEE PVDSDEDAQI

       570        580        590        600        610        620        630        640
QEMESGEQAA FMQQPFLEPT HTRALSVRQA PLAAVGMDGL EKHRLVSRTH SSPAASVLPH PAMDRPLQPG SATGIAYDPL

       650        660        670        680        690        700        710        720
MLKHQCVCGN STTHPEHAGR IQSIWSRLQE TGLLNKCERI QGRKASLEEI QLVHSEHHSL LYGTNPLDGQ KLDPRILLGD

       730        740        750        760        770        780        790        800
DSQKFFSSLP CGGLGVDSDT IWNELHSSGA ARMAVGCVIE LASKVASGEL KNGFAVVRPP GHHAEESTAM GFCFFNSVAI

       810        820        830        840        850        860        870        880
TAKYLRDQLN ISKILIVDLD VHHGNGTQQA FYADPSILYI SLHRYDEGNF FPGSGAPNEV GTGLGEGYNI NIAWTGGLDP

       890        900        910        920        930        940        950        960
PMGDVEYLEA FRTIVKPVAK EFDPDMVLVS AGFDALEGHT PPLGGYKVTA KCFGHLTKQL MTLADGRVVL ALEGGHDLTA

       970        980        990       1000       1010       1020
ICDASEACVN ALLGNELEPL AEDILHQSPN MNAVISLQKI IEIQSMSLKF S
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
819	1	706.2304	-210.02	2	39.7	13.1	1	1000-1011	K.IIEIQSMSLKFS.-	Oxidation: 7

Detailed Protein Report

Protein 921: POTE ankyrin domain family member A isoform 1 [Homo sapiens]

Accession: gi|50897294
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl, Oxidation

Score: 13.1
MW [kDa]: 51.2
pI: 6.2
Sequence Coverage [%]: 2.9
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MVAEVSPKLA	ASPMKKPFGF	RGKMGKWCCC	CFPCCRGSGK	NNMGAWRDHD	DSAFTEPRYH	VRREDLGKLH	RAAWWGEVPR
90	100	110	120	130	140	150	160
ADLIVMLRGP	GINKRDKKKR	TALHLACANG	NSEVVSLLLD	RQCQLHVFDS	KKRTALIKAV	QCQEDECALM	LLQHGTDPNL
170	180	190	200	210	220	230	240
PDMYGNTALH	YAVYNEDKLM	AKTLLLYGAD	IESKNKGGLT	PLLLAVHGQK	QRMVKFLIKK	KANLNALDRF	GRICQLLSDY
250	260	270	280	290	300	310	320
KENQMPNNSS	GNSNPEQDLK	LTSEEEPQRL	KGSENSQHEK	VTQEPDINKD	CDREVEEEMQ	KHGSNNVGLS	ENLTDGAAAG
330	340	350	360	370	380	390	400
NGDGGLVPQR	KSRKHENQQF	PNTEIEEYHR	PEKKSNEKNK	VKSQIHSVDN	LDDITWPSEI	ASEDYDLLFS	NYETFTLLIE
410	420	430	440	450	460		
QLKMDFNDSA	SLSKIQDAVI	SEEHLLELKN	SHYEQLTVEV	EQMENMVHVL	QK		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2257	1	557.1115	-149.12	3	58.1	13.1	1	24-36	K.MGKWCCCCFPCCR.G	Carbamidomethyl: 5, 11; Oxidation: 1

Detailed Protein Report

Protein 922: **transport and Golgi organization protein 6 homolog [Homo sapiens]**

Accession:	gi|153791502	**Score:**	13.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	120.7
Database Date:	2015-11-30	**pI:**	5.7
		Sequence Coverage [%]:	1.2
		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
2043	1	698.2867	-131.01	2	55.4	13.1	0	112-124	R.LAANFNPGKPNPR.T	

Detailed Protein Report

Protein 923: **PREDICTED: FYVE, RhoGEF and PH domain-containing protein 6 isoform X1 [Homo sapiens]**

Accession:	gi|530400569	**Score:**	13.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	155.9
Database Date:	2015-11-30	**pI:**	7.1
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MTSAAEIKKP	PVAPKPKFVV	ANNKPAPPPI	APKPDIVISS	VPQSTKKMKP	AIAPKPKVLK	TSPVREIGQS	PSRKIMLNLE
90	100	110	120	130	140	150	160
GHKQELAEST	DNFNCKYEGN	QSNDYISPMC	SCSSECIHKL	GHRENLCVKQ	LVLEPLEMNE	NLENSKIDET	LTIKTRSKCD
170	180	190	200	210	220	230	240
LYGEKAKNQG	GVVLKASVLE	EELKDALIHQ	MPPFISAQKH	RPTDSPEMNG	GCNSNGQFRI	EFADLSPSPS	SFEKVPDHHS
250	260	270	280	290	300	310	320
CHLQLPSDEC	EHFETCQDDS	EKSNNCFQSS	ELEALENGKR	STLISSDGVS	KKSEVKDLGP	LEIHLVPYTP	KFPTPKPRKT
330	340	350	360	370	380	390	400
RTARLLRQKC	VDTPSESTEE	PGNSDSSSSC	LTENSLKINK	ISVLHQNVLC	KQEQVDKMKL	GNKSELNMES	NSDAQDLVNS
410	420	430	440	450	460	470	480
QKAMCNETTS	FEKMAPSFDK	DSNLSSDSTT	VDGSSMSLAV	DEGTGFIRCT	VSMSLPKQLK	LTCNEHLQSG	RNLGVSAPQM
490	500	510	520	530	540	550	560
QKESVIKEEN	SLRIVPKKPQ	RHSLPATGVL	KKAASEELLE	KSSYPSSEEK	SSEKSLERNH	LQHLCAQNRG	VSSSFDMPKR
570	580	590	600	610	620	630	640
ASEKPVWKLP	HPILPFSGNP	EFLKSVTVSS	NSEPSTALTK	PRAKSLSAMD	VEKCTKPCKD	STKKNSFKKL	LSMKLSICFM
650	660	670	680	690	700	710	720
KSDFQKFWSK	SSQLGDTTTG	HLSSGEQKGI	ESDWQGLLVG	EEKRSKPIKA	YSTENYSLES	QKKRKKSRGQ	TSAANGLRAE
730	740	750	760	770	780	790	800
SLDDQMLSRE	SSSQAPYKSV	TSLCAPEYEN	IRHYEEIPEY	ENLPFIMAIR	KTQELEWQNS	SSMEDADANV	YEVEEPYEAP
810	820	830	840	850	860	870	880
DGQLQLGPRH	QHSSSGASQE	EQNDLGLGDL	PSDEEEIINS	SDEDDVSSES	SKGEPDPLED	KQDEDNGMKS	KVHHIAKEIM
890	900	910	920	930	940	950	960
SSEKVFVDVL	KLLHIDFRDA	VAHASRQLGK	PVIEDRILNQ	ILYYLPQLYE	LNRDLLKELE	ERMLHWTEQQ	RIADIFVKKG
970	980	990	1000	1010	1020	1030	1040
PYLKMYSTYI	KEFDKNIALL	DEQCKKNPGF	AAVVREFEMS	PRCANLALKH	YLLKPVQRIP	QYRLLLTDYL	KNLIEDAGDY
1050	1060	1070	1080	1090	1100	1110	1120
RDTQDALAVV	IEVANHANDT	MKQGDNFQKL	MQIQYSLNGH	HEIVQPGRVF	LKEGILMKLS	RKVMQPRMFF	LFNDALLYTT
1130	1140	1150	1160	1170	1180	1190	1200
PVQSGMYKLN	NMLSLAGMKV	RKPTQEAYQN	ELKIESVERS	FILSASSATE	RDEWLEAISR	AIEEYAKKRI	TFCPSRSLDE
1210	1220	1230	1240	1250	1260	1270	1280
ADSENKEEVS	PLGSKAPIWI	PDTRATMCMI	CTSEFTLTWR	RHHCRACGKI	VCQACSSNKY	GLDYLKNQPA	RVCEHCFQEL
1290	1300	1310	1320	1330	1340	1350	1360
QKLDHQHSPR	IGSPGNHKSP	SSALSSVLHS	IPSGRKQKKI	PAALKEVSAN	TEDSSMSGYL	YRSKGNKKPW	KHFWFVIKNK
1370	1380	1390					
VLYTYAASEV	DRSISGRHNI	VAVLVSSLL					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
867	1	819.8514	-51.08	2	40.4	13.0	0	739-752	K.SVTSLCAPEYENIR.H	Carbamidomethyl: 6

Protein 924: PREDICTED: coiled-coil domain-containing protein 150 isoform X1 [Homo sapiens]

Accession:	gi|578804109	**Score:**	13.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	126.4
Database Date:	2015-11-30	**pI:**	6.6
		Sequence Coverage [%]:	0.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDCKVHMETT	VSRPVLSPTH	INATASETFT	VLQQRMRIVE	EQTSSLRDDL	IMLDFGEKRG	YLEAPDCLED	LDSQKVISPI
90	100	110	120	130	140	150	160
QNEAICAGKT	DILWKNCEFL	VNRMCRLESL	MQSLKMNIFR	LQTEKDLNPQ	KTAFLKDRLN	AIQEEHSKDL	KLLHLEVMNL
170	180	190	200	210	220	230	240
RQQLRAVKEE	EDKAQDEVQR	LTATLKIASQ	TKKNAAIIEE	ELKTTKRKMN	LKIQELRRQL	AQEKYLRESL	EKSASAMLLK
250	260	270	280	290	300	310	320
IQEMGSTVEV	ERKQVHILQQ	NCIALRDSIQ	SAQELLAQEQ	KKKEELEIAT	SQLKSDLTSR	DDLISKLVEE	NKNLQISFNK
330	340	350	360	370	380	390	400
EHEENAYLRS	EIMSLHEASE	KAQVLNDQLT	KKCSELSCML	QTVTMEKARI	IADHQAILQV	EQKMMTQTFQ	EQNLLLDAAH
410	420	430	440	450	460	470	480
ASITNELQTV	QNEKTQLQAH	LDHLILEHNQ	CIQKAQDAEK	RTAVQKELLE	STIARLRGEL	EASMQEKKSL	LEEKERFQRE
490	500	510	520	530	540	550	560
VNKTEKEIVQ	ERCNLEKELA	KNKVDINTLT	HNLQTLEEEN	KHLADQMASL	ELQQVTSDYH	GLAQQKVEKI	TESKNKLAYE
570	580	590	600	610	620	630	640
NGKLQIKVKQ	LEEQVQSFTD	TSLQNDHLRK	MNKYLQTKYA	QVKSILERSK	EELSRTVKCR	NAALKESQKL	KEDLEAVEDR
650	660	670	680	690	700	710	720
ENKKVGNFQR	QLAEAKEDNC	KVTIMLENVL	ASHSKMQGAL	EKVQIELGRR	DSEIAGLKKE	RDLNQQRVQK	LEAEVDQWQA
730	740	750	760	770	780	790	800
RMLVMEDQHN	SEIESLQKAL	GVAREDNRKL	AMSLEQALQT	NNHLQTKLDH	IQEQLESKEL	ERQNLETFKD	RMTEESKVEA
810	820	830	840	850	860	870	880
ELHAERIEAL	RKQFQTERET	TKKVAQREVA	ELKKALDEAN	FRSVEVSRTN	RELRQKLAEL	EKILESNKEK	IKNQKTQIKL
890	900	910	920	930	940	950	960
HLSAKANNAQ	NIERMKQIEK	ELKQMELIKD	QYQKKNYEQS	LSIQRFVCEM	TNLQKEMQML	AKSQYDASVR	NKQQELHLEA
970	980	990	1000	1010	1020	1030	1040
ERKIRQELEN	RCQELEETVR	HLKKCKEATE	NTLKEASVES	EQITANLEEA	HRWFKHRFDG	LQLELTKNRL	QRPSGEDRWQ
1050	1060	1070	1080	1090			
EKDQDVKHDV	MSNQSVLHRW	ERKQNLRPMP	KKYHSEVQRK				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
533	1	524.1612	-224.39	2	36.3	13.0	1	493-501	R.CNLEKELAK.N	

Detailed Protein Report

Protein 925: PREDICTED: glutamate receptor ionotropic, kainate 2 isoform X2 [Homo sapiens]

Accession:	gi|530383627	**Score:**	13.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	96.9
Database Date:	2015-11-30	**pI:**	7.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGAEELAFRF	AVNTINRNRT	LLPNTTLTYD	TQKINLYDSF	EASKKACDQL	SLGVAAIFGP	SHSSSANAVQ	SICNALGVPH
90	100	110	120	130	140	150	160
IQTRWKHQVS	DNKDSFYVSL	YPDFSSLSRA	ILDLVQFFKW	KTVTVVYDDS	TGLIRLQELI	KAPSRYNLRL	KIRQLPADTK
170	180	190	200	210	220	230	240
DAKPLLKEMK	RGKEFHVIFD	CSHEMAAGIL	KQALAMGMMT	EYYHYIFTTL	DLFALDVEPY	RYSGVNMTGF	RILNTENTQV
250	260	270	280	290	300	310	320
SSIIEKWSME	RLQAPPKPDS	GLLDGFMTTD	AALMYDAVHV	VSVAVQQFPQ	MTVSSLQCNR	HKPWRFGTRF	MSLIKEAHWE
330	340	350	360	370	380	390	400
GLTGRITFNK	TNGLRTDFDL	DVISLKEEGL	EKIGTWDPAS	GLNMTESQKG	KPANITDSLS	NRSLIVTTIL	EEPYVLFKKS
410	420	430	440	450	460	470	480
DKPLYGNDRF	EGYCIDLLRE	LSTILGFTYE	IRLVEDGKYG	AQDDANGQWN	GMVRELIDHK	ADLAVAPLAI	TYVREKVIDF
490	500	510	520	530	540	550	560
SKPFMTLGIS	ILYRKPNGTN	PGVFSFLNPL	SPDIWMYILL	AYLGVSCVLF	VIARFSPYEW	YNPHPCNPDS	DVVENNFTLL
570	580	590	600	610	620	630	640
NSFWFGVGAL	MQQGSELMPK	ALSTRIVGGI	WWFFTLIIIS	SYTANLAAFL	TVERMESPID	SADDLAKQTK	IEYGAVEDGA
650	660	670	680	690	700	710	720
TMTFFKKSKI	STYDKMWAFM	SSRRQSVLVK	SNEEGIQRVL	TSDYAFLMES	TTIEFVTQRN	CNLTQIGGLI	DSKGYGVGTP
730	740	750	760	770	780	790	800
MGSPYRDKIT	IAILQLQEEG	KLHMMKEKWW	RGNGCPEEES	KEASALGVQN	IGGIFIVLAA	GLVLSVFVAV	GEFLYKSKKN
810	820	830	840	850	860		
AQLEKRSFCS	AMVEELRMSL	KCQRRLKHKP	QAPVIVKTEE	VINMHTFNDR	RLPGKETMA		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2002	1	704.2753	-62.09	2	55.1	13.0	0	615-627	R.MESPIDSADDLAK.Q	Oxidation: 1

Detailed Protein Report

Protein 926: 6-phosphogluconate dehydrogenase, decarboxylating [Homo sapiens]

Accession:	gi|40068518	**Score:**	13.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	53.1
Database Date:	2015-11-30	**pI:**	7.0
		Sequence Coverage [%]:	4.1
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MAQADIALIG LAVMGQNLIL NMNDHGFVVC AFNRTVSKVD DFLANEAKGT KVVGAQSLKE MVSKLKKPRR IILLVKAGQA
        90        100        110        120        130        140        150        160
VDDFIEKLVP LLDTGDIIID GGNSEYRDTT RRCRDLKAKG ILFVGSGVSG GEEGARYGPS LMPGGNKEAW PHIKTIFQGI
       170        180        190        200        210        220        230        240
AAKVGTGEPC CDWVGDEGAG HFVKMVHNGI EYGDMQLICE AYHLMKDVLG MAQDEMAQAF EDWNKTELDS FLIEITANIL
       250        260        270        280        290        300        310        320
KFQDTDGKHL LPKIRDSAGQ KGTGKWTAIS ALEYGVPVTL IGEAVFARCL SSLKDERIQA SKKLKGPQKF QFDGDKKSFL
       330        340        350        360        370        380        390        400
EDIRKALYAS KIISYAQGFM LLRQAATEFG WTLNYGGIAL MWRGGCIIRS VFLGKIKDAF DRNPELQNLL LDDFFKSAVE
       410        420        430        440        450        460        470        480
NCQDSWRRAV STGVQAGIPM PCFTTALSFY DGYRHEMLPA SLIQAQRDYF GAHTYELLAK PGQFIHTNWT GHGGTVSSSS
       490
YNA
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2781	1	1080.6827	110.97	2	65.2	13.0	0	88-107	K.LVPLLDTGDIIIDGGNSEYR.D	

Detailed Protein Report

Protein 927: PREDICTED: transmembrane protein 50A isoform X2 [Homo sapiens]

Accession:	gi|530360988	**Score:**	13.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	14.0
Database Date:	2015-11-30	**pI:**	4.8
		Sequence Coverage [%]:	21.4
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MSGFLEGLRC SECIDWGEKR NTIASIAAGV LFFTGWWIII DAAVIYPTMK DFNHSYHACG VIATIAFLMI NAVSNGQVRG
        90        100        110        120        130
DSYSEGCLGQ TEKDIVYPGI AVFFQNAFIF FGGLVFKFGR TEDLWQ
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1914	1	1023.9081	23.01	3	53.8	13.0	1	94-120	K.DIVYPGIAVFFQNAFIFFGGLVFKFGR.T	

Detailed Protein Report

Protein 928: transmembrane protein 14B isoform b [Homo sapiens]

Accession:	gi|189181734	**Score:**	13.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	8.6
Database Date:	2015-11-30	**pI:**	10.0
		Sequence Coverage [%]:	12.5
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MEKPLFPLVP LHWFGFGYTA LVVSGGIVGY VKTAATSVTF VGVMGMRSYY YGKFMPVGLI AGASLLMAAK VGVRMLMTSD
        90
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1706	1	1108.6371	79.54	1	51.3	13.0	1	71-80	K.VGVRMLMTSD.-	

Detailed Protein Report

Protein 929: PREDICTED: neurobeachin isoform X6 [Homo sapiens]

Accession:	gi|578824845	**Score:**	13.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	212.6
Database Date:	2015-11-30	**pI:**	5.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	0.6
		No. of unique Peptides:	1

Quantitation

MD:MU	**Median:** 0.47	**CV:** 0.00 %	**No. of Peptides:** 1

Detailed Protein Report

10	20	30	40	50	60	70	80
MASEKPGPGP	GLEPQPVGLI	AVGAAGGGGG	GSGGGGTGGS	GMGELRGASG	SGSVMLPAGM	INPSVPIRNI	RMKFAVLIGL
90	100	110	120	130	140	150	160
IQVGEVSNRD	IVETVLNLLV	GGEFDLEMNF	IIQDAESITC	MTELLEHCDV	TCQAEIWSMF	TAILRKSVRN	LQTSTEVGLI
170	180	190	200	210	220	230	240
EQVLLKMSAV	DDMIADLLVD	MLGVLASYSI	TVKELKLLFS	MLRGESGIWP	RHAVKLLSVL	NQMPQRHGPD	TFFNFPGCSA
250	260	270	280	290	300	310	320
AAIALPPIAK	WPYQNGFTLN	TWFRMDPLNN	INVDKDKPYL	YCFRTSKGVG	YSAHFVGNCL	IVTSLKSKGK	GFQHCVKYDF
330	340	350	360	370	380	390	400
QPRKWYMISI	VHIYNRWRNS	EIRCYVNGQL	VSYGDMAWHV	NTNDSYDKCF	LGSSETADAN	RVFCGQLGAV	YVFSEALNPA
410	420	430	440	450	460	470	480
QIFAIHQLGP	GYKSTFKFKS	ESDIHLAEHH	KQVLYDGKLA	SSIAFTYNAK	ATDAQLCLES	SPKENASIFV	HSPHALMLQD
490	500	510	520	530	540	550	560
VKAIVTHSIH	SAIHSIGGIQ	VLFPLFAQLD	NRQLNDSQVE	TTVCATLLAF	LVELLKSSVA	MQEQMLGGKG	FLVIGYLLEK
570	580	590	600	610	620	630	640
SSRVHITRAV	LEQFLSFAKY	LDGLSHGAPL	LKQLCDHILF	NPAIWIHTPA	KVQLSLYTYL	SAEFIGTATI	YTTIRRVGTV
650	660	670	680	690	700	710	720
LQLMHTLKYY	YWVINPADSS	GITPKGLDGP	RPSQKEIISL	RAFMLLFLKQ	LILKDRGVKE	DELQSILNYL	LTMHEDENIH
730	740	750	760	770	780	790	800
DVLQLLVALM	SEHPASMIPA	FDQRNGIRVI	YKLLASKSES	IWVQALKVLG	YFLKHLGHKR	KVEIMHTHSL	FTLLGERLML
810	820	830	840	850	860	870	880
HTNTVTVTTY	NTLYEILTEQ	VCTQVVHKPH	PEPDSTVKIQ	NPMILKVVAT	LLKNSTPSAE	LMEVRRLFLS	DMIKLFSNSR
890	900	910	920	930	940	950	960
ENRRCLLQCS	VWQDWMFSLG	YINPKNSEEQ	KITEMVYNIF	RILLYHAIKY	EWGGWRVWVD	TLSIAHSKVT	YEAHKEYLAK
970	980	990	1000	1010	1020	1030	1040
MYEEYQRQEE	ENIKKGKKGN	VSTISGLSSQ	TTGAKGGMEI	REIEDLSQSQ	SPESETDYPV	STDTRDLLMS	TKVSDDILGN
1050	1060	1070	1080	1090	1100	1110	1120
SDRPGSGVHV	EVHDLLVDIK	AEKVEATEVK	LDDMDLSPET	LVGGENGALV	EVESLLDNVY	SAAVEKLQNN	VHGSVGIIKK
1130	1140	1150	1160	1170	1180	1190	1200
NEEKDNGPLI	TLADEKEDLP	NSSTSFLFDK	IPKQEEKLLP	ELSSNHIIPN	IQDTQVHLGV	SDDLGLLAHM	TGSVDLTCTS
1210	1220	1230	1240	1250	1260	1270	1280
SIIEEKEFKI	HTTSDGMSSI	SERDLASSTK	GLEYAEMTAT	TLETESSSSK	IVPNIDAGSI	ISDTERSDDG	KESGKEIRKI
1290	1300	1310	1320	1330	1340	1350	1360
QTTTTTQAVQ	GRSITQQDRD	LRVDLGFRGM	PMTEEQRRQF	SPGPRTTMFR	IPEFKWSPMH	QRLLTDLLFA	LETDVHVWRS
1370	1380	1390	1400	1410	1420	1430	1440
HSTKSVMDFV	NSNENIIFVH	NTIHLISQMV	DNIIIACGGI	LPLLSAATSP	TGSKTELENI	EVTQGMSAET	AVTFLSRLMA
1450	1460	1470	1480	1490	1500	1510	1520
MVDVLVFASS	LNFSEIEAEK	NMSSGGLMRQ	CLRLVCCVAV	RNCLECRQRQ	RDRGNKSSHG	SSKPQEVPQS	VTATAASKTP
1530	1540	1550	1560	1570	1580	1590	1600
LENVPGNLSP	IKDPDRLLQD	VDINRLRAVV	FRDVDDSKQA	QFLALAVVYF	ISVLMVSKYR	DILEPQRETT	RTGSQPGRNI
1610	1620	1630	1640	1650	1660	1670	1680
RQEINSPTST	VVVIPSIPHP	SLNHGFLAKL	IPEQSFGHSF	YKETPAAFPD	TIKEKETPTP	GEDIQVESSI	PHTDSGIGEE
1690	1700	1710	1720	1730	1740	1750	1760
QVASILNGAE	LETSTGPDAM	SELLSTLSSE	VKKSQESLTE	NPSETLKPAT	SISSISQTKG	INVKEILKSL	VAAPVEIAEC
1770	1780	1790	1800	1810	1820	1830	1840
GPEPIPYPDP	ALKRETQAIL	PMQFHSFDRS	VVVPVKKPPP	GSLAVTTVGA	TTAGSGLPTG	STSNIFAATG	ATPKSMINTT
1850	1860	1870	1880	1890	1900	1910	1920
GAVDSGSSSS	SSSSSFVNGA	TSKNLPAVQT	VAPMPEDSAE	NMSITAKLER	ALEKVAPLLR	EIFVDFAPFL	SRTLLGSHGQ
1930	1940						
ELLIEEILVS	GGSL						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
1961	1	710.2813	-128.66	2	54.4	13.0	1	1470-1481	R.QCLRLVCCVAVR.N	Carbamidomethyl: 8	MD:MU	0.47

Detailed Protein Report

Protein 930: **PREDICTED: eukaryotic translation initiation factor 5B isoform X1 [Homo sapiens]**

Accession:	gi|530368915	**Score:**	13.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	138.6
Database Date:	2015-11-30	**pI:**	5.3
		Sequence Coverage [%]:	1.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGKKQKNKSE	DSTKDDIDLD	ALAAEIEGAG	AAKEQEPQKS	KGKKKKEKKK	QDFDEDDILK	ELEELSLEAQ	GIKADRETVA
90	100	110	120	130	140	150	160
VKPTENNEEE	FTSKDKKKKG	QKGKKQSFDD	NDSEELEDKD	SKSKKTAKPK	VEMYSGSDDD	DDFNKLPKKA	KGKAQKSNKK
170	180	190	200	210	220	230	240
WDGSEEDEDN	SKKIKERSRI	NSSGESGDES	DEFLQSRKGQ	KKNQKNKPGP	NIESGNEDDD	ASFKIKTVAQ	KKAEKKERER
250	260	270	280	290	300	310	320
KKRDEEKAKL	RKLKEKEELE	TGKKDQSKQK	ESQRKFEEET	VKSKVTVDTG	VIPASEEKAE	TPTAAEDDNE	GDKKKKDKKK
330	340	350	360	370	380	390	400
KKGEKEEKEK	EKKKGPSKAT	VKAMQEALAK	LKEEEERQKR	EEEERIKRLE	ELEAKRKEEE	RLEQEKRERK	KQKEKERKER
410	420	430	440	450	460	470	480
LKKEGKLLTK	SQREARARAE	ATLKLLQAQG	VEVPSKDSLP	KKRPIYEDKK	RKKIPQQLES	KEVSESMELC	AAVEVMEQGV
490	500	510	520	530	540	550	560
PEKEETPPPV	EPEEEDTEDA	GLDDWEAMAS	DEETEKVEGN	KVHIEVKENP	EEEEEEEEEE	EEDEESEEEE	EEEGESEGSE
570	580	590	600	610	620	630	640
GDEEDEKVSD	EKDSGKTLDK	KPSKEMSSDS	EYDSDDDRTK	EERAYDKAKR	RIEKRRLEHS	KNVNTEKLRA	PIICVLGHVD
650	660	670	680	690	700	710	720
TGKTKILDKL	RHTHVQDGEA	GGITQQIGAT	NVPLEAINEQ	TKMIKNFDRE	NVRIPGMLII	DTPGHESFSN	LRNRGSSLCD
730	740	750	760	770	780	790	800
IAILVVDIMH	GLEPQTIESI	NLLKSKKCPF	IVALNKIDRL	YDWKKSPDSD	VAATLKKQKK	NTKDEFEERA	KAIIVEFAQQ
810	820	830	840	850	860	870	880
GLNAALFYEN	KDPRTFVSLV	PTSAHTGDGM	GSLIYLLVEL	TQTMLSKRLA	HCEELRAQVM	EVKALPGMGT	TIDVILINGR
890	900	910	920	930	940	950	960
LKEGDTIIVP	GVEGPIVTQI	RGLLLPPPMK	ELRVKNQYEK	HKEVEAAQGV	KILGKDLEKT	LAGLPLLVAY	KEDEIPVLKD
970	980	990	1000	1010	1020	1030	1040
ELIHELKQTL	NAIKLEEKGV	YVQASTLGSL	EALLEFLKTS	EVPYAGINIG	PVHKKDVMKA	SVMLEHDPQY	AVILAFDVRI
1050	1060	1070	1080	1090	1100	1110	1120
ERDAQEMADS	LGVRIFSAEI	IYHLFDAFTK	YRQDYKKQKQ	EEFKHIAVFP	CKIKILPQYI	FNSRDPIVMG	VTVEAGQVKQ
1130	1140	1150	1160	1170	1180	1190	1200
GTPMCVPSKN	FVDIGIVTSI	EINHKQVDVA	KKGQEVCVKI	EPIPGESPKM	FGRHFEATDI	LVSKISRQSI	DALKDWFRDE
1210	1220						
MQKSDWQLIV	ELKKVFEII						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
129	1	680.3267	-74.77	2	31.0	13.0	2	765-777	K.KSPDSDVAATLKK.Q	

Detailed Protein Report

Protein 931: **vascular endothelial growth factor C preproprotein [Homo sapiens]**

Accession:	gi|4885653	**Score:**	13.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	46.9
Database Date:	2015-11-30	**pI:**	9.2
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.1
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MHLLGFFSVA CSLLAAALLP GPREAPAAAA AFESGLDLSD AEPDAGEATA YASKDLEEQL RSVSSVDELM TVLYPEYWKM

        90        100        110        120        130        140        150        160
YKCQLRKGGW QHNREQANLN SRTEETIKFA AAHYNTEILK SIDNEWRKTQ CMPREVCIDV GKEFGVATNT FFKPPCVSVY

       170        180        190        200        210        220        230        240
RCGGCCNSEG LQCMNTSTSY LSKTLFEITV PLSQGPKPVT ISFANHTSCR CMSKLDVYRQ VHSIIRRSLP ATLPQCQAAN

       250        260        270        280        290        300        310        320
KTCPTNYMWN NHICRCLAQE DFMFSSDAGD DSTDGFHDIC GPNKELDEET CQCVCRAGLR PASCGPHKEL DRNSCQCVCK

       330        340        350        360        370        380        390        400
NKLFPSQCGA NREFDENTCQ CVCKRTCPRN QPLNPGKCAC ECTESPQKCL LKGKKFHHQT CSCYRRPCTN RQKACEPGFS

       410        420
YSEEVCRCVP SYWKRPQMS
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1178	3	565.6313	-245.62	2	44.4	13.0	1	211-219	R.CMSKLDVYR.Q	Oxidation: 2

Detailed Protein Report

Protein 932: stromal interaction molecule 2 isoform 2 precursor [Homo sapiens]

Accession:	gi|281182822	**Score:**	13.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	83.9
Database Date:	2015-11-30	**pI:**	6.3
		Sequence Coverage [%]:	2.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLVLGLLVAG	AADGCELVPR	HLRGRRATGS	AATAASSPAA	AAGDSPALMT	DPCMSLSPPC	FTEEDRFSLE	ALQTIHKQMD
90	100	110	120	130	140	150	160
DDKDGGIEVE	ESDEFIREDM	KYKDATNKHS	HLHREDKHIT	IEDLWKRWKT	SEVHNWTLED	TLQWLIEFVE	LPQYEKNFRD
170	180	190	200	210	220	230	240
NNVKGTTLPR	IAVHEPSFMI	SQLKISDRSH	RQKLQLKALD	VVLFGPLTRP	PHNWMKDFIL	TVSIVIGVGG	CWFAYTQNKT
250	260	270	280	290	300	310	320
SKEHVAKMMK	DLESLQTAEQ	SLMDLQERLE	KAQEENRNVA	VEKQNLERKM	MDEINYAKEE	ACRLRELREG	AECELSRRQY
330	340	350	360	370	380	390	400
AEQELEQVRM	ALKKAEKEFE	LRSSWSVPDA	LQKWLQLTHE	VEVQYYNIKR	QNAEMQLAIA	KDEAEKIKKK	RSTVFGTLHV
410	420	430	440	450	460	470	480
AHSSSLDEVD	HKILEAKKAL	SELTTCLRER	LFRWQQIEKI	CGFQIAHNSG	LPSLTSSLYS	DHSWVVMPRV	SIPPYPIAGG
490	500	510	520	530	540	550	560
VDDLDEDTPP	IVSQFPGTMA	KPPGSLARSS	SLCRSRRSIV	PSSPQPQRAQ	LAPHAPHPSH	PRHPHHPQHT	PHSLPSPDPD
570	580	590	600	610	620	630	640
ILSVSSCPAL	YRNEEEEEAI	YFSAEKQWEV	PDTASECDSL	NSSIGRKQSP	PLSLEIYQTL	SPRKISRDEV	SLEDSSRGDS
650	660	670	680	690	700	710	720
PVTVDVSWGS	PDCVGLTETK	SMIFSPASKV	YNGILEKSCS	MNQLSSGIPV	PKPRHTSCSS	AGNDSKPVQE	APSVARISSI
730	740	750					
PHDLCHNGEK	SKKPSKIKSL	FKKKSK					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1585	1	942.4058	-100.34	2	49.7	13.0	1	661-677	K.SMIFSPASKVYNGILEK.S	

Detailed Protein Report

Protein 933: **kynurenine/alpha-aminoadipate aminotransferase, mitochondrial isoform b [Homo sapiens]**

Accession:	gi|7705897	**Score:**	12.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	47.3
Database Date:	2015-11-30	**pI:**	6.5
		Sequence Coverage [%]:	3.1
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|557878725	refseq_human (refseq_human_20140103.fasta)	kynurenine/alpha-aminoadipate aminotransferase, mitochondrial isoform b [Homo sapiens]
gi|33469970	refseq_human (refseq_human_20140103.fasta)	kynurenine/alpha-aminoadipate aminotransferase, mitochondrial isoform b [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MNYARFITAA SAARNPSPIR TMTDILSRGP KSMISLAGGL PNPNMFPFKT AVITVENGKT IQFGEEMMKR ALQYSPSAGI
        90        100        110        120        130        140        150        160
PELLSWLKQL QIKLHNPPTI HYPPSQGQMD LCVTSGSQQG LCKVFEMIIN PGDNVLLDEP AYSGTLQSLH PLGCNIINVA
       170        180        190        200        210        220        230        240
SDESGIVPDS LRDILSRWKP EDAKNPQKNT PKFLYTVPNG NNPTGNSLTS ERKKEIYELA RKYDFLIIED DPYYFLQFNK
       250        260        270        280        290        300        310        320
FRVPTFLSMD VDGRVIRADS FSKIISSGLR IGFLTGPKPL IERVILHIQV STLHPSTFNQ LMISQLLHEW GEEGFMAHVD
       330        340        350        360        370        380        390        400
RVIDFYSNQK DAILAADKW LTGLAEWHVP AAGMFLWIKV KGINDVKELI EEKAVKMGVL MLPGNAFYVD SSAPSPYLRA
       410        420        430
SFSSASPEQM DVAFQVLAQL IKESL
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
437	1	706.4564	114.32	2	34.8	12.9	1	2-14	M.NYARFITAASAAR.N	

Detailed Protein Report

Protein 934: protein AATF [Homo sapiens]

Accession:	gi|7657013	**Score:**	12.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	63.1
Database Date:	2015-11-30	**pI:**	4.7
		Sequence Coverage [%]:	2.7
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MAGPQPLALQ LEQLLNPRPS EADPEADPEE ATAARVIDRF DEGEDGEGDF LVVGSIRKLA SASLLDTDKR YCGKTTSRKA

        90        100        110        120        130        140        150        160
WNEDHWEQTL PGSSDEEISD EEGSGDEDSE GLGLEEYDED DLGAAEEQEC GDHRESKKSR SHSAKTPGFS VQSISDFEKF

       170        180        190        200        210        220        230        240
TKGMDDLGSS EEEEDEESGM EEGDDAEDSQ GESEEDRAGD RNSEDDGVVM TFSSVKVSEE VEKGRAVKNQ IALWDQLLEG

       250        260        270        280        290        300        310        320
RIKLQKALLT TNQLPQPDVF PLFKDKGGPE FSSALKNSHK ALKALLRSLV GLQEELLFQY PDTRYLVDGT KPNAGSEEIS

       330        340        350        360        370        380        390        400
SEDDELVEEK KQQRRRVPAK RKLEMEDYPS FMAKRFADFT VYRNRTLQKW HDKTKLASGK LGKGFGAFER SILTQIDHIL

       410        420        430        440        450        460        470        480
MDKERLLRRT QTKRSVYRVL GKPEPAAQPV PESLPGEPEI LPQAPANAHL KDLDEEIFDD DDFYHQLLRE LIERKTSSLD

       490        500        510        520        530        540        550        560
PNDQVAMGRQ WLAIQKLRSK IHKKVDRKAS KGRKLRFHVL SKLLSFMAPI DHTTMNDDAR TELYRSLFGQ LHPPDEGHGD

       570
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
501	1	599.6854	22.13	3	35.9	12.9	1	229-243	K.NQIALWDQLLEGRIK.L	

Detailed Protein Report

Protein 935: **PREDICTED: ligand-dependent nuclear receptor-interacting factor 1 isoform X2 [Homo sapiens]**

Accession:	gi|578799447	**Score:**	12.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	69.2
Database Date:	2015-11-30	**pI:**	10.3
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSNNLRRVFL	KPAEENSGNA	SRCVSGCMYQ	VVQTIGSDGK	NLLQLLPIPK	SSGNLIPLVQ	SSVMSDALKG	NTGKPVQVTF
90	100	110	120	130	140	150	160
QTQISSSSTS	ASVQLPIFQP	ASSSNYFLTR	TVDTSEKGRV	TSVGTGNFSS	SVSKVQSHGV	KIDGLTMQTF	AVPPSTQKDS
170	180	190	200	210	220	230	240
SFIVVNTQSL	PVTVKSPVLP	SGHHLQIPAH	AEVKSVPASS	LPPSVQQKIL	ATATTSTSGM	VEASQMPTVI	YVSPVNTVKN
250	260	270	280	290	300	310	320
VVTKNFQNIY	PKPVTEIAKP	VILNTTQIPK	NVATETQLKG	GQHSQAAPVK	WIFQDNLQPF	TPSLVPVKSS	NNVASKILKT
330	340	350	360	370	380	390	400
FVDRKNLGDN	TINMPPLSTI	DPSGTRSKNM	PIKDNALVMF	NGKVYLLAKK	GTDVLPSQID	QQNSVSPDTP	VRKDTLQTVS
410	420	430	440	450	460	470	480
SSPVTEISRE	VVNIVLAKSK	SSQMETKSLS	NTQLASMANL	RAEKNKVEKP	SPSTTNPHMN	QSSNYLKQSK	TLFTNPIFPV
490	500	510	520	530	540	550	560
GFSTGHNAPR	KVTAVIYARK	GSVLQSIEKI	SSSVDATTVT	SQQCVFRDQE	PKIHNEMAST	SDKGAQGRND	KKDSQGRSNK
570	580	590	600	610	620	630	640
ALHLKSDAEF	KKIFGLTKDL	RVCLTRIPDH	LTSGEGFDSF	SSLVKSGTYK	ETEFMVKEGE	RKQVAVRGED	LAIYRRREK

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
451	1	562.6268	-261.41	2	35.0	12.9	0	354-363	K.DNALVMFNGK.V	Oxidation: 6

Detailed Protein Report

Protein 936: PREDICTED: run domain Beclin-1 interacting and cysteine-rich containing protein isoform X5 [Homo sapiens]

Accession:	gi|578807915	**Score:**	12.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	93.5
Database Date:	2015-11-30	**pI:**	5.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.9
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578807917	refseq_human (refseq_human_20140103.fasta)	PREDICTED: run domain Beclin-1 interacting and cysteine-rich containing protein isoform X6 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MLQCLEAVEQ NNPRLLAQID ASMFARKHES PLLVTKSQSL TALPSSTYTP PNSYAQHSYF GSFSSLHQSV PNNGSERRST
        90        100        110        120        130        140        150        160
SFPLSGPPRK PQESRGHVSP AEDQTIQAPP VSVSALARDS PLTPNEMSSS TLTSPIEASW VSSQNDSPGD ASEGPEYLAI
       170        180        190        200        210        220        230        240
GNLDPRGRTA SCQSHSSNAE SSSSNLFSSS SSQKPDSAAS SLGDQEGGGE SQLSSVLRRS SFSEGQTLTV TSGAKKSHIR
       250        260        270        280        290        300        310        320
SHSDTSIASR GAPGGPRNIT IIVEDPIAES CNDKAKLRGP LPYSGQSSEV STPSSLYMEY EGGRYLCSGE GMFRRPSEGQ
       330        340        350        360        370        380        390        400
SLISYLSEQD FGSCADLEKE NAHFSISESL IAAIELMKCN MMSQCLEEEE VEEEDSDREI QELKQKIRLR RQQIRTKNLL
       410        420        430        440        450        460        470        480
PMYQEAEHGS FRVTSSSSQF SSRDSAQLSD SGSADEVDEF EIQDGSEGSN LTHISKNGLS VSLASMFSDA DIRRNTASSS
       490        500        510        520        530        540        550        560
KSFVSSQSFS HCFLHSTSAE AVAMGLLKQF EGMQLPAASE LEWLVPEHDA PQKLLPIPDS LPISPDDGQH ADIYKLRIRV
       570        580        590        600        610        620        630        640
RGNLEWAPPR PQIIFNVHPA PTRKIAVAKQ NYRCAGCGIR TDPDYIKRLR YCEYLGKYFC QCCHENAQMA IPSRVLRKWD
       650        660        670        680        690        700        710        720
FSKYYVSNFS KDLLIKIWND PLFNVQDINS ALYRKVKLLN QVRLLRVQLC HMKNMFKTCR LAKELLDSFD TVPGHLTEDL
       730        740        750        760        770        780        790        800
HLYSLNDLTA TRKGELGPRL AELTRAGATH VERCMLCQAK GFICEFCQNE DDIIFPFELH KCRTCEECKA CYHKACFKSG
       810        820        830        840        850
SCPRCERLQA RREALARQSL ESYLSDYEEE PAEALALEAA VLEAT
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1246	1	660.7639	71.36	3	45.2	12.9	2	678-693	K.LLNQVRLLRVQLCHMK.N	Oxidation: 15

Detailed Protein Report

Protein 937: transformer-2 protein homolog beta isoform 2 [Homo sapiens]

Accession:	gi|345197228	**Score:**	12.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	21.9
Database Date:	2015-11-30	**pI:**	10.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	11.2
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578807655	refseq_human (refseq_human_20140103.fasta)	PREDICTED: transformer-2 protein homolog beta isoform X2 [Homo sapiens]
gi|530375128	refseq_human (refseq_human_20140103.fasta)	PREDICTED: transformer-2 protein homolog beta isoform X1 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MSTRRRHVGN RANPDPNCCL GVFGLSLYTT ERDLREVFSK YGPIADVSIV YDQQSRRSRG FAFVYFENVD DAKEAKERAN
        90        100        110        120        130        140        150        160
GMELDGRRIR VDFSITKRPH TPTPGIYMGR PTYGSSRRRD YYDRGYDRGY DDRDYYSRSY RGGGGGGGGW RAAQDRDQIY
       170        180        190
RRRSPSPYYS RGGYRSRSRS RSYSPRRY
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
237	1	1202.1810	60.23	2	32.7	12.9	1	98-118	K.RPHTPTPGIYMGRPTYGSSRR.R	Oxidation: 11

Detailed Protein Report

Protein 938: protein FAM71C [Homo sapiens]

Accession:	gi|23503301	**Score:**	12.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	27.5
Database Date:	2015-11-30	**pI:**	6.7
		Sequence Coverage [%]:	10.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEDCCMLPYY	TAQSSPAMGM	FNTSMGKLQR	QLYKGEYTIF	RYAPMFESDF	IQISKRGEVI	DVHNRARMVT	MGIVRTSPCL
90	100	110	120	130	140	150	160
TLPDVMLLAR	PAAVCDNARC	GPATQKRESP	PAEILELTRL	LPLMFVKITI	HNSVKKQLHL	KLATGRSFYL	QLCPPSDASE
170	180	190	200	210	220	230	240
DLFVHWENLV	YILRPPVEAY	SDTRAILAGN	TLDSSVLEEV	QRSPVGYAMK	FCEEKEQFRI	SRLHMNAEMF	GSTYCDYTIE
250							
I							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1606	1	1052.1622	9.14	3	49.8	12.9	2	216-241	K.EQFRISRLHMNAEMFGSTYCDYTIEI.-	

BRUKER

Detailed Protein Report

Protein 939: PREDICTED: interleukin-20 receptor subunit beta isoform X1 [Homo sapiens]

Accession:	gi|578807489	**Score:**	12.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	29.6
Database Date:	2015-11-30	**pI:**	5.2
Modification(s):	Oxidation	**Sequence Coverage [%]:**	8.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MKHLLMWSPV	IAPGETVYYS	VEYQGEYESL	YTSHIWIPSS	WCSLTEGPEC	DVTDDITATV	PYNLRVRATL	GSQTSAWSIL
90	100	110	120	130	140	150	160
KHPFNRNSTI	LTRPGMEITK	DGFHLVIELE	DLGPQFEFLV	AYWRREPGAE	EHVKMVRSGG	IPVHLETMEP	GAAYCVKAQT
170	180	190	200	210	220	230	240
FVKAIGRYSA	FSQTECVEVQ	GEAIPLVLAL	FAFVGFMLIL	VVVPLFVWKM	GRLLQYSCCP	VVVLPDTLKI	TNSPQKLISC
250	260	270					
RREEVDACAT	AVMSPEELLR	AWIS					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2772	1	826.4371	39.66	3	66.0	12.9	1	135-157	K.MVRSGGIPVHLETMEPGAAYCVK.A	Oxidation: 1, 14

Detailed Protein Report

Protein 940: PREDICTED: autoimmune regulator isoform X1 [Homo sapiens]

Accession:	gi|530419216	**Score:**	12.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	36.5
Database Date:	2015-11-30	**pI:**	6.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	8.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MWLVYSSGAP	GTQQPARNRV	FFPIGMAPGG	VCWRPDGWGT	GGQGRISGPG	SMGAGQRLGS	SGTQRCCWGS	CFGKEVALRR
90	100	110	120	130	140	150	160
VLHPSPVCMG	VSCLCQKNED	ECAVCRDGGE	LICCDGCPRA	FHLACLSPPL	REIPSGTWRC	SSCLQATVQE	VQPRAEEPRP
170	180	190	200	210	220	230	240
QEPPVETPLP	PGLRSAGEEV	RGPPGEPLAG	MDTTLVYKHL	PAPPSAAPLP	GLDSSALHPL	LCVGPEGQQN	LAPGARCGVC
250	260	270	280	290	300	310	320
GDGTDVLRCT	HCAAAFHWRC	HFPAGTSRPG	TGLRCRSCSG	DVTPAPVEGV	LAPSPARLAP	GPAKDDTASH	EPALHRDDLE
330	340	350					
SLLSEHTFDG	ILQWAIQSMA	RPAAPFPS					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1699	1	1011.4214	-66.62	3	51.2	12.9	1	18-45	R.NRVFFPIGMAPGGVCWRPDGWGTGGQGR.I	Carbamidomethyl: 15

Detailed Protein Report

Protein 941: PREDICTED: solute carrier family 35 member B1 isoform X2 [Homo sapiens]

Accession: gi|578830240
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 12.9
MW [kDa]: 43.2
pI: 10.3
Sequence Coverage [%]: 6.9
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MRPLPPVGDV	RLELSPPPPL	LPVPVVSGSP	VGSSGRLMAS	SSSLVPDRLR	LPLCFLGVFV	CYFYYGILQE	KMTRVGPLLV
90	100	110	120	130	140	150	160
LPDACKQPIR	PRPWCHSRNT	VSSCLGTRGK	YGEGAKQETF	TFALTLVFIQ	CVINAVFAKI	LIQFFDTARV	DRTRSWLYAA
170	180	190	200	210	220	230	240
CSISYLGAMV	SSNSALQFVN	YPTQVLGKSC	KPIPVMLLGV	TLLKKKYPLA	KYLCVLLIVA	GVALFMYKPK	KVVGIEEHTV
250	260	270	280	290	300	310	320
GYGELLLLLS	LTLDGLTGVS	QDHMRAHYQT	GSNHMMLNIN	LWSTLLLGMG	ILFTGELWEF	LSFAERYPAI	IYNILLFGLT
330	340	350	360	370	380	390	400
SALGQSFIFM	TVVYFGPLTC	SIITTTRKFF	TILASVILFA	NPISPMQWVG	TVLVFLGLGL	DAKFGKGAKK	TSH

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2847	1	1080.8719	-36.05	3	66.0	12.9	2	72-98	K.MTRVGPLLVLPDACKQPIRPRPWCHSR.N	Carbamidomethyl: 14, 24

Detailed Protein Report

Protein 942: PREDICTED: glycerol-3-phosphate transporter isoform X4 [Homo sapiens]

Accession:	gi|530419282	**Score:**	12.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	45.6
Database Date:	2015-11-30	**pI:**	9.7
		Sequence Coverage [%]:	2.6
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 0.87	**CV:** 0.00 %	**No. of Peptides:**	1

10	20	30	40	50	60	70	80
MLASGAFTAL	FGLGYFYNIH	SFGFYVVTQV	INGLVQTTGW	PSVVTCLGNW	FGKGRRGLIM	GVWNSHTSVG	NILGSLIAGY
90	100	110	120	130	140	150	160
WVSTCWGLSF	VVPGAIVAAM	GIVCFLFLIE	HPNDVRCSST	LVTHSKGYEN	GTNRLRLQKQ	ILKSEKNKPL	DPEMQCLLLS
170	180	190	200	210	220	230	240
DGKGSIHPNH	VVILPGDGGS	GTAAISFTGA	LKIPGVIEFS	LCLLFAKLVS	YTFLFWLPLY	ITNVDHLDAK	KAGELSTLFD
250	260	270	280	290	300	310	320
VGGIFGGILA	GVISDRLEKR	ASTCGLMLLL	AAPTLYIFST	VSKMGLEATI	AMLLLSGALV	SGPYTLITTA	VSADLGTHKS
330	340	350	360	370	380	390	400
LKGNAHALST	VTAIIDGTGS	VGAALGPLLA	GLLSPSGWSN	VFYMLMFADA	CALLVSRPIF	SPIHLECRSL	WLCPNTGGTF
410	420	430					
SHAFLSYQRG	LGLPIFSKYA	WSKAPSLSD					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1899	1	612.7833	-24.65	2	53.8	12.9	1	419-429	K.YAWSKAPSLSD.-		MD:MU 0.87

Detailed Protein Report

Protein 943: sodium/potassium-transporting ATPase subunit alpha-2 proprotein [Homo sapiens]

Accession:	gi|4502271	**Score:**	12.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	112.2
Database Date:	2015-11-30	**pI:**	5.4
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.9
		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
26	1	803.7093	34.59	3	29.6	12.9	1	891-909	R.TMNDLEDSYGQEWTYEQRK.V	Oxidation: 2

Detailed Protein Report

Protein 944: **tudor domain-containing protein 5 isoform 3 [Homo sapiens]**

Accession:	gi|312283653	**Score:**	12.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	60.1
Database Date:	2015-11-30	**pI:**	5.1
		Sequence Coverage [%]:	5.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MANHDIPPDA	VPNKKLCRLP	PLDTSSLIGV	FVEYIISPSQ	FYIRIYSRDS	SELLEDMMIE	MRRCYSNQLV	SDRYVMPECF
90	100	110	120	130	140	150	160
IQPGHLCCVR	ISEDKWWYRV	IIHRVLEKQE	VEVFYPDFGN	IGIVQKSSLR	FLKCCYTKLP	AQAIPCSLAW	VRPVEEHWTS
170	180	190	200	210	220	230	240
KAILQFQKLC	GLKPLVGVVD	EYVDGILNIF	LCDTSSNEDV	YFHHVLRTEG	HAIVCRENIS	SKGFSELNPL	ALYTTSSGGP
250	260	270	280	290	300	310	320
EDIVLTELGY	PSQQHYFNED	RKISPQSKES	ELRILDEIPT	GMPCLESVTI	GDDIWDENWL	PLQAKMGKGG	DAASHLFTAS
330	340	350	360	370	380	390	400
LGGKNQYSSC	KEMPQKDWCF	STPKDTWDDS	WQPSGLVNGT	KVEVHKPEVL	GAQEKNTGTN	RTQKQLDING	SSDSSTLPKL
410	420	430	440	450	460	470	480
EEFCTSLTQS	EQSADGSQSE	PNNSQTQPKQ	IQLSTAAPCS	TTAVDDSAEK	PSGSVESSPE	ILKNEDFSSS	RAITLYKDKR
490	500	510	520	530	540		
QESVDQLSLI	LSYECQISQK	LYIPRSTATA	ALGAAARLAT	SRSLLHWYPS	VKRMEA		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
673	1	1106.2391	51.93	3	38.0	12.9	2	63-90	R.RCYSNQLVSDRYVMPECFIQPGHLCCVR.I	

Detailed Protein Report

Protein 945: centromere protein M isoform c [Homo sapiens]

Accession:	gi|158966691	**Score:**	12.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	6.3
Database Date:	2015-11-30	**pI:**	9.9
		Sequence Coverage [%]:	37.9
		No. of unique Peptides:	1

```
        10         20         30         40         50         60
MGRVWDLPGV LKVEGFRATM AQRLVRVLQI CAGHVPGVSA LNLLSLLRSS EGPSLEDL
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1172	1	1137.1797	15.76	2	44.3	12.9	0	27-48	R.VLQICAGHVPGVSALNLLSLLR.S	

Detailed Protein Report

Protein 946: **RING finger protein 122 [Homo sapiens]**

Accession: gi|38045931
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl, Oxidation

Score: 12.9
MW [kDa]: 17.5
pI: 9.6
Sequence Coverage [%]: 18.1
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MHPFQWCNGC	FCGLGLVSTN	KSCSMPPISF	QDLPLNIYMV	IFGTGIFVFM	LSLIFCCYFI	SKLRNQAQSE	RYGYKEVVLK
90	100	110	120	130	140	150	160
GDAKKLQLYG	QTCAVCLEDF	KGKDELGVLP	CQHAFHRKCL	VKWLEVRCVC	PMCNKPIASP	SEATQNIGIL	LDELV

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1390	1	1030.1245	-39.83	3	47.1	12.9	0	128-155	R.CVCPMCNKPIASPSEATQNIGILLDELV.-	Carbamidomethyl: 1, 3; Oxidation: 5

BRUKER

Detailed Protein Report

Protein 947: vesicular, overexpressed in cancer, prosurvival protein 1 isoform 3 [Homo sapiens]

Accession:	gi|546231038	**Score:**	12.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	18.9
Database Date:	2015-11-30	**pI:**	9.4
Modification(s):	Oxidation	**Sequence Coverage [%]:**	11.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLSETLGYLS	SVLLQCTEAK	KHCWYFEGLY	PTYYICRSYE	DCCGSRCCVR	ALSIQRLWYF	WFLLMMGVLF	CCGAGFFIRR
90	100	110	120	130	140	150	160
RMYPPPLIEE	PAFNVSYTRQ	PPNPGPGAQQ	PGPPYYTDPG	GPGMNPVGNS	MAMAFQVPPN	SPQGSVACPP	PPAYCNTPPP
170							
PYEQVVKAK							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1673	1	1101.4440	-101.03	2	50.7	12.9	0	1-20	-.MLSETLGYLSSVLLQCTEAK.K	Oxidation: 1

Detailed Protein Report

Protein 948: RNA-binding protein 47 isoform b [Homo sapiens]

Accession:	gi|148833511	**Score:**	12.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	56.9
Database Date:	2015-11-30	**pI:**	5.9
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	2.3
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|530376680	refseq_human (refseq_human_20140103.fasta)	PREDICTED: RNA-binding protein 47 isoform X9 [Homo sapiens]

10	20	30	40	50	60	70	80
MTAEDSTAAM	SSDSAAGSSA	KVPEGVAGAP	NEAALLALME	RTGYSMVQEN	GQRKYGGPPP	GWEGPHPQRG	CEVFVGKIPR
90	100	110	120	130	140	150	160
DVYEDELVPV	FEAVGRIYEL	RLMMDFDGKN	RGYAFVMYCH	KHEAKRAVRE	LNNYEIRPGR	LLGVCCSVDN	CRLFIGGIPK
170	180	190	200	210	220	230	240
MKKREEILEE	IAKVTEGVLD	VIVYASAADK	MKNRGFAFVE	YESHRAAAMA	RRKLMPGRIQ	LWGHQIAVDW	AEPEIDVDED
250	260	270	280	290	300	310	320
VMETVKILYV	RNLMIETTED	TIKKSFGQFN	PGCVERVKKI	RDYAFVHFTS	REDAVHAMNN	LNGTELEGSC	LEVTLAKPVD
330	340	350	360	370	380	390	400
KEQYSRYQKA	ARGGGAAEAA	QQPSYVYSCD	PYTLAYYGYP	YNALIGPNRD	YFVKVAIPAI	GAQYSMFPAA	PAPKMIEDGK
410	420	430	440	450	460	470	480
IHTVEHMISP	IAVQPDPASA	AAAAAAAAAA	AAAVIPTVST	PPPFQGRPIT	PVYTVAPNVQ	RIPTAGIYGA	SYVPFAAPAT
490	500	510	520	530			
ATIATLQKNA	AAAAAMYGGY	AGYIPQAFPA	AAIQVPIPDV	YQTY			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1602	1	781.3841	36.49	2	49.8	12.9	1	110-121	K.NRGYAFVMYCHK.H	Carbamidomethyl: 10; Oxidation: 8

Detailed Protein Report

Protein 949: **tyrosine-protein phosphatase non-receptor type 22 isoform 2 [Homo sapiens]**

Accession:	gi|301171662	**Score:**	12.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	85.1
Database Date:	2015-11-30	**pI:**	8.6
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	2.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDQREILQKF	LDEAQSKKIT	KEEFANEFLK	LKRQSTKYKA	DKTYPTTVAE	KPKNIKKNRY	KDILPYDYSR	VELSLITSDE
90	100	110	120	130	140	150	160
DSSYINANFI	KGVYGPKAYI	ATQGPLSTTL	LDFWRMIWEY	SVLIIVMACM	EYEMGKKKCE	RYWAEPGEMQ	LEFGPFSVSC
170	180	190	200	210	220	230	240
EAEKRKSDYI	IRTLKVKFNS	ETRTIYQFHY	KNWPDHDVPS	SIDPILELIW	DVRCYQEDDS	VPICIHCSAG	CGRTGVICAI
250	260	270	280	290	300	310	320
DYTWMLLKDG	SQAKHCIPEK	NHTLQADSYS	PNLPKSTTKA	AKMMNQQRTK	MEIKESSSFD	FRTSEISAKE	ELVLHPAKSS
330	340	350	360	370	380	390	400
TSFDFLELNY	SFDKNADTTM	KWQTKAFPIV	GEPLQKHQSL	DLGSLLFEGC	SNSKPVNAAG	RYFNSKVPIT	RTKSTPFELI
410	420	430	440	450	460	470	480
QQRETKEVDS	KENFSYLESQ	PHDSCFVEMQ	AQKVMHVSSA	ELNYSLPYDS	KHQIRNASNV	KHHDSSALGV	YSYIPLVENP
490	500	510	520	530	540	550	560
YFSSWPPSGT	SSKMSLDLPE	KQDGTVFPSS	LLPTSSTSLF	SYYNSHDSLS	LNSPTNISSL	LNQESAVLAT	APRIDDEIPP
570	580	590	600	610	620	630	640
PLPVRTPESF	IVVEEAGEFS	PNVPKSLSSA	VKVKIGTSLE	WGGTSEPKKF	DDSVILRPSK	SVKLRSPKSE	LHQDRSSPPP
650	660	670	680	690	700	710	720
PLPERTLESF	FLADEDCMQA	QSIETYSTSY	PDTMENSTSS	KQTLKTPGKS	FTRSKSLKIL	RNMKKSICNS	CPPNKPAESV
730	740	750	760				
QSNNSSSFLN	FGFANRFSKP	KGPRNPPPTW	NI				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1450	1	796.1201	70.21	3	47.9	12.9	1	234-254	R.TGVICAIDYTWMLLKDGSQAK.H	Carbamidomethyl: 5; Oxidation: 12

Detailed Protein Report

Protein 950: ataxin-3 isoform o [Homo sapiens]

Accession:	gi|258614025	**Score:**	12.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	17.3
Database Date:	2015-11-30	**pI:**	5.1
		Sequence Coverage [%]:	14.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MESIFHEKQE	GSLCAQHCLN	NLLQGEYFSP	VELSSIAHQL	DEEERMRMAE	GGVTSEDYRT	FLQQPSGNMD	DSGFFSIQVI
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
SNALKVWGLE	LILFNSPEYQ	RLRIDPINER	SFICNYKEHW	FTVRKLGKQT	AAKAATAAAA	AAAGGPIRTE	FTSM

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1220	1	1019.1330	50.19	2	44.8	12.9	2	126-148	K.LGKQTAAKAATAAAAAAAGGPIR.T	

Detailed Protein Report

Protein 951: myogenic factor 6 [Homo sapiens]

Accession:	gi|4505299	**Score:**	12.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	26.9
Database Date:	2015-11-30	**pI:**	5.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	5.8
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MMMDLFETGS YFFYLDGENV TLQPLEVAEG SPLYPGSDGT LSPCQDQMPP EAGSDSSGEE HVLAPPGLQP PHCPGQCLIW
        90        100        110        120        130        140        150        160
ACKTCKRKSA PTDRRKAATL RERRRLKKIN EAFEALKRRT VANPNQRLPK VEILRSAISY IERLQDLLHR LDQQEKMQEL
       170        180        190        200        210        220        230        240
GVDPFSYRPK QENLEGADFL RTCSSQWPSV SDHSRGLVIT AKEGGASIDS SASSSLRCLS SIVDSISSEE RKLPCVEEVV
       250
EK
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2534	1	841.8750	-46.34	2	61.7	12.9	0	157-170	K.MQELGVDPFSYRPK.Q	Oxidation: 1

Detailed Protein Report

Protein 952: **tripartite motif-containing protein 66 [Homo sapiens]**

Accession:	gi|209977097	**Score:**	12.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	134.6
Database Date:	2015-11-30	**pI:**	6.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MARNCSECKE	KRAAHILCTY	CNRWLCSSCT	EEHRHSPVPG	GPFFPRAQKG	SPGVNGGPGD	FTLYCPLHTQ	EVLKLFCETC
90	100	110	120	130	140	150	160
DMLTCHSCLV	VEHKEHRCRH	VEEVLQNQRM	LLEGVTTQVA	HKKSSLQTSA	KQIEDRIFEV	KHQHRKVENQ	IKMAKMVLMN
170	180	190	200	210	220	230	240
ELNKQANGLI	EELEGITNER	KRKLEQQLQS	IMVLNRQFEH	VQNFINWAVC	SKTSVPFLFS	KELIVFQMQR	LLETSCNTDP
250	260	270	280	290	300	310	320
GSPWSIRFTW	EPNFWTKQLA	SLGCITTEGG	QMSRADAPAY	GGLQGSSPFY	QSHQSPVAQQ	EALSHPSHKF	QSPAVCSSSV
330	340	350	360	370	380	390	400
CCSHCSPVSP	SLKGQVPPPS	IHPAHSFRQP	PEMVPQQLGS	LQCSALLPRE	KELACSPHPP	KLLQPWLETQ	PPVEQESTSQ
410	420	430	440	450	460	470	480
RLGQQLTSQP	VCIVPPQDVQ	QGAHAQPTLQ	TPSIQVQFGH	HQKLKLSHFQ	QQPQQQLPPP	PPPLPHPPPP	LPPPPQQPHP
490	500	510	520	530	540	550	560
PLPPSQHLAS	SQHESPPGPA	CSQNMDIMHH	KFELEEMQKD	LELLLQAQQP	SLQLSQTKSP	QHLQQTIVGQ	INYIVRQPAP
570	580	590	600	610	620	630	640
VQSQSQEETL	QATDEPPASQ	GSKPALPLDK	NTAAALPQAS	GEETPLSVPP	VDSTIQHSSP	NVVRKHSTSL	SIMGFSNTLE
650	660	670	680	690	700	710	720
MELSSTRLER	PLEPQIQSVS	NLTAGAPQAV	PSLLSAPPKM	VSSLTSVQNQ	AMPSLTTSHL	QTVPSLVHST	FQSMPNLISD
730	740	750	760	770	780	790	800
SPQAMASLAS	DHPQAGPSLM	SGHTQAVPSL	ATCPLQSIPP	VSDMQPETGS	SSSSGRTSGS	LCPRDGADPS	LENALCKVKL
810	820	830	840	850	860	870	880
EEPINLSVKK	PPLAPVVSTS	TALQQYQNPK	ECENFEQGAL	ELDAKENQSI	RAFNSEHKIP	YVRLERLKIC	AASSGEMPVF
890	900	910	920	930	940	950	960
KLKPQKNDQD	GSFLLIIECG	TESSSMSIKV	SQDRLSEATQ	APGLEGRKVT	VTSLAGQRPP	EVEGTSPEEH	RLIPRTPGAK
970	980	990	1000	1010	1020	1030	1040
KGPPAPIENE	DFCAVCLNGG	ELLCCDRCPK	VFHLSCHVPA	LLSFPGGEWV	CTLCRSLTQP	EMEYDCENAC	YNQPGMRASP
1050	1060	1070	1080	1090	1100	1110	1120
GLSMYDQKKC	EKLVLSLCCN	NLSLPFHEPV	SPLARHYYQI	IKRPMDLSII	RRKLQKKDPA	HYTTPEEVVS	DVRLMFWNCA
1130	1140	1150	1160	1170	1180	1190	1200
KFNYPDSEVA	EAGRCLEVFF	EGWLKEIYPE	KRFAQPRQED	SDSEEVSSES	GCSTPQGFPW	PPYMQEGIQP	KRRRRHMENE
1210	1220						
RAKRMSFRLA	NSISQV						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
862	1	942.1586	54.56	3	40.3	12.8	1	1098-1121	K.DPAHYTTPEEVVSDVRLMFWNCAK.F	Oxidation: 18

Detailed Protein Report

Protein 953: deoxycytidine kinase [Homo sapiens]

Accession:	gi|4503269	**Score:**	12.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	30.5
Database Date:	2015-11-30	**pI:**	5.0
		Sequence Coverage [%]:	2.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MATPPKRSCP	SFSASSEGTR	IKKISIEGNI	AAGKSTFVNI	LKQLCEDWEV	VPEPVARWCN	VQSTQDEFEE	LTMSQKNGGN
90	100	110	120	130	140	150	160
VLQMMYEKPE	RWSFTFQTYA	CLSRIRAQLA	SLNGKLKDAE	KPVLFFERSV	YSDRYIFASN	LYESECMNET	EWTIYQDWHD
170	180	190	200	210	220	230	240
WMNNQFGQSL	ELDGIIYLQA	TPETCLHRIY	LRGRNEEQGI	PLEYLEKLHY	KHESWLLHRT	LKTNFDYLQE	VPILTLDVNE
250	260	270					
DFKDKYESLV	EKVKEFLSTL						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2535	1	709.5600	258.43	1	62.1	12.8	0	255-260	K.EFLSTL.-	

Detailed Protein Report

Protein 954: **sestrin-2 [Homo sapiens]**

Accession:	gi|13899299	**Score:**	12.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	54.5
Database Date:	2015-11-30	**pI:**	5.5
		Sequence Coverage [%]:	2.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MIVADSECRA	ELKDYLRFAP	GGVGDSGPGE	EQRESRARRG	PRGPSAFIPV	EEVLREGAES	LEQHLGLEAL	MSSGRVDNLA
90	100	110	120	130	140	150	160
VVMGLHPDYF	TSFWRLHYLL	LHTDGPLASS	WRHYIAIMAA	ARHQCSYLVG	SHMAEFLQTG	GDPEWLLGLH	RAPEKLRKLS
170	180	190	200	210	220	230	240
EINKLLAHRP	WLITKEHIQA	LLKTGEHTWS	LAELIQALVL	LTHCHSLSSF	VFGCGILPEG	DADGSPAPQA	PTPPSEQSSP
250	260	270	280	290	300	310	320
PSRDPLNNSG	GFESARDVEA	LMERMQQLQE	SLLRDEGTSQ	EEMESRFELE	KSESLLVTPS	ADILEPSPHP	DMLCFVEDPT
330	340	350	360	370	380	390	400
FGYEDFTRRG	AQAPPTFRAQ	DYTWEDHGYS	LIQRLYPEGG	QLLDEKFQAA	YSLTYNTIAM	HSGVDTSVLR	RAIWNYIHCV
410	420	430	440	450	460	470	480
FGIRYDDYDY	GEVNQLLERN	LKVYIKTVAC	YPEKTTRRMY	NLFWRHFRHS	EKVHVNLLLL	EARMQAALLY	ALRAITRYMT
490							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
255	1	530.8805	-180.66	3	32.6	12.8	1	464-477	R.MQAALLYALRAITR.Y	

Detailed Protein Report

Protein 955: PREDICTED: fibroblast growth factor receptor substrate 3 isoform X1 [Homo sapiens]

Accession:	gi|578811367	**Score:**	12.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	31.0
Database Date:	2015-11-30	**pI:**	7.0
		Sequence Coverage [%]:	5.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGSCCSCLNR	DSVPDNHPTK	FKVTNVDDEG	VELGSGVMEL	TQSELVLHLH	RREAVRWPYL	CLRRYGYDSN	LFSFESGRRC
90	100	110	120	130	140	150	160
QTGQGIFAFK	CSRAEEIFNL	LQDLMQCNSI	NVMEEPVIIT	RNSHPAELDL	PRAPQPPNAL	GYTVSSFSNG	CPGEGPRFSA
170	180	190	200	210	220	230	240
PRRLSTSSLR	HPSLGEESTH	ALIAPDEQSH	TYVNTPASED	DHRRGRHCLQ	PLPEGQAPFL	PQARGPDQRD	PQVFLQPGQG
250	260	270	280	290			
SGLLCRRHGG	GTRCFPVLAG	VPRDISHRVS	WSVSRLGREG				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2113	1	899.3324	-89.81	2	56.6	12.8	1	64-78	R.RYGYDSNLFSFESGR.R	

Detailed Protein Report

Protein 956: **pre-mRNA-processing factor 17 [Homo sapiens]**

Accession:	gi|7706657	**Score:**	12.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	65.5
Database Date:	2015-11-30	**pI:**	6.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.4
		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
2547	1	885.0863	167.56	2	62.3	12.8	1	239-252	K.TILHVKEMYDYQGR.S	Oxidation: 8

Detailed Protein Report

Protein 957: PREDICTED: BMP-binding endothelial regulator protein isoform X3 [Homo sapiens]

Accession:	gi|530384519	**Score:**	12.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	52.5
Database Date:	2015-11-30	**pI:**	9.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.9
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MYQVFLHCQR KVFDLPFGSC LFRSDVYDNG SSFLYDNCTA CTCRDSTVVC KRKCSHPGGC DQGQEGCCEE CLLRVPPEDI
        90        100        110        120        130        140        150        160
KVCKFGNKIF QDGEMWSSIN CTICACVKGR TECRNKQCIP ISSCPQGKIL NRKGCCPICT EKPGVCTVFG DPHYNTFDGR
       170        180        190        200        210        220        230        240
TFNFQGTCQY VLTKDCSSPA SPFQVLVKND ARRTRSFSWT KSVELVLGES RVSLQQHLTV RWNGSRIALP CRAPHFHIDL
       250        260        270        280        290        300        310        320
DGYLLKVTTK AGLEISWDGD SFVEVMAAPH LKGKLCGLCG NYNGHKRDDL IGGDGNFKFD VDDFAESWRV ESNEFCNRPQ
       330        340        350        360        370        380        390        400
RKPVPELCQG TVKVKLRAHR ECQKLKSWEF QTCHSTVDYA TFYRSCVTDM CECPVHKNCY CESFLAYTRA CQREGIKVHW
       410        420        430        440        450        460        470
EPQQNCAATQ CKHGAVYDTC GPGCIKTCDN WNEIGPCNKP CVAGCHCPAN LVLHKGRCIK PVLCPQR
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1151	1	874.7151	21.78	3	44.0	12.8	2	52-74	K.RKCSHPGGCDQGQEGCCEECLLR.V	Carbamidomethyl: 3, 20

Detailed Protein Report

Protein 958: cytoplasmic FMR1-interacting protein 1 isoform b [Homo sapiens]

Accession:	gi|74271907	**Score:**	12.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	94.4
Database Date:	2015-11-30	**pI:**	6.7
		Sequence Coverage [%]:	1.6
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 1.34 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MAESLGSAEL	LRQLKSLGME	RLLHAVNTFL	RQSCTYLPLL	TFGGKTSFVS	LDVYGTEANC	SATSCSFPKA	AATWPRRQAP
90	100	110	120	130	140	150	160
GPLGELVRGP	PDQGVAEQSF	SHGLFEFGIT	NVPCIFSPPQ	MFPWIIQLYM	VRTMLESLIA	DKSGSKKTLR	SSLEGPTILD
170	180	190	200	210	220	230	240
IEKFHRESFF	YTHLINFSET	LQQCCDLSQL	WFREFFLELT	MGRRIQFPIE	MSMPWILTDH	ILETKEASMM	EYVLYSLDLY
250	260	270	280	290	300	310	320
NDSAHYALTR	FNKQFLYDEI	EAEVNLCFDQ	FVYKLADQIF	AYYKVMAGSL	LLDKRLRSEC	KNQGATIHLP	PSNRYETLLK
330	340	350	360	370	380	390	400
QRHVQLLGRS	IDLNRLITQR	VSAAMYKSLE	LAIGRFESED	LTSIVELDGL	LEINRMTHKL	LSRYLTLDGF	DAMFREANHN
410	420	430	440	450	460	470	480
VSAPYGRITL	HVFWELNYDF	LPNYCYNGST	NRFVRTVLPF	SQEFQRDKQP	NAQPQYLHGS	KALNLAYSSI	YGSYRNFVGP
490	500	510	520	530	540	550	560
PHFQVICRLL	GYQGIAVVME	ELLKVVKSLL	QGTILQYVKT	LMEVMPKICR	LPRHEYGSPG	ILEFFHHQLK	DIVEYAELKT
570	580	590	600	610	620	630	640
VCFQNLREVG	NAILFCLLIE	QSLSLEEVCD	LLHAAPFQNI	LPRVHVKEGE	RLDAKMKRLE	SKYAPLHLVP	LIERLGTPQQ
650	660	670	680	690	700	710	720
IAIAREGDLL	TKERLCCGLS	MFEVILTRIR	SFLDDPIWRG	PLPSNGVMHV	DECVEFHRLW	SAMQFVYCIP	VGTHEFTVEQ
730	740	750	760	770	780	790	800
CFGDGLHWAG	CMIIVLLGQQ	RRFAVLDFCY	HLLKVQKHDG	KDEIIKNVPL	KKMVERIRKF	QILNDEIITI	LDKYLKSGDG
810	820	830					
EGTPVEHVRC	FQPPIHQSLA	SS					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
199	1	797.8837	-38.98	2	32.2	12.8	1	436-448	R.TVLPFSQEFQRDK.Q		MD:MU 1.34

Detailed Protein Report

Protein 959: PREDICTED: protein SON isoform X3 [Homo sapiens]

Accession:	gi|578836658	**Score:**	12.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	228.0
Database Date:	2015-11-30	**pI:**	5.2
		Sequence Coverage [%]:	0.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MATNIEQIFR	SFVVSKFREI	QQELSSGRNE	GQLNGETNTP	IEGNQAGDAA	ASARSLPNEE	IVQKIEEVLS	GVLDTELRYK
90	100	110	120	130	140	150	160
PDLKEGSRKS	RCVSVQTDPT	DEIPTKKSKK	HKKHKNKKKK	KKKEKEKKYK	RQPEESESKT	KSHDDGNIDL	ESDSFLKFDS
170	180	190	200	210	220	230	240
EPSAVALELP	TRAFGPSETN	ESPAVVLEPP	VVSMEVSEPH	ILETLKPATK	TAELSVVSTS	VISEQSEQSV	AVMPEPSMTK
250	260	270	280	290	300	310	320
ILDSFAAAPV	PTTTLVLKSS	EPVVTMSVEY	QMKSVLKSVE	STSPEPSKIM	LVEPPVAKVL	EPSETLVVSS	ETPTEVYPEP
330	340	350	360	370	380	390	400
STSTTMDFPE	SSAIEALRLP	EQPVDVPSEI	ADSSMTRPQE	LPELPKTTAL	ELQESSVASA	MELPGPPATS	MPELQGPPVT
410	420	430	440	450	460	470	480
PVLELPGPSA	TPVPELPGPL	STPVPELPGP	PATAVPELPG	PSVTPVPQLS	QELPGLPAPS	MGLEPPQEVP	EPPVMAQELP
490	500	510	520	530	540	550	560
GLPLVTAAVE	LPEQPAVTVA	MELTEQPVTT	TELEQPVGMT	TVEHPGHPEV	TTATGLLGQP	EATMVLELPG	QPVATTALEL
570	580	590	600	610	620	630	640
PGQPSVTGVP	ELPGLPSATR	ALELSGQPVA	TGALELPGPL	MAAGALEFSG	QSGAAGALEL	LGQPLATGVL	ELPGQPGAPE
650	660	670	680	690	700	710	720
LPGQPVATVA	LEISVQSVVT	TSELSTMTVS	QSLEVPSTTA	LESYNTVAQE	LPTTLVGETS	VTVGVDPLMA	PESHILASNT
730	740	750	760	770	780	790	800
METHILASNT	MDSQMLASNT	MDSQMLASNT	MDSQMLASST	MDSQMLATSS	MDSQMLATSS	MDSQMLATST	MDSQMLATSS
810	820	830	840	850	860	870	880
MDSQMLATSS	MDSQMLATSS	MDSQMLATSS	MDSQMLATST	MDSQMLATST	MDSQMLATSS	MDSQMLASGT	MDSQMLASGT
890	900	910	920	930	940	950	960
MDAQMLASGT	MDAQMLASST	QDSAMLGSKS	PDPYRLAQDP	YRLAQDPYRL	GHDPYRLGHD	AYRLGQDPYR	LGHDPYRLTP
970	980	990	1000	1010	1020	1030	1040
DPYRMSPRPY	RIAPRSYRIA	PRPYRLAPRP	LMLASRRSMM	MSYAAERSMM	SSYERSMMSY	ERSMMSPMAE	RSMMSAYERS
1050	1060	1070	1080	1090	1100	1110	1120
MMSAYERSMM	SPMAERSMMS	AYERSMMSAY	ERSMMSPMAD	RSMMSMGADR	SMMSSYSAAD	RSMMSSYSAA	DRSMMSSYTA
1130	1140	1150	1160	1170	1180	1190	1200
DRSMMSMAAD	SYTDSYTDTY	TEAYMVPPLP	PEEPPTMPPL	PPEEPPMTPP	LPPEEPPEGP	ALPTEQSALT	AENTWPTEVP
1210	1220	1230	1240	1250	1260	1270	1280
SSPSEESVSQ	PEPPVSQSEI	SEPSAVPTDY	SVSASDPSVL	VSEAAVTVPE	PPPEPESSIT	LTPVESAVVA	EEHEVVPERP
1290	1300	1310	1320	1330	1340	1350	1360
VTCMVSETPA	MSAEPTVLAS	EPPVMSETAE	TFDSMRASGH	VASEVSTSLL	VPAVTTPVLA	ESILEPPAMA	APESSAMAVL
1370	1380	1390	1400	1410	1420	1430	1440
ESSAVTVLES	STVTVLESST	VTVLEPSVVT	VPEPPVVAEP	DYVTIPVPVV	SALEPSVPVL	EPAVSVLQPS	MIVSEPSVSV
1450	1460	1470	1480	1490	1500	1510	1520
QESTVTVSEP	AVTVSEQTQV	IPTEVAIEST	PMILESSIMS	SHVMKGINLS	SGDQNLAPEI	GMQEIALHSG	EEPHAEEHLK
1530	1540	1550	1560	1570	1580	1590	1600
GDFYESEHGI	NIDLNINNHL	IAKEMEHNTV	CAAGTSPVGE	IGEEKILPTS	ETKQRTVLDT	YPGVSEADAG	ETLSSTGPFA
1610	1620	1630	1640	1650	1660	1670	1680
LEPDATGTSK	GIEFTTASTL	SLVNKYDVDL	SLTTQDTEHD	MVISTSPSGG	SEADIEGPLP	AKDIHLDLPS	NNNLVSKDTE
1690	1700	1710	1720	1730	1740	1750	1760
EPLPVKESDQ	TLAALLSPKE	SSGGEKEVPP	PPKETLPDSG	FSANIEDINE	ADLVRPLLPK	DMERLTSLRA	GIEGPLLASD
1770	1780	1790	1800	1810	1820	1830	1840
VGRDRSAASP	VVSSMPERAS	ESSSEEKDDY	EIFVKVKDTH	EKSKKNKNRD	KGEKEKKRDS	SLRSRSKRSK	SSEHKSRKRT
1850	1860	1870	1880	1890	1900	1910	1920
SESRSRARKR	SSKSKSHRSQ	TRSRSRSRRR	RRSSRSRSKS	RGRRSVSKEK	RKRSPKHRSK	SRERKRKRSS	SRDNRKTVRA
1930	1940	1950	1960	1970	1980	1990	2000
RSRTPSRRSR	SHTPSRRRRS	RSVGRRRSFS	ISPSRRSRTP	SRRSRTPSRR	SRTPSRRSRT	PSRRSRTPSR	RSRTPSRRRR
2010	2020	2030	2040	2050	2060	2070	2080
SRSVVRRRSF	SISPVRLRRS	RTPLRRRFSR	SPIRRKRSRS	SERGRSPKRL	TDLDKAQLLE	IAKANAAAMC	AKAGVPLPPN
2090	2100	2110					
LKPAPPPTIE	EKVAKKSGGA	TIEELTEF					

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1493	1	513.1115	-200.27	2	48.3	12.8	0	1073-1081	R.SMMSPMADR.S	

Detailed Protein Report

Protein 960: chorionic somatomammotropin hormone-like 1 isoform 3 [Homo sapiens]

Accession:	gi|38201628	**Score:**	12.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	14.9
Database Date:	2015-11-30	**pI:**	5.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	10.9
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MEETQQKSNL ELLHISLLLI ESRLEPVRFL RSTFTNNLVY DTSDSDDYHL LKDLEEGIQM LMGRLEDGSH LTGQTLKQTY
        90        100        110        120        130
SKFDTNSHNH DALLKNYGLL HCFRKDMDKV ETFLRMVQCR SVEGSCGF
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1804	1	898.8338	-109.46	2	52.4	12.8	2	96-109	K.NYGLLHCFRKDMDK.V	Carbamidomethyl: 7

Detailed Protein Report

Protein 961: ankyrin repeat and zinc finger domain-containing protein 1 isoform 2 [Homo sapiens]

Accession:	gi|544346294	**Score:**	12.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	57.5
Database Date:	2015-11-30	**pI:**	10.3
		Sequence Coverage [%]:	1.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAAAGHFAGA	IFQGREVVTH	KTFHRYTVRA	KRGTAQGLRD	ARGGPSHSAG	ANLRRYNEAT	LYKDVRDLLA	GPSWAKALEE
90	100	110	120	130	140	150	160
AGTILLRAPR	SGRSLFFGGK	GAPLQRGDPR	LWDIPLATRR	PTFQELQRVL	HKLTTLHVYE	EDPREAVRLH	SPQTHWKTVR
170	180	190	200	210	220	230	240
EERKKPTEEE	IRKICRDEKE	ALGQNEESPK	QGSGSEGEDG	FQVELELVEL	TVGTLDLCES	EVLPKRRRRK	RNKKEKSRDQ
250	260	270	280	290	300	310	320
EAGAHRTLLQ	QTQEEEPSTQ	SSQAVAAPLG	PLLDEAKAPG	QPELWNALLA	ACRAGDVGVL	KLQLAPSPAD	PRVLSLLSAP
330	340	350	360	370	380	390	400
LGSGGFTLLH	AAAAAGRGSV	VRLLLEAGAD	PTVQDSRARP	PYTVAADKST	RNEFRRFMEK	NPDAYDYNKA	QVPGPLTPEM
410	420	430	440	450	460	470	480
EARQATRKRE	QKAARRQREE	QQQRQQEQEE	REREEQRRFA	ALSDREKRAL	AAERRLAAQL	GAPTSPIPDS	AIVNTRRCWS
490	500	510	520				
CGASLQGLTP	FHYLDFSFCS	TRCLQDHRRQ	AGRPSS				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
922	1	529.2971	18.15	2	41.1	12.8	0	67-76	R.DLLAGPSWAK.A	

Detailed Protein Report

Protein 962: **anaphase-promoting complex subunit 2 [Homo sapiens]**

Accession:	gi|7019327	**Score:**	12.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	93.8
Database Date:	2015-11-30	**pI:**	5.0
		Sequence Coverage [%]:	1.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAAAVVVAEG	DSDSRPGQEL	LVAWNTVSTG	LVPPAALGLV	SSRTSGAVPP	KEEELRAAVE	VLRGHGLHSV	LEEWFVEVLQ
90	100	110	120	130	140	150	160
NDLQANISPE	FWNAISQCEN	SADEPQCLLL	LLDAFGLLES	RLDPYLRSLE	LLEKWTRLGL	LMGTGAQGLR	EEVHTMLRGV
170	180	190	200	210	220	230	240
LFFSTPRTFQ	EMIQRLYGCF	LRVYMQSKRK	GEGGTDPELE	GELDSRYARR	RYYRLLQSPL	CAGCSSDKQQ	CWCRQALEQF
250	260	270	280	290	300	310	320
HQLSQVLHRL	SLLERVSAEA	VTTTLHQVTR	ERMEDRCRGE	YERSFLREFH	KWIERVVGWL	GKVFLQDGPA	RPASPEAGNT
330	340	350	360	370	380	390	400
LRRWRCHVQR	FFYRIYASLR	IEELFSIVRD	FPDSRPAIED	LKYCLERTDQ	RQQLLVSLKA	ALETRLLHPG	VNTCDIITLY
410	420	430	440	450	460	470	480
ISAIKALRVL	DPSMVILEVA	CEPIRRYLRT	REDTVRQIVA	GLTGDSDGTG	DLAVELSKTD	PASLETGQDS	EDDSGEPEDW
490	500	510	520	530	540	550	560
VPDPVDADPG	KSSSKRRSSD	IISLLVSIYG	SKDLFINEYR	SLLADRLLHQ	FSFSPEREIR	NVELLKLRFG	EAPMHFCEVM
570	580	590	600	610	620	630	640
LKDMADSRRI	NANIREEDEK	RPAEEQPPFG	VYAVILSSEF	WPPFKDEKLE	VPEDIRAALE	AYCKKYEQLK	AMRTLSWKHT
650	660	670	680	690	700	710	720
LGLVTMDVEL	ADRTLSVAVT	PVQAVILLYF	QDQASWTLEE	LSKAVKMPVA	LLRRRMSVWL	QQGVLREEPP	GTFSVIEEER
730	740	750	760	770	780	790	800
PQDRDNMVLI	DSDDESDSGM	ASQADQKEEE	LLLFWTYIQA	MLTNLESLSL	DRIYNMLRMF	VVTGPALAEI	DLQELQGYLQ
810	820	830					
KKVRDQQLVY	SAGVYRLPKN	CS					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2369	1	665.7303	-155.03	2	59.9	12.8	1	570-580	R.INANIREEDEK.R	

Detailed Protein Report

Protein 963: reticulon-2 isoform B [Homo sapiens]

Accession: gi|46255005
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 12.8
MW [kDa]: 51.4
pI: 4.8
Sequence Coverage [%]: 5.9
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MGQVLPVFAH	CKEAPSTASS	TPDSTEGGND	DSDFRELHTA	REFSEEDEEE	TTSQDWGTPR	ELTFSYIAFD	GVVGSGGRRD
90	100	110	120	130	140	150	160
STARRPRPQG	RSVSEPRDQH	PQPSLGDSLE	SIPSLSQSPE	PGRRGDPDTA	PPSERPLEDL	RLRLDHLGWV	ARGTGSGEDS
170	180	190	200	210	220	230	240
STSSSTPLED	EEPQEPNRLE	TGEAGEELDL	RLRLAQPSSP	EVLTPQLSPG	SGTPQAGTPS	PSRSRDSNSG	PEEPLLEEEE
250	260	270	280	290	300	310	320
KQWGPLEREP	VRGQCLDSTD	QLEFTVEPRL	LVADLLYWKD	TRTSGVVFTG	LMVSLLCLLH	FSIVSVAAHL	ALLLLCGTIS
330	340	350	360	370	380	390	400
LRVYRKVLQA	VHRGDGANPF	QAYLDVDLTL	TREQTERLSH	QITSRVVSAA	TQLRHFFLVE	DLVDSLKLAL	LFYILTFVGA
410	420	430	440	450	460	470	480
IFNGLTLLIL	GVIGLFTIPL	LYRQHQAQID	QYVGLVTNQL	SHIKAKIRAK	IPGTGALASA	AAAVSGSKAK	AE

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2220	1	1061.2430	20.21	3	58.0	12.8	2	125-152	R.GDPDTAPPSERPLEDLRLRLDHLGWVAR.G	

Detailed Protein Report

Protein 964: SLAM family member 5 isoform 1 precursor [Homo sapiens]

Accession:	gi|296434285	**Score:**	12.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	38.8
Database Date:	2015-11-30	**pI:**	6.7
		Sequence Coverage [%]:	4.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAQHHLWILL	LCLQTWPEAA	GKDSEIFTVN	GILGESVTFP	VNIQEPRQVK	IIAWTSKTSV	AYVTPGDSET	APVVTVTHRN
90	100	110	120	130	140	150	160
YYERIHALGP	NYNLVISDLR	MEDAGDYKAD	INTQADPYTT	TKRYNLQIYR	RLGKPKITQS	LMASVNSTCN	VTLTCSVEKE
170	180	190	200	210	220	230	240
EKNVTYNWSP	LGEEGNVLQI	FQTPEDQELT	YTCTAQNPVS	NNSDSISARQ	LCADIAMGFR	THHTGLLSVL	AMFFLLVLIL
250	260	270	280	290	300	310	320
SSVFLFRLFK	RRQGRIFPEG	SCLNTFTKNP	YAASKKTIYT	YIMASRNTQP	AESRIYDEIL	QSKVLPSKEE	PVNTVYSEVQ
330	340	350					
FADKMGKAST	QDSKPPGTSS	YEIVI					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1955	1	899.3551	-106.90	2	54.3	12.8	1	253-268	R.QGRIFPEGSCLNTFTK.N	

Detailed Protein Report

Protein 965: zinc phosphodiesterase ELAC protein 1 [Homo sapiens]

Accession: gi|8922122
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 12.8
MW [kDa]: 40.0
pI: 6.4
Sequence Coverage [%]: 7.4
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MSMDVTFLGT	GAAYPSPTRG	ASAVVLRCEG	ECWLFDCGEG	TQTQLMKSQL	KAGRITKIFI	THLHGDHFFG	LPGLLCTISL
90	100	110	120	130	140	150	160
QSGSMVSKQP	IEIYGPVGLR	DFIWRTMELS	HTELVFHYVV	HELVPTADQC	PAEELKEFAH	VNRADSPPKE	EQGRTILLDS
170	180	190	200	210	220	230	240
EENSYLLFDD	EQFVVKAFRL	FHRIPSFGFS	VVEKKRPGKL	NAQKLKDLGV	PPGPAYGKLK	NGISVVLENG	VTISPQDVLK
250	260	270	280	290	300	310	320
KPIVGRKICI	LGDCSGVVGD	GGVKLCFEAD	LLIHEATLDD	AQMDKAKEHG	HSTPQMAATF	AKLCRAKRLV	LTHFSQRYKP
330	340	350	360	370			
VALAREGETD	GIAELKKQAE	SVLDLQEVTL	AEDFMVISIP	IKK			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
122	1	1044.7808	-23.16	3	30.9	12.8	2	28-54	R.CEGECWLFDCGEGTQTQLMKSQLKAGR.I	Carbamidomethyl: 5, 10

Detailed Protein Report

Protein 966: myb-related transcription factor, partner of profilin [Homo sapiens]

Accession: gi|60460889
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 12.8
MW [kDa]: 42.5
pI: 10.8
Sequence Coverage [%]: 3.0
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MASAAAGEAE	ETTRLRKPRF	SFEENQILIR	EVRAHYPQLY	GAQSRRVSVA	ERRRVWDGIA	AKINGITSWK	RTGQEVQKRW
90	100	110	120	130	140	150	160
NDFKRRTKEK	LARVPHSTQG	AGPAAEDAFS	AEEETIFAIL	GPGVAAPGAG	AGAEEPPAAP	SSQPPPPSAC	PQRYVLSEDR
170	180	190	200	210	220	230	240
REDRRADTSA	HSKAGSSSPE	PWARPSCTPQ	EGGCPRPKER	ESPPPSALQP	VQLPRLALSP	PPPAPPLPPP	PPLAQVAPSP
250	260	270	280	290	300	310	320
PSPPPPPRPP	PTLSASDPSL	DFLRAQQETA	NAIRELAGTL	RQGLAKLSEA	LSALLPLLPG	TPVDSLPPPL	PPPPPPPPPP
330	340	350	360	370	380	390	400
RPVLPPPAPK	VEITPEPVSV	VAAVVDGAVV	AARGVIIAPR	SEEGAPRPPP	APLPPHDSPP	HKRRKGFPTR	KRRGRWKSP

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
674	1	628.8839	22.51	2	37.8	12.8	1	275-286	R.ELAGTLRQGLAK.L	

Detailed Protein Report

Protein 967: PREDICTED: protein FAM189A2 isoform X4 [Homo sapiens]

Accession:	gi|530391776	**Score:**	12.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	32.0
Database Date:	2015-11-30	**pI:**	8.0
		Sequence Coverage [%]:	4.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MERMVGPDVI	PLPHIYGARI	KGVEVFCPLD	PPPPYEAVVS	QMDQEQGSSF	QMSEGSEAAV	IPLDLGCTQV	TQDGDIPNIP
90	100	110	120	130	140	150	160
AEENASTSTP	SSTLVRPIRS	RRALPPLRTR	SKSDPVLHPS	EERAAPVLSC	EAATQTERRL	DLAAVTLRRG	LRSRASRCRP
170	180	190	200	210	220	230	240
RSLIDYKSYM	DTKLLVARFL	EQSSCTMTPD	IHELVENIKS	VLKSDEEHME	EAITSASFLE	QIMAPLQPST	SRAHKLPSRR
250	260	270	280	290			
QPGLLHLQSC	GDLHTFTPAG	RPRAERRPRR	VEAERPHSLI	GVIRETVL			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2134	1	788.3187	-168.98	2	56.6	12.8	0	271-284	R.VEAERPHSLIGVIR.E	

Detailed Protein Report

Protein 968: PREDICTED: neuroblastoma breakpoint family member 20 isoform X3 [Homo sapiens]

Accession:	gi|530429910	**Score:**	12.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	136.1
Database Date:	2015-11-30	**pI:**	4.5
		Sequence Coverage [%]:	1.4
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530433897	refseq_human (refseq_human_20140103.fasta)	PREDICTED: neuroblastoma breakpoint family member 20 isoform X5 [Homo sapiens]

10	20	30	40	50	60	70	80
MVVSAGHWSS	EKAEMNILEI	NETLRPQLPE	NKQQLRNLKE	KCFLTQLAGF	LANRQKKYKY	EECKDLIKFM	LRNERQFKEE
90	100	110	120	130	140	150	160
KLAEQLKQAE	ELRQYKVLVH	SQERELTQLK	EKLREGRDAS	RSLNEHLQAL	LTPDEPDKSQ	GQDLQEQLAE	GCRLAQHLVQ
170	180	190	200	210	220	230	240
KLSPENDEDE	DEDVQVEEDE	KVLESSAPRE	VQKTEESKVP	EDSLEECAIT	CSNSHGPCDS	NQPHKNIKIT	FEEDEVNSTL
250	260	270	280	290	300	310	320
VVDRESSHDE	CQDALNILPV	PGPTSSATNV	SMVVSAGPLS	GEKAAINILE	INEKLRPQLA	EKKQQFRNLK	EKCFLTQLAG
330	340	350	360	370	380	390	400
FLANQQNKYK	YEECKDLIKS	MLRNERQFKE	EKLAEQLKQA	EELRQYKVLV	HAQERELTQL	REKLREGRDA	SRSLNEHLQA
410	420	430	440	450	460	470	480
LLTPDEPDKS	QGQDLQEQLA	EGCRLAQHLV	QKLSPENDND	DDEDVQVEVA	EKVQKSSAPR	EMQKAEEKEV	PEDSLEECAI
490	500	510	520	530	540	550	560
TCSNSHGPYD	CNQPHRKTKI	TFEEDKVDST	LIGSSSHVEW	EDAVHIIPEN	ESDDEEEEEK	GPVSPRNLQE	SEEEEVPQES
570	580	590	600	610	620	630	640
WDEGYSTLSI	PPEMLASYKS	YSSTFHSLEE	QQVCMAVDIG	RHRWDQVKKE	DHEATGPRLS	RELLDEKGPE	VLQDSLDRCY
650	660	670	680	690	700	710	720
STPSGCLELT	DSCQPYRSAF	YVLEQQRVGL	AVDMDEIEKY	QEVEEDQDPS	CPRLSRELLD	EKEPEVLQDS	LGRCYSTPSG
730	740	750	760	770	780	790	800
YLELPDLGQP	YSSAVYSLEE	QYLGLALDVD	RIKKDQEEEE	DQGPPCPRLS	RELLEVVEPE	VLQDSLDRCY	STPSSCLEQP
810	820	830	840	850	860	870	880
DSCQPYGSSF	YALEEKHVGF	SLDVGEIEKK	GKGKKRRGRR	SKKERRRGRK	EGEEDQNPPC	PRLSRELLDE	KGPEVLQDSL
890	900	910	920	930	940	950	960
DRCYSTPSGC	LELTDSCQPY	RSAFYILEQQ	RVGLAVDMDE	IEKYQEVEED	QDPSCPRLSR	ELLDEKEPEV	LQDSLGRCYS
970	980	990	1000	1010	1020	1030	1040
TPSGYLELPD	LGQPYSSAVY	SLEEQYLGLA	LDVDRIKKDQ	EEEEDQGPPC	PRLSRELLEV	VEPEVLQDSL	DRCYSTPSSC
1050	1060	1070	1080	1090	1100	1110	1120
LEQPDSCQPY	GSSFYALEEK	HVGFSLDVGE	IEKKGKGKKR	RGRRSKKERR	RGRKEGEEDQ	NPPCPRLNSM	LMEVEEPEVL
1130	1140	1150	1160	1170	1180	1190	
QDSLDICYST	PSMYFELPDS	FQHYRSVFYS	FEEEHISFAL	YVDNRFFTLT	VTSLHLVFQM	GVIFPQ	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2087	1	958.8549	-151.09	2	56.0	12.7	2	182-198	K.VLESSAPREVQKTEESK.V	

Detailed Protein Report

Protein 969: galactose-3-O-sulfotransferase 2 [Homo sapiens]

Accession:	gi|124256491	**Score:**	12.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	46.1
Database Date:	2015-11-30	**pI:**	10.6
		Sequence Coverage [%]:	4.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MMSMLGGLQR	YFRVILLLLL	ALTLLLLAGF	LHSDLELDTP	LFGGQAEGPP	VTNIMFLKTH	KTASSTVLNI	LYRFAETHNL
90	100	110	120	130	140	150	160
SVALPAGSRV	HLGYPWLFLA	RYVEGVGSQQ	RFNIMCNHLR	FNLPQVQKVM	PNDTFYFSIL	RNPVFQLESS	FIYYKTYAPA
170	180	190	200	210	220	230	240
FRGAPSLDAF	LASPRTFYND	SRHLRNVYAK	NNMWFDFGFD	PNAQCEEGYV	RARIAEVERR	FRLVLIAEHL	DESLVLLRRR
250	260	270	280	290	300	310	320
LRWALDDVVA	FRLNSRSARS	VARLSPETRE	RARSWCALDW	RLYEHFNRTL	WAQLRAELGP	RRLRGEVERL	RARRRELASL
330	340	350	360	370	380	390	400
CLQDGGALKN	HTQIRDPRLR	PYQSGKADIL	GYNLRPGLDN	QTLGVCQRLV	MPELQYMARL	YALQFPEKPL	KNIPFLGA

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2191	1	1051.4626	-76.41	2	57.6	12.7	1	112-128	R.FNIMCNHLRFNLPQVQK.V	

Detailed Protein Report

Protein 970: PREDICTED: apoptosis-enhancing nuclease isoform X4 [Homo sapiens]

Accession: gi|578827297
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl
Score: 12.7
MW [kDa]: 40.2
pI: 12.0
Sequence Coverage [%]: 4.1
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MGPGRDDRRS	VSLPFSLKFP	ASMAGSQHEL	RPLQESLPFC	SRPPPRCQAG	STNQKRSWAG	AAVQRANRRA	VGAGLARACG
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
SCRLSGRHVQ	TGRDTRGFRL	LPHWKITPQA	SLAPSSELTG	MVPREAPESA	QCLCPSLTIP	NAKDVLRKRH	KRRSRQHQRF
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
MARKALLQEQ	GLLSMPPEPG	SSPLPTPFGA	ATATEAASSG	KQCLRAGSGS	APCSRRPAPG	KASGPLPSKC	VAIDCEMVGT
250	**260**	**270**	**280**	**290**	**300**	**310**	**320**
GPRGRVSELA	RCSIVSYHGN	VLYDKYIRPE	MPIADYRTRW	SGITRQHMRK	AVPFQVAQKE	ILKLLKGKVV	VGHALHNDFQ
330	**340**	**350**	**360**	**370**			
ALKYVHPRSQ	TRDTTYVPNF	LSEPGLHTRA	RVSLKDLALQ	LLHKKIQ			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
677	1	752.8492	-44.65	2	38.0	12.7	2	69-83	R.RAVGAGLARACGSCR.L	Carbamidomethyl: 11

Detailed Protein Report

Protein 971: kelch-like protein 14 [Homo sapiens]

Accession:	gi|55741643	**Score:**	12.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	70.7
Database Date:	2015-11-30	**pI:**	6.2
		Sequence Coverage [%]:	3.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSRSGDRTST	FDPSHSDNLL	HGLNLLWRKQ	LFCDVTLTAQ	GQQFHCHKAV	LASCSQYFRS	LFSSHPPLGG	GVGGQDGLGA
90	100	110	120	130	140	150	160
PKDQQQPPQQ	QPSQQQQPPP	QEEPGTPSSS	PDDKLLTSPR	AINNLVLQGC	SSIGLRLVLE	YLYTANVTLS	LDTVEEVLSV
170	180	190	200	210	220	230	240
SKILHIPQVT	KLCVQFLNDQ	ISVQNYKQVC	KIAALHGLEE	TKKLANKYLV	EDVLLLNFEE	MRALLDSLPP	PVESELALFQ
250	260	270	280	290	300	310	320
MSVLWLEHDR	ETRMQYAPDL	MKRLRFALIP	APELVERVQS	VDFMRTDPVC	QKLLLDAMNY	HLMPFRQHCR	QSLASRIRSN
330	340	350	360	370	380	390	400
KKMLLLVGGL	PPGPDRLPSN	LVQYYDDEKK	TWKILTIMPY	NSAHHCVVEV	ENFLFVLGGE	DQWNPNGKHS	TNFVSRYDPR
410	420	430	440	450	460	470	480
FNSWIQLPPM	QERRASFYAC	RLDKHLYVIG	GRNETGYLSS	VECYNLETNE	WRYVSSLPQP	LAAHAGAVHN	GKIYISGGVH
490	500	510	520	530	540	550	560
NGEYVPWLYC	YDPVMDVWAR	KQDMNTKRAI	HTLAVMNDRL	YAIGGNHLKG	FSHLDVMLVE	CYDPKGDQWN	ILQTPILEGR
570	580	590	600	610	620	630	
SGPGCAVLDD	SIYLVGGYSW	SMGAYKSSTI	CYCPEKGTWT	ELEGDVAEPL	AGPACVTVIL	PSCVPYNK	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2525	1	1155.0426	-61.91	2	61.5	12.7	1	204-222	K.LANKYLVEDVLLLNFEEMR.A	

Detailed Protein Report

Protein 972: testican-3 isoform 9 precursor [Homo sapiens]

Accession:	gi|324072875	**Score:**	12.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	35.6
Database Date:	2015-11-30	**pI:**	10.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLKVSAVLCV	CAAAWCSQSL	AAAAAVAAAG	GRSDGGNFLD	DKQWLTTISQ	YDKEVGQWNK	FRDDDYFRTW	SPGKPFDQAL
90	100	110	120	130	140	150	160
DPAKDPCLKM	KCSRHKVCIA	QDSQTAVCIS	HRRLTHRMKE	AGVDHRQWRG	PILSTCKQCP	VVYPSPVCGS	DGHTYSFQCK
170	180	190	200	210	220	230	240
LEYQACVLGK	QISVKCEGHC	PCPSDKPTST	SRNVKRACSD	LEFREVANRL	RDWFKALHES	GSQNKKTKTL	LRPERSRFDT
250	260	270	280	290	300	310	320
SILPICKDSL	GWMFNRLDTN	YDLLLDQSEL	RSIYLDKNEQ	CTKAFFNSCD	TYKDSLISNN	EWCYCFQRQQ	GKR

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1786	1	577.2453	-50.74	2	52.3	12.7	1	196-204	K.RACSDLEFR.E	Carbamidomethyl: 3

Detailed Protein Report

Protein 973: PREDICTED: zinc finger protein 569 isoform X2 [Homo sapiens]

Accession:	gi|530415811	**Score:**	12.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	60.4
Database Date:	2015-11-30	**pI:**	10.3
		Sequence Coverage [%]:	4.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MRKEHCEYNE	PVKSYGNSSS	HFVITPFKCN	HCGKGFNQTL	DLIRHLRIHT	GEKPYECSNC	RKAFSHKEKL	IKHYKIHSRE
90	100	110	120	130	140	150	160
QSYKCNECGK	AFIKMSNLIR	HQRIHTGEKP	YACKECEKSF	SQKSNLIDHE	KIHTGEKPYE	CNECGKAFSQ	KQSLIAHQKV
170	180	190	200	210	220	230	240
HTGEKPYACN	ECGKAFPRIA	SLALHMRSHT	GEKPYKCDKC	GKAFSQFSML	IIHVRIHTGE	KPYECNECGK	AFSQSSALTV
250	260	270	280	290	300	310	320
HMRSHTGEKP	YECKECRKAF	SHKKNFITHQ	KIHTREKPYE	CNECGKAFIQ	MSNLVRHQRI	HTGEKPYICK	ECGKAFSQKS
330	340	350	360	370	380	390	400
NLIAHEKIHS	GEKPYECNEC	GKAFSQKQNF	ITHQKVHTGE	KPYDCNECGK	AFSQIASLTL	HLRSHTGEKP	YECDKCGKAF
410	420	430	440	450	460	470	480
SQCSLLNLHM	RSHTGEKPYV	CNECGKAFSQ	RTSLIVHMRG	HTGEKPYECN	KCGKAFSQSS	SLTIHIRGHT	GEKPFDCSKC
490	500	510	520	530			
GKAFSQISSL	TLHMRKHTGE	KPYHCIECGK	AFSQKSHLVR	HQRIHTH			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
447	1	820.3791	-11.73	3	34.9	12.7	1	276-296	R.EKPYECNECGKAFIQMSNLVR.H	

Detailed Protein Report

Protein 974: **retinal-specific ATP-binding cassette transporter [Homo sapiens]**

Accession:	gi|105990541	**Score:**	12.7
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
2540	1	1045.0939	-285.62	1	62.2	12.7	0	1172-1182	K.GSEGTCSCSSK.G	

Detailed Protein Report

Protein 975: PREDICTED: sphingosine-1-phosphate phosphatase 1 isoform X1 [Homo sapiens]

Accession:	gi|578826162	**Score:**	12.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	45.6
Database Date:	2015-11-30	**pI:**	9.9
		Sequence Coverage [%]:	4.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSLRQRLAQL	VGRLQDPQKV	ARFQRLCGVE	APPRRSADRR	EDEKAEAPLA	GDPRLRGRQP	GAPGGPQPPG	SDRNQCPAKP
90	100	110	120	130	140	150	160
DGGGAPNGVR	NGLAAELGPA	SPRRAGALRR	NSLTGEEGQL	ARVSNWPLYC	LFCFGTELGN	ELFYILFFPF	WIWNLDPLVG
170	180	190	200	210	220	230	240
RRLVVIWVLV	MYLGQCTKDI	IRWPRPASPP	VVKLEVFYNS	EYSMPSTHAM	SGTAIPISMV	LLTYGRWQDI	IAGFLYTILI
250	260	270	280	290	300	310	320
LAVFYPFVDL	IDNFNQTHKY	APFIIIGLHL	ALGIFSFTLD	TWSTSRGDTA	EILGSGAGIA	CGSHVTYNMG	LVLDPSLDTL
330	340	350	360	370	380	390	400
PLAGPPITVT	LFGKAILRIL	IGMVFVLIIR	DVMKKITIPL	ACKIFNIPCD	DIRKARQHME	VELPYRYITY	GMVGFSITFF
410	420						
VPYIFFFIGI	S						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1865	1	682.2712	-143.24	3	53.4	12.7	1	356-373	K.ITIPLACKIFNIPCDDIR.K	

Detailed Protein Report

Protein 976: BTB/POZ domain-containing protein KCTD11 [Homo sapiens]

Accession:	gi|51036594	**Score:**	12.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	25.9
Database Date:	2015-11-30	**pI:**	6.2
		Sequence Coverage [%]:	6.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLGAMFRAGT	PMPPNLNSQG	GGHYFIDRDG	KAFRHILNFL	RLGRLDLPRG	YGETALLRAE	ADFYQIRPLL	DALRELEASQ
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
GTPAPTAALL	HADVDVSPRL	VHFSARRGPH	HYELSSVQVD	TFRANLFCTD	SECLGALRAR	FGVASGDRAE	GSPHFHLEWA
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
PRPVELPEVE	YGRLGLQPLW	TGGPGERREV	VGTPSFLEEV	LRVALEHGFR	LDSVFPDPED	LLNSRSLRFV	RH

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1788	1	806.7465	-161.16	2	52.3	12.7	0	124-138	R.ANLFCTDSECLGALR.A	

Detailed Protein Report

Protein 977: **PREDICTED: alpha-taxilin isoform X1 [Homo sapiens]**

Accession:	gi|530362064	**Score:**	12.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	43.3
Database Date:	2015-11-30	**pI:**	9.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MQTLNTLSTP	EEKLAALCKK	YAELLEEHRN	SQKQMKLLQK	KQSQLVQEKD	HLRGEHSKAV	LARSKLESLC	RELQRHNRSL
90	100	110	120	130	140	150	160
KEEGVQRARE	EEEKRKEVTS	HFQVTLNDIQ	LQMEQHNERN	SKLRQENMEL	AERLKKLIEQ	YELREEHIDK	VFKHKDLQQQ
170	180	190	200	210	220	230	240
LVDAKLQQAQ	EMLKEAEERH	QREKDFLLKE	AVESQRMCEL	MKQQETHLKQ	QLALYTEKFE	EFQNTLSKSS	EVFTTFKQEM
250	260	270	280	290	300	310	320
EKMTKKIKKL	EKETTMYRSR	WESSNKALLE	MAEEKTVRDK	ELEGLQVKIQ	RLEKLCRALQ	TERNDLNKRV	QDLSAGGQGS
330	340	350	360	370	380		
LTDSGPERRP	EGPGAQAPSS	PRVTEAPCYP	GAPSTEASGQ	TGPQEPTSAR	A		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2427	1	1056.2092	-246.91	1	60.7	12.6	1	238-245	K.QEMEKMTK.K	Oxidation: 3, 6

Detailed Protein Report

Protein 978: zinc finger protein 586 isoform b [Homo sapiens]

Accession:	gi|116812602	**Score:**	12.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	22.8
Database Date:	2015-11-30	**pI:**	10.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	9.5
		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
1529	1	1007.5953	57.03	2	48.9	12.6	2	2-21	M.AAAAALRAPAQVVGMEGKMR.Q	Oxidation: 19

Detailed Protein Report

Protein 979: PREDICTED: kinesin-like protein KIF3C isoform X1 [Homo sapiens]

Accession:	gi|578802893	**Score:**	12.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	89.3
Database Date:	2015-11-30	**pI:**	9.0
		Sequence Coverage [%]:	1.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MASKTKASEA	LKVVARCRPL	SRKEEAAGHE	QILTMDVKLG	QVTLRNPRAA	PGELPKTFTF	DAVYDASSKQ	ADLYDETVRP
90	100	110	120	130	140	150	160
LIDSVLQGFN	GTVFAYGQTG	TGKTYTMQGT	WVEPELRGVI	PNAFEHIFTH	ISRSQNQQYL	VRASYLEIYQ	EEIRDLLSKE
170	180	190	200	210	220	230	240
PGKRLELKEN	PETGVYIKDL	SSFVTKNVKE	IEHVMNLGNQ	TRAVGSTHMN	EVSSRSHAIF	IITVECSERG	SDGQDHIRVG
250	260	270	280	290	300	310	320
KLNLVDLAGS	ERQNKAGPNT	AGGAATPSSG	GGGGGGGSGG	GAGGERPKEA	SKINLSLSAL	GNVIAALAGN	RSTHIPYRDS
330	340	350	360	370	380	390	400
KLTRLLQDSL	GGNAKTIMVA	TLGPASHSYD	ESLSTLRFAN	RAKNIKNKPR	VNEDPKDTLL	REFQEEIARL	KAQLEKRGML
410	420	430	440	450	460	470	480
GKRPRRKSSR	RKKAVSAPPG	YPEGPVIEAW	VAEEEDDNNN	NHRPPQPILE	SALEKNMENY	LQEQKERLEE	EKAAIQDDRS
490	500	510	520	530	540	550	560
LVSEEKQKLL	EEKEKMLEDL	RREQQATELL	AAKYKAMESK	LLIGGRNIMD	HTNEQQKMLE	LKRQEIAEQK	RREREMQQEM
570	580	590	600	610	620	630	640
MLRDEETMEL	RGTYTSLQQE	VEVKTKKLKK	LYAKLQAVKA	EIQDQHDEYI	RVRQDLEEAQ	NEQTRELKLK	YLIIENFIPP
650	660	670	680	690	700	710	720
EEKNKIMNRL	FLDCEEEQWK	FQPLVPAGVS	SQMKKRPTSA	VGYKRPISQY	ARVAMAMGSH	PRYRAENIMF	LELDVSPPAV
730	740	750	760	770	780	790	800
FEMEFSHDQE	QDPRALHMER	LMRLDSFLER	PSTSKVRKSR	SWCQSPQRPP	PSTTHASLAS	ASLRPATVAD	HE

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2412	1	679.1732	-204.17	2	60.5	12.6	0	527-537	R.NIMDHTNEQQK.M	

Detailed Protein Report

Protein 980: PREDICTED: T-box transcription factor TBX22 isoform X4 [Homo sapiens]

Accession:	gi|578838386	**Score:**	12.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	39.7
Database Date:	2015-11-30	**pI:**	9.6
		Sequence Coverage [%]:	4.9
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578840717	refseq_human(refseq_human_20140103.fasta)	PREDICTED: T-box transcription factor TBX22 isoform X3 [Homo sapiens]

10	20	30	40	50	60	70	80
MALSSRARAF	SVEALVGRPS	KRKLQDPIQA	EQPELREKKG	GEEEEERRSS	AAGKSEPLAE	KQPKTEPSTS	ASSGCGSDSG
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
YGNSSESLEE	KDIQMELQGS	ELWKRFHDIG	TEMIITKAGR	RMFPSVRVKV	KGLDPGKQYH	VAIDVVPVDS	KRYRYVYHSS
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
QWMVAGNTDH	LCIIPRFYVH	PDSPCSGETW	MRQIISFDRM	KLTNNEMDDK	GHIILQSMHK	YKPRVHVIEQ	GSSVDLSQIQ
250	**260**	**270**	**280**	**290**	**300**	**310**	**320**
SLPTEGVKTF	SFKETEFTTV	TAYQNQQITK	LKIERNPFAK	GFRDTGRNRG	VLDGLLETYP	WRPSFTLDFK	TFGADTQILI
330	**340**	**350**	**360**				
EEGNKGKPSW	IIRLGRNLKR	FSSTHTLGME					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1901	1	682.2691	-146.50	3	53.8	12.6	2	138-154	K.QYHVAIDVVPVDSKRYR.Y	

Detailed Protein Report

Protein 981: PREDICTED: tyrosine-protein kinase transmembrane receptor ROR2 isoform X1 [Homo sapiens]

Accession:	gi|530391155	**Score:**	12.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	89.4
Database Date:	2015-11-30	**pI:**	6.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.0
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578817504	refseq_human (refseq_human_20140103.fasta)	PREDICTED: tyrosine-protein kinase transmembrane receptor ROR2 isoform X3 [Homo sapiens]

10	20	30	40	50	60	70	80
MKTITATGVL	FVRLGPTHSP	NHNFQDDYHE	DGFCQPYRGI	ACARFIGNRT	IYVDSLQMQG	EIENRITAAF	TMIGTSTHLS
90	100	110	120	130	140	150	160
DQCSQFAIPS	FCHFVFPLCD	ARSRTPKPRE	LCRDECEVLE	SDLCRQEYTI	ARSNPLILMR	LQLPKCEALP	MPESPDAANC
170	180	190	200	210	220	230	240
MRIGIPAERL	GRYHQCYNGS	GMDYRGTAST	TKSGHQCQPW	ALQHPHSHHL	SSTDFPELGG	GHAYCRNPGG	QMEGPWCFTQ
250	260	270	280	290	300	310	320
NKNVRMELCD	VPSCSPRDSS	KMGILYILVP	SIAIPLVIAC	LFFLVCMCRN	KQKASASTPQ	RRQLMASPSQ	DMEMPLINQH
330	340	350	360	370	380	390	400
KQAKLKEISL	SAVRFMEELG	EDRFGKVYKG	HLFGPAPGEQ	TQAVAIKTLK	DKAEGPLREE	FRHEAMLRAR	LQHPNVVCLL
410	420	430	440	450	460	470	480
GVVTKDQPLS	MIFSYCSHGD	LHEFLVMRSP	HSDVGSTDDD	RTVKSALEPP	DFVHLVAQIA	AGMEYLSSHH	VVHKDLATRN
490	500	510	520	530	540	550	560
VLVYDKLNVK	ISDLGLFREV	YAADYYKLLG	NSLLPIRWMA	PEAIMYGKFS	IDSDIWSYGV	VLWEVFSYGL	QPYCGYSNQD
570	580	590	600	610	620	630	640
VVEMIRNRQV	LPCPDDCPAW	VYALMIECWN	EFPSRRPRFK	DIHSRLRAWG	NLSNYNSSAQ	TSGASNTTQT	SSLSTSPVSN
650	660	670	680	690	700	710	720
VSNARYVGPK	QKAPPFPQPQ	FIPMKGQIRP	MVPPPQLYVP	VNGYQPVPAY	GAYLPNFYPV	QIPMQMAPQQ	VPPQMVPKPS
730	740	750	760	770	780	790	800
SHHSGSGSTS	TGYVTTAPSN	TSMADRAALL	SEGADDTQNA	PEDGAQSTVQ	EAEEEEEGSV	PETELLGDCD	TLQVDEAQVQ
810							
LEA							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2329	1	590.5024	-145.38	3	59.4	12.6	1	246-261	R.MELCDVPSCSPRDSSK.M	Oxidation: 1

Detailed Protein Report

Protein 982: **U3 small nucleolar RNA-associated protein 15 homolog isoform 2 [Homo sapiens]**

Accession:	gi|548923952	**Score:**	12.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	56.3
Database Date:	2015-11-30	**pI:**	9.7
		Sequence Coverage [%]:	2.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAGYKPVAIQ	TYPILGEKIT	QDTLYWNNYK	PPYNYAVTAS	SRIHIYGRYS	QEPIKTFSRF	KDTAYCATFR	QDGRLLVAGS
90	100	110	120	130	140	150	160
EDGGVQLFDI	SGRAPLRQFE	GHTKAVHTVD	FTADKYHVVS	GADDYTVKLW	DIPNSKEILT	FKEHSDYVRC	GCASKLNPDL
170	180	190	200	210	220	230	240
FITGSYDHTV	KMFDARTSES	VLSVEHGQPV	ESVLLFPSGG	LLVSAGGRYV	KVWDMLKGGQ	LLVSLKNHHK	TVTCLCLSSS
250	260	270	280	290	300	310	320
GQRLLSGSLD	RKVKVYSTTS	YKVVHSFDYA	ASILSLALAH	EDETIVVGMT	NGILSVKHRK	SEAKKESLPR	RRRPAYRTFI
330	340	350	360	370	380	390	400
KGKNYMKQRD	DILINRPAKK	HLELYDRDLK	HFRISKALDR	VLDPTCTIKT	PEITVSIIKE	LNRRGVLANA	LAGRDEKEIS
410	420	430	440	450	460	470	480
HVLNFLIRNL	SQPRFAPVLI	NAAEIIIDIY	LPVIGQSPVV	DKKFLLLQGL	VEKEIDYQRE	LLETLGMMDM	LFATMRRKEG
490	500						
TSVLEHTSDG	FPENKKIES						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
609	1	661.9075	142.03	2	37.2	12.6	1	60-70	R.FKDTAYCATFR.Q	

Detailed Protein Report

Protein 983: probable polypeptide N-acetylgalactosaminyltransferase 8 [Homo sapiens]

Accession:	gi|8393412	**Score:**	12.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	72.8
Database Date:	2015-11-30	**pI:**	9.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MMFWRKLPKA	LFIGLTLAIA	VNLLLVFSSK	GTLQNLFTGG	LHRELPLHLN	KRYGAVIKRL	SHLEVELQDL	KESMKLALRQ
90	100	110	120	130	140	150	160
QENVNSTLKR	AKDEVRPLLK	AMETKVNETK	KHKTQMKLFP	HSQLFRQWGE	DLSEAQQKAA	QDLFRKFGYN	AYLSNQLPLN
170	180	190	200	210	220	230	240
RTIPDTRDYR	CLRKTYPSQL	PSLSVILIFV	NEALSIIQRA	ITSIINRTPS	RLLKEIILVD	DFSSNGELKV	HLDEKIKLYN
250	260	270	280	290	300	310	320
QKYPGLLKII	RHPERKGLAQ	ARNTGWEAAT	ADVVAILDAH	IEVNVGWAEP	ILARIQEDRT	VIVSPVFDNI	RFDTFKLDKY
330	340	350	360	370	380	390	400
ELAVDGFNWE	LWCRYDALPQ	AWIDLHDVTA	PVKSPSIMGI	LAANRHFLGE	IGSLDGGMLI	YGGENVELSL	RVWQCGGKVE
410	420	430	440	450	460	470	480
ILPCSRIAHL	ERHHKPYALD	LTAALKRNAL	RVAEIWMDEH	KHMVYLAWNI	PLQNSGIDFG	DVSSRMALRE	KLKCKTFDWY
490	500	510	520	530	540	550	560
LKNVYPLLKP	LHTIVGYGRM	KNLLDENVCL	DQGPVPGNTP	IMYYCHEFSS	QNVYYHLTGE	LYVGQLIAEA	SASDRCLTDP
570	580	590	600	610	620	630	640
GKAEKPTLEP	CSKAAKNRLH	IYWDFKPGGA	VINRDTKRCL	EMKKDLLGSH	VLVLQTCSTQ	VWEIQHTVRD	WGQTNSQ

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1764	1	1273.4537	-105.56	1	52.0	12.6	0	432-441	R.VAEIWMDEHK.H	Oxidation: 6

Detailed Protein Report

Protein 984: cadherin EGF LAG seven-pass G-type receptor 1 precursor [Homo sapiens]

Accession:	gi|7656967	**Score:**	12.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	329.3
Database Date:	2015-11-30	**pI:**	5.5
		Sequence Coverage [%]:	0.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAPPPPPVLP	VLLLLAAAAA	LPAMGLRAAA	WEPRVPGGTR	AFALRPGCTY	AVGAACTPRA	PRELLDVGRD	GRLAGRRRVS
90	100	110	120	130	140	150	160
GAGRPLPLQV	RLVARSAPTA	LSRRLRARTH	LPGCGARARL	CGTGARLCGA	LCFPVPGGCA	AAQHSALAAP	TTLPACRCPP
170	180	190	200	210	220	230	240
RPRPRCPGRP	ICLPPGGSVR	LRLLCALRRA	AGAVRVGLAL	EAATAGTPSA	SPSPSPPLPP	NLPEARAGPA	RRARRGTSGR
250	260	270	280	290	300	310	320
GSLKFPMPNY	QVALFENEPA	GTLILQLHAH	YTIEGEEERV	SYYMEGLFDE	RSRGYFRIDS	ATGAVSTDSV	LDRETKETHV
330	340	350	360	370	380	390	400
LRVKAVDYST	PPRSATTYIT	VLVKDTNDHS	PVFEQSEYRE	RVRENLEVGY	EVLTIRASDR	DSPINANLRY	RVLGGAWDVF
410	420	430	440	450	460	470	480
QLNESSGVVS	TRAVLDREEA	AEYQLLVEAN	DQGRNPGPLS	ATATVYIEVE	DENDNYPQFS	EQNYVVQVPE	DVGLNTAVLR
490	500	510	520	530	540	550	560
VQATDRDQGQ	NAAIHYSILS	GNVAGQFYLH	SLSGILDVIN	PLDFEDVQKY	SLSIKAQDGG	RPPLINSSGV	VSVQVLDVND
570	580	590	600	610	620	630	640
NEPIFVSSPF	QATVLENVPL	GYPVVHIQAV	DADSGENARL	HYRLVDTAST	FLGGGSAGPK	NPAPTPDFPF	QIHNSSGWIT
650	660	670	680	690	700	710	720
VCAELDREEV	EHYSFGVEAV	DHGSPPMSSS	TSVSITVLDV	NDNDPVFTQP	TYELRLNEDA	AVGSSVLTLQ	ARDRDANSVI
730	740	750	760	770	780	790	800
TYQLTGGNTR	NRFALSSQRG	GGLITLALPL	DYKQEQQYVL	AVTASDGTRS	HTAHVLINVT	DANTHRPVFQ	SSHYTVSVSE
810	820	830	840	850	860	870	880
DRPVGTSIAT	LSANDEDTGE	NARITYVIQD	PVPQFRIDPD	SGTMYTMMEL	DYENQVAYTL	TIMAQDNGIP	QKSDTTTLEI
890	900	910	920	930	940	950	960
LILDANDNAP	QFLWDFYQGS	IFEDAPPSTS	ILQVSATDRD	SGPNGRLLYT	FQGGDDGDGD	FYIEPTSGVI	RTQRRLDREN
970	980	990	1000	1010	1020	1030	1040
VAVYNLWALA	VDRGSPTPLS	ASVEIQVTIL	DINDNAPMFE	KDELELFVEE	NNPVGSVVAK	IRANDPDEGP	NAQIMYQIVE
1050	1060	1070	1080	1090	1100	1110	1120
GDMRHFFQLD	LLNGDLRAMV	ELDFEVRREY	VLVVQATSAP	LVSRATVHIL	LVDQNDNPPV	LPDFQILFNN	YVTNKSNSFP
1130	1140	1150	1160	1170	1180	1190	1200
TGVIGCIPAH	DPDVSDSLNY	TFVQGNELRL	LLLDPATGEL	QLSRDLDNNR	PLEALMEVSV	SDGIHSVTAF	CTLRVTIITD
1210	1220	1230	1240	1250	1260	1270	1280
DMLTNSITVR	LENMSQEKFL	SPLLALFVEG	VAAVLSTTKD	DVFVFNVQND	TDVSSNILNV	TFSALLPGGV	RGQFFPSEDL
1290	1300	1310	1320	1330	1340	1350	1360
QEQIYLNRTL	LTTISTQRVL	PFDDNICLRE	PCENYMKCVS	VLRFDSSAPF	LSSTTVLFRP	IHPINGLRCR	CPPGFTGDYC
1370	1380	1390	1400	1410	1420	1430	1440
ETEIDLCYSD	PCGANGRCRS	REGGYTCECF	EDFTGEHCEV	DARSGRCANG	VCKNGGTCVN	LLIGGFHCVC	PPGEYERPYC
1450	1460	1470	1480	1490	1500	1510	1520
EVTTRSFPPQ	SFVTFRGLRQ	RFHFTISLTF	ATQERNGLLL	YNGRFNEKHD	FIALEIVDEQ	VQLTFSAGET	TTTVAPKVPS
1530	1540	1550	1560	1570	1580	1590	1600
GVSDGRWHSV	QVQYYNKPNI	GHLGLPHGPS	GEKMAVVTVD	DCDTTMAVRF	GKDIGNYSCA	AQGTQTGSKK	SLDLTGPLLL
1610	1620	1630	1640	1650	1660	1670	1680
GGVPNLPEDF	PVHNRQFVGC	MRNLSVDGKN	VDMAGFIANN	GTREGCAARR	NFCDGRRCQN	GGTCVNRWNM	YLCECPLRFG
1690	1700	1710	1720	1730	1740	1750	1760
GKNCEQAMPH	PQLFSGESVV	SWSDLNIIIS	VPWYLGLMFR	TRKEDSVLME	ATSGGPTSFR	LQILNNYLQF	EVSHGPSDVE
1770	1780	1790	1800	1810	1820	1830	1840
SVMLSGLRVT	DGEWHHLLIE	LKNVKEDSEM	KHLVTMTLDY	GMDQNKADIG	GMLPGLTVRS	VVVGGASEDK	VSVRRGFRGC
1850	1860	1870	1880	1890	1900	1910	1920
MQGVRMGGTP	TNVATLNMNN	ALKVRVKDGC	DVDDPCTSSP	CPPNSRCHDA	WEDYSCVCDK	GYLGINCVDA	CHLNPCENMG
1930	1940	1950	1960	1970	1980	1990	2000
ACVRSPGSPQ	GYVCECGPSH	YGPYCENKLD	LPCPRGWWGN	PVCGPCHCAV	SKGFDPDCNK	TNGQCQCKEN	YYKLLAQDTC
2010	2020	2030	2040	2050	2060	2070	2080
LPCDCFPHGS	HSRTCDMATG	QCACKPGVIG	RQCNRCDNPF	AEVTTLGCEV	IYNGCPKAFE	AGIWWPQTKF	GQPAAVPCPK
2090	2100	2110	2120	2130	2140	2150	2160
GSVGNAVRHC	SGEKGWLPPE	LFNCTTISFV	DLRAMNEKLS	RNETQVDGAR	ALQLVRALRS	ATQHTGTLFG	NDVRTAYQLL
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
155	1	855.3273	-115.70	2	31.7	12.6	0	715-730	R.DANSVITYQLTGGNTR.N	

Detailed Protein Report

Protein 985: zinc finger protein 329 [Homo sapiens]

Accession:	gi|71037407	**Score:**	12.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	61.7
Database Date:	2015-11-30	**pI:**	10.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.8
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578834898	refseq_human(refseq_human_20140103.fasta)	PREDICTED: zinc finger protein 329 isoform X4 [Homo sapiens]
gi|578834896	refseq_human(refseq_human_20140103.fasta)	PREDICTED: zinc finger protein 329 isoform X3 [Homo sapiens]
gi|578834894	refseq_human(refseq_human_20140103.fasta)	PREDICTED: zinc finger protein 329 isoform X2 [Homo sapiens]
gi|578834892	refseq_human(refseq_human_20140103.fasta)	PREDICTED: zinc finger protein 329 isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MRLKMTTRNF	PEREVPCDVE	VERFTREVPC	LSSLGDGWDC	ENQEGHLRQS	ALTLEKPGTQ	EAICEYPGFG	EHLIASSDLP
90	100	110	120	130	140	150	160
PSQRVLATNG	FHAPDSNVSG	LDCDPALPSY	PKSYADKRTG	DSDACGKGFN	HSMEVIHGRN	PVREKPYKYP	ESVKSFNHFT
170	180	190	200	210	220	230	240
SLGHQKIMKR	GKKSYEGKNF	ENIFTLSSSL	NENQRNLPGE	KQYRCTECGK	CFKRNSSLVL	HHRTHTGEKP	YTCNECGKSF
250	260	270	280	290	300	310	320
SKNYNLIVHQ	RIHTGEKPYE	CSKCGKAFSD	GSALTQHQRI	HTGEKPYECL	ECGKTFNRNS	SLILHQRTHT	GEKPYRCNEC
330	340	350	360	370	380	390	400
GKPFTDISHL	TVHLRIHTGE	KPYECSKCGK	AFRDGSYLTQ	HERTHTGEKP	FECAECGKSF	NRNSHLIVHQ	KIHSGEKPYE
410	420	430	440	450	460	470	480
CKECGKTFIE	SAYLIRHQRI	HTGEKPYGCN	QCQKLFRNIA	GLIRHQRTHT	GEKPYECNQC	GKAFRDSSCL	TKHQRIHTKE
490	500	510	520	530	540	550	
TPYQCPECGK	SFKQNSHLAV	HQRLHSREGP	SRCPQCGKMF	QKSSSLVRHQ	RAHLGEQPME	T	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1797	1	856.2884	-117.80	2	52.5	12.6	2	508-522	R.EGPSRCPQCGKMFQK.S	Oxidation: 12

Detailed Protein Report

Protein 986: PREDICTED: tau-tubulin kinase 2 isoform X5 [Homo sapiens]

Accession:	gi|578826647	**Score:**	12.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	129.8
Database Date:	2015-11-30	**pI:**	6.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	0.9
		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
1491	1	626.6231	-220.31	2	48.3	12.6	0	312-321	K.DVWEEMDANK.N	Oxidation: 6

Detailed Protein Report

Protein 987: PREDICTED: dual specificity protein kinase CLK3 isoform X4 [Homo sapiens]

Accession:	gi|530405373	**Score:**	12.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	31.9
Database Date:	2015-11-30	**pI:**	6.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	4.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSDWFNFHGH	MCIAFELLGK	NTFEFLKENN	FQPYPLPHVR	HMAYQLCHAL	RFLHENQLTH	TDLKPENILF	VNSEFETLYN
90	100	110	120	130	140	150	160
EHKSCEEKSV	KNTSIRVADF	GSATFDHEHH	TTIVATRHYR	PPEVILELGW	AQPCDVWSIG	CILFEYYRGF	TLFQTHENRE
170	180	190	200	210	220	230	240
HLVMMEKILG	PIPSHMIHRT	RKQKYFYKGG	LVWDENSSDG	RYVKENCKPL	KSYMLQDSLE	HVQLFDLMRR	MLEFDPAQRI
250	260	270					
TLAEALLHPF	FAGLTPEERS	FHTSRNPSR					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2272	1	693.7463	-203.34	2	58.7	12.6	0	168-179	K.ILGPIPSHMIHR.T	Oxidation: 9

Detailed Protein Report

Protein 988: spermatogenesis-associated protein 4 [Homo sapiens]

Accession:	gi|31543825	**Score:**	12.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	34.7
Database Date:	2015-11-30	**pI:**	10.4
		Sequence Coverage [%]:	6.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAAAGQEKGY	LTQTAAALDK	SPSLSPQLAA	PIRGRPKKCL	VYPHAPKSSR	LSRSVLRWLQ	GLDLSFFPRN	INRDFSNGFL
90	100	110	120	130	140	150	160
IAEIFCIYYP	WELELSSFEN	GTSLKVKLDN	WAQLEKFLAR	KKFKLPKELI	HGTIHCKAGV	PEILIEEVYT	LLTHREIKSI
170	180	190	200	210	220	230	240
QDDFVNFTDY	SYQMRLPLVS	RSTVSKSIKD	NIRLSELLSN	PNMLTNELKA	EFLILLHMLQ	RKLGRKLNPE	WFDVKPTVGE
250	260	270	280	290	300	310	
VTLNHLPAQA	SGRRYNLKVK	RGRVVPVLPN	IGSGGSSHRE	IHVKQAGQHS	YYSAMKPIRN	MDKKP	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2620	1	973.0041	-42.64	2	62.8	12.5	2	261-279	K.RGRVVPVLPNIGSGGSSHR.E	

Detailed Protein Report

Protein 989: PREDICTED: zinc finger protein 688 isoform X2 [Homo sapiens]

Accession:	gi|530407669	**Score:**	12.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	26.4
Database Date:	2015-11-30	**pI:**	10.8
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	8.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAPPPAPLLA	PRPGETRPGC	RKPGTVSFAD	VAVYFSPEEW	GCLRPAQRAL	YRDVMQETYG	HLGALGDVPN	RKEEEPEEVP
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
RAKGPRKAPV	KESPEVLVER	NPDPAISVAP	ARAQPPKNAA	WDPTTGAQPP	APIPSMDAQA	GQRRHVCTDC	GRRFTYPSLL
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
VSHRRMHSGE	RPFPCPECGM	RFKRKFAVEA	HQWIHRSCSG	GRRGRRPGIR	AVPRAPVRGD	RDPPVLFRHY	PDIFEECG

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2232	1	1129.1831	83.97	2	57.8	12.5	0	1-21	-.MAPPPAPLLAPRPGETRPGCR.K	Carbamidomethyl: 20; Oxidation: 1

Detailed Protein Report

Protein 990: **ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial precursor [Homo sapiens]**

Accession:	gi|7242140	**Score:**	12.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	69.2
Database Date:	2015-11-30	**pI:**	8.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.2
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 0.77 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MPSCGACTCG	AAAVRLITSS	LASAQRGISG	GRIHMSVLGR	LGTFETQILQ	RAPLRSFTET	PAYFASKDGI	SKDGSGDGNK
90	100	110	120	130	140	150	160
KSASEGSSKK	SGSGNSGKGG	NQLRCPKCGD	LCTHVETFVS	STRFVKCEKC	HHFFVVLSEA	DSKKSIIKEP	ESAAEAVKLA
170	180	190	200	210	220	230	240
FQQKPPPPPK	KIYNYLDKYV	VGQSFAKKVL	SVAVYNHYKR	IYNNIPANLR	QQAEVEKQTS	LTPRELEIRR	REDEYRFTKL
250	260	270	280	290	300	310	320
LQIAGISPHG	NALGASMQQQ	VNQQIPQEKR	GGEVLDSSHD	DIKLEKSNIL	LLGPTGSGKT	LLAQTLAKCL	DVPFAICDCT
330	340	350	360	370	380	390	400
TLTQAGYVGE	DIESVIAKLL	QDANYNVEKA	QQGIVFLDEV	DKIGSVPGIH	QLRDVGGEGV	QQGLLKLLEG	TIVNVPEKNS
410	420	430	440	450	460	470	480
RKLRGETVQV	DTTNILFVAS	GAFNGLDRII	SRRKNEKYLG	FGTPSNLGKG	RRAAAAADLA	NRSGESNTHQ	DIEEKDRLLR
490	500	510	520	530	540	550	560
HVEARDLIEF	GMIPEFVGRL	PVVVPLHSLD	EKTLVQILTE	PRNAVIPQYQ	ALFSMDKCEL	NVTEDALKAI	ARLALERKTG
570	580	590	600	610	620	630	640
ARGLRSIMEK	LLLEPMFEVP	NSDIVCVEVD	KEVVEGKKEP	GYIRAPTKES	SEEEYDSGVE	EEGWPRQADA	ANS

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
919	1	662.1519	-199.14	2	40.9	12.5	0	2-15	M.PSCGACTCGAAAVR.L	Carbamidomethyl: 3	MD:MU	0.77

Detailed Protein Report

Protein 991: **ATP-binding cassette sub-family C member 11 isoform b [Homo sapiens]**

Accession:	gi|21729876	**Score:**	12.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	150.0
Database Date:	2015-11-30	**pI:**	9.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MTRKRTYWVP	NSSGGLVNRG	IDIGDDMVSG	LIYKTYTLQD	GPWSQQERNP	EAPGRAAVPP	WGKYDAALRT	MIPFRPKPRF
90	100	110	120	130	140	150	160
PAPQPLDNAG	LFSYLTVSWL	TPLMIQSLRS	RLDENTIPPL	SVHDASDKNV	QRLHRLWEEE	VSRRGIEKAS	VLLVMLRFQR
170	180	190	200	210	220	230	240
TRLIFDALLG	ICFCIASVLG	PILIIPKILE	YSEEQLGNVV	HGVGLCFALF	LSECVKSLSF	SSSWIINQRT	AIRFRAAVSS
250	260	270	280	290	300	310	320
FAFEKLIQFK	SVIHITSGEA	ISFFTGDVNY	LFEGVCYGPL	VLITCASLVI	CSISSYFIIG	YTAFIAILCY	LLVFPLAVFM
330	340	350	360	370	380	390	400
TRMAVKAQHH	TSEVSDQRIR	VTSEVLTCIK	LIKMYTWEKP	FAKIIEDLRR	KERKLLEKCG	LVQSLTSITL	FIIPTVATAV
410	420	430	440	450	460	470	480
WVLIHTSLKL	KLTASMAFSM	LASLNLLRLS	VFFVPIAVKG	LTNSKSAVMR	FKKFFLQESP	VFYVQTLQDP	SKALVFEEAT
490	500	510	520	530	540	550	560
LSWQQTCPGI	VNGALELERN	GHASEGMTRP	RDALGPEEEG	NSLGPELHKI	NLVVSKGMML	GVCGNTGSGK	SSLLSAILEE
570	580	590	600	610	620	630	640
MHLLEGSVGV	QGSLAYVPQQ	AWIVSGNIRE	NILMGGAYDK	ARYLQVLHCC	SLNRDLELLP	FGDMTEIGER	GLNLSGGQKQ
650	660	670	680	690	700	710	720
RISLARAVYS	DRQIYLLDDP	LSAVDAHVGK	HIFEECIKKT	LRGKTVVLVT	HQLQYLEFCG	QIILLENGKI	CENGTHSELM
730	740	750	760	770	780	790	800
QKKGKYAQLI	QKMHKEATSD	MLQDTAKIAE	KPKVESQALA	TSLEESLNGN	AVPEHQLTQE	EEMEEGSLSW	RVYHHYIQAA
810	820	830	840	850	860	870	880
GGYMVSCIIF	FFVVLIVFLT	IFSFWWLSYW	LEQGSGTNSS	RESNGTMADL	GNIADNPQLS	FYQLVYGLNA	LLLICVGVCS
890	900	910	920	930	940	950	960
SGIFTKVTRK	ASTALHNKLF	NKVFRCPMSF	FDTIPIGRLL	NCFAGDLEQL	DQLLPIFSEQ	FLVLSLMVIA	VLLIVSVLSP
970	980	990	1000	1010	1020	1030	1040
YILLMGAIIM	VICFIYYMMF	KKAIGVFKRL	ENYSRSPLFS	HILNSLQGLS	SIHVYGKTED	FISQFKRLTD	AQNNYLLLFL
1050	1060	1070	1080	1090	1100	1110	1120
SSTRWMALRL	EIMTNLVTLA	VALFVAFGIS	STPYSFKVMA	VNIVLQLASS	FQATARIGLE	TEAQFTAVER	ILQYMKMCVS
1130	1140	1150	1160	1170	1180	1190	1200
EAPLHMEGTS	CPQGWPQHGE	IIFQDYHMKY	RDNTPTVLHG	INLTIRGHEV	VGIVGRTGSG	KSSLGMALFR	LVEPMAGRIL
1210	1220	1230	1240	1250	1260	1270	1280
IDGVDICSIG	LEDLRSKLSV	IPQDPVLLSG	TIRFNLDPFD	RHTDQQIWDA	LERTFLTKAI	ILIDEATASI	DMETDTLIQR
1290	1300	1310	1320	1330	1340	1350	
TIREAFQGCT	VLVIAHRVTT	VLNCDHILVM	GNGKVVEFDR	PEVLRKKPGS	LFAALMATAT	SSLR	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2294	1	869.2615	-150.95	2	59.0	12.5	1	733-747	K.MHKEATSDMLQDTAK.I	Oxidation: 1, 9

Detailed Protein Report

Protein 992: potassium voltage-gated channel subfamily A member 1 [Homo sapiens]

Accession:	gi|119395748	**Score:**	12.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	56.4
Database Date:	2015-11-30	**pI:**	4.9
		Sequence Coverage [%]:	2.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MTVMSGENVD	EASAAPGHPQ	DGSYPRQADH	DDHECCERVV	INISGLRFET	QLKTLAQFPN	TLLGNPKKRM	RYFDPLRNEY
90	100	110	120	130	140	150	160
FFDRNRPSFD	AILYYYQSGG	RLRRPVNVPL	DMFSEEIKFY	ELGEEAMEKF	REDEGFIKEE	ERPLPEKEYQ	RQVWLLFEYP
170	180	190	200	210	220	230	240
ESSGPARVIA	IVSVMVILIS	IVIFCLETLP	ELKDDKDFTG	TVHRIDNTTV	IYNSNIFTDP	FFIVETLCII	WFSFELVVRF
250	260	270	280	290	300	310	320
FACPSKTDFF	KNIMNFIDIV	AIIPYFITLG	TEIAEQEGNQ	KGEQATSLAI	LRVIRLVRVF	RIFKLSRHSK	GLQILGQTLK
330	340	350	360	370	380	390	400
ASMRELGLLI	FFLFIGVILF	SSAVYFAEAE	EAESHFSSIP	DAFWWAVVSM	TTVGYGDMYP	VTIGGKIVGS	LCAIAGVLTI
410	420	430	440	450	460	470	480
ALPVPVIVSN	FNYFYHRETE	GEEQAQLLHV	SSPNLASDSD	LSRRSSSTMS	KSEYMEIEED	MNNSIAHYRQ	VNIRTANCTT
490	500						
ANQNCVNKSK	LLTDV						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2837	1	673.3628	89.35	2	65.9	12.5	0	119-129	K.FYELGEEAMEK.F	

Detailed Protein Report

Protein 993: PREDICTED: uncharacterized protein C1orf194 isoform X4 [Homo sapiens]

Accession:	gi|578798360	**Score:**	12.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	21.3
Database Date:	2015-11-30	**pI:**	10.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	8.1
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MVSSQHFSAE AQECNSKSRA RSAERSLCSP RSFLPRGLPW SAARWRPPLR EFLCHRWLGS CLATETSAPN NWDPGSYASE
        90        100        110        120        130        140        150        160
AVLRLSGPPI PLKRVRHLAM PPTRDPFQQP TLDNDDSYLG ELRASKKLPY KNPTHLAQQQ EPWSRLNSTP TITSMRRDAY
       170        180        190
YFDPENQDPI PWRIFNPSHS THHFPG
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1672	1	881.8269	-144.73	2	50.7	12.5	2	22-36	R.SAERSLCSPRSFLPR.G	Carbamidomethyl: 7

Detailed Protein Report

Protein 994: **persephin precursor [Homo sapiens]**

Accession:	gi|4758974	**Score:**	12.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	16.6
Database Date:	2015-11-30	**pI:**	11.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	7.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAVGKFLLGS	LLLLSLQLGQ	GWGPDARGVP	VADGEFSSEQ	VAKAGGTWLG	THRPLARLRR	ALSGPCQLWS	LTLSVAELGL
90	100	110	120	130	140	150	160
GYASEEKVIF	RYCAGSCPRG	ARTQHGLALA	RLQGQGRAHG	GPCCRPTRYT	DVAFLDDRHR	WQRLPQLSAA	ACGCGG

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
476	1	599.1470	-198.93	2	35.3	12.5	1	92-102	R.YCAGSCPRGAR.T	Carbamidomethyl: 6

Detailed Protein Report

Protein 995: **PREDICTED: nidogen-1 isoform X1 [Homo sapiens]**

Accession:	gi|578802227	**Score:**	12.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	126.5
Database Date:	2015-11-30	**pI:**	5.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLASSSRIRA	AWTRALLLPL	LLAGPVGCLS	RQELFPFGPG	QGDLELEDGD	DFVSPALELS	GALRFYDRSD	IDAVYVTTNG
90	100	110	120	130	140	150	160
IIATSEPPAK	ESHPGLFPPT	FGAVAPFLAD	LDTTDGLGKV	YYREDLSPSI	TQRAAECVHR	GFPEISFQPS	SAVVVTWESV
170	180	190	200	210	220	230	240
APYQGPSRDP	DQKGKRNTFQ	AVLASSDSSS	YAIFLYPEDG	LQFHTTFSKK	ENNQVPAVVA	FSQGSVGFLW	KSNGAYNIFA
250	260	270	280	290	300	310	320
NDRESVENLA	KSSNSGQQGV	WVFEIGSPAT	TNGVVPADVI	LGTEDGAEYD	DEDEDYDLAT	TRLGLEDVGT	TPFSYKALRR
330	340	350	360	370	380	390	400
GGADTYSVPS	VLSPRRAATE	RPLGPPTERT	RSFQLAVETF	HQQHPQVIDV	DEVEETGVVF	SYNTDSRQTC	ANNRHQCSVH
410	420	430	440	450	460	470	480
AECRDYATGF	CCSCVAGYTG	NGRQCVAEGS	PQRVNGKVKG	RIFVGSSQVP	IVFENTDLHS	YVVMNHGRSY	TAISTIPETV
490	500	510	520	530	540	550	560
GYSLLPLAPV	GGIIGWMFAV	EQDGFKNGFS	ITGGEFTRQA	EVTFVGHPGN	LVIKQRFSGI	DEHGHLTIDT	ELEGRVPQIP
570	580	590	600	610	620	630	640
FGSSVHIEPY	TELYHYSTSV	ITSSSTREYT	VTEPERDGAS	PSRIYTYQWR	QTITFQECVH	DDSRPALPST	QQLSVDSVFV
650	660	670	680	690	700	710	720
LYNQEEKILR	YALSNSIGPV	REGSPDALQN	PCYIGTHGCD	TNAACRPGPR	TQFTCECSIG	FRGDGRTCYD	IDECSEQPSV
730	740	750	760	770	780	790	800
CGSHTICNNH	PGTFRCECVE	GYQFSDEGTC	VEVEKTRCQH	EREHILGAAG	ATDPQRPIPP	GLFVPECDAH	GHYAPTQCHG
810	820	830	840	850	860	870	880
STGYCWCVDR	DGREVEGTRT	RPGMTPPCLS	TVAPPIHQGP	AVPTAVIPLP	PGTHLLFAQT	GKIERLPLEG	NTMRKTEAKA
890	900	910	920	930	940	950	960
FLHVPAKVII	GLAFDCVDKM	VYWTDITEPS	IGRASLHGGE	PTTIIRQDLG	SPEGIAVDHL	GRNIFWTDSN	LDRIEVAKLD
970	980	990	1000	1010	1020	1030	1040
GTQRRVLFET	DLVNPRGIVT	DSVRGNLYWT	DWNRDNPKIE	TSYMDGTNRR	ILVQDDLGLP	NGLTFDAFSS	QLCWVDAGTN
1050	1060	1070	1080	1090	1100	1110	1120
RAECLNPSQP	SRRKALEGLQ	YPFAVTSYGK	NLYFTDWKMN	SVVALDLAIS	KETDAFQPHK	QTRLYGITTA	LSQCPQGHNY
1130	1140	1150	1160				
CSVNNGGCTH	LCLATPGSRT	CRCPDNTLGV	DCIEQK				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
181	1	796.2730	-106.98	2	31.7	12.4	0	1143-1156	R.CPDNTLGVDCIEQK.-	Carbamidomethyl: 10

Detailed Protein Report

Protein 996: **probable cation-transporting ATPase 13A1 [Homo sapiens]**

Accession:	gi|170016077	**Score:**	12.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	132.9
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
MAAAAAVGNA	VPCGARPCGV	RPDGQPKPGP	QPRALLAAGP	ALIANGDELV	AAVWPYRRLA	LLRRLTVLPF	AGLLYPAWLG
90	100	110	120	130	140	150	160
AAAAGCWGWG	SSWVQIPEAA	LLVLATICLA	HALTVLSGHW	SVHAHCALTC	TPEYDPSKAT	FVKVVPTPNN	GSTELVALHR
170	180	190	200	210	220	230	240
NEGEDGLEVL	SFEFQKIKYS	YDALEKKQFL	PVAFPVGNAF	SYYQSNRGFQ	EDSEIRAAEK	KFGSNKAEMV	VPDFSELFKE
250	260	270	280	290	300	310	320
RATAPFFVFQ	VFCVGLWCLD	EYWYYSVFTL	SMLVAFEASL	VQQQMRNMSE	IRKMGNKPHM	IQVYRSRKWR	PIASDEIVPG
330	340	350	360	370	380	390	400
DIVSIGRSPQ	ENLVPCDVLL	LRGRCIVDEA	MLTGESVPQM	KEPIEDLSPD	RVLDLQADSR	LHVIFGGTKV	VQHIPPQKAT
410	420	430	440	450	460	470	480
TGLKPVDSGC	VAYVLRTGFN	TSQGKLLRTI	LFGVKRVTAN	NLETFIFILF	LLVFAIAAAA	YVWIEGTKDP	SRNRYKLFLE
490	500	510	520	530	540	550	560
CTLILTSVVP	PELPIELSLA	VNTSLIALAK	LYMYCTEPFR	IPFAGKVEVC	CFDKTGTLTS	DSLVVRGVAG	LRDGKEVTPV
570	580	590	600	610	620	630	640
SSIPVETHRA	LASCHSLMQL	DDGTLVGDPL	EKAMLTAVDW	TLTKDEKVFP	RSIKTQGLKI	HQRFHFASAL	KRMSVLASYE
650	660	670	680	690	700	710	720
KLGSTDLCYI	AAVKGAPETL	HSMFSQCPPD	YHHIHTEISR	EGARVLALGY	KELGHLTHQQ	AREVKREALE	CSLKFVGFIV
730	740	750	760	770	780	790	800
VSCPLKADSK	AVIREIQNAS	HRVVMITGDN	PLTACHVAQE	LHFIEKAHTL	ILQPPSEKGR	QCEWRSIDGS	IVLPLARGSP
810	820	830	840	850	860	870	880
KALALEYALC	LTGDGLAHLQ	ATDPQQLLRL	IPHVQVFARV	APKQKEFVIT	SLKELGYVTL	MCGDGTNDVG	ALKHADVGVA
890	900	910	920	930	940	950	960
LLANAPERVV	ERRRRPRDSP	TLSNSGIRAT	SRTAKQRSGL	PPSEEQPTSQ	RDRLSQVLRD	LEDESTPIVK	LGDASIAAPF
970	980	990	1000	1010	1020	1030	1040
TSKLSSIQCI	CHVIKQGRCT	LVTTLQMFKI	LALNALILAY	SQSVLYLEGV	KFSDFQATLQ	GLLLAGCFLF	ISRSKPLKTL
1050	1060	1070	1080	1090	1100	1110	1120
SRERPLPNIF	NLYTILTVML	QFFVHFLSLV	YLYREAQARS	PEKQEQFVDL	YKEFEPSLVN	STVYIMAMAM	QMATFAINYK
1130	1140	1150	1160	1170	1180	1190	1200
GPPFMESLPE	NKPLVWSLAV	SLLAIIGLLL	GSSPDFNSQF	GLVDIPVEFK	LVIAQVLLLD	FCLALLADRV	LQFFLGTPKL
1210							
KVPS							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2027	1	1022.8890	-114.38	2	55.5	12.4	1	222-239	K.FGSNKAEMVVPDFSELFK.E	

Detailed Protein Report

Protein 997: PREDICTED: ras guanyl-releasing protein 3 isoform X2 [Homo sapiens]

Accession:	gi|530367447	**Score:**	12.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	64.9
Database Date:	2015-11-30	**pI:**	7.0
		Sequence Coverage [%]:	2.8
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 1.33 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MGSSGLGKAA	TLDELLCTCI	EMFDDNGELD	NSYLPRIVLL	MHRWYLSSTE	LAEKLLCMYR	NATGESCNEF	RLKICYFMRY
90	100	110	120	130	140	150	160
WILKFPAEFN	LDLGLIRMTE	EFREVASQLG	YEKHVSLIDI	SSIPSYDWMR	RVTQRKKVSK	KGKACLLFDH	LEPIELAEHL
170	180	190	200	210	220	230	240
TFLEHKSFRR	ISFTDYQSYV	IHGCLENNPT	LERSIALFNG	ISKWVQLMVL	SKPTPQQRAE	VITKFINVAK	KLLQLKNFNT
250	260	270	280	290	300	310	320
LMAVVGGLSH	SSISRLKETH	SHLSSEVTKN	WNEMTELVSS	NGNYCNYRKA	FADCDGFKIP	ILGVHLKDLI	AVHVIFPDWT
330	340	350	360	370	380	390	400
EENKVNIVKM	HQLSVTLSEL	VSLQNASHHL	EPNMDLINLL	TLSLDLYHTE	DDIYKLSLVL	EPRNSKSQPT	SPTTPNKPVV
410	420	430	440	450	460	470	480
PLEWALGVMP	KPDPTVINKH	IRKLVESVFR	NYDHDHDGYI	SQEDFESIAA	NFPFLDSFCV	LDKDQDGLIS	KDEMMAYFLR
490	500	510	520	530	540	550	560
AKSQLHCKMG	PGFIHNFQEM	TYLKPTFCEH	CAGFLWGIIK	QGYKCKDCGA	NCHKQCKDLL	VLACRRFARA	PSLSSGHGSL
570							
PGSPSLPPG							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2795	1	958.9896	34.46	2	65.4	12.4	1	98-113	R.MTEEFREVASQLGYEK.H		MD:MU 1.33

Detailed Protein Report

Protein 998: TBC1 domain family member 22A isoform b [Homo sapiens]

Accession:	gi|546231127	**Score:**	12.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	50.9
Database Date:	2015-11-30	**pI:**	5.6
		Sequence Coverage [%]:	3.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MASDGARKQF	WKRSNSKLPG	SLLRSTAKMP	TTPVKAKRVS	TFQEFESNTS	DAWDAGEDDD	ELLAMAAESL	NSEVVMETAN
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
RVLRNHSQRQ	GRPTLQEGPG	LQQKPRPEAE	PPSPPSGDLR	LVKSVSESHT	SCPAEELRRL	SWSGIPKPVR	PMTWKLLSGY
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
LPANVDRRPA	TLQRKQKEYF	AFIEHYYDSR	NDEVHQDTYR	QIHIDIPRMS	PEALILQPKV	TEIFERILFI	WAIRHPASGY
250	**260**	**270**	**280**	**290**	**300**	**310**	**320**
VQGINDLVTP	FFVVFICEYI	EAEEVDTVDV	SGVPAEVLCN	IEADTYWCMS	KLLDGIQDNY	TFAQPGIQMK	VKMLEELVSR
330	**340**	**350**	**360**	**370**	**380**	**390**	**400**
IDEQVHRHLD	QHEVRYLQFA	FRWMNNLLMR	EVPLRCTIRL	WDTYQSEPDG	FSHFHLYVCA	AFLVRWRKEI	LEEKDFQELL
410	**420**	**430**	**440**				
LFLQNLPTAH	WDDEDISLLL	AEAYRLKFAF	ADAPNHYKK				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1413	1	816.3918	26.50	2	47.3	12.4	0	124-138	K.SVSESHTSCPAEELR.R	

Detailed Protein Report

Protein 999: **PREDICTED: src kinase-associated phosphoprotein 1 isoform X2 [Homo sapiens]**

Accession:	gi|530413029	**Score:**	12.4
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
890	1	622.8509	51.55	2	40.6	12.4	0	1-11	-.MQAAALPEEIR.W	Oxidation: 1

Detailed Protein Report

Protein 1000: PREDICTED: nuclear pore membrane glycoprotein 210-like isoform X1 [Homo sapiens]

Accession:	gi|578801695	**Score:**	12.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	193.6
Database Date:	2015-11-30	**pI:**	7.1
		Sequence Coverage [%]:	0.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MVRALDAEGN	TFSSLAGMMF	EWSIAQDNES	AREELSSKIR	ILKYSEAEYA	PPIYIAEMEK	EEKQGDVILV	SGIRTGAAVV
90	100	110	120	130	140	150	160
KVRIHEPFYK	KVAAALIRLL	VLENIFLIPS	HDIYLLVGTY	IKYQVAKMVQ	GRVTEVKFPL	EHYILELQDH	RVALNGSHSE
170	180	190	200	210	220	230	240
KVAILDDKTA	MVTASQLGQT	NLVFVHKNVH	MRSVSGLPNC	TIYVVEPGFL	GFTVQPGNRW	SLEVGQVYVI	TVDVFDKSST
250	260	270	280	290	300	310	320
KVYISDNLRI	TYDFPKEYFE	EQLTTVNGSY	HIVKALKDGV	VVINASLTSI	IYQNKDIQPI	KFLIKHQQEV	KIYFPIMLTP
330	340	350	360	370	380	390	400
KFLAFPHHPM	GMLYRYKVQV	EGGSGNFTWT	SSNETVVIVT	TKGVVTAGQV	RGNSTVLARD	VQNPFRYGEI	KIHVLKLNKM
410	420	430	440	450	460	470	480
ELLPFHADVE	IGQIIEIPIA	MYHINKETKE	AMAFTDCSHL	SLDLNMDKQG	VFTLLKEGIQ	RPGPMHCSST	HIAAKSLGHT
490	500	510	520	530	540	550	560
LVTVSVNECD	KYLESSATFA	AYEPLKALNP	VEVALVTWQS	VKEMVFEGGP	RPWILEPSRF	FLELNAEKTE	KIGIAQVWLP
570	580	590	600	610	620	630	640
SKRKQNQYIY	RIQCLDLGEQ	VLTFRIGNHP	GVLNPSPAVE	VLQVRFICAH	PASMSVTPVY	KVPAGAQPCP	LPQHNKWLIP
650	660	670	680	690	700	710	720
VSRLRDTVLE	LAVFDQHRRK	FDNFSSLMLE	WKSSNETLAH	FEDYKSVEMV	AKDDGSGQTR	LHGHQILKVH	QIKGTVLIGV
730	740	750	760	770	780	790	800
NFVGYSEKKS	PKEISNLPRS	VDVELLLVDD	VTVVPENATI	YNHPDVKETF	SLVEGSGYFL	VNSSEQGVVT	ITYMEAESSV
810	820	830	840	850	860	870	880
ELVPLHPGFF	TLEVYDLCLA	FLGPATAHLR	VSDIQELELD	LIDKVEIDKT	VLVTVRVLGS	SKRPFQNKYF	RNMELKLQLA
890	900	910	920	930	940	950	960
SAIVTLTPME	QQDEYSENYI	LRATTIGQTT	LVAIAKDKMG	RKYTSTPRHI	EVFPPFRLLP	EKMTLIPMNM	MQVMSEGGPQ
970	980	990	1000	1010	1020	1030	1040
PQSIVHFSIS	NQTVAVVNRR	GQVTGKIVGT	AVVHGTIQTV	NEDTGKVIVF	SQDEVQIEVV	QLRAVRILAA	ATRLITATKM
1050	1060	1070	1080	1090	1100	1110	1120
PVYVMGVTST	QTPFSFSNAN	PGLTFHWSMS	KRDVLDLVPR	HSEVFLQLPV	EHNFAMVVHT	KAAGRTSIKV	TVHCMNSSSG
1130	1140	1150	1160	1170	1180	1190	1200
QFEGNLLELS	DEVQILVFEK	LQLFYPECQP	EQILMPINSQ	LKLHTNREGA	AFVSSRVLKC	FPNSSVIEED	GEGLLKAGSI
1210	1220	1230	1240	1250	1260	1270	1280
AGTAVLEVTS	IEPFGVNQTT	ITGVQVAPVT	YLRVSSQPKL	YTAQGRTLSA	FPLGMSLTFT	VQFYNSIGEK	FHTHNTQLYL
1290	1300	1310	1320	1330	1340	1350	1360
ALNRDDLLHI	GPGNKNYTYM	AQAVNRGLTL	VGLWDRRHPG	MADYIPVAVE	HAIEPDTKLT	FVGDIICFST	HLVSQHGEPG
1370	1380	1390	1400	1410	1420	1430	1440
IWMISANNIL	QTDIVTGVGV	ARSPGTAMIF	HDIPGVVKTY	REVVVNASSR	LMLSYDLKTY	LTNTLNSTVF	KLFITTGRNG
1450	1460	1470	1480	1490	1500	1510	1520
VNLKGFCTPN	QALAITKVLL	PATLMLCHVQ	FSNTLLDIPA	SKVFQVHSDF	SMEKGVYVCI	IKVRPQSEEL	LQALSVADTS
1530	1540	1550	1560	1570	1580	1590	1600
VYGWATLVSE	RSKNGMQRIL	IPFIPAFYIN	QSELVLSHKQ	DIGEIRVLGV	DRVLRKLEVI	SSSPVLVVAG	HSHSPLTPGL
1610	1620	1630	1640	1650	1660	1670	1680
AIYSVRVVNF	TSFQQMASPV	FINISCVLTS	QSEAVVVRAM	KDKLGADHCE	DSAILKRFTG	SYQILLLTLF	AVLASTASIF
1690	1700	1710	1720	1730	1740		
LAYNAFLNKI	QTVPVVYVPT	LGTPQPGFFN	STSSPPHFMS	LQPPLAQSRL	QHWLWSIRH		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1389	1	816.1017	158.52	2	47.0	12.4	1	903-918	R.ATTIGQTTLVAIAKDK.M	

Detailed Protein Report

Protein 1001: seizure 6-like protein 2 isoform 4 precursor [Homo sapiens]

Accession:	gi|166235140	**Score:**	12.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	86.8
Database Date:	2015-11-30	**pI:**	4.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGTPRAQHPP	PPQLLFLILL	SCPWIQGLPL	KEEEILPEPG	SETPTVASEA	LAELLHGALL	RRGPEMGYLP	GSDRDPTLAT
90	100	110	120	130	140	150	160
PPAGQTLAVP	SLPRATEPGT	GPLTTAVTPN	GVRGAGPTAP	ELLTPPPGTT	APPPPSPASP	GPPLGPEGGE	EETTTTIITT
170	180	190	200	210	220	230	240
TTVTTTVTSP	AYLLSCGFPP	RPAHGDVSVT	DLHPGGTATF	HCDSGYQLQG	EETLICLNGT	RPSWNGETPS	CMASCGGTIH
250	260	270	280	290	300	310	320
NATLGRIVSP	EPGGAVGPNL	TCRWVIEAAE	GRRLHLHFER	VSLDEDNDRL	MVRSGGSPLS	PVIYDSDMDD	VPERGLISDA
330	340	350	360	370	380	390	400
QSLYVELLSE	TPANPLLLSL	RFEAFEEDRC	FAPFLAHGNV	TTTDPEYRPG	ALATFSCLPG	YALEPPGPPN	AIECVDPTEP
410	420	430	440	450	460	470	480
HWNDTEPACK	AMCGGELSEP	AGVVLSPDWP	QSYSPGQDCV	WGVHVQEEKR	ILLQVEILNV	REGDMLTLFD	GDGPSARVLA
490	500	510	520	530	540	550	560
QLRGPQPRRR	LLSSGPDLTL	QFQAPPGPPN	PGLGQGFVLH	FKEVPRNDTC	PELPPPEWGW	RTASHGDLIR	GTVLTYQCEP
570	580	590	600	610	620	630	640
GYELLGSDIL	TCQWDLSWSA	APPACQKIMT	CADPGEIANG	HRTASDAGFP	VGSHVQYRCL	PGYSLEGAAM	LTCYSRDTGT
650	660	670	680	690	700	710	720
PKWSDRVPKC	ALKYEPCLNP	GVPENGYQTL	YKHHYQAGES	LRFFCYEGFE	LIGEVTITCV	PGHPSQWTSQ	PPLCKVAYEE
730	740	750	760	770	780	790	800
LLDNRKLEVT	QTTDPSRQLE	GGNLALAILL	PLGLVIVLGS	GVYIYYTKLQ	GKSLFGFSGS	HSYSPITVES	DFSNPLYEAG
810							
DTREYEVSI							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2089	2	862.3060	-159.34	2	56.0	12.4	0	247-263	R.IVSPEPGGAVGPNLTCR.W	Carbamidomethyl: 16

Detailed Protein Report

Protein 1002: acetyl-CoA carboxylase 1 isoform 3 [Homo sapiens]

Accession:	gi|38679971	**Score:**	12.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	259.5
Database Date:	2015-11-30	**pI:**	6.1
Modification(s):	Oxidation	**Sequence Coverage [%]:**	0.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEGSPEENKE	MRYYMLQRSS	MSGLHLVKQG	RDRKKIDSQR	DFTVASPAEF	VTRFGGNKVI	EKVLIANNGI	AAVKCMRSIR
90	100	110	120	130	140	150	160
RWSYEMFRNE	RAIRFVVMVT	PEDLKANAEY	IKMADHYVPV	PGGPNNNNYA	NVELILDIAK	RIPVQAVWAG	WGHASENPKL
170	180	190	200	210	220	230	240
PELLLKNGIA	FMGPPSQAMW	ALGDKIASSI	VAQTAGIPTL	PWSGSGLRVD	WQENDFSKRI	LNVPQELYEK	GYVKDVDDGL
250	260	270	280	290	300	310	320
QAAEEVGYPV	MIKASEGGGG	KGIRKVNNAD	DFPNLFRQVQ	AEVPGSPIFV	MRLAKQSRHL	EVQILADQYG	NAISLFGRDC
330	340	350	360	370	380	390	400
SVQRRHQKII	EEAPATIATP	AVFEHMEQCA	VKLAKMVGYV	SAGTVEYLYS	QDGSFYFLEL	NPRLQVEHPC	TEMVADVNLP
410	420	430	440	450	460	470	480
AAQLQIAMGI	PLYRIKDIRM	MYGVSPWGDS	PIDFEDSAHV	PCPRGHVIAA	RITSENPDEG	FKPSSGTVQE	LNFRSNKNVW
490	500	510	520	530	540	550	560
GYFSVAAAGG	LHEFADSQFG	HCFSWGENRE	EAISNMVVAL	KELSIRGDFR	TTVEYLIKLL	ETESFQMNRI	DTGWLDRLIA
570	580	590	600	610	620	630	640
EKVQAERPDT	MLGVVCGALH	VADVSLRNSV	SNFLHSLERG	QVLPAHTLLN	TVDVELIYEG	VKYVLKVTRQ	SPNSYVVIMN
650	660	670	680	690	700	710	720
GSCVEVDVHR	LSDGGLLLSY	DGSSYTTYMK	EEVDRYRITI	GNKTCVFEKE	NDPSVMRSPS	AGKLIQYIVE	DGGHVFAGQC
730	740	750	760	770	780	790	800
YAEIEVMKMV	MTLTAVESGC	IHYVKRPGAA	LDPGCVLAKM	QLDNPSKVQQ	AELHTGSLPR	IQSTALRGEK	LHRVFHYVLD
810	820	830	840	850	860	870	880
NLVNVMNGYC	LPDPFFSSKV	KDWVERLMKT	LRDPSLPLLE	LQDIMTSVSG	RIPPNVEKSI	KKEMAQYASN	ITSVLCQFPS
890	900	910	920	930	940	950	960
QQIANILDSH	AATLNRKSER	EVFFMNTQSI	VQLVQRYRSG	IRGHMKAVVM	DLLRQYLRVE	TQFQNGHYDK	CVFALREENK
970	980	990	1000	1010	1020	1030	1040
SDMNTVLNYI	FSHAQVTKKN	LLVTMLIDQL	CGRDPTLTDE	LLNILTELTQ	LSKTTNAKVA	LRARQVLIAS	HLPSYELRHN
1050	1060	1070	1080	1090	1100	1110	1120
QVESIFLSAI	DMYGHQFCIE	NLQKLILSET	SIFDVLPNFF	YHSNQVVRMA	ALEVYVRRAY	IAYELNSVQH	RQLKDNTCVV
1130	1140	1150	1160	1170	1180	1190	1200
EFQFMLPTSH	PNRGNIPTLN	RMSFSSNLNH	YGMTHVASVS	DVLLDNSFTP	PCQRMGGMVS	FRTFEDFVRI	FDEVMGCFSD
1210	1220	1230	1240	1250	1260	1270	1280
SPPQSPTFPE	AGHTSLYDED	KVPRDEPIHI	LNVAIKTDCD	IEDDRLAAMF	REFTQQNKAT	LVDHGIRRLT	FLVAQKDFRK
1290	1300	1310	1320	1330	1340	1350	1360
QVNYEVDRRF	HREFPKFFTF	RARDKFEEDR	IYRHLEPALA	FQLELNRMRN	FDLTAIPCAN	HKMHLYLGAA	KVEVGTEVTD
1370	1380	1390	1400	1410	1420	1430	1440
YRFFVRAIIR	HSDLVTKEAS	FEYLQNEGER	LLLEAMDELE	VAFNNTNVRT	DCNHIFLNFV	PTVIMDPSKI	EESVRSMVMR
1450	1460	1470	1480	1490	1500	1510	1520
YGSRLWKLRV	LQAELKINIR	LTPTGKAIPI	RLFLTNESGY	YLDISLYKEV	TDSRTAQIMF	QAYGDKQGPL	HGMLINTPYV
1530	1540	1550	1560	1570	1580	1590	1600
TKDLLQSKRF	QAQSLGTTYI	YDIPEMFRQS	LIKLWESMST	QAFLPSPPLP	SDMLTYTELV	LDDQGQLVHM	NRLPGGNEIG
1610	1620	1630	1640	1650	1660	1670	1680
MVAWKMTFKS	PEYPEGRDII	VIGNDITYRI	GSFGPQEDLL	FLRASELARA	EGIPRIYVSA	NSGARIGLAE	EIRHMFHVAW
1690	1700	1710	1720	1730	1740	1750	1760
VDPEDPYKGY	RYLYLTPQDY	KRVSALNSVH	CEHVEDEGES	RYKITDIIGK	EEGIGPENLR	GSGMIAGESS	LAYNEIITIS
1770	1780	1790	1800	1810	1820	1830	1840
LVTCRAIGIG	AYLVRLGQRT	IQVENSHLIL	TGAGALNKVL	GREVYTSNNQ	LGGIQIMHNN	GVTHCTVCDD	FEGVFTVLHW
1850	1860	1870	1880	1890	1900	1910	1920
LSYMPKSVHS	SVPLLNSKDP	IDRIIEFVPT	KTPYDPRWML	AGRPHPTQKG	QWLSGFFDYG	SFSEIMQPWA	QTVVVGRARL
1930	1940	1950	1960	1970	1980	1990	2000
GGIPVGVVAV	ETRTVELSIP	ADPANLDSEA	KIIQQAGQVW	FPDSAFKTYQ	AIKDFNREGL	PLMVFANWRG	FSGGMKDMYD
2010	2020	2030	2040	2050	2060	2070	2080
QVLKFGAYIV	DGLRECCQPV	LVYIPPQAEL	RGGSWVVIDS	SINPRHMEMY	ADRESRGSVL	EPEGTVEIKF	RRKDLVKTMR
2090	2100	2110	2120	2130	2140	2150	2160
RVDPVYIHLA	ERLGTPELST	AERKELENKL	KEREEFLIPI	YHQVAVQFAD	LHDTPGRMQE	KGVISDILDW	KTSRTFFYWR
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
411	2	537.6424	-263.75	2	34.5	12.4	0	19-28	R.SSMSGLHLVK.Q	Oxidation: 3

Detailed Protein Report

Protein 1003: PREDICTED: uncharacterized protein LOC100996412 [Homo sapiens]

Accession:	gi|530355840	**Score:**	12.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	22.5
Database Date:	2015-11-30	**pI:**	11.0
		Sequence Coverage [%]:	6.3
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 0.35 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MALQLRWFKH	RRPFFLLLIA	QLCVHWPPHL	PPDQRGFCLP	QHCQPGVFLD	SSPGPPSAPL	PPSALTSRPP	SLLLGNLAWV
90	100	110	120	130	140	150	160
GLPSQPSRLF	FLSLAACLAH	HCGQVSLSEN	TISSHHGPVY	KAVSHLPITS	DQIRTLRLWI	EADATVPGKP	HCPPIPALAS
170	180	190	200	210			
VPVRSCTMLL	SAILPSPALP	ACWSCIALHL	TDSYSTALAS	PKHTWPS			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
348	1	718.8478	-67.63	2	34.0	12.4	0	122-134	K.AVSHLPITSDQIR.T		MD:MU 0.35

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Detailed Protein Report

Protein 1004: PREDICTED: glycerol-3-phosphate acyltransferase 2, mitochondrial isoform X7 [Homo sapiens]

Accession:	gi|530368526	**Score:**	12.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	73.5
Database Date:	2015-11-30	**pI:**	10.1
		Sequence Coverage [%]:	3.6
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578803790	refseq_human (refseq_human_20140103.fasta)	PREDICTED: glycerol-3-phosphate acyltransferase 2, mitochondrial isoform X21 [Homo sapiens]

10	20	30	40	50	60	70	80
MATMLEGRCQ	TQPRSSPSGR	EASLWSSGFG	MKLEAVTPFL	GKYRPFVGRC	CQTCTPKSWE	SLFHRSITDL	GFCNVILVKE
90	100	110	120	130	140	150	160
ENTRFRGWLV	RRLCYFLWSL	EQHIPPCQDV	PQKIMESTGV	QNLLSGRVPG	GTGEGQVPDL	VKKEVQRILG	HIQAPPRPFL
170	180	190	200	210	220	230	240
VRLFSWALLR	FLNCLFLNVQ	LHKGQMKMVQ	KAAQAGLPLV	LLSTHKTLLD	GILLPFMLLS	QGLGVLRVAW	DSRACSPALR
250	260	270	280	290	300	310	320
ALLRKLGGLF	LPPEASLSLD	SSEGLLARAV	VQAVIEQLLV	SGQPLLIFLE	EPPGALGPRL	SALGQAWVGF	VVQAVQVGIV
330	340	350	360	370	380	390	400
PDALLVPVAV	TYDLVPDAPC	DIDHASAPLG	LWTGALAVLR	SLWSRWGCSH	RICSRVHLAQ	PFSLQEYIVS	ARSCWGGRQT
410	420	430	440	450	460	470	480
LEQLLQPIVL	GQCTAVPDTE	KEQEWTPITG	PLLALKEEDQ	LLVRRLSCHV	LSASVGSSAV	MSTAIMATLL	LFKHQKLLGE
490	500	510	520	530	540	550	560
FSWLTEEILL	RGFDVGFSGQ	LRSLLQHSLS	LLRAHVALLR	IRQGDLLVVP	QPGPGLTHLA	QLSAELLPVF	LSEAVGACAV
570	580	590	600	610	620	630	640
RGLLAGRVPP	QGPWELQGIL	LLSQNELYRQ	ILLLMHLLPQ	DLLLLKPCQS	SYCYCQEVLD	RLIQCGLLVA	EESWATQSSC
650	660	670	680				
SSSCRPPPRK	KGSSSVRTQS	SPSVLSGPSE	T				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
637	1	824.1210	-2.68	3	37.5	12.4	1	245-268	R.KLGGLFLPPEASLSLDSSEGLLAR.A	

Detailed Protein Report

Protein 1005: MAP kinase-activated protein kinase 3 [Homo sapiens]

Accession:	gi|4758700	**Score:**	12.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	43.0
Database Date:	2015-11-30	**pI:**	7.1
Modification(s):	Oxidation	**Sequence Coverage [%]:**	4.7
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|345441758	refseq_human (refseq_human_20140103.fasta)	MAP kinase-activated protein kinase 3 [Homo sapiens]
gi|345441756	refseq_human (refseq_human_20140103.fasta)	MAP kinase-activated protein kinase 3 [Homo sapiens]

10	20	30	40	50	60	70	80
MDGETAEEQG	GPVPPPVAPG	GPGLGGAPGG	RREPKKYAVT	DDYQLSKQVL	GLGVNGKVLE	CFHRRTGQKC	ALKLLYDSPK
90	100	110	120	130	140	150	160
ARQEVDHHWQ	ASGGPHIVCI	LDVYENMHHG	KRCLLIIMEC	MEGGELFSRI	QERGDQAFTE	REAAEIMRDI	GTAIQFLHSH
170	180	190	200	210	220	230	240
NIAHRDVKPE	NLLYTSKEKD	AVLKLTDFGF	AKETTQNALQ	TPCYTPYYVA	PEVLGPEKYD	KSCDMWSLGV	IMYILLCGFP
250	260	270	280	290	300	310	320
PFYSNTGQAI	SPGMKRRIRL	GQYGFPNPEW	SEVSEDAKQL	IRLLLKTDPT	ERLTITQFMN	HPWINQSMVV	PQTPLHTARV
330	340	350	360	370	380	390	
LQEDKDHWDE	VKEEMTSALA	TMRVDYDQVK	IKDLKTSNNR	LLNKRRKKQA	GSSSASQGCN	NQ	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2059	1	701.5898	-103.73	3	55.9	12.3	1	333-350	K.EEMTSALATMRVDYDQVK.I	Oxidation: 10

Detailed Protein Report

Protein 1006: Usher syndrome type-1G protein isoform 2 [Homo sapiens]

Accession:	gi|542133068	**Score:**	12.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	39.9
Database Date:	2015-11-30	**pI:**	9.4
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.1
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MAAMKGHMEC VRYLDSIAAK QSSLNPKLVG KLKDKAFREA ERRIRECAKL QRRHHERMER RYRRELAERS DTLSFSSLTS
        90        100        110        120        130        140        150        160
STLSRRLQHL ALGSHLPYSQ ATLHGTARGK TKMQKKLERR KQGGEGTFKV SEDGRKSARS LSGLQLGSDV MFVRQGTYAN
       170        180        190        200        210        220        230        240
PKEWGRAPLR DMFLSDEDSV SRATLAAEPA HSEVSTDSGH DSLFTRPGLG TMVFRRNYLS SGLHGLGRED GGLDGVGAPR
       250        260        270        280        290        300        310        320
GRLQSSPSLD DDSLGSANSL QDRSCGEELP WDELDLGLDE DLEPETSPLE TFLASLHMED FAALLRQEKI DLEALMLCSD
       330        340        350        360
LDLRSISVPL GPRKKILGAV RRRRQAMERP PALEDTEL
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
343	2	624.6712	-183.62	2	33.6	12.3	1	2-12	M.AAMKGHMECVR.Y	Oxidation: 7

Detailed Protein Report

Protein 1007: AT-rich interactive domain-containing protein 1A isoform b [Homo sapiens]

Accession:	gi|21264575	**Score:**	12.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	218.2
Database Date:	2015-11-30	**pI:**	6.1
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.2
		No. of unique Peptides:	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MAAQVAPAAA	SSLGNPPPPP	PSELKKAEQQ	QREEAGGEAA	AAAAAERGEM	KAAAGQESEG	PAVGPPQPLG	KELQDGAESN
90	100	110	120	130	140	150	160
GGGGGGGAGS	GGGPGAEPDL	KNSNGNAGPR	PALNNNLTEP	PGGGGGGSSD	GVGAPPHSAA	AALPPPAYGF	GQPYGRSPSA
170	180	190	200	210	220	230	240
VAAAAAAVFH	QQHGGQQSPG	LAALQSGGGG	GLEPYAGPQQ	NSHDHGFPNH	QYNSYYPNRS	AYPPPAPAYA	LSSPRGGTPG
250	260	270	280	290	300	310	320
SGAAAAAGSK	PPPSSSASAS	SSSSSFAQQR	FGAMGGGGPS	AAGGGTPQPT	ATPTLNQLLT	SPSSARGYQG	YPGGDYSGGP
330	340	350	360	370	380	390	400
QDGGAGKGPA	DMASQCWGAA	AAAAAAAAAS	GGAQQRSHHA	PMSPGSSGGG	GQPLARTPQP	SSPMDQMGKM	RPQPYGGTNP
410	420	430	440	450	460	470	480
YSQQQGPPSG	PQQGHGYPGQ	PYGSQTPQRY	PMTMQGRAQS	AMGGLSYTQQ	IPPYGQQGPS	GYGQQGQTPY	YNQQSPHPQQ
490	500	510	520	530	540	550	560
QQPPYSQQPP	SQTPHAQPSY	QQQPQSQPPQ	LQSSQPPYSQ	QPSQPPHQQS	PAPYPSQQST	TQQHPQSQPP	YSQPQAQSPY
570	580	590	600	610	620	630	640
QQQQPQQPAP	STLSQQAAYP	QPQSQQSQQT	AYSQQRFPPP	QELSQDSFGS	QASSAPSMTS	SKGGQEDMNL	SLQSRPSSLP
650	660	670	680	690	700	710	720
DLSGSIDDLP	MGTEGALSPG	VSTSGISSSQ	GEQSNPAQSP	FSPHTSPHLP	GIRGPSPSPV	GSPASVAQSR	SGPLSPAAVP
730	740	750	760	770	780	790	800
GNQMPPRPPS	GQSDSIMHPS	MNQSSIAQDR	GYMQRNPQMP	QYSSPQPGSA	LSPRQPSGGQ	IHTGMGSYQQ	NSMGSYGPQG
810	820	830	840	850	860	870	880
GQYGPQGGYP	RQPNYNALPN	ANYPSAGMAG	GINPMGAGGQ	MHGQPGIPPY	GTLPPGRMSH	ASMGNRPYGP	NMANMPPQVG
890	900	910	920	930	940	950	960
SGMCPPPGGM	NRKTQETAVA	MHVAANSIQN	RPPGYPNMNQ	GGMMGTGPPY	GQGINSMAGM	INPQGPPYSM	GGTMANNSAG
970	980	990	1000	1010	1020	1030	1040
MAASPEMMGL	GDVKLTPATK	MNNKADGTPK	TESKSKKSSS	STTTNEKITK	LYELGGEPER	KMWVDRYLAF	TEEKAMGMTN
1050	1060	1070	1080	1090	1100	1110	1120
LPAVGRKPLD	LYRLYVSVKE	IGGLTQVNKN	KKWRELATNL	NVGTSSSAAS	SLKKQYIQCL	YAFECKIERG	EDPPPDIFAA
1130	1140	1150	1160	1170	1180	1190	1200
ADSKKSQPKI	QPPSPAGSGS	MQGPQTPQST	SSSMAEGGDL	KPPTPASTPH	SQIPPLPGMS	RSNSVGIQDA	FNDGSDSTFQ
1210	1220	1230	1240	1250	1260	1270	1280
KRNSMTPNPG	YQPSMNTSDM	MGRMSYEPNK	DPYGSMRKAP	GSDPFMSSGQ	GPNGGMGDPY	SRAAGPGLGN	VAMGPRQHYP
1290	1300	1310	1320	1330	1340	1350	1360
YGGPYDRVRT	EPGIGPEGNM	STGAPQPNLM	PSNPDSGMYS	PSRYPPQQQQ	QQQQRHDSYG	NQFSTQGTPS	GSPFPSQQTT
1370	1380	1390	1400	1410	1420	1430	1440
MYQQQQQVSS	PAPLPRPMEN	RTSPSKSPFL	HSGMKMQKAG	PPVPASHIAP	APVQPPMIRR	DITFPPGSVE	ATQPVLKQRR
1450	1460	1470	1480	1490	1500	1510	1520
RLTMKDIGTP	EAWRVMMSLK	SGLLAESTWA	LDTINILLYD	DNSIMTFNLS	QLPGLLELLV	EYFRRCLIEI	FGILKEYEVG
1530	1540	1550	1560	1570	1580	1590	1600
DPGQRTLLDP	GRFSKVSSPA	PMEGGEEEEE	LLGPKLEEEE	EEEVVENDEE	IAFSGKDKPA	SENSEEKLIS	KFDKLPVKIV
1610	1620	1630	1640	1650	1660	1670	1680
QKNDPFVVDC	SDKLGRVQEF	DSGLLHWRIG	GGDTTEHIQT	HFESKTELLP	SRPHAPCPPA	PRKHVTTAEG	TPGTTDQEGP
1690	1700	1710	1720	1730	1740	1750	1760
PPDGPPEKRI	TATMDDMLST	RSSTLTEDGA	KSSEAIKESS	KFPFGISPAQ	SHRNIKILED	EPHSKDETPL	CTLLDWQDSL
1770	1780	1790	1800	1810	1820	1830	1840
AKRCVCVSNT	IRSLSFVPGN	DFEMSKHPGL	LLILGKLILL	HHKHPERKQA	PLTYEKEEEQ	DQGVSCNKVE	WWWDCLEMLR
1850	1860	1870	1880	1890	1900	1910	1920
ENTLVTLANI	SGQLDLSPYP	ESICLPVLDG	LLHWAVCPSA	EAQDPFSTLG	PNAVLSPQRL	VLETLSKLSI	QDNNVDLILA
1930	1940	1950	1960	1970	1980	1990	2000
TPPFSRLEKL	YSTMVRFLSD	RKNPVCREMA	VVLLANLAQG	DSLAARAIAV	QKGSIGNLLG	FLEDSLAATQ	FQQSQASLLH
2010	2020	2030	2040	2050	2060	2070	
MQNPPFEPTS	VDMMRRAARA	LLALAKVDEN	HSEFTLYESR	LLDISVSPLM	NSLVSQVICD	VLFLIGQS	

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

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2386	1	1023.7784	0.96	3	59.7	12.3	1	1817-1840	K.EEEQDQGVSCNKVEWWWDCLEMLR.E	Carbamidomethyl: 19

Detailed Protein Report

Protein 1008: PREDICTED: RNA-binding protein 6-like isoform X5 [Homo sapiens]

Accession:	gi|578841102	**Score:**	12.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	98.1
Database Date:	2015-11-30	**pI:**	10.4
		Sequence Coverage [%]:	0.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MKVGVQGLHV	NGGGAQGLHV	SGSGVTGTTG	QWRWGTGNTG	QWRWGHRHYR	SMEVESQGLQ	VNGGGSTETT	GQWRWSTGTT
90	100	110	120	130	140	150	160
GQWRWGHRDY	RSMQVGAQRL	QVNRGGDTGT	TGQCRWSHRD	YRSMEVGSQR	LQVNGGRVTE	TTGQWRWNTE	TTGQWRWEHR
170	180	190	200	210	220	230	240
DYRSIEVGTQ	GLQVNGGGAQ	RLQVKGGGVT	GTTGQWRWEH	RDYRSMEVGA	QRLQVNGGGD	TGTRGQWRWS	HREYRSMEVE
250	260	270	280	290	300	310	320
HRDYRSMEVE	SQGLQDNGGG	VTGTTGQWRW	STGTTGQWRW	SHRDYRSMEV	GHRDYRSMEV	EHRDYRSMEV	AQGLLLNGGG
330	340	350	360	370	380	390	400
AQGLQVNGGG	VTETTGQWRW	SIGTTRQWRW	STGTTGQWRW	GTETTGQWRW	GQKDCISMEV	EHRDYRSMEV	GAPGLHINGG
410	420	430	440	450	460	470	480
GAQGLQVNGG	GAQRLQVNGG	GAQGLQDNGG	GVQGLQVNGG	GVRGTKGQWR	WKHRDYRSME	VESQGLQVNG	CGVTGTTGQW
490	500	510	520	530	540	550	560
WWGHRDYRSM	EVGHRDYTSV	EVGSQGLQIN	GGGGTGTTRQ	WRWSHRDYRS	MEVGAQGLQF	NGGGGTGTTG	QWRWGTGTTG
570	580	590	600	610	620	630	640
QWRGSTGTTV	QWRWSTGTTG	QWRWGTGTTG	QWRWEHRDYR	SMEVGSQGLQ	VNGGGVTGTT	GQWRWTHSDY	RSMQVRHRDY
650	660	670	680	690	700	710	720
RLMEVGAQGL	QVNGGVAQGL	QVSGGGVTGS	TGQWRWGHRD	YRSMEVESQG	LQVNGGGGTG	TAGQCRWSTG	TTGQWRCSTE
730	740	750	760	770	780	790	800
TAGQWRWGTG	TTGQWRWSTE	TTGQWRWGHR	DYRSVEVEHR	DYRSVEVEYR	DYRSMEVGHR	DYRSVEVEHR	DYRSMEVESQ
810	820	830	840	850	860	870	880
RLQVNGGGVT	GTTGQWRWGT	GTTGQWRWST	ETACQWRWGT	ETTGQWRWSH	RDYRSMDVEY	RDYRSMEVGA	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1426	1	1011.7261	221.55	1	47.6	12.3	1	44-50	R.WGHRHYR.S	

Detailed Protein Report

Protein 1009: tensin-like C1 domain-containing phosphatase isoform 3 [Homo sapiens]

Accession:	gi|38787970	**Score:**	12.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	138.7
Database Date:	2015-11-30	**pI:**	7.1
		Sequence Coverage [%]:	1.0
		No. of unique Peptides:	1

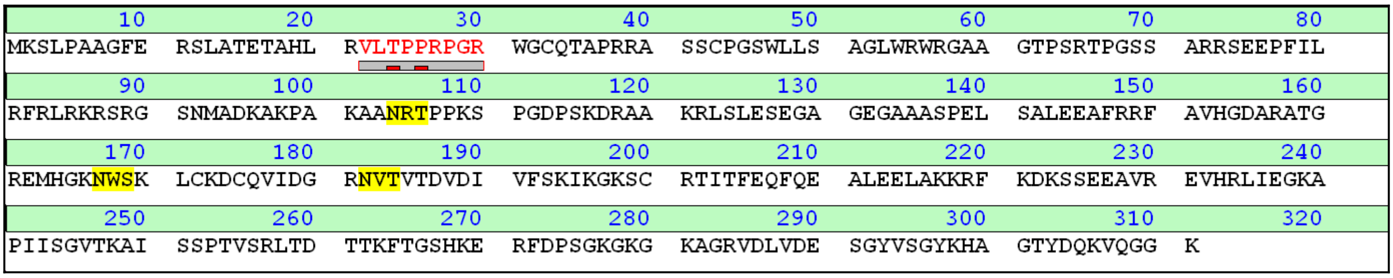
10	20	30	40	50	60	70	80
MERRWDLDLT	YVTERILAAA	FPARPDEQRH	RGHLRELAHV	LQSKHRDKYL	LFNLSEKRHD	LTRLNPKVQD	FGWPELHAPP
90	100	110	120	130	140	150	160
LDKLCSICKA	METWLSADPQ	HVVVLYCKGN	KGKLGVIVSA	YMHYSKISAG	ADQALATLTM	RKFCEDKVAT	ELQPSQRRYI
170	180	190	200	210	220	230	240
SYFSGLLSGS	IRMNSSPLFL	HYVLIPMLPA	FEPGTGFQPF	LKIYQSMQLV	YTSGVYHIAG	PGPQQLCISL	EPALLLKGDV
250	260	270	280	290	300	310	320
MVTCYHKGGR	GTDRTLVFRV	QFHTCTIHGP	QLTFPKDQLD	EAWTDERFPF	QASVEFVFSS	SPEKIKGSTP	RNDPSVSVDY
330	340	350	360	370	380	390	400
NTTEPAVRWD	SYENFNQHHE	DSVDGSLTHT	RGPLDGSPYA	QVQRPPRQTP	PAPSPEPPPP	PMLSVSSDSG	HSSTLTTEPA
410	420	430	440	450	460	470	480
AESPGRPPPT	AAERQELDRL	LGGCGVASGG	RGAGRETAIL	DDEEQPTVGG	GPHLGVYPGH	RPGLSRHCSC	RQGYREPCGV
490	500	510	520	530	540	550	560
PNGGYYRPEG	TLERRRLAYG	GYEGSPQGYA	EASMEKRRLC	RSLSEGLYPY	PPEMGKPATG	DFGYRAPGYR	EVVILEDPGL
570	580	590	600	610	620	630	640
PALYPCPACE	EKLALPTAAL	YGLRLEREAG	EGWASEAGKP	LLHPVRPGHP	LPLLLPACGH	HHAPMPDYSC	LKPPKAGEEG
650	660	670	680	690	700	710	720
HEGCSYTMCP	EGRYGHPGYP	ALVTYSYGGA	VPSYCPAYGR	VPHSCGSPGE	GRGYPSPGAH	SPRAGSISPG	SPPYPQSRKL
730	740	750	760	770	780	790	800
SYEIPTEEGG	DRYPLPGHLA	SAGPLASAES	LEPVSWREGP	SGHSTLPRSP	RDAPCSASSE	LSGPSTPLHT	SSPVQGKEST
810	820	830	840	850	860	870	880
RRQDTRSPTS	APTQRLSPGE	ALPPVSQAGT	GKAPELPSGS	GPEPLAPSPV	SPTFPPSSPS	DWPQERSPGG	HSDGASPRSP
890	900	910	920	930	940	950	960
VPTTLPGLRH	APWQGPRGPP	DSPDGSPLTP	VPSQMPWLVA	SPEPPQSSPT	PAFPLAASYD	TNGLSQPPLP	EKRHLPGPGQ
970	980	990	1000	1010	1020	1030	1040
QPGPWGPEQA	SSPARGISHH	VTFAPLLSDN	VPQTPEPPTQ	ESQSNVKFVQ	DTSKFWYKPH	LSRDQAIALL	KDKDPGAFLI
1050	1060	1070	1080	1090	1100	1110	1120
RDSHSFQGAY	GLALKVATPP	PSAQPWKGDP	VEQLVRHFLI	ETGPKGVKIK	GCPSEPYFGS	LSALVSQHSI	SPISLPCCLR
1130	1140	1150	1160	1170	1180	1190	1200
IPSKDPLEET	PEAPVPTNMS	TAADLLRQGA	ACSVLYLTSV	ETESLTGPQA	VARASSAALS	CSPRPTPAVV	HFKVSAQGIT
1210	1220	1230	1240	1250	1260	1270	1280
LTDNQRKLFF	RRHYPVNSIT	FSSTDPQDRR	WTNPDGTTSK	IFGFVAKKPG	SPWENVCHLF	AELDPDQPAG	AIVTFITKVL
1290							
LGQRK							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2463	1	701.7422	-179.06	2	60.7	12.3	0	1194-1206	K.VSAQGITLTDNQR.K	

Detailed Protein Report

Protein 1010: **PREDICTED: tubulin polymerization-promoting protein isoform X1 [Homo sapiens]**

Accession:	gi|530378674	**Score:**	12.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	33.8
Database Date:	2015-11-30	**pI:**	10.9
		Sequence Coverage [%]:	2.9
		No. of unique Peptides:	1



```
        10         20         30         40         50         60         70         80
MKSLPAAGFE RSLATETAHL RVLTPPRPGR WGCQTAPRRA SSCPGSWLLS AGLWRWRGAA GTPSRTPGSS ARRSEEPFIL
        90        100        110        120        130        140        150        160
RFRLRKRSRG SNMADKAKPA KAANRTPPKS PGDPSKDRAA KRLSLESEGA GEGAAASPEL SALEEAFRRF AVHGDARATG
       170        180        190        200        210        220        230        240
REMHGKNWSK LCKDCQVIDG RNVTVTDVDI VFSKIKGKSC RTITFEQFQE ALEELAKKRF KDKSSEEAVR EVHRLIEGKA
       250        260        270        280        290        300        310        320
PIISGVTKAI SSPTVSRLTD TTKFTGSHKE RFDPSGKGKG KAGRVDLVDE SGYVSGYKHA GTYDQKVQGG K
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2712	1	992.7958	197.25	1	65.1	12.3	0	22-30	R.VLTPPRPGR.W	

Detailed Protein Report

Protein 1011: protein orai-2 isoform b [Homo sapiens]

Accession:	gi|425854835	**Score:**	12.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	20.0
Database Date:	2015-11-30	**pI:**	7.0
		Sequence Coverage [%]:	4.0
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MVEVQLETQY QYPRPLLIAF SACTTVLVAV HLFALLISTC ILPNVEAVSN IHNLNSISES PHERMHPYIE LAWGFSTVLG
        90        100        110        120        130        140        150        160
ILLFLAEVVL LCWIKFLPVD ARRQPGPPPG PGSHTGWQAA LVSTIIMVPV GLIFVVFTIH FYRSLVRHKT ERHNREIEEL
       170        180
HKLKVQLDGH ERSLQVL
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1318	1	817.1630	-359.25	1	46.2	12.3	0	96-102	K.FLPVDAR.R	

Detailed Protein Report

Protein 1012: uncharacterized protein C10orf120 [Homo sapiens]

Accession:	gi|58218975	**Score:**	12.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	39.2
Database Date:	2015-11-30	**pI:**	10.2
		Sequence Coverage [%]:	3.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MIREWKNDCQ	RIEKQRASDT	MVQERKNEKP	VRIFNTNSSF	QDQAPTCCQE	DLSSASPLRI	WSKFYRSDPR	IALGKYSPLE
90	100	110	120	130	140	150	160
KEILRLGGIH	TIAARRLLAY	KQEEECRMLK	ELQLLSPDYK	QAMEYKKKHS	SPCAICVPLE	KIWTAKVIAP	LEAFKMPQRE
170	180	190	200	210	220	230	240
QVNVSKHIER	MRLARALGNH	QPLPYIERFT	RSSFLSGVGL	GPMAKNKARR	KEDNYDTHNC	DDANQDKKEE	AEGKNTKRRE
250	260	270	280	290	300	310	320
IKMNVVFKSK	EPKKCLTYHG	NDRKSFLPAK	KPERSIAGLT	NRNLFCISEF	PGDLMLMNQD	FISRRDHFSD	LVKTYSLEEE
330	340						
SIWKERMRKA	TPYHY						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1753	1	835.2741	-159.16	2	51.9	12.3	1	314-326	K.TYSLEEESIWKER.M	

Detailed Protein Report

Protein 1013: sperm-specific antigen 2 isoform 4 [Homo sapiens]

Accession: gi|566559898
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 12.3
MW [kDa]: 119.1
pI: 5.1
Sequence Coverage [%]: 1.3
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MNSTGSGKSS	GTVSSVSELL	ELYEEDPEEI	LYNLGFGRDE	PDIASKIPSR	FFNSSSFAKG	IDIKVFLSAQ	MQRMEVENPN
90	100	110	120	130	140	150	160
YALTSRFRQI	EVLTTVANAF	SSLYSQVSGT	PLQRIGSMSS	VTSNKETDPP	PPLTRSNTAN	RLMKTLSKLN	LCVDKTEKGE
170	180	190	200	210	220	230	240
SSSPSPSAEK	GKILNVSVIE	ESGNKNDQKS	QKIMKKKESS	SMLATVKEEV	SGSSAAVTEN	ADSDRISDEA	NSNFNQGTEN
250	260	270	280	290	300	310	320
EQSKETQSHE	SKLGEESGIV	ESKLDSDFNI	SSHSELENSS	ELKSVHISTP	EKEPCAPLTI	PSIRNIMTQQ	KDSFEMEEVQ
330	340	350	360	370	380	390	400
STEGEAPHVP	ATYQLGLTKS	KRDHLLRTAS	QHSDSSGFAE	DSTDCLSLNH	LQVQESLQAM	GSSADSCDSE	TTVTSLGEDL
410	420	430	440	450	460	470	480
ATPTAQDQPY	FNESEEESLV	PLQKGLEKAA	AVADKRKSGS	QDFPQCNTIE	NTGTKQSTCS	PGDHIIEITE	VEEDLFPAET
490	500	510	520	530	540	550	560
VELLREASAE	SDVGKSSESE	FTQYTTHHIL	KSLASIEAKC	SDMSSENTTG	PPSSMDRVNT	ALQRAQMKVC	SLSNQRMGRS
570	580	590	600	610	620	630	640
LLKSKDLLKQ	RYLFAKAGYP	LRRSQSLPTT	LLSPVRVVSS	VNVRLSPGKE	TRCSPPSFTY	KYTPEEEQEL	EKRVMEHDGQ
650	660	670	680	690	700	710	720
SLVKSTIFIS	PSSVKKEEAP	QSEAPRVEEC	HHGRTPTCSR	LAPPPMSQST	CSLHSIHSEW	QERPLCEHTR	TLSTHSVPNI
730	740	750	760	770	780	790	800
SGATCSAFAS	PFGCPYSHRH	ATYPYRVCSV	NPPSAIEMQL	RRVLHDIRNS	LQNLSQYPMM	RGPDPAAAPY	STQKSSVLPL
810	820	830	840	850	860	870	880
YENTFQELQV	MRRSLNLFRT	QMMDLELAML	RQQTMVYHHM	TEEERFEVDQ	LQGLRNSVRM	ELQDLELQLE	ERLLGLEEQL
890	900	910	920	930	940	950	960
RAVRMPSPFR	SSALMVTELM	QEQSYLKSEL	GLGLGEMGFE	IPPGESSESV	FSQATSESSS	VCSGPSHANR	RTGVPSTASV
970	980	990	1000	1010	1020	1030	1040
GKSKTPLVAR	KKVFRASVAL	TPTAPSRTGS	VQTPPDLESS	EEVDAAEGAP	EVVGPKSEVE	EGHGKLPSMP	AAEEMHKNVE
1050	1060	1070	1080	1090			
QDELQQVIRE	IKESIVGEIR	REIVSGLLAA	VSSSKASNSK	QDYH			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1851	1	917.8276	-74.46	2	53.2	12.3	0	832-845	R.QQTMVYHHMTEEER.F	Oxidation: 4

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Detailed Protein Report

Protein 1014: PREDICTED: sprT-like domain-containing protein Spartan isoform X3 [Homo sapiens]

Accession:	gi|578802337	**Score:**	12.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	50.2
Database Date:	2015-11-30	**pI:**	9.4
		Sequence Coverage [%]:	3.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDDDLMLALR	LQEEWNLQEA	ERDHAQESLS	LVDASWELVD	PTPDLQALFV	QFNDQFFWGQ	LEAVEVKWSV	RMTLCAGICS
90	100	110	120	130	140	150	160
YEGKGGMCSI	RLSEPLLKLR	PRKDLVEVYH	TFHDEVDEYR	RHWWRCNGPC	QHRPPYYGYV	KRATNREPSA	HDYWWAEHQK
170	180	190	200	210	220	230	240
TCGGTYIKIK	EPENYSKKGK	GKAKLGKEPV	LAAENKDKPN	RGEAQLVIPF	SGKGYVLGET	SNLPSPGKLI	TSHAINKTQD
250	260	270	280	290	300	310	320
LLNQNHSANA	VRPNSKIKVK	FEQNGSSKNS	HLVSPAVSNS	HQNVLSNYFP	RVSFANQKAF	RGVNGSPRIS	VTVGNIPKNS
330	340	350	360	370	380	390	400
VSSSSQRRVS	SSKISLRNSS	KVTESASVMP	SQDVSGSEDT	FPNKRPRLED	KTVFDNFFIK	KEQIKSSGND	PKYSTTTAQN
410	420	430	440	450			
SSSSSSQSKM	VNCPVCQNEV	LESQINEHLD	WCLEGDSIKV	KSEESL			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2692	1	848.1258	170.69	2	64.9	12.3	1	302-318	R.GVNGSPRISVTVGNIPK.N	

Detailed Protein Report

Protein 1015: PREDICTED: afadin isoform X15 [Homo sapiens]

Accession:	gi|578812779	**Score:**	12.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	185.3
Database Date:	2015-11-30	**pI:**	6.0
		Sequence Coverage [%]:	0.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSAGGRDEER	RKLADIIHHW	NANRLDLFEI	SQPTEDLEFH	GVMRFYFQDK	AAGNFATKCI	RVSSTATTQD	VIETLAEKFR
90	100	110	120	130	140	150	160
PDMRMLSSPK	YSLYEVHVSG	EERRLDIDEK	PLVVQLNWNK	DDREGRFVLK	NENDAIPPKK	AQSNGPEKQE	KEGVIQNFKR
170	180	190	200	210	220	230	240
TLSKKEKKEK	KKREKEALRQ	ASDKDDRPFQ	GEDVENSRLA	AEVYKDMPET	SFTRTISNPE	VVMKRRRQQK	LEKRMQEFRS
250	260	270	280	290	300	310	320
SDGRPDSGGT	LRIYADSLKP	NIPYKTILLS	TTDPADFAVA	EALEKYGLEK	ENPKDYCIAR	VMLPPGAQHS	DEKGAKEIIL
330	340	350	360	370	380	390	400
DDDECPLQIF	REWPSDKGIL	VFQLKRRPPD	HIPKKTKKHL	EGKTPKGKER	ADGSGYGSTL	PPEKLPYLVE	LSPGRRNHFA
410	420	430	440	450	460	470	480
YYNYHTYEDG	SDSRDKPKLY	RLQLSVTEVG	TEKLDDNSIQ	LFGPGIQPHH	CDLTNMDGVV	TVTPRSMDAE	TYVEGQRISE
490	500	510	520	530	540	550	560
TTMLQSGMKV	QFGASHVFKF	VDPSQDHALA	KRSVDGGLMV	KGPRHKPGIV	QETTFDLGGD	IHSGTALPTS	KSTTRLDSDR
570	580	590	600	610	620	630	640
VSSASSTAER	GMVKPMIRVE	QQPDYRRQES	RTQDASGPEL	ILPASIEFRE	SSEDSFLSAI	INYTNSSTVH	FKLSPTYVLY
650	660	670	680	690	700	710	720
MACRYVLSNQ	YRPDISPTER	THKVIAVVNK	MVSMMEGVIQ	EVDQVDQKQK	NIAGALAFWM	ANASELLNFI	KQDRDLSRIT
730	740	750	760	770	780	790	800
LDAQDVLAHL	VQMAFKYLVH	CLQSELNNYM	PAFLDDPEEN	SLQRPKIDDV	LHTLTGAMSL	LRRCRVNAAL	TIQLFSQLFH
810	820	830	840	850	860	870	880
FINMWLFNRL	VTDPDSGLCS	HYWGAIIRQQ	LGHIEAWAEK	QGLELAADCH	LSRIVQATTL	LTMDKYAPDD	IPNINSTCFK
890	900	910	920	930	940	950	960
LNSLQLQALL	QNYHCAPDEP	FIPTDLIENV	VTVAENTADE	LARSDGREVQ	LEEDPDLQLP	FLLPEDGYSC	DVVRNIPNGL
970	980	990	1000	1010	1020	1030	1040
QEFLDPLCQR	GFCRLIPHTR	SPGTWTIYFE	GADYESHLLR	ENTELAQPLR	KEPEIITVTL	KKQNGMGLSI	VAAKGAGQDK
1050	1060	1070	1080	1090	1100	1110	1120
LGIYVKSVVK	GGAADVDGRL	AAGDQLLSVD	GRSLVGLSQE	RAAELMTRTS	SVVTLEVAKQ	GAIYHGLATL	LNQPSPMMQR
1130	1140	1150	1160	1170	1180	1190	1200
ISDRRGSGKP	RPKSEGFELY	NNSTQNGSPE	SPQLPWAEYS	EPKKLPGDDR	LMKNRADHRS	SPNVANQPPS	PGGKSAYASG
1210	1220	1230	1240	1250	1260	1270	1280
TTAKITSVST	GNLCTEEQTP	PPRPEAYPIP	TQTYTREYFT	FPASKSQDRM	APPQNQWPNY	EEKPHMHTDS	NHSSIAIQRV
1290	1300	1310	1320	1330	1340	1350	1360
TRSQEELRED	KAYQLERHRI	EAAMDRKSDS	DMWINQSSSL	DSSTSSQEHL	NHSSKSVTPA	STLTKSGPGR	WKTPAAIPAT
1370	1380	1390	1400	1410	1420	1430	1440
PVAVSQPIRT	DLPPPPPPPP	VHYAGDFDGM	SMDLPLPPPP	SANQIGLPSA	QVAAAERRKR	EEHQRWYEKE	KARLEEERER
1450	1460	1470	1480	1490	1500	1510	1520
KRREQERKLG	QMRTQSLNPA	PFSPLTAQQM	KPEKPSTLQR	PQETVIRELQ	PQQQPRTIER	RDLQYITVSK	EELSSGDSLS
1530	1540	1550	1560	1570	1580	1590	1600
PDPWKRDAKE	KLEKQQQMHI	VDMLSKEIQE	LQSKPDRSAE	ESDRLRKLML	EWQFQKRLQE	SKQKDEDDEE	EEDDDVDTML
1610	1620	1630	1640				
IMQRLEAERR	ARQTAMPAIS	VLDLVCSCFF	PFGTFFLS				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1199	1	533.6590	-250.21	2	44.6	12.3	0	1502-1510	R.DLQYITVSK.E	

Detailed Protein Report

Protein 1016: PREDICTED: serine/threonine-protein kinase ULK2 isoform X1 [Homo sapiens]

Accession:	gi|578830126	**Score:**	12.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	110.3
Database Date:	2015-11-30	**pI:**	9.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.9
		No. of unique 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
2561	1	913.4770	71.20	2	62.0	12.3	0	721-739	R.TTSVGPSNSGGSLCAMSGR.V	Carbamidomethyl: 14

Detailed Protein Report

Protein 1017: potassium voltage-gated channel subfamily KQT member 2 isoform c [Homo sapiens]

Accession:	gi|26051260	**Score:**	12.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	93.0
Database Date:	2015-11-30	**pI:**	10.0
		Sequence Coverage [%]:	2.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MVQKSRNGGV	YPGPSGEKKL	KVGFVGLDPG	APDSTRDGAL	LIAGSEAPKR	GSILSKPRAG	GAGAGKPPKR	NAFYRKLQNF
90	100	110	120	130	140	150	160
LYNVLERPRG	WAFIYHAYVF	LLVFSCLVLS	VFSTIKEYEK	SSEGALYILE	IVTIVVFGVE	YFVRIWAAGC	CCRYRGWRGR
170	180	190	200	210	220	230	240
LKFARKPFCV	IDIMVLIASI	AVLAAGSQGN	VFATSALRSL	RFLQILRMIR	MDRRGGTWKL	LGSVVYAHSK	ELVTAWYIGF
250	260	270	280	290	300	310	320
LCLILASFLV	YLAEKGENDH	FDTYADALWW	GLITLTTIGY	GDKYPQTWNG	RLLAATFTLI	GVSFFALPAG	ILGSGFALKV
330	340	350	360	370	380	390	400
QEQHRQKHFE	KRRNPAAGLI	QSAWRFYATN	LSRTDLHSTW	QYYERTVTVP	MYRLIPPLNQ	LELLRNLKSK	SGLAFRKDPP
410	420	430	440	450	460	470	480
PEPSPSQKVS	LKDRVFSSPR	GVAAKGKGSP	QAQTVRRSPS	ADQSLEDSPS	KVPKSWSFGD	RSRARQAFRI	KGAASRQNSE
490	500	510	520	530	540	550	560
EASLPGEDIV	DDKSCPCEFV	TEDLTPGLKV	SIRAVCVMRF	LVSKRKFKES	LRPYDVMDVI	EQYSAGHLDM	LSRIKSLQSR
570	580	590	600	610	620	630	640
VDQIVGRGPA	ITDKDRTKGP	AEAELPEDPS	MMGRLGKVEK	QVLSMEKKLD	FLVNIYMQRM	GIPPTETEAY	FGAKEPEPAP
650	660	670	680	690	700	710	720
PYHSPEDSRE	HVDRHGCIVK	IVRSSSSTGQ	KNFSAPPAAP	PVQCPPSTSW	QPQSHPRQGH	GTSPVGDHGS	LVRIPPPPAH
730	740	750	760	770	780	790	800
ERSLSAYGGG	NRASMEFLRQ	EDTPGCRPPE	GNLRDSDTSI	SIPSVDHEEL	ERSFSGFSIS	QSKENLDALN	SCYAAVAPCA
810	820	830	840	850			
KVRPYIAEGE	SDTDSDLCTP	CGPPPRSATG	EGPFGDVGWA	GPRK			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1678	1	938.9348	-60.69	2	50.7	12.2	2	398-414	K.DPPPEPSPSQKVSLKDR.V	

Detailed Protein Report

Protein 1018: **hydroxymethylglutaryl-CoA synthase, mitochondrial isoform 2 precursor [Homo sapiens]**

Accession:	gi|260656028	**Score:**	12.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	52.4
Database Date:	2015-11-30	**pI:**	8.9
		Sequence Coverage [%]:	3.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MQRLLTPVKR	ILQLTRAVQE	TSLTPARLLP	VAHQRFSTAS	AVPLAKTDTW	PKDVGILALE	VYFPAQYVDQ	TDLEKYNNVE
90	100	110	120	130	140	150	160
AGKYTVGLGQ	TRMGFCSVQE	DINSLCLTVV	QRLMERIQLP	WDSVGRLEVG	TETIIDKSKA	VKTVLMELFQ	DSGNTDIEGI
170	180	190	200	210	220	230	240
DTTNACYGGT	ASLFNAANWM	ESSSWDGLRG	THMENVYDFY	KPNLASEYPI	VDGKLSIQCY	LRALDRCYTS	YRKKIQNQWK
250	260	270	280	290	300	310	320
QAGSDRPFTL	DDLQYMIFHT	PFCKMVQKSL	ARLMFNDFLS	ASSDTQTSLY	KGLEAFGGLK	LEDTYTNKDL	DKALLKASQD
330	340	350	360	370	380	390	400
MFDKKTKASL	YLSTHNGNMY	TSSLYGCLAS	LLSHHSAQEL	AGSRIGAFSY	GSGLAASFFS	FRVSQDAAPG	SPLDKLVSST
410	420	430	440	450	460	470	
SDLPKRLASR	KCVSPEEFTE	IMNQREQFYH	KVNFSPPGDT	NSLFPGTWYL	ERVDEQHRRK	YARRPV	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1251	1	940.5643	63.89	2	45.3	12.2	2	301-316	K.LEDTYTNKDLDKALLK.A	

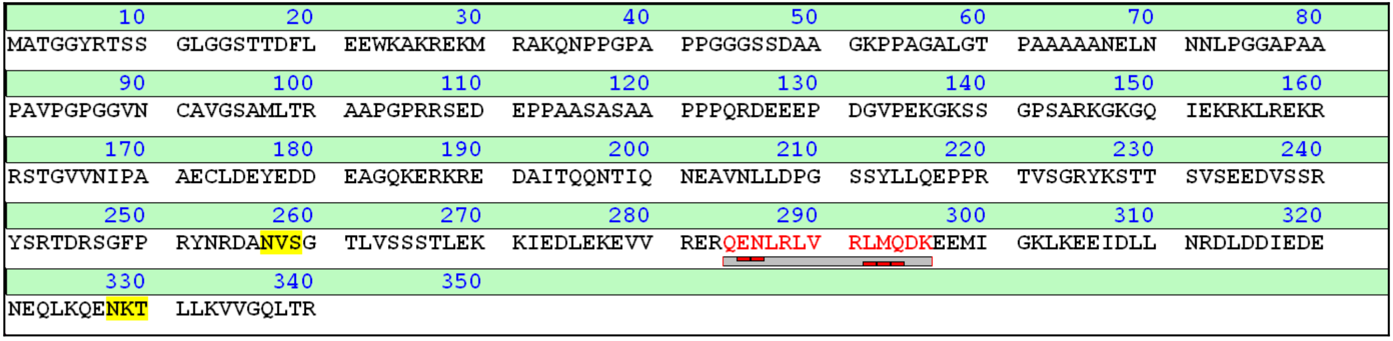
Detailed Protein Report

Protein 1019: PRKC apoptosis WT1 regulator protein [Homo sapiens]

Accession:	gi|55769533	**Score:**	12.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	36.5
Database Date:	2015-11-30	**pI:**	5.2
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.8
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578823825	refseq_human (refseq_human_20140103.fasta)	PREDICTED: PRKC apoptosis WT1 regulator protein isoform X1 [Homo sapiens]



```
        10         20         30         40         50         60         70         80
MATGGYRTSS GLGGSTTDFL EEWKAKREKM RAKQNPPGPA PPGGGSSDAA GKPPAGALGT PAAAAANELN NNLPGGAPAA
        90        100        110        120        130        140        150        160
PAVPGPGGVN CAVGSAMLTR AAPGPRRSED EPPAASASAA PPPQRDEEEP DGVPEKGKSS GPSARKGKGQ IEKRKLREKR
       170        180        190        200        210        220        230        240
RSTGVVNIPA AECLDEYEDD EAGQKERKRE DAITQQNTIQ NEAVNLLDPG SSYLLQEPPR TVSGRYKSTT SVSEEDVSSR
       250        260        270        280        290        300        310        320
YSRTDRSGFP RYNRDANVSG TLVSSSTLEK KIEDLEKEVV RERQENLRLV RLMQDKEEMI GKLKEEIDLL NRDLDDIEDE
       330        340        350
NEQLKQENKT LLKVVGQLTR
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
83	1	829.8813	-87.61	2	30.4	12.2	2	284-296	R.QENLRLVRLMQDK.E	Oxidation: 10

Detailed Protein Report

Protein 1020: PREDICTED: uncharacterized protein LOC101928647 [Homo sapiens]

Accession:	gi|530368444	**Score:**	12.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	25.5
Database Date:	2015-11-30	**pI:**	12.1
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	8.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEISLAGISA	CLRGLALLRG	EVTVLTLKSR	FQEAGDEAAP	FPNPRFCHLP	LLPFSKVQIT	GYPSGPATPS	FLIPDPSKYE
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
APRIWVSSCF	PCLVTRPVCR	GQRRELLPPH	GGAREPPKDR	AATAPHLLPI	PAPPARAQKE	PRPQPSRAGQ	PGAHLEGPGS
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
GRVAAASSPC	GSCCGLRVAP	APGSSSSRSP	TLHPFSTPLC	KSKAFRSSLG	AAAGAAKAAG	GAQQPSGSRG	GVARAAGEAP
250							
RCPARPPS							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
27	1	1182.5709	-22.85	2	29.6	12.2	1	84-103	R.IWVSSCFPCLVTRPVCRGQR.R	Carbamidomethyl: 9

Protein 1021: glutaredoxin-like protein C5orf63 isoform 2 [Homo sapiens]

Accession:	gi|256773203	**Score:**	12.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	13.4
Database Date:	2015-11-30	**pI:**	9.5
		Sequence Coverage [%]:	14.8
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MLWFQGNSMQ LARSSFGLFL RNCSASKTTL PVLTLFTKDP CPLCDEAKEV LKPYENRFIL QEVNITLPEN SVWYERYKFD
        90        100        110        120
IPVFHLNGQF LMMHRVNTSK LEKQLLKLEQ QSTGG
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2192	1	701.3305	-32.95	3	57.6	12.2	0	79-95	K.FDIPVFHLNGQFLMMHR.V	

Detailed Protein Report

Protein 1022: oxygen-regulated protein 1 [Homo sapiens]

Accession:	gi|5454016	**Score:**	12.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	240.5
Database Date:	2015-11-30	**pI:**	5.5
		Sequence Coverage [%]:	0.3
		No. of unique Peptides:	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MSDTPSTGFS	IIHPTSSEGQ	VPPPRHLSLT	HPVVAKRISF	YKSGDPQFGG	VRVVVNPRSF	KSFDALLDNL	SRKVPLPFGV
90	100	110	120	130	140	150	160
RNISTPRGRH	SITRLEELED	GESYLCSHGR	KVQPVDLDKA	RRRPRPWLSS	RAISAHSPPH	PVAVAAPGMP	RPPRSLVVFR
170	180	190	200	210	220	230	240
NGDPKTRRAV	LLSRRVTQSF	EAFLQHLTEV	MQRPVVKLYA	TDGRRVPSLQ	AVILSSGAVV	AAGREPFKPG	NYDIQKYLLP
250	260	270	280	290	300	310	320
ARLPGISQRV	YPKGNAKSES	RKISTHMSSS	SRSQIYSVSS	EKTHNNDCYL	DYSFVPEKYL	ALEKNDSQNL	PIYPSEDDIE
330	340	350	360	370	380	390	400
KSIIFNQDGT	MTVEMKVRFR	IKEEETIKWT	TTVSKTGPSN	NDEKSEMSFP	GRTESRSSGL	KLAACSFSAD	VSPMERSSNQ
410	420	430	440	450	460	470	480
EGSLAEEINI	QMTDQVAETC	SSASWENATV	DTDIIQGTQD	QAKHRFYRPP	TPGLRRVRQK	KSVIGSVTLV	SETEVQEKMI
490	500	510	520	530	540	550	560
GQFSYSEERE	SGENKSEYHM	FTHSCSKMSS	VSNKPVLVQI	NNNDQMEESS	LERKKENSLL	KSSAISAGVI	EITSQKMLEM
570	580	590	600	610	620	630	640
SHNNGLPSTI	SNNSIVEEDV	VDCVVLDNKT	GIKNFKTYGN	TNDRFSPISA	DATHFSSNNS	GTDKNISEAP	ASEASSTVTA
650	660	670	680	690	700	710	720
RIDRLINEFA	QCGLTKLPKN	EKKILSSVAS	KKKKKSRQQA	INSRYQDGQL	ATKGILNKNE	RINTKGRITK	EMIVQDSDSP
730	740	750	760	770	780	790	800
LKGGILCEED	LQKSDTVIES	NTFCSKSNLN	STISKNFHRN	KLNTTQNSKV	QGLLTKRKSR	SLNKISLGAP	KKREIGQRDK
810	820	830	840	850	860	870	880
VFPHNESKYC	KSTFENKSLF	HVFNILEQKP	KDFYAPQSQA	EVASGYLRGM	AKKSLVSKVT	DSHITLKSQK	KRKGDKVKAS
890	900	910	920	930	940	950	960
AILSKQHATT	RANSLASLKK	PDFPEAIAHH	SIQNYIQSWL	QNINPYPTLK	PIKSAPVCRN	ETSVVNCSNN	SFSGNDPHTN
970	980	990	1000	1010	1020	1030	1040
SGKISNFVME	SNKHITKIAG	LTGDNLCKEG	DKSFIANDTG	EEDLHETQVG	SLNDAYLVPL	HEHCTLSQSA	INDHNTKSHI
1050	1060	1070	1080	1090	1100	1110	1120
AAEKSGPEKK	LVYQEINLAR	KRQSVEAAIQ	VDPIEEETPK	DLLPVLMLHQ	LQASVPGIHK	TQNGVVQMPG	SLAGVPFHSA
1130	1140	1150	1160	1170	1180	1190	1200
ICNSSTNLLL	AWLLVLNLKG	SMNSFCQVDA	HKATNKSSET	LALLEILKHI	AITEEADDLK	AAVANLVEST	TSHFGLSEKE
1210	1220	1230	1240	1250	1260	1270	1280
QDMVPIDLSA	NCSTVNIQSV	PKCSENERTQ	GISSLDGGCS	ASEACAPEVC	VLEVTCSPCE	MCTVNKAYSP	KETCNPSDTF
1290	1300	1310	1320	1330	1340	1350	1360
FPSDGYGVDQ	TSMNKACFLG	EVCSLTDTVF	SDKACAQKEN	HTYEGACPID	ETYVPVNVCN	TIDFLNSKEN	TYTDNLDSTE
1370	1380	1390	1400	1410	1420	1430	1440
ELERGDDIQK	DLNILTDPEY	KNGFNTLVSH	QNVSNLSSCG	LCLSEKEAEL	DKKHSSLDDF	ENCSLRKFQD	ENAYTSFDME
1450	1460	1470	1480	1490	1500	1510	1520
EPRTSEEPGS	ITNSMTSSER	NISELESFEE	LENHDTDIFN	TVVNGGEQAT	EELIQEEVEA	SKTLELIDIS	SKNIMEEKRM
1530	1540	1550	1560	1570	1580	1590	1600
NGIIYEIISK	RLATPPSLDF	CYDSKQNSEK	ETNEGETKMV	KMMVKTMETG	SYSESSPDLK	KCIKSPVTSD	WSDYRPDSDS
1610	1620	1630	1640	1650	1660	1670	1680
EQPYKTSSDD	PNDSGELTQE	KEYNIGFVKR	AIEKLYGKAD	IIKPSFFPGS	TRKSQVCPYN	SVEFQCSRKA	SLYDSEGQSF
1690	1700	1710	1720	1730	1740	1750	1760
GSSEQVSSSS	SMLQEFQEER	QDKCDVSAVR	DNYCRGDIVE	PGTKQNDDSR	ILTDIEEGVL	IDKGKWLLKE	NHLLRMSSEN
1770	1780	1790	1800	1810	1820	1830	1840
PGMCGNADTT	SVDTLLDNNS	SEVPYSHFGN	LAPGPTMDEL	SSSELEELTQ	PLELKCNYFN	MPHGSDSEPF	HEDLLDVRNE
1850	1860	1870	1880	1890	1900	1910	1920
TCAKERIANH	HTEEKGSHQS	ERVCTSVTHS	FISAGNKVYP	VSDDAIKNQP	LPGSNMIHGT	LQEADSLDKL	YALCGQHCPI
1930	1940	1950	1960	1970	1980	1990	2000
LTVIIQPMNE	EDRGFAYRKE	SDIENFLGFY	LWMKIHPYLL	QTDKNVFREE	NNKASMRQNL	IDNAIGDIFD	QFYFSNTFDL
2010	2020	2030	2040	2050	2060	2070	2080
MGKRRKQKRI	NFLGLEEEGN	LKKFQPDLKE	RFCMNFLHTS	LLVVGNVDSN	TQDLSGQTNE	IFKAVDENNN	LLNNRFQGSR
2090	2100	2110	2120	2130	2140	2150	2160
TNLNQVVREN	INCHYFFEML	GQACLLDICQ	VETSLNISNR	NILELCMFEG	ENLFIWEEED	ILNLTDLESS	REQEDL

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
702	1	437.5923	-338.90	2	38.1	12.2	1	699-705	K.NERINTK.G	

Detailed Protein Report

Protein 1023: 28S ribosomal protein S18b, mitochondrial [Homo sapiens]

Accession:	gi|7662645	**Score:**	12.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	29.4
Database Date:	2015-11-30	**pI:**	10.2
		Sequence Coverage [%]:	7.4
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MAASVLNTVL RRLPMLSLFR GSHRVQVPLQ TLCTKAPSEE DSLSSVPISP YKDEPWKYLE SEEYQERYGS RPVWADYRRN
        90        100        110        120        130        140        150        160
HKGGVPPQRT RKTCIRRNKV VGNPCPICRD HKLHVDFRNV KLLEQFVCAH TGIIFYAPYT GVCVKQHKRL TQAIQKARDH
       170        180        190        200        210        220        230        240
GLLIYHIPQV EPRDLDFSTS HGAVSATPPA PTLVSGDPWY PWYNWKQPPE RELSRLRRLY QGHLQEESGP PPESMPKMPP
       250        260
RTPAEASSTG QTGPQSAL
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2160	1	1062.5356	26.98	2	57.2	12.2	0	219-237	R.LYQGHLQEESGPPPESMPK.M	

Detailed Protein Report

Protein 1024: **succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial precursor [Homo sapiens]**

Accession:	gi|4557817	**Score:**	12.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	56.1
Database Date:	2015-11-30	**pI:**	7.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAALKLLSSG	LRLCASARGS	GATWYKGCVC	SFSTSAHRHT	KFYTDPVEAV	KDIPDGATVL	VGGFGLCGIP	ENLIDALLKT
90	100	110	120	130	140	150	160
GVKGLTAVSN	NAGVDNFGLG	LLLRSKQIKR	MVSSYVGENA	EFERQYLSGE	LEVELTPQGT	LAERIRAGGA	GVPAFYTPTG
170	180	190	200	210	220	230	240
YGTLVQEGGS	PIKYNKDGSV	AIASKPREVR	EFNGQHFILE	EAITGDFALV	KAWKADRAGN	VIFRKSARNF	NLPMCKAAET
250	260	270	280	290	300	310	320
TVVEVEEIVD	IGAFAPEDIH	IPQIYVHRLI	KGEKYEKRIE	RLSIRKEGDG	EAKSAKPGDD	VRERIIKRAA	LEFEDGMYAN
330	340	350	360	370	380	390	400
LGIGIPLLAS	NFISPNITVH	LQSENGVLGL	GPYPRQHEAD	ADLINAGKET	VTILPGASFF	SSDESFAMIR	GGHVDLTMLG
410	420	430	440	450	460	470	480
AMQVSKYGDL	ANWMIPGKMV	KGMGGAMDLV	SSAKTKVVVT	MEHSAKGNAH	KIMEKCTLPL	TGKQCVNRII	TEKAVFDVDK
490	500	510	520	530			
KKGLTLIELW	EGLTVDDVQK	STGCDFAVSP	KLMPMQQIAN				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2541	1	914.0511	97.19	2	62.2	12.2	2	419-436	K.MVKGMGGAMDLVSSAKTK.V	Oxidation: 1

Detailed Protein Report

Protein 1025: mitotic-spindle organizing protein 2B [Homo sapiens]

Accession:	gi|46094070	**Score:**	12.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	16.2
Database Date:	2015-11-30	**pI:**	10.8
		Sequence Coverage [%]:	11.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAAQGVGPGP	GSAAPPGLEA	ARQKLALRRK	KVLSTEEMEL	YELAQAAGGA	IDPDVFKILV	DLLKLNVAPL	AVFQMLKSMC
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
AGQRLASEPQ	DPAAVSLPTS	SVPETRGRNK	GSAALGGALA	LAERSSREGS	SQRMPRQPSA	TRLPKGGGPG	KSPTRGST

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2459	1	856.6216	163.35	2	61.1	12.2	2	107-124	R.GRNKGSAALGGALALAER.S	

Detailed Protein Report

Protein 1026: tumor necrosis factor alpha-induced protein 8-like protein 1 [Homo sapiens]

Accession:	gi|269846912	**Score:**	12.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	20.8
Database Date:	2015-11-30	**pI:**	10.4
Modification(s):	Oxidation	**Sequence Coverage [%]:**	9.7
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530425099	refseq_human (refseq_human_20140103.fasta)	PREDICTED: tumor necrosis factor alpha-induced protein 8-like protein 1 isoform X1 [Homo sapiens]
gi|269846918	refseq_human (refseq_human_20140103.fasta)	tumor necrosis factor alpha-induced protein 8-like protein 1 [Homo sapiens]

10	20	30	40	50	60	70	80
MDTFSTKSLA	LQAQKKLLSK	MASKAVVAVL	VDDTSSEVLD	ELYRATREFT	RSRKEAQKML	KNLVKVALKL	GLLLRGDQLG
90	100	110	120	130	140	150	160
GEELALLRRF	RHRARCLAMT	AVSFHQVDFT	FDRRVLAAGL	LECRDLLHQA	VGPHLTAKSH	GRINHVFGHL	ADCDFLAALY
170	180	190					
GPAEPYRSHL	RRICEGLGRM	LDEGSL					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2788	1	702.0628	100.22	3	66.3	12.2	0	96-113	R.CLAMTAVSFHQVDFTFDR.R	Oxidation: 4

Detailed Protein Report

Protein 1027: tumor necrosis factor receptor superfamily member 25 isoform 12 precursor [Homo sapiens]

Accession:	gi|89142745	**Score:**	12.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	19.4
Database Date:	2015-11-30	**pI:**	6.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	8.8
		No. of unique Peptides:	1

```
         10          20          30          40          50          60          70          80
MEQRPRGCAA  VAAALLLVLL  GARAQGGTRS  PRCDCAGDFH  KKIGLFCCRG  CPAGHYLKAP  CTEPCGNSTC  LVCPQDTFLA
         90         100         110         120         130         140         150         160
WENHHNSECA  RCQACDEQAS  QVALENCSAV  ADTRCGCKPG  WFVECQVSQC  VSSSPFYCQP  CLDCGALHRH  TRLLCSRRDT
        170         180         190
DCGTCLPGFY  EHGDGCVSCP  T
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1768	1	897.9818	53.60	2	51.9	12.2	1	43-58	K.IGLFCCRGCPAGHYLK.A	Carbamidomethyl: 9

Detailed Protein Report

Protein 1028: PREDICTED: sodium/iodide cotransporter isoform X1 [Homo sapiens]

Accession:	gi|530415091	**Score:**	12.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	43.4
Database Date:	2015-11-30	**pI:**	5.2
		Sequence Coverage [%]:	2.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDFNPDPRSR	YTFWTFVVGG	TLVWLSMYGV	NQAQVQRYVA	CRTEKQAKLA	LLINQVGLFL	IVSSAACCGI	VMFVFYTDCD
90	100	110	120	130	140	150	160
PLLLGRISAP	DQYMPLLVLD	IFEDLPGVPG	LFLACAYSGT	LSTASTSINA	MAAVTVEDLI	KPRLRSLAPR	KLVIISKGLS
170	180	190	200	210	220	230	240
LIYGSACLTV	AALSSLLGGG	VLQGSFTVMG	VISGPLLGAF	ILGMFLPACN	TPGVLAGLGA	GLALSLWVAL	GATLYPPSEQ
250	260	270	280	290	300	310	320
TMRVLPSSAA	RCVALSVNAS	GLLDPALLPA	NDSSRAPSSG	MDASRPALAD	SFYAISYLYY	GALGTLTTVL	CGALISCLTG
330	340	350	360	370	380	390	400
PTKRSTLAPG	LLWWDLARQT	ASVAPKEEVA	ILDDNLVKGP	EELPTGNKKP	PGFLPTNEDR	LFFLGQKELE	GAGSWTPCVG
410	420						
HDGGRDQQET	NL						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1609	1	685.7648	-134.19	2	49.8	12.2	0	369-380	K.KPPGFLPTNEDR.L	

Detailed Protein Report

Protein 1029: PREDICTED: kinesin-like protein KIFC1 isoform X2 [Homo sapiens]

Accession:	gi|578811677	**Score:**	12.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	45.7
Database Date:	2015-11-30	**pI:**	10.6
		Sequence Coverage [%]:	3.4
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578842326	refseq_human (refseq_human_20140103.fasta)	PREDICTED: kinesin-like protein KIFC1 isoform X4 [Homo sapiens]
gi|578842083	refseq_human (refseq_human_20140103.fasta)	PREDICTED: kinesin-like protein KIFC1 isoform X2 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MDPQRSPLLE VKGNIELKRP LIKAPSQLPL SGSRLKRRPD QMEDGLEPEK KRTRGLGATT KITTSHPRVP SLTTVPQTQG
        90        100        110        120        130        140        150        160
QTTAQKVSKK TGPRCSTAIA TGLKNQKPVP AVPVQKSGTS GVPPMAGGKK PSKRPAWDLK GQLCDLNAEL KRCRERTQTL
       170        180        190        200        210        220        230        240
DQENQQLQDQ LRDAQQQVKA LGTERTTLEG HLAKVQAQAE QGQQELKNLR ACVLELEERL STQEGLVQEL QKKQVELQEE
       250        260        270        280        290        300        310        320
RRGLMSQLEE KEVDALLHLA RQNRAVARTA QNERSSRSHS VFQLQISGEH SSRGLQCGAP LSLVDLAGSE RLDPGLALGP
       330        340        350        360        370        380        390        400
GERERLRETQ AINSSLSTLG LVIMALSNKE SHVPYRNSKL TYLLQNSLGG SAKMLMFVNI SPLEENVSES LNSLRFASKV
       410        420
RLPPVSLVRT RGWL
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1826	1	740.3072	-124.40	2	52.9	12.2	1	312-325	R.LDPGLALGPGERER.L	

Detailed Protein Report

Protein 1030: glutaredoxin 2 isoform 2 precursor [Homo sapiens]

Accession:	gi|37537704	**Score:**	12.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	18.0
Database Date:	2015-11-30	**pI:**	10.0
		Sequence Coverage [%]:	12.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MIWRRAALAG	TRLVWSRSGS	AGWLDRAAGA	AGAAAAAASG	MESNTSSSLE	NLATAPVNQI	QETISDNCVV	IFSKTSCSYC
90	100	110	120	130	140	150	160
TMAKKLFHDM	NVNYKVVELD	LLEYGNQFQD	ALYKMTGERT	VPRIFVNGTF	IGGATDTHRL	HKEGKLLPLV	HQCYLKKSKR
170							
KEFQ							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1298	1	1115.7311	121.43	2	45.9	12.2	2	6-26	R.AALAGTRLVWSRSGSAGWLDR.A	

Detailed Protein Report

Protein 1031: keratinocyte-associated protein 3 [Homo sapiens]

Accession: gi|270265801

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Modification(s): Carbamidomethyl, Oxidation

Score: 12.1

MW [kDa]: 25.6

pI: 9.7

Sequence Coverage [%]: 5.4

No. of unique Peptides: 1

Quantitation

MD:MU	**Median:**	3.40	**CV:**	0.00 %	**No. of Peptides:**	1

Alias proteins:

Accession	Name	Description
gi|530367348	refseq_human (refseq_human_20140103.fasta)	PREDICTED: keratinocyte-associated protein 3 isoform X2 [Homo sapiens]
gi|530367346	refseq_human (refseq_human_20140103.fasta)	PREDICTED: keratinocyte-associated protein 3 isoform X1 [Homo sapiens]
gi|270265803	refseq_human (refseq_human_20140103.fasta)	keratinocyte-associated protein 3 [Homo sapiens]

10	20	30	40	50	60	70	80
MRRCSLCAFD	AARGPRRLMR	VGLALILVGH	VNLLLGAVLH	GTVLRHVANP	RGAVTPEYTV	ANVISVGSGL	LSVSVGLVAL
90	100	110	120	130	140	150	160
LASRNLLRPP	LHWVLLALAL	VNLLLSVACS	LGLLLAVSLT	VANGGRRLIA	DCHPGLLDPL	VPLDEGPGHT	DCPFDPTRIY
170	180	190	200	210	220	230	240
DTALALWIPS	LLMSAGEAAL	SGYCCVAALT	LRGVGPCRKD	GLQGQLEEMT	ELESPKCKRQ	ENEQLLDQNQ	EIRASQRSWV
250							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
558	1	786.7320	-166.72	2	36.3	12.1	2	1-13	-.MRRCSLCAFDAAR.G	Carbamidomethyl: 4; Oxidation: 1	MD:MU 3.40

Detailed Protein Report

Protein 1032: PREDICTED: kinesin-like protein KIF21A isoform X9 [Homo sapiens]

Accession:	gi|530400550	**Score:**	12.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	179.8
Database Date:	2015-11-30	**pI:**	6.1
		Sequence Coverage [%]:	0.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLGAPDESSV	RVAVRIRPQL	AKEKIEGCHI	CTSVTPGEPQ	VFLGKDKAFT	FDYVFDIDSQ	QEQIYIQCIE	KLIEGCFEGY
90	100	110	120	130	140	150	160
NATVFAYGQT	GAGKTYTMGT	GFDVNIVEEE	LGIISRAVKH	LFKSIEEKKH	IAIKNGLPAP	DFKVNAQFLE	LYNEEVLDLF
170	180	190	200	210	220	230	240
DTTRDIDAKS	KKSNIRIHED	STGGIYTVGV	TTRTVNTESE	MMQCLKLGAL	SRTTASTQMN	VQSSRSHAIF	TIHVCQTRVC
250	260	270	280	290	300	310	320
PQIDADNATD	NKIISESAQM	NEFETLTAKF	HFVDLAGSER	LKRTGATGER	AKEGISINCG	LLALGNVISA	LGDKSKRATH
330	340	350	360	370	380	390	400
VPYRDSKLTR	LLQDSLGGNS	QTIMIACVSP	SDRDFMETLN	TLKYANRARN	IKNKVMVNQD	RASQQINALR	SEITRLQMEL
410	420	430	440	450	460	470	480
MEYKTGKRII	DEEGVESIND	MFHENAMLQT	ENNNLRVRIK	AMQETVDALR	SRITQLVSDQ	ANHVLARAGE	GNEEISNMIH
490	500	510	520	530	540	550	560
SYIKEIEDLR	AKLLESEAVN	ENLRKNLTRA	TARAPYFSGS	STFSPTILSS	DKETIEIIDL	AKKDLEKLKR	KEKRKKKRLQ
570	580	590	600	610	620	630	640
KLEESNREER	SVAGKEDNTD	TDQEKKEEKG	VSERENNELE	VEESQEVSDH	EDEEEEEEEE	EDDIDGGESS	DESDSESDEK
650	660	670	680	690	700	710	720
ANYQADLANI	TCEIAIKQKL	IDELENSQKR	LQTLKKQYEE	KLMMLQHKIR	DTQLERDQVL	QNLGSVESYS	EEKAKKVRSE
730	740	750	760	770	780	790	800
YEKKLQAMNK	ELQRLQAAQK	EHARLLKNQS	QYEKQLKKLQ	QDVMEMKKTK	VRLMKQMKEE	QEKARLTESR	RNREIAQLKK
810	820	830	840	850	860	870	880
DQRKRDHQLR	LLEAQKRNQE	VVLRRKTEEV	TALRRQVRPM	SDKVAGKVTR	KLSSSDAPAQ	DTGSSAAAVE	TDASRTGAQQ
890	900	910	920	930	940	950	960
KMRIPVARVQ	ALPTPATNGN	RKKYQRKGLT	GRVFISKTAR	MKWQLLERRV	TDIIMQKMTI	SNMEADMNRL	LKQREELTKR
970	980	990	1000	1010	1020	1030	1040
REKLSKRREK	IVKENGEGDK	NVANINEEME	SLTANIDYIN	DSISDCQANI	MQMEEAKEEG	ETLDVTAVIN	ACTLTEARYL
1050	1060	1070	1080	1090	1100	1110	1120
LDHFLSMGIN	KGLQAAQKEA	QIKVLEGRLK	QTEITSATQN	QLLFHMLKEK	AELNPELDAL	LGHALQENVE	DSTDEDAPLN
1130	1140	1150	1160	1170	1180	1190	1200
SPGSEGSTLS	SDLMKLCGEV	KPKNKARRRT	TTQMELLYAD	SSELASDTST	GDASLPGPLT	PVAEGQEIGM	NTETSGTSAR
1210	1220	1230	1240	1250	1260	1270	1280
EKELSPPPGL	PSKIGSISRQ	SSLSEKKIPE	PSPVTRRKAY	EKAEKSKAKE	QKQGIINPFP	ASKGIRAFPL	QCIHIAEGHT
1290	1300	1310	1320	1330	1340	1350	1360
KAVLCVDSTD	DLLFTGSKDR	TCKVWNLVTG	QEIMSLGGHP	NNVVSVKYCN	YTSLVFTVST	SYIKVWDIRD	SAKCIRTLTS
1370	1380	1390	1400	1410	1420	1430	1440
SGQVTLGDAC	SASTSRTVAI	PSGENQINQI	ALNPTGTFLY	AASGNAVRMW	DLKRFQSTGK	LTGHLGPVMC	LTVDQISSGQ
1450	1460	1470	1480	1490	1500	1510	1520
DLIITGSKDH	YIKMFDVTEG	ALGTVSPTHN	FEPPHYDGIE	ALTIQGDNLF	SGSRDNGIKK	WDLTQKDLLQ	QVPNAHKDWV
1530	1540	1550	1560	1570	1580	1590	1600
CALGVVPDHP	VLLSGCRGGI	LKVWNMDTFM	PVGEMKGHDS	PINAICVNST	HIFTAADDRT	VRIWKARNLQ	DGQISDTGDL
1610							
GEDIASN							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
383	1	625.4008	133.02	2	34.4	12.1	1	759-768	K.LQQDVMEMKK.T	

Detailed Protein Report

Protein 1033: dexamethasone-induced Ras-related protein 1 isoform 2 [Homo sapiens]

Accession:	gi|317008582	**Score:**	12.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	13.8
Database Date:	2015-11-30	**pI:**	10.3
Modification(s):	Oxidation	**Sequence Coverage [%]:**	6.6
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 2.15 **CV:** 0.00 % **No. of Peptides:** 1

```
         10         20         30         40         50         60         70         80
MKLAAMIKKM CPSDSELSIP AKNCYRMVIL GSSKVGKTAI VSRFLTGRFE DAYTPTIEDF HRKFYSIRGE VYQLDILDTS
         90        100        110        120        130
GNHPFPAMRR LSILTDPRHQ VLPQEQNQGE RGRAPGHLRQ QG
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
574	1	469.1205	-305.92	2	36.8	12.1	1	1-8	-.MKLAAMIK.K	Oxidation: 1, 6	MD:MU 2.15

Detailed Protein Report

Protein 1034: PREDICTED: NADH-cytochrome b5 reductase 2 isoform X4 [Homo sapiens]

Accession:	gi|530395471	**Score:**	12.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	28.8
Database Date:	2015-11-30	**pI:**	10.4
Modification(s):	Oxidation	**Sequence Coverage [%]:**	7.8
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MNERRSARST RLQLGDAPAS APPRKHPPRT RPRVGAHEDP SLLLTITVTG VTVLVLVLKS MNSRRREPIT LQDPEAKYPL
        90        100        110        120        130        140        150        160
PLIEKEKISH NTRRFRFGLP SPDHVLGLPV GNYVQLLAKI DNELVVRAYT PVSSDDDRGF VDLIIKIYFK NVHPQYPEGG
       170        180        190        200        210        220        230        240
KMTQYLENMK IGETIFFRGP RGRLFYHGPG NLGIRPDQTS EPKKTLADHL GMIAGGTGIT PMLQLIRHIT KDPSDRTRMS
       250        260
LIFANQAGST AQASLLPT
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
13	1	1018.9359	-82.25	2	29.7	12.1	0	239-258	R.MSLIFANQAGSTAQASLLPT.-	Oxidation: 1

Detailed Protein Report

Protein 1035: PREDICTED: beta-chimaerin isoform X6 [Homo sapiens]

Accession:	gi|530384452	**Score:**	12.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	30.1
Database Date:	2015-11-30	**pI:**	6.5
		Sequence Coverage [%]:	3.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MRVTYRGLWH	PVHTFRGPHW	CEYCANFMWG	LIAQGVRCSD	CGLNVHKQCS	KHVPNDCQPD	LKRIKKVYCC	DLTTLVKAHN
90	100	110	120	130	140	150	160
TQRPMVVDIC	IREIEARGLK	SEGLYRVSGF	TEHIEDVKMA	FDRDGEKADI	SANVYPDINI	ITGALKLYFR	DLPIPVITYD
170	180	190	200	210	220	230	240
TYSKFIDAAK	ISNADERLEA	VHEVLMLLPP	AHYETLRYLM	IHLKKVTMNE	KDNFMNAENL	GIVFGPTLMR	PPEDSTLTTL
250	260	270					
HDMRYQKLIV	QILIENEDVL	F					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
446	1	538.2346	-3.64	2	34.9	12.1	0	38-47	R.CSDCGLNVHK.Q	

Detailed Protein Report

Protein 1036: **PREDICTED: 1-acyl-sn-glycerol-3-phosphate acyltransferase delta isoform X4 [Homo sapiens]**

Accession:	gi|530383876	**Score:**	12.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	27.3
Database Date:	2015-11-30	**pI:**	10.2
		Sequence Coverage [%]:	6.5
		No. of unique Peptides:	1

Quantitation

MD:MU	**Median:**	1.33	**CV:**	0.00 %	**No. of Peptides:**	1

Alias proteins:

Accession	**Name**	**Description**
gi|578812839	refseq_human(refseq_human_20140103.fasta)	PREDICTED: 1-acyl-sn-glycerol-3-phosphate acyltransferase delta isoform X8 [Homo sapiens]

10	20	30	40	50	60	70	80
MDLAGLLKSQ	FLCHLVFCYV	FIASGLIINT	IQLFTLLLWP	INKQLFRKIN	CRLSYCISSQ	LVMLLEWWSG	TECTIFTDPR
90	100	110	120	130	140	150	160
AYLKYGKENA	IVVLNHKFEI	DFLCGWSLSE	RFGLLGGSKV	LAKKELAYVP	IIGWMWYFTE	MVFCSRKWEQ	DRKTVATSLQ
170	180	190	200	210	220	230	240
HLRDYPEKYF	FLIHCEGTRF	TEKKHEISMQ	VARAKGLPRL	KHHLLPRTKG	FAITVRSLRN	VEIMKIQHCW	ES

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
862	1	945.8909	-77.27	2	40.2	12.1	1	169-183	K.YFFLIHCEGTRFTEK.K		MD:MU 1.33

Detailed Protein Report

Protein 1037: pleckstrin homology-like domain family B member 2 isoform c [Homo sapiens]

Accession:	gi|21955172	**Score:**	12.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	136.8
Database Date:	2015-11-30	**pI:**	7.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEEHSYIQKE	LDLQNGSLEE	DSVVHSVEND	SQNMMESLSP	KKYSSSLRFK	ANGDYSGSYL	TLSQPVPAKR	SPSPLGTSVR
90	100	110	120	130	140	150	160
SSPSLAKIQG	SKQFSYDGTD	KNIPMKPPTP	LLNTTSSLSG	YPLGRADFDH	YTGRDSERAL	RLSEKPPYSK	YSSRHKSHDN
170	180	190	200	210	220	230	240
VYSLGGLEGR	KASGSLLAMW	NGSSLSDAGP	PPISRSGAAS	MPSSPKQARK	MSIQDSLALQ	PKLTRHKELA	SENINLRTRK
250	260	270	280	290	300	310	320
YSSSSLSHMG	AYSRSLPRLY	RATENQLTPL	SLPPRNSLGN	SKRTKLGEKD	LPHSVIDNDN	YLNFSSLSSG	ALPYKTSASE
330	340	350	360	370	380	390	400
GNPYVSSTLS	VPASPRVARK	MLLASTSSCA	SDDFDQASYV	GTNPSHSLLA	GESDRVFATR	RNFSCGSVEF	DEADLESLRQ
410	420	430	440	450	460	470	480
ASGTPQPALR	ERKSSISSIS	GRDDLMDYHR	RQREERLREQ	EMERLERQRL	ETILSLCAEY	TKPDSRLSTG	TTVEDVQKIN
490	500	510	520	530	540	550	560
KELEKLQLSD	EESVFEEALM	SPDTRYRCHR	KDSLPDADLA	SCGSLSQSSA	SFFTPRSTRN	DELLSDLTRT	PPPPSSTFPK
570	580	590	600	610	620	630	640
ASSESSYLSI	LPKTPEGISE	EQRSQELAAM	EETRIVILNN	LEELKQKIKD	INDQMDESFR	ELDMECALLD	GEQKSETTEL
650	660	670	680	690	700	710	720
MKEKEILDHL	NRKIAELEKN	IVGEKTKDAD	LLDVESKHFE	DLEFQQLEHE	SRLDEEKENL	TQQLLREVAE	YQRNIVSRKE
730	740	750	760	770	780	790	800
KISALKKQAN	HIVQQAQREQ	DHFVKEKNNL	IMMLQREKEN	LCNLEKKYSS	LSGGKGFPVN	PNTLKEGYIS	VNEINEPCGN
810	820	830	840	850	860	870	880
STNLSPSTQF	PADADAVATE	PATAVLASQP	QSKEHFRSLE	ERKKQHKEGL	YLSDTLPRKK	TTSSISPHFS	SATMGRSITP
890	900	910	920	930	940	950	960
KAHLPLGQSN	SCGSVLPPSL	AAMAKDSESR	RMLRGYNHQQ	MSEGHRQKSE	FYNRTASESN	VYLNSFHYPD	HSYKDQAFDT
970	980	990	1000	1010	1020	1030	1040
LSLDSSDSME	TSISACSPDN	ISSASTSNIA	RIEEMERLLK	QAHAEKTRLL	ESREREMEAK	KRALEEEKRR	REILEKRLQE
1050	1060	1070	1080	1090	1100	1110	1120
ETSQRQKLIE	KEVKIRERQR	AQARPLTRYL	PVRKEDFDLR	SHVETAGHNI	DTCYHVSITE	KTCRGFLIKM	GGKIKTWKKR
1130	1140	1150	1160	1170	1180	1190	1200
WFVFDRNKRT	FSYYADKHET	KLKGVIYFQA	IEEVYYDHLK	NANKSPNPLL	TFSVKTHDRI	YYMVAPSPEA	MRIWMDVIVT
1210	1220						
GAEGYTHFLL							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
244	1	938.4223	1.97	2	32.4	12.1	1	912-926	R.MLRGYNHQQMSEGHR.Q	Oxidation: 1, 10

Detailed Protein Report

Protein 1038: PREDICTED: phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic subunit delta isoform isoform X7 [Homo sapiens]

Accession:	gi|578799247	**Score:**	12.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	116.2
Database Date:	2015-11-30	**pI:**	7.0
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	1.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPPGVDCPME	FWTKEENQSV	VVDFLLPTGV	YLNFPVSRNA	NLSTIKQLLW	HRAQYEPLFH	MLSGPEAYVF	TCINQTAEQQ
90	100	110	120	130	140	150	160
ELEDEQRRLC	DVQPFLPVLR	LVAREGDRVK	KLINSQISLL	IGKGLHEFDS	LCDPEVNDFR	AKMCQFCEEA	AARRQQLGWE
170	180	190	200	210	220	230	240
AWLQYSFPLQ	LEPSAQTWGP	GTLRLPNRAL	LVNVKFEGSE	ESFTFQVSTK	DVPLALMACA	LRKKATVFRQ	PLVEQPEDYT
250	260	270	280	290	300	310	320
LQVNGRHEYL	YGSYPLCQFQ	SNPAPQVQKP	RAKPPPIPAK	KPSSVSLWSL	EQPFRIELIQ	GSKVNADERM	KLVVQAGLFH
330	340	350	360	370	380	390	400
GNEMLCKTVS	SSEVSVCSEP	VWKQRLEFDI	NICDLPRMAR	LCFALYAVIE	KAKKARSTKK	KSKKADCPIA	WANLMLFDYK
410	420	430	440	450	460	470	480
DQLKTGERCL	YMWPSVPDEK	GELLNPTGTV	RSNPNTDSAA	ALLICLPEVA	PHPVYYPALE	KILELGRHSE	CVHVTEEEQL
490	500	510	520	530	540	550	560
QLREILERRG	SGELYEHEKD	LVWKLRHEVQ	EHFPEALARL	LLVTKWNKHE	DVAQMLYLLC	SWPELPVLSA	LELLDFSFPD
570	580	590	600	610	620	630	640
CHVGSFAIKS	LRKLTDDELF	QYLLQLVQVL	KYESYLDCEL	TKFLLDRALA	NRKIGHFLFW	HLRSEMHVPS	VALRFGLILE
650	660	670	680	690	700	710	720
AYCRGSTHHM	KVLMKQGEAL	SKLKALNDFV	KLSSQKTPKP	QTKELMHLCM	RQEAYLEALS	HLQSPLDPST	LLAEVCVEQC
730	740	750	760	770	780	790	800
TFMDSKMKPL	WIMYSNEEAG	SGGSVGIIFK	NGDDLRQDML	TLQMIQLMDV	LWKQEGLDLR	MTPYGCLPTG	DRTGLIEVVL
810	820	830	840	850	860	870	880
RSDTIANIQL	NKSNMAATAA	FNKDALLNWL	KSKNPGEALD	RAIEEFTLSC	AGYCVATYVL	GIGDRHSDNI	MIRESGQLFH
890	900	910	920	930	940	950	960
IDFGHFLGNF	KTKFGINRER	VPFILTYDFV	HVIQQGKTNN	SEKFERFRGY	CERAYTILRR	HGLLFLHLFA	LMRAAGLPEL
970	980	990	1000	1010	1020		
SCSKDIQYLK	DSLALGKTEE	EALKHFRVKF	NEALRESWKT	KVNWLAHNVS	KDNRQ		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2589	1	673.3601	12.11	2	62.9	12.1	0	211-222	K.DVPLALMACALR.K	Carbamidomethyl: 9; Oxidation: 7

Detailed Protein Report

Protein 1039: **endonuclease/exonuclease/phosphatase family domain-containing protein 1 [Homo sapiens]**

Accession: gi|71043966
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 12.1
MW [kDa]: 62.4
pI: 9.5
Sequence Coverage [%]: 3.2
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MGSTLGCHRS	IPRDPSDLSH	SRKFSAACNF	SNILVNQERL	NINTATEEEL	MTLPGVTRAV	ARSIVEYREY	IGGFKKVEDL
90	100	110	120	130	140	150	160
ALVSGVGATK	LEQVKFEICV	SSKGSSAQHS	PSSLRRDLLA	EQQPHHLATA	VPLTPRVNIN	TATPAQLMSV	RGLSEKMALS
170	180	190	200	210	220	230	240
IVDFRREHGP	FRSVEDLVRM	DGINAAFLDR	IRHQVFAERS	RPPSTHTNGG	LTFTAKPHPS	PTSLSLQSED	LDLPPGGPTQ
250	260	270	280	290	300	310	320
IISTRPSVEA	FGGTRDGRPV	LRLATWNLQG	CSVEKANNPG	VREVVCMTLL	ENSIKLLAVQ	ELLDREALEK	FCTELNQPTL
330	340	350	360	370	380	390	400
PNIRKWKGPR	GCWKAVVAEK	PSSQLQKGAG	YAGFLWDAAA	GMELRDAGSQ	ESSPSNGHGK	LAGPSPYLGR	FKVGSHDLTL
410	420	430	440	450	460	470	480
VNLHLAALTL	LGSENPSKNH	SDGHRLASFA	QTLQETLKGE	KDVIILGDFG	QGPDSNDYDI	LRKEKFHHLI	PAHTFTNIST
490	500	510	520	530	540	550	560
KNPQGSKSLD	NIWISKSLKK	VFTGHWAVVR	EGLTNPWIPD	NWSWGGVASE	HCPVLAEFYT	EKDWSKKDAP	RNGSGVALER
570							
SEANIKHER							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
983	1	984.1474	143.39	2	41.8	12.1	2	552-569	R.NGSGVALERSEANIKHER.-	

Detailed Protein Report

Protein 1040: glutamate receptor ionotropic, NMDA 2A isoform 2 precursor [Homo sapiens]

Accession:	gi|197313638	**Score:**	12.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	144.3
Database Date:	2015-11-30	**pI:**	6.3
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	1.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGRVGYWTLL	VLPALLVWRG	PAPSAAAEKG	PPALNIAVML	GHSHDVTERE	LRTLWGPEQA	AGLPLDVNVV	ALLMNRTDPK
90	100	110	120	130	140	150	160
SLITHVCDLM	SGARIHGLVF	GDDTDQEAVA	QMLDFISSHT	FVPILGIHGG	ASMIMADKDP	TSTFFQFGAS	IQQQATVMLK
170	180	190	200	210	220	230	240
IMQDYDWHVF	SLVTTIFPGY	REFISFVKTT	VDNSFVGWDM	QNVITLDTSF	EDAKTQVQLK	KIHSSVILLY	CSKDEAVLIL
250	260	270	280	290	300	310	320
SEARSLGLTG	YDFFWIVPSL	VSGNTELIPK	EFPSGLISVS	YDDWDYSLEA	RVRDGIGILT	TAASSMLEKF	SYIPEAKASC
330	340	350	360	370	380	390	400
YGQMERPEVP	MHTLHPFMVN	VTWDGKDLSF	TEEGYQVHPR	LVVIVLNKDR	EWEKVGKWEN	HTLSLRHAVW	PRYKSFSDCE
410	420	430	440	450	460	470	480
PDDNHLSIVT	LEEAPFVIVE	DIDPLTETCV	RNTVPCRKFV	KINNSTNEGM	NVKKCCKGFC	IDILKKLSRT	VKFTYDLYLV
490	500	510	520	530	540	550	560
TNGKHGKKVN	NVWNGMIGEV	VYQRAVMAVG	SLTINEERSE	VVDFSVPFVE	TGISVMVSRS	NGTVSPSAFL	EPFSASVWVM
570	580	590	600	610	620	630	640
MFVMLLIVSA	IAVFVFEYFS	PVGYNRNLAK	GKAPHGPSFT	IGKAIWLLWG	LVFNNSVPVQ	NPKGTTSKIM	VSVWAFFAVI
650	660	670	680	690	700	710	720
FLASYTANLA	AFMIQEEFVD	QVTGLSDKKF	QRPHDYSPPF	RFGTVPNGST	ERNIRNNYPY	MHQYMTKFNQ	KGVEDALVSL
730	740	750	760	770	780	790	800
KTGKLDAFIY	DAAVLNYKAG	RDEGCKLVTI	GSGYIFATTG	YGIALQKGSP	WKRQIDLALL	QFVGDGEMEE	LETLWLTGIC
810	820	830	840	850	860	870	880
HNEKNEVMSS	QLDIDNMAGV	FYMLAAAMAL	SLITFIWEHL	FYWKLRFCFT	GVCSDRPGLL	FSISRGIYSC	IHGVHIEEKK
890	900	910	920	930	940	950	960
KSPDFNLTGS	QSNMLKLLRS	AKNISSMSNM	NSSRMDSPKR	AADFIQRGSL	IMDMVSDKGN	LMYSDNRSFQ	GKESIFGDNM
970	980	990	1000	1010	1020	1030	1040
NELQTFVANR	QKDNLNNYVF	QGQHPLTLNE	SNPNTVEVAV	STESKANSRP	RQLWKKSVDS	IRQDSLSQNP	VSQRDEATAE
1050	1060	1070	1080	1090	1100	1110	1120
NRTHSLKSPR	YLPEEMAHSD	ISETSNRATC	HREPDNSKNH	KTKDNFKRSV	ASKYPKDCSE	VERTYLKTKS	SSPRDKIYTI
1130	1140	1150	1160	1170	1180	1190	1200
DGEKEPGFHL	DPPQFVENVT	LPENVDFPDP	YQDPSENFRK	GDSTLPMNRN	PLHNEEGLSN	NDQYKLYSKH	FTLKDKGSPH
1210	1220	1230	1240	1250	1260	1270	1280
SETSERYRQN	STHCRSCLSN	MPTYSGHFTM	RSPFKCDACL	RMGNLYDIDE	DQMLQETGMT	NAWLLGDAPR	TLTNTRCHPR
1290							
R							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2193	1	952.8178	-94.66	2	57.3	12.1	0	1216-1231	R.SCLSNMPTYSGHFTMR.S	Carbamidomethyl: 2; Oxidation: 6

Detailed Protein Report

Protein 1041: PREDICTED: zinc finger protein 584 isoform X4 [Homo sapiens]

Accession:	gi|530415952	**Score:**	12.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	16.1
Database Date:	2015-11-30	**pI:**	4.7
		Sequence Coverage [%]:	11.0
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MAGEAEGLVM FEDVTVYFSR EEWGLLNVTQ KGLYRDVMLE NFALVSSLGL APSRSPVFTQ LEDDEQSWVP SWVDVTPVSR
        90        100        110        120        130        140        150
AEARRGFGLG PACSCLSGLR LLIALLCICA ELSTVGDSVR VLKCAHILKQ MVCVEWRMRE PILSI
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
95	1	668.3014	-53.00	3	30.6	12.0	2	124-139	K.CAHILKQMVCVEWRMR.E	

Detailed Protein Report

Protein 1042: PREDICTED: kinesin-like protein KIF24 isoform X3 [Homo sapiens]

Accession:	gi|578816480	**Score:**	12.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	99.6
Database Date:	2015-11-30	**pI:**	8.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MYPSTGSGTH	PYSLQAKQTN	SATQGKTFKK	MQKKQHWIYL	EVTMGVKVLK	DSFIGNAKTC	MIANISPSHV	ATEHTLNTLR
90	100	110	120	130	140	150	160
YADRVKELKK	GIKCCTSVTS	RNRTSGNSSP	KRIQSSPGAL	SEDKCSPKKV	KLGFQQSLTV	AAPGSTRGKV	HPLTSHPPNI
170	180	190	200	210	220	230	240
PFTSAPKVSG	KRGGSRGSPS	QEWVIHASPV	KGTVRSGHVA	KKKPEESAPL	CSEKNRMGNK	TVLGWESRAS	GPGEGLVRGK
250	260	270	280	290	300	310	320
LSTKCKKVQT	VQPVQKQLVS	RVELSFGNAH	HRAEYSQDSQ	RGTPARPASE	AWTNIPPHQK	EREEHLRFYH	QQFQQPPLLQ
330	340	350	360	370	380	390	400
QKLKYQPLKR	SLRQYRPPEG	QLTNETPPLF	HSYSENHDGA	QVEELDDSDF	SEDSFSHISS	QRATKQRNTL	ENSEDSFFLH
410	420	430	440	450	460	470	480
QTWGQGPEKQ	VAERQQSLFS	SPRTGDKKDL	TKSWVDSRDP	INHRRAALDH	SCSPSKGPVD	WSRENSTSSG	PSPRDSLAEK
490	500	510	520	530	540	550	560
PYCSQVDFIY	RQERGGGSSF	DLRKDASQSE	VSGENEGNLP	SPEEDGFTIS	LSHVAVPGSP	DQRDTVTTPL	REVSADGPIQ
570	580	590	600	610	620	630	640
VTSTVKNGHA	VPGEDPRGQL	GTHAEYASGL	MSPLTMSLLE	NPDNEGSPPS	EQLVQDGATH	SLVAESTGGP	VVSHTVPSGD
650	660	670	680	690	700	710	720
QEAALPVSSA	TRHLWLSSSP	PDNKPGGDLP	ALSPSPIRQH	PADKLPSREA	DLGEACQSRE	TVLFSHEHMG	SEQYDADAEE
730	740	750	760	770	780	790	800
TGLDGSWGFP	GKPFTTIHMG	VPHSGPTLTP	RTGSSDVADQ	LWAQERKHPT	RLGWQEFGLS	TDPIKLPCNS	ENVTWLKPRP
810	820	830	840	850	860	870	880
ISRCLARPSS	PLVPSCSPKT	AGTLRQPTLE	QAQQVVIRAH	QEQLDEMAEL	GFKEETLMSQ	LASNDFEDFV	TQLDEIMVLK
890	900	910	920				
SKCIQSLRSQ	LQLYLTCHGP	TAAPEGTVPS					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2259	1	1023.8759	66.82	3	58.1	12.0	2	446-474	R.AALDHSCSPSKGPVDWSRENSTSSGPSPR.D	Carbamidomethyl: 7

Detailed Protein Report

Protein 1043: 28S ribosomal protein S31, mitochondrial [Homo sapiens]

Accession:	gi|186928854	**Score:**	12.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	45.3
Database Date:	2015-11-30	**pI:**	9.8
		Sequence Coverage [%]:	2.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MFPRVSTFLP	LRPLSRHPLS	SGSPETSAAA	IMLLTVRHGT	VRYRSSALLA	RTKNNIQRYF	GTNSVICSKK	DKQSVRTEET
90	100	110	120	130	140	150	160
SKETSESQDS	EKENTKKDLL	GIIKGMKVEL	STVNVRTTKP	PKRRPLKSLE	ATLGRLRRAT	EYAPKKRIEP	LSPELVAAAS
170	180	190	200	210	220	230	240
AVADSLPFDK	QTTKSELLSQ	LQQHEEESRA	QRDAKRPKIS	FSNIISDMKV	ARSATARVRS	RPELRIQFDE	GYDNYPGQEK
250	260	270	280	290	300	310	320
TDDLKKRKNI	FTGKRLNIFD	MMAVTKEAPE	TDTSPSLWDV	EFAKQLATVN	EQPLQNGFEE	LIQWTKEGKL	WEFPINNEAG
330	340	350	360	370	380	390	400
FDDDGSEFHE	HIFLEKHLES	FPKQGPIRHF	MELVTCGLSK	NPYLSVKQKV	EHIEWFRNYF	NEKKDILKES	NIQFN

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1539	1	660.8309	-18.83	2	48.9	12.0	1	385-395	K.DILKESNIQFN.-	

Detailed Protein Report

Protein 1044: PREDICTED: multidrug resistance-associated protein 1 isoform X6 [Homo sapiens]

Accession:	gi|578828091	**Score:**	12.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	156.6
Database Date:	2015-11-30	**pI:**	6.7
		Sequence Coverage [%]:	1.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MALRGFCSAD	GSDPLWDWNV	TWNTSNPDFT	KCFQNTVLVW	VPCFYLWACF	PFYFLYLSRH	DRGYIQMTPL	NKTKTNPCPE
90	100	110	120	130	140	150	160
SSASFLSRIT	FWWITGLIVR	GYRQPLEGSD	LWSLNKEDTS	EQVVPVLVKN	WKKECAKTRK	QPVKVVYSSK	DPAQPKESSK
170	180	190	200	210	220	230	240
VDANEEVEAL	IVKSPQKEWN	PSLFKVLYKT	FGPYFLMSFF	FKAIHDLMMF	SGPQILKLLI	KFVNDTKAPD	WQGYFYTVLL
250	260	270	280	290	300	310	320
FVTACLQTLV	LHQYFHICFV	SGMRIKTAVI	GAVYRKALVI	TNSARKSSTV	GEIVNLMSVD	AQRFMDLATY	INMIWSAPLQ
330	340	350	360	370	380	390	400
VILALYLLWL	NLGPSVLAGV	AVMVLMVPVN	AVMAMKTKTY	QVAHMKSKDN	RIKLMNEILN	GIKVLKLYAW	ELAFKDKVLA
410	420	430	440	450	460	470	480
IRQEELKVLK	KSAYLSAVGT	FTWVCTPFLV	ALCTFAVYVT	IDENNILDAQ	TAFVSLALFN	ILRFPLNILP	MVISSIVQAS
490	500	510	520	530	540	550	560
VSLKRLRIFL	SHEELEPDSI	ERRPVKDGGG	TNSITVRNAT	FTWARSDPPT	LNGITFSIPE	GALVAVVGQV	GCGKSSLLSA
570	580	590	600	610	620	630	640
LLAEMDKVEG	HVAIKGSVAY	VPQQAWIQND	SLRENILFGC	QLEEPYYRSV	IQACALLPDL	EILPSGDRTE	IGEKGVNLSG
650	660	670	680	690	700	710	720
GQKQRVSLAR	AVYSNADIYL	FDDPLSAVDA	HVGKHIFENV	IGPKGMLKNK	TRILVTHSMS	YLPQVDVIIV	MSGGKISEMG
730	740	750	760	770	780	790	800
SYQELLARDG	AFAEFLRTYA	STEQEQDAEE	NGVTGVSGPG	KEAKQMENGM	LVTDSAGKQL	QRQLSSSSSY	SGDISRHHNS
810	820	830	840	850	860	870	880
TAELQKAEAK	KEETWKLMEA	DKAQTGQVKL	SVYWDYMKAI	GLFISFLSIF	LFMCNHVSAL	ASNYWLSLWT	DDPIVNGTQE
890	900	910	920	930	940	950	960
HTKVRLSVYG	ALGISQGIAV	FGYSMAVSIG	GILASRCLHV	DLLHSILRSP	MSFFERTPSG	NLVNRFSKEL	DTVDSMIPEV
970	980	990	1000	1010	1020	1030	1040
IKMFMGSLFN	VIGACIVILL	ATPIAAIIIP	PLGLIYFFVQ	RFYVASSRQL	KRLESVSRSP	VYSHFNETLL	GVSVIRAFEE
1050	1060	1070	1080	1090	1100	1110	1120
QERFIHQSDL	KVDENQKAYY	PSIVANRWLA	VRLECVGNCI	VLFAALFAVI	SRHSLSAGLV	GLSVSYSLQV	TTYLNWLVRM
1130	1140	1150	1160	1170	1180	1190	1200
SSEMETNIVA	VERLKEYSET	EKEAPWQIQE	TAPPSSWPQV	GRVEFRNYCL	RYREDLDFVL	RHINVTINGG	EKVGIVGRTG
1210	1220	1230	1240	1250	1260	1270	1280
AGKSSLTLGL	FRINESAEGE	IIIDGINIAK	IGLHDLRFKI	TIIPQDPVLF	SGSLRMNLDP	FSQYSDEEVW	TSLELAHLKD
1290	1300	1310	1320	1330	1340	1350	1360
FVSALPDKLD	HECAEGGENL	SVGQRQLVCL	ARALLRKTKI	LVLDEATAAV	DLETDDLIQS	TIRTQFEDCT	VLTIAHRLNT
1370	1380	1390	1400	1410			
IMDYTRVIVL	DKGEIQEYGA	PSDLLQQRGL	FYSMAKDAGL	V			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1249	1	863.6787	164.53	2	45.2	12.0	2	372-386	R.IKLMNEILNGIKVLK.L	

Detailed Protein Report

Protein 1045: chondroitin sulfate glucuronyltransferase isoform 2 [Homo sapiens]

Accession:	gi|546231996	**Score:**	12.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	85.1
Database Date:	2015-11-30	**pI:**	8.9
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLSLARPPLP	PTGLRTSLSL	LRVSWIQGEG	EDPCVEAVGE	RGGPQNPDSR	ARLDQSDEDF	KPRIVPYYRD	PNKPYKKVLR
90	100	110	120	130	140	150	160
TRYIQTELGS	RERLLVAVLT	SRATLSTLAV	AVNRTVAHHF	PRLLYFTGQR	GARAPAGMQV	VSHGDERPAW	LMSETLRHLH
170	180	190	200	210	220	230	240
THFGADYDWF	FIMQDDTYVQ	APRLAALAGH	LSINQDLYLG	RAEEFIGAGE	QARYCHGGFG	YLLSRSLLLR	LRPHLDGCRG
250	260	270	280	290	300	310	320
DILSARPDEW	LGRCLIDSLG	VGCVSQHQGQ	QYRSFELAKN	RDPEKEGSSA	FLSAFAVHPV	SEGTLMYRLH	KRFSALELER
330	340	350	360	370	380	390	400
AYSEIEQLQA	QIRNLTVLTP	EGEAGLSWPV	GLPAPFTPHS	RFEVLGWDYF	TEQHTFSCAD	GAPKCPLQGA	SRADVGDALE
410	420	430	440	450	460	470	480
TALEQLNRRY	QPRLRFQKQR	LLNGYRRFDP	ARGMEYTLDL	LLECVTQRGH	RRALARRVSL	LRPLSRVEIL	PMPYVTEATR
490	500	510	520	530	540	550	560
VQLVLPLLVA	EAAAAPAFLE	AFAANVLEPR	EHALLTLLLV	YGPREGGRGA	PDPFLGVKAA	AAELERRYPG	TRLAWLAVRA
570	580	590	600	610	620	630	640
EAPSQVRLMD	VVSKKHPVDT	LFFLTTVWTR	PGPEVLNRCR	MNAISGWQAF	FPVHFQEFNP	ALSPQRSPPG	PPGAGPDPPS
650	660	670	680	690	700	710	720
PPGADPSRGA	PIGGRFDRQA	SAEGCFYNAD	YLAARARLAG	ELAGQEEEEA	LEGLEVMDVF	LRFSGLHLFR	AVEPGLVQKF
730	740	750	760	770			
SLRDCSPRLS	EELYHRCRLS	NLEGLGGRAQ	LAMALFEQEQ	ANST			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2366	1	938.2446	47.14	3	59.9	12.0	2	457-480	R.RVSLLRPLSRVEILPMPYVTEATR.V	Oxidation: 16

Detailed Protein Report

Protein 1046: **PREDICTED: zinc finger CCCH domain-containing protein 14 isoform X2 [Homo sapiens]**

Accession:	gi|530404628	**Score:**	12.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	80.0
Database Date:	2015-11-30	**pI:**	7.2
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEIGTEISRK	IRSAIKGKLQ	ELGAYVDEEL	PDYIMVMVAN	KKSQDQMTED	LSLFLGNNTI	RFTVWLHGVL	DKLRSVTTEP
90	100	110	120	130	140	150	160
SSLKSSDTNI	FDSNVPSNKS	NFSRGDERRH	EAAVPPLAIP	SARPEKRDSR	VSTSSQESKT	TNVRQTYDDG	AATRLMSTVK
170	180	190	200	210	220	230	240
PLREPAPSED	VIDIKPEPDD	LIDEDLNFVQ	ENPLSQKKPT	VTLTYGSSRP	SIEIYRPPAS	RNADSGVHLN	RLQFQQQQNS
250	260	270	280	290	300	310	320
IHAAKQLDMQ	SSWVYETGRL	CEPEVLNSLE	ETYSPFFRNN	SEKMSMEDEN	FRKRKLPVVS	SVVKVKKFNH	DGEEEEEDDD
330	340	350	360	370	380	390	400
YGSRTGSISS	SVSVPAKPER	RPSLPPSKQA	NKNLILKAIS	EAQESVTKTT	NYSTVPQKQT	LPVAPRTRTS	QEELLAEVVQ
410	420	430	440	450	460	470	480
GQSRTPRISP	PIKEEETKGD	SVEKNQDYYD	MESMVHADTR	SFILKKPKLS	EEVVVAPNQE	SGMKTADSLR	VLSGHLMQTR
490	500	510	520	530	540	550	560
DLVQPDKPAS	PKFIVTLDGV	PSPPGYMSDQ	EEDMCFEGMK	PVNQTAASNK	GLRGLLHPQQ	LHLLSRQLED	PNGSFSNAEM
570	580	590	600	610	620	630	640
SELSVAQKPE	KLLERCKYWP	ACKNGDECAY	HHPISPCKAF	PNCKFAEKCL	FVHPNCKYDA	KCTKPDCPFT	HVSRRIPVLS
650	660	670	680	690	700	710	720
PKPAVAPPAP	PSSSQLCRYF	PACKKMECPF	YHPKHCRFNT	QCTRPDCTFY	HPTINVPPRH	ALKWIRPQTS	E

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1725	1	1003.7849	-111.00	2	51.4	12.0	0	425-440	K.NQDYYDMESMVHADTR.S	Oxidation: 7, 10

Protein 1047: thioredoxin domain-containing protein 16 isoform 2 precursor [Homo sapiens]

Accession:	gi|237648961	**Score:**	12.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	93.0
Database Date:	2015-11-30	**pI:**	5.0
		Sequence Coverage [%]:	1.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MFSGFNVFRV	GISFVIMCIF	YMPTVNSLPE	LSPQKYFSTL	QPGKASLAYF	CQADSPRTSV	FLEELNEAVR	PLQDYGISVA
90	100	110	120	130	140	150	160
KVNCVKEEIS	RYCGKEKDLM	KAYLFKGNIL	LREFPTDTLF	DVNAIVAHVL	FEVKYITNLE	DLQNIENALK	GKANIIFSYV
170	180	190	200	210	220	230	240
RAIGIPEHRA	VMEAAFVYGT	TYQFVLTTEI	ALLESIGSED	VEYAHLYFFH	CKLVLDLTQQ	CRRTLMEQPL	TTLNIHLFIK
250	260	270	280	290	300	310	320
TMKAPLLTEV	AEDPQQVSTV	HLQLGLPLVF	IVSQQATYEA	DRRTAEWVAW	RLLGKAGVLL	LLRDSLEVNI	PQDANVVFKR
330	340	350	360	370	380	390	400
AEEGVPVEFL	VLHDVDLIIS	HVENNMHIEE	IQEDEDNDME	GPDIDVQDDE	VAETVFRDRK	RKLPLELTVE	LTEETFNATV
410	420	430	440	450	460	470	480
MASDSIVLFY	AGWQAVSMAF	LQSYIDVAVK	LKGTSTMLLT	RINCADWSDV	CTKQNVTEFP	IIKMYKKGEN	PVSYAGMLGT
490	500	510	520	530	540	550	560
EDLLKFIQLN	RISYPVNITS	IQEAEEYLSG	ELYKDLILYS	SVSVLGLFSP	TMKTAKEDFS	EAGNYLKGYV	ITGIYSEEDV
570	580	590	600	610	620	630	640
LLLSTKYAAS	LPALLLARHT	EGKIESIPLA	STHAQDIVQI	ITDALLEMFP	EITVENLPSY	FRLQKPLLIL	FSDGTVNPQY
650	660	670	680	690	700	710	720
KKAILTLVKQ	KYLDSFTPCW	LNLKNTPVGR	GILRAYFDPL	PPLPLLVLVN	LHSGGQVFAF	PSDQAIIEEN	LVLWLKKLEA
730	740	750	760	770	780	790	800
GLENHITILP	AQEWKPPLPA	YDFLSMIDAA	TSQRGTRKVP	KCMKETDVQE	NDKEQHEDKS	AVRKEPIETL	RIKHWNRSNW
810	820	830					
FKEAEKSFRR	DKELGCSKVN						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1399	1	720.3692	81.20	2	47.1	12.0	1	762-773	K.CMKETDVQENDK.E	

Detailed Protein Report

Protein 1048: uncharacterized protein LOC399693 [Homo sapiens]

Accession:	gi|42733592	**Score:**	12.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	103.0
Database Date:	2015-11-30	**pI:**	11.1
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPTLVVGTPP	TCLGDTPQPC	HKNSQRQGPF	SHGAPGRAAD	WKAVAKPRLC	APAAEDDVAA	LRWPGPSQQP	DPPWAAPHVV
90	100	110	120	130	140	150	160
GSDDLKEPGP	WGKACSLPMW	STGPEARDGD	SSVSSGRLSC	SSGGHDVCVS	WKERPPQVLG	PQQRPRKSDA	RLEQLRDKIR
170	180	190	200	210	220	230	240
AQAWQQGSCA	SLGTSAPSSA	SRLHKASTLT	LRRKGQEAKN	PPPAPECSGF	SILSAAERRV	EAKASHGQGR	ELSRVSQHQV
250	260	270	280	290	300	310	320
PVLREKPKRV	KSSSCKREKT	PKLPSPRRAA	KDKHKDEDSE	LVGVYAWRKG	QALVRSLLGP	PPVLRRHHSK	DPSRDPALTV
330	340	350	360	370	380	390	400
DLGDSEKVIA	AKCSPVCAQL	PDATSAHSDQ	QVSGNTPSLA	SFDQPATIQT	AMAILQDLRQ	QIQAGLELAQ	ARKGGQELGP
410	420	430	440	450	460	470	480
SKRRLQDVAG	RGRCRDPNAQ	SSFSKSPWAM	TERKHSSLER	ARSVHTWEPW	SSSTARESCP	QRAWGAQGQD	RSFQRPESPH
490	500	510	520	530	540	550	560
ERLGHFSQRP	WSALAGQACS	PQRAWGAQRQ	GPSSQRPGSP	PEKRSPFPQQ	PWSAVATQPC	PRRAWTACET	WEDPGPRLRN
570	580	590	600	610	620	630	640
PLERPSPPAQ	RPWSSSGVQR	AGPQGKGRGI	GSPVSAAKHA	LPRPTGSFPQ	NPLGKEKDTL	RPCPRSRGLL	GPSHSSESLR
650	660	670	680	690	700	710	720
EFMRQKAQAR	RRQALEEKAS	ALRTRELRSR	RLQEVYRQQR	EAVLGRAVPV	VSRTTPGIVT	FVPSSAQSGG	LEASGSLESP
730	740	750	760	770	780	790	800
VLEWSKVTSG	MVLGGQEAPG	SFCLCLNRAW	NHAETLDPPG	MGGPQDGRDA	PVLLSASPSL	GSLELQDLTT	RYLPRGMCIY
810	820	830	840	850	860	870	880
LDPKEAEHLG	TSSSLHLRHK	QAQLQALETT	AKVLKQRVDS	LTAKLQGAEA	PDTVRDPAVG	LLRSCPHSLP	AAPTLATPTL
890	900	910	920	930	940	950	960
ATPACPGALG	PNWGRGAPGE	WVSMQPQPLL	PPTYFLEGET	LSWGPSWEQQ	QSVSPRAHCE	SKPRGVSQAP	LLL

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
57	1	1119.8229	-19.69	3	30.1	12.0	2	443-471	R.SVHTWEPWSSSTARESCPQRAWGAQGQDR.S	Carbamidomethyl: 17

Detailed Protein Report

Protein 1049: PREDICTED: actin cytoskeleton-regulatory complex protein PAN1-like [Homo sapiens]

Accession:	gi|578844820	**Score:**	12.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	49.1
Database Date:	2015-11-30	**pI:**	6.3
		Sequence Coverage [%]:	3.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MERHSTQARP	EEALKLEQPP	MCKDREPTTA	SQSTGMATPR	SHPPLDTDAA	TSSQGPEDRP	ENVVAKPASA	EVEGPDGALS
90	100	110	120	130	140	150	160
QLPLAKFFPP	DNPTHQLQML	ERSLREEELR	AQHQAALLRL	REMALQEKTL	AELAWLEHRR	GCLDSKRDRA	VLAALVEKQQ
170	180	190	200	210	220	230	240
QALSRFEKEQ	REIQYLRHTQ	LFRHRDRKLL	LQHQRDVVSM	PGPVDILPIP	GPTDVVPAHE	LQAQAKLQQG	SSPKVKAAWE
250	260	270	280	290	300	310	320
GGSETSQQPE	ASLCPLTPCR	PSSSTSHRPQ	SSPASSKATR	PPTEQQDVTP	PQTTSDADGH	QQPPRPAWGE	DTHDPQGPLV
330	340	350	360	370	380	390	400
ESGSHVSQEP	GEQPRAPLLG	LQHVSPPDGQ	RLGPAFPAEE	AEGRLPTAQC	RSREVKEPPP	GKHPGNTAWA	STALDTSPTS
410	420	430	440	450			
SRACPRLELS	HWTRTESKED	GPWWPPTLAS	DPFTARRVAG	SISYRR			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1202	1	863.1498	168.34	2	44.6	12.0	1	150-165	R.AVLAALVEKQQQALSR.F	

Detailed Protein Report

Protein 1050: PREDICTED: RING finger protein 32 isoform X5 [Homo sapiens]

Accession: gi|578813915
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 12.0
MW [kDa]: 27.1
pI: 10.6
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
2582	1	834.4528	52.62	2	62.8	12.0	2	164-176	K.TCPLCRKNQYQTR.V	Carbamidomethyl: 2

Detailed Protein Report

Protein 1051: uncharacterized protein C2orf74 isoform 2 [Homo sapiens]

Accession:	gi|221139896	**Score:**	12.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	13.2
Database Date:	2015-11-30	**pI:**	5.2
Modification(s):	Oxidation	**Sequence Coverage [%]:**	11.3
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530367535	refseq_human (refseq_human_20140103.fasta)	PREDICTED: uncharacterized protein C2orf74 isoform X4 [Homo sapiens]
gi|530367533	refseq_human (refseq_human_20140103.fasta)	PREDICTED: uncharacterized protein C2orf74 isoform X3 [Homo sapiens]
gi|530367531	refseq_human (refseq_human_20140103.fasta)	PREDICTED: uncharacterized protein C2orf74 isoform X2 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MQVMNLNVPM RPGILVQRQS KEVLATPLEN RRDMEAEEEN QINEKQEPEN AGETGQEEDD GLQKIHTSVT RTPSVVESQK
        90        100        110        120
RPLKGVTFSR EVIVVDLGNE YPTPRSYTRE HKERK
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
209	1	797.8984	85.12	2	32.3	12.0	0	33-45	R.DMEAEEENQINEK.Q	Oxidation: 2

Detailed Protein Report

Protein 1052: PREDICTED: zinc finger protein 64 isoform X1 [Homo sapiens]

Accession:	gi|530418184	**Score:**	11.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	57.7
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
MKDMERHLKI	HTGDKPHKCE	VCGKCFSRKD	KLKTHMRCHT	GVKPYKCKTC	DYAAADSSSL	NKHLRIHSDE	RPFKCQICPY
90	100	110	120	130	140	150	160
ASRNSSQLTV	HLRSHTGDAP	FQCWLCSAKF	KISSDLKRHM	RVHSGEKPFK	CEFCNVRCTM	KGNLKSHIRI	KHSGNNFKCP
170	180	190	200	210	220	230	240
HCDFLGDSKA	TLRKHSRVHQ	SEHPEKCSEC	SYSCSSKAAL	RIHERIHCTD	RPFKCNYCSF	DTKQPSNLSK	HMKKFHGDMV
250	260	270	280	290	300	310	320
KTEALERKDT	GRQSSRQVAK	LDAKKSFHCD	ICDASFMRED	SLRSHKRQHS	EYSESKNSDV	TVLQFQIDPS	KQPATPLTVG
330	340	350	360	370	380	390	400
HLQVPLQPSQ	VPQFSEGRVK	IIVGHQVPQA	NTIVQAAAAA	VNIVPPALVA	QNPEELPGNS	RLQILRQVSL	IAPPQSSRCP
410	420	430	440	450	460	470	480
SEAGAMTQPA	VLLTTHEQTD	GATLHQTLIP	TASGGPQEGS	GNQTFITSSG	ITCTDFEGLN	ALIQEGTAEV	TVVSDGGQNI
490	500	510	520	530			
AVATTAPPVF	SSSSQQELPK	QTYSIIQGAA	HPALLCPADS	IPD			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
96	1	830.3615	4.91	2	30.6	11.9	1	265-278	K.KSFHCDICDASFMR.E	

Detailed Protein Report

Protein 1053: PREDICTED: triple functional domain protein isoform X2 [Homo sapiens]

Accession:	gi|578809984	**Score:**	11.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	292.2
Database Date:	2015-11-30	**pI:**	5.9
Modification(s):	Oxidation	**Sequence Coverage [%]:**	0.7
		No. of unique Peptides:	1

Detailed Protein Report

```
        10          20          30          40          50          60          70          80
MGKYLSLGTH  MTFQEVSQDG  KSLLDKLQRP  LTPGSSDSLT  ASANYSKAVH  HVLDVIHEVL  HHQRQLENIW  QHRKVRLHQR
        90         100         110         120         130         140         150         160
LQLCVFQQDV  QQVLDWIENH  GEAFLSKHTG  VGKSLHRARA  LQKRHEDFEE  VAQNTYTNAD  KLLEAAEQLA  QTGECDPEEI
       170         180         190         200         210         220         230         240
YQAAHQLEDR  IQDFVRRVEQ  RKILLDMSVS  FHTHVKELWT  WLEELQKELL  DDVYAESVEA  VQDLIKRFGQ  QQQTTLQVTV
       250         260         270         280         290         300         310         320
NVIKEGEDLI  QQLRDSAISS  NKTPHNSSIN  HIETVLQQLD  EAQSQMEELF  QERKIKLELF  LQLRIFERDA  IDIISDLESW
       330         340         350         360         370         380         390         400
NDELSQQMND  FDTEDLTIAE  QRLQHHADKA  LTMNNLTFDV  IHQGQDLLQY  VNEVQASGVE  LLCDRDVDMA  TRVQDLLEFL
       410         420         430         440         450         460         470         480
HEKQQELDLA  AEQHRKHLEQ  CVQLRHLQAE  VKQVLGWIRN  GESMLNAGLI  TASSLQEAEQ  LQREHEQFQH  AIEKTHQSAL
       490         500         510         520         530         540         550         560
QVQQKAEAML  QANHYDMDMI  RDCAEKVASH  WQQLMLKMED  RLKLVNASVA  FYKTSEQVCS  VLESLEQEYK  REEDWCGGAD
       570         580         590         600         610         620         630         640
KLGPNSETDH  VTPMISKHLE  QKEAFLKACT  LARRNADVFL  KYLHRNSVNM  PGMVTHIKAP  EQQVKNILNE  LFQRENRVLH
       650         660         670         680         690         700         710         720
YWTMRKRRLD  QCQQYVVFER  SAKQALEWIH  DNGEFYLSTH  TSTGSSIQHT  QELLKEHEEF  QITAKQTKER  VKLLIQLADG
       730         740         750         760         770         780         790         800
FCEKGHAHAA  EIKKCVTAVD  KRYRDFSLRM  EKYRTSLEKA  LGISSDSNKS  SKSLQLDIIP  ASIPGSEVKL  RDAAHELNEE
       810         820         830         840         850         860         870         880
KRKSARRKEF  IMAELIQTEK  AYVRDLRECM  DTYLWEMTSG  VEEIPPGIVN  KELIIFGNMQ  EIYEFHNNIF  LKELEKYEQL
       890         900         910         920         930         940         950         960
PEDVGHCFVT  WADKFQMYVT  YCKNKPDSTQ  LILEHAGSYF  DEIQQRHGLA  NSISSYLIKP  VQRITKYQLL  LKELLTCCEE
       970         980         990        1000        1010        1020        1030        1040
GKGEIKDGLE  VMLSVPKRAN  DAMHLSMLEG  FDENIESQGE  LILQESFQVW  DPKTLIRKGR  ERHLFLFEMS  LVFSKEVKDS
      1050        1060        1070        1080        1090        1100        1110        1120
SGRSKYLYKS  KLFTSELGVT  EHVEGDPCKF  ALWVGRTPTS  DNKIVLKASS  IENKQDWIKH  IREVIQERTI  HLKGALKEPI
      1130        1140        1150        1160        1170        1180        1190        1200
HIPKTAPATR  QKGRRDGEDL  DSQGDGSSQP  DTISIASRTS  QNTLDSDKLS  GGCELTVVIH  DFTACNSNEL  TIRRGQTVEV
      1210        1220        1230        1240        1250        1260        1270        1280
LERPHDKPDW  CLVRTTDRSP  AAEGLVPCGS  LCIAHSRSSM  EMEGIFNHKD  SLSVSSNDAS  PPASVASLQP  HMIGAQSSPG
      1290        1300        1310        1320        1330        1340        1350        1360
PKRPGNTLRK  WLTSPVRRLS  SGKADGHVKK  LAHKHKKSRE  VRKSADAGSQ  KDSDDSAATP  QDETVEERGR  NEGLSSGTLS
      1370        1380        1390        1400        1410        1420        1430        1440
KSSSSGMQSC  GEEEGEEGAD  AVPLPPPMAI  QQHSLLQPDS  QDDKASSRLL  VRPTSSETPS  AAELVSAIEE  LVKSKMALED
      1450        1460        1470        1480        1490        1500        1510        1520
RPSSLLVDQG  DSSSPSFNPS  DNSLLSSSSP  IDEMEERKSS  SLKRRHYVLQ  ELVETERDYV  RDLGYVVEGY  MALMKEDGVP
      1530        1540        1550        1560        1570        1580        1590        1600
DDMKGKDKIV  FGNIHQIYDW  HRDFFLGELE  KCLEDPEKLG  SLFVKHERRL  HMYIAYCQNK  PKSEHIVSEY  IDTFFEDLKQ
      1610        1620        1630        1640        1650        1660        1670        1680
RLGHRLQLTD  LLIKPVQRIM  KYQLLLKDFL  KYSKKASLDT  SELERAVEVM  CIVPRRCNDM  MNVGRLQGFD  GKIVAQGKLL
      1690        1700        1710        1720        1730        1740        1750        1760
LQDTFLVTDQ  DAGLLPRCRE  RRIFLFEQIV  IFSEPLDKKK  GFSMPGFLFK  NSIKVSCLCL  EENVENDPCK  FALTSRTGDV
      1770        1780        1790        1800        1810        1820        1830        1840
VETFILHSSS  PSVRQTWIHE  INQILENQRN  FLNALTSPIE  YQRNHSGGGG  GGGSGGSGGG  GGSGGGGAPS  GGSGHSGGPS
      1850        1860        1870        1880        1890        1900        1910        1920
SCGGAPSTSR  SRPSRIPQPV  RHHPPVLVSS  AASSQAEADK  MSGTSTPGPS  LPPPGAAPEA  GPSAPSRRPP  GADAEGSERE
      1930        1940        1950        1960        1970        1980        1990        2000
AEPIPKMKVL  ESPRKGAANA  SGSSPDAPAK  DARASLGTLP  LGKPRAGAAS  PLNSPLSSAV  PSLGKEPFPP  SSPLQKGGSF
      2010        2020        2030        2040        2050        2060        2070        2080
WSSIPASPAS  RPGSFTFPGD  SDSLQRQTPR  HAAPGKDTDR  MSTCSSASEQ  SVQSTQSNGS  ESSSSSNIST  MLVTHDYTAV
      2090        2100        2110        2120        2130        2140        2150        2160
KEDEINVYQG  EVVQILASNQ  QNMFLVFRAA  TDQCPAAEGW  IPGFVLGHTS  AVIVENPDGT  LKKSTSWHTA  LRLRKKSEKK
      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
970	1	752.3863	-19.92	3	41.7	11.9	2	1021-1038	R.ERHLFLFEMSLVFSKEVK.D	Oxidation: 9

Detailed Protein Report

Protein 1054: helicase SRCAP [Homo sapiens]

Accession:	gi|146219843	**Score:**	11.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	343.3
Database Date:	2015-11-30	**pI:**	5.6
		Sequence Coverage [%]:	0.5
		No. of unique Peptides:	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MQSSPSPAHP	QLPVLQTQMV	SDGMTGSNPV	SPASSSSPAS	SGAGGISPQH	IAQDSSLDGP	PGPPDGATVP	LEGFSLSQAA
90	100	110	120	130	140	150	160
DLANKGPKWE	KSHAEIAEQA	KHEAEIETRI	AELRKEGFWS	LKRLPKVPEP	PRPKGHWDYL	CEEMQWLSAD	FAQERRWKRG
170	180	190	200	210	220	230	240
VARKVVRMVI	RHHEEQRQKE	ERARREEQAK	LRRIASTMAK	DVRQFWSNVE	KVVQFKQQSR	LEEKRKKALD	LHLDFIVGQT
250	260	270	280	290	300	310	320
EKYSDLLSQS	LNQPLTSSKA	GSSPCLGSSS	AASSPPPPAS	RLDDEDGDFQ	PQEDEEEDDE	ETIEVEEQQE	GNDAEAQRRE
330	340	350	360	370	380	390	400
IELLRREGEL	PLEELLRSLP	PQLLEGPSSP	SQTPSSHDSD	TRDGPEEGAE	EEPPQVLEIK	PPPSAVTQRN	KQPWHPDEDD
410	420	430	440	450	460	470	480
EEFTANEEEA	EDEEDTIAAE	EQLEGEVDHA	MELSELAREG	ELSMEELLQQ	YAGAYAPGSG	SSEDEDEDEV	DANSSDCEPE
490	500	510	520	530	540	550	560
GPVEAEEPPQ	EDSSSQSDSV	EDRSEDEEDE	HSEEEETSGS	SASEESESEE	SEDAQSQSQA	DEEEEDDDFG	VEYLLARDEE
570	580	590	600	610	620	630	640
QSEADAGSGP	PTPGPTTLGP	KKEITDIAAA	AESLQPKGYT	LATTQVKTPI	PLLLRGQLRE	YQHIGLDWLV	TMYEKKLNGI
650	660	670	680	690	700	710	720
LADEMGLGKT	IQTISLLAHL	ACEKGNWGPH	LIIVPTSVML	NWEMELKRWC	PSFKILTYYG	AQKERKLKRQ	GWTKPNAFHV
730	740	750	760	770	780	790	800
CITSYKLVLQ	DHQAFRRKNW	RYLILDEAQN	IKNFKSQRWQ	SLLNFNSQRR	LLLTGTPLQN	SLMELWSLMH	FLMPHVFQSH
810	820	830	840	850	860	870	880
REFKEWFSNP	LTGMIEGSQE	YNEGLVKRLH	KVLRPFLLRR	VKVDVEKQMP	KKYEHVIRCR	LSKRQRCLYD	DFMAQTTTKE
890	900	910	920	930	940	950	960
TLATGHFMSV	INILMQLRKV	CNHPNLFDPR	PVTSPFITPG	ICFSTASLVL	RATDVHPLQR	IDMGRFDLIG	LEGRVSRYEA
970	980	990	1000	1010	1020	1030	1040
DTFLPRHRLS	RRVLLEVATA	PDPPPRPKPV	KMKVNRMLQP	VPKQEGRTVV	VVNNPRAPLG	PVPVRPPPGP	ELSAQPTPGP
1050	1060	1070	1080	1090	1100	1110	1120
VPQVLPASLM	VSASPAGPPL	IPASRPPGPV	LLPPLQPNSG	SLPQVLPSPL	GVLSGTSRPP	TPTLSLKPTP	PAPVRLSPAP
1130	1140	1150	1160	1170	1180	1190	1200
PPGSSSLLKP	LTVPPGYTFP	PAAATTTSTT	TATATTTAVP	APTPAPQRLI	LSPDMQARLP	SGEVVSIGQL	ASLAQRPVAN
1210	1220	1230	1240	1250	1260	1270	1280
AGGSKPLTFQ	IQGNKLTLTG	AQVRQLAVGQ	PRPLQRNVVH	LVSAGGQHHL	ISQPAHVALI	QAVAPTPGPT	PVSVLPSSTP
1290	1300	1310	1320	1330	1340	1350	1360
STTPAPTGLS	LPLAANQVPP	TMVNNTGVVK	IVVRQAPRDG	LTPVPPLAPA	PRPPSSGLPA	VLNPRPTLTP	GRLPTPTLGT
1370	1380	1390	1400	1410	1420	1430	1440
ARAPMPTPTL	VRPLLKLVHS	PSPEVSASAP	GAAPLTISSP	LHVPSSLPGP	ASSPMPIPNS	SPLASPVSST	VSVPLSSSLP
1450	1460	1470	1480	1490	1500	1510	1520
ISVPTTLPAP	ASAPLTIPIS	APLTVSASGP	ALLTSVTPPL	APVVPAAPGP	PSLAPSGASP	SASALTLGLA	TAPSLSSSQT
1530	1540	1550	1560	1570	1580	1590	1600
PGHPLLLAPT	SSHVPGLNST	VAPACSPVLV	PASALASPFP	SAPNPAPAQA	SLLAPASSAS	QALATPLAPM	AAPQTAILAP
1610	1620	1630	1640	1650	1660	1670	1680
SPAPPLAPLP	VLAPSPGAAP	VLASSQTPVP	VMAPSSTPGT	SLASASPVPA	PTPVLAPSST	QTMLPAPVPS	PLPSPASTQT
1690	1700	1710	1720	1730	1740	1750	1760
LALAPALAPT	LGGSSPSQTL	SLGTGNPQGP	FPTQTLSLTP	ASSLVPTPAQ	TLSLAPGPPL	GPTQTLSLAP	APPLAPASPV
1770	1780	1790	1800	1810	1820	1830	1840
GPAPAHTLTL	APASSSASLL	APASVQTLTL	SPAPVPTLGP	AAAQTLALAP	ASTQSPASQA	SSLVVSASGA	APLPVTMVSR
1850	1860	1870	1880	1890	1900	1910	1920
LPVSKDEPDT	LTLRSGPPSP	PSTATSFGGP	RPRRQPPPPP	RSPFYLDSLE	EKRKRQRSER	LERIFQLSEA	HGALAPVYGT
1930	1940	1950	1960	1970	1980	1990	2000
EVLDFCTLPQ	PVASPIGPRS	PGPSHPTFWT	YTEAAHRAVL	FPQQRLDQLS	EIIERFIFVM	PPVEAPPPSL	HACHPPPWLA
2010	2020	2030	2040	2050	2060	2070	2080
PRQAAFQEQL	ASELWPRARP	LHRIVCNMRT	QFPDLRLIQY	DCGKLQTLAV	LLRQLKAEGH	RVLIFTQMTR	MLDVLEQFLT
2090	2100	2110	2120	2130	2140	2150	2160
YHGHLYLRLD	GSTRVEQRQA	LMERFNADKR	IFCFILSTRS	GGVGVNLTGA	DTVVFYDSDW	NPTMDAQAQD	RCHRIGQTRD
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1273	1	863.9281	-68.36	2	45.5	11.9	2	3195-3209	R.RLVGTTNQGDQRILR.S	

Detailed Protein Report

Protein 1055: kinesin-like protein KIF1C [Homo sapiens]

Accession:	gi|40254834	**Score:**	11.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	122.9
Database Date:	2015-11-30	**pI:**	6.5
		Sequence Coverage [%]:	1.6
		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
1891	1	902.3321	-145.45	2	53.7	11.9	1	244-261	K.ISLVDLAGSERADSSGAR.G	

Detailed Protein Report

Protein 1056: PREDICTED: serine/threonine-protein phosphatase 2A regulatory subunit B'' subunit beta-like isoform X2 [Homo sapiens]

Accession:	gi|578840705	**Score:**	11.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	58.5
Database Date:	2015-11-30	**pI:**	4.8
		Sequence Coverage [%]:	5.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MRLRERSLRQ	DPDLRQELAS	LARGCDFVLP	SRFKKRLKAF	QQVQTRKEEP	LPPATSQSIP	TFYFPRGRPQ	DSVNVDAVIS
90	100	110	120	130	140	150	160
KIESTFARFP	HERATMDDMG	LVAKACGCPL	YWKGPLFYGA	GGERTGSVSV	HKFVAMWRKI	LQNCHDDAAK	FVHLLMSPGC
170	180	190	200	210	220	230	240
NYLVQEDFVP	FLQDVVNTHP	GLSFLKEASE	FHSRYITTVI	QRIFYAVNRS	WSGRITCAEL	RRSSFLQNVA	LLEEEADINQ
250	260	270	280	290	300	310	320
LTEFFSYEHF	YVIYCKFGEL	DTDHDLLIDA	DDLARHNDHA	LSTKMIDRIF	SGAVTRGRKV	QKEGKISYAD	FVWFLISEED
330	340	350	360	370	380	390	400
KKTPTSIEYW	FRCMDLDGDG	ALSMFELEYF	YEEQCRRLDS	MAIEALPFQD	CLCQMLDLVK	PRTEGKITLQ	DLKRCKLANV
410	420	430	440	450	460	470	480
FFDTFFNIEK	YLDHEQKEQI	SLLRDGDSGG	PELSDWEKYA	AEEYDILVAE	ETAGEPWEDG	FEAELSPVEQ	KLSALRSPLA
490	500	510					
QRPFFEAPSP	LGAVDLYEYA	CGDEDLEPL					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1250	1	1019.1193	-74.36	3	45.3	11.9	2	67-93	R.GRPQDSVNVDAVISKIESTFARFPHER.A	

Detailed Protein Report

Protein 1057: rho guanine nucleotide exchange factor 1 isoform 3 [Homo sapiens]

Accession:	gi|39777604	**Score:**	11.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	98.7
Database Date:	2015-11-30	**pI:**	5.3
		Sequence Coverage [%]:	1.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEDFARGAAS	PGPSRPGLVP	VSIIGAEDED	FENELETNSE	EQNSQFQSLE	QVKRRPAHLM	ALLQHVALQF	EPGPLVLRVP
90	100	110	120	130	140	150	160
VPPNVAFELD	RTRADLISED	VQRRFVQEVV	QSQQVAVGRQ	LEDFRSKRLM	GMTPWEQELA	QLEAWVGRDR	ASYEARERHV
170	180	190	200	210	220	230	240
AERLLMHLEE	MQHTISTDEE	KSAAVVNAIG	LYMRHLGVRT	KSGDKKSGRN	FFRKKVMGNR	RSDEPAKTKK	GLSSILDAAR
250	260	270	280	290	300	310	320
WNRGEPQVPD	FRHLKAEVDA	EKPGATDRKG	GVGMPSRDRN	IGAPGQDTPG	VSLHPLSLDS	PDREPGADAP	LELGDSSPQG
330	340	350	360	370	380	390	400
PMSLESLAPP	ESTDEGAETE	SPEPGDEGEP	GRSGLELEPE	EPPGWRELVP	PDTLHSLPKS	QVKRQEVISE	LLVTEAAHVR
410	420	430	440	450	460	470	480
MLRVLHDLFF	QPMAECLFFP	LEELQNIFPS	LDELIEVHSL	FLDRLMKRRQ	ESGYLIEEIG	DVLLARFDGA	EGSWFQKISS
490	500	510	520	530	540	550	560
RFCSRQSFAL	EQLKAKQRKD	PRFCAFVQEA	ESRPRCRRLQ	LKDMIPTEMQ	RLTKYPLLLQ	SIGQNTEEPT	EREKVELAAE
570	580	590	600	610	620	630	640
CCREILHHVN	QAVRDMEDLL	RLKDYQRRLD	LSHLRQSSDP	MLSEFKNLDI	TKKKLVHEGP	LTWRVTKDKA	VEVHVLLLDD
650	660	670	680	690	700	710	720
LLLLLQRQDE	RLLLKSHSRT	LTPTPDGKTM	LRPVLRLTSA	MTREVATDHK	AFYVLFTWDQ	EAQIYELVAQ	TVSERKNWCA
730	740	750	760	770	780	790	800
LITETAGSLK	VPAPASRPKP	RPSPSSTREP	LLSSSENGNG	GRETSPADAR	TERILSDLLP	FCRPGPEGQL	AATALRKVLS
810	820	830	840	850	860	870	880
LKQLLFPAEE	DNGAGPPRDG	DGVPGGGPLS	PARTQEIQEN	LLSLEETMKQ	LEELEEEFCR	LRPLLSQLGG	NSVPQPGCT

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1334	1	676.3054	-41.80	2	46.4	11.9	0	819-833	R.DGDGVPGGGPLSPAR.T	

Detailed Protein Report

Protein 1058: glutamate receptor 3 isoform 2 precursor [Homo sapiens]

Accession:	gi|163659858	**Score:**	11.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	101.0
Database Date:	2015-11-30	**pI:**	9.2
		Sequence Coverage [%]:	1.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MARQKKMGQS	VLRAVFFLVL	GLLGHSHGGF	PNTISIGGLF	MRNTVQEHSA	FRFAVQLYNT	NQNTTEKPFH	LNYHVDHLDS
90	100	110	120	130	140	150	160
SNSFSVTNAF	CSQFSRGVYA	IFGFYDQMSM	NTLTSFCGAL	HTSFVTPSFP	TDADVQFVIQ	MRPALKGAIL	SLLGHYKWEK
170	180	190	200	210	220	230	240
FVYLYDTERG	FSILQAIMEA	AVQNNWQVTA	RSVGNIKDVQ	EFRRIIEEMD	RRQEKRYLID	CEVERINTIL	EQVVILGKHS
250	260	270	280	290	300	310	320
RGYHYMLANL	GFTDILLERV	MHGGANITGF	QIVNNENPMV	QQFIQRWVRL	DEREFPEAKN	APLKYTSALT	HDAILVIAEA
330	340	350	360	370	380	390	400
FRYLRRQRVD	VSRRGSAGDC	LANPAVPWSQ	GIDIERALKM	VQVQGMTGNI	QFDTYGRRTN	YTIDVYEMKV	SGSRKAGYWN
410	420	430	440	450	460	470	480
EYERFVPFSD	QQISNDSASS	ENRTIVVTTI	LESPYVMYKK	NHEQLEGNER	YEGYCVDLAY	EIAKHVRIKY	KLSIVGDGKY
490	500	510	520	530	540	550	560
GARDPETKIW	NGMVGELVYG	RADIAVAPLT	ITLVREEVID	FSKPFMSLGI	SIMIKKPQKS	KPGVFSFLDP	LAYEIWMCIV
570	580	590	600	610	620	630	640
FAYIGVSVVL	FLVSRFSPYE	WHLEDNNEEP	RDPQSPPDPP	NEFGIFNSLW	FSLGAFMQQG	CDISPRSLSG	RIVGGVWWFF
650	660	670	680	690	700	710	720
TLIIISSYTA	NLAAFLTVER	MVSPIESAED	LAKQTEIAYG	TLDSGSTKEF	FRRSKIAVYE	KMWSYMKSAE	PSVFTKTTAD
730	740	750	760	770	780	790	800
GVARVRKSKG	KFAFLLESTM	NEYIEQRKPC	DTMKVGGNLD	SKGYGVATPK	GSALGNAVNL	AVLKLNEQGL	LDKLKNKWWY
810	820	830	840	850	860	870	880
DKGECGSGGG	DSKDKTSALS	LSNVAGVFYI	LVGGLGLAMM	VALIEFCYKS	RAESKRMKLT	KNTQNFKPAP	ATNTQNYATY
890	900						
REGYNVYGTE	SVKI						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2723	2	840.9077	-17.43	2	64.4	11.9	2	213-225	R.QEKRYLIDCEVER.I	

Detailed Protein Report

Protein 1059: PREDICTED: sushi domain-containing protein 3 isoform X1 [Homo sapiens]

Accession:	gi|578817174	**Score:**	11.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	24.9
Database Date:	2015-11-30	**pI:**	10.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	5.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPQCLREGTC	AKLRLPPQAT	FQVLRGNGAS	VGTVLMFRCP	SNHQMVGSGL	LTCTWKGSIA	EWSSGSPVCK	LVPPHETFGF
90	100	110	120	130	140	150	160
KVAVIASIVS	CAIILLMSMA	FLTCCLLKCV	KKSKRRRSNR	SAQLWSQLKD	EDLETVQAAY	LGLKHFNKPV	SGPSQAHDNH
170	180	190	200	210	220	230	240
SFTTDHGEST	SKLASVTRSV	DKDPGIPRAL	SLSGSSSSPQ	AQVMVHMANP	RQPLPASGLA	TGMPQQPAAY	ALG

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
589	1	697.2029	-172.10	2	36.9	11.9	1	1-12	-.MPQCLREGTCAK.L	Carbamidomethyl: 10

Detailed Protein Report

Protein 1060: transmembrane channel-like protein 1 [Homo sapiens]

Accession:	gi|21071070	**Score:**	11.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	87.7
Database Date:	2015-11-30	**pI:**	6.2
		Sequence Coverage [%]:	3.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSPKKVQIKV	EEKEDETEES	SSEEEEEVED	KLPRRESLRP	KRKRTRDVIN	EDDPEPEPED	EETRKAREKE	RRRRLKRGAE
90	100	110	120	130	140	150	160
EEEIDEEELE	RLKAELDEKR	QIIATVKCKP	WKMEKKIEVL	KEAKKFVSEN	EGALGKGKGK	RWFAFKMMMA	KKWAKFLRDF
170	180	190	200	210	220	230	240
ENFKAACVPW	ENKIKAIESQ	FGSSVASYFL	FLRWMYGVNM	VLFILTFSLI	MLPEYLWGLP	YGSLPRKTVP	RAEEASAANF
250	260	270	280	290	300	310	320
GVLYDFNGLA	QYSVLFYGYY	DNKRTIGWMN	FRLPLSYFLV	GIMCIGYSFL	VVLKAMTKNI	GDDGGGDDNT	FNFSWKVFTS
330	340	350	360	370	380	390	400
WDYLIGNPET	ADNKFNSITM	NFKEAITEEK	AAQVEENVHL	IRFLRFLANF	FVFLTLGGSG	YLIFWAVKRS	QEFAQQDPDT
410	420	430	440	450	460	470	480
LGWWEKNEMN	MVMSLLGMFC	PTLFDLFAEL	EDYHPLIALK	WLLGRIFALL	LGNLYVFILA	LMDEINNKIE	EEKLVKANIT
490	500	510	520	530	540	550	560
LWEANMIKAY	NASFSENSTG	PPFFVHPADV	PRGPCWETMV	GQEFVRLTVS	DVLTTYVTIL	IGDFLRACFV	RFCNYCWCWD
570	580	590	600	610	620	630	640
LEYGYPSYTE	FDISGNVLAL	IFNQGMIWMG	SFFAPSLPGI	NILRLHTSMY	FQCWAVMCCN	VPEARVFKAS	RSNNFYLGML
650	660	670	680	690	700	710	720
LLILFLSTMP	VLYMIVSLPP	SFDCGPFSGK	NRMFEVIGET	LEHDFPSWMA	KILRQLSNPG	LVIAVILVMV	LAIYYLNATA
730	740	750	760	770			
KGQKAANLDL	KKKMKMQALE	NKMRNKKMAA	ARAAAAAGRQ				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1300	1	1061.6254	28.57	3	45.9	11.9	2	363-389	R.FLRFLANFFVFLTLGGSGYLIFWAVKR.S	

Detailed Protein Report

Protein 1061: PREDICTED: chromobox protein homolog 7 isoform X1 [Homo sapiens]

Accession:	gi|530419688	**Score:**	11.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	17.9
Database Date:	2015-11-30	**pI:**	5.1
		Sequence Coverage [%]:	11.4
		No. of unique Peptides:	1

```
         10         20         30         40         50         60         70         80
MELSAIGEQV FAVESIRKKR VRKGKVEYLV KWKGWPPKYS TWEPEEHILD PRLVMAYEEK EERDRASGYR KRGPKPKRLL
         90        100        110        120        130        140        150        160
LQEPPAPDVL QAAGEWEPAA QPPEEEADAD LAEGPPPWTP ALPSSEVTVT DITANSITVT FREAQAAEGF FRDRSGKF
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2341	1	1002.7057	145.46	2	59.1	11.9	2	2-19	M.ELSAIGEQVFAVESIRKK.R	

Detailed Protein Report

Protein 1062: 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
Modification(s): Carbamidomethyl, Oxidation

Score: 11.9
MW [kDa]: 197.3
pI: 5.8
Sequence Coverage [%]: 0.7
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
1455	1	829.0640	130.95	2	48.0	11.9	2	575-587	R.KMCSQVLKHQLLR.V	Carbamidomethyl: 3; Oxidation: 2

Detailed Protein Report

Protein 1063: PREDICTED: AP-4 complex subunit mu-1 isoform X3 [Homo sapiens]

Accession: gi|530386622

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Score: 11.9

MW [kDa]: 25.3

pI: 10.0

Sequence Coverage [%]: 6.6

No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MRIGLTEEFC	VGKSELRGYG	PGIRVDEVSF	HSSVNLDEFE	SHRILRLQPP	QGELTVMRYQ	LSDDLPSPLP	FRLFPSVQWD
90	100	110	120	130	140	150	160
RGSGRLQVYL	KLRCDLLSKS	QALNVRLHLP	LPRGVVSLSQ	ELSSPEQKAE	LAEGALRWDL	PRVQGGSQLS	GLFQMDVPGP
170	180	190	200	210	220	230	
PGPPSHGLST	SASPLGLGPA	SLSFELPRHT	CSGLQVRFLR	LAFRPCGNAN	PHKWVRHLSH	SDAYVIRI	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1856	1	840.7923	-169.61	2	53.2	11.9	1	3-17	R.IGLTEEFCVGKSELR.G	

Detailed Protein Report

Protein 1064: prickle-like protein 1 [Homo sapiens]

Accession:	gi|222136678	**Score:**	11.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	94.2
Database Date:	2015-11-30	**pI:**	5.8
		Sequence Coverage [%]:	1.7
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|222136684	refseq_huma (refseq_human_20140103.fasta)	prickle-like protein 1 [Homo sapiens]
gi|222136682	refseq_huma (refseq_human_20140103.fasta)	prickle-like protein 1 [Homo sapiens]
gi|222136680	refseq_huma (refseq_human_20140103.fasta)	prickle-like protein 1 [Homo sapiens]

10	20	30	40	50	60	70	80
MPLEMEPKMS	KLAFGCQRSS	TSDDDSGCAL	EEYAWVPPGL	RPEQIQLYFA	CLPEEKVPYV	NSPGEKHRIK	QLLYQLPPHD
90	100	110	120	130	140	150	160
NEVRYCQSLS	EEEKKELQVF	SAQRKKEALG	RGTIKLLSRA	VMHAVCEQCG	LKINGGEVAV	FASRAGPGVC	WHPSCFVCFT
170	180	190	200	210	220	230	240
CNELLVDLIY	FYQDGKIHCG	RHHAELLKPR	CSACDEIIFA	DECTEAEGRH	WHMKHFCCLE	CETVLGGQRY	IMKDGRPFCC
250	260	270	280	290	300	310	320
GCFESLYAEY	CETCGEHIGV	DHAQMTYDGQ	HWHATEACFS	CAQCKASLLG	CPFLPKQGQI	YCSKTCSLGE	DVHASDSSDS
330	340	350	360	370	380	390	400
AFQSARSRDS	RRSVRMGKSS	RSADQCRQSL	LLSPALNYKF	PGLSGNADDT	LSRKLDDLSL	SRQGTSFASE	EFWKGRVEQE
410	420	430	440	450	460	470	480
TPEDPEEWAD	HEDYMTQLLL	KFGDKSLFQP	QPNEMDIRAS	EHWISDNMVK	SKTELKQNNQ	SLASKKYQSD	MYWAQSQDGL
490	500	510	520	530	540	550	560
GDSAYGSHPG	PASSRRLQEL	ELDHGASGYN	HDETQWYEDS	LECLSDLKPE	QSVRDSMDSL	ALSNITGASV	DGENKPRPSL
570	580	590	600	610	620	630	640
YSLQNFEEME	TEDCEKMSNM	GTLNSSMLHR	SAESLKSLSS	ELCPEKILPE	EKPVHLPVLR	RSKSQSRPQQ	VKFSDDVIDN
650	660	670	680	690	700	710	720
GNYDIEIRQP	PMSERTRRRV	YNFEERGSRS	HHHRRRRSRK	SRSDNALNLV	TERKYSPKDR	LRLYTPDNYE	KFIQNKSARE
730	740	750	760	770	780	790	800
IQAYIQNADL	YGQYAHATSD	YGLQNPGMNR	FLGLYGEDDD	SWCSSSSSSS	DSEEEGYFLG	QPIPQPRPQR	FAYYTDDLSS
810	820	830	840				
PPSALPTPQF	GQRTTKSKKK	KGHKGKNCII	S				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2548	1	834.1055	177.86	2	62.3	11.9	1	177-190	K.IHCGRHHAELLKPR.C	

Detailed Protein Report

Protein 1065: PREDICTED: HAUS augmin-like complex subunit 5 isoform X2 [Homo sapiens]

Accession: gi|578834213
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Score: 11.9
MW [kDa]: 62.7
pI: 10.1
Sequence Coverage [%]: 2.7
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MELAQEAREL	GCWAVEEMGV	PVAARAPEST	LRRLCLGQGA	DIWAYILQHV	HSQRTVKKIR	GNLLWYGHQD	SPQVRRKLEL
90	100	110	120	130	140	150	160
EAAVTRLRAE	IQELDQSLEL	MERDTEAQDT	AMEQARQHTQ	DTQRRALLLR	AQAGAMRRQQ	HTLRDPMQRL	QNQLRRLQDM
170	180	190	200	210	220	230	240
ERKAKVDVTF	GSLTSAALGL	EPVVLRDVRT	ACTLRAQFLQ	NLLLPQAKRG	SLPTPHDDHF	GTSYQQWLSS	VETLLTNHPP
250	260	270	280	290	300	310	320
GHVLAALEHL	AAEREAEIRS	LCSGDGLGDT	EISRPQAPDQ	SDSSQTLPSM	VHLIQEGWRT	VGVLVSQRST	LLKERQVLTQ
330	340	350	360	370	380	390	400
RLQGLVEEVE	RRVLGSSERQ	VLILGLRRCC	LWTELKALHD	QSQELQDAAG	HRQLLLRELQ	AKQQRILHWR	QLVEETQEQV
410	420	430	440	450	460	470	480
RLLIKGNSAS	KTRLCRSPGE	VLALVQRKVV	PTFEAVAPQS	RELLRCLEEE	VRHLPHILLG	TLLRHRPGEL	KPLPTVLPSI
490	500	510	520	530	540	550	560
HQLHPASPRG	SSFIALSHKL	GLPPGKASEL	LLPAAASLRQ	DLLLLQDQRS	LWCWDLLHMK	TSLPPGLPTQ	VPIVC

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1924	1	902.3552	-97.62	2	53.9	11.9	0	89-103	R.AEIQELDQSLELMER.D	

Detailed Protein Report

Protein 1066: PREDICTED: LOW QUALITY PROTEIN: armadillo repeat-containing protein 4-like [Homo sapiens]

Accession:	gi|578818723	**Score:**	11.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	24.5
Database Date:	2015-11-30	**pI:**	10.0
		Sequence Coverage [%]:	3.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MCKAKIILED	LSLESLDVFL	PNRNVLGYFK	GISFNEDQQK	EKDQLGKAPK	KEKAAALHKD	ISGSGKRSLE	KNQINFWRNQ
90	100	110	120	130	140	150	160
MTKRWEPSLN	WKTTVNYKGK	GSAKEIQEDK	HTGKLEKPRP	SVSHGRAQLL	RKSAEKIEET	VSDSSSESEE	DEEPPDHRQE
170	180	190	200	210	220		
ASADLPSEYW	QIQKLVKYLK	QKETSQNGRS	KRWARKQNTR	VIRSTIFDVG	KTS		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2526	1	410.2347	36.76	2	61.5	11.9	1	60-67	K.DISGSGKR.S	

Detailed Protein Report

Protein 1067: ras-related protein Rab-5C isoform a [Homo sapiens]

Accession:	gi|41393545	**Score:**	11.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	23.5
Database Date:	2015-11-30	**pI:**	9.5
		Sequence Coverage [%]:	6.5
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|41393614	refseq_human (refseq_human_20140103.fasta)	ras-related protein Rab-5C isoform a [Homo sapiens]

```
         10         20         30         40         50         60         70         80
MAGRGGAARP NGPAAGNKIC QFKLVLLGES AVGKSSLVLR FVKGQFHEYQ ESTIGAAFLT QTVCLDDTTV KFEIWDTAGQ
         90        100        110        120        130        140        150        160
ERYHSLAPMY YRGAQAAIVV YDITNTDTFA RAKNWVKELQ RQASPNIVIA LAGNKADLAS KRAVEFQEAQ AYADDNSLLF
        170        180        190        200        210        220
METSAKTAMN VNEIFMAIAK KLPKNEPQNA TGAPGRNRGV DLQENNPASR SQCCSN
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2013	1	698.2912	-157.69	2	55.1	11.8	0	122-135	R.QASPNIVIALAGNK.A	

Detailed Protein Report

Protein 1068: zinc finger protein 48 isoform 2 [Homo sapiens]

Accession:	gi|333805600	**Score:**	11.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	54.0
Database Date:	2015-11-30	**pI:**	11.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSDLVKHQRT	HTGEKPYKCG	VCGKGFGDSS	ARIKHQRTHS	GEKPYRARPP	AQGPPKIPRS	RIPAGERPTI	CGECGKSFRQ
90	100	110	120	130	140	150	160
SSDLVKHQRT	HTGEKPYKCG	ICGKGFGDSS	ARIKHQRTHR	GEQPPRPVVP	RRQPSRAATA	ATQGPKAQDK	PYICTDCGKR
170	180	190	200	210	220	230	240
FVLSCSLLSH	QRSHLGPKPF	GCDVCGKEFA	RGSDLVKHLR	VHTGEKPYLC	PECGKGFADS	SARVKHLRTH	SGERPHACPE
250	260	270	280	290	300	310	320
CDRTFSLSST	LLRHRLTHME	PQDFSFPGYP	LPALIPSPPP	PPLGTSPPLT	PRSPSHSGEP	FGLPGLEPEP	GGPQAGEPPP
330	340	350	360	370	380	390	400
PLAGDKPHKC	PECGKGFRRS	SDLVKHHRVH	TGEKPYLCPE	CGKGFADSSA	RVKHLRTHRG	ERARPPPPST	LLRPHNPPGP
410	420	430	440	450	460	470	480
VPMAPRPRVR	AQPSGPSQPH	VCGFCGKEFP	RSSDLVKHRR	THTGEKPYKC	AECGKGFGDS	SARIKHQRGH	LVLTPFGIGD
490	500						
GRARPLKQEA	ATGLE						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
139	1	707.7910	-32.11	2	31.5	11.8	1	99-112	K.CGICGKGFGDSSAR.I	Carbamidomethyl: 1

Detailed Protein Report

Protein 1069: dynein heavy chain domain-containing protein 1 isoform 2 [Homo sapiens]

Accession:	gi|222144247	**Score:**	11.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	68.6
Database Date:	2015-11-30	**pI:**	6.9
Modification(s):	Oxidation	**Sequence Coverage [%]:**	4.5
		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				
LVFDDHGQLS	HVPCVENMIQ	TLTGGLQSVK	TSALQVF				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1775	1	1023.8652	29.43	3	52.2	11.8	2	265-291	K.SSTGFSPETSFLDSQVMTALKMERYLK.K	Oxidation: 17

Detailed Protein Report

Protein 1070: MAD2L1-binding protein isoform 2 [Homo sapiens]

Accession: gi|7661918
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 11.8
MW [kDa]: 31.0
pI: 5.9
Sequence Coverage [%]: 5.1
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MAAPEAEVLS	SAAVPDLEWY	EKSEETHASQ	IELLETSSTQ	EPLNASEAFC	PRDCMVPVVF	PGPVSQEGCC	QFTCELLKHI
90	100	110	120	130	140	150	160
MYQRQQLPLP	YEQLKHFYRK	PSPQAEEMLK	KKPRATTEVS	SRKCQQALAE	LESVLSHLED	FFARTLVPRV	LILLGGNALS
170	180	190	200	210	220	230	240
PKEFYELDLS	LLAPYSVDQS	LSTAACLRRL	FRAIFMADAF	SELQAPPLMG	TVVMAQGHRN	CGEDWFRPKL	NYRVPSRGHK
250	260	270	280				
LTVTLSCGRP	SIRTTAWEDY	IWFQAPVTFK	GFRE				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1913	1	599.9134	-68.59	3	53.8	11.8	1	220-233	R.NCGEDWFRPKLNYR.V	

Detailed Protein Report

Protein 1071: putative uncharacterized protein C13orf35 [Homo sapiens]

Accession:	gi|46409504	**Score:**	11.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	13.4
Database Date:	2015-11-30	**pI:**	9.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	14.9
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MNSPEARLCV AQCRDSYPGC QPLKDTRAWA SSLKMDPAGL EGGPRDESRD EPPIRAQAAS WDQPQGCLTY KGRRSASGTQ

        90        100        110        120        130
KQLQLPDTLS SLLCWRGAIM VYIKVTVQTD DSNKLLSLLY R
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
199	1	666.6243	-81.39	3	31.9	11.8	1	97-114	R.GAIMVYIKVTVQTDDSNK.L	Oxidation: 4

Detailed Protein Report

Protein 1072: PREDICTED: ral GTPase-activating protein subunit alpha-1 isoform X15 [Homo sapiens]

Accession: gi|578825686
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 11.8
MW [kDa]: 180.2
pI: 6.0
Sequence Coverage [%]: 0.7
No. of unique Peptides: 1

Quantitation

MD:MU **Median:** 1.27 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MFSKKPHGDV	KKSTQKVLDT	KKDALTRLKH	LRIVIENAES	IDLKQFFDQH	FSHIYYVFFE	NFVTIEASLK	QKGHKSQREE
90	100	110	120	130	140	150	160
LDAILFIFEK	ILQLLPERIH	QRWQFHSIGL	ILKKLLHTGN	SLKIRREGVR	LFLLWLQALQ	NNCSKEQLWM	FSCLIPGFSA
170	180	190	200	210	220	230	240
PQSEHGPRTL	DNLINPPLNL	QETQVTIEEI	TPLVPPQSGD	KGQEDLTSYF	LEALLKYIVI	QVKSLEWKNK	ENQERGFSFL
250	260	270	280	290	300	310	320
FSHFKKYYLP	YIFPNICKEN	SLYHPILDIP	QMRPKPHYVV	IKKDAETNEA	IYCTKEPFIK	ARVIVIRWLV	SFWLEPKPHT
330	340	350	360	370	380	390	400
GPHIPGMEGE	VLPKNIQRAA	ASLVSREESK	NDNADKTDRT	TEPEQSHSNT	STLTEREPSS	SSLCSIDEEH	LTDIEIVRRV
410	420	430	440	450	460	470	480
FSSKRSNVNF	VTEIFRQAFL	LPICEAAAMR	KVVKVYQEWI	QQEEKPLFMQ	EPEEIVITSS	DLPCIENVTD	HDISMEEGEK
490	500	510	520	530	540	550	560
REEENGTNTA	DHVRNSSWAK	NGSYQGALHN	ASEEATEQNI	RAGTQAVLQV	FIINSSNIFL	LEPANEIKNL	LDEHTDMCKR
570	580	590	600	610	620	630	640
ILNIYRYMVV	QVSMDKKTWE	QMLLVLLRVT	ESVLKMPSQA	FLQFQGKKNM	TLAGRLAGPL	FQTLIVAWIK	ANLNVYISRE
650	660	670	680	690	700	710	720
LWDDLLSVLS	SLTYWEELAT	EWSLTMETLT	KVLARNLYSL	DLSDLPLDKL	SEQKQKKHKG	KGVGHEFQKV	SVDKSFSRGW
730	740	750	760	770	780	790	800
SRDQPGQAPM	RQRSATTTGS	PGTEKARSIV	RQKTVAMRSR	SIGECALPSA	YIRSAKSAPV	LIHTSKPFLP	DIVLTPLSDE
810	820	830	840	850	860	870	880
LSDIDDAQIL	PRSTRVRHFS	QSEETGNEVF	GALNEEQPLP	RSSSTSDILE	PFTVERAKGA	VPVIDSSSRH	APSLQSSTEA
890	900	910	920	930	940	950	960
SSITRSTESH	ITDTHSRESS	LEVGDSIYDH	LCHLIGPVEL	ADSAFEQIQY	IDLEGDDDLL	STLKEYFKEN	QENHSKNETG
970	980	990	1000	1010	1020	1030	1040
KDPASQEVTI	AVNRGERLSL	DKLECTDQET	ESENITSFVG	TPENLQFQKE	PNSAVFMSNI	APNQSDSFFR	TQTSEKSKQL
1050	1060	1070	1080	1090	1100	1110	1120
NTDKQPSEPS	LDSPCDKEKR	KHLYRQAATE	LDACVDVTLV	EKLKSVQINE	KITVPHVMRA	KKATLKAPVN	RRMPHVTSTS
1130	1140	1150	1160	1170	1180	1190	1200
KLSPTKRSLS	ETVTHRAKIM	KIATKKRNSV	HVTFRPSTES	VQFYNPLENK	EAPWKMRLRK	LGGFSSGSSN	SSTSNTHTST
1210	1220	1230	1240	1250	1260	1270	1280
NSATELVKPG	VYRPLDTLGT	ASVSSKTVKE	STEIPTTILQ	KEGIASSQLG	SRSTLRSSSH	EAGLQQGSLG	GVYKTVVHAL
1290	1300	1310	1320	1330	1340	1350	1360
SKPKANVSPQ	RQNRMPPEAP	LRDLYSHVMG	YFGRKAAVNK	EDMSQKLPPL	NSDIGGSSAN	VPDLMDEFIA	ERLRSGNAST
1370	1380	1390	1400	1410	1420	1430	1440
MTRRGSSPGS	LEIPKDLPDI	LNKQNQMRPI	DDPGVPSEWT	SPASAGSSDL	ISSDSHSDSF	SAFQYDGRKF	DNFGFGTDTG
1450	1460	1470	1480	1490	1500	1510	1520
VTSSADVDSG	SGHHQSAEEQ	EVASLTTLHI	DSETSSLNQQ	AFSAEVATIT	GSESASPVHS	PLGSRSQTPS	PSTLNIDHME
1530	1540	1550	1560	1570	1580	1590	1600
QKDLQLDEKL	HHSVLQTPDD	LEISEFPSEC	CSVMAGGTLT	GWHADVATVM	WRRMLGILGD	VNSIMDPEIH	AQVFDYLCEL
1610							
WQNLAKF							

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

			[ppm]								
800	1	709.3960	15.98	2	39.5	11.8	2	1-12	-.MFSKKPHGDVKK.S	Oxidation: 1	MD:MU 1.27

Detailed Protein Report

Protein 1073: transmembrane protein 126A isoform 1 [Homo sapiens]

Accession:	gi|14150017	**Score:**	11.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	21.5
Database Date:	2015-11-30	**pI:**	10.1
Modification(s):	Oxidation	**Sequence Coverage [%]:**	14.4
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MENHKSNNKE NITIVDISRK INQLPEAERN LLENGSVYVG LNAALCGLIA NSLFRRILNV TKARIAAGLP MAGIPFLTTD
        90        100        110        120        130        140        150        160
LTYRCFVSFP LNTGDLDCET CTITRSGLTG LVIGGLYPVF LAIPVNGGLA ARYQSALLPH KGNILSYWIR TSKPVFRKML
       170        180        190        200
FPILLQTMFS AYLGSEQYKL LIKALQLSEP GKEIH
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1779	1	1011.6290	57.94	3	52.1	11.8	2	57-84	R.ILNVTKARIAAGLPMAGIPFLTTDLTYR.C	Oxidation: 15

Detailed Protein Report

Protein 1074: 60S ribosomal protein L35 [Homo sapiens]

Accession: gi|6005860
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 11.8
MW [kDa]: 14.5
pI: 11.5
Sequence Coverage [%]: 8.9
No. of unique Peptides: 1

```
         10         20         30         40         50         60         70         80
MAKIKARDLR GKKKEELLKQ LDDLKVELSQ LRVAKVTGGA ASKLSKIRVV RKSIARVLTV INQTQKENLR KFYKGKKYKP
         90        100        110        120        130
LDLRPKKTRA MRRRLNKHEE NLKTKKQQRK ERLYPLRKYA VKA
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
593	1	509.6959	-200.58	2	36.7	11.8	1	36-46	K.VTGGAASKLSK.I	

Detailed Protein Report

Protein 1075: uncharacterized protein KIAA0195 [Homo sapiens]

Accession:	gi|157502197	**Score:**	11.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	151.1
Database Date:	2015-11-30	**pI:**	6.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	0.7
		No. of unique Peptides:	1

Quantitation

MD:MU	**Median:** 2.06	**CV:** 0.00 %	**No. of Peptides:** 1

10	20	30	40	50	60	70	80
MDLKEKHLGE	PPSALGLSTR	KALSVLKEQL	EAVLEGHLRE	RKKCLTWKEV	WRSSFLHHSN	RCSCFHWPGA	SLMLLAVLLL
90	100	110	120	130	140	150	160
LGCCGGQPAG	SRGVGLVNAS	ALFLLLLLNL	VLIGRQDRLK	RREVERRLRG	IIDQIQDALR	DGREIQWPSA	MYPDLHMPFA
170	180	190	200	210	220	230	240
PSWSLHWAYR	DGHLVNLPVS	LLVEGDIIAL	RPGQESFASL	RGIKDDEHIV	LEPGDLFPPF	SPPPSPRGEV	ERGPQSPQQH
250	260	270	280	290	300	310	320
RLFRVLETPV	IDNIRWCLDM	ALSRPVTALD	NERFTVQSVM	LHYAVPVVLA	GFLITNALRF	IFSAPGVTSW	QYTLLQLQVN
330	340	350	360	370	380	390	400
GVLPILPLLF	PVLWVLATAC	GEARVLAQMS	KASPSSLLAK	FSEDTLSSYT	EAVSSQEMLR	CIWGHFLRVL	GGTSPTLSHS
410	420	430	440	450	460	470	480
SSLLHSLGSV	TVLCCVDKQG	ILSWPNPSPE	TVLFFSGKVE	PPHSSHEDLT	DGLSTRSFCH	PEPHERDALL	AGSLNNTLHL
490	500	510	520	530	540	550	560
SNEQERGDWP	GEAPKPPEPY	SHHKAHGRSK	HPSGSNVSFS	RDTEGGEEEP	SKTQPGMESD	PYEAEDFVCD	YHLEMLSLSQ
570	580	590	600	610	620	630	640
DQQNPSCIQF	DDSNWQLHLT	SLKPLGLNVL	LNLCDASVTE	RLCRFSDHLC	NIALQESHSA	VLPVHVPWGL	CELARLIGFT
650	660	670	680	690	700	710	720
PGAKELFKQE	NHLALYRLPS	AETMKETSLG	RLSCVTKRRP	PLSHMISLFI	KDTTTSTEQM	LSHGTADVVL	EACTDFWDGA
730	740	750	760	770	780	790	800
DIYPLSGSDR	KKVLDFYQRA	CLSGYCSAFA	YKPMNCALSS	QLNGKCIELV	QVPGQSSIFT	MCELPSTIPI	KQNARRSSWS
810	820	830	840	850	860	870	880
SDEGIGEVLE	KEDCMQALSG	QIFMGMVSSQ	YQARLDIVRL	IDGLVNACIR	FVYFSLEDEL	KSKVFAEKMG	LETGWNCHIS
890	900	910	920	930	940	950	960
LTPNGDMPGS	EIPPSSPSHA	GSLHDDLNQV	SRDDAEGLLL	MEEEGHSDLI	SFQPTDSDIP	SFLEDSNRAK	LPRGIHQVRP
970	980	990	1000	1010	1020	1030	1040
HLQNIDNVPL	LVPLFTDCTP	ETMCEMIKIM	QEYGEVTCCL	GSSANLRNSC	LFLQSDISIA	LDPLYPSRCS	WETFGYATSI
1050	1060	1070	1080	1090	1100	1110	1120
SMAQASDGLS	PLQLSGQLNS	LPCSLTFRQE	ETISIIRLIE	QARHATYGIR	KCFLFLLQCQ	LTLVVIQFLS	CLVQLPPLLS
1130	1140	1150	1160	1170	1180	1190	1200
TTDILWLSCF	CYPLLSISLL	GKPPHSSIMS	MATGKNLQSI	PKKTQHYFLL	CFLLKFSLTI	SSCLICFGFT	LQSFCDSSRD
1210	1220	1230	1240	1250	1260	1270	1280
RNLTNCSSVM	LPSNDDRAPA	WFEDFANGLL	SAQKLTAALI	VLHTVFISIT	HVHRTKPLWR	KSPLTNLWWA	VTVPVVLLGQ
1290	1300	1310	1320	1330	1340	1350	1360
VVQTAVDLQL	WTHRDSHVHF	GLEDVPLLTW	LLGCLSLVLV	VVTNEIVKLH	EIRVRVRYQK	RQKLQFETKL	GMNSPF

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
1525	1	648.1346	-228.79	2	48.9	11.8	0	457-466	R.SFCHPEPHER.D	Carbamidomethyl: 3	MD:MU	2.06

Detailed Protein Report

Protein 1076: PREDICTED: bcl-2-binding component 3-like [Homo sapiens]

Accession:	gi|578822726	**Score:**	11.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	25.5
Database Date:	2015-11-30	**pI:**	12.2
		Sequence Coverage [%]:	5.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGKEEVEILI	LPMVQASSIA	WGQSGAAGPR	KPDQSGRLSR	QPPRPRHPAS	LAASGRACRP	GPHRLARARP	GGRPGGAASR
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
SAPLRGWSSP	RGSERKESGG	AGGCLTAESR	AGGAGRSTGS	LHAQGHALTT	AALQEAGTEP	PGAIGLFVKG	GAAATCHSSS
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
MSPARASTGH	LAQEKPCRSR	IQSAGIQQEC	QENSTQVCCL	LSCQVCGCTG	VLLMVEFKSP	VAKVPSRCEE	LQVLRGAGSC
250							
KVLKKTSRN							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
880	1	647.6499	-213.56	2	40.5	11.8	0	97-110	K.ESGGAGGCLTAESR.A	

Detailed Protein Report

Protein 1077: striatin-interacting protein 1 isoform 2 [Homo sapiens]

Accession:	gi|399154157	**Score:**	11.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	85.4
Database Date:	2015-11-30	**pI:**	6.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.5
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 2.06 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MNRKCFEEDF	RIHVTDKKWT	ELDTNQHRTH	AMRLLDGLEV	TAREKRLKVA	RAILYVAQGT	FGECSSEAEV	QSWMRYNIFL
90	100	110	120	130	140	150	160
LLEVGTFNAL	VELLNMEIDN	SAACSSAVRK	PAISLADSTD	LRVLLNIMYL	IVETVHQECE	GDKAEWRTMR	QTFRAELGSP
170	180	190	200	210	220	230	240
LYNNEPFAIM	LFGMVTKFCS	GHAPHFPMKK	VLLLLWKTVL	CTLGGFEELQ	SMKAEKRSIL	GLPPLPEDSI	KVIRNMRAAS
250	260	270	280	290	300	310	320
PPASASDLIE	QQQKRGRREH	KALIKQDNLD	AFNERDPYKA	DDSREEEEEN	DDDNSLEGET	FPLERDEVMP	PPLQHPQTDR
330	340	350	360	370	380	390	400
LTCPKGLPWA	PKVREKDIEM	FLESSRSKFI	GYTLGSDTNT	VVGLPRPIHE	SIKTLKQHKY	TSIAEVQAQM	EEEYLRSPLS
410	420	430	440	450	460	470	480
GGEEEVEQVP	AETLYQGLLP	SLPQYMIALL	KILLAAAPTS	KAKTDSINIL	ADVLPEEMPT	TVLQSMKLGV	DVNRHKEVIV
490	500	510	520	530	540	550	560
KAISAVLLLL	LKHFKLNHVY	QFEYMAQHLV	FANCIPLILK	FFNQNIMSYI	TAKNSISVLD	YPHCVVHELP	ELTAESLEAG
570	580	590	600	610	620	630	640
DSNQFCWRNL	FSCINLLRIL	NKLTKWKHSR	TMMLVVFKSA	PILKRALKVK	QAMMQLYVLK	LLKVQTKYLG	RQWRKSNMKT
650	660	670	680	690	700	710	720
MSAIYQKVRH	RLNDDWAYGN	DLDARPWDFQ	AEECALRANI	ERFNARRYDR	AHSNPDFLPV	DNCLQSVLGQ	RVDLPEDFQM
730	740	750					
NYDLWLEREV	FSKPISWEEL	LQ					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
1981	1	766.2302	-146.68	2	54.9	11.8	2	1-11	-.MNRKCFEEDFR.I	Carbamidomethyl: 5	MD:MU	2.06

Detailed Protein Report

Protein 1078: TBC1 domain family member 16 isoform d [Homo sapiens]

Accession:	gi|427918115	**Score:**	11.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	32.9
Database Date:	2015-11-30	**pI:**	5.9
Modification(s):	Oxidation	**Sequence Coverage [%]:**	4.7
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 2.19 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MKVAPDKTCM	QFSIRRPKLP	SSETHPEESM	YKRLGVSAWL	NHLNELGQVE	EEYKLRKAIF	FGGIDVSIRG	EVWPFLLRYY
90	100	110	120	130	140	150	160
SHESTSEERE	ALRLQKRKEY	SEIQQKRLSM	TPEEHRAFWR	NVQFTVDKDV	VRTDRNNQFF	RGEDNPNVES	MRRILLNYAV
170	180	190	200	210	220	230	240
YNPAVGYSQG	MSDLVAPILA	EVLDESDTFW	CFVGLMQNTI	FVSSPRDEDM	EKQLLYLREL	LRLTHVRFYQ	HLVSLGEDGL
250	260	270	280				
QMLFCHRWLL	LCFKREFPEA	EALRIWEACW	AHYQGADV				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
909	1	756.2387	-174.82	2	40.8	11.8	1	3-15	K.VAPDKTCMQFSIR.R	Oxidation: 8	MD:MU 2.19

Detailed Protein Report

Protein 1079: PREDICTED: myb/SANT-like DNA-binding domain-containing protein 2 isoform X4 [Homo sapiens]

Accession:	gi|530398384	**Score:**	11.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	38.0
Database Date:	2015-11-30	**pI:**	5.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	7.9
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578822380	refseq_human (refseq_human_20140103.fasta)	PREDICTED: myb/SANT-like DNA-binding domain-containing protein 2 isoform X8 [Homo sapiens]
gi|578822376	refseq_human (refseq_human_20140103.fasta)	PREDICTED: myb/SANT-like DNA-binding domain-containing protein 2 isoform X6 [Homo sapiens]
gi|578822374	refseq_human (refseq_human_20140103.fasta)	PREDICTED: myb/SANT-like DNA-binding domain-containing protein 2 isoform X5 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MEDYSQEDWG NHSQDLHGYP TDQELDEIPV TKRTLKIKQE SSEEAQKRDI MQNIVQILES VQLKWELFQS WTDFSRLHLS
        90        100        110        120        130        140        150        160
NKLAIFGIGY NTRWKEDIRY HYAEISSQVP LGKRLREYFN SEKPEGRIIM TRVQKMNWKN VYYKFLEITI SEARCLELHM
       170        180        190        200        210        220        230        240
EIDWIPIAHS KPTGGNVVQY LLPGGIPKSP GLYAIGYEEC IERPLSPHME QSSLDPGKEG RVDLETLSAQ ASLQVEIEPT
       250        260        270        280        290        300        310        320
RIIYCYLGIA EVRTLQQCLF LHFQANTKTF SKDWVGINGF LSQNCIVDPG VSPKSIYIKF VEVERDFLSA GSLVECLEKA
       330
IGYPLKFNN
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
975	1	955.7195	-97.68	3	41.8	11.7	1	269-294	K.TFSKDWVGINGFLSQNCIVDPGVSPK.S	Carbamidomethyl: 17

Detailed Protein Report

Protein 1080: SH2 domain-containing protein 4B isoform 2 [Homo sapiens]

Accession:	gi|224591408	**Score:**	11.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	36.4
Database Date:	2015-11-30	**pI:**	7.9
		Sequence Coverage [%]:	4.9
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 1.37 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MLPEDSGGSP	DAAASDKHIQ	WLLGADGEVW	VWIMGEGPGD	KPYEEISEEL	IAERARLQAQ	REAEELWRQK	EAEITKKFRD
90	100	110	120	130	140	150	160
ALANEKARIL	AEKWKVEMED	RKAAKVLEER	IHEEFKRKEE	EERKRGEEQI	RLQEEQRAKE	LYWTLKQAQL	HCQASEKEER
170	180	190	200	210	220	230	240
EWEEQLRRSK	AADEERSRRA	QRARDEYRHH	SLRAIQKGTV	AGLSSMFREL	GQSHEQEARL	YHHLPDPGLP	QPLALPVSRT
250	260	270	280	290	300	310	
WERPLRPVSR	DVIVRWFKEE	QLPRRAGFER	NTKFIAPWFH	GGNYHCFRRR	VTSGTLRTEG	QPTRLPSVV	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1450	1	783.3926	-44.00	2	47.8	11.7	1	194-208	R.AIQKGTVAGLSSMFR.E		MD:MU 1.37

Detailed Protein Report

Protein 1081: PREDICTED: deoxynucleoside triphosphate triphosphohydrolase SAMHD1 isoform X1 [Homo sapiens]

Accession:	gi|530418048	**Score:**	11.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	68.1
Database Date:	2015-11-30	**pI:**	6.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MQRADSEQPS	KRPRCDDSPR	TPSNTPSAEA	DWSPGLELHP	DYKTWGPEQV	CSFLRRGGFE	EPVLLKNIRE	NEITGALLPC
90	100	110	120	130	140	150	160
LDESRFENLG	VSSLGERKKL	LSYIQRLVQI	HVDTMKVIND	PIHGHIELHP	LLVRIIDTPQ	FQRLRYIKQL	GGGYYVFPGA
170	180	190	200	210	220	230	240
SHNRFEHSLG	VGYLAGCLVH	ALGEKQPELQ	ISERDVLCVQ	IAGLCHDLGH	GPFSHMFDGR	FIPLARPEVK	WTHEQGSVMM
250	260	270	280	290	300	310	320
FEHLINSNGI	KPVMEQYGLI	PEEDICFIKE	QIVGPLESPV	EDSLWPYKGR	PENKSFLYEI	VSNKRNGIDV	DKWDYFARDC
330	340	350	360	370	380	390	400
HHLGIQNNFD	YKRFIKFARV	CEVDNELRIC	ARDKEVGNLY	DMFHTRNSLH	RRAYQHKVGN	IIDTMITDAF	LKADDYIEIT
410	420	430	440	450	460	470	480
GAGGKKYRIS	TAIDDMEAYT	KLTDNIFLEI	LYSTDPKLKD	AREILKQIEY	RNLFKYVGET	QPTGQIKIKR	EDYESLPKEV
490	500	510	520	530	540	550	560
ASAKPKVLLD	VKLKAEDFIV	DVSQLLPEKF	AEQLIRVYCK	KVDRKSLYAA	RQYFVQWCAD	RNFTKPQDGD	VIAPLITPQK
570	580	590	600				
KEWNDSTSVQ	NPTRLREASK	SRVQLFKDDP	M				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1398	1	896.8326	-102.71	2	47.2	11.7	1	407-421	K.YRISTAIDDMEAYTK.L	Oxidation: 10

Detailed Protein Report

Protein 1082: PREDICTED: LOW QUALITY PROTEIN: zinc finger protein 806 [Homo sapiens]

Accession: gi|530369598

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Modification(s): Carbamidomethyl

Score: 11.7

MW [kDa]: 68.0

pI: 9.7

Sequence Coverage [%]: 0.0

No. of unique Peptides: 1

Alias proteins:

Accession	Name	Description
gi|530434464	refseq_human (refseq_human_20140103.fasta)	PREDICTED: LOW QUALITY PROTEIN: zinc finger protein 806 [Homo sapiens]

10	20	30	40	50	60	70	80
MIKFQERVTF	KDIAVIFTKE	ELAVLDKAQI	NLYQDVMLEN	FRNFISVDGI	KNNILNLQGK	GLIYLSQEEL	HCWKIWKQRI
90	100	110	120	130	140	150	160
RDLSVSQDYI	MNLQEQCSPH	LEDVSLCEEW	AGMSLQISEN	ENYVVNAIIK	NQDITAWQSL	TQVLTPESWR	KANIMTEPQK
170	180	190	200	210	220	230	240
SQGRYKGIYV	EEKLYRHARH	DESLNWTSRD	HHESQECKGE	DPGRHPNCGK	NLGMKSTVEQ	HHAVHVLPQP	FTCNNCGVAF
250	260	270	280	290	300	310	320
ADDTDPRVHH	STHLGEKSYK	CDQYGKNLSQ	SQYLIVHCKT	HSGETPYEFH	EWPTGCKQSS	DLPRCQKVPS	GDNPYKCKEC
330	340	350	360	370	380	390	400
GKGFRCNSSL	HNHHRVHTGE	MPYKCHVCGK	AFGFRSLPCI	HQGVHTGKKP	YKCEDCGKGF	EQSSNLLIHQ	RVHTGEKPYK
410	420	430	440	450	460	470	480
SSECGKCFSS	SSVLQVHWRF	HTGEKPYRCG	ECGKGFSQST	HLHIHQRVHT	GEKQYXCNVC	GKDFGYSSVL	HTHQRVHTAE
490	500	510	520	530	540	550	560
KPYKCEVCGK	CFSYSSYFHF	HQSNHTREKP	YKCDECGKGF	SWNSDLNVHL	RVHRGQRPCK	CKACGKGFSR	NSHLLAQQRV
570	580	590					
RIDKTQYTHC	EHGKDLLTHQ	RLHEQRETL					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
698	1	529.7363	24.47	2	38.1	11.7	0	0-0	.QYSCNVCGK.	Carbamidomethyl: 7

Detailed Protein Report

Protein 1083: dyslexia-associated protein KIAA0319 isoform b [Homo sapiens]

Accession:	gi|270265853	**Score:**	11.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	117.0
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
MTRLGWPSPC CARKQCSEGR TYSNAVISPN LETTRIMRVS HTFPVVDCTA ACCDLSSCDL AWWFEGRCYL VSCPHKENCE
        90        100        110        120        130        140        150        160
PKKMGPIRSY LTFVLRPVQR PAQLLDYGDM MLNRGSPSGI WGDSPEDIRK DLTFLGKDWG LEEMSEYSDD YRELEKDLLQ
       170        180        190        200        210        220        230        240
PSGKQEPRGS AEYTDWGLLP GSEGAFNSSV GDSPAVPAET QQDPELHYLN ESASTPAPKL PERSVLLPLP TTPSSGEVLE
       250        260        270        280        290        300        310        320
KEKASQLQEQ SSNSSGKEVL MPSHSLPPAS LELSSVTVEK SPVLTVTPGS TEHSIPTPPT SAAPSESTPS ELPISPTTAP
       330        340        350        360        370        380        390        400
RTVKELTVSA GDNLIITLPD NEVELKAFVA PAPPVETTYN YEWNLISHPT DYQGEIKQGH KQTLNLSQLS VGLYVFKVTV
       410        420        430        440        450        460        470        480
SSENAFGEGF VNVTVKPARR VNLPPVAVVS PQLQELTLPL TSALIDGSQS TDDTEIVSYH WEEINGPFIE EKTSVDSPVL
       490        500        510        520        530        540        550        560
RLSNLDPGNY SFRLTVTDSD GATNSTTAAL IVNNAVDYPP VANAGPNHTI TLPQNSITLN GNQSSDDHQI VLYEWSLGPG
       570        580        590        600        610        620        630        640
SEGKHVVMQG VQTPYLHLSA MQEGDYTFQL KVTDSSRQQS TAVVTVIVQP ENNRPPVAVA GPDKELIFPV ESATLDGSSS
       650        660        670        680        690        700        710        720
SDDHGIVFYH WEHVRGPSAV EMENIDKAIA TVTGLQVGTY HFRLTVKDQQ GLSSTSTLTV AVKKENNSPP RARAGGRHVL
       730        740        750        760        770        780        790        800
VLPNNSITLD GSRSTDDQRI VSYLWIRDGQ SPAAGDVIDG SDHSVALQLT NLVEGVYTFH LRVTDSQGAS DTDTATVEVQ
       810        820        830        840        850        860        870        880
PDPRKSGLVE LTLQVGVGQL TEQRKDTLVR QLAVLLNVLD SDIKVQKIRA HSDLSTVIVF YVQSRPPFKV LKAAEVARNL
       890        900        910        920        930        940        950        960
HMRLSKEKAD FLLFKVLRVD TAGCLLKCSG HGHCDPLTKR CICSHLWMEN LIQRYIWDGE SNCEWSIFYV TVLAFTLIVL
       970        980        990       1000       1010       1020       1030       1040
TGGFTWLCIC CCKRQKRTKI RKKTKYTILD NMDEQERMEL RPKYGIKHRS TEHNSSLMVS ESEFDSDQDT IFSREKMERG
      1050       1060       1070
NPKVSMNGSI RNGASFSYCS KDR
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2035	1	939.3035	-136.81	2	55.6	11.7	2	4-20	R.LGWPSPCCARKQCSEGR.T	

Detailed Protein Report

Protein 1084: PREDICTED: bone morphogenetic protein 5 isoform X3 [Homo sapiens]

Accession:	gi|530382406	**Score:**	11.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	39.5
Database Date:	2015-11-30	**pI:**	10.1
		Sequence Coverage [%]:	4.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MHLTVFLLKG	IVGFLWSCWV	LVGYAKGGLG	DNHVHSSFIY	RRLRNHERRE	IQREILSILG	LPHRPRPFSP	GKQASSAPLF
90	100	110	120	130	140	150	160
MLDLYNAMTN	EENPEESEYS	VRASLAEETR	GARKGYPASP	NGYPRRIQLS	RTTPLTTQSP	PLASLHDTNF	LNDADMVMSF
170	180	190	200	210	220	230	240
VNLVERDKDF	SHQRRHYKEF	RFDLTQIPHG	EAVTAAEFRI	YKDRSNNRFE	NETIKISIYQ	IIKEYTNRDA	DLFLLDTRKA
250	260	270	280	290	300	310	320
QALDVGWLVF	DITVTSNHWV	INPQNNLGLQ	LCAETGDGRS	INVKSAGLVG	RQGPQSKQPF	MVAFFKASEV	LLRSVRAANK
330	340	350					
RKNQNRNKSS	SHQDSSRMSS	VGGSSDVS					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2529	1	941.9279	-93.60	2	61.6	11.7	1	298-313	K.QPFMVAFFKASEVLLR.S	

Detailed Protein Report

Protein 1085: Krueppel-related zinc finger protein 1 [Homo sapiens]

Accession:	gi|32401441	**Score:**	11.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	75.1
Database Date:	2015-11-30	**pI:**	10.6
		Sequence Coverage [%]:	1.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MRVNHTVSTM	LPTCMVHRQT	MSCSGAGGIT	AFVAFRDVAV	YFTQEEWRLL	SPAQRTLHRE	VMLETYNHLV	SLEIPSSKPK
90	100	110	120	130	140	150	160
LIAQLERGEA	PWREERKCPL	DLCPESKPEI	QLSPSCPLIF	SSQQALSQHV	WLSHLSQLFS	SLWAGNPLHL	GKHYPEDQKQ
170	180	190	200	210	220	230	240
QQDPFCFSGK	AEWIQEGEDS	RLLFGRVSKN	GTSKALSSPP	EEQQPAQSKE	DNTVVDIGSS	PERRADLEET	DKVLHGLEVS
250	260	270	280	290	300	310	320
GFGEIKYEEF	GPGFIKESNL	LSLQKTQTGE	TPYMYTEWGD	SFGSMSVLIK	NPRTHSGGKP	YVCRECGRGF	TWKSNLITHQ
330	340	350	360	370	380	390	400
RTHSGEKPYV	CKDCGRGFTW	KSNLFTHQRT	HSGLKPYVCK	ECGQSFSLKS	NLITHQRAHT	GEKPYVCREC	GRGFRQHSHL
410	420	430	440	450	460	470	480
VRHKRTHSGE	KPYICRECEQ	GFSQKSHLIR	HLRTHTGEKP	YVCTECGRHF	SWKSNLKTHQ	RTHSGVKPYV	CLECGQCFSL
490	500	510	520	530	540	550	560
KSNLNKHQRS	HTGEKPFVCT	ECGRGFTRKS	TLSTHQRTHS	GEKPFVCAEC	GRGFNDKSTL	ISHQRTHSGE	KPFMCRECGR
570	580	590	600	610	620	630	640
RFRQKPNLFR	HKRAHSGAFV	CRECGQGFCA	KLTLIKHQRA	HAGGKPHVCR	ECGQGFSRQS	HLIRHQRTHS	GEKPYICRKC
650	660						
GRGFSRKSNL	IRHQRTHSG						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
952	1	584.2074	-228.39	2	41.5	11.7	1	564-572	R.QKPNLFRHK.R	

Detailed Protein Report

Protein 1086: PREDICTED: regulation of nuclear pre-mRNA domain-containing protein 2 isoform X3 [Homo sapiens]

Accession:	gi|530364450	**Score:**	11.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	76.0
Database Date:	2015-11-30	**pI:**	9.3
		Sequence Coverage [%]:	1.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAAGGGGGSS	KASSSSASSA	GALESSLDRK	FQSVTNTMES	IQGLSSWCIE	NKKHHSTIVY	HWMKWLRRSA	YPHRLNLFYL
90	100	110	120	130	140	150	160
ANDVIQNCKR	KNAIIFRESF	ADVLPEAAAL	VKDPSVSKSV	ERIFKIWEDR	NVYPEEMIVA	LREALSTTFK	TQKQLKENLN
170	180	190	200	210	220	230	240
KQPNKQWKKS	QTSTNPKAAL	KSKIVAEFRS	QALIEELLLY	KRSEDQIELK	EKQLSTMRVD	VCSTETLKCL	KDKTGGKKFS
250	260	270	280	290	300	310	320
KEFEEASSKL	EEFVNGLDKQ	VKNGPSLTEA	LENAGIFYEA	QYKEVKVVAN	AYKTFANRVN	NLKKKLDQLK	STLPDPEESP
330	340	350	360	370	380	390	400
VPSPSMDAPS	PTGSESPFQG	MGGEESQSPT	MESEKSATPE	PVTDNRDVED	MELSDVEDDG	SKIIVEDRKE	KPAEKSAVST
410	420	430	440	450	460	470	480
SVPTKPTENI	SKASSCTPVP	VTMTATPPLP	KPVNTSLSPS	PALALPNLAN	VDLAKISSIL	SSLTSVMKNT	GVSPASRPSP
490	500	510	520	530	540	550	560
GTPTSPSNLT	SGLKTPAPAT	TTSHNPLANI	LSKVEITPES	ILSALSKTQT	QSAPALQGLS	SLLQSVTGNP	VPASEAASQS
570	580	590	600	610	620	630	640
TSASPANTTV	STIKGRNLPS	SAQPFIPKSF	NYSPNSSTSE	VSSTSASKAS	IGQSPGLPST	TFKLPSNSLG	FTATHNTSPA
650	660	670	680	690	700	710	
APPTEVTICQ	SSEVSKPKLE	SESTSPSLEM	KIHNFLKEHP	CRSHGSPTHV	RRGESPGLHH	FHHVDD	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
657	1	593.6649	-208.22	2	37.5	11.7	0	356-366	K.SATPEPVTDNR.D	

Detailed Protein Report

Protein 1087: glutathione peroxidase 3 precursor [Homo sapiens]

Accession: gi|6006001
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 11.7
MW [kDa]: 25.6
pI: 9.1
Sequence Coverage [%]: 7.1
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MARLLQASCL	LSLLLAGFVS	QSRGQEKSKM	DCHGGISGTI	YEYGALTIDG	EEYIPFKQYA	GKYVLFVNVA	SYUGLTGQYI
90	100	110	120	130	140	150	160
ELNALQEELA	PFGLVILGFP	CNQFGKQEPG	ENSEILPTLK	YVRPGGGFVP	NFQLFEKGDV	NGEKEQKFYT	FLKNSCPPTS
170	180	190	200	210	220	230	
ELLGTSDRLF	WEPMKVHDIR	WNFEKFLVGP	DGIPIMRWHH	RTTVSNVKMD	ILSYMRRQAA	LGVKRK	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2604	1	973.9996	-12.90	2	62.6	11.7	1	186-201	K.FLVGPDGIPIMRWHHR.T	Oxidation: 11

Detailed Protein Report

Protein 1088: PREDICTED: histone-lysine N-methyltransferase 2D isoform X4 [Homo sapiens]

Accession:	gi|578824272	**Score:**	11.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	592.9
Database Date:	2015-11-30	**pI:**	5.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	0.3
		No. of unique Peptides:	1

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        10           20           30           40           50           60           70           80
MDSQKLAGED   KDSEPAADGP   AASEDPSATE   SDLPNPHVGE   VSVLSSGSPR   LQETPQDCSG   GPVRRCALCN   CGEPSLHGQR
        90          100          110          120          130          140          150          160
ELRRFELPFD   WPRCPVVSPG   GSPGPNEAVL   PSEDLSQIGF   PEGLTPAHLG   EPGGSCWAHH   WCAAWSAGVW   GQEGPELCGV
       170          180          190          200          210          220          230          240
DKAIFSGISQ   RCSHCTRLGA   SIPCRSPGCP   RLYHFPCATA   SGSFLSMKTL   QLLCPEHSEG   AAYLEEARCA   VCEGPGELCD
       250          260          270          280          290          300          310          320
LFFCTSCGHH   YHGACLDTAL   TARKRAGWQC   PECKVCQACR   KPGNDSKMLV   CETCDKGYHT   FCLKPPMEEL   PAHSWKCKAC
       330          340          350          360          370          380          390          400
RVCRACGAGS   AELNPNSEWF   ENYSLCHRCH   KAQGGQTIRS   VAEQHTPVCS   RFSPPEPGDT   PTDEPDALYV   ACQGQPKGGH
       410          420          430          440          450          460          470          480
VTSMQPKEPG   PLQCEAKPLG   KAGVQLEPQL   EAPLNEEMPL   LPPPEESPLS   PPPEESPTSP   PPEASRLSPP   PEELPASPLP
       490          500          510          520          530          540          550          560
EALHLSRPLE   ESPLSPPPEE   SPLSPPPESS   PFSPLEESPL   SPPEESPPSP   ALETPLSPPP   EASPLSPPFE   ESPLSPPPEE
       570          580          590          600          610          620          630          640
LPTSPPPEAS   RLSPPPEESP   MSPPPEESPM   SPPPEASRLF   PPFEESPLSP   PPEESPLSPP   PEASRLSPPP   EDSPMSPPPE
       650          660          670          680          690          700          710          720
ESPMSPPPEV   SRLSPLPVVS   RLSPPPEESP   LSPPPEESPT   SPPPEASRLS   PPPEDSPTSP   PPEDSPASPP   PEDSLMSLPL
       730          740          750          760          770          780          790          800
EESPLLPLPE   EPQLCPRSEG   PHLSPRPEEP   HLSPRPEEPH   LSPQAEEPHL   SPQPEEPCLC   AVPEEPHLSP   QAEGPHLSPQ
       810          820          830          840          850          860          870          880
PEELHLSPQT   EEPHLSPVPE   EPCLSPQPEE   SHLSPQSEEP   CLSPRPEESH   LSPELEKPPL   SPRPEKPPEE   PGQCPAPEEL
       890          900          910          920          930          940          950          960
PLFPPPGEPS   LSPLLGEPAL   SEPGEPPLSP   LPEELPLSPS   GEPSLSPQLM   PPDPLPPPLS   PIITAAAPPA   LSPLGELEYP
       970          980          990         1000         1010         1020         1030         1040
FGAKGDSDPE   SPLAAPILET   PISPPPEANC   TDPEPVPPMI   LPPSPGSPVG   PASPILMEPL   PPQCSPLLQH   SLVPQNSPPS
      1050         1060         1070         1080         1090         1100         1110         1120
QCSPPALPLS   VPSPLSPIGK   VVGVSDEAEL   HEMETEKVSE   PECPALEPSA   TSPLPSPMGD   LSCPAPSPAP   ALDDFSGLGE
      1130         1140         1150         1160         1170         1180         1190         1200
DTAPLDGIDA   PGSQPEPGQT   PGSLASELKG   SPVLLDPEEL   APVTPMEVYP   ECKQTAGQGS   PCEEQEEPRA   PVAPTPPTLI
      1210         1220         1230         1240         1250         1260         1270         1280
KSDIVNEISN   LSQGDASASF   PGSEPLLGSP   DPEGGGSLSM   ELGVSTDVSP   ARDEGSLRLC   TDSLPETDDS   LLCDAGTAIS
      1290         1300         1310         1320         1330         1340         1350         1360
GGKAEGEKGR   RRSSPARSRI   KQGRSSSFPG   RRRPRGGAHG   GRGRGRARLK   STASSIETLV   ADIDSSPSKE   EEEEDDDTMQ
      1370         1380         1390         1400         1410         1420         1430         1440
NTVVLFSNTD   KFVLMQDMCV   VCGSFGRGAE   GHLLACSQCS   QCYHPYCVNS   KITKVMLLKG   WRCVECIVCE   VCGQASDPSR
      1450         1460         1470         1480         1490         1500         1510         1520
LLLCDDCDIS   YHTYCLDPPL   LTVPKGGWKC   KWCVSCMQCG   AASPGFHCEW   QNSYTHCGPC   ASLVTCPICH   APYVEEDLLI
      1530         1540         1550         1560         1570         1580         1590         1600
QCRHCERWMH   AGCESLFTED   DVEQAADEGF   DCVSCQPYVV   KPVAPVAPPE   LVPMKVKEPE   PQYFRFEGVW   LTETGMALLR
      1610         1620         1630         1640         1650         1660         1670         1680
NLTMSPLHKR   RQRRGRLGLP   GEAGLEGSEP   SDALGPDDKK   DGDLDTDELL   KGEGGVEHME   CEIKLEGPVS   PDVEPGKEET
      1690         1700         1710         1720         1730         1740         1750         1760
EESKKRKRKP   YRPGIGGFMV   RQRKSHTRTK   KGPAAQAEVL   SGDGQPDEVI   PADLPAEGAV   EQSLAEGDEK   KKQQRRGRKK
      1770         1780         1790         1800         1810         1820         1830         1840
SKLEDMFPAY   LQEAFFGKEL   LDLSRKALFA   VGVGRPSFGL   GTPKAKGDGG   SERKELPTSQ   KGDDGPDIAD   EESRGLEGKA
      1850         1860         1870         1880         1890         1900         1910         1920
DTPGPEDGGV   KASPVPSDPE   KPGTPGEGML   SSDLDRISTE   ELPKMESKDL   QQLFKDVLGS   EREQHLGCGT   PGLEGSRTPL
      1930         1940         1950         1960         1970         1980         1990         2000
QRPFLQGGLP   LGNLPSSSPM   DSYPGLCQSP   FLDSRERGGF   FSPEPGEPDS   PWTGSGGTTP   STPTTPTTEG   EGDGLSYNQR
      2010         2020         2030         2040         2050         2060         2070         2080
SLQRWEKDEE   LGQLSTISPV   LYANINFPNL   KQDYPDWSSR   CKQIMKLWRK   VPAADKAPYL   QKAKDNRAAH   RINKVQKQAE
      2090         2100         2110         2120         2130         2140         2150         2160
SQINKQTKVG   DIARKTDRPA   LHLRIPPQPG   ALGSPPPAAA   PTIFIGSPTT   PAGLSTSADG   FLKPPAGSVP   GPDSPGELFL
      2170         2180         2190         2200         2210         2220         2230         2240
KLPPQVPAQV   PSQDPFGLAP   AYPLEPRFPT   APPTYPPYPS   PTGAPAQPPM   LGASSRPGAG   QPGEFHTTPP   GTPRHQPSTP
      2250         2260         2270         2280         2290         2300         2310         2320
DPFLKPRCPS   LDNLAVPESP   GVGGGKASEP   LLSPPPFGES   RKALEVKKEE   LGASSPSYGP   PNLGFVDSPS   SGTHLGGLEL
      2330         2340         2350         2360         2370         2380         2390         2400
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Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1758	1	851.2265	-164.30	2	51.9	11.7	0	66-80	R.CALCNCGEPSLHGQR.E	Carbamidomethyl: 4, 6

Detailed Protein Report

Protein 1089: sarcospan isoform 2 [Homo sapiens]

Accession:	gi|209529678	**Score:**	11.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	15.8
Database Date:	2015-11-30	**pI:**	9.4
		Sequence Coverage [%]:	9.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLCVSYQVDE	RTCIQFSMKL	LYFLLSALGL	TVCVLAVAFA	AHHYSQLTQF	TCETTLDSCQ	CKLPSSEPLS	RTFVYRDVTD
90	**100**	**110**	**120**	**130**	**140**	**150**	
CTSVTGTFKL	FLLIQMILNL	VCGLVCLLAC	FVMWKHRYQV	FYVGVRICSL	TASEGPQQKI		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2038	1	687.3353	27.66	2	55.6	11.7	0	77-89	R.DVTDCTSVTGTFK.L	

Detailed Protein Report

Protein 1090: putative sodium-coupled neutral amino acid transporter 10 isoform b [Homo sapiens]

Accession: gi|20070376
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 11.7
MW [kDa]: 83.3
pI: 5.8
Sequence Coverage [%]: 2.4
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	NQAASQLEGK	ASALQPPASG	PGSGSPLPQP	WGDAQVILGS
730	740	750	760	770	780	790	
PARPPFSFQP	PAEQTPRRAF	CSLPISSLLS	GNLLSALLPF	KHLRHRHMAC	DYRFISLAPL		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2229	1	701.2999	-60.69	3	57.7	11.7	0	275-293	R.VGFMMSVAVGFPMMILPCR.Q	Oxidation: 13

Detailed Protein Report

Protein 1091: PREDICTED: acyl-CoA synthetase short-chain family member 3, mitochondrial isoform X2 [Homo sapiens]

Accession: gi|530400836
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 11.7
MW [kDa]: 49.7
pI: 9.8
Sequence Coverage [%]: 3.7
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MKPSWLQCRK	VTSAGGLGGP	LPGSSPARGA	GAALRALVVP	GPRGGLGGRG	CRALSSGSGS	EYKTHFAASV	TDPERFWGKA
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
AEQISWYKPW	TKTLENKHSP	STRWFVEGML	NICYNAVDRH	IENGKGDKIA	IIYDSPVTNT	KATFTYKEVL	EQVSKLAGVL
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
VKHGIKKGDT	VVIYMPMIPQ	AMYTMLACAR	IGAIHSLIFG	GFASKELSSR	IDHVKPKVVV	TASFGIEPGR	RVEYVPLVEE
250	**260**	**270**	**280**	**290**	**300**	**310**	**320**
ALKIGQHKPD	KILIYNRPNM	EAVPLAPGRD	LDWDEEMAKA	QSHDCVPVLS	EHPLYILYTS	GTTGLPKGVI	RPTGGYAVML
330	**340**	**350**	**360**	**370**	**380**	**390**	**400**
HWSMSSIYGL	QPGEVWWAAS	DLGWVVGHSY	ICYGPLLHGN	TTVLYEGKPV	GTPDAGAYFR	VLAEHGVAAL	FTAPTAIRAI
410	**420**	**430**	**440**	**450**	**460**		
RQQDPGAALG	KQYSLTRFKT	LFVAGERCDV	ETLEWSKNVF	RVPVLDHWWQ	TGIKH		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2604	1	811.5526	117.82	2	63.2	11.7	2	36-52	R.ALVVPGPRGGLGGRGCR.A	

Detailed Protein Report

Protein 1092: zinc finger protein 721 [Homo sapiens]

Accession: gi|119120877
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 11.7
MW [kDa]: 106.4
pI: 10.4
Sequence Coverage [%]: 1.7
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MLENYRNLVS	LAMCSHFTQD	FLPVQGIEDS	FHKLILRRYE	KCGHDNLQLR	KGCKSMNVCK	VQKGVYNGIN	KCLSNTQSKI
90	100	110	120	130	140	150	160
FQCNARVKVF	SKFANSNKDK	TRHTGEKHFK	CNECGKSFQK	FSDLTQHKGI	HAGEKPYTCE	ERGKDFGWYT	DLNQHKKIHT
170	180	190	200	210	220	230	240
GEKPYKCEEC	GKAFNRSTNL	TAHKRIHNRE	KAYTGEDRDR	AFGWSTNLNE	YKKIHTGDKP	YKCKECGKAF	MHSSHLNKHE
250	260	270	280	290	300	310	320
KIHTGEKPYK	CKECGKVISS	SSSFAKHKRI	HTGEKPFKCL	ECGKAFNIST	TLTKHRRIHT	GEKPYTCEVC	GKAFRQSANL
330	340	350	360	370	380	390	400
YVHRRIHTGE	KPYTCGECGK	TFRQSANLYV	HRRIHTGEKP	YKCEDCGKAF	GRYTALNQHK	KIHTGEKPYK	CEECGKAFNS
410	420	430	440	450	460	470	480
STNLTAHKRI	HTREKPYTCE	DRGRAFGLST	NLNEYKKIHT	GDKPYKCKEC	GKAFIHSLHL	NKHEKIHTGK	KPYKCKQCGK
490	500	510	520	530	540	550	560
VITSSSSFAK	HKRIHTGEKP	FECLECGKAF	TSSTTLTKHR	RIHTGEKPYT	CEVCGKAFRQ	SAILYVHRRI	HTGEKPYTCE
570	580	590	600	610	620	630	640
ECGKTFRQSA	NLYVHRRIHT	GEKPYKCEEC	GKAFGRYTDL	NQHKKIHTGE	KLYKCEECGK	DFVWYTDLNQ	QKKIYTGEKP
650	660	670	680	690	700	710	720
YKCEECGKAF	APSTDLNQHT	KILTGEQSYK	CEECGKAFGW	SIALNQHKKI	HTGEKPYKCE	ECGKAFSRSR	NLTTHRRVHT
730	740	750	760	770	780	790	800
REKPYKCEDR	GRSFGWSTNL	NEYKKIHTGD	KLYKCKECGK	VFKQSSHLNR	HEKIHTGKKP	YKCKECGKVI	TSSSSFAKHK
810	820	830	840	850	860	870	880
RIHTGEKPFK	CLECGKAFTS	STTLTKHRRI	HTGEKPYTCE	ECGKAFRQSA	ILYVHRRIHT	GEKPYTCGEC	GKTFRQSANL
890	900	910	920	930			
YAHKKIHTGE	KPYTCGDCGK	TFRQSANLYA	HKKIHTGDKT	IQV			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1666	1	938.9110	-24.87	2	50.6	11.7	2	223-238	K.CKECGKAFMHSSHLNK.H	Carbamidomethyl: 1

Detailed Protein Report

Protein 1093: HHIP-like protein 1 isoform b precursor [Homo sapiens]

Accession:	gi|187936953	**Score:**	11.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	67.8
Database Date:	2015-11-30	**pI:**	5.3
		Sequence Coverage [%]:	2.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MARARAGALL	ALWVLGAAAH	PQCLDFRPPF	RPTQPLRLCA	QYSDFGCCDE	GRDAELTRRF	WALASRVDAA	EWAACAGYAR
90	100	110	120	130	140	150	160
DLLCQECSPY	AAHLYDAEDP	FTPLRTVPGL	CQDYCLDMWH	KCRGLFRHLS	TDQELWALEG	NLARFCRYLS	LDDTDYCFPY
170	180	190	200	210	220	230	240
LLVNKNLNSN	LGHVVADAKG	CLQLCLEEVA	NGLRNPVAMV	HARDGTHRFF	VAEQVGLVWA	YLPDRSRLGK	PFLNISRVVL
250	260	270	280	290	300	310	320
TSPWEGDERG	FLGIAFHPSF	QHNRRLYVYY	SVGIRSSEWI	RISEFRVSED	DENAVDHSSE	RIILEVKEPA	SNHNGGQLLF
330	340	350	360	370	380	390	400
GDDGYLYIFT	GDGGMAGDPF	GTFGNAQNKS	ALLGKVLRID	VDRKERGLPY	GIPPDNPFVG	DPAAQPEVYA	LGVRNMWRCS
410	420	430	440	450	460	470	480
FDRGDPSSGT	GRGRLFCGDV	GQNKFEEVDV	VERGGNYGWR	AREGFECYDR	SLCANTSLND	LLPIFAYPHT	VGKSVTGGYV
490	500	510	520	530	540	550	560
YRGCEYPNLN	GLYIFGDFMS	GRLMSLQENP	GTGQWQYSEI	CMGHGQTCEF	PGLINNYYPY	IISFGEDEAG	ELYFMSTGEP
570	580	590	600	610			
SATAPRGVVY	KIIDASSCKA	RSAMPGYVPA	PSVCSSLTSQ	PFILQWWK			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1490	1	670.7423	81.50	3	48.3	11.7	0	209-225	R.FFVAEQVGLVWAYLPDR.S	

Detailed Protein Report

Protein 1094: zinc finger protein ZIC 5 [Homo sapiens]

Accession:	gi|118766337	**Score:**	11.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	68.4
Database Date:	2015-11-30	**pI:**	9.9
		Sequence Coverage [%]:	1.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MFLKAGRGNK	VPPVRVYGPD	CVVLMEPPLS	KRNPPALRLA	DLATAQVQPL	QNMTGFPALA	GPPAHSQLRA	AVAHLRLRDL
90	100	110	120	130	140	150	160
GADPGVATTP	LGPEHMAQAS	TLGLSPPSQA	FPAHPEAPAA	AARAAALVAH	PGAGSYPCGG	GSSGAQPSAP	PPPAPPLPPT
170	180	190	200	210	220	230	240
PSPPPPPPPP	PPPALSGYTT	TNSGGGGSSG	KGHSRDFVLR	RDLSATAPAA	AMHGAPLGGE	QRSGTGSPQH	PAPPPHSAGM
250	260	270	280	290	300	310	320
FISASGTYAG	PDGSGGPALF	PALHDTPGAP	GGHPHPLNGQ	MRLGLAAAAA	AAAAELYGRA	EPPFAPRSGD	AHYGAVAAAA
330	340	350	360	370	380	390	400
AAALHGYGAV	NLNLNLAAAA	AAAAAGPGPH	LQHHAPPPAP	PPPPAPAQHP	HQHHPHLPGA	AGAFLRYMRQ	PIKQELICKW
410	420	430	440	450	460	470	480
IDPDELAGLP	PPPPPPPPPP	PPPPAGGAKP	CSKTFGTMHE	LVNHVTVEHV	GGPEQSSHVC	FWEDCPREGK	PFKAKYKLIN
490	500	510	520	530	540	550	560
HIRVHTGEKP	FPCPFPGCGK	VFARSENLKI	HKRTHTGEKP	FKCEFDGCDR	KFANSSDRKK	HSHVHTSDKP	YYCKIRGCDK
570	580	590	600	610	620	630	640
SYTHPSSLRK	HMKIHCKSPP	PSPGPLGYSS	VGTPVGAPLS	PVLDPARSHS	STLSPQVTNL	NEWYVCQASG	APSHLHTPSS
650	660	670					
NGTTSETEDE	EIYGNPEVVR	TIH					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2142	1	1052.3280	-209.35	1	57.0	11.7	2	531-539	R.KFANSSDRK.K	

Detailed Protein Report

Protein 1095: PREDICTED: protein Mpv17 isoform X2 [Homo sapiens]

Accession:	gi|530367613	**Score:**	11.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	13.7
Database Date:	2015-11-30	**pI:**	9.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	14.6
		No. of unique Peptides:	1

Quantitation

MD:MU	**Median:** 1.06	**CV:** 0.00 %	**No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MVSLGCGFVG PVVGGWYKVL DRFIPGTTKV DALKKMLLDQ GGFAPCFLGC FLPLVGALNG LSAQDNWAKL QRDYPDALIT
        90        100        110        120        130
NYYLWPAVQL ANFYLVPLHY RLAVVQCVAV IWNSYLSWKA HRL
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
40	1	712.6492	-92.66	3	30.2	11.6	0	102-119	R.LAVVQCVAVIWNSYLSWK.A	Carbamidomethyl: 6	MD:MU	1.06

Detailed Protein Report

Protein 1096: PREDICTED: protein naked cuticle homolog 1 isoform X1 [Homo sapiens]

Accession:	gi|530424451	**Score:**	11.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	40.9
Database Date:	2015-11-30	**pI:**	9.8
		Sequence Coverage [%]:	7.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MERVSEPCPG	SKKQLKFEEL	QCDVSMEEDS	RQEWTFTLYD	FDNNGKVTRE	DITSLLHTIY	EVVDSSVNHS	PTSSKMLRVK
90	100	110	120	130	140	150	160
LTVAPDGSQS	KRSVLVNQAD	LQSARPRAET	KPTEDLRSWE	KKQRAPLRFQ	GDSRLEQSGC	YHHCVDENIE	RRNHYLDLAG
170	180	190	200	210	220	230	240
IENYTSQFGP	GSPSVAQKSE	LPPRTSNPTR	SRSHEPEAIH	IPHRKPQGVD	PASFHFLDTP	IAKVSELQQR	LRGTQDGSKH
250	260	270	280	290	300	310	320
FVRSPKAQGK	SVGVGHVARG	ARNKPPLGPA	IPAVSPSAHL	AASPALLPSL	APLGHKKHKH	RAKESQQGCR	GLQAPLASGG
330	340	350	360	370			
PVLGREHLRE	LPALVVYESQ	AGQPVQRHEH	HHHHEHHHHY	HHFYQT			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
961	1	984.1419	-57.78	3	41.5	11.6	2	92-117	K.RSVLVNQADLQSARPRAETKPTEDLR.S	

Detailed Protein Report

Protein 1097: blood group Rh(CE) polypeptide isoform 4 [Homo sapiens]

Accession:	gi|301129229	**Score:**	11.6
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
944	1	955.6301	83.93	3	41.3	11.6	1	106-133	K.VVITLFSIRLATMSAMSVLISAGAVLGK.V	Oxidation: 13

Detailed Protein Report

Protein 1098: PREDICTED: neuronal PAS domain-containing protein 2 isoform X8 [Homo sapiens]

Accession:	gi|530368679	**Score:**	11.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	87.1
Database Date:	2015-11-30	**pI:**	6.6
		Sequence Coverage [%]:	1.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MYAYGFVGRC	APFPAEEGRT	FDLSEELGRS	VTREGTGTTR	LNSEPVPLLC	LPLLNCSRKN	CIENLMDEDE	KDRAKRASRN
90	100	110	120	130	140	150	160
KSEKKRRDQF	NVLIKELSSM	LPGNTRKMDK	TTVLEKVIGF	LQKHNEVSAQ	TEICDIQQDW	KPSFLSNEEF	TQLMLEALDG
170	180	190	200	210	220	230	240
FIIAVTTDGS	IIYVSDSITP	LLGHLPSDVM	DQNLLNFLPE	QEHSEVYKIL	SSHMLVTDSP	SPEYLKSDSD	LEFYCHLLRG
250	260	270	280	290	300	310	320
SLNPKEFPTY	EYIKFVGNFR	SYNNVMQFGK	GKSCCYRFLT	KGQQWIWLQT	HYYITYHQWN	SKPEFIVCTH	SVVSYADVRV
330	340	350	360	370	380	390	400
ERRQELALED	PPSEALHSSA	LKDKGSSLEP	RQHFNTLDVG	ASGLNTSHSP	SASSRSSHKS	SHTAMSEPTS	TPTKLMAEAS
410	420	430	440	450	460	470	480
TPALPRSATL	PQELPVPGLS	QAATMPAPLP	SPSSCDLTQQ	LLPQTVLQST	PAPMAQFSAQ	FSMFQTIKDQ	LEQRTRILQA
490	500	510	520	530	540	550	560
NIRWQQEELH	KIQEQLCLVQ	DSNVQMFLQQ	PAVSLSFSST	QRPEAQQQLQ	QRSAAVTQPQ	LGAGPQLPGQ	ISSAQVTSQH
570	580	590	600	610	620	630	640
LLRESSVIST	QGPKPMRSSQ	LMQSSGRSGS	SLVSPFSSAT	AALPPSLNLT	TPASTSQDAS	QCQPSPDFSH	DRQLRLLLSQ
650	660	670	680	690	700	710	720
PIQPMMPGSC	DARQPSEVSR	TGRQVKYAQS	QTVFQNPDAH	PANSSSAPMP	VLLMGQAVLH	PSFPASQPSP	LQPAQARQQP
730	740	750	760	770	780	790	
PQHYLQVQAP	TSLHSEQQDS	LLLSTYSQQP	GTLGYPQPPP	AQPQPLRPPR	RVSSLSESSG	LQQPPR	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
169	1	492.6415	18.04	3	31.8	11.6	1	111-123	K.TTVLEKVIGFLQK.H	

Detailed Protein Report

Protein 1099: peptidyl-prolyl cis-trans isomerase FKBP14 precursor [Homo sapiens]

Accession:	gi|8923659	**Score:**	11.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	24.2
Database Date:	2015-11-30	**pI:**	5.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	7.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MRLFLWNAVL	TLFVTSLIGA	LIPEPEVKIE	VLQKPFICHR	KTKGGDLMLV	HYEGYLEKDG	SLFHSTHKHN	NGQPIWFTLG
90	100	110	120	130	140	150	160
ILEALKGWDQ	GLKGMCVGEK	RKLIIPPALG	YGKEGKGKIP	PESTLIFNID	LLEIRNGPRS	HESFQEMDLN	DDWKLSKDEV
170	180	190	200	210	220		
KAYLKKEFEK	HGAVVNESHH	DALVEDIFDK	EDEDKDGFIS	AREFTYKHDE	L		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1519	1	949.1468	106.56	2	48.7	11.6	2	29-43	K.IEVLQKPFICHRKTK.G	Carbamidomethyl: 10

Detailed Protein Report

Protein 1100: eukaryotic translation initiation factor 1A, X-chromosomal [Homo sapiens]

Accession:	gi|4503499	**Score:**	11.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	16.5
Database Date:	2015-11-30	**pI:**	4.9
Modification(s):	Oxidation	**Sequence Coverage [%]:**	18.8
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MPKNKGKGGK NRRRGKNENE SEKRELVFKE DGQEYAQVIK MLGNGRLEAM CFDGVKRLCH IRGKLRKKVW INTSDIILVG
        90        100        110        120        130        140        150
LRDYQDNKAD VILKYNADEA RSLKAYGELP EHAKINETDT FGPGDDDEIQ FDDIGDDDED IDDI
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1437	1	1011.7959	-12.58	3	47.7	11.6	2	30-56	K.EDGQEYAQVIKMLGNGRLEAMCFDGVK.R	Oxidation: 12, 21

Detailed Protein Report

Protein 1101: rhomboid-related protein 1 isoform 1 [Homo sapiens]

Accession:	gi|523704585	**Score:**	11.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	41.7
Database Date:	2015-11-30	**pI:**	9.5
		Sequence Coverage [%]:	4.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDRSSLLQLI	QEQQLDPENT	GFIGADTFTG	LVHSHELPLD	PAKLDMLVAL	AQSNEQGQVC	YQELVDLISS	KRSSSFKRAI
90	100	110	120	130	140	150	160
ANGQRALPRD	GPLDEPGLGV	YKRFVRYVAY	EILPCEVDRR	WYFYRHRSCP	PPVFMASVTL	AQIIVFLCYG	ARLNKWVLQT
170	180	190	200	210	220	230	240
YHPEYMKSPL	VYHPGHRARA	WRFLTYMFMH	VGLEQLGFNA	LLQLMIGVPL	EMVHGLLRIS	LLYLAGVLAG	SLTVSITDMR
250	260	270	280	290	300	310	320
APVVGGSGGV	YALCSAHLAN	VVMNWAGMRC	PYKLLRMVLA	LVCMSSEVGR	AVWLRFSPPL	PASGPQPSFM	AHLAGAVVGV
330	340	350	360	370	380		
SMGLTILRSY	EERLRDQCGW	WVVLLAYGTF	LLFAVFWNVF	AYDLLGAHIP	PPP		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1780	1	898.8434	-152.71	2	52.1	11.6	1	86-102	R.ALPRDGPLDEPGLGVYK.R	

Detailed Protein Report

Protein 1102: signal-regulatory protein beta-1 isoform 3 precursor [Homo sapiens]

Accession:	gi|209529703	**Score:**	11.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	43.3
Database Date:	2015-11-30	**pI:**	8.8
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	6.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPVPASWPHL	PSPFLLMTLL	LGRLTGVAGE	EELQVIQPDK	SISVAAGESA	TLHCTVTSLI	PVGPIQWFRG	AGPGRELIYN
90	100	110	120	130	140	150	160
QKEGHFPRVT	TVSDLTKRNN	MDFSIRISNI	TPADAGTYYC	VKFRKGSPDH	VEFKSGAGTE	LSVRAKPSAP	VVSGPAARAT
170	180	190	200	210	220	230	240
PQHTVSFTCE	SHGFSPRDIT	LKWFKNGNEL	SDFQTNVDPA	GDSVSYSIHS	TAKVVLTRED	VHSQVICEVA	HVTLQGDPLR
250	260	270	280	290	300	310	320
GTANLSETIR	VPPTLEVTQQ	PVRAENQVNV	TCQVRKFYPQ	RLQLTWLENG	NVSRTETAST	LTENKDGTYN	WMSWLLVNVS
330	340	350	360	370	380	390	400
AHRDDVKLTC	QVEHDGQPAV	SKSHDLKVSA	HPKEQGSNTA	PGPALASAAP	LLIAFLLGPK	VLLVVGVSVI	YVYWKQKA

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1691	1	1023.7475	-74.15	3	51.1	11.6	2	99-124	R.NNMDFSIRISNITPADAGTYYCVKFR.K	Carbamidomethyl: 22; Oxidation: 3

Detailed Protein Report

Protein 1103: PREDICTED: SET domain-containing protein 5 isoform X12 [Homo sapiens]

Accession:	gi|530372821	**Score:**	11.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	147.3
Database Date:	2015-11-30	**pI:**	9.9
		Sequence Coverage [%]:	0.7
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 2.15 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MSRGKVIRLH	RRKQDNISGG	DSSATESWDE	ELSPSTVLYT	ATQHTPTSIT	LTVRRTKPKK	RKKSPEKGRA	APKTKKIKAF
90	100	110	120	130	140	150	160
REGSRKSLRM	KNSPSEAQNL	DENTTEGWEN	RIRLWTDQYE	EAFTNQYSAD	VQNALEQHLH	SSKEFVGKPT	ILDTINKTEL
170	180	190	200	210	220	230	240
ACNNTVIGSQ	MQLQLGRVTR	VQKHRKILRA	ARDLALDTLI	IEYRGKVMLR	QQFEVNGHFF	KKPYPFVLFY	SKFNGVEMCV
250	260	270	280	290	300	310	320
DARTFGNDAR	FIRRSCTPNA	EVRHMIADGM	IHLCIYAVSA	ITKDAEVTIA	FDYEYSNCNY	KVDCACHKGN	RNCPIQKRNP
330	340	350	360	370	380	390	400
NATELPLLPP	PPSLPTIGAE	TRRRKARRKE	LEMEQQNEAS	EENNDQQSQE	VPEKVTVSSD	HEEVDNPEEK	PEEEKEEVID
410	420	430	440	450	460	470	480
DQENLAHSRR	TREDRKVEAI	MHAFENLEKR	KKRRDQPLEQ	SNSDVEITTT	TSETPVGEET	KTEAPESEVS	NSVSNVTIPS
490	500	510	520	530	540	550	560
TPQSVGVNTR	RSSQAGDIAA	EKLVPKPPPA	KPSRPRPKSR	ISRYRTSSAQ	RLKRQKQANA	QQAELSQAAL	EEGGSNSLVT
570	580	590	600	610	620	630	640
PTEAGSLDSS	GENRPLTGSD	PTVVSITGSH	VNRAASKYPK	TKKYLVTEWL	NDKAEKQECP	VECPLRITTD	PTVLATTLNM
650	660	670	680	690	700	710	720
LPGLIHSPLI	CTTPKHYIRF	GSPFIPERRR	RPLLPDGTFS	SCKKRWIKQA	LEEGMTQTSS	VPQETRTQHL	YQSNENSSSS
730	740	750	760	770	780	790	800
SICKDNADLL	SPLKKWKSRY	LMEQNVTKLL	RPLSPVTPPP	PNSGSKSPQL	ATPGSSHPGE	EECRNGYSLM	FSPVTSLTTA
810	820	830	840	850	860	870	880
SRCNTPLQFE	LCHRKDLDLA	KVGYLDSNTN	SCADRPSLLN	SGHSDLAPHP	SLGPTSETGF	PSRSGDGHQT	LVRNSDQAFR
890	900	910	920	930	940	950	960
TEFNLMYAYS	PLNAMPRADG	LYRGSPLVGD	RKPLHLDGGY	CSPAEGFSSR	YEHGLMKDLS	RGSLSPGGER	ACEGVPSAPQ
970	980	990	1000	1010	1020	1030	1040
NPPQRKKVSL	LEYRKRKQEA	KENSAGGGGD	SAQSKSKSAG	AGQGSSNSVS	DTGAHGVQGS	SARTPSSPHK	KFSPSHSSMS
1050	1060	1070	1080	1090	1100	1110	1120
HLEAVSPSDS	RGTSSSHCRP	QENISSRWMV	PTSVERLREG	GSIPKVLRSS	VRVAQKGEPS	PTWESNITEK	DSDPADGEGP
1130	1140	1150	1160	1170	1180	1190	1200
ETLSSALSKG	ATVYSPSRYS	YQLLQCDSPR	TESQSLLQQS	SSPFRGHPTQ	SPGYSYRTTA	LRPGNPPSHG	SSESSLSSTS
1210	1220	1230	1240	1250	1260	1270	1280
YSSPAHPVST	DSLAPFTGTP	GYFSSQPHSG	NSTGSNLPRR	SCPSSAASPT	LQGPSDSPTS	DSVSQSSTGT	LSSTSFPQNS
1290	1300	1310	1320	1330	1340	1350	
RSSLPSDLRT	ISLPSAGQSA	VYQASRVSAV	SNSQHYPHRG	SGGVHQYRLQ	PLQGSGVKTQ	TGLS	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
539	1	469.1399	-214.38	2	36.1	11.6	0	1130-1138	K.GATVYSPSR.Y		MD:MU 2.15

Detailed Protein Report

Protein 1104: protein CASC5 isoform 2 [Homo sapiens]

Accession:	gi|444299651	**Score:**	11.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	262.5
Database Date:	2015-11-30	**pI:**	5.2
		Sequence Coverage [%]:	0.3
		No. of unique Peptides:	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MDGVSSEANE	ENDNIERPVR	RRHSSILKPP	RSPLQDLRGG	NERVQESNAL	RNKKNSRRVS	FADTIKVFQT	ESHMKIVRKS
90	100	110	120	130	140	150	160
EMEETETGEN	LLLIQNKKLE	DNYCEITGMN	TLLSAPIHTQ	MQQKEFSIIE	HTRERKHAND	QTVIFSDENQ	MDLTSSHTVM
170	180	190	200	210	220	230	240
ITKGLLDNPI	SEKSTKIDTT	SFLANLKLHT	EDSRMKKEVN	FSVDQNTSSE	NKIDFNDFIK	RLKTGKCSAF	PDVPDKENFE
250	260	270	280	290	300	310	320
IPIYSKEPNS	ASSTHQMHVS	LKEDENNSNI	TRLFREKDDG	MNFTQCHTAN	IQTLIPTSSE	TNSRESKGND	ITIYGNDFMD
330	340	350	360	370	380	390	400
LTFNHTLQIL	PATGNFSEIE	NQTQNAMDVT	TGYGTKASGN	KTVFKSKQNT	AFQDLSINSA	DKIHITRSHI	MGAETHIVSQ
410	420	430	440	450	460	470	480
TCNQDARILA	MTPESIYSNP	SIQGCKTVFY	SSCNDAMEMT	KCLSNMREEK	NLLKHDSNYA	KMYCNPDAMS	SLTEKTIYSG
490	500	510	520	530	540	550	560
EENMDITKSH	TVAIDNQIFK	QDQSNVQIAA	APTPEKEMML	QNLMTTSEDG	KMNVNCNSVP	HVSKERIQQS	LSNPLSISLT
570	580	590	600	610	620	630	640
DRKTELLSGE	NMDLTESHTS	NLGSQVPLAA	YNLAPESTSE	SHSQSKSSSD	ECEEITKSRN	EPFQRSDIIA	KNSLTDTWNK
650	660	670	680	690	700	710	720
DKDWVLKILP	YLDKDSPQSA	DCNQEIATSH	NIVYCGGVLD	KQITNRNTVS	WEQSLFSTTK	PLFSSGQFSM	KNHDTAISSH
730	740	750	760	770	780	790	800
TVKSVLGQNS	KLAEPLRKSL	SNPTPDYCHD	KMIICSEEEQ	NMDLTKSHTV	VIGFGPSELQ	ELGKTNLEHT	TGQLTTMNRQ
810	820	830	840	850	860	870	880
IAVKVEKCGK	SPIEKSGVLK	SNCIMDVLED	ESVQKPKFPK	EKQNVKIWGR	KSVGGPKIDK	TIVFSEDDKN	DMDITKSYTI
890	900	910	920	930	940	950	960
EINHRPLLEK	RDCHLVPLAG	TSETILYTCR	QDDMEITRSH	TTALECKTVS	PDEITTRPMD	KTVVFVDNHV	ELEMTESHTV
970	980	990	1000	1010	1020	1030	1040
FIDYQEKERT	DRPNFELSQR	KSLGTPTVIC	TPTEESVFFP	GNGESDRLVA	NDSQLTPLEE	WSNNRGPVEV	ADNMELSKSA
1050	1060	1070	1080	1090	1100	1110	1120
TCKNIKDVQS	PGFLNEPLSS	KSQRRKSLKL	KNDKTIVFSE	NHKNDMDITQ	SCMVEIDNES	ALEDKEDFHL	AGASKTILYS
1130	1140	1150	1160	1170	1180	1190	1200
CGQDDMEITR	SHTTALECKT	LLPNEIAIRP	MDKTVLFTDN	YSDLEVTDSH	TVFIDCQATE	KILEENPKFG	IGKGKNLGVS
1210	1220	1230	1240	1250	1260	1270	1280
FPKDNSCVQE	IAEKQALAVG	NKIVLHTEQK	QQLFAATNRT	TNEIIKFHSA	AMDEKVIGKV	VDQACTLEKA	QVESCQLNNR
1290	1300	1310	1320	1330	1340	1350	1360
DRRNVDFTSS	HATAVCGSSD	NYSCLPNVIS	CTDNLEGSAM	LLCDKDEEKA	NYCPVQNDLA	YANDFASEYY	LESEGQPLSA
1370	1380	1390	1400	1410	1420	1430	1440
PCPLLEKEEV	IQTSTKGQLD	CVITLHKDQD	LIKDPRNLLA	NQTLVYSQDL	GEMTKLNSKR	VSFKLPKDQM	KVYVDDIYVI
1450	1460	1470	1480	1490	1500	1510	1520
PQPHFSTDQP	PLPKKGQSSI	NKEEVILSKA	GNKSLNIIEN	SSAPICENKP	KILNSEEWFA	AACKKELKEN	IQTTNYNTAL
1530	1540	1550	1560	1570	1580	1590	1600
DFHSNSDVTK	QVIQTHVNAG	EAPDPVITSN	VPCFHSIKPN	LNNLNGKTGE	FLAFQTVHLP	PLPEQLLELG	NKAHNDMHIV
1610	1620	1630	1640	1650	1660	1670	1680
QATEIHNINI	ISSNAKDSRD	EENKKSHNGA	ETTSLPPKTV	FKDKVRRCSL	GIFLPRLPNK	RNCSVTGIDD	LEQIPADTTD
1690	1700	1710	1720	1730	1740	1750	1760
INHLETQPVS	SKDSGIGSVA	GKLNLSPSQY	INEENLPVYP	DEINSSDSIN	IETEEKALIE	TYQKEISPYE	NKMGKTCNSQ
1770	1780	1790	1800	1810	1820	1830	1840
KRTWVQEEED	IHKEKKIRKN	EIKFSDTTQD	REIFDHHTEE	DIDKSANSVL	IKNLSRTPSS	CSSSLDSIKA	DGTSLDFSTY
1850	1860	1870	1880	1890	1900	1910	1920
RSSQMESQFL	RDTICEESLR	EKLQDGRITI	REFFILLQVH	ILIQKPRQSN	LPGNFTVNTP	PTPEDLMLSQ	YVYRPKIQIY
1930	1940	1950	1960	1970	1980	1990	2000
REDCEARRQK	IEELKLSASN	QDKLLVDINK	NLWEKMRHCS	DKELKAFGIY	LNKIKSCFTK	MTKVFTHQGK	VALYGKLVQS
2010	2020	2030	2040	2050	2060	2070	2080
AQNEREKLQI	KIDEMDKILK	KIDNCLTEME	TETKNLEDEE	KNNPVEEWDS	EMRAAEKELE	QLKTEEEELQ	RNLLELEVQK
2090	2100	2110	2120	2130	2140	2150	2160
EQTLAQIDFM	QKQRNRTEEL	LDQLSLSEWD	VVEWSDDQAV	FTFVYDTIQL	TITFEESVVG	FPFLDKRYRK	IVDVNFQSLL
2170	2180	2190	2200	2210	2220	2230	2240
DEDQAPPSSL	LVHKLIFQYV	EEKESWKKTC	TTQHQLPKML	EEFSLVVHHC	RLLGEEIEYL	KRWGPNYNLM	NIDINNNELR
2250	2260	2270	2280	2290	2300	2310	2320
LLFSSSAAFA	KFEITLFLSA	YYPSVPLPST	IQNHVGNTSQ	DDIATILSKV	PLENNYLKNV	VKQIYQDLFQ	DCHFYH

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1404	1	816.5863	183.79	1	47.3	11.6	0	1984-1990	K.VFTHQGK.V	

Detailed Protein Report

Protein 1105: V-type proton ATPase subunit E 1 isoform c [Homo sapiens]

Accession:	gi|87159818	**Score:**	11.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	22.7
Database Date:	2015-11-30	**pI:**	7.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	5.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MALSDADVQK	QIKHMMAFIE	QEANEKAEEI	DAKAEEEFNI	EKGRLVQTQR	LKIMEYYEKK	EKQIEQQKKI	QMSNLMNQAR
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
LKVLRARDDL	ITGLYQLLEP	RMIVRCRKQD	FPLVKAAVQK	AIPMYKIATK	NDVDVQIDQE	SYLPEDIAGG	VEIYNGDRKI
170	**180**	**190**	**200**				
KVSNTLESRL	DLIAQQMMPE	VRGALFGANA	NRKFLD				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
428	1	645.8393	-21.26	2	35.0	11.5	2	106-115	R.CRKQDFPLVK.A	Carbamidomethyl: 1

Detailed Protein Report

Protein 1106: Krueppel-like factor 9 [Homo sapiens]

Accession:	gi|4557375	**Score:**	11.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	27.2
Database Date:	2015-11-30	**pI:**	9.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.5
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 5.20 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MSAAAYMDFV	AAQCLVSISN	RAAVPEHGVA	PDAERLRLPE	REVTKEHGDP	GDTWKDYCTL	VTIAKSLLDL	NKYRPIQTPS
90	100	110	120	130	140	150	160
VCSDSLESPD	EDMGSDSDVT	TESGSSPSHS	PEERQDPGSA	PSPLSLLHPG	VAAKGKHASE	KRHKCPYSGC	GKVYGKSSHL
170	180	190	200	210	220	230	240
KAHYRVHTGE	RPFPCTWPDC	LKKFSRSDEL	TRHYRTHTGE	KQFRCPLCEK	RFMRSDHLTK	HARRHTEFHP	SMIKRSKKAL
250							
ANAL							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
344	1	646.6642	-214.55	2	34.0	11.5	2	142-152	K.RHKCPYSGCGK.V	Carbamidomethyl: 4	MD:MU 5.20

Detailed Protein Report

Protein 1107: protein RRP5 homolog [Homo sapiens]

Accession:	gi|70980549	**Score:**	11.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	208.6
Database Date:	2015-11-30	**pI:**	9.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	0.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MANLEESFPR	GGTRKIHKPE	KAFQQSVEQD	NLFDISTEEG	STKRKKSQKG	PAKTKKLKIE	KRESSKSARE	KFEILSVESL
90	100	110	120	130	140	150	160
CEGMRILGCV	KEVNELELVI	SLPNGLQGFV	QVTEICDAYT	KKLNEQVTQE	QPLKDLLHLP	ELFSPGMLVR	CVVSSLGITD
170	180	190	200	210	220	230	240
RGKKSVKLSL	NPKNVNRVLS	AEALKPGMLL	TGTVSSLEDH	GYLVDIGVDG	TRAFLPLLKA	QEYIRQKNKG	AKLKVGQYLN
250	260	270	280	290	300	310	320
CIVEKVKGNG	GVVSLSVGHS	EVSTAIATEQ	QSWNLNNLLP	GLVVKAQVQK	VTPFGLTLNF	LTFFTGVVDF	MHLDPKKAGT
330	340	350	360	370	380	390	400
YFSNQAVRAC	ILCVHPRTRV	VHLSLRPIFL	QPGRPLTRLS	CQNLGAVLDD	VPVQGFFKKA	GATFRLKDGV	LAYARLSHLS
410	420	430	440	450	460	470	480
DSKNVFNPEA	FKPGNTHKCR	IIDYSQMDEL	ALLSLRTSII	EAQYLRYHDI	EPGAVVKGTV	LTIKSYGMLV	KVGEQMRGLV
490	500	510	520	530	540	550	560
PPMHLADILM	KNPEKKYHIG	DEVKCRVLLC	DPEAKKLMMT	LKKTLIESKL	PVITCYADAK	PGLQTHGFII	RVKDYGCIVK
570	580	590	600	610	620	630	640
FYNNVQGLVP	KHELSTEYIP	DPERVFYTGQ	VVKVVVLNCE	PSKERMLLSF	KLSSDPEPKK	EPAGHSQKKG	KAINIGQLVD
650	660	670	680	690	700	710	720
VKVLEKTKDG	LEVAVLPHNI	RAFLPTSHLS	DHVANGPLLH	HWLQAGDILH	RVLCLSQSEG	RVLLCRKPAL	VSTVEGGQDP
730	740	750	760	770	780	790	800
KNFSEIHPGM	LLIGFVKSIK	DYGVFIQFPS	GLSGLAPKAI	MSDKFVTSTS	DHFVEGQTVA	AKVTNVDEEK	QRMLLSLRLS
810	820	830	840	850	860	870	880
DCGLGDLAIT	SLLLLNQCLE	ELQGVRSLMS	NRDSVLIQTL	AEMTPGMFLD	LVVQEVLEDG	SVVFSGGPVP	DLVLKASRYH
890	900	910	920	930	940	950	960
RAGQEVESGQ	KKKVVILNVD	LLKLEVHVSL	HQDLVNRKAR	KLRKGSEHQA	IVQHLEKSFA	IASLVETGHL	AAFSLTSHLN
970	980	990	1000	1010	1020	1030	1040
DTFRFDSEKL	QVGQGVSLTL	KTTEPGVTGL	LLAVEGPAAK	RTMRPTQKDS	ETVDEDEEVD	PALTVGTIKK	HTLSIGDMVT
1050	1060	1070	1080	1090	1100	1110	1120
GTVKSIKPTH	VVVTLEDGII	GCIHASHILD	DVPEGTSPTT	KLKVGKTVTA	RVIGGRDMKT	FKYLPISHPR	FVRTIPELSV
1130	1140	1150	1160	1170	1180	1190	1200
RPSELEDGHT	ALNTHSVSPM	EKIKQYQAGQ	TVTCFLKKYN	VVKKWLEVEI	APDIRGRIPL	LLTSLSFKVL	KHPDKKFRVG
1210	1220	1230	1240	1250	1260	1270	1280
QALRATVVGP	DSSKTLLCLS	LTGPHKLEEG	EVAMGRVVKV	TPNEGLTVSF	PFGKIGTVSI	FHMSDSYSET	PLEDFVPQKV
1290	1300	1310	1320	1330	1340	1350	1360
VRCYILSTAD	NVLTLSLRSS	RTNPETKSKV	EDPEINSIQD	IKEGQLLRGY	VGSIQPHGVF	FRLGPSVVGL	ARYSHVSQHS
1370	1380	1390	1400	1410	1420	1430	1440
PSKKALYNKH	LPEGKLLTAR	VLRLNHQKNL	VELSFLPGDT	GKPDVLSASL	EGQLTKQEER	KTEAEERDQK	GEKKNQKRNE
1450	1460	1470	1480	1490	1500	1510	1520
KKNQKGQEEV	EMPSKEKQQP	QKPQAQKRGG	RECRESGSEQ	ERVSKKPKKA	GLSEEDDSLV	DVYYREGKEE	AEETNVLPKE
1530	1540	1550	1560	1570	1580	1590	1600
KQTKPAEAPR	LQLSSGFAWN	VGLDSLTPAL	PPLAESSDSE	EDEKPHQATI	KKSKKERELE	KQKAEKELSR	IEEALMDPGR
1610	1620	1630	1640	1650	1660	1670	1680
QPESADDFDR	LVLSSPNSSI	LWLQYMAFHL	QATEIEKARA	VAERALKTIS	FREEQEKLNV	WVALLNLENM	YGSQESLTKV
1690	1700	1710	1720	1730	1740	1750	1760
FERAVQYNEP	LKVFLHLADI	YAKSEKFQEA	GELYNRMLKR	FRQEKAVWIK	YGAFLLRRSQ	AAASHRVLQR	ALECLPSKEH
1770	1780	1790	1800	1810	1820	1830	1840
VDVIAKFAQL	EFQLGDAERA	KAIFENTLST	YPKRTDVWSV	YIDMTIKHGS	QKDVRDIFER	VIHLSLAPKR	MKFFFKRYLD
1850	1860	1870	1880				
YEKQHGTEKD	VQAVKAKALE	YVEAKSSVLE	D				

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

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1880	1	835.3213	-94.03	2	53.4	11.5	0	72-85	K.FEILSVESLCEGMR.I	Carbamidomethyl: 10

Detailed Protein Report

Protein 1108: PREDICTED: adenylate cyclase type 10 isoform X2 [Homo sapiens]

Accession:	gi|530365058	**Score:**	11.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	139.1
Database Date:	2015-11-30	**pI:**	6.5
		Sequence Coverage [%]:	1.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MNTPKEEFQD	WPIVRIAAHL	PDLIVYGHFS	PERPFMDYFD	GVLMFVDISG	FTAMTEKFSS	AMYMDRGAEQ	LVEILNYHIS
90	100	110	120	130	140	150	160
AIVEKVLIFG	GDILKFAGDA	LLALWRVERK	QLKNIITVVI	KCSLEIHGLF	ETQEWEEGLD	IRVKIGLAAG	HISMLVFGDE
170	180	190	200	210	220	230	240
THSHFLVIGQ	AVDDVRLAQN	MAQMNDVILS	PNCWQLCDRS	MIEIESVPDQ	RAVKVNFLKP	PPNFNFDEFF	TKCTTFMHYY
250	260	270	280	290	300	310	320
PSGEHKNLLR	LACTLKPDPE	LEMSLQKYVM	ESILKQIDNK	QLQGYLSELR	PVTIVFVNLM	FEDQDKAEEI	GPAIQDAYMH
330	340	350	360	370	380	390	400
ITSVLKIFQG	QINKVFMFDK	GCSFLCVFGF	PGEKVPDELT	HALECAMDIF	DFCSQVHKIQ	TVSIGVASGI	VFCGIVGHTV
410	420	430	440	450	460	470	480
RHEYTVIGQK	VNLAARMMMY	YPGIVTCDSV	TYNGSNLPAY	FFKELPKKVM	KGVADSGPLY	QYWGRTEKVM	FGMACLICNR
490	500	510	520	530	540	550	560
KEDYPLLGRN	KEINYFMYTM	KKFLISNSSQ	VLMYEGLPGY	GKSQILMKIE	YLAQGKNHRI	IAISLNKISF	HQTFYTIQMF
570	580	590	600	610	620	630	640
MANVLGLDTC	KHYKERQTNL	RNKVMTLLDE	KFYCLLNDIF	HVQFPISREI	SRMSTLKKQK	QLEILFMKIL	KLIVKEERII
650	660	670	680	690	700	710	720
FIIDEAQFVD	STSWRFMEKL	IRTLPIFIIM	SLCPFVNIPC	AAARAVIKNR	NTTYIVIGAV	QPNDISNKIC	LDLNVSCISK
730	740	750	760	770	780	790	800
ELDSYLGEGS	CGIPFYCEEL	LKNLEHHEVL	VFQQTESEEK	TNRTWNNLFK	YSIKLTEKLN	MVTLHSDKES	EEVCHLTSGV
810	820	830	840	850	860	870	880
RLKNLSPPTS	LKEISLIQLD	SMRLSHQMLV	RCAAIIGLTF	TTELLFEILP	CWNMKMMIKT	LATLVESNIF	YCFRNGKELQ
890	900	910	920	930	940	950	960
KALKQNDPSF	EVHYRSLSLK	PSEGMDHGEE	EQLRELENEV	IECHRIRFCN	PMMQKTAYEL	WLKDQRKAMH	LKCARFLEED
970	980	990	1000	1010	1020	1030	1040
AHRCDHCRGR	DFIPYHHFTV	NIRLNALDMD	AIKKMAMSHG	FKTEEKLILS	NSEIPETSAF	FPENRSPEEI	REKILNFFDH
1050	1060	1070	1080	1090	1100	1110	1120
VLTKMKTSDE	DIIPLESCQC	EEILEIVILP	LAHHFLALGE	NDKALYYFLE	IASAYLIFCD	NYMAYMYLNE	GQKLLKTLKK
1130	1140	1150	1160	1170	1180	1190	1200
DKSWSQTFES	ATFYSLKGEV	CFNMGQIVLA	KKMLRKALKL	LNRIFPYNLI	SLFLHIHVEK	NRHFHYVNRQ	AQESPPPGSL
1210							
RLT							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
249	1	679.3367	30.50	2	32.5	11.5	0	469-480	K.VMFGMACLICNR.K	

Detailed Protein Report

Protein 1109: syntaxin-10 isoform 3 [Homo sapiens]

Accession:	gi|410110902	**Score:**	11.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	27.5
Database Date:	2015-11-30	**pI:**	4.6
		Sequence Coverage [%]:	5.3
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MSLEDPFFVV RGEVQKAVNT ARGLYQRWCE LLQESAAVGR EELDWTTNEL RNGLRSIEWD LEDLEETIGI VEANPGKFKL
        90        100        110        120        130        140        150        160
PAGDLQERKV FVERMREAVQ EMKDHMVSPT AVAFLERNNR EILAGKPAAQ KSPSDLLDAS AVSATSRYIE EQQATQQLIM
       170        180        190        200        210        220        230        240
DEQDQQLEMV SGSIQVLKHM SGRVGEELDE QGIMLDAFAQ EMDHTQSRMD GVLRKLAKVS HMTSGESPQG RGQSWWGQVV
       250
GGTLSP
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2650	1	686.8825	94.84	2	63.2	11.5	0	219-231	K.VSHMTSGESPQGR.G	

Detailed Protein Report

Protein 1110: polyadenylate-binding protein 1 [Homo sapiens]

Accession:	gi|46367787	**Score:**	11.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	70.6
Database Date:	2015-11-30	**pI:**	10.0
		Sequence Coverage [%]:	3.0
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|530388906	refseq_human (refseq_human_20140103.fasta)	PREDICTED: polyadenylate-binding protein 1 isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MNPSAPSYPM	ASLYVGDLHP	DVTEAMLYEK	FSPAGPILSI	RVCRDMITRR	SLGYAYVNFQ	QPADAERALD	TMNFDVIKGK
90	100	110	120	130	140	150	160
PVRIMWSQRD	PSLRKSGVGN	IFIKNLDKSI	DNKALYDTFS	AFGNILSCKV	VCDENGSKGY	GFVHFETQEA	AERAIEKMNG
170	180	190	200	210	220	230	240
MLLNDRKVFV	GRFKSRKERE	AELGARAKEF	TNVYIKNFGE	DMDDERLKDL	FGKFGPALSV	KVMTDESGKS	KGFGFVSFER
250	260	270	280	290	300	310	320
HEDAQKAVDE	MNGKELNGKQ	IYVGRAQKKV	ERQTELKRKF	EQMKQDRITR	YQGVNLYVKN	LDDGIDDERL	RKEFSPFGTI
330	340	350	360	370	380	390	400
TSAKVMMEGG	RSKGFGFVCF	SSPEEATKAV	TEMNGRIVAT	KPLYVALAQR	KEERQAHLTN	QYMQRMASVR	AVPNPVINPY
410	420	430	440	450	460	470	480
QPAPPSGYFM	AAIPQTQNRA	AYYPPSQIAQ	LRPSPRWTAQ	GARPHPFQNM	PGAIRPAAPR	PPFSTMRPAS	SQVPRVMSTQ
490	500	510	520	530	540	550	560
RVANTSTQTM	GPRPAAAAAA	ATPAVRTVPQ	YKYAAGVRNP	QQHLNAQPQV	TMQQPAVHVQ	GQEPLTASML	ASAPPQEQKQ
570	580	590	600	610	620	630	640
MLGERLFPLI	QAMHPTLAGK	ITGMLLEIDN	SELLHMLESP	ESLRSKVDEA	VAVLQAHQAK	EAAQKAVNSA	TGVPTV

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1985	1	682.2638	-100.74	3	54.9	11.5	1	313-331	K.EFSPFGTITSAKVMMEGGR.S	

Detailed Protein Report

Protein 1111: arf-GAP with coiled-coil, ANK repeat and PH domain-containing protein 1 [Homo sapiens]

Accession:	gi|7661880	**Score:**	11.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	81.5
Database Date:	2015-11-30	**pI:**	8.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MTVKLDFEEC	LKDSPRFRAS	IELVEAEVSE	LETRLEKLLK	LGTGLLESGR	HYLAASRAFV	VGICDLARLG	PPEPMMAECL
90	100	110	120	130	140	150	160
EKFTVSLNHK	LDSHAELLDA	TQHTLQQQIQ	TLVKEGLRGF	REARRDFWRG	AESLEAALTH	NAEVPRRRAQ	EAEEAGAALR
170	180	190	200	210	220	230	240
TARAGYRGRA	LDYALQINVI	EDKRKFDIME	FVLRLVEAQA	THFQQGHEEL	SRLSQYRKEL	GAQLHQLVLN	SAREKRDMEQ
250	260	270	280	290	300	310	320
RHVLLKQKEL	GGEEPEPSLR	EGPGGLVMEG	HLFKRASNAF	KTWSRRWFTI	QSNQLVYQKK	YKDPVTVVVD	DLRLCTVKLC
330	340	350	360	370	380	390	400
PDSERRFCFE	VVSTSKSCLL	QADSERLLQL	WVSAVQSSIA	SAFSQARLDD	SPRGPGQGSG	HLAIGSAATL	GSGGMARGRE
410	420	430	440	450	460	470	480
PGGVGHVVAQ	VQSVDGNAQC	CDCREPAPEW	ASINLGVTLC	IQCSGIHRSL	GVHFSKVRSL	TLDSWEPELV	KLMCELGNVI
490	500	510	520	530	540	550	560
INQIYEARVE	AMAVKKPGPS	CSRQEKEAWI	HAKYVEKKFL	TKLPEIRGRR	GGRGRPRGQP	PVPPKPSIRP	RPGSLRSKPE
570	580	590	600	610	620	630	640
PPSEDLGSLH	PGALLFRASG	HPPSLPTMAD	ALAHGADVNW	VNGGQDNATP	LIQATAANSL	LACEFLLQNG	ANVNQADSAG
650	660	670	680	690	700	710	720
RGPLHHATIL	GHTGLACLFL	KRGADLGARD	SEGRDPLTIA	METANADIVT	LLRLAKMREA	EAAQGQAGDE	TYLDIFRDFS
730	740	750					
LMASDDPEKL	SRRSHDLHTL						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1185	1	984.5174	36.04	2	44.4	11.5	2	1-16	-.MTVKLDFEECLKDSPR.F	Carbamidomethyl: 10

Detailed Protein Report

Protein 1112: **myeloid leukemia factor 2 [Homo sapiens]**

Accession:	gi|4885487	**Score:**	11.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	28.1
Database Date:	2015-11-30	**pI:**	6.4
		Sequence Coverage [%]:	4.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MFRFMRDVEP	EDPMFLMDPF	AIHRQHMSRM	LSGGFGYSPF	LSITDGNMPG	TRPASRRMQQ	AGAVSPFGML	GMSGGFMDMF
90	100	110	120	130	140	150	160
GMMNDMIGNM	EHMTAGGNCQ	TFSSSTVISY	SNTGDGAPKV	YQETSEMRSA	PGGIRETRRT	VRDSDSGLEQ	MSIGHHIRDR
170	180	190	200	210	220	230	240
AHILQRSRNH	RTGDQEERQD	YINLDESEAA	AFDDEWRRET	SRFRQQRPLE	FRRLESSGAG	GRRAEGPPRL	AIQGPEDSPS
250							
RQSRRYDW							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1869	1	573.2178	-161.47	2	53.4	11.5	2	213-223	R.RLESSGAGGRR.A	

Detailed Protein Report

Protein 1113: long-chain-fatty-acid--CoA ligase 6 isoform f [Homo sapiens]

Accession:	gi|327412329	**Score:**	11.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	69.2
Database Date:	2015-11-30	**pI:**	7.8
		Sequence Coverage [%]:	2.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MQTQEILRIL	RLPELGDLGQ	FFRSLSATTL	DSGGARRSVI	GSGPQLLTHY	YDDARTMYQV	FRRGLSISGN	GPCLGFRKPK
90	100	110	120	130	140	150	160
QPYQWLSYQE	VADRAEFLGS	GLLQHNCKAC	TDQFIGVFAQ	NRPEWIIVEL	ACYTYSMVVV	PLYDTLGPGA	IRYIINTADI
170	180	190	200	210	220	230	240
STVIVDKPQK	AVLLLEHVER	KETPGLKLII	LMDPFEEALK	ERGQKCGVVI	KSMQAVEDCG	QENHQAPVPP	QPDDLSIVCF
250	260	270	280	290	300	310	320
TSGTTGNPKG	AMLTHGNVVA	DFSGFLKVTE	GDIRLLSDDM	KALCPTIFPV	VPRLLNRMYD	KIFSQANTPL	KRWLLEFAAK
330	340	350	360	370	380	390	400
RKQAEVRSGI	IRNDSIWDEL	FFNKIQASLG	GCVRMIVTGA	APASPTVLGF	LRAALGCQVY	EGYGQTECTA	GCTFTTPGDW
410	420	430	440	450	460	470	480
TSGHVGAPLP	CNHIKLVDVE	ELNYWACKGE	GEICVRGPNV	FKGYLKDPDR	TKEALDSDGW	LHTGDIGKWL	PAGTLKIIDR
490	500	510	520	530	540	550	560
KKHIFKLAQG	EYVAPEKIEN	IYIRSQPVAQ	IYVHGDSLKA	FLVGIVVPDP	EVMPSWAQKR	GIEGTYADLC	TNKDLKKAIL
570	580	590	600	610	620	630	
EDMVRLGKES	GLHSFEQVKA	IHIHSDMFSV	QNGLLTPTLK	AKRPELREYF	KKQIEELYSI	SM	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
631	1	766.4842	76.45	2	37.4	11.5	0	188-200	K.LIILMDPFEEALK.E	

Detailed Protein Report

Protein 1114: chloride intracellular channel protein 5 isoform a [Homo sapiens]

Accession: gi|166197662
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 11.5
MW [kDa]: 46.5
pI: 4.6
Sequence Coverage [%]: 7.1
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MNDEDYSTIY	DTIQNERTYE	VPDQPEENES	PHYDDVHEYL	RPENDLYATQ	LNTHEYDFVS	VYTIKGEETS	LASVQSEDRG
90	100	110	120	130	140	150	160
YLLPDEIYSE	LQEAHPGEPQ	EDRGISMEGL	YSSTQDQQLC	AAELQENGSV	MKEDLPSPSS	FTIQHSKAFS	TTKYSCYSDA
170	180	190	200	210	220	230	240
EGLEEKEGAH	MNPEIYLFVK	AGIDGESIGN	CPFSQRLFMI	LWLKGVVFNV	TTVDLKRKPA	DLHNLAPGTH	PPFLTFNGDV
250	260	270	280	290	300	310	320
KTDVNKIEEF	LEETLTPEKY	PKLAAKHRES	NTAGIDIFSK	FSAYIKNTKQ	QNNAALERGL	TKALKKLDDY	LNTPLPEEID
330	340	350	360	370	380	390	400
ANTCGEDKGS	RRKFLDGDEL	TLADCNLLPK	LHVVKIVAKK	YRNYDIPAEM	TGLWRYLKNA	YARDEFTNTC	AADSEIELAY
410	420						
ADVAKRLSRS							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2420	1	1045.2105	65.29	3	60.6	11.5	0	104-132	R.GISMEGLYSSTQDQQLCAAELQENGSVMK.E	Oxidation: 4

Detailed Protein Report

Protein 1115: presqualene diphosphate phosphatase [Homo sapiens]

Accession:	gi|66773040	**Score:**	11.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	32.2
Database Date:	2015-11-30	**pI:**	11.2
		Sequence Coverage [%]:	6.4
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MPSPRRSMEG RPLGVSASSS SSSPGSPAHG GGGGGSRFEF QSLLSSRATA VDPTCARLRA SESPVHRRGS FPLAAAGPSQ
        90        100        110        120        130        140        150        160
SPAPPLPEED RMDLNPSFLG IALRSLLAID LWLSKKLGVC AGESSSWGSV RPLMKLLEIS GHGIPWLLGT LYCLCRSDSW
       170        180        190        200        210        220        230        240
AGREVLMNLL FALLLDLLLV ALIKGLVRRR RPAHNQMDMF VTLSVDKYSF PSGHATRAAL MSRFILNHLV LAIPLRVLVV
       250        260        270        280        290        300
LWAFVLGLSR VMLGRHNVTD VAFGFFLGYM QYSIVDYCWL SPHNAPVLFL LWSQR
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
97	1	767.6746	-69.94	3	30.9	11.5	2	189-207	R.RRRPAHNQMDMFVTLSVDK.Y	

Detailed Protein Report

Protein 1116: PREDICTED: protein PRRC2C isoform X16 [Homo sapiens]

Accession:	gi|530364444	**Score:**	11.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	296.8
Database Date:	2015-11-30	**pI:**	9.4
		Sequence Coverage [%]:	0.5
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MSEKSGQSTK AKDGKKYATL SLFNTYKGKS LETQKTTVAA RHGLQSLGKV GISRRMPPPA NLPSLKAENK GNDPNVNIVP

        90        100        110        120        130        140        150        160
KDGTGWASKQ EQHEEEKTPE VPPAQPKPGV AAPPEVAPAP KSWASNKQGG QGDGIQVNSQ FQQEFPSLQA AGDQEKKEKE

       170        180        190        200        210        220        230        240
TNDDNYGPGP SLRPPNVACW RDGGKAAGSP SSSDQDEKLP GQDESTAGTS EQNDILKVVE KRIACGPPQA KLNGQQAALA

       250        260        270        280        290        300        310        320
SQYRAMMPPY MFQQYPRMTY PPLHGPMRFP PSLSETNKGL RGRGPPPSWA SEPERPSILS ASELKELDKF DNLDAEADEG

       330        340        350        360        370        380        390        400
WAGAQMEVDY TEQLNFSDDD EQGSNSPKEN NSEDQGSKAS ENNENKKETD EVSNTKSSSQ IPAQPSVAKV PYGKGPSFNQ

       410        420        430        440        450        460        470        480
ERGTSSHLPP PPKLLAQQHP PPDRQAVPGR PGPFPSKQQV ADEDEIWKQR RRQQSEISAA VERARKRREE EERRMEEQRK

       490        500        510        520        530        540        550        560
AACAEKLKRL DEKLGILEKQ PSPEEIRERE REKEREREKE LEKEQEQERE KEREKDRERQ QEKEKELEKE QEKQREMEKE

       570        580        590        600        610        620        630        640
RKQEKEKELE RQKEKEKELQ KMKEQEKECE LEKEREKLEE KIEPREPNLE PMVEKQESEN SCNKEEEPVF TRQDSNRSEK

       650        660        670        680        690        700        710        720
EATPVVHETE PESGSQPRPA VLSGYFKQFQ KSLPPRFQRQ QEQMKQQQWQ QQQQQGVLPQ TVPSQPSSST VPPPPHRPLY

       730        740        750        760        770        780        790        800
QPMQPHPQHL ASMGFDPRWL MMQSYMDPRM MSGRPAMDIP PIHPGMIPPK PLMRRDQMEG SPNSSESFEH IARSARDHAI

       810        820        830        840        850        860        870        880
SLSEPRMLWG SDPYPHAEPQ QATTPKATEE PEDVRSEAAL DQEQITAAYS VEHNQLEAHP KADFIRESSE AQVQKFLSRS

       890        900        910        920        930        940        950        960
VEDVRPHHTD ANNQSACFEA PDQKTLSAPQ EERISAVESQ PSRKRSVSHG SNHTQKPDEQ RSEPSAGIPK VTSRCIDSKE

       970        980        990       1000       1010       1020       1030       1040
PIERPEEKPK KEGFIRSSEG PKPEKVYKSK SETRWGPRPS SNRREEVNDR PVRRSGPIKK PVLRDMKEER EQRKEKEGEK

      1050       1060       1070       1080       1090       1100       1110       1120
AEKVTEKVVV KPEKTEKKDL PPPPPPPQPP APIQPQSVPP PIQPEAEKFP STETATLAQK PSQDTEKPLE PVSTVQVEPA

      1130       1140       1150       1160       1170       1180       1190       1200
VKTVNQQTMA APVVKEEKQP EKVISKDLVI ERPRPDSRPA VKKESTLPPR TYWKEARERD WFPDQGYRGR GRGEYYSRGR

      1210       1220       1230       1240       1250       1260       1270       1280
SYRGSYGGRG RGGRGHTRDY PQYRDNKPRA EHIPSGPLRQ REESETRSES SDFEVVPKRR RQRGSETDTD SEIHESASDK

      1290       1300       1310       1320       1330       1340       1350       1360
DSLSKGKLPK REERPENKKP VKPHSSFKPD NHVRIDNRLL EKPYVRDDDK AKPGFLPKGE PTRRGRGGTF RRGGRDPGGR

      1370       1380       1390       1400       1410       1420       1430       1440
PSRPSTLRRP AYRDNQWNPR QSEVPKPEDG EPPRRHEQFI PIAADKRPPK FERKFDPARE RPRRQRPTRP PRQDKPPRFR

      1450       1460       1470       1480       1490       1500       1510       1520
RLREREAASK SNEVVAVPTN GTVNNVAQEP VNTLGDISGN KTPDLSNQNS SDQANEEWET ASESSDFNER RERDEKKNAD

      1530       1540       1550       1560       1570       1580       1590       1600
LNAQTVVKVG ENVLPPKREI AKRSFSSQRP VDRQNRRGNN GPPKSGRNFS GPRNERRSGP PSKSGKRGPF DDQPAGTTGV

      1610       1620       1630       1640       1650       1660       1670       1680
DLINGSSAHH QEGVPNGTGQ KNSKDSTGKK REDPKPGPKK PKEKVDALSQ FDLNNYASVV IIDDHPEVTV IEDPQSNLND

      1690       1700       1710       1720       1730       1740       1750       1760
DGFTEVVSKK QQKRLQDEER RKKEEQVIQV WNKKNANEKG RSQTSKLPPR FAKKQATGIQ QAQSSASVPP LASAPLPPST

      1770       1780       1790       1800       1810       1820       1830       1840
SASVPASTSA PLPATLTPVP ASTSAPVPAS TLAPVLASTS APVPASPLAP VSASASVSAS VPASTSAAAI TSSSAPASAP

      1850       1860       1870       1880       1890       1900       1910       1920
APTPILASVS TPASVTILAS ASIPILASAL ASTSAPTPAP AASSPAAPVI TAPTIPASAP TASVPLAPAS ASAPAPAPTP

      1930       1940       1950       1960       1970       1980       1990       2000
VSAPNPAPPA PAQTQAQTHK PVQNPLQTTS QSSKQPPPSI RLPSAQTPNG TDYVASGKSI QTPQSHGTLT AELWDNKVAP

      2010       2020       2030       2040       2050       2060       2070       2080
PAVLNDISKK LGPISPPQPP SVSAWNKPLT SFGSAPSSEG AKNGQESGLE IGTDTIQFGA PASNGNENEV VPVLSEKSAD

      2090       2100       2110       2120       2130       2140       2150       2160
KIPEPKEQRQ KQPRAGPIKA QKLPDLSPVE NKEHKPGPIG KERSLKNRKV KDAQQVEPEG QEKPSPATVR STDPVTTKET

      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
1984	1	840.7858	-177.30	2	54.9	11.5	1	602-615	K.IEPREPNLEPMVEK.Q	

Detailed Protein Report

Protein 1117: Lebercilin [Homo sapiens]

Accession:	gi|170650670	**Score:**	11.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	80.5
Database Date:	2015-11-30	**pI:**	7.8
		Sequence Coverage [%]:	3.4
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530383030	refseq_human (refseq_human_20140103.fasta)	PREDICTED: Lebercilin isoform X2 [Homo sapiens]
gi|170650672	refseq_human (refseq_human_20140103.fasta)	lebercilin [Homo sapiens]

10	20	30	40	50	60	70	80
MGERAGSPGT	DQERKAGKHH	YSYLSDFETP	QSSGRSSLVS	SSPASVRRKN	PKRQTSDGQV	HHQAPRKPSP	KGLPNRKGVR
90	100	110	120	130	140	150	160
VGFRSQSLNR	EPLRKDTDLV	TKRILSARLL	KINELQNEVS	ELQVKLAELL	KENKSLKRLQ	YRQEKALNKF	EDAENEISQL
170	180	190	200	210	220	230	240
IFRHNNEITA	LKERLRKSQE	KERATEKRVK	DTESELFRTK	FSLQKLKEIS	EARHLPERDD	LAKKLVSAEL	KLDDTERRIK
250	260	270	280	290	300	310	320
ELSKNLELST	NSFQRQLLAE	RKRAYEAHDE	NKVLQKEVQR	LYHKLKEKER	ELDIKNIYSN	RLPKSSPNKE	KELALRKNAA
330	340	350	360	370	380	390	400
CQSDFADLCT	KGVQTMEDFK	PEEYPLTPET	IMCYENKWEE	PGHLTLDLQS	QKQDRHGEAG	ILNPIMEREE	KFVTDEELHV
410	420	430	440	450	460	470	480
VKQEVEKLED	EWEREELDKK	QKEKASLLER	EEKPEWETGR	YQLGMYPIQN	MDKLQGEEEE	RLKREMLLAK	LNEIDRELQD
490	500	510	520	530	540	550	560
SRNLKYPVLP	LLPDFESKLH	SPERSPKTYR	FSESSERLFN	GHHLQDISFS	TPKGEGQNSG	NVRSPASPNE	FAFGSYVPSF
570	580	590	600	610	620	630	640
AKTSERSNPF	SQKSSFLDFQ	RNSMEKLSKD	GVDLITRKEK	KANLMEQLFG	ASGSSTISSK	SSDPNSVASS	KGDIDPLNFL
650	660	670	680	690	700		
PGNKGSRDQE	HDEDEGFFLS	EGRSFNPNRH	RLKHADDKPA	VKAADSVEDE	IEEVALR		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
96	1	820.3387	-82.67	3	30.9	11.5	1	621-644	K.SSDPNSVASSKGDIDPLNFLPGNK.G	

Detailed Protein Report

Protein 1118: extracellular superoxide dismutase [Cu-Zn] precursor [Homo sapiens]

Accession:	gi|118582275	**Score:**	11.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	25.8
Database Date:	2015-11-30	**pI:**	6.2
		Sequence Coverage [%]:	3.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLALLCSCLL	LAAGASDAWT	GEDSAEPNSD	SAEWIRDMYA	KVTEIWQEVM	QRRDDDGALH	AACQVQPSAT	LDAAQPRVTG
90	100	110	120	130	140	150	160
VVLFRQLAPR	AKLDAFFALE	GFPTEPNSSS	RAIHVHQFGD	LSQGCESTGP	HYNPLAVPHP	QHPGDFGNFA	VRDGSLWRYR
170	180	190	200	210	220	230	240
AGLAASLAGP	HSIVGRAVVV	HAGEDDLGRG	GNQASVENGN	AGRRLACCVV	GVCGPGLWER	QAREHSERKK	RRRESECKAA
250							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2401	1	447.2391	62.99	2	60.4	11.5	2	233-240	R.RESECKAA.-	

Detailed Protein Report

Protein 1119: PREDICTED: collagen alpha-1(III) chain-like [Homo sapiens]

Accession:	gi|530436794	**Score:**	11.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	29.9
Database Date:	2015-11-30	**pI:**	10.7
		Sequence Coverage [%]:	4.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MTPSRAQEGP	PRVERAECGA	SAGALTIVSS	HGGDSDKDLC	ARTQIYGAQP	REDQMGSVEK	LTTSAFLSAK	PGSVPAPRPL
90	100	110	120	130	140	150	160
RRAPGLGKSI	DGEAGHSEAA	GEKGECGIPW	TEGQVWRPLE	RRASVASPGE	KGECGVPWRE	GRVWRPLDRR	GSVASPGEKG
170	180	190	200	210	220	230	240
QCGVPWREGG	VWRPLERRGS	VASPGEKGEC	GVPWREGPVW	RPLERRGEKG	ECGVPWREGG	VWRPLDRRGS	VASPGEKGEC
250	260	270	280				
GVRWREGRVW	YSLDRRGSVP	AALASQRHAL	LALPQPQG				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
355	1	528.6942	-187.78	2	34.1	11.5	0	257-267	R.GSVPAALASQR.H	

Detailed Protein Report

Protein 1120: epithelial splicing regulatory protein 1 isoform 5 [Homo sapiens]

Accession:	gi|170763533	**Score:**	11.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	67.2
Database Date:	2015-11-30	**pI:**	6.2
		Sequence Coverage [%]:	3.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MTASPDYLVV	LFGITAGATG	AKLGSDEKEL	ILLFWKVVDL	ANKKVGQLHE	VLVRPDQLEL	TEDCKEETKI	DVESLSSASQ
90	100	110	120	130	140	150	160
LDQALRQFNQ	SVSNELNIGV	GTSFCLCTDG	QLHVRQILHP	EASKKNVLLP	ECFYSFFDLR	KEFKKCCPGS	PDIDKLDVAT
170	180	190	200	210	220	230	240
MTEYLNFEKS	SSVSRYGASQ	VEDMGNIILA	MISEPYNHRF	SDPERVNYKF	ESGTCSKMEL	IDDNTVVRAR	GLPWQSSDQD
250	260	270	280	290	300	310	320
IARFFKGLNI	AKGGAALCLN	AQGRRNGEAL	VRFVSEEHRD	LALQRHKHHM	GTRYIEVYKA	TGEDFLKIAG	GTSNEVAQFL
330	340	350	360	370	380	390	400
SKENQVIVRM	RGLPFTATAE	EVVAFFGQHC	PITGGKEGIL	FVTYPDGRPT	GDAFVLFACE	EYAQNALRKH	KDLLGKRYIE
410	420	430	440	450	460	470	480
LFRSTAAEVQ	QVLNRFSSAP	LIPLPTPPII	PVLPQQFVPP	TNVRDCIRLR	GLPYAATIED	ILDFLGEFAT	DIRTHGVHMV
490	500	510	520	530	540	550	560
LNHQGRPSGD	AFIQMKSADR	AFMAAQKCHK	KNMKDRYVEV	FQCSAEEMNF	VLMGGTLNRN	GLSPPPCLSP	PSYTFPAPAA
570	580	590	600	610			
VIPTEAAIYQ	PSVILNPRAL	QPSTAYYPAG	TQLFMNYTAY	YPSV			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2627	1	863.9392	-38.81	2	62.9	11.5	1	247-264	K.GLNIAKGGAALCLNAQGR.R	

Detailed Protein Report

Protein 1121: PREDICTED: signal-induced proliferation-associated 1-like protein 2 isoform X8 [Homo sapiens]

Accession:	gi|578802290	**Score:**	11.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	188.3
Database Date:	2015-11-30	**pI:**	6.4
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSDPRQSQEE	KHKLGRASSK	FKDPPRIMQS	DDYFARKFKA	INGNMGPTTS	LNASNSNETG	GGGPANGTPA	VPKMGVRARV
90	100	110	120	130	140	150	160
SEWPPKKDCS	KELTCKALWE	SRSQTSYESI	TSVLQNGQSD	QSEGQQDEQL	DLDFVEAKYT	IGDIFVHSPQ	RGLHPIRQRS
170	180	190	200	210	220	230	240
NSDVTISDID	AEDVLDQNAV	NPNTGAALHR	EYGSTSSIDR	QGLSGENFFA	MLRGYRVENY	DHKAMVPFGF	PEFFRCDPAI
250	260	270	280	290	300	310	320
SPSLHAAAQI	SRGEFVRISG	LDYVDSALLM	GRDRDKPFKR	RLKSESVETS	LFRKLRTVKS	EHETFKFTSE	LEESRLERGI
330	340	350	360	370	380	390	400
RPWNCQRCFA	HYDVQSILFN	INEAMATRAN	VGKRKNITTG	ASAASQTQMP	TGQTGNCESP	LGSKEDLNSK	ENLDADEGDG
410	420	430	440	450	460	470	480
KSNDLVLSCP	YFRNETGGEG	DRRIALSRAN	SSSFSSGESC	SFESSLSSHC	TNAGVSVLEV	PRENQPIHRE	KVKRYIIEHI
490	500	510	520	530	540	550	560
DLGAYYYRKF	FYGKEHQNYF	GIDENLGPVA	VSIRREKVED	AKEKEGSQFN	YRVAFRTSEL	TTLRGAILED	AIPSTARHGT
570	580	590	600	610	620	630	640
ARGLPLKEVL	EYVIPELSIQ	CLRQASNSPK	VSEQLLKLDE	QGLSFQHKIG	ILYCKAGQST	EEEMYNNETA	GPAFEEFLDL
650	660	670	680	690	700	710	720
LGQRVRLKGF	SKYRAQLDNK	TDSTGTHSLY	TTYKDYELMF	HVSTLLPYMP	NNRQQLLRKR	HIGNDIVTIV	FQEPGALPFT
730	740	750	760	770	780	790	800
PKSIRSHFQH	VFVIVKVHNP	CTENVCYSVG	VSRSKDVPPF	GPPIPKGVTF	PKSAVFRDFL	LAKVINAENA	AHKSEKFRAM
810	820	830	840	850	860	870	880
ATRTRQEYLK	DLAENFVTTA	TVDTSVKFSF	ITLGAKKKEK	VKPRKDAHLF	SIGAIMWHVI	ARDFGQSADI	ECLLGISNEF
890	900	910	920	930	940	950	960
IMLIEKDSKN	VVFNCSCRDV	IGWTSGLVSI	KVFYERGECV	LLSSVDNCAE	DIREIVQRLV	IVTRGCETVE	MTLRRNGLGQ
970	980	990	1000	1010	1020	1030	1040
LGFHVNFEGI	VADVEPFGFA	WKAGLRQGSR	LVEICKVAVA	TLTHEQMIDL	LRTSVTVKVV	IIQPHDDGSP	RRGCSELCRI
1050	1060	1070	1080	1090	1100	1110	1120
PMVEYKLDSE	GTPCEYKTPF	RRNTTWHRVP	TPALQPLSRA	SPIPGTPDRL	PCQQLLQQAQ	AAIPRSTSFD	RKLPDGTRSS
1130	1140	1150	1160	1170	1180	1190	1200
PSNQSSSSDP	GPGGSGPWRP	QVGYDGCQSP	LLLEHQGSGP	LECDGARERE	DTMEASRHPE	TKWHGPPSKV	LGSYKERALQ
1210	1220	1230	1240	1250	1260	1270	1280
KDGSCKDSPN	KLSHIGDKSC	SSHSSSNTLS	SNTSSNSDDK	HFGSGDLMDP	ELLGLTYIKG	ASTDSGIDTA	PCMPATILGP
1290	1300	1310	1320	1330	1340	1350	1360
VHLAGSRSLI	HSRAEQWADA	ADVSGPDDEP	AKLYSVHGYA	STISAGSAAE	GSMGDLSEIS	SHSSGSHHSG	SPSAHCSKSS
1370	1380	1390	1400	1410	1420	1430	1440
GSLDSSKVYI	VSHSSGQQVP	GSMSKPYHRQ	GAVNKYVIGW	KKSEGSPPPE	EPEVTECPGM	YSEMDVMSTA	TQHQTVVGDA
1450	1460	1470	1480	1490	1500	1510	1520
VAETQHVLSK	EDFLKLMLPD	SPLVEEGRRK	FSFYGNLSPR	RSLYRTLSDE	SICSNRRGSS	FGSSRSSVLD	QALPNDILFS
1530	1540	1550	1560	1570	1580	1590	1600
TTPPYHSTLP	PRAHPAPSMG	SLRNEFWFSD	GSLSDKSKCA	DPGLMPLPDT	ATGLDWTHLV	DAARAFEDQR	VASFCTLTDM
1610	1620	1630	1640	1650	1660	1670	1680
QHGQDLEGAQ	ELPLCVDPGS	GKEFMDTTGE	RSPSPLTGKV	NQLELILRQL	QTDLRKEKQD	KAVLQAEVQH	LRQDNMRLQE
1690	1700	1710					
ESQTATAQLR	KFTEWFFTTI	DKKS					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1759	1	1057.1731	7.31	3	51.8	11.5	0	40-73	K.AINGNMGPTTSLNASNSNETGGGGPANGTPAVPK.M	Oxidation: 6

Detailed Protein Report

Protein 1122: NEDD4 family-interacting protein 2 isoform 2 [Homo sapiens]

Accession:	gi|239046743	**Score:**	11.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	34.1
Database Date:	2015-11-30	**pI:**	4.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	6.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MARRRSQRVC	ASGPSMLNSA	RGAPELLRGT	ATNAEVSAAA	AGATGSEELP	PGDRGCRNGG	GRGPAATTSS	TGVAVGAEHG
90	100	110	120	130	140	150	160
EDSLSRKPDP	EPGRMDHHQP	GTGRYQVLLN	EEDNSESSAI	EQPPTSNPAP	QIVQAASSAP	ALETDSSPPP	YSSITVEVPT
170	180	190	200	210	220	230	240
TSDTEVYGEF	YPVPPPYSVA	TSLPTYDEAE	KAKAAAMAAA	AAETSQRIQE	EECPPRDDFS	DADQLRVGND	GIFMLAFFTG
250	260	270	280	290	300	310	320
RYGAICGFGL	SLIKWILIVR	FSDYFTGYFN	GQYWLWWIFL	VLGLLLFFRG	FVNYLKVRNM	SESMAAAHRT	RYFFLL

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2111	1	1022.8759	-137.93	2	56.6	11.5	1	9-28	R.VCASGPSMLNSARGAPELLR.G	Oxidation: 8

Detailed Protein Report

Protein 1123: sorting nexin-5 isoform b [Homo sapiens]

Accession:	gi|540344544	**Score:**	11.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	34.9
Database Date:	2015-11-30	**pI:**	9.3
		Sequence Coverage [%]:	5.0
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MQKLGEGEGS MTKEEFAKMK QELEAEYLAV FKKTVSSHEV FLQRLSSHPV LSKDRNFHVF LEYDQDLSVR RKNTKEMFGG
        90        100        110        120        130        140        150        160
FFKSVVKSAD EVLFTGVKEV DDFFEQEKNF LINYYNRIKD SCVKADKMTR SHKNVADDYI HTAACLHSLA LEEPTVIKKY
       170        180        190        200        210        220        230        240
LLKVAELFEK LRKVEGRVSS DEDLKLTELL RYYMLNIEAA KDLLYRRTKA LIDYENSNKA LDKARLKSKD VKLAEAHQQE
       250        260        270        280        290        300
CCQKFEQLSE SAKEELINFK RKRVAAFRKN LIEMSELEIK HARNNVSLLQ SCIDLFKNN
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2099	1	938.3578	-137.94	2	56.1	11.5	1	192-206	R.YYMLNIEAAKDLLYR.R	

Detailed Protein Report

Protein 1124: PREDICTED: sphingomyelin phosphodiesterase 4 isoform X7 [Homo sapiens]

Accession:	gi|530369272	**Score:**	11.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	60.1
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
MWLHHYSLEM	YQKMQSPHAK	ESFTPTEEHV	LVVRLLLKHL	HAFANSLKPE	QASPSAHSHA	TSPLEEFKRA	AVPRFVQQKL
90	100	110	120	130	140	150	160
YLFLQHCFGH	WPLDASFRAV	LEMWLSYLQP	WRYAPDKQAP	GSDSQPRCVS	EKWAPFVQEN	LLMYTKLFVG	FLNRALRTDL
170	180	190	200	210	220	230	240
VSPKHALMVF	RVAKVFAQPN	LAEMIQKGEQ	LFLEPELVIP	HRQHRLFTAP	TFTGSFLSPW	PPAVTDASFK	VKSHVYSLEG
250	260	270	280	290	300	310	320
QDCKYTPMFG	PEARTLVLRL	AQLITQAKHT	AKSISDQCAE	SPAGHSFLSW	LGFSSMDTNG	SYTANDLDEM	GQDSVRKTDE
330	340	350	360	370	380	390	400
YLEKALEYLR	QIFRLSEAQL	RQFTLALGTT	QDENGKKQLP	DCIVGEDGLI	LTPLGRYQII	NGLRRFEIEY	QGDPELQPIR
410	420	430	440	450	460	470	480
SYEIASLVRT	LFRLSSAINH	RFAGQMAALC	SRDDFLGSFC	RYHLTEPGLA	SRHLLSPVGR	RQVAGHTRGP	RLSLRFLGSY
490	500	510	520	530	540		
RTLVSLLLAF	FVASLFCVGP	LPCTLLLTLG	YVLYASAMTL	LTERGKLHQP			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
730	1	683.3948	125.77	2	38.5	11.5	0	233-244	K.SHVYSLEGQDCK.Y	

Detailed Protein Report

Protein 1125: PREDICTED: zinc finger protein 638 isoform X4 [Homo sapiens]

Accession:	gi|530367482	**Score:**	11.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	134.5
Database Date:	2015-11-30	**pI:**	10.1
		Sequence Coverage [%]:	0.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPRDGVPAGN	TTPAAAQAAA	QSPDSATAGA	PQVLDSLKRF	VLFLENFAPL	VNSLNLGIAN	PLLLGPSPLH	FAQIKTQLAL
90	100	110	120	130	140	150	160
QQLNAVASHG	STPPYTLLNQ	AFLKIAMSRP	RFNPRGDFPL	QRPRAPNPSG	MRPPGPFMRP	GSMGLPRFYP	AGRARGIPHR
170	180	190	200	210	220	230	240
FAGHESYQNM	GPQRMNVQVT	QHRTDPRLTK	EKLDFHEAQQ	KKGKPHGSRW	DDEPHISASV	AVKQSSVTQV	TEQSPKVQSR
250	260	270	280	290	300	310	320
YTKESASSIL	ASFGLSNEDL	EELSRYPDEQ	LTPENMPLIL	RDIRMRKMGR	RLPNLPSQSR	NKETLGSEAV	SSNVIDYGHA
330	340	350	360	370	380	390	400
SKYGYTEDPL	EVRIYDPEIP	TDEVENEFQS	QQNISASVPN	PNVICNSMFP	VEDVFRQMDF	PGESSNNRSF	FSVESGTKMS
410	420	430	440	450	460	470	480
GLHISGGQSV	LEPIKSVNQS	INQTVSQTMS	QSLIPPSMNQ	QPFSSELISS	VSQQERIPHE	PVINSSNVHV	GSRGSKKNYQ
490	500	510	520	530	540	550	560
SQADIPIRSP	FGIVKASWLP	KFSHADAQKM	KRLPTPSMMN	DYYAASPRIF	PHLCSLCNVE	CSHLKDWIQH	QNTSTHIESC
570	580	590	600	610	620	630	640
RQLRQQYPDW	NPEILPSRRN	EGNRKENETP	RRRSHSPSPR	RSRRSSSSHR	FRRSRSPMHY	MYRPRSRSPR	ICHRFISRYR
650	660	670	680	690	700	710	720
SRSRSRSPYR	IRNPFRGSPK	CFRSVSPERM	SRRSVRSSDR	KKALEDVVQR	SGHGTEFNKQ	KHLEAADKGH	SPAQKPKTSS
730	740	750	760	770	780	790	800
GTKPSVKPTS	ATKSDSNLGG	HSIRCKSKNL	EDDTLSECKQ	VSDKAVSLQR	KLRKEQSLHY	GSVLLITELP	EDGCTEEDVR
810	820	830	840	850	860	870	880
KLFQPFGKVN	DVLIVPYRKE	AYLEMEFKEA	ITAIMKYIET	TPLTIKGKSV	KICVPGKKKA	QNKEVKKKTL	ESKKVSASTL
890	900	910	920	930	940	950	960
KRDADASKAV	EIVTSTSAAK	TGQAKASVAK	VNKSTGKSAS	SVKSVVTVAV	KGNKASIKTA	KSGGKKSLEA	KKTGNVKNKD
970	980	990	1000	1010	1020	1030	1040
SNKPVTIPEN	SEIKTSIEVK	ATENCAKEAI	SDAALEATEN	EPLNKETEEM	CVMLVSNLPN	KGYSVEEVYD	LAKPFGGLKD
1050	1060	1070	1080	1090	1100	1110	1120
ILILSSHKKA	YIEINRKAAE	SMVKFYTCFP	VLMDGNQLSI	SMAPENMNIK	DEEAIFITLV	KENDPEANID	TIYDRFVHLD
1130	1140	1150	1160	1170	1180	1190	1200
NLPEDGLQCV	LCVGLQFGKV	DHHVFISNRN	KAILQLDSPE	SAQSMYSFLK	QNPQNIGDHM	LTCSLSPKID	LPEVQIEHDP
1210							
ELEKES							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
450	1	658.3852	-7.72	2	35.3	11.4	1	809-819	K.VNDVLIVPYRK.E	

Detailed Protein Report

Protein 1126: olfactory receptor 5C1 [Homo sapiens]

Accession:	gi|53828676	**Score:**	11.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	35.0
Database Date:	2015-11-30	**pI:**	9.9
		Sequence Coverage [%]:	4.4
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MNSENLTRAA VAPAEFVLLG ITNRWDLRVA LFLTCLPVYL VSLLGNMGMA LLIRMDARLH TPMYFFLANL SLLDACYSSA
        90        100        110        120        130        140        150        160
IGPKMLVDLL LPRATIPYTA CALQMFVFAG LADTECCLLA AMAYDRYVAI RNPLLYTTAM SQRLCLALLG ASGLGGAVSA
       170        180        190        200        210        220        230        240
FVHTTLTFRL SFCRSRKINS FFCDIPPLLA ISCSDTSLNE LLLFAICGFI QTATVLAITV SYGFIAGAVI HMRSVEGSRR
       250        260        270        280        290        300        310        320
AASTGGSHLT AVAMMYGTLI FMYLRPSSSY ALDTDKMASV FYTLVIPSLN PLIYSLRNKE VKEALRQTWS RFHCPGQGSQ
       330
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
507	1	809.7240	-171.17	2	35.7	11.4	1	307-320	R.QTWSRFHCPGQGSQ.-	

Protein 1127: PREDICTED: A-kinase anchor protein 13 isoform X16 [Homo sapiens]

Accession:	gi|530407008	**Score:**	11.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	165.7
Database Date:	2015-11-30	**pI:**	6.5
		Sequence Coverage [%]:	1.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPDVKAEDEV	DFRASSISEE	VAVGSIAATL	KMKQGPMTQA	INRENWCTIE	PCPDAASLLA	SKQSPECENF	LDVGLGRECT
90	100	110	120	130	140	150	160
SKQGVLKRES	GSDSDLFHSP	SDDMDSIIFP	KPEEEHLACD	ITGSSSSTDD	TASLDRHSSH	GSDVSLSQIL	KPNRSRDRQS
170	180	190	200	210	220	230	240
LDGFYSHGMG	AEGRESESEP	ADPGDVEEEE	MDSITEVPAN	CSVLRSSMRS	LSPFRRHSWG	PGKNAASDAE	MNHRSSMRVL
250	260	270	280	290	300	310	320
GDVVRRPPIH	RRSFSLEGLT	GGAGVGNKPS	SSLEVSSANA	EELRHPFSGE	ERVDSLVSLS	EEDLESDQRE	HRMFDQQICH
330	340	350	360	370	380	390	400
RSKQQGFNYC	TSAISSPLTK	SISLMTISHP	GLDNSRPFHS	TFHNTSANLT	ESITEENYNF	LPHSPSKKDS	EWKSGTKVSR
410	420	430	440	450	460	470	480
TFSYIKNKMS	SSKKSKEKEK	EKDKIKEKEK	DSKDKEKDKK	TVNGHTFSSI	PVVGPISCSQ	CMKPFTNKDA	YTCANCSAFV
490	500	510	520	530	540	550	560
HKGCRESLAS	CAKVKMKQPK	GSLQAHDTSS	LPTVIMRNKP	SQPKERPRSA	VLLVDETATT	PIFANRRSQQ	SVSLSKSVSI
570	580	590	600	610	620	630	640
QNITGVGNDE	NMSNTWKFLS	HSTDSLNKIS	KVNESTESLT	DEGVGTDMNE	GQLLGDFEIE	SKQLEAESWS	RIIDSKFLKQ
650	660	670	680	690	700	710	720
QKKDVVKRQE	VIYELMQTEF	HHVRTLKIMS	GVYSQGMMAD	LLFEQQMVEK	LFPCLDELIS	IHSQFFQRIL	ERKKESLVDK
730	740	750	760	770	780	790	800
SEKNFLIKRI	GDVLVNQFSG	ENAERLKKTY	GKFCGQHNQS	VNYFKDLYAK	DKRFQAFVKK	KMSSSVVRRL	GIPECILLVT
810	820	830	840	850	860	870	880
QRITKYPVLF	QRILQCTKDN	EVEQEDLAQS	LSLVKDVIGA	VDSKVASYEK	KVRLNEIYTK	TDSKSIMRMK	SGQMFAKEDL
890	900	910	920	930	940	950	960
KRKKLVRDGS	VFLKNAAGRL	KEVQAVLLTD	ILVFLQEKDQ	KYIFASLDQK	STVISLKKLI	VREVAHEEKG	LFLISMGMTD
970	980	990	1000	1010	1020	1030	1040
PEMVEVHASS	KEERNSWIQI	IQDTINTLNR	DEDEGIPSEN	EEEKKMLDTR	ARELKDHFLL	PAEQLHQKDQ	KILLLLEEKE
1050	1060	1070	1080	1090	1100	1110	1120
MIFRDMAECS	TPLPEDCSPT	HSPRVLFRSN	TEEALKGGPL	MKSAINEVEI	LQGLVSGNLG	GTLGPTVSSP	IEQDVVGPVS
1130	1140	1150	1160	1170	1180	1190	1200
LPRRAETFGG	FDSHQMNASK	GGEKEEGDDG	QDLRRTESDS	GLKKGGNANL	VFMLKRNSEQ	VVQSVVHLYE	LLSALQGVVL
1210	1220	1230	1240	1250	1260	1270	1280
QQDSYIEDQK	LVLSERALTR	SLSRPSSLIE	QEKQRSLEKQ	RQDLANLQKQ	QAQYLEEKRR	REREWEARER	ELREREALLA
1290	1300	1310	1320	1330	1340	1350	1360
QREEEVQQGQ	QDLEKEREEL	QQKKGTYQYD	LERLRAAQKQ	LEREQEQLRR	EAERLSQRQT	ERDLCQVSHP	HTKLMRIPSF
1370	1380	1390	1400	1410	1420	1430	1440
FPSPEEPPSP	SAPSIAKSGS	LDSELSVSPK	RNSISRTHKD	KGPFHILSST	SQTNKGPEGQ	SQAPASTSAS	TRLFGLTKPK
1450	1460	1470	1480				
EKKEKKKKNK	TSRSQPGDGP	ASEVSAEGEE	IFC				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2281	1	557.4292	158.24	3	58.4	11.4	2	239-252	R.VLGDVVRRPPIHRR.S	

Detailed Protein Report

Protein 1128: coilin [Homo sapiens]

Accession: gi|4758024

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Score: 11.4

MW [kDa]: 62.6

pI: 10.0

Sequence Coverage [%]: 2.3

No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MAASETVRLR	LQFDYPPPAT	PHCTAFWLLV	DLNRCRVVTD	LISLIRQRFG	FSSGAFLGLY	LEGGLLPPAE	SARLVRDNDC
90	100	110	120	130	140	150	160
LRVKLEERGV	AENSVVISNG	DINLSLRKAK	KRAFQLEEGE	ETEPDCKYSK	KHWKSRENNN	NNEKVLDLEP	KAVTDQTVSK
170	180	190	200	210	220	230	240
KNKRKNKATC	GTVGDDNEEA	KRKSPKKKEK	CEYKKKAKNP	KSPKVQAVKD	WANQRCSSPK	GSARNSLVKA	KRKGSVSVCS
250	260	270	280	290	300	310	320
KESPSSSSES	ESCDESISDG	PSKVTLEARN	SSEKLPTELS	KEEPSTKNTT	ADKLAIKLGF	SLTPSKGKTS	GTTSSSSDSS
330	340	350	360	370	380	390	400
AESDDQCLMS	SSTPECAAGF	LKTVGLFAGR	GRPGPGLSSQ	TAGAAGWRRS	GSNGGGQAPG	ASPSVSLPAS	LGRGWGREEN
410	420	430	440	450	460	470	480
LFSWKGAKGR	GMRGRGRGRG	HPVSCVVNRS	TDNQRQQQLN	DVVKNSSTII	QNPVETPKKD	YSLLPLLAAA	PQVGEKIAFK
490	500	510	520	530	540	550	560
LLELTSSYSP	DVSDYKEGRI	LSHNPETQQV	DIEILSSLPA	LREPGKFDLV	YHNENGAEVV	EYAVTQESKI	TVFWKELIDP
570	580						
RLIIESPSNT	SSTEPA						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1773	1	835.3568	-43.51	2	52.0	11.4	2	132-144	K.HWKSRENNNNNEK.V	

Detailed Protein Report

Protein 1129: zinc finger and BTB domain-containing protein 10 isoform c [Homo sapiens]

Accession:	gi|460417313	**Score:**	11.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	64.9
Database Date:	2015-11-30	**pI:**	5.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MTRLERSSHR	TVICKVPGEL	VAREGKCASR	ARESEIPSEE	GYCDFNSRPN	ENSYCYQLLR	QLNEQRKKGI	LCDVSIVVSG
90	100	110	120	130	140	150	160
KIFKAHKNIL	VAGSRFFKTL	YCFSNKESPN	QNNTTHLDIA	AVQGFSVILD	FLYSGNLVLT	SQNAIEVMTV	ASYLQMSEVV
170	180	190	200	210	220	230	240
QTCRNFIKDA	LNISIKSEAP	ESVVVDYNNR	KPVNRDGLSS	SRDQKIASFW	ATRNLTNLAS	NVKIENDGCN	VDEGQIENYQ
250	260	270	280	290	300	310	320
MNDSSWVQDG	SPEMAENESE	GQTKVFIWNN	MGSQGIQETG	KTRRKNQTTK	RFIYNIPPNN	ETNLEDCSVM	QPPVAYPEEN
330	340	350	360	370	380	390	400
TLLIKEEPDL	DGALLSGPDG	DRNVNANLLA	EAGTSQDGGD	AGTSHDFKYG	LMPGPSNDFK	YGLIPGTSND	FKYGLIPGAS
410	420	430	440	450	460	470	480
NDFKYGLLPE	SWPKQETWEN	GESSLIMNKL	KCPHCSYVAK	YRRTLKRHLL	IHTGVRSFSC	DICGKLFTRR	EHVKRHSLVH
490	500	510	520	530	540	550	560
KKDKKYKCMV	CKKIFMLAAS	VGIRHGSRRY	GVCVDCADKS	QPGGQEGVDQ	GQDTEFPRDE	EYEENEVGEA	DEELVDDGED
570	580						
QNDPSRWDES	GEVCMSLDD						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1822	1	861.7800	-131.73	2	52.6	11.4	2	505-519	R.HGSRRYGVCVDCADK.S	Carbamidomethyl: 12

Detailed Protein Report

Protein 1130: **cytoplasmic tRNA 2-thiolation protein 1 [Homo sapiens]**

Accession:	gi|222537719	**Score:**	11.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	36.4
Database Date:	2015-11-30	**pI:**	11.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	8.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPAPPCASCH	AARAALRRPL	SGQALCGACF	CAAFEAEVLH	TVLAGRLLPP	GAVVAVGASG	GKDSTVLAHV	LRALAPRLGI
90	100	110	120	130	140	150	160
SLQLVAVDEG	IGGYRDAALA	AVRRQAARWE	LPLTVVAYED	LFGGWTMDAV	ARSTAGSGRS	RSCCTFCGVL	RRRALEEGAR
170	180	190	200	210	220	230	240
RVGATHIVTG	HNADDMAETV	LMNFLRGDAG	RLARGGGLGS	PGEGGALPRC	RPLQFASQKE	VVLYAHFRRL	DYFSEECVYA
250	260	270	280	290	300	310	320
PEAFRGHARD	LLKRLEAARP	SAVLDLVHSA	ERLALAPAAR	PPRPGACSRC	GALASRALCQ	ACALLDGLNR	GRPRLAIGKG
330	340	350					
RRGLDEEATP	GTPGDPARPP	ASKAVPTF					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1669	1	1061.1845	-12.16	3	50.6	11.4	1	105-132	R.QAARWELPLTVVAYEDLFGGWTMDAVAR.S	Oxidation: 23

Detailed Protein Report

Protein 1131: leukemia NUP98 fusion partner 1 [Homo sapiens]

Accession:	gi|146260273	**Score:**	11.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	21.3
Database Date:	2015-11-30	**pI:**	9.6
		Sequence Coverage [%]:	7.9
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MEHKDDDDDD VSFAKWMSSF WGHSWREEDQ RGLRERHRLQ ATSHRKTSLP CPLPVLPRIP SSDCHPRRHS HEDQEFRCRS
        90        100        110        120        130        140        150        160
HVRDYRKYSE DGSFKEPLES KGRSHSKIEK FSESFERQLC FRTKRSASLG PESRKERNER ECLRMEIKSR KKVEEERSSR
       170        180
KEEHGEAHMA PLFEKGPE
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
91	1	808.3744	-4.41	2	30.5	11.4	1	88-101	K.YSEDGSFKEPLESK.G	

Detailed Protein Report

Protein 1132: **PREDICTED: persulfide dioxygenase ETHE1, mitochondrial isoform X3 [Homo sapiens]**

Accession: gi|530416070
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 11.4
MW [kDa]: 14.4
pI: 6.0
Sequence Coverage [%]: 11.5
No. of unique Peptides: 1

Quantitation

MD:MU **Median:** 0.60 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MLALETRASP GHTPGCVTFV LNDHSMAFTG DALLIRGCGR TDFQQGCAKT LYHSVHEKIF TLPGDCLIYP AHDYHGFTVS
        90        100        110        120        130        140
TVEEERTLNP RLTLSCEEFV KIMGNLNLPK PQQIDFAVPA NMRCGVQTPT A
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
197	1	903.9342	-44.66	2	32.2	11.4	1	87-101	R.TLNPRLTLSCEEFVK.I	Carbamidomethyl: 10	MD:MU	0.60

BRUKER

Detailed Protein Report

Protein 1133: amiloride-sensitive sodium channel subunit beta [Homo sapiens]

Accession:	gi|124301196	**Score:**	11.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	72.6
Database Date:	2015-11-30	**pI:**	5.9
		Sequence Coverage [%]:	1.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MHVKKYLLKG	LHRLQKGPGY	TYKELLVWYC	DNTNTHGPKR	IICEGPKKKA	MWFLLTLLFA	ALVCWQWGIF	IRTYLSWEVS
90	100	110	120	130	140	150	160
VSLSVGFKTM	DFPAVTICNA	SPFKYSKIKH	LLKDLDELME	AVLERILAPE	LSHANATRNL	NFSIWNHTPL	VLIDERNPHH
170	180	190	200	210	220	230	240
PMVLDLFGDN	HNGLTSSSAS	EKICNAHGCK	MAMRLCSLNR	TQCTFRNFTS	ATQALTEWYI	LQATNIFAQV	PQQELVEMSY
250	260	270	280	290	300	310	320
PGEQMILACL	FGAEPCNYRN	FTSIFYPHYG	NCYIFNWGMT	EKALPSANPG	TEFGLKLILD	IGQEDYVPFL	ASTAGVRLML
330	340	350	360	370	380	390	400
HEQRSYPFIR	DEGIYAMSGT	ETSIGVLVDK	LQRMGEPYSP	CTVNGSEVPV	QNFYSDYNTT	YSIQACLRSC	FQDHMIRNCN
410	420	430	440	450	460	470	480
CGHYLYPLPR	GEKYCNNRDF	PDWAHCYSDL	QMSVAQRETC	IGMCKESCND	TQYKMTISMA	DWPSEASEDW	IFHVLSQERD
490	500	510	520	530	540	550	560
QSTNITLSRK	GIVKLNIYFQ	EFNYRTIEES	AANNIVWLLS	NLGGQFGFWM	GGSVLCLIEF	GEIIIDFVWI	TIIKLVALAK
570	580	590	600	610	620	630	640
SLRQRRAQAS	YAGPPPTVAE	LVEAHTNFGF	QPDTAPRSPN	TGPYPSEQAL	PIPGTPPPNY	DSLRLQPLDV	IESDSEGDAI
650							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1807	1	568.7511	-2.30	2	52.6	11.4	0	389-397	R.SCFQDHMIR.N	

Detailed Protein Report

Protein 1134: dnaJ homolog subfamily C member 14 [Homo sapiens]

Accession:	gi|119943096	**Score:**	11.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	78.5
Database Date:	2015-11-30	**pI:**	9.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.9
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 1.03 **CV:** 0.00 % **No. of Peptides:** 1

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	
1599	1	820.8799	15.70	2	49.7	11.4	2	552-564	R.EPKSARYCAECNR.L	Carbamidomethyl: 8, 11	MD:MU	1.03

Detailed Protein Report

Protein 1135: PREDICTED: multiple epidermal growth factor-like domains protein 6 isoform X4 [Homo sapiens]

Accession: gi|578798522
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 11.4
MW [kDa]: 135.9
pI: 5.9
Sequence Coverage [%]: 1.4
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MGASRDRGLA	ALWCLGLLGG	LARVAGTHYR	YLWRGCYPCH	LGQAGYPVSA	GDQRPDVDEC	RTHNGGCQHR	CVNTPGSYLC
90	100	110	120	130	140	150	160
ECKPGFRLHT	DSRTCLAINS	CALGNGGCQH	HCVQLTITRH	RCQCRPGFQL	QEDGRHCVRR	SPCANRNGSC	MHRCQVVRGL
170	180	190	200	210	220	230	240
ARCECHVGYQ	LAADGKACED	VDECAAGLAQ	CAHGCLNTQG	SFKCVCHAGY	ELGADGRQCY	RIEMEIVNSC	EANNGGCSHG
250	260	270	280	290	300	310	320
CSHTSAGPLC	TCPRGYELDT	DQRTCIDVDD	CADSPCCQQV	CTNNPGGYEC	GCYAGYRLSA	DGCGCEDVDE	CASSRGGCEH
330	340	350	360	370	380	390	400
HCTNLAGSFQ	CSCEAGYRLH	EDRRGCSPLE	EPMVDLDGEL	PFVRPLPHIA	VLQDELPQLF	QDDDVGADEE	EAELRGEHTL
410	420	430	440	450	460	470	480
TEKFVCLDDS	FGHDCSLTCD	DCRNGGTCLL	GLDGCDCPEG	WTGLICNETC	PPDTFGKNCS	FSCSCQNGGT	CDSVTGACRC
490	500	510	520	530	540	550	560
PPGVSGTNCE	DGCPKGYYGK	HCRKKCNCAN	RGRCHRLYGA	CLCDPGLYGR	FCHLTCPPWA	FGPGCSEECQ	CVQPHTQSCD
570	580	590	600	610	620	630	640
KRDGSCSCKA	GFRGERCQAE	CELGYFGPGC	WQACTCPVGV	ACDSVSGECG	KRCPAGFQGE	DCGQECPVGT	FGVNCSSSCS
650	660	670	680	690	700	710	720
CGGAPCHGVT	GQCRCPPGRT	GEDCEAECPQ	GHFGPGCEQR	CQCQHGAACD	HVSGACTCPA	GWRGTFCEHA	CPAGFFGLDC
730	740	750	760	770	780	790	800
RSACNCTAGA	ACDAVNGSCL	CPAGRRGPRC	AETCPAHTYG	HNCSQACACF	NGASCDPVHG	QCHCAPGWMG	PSCLQACPAG
810	820	830	840	850	860	870	880
LYGDNCRHSC	LCQNGGTCDP	VSGHCACPEG	WAGLACEKEC	LPRDVRAGCR	HSGGCLNGGL	CDPHTGRCLC	PAGWTGDKCQ
890	900	910	920	930	940	950	960
SPCLRGWFGE	ACAQRCSCPP	GAACHHVTGA	CRCPPGFTGS	GCEQACPPGS	FGEDCAQMCQ	CPGENPACHP	ATGTCSCAAG
970	980	990	1000	1010	1020	1030	1040
YHGPSCQQRC	PPGRYGPGCE	QLCGCLNGGS	CDAATGACRC	PTGFLGTDCN	LTCPQGRFGP	NCTHVCGCGQ	GAACDPVTGT
1050	1060	1070	1080	1090	1100	1110	1120
CLCPPGRAGV	RCERGCPQNR	FGVGCEHTCS	CRNGGLCHAS	NGSCSCGLGW	TGRHCELACP	PGRYGAACHL	ECSCHNNSTC
1130	1140	1150	1160	1170	1180	1190	1200
EPATGTCRCG	PGFYGQACEH	PCPPGFHGAG	CQGLCWCQHG	APCDPISGRC	LCPAGFHGHF	CERGCEPGSF	GEGCHQRCDC
1210	1220	1230	1240	1250	1260	1270	1280
DGGAPCDPVT	GLCLCPPGRS	GATCNLDCRR	GQFGPSCTLH	CDCGGGADCD	PVSGQCHCVD	GYMGPTCREG	GPLRLPENPS
1290	1300	1310					
LAQGSAGTLP	ASSRPTSRSG	GPARH					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1769	1	682.2402	-68.51	3	52.1	11.4	0	704-721	R.GTFCEHACPAGFFGLDCR.S	Carbamidomethyl: 4, 17

Detailed Protein Report

Protein 1136: putative protein FAM47C [Homo sapiens]

Accession:	gi|61966919	**Score:**	11.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	115.3
Database Date:	2015-11-30	**pI:**	6.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGDQRPQDRP	SSPGMDSTPW	YCDKPPSKYF	AKRKHRRLRF	PPVDTQNWVF	VTEGMDDFRY	GCQSPEDTLV	CRRDEFLLPK
90	100	110	120	130	140	150	160
ISLRGPQADP	KSRKKKLLKK	AALFSKLSPA	QPARKAFVEE	VEAQLMTKHP	LAMYPNLGED	MPPDLLLQVL	KPLDPERKLE
170	180	190	200	210	220	230	240
DAGSCEGQEK	TTDEPTEPGK	YPCGEFSPRP	PETRVSCLPP	EPPKTPVSSL	RPEPPETGVS	HLRPQPPKTQ	VSSLHLEPPE
250	260	270	280	290	300	310	320
TGVSHLRPEP	PKTQVSSLHL	EPPETGVSHL	YLEPPGTGVS	HLCPEPPKTR	VSHLHREPPE	TGVPDLCLEP	PKSRVSHLRP
330	340	350	360	370	380	390	400
EPSETGVSHL	HPEPPKTLVS	SLHPEPPETG	VSHLCPEPPE	TRVSPLRQLP	PEAGVSHLCP	EPPKTRVPPL	RPETPKNGVS
410	420	430	440	450	460	470	480
PLFPEPPKTR	ISNLRSEPPK	IGVSHLCLEP	PKTRGSHLRP	EPPETGVSHL	RPEPPKTRVS	SLHLEPPETG	VSHLCPEPPE
490	500	510	520	530	540	550	560
KDVSHLRPEP	PDTGVSHLCP	EPPKTRVSHL	RPEPSETGVS	HLRPEPPKIL	VSSLHQAPPE	SSVSHLRPEP	PETGVSHLRP
570	580	590	600	610	620	630	640
EPPKTRMYSL	RPEPPDTGVS	HLCPEPPKTR	VSSLPPEPPE	TGVSHLCPEP	PETRVSHLRP	EPPETGVSHL	RPEPPKTRMY
650	660	670	680	690	700	710	720
SLRPEPPNTG	VSHLCPEPPK	TRVSSLPPEP	PETGVSHLCP	EPPETRVSHL	RPEPPETGVS	RLHPEPPKTR	VSSLHAEPPE
730	740	750	760	770	780	790	800
SRVSHLCPEP	PETGVSHLRP	EPPKPRVSSL	RPEPLETRVS	HLRPEPPETG	VSHLHPELPK	PRVSSLHLEP	PKTRRVSSLR
810	820	830	840	850	860	870	880
LEPPKTGRVS	SLCPEPTKTG	ASHLKELFQE	GTSSTMECVS	DSLQRRHTSR	KLRDFKWAGD	LGVNEESISS	LFDFTPECRA
890	900	910	920	930	940	950	960
TYQDQKNKKA	NECSSGLKYS	MELDEMDEVK	FFSQEKDLDG	KIQNAPNSHS	AQHVKMGYGA	WYLKPKLGKK	LRSDEPLIDP
970	980	990	1000	1010	1020	1030	1040
KLVLEKPDEP	DILDGLYGPI	AFKDFILSKG	YEMPGIIQRL	FARRGWTYDS	VKTPIQRAMQ	VYKYKEDVTD	ASEED

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2436	1	822.6843	-57.00	3	60.8	11.4	0	567-588	R.MYSLRPEPPDTGVSHLCPEPPK.T	Oxidation: 1

Detailed Protein Report

Protein 1137: PREDICTED: transmembrane protein 129 isoform X1 [Homo sapiens]

Accession:	gi|530376215	**Score:**	11.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	32.5
Database Date:	2015-11-30	**pI:**	9.9
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	9.0
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578808304	refseq_human (refseq_human_20140103.fasta)	PREDICTED: transmembrane protein 129 isoform X3 [Homo sapiens]
gi|530376217	refseq_human (refseq_human_20140103.fasta)	PREDICTED: transmembrane protein 129 isoform X2 [Homo sapiens]

10	20	30	40	50	60	70	80
MCLAASEKRL	HALSQAPEAW	RLFLLLAVTL	PSIACILIYY	WSRDRWACHP	LARTLALYAL	PQSGWQAVAS	SVNTEFRRID
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
KFATGAPGAR	VIVTDTWVMK	VTTYRVHVAQ	QQDVHLTVTE	SRQHELSPDS	NLPVQLLTIR	VASTNPAVQA	FDIWLNSTEY
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
GELCEKLRAP	IRRAAHVVIH	QSLGDLFLET	FASLVEVNPA	YSVPSSQELE	ACIGCMQTRA	SVKLVKTCQE	AATGECQQCY
250	**260**	**270**	**280**	**290**			
CRPMWCLTCM	GKWFASRQDP	LRPDTWLASR	VPCPTCRARF	CILDVCTVR			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2066	1	1030.7798	45.77	3	56.0	11.4	0	227-252	K.TCQEAATGECQQCYCRPMWCLTCMGK.W	Carbamidomethyl: 10, 23; Oxidation: 18, 24

Detailed Protein Report

Protein 1138: PREDICTED: cell death activator CIDE-A isoform X1 [Homo sapiens]

Accession:	gi|578832070	**Score:**	11.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	13.7
Database Date:	2015-11-30	**pI:**	10.4
		Sequence Coverage [%]:	10.0
		No. of unique Peptides:	1

```
         10         20         30         40         50         60         70         80
MILEKGQKWM PGSQHVPTCS PPKRSGIARV TFDLYRLNPK DFIGCLNVKA TMYEMYSVSY DIRCTGLKGL LRSLLRFLSY
         90        100        110        120        130
SAQVTGQFLI YLGTYMLRVL DDKEERPSLR SQAKGRFTCG
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1540	1	699.3756	-6.91	2	48.9	11.4	1	25-36	R.SGIARVTFDLYR.L	

Detailed Protein Report

Protein 1139: ephrin type-A receptor 3 isoform b precursor [Homo sapiens]

Accession:	gi|32967314	**Score:**	11.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	60.9
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
MDCQLSILLL LSCSVLDSFG ELIPQPSNEV NLLDSKTIQG ELGWISYPSH GWEEISGVDE HYTPIRTYQV CNVMDHSQNN
        90        100        110        120        130        140        150        160
WLRTNWVPRN SAQKIYVELK FTLRDCNSIP LVLGTCKETF NLYYMESDDD HGVKFREHQF TKIDTIAADE SFTQMDLGDR
       170        180        190        200        210        220        230        240
ILKLNTEIRE VGPVNKKGFY LAFQDVGACV ALVSVRVYFK KCPFTVKNLA MFPDTVPMDS QSLVEVRGSC VNNSKEEDPP
       250        260        270        280        290        300        310        320
RMYCSTEGEW LVPIGKCSCN AGYEERGFMC QACRPGFYKA LDGNMKCAKC PPHSSTQEDG SMNCRCENNY FRADKDPPSM
       330        340        350        360        370        380        390        400
ACTRPPSSPR NVISNINETS VILDWSWPLD TGGRKDVTFN IICKKCGWNI KQCEPCSPNV RFLPRQFGLT NTTVTVTDLL
       410        420        430        440        450        460        470        480
AHTNYTFEID AVNGVSELSS PPRQFAAVSI TTNQAAPSPV LTIKKDRTSR NSISLSWQEP EHPNGIILDY EVKYYEKQEQ
       490        500        510        520        530        540
ETSYTILRAR GTNVTISSLK PDTIYVFQIR ARTAAGYGTN SRKFEFETSP DCMYYFNAV
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1965	1	856.8267	-91.14	2	54.7	11.4	0	242-256	R.MYCSTEGEWLVPIGK.C	

Detailed Protein Report

Protein 1140: spindle and kinetochore-associated protein 3 isoform 2 [Homo sapiens]

Accession:	gi|260763912	**Score:**	11.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	43.9
Database Date:	2015-11-30	**pI:**	4.7
		Sequence Coverage [%]:	4.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDPIRSFCGK	LRSLASTLDC	ETARLQRALD	GEESDFEDYP	MRILYDLHSE	VQTLKDDVNI	LLDKARLENQ	EGIDFIKATK
90	100	110	120	130	140	150	160
VLMEKNSMDI	MKIREYFQKY	GYSPRVKKNS	VHEQEAINSD	PELSNCENFQ	KTDVKDDLSD	PPVASSCISE	KSPRSPQLSD
170	180	190	200	210	220	230	240
FGLERYIVSQ	VLPNPPQAVN	NYKEEPVIVT	PPTKQSLVKV	LKTPKCALKM	DDFECVTPKL	EHFGISEYTM	CLNEDYTMGL
250	260	270	280	290	300	310	320
KNARNNKSEE	AIDTESRLND	NVFATPSPII	QQLEKSDAEY	TNSPLVPTFC	TPGLKIPSTK	NSIALVSTNY	PLSKTNSSSN
330	340	350	360	370	380	390	
DLEVEDRTSL	VLNSDTCFEN	LTDPSSPTIS	SYENLLRTPT	PPEVTKIPED	ILQKFQWIYP	TQKLNKMR	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1798	1	716.2952	-131.52	3	52.3	11.4	1	367-383	K.IPEDILQKFQWIYPTQK.L	

Detailed Protein Report

Protein 1141: PREDICTED: vezatin isoform X14 [Homo sapiens]

Accession: gi|578823956
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 11.4
MW [kDa]: 65.4
pI: 6.3
Sequence Coverage [%]: 2.1
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MLKEWAIKQG	ILLKVAETIK	SWIFFSQCNK	KDDLLHKLDI	GFRLDSLHTI	LQQEVLLQED	VELIELLDPS	ILSAGQSQQQ
90	100	110	120	130	140	150	160
ENGHLPTLCS	LATPNIWDLS	MLFAFISLLV	MLPTWWIVSS	WLVWGVILFV	YLVIRALRLW	RTAKLQVTLK	KYSVHLEDMA
170	180	190	200	210	220	230	240
TNSRAFTNLV	RKALRLIQET	EVISRGFTLV	SAACPFNKAG	QHPSQHLIGL	RKAVYRTLRA	NFQAARLATL	YMLKNYPLNS
250	260	270	280	290	300	310	320
ESDNVTNYIC	VVPFKELGLG	LSEEQISEEE	AHNFTDGFSL	PALKVLFQLW	VAQSSEFFRR	LALLLSTANS	PPGPLLTPAL
330	340	350	360	370	380	390	400
LPHRILSDVT	QGLPHAHSAC	LEELKRSYEF	YRYFETQHQS	VPQCLSKTQQ	KSRELNNVHT	AVRSLQLHLK	ALLNEVIILE
410	420	430	440	450	460	470	480
DELEKLVCTK	ETQELVSEAY	PILEQKLKLI	QPHVQASNNC	WEEAISQVDK	LLRRNTDKKG	KPEIACENPH	CTVVPLKQPT
490	500	510	520	530	540	550	560
LHIADKDPIP	EEQELEAYVD	DIDIDSDFRK	DDFYYLSQED	KERQKREHEE	SKRVLQELKS	VLGFKASEAE	RQKWKQLLFS
570							
DHGVKSAWN							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1627	1	698.3584	-25.47	2	50.2	11.4	1	372-383	K.SRELNNVHTAVR.S	

Detailed Protein Report

Protein 1142: DEP domain-containing protein 7 isoform 2 [Homo sapiens]

Accession:	gi|116256344	**Score:**	11.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	57.7
Database Date:	2015-11-30	**pI:**	7.8
		Sequence Coverage [%]:	2.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MRGLCEFYWQ	EFGIKGFSVA	QKPFGATYVW	SSIINTLQTQ	VEVKKRRHRL	KRHNDCFVGS	EAVDVIFSHL	IQNKYFGDVD
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
IPRAKVVRVC	QALMDYKVFE	AVPTKVFGKD	KKPTFEDSSC	SLYRFTTIPN	QDSQLGKENK	LYSPARYADA	LFKSSDIRSA
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
SLEDLWENLS	LKPANSPHVN	ISATLSPQVI	NEVWQEETIG	RLLQLVDLPL	LDSLLKQQEA	VPKIPQPKRQ	STMVNSSNYL
250	**260**	**270**	**280**	**290**	**300**	**310**	**320**
DRGILKAYSD	SQEDEWLSAA	IDCLEYLPDQ	MVVEISRSFP	EQPDRTDLVK	ELLFDAIGRY	YSSREPLLNH	LSDVHNGIAE
330	**340**	**350**	**360**	**370**	**380**	**390**	**400**
LLVNGKTEIA	LEATQLLLKL	LDFQNREEFR	RLLYFMAVAA	NPSEFKLQKE	SDNRMVVKRI	FSKAIVDNKN	LSKGKTDLLV
410	**420**	**430**	**440**	**450**	**460**	**470**	**480**
LFLMDHQKDV	FKIPGTLHKI	VSVKLMAIQN	GRDPNRDAGY	IYCQRIDQRD	YSNNTEKTTK	DELLNLLKTL	DEDSKLSAKE
490	**500**	**510**					
KKKLLGQFYK	CHPDIFIEHF	GD					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1968	1	766.2504	-183.77	2	54.7	11.4	1	278-290	R.SFPEQPDRTDLVK.E	

Detailed Protein Report

Protein 1143: PREDICTED: coiled-coil domain-containing protein 9 isoform X4 [Homo sapiens]

Accession:	gi|578834259	**Score:**	11.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	56.8
Database Date:	2015-11-30	**pI:**	5.4
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.4
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 1.34 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MAATLDLKSK	EEKDAELDKR	IEALRRKNEA	LIRRYQEIEE	DRKKAELEGV	AVTAPRKGRS	VEKENVAVES	EKNLGPSRRS
90	100	110	120	130	140	150	160
PGTPRPPGAS	KGGRTPPQQG	GRAGMGRASR	SWEGSPGEQP	RGGGAGGRGR	RGRGRGSPHL	SGAGDTSISD	RKSKEWEERR
170	180	190	200	210	220	230	240
RQNIEKMNEE	MEKIAEYERN	QREGVLEPNP	VRNFLDDPRR	RSGPLEESER	DRREESRRHG	RNWGGPDFER	VRCGLEHERQ
250	260	270	280	290	300	310	320
GRRAGLGSAG	DMTLSMTGRE	RSEYLRWKQE	REKIDQERLQ	RHRKPTGQWR	REWDAEKTDG	MFKDGPVPAH	EPSHRYDDQA
330	340	350	360	370	380	390	400
WARPPKPPTF	GEFLSQHKAE	ASSRRRRKSS	RPQAKAAPRA	YSDHDDRWET	KEGAASPAPE	TPQPTSPETS	PKETPMQPPE
410	420	430	440	450	460	470	480
IPAPAHRPPE	DEGEENEGEE	DEEWEDISED	EEEEEIEVEE	GGGQSAPAFP	ESGPSLRGTQ	EAEEEGSEAT	PEAGPEGQET
490	500	510					
AEITDFQRVR	FCKVVAAPPL	PGAAR					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
795	1	848.9510	49.56	2	39.5	11.4	1	243-259	R.RAGLGSAGDMTLSMTGR.E	Oxidation: 14	MD:MU 1.34

Detailed Protein Report

Protein 1144: zinc finger MYM-type protein 3 isoform 2 [Homo sapiens]

Accession:	gi|283837894	**Score:**	11.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	151.0
Database Date:	2015-11-30	**pI:**	6.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	0.8
		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
758	1	647.6599	-226.81	2	38.8	11.4	0	820-830	K.AAMCKPLMQNR.G	Oxidation: 3, 8

Detailed Protein Report

Protein 1145: deoxyribonuclease-1-like 1 precursor [Homo sapiens]

Accession:	gi|5803007	**Score:**	11.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	33.9
Database Date:	2015-11-30	**pI:**	5.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	6.0
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530430464	refseq_human (refseq_human_20140103.fasta)	PREDICTED: deoxyribonuclease-1-like 1 isoform X1 [Homo sapiens]
gi|58430946	refseq_human (refseq_human_20140103.fasta)	deoxyribonuclease-1-like 1 precursor [Homo sapiens]
gi|58430944	refseq_human (refseq_human_20140103.fasta)	deoxyribonuclease-1-like 1 precursor [Homo sapiens]
gi|58430942	refseq_human (refseq_human_20140103.fasta)	deoxyribonuclease-1-like 1 precursor [Homo sapiens]

10	20	30	40	50	60	70	80
MHYPTALLFL	ILANGAQAFR	ICAFNAQRLT	LAKVAREQVM	DTLVRILARC	DIMVLQEVVD	SSGSAIPLLL	RELNRFDGSG
90	100	110	120	130	140	150	160
PYSTLSSPQL	GRSTYMETYV	YFYRSHKTQV	LSSYVYNDED	DVFAREPFVA	QFSLPSNVLP	SLVLVPLHTT	PKAVEKELNA
170	180	190	200	210	220	230	240
LYDVFLEVSQ	HWQSKDVILL	GDFNADCASL	TKKRLDKLEL	RTEPGFHWVI	ADGEDTTVRA	STHCTYDRVV	LHGERCRSLL
250	260	270	280	290	300	310	
HTAAAFDFPT	SFQLTEEEAL	NISDHYPVEV	ELKLSQAHSV	QPLSLTVLLL	LSLLSPQLCP	AA	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
35	1	1080.5173	4.02	2	30.1	11.3	2	220-237	R.ASTHCTYDRVVLHGERCR.S	Carbamidomethyl: 5

Detailed Protein Report

Protein 1146: putative DNA repair and recombination protein RAD26-like [Homo sapiens]

Accession:	gi|58219008	**Score:**	11.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	81.0
Database Date:	2015-11-30	**pI:**	10.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.4
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MQPGSAPPPG RMDPSAPQPR AETSGKDIWH PGERCLAPSP DNGKLCEASI KSITVDENGK SFAVVLYADF QERKIPLKQL
        90        100        110        120        130        140        150        160
QEVKFVKDCP RNLIFDDEDL EKPYFPNRKF PSSSVAFKLS DNGDSIPYTI NRYLRDYQRE GTRFLYGHYI HGGGCILGDD
       170        180        190        200        210        220        230        240
MGLGKTVQVI SFLAAVLHKK GTREDIENNM PEFLLRSMKK EPLSSTAKKM FLIVAPLSVL YNWKDELDTW GYFRVTVLHG
       250        260        270        280        290        300        310        320
NRKDNELIRV KQRKCEIALT TYETLRLCLD ELNSLEWSAV IVDEAHRIKN PKARVTEVMK ALKCNVRIGL TGTILQNNMK
       330        340        350        360        370        380        390        400
ELWCVMDWAV PGLLGSGTYF KKQFSDPVEH GQRHTATKRE LATGRKAMQR LAKKMSGWFL RRTKTLIKDQ LPKKEDRMVY
       410        420        430        440        450        460        470        480
CSLTDFQKAV YQTVLETEDV TLILQSSEPC TCRSGQKRRN CCYKTNSHGE TVKTLYLSYL TVLQKVANHV ALLQAASTSK
       490        500        510        520        530        540        550        560
QQETLIKRIC DQVFSRFPDF VQKSKDAAFE TLSDPKYSGK MKVLQQLLNH CRKNRDKVLL FSFSTKLLDV LQQYCMASGL
       570        580        590        600        610        620        630        640
DYRRLDGSTK SEERLKIVKE FNSTQDVNIC LVSTMAGGLG LNFVGANVVV LFDPTWNPAN DLQAIDRAYR IGQCRDVKVL
       650        660        670        680        690        700        710        720
RLISLGTVEE IMYLRQIYKQ QLHCVVVGSE NAKRYFEAVQ GSKEHQGELF GIHNLFKFRS QGSCLTKDIL EV
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1853	1	682.2664	-96.93	3	53.2	11.3	0	547-563	K.LLDVLQQYCMASGLDYR.R	Carbamidomethyl: 9

Detailed Protein Report

Protein 1147: tripartite motif-containing protein 46 isoform 6 [Homo sapiens]

Accession: gi|538260579
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 11.3
MW [kDa]: 61.7
pI: 10.0
Sequence Coverage [%]: 3.3
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MAEGEDMQTF	TSIMDALVRI	STSMKNMEKE	LLCPVCQEMY	KQPLVLPCTH	NVCQACAREV	LGQQGYIGHG	GDPSSEPTSP
90	100	110	120	130	140	150	160
ASTPSTRSPR	LSRRTLPKPD	RLDRLLKSGF	GTYPGRKRGA	LHPQVIMFPC	PACQGDVELG	ERGLAGLFRN	LTLERVVERY
170	180	190	200	210	220	230	240
RQSVSVGGAI	LCQLCKPPPL	EATKGCTECR	ATFCNECFKL	FHPWGTQKAQ	HEPTLPTLSF	RPKGLMCPDH	KEEVTHYCKT
250	260	270	280	290	300	310	320
CQRLVCQLCR	VRRTHSGHKI	TPVLSAYQAL	KDKLTKSLTY	ILGNQDTVQT	QICELEEAVR	HTEVSGQQAK	EEVSQLVRGL
330	340	350	360	370	380	390	400
GAVLEEKRAS	LLQAIEECQQ	ERLARLSAQI	QEHRSLLDGS	GLVGYAQEVL	KETDQPCFVQ	AAKQLHNRIA	RATEALQTFR
410	420	430	440	450	460	470	480
PAASSSFRHC	QLDVGREMKL	LTELNFLRVP	EAPVIDTQRT	FAYDQIFLCW	RLPPHSPPAW	HYTVEFRRTD	VPAQPGPTRW
490	500	510	520	530	540	550	560
QRREEVRGTS	ALLENPDTGS	VYVLRVRGCN	KAGYGEYSED	VHLHTPPAPG	IQNLARRGGA	CLQFQLLGRL	R

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1266	1	1023.3521	-106.79	2	45.5	11.3	0	2-19	M.AEGEDMQTFTSIMDALVR.I	Oxidation: 6, 13

Detailed Protein Report

Protein 1148: methylthioribulose-1-phosphate dehydratase [Homo sapiens]

Accession:	gi|166235186	**Score:**	11.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	27.1
Database Date:	2015-11-30	**pI:**	6.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSGCDAREGD	CCSRRCGAQD	KEHPRYLIPE	LCKQFYHLGW	VTGTGGGISL	KHGDEIYIAP	SGVQKERIQP	EDMFVCDINE
90	100	110	120	130	140	150	160
KDISGPSPSK	KLKKSQCTPL	FMNAYTMRGA	GAVIHTHSKA	AVMATLLFPG	REFKITHQEM	IKGIKKCTSG	GYYRYDDMLV
170	180	190	200	210	220	230	240
VPIIENTPEE	KDLKDRMAHA	MNEYPDSCAV	LVRRHGVYVW	GETWEKAKTM	CECYDYLFDI	AVSMKKVGLD	PSQLPVGENG
250							
IV							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2673	1	826.1063	-212.47	1	64.6	11.3	0	8-14	R.EGDCCSR.R	Carbamidomethyl: 4

Detailed Protein Report

Protein 1149: putative tyrosine-protein phosphatase auxilin isoform 3 [Homo sapiens]

Accession:	gi|379030617	**Score:**	11.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	98.6
Database Date:	2015-11-30	**pI:**	7.1
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEPSYGGGLF	DMVKGGAGRL	FSNLKDNLKD	TLKDTSSRVI	QSVTSYTKGD	LDFTYVTSRI	IVMSFPLDNV	DIGFRNQVDD
90	100	110	120	130	140	150	160
IRSFLDSRHL	DHYTVYNLSP	KSYRTAKFHS	RVSECSWPIR	QAPSLHNLFA	VCRNMYNWLL	QNPKNVCVVH	CLDGRAASSI
170	180	190	200	210	220	230	240
LVGAMFIFCN	LYSTPGPAIR	LLYAKRPGIG	LSPSHRRYLG	YMCDLLADKP	YRPHFKPLTI	KSITVSPIPF	FNKQRNGCRP
250	260	270	280	290	300	310	320
YCDVLIGETK	IYSTCTDFER	MKEYRVQDGK	IFIPLNITVQ	GDVVVSMYHL	RSTIGSRLQA	KVTNTQIFQL	QFHTGFIPLD
330	340	350	360	370	380	390	400
TTVLKFTKPE	LDACDVPEKY	PQLFQVTLDV	ELQPHDKVID	LTPPWEHYCT	KDVNPSILFS	SHQEHQDTLA	LGGQAPIDIP
410	420	430	440	450	460	470	480
PDNPRHYGQS	GFFASLCWQD	QKSEKSFCEE	DHAALVNQES	EQSDDELLTL	SSPHGNANGD	KPHGVKKPSK	KQQEPAAPPP
490	500	510	520	530	540	550	560
PEDVDLLGLE	GSAMSNSFSP	PAAPPTNSEL	LSDLFGGGGA	AGPTQAGQSG	VEDVFHPSGP	ASTQSTPRRS	ATSTSASPTL
570	580	590	600	610	620	630	640
RVGEGATFDP	FGAPSKPSGQ	DLLGSFLNTS	SASSDPFLQP	TRSPSPTVHA	SSTPAVNIQP	DVSGGWDWHA	KPGGFGMGSK
650	660	670	680	690	700	710	720
SAATSPTGSS	HGTPTHQSKP	QTLDPFADLG	TLGSSSFASK	PTTPTGLGGG	FPPLSSPQKA	SPQPMGGGWQ	QGGAYNWQQP
730	740	750	760	770	780	790	800
QPKPQPSMPH	SSPQNRPNYN	VSFSAMPGGQ	NERGKGSSNL	EGKQKAADFE	DLLSGQGFNA	HKDKKGPRTI	AEMRKEEMAK
810	820	830	840	850	860	870	880
EMDPEKLKIL	EWIEGKERNI	RALLSTMHTV	LWAGETKWKP	VGMADLVTPE	QVKKVYRKAV	LVVHPDKATG	QPYEQYAKMI
890	900	910					
FMELNDAWSE	FENQGQKPLY						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1549	1	1052.1533	-35.54	3	49.1	11.3	2	108-133	K.FHSRVSECSWPIRQAPSLHNLFAVCR.N	Carbamidomethyl: 8, 25

Detailed Protein Report

Protein 1150: PREDICTED: phosphatidylinositide phosphatase SAC2 isoform X2 [Homo sapiens]

Accession:	gi|578819140	**Score:**	11.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	74.2
Database Date:	2015-11-30	**pI:**	8.5
		Sequence Coverage [%]:	2.0
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 1.10 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MELFQAKDHY ILQQGERALW CSRRDGGLQL RPATDLLLAW NPICLGLVEG VIGKIQLHSD LPWWLILIRQ KALVGKLPGD
        90        100        110        120        130        140        150        160
HEVCKVTKIA VLSLSEMEPQ DLELELCKKH HFGINKPEKI IPSPDDSKFL LKTFTHIKSN VSAPNKKKVK ESKEKEKLER
       170        180        190        200        210        220        230        240
RLLEELLKMF MDSESFYYSL TYDLTNSVQR QSTGERDGRP LWQKVDDRFF WNKYMIQDLT EIGTPDVDFW IIPMIQGFVQ
       250        260        270        280        290        300        310        320
IEELVVNYTE SSDDEKSSPE TPPQESTCVD DIHPRFLVAL ISRRSRHRAG MRYKRRGVDK NGNVANYVET EQLIHVHNHT
       330        340        350        360        370        380        390        400
LSFVQTRGSV PVFWSQVGYR YNPRPRLDRS EKETVAYFCA HFEEQLNIYK KQVIINLVDQ AGREKIIGDA YLKQVLLFNN
       410        420        430        440        450        460        470        480
SHLTYVSFDF HEHCRGMKFE NVQTLTDAIY DIILDMKWCW VDEAGVICKQ EGIFRVNCMD CLDRTNVVQA AIARVVMEQQ
       490        500        510        520        530        540        550        560
LKKLGVMPPE QPLPVKCNRI YQIMWANNGD SISRQYAGTA ALKGDFTRTG ERKLAGVMKD GVNSANRYYL NRFKDAYRQA
       570        580        590        600        610        620        630        640
VIDLMQGIPV TEDLYSIFTK EKEHEALHKE NQRSHQELIS QLLQSYMKLL LPDDEKFHGG WALIDCDPRK PPTLSTAGKR
       650
L
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1347	1	727.4089	-26.13	2	46.5	11.3	1	371-383	K.KQVIINLVDQAGR.E		MD:MU 1.10

Detailed Protein Report

Protein 1151: mitogen-activated protein kinase kinase kinase MLK4 [Homo sapiens]

Accession:	gi|155723000	**Score:**	11.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	113.9
Database Date:	2015-11-30	**pI:**	9.9
		Sequence Coverage [%]:	1.7
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 1.30 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MALRGAAGAT	DTPVSSAGGA	PGGSASSSST	SSGGSASAGA	GLWAALYDYE	ARGEDELSLR	RGQLVEVLSQ	DAAVSGDEGW
90	100	110	120	130	140	150	160
WAGQVQRRLG	IFPANYVAPC	RPAASPAPPP	SRPSSPVHVA	FERLELKELI	GAGGFGQVYR	ATWQGQEVAV	KAARQDPEQD
170	180	190	200	210	220	230	240
AAAAAESVRR	EARLFAMLRH	PNIIELRGVC	LQQPHLCLVL	EFARGGALNR	ALAAANAAPD	PRAPGPRRAR	RIPPHVLVNW
250	260	270	280	290	300	310	320
AVQIARGMLY	LHEEAFVPIL	HRDLKSSNIL	LLEKIEHDDI	CNKTLKITDF	GLAREWHRTT	KMSTAGTYAW	MAPEVIKSSL
330	340	350	360	370	380	390	400
FSKGSDIWSY	GVLLWELLTG	EVPYRGIDGL	AVAYGVAVNK	LTLPIPSTCP	EPFAKLMKEC	WQQDPHIRPS	FALILEQLTA
410	420	430	440	450	460	470	480
IEGAVMTEMP	QESFHSMQDD	WKLEIQQMFD	ELRTKEKELR	SREEELTRAA	LQQKSQEELL	KRREQQLAER	EIDVLERELN
490	500	510	520	530	540	550	560
ILIFQLNQEK	PKVKKRKGKF	KRSRLKLKDG	HRISLPSDFQ	HKITVQASPN	LDKRRSLNSS	SSSPPSSPTM	MPRLRAIQLT
570	580	590	600	610	620	630	640
SDESNKTWGR	NTVFRQEEFE	DVKRNFKKKG	CTWGPNSIQM	KDRTDCKERI	RPLSDGNSPW	STILIKNQKT	MPLASLFVDQ
650	660	670	680	690	700	710	720
PGSCEEPKLS	PDGLEHRKPK	QIKLPSQAYI	DLPLGKDAQR	ENPAEAESWE	EAASANAATV	SIEMTPTNSL	SRSPQRKKTE
730	740	750	760	770	780	790	800
SALYGCTVLL	ASVALGLDLR	ELHKAQAAEE	PLPKEEKKKR	EGIFQRASKS	RRSASPPTSL	PSTCGEASSP	PSLPLSSALG
810	820	830	840	850	860	870	880
ILSTPSFSTK	CLLQMDSEDP	LVDSAPVTCD	SEMLTPDFCP	TAPGSGREPA	LMPRLDTDCS	VSRNLPSSFL	QQTCGNVPYC
890	900	910	920	930	940	950	960
ASSKHRPSHH	RRTMSDGNPT	PTGATIISAT	GASALPLCPS	PAPHSHLPRE	VSPKKHSTVH	IVPQRRPASL	RSRSDLPQAY
970	980	990	1000	1010	1020	1030	1040
PQTAVSQLAQ	TACVVGRPGP	HPTQFLAAKE	RTKSHVPSLL	DADVEGQSRD	YTVPLCRMRS	KTSRPSIYEL	EKEFLS

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1556	1	853.3369	-142.17	2	49.3	11.3	1	205-222	R.GGALNRALAAANAAPDPR.A		MD:MU 1.30

Detailed Protein Report

Protein 1152: alpha-synuclein isoform NACP112 [Homo sapiens]

Accession:	gi|6806898	**Score:**	11.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	11.4
Database Date:	2015-11-30	**pI:**	9.0
		Sequence Coverage [%]:	11.6
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 3.93 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MDVFMKGLSK AKEGVVAAAE KTKQGVAEAA GKTKEGVLYV GSKTKEGVVH GVATVAEKTK EQVTNVGGAV VTGVTAVAQK
        90        100        110        120
TVEGAGSIAA ATGFVKKDQL GKEGYQDYEP EA
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
2558	1	648.3654	21.74	2	62.0	11.3	0	46-58	K.EGVVHGVATVAEK.T		MD:MU	3.93

Detailed Protein Report

Protein 1153: macrophage scavenger receptor types I and II isoform type 2 [Homo sapiens]

Accession:	gi|4505259	**Score:**	11.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	39.6
Database Date:	2015-11-30	**pI:**	5.3
		Sequence Coverage [%]:	4.5
		No. of unique Peptides:	1

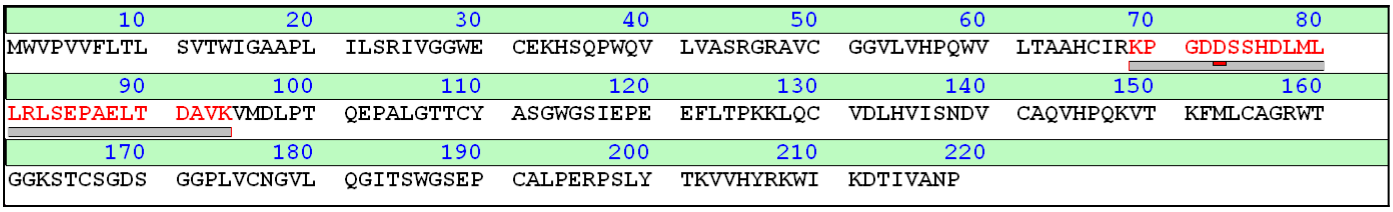
10	20	30	40	50	60	70	80
MEQWDHFHNQ	QEDTDSCSES	VKFDARSMTA	LLPPNPKNSP	SLQEKLKSFK	AALIALYLLV	FAVLIPLIGI	VAAQLLKWET
90	100	110	120	130	140	150	160
KNCSVSSTNA	NDITQSLTGK	GNDSEEEMRF	QEVFMEHMSN	MEKRIQHILD	MEANLMDTEH	FQNFSMTTDQ	RFNDILLQLS
170	180	190	200	210	220	230	240
TLFSSVQGHG	NAIDEISKSL	ISLNTTLLDL	QLNIENLNGK	IQENTFKQQE	EISKLEERVY	NVSAEIMAMK	EEQVHLEQEI
250	260	270	280	290	300	310	320
KGEVKVLNNI	TNDLRLKDWE	HSQTLRNITL	IQGPPGPPGE	KGDRGPTGES	GPRGFPGPIG	PPGLKGDRGA	IGFPGSRGLP
330	340	350	360				
GYAGRPGNSG	PKGQKGEKGS	GNTLRPVQLT	DHIRAGPS				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2549	1	913.4434	-93.02	2	61.8	11.3	2	242-257	K.GEVKVLNNITNDLRLK.D	

Detailed Protein Report

Protein 1154: prostate-specific antigen isoform 4 preproprotein [Homo sapiens]

Accession:	gi|71834855	**Score:**	11.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	23.7
Database Date:	2015-11-30	**pI:**	7.9
		Sequence Coverage [%]:	11.9
		No. of unique Peptides:	1



```
        10         20         30         40         50         60         70         80
MWVPVVFLTL SVTWIGAAPL ILSRIVGGWE CEKHSQPWQV LVASRGRAVC GGVLVHPQWV LTAAHCIRKP GDDSSHDLML
        90        100        110        120        130        140        150        160
LRLSEPAELT DAVKVMDLPT QEPALGTTCY ASGWGSIEPE EFLTPKKLQC VDLHVISNDV CAQVHPQKVT KFMLCAGRWT
       170        180        190        200        210        220
GGKSTCSGDS GGPLVCNGVL QGITSWGSEP CALPERPSLY TKVVHYRKWI KDTIVANP
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
801	1	1419.2740	37.23	2	39.6	11.3	1	69-94	R.KPGDDSSHDLMLLRLSEPAELTDAVK.V	

Detailed Protein Report

Protein 1155: **PREDICTED: 5'-AMP-activated protein kinase catalytic subunit alpha-1 isoform X1 [Homo sapiens]**

Accession:	gi|578809939	**Score:**	11.3
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

Quantitation

MD:MU **Median:** 0.75 **CV:** 0.00 % **No. of 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	Ratios	
174	1	424.2184	0.90	3	31.6	11.3	1	157-166	K.HMLQVDPMKR.A	Oxidation: 8	MD:MU	0.75

Detailed Protein Report

Protein 1156: **PREDICTED: deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial isoform X1 [Homo sapiens]**

Accession:	gi|530405491	**Score:**	11.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	28.2
Database Date:	2015-11-30	**pI:**	10.5
		Sequence Coverage [%]:	3.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAAGGAAPGK	SVQEQGPGLA	YTLGKMGARA	NKKSESKRAR	QPEAAARLKT	PTAPSSWGPR	ACAIPGLPGH	RLSTPLVRRR
90	100	110	120	130	140	150	160
LRLLPRSCSQ	DGRVFRVEAW	RTSGETPAIS	PSKRARPAEV	GGMQLRFARL	SEHATAPTRG	SARAAGYDLY	SAYDYTIPPM
170	180	190	200	210	220	230	240
EKAVVKTDIQ	IALPSGCYGR	VAPRSGLAAK	HFIDVGAGVI	DEDYRGNVGV	VLFNFGKEKF	EVKKGDRIAQ	LICERIFYPE
250	260	270					
IEEVQALDDT	ERGSGGFGST	GKN					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1436	1	699.6685	414.72	1	47.7	11.3	0	2-10	M.AAGGAAPGK.S	

Detailed Protein Report

Protein 1157: PREDICTED: transmembrane channel-like protein 6 isoform X4 [Homo sapiens]

Accession:	gi|530411463	**Score:**	11.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	64.8
Database Date:	2015-11-30	**pI:**	10.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPWRYALKRI	GGQFGSSVLS	YFLFLKTLLA	FNALLLLLLV	AFIMGPQVAF	PPALPGPAPV	CTGLELLTGA	GCFTHTVMYY
90	100	110	120	130	140	150	160
GHYSNATLNQ	PCGSPLDGSQ	CTPRVGGLPY	NMPLAYLSTV	GVSFFITCIT	LVYSMAHSFG	ESYRVGSTSG	IHAITVFCSW
170	180	190	200	210	220	230	240
DYKVTQKRAS	RLQQDNIRTR	LKELLAEWQL	RHSPRSVCGR	LRQAAVLGLV	WLLCLGTALG	CAVAVHVFSE	FMIQSPEAAG
250	260	270	280	290	300	310	320
QEAVLLVLPL	VVGLLNLGAP	YLCRVLAALE	PHDSPVLEVY	VAICRNLILK	LAILGTLCYH	WLGRRVGVLQ	GQCWEDFVGQ
330	340	350	360	370	380	390	400
ELYRFLVMDF	VLMLLDTLFG	ELVWRIISEK	KLKRRRKPEF	DIARNVLELI	YGQTLTWLGV	LFSPLLPAVQ	IIKLLLVFYV
410	420	430	440	450	460	470	480
KKTSLLANCQ	APRRPWLASH	MSTVFLTLLC	FPAFLGAAVF	LCYAVWQVKP	SSTCGPFRTL	DTMYEAGRVW	VRHLEAAGPR
490	500	510	520	530	540	550	560
VSWLPWVHRY	LMENTFFVFL	VSALLLAVIY	LNIQVVRGQR	KVICLLKEQI	SNEGEDKIFL	INKLHSIYER	KEREERSRVG
570	580						
TTEEAAAPPA	LLTDEQDA						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
300	1	646.8066	-31.67	4	33.4	11.3	1	145-167	R.VGSTSGIHAITVFCSWDYKVTQK.R	Carbamidomethyl: 14

Detailed Protein Report

Protein 1158: short-chain dehydrogenase/reductase family 42E member 1 [Homo sapiens]

Accession:	gi|116268111	**Score:**	11.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	44.3
Database Date:	2015-11-30	**pI:**	9.2
		Sequence Coverage [%]:	4.8
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530424544	refseq_human (refseq_human_20140103.fasta)	PREDICTED: short-chain dehydrogenase/reductase family 42E member 1 isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MDPKRSQKES	VLITGGSGYF	GFRLGCALNQ	NGVHVILFDI	SSPAQTIPEG	IKFIQGDIRH	LSDVEKAFQD	ADVTCVFHIA
90	100	110	120	130	140	150	160
SYGMSGREQL	NRNLIKEVNV	RGTDNILQVC	QRRRVPRLVY	TSTFNVIFGG	QVIRNGDESL	PYLPLHLHPD	HYSRTKSIAE
170	180	190	200	210	220	230	240
QKVLEANATP	LDRGDGVLRT	CALRPAGIYG	PGEQRHLPRI	VSYIEKGLFK	FVYGDPRSLV	EFVHVDNLVQ	AHILASEALR
250	260	270	280	290	300	310	320
ADKGHIASGQ	PYFISDGRPV	NNFEFFRPLV	EGLGYTFPST	RLPLTLVYCF	AFLTEMVHFI	LGRLYNFQPF	LTRTEVYKTG
330	340	350	360	370	380	390	400
VTHYFSLEKA	KKELGYKAQP	FDLQEAVEWF	KAHGHGRSSG	SRDSECFVWD	GLLVFLLIIA	VLMWLPSSVI	LSL

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2676	1	1045.0263	-17.77	2	63.6	11.3	2	5-23	K.RSQKESVLITGGSGYFGFR.L	

Detailed Protein Report

Protein 1159: elongator complex protein 1 [Homo sapiens]

Accession: gi|38569394
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 11.3
MW [kDa]: 150.2
pI: 5.6
Sequence Coverage [%]: 1.4
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MRNLKLFRTL	EFRDIQGPGN	PQCFSLRTEQ	GTVLIGSEHG	LIEVDPVSRE	VKNEVSLVAE	GFLPEDGSGR	IVGVQDLLDQ
90	100	110	120	130	140	150	160
ESVCVATASG	DVILCSLSTQ	QLECVGSVAS	GISVMSWSPD	QELVLLATGQ	QTLIMMTKDF	EPILEQQIHQ	DDFGESKFIT
170	180	190	200	210	220	230	240
VGWGRKETQF	HGSEGRQAAF	QMQMHESALP	WDDHRPQVTW	RGDGQFFAVS	VVCPETGARK	VRVWNREFAL	QSTSEPVAGL
250	260	270	280	290	300	310	320
GPALAWKPSG	SLIASTQDKP	NQQDIVFFEK	NGLLHGHFTL	PFLKDEVKVN	DLLWNADSSV	LAVWLEDLQR	EESSIPKTCV
330	340	350	360	370	380	390	400
QLWTVGNYHW	YLKQSLSFST	CGKSKIVSLM	WDPVTPYRLH	VLCQGWHYLA	YDWHWTTDRS	VGDNSSDLSN	VAVIDGNRVL
410	420	430	440	450	460	470	480
VTVFRQTVVP	PPMCTYQLLF	PHPVNQVTFL	AHPQKSNDLA	VLDASNQISV	YKCGDCPSAD	PTVKLGAVGG	SGFKVCLRTP
490	500	510	520	530	540	550	560
HLEKRYKIQF	ENNEDQDVNP	LKLGLLTWIE	EDVFLAVSHS	EFSPRSVIHH	LTAASSEMDE	EHGQLNVSSS	AAVDGVIISL
570	580	590	600	610	620	630	640
CCNSKTKSVV	LQLADGQIFK	YLWESPSLAI	KPWKNSGGFP	VRFPYPCTQT	ELAMIGEEEC	VLGLTDRCRF	FINDIEVASN
650	660	670	680	690	700	710	720
ITSFAVYDEF	LLLTTHSHTC	QCFCLRDASF	KTLQAGLSSN	HVSHGEVLRK	VERGSRIVTV	VPQDTKLVLQ	MPRGNLEVVH
730	740	750	760	770	780	790	800
HRALVLAQIR	KWLDKLMFKE	AFECMRKLRI	NLNLIYDHNP	KVFLGNVETF	IKQIDSVNHI	NLFFTELKEE	DVTKTMYPAP
810	820	830	840	850	860	870	880
VTSSVYLSRD	PDGNKIDLVC	DAMRAVMESI	NPHKYCLSIL	TSHVKKTTPE	LEIVLQKVHE	LQGNAPSDPD	AVSAEEALKY
890	900	910	920	930	940	950	960
LLHLVDVNEL	YDHSLGTYDF	DLVLMVAEKS	QKDPKEYLPF	LNTLKKMETN	YQRFTIDKYL	KRYEKAIGHL	SKCGPEYFPE
970	980	990	1000	1010	1020	1030	1040
CLNLIKDKNL	YNEALKLYSP	SSQQYQDISI	AYGEHLMQEH	MYEPAGLMFA	RCGAHEKALS	AFLTCGNWKQ	ALCVAAQLNF
1050	1060	1070	1080	1090	1100	1110	1120
TKDQLVGLGR	TLAGKLVEQR	KHIDAAMVLE	ECAQDYEEAV	LLLLEGAAWE	EALRLVYKYN	RLDIIETNVK	PSILEAQKNY
1130	1140	1150	1160	1170	1180	1190	1200
MAFLDSQTAT	FSRHKKRLLV	VRELKEQAQQ	AGLDDEVPHG	QESDLFSETS	SVVSGSEMSG	KYSHSNSRIS	ARSSKNRRKA
1210	1220	1230	1240	1250	1260	1270	1280
ERKKHSLKEG	SPLEDLALLE	ALSEVVQNTE	NLKDEVYHIL	KVLFLFEFDE	QGRELQKAFE	DTLQLMERSL	PEIWTLTYQQ
1290	1300	1310	1320	1330	1340		
NSATPVLGPN	STANSIMASY	QQQKTSVPVL	DAELFIPPKI	NRRTQWKLSL	LD		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2081	1	938.3438	-121.46	2	56.2	11.3	0	53-70	K.NEVSLVAEGFLPEDGSGR.I	

Detailed Protein Report

Protein 1160: **PREDICTED: nuclear receptor subfamily 2 group C member 2 isoform X1 [Homo sapiens]**

Accession: gi|530373071
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 11.2
MW [kDa]: 65.4
pI: 5.9
Sequence Coverage [%]: 2.0
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MTSPSPRIQI	ISTDSAVASP	QRIQIVTDQQ	TGQKIQIVTA	VDASGSPKQQ	FILTSPDGAG	TGKVILASPE	TSSAKQLIFT
90	100	110	120	130	140	150	160
TSDNLVPGRI	QIVTDSASVE	RLLGKTDVQR	PQVVEYCVVC	GDKASGRHYG	AVSCEGCKGF	FKRSVRKNLT	YSCRSNQDCI
170	180	190	200	210	220	230	240
INKHHRNRCQ	FCRLKKCLEM	GMKMESVQSE	RKPFDVQREK	PSNCAASTEK	IYIRKDLRSP	LIATPTFVAD	KDGARQTGLL
250	260	270	280	290	300	310	320
DPGMLVNIQQ	PLIREDGTVL	LATDSKAETS	QGALGTLANV	VTSLANLSES	LNNGDTSEIQ	PEDQSASEIT	RAFDTLAKAL
330	340	350	360	370	380	390	400
NTTDSSSSPS	LADGIDTSGG	GSIHVISRDQ	STPIIEVEGP	LLSDTHVTFK	LTMPSPMPEY	LNVHYICESA	SRLLFLSMHW
410	420	430	440	450	460	470	480
ARSIPAFQAL	GQDCNTSLVR	ACWNELFTLG	LAQCAQVMSL	STILAAIVNH	LQNSIQEDKL	SGDRIKQVME	HIWKLQEFCN
490	500	510	520	530	540	550	560
SMAKLDIDGY	EYAYLKAIVL	FSPDHPGLTS	TSQIEKFQEK	AQMELQDYVQ	KTYSEDTYRL	ARILVRLPAL	RLMSSNITEE
570	580	590	600				
LFFTGLIGNV	SIDSIIPYIL	KMETAEYNGQ	ITGASL				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1237	1	695.9289	-62.05	2	45.1	11.2	2	540-551	R.LARILVRLPALR.L	

Detailed Protein Report

Protein 1161: **heat shock-related 70 kDa protein 2 [Homo sapiens]**

Accession:	gi|13676857	**Score:**	11.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	70.0
Database Date:	2015-11-30	**pI:**	5.4
		Sequence Coverage [%]:	1.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSARGPAIGI	DLGTTYSCVG	VFQHGKVEII	ANDQGNRTTP	SYVAFTDTER	LIGDAAKNQV	AMNPTNTIFD	AKRLIGRKFE
90	100	110	120	130	140	150	160
DATVQSDMKH	WPFRVVSEGG	KPKVQVEYKG	ETKTFFPEEI	SSMVLTKMKE	IAEAYLGGKV	HSAVITVPAY	FNDSQRQATK
170	180	190	200	210	220	230	240
DAGTITGLNV	LRIINEPTAA	AIAYGLDKKG	CAGGEKNVLI	FDLGGGTFDV	SILTIEDGIF	EVKSTAGDTH	LGGEDFDNRM
250	260	270	280	290	300	310	320
VSHLAEEFKR	KHKKDIGPNK	RAVRRLRTAC	ERAKRTLSSS	TQASIEIDSL	YEGVDFYTSI	TRARFEELNA	DLFRGTLEPV
330	340	350	360	370	380	390	400
EKALRDAKLD	KGQIQEIVLV	GGSTRIPKIQ	KLLQDFFNGK	ELNKSINPDE	AVAYGAAVQA	AILIGDKSEN	VQDLLLLDVT
410	420	430	440	450	460	470	480
PLSLGIETAG	GVMTPLIKRN	TTIPTKQTQT	FTTYSDNQSS	VLVQVYEGER	AMTKDNNLLG	KFDLTGIPPA	PRGVPQIEVT
490	500	510	520	530	540	550	560
FDIDANGILN	VTAADKSTGK	ENKITITNDK	GRLSKDDIDR	MVQEAERYKS	EDEANRDRVA	AKNALESYTY	NIKQTVEDEK
570	580	590	600	610	620	630	640
LRGKISEQDK	NKILDKCQEV	INWLDRNQMA	EKDEYEHKQK	ELERVCNPII	SKLYQGGPGG	GSGGGGSGAS	GGPTIEEVD

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
440	1	563.2388	-158.27	2	34.8	11.2	2	255-264	K.DIGPNKRAVR.R	

Detailed Protein Report

Protein 1162: neurexophilin-1 precursor [Homo sapiens]

Accession:	gi|23097338	**Score:**	11.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	31.1
Database Date:	2015-11-30	**pI:**	9.6
		Sequence Coverage [%]:	2.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MQAACWYVLF	LLQPTVYLVT	CANLTNGGKS	ELLKSGSSKS	TLKHIWTESS	KDLSISRLLS	QTFRGKENDT	DLDLRYDTPE
90	100	110	120	130	140	150	160
PYSEQDLWDW	LRNSTDLQEP	RPRAKRRPIV	KTGKFKKMFG	WGDFHSNIKT	VKLNLLITGK	IVDHGNGTFS	VYFRHNSTGQ
170	180	190	200	210	220	230	240
GNVSVSLVPP	TKIVEFDLAQ	QTVIDAKDSK	SFNCRIEYEK	VDKATKNTLC	NYDPSKTCYQ	EQTQSHVSWL	CSKPFKVICI
250	260	270	280				
YISFYSTDYK	LVQKVCPDYN	YHSDTPYFPS	G				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
847	1	690.1561	-321.58	1	40.0	11.2	0	52-57	K.DLSISR.L	

Detailed Protein Report

Protein 1163: PREDICTED: serine/threonine-protein kinase TAO3 isoform X4 [Homo sapiens]

Accession:	gi|578823854	**Score:**	11.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	101.7
Database Date:	2015-11-30	**pI:**	7.3
		Sequence Coverage [%]:	1.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MRKGVLKDPE	IADLFYKDDP	EELFIGLHEI	GHGSFGAVYF	ATNAHTSEVV	AIKKMSYSGK	QTHEKWQDIL	KEVKFLRQLK
90	100	110	120	130	140	150	160
HPNTIEYKGC	YLKEHTAWLV	MEYCLGSASD	LLEVHKKPLQ	EVEIAAITHG	ALHGLAYLHS	HALIHRDIKA	GNILLTEPGQ
170	180	190	200	210	220	230	240
VKLADFGSAS	MASPANSFVG	TPYWMAPEVI	LAMDEGQYDG	KVDIWSLGIT	CIELAERKPP	LFNMNAMSAL	YHIAQNDSPT
250	260	270	280	290	300	310	320
LQSNEWTDSF	RRFVDYCLQK	IPQERPTSAE	LLRHDFVRRD	RPLRVLIDLI	QRTKDAVREL	DNLQYRKMKK	ILFQETRNGP
330	340	350	360	370	380	390	400
LNESQEDEED	SEHGTSLNRE	MDSLGSNHSI	PSMSVSTGSQ	SSSVNSMQEV	MDESSSELVM	MHDDESTINS	SSSVVHKKVG
410	420	430	440	450	460	470	480
FLVPSTEDHV	FIRDEAGHGD	PRPEPRPTQS	VQSQALHYRN	RERFATIKSA	SLVTRQIHEH	EQENELREQM	SGYKRMRRQH
490	500	510	520	530	540	550	560
QKQLIALENK	LKAEMDEHRL	KLQKEVETHA	NNSSIELEKL	AKKQVAIIEK	EAKVAAADEK	KFQQQILAQQ	KKDLTTFLES
570	580	590	600	610	620	630	640
QKKQYKICKE	KIKEEMNEDH	STPKKEKQER	ISKHKENLQH	TQAEEEAHLL	TQQRLYYDKN	CRFFKRKIMI	KRHEVEQQNI
650	660	670	680	690	700	710	720
REELNKKRTQ	KEMEHAMLIR	HDESTRELEY	RQLHTLQKLR	MDLIRLQHQT	ELENQLEYNK	RRERELHRKH	VMELRQQPKN
730	740	750	760	770	780	790	800
LKAMEMQIKK	QFQDTCKVQT	KQYKALKNHQ	LEVTPKNEHK	TILKTLKDEQ	TRKLAILAEQ	YEQSINEMMA	SQALRLDEAQ
810	820	830	840	850	860	870	880
EAECQALRLQ	LQQEMELLNA	YQSKIKMQTE	AQHERELQKL	EQRVSLRRAH	LEQKETLNVP	SQRNDVGCWG	G

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1644	1	803.6077	180.34	2	50.3	11.2	2	478-490	R.RQHQKQLIALENK.L	

Detailed Protein Report

Protein 1164: matrin-3 isoform c [Homo sapiens]

Accession:	gi|533112484	**Score:**	11.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	56.7
Database Date:	2015-11-30	**pI:**	5.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGDPFMLQQS	TNPAPGILGP	PPPSFHLGGP	AVGPRGNLGA	GNGNLQGPRH	MQKGRVETSR	VVHIMDFQRG	KNLRYQLLQL
90	100	110	120	130	140	150	160
VEPFGVISNH	LILNKINEAF	IEMATTEDAQ	AAVDYYTTTP	ALVFGKPVRV	HLSQKYKRIK	KPEGKPDQKF	DQKQELGRVI
170	180	190	200	210	220	230	240
HLSNLPHSGY	SDSAVLKLAE	PYGKIKNYIL	MRMKSQAFIE	METREDAMAM	VDHCLKKALW	FQGRCVKVDL	SEKYKKLVLR
250	260	270	280	290	300	310	320
IPNRGIDLLK	KDKSRKRSYS	PDGKESPSDK	KSKTDGSQKT	ESSTEGKEQE	EKSGEDGEKD	TKDDQTEQEP	NMLLESEDEL
330	340	350	360	370	380	390	400
LVDEEEAAAL	LESGSSVGDE	TDLANLGDVA	SDGKKEPSDK	AVKKDGSASA	AAKKKLKKVD	KIEELDQENE	AALENGIKNE
410	420	430	440	450	460	470	480
ENTEPGAESS	ENADDPNKDT	SENADGQSDE	NKDDYTIPDE	YRIGPYQPNV	PVGIDYVIPK	TGFYCKLCSL	FYTNEEVAKN
490	500	510					
THCSSLPHYQ	KLKKFLNKLA	EERRQKKET					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2783	1	973.5180	13.43	2	65.2	11.2	2	54-69	K.GRVETSRVVHIMDFQR.G	Oxidation: 12

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Detailed Protein Report

Protein 1165: PREDICTED: uncharacterized protein LOC101929393 [Homo sapiens]

Accession:	gi|530356822	**Score:**	11.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	20.3
Database Date:	2015-11-30	**pI:**	11.1
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	8.6
		No. of unique Peptides:	1

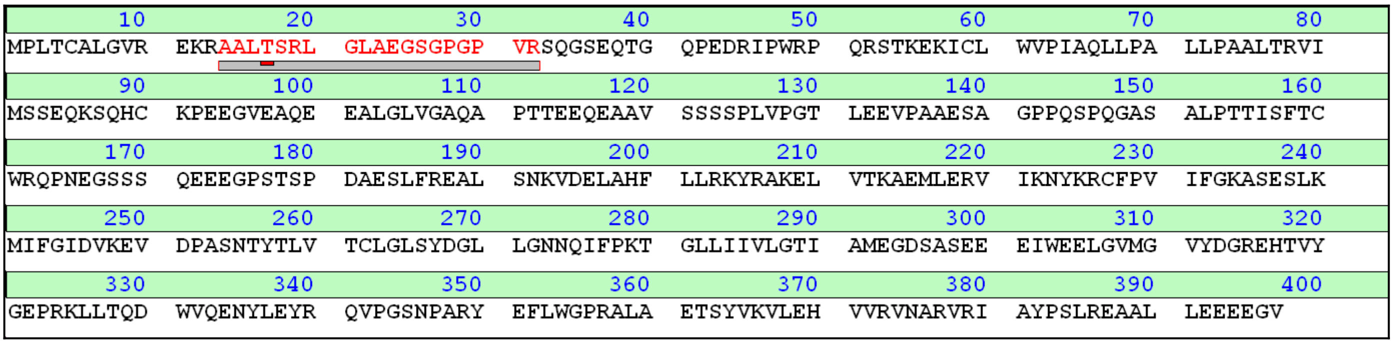
```
        10         20         30         40         50         60         70         80
MKLVEEVAGE EQPVRCTPCY AIEPPLERVE RKGARGQGSK KRSRGQRARS NGPAPAGDSR ASGFRLPGSG CLDPDRPLRD
        90        100        110        120        130        140        150        160
MSTAQDCSCW APAARSAGSA KPGPDRSFCK QSRCILGSLE GRACSERVQK QPRSSQHQVH WKCQATTSFM LLCDHLSKSR
       170        180        190
CQEPSLWPPW RDLSLGRDVL GCEAF
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2335	1	614.8205	-148.24	3	59.5	11.2	0	80-95	R.DMSTAQDCSCWAPAAR.S	Carbamidomethyl: 8, 10; Oxidation: 2

Detailed Protein Report

Protein 1166: PREDICTED: melanoma-associated antigen 4 isoform X1 [Homo sapiens]

Accession:	gi|530422789	**Score:**	11.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	43.5
Database Date:	2015-11-30	**pI:**	4.8
		Sequence Coverage [%]:	4.8
		No. of unique Peptides:	1



```
        10         20         30         40         50         60         70         80
MPLTCALGVR EKRAALTSRL GLAEGSGPGP VRSQGSEQTG QPEDRIPWRP QRSTKEKICL WVPIAQLLPA LLPAALTRVI
        90        100        110        120        130        140        150        160
MSSEQKSQHC KPEEGVEAQE EALGLVGAQA PTTEEQEAAV SSSSPLVPGT LEEVPAAESA GPPQSPQGAS ALPTTISFTC
       170        180        190        200        210        220        230        240
WRQPNEGSSS QEEEGPSTSP DAESLFREAL SNKVDELAHF LLRKYRAKEL VTKAEMLERV IKNYKRCFPV IFGKASESLK
       250        260        270        280        290        300        310        320
MIFGIDVKEV DPASNTYTLV TCLGLSYDGL LGNNQIFPKT GLLIIVLGTI AMEGDSASEE EIWEELGVMG VYDGREHTVY
       330        340        350        360        370        380        390        400
GEPRKLLTQD WVQENYLEYR QVPGSNPARY EFLWGPRALA ETSYVKVLEH VVRVNARVRI AYPSLREAAL LEEEEGV
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2785	1	905.0014	-1.19	2	66.2	11.2	1	14-32	R.AALTSRLGLAEGSGPGPVR.S	

Detailed Protein Report

Protein 1167: xin actin-binding repeat-containing protein 2 isoform 5 [Homo sapiens]

Accession:	gi|312433988	**Score:**	11.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	81.8
Database Date:	2015-11-30	**pI:**	6.3
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.0
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 1.75 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MARYQAAVSR	GDCRSFSANM	MEESEMCAVP	GGLAKVKKQF	EDEITSSRNT	FAQYQYQHQN	RSEQEAIHSS	QVGTSRSSQE
90	100	110	120	130	140	150	160
MARNEQEGSK	VQKIDVHGTE	MVSHLEKHTE	EVNQASQFHQ	YVQETVIDTP	EDEEIPKVST	KLLKEQFEKS	AQEKILYSDK
170	180	190	200	210	220	230	240
EMTTPAKQIK	KLLLQDKEIC	ILCQKTVYPM	ECLVADKQNF	HKSCFRCHHC	NSKLSLGNYA	SLHGQIYCKP	HFKQLFKSKG
250	260	270	280	290	300	310	320
NYDEGFGHKQ	HKDRWNCKNQ	SRSVDFIPNE	EPNMCKNIAE	NTLVPGDRNE	HLDAGNSEGQ	RNDLRKLGER	GKLKVIWPPS
330	340	350	360	370	380	390	400
KEIPKKTLPF	EEELKMSKPK	WPPEMTTLLS	PEFKSESLLE	DVRTPENKGQ	RQDHFPFLQP	YLQSTHVCQK	EDVIGIKEMK
410	420	430	440	450	460	470	480
MPEGRKDEKK	EGRKNVQDRP	SEAEDTKSNR	KSAMDLNDNN	NVIVQSAEKE	KNEKTNQTNG	AEVLQVTNTD	DEMMPENHKE
490	500	510	520	530	540	550	560
NLNKNNNNNY	VAVSYLNNCR	QKTSILEFLD	LLPLSSEAND	TANEYEIEKL	ENTSRISELL	GIFESEKTYS	RNVLAMALKK
570	580	590	600	610	620	630	640
QTDRAAAGSP	VQPAPKPSLS	RGLMVKGGSS	IISPDTNLLN	IKGSHSKSKN	LHFFFSNTVK	ITAFSKKNEN	IFNCDLIDSV
650	660	670	680	690	700	710	720
DQIKNMPCLD	LREFGKDVKP	WHVETTEAAR	NNENTGFDAL	SHECTAKPLF	PRVEVQSEQL	TVEEQIKRNR	CYSDTE

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2325	1	805.7815	-141.84	2	58.9	11.2	0	94-107	K.IDVHGTEMVSHLEK.H	Oxidation: 8	MD:MU 1.75

Detailed Protein Report

Protein 1168: PREDICTED: actin-related protein 5 isoform X4 [Homo sapiens]

Accession:	gi|530418407	**Score:**	11.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	51.3
Database Date:	2015-11-30	**pI:**	5.1
		Sequence Coverage [%]:	4.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAANVFPFRD	ARAAPDPVLE	AGPVAHGPLP	VPLVLDNGSF	QVRAGWACPG	QDPGPEPRLQ	FRAVCARGRG	GARGASGPQV
90	100	110	120	130	140	150	160
GNALGSLEPL	RWMLRSPFDR	NVPVNLELQE	LLLDYSFQHL	GVSSQGCVDH	PIVLTEAVCN	PLYSRQMMSE	LLFECYGIPK
170	180	190	200	210	220	230	240
VAYGIDSLFS	FYHNKPKNSM	CSGLIISSGY	QCTHVLPILE	GRLDAKNCKR	INLGGSQAAG	YLQRLLQLKY	PGHLAAITLS
250	260	270	280	290	300	310	320
RMEEILHEHS	YIAEDYVEEL	HKWRCPDYYE	NNVHKMQLPF	SSKLLGSTLT	SEEKQERRQQ	QLRRLQELNA	RRREEKLQLD
330	340	350	360	370	380	390	400
QERLDRLLYV	QELLEDGQMD	QFHKALIELN	MDSPEELQSY	IQKLSIAVEQ	AKQKILQAEV	NLEVDVVDSK	PETPDLEQLE
410	420	430	440	450	460		
PSLEDVESMN	DFDPLFSEET	PGVEKPVTTV	QHIISYLLGQ	KEFELQRLFS	SHLS		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2551	1	862.0295	80.32	2	62.4	11.2	0	74-91	R.GASGPQVGNALGSLEPLR.W	

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Detailed Protein Report

Protein 1169: minor histocompatibility protein HA-1 isoform 3 [Homo sapiens]

Accession: gi|537361054
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 11.2
MW [kDa]: 84.6
pI: 5.5
Sequence Coverage [%]: 0.8
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MGVGRKGGAG	ETESHPRIGL	ELASWLPHPQ	QEAESNLRKA	KQGYVQRCED	HDKARFLVAK	AEEEQAGSAP	GAGSTATKTL
90	100	110	120	130	140	150	160
DKRRRLEEEA	KNKAEEAMAT	YRTCVADAKT	QKQELEDTKV	TALRQIQEVI	RQSDQTIKSA	TISYYQMMHM	QTAPLPVHFQ
170	180	190	200	210	220	230	240
MLCESSKLYD	PGQQYASHVR	QLQRDQEPDV	HYDFEPHVSA	NAWSPVMRAR	KSSFNVSDVA	RPEAAGSPPE	EGGCTEGTPA
250	260	270	280	290	300	310	320
KDHRAGRGHQ	VHKSWPLSIS	DSDSGLDPGP	GAGDFKKFER	TSSSGTMSST	EELVDPDGGA	GASAFEQADL	NGMTPELPVA
330	340	350	360	370	380	390	400
VPSGPFRHEG	LSKAARTHRL	RKLRTPAKCR	ECNSYVYFQG	AECEECCLAC	HKKCLETLAI	QCGHKKLQGR	LQLFGQDFSH
410	420	430	440	450	460	470	480
AARSAPDGVP	FIVKKCVCEI	ERRALRTKGI	YRVNGVKTRV	EKLCQAFENG	KELVELSQAS	PHDISNVLKL	YLRQLPEPLI
490	500	510	520	530	540	550	560
SFRLYHELVG	LAKDSLKAEA	EAKAASRGRQ	DGSESEAVAV	ALAGRLRELL	RDLPPENRAS	LQYLLRHLRR	IVEVEQDNKM
570	580	590	600	610	620	630	640
TPGNLGIVFG	PTLLRPRPTE	ATVSLSSLVD	YPHQARVIET	LIVHYGLVFE	EEPEETPGGQ	DESSNQRAEV	VVQVPYLEAG
650	660	670	680	690	700	710	720
EAVVYPLQEA	AADGCRESRV	VSNDSDSDLE	EASELLSSSE	ASALGHLSFL	EQQQSEASLE	VASGSHSGSE	EQLEATARED
730	740	750	760	770	780		
GDGDEDGPAQ	QLSGFNTNQS	NNVLQAPLPP	MRLRGGRMTL	GSCRERQPEF	V		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
239	1	663.6255	399.22	1	32.4	11.2	1	1-6	-.MGVGRK.G	Oxidation: 1

Detailed Protein Report

Protein 1170: **fatty aldehyde dehydrogenase isoform 1 [Homo sapiens]**

Accession:	gi|73466520	**Score:**	11.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	57.6
Database Date:	2015-11-30	**pI:**	9.7
		Sequence Coverage [%]:	3.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MELEVRRVRQ	AFLSGRSRPL	RFRLQQLEAL	RRMVQEREKD	ILTAIAADLC	KSEFNVYSQE	VITVLGEIDF	MLENLPEWVT
90	100	110	120	130	140	150	160
AKPVKKNVLT	MLDEAYIQPQ	PLGVVLIIGA	WNYPFVLTIQ	PLIGAIAAGN	AVIIKPSELS	ENTAKILAKL	LPQYLDQDLY
170	180	190	200	210	220	230	240
IVINGGVEET	TELLKQRFDH	IFYTGNTAVG	KIVMEAAAKH	LTPVTLELGG	KSPCYIDKDC	DLDIVCRRIT	WGKYMNCGQT
250	260	270	280	290	300	310	320
CIAPDYILCE	ASLQNQIVWK	IKETVKEFYG	ENIKESPDYE	RIINLRHFKR	ILSLLEGQKI	AFGGETDEAT	RYIAPTVLTD
330	340	350	360	370	380	390	400
VDPKTKVMQE	EIFGPILPIV	PVKNVDEAIN	FINEREKPLA	LYVFSHNHKL	IKRMIDETSS	GGVTGNDVIM	HFTLNSFPFG
410	420	430	440	450	460	470	480
GVGSSGMGAY	HGKHSFDTFS	HQRPCLLKSL	KREGANKLRY	PPNSQSKVDW	GKFFLLKRFN	KEKLGLLLLT	FLGIVAAVLV
490	500	510					
KKYQAVLRRK	ALLIFLVVHR	LRWSSKQR					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1203	1	661.1025	-12.99	3	44.6	11.2	1	464-482	K.LGLLLLTFLGIVAAVLVKK.Y	

Detailed Protein Report

Protein 1171: mitogen-activated protein kinase 4 [Homo sapiens]

Accession: gi|89276769
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 11.2
MW [kDa]: 65.9
pI: 5.1
Sequence Coverage [%]: 3.1
No. of unique Peptides: 1

Alias proteins:

Accession	Name	Description
gi|530413856	refseq_human (refseq_human_20140103.fasta)	PREDICTED: mitogen-activated protein kinase 4 isoform X2 [Homo sapiens]

10	20	30	40	50	60	70	80
MAEKGDCIAS	VYGYDLGGRF	VDFQPLGFGV	NGLVLSAVDS	RACRKVAVKK	IALSDARSMK	HALREIKIIR	RLDHDNIVKV
90	100	110	120	130	140	150	160
YEVLGPKGTD	LQGELFKFSV	AYIVQEYMET	DLARLLEQGT	LAEEHAKLFM	YQLLRGLKYI	HSANVLHRDL	KPANIFISTE
170	180	190	200	210	220	230	240
DLVLKIGDFG	LARIVDQHYS	HKGYLSEGLV	TKWYRSPRLL	LSPNNYTKAI	DMWAAGCILA	EMLTGRMLFA	GAHELEQMQL
250	260	270	280	290	300	310	320
ILETIPVIRE	EDKDELLRVM	PSFVSSTWEV	KRPLRKLLPE	VNSEAIDFLE	KILTFNPMDR	LTAEMGLQHP	YMSPYSCPED
330	340	350	360	370	380	390	400
EPTSQHPFRI	EDEIDDIVLM	AANQSQLSNW	DTCSSRYPVS	LSSDLEWRPD	RCQDASEVQR	DPRAGSAPLA	EDVQVDPRKD
410	420	430	440	450	460	470	480
SHSSSERFLE	QSHSSMERAF	EADYGRSCDY	KVGSPSYLDK	LLWRDNKPHH	YSEPKLILDL	SHWKQAAGAP	PTATGLADTG
490	500	510	520	530	540	550	560
AREDEPASLF	LEIAQWVKST	QGGPEHASPP	ADDPERRLSA	SPPGRPAPVD	GGASPQFDLD	VFISRALKLC	TKPEDLPDNK
570	580	590					
LGDLNGACIP	EHPGDLVQTE	AFSKERW					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1554	1	977.3310	-137.30	2	49.1	11.2	0	209-226	K.AIDMWAAGCILAEMLTGR.M	Oxidation: 4, 14

Detailed Protein Report

Protein 1172: PREDICTED: calcineurin-binding protein cabin-1 isoform X12 [Homo sapiens]

Accession:	gi|578837055	**Score:**	11.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	134.8
Database Date:	2015-11-30	**pI:**	5.6
		Sequence Coverage [%]:	1.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MIRIAALNAS	STIEDDHEGS	FKSHKTQTKE	AQEAEAFALY	HKALDLQKHD	RFEESAKAYH	ELLEASLLRE	AVSSGDEKEG
90	100	110	120	130	140	150	160
LKHPGLILKY	STYKNLAQLA	AQREDLETAM	EFYLEAVMLD	STDVNLWYKI	GHVALRLIRI	PLARHAFEEG	LRCNPDHWPC
170	180	190	200	210	220	230	240
LDNLITVLYT	LSDYTTCLYF	ICKALEKDCR	YSKGLVLKEK	IFEEQPCLRK	DSLRMFLKCD	MSIHDVSVSA	AETQAIVDEA
250	260	270	280	290	300	310	320
LGLRKKRQAL	IVREKEPDLK	LVQPIPFFTW	KCLGESLLAM	YNHLTTCEPP	RPSLGKRIDL	SDYQDPSQPL	ESSMVVTPVN
330	340	350	360	370	380	390	400
VIQPSTVSTN	PAVAVAEPVV	SYTSVATTSF	PLHSPGLLET	GAPVGDISGG	DKSKKGVKRK	KISEESGETA	KRRSARVRNT
410	420	430	440	450	460	470	480
KCKKEEKVDF	QELLMKFLPS	RLRKLDPEEE	DDSFNNYEVQ	SEAKLESFPS	IGPQRLSFDS	ATFMESEKQD	VHEFLLENLT
490	500	510	520	530	540	550	560
NGGILELMMR	YLKAMGHKFL	VRWPPGLAEV	VLSVYHSWRR	HSTSLPNPLL	RDCSNKHIKD	MMLMSLSCME	LQLDQWLLTK
570	580	590	600	610	620	630	640
GRSSAVSPRN	CPAGMVNGRF	GPDFPGTHCL	GDLLQLSFAS	SQRDLFEDGW	LEFVVRVYWL	KARFLALQGD	MEQALENYDI
650	660	670	680	690	700	710	720
CTEMLQSSTA	IQVEAGAERR	DIVIRLPNLH	NDSVVSLEEI	DKNLKSLERC	QSLEEIQRLY	EAGDYKAVVH	LLRPTLCTSG
730	740	750	760	770	780	790	800
FDRAKHLEFM	TSIPERPAQL	LLLQDSLLRL	KDYRQCFECS	DVALNEAVQQ	MVNSGEAAAK	EEWVATVTQL	LMGIEQALSA
810	820	830	840	850	860	870	880
DSSGSILKVS	SSTTGLVRLT	NNLIQVIDCS	MAVQEEAKEP	HVSSVLPWII	LHRIIWQEED	TFHSLCHQQQ	LQNPAEEGMS
890	900	910	920	930	940	950	960
ETPMLPSSLM	LLNTAHEYLG	RRSWCCNSDG	ALLRFYVRVL	QKELAASTSE	DTHPYKEELE	TALEQCFYCL	YSFPSKKSKA
970	980	990	1000	1010	1020	1030	1040
RYLEEHSAQQ	VDLIWEDALF	MFEYFKPKTL	PEFDSYKTST	VSADLANLLK	RIATIVPRTE	RPALSLDKVS	AYIEGTSTEV
1050	1060	1070	1080	1090	1100	1110	1120
PCLPEGADPS	PPVVNELYYL	LADYHFKNKE	QSKAIKFYMH	DICICPNRFD	SWAGMALARA	SRIQDKLNSN	ELKSDGPIWK
1130	1140	1150	1160	1170	1180	1190	
HATPVLNCFR	RALEIDSSNL	SLWIEYGTMS	YALHSFASRQ	LKQWRGELPP	ELVQQWPQSW	AGWGLKLLP	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1719	1	786.6893	27.19	3	51.4	11.2	0	425-444	K.LDPEEEDDSFNNYEVQSEAK.L	

Detailed Protein Report

Protein 1173: retinol dehydrogenase 10 [Homo sapiens]

Accession:	gi|25282469	**Score:**	11.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	38.1
Database Date:	2015-11-30	**pI:**	7.9
		Sequence Coverage [%]:	2.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MNIVVEFFVV	TFKVLWAFVL	AAARWLVRPK	EKSVAGQVCL	ITGAGSGLGR	LFALEFARRR	ALLVLWDINT	QSNEETAGMV
90	100	110	120	130	140	150	160
RHIYRDLEAA	DAAALQAGNG	EEEILPHCNL	QVFTYTCDVG	KRENVYLTAE	RVRKEVGEVS	VLVNNAGVVS	GHHLLECPDE
170	180	190	200	210	220	230	240
LIERTMMVNC	HAHFWTTKAF	LPTMLEINHG	HIVTVASSLG	LFSTAGVEDY	CASKFGVVGF	HESLSHELKA	AEKDGIKTTL
250	260	270	280	290	300	310	320
VCPYLVDTGM	FRGCRIRKEI	EPFLPPLKPD	YCVKQAMKAI	LTDQPMICTP	RLMYIVTFMK	SILPFEAVVC	MYRFLGADKC
330	340	350					
MYPFIAQRKQ	ATNNNEAKNG	I					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
443	1	639.8800	7.68	2	34.9	11.2	2	51-60	R.LFALEFARRR.A	

Detailed Protein Report

Protein 1174: COP9 signalosome complex subunit 4 isoform 2 [Homo sapiens]

Accession:	gi|384367993	**Score:**	11.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	40.2
Database Date:	2015-11-30	**pI:**	6.5
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	4.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAAAVRQDLA	QLMNSSGSHK	DLAGKYRQIL	EKAIQLSGAE	QLEALKAFVE	AMVNENVSLV	ISRQLLTDFC	THLPNLPDST
90	100	110	120	130	140	150	160
AKEIYHFTLE	KIQPRVISFE	EQVASIRQHL	ASIYEKEEDW	RNAAQVLVGI	PLETGQKQYN	VDYKLETYLK	IARLYLEDDD
170	180	190	200	210	220	230	240
PVQAEAYINR	ASLLQNESTN	EQLQIHYKVC	YARVLDYRRK	FIEAAQRYNE	LSYKTIVHES	ERLEALKHAL	HCTILASAGQ
250	260	270	280	290	300	310	320
QRSRMLATLF	KDERCQQLAA	YGILEKMYLD	RIIRGNQLQE	FAAMLMPHQK	ATTADGSSIL	DRAVIEHNLL	SASKLYNNIT
330	340	350	360				
FEELGALLEI	PAAKHEKPCQ	RGISRSNHFV	SK				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2784	1	696.7062	37.74	3	65.2	11.2	1	255-271	R.CQQLAAYGILEKMYLDR.I	Carbamidomethyl: 1; Oxidation: 13

Detailed Protein Report

Protein 1175: PREDICTED: guanylate-binding protein 6 isoform X2 [Homo sapiens]

Accession:	gi|530361969	**Score:**	11.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	58.1
Database Date:	2015-11-30	**pI:**	6.0
		Sequence Coverage [%]:	4.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSTINHQALE	QLHYVTELTE	LIKAKSSPRP	DGVEDSTEFV	SFFPDFLWTV	RDFTLELKLN	GHPITEDEYL	ENALKLIQGN
90	100	110	120	130	140	150	160
NPRVQTSNFP	RECIRRFFPK	RKCFVFDRPT	NDKDLLANIE	KVSEKQLDPK	FQEQTNIFCS	YIFTHARTKT	LREGITVTGN
170	180	190	200	210	220	230	240
RLGTLAVTYV	EAINSGAVPC	LENAVITLAQ	RENSAAVQRA	ADYYSQQMAQ	RVKLPTDTLQ	ELLDMHAACE	REAIAIFMEH
250	260	270	280	290	300	310	320
SFKDENQEFQ	KKFMETTMNK	KGDFLLQNEE	SSVQYCQAKL	NELSKGLMES	ISAGSFSVPG	GHKLYMETKE	RIEQDYWQVP
330	340	350	360	370	380	390	400
RKGVKAKEVF	QRFLESQMVI	EESILQSDKA	LTDREKAVAV	DRAKKEAAEK	EQELLKQKLQ	EQQQQMEAQD	KSRKENIAQL
410	420	430	440	450	460	470	480
KEKLQMEREH	LLREQIMMLE	HTQKVQNDWL	HEGFKKKYEE	MNAEISQFKR	MIDTTKNDDT	PWIARTLDNL	ADELTAILSA
490	500	510					
PAKLIGHGVK	GVSSLFKKHK	LPF					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1393	1	927.1317	-42.53	3	47.0	11.2	1	2-25	M.STINHQALEQLHYVTELTELIKAK.S	

Detailed Protein Report

Protein 1176: pentatricopeptide repeat domain-containing protein 3, mitochondrial precursor [Homo sapiens]

Accession:	gi|38683855	**Score:**	11.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	78.5
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
MAVVSAVRWL	GLRSRLGQPL	TGRRAGLCEQ	ARSCRFYSGS	ATLSKVEGTD	VTGIEEVVIP	KKKTWDKVAV	LQALASTVNR
90	100	110	120	130	140	150	160
DTTAVPYVFQ	DDPYLMPASS	LESRSFLLAK	KSGENVAKFI	INSYPKYFQK	DIAEPHIPCL	MPEYFEPQIK	DISEAALKER
170	180	190	200	210	220	230	240
IELRKVKASV	DMFDQLLQAG	TTVSLETTNS	LLDLLCYYGD	QEPSTDYHFQ	QTGQSEALEE	ENDETSRRKA	GHQFGVTWRA
250	260	270	280	290	300	310	320
KNNAERIFSL	MPEKNEHSYC	TMIRGMVKHR	AYEQALNLYT	ELLNNRLHAD	VYTFNALIEA	TVCAINEKFE	EKWSKILELL
330	340	350	360	370	380	390	400
RHMVAQKVKP	NLQTFNTILK	CLRRFHVFAR	SPALQVLREM	KAIGIEPSLA	TYHHIIRLFD	QPGDPLKRSS	FIIYDIMNEL
410	420	430	440	450	460	470	480
MGKRFSPKDP	DDDKFFQSAM	SICSSLRDLE	LAYQVHGLLK	TGDNWKFIGP	DQHRNFYYSK	FFDLICLMEQ	IDVTLKWYED
490	500	510	520	530	540	550	560
LIPSAYFPHS	QTMIHLLQAL	DVANRLEVIP	KIWKDSKEYG	HTFRSDLREE	ILMLMARDKH	PPELQVAFAD	CAADIKSAYE
570	580	590	600	610	620	630	640
SQPIRQTAQD	WPATSLNCIA	ILFLRAGRTQ	EAWKMLGLFR	KHNKIPRSEL	LNELMDSAKV	SNSPSQAIEV	VELASAFSLP
650	660	670	680	690			
ICEGLTQRVM	SDFAINQEQK	EALSNLTALT	SDSDTDSSSD	SDSDTSEGK			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1587	1	820.8460	-154.50	2	49.6	11.2	1	345-358	R.FHVFARSPALQVLR.E	

Detailed Protein Report

Protein 1177: PREDICTED: zinc finger protein 62 homolog isoform X4 [Homo sapiens]

Accession:	gi|578811209	**Score:**	11.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	79.2
Database Date:	2015-11-30	**pI:**	10.4
		Sequence Coverage [%]:	2.3
		No. of unique 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
2131	1	938.3415	-116.92	2	56.8	11.2	2	317-332	K.RIHTREKPFGCDECGK.A	

Detailed Protein Report

Protein 1178: RNA-binding protein 40 [Homo sapiens]

Accession: gi|40538732
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 11.1
MW [kDa]: 58.5
pI: 8.5
Sequence Coverage [%]: 3.1
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MAAPEQPLAI	SRGCTSSSSL	SPPRGDRTLL	VRHLPAELTA	EEKEDLLKYF	GAQSVRVLSD	KGRLKHTAFA	TFPNEKAAIK
90	100	110	120	130	140	150	160
ALTRLHQLKL	LGHTLVVEFA	KEQDRVHSPC	PTSGSEKKKR	SDDPVEDDKE	KKELGYLTVE	NGIAPNHGLT	FPLNSCLKYM
170	180	190	200	210	220	230	240
YPPPSSTILA	NIVNALASVP	KFYVQVLHLM	NKMNLPTPFG	PITARPPMYE	DYMPLHAPLP	PTSPQPPEEP	PLPDEDEELS
250	260	270	280	290	300	310	320
SEESEYESTD	DEDRQRMNKL	MELANLQPKR	PKTIKQRHVR	KKRKIKDMLN	TPLCPSHSSL	HPVLLPSDVF	DQPQPVGNKR
330	340	350	360	370	380	390	400
IEFHISTDMP	AAFKKDLEKE	QNCEEKNHDL	PATEVDASNI	GFGKIFPKPN	LDITEEIKED	SDEMPSECIS	RRELEKGRIS
410	420	430	440	450	460	470	480
REEMETLSVF	RSYEPGEPNC	RIYVKNLAKH	VQEKDLKYIF	GRYVDFSSET	QRIMFDIRLM	KEGRMKGQAF	IGLPNEKAAA
490	500	510	520				
KALKEANGYV	LFGKPMVVQF	ARSARPKQDP	KEGKRKC				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1430	1	955.9503	-90.67	2	47.5	11.1	2	257-272	R.MNKLMELANLQPKRPK.T	

Protein 1179: dickkopf-related protein 3 precursor [Homo sapiens]

Accession:	gi|40548389	**Score:**	11.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	38.4
Database Date:	2015-11-30	**pI:**	4.4
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	7.4
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578820415	refseq_human (refseq_human_20140103.fasta)	PREDICTED: dickkopf-related protein 3 isoform X2 [Homo sapiens]
gi|66346689	refseq_human (refseq_human_20140103.fasta)	dickkopf-related protein 3 precursor [Homo sapiens]
gi|40548393	refseq_human (refseq_human_20140103.fasta)	dickkopf-related protein 3 precursor [Homo sapiens]

10	20	30	40	50	60	70	80
MQRLGATLLC	LLLAAAVPTA	PAPAPTATSA	PVKPGPALSY	PQEEATLNEM	FREVEELMED	TQHKLRSAVE	EMEAEEAAAK
90	100	110	120	130	140	150	160
ASSEVNLANL	PPSYHNETNT	DTKVGNNTIH	VHREIHKITN	NQTGQMVFSE	TVITSVGDEE	GRRSHECIID	EDCGPSMYCQ
170	180	190	200	210	220	230	240
FASFQYTCQP	CRGQRMLCTR	DSECCGDQLC	VWGHCTKMAT	RGSNGTICDN	QRDCQPGLCC	AFQRGLLFPV	CTPLPVEGEL
250	260	270	280	290	300	310	320
CHDPASRLLD	LITWELEPDG	ALDRCPCASG	LLCQPHSHSL	VYVCKPTFVG	SRDQDGEILL	PREVPDEYEV	GSFMEEVRQE
330	340	350	360				
LEDLERSLTE	EMALREPAAA	AAALLGGEEI					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2160	1	1045.4020	-30.23	3	56.9	11.1	2	176-201	R.MLCTRDSECCGDQLCVWGHCTKMATR.G	Carbamidomethyl: 3, 15, 20; Oxidation: 23

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Detailed Protein Report

Protein 1180: PREDICTED: uncharacterized protein LOC102723865 [Homo sapiens]

Accession:	gi|578795329	**Score:**	11.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	24.3
Database Date:	2015-11-30	**pI:**	12.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.7
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578843767	refseq_human (refseq_human_20140103.fasta)	PREDICTED: uncharacterized protein LOC102723865 [Homo sapiens]
gi|578810067	refseq_human (refseq_human_20140103.fasta)	PREDICTED: uncharacterized protein LOC102723865 [Homo sapiens]

10	20	30	40	50	60	70	80
MEIRSSHLPG	CLPPTIPRFL	KRAHQDSWLT	QRDALPAAGL	ARGNPRPPCY	SCRGIPAPRP	CHSGKGVPAP	RINQGEGIPA
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
HPGGSADPLR	SEARSGPQRR	CVPAPGSGTR	RGGGCRQPRS	RRPNPRHRDC	ASRGCRRTAA	LQLGAGAAAA	PVVAAVAAAA
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
RGPAGRRLGL	DARGSRGSLG	QAASRLRRLR	GSRICLDERC	SLAAVSLSVS	VQQEKGEKPA	KHYGADQCTC	CM

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2508	1	701.6144	-172.95	2	61.3	11.1	0	222-232	K.HYGADQCTCCM.-	Carbamidomethyl: 7, 9, 10

Detailed Protein Report

Protein 1181: PREDICTED: rho GTPase-activating protein 29 isoform X1 [Homo sapiens]

Accession:	gi|578800119	**Score:**	11.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	134.7
Database Date:	2015-11-30	**pI:**	6.1
		Sequence Coverage [%]:	0.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MERRDCFKEV	IHIRLEELLR	VLKSIMNKHQ	NLNSVDLQNA	AEMLTAKVKA	VNFTEVNEEN	KNDLFQEVFS	SIETLAFTFG
90	100	110	120	130	140	150	160
NILTNFLMGD	VGNDSLLRLP	VSRETKSFEN	VSVESVDSSS	EKGNFSPLEL	DNVLLKNTDS	IELALSYAKT	WSKYTKNIVS
170	180	190	200	210	220	230	240
WVEKKLNLEL	ESTRNMVKLA	EATRTNIGIQ	EFMPLQSLFT	NALLNDIESS	HLLQQTIAAL	QANKFVQPLL	GRKNEMEKQR
250	260	270	280	290	300	310	320
KEIKELWKQE	QNKMLEAENA	LKKAKLLCMQ	RQDEYEKAKS	SMFRAEEEHL	SSSGGLAKNL	NKQLEKKRRL	EEEALQKVEE
330	340	350	360	370	380	390	400
ANELYKVCVT	NVEERRNDLE	NTKREILAQL	RTLVFQCDLT	LKAVTVNLFH	MQHLQAASLA	DSLQSLCDSA	KLYDPGQEYS
410	420	430	440	450	460	470	480
EFVKATNSTE	EEKVDGNVNK	HLNSSQPSGF	GPANSLEDVV	RLPDSSNKIE	EDRCSNSADI	TGPSFIRSWT	FGMFSDSEST
490	500	510	520	530	540	550	560
GGSSESRSLD	SESISPGDFH	RKLPRTPSSG	TMSSADDLDE	REPPSPSETG	PNSLGTFKKT	LMSKAALTHK	FRKLRSPTKC
570	580	590	600	610	620	630	640
RDCEGIVVFQ	GVECEECLLV	CHRKCLENLV	IICGHQKLPG	KIHLFGAEFT	QVAKKEPDGI	PFILKICASE	IENRALCLQG
650	660	670	680	690	700	710	720
IYRVCGNKIK	TEKLCQALEN	GMHLVDISEF	SSHDICDVLK	LYLRQLPEPF	ILFRLYKEFI	DLAKEIQHVN	EEQETKKNSL
730	740	750	760	770	780	790	800
EDKKWPNMCI	EINRILLKSK	DLLRQLPASN	FNSLHFLIVH	LKRVVDHAEE	NKMNSKNLGV	IFGPSLIRPR	PTTAPITISS
810	820	830	840	850	860	870	880
LAEYSNQARL	VEFLITYSQK	IFDGSLQPQD	VMCSIGVVDQ	GCFPKPLLSP	EERDIERSMK	SLFFSSKEDI	HTSESESKIF
890	900	910	920	930	940	950	960
ERATSFEESE	RKQNALGKCD	ACLSDKAQLL	LDQEAESASQ	KIEDGKTPKP	LSLKSDRSTN	NVERHTPRTK	IRPVSLPVDR
970	980	990	1000	1010	1020	1030	1040
LLLASPPNER	NGRNMGNVNL	DKFCKNPAFE	GVNRKDAATT	VCSKFNGFDQ	QTLQKIQDKQ	YEQNSLTAKT	TMIMPSALQE
1050	1060	1070	1080	1090	1100	1110	1120
KGVTTSLQIS	GDHSINATQP	SKPYAEPVRS	VREASERRSS	DSYPLAPVRA	PRTLQPQHWT	TFYKPHAPII	SIRGNEEKPA
1130	1140	1150	1160	1170	1180	1190	1200
SPSAAVPPGT	DHDPHGLVVK	SMPDPDKASA	CPGQATGQPK	EDSEELGLPD	VNPMCQRPRL	KRMQQFEDLE	GEIPQFV

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
626	1	512.1199	-274.76	2	37.2	11.1	1	995-1004	R.KDAATTVCSK.F	

Detailed Protein Report

Protein 1182: **putative ATP-dependent Clp protease proteolytic subunit, mitochondrial precursor [Homo sapiens]**

Accession:	gi|5174419	**Score:**	11.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	30.2
Database Date:	2015-11-30	**pI:**	9.2
Modification(s):	Oxidation	**Sequence Coverage [%]:**	6.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MWPGILVGGA	RVASCRYPAL	GPRLAAHFPA	QRPPQRTLQN	GLALQRCLHA	TATRALPLIP	IVVEQTGRGE	RAYDIYSRLL
90	100	110	120	130	140	150	160
RERIVCVMGP	IDDSVASLVI	AQLLFLQSES	NKKPIHMYIN	SPGGVVTAGL	AIYDTMQYIL	NPICTWCVGQ	AASMGSLLLA
170	180	190	200	210	220	230	240
AGTPGMRHSL	PNSRIMIHQP	SGGARGQATD	IAIQAEEIMK	LKKQLYNIYA	KHTKQSLQVI	ESAMERDRYM	SPMEAQEFGI
250	260	270	280				
LDKVLVHPPQ	DGEDEPTLVQ	KEPVEAAPAA	EPVPAST				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2123	1	1023.3631	-103.43	2	56.7	11.1	1	227-243	R.DRYMSPMEAQEFGILDK.V	Oxidation: 7

Detailed Protein Report

Protein 1183: PREDICTED: F-box/LRR-repeat protein 4 isoform X1 [Homo sapiens]

Accession:	gi|530383594	**Score:**	11.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	67.5
Database Date:	2015-11-30	**pI:**	6.2
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	3.4
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MSPVFPMLTV LTMFYYICLR RRARTATRGE MMNTHRAIES NSQTSPLNAE VVQYAKEVVD FSSHYGSENS MSYTMWNLAG
        90        100        110        120        130        140        150        160
VPNVFPSSGD FTQTAVFRTY GTWWDQCPSA SLPFKRTPPN FQSQDYVELT FEQQVYPTAV HVLETYHPGA VIRILACSAN
       170        180        190        200        210        220        230        240
PYSPNPPAEV RWEILWSERP TKVNASQARQ FKPCIKQINF PTNLIRLEVN SSLLEYYTEL DAVVLHGVKD KPVLSLKTSL
       250        260        270        280        290        300        310        320
IDMNDIEDDA YAEKDGCGMD SLNKKFSSAV LGEGPNNGYF DKLPYELIQL ILNHLTLPDL CRLAQTCKLL SQHCCDPLQY
       330        340        350        360        370        380        390        400
IHLNLQPYWA KLDDTSLEFL QSRCTLVQWL NLSWTGNRGF ISVAGFSRFL KVCGSELVRL ELSCSHFLNE TCLEVISEMC
       410        420        430        440        450        460        470        480
PNLQALNLSS CDKLPPQAFN HIAKLCSLKR LVLYRTKVEI EDYDVIASMI GAKCKKLRTL DLWRCKNITE NGIAELASGC
       490        500        510        520        530        540        550        560
PLLEELDLGW CPTLQSSTGC FTRLAHQLPN LQKLFLTANR SVCDTDIDEL ACNCTRLQQL DILGTRMVSP ASLRKLLESC
       570        580        590        600
KDLSLLDVSF CSQIDNRAVL ELNASFPKVF IKKSFTQ
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1738	1	841.7160	-64.35	3	51.7	11.1	1	2-21	M.SPVFPMLTVLTMFYYICLRR.R	Carbamidomethyl: 17; Oxidation: 6

Detailed Protein Report

Protein 1184: tyrosine-protein kinase CSK [Homo sapiens]

Accession:	gi|4758078	**Score:**	11.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	50.7
Database Date:	2015-11-30	**pI:**	6.7
		Sequence Coverage [%]:	2.4
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530405396	refseq_human (refseq_human_20140103.fasta)	PREDICTED: tyrosine-protein kinase CSK isoform X1 [Homo sapiens]
gi|187475373	refseq_human (refseq_human_20140103.fasta)	tyrosine-protein kinase CSK [Homo sapiens]

10	20	30	40	50	60	70	80
MSAIQAAWPS	GTECIAKYNF	HGTAEQDLPF	CKGDVLTIVA	VTKDPNWYKA	KNKVGREGII	PANYVQKREG	VKAGTKLSLM
90	100	110	120	130	140	150	160
PWFHGKITRE	QAERLLYPPE	TGLFLVREST	NYPGDYTLCV	SCDGKVEHYR	IMYHASKLSI	DEEVYFENLM	QLVEHYTSDA
170	180	190	200	210	220	230	240
DGLCTRLIKP	KVMEGTVAAQ	DEFYRSGWAL	NMKELKLLQT	IGKGEFGDVM	LGDYRGNKVA	VKCIKNDATA	QAFLAEASVM
250	260	270	280	290	300	310	320
TQLRHSNLVQ	LLGVIVEEKG	GLYIVTEYMA	KGSLVDYLRS	RGRSVLGGDC	LLKFSLDVCE	AMEYLEGNNF	VHRDLAARNV
330	340	350	360	370	380	390	400
LVSEDNVAKV	SDFGLTKEAS	STQDTGKLPV	KWTAPEALRE	KKFSTKSDVW	SFGILLWEIY	SFGRVPYPRI	PLKDVVPRVE
410	420	430	440	450	460		
KGYKMDAPDG	CPPAVYEVMK	NCWHLDAAMR	PSFLQLREQL	EHIKTHELHL			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1966	2	616.2745	-102.45	2	54.5	11.1	0	57-67	R.EGIIPANYVQK.R	

Detailed Protein Report

Protein 1185: **spermatogenesis-associated protein 31D1 [Homo sapiens]**

Accession:	gi|48717285	**Score:**	11.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	175.5
Database Date:	2015-11-30	**pI:**	10.0
		Sequence Coverage [%]:	1.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MENILCFLNS	YTETGLSPDS	HWLDIDPNFI	CLSGLGLFIL	YLFYVVLTLY	SSPTEKNNDI	QKHQGRAKRR	RKGGTFKGFP
90	100	110	120	130	140	150	160
DWKSFQREEE	EERKLLSLLK	SFGPPVSCSP	RGQHHDTNHF	RRLLCPDPVC	RVCKRATADI	QQLLSWESLK	DAAPSVSPLA
170	180	190	200	210	220	230	240
SSASATESSF	TLASTPSATP	PEDLILSPRP	KASPPPPLIL	SPDLITTLAD	LFSPSPLRDP	LPPQPVSPLD	SKFPIDHSPP
250	260	270	280	290	300	310	320
QQLPFPLLPP	HHIERVESSL	QPEASLSLNT	IFSFGSTLCQ	DISQAMNPID	SCARHHGPPI	PSALPPEDCT	VTQSKSSLTI
330	340	350	360	370	380	390	400
LKTFPEMLSL	GGSGGSSTSA	PTIKGIDHSH	LASSEFTWWQ	PHAKDSFSSN	FVPSDFMEEL	LTLHSSEAFL	GGHSVANLIE
410	420	430	440	450	460	470	480
PVNISFLSHD	ILALLERQVK	KRGDFLMWKE	NGKKPGSFPK	QLRPNYQLNS	SRNMLTSIAV	KHDLAESFPF	WASKGKLEWQ
490	500	510	520	530	540	550	560
HIHQQPPHSK	CFEDHLEQKY	VQLFWGLPSL	HSESLHPTVL	VQRGHSSMFV	FFNGITNTSI	SHESPVLPPP	QPLSLPSTQP
570	580	590	600	610	620	630	640
LPLPQTLPQG	QSPHLTQVKS	LAQPQSPFRA	LLPSPLFLIR	ICGVCFHRPQ	NEARSLLPSE	INHLEWNVLQ	KVQESLWGLP
650	660	670	680	690	700	710	720
SVVQKSQEDF	CPPAPNPELV	RKSFKVHVPI	SIIPGDFPLS	SEVRKKLEQH	IRRRLIQRRW	GLPRRIHESL	SLLRPQSKIS
730	740	750	760	770	780	790	800
ELSVSERIHG	PLNISLVEGQ	RCNVLKKSAS	SFPRSFHERS	SNMLSMENVG	NYQGYSQETV	PKDHLLHGPE	TSSDKDLRSN
810	820	830	840	850	860	870	880
SERDLETHMM	HLSGNDSGVR	LGQKQLENAL	TVRLSKKFEE	INEGRMPGTV	HSSWHSVKQT	MSLPEKSHSQ	IKHRNLVTLV
890	900	910	920	930	940	950	960
SEDHCVDTSQ	EISFLSSNKQ	KMLEAHIKTF	RMRMLWGLPL	KVLESIEIFK	SKADLSTSFS	HFDLPSSATF	ISQGDSKDGV
970	980	990	1000	1010	1020	1030	1040
SKSRSRSTFQ	GEKLGTTSSV	PILDRPHPVS	SPVVQEGQGT	LRRQFSDTDH	DLIETDSKDG	ASTSLRRGTT	DFQSEKLDST
1050	1060	1070	1080	1090	1100	1110	1120
SSFPILGHSY	LVTSPVNQEK	QGTLRREFSD	TDNDLTESVR	TTEDGRQTFL	PPPHSIVDEV	SQKQTVLASR	CSAELPIMQA
1130	1140	1150	1160	1170	1180	1190	1200
GAGCESWDKR	KSSFHNVDRL	QGSRKTFPVT	NALQSQTRNN	LTTSKSGSCS	LTNVKASTSN	ETEIFPPRIS	VPQDPKSSYL
1210	1220	1230	1240	1250	1260	1270	1280
KNQMLSQLKL	VQRKHSQPQS	HFTDMSFALD	NLSSKDLLTN	SQGISSGDMG	TSQVVHVHLE	DSGIRVAQKQ	EPRVPTCVLQ
1290	1300	1310	1320	1330	1340	1350	1360
KCQVTNFPPA	VNRVSPVRPK	GGELDGGDAG	LGTSQRRRKS	LPVHNKTSGE	VLGSKSSPTL	KTQPPPENLF	RKWMKTSLQW
1370	1380	1390	1400	1410	1420	1430	1440
FNKPSISYEE	QESSWEKGSS	LSSCVQNIGR	VIRAAFTGTT	EAQKIRKDTR	EFLEEKLGHR	HGIDITCPQE	PLSFPVGLGK
1450	1460	1470	1480	1490	1500	1510	1520
AQHNPEVHVR	AEPVQGCPCN	YRAPSCKVTR	TKSCSQQAIF	VGQNYPTRIR	QIIDKDRQPQ	KVEAFKGKIL	CQSHPQSMPH
1530	1540	1550	1560	1570	1580		
RKPVPHPNPT	CRRQVSLVCP	AVPTSAKSPV	FSDVPFLTGQ	KMLPKHLQGG	KFPPTK		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1691	1	900.9255	-88.98	2	50.9	11.1	1	95-111	K.LLSLLKSFGPPVSCSPR.G	

Detailed Protein Report

Protein 1186: PREDICTED: zinc finger protein 608 isoform X4 [Homo sapiens]

Accession:	gi|530380059	**Score:**	11.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	133.1
Database Date:	2015-11-30	**pI:**	9.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	0.9
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 0.75 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MQLEGKGQLD	PIQTVDPLFT	VPAPPPPISS	SLTPQILPSY	FSPSSSNIAA	PVEQLLVRTR	SVGVNTCEVG	VVTEPECLGP
90	100	110	120	130	140	150	160
CEPGTSVNLE	GIVWHETEEG	VLVVNVTWRN	KTYVGTLLDC	TKHDWAPPRF	CESPTSDLEM	RGGRGRGKRA	RSAAAAPGSE
170	180	190	200	210	220	230	240
ASFTESRGLQ	NKNRGGANGK	GRRGSLNASG	RRTPPNCAAE	DIKASPSSTN	KRKNKPPMEL	DLNSSSEDNK	PGKRVRTNSR
250	260	270	280	290	300	310	320
STPTTPQGKP	ETTFLDQGCS	SPVLIDCPHP	NCNKKYKHIN	GLRYHQAHAH	LDPENKLEFE	PDSEDKISDC	EEGLSNVALE
330	340	350	360	370	380	390	400
CSEPSTSVSA	YDQLKAPASP	GAGNPPGTPK	GKRELMSNGP	GSIIGAKAGK	NSGKKKGLNN	ELNNLPVISN	MTAALDSCSA
410	420	430	440	450	460	470	480
ADGSLAAEMP	KLEAEGLIDK	KNLGDKEKGK	KATNCKTDKN	LSKLKSARPI	APAPAPTPPQ	LIAIPTATFT	TTTTGTIPGL
490	500	510	520	530	540	550	560
PSLTTTVVQA	TPKSPPLKPI	QPKPTIMGEP	ITVNPALVSL	KDKKKKEKRK	LKDKEGKETG	SPKMDAKLGK	LEDSKGASKD
570	580	590	600	610	620	630	640
LPGHFLKDHL	NKNEGLANGL	SESQESRMAS	IKAEADKVYT	FTDNAPSPSI	GSASRLECST	LVNGQAPMAP	LHVLTQNGAE
650	660	670	680	690	700	710	720
SSAAKTSSPA	YSDISDAADD	GGSDSRSEGM	RSKASSPSDI	ISSKDSVVKG	HSSTTAQSSQ	LKESHSPYYH	SYDPYYSPSY
730	740	750	760	770	780	790	800
MHPGQVGAPA	AGNSGSTQGM	KIKKESEEDA	EKKDKAEQLD	SKKVDHNSAS	LQPQHQSVIT	QRHPALAQSL	YYGQYAYGLY
810	820	830	840	850	860	870	880
MDQKSLMATS	PAYRQQYEKY	YEDQRLAEQK	MAQTGRGDCE	RKSELPLKEL	GKEETKQKNM	PSATISKAPS	TPEPNKNHSK
890	900	910	920	930	940	950	960
LGPSVPNKTE	ETGKSQLLSN	HQQQLQADSF	KAKQMENHQL	IKEAVEMKSV	MDSMKQTGVD	PTSRFKQDPD	SRTWHHYVYQ
970	980	990	1000	1010	1020	1030	1040
PKYLDQQKSE	ELDREKKLKE	DSPRKTPNKE	SGVPSLPVSL	TSIKEEPKEA	KHPDSQSMEE	SKLKNDDRKT	PVNWKDSRGT
1050	1060	1070	1080	1090	1100	1110	1120
RVAVSSPMSQ	HQSYIQYLHA	YPYPQMYDPS	HPAYRAVSPV	LMHSYPGAYL	SPGFHYPVYG	KMSGREETEK	VNTSPSVNTK
1130	1140	1150	1160	1170	1180	1190	1200
TTTESKALDL	LQQHANQYRS	KSPAPVEKAT	AEREREAERE	RDRHSPFGQR	HLHTHHHTHV	GMGYPLIPGQ	YDPFQGLTSA
1210	1220	1230					
ALVASQQVAA	QASASGMFPG	QRRE					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
205	1	635.8021	-29.77	2	32.3	11.1	0	112-122	K.TYVGTLLDCTK.H	Carbamidomethyl: 9	MD:MU 0.75

Detailed Protein Report

Protein 1187: adenosine receptor A2a [Homo sapiens]

Accession:	gi|5921992	**Score:**	11.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	44.7
Database Date:	2015-11-30	**pI:**	9.6
		Sequence Coverage [%]:	3.2
		No. of unique Peptides:	1

Quantitation

MD:MU	**Median:** 0.36		**CV:** 0.00 %		**No. of Peptides:**	1

Alias proteins:

Accession	Name	Description
gi|511772972	refseq_human (refseq_human_20140103.fasta)	adenosine receptor A2a [Homo sapiens]
gi|511772970	refseq_human (refseq_human_20140103.fasta)	adenosine receptor A2a [Homo sapiens]
gi|511772967	refseq_human (refseq_human_20140103.fasta)	adenosine receptor A2a [Homo sapiens]
gi|511772965	refseq_human (refseq_human_20140103.fasta)	adenosine receptor A2a [Homo sapiens]

10	20	30	40	50	60	70	80
MPIMGSSVYI	TVELAIAVLA	ILGNVLVCWA	VWLNSNLQNV	TNYFVVSLAA	ADIAVGVLAI	PFAITISTGF	CAACHGCLFI
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
ACFVLVLTQS	SIFSLLAIAI	DRYIAIRIPL	RYNGLVTGTR	AKGIIAICWV	LSFAIGLTPM	LGWNNCGQPK	EGKNHSQGCG
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
EGQVACLFED	VVPMNYMVYF	NFFACVLVPL	LLMLGVYLRI	FLAARRQLKQ	MESQPLPGER	ARSTLQKEVH	AAKSLAIIVG
250	**260**	**270**	**280**	**290**	**300**	**310**	**320**
LFALCWLPLH	IINCFTFFCP	DCSHAPLWLM	YLAIVLSHTN	SVVNPFIYAY	RIREFRQTFR	KIIRSHVLRQ	QEPFKAAGTS
330	**340**	**350**	**360**	**370**	**380**	**390**	**400**
ARVLAAHGSD	GEQVSLRLNG	HPPGVWANGS	APHPERRPNG	YALGLVSGGS	AQESQGNTGL	PDVELLSHEL	KGVCPEPPGL
410	**420**						
DDPLAQDGAG	VS						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
1218	1	695.7632	-135.29	2	44.9	11.0	1	310-322	R.QQEPFKAAGTSAR.V		MD:MU	0.36

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Detailed Protein Report

Protein 1188: muscarinic acetylcholine receptor M3 [Homo sapiens]

Accession:	gi|4502819	**Score:**	11.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	66.1
Database Date:	2015-11-30	**pI:**	10.0
		Sequence Coverage [%]:	3.1
		No. of unique Peptides:	1

Quantitation

MD:MU	**Median:**	1.33	**CV:**	0.00 %	**No. of Peptides:**	1

Alias proteins:

Accession	Name	Description
gi|578802131	refseq_human (refseq_human_20140103.fasta)	PREDICTED: muscarinic acetylcholine receptor M3 isoform X5 [Homo sapiens]
gi|530366001	refseq_human (refseq_human_20140103.fasta)	PREDICTED: muscarinic acetylcholine receptor M3 isoform X4 [Homo sapiens]
gi|530365999	refseq_human (refseq_human_20140103.fasta)	PREDICTED: muscarinic acetylcholine receptor M3 isoform X3 [Homo sapiens]
gi|530365997	refseq_human (refseq_human_20140103.fasta)	PREDICTED: muscarinic acetylcholine receptor M3 isoform X2 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MTLHNNSTTS PLFPNISSSW IHSPSDAGLP PGTVTHFGSY NVSRAAGNFS SPDGTTDDPL GGHTVWQVVF IAFLTGILAL
        90        100        110        120        130        140        150        160
VTIIGNILVI VSFKVNKQLK TVNNYFLLSL ACADLIIGVI SMNLFTTYII MNRWALGNLA CDLWLAIDYV ASNASVMNLL
       170        180        190        200        210        220        230        240
VISFDRYFSI TRPLTYRAKR TTKRAGVMIG LAWVISFVLW APAILFWQYF VGKRTVPPGE CFIQFLSEPT ITFGTAIAAF
       250        260        270        280        290        300        310        320
YMPVTIMTIL YWRIYKETEK RTKELAGLQA SGTEAETENF VHPTGSSRSC SSYELQQQSM KRSNRRKYGR CHFWFTTKSW
       330        340        350        360        370        380        390        400
KPSSEQMDQD HSSSDSWNNN DAAASLENSA SSDEEDIGSE TRAIYSIVLK LPGHSTILNS TKLPSSDNLQ VPEEELGMVD
       410        420        430        440        450        460        470        480
LERKADKLQA QKSVDDGGSF PKSFSKLPIQ LESAVDTAKT SDVNSSVGKS TATLPLSFKE ATLAKRFALK TRSQITKRKR
       490        500        510        520        530        540        550        560
MSLVKEKKAA QTLSAILLAF IITWTPYNIM VLVNTFCDSC IPKTFWNLGY WLCYINSTVN PVCYALCNKT FRTTFKMLLL
       570        580        590        600
CQCDKKKRRK QQYQQRQSVI FHKRAPEQAL
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
943	1	630.8946	-151.26	3	41.3	11.0	2	405-422	K.ADKLQAQKSVDDGGSFPK.S		MD:MU 1.33

Detailed Protein Report

Protein 1189: PREDICTED: NADPH oxidase 4 isoform X5 [Homo sapiens]

Accession:	gi|578822233	**Score:**	11.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	59.9
Database Date:	2015-11-30	**pI:**	10.0
		Sequence Coverage [%]:	1.0
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MNVLLFWKTF LLYNQGPEYH YLHQMLGLGL CLSRASASVL NLNCSLILLP MCRTLLAYLR GSQKVPSRRT RRLLDKSRTF
        90        100        110        120        130        140        150        160
HITCGVTICI FSGVHVAAHL VNALNFSVNY SEDFVELNAA RYRDEDPRKL LFTTVPGLTG VCMVVVLFLM ITASTYAIRV
       170        180        190        200        210        220        230        240
SNYDIFWYTH NLFFVFYMLL TLHVSGGLLK YQTNLDTHPP GCISLNRTSS QNISLPEYFS EHFHEPFPEG FSKPAEFTQH
       250        260        270        280        290        300        310        320
KFVKICMEEP RFQANFPQTW LWISGPLCLY CAERLYRYIR SNKPVTIISV MSHPSDVMEI RMVKENFKAR PGQYITLHCP
       330        340        350        360        370        380        390        400
SVSALENHPF TLTMCPTETK ATFGVHLKIV GDWTERFRDL LLPPSSQDSE ILPFIQSRNY PKDDWKPYKL RRLYFIWVCR
       410        420        430        440        450        460        470        480
DIQSFRWFAD LLCMLHNKFW QENRPDYVNI QLYLSQTDGI QKIIGEKYHA LNSRLFIGRP RWKLLFDEIA KYNRGKTVGV
       490        500        510        520
FCCGPNSLSK TLHKLSNQNN SYGTRFEYNK ESFS
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1019	1	700.1280	-288.50	1	42.3	11.0	0	506-510	R.FEYNK.E	

Detailed Protein Report

Protein 1190: calcium-activated chloride channel regulator 2 precursor [Homo sapiens]

Accession: gi|5729769
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 11.0
MW [kDa]: 103.9
pI: 6.6
Sequence Coverage [%]: 1.6
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MTQRSIAGPI	CNLKFVTLLV	ALSSELPFLG	AGVQLQDNGY	NGLLIAINPQ	VPENQNLISN	IKEMITEASF	YLFNATKRRV
90	100	110	120	130	140	150	160
FFRNIKILIP	ATWKANNNSK	IKQESYEKAN	VIVTDWYGAH	GDDPYTLQYR	GCGKEGKYIH	FTPNFLLNDN	LTAGYGSRGR
170	180	190	200	210	220	230	240
VFVHEWAHLR	WGVFDEYNND	KPFYINGQNQ	IKVTRCSSDI	TGIFVCEKGP	CPQENCIISK	LFKEGCTFIY	NSTQNATASI
250	260	270	280	290	300	310	320
MFMQSLSSVV	EFCNASTHNQ	EAPNLQNQMC	SLRSAWDVIT	DSADFHHSFP	MNGTELPPPP	TFSLVQAGDK	VVCLVLDVSS
330	340	350	360	370	380	390	400
KMAEADRLLQ	LQQAAEFYLM	QIVEIHTFVG	IASFDSKGEI	RAQLHQINSN	DDRKLLVSYL	PTTVSAKTDI	SICSGLKKGF
410	420	430	440	450	460	470	480
EVVEKLNGKA	YGSVMILVTS	GDDKLLGNCL	PTVLSSGSTI	HSIALGSSAA	PNLEELSRLT	GGLKFFVPDI	SNSNSMIDAF
490	500	510	520	530	540	550	560
SRISSGTGDI	FQQHIQLEST	GENVKPHHQL	KNTVTVDNTV	GNDTMFLVTW	QASGPPEIIL	FDPDGRKYYT	NNFITNLTFR
570	580	590	600	610	620	630	640
TASLWIPGTA	KPGHWTYTLN	NTHHSLQALK	VTVTSRASNS	AVPPATVEAF	VERDSLHFPH	PVMIYANVKQ	GFYPILNATV
650	660	670	680	690	700	710	720
TATVEPETGD	PVTLRLLDDG	AGADVIKNDG	IYSRYFFSFA	ANGRYSLKVH	VNHSPSISTP	AHSIPGSHAM	YVPGYTANGN
730	740	750	760	770	780	790	800
IQMNAPRKSV	GRNEEERKWG	FSRVSSGGSF	SVLGVPAGPH	PDVFPPCKII	DLEAVKVEEE	LTLSWTAPGE	DFDQGQATSY
810	820	830	840	850	860	870	880
EIRMSKSLQN	IQDDFNNAIL	VNTSKRNPQQ	AGIREIFTFS	PQISTNGPEH	QPNGETHESH	RIYVAIRAMD	RNSLQSAVSN
890	900	910	920	930	940	950	
IAQAPLFIPP	NSDPVPARDY	LILKGVLTAM	GLIGIICLII	VVTHHTLSRK	KRADKKENGT	KLL	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1242	1	786.5105	159.93	2	45.1	11.0	0	410-424	K.AYGSVMILVTSGDDK.L	Oxidation: 6

Detailed Protein Report

Protein 1191: unconventional myosin-VIIa isoform 2 [Homo sapiens]

Accession:	gi|189083802	**Score:**	11.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	250.1
Database Date:	2015-11-30	**pI:**	9.4
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.1
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MVILQQGDHV WMDLRLGQEF DVPIGAVVKL CDSGQVQVVD DEDNEHWISP QNATHIKPMH PTSVHGVEDM IRLGDLNEAG
        90        100        110        120        130        140        150        160
ILRNLLIRYR DHLIYTYTGS ILVAVNPYQL LSIYSPEHIR QYTNKKIGEM PPHIFAIADN CYFNMKRNSR DQCCIISGES
       170        180        190        200        210        220        230        240
GAGKTESTKL ILQFLAAISG QHSWIEQQVL EATPILEAFG NAKTIRNDNS SRFGKYIDIH FNKRGAIEGA KIEQYLLEKS
       250        260        270        280        290        300        310        320
RVCRQALDER NYHVFYCMLE GMSEDQKKKL GLGQASDYNY LAMGNCITCE GRVDSQEYAN IRSAMKVLMF TDTENWEISK
       330        340        350        360        370        380        390        400
LLAAILHLGN LQYEARTFEN LDACEVLFSP SLATAASLLE VNPPDLMSCL TSRTLITRGE TVSTPLSREQ ALDVRDAFVK
       410        420        430        440        450        460        470        480
GIYGRLFVWI VDKINAAIYK PPSQDVKNSR RSIGLLDIFG FENFAVNSFE QLCINFANEH LQQFFVRHVF KLEQEEYDLE
       490        500        510        520        530        540        550        560
SIDWLHIEFT DNQDALDMIA NKPMNIISLI DEESKFPKGT DTTMLHKLNS QHKLNANYIP PKNNHETQFG INHFAGIVYY
       570        580        590        600        610        620        630        640
ETQGFLEKNR DTLHGDIIQL VHSSRNKFIK QIFQADVAMG AETRKRSPTL SSQFKRSLEL LMRTLGACQP FFVRCIKPNE
       650        660        670        680        690        700        710        720
FKKPMLFDRH LCVRQLRYSG MMETIRIRRA GYPIRYSFVE FVERYRVLLP GVKPAYKQGD LRGTCQRMAE AVLGTHDDWQ
       730        740        750        760        770        780        790        800
IGKTKIFLKD HHDMLLEVER DKAITDRVIL LQKVIRGFKD RSNFLKLKNA ATLIQRHWRG HNCRKNYGLM RLGFLRLQAL
       810        820        830        840        850        860        870        880
HRSRKLHQQY RLARQRIIQF QARCRAYLVR KAFRHRLWAV LTVQAYARGM IARRLHQRLR AEYLWRLEAE KMRLAEEEKL
       890        900        910        920        930        940        950        960
RKEMSAKKAK EEAERKHQER LAQLAREDAE RELKEKEAAR RKKELLEQME RARHEPVNHS DMVDKMFGFL GTSGGLPGQE
       970        980        990       1000       1010       1020       1030       1040
GQAPSGFEDL ERGRREMVEE DLDAALPLPD EDEEDLSEYK FAKFAATYFQ GTTTHSYTRR PLKQPLLYHD DEGDQLAALA
      1050       1060       1070       1080       1090       1100       1110       1120
VWITILRFMG DLPEPKYHTA MSDGSEKIPV MTKIYETLGK KTYKRELQAL QGEGEAQLPE GQKKSSVRHK LVHLTLKKKS
      1130       1140       1150       1160       1170       1180       1190       1200
KLTEEVTKRL HDGESTVQGN SMLEDRPTSN LEKLHFIIGN GILRPALRDE IYCQISKQLT HNPSKSSYAR GWILVSLCVG
      1210       1220       1230       1240       1250       1260       1270       1280
CFAPSEKFVK YLRNFIHGGP PGYAPYCEER LRRTFVNGTR TQPPSWLELQ ATKSKKPIML PVTFMDGTTK TLLTDSATTA
      1290       1300       1310       1320       1330       1340       1350       1360
KELCNALADK ISLKDRFGFS LYIALFDKVS SLGSGSDHVM DAISQCEQYA KEQGAQERNA PWRLFFRKEV FTPWHSPSED
      1370       1380       1390       1400       1410       1420       1430       1440
NVATNLIYQQ VVRGVKFGEY RCEKEDDLAE LASQQYFVDY GSEMILERLL NLVPTYIPDR EITPLKTLEK WAQLAIAAHK
      1450       1460       1470       1480       1490       1500       1510       1520
KGIYAQRRTD AQKVKEDVVS YARFKWPLLF SRFYEAYKFS GPSLPKNDVI VAVNWTGVYF VDEQEQVLLE LSFPEIMAVS
      1530       1540       1550       1560       1570       1580       1590       1600
SSRGAKTTAP SFTLATIKGD EYTFTSSNAE DIRDLVVTFL EGLRKRSKYV VALQDNPNPA GEESGFLSFA KGDLIILDHD
      1610       1620       1630       1640       1650       1660       1670       1680
TGEQVMNSGW ANGINERTKQ RGDFPTDSVY VMPTVTMPPR EIVALVTMTP DQRQDVVRLL QLRTAEPEVR AKPYTLEEFS
      1690       1700       1710       1720       1730       1740       1750       1760
YDYFRPPPKH TLSRVMVSKA RGKDRLWSHT REPLKQALLK KLLGSEELSQ EACLAFIAVL KYMGDYPSKR TRSVNELTDQ
      1770       1780       1790       1800       1810       1820       1830       1840
IFEGPLKAEP LKDEAYVQIL KQLTDNHIRY SEERGWELLW LCTGLFPPSN ILLPHVQRFL QSRKHCPLAI DCLQRLQKAL
      1850       1860       1870       1880       1890       1900       1910       1920
RNGSRKYPPH LVEVEAIQHK TTQIFHKVYF PDDTDEAFEV ESSTKAKDFC QNIATRLLLK SSEGFSLFVK IADKVLSVPE
      1930       1940       1950       1960       1970       1980       1990       2000
NDFFFDFVRH LTDWIKKARP IKDGIVPSLT YQVFFMKKLW TTTVPGKDPM ADSIFHYYQE LPKYLRGYHK CTREEVLQLG
      2010       2020       2030       2040       2050       2060       2070       2080
ALIYRVKFEE DKSYFPSIPK LLRELVPQDL IRQVSPDDWK RSIVAYFNKH AGKSKEEAKL AFLKLIFKWP TFGSAFFEQT
      2090       2100       2110       2120       2130       2140       2150       2160
TEPNFPEILL IAINKYGVSL IDPKTKDILT THPFTKISNW SSGNTYFHIT IGNLVRGSKL LCETSLGYKM DDLLTSYISQ
      2170       2180
```

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1136	1	985.2085	56.47	3	43.8	11.0	1	1959-1983	K.LWTTTVPGKDPMADSIFHYYQELPK.Y	Oxidation: 12

Detailed Protein Report

Protein 1192: **PREDICTED: signal-induced proliferation-associated 1-like protein 1 isoform X6 [Homo sapiens]**

Accession:	gi|530403485	**Score:**	11.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	197.3
Database Date:	2015-11-30	**pI:**	9.2
Modification(s):	Oxidation	**Sequence Coverage [%]:**	0.6
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|545746375	refseq_human (refseq_human_20140103.fasta)	signal-induced proliferation-associated 1-like protein 1 isoform 3 [Homo sapiens]

Detailed Protein Report

10	20	30	40	50	60	70	80
MTSLKRSQTE	RPLATDRASV	VGTDGTPKVH	TDDFYMRRFR	SQNGSLGSSV	MAPVGPPRSE	GSHHITSTPG	VPKMGVRARI
90	100	110	120	130	140	150	160
ADWPPRKENI	KESSRSSQEI	ETSSCLDSLS	SKSSPVSQGS	SVSLNSNDSA	MLKSIQNTLK	NKTRPSENMD	SRFLMPEAYP
170	180	190	200	210	220	230	240
SSPRKALRRI	RQRSNSDITI	SELDVDSFDE	CISPTYKTGP	SLHREYGSTS	SIDKQGTSGE	SFFDLLKGYK	DDKSDRGPTP
250	260	270	280	290	300	310	320
TKLSDFLITG	GGKGSGFSLD	VIDGPISQRE	NLRLFKEREK	PLKRRSKSET	GDSSIFRKLR	NAKGEELGKS	SDLEDNRSED
330	340	350	360	370	380	390	400
SVRPWTCPKC	FAHYDVQSIL	FDLNEAIMNR	HNVIKRRNTT	TGASAAAVAS	LVSGPLSHSA	SFSSPMGSTE	DLNSKGSLSM
410	420	430	440	450	460	470	480
DQGDDKSNEL	VMSCPYFRNE	IGGEGERKIS	LSKSNSGSFS	GCESASFEST	LSSHCTNAGV	AVLEVPKENL	VLHLDRVKRY
490	500	510	520	530	540	550	560
IVEHVDLGAY	YYRKFFYQKE	HWNYFGADEN	LGPVAVSIRR	EKPDEMKENG	SPYNYRIIFR	TSELMTLRGS	VLEDAIPSTA
570	580	590	600	610	620	630	640
KHSTARGLPL	KEVLEHVVPE	LNVQCLRLAF	NTPKVTEQLM	KLDEQGLNYQ	QKVGIMYCKA	GQSTEEEMYN	NESAGPAFEE
650	660	670	680	690	700	710	720
FLQLLGERVR	LKGFEKYRAQ	LDTKTDSTGT	HSLYTTYKDY	EIMFHVSTML	PYTPNNKQQL	LRKRHIGNDI	VTIVFQEPGA
730	740	750	760	770	780	790	800
QPFSPKNIRS	HFQHVFVIVR	VHNPCSDSVC	YSVAVTRSRD	VPSFGPPIPK	GVTFPKSNVF	RDFLLAKVIN	AENAAHKSEK
810	820	830	840	850	860	870	880
FRAMATRTRQ	EYLKDLAEKN	VTNTPIDPSG	KFPFISLASK	KKEKSKPYPG	AELSSMGAIV	WAVRAEDYNK	AMELDCLLGI
890	900	910	920	930	940	950	960
SNEFIVLIEQ	ETKSVVFNCS	CRDVIGWTST	DTSLKIFYER	GECVSVGSFI	NIEEIKEIVK	RLQFVSKGCE	SVEMTLRRNG
970	980	990	1000	1010	1020	1030	1040
LGQLGFHVNY	EGIVADVEPY	GYAWQAGLRQ	GSRLVEICKV	AVATLSHEQM	IDLLRTSVTV	KVVIIPPHDD	CTPRRSCSET
1050	1060	1070	1080	1090	1100	1110	1120
YRMPVMEYKM	NEGVSYEFKF	PFRNNNKWQR	NASKGPHSPQ	VPSQVQSPMT	SRLNAGKGDG	KMPPPERAAN	IPRSISSDGR
1130	1140	1150	1160	1170	1180	1190	1200
PLERRLSPGS	DIYVTVSSMA	LARSQCRNSP	SNLSSSSDTG	SVGGTYRQKS	MPEGFGVSRR	SPASIDRQNT	QSDIGGSGKS
1210	1220	1230	1240	1250	1260	1270	1280
TPSWQRSEDS	IADQMEPTCH	LPAVSKVLPA	FRESPSGRLM	RQDPVVHLSP	NKQGHSDSHY	SSHSSSNTLS	SNASSAHSDE
1290	1300	1310	1320	1330	1340	1350	1360
KWYDGDRTES	ELNSYNYLQG	TSADSGIDTT	SYGPSHGSTA	SLGAATSSPR	SGPGKEKVAP	LWHSSSEVIS	MADRTLETES
1370	1380	1390	1400	1410	1420	1430	1440
HGLDRKTESS	LSLDIHSKSQ	AGSTPLTREN	STFSINDAAS	HTSTMSSRHS	ASPVVFTSAR	SSPKEELHPA	APSQLAPSFS
1450	1460	1470	1480	1490	1500	1510	1520
SSSSSSSGPR	SFYPRQGATS	KYLIGWKKPE	GTINSVGFMD	TRKRHQSDGN	EIAHTRLRAS	TRDLRASPKP	TSKSTIEEDL
1530	1540	1550	1560	1570	1580	1590	1600
KKLIDLESPT	PESQKSFKFH	ALSSPQSPFP	STPTSRRALH	RTLSDESIYN	SQREHFFTSR	ASLLDQALPN	DVLFSSTYPS
1610	1620	1630	1640	1650	1660	1670	1680
LPKSLPLRRP	SYTLGMKSLH	GEFSASDSSL	TDIQETRRQP	MPDPGLMPLP	DTAADLDWSN	LVDAAKAYEV	QRASFFAASD
1690	1700	1710	1720	1730	1740	1750	1760
ENHRPLSAAS	NSDQLEDQAL	AQMKPYSSKD	SSPTLASKVD	QLEGMLKMLR	EDLKKEKEDK	AHLQAEVQHL	REDNLRLQEE
1770	1780	1790					
SQNASDKLKK	FTEWVFNTID	MS					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
366	1	610.1431	-205.67	2	33.9	11.0	0	1050-1059	K.MNEGVSYEFK.F	Oxidation: 1

Detailed Protein Report

Protein 1193: transthyretin precursor [Homo sapiens]

Accession:	gi|4507725	**Score:**	11.0
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:	1

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
456	1	762.0068	189.66	2	35.3	11.0	1	55-68	R.KAADDTWEPFASGK.T	

Detailed Protein Report

Protein 1194: ephrin-B1 precursor [Homo sapiens]

Accession: gi|4758248
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 11.0
MW [kDa]: 38.0
pI: 9.8
Sequence Coverage [%]: 5.5
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MARPGQRWLG	KWLVAMVVWA	LCRLATPLAK	NLEPVSWSSL	NPKFLSGKGL	VIYPKIGDKL	DIICPRAEAG	RPYEYYKLYL
90	100	110	120	130	140	150	160
VRPEQAAACS	TVLDPNVLVT	CNRPEQEIRF	TIKFQEFSPN	YMGLEFKKHH	DYYITSTSNG	SLEGLENREG	GVCRTRTMKI
170	180	190	200	210	220	230	240
IMKVGQDPNA	VTPEQLTTSR	PSKEADNTVK	MATQAPGSRG	SLGDSDGKHE	TVNQEEKSGP	GASGGSSGDP	DGFFNSKVAL
250	260	270	280	290	300	310	320
FAAVGAGCVI	FLLIIIFLTV	LLLKLRKRHR	KHTQQRAAAL	SLSTLASPKG	GSGTAGTEPS	DIIIPLRTTE	NNYCPHYEKV
330	340	350					
SGDYGHPVYI	VQEMPPQSPA	NIYYKV					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1617	1	1071.2148	97.91	2	50.1	11.0	1	12-30	K.WLVAMVVWALCRLATPLAK.N	

Detailed Protein Report

Protein 1195: cyclin-dependent kinase 15 isoform 3 [Homo sapiens]

Accession:	gi|21040235	**Score:**	11.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	43.5
Database Date:	2015-11-30	**pI:**	7.2
		Sequence Coverage [%]:	4.9
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530370812	refseq_human (refseq_human_20140103.fasta)	PREDICTED: cyclin-dependent kinase 15 isoform X2 [Homo sapiens]

10	20	30	40	50	60	70	80
MTSFHPRGLQ	AARAQKFKSK	RPRSNSDCFQ	EEDLRQGFQW	RKSLPFGAAS	SYLNLEKLGE	GSYATVYKGI	SRINGQLVAL
90	100	110	120	130	140	150	160
KVISMNAEEG	VPFTAIREAS	LLKGLKHANI	VLLHDIIHTK	ETLTFVFEYM	HTDLAQYMSQ	HPGGLHPHNV	RLFMFQLLRG
170	180	190	200	210	220	230	240
LAYIHHQHVL	HRDLKPQNLL	ISHLGELKLA	DFGLARAKSI	PSQTYSSEVV	TLWYRPPDAL	LGATEYSSEL	DIWGAGCIFI
250	260	270	280	290	300	310	320
EMFQGQPLFP	GVSNILEQLE	KIWEVLGVPT	EDTWPGVSKL	PNYNPEWFPL	PTPRSLHVVW	NRLGRVPEAE	DLASQMLKGF
330	340	350	360	370	380	390	
PRDRVSAQEA	LVHDYFSALP	SQLYQLPDEE	SLFTVSGVRL	KPEMCDLLAS	YQKGHHPAQF	SKCW	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2792	1	1079.9998	-45.87	2	65.3	11.0	2	306-324	R.VPEAEDLASQMLKGFPRDR.V	

Protein 1196: PREDICTED: myoferlin isoform X3 [Homo sapiens]

Accession:	gi|578819249	**Score:**	11.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	221.1
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
MGGDGEEDEG	DEDRLDNAVR	GPGPKGPVGT	VSEAQLARRL	TKVKNSRRML	SNKPQDFQIR	VRVIEGRQLS	GNNIRPVVKV
90	100	110	120	130	140	150	160
HVCGQTHRTR	IKRGNNPFFD	ELFFYNVNMT	PSELMDEIIS	IRVYNSHSLR	ADCLMGEFKI	DVGFVYDEPG	HAVMRKWLLL
170	180	190	200	210	220	230	240
NDPEDTSSGS	KGYMKVSMFV	LGTGDEPPPE	RRDRDNDSDD	VESNLLLPAG	IALRWVTFLL	KIYRAEDIPQ	MDDAFSQTVK
250	260	270	280	290	300	310	320
EIFGGNADKK	NLVDPFVEVS	FAGKKVCTNI	IEKNANPEWN	QVVNLQIKFP	SVCEKIKLTI	YDWDRLTKND	VVGTTYLHLS
330	340	350	360	370	380	390	400
KIAASGGEVE	DFSSSGTGAA	SYTVNTGETE	VGFVPTFGPC	YLNLYGSPRE	YTGFPDPYDE	LNTGKGEGVA	YRGRILVELA
410	420	430	440	450	460	470	480
TFLEKTPPDK	KLEPISNDDL	LVVEKYQRRR	KYSLSAVFHS	ATMLQDVGEA	IQFEVSIGNY	GNKFDTTCKP	LASTTQYSRA
490	500	510	520	530	540	550	560
VFDGNYYYYL	PWAHTKPVVT	LTSYWEDISH	RLDAVNTLLA	MAERLQTNIE	ALKSGIQGKI	PANQLAELWL	KLIDEVIEDT
570	580	590	600	610	620	630	640
RYTLPLTEGK	ANVTVLDTQI	RKLRSRSLSQ	IHEAAVRMRS	EATDVKSTLA	EIEDWLDKLM	QLTEEPQNSM	PDIIIWMIRG
650	660	670	680	690	700	710	720
EKRLAYARIP	AHQVLYSTSG	ENASGKYCGK	TQTIFLKYPQ	EKNNGPKVPV	ELRVNIWLGL	SAVEKKFNSF	AEGTFTVFAE
730	740	750	760	770	780	790	800
MYENQALMFG	KWGTSGLVGR	HKFSDVTGKI	KLKREFFLPP	KGWEWEGEWI	VDPERSLLTE	ADAGHTEFTD	EVYQNESRYP
810	820	830	840	850	860	870	880
GGDWKPAEDT	YTDANGDKAA	SPSELTCPPG	WEWEDDAWSY	DINRAVDEKG	WEYGITIPPD	HKPKSWVAAE	KMYHTHRRRR
890	900	910	920	930	940	950	960
LVRKRKKDLT	QTASSTARAM	EELQDQEGWE	YASLIGWKFH	WKQRSSDTFR	RRRWRRKMAP	SETHGAAAIF	KLEGALGADT
970	980	990	1000	1010	1020	1030	1040
TEDGDEKSLE	KQKHSATTVF	GANTPIVSCN	FDRVYIYHLR	CYVYQARNLL	ALDKDSFSDP	YAHICFLHRS	KTTEIIHSTL
1050	1060	1070	1080	1090	1100	1110	1120
NPTWDQTIIF	DEVEIYGEPQ	TVLQNPPKVI	MELFDNDQVG	KDEFLGRSIF	SPVVKLNSEM	DITPKLLWHP	VMNGDKACGD
1130	1140	1150	1160	1170	1180	1190	1200
VLVTAELILR	GKDGSNLPIL	PPQRAPNLYM	VPQGIRPVVQ	LTAIEILAWG	LRNMKNFQMA	SITSPSLVVE	CGGERVESVV
1210	1220	1230	1240	1250	1260	1270	1280
IKNLKKTPNF	PSSVLFMKVF	LPKEELYMPP	LVIKVIDHRQ	FGRKPVVGQC	TIERLDRFRC	DPYAGKEDIV	PQLKASLLSA
1290	1300	1310	1320	1330	1340	1350	1360
PPCRDIVIEM	EDTKPLLASK	CLSSMSTALS	KMASPATVHL	TEKEEEIVDW	WSKFYASSGE	HEKCGQYIQK	GYSKLKIYNC
1370	1380	1390	1400	1410	1420	1430	1440
ELENVAEFEG	LTDFSDTFKL	YRGKSDENED	PSVVGEFKGS	FRIYPLPDDP	SVPAPPRQFR	ELPDSVPQEC	TVRIYIVRGL
1450	1460	1470	1480	1490	1500	1510	1520
ELQPQDNNGL	CDPYIKITLG	KKVIEDRDHY	IPNTLNPVFG	RMYELSCYLP	QEKDLKISVY	DYDTFTRDEK	VGETIIDLEN
1530	1540	1550	1560	1570	1580	1590	1600
RFLSRFGSHC	GIPEEYCVSG	VNTWRDQLRP	TQLLQNVARF	KGFPQPILSE	DGSRIRYGGR	DYSLDEFEAN	KILHQHLGAP
1610	1620	1630	1640	1650	1660	1670	1680
EERLALHILR	TQGLVPEHVE	TRTLHSTFQP	NISQGKLQMW	VDVFPKSLGP	PGPPFNITPR	KAKKYYLRVI	IWNTKDVILD
1690	1700	1710	1720	1730	1740	1750	1760
EKSITGEEMS	DIYVKGWIPG	NEENKQKTDV	HYRSLDGEGN	FNWRFVFPFD	YLPAEQLCIV	AKKEHFWSID	QTEFRIPPRL
1770	1780	1790	1800	1810	1820	1830	1840
IIQIWDNDKF	SLDDYLGFLE	LDLRHTIIPA	KSPEKCRLDM	IPDLKAMNPL	KAKTASLFEQ	KSMKGWWPCY	AEKDGARVMA
1850	1860	1870	1880	1890	1900	1910	1920
GKVEMTLEIL	NEKEADERPA	GKGRDEPNMN	PKLDLPNRPE	TSFLWFTNPC	KTMKFIVWRR	FKWVIIGLLF	LLILLLFVAV
1930	1940						
LLYSLPNYLS	MKIVKPNV						

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1791	1	1011.5611	83.52	3	52.2	11.0	1	938-967	K.MAPSETHGAAAIFKLEGALGADTTEDGDEK.S	

Detailed Protein Report

Protein 1197: 28S ribosomal protein S9, mitochondrial [Homo sapiens]

Accession:	gi|33188463	**Score:**	11.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	45.8
Database Date:	2015-11-30	**pI:**	10.1
		Sequence Coverage [%]:	3.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAAPCVSYGG	AVSYRLLLWG	RGSLARKQGL	WKTAAPELQT	NVRSQILRLR	HTAFVIPKKN	VPTSKRETYT	EDFIKKQIEE
90	100	110	120	130	140	150	160
FNIGKRHLAN	MMGEDPETFT	QEDIDRAIAY	LFPSGLFEKR	ARPVMKHPEQ	IFPRQRAIQW	GEDGRPFHYL	FYTGKQSYYS
170	180	190	200	210	220	230	240
LMHDVYGMLL	NLEKHQSHLQ	AKSLLPEKTV	TRDVIGSRWL	IKEELEEMLV	EKLSDLDYMQ	FIRLLEKLLT	SQCGAAEEEF
250	260	270	280	290	300	310	320
VQRFRRSVTL	ESKKQLIEPV	QYDEQGMAFS	KSEGKRKTAK	AEAIVYKHGS	GRIKVNGIDY	QLYFPITQDR	EQLMFPFHFV
330	340	350	360	370	380	390	400
DRLGKHDVTC	TVSGGGRSAQ	AGAIRLAMAK	ALCSFVTEDE	VEWMRQAGLL	TTDPRVRERK	KPGQEGARRK	FTWKKR

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
598	1	700.7029	-188.45	2	37.0	11.0	0	2-15	M.AAPCVSYGGAVSYR.L	

Detailed Protein Report

Protein 1198: Holliday junction recognition protein isoform c [Homo sapiens]

Accession: gi|545478902
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 11.0
MW [kDa]: 74.3
pI: 10.4
Sequence Coverage [%]: 2.0
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MLGTLRAMEG	EDVEDDQLLQ	KLRASRRRFQ	RRMQRLIEKY	NQPFEDTPVV	QMATLTYETP	QGLRIWGGRL	IKERNEGEIQ
90	100	110	120	130	140	150	160
CAGNRAGRDV	RVTPLPSLAS	PAVPAPGYCS	RISRKSPGDP	AKPASSPREW	DPLHPSSTDM	ALVPRNDSLS	LQETSSSSFL
170	180	190	200	210	220	230	240
SSQPFEDDDI	CNVTISDLYA	GMLHSMSRLL	STKPSSIIST	KTFIMQNWNS	RRRHRYKSRM	NKTYCKGARR	SQRSSKENFI
250	260	270	280	290	300	310	320
PCSEPVKGTG	ALRDCKNVLD	VSCRKTGLKL	EKAFLEVNRP	QIHKLDPSWK	ERKVTPSKYS	SLIYFDSSAT	YNLDEENRFR
330	340	350	360	370	380	390	400
TLKWLISPVK	IVSRPTIRQG	HGENRQREIE	IRFDQLHREY	CLSPRNQPRR	MCLPDSWAMN	MYRGGPASPG	GLQGLETRRL
410	420	430	440	450	460	470	480
SLPSSKAKAK	SLSEAFENLG	KRSLEAGRCL	PKSDSSSSLP	KTNPTHSATR	PQQTSDLHVQ	GNSSGIFRKS	VSPSKTLSVP
490	500	510	520	530	540	550	560
DKEVPGHGRN	RYDEIKEEFD	KLHQKYCLKS	PGQMTVPLCI	GVSTDKASME	VRYQTEGFLG	KLNPDPHFQG	FQKLPSSPLG
570	580	590	600	610	620	630	640
CRKSLLGSTA	IEAPSSTCVA	RAITRDGTRD	HQFPAKRPRL	SEPQGSGRQG	NSLGASDGVD	NTVRPGDQGS	SSQPNSEERG
650	660	670					
ENTSYRMEEK	SDFMLEKLET	KSV					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2872	1	703.3612	11.34	2	66.4	11.0	1	429-441	R.CLPKSDSSSSLPK.T	Carbamidomethyl: 1

Detailed Protein Report

Protein 1199: PREDICTED: transcription factor TFIIIB component B" homolog isoform X1 [Homo sapiens]

Accession:	gi|530430749	**Score:**	11.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	289.2
Database Date:	2015-11-30	**pI:**	4.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	0.5
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578810462	refseq_human (refseq_human_20140103.fasta)	PREDICTED: transcription factor TFIIIB component B" homolog isoform X4 [Homo sapiens]

10	20	30	40	50	60	70	80
MFRRARLSVK	PNVRPGVGAR	GSTASNPQRG	RESPRPPDPA	TDSASKPAEP	TDVPTVDFGG	AEPQEKAPRS	STEKTGGDND
90	100	110	120	130	140	150	160
VEESSRSSST	VSQRRKRISS	TSSLVKSSVS	VPSESHPLST	INQEAPQPTA	TSTKEKQPCS	DRYRIYKAQK	LREMLKEELR
170	180	190	200	210	220	230	240
KEKKQWKNKY	AINESQRPPD	RSKMTMRDFI	YYLPDNNPMT	SSLEQEKKTE	KPSTPVQTRE	QEGKSTPNAE	DNEMEEETDD
250	260	270	280	290	300	310	320
GPLLVPRVKV	AEDGSIILDE	ESLTVEVLRT	KGPCVVEEND	PIFERGSTTT	YSSFRKNYYS	KPWSNKETDM	FFLAISMVGT
330	340	350	360	370	380	390	400
DFSMIGQLFP	HRARIEIKNK	FKREEKTNGW	RIDKAFQEKR	PFDFDFFAHL	LQKVLAEEEK	RKQKSVKNHS	LKEKKSTKPR
410	420	430	440	450	460	470	480
KNVKVKKVAC	EGVNNDPDES	MSSRISDTER	SQKDAQTVEE	ESLTLSREDA	EQVALEVDLN	QKKRRRKKQD	GANELGVNNL
490	500	510	520	530	540	550	560
LENATVQAGP	SKGEKHKNKC	QAIRPELKEG	ECSKEQMLSC	TQNIDGIVGF	ASTEKVEKRT	DPILSLSNQQ	DATSVATESS
570	580	590	600	610	620	630	640
ESSTSDLPSF	EVGIRALCEV	NNAEGSCIEE	RNVDLKNNSL	EIDQTENVKP	MLRGRFQRPK	PNLSRAGKKS	VLSQGKTESE
650	660	670	680	690	700	710	720
SKNSHSKTSV	EKNHVEKDKM	NTLDILRMET	TERENPEAET	VSVLGEKNCL	QEGSQLKALR	PVQVRGRLQK	PKPNAGKAAE
730	740	750	760	770	780	790	800
RKEILISQEE	IGANVEKNEN	ESCADRDTPQ	HMEDQSRKDF	EEEDVILQPE	KNDSFQNVQP	DEPKVLNECL	SVQENNKANK
810	820	830	840	850	860	870	880
LNQVPILRTR	FQKPKPNIGR	GTGRREISSK	EEVLEKILVS	GEMAAALRET	VRLDTSPKEM	VPAEINTKEM	QSDLKETGRR
890	900	910	920	930	940	950	960
AISPREKILD	VIDDTIEMET	GLKAMGREIC	LREKTPEVID	ATEEIDKDLE	EAGRREISPQ	KNGPEEVKPL	GEVETDLKAT
970	980	990	1000	1010	1020	1030	1040
GNESSPREKT	PEVTDATEEI	DKNLEETGRR	KISPRENGPE	EVKPVDEMET	DLNATGRESS	PREKTPEVID	ATEEIDLEET
1050	1060	1070	1080	1090	1100	1110	1120
EREVSPQENG	LEEVKPLGEM	ETDLKATGRD	SFPRGKTPEV	IDAIEEIEID	LEETEREISP	QENGLEEVKP	LGEMQTDLKA
1130	1140	1150	1160	1170	1180	1190	1200
TGREISPREK	TPEVIDATEE	IDKDLEETGR	REISPEENGP	EEVKPVDEME	TDLKTTGREG	SSREKTREVI	DAAEVIETDL
1210	1220	1230	1240	1250	1260	1270	1280
EETEREISPQ	ENGPEEVKPV	GKMETDLKEI	REEISQREKV	LAEFSAIREK	EIDLKETGKR	DIPIMEKVSG	KMAVVEEMEA
1290	1300	1310	1320	1330	1340	1350	1360
DLKETGKENF	RERGSEEICV	TEEKVAELKQ	TGKTDISPRE	NELEETSTSR	QTDTHLMQSG	SNDFSAVPSL	DIQNISSEVL
1370	1380	1390	1400	1410	1420	1430	1440
SMMHTPVEEK	RNSEKEVSSH	FSHFKISSQT	HESDKTEVQG	IQSPDVPEQF	SDINLSKSLP	QEQKPLEIKP	APFVRSRFKR
1450	1460	1470	1480	1490	1500	1510	1520
PKPNLARAAL	KRETTESEKY	IYEKKSETKK	METIVMQENN	EQTDTLPSQH	DEASLMISRE	KDTLGHRNEE	AVILPCTQTE
1530	1540	1550	1560	1570	1580	1590	1600
RNLSPSNSCE	PKEESQSAPV	QKNDSVVSVG	TNNVNTFQQE	MKESVIQTAR	QVRGRLQRPR	PNIRKTGQRQ	IVDKGEAKGI
1610	1620	1630	1640	1650	1660	1670	1680
IKEGRTILPK	DETEKKVLTV	SNSQIETEIE	VPSSAVPEHR	MYENQSQVVL	VENLHVNKTN	ETIRHENKPY	VPSSAQMTRR
1690	1700	1710	1720	1730	1740	1750	1760
KFQKAKPNLG	RAHSKKEEPV	LEKVTTDQSK	EGKPEDHLLQ	KGASNTQLLL	KEKAELLTSL	EVSARKDCVG	SKESALAKID
1770	1780	1790	1800	1810	1820	1830	1840
AELEEVGPSR	RVGEETVGDN	SPSSVVEEQY	LNKLTSCPQP	LNETSYSKIA	LDGKTTISST	SEYERNRGER	RSHKKFKPNV
1850	1860	1870	1880	1890	1900	1910	1920
TRGRGSKRVR	GKTSKKEPRA	SKAMLVTLRA	SQEEDDDADD	FESDYEEESY	HLAPEEVNKA	PVFVPVGLRS	PEPVSAQIEE
1930	1940	1950	1960	1970	1980	1990	2000
TMEELEITVN	VPDVGCIAVV	EHELPNTDVT	TEEMKQEENL	SVPFEMTTSE	HIQDEPGTND	GSTEAAITLL	TMGDLVLQSE
2010	2020	2030	2040	2050	2060	2070	2080
ISSEQGDVGV	CIIPHVHSKD	KSHIPSSLDN	VNHKIVHECQ	ELSSPVITTS	PASFEENKIV	LEEQSSREEI	SLMEKVKENA
2090	2100	2110	2120	2130	2140	2150	2160
TPTRNTISKV	TSNLRIRSRL	AKPKPNLEKT	LGTNRLDDYQ	EVSSLCVTKG	AEMETQRETE	KNASKATELE	NKNLGPVTTA
2170	2180	2190	2200	2210	2220	2230	2240
ENKDQSKLAC	VHGIKGTSIS	SEVNLTERNE	NQEESSQEVH	MLSVAPVASS	ETGPCTLGLD	RGLGENSVEE	PQIKDSKGDS
2250	2260	2270	2280	2290	2300	2310	2320
VLTLPVPEYT	PTSIPEVQQE	NIINPQDLTV	NLVANVPQDG	EDEQAFILTL	VEIPANAVEE	FTDATAQFMP	NPLLPAPILV
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
2728	1	806.1966	-169.47	2	65.4	11.0	0	2392-2404	R.DDCQEYTTEVHSK.E	Carbamidomethyl: 3

Detailed Protein Report

Protein 1200: PREDICTED: supervillin isoform X15 [Homo sapiens]

Accession:	gi|578818557	**Score:**	11.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	209.9
Database Date:	2015-11-30	**pI:**	6.7
		Sequence Coverage [%]:	0.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MKPNVFGREK	SDFNKKNLSF	LGFPRQRKVS	SFQKEFSLED	KEQLANHERG	IDAQLLVALP	KVAELRQIFE	PKKKEFLEMK
90	100	110	120	130	140	150	160
RKERIARRLE	GIENDTQPIL	LQSCTGLVTH	RLLEEDTPRY	MRASDPASPH	IGRSNEEEET	SDSSLEKQTR	SKYCTETSGV
170	180	190	200	210	220	230	240
HGDSPYGSGT	MDTHSLESKA	ERIARYKAER	RRQLAEKYGL	TLDPEADSEY	LSRYTKSRKE	PDAVEKRGGK	SDKQEESSRD
250	260	270	280	290	300	310	320
ASSLYPGTET	MGLRTCAGES	KDYALHVGDG	SSDPEVLLNI	ENQRRGQELS	ATRQAHDLSP	AAESSSTFSF	SGRDSSFTEV
330	340	350	360	370	380	390	400
PRSPKHAHSS	SLQQAASRSP	SFGDPQLSPE	ARPRCTSHSE	TPTVDDEEKV	DERAKLSVAA	KRLLFREMEK	SFDEQNVPKR
410	420	430	440	450	460	470	480
RSRNTAVEQR	LRRLQDRSLT	QPITTEEVVI	AATLQASAHQ	KALAKDQTNE	GKELAEQGEP	DSSTLSLAEK	LALFNKLSQP
490	500	510	520	530	540	550	560
VSKAISTRNR	IDTRQRRMNA	RYQTQPVTLG	EVEQVQSGKL	IPFSPAVNTS	VSTVASTVAP	MYAGDLRTKP	PLDHNASATD
570	580	590	600	610	620	630	640
YKFSSSIENS	DSPVRSILKS	QAWQPLVEGS	ENKGMLREYG	ETESKRALTG	RDSGMEKYGS	FEEAEASYPI	LNRAREGDSH
650	660	670	680	690	700	710	720
KESKYAVPRR	GSLERANPPI	THLGDEPKEF	SMAKMNAQGN	LDLRDRLPFE	EKVEVENVMK	RKFSLRAAEF	GEPTSEQTGT
730	740	750	760	770	780	790	800
AAGKTIAQTT	APVSWKPQDS	SEQPQEKLCK	NPCAMFAAGE	IKTPTGEGLL	DSPSKTMSIK	ERLALLKKSG	EEDWRNRLSR
810	820	830	840	850	860	870	880
RQEGGKAPAS	SLHTQEAGRS	LIKKRVTESR	ESQMTIEERK	QLITVREEAW	KTRGRGAAND	STQFTVAGRM	VKKGLASPTA
890	900	910	920	930	940	950	960
ITPVASPICG	KTRGTTPVSK	PLEDIEARPD	MQLESDLKLD	RLETFLRRLN	NKVGGMHETV	LTVTGKSVKE	VMKPDDDETF
970	980	990	1000	1010	1020	1030	1040
AKFYRSVDYN	MPRSPVEMDE	DFDVIFDPYA	PKLTSSVAEH	KRAVRPKRRV	QASKNPLKML	AAREDLLQEY	TEQRLNVAFM
1050	1060	1070	1080	1090	1100	1110	1120
ESKRMKVEKM	SSNSNFSEVT	LAGLASKENF	SNVSLRSVNL	TEQNSNNSAV	PYKRLMLLQI	KGRRHVQTRL	VEPRASALNS
1130	1140	1150	1160	1170	1180	1190	1200
GDCFLLLSPH	CCFLWVGEFA	NVIEKAKASE	LATLIQTKRE	LGCRATYIQT	IEEGINTHTH	AAKDFWKLLG	GQTSYQSAGD
1210	1220	1230	1240	1250	1260	1270	1280
PKEDELYEAA	IIETNCIYRL	MDDKLVPDDD	YWGKIPKCSL	LQPKEVLVFD	FGSEVYVWHG	KEVTLAQRKI	AFQLAKHLWN
1290	1300	1310	1320	1330	1340	1350	1360
GTFDYENCDI	NPLDPGECNP	LIPRKGQGRP	DWAIFGRLTE	HNETILFKEK	FLDWTELKRS	NEKNPGELAQ	HKEDPRTDVK
1370	1380	1390	1400	1410	1420	1430	1440
AYDVTRMVSM	PQTTAGTILD	GVNVGRGYGL	VEGHDRRQFE	ITSVSVDVWH	ILEFDYSRLP	KQSIGQFHEG	DAYVVKWKFM
1450	1460	1470	1480	1490	1500	1510	1520
VSTAVGSRQK	GEHSVRAAGK	EKCVYFFWQG	RHSTVSEKGT	SALMTVELDE	ERGAQVQVLQ	GKEPPCFLQC	FQGGMVVHSG
1530	1540	1550	1560	1570	1580	1590	1600
RREEEEENVQ	SEWRLYCVRG	EVPVEGNLLE	VACHCSSLRS	RTSMVVLNVN	KALIYLWHGC	KAQAHTKEVG	RTAANKIKEQ
1610	1620	1630	1640	1650	1660	1670	1680
CPLEAGLHSS	SKVTIHECDE	GSEPLGFWDA	LGRRDRKAYD	CMLQDPGSFN	FAPRLFILSS	SSGDFAATEF	VYPARAPSVV
1690	1700	1710	1720	1730	1740	1750	1760
SSMPFLQEDL	YSAPQPALFL	VDNHHEVYLW	QGWWPIENKI	TGSARIRWAS	DRKSAMETVL	QYCKGKNLKK	PAPKSYLIHA
1770	1780	1790	1800	1810	1820	1830	1840
GLEPLTFTNM	FPSWEHREDI	AEITEMDTEV	SNQITLVEDV	LAKLCKTIYP	LADLLARPLP	EGVDPLKLEI	YLTDEDFEFA
1850	1860	1870					
LDMTRDEYNA	LPAWKQVNLK	KAKGLF					

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
874	1	903.4160	-143.87	2	40.5	11.0	1	50-66	R.GIDAQLLVALPKVAELR.Q	

Protein 1201: PREDICTED: serpin B13 isoform X1 [Homo sapiens]

Accession:	gi|530414214	**Score:**	11.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	45.3
Database Date:	2015-11-30	**pI:**	5.5
		Sequence Coverage [%]:	1.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDSLGAVSTR	LGFDLFKELK	KTNDGNIFFS	PVGILTAIGM	VLLGTRGATA	SQLEEVFHSE	KETKSSRIKA	EEKEVVRIKA
90	100	110	120	130	140	150	160
EGKEIENTEA	VHQQFQKFLT	EISKLTNDYE	LNITNRLFGE	KTYLFLQKYL	DYVEKYYHAS	LEPVDFVNAA	DESRKKINSW
170	180	190	200	210	220	230	240
VESKTNEKIK	DLFPDGSISS	STKLVLVNMV	YFKGQWDREF	KKENTKEEKF	WMNKSTSKSV	QMMTQSHSFS	FTFLEDLQAK
250	260	270	280	290	300	310	320
ILGIPYKNND	LSMFVLLPND	IDGLEKIIDK	ISPEKLVEWT	SPGHMEERKV	NLHLPRFEVE	DGYDLEAVLA	AMGMGDAFSE
330	340	350	360	370	380	390	400
HKADYSGMSS	GSGLYAQKFL	HSSFVAVTEE	GTEAAAATGI	GFTVTSAPGH	ENVHCNHPFL	FFIRHNESNS	ILFFGRFSSP
410							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1011	1	645.1242	-416.49	1	42.2	11.0	1	78-83	R.IKAEGK.E	

Detailed Protein Report

Protein 1202: cadherin-4 isoform 3 [Homo sapiens]

Accession:	gi|356640224	**Score:**	11.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	92.3
Database Date:	2015-11-30	**pI:**	4.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.4
		No. of unique Peptides:	1

Quantitation

MD:MU	**Median:**	2.35	**CV:**	0.00 %	**No. of Peptides:**	1	

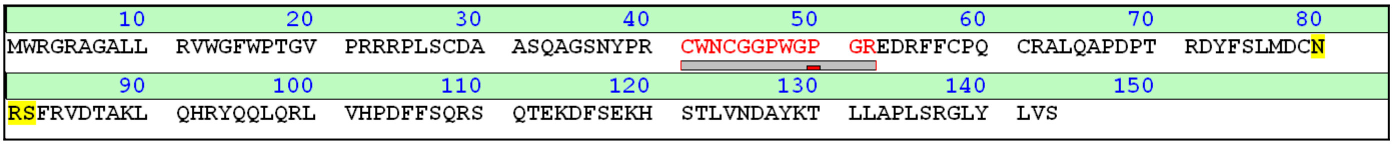
10	20	30	40	50	60	70	80
MDFKVGADGT	VFATRELQVP	SEQVAFTVTA	WDSQTAEKWD	AVVRLLVAQT	SSPHSGHKPQ	KGKKVVALDP	SPPPKDTLLP
90	100	110	120	130	140	150	160
WPQHQNANGL	RRRKRDWVIP	PINVPENSRG	PFPQQLVRIR	SDKDNDIPIR	YSITGVGADQ	PPMEVFSIDS	MSGRMYVTRP
170	180	190	200	210	220	230	240
MDREEHASYH	LRAHAVDMNG	NKVENPIDLY	IYVIDMNDNR	PEFINQVYNG	SVDEGSKPGT	YVMTVTANDA	DDSTTANGMV
250	260	270	280	290	300	310	320
RYRIVTQTPQ	SPSQNMFTIN	SETGDIVTVA	AGLDREKVQQ	YTVIVQATDM	EGNLNYGLSN	TATAIITVTD	VNDNPPEFTA
330	340	350	360	370	380	390	400
STFAGEVPEN	RVETVVANLT	VMDRDQPHSP	NWNAVYRIIS	GDPSGHFSVR	TDPVTNEGMV	TVVKAVDYEL	NRAFMLTVMV
410	420	430	440	450	460	470	480
SNQAPLASGI	QMSFQSTAGV	TISIMDINEA	PYFPSNHKLI	RLEEGVPPGT	VLTTFSAVDP	DRFMQQAVRY	SKLSDPASWL
490	500	510	520	530	540	550	560
HINATNGQIT	TAAVLDRESL	YTKNNVYEAT	FLAADNGIPP	ASGTGTLQIY	LIDINDNAPE	LLPKEAQICE	KPNLNAINIT
570	580	590	600	610	620	630	640
AADADVDPNI	GPYVFELPFV	PAAVRKNWTI	TRLNGDYAQL	SLRILYLEAG	MYDVPIIVTD	SGNPPLSNTS	IIKVKVCPCD
650	660	670	680	690	700	710	720
DNGDCTTIGA	VAAAGLGTGA	IVAILICILI	LLTMVLLFVM	WMKRREKERH	TKQLLIDPED	DVRDNILKYD	EEGGGEEDQD
730	740	750	760	770	780	790	800
YDLSQLQQPE	AMGHVPSKAP	GVRRVDERPV	GAEPQYPIRP	MVPHPGDIGD	FINEGLRAAD	NDPTAPPYDS	LLVFDYEGSG
810	820	830	840	850			
STAGSVSSLN	SSSSGDQDYD	YLNDWGPRFK	KLADMYGGGE	ED			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
1264	1	650.6734	-151.14	2	45.5	11.0	1	831-842	K.KLADMYGGGEED.-	Oxidation: 5	MD:MU	2.35

Detailed Protein Report

Protein 1203: PREDICTED: iron-sulfur cluster co-chaperone protein HscB, mitochondrial isoform X3 [Homo sapiens]

Accession:	gi|530419579	**Score:**	11.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	16.5
Database Date:	2015-11-30	**pI:**	11.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	8.4
		No. of unique Peptides:	1



```
         10         20         30         40         50         60         70         80
MWRGRAGALL RVWGFWPTGV PRRRPLSCDA ASQAGSNYPR CWNCGGPWGP GREDRFFCPQ CRALQAPDPT RDYFSLMDCN
         90        100        110        120        130        140        150
RSFRVDTAKL QHRYQQLQRL VHPDFFSQRS QTEKDFSEKH STLVNDAYKT LLAPLSRGLY LVS
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1921	1	673.7614	-26.92	2	54.1	11.0	0	41-52	R.CWNCGGPWGPGR.E	Carbamidomethyl: 1

Detailed Protein Report

Protein 1204: myelin transcription factor 1 [Homo sapiens]

Accession:	gi|17975763	**Score:**	11.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	122.3
Database Date:	2015-11-30	**pI:**	4.7
		Sequence Coverage [%]:	0.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSLENEDKRA	RTRSKALRGP	PETTAADLSC	PTPGCTGSGH	VRGKYSRHRS	LQSCPLAKKR	KLEGAEAEHL	VSKRKSHPLK
90	100	110	120	130	140	150	160
LALDEGYGVD	SDGSEDTEVK	DASVSDESEG	TLEGAEAETS	GQDEIHRPET	AEGRSPVKSH	FGSNPIGSAT	ASSKGSYSSY
170	180	190	200	210	220	230	240
QGIIATSLLN	LGQIAEETLV	EEDLGQAAKP	GPGIVHLLQE	AAEGAASEEG	EKGLFIQPED	AEEVVEVTTE	RSQDLCPQSL
250	260	270	280	290	300	310	320
EDAASEESSK	QKGILSHEEE	DEEEEEEEEE	EEEDEEEEEE	EEEEEEEEEE	EEEEEEEEEE	EEEEEEAAPD	VIFQEDTSHT
330	340	350	360	370	380	390	400
SAQKAPELRG	PESPSPKPEY	SVIVEVRSDD	DKDEDTHSRK	STVTDESEMQ	DMMTRGNLGL	LEQAIALKAE	QVRTVCEPGC
410	420	430	440	450	460	470	480
PPAEQSQLGL	GEPGKAAKPL	DTVRKSYYSK	DPSRAEKREI	KCPTPGCDGT	GHVTGLYPHH	RSLSGCPHKD	RIPPEILAMH
490	500	510	520	530	540	550	560
ENVLKCPTPG	CTGQGHVNSN	RNTHRSLSGC	PIAAAEKLAK	SHEKQQPQTG	DPSKSSSNSD	RILRPMCFVK	QLEVPPYGSY
570	580	590	600	610	620	630	640
RPNVAPATPR	ANLAKELEKF	SKVTFDYASF	DAQVFGKRML	APKIQTSETS	PKAFQCFDYS	QDAEAAHMAA	TAILNLSTRC
650	660	670	680	690	700	710	720
WEMPENLSTK	PQDLPSKSVD	IEVDENGTLD	LSMHKHRKRE	NAFPSSSSCS	SSPGVKSPDA	SQRHSSTSAP	SSSMTSPQSS
730	740	750	760	770	780	790	800
QASRQDEWDR	PLDYTKPSRL	REEEPEESEP	AAHSFASSEA	DDQEVSEENF	EERKYPGEVT	LTNFKLKFLS	KDIKKELLTC
810	820	830	840	850	860	870	880
PTPGCDGSGH	ITGNYASHRS	LSGCPLADKS	LRNLMAAHSA	DLKCPTPGCD	GSGHITGNYA	SHRSLSGCPR	AKKSGVKVAP
890	900	910	920	930	940	950	960
TKDDKEDPEL	MKCPVPGCVG	LGHISGKYAS	HRSASGCPLA	ARRQKEGSLN	GSSFSWKSLK	NEGPTCPTPG	CDGSGHANGS
970	980	990	1000	1010	1020	1030	1040
FLTHRSLSGC	PRATFAGKKG	KLSGDEVLSP	KFKTSDVLEN	DEEIKQLNQE	IRDLNESNSE	MEAAMVQLQS	QISSMEKNLK
1050	1060	1070	1080	1090	1100	1110	1120
NIEEENKLIE	EQNEALFLEL	SGLSQALIQS	LANIRLPHME	PICEQNFDAY	VSTLTDMYSN	QDPENKDLLE	SIKQAVRGIQ
1130							
V							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
302	1	1074.7296	122.86	1	33.5	11.0	1	50-59	R.SLQSCPLAKK.R	

Detailed Protein Report

Protein 1205: UBX domain-containing protein 7 [Homo sapiens]

Accession:	gi|149944496	**Score:**	10.9
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

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        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
1719	1	916.3061	-159.59	2	51.3	10.9	1	106-120	R.SIFDGFRDFQTETIR.Q	

Detailed Protein Report

Protein 1206: RIMS-binding protein 2 [Homo sapiens]

Accession:	gi|140561070	**Score:**	10.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	116.0
Database Date:	2015-11-30	**pI:**	5.0
		Sequence Coverage [%]:	1.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MREAAERRQQ	LQLEHDQALA	VLSAKQQEID	LLQKSKVREL	EEKCRTQSEQ	FNLLSRDLEK	FRQHAGKIDL	LGGSAVAPLD
90	100	110	120	130	140	150	160
ISTAPSKPFP	QFMNGLATSL	GKGQESAIGG	SSAIGEYIRP	LPQPGDRPEP	LSAKPTFLSR	SGSARCRSES	DMENERNSNT
170	180	190	200	210	220	230	240
SKQRYSGKVH	LCVARYSYNP	FDGPNENPEA	ELPLTAGKYL	YVYGDMDEDG	FYEGELLDGQ	RGLVPSNFVD	FVQDNESRLA
250	260	270	280	290	300	310	320
STLGNEQDQN	FINHSGIGLE	GEHILDLHSP	THIDAGITDN	SAGTLDVNID	DIGEDIVPYP	RKITLIKQLA	KSVIVGWEPP
330	340	350	360	370	380	390	400
AVPPGWGTVS	SYNVLVDKET	RMNLTLGSRT	KALIEKLNMA	ACTYRISVQC	VTSRGSSDEL	QCTLLVGKDV	VVAPSHLRVD
410	420	430	440	450	460	470	480
NITQISAQLS	WLPTNSNYSH	VIFLNEEEFD	IVKAARYKYQ	FFNLRPNMAY	KVKVLAKPHQ	MPWQLPLEQR	EKKEAFVEFS
490	500	510	520	530	540	550	560
TLPAGPPAPP	QDVTVQAGVT	PATIRVSWRP	PVLTPTGLSN	GANVTGYGVY	AKGQRVAEVI	FPTADSTAVE	LVRLRSLEAK
570	580	590	600	610	620	630	640
GVTVRTLSAQ	GESVDSAVAA	VPPELLVPPT	PHPRPAPQSK	PLASSGVPET	KDEHLGPHAR	MDEAWEQSRA	PGPVHGHMLE
650	660	670	680	690	700	710	720
PPVGPGRRSP	SPSRILPQPQ	GTPVSTTVAK	AMAREAAQRV	AESSRLEKRS	VFLERSSAGQ	YAASDEEDAY	DSPDFKRRGA
730	740	750	760	770	780	790	800
SVDDFLKGSE	LGKQPHCCHG	DEYHTESSRG	SDLSDIMEED	EEELYSEMQL	EDGGRRRPSG	TSHNALKILG	NPASAGRVDH
810	820	830	840	850	860	870	880
MGRRFPRGSA	GPQRSRPVTV	PSIDDYGRDR	LSPDFYEESE	TDPGAEELPA	RIFVALFDYD	PLTMSPNPDA	AEEELPFKEG
890	900	910	920	930	940	950	960
QIIKVYGDKD	ADGFYRGETC	ARLGLIPCNM	VSEIQADDEE	MMDQLLRQGF	LPLNTPVEKI	ERSRRSGRRH	SVSTRRMVAL
970	980	990	1000	1010	1020	1030	1040
YDYDPRESSP	NVDVEAELTF	CTGDIITVFG	EIDEDGFYYG	ELNGQKGLVP	SNFLEEVPDD	VEVYLSDAPS	HYSQDTPMRS
1050	1060						
KAKRKKSVHF	TP						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
665	1	639.3437	13.28	2	37.9	10.9	1	339-349	K.ETRMNLTLGSR.T	

Detailed Protein Report

Protein 1207: group 3 secretory phospholipase A2 precursor [Homo sapiens]

Accession:	gi|142976884	**Score:**	10.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	57.1
Database Date:	2015-11-30	**pI:**	10.8
		Sequence Coverage [%]:	2.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGVQAGLFGM	LGFLGVALGG	SPALRWYRTS	CHLTKAVPGN	PLGYLSFLAK	DAQGLALIHA	RWDAHRRLQS	CSWEDEPELT
90	100	110	120	130	140	150	160
AAYGALCAHE	TAWGSFIHTP	GPELQRALAT	LQSQWEACRA	LEESPAGARK	KRAAGQSGVP	GGGHQREKRG	WTMPGTLWCG
170	180	190	200	210	220	230	240
VGDSAGNSSE	LGVFQGPDLC	CREHDRCPQN	ISPLQYNYGI	RNYRFHTISH	CDCDTRFQQC	LQNQHDSISD	IVGVAFFNVL
250	260	270	280	290	300	310	320
EIPCFVLEEQ	EACVAWYWWG	GCRMYGTVPL	ARLQPRTFYN	ASWSSRATSP	TPSSRSPAPP	KPRQKQHLRK	GPPHQKGSKR
330	340	350	360	370	380	390	400
PSKANTTALQ	DPMVSPRLDV	APTGLQGPQG	GLKPQGARWV	CRSFRRHLDQ	CEHQIGPREI	EFQLLNSAQE	PLFHCNCTRR
410	420	430	440	450	460	470	480
LARFLRLHSP	PEVTNMLWEL	LGTTCFKLAP	PLDCVEGKNC	SRDPRAIRVS	ARHLRRLQQR	RHQLQDKGTD	ERQPWPSEPL
490	500	510					
RGPMSFYNQC	LQLTQAARRP	DRQQKSWSQ					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2728	1	741.8636	-14.06	2	64.4	10.9	2	461-472	R.RHQLQDKGTDER.Q	

Detailed Protein Report

Protein 1208: polycystic kidney disease protein 1-like 2 isoform d [Homo sapiens]

Accession:	gi|509155833	**Score:**	10.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	197.3
Database Date:	2015-11-30	**pI:**	6.0
		Sequence Coverage [%]:	0.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGEDSPVAMF	SWYLDNTPTE	QAEPLLDACR	LRGFWPRSLT	LLQSNTSTLL	LNSSFLQSRG	EVIRIRATAL	TRHAYGEDTY
90	100	110	120	130	140	150	160
VISTVPPREV	PACTIAPEEG	TVLTSFAIFC	NASTALGPLE	FCFCLESGSC	LHCGPEPALP	SVYLPLGEEN	NDFVLTVVIS
170	180	190	200	210	220	230	240
ATNRAGDTQQ	TQAMAKVALG	DTCVEDVAFQ	AAVSEKIPTA	LQGEGGPEQL	LQLAKAVSSM	LNQEHESQGS	GQSLSIDVRQ
250	260	270	280	290	300	310	320
KVREHVLGSL	SAVTTGLEDV	QRVQELAEVL	REVTCRSKEL	TPSAQWEASL	ALQHASEALL	TVSAKARPED	QRRQAATRDL
330	340	350	360	370	380	390	400
FQAVGSVLEA	SLSNRPEEPA	EASSSQIATV	LRLLRVMEHV	QTTLLLGKLP	GGLPAMLATP	SISVYTNRIQ	PWSWQGSSLR
410	420	430	440	450	460	470	480
PDAADSATFM	LPAASSLSSL	EGGQEPVDIK	IMSFPKSPFP	ARSHFDVSGT	VGGLRVTSPS	GQLIPVKNLS	ENIEILLPRH
490	500	510	520	530	540	550	560
SQRHSQPTVL	NLTSPEALWV	NVTSGEATLG	IQLHWRPDIA	LTLSLGYGYH	PNKSSYDAQT	HLVPMVAPDE	LPTWILSPQD
570	580	590	600	610	620	630	640
LRFGEGVYYL	TVVPESDLEP	APGRDLTVGI	TTFLSHCVFW	DEVQETWDDS	GCQVGPRTSP	YQTHCLCNHL	TFFGSTFLVM
650	660	670	680	690	700	710	720
SNAINIHQTA	ELFATFEDNP	VVVTTVGCLC	VVYVLVVIWA	RRKDAQDQAK	VKVTVLEDND	PFAQYHYLVT	VYTGHRRGAA
730	740	750	760	770	780	790	800
TSSKVTVTLY	GLDGEREPHH	LADPDTPVFE	RGAVDAFLLS	TLFPLGELRS	LRLWHDNSGD	RPSWYVSRVL	VYDLVMDRKW
810	820	830	840	850	860	870	880
YFLCNSWLSI	NVGDCVLDKV	FPVATEQDRK	QFSHLFFMKT	SAGFQDGHIW	YSIFSRCARS	SFTRVQRVSC	CFSLLLCTML
890	900	910	920	930	940	950	960
TSIMFWGVPK	DPAEQKMDLG	KIEFTWQEVM	IGLESSILMF	PINLLIVQIF	QNTRPRVAKE	QNTGKWDRGS	PNLTPSPQPM
970	980	990	1000	1010	1020	1030	1040
EDGLLTPEAV	TKDVSRIVSS	LFKALKVPSP	ALGWDSVNLM	DINSLLALVE	DVIYPQNTSG	QVFWEEAKKR	EDPVTLTLGS
1050	1060	1070	1080	1090	1100	1110	1120
SEMKEKSQCP	KPKAARSGPW	KDSAYRQCLY	LQLEHVEQEL	RLVGPRGFSQ	PHSHAQALRQ	LQTLKGGLGV	QPGTWAPAHA
1130	1140	1150	1160	1170	1180	1190	1200
SALQVSKPPQ	GLPWWCILVG	WLLVAATSGV	AAFFTMLYGL	HYGRASSLRW	LISMAVSFVE	SMFVTQPLKV	LGFAAFFALV
1210	1220	1230	1240	1250	1260	1270	1280
LKRVDDEEDT	VAPLPGHLLG	PDPYALFRAR	RNSSRDVYQP	PLTAAIEKMK	TTHLKEQKAF	ALIREILAYL	GFLWMLLLVA
1290	1300	1310	1320	1330	1340	1350	1360
YGQRDPSAYH	LNRHLQHSFT	RGFSGVLGFR	EFFKWANTTL	VSNLYGHPPG	FITDGNSKLV	GSAQIRQVRV	QESSCPLAQQ
1370	1380	1390	1400	1410	1420	1430	1440
PQAYLNGCRA	PYSLDAEDMA	DYGEGWNATT	LSEWQYQSQD	QRQGYPIWGK	LTVYRGGGYV	VPLGTDRQST	SRILRYLFDN
1450	1460	1470	1480	1490	1500	1510	1520
TWLDALTRAV	FVESTVYNAN	VNLFCIVTLT	LETSALGTFF	THAALQSLRL	YPFTDGWHPF	VVAAELIYFL	FLLYYMVVQG
1530	1540	1550	1560	1570	1580	1590	1600
KRMSKETWGY	FCSKWNLLEL	AIILASWSAL	AVFVKRAVLA	ERDLQRCRNH	REEGISFSET	AAADAALGYI	IAFLVLLSTV
1610	1620	1630	1640	1650	1660	1670	1680
KLWHLLRLNP	KMNMITAALR	RAWGDISGFM	IVILTMLLAY	SIASNLIFGW	KLRSYKTLFD	AAETMVSLQL	GIFNYEEVLD
1690	1700	1710	1720	1730	1740	1750	1760
YSPVLGSFLI	GSCIVFMTFV	VLNLFISVIL	VAFSEEQKYY	QLSEEGEIVD	LLLMKILSFL	GIKSKREEPG	SSREQPGSLS
1770	1780						
QTRHSRPAQA	LPKD						

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

Detailed Protein Report

	Cmpds.		[ppm]		[min]					
2032	1	616.2737	-47.55	2	55.3	10.9	1	891-901	K.DPAEQKMDLGK.I	

Detailed Protein Report

Protein 1209: zinc finger CCHC domain-containing protein 24 [Homo sapiens]

Accession:	gi|223633947	**Score:**	10.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	26.9
Database Date:	2015-11-30	**pI:**	9.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	7.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSLLSAIDTS	AASVYQPAQL	LNWVYLSLQD	THQASAFDAF	RPEPTAGAAP	PELAFGKGRP	EQLGSPLHSS	YLNSFFQLQR
90	100	110	120	130	140	150	160
GEALSNSVYK	GASPYGSLNN	IADGLSSLTE	HFSDLTLTSE	ARKPSKRPPP	NYLCHLCFNK	GHYIKDCPQA	RPKGEGLTPY
170	180	190	200	210	220	230	240
QGKKRCFGEY	KCPKCKRKWM	SGNSWANMGQ	ECIKCHINVY	PHKQRPLEKP	DGLDVSDQSK	EHPQHLCEKC	KVLGYYCRRV
250							
Q							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2518	1	1013.8383	-110.40	2	61.4	10.9	1	178-194	R.KWMSGNSWANMGQECIK.C	Carbamidomethyl: 15

Detailed Protein Report

Protein 1210: olfactory receptor 7G1 [Homo sapiens]

Accession:	gi|308737007	**Score:**	10.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	34.8
Database Date:	2015-11-30	**pI:**	9.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	7.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGPRNQTAVS	EFLLMKVTED	PELKLIPFSL	FLSMYLVTIL	GNLLILLAVI	SDSHLHTPMY	FLLFNLSFTD	ICLTTTTVPK
90	100	110	120	130	140	150	160
ILVNIQAQNQ	SITYTGCLTQ	ICLVLVFAGL	ESCFLAVMAY	DRYVAICHPL	RYTVLMNVHF	WGLLILLSMF	MSTMDALVQS
170	180	190	200	210	220	230	240
LMVLQLSFCK	NVEIPLFFCE	VVQVIKLACS	DTLINNILIY	FASSVFGAIP	LSGIIFSYSQ	IVTSVLRMPS	ARGKYKAFST
250	260	270	280	290	300	310	320
CGCHLSVFSL	FYGTAFGVYI	SSAVAESSRI	TAVASVMYTV	VPQMMNPFIY	SLRNKEMKKA	LRKLIGRLFP	F

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2334	1	921.7095	-100.50	3	59.5	10.9	0	270-293	R.ITAVASVMYTVVPQMMNPFIYSLR.N	Oxidation: 15, 16

Detailed Protein Report

Protein 1211: G2/mitotic-specific cyclin-B3 isoform 3 [Homo sapiens]

Accession: gi|90669307
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 10.9
MW [kDa]: 157.8
pI: 6.3
Sequence Coverage [%]: 1.9
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MLLPLPPQSS	KPVPKKSQSS	KIVPSHHDPS	EKTGENCQTK	ISPSSLQESP	SSLQGALKKR	SAFEDLTNAS	QCQPVQPKKE
90	100	110	120	130	140	150	160
ANKEFVKVVS	KKINRNTHAL	GLAKKNKRNL	KWHKLEVTPV	VASTTVVPNI	MEKPLILDIS	TTSKTPNTEE	ASLFRKPLVL
170	180	190	200	210	220	230	240
KEEPTIEDET	LINKSLSLKK	CSNHEEVSLL	EKLQPLQEES	DSDDAFVIEP	MTFKKTHKTE	EAAITKKTLS	LKKKMCASQR
250	260	270	280	290	300	310	320
KQSCQEESLA	VQDVNMEEDS	FFMESMSFKK	KPKTEESIPT	HKLSSLKKKC	TIYGKICHFR	KPPVLQTTIC	GAMSSIKKPT
330	340	350	360	370	380	390	400
TEKETLFQEL	SVLQEKHTTE	HEMSILKKSL	ALQKTNFKED	SLVKESLAFK	KKPSTEEAIM	MPVILKEQCM	TEGKRSRLKP
410	420	430	440	450	460	470	480
LVLQEITSGE	KSLIMKPLSI	KEKPSTEKES	FSQEPSALQK	KHTTQEEVSI	LKEPSSLLKS	PTEESPFDEA	LAFTKKCTIE
490	500	510	520	530	540	550	560
EAPPTKKPLI	LKRKHATQGT	MSHLKKPLIL	QTTSGEKSLI	KEPLPFKEEK	VSLKKKCTTQ	EMMSICPELL	DFQDMIGEDK
570	580	590	600	610	620	630	640
NSFFMEPMSF	RKNPTTEETV	LTKTSLSLQE	KKITQGKMSH	LKKPLVLQKI	TSEEESFYKK	LLPFKMKSTT	EEKFLSQEPS
650	660	670	680	690	700	710	720
ALKEKHTTLQ	EVSLSKESLA	IQEKATTEEE	FSQELFSLHV	KHTNKSGSLF	QEALVLQEKT	DAEEDSLKNL	LALQEKSTME
730	740	750	760	770	780	790	800
EESLINKLLA	LKEELSAEAA	TNIQTQLSLK	KKSTSHGKVF	FLKKQLALNE	TINEEEFLNK	QPLALEGYPS	IAEGETLFKK
810	820	830	840	850	860	870	880
LLAMQEEPSI	EKEAVLKEPT	IDTEAHFKEP	LALQEEPSTE	KEAVLKEPSV	DTEAHFKETL	ALQEKPSIEQ	EALFKRHSAL
890	900	910	920	930	940	950	960
WEKPSTEKET	IFKESLDLQE	KPSIKKETLL	KKPLALKMST	INEAVLFEDM	IALNEKPTTG	KELSFKEPLA	LQESPTYKED
970	980	990	1000	1010	1020	1030	1040
TFLKTLLVPQ	VGTSPNVSST	APESITSKSS	IATMTSVGKS	GTINEAFLFE	DMITLNEKPT	TGKELSFKEP	LALQESPTCK
1050	1060	1070	1080	1090	1100	1110	1120
EDTFLETFLI	PQIGTSPYVF	STTPESITEK	SSIATMTSVG	KSRTTTESSA	CESASDKPVS	PQAKGTPKEI	TPREDIDEDS
1130	1140	1150	1160	1170	1180	1190	1200
SDPSFNPMYA	KEIFSYMKER	EEQFILTDYM	NRQIEITSDM	RAILVDWLVE	VQVSFEMTHE	TLYLAVKLVD	LYLMKAVCKK
1210	1220	1230	1240	1250	1260	1270	1280
DKLQLLGATA	FMIAAKFEEH	NSPRVDDFVY	ICDDNYQRSE	VLSMEINILN	VLKCDINIPI	AYHFLRRYAR	CIHTNMKTLT
1290	1300	1310	1320	1330	1340	1350	1360
LSRYICEMTL	QEYHYVQEKA	SKLAAASLLL	ALYMKKLGYW	VPFLEHYSGY	SISELHPLVR	QLNKLLTFSS	YDSLKAVYYK
1370	1380	1390	1400				
YSHPVFFEVA	KIPALDMLKL	EEILNCDCEA	QGLVL				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1755	1	1011.7658	-30.21	3	51.8	10.9	2	535-560	K.KKCTTQEMMSICPELLDFQDMIGEDK.N	

Detailed Protein Report

Protein 1212: amphiregulin preproprotein [Homo sapiens]

Accession:	gi|4502199	**Score:**	10.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	27.9
Database Date:	2015-11-30	**pI:**	7.8
		Sequence Coverage [%]:	6.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MRAPLLPPAP	VVLSLLILGS	GHYAAGLDLN	DTYSGKREPF	SGDHSADGFE	VTSRSEMSSG	SEISPVSEMP	SSSEPSSGAD
90	100	110	120	130	140	150	160
YDYSEEYDNE	PQIPGYIVDD	SVRVEQVVKP	PQNKTESENT	SDKPKRKKKG	GKNGKNRRNR	KKKNPCNAEF	QNFCIHGECK
170	180	190	200	210	220	230	240
YIEHLEAVTC	KCQQEYFGER	CGEKSMKTHS	MIDSSLSKIA	LAAIAAFMSA	VILTAVAVIT	VQLRRQYVRK	YEGEAEERKK
250	260						
LRQENGNVHA	IA						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1180	1	977.2721	-136.69	2	44.3	10.9	0	144-160	K.NPCNAEFQNFCIHGECK.Y	

Detailed Protein Report

Protein 1213: E3 ubiquitin-protein ligase MSL2 isoform 2 [Homo sapiens]

Accession:	gi|224028284	**Score:**	10.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	54.3
Database Date:	2015-11-30	**pI:**	8.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.2
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578807532	refseq_human (refseq_human_20140103.fasta)	PREDICTED: E3 ubiquitin-protein ligase MSL2 isoform X3 [Homo sapiens]
gi|530374862	refseq_human (refseq_human_20140103.fasta)	PREDICTED: E3 ubiquitin-protein ligase MSL2 isoform X2 [Homo sapiens]
gi|530374860	refseq_human (refseq_human_20140103.fasta)	PREDICTED: E3 ubiquitin-protein ligase MSL2 isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MMMKPSCSWC	KDYEQFEENK	QLSILVNCYK	KLCEYITQTT	LARDIIEAVD	CSSDILALLN	DGSLFCEETE	KPSDSSFTLC
90	100	110	120	130	140	150	160
LTHSPLPSTS	EPTTDPQASL	SPMSESTLSI	AIGSSVINGL	PTYNGLSIDR	FGINIPSPEH	SNTIDVCNTV	DIKTEDLSDS
170	180	190	200	210	220	230	240
LPPVCDTVAT	DLCSTGIDIC	SFSEDIKPGD	SLLLSVEEVL	RSLETVSNTE	VCCPNLQPNL	EATVSNGPFL	QLSSQSLSHN
250	260	270	280	290	300	310	320
VFMSTSPALH	GLSCTAATPK	IAKLNRKRSR	SESDSEKVQP	LPISTIIRGP	TLGASAPVTV	KRESKISLQP	IATVPNGGTT
330	340	350	360	370	380	390	400
PKISKTVLLS	TKSMKKSHEH	GSKKSHSKTK	PGILKKDKAV	KEKIPSHHFM	PGSPTKTVYK	KPQEKKGCKC	GRATQNPSVL
410	420	430	440	450	460	470	480
TCRGQRCPCY	SNRKACLDCI	CRGCQNSYMA	NGEKKLEAFA	VPEKALEQTR	LTLGINVTSI	AVRNASTSTS	VINVTGSPVT
490	500	510					
TFLAASTHDD	KSLDEAIDMR	FDC					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
350	1	635.5383	-107.67	3	33.7	10.9	2	407-422	R.CPCYSNRKACLDCICR.G	Carbamidomethyl: 1

Detailed Protein Report

Protein 1214: PREDICTED: type II inositol 3,4-bisphosphate 4-phosphatase isoform X9 [Homo sapiens]

Accession:	gi|578809595	**Score:**	10.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	66.3
Database Date:	2015-11-30	**pI:**	5.6
		Sequence Coverage [%]:	3.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEIKEEGASE	EGQHFLPTAQ	ANDPGDCQFT	SIQKTPNEPQ	LEFILACKDL	VAPVRDRKLN	TLVQISVIHP	VEQSLTRYSS
90	100	110	120	130	140	150	160
TEIVEGTRDP	LFLTGVTFPS	EYPIYEETKI	KLTVYDVKDK	SHDTVRTSVL	PEHKDPPPEV	GRSFLGYASF	KVGELLKSKE
170	180	190	200	210	220	230	240
QLLVLSLRTS	DGGKVVGTIE	VSVVKMGEIE	DGEADHITTD	VQGQKCALVC	ECTAPESVSG	KDNLPFLNSV	LKNPVCKLYR
250	260	270	280	290	300	310	320
FPTSDNKWMR	IREQMSESIL	SFHIPKELIS	LHIKEDLCRN	QEIKELGELS	PHWDNLRKNV	LTHCDQMVNM	YQDILTELSK
330	340	350	360	370	380	390	400
ETGSSFKSSS	SKGEKTLEFV	PINLHLQRMQ	VHSPHLKDIS	SGIPQIDALY	DVITVGAPAA	HFQGFKNGGL	RKLLHRFETE
410	420	430	440	450	460	470	480
RRNTGYQFIY	YSPENTAKAK	EVLSNINQLQ	PLIATHADLL	LNSASQHSPD	SLKNSLKMLS	EKTELFVHAF	KDQLVRSALL
490	500	510	520	530	540	550	560
ALYTARPGGI	LKKPPSPKSS	TEESSPQDQP	PVMRGQDSIP	HHSDYDEEEW	DRVWANVGKS	LNCIIAMVDK	LIERDGGSEG
570	580	590	600				
SGGNNDGEKE	PSLTDAIPSH	PRGCDNGNNN	SYKLL				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2038	1	945.8225	-108.23	2	55.4	10.9	1	551-569	K.LIERDGGSEGSGGNNDGEK.E	

Detailed Protein Report

Protein 1215: PREDICTED: insulin receptor isoform X3 [Homo sapiens]

Accession:	gi|530425235	**Score:**	10.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	152.8
Database Date:	2015-11-30	**pI:**	5.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDIRNNLTRL	HELENCSVIE	GHLQILLMFK	TRPEDFRDLS	FPKLIMITDY	LLLFRVYGLE	SLKDLFPNLT	VIRGSRLFFN
90	100	110	120	130	140	150	160
YALVIFEMVH	LKELGLYNLM	NITRGSVRIE	KNNELCYLAT	IDWSRILDSV	EDNYIVLNKD	DNEECGDICP	GTAKGKTNCP
170	180	190	200	210	220	230	240
ATVINGQFVE	RCWTHSHCQK	VCPTICKSHG	CTAEGLCCHS	ECLGNCSQPD	DPTKCVACRN	FYLDGRCVET	CPPPYYHFQD
250	260	270	280	290	300	310	320
WRCVNFSFCQ	DLHHKCKNSR	RQGCHQYVIH	NNKCIPECPS	GYTMNSSNLL	CTPCLGPCPK	VCHLLEGEKT	IDSVTSAQEL
330	340	350	360	370	380	390	400
RGCTVINGSL	IINIRGGNNL	AAELEANLGL	IEEISGYLKI	RRSYALVSLS	FFRKLRLIRG	ETLEIGNYSF	YALDNQNLRQ
410	420	430	440	450	460	470	480
LWDWSKHNLT	ITQGKLFFHY	NPKLCLSEIH	KMEEVSGTKG	RQERNDIALK	TNGDQASCEN	ELLKFSYIRT	SFDKILLRWE
490	500	510	520	530	540	550	560
PYWPPDFRDL	LGFMLFYKEA	PYQNVTEFDG	QDACGSNSWT	VVDIDPPLRS	NDPKSQNHPG	WLMRGLKPWT	QYAIFVKTLV
570	580	590	600	610	620	630	640
TFSDERRTYG	AKSDIIYVQT	DATNPSVPLD	PISVSNSSSQ	IILKWKPPSD	PNGNITHYLV	FWERQAEDSE	LFELDYCLKG
650	660	670	680	690	700	710	720
LKLPSRTWSP	PFESEDSQKH	NQSEYEDSAG	ECCSCPKTDS	QILKELEESS	FRKTFEDYLH	NVVFVPRKTS	SGTGAEDPRP
730	740	750	760	770	780	790	800
SRKRRSLGDV	GNVTVAVPTV	AAFPNTSSTS	VPTSPEEHRP	FEKVVNKESL	VISGLRHFTG	YRIELQACNQ	DTPEERCSVA
810	820	830	840	850	860	870	880
AYVSARTMPE	AKADDIVGPV	THEIFENNVV	HLMWQEPKEP	NGLIVLYEVS	YRRYGDEELH	LCVSRKHFAL	ERGCRLRGLS
890	900	910	920	930	940	950	960
PGNYSVRIRA	TSLAGNGSWT	EPTYFYVTDY	LDVPSNIAKI	IIGPLIFVFL	FSVVIGSIYL	FLRKRQPDGP	LGPLYASSNP
970	980	990	1000	1010	1020	1030	1040
EYLSASDVFP	CSVYVPDEWE	VSREKITLLR	ELGQGSFGMV	YEGNARDIIK	GEAETRVAVK	TVNESASLRE	RIEFLNEASV
1050	1060	1070	1080	1090	1100	1110	1120
MKGFTCHHVV	RLLGVVSKGQ	PTLVVMELMA	HGDLKSYLRS	LRPEAENNPG	RPPPTLQEMI	QMAAEIADGM	AYLNAKKFVH
1130	1140	1150	1160	1170	1180	1190	1200
RDLAARNCMV	AHDFTVKIGD	FGMTRDIYET	DYYRKGGKGL	LPVRWMAPES	LKDGVFTTSS	DMWSFGVVLW	EITSLAEQPY
1210	1220	1230	1240	1250	1260	1270	1280
QGLSNEQVLK	FVMDGGYLDQ	PDNCPERVTD	LMRMCWQFNP	KMRPTFLEIV	NLLKDDLHPS	FPEVSFFHSE	ENKAPESEEL
1290	1300	1310	1320	1330	1340	1350	
EMEFEDMENV	PLDRSSHCQR	EEAGGRDGGS	SLGFKRSYEE	HIPYTHMNGG	KKNGRILTLP	RSNPS	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1935	1	865.8143	-91.73	2	54.3	10.9	0	991-1006	R.ELGQGSFGMVYEGNAR.D	Oxidation: 9

Detailed Protein Report

Protein 1216: PREDICTED: uncharacterized protein C9orf9 isoform X1 [Homo sapiens]

Accession:	gi|530427104	**Score:**	10.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	25.1
Database Date:	2015-11-30	**pI:**	10.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	10.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MNEVKESLRS	IEQKYKLFQQ	QQLTFTAALE	HCRENAHDKI	RPISSIGQVQ	SYMEHYCNSS	TDRRVLLMFL	DICSELNKLC
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
QHFEAVHSGT	PVTNNLLEKC	KTLVSQSNDL	SSLRAKYPHD	VVNHLSCDEA	RNHYGGVVSL	IPLILDLMKE	WIAHSEKLPR
170	**180**	**190**	**200**	**210**	**220**	**230**	
KVLQHVSEPQ	AHQESTRGAA	RPAQAIGTQP	RATKHKCRQL	TKASLKPRGC	SKPPWRPPGG	KL	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1647	1	1273.7336	18.18	2	50.5	10.9	2	199-221	R.QLTKASLKPRGCSKPPWRPPGGK.L	Carbamidomethyl: 12

Detailed Protein Report

Protein 1217: EGF-containing fibulin-like extracellular matrix protein 2 precursor [Homo sapiens]

Accession:	gi|320118911	**Score:**	10.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	49.4
Database Date:	2015-11-30	**pI:**	4.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLPCASCLPG	SLLLWALLLL	LLGSASPQDS	EEPDSYTECT	DGYEWDPDSQ	HCRDVNECLT	IPEACKGEMK	CINHYGGYLC
90	100	110	120	130	140	150	160
LPRSAAVIND	LHGEGPPPPV	PPAQHPNPCP	PGYEPDDQDS	CVDVDECAQA	LHDCRPSQDC	HNLPGSYQCT	CPDGYRKIGP
170	180	190	200	210	220	230	240
ECVDIDECRY	RYCQHRCVNL	PGSFRCQCEP	GFQLGPNNRS	CVDVNECDMG	APCEQRCFNS	YGTFLCRCHQ	GYELHRDGFS
250	260	270	280	290	300	310	320
CSDIDECSYS	SYLCQYRCIN	EPGRFSCHCP	QGYQLLATRL	CQDIDECESG	AHQCSEAQTC	VNFHGGYRCV	DTNRCVEPYI
330	340	350	360	370	380	390	400
QVSENRCLCP	ASNPLCREQP	SSIVHRYMTI	TSERSVPADV	FQIQATSVYP	GAYNAFQIRA	GNSQGDFYIR	QINNVSAMLV
410	420	430	440	450			
LARPVTGPRE	YVLDLEMVTM	NSLMSYRASS	VLRLTVFVGA	YTF			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2544	1	812.0217	172.08	2	62.3	10.9	0	71-83	K.CINHYGGYLCLPR.S	Carbamidomethyl: 1, 10

Detailed Protein Report

Protein 1218: PREDICTED: 1,5-anhydro-D-fructose reductase isoform X4 [Homo sapiens]

Accession:	gi|578818599	**Score:**	10.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	22.1
Database Date:	2015-11-30	**pI:**	6.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	8.2
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MGDIPAVGLS SWKASPGKVT EAVKEAIDAG YRHFDCAYFY HNEREVGAGI RCKIKEGAVR REDLFIATKP PHPEWIMSCS
        90        100        110        120        130        140        150        160
ELSFCLSHPR VQDLPLDESN MVIPSDTDFL DTWEAMEDLV ITGLVKNIGV SNFNHEQLER LLNKPGLRFK PLTNQILIRF
       170        180        190        200
QIQRNVIVIP GSITPSHIKE NIQVCYTLRG NAILRQ
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1457	1	960.4393	-73.19	2	47.9	10.9	1	180-195	K.ENIQVCYTLRGNAILR.Q	Carbamidomethyl: 6

Detailed Protein Report

Protein 1219: ribonucleoside-diphosphate reductase subunit M2 isoform 1 [Homo sapiens]

Accession:	gi|260064013	**Score:**	10.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	51.1
Database Date:	2015-11-30	**pI:**	6.1
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGRVGGMAQP	MGRAGAPKPM	GRAGSARRGR	FKGCWSEGSP	VHPVPAVLSW	LLALLRCAST	MLSLRVPLAP	ITDPQQLQLS
90	100	110	120	130	140	150	160
PLKGLSLVDK	ENTPPALSGT	RVLASKTARR	IFQEPTEPKT	KAAAPGVEDE	PLLRENPRRF	VIFPIEYHDI	WQMYKKAEAS
170	180	190	200	210	220	230	240
FWTAEEVDLS	KDIQHWESLK	PEERYFISHV	LAFFAASDGI	VNENLVERFS	QEVQITEARC	FYGFQIAMEN	IHSEMYSLLI
250	260	270	280	290	300	310	320
DTYIKDPKER	EFLFNAIETM	PCVKKKADWA	LRWIGDKEAT	YGERVVAFAA	VEGIFFSGSF	ASIFWLKKRG	LMPGLTFSNE
330	340	350	360	370	380	390	400
LISRDEGLHC	DFACLMFKHL	VHKPSEERVR	EIIINAVRIE	QEFLTEALPV	KLIGMNCTLM	KQYIEFVADR	LMLELGFSKV
410	420	430	440	450			
FRVENPFDFM	ENISLEGKTN	FFEKRVGEYQ	RMGVMSSPTE	NSFTLDADF			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
462	1	690.4221	146.85	2	35.4	10.9	1	1-13	-.MGRVGGMAQPMGR.A	Oxidation: 7, 11

Detailed Protein Report

Protein 1220: bcl-2-like protein 12 isoform 2 [Homo sapiens]

Accession:	gi|542133130	**Score:**	10.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	19.1
Database Date:	2015-11-30	**pI:**	12.2
		Sequence Coverage [%]:	10.8
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 0.41 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MGRPAGLFPP	LCPFLGFRPE	ACWERHMQIE	RAPSVPPFLR	WAGYRPGPVR	RRGKVELIKF	VRVQWRRPQV	EWRRRRWGPG
90	100	110	120	130	140	150	160
PGASMAGSEE	LGLREDTLRV	LAAFLRRGEA	AGSPVPTPPR	PSYSRLLCFG	GPAAGTAGPR	AAEISAQPRI	TGSPIDREGS
170	180						
HTAEAGGPAG	GGGRSH						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
320	2	846.3697	-9.38	2	33.7	10.9	1	158-176	R.EGSHTAEAGGPAGGGGRSH.-		MD:MU	0.41

Protein 1221: homeobox protein Nkx-2.6 [Homo sapiens]

Accession: gi|343183350
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 10.8
MW [kDa]: 32.1
pI: 10.7
Sequence Coverage [%]: 5.0
No. of unique Peptides: 1

```
        10         20         30         40         50         60         70         80
MLLSPVTSTP FSVKDILRLE RERSCPAASP HPRVRKSPEN FQYLRMDAEP RGSEVHNAGG GGGDRKLDGS EPPGGPCEAV
        90        100        110        120        130        140        150        160
LEMDAERMGE PQPGLNAASP LGGGTRVPER GVGNSGDSVR GGRSEQPKAR QRRKPRVLFS QAQVLALERR FKQQRYLSAP
       170        180        190        200        210        220        230        240
EREHLASALQ LTSTQVKIWF QNRRYKCKRQ RQDKSLELAG HPLTPRRVAV PVLVRDGKPC LGPGPGAPAF PSPYSAAVSP
       250        260        270        280        290        300        310
YSCYGGYSGA PYGAGYGTCY AGAPSGPAPH TPLASAGFGH GGQNATPQGH LAATLQGVRA W
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1544	1	853.3308	-117.62	2	49.1	10.8	2	19-33	R.LERERSCPAASPHPR.V	

Detailed Protein Report

Protein 1222: laminin subunit gamma-2 isoform b precursor [Homo sapiens]

Accession:	gi|157419140	**Score:**	10.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	121.5
Database Date:	2015-11-30	**pI:**	6.0
		Sequence Coverage [%]:	1.2
		No. of unique Peptides:	1

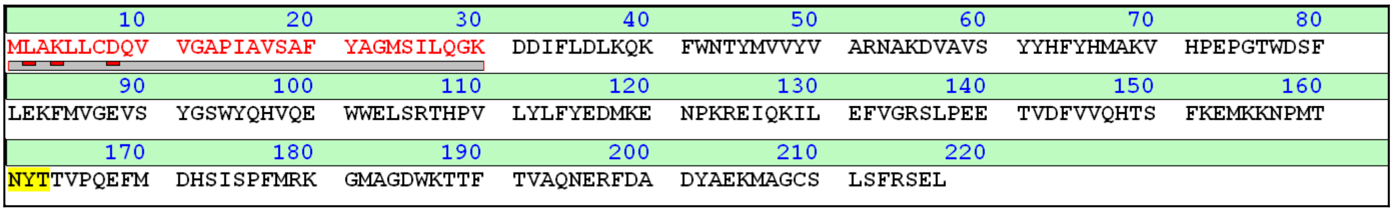
10	20	30	40	50	60	70	80
MPALWLGCCL	CFSLLLPAAR	ATSRREVCDC	NGKSRQCIFD	RELHRQTGNG	FRCLNCNDNT	DGIHCEKCKN	GFYRHRERDR
90	100	110	120	130	140	150	160
CLPCNCNSKG	SLSARCDNSG	RCSCKPGVTG	ARCDRCLPGF	HMLTDAGCTQ	DQRLLDSKCD	CDPAGIAGPC	DAGRCVCKPA
170	180	190	200	210	220	230	240
VTGERCDRCR	SGYYNLDGGN	PEGCTQCFCY	GHSASCRSSA	EYSVHKITST	FHQDVDGWKA	VQRNGSPAKL	QWSQRHQDVF
250	260	270	280	290	300	310	320
SSAQRLDPVY	FVAPAKFLGN	QQVSYGQSLS	FDYRVDRGGR	HPSAHDVILE	GAGLRITAPL	MPLGKTLPCG	LTKTYTFRLN
330	340	350	360	370	380	390	400
EHPSNNWSPQ	LSYFEYRRLL	RNLTALRIRA	TYGEYSTGYI	DNVTLISARP	VSGAPAPWVE	QCICPVGYKG	QFCQDCASGY
410	420	430	440	450	460	470	480
KRDSARLGPF	GTCIPCNCQG	GGACDPDTGD	CYSGDENPDI	ECADCPIGFY	NDPHDPRSCK	PCPCHNGFSC	SVMPETEEVV
490	500	510	520	530	540	550	560
CNNCPPGVTG	ARCELCADGY	FGDPFGEHGP	VRPCQPCQCN	NNVDPSASGN	CDRLTGRCLK	CIHNTAGIYC	DQCKAGYFGD
570	580	590	600	610	620	630	640
PLAPNPADKC	RACNCNPMGS	EPVGCRSDGT	CVCKPGFGGP	NCEHGAFSCP	ACYNQVKIQM	DQFMQQLQRM	EALISKAQGG
650	660	670	680	690	700	710	720
DGVVPDTELE	GRMQQAEQAL	QDILRDAQIS	EGASRSLGLQ	LAKVRSQENS	YQSRLDDLKM	TVERVRALGS	QYQNRVRDTH
730	740	750	760	770	780	790	800
RLITQMQLSL	AESEASLGNT	NIPASDHYVG	PNGFKSLAQE	ATRLAESHVE	SASNMEQLTR	ETEDYSKQAL	SLVRKALHEG
810	820	830	840	850	860	870	880
VGSGSGSPDG	AVVQGLVEKL	EKTKSLAQQL	TREATQAEIE	ADRSYQHSLR	LLDSVSRLQG	VSDQSFQVEE	AKRIKQKADS
890	900	910	920	930	940	950	960
LSSLVTRHMD	EFKRTQKNLG	NWKEEAQQLL	QNGKSGREKS	DQLLSRANLA	KSRAQEALSM	GNATFYEVES	ILKNLREFDL
970	980	990	1000	1010	1020	1030	1040
QVDNRKAEAE	EAMKRLSYIS	QKVSDASDKT	QQAERALGSA	AADAQRAKNG	AGEALEISSE	IEQEIGSLNL	EANVTADGAL
1050	1060	1070	1080	1090	1100	1110	1120
AMEKGLASLK	SEMREVEGEL	ERKELEFDTN	MDAVQMVITE	AQKVDTRAKN	AGVTIQDTLN	TLDGLLHLMG	M

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2722	1	772.4355	47.96	2	65.3	10.8	0	653-665	R.MQQAEQALQDILR.D	

Detailed Protein Report

Protein 1223: sulfotransferase 1A1 isoform b [Homo sapiens]

Accession:	gi|29540543	**Score:**	10.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	25.4
Database Date:	2015-11-30	**pI:**	5.8
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	13.8
		No. of unique Peptides:	1



```
        10         20         30         40         50         60         70         80
MLAKLLCDQV VGAPIAVSAF YAGMSILQGK DDIFLDLKQK FWNTYMVVYV ARNAKDVAVS YYHFYHMAKV HPEPGTWDSF
        90        100        110        120        130        140        150        160
LEKFMVGEVS YGSWYQHVQE WWELSRTHPV LYLFYEDMKE NPKREIQKIL EFVGRSLPEE TVDFVVQHTS FKEMKKNPMT
       170        180        190        200        210        220
NYTTVPQEFM DHSISPFMRK GMAGDWKTTF TVAQNERFDA DYAEKMAGCS LSFRSEL
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1792	1	1056.6546	89.16	3	52.4	10.8	1	1-30	-.MLAKLLCDQVVGAPIAVSAFYAGMSILQGK.D	Carbamidomethyl: 7; Oxidation: 24

Detailed Protein Report

Protein 1224: cytochrome P450 1B1 [Homo sapiens]

Accession:	gi|189491763	**Score:**	10.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	60.8
Database Date:	2015-11-30	**pI:**	10.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.2
		No. of unique Peptides:	1

Quantitation

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

10	20	30	40	50	60	70	80
MGTSLSPNDP	WPLNPLSIQQ	TTLLLLLSVL	ATVHVGQRLL	RQRRRQLRSA	PPGPFAWPLI	GNAAAVGQAA	HLSFARLARR
90	100	110	120	130	140	150	160
YGDVFQIRLG	SCPIVVLNGE	RAIHQALVQQ	GSAFADRPAF	ASFRVVSGGR	SMAFGHYSEH	WKVQRRAAHS	MMRNFFTRQP
170	180	190	200	210	220	230	240
RSRQVLEGHV	LSEARELVAL	LVRGSADGAF	LDPRPLTVVA	VANVMSAVCF	GCRYSHDDPE	FRELLSHNEE	FGRTVGAGSL
250	260	270	280	290	300	310	320
VDVMPWLQYF	PNPVRTVFRE	FEQLNRNFSN	FILDKFLRHC	ESLRPGAAPR	DMMDAFILSA	EKKAAGDSHG	GGARLDLENV
330	340	350	360	370	380	390	400
PATITDIFGA	SQDTLSTALQ	WLLLLFTRYP	DVQTRVQAEL	DQVVGRDRLP	CMGDQPNLPY	VLAFLYEAMR	FSSFVPVTIP
410	420	430	440	450	460	470	480
HATTANTSVL	GYHIPKDTVV	FVNQWSVNHD	PLKWPNPENF	DPARFLDKDG	LINKDLTSRV	MIFSVGKRRC	IGEELSKMQL
490	500	510	520	530	540	550	
FLFISILAHQ	CDFRANPNEP	AKMNFSYGLT	IKPKSFKVNV	TLRESMELLD	SAVQNLQAKE	TCQ	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
647	1	675.6947	-212.61	2	37.4	10.8	0	279-290	R.HCESLRPGAAPR.D	Carbamidomethyl: 2	MD:MU 0.64

Detailed Protein Report

Protein 1225: calcium/calmodulin-dependent protein kinase kinase 2 isoform 6 [Homo sapiens]

Accession:	gi|27437023	**Score:**	10.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	54.1
Database Date:	2015-11-30	**pI:**	7.0
		Sequence Coverage [%]:	5.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSSCVSSQPS	SNRAAPQDEL	GGRGSSSSES	QKPCEALRGL	SSLSIHLGME	SFIVVTECEP	GCAVDLGLAR	DRPLEADGQE
90	100	110	120	130	140	150	160
VPLDTSGSQA	RPHLSGRKLS	LQERSQGGLA	AGGSLDMNGR	CICPSLPYSP	VSSPQSSPRL	PRRPTVESHH	VSITGMQDCV
170	180	190	200	210	220	230	240
QLNQYTLKDE	IGKGSYGVVK	LAYNENDNTY	YAMKVLSKKK	LIRQAGFPRR	PPPRGTRPAP	GGCIQPRGPI	EQVYQEIAIL
250	260	270	280	290	300	310	320
KKLDHPNVVK	LVEVLDDPNE	DHLYMVFELV	NQGPVMEVPT	LKPLSEDQAR	FYFQDLIKGI	EYLHYQKIIH	RDIKPSNLLV
330	340	350	360	370	380	390	400
GEDGHIKIAD	FGVSNEFKGS	DALLSNTVGT	PAFMAPESLS	ETRKIFSGKA	LDVWAMGVTL	YCFVFGQCPF	MDERIMCLHS
410	420	430	440	450	460	470	480
KIKSQALEFP	DQPDIAEDLK	DLITRMLDKN	PESRIVVPEI	KILVKTMIRK	RSFGNPFEGS	RREERSLSAP	GNLLTKKPTR
490	500						
ECESLSELKT							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2098	1	966.7709	-4.81	3	56.4	10.8	0	370-394	K.ALDVWAMGVTLYCFVFGQCPFMDER.I	

Detailed Protein Report

Protein 1226: arylsulfatase A isoform b [Homo sapiens]

Accession:	gi|146229327	**Score:**	10.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	44.9
Database Date:	2015-11-30	**pI:**	5.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGMYPGVLVP	SSRGGLPLEE	VTVAEVLAAR	GYLTGMAGKW	HLGVGPEGAF	LPPHQGFHRF	LGIPYSHDQG	PCQNLTCFPP
90	100	110	120	130	140	150	160
ATPCDGGCDQ	GLVPIPLLAN	LSVEAQPPWL	PGLEARYMAF	AHDLMADAQR	QDRPFFLYYA	SHHTHYPQFS	GQSFAERSGR
170	180	190	200	210	220	230	240
GPFGDSLMEL	DAAVGTLMTA	IGDLGLLEET	LVIFTADNGP	ETMRMSRGGC	SGLLRCGKGT	TYEGGVREPA	LAFWPGHIAP
250	260	270	280	290	300	310	320
GVTHELASSL	DLLPTLAALA	GAPLPNVTLD	GFDLSPLLLG	TGKSPRQSLF	FYPSYPDEVR	GVFAVRTGKY	KAHFFTQGSA
330	340	350	360	370	380	390	400
HSDTTADPAC	HASSSLTAHE	PPLLYDLSKD	PGENYNLLGG	VAGATPEVLQ	ALKQLQLLKA	QLDAAVTFGP	SQVARGEDPA
410	420	430					
LQICCHPGCT	PRPACCHCPD	PHA					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2659	1	741.3515	-11.91	2	63.3	10.8	2	205-218	R.MSRGGCSGLLRCGK.G	Carbamidomethyl: 6

Detailed Protein Report

Protein 1227: calcium-binding and coiled-coil domain-containing protein 1 isoform 2 [Homo sapiens]

Accession:	gi|219521893	**Score:**	10.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	67.5
Database Date:	2015-11-30	**pI:**	4.5
		Sequence Coverage [%]:	2.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEESPLSRAP	SRGGVNFLNV	ARTYIPNTKV	ECHYTLPPGT	MPSASDWIGI	FKVEAACVRD	YHTFVWSSVP	ESTTDGSPIH
90	100	110	120	130	140	150	160
TSVQFQEPRP	MDELVTLEEA	DGGSDILLVV	PKATVLQNQL	DESQQERNDL	MQLKLQLEGQ	VTELRSRVQE	LERALATARQ
170	180	190	200	210	220	230	240
EHTELMEQYK	GISRSHGEIT	EERDILSRQQ	GDHVARILEL	EDDIQTISEK	VLTKEVELDR	LRDTVKALTR	EQEKLLGQLK
250	260	270	280	290	300	310	320
EVQADKEQSE	AELEPLKEQL	RGAQELAASS	QQKATLLGEE	LASAAAARDR	TIAELHRSRL	EVAEVNGRLA	ELGLHLKEEK
330	340	350	360	370	380	390	400
CQWSKERAGL	LQSVEAEKDK	ILKLSAEILR	LEKAVQEERT	QNQVFKTELA	REKDSSLVQL	SESKRELTEL	RSALRVLQKE
410	420	430	440	450	460	470	480
KEQLQEEKQE	LLEYMRKLEA	RLEKVADEKW	NEDATTEDEE	AAVGLSCPAA	LTDSEDESPE	DMRLPPYGLC	ERGDPGSSPA
490	500	510	520	530	540	550	560
GPREASPLVV	ISQPAPISPH	LSGPAEDSSS	DSEAEDEKSV	LMAAVQSGGE	EANLLLPELG	SAFYDMASGF	TVGTLSETST
570	580	590	600	610			
GGPATPTWKE	CPICKERFPA	ESDKDALEDH	MDGHFFFSTQ	DPFTFE			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
903	1	678.9131	43.92	2	40.8	10.8	1	148-159	R.VQELERALATAR.Q	

Detailed Protein Report

Protein 1228: **PREDICTED: threonylcarbamoyladenosine tRNA methylthiotransferase isoform X2 [Homo sapiens]**

Accession:	gi|578811764	**Score:**	10.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	47.7
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
MPSASCDTLL	DDIEDIVSQE	DSKPQDRHFV	RKDVVPKVRR	RNTQKYLQEE	ENSPPSDSTI	PGIQKIWIRT	WGCSHNNSDG
90	100	110	120	130	140	150	160
EYMAGQLAAY	GYKITENASD	ADLWLLNSCT	VKNPAEDHFR	NSIKKAQEEN	KKIVLAGCVP	QAQPRQDYLK	GLSIIGVQQI
170	180	190	200	210	220	230	240
DRVVEVVEET	IKGHSVRLLG	QKKDNGRRLG	GARLDLPKIR	KNPLIEIISI	NTGCLNACTY	CKTKHARGNL	ASYPIDELVD
250	260	270	280	290	300	310	320
RAKQSFQEGV	CEIWLTSEDT	GAYGRDIGTN	LPTLLWKLVE	VIPEGAMLRL	GMTNPPYILE	HLEEMAKILN	HPRVYAFLHI
330	340	350	360	370	380	390	400
PVQSASDSVL	MEMKREYCVA	DFKRVVDFLK	EKVPGITIAT	DIICGFPGET	DQDFQETVKL	VEEYKFPSLF	INQFYPRPGT
410	420	430					
PAAKMEQVPA	QVQHRNYWTV	LL					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1356	1	629.1525	-368.15	1	46.7	10.8	1	188-193	R.RLGGAR.L	

Detailed Protein Report

Protein 1229: PREDICTED: neurogenic locus notch homolog protein 3 isoform X1 [Homo sapiens]

Accession:	gi|530414885	**Score:**	10.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	238.2
Database Date:	2015-11-30	**pI:**	5.1
Modification(s):	Oxidation	**Sequence Coverage [%]:**	0.4
		No. of unique Peptides:	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MGPGARGRRR	RRRPMSPPPP	PPPVRALPLL	LLLAGPGAAA	PPCLDGSPCA	NGGRCTQLPS	REAACLCPPG	WVGERCQLED
90	100	110	120	130	140	150	160
PCHSGPCAGR	GVCQSSVVAG	TARFSCRCPR	GFRGPDCSLP	DPCLSSPCAH	GARCSVGPDG	RFLCSCPPGY	QGRSCRSDVD
170	180	190	200	210	220	230	240
ECRVGEPCRH	GGTCLNTPGS	FRCQCPAGYT	GPLCENPAVP	CAPSPCRNGG	TCRQSGDLTY	DCACLPGFEG	QNCEVNVDDC
250	260	270	280	290	300	310	320
PGHRCLNGGT	CVDGVNTYNC	QCPPEWTGQF	CTEDVDECQL	QPNACHNGGT	CFNTLGGHSC	VCVNGWTGES	CSQNIDDCAT
330	340	350	360	370	380	390	400
AVCFHGATCH	DRVASFYCAC	PMGKTGLLCH	LDDACVSNPC	HEDAICDTNP	VNGRAICTCP	PGFTGGACDQ	DVDECSIGAN
410	420	430	440	450	460	470	480
PCEHLGRCVN	TQGSFLCQCG	RGYTGPRCET	DVNECLSGPC	RNQATCLDRI	GQFTCICMAG	FTGTYCEVDI	DECQSSPCVN
490	500	510	520	530	540	550	560
GGVCKDRVNG	FSCTCPSGFS	GSTCQLDVDE	CASTPCRNGA	KCVDQPDGYE	CRCAEGFEGT	LCDRNVDDCS	PDPCHHGRCV
570	580	590	600	610	620	630	640
DGIASFSCAC	APGYTGTRCE	SQVDECRSQP	CRHGGKCLDL	VDKYLCRCPS	GTTGVNCEVN	IDDCASNPCT	FGVCRDGINR
650	660	670	680	690	700	710	720
YDCVCQPGFT	GPLCNVEINE	CASSPCGEGG	SCVDGENGFR	CLCPPGSLPP	LCLPPSHPCA	HEPCSHGICY	DAPGGFRCVC
730	740	750	760	770	780	790	800
EPGWSGPRCS	QSLARDACES	QPCRAGGTCS	SDGMGFHCTC	PPGVQGRQCE	LLSPCTPNPC	EHGGRCESAP	GQLPVCSCPQ
810	820	830	840	850	860	870	880
GWQDPCLNGG	SCQDGVGSFS	CSCLPGFAGP	RCARDVDECL	SNPCGPGTCT	DHVASFTCTC	PPGYGGFHCE	QDLPDCSPSS
890	900	910	920	930	940	950	960
CFNGGTCVDG	VNSFSCLCRP	GYTGAHCQHE	ADPCLSRPCL	HGGVCSAAHP	GFRCTCLESF	TGPQCQTLVD	WCSRQPCQNG
970	980	990	1000	1010	1020	1030	1040
GRCVQTGAYC	LCPPGWSGRL	CDIRSLPCRE	AAAQIGVRLE	QLCQAGGQCV	DEDSSHYCVC	PEGRTGSHCE	QEVDPCLAQP
1050	1060	1070	1080	1090	1100	1110	1120
CQHGGTCRGY	MGGYMCECLP	GYNGDNCEDD	VDECASQPCQ	HGGSCIDLVA	RYLCSCPPGT	LGVLCEINED	DCGPGPPLDS
1130	1140	1150	1160	1170	1180	1190	1200
GPRCLHNGTC	VDLVGGFRCT	CPPGYTGLRC	EADINECRSG	ACHAAHTRDC	LQDPGGGFRC	LCHAGFSGPR	CQTVLSPCES
1210	1220	1230	1240	1250	1260	1270	1280
QPCQHGGQCR	PSPGPGGGLT	FTCHCAQPFW	GPRCERVARS	CRELQCPVGV	PCQQTPRGPR	CACPPGLSGP	SCRSFPGSPP
1290	1300	1310	1320	1330	1340	1350	1360
GASNASCAAA	PCLHGGSCRP	APLAPFFRCA	CAQGWTGPRC	EAPAAAPEVS	EEPRCPRAAC	QAKRGDQRCD	RECNSPGCGW
1370	1380	1390	1400	1410	1420	1430	1440
DGGDCSLSVG	DPWRQCEALQ	CWRLFNNSRC	DPACSSPACL	YDNFDCHAGG	RERTCNPVYE	KYCADHFADG	RCDQGCNTEE
1450	1460	1470	1480	1490	1500	1510	1520
CGWDGLDCAS	EVPALLARGV	LVLTVLLPPE	ELLRSSADFL	QRLSAILRTS	LRFRLDAHGQ	AMVFPYHRPS	PGSEPRARRE
1530	1540	1550	1560	1570	1580	1590	1600
LAPEVIGSVV	MLEIDNRLCL	QSPENDHCFP	DAQSAADYLG	ALSAVERLDF	PYPLRDVRGE	PLEPPEPSVP	LLPLLVAGAV
1610	1620	1630	1640	1650	1660	1670	1680
LLLVILVLGV	MVARRKREHS	TLWFPEGFSL	HKDVASGHKG	RREPVGQDAL	GMKNMAKGES	LMGEVATDWM	DTECPEAKRL
1690	1700	1710	1720	1730	1740	1750	1760
KVEEPGMGAE	EAVDCRQWTQ	HHLVAADIRV	APAMALTPPQ	GDADADGMDV	NVRGPDGFTP	LMLASFCGGA	LEPMPTEEDE
1770	1780	1790	1800	1810	1820	1830	1840
ADDTSASIIS	DLICQGAQLG	ARTDRTGETA	LHLAARYARA	DAAKRLLDAG	ADTNAQDHSG	RTPLHTAVTA	DAQGVFQILI
1850	1860	1870	1880	1890	1900	1910	1920
RNRSTDLDAR	MADGSTALIL	AARLAVEGMV	EELIASHADV	NAVDELGKSA	LHWAAAVNNV	EATLALLKNG	ANKDMQDSKE
1930	1940	1950	1960	1970	1980	1990	2000
ETPLFLAARE	GSYEAAKLLL	DHFANREITD	HLDRLPRDVA	QERLHQDIVR	LLDQPSGPRS	PPGPHGLGPL	LCPPGAFLPG
2010	2020	2030	2040	2050	2060	2070	2080
LKAAQSGSKK	SRRPPGKAGL	GPQGPRGRGK	KLTLACPGPL	ADSSVTLSPV	DSLDSPRPFG	GPPASPGGFP	LEGPYAAATA
2090	2100	2110	2120	2130	2140	2150	2160
TAVSLAQLGG	PGRAGLGRQP	PGGCVLSLGL	LNPVAVPLDW	ARLPPPAPPG	PSFLLPLAPG	PQLLNPGTPV	SPQERPPPYL
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
1377	1	817.1361	-334.78	1	46.9	10.8	1	1-8	-.MGPGARGR.R	Oxidation: 1

Detailed Protein Report

Protein 1230: sister chromatid cohesion protein PDS5 homolog A isoform 3 [Homo sapiens]

Accession:	gi|155030220	**Score:**	10.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	69.0
Database Date:	2015-11-30	**pI:**	6.7
		Sequence Coverage [%]:	2.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDFTAQPKPA	TALCGVVSAD	GKIAYPPGVK	EITDKITTDE	MIKRLKMVVK	TFMDMDQDSE	DEKQQYLPLA	LHLASEFFLR
90	100	110	120	130	140	150	160
NPNKDVRLLV	ACCLADIFRI	YAPEAPYTSH	DKLKDIFLFI	TRQLKGLEDT	KSPQFNRYFY	LLENLAWVKS	YNICFELEDC
170	180	190	200	210	220	230	240
NEIFIQLFRT	LFSVINNSHN	KKVQMHMLDL	MSSIIMEGDG	VTQELLDSIL	INLIPAHKNL	NKQSFDLAKV	LLKRTVQTIE
250	260	270	280	290	300	310	320
ACIANFFNQV	LVLGRSSVSD	LSEHVFDLIQ	ELFAIDPHLL	LSVMPQLEFK	LKSNDGEERL	AVVRLLAKLF	GSKDSDLATQ
330	340	350	360	370	380	390	400
NRPLWQCFLG	RFNDIHVPVR	LESVKFASHC	LMNHPDLAKD	LTEYLKVRSH	DPEEAIRHDV	IVTIITAAKR	DLALVNDQLL
410	420	430	440	450	460	470	480
GFVRERTLDK	RWRVRKEAMM	GLAQLYKKYC	LHGEAGKEAA	EKVSWIKDKL	LHIYYQNSID	DKLLVEKIFA	QYLVPHNLET
490	500	510	520	530	540	550	560
EERMKCLYYL	YASLDPNAVK	ALNEMWKCQN	MLRSHVRELL	DLHKQPTSEA	NCSAMFGKLM	TIAKNLPDPG	KAQDFVKKFN
570	580	590	600	610			
QVLGDDEKLR	SQLELLISPT	CSCKQADICV	VSKSYFTLFL				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2709	1	735.9193	133.23	2	64.2	10.8	0	525-538	K.QPTSEANCSAMFGK.L	

Detailed Protein Report

Protein 1231: M-phase inducer phosphatase 2 isoform 7 [Homo sapiens]

Accession: gi|566559982
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 10.8
MW [kDa]: 53.7
pI: 5.8
Sequence Coverage [%]: 3.6
No. of unique Peptides: 1

Alias proteins:

Accession	Name	Description
gi|566559984	refseq_human (refseq_human_20140103.fasta)	M-phase inducer phosphatase 2 isoform 7 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MDSPSPMDPH MAEQTFEQAI QAASRIIRNE QFAIRRFQSM PVRLLGHSPV LRNITNSQAP DGRRKSEAGS GAASSSGEDK
        90        100        110        120        130        140        150        160
ENDGFVFKMP WKPTHPSSTH ALAEWASRRE AFAQRPSSAP DLMCLSPDRK MEVEELSPLA LGRFSLTPAE GDTEEDDGFV
       170        180        190        200        210        220        230        240
DILESDLKDD DAVPPGMESL ISAPLVKTLE KEEEKDLVMY SKCQRLFRSP SMPCSVIRPI LKRLERPQDR DTPVQNKRRR
       250        260        270        280        290        300        310        320
SVTPPEEQQE AEEPKARVLR SKSLCHDEIE NLLDSDHREL IGDYSKAFLL QTVDGKHQDL KYISPETMVA LLTGKFSNIV
       330        340        350        360        370        380        390        400
DKFVIVDCRY PYEYEGGHIK TAVNLPLERD AESFLLKSPI APCSLDKRVI LIFHCEFSSE RGPRMCRFIR ERDRAVNDYP
       410        420        430        440        450        460        470
SLYYPEMYIL KGGYKEFFPQ HPNFCEPQDY RPMNHEAFKD ELKTFRLKTR SWAGERSRRE LCSRLQDQ
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2473	1	812.2434	-170.71	2	60.8	10.8	2	64-80	R.RKSEAGSGAASSSGEDK.E	

Protein 1232: PREDICTED: methionine synthase isoform X7 [Homo sapiens]

Accession: gi|578802222

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Modification(s): Oxidation

Score: 10.8

MW [kDa]: 126.1

pI: 5.2

Sequence Coverage [%]: 0.9

No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MSPALQDLSQ	PEGLKKTLRD	EINAILQKRI	MVLDGGMGTM	IQREKLNEEH	FRGQEFKDHA	RPLKGNNDIL	SITQPDVIYQ
90	100	110	120	130	140	150	160
IHKEYLLAGA	DIIETNTFSS	TSIAQADYGL	EHLAYRMNMC	SAGVARKAAE	EVTLQTGIKR	FVAGALGPTN	KTLSVSPSVE
170	180	190	200	210	220	230	240
RPDYRNITFD	ELVEAYQEQA	KGLLDGGVDI	LLIETIFDTA	NAKAALFALQ	NLFEEKYAPR	PIFISGTIVD	KSGRTLSGQT
250	260	270	280	290	300	310	320
GEGFVISVSH	GEPLCIGLNC	ALGAAEMRPF	IEIIGKCTTA	YVLCYPNAGL	PNTFGDYDET	PSMMAKHLKD	FAMDGLVNIV
330	340	350	360	370	380	390	400
GGCCGSTPDH	IREIAEAVKN	CKPRVPPATA	FEGHMLLSGL	EPFRIGPYTN	FVNIGERCNV	AGSRKFAKLI	MAGNYEEALC
410	420	430	440	450	460	470	480
VAKVQVEMGA	QVLDVNMDDG	MLDGPSAMTR	FCNLIASEPD	IAKVPLCIDS	SNFAVIEAGL	KCCQGKCIVN	SISLKEGEDD
490	500	510	520	530	540	550	560
FLEKARKIKK	YGAAMVVMAF	DEEGQATETD	TKIRVCTRAY	HLLVKKLGFN	PNDIIFDPNI	LTIGTGMEEH	NLYAINFIHA
570	580	590	600	610	620	630	640
TKVIKETLPG	ARISGGLSNL	SFSFRGMEAI	REAMHGVFLY	HAIKSGMDMG	IVNAGNLPVY	DDIHKELLQL	CEDLIWNKDP
650	660	670	680	690	700	710	720
EATEKLLRYA	QTQGTGGKKV	IQTDEWRNGP	VEERLEYALV	KGIEKHIIED	TEEARLNQKK	YPRPLNIIEG	PLMNGMKIVG
730	740	750	760	770	780	790	800
DLFGAGKMFL	PQVIKSARVM	KKAVGHLIPF	MEKEREETRV	LNGTVEEEDP	YQGTIVLATV	KGDVHDIGKN	IVGVVLGCNN
810	820	830	840	850	860	870	880
FRVIDLGVMT	PCDKILKAAL	DHKADIIGLS	GLITPSLDEM	IFVAKEMERL	AIRIPLLIGG	ATTSKTHTAV	KIAPRYSAPV
890	900	910	920	930	940	950	960
IHVLDASKSV	VVCSQLLDEN	LKDEYFEEIM	EEYEDIRQDH	YESLKERRYL	PLSQARKSGF	QMDWLSEPHP	VKPTFIGTQV
970	980	990	1000	1010	1020	1030	1040
FEDYDLQKLV	DYIDWKPFFD	VWQLRGKYPN	RGFPKIFNDK	TVGGEARKVY	DDAHNMLNTL	ISQKKLRARG	VVGFWPAQSI
1050	1060	1070	1080	1090	1100	1110	1120
QDDIHLYAEA	AVPQAAEPIA	TFYGLRQQAE	KDSASTEPYY	CLSDFIAPLH	SGIRDYLGLF	AVACFGVEEL	SKAYEDDGDD
1130	1140						
YSSIMVKALG	DRLAESPSL						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1113	1	1071.2160	-207.16	1	43.5	10.8	0	117-126	R.MNMCSAGVAR.K	Oxidation: 1, 3

Detailed Protein Report

Protein 1233: 4-trimethylaminobutyraldehyde dehydrogenase [Homo sapiens]

Accession:	gi|115387104	**Score:**	10.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	56.3
Database Date:	2015-11-30	**pI:**	6.2
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MFLRAGLAAL	SPLLRSLRPS	PVAAMSTGTF	VVSQPLNYRG	GARVEPADAS	GTEKAFEPAT	GRVIATFTCS	GEKEVNLAVQ
90	100	110	120	130	140	150	160
NAKAAFKIWS	QKSGMERCRI	LLEAARIIRE	REDEIATMEC	INNGKSIFEA	RLDIDISWQC	LEYYAGLAAS	MAGEHIQLPG
170	180	190	200	210	220	230	240
GSFGYTRREP	LGVCVGIGAW	NYPFQIASWK	SAPALACGNA	MVFKPSPFTP	VSALLLAEIY	SEAGVPPGLF	NVVQGGAATG
250	260	270	280	290	300	310	320
QFLCQHPDVA	KVSFTGSVPT	GMKIMEMSAK	GIKPVTLELG	GKSPLIIFSD	CDMNNAVKGA	LMANFLTQGQ	VCCNGTRVFV
330	340	350	360	370	380	390	400
QKEILDKFTE	EVVKQTQRIK	IGDPLLEDTR	MGPLINRPHL	ERVLGFVKVA	KEQGAKVLCG	GDIYVPEDPK	LKDGYYMRPC
410	420	430	440	450	460	470	480
VLTNCRDDMT	CVKEEIFGPV	MSILSFDTEA	EVLERANDTT	FGLAAGVFTR	DIQRAHRVVA	ELQAGTCFIN	NYNVSPVELP
490	500	510	520				
FGGYKKSGFG	RENGRVTIEY	YSQLKTVCVE	MGDVESAF				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2653	1	701.8506	76.61	2	63.2	10.8	0	506-518	K.TVCVEMGDVESAF.-	Oxidation: 6

Detailed Protein Report

Protein 1234: sodium-dependent phosphate transport protein 2B isoform b [Homo sapiens]

Accession:	gi|295789158	**Score:**	10.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	75.5
Database Date:	2015-11-30	**pI:**	9.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.5
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|295789160	refseq_huma (refseq_human_20140103.fasta)	sodium-dependent phosphate transport protein 2B isoform b [Homo sapiens]

10	20	30	40	50	60	70	80
MAPWPELGDA	QPNPDKYLEG	AAGQQPTAPD	KSKETNKNNT	EAPVTKIELL	PSYSTATLID	EPTEVDDPWN	LPTLQDSGIK
90	100	110	120	130	140	150	160
WSERDTKGKI	LCFFQGIGRL	ILLLGFLYFF	VCSLDILSSA	FQLVGGKMAG	QFFSNSSIMS	NPLLGLVIGV	LVTVLVQSSS
170	180	190	200	210	220	230	240
TSTSIVVSMV	SSSLLTVRAA	IPIIMGANIG	TSITNTIVAL	MQVGDRSEFR	RAFAGATVHD	FFNWLSVLVL	LPVEVATHYL
250	260	270	280	290	300	310	320
EIITQLIVES	FHFKNGEDAP	DLLKVITKPF	TKLIVQLDKK	VISQIAMNDE	KAKNKSLVKI	WCKTFTNKTQ	INVTVPSTAN
330	340	350	360	370	380	390	400
CTSPSLCWTD	GIQNWTMKNV	TYKENIAKCQ	HIFVNFHLPD	LAVGTILLIL	SLLVLCGCLI	MIVKILGSVL	KGQVATVIKK
410	420	430	440	450	460	470	480
TINTDFPFPF	AWLTGYLAIL	VGAGMTFIVQ	SSSVFTSALT	PLIGIGVITI	ERAYPLTLGS	NIGTTTTAIL	AALASPGNAL
490	500	510	520	530	540	550	560
RSSLQIALCH	FFFNISGILL	WYPIPFTRLP	IRMAKGLGNI	SAKYRWFAVF	YLIIFFFLIP	LTVFGLSLAG	WRVLVGVGVP
570	580	590	600	610	620	630	640
VVFIIILVLC	LRLLQSRCPR	VLPKKLQNWN	FLPLWMRSLK	PWDAVVSKFT	GCFQMRCCCC	CRVCCRACCL	LCGCPKCCRC
650	660	670	680	690			
SKCCEDLEEA	QEGQDVPVKA	PETFDNITIS	REAQGEVPAS	DSKTECTAL			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
281	1	690.1846	-55.62	2	32.9	10.8	1	617-626	R.CCCCCRVCCR.A	Carbamidomethyl: 1, 2, 3, 4

Detailed Protein Report

Protein 1235: **neuronal acetylcholine receptor subunit alpha-4 isoform 1 precursor [Homo sapiens]**

Accession:	gi|4502827	**Score:**	10.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	69.9
Database Date:	2015-11-30	**pI:**	6.9
		Sequence Coverage [%]:	2.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MELGGPGAPR	LLPPLLLLLG	TGLLRASSHV	ETRAHAEERL	LKKLFSGYNK	WSRPVANISD	VVLVRFGLSI	AQLIDVDEKN
90	100	110	120	130	140	150	160
QMMTTNVWVK	QEWHDYKLRW	DPADYENVTS	IRIPSELIWR	PDIVLYNNAD	GDFAVTHLTK	AHLFHDGRVQ	WTPPAIYKSS
170	180	190	200	210	220	230	240
CSIDVTFFPF	DQQNCTMKFG	SWTYDKAKID	LVNMHSRVDQ	LDFWESGEWV	IVDAVGTYNT	RKYECCAEIY	PDITYAFVIR
250	260	270	280	290	300	310	320
RLPLFYTINL	IIPCLLISCL	TVLVFYLPSE	CGEKITLCIS	VLLSLTVFLL	LITEIIPSTS	LVIPLIGEYL	LFTMIFVTLS
330	340	350	360	370	380	390	400
IVITVFVLNV	HHRSPRTHTM	PTWVRRVFLD	IVPRLLLMKR	PSVVKDNCRR	LIESMHKMAS	APRFWPEPEG	EPPATSGTQS
410	420	430	440	450	460	470	480
LHPPSPSFCV	PLDVPAEPGP	SCKSPSDQLP	PQQPLEAEKA	SPHPSPGPCR	PPHGTQAPGL	AKARSLSVQH	MSSPGEAVEG
490	500	510	520	530	540	550	560
GVRCRSRSIQ	YCVPRDDAAP	EADGQAAGAL	ASRNTHSAEL	PPPDQPSPCK	CTCKKEPSSV	SPSATVKTRS	TKAPPPHLPL
570	580	590	600	610	620	630	
SPALTRAVEG	VQYIADHLKA	EDTDFSVKED	WKYVAMVIDR	IFLWMFIIVC	LLGTVGLFLP	PWLAGMI	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1862	1	917.8422	-125.92	2	53.3	10.8	1	98-112	K.LRWDPADYENVTSIR.I	

Detailed Protein Report

Protein 1236: probable histone-lysine N-methyltransferase PRDM7 [Homo sapiens]

Accession:	gi|148271100	**Score:**	10.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	55.7
Database Date:	2015-11-30	**pI:**	8.9
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.2
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530424650	refseq_human (refseq_human_20140103.fasta)	PREDICTED: probable histone-lysine N-methyltransferase PRDM7 isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MSPERSQEES	PEGDTERTER	KPMVKDAFKD	ISIYFTKEEW	AEMGDWEKTR	YRNVKMNYNA	LITVGLRATR	PAFMCHRRQA
90	100	110	120	130	140	150	160
IKLQVDDTED	SDEEWTPRQQ	VKPPWMAFRG	EQSKHQKGMP	KASFNNESSL	RELSGTPNLL	NTSDSEQAQK	PVSPPGEAST
170	180	190	200	210	220	230	240
SGQHSRLKLE	LRRKETEGKM	YSLRERKGHA	YKEISEPQDD	DYLYCEMCQN	FFIDSCAAHG	PPTFVKDSAV	DKGHPNRSAL
250	260	270	280	290	300	310	320
SLPPGLRIGP	SGIPQAGLGV	WNEASDLPLG	LHFGPYEGRI	TEDEEAANSG	YSWLITKGRN	CYEYVDGKDK	SSANWMRYVN
330	340	350	360	370	380	390	400
CARDDEEQNL	VAFQYHRQIF	YRTCRVIRPG	CELLVWSGDE	YGQELGIRSS	IEPAESLGQA	VNCWSGMGMS	MARNWASSGA
410	420	430	440	450	460	470	480
ASGRKSSWQG	ENQSQRSIHV	PHAVWPFQVK	NFSVNMWNAI	TPLRTSQDHL	QENFSNQRIP	AQGIRIRSGN	ILIHAAVMTK
490	500						
PKVKRSKKGP	NS						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
796	1	702.4202	76.83	2	39.3	10.8	0	99-109	R.QQVKPPWMAFR.G	Oxidation: 8

Detailed Protein Report

Protein 1237: PREDICTED: ubiquitin carboxyl-terminal hydrolase 45 isoform X6 [Homo sapiens]

Accession:	gi|530384124	**Score:**	10.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	51.0
Database Date:	2015-11-30	**pI:**	9.0
		Sequence Coverage [%]:	4.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MMKLEKKSKI	STVKDPFIDI	SLPIIEERVS	KPLLWGRMNK	YRSLRETDHD	RYSGNVTIEN	IHQPRAAKKH	SSSKDKSQLI
90	100	110	120	130	140	150	160
HDRKCIRKLS	SGETVTYQKN	ENLEMNGDSL	MFASLMNSES	RLNESPTDDS	EKEASHSESN	VDADSEPSES	ESASKQTGLF
170	180	190	200	210	220	230	240
RSSSGSGVQP	DGPLYPLSAG	KLLYTKETDS	GDKEMAEAIS	ELRLSSTVTG	DQDFDRENQP	LNISNNLCFL	EGKHLRSYSP
250	260	270	280	290	300	310	320
QNAFQTLSQS	YITTSKECSI	QSCLYQFTSM	ELLMGNNKLL	CENCTKNKQK	YQEETSFAEK	KVEGVYTNAR	KQLLISAVPA
330	340	350	360	370	380	390	400
VLILHLKRFH	QAGLSLRKVN	RHVDFPLMLD	LAPFCSATCK	NASVGDKVLY	GLYGIVEHSG	SMREGHYTAY	VKVRTPSRKL
410	420	430	440	450	460		
SEHNTKKKNV	PGLKAADNES	AGQWVHVSDT	YLQVVPESRA	LSAQAYLLFY	ERVL		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
331	1	847.0323	-20.10	3	33.5	10.7	0	257-278	K.ECSIQSCLYQFTSMELLMGNNK.L	

Detailed Protein Report

Protein 1238: PREDICTED: mucin-19-like isoform X15 [Homo sapiens]

Accession:	gi|578797289	**Score:**	10.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	49.8
Database Date:	2015-11-30	**pI:**	10.3
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEVGAQGLQV	NGGVEHRNYR	SMEVGAHGLQ	VNGGVEHRDY	KSMDVGPQGL	QVNGGGGTGT	SGQWRWGTWT	KGQWRWDRET
90	100	110	120	130	140	150	160
TGQWRWGHRD	YRSMEVGAQG	LHVSGDGVTG	TTGQWRWGHR	DYSSMEVGAQ	GLQVNGGGAQ	GLQVSGSGVT	GTTGQWRWGH
170	180	190	200	210	220	230	240
RDYRSLEVGA	QELQVNGGGG	TGTTGQWRWG	TGTTRQWRWS	HRDYRSMEVE	SQGLQVNGGG	GTGTAGQWRW	STGTTGQWRW
250	260	270	280	290	300	310	320
STGTTGQWRW	GTGTTGQWRC	STETTGQWRC	STETTGQWRW	GTGTTGQWRW	STETTGQWTW	STGTTGQWRW	GHRDYRSMEV
330	340	350	360	370	380	390	400
EHRDYRSMEV	EHRDYRSMEV	ESQGLQVNGG	GAERLQVNGR	GVQGLQVNGG	GAQRLQVNGG	GAQGLQVNGG	GAQRLQVNGG
410	420	430	440	450	460		
GVTGTTGQWT	WSIGTTGQWR	WGHRDYRSME	VGAEGLHVSG	GGAQRLGNGQ	LAGLGQ		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1877	1	599.5609	-112.71	3	53.3	10.7	0	1-17	-.MEVGAQGLQVNGGVEHR.N	Oxidation: 1

Detailed Protein Report

Protein 1239: methionine aminopeptidase 1D, mitochondrial precursor [Homo sapiens]

Accession:	gi|40385867	**Score:**	10.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	37.1
Database Date:	2015-11-30	**pI:**	6.4
		Sequence Coverage [%]:	4.8
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MAAPSGVHLL VRRGSHRIFS SPLNHIYLHK QSSSQQRRNF FFRRQRDISH SIVLPAAVSS AHPVPKHIKK PDYVTTGIVP
        90        100        110        120        130        140        150        160
DWGDSIEVKN EDQIQGLHQA CQLARHVLLL AGKSLKVDMT TEEIDALVHR EIISHNAYPS PLGYGGFPKS VCTSVNNVLC
       170        180        190        200        210        220        230        240
HGIPDSRPLQ DGDIINIDVT VYYNGYHGDT SETFLVGNVD ECGKKLVEVA RRCRDEAIAA CRAGAPFSVI GNTISHITHQ
       250        260        270        280        290        300        310        320
NGFQVCPHFV GHGIGSYFHG HPEIWHHAND SDLPMEEGMA FTIEPIITEG SPEFKVLEDA WTVVSLDNQR SAQFEHTVLI
       330        340
TSRGAQILTK LPHEA
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2526	1	856.9458	-54.55	2	62.0	10.7	2	2-17	M.AAPSGVHLLVRRGSHR.I	

Detailed Protein Report

Protein 1240: PREDICTED: AP-3 complex subunit beta-2 isoform X2 [Homo sapiens]

Accession:	gi|578827454	**Score:**	10.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	114.4
Database Date:	2015-11-30	**pI:**	5.4
Modification(s):	Oxidation	**Sequence Coverage [%]:**	0.9
		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
2291	1	974.3360	-251.91	1	58.9	10.7	1	17-25	R.IVAMIARGK.N	Oxidation: 4

Detailed Protein Report

Protein 1241: PREDICTED: cyclin-dependent kinase 12 isoform X3 [Homo sapiens]

Accession: gi|530412415
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 10.7
MW [kDa]: 139.4
pI: 10.1
Sequence Coverage [%]: 1.9
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MPNSERHGGK	KDGSGGASGT	LQPSSGGGSS	NSRERHRLVS	KHKRHKSKHS	KDMGLVTPEA	ASLGTVIKPL	VEYDDISSDS
90	100	110	120	130	140	150	160
DTFSDDMAFK	LDRRENDERR	GSDRSDRLHK	HRHHQHRRSR	DLLKAKQTEK	EKSQEVSSKS	GSMKDRISGS	SKRSNEETDD
170	180	190	200	210	220	230	240
YGKAQVAKSS	SKESRSSKLH	KEKTRKEREL	KSGHKDRSKS	HRKRETPKSY	KTVDSPKRRS	RSPHRKWSDS	SKQDDSPSGA
250	260	270	280	290	300	310	320
SYGQDYDLSP	SRSHTSSNYD	SYKKSPGSTS	RRQSVSPPYK	EPSAYQSSTR	SPSPYSRRQR	SVSPYSRRRS	SSYERSGSYS
330	340	350	360	370	380	390	400
GRSPSPYGRR	RSSSPFLSKR	SLSRSPLPSR	KSMKSRSRSP	AYSRHSSSHS	KKKRSSSRSR	HSSISPVRLP	LNSSLGAELS
410	420	430	440	450	460	470	480
RKKKERAAAA	AAAKMDGKES	KGSPVFLPRK	ENSSVEAKDS	GLESKKLPRS	VKLEKSAPDT	ELVNVTHLNT	EVKNSSDTGK
490	500	510	520	530	540	550	560
VKLDENSEKH	LVKDLKAQGT	RDSKPIALKE	EIVTPKETET	SEKETPPPLP	TIASPPPPLP	TTTPPPQTPP	LPPLPPIPAL
570	580	590	600	610	620	630	640
PQQPPLPPSQ	PAFSQVPASS	TSTLPPSTHS	KTSAVSSQAN	SQPPVQVSVK	TQVSVTAAIP	HLKTSTLPPL	PLPPLLPGDD
650	660	670	680	690	700	710	720
DMDSPKETLP	SKPVKKEKEQ	RTRHLLTDLP	LPPELPGGDL	SPPDSPEPKA	ITPPQQPYKK	RPKICCPRYG	ERRQTESDWG
730	740	750	760	770	780	790	800
KRCVDKFDII	GIIGEGTYGQ	VYKAKDKDTG	ELVALKKVRL	DNEKEGFPIT	AIREIKILRQ	LIHRSVVNMK	EIVTDKQDAL
810	820	830	840	850	860	870	880
DFKKDKGAFY	LVFEYMDHDL	MGLLESGLVH	FSEDHIKSFM	KQLMEGLEYC	HKKNFLHRDI	KCSNILLNNS	GQIKLADFGL
890	900	910	920	930	940	950	960
ARLYNSEESR	PYTNKVITLW	YRPPELLLGE	ERYTPAIDVW	SCGCILGELF	TKKPIFQANL	ELAQLELISR	LCGSPCPAVW
970	980	990	1000	1010	1020	1030	1040
PDVIKLPYFN	TMKPKKQYRR	RLREEFSFIP	SAALDLLDHM	LTLDPSKRCT	AEQTLQSDFL	KDVELSKMAP	PDLPHWQDCH
1050	1060	1070	1080	1090	1100	1110	1120
ELWSKKRRRQ	RQSGVVVEEP	PPSKTSRKET	TSGTSTEPVK	NSSPAPPQPA	PGKVESGAGD	AIGLADITQQ	LNQSELAVLL
1130	1140	1150	1160	1170	1180	1190	1200
NLLQSQTDLS	IPQMAQLLNI	HSNPEMQQQL	EALNQSISAL	TEATSQQQDS	ETMAPEESLK	EAPSAPVILP	SAEQTTLEAS
1210	1220	1230	1240	1250	1260		
STPADMQNIL	AVLLSQLMKT	QEPAGSLEEN	NSDKNSGPQG	PRRTPTMPQE	EAADGV		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1432	1	959.7733	-9.76	3	47.5	10.7	1	1022-1045	K.DVELSKMAPPDLPHWQDCHELWSK.K	Oxidation: 7

Detailed Protein Report

Protein 1242: PREDICTED: putative protein FAM157B-like [Homo sapiens]

Accession:	gi|578813822	**Score:**	10.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	27.5
Database Date:	2015-11-30	**pI:**	12.2
		Sequence Coverage [%]:	6.1
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 1.39 **CV:** 0.00 % **No. of Peptides:** 1

Alias proteins:

Accession	**Name**	**Description**
gi|578844171	refseq_human (refseq_human_20140103.fasta)	PREDICTED: putative protein FAM157B-like [Homo sapiens]
gi|578840953	refseq_human (refseq_human_20140103.fasta)	PREDICTED: putative protein FAM157B-like [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MGGGQRPMGL GSEFFRLLHD LHLLAFAMKR IWTSEIHRRG EATARPRAPE HPAPPATAVR GRDAASQNLK RRPGSGTDGL
        90        100        110        120        130        140        150        160
RLQGAEPSRL LRTYARGAVI PTGTPERAQP PPPQDPLGRR RWLSRNTWGP WPGTTQPPSP QLLRNDWGSC GFMVPEAARG
       170        180        190        200        210        220        230        240
KVFQDSQEGA HIRRETVSKS VCAEPWRHQR ARDPAPTNFP LKCQKQRGAS TSSGQHGGRV NLVFFIGCWN VIRVNVWSLL
       250
QCPETER
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
1583	1	798.3796	-14.25	2	49.5	10.7	0	2-16	M.GGGQRPMGLGSEFFR.L		MD:MU	1.39

Detailed Protein Report

Protein 1243: ventral anterior homeobox 1 isoform b [Homo sapiens]

Accession:	gi|40217622	**Score:**	10.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	21.0
Database Date:	2015-11-30	**pI:**	10.4
		Sequence Coverage [%]:	9.1
		No. of unique Peptides:	1

```
         10         20         30         40         50         60         70         80
MFGKPDKMDV RCHSDAEAAR VSKNAHKESR ESKGAEGNLP AAFLKEPQGA FSASGAAEDC NKSKSNSAAD PDYCRRILVR
         90        100        110        120        130        140        150        160
DAKGSIREII LPKGLDLDRP KRTRTSFTAE QLYRLEMEFQ RCQYVVGRER TELARQLNLS ETQANSEENN ERFKRGIKKQ
        170        180        190
KKKRKKEPAN DESRRGDSGG RGWQPL
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1749	1	841.2726	-103.58	2	51.8	10.7	0	46-62	K.EPQGAFSASGAAEDCNK.S	

Detailed Protein Report

Protein 1244: meiotic recombination protein SPO11 isoform b [Homo sapiens]

Accession:	gi|38201680	**Score:**	10.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	40.3
Database Date:	2015-11-30	**pI:**	10.1
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAFAPMGPEA	SFFDVLDRHR	ESLLAALRRG	GREPPTGGSR	LASRFEDSVG	LQMVSHCTTR	KIKSDSPKSA	QKFSLILKIL
90	100	110	120	130	140	150	160
SMIYKLVQSN	TYATKRDIYY	TDSQLFGNQT	VVDNIINDIS	CMLKVSRRSL	HILSTSKGLI	AGNLRYIEED	GTKVNCTCGA
170	180	190	200	210	220	230	240
TAVAVPSNIQ	GIRNLVTDAK	FVLIVEKDAT	FQRLLDDNFC	NKLSPCIMIT	GKGVPDLNTR	LLVKKLWDTF	HVPVFTLVDA
250	260	270	280	290	300	310	320
DPHGIEIMCI	YKYGSMSMSF	EAHHLTVPAI	RWLGLLPSDL	KRLNVPKDSL	IPLTKRDQMK	LDSILRRPYV	TCQPFWRKEM
330	340	350	360				
EIMADSKMKA	EIQALTFLSS	DYLSRVYLPN	KLKFGGWI				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
872	1	736.7983	-61.16	2	40.4	10.7	2	318-329	R.KEMEIMADSKMK.A	Oxidation: 6, 11

Detailed Protein Report

Protein 1245: uncharacterized protein C17orf98 [Homo sapiens]

Accession:	gi|122937325	**Score:**	10.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	17.6
Database Date:	2015-11-30	**pI:**	10.2
		Sequence Coverage [%]:	7.1
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 0.49 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MAYLSECRLR	LEKGFILDGV	AVSTAARAYG	RSRPKLWSAI	PPYNAQQDYH	ARSYFQSHVV	PPLLRKTDQD	HGGTGRDGWI
90	100	110	120	130	140	150	160
VDYIHIFGQG	QRYLNRRNWA	GTGHSLQQVT	GHDHYNADLK	PIDGFNGRFG	YRRNTPALRQ	STSVFGEVTH	FPLF

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
372	1	675.8993	38.72	2	34.3	10.7	2	129-139	R.FGYRRNTPALR.Q		MD:MU	0.49

Protein 1246: SH3 and multiple ankyrin repeat domains protein 2 isoform 2 [Homo sapiens]

Accession: gi|254911082
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 10.7
MW [kDa]: 135.6
pI: 5.5
Sequence Coverage [%]: 1.1
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MMMNVPGGGA	AAVMMTGYNN	GRCPRNSLYS	DCIIEEKTVV	LQKKDNEGFG	FVLRGAKADT	PIEEFTPTPA	FPALQYLESV
90	100	110	120	130	140	150	160
DEGGVAWQAG	LRTGDFLIEV	NNENVVKVGH	RQVVNMIRQG	GNHLVLKVVT	VTRNLDPDDT	ARKKAPPPPK	RAPTTALTLR
170	180	190	200	210	220	230	240
SKSMTSELEE	LVDKASVRKK	KDKPEEIVPA	SKPSRAAENM	AVEPRVATIK	QRPSSRCFPA	GSDMNSVYER	QGIAVMTPTV
250	260	270	280	290	300	310	320
PGSPKAPFLG	IPRGTMRRQK	SIDSRIFLSG	ITEEERQFLA	PPMLKFTRSL	SMPDTSEDIP	PPPQSVPPSP	PPPSPTTYNC
330	340	350	360	370	380	390	400
PKSPTPRVYG	TIKPAFNQNS	AAKVSPATRS	DTVATMMREK	GMYFRRELDR	YSLDSEDLYS	RNAGPQANFR	NKRGQMPENP
410	420	430	440	450	460	470	480
YSEVGKIASK	AVYVPAKPAR	RKGMLVKQSN	VEDSPEKTCS	IPIPTIIVKE	PSTSSSGKSS	QGSSMEIDPQ	APEPPSQLRP
490	500	510	520	530	540	550	560
DESLTVSSPF	AAAIAGAVRD	REKRLEARRN	SPAFLSTDLG	DEDVGLGPPA	PRTRPSMFPE	EGDFADEDSA	EQLSSPMPSA
570	580	590	600	610	620	630	640
TPREPENHFV	GGAEASAPGE	AGRPLNSTSK	AQGPESSPAV	PSASSGTAGP	GNYVHPLTGR	LLDPSSPLAL	ALSARDRAMK
650	660	670	680	690	700	710	720
ESQQGPKGEA	PKADLNKPLY	IDTKMRPSLD	AGFPTVTRQN	TRGPLRRQET	ENKYETDLGR	DRKGDDKKNM	LIDIMDTSQQ
730	740	750	760	770	780	790	800
KSAGLLMVHT	VDATKLDNAL	QEEDEKAEVE	MKPDSSPSEV	PEGVSETEGA	LQISAAPEPT	TVPGRTIVAV	GSMEEAVILP
810	820	830	840	850	860	870	880
FRIPPPPLAS	VDLDEDFIFT	EPLPPPLEFA	NSFDIPDDRA	ASVPALSDLV	KQKKSDTPQS	PSLNSSQPTN	SADSKKPASL
890	900	910	920	930	940	950	960
SNCLPASFLP	PPESFDAVAD	SGIEEVDSRS	SSDHHLETTS	TISTVSSIST	LSSEGGENVD	TCTVYADGQA	FMVDKPPVPP
970	980	990	1000	1010	1020	1030	1040
KPKMKPIIHK	SNALYQDALV	EEDVDSFVIP	PPAPPPPPGS	AQPGMAKVLQ	PRTSKLWGDV	TEIKSPILSG	PKANVISELN
1050	1060	1070	1080	1090	1100	1110	1120
SILQQMNREK	LAKPGEGLDS	PMGAKSASLA	PRSPEIMSTI	SGTRSTTVTF	TVRPGTSQPI	TLQSRPPDYE	SRTSGTRRAP
1130	1140	1150	1160	1170	1180	1190	1200
SPVVSPTEMN	KETLPAPLSA	ATASPSPALS	DVFSLPSQPP	SGDLFGLNPA	GRSRSPSPSI	LQQPISNKPF	TTKPVHLWTK
1210	1220	1230	1240	1250	1260	1270	
PDVADWLESL	NLGEHKEAFM	DNEIDGSHLP	NLQKEDLIDL	GVTRVGHRMN	IERALKQLLD	R	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2084	2	840.7946	-147.22	2	55.9	10.7	1	708-721	K.KNMLIDIMDTSQQK.S	Oxidation: 3

Detailed Protein Report

Protein 1247: lysM and putative peptidoglycan-binding domain-containing protein 2 isoform 1 [Homo sapiens]

Accession:	gi|23503313	**Score:**	10.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	23.4
Database Date:	2015-11-30	**pI:**	5.1
		Sequence Coverage [%]:	8.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MADSSPALSL	REGGPRAPRP	SAPSPPPRSR	SGSESEEAEL	SLSLARTKTR	SYGSTASVRA	PLGAGVIERH	VEHRVRAGDT
90	100	110	120	130	140	150	160
LQGIALKYGV	TMEQIKRANK	LFTNDCIFLK	KTLNIPVISE	KPLLFNGLNS	IDSPENETAD	NSFSQEEEPV	VAGEDLPPPS
170	180	190	200	210	220		
PQESDVQPVQ	PEEVSARDFL	QRLDLQIKLS	TQAAKKLKEE	SRDEESPYAT	SLYHS		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
932	1	636.7449	151.61	3	41.1	10.7	1	29-46	R.SRSGSESEEAELSLSLAR.T	

Detailed Protein Report

Protein 1248: **carcinoembryonic antigen-related cell adhesion molecule 16 precursor [Homo sapiens]**

Accession:	gi|291190766	**Score:**	10.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	45.8
Database Date:	2015-11-30	**pI:**	5.9
		Sequence Coverage [%]:	3.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MALTGYSWLL	LSATFLNVGA	EISITLEPAQ	PSEGDNVTLV	VHGLSGELLA	YSWYAGPTLS	VSYLVASYIV	STGDETPGPA
90	100	110	120	130	140	150	160
HTGREAVRPD	GSLDIQGILP	RHSGTYILQT	FNRQLQTEVG	YGHVQVHEIL	AQPTVLANST	ALVERRDTLR	LMCSSPSPTA
170	180	190	200	210	220	230	240
EVRWFFNGGA	LPVALRLGLS	PDGRVLARHG	IRREEAGAYQ	CEVWNPVSVS	RSEPINLTVY	FGPERVAILQ	DSTTRTGCTI
250	260	270	280	290	300	310	320
KVDFNTSLTL	WCVSRSCPEP	EYVWTFNGQA	LKNGQDHLNI	SSMTAAQEGT	YTCIAKNTKT	LLSGSASVVV	KLSAAAVATM
330	340	350	360	370	380	390	400
IVPVPTKPTE	GQDVTLTVQG	YPKDLLVYAW	YRGPASEPNR	LLSQLPSGTW	IAGPAHTGRE	VGFPNCSLLV	QKLNLTDTGR
410	420	430					
YTLKTVTVQG	KTETLEVELQ	VAPLG					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2150	1	820.7952	-138.29	2	56.7	10.7	0	242-255	K.VDFNTSLTLWCVSR.S	

Detailed Protein Report

Protein 1249: PREDICTED: glutamate receptor ionotropic, kainate 5 isoform X2 [Homo sapiens]

Accession:	gi|530416347	**Score:**	10.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	104.9
Database Date:	2015-11-30	**pI:**	9.4
		Sequence Coverage [%]:	1.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPAELLLLLI	VAFASPSCQV	LSSLRMAAIL	DDQTVCGRGE	RLALALAREQ	INGIIEVPAK	ARVEVDIFEL	QRDSQYETTD
90	100	110	120	130	140	150	160
TMCQILPKGV	VSVLGPSSSP	ASASTVSHIC	GEKEIPHIKV	GPEETPRLQY	LRFASVSLYP	SNEDVSLAVS	RILKSFNYPS
170	180	190	200	210	220	230	240
ASLICAKAEC	LLRLEELVRG	FLISKETLSV	RMLDDSRDPT	PLLKEIRDDK	VSTIIIDANA	SISHLILRKA	SELGMTSAFY
250	260	270	280	290	300	310	320
KYILTTMDFP	ILHLDGIVED	SSNILGFSMF	NTSHPFYPEF	VRSLNMSWRE	NCEASTYLGP	ALSAALMFDA	VHVVVSAVRE
330	340	350	360	370	380	390	400
LNRSQEIGVK	PLACTSANIW	PHGTSLMNYL	RMVEYDGLTG	RVEFNSKGQR	TNYTLRILEK	SRQGHREIGV	WYSNRTLAMN
410	420	430	440	450	460	470	480
ATTLDINLSQ	TLANKTLVVT	TILENPYVMR	RPNFQALSGN	ERFEGFCVDM	LRELAELLRF	RYRLRLVEDG	LYGAPEPNGS
490	500	510	520	530	540	550	560
WTGMVGELIN	RGRKPGYFSF	LDPFSPAVWL	FMLLAYLAVS	CVLFLAARLS	PYEWYNPHPC	LRARPHILEN	QYTLGNSLWF
570	580	590	600	610	620	630	640
PVGGFMQQGS	EIMPRALSTR	CVSGVWWAFT	LIIISSYTAN	LAAFLTVQRM	EVPVESADDL	ADQTNIEYGT	IHAGSTMTFF
650	660	670	680	690	700	710	720
QNSRYQTYQR	MWNYMQSKQP	SVFVKSTEEG	IARVLNSRYA	FLLESTMNEY	HRRLNCNLTQ	IGGLLDTKGY	GIGMPLGSPF
730	740	750	760	770	780	790	800
RDEITLAILQ	LQENNRLEIL	KRKWWEGGRC	PKEEDHRAKG	LGMENIGGIF	IVLICGLIIA	VFVAVMEFIW	STRRSAESEE
810	820	830	840	850	860	870	880
VSVCQEMLQE	LRHAVSCRKT	SRSRRRRRPG	GPSRALLSLR	AVREMRLSNG	KLYSAGAGGD	AGSAHGGPQR	LLDDPGPPSG
890	900	910	920	930	940	950	
ARPAAPTPCT	HVRVCQECRR	IQALRASGAG	APPRGLGVPA	EATSPPRPRP	GPAGPRELAE	HE	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
318	1	655.7866	-126.15	2	33.3	10.7	0	49-60	R.EQINGIIEVPAK.A	

Detailed Protein Report

Protein 1250: proteasome assembly chaperone 1 isoform b [Homo sapiens]

Accession:	gi|44680114	**Score:**	10.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	30.3
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
MAATFFGEVV	KAPCRAGTED	EEEEEEGRRE	TPEDREVRLQ	LARKREVRLL	RRQTKTSLEV	SLLEKYPCSK	FIIAIGNNAV
90	100	110	120	130	140	150	160
AFLSSFVMNS	GVWEEVGCAK	LWNEWCRTTD	TTHLSSTEAF	CVFYHLKSNP	SVFGSCPRKN	MQITILTCRH	VTDYKTSEST
170	180	190	200	210	220	230	240
GSLPSPFLRA	LKTQNFKDSA	CCPLLEQPNI	VHDLPAAVLS	YCQVWKIPAI	LYLCYTDVMK	LDLITVEAFK	PILSTRSLKG
250	260	270					
LVKNIPQSTE	ILKKLMTTNE	IQSNIYT					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1111	1	984.6997	106.49	1	43.5	10.7	1	36-43	R.EVRLQLAR.K	

Detailed Protein Report

Protein 1251: PREDICTED: ankyrin repeat domain-containing protein 42 isoform X6 [Homo sapiens]

Accession:	gi|530396729	**Score:**	10.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	21.6
Database Date:	2015-11-30	**pI:**	7.1
		Sequence Coverage [%]:	11.1
		No. of unique Peptides:	1

Quantitation

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

10	20	30	40	50	60	70	80
MPGVANSGPS	TSSRETANPC	SRKKVHFGSI	HDAVRAGDVK	QLSEIVVRGA	SINELDVLHK	FTPLHWAAHS	GSLECLHWLL
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
WHGADITHVT	TRGWTASHIA	AIRGQDACVQ	ALIMNGANLT	AQDDRGCTPL	HLAATHGHSF	TLQIMLRSGV	DPSVTDKREW
170	**180**	**190**	**200**				
RPVHYAAFHG	RLGCLQLLVK	WGCSIEDVDY	NGNLPEPP				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
28	1	1103.5007	-1.58	2	30.0	10.6	1	1-22	-.MPGVANSGPSTSSRETANPCSR.K		MD:MU 0.55

Detailed Protein Report

Protein 1252: PREDICTED: CAD protein isoform X4 [Homo sapiens]

Accession:	gi|530368098	**Score:**	10.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	235.9
Database Date:	2015-11-30	**pI:**	6.1
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	1.3
		No. of unique Peptides:	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MAALVLEDGS	VLRGQPFGAA	VSTAGEVVFQ	TGMVGYPEAL	TDPSYKAQIL	VLTYPLIGNY	GIPPDEMDEF	GLCKWFESSG
90	100	110	120	130	140	150	160
IHVAALVVGE	CCPTPSHWSA	TRTLHEWLQQ	HGIPGLQGVD	TRELTKKLRE	QGSLLGKLVQ	NGTEPSSLPF	LDPNARPLVP
170	180	190	200	210	220	230	240
EVSIKTPRVF	NTGGAPRILA	LDCGLKYNQI	RCLCQRGAEV	TVVPWDHALD	SQEYEGLFLS	NGPGDPASYP	SVVSTLSRVL
250	260	270	280	290	300	310	320
SEPNPRPVFG	ICLGHQLLAL	AIGAKTYKMR	YGNRGHNQPC	LLVGSGRCFL	TSQNHGFAVE	TDSLPADWAP	LFTNANDGSN
330	340	350	360	370	380	390	400
EGIVHNSLPF	FSVQFHPEHQ	AGPSDMELLF	DIFLETVKEA	TAGNPGGQTV	RERLTERLCP	PGIPTPGSGL	PPPRKVLILG
410	420	430	440	450	460	470	480
SGGLSIGQAG	EFDYSGSQAI	KALKEENIQT	LLINPNIATV	QTSQGLADKV	YFLPITPHYV	TQVIRNERPD	GVLLTFGGQT
490	500	510	520	530	540	550	560
ALNCGVELTK	AGVLARYGVR	VLGTPVETIE	LTEDRRAFAA	RMAEIGEHVA	PSEAANSLEQ	AQAAAERLGY	PVLVRAAFAL
570	580	590	600	610	620	630	640
GGLGSGFASN	REELSALVAP	AFAHTSQVLV	DKSLKGWKEI	EYEVVRDAYG	NCVTYYIIEV	NARLSRSSAL	ASKATGYPLA
650	660	670	680	690	700	710	720
YVAAKLALGI	PLPELRNSVT	GGTAAFEPSV	DYCVVKIPRW	DLSKFLRVST	KIGSCMKSVG	EVMGIGRSFE	EAFQKALRMV
730	740	750	760	770	780	790	800
DENCVGFDHT	VKPVSDMELE	TPTDKRIFVV	AAALWAGYSV	DRLYELTRID	RWFLHRMKRI	IAHAQLLEQH	RGQPLPPDLL
810	820	830	840	850	860	870	880
QQAKCLGFSD	KQIALAVLST	ELAVRKLRQE	LGICPAVKQI	DTVAAEWPAQ	TNYLYLTYWG	TTHDLTFRTP	HVLVLGSGVY
890	900	910	920	930	940	950	960
RIGSSVEFDW	CAVGCIQQLR	KMGYKTIMVN	YNPETVSTDY	DMCDRLYFDE	ISFEVVMDIY	ELENPEGVIL	SMGGQLPNNM
970	980	990	1000	1010	1020	1030	1040
AMALHRQQCR	VLGTSPEAID	SAENRFKFSR	LLDTIGISQP	QWRELSDLES	ARQFCQTVGY	PCVVRPSYVL	SGAAMNVAYT
1050	1060	1070	1080	1090	1100	1110	1120
DGDLERFLSS	AAAVSKEHPV	VISKFIQEAK	EIDVDAVASD	GVVAAIAISE	HVENAGVHSG	DATLVTPPQD	ITAKTLERIK
1130	1140	1150	1160	1170	1180	1190	1200
AIVHAVGQEL	QVTGPFNLQL	IAKDDQLKVI	ECNVRVSRSF	PFVSKTLGVD	LVALATRVIM	GEEVEPVGLM	TGSGVVGVKV
1210	1220	1230	1240	1250	1260	1270	1280
PQFSFSRLAG	ADVVLGVEMT	STGEVAGFGE	SRCEAYLKAM	LSTGFKIPKK	NILLTIGSYK	NKSELLPTVR	LLESLGYSLY
1290	1300	1310	1320	1330	1340	1350	1360
ASLGTADFYT	EHGVKVTAVD	WHFEEAVDGE	CPPQRSILEQ	LAEKNFELVI	NLSMRGAGGR	RLSSFVTKGY	RTRRLAADFS
1370	1380	1390	1400	1410	1420	1430	1440
VPLIIDIKCT	KLFVEALGQI	GPAPPLKVHV	DCMTSQKLVR	LPGLIDVHVH	LREPGGTHKE	DFASGTAAAL	AGGITMVCAM
1450	1460	1470	1480	1490	1500	1510	1520
PNTRPPIIDA	PALALAQKLA	EAGARCDFAL	FLGASSENAG	TLGTVAGSAA	GLKLYLNETF	SELRLDSVVQ	WMEHFETWPS
1530	1540	1550	1560	1570	1580	1590	1600
HLPIVAHAEQ	QTVAAVLMVA	QLTQRSVHIC	HVARKEEILL	IKAAKARGLP	VTCEVAPHHL	FLSHDDLERL	GPGKGEVRPE
1610	1620	1630	1640	1650	1660	1670	1680
LGSRQDVEAL	WENMAVIDCF	ASDHAPHTLE	EKCGSRPPPG	FPGLETMLPL	LLTAVSEGRL	SLDDLLQRLH	HNPRRIFHLP
1690	1700	1710	1720	1730	1740	1750	1760
PQEDTYVEVD	LEHEWTIPSH	MPFSKAHWTP	FEGQKVKGTV	RRVVLRGEVA	YIDGQVLVPP	GYGQDVRKWP	QGAVPQLPPS
1770	1780	1790	1800	1810	1820	1830	1840
APATSEMTTT	PERPRRGIPG	LPDGRFHLPP	RIHRASDPGL	PAEEPKEKSS	RKVAEPELMG	TPDGTCYPPP	PVPRQASPQN
1850	1860	1870	1880	1890	1900	1910	1920
LGTPGLLHPQ	TSPLLHSLVG	QHILSVQQFT	KDQMSHLFNV	AHTLRMMVQK	ERSLDILKGK	VMASMFYEVS	TRTSSSFAAA
1930	1940	1950	1960	1970	1980	1990	2000
MARLGGAVLS	FSEATSSVQK	GESLADSVQT	MSCYADVVVL	RHPQPGAVEL	AAKHCRRPVI	NAGDGVGEHP	TQALLDIFTI
2010	2020	2030	2040	2050	2060	2070	2080
REELGTVNGM	TITMVGDLKH	GRTVHSLACL	LTQYRVSLRY	VAPPSLRMPP	TVRAFVASRG	TKQEEFESIE	EALPDTDVLY
2090	2100	2110	2120	2130	2140	2150	2160
MTRIQKERFG	STQEYEACFG	QFILTPHIMT	RAKKKMVVMH	PMPRVNEISV	EVDSDPRAAY	FRQAENGMYI	RMALLATVLG
2170							

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1509	1	1061.8026	-76.29	3	48.7	10.6	2	1369-1397	K.CTKLFVEALGQIGPAPPLKVHVDCMTSQK.L	Carbamidomethyl: 1; Oxidation: 25

Detailed Protein Report

Protein 1253: bone morphogenetic protein 1 isoform 3 precursor [Homo sapiens]

Accession: gi|5453579
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 10.6
MW [kDa]: 111.2
pI: 6.5
Sequence Coverage [%]: 0.9
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	FSDKDECSKD	NGGCQQDCVN
730	740	750	760	770	780	790	800
TFGSYECQCR	SGFVLHDNKH	DCKEAGCDHK	VTSTSGTITS	PNWPDKYPSK	KECTWAISST	PGHRVKLTFM	EMDIESQPEC
810	820	830	840	850	860	870	880
AYDHLEVFDG	RDAKAPVLGR	FCGSKKPEPV	LATGSRMFLR	FYSDNSVQRK	GFQASHATEC	GGQVRADVKT	KDLYSHAQFG
890	900	910	920	930	940	950	960
DNNYPGGVDC	EWVIVAEEGY	GVELVFQTFE	VEEETDCGYD	YMELFDGYDS	TAPRLGRYCG	SGPPEEVYSA	GDSVLVKFHS
970	980	990					
DDTITKKGFH	LRYTSTKFQD	TLHSRK					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2126	1	1131.3250	-234.65	1	56.8	10.6	1	978-986	K.FQDTLHSRK.-	

Detailed Protein Report

Protein 1254: rho GTPase-activating protein 11A isoform 3 [Homo sapiens]

Accession:	gi|557128992	**Score:**	10.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	92.6
Database Date:	2015-11-30	**pI:**	9.9
		Sequence Coverage [%]:	2.3
		No. of unique Peptides:	1

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
2141	1	682.5590	-125.36	3	57.0	10.6	0	386-404	K.HNSNITSSPLSGDENNMTK.E	

Detailed Protein Report

Protein 1255: PREDICTED: palmitoyltransferase ZDHHC17 isoform X3 [Homo sapiens]

Accession:	gi|530399995	**Score:**	10.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	29.6
Database Date:	2015-11-30	**pI:**	5.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	7.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MQREEGFNTK	MADGPDEYDT	EAGCVPLLHP	EEIKPQSHYN	HGYGEPLGRK	THIDDYSTWD	IVKATQYGIY	ERCRELVEAG
90	100	110	120	130	140	150	160
YDVRQPDKEN	VTLLHWAAIN	NRIDLVKYYI	SKGAIVDQLG	GDLNSTPLHW	ATRQGHLSMV	VQLMKYGADP	SLIDGEGCSC
170	180	190	200	210	220	230	240
IHLAAQFGHT	SIVAYLIAKG	QDVDMMDQNG	MTPLMWAAYR	THSVDPTRLL	LTFNVSVNLG	DKYHKNTALH	WAVLAGNTTV
250	260	270					
ISLLLEAGAN	VDAQNIKAIL	RCHMAL					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
84	1	826.6636	-17.37	3	30.4	10.6	0	180-200	K.GQDVDMMDQNGMTPLMWAAYR.T	Oxidation: 6, 12, 16

Detailed Protein Report

Protein 1256: **PREDICTED: EF-hand calcium-binding domain-containing protein 7 isoform X1 [Homo sapiens]**

Accession:	gi|530363476	**Score:**	10.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	69.1
Database Date:	2015-11-30	**pI:**	6.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAISPRSDAT	FSSQKSTPSE	SPRTKKFPLT	EEEIFYMNCR	AAYLTVFKSS	LENIISKDQL	YLALQHAGRN	PSQKTINKYW
90	100	110	120	130	140	150	160
TPQTAKLNFD	DFCIILRKEK	PTSKAELLKS	FKQLDVNDDG	CILHTDLYKF	LTKRGEKMTR	EEVNAIINLA	DVNADGKFDY
170	180	190	200	210	220	230	240
IKFCKLYMTT	NEQCLKTTLE	KLEVDSKLMR	HQFGNHIEGS	PERDPSPVPK	PSPKITRKTD	PETFLNKGDT	RSSLLSATRK
250	260	270	280	290	300	310	320
FKTSVSFTVT	MGANGNRNSK	LMEPNLIKDW	QHMQSKGCFF	LEEDGEIISH	QYRMQIAQRS	MVYLTIKPLN	LSQVEGKPSP
330	340	350	360	370	380	390	400
WLSVDTALYI	LKENESQANL	QLVCFTELRN	REVFGWTGEL	GPGIYWLIPS	TTGCRLRKKI	KPVTDEAQLV	YRDETGELFL
410	420	430	440	450	460	470	480
TKEFKSTLSD	IFEVIDLDGN	GLLSLEEYNF	FELRTSGEKC	DEDAWAVCRE	NFDTKRNELT	RQGFMDLNLM	EANDREGDPC
490	500	510	520	530	540	550	560
DLWVTLHSMG	YNKALELTEA	CPFVIDIYAE	KCKPKIKAVH	MEACSGQLEK	AICKSVLSNG	DAKVMDGYEN	IIVHTYSCDT
570	580	590	600	610			
WITSVIENKS	DEKVIIHISN	ELSKNCINNR	GLNIFAVEVG	PKSTMP			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1835	1	835.2818	-104.41	2	52.8	10.6	0	462-475	R.QGFMDLNLMEANDR.E	Oxidation: 4

Detailed Protein Report

Protein 1257: dehydrogenase/reductase SDR family member 9 precursor [Homo sapiens]

Accession:	gi|22758144	**Score:**	10.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	35.2
Database Date:	2015-11-30	**pI:**	9.5
		Sequence Coverage [%]:	2.2
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|214010158	refseq_human(refseq_human_20140103.fasta)	dehydrogenase/reductase SDR family member 9 precursor [Homo sapiens]
gi|214010156	refseq_human(refseq_human_20140103.fasta)	dehydrogenase/reductase SDR family member 9 precursor [Homo sapiens]
gi|40548397	refseq_human(refseq_human_20140103.fasta)	dehydrogenase/reductase SDR family member 9 precursor [Homo sapiens]

10	20	30	40	50	60	70	80
MLFWVLGLLI	LCGFLWTRKG	KLKIEDITDK	YIFITGCDSG	FGNLAARTFD	KKGFHVIAAC	LTESGSTALK	AETSERLRTV
90	100	110	120	130	140	150	160
LLDVTDPENV	KRTAQWVKNQ	VGEKGLWGLI	NNAGVPGVLA	PTDWLTLEDY	REPIEVNLFG	LISVTLNMLP	LVKKAQGRVI
170	180	190	200	210	220	230	240
NVSSVGGRLA	IVGGGYTPSK	YAVEGFNDSL	RRDMKAFGVH	VSCIEPGLFK	TNLADPVKVI	EKKLAIWEQL	SPDIKQQYGE
250	260	270	280	290	300	310	320
GYIEKSLDKL	KGNKSYVNMD	LSPVVECMDH	ALTSLFPKTH	YAAGKDAKIF	WIPLSHMPAA	LQDFLLLKQK	AELANPKAV

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1476	1	742.1323	-373.15	1	48.2	10.6	0	311-317	K.AELANPK.A	

Detailed Protein Report

Protein 1258: ankyrin repeat family A protein 2 [Homo sapiens]

Accession:	gi|12746412	**Score:**	10.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	34.2
Database Date:	2015-11-30	**pI:**	4.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDTSTNLDIG	AQLIVEECPS	TYSLTGMPDI	KIEHPLDPNS	EEGSAQGVAM	GMKFILPNRF	DMNVCSRFVK	SLNEEDSKNI
90	100	110	120	130	140	150	160
QDQVNSDLEV	ASVLFKAECN	IHTSPSPGIQ	VRHVYTPSTT	KHFSPIKQST	TLTNKHRGNE	VSTTPLLANS	LSVHQLAAQG
170	180	190	200	210	220	230	240
EMLYLATRIE	QENVINHTDE	EGFTPLMWAA	AHGQIAVVEF	LLQNGADPQL	LGKGRESALS	LACSKGYTDI	VKMLLDCGVD
250	260	270	280	290	300	310	320
VNEYDWNGGT	PLLYAVHGNH	VKCVKMLLES	GADPTIETDS	GYNSMDLAVA	LGYRSVQQVI	ESHLLKLLQN	IKE

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2752	1	884.9908	63.41	2	65.7	10.6	1	54-67	K.FILPNRFDMNVCSR.F	Carbamidomethyl: 12

Detailed Protein Report

Protein 1259: PREDICTED: HMG domain-containing protein 3 isoform X3 [Homo sapiens]

Accession: gi|578810822
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 10.6
MW [kDa]: 109.9
pI: 6.3
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
2375	1	682.2879	-67.35	3	59.6	10.6	0	474-492	K.GGQNSLAGPQECWLLTASR.L	Carbamidomethyl: 12

Detailed Protein Report

Protein 1260: E3 ubiquitin-protein ligase HECTD3 [Homo sapiens]

Accession:	gi|157738609	**Score:**	10.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	97.1
Database Date:	2015-11-30	**pI:**	5.3
		Sequence Coverage [%]:	1.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAGPGPGAVL	ESPRQLLGRV	RFLAEAARSL	RAGRPLPAAL	AFVPREVLYK	LYKDPAGPSR	VLLPVWEAEG	LGLRVGAAGP
90	100	110	120	130	140	150	160
APGTGSGPLR	AARDSIELRR	GACVRTTGEE	LCNGHGLWVK	LTKEQLAEHL	GDCGLQEGWL	LVCRPAEGGA	RLVPIDTPNH
170	180	190	200	210	220	230	240
LQRQQQLFGV	DYRPVLRWEQ	VVDLTYSHRL	GSRPQPAEAY	AEAVQRLLYV	PPTWTYECDE	DLIHFLYDHL	GKEDENLGSV
250	260	270	280	290	300	310	320
KQYVESIDVS	SYTEEFNVSC	LTDSNADTYW	ESDGSQCQHW	VRLTMKKGTI	VKKLLLTVDT	TDDNFMPKRV	VVYGGEGDNL
330	340	350	360	370	380	390	400
KKLSDVSIDE	TLIGDVCVLE	DMTVHLPIIE	IRIVECRDDG	IDVRLRGVKI	KSSRQRELGL	NADLFQPTSL	VRYPRLEGTD
410	420	430	440	450	460	470	480
PEVLYRRAVL	LQRFIKILDS	VLHHLVPAWD	HTLGTFSEIK	QVKQFLLLSR	QRPGLVAQCL	RDSESSKPSF	MPRLYINRRL
490	500	510	520	530	540	550	560
AMEHRACPSR	DPACKNAVFT	QVYEGLKPSD	KYEKPLDYRW	PMRYDQWWEC	KFIAEGIIDQ	GGGFRDSLAD	MSEELCPSSA
570	580	590	600	610	620	630	640
DTPVPLPFFV	RTANQGNGTG	EARDMYVPNP	SCRDFAKYEW	IGQLMGAALR	GKEFLVLALP	GFVWKQLSGE	EVSWSKDFPA
650	660	670	680	690	700	710	720
VDSVLVKLLE	VMEGMDKETF	EFKFGKELTF	TTVLSDQQVV	ELIPGGAGIV	VGYGDRSRFI	QLVQKARLEE	SKEQVAAMQA
730	740	750	760	770	780	790	800
GLLKVVPQAV	LDLLTWQELE	KKVCGDPEVT	VDALRKLTRF	EDFEPSDSRV	QYFWEALNNF	TNEDRSRFLR	FVTGRSRLPA
810	820	830	840	850	860	870	
RIYIYPDKLG	YETTDALPES	STCSSTLFLP	HYASAKVCEE	KLRYAAYNCV	AIDTDMSPWE	E	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2262	1	682.8045	-92.58	2	58.2	10.6	0	75-90	R.VGAAGPAPGTGSGPLR.A	

Detailed Protein Report

Protein 1261: WAP four-disulfide core domain protein 8 precursor [Homo sapiens]

Accession:	gi|153946387	**Score:**	10.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	27.8
Database Date:	2015-11-30	**pI:**	10.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	10.0
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530418513	refseq_human (refseq_human_20140103.fasta)	PREDICTED: WAP four-disulfide core domain protein 8 isoform X1 [Homo sapiens]
gi|153946389	refseq_human (refseq_human_20140103.fasta)	WAP four-disulfide core domain protein 8 precursor [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MWTVRTEGGH FPLHSPTFSW RNVAFLLLLS LALEWTSAML TKKIKHKPGL CPKERLTCTT ELPDSCNTDF DCKEYQKCCF
        90        100        110        120        130        140        150        160
FACQKKCMDP FQEPCMLPVR HGNCNHEAQR WHFDFKNYRC TPFKYRGCEG NANNFLNEDA CRTACMLIVK DGQCPLFPFT
       170        180        190        200        210        220        230        240
ERKECPPSCH SDIDCPQTDK CCESRCGFVC ARAWTVKKGF CPRKPLLCTK IDKPKCLQDE ECPLVEKCCS HCGLKCMDPR
       250
R
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
288	1	881.8216	102.87	3	33.3	10.6	1	127-150	R.GCEGNANNFLNEDACRTACMLIVK.D	Carbamidomethyl: 15

Detailed Protein Report

Protein 1262: ubiquitin-like-conjugating enzyme ATG3 isoform 2 [Homo sapiens]

Accession: gi|523704487

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Score: 10.6

MW [kDa]: 35.4

pI: 4.6

Sequence Coverage [%]: 5.1

No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MQNVINTVKG	KALEVAEYLT	PVLKESKFKE	TGVITPEEFV	AAGDHLVHHC	PTWQWATGEE	LKVKAYLPTG	KQFLVTKNVP
90	100	110	120	130	140	150	160
CYKRCKQMEY	SDELEAIIEE	DDGDGGWVDT	YHNTGITGIT	EAVKEITLEN	KDNIRLQDCS	ALCEEEEDED	EGEAADMEEY
170	180	190	200	210	220	230	240
EESGLLETDE	ATLDTRKIVE	ACKAKTDAGG	EDAILQTRTY	DLYITYDKYY	QTPRLWLFGY	DEQRQPLTVE	HMYEDISQDH
250	260	270	280	290	300	310	320
VKKTVTIENH	PHLPPPPMCS	VHPCRHAEVM	KKIIETVAEG	GGELGVHMYP	SLYVRLVAKW	LLTIFFLRNL	V

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2808	1	973.5062	-99.59	2	65.5	10.6	2	296-311	R.LVAKWLLTIFFLRNLV.-	

Detailed Protein Report

Protein 1263: PREDICTED: UPF0600 protein C5orf51 isoform X2 [Homo sapiens]

Accession: gi|578809912
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 10.6
MW [kDa]: 25.7
pI: 5.5
Sequence Coverage [%]: 11.3
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MTYFEENKLV	DEDFPEDSSS	QKVKELISFL	SEPEILVKEN	NMHPKHCNLL	GDELLECLSW	RRGALLYMYC	HSLTKRREWL
90	100	110	120	130	140	150	160
LRKSSLLKKY	LLDGISYLLQ	MLNYRCPIQL	NEGVSFQDLD	TAKLLSAGIF	SDIHLLAMMY	SGEMCYWGSK	YCADQQPENH
170	180	190	200	210	220	230	
EVDTSVSGAG	CTTYKEPLDF	REVGEKILKK	YVSVCEGPLK	EQEWNTTNAK	QILNFFHHRC	N	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1594	1	920.8079	93.38	3	49.8	10.6	0	151-175	K.YCADQQPENHEVDTSVSGAGCTTYK.E	Carbamidomethyl: 2

Detailed Protein Report

Protein 1264: mitochondrial ribonuclease P protein 1 precursor [Homo sapiens]

Accession:	gi|117647226	**Score:**	10.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	47.3
Database Date:	2015-11-30	**pI:**	10.0
		Sequence Coverage [%]:	2.2
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 1.11 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MAAFLKMSVS	VNFFRPFTRF	LVPFTLHRKR	NNLTILQRYM	SSKIPAVTYP	KNESTPPSEE	LELDKWKTTM	KSSVQEECVS
90	100	110	120	130	140	150	160
TISSSKDEDP	LAATREFIEM	WRLLGREVPE	HITEEELKTL	MECVSNTAKK	KYLKYLYTKE	KVKKARQIKK	EMKAAAREEA
170	180	190	200	210	220	230	240
KNIKLLETTE	EDKQKNFLFL	RLWDRNMDIA	MGWKGAQAMQ	FGQPLVFDMA	YENYMKRKEL	QNTVSQLLES	EGWNRRNVDP
250	260	270	280	290	300	310	320
FHIYFCNLKI	DGALHRELVK	RYQEKWDKLL	LTSTEKSHVD	LFPKDSIIYL	TADSPNVMTT	FRHDKVYVIG	SFVDKSMQPG
330	340	350	360	370	380	390	400
TSLAKAKRLN	LATECLPLDK	YLQWEIGNKN	LTLDQMIRIL	LCLKNNGNWQ	EALQFVPKRK	HTGFLEISQH	SQEFINRLKK
410							
AKT							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
1651	1	494.2802	79.88	2	50.4	10.6	0	87-95	K.DEDPLAATR.E		MD:MU	1.11

Detailed Protein Report

Protein 1265: PREDICTED: centromere protein R isoform X2 [Homo sapiens]

Accession:	gi|578798787	**Score:**	10.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	32.6
Database Date:	2015-11-30	**pI:**	10.0
		Sequence Coverage [%]:	5.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MQSPSPNDPA	RNLGSADPER	TETAVLLLYR	GGGMARVVRE	GALLHQQEIG	AVLGLELPAR	SFARAHPDPS	SRGGCFRPAA
90	100	110	120	130	140	150	160
VGLTQRPARA	FHALAFPLAD	FLFSEVAGFV	LFSGSGAFPN	LRMPVKRSLK	LDGLLEENSF	DPSKITRKKS	VITYSPTTGT
170	180	190	200	210	220	230	240
CQMSLFASPT	SSEEQKHRNG	LSNEKRKKLN	HPSLTESKES	TTKDNDEFMM	LLSKVEKLSE	EIMEIMQNLS	SIQALEGSRE
250	260	270	280	290	300		
LENLIGISCA	SHFLKREMQK	TKELMTKVNK	QKLFEKSTGL	PHKDTSILKA	LRFEV		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2235	1	869.0977	107.21	2	58.2	10.5	2	277-292	K.STGLPHKDTSILKALR.F	

Detailed Protein Report

Protein 1266: uncharacterized protein C14orf105 isoform 5 [Homo sapiens]

Accession:	gi|545687738	**Score:**	10.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	17.0
Database Date:	2015-11-30	**pI:**	10.5
		Sequence Coverage [%]:	5.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MYFDIPLEHR	ETSIIKRHPP	QRLQKLEPID	LPRVITSGRL	LSQREARTMH	KAKVLEKKMQ	TPMYTSENRQ	YLHKMQVLEM
90	**100**	**110**	**120**	**130**	**140**	**150**	
IRKRQEAQME	LKKSLHGEAR	INKQSPRDHK	AKKTLQSTPR	NDDHDLLTML	PDEILNRGPG	QTHS	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
128	1	930.2523	-305.66	1	31.3	10.5	1	113-120	K.KTLQSTPR.N	

Detailed Protein Report

Protein 1267: liprin-beta-2 isoform 3 [Homo sapiens]

Accession:	gi|375151575	**Score:**	10.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	83.1
Database Date:	2015-11-30	**pI:**	9.3
		Sequence Coverage [%]:	2.0
		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
2318	1	938.4698	-37.91	2	59.3	10.5	2	154-168	K.DRRIEELTGLLNQYR.K	

Detailed Protein Report

Protein 1268: quinone oxidoreductase PIG3 isoform 2 [Homo sapiens]

Accession:	gi|332164791	**Score:**	10.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	25.4
Database Date:	2015-11-30	**pI:**	6.0
		Sequence Coverage [%]:	5.6
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578803300	refseq_human (refseq_human_20140103.fasta)	PREDICTED: quinone oxidoreductase PIG3 isoform X2 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MLAVHFDKPG GPENLYVKEV AKPSPGEGEV LLKVAASALN RADLMQRQGQ YDPPPGASNI LGLEASGHVA ELGPGCQGHW
        90        100        110        120        130        140        150        160
KIGDTAMALL PGGGQAQYVT VPEGLLMPIP EGLTLTQAAA IPEAWLTAFQ LLHLVGNVQA GDYVLIHAGL SGVGTAAIQL
       170        180        190        200        210        220        230        240
TRMAGAIPLV TAGSQKKLQM AEKLGAAAGF NYKKEDFSEA TLKFTKVQAN AGECFHGANS ASLLHGGPPT SAAGSGQNLP
       250
SDRNPGGP
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1177	1	758.4960	117.77	2	44.4	10.5	1	34-47	K.VAASALNRADLMQR.Q	

Detailed Protein Report

Protein 1269: huntingtin [Homo sapiens]

Accession:	gi|90903231	**Score:**	10.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	347.6
Database Date:	2015-11-30	**pI:**	5.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	0.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MATLEKLMKA	FESLKSFQQQ	QQQQQQQQQQ	QQQQQQQQQQ	PPPPPPPPPP	PQLPQPPPQA	QPLLPQPQPP	PPPPPPPPGP
90	100	110	120	130	140	150	160
AVAEEPLHRP	KKELSATKKD	RVNHCLTICE	NIVAQSVRNS	PEFQKLLGIA	MELFLLCSDD	AESDVRMVAD	ECLNKVIKAL
170	180	190	200	210	220	230	240
MDSNLPRLQL	ELYKEIKKNG	APRSLRAALW	RFAELAHLVR	PQKCRPYLVN	LLPCLTRTSK	RPEESVQETL	AAAVPKIMAS
250	260	270	280	290	300	310	320
FGNFANDNEI	KVLLKAFIAN	LKSSSPTIRR	TAAGSAVSIC	QHSRRTQYFY	SWLLNVLLGL	LVPVEDEHST	LLILGVLLTL
330	340	350	360	370	380	390	400
RYLVPLLQQQ	VKDTSLKGSF	GVTRKEMEVS	PSAEQLVQVY	ELTLHHTQHQ	DHNVVTGALE	LLQQLFRTPP	PELLQTLTAV
410	420	430	440	450	460	470	480
GGIGQLTAAK	EESGGRSRSG	SIVELIAGGG	SSCSPVLSRK	QKGKVLLGEE	EALEDDSESR	SDVSSSALTA	SVKDEISGEL
490	500	510	520	530	540	550	560
AASSGVSTPG	SAGHDIITEQ	PRSQHTLQAD	SVDLASCDLT	SSATDGDEED	ILSHSSSQVS	AVPSDPAMDL	NDGTQASSPI
570	580	590	600	610	620	630	640
SDSSQTTTEG	PDSAVTPSDS	SEIVLDGTDN	QYLGLQIGQP	QDEDEEATGI	LPDEASEAFR	NSSMALQQAH	LLKNMSHCRQ
650	660	670	680	690	700	710	720
PSDSSVDKFV	LRDEATEPGD	QENKPCRIKG	DIGQSTDDDS	APLVHCVRLL	SASFLLTGGK	NVLVPDRDVR	VSVKALALSC
730	740	750	760	770	780	790	800
VGAAVALHPE	SFFSKLYKVP	LDTTEYPEEQ	YVSDILNYID	HGDPQVRGAT	AILCGTLICS	ILSRSRFHVG	DWMGTIRTLT
810	820	830	840	850	860	870	880
GNTFSLADCI	PLLRKTLKDE	SSVTCKLACT	AVRNCVMSLC	SSSYSELGLQ	LIIDVLTLRN	SSYWLVRTEL	LETLAEIDFR
890	900	910	920	930	940	950	960
LVSFLEAKAE	NLHRGAHHYT	GLLKLQERVL	NNVVIHLLGD	EDPRVRHVAA	ASLIRLVPKL	FYKCDQGQAD	PVVAVARDQS
970	980	990	1000	1010	1020	1030	1040
SVYLKLLMHE	TQPPSHFSVS	TITRIYRGYN	LLPSITDVTM	ENNLSRVIAA	VSHELITSTT	RALTFGCCEA	LCLLSTAFPV
1050	1060	1070	1080	1090	1100	1110	1120
CIWSLGWHCG	VPPLSASDES	RKSCTVGMAT	MILTLLSSAW	FPLDLSAHQD	ALILAGNLLA	ASAPKSLRSS	WASEEEANPA
1130	1140	1150	1160	1170	1180	1190	1200
ATKQEEVWPA	LGDRALVPMV	EQLFSHLLKV	INICAHVLDD	VAPGPAIKAA	LPSLTNPPSL	SPIRRKGKEK	EPGEQASVPL
1210	1220	1230	1240	1250	1260	1270	1280
SPKKGSEASA	ASRQSDTSGP	VTTSKSSSLG	SFYHLPSYLK	LHDVLKATHA	NYKVTLDLQN	STEKFGGFLR	SALDVLSQIL
1290	1300	1310	1320	1330	1340	1350	1360
ELATLQDIGK	CVEEILGYLK	SCFSREPMMA	TVCVQQLLKT	LFGTNLASQF	DGLSSNPSKS	QGRAQRLGSS	SVRPGLYHYC
1370	1380	1390	1400	1410	1420	1430	1440
FMAPYTHFTQ	ALADASLRNM	VQAEQENDTS	GWFDVLQKVS	TQLKTNLTSV	TKNRADKNAI	HNHIRLFEPL	VIKALKQYTT
1450	1460	1470	1480	1490	1500	1510	1520
TTCVQLQKQV	LDLLAQLVQL	RVNYCLLDSD	QVFIGFVLKQ	FEYIEVGQFR	ESEAIIPNIF	FFLVLLSYER	YHSKQIIGIP
1530	1540	1550	1560	1570	1580	1590	1600
KIIQLCDGIM	ASGRKAVTHA	IPALQPIVHD	LFVLRGTNKA	DAGKELETQK	EVVVSMLLRL	IQYHQVLEMF	ILVLQQCHKE
1610	1620	1630	1640	1650	1660	1670	1680
NEDKWKRLSR	QIADIILPML	AKQQMHIDSH	EALGVLNTLF	EILAPSSLRP	VDMLLRSMFV	TPNTMASVST	VQLWISGILA
1690	1700	1710	1720	1730	1740	1750	1760
ILRVLISQST	EDIVLSRIQE	LSFSPYLISC	TVINRLRDGD	STSTLEEHSE	GKQIKNLPEE	TFSRFLLQLV	GILLEDIVTK
1770	1780	1790	1800	1810	1820	1830	1840
QLKVEMSEQQ	HTFYCQELGT	LLMCLIHIFK	SGMFRRITAA	ATRLFRSDGC	GGSFYTLDSL	NLRARSMITT	HPALVLLWCQ
1850	1860	1870	1880	1890	1900	1910	1920
ILLLVNHTDY	RWWAEVQQTP	KRHSLSSTKL	LSPQMSGEEE	DSDLAAKLGM	CNREIVRRGA	LILFCDYVCQ	NLHDSEHLTW
1930	1940	1950	1960	1970	1980	1990	2000
LIVNHIQDLI	SLSHEPPVQD	FISAVHRNSA	ASGLFIQAIQ	SRCENLSTPT	MLKKTLQCLE	GIHLSQSGAV	LTLYVDRLLC
2010	2020	2030	2040	2050	2060	2070	2080
TPFRVLARMV	DILACRRVEM	LLAANLQSSM	AQLPMEELNR	IQEYLQSSGL	AQRHQRLYSL	LDRFRLSTMQ	DSLSPSPPVS
2090	2100	2110	2120	2130	2140	2150	2160
SHPLDGDGHV	SLETVSPDKD	WYVHLVKSQC	WTRSDSALLE	GAELVNRIPA	EDMNAFMMNS	EFNLSLLAPC	LSLGMSEISG
2170	2180	2190	2200	2210	2220	2230	2240

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2586	1	836.2590	-135.02	1	62.8	10.5	0	2970-2976	K.GFPCEAR.V	Carbamidomethyl: 4

Detailed Protein Report

Protein 1270: voltage-dependent L-type calcium channel subunit alpha-1D isoform a [Homo sapiens]

Accession:	gi|4502527	**Score:**	10.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	247.4
Database Date:	2015-11-30	**pI:**	6.6
		Sequence Coverage [%]:	0.6
		No. of unique Peptides:	1

Detailed Protein Report

```
        10         20         30         40         50         60         70         80
MMMMMMMKKM QHQRQQQADH ANEANYARGT RLPLSGEGPT SQPNSSKQTV LSWQAAIDAA RQAKAAQTMS TSAPPPVGSL
        90        100        110        120        130        140        150        160
SQRKRQQYAK SKKQGNSSNS RPARALFCLS LNNPIRRACI SIVEWKPFDI FILLAIFANC VALAIYIPFP EDDSNSTNHN
       170        180        190        200        210        220        230        240
LEKVEYAFLI IFTVETFLKI IAYGLLLHPN AYVRNGWNLL DFVIVIVGLF SVILEQLTKE TEGGNHSSGK SGGFDVKALR
       250        260        270        280        290        300        310        320
AFRVLRPLRL VSGVPSLQVV LNSIIKAMVP LLHIALLVLF VIIIYAIIGL ELFIGKMHKT CFFADSDIVA EEDPAPCAFS
       330        340        350        360        370        380        390        400
GNGRQCTANG TECRSGWVGP NGGITNFDNF AFAMLTVFQC ITMEGWTDVL YWVNDAIGWE WPWVYFVSLI ILGSFFVLNL
       410        420        430        440        450        460        470        480
VLGVLSGEFS KEREKAKARG DFQKLREKQQ LEEDLKGYLD WITQAEDIDP ENEEEGGEEG KRNTSMPTSE TESVNTENVS
       490        500        510        520        530        540        550        560
GEGENRGCCG SLWCWWRRRG AAKAGPSGCR RWGQAISKSK LSRRWRRWNR FNRRRCRAAV KSVTFYWLVI VLVFLNTLTI
       570        580        590        600        610        620        630        640
SSEHYNQPDW LTQIQDIANK VLLALFTCEM LVKMYSLGLQ AYFVSLFNRF DCFVVCGGIT ETILVELEIM SPLGISVFRC
       650        660        670        680        690        700        710        720
VRLLRIFKVT RHWTSLSNLV ASLLNSMKSI ASLLLLLFLF IIIFSLLGMQ LFGGKFNFDE TQTKRSTFDN FPQALLTVFQ
       730        740        750        760        770        780        790        800
ILTGEDWNAV MYDGIMAYGG PSSSGMIVCI YFIILFICGN YILLNVFLAI AVDNLADAES LNTAQKEEAE EKERKKIARK
       810        820        830        840        850        860        870        880
ESLENKKNNK PEVNQIANSD NKVTIDDYRE EDEDKDPYPP CDVPVGEEEE EEEEDEPEVP AGPRPRRISE LNMKEKIAPI
       890        900        910        920        930        940        950        960
PEGSAFFILS KTNPIRVGCH KLINHHIFTN LILVFIMLSS AALAAEDPIR SHSFRNTILG YFDYAFTAIF TVEILLKMTT
       970        980        990       1000       1010       1020       1030       1040
FGAFLHKGAF CRNYFNLLDM LVVGVSLVSF GIQSSAISVV KILRVLRVLR PLRAINRAKG LKHVVQCVFV AIRTIGNIMI
      1050       1060       1070       1080       1090       1100       1110       1120
VTTLLQFMFA CIGVQLFKGK FYRCTDEAKS NPEECRGLFI LYKDGDVDSP VVRERIWQNS DFNFDNVLSA MMALFTVSTF
      1130       1140       1150       1160       1170       1180       1190       1200
EGWPALLYKA IDSNGENIGP IYNHRVEISI FFIIYIIIVA FFMMNIFVGF VIVTFQEQGE KEYKNCELDK NQRQCVEYAL
      1210       1220       1230       1240       1250       1260       1270       1280
KARPLRRYIP KNPYQYKFWY VVNSSPFEYM MFVLIMLNTL CLAMQHYEQS KMFNDAMDIL NMVFTGVFTV EMVLKVIAFK
      1290       1300       1310       1320       1330       1340       1350       1360
PKGYFSDAWN TFDSLIVIGS IIDVALSEAD PTESENVPVP TATPGNSEES NRISITFFRL FRVMRLVKLL SRGEGIRTLL
      1370       1380       1390       1400       1410       1420       1430       1440
WTFIKSFQAL PYVALLIAML FFIYAVIGMQ MFGKVAMRDN NQINRNNNFQ TFPQAVLLLF RCATGEAWQE IMLACLPGKL
      1450       1460       1470       1480       1490       1500       1510       1520
CDPESDYNPG EEYTCGSNFA IVYFISFYML CAFLIINLFV AVIMDNFDYL TRDWSILGPH HLDEFKRIWS EYDPEAKGRI
      1530       1540       1550       1560       1570       1580       1590       1600
KHLDVVTLLR RIQPPLGFGK LCPHRVACKR LVAMNMPLNS DGTVMFNATL FALVRTALKI KTEGNLEQAN EELRAVIKKI
      1610       1620       1630       1640       1650       1660       1670       1680
WKKTSMKLLD QVVPPAGDDE VTVGKFYATF LIQDYFRKFK KRKEQGLVGK YPAKNTTIAL QAGLRTLHDI GPEIRRAISC
      1690       1700       1710       1720       1730       1740       1750       1760
DLQDDEPEET KREEEDDVFK RNGALLGNHV NHVNSDRRDS LQQTNTTHRP LHVQRPSIPP ASDTEKPLFP PAGNSVCHNH
      1770       1780       1790       1800       1810       1820       1830       1840
HNHNSIGKQV PTSTNANLNN ANMSKAAHGK RPSIGNLEHV SENGHHSSHK HDREPQRRSS VKRTRYYETY IRSDSGDEQL
      1850       1860       1870       1880       1890       1900       1910       1920
PTICREDPEI HGYFRDPHCL GEQEYFSSEE CYEDDSSPTW SRQNYGYYSR YPGRNIDSER PRGYHHPQGF LEDDDSPVCY
      1930       1940       1950       1960       1970       1980       1990       2000
DSRRSPRRRL LPPTPASHRR SSFNFECLRR QSSQEEVPSS PIFPHRTALP LHLMQQQIMA VAGLDSSKAQ KYSPSHSTRS
      2010       2020       2030       2040       2050       2060       2070       2080
WATPPATPPY RDWTPCYTPL IQVEQSEALD QVNGSLPSLH RSSWYTDEPD ISYRTFTPAS LTVPSSFRNK NSDKQRSADS
      2090       2100       2110       2120       2130       2140       2150       2160
LVEAVLISEG LGRYARDPKF VSATKHEIAD ACDLTIDEME SAASTLLNGN VRPRANGDVG PLSHRQDYEL QDFGPGYSDE
      2170       2180       2190
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1214	1	565.6553	-248.62	2	44.8	10.5	2	500-511	R.GAAKAGPSGCRR.W	

Detailed Protein Report

Protein 1271: succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial precursor [Homo sapiens]

Accession:	gi|11321583	**Score:**	10.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	50.3
Database Date:	2015-11-30	**pI:**	7.7
		Sequence Coverage [%]:	2.8
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 2.03 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MAASMFYGRL	VAVATLRNHR	PRTAQRAAAQ	VLGSSGLFNN	HGLQVQQQQQ	RNLSLHEYMS	MELLQEAGVS	VPKGYVAKSP
90	100	110	120	130	140	150	160
DEAYAIAKKL	GSKDVVIKAQ	VLAGGRGKGT	FESGLKGGVK	IVFSPEEAKA	VSSQMIGKKL	FTKQTGEKGR	ICNQVLVCER
170	180	190	200	210	220	230	240
KYPRREYYFA	ITMERSFQGP	VLIGSSHGGV	NIEDVAAESP	EAIIKEPIDI	EEGIKKEQAL	QLAQKMGFPP	NIVESAAENM
250	260	270	280	290	300	310	320
VKLYSLFLKY	DATMIEINPM	VEDSDGAVLC	MDAKINFDSN	SAYRQKKIFD	LQDWTQEDER	DKDAAKANLN	YIGLDGNIGC
330	340	350	360	370	380	390	400
LVNGAGLAMA	TMDIIKLHGG	TPANFLDVGG	GATVHQVTEA	FKLITSDKKV	LAILVNIFGG	IMRCDVIAQG	IVMAVKDLEI
410	420	430	440	450	460	470	
KIPVVVRLQG	TRVDDAKALI	ADSGLKILAC	DDLDEAARMV	VKLSEIVTLA	KQAHVDVKFQ	LPI	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1749	1	785.8811	-26.88	2	51.7	10.5	2	275-287	K.INFDSNSAYRQKK.I		MD:MU 2.03

Detailed Protein Report

Protein 1272: ral GTPase-activating protein subunit beta isoform 2 [Homo sapiens]

Accession:	gi|544711150	**Score:**	10.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	166.4
Database Date:	2015-11-30	**pI:**	6.3
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MYSEWRSLHL	VIQNDQGHTS	VLHSYPESVG	REVANAVVRP	LGQVLGTPSV	AGSENLLKTD	KEVKWTMEVI	CYGLTLPLDG
90	100	110	120	130	140	150	160
ETVKYCVDVY	TDWIMALVLP	KDSIPLPVIK	EPNQYVQTIL	KHLQNLFVPR	QEQGSSQIRL	CLQVLRAIQK	LARESSLMAR
170	180	190	200	210	220	230	240
ETWEVLLLFL	LQINDILLAP	PTVQGGIAEN	LAEKLIGVLF	EVWLLACTRC	FPTPPYWKTA	KEMVANWRHH	PAVVEQWSKV
250	260	270	280	290	300	310	320
ICALTSRLLR	FTYGPSFPAF	KVPDEDASLI	PPEMDNECVA	QTWFRFLHML	SNPVDLSNPA	IISSTPKFQE	QFLNVSGMPQ
330	340	350	360	370	380	390	400
ELNQYPCLKH	LPQIFFRAMR	GISCLVDAFL	GISRPRSDSA	PPTPVNRLSM	PQSAAVSTTP	PHNRRHRAVT	VNKATMKTST
410	420	430	440	450	460	470	480
VSTAHASKVQ	HQTSSTSPLS	SPNQTSSEPR	PLPAPRRPKV	NSILNLFGSW	LFDAAFVHCK	LHNGINRDSS	MTAITTQASM
490	500	510	520	530	540	550	560
EFRRKGSQMS	TDTMVSNPMF	DASEFPDNYE	AGRAEACGTL	CRIFCSKKTG	EEILPAYLSR	FYMLLIQGLQ	INDYVCHPVL
570	580	590	600	610	620	630	640
ASVILNSPPL	FCCDLKGIDV	VVPYFISALE	TILPDRELSK	FKSYVNPTEL	RRSSINILLS	LLPLPHHFGT	VKSEVVLEGK
650	660	670	680	690	700	710	720
FSNDDSSSYD	KPITFLSLKL	RLVNILIGAL	QTETDPNNTQ	MILGAMLNIV	QDSALLEAIG	CQMEMGGGEN	NLKSHSRTNS
730	740	750	760	770	780	790	800
GISSASGGST	EPTTPDSERP	AQALLRDYDS	AAGLLIRSIH	LVTQRLNSQW	RQDMSISLAA	LELLSGLAKV	KVMVDSGDRK
810	820	830	840	850	860	870	880
RAISSVCTYI	VYQCSRPAPL	HSRDLHSMIV	AAFQCLCVWL	TEHPDMLDEK	DCLKEVLEIV	ELGISGSKSK	NNEQEVKYKG
890	900	910	920	930	940	950	960
DKEPNPASMR	VKDAAEATLT	CIMQLLGAFP	SPSGPASPCS	LVNETTLIKY	SRLPTINKHS	FRYFVLDNSV	ILAMLEQPLG
970	980	990	1000	1010	1020	1030	1040
NEQNDFFPSV	TVLVRGMSGR	LAWAQQLCLL	PRGAKANQKL	FVPEPRPVPK	NDVGFKYSVK	HRPFPEEVDK	IPFVKADLSI
1050	1060	1070	1080	1090	1100	1110	1120
PDLHEIVTEE	LEERHEKLRS	GMAQQIAYEI	HLEQQSEEEL	QKRSFPDPVT	DCKPPPPAQE	FQTARLFLSH	FGFLSLEALK
1130	1140	1150	1160	1170	1180	1190	1200
EPANSRLPPH	LIALDSTIPG	FFDDIGYLDL	LPCRPFDTVF	IFYMKPGQKT	NQEILKNVES	SRTVQPHFLE	FLLSLGWSVD
1210	1220	1230	1240	1250	1260	1270	1280
VGRHPGWTGH	VSTSWSINCC	DDGEGSQQEE	VISSEDIGAS	IFNGQKKVLY	YADALTEIAF	VVPSPVESLT	DSLESNISDQ
1290	1300	1310	1320	1330	1340	1350	1360
DSDSNMDLMP	GILKQPSLTL	ELFPNHTDNL	NSSQRLSPSS	RMRKLPQGRP	VPPLGPETRV	SVVWVERYDD	IENFPLSELM
1370	1380	1390	1400	1410	1420	1430	1440
TEISTGVETT	ANSSTSLRST	TLEKEVPVIF	IHPLNTGLFR	IKIQGATGKF	NMVIPLVDGM	IVSRRALGFL	VRQTVINICR
1450	1460	1470	1480	1490	1500		
RKRLESDSYS	PPHVRRKQKI	TDIVNKYRNK	QLEPEFYTSL	FQEVGLKNCS	S		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2029	1	682.2615	-118.35	3	55.3	10.5	0	85-101	K.YCVDVYTDWIMALVLPK.D	Oxidation: 11

Detailed Protein Report

Protein 1273: phosphatidylinositol 3-kinase catalytic subunit type 3 [Homo sapiens]

Accession:	gi|34761064	**Score:**	10.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	101.5
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
MGEAEKFHYI	YSCDLDINVQ	LKIGSLEGKR	EQKSYKAVLE	DPMLKFSGLY	QETCSDLYVT	CQVFAEGKPL	ALPVRTSYKA
90	100	110	120	130	140	150	160
FSTRWNWNEW	LKLPVKYPDL	PRNAQVALTI	WDVYGPGKAV	PVGGTTVSLF	GKYGMFRQGM	HDLKVWPNVE	ADGSEPTKTP
170	180	190	200	210	220	230	240
GRTSSTLSED	QMSRLAKLTK	AHRQGHMVKV	DWLDRLTFRE	IEMINESEKR	SSNFMYLMVE	FRCVKCDDKE	YGIVYYEKDG
250	260	270	280	290	300	310	320
DESSPILTSF	ELVKVPDPQM	SMENLVESKH	HKLARSLRSG	PSDHDLKPNA	ATRDQLNIIV	SYPPTKQLTY	EEQDLVWKFR
330	340	350	360	370	380	390	400
YYLTNQEKAL	TKFLKCVNWD	LPQEAKQALE	LLGKWKPMDV	EDSLELLSSH	YTNPTVRRYA	VARLRQADDE	DLLMYLLQLV
410	420	430	440	450	460	470	480
QALKYENFDD	IKNGLEPTKK	DSQSSVSENV	SNSGINSAEI	DSSQIITSPL	PSVSSPPPAS	KTKEVPDGEN	LEQDLCTFLI
490	500	510	520	530	540	550	560
SRACKNSTLA	NYLYWYVIVE	CEDQDTQQRD	PKTHEMYLNV	MRRFSQALLK	GDKSVRVMRS	LLAAQQTFVD	RLVHLMKAVQ
570	580	590	600	610	620	630	640
RESGNRKKKN	ERLQALLGDN	EKMNLSDVEL	IPLPLEPQVK	IRGIIPETAT	LFKSALMPAQ	LFFKTEDGGK	YPVIFKHGDD
650	660	670	680	690	700	710	720
LRQDQLILQI	ISLMDKLLRK	ENLDLKLTPY	KVLATSTKHG	FMQFIQSVPV	AEVLDTEGSI	QNFFRKYAPS	ENGPNGISAE
730	740	750	760	770	780	790	800
VMDTYVKSCA	GYCVITYILG	VGDRHLDNLL	LTKTGKLFHI	DFGYILGRDP	KPLPPPMKLN	KEMVEGMGGT	QSEQYQEFRK
810	820	830	840	850	860	870	880
QCYTAFLHLR	RYSNLILNLF	SLMVDANIPD	IALEPDKTVK	KVQDKFRLDL	SDEEAVHYMQ	SLIDESVHAL	FAAVVEQIHK
890							
FAQYWRK							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2742	2	703.3679	-39.75	2	65.6	10.5	2	178-189	K.LTKAHRQGHMVK.V	

Detailed Protein Report

Protein 1274: PREDICTED: kallikrein-2 isoform X2 [Homo sapiens]

Accession:	gi|578834440	**Score:**	10.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	29.6
Database Date:	2015-11-30	**pI:**	6.5
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	9.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGTLWGCPGA	PPVGAHSCPL	PKEVSRTLGS	GEGMAVSHRN	NSGMLPPGSL	LRNSQVWLGR	HNLFEPEDTG	QRVPVSHSFP
90	100	110	120	130	140	150	160
HPLYNMSLLK	HQSLRPDEDS	SHDLMLLRLS	EPAKITDVVK	VLGLPTQEPA	LGTTCYASGW	GSIEPEEFLR	PRSLQCVSLH
170	180	190	200	210	220	230	240
LLSNDMCARA	YSEKVTEFML	CAGLWTGGKD	TCGVSHPYSQ	HLEGKVRSCG	WCWTEEGQGL	AQGDSGGPLV	CNGVLQGITS
250	260	270	280				
WGPEPCALPE	KPAVYTKVVH	YRKWIKDTIA	ANP				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1240	1	926.5097	65.71	3	45.2	10.5	1	1-26	-.MGTLWGCPGAPPVGAHSCPLPKEVSR.T	Carbamidomethyl: 7, 18; Oxidation: 1

Detailed Protein Report

Protein 1275: zinc finger protein 668 isoform a [Homo sapiens]

Accession:	gi|289547677	**Score:**	10.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	67.9
Database Date:	2015-11-30	**pI:**	10.5
		Sequence Coverage [%]:	4.0
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|289547684	refseq_human (refseq_human_20140103.fasta)	zinc finger protein 668 isoform a [Homo sapiens]
gi|289547680	refseq_human (refseq_human_20140103.fasta)	zinc finger protein 668 isoform a [Homo sapiens]

10	20	30	40	50	60	70	80
MEVEAAEARS	PAPGYKRSGR	RYKCLSCTKT	FPNAPRAARH	AATHGPADCS	EEVAEVKPKP	ETEAKAEEAS	GEKVSGSAAK
90	100	110	120	130	140	150	160
PRPYACPLCP	KAYKTAPELR	SHGRSHTGEK	PFPCPECGRR	FMQPVCLRVH	LASHAGELPF	RCAHCPKAYG	ALSKLKIHQR
170	180	190	200	210	220	230	240
GHTGERPYAC	ADCGKSFADP	SVFRKHRRTH	AGLRPYSCER	CGKAYAELKD	LRNHERSHTG	ERPFLCSECG	KSFSRSSSLT
250	260	270	280	290	300	310	320
CHQRIHAAQK	PYRCPACGKG	FTQLSSYQSH	ERTHSGEKPF	LCPRCGRMFS	DPSSFRRHQR	AHEGVKPYHC	EKCGKDFRQP
330	340	350	360	370	380	390	400
ADLAMHRRVH	TGDRPFKCLQ	CDKTFVASWD	LKRHALVHSG	QRPFRCEECG	RAFAERASLT	KHSRVHSGER	PFHCNACGKS
410	420	430	440	450	460	470	480
FVVSSSLRKH	ERTHRSSEAA	GVPPAQELVV	GLALPVGVAG	ESSAAPAAGA	GLGDPPAGLL	GLPPESGGVM	ATQWQVVGMT
490	500	510	520	530	540	550	560
VEHVECQDAG	VREAPGPLEG	AGEAGGEEAD	EKPPQFVCRE	CKETFSTMTL	LRRHERSHPE	LRPFPCTQCG	KSFSDRAGLR
570	580	590	600	610	620		
KHSRTHSSVR	PYTCPHCPKA	FLSASDLRKH	ERTHPVPMGT	PTPLEPLVAL	LGMPEEGPA		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2114	1	900.3727	-52.43	3	56.3	10.5	2	161-185	R.GHTGERPYACADCGKSFADPSVFRK.H	

Detailed Protein Report

Protein 1276: ubiquitin-conjugating enzyme E2 variant 1 isoform h [Homo sapiens]

Accession:	gi|543583756	**Score:**	10.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	10.4
Database Date:	2015-11-30	**pI:**	10.0
		Sequence Coverage [%]:	7.7
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|543583762	refseq_human (refseq_human_20140103.fasta)	ubiquitin-conjugating enzyme E2 variant 1 isoform h [Homo sapiens]
gi|543583760	refseq_human (refseq_human_20140103.fasta)	ubiquitin-conjugating enzyme E2 variant 1 isoform h [Homo sapiens]

```
         10         20         30         40         50         60         70         80
MTIYENRIYS LKIECGPKYP EAPPFVRFVT KINMNGVNSS NGVVDPRAIS VLAKWQNSYS IKVVLQELRR LMMSKENMKL
         90        100
PQPPEGQCYS N
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1611	1	926.6153	189.17	1	50.0	10.5	0	1-7	-.MTIYENR.I	

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Detailed Protein Report

Protein 1277: zinc finger protein 486 [Homo sapiens]

Accession: gi|150170665
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 10.5
MW [kDa]: 53.6
pI: 10.1
Sequence Coverage [%]: 2.8
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MPGPLRSLEM	ESLQFRDVAV	EFSLEEWHCL	DTAQQNLYRD	VMLENYRHLV	FLGIIVSKPD	LITCLEQGIK	PLTMKRHEMI
90	100	110	120	130	140	150	160
AKPPVVCSHF	AQDLWPEQSI	KDSYQKVILR	KFEKCGHGNL	HFKKGCESVD	ECKLHKRGYN	GLNQCLTTTQ	SKIFQCGKYV
170	180	190	200	210	220	230	240
KVFHQFSNSK	RHKRRHTEKK	PLKYIEGDKA	FNQSSTHTTH	KKIDTGEKPY	KCEECGKAFN	RSSHLTTHKI	THTREKPYKC
250	260	270	280	290	300	310	320
EECGKVFKYF	SSFTTHKKIH	SGEKPYICEE	CGKAFMYPYT	LTTHKIIHTG	EQPYKCKECD	KAFNHPATLS	SHKKIHTGEK
330	340	350	360	370	380	390	400
PYTCDKCGKA	FISSSILSKH	EKIHTGEKPY	KCEECGKAFT	RSSHLTMHKI	IHTGEKPYKC	EECGKAFTWS	AGLHKHRRTH
410	420	430	440	450	460	470	
TGEKPYKCEE	CGKAYTTSSN	LTEHKTTHTG	EKPYKCKECG	KAFNWSSDLN	KHKRIHIGQK	PRT	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1341	1	699.4714	135.76	2	46.5	10.5	1	327-339	K.CGKAFISSSILSK.H	Carbamidomethyl: 1

Detailed Protein Report

Protein 1278: PREDICTED: long-chain fatty acid transport protein 1 isoform X1 [Homo sapiens]

Accession:	gi|578833253	**Score:**	10.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	73.9
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
MSVSVLAPAG	NKLLLPEKVL	LGLQDTRMRA	PGAGAASVVS	LALLWLLGLP	WTWSAAAALG	VYVGSGGWRF	LRIVCKTARR
90	100	110	120	130	140	150	160
DLFGLSVLIR	VRLELRRHQR	AGHTIPRIFQ	AVVQRQPERL	ALVDAGTGEC	WTFAQLDAYS	NAVANLFRQL	GFAPGDVVAI
170	180	190	200	210	220	230	240
FLEGRPEFVG	LWLGLAKAGM	EAALLNVNLR	REPLAFCLGT	SGAKALIFGG	EMVAAVAEVS	GHLGKSLIKF	CSGDLGPEGI
250	260	270	280	290	300	310	320
LPDTHLLDPL	LKEASTAPLA	QIPSKGMDDR	LFYIYTSGTT	GLPKAAIVVH	SRYYRMAAFG	HHAYRMQAAD	VLYDCLPLYH
330	340	350	360	370	380	390	400
SAGNIIGVGQ	CLIYGLTVVL	RKKFSASRFW	DDCIKYNCTV	VQYIGEICRY	LLKQPVREAE	RRHRVRLAVG	NGLRPAIWEE
410	420	430	440	450	460	470	480
FTERFGVRQI	GEFYGATECN	CSIANMDGKV	GSCGFNSRIL	PHVYPIRLVK	VNEDTMELLR	DAQGLCIPCQ	AGEPGLLVGQ
490	500	510	520	530	540	550	560
INQQDPLRRF	DGYVSESATS	KKIAHSVFSK	GDSAYLSGDV	LVMDELGYMY	FRDRSGDTFR	WRGENVSTTE	VEGVLSRLLG
570	580	590	600	610	620	630	640
QTDVAVYGVA	VPGVEGKAGM	AAVADPHSLL	DPNAIYQELQ	KVLAPYARPI	FLRLLPQVDT	TGTFKIQKTR	LQREGFDPRQ
650	660	670	680				
TSDRLFFLDL	KQGHYLPLNE	AVYTRICSGA	FAL				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
386	1	587.1707	-251.58	2	34.2	10.5	0	1-12	-.MSVSVLAPAGNK.L	

Detailed Protein Report

Protein 1279: E3 ubiquitin-protein ligase Praja-2 [Homo sapiens]

Accession:	gi|157412255	**Score:**	10.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	78.2
Database Date:	2015-11-30	**pI:**	4.1
		Sequence Coverage [%]:	2.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSQYTEKEPA	AMDQESGKAV	WPKPAGGYQT	ITGRRYGRRH	AYVSFKPCMT	RHERSLGRAG	DDYEVLELDD	VPKENSSGSS
90	100	110	120	130	140	150	160
PLDQVDSSLP	SEPIFEKSET	EIPTCGSALN	QTTESSQSFV	AVHHSEEGRD	TLGSSTNLHN	HSEGEYIPGA	CSASSVQNGI
170	180	190	200	210	220	230	240
ALVHTDSYDP	DGKHGEDNDH	LQLSAEVVEG	SRYQESLGNT	VFELENREAE	AYTGLSPPVP	SFNCEVRDEF	EELDSVPLVK
250	260	270	280	290	300	310	320
SSAGDTEFVH	QNSQEIQRSS	QDEMVSTKQQ	NNTSQERQTE	HSPEDAACGP	GHICSEQNTN	DREKNHGSSP	EQVVRPKVRK
330	340	350	360	370	380	390	400
LISSSQVDQE	TGFNRHEAKQ	RSVQRWREAL	EVEESGSDDL	LIKCEEYDGE	HDCMFLDPPY	SRVITQRETE	NNQMTSESGA
410	420	430	440	450	460	470	480
TAGRQEVDNT	FWNGCGDYYQ	LYDKDEDSSE	CSDGEWSASL	PHRFSGTEKD	QSSSDESWET	LPGKDENEPE	LQSDSSGPEE
490	500	510	520	530	540	550	560
ENQELSLQEG	EQTSLEEGEI	PWLQYNEVNE	SSSDEGNEPA	NEFAQPAFML	DGNNNLEDDS	SVSEDLDVDW	SLFDGFADGL
570	580	590	600	610	620	630	640
GVAEAISYVD	PQFLTYMALE	ERLAQAMETA	LAHLESLAVD	VEVANPPASK	ESIDGLPETL	VLEDHTAIGQ	EQCCPICCSE
650	660	670	680	690	700	710	
YIKDDIATEL	PCHHFFHKPC	VSIWLQKSGT	CPVCRRHFPP	AVIEASAAPS	SEPDPDAPPS	NDSIAEAP	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
151	1	716.1141	128.26	3	31.3	10.5	1	321-339	K.LISSSQVDQETGFNRHEAK.Q	

Detailed Protein Report

Protein 1280: PREDICTED: MAP7 domain-containing protein 1 isoform X7 [Homo sapiens]

Accession:	gi|578799442	**Score:**	10.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	85.5
Database Date:	2015-11-30	**pI:**	10.6
		Sequence Coverage [%]:	1.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MESGPRAELG	AGAPPAVVAR	TPPEPRPSPE	GDPSPPPPPM	SALVPDTPPD	TPPAMKNATS	SKQLPLEPES	PSGQVGPRPA
90	100	110	120	130	140	150	160
PPQEESPSSE	AKSRGPTPPA	MGPRDARPPR	RSSQPSPTAV	PASDSPPTKQ	EVKKAGERHK	LAKERREERA	KYLAAKKAVW
170	180	190	200	210	220	230	240
LEKEEKAKAL	REKQLQERRR	RLEEQRLKAE	QRRAALEERQ	RQKLEKNKER	YEAAIQRSVK	KTWAEIRQQR	WSWAGALHHS
250	260	270	280	290	300	310	320
SPGHKTNRSL	QLSAWESSIV	DRLMTPTLSF	LARSRSAVTL	PRNGRDQAVP	VCPRSASASP	LTPCSVTRSV	HRCAPAGERG
330	340	350	360	370	380	390	400
ERRKPNAGGS	PAPVRRRPEA	SPVQKKEKKD	KERENEKEKS	ALARERSLKK	RQSLPASPRA	RLSASTASEL	SPKSKARPSS
410	420	430	440	450	460	470	480
PSTSWHRPAS	PCPSPGPGHT	LPPKPPSPRG	TTASPKGRVR	RKEEAKESPS	AAGPEDKSQS	KRRASNEKES	AAPASPAPSP
490	500	510	520	530	540	550	560
APSPTPAPPQ	KEQPPAETPT	DAAVLTSPPA	PAPPVTPSKP	MAGTTDREEA	TRLLAEKRRQ	AREQREREEQ	ERRLQAERDK
570	580	590	600	610	620	630	640
RMREEQLARE	AEARAEREAE	ARRREEQEAR	EKAQAEQEEQ	ERLQKQKEEA	EARSREEAER	QRLEREKHFQ	QQEQERQERR
650	660	670	680	690	700	710	720
KRLEEIMKRT	RKSEVSETKK	QDSKEANANG	SSPEPVKAVE	ARSPGLQKEA	VQKEEPIPQE	PQWSLPSKEL	PASLVNGLQP
730	740	750	760	770	780		
LPAHQENGFS	TNGPSGDKSL	SRTPETLLPF	AEAEAFLKKA	VVQSPQVTEV	L		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1989	1	731.7759	-198.38	2	55.0	10.5	2	323-336	R.RKPNAGGSPAPVRR.R	

Detailed Protein Report

Protein 1281: protein Wnt-2b isoform WNT-2B2 [Homo sapiens]

Accession: gi|13518021
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 10.4
MW [kDa]: 43.7
pI: 11.0
Sequence Coverage [%]: 4.1
No. of unique Peptides: 1

```
        10         20         30         40         50         60         70         80
MLRPGGAEEA AQLPLRRASA PVPVPSPAAP DGSRASARLG LACLLLLLLL TLPARVDTSW WYIGALGARV ICDNIPGLVS
        90        100        110        120        130        140        150        160
RQRQLCQRYP DIMRSVGEGA REWIRECQHQ FRHHRWNCTT LDRDHTVFGR VMLRSSREAA FVYAISSAGV VHAITRACSQ
       170        180        190        200        210        220        230        240
GELSVCSCDP YTRGRHHDQR GDFDWGGCSD NIHYGVRFAK AFVDAKEKRL KDARALMNLH NNRCGRTAVR RFLKLECKCH
       250        260        270        280        290        300        310        320
GVSGSCTLRT CWRALSDFRR TGDYLRRRYD GAVQVMATQD GANFTAARQG YRRATRTDLV YFDNSPDYCV LDKAAGSLGT
       330        340        350        360        370        380        390        400
AGRVCSKTSK GTDGCEIMCC GRGYDTTRVT RVTQCECKFH WCCAVRCKEC RNTVDVHTCK APKKAEWLDQ T
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2539	1	863.0477	102.47	2	62.2	10.4	0	1-16	-.MLRPGGAEEAAQLPLR.R	Oxidation: 1

Detailed Protein Report

Protein 1282: PREDICTED: zinc finger protein 175 isoform X3 [Homo sapiens]

Accession:	gi|530417172	**Score:**	10.4
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:	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
30	1	1205.0059	-49.90	2	29.7	10.4	1	218-238	K.LSVYLTDHTGDIPCICKECGK.V	Carbamidomethyl: 16, 19

Detailed Protein Report

Protein 1283: probable ATP-dependent RNA helicase DDX41 [Homo sapiens]

Accession:	gi|21071032	**Score:**	10.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	69.8
Database Date:	2015-11-30	**pI:**	6.4
		Sequence Coverage [%]:	1.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEESEPERKR	ARTDEVPAGG	SRSEAEDEDD	EDYVPYVPLR	QRRQLLLQKL	LQRRRKGAAE	EEQQDSGSEP	RGDEDDIPLG
90	100	110	120	130	140	150	160
PQSNVSLLDQ	HQHLKEKAEA	RKESAKEKQL	KEEEKILESV	AEGRALMSVK	EMAKGITYDD	PIKTSWTPPR	YVLSMSEERH
170	180	190	200	210	220	230	240
ERVRKKYHIL	VEGDGIPPPI	KSFKEMKFPA	AILRGLKKKG	IHHPTPIQIQ	GIPTILSGRD	MIGIAFTGSG	KTLVFTLPVI
250	260	270	280	290	300	310	320
MFCLEQEKRL	PFSKREGPYG	LIICPSRELA	RQTHGILEYY	CRLLQEDSSP	LLRCALCIGG	MSVKEQMETI	RHGVHMMVAT
330	340	350	360	370	380	390	400
PGRLMDLLQK	KMVSLDICRY	LALDEADRMI	DMGFEGDIRT	IFSYFKGQRQ	TLLFSATMPK	KIQNFAKSAL	VKPVTINVGR
410	420	430	440	450	460	470	480
AGAASLDVIQ	EVEYVKEEAK	MVYLLECLQK	TPPPVLIFAE	KKADVDAIHE	YLLLKGVEAV	AIHGGKDQEE	RTKAIEAFRE
490	500	510	520	530	540	550	560
GKKDVLVATD	VASKGLDFPA	IQHVINYDMP	EEIENYVHRI	GRTGRSGNTG	IATTFINKAC	DESVLMDLKA	LLLEAKQKVP
570	580	590	600	610	620	630	
PVLQVLHCGD	ESMLDIGGER	GCAFCGGLGH	RITDCPKLEA	MQTKQVSNIG	RKDYLAHSSM	DF	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1392	1	627.0535	231.18	2	47.1	10.4	1	44-53	R.QLLLQKLLQR.R	

Detailed Protein Report

Protein 1284: dnaJ homolog subfamily C member 11 [Homo sapiens]

Accession:	gi|217035105	**Score:**	10.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	63.2
Database Date:	2015-11-30	**pI:**	9.2
		Sequence Coverage [%]:	2.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MATALSEEEL	DNEDYYSLLN	VRREASSEEL	KAAYRRLCML	YHPDKHRDPE	LKSQAERLFN	LVHQAYEVLS	DPQTRAIYDI
90	100	110	120	130	140	150	160
YGKRGLEMEG	WEVVERRRTP	AEIREEFERL	QREREERRLQ	QRTNPKGTIS	VGVDATDLFD	RYDEEYEDVS	GSSFPQIEIN
170	180	190	200	210	220	230	240
KMHISQSIEA	PLTATDTAIL	SGSLSTQNGN	GGGSINFALR	RVTSAKGWGE	LEFGAGDLQG	PLFGLKLFRN	LTPRCFVTTN
250	260	270	280	290	300	310	320
CALQFSSRGI	RPGLTTVLAR	NLDKNTVGYL	QWRWGIQSAM	NTSIVRDTKT	SHFTVALQLG	IPHSFALISY	QHKFQDDDQT
330	340	350	360	370	380	390	400
RVKGSLKAGF	FGTVVEYGAE	RKISRHSVLG	AAVSVGVPQG	VSLKVKLNRA	SQTYFFPIHL	TDQLLPSAMF	YATVGPLVVY
410	420	430	440	450	460	470	480
FAMHRLIIKP	YLRAQKEKEL	EKQRESAATD	VLQKKQEAES	AVRLMQESVR	RIIEAEESRM	GLIIVNAWYG	KFVNDKSRKS
490	500	510	520	530	540	550	560
EKVKVIDVTV	PLQCLVKDSK	LILTEASKAG	LPGFYDPCVG	EEKNLKVLYQ	FRGVLHQVMV	LDSEALRIPK	QSHRIDTDG

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2184	1	873.3319	-125.21	2	57.2	10.4	2	85-98	R.GLEMEGWEVVERRR.T	

Detailed Protein Report

Protein 1285: exocyst complex component 4 isoform a [Homo sapiens]

Accession:	gi|82546830	**Score:**	10.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	110.4
Database Date:	2015-11-30	**pI:**	6.1
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAAEAAGGKY	RSTVSKSKDP	SGLLISVIRT	LSTSDDVEDR	ENEKGRLEEA	YEKCDRDLDE	LIVQHYTELT	TAIRTYQSIT
90	100	110	120	130	140	150	160
ERITNSRNKI	KQVKENLLSC	KMLLHCKRDE	LRKLWIEGIE	HKHVLNLLDE	IENIKQVPQK	LEQCMASKHY	LSATDMLVSA
170	180	190	200	210	220	230	240
VESLEGPLLQ	VEGLSDLRLE	LHSKKMNLHL	VLIDELHRHL	YIKSTSRVVQ	RNKEKGKISS	LVKDASVPLI	DVTNLPTPRK
250	260	270	280	290	300	310	320
FLDTSHYSTA	GSSSVREINL	QDIKEDLELD	PEENSTLFMG	ILIKGLAKLK	KIPETVKAII	ERLEQELKQI	VKRSTTQVAD
330	340	350	360	370	380	390	400
SGYQRGENVT	VENQPRLLLE	LLELLFDKFN	AVAAAHSVVL	GYLQDTVVTP	LTQQEDIKLY	DMADVWVKIQ	DVLQMLLTEY
410	420	430	440	450	460	470	480
LDMKNTRTAS	EPSAQLSYAS	TGREFAAFFA	KKKPQRPKNS	LFKFESSSHA	ISMSAYLREQ	RRELYSRSGE	LQGGPDDNLI
490	500	510	520	530	540	550	560
EGGGTKFVCK	PGARNITVIF	HPLLRFIQEI	EHALGLGPAK	QCPLREFLTV	YIKNIFLNQV	LAEINKEIEG	VTKTSDPLKI
570	580	590	600	610	620	630	640
LANADTMKVL	GVQRPLLQST	IIVEKTVQDL	LNLMHDLSAY	SDQFLNMVCV	KLQEYKDTCT	AAYRGIVQSE	EKLVISASWA
650	660	670	680	690	700	710	720
KDDDISRLLK	SLPNWMNMAQ	PKQLRPKREE	EEDFIRAAFG	KESEVLIGNL	GDKLIPPQDI	LRDVSDLKAL	ANMHESLEWL
730	740	750	760	770	780	790	800
ASRTKSAFSN	LSTSQMLSPA	QDSHTNTDLP	PVSEQIMQTL	SELAKSFQDM	ADRCLLVLHL	EVRVHCFHYL	IPLAKEGNYA
810	820	830	840	850	860	870	880
IVANVESMDY	DPLVVKLNKD	ISAIEEAMSA	SLQQHKFQYI	FEGLGHLISC	ILINGAQYFR	RISESGIKKM	CRNIFVLQQN
890	900	910	920	930	940	950	960
LTNITMSREA	DLDFARQYYE	MLYNTADELL	NLVVDQGVKY	TELEYIHALT	LLHRSQTGVG	ELTTQNTRLQ	RLKEIICEQA
970	980						
AIKQATKDKK	ITTV						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2395	1	724.8481	15.80	2	59.8	10.4	0	651-662	K.SLPNWMNMAQPK.Q	Oxidation: 6, 8

Detailed Protein Report

Protein 1286: ATP-dependent DNA helicase PIF1 isoform b [Homo sapiens]

Accession:	gi|557357747	**Score:**	10.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	77.1
Database Date:	2015-11-30	**pI:**	11.7
		Sequence Coverage [%]:	1.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLSGIEAAAG	EYEDSELRCR	VAVEELSPGG	QPRRRQALRT	AELSLGRNER	RELMLRLQAP	GPAGRPRCFP	LRAARLFTRF
90	100	110	120	130	140	150	160
AEAGRSTLRL	PAHDTPGAGA	VQLLLSDCPP	DRLRRFLRTL	RLKLAAAPGP	GPASARAQLL	GPRPRDFVTI	SPVQPEERRL
170	180	190	200	210	220	230	240
RAATRVPDTT	LVKRPVEPQA	GAEPSTEAPR	WPLPVKRLSL	PSTKPQLSEE	QAAVLRAVLK	GQSIFFTGSA	GTGKSYLLKR
250	260	270	280	290	300	310	320
ILGSLPPTGT	VATASTGVAA	CHIGGTTLHA	FAGIGSGQAP	LAQCVALAQR	PGVRQGWLNC	QRLVIDEISM	VEADLFDKLE
330	340	350	360	370	380	390	400
AVARAVRQQN	KPFGGIQLII	CGDFLQLPPV	TKGSQPPRFC	FQSKSWKRCV	PVTLELTKVW	RQADQTFISL	LQAVRLGRCS
410	420	430	440	450	460	470	480
DEVTRQLQAT	ASHKVGRDGI	VATRLCTHQD	DVALTNERRL	QELPGKVHRF	EAMDSNPELA	STLDAQCPVS	QLLQLKLGAQ
490	500	510	520	530	540	550	560
VMLVKNLSVS	RGLVNGARGV	VVGFEAEGRG	LPQVRFLCGV	TEVIHADRWT	VQATGGQLLS	RQQLPLQLAW	AMSIHKSQGM
570	580	590	600	610	620	630	640
TLDCVEISLG	RVFASGQAYV	ALSRARSLQG	LRVLDFDPMA	VRCDPRVLHF	YATLRRGRSL	SLAAEGRGNE	DRCSGSSIRA
650	660	670	680	690	700	710	
LGGDWWGLRL	GAASKQRTEL	RCVSTARPSL	AQPRTNTLQS	LTKEHKLQNV	HPYFKLLFQG	INSVWGH	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1593	1	685.8528	-16.87	2	49.6	10.4	0	696-707	K.LLFQGINSVWGH.-	

Detailed Protein Report

Protein 1287: tetratricopeptide repeat protein 12 [Homo sapiens]

Accession:	gi|90669931	**Score:**	10.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	78.7
Database Date:	2015-11-30	**pI:**	5.4
		Sequence Coverage [%]:	2.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDADKEKDLQ	KFLKNVDEIS	NLIQEMNSDD	PVVQQKAVLE	TEKRLLLMEE	DQEEDECRTT	LNKTMISPPQ	TAMKSAEEIN
90	100	110	120	130	140	150	160
SEAFLASVEK	DAKERAKRRR	ENKVLADALK	EKGNEAFAEG	NYETAILRYS	EGLEKLKDMK	VLYTNRAQAY	MKLEDYEKAL
170	180	190	200	210	220	230	240
VDCEWALKCD	EKCTKAYFHM	GKANLALKNY	SVSRECYKKI	LEINPKLQTQ	VKGYLNQVDL	QEKADLQEKE	AHELLDSGKN
250	260	270	280	290	300	310	320
TAVTTKNLLE	TLSKPDQIPL	FYAGGIEILT	EMINECTEQT	LFRMHNGFSI	ISDNEVIRRC	FSTAGNDAVE	EMVCVSVLKL
330	340	350	360	370	380	390	400
WQAVCSRNEE	NQRVLVIHHD	RARLLAALLS	SKVLAIRQQS	FALLLHLAQT	ESGRSLIINH	LDLTRLLEAL	VSFLDFSDKE
410	420	430	440	450	460	470	480
ANTAMGLFTD	LALEERFQVW	FQANLPGVLP	ALTGVLKTDP	KVSSSSALCQ	CIAIMGNLSA	EPTTRRHMAA	CEEFGDGCLS
490	500	510	520	530	540	550	560
LLARCEEDVD	LFREVIYTLL	GLMMNLCLQA	PFVSEVWAVE	VSRRCLSLLN	SQDGGILTRA	AGVLSRTLSS	SLKIVEEALR
570	580	590	600	610	620	630	640
AGVVKKMMKF	LKTGGETASR	YAIKILAICT	NSYHEAREEV	IRLDKKLSVM	MKLLSSEDEV	LVGNAALCLG	NCMEVPNVAS
650	660	670	680	690	700	710	
SLLKTDLLQV	LLKLAGSDTQ	KTAVQVNAGI	ALGKLCTAEP	RFAAQLRKLH	GLEILNSTMK	YISDS	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2058	1	1051.3794	-99.24	2	55.9	10.4	0	300-319	R.CFSTAGNDAVEEMVCVSVLK.L	

Detailed Protein Report

Protein 1288: cGMP-specific 3',5'-cyclic phosphodiesterase isoform 1 [Homo sapiens]

Accession: gi|61744435

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Score: 10.4

MW [kDa]: 99.9

pI: 5.7

Sequence Coverage [%]: 1.3

No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MERAGPSFGQ	QRQQQQPQQQ	KQQQRDQDSV	EAWLDDHWDF	TFSYFVRKAT	REMVNAWFAE	RVHTIPVCKE	GIRGHTESCS
90	100	110	120	130	140	150	160
CPLQQSPRAD	NSAPGTPTRK	ISASEFDRPL	RPIVVKDSEG	TVSFLSDSEK	KEQMPLTPPR	FDHDEGDQCS	RLLELVKDIS
170	180	190	200	210	220	230	240
SHLDVTALCH	KIFLHIHGLI	SADRYSLFLV	CEDSSNDKFL	ISRLFDVAEG	STLEEVSNNC	IRLEWNKGIV	GHVAALGEPL
250	260	270	280	290	300	310	320
NIKDAYEDPR	FNAEVDQITG	YKTQSILCMP	IKNHREEVVG	VAQAINKKSG	NGGTFTEKDE	KDFAAYLAFC	GIVLHNAQLY
330	340	350	360	370	380	390	400
ETSLLENKRN	QVLLDLASLI	FEEQQSLEVI	LKKIAATIIS	FMQVQKCTIF	IVDEDCSDSF	SSVFHMECEE	LEKSSDTLTR
410	420	430	440	450	460	470	480
EHDANKINYM	YAQYVKNTME	PLNIPDVSKD	KRFPWTTENT	GNVNQQCIRS	LLCTPIKNGK	KNKVIGVCQL	VNKMEENTGK
490	500	510	520	530	540	550	560
VKPFNRNDEQ	FLEAFVIFCG	LGIQNTQMYE	AVERAMAKQM	VTLEVLSYHA	SAAEEETREL	QSLAAAVVPS	AQTLKITDFS
570	580	590	600	610	620	630	640
FSDFELSDLE	TALCTIRMFT	DLNLVQNFQM	KHEVLCRWIL	SVKKNYRKNV	AYHNWRHAFN	TAQCMFAALK	AGKIQNKLTD
650	660	670	680	690	700	710	720
LEILALLIAA	LSHDLDHRGV	NNSYIQRSEH	PLAQLYCHSI	MEHHHFDQCL	MILNSPGNQI	LSGLSIEEYK	TTLKIIKQAI
730	740	750	760	770	780	790	800
LATDLALYIK	RRGEFFELIR	KNQFNLEDPH	QKELFLAMLM	TACDLSAITK	PWPIQQRIAE	LVATEFFDQG	DRERKELNIE
810	820	830	840	850	860	870	880
PTDLMNREKK	NKIPSMQVGF	IDAICLQLYE	ALTHVSEDCF	PLLDGCRKNR	QKWQALAEQQ	EKMLINGESG	QAKRN	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1989	1	616.7715	-62.66	2	54.8	10.4	1	2-12	M.ERAGPSFGQQR.Q	

Detailed Protein Report

Protein 1289: zinc finger and SCAN domain-containing protein 26 isoform d [Homo sapiens]

Accession:	gi|566006134	**Score:**	10.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	31.5
Database Date:	2015-11-30	**pI:**	10.4
		Sequence Coverage [%]:	10.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEAHNEGSNL	ERHQAKPKEK	IEYKCSEREQ	RFIQHLDLIE	HASTHTGKKL	CESDVCQSSS	LTGHKKVLSR	EKGHQCHECG
90	100	110	120	130	140	150	160
KAFQRSSHLV	RHQKIHLGEK	PYQCNECGKV	FSQNAGLLEH	LRIHTGEKPY	LCIHCGKNFR	RSSHLNRHQR	IHSQEEPCEC
170	180	190	200	210	220	230	240
KECGKTFSQA	LLLTHHQRIH	SHSKSHQCNE	CGKAFSLTSD	LIRHHRIHTG	EKPFKCNICQ	KAFRLNSHLA	QHVRIHNEEK
250	260	270	280				
PYQCSECGEA	FRQRSGLFQH	QRYHHKDKLA					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2244	1	1061.7676	-92.40	3	58.3	10.4	1	95-122	K.IHLGEKPYQCNECGKVFSQNAGLLEHLR.I	

Detailed Protein Report

Protein 1290: G-protein coupled receptor 64 isoform 6 precursor [Homo sapiens]

Accession:	gi|296317297	**Score:**	10.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	106.3
Database Date:	2015-11-30	**pI:**	8.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MVFSVRQCGH	VGRTEEVLLT	FKIFLVIICL	HVVLVTSLEE	DTDNSSLSPP	PAKLSVVSFA	PSSNGTPEVE	TTSLNDVTLS
90	100	110	120	130	140	150	160
LLPSNETEKT	KITIVKTFNA	SGVKPQRNIC	NLSSICNDSA	FFRGEIMFQY	DKESTVPQNQ	HITNGTLTGV	LSLSELKRSE
170	180	190	200	210	220	230	240
LNKTLQTLSE	TYFIMCATAE	AQSTLNCTFT	IKLNNTMNAC	AVIAALERVK	IRPMEHCCCS	VRIPCPSSPE	ELEKLQCDLQ
250	260	270	280	290	300	310	320
DPIVCLADHP	RGPPFSSSQS	IPVVPRATVL	SQVPKATSFA	EPPDYSPVTH	NVPSPIGEIQ	PLSPQPSAPI	ASSPAIDMPP
330	340	350	360	370	380	390	400
QSETISSPMP	QTHVSGTPPP	VKASFSSPTV	SAPANVNTTS	APPVQTDIVN	TSSISDLENQ	VLQMEKALSL	GSLEPNLAGE
410	420	430	440	450	460	470	480
MINQVSRLLH	SPPDMLAPLA	QRLLKVVDDI	GLQLNFSNTT	ISLTSPSLAL	AVIRVNASSF	NTTTFVAQDP	ANLQVSLETQ
490	500	510	520	530	540	550	560
APENSIGTIT	LPSSLMNNLP	AHDMELASRV	QFNFFETPAL	FQDPSLENLS	LISYVISSSV	ANLTVRNLTR	NVTVTLKHIN
570	580	590	600	610	620	630	640
PSQDELTVRC	VFWDLGRNGG	RGGWSDNGCS	VKDRRLNETI	CTCSHLTSFG	VLLDLSRTSV	LPAQMMALTF	ITYIGCGLSS
650	660	670	680	690	700	710	720
IFLSVTLVTY	IAFEKIRRDY	PSKILIQLCA	ALLLLNLVFL	LDSWIALYKM	QGLCISVAVF	LHYFLLVSFT	WMGLEAFHMY
730	740	750	760	770	780	790	800
LALVKVFNTY	IRKYILKFCI	VGWGVPAVVV	TIILTISPDN	YGLGSYGKFP	NGSPDDFCWI	NNNAVFYITV	VGYFCVIFLL
810	820	830	840	850	860	870	880
NVSMFIVVLV	QLCRIKKKKQ	LGAQRKTSIQ	DLRSIAGLTF	LLGITWGFAF	FAWGPVNVTF	MYLFAIFNTL	QGFFIFIFYC
890	900	910	920	930	940	950	960
VAKENVRKQW	RRYLCCGKLR	LAENSGNAST	ERNGVSFSVQ	NGDVCLHDFT	GKQHMFNEKE	DSCNGKGRMA	LRRTSKRGSL
970							
HFIEQM							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1967	1	862.3053	-65.50	2	54.5	10.4	1	933-946	K.QHMFNEKEDSCNGK.G	Carbamidomethyl: 11

Detailed Protein Report

Protein 1291: BRI3-binding protein precursor [Homo sapiens]

Accession:	gi|19923665	**Score:**	10.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	27.8
Database Date:	2015-11-30	**pI:**	10.0
		Sequence Coverage [%]:	9.2
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MGARASGGPL ARAGLLLLLL LLLLLGLLAP GAQGARGRGG AEKNSYRRTV NTFSQSVSSL FGEDNVRAAQ KFLARLTERF
        90        100        110        120        130        140        150        160
VLGVDMFVET LWKVWTELLD VLGLDVSNLS QYFSPASVSS SPARALLLVG VVLLAYWFLS LTLGFTFSVL HVVFGRFFWI
       170        180        190        200        210        220        230        240
VRVVLFSMSC VYILHKYEGE PENAVLPLCF VVAVYFMTGP MGFYWRSSPS GPSNPSNPSV EEKLEHLEKQ VRLLNIRLNR
       250        260
VLESLDRSKD K
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1393	1	817.0674	1.39	3	47.1	10.4	1	207-229	R.SSPSGPSNPSNPSVEEKLEHLEK.Q	

Detailed Protein Report

Protein 1292: PREDICTED: uncharacterized protein C4orf50 [Homo sapiens]

Accession:	gi|530358255	**Score:**	10.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	97.6
Database Date:	2015-11-30	**pI:**	5.4
		Sequence Coverage [%]:	2.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPLLQGEASV	SKEGPESLSR	RERVEGYVWG	LRGGLSSENE	EVAPPATFSR	AHETKEPWPT	DSQLLAGKVR	ATGRTARGKE
90	100	110	120	130	140	150	160
ENQVWLGNAL	LLQGGSLEDK	GLEEEDEMPH	QEASGLGCRG	APEEPDSQEH	ESKEMLFFAG	ETGLPLFPRF	ALSVEGAEPT
170	180	190	200	210	220	230	240
DHGHPQAVSK	GHDRCALTID	ELAQDVEACF	QQLSTLQPGS	RGWQCSASAC	RGENWSFAQK	WHSGWERAHS	QQVWGNWGIC
250	260	270	280	290	300	310	320
SNEEAKSKES	GEGDKPGKTT	ALGTSEVPGN	PGTLPHWDEA	SPNPPQGPAE	PWGALERVRS	RFHQLISGLK	KQRSQILHDN
330	340	350	360	370	380	390	400
TKLHGDQERF	HERVCALERE	REREVTKISR	LERDNHRLVG	DISQLKKELD	QYLQAISDLE	DCNGKSYCKI	LELEEENETL
410	420	430	440	450	460	470	480
KGNLGQLQKA	TSESVRKSKD	TMEQVTLENW	KLQTLISELG	VSYKELIKDI	VLGIEDMIRA	LSGENEHLLR	RVHVLEREVT
490	500	510	520	530	540	550	560
LQRSTDQGRL	VRGREHLQGK	AKMHALDKEV	QVTPLTGQLL	SRACGPPLEE	EMSLAAGQTG	PSTGTGNSRR	GADSPPPSLV
570	580	590	600	610	620	630	640
WRNTGVANAL	QGNVSGAEVK	EAHLEKEEKR	PRCSVAQGQA	LSSLSNGPML	RDSEAEVTEE	DPRLRAQQLH	HRVLTLQCQL
650	660	670	680	690	700	710	720
RDQGAAHQAS	LDEATRLQEE	LQAKLEELQK	KQHEAKLAVT	PLKAKIASLV	RKCRERNRLI	THLLQELHRH	GLGNLLLSEL
730	740	750	760	770	780	790	800
AQNMLNDVAL	AEYTATFLAP	GVPETSHHLD	VKSEMTAALR	AQTYLLNPEM	DSVLQSSLSS	ESWPVPEPEW	PAQTAQLDSL
810	820	830	840	850	860	870	880
KLPLSLVSTL	DPGTCLAAVT	VEPGLPAQRL	QEKGGMPCPA	LQVDNVPAPS	ELLSPARILA	FHQELRQSIC	SNSQVHKSPL
890							
ELEM							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1506	1	1058.4824	21.34	2	48.5	10.4	1	202-220	R.GWQCSASACRGENWSFAQK.W	

Detailed Protein Report

Protein 1293: PREDICTED: sodium channel protein type 2 subunit alpha isoform X7 [Homo sapiens]

Accession:	gi|530370758	**Score:**	10.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	144.8
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
MCLIWDCCKP	WLKVKHLVNL	VVMDPFVDLA	ITICIVLNTL	FMAMEHYPMT	EQFSSVLSVG	NLVFTGIFTA	EMFLKIIAMD
90	100	110	120	130	140	150	160
PYYYFQEGWN	IFDGFIVSLS	LMELGLANVE	GLSVLRSFRL	LRVFKLAKSW	PTLNMLIKII	GNSVGALGNL	TLVLAIIVFI
170	180	190	200	210	220	230	240
FAVVGMQLFG	KSYKECVCKI	SNDCELPRWH	MHDFFHSFLI	VFRVLCGEWI	ETMWDCMEVA	GQTMCLTVFM	MVMVIGNLVV
250	260	270	280	290	300	310	320
LNLFLALLLS	SFSSDNLAAT	DDDNEMNNLQ	IAVGRMQKGI	DFVKRKIREF	IQKAFVRKQK	ALDEIKPLED	LNNKKDSCIS
330	340	350	360	370	380	390	400
NHTTIEIGKD	LNYLKDGNGT	TSGIGSSVEK	YVVDESDYMS	FINNPSLTVT	VPIAVGESDF	ENLNTEEFSS	ESDMEESKEK
410	420	430	440	450	460	470	480
LNATSSSEGS	TVDIGAPAEG	EQPEVEPEES	LEPEACFTED	CVRKFKCCQI	SIEEGKGKLW	WNLRKTCYKI	VEHNWFETFI
490	500	510	520	530	540	550	560
VFMILLSSGA	LAFEDIYIEQ	RKTIKTMLEY	ADKVFTYIFI	LEMLLKWVAY	GFQVYFTNAW	CWLDFLIVDV	SLVSLTANAL
570	580	590	600	610	620	630	640
GYSELGAIKS	LRTLRALRPL	RALSRFEGMR	VVVNALLGAI	PSIMNVLLVC	LIFWLIFSIM	GVNLFAGKFY	HCINYTTGEM
650	660	670	680	690	700	710	720
FDVSVVNNYS	ECKALIESNQ	TARWKNVKVN	FDNVGLGYLS	LLQVATFKGW	MDIMYAAVDS	RNVELQPKYE	DNLYMYLYFV
730	740	750	760	770	780	790	800
IFIIFGSFFT	LNLFIGVIID	NFNQQKKKFG	GQDIFMTEEQ	KKYYNAMKKL	GSKKPQKPIP	RPANKFQGMV	FDFVTKQVFD
810	820	830	840	850	860	870	880
ISIMILICLN	MVTMMVETDD	QSQEMTNILY	WINLVFIVLF	TGECVLKLIS	LRYYYFTIGW	NIFDFVVVIL	SIVGMFLAEL
890	900	910	920	930	940	950	960
IEKYFVSPTL	FRVIRLARIG	RILRLIKGAK	GIRTLLFALM	MSLPALFNIG	LLLFLVMFIY	AIFGMSNFAY	VKREVGIDDM
970	980	990	1000	1010	1020	1030	1040
FNFETFGNSM	ICLFQITTSA	GWDGLLAPIL	NSGPPDCDPD	KDHPGSSVKG	DCGNPSVGIF	FFVSYIIISF	LVVVNMYIAV
1050	1060	1070	1080	1090	1100	1110	1120
ILENFSVATE	ESAEPLSEDD	FEMFYEVWEK	FDPDATQFIE	FAKLSDFADA	LDPPLLIAKP	NKVQLIAMDL	PMVSGDRIHC
1130	1140	1150	1160	1170	1180	1190	1200
LDILFAFTKR	VLGESGEMDA	LRIQMEERFM	ASNPSKVSYE	PITTTLKRKQ	EEVSAIIIQR	AYRRYLLKQK	VKKVSSIYKK
1210	1220	1230	1240	1250	1260	1270	1280
DKGKECDGTP	IKEDTLIDKL	NENSTPEKTD	MTPSTTSPPS	YDSVTKPEKE	KFEKDKSEKE	DKGKDIRESK	K

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
390	1	704.6907	-199.27	2	34.2	10.4	0	336-350	K.DGNGTTSGIGSSVEK.Y	

Detailed Protein Report

Protein 1294: melanopsin isoform 1 [Homo sapiens]

Accession:	gi|15150803	**Score:**	10.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	52.6
Database Date:	2015-11-30	**pI:**	10.1
		Sequence Coverage [%]:	2.7
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 1.63 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MNPPSGPRVP	PSPTQEPSCM	ATPAPPSWWD	SSQSSISSLG	RLPSISPTAP	GTWAAAWVPL	PTVDVPDHAH	YTLGTVILLV
90	100	110	120	130	140	150	160
GLTGMLGNLT	VIYTFCRSRS	LRTPANMFII	NLAVSDFLMS	FTQAPVFFTS	SLYKQWLFGE	TGCEFYAFCG	ALFGISSMIT
170	180	190	200	210	220	230	240
LTAIALDRYL	VITRPLATFG	VASKRRAAFV	LLGVWLYALA	WSLPPFFGWS	AYVPEGLLTS	CSWDYMSFTP	AVRAYTMLLC
250	260	270	280	290	300	310	320
CFVFFLPLLI	IIYCYIFIFR	AIRETGRALQ	TFGACKGNGE	SLWQRQRLQS	ECKMAKIMLL	VILLFVLSWA	PYSAVALVAF
330	340	350	360	370	380	390	400
AGYAHVLTPY	MSSVPAVIAK	ASAIHNPIIY	AITHPKYRVA	IAQHLPCLGV	LLGVSRRHSR	PYPSYRSTHR	STLTSHTSNL
410	420	430	440	450	460	470	480
SWISIRRRQE	SLGSESEVGW	THMEAAAVWG	AAQQANGRSL	YGQGLEDLEA	KAPPRPQGHE	AETPGKTKGL	IPSQDPRM

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
831	1	711.9280	96.72	2	39.9	10.4	0	439-451	R.SLYGQGLEDLEAK.A		MD:MU 1.63

Detailed Protein Report

Protein 1295: von Willebrand factor preproprotein [Homo sapiens]

Accession:	gi|89191868	**Score:**	10.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	309.1
Database Date:	2015-11-30	**pI:**	5.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	0.8
		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
99	1	845.3517	-47.80	3	31.0	10.4	1	2289-2311	K.VNCTTQPCPTAKAPTCGLCEVAR.L	Carbamidomethyl: 8, 16, 19

Detailed Protein Report

Protein 1296: lysine-specific demethylase 4C isoform 3 [Homo sapiens]

Accession:	gi|226442893	**Score:**	10.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	91.8
Database Date:	2015-11-30	**pI:**	5.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEVAEVESPL	NPSCKIMTFR	PSMEEFREFN	KYLAYMESKG	AHRAGLAKVI	PPKEWKPRQC	YDDIDNLLIP	APIQQMVTGQ
90	100	110	120	130	140	150	160
SGLFTQYNIQ	KKAMTVKEFR	QLANSGKYCT	PRYLDYEDLE	RKYWKNLTFV	APIYGADING	SIYDEGVDEW	NIARLNTVLD
170	180	190	200	210	220	230	240
VVEEECGISI	EGVNTPYLYF	GMWKTTFAWH	TEDMDLYSIN	YLHFGEPKSW	YAIPPEHGKR	LERLAQGFFP	SSSQGCDAFL
250	260	270	280	290	300	310	320
RHKMTLISPS	VLKKYGIPFD	KITQEAGEFM	ITFPYGYHAG	FNHGFNCAES	TNFATVRWID	YGKVAKLCTC	RKDMVKISMD
330	340	350	360	370	380	390	400
IFVRKFQPDR	YQLWKQGKDI	YTIDHTKPTP	ASTPEVKAWL	QRRRKVRKAS	RSFQCARSTS	KRPKADEEEE	VSDEVDGAEV
410	420	430	440	450	460	470	480
PNPDSVTDDL	KVSEKSEAAV	KLRNTEASSE	EESSASRMQV	EQNLSDHIKL	SGNSCLSTSV	TEDIKTEDDK	AYAYRSVPSI
490	500	510	520	530	540	550	560
SSEADDSIPL	SSGYEKPEKS	DPSELSWPKS	PESCSSVAES	NGVLTEGEES	DVESHGNGLE	PGEIPAVPSG	ERNSFKVPSI
570	580	590	600	610	620	630	640
AEGENKTSKS	WRHPLSRPPA	RSPMTLVKQQ	APSDEELPEV	LSIEEEVEET	ESWAKPLIHL	WQTKSPNFAA	EQEYNATVAR
650	660	670	680	690	700	710	720
MKPHCAICTL	LMPYHKPDSS	NEENDARWET	KLDEVVTSEG	KTKPLIPEMC	FIYSEENIEY	SPPNAFLEED	GTSLLISCAK
730	740	750	760	770	780	790	800
CCVRVHASCY	GIPSHEICDG	WLCARCKRNA	WTAECCLCNL	RGGALKQTKN	NKWAHVMCAV	AVPEVRFTNV	PERTQIDVGR
810	820						
IPLQRLKLGR	LGI						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
168	1	855.2417	-169.95	2	31.8	10.4	1	748-761	K.RNAWTAECCLCNLR.G	Carbamidomethyl: 8

Detailed Protein Report

Protein 1297: PREDICTED: histone H2A deubiquitinase MYSM1 isoform X4 [Homo sapiens]

Accession:	gi|578798291	**Score:**	10.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	94.9
Database Date:	2015-11-30	**pI:**	5.3
		Sequence Coverage [%]:	1.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAAEEADVDI	EGDVVAAAGA	QPGSGENTAS	VLQKDHYLDS	SWRTENGLIP	WTLDNTISEE	NRAVIEKMLL	EEEYYLSKKS
90	100	110	120	130	140	150	160
QPEKVWLDQK	EDDKKYMKSL	QKTAKIMVHS	PTKPASYSVK	WTIEEKELFE	QGLAKFGRRW	TKISKLIGSR	TVLQVKSYAR
170	180	190	200	210	220	230	240
QYFKNKVKCG	LDKETPNQKT	GHNLQVKNED	KGTKAWTPSC	LRGRADPNLN	AVKIEKLSDD	EEVDITDEVD	ELSSQTPQKN
250	260	270	280	290	300	310	320
SSSDLLLDFP	NSKMHETNQG	EFITSDSQEA	LFSKSSRGCL	QNEKQDETLS	SSEITLWTEK	QSNGDKKSIE	LNDQKFNELI
330	340	350	360	370	380	390	400
KNCNKHDGRG	IIVDARQLPS	PEPCEIQKNL	NDNEMLFHSC	QMVEESHEEE	ELKPPEQEIE	IDRNIIQEEE	KQAIPEFFEG
410	420	430	440	450	460	470	480
RQAKTPERYL	KIRNYILDQW	EICKPKYLNK	TSVRPGLKNC	GDVNCIGRIH	TYLELIGAIN	FGCEQAVYNR	PQTVDKVRIR
490	500	510	520	530	540	550	560
DRKDAVEAYQ	LAQRLQSMRT	RRRRVRDPWG	NWCDAKDLEG	QTFEHLSAEE	LAKRREEEKG	RPVKSLKVPR	PTKSSFDPFQ
570	580	590	600	610	620	630	640
LIPCNFFSEE	KQEPFQVKVA	SEALLIMDLH	AHVSMAEVIG	LLGGRYSEVD	KVVEVCAAEP	CNSLSTGLQC	EMDPVSQTQA
650	660	670	680	690	700	710	720
SETLAVRGFS	VIGWYHSHPA	FDPNPSLRDI	DTQAKYQSYF	SRGGAKFIGM	IVSPYNRNNP	LPYSQITCLV	ISEEISPDGS
730	740	750	760	770	780	790	800
YRLPYKFEVQ	QMLEEPQWGL	VFEKTRWIIE	KYRLSHSVPM	DKIFRRDSDL	TCLQKLLECM	RKTLSKVTNC	FMAEEFLTEI
810	820	830					
ENLFLSNYKS	NQENGVTEEN	CTKELLM					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
189	1	614.3478	6.42	2	32.1	10.4	2	535-544	R.REEEKGRPVK.S	

Detailed Protein Report

Protein 1298: PREDICTED: nuclear receptor coactivator 5 isoform X2 [Homo sapiens]

Accession:	gi|530418236	**Score:**	10.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	48.2
Database Date:	2015-11-30	**pI:**	10.1
		Sequence Coverage [%]:	3.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MNTAPSRPSP	TRRDPYGFGD	SRDSRRDRSP	IRGSPRREPR	DGRNGRDARD	SRDIRDPRDL	RDHRHSRDLR	DHRDSRSVRD
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
VRDVRDLRDF	RDLRDSRDFR	DQRDPMYDRY	RDMRDSRDPM	YRREGSYDRY	LRMDDYCRRK	DDSYFDRYRD	SFDGRGPPGP
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
ESQSRAKERL	KREERRREEL	YRQYFEEIQR	RFDAERPVDC	SVIVVNKQTK	DYAESVGRKV	RDLGMVVDLI	FLNTEVSLSQ
250	**260**	**270**	**280**	**290**	**300**	**310**	**320**
ALEDVSRGGS	PFAIVITQQH	QIHRSCTVNI	MFGTPQEHRN	MPQADAMVLV	ARNYERYKNE	CREKEREEIA	RQAAKMADEA
330	**340**	**350**	**360**	**370**	**380**	**390**	**400**
ILQERERGGP	EEGVRGGHPP	AIQSLINLLA	DNRYLTAEET	DKIINYLRER	KERLMRSSTD	SLPGELRGRA	EARFPANHSG
410							
RPRVPR							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
163	1	896.0924	148.95	2	31.8	10.4	0	192-207	R.FDAERPVDCSVIVVNK.Q	

Detailed Protein Report

Protein 1299: disintegrin and metalloproteinase domain-containing protein 28 isoform 3 preproprotein [Homo sapiens]

Accession:	gi|54292117	**Score:**	10.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	61.2
Database Date:	2015-11-30	**pI:**	6.6
		Sequence Coverage [%]:	1.3
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 0.91 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MLQGLLPVSL	LLSVAVSAIK	ELPGVKKYEV	VYPIRLHPLH	KREAKEPEQQ	EQFETELKYK	MTINGKIAVL	YLKKNKNLLA
90	100	110	120	130	140	150	160
PGYTETYYNS	TGKEITTSPQ	IMDDCYYQGH	ILNEKVSDAS	ISTCRGLRGY	FSQGDQRYFI	EPLSPIHRDG	QEHALFKYNP
170	180	190	200	210	220	230	240
DEKNYDSTCG	MDGVLWAHDL	QQNIALPATK	LVKLKDRKVQ	EHEKYIEYYL	VLDNGEFKRY	NENQDEIRKR	VFEMANYVNM
250	260	270	280	290	300	310	320
LYKKLNTHVA	LVGMEIWTDK	DKIKITPNAS	FTLENFSKWR	GSVLSRRKRH	DIAQLITATE	LAGTTVGLAF	MSTMCSPYSV
330	340	350	360	370	380	390	400
GVVQDHSDNL	LRVAGTMAHE	MGHNFGMFHD	DYSCKCPSTI	CVMDKALSFY	IPTDFSSCSR	LSYDKFFEDK	LSNCLFNAPL
410	420	430	440	450	460	470	480
PTDIISTPIC	GNQLVEMGED	CDCGTSEECT	NICCDAKTCK	IKATFQCALG	ECCEKCQFKK	AGMVCRPAKD	ECDLPEMCNG
490	500	510	520	530	540	550	
KSGNCPDDRF	QVNGFPCHHG	KGHCLMGTCP	TLQEQCTELW	GPGRRTNPFP	CACAKENHFR		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
1056	1	770.2315	-318.65	1	42.8	10.4	1	21-27	K.ELPGVKK.Y		MD:MU	0.91

Protein 1300: inter-alpha-trypsin inhibitor heavy chain H6 precursor [Homo sapiens]

Accession:	gi|38348336	**Score:**	10.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	143.1
Database Date:	2015-11-30	**pI:**	9.6
		Sequence Coverage [%]:	0.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSGWRYLICV	SFLLTILLEL	TYQGPPVPAS	SSTKLLMTSY	SMRSTVVSRY	AHTLVTSVLF	NPHAEAHEAI	FDLDLPHLAF
90	100	110	120	130	140	150	160
ISNFTMTINN	KVYIAEVKEK	HQAKKIYEEA	HQQGKTAAHV	GIRDRESEKF	RISTSLAAGT	EVTFSLAYEE	LLQRHQGQYQ
170	180	190	200	210	220	230	240
LVVSLRPGQL	VKRLSIEVTV	SERTGISYVH	IPPLRTGRLR	TNAHASEVDS	PPSTRIERGE	TCVRITYCPT	LQDQSSISGS
250	260	270	280	290	300	310	320
GIMADFLVQY	DVVMEDIIGD	VQIYDDYFIH	YFAPRGLPPM	EKNVVFVIDV	SSSMFGTKME	QTKTAMNVIL	SDLQANDYFN
330	340	350	360	370	380	390	400
IISFSDTVNV	WKAGGSIQAT	IQNVHSAKDY	LHCMEADGWT	DVNSALLAAA	SVLNHSNQEP	GRGPSVGRIP	LIIFLTDGEP
410	420	430	440	450	460	470	480
TAGVTTPSVI	LSNVRQALGH	RVSLFSLAFG	DDADFTLLRR	LSLENRGIAR	RIYEDTDAAL	QLKGLYEEIS	MPLLADVRLN
490	500	510	520	530	540	550	560
YLGGLVGASP	WAVFPNYFGG	SELVVAGQVQ	PGKQELGIHL	AARGPKDQLL	VAHHSEGATN	NSQKAFGCPG	EPAPNVAHFI
570	580	590	600	610	620	630	640
RRLWAYVTIG	ELLDAHFQAR	DTTTRHLLAA	KVLNLSLEYN	FVTPLTSLVM	VQPKQASEET	RRQTSTSAGP	DTIMPSSSSR
650	660	670	680	690	700	710	720
HGLGVSTAQP	ALVPKVISPK	SRPVKPKFYL	SSTTTASTKK	MLSSKELEPL	GESPHTLSMP	TYPKAKIPAQ	QDSGTLAQPT
730	740	750	760	770	780	790	800
LRTKPTILVP	SNSGTLLPLK	PGSLSHQNPD	ILPTNSRTQV	PPVKPGIPAS	PKADTVKCVT	PLHSKPGAPS	HPQLGALTSQ
810	820	830	840	850	860	870	880
APKGLPQSRP	GVSTLQVPKY	PLHTRPRVPA	PKTRNNMPHL	GPGILLSKTP	KILLSLKPSA	PPHQISTSIS	LSKPETPNPH
890	900	910	920	930	940	950	960
MPQTPLPPRP	DRPRPPLPES	LSTFPNTISS	STGPSSTTTT	SVLGEPLPMP	FTPTLPPGRF	WHQYDLLPGP	QRTRQVLGPS
970	980	990	1000	1010	1020	1030	1040
RPGVPTMSLL	NSSRPTPEGS	PPNLPILLPS	SILPEAISLL	LLPEELELLS	ESMVESKFVE	SLNPPAFYTF	LTPDEDGSPN
1050	1060	1070	1080	1090	1100	1110	1120
WDGNSEEILG	GAGGSMESQG	SSVGLAKGTL	PSIFTFSSSV	DGDPHFVIQI	PHSEEKICFT	LNGHPGDLLQ	LIEDPKAGLH
1130	1140	1150	1160	1170	1180	1190	1200
VSGKLLGAPP	RPGHKDQTRT	YFQIITVTTD	KPRAYTITIS	RSSISLRGEG	TLRLSWDQPA	LLKRPQLELY	VAAAARLTLR
1210	1220	1230	1240	1250	1260	1270	1280
LGPYLEFLVL	RHRYRHPSTL	QLPHLGFYVA	NGSGLSPSAR	GLIGQFQHAD	IRLVTGPMGP	CLRRHHGPDV	PVILGKRLLK
1290	1300	1310	1320				
DSPRLLPRWA	SCWLVKRSHV	ELLLGHPYLS	YVL				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
451	1	690.4270	102.42	2	35.3	10.3	0	452-463	R.IYEDTDAALQLK.G	

Detailed Protein Report

Protein 1301: PREDICTED: SH3 and PX domain-containing protein 2A isoform X5 [Homo sapiens]

Accession:	gi|530394650	**Score:**	10.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	106.0
Database Date:	2015-11-30	**pI:**	9.5
		Sequence Coverage [%]:	1.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MILEQYVVVS	NYKKQENSEL	SLQAGEVVDV	IEKNESGWWF	VSTSEEQGWV	PATYLEAQNG	TRDDSDINTS	KTGEVSKRRK
90	100	110	120	130	140	150	160
AHLRRLDRRW	TLGGMVNRQH	SREEKYVTVQ	PYTSQSKDEI	GFEKGVTVEV	IRKNLEGWWY	IRYLGKEGWA	PASYLKKAKD
170	180	190	200	210	220	230	240
DLPTRKKNLA	GPVEIIGNIM	EISNLLNKKA	SGDKETPPAE	GEGHEAPIAK	KEISLPILCN	ASNGSAVGVP	DRTVSRLAQG
250	260	270	280	290	300	310	320
SPAVARIAPQ	RAQISSPNLR	TRPPPRRESS	LGFQLPKPPE	PPSVEVEYYT	IAEFQSCISD	GISFRGGQKA	EVIDKNSGGW
330	340	350	360	370	380	390	400
WYVQIGEKEG	WAPASYIDKR	KKPNLSRRTS	TLTRPKVPPP	APPSKPKEAE	EGPTGASESQ	DSPRKLKYEE	PEYDIPAFGF
410	420	430	440	450	460	470	480
DSEPELSEEP	VEDRASGERR	PAQPHRPSPA	SSLQRARFKV	GESSEDVALE	EETIYENEGF	RPYAEDTLSA	RGSSGDSDSP
490	500	510	520	530	540	550	560
GSSSLSLTRK	NSPKSGSPKS	SSLLKLKAEK	NAQAEMGKNH	SSASFSSSIT	INTTCCSSSS	SSSSSLSKTS	GDLKPRSASD
570	580	590	600	610	620	630	640
AGIRGTPKVR	AKKDADANAG	LTSCPRAKPS	VRPKPFLNRA	ESQSQEKMDI	STLRRQLRPT	GQLRGGLKGS	KSEDSELPPQ
650	660	670	680	690	700	710	720
TASEAPSEGS	RRSSSDLITL	PATTPPCPTK	KEWEGPATSY	MTCSAYQKVQ	DSEISFPAGV	EVQVLEKQES	GWWYVRFGEL
730	740	750	760	770	780	790	800
EGWAPSHYLV	LDENEQPDPS	GKELDTVPAK	GRQNEGKSDS	LEKIERRVQA	LNTVNQSKKA	TPPIPSKPPG	GFGKTSGTPA
810	820	830	840	850	860	870	880
VKMRNGVRQV	AVRPQSVFVS	PPPKDNNLSC	ALRRNESLTA	TDGLRGVRRN	SSFSTARSAA	AEAKGRLAER	AASQGSDSPL
890	900	910	920	930	940	950	960
LPAQRNSIPV	SPVRPKPIEK	SQFIHNNLKD	VYVSIADYEG	DEETAGFQEG	VSMEVLERNP	NGWWYCQILD	GVKPFKGWVP
970							
SNYLEKKN							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2762	1	665.3756	-3.39	2	64.9	10.3	1	768-779	R.VQALNTVNQSKK.A	

Detailed Protein Report

Protein 1302: ribosome biogenesis protein BOP1 [Homo sapiens]

Accession:	gi|21327667	**Score:**	10.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	83.6
Database Date:	2015-11-30	**pI:**	5.8
		Sequence Coverage [%]:	1.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAGSRGAGRT	AAPSVRPEKR	RSEPELEPEP	EPEPPLLCTS	PLSHSTGSDS	GVSDSEESVF	SGLEDSGSDS	SEDDDEGDEE
90	100	110	120	130	140	150	160
GEDGALDDEG	HSGIKKTTEE	QVQASTPCPR	TEMASARIGD	EYAEDSSDEE	DIRNTVGNVP	LEWYDDFPHV	GYDLDGRRIY
170	180	190	200	210	220	230	240
KPLRTRDELD	QFLDKMDDPD	YWRTVQDPMT	GRDLRLTDEQ	VALVRRLQSG	QFGDVGFNPY	EPAVDFFSGD	VMIHPVTNRP
250	260	270	280	290	300	310	320
ADKRSFIPSL	VEKEKVSRMV	HAIKMGWIQP	RRPRDPTPSF	YDLWAQEDPN	AVLGRHKMHV	PAPKLALPGH	AESYNPPPEY
330	340	350	360	370	380	390	400
LLSEEERLAW	EQQEPGERKL	SFLPRKFPSL	RAVPAYGRFI	QERFERCLDL	YLCPRQRKMR	VNVDPEDLIP	KLPRPRDLQP
410	420	430	440	450	460	470	480
FPTCQALVYR	GHSDLVRCLS	VSPGGQWLVS	GSDDGSLRLW	EVATARCVRT	VPVGGVVKSV	AWNPSPAVCL	VAAAVEDSVL
490	500	510	520	530	540	550	560
LLNPALGDRL	VAGSTDQLLS	AFVPPEEPPL	QPARWLEASE	EERQVGLRLR	ICHGKPVTQV	TWHGRGDYLA	VVLATQGHTQ
570	580	590	600	610	620	630	640
VLIHQLSRRR	SQSPFRRSHG	QVQRVAFHPA	RPFLLVASQR	SVRLYHLLRQ	ELTKKLMPNC	KWVSSLAVHP	AGDNVICGSY
650	660	670	680	690	700	710	720
DSKLVWFDLD	LSTKPYRMLR	HHKKALRAVA	FHPRYPLFAS	GSDDGSVIVC	HGMVYNDLLQ	NPLLVPVKVL	KGHVLTRDLG
730	740	750					
VLDVIFHPTQ	PWVFSSGADG	TVRLFT					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1359	1	649.4254	79.09	2	46.7	10.3	2	254-264	K.EKVSRMVHAIK.M	

Detailed Protein Report

Protein 1303: porphobilinogen deaminase isoform 4 [Homo sapiens]

Accession:	gi|384551656	**Score:**	10.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	33.2
Database Date:	2015-11-30	**pI:**	9.0
		Sequence Coverage [%]:	5.6
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MRVIRVGTRK SQLARIQTDS VVATLKASYP GLQFEIIAMS TTGDKILDTA LSKIGEKSLF TKELEHALEK NEVDLVVHSL
        90        100        110        120        130        140        150        160
KDLPTVLPPG FTIGAICKRE NPHDAVVFHP KFVGKTLETL PEKSVVGTSS LRRAAQLQRK FPHLEFRSIR GNLNTRLRKL
       170        180        190        200        210        220        230        240
DEQQEFSAII LATAGLQRMG WHNRVGQILH PEECMYAVGQ EGGCSVPVAV HTAMKDGQLY LTGGVWSLDG SDSIQETMQA
       250        260        270        280        290        300        310
TIHVPAQHED GPEDDPQLVG ITARNIPRGP QLAAQNLGIS LANLLLSKGA KNILDVARQL NDAH
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1460	1	620.0760	74.02	3	47.9	10.3	2	10-26	R.KSQLARIQTDSVVATLK.A	

Detailed Protein Report

Protein 1304: transcription factor HIVEP2 [Homo sapiens]

Accession:	gi|110347463	**Score:**	10.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	268.9
Database Date:	2015-11-30	**pI:**	6.5
		Sequence Coverage [%]:	0.7
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|530383649	refseq_human (refseq_human_20140103.fasta)	PREDICTED: transcription factor HIVEP2 isoform X2 [Homo sapiens]

10	20	30	40	50	60	70	80
MDTGDTALGQ	KATSRSGETD	KASGRWRQEQ	SAVIKMSTFG	SHEGQRQPQI	EPEQIGNTAS	AQLFGSGKLA	SPSEVVQQVA
90	100	110	120	130	140	150	160
EKQYPPHRPS	PYSCQHSLSF	PQHSLPQGVM	HSTKPHQSLE	GPPWLFPGPL	PSVASEDLFP	FPIHGHSGGY	PRKKISSLNP
170	180	190	200	210	220	230	240
AYSQYSQKSI	EQAEEAHKKE	HKPKKPGKYI	CPYCSRACAK	PSVLKKHIRS	HTGERPYPCI	PCGFSFKTKS	NLYKHRKSHA
250	260	270	280	290	300	310	320
HAIKAGLVPF	TESAVSKLDL	EAGFIDVEAE	IHSDGEQSTD	TDEESSLFAE	ASDKMSPGPP	IPLDIASRGG	YHGSLEESLG
330	340	350	360	370	380	390	400
GPMKVPILII	PKSGIPLPNE	SSQYIGPDML	PNPSLNTKAD	DSHTVKQKLA	LRLSEKKGQD	SEPSLNLLSP	HSKGSTDSGY
410	420	430	440	450	460	470	480
FSRSESAEQQ	ISPPNTNAKS	YEEIIFGKYC	RLSPRNALSV	TTTSQERAAM	GRKGIMEPLP	HVNTRLDVKM	FEDPVSQLIP
490	500	510	520	530	540	550	560
SKGDVDPSQT	SMLKSTKFNS	ESRQPQIIPS	SIRNEGKLYP	ANFQGSNPVL	LEAPVDSSPL	IRSNSVPTSS	ATNLTIPPSL
570	580	590	600	610	620	630	640
RGSHSFDERM	TGSDDVFYPG	TVGIPPQRML	RRQAAFELPS	VQEGHVEVEH	HGRMLKGISS	SSLKEKKLSP	GDRVGYDYDV
650	660	670	680	690	700	710	720
CRKPYKKWED	SETPKQNYRD	ISCLSSLKHG	GEYFMDPVVP	LQGVPSMFGT	TCENRKRRKE	KSVGDEEDTP	MICSSIVSTP
730	740	750	760	770	780	790	800
VGIMASDYDP	KLQMQEGVRS	GFAMAGHENL	SHGHTERFDP	CRPQLQPGSP	SLVSEESPSA	IDSDKMSDLG	GRKPPGNVIS
810	820	830	840	850	860	870	880
VIQHTNSLSR	PNSFERSESA	ELVACTQDKA	PSPSETCDSE	ISEAPVSPEW	APPGDGAESG	GKPSPSQQVQ	QQSYHTQPRL
890	900	910	920	930	940	950	960
VRQHNIQVPE	IRVTEEPDKP	EKEKEAQSKE	PEKPVEEFQW	PQRSETLSQL	PAEKLPPKKK	RLRLADMEHS	SGESSFESTG
970	980	990	1000	1010	1020	1030	1040
TGLSRSPSQE	SNLSHSSSFS	MSFEREETSK	LSALPKQDEF	GKHSEFLTVP	AGSYSLSVPG	HHHQKEMRRC	SSEQMPCPHP
1050	1060	1070	1080	1090	1100	1110	1120
AEVPEVRSKS	FDYGNLSHAP	VSGAAASTVS	PSRERKKCFL	VRQASFSGSP	EISQGEVGMD	QSVKQEQLEH	LHAGLRSGWH
1130	1140	1150	1160	1170	1180	1190	1200
HGPPAVLPPL	QQEDPGKQVA	GPCPPLSSGP	LHLAQPQIMH	MDSQESLRNP	LIQPTSYMTS	KHLPEQPHLF	PHQETIPFSP
1210	1220	1230	1240	1250	1260	1270	1280
IQNALFQFQY	PTVCMVHLPA	QQPPWWQAHF	PHPFAQHPQK	SYGKPSFQTE	IHSSYPLEHV	AEHTGKKPAE	YAHTKEQTYP
1290	1300	1310	1320	1330	1340	1350	1360
CYSGASGLHP	KNLLPKFPSD	QSSKSTETPS	EQVLQEDFAS	ANAGSLQSLP	GTVVPVRIQT	HVPSYGSVMY	TSISQILGQN
1370	1380	1390	1400	1410	1420	1430	1440
SPAIVICKVD	ENMTQRTLVT	NAAMQGIGFN	IAQVLGQHAG	LEKYPIWKAP	QTLPLGLESS	IPLCLPSTSD	SVATLGGSKR
1450	1460	1470	1480	1490	1500	1510	1520
MLSPASSLEL	FMETKQQKRV	KEEKMYGQIV	EELSAVELTN	SDIKKDLSRP	QKPQLVRQGC	ASEPKDGLQS	GSSSFSSLSP
1530	1540	1550	1560	1570	1580	1590	1600
SSSQDYPSVS	PSSREPFLPS	KEMLSGSRAP	LPGQKSSGPS	ESKESSDELD	IDETASDMSM	SPQSSSLPAG	DGQLEEEGKG
1610	1620	1630	1640	1650	1660	1670	1680
HKRPVGMLVR	MASAPSGNVA	DSTLLLTDMA	DFQQILQFPS	LRTTTTVSWC	FLNYTKPNYV	QQATFKSSVY	ASWCISSCNP
1690	1700	1710	1720	1730	1740	1750	1760
NPSGLNTKTT	LALLRSKQKI	TAEIYTLAAM	HRPGTGKLTS	SSAWKQFTQM	KPDASFLFGS	KLERKLVGNI	LKERGKGDIH
1770	1780	1790	1800	1810	1820	1830	1840
GDKDIGSKQT	EPIRIKIFEG	GYKSNEDYVY	VRGRGRGKYI	CEECGIRCKK	PSMLKKHIRT	HTDVRPYVCK	LCNFAFKTKG
1850	1860	1870	1880	1890	1900	1910	1920
NLTKHMKSKA	HMKKCLELGV	SMTSVDDTET	EEAENLEDLH	KAAEKHSMSS	ISTDHQFSDA	EESDGEDGDD	NDDDDEDEDD
1930	1940	1950	1960	1970	1980	1990	2000
FDDQGDLTPK	TRSRSTSPQP	PRFSSLPVNV	GAVPHGVPSD	SSLGHSSLIS	YLVTLPSIRV	TQLMTPSDSC	EDTQMTEYQR
2010	2020	2030	2040	2050	2060	2070	2080
LFQSKSTDSE	PDKDRLDIPS	CMDEECMLPS	EPSSSPRDFS	PSSHHSSPGY	DSSPCRDNSP	KRYLIPKGDL	SPRRHLSPRR
2090	2100	2110	2120	2130	2140	2150	2160
DLSPMRHLSP	RKEAALRREM	SQRDVSPRRH	LSPRRPVSPG	KDITARRDLS	PRRERRYMTT	IRAPSPRRAL	YHNPPLSMGQ
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2332	1	869.4368	43.79	2	59.0	10.3	0	1276-1291	K.EQTYPCYSGASGLHPK.N	

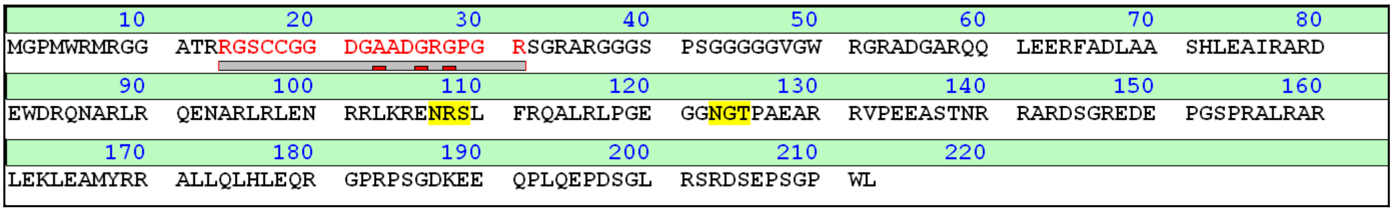
Detailed Protein Report

Protein 1305: tumor suppressor candidate gene 1 protein [Homo sapiens]

Accession:	gi|51944974	**Score:**	10.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	23.4
Database Date:	2015-11-30	**pI:**	11.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	8.5
		No. of unique Peptides:	1

Quantitation

MD:MU	**Median:** 1.30	**CV:** 0.00 %	**No. of 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	Ratios
1612	1	853.3687	3.55	2	49.9	10.3	2	14-31	R.RGSCCGGDGAADGRGPGR.S	Carbamidomethyl: 5	MD:MU 1.30

Detailed Protein Report

Protein 1306: **PREDICTED: LOW QUALITY PROTEIN: ubiquitin-conjugating enzyme E2 variant 1-like [Homo sapiens]**

Accession:	gi|578818188	**Score:**	10.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	15.9
Database Date:	2015-11-30	**pI:**	10.2
		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
997	1	932.4752	-21.83	3	42.0	10.3	2	0-0	.NTHLCKIVTKINTNGVDSSNVVVDPK.	

Detailed Protein Report

Protein 1307: **PREDICTED: receptor-type tyrosine-protein phosphatase U isoform X5 [Homo sapiens]**

Accession:	gi|578798179	**Score:**	10.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	132.6
Database Date:	2015-11-30	**pI:**	6.5
		Sequence Coverage [%]:	1.3
		No. of unique Peptides:	1

Quantitation

MD:MU	**Median:** 0.97	**CV:** 0.00 %	**No. of Peptides:** 1

10	20	30	40	50	60	70	80
MRSDLGVGAG	FEGDGQGQEP	PTPIAPPQLL	RAGPTYLIIQ	LNTNSIIGDG	PIVRKEIEYR	MARGPWAEVH	AVSLQTYKLW
90	100	110	120	130	140	150	160
HLDPDTEYEI	SVLLTRPGDG	GTGRPGPPLI	SRTKCAEPMR	APKGLAFAEI	QARQLTLQWE	PLGYNVTRCH	TYTVSLCYHY
170	180	190	200	210	220	230	240
TLGSSHNQTI	RECVKTEQGV	SRYTIKNLLP	YRNVHVRLVL	TNPEGRKEGK	EVTFQTDEDV	PSGIAAESLT	FTPLEDMIFL
250	260	270	280	290	300	310	320
KWEEPQEPNG	LITQYEISYQ	SIESSDPAVN	VPGPRRTISK	LRNETYHVFS	NLHPGTTYLF	SVRARTGKGF	GQAALTEITT
330	340	350	360	370	380	390	400
NISAPSFDYA	DMPSPLGESE	NTITVLLRPA	QGRGAPISVY	QVIVEEERAR	RLRREPGGQD	CFPVPLTFEA	ALARGLVHYF
410	420	430	440	450	460	470	480
GAELAASSLP	EAMPFTVGDN	QTYRGFWNPP	LEPRKAYLIY	FQAASHLKGE	TRLNCIRIAR	KAACKESKRP	LEVSQRSEEM
490	500	510	520	530	540	550	560
GLILGICAGG	LAVLILLLGA	IIVIIRKGKP	VNMTKATVNY	RQEKTHMMSA	VDRSFTDQST	LQEDERLGLS	FMDTHGYSTR
570	580	590	600	610	620	630	640
GDQRSGGVTE	ASSLLGGSPR	RPCGRKGSPY	HTGQLHPAVR	VADLLQHINQ	MKTAEGYGFK	QEYESFFEGW	DATKKKDKVK
650	660	670	680	690	700	710	720
GSRQEPMPAY	DRHRVKLHPM	LGDPNADYIN	ANYIDIRINR	EGYHRSNHFI	ATQGPKPEMV	YDFWRMVWQE	HCSSIVMITK
730	740	750	760	770	780	790	800
LVEVGRVKCS	RYWPEDSDTY	GDIKIMLVKT	ETLAEYVVRT	FALERRGYSA	RHEVRQFHFT	AWPEHGVPYH	ATGLLAFIRR
810	820	830	840	850	860	870	880
VKASTPPDAG	PIVIHCSAGT	GRTGCYIVLD	VMLDMAECEG	VVDIYNCVKT	LCSRRVNMIQ	TEEQYIFIHD	AILEACLCGE
890	900	910	920	930	940	950	960
TTIPVSEFKA	TYKEMIRIDP	QSNSSQLREE	FQTLNSVTPP	LDVEECSIAL	LPRNRDKNRS	MDVLPPDRCL	PFLISTDGDS
970	980	990	1000	1010	1020	1030	1040
NNYINAALTD	SYTRSAAFIV	TLHPLQSTTP	DFWRLVYDYG	CTSIVMLNQL	NQSNSAWPCL	QYWPEPGRQQ	YGLMEVEFMS
1050	1060	1070	1080	1090	1100	1110	1120
GTADEDLVAR	VFRVQNISRL	QEGHLLVRHF	QFLRWSAYRD	TPDSKKAFLH	LLAEVDKWQA	ESGDGRTIVH	CLNGGGRSGT
1130	1140	1150	1160	1170	1180		
FCACATVLEM	IRCHNLVDVF	FAAKTLRNYK	PNMVETMDQY	HFCYDVALEY	LEGLESR		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1388	1	844.8990	-55.98	2	47.0	10.3	0	354-368	R.GAPISVYQVIVEEER.A		MD:MU 0.97

Detailed Protein Report

Protein 1308: tectonin beta-propeller repeat-containing protein 1 [Homo sapiens]

Accession: gi|32698704

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Modification(s): Carbamidomethyl

Score: 10.3

MW [kDa]: 129.6

pI: 5.8

Sequence Coverage [%]: 1.3

No. of unique Peptides: 1

Alias proteins:

Accession	Name	Description
gi|530385707	refseq_human (refseq_human_20140103.fasta)	PREDICTED: tectonin beta-propeller repeat-containing protein 1 isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MPNSVLWAVD	LFGRVYTLST	AGQYWEMCKD	SQLEFKRVSA	TTQCCWGIAC	DNQVYVYVCA	SDVPIRRREE	AYENQRWNPM
90	100	110	120	130	140	150	160
GGFCEKLLLS	DRWGWSDVSG	LQHRPLDRVA	LPSPHWEWES	DWYVDENFGG	EPTEKGGWTY	AIDFPATYTK	DKKWNSCVRR
170	180	190	200	210	220	230	240
RKWIRYRRYK	SRDIWAKIPS	KDDPKELPDP	FNDLSVGGWE	ITEEPVGRLS	VWAVSLQGKV	WYREDVSHSN	PEGSSWSLLD
250	260	270	280	290	300	310	320
TPGEVVQISC	GPHDLLWATL	WEGQALVREG	INRSNPKGSS	WSIVEPPGSE	NGVMHISVGV	SVVWAVTKDW	KVWFRRGVNS
330	340	350	360	370	380	390	400
HNPCGTSWIE	MVGEMTMVNV	GMNDQVWGIG	CEDRAVYFRQ	GVTPSELSGK	TWKAIIAARE	CDRSHSGSSS	SLLSAGCFFG
410	420	430	440	450	460	470	480
DEVRGSGESA	PSDTDASSEV	ERPGPGQILP	AEPLDDSKNA	TGNSASGLGA	GRTAEDTVED	ACPAEGSREA	RPNTHPGPAP
490	500	510	520	530	540	550	560
TPAELPWTNI	DLKEAKKVPS	HSAAGFPETT	SLSSLGLLPL	GLEEPYGVDD	HPLWAWVSGG	GCVVEACAMP	RWFTVQAGLS
570	580	590	600	610	620	630	640
SSVHMLSLSI	TPAQTAAWRK	QIFQQLTERT	KRELENFRHY	EQAVEQSVWV	KTGALQWWCD	WKPHKWVDVR	LALEQFTGHD
650	660	670	680	690	700	710	720
GVRDSILFIY	YVVHEEKKYI	HIFLNEVVAL	VPVLNETKHS	FALYTPERTR	QRWPVRLAAA	TEQDMNDWLA	LLSLSCCESR
730	740	750	760	770	780	790	800
KVQGRPSPQA	IWSITCKGDI	FVSEPSPDLE	AHEHPLPCDQ	MFWRQMGGHL	RMVEANSRGV	VWGIGYDHTA	WVYTGGYGGG
810	820	830	840	850	860	870	880
CFQGLASSTS	NIYTQSDVKC	VHIYENQRWN	PVTGYTSRGL	PTDRYMWSDA	SGLQECTKAG	TKPPSLQWAW	VSDWFVDFSV
890	900	910	920	930	940	950	960
PGGTDQEGWQ	YASDFPASYH	GSKTMKDFVR	RRCWARKCKL	VTSGPWLEVP	PIALRDVSII	PESPGAEGSG	HSIALWAVSD
970	980	990	1000	1010	1020	1030	1040
KGDVLCRLGV	SELNPAGSSW	LHVGTDQPFA	SISIGACYQV	WAVARDGSAF	YRGSVYPSQP	AGDCWYHIPS	PPRQRLKQVS
1050	1060	1070	1080	1090	1100	1110	1120
AGQTSVYALD	ENGNLWYRQG	ITPSYPQGSS	WEHVSNNVCR	VSVGPLDQVW	VIANKVQGSH	SLSRGTVCHR	TGVQPHEPKG
1130	1140	1150	1160	1170			
HGWDYGIGGG	WDHISVRANA	TRAPRSSSQE	QEPSAPPEAH	GPVCC			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2289	1	840.8066	-136.06	2	58.5	10.3	1	1096-1110	K.VQGSHSLSRGTVCHR.T	Carbamidomethyl: 13

Detailed Protein Report

Protein 1309: THAP domain-containing protein 7 [Homo sapiens]

Accession:	gi|56788349	**Score:**	10.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	34.4
Database Date:	2015-11-30	**pI:**	10.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.9
		No. of unique Peptides:	1

Quantitation

MD:MU	**Median:**	2.07	**CV:**	0.00 %	**No. of Peptides:**	1

Alias proteins:

Accession	Name	Description
gi|56788351	refseq_human (refseq_human_20140103.fasta)	THAP domain-containing protein 7 [Homo sapiens]

10	20	30	40	50	60	70	80
MPRHCSAAGC	CTRDTRETRN	RGISFHRLPK	KDNPRRGLWL	ANCQRLDPSG	QGLWDPASEY	IYFCSKHFEE	DCFELVGISG
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
YHRLKEGAVP	TIFESFSKLR	RTTKTKGHSY	PPGPAEVSRL	RRCRKRCSEG	RGPTTPFSPP	PPADVTCFPV	EEASAPATLP
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
ASPAGRLEPG	LSSPFSDLLG	PLGAQADEAG	CSAQPSPERQ	PSPLEPRPVS	PSAYMLRLPP	PAGAYIQNEH	SYQVGSALLW
250	**260**	**270**	**280**	**290**	**300**	**310**	
KRRAEAALDA	LDKAQRQLQA	CKRREQRLRL	RLTKLQQERA	REKRAQADAR	QTLKEHVQDF	AMQLSSSMA	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
170	1	688.1530	-202.56	2	31.5	10.3	1	2-13	M.PRHCSAAGCCTR.D	Carbamidomethyl: 9, 10	MD:MU 2.07

Detailed Protein Report

Protein 1310: PREDICTED: phosphoglucomutase-2 isoform X1 [Homo sapiens]

Accession:	gi|578808564	**Score:**	10.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	53.0
Database Date:	2015-11-30	**pI:**	6.0
		Sequence Coverage [%]:	1.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSSQLILRPF	TVSHLKLCAG	IMITASHNPK	QDNGYKVYWD	NGAQIISPHD	KGISQAIEEN	LEPWPQAWDD	SLIDSSPLLH
90	100	110	120	130	140	150	160
NPSASINNDY	FEDLKKYCFH	RSVNRETKVK	FVHTSVHGVG	HSFVQSAFKA	FDLVPPEAVP	EQKDPDPEFP	TVKYPNPEEG
170	180	190	200	210	220	230	240
KGVLTLSFAL	ADKTKARIVL	ANDPDADRLA	VAEKQDSGEW	RVFSGNELGA	LLGWWLFTSW	KEKNQDRSAL	KDTYMLSSTV
250	260	270	280	290	300	310	320
SSKILRAIAL	KEGFHFEETL	TGFKWMGNRA	KQLIDQGKTV	LFAFEEAIGY	MCCPFVLDKD	GVSAAVISAE	LASFLATKNL
330	340	350	360	370	380	390	400
SLSQQLKAIY	VEYGYHITKA	SYFICHDQET	IKKLFENLRN	YDGKNNYPKA	CGKFEISAIR	DLTTGYDDSQ	PDKKAVLPTS
410	420	430	440	450	460	470	480
KSSQMITFTF	ANGGVATMRT	SGTEPKIKYY	AELCAPPGNS	DPEQLKKELN	ELVSAIEEHF	FQPQKYNLQP	KAD

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1347	1	497.6300	-225.67	2	46.5	10.3	1	365-373	K.NNYPKACGK.F	

Detailed Protein Report

Protein 1311: PREDICTED: tetraspanin-5 isoform X1 [Homo sapiens]

Accession:	gi|530377048	**Score:**	10.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	25.1
Database Date:	2015-11-30	**pI:**	4.5
		Sequence Coverage [%]:	5.5
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 0.27 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MSGKHYKGPE VSCCIKYFIF GFNVIFWFLG ITFLGIGLWA WNEKFSVFLG IIFFLELTAG VLAFVFKDWI KDQLYFFINN
        90        100        110        120        130        140        150        160
NIRAYRDDID LQNLIDFTQE YWQCCGAFGA DDWNLNIYFN CTDSNASRER CGVPFSCCTK DPAEDVINTQ CGYDARQKPE
       170        180        190        200        210        220
VDQQIVIYTK GCVPQFEKWL QDNLTIVAGI FIGIALLQIF GICLAQNLVS DIEAVRASW
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2405	1	665.1991	-138.24	2	60.4	10.3	1	129-140	R.ERCGVPFSCCTK.D		MD:MU 0.27

Detailed Protein Report

Protein 1312: keratin-associated protein 19-2 [Homo sapiens]

Accession:	gi|31791032	**Score:**	10.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	5.7
Database Date:	2015-11-30	**pI:**	9.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	36.5
		No. of unique Peptides:	1

```
        10         20         30         40         50         60
MCYGYGCGCG SFCRLGYGCG YEGCRYGCGH RGCGDGCCCP SCYRRYRFTG FY
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1176	1	704.1751	-100.37	3	44.4	10.3	1	26-44	R.YGCGHRGCGDGCCCPSCYR.R	Carbamidomethyl: 3, 17

Detailed Protein Report

Protein 1313: PREDICTED: zinc finger protein 197 isoform X2 [Homo sapiens]

Accession:	gi|578805510	**Score:**	10.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	96.1
Database Date:	2015-11-30	**pI:**	10.1
		Sequence Coverage [%]:	1.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MALMLLTAQP	QELVMFEEVS	VCFTSEEWAC	LGPIQRALYW	DVMLENYGNV	TSLEWETMTE	NEEVTSKPSS	SQRADSHKGT
90	100	110	120	130	140	150	160
SKRLQGSVPQ	VLDFEEECEW	QVLASQWGNE	TDERADTVKK	VSLCERDKKK	RTPPEKQGQK	WKELGDSLTF	GSAISESLIG
170	180	190	200	210	220	230	240
TEGKKFYKCD	MCCKHFNKIS	HLINHRRIHT	GEKPHKCKEC	GKGFIQRSSL	LMHLRNHSGE	KPYKCNECGK	AFSQSAYLLN
250	260	270	280	290	300	310	320
HQRIHTGEKP	YKCKECGKGF	YRHSGLIIHL	RRHSGERPYK	CNECGKVFSQ	NAYLIDHQRL	HKGEEPYKCN	KCQKAFILKK
330	340	350	360	370	380	390	400
SLILHQRIHS	GEKPYKCDEC	GKTFAQTTYL	IDHQRLHSAE	NPYKCKECGK	VFIRSKSLLL	HQRVHTEKKT	FGCKKCGKIF
410	420	430	440	450	460	470	480
SSKSNFIDHK	RMHSREKPYK	CTECGKAFTQ	SAYLFDHQRL	HNGEKPYECN	ECGKVFILKK	SLILHQRFHT	GENLYECKDC
490	500	510	520	530	540	550	560
GKVFGSNRNL	IDHERLHNGE	KPYECRECGK	TFIMSKSFMV	HQKLHTQEKA	YKCEDCGKAF	SYNSSLLVHR	RIHTGEKPFE
570	580	590	600	610	620	630	640
CSECGRAFSS	NRNLIEHKRI	HSGEKPYECD	ECGKCFILKK	SLIGHQRIHT	REKSYKCNDC	GKVFSYRSNL	IAHQRIHTGE
650	660	670	680	690	700	710	720
KPYACSECGK	GFTYNRNLIE	HQRIHSGEKT	YECHVCRKVL	TSSRNLMVHQ	RIHTGEKPYK	CNECGKDFSQ	NKNLVVHQRM
730	740	750	760	770	780	790	800
HTGEKPYECD	KCRKSFTSKR	NLVGHQRIHT	GEKPYGCNDC	SKVFRQRKNL	TVHQKIHTDE	KPCECDVSEK	EFSQTSNLHL
810	820	830					
QQKIHTIEEF	SWLQNTNESK	IEIQKI					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
926	1	539.7356	-166.84	2	41.1	10.3	2	312-320	K.CQKAFILKK.S	

Detailed Protein Report

Protein 1314: PREDICTED: EH domain-binding protein 1 isoform X4 [Homo sapiens]

Accession:	gi|530367409	**Score:**	10.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	108.6
Database Date:	2015-11-30	**pI:**	5.2
		Sequence Coverage [%]:	1.3
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 2.07 **CV:** 0.00 % **No. of Peptides:** 1

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	TEIVNQLNAL	SSLDEDQDDC	IKQANMRSAK
250	260	270	280	290	300	310	320
SASSSEELIN	KLNFLDEAEK	DLATVNSNPF	DDPDAAELNP	FGDPDSEEPI	TETASPRKTE	DSFYNNSYNP	FKEVQTPQYL
330	340	350	360	370	380	390	400
NPFDEPEAFV	TIKDSPPQST	KRKNIRPVDM	SKYLYADSSK	TEEEELDESN	PFYEPKSTPP	PNNLVNPVQE	LETERRVKRK
410	420	430	440	450	460	470	480
APAPPVLSPK	TGVLNENTVS	AGKDLSTSPK	PSPIPSPVLG	RKPNASQSLL	VWCKEVTKNY	RGVKITNFTT	SWRNGLSFCA
490	500	510	520	530	540	550	560
ILHHFRPDLI	DYKSLNPQDI	KENNKKAYDG	FASIGISRLL	EPSDMHRLLS	RQEELKERAR	VLLEQARRDA	ALKAGNKHNT
570	580	590	600	610	620	630	640
NTATPFCNRQ	LSDQQDEERR	RQLRERARQL	IAEARSGVKM	SELPSYGEMA	AEKLKERSKA	SGDENDNIEI	DTNEEIPEGF
650	660	670	680	690	700	710	720
VVGGGDELTN	LENDLDTPEQ	NSKLVDLKLK	KLLEVQPQVA	NSPSSAAQKA	VTESSEQDMK	SGTEDLRTER	LQKTTERFRN
730	740	750	760	770	780	790	800
PVVFSKDSTV	RKTQLQSFSQ	YIENRPEMKR	QRSIQEDTKK	GNEEKAAITE	TQRKPSEDEV	LNKGFKDTSQ	YVVGELAALE
810	820	830	840	850	860	870	880
NEQKQIDTRA	ALVEKRLRYL	MDTGRNTEEE	EAMMQEWFML	VNKKNALIRR	MNQLSLLEKE	HDLERRYELL	NRELRAMLAI
890	900	910	920	930	940	950	
EDWQKTEAQK	RREQLLLDEL	VALVNKRDAL	VRDLDAQEKQ	AEEEDEHLER	TLEQNKGKMA	KKEEKCVLQ	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
192	1	688.2999	-17.82	2	32.1	10.3	0	558-569	K.HNTNTATPFCNR.Q		MD:MU 2.07

Detailed Protein Report

Protein 1315: DNA helicase MCM9 isoform 2 [Homo sapiens]

Accession:	gi|23397546	**Score:**	10.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	44.0
Database Date:	2015-11-30	**pI:**	5.4
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	5.9
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MNSDQVTLVG QVFESYVSEY HKNDILLILK ERDEDAHYPV VVNAMTLFET NMEIGEYFNM FPSEVLTIFD SALRRSALTI
        90        100        110        120        130        140        150        160
LQSLSQPEAV SMKQNLHARI SGLPVCPELV REHIPKTKDV GHFLSVTGTV IRTSLVKVLE FERDYMCNKC KHVFVIKADF
       170        180        190        200        210        220        230        240
EQYYTFCRPS SCPSLESCDS SKFTCLSGLS SSPTRCRDYQ EIKIQEQVQR LSVGSIPRSM KVILEDDLVD SCKSGDDLTI
       250        260        270        280        290        300        310        320
YGIVMQRWKP FQQDVRCEVE IVLKANYIQV NNEQSSGIIM DEEVQKEFED FWEYYKSDPF AGRNVILASL CPQVFGMYLV
       330        340        350        360        370        380        390        400
KLAVAMVLAG GIQRTDATGT RVRGESHLLL VGDPGTGKSQ FLKYAAKITP RSVLTTGIGS TSAGIVCDNF K
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
754	1	859.6837	-112.34	3	38.8	10.3	2	211-233	R.LSVGSIPRSMKVILEDDLVDSCK.S	Carbamidomethyl: 22; Oxidation: 10

Detailed Protein Report

Protein 1316: voltage-dependent T-type calcium channel subunit alpha-1G isoform 14 [Homo sapiens]

Accession:	gi|38505268	**Score:**	10.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	240.8
Database Date:	2015-11-30	**pI:**	6.7
		Sequence Coverage [%]:	0.7
		No. of unique Peptides:	1

Quantitation

MD:MU	**Median:** 0.57	**CV:** 0.00 %	**No. of Peptides:** 1

Detailed Protein Report

```
        10         20         30         40         50         60         70         80
MDEEEDGAGA EESGQPRSFM RLNDLSGAGG RPGPGSAEKD PGSADSEAEG LPYPALAPVV FFYLSQDSRP RSWCLRTVCN
        90        100        110        120        130        140        150        160
PWFERISMLV ILLNCVTLGM FRPCEDIACD SQRCRILQAF DDFIFAFFAV EMVVKMVALG IFGKKCYLGD TWNRLDFFIV
       170        180        190        200        210        220        230        240
IAGMLEYSLD LQNVSFSAVR TVRVLRPLRA INRVPSMRIL VTLLLDTLPM LGNVLLLCFF VFFIFGIVGV QLWAGLLRNR
       250        260        270        280        290        300        310        320
CFLPENFSLP LSVDLERYYQ TENEDESPFI CSQPRENGMR SCRSVPTLRG DGGGGPPCGL DYEAYNSSSN TTCVNWNQYY
       330        340        350        360        370        380        390        400
TNCSAGEHNP FKGAINFDNI GYAWIAIFQV ITLEGWVDIM YFVMDAHSFY NFIYFILLII VGSFFMINLC LVVIATQFSE
       410        420        430        440        450        460        470        480
TKQRESQLMR EQRVRFLSNA STLASFSEPG SCYEELLKYL VYILRKAARR LAQVSRAAGV RVGLLSSPAP LGGQETQPSS
       490        500        510        520        530        540        550        560
SCSRSHRRLS VHHLVHHHHH HHHHYHLGNG TLRAPRASPE IQDRDANGSR RLMLPPPSTP ALSGAPPGGA ESVHSFYHAD
       570        580        590        600        610        620        630        640
CHLEPVRCQA PPPRSPSEAS GRTVGSGKVY PTVHTSPPPE TLKEKALVEV AASSGPPTLT SLNIPPGPYS SMHKLLETQS
       650        660        670        680        690        700        710        720
TGACQSSCKI SSPCLKADSG ACGPDSCPYC ARAGAGEVEL ADREMPDSDS EAVYEFTQDA QHSDLRDPHS RRQRSLGPDA
       730        740        750        760        770        780        790        800
EPSSVLAFWR LICDTFRKIV DSKYFGRGIM IAILVNTLSM GIEYHEQPEE LTNALEISNI VFTSLFALEM LLKLLVYGPF
       810        820        830        840        850        860        870        880
GYIKNPYNIF DGVIVVISVW EIVGQQGGGL SVLRTFRLMR VLKLVRFLPA LQRQLVVLMK TMDNVATFCM LLMLFIFIFS
       890        900        910        920        930        940        950        960
ILGMHLFGCK FASERDGDTL PDRKNFDSLL WAIVTVFQIL TQEDWNKVLY NGMASTSSWA ALYFIALMTF GNYVLFNLLV
       970        980        990       1000       1010       1020       1030       1040
AILVEGFQAE GDANKSESEP DFFSPSLDGD GDRKKCLALV SLGEHPELRK SLLPPLIIHT AATPMSLPKS TSTGLGEALG
      1050       1060       1070       1080       1090       1100       1110       1120
PASRRTSSSG SAEPGAAHEM KSPPSARSSP HSPWSAASSW TSRRSSRNSL GRAPSLKRRS PSGERRSLLS GEGQESQDEE
      1130       1140       1150       1160       1170       1180       1190       1200
ESSEEERASP AGSDHRHRGS LEREAKSSFD LPDTLQVPGL HRTASGRGSA SEHQDCNGKS ASGRLARALR PDDPPLDGDD
      1210       1220       1230       1240       1250       1260       1270       1280
ADDEGNLSKG ERVRAWIRAR LPACCLERDS WSAYIFPPQS RFRLLCHRII THKMFDHVVL VIIFLNCITI AMERPKIDPH
      1290       1300       1310       1320       1330       1340       1350       1360
SAERIFLTLS NYIFTAVFLA EMTVKVVALG WCFGEQAYLR SSWNVLDGLL VLISVIDILV SMVSDSGTKI LGMLRVLRLL
      1370       1380       1390       1400       1410       1420       1430       1440
RTLRPLRVIS RAQGLKLVVE TLMSSLKPIG NIVVICCAFF IIFGILGVQL FKGKFFVCQG EDTRNITNKS DCAEASYRWV
      1450       1460       1470       1480       1490       1500       1510       1520
RHKYNFDNLG QALMSLFVLA SKDGWVDIMY DGLDAVGVDQ QPIMNHNPWM LLYFISFLLI VAFFVLNMFV GVVVENFHKC
      1530       1540       1550       1560       1570       1580       1590       1600
RQHQEEEEAR RREEKRLRRL EKKRRSKEKQ MAEAQCKPYY SDYSRFRLLV HHLCTSHYLD LFITGVIGLN VVTMAMEHYQ
      1610       1620       1630       1640       1650       1660       1670       1680
QPQILDEALK ICNYIFTVIF VLESVFKLVA FGFRRFFQDR WNQLDLAIVL LSIMGITLEE IEVNASLPIN PTIIRIMRVL
      1690       1700       1710       1720       1730       1740       1750       1760
RIARVLKLLK MAVGMRALLD TVMQALPQVG NLGLLFMLLF FIFAALGVEL FGDLECDETH PCEGLGRHAT FRNFGMAFLT
      1770       1780       1790       1800       1810       1820       1830       1840
LFRVSTGDNW NGIMKDTLRD CDQESTCYNT VISPIYFVSF VLTAQFVLVN VVIAVLMKHL EESNKEAKEE AELEAELELE
      1850       1860       1870       1880       1890       1900       1910       1920
MKTLSPQPHS PLGSPFLWPG VEGPDSPDSP KPGALHPAAH ARSASHFSLE HPTMQPHPTE LPGPDLLTVR KSGVSRTHSL
      1930       1940       1950       1960       1970       1980       1990       2000
PNDSYMCRHG STAEGPLGHR GWGLPKAQSG SVLSVHSQPA DTSYILQLPK DAPHLLQPHS APTWGTIPKL PPPGRSPLAQ
      2010       2020       2030       2040       2050       2060       2070       2080
RPLRRQAAIR TDSLDVQGLG SREDLLAEEE PPSPRDLKKC YSVEAQSCQR RPTSWLDEQR RHSIAVSCLD SGSQPHLGTD
      2090       2100       2110       2120       2130       2140       2150       2160
PSNLGGQPLG GPGSRPKKKL SPPSITIDPP ESQGPRTPPS PGICLRRRAP SSDSKDPLAS GPPDSMAASP SPKKDVLSLS
      2170       2180
```

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
102	1	516.1595	-139.60	3	30.7	10.3	0	1046-1061	R.TSSSGSAEPGAAHEMK.S		MD:MU 0.57

Detailed Protein Report

Protein 1317: desmoglein-1 preproprotein [Homo sapiens]

Accession:	gi|119703744	**Score:**	10.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	113.7
Database Date:	2015-11-30	**pI:**	4.8
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	2.6
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MDWSFFRVVA MLFIFLVVVE VNSEFRIQVR DYNTKNGTIK WHSIRRQKRE WIKFAAACRE GEDNSKRNPI AKIHSDCAAN

        90        100        110        120        130        140        150        160
QQVTYRISGV GIDQPPYGIF VINQKTGEIN ITSIVDREVT PFFIIYCRAL NSMGQDLERP LELRVRVLDI NDNPPVFSMA

       170        180        190        200        210        220        230        240
TFAGQIEENS NANTLVMILN ATDADEPNNL NSKIAFKIIR QEPSDSPMFI INRNTGEIRT MNNFLDREQY GQYALAVRGS

       250        260        270        280        290        300        310        320
DRDGGADGMS AECECNIKIL DVNDNIPYME QSSYTIEIQE NTLNSNLLEI RVIDLDEEFS ANWMAVIFFI SGNEGNWFEI

       330        340        350        360        370        380        390        400
EMNERTNVGI LKVVKPLDYE AMQSLQLSIG VRNKAEFHHS IMSQYKLKAS AISVTVLNVI EGPVFRPGSK TYVVTGNMGS

       410        420        430        440        450        460        470        480
NDKVGDFVAT DLDTGRPSTT VRYVMGNNPA DLLAVDSRTG KLTLKNKVTK EQYNMLGGKY QGTILSIDDN LQRTCTGTIN

       490        500        510        520        530        540        550        560
INIQSFGNDD RTNTEPNTKI TTNTGRQEST SSTNYDTSTT STDSSQVYSS EPGNGAKDLL SDNVHFGPAG IGLLIMGFLV

       570        580        590        600        610        620        630        640
LGLVPFLMIC CDCGGAPRSA AGFEPVPECS DGAIHSWAVE GPQPEPRDIT TVIPQIPPDN ANIIECIDNS GVYTNEYGGR

       650        660        670        680        690        700        710        720
EMQDLGGGER MTGFELTEGV KTSGMPEICQ EYSGTLRRNS MRECREGGLN MNFMESYFCQ KAYAYADEDE GRPSNDCLLI

       730        740        750        760        770        780        790        800
YDIEGVGSPA GSVGCCSFIG EDLDDSFLDT LGPKFKKLAD ISLGKESYPD LDPSWPPQST EPVCLPQETE PVVSGHPPIS

       810        820        830        840        850        860        870        880
PHFGTTTVIS ESTYPSGPGV LHPKPILDPL GYGNVTVTES YTTSDTLKPS VHVHDNRPAS NVVVTERVVG PISGADLHGM

       890        900        910        920        930        940        950        960
LEMPDLRDGS NVIVTERVIA PSSSLPTSLT IHHPRESSNV VVTERVIQPT SGMIGSLSMH PELANAHNVI VTERVVSGAG

       970        980        990       1000       1010       1020       1030       1040
VTGISGTTGI SGGIGSSGLV GTSMGAGSGA LSGAGISGGG IGLSSLGGTA SIGHMRSSSD HHFNQTIGSA SPSTARSRIT

      1050
KYSTVQYSK
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1256	1	1018.4750	6.63	3	45.3	10.3	1	651-677	R.MTGFELTEGVKTSGMPEICQEYSGTLR.R	Carbamidomethyl: 19; Oxidation: 1, 15

Detailed Protein Report

Protein 1318: PREDICTED: cytochrome P450 2F1 isoform X2 [Homo sapiens]

Accession:	gi|578834042	**Score:**	10.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	50.6
Database Date:	2015-11-30	**pI:**	6.8
		Sequence Coverage [%]:	2.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDSISTAILL	LLLALVCLLL	TLSSRDKGKL	PPGPRPLSIL	GNLLLLCSQD	MLTSLTKLSK	EYGSMYTVHL	GPRRVVVLSG
90	100	110	120	130	140	150	160
YQAVKEALVD	QGEEFSGRGD	YPAFFNFTKG	NGIAFSSGDR	WKVLRQFSIQ	ILRNFGMGKR	SIEERILEEG	SFLLAELRKT
170	180	190	200	210	220	230	240
EGEPFDPTFV	LSRSVSNIIC	SVLFGSRFDY	DDERLLTIIR	LINDNFQIMS	SPWGELYDIF	PSLLDWVPGP	HQRIFQNFKC
250	260	270	280	290	300	310	320
LRDLIAHSVH	DHQASLDPRS	PRDFIQCFLT	KMAEEKEDPL	SHFHMDTLLM	TTHNLLFGGT	KTVSTTLHHA	FLALMKYPKV
330	340	350	360	370	380	390	400
QARVQEEIDL	VVGRARLPAL	KDRAAMPYTD	AVIHEVQRFA	DIIPMNLPHR	VTRDTAFRGF	LIPKGTDVIT	LLNTVHYDPS
410	420	430	440	450			
QFLTPQEFNP	EHFLDANQSF	KKSPAFMPFS	AALDAQRHSF	LLSTLLL			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
868	1	697.7757	-98.23	2	40.4	10.3	1	110-122	K.GNGIAFSSGDRWK.V	

Detailed Protein Report

Protein 1319: **UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 9 precursor [Homo sapiens]**

Accession:	gi|111160385	**Score:**	10.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	43.7
Database Date:	2015-11-30	**pI:**	10.1
		Sequence Coverage [%]:	6.5
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MRRRLRLRRD ALLTLLLGAS LGLLLYAQRD GAAPTASAPR GRGRAAPRPT PGPRAFQLPD AGAAPPAYEG DTPAPPTPTG
        90        100        110        120        130        140        150        160
PFDFARYLRA KDQRRFPLLI NQPHKCRGDG APGGRPDLLI AVKSVAEDFE RRQAVRQTWG AEGRVQGALV RRVFLLGVPR
       170        180        190        200        210        220        230        240
GAGSGGADEV GEGARTHWRA LLRAESLAYA DILLWAFDDT FFNLTLKEIH FLAWASAFCP DVRFVFKGDA DVFVNVGNLL
       250        260        270        280        290        300        310        320
EFLAPRDPAQ DLLAGDVIVH ARPIRTRASK YYIPEAVYGL PAYPAYAGGG GFVLSGATLH RLAGACAQVE LFPIDDVFLG
       330        340        350        360        370        380        390        400
MCLQRLRLTP EPHPAFRTFG IPQPSAAPHL STFDPCFYRE LVVVHGLSAA DIWLMWRLLH GPHGPACAHP QPVAAGPFQW
       410
DS
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1444	1	960.1132	-52.99	3	47.7	10.3	1	302-327	R.LAGACAQVELFPIDDVFLGMCLQRLR.L	

Protein 1320: PREDICTED: mediator of RNA polymerase II transcription subunit 14 isoform X3 [Homo sapiens]

Accession:	gi|530421646	**Score:**	10.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	148.5
Database Date:	2015-11-30	**pI:**	9.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	0.7
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MISSFLDQQA ILFVDTADRL ASLARDALVH ARLPSFAIPY AIDVLTTGSY PRLPTCIRDK IIPPDPITKI EKQATLHQLN
        90        100        110        120        130        140        150        160
QILRHRLVTT DLPPQLANLT VANGRVKFRV EGEFEATLTV MGDDPDVPWR LLKLEILVED KETGDGRALV HSMQISFIHQ
       170        180        190        200        210        220        230        240
LVQSRLFADE KPLQDMYNCL HSFCLSLQLE VLHSQTLMLI RERWGDLVQV ERYHAGKCLS LSVWNQQVLG RKTGTASVHK
       250        260        270        280        290        300        310        320
VTIKIDENDV SKPLQIFHDP PLPASDSKLV ERAMKIDHLS IEKLLIDSVH ARAHQKLQEL KAILRGFNAN ENSSIETALP
       330        340        350        360        370        380        390        400
ALVVPILEPC GNSECLHIFV DLHSGMFQLM LYGLDQATLD DMEKSVNDDM KRIIPWIQQL KFWLGQQRCK QSIKHLPTIS
       410        420        430        440        450        460        470        480
SETLQLSNYS THPIGNLSKN KLFIKLTRLP QYYIVVEMLE VPNKPTQLSY KYYFMSVNAA DREDSPAMAL LLQQFKENIQ
       490        500        510        520        530        540        550        560
DLVFRTKTGK QTRTNAKRKL SDDPCPVESK KTKRAGEMCA FNKVLAHFVA MCDTNMPFVG LRLELSNLEI PHQGVQVEGD
       570        580        590        600        610        620        630        640
GFSHAIRLLK IPPCKGITEE TQKALDRSLL DCTFRLQGRN NRTWVAELVF ANCPLNGTST REQGPSRHVY LTYENLLSEP
       650        660        670        680        690        700        710        720
VGGRKVVEMF LNDWNSIARL YECVLEFARS LPDIPAHLNI FSEVRVYNYR KLILCYGTTK GSSISIQWNS IHQKFHISLG
       730        740        750        760        770        780        790        800
TVGPNSGCSN CHNTILHQLQ EMFNKTPNVV QLLQVLFDTQ APLNAINKLP TVPMLGLTQR TNTAYQCFSI LPQSSTHIRL
       810        820        830        840        850        860        870        880
AFRNMYCIDI YCRSRGVVAI RDGAYSLFDN SKLVEGFYPA PGLKTFLNMF VDSNQDARRR SVNEDDNPPS PIGGDMMDSL
       890        900        910        920        930        940        950        960
ISQLQPPPQQ QPFPKQPGTS GAYPLTSPPT SYHSTVNQSP SMMHTQSPGN LHAASSPSGA LRAPSPASFV PTPPPSSHGI
       970        980        990       1000       1010       1020       1030       1040
SIGPGASFAS PHGTLDPSSP YTMVSPSGRA GNWPGSPQVS GPSPAARMPG MSPANPSLHS PVPDASHSPR AGTSSQTMPT
      1050       1060       1070       1080       1090       1100       1110       1120
NMPPPRKLPQ RSWAASIPTI LTHSALNILL LPSPTPGLVP GLAGSYLCSP LERFLGSVIM RRHLQRIIQQ ETLQLINSNE
      1130       1140       1150       1160       1170       1180       1190       1200
PGVIMFKTDA LKCRVALSPK TNQTLQLKVT PENAGQWKPD ELQVLEKFFE TRVAGPPFKA NTLIAFTKLL GAPTHILRDC
      1210       1220       1230       1240       1250       1260       1270       1280
VHIMKLELFP DQATQLKWNV QFCLTIPPSA PPIAPPGTPA VVLKSKMLFF LQLTQKTSVP PQEPVSIIVP IIYDMASGTT
      1290       1300       1310       1320       1330       1340
QQADIPRQQN SSVAAPMMVS NILKRFAEMN PPRQGECTIF AAVRDLMANL TLPPGGRP
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
623	1	675.6771	-160.57	2	37.1	10.3	0	804-813	R.NMYCIDIYCR.S	Carbamidomethyl: 9

Detailed Protein Report

Protein 1321: neuroendocrine convertase 1 isoform 3 [Homo sapiens]

Accession:	gi|295424145	**Score:**	10.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	49.3
Database Date:	2015-11-30	**pI:**	5.3
		Sequence Coverage [%]:	2.3
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MLDGIVTDAI EASSIGFNPG HVDIYSASWG PNDDGKTVEG PGRLAQKAFE YGVKQTSADL HNDCTETHTG TSASAPLAAG
        90        100        110        120        130        140        150        160
IFALALEANP NLTWRDMQHL VVWTSEYDPL ANNPGWKKNG AGLMVNSRFG FGLLNAKALV DLADPRTWRS VPEKKECVVK
       170        180        190        200        210        220        230        240
DNDFEPRALK ANGEVIIEIP TRACEGQENA IKSLEHVQFE ATIEYSRRGD LHVTLTSAAG TSTVLLAERE RDTSPNGFKN
       250        260        270        280        290        300        310        320
WDFMSVHTWG ENPIGTWTLR ITDMSGRIQN EGRIVNWKLI LHGTSSQPEH MKQPRVYTSY NTVQNDRRGV EKMVDPGEEQ
       330        340        350        360        370        380        390        400
PTQENPKENT LVSKSPSSSS VGGRRDELEE GAPSQAMLRL LQSAFSKNSP PKQSPKKSPS AKLNIPYENF YEALEKLNKP
       410        420        430        440        450
SQLKDSEDSL YNDYVDVFYN TKPYKHRDDR LLQALVDILN EEN
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1440	1	1018.7851	270.23	1	47.7	10.3	0	119-128	K.NGAGLMVNSR.F	

Detailed Protein Report

Protein 1322: sodium/hydrogen exchanger 4 precursor [Homo sapiens]

Accession:	gi|148727259	**Score:**	10.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	89.8
Database Date:	2015-11-30	**pI:**	9.4
		Sequence Coverage [%]:	1.5
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|530368639	refseq_human (refseq_human_20140103.fasta)	PREDICTED: sodium/hydrogen exchanger 4 isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MALQMFVTYS	PWNCLLLLVA	LECSEASSDL	NESANSTAQY	ASNAWFAAAS	SEPEEGISVF	ELDYDYVQIP	YEVTLWILLA
90	100	110	120	130	140	150	160
SLAKIGFHLY	HRLPGLMPES	CLLILVGALV	GGIIFGTDHK	SPPVMDSSIY	FLYLLPPIVL	EGGYFMPTRP	FFENIGSILW
170	180	190	200	210	220	230	240
WAVLGALINA	LGIGLSLYLI	CQVKAFGLGD	VNLLQNLLFG	SLISAVDPVA	VLAVFEEARV	NEQLYMMIFG	EALLNDGITV
250	260	270	280	290	300	310	320
VLYNMLIAFT	KMHKFEDIET	VDILAGCARF	IVVGLGGVLF	GIVFGFISAF	ITRFTQNISA	IEPLIVFMFS	YLSYLAAETL
330	340	350	360	370	380	390	400
YLSGILAITA	CAVTMKKYVE	ENVSQTSYTT	IKYFMKMLSS	VSETLIFIFM	GVSTVGKNHE	WNWAFICFTL	AFCQIWRAIS
410	420	430	440	450	460	470	480
VFALFYISNQ	FRTFPFSIKD	QCIIFYSGVR	GAGSFSLAFL	LPLSLFPRKK	MFVTATLVVI	YFTVFIQGIT	VGPLVRYLDV
490	500	510	520	530	540	550	560
KKTNKKESIN	EELHIRLMDH	LKAGIEDVCG	HWSHYQVRDK	FKKFDHRYLR	KILIRKNLPK	SSIVSLYKKL	EMKQAIEMVE
570	580	590	600	610	620	630	640
TGILSSTAFS	IPHQAQRIQG	IKRLSPEDVE	SIRDILTSNM	YQVRQRTLSY	NKYNLKPQTS	EKQAKEILIR	RQNTLRESMR
650	660	670	680	690	700	710	720
KGHSLPWGKP	AGTKNIRYLS	YPYGNPQSAG	RDTRAAGFSD	DDSSDPGSPS	ITFSACSRIG	SLQKQEAQEI	IPMKSLHRGR
730	740	750	760	770	780	790	800
KAFSFGYQRN	TSQEEYLGGV	RRVALRPKPL	FHAVDEEGES	GGESEGKASL	VEVRSRWTAD	HGHGRDHHRS	HSPLLQKK

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
534	1	451.4647	-195.32	3	36.3	10.3	0	730-741	R.NTSQEEYLGGVR.R	

Detailed Protein Report

Protein 1323: PREDICTED: nuclear receptor subfamily 4 group A member 2 isoform X2 [Homo sapiens]

Accession:	gi|530370487	**Score:**	10.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	59.8
Database Date:	2015-11-30	**pI:**	9.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.6
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530370489	refseq_human (refseq_human_20140103.fasta)	PREDICTED: nuclear receptor subfamily 4 group A member 2 isoform X3 [Homo sapiens]

10	20	30	40	50	60	70	80
MDNYSTGYDV	KPPCLYQMPL	SGQQSSIKVE	DIQMHNYQQH	SHLPPQSEEM	MPHSGSVYYK	PSSPPTPTTP	GFQVQHSPMW
90	100	110	120	130	140	150	160
DDPGSLHNFH	QNYVATTHMI	EQRKTPVSRL	SLFSFKQSPP	GTPVSSCQMR	FDGPLHVPMN	PEPAGSHHVV	DGQTFAVPNP
170	180	190	200	210	220	230	240
IRKPASMGFP	GLQIGHASQL	LDTQVPSPPS	RGSPSNEGLC	AVCGDNAACQ	HYGVRTCEGC	KGFFKRTVQK	NAKYVCLANK
250	260	270	280	290	300	310	320
NCPVDKRRRN	RCQYCRFQKC	LAVGMVKEVV	RTDSLKGRRG	RLPSKPKSPQ	EPSPPSPPVS	LISALVRAHV	DSNPAMTSLD
330	340	350	360	370	380	390	400
YSRFQANPDY	QMSGDDTQHI	QQFYDLLTGS	MEIIRGWAEK	IPGFADLPKA	DQDLLFESAF	LELFVLRLAY	RSNPVEGKLI
410	420	430	440	450	460	470	480
FCNGVVLHRL	QCVRGFGEWI	DSIVEFSSNL	QNMNIDISAF	SCIAALAMVT	ERHGLKEPKR	VEELQNKIVN	CLKDHVTFNN
490	500	510	520	530	540		
GGLNRPNYLS	KLLGKLPELR	TLCTQGLQRI	FYLKLEDLVP	PPAIIDKLFL	DTLPF		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1642	1	745.6928	-197.27	2	50.4	10.3	0	117-130	K.QSPPGTPVSSCQMR.F	Oxidation: 13

Detailed Protein Report

Protein 1324: 60S ribosomal protein L23 [Homo sapiens]

Accession:	gi|4506605	**Score:**	10.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	14.9
Database Date:	2015-11-30	**pI:**	11.2
Modification(s):	Oxidation	**Sequence Coverage [%]:**	14.3
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MSKRGRGGSS GAKFRISLGL PVGAVINCAD NTGAKNLYII SVKGIKGRLN RLPAAGVGDM VMATVKKGKP ELRKKVHPAV
        90        100        110        120        130        140        150
VIRQRKSYRR KDGVFLYFED NAGVIVNNKG EMKGSAITGP VAKECADLWP RIASNAGSIA
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2050	1	1044.4446	-106.91	2	55.5	10.3	2	47-66	K.GRLNRLPAAGVGDMVMATVK.K	Oxidation: 14, 16

Detailed Protein Report

Protein 1325: **serine/threonine-protein phosphatase 6 regulatory ankyrin repeat subunit C [Homo sapiens]**

Accession:	gi|157743284	**Score:**	10.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	115.0
Database Date:	2015-11-30	**pI:**	6.0
		Sequence Coverage [%]:	1.0
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 1.31 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MGILSITDQP	PLVQAIFSRD	VEEVRSLLSQ	KENINVLDQE	RRTPLHAAAY	VGDVPILQLL	LMSGANVNAK	DTLWLTPLHR
90	100	110	120	130	140	150	160
AAASRNEKVL	GLLLAHSADV	NARDKLWQTP	LHVAAANRAT	KCAEALAPLL	SSLNVADRSG	RSALHHAVHS	GHLETVNLLL
170	180	190	200	210	220	230	240
NKGASLNVCD	KKERQPLHWA	AFLGHLEVLK	LLVARGADLG	CKDRKGYGLL	HTAAASGQIE	VVKYLLRMGA	EIDEPNAFGN
250	260	270	280	290	300	310	320
TALHIACYLG	QDAVAIELVN	AGANVNQPND	KGFTPLHVAA	VSTNGALCLE	LLVNNGADVN	YQSKEGKSPL	HMAAIHGRFT
330	340	350	360	370	380	390	400
RSQILIQNGS	EIDCADKFGN	TPLHVAARYG	HELLISTLMT	NGADTARRGI	HDMFPLHLAV	LFGFSDCCRK	LLSSGQLYSI
410	420	430	440	450	460	470	480
VSSLSNEHVL	SAGFDINTPD	NLGRTCLHAA	ASGGNVECLN	LLLSSGADLR	RRDKFGRTPL	HYAAANGSYQ	CAVTLVTAGA
490	500	510	520	530	540	550	560
GVNEADCKGC	SPLHYAAASD	TYRRAEPHTP	SSHDAEEDEP	LKESRRKEAF	FCLEFLLDNG	ADPSLRDRQG	YTAVHYAAAY
570	580	590	600	610	620	630	640
GNRQNLELLL	EMSFNCLEDV	ESTIPVSPLH	LAAYNGHCEA	LKTLAETLVN	LDVRDHKGRT	ALFLATERGS	TECVEVLTAH
650	660	670	680	690	700	710	720
GASALIKERK	RKWTPLHAAA	ASGHTDSLHL	LIDSGERADI	TDVMDAYGQT	PLMLAIMNGH	VDCVHLLLEK	GSTADAADLR
730	740	750	760	770	780	790	800
GRTALHRGAV	TGCEDCLAAL	LDHDAFVLCR	DFKGRTPIHL	ASACGHTAVL	RTLLQAALST	DPLDAGVDYS	GYSPMHWASY
810	820	830	840	850	860	870	880
TGHEDCLELL	LEHSPFSYLE	GNPFTPLHCA	VINNQDSTTE	MLLGALGAKI	VNSRDAKGRT	PLHAAAFADN	VSGLRMLLQH
890	900	910	920	930	940	950	960
QAEVNATDHT	GRTALMTAAE	NGQTAAVEFL	LYRGKADLTV	LDENKNTALH	LACSKGHEKC	ALMILAETQD	LGLINATNSA
970	980	990	1000	1010	1020	1030	1040
LQMPLHIAAR	NGLASVVQAL	LSHGATVLAV	DEEGHTPALA	CAPNKDVADC	LALILSTMKP	FPPKDAVSPF	SFSLLKNCSI
1050	1060	1070	1080				
AAAKTVGGCG	ALPHGASCPY	SQERPGAIGL	DGCYSE				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
276	1	591.6792	-242.16	2	32.8	10.3	0	338-348	K.FGNTPLHVAAR.Y		MD:MU 1.31

Detailed Protein Report

Protein 1326: PREDICTED: TANK-binding kinase 1-binding protein 1 isoform X5 [Homo sapiens]

Accession:	gi|578831704	**Score:**	10.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	67.6
Database Date:	2015-11-30	**pI:**	5.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MESMFEDDIS	ILTQEALGPS	EVWLDSPGDP	SLGGDMCSAS	HFALITAYGD	IKERLGGLER	ENATLRRRLK	VYEIKYPLIS
90	100	110	120	130	140	150	160
DFGEEHGFSL	YEIKDGSLLE	VEKVSLQQRL	NQFQHELQKN	KEQEEQLGEM	IQAYEKLCVE	KSDLETELRE	MRALVETHLR
170	180	190	200	210	220	230	240
QICGLEQQLR	QQQGLQDAAF	SNLSPPPAPA	PPCTDLDLHY	LALRGGSGLS	HGWPGSTPSV	SDLERRRLEE	ALEAAQGEAR
250	260	270	280	290	300	310	320
GAQLREEQLQ	AECERLQGEL	KQLQETRAQD	LASNQSERDM	AWVKRVGDDQ	VNLALAYTEL	TEELGRLREL	SSLQGRILRT
330	340	350	360	370	380	390	400
LLQEQARSGG	QRHSPLSQRH	SPAPQCPSPS	PPARAAPPCP	PCQSPVPQRR	SPVPPCPSPQ	QRRSPASPSC	PSPVPQRRSP
410	420	430	440	450	460	470	480
VPPSCQSPSP	QRRSPVPPSC	PAPQPRPPPP	PPPGERTLAE	RAYAKPPSHH	VKAGFQGRRS	YSELAEGAAY	AGASPPWLQA
490	500	510	520	530	540	550	560
EAATLPKPRA	YGSELYGPGR	PLSPRRAFEG	IRLRFEKQPS	EEDEWAVPTS	PPSPEVGTIR	CASFCAGFPI	PESPAATAYA
570	580	590	600	610	620		
HAEHAQSWPS	INLLMETVGS	DIRSCPLCQL	GFPVGYPDDA	LIKHIDSHLE	NSKI		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2713	1	840.4021	-18.66	2	64.2	10.3	1	398-412	R.RSPVPPSCQSPSPQR.R	Carbamidomethyl: 8

Detailed Protein Report

Protein 1327: PREDICTED: potassium channel subfamily T member 2 isoform X3 [Homo sapiens]

Accession:	gi|578800878	**Score:**	10.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	85.7
Database Date:	2015-11-30	**pI:**	7.3
		Sequence Coverage [%]:	1.6
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 2.06 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MFSRQDHQTI	LRAWAVKDFA	PNCPLYVQIL	KPENKFHIKF	ADHVVCEEEF	KYAMLALNCI	CPATSTLITL	LVHTSRGQEG
90	100	110	120	130	140	150	160
QQSPEQWQKM	YGRCSGNEVY	HIVLEESTFF	AEYEGKSFTY	ASFHAHKKFG	VCLIGVRRED	NKNILLNPGP	RYIMNSTDIC
170	180	190	200	210	220	230	240
FYINITKEEN	SAFKNQDQQR	KSNVSRSFYH	GPSRLPVHSI	IASMGTVAID	LQDTSCRSAS	GPTLSLPTEG	SKEIRRPSIA
250	260	270	280	290	300	310	320
PVLEVADTSS	IQTCDLLSDQ	SEDETTPDEE	MSSNLEYAKG	YPPYSPYIGS	SPTFCHLLHE	KVPFCCLRLD	KSCQHNYYED
330	340	350	360	370	380	390	400
AKAYGFKNKL	IIVAAETAGN	GLYNFIVPLR	AYYRPKKELN	PIVLLLDNPP	DMHFLDAICW	FPMVYYMVGS	IDNLDDLLRC
410	420	430	440	450	460	470	480
GVTFAANMVV	VDKESTMSAE	EDYMADAKTI	VNVQTLFRLF	SSLSIITELT	HPANMRFMQF	RAKDCYSLAL	SKLEKKERER
490	500	510	520	530	540	550	560
GSNLAFMFRL	PFAAGRVFSI	SMLDTLLYQS	FVKDYMISIT	RLLLGLDTTP	GSGFLCSMKI	TADDLWIRTY	ARLYQKLCSS
570	580	590	600	610	620	630	640
TGDVPIGIYR	TESQKLTTSE	SRKIASQSQI	SISVEEWEDT	KDSKEQGHHR	SNHRNSTSSD	QSDHPLLRRK	SMQWARRLSR
650	660	670	680	690	700	710	720
KGPKHSGKTA	EKITQQRLNL	YRRSERQELA	ELVKNRMKHL	GLSTVGYDEM	NDHQSTLSYI	LINPSPDTRI	ELNDVVYLIR
730	740	750	760				
PDPLAYLPNS	EPSRRNSICN	VTGQDSREET	QL				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2024	1	766.2746	-155.24	2	55.2	10.3	1	1-12	-.MFSRQDHQTILR.A		MD:MU 2.06

Detailed Protein Report

Protein 1328: OCIA domain-containing protein 1 isoform 3 [Homo sapiens]

Accession:	gi|119874209	**Score:**	10.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	20.7
Database Date:	2015-11-30	**pI:**	8.9
		Sequence Coverage [%]:	7.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MNGRADFREP	NAEVPRPIPH	IGPDYIPTEE	ERRVFAECND	ESFWFRSVPL	AATSMLITQG	LISKGILSSH	PKYGSIPKLI
90	100	110	120	130	140	150	160
LACIMGYFAG	KLSYVKTCQE	KFKKLENSPL	GEALRSGQAR	RSSPPGHYYQ	KSKYDSSVSG	QSSFVTSPAA	DNIEMLPHYE
170	180	190					
PIPFSSSMNE	SAPTGITDHI	VQGRNFS					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2534	1	742.5453	172.78	2	62.1	10.2	1	65-78	K.GILSSHPKYGSIPK.L	

Detailed Protein Report

Protein 1329: mitochondrial import receptor subunit TOM70 [Homo sapiens]

Accession: gi|54607135
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 10.2
MW [kDa]: 67.4
pI: 6.9
Sequence Coverage [%]: 3.3
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MAASKPVEAA	VVAAAVPSSG	SGVGGGGTAG	PGTGGLPRWQ	LALAVGAPLL	LGAGAIYLWS	RQQRRREARG	RGDASGLKRN
90	100	110	120	130	140	150	160
SERKTPEGRA	SPAPGSGHPE	GPGAHLDMNS	LDRAQAAKNK	GNKYFKAGKY	EQAIQCYTEA	ISLCPTEKNV	DLSTFYQNRA
170	180	190	200	210	220	230	240
AAFEQLQKWK	EVAQDCTKAV	ELNPKYVKAL	FRRAKAHEKL	DNKKECLEDV	TAVCILEGFQ	NQQSMLLADK	VLKLLGKEKA
250	260	270	280	290	300	310	320
KEKYKNREPL	MPSPQFIKSY	FSSFTDDIIS	QPMLKGEKSD	EDKDKEGEAL	EVKENSGYLK	AKQYMEEENY	DKIISECSKE
330	340	350	360	370	380	390	400
IDAEGKYMAE	ALLLRATFYL	LIGNANAAKP	DLDKVISLKE	ANVKLRANAL	IKRGSMYMQQ	QQPLLSTQDF	NMAADIDPQN
410	420	430	440	450	460	470	480
ADVYHHRGQL	KILLDQVEEA	VADFDECIRL	RPESALAQAQ	KCFALYRQAY	TGNNSSQIQA	AMKGFEEVIK	KFPRCAEGYA
490	500	510	520	530	540	550	560
LYAQALTDQQ	QFGKADEMYD	KCIDLEPDNA	TTYVHKGLLQ	LQWKQDLDRG	LELISKAIEI	DNKCDFAYET	MGTIEVQRGN
570	580	590	600	610			
MEKAIDMFNK	AINLAKSEME	MAHLYSLCDA	AHAQTEVAKK	YGLKPPTL			

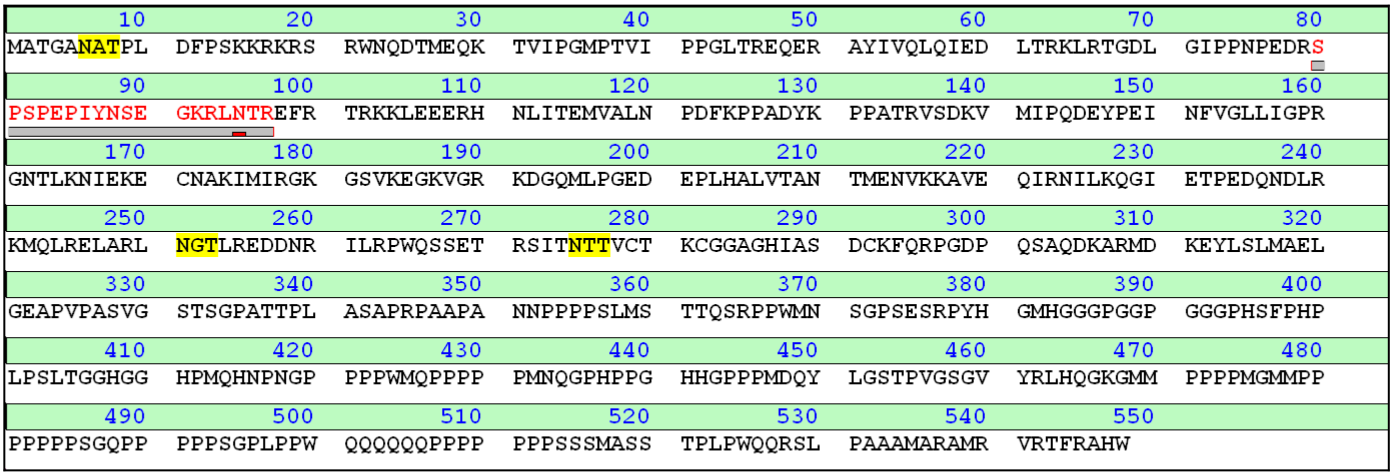
Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2380	1	1103.1407	111.53	2	60.1	10.2	0	475-494	R.CAEGYALYAQALTDQQQFGK.A	

Detailed Protein Report

Protein 1330: splicing factor 1 isoform 3 [Homo sapiens]

Accession: gi|42544123
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 10.2
MW [kDa]: 59.7
pI: 10.1
Sequence Coverage [%]: 3.3
No. of unique Peptides: 1



10	20	30	40	50	60	70	80
MATGANATPL	DFPSKKRKRS	RWNQDTMEQK	TVIPGMPTVI	PPGLTREQER	AYIVQLQIED	LTRKLRTGDL	GIPPNPEDRS
90	100	110	120	130	140	150	160
PSPEPIYNSE	GKRLNTREFR	TRKKLEEERH	NLITEMVALN	PDFKPPADYK	PPATRVSDKV	MIPQDEYPEI	NFVGLLIGPR
170	180	190	200	210	220	230	240
GNTLKNIEKE	CNAKIMIRGK	GSVKEGKVGR	KDGQMLPGED	EPLHALVTAN	TMENVKKAVE	QIRNILKQGI	ETPEDQNDLR
250	260	270	280	290	300	310	320
KMQLRELARL	NGTLREDDNR	ILRPWQSSET	RSITNTTVCT	KCGGAGHIAS	DCKFQRPGDP	QSAQDKARMD	KEYLSLMAEL
330	340	350	360	370	380	390	400
GEAPVPASVG	STSGPATTPL	ASAPRPAAPA	NNPPPPSLMS	TTQSRPPWMN	SGPSESRPYH	GMHGGGPGGP	GGGPHSFPHP
410	420	430	440	450	460	470	480
LPSLTGGHGG	HPMQHNPNGP	PPPWMQPPPP	PMNQGPHPPG	HHGPPPMDQY	LGSTPVGSGV	YRLHQGKGMM	PPPPMGMMPP
490	500	510	520	530	540	550	
PPPPPSGQPP	PPPSGPLPPW	QQQQQQPPPP	PPPSSSMASS	TPLPWQQRSL	PAAAMARAMR	VRTFRAHW	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1835	1	1022.8888	-132.35	2	53.0	10.2	2	80-97	R.SPSPEPIYNSEGKRLNTR.E	

Detailed Protein Report

Protein 1331: regulator of G-protein signaling 4 isoform 4 [Homo sapiens]

Accession:	gi|164664490	**Score:**	10.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	10.5
Database Date:	2015-11-30	**pI:**	9.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	18.3
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MCKGLAGLPA SCLRSAKDMK HRLGFLLQKS DSCEHNSSHN KKDKVVICQR VSQEEVKKWA ESLENLISHE CEPGFLHQGR
        90        100
DKPEHARAYN NLL
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
388	1	588.2883	-35.27	3	34.5	10.2	2	1-17	-.MCKGLAGLPASCLRSAK.D	Carbamidomethyl: 12

Detailed Protein Report

Protein 1332: uncharacterized protein LOC400863 [Homo sapiens]

Accession:	gi|572871229	**Score:**	10.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	14.6
Database Date:	2015-11-30	**pI:**	5.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	10.4
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MGTVIPHSPC GESGRAPDGW PKAAQRRSCE EEASGGSESR REPTCGCLSN SRRTWAAGSG VGEKQVDLEV LLQVERKGEF
        90        100        110        120        130        140
CKMLWGPLSS AAEAQLFLWL LLEQPVDQDV AHATPYIRSP FSDALSQLFA CTHL
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
930	1	770.6913	-164.74	2	41.2	10.2	1	27-40	R.RSCEEEASGGSESR.R	Carbamidomethyl: 3

Detailed Protein Report

Protein 1333: histone deacetylase 1 [Homo sapiens]

Accession:	gi|13128860	**Score:**	10.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	55.1
Database Date:	2015-11-30	**pI:**	5.2
		Sequence Coverage [%]:	2.7
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 0.71 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MAQTQGTRRK VCYYYDGDVG NYYYGQGHPM KPHRIRMTHN LLLNYGLYRK MEIYRPHKAN AEEMTKYHSD DYIKFLRSIR

        90        100        110        120        130        140        150        160
PDNMSEYSKQ MQRFNVGEDC PVFDGLFEFC QLSTGGSVAS AVKLNKQQTD IAVNWAGGLH HAKKSEASGF CYVNDIVLAI

       170        180        190        200        210        220        230        240
LELLKYHQRV LYIDIDIHHG DGVEEAFYTT DRVMTVSFHK YGEYFPGTGD LRDIGAGKGK YYAVNYPLRD GIDDESYEAI

       250        260        270        280        290        300        310        320
FKPVMSKVME MFQPSAVVLQ CGSDSLSGDR LGCFNLTIKG HAKCVEFVKS FNLPMLMLGG GGYTIRNVAR CWTYETAVAL

       330        340        350        360        370        380        390        400
DTEIPNELPY NDYFEYFGPD FKLHISPSNM TNQNTNEYLE KIKQRLFENL RMLPHAPGVQ MQAIPEDAIP EESGDEDEDD

       410        420        430        440        450        460        470        480
PDKRISICSS DKRIACEEEF SDSEEEGEGG RKNSSNFKKA KRVKTEDEKE KDPEEKKEVT EEEKTKEEKP EAKGVKEEVK

       490
LA
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
248	1	795.3819	1.58	2	32.5	10.2	2	452-464	K.DPEEKKEVTEEEK.T		MD:MU 0.71

Detailed Protein Report

Protein 1334: kelch-like protein 4 isoform 1 [Homo sapiens]

Accession:	gi|17017982	**Score:**	10.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	80.2
Database Date:	2015-11-30	**pI:**	6.4
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSVSGKKEFD	VKQILRLRWR	WFSHPFQGST	NTGSCLQQEG	YEHRGTPVQG	RLKSHSRDRN	GLKKSNSPVH	HNILAPVPGP
90	100	110	120	130	140	150	160
APAHQRAVQN	LQQHNLIVHF	QANEDTPKSV	PEKNLFKEAC	EKRAQDLEMM	ADDNIEDSTA	RLDTQHSEDM	NATRSEEQFH
170	180	190	200	210	220	230	240
VINHAEQTLR	KMENYLKEKQ	LCDVLLIAGH	LRIPAHRLVL	SAVSDYFAAM	FTNDVLEAKQ	EEVRMEGVDP	NALNSLVQYA
250	260	270	280	290	300	310	320
YTGVLQLKED	TIESLLAAAC	LLQLTQVIDV	CSNFLIKQLH	PSNCLGIRSF	GDAQGCTELL	NVAHKYTMEH	FIEVIKNQEF
330	340	350	360	370	380	390	400
LLLPANEISK	LLCSDDINVP	DEETIFHALM	QWVGHDVQNR	QGELGMLLSY	IRLPLLPPQL	LADLETSSMF	TGDLECQKLL
410	420	430	440	450	460	470	480
MEAMKYHLLP	ERRSMMQSPR	TKPRKSTVGA	LYAVGGMDAM	KGTTTIEKYD	LRTNSWLHIG	TMNGRRLQFG	VAVIDNKLYV
490	500	510	520	530	540	550	560
VGGRDGLKTL	NTVECFNPVG	KIWTVMPPMS	THRHGLGVAT	LEGPMYAVGG	HDGWSYLNTV	ERWDPEGRQW	NYVASMSTPR
570	580	590	600	610	620	630	640
STVGVVALNN	KLYAIGGRDG	SSCLKSMEYF	DPHTNKWSLC	APMSKRRGGV	GVATYNGFLY	VVGGHDAPAS	NHCSRLSDCV
650	660	670	680	690	700	710	720
ERYDPKGDSW	STVAPLSVPR	DAVAVCPLGD	KLYVVGGYDG	HTYLNTVESY	DAQRNEWKEE	VPVNIGRAGA	CVVVVKLP

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1263	1	857.8774	-59.82	2	45.4	10.2	1	425-441	R.KSTVGALYAVGGMDAMK.G	Oxidation: 16

Detailed Protein Report

Protein 1335: NEDD8-conjugating enzyme UBE2F isoform 3 [Homo sapiens]

Accession:	gi|507144081	**Score:**	10.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	17.5
Database Date:	2015-11-30	**pI:**	7.8
		Sequence Coverage [%]:	9.2
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 0.35 **CV:** 0.00 % **No. of Peptides:** 1

```
         10         20         30         40         50         60         70         80
MLTLASKLKR DDGLKGSRTA ATASDSTRRV SVRDKLLVKD EGYYQGGKFQ FETEVPDAYN MVPPKVKCLT KIWHPNITET
         90        100        110        120        130        140        150        160
GEICLSLLRE HSIDGTGWAP TRTLKDVVWG LNSLFTDLLN FDDPLNIEAA EHHLRDKEDF RNKVDDYIKR YAR
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
314	1	718.8197	-61.19	2	33.3	10.2	2	16-29	K.GSRTAATASDSTRR.V		MD:MU 0.35

Detailed Protein Report

Protein 1336: dipeptidase 3 isoform b precursor [Homo sapiens]

Accession:	gi|193211610	**Score:**	10.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	56.3
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
MIRTPLSASA	HRLLLPGSRG	RPPRNMQPTG	REGSRALSRR	YLRRLLLLLL	LLLLRQPVTR	AETTPGAPRA	LSTLGSPSLF
90	100	110	120	130	140	150	160
TTPGVPSALT	TPGLTTPGTP	KTLDLRGRAQ	ALMRSFPLVD	GHNDLPQVLR	QRYKNVLQDV	NLRNFSHGQT	SLDRLRDGLV
170	180	190	200	210	220	230	240
GAQFWSASVS	CQSQDQTAVR	LALEQIDLIH	RMCASYSELE	LVTSAEGLNS	SQKLACLIGV	EGGHSLDSSL	SVLRSFYVLG
250	260	270	280	290	300	310	320
VRYLTLTFTC	STPWAESSTK	FRHHMYTNVS	GLTSFGEKVV	EELNRLGMMI	DLSYASDTLI	RRVLEVSQAP	VIFSHSAARA
330	340	350	360	370	380	390	400
VCDNLLNVPD	DILQLLKNGG	IVMVTLSMGV	LQCNLLANVS	TVADHFDHIR	AVIGSEFIGI	GGNYDGTGRF	PQGLEDVSTY
410	420	430	440	450	460	470	480
PVLIEELLSR	SWSEEELQGV	LRGNLLRVFR	QVEKVREESR	AQSPVEAEFP	YGQLSTSCHS	HLVPQNGHQA	THLEVTKQPT
490	500	510	520				
NRVPWRSSNA	SPYLVPGLVA	AATIPTFTQW	LC				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2783	1	701.7137	-21.38	3	66.2	10.2	2	13-31	R.LLLPGSRGRPPRNMQPTGR.E	

Detailed Protein Report

Protein 1337: uncharacterized protein LOC101928436 [Homo sapiens]

Accession:	gi|558757363	**Score:**	10.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	11.5
Database Date:	2015-11-30	**pI:**	7.7
		Sequence Coverage [%]:	18.6
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|578798182	refseq_human (refseq_human_20140103.fasta)	PREDICTED: uncharacterized protein LOC101928436 isoform X1 [Homo sapiens]

```
         10         20         30         40         50         60         70         80
MRCVKSMAMD ANSLCVSGFK QLYTLMLSYT QQQFVTSLGN SSYSFELQPN FLSITALGLT LPEEKGKTQP ECPLKVKKCP
         90        100        110
HFYVQIVDLW NLHSTFDTAC DS
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2094	1	1023.8994	-81.91	2	56.1	10.1	2	2-20	M.RCVKSMAMDANSLCVSGFK.Q	

Detailed Protein Report

Protein 1338: myosin light chain kinase 2, skeletal/cardiac muscle [Homo sapiens]

Accession:	gi|14993776	**Score:**	10.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	64.6
Database Date:	2015-11-30	**pI:**	6.7
		Sequence Coverage [%]:	3.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MATENGAVEL	GIQNPSTDKA	PKGPTGERPL	AAGKDPGPPD	PKKAPDPPTL	KKDAKAPASE	KGDGTLAQPS	TSSQGPKGEG
90	100	110	120	130	140	150	160
DRGGGPAEGS	AGPPAALPQQ	TATPETSVKK	PKAEQGASGS	QDPGKPRVGK	KAAEGQAAAR	RGSPAFLHSP	SCPAIISSSE
170	180	190	200	210	220	230	240
KLLAKKPPSE	ASELTFEGVP	MTHSPTDPRP	AKAEEGKNIL	AESQKEVGEK	TPGQAGQAKM	QGDTSRGIEF	QAVPSEKSEV
250	260	270	280	290	300	310	320
GQALCLTARE	EDCFQILDDC	PPPPAPFPHR	MVELRTGNVS	SEFSMNSKEA	LGGGKFGAVC	TCMEKATGLK	LAAKVIKKQT
330	340	350	360	370	380	390	400
PKDKEMVLLE	IEVMNQLNHR	NLIQLYAAIE	TPHEIVLFME	YIEGGELFER	IVDEDYHLTE	VDTMVFVRQI	CDGILFMHKM
410	420	430	440	450	460	470	480
RVLHLDLKPE	NILCVNTTGH	LVKIIDFGLA	RRYNPNEKLK	VNFGTPEFLS	PEVVNYDQIS	DKTDMWSMGV	ITYMLLSGLS
490	500	510	520	530	540	550	560
PFLGDDDTET	LNNVLSGNWY	FDEETFEAVS	DEAKDFVSNL	IVKDQRARMN	AAQCLAHPWL	NNLAEKAKRC	NRRLKSQILL
570	580	590	600				
KKYLMKRRWK	KNFIAVSAAN	RFKKISSSGA	LMALGV				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2087	1	1022.8994	-78.95	2	56.2	10.1	1	62-82	K.GDGTLAQPSTSSQGPKGEGDR.G	

Detailed Protein Report

Protein 1339: PREDICTED: transmembrane protein 184B isoform X5 [Homo sapiens]

Accession:	gi|530419895	**Score:**	10.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	39.5
Database Date:	2015-11-30	**pI:**	8.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	5.5
		No. of unique Peptides:	1

Quantitation

MD:MU	**Median:**	0.37	**CV:**	0.00 %	**No. of Peptides:**	1	

Alias proteins:

Accession	Name	Description
gi|530419897	refseq_human (refseq_human_20140103.fasta)	PREDICTED: transmembrane protein 184B isoform X6 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MHLRCYSCPN EQRYIVRILF IVPIYAFDSW LSLLFFTNDQ YYVYFGTVRD CYEALVIYNF LSLCYEYLGG ESSIMSEIRG
        90        100        110        120        130        140        150        160
KPIESSCMYG TCCLWGKTYS IGFLRFCKQA TLQFCVVKPL MAVSTVVLQA FGKYRDGDFD VTSGYLYVTI IYNISVSLAL
       170        180        190        200        210        220        230        240
YALFLFYFAT RELLSPYSPV LKFFMVKSVI FLSFWQGMLL AILEKCGAIP KIHSARVSVG EGTVAAGYQD FIICVEMFFA
       250        260        270        280        290        300        310        320
ALALRHAFTY KVYADKRLDA QVPTYGPYGR CAPMKSISSS LKETMNPHDI VQDAIHNFSP AYQQYTQQST LEPGPTWRGG
       330        340        350
AHGLSRSHSL SGARDNEKTL LLSSDDEF
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1116	1	713.7679	112.87	3	43.6	10.1	2	257-275	K.RLDAQVPTYGPYGRCAPMK.S	Oxidation: 18	MD:MU 0.37

Detailed Protein Report

Protein 1340: F-box only protein 8 [Homo sapiens]

Accession:	gi|48928044	**Score:**	10.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	37.0
Database Date:	2015-11-30	**pI:**	8.7
		Sequence Coverage [%]:	4.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGQGLWRVVR	NQQLQQEGYS	EQGYLTREQS	RRMAASNISN	TNHRKQVQGG	IDIYHLLKAR	KSKEQEGFIN	LEMLPPELSF
90	100	110	120	130	140	150	160
TILSYLNATD	LCLASCVWQD	LANDELLWQG	LCKSTWGHCS	IYNKNPPLGF	SFRKLYMQLD	EGSLTFNANP	DEGVNYFMSK
170	180	190	200	210	220	230	240
GILDDSPKEI	AKFIFCTRTL	NWKKLRIYLD	ERRDVLDDLV	TLHNFRNQFL	PNALREFFRH	IHAPEERGEY	LETLITKFSH
250	260	270	280	290	300	310	320
RFCACNPDLM	RELGLSPDAV	YVLCYSLILL	SIDLTSPHVK	NKMSKREFIR	NTRRAAQNIS	EDFVGHLYDN	IYLIGHVAA

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
750	1	848.7476	-154.71	2	38.9	10.1	1	238-251	K.FSHRFCACNPDLMR.E	

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Detailed Protein Report

Protein 1341: PREDICTED: gamma-glutamyltransferase light chain 2 isoform X6 [Homo sapiens]

Accession:	gi|578837507	**Score:**	10.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	29.4
Database Date:	2015-11-30	**pI:**	6.1
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	4.5
		No. of unique Peptides:	1

Quantitation

MD:MU	**Median:** 0.44	**CV:** 0.00 %	**No. of Peptides:** 1

10	20	30	40	50	60	70	80
MAGGGRGGSC	NRYWKERGGH	KGRGRNRCPQ	WRQICPWITE	DSCSPAEVVH	NMTSEFFAAQ	LRAQISDDTT	HPISYYKPEF
90	100	110	120	130	140	150	160
YTPVDGGTAH	LSVVAEDGSA	VSATSTINLY	FGSKVRSPVS	EILFNDEMDD	FSSPNITNEF	GVPPSPANFI	QPGKQPLSSM
170	180	190	200	210	220	230	240
CPTIMVGQDG	QPPSHADHTP	MPQAIIYNLW	FGYDVKRAVE	EPRLHNQLLP	NVTTVERNID	QAVTAALETR	HHHTQIASTF
250	260	270					
IAVVQAIVRT	AGGWAAASDS	RKGGEPAGY					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
906	1	598.1145	-237.25	2	40.9	10.1	1	1-12	-.MAGGGRGGSCNR.Y	Carbamidomethyl: 10; Oxidation: 1	MD:MU 0.44

Detailed Protein Report

Protein 1342: centrosomal protein of 112 kDa isoform b [Homo sapiens]

Accession:	gi|82880654	**Score:**	10.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	24.5
Database Date:	2015-11-30	**pI:**	9.6
		Sequence Coverage [%]:	5.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MWASLSLDHP	SAKENQALRL	IEMREENGNV	PKTEQAGSLK	PLRDTGKSNL	KEKKANSKLK	QIEKEYTQKL	AKSSQIIAEL
90	100	110	120	130	140	150	160
QTTISSLKEE	NSQQQLAAER	RLQDVRQKFE	DEKKQLIRDN	DQAIKVLQDE	LENRSNQVRC	AEKKLQHKEL	ESQEQITYIR
170	180	190	200	210	220		
QEYETKLKGL	MPASLRQELE	DTISSLKSQV	NFLQKRASIL	QEELTTYQGR	R		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2475	1	701.6910	-200.17	2	60.9	10.1	0	89-100	K.EENSQQQLAAER.R	

Detailed Protein Report

Protein 1343: PREDICTED: fibroin heavy chain-like isoform X3 [Homo sapiens]

Accession:	gi|578832854	**Score:**	10.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	54.6
Database Date:	2015-11-30	**pI:**	4.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.4
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578846640	refseq_human (refseq_human_20140103.fasta)	PREDICTED: fibroin heavy chain-like isoform X3 [Homo sapiens]

10	20	30	40	50	60	70	80
MSGELAVCRV	TEGASCMSEL	AVWRVTEGAS	CMSGEPAVCR	VTEGASCMSG	ELAVWRVTEG	ASCMSGELAV	CRVTEGAGCM
90	100	110	120	130	140	150	160
SGELAVCRVT	EGASCMSGEL	AVCRVTEGAG	CMSGLLAVCR	VTEGAGCMSG	ELAVCRVTEG	ASCMSGELPV	WRVTEGAGCM
170	180	190	200	210	220	230	240
SGELAVCRVT	EGAGCMSGEL	AVCRVTEGAG	CMSGELAVCR	VTEGAGCMSG	ELTVCRVTEG	AGCMSGELAV	WRVTEGAGCM
250	260	270	280	290	300	310	320
SGELAVCRVT	EGAGCMSGEL	AVWRVTEGAG	CMSGELAVCR	VTEGASCMSG	ELPVWRVTEG	ASCMSGELAV	CRVTEGAGCM
330	340	350	360	370	380	390	400
SGELAVCRVT	EGAGCMSGEL	AVCRVTEGAG	CMSGELAVCR	VTEGAGCMSG	ELAVCRVTEG	AGCMSGELAV	CTVTEGASCM
410	420	430	440	450	460	470	480
SGELAVCRVT	EGARCMSGEP	AVWRVTEGAG	CMSGELAVWR	VTEGAGCMSG	ELAVWRVTEG	AGCMSGELAV	CTVTEGASCM
490	500	510	520	530	540	550	
SGELAVCRVT	EGPCCVSGEL	AVCRVTEGPC	CISGECIRSV	LICLIPDHVS	TQDTCVCVKG	VRS	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
315	1	881.3242	-98.81	3	33.3	10.1	1	1-24	-.MSGELAVCRVTEGASCMSELAVWR.V	Carbamidomethyl: 8

Detailed Protein Report

Protein 1344: dual specificity protein kinase CLK2 [Homo sapiens]

Accession:	gi|47717134	**Score:**	10.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	59.9
Database Date:	2015-11-30	**pI:**	10.2
		Sequence Coverage [%]:	1.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPHPRRYHSS	ERGSRGSYRE	HYRSRKHKRR	RSRSWSSSSD	RTRRRRREDS	YHVRSRSSYD	DRSSDRRVYD	RRYCGSYRRN
90	100	110	120	130	140	150	160
DYSRDRGDAY	YDTDYRHSYE	YQRENSSYRS	QRSSRRKHRR	RRRRSRTFSR	SSSHSSRRAK	SVEDDAEGHL	IYHVGDWLQE
170	180	190	200	210	220	230	240
RYEIVSTLGE	GTFGRVVQCV	DHRRGGARVA	LKIIKNVEKY	KEAARLEINV	LEKINEKDPD	NKNLCVQMFD	WFDYHGHMCI
250	260	270	280	290	300	310	320
SFELLGLSTF	DFLKDNNYLP	YPIHQVRHMA	FQLCQAVKFL	HDNKLTHTDL	KPENILFVNS	DYELTYNLEK	KRDERSVKST
330	340	350	360	370	380	390	400
AVRVVDFGSA	TFDHEHHSTI	VSTRHYRAPE	VILELGWSQP	CDVWSIGCII	FEYYVGFTLF	QTHDNREHLA	MMERILGPIP
410	420	430	440	450	460	470	480
SRMIRKTRKQ	KYFYRGRLDW	DENTSAGRYV	RENCKPLRRY	LTSEAEEHHQ	LFDLIESMLE	YEPAKRLTLG	EALQHPFFAR
490	500						
LRAEPPNKLW	DSSRDISR						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1198	1	985.2519	-184.18	1	44.6	10.1	1	55-62	R.SRSSYDDR.S	

Detailed Protein Report

Protein 1345: collagen alpha-1(XXV) chain isoform 3 [Homo sapiens]

Accession:	gi|366392941	**Score:**	10.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	63.3
Database Date:	2015-11-30	**pI:**	9.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLLKKHAGKG	GGREPRSEDP	TPAEQHCART	MPPCAVLAAL	LSVVAVVSCL	YLGVKTNDLQ	ARIAALESAK	GAPSIHLLPD
90	100	110	120	130	140	150	160
TLDHLKTMVQ	EKVERLLAQK	SYEHMAKIRI	AREAPSECNC	PAGPPGKRGK	RGRRGESGPP	GQPGPQGPPG	PKGDKGEQGD
170	180	190	200	210	220	230	240
QGPRGLPGFP	TVAALHSNQI	LTVKGDQGQA	GPPGPPGPPG	PRGPPGDTGK	DGPRGMPGVP	GEPGKPGEQG	LMGPLGPPGQ
250	260	270	280	290	300	310	320
KGSIGAPGIP	GMNGQKGEPG	LPGAVGQNGI	PGPKGEPGEQ	GEKGDAGENG	PKGDTGEKGD	PGSSAAGIKG	EPGESGRPGQ
330	340	350	360	370	380	390	400
KGEPGLPGLP	GLPGIKGEPG	FIGPQGEPGL	PGLPGTKGER	GEAGPPGRGE	RGEPGAPGPK	GDRGEKGDSG	AQGPRGPPGQ
410	420	430	440	450	460	470	480
KGDQGATEII	DYNGNLHEAL	QGPPGPPGPQ	GLQGPKGEQG	SPGIPGMDGE	QGLKGSKGDM	GDPGMTGEKG	GIGLPGLPGA
490	500	510	520	530	540	550	560
NGMKGEKGDS	GMPGPQGPSI	IGPPGPPGPH	GPPGPMGPHG	LPGPKGEPGL	NGVKGLKGEP	GQKGDRGPLG	LPGASGLDGK
570	580	590	600	610	620	630	640
PGSRGTDGPM	GPHGPAGPKG	ERGEKGAMGE	PGPRGPYGLP	GFPGPRGEKG	DLGEKGEKVT	SPSQHVPCLI	LLLLSALLFS
650							
LCDSI							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1307	1	835.3650	-11.55	2	45.9	10.1	1	113-128	R.EAPSECNCPAGPPGKR.G	Carbamidomethyl: 8

Detailed Protein Report

Protein 1346: PREDICTED: nuclear factor NF-kappa-B p100 subunit isoform X3 [Homo sapiens]

Accession: gi|578819504

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Score: 10.1

MW [kDa]: 92.6

pI: 5.6

Sequence Coverage [%]: 1.3

No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MESCYNPGLD	GIIEYDDFKL	NSSIVEPKEP	APETADGPYL	VIVEQPKQRG	FRFRYGCEGP	SHGGLPGASS	EKGRKTYPTV
90	100	110	120	130	140	150	160
KICNYEGPAK	IEVDLVTHSD	PPRAHAHSLV	GKQCSELGIC	AVSVGPKDMT	AQFNNLGVLH	VTKKNMMGTM	IQKLQRQRLR
170	180	190	200	210	220	230	240
SRPQGLTEAE	QRELEQEAKE	LKKVMDLSIV	RLRFSAFLRA	SDGSFSLPLK	PVISQPIHDS	KSPGASNLKI	SRMDKTAGSV
250	260	270	280	290	300	310	320
RGGDEVYLLC	DKVQKDDIEV	RFYEDDENGW	QAFGDFSPTD	VHKQYAIVFR	TPPYHKMKIE	RPVTVFLQLK	RKRGGDVSDS
330	340	350	360	370	380	390	400
KQFTYYPLVE	GGSLGFFPSS	LAYSPYQSGA	GPMGCYPGGG	GGAQMAATVP	SRDSGEEAAE	PSAPSRTPQC	EPQAPEMLQR
410	420	430	440	450	460	470	480
AREYNARLFG	LAQRSARALL	DYGVTADARA	LLAGQRHLLT	AQDENGDTPL	HLAIIHGQTS	VIEQIVYVIH	HAQDLGVVNL
490	500	510	520	530	540	550	560
TNHLHQTPLH	LAVITGQTSV	VSFLLRVGAD	PALLDRHGDS	AMHLALRAGA	GAPELLRALL	QSGAPAVPQL	LHMPDFEGLY
570	580	590	600	610	620	630	640
PVHLAVRARS	PECLDLLVDS	GAEVEATERQ	GGRTALHLAT	EMEELGLVTH	LVTKLRANVN	ARTFAGNTPL	HLAAGLGYPT
650	660	670	680	690	700	710	720
LTRLLLKAGA	DIHAENEEPL	CPLPSPPTSD	SDSDSEGPEK	DTRSSFRGHT	PLDLTCSTKV	KTLLLNAAQN	TMEPPLTPPS
730	740	750	760	770	780	790	800
PAGPGLSLGD	TALQNLEQLL	DGPEAQGSWA	ELAERLGLRS	LVDTYRQTTS	PSGSLLRSYE	LAGGDLAGLL	EALSDMGLEE
810	820	830	840	850	860		
GVRLLRGPET	RDKLPSTAEV	KEDSAYGSQS	VEQEAEKLGP	PPEPPGGLCH	GHPQPQVH		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
218	1	606.1428	-233.36	2	32.1	10.1	0	242-252	R.GGDEVYLLCDK.V	

Detailed Protein Report

Protein 1347: CUB domain-containing protein 2 precursor [Homo sapiens]

Accession:	gi|72384339	**Score:**	10.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	48.7
Database Date:	2015-11-30	**pI:**	5.8
		Sequence Coverage [%]:	2.9
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MLAEWGACLL LAVALLGPGL QAQAMEGVKC GGVLSAPSGN FSSPNFPRLY PYNTECSWLI VVAEGSSVLL TFHAFDLEYH
        90        100        110        120        130        140        150        160
DTCSFDFLEI YNGASPDKGN LLGRFCGKVP PPPFTSSWHV MSVIFHSDKH VASHGFSAGY QKDVCGGVLT GLSGVLTSPE
       170        180        190        200        210        220        230        240
YPNNYPNSME CHWVIRAAGP AHVKLVFVDF QVEGNEECTY DYVAVLGGPG PTRGHHYCGS TRPPTLVSLG HELQVVFKSD
       250        260        270        280        290        300        310        320
FNIGGRGFKA YYFSGECQEV YMAMRGNFSS PQYPSSYPNN IRCHWTIRLP PGYQVKVFFL DLDLEEPNSL TKTCDFDHLA
       330        340        350        360        370        380        390        400
AFDGASEEAP LLGNWCGHHL PPPVTSSHNQ LLLLLHTDRS TTRRGFSVAY IGGQLGCGSG STEGEGEALQ PQSLQSPSSI
       410        420        430        440        450
PPVCPAPPMN GLLQLLLHWL HPCPLSGPLR LDGTAPACFH YCRASFPSF
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1336	1	727.1974	-170.25	2	46.3	10.1	0	431-443	R.LDGTAPACFHYCR.A	

Protein 1348: putative ATP-dependent RNA helicase DHX30 isoform 1 [Homo sapiens]

Accession: gi|20336294
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 10.1
MW [kDa]: 133.9
pI: 9.8
Sequence Coverage [%]: 1.9
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MFSLDSFRKD	RAQHRQRQCK	LPPPRLPPMC	VNPTPGGTIS	RASRDLLKEF	PQPKNLLNSV	IGRALGISHA	KDKLVYVHTN
90	100	110	120	130	140	150	160
GPKKKKVTLH	IKWPKSVEVE	GYGSKKIDAE	RQAAAAACQL	FKGWGLLGPR	NELFDAAKYR	VLADRFGSPA	DSWWRPEPTM
170	180	190	200	210	220	230	240
PPTSWRQLNP	ESIRPGGPGG	LSRSLGREEE	EDEEEELEEG	TIDVTDFLSM	TQQDSHAPLR	DSRGSSFEMT	DDDSAIRALT
250	260	270	280	290	300	310	320
QFPLPKNLLA	KVIQIATSSS	TAKNLMQFHT	VGTKTKLSTL	TLLWPCPMTF	VAKGRRKAEA	ENKAAALACK	KLKSLGLVDR
330	340	350	360	370	380	390	400
NNEPLTHAMY	NLASLRELGE	TQRRPCTIQV	PEPILRKIET	FLNHYPVESS	WIAPELRLQS	DDILPLGKDS	GPLSDPITGK
410	420	430	440	450	460	470	480
PYVPLLEAEE	VRLSQSLLEL	WRRRGPVWQE	APQLPVDPHR	DTILNAIEQH	PVVVISGDTG	CGKTTRIPQL	LLERYVTEGR
490	500	510	520	530	540	550	560
GARCNVIITQ	PRRISAVSVA	QRVSHELGPS	LRRNVGFQVR	LESKPPSRGG	ALLFCTVGIL	LRKLQSNPSL	EGVSHVIVDE
570	580	590	600	610	620	630	640
VHERDVNTDF	LLILLKGLQR	LNPALRLVLM	SATGDNERFS	RYFGGCPVIK	VPGFMYPVKE	HYLEDILAKL	GKHQYLHRHR
650	660	670	680	690	700	710	720
HHESEDECAL	DLDLVTDLVL	HIDARGEPGG	ILCFLPGWQE	IKGVQQRLQE	ALGMHESKYL	ILPVHSNIPM	MDQKAIFQQP
730	740	750	760	770	780	790	800
PVGVRKIVLA	TNIAETSITI	NDIVHVVDSG	LHKEERYDLK	TKVSCLETVW	VSRANVIQRR	GRAGRCQSGF	AYHLFPRSRL
810	820	830	840	850	860	870	880
EKMVPFQVPE	ILRTPLENLV	LQAKIHMPEK	TAVEFLSKAV	DSPNIKAVDE	AVILLQEIGV	LDQREYLTTL	GQRLAHISTD
890	900	910	920	930	940	950	960
PRLAKAIVLA	AIFRCLHPLL	VVVSCLTRDP	FSSSLQNRAE	VDKVKALLSH	DSGSDHLAFV	RAVAGWEEVL	RWQDRSSREN
970	980	990	1000	1010	1020	1030	1040
YLEENLLYAP	SLRFIHGLIK	QFSENIYEAF	LVGKPSDCTL	ASAQCNEYSE	EEELVKGVLM	AGLYPNLIQV	RQGKVTRQGK
1050	1060	1070	1080	1090	1100	1110	1120
FKPNSVTYRT	KSGNILLHKS	TINREATRLR	SRWLTYFMAV	KSNGSVFVRD	SSQVHPLAVL	LLTDGDVHIR	DDGRRATISL
1130	1140	1150	1160	1170	1180	1190	1200
SDSDLLRLEG	DSRTVRLLKE	LRRALGRMVE	RSLRSELAAL	PPSVQEEHGQ	LLALLAELLR	GPCGSFDVRK	TADD

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
60	1	1220.0412	-85.90	2	30.1	10.1	2	26-48	R.LPPMCVNPTPGGTISRASRDLLK.E	Oxidation: 4

Detailed Protein Report

Protein 1349: PREDICTED: zinc finger protein 133 isoform X15 [Homo sapiens]

Accession:	gi|578835536	**Score:**	10.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	62.4
Database Date:	2015-11-30	**pI:**	10.9
		Sequence Coverage [%]:	4.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MQHVLCNHPP	WIFTCLCAEG	NIQPGDPGPG	DQEKQQQASE	GRPWSDQAEG	PEGEGAMPLF	GRTKKRTLGA	FSRPPQRQPV
90	100	110	120	130	140	150	160
SSRNGLRGVE	LEASPAQSGN	PEETDKLLKR	IEVLGFGTVN	CGECGLSFSK	MTNLLSHQRI	HSGEKPYVCG	VCEKGFSLKK
170	180	190	200	210	220	230	240
SLARHQKAHS	GEKPIVCREC	GRGFNRKSTL	IIHERTHSGE	KPYMCSECGR	GFSQKSNLII	HQRTHSGEKP	YVCRECGKGF
250	260	270	280	290	300	310	320
SQKSAVVRHQ	RTHLEEKTIV	CSDCGLGFSD	RSNLISHQRT	HSGEKPYACK	ECGRCFRQRT	TLVNHQRTHS	KEKPYVCGVC
330	340	350	360	370	380	390	400
GHSFSQNSTL	ISHRRTHTGE	KPYVCGVCGR	GFSLKSHLNR	HQNIHSGEKP	IVCKDCGRGF	SQQSNLIRHQ	RTHSGEKPMV
410	420	430	440	450	460	470	480
CGECGRGFSQ	KSNLVAHQRT	HSGERPYVCR	ECGRGFSHQA	GLIRHKRKHS	REKPYMCRQC	GLGFGNKSAL	ITHKRAHSEE
490	500	510	520	530	540	550	560
KPCVCRECGQ	GFLQKSHLTL	HQMTHTGEKP	YVCKTCGRGF	SLKSHLSRHR	KTTSVHHRLP	VQPDPEPCAG	QPSDSLYSL

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2415	1	919.8559	64.50	3	60.5	10.1	2	407-430	R.GFSQKSNLVAHQRTHSGERPYVCR.E	

Detailed Protein Report

Protein 1350: semaphorin-4A isoform 2 [Homo sapiens]

Accession:	gi|300863076	**Score:**	10.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	69.1
Database Date:	2015-11-30	**pI:**	6.3
		Sequence Coverage [%]:	2.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MIPWPASDRK	KSECAFKKKS	NEELQDSYLL	PISEDKVMEG	KGQSPFDPAH	KHTAVLVDGM	LYSGTMNNFL	GSEPILMRTL
90	100	110	120	130	140	150	160
GSQPVLKTDN	FLRWLHHDAS	FVAAIPSTQV	VYFFFEETAS	EFDFFERLHT	SRVARVCKND	VGGEKLLQKK	WTTFLKAQLL
170	180	190	200	210	220	230	240
CTQPGQLPFN	VIRHAVLLPA	DSPTAPHIYA	VFTSQWQVGG	TRSSAVCAFS	LLDIERVFKG	KYKELNKETS	RWTTYRGPET
250	260	270	280	290	300	310	320
NPRPGSCSVG	PSSDKALTFM	KDHFLMDEQV	VGTPLLVKSG	VEYTRLAVET	AQGLDGHSHL	VMYLGTTTGS	LHKAVVSGDS
330	340	350	360	370	380	390	400
SAHLVEEIQL	FPDPEPVRNL	QLAPTQGAVF	VGFSGGVWRV	PRANCSVYES	CVDCVLARDP	HCAWDPESRT	CCLLSAPNLN
410	420	430	440	450	460	470	480
SWKQDMERGN	PEWACASGPM	SRSLRPQSRP	QIIKEVLAVP	NSILELPCPH	LSALASYYWS	HGPAAVPEAS	STVYNGSLLL
490	500	510	520	530	540	550	560
IVQDGVGGLY	QCWATENGFS	YPVISYWVDS	QDQTLALDPE	LAGIPREHVK	VPLTRVSGGA	ALAAQQSYWP	HFVTVTVLFA
570	580	590	600	610	620	630	
LVLSGALIIL	VASPLRALRA	RGKVQGCETL	RPGEKAPLSR	EQHLQSPKEC	RTSASDVDAD	NNCLGTEVA	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1803	1	731.7464	-92.08	2	52.5	10.1	0	409-422	R.GNPEWACASGPMSR.S	

Detailed Protein Report

Protein 1351: NACHT, LRR and PYD domains-containing protein 5 [Homo sapiens]

Accession:	gi|158321897	**Score:**	10.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	134.3
Database Date:	2015-11-30	**pI:**	6.1
		Sequence Coverage [%]:	0.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MKVAGGLELG	AAALLSASPR	ALVTLSTGPT	CSILPKNPLF	PQNLSSQPCI	KMEGDKSLTF	SSYGLQWCLY	ELDKEEFQTF
90	100	110	120	130	140	150	160
KELLKKKSSE	STTCSIPQFE	IENANVECLA	LLLHEYYGAS	LAWATSISIF	ENMNLRTLSE	KARDDMKRHS	PEDPEATMTD
170	180	190	200	210	220	230	240
QGPSKEKVPG	ISQAVQQDSA	TAAETKEQEI	SQAMEQEGAT	AAETEEQEIS	QAMEQEGATA	AETEEQGHGG	DTWDYKSHVM
250	260	270	280	290	300	310	320
TKFAEEEDVR	RSFENTAADW	PEMQTLAGAF	DSDRWGFRPR	TVVLHGKSGI	GKSALARRIV	LCWAQGGLYQ	GMFSYVFFLP
330	340	350	360	370	380	390	400
VREMQRKKES	SVTEFISREW	PDSQAPVTEI	MSRPERLLFI	IDGFDDLGSV	LNNDTKLCKD	WAEKQPPFTL	IRSLLRKVLL
410	420	430	440	450	460	470	480
PESFLIVTVR	DVGTEKLKSE	VVSPRYLLVR	GISGEQRIHL	LLERGIGEHQ	KTQGLRAIMN	NRELLDQCQV	PAVGSLICVA
490	500	510	520	530	540	550	560
LQLQDVVGES	VAPFNQTLTG	LHAAFVFHQL	TPRGVVRRCL	NLEERVVLKR	FCRMAVEGVW	NRKSVFDGDD	LMVQGLGESE
570	580	590	600	610	620	630	640
LRALFHMNIL	LPDSHCEEYY	TFFHLSLQDF	CAALYYVLEG	LEIEPALCPL	YVEKTKRSME	LKQAGFHIHS	LWMKRFLFGL
650	660	670	680	690	700	710	720
VSEDVRRPLE	VLLGCPVPLG	VKQKLLHWVS	LLGQQPNATT	PGDTLDAFHC	LFETQDKEFV	RLALNSFQEV	WLPINQNLDL
730	740	750	760	770	780	790	800
IASSFCLQHC	PYLRKIRVDV	KGIFPRDESA	EACPVVPLWM	RDKTLIEEQW	EDFCSMLGTH	PHLRQLDLGS	SILTERAMKT
810	820	830	840	850	860	870	880
LCAKLRHPTC	KIQTLMFRNA	QITPGVQHLW	RIVMANRNLR	SLNLGGTHLK	EEDVRMACEA	LKHPKCLLES	LRLDCCGLTH
890	900	910	920	930	940	950	960
ACYLKISQIL	TTSPSLKSLS	LAGNKVTDQG	VMPLSDALRV	SQCALQKLIL	EDCGITATGC	QSLASALVSN	RSLTHLCLSN
970	980	990	1000	1010	1020	1030	1040
NSLGNEGVNL	LCRSMRLPHC	SLQRLMLNQC	HLDTAGCGFL	ALALMGNSWL	THLSLSMNPV	EDNGVKLLCE	VMREPSCHLQ
1050	1060	1070	1080	1090	1100	1110	1120
DLELVKCHLT	AACCESLSCV	ISRSRHLKSL	DLTDNALGDG	GVAALCEGLK	QKNSVLARLG	LKACGLTSDC	CEALSLALSC
1130	1140	1150	1160	1170	1180	1190	1200
NRHLTSLNLV	QNNFSPKGMM	KLCSAFACPT	SNLQIIGLWK	WQYPVQIRKL	LEEVQLLKPR	VVIDGSWHSF	DEDDRYWWKN
1210							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
692	1	454.6453	-240.71	2	38.0	10.1	0	812-818	K.IQTLMFR.N	

Detailed Protein Report

Protein 1352: zinc finger protein 227 isoform d [Homo sapiens]

Accession:	gi|574584777	**Score:**	10.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	80.4
Database Date:	2015-11-30	**pI:**	10.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
METLQKFALK	YLSNQELSCW	QIWKQVASEL	TRCLQGKSSQ	LLQGDSIQVS	ENENNIMNPK	GDSSIYIENQ	EFPFWRTQHS
90	100	110	120	130	140	150	160
CGNTYLSESQ	IQSRGKQIDV	KNNLQIHEDF	MKKSPFHEHI	KTDTEPKPCK	GNEYGKIISD	GSNQKLPLGE	KPHPCGECGR
170	180	190	200	210	220	230	240
GFSYSPRLPL	HPNVHTGEKC	FSQSSHLRTH	QRIHPGEKLN	RCHESGDCFN	KSSFHSYQSN	HTGEKSYRCD	SCGKGFSSST
250	260	270	280	290	300	310	320
GLIIHYRTHT	GEKPYKCEEC	GKCFSQSSNF	QCHQRVHTEE	KPYKCEECGK	GFGWSVNLRV	HQRVHRGEKP	YKCEECGKGF
330	340	350	360	370	380	390	400
TQAAHFHIHQ	RVHTGEKPYK	CDVCGKGFSH	NSPLICHRRV	HTGEKPYKCE	ACGKGFTRNT	DLHIHFRVHT	GEKPYKCKEC
410	420	430	440	450	460	470	480
GKGFSQASNL	QVHQNVHTGE	KRFKCETCGK	GFSQSSKLQT	HQRVHTGEKP	YRCDVCGKDF	SYSSNLKLHQ	VIHTGEKPYK
490	500	510	520	530	540	550	560
CEECGKGFSW	RSNLHAHQRV	HSGEKPYKCE	QCDKSFSQAI	DFRVHQRVHT	GEKPYKCGVC	GKGFSQSSGL	QSHQRVHTGE
570	580	590	600	610	620	630	640
KPYKCDVCGK	GFRYSSQFIY	HQRGHTGEKP	YKCEECGKGF	GRSLNLRHHQ	RVHTGEKPHI	CEECGKAFSL	PSNLRVHLGV
650	660	670	680	690	700	710	
HTREKLFKCE	ECGKGFSQSA	RLEAHQRVHT	GEKPYKCDIC	DKDFRHRSRL	TYHQKVHTGK	KL	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2710	1	709.8328	38.38	2	65.1	10.1	1	425-437	K.CETCGKGFSQSSK.L	Carbamidomethyl: 1

Detailed Protein Report

Protein 1353: homeobox protein TGIF1 isoform d [Homo sapiens]

Accession:	gi|28178851	**Score:**	10.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	27.7
Database Date:	2015-11-30	**pI:**	9.8
		Sequence Coverage [%]:	6.0
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530424923	refseq_human (refseq_human_20140103.fasta)	PREDICTED: homeobox protein TGIF1 isoform X2 [Homo sapiens]
gi|522838246	refseq_human (refseq_human_20140103.fasta)	homeobox protein TGIF1 isoform d [Homo sapiens]
gi|28178857	refseq_human (refseq_human_20140103.fasta)	homeobox protein TGIF1 isoform d [Homo sapiens]
gi|28178855	refseq_human (refseq_human_20140103.fasta)	homeobox protein TGIF1 isoform d [Homo sapiens]
gi|28178853	refseq_human (refseq_human_20140103.fasta)	homeobox protein TGIF1 isoform d [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MDIPLDLSSS AGSGKRRRRG NLPKESVQIL RDWLYEHRYN AYPSEQEKAL LSQQTHLSTL QVCNWFINAR RRLLPDMLRK
        90        100        110        120        130        140        150        160
DGKDPNQFTI SRRGAKISET SSVESVMGIK NFMPALEETP FHSCTAGPNP TLGRPLSPKP SSPGSVLARP SVICHTTVTA
       170        180        190        200        210        220        230        240
LKDVPFSLCQ SVGVGQNTDI QQIAAKNFTD TSLMYPEDTC KSGPSTNTQS GLFNTPPPTP PDLNQDFSGF QLLVDVALKR
       250        260
AAEMELQAKL TA
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1081	1	751.8650	-38.72	2	43.1	10.1	1	2-16	M.DIPLDLSSSAGSGKR.R	

Detailed Protein Report

Protein 1354: retinoic acid receptor responder protein 3 [Homo sapiens]

Accession:	gi|149588791	**Score:**	10.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	18.2
Database Date:	2015-11-30	**pI:**	9.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	7.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MASPHQEPKP	GDLIEIFRLG	YEHWALYIGD	GYVIHLAPPS	EYPGAGSSSV	FSVLSNSAEV	KRERLEDVVG	GCCYRVNNSL
90	100	110	120	130	140	150	160
DHEYQPRPVE	VIISSAKEMV	GQKMKYSIVS	RNCEHFVTQL	RYGKSRCKQV	EKAKVEVGVA	TALGILVVAG	CSFAIRRYQK
170							
KATA							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2835	1	826.4327	34.55	2	65.9	10.0	1	112-124	R.NCEHFVTQLRYGK.S	Carbamidomethyl: 2

Detailed Protein Report

Protein 1355: PREDICTED: F-box/WD repeat-containing protein 1A isoform X1 [Homo sapiens]

Accession:	gi|530394581	**Score:**	10.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	37.0
Database Date:	2015-11-30	**pI:**	9.2
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	4.9
		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
1902	1	1023.9142	-73.12	2	53.7	10.0	2	1-16	-.MTIESNWRCGRHSLQR.I	Carbamidomethyl: 9; Oxidation: 1

Detailed Protein Report

Protein 1356: **PREDICTED: zinc finger and SCAN domain-containing protein 12 isoform X3 [Homo sapiens]**

Accession:	gi|578812153	**Score:**	10.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	65.7
Database Date:	2015-11-30	**pI:**	6.2
		Sequence Coverage [%]:	3.0
		No. of unique Peptides:	1

Quantitation

MD:MU **Median:** 0.49 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MASTWAIQAH	MDQDEPLEVK	IEEEKYTTRQ	DWDLRKNNTH	SREVFRQYFR	QFCYQETSGP	REALSRLREL	CHQWLRPETH
90	100	110	120	130	140	150	160
TKEQILELLV	LEQFLTILPE	ELQAWVQEQH	PESGEEVVTV	LEDLERELDE	PGEQVSVHTG	EQEMFLQETV	RLRKEGEPSM
170	180	190	200	210	220	230	240
SLQSMKAQPK	YESPELESQQ	EQVLDVETGN	EYGNLKQEVS	EEMEPHGKTS	SKFENDMSKS	ARCGETREPE	EITEEPSACS
250	260	270	280	290	300	310	320
REDKQPTCDE	NGVSLTENSD	HTEHQRICPG	EESYGCDDCG	KAFSQHSHLI	EHQRIHTGDR	PYKCEECGKA	FRGRTVLIRH
330	340	350	360	370	380	390	400
KIIHTGEKPY	KCNECGKAFG	RWSALNQHQR	LHTGEKHYHC	NDCGKAFSQK	AGLFHHIKIH	TRDKPYQCTQ	CNKSFSRRSI
410	420	430	440	450	460	470	480
LTQHQGVHTG	AKPYECNECG	KAFVYNSSLV	SHQEIHHKEK	CYQCKECGKS	FSQSGLIQHQ	RIHTGEKPYK	CDVCEKAFIQ
490	500	510	520	530	540	550	560
RTSLTEHQRI	HTGERPYKCD	KCGKAFTQRS	VLTEHQRIHT	GERPYKCDEC	GNAFRGITSL	IQHQRIHTGE	KPYQCDECGK
570							
AFRQR							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
224	1	666.0908	127.27	3	32.5	10.0	0	422-438	K.AFVYNSSLVSHQEIHHK.E		MD:MU 0.49

Detailed Protein Report

Protein 1357: PREDICTED: FCH and double SH3 domains protein 1 isoform X2 [Homo sapiens]

Accession:	gi|578810932	**Score:**	10.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	72.0
Database Date:	2015-11-30	**pI:**	5.1
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MQPPPRKVKP	AQEVKLRFLE	QLSILQTWQQ	READLLEDIR	SYSKQRAAIE	REYGQALQKL	AGPFLKREGH	RSGEMDSRGR
90	100	110	120	130	140	150	160
TVFGAWRCLL	DATVAGGQTR	LQASDRYRDL	AGGTGRSAKE	QVLRKGTENL	QRAQAEVLQS	VRELSRSRKL	YGQRERVWAL
170	180	190	200	210	220	230	240
AQEKAADVQA	RLNRSDHGIF	HSRTSLQKLS	TKALVSELSE	HLRDPLTSLS	HTELEAAEVI	LEHAHRGEQT	TSQVSWEQDL
250	260	270	280	290	300	310	320
KLFLQEPGVF	SPTPPQQFQP	AGTDQVCVLE	WGAEGVAGKS	GLEKEVQRLT	SRAARDYKIQ	NHGHRVLQRL	EQRRQQASER
330	340	350	360	370	380	390	400
EAPSIEQRLQ	EVRESIRRAQ	VSQVKGAARL	ALLQGAGLDV	ERWLKPAMTQ	AQDEVEQERR	LSEARLSQRD	LSPTAEDAEL
410	420	430	440	450	460	470	480
SDFEECEETG	ELFEEPAPQA	LATRALPCPA	HVVFRYQAGR	EDELTITEGE	WLEVIEEGDA	DEWVKARNQH	GEVGFVPERY
490	500	510	520	530	540	550	560
LNFPDLSLPE	SSQDSDNPCG	AEPTAFLAQA	LYSYTGQSAE	ELSFPEGALI	RLLPRAQDGV	DDGFWRGEFG	GRVGVFPSLL
570	580	590	600	610	620	630	640
VEELLGPPGP	PELSDPEQML	PSPSPPSFSP	PAPTSVLDGP	PAPVLPGDKA	LDFPGFLDMM	APRLRPMRPP	PPPPAKAPDP
650							
GHPDPLT							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2505	1	735.3915	-44.40	2	61.8	10.0	0	624-636	R.LRPMRPPPPPPAK.A	Oxidation: 4

Detailed Protein Report

Protein 1358: kell blood group glycoprotein [Homo sapiens]

Accession:	gi|4557691	**Score:**	10.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	82.8
Database Date:	2015-11-30	**pI:**	9.1
		Sequence Coverage [%]:	1.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEGGDQSEEE	PRERSQAGGM	GTLWSQESTP	EERLPVEGSR	PWAVARRVLT	AILILGLLLC	FSVLLFYNFQ	NCGPRPCETS
90	100	110	120	130	140	150	160
VCLDLRDHYL	ASGNTSVAPC	TDFFSFACGR	AKETNNSFQE	LATKNKNRLR	RILEVQNSWH	PGSGEEKAFQ	FYNSCMDTLA
170	180	190	200	210	220	230	240
IEAAGTGPLR	QVIEELGGWR	ISGKWTSLNF	NRTLRLLMSQ	YGHFPFFRAY	LGPHPASPHT	PVIQIDQPEF	DVPLKQDQEQ
250	260	270	280	290	300	310	320
KIYAQIFREY	LTYLNQLGTL	LGGDPSKVQE	HSSLSISITS	RLFQFLRPLE	QRRAQGKLFQ	MVTIDQLKEM	APAIDWLSCL
330	340	350	360	370	380	390	400
QATFTPMSLS	PSQSLVVHDV	EYLKNMSQLV	EEMLLKQRDF	LQSHMILGLV	VTLSPALDSQ	FQEARRKLSQ	KLRELTEQPP
410	420	430	440	450	460	470	480
MPARPRWMKC	VEETGTFFEP	TLAALFVREA	FGPSTRSAAM	KLFTAIRDAL	ITRLRNLPWM	NEETQNMAQD	KVAQLQVEMG
490	500	510	520	530	540	550	560
ASEWALKPEL	ARQEYNDIQL	GSSFLQSVLS	CVRSLRARIV	QSFLQPHPQH	RWKVSPWDVN	AYYSVSDHVV	VFPAGLLQPP
570	580	590	600	610	620	630	640
FFHPGYPRAV	NFGAAGSIMA	HELLHIFYQL	LLPGGCLACD	NHALQEAHLC	LKRHYAAFPL	PSRTSFNDSL	TFLENAADVG
650	660	670	680	690	700	710	720
GLAIALQAYS	KRLLRHHGET	VLPSLDLSPQ	QIFFRSYAQV	MCRKPSPQDS	HDTHSPPHLR	VHGPLSSTPA	FARYFRCARG
730	740						
ALLNPSSRCQ	LW						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
941	1	593.7466	-114.09	2	41.3	10.0	0	171-180	R.QVIEELGGWR.I	

Detailed Protein Report

Protein 1359: PREDICTED: binder of sperm protein homolog 1 isoform X2 [Homo sapiens]

Accession:	gi|578833811	**Score:**	10.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	15.3
Database Date:	2015-11-30	**pI:**	8.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	13.1
		No. of unique Peptides:	1

```
        10          20          30          40          50          60          70          80
MARHMGLLLV  WVCLIRGVVG  GVVGAVFNVL  EEDELSSTVD  GECVFPFHYK  NGTYYDCIKS  KARHKWCSLN  KTYEGYWKFC
        90         100         110         120         130         140
SAEDFANCVF  PFWYRRLIYW  ECTDDGEAFG  KKWCSLTKNF  NKDRIWKYCE
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2210	1	1044.3865	-105.22	2	57.5	10.0	2	96-112	R.RLIYWECTDDGEAFGKK.W	Carbamidomethyl: 7

Detailed Protein Report

Protein 1360: PREDICTED: protoporphyrinogen oxidase isoform X6 [Homo sapiens]

Accession:	gi|530364988	**Score:**	10.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	38.5
Database Date:	2015-11-30	**pI:**	9.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	9.0
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578801162	refseq_human (refseq_human_20140103.fasta)	PREDICTED: protoporphyrinogen oxidase isoform X11 [Homo sapiens]

10	20	30	40	50	60	70	80
MRLCTVLPSA	ALDLSPSLTL	KVASLAMDSL	CRGVFAGNSR	ELSIRSCFPS	LFQAEQTHRS	ILLGLLLGAG	RTPQPDSALI
90	100	110	120	130	140	150	160
RQALAERWSQ	WSLRGGLEML	PQALETHLTS	RGVSVLRGQP	VCGLSLQAEG	RWKVSLRDSS	LEADHVISAI	PASVLSELLP
170	180	190	200	210	220	230	240
AEAAPLARAL	SAITAVSVAV	VNLQYQGAHL	PVQGFGHLVP	SSEDPGVLGI	VYDSVAFPEQ	DGSPPGLRVT	VMLGGSWLQT
250	260	270	280	290	300	310	320
LEASGCVLSQ	ELFQQRAQEA	AATQLGLKEM	PSHCLVHLHK	TKNQLKWRQS	HDRTVEWPKE	YPGRSRKQAP	SILHVPGCQL
330	340	350	360				
LRCRDRDHLG	AVSEQPRSSA	ESRVGVASST	FSTFPLF				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2164	1	1131.3015	31.86	3	56.9	10.0	2	1-32	-.MRLCTVLPSAALDLSPSLTLKVASLAMDSLCR.G	Oxidation: 27

Detailed Protein Report

Protein 1361: phosphoserine aminotransferase isoform 2 [Homo sapiens]

Accession:	gi|10863955	**Score:**	10.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	35.2
Database Date:	2015-11-30	**pI:**	6.3
		Sequence Coverage [%]:	2.2
		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
1777	1	917.3037	-164.85	1	52.2	10.0	0	318-324	K.FLEMHQL.-	

Detailed Protein Report

Protein 1362: **disintegrin and metalloproteinase domain-containing protein 21 preproprotein [Homo sapiens]**

Accession:	gi|333033779	**Score:**	10.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	80.8
Database Date:	2015-11-30	**pI:**	6.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAVDGTLVYI	RVTLLLLWLG	VFLSISGYCQ	AGPSQHFTSP	EVVIPLKVIS	RGRSAKAPGW	LSYSLRFGGQ	KHVVHMRVKK
90	100	110	120	130	140	150	160
LLVSRHLPVF	TYTDDRALLE	DQLFIPDDCY	YHGYVEAAPE	SLVVFSACFG	GFRGVLKISG	LTYEIEPIRH	SATFEHLVYK
170	180	190	200	210	220	230	240
INSNETQFPA	MRCGLTEKEV	ARQQLEFEEA	ENSALEPKSA	GDWWTHAWFL	ELVVVVNHDF	FIYSQSNISK	VQEDVFLVVN
250	260	270	280	290	300	310	320
IVDSMYKQLG	TYIILIGIEI	WNQGNVFPMT	SIEQVLNDFS	QWKQISLSQL	QHDAAHMFIK	NSLISILGLA	YVAGICRPPI
330	340	350	360	370	380	390	400
DCGVDNFQGD	TWSLFANTVA	HELGHTLGMQ	HDEEFCFCGE	RGCIMNTFRV	PAEKFTNCSY	ADFMKTTLNQ	GSCLHNPPRL
410	420	430	440	450	460	470	480
GEIFMLKRCG	NGVVEREEQC	DCGSVQQCEQ	DACCLLNCTL	RPGAACAFGL	CCKDCKFMPS	GELCRQEVNE	CDLPEWCNGT
490	500	510	520	530	540	550	560
SHQCPEDRYV	QDGIPCSDSA	YCYQKRCNNH	DQHCREIFGK	DAKSASQNCY	KEINSQGNRF	GHCGINGTTY	LKCHISDVFC
570	580	590	600	610	620	630	640
GRVQCENVRD	IPLLQDHFTL	QHTHINGVTC	WGIDYHLRMN	ISDIGEVKDG	TVCGPGKICI	HKKCVSLSVL	SHVCLPETCN
650	660	670	680	690	700	710	720
MKGICNNKHH	CHCGYGWSPP	YCQHRGYGGS	IDSGPASAKR	GVFLPLIVIP	SLSVLTFLFT	VGLLMYLRQC	SGPKETKAHS
730							
SG							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
458	1	592.1571	-119.04	2	35.0	10.0	0	507-515	R.CNNHDQHCR.E	Carbamidomethyl: 8

Detailed Protein Report

Protein 1363: BTB/POZ domain-containing protein KCTD18 [Homo sapiens]

Accession:	gi|45387953	**Score:**	10.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	46.7
Database Date:	2015-11-30	**pI:**	9.9
		Sequence Coverage [%]:	2.1
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|530369815	refseq_human(refseq_human_20140103.fasta)	PREDICTED: BTB/POZ domain-containing protein KCTD18 isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MEGHKAEEEV	LDVLRLNVGG	CIYTARRESL	CRFKDSMLAS	MFSGRFPLKT	DESGACVIDR	DGRLFKYLLD	YLHGEVQIPT
90	100	110	120	130	140	150	160
DEQTRIALQE	EADYFGIPYP	YSLSDHLANE	METYSLRSNI	ELKKALTDFC	DSYGLVCNKP	TVWVLHYLNT	SGASCESRII
170	180	190	200	210	220	230	240
GVYATKTDGT	DAIEKQLGGR	IHSKGIFKRE	AGNNVQYIWS	YYSVAELKKM	MDAFDAWEGK	GVSYWRVPHE	LIECWTLEER
250	260	270	280	290	300	310	320
PLLGSLRHMA	PIRKRRLITF	NEADESVNYK	TGPKPVRFLG	PSTSTQIKVK	NSASVTVSPA	SAIQTSAGAT	ANRFQSGSRR
330	340	350	360	370	380	390	400
KAAQRSAPSR	ATALVGTGAP	GHPQASPGAA	SAENGGTHLP	PAKVLLSDKK	PTPQRVIKLK	RTPLCATAPC	LPSPTATRQA
410	420	430					
NSLKPLPGEA	ARALGVRTEN	GKNKGN					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
588	1	472.1621	-200.95	2	36.9	10.0	1	322-330	K.AAQRSAPSR.A	

Detailed Protein Report

Protein 1364: interferon omega-1 precursor [Homo sapiens]

Accession: gi|4504605
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 10.0
MW [kDa]: 22.3
pI: 10.1
Sequence Coverage [%]: 8.2
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MALLFPLLAA	LVMTSYSPVG	SLGCDLPQNH	GLLSRNTLVL	LHQMRRISPF	LCLKDRRDFR	FPQEMVKGSQ	LQKAHVMSVL
90	100	110	120	130	140	150	160
HEMLQQIFSL	FHTERSSAAW	NMTLLDQLHT	GLHQQLQHLE	TCLLQVVGEG	ESAGAISSPA	LTLRRYFQGI	RVYLKEKKYS
170	180	190	200				
DCAWEVVRME	IMKSLFLSTN	MQERLRSKDR	DLGSS				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1937	1	682.2708	-81.85	3	54.3	10.0	2	158-173	K.KYSDCAWEVVRMEIMK.S	Carbamidomethyl: 5