Detailed Protein Report

Project Info

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

Sample Info & Protocols

Name: id-DOWN **Date:** Dec 10, 2015
Fraction:
Volume: **Concentration:**
Note:
Buffer: **Organism:**

Search Result Info

Search Result	Location	Search Engine	Database
ZT_human_PE_2015-12-10 16:24:32	/teeth-151208/id-DOWN/"Combined MS/MS spectra"	Mascot	refseq_human

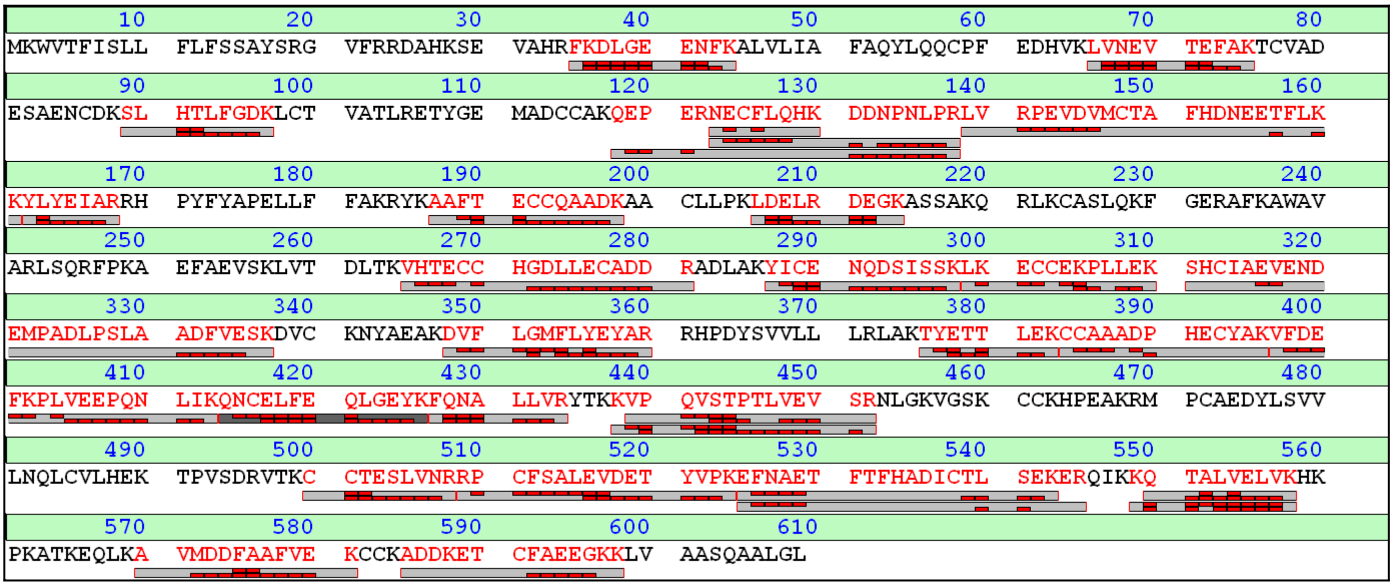
Protein 1: serum albumin preproprotein [Homo sapiens]

Accession: gi\|4502027
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl, Oxidation

Score: 1455.3
MW [kDa]: 69.3
pI: 5.9
Sequence Coverage [%]: 55.5
No. of unique Peptides: 30

Quantitation

mdown:qdown **Median:** 1.04 **CV:** 57.29 % **No. of Peptides:** 18
Wdown:Qdown **Median:** 0.59 **CV:** 92.33 % **No. of Peptides:** 18



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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
298	12	613.8004	-9.46	2	32.4	71.1	1	35-44	R.FKDLGEENFK.A		Wdown:Qdown 1.02 mdown:qdown 1.23
600	16	575.1620	-259.21	2	36.4	63.2	0	66-75	K.LVNEVTEFAK.T		Wdown:Qdown 0.99 mdown:qdown 3.00
357	7	509.1363	-266.02	2	33.8	49.0	0	89-97	K.SLHTLFGDK.L		Wdown:Qdown 1.33 mdown:qdown 0.62
171	1	659.8150	4.22	4	31.4	26.5	2	118-138	K.QEPERNECFLQHKDDNPNLPR.L	Carbamidomethyl: 8	
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	Wdown:Qdown 0.83 mdown:qdown 0.76

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1425	1	695.3249	-29.21	4	46.6	14.9	1	139-161	R. LVRPEVDVMCTAFHDNEETFLKK. Y	Carbamidomethyl: 10	
532	9	464.1198	-281.27	2	35.3	30.2	0	162-168	K.YLYEIAR.R		Wdown:Qdown 0.79 mdown:qdown 1.28
33	3	686.2794	-11.06	2	29.6	70.0	0	187-198	K.AAFTECCQAADK.A	Carbamidomethyl: 6, 7	
20	5	537.7465	-52.90	2	29.5	44.4	1	206-214	K.LDELRDEGK.A		Wdown:Qdown 0.46 mdown:qdown 0.80
235	5	696.2743	-13.94	3	31.7	57.7	0	265-281	K.VHTECCHGDLLECADDR.A	Carbamidomethyl: 5, 6, 13	Wdown:Qdown 1.57 mdown:qdown 0.83
43	6	722.3176	-9.77	2	29.9	70.8	0	287-298	K.YICENQDSISSK.L	Carbamidomethyl: 3	mdown:qdown 0.86 Wdown:Qdown 0.45
75	2	773.8989	-4.03	2	30.2	28.9	1	299-310	K.LKECCEKPLLEK.S	Carbamidomethyl: 4, 5	Wdown:Qdown 0.73 mdown:qdown 0.81
2988	1	992.1219	2.21	3	66.1	32.9	0	311-337	K. SHCIAEVENDEMPADLPSLAADFV D	Carbamidomethyl: 3	
2549	3	820.4166	26.51	2	60.1	54.2	0	348-360	K.DVFLGMFLYEYAR.R	Oxidation: 6	
42	1	492.7365	-23.11	2	29.7	28.1	0	376-383	K.TYETTLEK.C		Wdown:Qdown 0.55
3	5	776.7905	-15.51	2	28.9	31.9	0	384-396	K.CCAAADPHECYAK.V	Carbamidomethyl: 1, 2, 10	mdown:qdown 1.78
2246	52	682.3456	-35.78	3	56.6	62.3	0	397-413	K.VFDEFKPLVEEPQNLIK.Q		
1582	31	829.3539	-31.44	2	48.3	77.6	0	414-426	K.QNCELFEQLGEYK.F	Carbamidomethyl: 3	Wdown:Qdown 0.15
855	16	480.6439	-293.27	2	39.2	53.0	0	427-434	K.FQNALLVR.Y		Wdown:Qdown 0.17 mdown:qdown 2.77
783	8	820.4638	-10.68	2	38.6	67.6	1	438-452	K.KVPQVSTPTLVEVSR.N		mdown:qdown 0.74 Wdown:Qdown 0.22
1019	2	756.4151	-13.09	2	41.5	37.1	0	439-452	K.VPQVSTPTLVEVSR.N		mdown:qdown 1.44 Wdown:Qdown 0.34
57	4	569.7652	22.14	2	29.9	51.3	0	500-508	K.CCTESLVNR.R	Carbamidomethyl: 1, 2	
1753	6	637.6399	-13.90	3	50.5	67.0	0	509-524	R.RPCFSALEVDETYVPK.E	Carbamidomethyl: 3	Wdown:Qdown 0.17 mdown:qdown 0.31
2255	7	753.9716	-54.07	3	56.7	52.9	0	525-543	K.EFNAETFTFHADICTLSEK.E	Carbamidomethyl: 14	
2154	1	848.9827	-91.45	3	55.4	11.2	1	525-545	K.EFNAETFTFHADICTLSEKER. Q	Carbamidomethyl: 14	mdown:qdown 0.86
421	2	564.7074	-257.77	2	34.6	52.0	1	549-558	K.KQTALVELVK.H		Wdown:Qdown 0.71 mdown:qdown 0.91
860	15	500.8124	13.72	2	39.6	52.8	0	550-558	K.QTALVELVK.H		mdown:qdown 0.90
2105	55	671.7288	-137.21	2	54.9	98.5	0	570-581	K.AVMDDFAAFVEK.C		Wdown:Qdown 1.72
21	2	543.2367	-19.25	3	29.6	43.1	2	585-598	K.ADDKETCFAEEGKK.L	Carbamidomethyl: 7	Wdown:Qdown 1.67 mdown:qdown 1.85

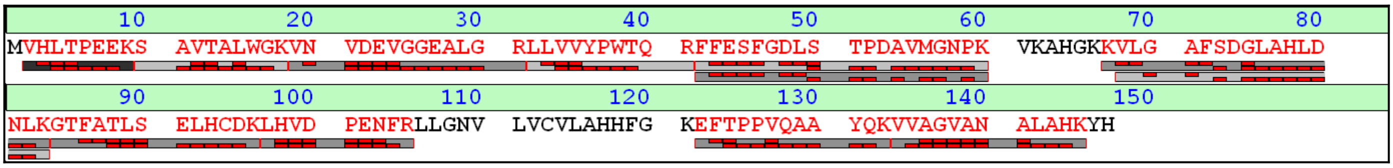
Detailed Protein Report

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

Accession:	gi|4504349	**Score:**	732.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	16.0
Database Date:	2015-11-30	**pI:**	6.9
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	83.0
		No. of unique Peptides:	12

Quantitation

mdown:qdown	**Median:**	0.66	**CV:**	88.03 %	**No. of Peptides:**	6
Wdown:Qdown	**Median:**	0.10	**CV:**	57.84 %	**No. of Peptides:**	5



Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
47	2	476.7443	-29.87	2	29.8	25.8	0	2-9	M.VHLTPEEK.S		
701	5	466.7367	-57.79	2	37.6	58.3	0	10-18	K.SAVTALWGK.V		mdown:qdown 0.34 Wdown:Qdown 0.07
391	7	657.8281	-12.11	2	34.2	66.6	0	19-31	K.VNVDEVGGEALGR.L		Wdown:Qdown 0.17 mdown:qdown 0.64
2103	16	637.8031	-99.32	2	56.4	50.0	0	32-41	R.LLVVYPWTQR.F		
2217	12	1029.8793	-95.37	2	56.2	51.5	0	42-60	R.FFESFGDLSTPDAVMGNPK.V		mdown:qdown 3.03
1677	1	1037.9101	-62.48	2	49.6	60.1	0	42-60	R.FFESFGDLSTPDAVMGNPK.V	Oxidation: 15	
2072	17	599.9066	-155.81	3	54.5	102.5	1	67-83	K.KVLGAFSDGLAHLDNLK.G		
2939	17	557.3045	4.87	3	65.5	94.6	0	68-83	K.VLGAFSDGLAHLDNLK.G		
595	2	739.7263	-168.37	2	36.3	53.2	0	84-96	K.GTFATLSELHCDK.L	Carbamidomethyl: 11	Wdown:Qdown 0.06 mdown:qdown 0.48
237	11	563.6399	-258.57	2	32.1	37.3	0	97-105	K.LHVDPENFR.L		mdown:qdown 0.81 Wdown:Qdown 0.19
563	3	689.7251	-186.44	2	35.9	45.0	0	122-133	K.EFTPPVQAAYQK.V		Wdown:Qdown 0.06 mdown:qdown 0.31
213	3	575.2065	-233.10	2	31.9	88.0	0	134-145	K.VVAGVANALAHK.Y		

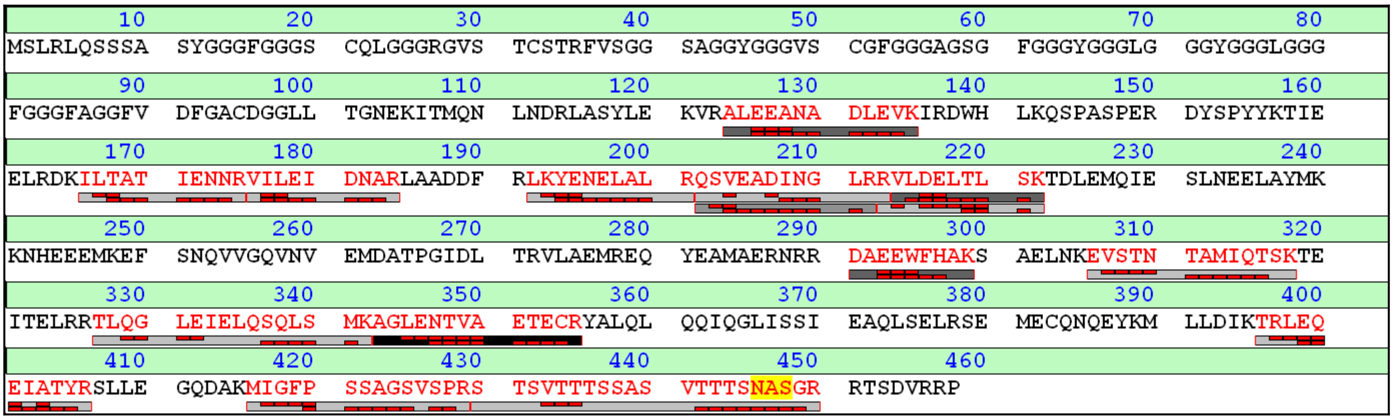
Detailed Protein Report

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

Accession:	gi|131412225	**Score:**	661.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	49.5
Database Date:	2015-11-30	**pI:**	4.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	34.7
		No. of unique Peptides:	15

Quantitation

mdown:qdown	**Median:**	0.69	**CV:**	42.42 %	**No. of Peptides:**	12
Wdown:Qdown	**Median:**	2.00	**CV:**	67.65 %	**No. of Peptides:**	11



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	3	651.1939	-213.19	2	32.7	78.3	0	124-135	R.ALEEANADLEVK.I		mdown:qdown 1.21
288	1	572.8039	-27.55	2	32.3	45.4	0	166-175	K.ILTATIENNR.V		Wdown:Qdown 0.81 mdown:qdown 1.32
528	7	521.6763	-233.65	2	35.9	61.6	0	176-184	R.VILEIDNAR.L		Wdown:Qdown 2.79 mdown:qdown 0.61
342	4	624.7261	-199.84	2	33.4	46.8	1	192-201	R.LKYENELALR.Q		mdown:qdown 0.51 Wdown:Qdown 1.80
379	5	601.3190	11.24	2	34.1	54.4	0	202-212	R.QSVEADINGLR.R		mdown:qdown 0.76
235	1	679.3515	-16.64	2	32.3	26.4	1	202-213	R.QSVEADINGLRR.V		Wdown:Qdown 2.65 mdown:qdown 0.51
686	1	587.3207	-42.26	2	37.1	41.5	1	213-222	R.RVLDELTLSK.T		mdown:qdown 0.46
809	4	509.1457	-293.16	2	38.6	50.8	0	214-222	R.VLDELTLSK.T		Wdown:Qdown 0.84 mdown:qdown 0.64
467	1	566.6136	-252.15	2	34.5	12.6	0	291-299	R.DAEEWFHAK.S		Wdown:Qdown 3.86 mdown:qdown 1.18
173	1	705.3260	-34.92	2	30.9	13.5	0	306-318	K.EVSTNTAMIQTSK.T		Wdown:Qdown 4.32
2903	1	909.4716	-17.49	2	65.4	28.3	0	327-342	R.TLQGLEIELQSQLSMK.A		Wdown:Qdown 2.40
142	2	725.3217	-19.13	2	31.2	69.4	0	343-355	K.AGLENTVAETECR.Y	Carbamidomethyl: 12	Wdown:Qdown 3.00 mdown:qdown 0.72
258	3	690.3402	-39.52	2	32.4	52.8	1	396-406	K.TRLEQEIATYR.S		Wdown:Qdown 2.61 mdown:qdown 0.76
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		Wdown:Qdown 0.71 mdown:qdown 0.32

Detailed Protein Report

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

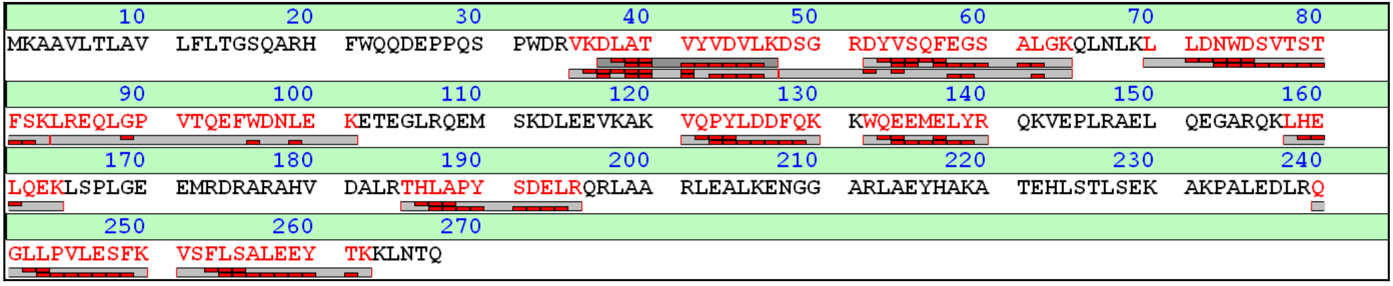
Accession:	gi|4557321	**Score:**	494.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	30.8
Database Date:	2015-11-30	**pI:**	5.5
		Sequence Coverage [%]:	45.7
		No. of unique Peptides:	12

Quantitation

mdown:qdown	**Median:**	1.63	**CV:**	30.66 %	**No. of Peptides:**	2
Wdown:Qdown	**Median:**	0.86	**CV:**	124.09 %	**No. of Peptides:**	4

Alias proteins:

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



10 20 30 40 50 60 70 80
MKAAVLTLAV LFLTGSQARH FWQQDEPPQS PWDRVKDLAT VYVDVLKDSG RDYVSQFEGS ALGKQLNLKL LDNWDSVTST

90 100 110 120 130 140 150 160
FSKLREQLGP VTQEFWDNLE KETEGLRQEM SKDLEEVKAK VQPYLDDFQK KWQEEMELYR QKVEPLRAEL QEGARQKLHE

170 180 190 200 210 220 230 240
LQEKLSPLGE EMRDRARAHV DALRTHLAPY SDELRQRLAA RLEALKENGG ARLAEYHAKA TEHLSTLSEK AKPALEDLRQ

250 260 270
GLLPVLESFK VSFLSALEEY TKKLNTQ

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1873	4	731.8942	-48.16	2	52.1	53.6	1	35-47	R.VKDLATVYVDVLK.D		
2093	3	618.2734	-120.22	2	54.7	58.3	0	37-47	K.DLATVYVDVLK.D		
805	1	908.4284	-0.73	2	38.9	11.7	1	48-64	K.DSGRDYVSQFEGSALGK.Q		Wdown:Qdown 0.52
943	3	700.8438	7.87	2	40.6	38.3	0	52-64	R.DYVSQFEGSALGK.Q		Wdown:Qdown 0.25
1807	8	806.8737	-27.99	2	51.3	94.1	0	70-83	K.LLDNWDSVTSTFSK.L		
2784	1	734.7111	-0.04	3	66.2	16.8	1	84-101	K.LREQLGPVTQEFWDNLEK.E		
681	5	626.6736	-224.11	2	37.1	28.6	0	121-130	K.VQPYLDDFQK.K		
860	1	642.2972	11.37	2	39.2	28.3	0	132-140	K.WQEEMELYR.Q		Wdown:Qdown 3.28 mdown:qdown 2.21
1373	1	896.6035	133.69	1	46.9	10.1	0	158-164	K.LHELQEK.L		
311	3	651.3061	-33.42	2	32.6	52.7	0	185-195	R.THLAPYSDELR.Q		Wdown:Qdown 1.30 mdown:qdown 1.21
2427	8	615.8382	-32.66	2	58.7	41.3	0	240-250	R.QGLLPVLESFK.V		
2300	6	693.8302	-44.61	2	57.2	61.0	0	251-262	K.VSFLSALEEYTK.K		

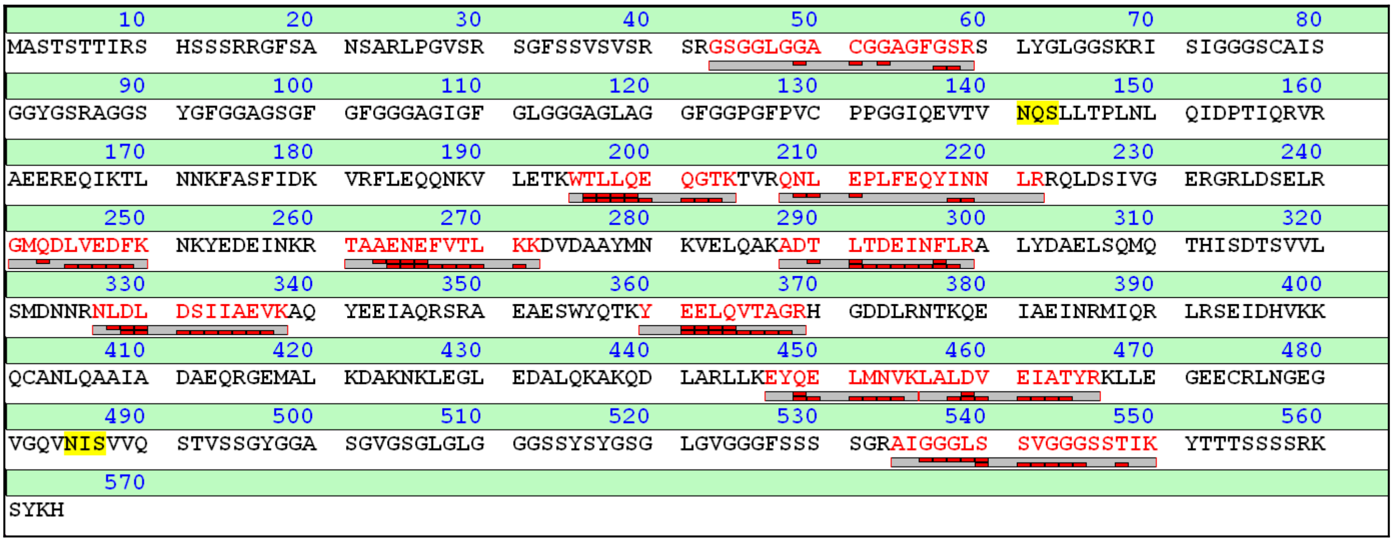
Detailed Protein Report

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

Accession:	gi|5031839	**Score:**	479.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	60.0
Database Date:	2015-11-30	**pI:**	8.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	23.9
		No. of unique Peptides:	11

Quantitation

mdown:qdown	**Median:**	0.60	**CV:**	168.38 %	**No. of Peptides:**	6
Wdown:Qdown	**Median:**	1.09	**CV:**	87.16 %	**No. of Peptides:**	5



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        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
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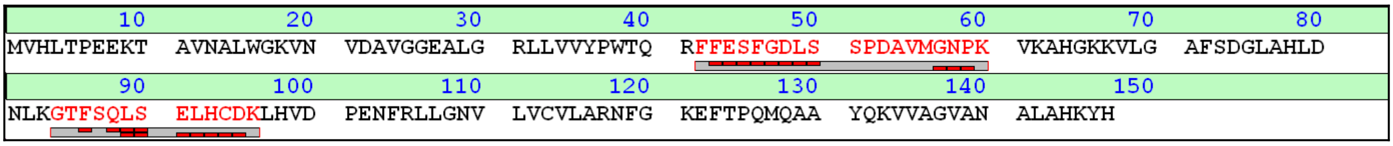
Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
902	1	712.9682	207.39	2	39.8	10.1	0	43-59	R.GSGGLGGACGGAGFGSR.S	Carbamidomethyl: 9	
910	11	602.3097	-20.53	2	39.9	44.2	0	195-204	K.WTLLQEQGTK.T		Wdown:Qdown 0.86 mdown:qdown 0.45
2397	1	945.9922	3.32	2	58.3	17.5	0	208-222	R.QNLEPLFEQYINNLR.R		
1215	2	591.1296	-252.65	2	44.9	47.4	0	241-250	R.GMQDLVEDFK.N		mdown:qdown 2.16
212	1	675.8653	-2.24	2	32.0	57.5	1	261-272	R.TAAENEFVTLKK.D		Wdown:Qdown 2.26 mdown:qdown 0.75
1892	10	704.2620	-138.19	2	53.7	69.2	0	288-299	K.ADTLTDEINFLR.A		
2868	18	665.3564	-15.34	2	65.0	82.6	0	327-338	R.NLDLDSIIAEVK.A		Wdown:Qdown 1.64
145	3	583.2816	-24.68	2	31.1	63.8	0	360-369	K.YEELQVTAGR.H		mdown:qdown 1.13 Wdown:Qdown 1.72
303	1	577.1338	-255.87	2	33.1	22.3	0	447-455	K.EYQELMNVK.L		mdown:qdown 1.02
2191	11	632.2117	-219.91	2	56.0	48.4	0	456-466	K.LALDVEIATYR.K		
359	1	724.3637	-37.90	2	33.6	16.6	0	534-550	R.AIGGGLSSVGGGSSTIK.Y		Wdown:Qdown 0.28 mdown:qdown 0.06

Protein 6: hemoglobin subunit delta [Homo sapiens]

Accession:	gi|4504351	**Score:**	462.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	16.0
Database Date:	2015-11-30	**pI:**	9.1
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	59.9
		No. of unique Peptides:	2


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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2232	1	1030.8450	-118.44	2	56.4	33.3	0	42-60	R.FFESFGDLSSPDAVMGNPK.V	Oxidation: 15
1086	2	761.3593	7.32	2	42.3	31.4	0	84-96	K.GTFSQLSELHCDK.L	Carbamidomethyl: 11

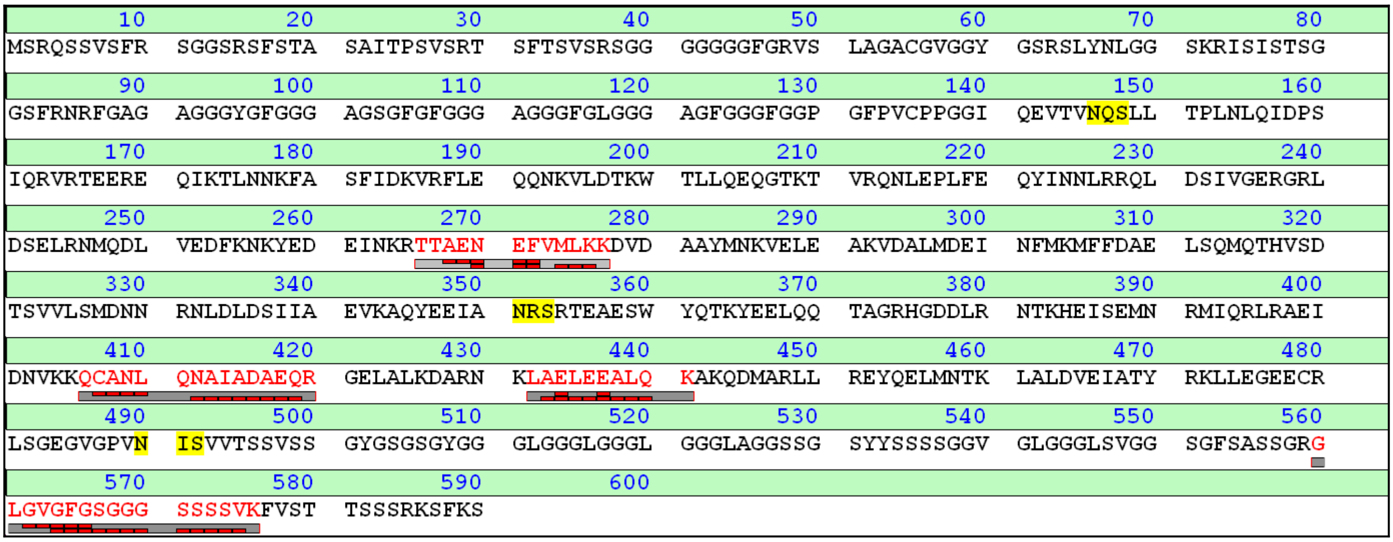
Detailed Protein Report

Protein 7: keratin, type II cytoskeletal 5 [Homo sapiens]

Accession:	gi|119395754	**Score:**	385.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	62.3
Database Date:	2015-11-30	**pI:**	8.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	17.3
		No. of unique Peptides:	4

Quantitation

mdown:qdown	**Median:**	0.46	**CV:**	12.37 %	**No. of Peptides:**	4
Wdown:Qdown	**Median:**	3.63	**CV:**	71.17 %	**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		mdown:qdown 0.38
553	1	851.4187	19.30	2	36.2	57.4	0	406-420	K.QCANLQNAIADAEQR.G	Carbamidomethyl: 2	mdown:qdown 0.48
804	1	572.1668	-261.37	2	38.5	48.3	0	432-441	K.LAELEEALQK.A		Wdown:Qdown 6.89 mdown:qdown 0.53
334	3	720.3453	-20.22	2	33.5	59.4	0	560-576	R.GLGVGFGSGGGSSSSVK.F		mdown:qdown 0.48 Wdown:Qdown 1.92

Detailed Protein Report

Protein 8: hemoglobin subunit alpha [Homo sapiens]

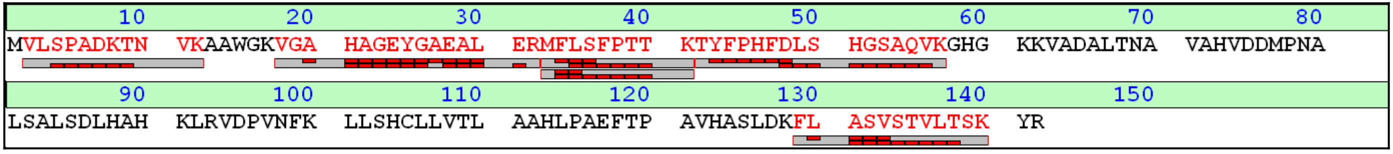
Accession:	gi|4504345	**Score:**	376.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	15.2
Database Date:	2015-11-30	**pI:**	9.4
Modification(s):	Oxidation	**Sequence Coverage [%]:**	44.4
		No. of unique Peptides:	6

Quantitation

mdown:qdown	**Median:**	0.87	**CV:**	366.85 %	**No. of Peptides:**	2
Wdown:Qdown	**Median:**	0.13	**CV:**	64.98 %	**No. of Peptides:**	2

Alias proteins:

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



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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
39	1	586.3399	3.78	2	29.7	55.0	1	2-12	M.VLSPADKTNVK.A		
111	9	765.3757	6.39	2	30.7	80.1	0	18-32	K.VGAHAGEYGAEALER.M		Wdown:Qdown 0.24
1149	2	544.2847	11.90	2	43.1	35.6	0	33-41	R.MFLSFPTTK.T	Oxidation: 1	
1779	24	536.2595	-39.76	2	50.9	56.7	0	33-41	R.MFLSFPTTK.T		mdown:qdown 4.44
1032	12	917.4300	-21.34	2	41.7	79.5	0	42-57	K.TYFPHFDLSHGSAQVK.G		Wdown:Qdown 0.07 mdown:qdown 0.17
1623	13	626.8522	-14.06	2	49.0	69.7	0	129-140	K.FLASVSTVLTSK.Y		

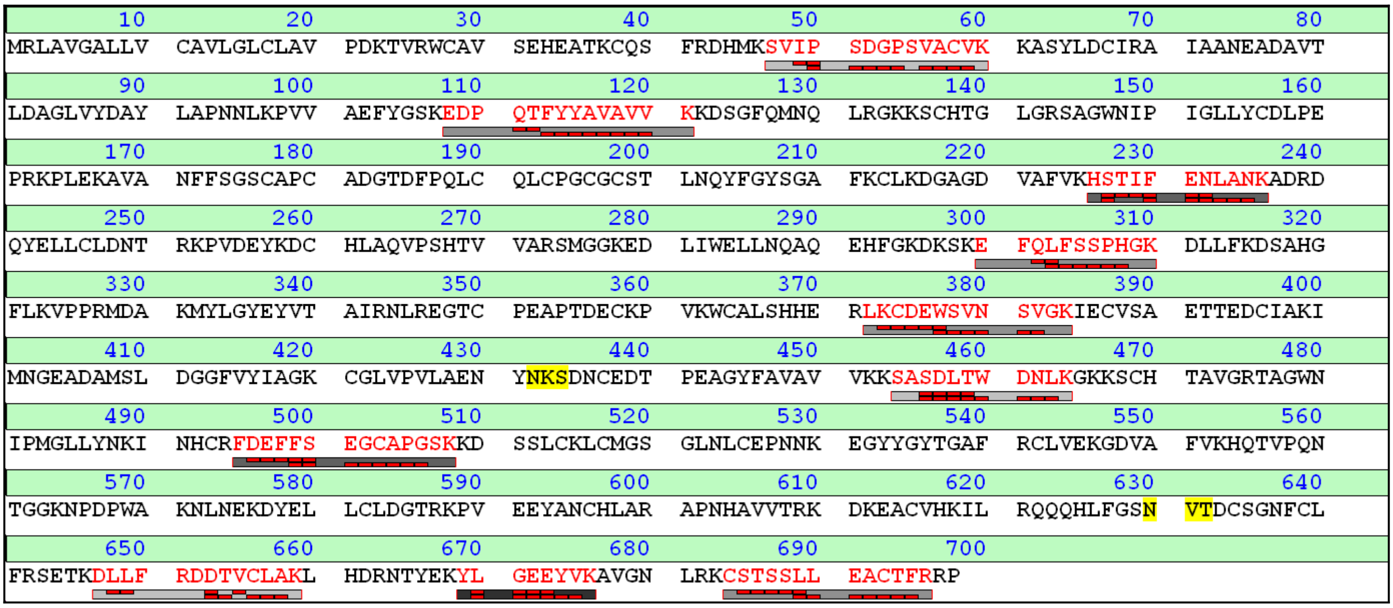
Detailed Protein Report

Protein 9: serotransferrin precursor [Homo sapiens]

Accession:	gi|4557871	**Score:**	375.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	77.0
Database Date:	2015-11-30	**pI:**	7.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	17.5
		No. of unique Peptides:	10

Quantitation

mdown:qdown	**Median:**	0.71	**CV:**	25.98 %	**No. of Peptides:**	7
Wdown:Qdown	**Median:**	0.68	**CV:**	50.84 %	**No. of Peptides:**	7



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
610	1	708.3500	-19.16	2	36.2	66.2	0	47-60	K.SVIPSDGPSVACVK.K	Carbamidomethyl: 12	mdown:qdown 0.73 Wdown:Qdown 0.87
1759	1	815.3781	-41.02	2	50.7	25.1	0	108-121	K.EDPQTFYYAVAVVK.K		
400	1	637.3157	-23.07	2	34.3	35.7	0	226-236	K.HSTIFENLANK.A		Wdown:Qdown 1.19 mdown:qdown 1.01
1032	2	638.7248	-148.43	2	41.4	30.2	0	300-310	K.EFQLFSSPHGK.D		
229	1	761.3746	3.44	2	32.3	48.1	1	372-384	R.LKCDEWSVNSVGK.I	Carbamidomethyl: 3	mdown:qdown 0.55 Wdown:Qdown 0.81
708	2	625.2611	-72.75	2	37.7	48.9	0	454-464	K.SASDLTWDNLK.G		mdown:qdown 0.46 Wdown:Qdown 0.33
817	2	789.3225	-12.58	2	39.0	49.5	0	495-508	R.FDEFFSEGCAPGSK.K	Carbamidomethyl: 9	mdown:qdown 0.87 Wdown:Qdown 1.21
1439	1	783.3662	-47.33	2	46.8	10.9	1	647-659	K.DLLFRDDTVCLAK.L	Carbamidomethyl: 10	Wdown:Qdown 0.41 mdown:qdown 0.82
232	3	500.6172	-271.08	2	32.1	36.9	0	669-676	K.YLGEEYVK.A		mdown:qdown 0.69 Wdown:Qdown 0.49
915	1	766.3408	-8.88	2	40.2	24.0	0	684-696	K.CSTSSLLEACTFR.R	Carbamidomethyl: 1, 10	

Detailed Protein Report

Protein 10: keratin, type I cytoskeletal 15 [Homo sapiens]

Accession:	gi|24430190	**Score:**	337.7
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

mdown:qdown	**Median:**	1.55	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	4.68	**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	5	515.1698	-253.80	2	39.5	44.9	0	215-223	R.VLDELTLAR.T		Wdown:Qdown 4.68 mdown:qdown 1.55

Detailed Protein Report

Protein 11: titin isoform IC [Homo sapiens]

Accession:	gi|388998877	**Score:**	303.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	3992.1
Database Date:	2015-11-30	**pI:**	6.0
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	0.9
		No. of unique Peptides:	23

Quantitation

mdown:qdown	**Median:**	0.58	**CV:**	49.87 %	**No. of Peptides:**	3
Wdown:Qdown	**Median:**	1.11	**CV:**	127.57 %	**No. of Peptides:**	4

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1676	1	839.3937	-10.73	2	49.5	10.3	2	1417-1431	R.MSPARMSPARMSPAR.M	Oxidation: 6, 11	Wdown:Qdown 0.30 mdown:qdown 0.35
1459	1	851.5485	120.85	2	48.0	14.8	0	7427-7441	K.DIEQTVGLPVTLTCR.L	Carbamidomethyl: 14	
2713	1	698.3756	114.21	2	62.8	14.9	0	8326-8337	K.VDHSDVGEYSCK.A	Carbamidomethyl: 11	
967	1	752.8772	-83.84	2	40.6	12.6	2	10852-10864	K.VPEEPKKPVPEKK.V		
1296	1	640.2561	-89.77	2	45.9	12.9	1	10963-10972	K.EVTIMEEKER.A	Oxidation: 5	
2926	1	713.8984	-28.68	2	65.7	11.1	1	11452-11464	K.VEPPPPPKVPEIK.K		
1036	8	555.3376	91.87	2	41.5	15.1	0	13889-13899	K.GTAIFACDIAK.D		Wdown:Qdown 2.51
2424	1	822.3339	-55.35	2	60.7	10.9	2	14955-14967	R.EKEMARFECELSR.E	Oxidation: 4	
2695	1	805.4194	19.35	2	64.9	15.3	2	14961-14973	R.FECELSRENAKVK.W	Carbamidomethyl: 3	
798	5	481.1628	-199.39	2	38.5	12.9	0	15703-15710	K.TWVLATDR.A		Wdown:Qdown 3.26
1108	1	540.7821	22.96	2	42.5	15.6	1	17633-17641	K.EIREGADYK.L		mdown:qdown 1.09
2888	1	900.4707	-22.65	2	64.8	13.7	0	18003-18018	K.NETVIEKPTDALQITK.E		
2673	3	813.4051	24.69	2	61.8	13.6	0	19641-19653	R.VPDLLEGCQYEFR.V	Carbamidomethyl: 8	
2371	2	805.2633	-115.33	2	60.0	12.7	0	28749-28761	R.EEEPLFDIDSEMR.K		
1812	1	658.3022	-97.61	2	52.7	11.3	0	29853-29864	K.AGEDVQVLIPFK.G		
2869	1	710.3695	-29.92	2	65.0	10.9	0	30145-30156	R.IGHNVHLELPYK.G		
2745	1	656.8669	67.42	2	62.7	10.9	0	30994-31005	K.YTLTVENNSGSK.S		
2485	1	862.3731	-106.42	2	61.5	10.8	0	31629-31646	R.AGSDLVLDAAVGGKPEPK.I		
98	1	529.8207	-183.86	3	30.5	11.1	1	32923-32936	K.DDGGSRVTGYYIER.K		
2686	1	937.4503	-21.14	2	62.5	12.9	0	33057-33072	K.QFTIGGLLEATEYEFR.V		
496	1	677.6900	21.58	3	35.5	11.2	2	33663-33680	K.DAGFYVVCAKNRFGIDQK.T		
37	1	731.6663	-74.70	3	29.7	10.4	2	35370-35388	K.TNLQFMGQAFKSIHEKVSK.I		Wdown:Qdown 0.61 mdown:qdown 0.52
1561	1	745.7829	-73.36	2	49.4	15.1	0	35482-35495	K.TDTSDSGLYTCTVK.N		

BRUKER

Detailed Protein Report

Protein 12: keratin, type I cytoskeletal 14 [Homo sapiens]

Accession:	gi|15431310	**Score:**	300.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	51.6
Database Date:	2015-11-30	**pI:**	4.9
Modification(s):	Oxidation	**Sequence Coverage [%]:**	17.8
		No. of unique Peptides:	4

Quantitation

mdown:qdown	**Median:**	1.20	**CV:**	147.60 %	**No. of Peptides:**	3
Wdown:Qdown	**Median:**	0.24	**CV:**	67.67 %	**No. of Peptides:**	2

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
121	2	713.3373	-20.71	2	30.8	66.0	0	42-56	R.APSTYGGGLSVSSSR.F		
639	1	680.8203	-49.04	2	36.6	15.5	1	212-223	R.MSVEADINGLRR.V		mdown:qdown 0.43 Wdown:Qdown 0.44
1899	3	586.6929	-125.55	2	52.2	33.2	0	301-309	K.DAEEWFFTK.T		mdown:qdown 5.28
1027	2	636.9803	-7.37	3	41.6	10.2	0	337-352	R.TMQNLEIELQSQLSMK.A	Oxidation: 15	mdown:qdown 0.77 Wdown:Qdown 0.13

Detailed Protein Report

Protein 13: **keratin, type II cytoskeletal 75 [Homo sapiens]**

Accession:	gi|153791158	**Score:**	247.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	59.5
Database Date:	2015-11-30	**pI:**	8.7
		Sequence Coverage [%]:	8.2
		No. of unique Peptides:	1

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
566	2	678.9555	96.02	2	35.7	53.0	1	413-424	K.LVDLEEALQKAK.Q	

Detailed Protein Report

Protein 14: alpha-1-antitrypsin precursor [Homo sapiens]

Accession:	gi|50363217	**Score:**	244.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	46.7
Database Date:	2015-11-30	**pI:**	5.3
		Sequence Coverage [%]:	23.0
		No. of unique Peptides:	5

Quantitation

mdown:qdown	**Median:**	1.75	**CV:**	13.54 %	**No. of Peptides:**	3
Wdown:Qdown	**Median:**	0.63	**CV:**	72.71 %	**No. of Peptides:**	3

Alias proteins:

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

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2910	3	858.7649	-23.64	3	65.6	35.3	0	126-149	R. TLNQPDSQLQLTTGNGLFLSEGLK L		
722	1	729.3434	-11.09	3	37.9	16.3	1	161-179	K.LYHSEAFTVNFGDTEEAKK.Q		Wdown:Qdown 0.32
762	1	601.9916	0.24	3	38.4	25.3	0	284-298	K.LQHLENELTHDIITK.F		mdown:qdown 1.97
904	4	555.7989	-12.32	2	39.8	70.1	0	315-324	K.LSITGTYDLK.S		Wdown:Qdown 0.51 mdown:qdown 1.88
1068	4	508.1796	-258.32	2	42.1	41.2	0	325-334	K.SVLGQLGITK.V		mdown:qdown 1.45 Wdown:Qdown 1.52

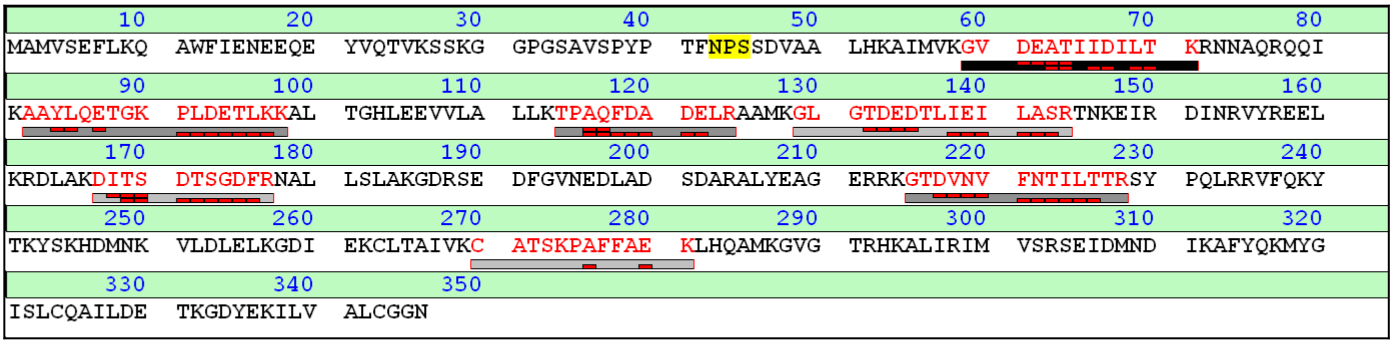
Detailed Protein Report

Protein 15: annexin A1 [Homo sapiens]

Accession:	gi|4502101	**Score:**	234.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	38.7
Database Date:	2015-11-30	**pI:**	6.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	27.2
		No. of unique Peptides:	7

Quantitation

mdown:qdown	**Median:**	2.22	**CV:**	104.73 %	**No. of Peptides:**	3
Wdown:Qdown	**Median:**	2.63	**CV:**	93.07 %	**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
2228	1	694.3075	-115.27	2	56.3	17.4	0	59-71	K.GVDEATIIDILTK.R		
537	1	635.6517	-48.42	3	35.3	22.1	1	82-98	K.AAYLQETGKPLDETLKK.A		
352	1	631.8010	-5.09	2	33.8	31.5	0	114-124	K.TPAQFDADELR.A		Wdown:Qdown 2.57 mdown:qdown 1.16
2453	2	851.9230	-27.64	2	59.0	48.1	0	129-144	K.GLGTDEDTLIEILASR.T		
174	2	607.2652	-8.28	2	30.9	68.2	0	167-177	K.DITSDTSGDFR.N		Wdown:Qdown 6.99 mdown:qdown 7.48
2388	1	775.8834	-37.22	2	58.2	36.2	0	215-228	K.GTDVNVFNTILTTR.S		Wdown:Qdown 1.01 mdown:qdown 1.26
2020	1	678.7710	-93.49	2	55.4	10.5	0	270-281	K.CATSKPAFFAEK.L	Carbamidomethyl: 1	

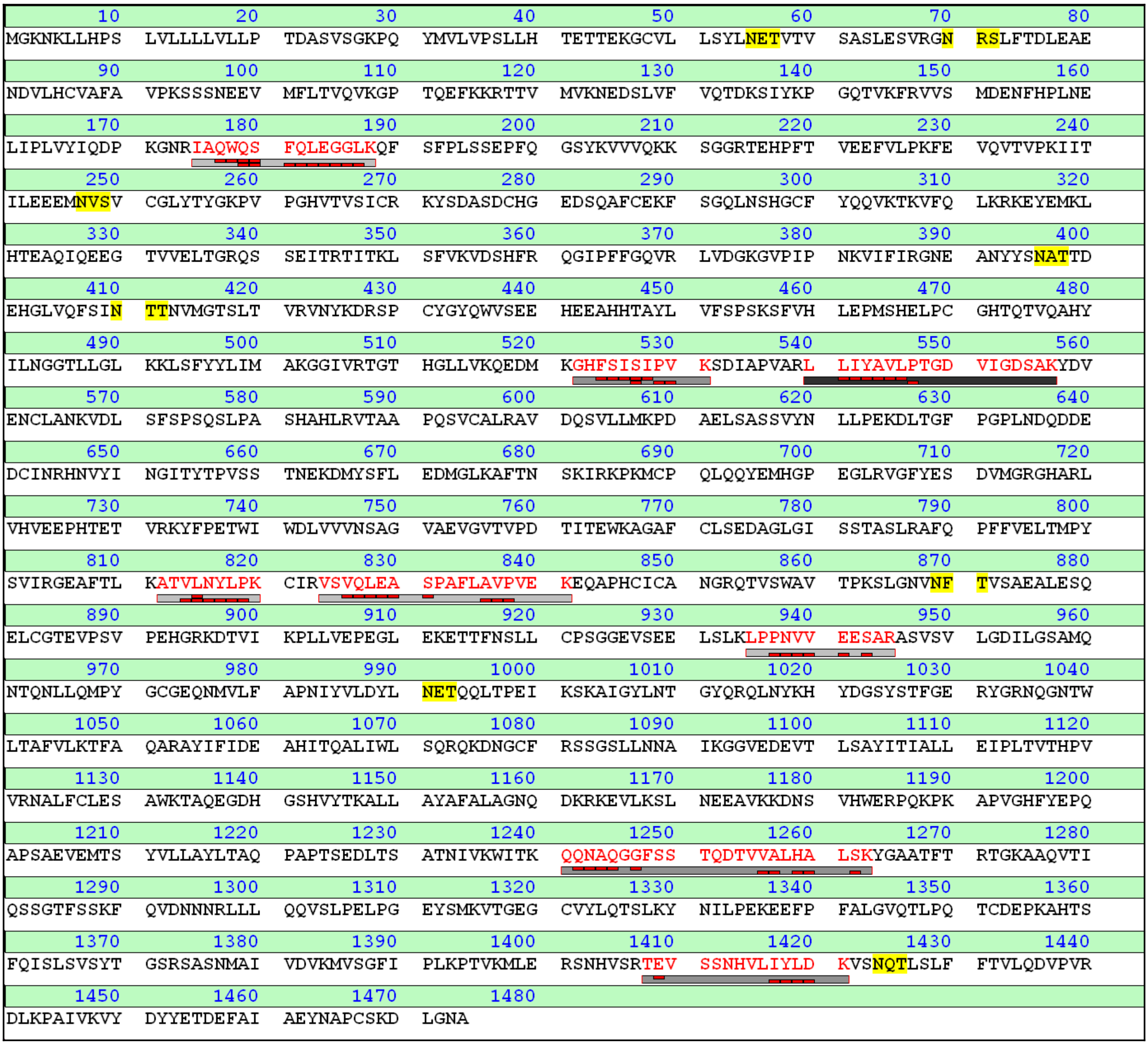
Detailed Protein Report

Protein 16: alpha-2-macroglobulin precursor [Homo sapiens]

Accession:	gi|66932947	**Score:**	220.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	163.2
Database Date:	2015-11-30	**pI:**	6.0
		Sequence Coverage [%]:	7.9
		No. of unique Peptides:	8

Quantitation

mdown:qdown	**Median:**	1.56	**CV:**	27.61 %	**No. of Peptides:**	2
Wdown:Qdown	**Median:**	1.15	**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
1683	5	802.8311	-117.18	2	49.7	41.2	0	175-188	R.IAQWQSFQLEGGLK.Q		
980	1	542.6642	-270.62	2	41.0	12.6	0	522-531	K.GHFSISIPVK.S		
2454	1	922.9898	-34.93	2	59.0	33.4	0	540-557	R.LLIYAVLPTGDVIGDSAK.Y		
1177	1	509.7828	-34.15	2	43.4	37.2	0	812-820	K.ATVLNYLPK.C		
2405	1	942.4446	-87.99	2	58.4	18.6	0	824-841	R.VSVQLEASPAFLAVPVEK.E		

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
234	1	605.7801	-74.07	2	32.3	35.4	0	935-945	K.LPPNVVEESAR.A		Wdown:Qdown 1.15 mdown:qdown 2.04
1151	1	796.4102	8.78	3	43.1	23.4	0	1241-1263	K.QQNAQGGFSSTQDTVVALHALSK.Y		
891	2	809.4242	-4.39	2	39.9	18.3	0	1408-1421	R.TEVSSNHVLIYLDK.V		mdown:qdown 1.19

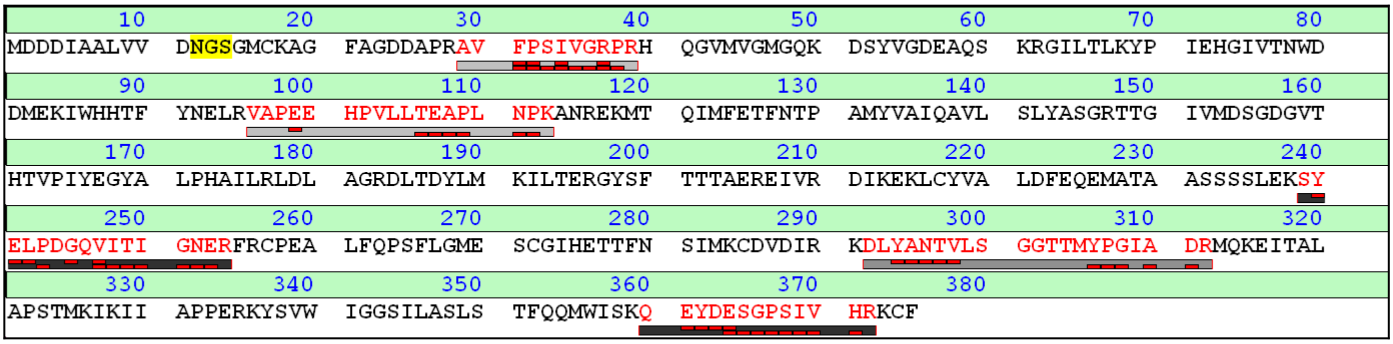
Detailed Protein Report

Protein 17: actin, cytoplasmic 1 [Homo sapiens]

Accession:	gi|4501885	**Score:**	215.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	41.7
Database Date:	2015-11-30	**pI:**	5.2
		Sequence Coverage [%]:	21.1
		No. of unique Peptides:	5

Quantitation

mdown:qdown	**Median:**	1.44	**CV:**	61.08 %	**No. of Peptides:**	5
Wdown:Qdown	**Median:**	1.30	**CV:**	21.84 %	**No. of Peptides:**	2



```
        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
659	3	599.7070	-249.11	2	36.8	51.4	0	29-39	R.AVFPSIVGRPR.H		mdown:qdown 1.29
2136	3	651.9448	-125.01	3	55.3	28.9	0	96-113	R.VAPEEHPVLLTEAPLNPK.A		mdown:qdown 3.26
1678	5	895.8924	-63.80	2	49.5	48.9	0	239-254	K.SYELPDGQVITIGNER.F		mdown:qdown 0.69 Wdown:Qdown 1.05
2043	1	1107.8969	-127.87	2	54.1	33.7	0	292-312	K.DLYANTVLSGGTTMYPGIADR.M		mdown:qdown 0.95
74	2	758.8545	-0.57	2	30.1	53.0	0	360-372	K.QEYDESGPSIVHR.K		Wdown:Qdown 1.61 mdown:qdown 2.23

Detailed Protein Report

Protein 18: keratin, type II cytoskeletal 4 [Homo sapiens]

Accession:	gi|331999954	**Score:**	179.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	56.1
Database Date:	2015-11-30	**pI:**	6.2
		Sequence Coverage [%]:	10.2
		No. of unique Peptides:	6

Quantitation

mdown:qdown	**Median:**	0.69	**CV:**	18.18 %	**No. of Peptides:**	3
Wdown:Qdown	**Median:**	1.59	**CV:**	54.27 %	**No. of Peptides:**	3

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
950	1	603.8017	-33.37	2	40.4	11.5	0	235-245	R.TAAENDFVVLK.K		Wdown:Qdown 0.78 mdown:qdown 0.88
530	2	667.8552	-21.26	2	35.2	56.2	1	235-246	R.TAAENDFVVLKK.D		mdown:qdown 0.64 Wdown:Qdown 2.40
1586	2	703.8014	-85.66	2	49.7	20.9	0	262-273	K.VDSLNDEINFLK.V		
2400	2	679.3689	-1.20	2	60.3	33.7	0	301-312	R.NLDLDSIIAEVR.A		
365	2	678.3483	-55.17	2	33.6	39.9	1	401-412	K.RVELEAALQQAK.E		mdown:qdown 0.58 Wdown:Qdown 2.17
1796	1	599.9815	-22.51	3	51.1	17.3	1	402-417	R.VELEAALQQAKEELAR.M		

Detailed Protein Report

Protein 19: keratin, type II cytoskeletal 2 epidermal [Homo sapiens]

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

Score: 176.3
MW [kDa]: 65.4
pI: 8.9
Sequence Coverage [%]: 5.5
No. of unique Peptides: 1

Quantitation

mdown:qdown	**Median:**	1.08	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.55	**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		Wdown:Qdown 0.55 mdown:qdown 1.08

Protein 20: PREDICTED: POTE ankyrin domain family member E isoform X1 [Homo sapiens]

Accession: gi|578804361
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 164.6
MW [kDa]: 76.6
pI: 4.9
Sequence Coverage [%]: 8.6
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MSQELEINKD	GDREVEEEMK	KHESNNVGLL	ENLTNGVTAG	NGDNGLIPQR	KSRTPENQQF	PDNESEEYHR	ICELLSDYKE
90	100	110	120	130	140	150	160
KQMPKYSSEN	SNPEQDLKLT	SEEESQRLKG	SENGQPEKRS	QEPEINKDGD	RELENFMAIE	EMKKHGSTHV	GFPENLTNGA
170	180	190	200	210	220	230	240
TAGNGDDGLI	PPRKSRTPES	QQFPDTENEE	YHSDEQNDTQ	KQFCEEQNTG	ILHDEILIHE	EKQIEVVEKM	NSELSLSCKK
250	260	270	280	290	300	310	320
EKDVLHENST	LREEIAMLRL	ELDTMKHQSQ	LREKKYLEDI	ESVKKKNDNL	LKALQLNELT	MDDDTAVLVI	DNGSGMCKAG
330	340	350	360	370	380	390	400
FAGDDAPRAV	FPSIVGRPRQ	QGMMGGMHQK	ESYVGKEAQS	KRGILTLKYP	MEHGIITNWD	DMEKIWHHTF	YNELRVAPEE
410	420	430	440	450	460	470	480
HPILLTEAPL	NPKANREKMT	QIMFETFNTP	AMYVAIQAVP	SLYTSGRTTG	IVMDSGDGVT	HTVPIYEGNA	LPHATLRLDL
490	500	510	520	530	540	550	560
AGRELPDYLM	KILTERGYRF	TTMAEREIVR	DIKEKLCYVA	LDFEQEMATA	ASSSSLEKSY	ELPDGQVITI	GNERFRCPEA
570	580	590	600	610	620	630	640
LFQPCFLGME	SCGIHETTFN	SIMKSDVDIR	KDLYTNTVLS	GGTTMYPGMA	HRMQKEIAAL	APSMMKIRII	APPKRKYSVW
650	660	670	680				
VGGSILASLS	TFQQMWISKQ	EYDESGPSIV	HRKCF				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1146	1	984.4853	-59.25	2	43.0	11.3	0	396-413	R.VAPEEHPILLTEAPLNPK.A	

Detailed Protein Report

Protein 21: **keratin, type II cytoskeletal 1 [Homo sapiens]**

Accession:	gi|119395750	**Score:**	154.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	66.0
Database Date:	2015-11-30	**pI:**	8.8
		Sequence Coverage [%]:	9.9
		No. of unique Peptides:	3

```
        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
1307	1	738.3615	-22.47	2	45.1	53.5	0	212-223	K.WELLQQVDTSTR.T	
2843	2	651.8509	-15.86	2	64.1	16.0	0	344-355	R.SLDLDSIIAEVK.A	
1168	1	922.9918	16.42	2	44.2	12.8	1	417-432	K.KQISNLQQSISDAEQR.G	

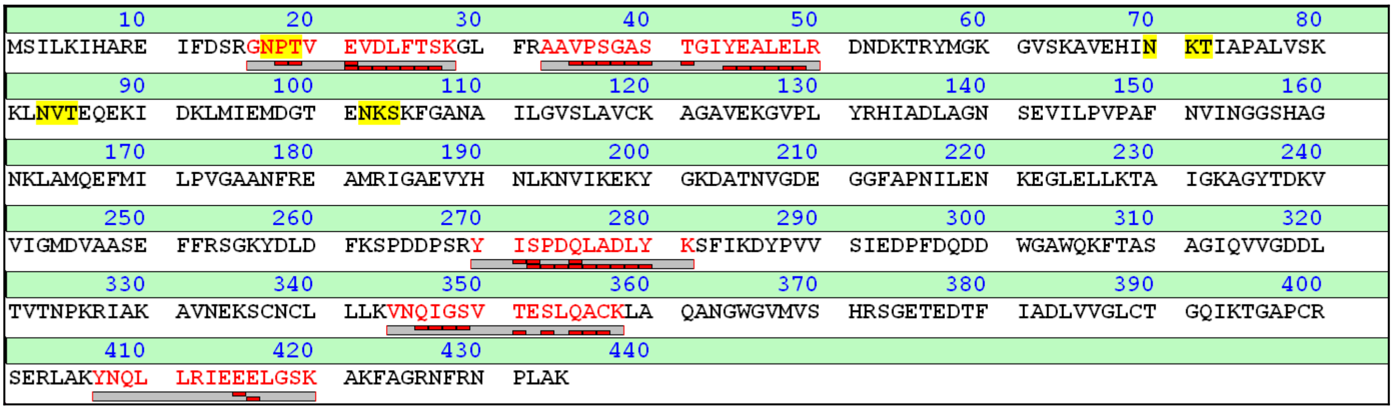
Detailed Protein Report

Protein 22: alpha-enolase isoform 1 [Homo sapiens]

Accession:	gi|4503571	**Score:**	146.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	47.1
Database Date:	2015-11-30	**pI:**	7.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	16.6
		No. of unique Peptides:	5

Quantitation

mdown:qdown	**Median:**	0.67	**CV:**	33.45 %	**No. of Peptides:**	2
Wdown:Qdown	**Median:**	1.72	**CV:**	51.45 %	**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
1541	1	703.8713	13.64	2	47.8	10.1	0	16-28	R.GNPTVEVDLFTSK.G		
2401	2	902.9549	-22.96	2	58.7	34.1	0	33-50	R.AAVPSGASTGIYEALELR.D		
1993	5	713.2706	-134.70	2	53.4	51.9	0	270-281	R.YISPDQLADLYK.S		
584	1	817.3947	-24.01	2	36.2	33.0	0	344-358	K.VNQIGSVTESLQACK.L	Carbamidomethyl: 14	Wdown:Qdown 1.06 mdown:qdown 0.48
307	1	846.3647	-102.88	2	33.2	17.4	1	407-420	K.YNQLLRIEEELGSK.A		mdown:qdown 0.92 Wdown:Qdown 2.78

Detailed Protein Report

Protein 23: actin, aortic smooth muscle [Homo sapiens]

Accession:	gi|4501883	**Score:**	130.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	42.0
Database Date:	2015-11-30	**pI:**	5.1
		Sequence Coverage [%]:	15.4
		No. of unique Peptides:	2

Quantitation

mdown:qdown	**Median:**	2.74	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.67	**CV:**	0.00 %	**No. of Peptides:**	1

Alias proteins:

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

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2088	1	652.6205	-100.50	3	54.7	15.4	0	98-115	R.VAPEEHPTLLTEAPLNPK.A		
267	1	750.8467	-14.36	2	32.1	15.2	0	362-374	K.QEYDEAGPSIVHR.K		Wdown:Qdown 0.67 mdown:qdown 2.74

Detailed Protein Report

Protein 24: **beta-actin-like protein 2 [Homo sapiens]**

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

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

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

Detailed Protein Report

Protein 25: pyruvate kinase PKM isoform f [Homo sapiens]

Accession: gi|332164781
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 119.1
MW [kDa]: 58.5
pI: 8.7
Sequence Coverage [%]: 9.9
No. of unique Peptides: 4

Quantitation

mdown:qdown **Median:** 0.45 **CV:** 16.33 % **No. of Peptides:** 2
Wdown:Qdown **Median:** 2.15 **CV:** 39.88 % **No. of Peptides:** 2

```
        10         20         30         40         50         60         70         80
MTSAAMSKPH SEAGTAFIQT QQLHAAMADT FLEHMCRLDI DSPPITARNT GIICTIGPAS RSVETLKEMI KSGMNVARLN
        90        100        110        120        130        140        150        160
FSHGTHEYHA ETIKNVRTAT ESFASDPILY RPVAVALDTK GPEIRTGLIK GSGTAEVELK KGATLKITLD NAYMEKCDEN
       170        180        190        200        210        220        230        240
ILWLDYKNIC KVVEVGSKIY VDDGLISLQV KQKGADFLVT EVENGGSLGS KKGVNLPGAA VDLPAVSEKD IQDLKFGVEQ
       250        260        270        280        290        300        310        320
DVDMVFASFI RKASDVHEVR KVLGEKGKNI KIISKIENHE GVRRFDEILE ASDGIMVARG DLGIEIPAEK VFLAQKMMIG
       330        340        350        360        370        380        390        400
RCNRAGKPVI CATQMLESMI KKPRPTRAEG SDVANAVLDG ADCIMLSGET AKGDYPLEAV RMQHLIAREA EAAMFHRKLF
       410        420        430        440        450        460        470        480
EELVRASSHS TDLMEAMAMG SVEASYKCLA AALIVLTESG RSAHQVARYR PRAPIIAVTR NPQTARQAHL YRGIFPVLCK
       490        500        510        520        530        540
DPVQEAWAED VDLRVNFAMN VGKARGFFKK GDVVIVLTGW RPGSGFTNTM RVVPVP
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
859	2	599.3167	-17.70	2	39.2	51.2	0	38-48	R.LDIDSPPITAR.N		Wdown:Qdown 3.15 mdown:qdown 0.39
566	1	680.2094	-215.66	2	36.4	14.7	0	49-61	R.NTGIICTIGPASR.S	Carbamidomethyl: 6	
111	1	628.6466	11.60	3	30.8	41.8	0	79-94	R.LNFSHGTHEYHAETIK.N		Wdown:Qdown 1.46 mdown:qdown 0.53
2063	1	731.7933	-161.16	2	54.4	11.5	0	179-191	K.IYVDDGLISLQVK.Q		

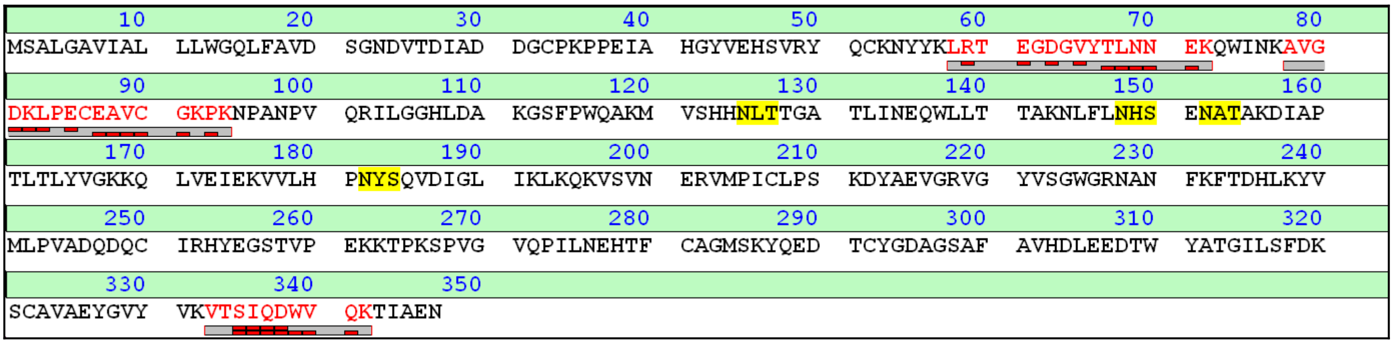
Detailed Protein Report

Protein 26: **haptoglobin isoform 2 preproprotein [Homo sapiens]**

Accession:	gi|186910296	**Score:**	114.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	38.4
Database Date:	2015-11-30	**pI:**	6.1
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	12.1
		No. of unique Peptides:	3

Quantitation

mdown:qdown	**Median:**	0.85	**CV:**	28.22 %	**No. of Peptides:**	2
Wdown:Qdown	**Median:**	0.57	**CV:**	18.62 %	**No. of Peptides:**	2



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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
136	2	854.8916	-43.33	2	31.0	42.7	1	58-72	K.LRTEGDGVYTLNNEK.Q		mdown:qdown 1.12 Wdown:Qdown 0.69
83	2	619.9584	-31.73	3	30.3	42.3	1	78-94	K.AVGDKLPECEAVCGKPK.N	Carbamidomethyl: 9, 13	Wdown:Qdown 0.48 mdown:qdown 0.64
819	1	602.3169	-8.58	2	38.7	29.6	0	333-342	K.VTSIQDWVQK.T		

Detailed Protein Report

Protein 27: PREDICTED: nebulin isoform X22 [Homo sapiens]

Accession:	gi|530370465	**Score:**	114.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	961.5
Database Date:	2015-11-30	**pI:**	9.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.2
		No. of unique Peptides:	7

Quantitation

mdown:qdown	**Median:**	1.64	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.66	**CV:**	0.00 %	**No. of Peptides:**	1

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	Ratios
2522	1	885.4523	-25.95	2	62.0	17.0	2	407-421	K.FKLDTVLQNFSSDKK.Y		
415	3	544.7701	86.52	2	34.2	12.0	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	
1176	2	729.3599	-9.93	2	43.4	18.3	1	3617-3628	R.KAYDLQSDNLYK.S		Wdown:Qdown 0.66 mdown:qdown 1.64
993	1	662.3199	-62.62	2	41.2	12.9	2	7204-7214	K.VKDEVSDLKYK.E		
624	1	607.8333	-21.30	2	36.4	10.4	2	7714-7723	K.RDLELEVKGR.G		
2801	1	994.5013	20.67	2	63.5	13.2	1	8000-8015	K.LNQENFSSVLYKENMR.K	Oxidation: 15	

Detailed Protein Report

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

Accession:	gi|4504517	**Score:**	107.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	22.8
Database Date:	2015-11-30	**pI:**	6.0
		Sequence Coverage [%]:	21.5
		No. of unique Peptides:	3

Quantitation

mdown:qdown **Median:** 1.04 **CV:** 0.00 % **No. of Peptides:** 1

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1668	7	582.3006	-23.03	2	50.8	56.0	0	28-37	R.LFDQAFGLPR.L		
1666	3	953.4317	-71.06	2	49.5	35.6	0	172-188	K.LATQSNEITIPVTFESR.A		mdown:qdown 1.04
2886	2	822.4678	63.76	2	64.8	15.6	1	189-205	R.AQLGGPEAAKSDETAAK.-		

Protein 29: cadherin EGF LAG seven-pass G-type receptor 3 precursor [Homo sapiens]

Accession:	gi|145309304	**Score:**	103.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	358.0
Database Date:	2015-11-30	**pI:**	6.2
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	3.0
		No. of unique Peptides:	7

Quantitation

Wdown:Qdown	**Median:**	0.31	**CV:**	0.00 %	**No. of Peptides:**	1	

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1647	5	942.4685	14.29	2	49.1	22.8	1	232-250	R.RNCLPGASGSGPELDSAPR.T		
2841	1	648.3701	87.56	1	64.1	13.5	0	1513-1518	R.CEVAAR.S		
2719	1	964.4996	-2.09	2	62.9	13.4	2	1519-1534	R.SFPPSSFVMFRGLRQR.F	Oxidation: 9	
2229	1	956.4132	-125.14	2	56.5	12.5	1	2144-2162	K.FGVLATVPCPRGALGAAVR.L	Carbamidomethyl: 9	
942	1	470.6329	-182.64	2	40.6	10.3	0	2331-2338	R.MEHPSSPR.G		Wdown:Qdown 0.31
2129	1	698.8200	-38.23	2	55.2	13.9	2	2331-2342	R.MEHPSSPRGARR.Y	Oxidation: 1	
118	1	1069.1641	-33.12	3	30.2	17.4	1	3083-3111	R.ERLEEAPAPVLRPLSRPGSQECM L	Carbamidomethyl: 22; Oxidation: 23	

Detailed Protein Report

Protein 30: PREDICTED: dystonin isoform X9 [Homo sapiens]

Accession:	gi|530382434	**Score:**	101.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	872.0
Database Date:	2015-11-30	**pI:**	5.0
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	1.3
		No. of unique Peptides:	6

Quantitation

mdown:qdown	**Median:**	0.81	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.70	**CV:**	0.00 %	**No. of Peptides:**	1

10	20	30	40	50	60	70	80
MSSGNASYRC	SMSSSADFSD	EDDFSQKSGS	ASPAPGDTLP	WNLPKHERSK	RKIQGGSVLD	PAERAVLRIA	DERDKVQKKT
90	100	110	120	130	140	150	160
FTKWINQHLM	KVRKHVNDLY	EDLRDGHNLI	SLLEVLSGDT	LPRERDFLKT	LRLVSATEAC	EYEQHEDVED	EDKGPREKGR
170	180	190	200	210	220	230	240
MRFHRLQNVQ	IALDYLKRRQ	VKLVNIRNDD	ITDGNPKLTL	GLIWTIILHF	QISDIHVTGE	SEDMSAKERL	LLWTQQATEG
250	260	270	280	290	300	310	320
YAGIRCENFT	TCWRDGKLFN	AIIHKYRPDL	IDMNTVAVQS	NLANLEHAFY	VAEKIGVIRL	LDPEDVDVSS	PDEKSVITYV
330	340	350	360	370	380	390	400
SSLYDAFPKV	PEGGEGIGAN	DVEVKWIEYQ	NMVNYLIQWI	RHHVTTMSER	TFPNNPVELK	ALYNQYLQFK	ETEIPPKETE
410	420	430	440	450	460	470	480
KSKIKRLYKL	LEIWIEFGRI	KLLQGYHPND	IEKEWGKLII	AMLEREKALR	PEVERLEMLQ	QIANRVQRDS	VICEDKLILA
490	500	510	520	530	540	550	560
GNALQSDSKR	LESGVQFQNE	AEIAGYILEC	ENLLRQHVID	VQILIDGKYY	QADQLVQRVA	KLRDEIMALR	NECSSVYSKG
570	580	590	600	610	620	630	640
RILTTEQTKL	MISGITQSLN	SGFAQTLHPS	LTSGLTQSLT	PSLTSSSMTS	GLSSGMTSRL	TPSVTPAYTP	GFPSGLVPNF
650	660	670	680	690	700	710	720
SSGVEPNSLQ	TLKLMQIRKP	LLKSSLLDQN	LTEEEINMKF	VQDLLNWVDE	MQVQLDRTEW	GSDLPSVESH	LENHKNVHRA
730	740	750	760	770	780	790	800
IEEFESSLKE	AKISEIQMTA	PLKLTYAEKL	HRLESQYAKL	LNTSRNQERH	LDTLHNFVSR	ATNELIWLNE	KEEEEVAYDW
810	820	830	840	850	860	870	880
SERNTNIARK	KDYHAELMRE	LDQKEENIKS	VQEIAEQLLL	ENHPARLTIE	AYRAAMQTQW	SWILQLCQCV	EQHIKENTAY
890	900	910	920	930	940	950	960
FEFFNDAKEA	TDYLRNLKDA	IQRKYSCDRS	SSIHKLEDLV	QESMEEKEEL	LQYKSTIANL	MGKAKTIIQL	KPRNSDCPLK
970	980	990	1000	1010	1020	1030	1040
TSIPIKAICD	YRQIEITIYK	DDECVLANNS	HRAKWKVISP	TGNEAMVPSV	CFTVPPPNKE	AVDLANRIEQ	QYQNVLTLWH
1050	1060	1070	1080	1090	1100	1110	1120
ESHINMKSVV	SWHYLINEID	RIRASNVASI	KTMLPGEHQQ	VLSNLQSRFE	DFLEDSQESQ	VFSGSDITQL	EKEVNVCKQY
1130	1140	1150	1160	1170	1180	1190	1200
YQELLKSAER	EEQEESVYNL	YISEVRNIRL	RLENCEDRLI	RQIRTPLERD	DLHESVFRIT	EQEKLKKELE	RLKDDLGTIT
1210	1220	1230	1240	1250	1260	1270	1280
NKCEEFFSQA	AASSSVPTLR	SELNVVLQNM	NQVYSMSSTY	IDKLKTVNLV	LKNTQAAEAL	VKLYETKLCE	EEAVIADKNN
1290	1300	1310	1320	1330	1340	1350	1360
IENLISTLKQ	WRSEVDEKRQ	VFHALEDELQ	KAKAISDEMF	KTYKERDLDF	DWHKEKADQL	VERWQNVHVQ	IDNRLRDLEG
1370	1380	1390	1400	1410	1420	1430	1440
IGKSLKYYRD	TYHPLDDWIQ	QVETTQRKIQ	ENQPENSKTL	ATQLNQQKML	VSEIEMKQSK	MDECQKYAEQ	YSATVKDYEL
1450	1460	1470	1480	1490	1500	1510	1520
QTMTYRAMVD	SQQKSPVKRR	RMQSSADLII	QEFMDLRTRY	TALVTLMTQY	IKFAGDSLKR	LEEEEKSLEE	EKKEHVEKAK
1530	1540	1550	1560	1570	1580	1590	1600
ELQKWVSNIS	KTLKDAEKAG	KPPFSKQKIS	SEEISTKKEQ	LSEALQTIQL	FLAKHGDKMT	DEERNELEKQ	VKTLQESYNL
1610	1620	1630	1640	1650	1660	1670	1680
LFSESLKQLQ	ESQTSGDVKV	EEKLDKVIAG	TIDQTTGEVL	SVFQAVLRGL	IDYDTGIRLL	ETQLMISGLI	SPELRKCFDL
1690	1700	1710	1720	1730	1740	1750	1760
KDAKSHGLID	EQILCQLKEL	SKAKEIISAA	SPTTIPVLDA	LAQSMITESM	AIKVLEILLS	TGSLVIPATG	EQLTLQKAFQ
1770	1780	1790	1800	1810	1820	1830	1840
QNLVSSALFS	KVLERQNMCK	DLIDPCTSEK	VSLIDMVQRS	TLQENTGMWL	LPVRPQEGGR	ITLKCGRNIS	ILRAAHEGLI
1850	1860	1870	1880	1890	1900	1910	1920
DRETMFRLLS	AQLLSGGLIN	SNSGQRMTVE	EAVREGVIDR	DTASSILTYQ	VQTGGIIQSN	PAKRLTVDEA	VQCDLITSSS
1930	1940	1950	1960	1970	1980	1990	2000
ALLVLEAQRG	YVGLIWPHSG	EIFPTSSSLQ	QELITNELAY	KILNGRQKIA	ALYIPESSQV	IGLDAAKQLG	IIDNNTASIL
2010	2020	2030	2040	2050	2060	2070	2080
KNITLPDKMP	DLGDLEACKN	ARRWLSFCKF	QPSTVHDYRQ	EEDVFDGEEP	VTTQTSEETK	KLFLSYLMIN	SYMDANTGQR
2090	2100	2110	2120	2130	2140	2150	2160
LLLYDGDLDE	AVGMLLEGCH	AEFDGNTAIK	ECLDVLSSSG	VFLNNASGRE	KDECTATPSS	FNKCHCGEPE	HEETPENRKC
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	542-550	K.LRDEIMALR.N		Wdown:Qdown 0.70 mdown:qdown 0.81
1982	1	927.8655	-42.70	2	53.4	10.5	1	1776-1790	R.QNMCKDLIDPCTSEK.V	Carbamidomethyl: 4, 11; Oxidation: 3	
103	1	822.3979	-76.79	2	30.5	11.5	2	3803-3816	K.LNEAKIKCEQLNLK.A		
779	1	1105.2011	129.15	2	38.2	12.7	2	4203-4221	K.TLDDIVGRYEDLSKSVNER.N		
2450	1	684.2042	-212.00	2	61.0	10.9	1	4940-4951	K.EEQNKSHPISAK.L		
2575	1	588.6984	-194.01	2	60.9	10.5	0	6226-6235	K.LLDVMELAEK.F	Oxidation: 5	

Detailed Protein Report

Protein 31: **PREDICTED: plectin isoform X7 [Homo sapiens]**

Accession:	gi|530389155	**Score:**	101.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	514.1
Database Date:	2015-11-30	**pI:**	5.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.3
		No. of unique Peptides:	4

Quantitation

mdown:qdown	**Median:**	0.40	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.34	**CV:**	0.00 %	**No. of Peptides:**	1

10	20	30	40	50	60	70	80
MDPSRAIQNE	ISSLKDERDR	VQKKTFTKWV	NKHLIKHWRA	EAQRHISDLY	EDLRDGHNLI	SLLEVLSGDS	LPREKGRMRF
90	100	110	120	130	140	150	160
HKLQNVQIAL	DYLRHRQVKL	VNIRNDDIAD	GNPKLTLGLI	WTIILHFQIS	DIQVSGQSED	MTAKEKLLLW	SQRMVEGYQG
170	180	190	200	210	220	230	240
LRCDNFTSSW	RDGRLFNAII	HRHKPLLIDM	NKVYRQTNLE	NLDQAFSVAE	RDLGVTRLLD	PEDVDVPQPD	EKSIITYVSS
250	260	270	280	290	300	310	320
LYDAMPRVPD	VQDGVRANEL	QLRWQEYREL	VLLLLQWMRH	HTAAFEERRF	PSSFEEIEIL	WSQFLKFKEM	ELPAKEADKN
330	340	350	360	370	380	390	400
RSKGIYQSLE	GAVQAGQLKV	PPGYHPLDVE	KEWGKLHVAI	LEREKQLRSE	FERLECLQRI	VTKLQMEAGL	CEEQLNQADA
410	420	430	440	450	460	470	480
LLQSDVRLLA	AGKVPQRAGE	VERDLDKADS	MIRLLFNDVQ	TLKDGRHPQG	EQMYRRVYRL	HERLVAIRTE	YNLRLKAGVA
490	500	510	520	530	540	550	560
APATQVAQVT	LQSVQRRPEL	EDSTLRYLQD	LLAWVEENQH	RVDGAEWGVD	LPSVEAQLGS	HRGLHQSIEE	FRAKIERARS
570	580	590	600	610	620	630	640
DEGQLSPATR	GAYRDCLGRL	DLQYAKLLNS	SKARLRSLES	LHSFVAAATK	ELMWLNEKEE	EEVGFDWSDR	NTNMTAKKES
650	660	670	680	690	700	710	720
YSALMRELEL	KEKKIKELQN	AGDRLLREDH	PARPTVESFQ	AALQTQWSWM	LQLCCCIEAH	LKENAAYFQF	FSDVREAEGQ
730	740	750	760	770	780	790	800
LQKLQEALRR	KYSCDRSATV	TRLEDLLQDA	QDEKEQLNEY	KGHLSGLAKR	AKAVVQLKPR	HPAHPMRGRL	PLLAVCDYKQ
810	820	830	840	850	860	870	880
VEVTVHKGDE	CQLVGPAQPS	HWKVLSSSGS	EAAVPSVCFL	VPPPNQEAQE	AVTRLEAQHQ	ALVTLWHQLH	VDMKSLLAWQ
890	900	910	920	930	940	950	960
SLRRDVQLIR	SWSLATFRTL	KPEEQRQALH	SLELHYQAFL	RDSQDAGGFG	PEDRLMAERE	YGSCSHHYQQ	LLQSLEQGAQ
970	980	990	1000	1010	1020	1030	1040
EESRCQRCIS	ELKDIRLQLE	ACETRTVHRL	RLPLDKEPAR	ECAQRIAEQQ	KAQAEVEGLG	KGVARLSAEA	EKVLALPEPS
1050	1060	1070	1080	1090	1100	1110	1120
PAAPTLRSEL	ELTLGKLEQV	RSLSAIYLEK	LKTISLVIRG	TQGAEEVLRA	HEEQLKEAQA	VPATLPELEA	TKASLKKLRA
1130	1140	1150	1160	1170	1180	1190	1200
QAEAQQPTFD	ALRDELRGAQ	EVGERLQQRH	GERDVEVERW	RERVAQLLER	WQAVLAQTDV	RQRELEQLGR	QLRYYRESAD
1210	1220	1230	1240	1250	1260	1270	1280
PLGAWLQDAR	RRQEQIQAMP	LADSQAVREQ	LRQEQALLEE	IERHGEKVEE	CQRFAKQYIN	AIKDYELQLV	TYKAQLEPVA
1290	1300	1310	1320	1330	1340	1350	1360
SPAKKPKVQS	GSESVIQEYV	DLRTHYSELT	TLTSQYIKFI	SETLRRMEEE	ERLAEQQRAE	ERERLAEVEA	ALEKQRQLAE
1370	1380	1390	1400	1410	1420	1430	1440
AHAQAKAQAE	REAKELQQRM	QEEVVRREEA	AVDAQQQKRS	IQEELQQLRQ	SSEAEIQAKA	RQAEAAERSR	LRIEEEIRVV
1450	1460	1470	1480	1490	1500	1510	1520
RLQLEATERQ	RGGAEGELQA	LRARAEEAEA	QKRQAQEEAE	RLRRQVQDES	QRKRQAEVEL	ASRVKAEAEA	AREKQRALQA
1530	1540	1550	1560	1570	1580	1590	1600
LEELRLQAEE	AERRLRQAEV	ERARQVQVAL	ETAQRSAEAE	LQSKRASFAE	KTAQLERSLQ	EEHVAVAQLR	EEAERRAQQQ
1610	1620	1630	1640	1650	1660	1670	1680
AEAERAREEA	ERELERWQLK	ANEALRLRLQ	AEEVAQQKSL	AQAEAEKQKE	EAEREARRRG	KAEEQAVRQR	ELAEQELEKQ
1690	1700	1710	1720	1730	1740	1750	1760
RQLAEGTAQQ	RLAAEQELIR	LRAETEQGEQ	QRQLLEEELA	RLQREAAAAT	QKRQELEAEL	AKVRAEMEVL	LASKARAEEE
1770	1780	1790	1800	1810	1820	1830	1840
SRSTSEKSKQ	RLEAEAGRFR	ELAEEAARLR	ALAEEAKRQR	QLAEEDAARQ	RAEAERVLAE	KLAAIGEATR	LKTEAEIALK
1850	1860	1870	1880	1890	1900	1910	1920
EKEAENERLR	RLAEDEAFQR	RRLEEQAAQH	KADIEERLAQ	LRKASDSELE	RQKGLVEDTL	RQRRQVEEEI	LALKASFEKA
1930	1940	1950	1960	1970	1980	1990	2000
AAGKAELELE	LGRIRSNAED	TLRSKEQAEL	EAARQRQLAA	EEERRRREAE	ERVQKSLAAE	EEAARQRKAA	LEEVERLKAK
2010	2020	2030	2040	2050	2060	2070	2080
VEEARRLRER	AEQESARQLQ	LAQEAAQKRL	QAEEKAHAFA	VQQKEQELQQ	TLQQEQSVLD	QLRGEAEAAR	RAAEEAEEAR
2090	2100	2110	2120	2130	2140	2150	2160
VQAEREAAQS	RRQVEEAERL	KQSAEEQAQA	RAQAQAAAEK	LRKEAEQEAA	RRAQAEQAAL	RQKQAADAEM	EKHKKFAEQT
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
1213	1	713.6809	-62.89	3	43.8	10.9	2	2258-2277	K.QVAEEAARLSVAAQEAARLR.Q		
1692	1	582.1401	-225.95	2	51.1	12.2	0	2358-2367	R.QLEMSAEAER.L		
42	1	768.2950	-141.23	2	29.9	18.7	1	3585-3598	R.AQLMADFQAGRVTK.E		mdown:qdown 0.40 Wdown:Qdown 0.34
1932	1	1021.8810	-139.60	2	52.6	12.9	2	3847-3864	R.CRRDDGTGQLLLPLSDAR.K	Carbamidomethyl: 1	

Detailed Protein Report

Protein 32: **lactotransferrin isoform 2 [Homo sapiens]**

Accession:	gi|312433998	**Score:**	100.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	73.1
Database Date:	2015-11-30	**pI:**	9.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	5.4
		No. of unique Peptides:	3

Quantitation

mdown:qdown	**Median:**	0.43	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	2.01	**CV:**	0.00 %	**No. of Peptides:**	1

```
        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
1629	2	695.8567	-18.94	2	48.9	36.9	0	76-88	K.GGSFQLNELQGLK.S		
852	1	598.3199	18.32	2	40.1	36.0	0	261-271	K.FQLFGSPSGQK.D		mdown:qdown 0.43
2950	4	668.3368	-23.49	2	66.0	27.5	0	543-554	K.LADFALLCLDGK.R	Carbamidomethyl: 8	Wdown:Qdown 2.01

Detailed Protein Report

Protein 33: **keratin, type I cytoskeletal 19 [Homo sapiens]**

Accession:	gi|24234699	**Score:**	100.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	44.1
Database Date:	2015-11-30	**pI:**	4.9
Modification(s):	Oxidation	**Sequence Coverage [%]:**	13.5
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MTSYSYRQSS ATSSFGGLGG GSVRFGPGVA FRAPSIHGGS GGRGVSVSSA RFVSSSSSGA YGGGYGGVLT ASDGLLAGNE

        90        100        110        120        130        140        150        160
KLTMQNLNDR LASYLDKVRA LEAANGELEV KIRDWYQKQG PGPSRDYSHY YTTIQDLRDK ILGATIENSR IVLQIDNARL

       170        180        190        200        210        220        230        240
AADDFRTKFE TEQALRMSVE ADINGLRRVL DELTLARTDL EMQIEGLKEE LAYLKKNHEE EISTLRGQVG GQVSVEVDSA

       250        260        270        280        290        300        310        320
PGTDLAKILS DMRSQYEVMA EQNRKDAEAW FTSRTEELNR EVAGHTEQLQ MSRSEVTDLR RTLQGLEIEL QSQLSMKAAL

       330        340        350        360        370        380        390        400
EDTLAETEAR FGAQLAHIQA LISGIEAQLG DVRADSERQN QEYQRLMDIK SRLEQEIATY RSLLEGQEDH YNNLSASKVL

       410
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1981	1	1051.4041	-77.63	2	53.4	11.4	1	248-264	K.ILSDMRSQYEVMAEQNR.K	Oxidation: 5, 12

Protein 34: dynein heavy chain 1, axonemal [Homo sapiens]

Accession:	gi|197927452	**Score:**	87.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	487.2
Database Date:	2015-11-30	**pI:**	5.5
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	2.0
		No. of unique Peptides:	6

Quantitation

mdown:qdown	**Median:**	1.42	**CV:**	70.92 %	**No. of Peptides:**	2

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
405	3	565.3234	-64.51	2	34.1	17.4	2	596-604	K.LRKLMELVK.Y		
2181	1	990.9291	-65.49	2	55.9	12.3	2	1828-1844	R.EACRNSNLKDVEGFLTK.C	Carbamidomethyl: 3	
870	1	573.1350	-254.46	2	40.3	10.7	1	2478-2486	R.DRLVNEEDR.S		mdown:qdown 2.69
318	1	715.6717	-189.89	2	32.7	11.8	0	2496-2506	R.CMEQWEVTFNK.V	Oxidation: 2	
972	1	730.6935	389.04	1	40.6	12.0	0	3422-3428	K.AAEIQAK.V		mdown:qdown 0.75
41	1	706.3121	-81.89	3	29.9	12.9	2	3699-3718	K.KLSAISLGQGQGPRAEAMMR.S	Oxidation: 18	

Detailed Protein Report

Protein 35: fibrillin-2 precursor [Homo sapiens]

Accession:	gi|66346695	**Score:**	83.7
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 [%]:**	2.0
		No. of unique Peptides:	5

Quantitation

mdown:qdown	**Median:**	1.53	**CV:**	38.07 %	**No. of Peptides:**	2
Wdown:Qdown	**Median:**	3.53	**CV:**	7.35 %	**No. of Peptides:**	2

Detailed Protein Report

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

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
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	
472	1	516.1120	-268.37	2	34.5	12.2	0	1884-1893	K.LSPNGACVDR.N		mdown:qdown 1.06 Wdown:Qdown 3.80
281	1	477.4617	-193.67	3	32.2	10.8	0	2436-2448	K.ICPHGPGYTTDGR.D	Carbamidomethyl: 2	
304	4	642.1738	-171.43	2	33.2	24.4	1	2529-2539	K.TCKDLDECQTK.Q		Wdown:Qdown 3.28 mdown:qdown 2.21

Detailed Protein Report

Protein 36: plastin-2 [Homo sapiens]

Accession:	gi|167614506	**Score:**	83.3
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 [%]:**	12.1
		No. of unique Peptides:	5

Quantitation

Wdown:Qdown **Median:** 1.14 **CV:** 0.00 % **No. of Peptides:** 1

Alias proteins:

Accession	Name	Description
gi|530402335	refseq_human (refseq_human_20140103.fasta)	PREDICTED: plastin-2 isoform X2 [Homo sapiens]

10	20	30	40	50	60	70	80
MARGSVSDEE	MMELREAFAK	VDTDGNGYIS	FNELNDLFKA	ACLPLPGYRV	REITENLMAT	GDLDQDGRIS	FDEFIKIFHG
90	100	110	120	130	140	150	160
LKSTDVAKTF	RKAINKKEGI	CAIGGTSEQS	SVGTQHSYSE	EEKYAFVNWI	NKALENDPDC	RHVIPMNPNT	NDLFNAVGDG
170	180	190	200	210	220	230	240
IVLCKMINLS	VPDTIDERTI	NKKKLTPFTI	QENLNLALNS	ASAIGCHVVN	IGAEDLKEGK	PYLVLGLLWQ	VIKIGLFADI
250	260	270	280	290	300	310	320
ELSRNEALIA	LLREGESLED	LMKLSPEELL	LRWANYHLEN	AGCNKIGNFS	TDIKDSKAYY	HLLEQVAPKG	DEEGVPAVVI
330	340	350	360	370	380	390	400
DMSGLREKDD	IQRAECMLQQ	AERLGCRQFV	TATDVVRGNP	KLNLAFIANL	FNRYPALHKP	ENQDIDWGAL	EGETREERTF
410	420	430	440	450	460	470	480
RNWMNSLGVN	PRVNHLYSDL	SDALVIFQLY	EKIKVPVDWN	RVNKPPYPKL	GGNMKKLENC	NYAVELGKNQ	AKFSLVGIGG
490	500	510	520	530	540	550	560
QDLNEGNRTL	TLALIWQLMR	RYTLNILEEI	GGGQKVNDDI	IVNWVNETLR	EAKKSSSISS	FKDPKISTSL	PVLDLIDAIQ
570	580	590	600	610	620	630	
PGSINYDLLK	TENLNDDEKL	NNAKYAISMA	RKIGARVYAL	PEDLVEVNPK	MVMTVFACLM	GKGMKRV	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2609	1	658.3945	34.02	2	61.3	14.5	1	77-88	K.IFHGLKSTDVAK.T		
545	1	652.1661	-227.16	2	36.1	14.5	0	402-412	R.NWMNSLGVNPR.V	Oxidation: 3	Wdown:Qdown 1.14
1806	1	649.7882	-96.92	2	52.6	11.2	2	531-542	R.EAKKSSSISSFK.D		
2231	1	793.3805	-58.93	2	56.5	14.2	0	597-610	R.VYALPEDLVEVNPK.M		
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 37: splicing factor, proline- and glutamine-rich [Homo sapiens]

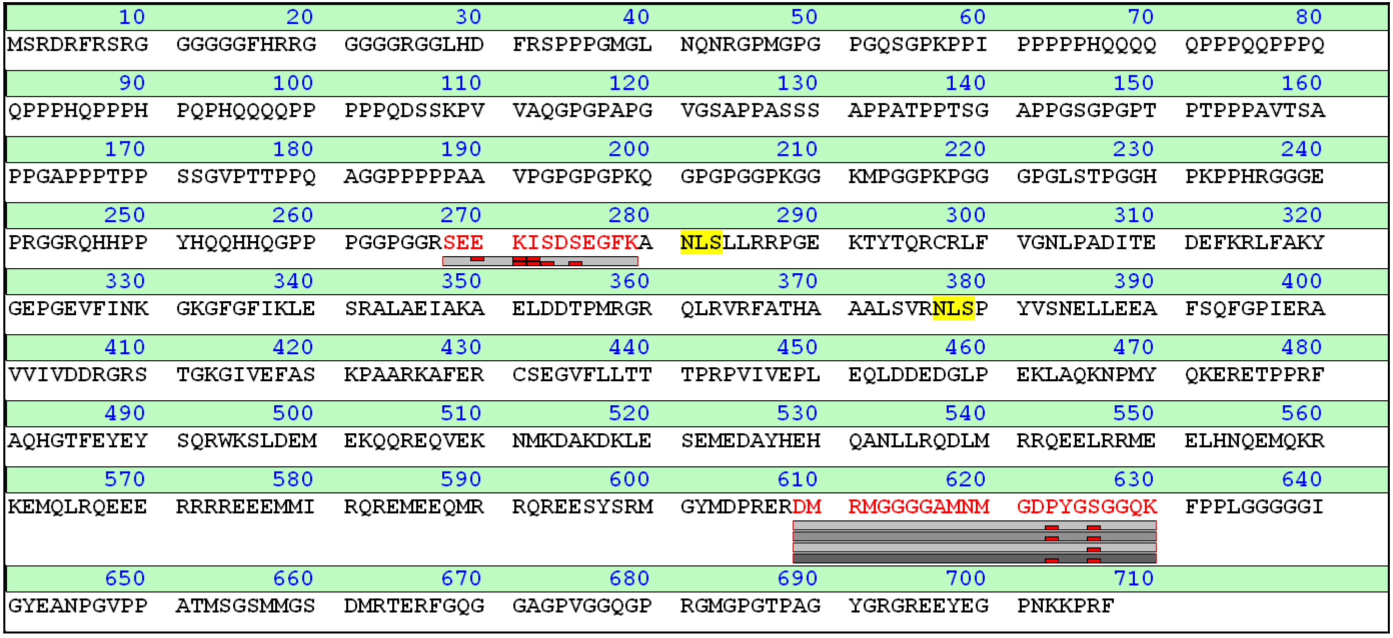
Accession:	gi|4826998	**Score:**	81.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	76.1
Database Date:	2015-11-30	**pI:**	9.9
Modification(s):	Oxidation	**Sequence Coverage [%]:**	4.8
		No. of unique Peptides:	5

Quantitation

mdown:qdown	**Median:**	0.44	**CV:**	28.48 %	**No. of Peptides:**	2
Wdown:Qdown	**Median:**	1.11	**CV:**	74.66 %	**No. of Peptides:**	2

Alias proteins:

Accession	Name	Description
gi|530363144	refseq_human (refseq_human_20140103.fasta)	PREDICTED: splicing factor, proline- and glutamine-rich isoform X3 [Homo sapiens]
gi|530363142	refseq_human (refseq_human_20140103.fasta)	PREDICTED: splicing factor, proline- and glutamine-rich isoform X2 [Homo sapiens]
gi|530363140	refseq_human (refseq_human_20140103.fasta)	PREDICTED: splicing factor, proline- and glutamine-rich isoform X1 [Homo sapiens]



```
        10         20         30         40         50         60         70         80
MSRDRFRSRG GGGGGFHRRG GGGGRGGLHD FRSPPPGMGL NQNRGPMGPG PGQSGPKPPI PPPPPHQQQQ QPPPQQPPPQ
        90        100        110        120        130        140        150        160
QPPPHQPPPH PQPHQQQQPP PPPQDSSKPV VAQGPGPAPG VGSAPPASSS APPATPPTSG APPGSGPGPT PTPPPAVTSA
       170        180        190        200        210        220        230        240
PPGAPPPTPP SSGVPTTPPQ AGGPPPPPAA VPGPGPGPKQ GPGPGGPKGG KMPGGPKPGG GPGLSTPGGH PKPPHRGGGE
       250        260        270        280        290        300        310        320
PRGGRQHHPP YHQQHHQGPP PGGPGGRSEE KISDSEGFKA NLSLLRRPGE KTYTQRCRLF VGNLPADITE DEFKRLFAKY
       330        340        350        360        370        380        390        400
GEPGEVFINK GKGFGFIKLE SRALAEIAKA ELDDTPMRGR QLRVRFATHA AALSVRNLSP YVSNELLEEA FSQFGPIERA
       410        420        430        440        450        460        470        480
VVIVDDRGRS TGKGIVEFAS KPAARKAFER CSEGVFLLTT TPRPVIVEPL EQLDDEDGLP EKLAQKNPMY QKERETPPRF
       490        500        510        520        530        540        550        560
AQHGTFEYEY SQRWKSLDEM EKQQREQVEK NMKDAKDKLE SEMEDAYHEH QANLLRQDLM RRQEELRRME ELHNQEMQKR
       570        580        590        600        610        620        630        640
KEMQLRQEEE RRRREEEMMI RQREMEEQMR RQREESYSRM GYMDPRERDM RMGGGGAMNM GDPYGSGGQK FPPLGGGGGI
       650        660        670        680        690        700        710
GYEANPGVPP ATMSGSMMGS DMRTERFGQG GAGPVGGQGP RGMGPGTPAG YGRGREEYEG PNKKPRF
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
376	6	678.1939	-185.67	2	34.0	29.1	1	268-279	R.SEEKISDSEGFK.A		mdown:qdown 0.58 Wdown:Qdown 2.17
14	1	1103.5206	70.68	2	29.5	14.3	1	609-630	R. DMRMGGGGAMNMGDPYGSGGQ F	Oxidation: 2, 12	
18	2	736.0042	54.34	3	29.4	11.7	1	609-630	R. DMRMGGGGAMNMGDPYGSGGQ F	Oxidation: 2, 10	Wdown:Qdown 0.57 mdown:qdown 0.33
20	2	735.9950	41.81	3	29.6	11.7	1	609-630	R. DMRMGGGGAMNMGDPYGSGGQ F	Oxidation: 4, 10	
8	2	736.0117	64.51	3	29.3	14.9	1	609-630	R. DMRMGGGGAMNMGDPYGSGGQ F	Oxidation: 4, 12	

Detailed Protein Report

Protein 38:	**PREDICTED: dynein heavy chain 3, axonemal isoform X1 [Homo sapiens]**		
Accession:	gi|578828592	**Score:**	81.1
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 [%]:**	2.0
		No. of unique Peptides:	3

Detailed Protein Report

10	20	30	40	50	60	70	80
MGDMDCSSQK	IAKSDSIHHM	SHSQGQPELP	PLPASANEEP	SGLYQTVMSH	SFYPPLMQRT	SWTLAAPFKE	QHHHRGPSDS
90	100	110	120	130	140	150	160
IANNYSLMAQ	DLKLKDLLKV	YQPATISVPR	DRTGQGLPSS	GNRSSSEPMR	KKTKFSSRNK	EDSTRIKLAF	KTSIFSPMKK
170	180	190	200	210	220	230	240
EVKTSLTFPG	SRPMSPEQQL	DVMLQQEMEM	ESKEKKPSES	DLERYYYYLT	NGIRKDMIAP	EEGEVMVRIS	KLISNTLLTS
250	260	270	280	290	300	310	320
PFLEPLMVVL	VQEKENDYYC	SLMKSIVDYI	LMDPMERKRL	FIESIPRLFP	QRVIRAPVPW	HSVYRSAKKW	NEEHLHTVNP
330	340	350	360	370	380	390	400
MMLRLKELWF	AEFRDLRFVR	TAEILAGKLP	LQPQEFWDVI	QKHCLEAHQT	LLNKWIPTCA	QLFTSRKEHW	IHFAPKSNYD
410	420	430	440	450	460	470	480
SSRNIEEYFA	SVASFMSLQL	RELVIKSLED	LVSLFMIHKD	GNDFKEPYQE	MKFFIPQLIM	IKLEVSEPII	VFNPSFDGCW
490	500	510	520	530	540	550	560
ELIRDSFLEI	IKNSNGIPKV	ESVLFPELKG	YNLLLGTVNA	EEKLVSDFLI	QTFKVFQKNQ	VGPCKYLNVY	KKYVDLLDNT
570	580	590	600	610	620	630	640
AEQNIAAFLK	ENHDIDDFVT	KINAIKKRRN	EIASMNITVP	LAMFCLDATA	LNHDLCERAQ	NLKDHLIQFQ	VDVNRDTNTS
650	660	670	680	690	700	710	720
ICNQYSHIAD	KVSEVPANTK	ELVSLIEFLK	KSSAVTVFKL	RRQLRDASER	LEFLMDYADL	PYEDIKLNST	LFLWPDQIED
730	740	750	760	770	780	790	800
IFDNSRNLLL	HKRDQAEMDL	IKRCSEFELR	LEGYHRELES	FRKREVMTTE	EMKHNVEKLN	ELSKNLNRAF	AEFELINKEE
810	820	830	840	850	860	870	880
ELLEKEKSTY	PLLQAMLKNK	VPYEQLWSTA	YEFSIKSEEW	MNGPLFLLNA	EQIAEEIGNM	WRTTYKLIKT	LSDVPAPRRL
890	900	910	920	930	940	950	960
AENVKIKIDK	FKQYIPILSI	SCNPGMKDRH	WQQISEIVGY	EIKPTETTCL	SNMLEFGFGK	FVEKLEPIGA	AASKEYSLEK
970	980	990	1000	1010	1020	1030	1040
NLDRMKLDWV	NVTFSFVKYR	DTDTNILCAI	DDIQMLLDDH	VIKTQTMCGS	PFIKPIEAEC	RKWEEKLIRI	QDNLDAWLKC
1050	1060	1070	1080	1090	1100	1110	1120
QATWLYLEPI	FSSEDIIAQM	PEEGRKFGIV	DSYWKSLMSQ	AVKDNRILVA	ADQPRMAEKL	QEANFLLEDI	QKGLNDYLEK
1130	1140	1150	1160	1170	1180	1190	1200
KRLFFPRFFF	LSNDELLEIL	SETKDPLRVQ	PHLKKCFEGI	AKLEFTDNLE	IVGMISSEKE	TVPFIQKIYP	ANAKGMVEKW
1210	1220	1230	1240	1250	1260	1270	1280
LQQVEQMMLA	SMREVIGLGI	EAYVKVPRNH	WVLQWPGQVV	ICVSSIFWTQ	EVSQALAENT	LLDFLKKSND	QIAQIVQLVR
1290	1300	1310	1320	1330	1340	1350	1360
GKLSSGARLT	LGALTVIDVH	ARDVVAKLSE	DRVSDLNDFQ	WISQLRYYWV	AKDVQVQIIT	TEALYGYEYL	GNSPRLVITP
1370	1380	1390	1400	1410	1420	1430	1440
LTDRCYRTLM	GALKLNLGGA	PEGPAGTGKT	ETTKDLAKAL	AKQCVVFNCS	DGLDYKAMGK	FFKGLAQAGA	WACFDEFNRI
1450	1460	1470	1480	1490	1500	1510	1520
EVEVLSVVAQ	QILSIQQAII	RKLKTFIFEG	TELSLNPTCA	VFITMNPGYA	GRAELPDNLK	ALFRTVAMMV	PDYALIGEIS
1530	1540	1550	1560	1570	1580	1590	1600
LYSMGFLDSR	SLAQKIVATY	RLCSEQLSSQ	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
565	1	607.8337	-71.29	2	35.7	10.9	1	1562-1573	K.SVLTAAGNLKLK.Y	
315	1	1201.1883	61.60	2	32.6	16.3	1	2128-2150	K.DTTRLDIVDMLLVTAMGPPGGGR.N	Oxidation: 10

Detailed Protein Report

Protein 39: glyceraldehyde-3-phosphate dehydrogenase isoform 1 [Homo sapiens]

Accession:	gi|7669492	**Score:**	80.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	36.0
Database Date:	2015-11-30	**pI:**	9.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	13.7
		No. of unique Peptides:	3

Quantitation

mdown:qdown	**Median:**	0.50	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.36	**CV:**	136.48 %	**No. of Peptides:**	2

10	20	30	40	50	60	70	80
MGKVKVGVNG	FGRIGRLVTR	AAFNSGKVDI	VAINDPFIDL	NYMVYMFQYD	STHGKFHGTV	KAENGKLVIN	GNPITIFQER
90	100	110	120	130	140	150	160
DPSKIKWGDA	GAEYVVESTG	VFTTMEKAGA	HLQGGAKRVI	ISAPSADAPM	FVMGVNHEKY	DNSLKIISNA	SCTTNCLAPL
170	180	190	200	210	220	230	240
AKVIHDNFGI	VEGLMTTVHA	ITATQKTVDG	PSGKLWRDGR	GALQNIIPAS	TGAAKAVGKV	IPELNGKLTG	MAFRVPTANV
250	260	270	280	290	300	310	320
SVVDLTCRLE	KPAKYDDIKK	VVKQASEGPL	KGILGYTEHQ	VVSSDFNSDT	HSSTFDAGAG	IALNDHFVKL	ISWYDNEFGY
330	340						
SNRVVDLMAH	MASKE						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
703	1	917.4101	-58.22	2	37.6	39.4	0	146-162	K.IISNASCTTNCLAPLAK.V	Carbamidomethyl: 7, 11	mdown:qdown 0.50 Wdown:Qdown 1.00
904	2	706.3818	-24.09	2	40.1	26.3	0	201-215	R.GALQNIIPASTGAAK.A		Wdown:Qdown 0.13
2067	1	882.3181	-98.33	2	54.4	15.0	0	310-323	K.LISWYDNEFGYSNR.V		

Detailed Protein Report

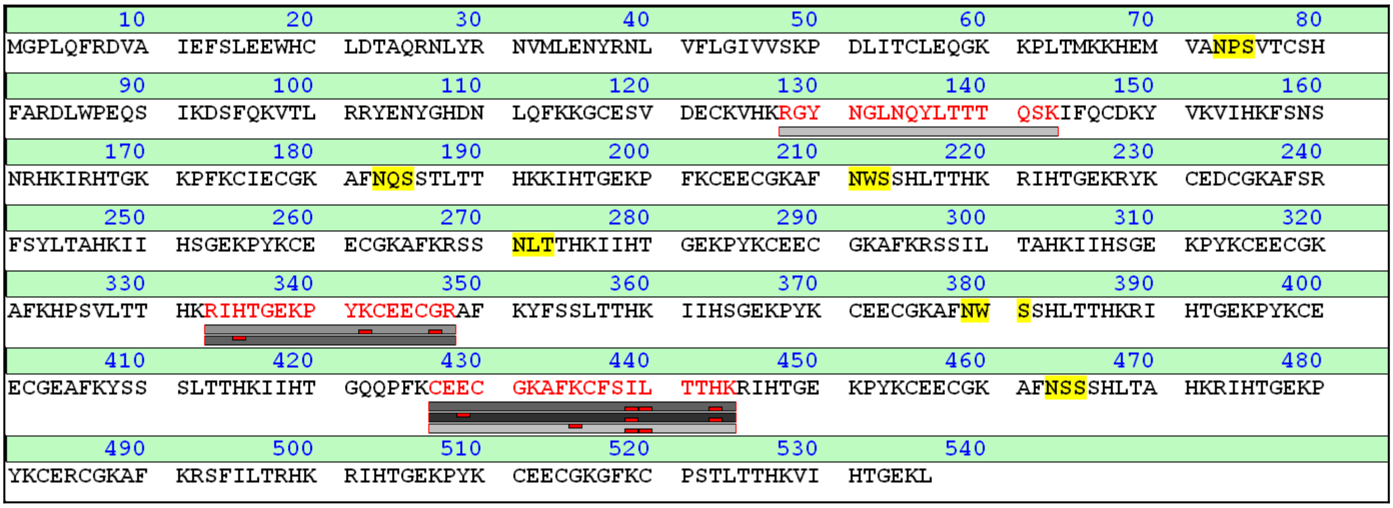
Protein 40: **zinc finger protein 737 [Homo sapiens]**

Accession: gi|226530355
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 78.7
MW [kDa]: 61.9
pI: 10.3
Sequence Coverage [%]: 9.3
No. of unique Peptides: 6

Quantitation

Wdown:Qdown **Median:** 3.24 **CV:** 0.00 % **No. of Peptides:** 1



```
        10         20         30         40         50         60         70         80
MGPLQFRDVA IEFSLEEWHC LDTAQRNLYR NVMLENYRNL VFLGIVVSKP DLITCLEQGK KPLTMKKHEM VANPSVTCSH
        90        100        110        120        130        140        150        160
FARDLWPEQS IKDSFQKVTL RRYENYGHDN LQFKKGCESV DECKVHKRGY NGLNQYLTTT QSKIFQCDKY VKVIHKFSNS
       170        180        190        200        210        220        230        240
NRHKIRHTGK KPFKCIECGK AFNQSSTLTT HKKIHTGEKP FKCEECGKAF NWSSHLTTHK RIHTGEKRYK CEDCGKAFSR
       250        260        270        280        290        300        310        320
FSYLTAHKII HSGEKPYKCE ECGKAFKRSS NLTTHKIIHT GEKPYKCEEC GKAFKRSSIL TAHKIIHSGE KPYKCEECGK
       330        340        350        360        370        380        390        400
AFKHPSVLTT HKRIHTGEKP YKCEECGRAF KYFSSLTTHK IIHSGEKPYK CEECGKAFNW SSHLTTHKRI HTGEKPYKCE
       410        420        430        440        450        460        470        480
ECGEAFKYSS SLTTHKIIHT GQQPFKCEEC GKAFKCFSIL TTHKRIHTGE KPYKCEECGK AFNSSSHLTA HKRIHTGEKP
       490        500        510        520        530        540
YKCERCGKAF KRSFILTRHK RIHTGEKPYK CEECGKGFKC PSTLTTHKVI HTGEKL
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2780	1	922.4553	-14.26	2	66.1	16.9	1	128-143	K.RGYNGLNQYLTTTQSK.I		
2919	1	981.9597	-7.66	2	65.7	10.8	2	333-348	K.RIHTGEKPYKCEECGR.A	Carbamidomethyl: 11	
2966	1	953.4397	-17.72	2	66.3	13.9	2	333-348	K.RIHTGEKPYKCEECGR.A		Wdown:Qdown 3.24
1955	1	1022.8979	-86.37	2	54.5	10.5	2	427-444	K.CEECGKAFKCFSILTTHK.R		
2022	1	1051.4074	-85.21	2	53.9	10.6	2	427-444	K.CEECGKAFKCFSILTTHK.R	Carbamidomethyl: 10	
2081	3	1051.4297	-64.07	2	54.6	15.9	2	427-444	K.CEECGKAFKCFSILTTHK.R	Carbamidomethyl: 1	

Detailed Protein Report

Protein 41: TNF receptor-associated factor 2 [Homo sapiens]

Accession:	gi|22027612	**Score:**	77.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	55.8
Database Date:	2015-11-30	**pI:**	9.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	9.2
		No. of unique Peptides:	2

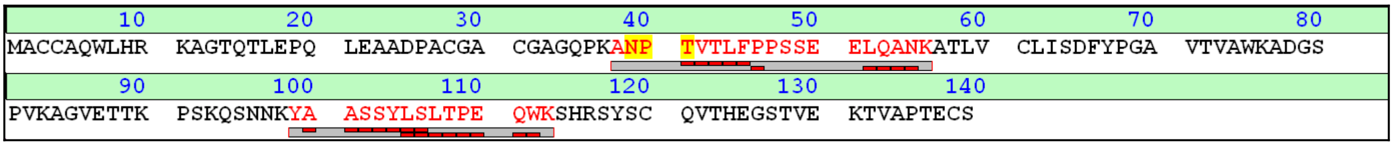
10	20	30	40	50	60	70	80
MAAASVTPPG	SLELLQPGFS	KTLLGTKLEA	KYLCSACRNV	LRRPFQAQCG	HRYCSFCLAS	ILSSGPQNCA	ACVHEGIYEE
90	100	110	120	130	140	150	160
GISILESSSA	FPDNAARREV	ESLPAVCPSD	GCTWKGTLKE	YESCHEGRCP	LMLTECPACK	GLVRLGEKER	HLEHECPERS
170	180	190	200	210	220	230	240
LSCRHCRAPC	CGADVKAHHE	VCPKFPLTCD	GCGKKKIPRE	KFQDHVKTCG	KCRVPCRFHA	IGCLETVEGE	KQQEHEVQWL
250	260	270	280	290	300	310	320
REHLAMLLSS	VLEAKPLLGD	QSHAGSELLQ	RCESLEKKTA	TFENIVCVLN	REVERVAMTA	EACSRQHRLD	QDKIEALSSK
330	340	350	360	370	380	390	400
VQQLERSIGL	KDLAMADLEQ	KVLEMEASTY	DGVFIWKISD	FARKRQEAVA	GRIPAIFSPA	FYTSRYGYKM	CLRIYLNGDG
410	420	430	440	450	460	470	480
TGRGTHLSLF	FVVMKGPNDA	LLRWPFNQKV	TLMLLDQNNR	EHVIDAFRPD	VTSSSFQRPV	NDMNIASGCP	LFCPVSKMEA
490	500	510					
KNSYVRDDAI	FIKAIVDLTG	L					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2037	1	1051.4158	-90.99	2	54.1	10.8	1	214-231	R.VPCRFHAIGCLETVEGEK.Q	Carbamidomethyl: 3, 10
2147	1	1022.9076	-91.14	2	57.0	15.3	1	214-231	R.VPCRFHAIGCLETVEGEK.Q	Carbamidomethyl: 10

Detailed Protein Report

Protein 42: **immunoglobulin lambda-like polypeptide 5 isoform 2 [Homo sapiens]**

Accession:	gi|372466586	**Score:**	77.0
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
1891	3	1021.8855	-134.81	2	52.1	22.0	0	38-56	K.ANPTVTLFPPSSEELQANK.A	
1753	11	872.4147	-21.04	2	50.6	55.0	0	99-113	K.YAASSYLSLTPEQWK.S	

Detailed Protein Report

Protein 43: **PREDICTED: DNA-directed RNA polymerase, mitochondrial isoform X1 [Homo sapiens]**

Accession:	gi|530425287	**Score:**	75.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	145.0
Database Date:	2015-11-30	**pI:**	10.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.6
		No. of unique Peptides:	3

```
        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	
125	1	793.8591	-42.14	2	30.8	18.8	1	158-172	K.VQMGAKDATPVPCGR.W	Carbamidomethyl: 13
2603	1	678.4838	186.95	1	63.1	15.6	0	1227-1231	R.EQFVR.L	

Detailed Protein Report

Protein 44: keratin, type II cytoskeletal 1b [Homo sapiens]

Accession:	gi|194018511	**Score:**	75.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	61.9
Database Date:	2015-11-30	**pI:**	5.6
		Sequence Coverage [%]:	9.0
		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
2213	1	1103.9435	-56.00	2	56.2	13.0	0	18-41	R.VYSTSSSAGSGGGSPAVGSVCYAR.G	

Detailed Protein Report

Protein 45: PREDICTED: zinc finger protein 665 isoform X5 [Homo sapiens]

Accession:	gi|578834915	**Score:**	72.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	76.3
Database Date:	2015-11-30	**pI:**	10.3
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	7.5
		No. of unique Peptides:	5

Quantitation

Wdown:Qdown **Median:** 0.88 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MVCPCSGLLL	AVGGMPPRCQ	GRTLEEEEEE	GKGVRDGSSS	DISCKCVNTD	LPPKGKNNMG	EAFYTVKLER	LESCDTVGLS
90	100	110	120	130	140	150	160
FQEVQKNTYD	FECQWKDDEG	NYKTVLMLQK	ENLPGRRAQR	DRRAAGNRHI	ENQLGVSFQS	HLPELQQFQH	EGKIYEYNQV
170	180	190	200	210	220	230	240
EKSPNNRGKH	YKCDECGKVF	SQNSRLTSHK	RIHTGEKPYQ	CNKCGKAFTV	RSNLTIHQVI	HTGEKPYKCN	ECGKVFSQPS
250	260	270	280	290	300	310	320
NLAGHQRIHT	GEKPYKCNEC	GKAFRAHSKL	TTHQVIHTGE	KPYKCKECGK	CFTQNSHLAS	HRRIHTGEKP	YKCNECGKAF
330	340	350	360	370	380	390	400
SVRSSLTTHQ	TIHTGEKPYK	CNECGKVFRH	NSYLAKHRRI	HTGEKPYKCN	ECGKAFSMHS	NLTKHQIIHT	GEKPFKCNEC
410	420	430	440	450	460	470	480
VKVFTQYSHL	ANHRRIHTGE	KPYRCDECGK	AFSVRSSLTT	HQAIHTGEKP	YKCNDCGKVF	TQNSHLASHR	GIHSGEKPYK
490	500	510	520	530	540	550	560
CDECGKAFSQ	TSQLARHWRV	HTGEKPYKCN	ECGKAFSVHS	SLTIHQTIHT	GQKPYKCNDC	GKVFRHNSYL	AIHQRIHTGE
570	580	590	600	610	620	630	640
KPYKCNECGK	AFSVHSNLAT	HQVIHTGEKP	YKCNECGKVF	TQNSHLANHR	RIHTGEKPYR	CNECGKAFSV	RSTLTTHMAV
650	660	670	680				
HTGDKPYKCN	QCGKVFTQNS	NLAKHRRIHS	G				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2105	6	937.3619	-106.09	2	56.5	15.4	0	1-18	-.MVCPCSGLLLAVGGMPPR.C	Carbamidomethyl: 5; Oxidation: 15	Wdown:Qdown 0.88
2957	4	937.4644	3.23	2	66.1	16.2	0	1-18	-.MVCPCSGLLLAVGGMPPR.C	Carbamidomethyl: 3; Oxidation: 15	
2976	1	754.4009	45.80	3	66.4	15.0	1	1-22	-. MVCPCSGLLLAVGGMPPRCQGR. T	Oxidation: 1	
1877	2	1057.5274	21.10	3	52.1	10.3	2	453-480	K. CNDCGKVFTQNSHLASHRGIHSG C	Carbamidomethyl: 4	
1830	2	1057.5034	-1.56	3	51.5	15.7	2	453-480	K. CNDCGKVFTQNSHLASHRGIHSG C	Carbamidomethyl: 1	

Detailed Protein Report

Protein 46: PREDICTED: protein AHNAK2 isoform X1 [Homo sapiens]

Accession:	gi|530403029	**Score:**	72.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	605.3
Database Date:	2015-11-30	**pI:**	5.1
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.4
		No. of unique Peptides:	5

Quantitation

mdown:qdown	**Median:**	7.41	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.50	**CV:**	0.00 %	**No. of Peptides:**	1

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

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
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		Wdown:Qdown 0.50 mdown:qdown 7.41
597	1	1230.6275	14.93	2	36.8	18.6	1	685-707	K.AEVTAPDVKMSLSSMEVDVQAPRA		
2190	3	648.2929	-93.26	2	56.0	10.4	1	5599-5610	R.FPKLGFSSSPTK.K		
1331	1	1023.0328	-5.50	2	45.4	12.2	1	5662-5679	R.VMVTSAARTELILPEQDR.K	Oxidation: 2	

Protein 47: centromere protein F [Homo sapiens]

Accession:	gi|55770834	**Score:**	71.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	357.3
Database Date:	2015-11-30	**pI:**	4.9
		Sequence Coverage [%]:	1.9
		No. of unique Peptides:	3

Quantitation

mdown:qdown	**Median:**	1.50	**CV:**	63.88 %	**No. of Peptides:**	2
Wdown:Qdown	**Median:**	1.57	**CV:**	0.00 %	**No. of Peptides:**	1

Detailed Protein Report

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	KLKEREREND	SLKDKVENLE
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
104	2	1043.8924	-98.05	2	30.5	15.3	0	128-147	R.SQQAAQSADVSLNPCNTPQK.I		Wdown:Qdown 1.57 mdown:qdown 0.83
1209	1	573.1437	-261.24	2	43.6	14.6	0	981-990	K.EINASLNQEK.M		mdown:qdown 2.69
2721	2	974.5198	32.44	2	63.0	14.2	1	2466-2482	K.AKEQNLSSQVECLELEK.A		

Detailed Protein Report

Protein 48: neurogenic locus notch homolog protein 1 preproprotein [Homo sapiens]

Accession:	gi|148833508	**Score:**	70.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	272.3
Database Date:	2015-11-30	**pI:**	4.8
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	2.2
		No. of unique Peptides:	5

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	AAAFVLLFFV	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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1878	2	716.0566	111.85	3	52.1	10.3	1	1331-1350	R.GFICKCPAGFEGATCENDAR.T	Carbamidomethyl: 6
1825	2	715.9982	30.20	3	51.5	11.6	1	1331-1350	R.GFICKCPAGFEGATCENDAR.T	Carbamidomethyl: 4
1618	4	697.0380	98.52	3	48.9	15.1	1	1331-1350	R.GFICKCPAGFEGATCENDAR.T	
2040	1	841.7905	116.85	3	55.6	14.8	0	1855-1877	R.MSAMAPTPPQGEVDADCMDVNVR.G	Carbamidomethyl: 17; Oxidation: 1, 4
2914	9	698.3691	-7.48	2	65.6	18.9	0	1992-2004	R.MHDGTTPLILAAR.L	

Detailed Protein Report

Protein 49: dynein heavy chain 17, axonemal [Homo sapiens]

Accession:	gi|256542310	**Score:**	70.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	509.0
Database Date:	2015-11-30	**pI:**	5.4
		Sequence Coverage [%]:	1.6
		No. of unique Peptides:	3

10	20	30	40	50	60	70	80
MTMAPDVRLE	YLEEVASIVL	KFKPDKWSKL	IGAEENVALF	TEFFEKPDVQ	VLVLTLNAAG	MIIPCLGFPQ	SLKSKGVYFI
90	100	110	120	130	140	150	160
KTKSENINKD	NYRARLLYGD	ISPTPVDQLI	AVVEEVLSSL	LNQSENMAGW	PQVVSEDIVK	QVHRLKNEMF	VMSGKIKGKT
170	180	190	200	210	220	230	240
LLPIPEHLGS	LDGTLESMER	IPSSLDNLLL	HAIETTIIDW	SHQIRDVLSK	DSAQALLDGL	HPLPQVEFEF	WDTRLLNLKC
250	260	270	280	290	300	310	320
IHEQLNRPKV	NKIVEILEKA	KSCYWPALQN	VYTNVTEGLK	EANDIVLYLK	PLRILLEEME	QADFTMLPTF	IAKVLDTICF
330	340	350	360	370	380	390	400
IWATSEYYNT	PARIIVILQE	FCNQIIEMTR	TFLSPEEVLK	GLQGEIEEVL	SGISLAVNVL	KELYQTYDFC	CVNMKLFFKD
410	420	430	440	450	460	470	480
KEPVPWEFPS	SLAFSRINSF	FQRIQTIEEL	YKTAIEFLKL	EKIELGGVRG	NLLGSLVTRI	YDEVFELVKV	FADCKYDPLD
490	500	510	520	530	540	550	560
PGDSNFDRDY	ADFEIKIQDL	DRRLATIFCQ	GFDDCSCIKS	SAKLLYMCGG	LMERPLILAE	VAPRYSVMLE	LFDAELDNAK
570	580	590	600	610	620	630	640
ILYDAQMAAS	EEGNIPLIHK	NMPPVAGQLK	WSLELQERLE	VSMKHLKHVE	HPVMSGAEAK	LTYQKYDEMM	ELLRCHREKI
650	660	670	680	690	700	710	720
YQQWVAGVDQ	DCHFNLGQPL	ILRDAASNLI	HVNFSKALVA	VLREVKYLNF	QQQKEIPDSA	ESLFSENETF	RKFVGNLELI
730	740	750	760	770	780	790	800
VGWYNEIKTI	VKAVEFLLIK	SELEAIDVKL	LSAETTLFWN	GEGVFQYIQE	VREILHNLQN	RMQKAKQNIE	GISQAMKDWS
810	820	830	840	850	860	870	880
ANPLFERKDN	KKEALLDLDG	RIANLNKRYA	AVRDAGVKIQ	AMVAENAELF	RADTLSLPWK	DYVIYIDDMV	LDEFDQFIRK
890	900	910	920	930	940	950	960
SLSFLMDNMV	IDESIAPLFE	IRMELDEDGL	TFNPTLEVGS	DRGFLALIEG	LVNDIYNVAR	LIPRLAKDRM	NYKMDLEDNT
970	980	990	1000	1010	1020	1030	1040
DLIEMREEVS	SLVINAMKEA	EEYQDSFERY	SYLWTDNLQE	FMKNFLIYGC	AVTAEDLDTW	TDDTIPKTPP	TLAQFQEQID
1050	1060	1070	1080	1090	1100	1110	1120
SYEKLYEEVS	KCENTKVFHG	WLQCDCRPFK	QALLSTIRRW	GFMFKRHLSN	HVTNSLADLE	AFMKVARMGL	TKPLKEGDYD
1130	1140	1150	1160	1170	1180	1190	1200
GLVEVMGHLM	KVKERQAATD	NMFEPLKQTI	ELLKTYGEEM	PEEIHLKLQE	LPEHWANTKK	LAIQVKLTVA	PLQANEVSIL
1210	1220	1230	1240	1250	1260	1270	1280
RRKCQQFELK	QHEFRERFRR	EAPFSFSDPN	PYKSLNKQQK	SISAMEGIME	ALSKSGGLFE	VPVPDYKQLK	ACHREVRLLK
1290	1300	1310	1320	1330	1340	1350	1360
ELWDMVVVVN	TSIEDWKTTK	WKDINVEQMD	IDCKKFAKDM	RSLDKEMKTW	DAFVGLDNTV	KNVITSLRAV	SELQNPAIRE
1370	1380	1390	1400	1410	1420	1430	1440
RHWQQLMQAT	QVKFKMSEET	TLADLLQLNL	HSYEDEVRNI	VDKAVKESGM	EKVLKALDST	WSMMEFQHEP	HPRTGTMMLK
1450	1460	1470	1480	1490	1500	1510	1520
SSEVLVETLE	DNQVQLQNLM	MSKYLAHFLK	EVTSWQQKLS	TADSVISIWF	EVQRTWSHLE	SIFIGSEDIR	TQLPGDSQRF
1530	1540	1550	1560	1570	1580	1590	1600
DDINQEFKAL	MEDAVKTPNV	VEATSKPGLY	NKLEALKKSL	AICEKALAEY	LETKRLAFPR	FYFVSSADLL	DILSNGNDPV
1610	1620	1630	1640	1650	1660	1670	1680
EVSRHLSKLF	DSLCKLKFRL	DASDKPLKVG	LGMYSKEDEY	MVFDQECDLS	GQVEVWLNRV	LDRMCSTLRH	EIPEAVVTYE
1690	1700	1710	1720	1730	1740	1750	1760
EKPREQWILD	YPAQVALTCT	QIWWTTEVGL	AFARLEEGYE	NAIRDYNKKQ	ISQLNVLITL	LMGNLNAGDR	MKIMTICTID
1770	1780	1790	1800	1810	1820	1830	1840
VHARDVVAKM	IVAKVESSQA	FTWQAQLRHR	WDEEKRHCFA	NICDAQIQYS	YEYLGNTPRL	VITPLTDRCY	ITLTQSLHLI
1850	1860	1870	1880	1890	1900	1910	1920
MGGAPAGPAG	TGKTETTKDL	GRALGTMVYV	FNCSEQMDYK	SCGNIYKGLA	QTGAWGCFDE	FNRISVEVLS	VIAVQVKCVQ
1930	1940	1950	1960	1970	1980	1990	2000
DAIRAKKKAF	NFLGEIIGLI	PTVGIFITMN	PGYAGRAELP	ENLKALFRPC	AMVVPDFELI	CEIMLMAEGF	LEARLLARKF
2010	2020	2030	2040	2050	2060	2070	2080
ITLYTLCKEL	LSKQDHYDWG	LRAIKSVLVV	AGSLKRGDPS	RAEDQVLMRA	LRDFNIPKIV	TDDLPVFMGL	IGDLFPALDV
2090	2100	2110	2120	2130	2140	2150	2160
PRKRDLNFEK	IIKQSIVELK	LQAEDSFVLK	VVQLEELLQV	RHSVFIVGNA	GSGKSQVLKS	LNKTYQNLKR	KPVAVDLDPK
2170	2180	2190	2200	2210	2220	2230	2240

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1870	1	704.2582	-146.54	2	53.4	13.7	0	1255-1267	K.SGGLFEVPVPDYK.Q	
2850	1	869.4224	-91.80	2	64.2	14.1	0	3728-3742	K.LIFLAQVTFQVLSMK.K	
637	1	635.8011	-148.78	2	36.5	10.8	2	4247-4257	R.RSLKELNLGLK.G	

Detailed Protein Report

Protein 50: zinc finger protein 492 [Homo sapiens]

Accession:	gi|148806865	**Score:**	69.5
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 [%]:**	11.3
		No. of unique Peptides:	3

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
1839	1	582.2374	12.53	2	53.0	13.4	1	84-92	K.YCKSMDECK.V	Carbamidomethyl: 8
1912	1	621.2738	-20.17	2	54.0	13.3	1	195-204	K.KPYKCEECGK.A	Carbamidomethyl: 5
2688	1	992.0980	-39.40	3	64.8	18.1	2	495-519	R.HKMIHTGEKLYKPESCNNACDNIAK.I	Carbamidomethyl: 16, 20; Oxidation: 3

Detailed Protein Report

Protein 51:	**PREDICTED: neuroblast differentiation-associated protein AHNAK isoform X6 [Homo sapiens]**		
Accession:	gi|530397289	**Score:**	68.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	580.3
Database Date:	2015-11-30	**pI:**	5.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.2
		No. of unique Peptides:	4

Quantitation

mdown:qdown	**Median:**	0.54	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	1.31	**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

Detailed Protein Report

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		Wdown:Qdown 1.31 mdown:qdown 0.54

Detailed Protein Report

Protein 52: PREDICTED: rho GTPase-activating protein 26 isoform X13 [Homo sapiens]

Accession:	gi|578810840	**Score:**	68.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	71.6
Database Date:	2015-11-30	**pI:**	9.8
		Sequence Coverage [%]:	8.4
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MKRETRRSAF	CVQGWSGGDP	ARVVLWGSAG	GRGRARHAGV	PAVGPECRAR	RSQRADPIVS	TAPAPLGAEL	LSLECPTVRM
90	100	110	120	130	140	150	160
ERALPRGRCL	PLGKDLSSAK	RKFADSLNEF	KFQCIGDAET	DDEMCIARSL	QEFATVLRNL	EDERIRMIEN	ASEVLITPLE
170	180	190	200	210	220	230	240
KFRKEQIGAA	KEAKKKYDKE	TEKYCGILEK	HLNLSSKKKE	SQLQEADSQV	DLVRQHFYEV	SLEYVFKVQE	VQERKMFEFV
250	260	270	280	290	300	310	320
EPLLAFLQGL	FTFYHHGYEL	AKDFGDFKTQ	LTISIQNTRN	RFEGTRSEVE	SLMKKMKENP	LEHKTISPYT	MEGYLYVQEK
330	340	350	360	370	380	390	400
RHFGTSWVKH	YCTYQRDSKQ	ITMVPFDQKS	GGKGGEDESV	ILKSCTRRKT	DSIEKRFCFD	VEAVDRPGVI	TMQALSEEDR
410	420	430	440	450	460	470	480
RLWMEAMDGR	EPVYNSNKDS	QSEGTAQLDS	IGFSIIRKCI	HAVETRGINE	QGLYRIVGVN	SRVQKLLSVL	MDPKTASETE
490	500	510	520	530	540	550	560
TDICAEWEIK	TITSALKTYL	RMLPGPLMMY	QFQRSFIKAA	KLENQESRVS	EIHSLVHRLP	EKNRQMLQLL	MNHLANSAFV
570	580	590	600	610	620	630	
SLSHYCIRYA	GGLGKKCVKC	SLQWRTAANA	RWPSQRMLGK	CSCNQATKQS	FQGDFTYGDQ	GQIGVCCP	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1954	9	710.2864	-113.94	2	54.5	21.4	1	35-48	R.ARHAGVPAVGPECR.A	
286	1	716.6484	355.53	1	32.9	20.0	0	165-171	K.EQIGAAK.E	

Protein 53: zymogen granule protein 16 homolog B precursor [Homo sapiens]

Accession: gi|94536866
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 68.1
MW [kDa]: 22.7
pI: 7.6
Sequence Coverage [%]: 14.4
No. of unique Peptides: 2

Quantitation

mdown:qdown **Median:** 2.33 **CV:** 0.00 % **No. of Peptides:** 1
Wdown:Qdown **Median:** 2.74 **CV:** 0.00 % **No. of Peptides:** 1

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2510	2	464.1779	-296.31	2	60.1	35.2	0	79-87	R.VSVGLLLVK.S		
1743	6	1095.0646	-10.46	2	50.3	32.9	0	101-121	K.LGALGGNTQEVTLQPGEYITK.V		Wdown:Qdown 2.74 mdown:qdown 2.33

Detailed Protein Report

Protein 54: PREDICTED: keratin, type I cytoskeletal 24 isoform X1 [Homo sapiens]

Accession:	gi|578830527	**Score:**	67.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	46.1
Database Date:	2015-11-30	**pI:**	4.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	4.9
		No. of unique Peptides:	1

Quantitation

Wdown:Qdown **Median:** 0.97 **CV:** 0.00 % **No. of Peptides:** 1

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
587	1	512.7149	-24.47	2	35.9	12.9	0	367-376	R.NSGSVNMGSR.D	Oxidation: 7	Wdown:Qdown 0.97

Detailed Protein Report

Protein 55: **macrophage mannose receptor 1 precursor [Homo sapiens]**

Accession:	gi|4505245	**Score:**	66.0
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 [%]:**	4.9
		No. of unique Peptides:	5

Quantitation

mdown:qdown	**Median:** 0.16	**CV:** 0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:** 0.51	**CV:** 117.59 %	**No. of Peptides:**	2

```
        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	Ratios
1884	1	621.2922	12.19	2	53.6	15.7	1	95-103	K.SEFQKWECK.N	Carbamidomethyl: 8	
1638	1	1069.9824	-53.73	2	49.0	18.2	2	324-341	K.NAKWENLECVQKLGYICK.K		Wdown:Qdown 0.20 mdown:qdown 0.16
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	

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
196	1	651.1714	-173.27	2	31.8	10.9	1	819-829	K.ETMDNARAFCK.R	Oxidation: 3	Wdown:Qdown 1.30

Detailed Protein Report

Protein 56: dystrophin Dp260-2 isoform [Homo sapiens]

Accession:	gi|5032291	**Score:**	65.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	270.9
Database Date:	2015-11-30	**pI:**	5.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.4
		No. of unique Peptides:	5

Quantitation

Wdown:Qdown	**Median:**	0.50	**CV:**	3.56 %	**No. of Peptides:**	2

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
129	1	619.6434	29.86	3	30.9	11.2	2	392-407	R.DQAANLMANRGDHCRK.L	Carbamidomethyl: 14	Wdown:Qdown 0.48
2949	1	735.4039	12.58	2	65.6	12.3	1	482-493	K.ELLQRGDNLQQR.I		
982	1	712.1299	-301.49	1	41.8	17.8	1	747-751	K.MYKDR.Q		Wdown:Qdown 0.52
1755	1	636.2889	-138.71	2	51.9	13.1	1	951-960	K.LKQTNLQWIK.V		
1813	1	785.8684	-31.80	2	51.3	11.2	0	1315-1327	K.VHMITENINASWR.S		

Detailed Protein Report

Protein 57: PREDICTED: uncharacterized protein KIAA1551 isoform X1 [Homo sapiens]

Accession:	gi|530399223	**Score:**	65.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	194.7
Database Date:	2015-11-30	**pI:**	9.7
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	2.5
		No. of unique Peptides:	4

```
        10         20         30         40         50         60         70         80
MNWNEKPKSA TLPPLYPKSQ PPFLHQSLIN QITTTSQSSF SYPGSNQEAC MYPGNSNPIS QPLLNIQNYP QQISVSDMHN
        90        100        110        120        130        140        150        160
GTVVASHTSV ERITYANVNG PKQLTHNLQM SSGVTQNVWL NSPMRNPVHS HIGATVSHQT DFGANVPNMP ALQSQLITSD
       170        180        190        200        210        220        230        240
TYSMQMQMIP SNSTRLPVAY QGNQGLNQSF SEQQVDWTQQ CISKGLTYPD YRPPPKLYRY SPQSFLPDST IQKQNFIPHT
       250        260        270        280        290        300        310        320
SLQVKNSQLL NSVLTLPSRQ TSAVPSQQYA TQTDKRPPPP PYNCRYGSQP LQSTQHITKH LSMEVPQSRE MLSSEIRTSF
       330        340        350        360        370        380        390        400
QQQWQNPNEN VSTIGNFTNL KVNTNSKQPF NSPIRSSVDG VQTLAQTNEE KIMDSCNPTS NQVLDTSVAK EKLVRDIKTL
       410        420        430        440        450        460        470        480
VEIKQKFSEL ARKIKINKDL LMAAGCIKMT NTSYSEPAQN SKLSLKQTAK IQSGPQITPV MPENAERQTP TVVESAETNK
       490        500        510        520        530        540        550        560
TQCMLNSDIQ EVNCRRFNQV DSVLPNPVYS EKRPMPDSSH DVKVLTSKTS AVEMTQAVLN TQLSSENVTK VEQNSPAVCE
       570        580        590        600        610        620        630        640
TISVPKSMST EEYKSKIQNE NMLLLALLSQ ARKTQKTVLK DANQTIQDSK PDSCEMNPNT QMTGNQLNLK NMETPSTSNV
       650        660        670        680        690        700        710        720
SGRVLDNSFC SGQESSTKGM PAKSDSSCSM EVLATCLSLW KKQPSDTAKE KECDKLRTNT TAVGISKPAN IHVKSPCSVV
       730        740        750        760        770        780        790        800
GNSNSQNKIS NPSQQTALSM VMHNYESSGI NITKGTELQI AVVSPLVLSE VKTLSVKGIT PAVLPETVYP VIKEGSVCSL
       810        820        830        840        850        860        870        880
QNQLAENAKA TAALKVDVSG PVASTATSTK IFPLTQKEKQ NESTNGNSEV TPNVNQGKHN KLESAIHSPM NDQQISQESR
       890        900        910        920        930        940        950        960
NSTVVSSDTL QIDNICSLVE GDTSYNSQIA KIFSSLPLKM VEPQKPSLPN QQGIGSREPE KQLDNTTENK DFGFQKDKPV
       970        980        990       1000       1010       1020       1030       1040
QCTDVSHKIC DQSKSEPPLE SSFNNLETNR VILEKSSLEH ATEKSTANDT CSSAAIQEDI YPQEIDASSN YTPQDPARNE
      1050       1060       1070       1080       1090       1100       1110       1120
IHSDKAPVLY LHDQLSELLK EFPYGIEAVN TREGSVGQQT TYQTSEDQTA DKTSSDSKDP ADQIQITILS SEQMKEIFPE
      1130       1140       1150       1160       1170       1180       1190       1200
QDDQPYVVDK LAEPQKEEPI TEVVSQCDLQ APAAGQSRDS VILDSEKDDI HCCALGWLSM VYEGVPQCQC NSIKNSSSEE
      1210       1220       1230       1240       1250       1260       1270       1280
EKQKEQCSPL DTNSCKQGER TSDRDVTVVQ FKSLVNNPKT PPDGKSHFPE LQDDSRKDTP KTKHKSLPRT EQELVAGQFS
      1290       1300       1310       1320       1330       1340       1350       1360
SKCDKLNPLQ NHKRKKLRFH EVTFHSSNKM TASYEQASQE TRQKKHVTQN SRPLKTKTAF LPNKDVYKKH SSLGQSLSPE
      1370       1380       1390       1400       1410       1420       1430       1440
KIKLKLKSVS FKQKRKLDQG NVLDMEVKKK KHDKQEQKGS VGATFKLGDS LSNPNERAIV KEKMVSNTKS VDTKASSSKF
      1450       1460       1470       1480       1490       1500       1510       1520
SRILTPKEYL QRQKHKEALS NKASKKICVK NVPCDSEHMR PSKLAVQVES CGKSNEKHSS GVQTSKESLN GLTSHGKNLK
      1530       1540       1550       1560       1570       1580       1590       1600
IHHSQESKTY NILRNVKEKV GGKQPDKIWI DKTKLDKLTN ISNEAQFSQM PPQVKDQKKL YLNRVGFKCT ERESISLTKL
      1610       1620       1630       1640       1650       1660       1670       1680
ESSPRKLHKD KRQENKHKTF LPVKGNTEKS NMLEFKLCPD ILLKNTNSVE ERKDVKPHPR KEQAPLQVSG IKSTKEDWLK
      1690       1700       1710       1720       1730       1740       1750
FVATKKRTQK DSQERDNVNS RLSKRSFSAD GFEMLQNPVK DSKEMFQTYK QMYLEKRSRS LGSSPVK
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2628	1	644.4984	138.82	1	63.6	19.8	1	391-395	K.EKLVR.D	
2689	1	731.8632	-38.63	2	64.8	14.6	1	416-428	K.INKDLLMAAGCIK.M	Carbamidomethyl: 11;

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
										Oxidation: 7
2776	1	710.3755	7.84	2	63.8	11.0	0	816-830	K.VDVSGPVASTATSTK.I	
258	1	585.2801	-84.98	2	32.0	19.7	0	1662-1672	K.EQAPLQVSGIK.S	

Detailed Protein Report

Protein 58: ubiquitin carboxyl-terminal hydrolase 34 [Homo sapiens]

Accession:	gi|110347427	**Score:**	64.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	404.0
Database Date:	2015-11-30	**pI:**	5.4
		Sequence Coverage [%]:	1.7
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MCENCADLVE	VLNEISDVEG	GDGLQLRKEH	TLKIFTYINS	WTQRQCLCCF	KEYKHLEIFN	QVVCALINLV	IAQVQVLRDQ
90	100	110	120	130	140	150	160
LCKHCTTINI	DSTWQDESNQ	AEEPLNIDRE	CNEGSTERQK	SIEKKSNSTR	ICNLTEEESS	KSSDPFSLWS	TDEKEKLLLC
170	180	190	200	210	220	230	240
VAKIFQIQFP	LYTAYKHNTH	PTIEDISTQE	SNILGAFCDM	NDVEVPLHLL	RYVCLFCGKN	GLSLMKDCFE	YGTPETLPFL
250	260	270	280	290	300	310	320
IAHAFITVVS	NIRIWLHIPA	VMQHIIPFRT	YVIRYLCKLS	DQELRQSAAR	NMADLMWSTV	KEPLDTTLCF	DKESLDLAFK
330	340	350	360	370	380	390	400
YFMSPTLTMR	LAGLSQITNQ	LHTFNDVCNN	ESLVSDTETS	IAKELADWLI	SNNVVEHIFG	PNLHIEIIKQ	CQVILNFLAA
410	420	430	440	450	460	470	480
EGRLSTQHID	CIWAAAQLKH	CSRYIHDLFP	SLIKNLDPVP	LRHLLNLVSA	LEPSVHTEQT	LYLASMLIKA	LWNNALAAKA
490	500	510	520	530	540	550	560
QLSKQSSFAS	LLNTNIPIGN	KKEEEELRRT	APSPWSPAAS	PQSSDNSDTH	QSGGSDIEMD	EQLINRTKHV	QQRLSDTEES
570	580	590	600	610	620	630	640
MQGSSDETAN	SGEDGSSGPG	SSSGHSDGSS	NEVNSSHASQ	SAGSPGSEVQ	SEDIADIEAL	KEEDEDDDHG	HNPPKSSCGT
650	660	670	680	690	700	710	720
DLRNRKLESQ	AGICLGDSQG	MSERNGTSSG	TGKDLVFNTE	SLPSVDNRMR	MLDACSHSED	PEHDISGEMN	ATHIAQGSQE
730	740	750	760	770	780	790	800
SCITRTGDFL	GETIGNELFN	CRQFIGPQHH	HHHHHHHHHH	DGHMVDDMLS	ADDVSCSSSQ	VSAKSEKNMA	DFDGEESGCE
810	820	830	840	850	860	870	880
EELVQINSHA	ELTSHLQQHL	PNLASIYHEH	LSQGPVVHKH	QFNSNAVTDI	NLDNVCKKGN	TLLWDIVQDE	DAVNLSEGLI
890	900	910	920	930	940	950	960
NEAEKLLCSL	VCWFTDRQIR	MRFIEGCLEN	LGNNRSVVIS	LRLLPKLFGT	FQQFGSSYDT	HWITMWAEKE	LNMMKLFFDN
970	980	990	1000	1010	1020	1030	1040
LVYYIQTVRE	GRQKHALYSH	SAEVQVRLQF	LTCVFSTLGS	PDHFRLSLEQ	VDILWHCLVE	DSECYDDALH	WFLNQVRSKD
1050	1060	1070	1080	1090	1100	1110	1120
QHAMGMETYK	HLFLEKMPQL	KPETISMTGL	NLFQHLCNLA	RLATSAYDGC	SNSELCGMDQ	FWGIALRAQS	GDVSRAAIQY
1130	1140	1150	1160	1170	1180	1190	1200
INSYYINGKT	GLEKEQEFIS	KCMESLMIAS	SSLEQESHSS	LMVIERGLLM	LKTHLEAFRR	RFAYHLRQWQ	IEGTGISSHL
1210	1220	1230	1240	1250	1260	1270	1280
KALSDKQSLP	LRVVCQPAGL	PDKMTIEMYP	SDQVADLRAE	VTHWYENLQK	EQINQQAQLQ	EFGQSNRKGE	FPGGLMGPVR
1290	1300	1310	1320	1330	1340	1350	1360
MISSGHELTT	DYDEKALHEL	GFKDMQMVFV	SLGAPRRERK	GEGVQLPASC	LPPPQKDNIP	MLLLLQEPHL	TTLFDLLEML
1370	1380	1390	1400	1410	1420	1430	1440
ASFKPPSGKV	AVDDSESLRC	EELHLHAENL	SRRVWELLML	LPTCPNMLMA	FQNISDEQSN	DGFNWKELLK	IKSAHKLLYA
1450	1460	1470	1480	1490	1500	1510	1520
LEIIEALGKP	NRRIRRESTG	SYSDLYPDSD	DSSEDQVENS	KNSWSCKFVA	AGGLQQLLEI	FNSGILEPKE	QESWTVWQLD
1530	1540	1550	1560	1570	1580	1590	1600
CLACLLKLIC	QFAVDPSDLD	LAYHDVFAWS	GIAESHRKRT	WPGKSRKAAG	DHAKGLHIPR	LTEVFLVLVQ	GTSLIQRLMS
1610	1620	1630	1640	1650	1660	1670	1680
VAYTYDNLAP	RVLKAQSDHR	SRHEVSHYSM	WLLVSWAHCC	SLVKSSLADS	DHLQDWLKKL	TLLIPETAVR	HESCSGLYKL
1690	1700	1710	1720	1730	1740	1750	1760
SLSGLDGGDS	INRSFLLLAA	STLLKFLPDA	QALKPIRIDD	YEEEPILKPG	CKEYFWLLCK	LVDNIHIKDA	SQTTLLDLDA
1770	1780	1790	1800	1810	1820	1830	1840
LARHLADCIR	SREILDHQDG	NVEDDGLTGL	LRLATSVVKH	KPPFKFSREG	QEFLRDIFNL	LFLLPSLKDR	QQPKCKSHSS
1850	1860	1870	1880	1890	1900	1910	1920
RAAAYDLLVE	MVKGSVENYR	LIHNWVMAQH	MQSHAPYKWD	YWPHEDVRAE	CRFVGLTNLG	ATCYLASTIQ	QLYMIPEARQ
1930	1940	1950	1960	1970	1980	1990	2000
AVFTAKYSED	MKHKTTLLEL	QKMFTYLMES	ECKAYNPRPF	CKTYTMDKQP	LNTGEQKDMT	EFFTDLITKI	EEMSPELKNT
2010	2020	2030	2040	2050	2060	2070	2080
VKSLFGGVIT	NNVVSLDCEH	VSQTAEEFYT	VRCQVADMKN	IYESLDEVTI	KDTLEGDNMY	TCSHCGKKVR	AEKRACFKKL
2090	2100	2110	2120	2130	2140	2150	2160
PRILSFNTMR	YTFNMVTMMK	EKVNTHFSFP	LRLDMTPYTE	DFLMGKSERK	EGFKEVSDHS	KDSESYEYDL	IGVTVHTGTA
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2681	1	1079.0243	41.33	2	64.7	12.9	2	2052-2070	K.DTLEGDNMYTCSHCGKKVR.A	
597	2	642.8360	18.78	2	36.1	18.4	0	2940-2950	R.SCWTTLISAFR.I	

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Detailed Protein Report

Protein 59: PREDICTED: uncharacterized protein LOC101927628 [Homo sapiens]

Accession: gi|578827891
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 63.5
MW [kDa]: 109.0
pI: 12.3
Sequence Coverage [%]: 7.8
No. of unique Peptides: 5

10	20	30	40	50	60	70	80
MEESAEQAQR	RDETRVGRRR	HSWRSRQSRQ	TKEFIFSELL	SNLYSRRNLQ	TLVEESAEQA	QRCDEMLLLR	AAVQPALAWE
90	100	110	120	130	140	150	160
REDTRGGVGR	AGRPRSSSSQ	SCCPTCTHVG	TSRHSWRRRQ	SRQTKEFIFS	ELLSNLHSRG	NEKTLVKASA	EKADQGVHLL
170	180	190	200	210	220	230	240
RAAVQPALAW	EREDTRGGVG	RAGRPRSSSS	QSCCPNCTRV	GTRRHSWRSR	QSRQTKEFIF	SELLSNLYSR	RNLQTLVEES
250	260	270	280	290	300	310	320
AEQAQRCDEM	LLLRAAVQPA	LAWEREDTRG	GVGRAGRPRS	SSSQSCCPTC	TRVGTRRHSW	RRRQSRQTKE	FIFSELLSNL
330	340	350	360	370	380	390	400
HSRGNEKTLM	EESAEQAQRR	DETRVGRRRH	SWRSRQSRQT	KEFIFSELLS	NLYSHRNLQT	LVEESAEQAQ	RCDEMLLLRA
410	420	430	440	450	460	470	480
AVQPALAWER	EDTRGGVGRA	GRPRSSSSQS	CCPTCTHVGT	SRHSWRRRQS	RQTKEFIFSE	LLSNLHSRGN	EKTLVKASAE
490	500	510	520	530	540	550	560
KADQGVHLLR	AAVQPALAWE	REDTRGGVGR	AGRPRSSSSQ	SCCPNCTRVG	TRRHSWRSRQ	SRHRGVTRLA	WEEEDTPGGV
570	580	590	600	610	620	630	640
GRAGRPRSSS	SRSCCPTCTR	VGTCRHLWRS	RQSRHSGATR	CCFSELLSNL	HSRGNKKTLV	EALAEQADQG	VHLLRAAVQP
650	660	670	680	690	700	710	720
VLAWEREDTR	GGVGRAGRPR	SSSSQSCCPT	CTRVGTRRHS	CRSRQSRHSG	VTRLAWEEED	IPGGVGRAGR	ARSSSSRSCC
730	740	750	760	770	780	790	800
PTCTRVGTCR	HLWRSRQSRH	SGATRCCFSE	LLSNLHSRGN	QKTLVEASAE	QADQGVHLLR	AAVQPVLAWE	REDTRGGVGR
810	820	830	840	850	860	870	880
AGRPRSSSSQ	SCCPTCTRVG	TRRHSWRSRP	SRHSGVTRLA	WEEEDTPGGV	GRAGRPRSSS	SRSCCPTCTR	VGTCRHLWRS
890	900	910	920	930	940	950	960
RQSRHSGATR	CCFSELLSNL	HWRGNEKTLV	EASAEQADQG	VHLLRAAVQP	VLAWERADTR	GGVGRAGRPR	NSSSQSCCPT
970	980						
CTRVGMRRHS							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2702	1	856.8935	-53.50	2	65.0	10.9	1	71-85	R.AAVQPALAWEREDTR.G	
254	1	977.7698	-10.85	3	31.9	11.3	2	91-117	R.AGRPRSSSSQSCCPTCTHVGTSRHSWR.R	
2075	3	937.3867	-15.36	2	54.5	13.9	1	280-296	R.SSSSQSCCPTCTRVGTR.R	Carbamidomethyl: 7, 8
2276	2	937.4372	47.94	2	56.9	12.7	1	951-967	R.NSSSQSCCPTCTRVGMR.R	Carbamidomethyl: 8
2316	1	937.2798	-119.93	2	57.4	14.7	1	951-967	R.NSSSQSCCPTCTRVGMR.R	Carbamidomethyl: 7

Detailed Protein Report

Protein 60: hemoglobin subunit epsilon [Homo sapiens]

Accession:	gi|4885393	**Score:**	63.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	16.2
Database Date:	2015-11-30	**pI:**	9.4
		Sequence Coverage [%]:	15.0
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	7.41	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.50	**CV:**	0.00 %	**No. of Peptides:**	1

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2140	3	596.7831	-152.64	2	55.3	13.5	0	134-145	K.LVSAVAIALAHK.Y		Wdown:Qdown 0.50 mdown:qdown 7.41

Detailed Protein Report

Protein 61: dynein heavy chain 11, axonemal [Homo sapiens]

Accession:	gi|459642365	**Score:**	63.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	520.0
Database Date:	2015-11-30	**pI:**	6.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.4
		No. of unique Peptides:	5

Detailed Protein Report

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

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
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	
882	1	647.8007	-79.74	2	39.8	12.8	2	1437-1446	R.LHRVEDDVRR.I	
36	1	779.3158	-100.01	2	29.7	10.1	1	2083-2095	R.GDKNRPEDQVLMR.A	
1863	1	965.8216	-153.66	2	53.3	12.4	2	4470-4484	R.QETKQTYECPVYRTK.L	Carbamidomethyl: 9

Detailed Protein Report

Protein 62: fibrillin-1 precursor [Homo sapiens]

Accession:	gi|281485550	**Score:**	63.1
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 [%]:**	2.3
		No. of unique Peptides:	4

Quantitation

mdown:qdown	**Median:**	0.87	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.57	**CV:**	87.02 %	**No. of Peptides:**	2

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
25	1	796.8073	-13.58	2	29.5	12.2	0	166-179	R.CACTYGFTGPQCER.D	Carbamidomethyl: 1	Wdown:Qdown 0.27
1152	1	991.7003	-40.24	3	44.0	14.6	1	356-380	K. MQCCCDAGRCWSPGVTVAPEM A	Carbamidomethyl: 3, 4, 5, 22; Oxidation: 1, 21	
2800	1	913.4636	99.50	2	63.5	13.3	0	1178-1192	K.YQCACNPGYHSTPDR.L	Carbamidomethyl: 3, 5	
976	9	635.1635	-177.36	2	40.7	23.1	1	2482-2492	R.SCKDLDECATK.Q	Carbamidomethyl: 8	Wdown:Qdown 1.21 mdown:qdown 0.87

Detailed Protein Report

Protein 63: **coagulation factor VIII isoform a precursor [Homo sapiens]**

Accession:	gi|4503647	**Score:**	63.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	266.8
Database Date:	2015-11-30	**pI:**	7.0
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	3.8
		No. of unique Peptides:	4

Quantitation

mdown:qdown	**Median:**	0.79	**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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2170	1	937.3499	-130.54	2	55.7	11.5	0	1-15	-.MQIELSTCFFLCLLR.F	Carbamidomethyl: 12	mdown:qdown 0.79
2041	1	856.8157	-171.77	2	55.6	11.8	2	1060-1073	K.KVTPLIHDRMLMDK.N	Oxidation: 12	
2184	1	1061.5230	-9.68	3	57.5	13.4	0	1523-1553	K.DLFPTETSNGSPGHLDLVEGSLLQW		
2720	1	710.3296	-131.82	2	65.3	14.5	0	2092-2104	K.VDLLAPMIIHGIK.T		

Detailed Protein Report

Protein 64: profilin-1 [Homo sapiens]

Accession:	gi|4826898	**Score:**	62.6
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

mdown:qdown	**Median:**	1.19	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	1.07	**CV:**	0.00 %	**No. of Peptides:**	1

```
         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
2934	9	822.4733	1.65	2	65.5	46.8	0	39-54	K.TFVNITPAEVGVLVGK.D		
1495	1	850.7379	-173.16	2	48.5	15.9	2	128-140	K.CYEMASHLRRSQY.-	Carbamidomethyl: 1	mdown:qdown 1.19 Wdown:Qdown 1.07

Detailed Protein Report

Protein 65: **PREDICTED: probable E3 ubiquitin-protein ligase MYCBP2 isoform X2 [Homo sapiens]**

Accession:	gi|530402184	**Score:**	62.5
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 [%]:**	1.9
		No. of unique Peptides:	3

Detailed Protein Report

```
        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
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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
1222	1	927.2551	104.81	3	44.9	11.3	1	1184-1209	R.ALTTRSHAALHILGCLDTLAAMQDLK.M	Oxidation: 22
1800	1	658.7973	-153.52	2	52.5	13.4	1	1909-1921	R.ALSVVSTVVRASK.D	
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 66: low-density lipoprotein receptor-related protein 2 precursor [Homo sapiens]

Accession:	gi|126012573	**Score:**	61.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	521.6
Database Date:	2015-11-30	**pI:**	4.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.5
		No. of unique Peptides:	4

Detailed Protein Report

10	20	30	40	50	60	70	80
MDRGPAAVAC	TLLLALVACL	APASGQECDS	AHFRCGSGHC	IPADWRCDGT	KDCSDDADEI	GCAVVTCQQG	YFKCQSEGQC
90	100	110	120	130	140	150	160
IPNSWVCDQD	QDCDDGSDER	QDCSQSTCSS	HQITCSNGQC	IPSEYRCDHV	RDCPDGADEN	DCQYPTCEQL	TCDNGACYNT
170	180	190	200	210	220	230	240
SQKCDWKVDC	RDSSDEINCT	EICLHNEFSC	GNGECIPRAY	VCDHDNDCQD	GSDEHACNYP	TCGGYQFTCP	SGRCIYQNWV
250	260	270	280	290	300	310	320
CDGEDDCKDN	GDEDGCESGP	HDVHKCSPRE	WSCPESGRCI	SIYKVCDGIL	DCPGREDENN	TSTGKYCSMT	LCSALNCQYQ
330	340	350	360	370	380	390	400
CHETPYGGAC	FCPPGYIINH	NDSRTCVEFD	DCQIWGICDQ	KCESRPGRHL	CHCEEGYILE	RGQYCKANDS	FGEASIIFSN
410	420	430	440	450	460	470	480
GRDLLIGDIH	GRSFRILVES	QNRGVAVGVA	FHYHLQRVFW	TDTVQNKVFS	VDINGLNIQE	VLNVSVETPE	NLAVDWVNNK
490	500	510	520	530	540	550	560
IYLVETKVNR	IDMVNLDGSY	RVTLITENLG	HPRGIAVDPT	VGYLFFSDWE	SLSGEPKLER	AFMDGSNRKD	LVKTKLGWPA
570	580	590	600	610	620	630	640
GVTLDMISKR	VYWVDSRFDY	IETVTYDGIQ	RKTVVHGGSL	IPHPFGVSLF	EGQVFFTDWT	KMAVLKANKF	TETNPQVYYQ
650	660	670	680	690	700	710	720
ASLRPYGVTV	YHSLRQPYAT	NPCKDNNGGC	EQVCVLSHRT	DNDGLGFRCK	CTFGFQLDTD	ERHCIAVQNF	LIFSSQVAIR
730	740	750	760	770	780	790	800
GIPFTLSTQE	DVMVPVSGNP	SFFVGIDFDA	QDSTIFFSDM	SKHMIFKQKI	DGTGREILAA	NRVENVESLA	FDWISKNLYW
810	820	830	840	850	860	870	880
TDSHYKSISV	MRLADKTRRT	VVQYLNNPRS	VVVHPFAGYL	FFTDWFRPAK	IMRAWSDGSH	LLPVINTTLG	WPNGLAIDWA
890	900	910	920	930	940	950	960
ASRLYWVDAY	FDKIEHSTFD	GLDRRRLGHI	EQMTHPFGLA	IFGEHLFFTD	WRLGAIIRVR	KADGGEMTVI	RSGIAYILHL
970	980	990	1000	1010	1020	1030	1040
KSYDVNIQTG	SNACNQPTHP	NGDCSHFCFP	VPNFQRVCGC	PYGMRLASNH	LTCEGDPTNE	PPTEQCGLFS	FPCKNGRCVP
1050	1060	1070	1080	1090	1100	1110	1120
NYYLCDGVDD	CHDNSDEQLC	GTLNNTCSSS	AFTCGHGECI	PAHWRCDKRN	DCVDGSDEHN	CPTHAPASCL	DTQYTCDNHQ
1130	1140	1150	1160	1170	1180	1190	1200
CISKNWVCDT	DNDCGDGSDE	KNCNSTETCQ	PSQFNCPNHR	CIDLSFVCDG	DKDCVDGSDE	VGCVLNCTAS	QFKCASGDKC
1210	1220	1230	1240	1250	1260	1270	1280
IGVTNRCDGV	FDCSDNSDEA	GCPTRPPGMC	HSDEFQCQED	GICIPNFWEC	DGHPDCLYGS	DEHNACVPKT	CPSSYFHCDN
1290	1300	1310	1320	1330	1340	1350	1360
GNCIHRAWLC	DRDNDCGDMS	DEKDCPTQPF	RCPSWQWQCL	GHNICVNLSV	VCDGIFDCPN	GTDESPLCNG	NSCSDFNGGC
1370	1380	1390	1400	1410	1420	1430	1440
THECVQEPFG	AKCLCPLGFL	LANDSKTCED	IDECDILGSC	SQHCYNMRGS	FRCSCDTGYM	LESDGRTCKV	TASESLLLLV
1450	1460	1470	1480	1490	1500	1510	1520
ASQNKIIADS	VTSQVHNIYS	LVENGSYIVA	VDFDSISGRI	FWSDATQGKT	WSAFQNGTDR	RVVFDSSIIL	TETIAIDWVG
1530	1540	1550	1560	1570	1580	1590	1600
RNLYWTDYAL	ETIEVSKIDG	SHRTVLISKN	LTNPRGLALD	PRMNEHLLFW	SDWGHHPRIE	RASMDGSMRT	VIVQDKIFWP
1610	1620	1630	1640	1650	1660	1670	1680
CGLTIDYPNR	LLYFMDSYLD	YMDFCDYNGH	HRRQVIASDL	IIRHPYALTL	FEDSVYWTDR	ATRRVMRANK	WHGGNQSVVM
1690	1700	1710	1720	1730	1740	1750	1760
YNIQWPLGIV	AVHPSKQPNS	VNPCAFSRCS	HLCLLSSQGP	HFYSCVCPSG	WSLSPDLLNC	LRDDQPFLIT	VRQHIIFGIS
1770	1780	1790	1800	1810	1820	1830	1840
LNPEVKSNDA	MVPIAGIQNG	LDVEFDDAEQ	YIYWVENPGE	IHRVKTDGTN	RTVFASISMV	GPSMNLALDW	ISRNLYSTNP
1850	1860	1870	1880	1890	1900	1910	1920
RTQSIEVLTL	HGDIRYRKTL	IANDGTALGV	GFPIGITVDP	ARGKLYWSDQ	GTDSGVPAKI	ASANMDGTSV	KTLFTGNLEH
1930	1940	1950	1960	1970	1980	1990	2000
LECVTLDIEE	QKLYWAVTGR	GVIERGNVDG	TDRMILVHQL	SHPWGIAVHD	SFLYYTDEQY	EVIERVDKAT	GANKIVLRDN
2010	2020	2030	2040	2050	2060	2070	2080
VPNLRGLQVY	HRRNAAESSN	GCSNNMNACQ	QICLPVPGGL	FSCACATGFK	LNPDNRSCSP	YNSFIVVSML	SAIRGFSLEL
2090	2100	2110	2120	2130	2140	2150	2160
SDHSETMVPV	AGQGRNALHV	DVDVSSGFIY	WCDFSSSVAS	DNAIRRIKPD	GSSLMNIVTH	GIGENGVRGI	AVDWVAGNLY
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
573	1	656.8903	-140.87	3	35.8	15.5	1	279-295	R.CISIYKVCDGILDCPGR.E	Carbamidomethyl: 1, 8
1173	1	786.4695	28.78	1	44.3	12.4	0	776-782	R.EILAANR.V	
1012	1	974.7041	-35.28	3	41.2	13.1	1	1173-1199	K.DCVDGSDEVGCVLNCTASQFKCASGDK.C	Carbamidomethyl: 11, 15, 22
23	1	788.3643	33.00	3	29.6	20.9	0	3797-3816	R.TCHPEYFQCTSGHCVHSELK.C	Carbamidomethyl: 2

Detailed Protein Report

Protein 67: **PREDICTED: RANBP2-like and GRIP domain-containing protein 8 isoform X4 [Homo sapiens]**

Accession:	gi|530369360	**Score:**	61.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	166.0
Database Date:	2015-11-30	**pI:**	6.2
		Sequence Coverage [%]:	4.7
		No. of unique Peptides:	3

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	ILDAVNGNIE	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	LQAQDIRGRK	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	GVAGASDTTI	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
SPCGKIAVAV	LEEITRERTD	VIQGDDVADA	ASEVEVSSTS	ETTTKAVVSP	PKFVFVSESV	KRIFSSEKSK	PFAFGNSSAT
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	EEENPSRSSG				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2775	1	557.2986	22.82	3	63.1	14.9	1	623-638	K.STKEGFSIPVSADGFK.F	
1997	1	648.7895	-86.66	2	53.5	11.3	1	1114-1124	R.DQVLKLCANHR.I	
1535	1	1023.6824	101.59	2	49.0	12.2	1	1429-1445	K.NVLLQFIFLKPGSERER.L	

Detailed Protein Report

Protein 68: **PREDICTED: E3 ubiquitin-protein ligase HERC2 isoform X5 [Homo sapiens]**

Accession:	gi|578827509	**Score:**	59.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	517.6
Database Date:	2015-11-30	**pI:**	5.9
		Sequence Coverage [%]:	1.0
		No. of unique Peptides:	3

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Detailed Protein Report

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

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
445	2	592.8266	-45.39	2	34.9	13.6	1	568-577	K.LQDLDVVKVR.C	
2175	1	1031.4134	-71.31	2	55.8	19.5	1	2684-2701	R.CHSSQPGMLLDSWSRMVK.S	
360	1	543.1311	-259.95	2	33.8	14.2	0	3920-3930	K.LYATGYGAGGR.L	

Detailed Protein Report

Protein 69: complement C3 precursor [Homo sapiens]

Accession:	gi|115298678	**Score:**	59.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	187.0
Database Date:	2015-11-30	**pI:**	6.0
		Sequence Coverage [%]:	2.8
		No. of unique Peptides:	3

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2933	1	940.0026	13.02	2	65.4	22.8	0	226-241	K.EYVLPSFEVIVEPTEK.F	
2727	4	701.3852	-51.38	2	62.5	16.6	0	892-904	K.SSLSVPYVIVPLK.T	
1782	3	1086.9427	-40.31	2	50.9	20.1	2	1505-1522	K.LCRDELCRCAEENCFIQK.S	

Detailed Protein Report

Protein 70: fibrinogen beta chain isoform 2 preproprotein [Homo sapiens]

Accession:	gi|296080754	**Score:**	59.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	49.9
Database Date:	2015-11-30	**pI:**	9.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	5.8
		No. of unique Peptides:	2

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1961	3	893.2648	-149.91	2	53.0	20.5	0	255-269	K.NYCGLPGEYWLGNDK.I	Carbamidomethyl: 3
656	1	620.1188	-231.67	2	36.8	38.6	0	368-377	K.EDGGGWWYNR.C	

Detailed Protein Report

Protein 71: PDZ domain-containing protein 4 [Homo sapiens]

Accession: gi|46559761
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl, Oxidation

Score: 59.0
MW [kDa]: 86.1
pI: 5.7
Sequence Coverage [%]: 10.5
No. of unique Peptides: 2

10	20	30	40	50	60	70	80
MGCNMCVVQK	PEEQYKVMLQ	VNGKELSKLS	QEQTLQALRS	SKEPLVIQVL	RRSPRLRGDS	SCHDLQLVDS	GTQTDITFEH
90	100	110	120	130	140	150	160
IMALGKLRPP	TPPMVILEPP	PISHEYYDPA	EFMEGGPQEA	DRLDELEYEE	VELYKSSHRD	KLGLMVCYRT	DDEEDLGIYV
170	180	190	200	210	220	230	240
GEVNPNSIAA	KDGRIREGDR	IIQINGVDVQ	NREEAVAILS	QEENTNISLL	VARPESQLAK	RWKDSDRDDF	LDDFGSENEG
250	260	270	280	290	300	310	320
ELRARKLKSP	PAQQPGNEEE	KGAPDAGPGL	SNSQELDSGV	GRTDESTRNE	ESSEHDLLGD	EPPSSTNTPG	SLRKFGLQGD
330	340	350	360	370	380	390	400
ALQSRDFHFS	MDSLLAEGAG	LGGGDVPGLT	DEEYERYREL	LEIKCHLENG	NQLGLLFPRA	SGGNSALDVN	RNESLGHEMA
410	420	430	440	450	460	470	480
MLEEELRHLE	FKCRNILRAQ	KMQQLRERCM	KAWLLEEESL	YDLAASEPKK	HELSDISELP	EKSDKDSTSA	YNTGESCRST
490	500	510	520	530	540	550	560
PLLVEPLPES	PLRRAMAGNS	NLNRTPPGPA	VATPAKAAPP	PGSPAKFRSL	SRDPEAGRRQ	HAEERGRRNP	KTGLTLERVG
570	580	590	600	610	620	630	640
PESSPYLSRR	HRGQGQEGEH	YHSCVQLAPT	RGLEELGHGP	LSLAGGPRVG	GVAAAATEAP	RMEWKVKVRS	DGTRYVAKRP
650	660	670	680	690	700	710	720
VRDRLLKARA	LKIREERSGM	TTDDDAVSEM	KMGRYWSKEE	RKQHLIRARE	QRKRREFMMQ	SRLECLREQQ	NGDSKPELNI
730	740	750	760	770			
IALSHRKTMK	KRNKKILDNW	ITIQEMLAHG	ARSADGKRVY	NPLLSVTTV			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2759	1	905.4805	55.19	3	65.8	12.2	1	2-24	M.GCNMCVVQKPEEQYKVMLQVNGK.E	Carbamidomethyl: 2; Oxidation: 4, 17
450	1	1100.7316	-85.85	3	34.6	14.6	0	326-356	R.DFHFSMDSLLAEGAGLGGGDVPGLTDEEYER.Y	Oxidation: 6

Detailed Protein Report

Protein 72: tenascin-X isoform 1 precursor [Homo sapiens]

Accession:	gi|188528648	**Score:**	58.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	457.9
Database Date:	2015-11-30	**pI:**	4.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.6
		No. of unique Peptides:	4

Detailed Protein Report

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

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2799	1	732.8911	134.58	2	64.1	13.0	1	725-737	R.GRGECHDGSCVCK.D	Carbamidomethyl: 10, 12
1929	1	890.3591	-119.35	2	52.8	13.5	1	1418-1435	R.VGGKESEVTVGGLEPGHK.Y	
2906	1	557.9675	41.54	3	65.1	15.9	0	2141-2157	R.VGGEESEVTVGGLEPGR.K	
2882	1	981.9684	-29.71	2	65.2	15.6	1	2349-2366	R.VPGHEDRVTISGLEPDNK.Y	

Detailed Protein Report

Protein 73: PREDICTED: caspase-10 isoform X1 [Homo sapiens]

Accession:	gi|530371069	**Score:**	57.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	58.8
Database Date:	2015-11-30	**pI:**	6.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	9.8
		No. of unique Peptides:	3

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	KTFLEALPES	WQNKHAGSNG
250	260	270	280	290	300	310	320
NRATNGAPSL	VSRGMQGASA	NTLNSETSTK	RAAVYRMNRN	HRGLCVIVNN	HSFTSLKDRQ	GTHKDAEILS	HVFQWLGFTV
330	340	350	360	370	380	390	400
HIHNNVTKVE	MEMVLQKQKC	NPAHADGDCF	VFCILTHGRF	GAVYSSDEAL	IPIREIMSHF	TALQCPRLAE	KPKLFFIQAC
410	420	430	440	450	460	470	480
QGEEIQPSVS	IEADALNPEQ	APTSLQDSIP	AEADFLLGLA	TVPGYVSFRH	VEEGSWYIQS	LCNHLKKLVP	RHEDILSILT
490	500	510	520	530			
AVNDDVSRRV	DKQGTKKQMP	QPAFTLRKKL	VFPVPLDALS	L			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2857	12	710.3665	-46.32	2	64.9	19.3	1	133-144	K.DMIFLLKDSLPK.T	
1677	1	933.3261	-154.07	2	50.9	26.9	1	235-253	K.HAGSNGNRATNGAPSLVSR.G	
2646	1	1145.5422	35.87	2	61.8	11.6	0	340-359	K.CNPAHADGDCFVFCILTHGR.F	Carbamidomethyl: 10, 14

Detailed Protein Report

Protein 74: PREDICTED: NEDD8 ultimate buster 1 isoform X1 [Homo sapiens]

Accession:	gi|530387030	**Score:**	57.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	73.2
Database Date:	2015-11-30	**pI:**	6.2
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	4.9
		No. of unique Peptides:	2

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	AKRAETVVDP	EMTPYLDIAN
250	260	270	280	290	300	310	320
QTGRSIRIPP	SERKALMLAM	GYHEKGRAFL	KRKEYGIALP	CLLDADKYFC	ECCRELLDTV	DNYAVLQLDI	VWCYFRLEQL
330	340	350	360	370	380	390	400
ECLDDAEKKL	NLAQKCFKNC	YGENHQRLVH	IKGNCGKEKV	LFLRLYLLQG	IRNYHSGNDV	EAYEYLNKAR	QLFKELYIDP
410	420	430	440	450	460	470	480
SKVDNLLQLG	FTAQEARLGL	RACDGNVDHA	ATHITNRREE	LAQIRKEEKE	KKRRRLENIR	FLKGMGYSTH	AAQQVLHAAS
490	500	510	520	530	540	550	560
GNLDEALKIL	LSNPQMWWLN	DSNPETDNRQ	ESPSQENIDR	LVYMGFDALV	AEAALRVFRG	NVQLAAQTLA	HNGGSLPPEL
570	580	590	600	610	620	630	640
PLSPEDSLSP	PATSPSDSAG	TSSASTDEDM	ETEAVNEILE	DIPEHEEDYL	DSTLEDEEII	IAEYLSYVEN	RKSATKKN

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2521	1	648.3547	69.36	2	62.0	10.7	0	255-265	K.ALMLAMGYHEK.G	Oxidation: 3, 6
2062	1	625.2581	-159.60	2	54.4	16.1	2	329-338	K.KLNLAQKCFK.N	Carbamidomethyl: 8

Detailed Protein Report

Protein 75: centrosomal protein of 290 kDa [Homo sapiens]

Accession:	gi|109255234	**Score:**	57.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	290.2
Database Date:	2015-11-30	**pI:**	5.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.0
		No. of unique Peptides:	5

Quantitation

mdown:qdown	**Median:**	0.41	**CV:**	41.53 %	**No. of Peptides:**	2

Detailed Protein Report

10	20	30	40	50	60	70	80
MPPNINWKEI	MKVDPDDLPR	QEELADNLLI	SLSKVEVNEL	KSEKQENVIH	LFRITQSLMK	MKAQEVELAL	EEVEKAGEEQ
90	100	110	120	130	140	150	160
AKFENQLKTK	VMKLENELEM	AQQSAGGRDT	RFLRNEICQL	EKQLEQKDRE	LEDMEKELEK	EKKVNEQLAL	RNEEAENENS
170	180	190	200	210	220	230	240
KLRRENKRLK	KKNEQLCQDI	IDYQKQIDSQ	KETLLSRRGE	DSDYRSQLSK	KNYELIQYLD	EIQTLTEANE	KIEVQNQEMR
250	260	270	280	290	300	310	320
KNLEESVQEM	EKMTDEYNRM	KAIVHQTDNV	IDQLKKENDH	YQLQVQELTD	LLKSKNEEDD	PIMVAVNAKV	EEWKLILSSK
330	340	350	360	370	380	390	400
DDEIIEYQQM	LHNLREKLKN	AQLDADKSNV	MALQQGIQER	DSQIKMLTEQ	VEQYTKEMEK	NTCIIEDLKN	ELQRNKGAST
410	420	430	440	450	460	470	480
LSQQTHMKIQ	STLDILKEKT	KEAERTAELA	EADAREKDKE	LVEALKRLKD	YESGVYGLED	AVVEIKNCKN	QIKIRDREIE
490	500	510	520	530	540	550	560
ILTKEINKLE	LKISDFLDEN	EALRERVGLE	PKTMIDLTEF	RNSKHLKQQQ	YRAENQILLK	EIESLEEERL	DLKKKIRQMA
570	580	590	600	610	620	630	640
QERGKRSATS	GLTTEDLNLT	ENISQGDRIS	ERKLDLLSLK	NMSEAQSKNE	FLSRELIEKE	RDLERSRTVI	AKFQNKLKEL
650	660	670	680	690	700	710	720
VEENKQLEEG	MKEILQAIKE	MQKDPDVKGG	ETSLIIPSLE	RLVNAIESKN	AEGIFDASLH	LKAQVDQLTG	RNEELRQELR
730	740	750	760	770	780	790	800
ESRKEAINYS	QQLAKANLKI	DHLEKETSLL	RQSEGSNVVF	KGIDLPDGIA	PSSASIINSQ	NEYLIHLLQE	LENKEKKLKN
810	820	830	840	850	860	870	880
LEDSLEDYNR	KFAVIRHQQS	LLYKEYLSEK	ETWKTESKTI	KEEKRKLEDQ	VQQDAIKVKE	YNNLLNALQM	DSDEMKKILA
890	900	910	920	930	940	950	960
ENSRKITVLQ	VNEKSLIRQY	TTLVELERQL	RKENEKQKNE	LLSMEAEVCE	KIGCLQRFKE	MAIFKIAALQ	KVVDNSVSLS
970	980	990	1000	1010	1020	1030	1040
ELELANKQYN	ELTAKYRDIL	QKDNMLVQRT	SNLEHLECEN	ISLKEQVESI	NKELEITKEK	LHTIEQAWEQ	ETKLGNESSM
1050	1060	1070	1080	1090	1100	1110	1120
DKAKKSITNS	DIVSISKKIT	MLEMKELNER	QRAEHCQKMY	EHLRTSLKQM	EERNFELETK	FAELTKINLD	AQKVEQMLRD
1130	1140	1150	1160	1170	1180	1190	1200
ELADSVSKAV	SDADRQRILE	LEKNEMELKV	EVSKLREISD	IARRQVEILN	AQQQSRDKEV	ESLRMQLLDY	QAQSDEKSLI
1210	1220	1230	1240	1250	1260	1270	1280
AKLHQHNVSL	QLSEATALGK	LESITSKLQK	MEAYNLRLEQ	KLDEKEQALY	YARLEGRNRA	KHLRQTIQSL	RRQFSGALPL
1290	1300	1310	1320	1330	1340	1350	1360
AQQEKFSKTM	IQLQNDKLKI	MQEMKNSQQE	HRNMENKTLE	MELKLKGLEE	LISTLKDTKG	AQKVINWHMK	IEELRLQELK
1370	1380	1390	1400	1410	1420	1430	1440
LNRELVKDKE	EIKYLNNIIS	EYERTISSLE	EEIVQQNKFH	EERQMAWDQR	EVDLERQLDI	FDRQQNEILN	AAQKFEEATG
1450	1460	1470	1480	1490	1500	1510	1520
SIPDPSLPLP	NQLEIALRKI	KENIRIILET	RATCKSLEEK	LKEKESALRL	AEQNILSRDK	VINELRLRLP	ATAEREKLIA
1530	1540	1550	1560	1570	1580	1590	1600
ELGRKEMEPK	SHHTLKIAHQ	TIANMQARLN	QKEEVLKKYQ	RLLEKAREEQ	REIVKKHEED	LHILHHRLEL	QADSSLNKFK
1610	1620	1630	1640	1650	1660	1670	1680
QTAWDLMKQS	PTPVPTNKHF	IRLAEMEQTV	AEQDDSLSSL	LVKLKKVSQD	LERQREITEL	KVKEFENIKL	QLQENHEDEV
1690	1700	1710	1720	1730	1740	1750	1760
KKVKAEVEDL	KYLLDQSQKE	SQCLKSELQA	QKEANSRAPT	TTMRNLVERL	KSQLALKEKQ	QKALSRALLE	LRAEMTAAAE
1770	1780	1790	1800	1810	1820	1830	1840
ERIISATSQK	EAHLNVQQIV	DRHTRELKTQ	VEDLNENLLK	LKEALKTSKN	RENSLTDNLN	DLNNELQKKQ	KAYNKILREK
1850	1860	1870	1880	1890	1900	1910	1920
EEIDQENDEL	KRQIKRLTSG	LQGKPLTDNK	QSLIEELQRK	VKKLENQLEG	KVEEVDLKPM	KEKNAKEELI	RWEEGKKWQA
1930	1940	1950	1960	1970	1980	1990	2000
KIEGIRNKLK	EKEGEVFTLT	KQLNTLKDLF	AKADKEKLTL	QRKLKTTGMT	VDQVLGIRAL	ESEKELEELK	KRNLDLENDI
2010	2020	2030	2040	2050	2060	2070	2080
LYMRAHQALP	RDSVVEDLHL	QNRYLQEKLH	ALEKQFSKDT	YSKPSISGIE	SDDHCQREQE	LQKENLKLSS	ENIELKFQLE
2090	2100	2110	2120	2130	2140	2150	2160
QANKDLPRLK	NQVRDLKEMC	EFLKKEKAEV	QRKLGHVRGS	GRSGKTIPEL	EKTIGLMKKV	VEKVQRENEQ	LKKASGILTS
2170	2180	2190	2200	2210	2220	2230	2240

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2146	2	937.4291	-49.48	2	55.4	15.4	2	115-129	R.NEICQLEKQLEQKDR.E		
1969	1	703.7594	-155.73	2	54.7	10.7	0	1966-1978	K.TTGMTVDQVLGIR.A	Oxidation: 4	
1615	1	494.1461	-276.33	2	50.1	10.7	2	2106-2113	K.EKAEVQRK.L		mdown:qdown 0.61
1421	1	846.6046	174.69	1	47.5	10.1	0	2387-2393	K.DLETQLK.M		mdown:qdown 0.28
1648	1	858.4049	-102.70	1	49.1	10.3	0	2438-2444	K.NILLEEK.V		

Detailed Protein Report

Protein 76:	**PREDICTED: ankyrin repeat domain-containing protein 11 isoform X3 [Homo sapiens]**		
Accession:	gi|578828957	**Score:**	56.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	293.2
Database Date:	2015-11-30	**pI:**	6.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.3
		No. of unique Peptides:	4

Quantitation

mdown:qdown	**Median:** 3.05	**CV:** 0.00 %	**No. of Peptides:** 1

10	20	30	40	50	60	70	80
MPPAQSLLWC	CKAGTLLEAP	WHEMEVPRSK	KKEKQGPERK	RIKKEPVTRK	AGLLFGMGLS	GIRAGYPLSE	RQQVALLMQM
90	100	110	120	130	140	150	160
TAEESANSPV	DTTPKHPSQS	TVCQKGTPNS	ASKTKDKVNK	RNERGETRLH	RAAIRGDARR	IKELISEGAD	VNVKDFAGWT
170	180	190	200	210	220	230	240
ALHEACNRGY	YDVAKQLLAA	GAEVNTKGLD	DDTPLHDAAN	NGHYKVVKLL	LRYGGNPQQS	NRKGETPLKV	ANSPTMVNLL
250	260	270	280	290	300	310	320
LGKGTYTSSE	ESSTESSEEE	DAPSFAPSSS	VDGNNTDSEF	EKGLKHKAKN	PEPQKATAPV	KDEYEFDEDD	EQDRVPPVDD
330	340	350	360	370	380	390	400
KHLLKKDYRK	ETKSNSFISI	PKMEVKSYTK	NNTIAPKKAS	HRILSDTSDE	EDASVTVGTG	EKLRLSAHTI	LPGSKTREPS
410	420	430	440	450	460	470	480
NAKQQKEKNK	VKKKRKKETK	GREVRFGKRS	DKFCSSESES	ESSESGEDDR	DSLGSSGCLK	GSPLVLKDPS	LFSSLSASST
490	500	510	520	530	540	550	560
SSHGSSAAQK	QNPSHTDQHT	KHWRTDNWKT	ISSPAWSEVS	SLSDSTRTRL	TSESDYSSEG	SSVESLKPVR	KRQEHRKRAS
570	580	590	600	610	620	630	640
LSEKKSPFLS	SAEGAVPKLD	KEGKVVKKHK	TKHKHKNKEK	GQCSISQELK	LKSFTYEYED	SKQKSDKAIL	LENDLSTENK
650	660	670	680	690	700	710	720
LKVLKHDRDH	FKKEEKLSKM	KLEEKEWLFK	DEKSLKRIKD	TNKDISRSFR	EEKDRSNKAE	KERSLKEKSP	KEEKLRLYKE
730	740	750	760	770	780	790	800
ERKKKSKDRP	SKLEKKNDLK	EDKISKEKEK	IFKEDKEKLK	KEKVYREDSA	FDEYCNKNQF	LENEDTKFSL	SDDQRDRWFS
810	820	830	840	850	860	870	880
DLSDSSFDFK	GEDSWDSPVT	DYRDMKSDSV	AKLILETVKE	DSKERRRDSR	AREKRDYREP	FFRKKDRDYL	DKNSEKRKEQ
890	900	910	920	930	940	950	960
TEKHKSVPGY	LSEKDKKRRE	SAEAGRDRKD	ALESCKERRD	GRAKPEEAHR	EELKECGCES	GFKDKSDGDF	GKGLEPWERH
970	980	990	1000	1010	1020	1030	1040
HPAREKEKKD	GPDKERKEKT	KPERYKEKSS	DKDKSEKSIL	EKCQKDKEFD	KCFKEKKDTK	EKHKDTHGKD	KERKASLDQG
1050	1060	1070	1080	1090	1100	1110	1120
KEKKEKAFPG	IISEDFSEKK	DDKKGKEKSW	YIADIFTDES	EDDRDSCMGS	GFKMGEASDL	PRTDGLQEKE	EGREAYASDR
1130	1140	1150	1160	1170	1180	1190	1200
HRKSSDKQHP	ERQKDKEPRD	RRKDRGAADA	GRDKKEKVFE	KHKEKKDKES	TEKYKDRKDR	ASVDSTQDKK	NKQKLPEKAE
1210	1220	1230	1240	1250	1260	1270	1280
KKHAAEDKAK	SKHKEKSDKE	HSKERKSSRS	ADAEKSLLEK	LEEEALHEYR	EDSNDKISEV	SSDSFTDRGQ	EPGLTAFLEV
1290	1300	1310	1320	1330	1340	1350	1360
SFTEPPGDDK	PRESACLPEK	LKEKERHRHS	SSSSKKSHDR	ERAKKEKAEK	KEKGEDYKEG	GSRKDSGQYE	KDFLEADAYG
1370	1380	1390	1400	1410	1420	1430	1440
VSYNMKADIE	DELDKTIELF	STEKKDKNDS	EREPSKKIEK	ELKPYGSSAI	NILKEKKKRE	KHREKWRDEK	ERHRDRHADG
1450	1460	1470	1480	1490	1500	1510	1520
LLRHHRDELL	RHHRDEQKPA	TRDKDSPPRV	LKDKSRDEGP	RLGDAKLKEK	FKDGAEKEKG	DPVKMSNGND	KVAPSKDPGK
1530	1540	1550	1560	1570	1580	1590	1600
KDARPREKLL	GDGDLMMTSF	ERMLSQKDLE	IEERHKRHKE	RMKQMEKLRH	RSGDPKLKEK	AKPADDGRKK	GLDIPAKKPP
1610	1620	1630	1640	1650	1660	1670	1680
GLDPPFKDKK	LKESTPIPPA	AENKLHPASG	ADSKDWLAGP	HMKEVLPASP	RPDQSRPTGV	PTPTSVLSCP	SYEEVMHTPR
1690	1700	1710	1720	1730	1740	1750	1760
TPSCSADDYA	DLVFDCADSQ	HSTPVPTAPT	SACSPSFFDR	FSVASSGLSE	NASQAPARPL	STNLYRSVSV	DIRRTPEEEF
1770	1780	1790	1800	1810	1820	1830	1840
SVGDKLFRQQ	SVPAASSYDS	PMPPSMEDRA	PLPPVPAEKF	ACLSPGYYSP	DYGLPSPKVD	ALHCPPAAVV	TVTPSPEGVF
1850	1860	1870	1880	1890	1900	1910	1920
SSLQAKPSPS	PRAELLVPSL	EGALPPDLDT	SEDQQATAAI	IPPEPSYLEP	LDEGPFSAVI	TEEPVEWAHP	SEQALASSLI
1930	1940	1950	1960	1970	1980	1990	2000
GGTSENPVSW	PVGSDLLLKS	PQRFPESPKR	FCPADPLHSA	APGPFSASEA	PYPAPPASPA	PYALPVAEPG	LEDVKDGVDA
2010	2020	2030	2040	2050	2060	2070	2080
VPAAISTSEA	APYAPPSGLE	SFFSNCKSLP	EAPLDVAPEP	ACVAAVAQVE	ALGPLENSFL	DGSRGLSHLG	QVEPVPWADA
2090	2100	2110	2120	2130	2140	2150	2160
FAGPEDDLDL	GPFSLPELPL	QTKDAADGEA	EPVEESLAPP	EEMPPGAPGV	INGGDVSTVV	AEEPPALPPD	QASTRLPAEL
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
2918	1	1155.0468	-67.97	2	65.2	13.4	2	50-71	R.KAGLLFGMGLSGIRAGYPLSER.Q	Oxidation: 8	
1383	2	637.4051	150.05	3	45.8	14.2	0	510-527	K.TISSPAWSEVSSLSDSTR.T		mdown:qdown 3.05
313	2	501.1733	-259.03	2	33.0	13.5	2	1482-1490	R.LGDAKLKEK.F		
2584	1	658.2319	-130.00	2	61.0	15.1	0	2381-2391	K.LDAIEPYHSDR.A		

Detailed Protein Report

Protein 77:	**hemicentin-1 precursor [Homo sapiens]**		
Accession:	gi|118572606	**Score:**	56.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	613.0
Database Date:	2015-11-30	**pI:**	6.1
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.3
		No. of unique Peptides:	3

Quantitation

Wdown:Qdown	**Median:** 6.26	**CV:** 0.00 %	**No. of Peptides:** 1

10	20	30	40	50	60	70	80
MISWEVVHTV	FLFALLYSSL	AQDASPQSEI	RAEEIPEGAS	TLAFVFDVTG	SMYDDLVQVI	EGASKILETS	LKRPKRPLFN
90	100	110	120	130	140	150	160
FALVPFHDPE	IGPVTITTDP	KKFQYELREL	YVQGGGDCPE	MSIGAIKIAL	EISLPGSFIY	VFTDARSKDY	RLTHEVLQLI
170	180	190	200	210	220	230	240
QQKQSQVVFV	LTGDCDDRTH	IGYKVYEEIA	STSSGQVFHL	DKKQVNEVLK	WVEEAVQASK	VHLLSTDHLE	QAVNTWRIPF
250	260	270	280	290	300	310	320
DPSLKEVTVS	LSGPSPMIEI	RNPLGKLIKK	GFGLHELLNI	HNSAKVVNVK	EPEAGMWTVK	TSSSGRHSVR	ITGLSTIDFR
330	340	350	360	370	380	390	400
AGFSRKPTLD	FKKTVSRPVQ	GIPTYVLLNT	SGISTPARID	LLELLSISGS	SLKTIPVKYY	PHRKPYGIWN	ISDFVPPNEA
410	420	430	440	450	460	470	480
FFLKVTGYDK	DDYLFQRVSS	VSFSSIVPDA	PKVTMPEKTP	GYYLQPGQIP	CSVDSLLPFT	LSFVRNGVTL	GVDQYLKESA
490	500	510	520	530	540	550	560
SVNLDIAKVT	LSDEGFYECI	AVSSAGTGRA	QTFFDVSEPP	PVIQVPNNVT	VTPGERAVLT	CLIISAVDYN	LTWQRNDRDV
570	580	590	600	610	620	630	640
RLAEPARIRT	LANLSLELKS	VKFNDAGEYH	CMVSSEGGSS	AASVFLTVQE	PPKVTVMPKN	QSFTGGSEVS	IMCSATGYPK
650	660	670	680	690	700	710	720
PKIAWTVNDM	FIVGSHRYRM	TSDGTLFIKN	AAPKDAGIYG	CLASNSAGTD	KQNSTLRYIE	APKLMVVQSE	LLVALGDITV
730	740	750	760	770	780	790	800
MECKTSGIPP	PQVKWFKGDL	ELRPSTFLII	DPLLGLLKIQ	ETQDLDAGDY	TCVAINEAGR	ATGKITLDVG	SPPVFIQEPA
810	820	830	840	850	860	870	880
DVSMEIGSNV	TLPCYVQGYP	EPTIKWRRLD	NMPIFSRPFS	VSSISQLRTG	ALFILNLWAS	DKGTYICEAE	NQFGKIQSET
890	900	910	920	930	940	950	960
TVTVTGLVAP	LIGISPSVAN	VIEGQQLTLP	CTLLAGNPIP	ERRWIKNSAM	LLQNPYITVR	SDGSLHIERV	QLQDGGEYTC
970	980	990	1000	1010	1020	1030	1040
VASNVAGTNN	KTTSVVVHVL	PTIQHGQQIL	STIEGIPVTL	PCKASGNPKP	SVIWSKKGEL	ISTSSAKFSA	GADGSLYVVS
1050	1060	1070	1080	1090	1100	1110	1120
PGGEESGEYV	CTATNTAGYA	KRKVQLTVYV	RPRVFGDQRG	LSQDKPVEIS	VLAGEEVTLP	CEVKSLPPPI	ITWAKETQLI
1130	1140	1150	1160	1170	1180	1190	1200
SPFSPRHTFL	PSGSMKITET	RTSDSGMYLC	VATNIAGNVT	QAVKLNVHVP	PKIQRGPKHL	KVQVGQRVDI	PCNAQGTPLP
1210	1220	1230	1240	1250	1260	1270	1280
VITWSKGGST	MLVDGEHHVS	NPDGTLSIDQ	ATPSDAGIYT	CVATNIAGTD	ETEITLHVQE	PPTVEDLEPP	YNTTFQERVA
1290	1300	1310	1320	1330	1340	1350	1360
NQRIEFPCPA	KGTPKPTIKW	LHNGRELTGR	EPGISILEDG	TLLVIASVTP	YDNGEYICVA	VNEAGTTERK	YNLKVHVPPV
1370	1380	1390	1400	1410	1420	1430	1440
IKDKEQVTNV	SVLLNQLTNL	FCEVEGTPSP	IIMWYKDNVQ	VTESSTIQTV	NNGKILKLFR	ATPEDAGRYS	CKAINIAGTS
1450	1460	1470	1480	1490	1500	1510	1520
QKYFNIDVLV	PPTIIGTNFP	NEVSVVLNRD	VALECQVKGT	PFPDIHWFKD	GKPLFLGDPN	VELLDRGQVL	HLKNARRNDK
1530	1540	1550	1560	1570	1580	1590	1600
GRYQCTVSNA	AGKQAKDIKL	TIYIPPSIKG	GNVTTDISVL	INSLIKLECE	TRGLPMPAIT	WYKDGQPIMS	SSQALYIDKG
1610	1620	1630	1640	1650	1660	1670	1680
QYLHIPRAQV	SDSATYTCHV	ANVAGTAEKS	FHVDVYVPPM	IEGNLATPLN	KQVVIAHSLT	LECKAAGNPS	PILTWLKDGV
1690	1700	1710	1720	1730	1740	1750	1760
PVKANDNIRI	EAGGKKLEIM	SAQEIDRGQY	ICVATSVAGE	KEIKYEVDVL	VPPAIEGGDE	TSYFIVMVNN	LLELDCHVTG
1770	1780	1790	1800	1810	1820	1830	1840
SPPPTIMWLK	DGQLIDERDG	FKILLNGRKL	VIAQAQVSNT	GLYRCMAANT	AGDHKKEFEV	TVHVPPTIKS	SGLSERVVVK
1850	1860	1870	1880	1890	1900	1910	1920
YKPVALQCIA	NGIPNPSITW	LKDDQPVNTA	QGNLKIQSSG	RVLQIAKTLL	EDAGRYTCVA	TNAAGETQQH	IQLHVHEPPS
1930	1940	1950	1960	1970	1980	1990	2000
LEDAGKMLNE	TVLVSNPVQL	ECKAAGNPVP	VITWYKDNRL	LSGSTSMTFL	NRGQIIDIES	AQISDAGIYK	CVAINSAGAT
2010	2020	2030	2040	2050	2060	2070	2080
ELFYSLQVHV	APSISGSNNM	VAVVVNNPVR	LECEARGIPA	PSLTWLKDGS	PVSSFSNGLQ	VLSGGRILAL	TSAQISDTGR
2090	2100	2110	2120	2130	2140	2150	2160
YTCVAVNAAG	EKQRDIDLRV	YVPPNIMGEE	QNVSVLISQA	VELLCQSDAI	PPPTLTWLKD	GHPLLKKPGL	SISENRSVLK
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2962	1	1019.9724	-61.55	2	66.2	12.4	0	1188-1206	R.VDIPCNAQGTPLPVITWSK.G		
1984	1	883.9757	-72.13	3	53.5	15.0	1	5183-5205	R.RTSDGLSCQDINECQESSPCHQRC	Carbamidomethyl: 8	
1025	1	676.6792	37.90	3	41.3	16.6	2	5247-5264	K.NTRGGYKCIDLCPNGMTK.A	Carbamidomethyl: 8	Wdown:Qdown 6.26

Detailed Protein Report

Protein 78:	**coiled-coil domain-containing protein 168 [Homo sapiens]**		
Accession:	gi|226246554	**Score:**	56.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	801.4
Database Date:	2015-11-30	**pI:**	9.6
		Sequence Coverage [%]:	0.9
		No. of unique Peptides:	2

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

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2780	1	701.4146	-7.24	2	63.2	11.0	2	2385-2396	R.KIILNPKCLTMK.E	
2491	1	974.1939	35.72	3	59.5	10.7	2	5658-5682	R.DEDIYFTGFGTIRSGKRPEWLFTGK.K	

Detailed Protein Report

Protein 79: PREDICTED: centrosomal protein of 290 kDa isoform X4 [Homo sapiens]

Accession:	gi|530400856	**Score:**	55.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	234.7
Database Date:	2015-11-30	**pI:**	6.1
		Sequence Coverage [%]:	2.1
		No. of unique Peptides:	1

Detailed Protein Report

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        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

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1190	3	500.7991	-35.31	2	43.5	14.1	2	2-9	M.QKLSLRQK.S	

Detailed Protein Report

Protein 80: **PREDICTED: striated muscle preferentially expressed protein kinase isoform X14 [Homo sapiens]**

Accession:	gi|578803490	**Score:**	55.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	283.5
Database Date:	2015-11-30	**pI:**	9.4
		Sequence Coverage [%]:	1.8
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	0.31	**CV:**	0.00 %	**No. of Peptides:**	1

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

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
92	1	531.9231	-79.62	3	30.5	25.4	2	2089-2103	R.GPLLESLGGRARDPR.M		mdown:qdown 0.31

Detailed Protein Report

Protein 81: **PREDICTED: LOW QUALITY PROTEIN: ubiquitin carboxyl-terminal hydrolase 17-like protein 20 [Homo sapiens]**

Accession: gi|578843530
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 55.8
MW [kDa]: 38.1
pI: 9.8
Sequence Coverage [%]: 6.0
No. of unique Peptides: 3

10	20	30	40	50	60	70	80
MEDDSLYLGA	SAKVLILVLK	RFSDVTGNKI	AKNVQYPECL	DMQPYMSQPN	TGPLVYVLYA	VLVHAGWSCH	NGHYFSYVKA
90	100	110	120	130	140	150	160
QEGQWYKMDD	AEVTASSITS	VLSQQAYVLF	YIQKSEWERH	SESVSRGREP	RALGAEDTDR	RATQGELKRD	HPCLQAPELD
170	180	190	200	210	220	230	240
EHLVERATQE	STLDHWKFLQ	EQNKTKPEFN	VRKVEGTLPP	DVLVIHQSXY	KCGMKNHHPE	QQSSLLNLSS	TTPTHQESMN
250	260	270	280	290	300	310	320
TGTLASLRGR	ARRSKGKNKH	SKRALLVCQX	SQWKYRPTRT	VIKVDQPQRK	AAQGTTQGSV	EPQNLGRNPA	QAPKCAYEQG
330	340						
LRVTTLYIRH	RKPSDG						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1896	1	599.9585	-51.71	3	52.4	13.5	2	260-274	K.HSKRALLVCQNSQWK.Y	
2567	1	709.8660	-0.12	2	62.5	14.7	0	264-274	R.ALLVCQWSQWK.Y	Carbamidomethyl: 5
1491	1	981.6005	60.92	2	47.4	15.8	1	264-279	R.ALLVCQISQWKYRPTR.T	

Detailed Protein Report

Protein 82: intersectin-1 isoform ITSN-I [Homo sapiens]

Accession: gi|47717123
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 55.5
MW [kDa]: 195.3
pI: 8.5
Sequence Coverage [%]: 2.7
No. of unique Peptides: 2

Quantitation

mdown:qdown **Median:** 0.83 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MAQFPTPFGG	SLDIWAITVE	ERAKHDQQFH	SLKPISGFIT	GDQARNFFFQ	SGLPQPVLAQ	IWALADMNND	GRMDQVEFSI
90	100	110	120	130	140	150	160
AMKLIKLKLQ	GYQLPSALPP	VMKQQPVAIS	SAPAFGMGGI	ASMPPLTAVA	PVPMGSIPVV	GMSPTLVSSV	PTAAVPPLAN
170	180	190	200	210	220	230	240
GAPPVIQPLP	AFAHPAATLP	KSSSFSRSGP	GSQLNTKLQK	AQSFDVASVP	PVAEWAVPQS	SRLKYRQLFN	SHDKTMSGHL
250	260	270	280	290	300	310	320
TGPQARTILM	QSSLPQAQLA	SIWNLSDIDQ	DGKLTAEEFI	LAMHLIDVAM	SGQPLPPVLP	PEYIPPSFRR	VRSGSGISVI
330	340	350	360	370	380	390	400
SSTSVDQRLP	EEPVLEDEQQ	QLEKKLPVTF	EDKKRENFER	GNLELEKRRQ	ALLEQQRKEQ	ERLAQLERAE	QERKERERQE
410	420	430	440	450	460	470	480
QERKRQLELE	KQLEKQRELE	RQREEERRKE	IERREAAKRE	LERQRQLEWE	RNRRQELLNQ	RNKEQEDIVV	LKAKKKTLEF
490	500	510	520	530	540	550	560
ELEALNDKKH	QLEGKLQDIR	CRLTTQRQEI	ESTNKSRELR	IAEITHLQQQ	LQESQQMLGR	LIPEKQILND	QLKQVQQNSL
570	580	590	600	610	620	630	640
HRDSLVTLKR	ALEAKELARQ	HLRDQLDEVE	KETRSKLQEI	DIFNNQLKEL	REIHNKQQLQ	KQKSMEAERL	KQKEQERKII
650	660	670	680	690	700	710	720
ELEKQKEEAQ	RRAQERDKQW	LEHVQQEDEH	QRPRKLHEEE	KLKREESVKK	KDGEEKGKQE	AQDKLGRLFH	QHQEPAKPAV
730	740	750	760	770	780	790	800
QAPWSTAEKG	PLTISAQENV	KVVYYRALYP	FESRSHDEIT	IQPGDIVMVK	GEWVDESQTG	EPGWLGGELK	GKTGWFPANY
810	820	830	840	850	860	870	880
AEKIPENEVP	APVKPVTDST	SAPAPKLALR	ETPAPLAVTS	SEPSTTPNNW	ADFSSTWPTS	TNEKPETDNW	DAWAAQPSLT
890	900	910	920	930	940	950	960
VPSAGQLRQR	SAFTPATATG	SSPSPVLGQG	EKVEGLQAQA	LYPWRAKKDN	HLNFNKNDVI	TVLEQQDMWW	FGEVQGQKGW
970	980	990	1000	1010	1020	1030	1040
FPKSYVKLIS	GPIRKSTSMD	SGSSESPASL	KRVASPAAKP	VVSGEEFIAM	YTYESSEQGD	LTFQQGDVIL	VTKKDGDWWT
1050	1060	1070	1080	1090	1100	1110	1120
GTVGDKAGVF	PSNYVRLKDS	EGSGTAGKTG	SLGKKPEIAQ	VIASYTATGP	EQLTLAPGQL	ILIRKKNPGG	WWEGELQARG
1130	1140	1150	1160	1170	1180	1190	1200
KKRQIGWFPA	NYVKLLSPGT	SKITPTEPPK	STALAAVCQV	IGMYDYTAQN	DDELAFNKGQ	IINVLNKEDP	DWWKGEVNGQ
1210	1220	1230	1240	1250	1260	1270	1280
VGLFPSNYVK	LTTDMDPSQQ	WCSDLHLLDM	LTPTERKRQG	YIHELIVTEE	NYVNDLQLVT	EIFQKPLMES	ELLTEKEVAM
1290	1300	1310	1320	1330	1340	1350	1360
IFVNWKELIM	CNIKLLKALR	VRKKMSGEKM	PVKMIGDILS	AQLPHMQPYI	RFCSRQLNGA	ALIQQKTDEA	PDFKEFVKRL
1370	1380	1390	1400	1410	1420	1430	1440
AMDPRCKGMP	LSSFILKPMQ	RVTRYPLIIK	NILENTPENH	PDHSHLKHAL	EKAEELCSQV	NEGVREKENS	DRLEWIQAHV
1450	1460	1470	1480	1490	1500	1510	1520
QCEGLSEQLV	FNSVTNCLGP	RKFLHSGKLY	KAKSNKELYG	FLFNDFLLLT	QITKPLGSSG	TDKVFSPKSN	LQYKMYKTPI
1530	1540	1550	1560	1570	1580	1590	1600
FLNEVLVKLP	TDPSGDEPIF	HISHIDRVYT	LRAESINERT	AWVQKIKAAS	ELYIETEKKK	REKAYLVRSQ	RATGIGRLMV
1610	1620	1630	1640	1650	1660	1670	1680
NVVEGIELKP	CRSHGKSNPY	CEVTMGSQCH	ITKTIQDTLN	PKWNSNCQFF	IRDLEQEVLC	ITVFERDQFS	PDDFLGRTEI
1690	1700	1710	1720	1730			
RVADIKKDQG	SKGPVTKCLL	LHEVPTGEIV	VRLDLQLFDE	P			

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1569	1	788.7801	-144.71	2	49.5	15.7	2	584-596	R.DQLDEVEKETRSK.L		
2785	1	874.5334	88.10	1	63.9	14.2	1	1359-1365	K.RLAMDPR.C	Oxidation: 4	mdown:qdown 0.83

Detailed Protein Report

Protein 83: histone-lysine N-methyltransferase, H3 lysine-36 and H4 lysine-20 specific isoform b [Homo sapiens]

Accession:	gi|19923586	**Score:**	55.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	296.5
Database Date:	2015-11-30	**pI:**	9.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.1
		No. of unique Peptides:	2

Quantitation

mdown:qdown	**Median:**	0.50	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.47	**CV:**	0.00 %	**No. of Peptides:**	1

Alias proteins:

Accession	**Name**	**Description**
gi|578811198	refseq_human (refseq_human_20140103.fasta)	PREDICTED: histone-lysine N-methyltransferase, H3 lysine-36 and H4 lysine-20 specific isoform X5 [Homo sapiens]
gi|530381144	refseq_human (refseq_human_20140103.fasta)	PREDICTED: histone-lysine N-methyltransferase, H3 lysine-36 and H4 lysine-20 specific isoform X1 [Homo sapiens]

Detailed Protein Report

10	20	30	40	50	60	70	80
MDQTCELPRR	NCLLPFSNPV	NLDAPEDKDS	PFGNGQSNFS	EPLNGCTMQL	STVSGTSQNA	YGQDSPSCYI	PLRRLQDLAS
90	100	110	120	130	140	150	160
MINVEYLNGS	ADGSESFQDP	EKSDSRAQTP	IVCTSLSPGG	PTALAMKQEP	SCNNSPELQV	KVTKTIKNGF	LHFENFTCVD
170	180	190	200	210	220	230	240
DADVDSEMDP	EQPVTEDESI	EEIFEETQTN	ATCNYETKSE	NGVKVAMGSE	QDSTPESRHG	AVKSPFLPLA	PQTETQKNKQ
250	260	270	280	290	300	310	320
RNEVDGSNEK	AALLPAPFSL	GDTNITIEEQ	LNSINLSFQD	DPDSSTSTLG	NMLELPGTSS	SSTSQELPFC	QPKKKSTPLK
330	340	350	360	370	380	390	400
YEVGDLIWAK	FKRRPWWPCR	ICSDPLINTH	SKMKVSNRRP	YRQYYVEAFG	DPSERAWVAG	KAIVMFEGRH	QFEELPVLRR
410	420	430	440	450	460	470	480
RGKQKEKGYR	HKVPQKILSK	WEASVGLAEQ	YDVPKGSKNR	KCIPGSIKLD	SEEDMPFEDC	TNDPESEHDL	LLNGCLKSLA
490	500	510	520	530	540	550	560
FDSEHSADEK	EKPCAKSRAR	KSSDNPKRTS	VKKGHIQFEA	HKDERRGKIP	ENLGLNFISG	DISDTQASNE	LSRIANSLTG
570	580	590	600	610	620	630	640
SNTAPGSFLF	SSCGKNTAKK	EFETSNGDSL	LGLPEGALIS	KCSREKNKPQ	RSLVCGSKVK	LCYIGAGDEE	KRSDSISICT
650	660	670	680	690	700	710	720
TSDDGSSDLD	PIEHSSESDN	SVLEIPDAFD	RTENMLSMQK	NEKIKYSRFA	ATNTRVKAKQ	KPLISNSHTD	HLMGCTKSAE
730	740	750	760	770	780	790	800
PGTETSQVNL	SDLKASTLVH	KPQSDFTNDA	LSPKFNLSSS	ISSENSLIKG	GAANQALLHS	KSKQPKFRSI	KCKHKENPVM
810	820	830	840	850	860	870	880
AEPPVINEEC	SLKCCSSDTK	GSPLASISKS	GKVDGLKLLN	NMHEKTRDSS	DIETAVVKHV	LSELKELSYR	SLGEDVSDSG
890	900	910	920	930	940	950	960
TSKPSKPLLF	SSASSQNHIP	IEPDYKFSTL	LMMLKDMHDS	KTKEQRLMTA	QNLVSYRSPG	RGDCSTNSPV	GVSKVLVSGG
970	980	990	1000	1010	1020	1030	1040
STHNSEKKGD	GTQNSANPSP	SGGDSALSGE	LSASLPGLLS	DKRDLPASGK	SRSDCVTRRN	CGRSKPSSKL	RDAFSAQMVK
1050	1060	1070	1080	1090	1100	1110	1120
NTVNRKALKT	ERKRKLNQLP	SVTLDAVLQG	DRERGGSLRG	GAEDPSKEDP	LQIMGHLTSE	DGDHFSDVHF	DSKVKQSDPG
1130	1140	1150	1160	1170	1180	1190	1200
KISEKGLSFE	NGKGPELDSV	MNSENDELNG	VNQVVPKKRW	QRLNQRRTKP	RKRMNRFKEK	ENSECAFRVL	LPSDPVQEGR
1210	1220	1230	1240	1250	1260	1270	1280
DEFPEHRTPS	ASILEEPLTE	QNHADCLDSA	GPRLNVCDKS	SASIGDMEKE	PGIPSLTPQA	ELPEPAVRSE	KKRLRKPSKW
1290	1300	1310	1320	1330	1340	1350	1360
LLEYTEEYDQ	IFAPKKKQKK	VQEQVHKVSS	RCEEESLLAR	GRSSAQNKQV	DENSLISTKE	EPPVLEREAP	FLEGPLAQSE
1370	1380	1390	1400	1410	1420	1430	1440
LGGGHAELPQ	LTLSVPVAPE	VSPRPALESE	ELLVKTPGNY	ESKRQRKPTK	KLLESNDLDP	GFMPKKGDLG	LSKKCYEAGH
1450	1460	1470	1480	1490	1500	1510	1520
LENGITESCA	TSYSKDFGGG	TTKIFDKPRK	RKRQRHAAAK	MQCKKVKNDD	SSKEIPGSEG	ELMPHRTATS	PKETVEEGVE
1530	1540	1550	1560	1570	1580	1590	1600
HDPGMPASKK	MQGERGGGAA	LKENVCQNCE	KLGELLLCEA	QCCGAFHLEC	LGLTEMPRGK	FICNECRTGI	HTCFVCKQSG
1610	1620	1630	1640	1650	1660	1670	1680
EDVKRCLLPL	CGKFYHEECV	QKYPPTVMQN	KGFRCSLHIC	ITCHAANPAN	VSASKGRLMR	CVRCPVAYHA	NDFCLAAGSK
1690	1700	1710	1720	1730	1740	1750	1760
ILASNSIICP	NHFTPRRGCR	NHEHVNVSWC	FVCSEGGSLL	CCDSCPAAFH	RECLNIDIPE	GNWYCNDCKA	GKKPHYREIV
1770	1780	1790	1800	1810	1820	1830	1840
WVKVGRYRWW	PAEICHPRAV	PSNIDKMRHD	VGEFPVLFFG	SNDYLWTHQA	RVFPYMEGDV	SSKDKMGKGV	DGTYKKALQE
1850	1860	1870	1880	1890	1900	1910	1920
AAARFEELKA	QKELRQLQED	RKNDKKPPPY	KHIKVNRPIG	RVQIFTADLS	EIPRCNCKAT	DENPCGIDSE	CINRMLLYEC
1930	1940	1950	1960	1970	1980	1990	2000
HPTVCPAGGR	CQNQCFSKRQ	YPEVEIFRTL	QRGWGLRTKT	DIKKGEFVNE	YVGELIDEEE	CRARIRYAQE	HDITNFYMLT
2010	2020	2030	2040	2050	2060	2070	2080
LDKDRIIDAG	PKGNYARFMN	HCCQPNCETQ	KWSVNGDTRV	GLFALSDIKA	GTELTFNYNL	ECLGNGKTVC	KCGAPNCSGF
2090	2100	2110	2120	2130	2140	2150	2160
LGVRPKNQPI	ATEEKSKKFK	KKQQGKRRTQ	GEITKEREDE	CFSCGDAGQL	VSCKKPGCPK	VYHADCLNLT	KRPAGKWECP
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1166	2	509.6492	-167.89	2	43.2	11.3	0	2-9	M.DQTCELPR.R	Carbamidomethyl: 4	
617	1	459.6161	-280.24	2	37.0	16.5	1	491-498	K.EKPCAKSR.A		mdown:qdown 0.50 Wdown:Qdown 0.47

Detailed Protein Report

Protein 84: PREDICTED: dynein heavy chain 12, axonemal isoform X1 [Homo sapiens]

Accession:	gi|578805765	**Score:**	55.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	454.9
Database Date:	2015-11-30	**pI:**	5.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.6
		No. of unique Peptides:	3

Quantitation

mdown:qdown	**Median:**	0.23	**CV:**	37.24 %	**No. of Peptides:**	2
Wdown:Qdown	**Median:**	0.34	**CV:**	56.08 %	**No. of Peptides:**	2

```
        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  MCSTVMEQIK  AFKEYIPTVS  ILCNPGMRAR
       810         820         830         840         850         860         870         880
HWKQISEIVG  YDLTPDSGTT  LRKVLKLNLT  PYLEQFEVIS  AGASKEFSLE  KAMNTMIGTW  EDIAFHISLY  RDTGVCILSS
       890         900         910         920         930         940         950         960
VDEIQAILDD  QIIKTQTMRG  SPFIKPFEHE  IKAWEDRLIR  IQETIDEWLK  VQAQWLYLEP  IFCSEDIMQQ  MPEEGRQFQT
       970         980         990        1000        1010        1020        1030        1040
VDRHWRDIMK  FCAKDPKVLA  ATSLTGLLEK  LQNCNELLEK  IMKGLNAYLE  KKRLFFPRFF  FLSNDEMLEI  LSETKDPLRV
      1050        1060        1070        1080        1090        1100        1110        1120
QPHLKKCFEG  IAKLEFLPNL  DIKAMYSSEG  ERVELIALIS  TSAARGAVEK  WLIQVEDLML  RSVHDVIAAA  RLAYPESARR
      1130        1140        1150        1160        1170        1180        1190        1200
DWVREWPGQV  VLCISQMFWT  SETQEVISGG  TEGLKKYYKE  LQNQLNEIVE  LVRGKLSKQT  RTTLGALVTI  DVHARDVVMD
      1210        1220        1230        1240        1250        1260        1270        1280
MIKMGVSHDT  DFLWLAQLRY  YWENENARVR  IINCNVKYAY  EYLGNSPRLV  ITPLTDRCYR  TLIGAFYLNL  GGAPEGPAGT
      1290        1300        1310        1320        1330        1340        1350        1360
GKTETTKDLA  KALAVQCVVF  NCSDGLDYLA  MGKFFKGLAS  SGAWACFDEF  NRIELEVLSV  VAQQILCIQR  AIQQKLVVFV
      1370        1380        1390        1400        1410        1420        1430        1440
FEGTELKLNP  NCFVAITMNP  GYAGRSELPD  NLKVLFRTVA  MMVPNYALIA  EISLYSYGFL  NARPLSVKIV  MTYRLCSEQL
      1450        1460        1470        1480        1490        1500        1510        1520
SSQFHYDYGM  RAVKAVLVAA  GNLKLKYPNE  NEDILLLRSI  KDVNEPKFLS  HDIPLFNGIT  SDLFPGIKLP  EADYHEFLEC
      1530        1540        1550        1560        1570        1580        1590        1600
AHEACNVHNL  QPVKFFLEKI  IQTYEMMIVR  HGFMLVGEPF  AAKTKVLHVL  ADTLTLMNEH  GYGEEEKVIY  RTVNPKSITM
      1610        1620        1630        1640        1650        1660        1670        1680
GQLFGQFDPV  SHEWTDGIVA  NTFREFALSE  TPDRKWVVFD  GPIDTLWIES  MNTVLDDNKK  LCLMSGEIIQ  MSPQMSLIFE
      1690        1700        1710        1720        1730        1740        1750        1760
TMDLSQASPA  TVSRCGMIYL  EPSQLGWEPL  VSSWLNSLKG  PLCEPEYQAL  LRGLFAWLIP  PSLNQRVELF  QLNYLYTTIV
      1770        1780        1790        1800        1810        1820        1830        1840
SKILKILITF  RISNYFKYVP  LKTQCTFIKF  FLHQQACFIF  SLIWSIGGSC  DTDGRRVFDT  FIRLIILGKD  DENPVPDSVG
      1850        1860        1870        1880        1890        1900        1910        1920
KWECPFDEKG  LVYDYMYELK  NKGRWVHWNE  LIKNTNLGDK  QIKIQDIIVP  TMDTIRYTFL  MDLSITYAKP  LLFVGPTGTG
      1930        1940        1950        1960        1970        1980        1990        2000
KSVYVKDKLM  NHLEKDQYFP  FYINLSARTS  ANQVQNIIMA  RLDKRRKGVF  GPPMGKKCII  FIDDMNMPAL  EKYGAQPPIE
      2010        2020        2030        2040        2050        2060        2070        2080
LLRQFFDCGH  WYDLKDTSKI  TLVDIELIAA  MGPPGGGRNP  VTPRCIRHFN  ICSINSFSDE  TMVRIFSSIV  AFYLRTHEFP
      2090        2100        2110        2120        2130        2140        2150        2160
PEYFVIGNQI  VNGTMEIYKQ  SVENLLPTPT  KSHYTFNLRD  FSRVIRGCLL  IERDAVANKH  TMIRLFVHEV  LRVFYDRLIN
      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
47	1	1103.4984	-39.62	2	29.9	12.9	1	73-91	R.TPLLPPPDYPQTMTSEMKK.K	Oxidation: 13, 17	Wdown:Qdown 0.57 mdown:qdown 0.33
1482	1	681.7771	64.45	3	47.3	18.6	2	267-284	K.VINLFTKKEALEGVKPEK.L		
1201	1	1070.0173	-20.70	2	43.7	12.3	1	583-600	K.INPIFDENDELIENAKHK.K		Wdown:Qdown 0.20 mdown:qdown 0.16

Detailed Protein Report

Protein 85: fibrinogen gamma chain isoform gamma-A precursor [Homo sapiens]

Accession:	gi|70906437	**Score:**	54.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	49.5
Database Date:	2015-11-30	**pI:**	5.7
		Sequence Coverage [%]:	4.8
		No. of unique Peptides:	2

Quantitation

mdown:qdown	**Median:**	0.52	**CV:**	98.68 %	**No. of Peptides:**	2
Wdown:Qdown	**Median:**	0.89	**CV:**	37.40 %	**No. of Peptides:**	2

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
176	1	757.3345	-43.89	2	31.4	25.9	0	135-146	R.YLQEIYNSNNQK.I		Wdown:Qdown 0.62 mdown:qdown 1.19
329	1	559.1487	-212.08	2	33.2	28.9	0	274-282	R.VELEDWNGR.T		Wdown:Qdown 1.28 mdown:qdown 0.23

Detailed Protein Report

Protein 86: stAR-related lipid transfer protein 9 [Homo sapiens]

Accession:	gi|270265793	**Score:**	54.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	516.0
Database Date:	2015-11-30	**pI:**	5.9
		Sequence Coverage [%]:	1.0
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MANVQVAVRV	RPLSKRETKE	GGRIIVEVDG	KVAKIRNLKV	DNRPDGFGDS	REKVMAFGFD	YCYWSVNPED	PQYASQDVVF
90	100	110	120	130	140	150	160
QDLGMEVLSG	VAKGYNICLF	AYGQTGSGKT	YTMLGTPASV	GLTPRICEGL	FVREKDCASL	PSSCRIKVSF	LEIYNERVRD
170	180	190	200	210	220	230	240
LLKQSGQKKS	YTLRVREHPE	MGPYVQGLSQ	HVVTNYKQVI	QLLEEGIANR	ITAATHVHEA	SSRSHAIFTI	HYTQAILENN
250	260	270	280	290	300	310	320
LPSEMASKIN	LVDLAGSERA	DPSYCKDRIA	EGANINKSLV	TLGIVISTLA	QNSQVFSSCQ	SLNSSVSNGG	DSGILSSPSG
330	340	350	360	370	380	390	400
TSSGGAPSRR	QSYIPYRDSV	LTWLLKDSLG	GNSKTIMVAT	VSPAHTSYSE	TMSTLRYASS	AKNIINKPRV	NEDANLKLIR
410	420	430	440	450	460	470	480
ELREEIERLK	ALLLSFELRN	FSSLSDENLK	ELVLQNELKI	DQLTKDWTQK	WNDWQALMEH	YSVDINRRRA	GVVIDSSLPH
490	500	510	520	530	540	550	560
LMALEDDVLS	TGVVLYHLKE	GTTKIGRIDS	DQEQDIVLQG	QWIERDHCTI	TSACGVVVLR	PARGARCTVN	GREVTASCRL
570	580	590	600	610	620	630	640
TQGAVITLGK	AQKFRFNHPA	EAAVLRQRRQ	VGEAAAGRGS	LEWLDLDGDL	AASRLGLSPL	LWKERRALEE	QCDEDHQTPR
650	660	670	680	690	700	710	720
DGETSHRAQI	QQQQSYVEDL	RHQILAEEIR	AAKELEFDQA	WISQQIKENQ	QCLLREETWL	ASLQQQQQED	QVAEKELEAS
730	740	750	760	770	780	790	800
VALDAWLQTD	PEIQPSPFVQ	SQKRVVHLQL	LRRHTLRAAE	RNVRRKKVSF	QLERIIKKQR	LLEAQKRLEK	LTTLCWLQDD
810	820	830	840	850	860	870	880
STQEPPYQVL	SPDATVPRPP	CRSKLTSCSS	LSPQRLCSKH	MPQLHSIFLS	WDPSTTLPPR	PDPTHQTSEK	TSSEEHLPQA
890	900	910	920	930	940	950	960
ASYPARTGCL	RKNGLHSSGH	GQPCTARAAL	ARKGASAPDA	CLTMSPNSVG	IQEMEMGVKQ	PHQMVSQGLA	SLRKSANKLK
970	980	990	1000	1010	1020	1030	1040
PRHEPKIFTS	TTQTRGAKGL	ADPSHTQAGW	RKEGNLGTHK	AAKGASCNSL	YPHGPRQTAG	HGKAVKTFWT	EYKPPSPSRA
1050	1060	1070	1080	1090	1100	1110	1120
SKRHQRVLAT	RVRNITKKSS	HLPLGSPLKR	QQNTRDPDTM	VPLTDFSPVM	DHSREKDNDL	SDTDSNYSLD	SLSCVYAKAL
1130	1140	1150	1160	1170	1180	1190	1200
IEPLKPEERK	WDFPEPENSE	SDDSQLSEDS	LAEKRYQSPK	NRLGGNRPTN	NRGQPRTRTR	ASVRGFTAAS	DSDLLAQTHR
1210	1220	1230	1240	1250	1260	1270	1280
SFSLDSLIDA	EEELGEDQQE	EPFPGSADEI	PTETFWHLED	SSLPVMDQEA	ICRLGPINYR	TAARLDAVLP	MSSSFYLDPQ
1290	1300	1310	1320	1330	1340	1350	1360
FQPHCELQPH	CELQPHCELQ	PHCEQAESQV	EPSYSEQADS	LQGMQLSRES	PLMSMDSWFS	CDSKINPSSP	PGIVGSLCPS
1370	1380	1390	1400	1410	1420	1430	1440
PDMQEFHSCK	GERPGYWPNT	EELKPSDAET	VLPYSSKLHQ	GSTELLCSAR	DEHTASAADT	SRLSLWGIQR	LIQPGADGTF
1450	1460	1470	1480	1490	1500	1510	1520
QGRCIPDMTQ	QGSSEASHNS	SVSNVLAASA	TTLTHVGSTH	ERDWSALQQK	YLLELSCPVL	EAIGAPKPAY	PYLEEDSGSL
1530	1540	1550	1560	1570	1580	1590	1600
AQASSKGGDT	LLPVGPRVSS	NLNLNNFPVH	LSRIRRLRAE	KEQDSLNAKL	EGVSDFFSTS	EKEASYDETY	SADLESLSAS
1610	1620	1630	1640	1650	1660	1670	1680
RSTNAQVFAT	ENAIPDSMTE	ACEVKQNNLE	ECLQSCRKPG	LMTSSDEDFF	QKNACHSNVT	TATKADHWSQ	GWAPLRKNSA
1690	1700	1710	1720	1730	1740	1750	1760
VQPGQLSPDS	HYPLEEEKTD	CQESSKEAVR	RHINVSFALP	SGPELYLHSA	PWNPLSSSLQ	PPLLETFYVT	KSRDALTETA
1770	1780	1790	1800	1810	1820	1830	1840
LEIPACREVR	VPSPPPREAW	GFGHNHQALQ	GAYLKNNLPV	LLQNQNSKIA	SSQQVTAEIP	VDLNTREVIR	ESGKCPGNIT
1850	1860	1870	1880	1890	1900	1910	1920
EESHDSVYSS	VTQNRHFLPS	TSTKVCEFEN	QVVILNKKHS	FPALEGGEVT	AQSCCGASSD	STESGKSLLF	RESEAREEEE
1930	1940	1950	1960	1970	1980	1990	2000
LDQNTVLRQT	INVSLEKDMP	GESAVSLKSR	SVDRRVSSPV	MVAQGGGPTP	KWEGKNETGL	LEKGLRPKDS	SEEFKLPGTK
2010	2020	2030	2040	2050	2060	2070	2080
PAYERFQLVA	CPQERNPSEC	KSQEMLNPNR	EPSGKKQNKR	VNNTDEMARL	IRSVMQLENG	ILEIESKQNK	QVHASHTPGT
2090	2100	2110	2120	2130	2140	2150	2160
DKELVFQDQK	EQEKTDHAFR	PDSSGNPLPS	KDQPSSPRQT	DDTVFRDSEA	GAMEVNSIGN	HPQVQKITPN	PFRSREGVRE
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2847	1	665.3691	57.41	2	64.1	17.6	0	2192-2202	R.EFTNTSLHPQR.M	
1886	1	863.9273	-37.56	2	52.2	12.3	1	2739-2754	K.KVVAALPSQAPYDDPR.V	

Detailed Protein Report

Protein 87: phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 1 isoform b [Homo sapiens]

Accession:	gi|40254823	**Score:**	54.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	133.1
Database Date:	2015-11-30	**pI:**	7.9
		Sequence Coverage [%]:	4.0
		No. of unique Peptides:	2

Quantitation

mdown:qdown	**Median:**	1.45	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	1.00	**CV:**	0.00 %	**No. of Peptides:**	1

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        10         20         30         40         50         60         70         80
MVPCWNHGNI TRSKAEELLS RTGKDGSFLV RASESISRAY ALCVLYRNCV YTYRILPNED DKFTVQASEG VSMRFFTKLD
        90        100        110        120        130        140        150        160
QLIEFYKKEN MGLVTHLQYP VPLEEEDTGD DPEEDTESVV SPPELPPRNI PLTASSCEAK EVPFSNENPR ATETSRPSLS
       170        180        190        200        210        220        230        240
ETLFQRLQSM DTSGLPEEHL KAIQDYLSTQ LAQDSEFVKT GSSSLPHLKK LTTLLCKELY GEVIRTLPSL ESLQRLFDQQ
       250        260        270        280        290        300        310        320
LSPGLRPRPQ VPGEANPINM VSKLSQLTSL LSSIEDKVKA LLHEGPESPH RPSLIPPVTF EVKAESLGIP QKMQLKVDVE
       330        340        350        360        370        380        390        400
SGKLIIKKSK DGSEDKFYSH KKILQLIKSQ KFLNKLVILV ETEKEKILRK EYVFADSKKR EGFCQLLQQM KNKHSEQPEP
       410        420        430        440        450        460        470        480
DMITIFIGTW NMGNAPPPKK ITSWFLSKGQ GKTRDDSADY IPHDIYVIGT QEDPLSEKEW LEILKHSLQE ITSVTFKTVA
       490        500        510        520        530        540        550        560
IHTLWNIRIV VLAKPEHENR ISHICTDNVK TGIANTLGNK GAVGVSFMFN GTSLGFVNSH LTSGSEKKLR RNQNYMNILR
       570        580        590        600        610        620        630        640
FLALGDKKLS PFNITHRFTH LFWFGDLNYR VDLPTWEAET IIQKIKQQQY ADLLSHDQLL TERREQKVFL HFEEEEITFA
       650        660        670        680        690        700        710        720
PTYRFERLTR DKYAYTKQKA TGMKYNLPSW CDRVLWKSYP LVHVVCQSYG STSDIMTSDH SPVFATFEAG VTSQFVSKNG
       730        740        750        760        770        780        790        800
PGTVDSQGQI EFLRCYATLK TKSQTKFYLE FHSSCLESFV KSQEGENEEG SEGELVVKFG ETLPKLKPII SDPEYLLDQH
       810        820        830        840        850        860        870        880
ILISIKSSDS DESYGEGCIA LRLEATETQL PIYTPLTHHG ELTGHFQGEI KLQTSQGKTR EKLYDFVKTE RDESSGPKTL
       890        900        910        920        930        940        950        960
KSLTSHDPMK QWEVTSRAPP CSGSSITEII NPNYMGVGPF GPPMPLHVKQ TLSPDQQPTA WSYDQPPKDS PLGPCRGESP
       970        980        990       1000       1010       1020       1030       1040
PTPPGQPPIS PKKFLPSTAN RGLPPRTQES RPSDLGKNAG DTLPQEDLPL TKPEMFENPL YGSLSSFPKP APRKDQESPK
      1050       1060       1070       1080       1090       1100       1110       1120
MPRKEPPPCP EPGILSPSIV LTKAQEADRG EGPGKQVPAP RLRSFTCSSS AEGRAAGGDK SQGKPKTPVS SQAPVPAKRP
      1130       1140       1150       1160       1170       1180       1190
IKPSRSEINQ QTPPTPTPRP PLPVKSPAVL HLQHSKGRDY RDNTELPHHG KHRPEEGPPG PLGRTAMQ
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
499	3	584.8345	31.59	2	35.6	27.2	0	79-87	K.LDQLIEFYK.K		Wdown:Qdown 1.00 mdown:qdown 1.45
1543	1	1008.6543	64.47	2	49.1	16.6	1	1107-1125	K.TPVSSQAPVPAKRPIKPSR.S		

Detailed Protein Report

Protein 88: PREDICTED: integrin beta-7 isoform X3 [Homo sapiens]

Accession: gi|578823673

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Modification(s): Carbamidomethyl

Score: 54.2

MW [kDa]: 85.0

pI: 5.7

Sequence Coverage [%]: 6.6

No. of unique Peptides: 4

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
2734	1	772.4219	-54.41	2	65.4	16.0	1	200-213	K.TVLPFVSTVPSKLR.H	
2949	1	1019.4212	-21.13	3	66.0	11.9	2	569-594	R.HEGILCGGFGRCQCGVCHCHANRTGR.A	Carbamidomethyl: 6, 12, 14, 17, 19
143	1	722.7732	-4.06	2	30.5	13.0	0	580-591	R.CQCGVCHCHANR.T	Carbamidomethyl: 1, 3

Detailed Protein Report

Protein 89: PREDICTED: keratin, type I cytoskeletal 26 isoform X2 [Homo sapiens]

Accession:	gi|578830847	**Score:**	53.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	51.6
Database Date:	2015-11-30	**pI:**	4.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	10.5
		No. of unique Peptides:	4

Quantitation

mdown:qdown **Median:** 0.46 **CV:** 0.00 % **No. of Peptides:** 1

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
108	1	557.2530	-43.29	2	30.6	12.5	1	1-10	-.MSFRLSGGSR.R	Oxidation: 1	
559	1	625.3768	63.05	2	35.6	11.4	0	368-377	K.LEYEQLLDVK.I		mdown:qdown 0.46
1697	1	905.3389	-109.42	2	49.8	10.8	1	383-397	K.EIDIYCNLLDGEERK.S		
2812	1	753.3845	-13.35	2	64.3	19.2	1	405-418	K.SKGYRPVNSGNQAK.E		

Detailed Protein Report

Protein 90: PREDICTED: zinc finger protein 729 isoform X1 [Homo sapiens]

Accession: gi|578832877
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 53.6
MW [kDa]: 144.0
pI: 10.5
Sequence Coverage [%]: 3.3
No. of unique Peptides: 2

10	20	30	40	50	60	70	80
MAASLRDCAG	TTGGASGENP	DSGCGFMNGK	SFGPGPLTFR	DVTIEFSLEE	WQCLDTVQQN	LYRDVMLENY	RNLVFLGMAV
90	100	110	120	130	140	150	160
FKPDLITCLK	QGKEPWNMKR	HEMVTKPPVM	RSHFTQDLWP	DQSTKDSFQE	VILRTYARCG	HKNLRLRKDC	KSANEGKMHK
170	180	190	200	210	220	230	240
EGYNKLNQCR	TATQRKIFQC	NKHMKVFHKY	SNRNKVRHTK	KKTFKCIKCS	KSFFMLSCLI	RHKRIHIRQN	IYKCEERGKA
250	260	270	280	290	300	310	320
FKSFSTLTKH	KIIHTEDKPY	KYKKCGNAFK	FSSTFTKHKR	IHTGETPFRC	EECGKAFNQS	SNLTDHKRIH	TGEKTYKCEE
330	340	350	360	370	380	390	400
CGKAFKGSSN	FNAHKVIHTA	EKPYKCEDCG	KTFNHFSALR	KHKIIHTGKK	PYKREECGKA	FSQSSTLRKH	EIIHTGEKPY
410	420	430	440	450	460	470	480
KCEECGKAFK	WSSKLTVHKV	VHTGEKPYKC	EECGKAFSQF	STLKKHKIIH	TGKKPYKCEE	CGKAFNSSST	LMKHKIIHTG
490	500	510	520	530	540	550	560
EKPYKCEECG	KAFRQSSHLT	RHKAIHTGEK	PYKCEECGKA	FNHFSDLRRH	KIIHTGKKPY	KCEECGKAFS	QSSTLRNHQI
570	580	590	600	610	620	630	640
IHTGEKPYKC	EECGKAFKWS	SKLTVHKVIH	TGEKPCKCEE	CGKAFKHFSA	LRKHKVIHTR	EKLYKCEECG	KAFNNSSILA
650	660	670	680	690	700	710	720
KHKIIHTGKK	PYKCEECGKA	FRQSSHLTRH	KAIHTGEKPY	KCEECGKAFS	HFSALRRHKI	IHTGKKPYKC	EECGKAFSHF
730	740	750	760	770	780	790	800
SALRRHKIIH	TGEKPYKCEE	CGKAFKWSSK	LTVHKVIHTR	EKLYKCEECV	KAFNSFSALM	KHKVIHTGEK	PYKCEECGKA
810	820	830	840	850	860	870	880
FKWSSKLTVH	KVIHTGEKPC	KCEECGKAFK	HFSALRKHKV	IHTGKKPYKC	EECGKAFSQS	SSLRKHEIIH	SGEKPYKCEE
890	900	910	920	930	940	950	960
CGKAFKWLSK	LTVHKVIHTA	EKPCKCEECG	KAFKHFSALR	KHKIIHTGKK	PYKCEECGKA	FNDSSTLMKH	KIIHTGKKPY
970	980	990	1000	1010	1020	1030	1040
KCAECGKAFK	QSSHLTRHKA	IHTGEKPYKC	EECGKDFNNS	STLKKHKLIH	TREKLYKCEE	CVKAFNNFSA	LMKHKIIHTG
1050	1060	1070	1080	1090	1100	1110	1120
EKPYKCEECG	KAFKWSSKLT	EHKVIHTGEK	PCKCEECDKA	FKHFSALRKH	KVIHTGKKPY	QCDECGKAFN	NSSTLTKHKI
1130	1140	1150	1160	1170	1180	1190	1200
IHTGEKPYKC	EECGKAFSQS	SILTKHKIIH	SVEKPYKCEE	CGKAFNQSSH	LTRHKTIHTG	EKPYKCEECG	KAFIQCSYLI
1210	1220	1230	1240	1250			
RHKTIHTREK	PTNVKKVPKL	LSNPHTLLDK	TIHTGEKPYK	CEECAKAF			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1895	1	704.7670	-172.25	2	52.2	13.8	1	502-513	R.HKAIHTGEKPYK.C	
2677	1	665.3406	42.21	2	61.8	13.9	2	621-631	R.EKLYKCEECGK.A	

Detailed Protein Report

Protein 91: GRIP and coiled-coil domain-containing protein 1 [Homo sapiens]

Accession:	gi|22208850	**Score:**	53.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	87.8
Database Date:	2015-11-30	**pI:**	5.2
		Sequence Coverage [%]:	6.5
		No. of unique Peptides:	3

Quantitation

mdown:qdown	**Median:**	1.36	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.90	**CV:**	41.33 %	**No. of Peptides:**	2

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	LEHQHQQEAD	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
165	1	635.8027	-9.05	2	31.3	11.3	1	180-190	K.SRMEASYLADK.K		Wdown:Qdown 1.34 mdown:qdown 1.36
1918	2	572.7243	-166.46	2	54.0	17.8	1	344-353	R.KTALAEDQLR.Q		
55	1	1096.9659	-93.00	2	30.1	11.7	0	363-382	R.VAALENQISEVSELLGTYEK.A		Wdown:Qdown 0.61

Detailed Protein Report

Protein 92: PREDICTED: kinesin-like protein KIF13B isoform X2 [Homo sapiens]

Accession:	gi|530387685	**Score:**	53.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	195.4
Database Date:	2015-11-30	**pI:**	5.4
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.5
		No. of unique Peptides:	2

Alias proteins:

Accession	Name	Description
gi|578815259	refseq_human (refseq_human_20140103.fasta)	PREDICTED: kinesin-like protein KIF13B isoform X4 [Homo sapiens]
gi|578815257	refseq_human (refseq_human_20140103.fasta)	PREDICTED: kinesin-like protein KIF13B isoform X3 [Homo sapiens]

10	20	30	40	50	60	70	80
MDESVKEKYA	GQDIVFKCLG	ENILQNAFDG	YNACIFAYGQ	TGSGKSYTMM	GTADQPGLIP	RLCSGLFERT	QKEENEEQSF
90	100	110	120	130	140	150	160
KVEVSYMEIY	NEKVRDLLDP	KGSRQTLKVR	EHSVLGPYVD	GLSKLAVTSY	KDIESLMSEG	NKSRTVAATN	MNEESSRSHA
170	180	190	200	210	220	230	240
VFKITLTHTL	YDVKSGTSGE	KVGKLSLVDL	AGSERATKTG	AAGDRLKEGS	NINKSLTTLG	LVISALADQS	AGKNKNKFVP
250	260	270	280	290	300	310	320
YRDSVLTWLL	KDSLGGNSKT	AMVATVSPAA	DNYDETLSTL	RYADRAKHIV	NHAVVNEDPN	ARIIRDLREE	VEKLREQLTK
330	340	350	360	370	380	390	400
AEAMKSPELK	DRLEESEKLI	QEMTVTWEEK	LRKTEEIAQE	RQKQLESLGI	SLQSSGIKVG	DDKCFLVNLN	ADPALNELLV
410	420	430	440	450	460	470	480
YYLKEHTLIG	SANSQDIQLC	GMGILPEHCI	IDITSEGQVM	LTPQKNTRTF	VNGSSVSSPI	QLHHGDRILW	GNNHFFRLNL
490	500	510	520	530	540	550	560
PKKKKKAERE	DEDQDPSMKN	ENSSEQLDVD	GDSSSEVSSE	VNFNYEYAQM	EVTMKALGSN	DPMQSILNSL	EQQHEEEKRS
570	580	590	600	610	620	630	640
ALERQRLMYE	HELEQLRRRL	SPEKQNCRSM	DRFSFHSPSA	QQRLRQWAEE	REATLNNSLM	RLREQIVKAN	LLVREANYIA
650	660	670	680	690	700	710	720
EELDKRTEYK	VTLQIPASSL	DANRKRGSLL	SEPAIQVRRK	GKGKQIWSLE	KLDNRLLDMR	DLYQEWKECE	EDNPVIRSYF
730	740	750	760	770	780	790	800
KRADPFYDEQ	ENHSLIGVAN	VFLESLFYDV	KLQYAVPIIN	QKGEVAGRLH	VEVMRLSGDV	GERIAGGDEV	AEVSFEKETQ
810	820	830	840	850	860	870	880
ENKLVCMVKI	LQATGLPQHL	SHFVFCKYSF	WDQQEPVIVA	PEVDTSSSSV	SKEPHCMVVF	DHCNEFSVNI	TEDFIEHLSE
890	900	910	920	930	940	950	960
GALAIEVYGH	KINDPRKNPA	LWDLGIIQAK	TRSLRDRWSE	VTRKLEFWVQ	ILEQNENGEY	CPVEVISAKD	VPTGGIFQLR
970	980	990	1000	1010	1020	1030	1040
QGQSRRVQVE	VKSVQESGTL	PLMEECILSV	GIGCVKVRPL	RAPRTHETFH	EEEEDMDSYQ	DRDLERLRRK	WLNALTKRQE
1050	1060	1070	1080	1090	1100	1110	1120
YLDQQLQKLV	SKRDKTEDDA	DREAQLLEMR	LTLTEERNAV	MVPSAGSGIP	GAPAEWTPVP	GMETHIPVIF	LDLNADDFSS
1130	1140	1150	1160	1170	1180	1190	1200
QDNLDDPEAG	GWDATLTGEE	EEEFFELQIV	KQHDGEVKAE	ASWDSAVHGC	PQLSRGTPVD	ERLFLIVRVT	VQLSHPADMQ
1210	1220	1230	1240	1250	1260	1270	1280
LVLRKRICVN	VHGRQGFAQS	LLKKMSHRSS	IPGCGVTFEI	VSNIPEDAQG	VEEREALARM	AANVENPASA	DSEAYIEKYL
1290	1300	1310	1320	1330	1340	1350	1360
RSVLAVENLL	TLDRLRQEVA	VKEQLTGKGK	LSRRSISSPN	VNRLSGSRQD	LIPSYSLGSN	KGRWESQQDV	SQTTVSRGIA
1370	1380	1390	1400	1410	1420	1430	1440
PAPALSVSPQ	NNHSPDPGLS	NLAASYLNPV	KSFVPQMPKL	LKSLFPVRDE	KRGKRPSPLA	HQPVPRIMVQ	SASPDIRVTR
1450	1460	1470	1480	1490	1500	1510	1520
MEEAQPEMGP	DVLVQTMGAP	ALKICDKPAK	VPSPPPVIAV	TAVTPAPEAQ	DGPPSPLSEA	SSGYFSHSVS	TATLSDALGP
1530	1540	1550	1560	1570	1580	1590	1600
GLDAAAPPGS	MPTAPEAEPE	APISHPPPPT	AVPAEEPPGP	QQLVSPGRER	PDLEAPAPGS	PFRVRRVRAS	ELRSFSRMLA
1610	1620	1630	1640	1650	1660	1670	1680
GDPGCSPGAE	GNAPAPGAGG	QALASDSEEA	DEVPEWLREG	EFVTVGAHKT	GVVRYVGPAD	FQEGTWVGVE	LDLPSGKNDG
1690	1700	1710	1720	1730	1740	1750	1760
SIGGKQYFRC	NPGYGLLVRP	SRVRRATGPV	RRRSTGLRLG	APEARRSATL	SGSATNLASL	TAALAKADRS	HKNPENRKSW
1770							
AS							

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	94-101	K.VRDLLDPK.G	
1541	1	513.1056	-215.54	2	48.0	12.4	1	585-592	K.QNCRSMDR.F	Oxidation: 6

Detailed Protein Report

Protein 93: PREDICTED: MAX gene-associated protein isoform X16 [Homo sapiens]

Accession:	gi|578826753	**Score:**	53.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	290.2
Database Date:	2015-11-30	**pI:**	8.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.6
		No. of unique Peptides:	2

Quantitation

Wdown:Qdown	**Median:**	1.85	**CV:**	0.00 %	**No. of Peptides:**	1

10	20	30	40	50	60	70	80
MFKLDTGKMP	VVYLEPCAVT	RSTVKISELP	DNMLSTSRKD	KSSMLAELEY	LPTYIENSNE	TAFCLGKESE	NGLRKHSPDL
90	100	110	120	130	140	150	160
RVVQKYPLLK	EPQWKYPDIS	DSISTERILD	DSKDSVGDSL	SGKEDLGRKR	TTMLKIATAA	KVVNANQNAS	PNVPGKRGRP
170	180	190	200	210	220	230	240
RKLKLCKAGR	PPKNTGKSLI	STKNTPVSPG	STFPDVKPDL	EDVDGVLFVS	FESKEALDIH	AVDGTTEESS	SLQASTTNDS
250	260	270	280	290	300	310	320
GYRARISQLE	KELIEDLKTL	RHKQVIHPGL	QEVGLKLNSV	DPTMSIDLKY	LGVQLPLAPA	TSFPFWNLTG	TNPASPDAGF
330	340	350	360	370	380	390	400
PFVSRTGKTN	DFTKIKGWRG	KFHSASASRN	EGGNSESSLK	NRSAFCSDKL	DEYLENEGKL	METSMGFSSN	APTSPVVYQL
410	420	430	440	450	460	470	480
PTKSTSYVRT	LDSVLKKQST	ISPSTSYSLK	PHSVPPVSRK	AKSQNRQATF	SGRTKSSYKS	ILPYPVSPKQ	KYSHVILGDK
490	500	510	520	530	540	550	560
VTKNSSGIIS	ENQANNFVVP	TLDENIFPKQ	ISLRQAQQQQ	QQQQGSRPPG	LSKSQVKLMD	LEDCALWEGK	PRTYITEERA
570	580	590	600	610	620	630	640
DVSLTTLLTA	QASLKTKPIH	TIIRKRAPPC	NNDFCRLGCV	CSSLALEKRQ	PAHCRRPDCM	FGCTCLKRKV	VLVKGGSKTK
650	660	670	680	690	700	710	720
HFQRKAAHRD	PVFYDTLGEE	AREEEEGIRE	EEEQLKEKKK	RKKLEYTICE	TEPEQPVRHY	PLWVKVEGEV	DPEPVYIPTP
730	740	750	760	770	780	790	800
SVIEPMKPLL	LPQPEVLSPT	VKGKLLTGIK	SPRSYTPKPN	PVIREEDKDP	VYLYFESMMT	CARVRVYERK	KEDQRQPSSS
810	820	830	840	850	860	870	880
SSPSPSFQQQ	TSCHSSPENH	NNAKEPDSEQ	QPLKQLTCDL	EDDSDKLQEK	SWKSSCNEGE	SSSTSYMHQR	SPGGPTKLIE
890	900	910	920	930	940	950	960
IISDCNWEED	RNKILSILSQ	HINSNMPQSL	KVGSFIIELA	SQRKSRGEKN	PPVYSSRVKI	SMPSCQDQDD	MAEKSGSETP
970	980	990	1000	1010	1020	1030	1040
DGPLSPGKME	DISPVQTDAL	DSVRERLHGG	KGLPFYAGLS	PAGKLVAYKR	KPSSSTSGLI	QVNGKSYPQA	KLLLGQMGAL
1050	1060	1070	1080	1090	1100	1110	1120
HPANRLAAYI	TGRLRPSVLD	LSTLSTVISK	VASNAKVAAS	RKPRTLLPST	SNSKMASSSG	TATNRPGKNL	KAFVPAKRPI
1130	1140	1150	1160	1170	1180	1190	1200
AARPSPGGVF	TQFVMSKVGA	LQQKIPGVST	PQTLAGTQKF	SIRPSPVMVV	TPVVSSEPVQ	VCSPVTAAVT	TTTPQVFLEN
1210	1220	1230	1240	1250	1260	1270	1280
TTAVTPMTAI	SDVETKETTY	SSGATTTGVV	EVSETNTSTS	VTSTQSTATV	NLTKTTGITT	PVASVAFPKS	LVASPSTITL
1290	1300	1310	1320	1330	1340	1350	1360
PVASTASTSL	VVVTAAASSS	MVTTPTSSLG	SVPIILSGIN	GSPPVSQRPE	NAAQIPVATP	QVSPNTVKRA	GPRLLLIPVQ
1370	1380	1390	1400	1410	1420	1430	1440
QGSPTLRPVS	NTQLQGHRMV	LQPVRSPSGM	NLFRHPNGQI	VQLLPLHQLR	GSNTQPNLQP	VMFRNPGSVM	GIRLPAPSKP
1450	1460	1470	1480	1490	1500	1510	1520
SETPPSSTSS	SAFSVMNPVI	QAVGSSSAVN	VITQAPSLLS	SGASFVSQAG	TLTLRISPPE	PQSFASKTGS	ETKITYSSGG
1530	1540	1550	1560	1570	1580	1590	1600
QPVGTASLIP	LQSGSFALLQ	LPGQKPVPSS	ILQHVASLQM	KRESQNPDQK	DETNSIKREQ	ETKKVLQSEG	EAVDPEANVI
1610	1620	1630	1640	1650	1660	1670	1680
KQNSGAATSE	ETLNDSLEDR	GDHLDEECLP	EEGCATVKPS	EHSCITGSHT	DQDYKDVNEE	YGARNRKSSK	EKVAVLEVRT
1690	1700	1710	1720	1730	1740	1750	1760
ISEKASNKTV	QNLSKVQHQK	LGDVKVEQQK	GFDNPEENSS	EFPVTFKEES	KFELSGSKVM	EQQSNLQPEA	KEKECGDSLE
1770	1780	1790	1800	1810	1820	1830	1840
KDRERWRKHL	KGPLTRKCVG	ASQECKKEAD	EQLIKETKTC	QENSDVFQQE	QGISDLLGKS	GITEDARVLK	TECDSWSRIS
1850	1860	1870	1880	1890	1900	1910	1920
NPSAFSIVPR	RAAKSSRGNG	HFQGHLLLPG	EQIQPKQEKK	GGRSSADFTV	LDLEEDDEDD	NEKTDDSIDE	IVDVVSDYQS
1930	1940	1950	1960	1970	1980	1990	2000
EEVDDVEKVN	NCVEYIEDDE	EHVDIETVEE	LSEEINVAHL	KTTAAHTQSF	KQPSCTHISA	DEKAAERSRK	APPIPLKLKP
2010	2020	2030	2040	2050	2060	2070	2080
DYWSDKLQKE	AEAFAYYRRT	HTANERRRRG	EMRDLFEKLK	ITLGLLHSSK	VSKSLILTRA	FSEIQGLTDQ	ADKLIGQKNL
2090	2100	2110	2120	2130	2140	2150	2160
LTRKRNILIR	KVSSLSGKTE	EVVLKKLEYI	YAKQQALEAQ	KRKKKMGSDE	FDISPRISKQ	QEGSSASSVD	LGQMFINNRR
2170	2180	2190	2200	2210	2220	2230	2240

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1840	1	899.4842	21.23	2	51.7	12.0	0	1585-1601	K.VLQSEGEAVDPEANVIK.Q		
238	1	897.4097	-91.61	2	31.7	17.0	1	2603-2620	K.VMPCLAPIAAKVGSVGHK.M	Oxidation: 2	Wdown:Qdown 1.85

Detailed Protein Report

Protein 94: E3 ubiquitin-protein ligase UBR5 isoform 2 [Homo sapiens]

Accession:	gi|544583486	**Score:**	53.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	309.0
Database Date:	2015-11-30	**pI:**	5.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.4
		No. of unique Peptides:	3

Quantitation

mdown:qdown	**Median:**	0.46	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	7.90	**CV:**	0.00 %	**No. of Peptides:**	1

10	20	30	40	50	60	70	80
MTSIHFVVHP	LPGTEDQLND	RLREVSEKLN	KYNLNSHPPL	NVLEQATIKQ	CVVGPNHAAF	LLEDGRVCRI	GFSVQPDRLE
90	100	110	120	130	140	150	160
LGKPDNNDGS	KLNSNSGAGR	TSRPGRTSDS	PWFLSGSETL	GRLAGNTLGS	RWSSGVGGSG	GGSSGRSSAG	ARDSRRQTRV
170	180	190	200	210	220	230	240
IRTGRDRGSG	LLGSQPQPVI	PASVIPEELI	SQAQVVLQGK	SRSVIIRELQ	RTNLDVNLAV	NNLLSRDDED	GDDGDDTASE
250	260	270	280	290	300	310	320
SYLPGEDLMS	LLDADIHSAH	PSVIIDADAM	FSEDISYFGY	PSFRRSSLSR	LGSSRVLLLP	LERDSELLRE	RESVLRLRER
330	340	350	360	370	380	390	400
RWLDGASFDN	ERGSTSKEGE	PNLDKKNTPV	QSPVSLGEDL	QWWPDKDGTK	FICIGALYSE	LLAVSSKGEL	YQWKWSESEP
410	420	430	440	450	460	470	480
YRNAQNPSLH	HPRATFLGLT	NEKIVLLSAN	SIRATVATEN	NKVATWVDET	LSSVASKLEH	TAQTYSELQG	ERIVSLHCCA
490	500	510	520	530	540	550	560
LYTCAQLENS	LYWWGVVPFS	QRKKMLEKAR	AKNKKPKSSA	GISSMPNITV	GTQVCLRNNP	LYHAGAVAFS	ISAGIPKVGV
570	580	590	600	610	620	630	640
LMESVWNMND	SCRFQLRSPE	SLKNMEKASK	TTEAKPESKQ	EPVKTEMGPP	PSPASTCSDA	SSIASSASMP	YKRRRSTPAP
650	660	670	680	690	700	710	720
KEEEKVNEEQ	WSLREVVFVE	DVKNVPVGKV	LKVDGAYVAV	KFPGTSSNTN	CQNSSGPDAD	PSSLLQDCRL	LRIDELQVVK
730	740	750	760	770	780	790	800
TGGTPKVPDC	FQRTPKKLCI	PEKTEILAVN	VDSKGVHAVL	KTGNWVRYCI	FDLATGKAEQ	ENNFPTSSIA	FLGQNERNVA
810	820	830	840	850	860	870	880
IFTAGQESPI	ILRDGNGTIY	PMAKDCMGGI	RDPDWLDLPP	ISSLGMGVHS	LINLPANSTI	KKKAAVIIMA	VEKQTLMQHI
890	900	910	920	930	940	950	960
LRCDYEACRQ	YLMNLEQAVV	LEQNLQMLQT	FISHRCDGNR	NILHACVSVC	FPTSNKETKE	EEEAERSERN	TFAERLSAVE
970	980	990	1000	1010	1020	1030	1040
AIANAISVVS	SNGPGNRAGS	SSSRSLRLRE	MMRRSLRAAG	LGRHEAGASS	SDHQDPVSPP	IAPPSWVPDP	PAMDPDGDID
1050	1060	1070	1080	1090	1100	1110	1120
FILAPAVGSL	TTAATGTGQG	PSTSTIPGPS	TEPSVVESKD	RKANAHFILK	LLCDSVVLQP	YLRELLSAKD	ARGMTPFMSA
1130	1140	1150	1160	1170	1180	1190	1200
VSGRAYPAAI	TILETAQKIA	KAEISSSEKE	EDVFMGMVCP	SGTNPDDSPL	YVLCCNDTCS	FTWTGAEHIN	QDIFECRTCG
1210	1220	1230	1240	1250	1260	1270	1280
LLESLCCCTE	CARVCHKGHD	CKLKRTSPTA	YCDCWEKCKC	KTLIAGQKSA	RLDLLYRLLT	ATNLVTLPNS	RGEHLLLFLV
1290	1300	1310	1320	1330	1340	1350	1360
QTVARQTVEH	CQYRPPRIRE	DRNRKTASPE	DSDMPDHDLE	PPRFAQLALE	RVLQDWNALK	SMIMFGSQEN	KDPLSASSRI
1370	1380	1390	1400	1410	1420	1430	1440
GHLLPEEQVY	LNQQSGTIRL	DCFTHCLIVK	CTADILLLDT	LLGTLVKELQ	NKYTPGRREE	AIAVTMRFLR	SVARVFVILS
1450	1460	1470	1480	1490	1500	1510	1520
VEMASSKKKN	NFIPQPIGKC	KRVFQALLPY	AVEELCNVAE	SLIVPVRMGI	ARPTAPFTLA	STSIDAMQGS	EELFSVEPLP
1530	1540	1550	1560	1570	1580	1590	1600
PRPSSDQSSS	SSQSQSSYII	RNPQQRRISQ	SQPVRGRDEE	QDDIVSADVE	EVEVVEGVAG	EEDHHDEQEE	HGEENAEAEG
1610	1620	1630	1640	1650	1660	1670	1680
QHDEHDEDGS	DMELDLLAAA	ETESDSESNH	SNQDNASGRR	SVVTAATAGS	EAGASSVPAF	FSEDDSQSND	SSDSDSSSSQ
1690	1700	1710	1720	1730	1740	1750	1760
SDDIEQETFM	LDEPLERTTN	SSHANGAAQA	PRSMQWAVRN	TQHQRAASTA	PSSTSTPAAS	SAGLIYIDPS	NLRRSGTIST
1770	1780	1790	1800	1810	1820	1830	1840
SAAAAAAALE	ASNASSYLTS	ASSLARAYSI	VIRQISDLMG	LIPKYNHLVY	SQIPAAVKLT	YQDAVNLQNY	VEEKLIPTWN
1850	1860	1870	1880	1890	1900	1910	1920
WMVSIMDSTE	AQLRYGSALA	SAGDPGHPNH	PLHASQNSAR	RERMTAREEA	SLRTLEGRRR	ATLLSARQGM	MSARGDFLNY
1930	1940	1950	1960	1970	1980	1990	2000
ALSLMRSHND	EHSDVLPVLD	VCSLKHVAYV	FQALIYWIKA	MNQQTTLDTP	QLERKRTREL	LELGIDNEDS	EHENDDDTNQ
2010	2020	2030	2040	2050	2060	2070	2080
SATLNDKDDD	SLPAETGQNH	PFFRRSDSMT	FLGCIPPNPF	EVPLAEAIPL	ADQPHLLQPN	ARKEDLFGRP	SQGLYSSSAS
2090	2100	2110	2120	2130	2140	2150	2160
SGKCLMEVTV	DRNCLEVLPT	KMSYAANLKN	VMNMQNRQKK	EGEEQPVLPE	ETESSKPGPS	AHDLAAQLKS	SLLAEIGLTE
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1093	1	647.6752	-180.54	2	42.2	14.8	0	132-146	R.WSSGVGGSGGGSSGR.S		Wdown:Qdown 7.90 mdown:qdown 0.46
31	1	712.9884	0.22	3	29.6	11.4	1	1305-1323	R.KTASPEDSDMPDHDLEPPR.F		
2778	1	958.9830	42.28	2	66.1	16.7	1	2102-2117	K.MSYAANLKNVMNMQNR.Q	Oxidation: 11, 13	

Detailed Protein Report

Protein 95: neuralized-like protein 4 isoform 2 [Homo sapiens]

Accession:	gi|53829368	**Score:**	52.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	166.6
Database Date:	2015-11-30	**pI:**	5.5
		Sequence Coverage [%]:	2.4
		No. of unique Peptides:	4

Quantitation

mdown:qdown **Median:** 0.11 **CV:** 0.00 % **No. of Peptides:** 1

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
760	1	856.2336	-324.05	1	38.9	11.7	1	493-499	R.RNNAILR.A		
512	1	457.1269	-288.36	2	35.0	10.5	0	500-508	R.ALSPEGALR.R		mdown:qdown 0.11
2675	1	715.3668	-42.44	2	61.8	10.6	1	1139-1151	K.NILLSNGNRTATR.V		

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1492	1	555.2127	-156.80	2	47.2	20.0	2	1372-1380	K.LRGDEAHRR.R		

Protein 96: zinc finger protein 281 isoform 2 [Homo sapiens]

Accession: gi|526253066
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 52.7
MW [kDa]: 93.2
pI: 9.3
Sequence Coverage [%]: 2.6
No. of unique Peptides: 2

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
2653	1	811.8976	73.50	2	64.2	24.6	1	311-323	K.CDTCQQYFSRTDR.L	
768	2	495.2668	-36.55	2	38.4	28.1	1	372-380	K.SKSIAIENK.E	

Detailed Protein Report

Protein 97: **prolactin-inducible protein precursor [Homo sapiens]**

Accession:	gi|4505821	**Score:**	52.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	16.6
Database Date:	2015-11-30	**pI:**	9.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	18.5
		No. of unique Peptides:	2

Quantitation

mdown:qdown	**Median:**	0.55	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	1.61	**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		Wdown:Qdown 1.61 mdown:qdown 0.55
2317	1	805.9036	-28.46	2	57.6	24.3	0	119-133	R.ELGICPDDAAVIPIK.N	Carbamidomethyl: 5	

Detailed Protein Report

Protein 98: **short transient receptor potential channel 4 isoform zeta [Homo sapiens]**

Accession:	gi|209863032	**Score:**	52.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	92.2
Database Date:	2015-11-30	**pI:**	9.3
Modification(s):	Oxidation	**Sequence Coverage [%]:**	4.9
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	1.09	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	1.24	**CV:**	0.00 %	**No. of Peptides:**	1

10	20	30	40	50	60	70	80
MAQFYYKRNV	NAPYRDRIPL	RIVRAESELS	PSEKAYLNAV	EKGDYASVKK	SLEEAEIYFK	ININCIDPLG	RTALLIAIEN
90	100	110	120	130	140	150	160
ENLELIELLL	SFNVYVGDAL	LHAIRKEVVG	AVELLLNHKK	PSGEKQFVAQ	PNCQQLLASR	WYDEFPGWRR	RHWAVKMVTC
170	180	190	200	210	220	230	240
FIIGLLFPVF	SVCYLIAPKS	PLGLFIRKPF	IKFICHTASY	LTFLFLLLLA	SQHIDRSDLN	RQGPPPTIVE	WMILPWVLGF
250	260	270	280	290	300	310	320
IWGEIKQMWD	GGLQDYIHDW	WNLMDFVMNS	LYLATISLKI	VAFVKYSALN	PRESWDMWHP	TLVAEALFAI	ANIFSSLRLI
330	340	350	360	370	380	390	400
SLFTANSHLG	PLQISLGRML	LDILKFLFIY	CLVLLAFANG	LNQLYFYYEE	TKGLTCKGIR	CEKQNNAFST	LFETLQSLFW
410	420	430	440	450	460	470	480
SIFGLINLYV	TNVKAQHEFT	EFVGATMFGT	YNVISLVVLL	NMLIAMMNNS	YQLIADHADI	EWKFARTKLW	MSYFEEGGTL
490	500	510	520	530	540	550	560
PTPFNVIPSP	KSLWYLIKWI	WTHLCKKKMR	RKPESFGTIG	RRAADNLRRH	HQYQEVMRNL	VKRYVAAMIR	DAKTEEGLTE
570	580	590	600	610	620	630	640
ENFKELKQDI	SSFRFEVLGL	LRGSKLSTIQ	SANASKESSN	SADSDEKSDS	EGNSKDKKKN	FSLFDLTTLI	HPRSAAIASE
650	660	670	680	690	700	710	720
RHNISNGSAL	VVQEPPREKQ	RKVNFVTDIK	NFGLFHRRSK	QNAAEQNANQ	IFSVSEEVAR	QQAAGPLERN	IQLESRGLAS
730	740	750	760	770	780	790	800
RGDLSIPGLS	EQCVLVDHRE	RNTDTLGLQV	GKRVCPFKSE	KVVVEDTVPI	IPKEKHAKEE	DSSIDYDLNL	PDTVTHEDYV
810							
TTRL							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
117	1	849.3965	-40.26	2	30.9	18.1	1	530-542	R.HHQYQEVMRNLVK.R	Oxidation: 8	Wdown:Qdown 1.24 mdown:qdown 1.09

Detailed Protein Report

Protein 99: desmoplakin isoform I [Homo sapiens]

Accession:	gi|58530840	**Score:**	52.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	331.6
Database Date:	2015-11-30	**pI:**	6.4
		Sequence Coverage [%]:	1.7
		No. of unique Peptides:	2

Quantitation

mdown:qdown	**Median:** 1.44	**CV:** 0.00 %	**No. of Peptides:** 1

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

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2423	1	837.8362	-126.41	2	60.6	16.4	2	1545-1558	R.VSQERTVKDQDITR.F		
1485	1	600.4356	127.57	2	47.3	10.5	2	1819-1828	K.IKVLEQDKAR.L		mdown:qdown 1.44

Detailed Protein Report

Protein 100: **guanine nucleotide-binding protein-like 3-like protein [Homo sapiens]**

Accession:	gi|9506611	**Score:**	51.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	65.5
Database Date:	2015-11-30	**pI:**	9.5
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	10.1
		No. of unique Peptides:	2

Alias proteins:

Accession	Name	Description
gi|296317324	refseq_human (refseq_human_20140103.fasta)	guanine nucleotide-binding protein-like 3-like protein [Homo sapiens]

10	20	30	40	50	60	70	80
MMKLRHKNKK	PGEGSKGHKK	ISWPYPQPAK	QNGKKATSKV	PSAPHFVHPN	DHANREAELK	KKWVEEMREK	QQAAREQERQ
90	100	110	120	130	140	150	160
KRRTIESYCQ	DVLRRQEEFE	HKEEVLQELN	MFPQLDDEAT	RKAYYKEFRK	VVEYSDVILE	VLDARDPLGC	RCFQMEEAVL
170	180	190	200	210	220	230	240
RAQGNKKLVL	VLNKIDLVPK	EVVEKWLDYL	RNELPTVAFK	ASTQHQVKNL	NRCSVPVDQA	SESLLKSKAC	FGAENLMRVL
250	260	270	280	290	300	310	320
GNYCRLGEVR	THIRVGVVGL	PNVGKSSLIN	SLKRSRACSV	GAVPGITKFM	QEVYLDKFIR	LLDAPGIVPG	PNSEVGTILR
330	340	350	360	370	380	390	400
NCVHVQKLAD	PVTPVETILQ	RCNLEEISNY	YGVSGFQTTE	HFLTAVAHRL	GKKKKGGLYS	QEQAAKAVLA	DWVSGKISFY
410	420	430	440	450	460	470	480
IPPPATHTLP	THLSAEIVKE	MTEVFDIEDT	EQANEDTMEC	LATGESDELL	GDTDPLEMEI	KLLHSPMTKI	ADAIENKTTV
490	500	510	520	530	540	550	560
YKIGDLTGYC	TNPNRHQMGW	AKRNVDHRPK	SNSMVDVCSV	DRRSVLQRIM	ETDPLQQGQA	LASALKNKKK	MQKRADKIAS
570	580	590					
KLSDSMMSAL	DLSGNADDGV	GD					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2071	1	1023.8928	-74.38	2	54.5	11.7	1	229-245	K.ACFGAENLMRVLGNYCR.L	Carbamidomethyl: 2, 16; Oxidation: 9
2097	1	701.2282	-87.20	3	56.4	10.9	0	562-582	K.LSDSMMSALDLSGNADDGVGD.-	Oxidation: 5, 6

Detailed Protein Report

Protein 101: PREDICTED: tetratricopeptide repeat protein 13 isoform X7 [Homo sapiens]

Accession:	gi|578802328	**Score:**	51.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	57.4
Database Date:	2015-11-30	**pI:**	9.3
		Sequence Coverage [%]:	10.8
		No. of unique Peptides:	3

Quantitation

mdown:qdown	**Median:**	2.05	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	5.78	**CV:**	0.00 %	**No. of 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	Ratios
1705	1	820.8385	-139.02	2	49.9	10.6	1	234-247	R.SLSRGFNNHINLIR.G		
549	2	730.3654	19.41	2	36.2	15.9	0	328-340	K.EYDGFTITITGDK.V		Wdown:Qdown 5.78 mdown:qdown 2.05
2198	1	905.3670	-138.71	2	56.0	12.3	0	410-428	R.GSSVIAYSVIVGALMASGK.E		

Detailed Protein Report

Protein 102: PREDICTED: ubiquitin-protein ligase E3C isoform X3 [Homo sapiens]

Accession:	gi|530387311	**Score:**	51.9
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:	4

Quantitation

mdown:qdown **Median:** 1.08 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MFSFEGDFKT RPKVSLGGAS RKEEKASLLH RTQEERRKRE EERRRLKNAI IIQSFIRGYR DRKQQYSIQR SAFDRCATLS
        90        100        110        120        130        140        150        160
QSGGAFPIAN GPNLTLLVRQ LLFFYKQNED SKRLIWLYQN LIKHSSLFVK QLDGSERLTC LFQIKRLMSL CCRLLQNCND
       170        180        190        200        210        220        230        240
DSLNVALPMR MLEVFSSENT YLPVLQDASY VVSVIEQILH YMIHNGYYRS LYLLINSKLP SSIEYSDLSR VPIAKILLEN
       250        260        270        280        290        300        310        320
VLKPLHFTYN SCPEGARQQV FTAFTEEFLA APFTDQIFHF IIPALADAQT VFPYEPFLNA LLLIESRCSR KSGGAPWLFY
       330        340        350        360        370        380        390        400
FVLTVGENYL GALSEEGLLV YLRVLQTFLS QLPVSPASAS CHDSASDSEE ESEEADKPSS PEDGRLSVSY ITEECLKKLD
       410        420        430        440        450        460        470        480
TKQQTNTLLN LVWRDSASEE VFTTMASVCH TLMVQHRMMV PKVRLLYSLA FNARFLRHLW FLISSMSTRM ITGSMVPLLQ
       490        500        510        520        530        540        550        560
VISRGSPMSF EDSSRIIPLF YLFSSLFSHS LISIHDNEFF GDPIEVVGQR QSSMMPFTLE ELIMLSRCLR DACLGIIKLA
       570        580        590        600        610        620        630        640
YPETKPEVRE EYITAFQSIG VTTSSEMQQC IQMEQKRWIQ LFKVITNLVK MLKSRDTRRN FCPPNHWLSE QEDIKADKIF
       650        660        670        680        690        700        710        720
QRLIYADKQE VQGDGPFLDG INVTIRRNYI YEDAYDKLSP ENEPDLKKRI RVHLLNAHGL DEAGIDGGGI FREFLNELLK
       730        740        750        760        770        780        790        800
SGFNPNQGFF KTTNEGLLYP NPAAQMLVGD SFARHYYFLG RMLGKALYEN MLVELPFAGF FLSKLLGTSA DVDIHHLASL
       810        820        830        840        850        860        870        880
DPEVYKNLLF LKSYEDDVEE LGLNFTVVNN DLGEAQVVEL KFGGKDIPVT SANRIAYIHL VADYRLNRQI RQHCLAFRQG
       890        900        910        920        930        940        950        960
LANVVSLEWL RMFDQQEIQV LISGAQVPIS LEDLKSFTNY SGGYSADHPV IKVFWRVVEG FTDEEKRKLL KFVTSCSRPP
       970        980        990       1000       1010       1020       1030
LLGFKELYPA FCIHNGGSDL ERLPTASTCM NLLKLPEFYD ETLLRSKLLY AIECAAGFEL S
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2476	4	817.2871	-207.41	1	61.3	12.6	0	124-130	K.HSSLFVK.Q		mdown:qdown 1.08
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	
2795	1	874.5325	111.23	1	64.0	11.6	0	872-878	R.QHCLAFR.Q		

Detailed Protein Report

Protein 103: PREDICTED: neuron navigator 2 isoform X5 [Homo sapiens]

Accession:	gi|578820908	**Score:**	51.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	264.1
Database Date:	2015-11-30	**pI:**	9.8
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	2.0
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MPAILVASKM	KSGLPKPVHS	AAPILHVPPA	RAGPQPCYLK	LGSKVEVSKT	TYPSQIPLKS	QVLQGLQEPA	GEGLPLRKSG
90	100	110	120	130	140	150	160
SVENGFDTQI	YTDWANHYLA	KSGHKRLIRD	LQQDVTDGVL	LAQIIQVVAN	EKIEDINGCP	KNRSQMIENI	DACLNFLAAK
170	180	190	200	210	220	230	240
GINIQGLSAE	EIRNGNLKAI	LGLFFSLSRY	KQQQQQPQKQ	HLSSPLPPAV	SQVAGAPSQC	QAGTPQQQVP	VTPQAPCQPH
250	260	270	280	290	300	310	320
QPAPHQQSKA	QAEMQSSASS	KDSSQSKIIR	FTLGQKKISR	LPGPTARVSA	AGSEAKTRGG	STTANNRRSQ	SFNNYDKSKP
330	340	350	360	370	380	390	400
VTSPPPPPSS	HEKEPLASSA	SSHPGMSDNA	PASLESGSSS	TPTNCSTSSA	IPQPGAATKP	WRSKSLSVKH	SATVSMLSVK
410	420	430	440	450	460	470	480
PPGPEAPRPT	PEAMKPAPNN	QKSMLEKLKL	FNSKGGSKAG	EGPGSRDTSC	ERLETLPSFE	ESEELEAASR	MLTTVGPASS
490	500	510	520	530	540	550	560
SPKIALKGIA	QRTFSRALTN	KKSSLKGNEK	EKEKQQREKD	KEKSKDLAKR	ASVTERLDLK	EEPKEDPSGA	AVPEMPKKSS
570	580	590	600	610	620	630	640
KIASFIPKGG	KLNSAKKEPM	APSHSGIPKP	GMKSMPGKSP	SAPAPSKEGE	RSRSGKLSSG	LPQQKPQLDG	RHSSSSSSLA
650	660	670	680	690	700	710	720
SSEGKGPGGT	TLNHSISSQT	VSGSVGTTQT	TGSNTVSVQL	PQPQQQYNHP	NTATVAPFLY	RSQTDTEGNV	TAESSSTGVS
730	740	750	760	770	780	790	800
VEPSHFTKTG	QPALEELTGE	DPEARRLRTV	KNIADLRQNL	EETMSSLRGT	QVTHSTLETT	FDTNVTTEMS	GRSILSLTGR
810	820	830	840	850	860	870	880
PTPLSWRLGQ	SSPRLQAGDA	PSMGNGYPPR	ANASRFINTE	SGRYVYSAPL	RRQLASRGSS	VCHVDVSDKA	GDEMDLEGIS
890	900	910	920	930	940	950	960
MDAPGYMSDG	DVLSKNIRTD	DITSGYMTDG	GLGLYTRRLN	RLPDGMAVVR	ETLQRNTSLG	LGDADSWDDS	SSVSSGISDT
970	980	990	1000	1010	1020	1030	1040
IDNLSTDDIN	TSSSISSYAN	TPASSRKNLD	VQTDAEKHSQ	VERNSLWSGD	DVKKSDGGSD	SGIKMEPGSK	WRRNPSDVSD
1050	1060	1070	1080	1090	1100	1110	1120
ESDKSTSGKK	NPVISQTGSW	RRGMTAQVGI	TMPRTKPSAP	AGALKTPGTG	KTDDAKVSEK	GRLSPKASQV	KRSPSDAGRS
1130	1140	1150	1160	1170	1180	1190	1200
SGDESKKPLP	SSSRTPTANA	NSFGFKKQSG	SAAGLAMITA	SGVTVTSRSA	TLGKIPKSSA	LVSRSAGRKS	SMDGAQNQDD
1210	1220	1230	1240	1250	1260	1270	1280
GYLALSSRTN	LQYRSLPRPS	KSNSRNGAGN	RSSTSSIDSN	ISSKSAGLPV	PKLREPSKTA	LGSSLPGLVN	QTDKEKGISS
1290	1300	1310	1320	1330	1340	1350	1360
DNESVASCNS	VKVNPAAQPV	SSPAQTSLQP	GAKYPDVASP	TLRRLFGGKP	TKQVPIATAE	NMKNSVVISN	PHATMTQQGN
1370	1380	1390	1400	1410	1420	1430	1440
LDSPSGSGVL	SSGSSSPLYS	KNVDLNQSPL	ASSPSSAHSA	PSNSLTWGTN	ASSSSAVSKD	GLGFQSVSSL	HTSCESIDIS
1450	1460	1470	1480	1490	1500	1510	1520
LSSGGVPSHN	SSTGLIASSK	DDSLTPFVRT	NSVKTTLSES	PLSSPAASPK	FCRSTLPRKQ	DSDPHLDRNT	LPKKGLRYTP
1530	1540	1550	1560	1570	1580	1590	1600
TSQLRTQEDA	KEWLRSHSAG	GLQDTAANSP	FSSGSSVTSP	SGTRFNFSQL	ASPTTVTQMS	LSNPTMLRTH	SLSNADGQYD
1610	1620	1630	1640	1650	1660	1670	1680
PYTDSRFRNS	SMSLDEKSRT	MSRSGSFRDG	FEEVHGSSLS	LVSSTSSVYS	TPEEKCQSEI	RKLRRELDAS	QEKVSALTTQ
1690	1700	1710	1720	1730	1740	1750	1760
LTANAHLVAA	FEQSLGNMTI	RLQSLTMTAE	QKDSELNELR	KTIELLKKQN	AAAQAAINGV	INTPELNCKG	NGTAQSADLR
1770	1780	1790	1800	1810	1820	1830	1840
IRRQHSSDSV	SSINSATSHS	SVGSNIESDS	KKKKRKNWVN	ELRSSFKQAF	GKKKSPKSAS	SHSDIEEMTD	SSLPSSPKLP
1850	1860	1870	1880	1890	1900	1910	1920
HNGSTGSTPL	LRNSHSNSLI	SECMDSEAET	VMQLRNELRD	KEMKLTDIRL	EALSSAHQLD	QLREAMNRMQ	SEIEKLKAEN
1930	1940	1950	1960	1970	1980	1990	2000
DRLKSESQGS	GCSRAPSQVS	ISASPRQSMG	LSQHSLNLTE	STSLDMLLDD	TGECSARKEG	GRHVKIVVSF	QEEMKWKEDS
2010	2020	2030	2040	2050	2060	2070	2080
RPHLFLIGCI	GVSGKTKWDV	LDGVVRRLFK	EYIIHVDPVS	QLGLNSDSVL	GYSIGEIKRS	NTSETPELLP	CGYLVGENTT
2090	2100	2110	2120	2130	2140	2150	2160
ISVTVKGLAE	NSLDSLVFES	LIPKPILQRY	VSLLIEHRRI	ILSGPSGTGK	TYLANRLSEY	IVLREGRELT	DGVIATFNVD
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	435-452	K.GGSKAGEGPGSRDTSCER.L	Carbamidomethyl: 16
2463	1	647.1849	-205.84	2	61.2	24.0	0	1063-1074	R.GMTAQVGITMPR.T	Oxidation: 2, 10

Detailed Protein Report

Protein 104: Alstrom syndrome protein 1 [Homo sapiens]

Accession:	gi|110349786	**Score:**	51.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	460.9
Database Date:	2015-11-30	**pI:**	5.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.3
		No. of unique Peptides:	2

Detailed Protein Report

```
        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
312	1	862.8548	-22.20	2	33.0	10.7	1	340-352	R.YDDLCSYMSWKTR.K	Carbamidomethyl: 5
1836	4	863.4125	-60.24	2	51.6	18.6	1	3791-3805	R.LIQAFGHERVCLSPR.R	

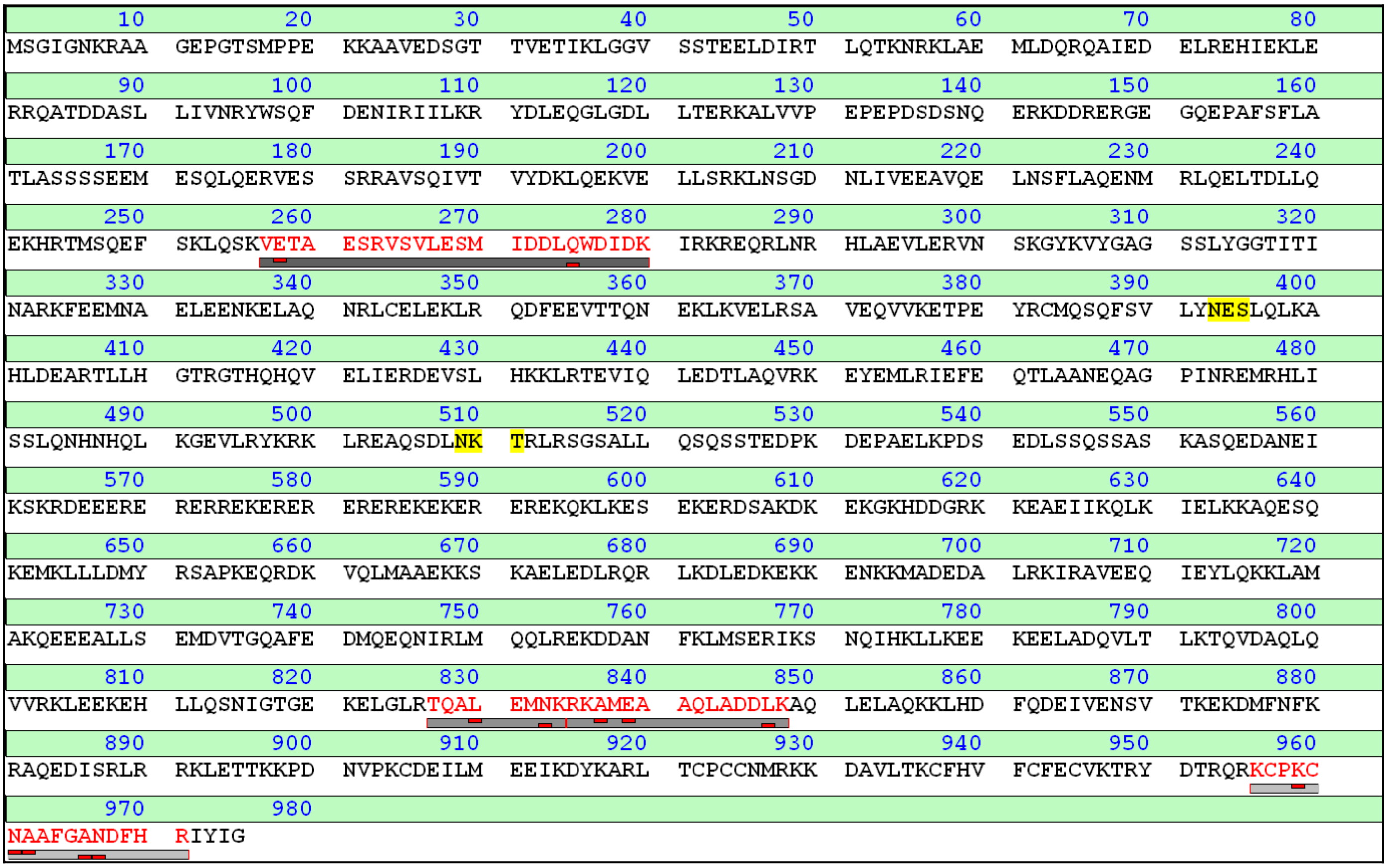
Detailed Protein Report

Protein 105: E3 ubiquitin-protein ligase BRE1A [Homo sapiens]

Accession:	gi|34878777	**Score:**	51.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	113.6
Database Date:	2015-11-30	**pI:**	5.6
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	6.4
		No. of unique Peptides:	4

Quantitation

mdown:qdown	**Median:**	1.17	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	3.32	**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
1337	1	926.7938	6.01	3	45.5	12.7	1	257-280	K.VETAESRVSVLESMIDDLQWDIDK.I		
463	1	475.6020	-277.84	2	35.1	11.6	0	827-834	R.TQALEMNK.R	Oxidation: 6	Wdown:Qdown 3.32 mdown:qdown 1.17
2961	1	788.3914	-25.63	2	65.8	15.7	2	835-848	K.RKAMEAAQLADDLK.A	Oxidation: 4	
1898	1	918.3471	-84.86	2	52.4	11.4	2	956-971	R.KCPKCNAAFGANDFHR.I	Carbamidomethyl: 5	

Detailed Protein Report

Protein 106: **protein FAM115C isoform B [Homo sapiens]**

Accession:	gi|293651621	**Score:**	51.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	90.6
Database Date:	2015-11-30	**pI:**	8.9
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.8
		No. of unique Peptides:	4

Quantitation

mdown:qdown	**Median:**	1.85	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.60	**CV:**	0.00 %	**No. of Peptides:**	2

```
        10         20         30         40         50         60         70         80
MKIFQKEFKF ILKKCTPIQK YREENGNSSS SPHHQLQSHA SGPRYGEDVR QDQQQLLEGI SELDIRTGGV PSQLLVHGAL
        90        100        110        120        130        140        150        160
AFPLGLDASL NCFLAAAHYG RGRVVLAAHE CLLCAPKMGP FLLNAVRWLA RGQTGKVGVN TNLKDLCPLL SEHGLQCSLE
       170        180        190        200        210        220        230        240
PHLNSDLCVY CCKAYSDKEA KQLQEFVAEG GGLLIGGQAW WWASQNPGHC PLAGFPGNII LNCFGLSILP QTLKAGCFPV
       250        260        270        280        290        300        310        320
PTPEMRSYHF RKALSQFQAI LNHENGNLEK SCLAKLRVDG AAFLQIPAEG VPAYISLHRL LRKMLRGSGL PAVSRENPVA
       330        340        350        360        370        380        390        400
SDSYEAAVLS LATGLAHSGT DCSQLAQGLG TWTCSSSLYP SKHPITVEIN GINPESHSVI QVGMQWRDLS SCNLHLLGLS
       410        420        430        440        450        460        470        480
NSSLSASCVA GTTGTRHHAW LIFVFLVERE FHRKGNNDCW VSTGLYLLEG QNAEVSLSEA AASAGLRVQI GCHTDDLTKA
       490        500        510        520        530        540        550        560
RKLSRAPVVT HQCWMDRTER SVSCLWGGLL YVIVPKGSQL GPVPVTIRGA VPAPYYKLGK TSLEEWKRQM QENLAPWGEL
       570        580        590        600        610        620        630        640
ATDNIILTVP TTNLQALKDP EPVLRLWDEM MQAVARLAAE PFPFRRPERI VADVQISAGW MHSGYPIMCH LESVKEIINE
       650        660        670        680        690        700        710        720
MDMRSRGVWG PIHELGHNQQ RHGWEFPPHT TEATCNLWSV YVHETVLGIP RAQAHEALSP PERERRIKAH LGKGAPLCDW
       730        740        750        760        770        780        790        800
NVWTALETYL QLQEAFGWEP FTQLFAEYQT LSHLPKDNTG RMNLWVKKFS EKVKKNLVPF FEAWGWPIQK EVADSLASLP
       810        820
EWQENPMQVY LRARK
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
7	1	689.3232	-60.71	1	29.3	10.0	0	15-20	K.CTPIQK.Y		
126	1	822.3680	-116.44	2	30.8	17.1	1	118-131	K.MGPFLLNAVRWLAR.G		
495	2	705.1921	-194.39	2	35.1	10.8	1	636-646	K.EIINEMDMRSR.G	Oxidation: 6	Wdown:Qdown 0.60
738	2	705.1981	-185.90	2	37.8	13.4	1	636-646	K.EIINEMDMRSR.G	Oxidation: 8	Wdown:Qdown 0.60

Detailed Protein Report

Protein 107: **PREDICTED: unhealthy ribosome biogenesis protein 2 homolog isoform X1 [Homo sapiens]**

Accession:	gi|530366678	**Score:**	51.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	166.5
Database Date:	2015-11-30	**pI:**	6.9
		Sequence Coverage [%]:	2.6
		No. of unique Peptides:	1

Quantitation

mdown:qdown **Median:** 1.55 **CV:** 0.00 % **No. of 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	Ratios
598	1	661.8686	26.39	2	36.8	13.9	2	12-22	K.LKSKTTSWEDK.L		mdown:qdown 1.55

Detailed Protein Report

Protein 108: PREDICTED: serine/threonine-protein kinase 31 isoform X3 [Homo sapiens]

Accession:	gi|578813577	**Score:**	51.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	95.7
Database Date:	2015-11-30	**pI:**	4.8
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	4.2
		No. of unique Peptides:	3

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
452	1	524.1225	-252.65	2	34.6	17.8	0	551-559	R.DLLDAEPMK.E	Oxidation: 8
249	3	592.1348	-240.88	2	32.3	18.3	0	581-591	K.GYSVDVDTEAK.V	
2669	1	948.3641	-79.89	2	64.6	15.1	2	817-831	K.EEEIKTENLDKCMEK.T	Carbamidomethyl: 12

Detailed Protein Report

Protein 109: Fanconi anemia group I protein isoform 2 [Homo sapiens]

Accession:	gi|82830440	**Score:**	51.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	142.5
Database Date:	2015-11-30	**pI:**	6.3
		Sequence Coverage [%]:	3.3
		No. of unique Peptides:	3

Quantitation

mdown:qdown	**Median:**	1.85	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	1.67	**CV:**	0.00 %	**No. of Peptides:**	1

10	20	30	40	50	60	70	80
MDQKILSLAA	EKTADKLQEF	LQTLREGDLT	NLLQNQAVKG	KVAGALLRAI	FKGSPCSEEA	GTLRRRKIYT	CCIQLVESGD
90	100	110	120	130	140	150	160
LQKEIASEII	GLLMLEAHHF	PGPLLVELAN	EFISAVREGS	LVNGKSLELL	PIILTALATK	KENLAYGKGV	LSGEECKKQL
170	180	190	200	210	220	230	240
INTLCSGRWD	QQYVIQLTSM	FKDVPLTAEE	VEFVVEKALS	MFSKMNLQEI	PPLVYQLLVL	SSKGSRKSVL	EGIIAFFSAL
250	260	270	280	290	300	310	320
DKQHNEEQSG	DELLDVVTVP	SGELRHVEGT	IILHIVFAIK	LDYELGRELV	KHLKVGQQGD	SNNNLSPFSI	ALLLSVTRIQ
330	340	350	360	370	380	390	400
RFQDQVLDLL	KTSVVKSFKD	LQLLQGSKFL	QNLVPHRSYV	STMILEVVKN	SVHSWDHVTQ	GLVELGFILM	DSYGPKKVLD
410	420	430	440	450	460	470	480
GKTIETSPSL	SRMPNQHACK	LGANILLETF	KIHEMIRQEI	LEQVLNRVVT	RASSPISHFL	DLLSNIVMYA	PLVLQSCSSK
490	500	510	520	530	540	550	560
VTEAFDYLSF	LPLQTVQRLL	KAVQPLLKVS	MSMRDCLILV	LRKAMFANQL	DARKSAVAGF	LLLLKNFKVL	GSLSSSQCSQ
570	580	590	600	610	620	630	640
SLSVSQVHVD	VHSHYNSVAN	ETFCLEIMDS	LRRCLSQQAD	VRLMLYEGFY	DVLRRNSQLA	NSVMQTLLSQ	LKQFYEPKPD
650	660	670	680	690	700	710	720
LLPPLKLEAC	ILTQGDKISL	QEPLDYLLCC	IQHCLAWYKN	TVIPLQQGEE	EEEEEEAFYE	DLDDILESIT	NRMIKSELED
730	740	750	760	770	780	790	800
FELDKSADFS	QSTSIGIKNN	ICAFLVMGVC	EVLIEYNFSI	SSFSKNRFED	ILSLFMCYKK	LSDILNEKAG	KAKTKMANKT
810	820	830	840	850	860	870	880
SDSLLSMKFV	SSLLTALFRV	LLWRYTSIPT	SVEESGKKEK	GKSISLLCLE	GLQKIFSAVQ	QFYQPKIQQF	LRALDVTDKE
890	900	910	920	930	940	950	960
GEEREDADVS	VTQRTAFQIR	QFQRSLLNLL	SSQEEDFNSK	EALLLVTVLT	SLSKLLEPSS	PQFVQMLSWT	SKICKENSRE
970	980	990	1000	1010	1020	1030	1040
DALFCKSLMN	LLFSLHVSYK	SPVILLRDLS	QDIHGHLGDI	DQDVEVEKTN	HFAIVNLRTA	APTVCLLVLS	QAEKVLEEVD
1050	1060	1070	1080	1090	1100	1110	1120
WLITKLKGQV	SQETLSEEAS	SQATLPNQPV	EKAIIMQLGT	LLTFFHELVQ	TALPSGSCVD	TLLKDLCKMY	TTLTALVRYY
1130	1140	1150	1160	1170	1180	1190	1200
LQVCQSSGGI	PKNMEKLVKL	SGSHLTPLCY	SFISYVQNKS	KSLNYTGEKK	EKPAAVATAM	ARVLRETKPI	PNLIFAIEQY
1210	1220	1230	1240	1250	1260	1270	
EKFLIHLSKK	SKVNLMQHMK	LSTSRDFKIK	GNILDMVLRE	DGEDENEEGT	ASEHGGQNKE	PAKKKRKK	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
426	3	658.3901	11.29	2	34.4	22.4	2	780-791	K.KLSDILNEKAGK.A		
1909	2	918.3239	-154.66	2	52.5	13.3	1	885-900	R.EDADVSVTQRTAFQIR.Q		
13	1	814.3623	-84.24	2	29.4	15.2	1	1105-1118	K.DLCKMYTTLTALVR.Y		Wdown:Qdown 1.67 mdown:qdown 1.85

Detailed Protein Report

Protein 110: **PREDICTED: histone-lysine N-methyltransferase 2A isoform X2 [Homo sapiens]**

Accession:	gi|578822197	**Score:**	51.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	292.4
Database Date:	2015-11-30	**pI:**	6.6
		Sequence Coverage [%]:	1.3
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MSRPLGLNPN	RPPLQLPGSQ	ASRSPSQHWS	SRLSHLLQDR	QEKKFPKPLL	VSPRKSSLHH	QNQEKPPPVN	KQENAGTLNI
90	100	110	120	130	140	150	160
LSTLSNGNSS	KQKIPADGVH	RIRVDFKEDC	EAENVWEMGG	LGILTSVPIT	PRVVCFLCAS	SGHVEFVYCQ	VCCEPFHKFC
170	180	190	200	210	220	230	240
LEENERPLED	QLENWCCRRC	KFCHVCGRQH	QATKQLLECN	KCRNSYHPEC	LGPNYPTKPT	KKKKVWICTK	CVRCKSCGST
250	260	270	280	290	300	310	320
TPGKGWDAQW	SHDFSLCHDC	AKLFAKGNFC	PLCDKCYDDD	DYESKMMQCG	KCDRWVHSKC	ENLSGTEDEM	YEILSNLPES
330	340	350	360	370	380	390	400
VAYTCVNCTE	RHPAEWRLAL	EKELQISLKQ	VLTALLNSRT	TSHLLRYRQA	AKPPDLNPET	EESIPSRSSP	EGPDPPVLTE
410	420	430	440	450	460	470	480
VSKQDDQQPL	DLEGVKRKMD	QGNYTSVLEF	SDDIVKIIQA	AINSDGGQPE	IKKANSMVKS	FFIRQMERVF	PWFSVKKSRF
490	500	510	520	530	540	550	560
WEPNKVSSNS	GMLPNAVLPP	SLDHNYAQWQ	EREENSHTEQ	PPLMKKIIPA	PKPKGPGEPD	SPTPLHPPTP	PILSTDRSRE
570	580	590	600	610	620	630	640
DSPELNPPPG	IEDNRQCALC	LTYGDDSAND	AGRLLYIGQN	EWTHVNCALW	SAEVFEDDDG	SLKNVHMAVI	RGKQLRCEFC
650	660	670	680	690	700	710	720
QKPGATVGCC	LTSCTSNYHF	MCSRAKNCVF	LDDKKVYCQR	HRDLIKGEVV	PENGFEVFRR	VFVDFEGISL	RRKFLNGLEP
730	740	750	760	770	780	790	800
ENIHMMIGSM	TIDCLGILND	LSDCEDKLFP	IGYQCSRVYW	STTDARKRCV	YTCKIVECRP	PVVEPDINST	VEHDENRTIA
810	820	830	840	850	860	870	880
HSPTSFTESS	SKESQNTAEI	ISPPSPDRPP	HSQTSGSCYY	HVISKVPRIR	TPSYSPTQRS	PGCRPLPSAG	SPTPTTHEIV
890	900	910	920	930	940	950	960
TVGDPLLSSG	LRSIGSRRHS	TSSLSPQRSK	LRIMSPMRTG	NTYSRNNVSS	VSTTGTATDL	ESSAKVVDHV	LGPLNSSTSL
970	980	990	1000	1010	1020	1030	1040
GQNTSTSSNL	QRTVVTVGNK	NSHLDGSSSS	EMKQSSASDL	VSKSSSLKGE	KTKVLSSKSS	EGSAHNVAYP	GIPKLAPQVH
1050	1060	1070	1080	1090	1100	1110	1120
NTTSRELNVS	KIGSFAEPSS	VSFSSKEALS	FPHLHLRGQR	NDRDQHTDST	QSANSSPDED	TEVKTLKLSG	MSNRSSIINE
1130	1140	1150	1160	1170	1180	1190	1200
HMGSSSRDRR	QKGKKSCKET	FKEKHSSKSF	LEPGQVTTGE	EGNLKPEFMD	EVLTPEYMGQ	RPCNNVSSDK	IGDKGLSMPG
1210	1220	1230	1240	1250	1260	1270	1280
VPKAPPMQVE	GSAKELQAPR	KRTVKVTLTP	LKMENESQSK	NALKESSPAS	PLQIESTSPT	EPISASENPG	DGPVAQPSPN
1290	1300	1310	1320	1330	1340	1350	1360
NTSCQDSQSN	NYQNLPVQDR	NLMLPDGPKP	QEDGSFKRRY	PRRSARARSN	MFFGLTPLYG	VRSYGEEDIP	FYSSSTGKKR
1370	1380	1390	1400	1410	1420	1430	1440
GKRSAEGQVD	GADDLSTSDE	DDLYYYNFTR	TVISSGGEER	LASHNLFREE	EQCDLPKISQ	LDGVDDGTES	DTSVTATTRK
1450	1460	1470	1480	1490	1500	1510	1520
SSQIPKRNGK	ENGTENLKID	RPEDAGEKEH	VTKSSVGHKN	EPKMDNCHSV	SRVKTQGQDS	LEAQLSSLES	SRRVHTSTPS
1530	1540	1550	1560	1570	1580	1590	1600
DKNLLDTYNT	ELLKSDSDNN	NSDDCGNILP	SDIMDFVLKN	TPSMQALGES	PESSSSELLN	LGEGLGLDSN	REKDMGLFEV
1610	1620	1630	1640	1650	1660	1670	1680
FSQQLPTTEP	VDSSVSSSIS	AEEQFELPLE	LPSDLSVLTT	RSPTVPSQNP	SRLAVISDSG	EKRVTITEKS	VASSESDPAL
1690	1700	1710	1720	1730	1740	1750	1760
LSPGVDPTPE	GHMTPDHFIQ	GHMDADHISS	PPCGSVEQGH	GNNQDLTRNS	STPGLQVPVS	PTVPIQNQKY	VPNSTDSPGP
1770	1780	1790	1800	1810	1820	1830	1840
SQISNAAVQT	TPPHLKPATE	KLIVVNQNMQ	PLYVLQTLPN	GVTQKIQLTS	SVSSTPSVME	TNTSVLGPMG	GGLTLTTGLN
1850	1860	1870	1880	1890	1900	1910	1920
PSLPTSQSLF	PSASKGLLPM	SHHQHLHSFP	AATQSSFPPN	ISNPPSGLLI	GVQPPPDPQL	LVSESSQRTD	LSTTVATPSS
1930	1940	1950	1960	1970	1980	1990	2000
GLKKRPISRL	QTRKNKKLAP	SSTPSNIAPS	DVVSNMTLIN	FTPSQLPNHP	SLLDLGSLNT	SSHRTVPNII	KRSKSSIMYF
2010	2020	2030	2040	2050	2060	2070	2080
EPAPLLPQSV	GGTAATAAGT	STISQDTSHL	TSGSVSGLAS	SSSVLNVVSM	QTTTTPTSSA	SVPGHVTLTN	PRLLGTPDIG
2090	2100	2110	2120	2130	2140	2150	2160
SISNLLIKAS	QQSLGIQDQP	VALPPSSGMF	PQLGTSQTPS	TAAITAASSI	CVLPSTQTTG	ITAASPSGEA	DEHYQLQHVN
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
11	1	820.3475	-49.73	1	29.3	12.9	1	2443-2448	K.HCRNYK.F	
2967	2	753.3836	9.44	2	66.3	16.1	1	2476-2488	R.KSAFDMFNFLASK.H	

Detailed Protein Report

Protein 111: mucin-19 precursor [Homo sapiens]

Accession:	gi|533112494	**Score:**	50.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	804.8
Database Date:	2015-11-30	**pI:**	4.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	0.9
		No. of unique Peptides:	3

```
        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
```

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2638	1	937.4152	-21.95	2	61.7	11.6	2	1085-1100	K.YNVKACNSSCRSLSER.D	Carbamidomethyl: 10
1442	1	1061.4940	-55.50	2	47.8	12.0	1	6074-6097	R.SSAGVTGTTGLSAKSGTSIPSAGK.T	
2090	1	1131.3695	-118.05	2	56.3	11.2	1	8209-8227	K.LVKFQSNDTCCEIGYCEPR.T	Carbamidomethyl: 10

BRUKER

Detailed Protein Report

Protein 112: sorting nexin-8 [Homo sapiens]

Accession:	gi|23943858	**Score:**	50.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	52.5
Database Date:	2015-11-30	**pI:**	7.2
Modification(s):	Oxidation	**Sequence Coverage [%]:**	9.2
		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 113: PREDICTED: nesprin-2 isoform X6 [Homo sapiens]

Accession:	gi|530403362	**Score:**	50.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	795.8
Database Date:	2015-11-30	**pI:**	5.1
		Sequence Coverage [%]:	0.7
		No. of unique Peptides:	3

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
289	1	715.8764	45.86	2	32.3	10.0	0	1817-1828	K.QYESVSDLFNTK.K	
2908	1	922.9773	-1.53	2	65.5	11.3	1	3576-3590	K.ELVQTEIQERHSFTK.E	
1518	1	882.6077	144.13	2	48.8	11.3	2	3618-3632	K.SEQFEELQSILKKGK.L	

Detailed Protein Report

Protein 114: dynein heavy chain 6, axonemal [Homo sapiens]

Accession:	gi|194353966	**Score:**	50.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	475.7
Database Date:	2015-11-30	**pI:**	5.6
		Sequence Coverage [%]:	1.3
		No. of unique Peptides:	3

Alias proteins:

Accession	**Name**	**Description**
gi|578802753	refseq_human (refseq_human_20140103.fasta)	PREDICTED: dynein heavy chain 6, axonemal isoform X1 [Homo sapiens]

Detailed Protein Report

10	20	30	40	50	60	70	80
MTFRATDSEF	DLTNIEEYAE	NSALSRLNNI	KAKQRVSYVT	STENESDTQI	LTFRHITKAQ	EKTRKRQQPI	KLEPLPVLKV
90	100	110	120	130	140	150	160
YQDHKQPEYI	HEQNRFQLMT	AGIIKRPVSI	AKKSFATSST	QFLEHQDAVK	KMQIHRPYVE	VFSPSPPKLP	HTGIGKRGLF
170	180	190	200	210	220	230	240
GTRSSAYPKY	TFHDREEVVK	ANIRDPLQII	KIIRENEHLG	FLYMIPAVPR	SSIEYDTYNL	KVVSYENINK	NDYYTISQRA
250	260	270	280	290	300	310	320
VTHIYNEDIE	FIEIDRWEQE	YLYHRELTKI	PIFSLFRKWK	AFSVWRKNVR	SKKITGCQKS	LQKNLFIVNP	HLRPALLKIN
330	340	350	360	370	380	390	400
ELCYHLSFMG	LCYIEKCHTY	TLQEFKAAQV	IRLAEVTERL	GEFRNEAKYV	VRRACRFALR	AAGFVPDDCA	FGPFEDYHKV
410	420	430	440	450	460	470	480
QSSGSFINTP	HELPTYGDSE	KMTYTEQASK	RHYCMRLTCF	IRLNDYLIEN	TMHILTVNAV	NSLLNHLTDK	LKRTPSADVI
490	500	510	520	530	540	550	560
QKWITEEKPE	VPDKKGTLMV	EKQEEDESLI	PMFLTELMLT	VQSLLFEPSL	EDFLDGILGA	VNHCQNTVLS	VPNLVPDSYF
570	580	590	600	610	620	630	640
DAFTSPYINN	KLEGKTCGTG	PSLAAVFEDD	KNFHTIISQI	KETIQAAFES	ARIYAATFEK	FQIFFKENES	LDLQALKLQE
650	660	670	680	690	700	710	720
PDINFFSEQL	EKYHKQHKDA	VALRPTRNVG	LLLIDTRLLR	EKLIPSPLRC	LEVLNFMLPR	QSKKKVDAII	FEAQDAEYKL
730	740	750	760	770	780	790	800
EFVPTTTTEY	VHSLLFLDEI	QERIESLEDE	GNIVTQMYKL	MEQYQVPTPP	EDFAVFATMK	PSIVAVRNAI	DKSVGDRESS
810	820	830	840	850	860	870	880
IKQFCVHLGS	DLEELNNEVN	EVKLQAQDPQ	ILDISADQDK	IRLILNNLQS	VLADLQKRAF	QYKSYQKNFK	VEVSKFEALE
890	900	910	920	930	940	950	960
EVSAELKLKQ	LLWDSFSEWD	KLQQEWLKSK	FDCLDPEVLN	GQVSKYAKFV	TQLEKGLPPN	SVVPQLKYKV	EKMKEKLPVI
970	980	990	1000	1010	1020	1030	1040
IDLRNPTLKA	RHWAAIEQTV	DATLVDAEIP	LTLERLSQLH	VFDFGQEIQD	ISGQASGEAA	LEAILKKVED	SWKTTEFVIL
1050	1060	1070	1080	1090	1100	1110	1120
PHRDSKDVFI	LGGTDDIQVL	LDDSTINVAT	LASSRYLGPL	KTRVDEWQKQ	LALFNQTLEE	WLTCQRNWLY	LESIFNAPDI
1130	1140	1150	1160	1170	1180	1190	1200
QRQLPAEAKM	FLQVDKSWKE	IMRKVNRLPN	ALRAATQPGL	LETFQNNNAL	LDQIQKCLEA	YLESKRVIFP	RFYFLSNDEL
1210	1220	1230	1240	1250	1260	1270	1280
LEILAQTRNP	QAVQPHLRKC	FDSISKLEFA	LMPPAEGKIP	GIDGEPEKVY	TNDILAMLSP	EGERVSLGKG	LKARGNVEEW
1290	1300	1310	1320	1330	1340	1350	1360
LGKVEEAMFT	SLRRLCKAAI	ADYQGKLRTD	WVVAGHPSQV	ILTVSQIMWC	RDLTECLETE	HSNHIQALKN	FEKVNFERLN
1370	1380	1390	1400	1410	1420	1430	1440
ALAAIVQGSL	PKLHRNILTA	LITIDVHARD	IVTELVQSKV	ETVESFDWQR	QLRYYWDIDL	DNCVARMALS	QYTYGYEYLG
1450	1460	1470	1480	1490	1500	1510	1520
ACPRLVITPL	TDRCYLCLMG	ALQLDLGGAP	AGPAGTGKTE	TTKDLAKALA	IQCVVFNCSD	GLDYKMMGRF	FSGLAQSGAW
1530	1540	1550	1560	1570	1580	1590	1600
CCFDEFNRID	IEVLSVIAQQ	LITIRNAKAA	KLSRFMFEGR	EIKLVMTCAA	FITMNPGYAG	RTELPDNLKA	LFRPFAMMVP
1610	1620	1630	1640	1650	1660	1670	1680
NYALIAEVIL	YSEGFESSKI	LARKMTQMYK	LCSEQLSQQD	HYDFGMRAVK	SVLVMAGSLK	RENPDLNEDV	VLIRALQDSN
1690	1700	1710	1720	1730	1740	1750	1760
LPKFLTDDAL	LFSGIISDLF	PGVQIPEHDY	GILQSTIVDV	MNRQNLQPEM	CMVRKVIQFY	ETMLVRHGVM	LVGPTGGGKT
1770	1780	1790	1800	1810	1820	1830	1840
TVYRILAETL	GNLQKLGIEN	SFYQAVKTYV	LNPKSITMGE	LYGEVNNLTL	EWKDGLMALS	VRAAVNDTSE	DHKWIISDGP
1850	1860	1870	1880	1890	1900	1910	1920
VDALWIENMN	TVLDDNKMLC	LANSERIKLT	PQIHMLFEVQ	DLRVASPATV	SRCGMVFVDP	EELKWMPYVK	TWMKGISKKL
1930	1940	1950	1960	1970	1980	1990	2000
TEETQEYILN	LFQRYVDEGL	HFINKKCSQA	IPQVDISKVT	TLCCLLESLI	LGKDGVNLAM	EQTKLNTILC	QTFVFCYLWS
2010	2020	2030	2040	2050	2060	2070	2080
LGGNLTENYY	DSFDTFIRTQ	FDDNPDARLP	NSGDLWSIHM	DFDTKRLDPW	ERIIPTFKYN	RDVPFFEMLV	PTTDTVRYGY
2090	2100	2110	2120	2130	2140	2150	2160
LMEKLLAVKH	SVLFTGITGV	GKSVIAKGLL	NKIQESAGYV	PVYLNFSAQT	SSARTQEIIE	SKLERKRKNI	LGAPGNKRIV
2170	2180	2190	2200	2210	2220	2230	2240

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2662	1	698.0710	213.61	2	62.1	10.4	0	1359-1372	R.LNALAAIVQGSLPK.L	
2264	1	1011.7667	170.21	1	56.8	10.2	1	2148-2157	R.KNILGAPGNK.R	
2924	1	1015.5128	-43.32	2	65.3	18.0	2	2905-2922	K.LRAAQAELDITMATLREK.Q	

Detailed Protein Report

Protein 115: **PREDICTED: obscurin isoform X31 [Homo sapiens]**

Accession:	gi|578802370	**Score:**	50.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	877.0
Database Date:	2015-11-30	**pI:**	5.6
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	0.7
		No. of unique Peptides:	4

Detailed Protein Report

10	20	30	40	50	60	70	80
MDQPQFSGAP	RFLTRPKAFV	VSVGKDATLS	CQIVGNPTPQ	VSWEKDQQPV	AAGARFRLAQ	DGDLYRLTIL	DLALGDSGQY
90	100	110	120	130	140	150	160
VCRARNAIGE	AFAAVGLQVD	AEAACAEQAP	HFLLRPTSIR	VREGSEATFR	CRVGGSPRPA	VSWSKDGRRL	GEPDGPRVRV
170	180	190	200	210	220	230	240
EELGEASALR	IRAARPRDGG	TYEVRAENPL	GAASAAAALV	VDSDAADTAS	RPGTSTAALL	AHLQRRREAM	RAEGAPASPP
250	260	270	280	290	300	310	320
STGTRTCTVT	EGKHARLSCY	VTGEPKPETV	WKKDGQLVTE	GRRHVVYEDA	QENFVLKILF	CKQSDRGLYT	CTASNLVGQT
330	340	350	360	370	380	390	400
YSSVLVVVRE	PAVPFKKRLQ	DLEVREKESA	TFLCEVPQPS	TEAAWFKEET	RLWASAKYGI	EEEGTERRLT	VRNVSADDDA
410	420	430	440	450	460	470	480
VYICETPEGS	RTVAELAVQG	NLLRKLPRKT	AVRVGDTAMF	CVELAVPVGP	VHWLRNQEEV	VAGGRVAISA	EGTRHTLTIS
490	500	510	520	530	540	550	560
QCCLEDVGQV	AFMAGDCQTS	TQFCVSAPRK	PPLQPPVDPV	VKARMESSVI	LSWSPPPHGE	RPVTIDGYLV	EKKKLGTYTW
570	580	590	600	610	620	630	640
IRCHEAEWVA	TPELTVADVA	EEGNFQFRVS	ALNSFGQSPY	LEFPGTVHLA	PKLAVRTPLK	AVQAVEGGEV	TFSVDLTVAS
650	660	670	680	690	700	710	720
AGEWFLDGQA	LKASSVYEIH	CDRTRHTLTI	REVPASLHGA	QLKFVANGIE	SSIRMEVRAA	PGLTANKPPA	AAAREVLARL
730	740	750	760	770	780	790	800
HEEAQLLAEL	SDQAAAVTWL	KDGRTLSPGP	KYEVQASAGR	RVLLVRDVAR	DDAGLYECVS	RGGRIAYQLS	VQGLARFLHK
810	820	830	840	850	860	870	880
DMAGSCVDAV	AGGPAQFECE	TSEAHVHVHW	YKDGMELGHS	GERFLQEDVG	TRHRLVAATV	TRQDEGTYSC	RVGEDSVDFR
890	900	910	920	930	940	950	960
LRVSEPKAVF	AKEQPACREV	QAEVGASATL	SCEVAQDQME	VTWYKDGKKL	SSSSKVHVEA	VGCMRRLVVQ	QVGQADSGEY
970	980	990	1000	1010	1020	1030	1040
SCEARGQRVS	FRLDVAEPKV	VFAKEQLARR	KLQAEAGASA	TLSCEVAQAQ	TEVTWYKDGK	KLSSSSKVCM	EATGCTRRLV
1050	1060	1070	1080	1090	1100	1110	1120
VQQAGQADAG	EYSCEAGGQR	LSFHLDVKEP	KVVFAKDQVA	HSEVQAEAGA	SATLSCEVAQ	AQTEVMWYKD	GKKLSSSLKV
1130	1140	1150	1160	1170	1180	1190	1200
HVEAKGCRRR	LVVQQAGKTD	AGDYSCEARG	QRVSFRLHIT	EPKMMFAKEQ	SVHNEVQAEA	GASAMLSCEV	AQAQTEVTWY
1210	1220	1230	1240	1250	1260	1270	1280
KDGKKLSSSS	KVGMEVKGCT	RRLVLPQAGK	ADAGEYSCEA	GGQRVSFHLH	ITEPKGVFAK	EQSVHNEVQA	EAGTTAMLSC
1290	1300	1310	1320	1330	1340	1350	1360
EVAQPQTEVT	WYKDGKKLSS	SSKVRMEVKG	CTRRLVVQQV	GKADAGEYSC	EAGGQRVSFQ	LHITEPKAVF	AKEQLVHNEV
1370	1380	1390	1400	1410	1420	1430	1440
RTEAGASATL	SCEVAQAQTE	VTWYKDGKKL	SSSSKVRIEA	AGCMRQLVVQ	QAGQADAGEY	TCEAGGQRLS	FHLDVSEPKA
1450	1460	1470	1480	1490	1500	1510	1520
VFAKEQLAHR	KVQAEAGAIA	TLSCEVAQAQ	TEVTWYKDGK	KLSSSSKVRM	EAVGCTRRLV	VQQACQADTG	EYSCEAGGQR
1530	1540	1550	1560	1570	1580	1590	1600
LSFSLDVAEP	KVVFAKEQPV	HREVQAQAGA	STTLSCEVAQ	AQTEVMWYKD	GKKLSFSSKV	RMEAVGCTRR	LVVQQAGQAV
1610	1620	1630	1640	1650	1660	1670	1680
AGEYSCEAGS	QRLSFHLHVA	EPKAVFAKEQ	PASREVQAEA	GTSATLSCEV	AQAQTEVTWY	KDGKKLSSSS	KVRMEAVGCT
1690	1700	1710	1720	1730	1740	1750	1760
RRLVVQEAGQ	ADAGEYSCKA	GDQRLSFHLH	VAEPKVVFAK	EQPAHREVQA	EAGASATLSC	EVAQAQTEVT	WYKDGKKLSS
1770	1780	1790	1800	1810	1820	1830	1840
SSKVRVEAVG	CTRRLVVQQA	GQAEAGEYSC	EAGGQQLSFR	LQVAEPKAVF	AKEQVVFAKD	QPVHREVQAE	AGTSTMLSCE
1850	1860	1870	1880	1890	1900	1910	1920
VAQAQTEVMW	YKDGKKLSSS	SKMRVEAVGC	TRRLVVQEAG	QADAGEYSCE	AGGQRLSFHL	HVAEPKVVFA	KEQPACREVQ
1930	1940	1950	1960	1970	1980	1990	2000
AEAGASATLS	CEVAQGQMEV	TWYKDGKKLS	SSSKVHMEAS	GYTRRLVVQQ	AGQADAGEYS	CEAGGQRLSF	RLHVAELEPQ
2010	2020	2030	2040	2050	2060	2070	2080
ISERPCRREP	LVVKEHEDII	LTATLATPSA	ATVTWLKDGV	EIRRSKRHET	ASQGDTHTLT	VHGAQVLDSA	IYSCRVGAEG
2090	2100	2110	2120	2130	2140	2150	2160
QDFPVQVEEV	AAKFCRLLEP	VCGELGGTVT	LACELSPACA	EVVWRCGNTQ	LRVGKRFQMV	AEGPVRSLTV	LGLRAEDAGE
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1941	1	643.2925	-112.28	2	54.4	13.1	2	338-347	K.RLQDLEVREK.E	
2890	1	922.9785	45.19	2	65.3	10.6	2	1021-1037	K.KLSSSSKVCMEATGCTR.R	Carbamidomethyl: 15
2923	1	951.4595	12.61	2	65.7	13.9	2	1021-1037	K.KLSSSSKVCMEATGCTR.R	Carbamidomethyl: 9, 15
1563	1	927.4401	-8.97	3	48.2	13.0	1	5415-5440	R.EDSGQYAAYISNAMGAAYSSARLLVR.G	Oxidation: 14

Detailed Protein Report

Protein 116: sacsin isoform 2 [Homo sapiens]

Accession:	gi|491227401	**Score:**	50.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	504.2
Database Date:	2015-11-30	**pI:**	6.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.5
		No. of unique Peptides:	3

10	20	30	40	50	60	70	80
MAPYQGPALY	VYNNAVFTPE	DWHGIQEIAR	SRKKDDPLKV	GRFGIGFNSV	YHITDVPCIF	SGDQIGMLDP	HQTLFGPHES
90	100	110	120	130	140	150	160
GQCWNLKDDS	KEISELSDQF	APFVGIFGST	KETFINGNFP	GTFFRFPLRL	QPSQLSSNLY	NKQKVLELFE	SFRADADTVL
170	180	190	200	210	220	230	240
LFLKSVQDVS	LYVREADGTE	KLVFRVTSSE	SKALKHERPN	SIKILGTAIS	NYCKKTPSNN	ITCVTYHVNI	VLEEESTKDA
250	260	270	280	290	300	310	320
QKTSWLVCNS	VGGRGISSKL	DSLADELKFV	PIIGIAMPLS	SRDDEAKGAT	SDFSGKAFCF	LPLPPGEESS	TGLPVHISGF
330	340	350	360	370	380	390	400
FGLTDNRRSI	KWRELDQWRD	PAALWNEFLV	MNVVPKAYAT	LILDSIKRLE	MEKSSDFPLS	VDVIYKLWPE	ASKVKVHWQP
410	420	430	440	450	460	470	480
VLEPLFSELL	QNAVIYSISC	DWVRLEQVYF	SELDENLEYT	KTVLNYLQSS	GKQIAKVPGN	VDAAVQLTAA	SGTTPVRKVT
490	500	510	520	530	540	550	560
PAWVRQVLRK	CAHLGCAEEK	LHLLEFVLSD	QAYSELLGLE	LLPLQNGNFV	PFSSSVSDQD	VIYITSAEYP	RSLFPSLEGR
570	580	590	600	610	620	630	640
FILDNLKPHL	VAALKEAAQT	RGRPCTQLQL	LNPERFARLI	KEVMNTFWPG	RELIVQWYPF	DENRNHPSVS	WLKMVWKNLY
650	660	670	680	690	700	710	720
IHFSEDLTLF	DEMPLIPRTI	LEEGQTCVEL	IRLRIPSLVI	LDDESEAQLP	EFLADIVQKL	GGFVLKKLDA	SIQHPLIKKY
730	740	750	760	770	780	790	800
IHSPLPSAVL	QIMEKMPLQK	LCNQITSLLP	THKDALRKFL	ASLTDSSEKE	KRIIQELAIF	KRINHSSDQG	ISSYTKLKGC
810	820	830	840	850	860	870	880
KVLHHTAKLP	ADLRLSISVI	DSSDEATIRL	ANMLKIEQLK	TTSCLKLVLK	DIENAFYSHE	EVTQLMLWVL	ENLSSLKNEN
890	900	910	920	930	940	950	960
PNVLEWLTPL	KFIQISQEQM	VSAGELFDPD	IEVLKDLFCN	EEGTYFPPSV	FTSPDILHSL	RQIGLKNEAS	LKEKDVVQVA
970	980	990	1000	1010	1020	1030	1040
KKIEALQVGA	CPDQDVLLKK	AKTLLLVLNK	NHTLLQSSEG	KMTLKKIKWV	PACKERPPNY	PGSLVWKGDL	CNLCAPPDMC
1050	1060	1070	1080	1090	1100	1110	1120
DVGHAILIGS	SLPLVESIHV	NLEKALGIFT	KPSLSAVLKH	FKIVVDWYSS	KTFSDEDYYQ	FQHILLEIYG	FMHDHLNEGK
1130	1140	1150	1160	1170	1180	1190	1200
DSFRALKFPW	VWTGKKFCPL	AQAVIKPIHD	LDLQPYLHNV	PKTMAKFHQL	FKVCGSIEEL	TSDHISMVIQ	KIYLKSDQDL
1210	1220	1230	1240	1250	1260	1270	1280
SEQESKQNLH	LMLNIIRWLY	SNQIPASPNT	PVPIHHSKNP	SKLIMKPIHE	CCYCDIKVDD	LNDLLEDSVE	PIILVHEDIP
1290	1300	1310	1320	1330	1340	1350	1360
MKTAEWLKVP	CLSTRLINPE	NMGFEQSGQR	EPLTVRIKNI	LEEYPSVSDI	FKELLQNADD	ANATECSFLI	DMRRNMDIRE
1370	1380	1390	1400	1410	1420	1430	1440
NLLDPGMAAC	HGPALWSFNN	SQFSDSDFVN	ITRLGESLKR	GEVDKVGKFG	LGFNSVYHIT	DIPIIMSREF	MIMFDPNINH
1450	1460	1470	1480	1490	1500	1510	1520
ISKHIKDKSN	PGIKINWSKQ	QKRLRKFPNQ	FKPFIDVFGC	QLPLTVEAPY	SYNGTLFRLS	FRTQQEAKVS	EVSSTCYNTA
1530	1540	1550	1560	1570	1580	1590	1600
DIYSLVDEFS	LCGHRLIIFT	QSVKSMYLKY	LKIEETNPSL	AQDTVIIKKK	SCSSKALNTP	VLSVLKEAAK	LMKTCSSSNK
1610	1620	1630	1640	1650	1660	1670	1680
KLPSDEPKSS	CILQITVEEF	HHVFRRIADL	QSPLFRGPDD	DPAALFEMAK	SGQSKKPSDE	LSQKTVECTT	WLLCTCMDTG
1690	1700	1710	1720	1730	1740	1750	1760
EALKFSLSES	GRRLGLVPCG	AVGVQLSEIQ	DQKWTVKPHI	GEVFCYLPLR	IKTGLPVHIN	GCFAVTSNRK	EIWKTDTKGR
1770	1780	1790	1800	1810	1820	1830	1840
WNTTFMRHVI	VKAYLQVLSV	LRDLATSGEL	MDYTYYAVWP	DPDLVHDDFS	VICQGFYEDI	AHGKGKELTK	VFSDGSTWVS
1850	1860	1870	1880	1890	1900	1910	1920
MKNVRFLDDS	ILKRRDVGSA	AFKIFLKYLK	KTGSKNLCAV	ELPSSVKLGF	EEAGCKQILL	ENTFSEKQFF	SEVFFPNIQE
1930	1940	1950	1960	1970	1980	1990	2000
IEAELRDPLM	IFVLNEKVDE	FSGVLRVTPC	IPCSLEGHPL	VLPSRLIHPE	GRVAKLFDIK	DGRFPYGSTQ	DYLNPIILIK
2010	2020	2030	2040	2050	2060	2070	2080
LVQLGMAKDD	ILWDDMLERA	VSVAEINKSD	HVAACLRSSI	LLSLIDEKLK	IRDPRAKDFA	AKYQTIRFLP	FLTKPAGFSL
2090	2100	2110	2120	2130	2140	2150	2160
DWKGNSFKPE	TMFAATDLYT	AEHQDIVCLL	QPILNENSHS	FRGCGSVSLA	VKEFLGLLKK	PTVDLVINQL	KEVAKSVDDG
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2078	1	1029.6855	128.38	2	56.1	10.5	0	1714-1730	K.WTVKPHIGEVFCYLPLR.I	
71	1	845.3572	-104.63	2	30.3	12.1	1	1872-1887	K.TGSKNLCAVELPSSVK.L	Carbamidomethyl: 7
2171	1	1022.8841	-140.49	2	57.3	14.3	2	2331-2348	K.DTTVKYCHADIPREVAVK.L	

Detailed Protein Report

Protein 117: peroxisome biogenesis factor 1 isoform 3 [Homo sapiens]

Accession:	gi|544186104	**Score:**	50.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	119.5
Database Date:	2015-11-30	**pI:**	5.7
		Sequence Coverage [%]:	3.4
		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
1127	6	1207.8838	99.74	1	42.8	28.3	2	233-242	K.IPRSLKLQPR.E	

Detailed Protein Report

Protein 118: peroxiredoxin-2 [Homo sapiens]

Accession:	gi|32189392	**Score:**	50.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	21.9
Database Date:	2015-11-30	**pI:**	5.6
		Sequence Coverage [%]:	5.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MASGNARIGK	PAPDFKATAV	VDGAFKEVKL	SDYKGKYVVL	FFYPLDFTFV	CPTEIIAFSN	RAEDFRKLGC	EVLGVSVDSQ
90	100	110	120	130	140	150	160
FTHLAWINTP	RKEGGLGPLN	IPLLADVTRR	LSEDYGVLKT	DEGIAYRGLF	IIDGKGVLRQ	ITVNDLPVGR	SVDEALRLVQ
170	180	190	200				
AFQYTDEHGE	VCPAGWKPGS	DTIKPNVDDS	KEYFSKHN				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
766	1	606.3268	-23.04	2	38.4	50.1	0	140-150	R.QITVNDLPVGR.S	

Detailed Protein Report

Protein 119: myotubularin-related protein 5 [Homo sapiens]

Accession:	gi|239735519	**Score:**	49.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	210.9
Database Date:	2015-11-30	**pI:**	6.7
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	2.0
		No. of unique Peptides:	3

Quantitation

mdown:qdown	**Median:**	0.57	**CV:**	11.37 %	**No. of Peptides:**	2
Wdown:Qdown	**Median:**	0.76	**CV:**	104.20 %	**No. of Peptides:**	3

Detailed Protein Report

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	HMGSHVPSPR
1290	1300	1310	1320	1330	1340	1350	1360
ARVTTLSNPM	AASASRRTAP	RGKWGSVRTS	GRSSGLGTDV	GSRLAGRDAL	APPQANGGPP	DPGFLRPQRA	ALYILGDKAQ
1370	1380	1390	1400	1410	1420	1430	1440
LKGVRSDPLQ	QWELVPIEVF	EARQVKASFK	KLLKACVPGC	PAAEPSPASF	LRSLEDSEWL	IQIHKLLQVS	VLVVELLDSG
1450	1460	1470	1480	1490	1500	1510	1520
SSVLVGLEDG	WDITTQVVSL	VQLLSDPFYR	TLEGFRLLVE	KEWLSFGHRF	SHRGAHTLAG	QSSGFTPVFL	QFLDCVHQVH
1530	1540	1550	1560	1570	1580	1590	1600
LQFPMEFEFS	QFYLKFLGYH	HVSRRFRTFL	LDSDYERIEL	GLLYEEKGER	RGQVPCRSVW	EYVDRLSKRT	PVFHNYMYAP
1610	1620	1630	1640	1650	1660	1670	1680
EDAEVLRPYS	NVSNLKVWDF	YTEETLAEGP	PYDWELAQGP	PEPPEEERSD	GGAPQSRRRV	VWPCYDSCPR	AQPDAISRLL
1690	1700	1710	1720	1730	1740	1750	1760
EELQRLETEL	GQPAERWKDT	WDRVKAAQRL	EGRPDGRGTP	SSLLVSTAPH	HRRSLGVYLQ	EGPVGSTLSL	SLDSDQSSGS
1770	1780	1790	1800	1810	1820	1830	1840
TTSGSRQAAR	RSTSTLYSQF	QTAESENRSY	EGTLYKKGAF	MKPWKARWFV	LDKTKHQLRY	YDHRVDTECK	GVIDLAEVEA
1850	1860	1870	1880	1890	1900		
VAPGTPTMGA	PKTVDEKAFF	DVKTTRRVYN	FCAQDVPSAQ	QWVDRIQSCL	SDA		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
280	1	591.8074	33.08	2	32.6	12.3	1	242-251	R.SYQRLADACR.G		Wdown:Qdown 0.25 mdown:qdown 0.64
1064	3	751.8788	61.27	2	42.0	11.0	1	1116-1128	R.MTMSSLVERACCR.D	Oxidation: 3	Wdown:Qdown 0.87
348	1	800.7371	-149.37	2	33.7	13.1	1	1116-	R.MTMSSLVERACCR.D	Carbamidomethyl: 11, 12	mdown:qdown 0.51

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
								1128			Wdown:Qdown 2.02

Detailed Protein Report

Protein 120: spectrin beta chain, non-erythrocytic 1 isoform 2 [Homo sapiens]

Accession:	gi|112382252	**Score:**	49.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	251.2
Database Date:	2015-11-30	**pI:**	5.3
		Sequence Coverage [%]:	1.9
		No. of unique Peptides:	2

Quantitation

mdown:qdown	**Median:**	0.88	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	3.94	**CV:**	0.00 %	**No. of Peptides:**	1

10	20	30	40	50	60	70	80
MELQRTSSIS	GPLSPAYTGQ	VPYNYNQLEG	RFKQLQDERE	AVQKKTFTKW	VNSHLARVSC	RITDLYTDLR	DGRMLIKLLE
90	100	110	120	130	140	150	160
VLSGERLPKP	TKGRMRIHCL	ENVDKALQFL	KEQRVHLENM	GSHDIVDGNH	RLTLGLIWTI	ILRFQIQDIS	VETEDNKEKK
170	180	190	200	210	220	230	240
SAKDALLLWC	QMKTAGYPNV	NIHNFTTSWR	DGMAFNALIH	KHRPDLIDFD	KLKKSNAHYN	LQNAFNLAEQ	HLGLTKLLDP
250	260	270	280	290	300	310	320
EDISVDHPDE	KSIITYVVTY	YHYFSKMKAL	AVEGKRIGKV	LDNAIETEKM	IEKYESLASD	LLEWIEQTII	ILNNRKFANS
330	340	350	360	370	380	390	400
LVGVQQQLQA	FNTYRTVEKP	PKFTEKGNLE	VLLFTIQSKM	RANNQKVYMP	REGKLISDIN	KAWERLEKAE	HERELALRNE
410	420	430	440	450	460	470	480
LIRQEKLEQL	ARRFDRKAAM	RETWLSENQR	LVSQDNFGFD	LPAVEAATKK	HEAIETDIAA	YEERVQAVVA	VARELEAENY
490	500	510	520	530	540	550	560
HDIKRITARK	DNVIRLWEYL	LELLRARRQR	LEMNLGLQKI	FQEMLYIMDW	MDEMKVLVLS	QDYGKHLLGV	EDLLQKHTLV
570	580	590	600	610	620	630	640
EADIGIQAER	VRGVNASAQK	FATDGEGYKP	CDPQVIRDRV	AHMEFCYQEL	CQLAAERRAR	LEESRRLWKF	FWEMAEEEGW
650	660	670	680	690	700	710	720
IREKEKILSS	DDYGKDLTSV	MRLLSKHRAF	EDEMSGRSGH	FEQAIKEGED	MIAEEHFGSE	KIRERIIYIR	EQWANLEQLS
730	740	750	760	770	780	790	800
AIRKKRLEEA	SLLHQFQADA	DDIDAWMLDI	LKIVSSSDVG	HDEYSTQSLV	KKHKDVAEEI	ANYRPTLDTL	HEQASALPQE
810	820	830	840	850	860	870	880
HAESPDVRGR	LSGIEERYKE	VAELTRLRKQ	ALQDTLALYK	MFSEADACEL	WIDEKEQWLN	NMQIPEKLED	LEVIQHRFES
890	900	910	920	930	940	950	960
LEPEMNNQAS	RVAVVNQIAR	QLMHSGHPSE	KEIKAQQDKL	NTRWSQFREL	VDRKKDALLS	ALSIQNYHLE	CNETKSWIRE
970	980	990	1000	1010	1020	1030	1040
KTKVIESTQD	LGNDLAGVMA	LQRKLTGMER	DLVAIEAKLS	DLQKEAEKLE	SEHPDQAQAI	LSRLAEISDV	WEEMKTTLKN
1050	1060	1070	1080	1090	1100	1110	1120
REASLGEASK	LQQFLRDLDD	FQSWLSRTQT	AIASEDMPNT	LTEAEKLLTQ	HENIKNEIDN	YEEDYQKMRD	MGEMVTQGQT
1130	1140	1150	1160	1170	1180	1190	1200
DAQYMFLRQR	LQALDTGWNE	LHKMWENRQN	LLSQSHAYQQ	FLRDTKQAEA	FLNNQEYVLA	HTEMPTTLEG	AEAAIKKQED
1210	1220	1230	1240	1250	1260	1270	1280
FMTTMDANEE	KINAVVETGR	RLVSDGNINS	DRIQEKVDSI	DDRHRKNRET	ASELLMRLKD	NRDLQKFLQD	CQELSLWINE
1290	1300	1310	1320	1330	1340	1350	1360
KMLTAQDMSY	DEARNLHSKW	LKHQAFMAEL	ASNKEWLDKI	EKEGMQLISE	KPETEAVVKE	KLTGLHKMWE	VLESTTQTKA
1370	1380	1390	1400	1410	1420	1430	1440
QRLFDANKAE	LFTQSCADLD	KWLHGLESQI	QSDDYGKDLT	SVNILLKKQQ	MLENQMEVRK	KEIEELQSQA	QALSQEGKST
1450	1460	1470	1480	1490	1500	1510	1520
DEVDSKRLTV	QTKFMELLEP	LNERKHNLLA	SKEIHQFNRD	VEDEILWVGE	RMPLATSTDH	GHNLQTVQLL	IKKNQTLQKE
1530	1540	1550	1560	1570	1580	1590	1600
IQGHQPRIDD	IFERSQNIVT	DSSSLSAEAI	RQRLADLKQL	WGLLIEETEK	RHRRLEEAHR	AQQYYFDAAE	AEAWMSEQEL
1610	1620	1630	1640	1650	1660	1670	1680
YMMSEEKAKD	EQSAVSMLKK	HQILEQAVED	YAETVHQLSK	TSRALVADSH	PESERISMRQ	SKVDKLYAGL	KDLAEERRGK
1690	1700	1710	1720	1730	1740	1750	1760
LDERHRLFQL	NREVDDLEQW	IAEREVVAGS	HELGQDYEHV	TMLQERFREF	ARDTGNIGQE	RVDTVNHLAD	ELINSGHSDA
1770	1780	1790	1800	1810	1820	1830	1840
ATIAEWKDGL	NEAWADLLEL	IDTRTQILAA	SYELHKFYHD	AKEIFGRIQD	KHKKLPEELG	RDQNTVETLQ	RMHTTFEHDI
1850	1860	1870	1880	1890	1900	1910	1920
QALGTQVRQL	QEDAARLQAA	YAGDKADDIQ	KRENEVLEAW	KSLLDACESR	RVRLVDTGDK	FRFFSMVRDL	MLWMEDVIRQ
1930	1940	1950	1960	1970	1980	1990	2000
IEAQEKPRDV	SSVELLMNNH	QGIKAEIDAR	NDSFTTCIEL	GKSLLARKHY	ASEEIKEKLL	QLTEKRKEMI	DKWEDRWEWL
2010	2020	2030	2040	2050	2060	2070	2080
RLILEVHQFS	RDASVAEAWL	LGQEPYLSSR	EIGQSVDEVE	KLIKRHEAFE	KSAATWDERF	SALERLTTLE	LLEVRRQQEE
2090	2100	2110	2120	2130	2140	2150	2160
EERKRRPPSP	EPSTKVSEEA	ESQQQWDTSK	GEQVSQNGLP	AEQGSPRVSY	RSQTYQNYKN	FNSRRTASDQ	PWSGL

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
418	6	607.8310	-55.05	2	34.3	14.1	2	820-829	K.EVAELTRLRK.Q		
601	2	548.1743	-250.21	2	36.1	12.2	0	1087-1095	K.LLTQHENIK.N		mdown:qdown 0.88 Wdown:Qdown 3.94

Detailed Protein Report

Protein 121: aldehyde oxidase [Homo sapiens]

Accession:	gi|71773480	**Score:**	49.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	147.8
Database Date:	2015-11-30	**pI:**	6.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDRASELLFY	VNGRKVIEKN	VDPETMLLPY	LRKKLRLTGT	KYGCGGGGCG	ACTVMISRYN	PITKRIRHHP	ANACLIPICS
90	100	110	120	130	140	150	160
LYGAAVTTVE	GIGSTHTRIH	PVQERIAKCH	GTQCGFCTPG	MVMSIYTLLR	NHPEPTLDQL	TDALGGNLCR	CTGYRPIIDA
170	180	190	200	210	220	230	240
CKTFCKTSGC	CQSKENGVCC	LDQGINGLPE	FEEGSKTSPK	LFAEEEFLPL	DPTQELIFPP	ELMIMAEKQS	QRTRVFGSER
250	260	270	280	290	300	310	320
MMWFSPVTLK	ELLEFKFKYP	QAPVIMGNTS	VGPEVKFKGV	FHPVIISPDR	IEELSVVNHA	YNGLTLGAGL	SLAQVKDILA
330	340	350	360	370	380	390	400
DVVQKLPEEK	TQMYHALLKH	LGTLAGSQIR	NMASLGGHII	SRHPDSDLNP	ILAVGNCTLN	LLSKEGKRQI	PLNEQFLSKC
410	420	430	440	450	460	470	480
PNADLKPQEI	LVSVNIPYSR	KWEFVSAFRQ	AQRQENALAI	VNSGMRVFFG	EGDGIIRELC	ISYGGVGPAT	ICAKNSCQKL
490	500	510	520	530	540	550	560
IGRHWNEQML	DIACRLILNE	VSLLGSAPGG	KVEFKRTLII	SFLFKFYLEV	SQILKKMDPV	HYPSLADKYE	SALEDLHSKH
570	580	590	600	610	620	630	640
HCSTLKYQNI	GPKQHPEDPI	GHPIMHLSGV	KHATGEAIYC	DDMPLVDQEL	FLTFVTSSRA	HAKIVSIDLS	EALSMPGVVD
650	660	670	680	690	700	710	720
IMTAEHLSDV	NSFCFFTEAE	KFLATDKVFC	VGQLVCAVLA	DSEVQAKRAA	KRVKIVYQDL	EPLILTIEES	IQHNSSFKPE
730	740	750	760	770	780	790	800
RKLEYGNVDE	AFKVVDQILE	GEIHMGGQEH	FYMETQSMLV	VPKGEDQEMD	VYVSTQFPKY	IQDIVASTLK	LPANKVMCHV
810	820	830	840	850	860	870	880
RRVGGAFGGK	VLKTGIIAAV	TAFAANKHGR	AVRCVLERGE	DMLITGGRHP	YLGKYKAGFM	NDGRILALDM	EHYSNAGASL
890	900	910	920	930	940	950	960
DESLFVIEMG	LLKMDNAYKF	PNLRCRGWAC	RTNLPSNTAF	RGFGFPQAAL	ITESCITEVA	AKCGLSPEKV	RIINMYKEID
970	980	990	1000	1010	1020	1030	1040
QTPYKQEINA	KNLIQCWREC	MAMSSYSLRK	VAVEKFNAEN	YWKKKGLAMV	PLKFPVGLGS	RAAGQAAALV	HIYLDGSVLV
1050	1060	1070	1080	1090	1100	1110	1120
THGGIEMGQG	VHTKMIQVVS	RELRMPMSNV	HLRGTSTETV	PNANISGGSV	VADLNGLAVK	DACQTLLKRL	EPIISKNPKG
1130	1140	1150	1160	1170	1180	1190	1200
TWKDWAQTAF	DESINLSAVG	YFRGYESDMN	WEKGEGQPFE	YFVYGAACSE	VEIDCLTGDH	KNIRTDIVMD	VGCSINPAID
1210	1220	1230	1240	1250	1260	1270	1280
IGQIEGAFIQ	GMGLYTIEEL	NYSPQGILHT	RGPDQYKIPA	ICDMPTELHI	ALLPPSQNSN	TLYSSKGLGE	SGVFLGCSVF
1290	1300	1310	1320	1330	1340		
FAIHDAVSAA	RQERGLHGPL	TLNSPLTPEK	IRMACEDKFT	KMIPRDEPGS	YVPWNVPI		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2110	1	938.3880	-65.37	2	55.0	10.6	1	151-166	R.CTGYRPIIDACKTFCK.T	Carbamidomethyl: 11

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Detailed Protein Report

Protein 122: zinc finger protein 540 isoform a [Homo sapiens]

Accession:	gi|22749241	**Score:**	48.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	77.0
Database Date:	2015-11-30	**pI:**	10.5
		Sequence Coverage [%]:	7.4
		No. of unique Peptides:	3

Alias proteins:

Accession	**Name**	**Description**
gi|288557351	refseq_human (refseq_human_20140103.fasta)	zinc finger protein 540 isoform a [Homo sapiens]

10	20	30	40	50	60	70	80
MAHALVTFRD	VAIDFSQKEW	ECLDTTQRKL	YRDVMLENYN	NLVSLGYSGS	KPDVITLLEQ	GKEPCVVARD	VTGRQCPGLL
90	100	110	120	130	140	150	160
SRHKTKKLSS	EKDIHEISLS	KESIIEKSKT	LRLKGSIFRN	EWQNKSEFEG	QQGLKERSIS	QKKIVSKKMS	TDRKRPSFTL
170	180	190	200	210	220	230	240
NQRIHNSEKS	CDSHLVQHGK	IDSDVKHDCK	ECGSTFNNVY	QLTLHQKIHT	GEKSCKCEKC	GKVFSHSYQL	TLHQRFHTGE
250	260	270	280	290	300	310	320
KPYECQECGK	TFTLYPQLNR	HQKIHTGKKP	YMCKKCDKGF	FSRLELTQHK	RIHTGKKSYE	CKECGKVFQL	IFYFKEHERI
330	340	350	360	370	380	390	400
HTGKKPYECK	ECGKAFSVCG	QLTRHQKIHT	GVKPYECKEC	GKTFRLSFYL	TEHRRTHAGK	KPYECKECGK	SFNVRGQLNR
410	420	430	440	450	460	470	480
HKTIHTGIKP	FACKVCEKAF	SYSGDLRVHS	RIHTGEKPYE	CKECGKAFML	RSVLTEHQRL	HTGVKPYECK	ECGKTFRVRS
490	500	510	520	530	540	550	560
QISLHKKIHT	DVKPYKCVRC	GKTFRFGFYL	TEHQRIHTGE	KPYKCKECGK	AFIRRGNLKE	HLKIHSGLKP	YDCKECGKSF
570	580	590	600	610	620	630	640
SRRGQFTEHQ	KIHTGVKPYK	CKECGKAFSR	SVDLRIHQRI	HTGEKPYECK	QCGKAFRLNS	HLTEHQRIHT	GEKPYECKVC
650	660	670					
RKAFRQYSHL	YQHQKTHNVI						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2641	1	701.3872	28.83	2	61.3	12.6	1	70-82	R.DVTGRQCPGLLSR.H	
765	1	541.3095	42.61	3	38.4	11.9	1	303-315	K.ECGKVFQLIFYFK.E	
848	2	946.4705	3.74	2	39.4	11.1	2	331-347	K.ECGKAFSVCGQLTRHQK.I	

Detailed Protein Report

Protein 123: **PREDICTED: extracellular matrix protein FRAS1 isoform X2 [Homo sapiens]**

Accession:	gi|578809381	**Score:**	48.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	438.5
Database Date:	2015-11-30	**pI:**	5.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.4
		No. of unique Peptides:	2

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        10         20         30         40         50         60         70         80
MGVLKVWLGL ALALAEFAVL PHHSEGACVY QDSLLADATI WKPDSCQSCR CHGDIVICKP AVCRNPQCAF EKGEVLQIAA

        90        100        110        120        130        140        150        160
NQCCPECVLR TPGSCHHEKK IHEHGTEWAS SPCSVCSCNH GEVRCTPQPC PPLSCGHQEL AFIPEGSCCP VCVGLGKPCS

       170        180        190        200        210        220        230        240
YEGHVFQDGE DWRLSRCAKC LCRNGVAQCF TAQCQPLFCN QDETVVRVPG KCCPQCSARS CSAAGQVYEH GEQWSENACT

       250        260        270        280        290        300        310        320
TCICDRGEVR CHKQACLPLR CGKGQSRARR HGQCCEECVS PAGSCSYDGV VRYQDEMWKG SACEFCMCDH GQVTCQTGEC

       330        340        350        360        370        380        390        400
AKVECARDEE LIHLDGKCCP ECISRNGYCV YEETGEFMSS NASEVKRIPE GEKWEDGPCK VCECRGAQVT CYEPSCPPCP

       410        420        430        440        450        460        470        480
VGTLALEVKG QCCPDCTSVH CHPDCLTCSQ SPDHCDLCQD PTKLLQNGWC VHSCGLGFYQ AGSLCLACQP QCSTCTSGLE

       490        500        510        520        530        540        550        560
CSSCQPPLLM RHGQCVPTCG DGFYQDRHSC AVCHESCAGC WGPTEKHCLA CRDPLHVLRD GGCESSCGKG FYNRQGTCSA

       570        580        590        600        610        620        630        640
CDQSCDSCGP SSPRCLTCTE KTVLHDGKCM SECPGGYYAD ATGRCKACHS SCLACMGPAP SHCTGCKKPE EGLQVEQLSD

       650        660        670        680        690        700        710        720
VGIPSGECLA QCRAHFYLES TGICEACHQS CFRCAGKSPH NCTDCGPSHV LLDGQCLSQC PDGYFHQEGS CTECHPTCRQ

       730        740        750        760        770        780        790        800
CHGPLESDCI SCYPHISLTN GNCRTSCREE QFLNLVGYCA DCHHLCQHCA ADLHNTGSIC LRCQNAHYLL LGDHCVPDCP

       810        820        830        840        850        860        870        880
SGYYAERGAC KKCHSSCRTC QGRGPFSCSS CDTNLVLSHT GTCSTTCFPG HYLDDNHVCQ PCNTHCGSCD SQASCTSCRD

       890        900        910        920        930        940        950        960
PNKVLLFGEC QYESCAPQYY LDFSTNTCKE CDWSCSACSG PLKTDCLQCM DGYVLQDGAC VEQCLSSFYQ DSGLCKNCDS

       970        980        990       1000       1010       1020       1030       1040
YCLQCQGPHE CTRCKGPFLL LEAQCVQECG KGYFADHAKH KCTACPQGCL QCSHRDRCHL CDHGFFLKSG LCVYNCVPGF

      1050       1060       1070       1080       1090       1100       1110       1120
SVHTSNETCS GKIHTPSLHV NGSLILPIGS IKPLDFSLLN VQDQEGRVED LLFHVVSTPT NGQLVLSRNG KEVQLDKAGR

      1130       1140       1150       1160       1170       1180       1190       1200
FSWKDVNEKK VRFVHSKEKL RKGYLFLKIS DQQFFSEPQL INIQAFSTQA PYVLRNEVLH ISRGERATIT TQMLDIRDDD

      1210       1220       1230       1240       1250       1260       1270       1280
NPQDVVIEII DPPLHGQLLQ TLQSPATPIY QFQLDELSRG LLHYAHDGSD STSDVAVLQA NDGHSFHNIL FQVKTVPQND

      1290       1300       1310       1320       1330       1340       1350       1360
RGLQLVANSM VWVPEGGMLQ ITNRILQAEA PGASAEEIIY KITQDYPQFG EVVLLVNMPA DSPADEGQHL PDGRTATPTS

      1370       1380       1390       1400       1410       1420       1430       1440
TFTQQDINEG IVWYRHSGAP AQSDSFRFEV SSASNAQTRL ESHMFNIAIL PQTPEAPKVS LEASLHMTAR EDGLTVIQPH

      1450       1460       1470       1480       1490       1500       1510       1520
SLSFINSEKP SGKIVYNITL PLHPNQGIIE HRDHPHSPIR YFTQEDINQG KVMYRPPPAA PHLQELMAFS FAGLPESVKF

      1530       1540       1550       1560       1570       1580       1590       1600
HFTVSDGEHT SPEMVLTIHL LPSDQQLPVF QVTAPRLAVS PGGSTSVGLQ VVVRDAETAP KELFFELRRP PQHGVLLKHT

      1610       1620       1630       1640       1650       1660       1670       1680
AEFRRPMATG DTFTYEDVEK NALQYIHDGS STREDSMEIS VTDGLTVTML EVRVEVSLSE DRGPRLAAGS SLSITVASKS

      1690       1700       1710       1720       1730       1740       1750       1760
TAIITRSHLA YVDDSSPDPE IWIQLNYLPS YGTLLRISGS EVEELSEVSN FTMEDINNKK IRYSAVFETD GHLVTDSFYF

      1770       1780       1790       1800       1810       1820       1830       1840
SVSDMDHNHL DNQIFTIMIT PAENPPPVIA FADLITVDEG GRAPLSFHHF FATDDDDNLQ RDAIIKLSAL PKYGCIENTG

      1850       1860       1870       1880       1890       1900       1910       1920
TGDRFGPETA SDLEASFPIQ DVLENYIYYF QSVHESIEPT HDIFSFYVSD GTSRSEIHSI NITIERKNDE PPRMTLQPLR

      1930       1940       1950       1960       1970       1980       1990       2000
VQLSSGVVIS NSSLSLQDLD TPDNELIFVL TKKPDHGHVL WRQTASEPLE NGRVLVQGST FTYQDILAGL VGYVPSVPGM

      2010       2020       2030       2040       2050       2060       2070       2080
VVDEFQFSLT DGLHVDTGRM KIYTELPASD TPHLAINQGL QLSAGSVARI TEQHLKVTDI DSDDHQVMYI MKEDPGAGRL

      2090       2100       2110       2120       2130       2140       2150       2160
QMMKHGNLEQ ISIKGPIRSF TQADISQGHV EYSHGTGEPG GSFAFKFDVV DGEGNRLIDK SFSISILEDK SPPVITTNKG

      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
2609	1	1176.3241	-122.97	2	60.9	16.9	1	605-627	R.CKACHSSCLACMGPAPSHCTGCK.K	Carbamidomethyl: 1
30	1	1096.9812	-111.34	2	29.6	16.6	2	2080-2098	R.LQMMKHGNLEQISIKGPIR.S	

Detailed Protein Report

Protein 124: PREDICTED: collagen alpha-1(XIV) chain isoform X1 [Homo sapiens]

Accession:	gi|530389313	**Score:**	48.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	191.8
Database Date:	2015-11-30	**pI:**	5.1
		Sequence Coverage [%]:	2.7
		No. of unique Peptides:	3

Quantitation

mdown:qdown	**Median:**	0.60	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.46	**CV:**	0.00 %	**No. of Peptides:**	1

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1886	10	673.2683	-119.28	2	53.6	15.8	0	208-218	R.IEWHLNAFSTK.D		
64	1	809.3817	-76.89	2	30.0	10.1	1	740-754	R.NLVVGDETTSSLRVK.W		mdown:qdown 0.60 Wdown:Qdown 0.46
2197	1	585.1748	-243.43	2	57.7	10.6	0	826-836	K.TLPSSGPQNLR.V		

Detailed Protein Report

Protein 125: PREDICTED: A-kinase anchor protein 9 isoform X3 [Homo sapiens]

Accession:	gi|578813854	**Score:**	48.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	447.3
Database Date:	2015-11-30	**pI:**	4.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	0.8
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MEDEERQKKL	EAGKAKLAQF	RQRKAQSDGQ	SPSKKQKKKR	KTSSSKHDVS	AHHDLNIDQS	QCNEMYINSS	QRVESTVIPE
90	100	110	120	130	140	150	160
STIMRTLHSG	EITSHEQGFS	VELESEISTT	ADDCSSEVNG	CSFVMRTGKP	TNLLREEEFG	VDDSYSEQGA	QDSPTHLEMM
170	180	190	200	210	220	230	240
ESELAGKQHE	IEELNRELEE	MRVTYGTEGL	QQLQEFEAAI	KQRDGIITQL	TANLQQARRE	KDETMREFLE	LTEQSQKLQI
250	260	270	280	290	300	310	320
QFQQLQASET	LRNSTHSSTA	ADLLQAKQQI	LTHQQQLEEQ	DHLLEDYQKK	KEDFTMQISF	LQEKIKVYEM	EQDKKVENSN
330	340	350	360	370	380	390	400
KEEIQEKETI	IEELNTKIIE	EEKKTLELKD	KLTTADKLLG	ELQEQIVQKN	QEIKNMKLEL	TNSKQKERQS	SEEIKQLMGT
410	420	430	440	450	460	470	480
VEELQKRNHK	DSQFETDIVQ	RMEQETQRKL	EQLRAELDEM	YGQQIVQMKQ	ELIRQHMAQM	EEMKTRHKGE	MENALRSYSN
490	500	510	520	530	540	550	560
ITVNEDQIKL	MNVAINELNI	KLQDTNSQKE	KLKEELGLIL	EEKCALQRQL	EDLVEELSFS	REQIQRARQT	IAEQESKLNE
570	580	590	600	610	620	630	640
AHKSLSTVED	LKAEIVSASE	SRKELELKHE	AEVTNYKIKL	EMLEKEKNAV	LDRMAESQEA	ELERLRTQLL	FSHEEELSKL
650	660	670	680	690	700	710	720
KEDLEIEHRI	NIEKLKDNLG	IHYKQQIDGL	QNEMSQKIET	MQFEKDNLIT	KQNQLILEIS	KLKDLQQSLV	NSKSEEMTLQ
730	740	750	760	770	780	790	800
INELQKEIEI	LRQEEKEKGT	LEQEVQELQL	KTELLEKQMK	EKENDLQEKF	AQLEAENSIL	KDEKKTLEDM	LKIHTPVSQE
810	820	830	840	850	860	870	880
ERLIFLDSIK	SKSKDSVWEK	EIEILIEENE	DLKQQCIQLN	EEIEKQRNTF	SFAEKNFEVN	YQELQEEYAC	LLKVKDDLED
890	900	910	920	930	940	950	960
SKNKQELEYK	SKLKALNEEL	HLQRINPTTV	KMKSSVFDED	KTFVAETLEM	GEVVEKDTTE	LMEKLEVTKR	EKLELSQRLS
970	980	990	1000	1010	1020	1030	1040
DLSEQLKQKH	GEISFLNEEV	KSLKQEKEQV	SLRCRELEII	INHNRAENVQ	SCDTQVSSLL	DGVVTMTSRG	AEGSVSKVNK
1050	1060	1070	1080	1090	1100	1110	1120
SFGEESKIMV	EDKVSFENMT	VGEESKQEQL	ILDHLPSVTK	ESSLRATQPS	ENDKLQKELN	VLKSEQNDLR	LQMEAQRICL
1130	1140	1150	1160	1170	1180	1190	1200
SLVYSTHVDQ	VREYMENEKD	KALCSLKEEL	IFAQEEKIKE	LQKIHQLELQ	TMKTQETGDE	GKPLHLLIGK	LQKAVSEECS
1210	1220	1230	1240	1250	1260	1270	1280
YFLQTLCSVL	GEYYTPALKC	EVNAEDKENS	GDYISENEDP	ELQDYRYEVQ	DFQENMHTLL	NKVTEEYNKL	LVLQTRLSKI
1290	1300	1310	1320	1330	1340	1350	1360
WGQQTDGMKL	EFGEENLPKE	ETEFLSIHSQ	MTNLEDIDVN	HKSKLSSLQD	LEKTKLEEQV	QELESLISSL	QQQLKETEQN
1370	1380	1390	1400	1410	1420	1430	1440
YEAEIHCLQK	RLQAVSESTV	PPSLPVDSVV	ITESDAQRTM	YPGSCVKKNI	DGTIEFSGEF	GVKEETNIVK	LLEKQYQEQL
1450	1460	1470	1480	1490	1500	1510	1520
EEEVAKVIVS	MSIAFAQQTE	LSRISGGKEN	TASSKQAHAV	CQQEQHYFNE	MKLSQDQIGF	QTFETVDVKF	KEEFKPLSKE
1530	1540	1550	1560	1570	1580	1590	1600
LGEHGKEILL	SNSDPHDIPE	SKDCVLTISE	EMFSKDKTFI	VRQSIHDEIS	VSSMDASRQL	MLNEEQLEDM	RQELVRQYQE
1610	1620	1630	1640	1650	1660	1670	1680
HQQATELLRQ	AHMRQMERQR	EDQEQLQEEI	KRLNRQLAQN	GNENQGEVEE	QTFKEKELDR	KPEDVPPEIL	SNERYALQKA
1690	1700	1710	1720	1730	1740	1750	1760
NNRLLKILLE	VVKTTAAVEE	TIGRHVLGIL	DRSSKSQSSA	SLIWRSEAEA	SVKSCVHEEH	TRVTDESIPS	YSGSDMPRND
1770	1780	1790	1800	1810	1820	1830	1840
INMWSKVTEE	GTELSQRLVR	SGFAGTEIDP	ENEELMLNIS	SRLQAAVEKL	LEAISETSSQ	LEHAKVTQTE	LMRESFRQKQ
1850	1860	1870	1880	1890	1900	1910	1920
EATESLKCQE	ELRERLHEES	RAREQLAVEL	SKAEGVIDGY	ADEKTLFERQ	IQEKTDIIDR	LEQELLCASN	RLQELEAEQQ
1930	1940	1950	1960	1970	1980	1990	2000
QIQEERELLS	RQKEAMKAEA	GPVEQQLLQE	TEKLMKEKLE	VQCQAEKVRD	DLQKQVKALE	IDVEEQVSRF	IELEQEKNTE
2010	2020	2030	2040	2050	2060	2070	2080
LMDLRQQNQA	LEKQLEKMRK	FLDEQAIDRE	HERDVFQQEI	QKLEQQLKVV	PRFQPISEHQ	TREVEQLANH	LKEKTDKCSE
2090	2100	2110	2120	2130	2140	2150	2160
LLLSKEQLQR	DIQERNEEIE	KLEFRVRELE	QALLVSADTF	QKVEDRKHFG	AVEAKPELSL	EVQLQAERDA	IDRKEKEITN
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
27	4	768.2815	-117.99	2	29.6	16.0	2	758-769	K.QMKEKENDLQEK.F	Oxidation: 2
49	1	819.8727	-87.95	2	29.3	12.5	1	3738-3751	R.WHRVTGSVSININR.D	

Detailed Protein Report

Protein 126: phospholipase B1, membrane-associated isoform 2 precursor [Homo sapiens]

Accession:	gi|283436114	**Score:**	48.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	161.6
Database Date:	2015-11-30	**pI:**	5.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.0
		No. of unique Peptides:	3

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
428	3	587.8118	72.68	2	34.7	11.5	0	43-52	K.NSPFPCNPNK.L	Carbamidomethyl: 6
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 127: eukaryotic translation initiation factor 4 gamma 3 isoform 1 [Homo sapiens]

Accession:	gi|311771714	**Score:**	48.0
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 [%]:**	2.8
		No. of unique Peptides:	3

```
        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
1921	1	781.2702	-157.47	2	52.7	13.1	0	857-870	K.VPMADKPGNTVNFR.K	Oxidation: 3
2882	1	938.5029	13.03	2	64.8	15.4	1	940-955	K.MLTEAIMHDCVVKLLK.N	Oxidation: 1, 7

Detailed Protein Report

Protein 128: **transcription factor HIVEP3 isoform b [Homo sapiens]**

Accession:	gi|189181750	**Score:**	47.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	259.2
Database Date:	2015-11-30	**pI:**	8.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.8
		No. of unique Peptides:	2

Quantitation

mdown:qdown	**Median:**	0.97	**CV:**	0.00 %	**No. of 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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2516	1	941.4560	-33.22	2	61.9	13.2	2	635-651	K.GLKTKGVIYECNICGAR.Y	Carbamidomethyl: 11	
22	1	657.3901	133.33	2	28.9	15.8	1	1752-1762	R.GKYVCEECGIR.C	Carbamidomethyl: 5	mdown:qdown 0.97

Detailed Protein Report

Protein 129: PREDICTED: uncharacterized protein LOC101929845 [Homo sapiens]

Accession:	gi|578845877	**Score:**	47.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	90.2
Database Date:	2015-11-30	**pI:**	12.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	9.3
		No. of unique Peptides:	2

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
2221	1	1032.3950	-68.06	2	56.4	11.4	2	1-18	-.MEESAEQAPRCDETRVGR.R	
48	1	1220.0219	-37.76	2	30.0	11.4	2	33-56	R.AGTAVRRDAASQSCCPTCTGVATR.R	Carbamidomethyl: 14

Detailed Protein Report

Protein 130: mis18-binding protein 1 [Homo sapiens]

Accession:	gi|42415492	**Score:**	47.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	129.0
Database Date:	2015-11-30	**pI:**	9.9
Modification(s):	Oxidation	**Sequence Coverage [%]:**	5.6
		No. of unique Peptides:	3

Alias proteins:

Accession	**Name**	**Description**
gi|530404134	refseq_human (refseq_human_20140103.fasta)	PREDICTED: mis18-binding protein 1 isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MIATPLKHSR	IYLPPEASSQ	RRNLPMDAIF	FDSIPSGTLT	PVKDLVKYQN	SSLKLNDHKK	NQFLKMTTFN	NKNIFQSTML
90	100	110	120	130	140	150	160
TEATTSNSSL	DISAIKPNKD	GLKNKANYES	PGKIFLRMKE	KVLRDKQEQP	SRNSSLLEPQ	KSGNNETFTP	NRVEKKKLQH
170	180	190	200	210	220	230	240
TYLCEEKENN	KSFQSDDSSL	RASVQGVPLE	SSNNDIFLPV	KQKIQCQQEK	KAPLHNLTYE	LPTLNQEQEN	FLAVEARNKT
250	260	270	280	290	300	310	320
LTRAQLAKQI	FHSKESIVAT	TKSKKDTFVL	ESVDSADEQF	QNTNAETLST	NCIPIKNGSL	LMVSDSERTT	EGTSQQKVKE
330	340	350	360	370	380	390	400
GNGKTVPGET	GLPGSMKDTC	KIVLATPRLH	ITIPRRSKRN	ISKLSPPRIF	QTVTNGLKKN	QVVQLQEWMI	KSINNNTAIC
410	420	430	440	450	460	470	480
VEGKLIDVTN	IYWHSNVIIE	RIEHNKLRTI	SGNVYILKGM	IDQISMKEAG	YPNYLIRKFM	FGFPENWKEH	IDNFLEQLRA
490	500	510	520	530	540	550	560
GEKNREKTKQ	KQKTGRSVRD	IRKSMKNDAR	ENQTDTAQRA	TTTYDFDCDN	LELKSNKHSE	SPGATELNMC	HSNCQNKPTL
570	580	590	600	610	620	630	640
RFPDDQVNNT	IQNGGGDDLS	NQELIGKKEY	KMSSKKLKIG	ERTNERIIKS	QKQETTEELD	VSIDILTSRE	QFFSDEERKY
650	660	670	680	690	700	710	720
MAINQKKAYI	LVTPLKSRKV	IEQRCMRYNL	SAGTIKAVTD	FVIPECQKKS	PISKSMGTLE	NTFEGHKSKN	KEDCDERDLL
730	740	750	760	770	780	790	800
TVNRKIKISN	LEKEQMLTSD	FKKNTRLLPK	LKKIENQVAM	SFYKHQSSPD	LSSEESETEK	EIKRKAEVKK	TKAGNTKEAV
810	820	830	840	850	860	870	880
VHLRKSTRNT	SNIPVILEPE	TEESENEFYI	KQKKARPSVK	ETLQKSGVRK	EFPITEAVGS	DKTNRHPLEC	LPGLIQDKEW
890	900	910	920	930	940	950	960
NEKELQKLHC	AFASLPKHKP	GFWSEVAAAV	GSRSPEECQR	KYMENPRGKG	SQKHVTKKKP	ANSKGQNGKR	GDADQKQTIK
970	980	990	1000	1010	1020	1030	1040
ITAKVGTLKR	KQQMREFLEQ	LPKDDHDDFF	STTPLQHQRI	LLPSFQDSED	DDDILPNMDK	NPTTPSSVIF	PLVKTPQCQH
1050	1060	1070	1080	1090	1100	1110	1120
VSPGMLGSIN	RNDCDKYVFR	MQKYHKSNGG	IVWGNIKKKL	VETDFSTPTP	RRKTPFNTDL	GENSGIGKLF	TNAVESLDEE
1130	1140						
EKDYYFSNSD	SA						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1865	1	1057.5367	-22.09	2	52.0	12.7	0	182-201	R.ASVQGVPLESSNNDIFLPVK.Q	
2837	1	868.9237	11.97	2	64.0	11.5	1	325-341	K.TVPGETGLPGSMKDTCK.I	Oxidation: 12
2772	1	733.8764	59.69	2	63.7	13.0	0	695-707	K.SMGTLENTFEGHK.S	Oxidation: 2

BRUKER

Detailed Protein Report

Protein 131: OTU domain-containing protein 7B [Homo sapiens]

Accession:	gi|118026942	**Score:**	47.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	92.5
Database Date:	2015-11-30	**pI:**	6.3
Modification(s):	Oxidation	**Sequence Coverage [%]:**	6.2
		No. of unique Peptides:	3

Alias proteins:

Accession	Name	Description
gi|578801304	refseq_human(refseq_human_20140103.fasta)	PREDICTED: OTU domain-containing protein 7B isoform X5 [Homo sapiens]
gi|578801302	refseq_human(refseq_human_20140103.fasta)	PREDICTED: OTU domain-containing protein 7B isoform X4 [Homo sapiens]
gi|578801300	refseq_human(refseq_human_20140103.fasta)	PREDICTED: OTU domain-containing protein 7B isoform X3 [Homo sapiens]

10	20	30	40	50	60	70	80
MTLDMDAVLS	DFVRSTGAEP	GLARDLLEGK	NWDVNAALSD	FEQLRQVHAG	NLPPSFSEGS	GGSRTPEKGF	SDREPTRPPR
90	100	110	120	130	140	150	160
PILQRQDDIV	QEKRLSRGIS	HASSSIVSLA	RSHVSSNGGG	GGSNEHPLEM	PICAFQLPDL	TVYNEDFRSF	IERDLIEQSM
170	180	190	200	210	220	230	240
LVALEQAGRL	NWWVSVDPTS	QRLLPLATTG	DGNCLLHAAS	LGMWGFHDRD	LMLRKALYAL	MEKGVEKEAL	KRRWRWQQTQ
250	260	270	280	290	300	310	320
QNKESGLVYT	EDEWQKEWNE	LIKLASSEPR	MHLGTNGANC	GGVESSEEPV	YESLEEFHVF	VLAHVLRRPI	VVVADTMLRD
330	340	350	360	370	380	390	400
SGGEAFAPIP	FGGIYLPLEV	PASQCHRSPL	VLAYDQAHFS	ALVSMEQKEN	TKEQAVIPLT	DSEYKLLPLH	FAVDPGKGWE
410	420	430	440	450	460	470	480
WGKDDSDNVR	LASVILSLEV	KLHLLHSYMN	VKWIPLSSDA	QAPLAQPESP	TASAGDEPRS	TPESGDSDKE	SVGSSSTSNE
490	500	510	520	530	540	550	560
GGRRKEKSKR	DREKDKKRAD	SVANKLGSFG	KTLGSKLKKN	MGGLMHSKGS	KPGGVGTGLG	GSSGTETLEK	KKKNSLKSWK
570	580	590	600	610	620	630	640
GGKEEAAGDG	PVSEKPPAES	VGNGGSKYSQ	EVMQSLSILR	TAMQGEGKFI	FVGTLKMGHR	HQYQEEMIQR	YLSDAEERFL
650	660	670	680	690	700	710	720
AEQKQKEAER	KIMNGGIGGG	PPPAKKPEPD	AREEQPTGPP	AESRAMAFST	GYPGDFTIPR	PSGGGVHCQE	PRRQLAGGPC
730	740	750	760	770	780	790	800
VGGLPPYATF	PRQCPPGRPY	PHQDSIPSLE	PGSHSKDGLH	RGALLPPPYR	VADSYSNGYR	EPPEPDGWAG	GLRGLPPTQT
810	820	830	840	850			
KCKQPNCSFY	GHPETNNFCS	CCYREELRRR	EREPDGELLV	HRF			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2718	1	1175.5515	-33.60	2	62.4	11.6	0	348-368	R.SPLVLAYDQAHFSALVSMEQK.E	Oxidation: 18
2130	1	1052.4295	-112.31	2	56.8	17.0	1	529-551	K.GSKPGGVGTGLGGSSGTETLEKK.K	
917	1	491.6624	-132.38	2	40.3	18.8	0	631-638	R.YLSDAEER.F	

Detailed Protein Report

Protein 132: MAP/microtubule affinity-regulating kinase 4 isoform 2 [Homo sapiens]

Accession:	gi|33636756	**Score:**	47.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	75.3
Database Date:	2015-11-30	**pI:**	10.5
		Sequence Coverage [%]:	3.8
		No. of unique Peptides:	1

Quantitation

mdown:qdown **Median:** 0.40 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MSSRTVLAPG	NDRNSDTHGT	LGSGRSSDKG	PSWSSRSLGA	RCRNSIASCP	EEQPHVGNYR	LLRTIGKGNF	AKVKLARHIL
90	100	110	120	130	140	150	160
TGREVAIKII	DKTQLNPSSL	QKLFREVRIM	KGLNHPNIVK	LFEVIETEKT	LYLVMEYASA	GEVFDYLVSH	GRMKEKEARA
170	180	190	200	210	220	230	240
KFRQIVSAVH	YCHQKNIVHR	DLKAENLLLD	AEANIKIADF	GFSNEFTLGS	KLDTFCGSPP	YAAPELFQGK	KYDGPEVDIW
250	260	270	280	290	300	310	320
SLGVILYTLV	SGSLPFDGHN	LKELRERVLR	GKYRVPFYMS	TDCESILRRF	LVLNPAKRCT	LEQIMKDKWI	NIGYEGEELK
330	340	350	360	370	380	390	400
PYTEPEEDFG	DTKRIEVMVG	MGYTREEIKE	SLTSQKYNEV	TATYLLLGRK	TEEGGDRGAP	GLALARVRAP	SDTTNGTSSS
410	420	430	440	450	460	470	480
KGTSHSKGQR	SSSSTYHRQR	RHSDFCGPSP	APLHPKRSPT	STGEAELKEE	RLPGRKASCS	TAGSGSRGLP	PSSPMVSSAH
490	500	510	520	530	540	550	560
NPNKAEIPER	RKDSTSTPNN	LPPSMMTRRN	TYVCTERPGA	ERPSLLPNGK	ENSSGTPRVP	PASPSSHSLA	PPSGERSRLA
570	580	590	600	610	620	630	640
RGSTIRSTFH	GGQVRDRRAG	GGGGGGVQNG	PPASPTLAHE	AAPLPAGRPR	PTTNLFTKLT	SKLTRRVTLD	PSKRQNSNRC
650	660	670	680	690			
VSGASLPQGS	KIRSQTNLRE	SGDLRSQVAI	YLGIKRKPPP	GCSDSPGV			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1367	1	388.0811	-379.40	2	45.6	16.7	1	106-111	R.EVRIMK.G		mdown:qdown 0.40

Detailed Protein Report

Protein 133: PREDICTED: dmX-like protein 2 isoform X3 [Homo sapiens]

Accession:	gi|530405585	**Score:**	47.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	291.5
Database Date:	2015-11-30	**pI:**	5.9
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	1.7
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MHLHQVLTGA	VNPGDNCYSV	GSVGDVPFTA	YGSGCDIVIL	ANDFECVQII	PGAKHGNIQV	SCVECSNQQG	RIAASYGNAV
90	100	110	120	130	140	150	160
CIFEPLGINS	HKRNCQLKCQ	WLKTGQFFLS	SVTYNLAWDP	QDNRLLTATD	SIQLWAPPGD	DILEEEEEID	NTVPPVLNDW
170	180	190	200	210	220	230	240
KCVWQCKTSV	SVHLMEWSPD	GEYFATAGKD	DCLLKVWYPM	TGWKSSIIPQ	DHHEVKRRQS	STQFSFVYLA	HPRAVTGFSW
250	260	270	280	290	300	310	320
RKTSKYMPRG	SVCNVLLTSC	HDGVCRLWAE	TLLPEDCLLG	EQICETTTSS	IASSLSHAGR	HKDRIQHALE	TIHHLKNLRK
330	340	350	360	370	380	390	400
GQRRSSVLVT	HAELMPDQTA	MHEVQRHISH	HANALCHFHI	AASINPATDI	PNVLVGTAFN	VDDGNGGFVV	HWLNNKEFHF
410	420	430	440	450	460	470	480
TSSTEVFMHQ	LRKLSDKQVD	HENDDADRED	EEHSQEDRER	GLHMKLDHDL	SLDRESEAGT	GSSEHEDGER	EGSPRTYSRL
490	500	510	520	530	540	550	560
SVPMPLPTVL	LDRKIETLLT	EWNKNPDMLF	TIHPVDGTFL	VWHVKYLDEY	NPGIFRQVQV	SFSSRIPVAF	PSGDASSLSK
570	580	590	600	610	620	630	640
NIMMYACINA	TKDSHHTLLH	QEGMSVGSPH	GSQPHSRSHS	THMNILAPTV	MMISKHIDGS	LNQWAVTFAD	KSAFTTVLTV
650	660	670	680	690	700	710	720
SHKFRYCGHR	FHLNDLACHS	VLPLLLTSSH	HNALLTPELD	CQWDSDNKLS	RLMDPVKHIK	GSSKQPLRNA	ATRTFHDPNA
730	740	750	760	770	780	790	800
IYSELILWRV	DPIGPLSYTG	GVSELARINS	LHTSAFSNVA	WLPTLIPSYC	LGTYCNSASA	CFVASDGKNL	RLYQAVVDAR
810	820	830	840	850	860	870	880
KLLDELSDPE	SSKLIGEVFN	IVSQQSTARP	GCIIELDAIT	NQCGSNTQLL	HVFQEDFIIG	YKPHKEDMEK	KETEIFFQPS
890	900	910	920	930	940	950	960
QGYRPPPFSE	KFFLVVIEKD	SNNNSILHMW	HLHLKSVQAC	LAKASEGASS	ESLLSVPGQK	NVDSSPETSP	SVSPMPHSSS
970	980	990	1000	1010	1020	1030	1040
IANLQTASKL	ILSSRLVYSQ	PLDLPESVEV	IRATPSAGHL	SSSSIYPVCL	APYLVVTTCS	DNKVRFWKCC	MEANPECNKS
1050	1060	1070	1080	1090	1100	1110	1120
DEKEIYHWKR	WPLMNDEGED	NSSTVSIVGR	PVAVSCSYTG	RLAVAYKQPI	HHNGFVSKEF	SMHVCIFECE	STGGSEWVLE
1130	1140	1150	1160	1170	1180	1190	1200
QTIHLDDLVK	VGSVLDSRVS	VDSNLFVYSK	SDALLSKDRY	LIPNIKHLVH	LDWVSKEDGS	HILTVGVGAN	IFMYGRLSGI
1210	1220	1230	1240	1250	1260	1270	1280
VTEQTNSKDG	VAVITLPLGG	SIKQGVKSRW	VLLRSIDLVS	SVDGTPSLPV	SLSWVRDGIL	VVGMDCEMHV	YAQWKHAVKF
1290	1300	1310	1320	1330	1340	1350	1360
GDTEADSSNA	EEAAMQDHST	FKSNMLARKS	VVEGTAISDD	VFCSPTVIQD	GGLFEAAHVL	SPTLPQYHPT	QLLELMDLGK
1370	1380	1390	1400	1410	1420	1430	1440
VRRAKAILSH	LVKCIAGEVA	IVRDPDAGEG	TKRHLSRTIS	VSGSTAKETV	TVGKDGTRDY	TEIDSIPPLP	LYALLAADQD
1450	1460	1470	1480	1490	1500	1510	1520
TSYRISEEST	KIPQSYEDQT	VSQPEDQYSE	LFQIQDIPTD	DIDLEPEKRE	NKSKVINLSQ	YGPAYFGQEH	ARVLSSHLMH
1530	1540	1550	1560	1570	1580	1590	1600
SSLPGLTRLE	QMFLVALADT	VATTSTELDE	SRDKSCSGRD	TLDECGLRYL	LAMRLHTCLL	TSLPPLYRVQ	LLHQGVSTCH
1610	1620	1630	1640	1650	1660	1670	1680
FAWAFHSEAE	EELINMIPAI	QRGDPQWSEL	RAMGIGWWVR	NINTLRRCIE	KVAKASFQRN	NDALDAALFY	LSMKKKAVVW
1690	1700	1710	1720	1730	1740	1750	1760
GLFRSQHDEK	MTTFFSHNFN	EDRWRKAALK	NAFSLLGKQR	FEQSAAFFLL	AGSLKDAIEV	CLEKMEDIQL	AMVIARLYES
1770	1780	1790	1800	1810	1820	1830	1840
EFETSSTYIS	ILNQKILGCQ	KDGSGFSCKR	LHPDPFLRSL	AYWVMKDYTR	ALDTLLEQTP	KEDDEHQVII	KSCNPVAFSF
1850	1860	1870	1880	1890	1900	1910	1920
YNYLRTHPLL	IRRNLASPEG	TLATLGLKTE	KNFVDKINLI	ERKLFFTTAN	AHFKVGCPVL	ALEVLSKIPK	VTKTSALSAK
1930	1940	1950	1960	1970	1980	1990	2000
KDQPDFISHR	MDDVPSHSKA	LSDGNGSSGI	EWSNVTSSQY	DWSQPIVKVD	EEPLNLDWGE	DHDSALDEEE	DDAVGLVMKS
2010	2020	2030	2040	2050	2060	2070	2080
TDAREKDKQS	DQKASDPNML	LTPQEEDDPE	GDTEVDVIAE	QLKFRACLKI	LMTELRTLAT	GYEVDGGKLR	FQLYNWLEKE
2090	2100	2110	2120	2130	2140	2150	2160
IAALHEICNH	ESVIKEYSSK	TYSKVESDLL	DQEEMVDKPD	IGSYERHQIE	RRRLQAKREH	AERRKSWLQK	NQDLLRVFLS
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
951	1	677.3400	9.12	3	40.4	17.0	0	598-615	R.SHSTHMNILAPTVMMISK.H	Oxidation: 14, 15
1839	1	780.2904	-91.58	2	51.5	14.1	1	2574-2588	R.VSCSSHRGVPGGMGR.K	Carbamidomethyl: 3; Oxidation: 13

Detailed Protein Report

Protein 134: collagen alpha-2(XI) chain isoform 2 preproprotein [Homo sapiens]

Accession: gi|111118972
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 47.3
MW [kDa]: 162.1
pI: 8.8
Sequence Coverage [%]: 2.8
No. of unique Peptides: 2

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	QEPQSQDPTP	GEEEEILESS	LLPPLEEAAH	GPRGLKGEKG	EPAVLEPGML	VEGPPGPEGP
330	340	350	360	370	380	390	400
AGLIGPPGIQ	GNPGPVGDPG	ERGPPGRAGL	PGSDGAPGPP	GTSLMLPFRF	GSGGGDKGPV	VAAQEAQAQA	ILQQARLALR
410	420	430	440	450	460	470	480
GPPGPMGYTG	RPGPLGQPGS	PGLKGESGDL	GPQGPRGPQG	LTGPPGKAGR	RGRAGADGAR	GMPGDPGVKG	DRGFDGLPGL
490	500	510	520	530	540	550	560
PGEKGHRGDT	GAQGLPGPPG	EDGERGDDGE	IGPRGLPGES	GPRGLLGPKG	PPGIPGPPGV	RGMDGPQGPK	GSLGPQGEPG
570	580	590	600	610	620	630	640
PPGQQGTPGT	QGLPGPQGAI	GPHGEKGPQG	KPGLPGMPGS	DGPPGHPGKE	GPPGTKGNQG	PSGPQGPLGY	PGPRGVKGVD
650	660	670	680	690	700	710	720
GIRGLKGHKG	EKGEDGFPGF	KGDIGVKGDR	GEVGVPGSRG	EDGPEGPKGR	TGPTGDPGPP	GLMGEKGKLG	VPGLPGYPGR
730	740	750	760	770	780	790	800
QGPKGSLGFP	GFPGASGEKG	ARGLSGKSGP	RGERGPTGPR	GQRGPRGATG	KSGAKGTSGG	DGPHGPPGER	GLPGPQGPNG
810	820	830	840	850	860	870	880
FPGPKGPPGP	PGKDGLPGHP	GQRGEVGFQG	KTGPPGPPGV	VGPQGAAGET	GPMGERGHPG	PPGPPGEQGL	PGTAGKEGTK
890	900	910	920	930	940	950	960
GDPGPPGAPG	KDGPAGLRGF	PGERGLPGTA	GGPGLKGNEG	PSGPPGPAGS	PGERGAAGSG	GPIGPPGRPG	PQGPPGAAGE
970	980	990	1000	1010	1020	1030	1040
KGVPGEKGPI	GPTGRDGVQG	PVGLPGPAGP	PGVAGEDGDK	GEVGDPGQKG	TKGNKGEHGP	PGPPGPIGPV	GQPGAAGADG
1050	1060	1070	1080	1090	1100	1110	1120
EPGARGPQGH	FGAKGDEGTR	GFNGPPGPIG	LQGLPGPSGE	KGETGDVGPM	GPPGPPGPRG	PAGPNGADGP	QGPPGGVGNL
1130	1140	1150	1160	1170	1180	1190	1200
GPPGEKGEPG	ESGSPGIQGE	PGVKGPRGER	GEKGESGQPG	EPGPPGPKGP	TGDDGPKGNP	GPVGFPGDPG	PPGEGGPRGQ
1210	1220	1230	1240	1250	1260	1270	1280
DGAKGDRGED	GEPGQPGSPG	PTGENGPPGP	LGKRGPAGSP	GSEGRQGGKG	AKGDPGAIGA	PGKTGPVGPA	GPAGKPGPDG
1290	1300	1310	1320	1330	1340	1350	1360
LRGLPGSVGQ	QGRPGATGQA	GPPGPVGPPG	LPGLRGDAGA	KGEKGHPGLI	GLIGPPGEQG	EKGDRGLPGP	QGSPGQKGEM
1370	1380	1390	1400	1410	1420	1430	1440
GIPGASGPIG	PGGPPGLPGP	AGPKGAKGAT	GPGGPKGEKG	VQGPPGHPGP	PGEVIQPLPI	QMPKKTRRSV	DGSRLMQEDE
1450	1460	1470	1480	1490	1500	1510	1520
AIPTGGAPGS	PGGLEEIFGS	LDSLREEIEQ	MRRPTGTQDS	PARTCQDLKL	CHPELPDGEY	WVDPNQGCAR	DAFRVFCNFT
1530	1540	1550	1560	1570	1580	1590	1600
AGGETCVTPR	DDVTQFSYVD	SEGSPVGVVQ	LTFLRLLSVS	AHQDVSYPCS	GAARDGPLRL	RGANEDELSP	ETSPYVKEFR
1610	1620	1630	1640	1650	1660		
DGCQTQQGRT	VLEVRTPVLE	QLPVLDASFS	DLGAPPRRGG	VLLGPVCFMG			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2871	3	645.8309	-41.94	2	64.6	23.7	1	158-169	K.GQSVTLIVDCKK.R	
2503	1	862.3584	-77.51	2	61.7	12.3	1	689-706	K.GRTGPTGDPGPPGLMGEK.G	

Detailed Protein Report

Protein 135: PREDICTED: nesprin-1 isoform X17 [Homo sapiens]

Accession:	gi|578812600	**Score:**	47.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	1006.9
Database Date:	2015-11-30	**pI:**	5.3
Modification(s):	Oxidation	**Sequence Coverage [%]:**	0.6
		No. of unique Peptides:	4

Quantitation

mdown:qdown	**Median:** 1.08	**CV:** 0.00 %	**No. of Peptides:** 1

Detailed Protein Report

10	20	30	40	50	60	70	80
MATSRGASRC	PRDIANVMQR	LQDEQEIVQK	RTFTKWINSH	LAKRKPPMVV	DDLFEDMKDG	VKLLALLEVL	SGQKLPCEQG
90	100	110	120	130	140	150	160
RRMKRIHAVA	NIGTALKFLE	GRKSMHRGSP	IKLVNINSTD	IADGRPSIVL	GLMWTIILYF	QIEELTSNLP	QLQSLSSSAS
170	180	190	200	210	220	230	240
SVDSIVSSET	PSPPSKRKVT	TKIQGNAKKA	LLKWVQYTAG	KQTGIEVKDF	GKSWRSGVAF	HSVIHAIRPE	LVDLETVKGR
250	260	270	280	290	300	310	320
SNRENLEDAF	TIAETELGIP	RLLDPEDVDV	DKPDEKSIMT	YVAQFLKHYP	DIHNASTDGQ	EDDEILPGFP	SFANSVQNFK
330	340	350	360	370	380	390	400
REDRVIFKEM	KVWIEQFERD	LTRAQMVESN	LQDKYQSFKH	FRVQYEMKRK	QIEHLIQPLH	RDGKLSLDQA	LVKQSWDRVT
410	420	430	440	450	460	470	480
SRLFDWHIQL	DKSLPAPLGT	IGAWLYRAEV	ALREEITVQQ	VHEETANTIQ	RKLEQHKDLL	QNTDAHKRAF	HEIYRTRSVN
490	500	510	520	530	540	550	560
GIPVPPDQLE	DMAERFHFVS	STSELHLMKM	EFLELKYRLL	SLLVLAESKL	KSWIIKYGRR	ESVEQLLQNY	VSFIENSKFF
570	580	590	600	610	620	630	640
EQYEVTYQIL	KQTAEMYVKA	DGSVEEAENV	MKFMNETTAQ	WRNLSVEVRS	VRSMLEEVIS	NWDRYGNTVA	SLQAWLEDAE
650	660	670	680	690	700	710	720
KMLNQSENAK	KDFFRNLPHW	IQQHTAMNDA	GNFLIETCDE	MVSRDLKQQL	LLLNGRWREL	FMEVKQYAQA	DEMDRMKKEY
730	740	750	760	770	780	790	800
TDCVVTLSAF	ATEAHKKLSE	PLEVSFMNVK	LLIQDLEDIE	QRVPVMDAQY	KIITKTAHLI	TKESPQEEGK	EMFATMSKLK
810	820	830	840	850	860	870	880
EQLTKVKECY	SPLLYESQQL	LIPLEELEKQ	MTSFYDSLGK	INEIITVLER	EAQSSALFKQ	KHQELLACQE	NCKKTLTLIE
890	900	910	920	930	940	950	960
KGSQSVQKFV	TLSNVLKHFD	QTRLQRQIAD	IHVAFQSMVK	KTGDWKKHVE	TNSRLMKKFE	ESRAELEKVL	RIAQEGLEEK
970	980	990	1000	1010	1020	1030	1040
GDPEELLRRH	TEFFSQLDQR	VLNAFLKACD	ELTDILPEQE	QQGLQEAVRK	LHKQWKDLQG	EAPYHLLHLK	IDVEKNRFLA
1050	1060	1070	1080	1090	1100	1110	1120
SVEECRTELD	RETKLMPQEG	SEKIIKEHRV	FFSDKGPHHL	CEKRLQLIEE	LCVKLPVRDP	VRDTPGTCHV	TLKELRAAID
1130	1140	1150	1160	1170	1180	1190	1200
STYRKLMEDP	DKWKDYTSRF	SEFSSWISTN	ETQLKGIKGE	AIDTANHGEV	KRAVEEIRNG	VTKRGETLSW	LKSRLKVLTE
1210	1220	1230	1240	1250	1260	1270	1280
VSSENEAQKQ	GDELAKLSSS	FKALVTLLSE	VEKMLSNFGD	CVQYKEIVKN	SLEELISGSK	EVQEQAEKIL	DTENLFEAQQ
1290	1300	1310	1320	1330	1340	1350	1360
LLLHHQQKTK	RISAKKRDVQ	QQIAQAQQGE	GGLPDRGHEE	LRKLESTLDG	LERSRERQER	RIQVTLRKWE	RFETNKETVV
1370	1380	1390	1400	1410	1420	1430	1440
RYLFQTGSSH	ERFLSFSSLE	SLSSELEQTK	EFSKRTESIA	VQAENLVKEA	SEIPLGPQNK	QLLQQQAKSI	KEQVKKLEDT
1450	1460	1470	1480	1490	1500	1510	1520
LEEDIKTMEM	VKTKWDHFGS	NFETLSVWIT	EKEKELNALE	TSSSAMDMQI	SQIKVTIQEI	ESKLSSIVGL	EEEAQSFAQF
1530	1540	1550	1560	1570	1580	1590	1600
VTTGESARIK	AKLTQIRRYG	EELREHAQCL	EGTILGHLSQ	QQKFEENLRK	IQQSVSEFED	KLAVPIKICS	SATETYKVLQ
1610	1620	1630	1640	1650	1660	1670	1680
EHMDLCQALE	SLSSAITAFS	ASARKVVNRD	SCVQEAAALQ	QQYEDILRRA	KERQTALENL	LAHWQRLEKE	LSSFLTWLER
1690	1700	1710	1720	1730	1740	1750	1760
GEAKASSPEM	DISADRVKVE	GELQLIQALQ	NEVVSQASFY	SKLLQLKESL	FSVASKDDVK	MMKLHLEQLD	ERWRDLPQII
1770	1780	1790	1800	1810	1820	1830	1840
NKRINFLQSV	VAEHQQFDEL	LLSFSVWIKL	FLSELQTTSE	ISIMDHQVAL	TRHKDHAAEV	ESKKGELQSL	QGHLAKLGSL
1850	1860	1870	1880	1890	1900	1910	1920
GRAEDLHLLQ	GKAEDCFQLF	EEASQVVERR	QLALSHLAEF	LQSHASLSGI	LRQLRQTVEA	TNSMNKNESD	LIEKDLNDAL
1930	1940	1950	1960	1970	1980	1990	2000
QNAKALESAA	VSLDGILSKA	QYHLKIGSSE	QRTSCRATAD	QLCGEVERIQ	NLLGTKQSEA	DALAVLKKAF	QDQKEELLKS
2010	2020	2030	2040	2050	2060	2070	2080
IEDIEERTDK	ERLKEPTRQA	LQQRLRVFNQ	LEDELNSHEH	ELCWLKDKAK	QIAQKDVAFA	PEVDREINRL	EVTWDDTKRL
2090	2100	2110	2120	2130	2140	2150	2160
IHENQGQCCG	LIDLMREYQN	LKSAVSKVLE	NASSVIVTRT	TIKDQEDLKW	AFSKHETAKN	KMNYKQKDLD	NFTSKGKHLL
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1807	1	945.8341	-138.33	2	51.1	10.6	2	1681-1698	R.GEAKASSPEMDISADRVK.V		
742	1	524.3579	134.01	2	37.8	10.5	1	2443-2452	R.TGDSKVLEAK.L		
543	1	567.1646	-233.64	2	36.1	11.3	0	5483-5492	K.LMELDAAVQK.F	Oxidation: 2	mdown:qdown 1.08
2878	1	913.4666	-41.53	2	65.2	14.8	1	7089-7104	K.EVEKIEQNGLALIQNK.K		

Detailed Protein Report

Protein 136: PREDICTED: LOW QUALITY PROTEIN: hemicentin-2 [Homo sapiens]

Accession:	gi|578818143	**Score:**	47.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	546.0
Database Date:	2015-11-30	**pI:**	5.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.1
		No. of unique Peptides:	2

Detailed Protein Report

```
        10         20         30         40         50         60         70         80
MMPGAPLLRL LTAVSAAVAV AVAGAPGTVM PPTTGDATLA FVFDVTGSMW DELMQVIDGA SRILERSLSR RSQAIANYAL
        90        100        110        120        130        140        150        160
VPFHDPDIGP VTLTADPTVF QRELRELYVQ GGGDCPEMSV GAIKAAVEVA NPGSFIYVFS DARAKDYHKK EELLRLLQLK
       170        180        190        200        210        220        230        240
QSQVVFVLTG DCGDRTHPGY LAYEEIAATS SGQVFHLDKQ QVTEVLKWVE SAIQASKVHL LSTDHEEEGE HTWRLPFDPS
       250        260        270        280        290        300        310        320
LKEVTISLSG PGPEIEVQDP LGRILQEDEG LNVLLNIPDS AKVVAFKPEH PGLWSIKVYS SGRHSVRITG VSNIDFRAGF
       330        340        350        360        370        380        390        400
STQPLLDLNH TLEWPLQGVP ISLVINSTGL KAPGRLDSVE LAQSSGKPLL TLPTKPLSNG STHQLWGGPP FHTPKERFYL
       410        420        430        440        450        460        470        480
KVKGKDHEGN PLLRVSGVSY SGVAPGAPLV SMAPRIHGYL HQPLLVSCSV HSALPFRLQL RRGEARLGEE RHFQESGNSS
       490        500        510        520        530        540        550        560
WEILRASKAE EGTYECTAVS RAGTGRAKAQ IVVTDPPPQL VPAPNVTVSP GETAVLSCRV LGEAPYNLTW VRDWRVLPAS
       570        580        590        600        610        620        630        640
TGRVAQLADL SLEISGIIPT DGGRYQCVAS NANGVTRASV WLLVREAPQV SIHTSSQHFS QGVEVKVSCS ASGYPTPHIS
       650        660        670        680        690        700        710        720
WSRESQALQE DSRIHVDAQG TLIIQGVAPE DAGNYSCQAT NEVGTDQETV TLYYTDPPSV SAVNAVVLVA VGEEAVLVCE
       730        740        750        760        770        780        790        800
ASGVPPPRVI WYRGGLEMIL APEGSSSGKL RIPAAQERDA GTYTCRAVNE LGDASAEIQL AVGHAPQLTE LPRDVTVELG
       810        820        830        840        850        860        870        880
RSALLACRAT GRPPPTVTWR RGDGQPLGLR LGAGRGSRSR QPDSGVLFFE SVAPEDQAPY VCEARNVFGK VQAEARLIVT
       890        900        910        920        930        940        950        960
GHAPPQIASS APTVRVLEGQ PVSLPCIVLA GRPLPERHWL KDGRPLPPGS RHSIRADGSL HLDRALQEHA GRYSCVATNT
       970        980        990       1000       1010       1020       1030       1040
AGSQHRDVEL VVQVPPRIHP TATHHITNEG VAASLPCVAS GVPAPTITWT KETNALTSRG PHYNVSKEGT LLIAQPSAQD
      1050       1060       1070       1080       1090       1100       1110       1120
AGAYVCTATN TVGFSSQEMR LSVNTKPRIH MNGSRNADVP LQVTAKAGEE VTLDCEAKGS PPPLVTWTKD SRPVPPITNR
      1130       1140       1150       1160       1170       1180       1190       1200
YGLLPSGSLR LAQVQVGDSG HYECTASNPA GSASHRYVLG VQVPPQVQPG PRVLKVLVGE ALDLNCVAEG NPEPQLSWSK
      1210       1220       1230       1240       1250       1260       1270       1280
DGVVLQGRGP QGSVHFAAIR TSDAGRYRCE ASNSAGVDAW EVELRVLEPP HWGADETSGL LERVAGENAS LPCPARGTPK
      1290       1300       1310       1320       1330       1340       1350       1360
PQVTWRKGPS SEPLHGQPGV AVLEEGSLFL ASVSPADSGD YECQATNEVG STSRRAKLVV YVPPSIREDG RKANVSGMAG
      1370       1380       1390       1400       1410       1420       1430       1440
QSLTLECDAN GFPVPEIVWL KDAQLIPKVG GHRLLDEGQS LHFPRIQEGD SGLYSCRAEN QAGTAQRDFH LLVLTPPSVL
      1450       1460       1470       1480       1490       1500       1510       1520
GAGAAQEVLG LAGADVELQC WTSGVPTPQV EWTKDRQPVL PGGPHLQVQE DGQVLRITGS HVGDEGRYQC VAFSPAGQQA
      1530       1540       1550       1560       1570       1580       1590       1600
RDFQLRVHAP PTIWGSNETG EVAVMEDHLV QLLCEARGVP TPNITWFKDG ALLPTSTKVV YTRGGRQLQL GRAQSSDAGV
      1610       1620       1630       1640       1650       1660       1670       1680
YTCKASNAVG AAEKATRLDV YVPPTIEGAG GRPYVVKAVA GRPVALECVA RGHPSPTLSW HHEGLPVAES NESRLETDGS
      1690       1700       1710       1720       1730       1740       1750       1760
VLRLESPGEA SSGLYSCVAS SPAGEAVLQY SVEVQVPPQL LVAEGLGQVT TIVGQPLELP CQASGSPVPT IQWLQNGRPA
      1770       1780       1790       1800       1810       1820       1830       1840
EELAGVQVAS QGTTLHIDHV ELDHSGLFAC QATNEAGTAG AEVEVSVHGE WAPGVLEVPI GQYHWGXEHH SSFPAACDPP
      1850       1860       1870       1880       1890       1900       1910       1920
VHRGWGAHPK PPLVEGWCSP GSLWGEPTGI PVAYSLPPPL QIEKVDLRDE GIYTCAATNL AGESKREVAL KVLVPPNIEP
      1930       1940       1950       1960       1970       1980       1990       2000
GPVNKAVLEN ASVTLECLAS GVPPPDVSWF KGHQPVSSWM GVTVSVDGRV LRIEQAQLSD AGSYRCVASN VAGSTELRYG
      2010       2020       2030       2040       2050       2060       2070       2080
LRVNVPPRIT LPPSLPGPVL VNTPVRLTCN ATGAPSPTLM WLKDGNPVSP AGTPGLQVFP GGRVLTLASA RASDSGRYSC
      2090       2100       2110       2120       2130       2140       2150       2160
VAVSAVGEDR QDVVLQVHMP PSILGEELNV SVVANESVAL ECQSHAMPPP VLSWWKDGRP LEPRPGVHLS ADKALLQVDR
      2170       2180       2190       2200       2210       2220       2230       2240
```

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2115	1	840.8591	-53.51	2	56.6	14.6	0	161-175	K.QSQVVFVLTGDCGDR.T	Carbamidomethyl: 12
61	1	623.8088	95.46	5	29.5	12.6	2	866-895	R.NVFGKVQAEARLIVTGHAPPQIASSAPTVR.V	

Detailed Protein Report

Protein 137: keratin, type II cuticular Hb4 [Homo sapiens]

Accession:	gi|15431316	**Score:**	47.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	64.8
Database Date:	2015-11-30	**pI:**	9.0
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	5.8
		No. of unique Peptides:	2

Quantitation

mdown:qdown **Median:** 1.41 **CV:** 0.00 % **No. of 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	Ratios
553	1	607.3109	-5.53	2	35.5	13.1	0	54-64	R.SVITFGSYSPR.I		
603	2	652.6252	-207.98	2	36.9	13.1	0	79-91	R.FGAGCGMGFGDGR.G	Carbamidomethyl: 5; Oxidation: 7	mdown:qdown 1.41

Detailed Protein Report

Protein 138: PREDICTED: PR domain zinc finger protein 16 isoform X3 [Homo sapiens]

Accession:	gi|530360370	**Score:**	47.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	129.7
Database Date:	2015-11-30	**pI:**	5.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.5
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MRSKARARKL	AKSDGDVVNN	MYEPNRDLLA	SHSAEDEAED	SAMSPIPVGP	PSPFPTSEDF	TPKEGSPYEA	PVYIPEDIPI
90	100	110	120	130	140	150	160
PADFELRESS	IPGAGLGVWA	KRKMEAGERL	GPCVVVPRAA	AKETDFGWEQ	ILTDVEVSPQ	EGCITKQISE	DLGSEKFCVD
170	180	190	200	210	220	230	240
ANQAGAGSWL	KYIRVACSCD	DQNLTMCQIS	EQIYYKVIKD	IEPGEELLVH	VKEGVYPLGT	VPPGLDEEPT	FRCDECDELF
250	260	270	280	290	300	310	320
QSKLDLRRHK	KYTCGSVGAA	LYEGLAEELK	PEGLGGGSGQ	AHECKDCERM	FPNKYSLEQH	MVIHTEEREY	KCDQCPKAFN
330	340	350	360	370	380	390	400
WKSNLIRHQM	SHDSGKRFEC	ENCVKVFTDP	SNLQRHIRSQ	HVGARAHACP	DCGKTFATSS	GLKQHKHIHS	TVKPFICEVC
410	420	430	440	450	460	470	480
HKSYTQFSNL	CRHKRMHADC	RTQIKCKDCG	QMFSTTSSLN	KHRRFCEGKN	HYTPGGIFAP	GLPLTPSPMM	DKAKPSPSLN
490	500	510	520	530	540	550	560
HASLGFNEYF	PSRPHPGSLP	FSTAPPTFPA	LTPGFPGIFP	PSLYPRPPLL	PPTSLLKSPL	NHTQDAKLPS	PLGNPALPLV
570	580	590	600	610	620	630	640
SAVSNSSQGT	TAAAGPEEKF	ESRLEDSCVE	KLKTRSSDMS	DGSDFEDVNT	TTGTDLDTTT	GTGSDLDSDV	DSDPDKDKGK
650	660	670	680	690	700	710	720
GKSAEGQPKF	GGGLAPPGAP	NSVAEVPVFY	SQHSFFPPPD	EQLLTATGAA	GDSIKAIASI	AEKYFGPGFM	GMQEKKLGSL
730	740	750	760	770	780	790	800
PYHSAFPFQF	LPNFPHSLYP	FTDRALAHNL	LVKAEPKSPR	DALKVGGPSA	ECPFDLTTKP	KDVKPILPMP	KGPSAPASGE
810	820	830	840	850	860	870	880
EQPLDLSIGS	RARASQNGGG	REPRKNHVYG	ERKLGAGEGL	PQVCPARMPQ	QPPLHYAKPS	PFFMDPIYSR	VEKRKVTDPV
890	900	910	920	930	940	950	960
GALKEKYLRP	SPLLFHPQMS	AIETMTEKLE	SFAAMKADSG	SSLQPLPHHP	FNFRSPPPTL	SDPILRKGKE	RYTCRYCGKI
970	980	990	1000	1010	1020	1030	1040
FPRSANLTRH	LRTHTGEQPY	RCKYCDRSFS	ISSNLQRHVR	NIHNKEKPFK	CHLCNRCFGQ	QTNLDRHLKK	HEHENAPVSQ
1050	1060	1070	1080	1090	1100	1110	1120
HPGVLTNHLG	TSASSPTSES	DNHALLDEKE	DSYFSEIRNF	IANSEMNQAS	TRTEKRADMQ	IVDGSAQCPG	LASEKQEDVE
1130	1140	1150	1160	1170	1180		
EEDDDDLEED	DEDSLAGKSQ	DDTVSPAPEP	QAAYEDEEDE	EPAASLAVGF	DHTRRHMQ		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1511	1	1005.9710	-61.06	2	47.6	21.5	2	104-122	K.MEAGERLGPCVVVPRAAAK.E	Carbamidomethyl: 10
2972	1	646.8226	-64.07	2	66.4	11.8	0	935-946	R.SPPPTLSDPILR.K	

Detailed Protein Report

Protein 139: myosin-9 [Homo sapiens]

Accession:	gi|12667788	**Score:**	47.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	226.4
Database Date:	2015-11-30	**pI:**	5.4
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.6
		No. of unique Peptides:	3

Quantitation

Wdown:Qdown	**Median:**	0.74	**CV:**	125.52 %	**No. of Peptides:**	2

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
573	1	472.1766	-189.39	2	36.0	12.4	0	31-38	K.LVWVPSDK.S		Wdown:Qdown 0.28
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-	K.QRSMAVAARK.K	Oxidation: 4	Wdown:Qdown 1.96

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
								1613			

Detailed Protein Report

Protein 140:	**PREDICTED: chromodomain-helicase-DNA-binding protein 7 isoform X4 [Homo sapiens]**		
Accession:	gi|578815680	**Score:**	47.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	214.1
Database Date:	2015-11-30	**pI:**	5.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.6
		No. of unique Peptides:	3

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 Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2753	2	937.4586	-76.18	2	63.4	14.1	2	343-360	K.ASLKLGLDKAVLQSMSGR.E	
1713	1	806.6994	-162.85	2	51.4	15.5	0	750-765	R.GTDMLADGGDGGEFDR.E	
2811	1	995.0043	51.30	2	63.6	17.4	0	995-1010	K.LCQPSLDLPEWWECGR.H	Carbamidomethyl: 14

Detailed Protein Report

Protein 141: PREDICTED: rho guanine nucleotide exchange factor 5-like, partial [Homo sapiens]

Accession:	gi|578844357	**Score:**	46.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	165.0
Database Date:	2015-11-30	**pI:**	5.4
		Sequence Coverage [%]:	2.9
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
FSIIPEAPMR	SSQVSALGLE	AQEDEDPSYK	WREEHRLSAT	QQSELRDVCD	YAIETMPSFP	KEGSADVEPN	QESLVAEACD
90	100	110	120	130	140	150	160
TPEHWEAVPQ	SLAGRQARTL	APPELWACPI	QSEHLDMAPF	SSDLGSEEEE	VEFWPGLTSL	TLGSGQAEEE	EETSSDNSGQ
170	180	190	200	210	220	230	240
TRYYSPCEEH	PAETNQNEGS	ESGTIRQGEE	LPPEELQESQ	GLLHPQEVQV	LEEQGQQEAG	FRGEGTLRED	VCADGLLGEE
250	260	270	280	290	300	310	320
QMIEQVNDEK	GEQKQKQEQV	QDVMLGRQGE	RMGLTGEPEG	LNDGEWEQED	MERKAQGQGG	PEQGEERKRE	LQVPEENRAD
330	340	350	360	370	380	390	400
SQDEKSQIFL	GKSEEVTGKQ	EDHGIKEKGV	PVSGQEAKEP	ESWDGGRLGA	VGRARSREEE	NEHHGPSMPA	LIAPEDSPHC
410	420	430	440	450	460	470	480
DLFPGASYLM	TQIPGTQTES	RAEELSPAAL	SPSLEPIRCS	HQPISLLGSF	LTEESPDKEI	DQNSQQEGSR	LRKGTVSSQG
490	500	510	520	530	540	550	560
TEVVFASASV	TPPRTPDSAP	PSPAEAYPIT	PASVSARPPV	AFPRRETSCA	ARAPETASAP	LSMDDPSPCG	TSEMCPAALY
570	580	590	600	610	620	630	640
GFPSTGTSPP	RPPANSTGTV	QHLRSDSFPG	SHRTEQTPDL	VGMLLSYSHS	ELPQRPPKPA	IYSSVTPRRD	RRSGRDYSTV
650	660	670	680	690	700	710	720
SASPTALSTL	KQDSQESISN	LERPSSPPSI	QPWVSPHNPA	FATESPAYGS	SPSFVSMEDV	RIHEPLPPPP	PQRRDTHPSV
730	740	750	760	770	780	790	800
VETDGHARVV	VPTLKQHSHP	PPLALGSGLH	APHKGPLPQA	SDPAVARQHR	PLPSTPDSSH	HAQATPRWRY	NKPLPPTPDL
810	820	830	840	850	860	870	880
PQPHLPPISA	PGSSRIYRPL	PPLPIIDPPT	EPPPLPPKSR	GRSRSTRGGH	MNSGGHAKTR	PACQDWTVPL	PASAGRTSWP
890	900	910	920	930	940	950	960
PATARSTESF	TSTSRSKSEV	SPGMAFSNMT	NFLCPSSPTT	PWTPELQGPT	SKDEAGVSEH	PEAPAREPLR	RTTPQQGASG
970	980	990	1000	1010	1020	1030	1040
PGRSPVGQAR	QPEKPSHLHL	EKASSWPHRR	DSGRPPGDSS	GQAVAPSEGA	NKHKGWSRQG	LRRPSILPEG	SSDSRGPAVE
1050	1060	1070	1080	1090	1100	1110	1120
KHPGPSDTVV	FREKKPKEVM	GGFSRRCSKL	INSSQLLYQE	YSDVVLNKEI	QSQQRLESLS	ETPGPSSPRQ	PRKALVSSES
1130	1140	1150	1160	1170	1180	1190	1200
YLQRLSMASS	GSLWQEIPVV	RNSTVLLSMT	HEDQKLQEVK	FELIVSEASY	LRSLNIAVDH	FQLSTSLRAT	LSNQEHQWLF
1210	1220	1230	1240	1250	1260	1270	1280
SRLQDVRDVS	ATFLSDLEEN	FENNIFSFQV	CDVVLNHAPD	FRRVYLPYVT	NQTYQERTFQ	SLMNSNSNFR	EVLEKLESDP
1290	1300	1310	1320	1330	1340	1350	1360
VCQRLSLKSF	LILPFQRITR	LKLLLQNILK	RTQPGSSEEA	EATKAHHALE	QLIRDCNNNV	QSMRRTEELI	YLSQKIEFEC
1370	1380	1390	1400	1410	1420	1430	1440
KIFPLISQSR	WLVKSGELTA	LEFSASPGLR	RKLNTRPVHL	HLFNDCLLLS	RPREGSRFLV	FDHAPFSSIR	GEKCEMKLHG
1450	1460	1470	1480	1490	1500		
PHKNLFRLFL	RQNTQGAQAE	FLFRTETQSE	KLRWISALAM	PREELDLLEC	YTM		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2416	1	447.0974	-266.42	2	60.5	12.0	1	525-532	R.RETSCAAR.A	
1626	1	1058.4994	-29.00	2	49.0	12.0	2	933-951	K.DEAGVSEHPEAPAREPLRR.T	

Detailed Protein Report

Protein 142: numb-like protein [Homo sapiens]

Accession:	gi|10863899	**Score:**	46.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	64.9
Database Date:	2015-11-30	**pI:**	10.1
		Sequence Coverage [%]:	9.9
		No. of unique Peptides:	3

Quantitation

mdown:qdown **Median:** 1.04 **CV:** 0.00 % **No. of Peptides:** 1

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	Ratios
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		
2024	2	788.7867	-185.87	2	53.8	13.7	2	308-321	R.GFPALSQKNSPFKR.Q		mdown:qdown 1.04

Detailed Protein Report

Protein 143: PREDICTED: zinc finger protein 708 isoform X1 [Homo sapiens]

Accession:	gi|578833563	**Score:**	46.4
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:	2

Quantitation

mdown:qdown	**Median:**	2.04	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	1.15	**CV:**	0.00 %	**No. of Peptides:**	1

```
        10         20         30         40         50         60         70         80
MKRHEMAAKP PAMCSHFAKD LRPEQYIKNS FQQVILRRYG KCGYQKGCKS VDEHKLHKGG HKGLNRCVTT TQSKIVQCDK
        90        100        110        120        130        140        150        160
YVKVFHKYSN AKRHKIRHTG KNPFKCKECG KSFCMLSQLT QHEIIHTGEK PYKCEECGKA FKKSSNLTNH KIIHTGEKPY
       170        180        190        200        210        220        230        240
KCEECGKAFN QSSTLTRHKI IHTGEKLYKC EECGKAFNRS SNLTKHKIVH TGEKPYKCEE CGKAFKQSSN LTNHKKIHTG
       250        260        270        280        290        300        310        320
EKPYKCGECG KAFTLSSHLT THKRIHTGEK PYKCEECGKA FSVFSTLTKH KIIHTEEKPY KCEECGKAFN RSSHLTNHKV
       330        340        350        360        370        380        390        400
IHTGEKPYKC EECGKAFTKS STLTYHKVIH TGKKPYKCEE CGKAFSIFSI LTKHKVIHTE DKPYKCEECG KTFNYSSNFT
       410        420        430        440        450        460        470        480
NHKKIHTGEK PYKCEECGKS FILSSHLTTH KIIHTGEKPY KCKECGKAFN QSSTLMKHKI IHTGEKPYKC EECGKAFNQS
       490        500
PNLTKHKRIH TKEKPYKCK
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
328	4	605.6684	-199.06	2	32.8	13.8	2	102-111	K.NPFKCKECGK.S	Carbamidomethyl: 8	Wdown:Qdown 1.15 mdown:qdown 2.04
1130	6	586.6095	-252.07	2	43.8	19.3	1	330-339	K.CEECGKAFTK.S	Carbamidomethyl: 4	

Detailed Protein Report

Protein 144: **rap guanine nucleotide exchange factor 3 isoform b [Homo sapiens]**

Accession: gi|20070215
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl, Oxidation

Score: 46.3
MW [kDa]: 99.3
pI: 8.6
Sequence Coverage [%]: 2.5
No. of unique Peptides: 2

Quantitation

mdown:qdown **Median:** 0.50 **CV:** 6.46 % **No. of Peptides:** 2

Alias proteins:

Accession	Name	Description
gi|148747862	refseq_human(refseq_human_20140103.fasta)	rap guanine nucleotide exchange factor 3 isoform b [Homo sapiens]

10	20	30	40	50	60	70	80
MVLRRMHRPR	SCSYQLLLEH	QRPSCIQGLR	WTPLTNSEES	LDFSESLEQA	STERVLRAGR	QLHRHLLATC	PNLIRDRKYH
90	100	110	120	130	140	150	160
LRLYRQCCSG	RELVDGILAL	GLGVHSRSQV	VGICQVLLDE	GALCHVKHDW	AFQDRDAQFY	RFPGPEPEPV	GTHEMEEELA
170	180	190	200	210	220	230	240
EAVALLSQRG	PDALLTVALR	KPPGQRTDEE	LDLIFEELLH	IKAVAHLSNS	VKRELAAVLL	FEPHSKAGTV	LFSQGDKGTS
250	260	270	280	290	300	310	320
WYIIWKGSVN	VVTHGKGLVT	TLHEGDDFGQ	LALVNDAPRA	ATIILREDNC	HFLRVDKQDF	NRIIKDVEAK	TMRLEEHGKV
330	340	350	360	370	380	390	400
VLVLERASQG	AGPSRPPTPG	RNRYTVMSGT	PEKILELLLE	AMGPDSSAHD	PTETFLSDFL	LTHRVFMPSA	QLCAALLHHF
410	420	430	440	450	460	470	480
HVEPAGGSEQ	ERSTYVCNKR	QQILRLVSQW	VALYGSMLHT	DPVATSFLQK	LSDLVGRDTR	LSNLLREQWP	ERRRCHRLEN
490	500	510	520	530	540	550	560
GCGNASPQMK	ARNLPVWLPN	QDEPLPGSSC	AIQVGDKVPY	DICRPDHSVL	TLQLPVTASV	REVMAALAQE	DGWTKGQVLV
570	580	590	600	610	620	630	640
KVNSAGDAIG	LQPDARGVAT	SLGLNERLFV	VNPQEVHELI	PHPDQLGPTV	GSAEGLDLVS	AKDLAGQLTD	HDWSLFNSIH
650	660	670	680	690	700	710	720
QVELIHYVLG	PQHLRDVTTA	NLERFMRRFN	ELQYWVATEL	CLCPVPGPRA	QLLRKFIKLA	AHLKEQKNLN	SFFAVMFGLS
730	740	750	760	770	780	790	800
NSAISRLAHT	WERLPHKVRK	LYSALERLLD	PSWNHRVYRL	ALAKLSPPVI	PFMPLLLKDM	TFIHEGNHTL	VENLINFEKM
810	820	830	840	850	860	870	880
RMMARAARML	HHCRSHNPVP	LSPLRSRVSH	LHEDSQVARI	STCSEQSLST	RSPASTWAYV	QQLKVIDNQR	ELSRLSRELE
890							
P							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
870	1	711.3337	31.93	2	39.7	13.9	0	478-490	R.LENGCGNASPQMK.A	Carbamidomethyl: 5; Oxidation: 12	mdown:qdown 0.47
997	3	555.1971	-145.78	2	41.0	15.0	2	800-808	K.MRMMARAAR.M	Oxidation: 1	mdown:qdown 0.54

Detailed Protein Report

Protein 145: transformation/transcription domain-associated protein isoform 2 [Homo sapiens]

Accession:	gi|4507691	**Score:**	46.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	434.1
Database Date:	2015-11-30	**pI:**	9.3
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.5
		No. of unique Peptides:	2

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

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
2507	1	913.4337	-85.65	2	61.8	14.5	2	2373-2387	R.EKSILLVKMMTYIEK.R	

Detailed Protein Report

Protein 146: alpha-1-acid glycoprotein 2 precursor [Homo sapiens]

Accession:	gi|4505529	**Score:**	46.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	23.6
Database Date:	2015-11-30	**pI:**	4.9
		Sequence Coverage [%]:	5.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MALSWVLTVL	SLLPLLEAQI	PLCANLVPVP	ITNATLDRIT	GKWFYIASAF	RNEEYNKSVQ	EIQATFFYFT	PNKTEDTIFL
90	100	110	120	130	140	150	160
REYQTRQNQC	FYNSSYLNVQ	RENGTVSRYE	GGREHVAHLL	FLRDTKTLMF	GSYLDDEKNW	GLSFYADKPE	TTKEQLGEFY
170	180	190	200	210			
EALDCLCIPR	SDVMYTDWKK	DKCEPLEKQH	EKERKQEEGE	S			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1023	3	617.8379	-30.01	2	41.5	46.2	0	114-123	R.EHVAHLLFLR.D	

Detailed Protein Report

Protein 147: uncharacterized protein C4orf21 [Homo sapiens]

Accession:	gi|254826809	**Score:**	46.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	236.5
Database Date:	2015-11-30	**pI:**	5.8
		Sequence Coverage [%]:	2.1
		No. of unique Peptides:	2

Quantitation

mdown:qdown	**Median:**	1.15	**CV:**	0.00 %	**No. of Peptides:**	1

Alias proteins:

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

Detailed Protein Report

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

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2940	2	973.5071	-8.25	2	65.5	10.8	1	167-183	K.KDVNNILADPENIVTYK.N		mdown:qdown 1.15
2930	7	698.3835	-51.56	2	65.8	21.0	1	282-294	K.QPQGSLKIATKPK.Y		

Detailed Protein Report

Protein 148: serine/threonine-protein kinase Nek1 isoform 5 [Homo sapiens]

Accession:	gi|313661434	**Score:**	45.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	138.0
Database Date:	2015-11-30	**pI:**	5.4
		Sequence Coverage [%]:	5.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEKYVRLQKI	GEGSFGKAIL	VKSTEDGRQY	VIKEINISRM	SSKEREESRR	EVAVLANMKH	PNIVQYRESF	EENGSLYIVM
90	100	110	120	130	140	150	160
DYCEGGDLFK	RINAQKGVLF	QEDQILDWFV	QICLALKHVH	DRKILHRDIK	SQNIFLTKDG	TVQLGDFGIA	RVLNSTVELA
170	180	190	200	210	220	230	240
RTCIGTPYYL	SPEICENKPY	NNKSDIWALG	CVLYELCTLK	HAFEAGSMKN	LVLKIISGSF	PPVSLHYSYD	LRSLVSQLFK
250	260	270	280	290	300	310	320
RNPRDRPSVN	SILEKGFIAK	RIEKFLSPQL	IAEEFCLKTF	SKFGSQPIPA	KRPASGQNSI	SVMPAQKITK	PAAKYGIPLA
330	340	350	360	370	380	390	400
YKKYGDKKLH	EKKPLQKHKQ	AHQTPEKRVN	TGEERRKISE	EAARKRRLEF	IEKEKKQKDQ	IISLMKAEQM	KRQEKERLER
410	420	430	440	450	460	470	480
INRAREQGWR	NVLSAGGSGE	VKAPFLGSGG	TIAPSSFSSR	GQYEHYHAIF	DQMQQQRAED	NEAKWKREIY	GRGLPERQKG
490	500	510	520	530	540	550	560
QLAVERAKQV	EEFLQRKREA	MQNKARAEGH	MVYLARLRQI	RLQNFNERQQ	IKAKLRGEKK	EANHSEGQEG	SEEADMRRKK
570	580	590	600	610	620	630	640
IESLKAHANA	RAAVLKEQLE	RKRKEAYERE	KKVWEEHLVA	KGVKSSDVSP	PLGQHETGGS	PSKQQMRSVI	SVTSALKEVG
650	660	670	680	690	700	710	720
VDSSLTDTRE	TSEEMQKTNN	AISSKREILR	RLNENLKAQE	DEKGKQNLSD	TFEINVHEDA	KEHEKEKSVS	SDRKKWEAGG
730	740	750	760	770	780	790	800
QLVIPLDELT	LDTSFSTTER	HTVGEVIKLG	PNGSPRRAWG	KSPTDSVLKI	LGEAELQLQT	ELLENTTIRS	EISPEGEKYK
810	820	830	840	850	860	870	880
PLITGEKKVQ	CISHEINPSA	IVDSPVETKS	PEFSEASPQM	SLKLEGNLEE	PDDLETEILQ	EPSGTNKDES	LPCTITDVWI
890	900	910	920	930	940	950	960
SEEKETKETQ	SADRITIQEN	EVSEDGVSST	VDQLSDIHIE	PGTNDSQHSK	CDVDKSVQPE	PFFHKVVHSE	HLNLVPQVQS
970	980	990	1000	1010	1020	1030	1040
VQCSPEESFA	FRSHSHLPPK	NKNKNSLLIG	LSTGLFDANN	PKMLRTCSLP	DLSKLFRTLM	DVPTVGDVRQ	DNLEIDEIED
1050	1060	1070	1080	1090	1100	1110	1120
ENIKEGPSDS	EDIVFEETDT	DLQELQASME	QLLREQPGEE	YSEEEESVLK	NSDVEPTANG	TDVADEDDNP	SSESALNEEW
1130	1140	1150	1160	1170	1180	1190	1200
HSDNSDGEIA	SECECDSVFN	HLEELRLHLE	QEMGFEKFFE	VYEKIKAIHE	DEDENIEICS	KIVQNILGNE	HQHLYAKILH
1210	1220						
LVMADGAYQE	DNDE						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
894	1	946.4617	-25.43	3	40.0	16.1	1	411-440	R.NVLSAGGSGEVKAPFLGSGGTIAPSSFSSR.G	

Detailed Protein Report

Protein 149: neutrophil defensin 1 preproprotein [Homo sapiens]

Accession:	gi|4758146	**Score:**	45.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	10.2
Database Date:	2015-11-30	**pI:**	7.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	9.6
		No. of unique Peptides:	1

Quantitation

mdown:qdown **Median:** 1.15 **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	2	493.6493	-220.14	2	30.7	45.9	0	70-78	R.IPACIAGER.R	Carbamidomethyl: 4	mdown:qdown 1.15

Detailed Protein Report

Protein 150: **PREDICTED: chromodomain-helicase-DNA-binding protein 4 isoform X6 [Homo sapiens]**

Accession:	gi|578822562	**Score:**	45.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	216.7
Database Date:	2015-11-30	**pI:**	5.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.5
		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
2537	2	649.8872	-125.27	3	60.0	13.8	0	1005-1021	K.CCNHPYLFPVAAMEAPK.M	Carbamidomethyl: 2
2522	2	649.8743	-145.17	3	59.8	13.9	0	1005-1021	K.CCNHPYLFPVAAMEAPK.M	Carbamidomethyl: 1

Detailed Protein Report

Protein 151: PREDICTED: transmembrane channel-like protein 8 isoform X4 [Homo sapiens]

Accession:	gi|578830481	**Score:**	45.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	45.7
Database Date:	2015-11-30	**pI:**	10.7
		Sequence Coverage [%]:	4.2
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MLLPRSVSSE RAPGVPEPEE LWEAEMERLR GSGTPVRGLP YAMMDKRLIW QLREPAGVQT LRWQRWQRRR QTVERRLREA
        90        100        110        120        130        140        150        160
AQRLARGLGL WEGALYEIGG LFGTGIRSYF TFLRFLLLLN LLSLLLTASF VLLPLVWLRP PDPGPTLNLT LQCPGSRQSP
       170        180        190        200        210        220        230        240
PGVLRFHNQL WHVLTGRAFT NTYLFYGAYR VGPESSSVYS IRLAYLLSPL ACLLLCFCGT LRRMVKGLPQ KTLLGQGYQA
       250        260        270        280        290        300        310        320
PLSAKVFSSW DFCIRVQEAA TIKKHEISNE FKVELEEGRR FQLMQQQTRA QTACRLLSYL RVNVLNGLLV VGAISAIFWA
       330        340        350        360        370        380        390        400
TKYSQDNKEV SGVPVSAAPV PAPWGHRPGQ LPGSPAVHIS GPAGELPSQH GGQPHSDLVR GAEAGQLGDV LRLPGSDHTV
       410
HWQRQEQL
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
704	1	457.7465	-33.68	2	37.6	18.2	1	79-86	R.EAAQRLAR.G	

Detailed Protein Report

Protein 152: dynein heavy chain 10, axonemal [Homo sapiens]

Accession:	gi|198442844	**Score:**	45.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	514.5
Database Date:	2015-11-30	**pI:**	5.6
		Sequence Coverage [%]:	1.0
		No. of unique Peptides:	2

Quantitation

mdown:qdown	**Median:**	0.91	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	1.20	**CV:**	0.00 %	**No. of Peptides:**	1

10	20	30	40	50	60	70	80
MVPEEVEVEI	DEIPVLSEEG	EEEEETYSQK	VESVDKVRAK	RVSLRTESLG	QPLNREDEEM	DKEISEKLPS	KRTAKHIMEK
90	100	110	120	130	140	150	160
MHLHMLCTPL	PEEFLDQNVV	FFLRNTKEAI	SEATDMKEAM	EIMPETLEYG	IINANVLHFL	KNIICQVFLP	ALSFNQHRTS
170	180	190	200	210	220	230	240
TTVGVTSGEV	SNSSEHESDL	PPMPGEAVEY	HSIQLIRDEF	LMNVQKFASN	IQRTMQQLEG	EIKLEMPIIS	VEGEVSDLAA
250	260	270	280	290	300	310	320
DPETVDILEQ	CVINWLNQIS	TAVEAQLKKT	PQGKGPLAEI	EFWRERNATL	SALHEQTKLP	IVRKVLDVIK	ESDSMLVANL
330	340	350	360	370	380	390	400
QPVFTELFKF	HTEASDNVRF	LSTVERYFKN	ITHGSGFHVV	LDTIPAMMSA	LRMVWIISRH	YNKDERMIPL	MERIAWEIAE
410	420	430	440	450	460	470	480
RVCRVVNLRT	LFKENRASAQ	SKTLEARNTL	RLWKKAYFDT	RAKIEASGRE	DRWEFDRKRL	FERTDYMATI	CQDLSDVLQI
490	500	510	520	530	540	550	560
LEEFYNIFGP	ELKAVTGDPK	RIDDVLCRVD	GLVTPMENLT	FDPFSIKSSQ	FWKYVMDEFK	IEVLIDIINK	IFVQNLENPP
570	580	590	600	610	620	630	640
LYKNHPPVAG	AIYWERSLFF	RIKHTILRFQ	EVQEILDSDR	GQEVKQKYLE	VGRTMKEYED	RKYEQWMEVT	EQVLPALMKK
650	660	670	680	690	700	710	720
SLLTKSSIAT	EEPSTLERGA	VFAINFSPAL	REIINETKYL	EQLGFTVPEL	ARNVALQEDK	FLRYTAGIQR	MLDHYHMLIG
730	740	750	760	770	780	790	800
TLNDAESVLL	KDHSQELLRV	FRSGYKRLNW	NSLGIGDYIT	GCKQAIGKFE	SLVHQIHKNA	DDISSRLTLI	EAINLFKYPA
810	820	830	840	850	860	870	880
AKSEEELPGV	KEFFEHIERE	RASDVDHMVR	WYLAIGPLLT	KVEGLVVHTN	TGKAPKLASY	YKYWEKKIYE	VLTKLILKNL
890	900	910	920	930	940	950	960
QSFNSLILGN	VPLFHTETIL	TAPEIILHPN	TNEIDKMCFH	CVRNCVEITK	HFVRWMNGSC	IECPPQKGEE	EEVVIINFYN
970	980	990	1000	1010	1020	1030	1040
DISLNPQIIE	QAVMIPQNVH	RILINLMKYL	QKWKRYRPLW	KLDKAIVMEK	FAAKKPPCVA	YDEKLQFYSK	IAYEVMRHPL
1050	1060	1070	1080	1090	1100	1110	1120
IKDEHCIRLQ	LRHLANTVQE	NAKSWVISLG	KLLNESAKEE	LYNLHEEMEH	LAKNLRKIPN	TLEDLKFVLA	TIAEIRSKSL
1130	1140	1150	1160	1170	1180	1190	1200
VMELRYRDVQ	ERYRTMAMYN	LFPPDAEKEL	VDKIESIWSN	LFNDSVNVEH	ALGDIKRTFT	ELTRGEIMNY	RVQIEEFAKR
1210	1220	1230	1240	1250	1260	1270	1280
FYSEGPGSVG	DDLDKGVELL	GVYERELARH	EKSRQELANA	EKLFDLPITM	YPELLKVQKE	MSGLRMIYEL	YEGLKVAKEE
1290	1300	1310	1320	1330	1340	1350	1360
WSQTLWINLN	VQILQEGIEG	FLRALRKLPR	PVRGLSVTYY	LEAKMKAFKD	SIPLLLDLKN	EALRDRHWKE	LMEKTSVFFE
1370	1380	1390	1400	1410	1420	1430	1440
MTETFTLENM	FAMELHKHTD	VLNEIVTAAI	KEVAIEKAVK	EILDTWENMK	FTVVKYCKGT	QERGYILGSV	DEIIQSLDDN
1450	1460	1470	1480	1490	1500	1510	1520
TFNLQSISGS	RFVGPFLQTV	HKWEKTLSLI	GEVIEIWMLV	QRKWMYLESI	FIGGDIRSQL	PEEAKKFDNI	DKVFKRIMGE
1530	1540	1550	1560	1570	1580	1590	1600
TLKDPVIKRC	CEAPNRLSDL	QNVSEGLEKC	QKSLNDYLDS	KRNAFPRFFF	ISDDELLSIL	GSSDPLCVQE	HMIKMYDNIA
1610	1620	1630	1640	1650	1660	1670	1680
SLRFNDGDSG	EKLVSAMISA	EGEVMEFRKI	LRAEGRVEDW	MTAVLNEMRR	TNRLITKEAI	FRYCEDRSRV	DWMLLYQGMV
1690	1700	1710	1720	1730	1740	1750	1760
VLAASQVWWT	WEVEDVFHKA	QKGEKQAMKN	YGRKMHRQID	ELVTRITMPL	SKNDRKKYNT	VLIIDVHARD	IVDSFIRGSI
1770	1780	1790	1800	1810	1820	1830	1840
LEAREFDWES	QLRFYWDREP	DELNIRQCTG	TFGYGYEYMG	LNGRLVITPL	TDRIYLTLTQ	ALSMYLGGAP	AGPAGTGKTE
1850	1860	1870	1880	1890	1900	1910	1920
TTKDLAKALG	LLCVVTNCGE	GMDYRAVGKI	FSGLAQCGAW	GCFDEFNRID	ASVLSVISSQ	IQTIRNALIH	QLTTFQFEGQ
1930	1940	1950	1960	1970	1980	1990	2000
EISLDSRMGI	FITMNPGYAG	RTELPESVKA	LFRPVVVIVP	DLQQICEIML	FSEGFLEAKT	LAKKMTVLYK	LAREQLSKQY
2010	2020	2030	2040	2050	2060	2070	2080
HYDFGLRALK	SVLVMAGELK	RGSSDLREDV	VLMRALRDMN	LPKFVFEDVP	LFLGLISDLF	PGLDCPRVRY	PDFNDAVEQV
2090	2100	2110	2120	2130	2140	2150	2160
LEENGYAVLP	IQVDKVVQMF	ETMLTRHTTM	VVGPTRGGKS	VVINTLCQAQ	TKLGLTTKLY	ILNPKAVSVI	ELYGILDPTT
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1629	1	711.6687	-76.59	3	49.1	10.5	1	779-797	K.NADDISSRLTLIEAINLFK.Y		
115	1	679.8485	-38.99	2	30.8	24.0	0	2662-2673	R.VFNGLVLTNPER.F		Wdown:Qdown 1.20 mdown:qdown 0.91

Detailed Protein Report

Protein 153: **PREDICTED: pyridine nucleotide-disulfide oxidoreductase domain-containing protein 2 isoform X1 [Homo sapiens]**

Accession:	gi|578819959	**Score:**	45.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	61.0
Database Date:	2015-11-30	**pI:**	6.3
		Sequence Coverage [%]:	8.6
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MAASGRGLCK	AVAASPFPAW	RRDNTEARGG	LKPEYDAVVI	GAGHNGLVAA	AYLQRLGVNT	AVFERRHVIG	GAAVTEEIIP
90	100	110	120	130	140	150	160
GFKFSRASYL	LSLLRPQIYT	DLELKKHGLR	LHLRNPYSFT	PMLEEGAGSK	VPRCLLLGTD	MAENQKQIAQ	FSQKDAQVFP
170	180	190	200	210	220	230	240
KYEEFMHRLA	LAIDPLLDAA	PVDMAAFQHG	SLLQRMRSLS	TLKPLLKAGR	ILGAQLPRYY	EVLTAPITKV	LDQWFESEPL
250	260	270	280	290	300	310	320
KATLATDAVI	GAMTSPHTPG	SGYVLLHHVM	GGLEGMQGAW	GYVQGGMGAL	SDAIASSATT	HGASIFTEKT	VAKVQVNSEG
330	340	350	360	370	380	390	400
CVQGVVLEDG	TEVRSKMVLS	NTSPQITFLK	LTPQEWLPEE	FLERISQLDT	RSPVTKINVA	VDRLPSFLAA	PNAPRGQPLP
410	420	430	440	450	460	470	480
HHQCSIHLNC	EDTLLLHQAF	EDAMDGLPSH	RPVIELCIPS	SLDPTLAPPG	CHVVSLFTQY	MPYTLAGGKA	WDEQERDAYA
490	500	510	520	530	540	550	560
DRVFDCIEVY	APGFKDSVVG	RDILTPPDLE	RIFGLPGGNI	FHCAMSLDQL	YFARPVPLHS	GYRCPLQGLY	LCGSGAHPGF
570							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2627	1	869.6010	138.74	2	61.1	14.0	0	67-83	R.HVIGGAAVTEEIIPGFK.F	
2482	1	836.1552	175.38	2	59.3	13.8	2	196-210	R.MRSLSTLKPLLKAGR.I	

Detailed Protein Report

Protein 154: astrotactin-1 isoform 2 precursor [Homo sapiens]

Accession:	gi|46488921	**Score:**	45.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	135.0
Database Date:	2015-11-30	**pI:**	4.9
		Sequence Coverage [%]:	5.1
		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	

BRUKER

Detailed Protein Report

Protein 155: PREDICTED: armadillo repeat-containing protein 3 isoform X3 [Homo sapiens]

Accession:	gi|530392014	**Score:**	45.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	86.5
Database Date:	2015-11-30	**pI:**	5.8
		Sequence Coverage [%]:	2.6
		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 156: zinc finger protein 646 [Homo sapiens]

Accession:	gi|215820619	**Score:**	45.0
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 [%]:**	2.2
		No. of unique Peptides:	3

Quantitation

mdown:qdown	**Median:**	1.04	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.80	**CV:**	0.00 %	**No. of Peptides:**	1

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	Ratios
2876	1	899.9560	111.44	2	64.7	16.6	0	1-15	-.MEDTPPSLSCSDCQR.H	Carbamidomethyl: 10, 13; Oxidation: 1	
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	mdown:qdown 1.04 Wdown:Qdown 0.80

Detailed Protein Report

Protein 157: DNA-dependent protein kinase catalytic subunit isoform 2 [Homo sapiens]

Accession:	gi|126032350	**Score:**	45.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	465.2
Database Date:	2015-11-30	**pI:**	6.9
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	0.8
		No. of unique Peptides:	3

Quantitation

mdown:qdown	**Median:**	1.23	**CV:**	0.00 %	**No. of Peptides:**	1

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1341	1	473.1526	-298.22	2	45.3	12.1	0	1643-1651	K.MAVLALLAK.I	Oxidation: 1	
698	1	512.2692	-22.73	2	37.6	10.8	0	2434-2441	K.VCLDIIYK.M	Carbamidomethyl: 2	mdown:qdown 1.23
2232	1	937.4206	-14.54	2	56.5	22.1	1	3682-3696	K.ECSPWMSDFKVEFLR.N		

Detailed Protein Report

Protein 158: **PREDICTED: cyclin-dependent kinase 7 isoform X1 [Homo sapiens]**

Accession:	gi|530379082	**Score:**	44.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	32.7
Database Date:	2015-11-30	**pI:**	9.8
		Sequence Coverage [%]:	11.4
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|530430719	refseq_human (refseq_human_20140103.fasta)	PREDICTED: cyclin-dependent kinase 7 isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MRSWTSLGRD	SLPPFTRPEI	RTPTKLSPLR	KSNLDIDQKL	KMVIIKDNSL	VLTPSHIKAY	MLMTLQGLEY	LHQHWILHRD
90	100	110	120	130	140	150	160
LKPNNLLLDE	NGVLKLADFG	LAKSFGSPNR	AYTHQVVTRW	YRAPELLFGA	RMYGVGVDMW	AVGCILAELL	LRVPFLPGDS
170	180	190	200	210	220	230	240
DLDQLTRIFE	TLGTPTEEQW	PDMCSLPDYV	TFKSFPGIPL	HHIFSAAGDD	LLDLIQGLFL	FNPCARITAT	QALKMKYFSN
250	260	270	280	290			
RPGPTPGCQL	PRPNCPVETL	KEQSNPALAI	KRKRTEALEQ	GGLPKKLIF			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
50	1	662.2443	-185.28	2	29.3	10.8	0	47-58	K.DNSLVLTPSHIK.A	

Detailed Protein Report

Protein 159: PREDICTED: ankyrin repeat domain-containing protein 26 isoform X7 [Homo sapiens]

Accession:	gi|578818368	**Score:**	44.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	187.0
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
MKKIFSKKGE	SPLGSFARRQ	RSSAGGGGEP	GEGAYSQPGY	HVRDRDLGKI	HKAASAGNVA	KVQQILLLRK	NGLNDRDKMN
90	100	110	120	130	140	150	160
RTALHLACAN	GHPEVVTLLV	DRKCQLNVCD	NENRTALMKA	VQCQEEKCAT	ILLEHGADPN	LADVHGNTAL	HYAVYNEDIS
170	180	190	200	210	220	230	240
VATKLLLYDA	NIEAKNKDDL	TPLLLAVSGK	KQQMVEFLIK	KKANVNAVDK	LESSHQLISE	YKEERIPKHS	SQNSNSVDES
250	260	270	280	290	300	310	320
SEDSLSRLSG	KPGVDDSWPT	SDDEDLNFDT	KNVPKPSLAK	LMTASQQSRK	NLEATYGTVR	TGNRTLFEDR	DSDSQDEVVV
330	340	350	360	370	380	390	400
ESLPTTSIKV	QCFSHPTYQS	PDLLPKPSHK	SLANPGLMKE	EPTKPGIAKK	ENGIDIIESA	PLEQTNNDNL	TYVDEVHKNN
410	420	430	440	450	460	470	480
RSDMMSALGL	GQEEDIESPW	DSESISENFP	QKYVDPLAGA	ADGKEKNIGN	EQAEDVFYIP	SCMSGSRNFK	MAKLEDTRNV
490	500	510	520	530	540	550	560
GMPVAHMESP	ERYLHLKPTI	EMKDSVPNKA	GGMKDVQTSK	AAEHDLEVAS	EEEQEREGSE	NNQPQDKVIL	KTCTLTEKTS
570	580	590	600	610	620	630	640
EKQNKQINRP	LSCLQKMSQE	PELNKECDRE	DVSVYSGLPC	VQNDEEMWTK	QGKLEWKNNL	KLITNELKQS	CGETCEKYKI
650	660	670	680	690	700	710	720
TASPGEESLH	DNSKGGTNLK	EIPSSLTNNI	LDCDEKDSPV	SVLFQALPEQ	KVLSLENGFS	FPSYSGSPEY	ACQSSSKPYL
730	740	750	760	770	780	790	800
NENKLGHENV	NKPDTEHVFN	TDENFYNDTE	NKKVRNPEVV	TGVMKEEFDK	TKNMNRNTTN	WKLDIRRVPQ	YSDPKRPFDL
810	820	830	840	850	860	870	880
ICSKEMNHMF	HIKRHSISAG	TDAYKKTKPI	QNLFQKPLYD	HCSANNYKSM	EPELENVRSS	PPRGDRTSKV	SLKEELQQDM
890	900	910	920	930	940	950	960
QRFKNEIGML	KVEFQALEKE	KVQLQKEVEE	ERKKHRNNEM	EVSANIHDGA	TDDAEDDDDD	DGLIQKRKSG	ETDHQQFPRK
970	980	990	1000	1010	1020	1030	1040
ENKEYASSGP	ALQMKEVKST	EKEKRTSKES	VNSPVFGKAS	LLTGGLLQVD	DDSSLSEIDE	DEGRPTKKTS	NEKNKVKNQI
1050	1060	1070	1080	1090	1100	1110	1120
QSMDDVDDLT	QSSETASEDC	ELPHSSYKNF	MLLIEQLGME	CKDSVSLLKI	QDAALSCERL	LELKKNHCEL	LTVKIKKMED
1130	1140	1150	1160	1170	1180	1190	1200
KVNVLQRELS	ETKEIKSQLE	HQKVEWEREL	CSLRFSLNQE	EEKRRNADTL	YEKIREQLRR	KEEQYRKEVE	VKQQLELSLQ
1210	1220	1230	1240	1250	1260	1270	1280
TLEMELRTVK	SNLNQVVQER	NDAQRQLSRE	QNARMLQDGI	LTNHLSKQKE	IEMAQKKMNS	ENSHSHEEEK	DLSHKNSMLQ
1290	1300	1310	1320	1330	1340	1350	1360
EEIAMLRLEI	DTIKNQNQEK	EKKCFEDLKI	VKEKNEDLQK	TIKQNEETLT	QTISQYNGRL	SVLTAENAML	NSKLENEKQS
1370	1380	1390	1400	1410	1420	1430	1440
KERLEAEVES	YHSRLAAAIH	DRDQSETSKR	ELELAFQRAR	DECSRLQDKM	NFDVSNLKDN	NEILSQQLFK	TESKLNSLEI
1450	1460	1470	1480	1490	1500	1510	1520
EFHHTRDALR	EKTLGLERVQ	KDLSQTQCQM	KEMEQKYQNE	QVKVNKYIGK	QESVEERLSQ	LQSENMLLRQ	QLDDAHNKAD
1530	1540	1550	1560	1570	1580	1590	1600
NKEKTVINIQ	DQFHAIVQKL	QAESEKQSLL	LEERNKELIS	ECNHLKERQY	QYENEKAERE	VVVRQLQQEL	ADTLKKQSMS
1610	1620	1630	1640				
EASLEVTSRY	RINLEDETQD	LKKKLGQIRN	QSWDP				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1740	1	555.2376	-81.69	2	51.7	17.4	1	1165-1173	R.RNADTLYEK.I	

Detailed Protein Report

Protein 160: PREDICTED: dolichyl-phosphate beta-glucosyltransferase isoform X1 [Homo sapiens]

Accession: gi|530402309
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl, Oxidation

Score: 44.8
MW [kDa]: 32.8
pI: 10.1
Sequence Coverage [%]: 16.8
No. of unique Peptides: 2

```
        10          20          30          40          50          60          70          80
MAPLLLQLAV  LGAALAAAAL  VLISIVAFTT  ATKMPALHRH  EEEKFFLNAK  GQKETLPSIW  DSPTKQLSVV  VPSYNEEKRL
        90         100         110         120         130         140         150         160
PVMMDEALSY  LEKRQKRDPA  FTYEVIVVDD  GSKDQTSKVA  FKYCQKYGSD  KVRVITLVKN  RGKGGAIRMN  QMAIACGSRA
       170         180         190         200         210         220         230         240
HLEKESIAQR  SYFRTLLMYG  FHFLVWFLCV  KGIRDTQCGF  KLFTREAASR  TFSSLHVERW  AFDVELLYIA  QFFKIPIAEI
       250         260         270         280         290
AVNWTEIEGS  KLVPFWSWLQ  MGKDLLFIRL  RYLTGAWRLE  QTRKMN
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2024	1	687.3070	-64.03	2	55.4	10.8	0	54-65	K.ETLPSIWDSPTK.Q	
153	1	635.8187	75.84	2	31.1	11.0	0	149-159	R.MNQMAIACGSR.A	Carbamidomethyl: 8; Oxidation: 1, 4

Detailed Protein Report

Protein 161: **PREDICTED: arf-GAP with Rho-GAP domain, ANK repeat and PH domain-containing protein 3 isoform X7 [Homo sapiens]**

Accession:	gi|578810904	**Score:**	44.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	149.1
Database Date:	2015-11-30	**pI:**	6.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
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
164	1	715.8153	8.42	2	31.4	24.0	0	170-181	R.DMWCSTLQSCLK.E	Oxidation: 2

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Detailed Protein Report

Protein 162: **protein FAM194B [Homo sapiens]**

Accession:	gi|210147567	**Score:**	44.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	81.6
Database Date:	2015-11-30	**pI:**	4.6
		Sequence Coverage [%]:	4.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSAENNQLSG	ASPPHPPTTP	QYSTQNLPSE	KEDTEVELDE	ESLQDESPFS	PEGESLEDKE	YLEEEEDLEE	EEYLGKEEYL
90	100	110	120	130	140	150	160
KEEEYLGKEE	HLEEEEYLEK	AGYLEEEEYI	EEEEYLGKEG	YLEEEEYLGK	EEHLEEEEYL	GKEGYLEKED	YIEEVDYLGK
170	180	190	200	210	220	230	240
KAYLEEEEYL	GKKSYLEEEK	ALEKEENLEE	EEALEKEENL	DGKENLYKKY	LKEPKASYSS	QTMLLRDARS	PDAGPSQVTT
250	260	270	280	290	300	310	320
FLTVPLTFAT	PSPVSESATE	SSELLLTLYR	RSQASQTDWC	YDRTAVKSLK	SKSETEQETT	TKLAPEEHVN	TKVQQKKEEN
330	340	350	360	370	380	390	400
VLEFASKENF	WDGITDESID	KLEVEDLDEN	FLNSSYQTVF	KTIIKEMAAH	NELEEDFDIP	LTKLLESENR	WKLVIMLKKN
410	420	430	440	450	460	470	480
YEKFKETILR	IKRRREAQKL	TEMTSFTFHL	MSKPTPEKPE	TEEIQKPQRV	VHHRKKLERD	KEWIQKKTVV	HQGDGKLILY
490	500	510	520	530	540	550	560
PNKNVYQILF	PDGTGQIHYP	SGNLAMLILY	AKMKKFTYII	LEDSLEGRIR	ALINNSGNAT	FYDENSDIWL	NLSSNLGYYF
570	580	590	600	610	620	630	640
PKDKRQKAWN	WWNLNIHVHA	PPVQPISLKI	NEYIQVQIRS	QDKIIFCFTY	EQKQICLNLG	TRYKFVIPEV	LSEMKKKTIL
650	660	670	680	690	700		
EAEPGPTAQK	IRVLLGKMNR	LLNYATTPDL	ENFIEAVSIS	LMDNKYLKKM	LSKLWF		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2001	1	876.8626	-126.17	2	53.7	10.2	2	462-476	K.EWIQKKTVVHQGDGK.L	

Detailed Protein Report

Protein 163: ATP-binding cassette sub-family A member 13 [Homo sapiens]

Accession:	gi|31657092	**Score:**	44.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	575.8
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
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 164: GDNF family receptor alpha-like precursor [Homo sapiens]

Accession:	gi|148231468	**Score:**	44.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	44.5
Database Date:	2015-11-30	**pI:**	9.6
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	7.1
		No. of unique Peptides:	3

10	20	30	40	50	60	70	80
MIVFIFLAMG	LSLENEYTSQ	TNNCTYLREQ	CLRDANGCKH	AWRVMEDACN	DSDPGDPCKM	RNSSYCNLSI	QYLVESNFQF
90	100	110	120	130	140	150	160
KECLCTDDFY	CTVNKLLGKK	CINKSDNVKE	DKFKWNLTTR	SHHGFKGMWS	CLEVAEACVG	DVVCNAQLAS	YLKACSANGN
170	180	190	200	210	220	230	240
PCDLKQCQAA	IRFFYQNIPF	NIAQMLAFCD	CAQSDIPCQQ	SKEALHSKTC	AVNMVPPPTC	LSVIRSCQND	ELCRRHYRTF
250	260	270	280	290	300	310	320
QSKCWQRVTR	KCHEDENCIS	TLSKQDLTCS	GSDDCKAAYI	DILGTVLQVQ	CTCRTITQSE	ESLCKIFQHM	LHRKSCFNYP
330	340	350	360	370	380	390	400
TLSNVKGMAL	YTRKHANKIT	LTGFHSPFNG	EVIYAAMCMT	VTCGILLLVM	VKLRTSRISS	KARDPSSIQI	PGEL

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2904	2	937.4573	-13.81	2	65.5	12.0	0	209-225	K.TCAVNMVPPPTCLSVIR.S	Carbamidomethyl: 2; Oxidation: 6
2943	1	937.4648	-5.86	2	66.0	16.3	0	209-225	K.TCAVNMVPPPTCLSVIR.S	Carbamidomethyl: 12; Oxidation: 6
2830	1	648.3562	69.68	2	63.9	15.9	0	295-305	R.TITQSEESLCK.I	Carbamidomethyl: 10

Detailed Protein Report

Protein 165: PREDICTED: autoimmune regulator isoform X1 [Homo sapiens]

Accession:	gi|530419216	**Score:**	44.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	36.5
Database Date:	2015-11-30	**pI:**	6.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	14.9
		No. of unique Peptides:	3

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
1351	1	669.2815	20.48	2	45.7	14.6	0	107-119	R.DGGELICCDGCPR.A	
2864	1	651.8581	112.84	2	64.5	16.6	0	249-259	R.CTHCAAAFHWR.C	

Detailed Protein Report

Protein 166: PREDICTED: androglobin isoform X1 [Homo sapiens]

Accession:	gi|578812976	**Score:**	44.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	189.6
Database Date:	2015-11-30	**pI:**	9.1
		Sequence Coverage [%]:	2.3
		No. of unique Peptides:	2

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

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

Detailed Protein Report

Protein 167: putative ribosomal RNA methyltransferase NOP2 isoform 4 [Homo sapiens]

Accession:	gi|385198063	**Score:**	43.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	69.6
Database Date:	2015-11-30	**pI:**	6.2
		Sequence Coverage [%]:	6.2
		No. of unique Peptides:	2

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
2658	1	625.2870	-81.65	2	61.5	11.2	1	442-452	R.QFPKVVGGFDR.V	
2674	1	933.1060	151.43	2	64.6	13.8	0	583-599	K.FSNSIPQSQTDGVLLCR.S	

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Detailed Protein Report

Protein 168: FERM, RhoGEF and pleckstrin domain-containing protein 2 isoform b [Homo sapiens]

Accession:	gi|545478372	**Score:**	43.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	73.2
Database Date:	2015-11-30	**pI:**	9.6
		Sequence Coverage [%]:	7.7
		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	KVFQLHEGHV
650							
AGVTKME							

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

Accession:	gi|530402705	**Score:**	43.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	95.8
Database Date:	2015-11-30	**pI:**	9.3
		Sequence Coverage [%]:	4.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
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
1492	1	450.0889	-279.87	2	48.4	13.5	0	43-50	K.NCLGPHMK.F	

Detailed Protein Report

Protein 170: PREDICTED: coiled-coil domain-containing protein 91 isoform X6 [Homo sapiens]

Accession:	gi|578822930	**Score:**	43.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	51.6
Database Date:	2015-11-30	**pI:**	5.4
Modification(s):	Oxidation	**Sequence Coverage [%]:**	5.8
		No. of unique Peptides:	2

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
1931	4	1022.8987	-73.55	2	54.2	16.6	0	1-16	-.MWVQQHRPENTFGDQR.E	Oxidation: 1
1996	1	665.3129	-29.71	2	55.1	11.2	2	203-212	K.HKQELEDMRK.A	Oxidation: 8

Detailed Protein Report

Protein 171: **complement C4-A isoform 2 preproprotein [Homo sapiens]**

Accession:	gi|356582273	**Score:**	43.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	187.6
Database Date:	2015-11-30	**pI:**	6.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.7
		No. of unique Peptides:	2

```
        10          20          30          40          50          60          70          80
MRLLWGLIWA  SSFFTLSLQK  PRLLLFSPSV  VHLGVPLSVG  VQLQDVPRGQ  VVKGSVFLRN  PSRNNVPCSP  KVDFTLSSER
        90         100         110         120         130         140         150         160
DFALLSLQVP  LKDAKSCGLH  QLLRGPEVQL  VAHSPWLKDS  LSRTTNIQGI  NLLFSSRRGH  LFLQTDQPIY  NPGQRVRYRV
       170         180         190         200         210         220         230         240
FALDQKMRPS  TDTITVMVEN  SHGLRVRKKE  VYMPSSIFQD  DFVIPDISEP  GTWKISARFS  DGLESNSSTQ  FEVKKYVLPN
       250         260         270         280         290         300         310         320
FEVKITPGKP  YILTVPGHLD  EMQLDIQARY  IYGKPVQGVA  YVRFGLLDED  GKKTFFRGLE  SQTKLVNGQS  HISLSKAEFQ
       330         340         350         360         370         380         390         400
DALEKLNMGI  TDLQGLRLYV  AAAIIESPGG  EMEEAELTSW  YFVSSPFSLD  LSKTKRHLVP  GAPFLLQALV  REMSGSPASG
       410         420         430         440         450         460         470         480
IPVKVSATVS  SPGSVPEVQD  IQQNTDGSGQ  VSIPIIIPQT  ISELQLSVSA  GSPHPAIARL  TVAAPPSGGP  GFLSIERPDS
       490         500         510         520         530         540         550         560
RPPRVGDTLN  LNLRAVGSGA  TFSHYYYMIL  SRGQIVFMNR  EPKRTLTSVS  VFVDHHLAPS  FYFVAFYYHG  DHPVANSLRV
       570         580         590         600         610         620         630         640
DVQAGACEGK  LELSVDGAKQ  YRNGESVKLH  LETDSLALVA  LGALDTALYA  AGSKSHKPLN  MGKVFEAMNS  YDLGCGPGGG
       650         660         670         680         690         700         710         720
DSALQVFQAA  GLAFSDGDQW  TLSRKRLSCP  KEKTTRKKRN  VNFQKAINEK  LGQYASPTAK  RCCQDGVTRL  PMMRSCEQRA
       730         740         750         760         770         780         790         800
ARVQQPDCRE  PFLSCCQFAE  SLRKKSRDKG  QAGLQRALEI  LQEEDLIDED  DIPVRSFFPE  NWLWRVETVD  RFQILTLWLP
       810         820         830         840         850         860         870         880
DSLTTWEIHG  LSLSKTKGLC  VATPVQLRVF  REFHLHLRLP  MSVRRFEQLE  LRPVLYNYLD  KNLTVSVHVS  PVEGLCLAGG
       890         900         910         920         930         940         950         960
GGLAQQVLVP  AGSARPVAFS  VVPTAAAAVS  LKVVARGSFE  FPVGDAVSKV  LQIEKEGAIH  REELVYELNP  LDHRGRTLEI
       970         980         990        1000        1010        1020        1030        1040
PGNSDPNMIP  DGDFNSYVRV  TASDPLDTLG  SEGALSPGGV  ASLLRLPRGC  GEQTMIYLAP  TLAASRYLDK  TEQWSTLPPE
      1050        1060        1070        1080        1090        1100        1110        1120
TKDHAVDLIQ  KGYMRIQQFR  KADGSYAAWL  SRDSSTWLTA  FVLKVLSLAQ  EQVGGSPEKL  QETSNWLLSQ  QQADGSFQDP
      1130        1140        1150        1160        1170        1180        1190        1200
CPVLDRSMQG  GLVGNDETVA  LTAFVTIALH  HGLAVFQDEG  AEPLKQRVEA  SISKANSFLG  EKASAGLLGA  HAAAITAYAL
      1210        1220        1230        1240        1250        1260        1270        1280
TLTKAPVDLL  GVAHNNLMAM  AQETGDNLYW  GSVTGSQSNA  VSPTPAPRNP  SDPMPQAPAL  WIETTAYALL  HLLLHEGKAE
      1290        1300        1310        1320        1330        1340        1350        1360
MADQASAWLT  RQGSFQGGFR  STQDTVIALD  ALSAYWIASH  TTEERGLNVT  LSSTGRNGFK  SHALQLNNRQ  IRGLEEELQF
      1370        1380        1390        1400        1410        1420        1430        1440
SLGSKINVKV  GGNSKGTLKV  LRTYNVLDMK  NTTCQDLQIE  VTVKGHVEYT  MEANEDYEDY  EYDELPAKDD  PDAPLQPVTP
      1450        1460        1470        1480        1490        1500        1510        1520
LQLFEGRRNR  RRREAPKLTS  LSDRYVSHFE  TEGPHVLLYF  DSVPTSRECV  GFEAVQEVPV  GLVQPASATL  YDYYNPERRC
      1530        1540        1550        1560        1570        1580        1590        1600
SVFYGAPSKS  RLLATLCSAE  VCQCAEGKCP  RQRRALERGL  QDEDGYRMKF  ACYYPRVEYG  FQVKVLREDS  RAAFRLFETK
      1610        1620        1630        1640        1650        1660        1670        1680
ITQVLHFTKD  VKAAANQMRN  FLVRASCRLR  LEPGKEYLIM  GLDGATYDLE  GHPQYLLDSN  SWIEEMPSER  LCRSTRQRAA
      1690        1700
CAQLNDFLQE  YGTQGCQV
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1978	2	656.8089	-24.39	2	54.8	11.3	1	60-71	R.NPSRNNVPCSPK.V	
946	1	872.2583	-156.84	2	40.6	12.5	0	730-743	R.EPFLSCCQFAESLR.K	Carbamidomethyl: 6, 7

Detailed Protein Report

Protein 172: PREDICTED: protein PRR14L isoform X4 [Homo sapiens]

Accession:	gi|578837142	**Score:**	43.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	219.9
Database Date:	2015-11-30	**pI:**	6.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.4
		No. of unique Peptides:	3

Quantitation

mdown:qdown	**Median:**	0.17	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.07	**CV:**	0.00 %	**No. of Peptides:**	1

Detailed Protein Report

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1682	1	917.4150	-55.34	2	49.6	13.4	2	245-260	R.SERGGPFLFNAREPEK.E		Wdown:Qdown 0.07 mdown:qdown 0.17
140	1	793.8794	36.37	2	31.0	13.1	0	632-646	K.NVSQENMCSASAAFK.S		

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1702	2	867.8891	-25.32	2	49.8	17.0	1	1316-1331	R.KDTESCTSPCLLGAPR.K	Carbamidomethyl: 10	

Detailed Protein Report

Protein 173: RB1-inducible coiled-coil protein 1 isoform 2 [Homo sapiens]

Accession: gi|134304846
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 43.2
MW [kDa]: 182.7
pI: 5.2
Sequence Coverage [%]: 1.9
No. of unique Peptides: 3

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1272	1	673.3365	-36.20	2	45.6	18.3	1	1228-1238	R.EQLIQKLNCEK.D	

Detailed Protein Report

Protein 174: PREDICTED: leucine-rich repeat-containing protein 16C isoform X1 [Homo sapiens]

Accession:	gi|530423607	**Score:**	43.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	148.1
Database Date:	2015-11-30	**pI:**	6.1
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.8
		No. of unique Peptides:	2

Quantitation

mdown:qdown **Median:** 1.82 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MAQTPDGISC	ELRGEITRFL	WPKEVELLLK	TWLPGEGAVQ	NHVLALLRWR	AYLLHTTCLP	LRVDCTFSYL	EVQAMALQET
90	100	110	120	130	140	150	160
PPQVTFELES	LRELVLEFPG	VAALEQLAQH	VAAAIKKVFP	RSTLGKLFRR	PTPASMLARL	ERSSPSESTD	PCSPCGGFLE
170	180	190	200	210	220	230	240
TYEALCDYNG	FPFREEIQWD	VDTIYHRQGC	RHFSLGDFSH	LGSRDLALSV	AALSYNLWFR	CLSCVDMKLS	LEVSEQILHM
250	260	270	280	290	300	310	320
MSQSSHLEEL	VLETCSLRGD	FVRRLAQALA	GHSSSGLREL	SLAGNLLDDR	GMTALSRHLE	RCPGALRRLS	LAQTGLTPRG
330	340	350	360	370	380	390	400
MRALGRALAT	NAAFDSTLTH	LDLSGNPGAL	GASEDSGGLY	SFLSRPNVLS	FLNLAGTDTA	LDTLFAAVSR	GCCTSLTHLD
410	420	430	440	450	460	470	480
ASRNVFSRTK	SRAAPAALQL	FLSRARTLRH	LGLAGCKLPP	DALRALLDGL	ALNTHLRDLH	LDLSACELRS	AGAQVIQDLV
490	500	510	520	530	540	550	560
CDAGAVSSLD	LADNGFGSDM	VTLVLAIGRS	RSLRHVALGR	NFNVRCKETL	DDVLHRIVQL	MQDDDCPLQS	LSVAESRLKL
570	580	590	600	610	620	630	640
GASVLLRALA	TNPNLTALDI	SGNAMGDAGA	KLLAKALRVN	SRLRSVVWDR	NHTSALGLLD	VAQALEQNHS	LKAMPLPLND
650	660	670	680	690	700	710	720
VAQAQRSRPE	LTARAVHQIQ	ACLLRNNRAD	PASSDHTTRL	QPLGLVSDPS	EQEVNELCQS	VQEHVELLGC	GAGPQGEAAV
730	740	750	760	770	780	790	800
RQAEDAIQNA	NFSLSILPIL	YEAGSSPSHH	WQLGQKLEGL	LRQVGEVCRQ	DIQDFTQATL	DTARSLCPQM	LQGSSWREQL
810	820	830	840	850	860	870	880
EGVLAGSRGL	PELLPEQLLQ	DAFTRLRDMR	LSITGTLAES	IVAQALAGLS	AARDQLVESL	AQQATVTMPP	ALPAPDGGEP
890	900	910	920	930	940	950	960
SLLEPGELEG	LFFPEEKEEE	KEKDDSPPQK	WPELSHGLHL	VPFIHSAAEE	AEPEPELAAP	GEDAEPQAGP	SARGSPSPAA
970	980	990	1000	1010	1020	1030	1040
PGPPAGPLPR	MDLPLAGQPL	RHPTRARPRP	RRQHHHRPPP	GGPQVPPALP	QEGNGLSARV	DEGVEEFFSK	RLIQQDRLWA
1050	1060	1070	1080	1090	1100	1110	1120
PEEDPATEGG	ATPVPRTLRK	KLGTLFAFKK	PRSTRGPRTD	LETSPGAAPR	TRKTTFGDLL	RPPTRPSRGE	ELGGAEGDTS
1130	1140	1150	1160	1170	1180	1190	1200
SPDPAGRSRP	RYTRDSKAYS	MILLPAEEEA	TLGARPDKRR	PLERGETELA	PSFEQRVQVM	LQRIGVSRGS	GGAEGKRKQS
1210	1220	1230	1240	1250	1260	1270	1280
KDGEIKKAGS	DGDIMDSSTE	APPISIKSRT	HSVSADPSCR	PGPGSQGPES	ATWKTLGQQL	NAELRSRGWG	QQDGPGPPSP
1290	1300	1310	1320	1330	1340	1350	1360
GQSPSPCRTS	PSPDSLGLPE	DPCLGPRNEE	RPLRLQRSPV	LKRRPKLEAP	PSPSLGSGLG	TEPLPPQPTE	PSSPERSPPS
1370	1380						
PATDQRGGGP	NP						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2608	1	698.3486	-78.93	2	61.3	15.4	2	425-437	R.ARTLRHLGLAGCK.L		mdown:qdown 1.82
2909	1	682.3620	-10.00	3	65.1	17.7	2	1177-1196	R.VQVMLQRIGVSRGSGGAEGK.R	Oxidation: 4	

Detailed Protein Report

Protein 175: PREDICTED: amphiphysin isoform X1 [Homo sapiens]

Accession:	gi|578813410	**Score:**	43.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	134.8
Database Date:	2015-11-30	**pI:**	4.3
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	3.7
		No. of unique Peptides:	2

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
2902	1	836.7384	18.81	3	65.4	13.6	2	93-112	R.EDVKMVGEKCDVLWEDFHQK.L	Carbamidomethyl: 10; Oxidation: 5
1311	1	1115.7434	90.99	1	46.1	17.0	1	751-760	R.DKNQAVLSIK.L	

Detailed Protein Report

Protein 176: PREDICTED: protein unc-13 homolog B isoform X1 [Homo sapiens]

Accession:	gi|578816361	**Score:**	43.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	268.9
Database Date:	2015-11-30	**pI:**	5.4
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	1.7
		No. of unique Peptides:	3

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

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	
2064	1	753.2991	-61.50	2	55.9	14.2	0	1327-1338	K.CQDLLNADCLQR.A	Carbamidomethyl: 1, 9
2797	1	937.4532	-3.05	2	64.1	17.3	1	1934-1948	K.LECPDPSILAHYMRR.F	Carbamidomethyl: 3; Oxidation: 13

Detailed Protein Report

Protein 177: PREDICTED: AP-3 complex subunit beta-2 isoform X2 [Homo sapiens]

Accession:	gi|578827454	**Score:**	43.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	114.4
Database Date:	2015-11-30	**pI:**	5.4
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.9
		No. of unique Peptides:	2

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
2503	2	974.2875	-301.77	1	59.6	11.1	1	17-25	R.IVAMIARGK.N	Oxidation: 4
619	1	677.3962	18.75	2	36.6	11.7	1	77-88	K.DPNQLIRASALR.V	

Detailed Protein Report

Protein 178: PREDICTED: muskelin isoform X4 [Homo sapiens]

Accession:	gi|578814266	**Score:**	43.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	80.3
Database Date:	2015-11-30	**pI:**	6.1
		Sequence Coverage [%]:	6.3
		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	
2818	1	989.4652	-27.99	2	64.4	13.5	2	597-614	K.VHYLFGGNPGKSCSPKMR.L	

Detailed Protein Report

Protein 179: **zinc finger protein 605 isoform 1 [Homo sapiens]**

Accession:	gi|34222391	**Score:**	43.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	74.3
Database Date:	2015-11-30	**pI:**	10.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	9.0
		No. of unique Peptides:	4

Quantitation

mdown:qdown	**Median:**	0.80	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	1.64	**CV:**	0.00 %	**No. of Peptides:**	1

```
        10         20         30         40         50         60         70         80
MIQSQISFED VAVDFTLEEW QLLNPTQKNL YRDVMLENYS NLVFLEVWLD NPKMWLRDNQ DNLKSMERGH KYDVFGKIFN
        90        100        110        120        130        140        150        160
SSINIVHVGL RSHKCGTGEK SLKCPFDLLI PKNNCERKKI DELNKKLLFC IKPGRTHGGI KYCDCSTCRK SSNEEPWLTA
       170        180        190        200        210        220        230        240
NHITHTGVYL CMECGRFFNK KSQLVIHQRT HTGEKPYQCS ECGKAFSQKS LLTVHQRTHS GEKPHGCSEC QKAFSRKSLL
       250        260        270        280        290        300        310        320
ILHQRIHTGE KPYGCSECGK AFSRKSQLKR HQITHTIEKP YSCSECGKAF SQKLKLITHQ RAHTGEKPYP CSHCGKAFFW
       330        340        350        360        370        380        390        400
KSQLITHQRT HTGKKPYGCG ECQKAFSRNS LLIRHQRIHT GEKPYECNEC GEAFIRKPQL IKHQITHTGE KNYRCSDCEE
       410        420        430        440        450        460        470        480
AFFKKSELIR HQKIHLGEKP YGCIQCGKTF FGKSQLLTHH RTHTGEKPYE CSECGKAFTQ KSSLISHQRT HTGEKPYECS
       490        500        510        520        530        540        550        560
ECRKTFSEKS SLIHHQRTHT GEKPFECSEC RKAFAWKPQL LRHQRIHTGE KPYECSECGK AFVQKVQLIK HQRNHTGEKT
       570        580        590        600        610        620        630        640
YGCSDCAKAF FEKAQLIIHQ RIHTGERPYK CGECGKSFTR KSHLMRHQRI HTGDKYYGCN ECGTTFNRKS QLMIHQRNHI
       650
I
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2421	1	863.4315	78.18	2	58.6	10.2	0	442-456	R.THTGEKPYECSECGK.A	Carbamidomethyl: 13	
1971	1	1079.8531	-128.17	2	53.3	10.5	1	523-540	R.HQRIHTGEKPYECSECGK.A	Carbamidomethyl: 16	
1972	1	665.2897	-23.77	2	54.8	11.9	2	591-601	K.CGECGKSFTRK.S	Carbamidomethyl: 1, 4	Wdown:Qdown 1.64 mdown:qdown 0.80
1767	1	856.7921	-80.88	2	52.1	10.3	1	616-629	K.YYGCNECGTTFNRK.S	Carbamidomethyl: 4	

Detailed Protein Report

Protein 180: PREDICTED: testis-specific gene 10 protein isoform X9 [Homo sapiens]

Accession:	gi|578804973	**Score:**	42.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	103.2
Database Date:	2015-11-30	**pI:**	5.3
		Sequence Coverage [%]:	3.9
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	1.21	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	1.07	**CV:**	0.00 %	**No. of Peptides:**	1

```
        10         20         30         40         50         60         70         80
MSSGQDGGPR SPGRDPELQV EAAEVTTKEY DFGLGAPVSE AENYQNTLQL EQEVRNQDRF ISTLKLQIED LKQTNHGLEE
        90        100        110        120        130        140        150        160
YVRKLLDSKE VVSSQVDDLT SHNEHLCKEL IKIDQLAEQL EKEKNFVVDS ANKELEEAKI DLICQQNNII VLEDTIKRLK
       170        180        190        200        210        220        230        240
SIILDTEKAQ NKSPSRLDSF VKTLEADKDH YKSEAQHLRK MMRSRSKSPR RPSPTARGAN CDVELLKTTT RDREELKCML
       250        260        270        280        290        300        310        320
EKYERHLAEI QGNVKVLKSE RDKIFLLYEQ AQEEITRLRR EMMKSCKSPK STTAHAILRR VETERDVAFT DLRRMTTERD
       330        340        350        360        370        380        390        400
SLRERLKIAQ ETAFNEKAHL EQRIEELECT VHNLDDERME QMSNMTLMKE TISTVEKEMK SLARKAMDTE SELGRQKAEN
       410        420        430        440        450        460        470        480
NSLRLLYENT EKDLSDTQRH LAKKKYELQL TQEKIMCLDE KIDNFTRQNI AQREEISILG GTLNDLAKEK ECLQACLDKK
       490        500        510        520        530        540        550        560
SENIASLGES LAMKEKTISG MKNIIAEMEQ ASRQCTEALI VCEQDVSRMR RQLDETNDEL AQIARERDIL AHDNDNLQEQ
       570        580        590        600        610        620        630        640
FAKAKQENQA LSKKLNDTHN ELNDIKQKVQ DTNLEVNKLK NILKSEESEN RQMMEQLRKA NEDAENWENK ARQSEADNNT
       650        660        670        680        690        700        710        720
LKLELITAEA EGNRLKEKVD SLNREVEQHL NAERSYKSQI STLHKSVVKM EEELQKVQFE KVSALADLSS TRELCIKLDS
       730        740        750        760        770        780        790        800
SKELLNRQLV AKDQEIEMRE NELDSAHSEI ELLRSQMANE RISMQNLEAL LVANRDKEYQ SQIALQEKES EIQLLKEHLC
       810        820        830        840        850        860        870        880
LAENKMAIQS RDVAQFRNVV TQLEADLDIT KRQLGTERFE RERAVQELRR QNYSSNAYHM SSTMKPNTKC HSPERAHHRS
       890        900
PDRGLDRSLE E
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1178	1	760.8598	-40.38	2	43.4	12.7	1	218-231	R.GANCDVELLKTTTR.D		Wdown:Qdown 1.07 mdown:qdown 1.21

BRUKER

Detailed Protein Report

Protein 181: **PREDICTED: N-alpha-acetyltransferase 15, NatA auxiliary subunit isoform X1 [Homo sapiens]**

Accession: gi|530378196
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 42.8
MW [kDa]: 101.1
pI: 7.8
Sequence Coverage [%]: 5.1
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MPAVSLPPKE	NALFKRILRC	YEHKQYRNGL	KFCKQILSNP	KFAEHGETLA	MKGLTLNCLG	KKEEAYELVR	RGLRNDLKSH
90	100	110	120	130	140	150	160
VCWHVYGLLQ	RSDKKYDEAI	KCYRNALKWD	KDNLQILRDL	SLLQIQMRDL	EGYRETRYQL	LQLRPAQRAS	WIGYAIAYHL
170	180	190	200	210	220	230	240
LEDYEMAAKI	LEEFRKTQQT	SPDKVDYEYS	ELLLYQNQVL	REAGLYREAL	EHLCTYEKQI	CDKLAVEETK	GELLLQLCRL
250	260	270	280	290	300	310	320
EDAADVYRGL	QERNPENWAY	YKGLEKALKP	ANMLERLKIY	EEAWTKYPRG	LVPRRLPLNF	LSGEKFKECL	DKFLRMNFSK
330	340	350	360	370	380	390	400
GCPPVFNTLR	SLYKDKEKVA	IIEELVVGYE	TSLKSCRLFN	PNDDGKEEPP	TTLLWVQYYL	AQHYDKIGQP	SIALEYINTA
410	420	430	440	450	460	470	480
IESTPTLIEL	FLVKAKIYKH	AGNIKEAARW	MDEAQALDTA	DRFINSKCAK	YMLKANLIKE	AEEMCSKFTR	EGTSAVENLN
490	500	510	520	530	540	550	560
EMQCMWFQTE	CAQAYKAMNK	FGEALKKCHE	IERHFIEITD	DQFDFHTYCM	RKITLRSYVD	LLKLEDVLRQ	HPFYFKAARI
570	580	590	600	610	620	630	640
AIEIYLKLHD	NPLTDENKEH	EADTANMSDK	ELKKLRNKQR	RAQKKAQIEE	EKKNAEKEKQ	QRNQKKKKDD	DDEEIGGPKE
650	660	670	680	690	700	710	720
ELIPEKLAKV	ETPLEEAIKF	LTPLKNLVKN	KIETHLFAFE	IYFRKEKFLL	MLQSVKRAFA	IDSSHPWLHE	CMIRLFNTVC
730	740	750	760	770	780	790	800
ESKDLSDTVR	TVLKQEMNRL	FGATNPKNFN	ETFLKRNSDS	LPHRLSAAKM	VYYLDPSSQK	RAIELATTLD	ESLTNRNLQT
810	820	830	840	850	860	870	
CMEVLEALYD	GSLGDCKEAA	EIYRANCHKL	FPYALAFMPP	GYEEDMKITV	NGDSSAEAEE	LANEI	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2297	1	863.8705	-61.74	2	57.2	20.5	1	316-330	R.MNFSKGCPPVFNTLR.S	Oxidation: 1

Detailed Protein Report

Protein 182: probable ATP-dependent RNA helicase DDX58 [Homo sapiens]

Accession:	gi|27881482	**Score:**	42.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	106.5
Database Date:	2015-11-30	**pI:**	6.0
Modification(s):	Oxidation	**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 183: PREDICTED: uncharacterized protein LOC102724905 [Homo sapiens]

Accession:	gi|578835678	**Score:**	42.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	22.0
Database Date:	2015-11-30	**pI:**	10.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	16.7
		No. of unique Peptides:	2

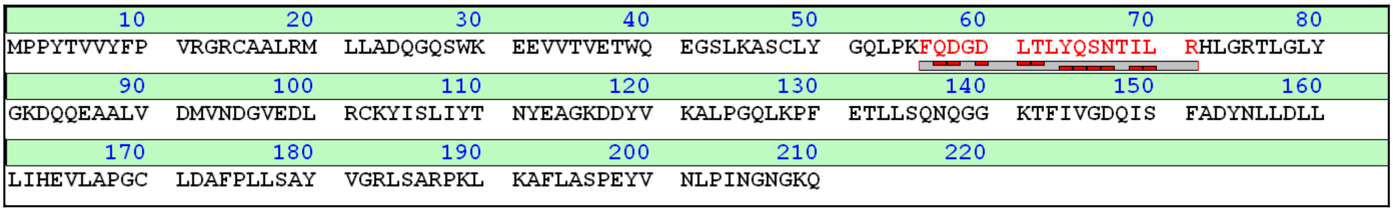
10	20	30	40	50	60	70	80
MKCSTSNCII	SIKDYTSIRI	NVAEVDKVTS	RFNGQFKTYA	FGGSPGTGVT	GGKGREGGRS	FCAGEGNERN	GKGTAGCEAR
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
DVPGSAAGPA	RGRAAPLHPA	PGPPLRGAIL	QAAVAGTGGG	GCSGHCGAEA	RRQDGNHASC	SQLGLDSTNG	DFSYGFELGP
170	**180**	**190**	**200**	**210**	**220**		
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
1810	1	641.7727	-58.27	2	52.6	13.4	0	3-13	K.CSTSNCIISIK.D	Carbamidomethyl: 1, 6

Detailed Protein Report

Protein 184: glutathione S-transferase P [Homo sapiens]

Accession:	gi|4504183	**Score:**	42.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	23.3
Database Date:	2015-11-30	**pI:**	5.3
		Sequence Coverage [%]:	7.6
		No. of unique Peptides:	1



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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1632	1	942.4899	12.06	2	49.1	42.5	0	56-71	K.FQDGDLTLYQSNTILR.H	

Detailed Protein Report

Protein 185: mitochondrial intermediate peptidase [Homo sapiens]

Accession:	gi|156105687	**Score:**	42.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	80.6
Database Date:	2015-11-30	**pI:**	6.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	5.2
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MLCVGRLGGL	GARAAALPPR	RAGRGSLEAG	IRARRVSTSW	SPVGAAFNVK	PQGSRLDLFG	ERRGLFGVPE	LSAPEGFHIA
90	100	110	120	130	140	150	160
QEKALRKTEL	LVDRACSTPP	GPQTVLIFDE	LSDSLCRVAD	LADFVKIAHP	EPAFREAAEE	ACRSIGTMVE	KLNTNVDLYQ
170	180	190	200	210	220	230	240
SLQKLLADKK	LVDSLDPETR	RVAELFMFDF	EISGIHLDKE	KRKRAVDLNV	KILDLSSTFL	MGTNFPNKIE	KHLLPEHIRR
250	260	270	280	290	300	310	320
NFTSAGDHII	IDGLHAESPD	DLVREAAYKI	FLYPNAGQLK	CLEELLSSRD	LLAKLVGYST	FSHRALQGTI	AKNPETVMQF
330	340	350	360	370	380	390	400
LEKLSDKLSE	RTLKDFEMIR	GMKMKLNPQN	SEVMPWDPPY	YSGVIRAERY	NIEPSLYCPF	FSLGACMEGL	NILLNRLLGI
410	420	430	440	450	460	470	480
SLYAEQPAKG	EVWSEDVRKL	AVVHESEGLL	GYIYCDFFQR	ADKPHQDCHF	TIRGGRLKED	GDYQLPVVVL	MLNLPRSSRS
490	500	510	520	530	540	550	560
SPTLLTPGMM	ENLFHEMGHA	MHSMLGRTRY	QHVTGTRCPT	DFAEVPSILM	EYFANDYRVV	NQFARHYQTG	QPLPKNMVSR
570	580	590	600	610	620	630	640
LCESKKVCAA	ADMQLQVFYA	TLDQIYHGKH	PLRNSTTDIL	KETQEKFYGL	PYVPNTAWQL	RFSHLVGYGA	RYYSYLMSRA
650	660	670	680	690	700	710	720
VASMVWKECF	LQDPFNRAAG	ERYRREMLAH	GGGREPMLMV	EGMLQKCPSV	DDFVSALVSD	LDLDFETFLM	DSE

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2189	1	993.8848	-92.03	2	56.0	11.7	1	632-647	R.YYSYLMSRAVASMVWK.E	Oxidation: 6, 13
3000	4	703.3599	16.84	2	66.4	13.5	0	675-686	R.EPMLMVEGMLQK.C	

Protein 186: PREDICTED: microtubule-actin cross-linking factor 1 isoform X21 [Homo sapiens]

Accession:	gi|578798822	**Score:**	42.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	853.1
Database Date:	2015-11-30	**pI:**	5.2
		Sequence Coverage [%]:	0.5
		No. of unique Peptides:	2

Quantitation

Wdown:Qdown	**Median:** 1.17	**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

Detailed Protein Report

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		Wdown:Qdown 1.17
1103	1	1355.1276	184.19	1	42.5	16.9	2	2167-2178	K.LQVQVKKTLGIK.L		

Detailed Protein Report

Protein 187: PREDICTED: zinc finger protein 554 isoform X2 [Homo sapiens]

Accession:	gi|578832959	**Score:**	42.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	43.7
Database Date:	2015-11-30	**pI:**	9.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	10.8
		No. of unique Peptides:	2

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
2493	4	741.8586	-20.96	2	61.6	20.5	0	266-277	K.SFCQSSYLILHK.R	Carbamidomethyl: 3

Detailed Protein Report

Protein 188: smoothelin isoform e [Homo sapiens]

Accession: gi|333360860
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 42.0
MW [kDa]: 104.8
pI: 9.9
Sequence Coverage [%]: 3.9
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
2098	2	938.2855	-133.64	2	54.8	13.7	0	1-19	-.MGGMGTPGDLHAACPSTTR.R	Oxidation: 1
1621	1	502.6927	-108.16	2	50.1	15.3	1	523-532	K.DGRGQASTGR.V	

Detailed Protein Report

Protein 189: TRIO and F-actin-binding protein isoform 1 [Homo sapiens]

Accession:	gi|88501740	**Score:**	42.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	74.0
Database Date:	2015-11-30	**pI:**	6.5
		Sequence Coverage [%]:	8.9
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MGGWKGPGQR	RGKEGPEARR	RAAERGGGGG	GGGVPAPRSP	AREPRPRSCL	LLPPPWGAAM	TPDLLNFKKG	WMSILDEPGE
90	100	110	120	130	140	150	160
PPSPSLTTTS	TSQWKKHWFV	LTDSSLKYYR	DSTAEEADEL	DGEIDLRSCT	DVTEYAVQRN	YGFQIHTKDA	VYTLSAMTSG
170	180	190	200	210	220	230	240
IRRNWIEALR	KTVRPTSAPD	VTKLSDSNKE	NALHSYSTQK	GPLKAGEQRA	GSEVISRGGP	RKADGQRQAL	DYVELSPLTQ
250	260	270	280	290	300	310	320
ASPQRARTPA	RTPDRLAKQE	ELERDLAQRS	EERRKWFEAT	DSRTPEVPAG	EGPRRGLGAP	LTEDQQNRLS	EEIEKKWQEL
330	340	350	360	370	380	390	400
EKLPLRENKR	VPLTALLNQS	RGERRGPPSD	GHEALEKEVQ	ALRAQLEAWR	LQGEAPQSAL	RSQEDGHIPP	GYISQEACER
410	420	430	440	450	460	470	480
SLAEMESSHQ	QVMEELQRHH	ERELQRLQQE	KEWLLAEETA	ATASAIEAMK	KAYQEELSRE	LSKTRSLQQG	PDGLRKQHQS
490	500	510	520	530	540	550	560
DVEALKRELQ	VLSEQYSQKC	LEIGALMRQA	EEREHTLRRC	QQEGQELLRH	NQELHGRLSE	EIDQLRGFIA	SQGMGNGCGR
570	580	590	600	610	620	630	640
SNERSSCELE	VLLRVKENEL	QYLKKEVQCL	RDELQMMQKD	KRFTSGKYQD	VYVELSHIKT	RSEREIEQLK	EHLRLAMAAL
650	660						
QEKESMRNSL	AE						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2143	1	1051.3799	-114.76	2	55.3	12.5	1	276-294	K.WFEATDSRTPEVPAGEGPR.R	
1759	1	920.8290	-90.65	2	52.0	12.2	1	547-564	R.GFIASQGMGNGCGRSNER.S	

Detailed Protein Report

Protein 190: ranBP2-like and GRIP domain-containing protein 4 [Homo sapiens]

Accession:	gi|211059431	**Score:**	41.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	197.2
Database Date:	2015-11-30	**pI:**	5.9
		Sequence Coverage [%]:	2.7
		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	AAVAQGEE

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 191: testis-specific serine/threonine-protein kinase 2 [Homo sapiens]

Accession:	gi|194294513	**Score:**	41.8
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

Quantitation

mdown:qdown **Median:** 2.21 **CV:** 0.00 % **No. of Peptides:** 1

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
174	2	642.2924	-49.65	2	31.4	20.1	2	293-302	K.YRAECKLDTK.T	Carbamidomethyl: 5	mdown:qdown 2.21

Detailed Protein Report

Protein 192: **PREDICTED: latrophilin-1 isoform X5 [Homo sapiens]**

Accession:	gi|578833089	**Score:**	41.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	96.9
Database Date:	2015-11-30	**pI:**	6.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	6.1
		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 193: xylosyltransferase 1 precursor [Homo sapiens]

Accession:	gi|28269693	**Score:**	41.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	107.5
Database Date:	2015-11-30	**pI:**	10.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	5.3
		No. of unique Peptides:	3

Quantitation

mdown:qdown	**Median:**	0.48	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	1.47	**CV:**	0.00 %	**No. of Peptides:**	1

```
        10         20         30         40         50         60         70         80
MVAAPCARRL ARRSHSALLA ALTVLLLQTL VVWNFSSLDS GAGERRGGAA VGGGEQPPPA PAPRRERRDL PAEPAAARGG
        90        100        110        120        130        140        150        160
GGGGGGGGGG RGPQARARGG GPGEPRGQQP ASRGALPARA LDPHPSPLIT LETQDGYFSH RPKEKVRTDS NNENSVPKDF
       170        180        190        200        210        220        230        240
ENVDNSNFAP RTQKQKHQPE LAKKPPSRQK ELLKRKLEQQ EKGKGHTFPG KGPGEVLPPG DRAAANSSHG KDVSRPPHAR
       250        260        270        280        290        300        310        320
KTGGSSPETK YDQPPKCDIS GKEAISALSR AKSKHCRQEI GETYCRHKLG LLMPEKVTRF CPLEGKANKN VQWDEDSVEY
       330        340        350        360        370        380        390        400
MPANPVRIAF VLVVHGRASR QLQRMFKAIY HKDHFYYIHV DKRSNYLHRQ VLQVSRQYSN VRVTPWRMAT IWGGASLLST
       410        420        430        440        450        460        470        480
YLQSMRDLLE MTDWPWDFFI NLSAADYPIR TNDQLVAFLS RYRDMNFLKS HGRDNARFIR KQGLDRLFLE CDAHMWRLGD
       490        500        510        520        530        540        550        560
RRIPEGIAVD GGSDWFLLNR RFVEYVTFST DDLVTKMKQF YSYTLLPAES FFHTVLENSP HCDTMVDNNL RITNWNRKLG
       570        580        590        600        610        620        630        640
CKCQYKHIVD WCGCSPNDFK PQDFHRFQQT ARPTFFARKF EAVVNQEIIG QLDYYLYGNY PAGTPGLRSY WENVYDEPDG
       650        660        670        680        690        700        710        720
IHSLSDVTLT LYHSFARLGL RRAETSLHTD GENSCRYYPM GHPASVHLYF LADRFQGFLI KHHATNLAVS KLETLETWVM
       730        740        750        760        770        780        790        800
PKKVFKIASP PSDFGRLQFS EVGTDWDAKE RLFRNFGGLL GPMDEPVGMQ KWGKGPNVTV TVIWVDPVNV IAATYDILIE
       810        820        830        840        850        860        870        880
STAEFTHYKP PLNLPLRPGV WTVKILHHWV PVAETKFLVA PLTFSNRQPI KPEEALKLHN GPLRNAYMEQ SFQSLNPVLS
       890        900        910        920        930        940        950        960
LPINPAQVEQ ARRNAASTGT ALEGWLDSLV GGMWTAMDIC ATGPTACPVM QTCSQTAWSS FSPDPKSELG AVKPDGRLR
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
87	1	669.7442	115.37	3	29.8	12.8	2	68-91	R. RDLPAEPAAARGGGGGGGGGG G		
1789	1	916.3008	-236.11	1	52.4	13.7	0	289-296	K.LGLLMPEK.V	Oxidation: 5	Wdown:Qdown 1.47 mdown:qdown 0.48
2109	1	701.2880	-90.93	3	56.5	15.4	0	388-406	R.MATIWGGASLLSTYLQSMR.D	Oxidation: 18	

Detailed Protein Report

Protein 194: **PREDICTED: cleavage and polyadenylation specificity factor subunit 1 isoform X1 [Homo sapiens]**

Accession: gi|578815943
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 41.8
MW [kDa]: 160.4
pI: 5.9
Sequence Coverage [%]: 2.4
No. of unique Peptides: 1

```
        10         20         30         40         50         60         70         80
MYAVYKQAHP PTGLEFSMYC NFFNNSERNL VVAGTSQLYV YRLNRDAEAL TKNDRSTEGK AHREKLELAA SFSFFGNVMS

        90        100        110        120        130        140        150        160
MASVQLAGAK RDALLLSFKD AKLSVVEYDP GTHDLKTLSL HYFEEPELRD GFVQNVHTPR VRVDPDGRCA AMLVYGTRLV

       170        180        190        200        210        220        230        240
VLPFRRESLA EEHEGLVGEG QRSSFLPSYI IDVRALDEKL LNIIDLQFLH GYYEPTLLIL FEPNQTWPGR VAVRQDTCSI

       250        260        270        280        290        300        310        320
VAISLNITQK VHPVIWSLTS LPFDCTQALA VPKPIGGVVV FAVNSLLYLN QSVPPYGVAL NSLTTGTTAF PLRTQEGVRI

       330        340        350        360        370        380        390        400
TLDCAQATFI SYDKMVISLK GGEIYVLTLI TDGMRSVRAF HFDKAAASVL TTSMVTMEPG YLFLGSRLGN SLLLKYTEKL

       410        420        430        440        450        460        470        480
QEPPASAVRE AADKEEPPSK KKRVDATAGW SAAGKSVPQD EVDEIEVYGS EAQSGTQLAT YSFEVCDSIL NIGPCANAAV

       490        500        510        520        530        540        550        560
GEPAFLSEEF QNSPEPDLEI VVCSGHGKNG ALSVLQKSIR PQVVTTFELP GCYDMWTVIA PVRKEEEDNP KGEGTEQEPS

       570        580        590        600        610        620        630        640
TTPEADDDGR RHGFLILSRE DSTMILQTGQ EIMELDTSGF ATQGPTVFAG NIGDNRYIVQ VSPLGIRLLE GVNQLHFIPV

       650        660        670        680        690        700        710        720
DLGAPIVQCA VADPYVVIMS AEGHVTMFLL KSDSYGGRHH RLALHKPPLH HQSKVITLCL YRDLSGMFTT ESRLGGARDE

       730        740        750        760        770        780        790        800
LGGRSGPEAE GLGSETSPTV DDEEEMLYGD SGSLFSPSKE EARRSSQPPA DRDPAPFRAE PTHWCLLVRE NGTMEIYQLP

       810        820        830        840        850        860        870        880
DWRLVFLVKN FPVGQRVLVD SSFGQPTTQG EARREEATRQ GELPLVKEVL LVALGSRQSR PYLLVHVDQE LLIYEAFPHD

       890        900        910        920        930        940        950        960
SQLGQGNLKV RFKKVPHNIN FREKKPKPSK KKAEGGGAEE GAGARGRVAR FRYFEDIYGY SGVFICGPSP HWLLVTGRGA

       970        980        990       1000       1010       1020       1030       1040
LRLHPMAIDG PVDSFAPFHN VNCPRGFLYF NRQGELRISV LPAYLSYDAP WPVRKIPLRC TAHYVAYHVE SKVYAVATST

      1050       1060       1070       1080       1090       1100       1110       1120
NTPCARIPRM TGEEKEFETI ERDERYIHPQ QEAFSIQLIS PVSWEAIPNA RIELQEWEHV TCMKTVSLRS EETVSGLKGY

      1130       1140       1150       1160       1170       1180       1190       1200
VAAGTCLMQG EEVTCRGRIL IMDVIEVVPE PGQPLTKNKF KVLYEKEQKG PVTALCHCNG HLVSAIGQKI FLWSLRASEL

      1210       1220       1230       1240       1250       1260       1270       1280
TGMAFIDTQL YIHQMISVKN FILAADVMKS ISLLRYQEES KTLSLDAKPL EVYSVDFMVD NAQLGFLVSD RDRNLMVYMY

      1290       1300       1310       1320       1330       1340       1350       1360
LPEAKESFGG MRLLRRADFH VGAHVNTFWR TPCRGATEGL SKKSVVWENK HITWFATLDG GIGLLLPMQE KTYRRLLMLQ

      1370       1380       1390       1400       1410       1420       1430       1440
NALTTMLPHH AGLNPRAFRM LHVDRRTLQN AVRNVLDGEL LNRYLYLSTM ERSELAKKIG TTPDIILDDL LETDRVTAHF

      1450
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2457	1	596.2158	-123.37	2	61.1	10.4	0	1404- 1412	R.YLYLSTMER.S	Oxidation: 7

Detailed Protein Report

Protein 195: talin-1 [Homo sapiens]

Accession:	gi|223029410	**Score:**	41.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	269.6
Database Date:	2015-11-30	**pI:**	5.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.4
		No. of unique Peptides:	2

Quantitation

mdown:qdown	**Median:**	0.35	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.07	**CV:**	0.00 %	**No. of Peptides:**	1

```
        10         20         30         40         50         60         70         80
MVALSLKISI GNVVKTMQFE PSTMVYDACR IIRERIPEAP AGPPSDFGLF LSDDDPKKGI WLEAGKALDY YMLRNGDTME
        90        100        110        120        130        140        150        160
YRKKQRPLKI RMLDGTVKTI MVDDSKTVTD MLMTICARIG ITNHDEYSLV RELMEEKKEE ITGTLRKDKT LLRDEKKMEK
       170        180        190        200        210        220        230        240
LKQKLHTDDE LNWLDHGRTL REQGVEEHET LLLRRKFFYS DQNVDSRDPV QLNLLYVQAR DDILNGSHPV SFDKACEFAG
       250        260        270        280        290        300        310        320
FQCQIQFGPH NEQKHKAGFL DLKDFLPKEY VKQKGERKIF QAHKNCGQMS EIEAKVRYVK LARSLKTYGV SFFLVKEKMK
       330        340        350        360        370        380        390        400
GKNKLVPRLL GITKECVMRV DEKTKEVIQE WNLTNIKRWA ASPKSFTLDF GDYQDGYYSV QTTEGEQIAQ LIAGYIDIIL
       410        420        430        440        450        460        470        480
KKKKSKDHFG LEGDEESTML EDSVSPKKST VLQQQYNRVG KVEHGSVALP AIMRSGASGP ENFQVGSMPP AQQQITSGQM
       490        500        510        520        530        540        550        560
HRGHMPPLTS AQQALTGTIN SSMQAVQAAQ ATLDDFDTLP PLGQDAASKA WRKNKMDESK HEIHSQVDAI TAGTASVVNL
       570        580        590        600        610        620        630        640
TAGDPAETDY TAVGCAVTTI SSNLTEMSRG VKLLAALLED EGGSGRPLLQ AAKGLAGAVS ELLRSAQPAS AEPRQNLLQA
       650        660        670        680        690        700        710        720
AGNVGQASGE LLQQIGESDT DPHFQDALMQ LAKAVASAAA ALVLKAKSVA QRTEDSGLQT QVIAAATQCA LSTSQLVACT
       730        740        750        760        770        780        790        800
KVVAPTISSP VCQEQLVEAG RLVAKAVEGC VSASQAATED GQLLRGVGAA ATAVTQALNE LLQHVKAHAT GAGPAGRYDQ
       810        820        830        840        850        860        870        880
ATDTILTVTE NIFSSMGDAG EMVRQARILA QATSDLVNAI KADAEGESDL ENSRKLLSAA KILADATAKM VEAAKGAAAH
       890        900        910        920        930        940        950        960
PDSEEQQQRL REAAEGLRMA TNAAAQNAIK KKLVQRLEHA AKQAAASATQ TIAAAQHAAS TPKASAGPQP LLVQSCKAVA
       970        980        990       1000       1010       1020       1030       1040
EQIPLLVQGV RGSQAQPDSP SAQLALIAAS QSFLQPGGKM VAAAKASVPT IQDQASAMQL SQCAKNLGTA LAELRTAAQK
      1050       1060       1070       1080       1090       1100       1110       1120
AQEACGPLEM DSALSVVQNL EKDLQEVKAA ARDGKLKPLP GETMEKCTQD LGNSTKAVSS AIAQLLGEVA QGNENYAGIA
      1130       1140       1150       1160       1170       1180       1190       1200
ARDVAGGLRS LAQAARGVAA LTSDPAVQAI VLDTASDVLD KASSLIEEAK KAAGHPGDPE SQQRLAQVAK AVTQALNRCV
      1210       1220       1230       1240       1250       1260       1270       1280
SCLPGQRDVD NALRAVGDAS KRLLSDSLPP STGTFQEAQS RLNEAAAGLN QAATELVQAS RGTPQDLARA SGRFGQDFST
      1290       1300       1310       1320       1330       1340       1350       1360
FLEAGVEMAG QAPSQEDRAQ VVSNLKGISM SSSKLLLAAK ALSTDPAAPN LKSQLAAAAR AVTDSINQLI TMCTQQAPGQ
      1370       1380       1390       1400       1410       1420       1430       1440
KECDNALREL ETVRELLENP VQPINDMSYF GCLDSVMENS KVLGEAMTGI SQNAKNGNLP EFGDAISTAS KALCGFTEAA
      1450       1460       1470       1480       1490       1500       1510       1520
AQAAYLVGVS DPNSQAGQQG LVEPTQFARA NQAIQMACQS LGEPGCTQAQ VLSAATIVAK HTSALCNSCR LASARTTNPT
      1530       1540       1550       1560       1570       1580       1590       1600
AKRQFVQSAK EVANSTANLV KTIKALDGAF TEENRAQCRA ATAPLLEAVD NLSAFASNPE FSSIPAQISP EGRAAMEPIV
      1610       1620       1630       1640       1650       1660       1670       1680
ISAKTMLESA GGLIQTARAL AVNPRDPPSW SVLAGHSRTV SDSIKKLITS MRDKAPGQLE CETAIAALNS CLRDLDQASL
      1690       1700       1710       1720       1730       1740       1750       1760
AAVSQQLAPR EGISQEALHT QMLTAVQEIS HLIEPLANAA RAEASQLGHK VSQMAQYFEP LTLAAVGAAS KTLSHPQQMA
      1770       1780       1790       1800       1810       1820       1830       1840
LLDQTKTLAE SALQLLYTAK EAGGNPKQAA HTQEALEEAV QMMTEAVEDL TTTLNEAASA AGVVGGMVDS ITQAINQLDE
      1850       1860       1870       1880       1890       1900       1910       1920
GPMGEPEGSF VDYQTTMVRT AKAIAVTVQE MVTKSNTSPE ELGPLANQLT SDYGRLASEA KPAAVAAENE EIGSHIKHRV
      1930       1940       1950       1960       1970       1980       1990       2000
QELGHGCAAL VTKAGALQCS PSDAYTKKEL IECARRVSEK VSHVLAALQA GNRGTQACIT AASAVSGIIA DLDTTIMFAT
      2010       2020       2030       2040       2050       2060       2070       2080
AGTLNREGTE TFADHREGIL KTAKVLVEDT KVLVQNAAGS QEKLAQAAQS SVATITRLAD VVKLGAASLG AEDPETQVVL
      2090       2100       2110       2120       2130       2140       2150       2160
INAVKDVAKA LGDLISATKA AAGKVGDDPA VWQLKNSAKV MVTNVTSLLK TVKAVEDEAT KGTRALEATT EHIRQELAVF
      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
509	2	501.1523	-279.76	2	35.2	14.2	1	58-66	K.KGIWLEAGK.A		mdown:qdown 0.35 Wdown:Qdown 0.07
2760	1	698.3753	1.48	2	63.5	13.0	0	442-454	K.VEHGSVALPAIMR.S	Oxidation: 12	

Detailed Protein Report

Protein 196: **sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform a [Homo sapiens]**

Accession:	gi|4502285	**Score:**	41.7
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 [%]:**	3.4
		No. of unique Peptides:	2

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
1931	1	709.7683	-152.59	2	52.8	13.6	1	511-523	K.MFVKGAPEGVIDR.C	
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 197: ATPase family AAA domain-containing protein 2 [Homo sapiens]

Accession: gi|24497618
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 41.6
MW [kDa]: 158.5
pI: 5.9
Sequence Coverage [%]: 2.8
No. of unique Peptides: 2

Quantitation

Wdown:Qdown **Median:** 0.88 **CV:** 0.00 % **No. of Peptides:** 1

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2101	1	1057.6924	66.12	1	54.8	10.3	2	38-47	R.RLRSAGAAQK.K		
2087	6	937.3467	-131.35	2	54.7	19.5	0	407-424	K.IGASLADVDPMQLDSSVR.F		Wdown:Qdown 0.88

Detailed Protein Report

Protein 198: endothelin-2 preproprotein [Homo sapiens]

Accession: gi|4503463
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 41.5
MW [kDa]: 19.9
pI: 12.1
Sequence Coverage [%]: 10.1
No. of unique Peptides: 1

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2155	1	1051.4608	-0.17	2	55.5	16.2	2	95-112	R.RCQCSSARDPACATFCLR.R	Carbamidomethyl: 12, 16

Detailed Protein Report

Protein 199: Fanconi anemia group M protein [Homo sapiens]

Accession:	gi|74959747	**Score:**	41.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	232.0
Database Date:	2015-11-30	**pI:**	5.7
		Sequence Coverage [%]:	2.7
		No. of unique Peptides:	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MSGRQRTLFQ	TWGSSISRSS	GTPGCSSGTE	RPQSPGSSKA	PLPAAAEAQL	ESDDDVLLVA	AYEAERQLCL	ENGGFCTSAG
90	100	110	120	130	140	150	160
ALWIYPTNCP	VRDYQLHISR	AALFCNTLVC	LPTGLGKTFI	AAVVMYNFYR	WFPSGKVVFM	APTKPLVTQQ	IEACYQVMGI
170	180	190	200	210	220	230	240
PQSHMAEMTG	STQASTRKEI	WCSKRVLFLT	PQVMVNDLSR	GACPAAEIKC	LVIDEAHKAL	GNYAYCQVVR	ELVKYTNHFR
250	260	270	280	290	300	310	320
ILALSATPGS	DIKAVQQVIT	NLLIGQIELR	SEDSPDILTY	SHERKVEKLI	VPLGEELAAI	QKTYIQILES	FARSLIQRNV
330	340	350	360	370	380	390	400
LMRRDIPNLT	KYQIILARDQ	FRKNPSPNIV	GIQQGIIEGE	FAICISLYHG	YELLQQMGMR	SLYFFLCGIM	DGTKGMTRSK
410	420	430	440	450	460	470	480
NELGRNEDFM	KLYNHLECMF	ARTRSTSANG	ISAIQQGDKN	KKFVYSHPKL	KKLEEVVIEH	FKSWNAENTT	EKKRDETRVM
490	500	510	520	530	540	550	560
IFSSFRDSVQ	EIAEMLSQHQ	PIIRVMTFVG	HASGKSTKGF	TQKEQLEVVK	QFRDGGYNTL	VSTCVGEEGL	DIGEVDLIIC
570	580	590	600	610	620	630	640
FDSQKSPIRL	VQRMGRTGRK	RQGRIVIILS	EGREERIYNQ	SQSNKRSIYK	AISSNRQVLH	FYQRSPRMVP	DGINPKLHKM
650	660	670	680	690	700	710	720
FITHGVYEPE	KPSRNLQRKS	SIFSYRDGMR	QSSLKKDWFL	SEEEFKLWNR	LYRLRDSDEI	KEITLPQVQF	SSLQNEENKP
730	740	750	760	770	780	790	800
AQESTTGIHQ	LSLSEWRLWQ	DHPLPTHQVD	HSDRCRHFIG	LMQMIEGMRH	EEGECSYELE	VESYLQMEDV	TSTFIAPRNE
810	820	830	840	850	860	870	880
SNNLASDTFI	THKKSSFIKN	INQGSSSSVI	ESDEECAEIV	KQTHIKPTKI	VSLKKKVSKE	IKKDQLKKEN	NHGIIDSVDN
890	900	910	920	930	940	950	960
DRNSTVENIF	QEDLPNDKRT	SDTDEIAATC	TINENVIKEP	CVLLTECQFT	NKSTSSLAGN	VLDSGYNSFN	DEKSVSSNLF
970	980	990	1000	1010	1020	1030	1040
LPFEEELYIV	RTDDQFYNCH	SLTKEVLANV	ERFLSYSPPP	LSGLSDLEYE	IAKGTALENL	LFLPCAEHLR	SDKCTCLLSH
1050	1060	1070	1080	1090	1100	1110	1120
SAVNSQQNLE	LNSLKCINYP	SEKSCLYDIP	NDNISDEPSL	CDCDVHKHNQ	NENLVPNNRV	QIHRSPAQNL	VGENNHDVDN
1130	1140	1150	1160	1170	1180	1190	1200
SDLPVLSTDQ	DESLLLFEDV	NTEFDDVSLS	PLNSKSESLP	VSDKTAISET	PLVSQFLISD	ELLLDNNSEL	QDQITRDANS
1210	1220	1230	1240	1250	1260	1270	1280
FKSRDQRGVQ	EEKVKNHEDI	FDCSRDLFSV	TFDLGFCSPD	SDDEILEHTS	DSNRPLDDLY	GRYLEIKEIS	DANYVSNQAL
1290	1300	1310	1320	1330	1340	1350	1360
IPRDHSKNFT	SGTVIIPSNE	DMQNPNYVHL	PLSAAKNEEL	LSPGYSQFSL	PVQKKVMSTP	LSKSNTLNSF	SKIRKEILKT
1370	1380	1390	1400	1410	1420	1430	1440
PDSSKEKVNL	QRFKEALNST	FDYSEFSLEK	SKSSGPMYLH	KSCHSVEDGQ	LLTSNESEDD	EIFRRKVKRA	KGNVLNSPED
1450	1460	1470	1480	1490	1500	1510	1520
QKNSEVDSPL	HAVKKRRFPI	NRSELSSSDE	SENFPKPCSQ	LEDFKVCNGN	ARRGIKVPKR	QSHLKHVARK	FLDDEAELSE
1530	1540	1550	1560	1570	1580	1590	1600
EDAEYVSSDE	NDESENEQDS	SLLDFLNDET	QLSQAINDSE	MRAIYMKSLR	SPMMNNKYKM	IHKTHKNINI	FSQIPEQDET
1610	1620	1630	1640	1650	1660	1670	1680
YLEDSFCVDE	EESCKGQSSE	EEVCVDFNLI	TDDCFANSKK	YKTRRAVMLK	EMMEQNCAHS	KKKLSRIILP	DDSSEEENNV
1690	1700	1710	1720	1730	1740	1750	1760
NDKRESNIAV	NPSTVKKNKQ	QDHCLNSVPS	GSSAQSKVRS	TPRVNPLAKQ	SKQTSLNLKD	TISEVSDFKP	QNHNEVQSTT
1770	1780	1790	1800	1810	1820	1830	1840
PPFTTVDSQK	DCRKFPVPQK	DGSALEDSST	SGASCSKSRP	HLAGTHTSLR	LPQEGKGTCI	LVGGHEITSG	LEVISSLRAI
1850	1860	1870	1880	1890	1900	1910	1920
HGLQVEVCPL	NGCDYIVSNR	MVVERRSQSE	MLNSVNKNKF	IEQIQHLQSM	FERICVIVEK	DREKTGDTSR	MFRRTKSYDS
1930	1940	1950	1960	1970	1980	1990	2000
LLTTLIGAGI	RILFSSCQEE	TADLLKELSL	VEQRKNVGIH	VPTVVNSNKS	EALQFYLSIP	NISYITALNM	CHQFSSVKRM
2010	2020	2030	2040	2050			
ANSSLQEISM	YAQVTHQKAE	EIYRYIHYVF	DIQMLPNDLN	QDRLKSDI			

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
2013	1	687.7835	-136.48	2	55.3	11.0	2	1356-1367	K.EILKTPDSSKEK.V	

Detailed Protein Report

Protein 200: cystatin-S precursor [Homo sapiens]

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

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

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

Detailed Protein Report

Protein 201: PREDICTED: ATPase family AAA domain-containing protein 2B isoform X1 [Homo sapiens]

Accession:	gi|578802946	**Score:**	41.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	166.4
Database Date:	2015-11-30	**pI:**	6.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.4
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	0.92	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	4.19	**CV:**	0.00 %	**No. of Peptides:**	1

10	20	30	40	50	60	70	80
MVNTRKSSLR	LLGSKSPGPG	PGPGAGAEPG	ATGGSSHFIS	SRTRSSKTRA	ASCPAAKAGG	SGGAGVTLDE	ARKVEVDGSL
90	100	110	120	130	140	150	160
SDSHVSPPAK	RTLKQPDSVC	KDKSKSRSTG	QREEWNLSTG	QARLTSQPGA	TLPNGHSGLS	LRSHPLRGEK	KGDGDLSCIN
170	180	190	200	210	220	230	240
GDMEVRKSCR	SRKNRFESVN	QSLLFDQLVN	STAEAVLQEM	DNINIRRNRR	SGEVERLRMW	TDTEFENMDM	YSRVKRRRKS
250	260	270	280	290	300	310	320
LRRNSYGIQN	HHEVSTEGEE	EARTSKLLPL	EKISIESQEE	DGDIEVEEAE	GEENDRPYNL	RQRKTVDRYQ	APPIVPAHQK
330	340	350	360	370	380	390	400
KRENTLFDIH	RSPARRSHIR	RKKHAIHSSD	TTSSDEERFE	RRKSKSMARA	RNRCLPMNFR	AEDLASGILR	ERVKVGASLA
410	420	430	440	450	460	470	480
DVDPMNIDKS	VRFDSIGGLS	HHIHALKEMV	VFPLLYPEIF	EKFKIQPPRG	CLFYGPPGTG	KTLVARALAN	ECSQGDKKVA
490	500	510	520	530	540	550	560
FFMRKGADCL	SKWVGESERQ	LRLLFDQAYL	MRPSIIFFDE	IDGLAPVRSS	RQDQIHSSIV	STLLALMDGL	DNRGEIVVIG
570	580	590	600	610	620	630	640
ATNRLDSIDP	ALRRPGRFDR	EFLFNLPDQK	ARKHILQIHT	RDWNPKLSDA	FLGELAEKCV	GYCGADIKAL	CTEAALIALR
650	660	670	680	690	700	710	720
RRYPQIYASS	HKLQLDVSSI	VLSAQDFYHA	MQNIVPASQR	AVMSSGHALS	PIIRPLLERS	FNNILAVLQK	VFPHAEISQS
730	740	750	760	770	780	790	800
DKKEDIETLI	LEDSEDENAL	SIFETNCHSG	SPKKQSSSAA	IHKPYLHFTM	SPYHQPTSYR	PRLLLSGERG	SGQTSHLAPA
810	820	830	840	850	860	870	880
LLHTLERFSV	HRLDLPALYS	VSAKTPEESC	AQIFREARRT	VPSIVYMPHI	GDWWEAVSET	VRATFLTLLQ	DIPSFSPIFL
890	900	910	920	930	940	950	960
LSTSETMYSE	LPEEVKCIFR	IQYEEVLYIQ	RPIEEDRRKF	FQELILNQAS	MAPPRRKHAA	LCAMEVLPLA	LPSPPRQLSE
970	980	990	1000	1010	1020	1030	1040
SEKSRMEDQE	ENTLRELRLF	LRDVTKRLAT	DKRFNIFSKP	VDIEEVSDYL	EVIKEPMDLS	TVITKIDKHN	YLTAKDFLKD
1050	1060	1070	1080	1090	1100	1110	1120
IDLICSNALE	YNPDKDPGDK	IIRHRACTLK	DTAHAIIAAE	LDPEFNKLCE	EIKEARIKRG	LSVTSEQINP	HSTGARKTET
1130	1140	1150	1160	1170	1180	1190	1200
RVEEAFRHKQ	RNPMDVWHNS	ANKCAFRVRR	KSRRRSQWGK	GIIKKRKVNN	LKKDEEDTKF	ADYENHTEDR	KLLENGEFEV
1210	1220	1230	1240	1250	1260	1270	1280
STDCHEENGE	ETGDLSMTND	ESSCDIMDLD	QGQRLNNGAG	TKENFASTEE	ESSNESLLVN	SSSSLNPEQT	SRKETFLKGN
1290	1300	1310	1320	1330	1340	1350	1360
CLNGEASTDS	FEGIPVLECQ	NGKLEVVSFC	DSGDKCSSEQ	KILLEDQSKE	KPETSTENHG	DDLEKLEALE	CSNNEKLEPG
1370	1380	1390	1400	1410	1420	1430	1440
SDVEVKDAEL	DKEGASKVKK	YRKLILEQAK	TTSLELVPEE	PSEPVPPLIV	DRERLKKLLD	LLVDKSNNLA	VDQLERLYSL
1450	1460	1470	1480				
LSQCIYRHRK	DYDKSQLVEE	MERTVHMFET	FL				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
987	1	574.1653	-221.32	2	40.8	18.3	1	1088-1096	K.LCEEIKEAR.I	Carbamidomethyl: 2	mdown:qdown 0.92 Wdown:Qdown 4.19

Detailed Protein Report

Protein 202: PREDICTED: thyroglobulin isoform X10 [Homo sapiens]

Accession:	gi|578816124	**Score:**	41.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	302.4
Database Date:	2015-11-30	**pI:**	5.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.5
		No. of unique Peptides:	2

Quantitation

mdown:qdown	**Median:**	0.75	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.79	**CV:**	118.24 %	**No. of Peptides:**	2

Detailed Protein Report

10	20	30	40	50	60	70	80
MALVLEIFTL	LASICWVSAN	IFEYQVDAQP	LRPCELQRET	AFLKQADYVP	QCAEDGSFQT	VQCQNDGRSC	WCVGANGSEV
90	100	110	120	130	140	150	160
LGSRQPGRPV	ACLSFCQLQK	QQILLSGYIN	STDTSYLPQC	QDSGDYAPVQ	CDVQQVQCWC	VDAEGMEVYG	TRQLGRPKRC
170	180	190	200	210	220	230	240
PRSCEIRNRR	LLHGVGDKSP	PQCSAEGEFM	PVQCKFVNTT	DMMIFDLVHS	YNRFPDAFVT	FSSFQRRFPE	VSGYCHCADS
250	260	270	280	290	300	310	320
QGRELAETGL	ELLLDEIYDT	IFAGLDLPST	FTETTLYRIL	QRRFLAVQSV	ISGRFRCPTK	CEVERFTATS	FGHPYVPSCR
330	340	350	360	370	380	390	400
RNGDYQAVQC	QTEGPCWCVD	AQGKEMHGTR	QQGEPPSCAE	GQSCASERQQ	ALSRLYFGTS	GYFSQHDLFS	SPEKRWASPR
410	420	430	440	450	460	470	480
VARFATSCPP	TIKELFVDSG	LLRPMVEGQS	QQFSVSENLL	KEAIRAIFPS	RGLARLALQF	TTNPKRLQQN	LFGGKFLVNV
490	500	510	520	530	540	550	560
GQFNLSGALG	TRGTFNFSQF	FQQLGLASFL	NGGRQEDLAK	PLSVGLDSNS	STGTPEAAKK	DGTMNKPTVG	SFGFEINLQE
570	580	590	600	610	620	630	640
NQNALKFLAS	LLELPEFLLF	LQHAISVPED	VARDLGDVME	TVLSSQTCEQ	TPERLFVPSC	TTEGSYEDVQ	CFSGECWCVN
650	660	670	680	690	700	710	720
SWGKELPGSR	VRGGQPRCPT	DCEKQRARMQ	SLMGSQPAGS	TLFVPACTSE	GHFLPVQCFN	SECYCVDAEG	QAIPGTRSAI
730	740	750	760	770	780	790	800
GKPKKCPTPC	QLQSEQAFLR	TVQALLSNSS	MLPTLSDTYI	PQCSTDGQWR	QVQCNGPPEQ	VFELYQRWEA	QNKGQDLTPA
810	820	830	840	850	860	870	880
KLLVKIMSYR	EAASGNFSLF	IQSLYEAGQQ	DVFPVLSQYP	SLQDVPLAAL	EGKRPQPREN	ILLEPYLFWQ	ILNGQLSQYP
890	900	910	920	930	940	950	960
GSYSDFSTPL	AHFDLRNCWC	VDEAGQELEG	MRSEPSKLPT	CPGSCEEAKL	RVLQFIRETE	EIVSASNSSR	FPLGESFLVA
970	980	990	1000	1010	1020	1030	1040
KGIRLRNEDL	GLPPLFPPRE	AFAEQFLRGS	DYAIRLAAQS	TLSFYQRRRF	SPDDSAGASA	LLRSGPYMPQ	CDAFGSWEPV
1050	1060	1070	1080	1090	1100	1110	1120
QCHAGTGHCW	CVDEKGGFIP	GSLTARSLQI	PQCPTTCEKS	RTSGLLSSWK	QARSQENPSP	KDLFVPACLE	TGEYARLQAS
1130	1140	1150	1160	1170	1180	1190	1200
GAGTWCVDPA	SGEELRPGSS	SSAQCPSLCN	VLKSGVLSRR	VSPGYVPACR	AEDGGFSPVQ	CDQAQGSCWC	VMDSGEEVPG
1210	1220	1230	1240	1250	1260	1270	1280
TRVTGGQPAC	ESPRCPLPFN	ASEVVGGTIL	CETISGPTGS	AMQQCQLLCR	QGSWSVFPPG	PLICSLESGR	WESQLPQPRA
1290	1300	1310	1320	1330	1340	1350	1360
CQRPQLWQTI	QTQGHFQLQL	PPGKMCSADY	ADLLQTFQVF	ILDELTARGF	CQIQVKTFGT	LVSIPVCNNS	SVQVGCLTRE
1370	1380	1390	1400	1410	1420	1430	1440
RLGVNVTWKS	RLEDIPVASL	PDLHDIERAL	VGKDLLGRFT	DLIQSGSFQL	HLDSKTFPAE	TIRFLQGDHF	GTSPRTWFGC
1450	1460	1470	1480	1490	1500	1510	1520
SEGFYQVLTS	EASQDGLGCV	KCPEGSYSQD	EECIPCPVGF	YQEQAGSLAC	VPCPVGRTTI	SAGAFSQTHC	VTDCQRNEAG
1530	1540	1550	1560	1570	1580	1590	1600
LQCDQNGQYR	ASQKDRGSGK	AFCVDGEGRR	LPWWETEAPL	EDSQCLMMQK	FEKVPESKVI	FDANAPVAVR	SKVPDSEFPV
1610	1620	1630	1640	1650	1660	1670	1680
MQCLTDCTED	EACSFFTVST	TEPEISCDFY	AWTSDNVACM	TSDQKRDALG	NSKATSFGSL	RCQVKVRSHG	QDSPAVYLKK
1690	1700	1710	1720	1730	1740	1750	1760
GQGSTTTLQK	RFEPTGFQNM	LSGLYNPIVF	SASGANLTDA	HLFCLLACDR	DLCCDGFVLT	QVQGGAIICG	LLSSPSVLLC
1770	1780	1790	1800	1810	1820	1830	1840
NVKDWMDPSE	AWANATCPGV	TYDQESHQVI	LRLGDQEFIK	SLTPLEGTQD	TFTNFQQVYL	WKDSDMGSRP	ESMGCRKDTV
1850	1860	1870	1880	1890	1900	1910	1920
PRPASPTEAG	LTTELFSPVD	LNQVIVNGNQ	SLSSQKHWLF	KHLFSAQQAN	LWCLSRCVQE	HSFCQLAEIT	ESASLYFTCT
1930	1940	1950	1960	1970	1980	1990	2000
LYPEAQVCDD	IMESNAQGCR	LILPQMPKAL	FRKKVILEDK	VKNFYTRLPF	QKLMGISIRN	KVPMSEKSIS	NGFFECERRC
2010	2020	2030	2040	2050	2060	2070	2080
DADPCCTGFG	FLNVSQLKGG	EVTCLTLNSL	GIQMCSEENG	GAWRILDCGS	PDIEVHTYPF	GWYQKPMSLD	SWQSLALSSV
2090	2100	2110	2120	2130	2140	2150	2160
VVDPSIRHFD	VAHVSTAATS	NFSAVRDLCL	SECSQHEACL	ITTLQTQPGA	VRCMFYADTQ	SCTHSLQGQN	CRLLLREEAT
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
865	1	623.9049	-34.22	3	40.3	10.8	0	228-243	R.FPEVSGYCHCADSQGR.E	Carbamidomethyl: 8, 10	Wdown:Qdown 2.01 mdown:qdown 0.75
1861	1	719.7564	-125.05	2	51.8	13.2	2	1537-1550	R.GSGKAFCVDGEGRR.L		Wdown:Qdown 0.31

Detailed Protein Report

Protein 203: **structural maintenance of chromosomes protein 4 isoform 2 [Homo sapiens]**

Accession:	gi|570700827	**Score:**	41.0
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
452	5	862.8266	-126.10	2	34.3	30.1	2	457-471	R.EKELMGFSKSVNEAR.S	

Detailed Protein Report

Protein 204: small proline-rich protein 2E [Homo sapiens]

Accession:	gi|83582817	**Score:**	41.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	7.8
Database Date:	2015-11-30	**pI:**	10.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	18.1
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	1.02	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	1.76	**CV:**	0.00 %	**No. of Peptides:**	1

```
         10         20         30         40         50         60         70         80
MSYQQQQCKQ PCQPPPVCPT PKCPEPCPPP KCPEPCPPPK CPQPCPPQQC QQKCPPVTPS PPCQPKCPPK SK
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
85	3	753.3519	-18.26	2	30.5	41.0	0	10-22	K.QPCQPPPVCPTPK.C	Carbamidomethyl: 3, 9	Wdown:Qdown 1.76 mdown:qdown 1.02

Detailed Protein Report

Protein 205: prosaposin isoform a preproprotein [Homo sapiens]

Accession:	gi|11386147	**Score:**	40.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	58.1
Database Date:	2015-11-30	**pI:**	4.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.9
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MYALFLLASL	LGAALAGPVL	GLKECTRGSA	VWCQNVKTAS	DCGAVKHCLQ	TVWNKPTVKS	LPCDICKDVV	TAAGDMLKDN
90	100	110	120	130	140	150	160
ATEEEILVYL	EKTCDWLPKP	NMSASCKEIV	DSYLPVILDI	IKGEMSRPGE	VCSALNLCES	LQKHLAELNH	QKQLESNKIP
170	180	190	200	210	220	230	240
ELDMTEVVAP	FMANIPLLLY	PQDGPRSKPQ	PKDNGDVCQD	CIQMVTDIQT	AVRTNSTFVQ	ALVEHVKEEC	DRLGPGMADI
250	260	270	280	290	300	310	320
CKNYISQYSE	IAIQMMMHMQ	PKEICALVGF	CDEVKEMPMQ	TLVPAKVASK	NVIPALELVE	PIKKHEVPAK	SDVYCEVCEF
330	340	350	360	370	380	390	400
LVKEVTKLID	NNKTEKEILD	AFDKMCSKLP	KSLSEECQEV	VDTYGSSILS	ILLEEVSPEL	VCSMLHLCSG	TRLPALTVHV
410	420	430	440	450	460	470	480
TQPKDGGFCE	VCKKLVGYLD	RNLEKNSTKQ	EILAALEKGC	SFLPDPYQKQ	CDQFVAEYEP	VLIEILVEVM	DPSFVCLKIG
490	500	510	520	530			
ACPSAHKPLL	GTEKCIWGPS	YWCQNTETAA	QCNAVEHCKR	HVWN			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2867	11	869.4159	28.09	2	64.6	19.3	0	93-107	K.TCDWLPKPNMSASCK.E	Carbamidomethyl: 2
1784	4	840.7706	-131.02	2	52.3	21.6	0	93-107	K.TCDWLPKPNMSASCK.E	

Detailed Protein Report

Protein 206: PREDICTED: hormone-sensitive lipase isoform X1 [Homo sapiens]

Accession:	gi|530416587	**Score:**	40.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	108.8
Database Date:	2015-11-30	**pI:**	6.2
		Sequence Coverage [%]:	3.6
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MEPGSKSVSR	SDWQPEPHQR	PITPLEPGPE	KTPIAQPESK	TLQGSNTQQK	PASNQRPLTQ	QETPAQHDAE	SQKEPRAQQK
90	100	110	120	130	140	150	160
SASQEEFLAP	QKPAPQQSPY	IQRVLLTQQE	AASQQGPGLG	KESITQQEPA	LRQRHVAQPG	PGPGEPPPAQ	QEAESTPAAQ
170	180	190	200	210	220	230	240
AKPGAKREPS	APTESTSQET	PEQSDKQTTP	VQGAKSKQGS	LTELGFLTKL	QELSIQRSAL	EWKALSEWVT	DSESESDVGS
250	260	270	280	290	300	310	320
SSDTDSPATM	GGMVAQGVKL	GFKGKSGYKV	MSGYSGTSPH	EKTSARNHRH	YQDTASRLIH	NMDLRTMTQS	LVTLAEDNIA
330	340	350	360	370	380	390	400
FFSSQGPGET	AQRLSGVFAG	VREQALGLEP	ALGRLLGVAH	LFDLDPETPA	NGYRSLVHTA	RCCLAHLLHK	SRYVASNRRS
410	420	430	440	450	460	470	480
IFFRTSHNLA	ELEAYLAALT	QLRALVYYAQ	RLLVTNRPGV	LFFEGDEGLT	ADFLREYVTL	HKGCFYGRCL	GFQFTPAIRP
490	500	510	520	530	540	550	560
FLQTISIGLV	SFGEHYKRNE	TGLSVAASSL	FTSGRFAIDP	ELRGAEFERI	TQNLDVHFWK	AFWNITEMEV	LSSLANMASA
570	580	590	600	610	620	630	640
TVRVSRLLSL	PPEAFEMPLT	ADPTLTVTIS	PPLAHTGPGP	VLVRLISYDL	REGQDSEELS	SLIKSNGQRS	LELWPRPQQA
650	660	670	680	690	700	710	720
PRSRSLIVHF	HGGGFVAQTS	RSHEPYLKSW	AQELGAPIIS	IDYSLAPEAP	FPRALEECFF	AYCWAIKHCA	LLGAKTEDHS
730	740	750	760	770	780	790	800
NSDQKALGMM	GLVRRDTALL	LRDFRLGASS	WLNSFLELSG	RKSQKMSEPI	AEPMRRSVSE	AALAQPQGPL	GTDSLKNLTL
810	820	830	840	850	860	870	880
RDLSLRGNSE	TSSDTPEMSL	SAETLSPSTP	SDVNFLLPPE	DAGEEAEAKN	ELSPMDRGLG	VRAAFPEGFH	PRRSSQGATQ
890	900	910	920	930	940	950	960
MPLYSSPIVK	NPFMSPLLAP	DSMLKSLPPV	HIVACALDPM	LDDSVMLARR	LRNLGQPVTL	RVVEDLPHGF	LTLAALCRET
970	980	990	1000	1010			
RQAAELCVER	IRLVLTPPAG	AGPSGETGAA	GVDGGCGGRH				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2789	2	1023.0413	-12.46	2	63.3	21.9	2	375-392	R.SLVHTARCCLAHLLHKSR.Y	
1528	1	977.3724	-87.41	2	48.9	18.9	1	708-725	K.HCALLGAKTEDHSNSDQK.A	

Detailed Protein Report

Protein 207: **1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase epsilon-1 isoform 2 [Homo sapiens]**

Accession:	gi|260166694	**Score:**	40.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	223.7
Database Date:	2015-11-30	**pI:**	6.2
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	1.7
		No. of unique Peptides:	2

Quantitation

mdown:qdown	**Median:**	0.51	**CV:**	0.00 %	**No. of Peptides:**	1	

Detailed Protein Report

```
        10         20         30         40         50         60         70         80
MVSEGSAAGR DFAGMEEVRQ LHVRFCKGIK IWHQAWFLCS LLGREPQERE AGCQLWLCTL SAVLKVGWLF PLSEVPNFTL

        90        100        110        120        130        140        150        160
LKDGCGCWRL KEDQIYNAVR REETENTVGS LLHFLTKLPA SETAHGRISV GPCLKQCVRD TVCEYRATLQ RTSISQYITG

       170        180        190        200        210        220        230        240
SLLEATTSLG ARSGLLSTFG GSTGRMMLKE RQPGPSVANS NALPSSSAGI SKELIDLQPL IQFPEEVASI LMEQEQTIYR

       250        260        270        280        290        300        310        320
RVLPVDYLCF LTRDLGTPEC QSSLPCLKAS ISASILTTQN GEHNALEDLV MRFNEVSSWV TWLILTAGSM EEKREVFSYL

       330        340        350        360        370        380        390        400
VHVAKCCWNM GNYNAVMEFL AGLRSRKVLK MWQFMDQSDI ETMRSLKDAM AQHESSCEYR KVVTRALHIP GCKVVPFCGV

       410        420        430        440        450        460        470        480
FLKELCEVLD GASGLMKLCP RYNSQEETLE FVADYSGQDN FLQRVGQNGL KNSEKESTVN SIFQVIRSCN RSLETDEEDS

       490        500        510        520        530        540        550        560
PSEGNSSRKS SLKDKSRWQF IIGDLLDSDN DIFEQSKEYD SHGSEDSQKA FDHGTELIPW YVLSIQADVH QFLLQGATVI

       570        580        590        600        610        620        630        640
HYDQDTHLSA RCFLQLQPDN STLTWVKPTT ASPASSKAKL GVLNNTAEPG KFPLLGNAGL SSLTEGVLDL FAVKAVYMGH

       650        660        670        680        690        700        710        720
PGIDIHTVCV QNKLGSMFLS ETGVTLLYGL QTTDNRLLHF VAPKHTAKML FSGLLELTRA VRKMRKFPDQ RQQWLRKQYV

       730        740        750        760        770        780        790        800
SLYQEDGRYE GPTLAHAVEL FGGRRWSARN PSPGTSAKNA EKPNMQRNNT LGISTTKKKK KILMRGESGE VTDDEMATRK

       810        820        830        840        850        860        870        880
AKMHKECRSR SGSDPQDINE QEESEVNAIA NPPNPLPSRR AHSLTTAGSP NLAAGTSSPI RPVSSPVLSS SNKSPSSAWS

       890        900        910        920        930        940        950        960
SSSWHGRIKG GMKGFQSFMV SDSNMSFVEF VELFKSFSVR SRKDLKDLFD VYAVPCNRSG SESAPLYTNL TIDENTSDLQ

       970        980        990       1000       1010       1020       1030       1040
PDLDLLTRNV SDLGLFIKSK QQLSDNQRQI SDAIAAASIV TNGTGIESTS LGIFGVGILQ LNDFLVNCQG EHCTYDEILS

      1050       1060       1070       1080       1090       1100       1110       1120
IIQKFEPSIS MCHQGLMSFE GFARFLMDKE NFASKNDESQ ENIKELQLPL SYYYIESSHN TYLTGHQLKG ESSVELYSQV

      1130       1140       1150       1160       1170       1180       1190       1200
LLQGCRSVEL DCWDGDDGMP IIYHGHTLTT KIPFKEVVEA IDRSAFINSD LPIIISIENH CSLPQQRKMA EIFKTVFGEK

      1210       1220       1230       1240       1250       1260       1270       1280
LVTKFLFETD FSDDPMLPSP DQLRKKVLLK NKKLKAHQTP VDILKQKAHQ LASMQVQAYN GGNANPRPAN NEEEEDEEDE

      1290       1300       1310       1320       1330       1340       1350       1360
YDYDYESLSD DNILEDRPEN KSCNDKLQFE YNEEIPKRIK KADNSACNKG KVYDMELGEE FYLDQNKKES RQIAPELSDL

      1370       1380       1390       1400       1410       1420       1430       1440
VIYCQAVKFP GLSTLNASGS SRGKERKSRK SIFGNNPGRM SPGETASFNK TSGKSSCEGI RQTWEESSSP LNPTTSLSAI

      1450       1460       1470       1480       1490       1500       1510       1520
IRTPKCYHIS SLNENAAKRL CRRYSQKLTQ HTACQLLRTY PAATRIDSSN PNPLMFWLHG IQLVALNYQT DDLPLHLNAA

      1530       1540       1550       1560       1570       1580       1590       1600
MFEANGGCGY VLKPPVLWDK NCPMYQKFSP LERDLDSMDP AVYSLTIVSG QNVCPSNSMG SPCIEVDVLG MPLDSCHFRT

      1610       1620       1630       1640       1650       1660       1670       1680
KPIHRNTLNP MWNEQFLFHV HFEDLVFLRF AVVENNSSAV TAQRIIPLKA LKRGYRHLQL RNLHNEVLEI SSLFINSRRM

      1690       1700       1710       1720       1730       1740       1750       1760
EENSSGNTMS ASSMFNTEER KCLQTHRVTV HGVPGPEPFT VFTINGGTKA KQLLQQILTN EQDIKPVTTD YFLMEEKYFI

      1770       1780       1790       1800       1810       1820       1830       1840
SKEKNECRKQ PFQRAIGPEE EIMQILSSWF PEEGYMGRIV LKTQQENLEE KNIVQDDKEV ILSSEEESFF VQVHDVSPEQ

      1850       1860       1870       1880       1890       1900       1910       1920
PRTVIKAPRV STAQDVIQQT LCKAKYSYSI LSNPNPSDYV LLEEVVKDTT NKKTTTPKSS QRVLLDQECV FQAQSKWKGA

      1930       1940       1950       1960       1970       1980       1990       2000
GKFILKLKEQ VQASREDKKK GISFASELKK LTKSTKQPRG LTSPSQLLTS ESIQTKEEKP VGGLSSSDTM DYRQ
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2773	1	648.3579	4.41	2	63.1	11.0	0	689-699	K.MLFSGLLELTR.A	Oxidation: 1	
547	1	624.6856	-218.06	2	35.5	11.3	2	1319-1329	R.IKKADNSACNK.G	Carbamidomethyl: 9	mdown:qdown 0.51

Detailed Protein Report

Protein 208: cornifin-A [Homo sapiens]

Accession:	gi|45827734	**Score:**	40.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	9.9
Database Date:	2015-11-30	**pI:**	10.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	15.7
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	0.90	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	2.67	**CV:**	0.00 %	**No. of Peptides:**	1

Alias proteins:

Accession	Name	Description
gi|315360635	refseq_human (refseq_human_20140103.fasta)	cornifin-A [Homo sapiens]

```
         10         20         30         40         50         60         70         80
MNSQQQKQPC TPPPQPQQQQ VKQPCQPPPQ EPCIPKTKEP CHPKVPEPCH PKVPEPCQPK VPEPCQPKVP EPCPSTVTPA
         90
PAQQKTKQK
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
243	2	838.3874	-15.29	2	31.8	40.7	0	23-36	K.QPCQPPPQEPCIPK.T	Carbamidomethyl: 3, 11	Wdown:Qdown 2.67 mdown:qdown 0.90

Detailed Protein Report

Protein 209: PREDICTED: cytosolic carboxypeptidase 2 isoform X4 [Homo sapiens]

Accession: gi|530395811

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Modification(s): Oxidation

Score: 40.6

MW [kDa]: 90.6

pI: 9.4

Sequence Coverage [%]: 5.6

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 210: **elongation factor 1-alpha 2 [Homo sapiens]**

Accession:	gi|4503475	**Score:**	40.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	50.4
Database Date:	2015-11-30	**pI:**	9.7
		Sequence Coverage [%]:	4.3
		No. of unique Peptides:	1

Quantitation

Wdown:Qdown **Median:** 1.32 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MGKEKTHINI	VVIGHVDSGK	STTTGHLIYK	CGGIDKRTIE	KFEKEAAEMG	KGSFKYAWVL	DKLKAERERG	ITIDISLWKF
90	100	110	120	130	140	150	160
ETTKYYITII	DAPGHRDFIK	NMITGTSQAD	CAVLIVAAGV	GEFEAGISKN	GQTREHALLA	YTLGVKQLIV	GVNKMDSTEP
170	180	190	200	210	220	230	240
AYSEKRYDEI	VKEVSAYIKK	IGYNPATVPF	VPISGWHGDN	MLEPSPNMPW	FKGWKVERKE	GNASGVSLLE	ALDTILPPTR
250	260	270	280	290	300	310	320
PTDKPLRLPL	QDVYKIGGIG	TVPVGRVETG	ILRPGMVVTF	APVNITTEVK	SVEMHHEALS	EALPGDNVGF	NVKNVSVKDI
330	340	350	360	370	380	390	400
RRGNVCGDSK	SDPPQEAAQF	TSQVIILNHP	GQISAGYSPV	IDCHTAHIAC	KFAELKEKID	RRSGKKLEDN	PKSLKSGDAA
410	420	430	440	450	460	470	
IVEMVPGKPM	CVESFSQYPP	LGRFAVRDMR	QTVAVGVIKN	VEKKSGGAGK	VTKSAQKAQK	AGK	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
668	1	488.2507	-58.30	2	36.9	28.2	0	248-255	R.LPLQDVYK.I		Wdown:Qdown 1.32

Detailed Protein Report

Protein 211: PREDICTED: serine/threonine-protein kinase mTOR isoform X2 [Homo sapiens]

Accession:	gi|530360520	**Score:**	40.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	263.7
Database Date:	2015-11-30	**pI:**	6.8
		Sequence Coverage [%]:	1.2
		No. of unique Peptides:	3

Quantitation

mdown:qdown	**Median:**	1.03	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	14.16	**CV:**	0.00 %	**No. of Peptides:**	1

10	20	30	40	50	60	70	80
MQKPQWYRHT	FEEAEKGFDE	TLAKEKGMNR	DDRIHGALLI	LNELVRISSM	EGERLREEME	EITQQQLVHD	KYCKDLMGFG
90	100	110	120	130	140	150	160
TKPRHITPFT	SFQAVQPQQS	NALVGLLGYS	SHQGLMGFGT	SPSPAKSTLV	ESRCCRDLME	EKFDQVCQWV	LKCRNSKNSL
170	180	190	200	210	220	230	240
IQMTILNLLP	RLAAFRPSAF	TDTQYLQDTM	NHVLSCVKKE	KERTAAFQAL	GLLSVAVRSE	FKVYLPRVLD	IIRAALPPKD
250	260	270	280	290	300	310	320
FAHKRQKAMQ	VDATVFTCIS	MLARAMGPGI	QQDIKELLEP	MLAVGLSPAL	TAVLYDLSRQ	IPQLKKDIQD	GLLKMLSLVL
330	340	350	360	370	380	390	400
MHKPLRHPGM	PKGLAHQLAS	PGLTTLPEAS	DVGSITLALR	TLGSFEFEGH	SLTQFVRHCA	DHFLNSEHKE	IRMEAARTCS
410	420	430	440	450	460	470	480
RLLTPSIHLI	SGHAHVVSQT	AVQVVADVLS	KLLVVGITDP	DPDIRYCVLA	SLDERFDAHL	AQAENLQALF	VALNDQVFEI
490	500	510	520	530	540	550	560
RELAICTVGR	LSSMNPAFVM	PFLRKMLIQI	LTELEHSGIG	RIKEQSARML	GHLVSNAPRL	IRPYMEPILK	ALILKLKDPD
570	580	590	600	610	620	630	640
PDPNPGVINN	VLATIGELAQ	VSGLEMRKWV	DELFIIIMDM	LQDSSLLAKR	QVALWTLGQL	VASTGYVVEP	YRKYPTLLEV
650	660	670	680	690	700	710	720
LLNFLKTEQN	QGTRREAIRV	LGLLGALDPY	KHKVNIGMID	QSRDASAVSL	SESKSSQDSS	DYSTSEMLVN	MGNLPLDEFY
730	740	750	760	770	780	790	800
PAVSMVALMR	IFRDQSLSHH	HTMVVQAITF	IFKSLGLKCV	QFLPQVMPTF	LNVIRVCDGA	IREFLFQQLG	MLVSFVKSHI
810	820	830	840	850	860	870	880
RPYMDEIVTL	MREFWVMNTS	IQSTIILLIE	QIVVALGGEF	KLYLPQLIPH	MLRVFMHDNS	PGRIVSIKLL	AAIQLFGANL
890	900	910	920	930	940	950	960
DDYLHLLLPP	IVKLFDAPEA	PLPSRKAALE	TVDRLTESLD	FTDYASRIIH	PIVRTLDQSP	ELRSTAMDTL	SSLVFQLGKK
970	980	990	1000	1010	1020	1030	1040
YQIFIPMVNK	VLVRHRINHQ	RYDVLICRIV	KGYTLADEEE	DPLIYQHRML	RSGQGDALAS	GPVETGPMKK	LHVSTINLQK
1050	1060	1070	1080	1090	1100	1110	1120
AWGAARRVSK	DDWLEWLRRL	SLELLKDSSS	PSLRSCWALA	QAYNPMARDL	FNAAFVSCWS	ELNEDQQDEL	IRSIELALTS
1130	1140	1150	1160	1170	1180	1190	1200
QDIAEVTQTL	LNLAEFMEHS	DKGPLPLRDD	NGIVLLGERA	AKCRAYAKAL	HYKELEFQKG	PTPAILESLI	SINNKLQQPE
1210	1220	1230	1240	1250	1260	1270	1280
AAAGVLEYAM	KHFGELEIQA	TWYEKLHEWE	DALVAYDKKM	DTNKDDPELM	LGRMRCLEAL	GEWGQLHQQC	CEKWTLVNDE
1290	1300	1310	1320	1330	1340	1350	1360
TQAKMARMAA	AAAWGLGQWD	SMEEYTCMIP	RDTHDGAFYR	AVLALHQDLF	SLAQQCIDKA	RDLLDAELTA	MAGESYSRAY
1370	1380	1390	1400	1410	1420	1430	1440
GAMVSCHMLS	ELEEVIQYKL	VPERREIIRQ	IWWERLQGCQ	RIVEDWQKIL	MVRSLVVSPH	EDMRTWLKYA	SLCGKSGRLA
1450	1460	1470	1480	1490	1500	1510	1520
LAHKTLVLLL	GVDPSRQLDH	PLPTVHPQVT	YAYMKNMWKS	ARKIDAFQHM	QHFVQTMQQQ	AQHAIATEDQ	QHKQELHKLM
1530	1540	1550	1560	1570	1580	1590	1600
ARCFLKLGEW	QLNLQGINES	TIPKVLQYYS	AATEHDRSWY	KAWHAWAVMN	FEAVLHYKHQ	NQARDEKKKL	RHASGANITN
1610	1620	1630	1640	1650	1660	1670	1680
ATTAATTAAT	ATTTASTEGS	NSESEAESTE	NSPTPSPLQK	KVTEDLSKTL	LMYTVPAVQG	FFRSISLSRG	NNLQDTLRVL
1690	1700	1710	1720	1730	1740	1750	1760
TLWFDYGHWP	DVNEALVEGV	KAIQIDTWLQ	VIPQLIARID	TPRPLVGRLI	HQLLTDIGRY	HPQALIYPLT	VASKSTTTAR
1770	1780	1790	1800	1810	1820	1830	1840
HNAANKILKN	MCEHSNTLVQ	QAMMVSEELI	RVAILWHEMW	HEGLEEASRL	YFGERNVKGM	FEVLEPLHAM	MERGPQTLKE
1850	1860	1870	1880	1890	1900	1910	1920
TSFNQAYGRD	LMEAQEWCRK	YMKSGNVKDL	TQAWDLYYHV	FRRISKQLPQ	LTSLELQYVS	PKLLMCRDLE	LAVPGTYDPN
1930	1940	1950	1960	1970	1980	1990	2000
QPIIRIQSIA	PSLQVITSKQ	RPRKLTLMGS	NGHEFVFLLK	GHEDLRQDER	VMQLFGLVNT	LLANDPTSLR	KNLSIQRYAV
2010	2020	2030	2040	2050	2060	2070	2080
IPLSTNSGLI	GWVPHCDTLH	ALIRDYREKK	KILLNIEHRI	MLRMAPDYDH	LTLMQKVEVF	EHAVNNTAGD	DLAKLLWLKS
2090	2100	2110	2120	2130	2140	2150	2160
PSSEVWFDRR	TNYTRSLAVM	SMVGYILGLG	DRHPSNLMLD	RLSGKILHID	FGDCFEVAMT	REKFPEKIPF	RLTRMLTNAM
2170	2180	2190	2200	2210	2220	2230	2240

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1142	1	586.6322	-235.21	2	43.9	12.9	0	1840-1849	K.ETSFNQAYGR.D		mdown:qdown 1.03
1911	1	704.7631	-82.23	2	52.4	11.2	1	1850-1860	R.DLMEAQEWCRK.Y		
559	1	472.6946	-192.04	2	35.8	16.4	2	2277-2284	R.VRDKLTGR.D		

Detailed Protein Report

Protein 212: **PREDICTED: bromodomain-containing protein 1 isoform X12 [Homo sapiens]**

Accession:	gi|578837129	**Score:**	40.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	110.4
Database Date:	2015-11-30	**pI:**	9.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	5.3
		No. of unique Peptides:	2

```
        10         20         30         40         50         60         70         80
MKSFTAPWER VGFQGLLVVR ATQDFAVEGK MTGNHYQMRR KGRCHRGSAA RHPSSPCSVK HSPTRETLTY AQAQRMVEIE
        90        100        110        120        130        140        150        160
IEGRLHRISI FDPLEIILED DLTAQEMSEC NSNKENSERP PVCLRTKRHK NNRVKKKNEA LPSAHGTPAS ASALPEPKVR
       170        180        190        200        210        220        230        240
IVEYSPPSAP RRPPVYYKFI EKSAEELDNE VEYDMDEEDY AWLEIVNEKR KGDCVPAVSQ SMFEFLMDRF EKESHCENQK
       250        260        270        280        290        300        310        320
QGEQQSLIDE DAVCCICMDG ECQNSNVILF CDMCNLAVHQ ECYGVPYIPE GQWLCRHCLQ SRARPADCVL CPNKGGAFKK
       330        340        350        360        370        380        390        400
TDDDRWGHVV CALWIPEVGF ANTVFIEPID GVRNIPPARW KLTCYLCKQK GVGACIQCHK ANCYTAFHVT CAQKAGLYMK
       410        420        430        440        450        460        470        480
MEPVKELTGG GTTFSVRKTA YCDVHTPPGC TRRPLNIYGD VEMKNGVCRK ESSVKTVRST SKVRKKAKKA KKALAEPCAV
       490        500        510        520        530        540        550        560
LPTVCAPYIP PQRLNRIANQ VAIQRKKQFV ERAHSYWLLK RLSRNGAPLL RRLQSSLQSQ RSSQQRENDE EMKAAKEKLK
       570        580        590        600        610        620        630        640
YWQRLRHDLE RARLLIELLR KREKLKREQV KVEQVAMELR LTPLTVLLRS VLDQLQDKDP ARIFAQPVSL KEVPDYLDHI
       650        660        670        680        690        700        710        720
KHPMDFATMR KRLEAQGYKN LHEFEEDFDL IIDNCMKYNA RDTVFYRAAV RLRDQGGVVL RQARREVDSI GLEEASGMHL
       730        740        750        760        770        780        790        800
PERPAAAPRR PFSWEDVDRL LDPANRAHLG LEEQLRELLD MLDLTCAMKS SGSRSKRAKL LKKEIALLRN KLSQQHSQPL
       810        820        830        840        850        860        870        880
PTGPGLEGFE EDGAALGPEA GEEGDKSPPK LEPSDALPLP SNSETNSEPP TLKPVELNPE QSKLFKRVTF DNESHSACTQ
       890        900        910        920        930        940        950        960
SALVSGRPPE PTRASSGDVP AAAASAVAEP ASDVNRRTSV LFCKSKSSFR GWRLFCSQGK GRGAHAETPR WRRSPQESAW
       970        980
TQVLTLTTNV LGSSLFGP
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
832	1	902.3468	-117.98	2	39.2	13.7	1	303-319	R.ARPADCVLCPNKGGAFK.K	Carbamidomethyl: 6
1578	2	873.9352	-97.55	2	48.2	14.4	2	567-580	R.HDLERARLLIELLR.K	

Detailed Protein Report

Protein 213: **PREDICTED: matrix extracellular phosphoglycoprotein isoform X1 [Homo sapiens]**

Accession:	gi|578809281	**Score:**	39.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	62.1
Database Date:	2015-11-30	**pI:**	9.4
Modification(s):	Oxidation	**Sequence Coverage [%]:**	4.9
		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 214: hemopexin precursor [Homo sapiens]

Accession:	gi|11321561	**Score:**	39.8
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:	2

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
2360	1	1073.7380	-84.18	3	59.8	17.0	0	290-317	R.DGWHSWPIAHQWPQGPSAVDAAFSWEEK.L	
1592	2	919.4423	-5.15	2	48.6	22.8	0	387-402	K.SGAQATWTELPWPHEK.V	

Detailed Protein Report

Protein 215: centrosomal protein of 55 kDa [Homo sapiens]

Accession:	gi|187608537	**Score:**	39.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	54.1
Database Date:	2015-11-30	**pI:**	6.6
		Sequence Coverage [%]:	5.0
		No. of unique Peptides:	2

Quantitation

mdown:qdown	**Median:**	0.36	**CV:**	26.65 %	**No. of Peptides:**	2
Wdown:Qdown	**Median:**	0.51	**CV:**	0.00 %	**No. of Peptides:**	1

Alias proteins:

Accession	**Name**	**Description**
gi|187608545	refseq_human (refseq_human_20140103.fasta)	centrosomal protein of 55 kDa [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MSSRSTKDLI KSKWGSKPSN SKSETTLEKL KGEIAHLKTS VDEITSGKGK LTDKERHRLL EKIRVLEAEK EKNAYQLTEK
        90        100        110        120        130        140        150        160
DKEIQRLRDQ LKARYSTTAL LEQLEETTRE GERREQVLKA LSEEKDVLKQ QLSAATSRIA ELESKTNTLR LSQTVAPNCF
       170        180        190        200        210        220        230        240
NSSINNIHEM EIQLKDALEK NQQWLVYDQQ REVYVKGLLA KIFELEKKTE TAAHSLPQQT KKPESEGYLQ EEKQKCYNDL
       250        260        270        280        290        300        310        320
LASAKKDLEV ERQTITQLSF ELSEFRRKYE ETQKEVHNLN QLLYSQRRAD VQHLEDDRHK TEKIQKLREE NDIARGKLEE
       330        340        350        360        370        380        390        400
EKKRSEELLS QVQFLYTSLL KQQEEQTRVA LLEQQMQACT LDFENEKLDR QHVQHQLHVI LKELRKARNQ ITQLESLKQL
       410        420        430        440        450        460        470
HEFAITEPLV TFQGETENRE KVAASPKSPT AALNESLVEC PKCNIQYPAT EHRDLLVHVE YCSK
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1005	1	423.6388	-147.47	2	41.1	17.5	0	309-315	R.EENDIAR.G		mdown:qdown 0.28 Wdown:Qdown 0.51
398	1	587.3194	-13.57	2	34.3	10.3	0	389-398	R.NQITQLESLK.Q		mdown:qdown 0.46

Detailed Protein Report

Protein 216: **PREDICTED: histone-lysine N-methyltransferase setd3 isoform X3 [Homo sapiens]**

Accession:	gi|530404751	**Score:**	39.7
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:	1

Quantitation

mdown:qdown **Median:** 0.54 **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		mdown:qdown 0.54

Detailed Protein Report

Protein 217: 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:	1

Detailed Protein Report

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
1917	1	902.8454	-85.60	2	54.0	12.9	0	3678-3694	R.SMSDPKPLSPTADESSR.A	

Detailed Protein Report

Protein 218: sodium-driven chloride bicarbonate exchanger isoform 2 [Homo sapiens]

Accession: gi|155722998
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 39.6
MW [kDa]: 122.6
pI: 5.9
Sequence Coverage [%]: 2.8
No. of unique Peptides: 1

Quantitation

Wdown:Qdown **Median:** 0.41 **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	TVDFSKVDLH	FMKKIPPGAE	ASNILVGELE	FLDRTVVAFV
330	340	350	360	370	380	390	400
RLSPAVLLQG	LAEVPIPTRF	LFILLGPLGK	GQQYHEIGRS	IATLMTDEVF	HDVAYKAKDR	NDLVSGIDEF	LDQVTVLPPG
410	420	430	440	450	460	470	480
EWDPSIRIEP	PKNVPSQEKR	KIPAVPNGTA	AHGEAEPHGG	HSGPELQRTG	RIFGGLILDI	KRKAPYFWSD	FRDAFSLQCL
490	500	510	520	530	540	550	560
ASFLFLYCAC	MSPVITFGGL	LGEATEGRIS	AIESLFGASM	TGIAYSLFGG	QPLTILGSTG	PVLVFEKILF	KFCKEYGLSY
570	580	590	600	610	620	630	640
LSLRASIGLW	TATLCIILVA	TDASSLVCYI	TRFTEEAFAS	LICIIFIYEA	LEKLFELSEA	YPINMHNDLE	LLTQYSCNCV
650	660	670	680	690	700	710	720
EPHNPSNGTL	KEWRESNISA	SDIIWENLTV	SECKSLHGEY	VGRACGHDHP	YVPDVLFWSV	ILFFSTVTLS	ATLKQFKTSR
730	740	750	760	770	780	790	800
YFPTKVRSIV	SDFAVFLTIL	CMVLIDYAIG	IPSPKLQVPS	VFKPTRDDRG	WFVTPLGPNP	WWTVIAAIIP	ALLCTILIFM
810	820	830	840	850	860	870	880
DQQITAVIIN	RKEHKLKKGC	GYHLDLLMVA	VMLGVCSIMG	LPWFVAATVL	SITHVNSLKL	ESECSAPGEQ	PKFLGIREQR
890	900	910	920	930	940	950	960
VTGLMIFILM	GSSVFMTSIL	KFIPMPVLYG	VFLYMGASSL	KGIQFFDRIK	LFWMPAKHQP	DFIYLRHVPL	RKVHLFTIIQ
970	980	990	1000	1010	1020	1030	1040
MSCLGLLWII	KVSRAAIVFP	MMVLALVFVR	KLMDLLFTKR	ELSWLDDLMP	ESKKKKLEDA	EKEEEQSMLA	MEDEGTVQLP
1050	1060	1070	1080	1090			
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
1399	1	783.2967	-72.60	2	47.2	11.8	0	1047-1060	R.DDPSVINISDEMSK.T	Oxidation: 12	Wdown:Qdown 0.41

Detailed Protein Report

Protein 219: **PREDICTED: polyamine-modulated factor 1-binding protein 1 isoform X2 [Homo sapiens]**

Accession:	gi|530424400	**Score:**	39.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	94.2
Database Date:	2015-11-30	**pI:**	5.6
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	5.1
		No. of unique Peptides:	2

Quantitation

mdown:qdown	**Median:**	1.46	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	2.39	**CV:**	0.00 %	**No. of Peptides:**	1

10	20	30	40	50	60	70	80
MKDEAGERDR	EVSSLNSKLL	SLQLDIKNLH	DVCKRQRKTL	QDNQLCMEEA	MNSSHDKKQA	QALAFEESEV	EFGSSKQCHL
90	100	110	120	130	140	150	160
RQLQQLKKKL	LVLQQELEFH	TEELQTSYYS	LRQYQSILEK	QTSDLVLLHH	HCKLKEDEVI	LYEEEMGNHN	ENTGEKLHLA
170	180	190	200	210	220	230	240
QEQLALAGDK	IASLERSLNL	YRDKYQSSLS	NIELLECQVK	MLQGELGGIM	GQEPENKGDH	SKVRIYTSPC	MIQEHQETQK
250	260	270	280	290	300	310	320
RLSEVWQKVS	QQDDLIQELR	NKLACSNALV	LEREKALIKL	QADFASCTAT	HRYPPSSSEE	CEDIKKILKH	LQEQKDSQCL
330	340	350	360	370	380	390	400
HVEEYQNLVK	DLRVELEAVS	EQKRNIMKDM	MKLELDLHGL	REETSAHIER	KDKDITILQC	RLQELQLEFT	ETQKLTLKKD
410	420	430	440	450	460	470	480
KFLQEKDEML	QELEKKLTQV	QNSLLKKEKE	LEKQQCMATE	LEMTVKEAKQ	DKSKEAECKA	LQAEVQKLKN	SLEEAKQQER
490	500	510	520	530	540	550	560
LAAQQAAQCK	EEAALAGCHL	EDTQRKLQKG	LLLDKQKADT	IQELQRELQM	LQKESSMAEK	EQTSNRKRVE	ELSLELSEAL
570	580	590	600	610	620	630	640
RKLENSDKEK	RQLQKTVAEQ	DMKMNDMLDR	IKHQHREQGS	IKCKLEEDLQ	EATKLLEDKR	EQLKKSKEHE	KLMEGELEAL
650	660	670	680	690	700	710	720
RQEFKKKDKT	LKENSRKLEE	ENENLRAELQ	CCSTQLESSL	NKYNTSQQVI	QDLNKEIALQ	KESLMSLQAQ	LDKALQKEKH
730	740	750	760	770	780	790	800
YLQTTITKEA	YDALSRKSAA	CQDDLTQALE	KLNHVTSETK	SLQQSLTQTQ	EKKAQLEEEI	IAYEERMKKL	NTELRKLRGF
810							
HQESELE							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
293	1	477.5768	-43.77	3	32.4	14.6	1	261-273	R.NKLACSNALVLER.E		mdown:qdown 1.46 Wdown:Qdown 2.39
1797	1	638.2204	-122.59	3	51.0	12.7	1	434-449	K.QQCMATELEMTVKEAK.Q	Carbamidomethyl: 3; Oxidation: 4	

Detailed Protein Report

Protein 220: **PREDICTED: serine/arginine repetitive matrix protein 1 isoform X3 [Homo sapiens]**

Accession:	gi|530360787	**Score:**	39.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	103.7
Database Date:	2015-11-30	**pI:**	12.4
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.4
		No. of unique Peptides:	2

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	SPRRRKSRSP	SPRRRSSPVR	RERKRSHSRS	PRHRTKSRSP	SPAPEKKEKT	PELPEPSVKV	KEPSVQEATS
250	260	270	280	290	300	310	320
TSDILKVPKP	EPIPEPKEPS	PEKNSKKEKE	KEKTRPRSRS	RSKSRSRTRS	RSPSHTRPRR	RHRSRSRSYS	PRRRPSPRRR
330	340	350	360	370	380	390	400
PSPRRRTPPR	RMPPPPRHRR	SRSPVRRRRR	SSASLSGSSS	SSSSSRSRSP	PKKPPKRTSS	PPRKTRRLSP	SASPPRRRHR
410	420	430	440	450	460	470	480
PSPPATPPPK	TRHSPTPQQS	NRTRKSRVSV	SPGRTSVTKH	KGTEKRESPS	PAPKPRKVEL	SESEEDKGGK	MAAADSVQQR
490	500	510	520	530	540	550	560
RQYRRQNQQS	SSDSGSSSSS	EDERPKRSHV	KNGEVGRRRR	HSPSRSASPS	PRKRQKETSP	RMQMGKRWQS	PVTKSGRRRR
570	580	590	600	610	620	630	640
SPSPPPTRRR	RSPSPAPPPR	RRRTPTPPPR	RRTPSPPPRR	RSPSPRRYSP	PIQRRYSPSP	PPKRRTASPP	PPPKRRASPS
650	660	670	680	690	700	710	720
PPPKRRVSHS	PPPKQRSSPV	TKRRSPSLSS	KHRKGSSPSR	STREARSPQP	NKRHSPSPRP	RAPQTSSSPP	PVRRGASSSP
730	740	750	760	770	780	790	800
QRRQSPSPST	RPIRRVSRTP	EPKKIKKAAS	PSPQSVRRVS	SSRSVSGSPE	PAAKKPPAPP	SPVQSQSPST	NWSPAVPVKK
810	820	830	840	850	860	870	880
AKSPTPSPSP	PRNSDQEGGG	KKKKKKKDKK	HKKDKKHKKH	KKHKKEKAVA	AAAAAAVTPA	AIAAATTTLA	QEEPVAAPEP
890	900	910	920				
KKETESEAED	NLDDLEKHLR	EKALRSMRKA	QVSPQS				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2594	1	741.8530	-30.71	2	63.0	14.5	0	84-96	K.MMQINLTGFLNGK.N	Oxidation: 1
1844	1	590.7772	1.91	2	53.1	11.4	1	537-546	K.ETSPRMQMGK.R	Oxidation: 6

Detailed Protein Report

Protein 221: A disintegrin and metalloproteinase with thrombospondin motifs 20 preproprotein [Homo sapiens]

Accession:	gi|124430557	**Score:**	39.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	214.6
Database Date:	2015-11-30	**pI:**	7.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.7
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	0.57	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.97	**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	Wdown:Qdown 0.97 mdown:qdown 0.57

Detailed Protein Report

Protein 222: PREDICTED: zinc finger protein DZIP1 isoform X5 [Homo sapiens]

Accession:	gi|578825194	**Score:**	39.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	101.9
Database Date:	2015-11-30	**pI:**	6.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.4
		No. of unique Peptides:	2

Quantitation

mdown:qdown **Median:** 1.04 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MQAEAADWFS	SMVRGGRPGR	PRRGCRAGEN	RGFPGPPAPQ	PARPPSPPPA	ALSLCPPQPF	QKHVYYPLAS	GPEGPDVAVA
90	100	110	120	130	140	150	160
AAAAGAASMA	CAPPSAASGP	LPFFQFRPRL	ESVDWRRLSA	IDVDKVAGAV	DVLTLQENIM	NITFCKLEDE	KCPHCQSGVD
170	180	190	200	210	220	230	240
PVLLKLIRLA	QFTIEYLLHS	QEFLTSQLHT	LEERLRLSHC	DGEQSKKLLT	KQAGEIKTLK	EECKRRKKMI	STQQLMIEAK
250	260	270	280	290	300	310	320
ANYYQCHFCD	KAFMNQAFLQ	SHIQRRHTEE	NSHFEYQKNA	QIEKLRSEIV	VLKEELQLTR	SELEAAHHAS	AVRFSKEYEM
330	340	350	360	370	380	390	400
QKTKEEDFLK	LFDRWKEEEK	EKLVDEMEKV	KEMFMKEFKE	LTSKNSALEY	QLSEIQKSNM	QIKSNIGTLK	DAHEFKEDRS
410	420	430	440	450	460	470	480
PYPQDFHNVM	QLLDSQESKW	TARVQAIHQE	HKKEKGRLLS	HIEKLRTSMI	DDLNASNVFY	KKRIEELGQR	LQEQNELIIT
490	500	510	520	530	540	550	560
QRQQIKDFTC	NPLNSISEPK	EQAFSSHILE	PIEELSEEEK	GRENEQKLNN	NKMHLRKALK	SNSSLTKGLR	TMVEQNLMEK
570	580	590	600	610	620	630	640
LETLGINADI	RGISSDQLHR	VLKSVESERH	KQEREIPNFH	QIREFLEHQV	SCKIEEKALL	SSDQCSVSQM	DTLSTGEVPK
650	660	670	680	690	700	710	720
MIQLPSKNRQ	LIRQKAVSTD	RTSVPKIKKN	VMEDPFPRKS	STITTPPFSS	EEEQEDDDLI	RAYASPGPLP	VPPPQNKGSF
730	740	750	760	770	780	790	800
GKNTVKSDAD	GTEGSEIEDT	DDSPKPAGVA	VKTPTEKVEK	MFPHRKNVNK	PVGGTNVPEM	FIKKEELQEL	KCADVEDEDW
810	820	830	840	850	860	870	880
DISSLEEEIS	LGKKSGKEQK	EPPPAKNEPH	FAHVLNAWGA	FNPKGPKGEG	LLLSPLIQAR	SIFLLVVFHL	YKYLINLCWY
890	900						
IIRQKSCQCF	LYVI						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1639	1	1023.6248	76.10	1	49.2	11.8	1	818-826	K.EQKEPPPAK.N		mdown:qdown 1.04
2531	1	595.3252	88.36	2	62.1	10.6	0	886-894	K.SCQCFLYVI.-	Carbamidomethyl: 2, 4	

Detailed Protein Report

Protein 223: RNA polymerase II transcription factor SIII subunit A2 [Homo sapiens]

Accession:	gi|45439357	**Score:**	39.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	83.9
Database Date:	2015-11-30	**pI:**	10.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.9
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MAAGSTTLHA	VEKLQVRLAT	KTEPKKLEKY	LQKLSALPMT	ADILAETGIR	KTVKRLRKHQ	HVGDFARDLA	ARWKKLVLVD
90	100	110	120	130	140	150	160
RNTRPGPQDP	EESASRQRFG	EALQDQEKAW	GFPENATAPR	SPSHSPEHRR	TARRTPPGQQ	RPHPRSHSRE	PRAERKCPRI
170	180	190	200	210	220	230	240
APADSGRYRA	SPTRTAPLRM	PEGPEPAAPG	KQPGRGHTHA	AQGGPLLCPG	CQGQPQGKAV	VSHSKGHKSS	RQEKRPLCAQ
250	260	270	280	290	300	310	320
GDWHSPTLIR	EKSCGACLRE	ETPRMPSWAS	ARDRQPSDFK	TDKEGGQAGS	GQRVPALEEA	PDSHQKRPQH	SHSNKKRPSL
330	340	350	360	370	380	390	400
DGRDPGNGTH	GLSPEEKEQL	SNDRETQEGK	PPTAHLDRTS	VSSLSEVEEV	DMAEEFEQPT	LSCEKYLTYD	QLRKQKKKTG
410	420	430	440	450	460	470	480
KSATTALGDK	QRKANESKGT	RESWDSAKKL	PPVQESQSER	LQAAGADSAG	PKTVPSHVFS	ELWDLSEAWM	QANYDPLSDS
490	500	510	520	530	540	550	560
DSMTSQAKPE	ALSSPKFREE	AAFPGRRVNA	KMPVYSGSRP	ACQLQVPTLR	QQCAQVLRNN	PDALSDVGEV	PYWVLEPVLE
570	580	590	600	610	620	630	640
GWRPDQLYRR	KKDNHALVRE	TDELRRNHCF	QDFKEEKPQE	NKTWREQYLR	LPDAPEQRLR	VMTTNIRSAR	GNNPNGREAK
650	660	670	680	690	700	710	720
MICFKSVAKT	PYDTSRRQEK	SAGDADPENG	EIKPASKPAG	SSHTPSSQSS	SGGGRDSSSS	ILRWLPEKRA	NPCLSSSNEH
730	740	750	760				
AAPAAKTRKQ	AAKKVAPLMA	KAIRDYKRRF	SRR				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
687	1	512.1344	-204.56	2	37.4	13.3	1	251-259	R.EKSCGACLR.E	Carbamidomethyl: 4
436	1	734.3141	-70.58	3	34.5	10.6	2	422-440	R.ESWDSAKKLPPVQESQSER.L	

Detailed Protein Report

Protein 224: protein inscuteable homolog isoform d [Homo sapiens]

Accession:	gi|507417931	**Score:**	39.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	57.2
Database Date:	2015-11-30	**pI:**	5.4
		Sequence Coverage [%]:	9.6
		No. of unique Peptides:	1

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2332	1	952.9342	-79.33	2	57.6	13.0	1	2-19	M.MALPGGRHLDSVTLPGQR.L	

Detailed Protein Report

Protein 225: **PREDICTED: splicing regulatory glutamine/lysine-rich protein 1 isoform X2 [Homo sapiens]**

Accession: gi|530379166
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 39.4
MW [kDa]: 43.4
pI: 11.1
Sequence Coverage [%]: 6.4
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MTPQAAAKEL	EEVMKRVREA	QSFISAAIEP	ESGKSNERKG	GRSRSHTRSK	SRSSSKSHSR	RKRSQSKHRS	RSHNRSRSRQ
90	100	110	120	130	140	150	160
KDRRRSKSPH	KKRSKSRERR	KSRSRSHSRD	KRKDTREKIK	EKERVKEKDR	EKEREREKER	EKEKERGKNK	DRDKEREKDR
170	180	190	200	210	220	230	240
EKDKEKDRER	EREKEHEKDR	DKEKEKEQDK	EKEREKDRSK	EIDEKRKKDK	KSRTPPRSYN	ASRRSRSSSR	ERRRRRSRSS
250	260	270	280	290	300	310	320
SRSPRTSKTI	KRKSSRSPSP	RSRNKKDKKR	EKERDHISER	RERERSTSMR	KSSNDRDGKE	KLEKNSTSLK	EKEHNKEPDS
330	340	350	360				
SVSKEVDDKD	APRTEENKIQ	HNGNCQLNEE	NLSTKTEAV				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2747	1	807.3929	1.22	2	65.6	17.1	2	311-324	K.EKEHNKEPDSSVSK.E	

Protein 226: latent-transforming growth factor beta-binding protein 4 isoform b [Homo sapiens]

Accession:	gi|110347412	**Score:**	39.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	169.3
Database Date:	2015-11-30	**pI:**	5.0
		Sequence Coverage [%]:	2.5
		No. of unique Peptides:	3

Quantitation

mdown:qdown **Median:** 0.11 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MGDVKALLFV	AAARARRLGG	AAASESLAVS	EAFCRVRSCQ	PKKCAGPQRC	LNPVPAVPSP	SPSVRKRQVS	LNWQPLTLQE
90	100	110	120	130	140	150	160
ARALLKRRRP	RGPGGRGLLR	RRPPQRAPAG	KAPVLCPLIC	HNGGVCVKPD	RCLCPPDFAG	KFCQLHSSGA	RPPAPAVPGL
170	180	190	200	210	220	230	240
TRSVYTMPLA	NHRDDEHGVA	SMVSVHVEHP	QEASVVVHQV	ERVSGPWEEA	DAEAVARAEA	AARAEAAAPY	TVLAQSAPRE
250	260	270	280	290	300	310	320
DGYSDASGFG	YCFRELRGGE	CASPLPGLRT	QEVCCRGAGL	AWGVHDCQLC	SERLGNSERV	SAPDGPCPTG	FERVNGSCED
330	340	350	360	370	380	390	400
VDECATGGRC	QHGECANTRG	GYTCVCPDGF	LLDSSRSSCI	SQHVISEAKG	PCFRVLRDGG	CSLPILRNIT	KQICCCSRVG
410	420	430	440	450	460	470	480
KAWGRGCQLC	PPFGSEGFRE	ICPAGPGYHY	SASDLRYNTR	PLGQEPPRVS	LSQPRTLPAT	SRPSAGFLPT	HRLEPRPEPR
490	500	510	520	530	540	550	560
PDPRPGPELP	LPSIPAWTGP	EIPESGPSSG	MCQRNPQVCG	PGRCISRPSG	YTCACDSGFR	LSPQGTRCID	VDECRRVPPP
570	580	590	600	610	620	630	640
CAPGRCENSP	GSFRCVCGPG	FRAGPRAAEC	LDVDECHRVP	PPCDLGRCEN	TPGSFLCVCP	AGYQAAPHGA	SCQDVDECTQ
650	660	670	680	690	700	710	720
SPGLCGRGAC	KNLPGSFRCV	CPAGFRGSAC	EEDVDECAQE	PPPCGPGRCD	NTAGSFHCAC	PAGFRSRGPG	APCQDVDECA
730	740	750	760	770	780	790	800
RSPPPCTYGR	CENTEGSFQC	VCPMGFQPNT	AGSECEDVDE	CENHLACPGQ	ECVNSPGSFQ	CRTCPSGHHL	HRGRCTDVDE
810	820	830	840	850	860	870	880
CSSGAPPCGP	HGHCTNTEGS	FRCSCAPGYR	APSGRPGPCA	DVNECLEGDF	CFPHGECLNT	DGSFACTCAP	GYRPGPRGAS
890	900	910	920	930	940	950	960
CLDVDECSEE	DLCQSGICTN	TDGSFECICP	PGHRAGPDLA	SCLDVDECRE	RGPALCGSQR	CENSPGSYRC	VRDCDPGYHA
970	980	990	1000	1010	1020	1030	1040
GPEGTCDDVD	ECQEYGPEIC	GAQRCENTPG	SYRCTPACDP	GYQPTPGGGC	QDVDECRNRS	FCGAHAVCQN	LPGSFQCLCD
1050	1060	1070	1080	1090	1100	1110	1120
QGYEGARDGR	HCVDVNECET	LQGVCGAALC	ENVEGSFLCV	CPNSPEEFDP	MTGRCVPPRT	SAGTFPGSQP	QAPASPVLPA
1130	1140	1150	1160	1170	1180	1190	1200
RPPPPPLPRR	PSTPRQGPVG	SGRRECYFDT	AAPDACDNIL	ARNVTWQECC	CTVGEGWGSG	CRIQQCPGTE	TAEYQSLCPH
1210	1220	1230	1240	1250	1260	1270	1280
GRGYLAPSGD	LSLRRDVDEC	QLFRDQVCKS	GVCVNTAPGY	SCYCSNGYYY	HTQRLECIDN	DECADEEPAC	EGGRCVNTVG
1290	1300	1310	1320	1330	1340	1350	1360
SYHCTCEPPL	VLDGSQRRCV	SNESQSLDDN	LGVCWQEVGA	DLVCSHPRLD	RQATYTECCC	LYGEAWGMDC	ALCPAQDSDD
1370	1380	1390	1400	1410	1420	1430	1440
FEALCNVLRP	PAYSPPRPGG	FGLPYEYGPD	LGPPYQGLPY	GPELYPPPAL	PYDPYPPPPG	PFARREAPYG	APRFDMPDFE
1450	1460	1470	1480	1490	1500	1510	1520
DDGGPYGESE	APAPPGPGTR	WPYRSRDTRR	SFPEPEEPPE	GGSYAGSLAE	PYEELEAEEC	GILDGCTNGR	CVRVPEGFTC
1530	1540	1550	1560	1570	1580	1590	
RCFDGYRLDM	TRMACVDINE	CDEAEAASPL	CVNARCLNTD	GSFRCICRPG	FAPTHQPHHC	APARPRA	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
398	1	646.4124	27.70	2	34.0	10.5	2	89-100	R.RPRGPGGRGLLR.R		
1055	1	941.2810	-147.80	2	42.8	15.8	1	932-949	R.GPALCGSQRCENSPGSYR.C		
373	1	457.1205	-287.06	2	34.0	13.0	1	1136-1144	R.QGPVGSGRR.E		mdown:qdown 0.11

Detailed Protein Report

Protein 227: PREDICTED: neuroblastoma breakpoint family member 3 isoform X2 [Homo sapiens]

Accession:	gi|578799908	**Score:**	39.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	67.0
Database Date:	2015-11-30	**pI:**	4.2
Modification(s):	Oxidation	**Sequence Coverage [%]:**	5.9
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578799910	refseq_human (refseq_human_20140103.fasta)	PREDICTED: neuroblastoma breakpoint family member 3 isoform X3 [Homo sapiens]

10	20	30	40	50	60	70	80
MVVSAGPWSG	EKAEMNILEI	NKKSRPQLAE	NKQQFRNLKQ	KCLVTQVAYF	LANRQNNYDY	EDCKDLIKSM	LRDERLLTEE
90	100	110	120	130	140	150	160
KLAEELGQAE	ELRQYKVLVH	SQERELTQLR	EKLQEGRDAS	RSLNQHLQAL	LTPDEPDNSQ	GRDLREQLAE	GCRLAQHLVQ
170	180	190	200	210	220	230	240
KLSPENDDDE	DEDVKVEEAE	KVQELYAPRE	VQKAEEKEVP	EDSLEECAIT	CSNSHHPCES	NQPYGNTRIT	FEEDQVDSTL
250	260	270	280	290	300	310	320
IDSSSHDEWL	DAVCIIPENE	SDHEQEEEKG	PVSPRNLQES	EEEEAPQESW	DEGDWTLSIP	PDMSASYQSD	RSTFHSVEEQ
330	340	350	360	370	380	390	400
QVGLALDIGR	HWCDQVKKED	QEATSPRLSR	ELLDEKEPEV	LQDSLDRFYS	TPFEYLELPD	LCQPYRSDFY	SLQEQHLGLA
410	420	430	440	450	460	470	480
LDLDRMKKDQ	EEEEDQGPPC	PRLSRELPEV	VEPEDLQDSL	DRWYSTPFSY	PELPDSCQPY	GSCFYSLEEE	HVGFSLDVDE
490	500	510	520	530	540	550	560
IEKYQEGEED	QKPPCPRLNE	VLMEAEEPEV	LQDSLDRCYS	TTSTYFQLHA	SFQQYRSAFY	SFEEQDVSLA	LDVDNRFFTL
570	580						
TVIRHHLAFQ	MGVIFPH						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1974	2	696.2762	-133.49	2	54.8	13.9	2	65-75	K.DLIKSMLRDER.L	Oxidation: 6

Detailed Protein Report

Protein 228: PREDICTED: focal adhesion kinase 1 isoform X12 [Homo sapiens]

Accession:	gi|530389222	**Score:**	39.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	108.1
Database Date:	2015-11-30	**pI:**	5.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	4.2
		No. of unique Peptides:	2

Quantitation

mdown:qdown **Median:** 1.25 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MEMLLMSGYE LRIRYLPKGF LNQFTEDKPT LNFFYQQVKS DYMLEIADQV DQEIALKLGC LEIRRSYWEM RGNALEKKSN

        90        100        110        120        130        140        150        160
YEVLEKDVGL KRFFPKSLLD SVKAKTLRKL IQQTFRQFAN LNREESILKF FEILSPVYRF DKECFKCALG SSWIISVELA

       170        180        190        200        210        220        230        240
IGPEEGISYL TDKGCNPTHL ADFTQVQTIQ YSNSEDKDRK GMLQLKIAGA PEPLTVTAPS LTIAENMADL IDGYCRLVNG

       250        260        270        280        290        300        310        320
TSQSFIIRPQ KEGERALPSI PKLANSEKQG MRTHAVSVSD EISGDETDDY AEIIDEEDTY TMPSKSYGID EARDYEIQRE

       330        340        350        360        370        380        390        400
RIELGRCIGE GQFGDVHQGI YMSPENPALA VAIKTCKNCT SDSVREKFLQ EALTMRQFDH PHIVKLIGVI TENPVWIIME

       410        420        430        440        450        460        470        480
LCTLGELRSF LQVRKYSLDL ASLILYAYQL STALAYLESK RFVHRDIAAR NVLVSSNDCV KLGDFGLSRY MEDSTYYKAS

       490        500        510        520        530        540        550        560
KGKLPIKWMA PESINFRRFT SASDVWMFGV CMWEILMHGV KPFQGVKNND VIGRIENGER LPMPPNCPPT LYSLMTKCWA

       570        580        590        600        610        620        630        640
YDPSRRPRFT ELKAQLSTIL EEEKAQQEER MRMESRRQAT VSWDSGGSDE APPKPSRPGY PSPRSSEGFY PSPQHMVQTN

       650        660        670        680        690        700        710        720
HYQVSGYPGS HGITAMAGSI YPGQASLLDQ TDSWNHRPQE IAMWQPNVED STVLDLRGIG QVLPTHLMEE RLIRQQQEME

       730        740        750        760        770        780        790        800
EDQRWLEKEE RFLKPDVRLS RGSIDREDGS LQGPIGNQHI YQPVGKPDPA APPKKPPRPG APGHLGSLAS LSSPADSYNE

       810        820        830        840        850        860        870        880
GVKPWRLQPQ EISPPPTANL DRSNDKVYEN VTGLVKAVIE MSSKIQPAPP EEYVPMVKEV GLALRTLLAT VDETIPLLPA

       890        900        910        920        930        940        950        960
STHREIEMAQ KLLNSDLGEL INKMKLAQQY VMTSLQQEYK KQMLTAAHAL AVDAKNLLDV IDQARLKMLG QTRPH
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2249	1	937.4207	-94.13	2	56.6	13.7	2	484-498	K.LPIKWMAPESINFRR.F	Oxidation: 6	
2062	1	720.2626	-173.22	2	54.3	10.7	0	922-935	K.QMLTAAHALAVDAK.N		mdown:qdown 1.25

Detailed Protein Report

Protein 229: **PREDICTED: p21-activated protein kinase-interacting protein 1 isoform X2 [Homo sapiens]**

Accession:	gi|578811766	**Score:**	39.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	41.4
Database Date:	2015-11-30	**pI:**	10.1
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	7.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLEQQWTLVA	DFTHHAHTAS	LSAVAVNSRF	VVTGSKDETI	HIYDMKKKIE	HGALVHHSGT	ITCLKFYGNR	HLISGAEDGL
90	100	110	120	130	140	150	160
ICIWDAKKWE	CLKSIKAHKG	QVTFLSIHPS	GKLALSVGTD	KTLRTWNLVE	GRSAFIKNIK	QNAHIVEWSP	RGEQYVVIIQ
170	180	190	200	210	220	230	240
NKIDIYQLDT	ASISGTITNE	KRISSVKFLS	ESVLAVAGDE	EVIRFFDCDS	LVCLCEFKAH	ENRVKDMFSF	EIPEHHVIVS
250	260	270	280	290	300	310	320
ASSDGFIKMW	KLKQDKKVPP	SLLCEINTNA	RLTCLGVWLD	KVADMKESLP	PAAEPSPVSK	EQSKIGKKEP	GDTVHKEEKR
330	340	350	360	370			
SKPNTKKRGL	TGDSKKATKE	SGLISTKKRK	MVEMLEKKRK	KKKIKTMQ			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2184	1	778.2730	-90.09	3	55.8	13.6	1	205-223	R.FFDCDSLVCLCEFKAHENR.V	Carbamidomethyl: 11

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Detailed Protein Report

Protein 230: 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):	Oxidation	**Sequence Coverage [%]:**	2.5
		No. of unique Peptides:	2

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
2215	1	682.1038	136.60	3	57.9	10.1	1	1122-1137	K.WLYNEYVTELPAFKDR.V	

Detailed Protein Report

Protein 231: **latent-transforming growth factor beta-binding protein 4 isoform c precursor [Homo sapiens]**

Accession:	gi|110347437	**Score:**	39.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	165.6
Database Date:	2015-11-30	**pI:**	4.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAGGVRLLWV	SLLVLLAQLG	PQPGLGRLGE	RLRVRFTPVV	CGLRCVHGPT	GSRCTPTCAP	RNATSVDSGA	PGGAAPGGPG
90	100	110	120	130	140	150	160
FRAFLCPLIC	HNGGVCVKPD	RCLCPPDFAG	KFCQLHSSGA	RPPAPAVPGL	TRSVYTMPLA	NHRDDEHGVA	SMVSVHVEHP
170	180	190	200	210	220	230	240
QEASVVVHQV	ERVSGPWEEA	DAEAVARAEA	AARAEAAAPY	TVLAQSAPRE	DGYSDASGFG	YCFRELRGGE	CASPLPGLRT
250	260	270	280	290	300	310	320
QEVCCRGAGL	AWGVHDCQLC	SERLGNSERV	SAPDGPCPTG	FERVNGSCED	VDECATGGRC	QHGECANTRG	GYTCVCPDGF
330	340	350	360	370	380	390	400
LLDSSRSSCI	SQHVISEAKG	PCFRVLRDGG	CSLPILRNIT	KQICCCSRVG	KAWGRGCQLC	PPFGSEGFRE	ICPAGPGYHY
410	420	430	440	450	460	470	480
SASDLRYNTR	PLGQEPPRVS	LSQPRTLPAT	SRPSAGFLPT	HRLEPRPEPR	PDPRPGPELP	LPSIPAWTGP	EIPESGPSSG
490	500	510	520	530	540	550	560
MCQRNPQVCG	PGRCISRPSG	YTCACDSGFR	LSPQGTRCID	VDECRRVPPP	CAPGRCENSP	GSFRCVCGPG	FRAGPRAAEC
570	580	590	600	610	620	630	640
LDVDECHRVP	PPCDLGRCEN	TPGSFLCVCP	AGYQAAPHGA	SCQDVDECTQ	SPGLCGRGAC	KNLPGSFRCV	CPAGFRGSAC
650	660	670	680	690	700	710	720
EEDVDECAQE	PPPCGPGRCD	NTAGSFHCAC	PAGFRSRGPG	APCQDVDECA	RSPPPCTYGR	CENTEGSFQC	VCPMGFQPNT
730	740	750	760	770	780	790	800
AGSECEDVDE	CENHLACPGQ	ECVNSPGSFQ	CRTCPSGHHL	HRGRCTDVDE	CSSGAPPCGP	HGHCTNTEGS	FRCSCAPGYR
810	820	830	840	850	860	870	880
APSGRPGPCA	DVNECLEGDF	CFPHGECLNT	DGSFACTCAP	GYRPGPRGAS	CLDVDECSEE	DLCQSGICTN	TDGSFECICP
890	900	910	920	930	940	950	960
PGHRAGPDLA	SCLDVDECRE	RGPALCGSQR	CENSPGSYRC	VRDCDPGYHA	GPEGTCDDVD	ECQEYGPEIC	GAQRCENTPG
970	980	990	1000	1010	1020	1030	1040
SYRCTPACDP	GYQPTPGGGC	QDVDECRNRS	FCGAHAVCQN	LPGSFQCLCD	QGYEGARDGR	HCVDVNECET	LQGVCGAALC
1050	1060	1070	1080	1090	1100	1110	1120
ENVEGSFLCV	CPNSPEEFDP	MTGRCVPPRT	SAGTFPGSQP	QAPASPVLPA	RPPPPPLPRR	PSTPRQGPVG	SGRRECYFDT
1130	1140	1150	1160	1170	1180	1190	1200
AAPDACDNIL	ARNVTWQECC	CTVGEGWGSG	CRIQQCPGTE	TAEYQSLCPH	GRGYLAPSGD	LSLRRDVDEC	QLFRDQVCKS
1210	1220	1230	1240	1250	1260	1270	1280
GVCVNTAPGY	SCYCSNGYYY	HTQRLECIDN	DECADEEPAC	EGGRCVNTVG	SYHCTCEPPL	VLDGSQRRCV	SNESQSLDDN
1290	1300	1310	1320	1330	1340	1350	1360
LGVCWQEVGA	DLVCSHPRLD	RQATYTECCC	LYGEAWGMDC	ALCPAQDSDD	FEALCNVLRP	PAYSPPRPGG	FGLPYEYGPD
1370	1380	1390	1400	1410	1420	1430	1440
LGPPYQGLPY	GPELYPPPAL	PYDPYPPPPG	PFARREAPYG	APRFDMPDFE	DDGGPYGESE	APAPPGPGTR	WPYRSRDTRR
1450	1460	1470	1480	1490	1500	1510	1520
SFPEPEEPPE	GGSYAGSLAE	PYEELEAEEC	GILDGCTNGR	CVRVPEGFTC	RCFDGYRLDM	TRMACVDINE	CDEAEAASPL
1530	1540	1550	1560				
CVNARCLNTD	GSFRCICRPG	FAPTHQPHHC	APARPRA				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1901	1	900.3202	-98.12	2	52.4	10.3	1	45-61	R.CVHGPTGSRCTPTCAPR.N	Carbamidomethyl: 10

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Detailed Protein Report

Protein 232: SURP and G-patch domain-containing protein 2 [Homo sapiens]

Accession: gi|224282117
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 39.0
MW [kDa]: 120.1
pI: 7.0
Sequence Coverage [%]: 4.4
No. of unique Peptides: 2

Alias proteins:

Accession	Name	Description
gi|224282119	refseq_human (refseq_human_20140103.fasta)	SURP and G-patch domain-containing protein 2 [Homo sapiens]

```
        10          20          30          40          50          60          70          80
MAARRITQET  FDAVLQEKAK  RYHMDASGEA  VSETLQFKAQ  DLLRAVPRSR  AEMYDDVHSD  GRYSLSGSVA  HSRDAGREGL
        90         100         110         120         130         140         150         160
RSDVFPGPSF  RSSNPSISDD  SYFRKECGRD  LEFSHSDSRD  QVIGHRKLGH  FRSQDWKFAL  RGSWEQDFGH  PVSQESSWSQ
       170         180         190         200         210         220         230         240
EYSFGPSAVL  GDFGSSRLIE  KECLEKESRD  YDVDHPGEAD  SVLRGGSQVQ  ARGRALNIVD  QEGSLLGKGE  TQGLLTAKGG
       250         260         270         280         290         300         310         320
VGKLVTLRNV  STKKIPTVNR  ITPKTQGTNQ  IQKNTPSPDV  TLGTNPGTED  IQFPIQKIPL  GLDLKNLRLP  RRKMSFDIID
       330         340         350         360         370         380         390         400
KSDVFSRFGI  EIIKWAGFHT  IKDDIKFSQL  FQTLFELETE  TCAKMLASFK  CSLKPEHRDF  CFFTIKFLKH  SALKTPRVDN
       410         420         430         440         450         460         470         480
EFLNMLLDKG  AVKTKNCFFE  IIKPFDKYIM  RLQDRLLKSV  TPLLMACNAY  ELSVKMKTLS  NPLDLALALE  TTNSLCRKSL
       490         500         510         520         530         540         550         560
ALLGQTFSLA  SSFRQEKILE  AVGLQDIAPS  PAAFPNFEDS  TLFGREYIDH  LKAWLVSSGC  PLQVKKAEPE  PMREEEKMIP
       570         580         590         600         610         620         630         640
PTKPEIQAKA  PSSLSDAVPQ  RADHRVVGTI  DQLVKRVIEG  SLSPKERTLL  KEDPAYWFLS  DENSLEYKYY  KLKLAEMQRM
       650         660         670         680         690         700         710         720
SENLRGADQK  PTSADCAVRA  MLYSRAVRNL  KKKLLPWQRR  GLLRAQGLRG  WKARRATTGT  QTLLSSGTRL  KHHGRQAPGL
       730         740         750         760         770         780         790         800
SQAKPSLPDR  NDAAKDCPPD  PVGPSPQDPS  LEASGPSPKP  AGVDISEAPQ  TSSPCPSADI  DMKTMETAEK  LARFVAQVGP
       810         820         830         840         850         860         870         880
EIEQFSIENS  TDNPDLWFLH  DQNSSAFKFY  RKKVFELCPS  ICFTSSPHNL  HTGGGDTTGS  QESPVDLMEG  EAEFEDEPPP
       890         900         910         920         930         940         950         960
REAELESPEV  MPEEEDEDDE  DGGEEAPAPG  GAGKSEGSTP  ADGLPGEAAE  DDLAGAPALS  QASSGTCFPR  KRISSKSLKV
       970         980         990        1000        1010        1020        1030        1040
GMIPAPKRVC  LIQEPKVHEP  VRIAYDRPRG  RPMSKKKKPK  DLDFAQQKLT  DKNLGFQMLQ  KMGWKEGHGL  GSLGKGIREP
      1050        1060        1070        1080        1090
VSVGTPSEGE  GLGADGQEHK  EDTFDVFRQR  MMQMYRHKRA  NK
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2696	1	835.4525	-15.26	2	62.1	11.4	1	213-228	R.GRALNIVDQEGSLLGK.G	
1971	6	948.3560	-134.88	2	53.1	17.6	0	439-455	K.SVTPLLMACNAYELSVK.M	Carbamidomethyl: 9

Detailed Protein Report

Protein 233: PREDICTED: protein FAM186A isoform X1 [Homo sapiens]

Accession:	gi|578823289	**Score:**	38.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	262.1
Database Date:	2015-11-30	**pI:**	9.1
		Sequence Coverage [%]:	1.4
		No. of unique Peptides:	1

Quantitation

Wdown:Qdown	**Median:** 0.34	**CV:** 0.00 %	**No. of Peptides:** 1

10	20	30	40	50	60	70	80
MFFKMKNEID	NDPESEKCIK	DSTIMRREPQ	NILSPLMLPN	LEIPFSVKDI	ISRIERAQLH	RAREDIDMQL	SEIMNNVHRI
90	100	110	120	130	140	150	160
MTRYTLVFNS	SSERNVSLTE	HKKKQRTNFL	EKMATYAKTI	EIREKTLANI	LAWLEEWNDV	LSEMTLMDVD	EHHHWIAQME
170	180	190	200	210	220	230	240
LLPDTLKAIE	NNVKILSRFS	TSFLDEKKKQ	KKKILSRGTL	WKSWKERVIK	RPSTARALRP	DQMISDQLAT	NTKVSEIQGM
250	260	270	280	290	300	310	320
LQELIGTTMF	STLENNAIKY	ISSTIVNLST	ALSMLNDELK	CVNFQSSTVY	AHETSEAEKE	LSLKIIRDLS	NENEMLQQKL
330	340	350	360	370	380	390	400
QDAEEKCEQL	IRSKIVIEQL	YAKLSTSSTL	KVLPGPSPQS	SRAIIKVGDT	EDNMDNILDK	ELENIVDEVQ	RKETKDSGIK
410	420	430	440	450	460	470	480
WDSTISYTAQ	AERTPDLTEL	RQQPVASEDI	SEDSTKDNVS	LKKGDFYQED	ETDEYQSWKR	SHKKATYVYE	TSGPNLSDNK
490	500	510	520	530	540	550	560
SGQKVSEAKP	SQYYELQVLK	KKRKEMKSFS	EDKSKSPTEA	KRKHLSLTET	KSQGGKSGTS	MMMLEQFRKV	KRESPFDKRP
570	580	590	600	610	620	630	640
TAAEIKVEPT	TESLDKEGKG	EIRSLVEPLS	MIQFDDTAEP	QKGKIKGKKH	HISSGTITSK	EEKTEEKEEL	TKQVKSHQLV
650	660	670	680	690	700	710	720
KSLSRVAKET	SESTRVLESP	DGKSEQSNLE	EFQEAIMAFL	KQKIDNIGKA	FDKKTVPKEE	ELLKRAEAEK	LGIIKAKMEE
730	740	750	760	770	780	790	800
YFQKVAETVT	KILRKYKDTK	KEEQVGEKPI	KQKKVVSFMP	GLHFQKSPIS	AKSESSTLLS	YESTDPVINN	LIQMILAEIE
810	820	830	840	850	860	870	880
SERDIPTVST	VQKDHKEKEK	QRQEQYLQEG	QEQMSGMSLK	QQLLGERNLL	KEHYEKISEN	WEEKKAWLQM	KEGKQEQQSQ
890	900	910	920	930	940	950	960
KQWQEEEMWK	EEQKQATPKQ	AEQEEKQKQR	GQEEEELPKS	SLQRLEEGTQ	KMKTQGLLLE	KENGQMRQIQ	KEAKHLGPHR
970	980	990	1000	1010	1020	1030	1040
RREKGKEKQK	PERGLEDLER	QIKTKDQMQM	KETQPKELEK	MVIQTPMTLS	PRWKSVLKDV	QRSYEGKEFQ	RNLKTLENLP
1050	1060	1070	1080	1090	1100	1110	1120
DEKEPISITP	PPSLQYSLPG	ALPISGQPLT	KCIHLTPQQA	QEVGITLTPQ	QAQAQGITLT	LQQAQELGIP	LTPQQAQALE
1130	1140	1150	1160	1170	1180	1190	1200
ILFTPQQAQA	LGIPLTPQQT	QVQGITLTPQ	QDQAPGISLT	TQQAQKLGIP	LTPQQAQALG	IPLTPQQAQE	LGIPLTPQQA
1210	1220	1230	1240	1250	1260	1270	1280
QALRVSLTPQ	QAQELGIPLT	PQQAQALGIT	LTLQQAQQLG	IPLTPQQAQA	LGITLTPKQV	QELGIPLTPQ	QAQALGITLT
1290	1300	1310	1320	1330	1340	1350	1360
PKQAQELGIP	LNPQQAQTLG	IPLTPKQAQA	LGIPFTPQQA	QALGIPLTPQ	QAQTQEITLT	PQQAQALGMP	LTTQQAQELG
1370	1380	1390	1400	1410	1420	1430	1440
IPLTPQHAQA	LGMPLTTQQA	QELGIPLTPQ	QAQALGMPLT	TQQAQELGIP	LTPQQAQELG	IPFTPQQAQA	QEITLTPQQA
1450	1460	1470	1480	1490	1500	1510	1520
QALGMPLTAQ	QAQELGITLT	PQQAQELGIP	LTPQQAQALG	IPLIPPQAQE	LGIPLTPQQA	QALGILLIPP	QAQELGIPLT
1530	1540	1550	1560	1570	1580	1590	1600
PQQAQALGIP	LIPPQAQELG	IPLTPQQVQA	LGIPLIPPQA	QELEIPLTPQ	QAQALGIPLT	PQQAQELGIP	LTPQQAQELG
1610	1620	1630	1640	1650	1660	1670	1680
IPLTPQQAQA	QGIPLTPQQA	QALGISLTPQ	QAQAQGITLT	PQQAQALGVP	ITPVNAWVSA	VTLTSEQTHA	LESPMNLEQA
1690	1700	1710	1720	1730	1740	1750	1760
QEQLLKLGVP	LTLDKAHTLG	SPLTLKQVQW	SHRPFQKSKA	SLPTGQSIIS	RLSPSLRLSL	ASSAPTAEKS	SIFGVSSTPL
1770	1780	1790	1800	1810	1820	1830	1840
QISRVPLNQG	PFAPGKPLEM	GILSEPGKLG	APQTLRSSGQ	TLVYGGQSTS	AQFPAPQAPP	SPGQLPISRA	PPTPGQPFIA
1850	1860	1870	1880	1890	1900	1910	1920
GVPPTSGQIP	SLWAPLSPGQ	PLVPEASSIP	GDLLESGPLT	FSEQLQEFQP	PATAEQSPYL	QAPSTPGQHL	ATWTLPGRAS
1930	1940	1950	1960	1970	1980	1990	2000
SLWIPPTSRH	PPTLWPSPAP	GKPQKSWSPS	VAKKRLAIIS	SLKSKSVLIH	PSAPDFKVAQ	VPFTTKKFQM	SEVSDTSEET
2010	2020	2030	2040	2050	2060	2070	2080
QILRDTFAIE	SFRTFQSHFT	KYRTPVYQTP	YTDERALLTL	MKPTTSPSSL	TTLLRTSQIS	PLEWYQKSRF	PPIDKPWILS
2090	2100	2110	2120	2130	2140	2150	2160
SVSDTKKPKV	MVPPSSPQEL	EEKRYFVDVE	AQKKNLILLN	QAIKTCGLPS	QLHTMARTLI	IEILHMDTVQ	LGYLFRKYIA
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
82	1	724.8160	-30.23	2	30.3	10.0	0	308-319	R.DLSNENEMLQQK.L		Wdown:Qdown 0.34

Detailed Protein Report

Protein 234: replication factor C subunit 1 isoform 1 [Homo sapiens]

Accession:	gi|32528306	**Score:**	38.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	128.1
Database Date:	2015-11-30	**pI:**	9.9
		Sequence Coverage [%]:	3.5
		No. of unique Peptides:	2

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
991	1	530.7704	-72.90	2	41.2	10.7	2	42-50	K.EIKVNSSRK.E	
6	1	776.7890	-162.05	2	28.8	17.4	1	776-789	R.VEQIKGAMMSIAFK.E	

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Detailed Protein Report

Protein 235: zinc finger protein 275 [Homo sapiens]

Accession:	gi|298231195	**Score:**	38.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	37.0
Database Date:	2015-11-30	**pI:**	10.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	9.7
		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 236: zinc finger protein 841 [Homo sapiens]

Accession: gi|211057416
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 38.7
MW [kDa]: 106.0
pI: 10.4
Sequence Coverage [%]: 6.1
No. of unique Peptides: 2

10	20	30	40	50	60	70	80
MALPQGSLTF	RDVAVEFSQE	EWKCLDPVQK	ALYRDVMLEN	YRNLGFLGLC	LPDLNIISML	EQGKEPWTVV	SQVKIARNPN
90	100	110	120	130	140	150	160
CGECMKGVIT	GISPKCVIKE	LPPIQNSNTG	EKFQAVMLEG	HESYDTENFY	FREIRKNLQE	VDFQWKDGEI	NYKEGPMTHK
170	180	190	200	210	220	230	240
NNLTGQRVRH	SQGDVENKHM	ENQLILRFQS	GLGELQKFQT	AEKIYGCNQI	ERTVNNCFLA	SPLQRIFPGV	QTNISRKYGN
250	260	270	280	290	300	310	320
DFLQLSLPTQ	DEKTHIREKP	YIGNECGKAF	RVSSSLINHQ	MIHTTEKPYR	CNESGKAFHR	GSLLTVHQIV	HTRGKPYQCD
330	340	350	360	370	380	390	400
VCGRIFRQNS	DLVNHRRSHT	GDKPYICNEC	GKSFSKSSHL	AVHQRIHTGE	KPYKCNRCGK	CFSQSSSLAT	HQTVHTGDKP
410	420	430	440	450	460	470	480
YKCNECGKTF	KRNSSLTAHH	IIHAGKKPYT	CDVCGKVFYQ	NSQLVRHQII	HTGETPYKCN	ECGKVFFQRS	RLAGHRRIHT
490	500	510	520	530	540	550	560
GEKPYKCNEC	GKVFSQHSHL	AVHQRVHTGE	KPYKCNECGK	AFNWGSLLTV	HQRIHTGEKP	YKCNVCGKVF	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
2885	1	1129.0588	-29.01	2	64.8	11.2	1	179-197	K.HMENQLILRFQSGLGELQK.F	Oxidation: 2
1460	1	1011.7530	-79.39	3	48.0	16.8	2	590-616	R.MHTGEKPYKCNVCGKVFIDSGNLSIHR.R	

Detailed Protein Report

Protein 237: G2/mitotic-specific cyclin-B3 isoform 3 [Homo sapiens]

Accession:	gi|90669307	**Score:**	38.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	157.8
Database Date:	2015-11-30	**pI:**	6.3
		Sequence Coverage [%]:	3.4
		No. of unique Peptides:	3

Quantitation

mdown:qdown **Median:** 0.38 **CV:** 0.00 % **No. of 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	Ratios
1030	1	670.7981	-53.16	2	41.6	10.6	1	290-300	K.CTIYGKICHFR.K		mdown:qdown 0.38
2723	1	639.3585	-37.42	2	62.4	12.0	2	348-358	K.KSLALQKTNFK.E		
1809	2	1011.7628	-33.19	3	51.3	16.1	2	535-560	K. KKCTTQEMMSICPELLDFQDMIGE N		

Detailed Protein Report

Protein 238: ankyrin-1 isoform 2 [Homo sapiens]

Accession:	gi|70780355	**Score:**	38.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	188.9
Database Date:	2015-11-30	**pI:**	6.2
		Sequence Coverage [%]:	1.4
		No. of unique Peptides:	2

Quantitation

mdown:qdown	**Median:**	1.76	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	3.16	**CV:**	0.00 %	**No. of Peptides:**	1

10	20	30	40	50	60	70	80
MPYSVGFREA	DAATSFLRAA	RSGNLDKALD	HLRNGVDINT	CNQNGLNGLH	LASKEGHVKM	VVELLHKEII	LETTTKKGNT
90	100	110	120	130	140	150	160
ALHIAALAGQ	DEVVRELVNY	GANVNAQSQK	GFTPLYMAAQ	ENHLEVVKFL	LENGANQNVA	TEDGFTPLAV	ALQQGHENVV
170	180	190	200	210	220	230	240
AHLINYGTKG	KVRLPALHIA	ARNDDTRTAA	VLLQNDPNPD	VLSKTGFTPL	HIAAHYENLN	VAQLLLNRGA	SVNFTPQNGI
250	260	270	280	290	300	310	320
TPLHIASRRG	NVIMVRLLLD	RGAQIETKTK	DELTPLHCAA	RNGHVRISEI	LLDHGAPIQA	KTKNGLSPIH	MAAQGDHLDC
330	340	350	360	370	380	390	400
VRLLLQYDAE	IDDITLDHLT	PLHVAAHCGH	HRVAKVLLDK	GAKPNSRALN	GFTPLHIACK	KNHVRVMELL	LKTGASIDAV
410	420	430	440	450	460	470	480
TESGLTPLHV	ASFMGHLPIV	KNLLQRGASP	NVSNVKVETP	LHMAARAGHT	EVAKYLLQNK	AKVNAKAKDD	QTPLHCAARI
490	500	510	520	530	540	550	560
GHTNMVKLLL	ENNANPNLAT	TAGHTPLHIA	AREGHVETVL	ALLEKEASQA	CMTKKGFTPL	HVAAKYGKVR	VAELLLERDA
570	580	590	600	610	620	630	640
HPNAAGKNGL	TPLHVAVHHN	NLDIVKLLLP	RGGSPHSPAW	NGYTPLHIAA	KQNQVEVARS	LLQYGGSANA	ESVQGVTPLH
650	660	670	680	690	700	710	720
LAAQEGHAEM	VALLLSKQAN	GNLGNKSGLT	PLHLVAQEGH	VPVADVLIKH	GVMVDATTRM	GYTPLHVASH	YGNIKLVKFL
730	740	750	760	770	780	790	800
LQHQADVNAK	TKLGYSPLHQ	AAQQGHTDIV	TLLLKNGASP	NEVSSDGTTP	LAIAKRLGYI	SVTDVLKVVT	DETSFVLVSD
810	820	830	840	850	860	870	880
KHRMSFPETV	DEILDVSEDE	GEELISFKAE	RRDSRDVDEE	KELLDFVPKL	DQVVESPAIP	RIPCAMPETV	VIRSEEQEQA
890	900	910	920	930	940	950	960
SKEYDEDSLI	PSSPATETSD	NISPVASPVH	TGFLVSFMVD	ARGGSMRGSR	HNGLRVVIPP	RTCAAPTRIT	CRLVKPQKLS
970	980	990	1000	1010	1020	1030	1040
TPPPLAEEEG	LASRIIALGP	TGAQFLSPVI	VEIPHFASHG	RGDRELVVLR	SENGSVWKEH	RSRYGESYLD	QILNGMDEEL
1050	1060	1070	1080	1090	1100	1110	1120
GSLEELEKKR	VCRIITTDFP	LYFVIMSRLC	QDYDTIGPEG	GSLKSKLVPL	VQATFPENAV	TKRVKLALQA	QPVPDELVTK
1130	1140	1150	1160	1170	1180	1190	1200
LLGNQATFSP	IVTVEPRRRK	FHRPIGLRIP	LPPSWTDNPR	DSGEGDTTSL	RLLCSVIGGT	DQAQWEDITG	TTKLVYANEC
1210	1220	1230	1240	1250	1260	1270	1280
ANFTTNVSAR	FWLSDCPRTA	EAVNFATLLY	KELTAVPYMA	KFVIFAKMND	PREGRLRCYC	MTDDKVDKTL	EQHENFVEVA
1290	1300	1310	1320	1330	1340	1350	1360
RSRDIEVLEG	MSLFAELSGN	LVPVKKAAQQ	RSFHFQSFRE	NRLAMPVKVR	DSSREPGGSL	SFLRKAMKYE	DTQHILCHLN
1370	1380	1390	1400	1410	1420	1430	1440
ITMPPCAKGS	GAEDRRRTPT	PLALRYSILS	ESTPGSLSGT	EQAEMKMAVI	SEHLGLSWAE	LARELQFSVE	DINRIRVENP
1450	1460	1470	1480	1490	1500	1510	1520
NSLLEQSVAL	LNLWVIREGQ	NANMENLYTA	LQSIDRGEIV	NMLEGSGRQS	RNLKPDRRHT	DRDYSLSPSQ	MNGHQRGQAR
1530	1540	1550	1560	1570	1580	1590	1600
ITHSPTVSQV	TERSQDRLQD	WDADGSIVSY	LQDAAQGSWQ	EEVTQGPHSF	QGTSTMTEGL	EPGGSQEYEK	VLVSVSEHTW
1610	1620	1630	1640	1650	1660	1670	1680
TEQPEAESSQ	ADRDRRQQGQ	EEQVQEAKNT	FTQVVQGNEF	QNIPGEQVTE	EQFTDEQGNI	VTKKIIRKVV	RQIDLSSADA
1690	1700	1710	1720				
AQEHEEVTVE	GPLEDPSELE	VDIDYFMKHS	KDHTSTPNP				

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1714	2	917.4108	-124.71	2	50.0	23.4	1	287-303	R.ISEILLDHGAPIQAKTK.N		
2592	3	449.6181	-325.55	2	61.1	15.2	1	1492-1498	R.NLKPDRR.H		Wdown:Qdown 3.16 mdown:qdown 1.76

Detailed Protein Report

Protein 239: PREDICTED: testis-expressed sequence 2 protein isoform X4 [Homo sapiens]

Accession:	gi|530412523	**Score:**	38.6
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 [%]:**	3.2
		No. of unique Peptides:	2

Quantitation

mdown:qdown	**Median:**	0.67	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.16	**CV:**	0.00 %	**No. of Peptides:**	1

10	20	30	40	50	60	70	80
MTSLYGRHAE	KTTDMPKPSA	PKVHVQRSVS	RDTIAIHFSA	SGEEEEEEEE	EFREYFEEGL	DDQSIVTGLE	AKEDLYLEPQ
90	100	110	120	130	140	150	160
VGHDPAGPAA	SPVLADGLSV	SQAPAILPVS	KNTVKLLESP	VPAAQVLSTV	PLAVSPGSSS	SGPLASSPSV	SSLSEQKTSS
170	180	190	200	210	220	230	240
SSPLSSPSKS	PILSSSASTS	TLSSAKPFMS	LVKSLSTEVE	PKESPHPARH	RHLMKTLVKS	LSTDTSRQES	DTVSYKPPDS
250	260	270	280	290	300	310	320
KLNLHLFKQF	TQPRNTGGDS	KTAPSSPLTS	PSDTRSFFKV	PEMEAKIEDT	KRRLSEVIYE	PFQLLSKIIG	EESGSHRPKA
330	340	350	360	370	380	390	400
LSSSASELSN	LSSLNGHLES	NNNYSIKEEE	CDSEGDGYGS	DSNIPRSDHP	KSTGEPTREI	ELKSSQGSSL	KDLGLKTSSL
410	420	430	440	450	460	470	480
VLEKCSLSAL	VSKEDEEFCE	LYTEDFDLET	EGESKVDKLS	DIPLKPEVLA	EDGVVLDSED	EVDSAVQHPE	LPVKTLGFFI
490	500	510	520	530	540	550	560
MCVYVYLILP	LPHYVSGLFL	GIGLGFMTAV	CVIWFFTPPS	AHKYHKLHKN	LRHWNTRSLD	IKEPEILKGW	MNEIYNYDPE
570	580	590	600	610	620	630	640
TYHATLTHSV	FVRLEGGTLR	LSKPNKNISR	RASYNEPKPE	VTYISQKIYD	LSDSKIYLVP	KTLARKRIWN	KKYPICIELG
650	660	670	680	690	700	710	720
QQDDFMSKAQ	TDKETSEEKP	PAEGSEDPKK	PPRPQEGTRS	SQRDQILYLF	GRTGREKEEW	FRRFILASKL	KSEIKKSSGV
730	740	750	760	770	780	790	800
SGGKPGLLPA	HSRHNSPSGH	LTHSRSSSKG	SVEEIMSQPK	QKELAGSVRQ	KMLLDYSVYM	GRCVPQESRS	PQRSPLQSAE
810	820	830	840	850	860	870	880
SSPTAGKKLP	EVPPSEEEEQ	EAWVNALLGR	IFWDFLGEKY	WSDLVSKKIQ	MKLSKIKLPY	FMNELTLTEL	DMGVAVPKIL
890	900	910	920	930	940	950	960
QAFKPYVDHQ	GLWIDLEMSY	NGSFLMTLET	KMNLTKLGKE	PLVEALKVGE	IGKEGPRAFC	LADSDEESSS	AGSSEEDDAP
970	980	990	1000	1010	1020	1030	1040
EPSGGDKQLL	PGAEGYVGGH	RTSKIMRFVD	KITKSKYFQK	ATETEFIKKK	IEEVSNTPLL	LTVEVQECRG	TLAVNIPPPP
1050	1060	1070	1080	1090	1100	1110	1120
TDRVWYGFRK	PPHVELKARP	KLGEREVTLV	HVTDWIEKKL	EQEFQKVFVM	PNMDDVYITI	MHSAMDPRST	SCLLKDPPVE
1130							
AADQP							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1076	1	581.1694	-231.84	2	41.9	12.9	1	2-11	M.TSLYGRHAEK.T		mdown:qdown 0.67
2499	1	1044.5086	15.43	2	61.7	15.0	1	632-648	K.KYPICIELGQQDDFMSK.A	Carbamidomethyl: 5; Oxidation: 15	Wdown:Qdown 0.16

Detailed Protein Report

Protein 240: bone morphogenetic protein 1 isoform 3 precursor [Homo sapiens]

Accession:	gi|5453579	**Score:**	38.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	111.2
Database Date:	2015-11-30	**pI:**	6.5
		Sequence Coverage [%]:	3.4
		No. of unique Peptides:	3

Quantitation

mdown:qdown **Median:** 0.63 **CV:** 0.00 % **No. of 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	Ratios
556	1	658.3907	22.79	2	35.8	11.5	2	303-314	R.TRLSKGDIAQAR.K		mdown:qdown 0.63
2634	3	753.8426	-101.90	2	61.7	16.4	1	525-537	R.LWLKFVSDGSINK.A		
2126	1	1131.3250	-234.65	1	56.8	10.6	1	978-986	K.FQDTLHSRK.-		

Detailed Protein Report

Protein 241: F-box only protein 41 [Homo sapiens]

Accession:	gi|289803020	**Score:**	38.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	94.4
Database Date:	2015-11-30	**pI:**	9.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.7
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	1.17	**CV:**	0.00 %	**No. of 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	Ratios
2879	2	813.9356	28.83	2	65.2	12.4	1	568-580	R.TLLHAAEVCRDWR.F	Carbamidomethyl: 9	mdown:qdown 1.17

Detailed Protein Report

Protein 242: **chromosome-associated kinesin KIF4A [Homo sapiens]**

Accession:	gi|116686122	**Score:**	38.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	139.8
Database Date:	2015-11-30	**pI:**	5.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.5
		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
2387	1	1051.5184	80.34	2	58.2	16.1	2	1082-1100	K.NIQGCSCKGWCGNKQCGCR.K	Carbamidomethyl: 11
2074	1	701.2275	-91.47	3	56.1	10.6	2	1082-1100	K.NIQGCSCKGWCGNKQCGCR.K	Carbamidomethyl: 18

Detailed Protein Report

Protein 243: ubiquilin-like protein [Homo sapiens]

Accession: gi|145580580

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Modification(s): Oxidation

Score: 38.3

MW [kDa]: 52.9

pI: 5.6

Sequence Coverage [%]: 8.8

No. of unique Peptides: 2

Quantitation

mdown:qdown	**Median:**	1.36	**CV:**	31.66 %	**No. of Peptides:**	2
Wdown:Qdown	**Median:**	0.78	**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	mdown:qdown 1.00 Wdown:Qdown 0.78
2144	1	953.3984	-72.07	2	57.0	10.6	1	358-375	K.ANTAMISTKGQSHICATR.Q	Oxidation: 5	mdown:qdown 1.85

Detailed Protein Report

Protein 244: 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:	1

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

Detailed Protein Report

Protein 245: death-inducer obliterator 1 isoform c [Homo sapiens]

Accession:	gi|301129165	**Score:**	38.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	243.7
Database Date:	2015-11-30	**pI:**	8.9
		Sequence Coverage [%]:	1.2
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|301129170	refseq_human (refseq_human_20140103.fasta)	death-inducer obliterator 1 isoform c [Homo sapiens]

10	20	30	40	50	60	70	80
MDDKGDPSNE	EAPKAIKPTS	KEFRKTWGFR	RTTIAKREGA	GDAEADPLEP	PPPQQQLGLS	LRRSGRQPKR	TERVEQFLTI
90	100	110	120	130	140	150	160
ARRRGRRSMP	VSLEDSGEPT	SCPATDAETA	SEGSVESASE	TRSGPQSAST	AVKERPASSE	KVKGGDDHDD	TSDSDSDGLT
170	180	190	200	210	220	230	240
LKELQNRLRR	KREQEPTERP	LKGIQSRLRK	KRREEGPAET	VGSEASDTVE	GVLPSKQEPE	NDQGVVSQAG	KDDRESKLEG
250	260	270	280	290	300	310	320
KAAQDIKDEE	PGDLGRPKPE	CEGYDPNALY	CICRQPHNNR	FMICCDRCEE	WFHGDCVGIS	EARGRLLERN	GEDYICPNCT
330	340	350	360	370	380	390	400
ILQVQDETHS	ETADQQEAKW	RPGDADGTDC	TSIGTIEQKS	SEDQGIKGRI	EKAANPSGKK	KLKIFQPVIE	APGASKCIGP
410	420	430	440	450	460	470	480
GCCHVAQPDS	VYCSNDCILK	HAAATMKFLS	SGKEQKPKPK	EKMKMKPEKP	SLPKCGAQAG	IKISSVHKRP	APEKKETTVK
490	500	510	520	530	540	550	560
KAVVVPARSE	ALGKEAACES	STPSWASDHN	YNAVKPEKTA	APSPSLLYKS	TKEDRRSEEK	AAAMAASKKT	APPGSAVGKQ
570	580	590	600	610	620	630	640
PAPRNLVPKK	SSFANVAAAT	PAIKKPPSGF	KGTIPKRPWL	SATPSSGASA	ARQAGPAPAA	ATAASKKFPG	SAALVGAVRK
650	660	670	680	690	700	710	720
PVVPSVPMAS	PAPGRLGAMS	AAPSQPNSQI	RQNIRRSLKE	ILWKRVNDSD	DLIMTENEVG	KIALHIEKEM	FNLFQVTDNR
730	740	750	760	770	780	790	800
YKSKYRSIMF	NLKDPKNQGL	FHRVLREEIS	LAKLVRLKPE	ELVSKELSTW	KERPARSVME	SRTKLHNESK	KTAPRQEAIP
810	820	830	840	850	860	870	880
DLEDSPPVSD	SEEQQESARA	VPEKSTAPLL	DVFSSMLKDT	TSQHRAHLFD	LNCKICTGQV	PSAEDEPAPK	KQKLSASVKK
890	900	910	920	930	940	950	960
EDLKSKHDSS	APDPAPDSAD	EVMPEAVPEV	ASEPGLESAS	HPNVDRTYFP	GPPGDGHPEP	SPLEDLSPCP	ASCGSGVVTT
970	980	990	1000	1010	1020	1030	1040
VTVSGRDPRT	APSSSCTAVA	SAASRPDSTH	MVEARQDVPK	PVLTSVMVPK	SILAKPSSSP	DPRYLSVPPS	PNISTSESRS
1050	1060	1070	1080	1090	1100	1110	1120
PPEGDTTLFL	SRLSTIWKGF	INMQSVAKFV	TKAYPVSGCF	DYLSEDLPDT	IHIGGRIAPK	TVWDYVGKLK	SSVSKELCLI
1130	1140	1150	1160	1170	1180	1190	1200
RFHPATEEEE	VAYISLYSYF	SSRGRFGVVA	NNNRHVKDLY	LIPLSAQDPV	PSKLLPFEGP	GLESPRPNII	LGLVICQKIK
1210	1220	1230	1240	1250	1260	1270	1280
RPANSGELDK	MDEKRTRLQP	EEADVPAYPK	VATVPQSEKK	PSKYPLCSAD	AAVSTTPPGS	PPPPPPLPEP	PVLKVLSSLK
1290	1300	1310	1320	1330	1340	1350	1360
PAAPSPATAA	TTAAAASTAA	SSTASSASKT	ASPLEHILQT	LFGKKKSFDP	SAREPPGSTA	GLPQEPKTTA	EDGVPAPPLL
1370	1380	1390	1400	1410	1420	1430	1440
DPIVQQFGQF	SKDKALEEEE	DDRPYDPEEE	YDPERAFDTQ	LVERGRRHEV	ERAPEAAAAE	REEVAYDPED	ETILEEAKVT
1450	1460	1470	1480	1490	1500	1510	1520
VDDLPNRMCA	DVRRNSVERP	AEPVAGAATP	SLVEQQKMLE	ELNKQIEEQK	RQLEEQEEAL	RQQRAAVGVS	MAHFSVSDAL
1530	1540	1550	1560	1570	1580	1590	1600
MSPPPKSSLP	KAELFQQEQQ	SADKPASLPP	ASQASNHRDP	RQARRLATET	GEGEGEPLSR	LSARGAQGAL	PERDASRGGL
1610	1620	1630	1640	1650	1660	1670	1680
VGQAPMPVPE	EKEPASSPWA	SGEKPPAGSE	QDGWKAEPGE	GTRPATVGDS	SARPARRVLL	PTPPCGALQP	GFPLQHDGER
1690	1700	1710	1720	1730	1740	1750	1760
DPFTCPGFAS	QDKALGSAQY	EDPRNLHSAG	RSSSPAGETE	GDREPQARPG	EGTAPLPPPG	QKVGGSQPPF	QGQREPGPHA
1770	1780	1790	1800	1810	1820	1830	1840
LGMSGLHGPN	FPGPRGPAPP	FPEENIASND	GPRGPPPARF	GAQKGPIPSL	FSGQHGPPPY	GDSRGPSPSY	LGGPRGVAPS
1850	1860	1870	1880	1890	1900	1910	1920
QFEERKDPHG	EKREFQDAPY	NEVTGAPAQF	EGTEQAPFLG	SRGGAPFQFG	GQRRPLLSQL	KGPRGGPPPS	QFGGQRGPPP
1930	1940	1950	1960	1970	1980	1990	2000
GHFVGPRGPH	PSQFETARGP	HPNQFEGPRG	QAPNFMPGPR	GIQPQQFEDQ	RVHSPPRFTN	QRAPAPLQFG	GLRGSAPFSE
2010	2020	2030	2040	2050	2060	2070	2080
KNEQTPSRFH	FQGQAPQVMK	PGPRPLLELP	SHPPQHRKDR	WEEAGPPSAL	SSSAPGQGPE	ADGQWASADF	REGKGHEYRN
2090	2100	2110	2120	2130	2140	2150	2160
QTFEGRQRER	FDVGPKEKPL	EEPDAQGRAS	EDRRRERERG	RNWSRERDWD	RPREWDRHRD	KDSSRDWDRN	RERSANRDRE
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
62	1	675.3854	58.70	2	29.5	15.9	2	536-548	R.RSEEKAAAMAASK.K	

Detailed Protein Report

Protein 246: ubiquitin carboxyl-terminal hydrolase 43 isoform 2 [Homo sapiens]

Accession:	gi|389616163	**Score:**	38.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	122.2
Database Date:	2015-11-30	**pI:**	10.2
		Sequence Coverage [%]:	2.5
		No. of unique 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
2554	5	812.4077	-74.32	2	62.4	18.3	2	1042-1056	R.IPEGLARGLGSRLER.D	

Detailed Protein Report

Protein 247: PREDICTED: sperm flagellar protein 2 isoform X5 [Homo sapiens]

Accession: gi|578810001
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 38.1
MW [kDa]: 176.7
pI: 5.7
Sequence Coverage [%]: 3.4
No. of unique Peptides: 3

Quantitation

mdown:qdown **Median:** 0.35 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MSEILCQWLN KELKVSRTVS PKSFAKAFSS GYLLGEVLHK FELQDDFSEF LDSRVSSAKL NNFSRLEPTL NLLGVQFDQN
        90        100        110        120        130        140        150        160
VAHGIITEKP GVATKLLYQL YIALQKKKKS GLTGVEMQTM QRLTNLRLQN MKSDTFQERL RHMIPRQTDF NLMRITYRFQ
       170        180        190        200        210        220        230        240
EKYKHVKEDL AHLHFEKLER FQKLKEEQRC FDIEKQYLNR RRQNEIMAKI QAAIIQIPKP ASNRTLKALE AQKMMKKKKE
       250        260        270        280        290        300        310        320
AEDVADEIKK FEALIKKDLQ AKESASKTSL DTAGQTTTDL LNTYSDDEYI KKIQKRLEED AFAREQREKR RRKLLMDQLI
       330        340        350        360        370        380        390        400
AHEAQEEAYR EEQLINRLMR QSQQERRIAV QLMHVRHEKE VLWQNRIFRE KQHEERRLKD FQDALDREAA LAKQAKIDFE
       410        420        430        440        450        460        470        480
EQFLKEKRFH DQIAVERAQA RYEKHYSVCA EILDQIVDLS TKVADYRMLT NNLIPYKLMH DWKELFFNAK PIYEQASVKT
       490        500        510        520        530        540        550        560
LPANPSREQL TELEKRDLLD TNDYEEYKNM VGEWALPEEM VDNLPPSNNC ILGHILHRLA EKSLPPRAES TTPELPSFAV
       570        580        590        600        610        620        630        640
KGCLLGKTLS GKTTILRSLQ KDFPIQILSI DTLVQEAIQA FHDNEKVSEV LPIQKNDEED ALPVLQEEIK ESQDPQHVFS
       650        660        670        680        690        700        710        720
AGPVSDEVLP ETEGETMLSA NADKTPKAEE VKSSDSFLKL TTRAQLGAKS EQLLKKGKSI PDVLLVDIIV NAINEIPVNQ
       730        740        750        760        770        780        790        800
DCILDGFPMT LNQAQLLEEA LTGCNRNLTE VERKKAQKST LAIDPATSKE IPLPSPAFDF VILLDVSDTS SMSRMNDIIA
       810        820        830        840        850        860        870        880
EELSYKTAHE DISQRVAAEN QDKDGDQNLR DQIQHRIIGF LDNWPLLEQW FSEPENILIK INAEIDKESL CEKVKEILTT
       890        900        910        920        930        940        950        960
EIAKKKNKVE KKLEEKEAEK KAAASLAELP LPTPPPAPPP EPEKEKEIHQ SHVASKTPTA KGKPQSEAPH GKQESLQEGK
       970        980        990       1000       1010       1020       1030       1040
GKKGETALKR KGSPKGKSSG GKVPVKKSPA DSTDTSPVAI VPQPPKPGSE EWVYVNEPVP EEMPLFLVPY WELIENSYIN
      1050       1060       1070       1080       1090       1100       1110       1120
TIKTVLRHLR EDQHTVLAYL YEIRTSFQEF LKRPDHKQDF VAQWQADFNS LPDDLWDDEE TKAELHQRVN DLRDRLWDIC
      1130       1140       1150       1160       1170       1180       1190       1200
DARKEEAEQE RLDIINESWL QDTLGMTMNH FFSLMQAELN RFQDTKRLLQ DYYWGMESKI PVEDNKRFTR IPLVQLDSKD
      1210       1220       1230       1240       1250       1260       1270       1280
NSESQLRIPL VPRISISLET VTPKPKTKSV LKGKMDNSLE NVESNFEADE KLVMDTWQQA SLAVSHMVAA EIHQRLMEEE
      1290       1300       1310       1320       1330       1340       1350       1360
KENQPADPKE KSPQMGANKK VKKEPPKKKQ EDKKPKGKSP PMAEATPVIV TTEEIAEIKR KNELRVKIKE EHLAALQFEE
      1370       1380       1390       1400       1410       1420       1430       1440
IATQFRLELI KTKALALLED LVTKVVDVYK LMEKWLGERY LNEMASTEKL TDVARYHIET STKIQNELYL SQEDFFINGN
      1450       1460       1470       1480       1490       1500       1510       1520
IKVFPDPPPS IRPPPVEKEE DGTLTIEQLD SLRDQFLDMA PKECSENCFQ RPSPSTCDAF SNRRQEVASW ITGSPPELSQ
      1530       1540
GISCNCSATA LSRQRQK
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2952	1	973.5048	-25.95	2	66.1	10.6	2	2-17	M.SEILCQWLNKELKVSR.T		
1496	1	1006.5889	17.49	3	47.4	12.9	2	1200-1226	K. DNSESQLRIPLVPRISISLETVTPKP T		

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1569	1	480.6396	-230.14	2	48.1	14.6	1	1292-1300	K.SPQMGANKK.V		mdown:qdown 0.35

Detailed Protein Report

Protein 248: 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 249: 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 250: biorientation of chromosomes in cell division protein 1-like 1 [Homo sapiens]

Accession:	gi|87299628	**Score:**	38.0
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

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 251: PREDICTED: disks large homolog 5 isoform X3 [Homo sapiens]

Accession:	gi|578819987	**Score:**	38.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	176.9
Database Date:	2015-11-30	**pI:**	6.5
		Sequence Coverage [%]:	1.6
		No. of unique Peptides:	2

Quantitation

Wdown:Qdown	**Median:**	4.10	**CV:**	0.00 %	**No. of Peptides:**	1

Alias proteins:

Accession	Name	Description
gi|578839810	refseq_human (refseq_human_20140103.fasta)	PREDICTED: disks large homolog 5 isoform X3 [Homo sapiens]

10	20	30	40	50	60	70	80
MEPQRRELLA	QCQQSLAQAM	TEVEAVLGLL	EAAGALSPGE	RRQLDEEAGG	AKAELLLKLL	LAKERDHFQD	LRAALEKTQP
90	100	110	120	130	140	150	160
HLLPILYLNG	VVGPPQPAEG	AGSTYSVLST	MPSDSESSSS	LSSVGTTGKA	PSPPPLLTDQ	QVNEKVENLS	IQLRLMTRER
170	180	190	200	210	220	230	240
NELRKRLAFA	THGTAFDKRP	YHRLNPDYER	LKIQCVRAMS	DLQSLQNQHT	NALKRCEEVA	KETDFYHTLH	SRLLSDQTRL
250	260	270	280	290	300	310	320
KDDVDMLRRE	NGQLLRERNL	LQQSWEDMKR	LHEEDQKEIG	DLRAQQQQVL	KHNGSSEILN	KLYDTAMDKL	EVVKKDYDAL
330	340	350	360	370	380	390	400
RKRYSEKVAI	HNADLSRLEQ	LGEENQRLLK	QTEMLTQQRD	TAIQLQHQCA	LSLRRFEAIH	HELNKATAQN	KDLQWEMELL
410	420	430	440	450	460	470	480
QSELTELRTT	QVKTAKESEK	YREERDAVYS	EYKLIMSERD	QVISELDKLQ	TEVELAESKL	KSSTSEKKAA	NEEMEALRQI
490	500	510	520	530	540	550	560
KDTVTMDAGR	ANKEVEILRK	QCKALCQELK	EALQEADVAK	CRRDWAFQER	DKIVAERDSI	RTLCDNLRRE	RDRAVSELAE
570	580	590	600	610	620	630	640
ALRSLDDTRK	QKNDVSRELK	ELKEQMESQL	EKEARFRQLM	AHSSHDSAID	TDSMEWETEV	VEFERETEDI	DLKALGFDMA
650	660	670	680	690	700	710	720
EGVNEPCFPG	DCGIFVTKVD	KGSIADGRLR	VNDWLLRIND	VDLINKDKKQ	AIKALLNGEG	AINMVVRRRK	SLGGKVVTPL
730	740	750	760	770	780	790	800
HINLSGQKDS	GISLENGVYA	AAVLPGSPAA	KEGSLAVGDR	IVAINGIALD	NKSLNECESL	LRSCQDSLTL	SLLKEQKCVP
810	820	830	840	850	860	870	880
ASGELSPELQ	EWAPYSPGHS	SRHSNPPLYP	SRPSVGTVPR	SLTPSTTVSS	ILRNPIYTVR	SHRVGPCSSP	PAARDAGPQG
890	900	910	920	930	940	950	960
LHPSVQHQGR	LSLDLSHRTC	SDYSEMRATH	GSNSLPSSAR	LGSSSNLQFK	AERIKIPSTP	RYPRSVVGSE	RGSVSHSECS
970	980	990	1000	1010	1020	1030	1040
TPPQSPLNID	TLSSCSQSQT	SASTLPRIAV	NPASLGERRK	DRPYVEEPRH	VKVQKGSEPL	GISIVSGEKG	GIYVSKVTVG
1050	1060	1070	1080	1090	1100	1110	1120
SIAHQAGLEY	GDQLLEFNGI	NLRSATEQQA	RLIIGQQCDT	ITILAQYNPH	VHQLSSHSRS	SSHLDPAGTH	STLQGSGTTT
1130	1140	1150	1160	1170	1180	1190	1200
PEHPSVIDPL	MEQDEGPSTP	PAKQSSSRIA	GDANKKTLEP	RVVFIKKSQL	ELGVHLCGGN	LHGVFVAEVE	DDSPAKGPDG
1210	1220	1230	1240	1250	1260	1270	1280
LVPGDLILEY	GSLDVRNKTV	EEVYVEMLKP	RDGVRLKVQY	RPEEFTKAKG	LPGDSFYIRA	LYDRLADVEQ	ELSFKKDDIL
1290	1300	1310	1320	1330	1340	1350	1360
YVDDTLPQGT	FGSWMAWQLD	ENAQKIQRGQ	IPSKYVMDQE	FSRRLSMSEV	KDDNSATKTL	SAAARRSFFR	RKHKHKRSGS
1370	1380	1390	1400	1410	1420	1430	1440
KDGKDLLALD	AFSSDSIPLF	EDSVSLAYQR	VQKVDCTALR	PVLILGPLLD	VVKEMLVNEA	PGKFCRCPLE	VMKASQQAIE
1450	1460	1470	1480	1490	1500	1510	1520
RGVKDCLFVD	YKRRSGHFDV	TTVASIKEIT	EKNRHCLLDI	APHAIERLHH	MHIYPIVIFI	HYKSAKHIKE	QRDPIYLRDK
1530	1540	1550	1560	1570	1580		
VTQRHSKEQF	EAAQKLEQEY	SRYFTGVIQG	GALSSICTQI	LAMVNQEQNK	VLWIPACPL		

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2115	1	916.8144	-155.80	2	55.0	10.3	2	257-270	R.ERNLLQQSWEDMKR.L		Wdown:Qdown 4.10
1673	1	662.2991	-86.48	2	49.4	14.9	1	1248-1259	K.AKGLPGDSFYIR.A		

Detailed Protein Report

Protein 252: PREDICTED: cyclin-dependent kinase-like 1 isoform X1 [Homo sapiens]

Accession: gi|530404810
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 37.9
MW [kDa]: 108.9
pI: 9.8
Sequence Coverage [%]: 3.9
No. of unique Peptides: 1

Quantitation

mdown:qdown	**Median:**	0.56	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.15	**CV:**	0.00 %	**No. of Peptides:**	1

10	20	30	40	50	60	70	80
MELSTDTGWN	QKSNFPPCDS	RVSKEEAQLP	FPTPSSYGAD	SSNQTYAHKS	QSEREQHKEV	RAVLNHCSGL	DGGEESGLCG
90	100	110	120	130	140	150	160
TSTRIDAGTG	NGTDDKVTDQ	HRHRRCLQGT	KGNNRGSEVW	GLLLQGNVDR	SGGAPSAGVL	LRRRGYSCAL	HGLRKFANLA
170	180	190	200	210	220	230	240
GLLSRQQDSA	RGVSHHSRLK	IHFKKIYSSM	MEKYEKIGKI	GEGSYGVVFK	CRNRDTGQIV	AIKKFLESED	DPVIKKIALR
250	260	270	280	290	300	310	320
EIRMLKAPSP	YAAEPSLCGM	KMVRRGKKEF	LPAVAEKVDA	PSGVGGQGQD	SVTVGSLGRR	STYGRKQEKQ	VRQREGIIYC
330	340	350	360	370	380	390	400
YVAVLLRIYY	FDQGCVAREE	EQFQELVFGP	FCHIGSYFTG	HRTNVRPYIL	LLSRPSPFKT	AAGTYEAGLV	ILECSYFLAE
410	420	430	440	450	460	470	480
QEPYCPTQAL	QQPHPIIGPW	ALEGGGVESK	EDRHPPPKEA	PASCEGFLRS	AVPKQAYTPF	KTSPDKRLSD	CVATPPWAPP
490	500	510	520	530	540	550	560
TPLIISSGVL	VAICSMIDPV	PEFHSEGLLA	KATSGSAGIL	VWIFLCNDAF	IYGKYILRSG	VLWVRGLPGF	KSEAAALCHK
570	580	590	600	610	620	630	640
CYSSADPKRE	QQQDLLQRVK	EQSFHSVNGA	QARHKGSPSP	HQTQEPSWPH	PVDPTPGHRW	SCLPVPCRAP	ALLSPWVVDG
650	660	670	680	690	700	710	720
TGCCGAGGGS	DRGGSAAQEP	TQLKHPNLVN	LLEVFRRKRR	LHLVFEYCDH	TVLHELDRYQ	RGICNIFVCT	GRRLGEHTEA
730	740	750	760	770	780	790	800
LSKKKKKGGG	GPFLKLRAAS	CRITLFKNVG	CGLETTGDLS	LNSGGGAASR	GVAAALRALV	CGTELTSSDS	PQRCIHRDVK
810	820	830	840	850	860	870	880
PENILITKHS	VIKLCDFGFA	RLLTGPSDYY	TDYVATRWYR	SPELLVGDTQ	YGPPVDVWAI	GCVFAELLSG	VPLWPGKSDV
890	900	910	920	930	940	950	960
DQLYLIRKTL	GDLIPRHQQV	FSTNQYFSGV	KIPDPEDMSL	CLSVTLTEGG	LLASGAVKRS	QMGSSVSQAT	SWPHPDIVAE
970	980	990	1000				
TAELDDIAMA	RQTPVMLRFN	RQKEQEKYLS	YGA				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
317	1	442.6411	-276.80	2	33.0	10.9	0	889-896	K.TLGDLIPR.H		Wdown:Qdown 0.15 mdown:qdown 0.56

Detailed Protein Report

Protein 253: **neuropeptides B/W receptor type 1 [Homo sapiens]**

Accession:	gi|53828924	**Score:**	37.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	36.1
Database Date:	2015-11-30	**pI:**	10.1
		Sequence Coverage [%]:	7.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDNASFSEPW	PANASGPDPA	LSCSNASTLA	PLPAPLAVAV	PVVYAVICAV	GLAGNSAVLY	VLLRAPRMKT	VTNLFILNLA
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
IADELFTLVL	PINIADFLLR	QWPFGELMCK	LIVAIDQYNT	FSSLYFLTVM	SADRYLVVLA	TAESRRVAGR	TYSAARAVSL
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
AVWGIVTLVV	LPFAVFARLD	DEQGRRQCVL	VFPQPEAFWW	RASRLYTLVL	GFAIPVSTIC	VLYTTLLCRL	HAMRLDSHAK
250	**260**	**270**	**280**	**290**	**300**	**310**	**320**
ALERAKKRVT	FLVVAILAVC	LLCWTPYHLS	TVVALTTDLP	QTPLVIAISY	FITSLSYANS	CLNPFLYAFL	DASFRRNLRQ
330							
LITCRAAA							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
408	1	604.3472	17.95	2	34.1	23.5	2	146-156	R.RVAGRTYSAAR.A	

Detailed Protein Report

Protein 254: histone H4 [Homo sapiens]

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

Score: 37.9
MW [kDa]: 11.4
pI: 11.8
Sequence Coverage [%]: 7.8
No. of unique 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
1347	10	495.2734	-38.66	2	45.6	37.9	0	61-68	K.VFLENVIR.D	

Detailed Protein Report

Protein 255: PREDICTED: centlein isoform X1 [Homo sapiens]

Accession:	gi|530389965	**Score:**	37.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	162.0
Database Date:	2015-11-30	**pI:**	8.8
		Sequence Coverage [%]:	2.6
		No. of unique Peptides:	3

Quantitation

mdown:qdown	**Median:**	1.15	**CV:**	55.25 %	**No. of Peptides:**	2
Wdown:Qdown	**Median:**	2.15	**CV:**	86.23 %	**No. of Peptides:**	2

10	20	30	40	50	60	70	80
MAARSPPSPH	PSPPARQLGP	RSPRVGRGAE	VHAMRSEASG	FAGAAREVVA	DESDKIWVGE	EGSGGRRGPG	GAAPAHAPLL
90	100	110	120	130	140	150	160
SAPMGSRRLE	GISVEEAMVT	RTQLLEEELS	SLKEELALCQ	ADKEFVWSLW	KRLQVTNPDL	TQVVSLVVER	EKQKSEAKDR
170	180	190	200	210	220	230	240
KVLEILQVKD	AKIQEFEQRE	SVLKQEINDL	VKRKIAVDEE	NAFLRKEFSD	LEKKFKDKSQ	EIKDTKECVQ	NKEEQNRLVI
250	260	270	280	290	300	310	320
KNLEEENKKL	STRCTDLLND	LEKLRKQEAH	LRKEKYSTDA	KIKTFEDNLI	EARKEVEVSQ	SKYNALSLQL	SNKQTELIQK
330	340	350	360	370	380	390	400
DMDITLVRKE	LQELQNLYKQ	NSTHTAQQAE	LIQQLQVLNM	DTQKVLRNQE	DVHTAESISY	QKLYNELHIC	FETTKSNEAM
410	420	430	440	450	460	470	480
LRQSVTNLQD	QLLQKEQENA	KLKEKLQESQ	GAPLPLPQES	DPDYSAQVPH	RPSLSSLETL	MVSQKSEIEY	LQEKLKIANE
490	500	510	520	530	540	550	560
KLSENISANK	GFSRKSIMTS	AEGKHKEPPV	KRSRSLSPKS	SFTDSEELQK	LRKAERKIEN	LEKALQLKSQ	ENDELRDAHE
570	580	590	600	610	620	630	640
KRKERLQMLQ	TNYRAVKEQL	KQWEEGSGMT	EIRKIKRADP	QQLRQEDSDA	VWNELAYFKR	ENQELMIQKM	NLEEELDELK
650	660	670	680	690	700	710	720
VHISIDKAAI	QELNRCVAER	REEQLFRSGE	DDEVKRSTPE	KNGKEMLEQT	LQKVTELENR	LKSFEKRSRK	LKEGNKKLMK
730	740	750	760	770	780	790	800
ENDFLKSLLK	QQQEDTETRE	KELEQIIKGS	KDVEKENTEL	QVKISELETE	VTSLRRQVAE	ANALRNENEE	LINPMEKSHQ
810	820	830	840	850	860	870	880
SADRAKSEMA	TMKVRSGRYD	CKTTMTKVKF	KAAKKNCSVG	RHHTVLNHSI	KVMSNVFENL	SKDGWEDVSE	SSDSEAQTSQ
890	900	910	920	930	940	950	960
TLGTIIVETS	QKISPTEDGK	DQKESDPTED	SQTQGKEIVQ	TYLNIDGKTP	KDYFHDKNAK	KPTFQKKNCK	MQKSSHTAVP
970	980	990	1000	1010	1020	1030	1040
TRVNREKYKN	ITAQKSSSNI	ILLRERIISL	QQQNSVLQNA	KKTAELSVKE	YKEVNEKLLH	QQQVSDQRFQ	TSRQTIKKLN
1050	1060	1070	1080	1090	1100	1110	1120
LDLAGLRKEK	EDLLKKLESS	SEITSLAEEN	SQVTFPRIQV	TSLSPSRSMD	LEMKQLQYKL	KNATNELTKQ	SSNVKTLKFE
1130	1140	1150	1160	1170	1180	1190	1200
LLAKEEHIKE	MHEKISRMER	DITMKRHLIE	DLKFRQKVNL	ESNKSFSEML	QNLDKKVKTL	TEECSNKKVS	IDSLKQRLNV
1210	1220	1230	1240	1250	1260	1270	1280
AVKEKSQYEQ	MYQKSKEELE	KKDLKLTLLV	SRISETESAM	AEIETAASKQ	LQELALQSEQ	VLEGAQKTLL	LANEKVEEFT
1290	1300	1310	1320	1330	1340	1350	1360
TFVKALAKEL	QNDVHVVRRQ	IRELKKMKKN	RDACKTSTHK	AQTLAASILN	ISRSDLEEIL	DTEDQVEIEK	TKIDAENDKE
1370	1380	1390	1400	1410			
WMLYIQKLLE	GQLPFASYLL	EAVLEKINEK	KKLVEGYFTI	MKDIR			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
255	1	795.3881	-39.33	2	32.4	10.8	1	88-101	R.RLEGISVEEAMVTR.T		Wdown:Qdown 1.02 mdown:qdown 0.69
1953	1	643.3047	-169.45	1	54.5	11.9	0	1198-1203	R.LNVAVK.E		mdown:qdown 1.93 Wdown:Qdown 4.53
2736	1	683.3656	57.65	3	65.5	15.2	2	1206-1221	K.SQYEQMYQKSKEELEK.K		

Detailed Protein Report

Protein 256: PREDICTED: dedicator of cytokinesis protein 6 isoform X3 [Homo sapiens]

Accession:	gi|578833402	**Score:**	37.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	232.6
Database Date:	2015-11-30	**pI:**	6.3
		Sequence Coverage [%]:	1.4
		No. of unique Peptides:	2

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	RILASKAIDC	NSSRASSYLE	GSSSAPPATQ	LRPTVQKLLH	EELALQWVVS	SSAVREAILQ
970	980	990	1000	1010	1020	1030	1040
HAWFFFQLMV	KSMALHLLLG	QRLDTPRKLR	FPGRFLDDIT	ALVGSVGLEV	ITRVHKDVEL	AEHLNASLAF	FLSDLLSLVD
1050	1060	1070	1080	1090	1100	1110	1120
RGFVFSLVRA	HYKQVATRLQ	SSPNPAALLT	LRMEFTRILC	SHEHYVTLNL	PCCPLSPPAS	PSPSVSSTTS	QSSTFSSQAP
1130	1140	1150	1160	1170	1180	1190	1200
DPKVTSMFEL	SGPFRQQHFL	AGLLLTELAL	ALEPEAEGAF	LLHKKAISAV	HSLLCGHDTD	PRYAEATVKA	RVAELYLPLL
1210	1220	1230	1240	1250	1260	1270	1280
SIARDTLPRL	HDFAEGPGQR	SRLASMLDSD	TEGEGDIAGT	INPSVAMAIA	GGPLAPGSRA	SISQGPPTAS	RAGCALSAES
1290	1300	1310	1320	1330	1340	1350	1360
SRTLLACVLW	VLKNTEPALL	QRWATDLTLP	QLGRLLDLLY	LCLAAFEYKG	KKAFERINSL	TFKKSLDMKA	RLEEAILGTI
1370	1380	1390	1400	1410	1420	1430	1440
GARQEMVRRS	RERSPFGNPE	NVRWRKSVTH	WKQTSDRVDK	TKDEMEHEAL	VEGNLATEAS	LVVLDTLEII	VQTVMLSEAR
1450	1460	1470	1480	1490	1500	1510	1520
ESVLGAVLKV	VLYSLGSAQS	ALFLQHGLAT	QRALVSKFPE	LLFEEDTELC	ADLCLRLLRH	CGSRISTIRT	HASASLYLLM
1530	1540	1550	1560	1570	1580	1590	1600
RQNFEIGHNF	ARVKMQVTMS	LSSLVGTTQN	FSEEHLRRSL	KTILTYAEED	MGLRDSTFAE	QVQDLMFNLH	MILTDTVKMK
1610	1620	1630	1640	1650	1660	1670	1680
EHQEDPEMLI	DLMYRIARGY	QGSPDLRLTW	LQNMAGKHAE	LGNHAEAAQC	MVHAAALVAE	YLALLEDHRH	LPVGCVSFQN
1690	1700	1710	1720	1730	1740	1750	1760
ISSNVLEESA	ISDDILSPDE	EGFCSGKHFT	ELGLVGLLEQ	AAGYFTMGGL	YEAVNEVYKN	LIPILEAHRD	YKKLAAVHGK
1770	1780	1790	1800	1810	1820	1830	1840
LQEAFTKIMH	QSSGWERVFG	TYFRVGFYGA	HFGDLDEQEF	VYKEPSITKL	AEISHRLEEF	YTERFGDDVV	EIIKDSNPVD
1850	1860	1870	1880	1890	1900	1910	1920
KSKLDSQKAY	IQITYVEPYF	DTYELKDRVT	YFDRNYGLRT	FLFCTPFTPD	GRAHGELPEQ	HKRKTLLSTD	HAFPYIKTRI
1930	1940	1950	1960	1970	1980	1990	2000
RVCHREETVL	TPVEVAIEDM	QKKTRELAFA	TEQDPPDAKM	LQMVLQGSVG	PTVNQGPLEV	AQVFLAEIPE	DPKLFRHHNK
2010	2020	2030	2040	2050	2060	2070	2080
LRLCFKDFCK	KCEDALRKNK	ALIGPDQKEY	HRELERNYCR	LREALQPLLT	QRLPQLMAPT	PPGLRNSLNR	ASFRKADL

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
1750	1	628.2499	-105.50	2	51.8	11.8	2	28-38	R.ERSGSPHSSRR.C	
2956	1	753.3925	-14.65	2	66.1	10.4	0	1905-1917	K.TLLSTDHAFPYIK.T	

Detailed Protein Report

Protein 257: PREDICTED: utrophin isoform X8 [Homo sapiens]

Accession:	gi|578812959	**Score:**	37.8
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 258: zinc finger CCCH domain-containing protein 13 [Homo sapiens]

Accession: gi|116008442
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 37.8
MW [kDa]: 184.8
pI: 10.0
Sequence Coverage [%]: 1.9
No. of unique Peptides: 2

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
1864	1	606.2622	-6.93	2	53.3	12.3	2	475-483	R.DMRDSREMR.D	Oxidation: 8
1287	1	795.9839	117.71	2	45.8	13.8	2	528-540	R.SYGRNHLREESSR.T	

Detailed Protein Report

Protein 259: **PREDICTED: 1-acyl-sn-glycerol-3-phosphate acyltransferase gamma isoform X1 [Homo sapiens]**

Accession: gi|530419317
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl, Oxidation

Score: 37.7
MW [kDa]: 52.2
pI: 9.9
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 260: **PREDICTED: WD repeat-containing protein 88 isoform X1 [Homo sapiens]**

Accession:	gi|578833944	**Score:**	37.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	31.0
Database Date:	2015-11-30	**pI:**	6.8
		Sequence Coverage [%]:	9.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MASPPRCSPT	AHDRECKLPP	PSAPASEYCP	GKLSWGTMAR	ALGRFKLSIP	HTHLLATLDP	LALDREPPPH	LLPEKHQVPE
90	100	110	120	130	140	150	160
KLIWGDQDPL	SKIPFKILSG	HEHAVSTCHF	CVDDTKLLSG	SYDCTVKLWD	PVDGSVVRDF	EHRPKAPVVE	CSITGDSSRV
170	180	190	200	210	220	230	240
IAASYDKTVR	AWDLETGKLL	WKVRYDTFIV	SCKFSPDGKY	VVSGFDVDHG	ICIMDAENIT	TVSVIKDHHT	RSITSCCFDP
250	260	270	280				
DSQRVASVSL	DRCIKIWDVT	SQATLLTITK	LFSHFWRV				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2091	1	757.2566	-151.54	2	54.7	16.0	0	18-32	K.LPPPSAPASEYCPGK.L	

Detailed Protein Report

Protein 261: TPR and ankyrin repeat-containing protein 1 [Homo sapiens]

Accession:	gi|257467636	**Score:**	37.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	336.0
Database Date:	2015-11-30	**pI:**	6.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.6
		No. of unique Peptides:	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MWDPRAARVP	PRDLAVLLCN	KSNAFFSLGK	WNEAFVAAKE	CLQWDPTYVK	GYYRAGYSLL	RLHQPYEAAR	MFFEGLRLVQ
90	100	110	120	130	140	150	160
RSQDQAPVAD	FLVGVFTTMS	SDSIVLQSFL	PCFDHIFTTG	FPTEVWQSVI	EKLAKKGLWH	SFLLLSAKKD	RLPRNIHVPE
170	180	190	200	210	220	230	240
LSLKSLFEKY	VFIGLYEKME	QVPKLVQWLI	SIGASVETIG	PYPLHALMRL	CIQARENHLF	RWLMDHKPEW	KGRINQKDGD
250	260	270	280	290	300	310	320
GCTVLHVVAA	HSPGYLVKRQ	TEDVQMLLRF	GADPTLLDRQ	SRSVVDVLKR	NKNFKAIEKI	NSHLEKLATC	SKDLSGFSNG
330	340	350	360	370	380	390	400
DGPTSENDIF	RKVLEQLVKY	MNSGNRLLHK	NFLKQEVVQR	FLRLLSTLQE	IPPDLVCDIN	QDCATTVFKF	LLEKQRWPEV
410	420	430	440	450	460	470	480
LLLLTRKVSG	EPPLGDCLIK	DCNFSDLDIC	TIIPHLSTWD	QRKKQLLGCL	IDSGALPDGL	QESQERPVVT	CLKHEDFELA
490	500	510	520	530	540	550	560
FLLLTKGADP	RAISLTEGDT	PLHAALHIFL	EIKADIGFSF	LSHLLDLFWS	NPTEFDYLNP	NVQDSNGNTL	MHILFQKGML
570	580	590	600	610	620	630	640
KRVKKLLDLL	VKFDINFNLK	NKEGKDARHR	IKKNDSLLLA	WNKALMENRR	RSRQDSAAHL	GKLSKSTAPG	HTSQLKSQGS
650	660	670	680	690	700	710	720
FKSVPCGATA	RTLPEGSAVP	DSWETLPGTQ	VTRKEPGALR	PCSLRDCLMQ	DITVLIQQVE	VDPSFPEDCL	QSSEPLEAGA
730	740	750	760	770	780	790	800
GKEGKKDDKP	TLGAGAPDCS	EVGEGHAQVG	LGALQLVPDD	NRGKEGNDDQ	DDWSTQEIEA	CLQDFDNMTW	EIECTSEMLK
810	820	830	840	850	860	870	880
KLSSKVMTKV	IKKKIILAIQ	QLGNGEWTQG	LQKRLKHLKG	SIQLFEAKLD	KGARMLWELA	IDFSPRCSEN	PEKIIATEQN
890	900	910	920	930	940	950	960
TCAMEKSGRI	YTEIIRIWDI	VLDHCKLADS	IKAICNAYNR	GLSCVLRKKL	KGINKGQVSA	NMKIQKRIPR	CYVEDTEAEK
970	980	990	1000	1010	1020	1030	1040
GREHVNPEYF	PPASAVETEY	NIMKFHSFST	NMAFNILNDT	TATVEYPFRV	GELEYAVIDL	NPRPLEPIIL	IGRSGTGKTT
1050	1060	1070	1080	1090	1100	1110	1120
CCLYRLWKKF	HVYWEKAEQA	GSPLLAKQVW	LKRRLEVEPG	KESPGGEEEE	EEEDEEEEDS	IEVETVESID	EQEYEACAGG
1130	1140	1150	1160	1170	1180	1190	1200
AGVEPAGDGQ	AAEVCAPEHP	HQLEHLHQIF	VTKNHVLCQE	VQRNFIELSK	STKATSHYKP	LDPNIHKLQD	LRDENFPLFV
1210	1220	1230	1240	1250	1260	1270	1280
TSKQLLLLLD	ASLPKPFFLR	NEDGSLKRTI	IGWSAQEEST	IPSWQEDEEE	AEVDGDYSEE	DKAVEMRTGD	SDPRVYVTFE
1290	1300	1310	1320	1330	1340	1350	1360
VFKNEIWPKM	TKGRTAYNPA	LIWKEIKSFL	KGSFEALSCP	HGRLTEEVYK	KLGRKRCPNF	KEDRSEIYSL	FSLYQQIRSQ
1370	1380	1390	1400	1410	1420	1430	1440
KGYFDEEDVL	YNISRRLSKL	RVLPWSIHEL	YGDEIQDFTQ	AELALLMKCI	NDPNSMFLTG	DTAQSIMKGV	AFRFSDLRSL
1450	1460	1470	1480	1490	1500	1510	1520
FHYASRNTID	KQCAVRKPKK	IHQLYQNYRS	HSGILNLASG	VVDLLQFYFP	ESFDRLPRDS	GLFDGPKPTV	LESCSVSDLA
1530	1540	1550	1560	1570	1580	1590	1600
ILLRGNKRKT	QPIEFGAHQV	ILVANETAKE	KIPEELGLAL	VLTIYEAKGL	EFDDVLLYNF	FTDSEAYKEW	KIISSFTPTS
1610	1620	1630	1640	1650	1660	1670	1680
TDSREENRPL	VEVPLDKPGS	SQGRSLMVNP	EMYKLLNGEL	KQLYTAITRA	RVNLWIFDEN	REKRAPAFKY	FIRRDFVQVV
1690	1700	1710	1720	1730	1740	1750	1760
KTDENKDFDD	SMFVKTSTPA	EWIAQGDYYA	KHQCWKVAAK	CYQKGGAFEK	EKLALAHDTA	LSMKSKKVSP	KEKQLEYLEL
1770	1780	1790	1800	1810	1820	1830	1840
AKTYLECKEP	TLSLKCLSYA	KEFQLSAQLC	ERLGKIRDAA	YFYKRSQCYK	DAFRCFEQIQ	EFDLALKMYC	QEELFEEAAI
1850	1860	1870	1880	1890	1900	1910	1920
AVEKYEEMLK	TKTLPISKLS	YSASQFYLEA	AAKYLSANKM	KEMMAVLSKL	DIEDQLVFLK	SRKRLAEAAD	LLNREGRREE
1930	1940	1950	1960	1970	1980	1990	2000
AALLMKQHGC	LLEAARLTAD	KDFQASCLLG	AARLNVARDS	DIEHTKDILR	EALDICYQTG	QLSGIAEAHF	LQGVILRDFQ
2010	2020	2030	2040	2050	2060	2070	2080
KLRDAFFKFD	TLNHSAGVVE	ALYEAASQCE	AEPEKILGLA	PGGLEILLSL	VRALKRVTNN	AEKEMVKSCF	EFFGISQVDA
2090	2100	2110	2120	2130	2140	2150	2160
KYCQIAQNDP	GPILRIIFDL	DLNLREKKTK	DHFLIMTDQV	KLALNKHLLG	RLCQITRSLL	GKTYRGVCMR	FIVGLKCEDE
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
770	1	573.6008	-82.93	3	39.0	12.7	2	2682-2695	R.ACLVVSLCISWRRR.V	Carbamidomethyl: 8

Detailed Protein Report

Protein 262: rapamycin-insensitive companion of mTOR isoform 3 [Homo sapiens]

Accession:	gi|550544215	**Score:**	37.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	155.8
Database Date:	2015-11-30	**pI:**	6.8
		Sequence Coverage [%]:	1.8
		No. of unique Peptides:	1

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2622	1	658.3808	-6.32	2	61.5	16.9	2	182-193	R.LRASAALNCLKR.F	

Detailed Protein Report

Protein 263:	**PREDICTED: receptor-type tyrosine-protein phosphatase delta isoform X16 [Homo sapiens]**		
Accession:	gi|578816637	**Score:**	37.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	211.2
Database Date:	2015-11-30	**pI:**	6.2
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.0
		No. of unique Peptides:	2

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
1854	2	1074.5548	-28.36	2	51.8	13.8	2	1040-1060	R.GNSAGGLQHRVTAKTAPDVLR.T	

Detailed Protein Report

Protein 264: 14-3-3 protein zeta/delta [Homo sapiens]

Accession:	gi|4507953	**Score:**	37.3
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:	1

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
2523	1	709.8534	-14.08	2	62.0	10.3	0	92-103	R.DICNDVLSLLEK.F	Carbamidomethyl: 3

Detailed Protein Report

Protein 265: PREDICTED: serine/threonine-protein phosphatase 4 regulatory subunit 4 isoform X1 [Homo sapiens]

Accession:	gi|530404339	**Score:**	37.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	87.3
Database Date:	2015-11-30	**pI:**	9.4
		Sequence Coverage [%]:	7.0
		No. of unique Peptides:	2

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	
2420	1	701.3590	-21.14	3	58.6	13.0	0	498-515	K.YFFLPAIELTHDPVANVR.M	

Detailed Protein Report

Protein 266: **E3 ubiquitin-protein ligase RNF213 isoform 3 [Homo sapiens]**

Accession:	gi|366039979	**Score:**	37.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	591.0
Database Date:	2015-11-30	**pI:**	6.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	0.7
		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	EAVSSACQSQ	TSILQGFSYS	DLRKFGIVLS	AVITKSWPRT
1050	1060	1070	1080	1090	1100	1110	1120
ADNFNDILKH	LLTLADVKHV	FRLCGTDEKI	LANVTEDAKR	LIAVADSVLT	KVVGDLLSGT	ILVGQLELII	KHKNQFLDIW
1130	1140	1150	1160	1170	1180	1190	1200
QLREKSLSPQ	DEQCAVEEAL	DWRREELLLL	KKEKRCVDSL	LKMCGNVKHL	IQVDFGVLAV	RHSQDLSSKR	LNDTVTVRLS
1210	1220	1230	1240	1250	1260	1270	1280
TSSNSQRATH	YHLSSQVQEM	AGKIDLLRDS	HIFQLFWREA	AEPLSEPKED	QEAAELLSEP	EEESERHILE	LEEVYDYLYQ
1290	1300	1310	1320	1330	1340	1350	1360
PSYRKFIKLH	QDLKSGEVTL	AEIDVIFKDF	VNKYTDLDSE	LKIMCTVDHQ	DQRDWIKDRV	EQIKEYHHLH	QAVHAAKVIL
1370	1380	1390	1400	1410	1420	1430	1440
QVKESLGLNG	DFSVLNTLLN	FTDNFDDFRR	ETLDQINQEL	IQAKKLLQDI	SEARCKGLQA	LSLRKEFICW	VREALGGINE
1450	1460	1470	1480	1490	1500	1510	1520
LKVFVDLASI	SAGENDIDVD	RVACFHDAVQ	GYASLLFKLD	PSVDFSAFMK	HLKKLWKALD	KDQYLPRKLC	DSARNLEWLK
1530	1540	1550	1560	1570	1580	1590	1600
TVNESHGSVE	RSSLTLATAI	NQRGIYVIQA	PKGGQKISPD	TVLHLILPES	PGSHEESREY	SLEEVKELLN	KLMLMSGKKD
1610	1620	1630	1640	1650	1660	1670	1680
RNNTEVERFS	EVFCSVQRLS	QAFIDLHSAG	NMLFRTWIAM	AYCSPKQGVS	LQMDFGLDLV	TELKEGGDVT	ELLAALCRQM
1690	1700	1710	1720	1730	1740	1750	1760
EHFLDSWKRF	VTQKRMEHFY	LNFYTAEQLV	YLSTELRKQP	PSDAALTMLS	FIKSNCTLRD	VLRASVGCGS	EAARYRMRRV
1770	1780	1790	1800	1810	1820	1830	1840
MEELPLMLLS	EFSLVDKLRI	IMEQSMRCLP	AFLPDCLDLE	TLGHCLAHLA	GMGGSPVERC	LPRGLQVGQP	NLVVCGHSEV
1850	1860	1870	1880	1890	1900	1910	1920
LPAALAVYMQ	TPSQPLPTYD	EVLLCTPATT	FEEVALLLRR	CLTLGSLGHK	VYSLLFADQL	SYEVARQAEE	LFHNLCTQQH
1930	1940	1950	1960	1970	1980	1990	2000
REDYQLVMVC	DGDWEHCYLP	SAFSQHKVFV	TPQAPLEAIQ	AYLAGHYRVP	KQTLSAAAVF	NDRLCVGIVA	SERAGVGKSL
2010	2020	2030	2040	2050	2060	2070	2080
YVKRLHDKMK	MQLNVKNVPL	KTIRLIDPQV	DESRVLGALL	PFLDAQYQKV	PVLFHLDVTS	SVQTGIWVFL	FKLLILQYLM
2090	2100	2110	2120	2130	2140	2150	2160
DINGKMWLRN	PCHLYIVEIL	ERRTSVPSRS	SSALRTRVPQ	FSFLDIFPKV	TCRPPKEVID	MELSALRSDT	EPGMDLWEFC
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2481	1	856.9085	-24.89	2	61.4	13.6	1	4661-4674	R.LLNFDTELSTKEMR.N	Oxidation: 13

Detailed Protein Report

Protein 267: condensin complex subunit 1 [Homo sapiens]

Accession: gi|178056552
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 37.1
MW [kDa]: 157.1
pI: 6.2
Sequence Coverage [%]: 3.7
No. of unique Peptides: 2

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	
1660	1	927.4336	-29.14	3	49.5	11.3	2	286-310	K.CPQELSRDPSGTKGFAAFLTELAER.V	Carbamidomethyl: 1

Detailed Protein Report

Protein 268: zinc finger protein castor homolog 1 isoform a [Homo sapiens]

Accession:	gi|119709834	**Score:**	37.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	189.9
Database Date:	2015-11-30	**pI:**	6.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.4
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578799307	refseq_human (refseq_human_20140103.fasta)	PREDICTED: zinc finger protein castor homolog 1 isoform X2 [Homo sapiens]

Detailed Protein Report

10	20	30	40	50	60	70	80
MDLGTAEGTR	CTDPPAGKPA	MAPKRKGGLK	LNAICAKLSR	QVVVEKRADA	GSHTEGSPSQ	PRDQERSGPE	SGAARAPRSE
90	100	110	120	130	140	150	160
EDKRRAVIEK	WVNGEYSEEP	APTPVLGRIA	REGLELPPEG	VYMVQPQGCS	DEEDHAEEPS	KDGGALEEKD	SDGAASKEDS
170	180	190	200	210	220	230	240
GPSTRQASGE	ASSLRDYAAS	TMTEFLGMFG	YDDQNTRDEL	ARKISFEKLH	AGSTPEAATS	SMLPTSEDTL	SKRARFSKYE
250	260	270	280	290	300	310	320
EYIRKLKAGE	QLSWPAPSTK	TEERVGKEVV	GTLPGLRLPS	STAHLETKAT	ILPLPSHSSV	QMQNLVARAS	KYDFFIQKLK
330	340	350	360	370	380	390	400
TGENLRPQNG	STYKKPSKYD	LENVKYLHLF	KPGEGSPDMG	GAIAFKTGKV	GRPSKYDVRG	IQKPGPAKVP	PTPSLAPAPL
410	420	430	440	450	460	470	480
ASVPSAPSAP	GPGPEPPASL	SFNTPEYLKS	TFSKTDSITT	GTVSTVKNGL	PTDKPAVTED	VNIYQKYIAR	FSGSQHCGHI
490	500	510	520	530	540	550	560
HCAYQYREHY	HCLDPECNYQ	RFTSKQDVIR	HYNMHKKRDN	SLQHGFMRFS	PLDDCSVYYH	GCHLNGKSTH	YHCMQVGCNK
570	580	590	600	610	620	630	640
VYTSTSDVMT	HENFHKKNTQ	LINDGFQRFR	ATEDCGTADC	QFYGQKTTHF	HCRRPGCTFT	FKNKCDIEKH	KSYHIKDDAY
650	660	670	680	690	700	710	720
AKDGFKKFYK	YEECKYEGCV	YSKATNHFHC	IRAGCGFTFT	STSQMTSHKR	KHERRHIRSS	GALGLPPSLL	GAKDTEHEES
730	740	750	760	770	780	790	800
SNDDLVDFSA	LSSKNSSLSA	SPTSQQSSAS	LAAATAATEA	GPSATKPPNS	KISGLLPQGL	PGSIPLALAL	SNSGLPTPTP
810	820	830	840	850	860	870	880
YFPILAGRGS	TSLPVGTPSL	LGAVSSGSAA	SATPDTPTLV	ASGAGDSAPV	AAASVPAPPA	SIMERISASK	GLISPMMARL
890	900	910	920	930	940	950	960
AAAALKPSAT	FDPGSGQQVT	PARFPPAQVK	PEPGESTGAP	GPHEASQDRS	LDLTVKEPSN	ESNGHAVPAN	SSLLSSLMNK
970	980	990	1000	1010	1020	1030	1040
MSQGNPGLGS	LLNIKAEAEG	SPAAEPSPFL	GKAVKALVQE	KLAEPWKVYL	RRFGTKDFCD	GQCDFLHKAH	FHCVVEECGA
1050	1060	1070	1080	1090	1100	1110	1120
LFSTLDGAIK	HANFHFRTEG	GAAKGNTEAA	FPASAAETKP	PMAPSSPPVP	PVTTATVSSL	EGPAPSPASV	PSTPTLLAWK
1130	1140	1150	1160	1170	1180	1190	1200
QLASTIPQMP	QIPASVPHLP	ASPLATTSLE	NAKPQVKPGF	LQFQENDPCL	ATDCKYANKF	HFHCLFGNCK	YVCKTSGKAE
1210	1220	1230	1240	1250	1260	1270	1280
SHCLDHINPN	NNLVNVRDQF	AYYSLQCLCP	NQHCEFRMRG	HYHCLRTGCY	FVTNITTKLP	WHIKKHEKAE	RRAANGFKYF
1290	1300	1310	1320	1330	1340	1350	1360
TKREECGRLG	CKYNQVNSHF	HCIREGCQFS	FLLKHQMTSH	ARKHMRRMLG	KNFDRVPPSQ	GPPGLMDAET	DECMDYTGCS
1370	1380	1390	1400	1410	1420	1430	1440
PGAMSSESST	MDRSCSSTPV	GNESTAAGNT	ISMPTASGAK	KRFWIIEDMS	PFGKRRKTAS	SRKMLDEGMM	LEGFRRFDLY
1450	1460	1470	1480	1490	1500	1510	1520
EDCKDAACQF	SLKVTHYHCT	RENCGYKFCG	RTHMYKHAQH	HDRVDNLVLD	DFKRFKASLS	CHFADCPFSG	TSTHFHCLRC
1530	1540	1550	1560	1570	1580	1590	1600
RFRCTDSTKV	TAHRKHHGKQ	DVISAAGFCQ	FSSSADCAVP	DCKYKLKCSH	FHCTFPGCRH	TVVGMSQMDS	HKRKHEKQER
1610	1620	1630	1640	1650	1660	1670	1680
GEPAAEGPAP	GPPISLDGSL	SLGAEPGSLL	FLQSAAAGLG	LALGDAGDPG	PPDAAAPGPR	EGAAAAAAAA	GESSQEDEEE
1690	1700	1710	1720	1730	1740	1750	1760
ELELPEEEAE	DDEDEDDDED	DDDEDDDEDD	DDEDLRTDSE	ESLPEAAAEA	AGAGARTPAL	AALAALGAPG	PAPTAASSP

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2568	2	673.3695	74.26	2	62.6	11.8	2	1279-1288	K.YFTKREECGR.L	Carbamidomethyl: 8

Detailed Protein Report

Protein 269: protein kinase C delta type [Homo sapiens]

Accession: gi|31377782

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Modification(s): Oxidation

Score: 36.8

MW [kDa]: 77.5

pI: 8.9

Sequence Coverage [%]: 6.4

No. of unique Peptides: 2

Alias proteins:

Accession	Name	Description
gi|578806373	refseq_human (refseq_human_20140103.fasta)	PREDICTED: protein kinase C delta type isoform X3 [Homo sapiens]
gi|578806371	refseq_human (refseq_human_20140103.fasta)	PREDICTED: protein kinase C delta type isoform X2 [Homo sapiens]
gi|47157325	refseq_human (refseq_human_20140103.fasta)	protein kinase C delta type [Homo sapiens]

10	20	30	40	50	60	70	80
MAPFLRIAFN	SYELGSLQAE	DEANQPFCAV	KMKEALSTER	GKTLVQKKPT	MYPEWKSTFD	AHIYEGRVIQ	IVLMRAAEEP
90	100	110	120	130	140	150	160
VSEVTVGVSV	LAERCKKNNG	KAEFWLDLQP	QAKVLMSVQY	FLEDVDCKQS	MRSEDEAKFP	TMNRRGAIKQ	AKIHYIKNHE
170	180	190	200	210	220	230	240
FIATFFGQPT	FCSVCKDFVW	GLNKQGYKCR	QCNAAIHKKC	IDKIIGRCTG	TAANSRDTIF	QKERFNIDMP	HRFKVHNYMS
250	260	270	280	290	300	310	320
PTFCDHCGSL	LWGLVKQGLK	CEDCGMNVHH	KCREKVANLC	GINQKLLAEA	LNQVTQRASR	RSDSASSEPV	GIYQGFEKKT
330	340	350	360	370	380	390	400
GVAGEDMQDN	SGTYGKIWEG	SSKCNINNFI	FHKVLGKGSF	GKVLLGELKG	RGEYFAIKAL	KKDVVLIDDD	VECTMVEKRV
410	420	430	440	450	460	470	480
LTLAAENPFL	THLICTFQTK	DHLFFVMEFL	NGGDLMYHIQ	DKGRFELYRA	TFYAAEIMCG	LQFLHSKGII	YRDLKLDNVL
490	500	510	520	530	540	550	560
LDRDGHIKIA	DFGMCKENIF	GESRASTFCG	TPDYIAPEIL	QGLKYTFSVD	WWSFGVLLYE	MLIGQSPFHG	DDEDELFESI
570	580	590	600	610	620	630	640
RVDTPHYPRW	ITKESKDILE	KLFEREPTKR	LGVTGNIKIH	PFFKTINWTL	LEKRRLEPPF	RPKVKSPRDY	SNFDQEFLNE
650	660	670	680				
KARLSYSDKN	LIDSMDQSAF	AGFSFVNPKF	EHLLED				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2648	1	937.4596	47.34	2	61.9	14.1	1	319-336	K.KTGVAGEDMQDNSGTYGK.I	Oxidation: 9
2810	1	648.3524	-55.50	2	63.6	10.4	2	614-623	K.RRLEPPFRPK.V	

Detailed Protein Report

Protein 270: ryanodine receptor 3 isoform 2 [Homo sapiens]

Accession:	gi|345842488	**Score:**	36.8
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 [%]:**	1.0
		No. of unique Peptides:	3

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
58	1	845.3504	-92.64	3	29.9	13.1	2	382-402	R.KVILHQEGHMDDGLTLQRCQR.E	Carbamidomethyl: 19
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 271: toll-like receptor 9 precursor [Homo sapiens]

Accession:	gi|8394456	**Score:**	36.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	115.8
Database Date:	2015-11-30	**pI:**	9.7
		Sequence Coverage [%]:	3.2
		No. of unique Peptides:	3

Quantitation

mdown:qdown	**Median:**	0.74	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.60	**CV:**	0.00 %	**No. of Peptides:**	1

10	20	30	40	50	60	70	80
MGFCRSALHP	LSLLVQAIML	AMTLALGTLP	AFLPCELQPH	GLVNCNWLFL	KSVPHFSMAA	PRGNVTSLSL	SSNRIHHLHD
90	100	110	120	130	140	150	160
SDFAHLPSLR	HLNLKWNCPP	VGLSPMHFPC	HMTIEPSTFL	AVPTLEELNL	SYNNIMTVPA	LPKSLISLSL	SHTNILMLDS
170	180	190	200	210	220	230	240
ASLAGLHALR	FLFMDGNCYY	KNPCRQALEV	APGALLGLGN	LTHLSLKYNN	LTVVPRNLPS	SLEYLLLSYN	RIVKLAPEDL
250	260	270	280	290	300	310	320
ANLTALRVLD	VGGNCRRCDH	APNPCMECPR	HFPQLHPDTF	SHLSRLEGLV	LKDSSLSWLN	ASWFRGLGNL	RVLDLSENFL
330	340	350	360	370	380	390	400
YKCITKTKAF	QGLTQLRKLN	LSFNYQKRVS	FAHLSLAPSF	GSLVALKELD	MHGIFFRSLD	ETTLRPLARL	PMLQTLRLQM
410	420	430	440	450	460	470	480
NFINQAQLGI	FRAFPGLRYV	DLSDNRISGA	SELTATMGEA	DGGEKVWLQP	GDLAPAPVDT	PSSEDFRPNC	STLNFTLDLS
490	500	510	520	530	540	550	560
RNNLVTVQPE	MFAQLSHLQC	LRLSHNCISQ	AVNGSQFLPL	TGLQVLDLSH	NKLDLYHEHS	FTELPRLEAL	DLSYNSQPFG
570	580	590	600	610	620	630	640
MQGVGHNFSF	VAHLRTLRHL	SLAHNNIHSQ	VSQQLCSTSL	RALDFSGNAL	GHMWAEGDLY	LHFFQGLSGL	IWLDLSQNRL
650	660	670	680	690	700	710	720
HTLLPQTLRN	LPKSLQVLRL	RDNYLAFFKW	WSLHFLPKLE	VLDLAGNQLK	ALTNGSLPAG	TRLRRLDVSC	NSISFVAPGF
730	740	750	760	770	780	790	800
FSKAKELREL	NLSANALKTV	DHSWFGPLAS	ALQILDVSAN	PLHCACGAAF	MDFLLEVQAA	VPGLPSRVKC	GSPGQLQGLS
810	820	830	840	850	860	870	880
IFAQDLRLCL	DEALSWDCFA	LSLLAVALGL	GVPMLHHLCG	WDLWYCFHLC	LAWLPWRGRQ	SGRDEDALPY	DAFVVFDKTQ
890	900	910	920	930	940	950	960
SAVADWVYNE	LRGQLEECRG	RWALRLCLEE	RDWLPGKTLF	ENLWASVYGS	RKTLFVLAHT	DRVSGLLRAS	FLLAQQRLLE
970	980	990	1000	1010	1020	1030	1040
DRKDVVVLVI	LSPDGRRSRY	VRLRQRLCRQ	SVLLWPHQPS	GQRSFWAQLG	MALTRDNHHF	YNRNFCQGPT	AE

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1901	1	698.8088	-121.07	2	52.3	10.8	0	235-247	K.LAPEDLANLTALR.V		
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		mdown:qdown 0.74 Wdown:Qdown 0.60

Detailed Protein Report

Protein 272: tRNA wybutosine-synthesizing protein 1 homolog B isoform 1 [Homo sapiens]

Accession:	gi|224282123	**Score:**	36.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	76.9
Database Date:	2015-11-30	**pI:**	5.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	5.2
		No. of unique Peptides:	2

Quantitation

Wdown:Qdown **Median:** 1.27 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MDPSADTWDL	SSPLISLWIN	RFYIYLGFAV	SISLWICVQI	VIEMQGFATV	LAEAVTSLDL	PVAIINLKEY	DPDDHLIEEV
90	100	110	120	130	140	150	160
TSKNVCVFLV	ATYTDGLPTE	SAEWFCKWLE	EASIDFRFGK	TYLKGMRDAV	FGLGNSAYAS	HFNKVGKNVD	KWLWMLGVHR
170	180	190	200	210	220	230	240
VMSRGEGDCD	VVKSKHGSIE	ANFRAWKTKF	ISQLQALQKG	ERKKSCGGHC	KKGKCESHQH	GSEEREEGSQ	EQDELHHRDT
250	260	270	280	290	300	310	320
KEEEPFESSS	EEEFGGEDHQ	SLNSIVDVED	LGKIMDHVKK	EKREKEQQEE	KSGLFRNMGR	NEDGERRAMI	TPALREALTK
330	340	350	360	370	380	390	400
QVDAPRERSL	LQTHILWNES	HRCMETTPSL	ACANKCVFCW	WHHNNPVGTE	WLWKMDQPEM	ILKEAIENHQ	NMIKQFKGVP
410	420	430	440	450	460	470	480
GVKAERFEEG	MTVKHCALSL	VGEPIMYPEI	NRFLKLLHQC	KISSFLVTNA	QFPAEIRNLE	PVTQLYVSVD	ASTKDSLKKI
490	500	510	520	530	540	550	560
DRPLFKDFWQ	QFLDSLKALA	VKQQRTVYRL	TLVKAWNVDE	LQAYAQLVSL	GNPDFIEVKG	VTYCRESSAS	SLTMAHVPWH
570	580	590	600	610	620	630	640
EEVVQFVREL	VDLIPEYEIA	CEHEHSNCLL	IAHRKFKIGG	EWWTWIDYNR	FQELIQEYED	SGGSKTFSAK	DYMARTPHWA
650	660	670					
LFGANERSFD	PKDTRHQRKN	KSKAISGC					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
912	1	697.8084	-22.08	2	39.9	10.4	1	161-173	R.VMSRGEGDCDVVK.S		Wdown:Qdown 1.27
2915	3	713.3417	41.37	2	65.2	16.0	0	343-355	R.CMETTPSLACANK.C	Carbamidomethyl: 10	

Detailed Protein Report

Protein 273: retinal dehydrogenase 1 [Homo sapiens]

Accession:	gi|21361176	**Score:**	36.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	54.8
Database Date:	2015-11-30	**pI:**	6.3
		Sequence Coverage [%]:	6.0
		No. of unique Peptides:	1

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2975	1	953.4552	-84.55	2	66.4	23.6	2	242-260	K.VAFTGSTEVGKLIKEAAGK.S	

Detailed Protein Report

Protein 274: **PREDICTED: LIM/homeobox protein Lhx9 isoform X2 [Homo sapiens]**

Accession:	gi|530365098	**Score:**	36.6
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 [%]:**	13.6
		No. of unique Peptides:	2

Quantitation

mdown:qdown **Median:** 0.95 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MEIVGCRAED	NSCPFRPPAM	LFHGISGGHI	QGIMEEMERR	SKTEARLAKG	AQLNGRDAGM	PPLSPEKPAL	CAGCGGKISD
90	100	110	120	130	140	150	160
RYYLLAVDKQ	WHLRCLKCCE	CKLALESELT	CFAKDGSIYC	KEDYYRRFSV	QRCARCHLGI	SASEMVMRAR	DSVYHLSCFT
170	180	190	200	210	220	230	240
CSTCNKTLTT	GDHFGMKDSL	VYCRAHFETL	LQGEYPPQLS	YTELAAKSGG	LALPYFNGTG	TVQKGRPRKR	KSPALGVDIV
250	260	270	280	290	300	310	320
NYNSGCNENE	ADHLDRDQQP	YPPSQKTKRM	RTSFKHHQLR	TMKSYFAINH	NPDAKDLKQL	AQKTGLTKRV	LQGEQILGHY
330	340						
SQTSRRLKIP							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
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	mdown:qdown 0.95

Detailed Protein Report

Protein 275: PREDICTED: NMDA receptor-regulated protein 2 isoform X4 [Homo sapiens]

Accession:	gi|530406441	**Score:**	36.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	86.5
Database Date:	2015-11-30	**pI:**	6.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.1
		No. of unique Peptides:	3

10	20	30	40	50	60	70	80
MSSKMVISEP	GLNWDISPKN	GLKTFFSREN	YKDHSMAPSL	KELRVLSNRR	IGENLNASAS	SVENEPAVSS	ATQAKEKVKT
90	100	110	120	130	140	150	160
TIGMVLLPKP	RVPYPRFSRF	SQREQRSYVD	LLVKYAKIPA	NSKAVGINKN	DYLQYLDMKK	HVNEEVTEFL	KFLQNSAKKC
170	180	190	200	210	220	230	240
AQDYNMLSDD	ARLFTEKILR	ACIEQVKKYS	EFYTLHEVTS	LMGFFPFRVE	MGLKLEKTLL	ALGSVKYVKT	VFPSMPIKLQ
250	260	270	280	290	300	310	320
LSKDDIATIE	TSEQTAEAMH	YDISKDPNAE	KLVSRYHPQI	ALTSQSLFTL	LNNHGPTYKE	QWEIPVCIQV	IPVAGSKPVK
330	340	350	360	370	380	390	400
VIYINSPLPQ	KKMTMRERNQ	IFHEVPLKFM	MSKNTSVPVS	AVFMDKPEEF	ISEMDMSCEV	NECRKIESLE	NLYLDFDDDV
410	420	430	440	450	460	470	480
TELETFGVTT	TKVSKSPSPA	STSTVPNMTD	APTAPKAGTT	TVAPSAPDIS	ANSRSLSQIL	MEQLQKEKQL	VTGMDGGPEE
490	500	510	520	530	540	550	560
CKNKDDQGFE	SCEKVSNSDK	PLIQDSDLKT	SDALQLENSQ	EIETSNKNDM	TIDILHADGE	RPNVLENLDN	SKEKTVGSEA
570	580	590	600	610	620	630	640
AKTEDTVLCS	SDTDEECLII	DTECKNNSDG	KTAVVGSNLS	SRPASPNSSS	GQASVGNQTN	TACSPEESCV	LKKPIKRVYK
650	660	670	680	690	700	710	720
KFDPVGEILK	MQDELLKPIS	RKVPELPLMN	LENSKQPSVS	EQLSGPSDSS	SWPKSGWPSA	FQKPKGRLPY	ELQDYVEDTS
730	740	750	760	770	780		
EYLAPQEGNF	VYKLFSLQDL	LLLVRCSVQR	IETRPRSKKR	KKIRRLTALR	NC		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1819	1	649.7840	-134.37	2	52.7	13.7	1	107-117	R.SYVDLLVKYAK.I	
9	1	650.7714	-185.46	2	29.3	12.0	2	178-188	K.ILRACIEQVKK.Y	
1355	1	607.6081	-208.99	2	45.5	10.8	0	485-494	K.DDQGFESCEK.V	Carbamidomethyl: 8

Detailed Protein Report

Protein 276: myeloid zinc finger 1 isoform 1 [Homo sapiens]

Accession:	gi|37622341	**Score:**	36.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	82.0
Database Date:	2015-11-30	**pI:**	10.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	7.2
		No. of unique Peptides:	1

Alias proteins:

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

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

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

Detailed Protein Report

Protein 277: PREDICTED: probable E3 ubiquitin-protein ligase HERC1 isoform X6 [Homo sapiens]

Accession:	gi|530406610	**Score:**	36.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	524.9
Database Date:	2015-11-30	**pI:**	5.7
		Sequence Coverage [%]:	1.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2832	1	923.8157	-4.48	3	64.6	12.0	1	487-513	R.NIPTLVKDISNVGEVSCGSSHTIALSK.D	

Detailed Protein Report

Protein 278: PREDICTED: peroxisomal acyl-coenzyme A oxidase 2 isoform X2 [Homo sapiens]

Accession:	gi|530373234	**Score:**	36.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	68.7
Database Date:	2015-11-30	**pI:**	8.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	6.5
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MTQNERYKAA	MRRAFHIRLI	ARRLGWLEDG	RELGYAYRAL	SGDVALNIHR	VFVRALRSLG	SEEQIAKWDP	LCKNIQIIAT
90	100	110	120	130	140	150	160
YAQTELGHGT	YLQGLETEAT	YDAATQEFVI	HSPTLTATKW	WPGDLGRSAT	HALVQAQLIC	SGARRGMHAF	IVPIRSLQDH
170	180	190	200	210	220	230	240
TPLPGIIIGD	IGPKMDFDQT	DNGFLQLNHV	RVPRENMLSR	FAQVLPDGTY	VKLGTAQSNY	LPMVVVRVEL	LSGEILPILQ
250	260	270	280	290	300	310	320
KACVIAMRYS	VIRRQSRLRP	SDPEAKVLDY	QTQQQKLFPQ	LAISYAFHFL	AVSLLEFFQH	SYTAILNQDF	SFLPELHALS
330	340	350	360	370	380	390	400
TGMKAMMSEF	CTQGAEMCRR	ACGGHGYSKL	SGLPSLVTKL	SASCTYEGEN	TVLYLQVARF	LVKSYLQTQM	SPGSTPQRSL
410	420	430	440	450	460	470	480
SPSVAYLTAP	DLARCPAQRA	ADFLCPELYT	TAWAHVAVRL	IKDSVQHLQT	LTQSGADQHE	AWNQTTVIHL	QAAKVHCYYV
490	500	510	520	530	540	550	560
TVKGFTEALE	KLENEPAIQQ	VLKRLCDLHA	IHGILTNSGD	FLHDAFLSGA	QVDMARTAYL	DLLRLIRKDA	ILLTDAFDFT
570	580	590	600	610	620		
DQCLNSALGC	YDGNVYERLF	QWAQKSPTNT	QENPAYEEYI	RPLLQSWRSK	L		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1349	1	945.2230	-270.57	1	45.4	11.1	0	24-31	R.LGWLEDGR.E	
2448	1	863.7544	-77.93	2	58.9	15.3	0	325-339	K.AMMSEFCTQGAEMCR.R	Oxidation: 2, 13

Detailed Protein Report

Protein 279: PREDICTED: centrosome-associated protein CEP250 isoform X4 [Homo sapiens]

Accession:	gi|530417804	**Score:**	36.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	208.3
Database Date:	2015-11-30	**pI:**	4.9
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.7
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MEAAEQARNA	LQVDLAEAEK	RREALWEKNT	HLEAQLQKAE	EAGAELQADL	RDIQEEKEEI	QKKLSESRHQ	QEAATTQLEQ
90	100	110	120	130	140	150	160
LHQEAKRQEE	VLARAVQEKE	ALVREKAALE	VRLQAVERDR	QDLAEQLQGL	SSAKELLESS	LFEAQQQNSV	IEVTKGQLEV
170	180	190	200	210	220	230	240
QIQTVTQAKE	VIQGEVRCLK	LELDTERSQA	EQERDAAARQ	LAQAEQEGKT	ALEQQKAAHE	KEVNQLREKW	EKERSWHQQE
250	260	270	280	290	300	310	320
LAKALESLER	EKMELEMRLK	EQQTEMEAIQ	AQREEERTQA	ESALCQMQLE	TEKERVSLLE	TLLQTQKELA	DASQQLERLR
330	340	350	360	370	380	390	400
QDMKVQKLKE	QETTGILQTQ	LQEAQRELKE	AARQHRDDLA	ALQEESSSLL	QDKMDLQKQV	EDLKSQLVAQ	DDSQRLVEQE
410	420	430	440	450	460	470	480
VQEKLRETQE	YNRIQKELER	EKASLTLSLM	EKEQRLLVLQ	EADSIRQQEL	SALRQDMQEA	QGEQKELSAQ	MELLRQEVKE
490	500	510	520	530	540	550	560
KEADFLAQEA	QLLEELEASH	ITEQQLRASL	WAQEAKAAQL	QLRLRSTESQ	LEALAAEQQP	GNQAQAQAQL	ASLYSALQQA
570	580	590	600	610	620	630	640
LGSVCESRPE	LSGGGDSAPS	VWGLEPDQNG	ARSLFKRGPL	LTALSAEAVA	SALHKLHQDL	WKTQQTRDVL	RDQVQKLEER
650	660	670	680	690	700	710	720
LTDTEAEKSQ	VHTELQDLQR	QLSQNQEEKS	KWEGKQNSLE	SELMELHETM	ASLQSRLRRA	ELQRMEAQGE	RELLQAAKEN
730	740	750	760	770	780	790	800
LTAQVEHLQA	AVVEARAQAS	AAGILEEDLR	TARSALKLKN	EEVESERERA	QALQEQGELK	VAQGKALQEN	LALLTQTLAE
810	820	830	840	850	860	870	880
REEEVETLRG	QIQELEKQRE	MQKAALELLS	LDLKKRNQEV	DLQQEQIQEL	EKCRSVLEHL	PMAVQEREQK	LTVQREQIRE
890	900	910	920	930	940	950	960
LEKDRETQRN	VLEHQLLELE	KKDQMIESQR	GQVQDLKKQL	VTLECLALEL	EENHHKMECQ	QKLIKELEGQ	RETQRVALTH
970	980	990	1000	1010	1020	1030	1040
LTLDLEERSQ	ELQAQSSQIH	DLESHSTVLA	RELQERDQEV	KSQREQIEEL	QRQKEHLTQD	LERRDQELML	QKERIQVLED
1050	1060	1070	1080	1090	1100	1110	1120
QRTRQTKILE	EDLEQIKLSL	RERGRELTTQ	RQLMQERAEE	GKGPSKAQRG	SLEHMKLILR	DKEKEVECQQ	EHIHELQELK
1130	1140	1150	1160	1170	1180	1190	1200
DQLEQQLQGL	HRKVGETSLL	LSQREQEIVV	LQQQLQEARE	QGELKEQSLQ	SQLDEAQRAL	AQRDQELEAL	QQEQQQAQGQ
1210	1220	1230	1240	1250	1260	1270	1280
EERVKEKADA	LQGALEQAHM	TLKERHGELQ	DHKEQARRLE	EELAVEGRRV	QALEEVLGDL	RAESREQEKA	LLALQQQCAE
1290	1300	1310	1320	1330	1340	1350	1360
QAQEHEVETR	ALQDSWLQAQ	AVLKERDQEL	EALRAESQSS	RHQEEAARAR	AEALQEALGK	AHAALQGKEQ	HLLEQAELSR
1370	1380	1390	1400	1410	1420	1430	1440
SLEASTATLQ	ASLDACQAHS	RQLEEALRIQ	EGEIQDQDLR	YQEDVQQLQQ	ALAQRDEELR	HQQEREQLLE	KSLAQRVQEN
1450	1460	1470	1480	1490	1500	1510	1520
MIQEKQNLGQ	EREEEEIRGL	HQSVRELQLT	LAQKEQEILE	LRETQQRNNL	EALPHSHKTS	PMEEQSLKLD	SLEPRLQREL
1530	1540	1550	1560	1570	1580	1590	1600
ERLQAALRQT	EAREIEWREK	AQDLALSLAQ	TKASVSSLQE	VAMFLQASVL	ERDSEQQRLQ	DELELTRRAL	EKERLHSPGA
1610	1620	1630	1640	1650	1660	1670	1680
TSTAELGSRG	EQGVQLGEVS	GVEAEPSPDG	MEKQSWRQRL	EHLQQAVARL	EIDRSRLQRH	NVQLRSTLEQ	VERERRKLKR
1690	1700	1710	1720	1730	1740	1750	1760
EAMRAAQAGS	LEISKATASS	PTQQDGRGQK	NSDAKCVAEL	QKEVVLLQAQ	LTLERKQKQD	YITRSAQTSR	ELAGLHHSLS
1770	1780	1790	1800	1810	1820		
HSLLAVAQAP	EATVLEAETR	RLDESLTQSL	TSPGPVLLHP	SPSTTQAASR			

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

	Cmpds.		[ppm]		[min]					
813	1	683.3344	-49.61	2	39.0	12.1	1	421-432	R.EKASLTLSLMEK.E	Oxidation: 10
1397	1	926.5056	55.39	3	46.2	12.2	2	1681-1707	R.EAMRAAQAGSLEISKATASSPTQQDGR.G	Oxidation: 3

Detailed Protein Report

Protein 280: T-complex protein 11 homolog isoform 3 [Homo sapiens]

Accession:	gi|387849264	**Score:**	36.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	56.8
Database Date:	2015-11-30	**pI:**	5.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	5.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MTRGGGGGDT	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 281: kinesin-like protein KIF26B [Homo sapiens]

Accession:	gi|124430752	**Score:**	36.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	223.7
Database Date:	2015-11-30	**pI:**	9.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.5
		No. of unique Peptides:	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MNSVAGNKER	LAVSTRGKKY	GVNEVCSPTK	PAAPFSPESW	YRKAYEESRA	GSRPTPEGAG	SALGSSGTPS	PGSGTSSPSS
90	100	110	120	130	140	150	160
FTGSPGPASP	GIGTSSPGSL	GGSPGFGTGS	PGSGSGGGSS	PGSDRGVWCE	NCNARLVELK	RQALRLLLPG	PFPGKDPAFS
170	180	190	200	210	220	230	240
AVIHDKLQVP	NTIRKAWNDR	DNRCDICATH	LNQLKQEAIQ	MVLTLEQAAG	SEHYDASPCS	PPPLSNIPTL	VGSRHVGGLQ
250	260	270	280	290	300	310	320
QPRDWAFVPA	PCATSNYTGF	ANKHGSKPSS	LGVSNGAEKK	SGSPTHQAKV	SLQMATSPSN	GNILNSVAIQ	AHQYLDGTWS
330	340	350	360	370	380	390	400
LSRTNGVTLY	PYQISQLMTE	SSREGLTEAV	LNRYNADKPS	ACSVPASQGS	CVASETSTGT	SVAASFFARA	AQKLNLSSKK
410	420	430	440	450	460	470	480
KKHRPSTSSA	AEPPLFATSF	SGILQTSPPP	APPCLLRAVN	KVKDTPGLGK	VKVMLRICST	LARDTSESSS	FLKVDPRKKQ
490	500	510	520	530	540	550	560
ITLYDPLTCG	GQNAFQKRGN	QVPPKMFAFD	AVFPQDASQA	EVCAGTVAEV	IQSVVNGADG	CVFCFGHAKL	GKSYTMIGKD
570	580	590	600	610	620	630	640
DSMQNLGIIP	CAISWLFKLI	NERKEKTGAR	FSVRVSAVEV	WGKEENLRDL	LSEVATGSLQ	DGQSPGVYLC	EDPICGTQLQ
650	660	670	680	690	700	710	720
NQSELRAPTA	EKAAFFLDAA	IASRRSHQQD	CDEDDHRNSH	VFFTLHIYQY	RMEKSGKGGM	SGGRSRLHLI	DLGSCVKALS
730	740	750	760	770	780	790	800
KNREGGSGLC	LSLSALGNVI	LALVNGSKHI	PYKESKLAML	LRESLGNMNC	RTTMIAHISA	AVGSYAETLS	TIQIASRVLR
810	820	830	840	850	860	870	880
MKKKKTKYTS	SSSGGESSCE	EGRMRRPTQL	RPFHTRATVD	PDFPIAHLSS	DPDYSSSSEQ	SCDTVIYIGP	NGTALSDKEL
890	900	910	920	930	940	950	960
TDNEGPPDFV	PIVPALQKTR	GDSRPAEAGE	AAAGKSERDC	LKCNTFAELQ	ERLDCIDGSE	EPSSFPFEEL	PAQFGPEQAS
970	980	990	1000	1010	1020	1030	1040
RGPRLSQAAG	ASPLSESDKE	DNGSEGQLTN	REGPELPASK	MQRSHSPVPA	AAPAHSPSPA	SPRSVPGSSS	QHSASPLVQS
1050	1060	1070	1080	1090	1100	1110	1120
PSLQSSRESL	NSCGFVEGKP	RPMGSPRLGI	ASLSKTSEYK	PPSSPSQRCK	VYTQKGVLPS	PAPLPPSSKD	SGVASRESLL
1130	1140	1150	1160	1170	1180	1190	1200
QPEVRTPPVG	MSPQVLKKSM	SAGSEGFPET	PVDDEQQAAT	PSESKKEILS	TTMVTVQQPL	ELNGEDELVF	TLVEELTISG
1210	1220	1230	1240	1250	1260	1270	1280
VLDSGRPTSI	ISFNSDCSAR	ALASGSRPVS	IISSISEDLE	CYSSTAPVSE	VSITQFLPLP	KMSLDEKAQD	AGSRRSSISS
1290	1300	1310	1320	1330	1340	1350	1360
WLSEMSAGSE	GEQSCHSFIA	QTCFGHGEAM	AEPVASEFVS	SLQNTAVVCR	EKPKASPDNL	LILSEMGDDS	FNKAAPIKGC
1370	1380	1390	1400	1410	1420	1430	1440
KISTVSKAMV	TISNTANLSS	CEGYIPMKTN	ITVYPCIAMS	PRNIQEPEAP	TATPKAGPTL	AQSRESKENS	AKKEMKFEDP
1450	1460	1470	1480	1490	1500	1510	1520
WLKREEEVKK	ETAHPNEEGM	MRCETATGPS	NAETRAEQEQ	DGKPSPGDRL	SSSSGEVSAS	PVTDNFRRVV	DGCEMALPGL
1530	1540	1550	1560	1570	1580	1590	1600
ATQSPVHPNK	SVKSSSLPRA	FQKASRQEEP	DSLSYYCAAE	TNGVGAASGT	PPSKATLEGK	VASPKHCVLA	RPKGTPPLPP
1610	1620	1630	1640	1650	1660	1670	1680
VRKSSLDQKN	RASPQHSASG	SGTSSPLNQP	AAFPAGLPDE	PSGKTKDASS	SSKLFSAKLE	QLASRSNSLG	RATVSHYECL
1690	1700	1710	1720	1730	1740	1750	1760
SLERAESLSS	VSSRLHAGKD	GTMPRAGRSL	GRSAGTSPPS	SGASPKAGQS	KISAVSRLLL	ASPRARGPSA	STTKTLSFST
1770	1780	1790	1800	1810	1820	1830	1840
KSLPQAVGQG	SSSPPGGKHT	PWSTQSLSRN	RSSGLASKLP	LRAVSGRISE	LLQGGAGARG	LQLRAGPEAE	ARGGALAEDE
1850	1860	1870	1880	1890	1900	1910	1920
PAAAHLLPSP	YSKITPPRRP	HRCSSGHGSD	NSSVLSGELP	PAMGKTALFY	HSGGSSGYES	VMRDSEATGS	ASSAQDSTSE
1930	1940	1950	1960	1970	1980	1990	2000
NSSSVGGRCR	SLKTPKKRSN	PGSQRRRLIP	ALSLDTSSPV	RKPPNSTGVR	WVDGPLRSSP	RGLGEPFEIK	VYEIDDVERL
2010	2020	2030	2040	2050	2060	2070	2080
QRRRGGASKE	AMCFNAKLKI	LEHRQQRIAE	VRAKYEWLMK	ELEATKQYLM	LDPNKWLSEF	DLEQVWELDS	LEYLEALECV
2090	2100	2110					
TERLESRVNF	CKAHLMMITC	FDITSRRR					

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2229	1	597.6218	-9.28	3	56.3	11.5	1	126-140	R.GVWCENCNARLVELK.R	Carbamidomethyl: 7

Detailed Protein Report

Protein 282: PREDICTED: protein unc-13 homolog C isoform X2 [Homo sapiens]

Accession:	gi|530405878	**Score:**	36.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	247.7
Database Date:	2015-11-30	**pI:**	5.6
		Sequence Coverage [%]:	1.4
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	0.38	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	1.31	**CV:**	0.00 %	**No. of Peptides:**	1

10	20	30	40	50	60	70	80
MVANFFKSLI	LPYIHKLCKG	MFTKKLGNTN	KNKEYRQQKK	DQDFPTAGQT	KSPKFSYTFK	STVKKIAKCS	STHNLSTEED
90	100	110	120	130	140	150	160
EASKEFSLSP	TFSYRVAIAN	GLQKNAKVTN	SDNEDLLQEL	SSIESSYSES	LNELRSSTEN	QAQSTHTMPV	RRNRKSSSSL
170	180	190	200	210	220	230	240
APSEGSSDGE	RTLHGLKLGA	LRKLRKWKKS	QECVSSDSEL	STMKKSWGIR	SKSLDRTVRN	PKTNALEPGF	SSSGCISQTH
250	260	270	280	290	300	310	320
DVMEMIFKEL	QGISQIETEL	SELRGHVNAL	KHSIDEISSS	VEVVQSEIEQ	LRTGFVQSRR	ETRDIHDYIK	HLGHMGSKAS
330	340	350	360	370	380	390	400
LRFLNVTEER	FEYVESVVYQ	ILIDKMGFSD	APNAIKIEFA	QRIGHQRDCP	NAKPRPILVY	FETPQQRDSV	LKKSYKLKGT
410	420	430	440	450	460	470	480
GIGISTDILT	HDIRERKEKG	IPSSQTYESM	AIKLSTPEPK	IKKNNWQSPD	DSDEDLESDL	NRNSYAVLSK	SELLTKGSTS
490	500	510	520	530	540	550	560
KPSSKSHSAR	SKNKTANSSR	ISNKSDYDKI	SSQLPESDIL	EKQTTTHYAD	ATPLWHSQSD	FFTAKLSRSE	SDFSKLCQSY
570	580	590	600	610	620	630	640
SEDFSENQFF	TRTNGSSLLS	SSDRELWQRK	QEGTATLYDS	PKDQHLNGGV	QGIQGQTETE	NTETVDSGMS	NGMVCASGDR
650	660	670	680	690	700	710	720
SHYSDSQLSL	HEDLSPWKEW	NQGADLGLDS	STQEGFDYET	NSLFDQQLDV	YNKDLEYLGK	CHSDLQDDSE	SYDLTQDDNS
730	740	750	760	770	780	790	800
SPCPGLDNEP	QGQWVGQYDS	YQGANSNELY	QNQNQLSMMY	RSQSELQSDD	SEDAPPKSWH	SRLSIDLSDK	TFSFPKFGST
810	820	830	840	850	860	870	880
LQRAKSALEV	VWNKSTQSLS	GYEDSGSSLM	GRFRTLSQST	ANESSTTLDS	DVYTEPYYYK	AEDEEDYTEP	VADNETDYVE
890	900	910	920	930	940	950	960
VMEQVLAKLE	NRTSITETDE	QMQAYDHLSY	ETPYETPQDE	GYDGPADDMV	SEEGLEPLNE	TSAEMEIRED	ENQNIPEQPV
970	980	990	1000	1010	1020	1030	1040
EITKPKRIRP	SFKEAALRAY	KKQMAELEEK	ILAGDSSSVD	EKARIVSGND	LDASKFSALQ	VCGGAGGGLY	GIDSMPDLRR
1050	1060	1070	1080	1090	1100	1110	1120
KKTLPIVRDV	AMTLAARKSG	LSLAMVIRTS	LNNEELKMHV	FKKTLQALIY	PMSSTIPHNF	EVWTATTPTY	CYECEGLLWG
1130	1140	1150	1160	1170	1180	1190	1200
IARQGMKCLE	CGVKCHEKCQ	DLLNADCLQR	AAEKSSKHGA	EDKTQTIITA	MKERMKIREK	NRPEVFEVIQ	EMFQISKEDF
1210	1220	1230	1240	1250	1260	1270	1280
VQFTKAAKQS	VLDGTSKWSA	KITITVVSAQ	GLQAKDKTGS	SDPYVTVQVG	KNKRRTKTIF	GNLNPVWDEK	FYFECHNSTD
1290	1300	1310	1320	1330	1340	1350	1360
RIKVRVWDED	DDIKSRVKQH	FKKESDDFLG	QTIVEVRTLS	GEMDVWYNLE	KRTDKSAVSG	AIRLKINVEI	KGEEKVAPYH
1370	1380	1390	1400	1410	1420	1430	1440
IQYTCLHENL	FHYLTEVKSN	GGVKIPEVKG	DEAWKVFFDD	ASQEIVDEFA	MRYGIESIYQ	AMTHFSCLSS	KYMCPGVPAV
1450	1460	1470	1480	1490	1500	1510	1520
MSTLLANINA	FYAHTTVSTN	IQVSASDRFA	ATNFGREKFI	KLLDQLHNSL	RIDLSKYREN	FPASNTERLQ	DLKSTVDLLT
1530	1540	1550	1560	1570	1580	1590	1600
SITFFRMKVL	ELQSPPKASM	VVKDCVRACL	DSTYKYIFDN	CHELYSQLTD	PSKKQDIPRE	DQGPTTKNLD	FWPQLITLMV
1610	1620	1630	1640	1650	1660	1670	1680
TIIDEDKTAY	TPVLNQFPQE	LNMGKISAEI	MWTLFALDMK	YALEEHENQR	LCKSTDYMNL	HFKVKWFYNE	YVRELPAFKD
1690	1700	1710	1720	1730	1740	1750	1760
AVPEYSLWFE	PFVMQWLDEN	EDVSMEFLHG	ALGRDKKDGF	QQTSEHALFS	CSVVDVFAQL	NQSFEIIKKL	ECPNPEALSH
1770	1780	1790	1800	1810	1820	1830	1840
LMRRFAKTIN	KVLLQYAAIV	SSDFSSHCDK	ENVLDSEAST	ILKELQVKLS	GVLDELSVTY	GESFQVIIEE	CIKQMSFELN
1850	1860	1870	1880	1890	1900	1910	1920
QMRANGNTTS	NKNSAAMDAE	IVLRSLMDFL	DKTLSLSAKI	CEKTVLKRVL	KELWKLVLNK	IEKQIVLPPL	TDQTGPQMIF
1930	1940	1950	1960	1970	1980	1990	2000
IAAKDLGQLS	KLKEHMIRED	ARGLTPRQCA	IMEVVLATIK	QYFHAGGNGL	KKNFLEKSPD	LQSLRYALSL	YTQTTDALIK
2010	2020	2030	2040	2050	2060	2070	2080
KFIDTQTSQS	RSSKDAVGQI	SVHVDITATP	GTGDHKVTVK	VIAINDLNWQ	TTAMFRPFVE	VCILGPNLGD	KKRKQGTKTK
2090	2100	2110	2120	2130	2140	2150	2160
SNTWSPKYNE	TFQFILGKEN	RPGAYELHLS	VKDYCFARED	RIIGMTVIQL	QNIAEKGSYG	AWYPLLKNIS	MDETGLTILR
2170	2180	2190					
ILSQRTSDDV	AKEFVRLKSE	TRSTEESA					

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

Detailed Protein Report

	Cmpds.		[ppm]		[min]						
1046	1	742.4006	68.40	2	41.8	12.0	1	1497- 1508	K.YRENFPASNTER.L		Wdown:Qdown 1.31 mdown:qdown 0.38

Detailed Protein Report

Protein 283: PDZ domain-containing RING finger protein 4 isoform 2 [Homo sapiens]

Accession: gi|142976783

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Score: 36.1

MW [kDa]: 89.0

pI: 5.0

Sequence Coverage [%]: 3.2

No. of unique Peptides: 2

Quantitation

mdown:qdown	**Median:**	1.40	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	1.42	**CV:**	0.00 %	**No. of Peptides:**	1

10	20	30	40	50	60	70	80
MGCNLCTFQK	REEHYKLLYE	VSQVNGKDLS	KATHEEAVEA	FRNAKEPIVV	QVLRRTPLSR	PAYGMASEVQ	LMNASTQTDI
90	100	110	120	130	140	150	160
TFEHIMALAK	LRPPTPPVPD	ICPFLLSDSC	HSLHPMEHEF	YEDNEYISSL	PADADRTEDF	EYEEVELCRV	SSQEKLGLTV
170	180	190	200	210	220	230	240
CYRTDDEEDT	GIYVSEVDPN	SIAAKDGRIR	EGDRILQING	EDVQNREEAV	ALLSNDECKR	IVLLVARPEI	QLDEGWLEDE
250	260	270	280	290	300	310	320
RNEFLEELNL	EMLEEEHNEA	MQPTANEVEQ	PKKQEEEEGT	TDTATSSSNN	HEKDSGVGRT	DESLRNDESS	EQENAAEDPN
330	340	350	360	370	380	390	400
STSLKSKRDL	GQSQDTLGSV	ELQYNESLVS	GEYIDSDCIG	NPDEDCERFR	QLLELKCKIR	NHGEYDLYYS	SSTIECNQGE
410	420	430	440	450	460	470	480
QEGVEHELQL	LNEELRNIEL	ECQNIMQAHR	LQKVTDQYGD	IWTLHDGGFR	NYNTSIDMQR	GKLDDIMEHP	EKSDKDSSSA
490	500	510	520	530	540	550	560
YNTAESCRST	PLTVDRSPDS	SLPRVINLTN	KKNLRSTMAA	TQSSSGQSSK	ESTSTKAKTT	EQGCSAESKE	KVLEGSKLPD
570	580	590	600	610	620	630	640
QEKAVSEHIP	YLSPYHSSSY	RYANIPAHAR	HYQSYMQLIQ	QKSAVEYAQS	QLSLVSMCKE	SQKCSEPKME	WKVKIRSDGT
650	660	670	680	690	700	710	720
RYITKRPVRD	RILKERALKI	KEERSGMTTD	DDTMSEMKMG	RYWSKEERKQ	HLVRAKEQRR	RREFMMRSRL	ECLKESPQSG
730	740	750	760	770	780		
SEGKKEINII	ELSHKKMMKK	RNKKILDNWM	TIQELMTHGA	KSPDGTRVHN	AFLSVTTV		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
652	2	639.3334	-62.76	2	37.0	25.9	2	369-378	R.FRQLLELKCK.I		Wdown:Qdown 1.42 mdown:qdown 1.40
2536	1	821.0789	154.65	2	60.0	10.2	1	497-511	R.SPDSSLPRVINLTNK.K		

Detailed Protein Report

Protein 284: nuclear receptor coactivator 3 isoform d [Homo sapiens]

Accession:	gi|291490685	**Score:**	36.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	154.3
Database Date:	2015-11-30	**pI:**	7.0
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	4.2
		No. of unique Peptides:	3

Quantitation

mdown:qdown	**Median:**	0.74	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.60	**CV:**	0.00 %	**No. of Peptides:**	1

```
        10         20         30         40         50         60         70         80
MSGLGENLDP LASDSRKRKL PCDTPGQGLT CSGEKRRREQ ESKYIEELAE LISANLSDID NFNVKPDKCA ILKETVRQIR
        90        100        110        120        130        140        150        160
QIKEQGKTIS NDDDVQKADV SSTGQGVIDK DSLGPLLLQA LDGFLFVVNR DGNIVFVSEN VTQYLQYKQE DLVNTSVYNI
       170        180        190        200        210        220        230        240
LHEEDRKDFL KNLPKSTVNG VSWTNETQRQ KSHTFNCRML MKTPHDILED INASPEMRQR YETMQCFALS QPRAMMEEGE
       250        260        270        280        290        300        310        320
DLQSCMICVA RRITTGERTF PSNPESFITR HDLSGKVVNI DTNSLRSSMR PGFEDIIRRC IQRFFSLNDG QSWSQKRHYQ
       330        340        350        360        370        380        390        400
EVTSDGIFSP TAYLNGHAET PVYRFSLADG TIVTAQTKSK LFRNPVTNDR HGFVSTHFLQ REQNGYRPNP NPVGQGIRPP
       410        420        430        440        450        460        470        480
MAGCNSSVGG MSMSPNQGLQ MPSSRAYGLA DPSTTGQMSG ARYGGSSNIA SLTPGPGMQS PSSYQNNNYG LNMSSPPHGS
       490        500        510        520        530        540        550        560
PGLAPNQQNI MISPRNRGSP KIASHQFSPV AGVHSPMASS GNTGNHSFSS SSLSALQAIS EGVGTSLLST LSSPGPKLDN
       570        580        590        600        610        620        630        640
SPNMNITQPS KVSNQDSKSP LGFYCDQNPV ESSMCQSNSR DHLSDKESKE SSVEGAENQR GPLESKGHKK LLQLLTCSSD
       650        660        670        680        690        700        710        720
DRGHSSLTNS PLDSSCKESS VSVTSPSGVS SSTSGGVSST SNMHGSLLQE KHRILHKLLQ NGNSPAEVAK ITAEATGKDT
       730        740        750        760        770        780        790        800
SSITSCGDGN VVKQEQLSPK KKENNALLRY LLDRDDPSDA LSKELQPQVE GVDNKMSQCT SSTIPSSSQE KDPKIKTETS
       810        820        830        840        850        860        870        880
EEGSGDLDNL DAILGDLTSS DFYNNSISSN GSHLGTKQQV FQGTNSLGLK SSQSVQSIRP PYNRAVSLDS PVSVGSSPPV
       890        900        910        920        930        940        950        960
KNISAFPMLP KQPMLGGNPR MMDSQENYGS SMGDWGLPNS KAGRMEPMNS NSMGRPGGDY NTSLPRPALG GSIPTLPLRS
       970        980        990       1000       1010       1020       1030       1040
NSIPGARPVL QQQQQMLQMR PGEIPMGMGA NPYGQAAASN QLGSWPDGML SMEQVSHGTQ NRPLLRNSLD DLVGPPSNLE
      1050       1060       1070       1080       1090       1100       1110       1120
GQSDERALLD QLHTLLSNTD ATGLEEIDRA LGIPELVNQG QALEPKQDAF QGQEAAVMMD QKAGLYGQTY PAQGPPMQGG
      1130       1140       1150       1160       1170       1180       1190       1200
FHLQGQSPSF NSMMNQMNQQ GNFPLQGMHP RANIMRPRTN TPKQLRMQLQ QRLQGQQFLN QSRQALELKM ENPTAGGAAV
      1210       1220       1230       1240       1250       1260       1270       1280
MRPMMQPQQG FLNAQMVAQR SRELLSHHFR QQRVAMMMQQ QQQQQQQQQQ QQQQQQQQQQ QQQQQQQTQA FSPPPNVTAS
      1290       1300       1310       1320       1330       1340       1350       1360
PSMDGLLAGP TMPQAPPQQF PYQPNYGMGQ QPDPAFGRVS SPPNAMMSSR MGPSQNPMMQ HPQAASIYQS SEMKGWPSGN
      1370       1380       1390       1400       1410       1420
LARNSSFSQQ QFAHQGNPAV YSMVHMNGSS GHMGQMNMNP MPMSGMPMGP DQKYC
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
544	1	630.6481	4.75	3	35.4	14.2	2	18-35	K.RKLPCDTPGQGLTCSGEK.R		mdown:qdown 0.74 Wdown:Qdown 0.60
286	1	881.1736	82.04	3	32.7	11.0	2	199-220	R. MLMKTPHDILEDINASPEMRQR. Y	Oxidation: 19	
787	1	1115.0348	46.39	2	38.7	10.9	1	234-252	R.AMMEEGEDLQSCMICVARR.I	Carbamidomethyl: 15	

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Detailed Protein Report

Protein 285: PREDICTED: uncharacterized protein LOC102723569 isoform X1 [Homo sapiens]

Accession:	gi|578835246	**Score:**	36.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	28.7
Database Date:	2015-11-30	**pI:**	10.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	15.3
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	0.37	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	1.53	**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
169	1	826.3632	-11.95	3	30.9	10.2	0	223-244	K.CWLQGTESSPCHSPCYPLGNLK.G	Carbamidomethyl: 11	mdown:qdown 0.37 Wdown:Qdown 1.53

Detailed Protein Report

Protein 286: PREDICTED: collagen alpha-4(IV) chain isoform X9 [Homo sapiens]

Accession: gi|578803629
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 36.0
MW [kDa]: 135.0
pI: 10.1
Sequence Coverage [%]: 3.8
No. of unique Peptides: 2

Quantitation

mdown:qdown **Median:** 7.48 **CV:** 0.00 % **No. of Peptides:** 1
Wdown:Qdown **Median:** 1.74 **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
464	3	607.1279	-228.90	2	34.7	14.4	0	1142-1153	R.GQPGEMGDPGPR.G	Oxidation: 6	mdown:qdown 7.48 Wdown:Qdown 1.74
950	1	984.1390	132.77	2	41.4	10.5	1	1230-1252	K. GPPGPPGSSGPPGPAGATGRAP D		

Detailed Protein Report

Protein 287: stromal interaction molecule 2 isoform 2 precursor [Homo sapiens]

Accession:	gi|281182822	**Score:**	36.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	83.9
Database Date:	2015-11-30	**pI:**	6.3
		Sequence Coverage [%]:	6.0
		No. of unique Peptides:	1

Quantitation

Wdown:Qdown **Median:** 1.24 **CV:** 0.00 % **No. of 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	Ratios
1585	1	942.4058	-100.34	2	49.7	13.0	1	661-677	K.SMIFSPASKVYNGILEK.S		Wdown:Qdown 1.24

Detailed Protein Report

Protein 288: **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 289: **PREDICTED: Fanconi anemia-associated protein of 100 kDa isoform X2 [Homo sapiens]**

Accession:	gi|578831470	**Score:**	35.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	77.0
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
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 290: protein-tyrosine kinase 2-beta isoform b [Homo sapiens]

Accession:	gi|27886588	**Score:**	35.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	111.1
Database Date:	2015-11-30	**pI:**	5.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSGVSEPLSR	VKLGTLRRPE	GPAEPMVVVP	VDVEKEDVRI	LKVCFYSNSF	NPGKNFKLVK	CTVQTEIREI	ITSILLSGRI
90	100	110	120	130	140	150	160
GPNIRLAECY	GLRLKHMKSD	EIHWLHPQMT	VGEVQDKYEC	LHVEAEWRYD	LQIRYLPEDF	MESLKEDRTT	LLYFYQQLRN
170	180	190	200	210	220	230	240
DYMQRYASKV	SEGMALQLGC	LELRRFFKDM	PHNALDKKSN	FELLEKEVGL	DLFFPKQMQE	NLKPKQFRKM	IQQTFQQYAS
250	260	270	280	290	300	310	320
LREEECVMKF	FNTLAGFANI	DQETYRCELI	QGWNITVDLV	IGPKGIRQLT	SQDAKPTCLA	EFKQIRSIRC	LPLEEGQAVL
330	340	350	360	370	380	390	400
QLGIEGAPQA	LSIKTSSLAE	AENMADLIDG	YCRLQGEHQG	SLIIHPRKDG	EKRNSLPQIP	MLNLEARRSH	LSESCSIESD
410	420	430	440	450	460	470	480
IYAEIPDETL	RRPGGPQYGI	AREDVVLNRI	LGEGFFGEVY	EGVYTNHKGE	KINVAVKTCK	KDCTLDNKEK	FMSEAVIMKN
490	500	510	520	530	540	550	560
LDHPHIVKLI	GIIEEEPTWI	IMELYPYGEL	GHYLERNKNS	LKVLTLVLYS	LQICKAMAYL	ESINCVHRDI	AVRNILVASP
570	580	590	600	610	620	630	640
ECVKLGDFGL	SRYIEDEDYY	KASVTRLPIK	WMSPESINFR	RFTTASDVWM	FAVCMWEILS	FGKQPFFWLE	NKDVIGVLEK
650	660	670	680	690	700	710	720
GDRLPKPDLC	PPVLYTLMTR	CWDYDPSDRP	RFTELVCSLS	DVYQMEKDIA	MEQERNARYR	TPKILEPTAF	QEPPPKPSRP
730	740	750	760	770	780	790	800
KYRPPPQTNL	LAPKLQFQEE	DFIQPSSREE	AQQLWEAEKV	KMRQILDKQQ	KQMVEDYQWL	RQEEKSLDPM	VYMNDKSPLT
810	820	830	840	850	860	870	880
PEKEVGYLEF	TGPPQKPPRL	GAQSIQPTAN	LDRTDDLVYL	NVMELVRAVL	ELKNELCQLP	PEGYVVVVKN	VGLTLRKLIG
890	900	910	920	930	940	950	960
SVDDLLPSLP	SSSRTEIEGT	QKLLNKDLAE	LINKMRLAQQ	NAVTSLSEEC	KRQMLTASHT	LAVDAKNLLD	AVDQAKVLAN
970							
LAHPPAE							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
458	1	544.1530	-199.80	2	34.7	10.3	0	471-479	K.FMSEAVIMK.N	Oxidation: 2, 8

Detailed Protein Report

Protein 291: prolow-density lipoprotein receptor-related protein 1 precursor [Homo sapiens]

Accession:	gi|126012562	**Score:**	35.9
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 [%]:**	1.1
		No. of unique Peptides:	1

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
127	1	849.3809	-43.54	2	30.9	15.1	1	1560-1573	R.TVSCACPHLMKLHK.D	Carbamidomethyl: 4, 6; Oxidation: 10

Detailed Protein Report

Protein 292: PREDICTED: cortactin-binding protein 2 isoform X1 [Homo sapiens]

Accession:	gi|530386508	**Score:**	35.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	179.5
Database Date:	2015-11-30	**pI:**	9.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.1
		No. of unique Peptides:	2

Quantitation

mdown:qdown **Median:** 2.68 **CV:** 102.48 % **No. of Peptides:** 2

```
        10          20          30          40          50          60          70          80
MIWCLHPQKK  KEFDVDTLSK  SELRMLLSVM  EGELEARDLV  IEALRARRKE  VFIQERYGRF  NLNDPFLALQ  RDYEAGAGDK
        90         100         110         120         130         140         150         160
EKKPVCTNPL  SILEAVMAHC  KKMQERMSAQ  LAAAESRQKK  LEMEKLQLQA  LEQEHKKLAA  RLEEERGKNK  QVVLMLVKEC
       170         180         190         200         210         220         230         240
KQLSGKVIEE  AQKLEDVMAK  LEEEKKKTNE  LEEELSAEKR  RSTEMEAQME  KQLSEFDTER  EQLRAKLNRE  EAHTTDLKEE
       250         260         270         280         290         300         310         320
IDKMRKMIEQ  LKRGSDSKPS  LSLPRKTKDR  RLVSISVGTE  GTVTRSVACQ  TDLVTENADH  MKKLPLTMPV  KPSTGSPLVS
       330         340         350         360         370         380         390         400
ANAKGSVCTS  ATMARPGIDR  QASYGDLIGA  SVPAFPPPSA  NKIEENGPST  GSTPDPTSST  PPLPSNAAPP  TAQTPGIAPQ
       410         420         430         440         450         460         470         480
NSQAPPMHSL  HSPCANTSLH  PGLNPRIQAA  RFRFQGNAND  PDQNGNTTQS  PPSRDVSPTS  RDNLVAKQLA  RNTVTQALSR
       490         500         510         520         530         540         550         560
FTSPQAGAPS  RPGVPPTGDV  GTHPPVGRTS  LKTHGVARVD  RGNPPPIPPK  KPGLSQTPSP  PHPQLKVIID  SSRASNTGAK
       570         580         590         600         610         620         630         640
VDNKTVASTP  SSLPQGNRVI  NEENLPKSSS  PQLPPKPSID  LTVAPAGCAV  SALATSQVGA  WPAATPGLNQ  PACSDSSLVI
       650         660         670         680         690         700         710         720
PTTIAFCSSI  NPVSASSCRP  GASDSLLVTA  SGWSPSLTPL  LMSGGPAPLA  GRPTLLQQAA  AQGNVTLLSM  LLNEEGLDIN
       730         740         750         760         770         780         790         800
YSCEDGHSAL  YSAAKNGHTD  CVRLLLSAEA  QVNAADKNGF  TPLCAAAAQG  HFECVELLIS  YDANINHAAD  GGQTPLYLAC
       810         820         830         840         850         860         870         880
KNGNKECIKL  LLEAGTNRSV  KTTDGWTPVH  AAVDTGNVDS  LKLLMYHRIP  AHGNSFNEEE  SESSVFDLDG  GEESPEGISK
       890         900         910         920         930         940         950         960
PVVPADLINH  ANREGWTAAH  IAASKGFKNC  LEILCRHGGL  EPERRDKCNR  TVHDVATDDC  KHLLENLNAL  KIPLRISVGE
       970         980         990        1000        1010        1020        1030        1040
IEPSNYGSDD  LECENTICAL  NIRKQTSWDD  FSKAVSQALT  NHFQAISSDG  WWSLEDVTCN  NTTDSNIGLS  ARSIRSITLG
      1050        1060        1070        1080        1090        1100        1110        1120
NVPWSVGQSF  AQSPWDFMRK  NKAEHITVLL  SGPQEGCLSS  VTYASMIPLQ  MMQNYLRLVE  QYHNVIFHGP  EGSLQDYIVH
      1130        1140        1150        1160        1170        1180        1190        1200
QLALCLKHRQ  MAAGFSCEIV  RAEVDAGFSK  EQLLDLFISS  ACLIPVKQSP  SKKKIIIILE  NLEKSSLSEL  LRDFLAPLEN
      1210        1220        1230        1240        1250        1260        1270        1280
RSTESPCTFQ  KGNGLSECYY  FHENCFLMGT  IAKACLQGSD  LLVQQHFRWV  QLRWDGEPMQ  GLLQRFLRRK  VVNKFKGQAP
      1290        1300        1310        1320        1330        1340        1350        1360
SPCDPVCKIV  DWALSVWRQL  NSCLARLGTP  EALLGPKYFL  SCPVVPGHAQ  VTVKWMSKLW  NGVIAPRVQE  AILSRASVKR
      1370        1380        1390        1400        1410        1420        1430        1440
QPGFGQTTAK  RHPSQGQQAV  VKAALSILLN  KAVLHGCPLP  RAELDQHTAD  FKGGSFPLSI  VSSYNTCNKK  KGESGAWRKV
      1450        1460        1470        1480        1490        1500        1510        1520
NTSPRRKSGR  FSLPTWNKPD  LSTEGMKNKT  ISQLNCNRNA  SLSKQKSLEN  DLSLTLNLDQ  RLSLGSDDEA  DLVKELQSMC
      1530        1540        1550        1560        1570        1580        1590        1600
SSKSESDISK  IADSRDDLRM  FDSSGNNPVL  SATINNLRMP  VSQKEVSPLS  SHQTTECSNS  KSKTELGVSR  VKSFLPVPRS
      1610        1620        1630        1640        1650
KVTQCSQNTK  RSSSSSNTRQ  IEINNNSKEV  NWNLHKNEHL  EKPNK
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
493	1	464.6529	-266.41	2	34.8	10.9	0	38-45	R.DLVIEALR.A		mdown:qdown 6.24

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2703	3	973.4604	-78.66	2	65.0	13.9	0	1151-1167	K.EQLLDLFISSACLIPVK.Q	Carbamidomethyl: 12	mdown:qdown 1.15

Detailed Protein Report

Protein 293: sodium channel protein type 7 subunit alpha [Homo sapiens]

Accession:	gi|111378393	**Score:**	35.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	193.4
Database Date:	2015-11-30	**pI:**	9.1
		Sequence Coverage [%]:	1.4
		No. of unique Peptides:	1

Quantitation

Wdown:Qdown	**Median:**	4.16	**CV:**	0.00 %	**No. of Peptides:**	1

Alias proteins:

Accession	Name	Description
gi|578804726	refseq_human (refseq_human_20140103.fasta)	PREDICTED: sodium channel protein type 7 subunit alpha isoform X3 [Homo sapiens]
gi|578804724	refseq_human (refseq_human_20140103.fasta)	PREDICTED: sodium channel protein type 7 subunit alpha isoform X2 [Homo sapiens]
gi|578804722	refseq_human (refseq_human_20140103.fasta)	PREDICTED: sodium channel protein type 7 subunit alpha isoform X1 [Homo sapiens]

Detailed Protein Report

10	20	30	40	50	60	70	80
MLASPEPKGL	VPFTKESFEL	IKQHIAKTHN	EDHEEEDLKP	TPDLEVGKKL	PFIYGNLSQG	MVSEPLEDVD	PYYYKKKNTF
90	100	110	120	130	140	150	160
IVLNKNRTIF	RFNAASILCT	LSPFNCIRRT	TIKVLVHPFF	QLFILISVLI	DCVFMSLTNL	PKWRPVLENT	LLGIYTFEIL
170	180	190	200	210	220	230	240
VKLFARGVWA	GSFSFLGDPW	NWLDFSVTVF	EVIIRYSPLD	FIPTLQTART	LRILKIIPLN	QGLKSLVGVL	IHCLKQLIGV
250	260	270	280	290	300	310	320
IILTLFFLSI	FSLIGMGLFM	GNLKHKCFRW	PQENENETLH	NRTGNPYYIR	ETENFYYLEG	ERYALLCGNR	TDAGQCPEGY
330	340	350	360	370	380	390	400
VCVKAGINPD	QGFTNFDSFG	WALFALFRLM	AQDYPEVLYH	QILYASGKVY	MIFFVVVSFL	FSFYMASLFL	GILAMAYEEE
410	420	430	440	450	460	470	480
KQRVGEISKK	IEPKFQQTGK	ELQEGNETDE	AKTIQIEMKK	RSPISTDTSL	DVLEDATLRH	KEELEKSKKI	CPLYWYKFAK
490	500	510	520	530	540	550	560
TFLIWNCSPC	WLKLKEFVHR	IIMAPFTDLF	LIICIILNVC	FLTLEHYPMS	KQTNTLLNIG	NLVFIGIFTA	EMIFKIIAMH
570	580	590	600	610	620	630	640
PYGYFQVGWN	IFDSMIVFHG	LIELCLANVA	GMALLRLFRM	LRIFKLGKYW	PTFQILMWSL	SNSWVALKDL	VLLLFTFIFF
650	660	670	680	690	700	710	720
SAAFGMKLFG	KNYEEFVCHI	DKDCQLPRWH	MHDFFHSFLN	VFRILCGEWV	ETLWDCMEVA	GQSWCIPFYL	MVILIGNLLV
730	740	750	760	770	780	790	800
LYLFLALVSS	FSSCKDVTAE	ENNEAKNLQL	AVARIKKGIN	YVLLKILCKT	QNVPKDTMDH	VNEVYVKEDI	SDHTLSELSN
810	820	830	840	850	860	870	880
TQDFLKDKEK	SSGTEKNATE	NESQSLIPSP	SVSETVPIAS	GESDIENLDN	KEIQSKSGDG	GSKEKIKQSS	SSECSTVDIA
890	900	910	920	930	940	950	960
ISEEEEMFYG	GERSKHLKNG	CRRGSSLGQI	SGASKKGKIW	QNIRKTCCKI	VENNWFKCFI	GLVTLLSTGT	LAFEDIYMDQ
970	980	990	1000	1010	1020	1030	1040
RKTIKILLEY	ADMIFTYIFI	LEMLLKWMAY	GFKAYFSNGW	YRLDFVVVIV	FCLSLIGKTR	EELKPLISMK	FLRPLRVLSQ
1050	1060	1070	1080	1090	1100	1110	1120
FERMKVVVRA	LIKTTLPTLN	VFLVCLMIWL	IFSIMGVDLF	AGRFYECIDP	TSGERFPSSE	VMNKSRCESL	LFNESMLWEN
1130	1140	1150	1160	1170	1180	1190	1200
AKMNFDNVGN	GFLSLLQVAT	FNGWITIMNS	AIDSVAVNIQ	PHFEVNIYMY	CYFINFIIFG	VFLPLSMLIT	VIIDNFNKHK
1210	1220	1230	1240	1250	1260	1270	1280
IKLGGSNIFI	TVKQRKQYRR	LKKLMYEDSQ	RPVPRPLNKL	QGFIFDVVTS	QAFNVIVMVL	ICFQAIAMMI	DTDVQSLQMS
1290	1300	1310	1320	1330	1340	1350	1360
IALYWINSIF	VMLYTMECIL	KLIAFRCFYF	TIAWNIFDFM	VVIFSITGLC	LPMTVGSYLV	PPSLVQLILL	SRIIHMLRLG
1370	1380	1390	1400	1410	1420	1430	1440
KGPKVFHNLM	LPLMLSLPAL	LNIILLIFLV	MFIYAVFGMY	NFAYVKKEAG	INDVSNFETF	GNSMLCLFQV	AIFAGWDGML
1450	1460	1470	1480	1490	1500	1510	1520
DAIFNSKWSD	CDPDKINPGT	QVRGDCGNPS	VGIFYFVSYI	LISWLIIVNM	YIVVVMEFLN	IASKKKNKTL	SEDDFRKFFQ
1530	1540	1550	1560	1570	1580	1590	1600
VWKRFDPDRT	QYIDSSKLSD	FAAALDPPLF	MAKPNKGQLI	ALDLPMAVGD	RIHCLDILLA	FTKRVMGQDV	RMEKVVSEIE
1610	1620	1630	1640	1650	1660	1670	1680
SGFLLANPFK	ITCEPITTTL	KRKQEAVSAT	IIQRAYKNYR	LRRNDKNTSD	IHMIDGDRDV	HATKEGAYFD	KAKEKSPIQS
1690							
QI							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
235	1	627.3257	-128.41	2	32.1	15.7	2	747-757	K.NLQLAVARIKK.G		Wdown:Qdown 4.16

Detailed Protein Report

Protein 294: PREDICTED: dedicator of cytokinesis protein 11 isoform X2 [Homo sapiens]

Accession:	gi|530422336	**Score:**	35.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	235.7
Database Date:	2015-11-30	**pI:**	8.1
Modification(s):	Oxidation	**Sequence Coverage [%]:**	0.5
		No. of unique Peptides:	2

Detailed Protein Report

10	20	30	40	50	60	70	80
MFKEKAKVVE	PLDYENVIAQ	RKTQIYSDPL	RDLLMFPMED	ISISVIGRQR	RTVQSTVPED	AEKRAQSLFV	KECIKTYSTD
90	100	110	120	130	140	150	160
WHVVNYKYED	FSGDFRMLPC	KSLRPEKIPN	HVFEIDEDCE	KDEDSSSLCS	QKGGVIKQGW	LHKANVNSTI	TVTMKVFKRR
170	180	190	200	210	220	230	240
YFYLTQLPDG	SYILNSYKDE	KNSKESKGCI	YLDACIDVVQ	CPKMRRHAFE	LKMLDKYSHY	LAAETEQEME	EWLITLKKII
250	260	270	280	290	300	310	320
QINTDSLVQE	KKETVETAQD	DETSSQGKAE	NIMASLERSM	HPELMKYGRE	TEQLNKLSRG	DGRQNLFSFD	SEVQRLDFSG
330	340	350	360	370	380	390	400
IEPDIKPFEE	KCNKRFLVNC	HDLTFNILGQ	IGDNAKGPPT	NVEPFFINLA	LFDVKNNCKI	SADFHVDLNP	PSVREMLWGS
410	420	430	440	450	460	470	480
STQLASDGSP	KGSSPESYIH	GIAESQLRYI	QQGIFSVTNP	HPEIFLVARI	EKVLQGNITH	CAEPYIKNSD	PVKTAQKVHR
490	500	510	520	530	540	550	560
TAKQVCSRLG	QYRMPFAWAA	RPIFKDTQGS	LDLDGRFSPL	YKQDSSKLSS	EDILKLLSEY	KKPEKTKLQI	IPGQLNITVE
570	580	590	600	610	620	630	640
CVPVDLSNCI	TSSYVPLKPF	EKNCQNITVE	VEEFVPEMTK	YCYPFTIYKN	HLYVYPLQLK	YDSQKTFAKA	RNIAVCVEFR
650	660	670	680	690	700	710	720
DSDESDASAL	KCIYGKPAGS	VFTTNAYAVV	SHHNQNPEFY	DEIKIELPIH	LHQKHHLLFT	FYHVSCEINT	KGTTKKQDTV
730	740	750	760	770	780	790	800
ETPVGFAWVP	LLKDGRIITF	EQQLPVSANL	PPGYLNLNDA	ESRRQCNVDI	KWVDGAKPLL	KIKSHLESTI	YTQDLHVHKF
810	820	830	840	850	860	870	880
FHHCQLIQSG	SKEVPGELIK	YLKCLHAMEI	QVMIQFLPVI	LMQLFRVLTN	MTHEDDVPIN	CTMVLLHIVS	KCHEEGLDSY
890	900	910	920	930	940	950	960
LRSFIKYSFR	PEKPSAPQAQ	LIHETLATTM	IAILKQSADF	LSINKLLKYS	WFFFEIIAKS	MATYLLEENK	IKLPRGQRFP
970	980	990	1000	1010	1020	1030	1040
ETYHHVLHSL	LLAIIPHVTI	RYAEIPDESR	NVNYSLASFL	KRCLTLMDRG	FIFNLINDYI	SGFSPKDPKV	LAEYKFEFLQ
1050	1060	1070	1080	1090	1100	1110	1120
TICNHEHYIP	LNLPMAFAKP	KLQRVQDFFS	FAVDRLTSVD	SNLEYSLSDE	YCKHHFLVGL	LLRETSIALQ	DNYEIRYTAI
1130	1140	1150	1160	1170	1180	1190	1200
SVIKNLLIKH	AFDTRYQHKN	QQAKIAQLYL	PFVGLLLENI	QRLAGRDTLY	SCAAMPNSAS	RDEFPCGFTS	PANRGSLSTD
1210	1220	1230	1240	1250	1260	1270	1280
KDTAYGSFQN	GHGIKREDSR	GSLIPEGATG	FPDQGNTGEN	TRQSSTRSSV	SQYNRLDQYE	IRSLLMCYLY	IVKMISEDTL
1290	1300	1310	1320	1330	1340	1350	1360
LTYWNKVSPQ	ELINILILLE	VCLFHFRYMG	KRNIARVHDA	WLSKHFGIDR	KSQTMPALRN	RSGVMQARLQ	HLSSLESSFT
1370	1380	1390	1400	1410	1420	1430	1440
LNHSSTTTEA	DIFHQALLEG	NTATEVSLTV	LDTISFFTQC	FKTQLLNNDG	HNPLMKKVFD	IHLAFLKNGQ	SEVSLKHVFA
1450	1460	1470	1480	1490	1500	1510	1520
SLRAFISKFP	SAFFKGRVNM	CAAFCYEVLK	CCTSKISSTR	NEASALLYLL	MRNNFEYTKR	KTFLRTHLQI	IIAVSQLIAD
1530	1540	1550	1560	1570	1580	1590	1600
VALSGGSRFQ	ESLFIINNFA	NSDRPMKATA	FPAEVKDLTK	RIRTVLMATA	QMKEHEKDPE	MLIDLQYSLA	KSYASTPELR
1610	1620	1630	1640	1650	1660	1670	1680
KTWLDSMAKI	HVKNGDFSEA	AMCYVHVAAL	VAEFLHRKKL	FPNGCSAFKK	ITPNIDEEGA	MKEDAGMMDV	HYSEEVLLEL
1690	1700	1710	1720	1730	1740	1750	1760
LEQCVDGLWK	AERYEIISEI	SKLIVPIYEK	RREFEKLTQV	YRTLHGAYTK	ILEVMHTKKR	LLGTFFRVAF	YGQSFFEEED
1770	1780	1790	1800	1810	1820	1830	1840
GKEYIYKEPK	LTGLSEISLR	LVKLYGEKFG	TENVKIIQDS	DKVNAKELDP	KYAHIQVTYV	KPYFDDKELT	ERKTEFERNH
1850	1860	1870	1880	1890	1900	1910	1920
NISRFVFEAP	YTLSGKKQGC	IEEQCKRRTI	LTTSNSFPYV	KKRIPINCEQ	QINLKPIDVA	TDEIKDKTAE	LQKLCSSTDV
1930	1940	1950	1960	1970	1980	1990	2000
DMIQLQLKLQ	GCVSVQVNAG	PLAYARAFLN	DSQASKYPPK	KVSELKDMFR	KFIQACSIAL	ELNERLIKED	QVEYHEGLKS
2010	2020	2030	2040	2050	2060		
NFRDMVKELS	DIIHEQILQE	DTMHSPWMSN	TLHVFCAISG	TSSDRGYGSP	RYAEV		

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

	Cmpds.		[ppm]		[min]					
2375	3	682.7793	-68.50	2	58.1	17.0	1	279-289	R.SMHPELMKYGR.E	Oxidation: 7
1995	1	682.7325	-137.16	2	53.4	18.8	1	279-289	R.SMHPELMKYGR.E	Oxidation: 2

Detailed Protein Report

Protein 295: PREDICTED: GRAM domain-containing protein 1C isoform X2 [Homo sapiens]

Accession:	gi|530374810	**Score:**	35.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	69.6
Database Date:	2015-11-30	**pI:**	6.9
		Sequence Coverage [%]:	4.8
		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 296: 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

mdown:qdown	**Median:**	0.50	**CV:**	14.84 %	**No. of Peptides:**	2
Wdown:Qdown	**Median:**	0.88	**CV:**	0.00 %	**No. of Peptides:**	1

```
        10         20         30         40         50         60         70         80
MQTSSPTTRL FLRIKEKSLK EEKIIIVKEF EKITKPGEME KKMKILREST EELRKEIMQK KLEIKNLRED LASKQKQLLK
        90        100        110        120        130        140        150        160
EQKELEELLG HQVVLKDEVA HHQTIPVQIG KEIEKITRKK VEMEKKKIVL EQEVKTLNDS LKKVENKVSA IVDEKENVIK
       170        180        190        200        210        220        230        240
EVEGKRALLE IKEREHNQLV KLLELARENE ATSLTERGIL DLNLRNSLID KQNYHDELSR KQREKERDFR NLRKMELLLK
       250        260        270        280        290        300        310        320
VSWDALRQTQ ALHQRLLLEM EAIPKDDSTL SERRELHKE  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	mdown:qdown 0.58
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		Wdown:Qdown 0.88 mdown:qdown 0.43

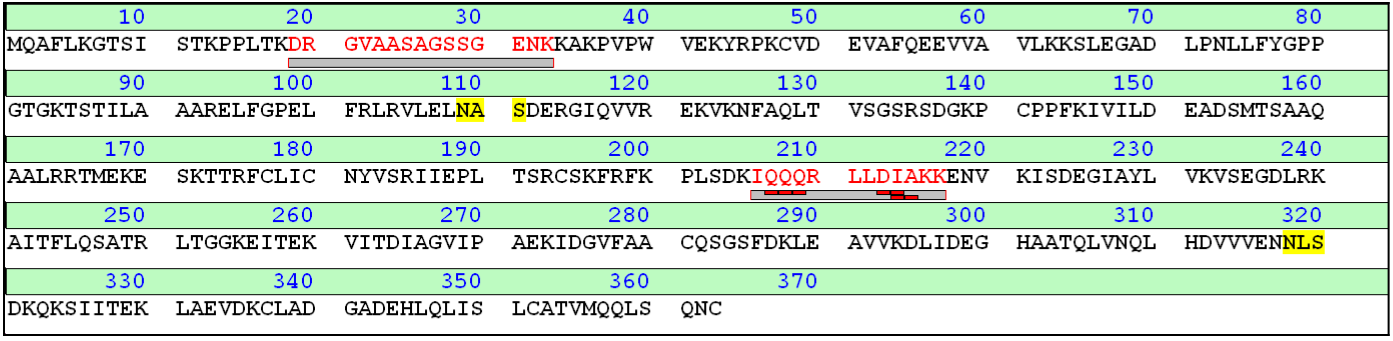
Detailed Protein Report

Protein 297: replication factor C subunit 4 [Homo sapiens]

Accession:	gi|4506491	**Score:**	35.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	39.7
Database Date:	2015-11-30	**pI:**	9.3
		Sequence Coverage [%]:	7.4
		No. of unique Peptides:	2

Alias proteins:

Accession	**Name**	**Description**
gi|31881687	refseq_human (refseq_human_20140103.fasta)	replication factor C subunit 4 [Homo sapiens]



```
        10         20         30         40         50         60         70         80
MQAFLKGTSI STKPPLTKDR GVAASAGSSG ENKKAKPVPW VEKYRPKCVD EVAFQEEVVA VLKKSLEGAD LPNLLFYGPP
        90        100        110        120        130        140        150        160
GTGKTSTILA AARELFGPEL FRLRVLELNA SDERGIQVVR EKVKNFAQLT VSGSRSDGKP CPPFKIVILD EADSMTSAAQ
       170        180        190        200        210        220        230        240
AALRRTMEKE SKTTRFCLIC NYVSRIIEPL TSRCSKFRFK PLSDKIQQQR LLDIAKKENV KISDEGIAYL VKVSEGDLRK
       250        260        270        280        290        300        310        320
AITFLQSATR LTGGKEITEK VITDIAGVIP AEKIDGVFAA CQSGSFDKLE AVVKDLIDEG HAATQLVNQL HDVVVENNLS
       330        340        350        360        370
DKQKSIITEK LAEVDKCLAD GADEHLQLIS LCATVMQQLS QNC
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2686	2	703.3641	38.67	2	64.8	15.8	1	19-33	K.DRGVAASAGSSGENK.K	
1817	2	727.2971	-204.84	2	51.2	19.9	2	206-217	K.IQQQRLLDIAKK.E	

Detailed Protein Report

Protein 298: CCR4-NOT transcription complex subunit 1 isoform a [Homo sapiens]

Accession:	gi|42716275	**Score:**	35.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	266.8
Database Date:	2015-11-30	**pI:**	6.7
		Sequence Coverage [%]:	1.3
		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	QSKMKPSDLS	QVWPEANQHF	SKEIDDEANS	YFQRIYNHPP	HPTMSVDEVL	EMLQRFKDST
890	900	910	920	930	940	950	960
IKREREVFNC	MLRNLFEEYR	FFPQYPDKEL	HITACLFGGI	IEKGLVTYMA	LGLALRYVLE	ALRKPFGSKM	YYFGIAALDR
970	980	990	1000	1010	1020	1030	1040
FKNRLKDYPQ	YCQHLASISH	FMQFPHHLQE	YIEYGQQSRD	PPVKMQGSIT	TPGSIALAQA	QAQAQVPAKA	PLAGQVSTMV
1050	1060	1070	1080	1090	1100	1110	1120
TTSTTTTVAK	TVTVTRPTGV	SFKKDVPPSI	NTTNIDTLLV	ATDQTERIVE	PPENIQEKIA	FIFNNLSQSN	MTQKVEELKE
1130	1140	1150	1160	1170	1180	1190	1200
TVKEEFMPWV	SQYLVMKRVS	IEPNFHSLYS	NFLDTLKNPE	FNKMVLNETY	RNIKVLLTSD	KAAANFSDRS	LLKNLGHWLG
1210	1220	1230	1240	1250	1260	1270	1280
MITLAKNKPI	LHTDLDVKSL	LLEAYVKGQQ	ELLYVVPFVA	KVLESSIRSV	VFRPPNPWTM	AIMNVLAELH	QEHDLKLNLK
1290	1300	1310	1320	1330	1340	1350	1360
FEIEVLCKNL	ALDINELKPG	NLLKDKDRLK	NLDEQLSAPK	KDVKQPEELP	PITTTTTSTT	PATNTTCTAT	VPPQPQYSYH
1370	1380	1390	1400	1410	1420	1430	1440
DINVYSLAGL	APHITLNPTI	PLFQAHPQLK	QCVRQAIERA	VQELVHPVVD	RSIKIAMTTC	EQIVRKDFAL	DSEESRMRIA
1450	1460	1470	1480	1490	1500	1510	1520
AHHMMRNLTA	GMAMITCREP	LLMSISTNLK	NSFASALRTA	SPQQREMMDQ	AAAQLAQDNC	ELACCFIQKT	AVEKAGPEMD
1530	1540	1550	1560	1570	1580	1590	1600
KRLATEFELR	KHARQEGRRY	CDPVVLTYQA	ERMPEQIRLK	VGGVDPKQLA	VYEEFARNVP	GFLPTNDLSQ	PTGFLAQPMK
1610	1620	1630	1640	1650	1660	1670	1680
QAWATDDVAQ	IYDKCITELE	QHLHAIPPTL	AMNPQAQALR	SLLEVVVLSR	NSRDAIAALG	LLQKAVEGLL	DATSGADADL
1690	1700	1710	1720	1730	1740	1750	1760
LLRYRECHLL	VLKALQDGRA	YGSPWCNKQI	TRCLIECRDE	YKYNVEAVEL	LIRNHLVNMQ	QYDLHLAQSM	ENGLNYMAVA
1770	1780	1790	1800	1810	1820	1830	1840
FAMQLVKILL	VDERSVAHVT	EADLFHTIET	LMRINAHSRG	NAPEGLPQLM	EVVRSNYEAM	IDRAHGGPNF	MMHSGISQAS
1850	1860	1870	1880	1890	1900	1910	1920
EYDDPPGLRE	KAEYLLREWV	NLYHSAAAGR	DSTKAFSAFV	GQMHQQGILK	TDDLITRFFR	LCTEMCVEIS	YRAQAEQQHN
1930	1940	1950	1960	1970	1980	1990	2000
PAANPTMIRA	KCYHNLDAFV	RLIALLVKHS	GEATNTVTKI	NLLNKVLGIV	VGVLLQDHDV	RQSEFQQLPY	HRIFIMLLLE
2010	2020	2030	2040	2050	2060	2070	2080
LNAPEHVLET	INFQTLTAFC	NTFHILRPTK	APGFVYAWLE	LISHRIFIAR	MLAHTPQQKG	WPMYAQLLID	LFKYLAPFLR
2090	2100	2110	2120	2130	2140	2150	2160
NVELTKPMQI	LYKGTLRVLL	VLLHDFPEFL	CDYHYGFCDV	IPPNCIQLRN	LILSAFPRNM	RLPDPFTPNL	KVDMLSEINI
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
585	1	603.8101	58.84	2	36.2	10.4	0	2365-2376	K.QAQQVMEGTGAS.-	

Detailed Protein Report

Protein 299: **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 300: pogo transposable element with ZNF domain isoform 3 [Homo sapiens]

Accession:	gi|302699211	**Score:**	35.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	145.2
Database Date:	2015-11-30	**pI:**	6.8
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	2.1
		No. of unique Peptides:	3

Quantitation

mdown:qdown **Median:** 0.84 **CV:** 0.00 % **No. of Peptides:** 1

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
240	1	732.8262	-63.03	2	31.7	14.2	1	285-296	R.CNAQFRVTEALR.G	Carbamidomethyl: 1	mdown:qdown 0.84
2117	1	990.8950	2.39	2	55.0	10.3	1	297-312	R.GHMCYCCPEMVEYQKK.G	Oxidation: 3, 10	
2186	1	1031.8206	-95.59	2	55.9	11.0	1	297-312	R.GHMCYCCPEMVEYQKK.G	Carbamidomethyl: 4, 6	

Detailed Protein Report

Protein 301: testis- and ovary-specific PAZ domain-containing protein 1 [Homo sapiens]

Accession: gi|222537754
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 35.5
MW [kDa]: 190.8
pI: 9.1
Sequence Coverage [%]: 3.2
No. of unique Peptides: 3

Quantitation

mdown:qdown	**Median:**	1.11	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	1.14	**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
```

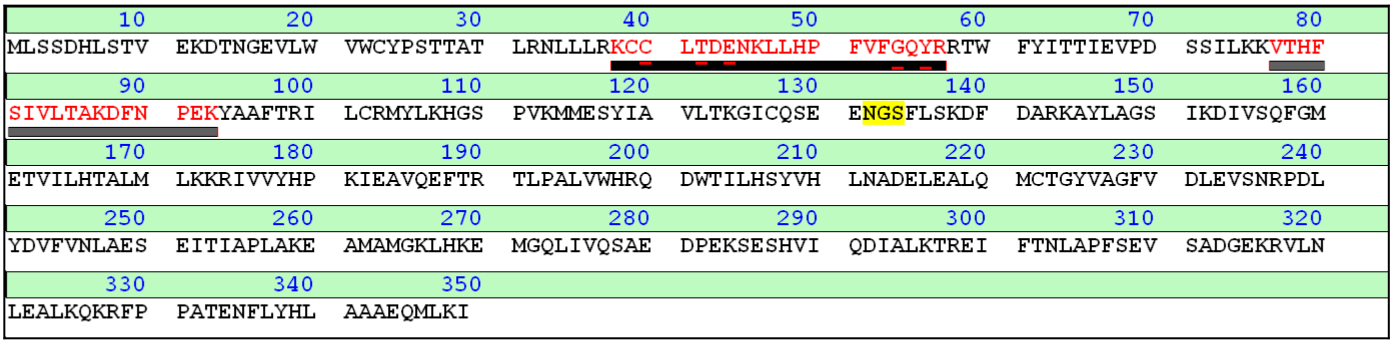
Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2728	1	913.4776	71.07	2	62.5	11.3	1	25-44	K. RQAPGPGAAGGCGPEAGGCR. E	Carbamidomethyl: 19	
934	1	872.4494	41.89	2	40.5	10.6	0	749-764	R.NSVTPVQASSDSFYNK.K		
64	1	1068.4736	-22.86	2	30.2	13.6	1	1114-1131	K.FAHVPEQGDEKVCMDVFK.K	Carbamidomethyl: 13	Wdown:Qdown 1.14 mdown:qdown 1.11

Detailed Protein Report

Protein 302: PREDICTED: protein FAM45A isoform X1 [Homo sapiens]

Accession:	gi|530393695	**Score:**	35.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	39.8
Database Date:	2015-11-30	**pI:**	6.3
		Sequence Coverage [%]:	10.6
		No. of unique Peptides:	2



```
        10         20         30         40         50         60         70         80
MLSSDHLSTV EKDTNGEVLW VWCYPSTTAT LRNLLLRKCC LTDENKLLHP FVFGQYRRTW FYITTIEVPD SSILKKVTHF
        90        100        110        120        130        140        150        160
SIVLTAKDFN PEKYAAFTRI LCRMYLKHGS PVKMMESYIA VLTKGICQSE ENGSFLSKDF DARKAYLAGS IKDIVSQFGM
       170        180        190        200        210        220        230        240
ETVILHTALM LKKRIVVYHP KIEAVQEFTR TLPALVWHRQ DWTILHSYVH LNADELEALQ MCTGYVAGFV DLEVSNRPDL
       250        260        270        280        290        300        310        320
YDVFVNLAES EITIAPLAKE AMAMGKLHKE MGQLIVQSAE DPEKSESHVI QDIALKTREI FTNLAPFSEV SADGEKRVLN
       330        340        350
LEALKQKRFP PATENFLYHL AAAEQMLKI
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2766	1	804.4142	11.70	3	63.0	10.7	2	38-57	R.KCCLTDENKLLHPFVFGQYR.R	
2881	2	973.5257	3.04	2	64.8	12.2	1	77-93	K.VTHFSIVLTAKDFNPEK.Y	

Detailed Protein Report

Protein 303: cytoplasmic dynein 1 heavy chain 1 [Homo sapiens]

Accession:	gi|33350932	**Score:**	35.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	532.1
Database Date:	2015-11-30	**pI:**	6.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	0.6
		No. of unique Peptides:	2

Quantitation

Wdown:Qdown	**Median:** 2.42	**CV:** 0.00 %	**No. of Peptides:** 1

Detailed Protein Report

10	20	30	40	50	60	70	80
MSEPGGGGGE	DGSAGLEVSA	VQNVADVSVL	QKHLRKLVPL	LLEDGGEAPA	ALEAALEEKS	ALEQMRKFLS	DPQVHTVLVE
90	100	110	120	130	140	150	160
RSTLKEDVGD	EGEEEKEFIS	YNINIDIHYG	VKSNSLAFIK	RTPVIDADKP	VSSQLRVLTL	SEDSPYETLH	SFISNAVAPF
170	180	190	200	210	220	230	240
FKSYIRESGK	ADRDGDKMAP	SVEKKIAELE	MGLLHLQQNI	EIPEISLPIH	PMITNVAKQC	YERGEKPKVT	DFGDKVEDPT
250	260	270	280	290	300	310	320
FLNQLQSGVN	RWIREIQKVT	KLDRDPASGT	ALQEISFWLN	LERALYRIQE	KRESPEVLLT	LDILKHGKRF	HATVSFDTDT
330	340	350	360	370	380	390	400
GLKQALETVN	DYNPLMKDFP	LNDLLSATEL	DKIRQALVAI	FTHLRKIRNT	KYPIQRALRL	VEAISRDLSS	QLLKVLGTRK
410	420	430	440	450	460	470	480
LMHVAYEEFE	KVMVACFEVF	QTWDDEYEKL	QVLLRDIVKR	KREENLKMVW	RINPAHRKLQ	ARLDQMRKFR	RQHEQLRAVI
490	500	510	520	530	540	550	560
VRVLRPQVTA	VAQQNQGEVP	EPQDMKVAEV	LFDAADANAI	EEVNLAYENV	KEVDGLDVSK	EGTEAWEAAM	KRYDERIDRV
570	580	590	600	610	620	630	640
ETRITARLRD	QLGTAKNANE	MFRIFSRFNA	LFVRPHIRGA	IREYQTQLIQ	RVKDDIESLH	DKFKVQYPQS	QACKMSHVRD
650	660	670	680	690	700	710	720
LPPVSGSIIW	AKQIDRQLTA	YMKRVEDVLG	KGWENHVEGQ	KLKQDGDSFR	MKLNTQEIFD	DWARKVQQRN	LGVSGRIFTI
730	740	750	760	770	780	790	800
ESTRVRGRTG	NVLKLKVNFL	PEIITLSKEV	RNLKWLGFRV	PLAIVNKAHQ	ANQLYPFAIS	LIESVRTYER	TCEKVEERNT
810	820	830	840	850	860	870	880
ISLLVAGLKK	EVQALIAEGI	ALVWESYKLD	PYVQRLAETV	FNFQEKVDDL	LIIEEKIDLE	VRSLETCMYD	HKTFSEILNR
890	900	910	920	930	940	950	960
VQKAVDDLNL	HSYSNLPIWV	NKLDMEIERI	LGVRLQAGLR	AWTQVLLGQA	EDKAEVDMDT	DAPQVSHKPG	GEPKIKNVVH
970	980	990	1000	1010	1020	1030	1040
ELRITNQVIY	LNPPIEECRY	KLYQEMFAWK	MVVLSLPRIQ	SQRYQVGVHY	ELTEEEKFYR	NALTRMPDGP	VALEESYSAV
1050	1060	1070	1080	1090	1100	1110	1120
MGIVSEVEQY	VKVWLQYQCL	WDMQAENIYN	RLGEDLNKWQ	ALLVQIRKAR	GTFDNAETKK	EFGPVVIDYG	KVQSKVNLKY
1130	1140	1150	1160	1170	1180	1190	1200
DSWHKEVLSK	FGQMLGSNMT	EFHSQISKSR	QELEQHSVDT	ASTSDAVTFI	TYVQSLKRKI	KQFEKQVELY	RNGQRLLEKQ
1210	1220	1230	1240	1250	1260	1270	1280
RFQFPPSWLY	IDNIEGEWGA	FNDIMRRKDS	AIQQQVANLQ	MKIVQEDRAV	ESRTTDLLTD	WEKTKPVTGN	LRPEEALQAL
1290	1300	1310	1320	1330	1340	1350	1360
TIYEGKFGRL	KDDREKCAKA	KEALELTDTG	LLSGSEERVQ	VALEELQDLK	GVWSELSKVW	EQIDQMKEQP	WVSVQPRKLR
1370	1380	1390	1400	1410	1420	1430	1440
QNLDALLNQL	KSFPARLRQY	ASYEFVQRLL	KGYMKINMLV	IELKSEALKD	RHWKQLMKRL	HVNWVVSELT	LGQIWDVDLQ
1450	1460	1470	1480	1490	1500	1510	1520
KNEAIVKDVL	LVAQGEMALE	EFLKQIREVW	NTYELDLVNY	QNKCRLIRGW	DDLFNKVKEH	INSVSAMKLS	PYYKVFEEDA
1530	1540	1550	1560	1570	1580	1590	1600
LSWEDKLNRI	MALFDVWIDV	QRRWVYLEGI	FTGSADIKHL	LPVETQRFQS	ISTEFLALMK	KVSKSPLVMD	VLNIQGVQRS
1610	1620	1630	1640	1650	1660	1670	1680
LERLADLLGK	IQKALGEYLE	RERSSFPRFY	FVGDEDLLEI	IGNSKNVAKL	QKHFKKMFAG	VSSIILNEDN	SVVLGISSRE
1690	1700	1710	1720	1730	1740	1750	1760
GEEVMFKTPV	SITEHPKINE	WLTLVEKEMR	VTLAKLLAES	VTEVEIFGKA	TSIDPNTYIT	WIDKYQAQLV	VLSAQIAWSE
1770	1780	1790	1800	1810	1820	1830	1840
NVETALSSMG	GGGDAAPLHS	VLSNVEVTLN	VLADSVLMEQ	PPLRRRKLEH	LITELVHQRD	VTRSLIKSKI	DNAKSFEWLS
1850	1860	1870	1880	1890	1900	1910	1920
QMRFYFDPKQ	TDVLQQLSIQ	MANAKFNYGF	EYLGVQDKLV	QTPLTDRCYL	TMTQALEARL	GGSPFGPAGT	GKTESVKALG
1930	1940	1950	1960	1970	1980	1990	2000
HQLGRFVLVF	NCDETFDFQA	MGRIFVGLCQ	VGAWGCFDEF	NRLEERMLSA	VSQQVQCIQE	ALREHSNPNY	DKTSAPITCE
2010	2020	2030	2040	2050	2060	2070	2080
LLNKQVKVSP	DMAIFITMNP	GYAGRSNLPD	NLKKLFRSLA	MTKPDRQLIA	QVMLYSQGFR	TAEVLANKIV	PFFKLCDEQL
2090	2100	2110	2120	2130	2140	2150	2160
SSQSHYDFGL	RALKSVLVSA	GNVKRERIQK	IKREKEERGE	AVDEGEIAEN	LPEQEILIQS	VCETMVPKLV	AEDIPLLFSL
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
1836	1	805.7966	-107.51	2	53.0	18.5	1	570-583	R.DQLGTAKNANEMFR.I	Oxidation: 12	Wdown:Qdown 2.42
1465	1	671.4099	30.99	2	47.1	16.6	2	705-716	R.KVQQRNLGVSGR.I		

Detailed Protein Report

Protein 304: PREDICTED: protein THEMIS isoform X2 [Homo sapiens]

Accession:	gi|578812733	**Score:**	35.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	62.5
Database Date:	2015-11-30	**pI:**	5.8
		Sequence Coverage [%]:	4.0
		No. of unique Peptides:	2

Quantitation

mdown:qdown **Median:** 1.29 **CV:** 0.00 % **No. of Peptides:** 1

Alias proteins:

Accession	Name	Description
gi|578839551	refseq_human (refseq_human_20140103.fasta)	PREDICTED: protein THEMIS isoform X2 [Homo sapiens]

10	20	30	40	50	60	70	80
MEEITRTIHI	GPSRLGHPCF	YHQKDIKLEN	LIIKQGEQIM	LNSVEEIDGE	IMVSCAVARN	HQTHSFNLPL	SQEGEFYECE
90	100	110	120	130	140	150	160
DERIYTLKEI	VEWKIPKNRT	RTVNLTDFSN	KWDSTNPFPK	DFYGTLILKP	VYEIQGVMKF	RKDIIRILPS	LDVEVKDITD
170	180	190	200	210	220	230	240
SYDANWFLQL	LSTEDLFEMT	SKEFPIVTEV	IEAPEGNHLP	QSILQPGKTI	VIHKKYQASR	ILASEIRSNF	PKRHFLIPTS
250	260	270	280	290	300	310	320
YKGKFKRRPR	EFPTAYDLEI	AKSEKEPLHV	VATKAFHSPH	DKLSSVSVGD	QFLVHQSETT	EVLCEGIKKV	VNVLACEKIL
330	340	350	360	370	380	390	400
KKSYEAALLP	LYMEGGFVEV	IHDKKQYPIS	ELCKQFRLPF	NVKVSVRDLS	IEEDVLAATP	GLQLEEDITD	SYLLISDFAN
410	420	430	440	450	460	470	480
PTECWEIPVG	RLNMTVQLVS	NFSRDAEPFL	VRTLVEEITE	EQYYMMRRYE	SSASHPPPRP	PKHPSVEETK	LTLLTLAEER
490	500	510	520	530	540	550	
TVDLPKSPKR	HHVDITKKLH	PNQAGLDSKV	LIGSQNDLVD	EEKERSNRGA	TAIAETFKNE	KHQK	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
500	1	599.8540	-33.23	2	35.6	16.2	1	25-34	K.DIKLENLIIK.Q		mdown:qdown 1.29
2974	2	698.3723	10.43	2	66.4	18.9	1	100-111	R.TRTVNLTDFSNK.W		

Detailed Protein Report

Protein 305: **A-kinase anchor protein 2 isoform 2 [Homo sapiens]**

Accession:	gi|211971074	**Score:**	35.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	94.6
Database Date:	2015-11-30	**pI:**	4.9
		Sequence Coverage [%]:	3.0
		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 306: guanylate cyclase soluble subunit alpha-3 isoform D [Homo sapiens]

Accession:	gi|194595482	**Score:**	35.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	70.1
Database Date:	2015-11-30	**pI:**	7.8
		Sequence Coverage [%]:	5.6
		No. of unique Peptides:	2

Quantitation

mdown:qdown	**Median:**	0.88	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	3.94	**CV:**	0.00 %	**No. of Peptides:**	1

```
        10         20         30         40         50         60         70         80
MFCTKLKDLK ITGECPFSLL APGQVPNESS EEAAGSSESC KATVPICQDI PEKNIQESLP QRKTSRSRVY LHTLAESICK
        90        100        110        120        130        140        150        160
LIFPEFERLN VALQRTLAKH KIKESRKSLE REDFEKTIAE QAVAAGVPVE VIKESLGEEV FKICYEEDEN ILGVVGGTLK
       170        180        190        200        210        220        230        240
DFLNSFSTLL KQSSHCQEAG KRGRLEDASI LCLDKEDDFL HVYYFFPKRT TSLILPGIIK AAAHVLYETE VEVSLMPPCF
       250        260        270        280        290        300        310        320
HNDCSEFVNQ PYLLYSVHMK STKPSLSPSK PQSSLVIPTS LFCKTFPFHF MFDKDMTILQ FGNGIRRLMN RRDFQGKPNF
       330        340        350        360        370        380        390        400
EEYFEILTPK INQTFSGIMT MLNMQFVVRV RRWDNSVKKS SRVMDLKGQM IYIVESSAIL FLGSPCVDRL EDFTGRGLYL
       410        420        430        440        450        460        470        480
SDIPIHNALR DVVLIGEQAR AQDGLKKRLG KLKATLEQAH QALEEEKKKT VDLLCSIFPC EVAQQLWQGQ VVQAKKFSNV
       490        500        510        520        530        540        550        560
TMLFSDIVGF TAICSQCSPL QVITMLNALY TRFDQQCGEL DVYKVETIGD AYCVAGGLHK ESDTHAVQIA LMALKMMELS
       570        580        590        600        610        620        630
DEVMSPHGEP IKMRIGLHSG SVFAGVVGVK MPRYCLFGNN VTLANKFESC SVPRKINVSP TTYR
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
289	1	548.1845	-238.23	2	32.7	11.4	2	2-10	M.FCTKLKDLK.I		mdown:qdown 0.88 Wdown:Qdown 3.94
2692	1	848.1258	162.49	2	64.9	11.8	0	117-133	K.TIAEQAVAAGVPVEVIK.E		

Detailed Protein Report

Protein 307: glutamate receptor ionotropic, kainate 3 precursor [Homo sapiens]

Accession:	gi|28605145	**Score:**	35.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	104.0
Database Date:	2015-11-30	**pI:**	7.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MTAPWRRLRS	LVWEYWAGLL	VCAFWIPDSR	GMPHVIRIGG	IFEYADGPNA	QVMNAEEHAF	RFSANIINRN	RTLLPNTTLT
90	100	110	120	130	140	150	160
YDIQRIHFHD	SFEATKKACD	QLALGVVAIF	GPSQGSCTNA	VQSICNALEV	PHIQLRWKHH	PLDNKDTFYV	NLYPDYASLS
170	180	190	200	210	220	230	240
HAILDLVQYL	KWRSATVVYD	DSTGLIRLQE	LIMAPSRYNI	RLKIRQLPID	SDDSRPLLKE	MKRGREFRII	FDCSHTMAAQ
250	260	270	280	290	300	310	320
ILKQAMAMGM	MTEYYHFIFT	TLDLYALDLE	PYRYSGVNLT	GFRILNVDNP	HVSAIVEKWS	MERLQAAPRS	ESGLLDGVMM
330	340	350	360	370	380	390	400
TDAALLYDAV	HIVSVCYQRA	PQMTVNSLQC	HRHKAWRFGG	RFMNFIKEAQ	WEGLTGRIVF	NKTSGLRTDF	DLDIISLKED
410	420	430	440	450	460	470	480
GLEKVGVWSP	ADGLNITEVA	KGRGPNVTDS	LTNRSLIVTT	VLEEPFVMFR	KSDRTLYGND	RFEGYCIDLL	KELAHILGFS
490	500	510	520	530	540	550	560
YEIRLVEDGK	YGAQDDKGQW	NGMVKELIDH	KADLAVAPLT	ITHVREKAID	FSKPFMTLGV	SILYRKPNGT	NPSVFSFLNP
570	580	590	600	610	620	630	640
LSPDIWMYVL	LAYLGVSCVL	FVIARFSPYE	WYDAHPCNPG	SEVVENNFTL	LNSFWFGMGS	LMQQGSELMP	KALSTRIIGG
650	660	670	680	690	700	710	720
IWWFFTLIII	SSYTANLAAF	LTVERMESPI	DSADDLAKQT	KIEYGAVKDG	ATMTFFKKSK	ISTFEKMWAF	MSSKPSALVK
730	740	750	760	770	780	790	800
NNEEGIQRAL	TADYALLMES	TTIEYVTQRN	CNLTQIGGLI	DSKGYGIGTP	MGSPYRDKIT	IAILQLQEED	KLHIMKEKWW
810	820	830	840	850	860	870	880
RGSGCPEEEN	KEASALGIQK	IGGIFIVLAA	GLVLSVLVAV	GEFVYKLRKT	AEREQRSFCS	TVADEIRFSL	TCQRRVKHKP
890	900	910	920				
QPPMMVKTDA	VINMHTFNDR	RLPGKDSMAC	STSLAPVFP				

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	666-678	R.MESPIDSADDLAK.Q	Oxidation: 1

Detailed Protein Report

Protein 308: **aldo-keto reductase family 1 member C2 isoform 2 [Homo sapiens]**

Accession:	gi|207028673	**Score:**	35.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	15.7
Database Date:	2015-11-30	**pI:**	8.9
		Sequence Coverage [%]:	23.7
		No. of unique Peptides:	1

```
         10         20         30         40         50         60         70         80
MDSKYQCVKL NDGHFMPVLG FGTYAPAEVP KSKALEAVKL AIEAGFHHID SAHVYNNEEQ VGLAIRSKIA DGSVKREDIF
         90        100        110        120        130        140
YTSKLWSNSH RPELVRPALE RSLKNLQLDY VDLYLIHFPV SVKEDIGILT WKKSPKHNS
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2935	1	859.1202	17.35	3	65.9	17.7	1	10-33	K.LNDGHFMPVLGFGTYAPAEVPKSK.A	

Detailed Protein Report

Protein 309: dnaJ homolog subfamily C member 14 [Homo sapiens]

Accession: gi|119943096
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl, Oxidation

Score: 34.9
MW [kDa]: 78.5
pI: 9.4
Sequence Coverage [%]: 5.7
No. of unique Peptides: 3

Quantitation

mdown:qdown **Median:** 1.37 **CV:** 10.31 % **No. of Peptides:** 2
Wdown:Qdown **Median:** 1.17 **CV:** 81.46 % **No. of Peptides:** 3

```
        10         20         30         40         50         60         70         80
MAQKHPGERG LYGAHHSGGA SLRTLGPSVD PEIPSFSGLR DSAGTAPNGT RCLTEHSGPK HTQHPNPAHW LDPSHGPPGG
        90        100        110        120        130        140        150        160
PGPPRDAEDP DQSETSSEEE SGVDQELSKE NETGNQKDGN SFLSIPSACN CQGTPGIPEG PYSEGGNGSS SNFCHHCTSP
       170        180        190        200        210        220        230        240
ALGEDELEEE YDDEESLKFP SDFSRVSSGK KPPSRRQRHR FPTKEDTREG GRRDPRSPGR HRLGRKRSQA DKRKGLGLWG
       250        260        270        280        290        300        310        320
AEELCQLGQA GFWWLIELLV LVGEYVETCG HLIYACRQLK SSDLDLFRVW MGVWTGRLGG WAQVMFQFLS QGFYCGVGLF
       330        340        350        360        370        380        390        400
TRFLKLLGAL LLLALALFLG FLQLGWRFLV GLGDRLGWRD KATWLFSWLD SPALQRCLTL LRDSRPWQRL VRIVQWGWLE
       410        420        430        440        450        460        470        480
LPWVKQNINR QGNAPVASGR YCQPEEEVAR LLTMAGVPED ELNPFHVLGV EATASDVELK KAYRQLAVMV HPDKNHHPRA
       490        500        510        520        530        540        550        560
EEAFKVLRAA WDIVSNAEKR KEYEMKRMAE NELSRSVNEF LSKLQDDLKE AMNTMMCSRC QGKHRRFEMD REPKSARYCA
       570        580        590        600        610        620        630        640
ECNRLHPAEE GDFWAESSML GLKITYFALM DGKVYDITEW AGCQRVGISP DTHRVPYHIS FGSRIPGTRG RQRATPDAPP
       650        660        670        680        690        700        710
ADLQDFLSRI FQVPPGQMPN GNFFAAPQPA PGAAAASKPN STVPKGEAKP KRRKKVRRPF QR
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2138	1	661.2888	-106.46	2	55.3	10.6	1	278-288	R.QLKSSDLDLFR.V		Wdown:Qdown 2.63
2317	1	951.3323	-86.76	2	57.4	10.0	1	524-539	K.LQDDLKEAMNTMMCSR.C	Oxidation: 12	Wdown:Qdown 0.46 mdown:qdown 1.52
1717	3	820.8378	-35.57	2	50.0	14.3	2	552-564	R.EPKSARYCAECNR.L	Carbamidomethyl: 8, 11	Wdown:Qdown 1.30 mdown:qdown 1.23

Detailed Protein Report

Protein 310: **PREDICTED: inositol 1,4,5-trisphosphate receptor type 2 isoform X1 [Homo sapiens]**

Accession: gi|578822836
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 34.9
MW [kDa]: 212.9
pI: 6.3
Sequence Coverage [%]: 2.2
No. of unique Peptides: 2

10	20	30	40	50	60	70	80
MTEKMSSFLY	IGDIVSLYAE	GSVNGFISTL	GLVDDRCVVH	PEAGDLANPP	KKFRDCLFKV	CPMNRYSAQK	QYWKAKQAKQ
90	100	110	120	130	140	150	160
GNHTEAALLK	KLQHAAELEQ	KQNESENKKL	LGEIVKYSNV	IQLLHIKSNK	YLTVNKRLPA	LLEKNAMRVS	LDAAGNEGSW
170	180	190	200	210	220	230	240
FYIHPFWKLR	SEGDNIVVGD	KVVLMPVNAG	QPLHASNIEL	LDNPGCKEVN	AVNCNTSWKI	TLFMKYSSYR	EDVLKGGDVV
250	260	270	280	290	300	310	320
RLFHAEQEKF	LTCDEYEKKQ	HIFLRTTLRQ	SATSATSSKA	LWEIEVVHHD	PCRGGAGQWN	SLFRFKHLAT	GNYLAAELNP
330	340	350	360	370	380	390	400
DYRDAQNEGK	NVRDGVPPTS	KKKRQAGEKI	MYTLVSVPHG	NDIASLFELD	ATTLQRADCL	VPRNSYVRLR	HLCTNTWVTS
410	420	430	440	450	460	470	480
TSIPIDTDEE	RPVMLKIGTC	QTKEDKEAFA	IVSVPLSEVR	DLDFANDANK	VLATTVKKLE	NGTITQNERR	FVTKLLEDLI
490	500	510	520	530	540	550	560
FFVADVPNNG	QEVLDVVITK	PNRERQKLMR	EQNILAQVFG	ILKAPFKEKA	GEGSMLRLED	LGDQRYAPYK	YMLRLCYRVL
570	580	590	600	610	620	630	640
RHSQQDYRKN	QEYIAKNFCV	MQSQIGYDIL	AEDTITALLH	NNRKLLEKHI	TAKEIETFVS	LLRRNREPRF	LDYLSDLCVS
650	660	670	680	690	700	710	720
NTTAIPVTQE	LICKFMLSPG	NADILIQTKV	VSMQADNPME	SSILSDDIDD	EEVWLYWIDS	NKEPHGKAIR	HLAQEAKEGT
730	740	750	760	770	780	790	800
KADLEVLTYY	RYQLNLFARM	CLDRQYLAIN	QISTQLSVDL	ILRCVSDESL	PFDLRASFCR	LMLHMHVDRD	PQESVVPVRY
810	820	830	840	850	860	870	880
ARLWTEIPTK	ITIHEYDSIT	DSSRNDMKRK	FALTMEFVEE	YLKEVVNQPF	PFGDKEKNKL	TFEVVHLARN	LIYFGFYSFS
890	900	910	920	930	940	950	960
ELLRLTRTLL	AILDIVQAPM	SSYFERLSKF	QDGGNNVMRT	IHGVGEMMTQ	MVLSRGSIFP	MSVPDVPPSI	HPSKQGSPTE
970	980	990	1000	1010	1020	1030	1040
HEDVTVMDTK	LKIIEILQFI	LSVRLDYRIS	YMLSIYKKEF	GEDNDNAETS	ASGSPDTLLP	SAIVPDIDEI	AAQAETMFAG
1050	1060	1070	1080	1090	1100	1110	1120
RKEKNPVQLD	DEGGRTFLRV	LIHLIMHDYP	PLLSGALQLL	FKHFSQRAEV	LQAFKQVQLL	VSNQDVDNYK	QIKADLDQLR
1130	1140	1150	1160	1170	1180	1190	1200
LTVEKSELWV	EKSSNYENGE	IGESQVKGGE	EPIEESNILS	PVQDGTKKPQ	IDSNKSNNYR	IVKEILIRLS	KLCVQNKKCR
1210	1220	1230	1240	1250	1260	1270	1280
NQHQRLLKNM	GAHSVVLDLL	QIPYEKNDEK	MNEVMNLAHT	FLQNFCRGNP	QNQVLLHKHL	NLFLTPGLLE	AETMRHIFMN
1290	1300	1310	1320	1330	1340	1350	1360
NYHLCNEISE	RVVQHFVHCI	ETHGRHVEYL	RFLQTIVKAD	GKYVKKCQDM	VMTELINGGE	DVLIFYNDRA	SFPILLHMMC
1370	1380	1390	1400	1410	1420	1430	1440
SERDRGDESG	PLAYHITLVE	LLAACTEGKN	VYTEIKCNSL	LPLDDIVRVV	THDDCIPEVK	IAYVNFVNHC	YVDTEVEMKE
1450	1460	1470	1480	1490	1500	1510	1520
IYTSNHIWKL	FENFLVDMAR	VCNTTTDRKH	ADIFLEKCVT	ESIMNIVSGF	FNSPFSDNST	SLQTHQPVFI	QLLQSAFRIY
1530	1540	1550	1560	1570	1580	1590	1600
NCTWPNPAQK	ASVESCIRTL	AEVAKNRGIA	IPVDLDSQVN	TLFMKSHSNM	VQRAAMGWRL	SARSGPRFKE	ALGGPAWDYR
1610	1620	1630	1640	1650	1660	1670	1680
NIIEKLQDVV	ASLEHQFSPM	MQAEFSVLVD	VLYSPELLFP	EGSDARIRCG	AFMSKLINHT	KKLMEKEEKL	CIKILQTLRE
1690	1700	1710	1720	1730	1740	1750	1760
MLEKKDSFVE	EGNTLRKILL	NRYFKGDYSI	GVNGHLSGAY	SKTAQVGGSF	SGQDSDKMGI	SMSDIQCLLD	KEGASELVID
1770	1780	1790	1800	1810	1820	1830	1840
VIVNTKNDRI	FSEGIFLGIA	LLEGGNTQTQ	YSFYQQLHEQ	KKSEKFFKVL	YDRMKAAQKE	IRSTVTVNTI	DLGNKKRDDD
1850	1860	1870					
NELMTSGPRM	REFWSWGDPK	TALQD					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2130	3	648.2779	-125.55	2	55.2	13.9	2	1199-1208	K.CRNQHQRLLK.N	
1156	1	867.9132	-54.78	2	43.1	10.9	2	1647-1661	R.IRCGAFMSKLINHTK.K	Oxidation: 7

Detailed Protein Report

Protein 311: dynein heavy chain 2, axonemal [Homo sapiens]

Accession:	gi|75677365	**Score:**	34.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	507.4
Database Date:	2015-11-30	**pI:**	5.9
		Sequence Coverage [%]:	0.9
		No. of unique Peptides:	2

Alias proteins:

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

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

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
58	1	827.0195	-82.92	3	30.1	13.2	1	1393-1414	R.LRGTEEVFQALEDNQVALSTMK.A	
312	1	712.8533	-32.33	2	33.2	10.2	2	3248-3258	K.LEMLKKQYDEK.L	

Detailed Protein Report

Protein 312: **PREDICTED: hephaestin isoform X3 [Homo sapiens]**

Accession:	gi|578838557	**Score:**	34.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	97.3
Database Date:	2015-11-30	**pI:**	5.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	4.1
		No. of unique Peptides:	2

```
        10         20         30         40         50         60         70         80
MWAMESGHLL WALLFMQSLW PQLTDGATRV YYLGIRDVQW NYAPKGRNVI TNQPLDSDIV ASSFLKSDKN RIGGTYKKTI
        90        100        110        120        130        140        150        160
YKEYKDDSYT DEVAQPAWLG FLGPVLQAEV GDVILIHLKN FATRPYTIHP HGVFYEKDSE GSLYPDGSSG PLKADDSVPP
       170        180        190        200        210        220        230        240
GGSHIYNWTI PEGHAPTDAD PACLTWIYHS HVDAPRDIAT GLIGPLITCK RGALDGNSPP QRQDVDHDFF LLFSVVDENL
       250        260        270        280        290        300        310        320
SWHLNENIAT YCSDPASVDK EDETFQESNR MHAINGFVFG NLPELNMCAQ KRVAWHLFGM GNEIDVHTAF FHGQMLTTRG
       330        340        350        360        370        380        390        400
HHTDVANIFP ATFVTAEMVP WEPGTWLISC QVNSHFRDGM QALYKVKSCS MAPPVDLLTG KVRQYFIEAH EIQWDYGPMG
       410        420        430        440        450        460        470        480
HDGSTGKNLR EPGSISDKFF QKSSSRIGGT YWKVRYEAFQ DETFQEKMHL EEDRHLGILG PVIRAEVGDT IQVVFYNRAS
       490        500        510        520        530        540        550        560
QPFSMQPHGV FYEKDYEGTV YNDGTFEIYC QAGSHREAGM RAIYNVSQCP GHQATPRQRY QAARIYYIMA EEVEWDYCPD
       570        580        590        600        610        620        630        640
RSWEREWHNQ SEKDSYGYIF LSNKDGLLGS RYKKAVFREY TDGTFRIPRP RTGPEEHLGI LGPLIKGEVG DILTVVFKNN
       650        660        670        680        690        700        710        720
ASRPYSVHAH GVLESTTVWP LAAEPAINGK LYANLRGLTM YQGERVAWYM LAMGQDVDLH TIHFHAESFL YRNGENYRAD
       730        740        750        760        770        780        790        800
VVDLFPGTFE VVEMVASNPG TWLMHCHVTD HVHAGMETLF TVFSRTEHLS PLTVITKETE KAVPPRDIEE GNVKMLGMQI
       810        820        830        840        850        860
PIKNVEMLAS VLVAISVTLL LVVLALGGVV WYQHRQRKLR RNRRSILDDS FKLLSFKQ
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2643	1	784.0056	-47.59	3	61.3	13.5	0	271-291	R.MHAINGFVFGNLPELNMCAQK.R	Oxidation: 17
1824	2	805.8049	-133.19	2	52.8	21.4	0	465-478	R.AEVGDTIQVVFYNR.A	

Detailed Protein Report

Protein 313: acyl-protein thioesterase 2 [Homo sapiens]

Accession:	gi|9966764	**Score:**	34.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	24.7
Database Date:	2015-11-30	**pI:**	6.9
Modification(s):	Oxidation	**Sequence Coverage [%]:**	12.6
		No. of unique Peptides:	2

```
         10          20          30          40          50          60          70          80
MCGNTMSVPL  LTDAATVSGA  ERETAAVIFL  HGLGDTGHSW  ADALSTIRLP  HVKYICPHAP  RIPVTLNMKM  VMPSWFDLMG
         90         100         110         120         130         140         150         160
LSPDAPEDEA  GIKKAAENIK  ALIEHEMKNG  IPANRIVLGG  FSQGGALSLY  TALTCPHPLA  GIVALSCWLP  LHRAFPQAAN
        170         180         190         200         210         220         230         240
GSAKDLAILQ  CHGELDPMVP  VRFGALTAEK  LRSVVTPARV  QFKTYPGVMH  SSCPQEMAAV  KEFLEKLLPP  V
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1333	1	1061.5792	39.36	1	46.4	21.3	0	154-164	R.AFPQAANGSAK.D	
1865	2	984.3384	-99.79	2	51.8	13.6	0	204-221	K.TYPGVMHSSCPQEMAAVK.E	Oxidation: 6, 14

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Detailed Protein Report

Protein 314: PREDICTED: integrin beta-8 isoform X2 [Homo sapiens]

Accession:	gi|530384769	**Score:**	34.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	71.2
Database Date:	2015-11-30	**pI:**	9.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.7
		No. of unique Peptides:	1

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
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 315: **scm-like with four MBT domains protein 1 [Homo sapiens]**

Accession:	gi|53692193	**Score:**	34.8
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:	1

Quantitation

Wdown:Qdown	**Median:**	1.64	**CV:**	0.00 %	**No. of Peptides:**	1

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	Ratios
2349	1	873.4186	-61.16	2	57.8	11.0	1	46-61	R.LQNGFAPGMKLEVAVR.T	Oxidation: 9	Wdown:Qdown 1.64

Detailed Protein Report

Protein 316: PREDICTED: dedicator of cytokinesis protein 5 isoform X2 [Homo sapiens]

Accession:	gi|530388077	**Score:**	34.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	119.2
Database Date:	2015-11-30	**pI:**	7.9
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	3.9
		No. of unique Peptides:	3

Quantitation

mdown:qdown **Median:** 1.06 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MDLIRPRVSL	VCQIVRVGHM	ELKEGKKHTC	GLRRPFGVAV	MDITDIIHGK	VDDEEKQHFI	PFQQIAMETY	IRQRQLIMSP
90	100	110	120	130	140	150	160
LITSHVIGEN	EPLTSVLNKV	IAAKEVNHKG	QGLWVSLKLL	PGDLTQVQKN	FSHLVDRSTA	IARKMGFPEI	ILPGDVRNDI
170	180	190	200	210	220	230	240
YVTLIHGEFD	KGKKKTPKNV	EVTMSVHDEE	GKLLEKAIHP	GAGYEGISEY	KSVVYYQVKQ	PCWYETVKVS	IAIEEVTRCH
250	260	270	280	290	300	310	320
IRFTFRHRSS	QETRDKSERA	FGVAFVKLMN	PDGTTLQDGR	HDLVVYKGDN	KKMEDAKFYL	TLPGTKMEME	EKELQASKNL
330	340	350	360	370	380	390	400
VTFTPSKDST	KDSFQIATLI	CSTKLTQNVD	LLGLLNWRSN	SQNIKHNLKK	LMEVDGGEIV	KFLQDTLDAL	FNIMMEMSDS
410	420	430	440	450	460	470	480
ETYDFLVFDA	LVFIISLIGD	IKFQHFNPVL	ETYIYKHFSA	TLAYVKLSKV	LNFYVANADD	SSKTELLFAA	LKALKYLFRF
490	500	510	520	530	540	550	560
IIQSRVLYLR	FYGQSKDGDE	FNNSIRQLFL	AFNMLMDRPL	EEAVKIKGAA	LKYLPSIIND	VKLVFDPVEL	SVLFCKFIQS
570	580	590	600	610	620	630	640
IPDNQLVRQK	LNCMTKIVES	TLFRQSECRE	VLLPLLTDQL	SGQLDDNSNK	PDHEASSQLL	SNILEVLDRK	DVGATAVHIQ
650	660	670	680	690	700	710	720
LIMERLLRRI	NRTVIGMNRQ	SPHIGSFVAC	MIALLQQMDD	SHYSHYISTF	KTRQDIIDFL	METFIMFKDL	IGKNVYAKDW
730	740	750	760	770	780	790	800
MVMNMTQNRV	FLRAINQFAE	VLTRFFMDQA	SFELQLWNNY	FHLAVAFLTH	ESLQLETFSQ	AKRNKIVKKY	GDMRKEIGFR
810	820	830	840	850	860	870	880
IRDMWYNLGP	HKIKFIPSMV	GPILEVTLTP	EVELRKATIP	IFFDMMQCEF	NFSGNGNFHM	FENELITKLD	QEVEGGRGDE
890	900	910	920	930	940	950	960
QYKVLLEKLL	LEHCRKHKYL	SSSGEVFALL	VSSLLENLLD	YRTIIMQDES	KENRMSCTVN	VLNFYKEKKR	EDIYIRYLYK
970	980	990	1000	1010	1020	1030	1040
LRDLHRDCEN	YTEAAYTLLL	HAELLQVNGS	ESLFQQGGVQ	CPFRLNSIHF	MILMGKNFIP	GISFYTSFFS	SF

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1026	1	583.6927	-110.67	2	41.3	11.4	0	497-506	K.DGDEFNNSIR.Q		
1143	2	630.9795	-7.44	3	43.0	11.9	0	694-708	R.QDIIDFLMETFIMFK.D		
862	1	945.8909	-57.70	2	40.2	11.6	1	932-946	K.ENRMSCTVNVLNFYK.E	Carbamidomethyl: 6; Oxidation: 4	mdown:qdown 1.06

Detailed Protein Report

Protein 317: trinucleotide repeat-containing gene 6B protein isoform 3 [Homo sapiens]

Accession:	gi|67782330	**Score:**	34.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	109.3
Database Date:	2015-11-30	**pI:**	7.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.3
		No. of unique Peptides:	2

Quantitation

mdown:qdown	**Median:**	1.02	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.13	**CV:**	0.00 %	**No. of Peptides:**	1

10	20	30	40	50	60	70	80
MQTNEGEVSE	ESSSKVEQED	FVMEGHGKTP	PPGEESKQEK	EQEREEQLME	DKKRKKEDKK	KKEATQKVTE	QKTKVPEVTK
90	100	110	120	130	140	150	160
PSLSQPTAAS	PIGSSPSPPV	NGGNNAKRVA	VPNGQPPSAA	RYMPREVPPR	FRCQQDHKVL	LKRGQPPPPS	CMLLGGGAGP
170	180	190	200	210	220	230	240
PPCTAPGANP	NNAQVTGALL	QSESGTAPVW	SKSTPPAPDN	GTSAWGEPNE	SSPGWGEMDD	TGASTTGWGN	TPANAPNAMK
250	260	270	280	290	300	310	320
PNSKSMQDGW	GESDGPVTGA	RHPSWEEEED	GGVWNTTGSQ	GSASSHNSAS	WGQGGKKQMK	CSLKGGNNDS	WMNPLAKQFS
330	340	350	360	370	380	390	400
NMGLLSQTED	NPSSKMDLSV	GSLSDKKFDV	DKRAMNLGDF	NDIMRKDRSG	FRPPNSKDMG	TTDSGPYFEK	GGSHGLFGNS
410	420	430	440	450	460	470	480
TAQSRGLHTP	VQPLNSSPSL	RAQVPPQFIS	PQVSASMLKQ	FPNSGLSPGL	FNVGPQLSPQ	QIAMLSQLPQ	IPQFQLACQL
490	500	510	520	530	540	550	560
LLQQQQQQL	LQNQRKISQA	VRQQQEQQLA	RMVSALQQQQ	QQQQRQPGMK	HSPSHPVGPK	PHLDNMVPNA	LNVGLPDLQT
570	580	590	600	610	620	630	640
KGPIPGYGSG	FSSGGMDYGM	VGGKEAGTES	RFKQWTSMME	GLPSVATQEA	NMHKNGAIVA	PGKTRGGSPY	NQFDIIPGDT
650	660	670	680	690	700	710	720
LGGHTGPAGD	SWLPAKSPPT	NKIGSKSSNA	SWPPEFQPGV	PWKGIQNIDP	ESDPYVTPGS	VLGGTATSPI	VDTDHQLLRD
730	740	750	760	770	780	790	800
NTTGSNSSLN	TSLPSPGAWP	YSASDNSFTN	VHSTSAKFPD	YKSTWSPDPI	GHNPTHLSNK	MWKNHISSRN	TTPLPRPPPG
810	820	830	840	850	860	870	880
LTNPKPSSPW	SSTAPRSVRG	WGTQDSRLAS	ASTWSDGGSV	RPSYWLVLHN	LTPQIDGSTL	RTICMQHGPL	LTFHLNLTQG
890	900	910	920	930	940	950	960
TALIRYSTKQ	EAAKAQTALH	MCVLGNTTIL	AEFATDDEVS	RFLAQAQPPT	PAATPSAPAA	GWQSLETGQN	QSDPVGPALN
970	980	990	1000	1010	1020	1030	
LFGGSTGLGQ	WSSSAGGSSG	ADLAGASLWG	PPNYSSSLWG	VPTVEDPHRM	GSPAPLLPGD	LLGGGSDSI	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1277	1	829.2282	-142.65	2	45.6	10.2	0	1-15	-.MQTNEGEVSEESSSK.V	Oxidation: 1	
433	6	564.6888	-181.74	2	34.7	24.6	0	503-511	R.QQQEQQLAR.M		Wdown:Qdown 0.13 mdown:qdown 1.02

Detailed Protein Report

Protein 318: **uncharacterized aarF domain-containing protein kinase 2 [Homo sapiens]**

Accession:	gi|32261307	**Score:**	34.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	68.9
Database Date:	2015-11-30	**pI:**	10.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	7.7
		No. of unique Peptides:	3

Quantitation

mdown:qdown **Median:** 0.21 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MVAPWRVSVR	VCLSHLRCFE	LRQGLSLLRP	SECPRDARLC	WLLLGTLPKV	VSLCGDVGEG	APDVLSRRRV	RCSGAAGAGP
90	100	110	120	130	140	150	160
AESLPRAGPL	GGVFLHLRLW	LRAGALLVKF	FPLLLLYPLT	YLAPSVSTLW	LHLLLKATET	SGPTYIKLGQ	WASTRRDLFS
170	180	190	200	210	220	230	240
EAFCAQFSKL	HVRVTPHPWT	HTERFLRQAF	GDDWGSILSF	ENREPVGSGC	VAQVYKAYAN	TAFLETDSVQ	RLGRASCLPP
250	260	270	280	290	300	310	320
FSHTGAVGGL	RELFGYLGNG	RKPPENLADQ	SFLERLLLPK	ADLVGSNAGV	SRAQVPGHQP	EATNLISVAV	KVLHPGLLAQ
330	340	350	360	370	380	390	400
VHMDLLLMKI	GSRVLGVLPG	IKWLSLPEIV	EEFEKLMVQQ	IDLRYEAQNL	EHFQVNFRNV	KAVKFPTPLR	PFVTREVLVE
410	420	430	440	450	460	470	480
TYEESVPVSS	YQQAGIPVDL	KRKIARLGIN	MLLKMIFVDN	FVHADLHPGN	ILVQGANGLS	SSQEAQLQQA	DICDTLVVAV
490	500	510	520	530	540	550	560
PSSLCPLRLV	LLDAGIVAEL	QAPDLRNFRA	VFMAVVMGQG	QRVAELILHH	ARASECRDVE	GFKTEMAMLV	TQARKNTITL
570	580	590	600	610	620	630	
EKLHVSSLLS	SVFKLLMTHK	VKLESNFASI	VFAIMVLEGL	GRSLDPKLDI	LEAARPFLLT	GPVCPP	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2782	2	835.4333	6.80	2	63.2	13.6	0	235-251	R.ASCLPPFSHTGAVGGLR.E		
2955	1	953.4514	-107.61	2	66.1	10.5	0	489-506	R.LVLLDAGIVAELQAPDLR.N		
2880	1	713.3447	-10.93	2	64.7	10.8	0	510-522	R.AVFMAVVMGQGQR.V	Oxidation: 4, 8	mdown:qdown 0.21

Detailed Protein Report

Protein 319: microtubule-associated protein 6 isoform 1 [Homo sapiens]

Accession:	gi|48375173	**Score:**	34.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	86.5
Database Date:	2015-11-30	**pI:**	9.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.8
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MAWPCITRAC	CIARFWNQLD	KADIAVPLVF	TKYSEATEHP	GAPPQPPPPQ	QQAQPALAPP	SARAVAIETQ	PAQGELDAVA
90	100	110	120	130	140	150	160
RATGPAPGPT	GEREPAAGPG	RSGPGPGLGS	GSTSGPADSV	MRQDYRAWKV	QRPEPSCRPR	SEYQPSDAPF	ERETQYQKDF
170	180	190	200	210	220	230	240
RAWPLPRRGD	HPWIPKPVQI	SAASQASAPI	LGAPKRRPQS	QERWPVQAAA	EAREQEAAPG	GAGGLAAGKA	SGADERDTRR
250	260	270	280	290	300	310	320
KAGPAWIVRR	AEGLGHEQTP	LPAAQAQVQA	TGPEAGRGRA	AADALNRQIR	EEVASAVSSS	YRNEFRAWTD	IKPVKPIKAK
330	340	350	360	370	380	390	400
PQYKPPDDKM	VHETSYSAQF	KGEASKPTTA	DNKVIDRRRI	RSLYSEPFKE	PPKVEKPSVQ	SSKPKKTSAS	HKPTRKAKDK
410	420	430	440	450	460	470	480
QAVSGQAAKK	KSAEGPSTTK	PDDKEQSKEM	NNKLAEAKES	LAQPVSDSSK	TQGPVATEPD	KDQGSVVPGL	LKGQGPMVQE
490	500	510	520	530	540	550	560
PLKKQGSVVP	GPPKDLGPMI	PLPVKDQDHT	VPEPLKNESP	VISAPVKDQG	PSVPVPPKNQ	SPMVPAKVKD	QGSVVPESLK
570	580	590	600	610	620	630	640
DQGPRIPEPV	KNQAPMVPAP	VKDEGPMVSA	SVKDQGPMVS	APVKDQGPIV	PAPVKGEGPI	VPAPVKDEGP	MVSAPIKDQD
650	660	670	680	690	700	710	720
PMVPEHPKDE	SAMATAPIKN	QGSMVSEPVK	NQGLVVSGPV	KDQDVVVPEH	AKVHDSAVVA	PVKNQGPVVP	ESVKNQDPIL
730	740	750	760	770	780	790	800
PVLVKDQGPT	VLQPPKNQGR	IVPEPLKNQV	PIVPVPLKDQ	DPLVPVPAKD	QGPAVPEPLK	TQGPRDPQLP	TVSPLPRVMI
810	820						
PTAPHTEYIE	SSP						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1658	1	1045.0497	8.34	2	49.4	18.6	1	528-547	K.DQGPSVPVPPKNQSPMVPAK.V	Oxidation: 16
1905	5	572.7262	-106.04	2	53.9	16.3	0	594-604	K.DQGPMVSAPVK.D	Oxidation: 5

Detailed Protein Report

Protein 320: **uncharacterized protein C9orf172 [Homo sapiens]**

Accession:	gi|148762978	**Score:**	34.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	106.6
Database Date:	2015-11-30	**pI:**	10.2
		Sequence Coverage [%]:	3.1
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MTRTDPPDLL	VSTVYQDIKV	ATPGPASKCS	PCERSVARPA	EPAPFNKRHC	RSFDFLEALD	GPAMETLPEP	PPPESAVPRA
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
RTREAEPRRR	ARSKSAPRAP	PGLTPAPASP	PVLPRRGREA	QRAARAEASP	RREPAYPALR	ALANELHPIK	LQPQRGGPGR
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
VAPLCAAAGR	CAPPEPPAGP	APHVRCRLDI	KPDDAVLQHA	TRGSRSCGPT	EAAHWARPAP	QFHGLTVPGP	RHMALSRTPT
250	**260**	**270**	**280**	**290**	**300**	**310**	**320**
PSDSYCADPR	AFYCDGPLPG	PRDYAERRSL	PFTTPPGPTQ	FFYTEEPQGF	RGSFAASPGP	TFDAYYPRPY	PSEELSGPSP
330	**340**	**350**	**360**	**370**	**380**	**390**	**400**
RRMGGYYAGE	VRTFPIQEPP	SRSYYGEAPR	AYGLPYGPRY	VPEEPRAHST	ARPFYTEDFG	RYRERDVLAR	TYPHPRSSPA
410	**420**	**430**	**440**	**450**	**460**	**470**	**480**
WADWGPRPYR	TLQVVPPSDP	DPLLASWHGG	TGTSPPRLAT	DSRHYSRSWD	NILAPGPRRE	DPLGRGRSYE	NLLGREVREP
490	**500**	**510**	**520**	**530**	**540**	**550**	**560**
RGVSPEGRRP	PVVVNLSTSP	RRYAALSLSE	TSLTEKGRAG	EGLGRNWYVT	PEITITDNDL	RATERPSARA	WELPGGRTRP
570	**580**	**590**	**600**	**610**	**620**	**630**	**640**
PPHAAPDGPT	SGRQRSLEQL	DELITDLVID	SRPTAGQASE	PAADCLGPQL	RRLLDSRPAG	SGAPALAPPR	SPPASAGSAE
650	**660**	**670**	**680**	**690**	**700**	**710**	**720**
EPAAPGEAAD	ASPEPSADED	DLMTCSNARC	RRTETMFNAC	LYFKSCHSCY	TYYCSRLCRR	EDWDAHKARC	VYGRVGSVCR
730	**740**	**750**	**760**	**770**	**780**	**790**	**800**
HVLQFCRDSG	PVHRAFSRIA	RVGFLSRGRG	VLFLGFPSPG	SADNFLRFGL	EGLLLSPTYL	SLRELATHAA	PLGSYARELA
810	**820**	**830**	**840**	**850**	**860**	**870**	**880**
AAGRLYEPAE	CFLLSVSVAV	GPGTAPPGTP	ALPAPAPRSH	GPTVRKFAKV	ALAAGSPARP	PPARSREPDM	ETLILTPPPG
890	**900**	**910**	**920**	**930**	**940**	**950**	**960**
TAGLDQDGEA	GRRAREVAFI	HIQRELRLRG	VFLRHEFPRV	YEQLCEFVEA	NRRFTPTTIY	PTDRRTGRPF	MCMIMAASEP
970	**980**						
RALDWVASAN	LLDDIM						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2104	1	977.4132	-55.55	2	54.9	10.8	1	945-961	R.RTGRPFMCMIMAASEPR.A	
1808	3	599.9802	55.20	3	51.3	13.7	0	946-961	R.TGRPFMCMIMAASEPR.A	

Detailed Protein Report

Protein 321: integrin beta-4 isoform 3 precursor [Homo sapiens]

Accession:	gi|54607033	**Score:**	34.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	194.9
Database Date:	2015-11-30	**pI:**	5.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.2
		No. of unique Peptides:	1

Alias proteins:

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

Detailed Protein Report

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2157	1	841.3003	-27.93	2	57.2	16.5	1	47-59	K.DCAYCTDEMFRDR.R	Carbamidomethyl: 2

Detailed Protein Report

Protein 322: **tumor protein D54 isoform g [Homo sapiens]**

Accession:	gi|345197262	**Score:**	34.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	19.5
Database Date:	2015-11-30	**pI:**	6.2
		Sequence Coverage [%]:	9.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDSAGQDINL	NSPNKGLLSD	SMTDVPVDTG	VEEEIVTLRQ	VLAAKERHCG	ELKRRLGLST	LGELKQNLSR	SWHDVQVSSA
90	100	110	120	130	140	150	160
YVKTSEKLGE	WNEKVTQSDL	YKKTQETLSQ	AGQKTSAALS	TVGSAISRKL	GDMRNSATFK	SFEDRVGTIK	SKVVGDRENG
170	180	190					
SDNLPSSAGS	GDKPLSDPAP	F					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2523	1	1052.4103	-115.77	2	59.8	34.7	1	66-83	K.QNLSRSWHDVQVSSAYVK.T	

Detailed Protein Report

Protein 323: **PREDICTED: latent-transforming growth factor beta-binding protein 1 isoform X5 [Homo sapiens]**

Accession:	gi|530367595	**Score:**	34.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	134.0
Database Date:	2015-11-30	**pI:**	9.1
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	4.3
		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 324: transcription regulator protein BACH1 [Homo sapiens]

Accession:	gi|4502353	**Score:**	34.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	81.9
Database Date:	2015-11-30	**pI:**	4.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.7
		No. of unique Peptides:	2

Quantitation

mdown:qdown	**Median:**	0.64	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	2.40	**CV:**	0.00 %	**No. of Peptides:**	1

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	Ratios
504	1	667.7055	-215.81	2	35.6	22.1	1	615-626	K.QNLTGLCQKVCK.E		mdown:qdown 0.64 Wdown:Qdown 2.40
1770	1	851.2192	-170.05	2	52.1	12.5	0	717-731	R.QSGGISDFCQQMTDK.C	Carbamidomethyl: 9	

Detailed Protein Report

Protein 325: **PREDICTED: DNA polymerase kappa isoform X3 [Homo sapiens]**

Accession:	gi|530379363	**Score:**	34.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	57.6
Database Date:	2015-11-30	**pI:**	9.2
Modification(s):	Oxidation	**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 326: retinoic acid-induced protein 1 [Homo sapiens]

Accession:	gi|40807477	**Score:**	34.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	203.2
Database Date:	2015-11-30	**pI:**	9.9
		Sequence Coverage [%]:	0.8
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:** 0.69	**CV:** 0.00 %	**No. of Peptides:** 1

Detailed Protein Report

```
        10         20         30         40         50         60         70         80
MQSFRERCGF HGKQQNYQQT SQETSRLENY RQPSQAGLSC DRQRLLAKDY YNPQPYPSYE GGAGTPSGTA AAVAADKYHR
        90        100        110        120        130        140        150        160
GSKALPTQQG LQGRPAFPGY GVQDSSPYPG RYAGEESLQA WGAPQPPPPQ PQPLPAGVAK YDENLMKKTA VPPSRQYAEQ
       170        180        190        200        210        220        230        240
GAQVPFRTHS LHVQQPPPPQ QPLAYPKLQR QKLQNDIASP LPFPQGTHFP QHSQSFPTSS TYSSSVQGGG QGAHSYKSCT
       250        260        270        280        290        300        310        320
APTAQPHDRP LTASSSLAPG QRVQNLHAYQ SGRLSYDQQQ QQQQQQQQQQ QALQSRHHAQ ETLHYQNLAK YQHYGQQGQG
       330        340        350        360        370        380        390        400
YCQPDAAVRT PEQYYQTFSP SSSHSPARSV GRSPSYSSTP SPLMPNLENF PYSQQPLSTG AFPAGITDHS HFMPLLNPSP
       410        420        430        440        450        460        470        480
TDATSSVDTQ AGNCKPLQKD KLPENLLSDL SLQSLTALTS QVENISNTVQ QLLLSKAAVP QKKGVKNLVS RTPEQHKSQH
       490        500        510        520        530        540        550        560
CSPEGSGYSA EPAGTPLSEP PSSTPQSTHA EPQEADYLSG SEDPLERSFL YCNQARGSPA RVNSNSKAKP ESVSTCSVTS
       570        580        590        600        610        620        630        640
PDDMSTKSDD SFQSLHGSLP LDSFSKFVAG ERDCPRLLLS ALAQEDLASE ILGLQEAIGE KADKAWAEAP SLVKDSSKPP
       650        660        670        680        690        700        710        720
FSLENHSACL DSVAKSAWPR PGEPEALPDS LQLDKGGNAK DFSPGLFEDP SVAFATPDPK KTTGPLSFGT KPTLGVPAPD
       730        740        750        760        770        780        790        800
PTTAAFDCFP DTTAASSADS ANPFAWPEEN LGDACPRWGL HPGELTKGLE QGGKASDGIS KGDTHEASAC LGFQEEDPPG
       810        820        830        840        850        860        870        880
EKVASLPGDF KQEEVGGVKE EAGGLLQCPE VAKADRWLED SRHCCSTADF GDLPLLPPTS RKEDLEAEEE YSSLCELLGS
       890        900        910        920        930        940        950        960
PEQRPGMQDP LSPKAPLICT KEEVEEVLDS KAGWGSPCHL SGESVILLGP TVGTESKVQS WFESSLSHMK PGEEGPDGER
       970        980        990       1000       1010       1020       1030       1040
APGDSTTSDA SLAQKPNKPA VPEAPIAKKE PVPRGKSLRS RRVHRGLPEA EDSPCRAPVL PKDLLLPESC TGPPQGQMEG
      1050       1060       1070       1080       1090       1100       1110       1120
AGAPGRGASE GLPRMCTRSL TALSEPRTPG PPGLTTTPAP PDKLGGKQRA AFKSGKRVGK PSPKAASSPS NPAALPVASD
      1130       1140       1150       1160       1170       1180       1190       1200
SSPMGSKTKE TDSPSTPGKD QRSMILRSRT KTQEIFHSKR RRPSEGRLPN CRATKKLLDN SHLPATFKVS SSPQKEGRVS
      1210       1220       1230       1240       1250       1260       1270       1280
QRARVPKPGA GSKLSDRPLH ALKRKSAFMA PVPTKKRNLV LRSRSSSSSN ASGNGGDGKE ERPEGSPTLF KRMSSPKKAK
      1290       1300       1310       1320       1330       1340       1350       1360
PTKGNGEPAT KLPPPETPDA CLKLASRAAF QGAMKTKVLP PRKGRGLKLE AIVQKITSPS LKKFACKAPG ASPGNPLSPS
      1370       1380       1390       1400       1410       1420       1430       1440
LSDKDRGLKG AGGSPVGVEE GLVNVGTGQK LPTSGADPLC RNPTNRSLKG KLMNSKKLSS TDCFKTEAFT SPEALQPGGT
      1450       1460       1470       1480       1490       1500       1510       1520
ALAPKKRSRK GRAGAHGLSK GPLEKRPYLG PALLLTPRDR ASGTQGASED NSGGGGKKPK MEELGLASQP PEGRPCQPQT
      1530       1540       1550       1560       1570       1580       1590       1600
RAQKQPGHTN YSSYSKRKRL TRGRAKNTTS SPCKGRAKRR RQQQVLPLDP AEPEIRLKYI SSCKRLRSDS RTPAFSPFVR
      1610       1620       1630       1640       1650       1660       1670       1680
VEKRDAFTTI CTVVNSPGDA PKPHRKPSSS ASSSSSSSSF SLDAAGASLA TLPGGSILQP RPSLPLSSTM HLGPVVSKAL
      1690       1700       1710       1720       1730       1740       1750       1760
STSCLVCCLC QNPANFKDLG DLCGPYYPEH CLPKKKPKLK EKVRPEGTCE EASLPLERTL KGPECAAAAT AGKPPRPDGP
      1770       1780       1790       1800       1810       1820       1830       1840
ADPAKQGPLR TSARGLSRRL QSCYCCDGRE DGGEEAAPAD KGRKHECSKE APAEPGGEAQ EHWVHEACAV WTGGVYLVAG
      1850       1860       1870       1880       1890       1900       1910
KLFGLQEAMK VAVDMMCSSC QEAGATIGCC HKGCLHTYHY PCASDAGCIF IEENFSLKCP KHKRLP
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
95	1	510.4790	-193.63	3	30.4	18.7	2	1790-1804	R.EDGGEEAAPADKGRK.H		mdown:qdown 0.69

Detailed Protein Report

Protein 327: **MAP7 domain-containing protein 2 isoform 4 [Homo sapiens]**

Accession:	gi|270483747	**Score:**	34.4
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 328: mucin-2 precursor [Homo sapiens]

Accession:	gi|557129045	**Score:**	34.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	539.8
Database Date:	2015-11-30	**pI:**	5.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	0.8
		No. of unique 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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2678	1	857.6944	26.58	3	64.7	10.2	0	616-637	K.YDTCNCQNNEDCLCAALSSYAR.A	Carbamidomethyl: 4, 12

Detailed Protein Report

Protein 329: 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

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 330: PREDICTED: CAD protein isoform X4 [Homo sapiens]

Accession:	gi|530368098	**Score:**	34.2
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 [%]:**	2.7
		No. of unique Peptides:	2

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
2542	1	836.1207	149.60	2	60.1	10.3	1	1354-1368	R.RLAADFSVPLIIDIK.C	
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 331: PREDICTED: centriolin isoform X3 [Homo sapiens]

Accession:	gi|578817016	**Score:**	34.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	258.5
Database Date:	2015-11-30	**pI:**	5.3
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MKKGSQQKIF	SKAKIPSSSH	SPIPSSMSNM	RSRSLSPLIG	SETLPFHSGG	QWCEQVEIAD	ENNMLLDYQD	HKGADSHAGV
90	100	110	120	130	140	150	160
RYITEALIKK	LTKQDNLALI	KSLNLSLSKD	GGKKFKYIEN	LEKCVKLEVL	NLSYNLIGKI	EKLDKLLKLR	ELNLSYNKIS
170	180	190	200	210	220	230	240
KIEGIENMCN	LQKLNLAGNE	IEHIPVWLGK	KLKSLRVLNL	KGNKISSLQD	ISKLKPLQDL	ISLILVENPV	VTLPHYLQFT
250	260	270	280	290	300	310	320
IFHLRSLESL	EGQPVTTQDR	QEAFERFSLE	EVERLERDLE	KKMIETEELK	SKQTRFLEEI	KNQDKLNKSL	KEEAMLQKQS
330	340	350	360	370	380	390	400
CEELKSDLNT	KNELLKQKTI	ELTRACQKQY	ELEQELAFYK	IDAKFEPLNY	YPSEYAEIDK	APDESPYIGK	SRYKRNMFAT
410	420	430	440	450	460	470	480
ESYIIDSAQA	VQIKKMEPDE	QLRNDHMNLR	GHTPLDTQLE	DKEKKISAAQ	TRLSELHDEI	EKAEQQILRA	TEEFKQLEEA
490	500	510	520	530	540	550	560
IQLKKISEAG	KDLLYKQLSG	RLQLVNKLRQ	EALDLELQME	KQKQEIAGKQ	KEIKDLQIAI	DSLDSKDPKH	SHMKAQKSGK
570	580	590	600	610	620	630	640
EQQLDIMNKQ	YQQLESRLDE	ILSRIAKETE	EIKDLEEQLT	EGQIAANEAL	KKDLEGVISG	LQEYLGTIKG	QATQAQNECR
650	660	670	680	690	700	710	720
KLRDEKETLL	QRLTEVEQER	DQLEIVAMDA	ENMRKELAEL	ESALQEQHEV	NASLQQTQGD	LSAYEAELEA	RLNLRDAEAN
730	740	750	760	770	780	790	800
QLKEELEKVT	RLTQLEQSAL	QAELEKERQA	LKNALGKAQF	SEEKEQENSE	LHAKLKHLQD	DNNLLKQQLK	DFQNHLNHVV
810	820	830	840	850	860	870	880
DGLVRPEEVA	ARVDELRRKL	KLGTGEMNIH	SPSDVLGKSL	ADLQKQFSEI	LARSKWERDE	AQVRERKLQE	EMALQQEKLA
890	900	910	920	930	940	950	960
TGQEEFRQAC	ERALEARMNF	DKRQHEARIQ	QMENEIHYLQ	ENLKSMEEIQ	GLTDLQLQEA	DEEKERILAQ	LRELEKKKKL
970	980	990	1000	1010	1020	1030	1040
EDAKSQEQVF	GLDKELKKLK	KAVATSDKLA	TAELTIAKDQ	LKSLHGTVMK	INQERAEELQ	EAERFSRKAA	QAARDLTRAE
1050	1060	1070	1080	1090	1100	1110	1120
AEIELLQNLL	RQKGEQFRLE	MEKTGVGTGA	NSQVLEIEKL	NETMERQRTE	IARLQNVLDL	TGSDNKGGFE	NVLEEIAELR
1130	1140	1150	1160	1170	1180	1190	1200
REVSYQNDYI	SSMADPFKRR	GYWYFMPPPP	SSKVSSHSSQ	ATKDSGVGLK	YSASTPVRKP	RPGQQDGKEG	SQPPPASGYW
1210	1220	1230	1240	1250	1260	1270	1280
VYSPIRSGLH	KLFPSRDADS	GGDSQEESEL	DDQEEPPFVP	PPGYMMYTVL	PDGSPVPQGM	ALYAPPPPLP	NNSRPLTPGT
1290	1300	1310	1320	1330	1340	1350	1360
VVYGPPPAGA	PMVYGPPPPN	FSIPFIPMGV	LHCNVPEHHN	LENEVSRLED	IMQHLKSKKR	EERWMRASKR	QSEKEMEELH
1370	1380	1390	1400	1410	1420	1430	1440
HNIDDLLQEK	KSLECEVEEL	HRTVQKRQQQ	KDFIDGNVES	LMTELEIEKS	LKHHEDIVDE	IECIEKTLLK	RRSELREADR
1450	1460	1470	1480	1490	1500	1510	1520
LLAEAESELS	CTKEKTKNAV	EKFTDAKRSL	LQTESDAEEL	ERRAQETAVN	LVKADQQLRS	LQADAKDLEQ	HKIKQEEILK
1530	1540	1550	1560	1570	1580	1590	1600
EINKIVAAKD	SDFQCLSKKK	EKLTEELQKL	QKDIEMAERN	EDHHLQVLKE	SEVLLQAKRA	ELEKLKSQVT	SQQQEMAVLD
1610	1620	1630	1640	1650	1660	1670	1680
RQLGHKKEEL	HLLQGSMVQA	KADLQEALRL	GETEVTEKCN	HIREVKSLLE	ELSFQKGELN	VQISERKTQL	TLIKQEIEKE
1690	1700	1710	1720	1730	1740	1750	1760
EENLQVVLRQ	MSKHKTELKN	ILDMLQLENH	ELQGLKLQHD	QRVSELEKTQ	VAVLEEKLEL	ENLQQISQQQ	KGEIEWQKQL
1770	1780	1790	1800	1810	1820	1830	1840
LERDKREIER	MTAESRALQS	CVECLSKEKE	DLQEKCDIWE	KKLAQTKRVL	AAAEENSKME	QSNLEKLELN	VRKLQQELDQ
1850	1860	1870	1880	1890	1900	1910	1920
LNRDKLSLHN	DISAMQQQLQ	EKREAVNSLQ	EELANVQDHL	NLAKQDLLHT	TKHQDVLLSE	QTRLQKDISE	WANRFEDCQK
1930	1940	1950	1960	1970	1980	1990	2000
EEETKQQQLQ	VLQNEIEENK	LKLVQQEMMF	QRLQKERESE	ESKLETSKVT	LKEQQHQLEK	ELTDQKSKLD	QVLSKVLAAE
2010	2020	2030	2040	2050	2060	2070	2080
ERVRTLQEEE	RWCESLEKTL	SQTKRQLSER	EQQLVEKSGE	LLALQKEADS	MRADFSLLRN	QFLTERKKAE	KQVASLKEAL
2090	2100	2110	2120	2130	2140	2150	2160
KIQRSQLEKN	LLFLPELPAD	LEAILERNEN	LEGELESLKE	NLPFTMNEGP	FEEKLNFSQV	HIMDEHWRGE	ALREKLRHRE
2170	2180	2190	2200	2210	2220	2230	2240
DRLKAQLRHC	MSKQAEVLIK	GKRQTEGTLH	SLRRQVDALG	ELVTSTSADS	ASSPSLSQLE	SSLTEDSQLG	QNQEKNASAR
2250							

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2056	1	1029.5727	91.82	2	55.8	13.5	2	415-430	K.KMEPDEQLRNDHMNLR.G	Oxidation: 2, 13

Detailed Protein Report

Protein 332: **PREDICTED: rootletin-like [Homo sapiens]**

Accession:	gi|578843302	**Score:**	34.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	147.5
Database Date:	2015-11-30	**pI:**	5.5
		Sequence Coverage [%]:	3.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MRAAIERRWR	REQELCLQLK	SSQALVASLQ	EQLSESRREL	WAAQKLQQER	AREQAREREA	LRGQLEAQRL	EVQQCRASCK
90	100	110	120	130	140	150	160
LLGREKAALE	MVVEELKGKA	DAADAEKQGL	EAEAAELQRS	LLLQAERREE	LALRRERSCR	ALETSQGRLQ	QLEEKVSGLR
170	180	190	200	210	220	230	240
EELASVREAL	STAQLQRDVV	ESEREGLRSA	LARAECSNAD	LELLVRRLKS	EGVEQRDSLA	AMAALMEGLA	QDKSALNHLA
250	260	270	280	290	300	310	320
LQLEQERDQL	REQRKTLEQE	RARAGEQLAQ	AEQQLALERA	ERRGLQQACG	RLEQRQEQLE	GQAALLGREK	AQLQEQVGQV
330	340	350	360	370	380	390	400
TCQKQALEEQ	LAQSLQDQEA	QMGTLQQALQ	GKDALSEERA	QLLAKQEALE	RQGRLAAEEA	ADLRVERDSL	ESSLLEAQQL
410	420	430	440	450	460	470	480
ATKLQEQLEE	EARSAGLARQ	ALQVEMEQLQ	SDWEVQEMKL	RQDTVRLQRQ	VAQQEREAQR	ALESQALAHR	EALAQLQREK
490	500	510	520	530	540	550	560
ETLSLTLAEE	KEVARCQLEQ	EKELVTKSAA	EREALKGEIQ	SLKQERDESL	LQLEHKMQQA	LSLKETERSL	LSEELSRARR
570	580	590	600	610	620	630	640
TLERVQQEAQ	SQQEQAQATI	SATTEELKAL	QAQFEDAITA	HQRETTALRE	SLQDLAAERG	DVEREVRGRA	GGLLGMPEDR
650	660	670	680	690	700	710	720
RKQGRRKVSF	QQISKSGPVS	DHTGKQNEIA	KLGAAGGGGG	GGVERAERLR	AQLTVAQEGL	AALRQELQGV	EESREGLHRE
730	740	750	760	770	780	790	800
AQEARRALSD	EAREKDVLLL	FNSELRATIC	RAEQEKASFK	RSKEEKEQKL	LILEEAQAAL	QQEASALRAH	LWELEQAGGD
810	820	830	840	850	860	870	880
ARQELRELHR	QVLGLQRKLA	EVEAAGEAHG	QRLQEHLRES	RGAEQTLRAE	LHSVTRKLQE	ASGVADALQA	RLDQACHRIH
890	900	910	920	930	940	950	960
SLEQELAQAE	GARQDAEAQL	GRLCSTLRRG	LGLQRQSPWA	SPEQPGSPTK	GSDSSQALPG	QQGTSPPARP	HSPLRWPSPT
970	980	990	1000	1010	1020	1030	1040
PGGRSSELMD	VATVQDILRD	FVQKLREAQR	ERDDSRIQMA	TLSSRLSEAE	CRCARAQSRV	GQLQKALAEA	EEGQRRVEGA
1050	1060	1070	1080	1090	1100	1110	1120
LSSARAARAL	QKEALRRLEL	EHLASVRAAG	QEKRRLQEQL	ETLRQALEES	RRHSQGLAKQ	GKLLEEQLTN	LEHRCQKAEV
1130	1140	1150	1160	1170	1180	1190	1200
SLEPLRQVLC	RPQRLSGGQE	AAEAQAERRV	LQEQTAALRT	ERARLQGELA	ALRAQLAQME	QETLKREEDV	ARLGAEKEQL
1210	1220	1230	1240	1250	1260	1270	1280
DQSLNSLHQE	VDGALRQNQQ	LQAQMTEMEQ	AHTQRLQDLT	AQHQRDLATE	AERLHGARPQ	ATQALESQEW	THQQRVKVLE
1290	1300	1310	1320				
EQVASLKEQL	DQEVQWRQQA	HLGQAFQTGQ					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2904	2	973.5046	-21.62	2	65.1	13.6	2	479-495	R.EKETLSLTLAEEKEVAR.C	

Detailed Protein Report

Protein 333: **PREDICTED: transforming acidic coiled-coil-containing protein 3 isoform X2 [Homo sapiens]**

Accession:	gi|530375987	**Score:**	34.1
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

Quantitation

mdown:qdown **Median:** 1.72 **CV:** 0.00 % **No. of 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	Ratios
1875	1	917.8351	-120.99	2	53.5	12.8	1	464-478	K.ENEELTRICDDLISK.M	Carbamidomethyl: 9	mdown:qdown 1.72

Detailed Protein Report

Protein 334: PREDICTED: F-box/WD repeat-containing protein 8 isoform X2 [Homo sapiens]

Accession:	gi|530401261	**Score:**	34.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	46.4
Database Date:	2015-11-30	**pI:**	5.5
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	7.7
		No. of unique Peptides:	2

Alias proteins:

Accession	Name	Description
gi|530401263	refseq_human (refseq_human_20140103.fasta)	PREDICTED: F-box/WD repeat-containing protein 8 isoform X3 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MRCCGTGCAS RKGTFRIAAS LTILAGSSSS KSAEPRNTCY EPTGRYTSGD VRVWDTRTWD YVAPFLESED EEDEPGMQPN
        90        100        110        120        130        140        150        160
VSFVRINSSL AVAAYEDGFL NIWDLRTGKY PVHRFEHDAR IQALALSQDD ATVATASAFD VVMLSPNEEG YWQIAAEFEV
       170        180        190        200        210        220        230        240
PKLVQYLEIV PETRRYPVAV AAAGDLMYLL KAEDSARTLL YAHGPPVTCL DVSANQVAFG VQGLGWVYEG SKILVYSLEA
       250        260        270        280        290        300        310        320
GRRLLKLGNV LRDFTCVNLS DSPPNLMVSG NMDGRVRIHD LRSGNIALSL SAHQLRVSAV QMDDWKIVSG GEEGLVSVWD
       330        340        350        360        370        380        390        400
YRMNQKLWEV YSGHPVQHIS FSSHSLITAN VPYQTVMRNA DLDSFTTHRR HRGLIRAYEF AVDQLAFQSP LPVCRSSCDA
       410        420
MATHYYDLAL AFPYNHV
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2655	2	673.3551	106.75	2	64.3	12.0	2	1-12	-.MRCCGTGCASRK.G	Carbamidomethyl: 3; Oxidation: 1
2701	1	973.4995	-32.63	2	62.2	10.8	1	17-36	R.IAASLTILAGSSSSKSAEPR.N	

Detailed Protein Report

Protein 335: insulin receptor-related protein precursor [Homo sapiens]

Accession: gi|31657140
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 34.0
MW [kDa]: 143.6
pI: 6.0
Sequence Coverage [%]: 2.1
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	2	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	

BRUKER

Detailed Protein Report

Protein 336: storkhead-box protein 1 isoform a [Homo sapiens]

Accession:	gi|63025200	**Score:**	33.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	110.9
Database Date:	2015-11-30	**pI:**	8.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.2
		No. of unique Peptides:	2

Alias proteins:

Accession	Name	Description
gi|194328691	refseq_huma (refseq_human_20140103.fasta)	storkhead-box protein 1 isoform a [Homo sapiens]

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	KHYPGIAIPS
170	180	190	200	210	220	230	240
EDILYTTLGT	LIKERKIYHT	GEGYFIVTPQ	TYFITNTTTQ	ENKRMLPSDE	SRLMPASMTY	LVSMESCAES	AQENAAPISH
250	260	270	280	290	300	310	320
CQSCQCFRDM	HTQDVQEAPV	AAEVTRKSHR	GLGESVSWVQ	NGAVSVSAEH	HICESTKPLP	YTRDKEKGKK	FGFSLLWRSL
330	340	350	360	370	380	390	400
SRKEKPKTEH	SSFSAQFPPE	EWPVRDEDDL	DNIPRDVEHE	IIKRINPILT	VDNLIKHTVL	MQKYEEQKKY	NSQGTSTDML
410	420	430	440	450	460	470	480
TIGHKYPSKE	GVKKRQGLSA	KPQGQGHSRR	DRHKARNQGS	EFQPGSIRLE	KHPKLPATQP	IPRIKSPNEM	VGQKPLGEIT
490	500	510	520	530	540	550	560
TVLGSHLIYK	KRISNPFQGL	SHRGSTISKG	HKIQKTSDLK	PSQTGPKEKP	FQKPRSLDSS	RIFDGKAKEP	YAEQPNDKME
570	580	590	600	610	620	630	640
AESIYINDPT	VKPINDDFRG	HLFSHPQQSM	LQNDGKCCPF	MESMLRYEVY	GGENEVIPEV	LRKSHSHFDK	LGETKQTPHS
650	660	670	680	690	700	710	720
LPSRGASFSD	RTPSACRLVD	NTIHQFQNLG	LLDYPVGVNP	LRQAARQDKD	SEELLRKGFV	QDAETTSLEN	EQLSNDDQAL
730	740	750	760	770	780	790	800
YQNEVEDDDG	ACSSLYLEED	DISENDDLRQ	MLPGHSQYSF	TGGSQGNHLG	KQKVIERSLT	EYNSTMERVE	SQVLKRNECY
810	820	830	840	850	860	870	880
KPTGLHATPG	ESQEPNLSAE	SCGLNSGAQF	GFNYEEEPSV	AKCVQASAPA	DERIFDYYSA	RKASFEAEVI	QDTIGDTGKK
890	900	910	920	930	940	950	960
PASWSQSPQN	QEMRKHFPQK	FQLFNTSHMP	VLAQDVQYEH	SHLEGTENHS	MAGDSGIDSP	RTQSLGSNNS	VILDGLKRRQ
970	980	990					
NFLQNVEGTK	SSQPLTSNSL	LPLTPVINV					

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
2951	1	823.4152	-31.89	2	66.1	15.5	0	942-957	R.TQSLGSNNSVILDGLK.R	

Detailed Protein Report

Protein 337: ubiquitin carboxyl-terminal hydrolase 6 [Homo sapiens]

Accession:	gi|109638751	**Score:**	33.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	158.6
Database Date:	2015-11-30	**pI:**	8.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	4.1
		No. of unique Peptides:	3

Alias proteins:

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

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1774	8	673.2348	-219.99	2	52.2	11.9	2	89-99	K.HSSKLIDRVYK.G	
2932	1	965.1226	-27.88	3	65.8	10.3	0	218-244	R.HSLPGFHSPNGGTVQGLQDQQEHVVPK.S	
2697	1	1175.5508	58.82	2	62.1	11.6	1	1039-1058	R.AFTSEEELGESEMYYCSKCK.T	Oxidation: 13

Protein 338: prostate tumor-overexpressed gene 1 protein [Homo sapiens]

Accession:	gi|33695090	**Score:**	33.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	46.8
Database Date:	2015-11-30	**pI:**	11.6
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	9.6
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530416718	refseq_human (refseq_human_20140103.fasta)	PREDICTED: prostate tumor-overexpressed gene 1 protein isoform X3 [Homo sapiens]
gi|530416716	refseq_human (refseq_human_20140103.fasta)	PREDICTED: prostate tumor-overexpressed gene 1 protein isoform X2 [Homo sapiens]

10	20	30	40	50	60	70	80
MVRPRRAPYR	SGAGGPLGGR	GRPPRPLVVR	AVRSRSWPAS	PRGPQPPRIR	ARSAPPMEGA	RVFGALGPIG	PSSPGLTLGG
90	100	110	120	130	140	150	160
LAVSEHRLSN	KLLAWSGVLE	WQEKRRPYSD	STAKLKRTLP	CQAYVNQGEN	LETDQWPQKL	IMQLIPQQLL	TTLGPLFRNS
170	180	190	200	210	220	230	240
QLAQFHFTNR	DCDSLKGLCR	IMGNGFAGCM	LFPHISPCEV	RVLMLLYSSK	KKIFMGLIPY	DQSGFVSAIR	QVITTRKQAV
250	260	270	280	290	300	310	320
GPGGVNSGPV	QIVNNKFLAW	SGVMEWQEPR	PEPNSRSKRW	LPSHVYVNQG	EILRTEQWPR	KLYMQLIPQQ	LLTTLVPLFR
330	340	350	360	370	380	390	400
NSRLVQFHFT	KDLETLKSLC	RIMDNGFAGC	VHFSYKASCE	IRVLMLLYSS	EKKIFIGLIP	HDQGNFVNGI	RRVIANQQQV
410	420						
LQRNLEQEQQ	QRGMGG						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2316	1	974.1925	62.96	3	59.2	21.5	2	332-356	K.DLETLKSLCRIMDNGFAGCVHFSYK.A	Carbamidomethyl: 19; Oxidation: 12

Detailed Protein Report

Protein 339: glycerol-3-phosphate dehydrogenase, mitochondrial precursor [Homo sapiens]

Accession:	gi|285002231	**Score:**	33.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	80.8
Database Date:	2015-11-30	**pI:**	8.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	5.9
		No. of unique Peptides:	3

Alias proteins:

Accession	Name	Description
gi|530370176	refseq_human (refseq_human_20140103.fasta)	PREDICTED: glycerol-3-phosphate dehydrogenase, mitochondrial isoform X1 [Homo sapiens]
gi|285002233	refseq_human (refseq_human_20140103.fasta)	glycerol-3-phosphate dehydrogenase, mitochondrial precursor [Homo sapiens]

10	20	30	40	50	60	70	80
MAFQKAVKGT	ILVGGGALAT	VLGLSQFAHY	RRKQMNLAYV	KAADCISEPV	NREPPSREAQ	LLTLQNTSEF	DILVIGGGAT
90	100	110	120	130	140	150	160
GSGCALDAVT	RGLKTALVER	DDFSSGTSSR	STKLIHGGVR	YLQKAIMKLD	IEQYRMVKEA	LHERANLLEI	APHLSAPLPI
170	180	190	200	210	220	230	240
MLPVYKWWQL	PYYWVGIKLY	DLVAGSNCLK	SSYVLSKSRA	LEHFPMLQKD	KLVGAIVYYD	GQHNDARMNL	AIALTAARYG
250	260	270	280	290	300	310	320
AATANYMEVV	SLLKKTDPQT	GKVRVSGARC	KDVLTGQEFD	VRAKCVINAT	GPFTDSVRKM	DDKDAAAICQ	PSAGVHIVMP
330	340	350	360	370	380	390	400
GYYSPESMGL	LDPATSDGRV	IFFLPWQKMT	IAGTTDTPTD	VTHHPIPSEE	DINFILNEVR	NYLSCDVEVR	RGDVLAAWSG
410	420	430	440	450	460	470	480
IRPLVTDPKS	ADTQSISRNH	VVDISESGLI	TIAGGKWTTY	RSMAEDTINA	AVKTHNLKAG	PSRTVGLFLQ	GGKDWSPTLY
490	500	510	520	530	540	550	560
IRLVQDYGLE	SEVAQHLAAT	YGDKAFEVAK	MASVTGKRWP	IVGVRLVSEF	PYIEAEVKYG	IKEYACTAVD	MISRRTRLAF
570	580	590	600	610	620	630	640
LNVQAAEEAL	PRIVELMGRE	LNWDDYKKQE	QLETARKFLY	YEMGYKSRSE	QLTDRSEISL	LPSDIDRYKK	RFHKFDADQK
650	660	670	680	690	700	710	720
GFITIVDVQR	VLESINVQMD	ENTLHEILNE	VDLNKNGQVE	LNEFLQLMSA	IQKGRVSGSR	LAILMKTAEE	NLDRRVPIPV
730							
DRSCGGL							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1028	1	863.9268	-97.49	2	41.6	10.0	2	114-128	K.LIHGGVRYLQKAIMK.L	
29	1	706.3122	-81.53	3	29.6	11.9	1	179-197	K.LYDLVAGSNCLKSSYVLSK.S	Carbamidomethyl: 10
2822	1	607.3358	86.08	2	64.4	11.7	0	598-606	K.FLYYEMGYK.S	

Detailed Protein Report

Protein 340: leukocyte receptor cluster member 1 [Homo sapiens]

Accession: gi|24308289
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 33.6
MW [kDa]: 30.5
pI: 10.1
Sequence Coverage [%]: 7.6
No. of unique Peptides: 1

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 341: **PREDICTED: regulator of G-protein signaling 3 isoform X5 [Homo sapiens]**

Accession:	gi|578817739	**Score:**	33.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	68.1
Database Date:	2015-11-30	**pI:**	9.9
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	6.9
		No. of unique Peptides:	3

10	20	30	40	50	60	70	80
MEWLSPDIAL	PRRDEWTQTS	PARKRITHAK	VQGAGQLRLS	IDAQDRVLLL	HIIEGKGLIS	KQPGTCDPYV	KISLIPEDSR
90	100	110	120	130	140	150	160
LRHQKTQTVP	DCRDPAFHEH	FFFPVQEEDD	QKRLLVTVWN	RASQSRQSGL	IGCMSFGVKS	LLTPDKEISG	WYYLLGEHLG
170	180	190	200	210	220	230	240
RTKHLKVARR	RLRPLRDPLL	RMPGGGDTEN	GKKLKITIPR	GKDGFGFTIC	CDSPVRVQAV	DSGGPAERAG	LQQLDTVLQL
250	260	270	280	290	300	310	320
NERPVEHWKC	VELAHEIRSC	PSEIILLVWR	MVPQVKPGPD	GGVLRRASCK	STHDLQSPPN	KREKNCTHGV	QARPEQRHSC
330	340	350	360	370	380	390	400
HLVCDSSDGL	LLGGWERYTE	VAKRGGQHTL	PALSRATAPT	DPNYIILAPL	NPGSQLLRPV	YQEDTIPEES	GSPSKGKSYT
410	420	430	440	450	460	470	480
GLGKKSRLMK	TVQTMKGHGN	YQNCPVVRPH	ATHSSYGTYV	TLAPKVLVFP	VFVQPLDLCN	PARTLLLSEE	LLLYEGRNKA
490	500	510	520	530	540	550	560
AEVTLFAYSD	LLLFTKEDEP	GRCDVLRNPL	YLQSVKLQEG	SSEDLKFCVL	YLAEKAECLF	TLEAHSQEQK	KRVCWCLSEN
570	580	590	600	610	620		
IAKQQQLAAS	PPDSKKLHPF	GSLQQEMGPV	NSTNATQDRS	FTSPGQTLIG			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2171	1	576.2313	-138.85	3	55.7	10.6	1	31-46	K.VQGAGQLRLSIDAQDR.V	
27	4	819.8677	-73.87	2	29.0	12.2	2	81-93	R.LRHQKTQTVPDCR.D	Carbamidomethyl: 12
1945	1	700.2356	-147.65	2	54.4	10.8	0	127-139	R.QSGLIGCMSFGVK.S	Carbamidomethyl: 7; Oxidation: 8

Detailed Protein Report

Protein 342: KRR1 small subunit processome component homolog [Homo sapiens]

Accession:	gi|117676403	**Score:**	33.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	43.6
Database Date:	2015-11-30	**pI:**	10.3
		Sequence Coverage [%]:	6.3
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	1.15	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	1.28	**CV:**	0.00 %	**No. of Peptides:**	1

10	20	30	40	50	60	70	80
MASPSLERPE	KGAGKSEFRN	QKPKPENQDE	SELLTVPDGW	KEPAFSKEDN	PRGLLEESSF	ATLFPKYREA	YLKECWPLVQ
90	100	110	120	130	140	150	160
KALNEHHVNA	TLDLIEGSMT	VCTTKKTFDP	YIIIRARDLI	KLLARSVSFE	QAVRILQDDV	ACDIIKIGSL	VRNKERFVKR
170	180	190	200	210	220	230	240
RQRLIGPKGS	TLKALELLTN	CYIMVQGNTV	SAIGPFSGLK	EVRKVVLDTM	KNIHPIYNIK	SLMIKRELAK	DSELRSQSWE
250	260	270	280	290	300	310	320
RFLPQFKHKN	VNKRKEPKKK	TVKKEYTPFP	PPQPESQIDK	ELASGEYFLK	ANQKKRQKME	AIKAKQAEAI	SKRQEERNKA
330	340	350	360	370	380	390	
FIPPKEKPIV	KPKEASTETK	IDVASIKEKV	KKAKNKKLGA	LTAEEIALKM	EADEKKKKKK	K	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2913	2	973.5096	1.50	2	65.6	13.8	2	2-19	M.ASPSLERPEKGAGKSEFR.N		Wdown:Qdown 1.28 mdown:qdown 1.15

Detailed Protein Report

Protein 343: **PREDICTED: centrosomal protein KIAA1731 isoform X7 [Homo sapiens]**

Accession:	gi|578822447	**Score:**	33.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	268.9
Database Date:	2015-11-30	**pI:**	5.4
		Sequence Coverage [%]:	1.0
		No. of unique Peptides:	2

Detailed Protein Report

10	20	30	40	50	60	70	80
MERFEKAHVR	GFQAMKKIHL	AQNQEKLMKE	LKQLQQEDLA	RRRQTVAQMP	PQLVELPYKR	SEMKEDWQRE	LEFAFEDMYN
90	100	110	120	130	140	150	160
ADRKVKGNLI	LHLEPEPLPT	VTNQIQDEEL	DLSMEQENLG	AAEDLPVTEA	EICSSETDVP	LVMKTQQIPS	KVLFKKLLNK
170	180	190	200	210	220	230	240
IRSQKSLWTI	KSMSEDESEM	ITTVSEIESK	APTVESGTIA	SKERTLSSGQ	EQVVESDTLT	IESGPLASED	KPLSCGTNSG
250	260	270	280	290	300	310	320
KEQEINETLP	ITTVAQSSVL	LHPQEAAARI	RMSARQKQIM	EIEEQKQKQL	ELLEQIEQQK	LRLETDCFRA	QLEEEKRKKT
330	340	350	360	370	380	390	400
QPTGVGCRKS	HHYINHLVGI	APASCPVISD	EDSHRQMIRN	YQHQLLQQNR	LHRQSVETAR	KQLLEYQTML	KGRCPSVSAP
410	420	430	440	450	460	470	480
SLITDSVISV	PSWKSERPTA	ISEHWDQGQR	LKLSPNKYQP	IQPIQTSKLE	QDHFQVARQN	HFPQRQVETT	ETLRASDILT
490	500	510	520	530	540	550	560
NQALESQEHL	RQFSQTETQQ	RDYKLVPKDS	ETLSRALSHD	RQLISQDARK	ISETFGATTF	QSLESQQLFS	ENSENISYHL
570	580	590	600	610	620	630	640
TEPSSFVPLV	PQHSFSSLPV	KVESGKIQEP	FSAMSKSTVS	TSHSIISQMH	DRPLLPSENI	TAQQGNMKAL	QEQLDLQKKV
650	660	670	680	690	700	710	720
LQATQEAQEQ	LLLCKQKEVE	QQTGLSVFLP	LVTPDSSALL	PSAKADLGRI	QESSPTKNNI	AVSSDHHVIS	QLQDKRLSLS
730	740	750	760	770	780	790	800
QPILSQQNNF	KFLQEQLNIQ	KDSLQARREA	QEVLYVHKQS	ELDRRVCSEQ	AEPSFPFQVA	QHTFTSLPSA	DTKSGKIQEQ
810	820	830	840	850	860	870	880
HSSKSEKGLV	SCQSDIPISQ	DGSLSFLQQF	LPLHDSLKLL	QEQLTKQRDT	LQARHEAQVE	LLLHRQRDLG	DSKSGLVSSS
890	900	910	920	930	940	950	960
SSPVVVQHSV	ASQASAKAEP	RRIQELYLSE	KENVGPSCHL	IIPTFQDKSL	SFPQHSLAQQ	ENLTILQEQS	QIQRVILGAK
970	980	990	1000	1010	1020	1030	1040
EGTQEFVHTE	SELEKRISSE	QTGTSSSLSQ	VDESERFQEC	ISIKSDSTIP	LSHPKIPRCQ	ERLLRVSQHM	LPLQDNLEEH
1050	1060	1070	1080	1090	1100	1110	1120
QAWLDTEKEA	FHFSQKTQEN	TSSEQTGSSS	FIPQLVQLSF	TSLASAESGT	ILEPLFTESE	SKIFSSHLQI	PQLQDRLLRI
1130	1140	1150	1160	1170	1180	1190	1200
SQLIQPQQDN	LKALQEQLAT	QREAIILARQ	EAREELLLHQ	SEWEGRISPE	QVDTSSLPLV	PQHSFASLPL	NESERNQEPC
1210	1220	1230	1240	1250	1260	1270	1280
SINSDNIVSS	GHSEIPTLPD	GLLGLSHLVL	PQQDNLIALE	EHLHAQTDFL	PSIEKTQKEL	VLSKPCKFEE	KVSSEHFIQS
1290	1300	1310	1320	1330	1340	1350	1360
HHGDLQALQQ	QLDTQKKAIR	SIQEVQEELL	LQRLSELEKR	VSSEQVCSSS	FVSQVPVADS	ERTQKSFPTK	SNDTLPSSHR
1370	1380	1390	1400	1410	1420	1430	1440
EIPRLQDRLL	SLSKPILPQQ	DNMTAQLDAQ	REVMYSYEKP	QEELSLNKQR	KLNKSESAEH	TIPSLFLPKE	TEHSFIPLPF
1450	1460	1470	1480	1490	1500	1510	1520
AEAKPKSTCE	LYSSQNEHAA	PPSNPVIPGF	QDRLLSFSQS	VLTQQDNLGL	QKQLDLQREV	LHYSQKAQEK	LLVQRQTALQ
1530	1540	1550	1560	1570	1580	1590	1600
QQIQKHEETL	KDFFKDSQIS	KPTVENDLKT	QKMGQLRDWF	PNTQDLAGND	QENIRHADRN	NSDDNHLASE	DTSAKQSGEH
1610	1620	1630	1640	1650	1660	1670	1680
LEKDLGRRSS	KPPVAKVKCG	LDLNQHELSA	IQEVESPAIG	RTSILGKPGI	YEDRDPLRVS	ISREQSFFGS	PLAHDPFSCL
1690	1700	1710	1720	1730	1740	1750	1760
QLVGQENVCG	DDYDEAVKLK	ESVVENHAVL	SYAVEEEHAY	LGPTVKPDDK	AKTLSYEPLS	SATVSTGSLL	SYENTDLSLT
1770	1780	1790	1800	1810	1820	1830	1840
DPESFSEHMD	DSKQESTTSK	EEETNIISSI	VPSTQDIYQR	QNSSDVHKSL	LPAVDETTCG	HTHFQQMIDK	YINEANLIPE
1850	1860	1870	1880	1890	1900	1910	1920
KTDLQELEHI	FPNLHHQLFK	PLEPHPDFDL	SSSSSGISPD	NRDFYQRSDS	SSESHCATGL	SKSTVYFTAL	RRTSMHSSLN
1930	1940	1950	1960	1970	1980	1990	2000
TSPNQQPDTN	LAHVGAHSFA	TENIIGGSEQ	CFEQLQPEYS	SQEESQHADL	PSIFSIEARD	SSQGMKNQNY	PSEEHTEILQ
2010	2020	2030	2040	2050	2060	2070	2080
NKKKIVHFQL	SIGNLSSVYS	SSDEANVFDQ	LNVQHSTPCG	SNSSECSTKH	QLESRKESMG	FEELSKRGVV	TMLQSQGLIE
2090	2100	2110	2120	2130	2140	2150	2160
DNKNETCRVL	DINPQVEETD	SRLCVRTVEM	GTSIQAPYSL	TTQNEKYFEN	SAETDIPKIT	KKLSQLGESE	LFASSGSFSL
2170	2180	2190	2200	2210	2220	2230	2240

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
131	1	608.2888	-54.72	2	30.9	17.7	0	749-758	R.EAQEVLYVHK.Q	
2043	1	709.3053	-139.25	2	55.7	15.7	1	2299-2311	K.EKPSISSSVSRLK.G	

Detailed Protein Report

Protein 344: keratin, type II cytoskeletal 8 isoform 2 [Homo sapiens]

Accession:	gi|4504919	**Score:**	33.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	53.7
Database Date:	2015-11-30	**pI:**	5.4
		Sequence Coverage [%]:	4.6
		No. of unique Peptides:	1

Quantitation

mdown:qdown **Median:** 1.08 **CV:** 0.00 % **No. of Peptides:** 1

Alias proteins:

Accession	**Name**	**Description**
gi|372466577	refseq_human (refseq_human_20140103.fasta)	keratin, type II cytoskeletal 8 isoform 2 [Homo sapiens]

10	20	30	40	50	60	70	80
MSIRVTQKSY	KVSTSGPRAF	SSRSYTSGPG	SRISSSSFSR	VGSSNFRGGL	GGGYGGASGM	GGITAVTVNQ	SLLSPLVLEV
90	100	110	120	130	140	150	160
DPNIQAVRTQ	EKEQIKTLNN	KFASFIDKVR	FLEQQNKMLE	TKWSLLQQQK	TARSNMDNMF	ESYINNLRRQ	LETLGQEKLK
170	180	190	200	210	220	230	240
LEAELGNMQG	LVEDFKNKYE	DEINKRTEME	NEFVLIKKDV	DEAYMNKVEL	ESRLEGLTDE	INFLRQLYEE	EIRELQSQIS
250	260	270	280	290	300	310	320
DTSVVLSMDN	SRSLDMDSII	AEVKAQYEDI	ANRSRAEAES	MYQIKYEELQ	SLAGKHGDDL	RRTKTEISEM	NRNISRLQAE
330	340	350	360	370	380	390	400
IEGLKGQRAS	LEAAIADAEQ	RGELAIKDAN	AKLSELEAAL	QRAKQDMARQ	LREYQELMNV	KLALDIEIAT	YRKLLEGEES
410	420	430	440	450	460	470	480
RLESGMQNMS	IHTKTTSGYA	GGLSSAYGGL	TSPGLSYSLG	SSFGSGAGSS	SFSRTSSSRA	VVVKKIETRD	GKLVSESSDV
490							
LPK							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
447	1	738.2345	-160.13	2	34.2	11.1	0	402-414	R.LESGMQNMSIHTK.T		mdown:qdown 1.08

Detailed Protein Report

Protein 345: **PREDICTED: EGF-containing fibulin-like extracellular matrix protein 1 isoform X2 [Homo sapiens]**

Accession:	gi|530367362	**Score:**	33.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	59.3
Database Date:	2015-11-30	**pI:**	9.5
		Sequence Coverage [%]:	9.8
		No. of unique Peptides:	2

Quantitation

Wdown:Qdown **Median:** 1.24 **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
952	1	824.0174	-86.17	3	40.4	12.7	2	2-24	M.STCPLWRGVPASLGNEELAREGKR		
555	1	676.8735	43.07	2	36.3	10.5	0	110-122	R.SAAAQVFLLCCAR.N		Wdown:Qdown 1.24

Detailed Protein Report

Protein 346: PREDICTED: keratin, type II cuticular Hb3 isoform X1 [Homo sapiens]

Accession:	gi|530400232	**Score:**	33.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	49.6
Database Date:	2015-11-30	**pI:**	5.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	7.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MTCGFNSIGC	GFRPGNFSCV	SACGPRPSRC	CITAAPYRGI	SCYRGLTGGF	GSHSVCGGFR	AGSCGRSFGY	RSGGVCGPSP
90	100	110	120	130	140	150	160
PCITTVSVNE	SLLTPLNLEI	DPNAQCVKQE	EKEQIKSLNS	RFAAFIDKVR	FLEQQNKLLE	TKLQFYQNRE	CCQSNLEPLF
170	180	190	200	210	220	230	240
AGYIETLRRE	AECVEADSGR	LASELNHVQE	VLEGYKKKYE	EEVALRATAE	NEFVALKKDV	DCAYLRKSDL	EANVEALIQE
250	260	270	280	290	300	310	320
IDFLRRLYEE	EIRILQSHIS	DTSVVVKLDN	SRDLNMDCIV	AEIKAQYDDI	ATRSRAEAES	WYRSKCEEMK	ATVIRHGETL
330	340	350	360	370	380	390	400
RRTKEEINEL	NRMIQRLTAE	VENAKCQNSK	LEAAVAQSEQ	QGEAALSDAR	CKLAELEGAL	QKAKQDMACL	IREYQEVMNS
410	420	430	440	450			
KLGLDIEIAT	YRRLLEGEEQ	RLCEGVEAAA	PGVGLCAGIS	ACRAPGR			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2096	1	1052.4199	-78.76	2	54.8	12.5	0	422-443	R.LCEGVEAAAPGVGLCAGISACR.A	Carbamidomethyl: 2

Detailed Protein Report

Protein 347:	**PREDICTED: filamin-B isoform X6 [Homo sapiens]**		
Accession:	gi|530372129	**Score:**	33.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	233.6
Database Date:	2015-11-30	**pI:**	5.2
		Sequence Coverage [%]:	1.1
		No. of unique Peptides:	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MPVTEKDLAE	DAPWKKIQQN	TFTRWCNEHL	KCVNKRIGNL	QTDLSDGLRL	IALLEVLSQK	RMYRKYHQRP	TFRQMQLENV
90	100	110	120	130	140	150	160
SVALEFLDRE	SIKLVSIDSK	AIVDGNLKLI	LGLVWTLILH	YSISMPVWED	EGDDDAKKQT	PKQRLLGWIQ	NKIPYLPITN
170	180	190	200	210	220	230	240
FNQNWQDGKA	LGALVDSCAP	GLCPDWESWD	PQKPVDNARE	AMQQADDWLG	VPQVITPEEI	IHPDVDEHSV	MTYLSQFPKA
250	260	270	280	290	300	310	320
KLKPGAPLKP	KLNPKKARAY	GRGIEPTGNM	VKQPAKFTVD	TISAGQGDVM	VFVEDPEGNK	EEAQVTPDSD	KNKTYSVEYL
330	340	350	360	370	380	390	400
PKVTGLHKVT	VLFAGQHISK	SPFEVSVDKA	QGDASKVTAK	GPGLEAVGNI	ANKPTYFDIY	TAGAGVGDIG	VEVEDPQGKN
410	420	430	440	450	460	470	480
TVELLVEDKG	NQVYRCVYKP	MQPGPHVVKI	FFAGDTIPKS	PFVVQVGEAC	NPNACRASGR	GLQPKGVRIR	ETTDFKVDTK
490	500	510	520	530	540	550	560
AAGSGELGVT	MKGPKGLEEL	VKQKDFLDGV	YAFEYYPSTP	GRYSIAITWG	GHHIPKSPFE	VQVGPEAGMQ	KVRAWGPGLH
570	580	590	600	610	620	630	640
GGIVGRSADF	VVESIGSEVG	SLGFAIEGPS	QAKIEYNDQN	DGSCDVKYWP	KEPGEYAVHI	MCDDEDIKDS	PYMAFIHPAT
650	660	670	680	690	700	710	720
GGYNPDLVRA	YGPGLEKSGC	IVNNLAEFTV	DPKDAGKAPL	KIFAQDGEGQ	RIDIQMKNRM	DGTYACSYTP	VKAIKHTIAV
730	740	750	760	770	780	790	800
VWGGVNIPHS	PYRVNIGQGS	HPQKVKVFGP	GVERSGLKAN	EPTHFTVDCT	EAGEGDVSVG	IKCDARVLSE	DEEDVDFDII
810	820	830	840	850	860	870	880
HNANDTFTVK	YVPPAAGRYT	IKVLFASQEI	PASPFRVKVD	PSHDASKVKA	EGPGLSKAGV	ENGKPTHFTV	YTKGAGKAPL
890	900	910	920	930	940	950	960
NVQFNSPLPG	DAVKDLDIID	NYDYSHTVKY	TPTQQGNMQV	LVTYGGDPIP	KSPFTVGVAA	PLDLSKIKLN	GLENRVEVGK
970	980	990	1000	1010	1020	1030	1040
DQEFTVDTRG	AGGQGKLDVT	ILSPSRKVVP	CLVTPVTGRE	NSTAKFIPRE	EGLYAVDVTY	DGHPVPGSPY	TVEASLPPDP
1050	1060	1070	1080	1090	1100	1110	1120
SKVKAHGPGL	EGGLVGKPAE	FTIDTKGAGT	GGLGLTVEGP	CEAKIECSDN	GDGTCSVSYL	PTKPGEYFVN	ILFEEVHIPG
1130	1140	1150	1160	1170	1180	1190	1200
SPFKADIEMP	FDPSKVVASG	PGLEHGKVGE	AGLLSVDCSE	AGPGALGLEA	VSDSGTKAEV	SIQNNKDGTY	AVTYVPLTAG
1210	1220	1230	1240	1250	1260	1270	1280
MYTLTMKYGG	ELVPHFPARV	KVEPAVDTSR	IKVFGPGIEG	KDVFREATTD	FTVDSRPLTQ	VGGDHIKAHI	ANPSGASTEC
1290	1300	1310	1320	1330	1340	1350	1360
FVTDNADGTY	QVEYTPFEKG	LHVVEVTYDD	VPIPNSPFKV	AVTEGCQPSR	VQAQGPGLKE	AFTNKPNVFT	VVTRGAGIGG
1370	1380	1390	1400	1410	1420	1430	1440
LGITVEGPSE	SKINCRDNKD	GSCSAEYIPF	APGDYDVNIT	YGGAHIPGSP	FRVPVKDVVD	PSKVKIAGPG	LGSGVRARVL
1450	1460	1470	1480	1490	1500	1510	1520
QSFTVDSSKA	GLAPLEVRVL	GPRADDTDSQ	SWRSPLKALS	EFFKGDPKGD	FNKTGLVEPV	NVVDNGDGTH	TVTYTPSQEG
1530	1540	1550	1560	1570	1580	1590	1600
PYMVSVKYAD	EEIPRSPFKV	KVLPTYDASK	VTASGPGLSS	YGVPASLPVD	FAIDARDAGE	GLLAVQITDQ	EGKPKRAIVH
1610	1620	1630	1640	1650	1660	1670	1680
DNKDGTYAVT	YIPDKTGRYM	IGVTYGGDDI	PLSPYRIRAT	QTGDASKCLA	TGPGIASTVK	TGEEVGFVVD	AKTAGKGKVT
1690	1700	1710	1720	1730	1740	1750	1760
CTVLTPDGTE	AEADVIENED	GTYDIFYTAA	KPGTYVIYVR	FGGVDIPNSP	FTVMATDGEV	TAVEEAPVNA	CPPGFRPWVT
1770	1780	1790	1800	1810	1820	1830	1840
EEAYVPVSDM	NGLGFKPFDL	VIPFAVRKGE	ITGEVHMPSG	KTATPEIVDN	KDGTVTVRYA	PTEVGLHEMH	IKYMGSHIPE
1850	1860	1870	1880	1890	1900	1910	1920
SPLQFYVNYP	NSGSVSAYGP	GLVYGVANKT	ATFTIVTEDA	GEGGLDLAIE	GPSKAEISCI	DNKDGTCTVT	YLPTLPGDYS
1930	1940	1950	1960	1970	1980	1990	2000
ILVKYNDKHI	PGSPFTAKIT	DDSRRCSQVK	LGSAADFLLD	ISETDLSSLT	ASIKAPSGRD	EPCLLKRLPN	NHIGISFIPR
2010	2020	2030	2040	2050	2060	2070	2080
EVGEHLVSIK	KNGNHVANSP	VSIMVVQSEI	GDARRAKVYG	RGLSEGRTFE	MSDFIVDTRD	AGYGGISLAV	EGPSKVDIQT
2090	2100	2110	2120	2130	2140	2150	2160
EDLEDGTCKV	SYFPTVPGVY	IVSTKFADEH	VPGSPFTVKI	SGEGRVKESI	TRTSRAPSVA	TVGSICDLNL	KIPGVRVMNC
2170	2180						

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
171	1	614.7837	-134.87	2	30.9	13.4	1	977-987	K.LDVTILSPSRK.V	

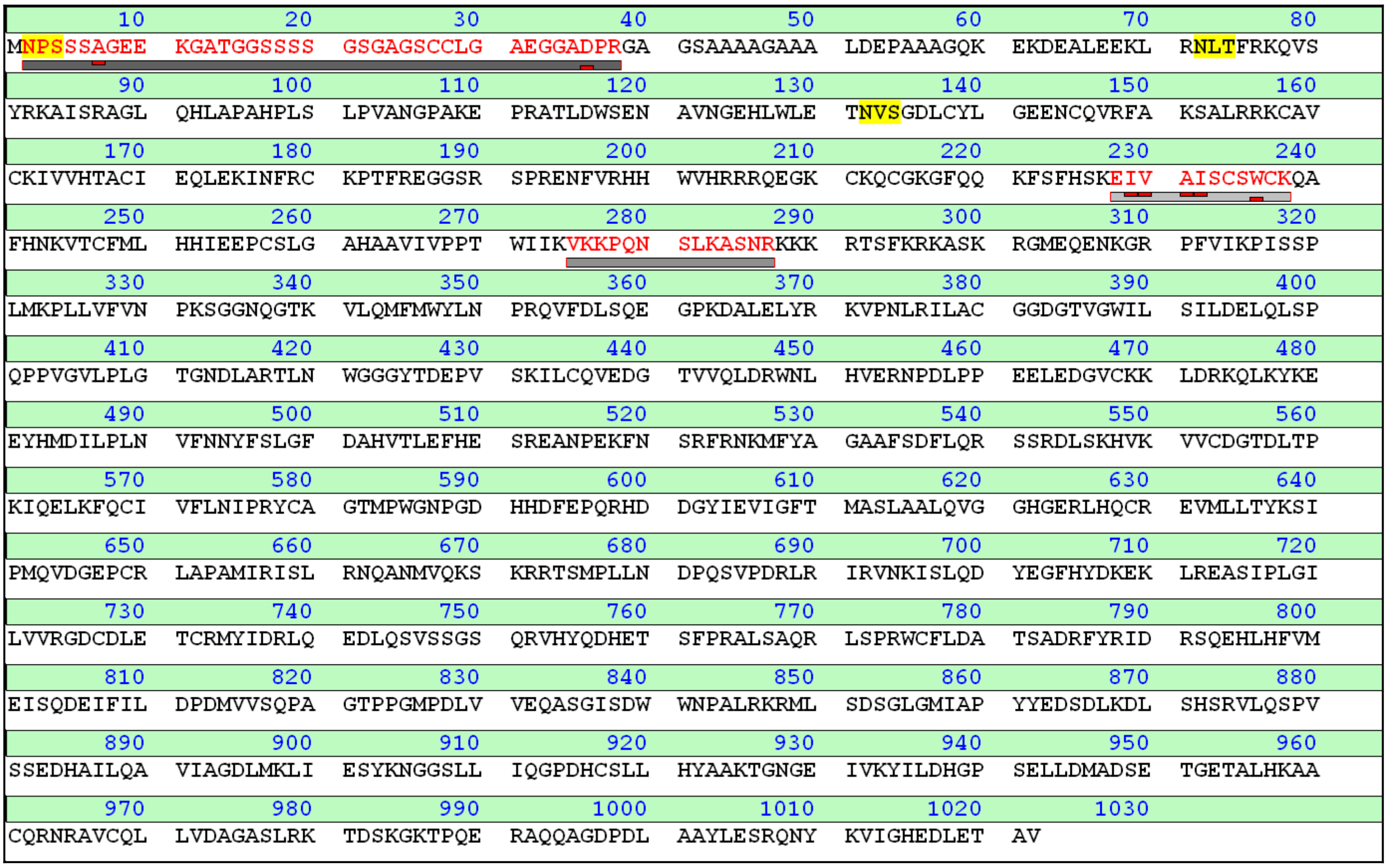
Detailed Protein Report

Protein 348: PREDICTED: diacylglycerol kinase iota isoform X2 [Homo sapiens]

Accession:	gi|578814735	**Score:**	33.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	113.9
Database Date:	2015-11-30	**pI:**	9.1
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	6.0
		No. of unique Peptides:	3

Quantitation

mdown:qdown	**Median:**	1.70	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	1.24	**CV:**	0.00 %	**No. of Peptides:**	1



```
         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	Ratios
1635	1	1100.4411	-20.69	3	50.3	12.6	1	2-38	M. NPSSSAGEEKGATGGSSSSGSGA G	Carbamidomethyl: 26	
800	2	451.4498	-220.69	3	38.5	10.1	0	228-238	K.EIVAISCSWCK.Q	Carbamidomethyl: 7, 10	Wdown:Qdown 1.24 mdown:qdown 1.70
2495	1	735.4148	-22.06	2	61.6	10.5	2	275-287	K.VKKPQNSLKASNR.K		

Detailed Protein Report

Protein 349: **serine/threonine-protein kinase 3 isoform 2 [Homo sapiens]**

Accession: gi|372622373
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 33.2
MW [kDa]: 59.4
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 350: uncharacterized protein C2orf78 [Homo sapiens]

Accession:	gi|122937341	**Score:**	33.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	100.1
Database Date:	2015-11-30	**pI:**	9.7
		Sequence Coverage [%]:	2.7
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	0.43	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.88	**CV:**	0.00 %	**No. of Peptides:**	1

Alias proteins:

Accession	Name	Description
gi|530367561	refseq_human (refseq_human_20140103.fasta)	PREDICTED: uncharacterized protein C2orf78 isoform X1 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MHWLASATQT SASIVSSSLL SAVDVSSSLT MSEYFQNTSL PGTANSRQFS LPVVSNAAFL TGSISNFSRA SAPAISSAWL
        90        100        110        120        130        140        150        160
QPSASGTSFQ PLMGSAYLYQ HSSTTMLSGV TGQSHICTSA ASYPGVFEWD STASTVKKSS SLRDFTVTVI DQNTAVSSMS
       170        180        190        200        210        220        230        240
MTAQYYKTSD TNTMVPLYPS LSASLVQGTL TQIPNQQGHN LSLPCQIGSQ VYYYNQGTLG PQLSCLQSYG SVSYTGYRAS
       250        260        270        280        290        300        310        320
AHQPEMVMVL KEVQPTNVLP PVSTSGMYYS VSSQPITETS VQVMETSLGM DTSLGLQSPS QTFCLPQTPE FSKSFSSRNT
       330        340        350        360        370        380        390        400
QTLESNPSPE LGDISITPVQ SPTNLLTLSP APSQEKNENE NLDEIKTNLS KPLDVHQILI GNQDPPLLPV EIPDIHPLLA
       410        420        430        440        450        460        470        480
CIDPLGQEEQ PGSENANLRN KSLSLEDQGI FENGIESSSD LADITTWVED TYLPPIFSSL QDLDQPESPS AKKAKDTSAI
       490        500        510        520        530        540        550        560
KVNQVQEKSC VIKGHSDQVR KNKHKASEPI QGAPKAKIQP KNPECLLERE VVVGSATVSN SASVNKAKHS SNKPHKAASS
       570        580        590        600        610        620        630        640
RISKTKSHGQ EKTKGNRKNS SKKSEESKQS GKKVKVEEKQ TIPNMKRKKN QPELSQKTLK KPRSSLGMHM LESVQVFHAL
       650        660        670        680        690        700        710        720
GKKIDMKTGF SSSRTLGSSS NTQNRQPFPA LKPWLDIQHE GKGPEKIQVK AQKLDGSAEK ECTSPSHSEL PPPGKVKLIP
       730        740        750        760        770        780        790        800
LPFLTLDQPQ ARHVSRRPNP LASRRPAVAY PARPDSTNSA QSNAVNPSRP APTNTSLTGP ATPAQPISAK ATQPSSANPT
       810        820        830        840        850        860        870        880
QPTVPQSAAS RPSAYKTSSC SSLQREPVST AVTSLRSLPK PQNQFLIQDF SLQPRPWRKP TVPEPVMSTP ITEEQRPERE
       890        900        910        920        930
AMKRKAQQER ENAAKYTSLG KVQFFIERER DMEIAEYYGY TI
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
273	1	572.6538	-235.90	2	32.1	17.4	1	886-895	K.AQQERENAAK.Y		Wdown:Qdown 0.88 mdown:qdown 0.43

Detailed Protein Report

Protein 351: E3 SUMO-protein ligase CBX4 [Homo sapiens]

Accession:	gi|55770830	**Score:**	33.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	61.3
Database Date:	2015-11-30	**pI:**	10.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	6.1
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MELPAVGEHV	FAVESIEKKR	IRKGRVEYLV	KWRGWSPKYN	TWEPEENILD	PRLLIAFQNR	ERQEQLMGYR	KRGPKPKPLV
90	100	110	120	130	140	150	160
VQVPTFARRS	NVLTGLQDSS	TDNRAKLDLG	AQGKGQGHQY	ELNSKKHHQY	QPHSKERAGK	PPPPGKSGKY	YYQLNSKKHH
170	180	190	200	210	220	230	240
PYQPDPKMYD	LQYQGGHKEA	PSPTCPDLGA	KSHPPDKWAQ	GAGAKGYLGA	VKPLAGAAGA	PGKGSEKGPP	NGMMPAPKEA
250	260	270	280	290	300	310	320
VTGNGIGGKM	KIVKNKNKNG	RIVIVMSKYM	ENGMQAVKIK	SGEVAEGEAR	SPSHKKRAAD	ERHPPADRTF	KKAAGAEEKK
330	340	350	360	370	380	390	400
VEAPPKRREE	EVSGVSDPQP	QDAGSRKLSP	TKEAFGEQPL	QLTTKPDLLA	WDPARNTHPP	SHHPHPHPHH	HHHHHHHHHH
410	420	430	440	450	460	470	480
AVGLNLSHVR	KRCLSETHGE	REPCKKRLTA	RSISTPTCLG	GSPAAERPAD	LPPAAALPQP	EVILLDSDLD	EPIDLRCVKT
490	500	510	520	530	540	550	560
RSEAGEPPSS	LQVKPETPAS	AAVAVAAAAA	PTTTAEKPPA	EAQDEPAESL	SEFKPFFGNI	IITDVTANCL	TVTFKEYVTV
570							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1064	1	500.6481	-289.29	2	42.9	11.2	1	105-114	R.AKLDLGAQGK.G	
443	1	699.2695	-110.76	3	34.5	10.6	1	228-249	K.GPPNGMMPAPKEAVTGNGIGGK.M	Oxidation: 6

Detailed Protein Report

Protein 352: membrane-bound transcription factor site-1 protease preproprotein [Homo sapiens]

Accession:	gi|4506775	**Score:**	33.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	117.7
Database Date:	2015-11-30	**pI:**	9.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.4
		No. of unique Peptides:	2

Quantitation

mdown:qdown	**Median:**	1.41	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	1.20	**CV:**	0.00 %	**No. of 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	Ratios
1660	1	612.4256	151.20	3	49.3	12.0	1	387-404	R.MKPDIVTYGAGVRGSGVK.G		Wdown:Qdown 1.20 mdown:qdown 1.41
1464	1	742.6304	-61.81	3	48.1	21.1	1	645-662	R.MKNDPLDWNGDHIHTNFR.D	Oxidation: 1	

Detailed Protein Report

Protein 353: **zinc finger protein 674 isoform 1 [Homo sapiens]**

Accession:	gi|89994742	**Score:**	33.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	67.2
Database Date:	2015-11-30	**pI:**	10.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	8.6
		No. of unique Peptides:	2

Quantitation

Wdown:Qdown **Median:** 0.33 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MAMSQESLTF	KDVFVDFTLE	EWQQLDSAQK	NLYRDVMLEN	YSHLVSVGHL	VGKPDVIFRL	GPGDESWMAD	GGTPVRTCAG
90	100	110	120	130	140	150	160
EDRPEVWEVD	EQIDHYKESQ	DKFLWQAAFI	GKETLKDESG	QECKICRKII	YLNTDFVSVK	QRLPKYYSWE	RCSKHHLNFL
170	180	190	200	210	220	230	240
GQNRSYVRKK	DDGCKAYWKV	CLHYNLHKAQ	PAERFFDPNQ	RGKALHQKQA	LRKSQRSQTG	EKLYKCTECG	KVFIQKANLV
250	260	270	280	290	300	310	320
VHQRTHTGEK	PYECCECAKA	FSQKSTLIAH	QRTHTGEKPY	ECSECGKTFI	QKSTLIKHQR	THTGEKPFVC	DKCPKAFKSS
330	340	350	360	370	380	390	400
YHLIRHEKTH	IRQAFYKGIK	CTTSSLIYQR	IHTSEKPQCS	EHGKASDEKP	SPTKHWRTHT	KENIYECSKC	GKSFRGKSHL
410	420	430	440	450	460	470	480
SVHQRIHTGE	KPYECSICGK	TFSGKSHLSV	HHRTHTGEKP	YECRRCGKAF	GEKSTLIVHQ	RMHTGEKPYK	CNECGKAFSE
490	500	510	520	530	540	550	560
KSPLIKHQRI	HTGERPYECT	DCKKAFSRKS	TLIKHQRIHT	GEKPYKCSEC	GKAFSVKSTL	IVHHRTHTGE	KPYECRDCGK
570	580	590					
AFSGKSTLIK	HQRSHTGDKN	L					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2101	1	599.9147	-53.58	3	56.4	11.0	2	378-392	R.THTKENIYECSKCGK.S	Carbamidomethyl: 10	Wdown:Qdown 0.33
1639	1	1136.1099	81.18	2	50.4	11.8	2	546-565	R.THTGEKPYECRDCGKAFSGK.S	Carbamidomethyl: 13	

Detailed Protein Report

Protein 354: PREDICTED: serine/arginine repetitive matrix protein 2 isoform X3 [Homo sapiens]

Accession:	gi|530407861	**Score:**	32.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	281.3
Database Date:	2015-11-30	**pI:**	12.6
		Sequence Coverage [%]:	0.9
		No. of unique Peptides:	2

Quantitation

mdown:qdown	**Median:**	0.54	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.36	**CV:**	0.00 %	**No. of Peptides:**	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MYNGIGLPTP	RGSGTNGYVQ	RNLSLVRGRR	GERPDYKGEE	ELRRLEAALV	KRPNPDILDH	ERKRRVELRC	LELEEMMEEQ
90	100	110	120	130	140	150	160
GYEEQQIQEK	VATFRLMLLE	KDVNPGGKEE	TPGQRPAVTE	THQLAELNEK	KNERLRAAFG	ISDSYVDGSS	FDPQRRAREA
170	180	190	200	210	220	230	240
KQPAPEPPKP	YSLVRESSSS	RSPTPKQKKK	KKKKDRGRRS	ESSSPRRERK	KSSKKKKHRS	ESESKKRKHR	SPTPKSKRKS
250	260	270	280	290	300	310	320
KDKKRKRSRS	TTPAPKSRRA	HRSTSADSAS	SSDTSRSRSR	SAAAKTHTTA	LAGRSPSPAS	GRRGEGDAPF	SEPGTTSTQR
330	340	350	360	370	380	390	400
PSSPETATKQ	PSSPYEDKDK	DKKEKSATRP	SPSPERSSTG	PEPPAPTPLL	AERHGGSPQP	LATTPLSQEP	VNPPSEASPT
410	420	430	440	450	460	470	480
RDRSPPKSPE	KLPQSSSSES	SPPSPQPTKV	SRHASSSPES	PKPAPAPGSH	REISSSPTSK	NRSHGRAKRD	KSHSHTPSRR
490	500	510	520	530	540	550	560
MGRSRSPATA	KRGRSRSRTP	TKRGHSRSRS	PQWRRSRSAQ	RWGRSRSPQR	RGRSRSPQRP	GWSRSRNTQR	RGRSRSARRG
570	580	590	600	610	620	630	640
RSHSRSPATR	GRSRSRTPAR	RGRSRSRTPA	RRRSRSRTPT	RRRSRSRTPA	RRGRSRSRTP	ARRRSRTRSP	VRRRSRSRSP
650	660	670	680	690	700	710	720
ARRSGRSRSR	TPARRGRSRS	RTPARRGRSR	SRTPARRSGR	SRSRTPARRG	RSRSRTPRRG	RSRSRSLVRR	GRSHSRTPQR
730	740	750	760	770	780	790	800
RGRSGSSSER	KNKSRTSQRR	SRSNSSPEMK	KSRISSRRSR	SLSSPRSKAK	SRLSLRRSLS	GSSPCPKQKS	QTPPRRSRSG
810	820	830	840	850	860	870	880
SSQPKAKSRT	PPRRSRSSSS	PPPKQKSKTP	SRQSHSSSSP	HPKVKSGTPP	RQGSITSPQA	NEQSVTPQRR	SCFESSPDPE
890	900	910	920	930	940	950	960
LKSRTPSRHS	CSGSSPPRVK	SSTPPRQSPS	RSSSPQPKVK	AIISPRQRSH	SGSSSPSPSR	VTSRTTPRRS	RSVSPCSNVE
970	980	990	1000	1010	1020	1030	1040
SRLLPRYSHS	GSSSPDTKVK	PETPPRQSHS	GSISPYPKVK	AQTPPGPSLS	GSKSPCPQEK	SKDSLVQSCP	GSLSLCAGVK
1050	1060	1070	1080	1090	1100	1110	1120
SSTPPGESYF	GVSSLQLKGQ	SQTSPDHRSD	TSSPEVRQSH	SESPSLQSKS	QTSPKGGRSR	SSSPVTELAS	RSPIRQDRGE
1130	1140	1150	1160	1170	1180	1190	1200
FSASPMLKSG	MSPEQSRFQS	DSSSYPTVDS	NSLLGQSRLE	TAESKEKMAL	PPQEDATASP	PRQKDKFSPF	PVQDRPESSL
1210	1220	1230	1240	1250	1260	1270	1280
VFKDTLRTPP	RERSGAGSSP	ETKEQNSALP	TSSQDEELME	VVEKSEEPAG	QILSHLSSEL	KEMSTSNFES	SPEVEERPAV
1290	1300	1310	1320	1330	1340	1350	1360
SLTLDQSQSQ	ASLEAVEVPS	MASSWGGPHF	SPEHKELSNS	PLRENSFGSP	LEFRNSGPLG	TEMNTGFSSE	VKEDLNGPFL
1370	1380	1390	1400	1410	1420	1430	1440
NQLETDPSLD	MKEQSTRSSG	HSSSELSPDA	VEKAGMSSNQ	SISSPVLDAV	PRTPSRERSS	SASSPEMKDG	LPRTPSRRSR
1450	1460	1470	1480	1490	1500	1510	1520
SGSSPGLRDG	SGTPSRHSLS	GSSPGMKDIP	RTPSRGRSEC	DSSPEPKALP	QTPRPRSRSP	SSPELNNKCL	TPQRERSGSE
1530	1540	1550	1560	1570	1580	1590	1600
SSVDQKTVAR	TPLGQRSRSG	SSQELDVKPS	ASPQERSESD	SSPDSKAKTR	TPLRQRSRSG	SSPEVDSKSR	LSPRRSRSGS
1610	1620	1630	1640	1650	1660	1670	1680
SPEVKDKPRA	APRAQSGSDS	SPEPKAPAPR	ALPRRSRSGS	SSKGRGPSPE	GSSSTESSPE	HPPKSRTARR	GSRSSPEPKT
1690	1700	1710	1720	1730	1740	1750	1760
KSRTPPRRRS	SRSSPELTRK	ARLSRRSRSA	SSSPETRSRT	PPRHRRSPSV	SSPEPAEKSR	SSRRRRSASS	PRTKTTSRRG
1770	1780	1790	1800	1810	1820	1830	1840
RSPSPKPRGL	QRSRSRSRRE	KTRTTRRRDR	SGSSQSTSRR	RQRSRSRSRV	TRRRRGGSGY	HSRSPARQES	SRTSSRRRRG
1850	1860	1870	1880	1890	1900	1910	1920
RSRTPPTSRK	RSRSRTSPAP	WKRSRSRASP	ATHRRSRSRT	PLISRRRSRS	RTSPVSRRRS	RSRTSVTRRR	SRSRASPVSR
1930	1940	1950	1960	1970	1980	1990	2000
RRSRSRTPPV	TRRRSRSRTP	TTRRRSRSRT	PPVTRRRSRS	RTPPVTRRRS	RSRTSPITRR	RSRSRTSPVT	RRRSRSRTSP
2010	2020	2030	2040	2050	2060	2070	2080
VTRRRSRSRT	SPVTRRRSRS	RTPPAIRRRS	RSRTPLLPRK	RSRSRSPLAI	RRRSRSRTPR	TARGKRSLTR	SPPAIRRRSA
2090	2100	2110	2120	2130	2140	2150	2160
SGSSSDRSRS	ATPPATRNHS	GSRTPPVALN	SSRMSCFSRP	SMSPTPLDRC	RSPGMLEPLG	SSRTPMSVLQ	QAGGSMMDGP
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2951	7	703.3519	-15.42	2	65.6	16.8	1	833-845	R.QSHSSSSPHPKVK.S		
873	1	491.7878	51.39	2	39.7	16.0	1	1866-1874	R.SRASPATHR.R		Wdown:Qdown 0.36 mdown:qdown 0.54

Detailed Protein Report

Protein 355: 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: 32.8
MW [kDa]: 141.7
pI: 5.7
Sequence Coverage [%]: 1.1
No. of unique Peptides: 2

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
2899	3	840.9173	97.31	2	65.0	13.7	0	168-182	K.YMGQMCGLCGNFDGK.V	Carbamidomethyl: 6
1896	3	840.7895	-54.74	2	53.8	19.2	0	168-182	K.YMGQMCGLCGNFDGK.V	Carbamidomethyl: 9

Detailed Protein Report

Protein 356: **PREDICTED: pleckstrin homology domain-containing family A member 4 isoform X3 [Homo sapiens]**

Accession:	gi|530416942	**Score:**	32.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	65.5
Database Date:	2015-11-30	**pI:**	10.7
		Sequence Coverage [%]:	7.4
		No. of unique Peptides:	3

Quantitation

mdown:qdown	**Median:**	0.66	**CV:**	30.90 %	**No. of Peptides:**	3
Wdown:Qdown	**Median:**	4.13	**CV:**	0.00 %	**No. of Peptides:**	1

10	20	30	40	50	60	70	80
MEGSRPRSSL	SLASSASTIS	SLSSLSPKKP	TRAVNKIHAF	GKRGNALRRD	PNLPVHIRGW	LHKQDSSGLR	LWKRRWFVLS
90	100	110	120	130	140	150	160
GHCLFYYKDS	REESVLGSVL	LPSYNIRPDG	PGAPRGRRFT	FTAEHPGMRT	YVLAADTLED	LRGWLRALGR	ASRAEGDDYG
170	180	190	200	210	220	230	240
QPRSPARPQP	GEGPGGPGGP	PEVSRGEEGR	ISESPEVTRL	SRGRGRPRLL	TPSPTTDLHS	GLQMRRARSP	DLFTPLSRPP
250	260	270	280	290	300	310	320
SPLSLPRPRS	APARRPPAPS	GDTAPPARPH	TPLSRIDVRP	PLDWGPQRQT	LSRPPTPRRG	PPSEAGGGKP	PRSPQHWSQE
330	340	350	360	370	380	390	400
PRTQAHSGSP	TYLQLPPRPP	GTRASMVLLP	GPPLESTFHQ	SLETDTLLTK	LCGQDRLLRR	LQEEIDQKQE	EKEQLEAALE
410	420	430	440	450	460	470	480
LTRQQLGQAT	REAGAPGRAW	GRQRLLQDRL	VSVRATLCHL	TQERERVWDT	YSGLEQELGT	LRETLEYLLH	LGSPQDRVSA
490	500	510	520	530	540	550	560
QQQLWMVEDT	LAGLGGPQKP	PPHTEPDSPS	PVLQGEESSE	RESLPESLEL	SSPRSPETDW	GRPPGGDKDL	ASPHLGLGSP
570	580	590	600				
RVSRASSPEG	RHLPSPQLGT	KKYGSITDWP	ALRSM				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
361	2	711.1755	-208.54	2	33.6	11.6	1	151-163	R.ASRAEGDDYGQPR.S		Wdown:Qdown 4.13 mdown:qdown 0.43
375	1	603.6767	-228.84	2	33.8	10.1	0	300-312	R.GPPSEAGGGKPPR.S		mdown:qdown 0.88
1037	1	945.4829	-32.03	2	41.7	11.1	2	565-582	R.ASSPEGRHLPSPQLGTKK.Y		mdown:qdown 0.74

Detailed Protein Report

Protein 357: H/ACA ribonucleoprotein complex subunit 4 isoform 3 [Homo sapiens]

Accession: gi|570700851
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 32.8
MW [kDa]: 47.6
pI: 10.0
Sequence Coverage [%]: 6.7
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MADAEVIILP	KKHKKKKERK	SLPEEDVAEI	QHAEEFLIKP	ESKVAKLDTS	QWPLLLKNFD	KLNVRTTHYT	PLACGSNPLK
90	100	110	120	130	140	150	160
REIGDYIRTG	FINLDKPSNP	SSHEVVAWIR	RILRVEKTGH	SGTLDPKVTG	CLIVCIERAT	RLVKSQQSAG	KEYVGIVRLH
170	180	190	200	210	220	230	240
NAIEGGTQLS	RALETLTGAL	FQRPPLIAAV	KRQLRVRTIY	ESKMIEYDPE	RRLGIFWVSC	EAGTYIRTLC	VHLGLLLGVG
250	260	270	280	290	300	310	320
GQMQELRRVR	SGVMSEKDHM	VTMHDVLDAQ	WLYDNHKDES	YLRRVVYPLE	KLLTSHKRLV	MKDSAVNAIC	YGAKIMLPGV
330	340	350	360	370	380	390	400
LRYEDGIEVN	QEIVVITTKG	EAICMAIALM	TTAVISTCDH	GIVAKIKRVI	MERDTYPRKW	GLGPKASQKK	LMIKQGLLDK
410	420	430					
HGKPTDSTPA	TWKQEYVDYR						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1944	1	618.9252	-105.31	3	53.0	18.6	2	298-314	K.RLVMKDSAVNAICYGAK.I	Oxidation: 4

Detailed Protein Report

Protein 358: PREDICTED: kinesin-like protein KIF23 isoform X8 [Homo sapiens]

Accession:	gi|578827640	**Score:**	32.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	56.1
Database Date:	2015-11-30	**pI:**	9.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	10.7
		No. of unique Peptides:	1

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2419	1	1051.5349	69.41	2	58.6	10.1	0	240-258	R.SNSCSSISVASCISEWEQK.I	Carbamidomethyl: 12

Detailed Protein Report

Protein 359: fanconi-associated nuclease 1 isoform b [Homo sapiens]

Accession:	gi|226246525	**Score:**	32.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	59.5
Database Date:	2015-11-30	**pI:**	6.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	7.3
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|226246529	refseq_huma (refseq_human_20140103.fasta)	fanconi-associated nuclease 1 isoform b [Homo sapiens]
gi|226246527	refseq_huma (refseq_human_20140103.fasta)	fanconi-associated nuclease 1 isoform b [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		
AKTFHLVNPN	GQKQQLVDAF	LKLAKQRSVC	TWGKNKPGIG	AVILKRFCWL	LLQ		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
443	1	874.1657	67.87	3	34.2	13.4	2	25-49	K.KASNSIISCFNNAPPAKLACPVCSK.M	Carbamidomethyl: 20

Detailed Protein Report

Protein 360: cystatin-B [Homo sapiens]

Accession:	gi|4503117	**Score:**	32.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	11.1
Database Date:	2015-11-30	**pI:**	7.9
		Sequence Coverage [%]:	12.2
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	0.39	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	2.00	**CV:**	0.00 %	**No. of Peptides:**	1

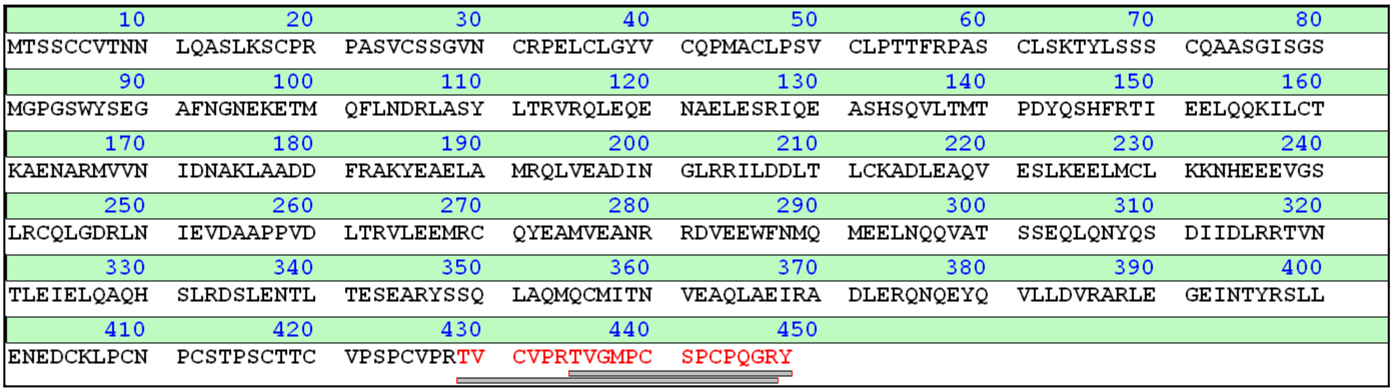
10	20	30	40	50	60	70	80
MMCGAPSATQ	PATAETQHIA	DQVRSQLEEK	ENKKFPVFKA	VSFKSQVVAG	TNYFIKVHVG	DEDFVHLRVF	QSLPHENKPL
90	100						
TLSNYQTNKA	KHDELTYF						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
953	2	663.8439	-18.59	2	40.4	32.7	0	45-56	K.SQVVAGTNYFIK.V		Wdown:Qdown 2.00 mdown:qdown 0.39

Detailed Protein Report

Protein 361: keratin, type I cuticular Ha2 [Homo sapiens]

Accession:	gi|116488398	**Score:**	32.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	50.3
Database Date:	2015-11-30	**pI:**	4.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.5
		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
63	1	518.2825	104.44	3	30.0	10.0	1	435-448	R.TVGMPCSPCPQGRY.-	Carbamidomethyl: 6

Detailed Protein Report

Protein 362: **elongator complex protein 1 [Homo sapiens]**

Accession: gi|38569394
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 32.5
MW [kDa]: 150.2
pI: 5.6
Sequence Coverage [%]: 2.3
No. of unique Peptides: 2

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	
2670	2	625.3045	66.40	2	61.7	21.2	0	453-464	K.CGDCPSADPTVK.L	Carbamidomethyl: 4

Detailed Protein Report

Protein 363: PREDICTED: multiple epidermal growth factor-like domains protein 6 isoform X4 [Homo sapiens]

Accession:	gi|578798522	**Score:**	32.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	135.9
Database Date:	2015-11-30	**pI:**	5.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.4
		No. of unique Peptides:	2

```
        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
12	1	1103.5102	57.86	2	29.4	10.6	0	1198-1219	R.CDCDGGAPCDPVTGLCLCPPGR.S	Carbamidomethyl: 16

Detailed Protein Report

Protein 364: C3 and PZP-like alpha-2-macroglobulin domain-containing protein 8 [Homo sapiens]

Accession:	gi|118600977	**Score:**	32.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	211.2
Database Date:	2015-11-30	**pI:**	6.2
		Sequence Coverage [%]:	1.8
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	0.69	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	1.61	**CV:**	0.00 %	**No. of Peptides:**	1

Detailed Protein Report

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
968	1	820.0912	-24.82	3	40.6	16.4	1	1285-1306	K.SWIIQQQQADGSFLAVGRVLNK.D		Wdown:Qdown 1.61 mdown:qdown 0.69

Detailed Protein Report

Protein 365: PREDICTED: serine/threonine-protein kinase B-raf isoform X2 [Homo sapiens]

Accession: gi|530387108
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 32.4
MW [kDa]: 83.9
pI: 7.9
Sequence Coverage [%]: 2.1
No. of unique Peptides: 1

Quantitation

mdown:qdown **Median:** 0.64 **CV:** 0.00 % **No. of Peptides:** 1
Wdown:Qdown **Median:** 0.48 **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	IQNFQCIS				

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	Wdown:Qdown 0.48 mdown:qdown 0.64

Detailed Protein Report

Protein 366: protein FAM104A isoform 3 [Homo sapiens]

Accession:	gi|574956994	**Score:**	32.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	9.8
Database Date:	2015-11-30	**pI:**	12.7
		Sequence Coverage [%]:	40.8
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MGGRGADAGS SGGTGPTEGY SPPAASTRAA ARAKARGGGR GGRRNTTPSV PSLRGAAPRS FHPPAAMSER LRPSLQAVTV
        90        100        110
VGAAAAAAAA SIARTGPAGR KAA
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2594	1	974.3959	-62.39	3	60.7	16.5	2	1-32	-.MGGRGADAGSSGGTGPTEGYSPPAASTRAAAR.A	

Detailed Protein Report

Protein 367: PREDICTED: HMG box transcription factor BBX isoform X10 [Homo sapiens]

Accession:	gi|578807613	**Score:**	32.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	98.5
Database Date:	2015-11-30	**pI:**	9.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MKGSNRNKDH	SAEGEGVGKR	PKRKCLQWHP	LLAKKLLDFS	EEEEEEDEEE	DIDKVQLLGA	DGLEQDVGET	EDDESPEQRA
90	100	110	120	130	140	150	160
RRPMNAFLLF	CKRHRSLVRQ	EHPRLDNRGA	TKILADWWAV	LDPKEKQKYT	DMAKEYKDAF	MKANPGYKWC	PTTNKPVKSP
170	180	190	200	210	220	230	240
TPTVNPRKKL	WAFPSDSSRD	LPSPKKAKTE	EMPQLNFGMA	DPTQMGGLSM	LLLAGEHALG	TPEVSSGTCR	PDVSESPELR
250	260	270	280	290	300	310	320
QKSPLFQFAE	ISSSTSHSDA	STKQCQTSAL	FQFAEISSNT	SQLGGAEPVK	RCGKSALFQL	AEMCLASEGM	KMEESKLIKA
330	340	350	360	370	380	390	400
KESDGGRIKE	LEKGKEEKEI	KMEKTDETRL	QKEAEFEKSA	KENLRDSKEL	RNFEALQIDD	IMAIKMEDPK	EIRKEELEED
410	420	430	440	450	460	470	480
HKCSHFPDFS	YSASSKIIIS	DVPSRKDHMC	HPHGIMIIED	PAALNKPEKL	KKKKKKSKMD	RHGNDKSTPK	KTCKKRQSSE
490	500	510	520	530	540	550	560
SDIESVIYTI	EAVAKGDWGI	EKLGDTPRKK	VRTSSSGKGS	ILDAKPPKKK	VKSREKKMSK	EKSSDTTKES	RPPDFISISA
570	580	590	600	610	620	630	640
SKNISGETPE	GIKAEPLTPM	EDALPPSLSG	QAKPEDSDCH	RKIETCGSRK	SERSCKGALY	KTLVSEGMLT	SLRANVDRGK
650	660	670	680	690	700	710	720
RSSGKGNSSD	HEGCWNEESW	TFSQSGTSGS	KKFKKTKPKE	DCLLGSAKLD	EEFEKKFNSL	PQYSPVTFDR	KCVPVPRKKK
730	740	750	760	770	780	790	800
KTGNVSSEPT	KTSKGSGDKW	SNKQLFLDAI	HPTEEPTTTQ	EPLVGSQKRK	ARKTKITHLV	RTADGRVSPA	GGTLDDKPKE
810	820	830	840	850	860	870	880
QLQRSLPKAT	ETDCNDKCSH	NTEVGETRSS	TPEMPAVSAF	FSLAALAEVA	AMENVHRGQR	STPLTHDGQP	KEMPQAPVLI
890							
SCADQ							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2908	1	939.4942	3.35	2	65.1	16.7	1	622-638	K.TLVSEGMLTSLRANVDR.G	Oxidation: 7

Detailed Protein Report

Protein 368: PREDICTED: cytoplasmic tyrosine-protein kinase BMX isoform X1 [Homo sapiens]

Accession:	gi|578837945	**Score:**	32.3
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:	2

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
1584	1	1022.9716	-60.15	2	49.7	16.6	1	559-576	R.YVLDDQYVSSVGTKFPVK.W	
2432	1	701.1001	113.81	3	58.7	15.7	0	592-609	K.SDVWAFGILMWEVFSLGK.Q	Oxidation: 10

Detailed Protein Report

Protein 369: **PREDICTED: conserved oligomeric Golgi complex subunit 7 isoform X2 [Homo sapiens]**

Accession:	gi|530409377	**Score:**	32.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	79.1
Database Date:	2015-11-30	**pI:**	5.2
		Sequence Coverage [%]:	5.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPKVLRDVEA	LKQEASFLKE	QMILVKEDIK	KFEQDTSQSM	QVLVEIDQVK	SRMQLAAESL	QEADKWSTLS	ADIEETFKTQ
90	100	110	120	130	140	150	160
DIAVISAKLT	GMQNSLMMLV	DTPDYSEKCV	HLEALKNRLE	ALASPQIVAA	FTSQAVDQSK	VFVKVFTEID	RMPQLLAYYY
170	180	190	200	210	220	230	240
KCHKVQLLAA	WQELCQSDLS	LDRQLTGLYD	ALLGAWHTQI	QWATQVFQKP	HEVVMVLLIQ	TLGALMPSLP	SCLSNGVERA
250	260	270	280	290	300	310	320
GPEQELTRLL	EFYDATAHFA	KGLEMALLPH	LHEHNLVKVT	ELVDAVYDPY	KPYQLKYGDM	EESNLLIQMS	AVPLEHGEVI
330	340	350	360	370	380	390	400
DCVQELSHSV	NKLFGLASAA	VDRCVRFTNG	LGTCGLLSAL	KSLFAKYVSD	FTSTLQSIRK	KCKLDHIPPN	SLFQEDWTAF
410	420	430	440	450	460	470	480
QNSIRIIATC	GELLRHCGDF	EQQLANRILS	TAGKYLSDSC	SPRSLAGFQE	SILTDKKNSA	KNPWQEYNYL	QKDNPAEYAS
490	500	510	520	530	540	550	560
LMEILYTLKE	KGSSNHNLLA	APRAALTRLN	QQAHQLAFDS	VFLRIKQQLL	LISKMDSWNT	AGIGETLTDE	LPAFSLTPLE
570	580	590	600	610	620	630	640
YISNIGQYIM	SLPLNLEPFV	TQEDSALELA	LHAGKLPFPP	EQGDELPELD	NMADNWLGSI	ARATMQTYCD	AILQIPELSP
650	660	670	680	690	700	710	
HSAKQLATDI	DYLINVMDAL	GLQPSRTLQH	IVTLLKTRPE	DYRQVSKGLP	RRLATTVATM	RSVNY	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1449	1	946.3990	-84.94	3	46.6	13.1	2	27-50	K.EDIKKFEQDTSQSMQVLVEIDQVK.S	

Detailed Protein Report

Protein 370: **PREDICTED: insulin-like growth factor 1 receptor isoform X2 [Homo sapiens]**

Accession:	gi|530407102	**Score:**	32.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	141.1
Database Date:	2015-11-30	**pI:**	5.4
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	3.7
		No. of unique Peptides:	3

10	20	30	40	50	60	70	80
MTNLKDIGLY	NLRNITRGAI	RIEKNADLCY	LSTVDWSLIL	DAVSNNYIVG	NKPPKECGDL	CPGTMEEKPM	CEKTTINNEY
90	100	110	120	130	140	150	160
NYRCWTTNRC	QKMCPSTCGK	RACTENNECC	HPECLGSCSA	PDNDTACVAC	RHYYYAGVCV	PACPPNTYRF	EGWRCVDRDF
170	180	190	200	210	220	230	240
CANILSAESS	DSEGFVIHDG	ECMQECPSGF	IRNGSQSMYC	IPCEGPCPKV	CEEEKKTKTI	DSVTSAQMLQ	GCTIFKGNLL
250	260	270	280	290	300	310	320
INIRRGNNIA	SELENFMGLI	EVVTGYVKIR	HSHALVSLSF	LKNLRLILGE	EQLEGNYSFY	VLDNQNLQQL	WDWDHRNLTI
330	340	350	360	370	380	390	400
KAGKMYFAFN	PKLCVSEIYR	MEEVTGTKGR	QSKGDINTRN	NGERASCESD	VLHFTSTTTS	KNRIIITWHR	YRPPDYRDLI
410	420	430	440	450	460	470	480
SFTVYYKEAP	FKNVTEYDGQ	DACGSNSWNM	VDVDLPPNKD	VEPGILLHGL	KPWTQYAVYV	KAVTLTMVEN	DHIRGAKSEI
490	500	510	520	530	540	550	560
LYIRTNASVP	SIPLDVLSAS	NSSSQLIVKW	NPPSLPNGNL	SYYIVRWQRQ	PQDGYLYRHN	YCSKDKIPIR	KYADGTIDIE
570	580	590	600	610	620	630	640
EVTENPKTEV	CGGEKGPCCA	CPKTEAEKQA	EKEEAEYRKV	FENFLHNSIF	VPRPERKRRD	VMQVANTTMS	SRSRNTTAAD
650	660	670	680	690	700	710	720
TYNITDPEEL	ETEYPFFESR	VDNKERTVIS	NLRPFTLYRI	DIHSCNHEAE	KLGCSASNFV	FARTMPAEGA	DDIPGPVTWE
730	740	750	760	770	780	790	800
PRPENSIFLK	WPEPENPNGL	ILMYEIKYGS	QVEDQRECVS	RQEYRKYGGA	KLNRLNPGNY	TARIQATSLS	GNGSWTDPVF
810	820	830	840	850	860	870	880
FYVQAKTGYE	NFIHLIIALP	VAVLLIVGGL	VIMLYVFHRK	RNNSRLGNGV	LYASVNPEYF	SAADVYVPDE	WEVAREKITM
890	900	910	920	930	940	950	960
SRELGQGSFG	MVYEGVAKGV	VKDEPETRVA	IKTVNEAASM	RERIEFLNEA	SVMKEFNCHH	VVRLLGVVSQ	GQPTLVIMEL
970	980	990	1000	1010	1020	1030	1040
MTRGDLKSYL	RSLRPEMENN	PVLAPPSLSK	MIQMAGEIAD	GMAYLNANKF	VHRDLAARNC	MVAEDFTVKI	GDFGMTRDIY
1050	1060	1070	1080	1090	1100	1110	1120
ETDYYRKGGK	GLLPVRWMSP	ESLKDGVFTT	YSDVWSFGVV	LWEIATLAEQ	PYQGLSNEQV	LRFVMEGGLL	DKPDNCPDML
1130	1140	1150	1160	1170	1180	1190	1200
FELMRMCWQY	NPKMRPSFLE	IISSIKEEME	PGFREVSFYY	SEENKLPEPE	ELDLEPENME	SVPLDPSASS	SSLPLPDRHS
1210	1220	1230	1240	1250			
GHKAENGPGP	GVLVLRASFD	ERQPYAHMNG	GRKNERALPL	PQSSTC			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1818	1	697.0290	127.81	3	51.4	10.3	0	56-73	K.ECGDLCPGTMEEKPMCEK.T	Carbamidomethyl: 16; Oxidation: 10, 15
1420	1	669.8545	-38.10	2	46.5	11.2	0	271-282	R.HSHALVSLSFLK.N	
2019	1	660.9088	-130.71	3	53.8	10.8	1	325-340	K.MYFAFNPKLCVSEIYR.M	

Detailed Protein Report

Protein 371: 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:	1

10	20	30	40	50	60	70	80
MDDDSLDELV	ARSPGPDGHP	QVGPADPAES	SVGSSGDSGD	DSDSEHGDGT	DGEDEGASEE	EDLEDRSGSE	DSEDDGETLL
90	100	110	120	130	140	150	160
EVAGTQGKLE	AAGSFNSDDD	AESCPICLNA	FRDQAVGTPE	NCAHYFCLDC	IVEWSKNANS	CPVDRTLFKC	ICIRAQFGGK
170	180	190	200	210	220	230	240
ILRKIPVENT	KASEEEEDPT	FCEVCGRSDR	EDRLLLCDGC	DAGYHMECLD	PPLQEVPVDE	WFCPECAAPG	VVLAADAGPV
250	260	270	280	290	300	310	320
SEEEVSLLLA	DVVPTTSRLR	PRAGRTRAIA	RTRQSERVRA	TVNRNRISTA	RRVQHTPGRL	GSSLLDEAIE	AVATGLSTAV
330	340	350	360	370	380	390	400
YQRPLTPRTP	ARRKRKTRRR	KKVPGRKKTP	SGPSAKSKSS	ATRSKKRQHR	VKKRRGKKVK	SEATTRSRIA	RTLGLRRPVH
410	420	430	440	450	460	470	480
SSCIPSVLKP	VEPSLGLLRA	DIGAASLSLF	GDPYELDPFD	SSEELSANPL	SPLSAKRRAL	SRSALQSHQP	VARPVSVGLS
490	500	510	520	530	540	550	560
RRRLPAAVPE	PDLEEEPVPD	LLGSILSGQS	LLMLGSSDVI	IHRDGSLSAK	RAAPVSFQRN	SGSLSRGEEG	FKGCLQPRAL
570	580	590	600	610	620	630	640
PSGSPAQGPS	GNRPQSTGLS	CQGRSRTPAR	TAGAPVRLDL	PAAPGAVQAR	NLSNGSVPGF	RQSHSPWFNG	TNKHTLPLAS
650	660	670	680	690	700	710	720
AASKISSRDS	KPPCRSVVPG	PPLKPAPRRT	DISELPRIPK	IRRDDGGGRR	DAAPAHGQSI	EIPSACISRL	TGREGTGQPG
730	740	750	760	770	780	790	800
RGTRAESEAS	SRVPREPGVH	TGSSRPPAPS	SHGSLAPLGP	SRGKGVGSTF	ESFRINIPGN	MAHSSQLSSP	GFCNTFRPVD
810	820	830	840	850	860	870	880
DKEQRKENPS	PLFSIKKTKQ	LRSEVYDPSD	PTGSDSSAPG	SSPERSGPGL	LPSEITRTIS	INSPKAQTVQ	AVRCVTSYTV
890	900	910	920	930	940	950	960
ESIFGTEPEP	PLGPSSAMSK	LRGAVAAEGA	SDTEREEPTE	SQGLAARLRR	PSPPEPWDEE	DGASCSTFFG	SEERTVTCVT
970	980	990	1000	1010	1020	1030	1040
VVEPEAPPSP	DVLQAATHRV	VELRPPSRSR	STSSSRSRKK	AKRKRVSREH	GRTRSGTRSE	SRDRSSRSAS	PSVGEERPRR
1050	1060	1070	1080	1090	1100	1110	1120
QRSKAKSRRS	SSDRSSSRER	AKRKKAKDKS	REHRRGPWGH	SRRTSRSRSG	SPGSSSYEHY	ESRKKKKRRS	ASRPRGRECS
1130	1140	1150	1160	1170	1180	1190	1200
PTSSLERLCR	HKHQRERSHE	RPDRKESVAW	PRDRRKRRSR	SPSSEHRARE	HRRPRSREKW	PQTRSHSPER	KGAVREASPA
1210	1220	1230	1240	1250	1260	1270	1280
PLAQGEPGRE	DLPTRLPALG	EAHVSPEVAT	ADKAPLQAPP	VLEVAAECEP	DDLDLDYGDS	VEAGHVFDDF	SSDAVFIQLD
1290	1300	1310	1320	1330	1340	1350	1360
DMSSPPSPES	TDSSPERDFP	LKPALPPASL	AVAAIQREVS	LMHDEDPSQP	PPLPEGTQEP	HLLRPDAAEK	AEAPSSPDVA
1370	1380	1390	1400	1410	1420	1430	1440
PAGKEDSPSA	SGRVQEAARP	EEVVSQTPLL	RSRALVKRVT	WNLQESESSA	PAEDRAPRAP	LHRPQKPREG	AWDMEDVAPT
1450	1460	1470	1480	1490	1500	1510	1520
GVRQVFSELP	FPSHVLPEPG	FPDTDPSQVY	SPGLPPAPAQ	PSSIPPCALV	SQPTVQFILQ	GSLPLVGCGA	AQTLAPVPAA
1530	1540	1550	1560	1570	1580	1590	1600
LTPASEPASQ	ATAASNSEEK	TPAPRLAAEK	TKKEEYMKKL	HMQERAVEEV	KLAIKPFYQK	REVTKEEYKD	ILRKAVQKIC
1610	1620	1630	1640	1650			
HSKSGEINPV	KVANLVKAYV	DKYRHMRRHK	KPEAGEEPPT	QGAEG			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1686	1	697.6744	-192.66	2	51.0	20.4	0	1-12	-.MDDDSLDELVAR.S	Oxidation: 1

Detailed Protein Report

Protein 372: NACHT, LRR and PYD domains-containing protein 2 isoform 3 [Homo sapiens]

Accession:	gi|291463280	**Score:**	32.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	117.8
Database Date:	2015-11-30	**pI:**	5.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.4
		No. of unique Peptides:	3

Quantitation

Wdown:Qdown **Median:** 0.59 **CV:** 0.00 % **No. of Peptides:** 1

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	Ratios
1358	1	727.3750	-33.15	2	45.7	10.3	1	710-722	R.VVFKNISPADAHR.N		Wdown:Qdown 0.59
1270	1	419.0769	-336.69	2	44.6	11.0	0	864-870	K.FLCEGLR.Y		
1197	1	786.4909	152.63	2	44.6	10.8	1	864-875	K.FLCEGLRYPECK.L	Carbamidomethyl: 3, 11	

Detailed Protein Report

Protein 373: integrin beta-1-binding protein 2 [Homo sapiens]

Accession:	gi|6912438	**Score:**	32.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	38.4
Database Date:	2015-11-30	**pI:**	4.9
		Sequence Coverage [%]:	8.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSLLCRNKGC	GQHFDPNTNL	PDSCCHHPGV	PIFHDALKGW	SCCRKRTVDF	SEFLNIKGCT	MGPHCAEKLP	EAPQPEGPAT
90	100	110	120	130	140	150	160
SSSLQEQKPL	NVIPKSAETL	RRERPKSELP	LKLLPLNISQ	ALEMALEQKE	LDQEPGAGLD	SLIRTGSSCQ	NPGCDAVYQG
170	180	190	200	210	220	230	240
PESDATPCTY	HPGAPRFHEG	MKSWSCCGIQ	TLDFGAFLAQ	PGCRVGRHDW	GKQLPASCRH	DWHQTDSLVV	VTVYGQIPLP
250	260	270	280	290	300	310	320
AFNWVKASQT	ELHVHIVFDG	NRVFQAQMKL	WGVINVEQSS	VFLMPSRVEI	SLVKADPGSW	AQLEHPDALA	KKARAGVVLE
330	340	350					
MDEEESDDSD	DDLSWTEEEE	EEEAMGE					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
297	1	861.8427	115.33	3	32.8	21.3	2	46-68	K.RTVDFSEFLNIKGCTMGPHCAEK.L	

Detailed Protein Report

Protein 374: deoxyribonuclease-1-like 2 precursor [Homo sapiens]

Accession:	gi|4503347	**Score:**	32.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	32.8
Database Date:	2015-11-30	**pI:**	4.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	8.0
		No. of unique Peptides:	2

Alias proteins:

Accession	**Name**	**Description**
gi|578828006	refseq_human (refseq_human_20140103.fasta)	PREDICTED: deoxyribonuclease-1-like 2 isoform X3 [Homo sapiens]
gi|530407699	refseq_human (refseq_human_20140103.fasta)	PREDICTED: deoxyribonuclease-1-like 2 isoform X2 [Homo sapiens]

10	20	30	40	50	60	70	80
MGGPRALLAA	LWALEAAGTA	ALRIGAFNIQ	SFGDSKVSDP	ACGSIIAKIL	AGYDLALVQE	VRDPDLSAVS	ALMEQINSVS
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
EHEYSFVSSQ	PLGRDQYKEM	YLFVYRKDAV	SVVDTYLYPD	PEDVFSREPF	VVKFSAPGTG	ERAPPLPSRR	ALTPPPLPAA
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
AQNLVLIPLH	AAPHQAVAEI	DALYDVYLDV	IDKWGTDDML	FLGDFNADCS	YVRAQDWAAI	RLRSSEVFKW	LIPDSADTTV
250	**260**	**270**	**280**	**290**	**300**		
GNSDCAYDRI	VACGARLRRS	LKPQSATVHD	FQEEFGLDQT	QALAISDHFP	VEVTLKFHR		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1794	1	568.7414	-60.72	2	52.4	15.0	0	99-106	K.EMYLFVYR.K	Oxidation: 2
1326	1	939.1023	103.59	2	45.3	17.0	2	214-229	R.AQDWAAIRLRSSEVFK.W	

Detailed Protein Report

Protein 375: Golgi apparatus protein 1 isoform 3 precursor [Homo sapiens]

Accession:	gi|224586817	**Score:**	32.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	134.5
Database Date:	2015-11-30	**pI:**	6.5
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	1.4
		No. of unique Peptides:	1

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

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

Detailed Protein Report

Protein 376: DNA endonuclease RBBP8 isoform b [Homo sapiens]

Accession:	gi|42718017	**Score:**	31.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	98.4
Database Date:	2015-11-30	**pI:**	6.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MNISGSSCGS	PNSADTSSDF	KDLWTKLKEC	HDREVQGLQV	KVTKLKQERI	LDAQRLEEFF	TKNQQLREQQ	KVLHETIKVL
90	100	110	120	130	140	150	160
EDRLRAGLCD	RCAVTEEHMR	KKQQEFENIR	QQNLKLITEL	MNERNTLQEE	NKKLSEQLQQ	KIENDQQHQA	AELECEEDVI
170	180	190	200	210	220	230	240
PDSPITAFSF	SGVNRLRRKE	NPHVRYIEQT	HTKLEHSVCA	NEMRKVSKSS	THPQHNPNEN	EILVADTYDQ	SQSPMAKAHG
250	260	270	280	290	300	310	320
TSSYTPDKSS	FNLATVVAET	LGLGVQEESE	TQGPMSPLGD	ELYHCLEGNH	KKQPFEESTR	NTEDSLRFSD	STSKTPPQEE
330	340	350	360	370	380	390	400
LPTRVSSPVF	GATSSIKSGL	DLNTSLSPSL	LQPGKKKHLK	TLPFSNTCIS	RLEKTRSKSE	DSALFTHHSL	GSEVNKIIIQ
410	420	430	440	450	460	470	480
SSNKQILINK	NISESLGEQN	RTEYGKDSNT	DKHLEPLKSL	GGRTSKRKKT	EEESEHEVSC	PQASFDKENA	FPFPMDNQFS
490	500	510	520	530	540	550	560
MNGDCVMDKP	LDLSDRFSAI	QRQEKSQGSE	TSKNKFRQVT	LYEALKTIPK	GFSSSRKASD	GNCTLPKDSP	GEPCSQECII
570	580	590	600	610	620	630	640
LQPLNKCSPD	NKPSLQIKEE	NAVFKIPLRP	RESLETENVL	DDIKSAGSHE	PIKIQTRSDH	GGCELASVLQ	LNPCRTGKIK
650	660	670	680	690	700	710	720
SLQNNQDVSF	ENIQWSIDPG	ADLSQYKMDV	TVIDTKDGSQ	SKLGGETVDM	DCTLVSETVL	LKMKKQEQKG	EKSSNEERKM
730	740	750	760	770	780	790	800
NDSLEDMFDR	TTHEEYESCL	ADSFSQAADE	EEELSTATKK	LHTHGDKQDK	VKQKAFVEPY	FKGDESIMQI	CQQKKEKRNW
810	820	830	840	850	860	870	
LPAQDTDSAT	FHPTHQRIFG	KLVFLPLRLV	WKEVILRKIL	ILVLVQKDVS	LTTQYFLQKA	RSRRHRR	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2621	1	673.3610	86.09	2	63.5	12.5	0	194-204	K.LEHSVCANEMR.K	Carbamidomethyl: 6

Detailed Protein Report

Protein 377: **PREDICTED: mediator of RNA polymerase II transcription subunit 12 isoform X3 [Homo sapiens]**

Accession:	gi|530421861	**Score:**	31.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	240.6
Database Date:	2015-11-30	**pI:**	6.7
		Sequence Coverage [%]:	1.5
		No. of unique Peptides:	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MAAFGILSYE	HRPLKRPRLG	PPDVYPQDPK	QKEDELTALN	VKQGFNNQPA	VSGDEHGSAK	NVSFNPAKIS	SNFSSIIAEK
90	100	110	120	130	140	150	160
LRCNTLPDTG	RRKPQVNQKD	NFWLVTARSQ	SAINTWFTDL	AGTKPLTQLA	KKVPIFSKKE	EVFGYLAKYT	VPVMRAAWLI
170	180	190	200	210	220	230	240
KMTCAYYAAI	SETKVKKRHV	DPFMEWTQII	TKYLWEQLQK	MAEYYRPGPA	GSGGCGSTIG	PLPHDVEVAI	RQWDYTEKLA
250	260	270	280	290	300	310	320
MFMFQDGMLD	RHEFLTWVLE	CFEKIRPGED	ELLKLLLPLL	LRYSGEFVQS	AYLSRRLAYF	CTRRLALQLD	GVSSHSSHVI
330	340	350	360	370	380	390	400
SAQSTSTLPT	TPAPQPPTSS	TPSTPFSDLL	MCPQHRPLVF	GLSCILQTIL	LCCPSALVWH	YSLTDSRIKT	GSPLDHLPIA
410	420	430	440	450	460	470	480
PSNLPMPEGN	SAFTQQVRAK	LREIEQQIKE	RGQAVEVRWS	FDKCQEATAG	FTIGRVLHTL	EVLDSHSFER	SDFSNSLDSL
490	500	510	520	530	540	550	560
CNRIFGLGPS	KDGHEISSDD	DAVVSLLCEW	AVSCKRSGRH	RAMVVAKLLE	KRQAEIEAER	CGESEAADEK	GSIASGSLSA
570	580	590	600	610	620	630	640
PSAPIFQDVL	LQFLDTQAPM	LTDPRSESER	VEFFNLVLLF	CELIRHDVFS	HNMYTCTLIS	RGDLAFGAPG	PRPPSPFDDP
650	660	670	680	690	700	710	720
ADDPEHKEAE	GSSSSKLEDP	GLSESMDIDP	SSSVLFEDME	KPDFSLFSPT	MPCEGKGSPS	PEKPDVEKEV	KPPPKEKIEG
730	740	750	760	770	780	790	800
TLGVLYDQPR	HVQYATHFPI	PQEESCSHEC	NQRLVVLFGV	GKQRDDARHA	IKKITKDILK	VLNRKGTAET	DQLAPIVPLN
810	820	830	840	850	860	870	880
PGDLTFLGGE	DGQKRRRNRP	EAFPTAEDIF	AKFQHLSHYD	QHQVTAQVSR	NVLEQITSFA	LGMSYHLPLV	QHVQFIFDLM
890	900	910	920	930	940	950	960
EYSLSISGLI	DFAIQLLNEL	SVVEAELLLK	SSDLVGSYTT	SLCLCIVAVL	RHYHACLILN	QDQMAQVFEG	LCGVVKHGMN
970	980	990	1000	1010	1020	1030	1040
RSDGSSAERC	ILAYLYDLYT	SCSHLKNKFG	ELFSDFCSKV	KNTIYCNVEP	SESNMRWAPE	FMIDTLENPA	AHTFTYTGLG
1050	1060	1070	1080	1090	1100	1110	1120
KSLSENPANR	YSFVCNALMH	VCVGHHDPDR	VNDIAILCAE	LTGYCKSLSA	EWLGVLKALC	CSSNNGTCGF	NDLLCNVDVS
1130	1140	1150	1160	1170	1180	1190	1200
DLSFHDSLAT	FVAILIARQC	LLLEDLIRCA	AIPSLLNAAC	SEQDSEPGAR	LTCRILLHLF	KTPQLNPCQS	DGNKPTVGIR
1210	1220	1230	1240	1250	1260	1270	1280
SSCDRHLLAA	SQNRIVDGAV	FAVLKAVFVL	GDAELKGSGF	TVTGGTEELP	EEEGGGGSGG	RRQGGRNISV	ETASLDVYAK
1290	1300	1310	1320	1330	1340	1350	1360
YVLRSICQQE	WVGERCLKSL	CEDSNDLQDP	VLSSAQAQRL	MQLICYPHRL	LDNEDGENPQ	RQRIKRILQN	LDQWTMRQSS
1370	1380	1390	1400	1410	1420	1430	1440
LELQLMIKQT	PNNEMNSLLE	NIAKATIEVF	QQSAETGSSS	GSTASNMPSS	SKTKPVLSSL	ERSGVWLVAP	LIAKLPTSVQ
1450	1460	1470	1480	1490	1500	1510	1520
GHVLKAAGEE	LEKGQHLGSS	SRKERDRQKQ	KSMSLLSQQP	FLSLVLTCLK	GQDEQREGLL	TSLYSQVHQI	VNNWRDDQYL
1530	1540	1550	1560	1570	1580	1590	1600
DDCKPKQLMH	EALKLRLNLV	GGMFDTVQRS	TQQTTEWAML	LLEIIISGTV	DMQSNNELFT	TVLDMLSVLI	NGTLAADMSS
1610	1620	1630	1640	1650	1660	1670	1680
ISQGSMEENK	RAYMNLAKKL	QKELGERQSD	SLEKVRQLLP	LPKQTRDVIT	CEPQGSLIDT	KGNKIAGFDS	IFKKEGLQVS
1690	1700	1710	1720	1730	1740	1750	1760
TKQKISPWDL	FEGLKPSAPL	SWGWFGTVRV	DRRVARGEEQ	QRLLLYHTHL	RPRPRAYYLE	PLPLPPEDEE	PPAPTLLEPE
1770	1780	1790	1800	1810	1820	1830	1840
KKAPEPPKTD	KPGAAPPSTE	ERKKKSTKGK	KRSQPATKTE	DYGMGPGRSG	PYGVTVPPDL	LHHPNPGSIT	HLNYRQGSIG
1850	1860	1870	1880	1890	1900	1910	1920
LYTQNQPLPA	GGPRVDPYRP	VRLPMQKLPT	RPTYPGVLPT	TMTGVMGLEP	SSYKTSVYRQ	QQPAVPQGQR	LRQQLQAKIQ
1930	1940	1950	1960	1970	1980	1990	2000
SQGMLGQSSV	HQMTPSSSYG	LQTSQGYTPY	VSHVGLQQHT	GPADPTRHLQ	QRPSGYVHQQ	APTYGHGLTS	TQRFSHQTLQ
2010	2020	2030	2040	2050	2060	2070	2080
QTPMISTMTP	MSAQGVQAGV	RSTAILPEQQ	QQQQQQQQQQ	QQQQQQQQQQ	QQQQYHIRQQ	QQQQILRQQQ	QQQQQQQQQQ
2090	2100	2110	2120	2130	2140	2150	2160
QQQQQQQQQQ	QQQHQQQQQQ	QAAPPQPQPQ	SQPQFQRQGL	QQTQQQQQTA	ALVRQLQQQL	SNTQPQPSTN	IFGRY

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1964	5	753.7894	-104.99	2	54.7	14.5	1	989-1001	K.FGELFSDFCSKVK.N	

Detailed Protein Report

Protein 378: PREDICTED: uncharacterized protein LOC102725205, partial [Homo sapiens]

Accession:	gi|578845222	**Score:**	31.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	95.5
Database Date:	2015-11-30	**pI:**	6.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.3
		No. of unique Peptides:	3

```
        10         20         30         40         50         60         70         80
TLSHTLHPPT HTPNLTHSTH THTTPPTHTP HPTHHSTPLT HSTPHTSHTH STPLTHSTPH SWAAKSLERL LWVVASSPPR

        90        100        110        120        130        140        150        160
RTAVVGRIPG AGMPAGAGGP ACRCPCLSRV GWRDLDAEPS SQEFRQLSLD SHQVAAFQTE MECWARGSGM DATEPLCCDC

       170        180        190        200        210        220        230        240
QTSDLVCWSQ QGHQGPERGA LGSLEEPGLL SAREAWPVSC SSIFLEVSGR RLESRMPPGG AAINISPGDK RTNQSPAGYR

       250        260        270        280        290        300        310        320
GEDKSGKRLM SELWLQVAAA RDGLQDFPGL LVAGRGSSSG DWSERAYGWE LEELMEKRGR VGWSSREALW SGEGEEEPNK

       330        340        350        360        370        380        390        400
EKQQSTWNIS IPPSKAVLEE QPQSPIVPKS GKSVKTFIRN RYEPAKRCEE LICAELIRMN KVTTDSAMGI ADKDLSEELQ

       410        420        430        440        450        460        470        480
HRLQHALASL QVAQGEDLTA DIMYSPSASE PLPFMQCDGE QETGTASPIW LWNLWAGESH PHGVHALATL GWEGPMVNAG

       490        500        510        520        530        540        550        560
EKVQEEEGAP ATGPSCGQHR EGCCGGEDVG VEGCGGGHLL ALGCPSKTLT ARGILPVGGA ASTTSLQEAM FVFRTTLIRA

       570        580        590        600        610        620        630        640
VGCKEQRPLK GEGGAVKDVE SRRCAGLWFR EPCGRQVKME LHKSAGETPG KLKVEYADGG MPEARLWEGT HIFETKVKLS

       650        660        670        680        690        700        710        720
TVIHEAAVQW PSGDIEKTHL SSGLFSELIR GLCSFDMFLP DTVVCWPLPW SAFHPVLLQT MSAPGLSPAL DPLCPQLLAD

       730        740        750        760        770        780        790        800
LGSEKQSCPS REFGWGLAEV PSVSNLCKGG LALQAADGGS GGGVRTPSYY LNECMGITAA LYEHLKTTLS NPSFSKEKES

       810        820        830        840        850        860        870        880
VNFPFSMHEV TGVCHSGGPV FKKNREETVR LSAGGAARQK ELMLYPVVSF PKGLHQLPSF LALIMTISVV TSLLSKESIF

       890
SSCQE
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2662	1	933.9882	34.09	2	64.5	10.3	0	194-210	R.EAWPVSCSSIFLEVSGR.R	
992	2	647.6724	-181.96	2	40.9	10.3	0	614-625	K.VEYADGGMPEAR.L	
2897	1	655.6487	-212.02	2	65.0	11.2	0	614-625	K.VEYADGGMPEAR.L	Oxidation: 8

Detailed Protein Report

Protein 379: transient receptor potential cation channel subfamily M member 8 [Homo sapiens]

Accession: gi|109689695
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 31.7
MW [kDa]: 127.6
pI: 7.0
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 380: **PREDICTED: transcription factor TFIIIB component B" homolog isoform X2 [Homo sapiens]**

Accession:	gi|578840763	**Score:**	31.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	289.3
Database Date:	2015-11-30	**pI:**	4.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.5
		No. of unique Peptides:	2

Quantitation

mdown:qdown	**Median:**	1.23	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	1.02	**CV:**	0.00 %	**No. of Peptides:**	1

10	20	30	40	50	60	70	80
MFRRARLSVK	PNVRPGVGAR	GSTASNPQRG	RESPRPPEPA	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	Ratios
138	1	613.7562	-197.90	2	31.0	10.7	1	1438-1447	R.FKRPKPNLAR.A		Wdown:Qdown 1.02 mdown:qdown 1.23
2728	1	806.1966	-169.47	2	65.4	11.0	0	2392-2404	R.DDCQEYTTEVHSK.E	Carbamidomethyl: 3	

Detailed Protein Report

Protein 381: **PREDICTED: arf-GAP with GTPase, ANK repeat and PH domain-containing protein 3 isoform X2 [Homo sapiens]**

Accession:	gi|530386889	**Score:**	31.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	61.7
Database Date:	2015-11-30	**pI:**	11.8
		Sequence Coverage [%]:	5.2
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MERGWPQGDS CPGERPAACR RAHSVCDSLD LHGASAGRAA AALQAALCAA SEQPARPRSV CSGGPEPPPT GARGLLLGLL
        90        100        110        120        130        140        150        160
RPRLGRRGLA PSGPPVSPAP SPASSPAPTR RSRTRGEPTP RPRPASMTFL EVNRLELAAA EAPGAGLGRA GSAGFLRGAA
       170        180        190        200        210        220        230        240
LWSSQRWPVL RGGRGPEGPR RGLAALRKSF SFRLRRGQEV RRSESGLLAR PPRARTRSDG DAGSLGAFPS RRDLLGSDAP
       250        260        270        280        290        300        310        320
RAAPEPGRPR TAAGLWRLLT SRFRRREPAP AAPLWGRRAA AAPELLRAPS DSFVNSQEWT LSRSVPELKV GIVGNLSSGK
       330        340        350        360        370        380        390        400
SALVHRYLTG TYVQEESPEG GRFKKEIVVD GQSYLLLIRD EGGPPELQFA AWVDAVVFVF SLEDEISFQT VYNYFLRLCS
       410        420        430        440        450        460        470        480
FRNASEVPMV LVGTQDAISA ANPRVIDDSR ARKLSTDLKR CTYYETCATY GLNVERVFQD VAQKVVALRK KQQLAIGPCK
       490        500        510        520        530        540        550        560
SLPNSPSHSA VSAASIPAVH INQATNGGGS AFSDYSSSVP STPSISQREL RIETIAASST PTPIRKQSKR RSNIFTICAT
       570        580
VSNFSSTKRP FQLLPN
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1530	1	873.6409	147.98	2	47.7	10.1	1	345-359	K.KEIVVDGQSYLLLIR.D	

Detailed Protein Report

Protein 382: ras and Rab interactor 2 isoform 2 [Homo sapiens]

Accession:	gi|18466802	**Score:**	31.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	100.1
Database Date:	2015-11-30	**pI:**	6.1
		Sequence Coverage [%]:	2.0
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578835435	refseq_human (refseq_human_20140103.fasta)	PREDICTED: ras and Rab interactor 2 isoform X10 [Homo sapiens]
gi|578835433	refseq_human (refseq_human_20140103.fasta)	PREDICTED: ras and Rab interactor 2 isoform X9 [Homo sapiens]
gi|578835431	refseq_human (refseq_human_20140103.fasta)	PREDICTED: ras and Rab interactor 2 isoform X8 [Homo sapiens]
gi|578835429	refseq_human (refseq_human_20140103.fasta)	PREDICTED: ras and Rab interactor 2 isoform X7 [Homo sapiens]
gi|530425753	refseq_human (refseq_human_20140103.fasta)	PREDICTED: ras and Rab interactor 2 isoform X3 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MTAWTMGARG LDKRGSFFKL IDTIASEIGE LKQEMVRTDV NLENGLEPAE THSMVRHKDG GYSEEEDVKT CARDSGYDSL
        90        100        110        120        130        140        150        160
SNRLSILDRL LHTHPIWLQL SLSEEEAAEV LQAQPPGIFL VHKSTKMQKK VLSLRLPCEF GAPLKEFAIK ESTYTFSLEG
       170        180        190        200        210        220        230        240
SGISFADLFR LIAFYCISRD VLPFTLKLPY AISTAKSEAQ LEELAQMGLN FWSSPADSKP PNLPPPHRPL SSDGVCPASL
       250        260        270        280        290        300        310        320
RQLCLINGVH SIKTRTPSEL ECSQTNGALC FINPLFLKVH SQDLSGGLKR PSTRTPNANG TERTRSPPPR PPPPAINSLH
       330        340        350        360        370        380        390        400
TSPRLARTET QTSMPETVNH NKHGNVALPG TKPTPIPPPR LKKQASFLEA EGGAKTLSGG RPGAGPELEL GTAGSPGGAP
       410        420        430        440        450        460        470        480
PEAAPGDCTR APPPSSESRP PCHGGRQRLS DMSISTSSSD SLEFDRSMPL FGYEADTNSS LEDYEGESDQ ETMAPPIKSK
       490        500        510        520        530        540        550        560
KKRSSSFVLP KLVKSQLQKV SGVFSSFMTP EKRMVRRIAE LSRDKCTYFG CLVQDYVSFL QENKECHVSS TDMLQTIRQF
       570        580        590        600        610        620        630        640
MTQVKNYLSQ SSELDPPIES LIPEDQIDVV LEKAMHKCIL KPLKGHVEAM LKDFHMADGS WKQLKENLQL VRQRNPQELG
       650        660        670        680        690        700        710        720
VFAPTPDFVD VEKIKVKFMT MQKMYSPEKK VMLLLRVCKL IYTVMENNSG RMYGADDFLP VLTYVIAQCD MLELDTEIEY
       730        740        750        760        770        780        790        800
MMELLDPSLL HGEGGYYLTS AYGALSLIKN FQEEQAARLL SSETRDTLRQ WHKRRTTNRT IPSVDDFQNY LRVAFQEVNS
       810        820        830        840        850        860        870        880
GCTGKTLLVR PYIITEDVCQ ICAEKFKVGD PEEYSLFLFV DETWQQLAED TYPQKIKAEL HSRPQPHIFH FVYKRIKNDP
       890        900
YGIIFQNGEE DLTTS
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2319	1	719.3506	-2.64	2	57.7	16.1	1	1-13	-.MTAWTMGARGLDK.R	

Detailed Protein Report

Protein 383: mothers against decapentaplegic homolog 3 isoform 1 [Homo sapiens]

Accession:	gi|5174513	**Score:**	31.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	48.0
Database Date:	2015-11-30	**pI:**	6.8
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	7.1
		No. of unique Peptides:	2

Quantitation

mdown:qdown **Median:** 0.97 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MSSILPFTPP	IVKRLLGWKK	GEQNGQEEKW	CEKAVKSLVK	KLKKTGQLDE	LEKAITTQNV	NTKCITIPRS	LDGRLQVSHR
90	100	110	120	130	140	150	160
KGLPHVIYCR	LWRWPDLHSH	HELRAMELCE	FAFNMKKDEV	CVNPYHYQRV	ETPVLPPVLV	PRHTEIPAEF	PPLDDYSHSI
170	180	190	200	210	220	230	240
PENTNFPAGI	EPQSNIPETP	PPGYLSEDGE	TSDHQMNHSM	DAGSPNLSPN	PMSPAHNNLD	LQPVTYCEPA	FWCSISYYEL
250	260	270	280	290	300	310	320
NQRVGETFHA	SQPSMTVDGF	TDPSNSERFC	LGLLSNVNRN	AAVELTRRHI	GRGVRLYYIG	GEVFAECLSD	SAIFVQSPNC
330	340	350	360	370	380	390	400
NQRYGWHPAT	VCKIPPGCNL	KIFNNQEFAA	LLAQSVNQGF	EAVYQLTRMC	TIRMSFVKGW	GAEYRRQTVT	STPCWIELHL
410	420	430					
NGPLQWLDKV	LTQMGSPSIR	CSSVS					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1610	1	1100.1365	-2.93	2	50.0	20.3	2	1-19	-.MSSILPFTPPIVKRLLGWK.K	Oxidation: 1	
1152	2	644.3310	-22.52	2	43.1	11.4	1	64-74	K.CITIPRSLDGR.L	Carbamidomethyl: 1	mdown:qdown 0.97

Detailed Protein Report

Protein 384: serine/threonine-protein kinase WNK3 isoform 2 [Homo sapiens]

Accession:	gi|50845416	**Score:**	31.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	191.7
Database Date:	2015-11-30	**pI:**	5.4
		Sequence Coverage [%]:	2.8
		No. of unique Peptides:	2

Alias proteins:

Accession	**Name**	**Description**
gi|578838231	refseq_human (refseq_human_20140103.fasta)	PREDICTED: serine/threonine-protein kinase WNK3 isoform X2 [Homo sapiens]
gi|578838229	refseq_human (refseq_human_20140103.fasta)	PREDICTED: serine/threonine-protein kinase WNK3 isoform X1 [Homo sapiens]

Detailed Protein Report

10	20	30	40	50	60	70	80
MATDSGDPAS	TEDSEKPDGI	SFENRVPQVA	ATLTVEARLK	EKNSTFSASG	ETVERKRFFR	KSVEMTEDDK	VAESSPKDER
90	100	110	120	130	140	150	160
IKAAMNIPRV	DKLPSNVLRG	GQEVKYEQCS	KSTSEISKDC	FKEKNEKEME	EEAEMKAVAT	SPSGRFLKFD	IELGRGAFKT
170	180	190	200	210	220	230	240
VYKGLDTETW	VEVAWCELQD	RKLTKAEQQR	FKEEAEMLKG	LQHPNIVRFY	DSWESILKGK	KCIVLVTELM	TSGTLKTYLK
250	260	270	280	290	300	310	320
RFKVMKPKVL	RSWCRQILKG	LQFLHTRTPP	IIHRDLKCDN	IFITGPTGSV	KIGDLGLATL	MRTSFAKSVI	GTPEFMAPEM
330	340	350	360	370	380	390	400
YEEHYDESVD	VYAFGMCMLE	MATSEYPYSE	CQNAAQIYRK	VTSGIKPASF	NKVTDPEVKE	IIEGCIRQNK	SERLSIRDLL
410	420	430	440	450	460	470	480
NHAFFAEDTG	LRVELAEEDD	CSNSSLALRL	WVEDPKKLKG	KHKDNEAIEF	SFNLETDTPE	EVAYEMVKSG	FFHESDSKAV
490	500	510	520	530	540	550	560
AKSIRDRVTP	IKKTREKKPA	GCLEERRDSQ	CKSMGNVFPQ	PQNTTLPLAP	AQQTGAECEE	TEVDQHVRQQ	LLQRKPQQHC
570	580	590	600	610	620	630	640
SSVTGDNLSE	AGAASVIHSD	TSSQPSVAYS	SNQTMGSQMV	SNIPQAEVNV	PGQIYSSQQL	VGHYQQVSGL	QKHSKLTQPQ
650	660	670	680	690	700	710	720
ILPLVQGQST	VLPVHVLGPT	VVSQPQVSPL	TVQKVPQIKP	VSQPVGAEQQ	AALLKPDLVR	SLNQDVATTK	ENVSSPDNPS
730	740	750	760	770	780	790	800
GNGKQDRIKQ	RRASCPRPEK	GTKFQLTVLQ	VSTSGDNMVE	CQLETHNNKM	VTFKFDVDGD	APEDIADYMV	EDNFVLESEK
810	820	830	840	850	860	870	880
EKFVEELRAI	VGQAQEILHV	HFATERATGV	DSITVDSNSS	QTGSSEQVQI	NSTSTQTSNE	SAPQSSPVGR	WRFCINQTIR
890	900	910	920	930	940	950	960
NRETQSPPSL	QHSMSAVPGR	HPLPSPKNTS	NKEISRDTLL	TIENNPCHRA	LFTSKSEHKD	VVDGKISECA	SVETKQPAIL
970	980	990	1000	1010	1020	1030	1040
YQVEDNRQIM	APVTNSSSYS	TTSVRAVPAE	CEGLTKQASI	FIPVYPCHQT	ASQADALMSH	PGESTQTSGN	SLTTLAFDQK
1050	1060	1070	1080	1090	1100	1110	1120
PQTLSVQQPA	MDAEFISQEG	ETTVNTEASS	PKTVIPTQTP	GLEPTTLQPT	TVLESDGERP	PKLEFADNRI	KTLDEKLRNL
1130	1140	1150	1160	1170	1180	1190	1200
LYQEHSISSI	YPESQKDTQS	IDSPFSSSAE	DTLSCPVTEV	IAISHCGIKD	SPVQSPNFQQ	TGSKLLSNVA	ASQPANISVF
1210	1220	1230	1240	1250	1260	1270	1280
KRDLNVITSV	PSELCLHEMS	SDASLPGDPE	AYPAAVSSGG	AIHLQTGVET	EEMRSAIAPD	PIPLTRESTA	DTRALNRCKA
1290	1300	1310	1320	1330	1340	1350	1360
MSGSFQRGRF	QVITIPQQQS	AKMTSFGIEH	ISVFSETNHS	SEEAFIKTAK	SQLVEIEPAT	QNPKTSFSYE	KLQALQETCK
1370	1380	1390	1400	1410	1420	1430	1440
ENKGVPKQGD	NFLSFSAACE	TDVSSVTPEK	EFEETSATGS	SMQSGSELLL	KEREILTAGK	QPSSDSEFSA	SLAGSGKSVA
1450	1460	1470	1480	1490	1500	1510	1520
KTGPESNQCL	PHHEEQAYAQ	TQSSLFYSPS	SPMSSDDESE	IEDEDLKVEL	QRLREKHIQE	VVNLQTQQNK	ELQELYERLR
1530	1540	1550	1560	1570	1580	1590	1600
SIKDSKTQST	EIPLPPASPR	RPRSFKSKLR	SRPQSLTHVD	NGIVATDPLC	VESNAASCQQ	SPASKKGMFT	DDLHKLVDDW
1610	1620	1630	1640	1650	1660	1670	1680
TKEAVGNSLI	KPSLNQLKQS	QHKLETENWN	KVSENTPSTM	GYTSTWISSL	SQIRGAVPTS	LPQGLSLPSF	PGPLSSYGMP
1690	1700	1710	1720	1730	1740	1750	
HVCQYNAVAG	AGYPVQWVGI	SGTTQQSVVI	PAQSGGPFQP	GMNMQAFPTS	SVQNPATIPP	GPK	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1147	1	956.4746	-119.29	1	43.0	10.6	2	486-493	R.DRVTPIKK.T	
1472	1	918.1282	-10.85	3	46.9	10.8	2	1414-1441	R.EILTAGKQPSSDSEFSASLAGSGKSVAK.T	

Detailed Protein Report

Protein 385: PREDICTED: putative tripartite motif-containing protein 61 isoform X1 [Homo sapiens]

Accession:	gi|578809113	**Score:**	31.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	55.4
Database Date:	2015-11-30	**pI:**	9.5
		Sequence Coverage [%]:	6.4
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578809117	refseq_human (refseq_human_20140103.fasta)	PREDICTED: putative tripartite motif-containing protein 61 isoform X3 [Homo sapiens]
gi|578809115	refseq_human (refseq_human_20140103.fasta)	PREDICTED: putative tripartite motif-containing protein 61 isoform X2 [Homo sapiens]

10	20	30	40	50	60	70	80
MEFVTALADL	RAEASCPICL	DYLKDPVTIS	CGHNFCLSCI	IMSWKDLHDS	FPCPFCHFCC	PERKFISNPQ	LGSLTEIAKQ
90	100	110	120	130	140	150	160
LQIRSKKRKR	QEEKHVCKKH	NQVLTFFCQK	DLELLCPRCS	LSTDHQHHCV	WPIKKAASYH	RKKLEEYNAP	WKERVELIEK
170	180	190	200	210	220	230	240
VITMQTRKSL	ELKKKVKHRA	EEVKSEFEQL	RLFLQNEQET	VLRQLQDEEM	DILAQLNESL	TKFSDYTSSL	KYLLKEIESI
250	260	270	280	290	300	310	320
YVKSELELLA	NVKDIYHRYE	NLKFPELFLF	KLKKYGYHLP	PQYSGLDKII	KRFQVDVILD	PETAHRKLIV	SEDRKTVRYG
330	340	350	360	370	380	390	400
NTTQNVPHNP	RRFYLLPAVL	GSKGYSCGRQ	YWEVEVKDKP	EWILGVCNDC	LPRRRKSQPI	LVQDGLWGIW	RSSQNNYIVL
410	420	430	440	450	460	470	480
GHREIILLPQ	VIPSKIGIFL	DYEMNEVSFY	NLNDRSLLYT	FNDNFTGALW	PYFYTGTDSK	PLKISTVTDS	E

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1483	1	620.0670	154.80	3	47.3	17.2	0	358-373	K.DKPEWILGVCNDCLPR.R	

Detailed Protein Report

Protein 386: tetratricopeptide repeat protein 37 [Homo sapiens]

Accession:	gi|7662078	**Score:**	31.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	175.4
Database Date:	2015-11-30	**pI:**	8.1
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.5
		No. of unique Peptides:	1

Quantitation

mdown:qdown **Median:** 1.29 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MSSKEVKTAL	KSARDAIRNK	EYKEALKHCK	TVLKQEKNNY	NAWVFIGVAA	AELEQPDQAQ	SAYKKAAELE	PDQLLAWQGL
90	100	110	120	130	140	150	160
ANLYEKYNHI	NAKDDLPGVY	QKLLDLYESV	DKQKWCDVCK	KLVDLYYQEK	KHLEVARTWH	KLIKTRQEQG	AENEELHQLW
170	180	190	200	210	220	230	240
RKLTQFLAES	TEDQNNETQQ	LLFTAFENAL	GLSDKIPSED	HQVLYRHFIQ	SLSKFPHESA	RLKKACEGMI	NIYPTVQYPL
250	260	270	280	290	300	310	320
EVLCLHLIES	GNLTDEGQQY	CCRLVEMDSK	SGPGLIGLGI	KALQDKKYED	AVRNLTEGLK	ESPVCTSGWY	HLAEAQVKMH
330	340	350	360	370	380	390	400
RPKEAVLSCS	QALKIVDNLG	ASGNSLYQRN	LCLHLKAEAL	IKLSDYDSSE	EAIRTLDQIS	DADNIPGLLV	LKSLAYRNKG
410	420	430	440	450	460	470	480
SFDEAAKIME	DLLSSYPDLA	EVHALEALIH	FTKKDYLQAE	KCFQRALEKD	TEVAEYHYQL	GLTYWFMGEE	TRKDKTKALT
490	500	510	520	530	540	550	560
HFLKAARLDT	YMGKVFCYLG	HYYRDVVGDK	NRARGCYRKA	FELDDTDAES	GAAAVDLSVE	LEDMEMALAI	LTTVTQKASA
570	580	590	600	610	620	630	640
GTAKWAWLRR	GLYYLKAGQH	SQAVADLQAA	LRADPKDFNC	WESLGEAYLS	RGGYTTALKS	FTKASELNPE	SIYSVFKVAA
650	660	670	680	690	700	710	720
IQQILGKYKE	AVAQYQMIIK	KKEDYVPALK	GLGECHLMMA	KAALVDYLDG	KAVDYIEKAL	EYFTCALQHR	ADVSCLWKLA
730	740	750	760	770	780	790	800
GDACTCLYAV	APSKVNVHVL	GVLLGQKEGK	QVLKKNELLH	LGGRCYGRAL	KLMSTSNTWC	DLGINYYRQA	QHLAETGSNM
810	820	830	840	850	860	870	880
NDLKELLEKS	LHCLKKAVRL	DSNNHLYWNA	LGVVACYSGI	GNYALAQHCF	IKSIQSEQIN	AVAWTNLGVL	YLTNENIEQA
890	900	910	920	930	940	950	960
HEAFKMAQSL	DPSYLMCWIG	QALIAEAVGS	YDTMDLFRHT	TELNMHTEGA	LGYAYWVCTT	LQDKSNRETE	LYQYNILQMN
970	980	990	1000	1010	1020	1030	1040
AIPAAQVILN	KYVERIQNYA	PAFTMLGYLN	EHLQLKKEAA	NAYQRAILLL	QTAEDQDTYN	VAIRNYGRLL	CSTGEYDKAI
1050	1060	1070	1080	1090	1100	1110	1120
QAFKSTPLEV	LEDIIGFALA	LFMKGLYKES	SKAYERALSI	VESEQDKAHI	LTALAITEYK	QGKTDVAKTL	LFKCSILKEP
1130	1140	1150	1160	1170	1180	1190	1200
TTESLQALCA	LGLAMQDATL	SKAALNELLK	HIKHKDSNYQ	RCLLTSAIYA	LQGRSVAVQK	QISKAVHSNP	GDPALWSLLS
1210	1220	1230	1240	1250	1260	1270	1280
RVVAQYAQRN	AKGGVVAGNV	AHILDSNHGK	KALLYTAVNQ	LAMGSSSAED	EKNTALKTIQ	KAALLSPGDP	AIWAGLMAAC
1290	1300	1310	1320	1330	1340	1350	1360
HADDKLALVN	NTQPKRIDLY	LALLSAVSAS	IKDEKFFENY	NQSLEKWSLS	QAVTGLIDTG	RISEAETLCT	KNLKSNPDQP
1370	1380	1390	1400	1410	1420	1430	1440
AVILLLRQVQ	CKPLLESQKP	LPDAVLEELQ	KTVMSNSTSV	PAWQWLAHVY	QSQGMMRAAE	MCYRKSLQLA	SQRGSWSGKL
1450	1460	1470	1480	1490	1500	1510	1520
SSLLRLALLA	LKVCMANISN	DHWPSLVQEA	TTEALKLCFC	PLAVLLQALL	QFKRKMGARE	TRRLLERVVY	QPGYPKSIAS
1530	1540	1550	1560	1570			
TARWYLLRHL	YAKDDYELID	VLVNNAKTHG	DTRALELNQR	LSSQ			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1224	1	533.6546	-167.61	2	44.0	14.5	1	113-120	K.QKWCDVCK.K	Carbamidomethyl: 7	mdown:qdown 1.29

Detailed Protein Report

Protein 387: keratin, type II cuticular Hb2 [Homo sapiens]

Accession:	gi|27477127	**Score:**	31.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	56.6
Database Date:	2015-11-30	**pI:**	6.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	5.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSYHSFQPGS	RCGSQSFSSY	SAVMPRMVTH	YAVSKGPCRP	GGGRGLRALG	CLGSRSLCNV	GFGRPRVASR	CGGTLPGFGY
90	100	110	120	130	140	150	160
RLGATCGPSA	CITPVTINES	LLVPLALEID	PTVQRVKRDE	KEQIKCLNNR	FASFINKVRF	LEQKNKLLET	KWNFMQQQRC
170	180	190	200	210	220	230	240
CQTNIEPIFE	GYISALRRQL	DCVSGDRVRL	ESELCSLQAA	LEGYKKKYEE	ELSLRPCVEN	EFVALKKDVD	TAFLMKADLE
250	260	270	280	290	300	310	320
TNAEALVQEI	DFLKSLYEEE	ICLLQSQISE	TSVIVKMDNS	RELDVDGIIA	EIKAQYDDIA	SRSKAEAEAW	YQCRYEELRV
330	340	350	360	370	380	390	400
TAGNHCDNLR	NRKNEILEMN	KLIQRLQQET	ENVKAQRCKL	EGAIAEAEQQ	GEAALNDAKC	KLAGLEEALQ	KAKQDMACLL
410	420	430	440	450	460	470	480
KEYQEVMNSK	LGLDIEIATY	RRLLEGEEHR	LCEGIGPVNI	SVSSSKGAFL	YEPCGVSTPV	LSTGVLRSNG	GCSIVGTGEL
490	500	510	520				
YVPCEPQGLL	SCGSGRKSSM	TLGAGGSSPS	HKH				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1841	1	1057.4972	-8.19	2	51.7	10.5	0	160-177	R.CCQTNIEPIFEGYISALR.R	Carbamidomethyl: 2

Detailed Protein Report

Protein 388: 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

Detailed Protein Report

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

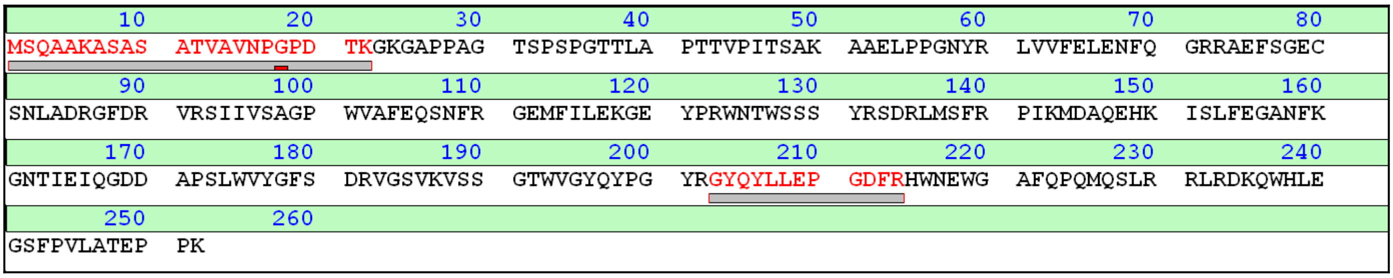
Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1821	1	920.3533	-110.00	2	52.8	20.0	2	2474-2489	R.EAHKQVTCENSPKSPK.V	Carbamidomethyl: 8

Detailed Protein Report

Protein 389: beta-crystallin B1 [Homo sapiens]

Accession: gi|4503061
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 31.3
MW [kDa]: 28.0
pI: 9.2
Sequence Coverage [%]: 13.5
No. of unique Peptides: 2



```
        10         20         30         40         50         60         70         80
MSQAAKASAS ATVAVNPGPD TKGKGAPPAG TSPSPGTTLA PTTVPITSAK AAELPPGNYR LVVFELENFQ GRRAEFSGEC
        90        100        110        120        130        140        150        160
SNLADRGFDR VRSIIVSAGP WVAFEQSNFR GEMFILEKGE YPRWNTWSSS YRSDRLMSFR PIKMDAQEHK ISLFEGANFK
       170        180        190        200        210        220        230        240
GNTIEIQGDD APSLWVYGFS DRVGSVKVSS GTWVGYQYPG YRGYQYLLEP GDFRHWNEWG AFQPQMQSLR RLRDKQWHLE
       250        260
GSFPVLATEP PK
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2177	1	1051.4295	-96.54	2	55.7	20.8	1	1-22	-.MSQAAKASASATVAVNPGPDTK.G	
2974	1	729.3714	20.28	2	65.9	10.5	0	203-214	R.GYQYLLEPGDFR.H	

Detailed Protein Report

Protein 390: **wee1-like protein kinase 2 [Homo sapiens]**

Accession:	gi|157738687	**Score:**	31.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	62.9
Database Date:	2015-11-30	**pI:**	6.1
		Sequence Coverage [%]:	5.5
		No. of unique Peptides:	2

```
        10         20         30         40         50         60         70         80
MDDKDIDKEL RQKLNFSYCE ETEIEGQKKV EESREASSQT PEKGEVQDSE AKGTPPWTPL SNVHELDTSS EKDKESPDQI
        90        100        110        120        130        140        150        160
LRTPVSHPLK CPETPAQPDS RSKLLPSDSP STPKTMLSRL VISPTGKLPS RGPKHLKLTP APLKDEMTSL ALVNINPFTP
       170        180        190        200        210        220        230        240
ESYKKLFLQS GGKRKIRGDL EEAGPEEGKG GLPAKRCVLR ETNMASRYEK EFLEVEKIGV GEFGTVYKCI KRLDGCVYAI
       250        260        270        280        290        300        310        320
KRSMKTFTEL SNENSALHEV YAHAVLGHHP HVVRYYSSWA EDDHMIIQNE YCNGGSLQAA ISENTKSGNH FEEPKLKDIL
       330        340        350        360        370        380        390        400
LQISLGLNYI HNSSMVHLDI KPSNIFICHK MQSESSGVIE EVENEADWFL SANVMYKIGD LGHATSINKP KVEEGDSRFL
       410        420        430        440        450        460        470        480
ANEILQEDYR HLPKADIFAL GLTIAVAAGA ESLPTNGAAW HHIRKGNFPD VPQELSESFS SLLKNMIQPD AEQRPSAAAL
       490        500        510        520        530        540        550        560
ARNTVLRPSL GKTEELQQQL NLEKFKTATL ERELREAQQA QSPQGYTHHG DTGVSGTHTG SRSTKRLVGG KSARSSSFTS
       570
GEREPLH
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1295	2	1023.3898	-86.03	2	45.9	14.1	1	12-28	R.QKLNFSYCEETEIEGQK.K	
135	1	725.9700	90.61	2	30.9	17.2	0	378-391	K.IGDLGHATSINKPK.V	

Detailed Protein Report

Protein 391: cytoplasmic phosphatidylinositol transfer protein 1 isoform b [Homo sapiens]

Accession:	gi|32307142	**Score:**	31.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	31.7
Database Date:	2015-11-30	**pI:**	5.3
		Sequence Coverage [%]:	11.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLLKEYRICM	PLTVDEYKIG	QLYMISKHSH	EQSDRGEGVE	VVQNEPFEDP	HHGNGQFTEK	RVYLNSKLPS	WARAVVPKIF
90	100	110	120	130	140	150	160
YVTEKAWNYY	PYTITEYTCS	FLPKFSIHIE	TKYEDNKGSN	DTIFDNEAKD	VEREVCFIDI	ACDEIPERYY	KESEDPKHFK
170	180	190	200	210	220	230	240
SEKTGRGQLR	EGWRDSHQPI	MCSYKLVTVK	FEVWGLQTRV	EQFVHKVVRD	ILLIGHRQAF	AWVDEWYDMT	MDDVREYEKN
250	260	270					
MHEQTNIKVC	NQHSSPVDDI	ESHAQTST					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
38	1	918.9134	2.10	2	29.2	16.1	1	171-185	R.EGWRDSHQPIMCSYK.L	

Detailed Protein Report

Protein 392: **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: 31.2
MW [kDa]: 53.6
pI: 10.1
Sequence Coverage [%]: 9.5
No. of unique Peptides: 3

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
2109	1	1065.5116	14.23	2	54.9	10.5	2	296-313	K.CKECDKAFNHPATLSSHK.K	Carbamidomethyl: 1, 4
2242	1	961.4221	-46.22	2	56.7	10.2	2	314-329	K.KIHTGEKPYTCDKCGK.A	Carbamidomethyl: 11, 14
1341	1	699.4714	135.76	2	46.5	10.5	1	327-339	K.CGKAFISSSILSK.H	Carbamidomethyl: 1

Detailed Protein Report

Protein 393: **pyrroline-5-carboxylate reductase 2 isoform 2 [Homo sapiens]**

Accession:	gi|410991931	**Score:**	31.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	25.9
Database Date:	2015-11-30	**pI:**	10.2
		Sequence Coverage [%]:	14.2
		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 394: PREDICTED: zinc finger protein 649 isoform X1 [Homo sapiens]

Accession: gi|530417068
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 31.1
MW [kDa]: 40.8
pI: 10.5
Sequence Coverage [%]: 10.8
No. of unique Peptides: 2

10	20	30	40	50	60	70	80
MPTEIEFPES	RKPISTKSQF	LKHQQTHNIE	KAHECTDCGK	AFLKKSQLTE	HKRIHTGKKP	HVCSLCGKAF	YKKYRLTEHE
90	100	110	120	130	140	150	160
RAHRGEKPHG	CSLCGKAFYK	RYRLTEHERA	HKGEKPYGCS	ECGKAFPRKS	ELTEHQRIHT	GIKPHQCSEC	GRAFSRKSLL
170	180	190	200	210	220	230	240
VVHQRTHTGE	KPHTCSECGK	GFIQKGNLNI	HQRTHTGEKP	YGCIDCGKAF	SQKSCLVAHQ	RYHTGKTPFV	CPECGQPCSQ
250	260	270	280	290	300	310	320
KSGLIRHQKI	HSGEKPYKCS	DCGKAFLTKT	MLIVHHRTHT	GERPYGCDEC	EKAYFYMSCL	VKHKRIHSRE	KRGDSVKVEN
330	340	350	360	370			
PSTASHSLSP	SEHVQGKSPV	NMVTVAMVAG	QCEFAHILHS				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2142	1	882.4021	-87.85	2	55.4	12.7	2	53-68	K.RIHTGKKPHVCSLCGK.A	
1729	1	848.5007	100.59	3	51.6	18.4	2	227-249	K.TPFVCPECGQPCSQKSGLIRHQK.I	

Detailed Protein Report

Protein 395: PREDICTED: zinc finger protein 468 isoform X2 [Homo sapiens]

Accession: gi|578835091
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 31.0
MW [kDa]: 54.3
pI: 10.3
Sequence Coverage [%]: 4.5
No. of unique Peptides: 2

Quantitation

Wdown:Qdown **Median:** 0.19 **CV:** 0.00 % **No. of Peptides:** 1

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	Ratios
1828	4	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		Wdown:Qdown 0.19

Detailed Protein Report

Protein 396: **PREDICTED: zinc finger CCCH domain-containing protein 7A isoform X4 [Homo sapiens]**

Accession:	gi|530407964	**Score:**	30.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	67.6
Database Date:	2015-11-30	**pI:**	9.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.6
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MNGPGSLFAS	ENFLGISSQP	RNDFGNFFGS	AVTKPSSSVT	PRHPLEGTHE	LRQACQICFV	KSGPKLMDFT	YHANIDHKCK
90	100	110	120	130	140	150	160
KDILIGRIKN	VEDKSWKKIR	PRPTKTNYEG	PYYICKDVAA	EEECRYSGHC	TFAYCQEEID	VWTLERKGAF	SREAFFGGNG
170	180	190	200	210	220	230	240
KINLTVFKLL	QEHLGEFIFL	CEKCFDHKPR	MISKRNKDNS	TACSHPVTKH	EFEDNKCLVH	ILRETTVKYS	KIRSFHGQCQ
250	260	270	280	290	300	310	320
LDLCRHEVRY	GCLREDECFY	AHSLVELKVW	IMQNETGISH	DAIAQESKRY	WQNLEANVPG	AQVLGNQIMP	GFLNMKIKFV
330	340	350	360	370	380	390	400
CAQCLRNGQV	IEPDKNRKYC	SAKARHSWTK	DRRAMRVMSI	ERKKWMNIRP	LPTKKQMPLQ	FDLCNHIASG	KKCQYVGNCS
410	420	430	440	450	460	470	480
FAHSPEEREV	WTYMKENGIQ	DMEQFYELWL	KSQKNEKSED	IASQSNKENG	KQIHMPTDYA	EVTVDFHCWM	CGKNCNSEKQ
490	500	510	520	530	540	550	560
WQGHISSEKH	KEKVFHTEDD	QYCWQHRFPT	GYFSICDRYM	NGTCPEGNSC	KFAHGNAELH	EWEERRDALK	MKLNKARKDH
570	580	590					
LIGPNDNDFG	KYSFLFKDLN						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2596	1	658.6717	-192.67	2	61.1	11.2	0	198-209	K.DNSTACSHPVTK.H	Carbamidomethyl: 6
202	1	999.6888	178.38	1	31.7	19.7	0	327-335	R.NGQVIEPDK.N	

Detailed Protein Report

Protein 397: LIM/homeobox protein Lhx1 [Homo sapiens]

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

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

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

Detailed Protein Report

Protein 398: **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:	1

10	20	30	40	50	60	70	80
MKFVAHAVSF	TIFLGLLVVN	ASDRFEGVKT	LPNETFTDYP	KQIFRVKTTQ	FSWTEMLIMK	WVLGMIWSEC	KEIWEEGPRE
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
YVLHLWNLLD	FGMLSIFVAS	FTARFMAFLK	ATEAQLYVDQ	HVQDDTLHNV	SLPPEVAYFT	YARDKWWPSD	PQIISEGLYA
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
IAVVLSFSRI	AYILPANESF	GPLQISLGRT	VKDIFKFMVI	FIMVFVAFMI	GMFNLYSYYR	GAKYNPAFTT	VEESFKTLFW
250	**260**	**270**	**280**	**290**	**300**	**310**	**320**
SIFGLSEVIS	VVLKYDHKFI	ENIGYVLYGV	YNVTMVVVLL	NMLIAMINNS	YQEIEEDADV	EWKFARAKLW	LSYFDEGRTL
330	**340**	**350**	**360**	**370**	**380**	**390**	**400**
PAPFNLVPSP	KSFYYLIMRI	KMCLIKLCKS	KAKSCENDLE	MGMLNSKFKK	TRYQAGMRNS	ENLTANNTLS	KPTRYQKIMK
410	**420**	**430**	**440**	**450**	**460**	**470**	**480**
RLIKRYVLKA	QVDRENDEVN	EGELKEIKQD	ISSLRYELLE	EKSQATGELA	DLIQQLSEKF	GKNLNKDHLR	VNKGKDI

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
965	1	607.1283	-333.12	1	41.6	14.2	0	342-346	K.MCLIK.L	

Detailed Protein Report

Protein 399: pre-mRNA 3' end processing protein WDR33 isoform 1 [Homo sapiens]

Accession: gi|56243590
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 30.8
MW [kDa]: 145.8
pI: 9.9
Sequence Coverage [%]: 2.5
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MATEIGSPPR	FFHMPRFQHQ	APRQLFYKRP	DFAQQQAMQQ	LTFDGKRMRK	AVNRKTIDYN	PSVIKYLENR	IWQRDQRDMR
90	100	110	120	130	140	150	160
AIQPDAGYYN	DLVPPIGMLN	NPMNAVTTKF	VRTSTNKVKC	PVFVVRWTPE	GRRLVTGASS	GEFTLWNGLT	FNFETILQAH
170	180	190	200	210	220	230	240
DSPVRAMTWS	HNDMWMLTAD	HGGYVKYWQS	NMNNVKMFQA	HKEAIREASF	SPTDNKFATC	SDDGTVRIWD	FLRCHEERIL
250	260	270	280	290	300	310	320
RGHGADVKCV	DWHPTKGLVV	SGSKDSQQPI	KFWDPKTGQS	LATLHAHKNT	VMEVKLNLNG	NWLLTASRDH	LCKLFDIRNL
330	340	350	360	370	380	390	400
KEELQVFRGH	KKEATAVAWH	PVHEGLFASG	GSDGSLLFWH	VGVEKEVGGM	EMAHEGMIWS	LAWHPLGHIL	CSGSNDHTSK
410	420	430	440	450	460	470	480
FWTRNRPGDK	MRDRYNLNLL	PGMSEDGVEY	DDLEPNSLAV	IPGMGIPEQL	KLAMEQEQMG	KDESNEIEMT	IPGLDWGMEE
490	500	510	520	530	540	550	560
VMQKDQKKVP	QKKVPYAKPI	PAQFQQAWMQ	NKVPIPAPNE	VLNDRKEDIK	LEEKKKTQAE	IEQEMATLQY	TNPQLLEQLK
570	580	590	600	610	620	630	640
IERLAQKQVE	QIQPPPSSGT	PLLGPQPFPG	QGPMSQIPQG	FQQPHPSQQM	PMNMAQMGPP	GPQGQFRPPG	PQGQMGPQGP
650	660	670	680	690	700	710	720
PLHQGGGGPQ	GFMGPQGPQG	PPQGLPRPQD	MHGPQGMQRH	PGPHGPLGPQ	GPPGPQGSSG	PQGHMGPQGP	PGPQGHIGPQ
730	740	750	760	770	780	790	800
GPPGPQGHLG	PQGPPGTQGM	QGPPGPRGMQ	GPPHPHGIQG	GPGSQGIQGP	VSQGPLMGLN	PRGMQGPPGP	RENQGPAPQG
810	820	830	840	850	860	870	880
MIMGHPPQEM	RGPHPPGGLL	GHGPQEMRGP	QEIRGMQGPP	PQGSMLGPPQ	ELRGPPGSQS	QQGPPQGSLG	PPPQGGMQGP
890	900	910	920	930	940	950	960
PGPQGQQNPA	RGPHPSQGPI	PFQQQKTPLL	GDGPRAPFNQ	EGQSTGPPPL	IPGLGQQGAQ	GRIPPLNPGQ	GPGPNKGDSR
970	980	990	1000	1010	1020	1030	1040
GPPNHHMGPM	SERRHEQSGG	PEHGPERGPF	RGGQDCRGPP	DRRGPHPDFP	DDFSRPDDFH	PDKRFGHRLR	EFEGRGGPLP
1050	1060	1070	1080	1090	1100	1110	1120
QEEKWRRGGP	GPPFPPDHRE	FSEGDGRGAA	RGPPGAWEGR	RPGDERFPRD	PEDPRFRGRR	EESFRRGAPP	RHEGRAPPRG
1130	1140	1150	1160	1170	1180	1190	1200
RDGFPGPEDF	GPEENFDASE	EAARGRDLRG	RGRGTPRGGR	KGLLPTPDEF	PRFEGGRKPD	SWDGNREPGP	GHEHFRDTPR
1210	1220	1230	1240	1250	1260	1270	1280
PDHPPHDGHS	PASRERSSSL	QGMDMASLPP	RKRPWHDGPG	TSEHREMEAP	GGPSEDRGGK	GRGGPGPAQR	VPKSGRSSSL
1290	1300	1310	1320	1330	1340		
DGEHHDGYHR	DEPFGGPPGS	GTPSRGGRSG	SNWGRGSNMN	SGPPRRGASR	GGGRGR		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2698	1	937.4703	7.09	2	62.7	13.8	1	1-16	-.MATEIGSPPRFFHMPR.F	

Detailed Protein Report

Protein 400: thrombospondin type-1 domain-containing protein 7B [Homo sapiens]

Accession:	gi|122937257	**Score:**	30.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	175.5
Database Date:	2015-11-30	**pI:**	9.1
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	2.5
		No. of unique Peptides:	2

Quantitation

mdown:qdown	**Median:**	2.43	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.71	**CV:**	0.00 %	**No. of 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	Ratios
122	1	981.4639	-1.83	2	30.8	11.7	0	822-838	K.QTNGMPLLVQECTVPCR.E	Carbamidomethyl: 16; Oxidation: 5	Wdown:Qdown 0.71 mdown:qdown 2.43
1180	1	883.7188	-3.03	3	44.4	19.1	1	1443-	R.	Carbamidomethyl: 2, 6, 13	

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
								1465	QCIPACRKPFSYCTQGGVCGCEKG		

Detailed Protein Report

Protein 401: centrosome-associated protein 350 [Homo sapiens]

Accession:	gi|171184451	**Score:**	30.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	350.7
Database Date:	2015-11-30	**pI:**	5.9
		Sequence Coverage [%]:	1.2
		No. of unique Peptides:	2

Quantitation

mdown:qdown	**Median:**	0.70	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.75	**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
2836	5	973.5061	1.61	2	64.6	19.7	1	329-347	K.VATAPPAPAYKGFNPSETK.I		
316	1	966.9340	-27.85	2	33.3	11.1	2	1795-1812	K.LKSAGESKLDSHSDDDTK.D		Wdown:Qdown 0.75 mdown:qdown 0.70

Detailed Protein Report

Protein 402: myosin-IIIb isoform 1 [Homo sapiens]

Accession:	gi|284172510	**Score:**	30.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	148.5
Database Date:	2015-11-30	**pI:**	8.7
		Sequence Coverage [%]:	3.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MKHLYGLFHY	NPMMLGLESL	PDPTDTWEII	ETIGKGTYGK	VYKVTNKRDG	SLAAVKILDP	VSDMDEEIEA	EYNILQFLPN
90	100	110	120	130	140	150	160
HPNVVKFYGM	FYKADHCVGG	QLWLVLELCN	GGSVTELVKG	LLRCGQRLDE	AMISYILYGA	LLGLQHLHNN	RIIHRDVKGN
170	180	190	200	210	220	230	240
NILLTTEGGV	KLVDFGVSAQ	LTSTRLRRNT	SVGTPFWMAP	EVIACEQQYD	SSYDARCDVW	SLGITAIELG	DGDPPLFDMH
250	260	270	280	290	300	310	320
PVKTLFKIPR	NPPPTLLHPE	KWCEEFNHFI	SQCLIKDFER	RPSVTHLLDH	PFIKGVHGKV	LFLQKQLAKV	LQDQKHQNPV
330	340	350	360	370	380	390	400
AKTRHERMHT	RRPYHVEDAE	KYCLEDDLVN	LEVLDEDTII	HQLQKRYADL	LIYTYVGDIL	IALNPFQNLS	IYSPQFSRLY
410	420	430	440	450	460	470	480
HGVKRASNPP	HIFASADAAY	QCMVTLSKDQ	CIVISGESGS	GKTESAHLIV	QHLTFLGKAN	NQTLREKILQ	VNSLVEAFGN
490	500	510	520	530	540	550	560
SCTAINDNSS	RFGKYLEMMF	TPTGVVMGAR	ISEYLLEKSR	VIKQAAREKN	FHIFYYIYAG	LHHQKKLSDF	RLPEEKPPRY
570	580	590	600	610	620	630	640
IADETGRVMH	DITSKESYRR	QFEAIQHCFR	IIGFTDKEVH	SVYRILAGIL	NIGNIEFAAI	SSQHQTDKSE	VPNAEALQNA
650	660	670	680	690	700	710	720
ASVLCISPEE	LQEALTSHCV	VTRGETIIRA	NTVDRAADVR	DAMSKALYGR	LFSWIVNRIN	TLLQPDENIC	SAGGGMNVGI
730	740	750	760	770	780	790	800
LDIFGFENFQ	RNSFEQLCIN	IANEQIQYYF	NQHVFALEQM	EYQNEGIDAV	PVEYEDNRPL	LDMFLQKPLG	LLALLDEESR
810	820	830	840	850	860	870	880
FPQATDQTLV	DKFEDNLRCK	YFWRPKGVEL	CFGIQHYAGK	VLYDASGVLE	KNRDTLPADV	VVVLRTSENK	LLQQLFSIPL
890	900	910	920	930	940	950	960
TKTGNLAQTR	ARITVASSSL	PPHFSAGKAK	VDTLEVIRHP	EETTNMKRQT	VASYFRYSLM	DLLSKMVVGQ	PHFVRCIKPN
970	980	990	1000	1010	1020	1030	1040
DDREALQFSR	ERVLAQLRST	GILETVSIRR	QGYSHRILFE	EFVKRYYYLA	FTAHQTPLAS	KESCVAILEK	SRLDHWVLGK
1050	1060	1070	1080	1090	1100	1110	1120
TKVFLKYYHV	EQLNLLLREV	IGRVVVLQAY	TKGWLGARRY	KRVREKREKG	AIAIQSGDTS	NQSSGPHSPV	AAGTRGSAEV
1130	1140	1150	1160	1170	1180	1190	1200
QDCSEPGDHK	VLRGSVHRRS	HSQAESNNGR	TQTSSNSPAV	TEKNGHSQAQ	SSPKGCDIFA	GHANKHSVSG	TDLLSSRICH
1210	1220	1230	1240	1250	1260	1270	1280
PAPDQQGLSL	WGAPQKPGSE	NGLAQKHRTP	RRRCQQPKML	SSPEDTMYYN	QLNGTLEYQG	SKRKPRKLGQ	IKVLDGEDEY
1290	1300	1310	1320				
YKSLSPVDCI	PEENNSAHPS	FFSSSSKGDS	FAQH				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1349	2	926.7733	-30.95	3	45.6	14.9	1	495-518	K.YLEMMFTPTGVVMGARISEYLLEK.S	

Detailed Protein Report

Protein 403:	**PREDICTED: probable JmjC domain-containing histone demethylation protein 2C isoform X6 [Homo sapiens]**		
Accession:	gi|530393271	**Score:**	30.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	250.9
Database Date:	2015-11-30	**pI:**	9.0
		Sequence Coverage [%]:	0.9
		No. of unique Peptides:	1

Detailed Protein Report

10	20	30	40	50	60	70	80
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
1263	1	1019.5782	7.40	1	45.5	17.4	1	1912-1919	K.KMNISLWK.A	

Detailed Protein Report

Protein 404: **PREDICTED: probable tubulin polyglutamylase TTLL2 isoform X1 [Homo sapiens]**

Accession:	gi|578812991	**Score:**	30.6
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

Quantitation

mdown:qdown **Median:** 2.82 **CV:** 0.00 % **No. of Peptides:** 1

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
531	1	542.2992	-6.22	2	35.3	12.3	1	239-248	K.IKEVIGHGCK.W		mdown:qdown 2.82
89	1	647.9192	-109.54	3	30.5	18.2	1	447-463	K.TLMPYASLFQSHSCKTK.T		

Detailed Protein Report

Protein 405: zinc-binding alcohol dehydrogenase domain-containing protein 2 [Homo sapiens]

Accession:	gi|28557745	**Score:**	30.4
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:	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
26	6	1068.4724	-95.51	2	29.6	14.6	2	1-19	-.MLRLVPTGARAIVDMSYAR.H	Oxidation: 1

Detailed Protein Report

Protein 406: DNA-directed RNA polymerase I subunit RPA49 isoform 2 [Homo sapiens]

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

Quantitation

mdown:qdown	**Median:**	4.15	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	1.18	**CV:**	0.00 %	**No. of Peptides:**	1

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
182	1	688.3002	4.63	2	31.0	12.9	0	65-76	K.MDSCIEAFGTTK.Q	Carbamidomethyl: 4; Oxidation: 1	Wdown:Qdown 1.18 mdown:qdown 4.15

Detailed Protein Report

Protein 407: calcium-binding mitochondrial carrier protein SCaMC-1 isoform 2 [Homo sapiens]

Accession:	gi|47458041	**Score:**	30.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	51.3
Database Date:	2015-11-30	**pI:**	5.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	7.2
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	0.57	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	1.08	**CV:**	0.00 %	**No. of Peptides:**	1

10	20	30	40	50	60	70	80
MDSLYGDLFW	YLDYNKDGTL	DIFELQEGLE	DVGAIQSLEE	AKKIFTTGDV	NKDGKLDFEE	FMKYLKDHEK	KMKLAFKSLD
90	100	110	120	130	140	150	160
KNNDGKIEAS	EIVQSLQTLG	LTISEQQAEL	ILQSIDVDGT	MTVDWNEWRD	YFLFNPVTDI	EEIIRFWKHS	TGIDIGDSLT
170	180	190	200	210	220	230	240
IPDEFTEDEK	KSGQWWRQLL	AGGIAGAVSR	TSTAPLDRLK	IMMQVHGSKS	DKMNIFGGFR	QMVKEGGIRS	LWRGNGTNVI
250	260	270	280	290	300	310	320
KIAPETAVKF	WAYEQYKKLL	TEEGQKIGTF	ERFISGSMAG	ATAQTFIYPM	EVMKTRLAVG	KTGQYSGIYD	CAKKILKHEG
330	340	350	360	370	380	390	400
LGAFYKGYVP	NLLGIIPYAG	IDLAVYELLK	SYWLDNFAKD	SVNPGVMVLL	GCGALSSTCG	QLASYPLALV	RTRMQAQAML
410	420	430	440	450	460		
EGSPQLNMVG	LFRRIISKEG	IPGLYRGITP	NFMKVLPAVG	ISYVVYENMK	QTLGVTQK		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
9	1	803.7023	-37.89	3	29.3	14.8	1	394-414	R. MQAQAMLEGSPQLNMVGLFRR. I	Oxidation: 1, 15	mdown:qdown 0.57 Wdown:Qdown 1.08

Detailed Protein Report

Protein 408: armadillo repeat-containing X-linked protein 2 [Homo sapiens]

Accession:	gi|7662162	**Score:**	30.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	65.6
Database Date:	2015-11-30	**pI:**	9.3
		Sequence Coverage [%]:	5.7
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|532691767	refseq_human (refseq_human_20140103.fasta)	armadillo repeat-containing X-linked protein 2 [Homo sapiens]
gi|530433311	refseq_human (refseq_human_20140103.fasta)	PREDICTED: armadillo repeat-containing X-linked protein 2 isoform X9 [Homo sapiens]
gi|530433309	refseq_human (refseq_human_20140103.fasta)	PREDICTED: armadillo repeat-containing X-linked protein 2 isoform X8 [Homo sapiens]
gi|530433307	refseq_human (refseq_human_20140103.fasta)	PREDICTED: armadillo repeat-containing X-linked protein 2 isoform X7 [Homo sapiens]
gi|530433305	refseq_human (refseq_human_20140103.fasta)	PREDICTED: armadillo repeat-containing X-linked protein 2 isoform X6 [Homo sapiens]
gi|530433303	refseq_human (refseq_human_20140103.fasta)	PREDICTED: armadillo repeat-containing X-linked protein 2 isoform X5 [Homo sapiens]
gi|530433299	refseq_human (refseq_human_20140103.fasta)	PREDICTED: armadillo repeat-containing X-linked protein 2 isoform X3 [Homo sapiens]
gi|530433297	refseq_human (refseq_human_20140103.fasta)	PREDICTED: armadillo repeat-containing X-linked protein 2 isoform X2 [Homo sapiens]
gi|530433295	refseq_human (refseq_human_20140103.fasta)	PREDICTED: armadillo repeat-containing X-linked protein 2 isoform X1 [Homo sapiens]
gi|29540562	refseq_human (refseq_human_20140103.fasta)	armadillo repeat-containing X-linked protein 2 [Homo sapiens]

10	20	30	40	50	60	70	80
MSRVRDAGCV	AAGIVIGAGA	WYCVYKYTRG	RDQTKKRMAK	PKNRAVAGTG	ARARAGLRAG	FTIDLGSGFS	PPTPVRAEAE
90	100	110	120	130	140	150	160
DRAQDEASAL	DTVGAEAVAP	AASSAEAQSG	AGSQAQEADG	AGVGPKAESV	VGAAMASAIA	PPPGVTEALG	AAEAPAMAGA
170	180	190	200	210	220	230	240
PKVAEAPREA	ETSRAAVPPG	TVVPTEAAAP	TEVTEGPGVA	APTKVAEAPG	VASPTEAAEA	PVPATPTGAA	APTGAAESPG
250	260	270	280	290	300	310	320
TSGSPRTAVV	PGTSAAKKAT	PGAHTGAIPK	ATSATGAVPK	GGGKGVTRSR	NGGKGKGKKS	KVEVDELGMG	FRPGDGAAAA
330	340	350	360	370	380	390	400
AAASANGGQA	FLAEVPDSEE	GESGWTDTES	DSDSEPETQR	RGRGRRPVAM	QKRPFPYEID	EILGVRDLRK	VLALLQKSDD
410	420	430	440	450	460	470	480
PFIQQVALLT	LSNNANYSCN	QETIRKLGGL	PIIANMINKT	DPHIKEKALM	AMNNLSENYE	NQGRLQVYMN	KVMDDIMASN
490	500	510	520	530	540	550	560
LNSAVQVVGL	KFLTNMTITN	DYQHLLVNSI	ANFFRLLSQG	GGKIKVEILK	ILSNFAENPD	MLKKLLSTQV	PASFSSLYNS
570	580	590	600	610	620	630	640
YVESEILINA	LTLFEIIYDN	LRAEVFNYRE	FNKGSLFYLC	TTSGVCVKKI	RALANHHDLL	VKVKVIKLVN	KF

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2790	1	853.4116	-28.91	2	63.3	15.1	1	594-609	K.GSLFYLCTTSGVCVKK.I	

Detailed Protein Report

Protein 409: intraflagellar transport protein 122 homolog isoform 7 [Homo sapiens]

Accession: gi|526253060
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 30.3
MW [kDa]: 118.4
pI: 6.8
Sequence Coverage [%]: 2.3
No. of unique Peptides: 2

10	20	30	40	50	60	70	80
MFNGIISIRN	KNGEEKVKIE	RPGGSLSPIW	SICWNPSREE	RNDILAVADW	GQKVSFYQLS	GKQIGKDRAL	NFDPCCISYF
90	100	110	120	130	140	150	160
TKGEYILLGG	SDKQVSLFTK	DGVRLGTVGE	QNSWVWTCQA	KPDSNYVVVG	CQDGTISFYQ	LIFSTVHGLY	KDRYAYRDSM
170	180	190	200	210	220	230	240
TDVIVQHLIT	EQKVRIKCKE	LVKKIAIYRN	RLAIQLPEKI	LIYELYSEDL	SDMHYRVKEK	IIKKFECNLL	VVCANHIILC
250	260	270	280	290	300	310	320
QEKRLQCLSF	SGVKEREWQM	ESLIRYIKVI	GGPPGREGLL	VGLKNGQILK	IFVDNLFAIV	LLKQATAVRC	LDMSASRKKL
330	340	350	360	370	380	390	400
AVVDENDTCL	VYDIDTKELL	FQEPNANSVA	WNTQCEDMLC	FSGGGYLNIK	ASTFPVHRQK	LQGFVVGYNG	SKIFCLHVFS
410	420	430	440	450	460	470	480
ISAVEVPQSA	PMYQYLDRKL	FKEAYQIACL	GVTDTDWREL	AMEALEGLDF	ETAKKAFIRV	QDLRYLELIS	SIEERKKRGE
490	500	510	520	530	540	550	560
TNNDLFLADV	FSYQGKFHEA	AKLYKRSGHE	NLALEMYTDL	CMFEYAKDFL	GSGDPKETKM	LITKQADWAR	NIKEPKAAVE
570	580	590	600	610	620	630	640
MYISAGEHVK	AIEICGDHGW	VDMLIDIARK	LDKAEREPLL	LCATYLKKLD	SPGYAAETYL	KMGDLKSLVQ	LHVETQRWDE
650	660	670	680	690	700	710	720
AFALGEKHPE	FKDDIYMPYA	QWLAENDRFE	EAQKAFHKAG	RQREAVQVLE	QLTNNAVAES	RFNDAAYYYW	MLSMQCLDIA
730	740	750	760	770	780	790	800
QDPAQKDTML	GKFYHFQRLA	ELYHGYHAIH	RHTEDPFSVH	RPETLFNISR	FLLHSLPKDT	PSGISKVKIL	FTLAKQSKAL
810	820	830	840	850	860	870	880
GAYRLARHAY	DKLRGLYIPA	RFQKSIELGT	LTIRAKPFHD	SEELVPLCYR	CSTNNPLLNN	LGNVCINCRQ	PFIFSASSYD
890	900	910	920	930	940	950	960
VLHLVEFYLE	EGITDEEAIS	LIDLEVLRPK	RDDRQLEIAN	NSSQILRLVE	TKDSIGDEDP	FTAKLSFEQG	GSEFVPVVVS
970	980	990	1000	1010	1020	1030	1040
RLVLRSMSRR	DVLIKRWPPP	LRWQYFRSLL	PDASITMCPS	CFQMFHSEDY	ELLVLQHGCC	PYCRRCKDDP	GP

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2627	3	665.3628	29.07	2	61.5	19.4	0	42-53	R.NDILAVADWGQK.V	
2085	1	731.3255	-153.98	2	56.2	10.9	2	813-824	K.LRGLYIPARFQK.S	

Detailed Protein Report

Protein 410: **protein limb expression 1 homolog [Homo sapiens]**

Accession:	gi|167466286	**Score:**	30.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	31.9
Database Date:	2015-11-30	**pI:**	5.3
		Sequence Coverage [%]:	8.5
		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 411:	**CMP-N-acetylneuraminate-beta-1,4-galactoside alpha-2,3-sialyltransferase isoform n [Homo sapiens]**
Accession:	gi|394953753
Database:	refseq_human(refseq_human_20140103.fasta)
Database Date:	2015-11-30
Modification(s):	Carbamidomethyl

Score:	30.3
MW [kDa]:	26.7
pI:	10.2
Sequence Coverage [%]:	10.4
No. of unique Peptides:	2

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
146	2	657.8165	-71.56	2	31.1	10.8	0	113-125	R.CIIVGNGGVLANK.S	Carbamidomethyl: 1
2295	3	1131.4541	-161.50	1	57.1	19.5	1	220-230	K.ARVITDLSSGI.-	

Detailed Protein Report

Protein 412: **PREDICTED: PR domain zinc finger protein 1 isoform X1 [Homo sapiens]**

Accession:	gi|530383954	**Score:**	30.2
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
1540	3	598.8105	61.20	2	47.8	11.5	0	129-138	R.GSPEMPFYPR.V	Oxidation: 5

Detailed Protein Report

Protein 413: **PREDICTED: nuclear receptor subfamily 1 group D member 2 isoform X1 [Homo sapiens]**

Accession:	gi|530373510	**Score:**	30.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	45.6
Database Date:	2015-11-30	**pI:**	9.9
Modification(s):	Oxidation	**Sequence Coverage [%]:**	9.8
		No. of unique Peptides:	1

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1576	1	1011.7169	-72.08	3	49.6	10.7	1	96-124	K.FSGMVLLCKVCGDVASGFHYGVHACEGCK.G	Oxidation: 4

Detailed Protein Report

Protein 414: telomerase protein component 1 [Homo sapiens]

Accession:	gi|21536371	**Score:**	30.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	290.3
Database Date:	2015-11-30	**pI:**	9.2
		Sequence Coverage [%]:	0.9
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530404542	refseq_human (refseq_human_20140103.fasta)	PREDICTED: telomerase protein component 1 isoform X1 [Homo sapiens]

Detailed Protein Report

10	20	30	40	50	60	70	80
MEKLHGHVSA	HPDILSLENR	CLAMLPDLQP	LEKLHQHVST	HSDILSLKNQ	CLATLPDLKT	MEKPHGYVSA	HPDILSLENQ
90	100	110	120	130	140	150	160
CLATLSDLKT	MEKPHGHVSA	HPDILSLENR	CLATLSSLKS	TVSASPLFQS	LQISHMTQAD	LYRVNNSNCL	LSEPPSWRAQ
170	180	190	200	210	220	230	240
HFSKGLDLST	CPIALKSISA	TETAQEATLG	RWFDSEEKKG	AETQMPSYSL	SLGEEEEVED	LAVKLTSGDS	ESHPEPTDHV
250	260	270	280	290	300	310	320
LQEKKMALLS	LLCSTLVSEV	NMNNTSDPTL	AAIFEICREL	ALLEPEFILK	ASLYARQQLN	VRNVANNILA	IAAFLPACRP
330	340	350	360	370	380	390	400
HLRRYFCAIV	QLPSDWIQVA	ELYQSLAEGD	KNKLVPLPAC	LRTAMTDKFA	QFDEYQLAKY	NPRKHRAKRH	PRRPPRSPGM
410	420	430	440	450	460	470	480
EPPFSHRCFP	RYIGFLREEQ	RKFEKAGDTV	SEKKNPPRFT	LKKLVQRLHI	HKPAQHVQAL	LGYRYPSNLQ	LFSRSRLPGP
490	500	510	520	530	540	550	560
WDSSRAGKRM	KLSRPETWER	ELSLRGNKAS	VWEELIENGK	LPFMAMLRNL	CNLLRVGISS	RHHELILQRL	QHAKSVIHSR
570	580	590	600	610	620	630	640
QFPFRFLNAH	DAIDALEAQL	RNQALPFPSN	ITLMRRILTR	NEKNRPRRRF	LCHLSRQQLR	MAMRIPVLYE	QLKREKLRVH
650	660	670	680	690	700	710	720
KARQWKYDGE	MLNRYRQALE	TAVNLSVKHS	LPLLPGRTVL	VYLTDANADR	LCPKSNPQGP	PLNYALLLIG	MMITRAEQVD
730	740	750	760	770	780	790	800
VVLCGGDTLK	TAVLKAEEGI	LKTAIKLQAQ	VQEFDENDGW	SLNTFGKYLL	SLAGQRVPVD	RVILLGQSMD	DGMINVAKQL
810	820	830	840	850	860	870	880
YWQRVNSKCL	FVGILLRRVQ	YLSTDLNPND	VTLSGCTDAI	LKFIAEHGAS	HLLEHVGQMD	KIFKIPPPPG	KTGVQSLRPL
890	900	910	920	930	940	950	960
EEDTPSPLAP	VSQQGWRSIR	LFISSTFRDM	HGERDLLLRS	VLPALQARAA	PHRISLHGID	LRWGVTEEET	RRNRQLEVCL
970	980	990	1000	1010	1020	1030	1040
GEVENAQLFV	GILGSRYGYI	PPSYNLPDHP	HFHWAQQYPS	GRSVTEMEVM	QFLNRNQRLQ	PSAQALIYFR	DSSFLSSVPD
1050	1060	1070	1080	1090	1100	1110	1120
AWKSDFVSES	EEAARRISEL	KSYLSRQKGI	TCRRYPCEWG	GVAAGRPYVG	GLEEFGQLVL	QDVWNMIQKL	YLQPGALLEQ
1130	1140	1150	1160	1170	1180	1190	1200
PVSIPDDDLV	QATFQQLQKP	PSPARPRLLQ	DTVQRLMLPH	GRLSLVTGQS	GQGKTAFLAS	LVSALQAPDG	AKVASLVFFH
1210	1220	1230	1240	1250	1260	1270	1280
FSGARPDQGL	ALTLLRRLCT	YLRGQLKEPG	ALPSTYRSLV	WELQQRLLPK	SAESLHPGQT	QVLIIDGADR	LVDQNGQLIS
1290	1300	1310	1320	1330	1340	1350	1360
DWIPKKLPRC	VHLVLSVSSD	AGLGETLEQS	QGAHVLALGP	LEASARARLV	REELALYGKR	LEESPFNNQM	RLLLVKRESG
1370	1380	1390	1400	1410	1420	1430	1440
RPLYLRLVTD	HLRLFTLYEQ	VSERLRTLPA	TVPLLLQHIL	STLEKEHGPD	VLPQALTALE	VTRSGLTVDQ	LHGVLSVWRT
1450	1460	1470	1480	1490	1500	1510	1520
LPKGTKSWEE	AVAAGNSGDP	YPMGPFACLV	QSLRSLLGEG	PLERPGARLC	LPDGPLRTAA	KRCYGKRPGL	EDTAHILIAA
1530	1540	1550	1560	1570	1580	1590	1600
QLWKTCDADA	SGTFRSCPPE	ALGDLPYHLL	QSGNRGLLSK	FLTNLHVVAA	HLELGLVSRL	LEAHALYASS	VPKEEQKLPE
1610	1620	1630	1640	1650	1660	1670	1680
ADVAVFRTFL	RQQASILSQY	PRLLPQQAAN	QPLDSPLCHQ	ASLLSRRWHL	QHTLRWLNKP	RTMKNQQSSS	LSLAVSSSPT
1690	1700	1710	1720	1730	1740	1750	1760
AVAFSTNGQR	AAVGTANGTV	YLLDLRTWQE	EKSVVSGCDG	ISACLFLSDD	TLFLTAFDGL	LELWDLQHGC	RVLQTKAHQY
1770	1780	1790	1800	1810	1820	1830	1840
QITGCCLSPD	CRLLATVCLG	GCLKLWDTVR	GQLAFQHTYP	KSLNCVAFHP	EGQVIATGSW	AGSISFFQVD	GLKVTKDLGA
1850	1860	1870	1880	1890	1900	1910	1920
PGASIRTLAF	NVPGGVVAVG	RLDSMVELWA	WREGARLAAF	PAHHGFVAAA	LFLHAGCQLL	TAGEDGKVQV	WSGSLGRPRG
1930	1940	1950	1960	1970	1980	1990	2000
HLGSLSLSPA	LSVALSPDGD	RVAVGYRADG	IRIYKISSGS	QGAQGQALDV	AVSALAWLSP	KVLVSGAEDG	SLQGWALKEC
2010	2020	2030	2040	2050	2060	2070	2080
SLQSLWLLSR	FQKPVLGLAT	SQELLASASE	DFTVQLWPRQ	LLTRPHKAED	FPCGTELRGH	EGPVSCCSFS	TDGGSLATGG
2090	2100	2110	2120	2130	2140	2150	2160
RDRSLLCWDV	RTPKTPVLIH	SFPACHRDWV	TGCAWTKDNL	LISCSSDGSV	GLWDPESGQR	LGQFLGHQSA	VSAVAAVEEH
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1409	1	630.7535	142.03	3	46.2	11.3	2	610-624	R.FLCHLSRQQLRMAMR.I	

Detailed Protein Report

Protein 415: uncharacterized protein C5orf55 precursor [Homo sapiens]

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

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1854	1	829.2700	-158.89	2	51.7	10.9	0	98-113	R.GPAAQVLENECGSLGR.A	Carbamidomethyl: 11

Protein 416: PREDICTED: pericentriolar material 1 protein isoform X28 [Homo sapiens]

Accession:	gi|578815347	**Score:**	30.0
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
54	2	809.3848	-118.90	2	29.9	12.2	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 417: protein FAM83G [Homo sapiens]

Accession:	gi|115392150	**Score:**	30.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	90.8
Database Date:	2015-11-30	**pI:**	5.9
		Sequence Coverage [%]:	2.3
		No. of unique Peptides:	2

Quantitation

mdown:qdown	**Median:**	1.11	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.80	**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
1617	1	712.0414	-43.20	3	48.9	13.8	2	33-51	R.LALEALVARGRDAFYEVLK.R		
568	5	492.7372	-37.03	2	35.9	16.2	0	44-51	R.DAFYEVLK.R		Wdown:Qdown 0.80 mdown:qdown 1.11

Detailed Protein Report

Protein 418: nuclear receptor coactivator 4 isoform 3 [Homo sapiens]

Accession:	gi|14149617	**Score:**	30.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	69.7
Database Date:	2015-11-30	**pI:**	5.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	5.2
		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
88	1	1103.5131	90.47	2	29.8	12.6	0	406-424	R.ANEPCTSFAECVCDENCEK.E	Carbamidomethyl: 5, 17

Detailed Protein Report

Protein 419: MLX-interacting protein [Homo sapiens]

Accession:	gi|111955326	**Score:**	30.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	101.1
Database Date:	2015-11-30	**pI:**	9.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAADVFMCSP	RRPRSRGRQV	LLKPQVSEDD	DDSDTDEPSP	PPASGAATPA	RAHASAAPPP	PRAGPGREEP	PRRQQIIHSG
90	100	110	120	130	140	150	160
HFMVSSPHRE	HPPKKGYDFD	TVNKQTCQTY	SFGKTSSCHL	SIDASLTKLF	ECMTLAYSGK	LVSPKWKNFK	GLKLQWRDKI
170	180	190	200	210	220	230	240
RLNNAIWRAW	YMQYLEKRKN	PVCHFVTPLD	GSVDVDEHRR	PEAITTEGKY	WKSRIEIVIR	EYHKWRTYFK	KRLQQHKDED
250	260	270	280	290	300	310	320
LSSLVQDDDM	LYWHKHGDGW	KTPVPMEEDP	LLDTDMLMSE	FSDTLFSTLS	SHQPVAWPNP	REIAHLGNAD	MIQPGLIPLQ
330	340	350	360	370	380	390	400
PNLDFMDTFE	PFQDLFSSSR	SIFGSMLPAS	ASAPVPDPNN	PPAQESILPT	TALPTVSLPD	SLIAPPTAPS	LAHMDEQGCE
410	420	430	440	450	460	470	480
HTSRTEDPFI	QPTDFGPSEP	PLSVPQPFLP	VFTMPLLSPS	PAPPPISPVL	PLVPPPATAL	NPPAPPTFHQ	PQKFAGVNKA
490	500	510	520	530	540	550	560
PSVITHTASA	TLTHDAPATT	FSQSQGLVIT	THHPAPSAAP	CGLALSPVTR	PPQPRLTFVH	PKPVSLTGGR	PKQPHKIVPA
570	580	590	600	610	620	630	640
PKPEPVSLVL	KNARIAPAAF	SGQPQAVIMT	SGPLKREGML	ASTVSQSNVV	IAPAAIARAP	GVPEFHSSIL	VTDLGHGTSS
650	660	670	680	690	700	710	720
PPAPVSRLFP	STAQDPLGKG	EQVPLHGGSP	QVTVTGPSRD	CPNSGQASPC	ASEQSPSPQS	PQNNCSGKSD	PKNVAALKNR
730	740	750	760	770	780	790	800
QMKHISAEQK	RRFNIKMCFD	MLNSLISNNS	KLTSHAITLQ	KTVEYITKLQ	QERGQMQEEA	RRLREEIEEL	NATIISCQQL
810	820	830	840	850	860	870	880
LPATGVPVTR	RQFDHMKDMF	DEYVKTRTLQ	NWKFWIFSII	IKPLFESFKG	MVSTSSLEEL	HRTALSWLDQ	HCSLPILRPM
890	900	910	920				
VLSTLRQLST	STSILTDPAQ	LPEQASKAVT	RIGKRLGES				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
717	1	866.9167	32.26	2	37.8	13.5	0	737-751	K.MCFDMLNSLISNNSK.L	Oxidation: 1

Detailed Protein Report

Protein 420: PREDICTED: neurexin-2-beta isoform X15 [Homo sapiens]

Accession:	gi|578821888	**Score:**	29.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	133.0
Database Date:	2015-11-30	**pI:**	5.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEGPAHLTLN	SEVGSLLFSE	GGAGRGGAGD	VHQPTKGKEE	FVATFKGNEF	FCYDLSHNPI	QSSTDEITLA	FRTLQRNGLM
90	100	110	120	130	140	150	160
LHTGKSADYV	NLSLKSGAVW	LVINLGSGAF	EALVEPVNGK	FNDNAWHDVR	VTRNLRQVTI	SVDGILTTTG	YTQEDYTMLG
170	180	190	200	210	220	230	240
SDDFFYIGGS	PNTADLPGSP	VSNNFMGCLK	DVVYKNNDFK	LELSRLAKEG	DPKMKLQGDL	SFRCEDVAAL	DPVTFESPEA
250	260	270	280	290	300	310	320
FVALPRWSAK	RTGSISLDFR	TTEPNGLLLF	SQGRRAGGGA	GSHSSAQRAD	YFAMELLDGH	LYLLLDMGSG	GIKLRASSRK
330	340	350	360	370	380	390	400
VNDGEWCHVD	FQRDGRKGSI	SVNSRSTPFL	ATGDSEILDL	ESELYLGGLP	EGGRVDLPLP	PEVWTAALRA	GYVGCVRDLF
410	420	430	440	450	460	470	480
IDGRSRDLRG	LAEAQGAVGV	APFCSRETLK	QCASAPCRNG	GVCREGWNRF	ICDCIGTGFL	GRVCEREATV	LSYDGSMYMK
490	500	510	520	530	540	550	560
IMLPNAMHTE	AEDVSLRFMS	QRAYGLMMAT	TSRESADTLR	LELDGGQMKL	TVNLDCLRVG	CAPSKGPETL	FAGHKLNDNE
570	580	590	600	610	620	630	640
WHTVRVVRRG	KSLQLSVDNV	TVEGQMAGAH	MRLEFHNIET	GIMTERRFIS	VVPSNFIGHL	SGLVFNGQPY	MDQCKDGDIT
650	660	670	680	690	700	710	720
YCELNARFGL	RAIVADPVTF	KSRSSYLALA	TLQAYASMHL	FFQFKTTAPD	GLLLFNSGNG	NDFIVIELVK	GYIHYVFDLG
730	740	750	760	770	780	790	800
NGPSLMKGNS	DKPVNDNQWH	NVVVSRDPGN	VHTLKIDSRT	VTQHSNGARN	LDLKGELYIG	GLSKNMFSNL	PKLVASRDGF
810	820	830	840	850	860	870	880
QGCLASVDLN	GRLPDLIADA	LHRIGQVERG	CDGPSTTCTE	ESCANQGVCL	QQWDGFTCDC	TMTSYGGPVC	NDPGTTYIFG
890	900	910	920	930	940	950	960
KGGALITYTW	PPNDRPSTRM	DRLAVGFSTH	QRSAVLVRVD	SASGLGDYLQ	LHIDQGTVGV	IFNVGTDDIT	IDEPNAIVSD
970	980	990	1000	1010	1020	1030	1040
GKYHVVRFTR	SGGNATLQVD	SWPVNERYPA	GRQLTIFNSQ	AAIKIGGRDQ	GRPFQGQVSG	LYYNGLKVLA	LAAESDPNVR
1050	1060	1070	1080	1090	1100	1110	1120
TEGHLRLVGE	GPSVLLSAET	TATTLLADMA	TTIMETTTTM	ATTTTRRGRS	PTLRDSTTQN	TDDLLVASAE	CPSDDEDLEE
1130	1140	1150	1160	1170	1180	1190	1200
CEPSTANPTG	PGERGPPGAV	EVIRESSSTT	GMVVGIVAAA	ALCILILLYA	MYKYRNRDEG	SYQVDQSRNY	ISNSAQSNGA
1210	1220	1230					
VVKEKAPAAP	KTPSKAKKNK	DKEYYV					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2853	1	650.6072	-52.95	3	64.3	10.2	2	427-444	R.ETLKQCASAPCRNGGVCR.E	Carbamidomethyl: 6

Detailed Protein Report

Protein 421: 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 422: PREDICTED: zinc finger protein 280D isoform X2 [Homo sapiens]

Accession:	gi|530406054	**Score:**	29.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	110.5
Database Date:	2015-11-30	**pI:**	10.7
		Sequence Coverage [%]:	1.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MTFSLSKPTD	WGSLHTRRAR	NARLLACKFR	AVRILGLPPG	HTSQQLAPTW	RQGPGPRPGP	ARGGARGSSR	ARDAAHMPVP
90	100	110	120	130	140	150	160
ASRVGEKTGS	SDTGRLTRSL	PMRQRAGCTR	APPFPRLGCQ	LRNGSRRRRR	SVVFRAPPFP	PPLSPPPQGS	SQADPLRSRK
170	180	190	200	210	220	230	240
ENRNNLLACL	ESHGNSKMAE	LFMECEEEEL	EPWQKKVKEV	EDDDDDEPIF	VGEISSSKPA	ISNILNRVNP	SSYSRGLKNG
250	260	270	280	290	300	310	320
ALSRGITAAF	KPTSQHYTNP	TSNPVPASPI	NFHPESRSSD	SSVIVQPFSK	PGYITNSSRV	VSNKSSELLF	DLTQDTGLSH
330	340	350	360	370	380	390	400
YQGGPTLSMA	GMSESSFLSK	RPSTSEVNNV	NPKKPKPSES	VSGANSSAVL	PSVKSPSVTS	SQAMLAKGTN	TSSNQSKNGT
410	420	430	440	450	460	470	480
PFPRACPKCN	IHFNLLDPLK	NHMKYCCPDM	INNFLGLAKT	EFSSTVNKNT	TIDSEKGKLI	MLVNDFYYGK	HEGDVQEEQK
490	500	510	520	530	540	550	560
THTTFKCFSC	LKILKNNIRF	MNHMKHHLEL	EKQSSESWEN	HTTCQHCYRQ	FPTPFQLQCH	IESTHTPHEF	STICKICELS
570	580	590	600	610	620	630	640
FETEHVLLQH	MKDNHKPGEM	PYVCQVCNYR	SSSFSDVETH	FRTSHENTKN	LLCPFCLKVI	KIATPYMHHY	MKHQKKGIHR
650	660	670	680	690	700	710	720
CTKCRLQFLT	CKEKMDHKTQ	HHRTFIKPKQ	LEGLPPGTKV	TIRASVGPLQ	SGASPTPSIS	ASASTLQLSP	PRTKNITAKN
730	740	750	760	770	780	790	800
PAKSNTSKPN	TVKSNASKPN	TSKPNGSKSK	YKPKISNMQK	KQSTLASSNK	KSKVNTALRN	LRYRRGIHKC	IECCSEIKDF
810	820	830	840	850	860	870	880
ANHFPTYVHC	SFCRYNTSCS	KAYVNHMMSF	HSNRPSKRFC	IFKKHSENLR	GITLVCLNCD	FLSDVSGLDN	MATHLSQHKT
890	900	910	920	930	940	950	960
HTCQVVMQKV	SVCIPTSEHL	SECRSSPEIS	KNIQGIPGQC	PPSMDTTDAC	SLFPRNVNNL	TVGPALRLWP	QEIRSWGDSL
970	980	990	1000				
STWLASHKAD	VVWPEMALRP	TKLSILPTGG	FGL				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
44	1	634.4553	151.04	2	29.2	11.9	0	936-947	R.NVNNLTVGPALR.L	

Detailed Protein Report

Protein 423: PREDICTED: RING finger protein 17 isoform X9 [Homo sapiens]

Accession:	gi|578824965	**Score:**	29.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	174.6
Database Date:	2015-11-30	**pI:**	5.1
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.6
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MLDTNTAEEI	DEALNTAHHS	FEQLSIAGKA	LEHMQKQTIE	ERERVIEVVE	KQFDQLLAFF	DSRKKNLCEE	FARTTDDYLS
90	100	110	120	130	140	150	160
NLIKAKSYIE	EKKNNLNAAM	NIARALQLSP	SLRTYCDLNQ	IIRTLQLTSD	SELAQVSSPQ	LRNPPRLSVN	CSEIICMFNN
170	180	190	200	210	220	230	240
MGKIEFRDST	KCYPQENEIR	QNVQKKYNNK	KELSCYDTYP	PLEKKKVDMS	VLTSEAPPPP	LQPETNDVHL	EAKNFQPQKD
250	260	270	280	290	300	310	320
VATASPKTIA	VLPQMGSSPD	VIIEEIIEDN	VESSAELVFV	SHVIDPCHFY	IRKYSQIKDA	KVLEKKVNEF	CNRSSHLDPS
330	340	350	360	370	380	390	400
DILELGARIF	VSSIKNGMWC	RGTITELIPI	EGRNTRKPCS	PTRLFVHEVA	LIQIFMVDFG	NSEVLIVTGV	VDTHVRPEHS
410	420	430	440	450	460	470	480
AKQHIALNDL	CLVLRKSEPY	TEGLLKDIQP	LAQPCSLKDI	VPQNSNEGWE	EEAKVEFLKM	VNNKAVSMKV	FREEDGVLIV
490	500	510	520	530	540	550	560
DLQKPPPNKI	SSDMPVSLRD	ALVFMELAKF	KSQSLRSHFE	KNTTLHYHPP	ILPKEMTDVS	VTVCHINSPG	DFYLQLIEGL
570	580	590	600	610	620	630	640
DILFLLKTIE	EFYKSEDGEN	LEILCPVQDQ	ACVAKFEDGI	WYRAKVIELN	HWESCWKSCI	DRTKQQKLII	QKPVNSSLML
650	660	670	680	690	700	710	720
TVCLSHAILI	VKVQIKGLPG	HQEVEVKYVD	FGNTAKITIK	DVRKIKDEFL	NAPEKAIKCK	LAYIEPYKRT	MQWSKEAKEK
730	740	750	760	770	780	790	800
FEEKAQDKFM	TCSVIKILED	NVLLVELFDS	LGAPEMTTTS	INDQLVKEGL	ASYEIGYILK	DNSQKHIEVW	DPSPEEIISN
810	820	830	840	850	860	870	880
EVHNLNPVSA	KSLPNENFQS	LYNKELPVHI	CNVISPEKIY	VQWLLTENLL	NSLEEKMIAA	YENSKWEPVK	WENDMHCAVK
890	900	910	920	930	940	950	960
IQDKNQWRRG	QIIRMVTDTL	VEVLLYDVGV	ELVVNVDCLR	KLEENLKTMG	RLSLECSLVD	IRPAGGSDKW	TATACDCLSL
970	980	990	1000	1010	1020	1030	1040
YLTGAVATII	LQVDSEENNT	TWPLPVKIFC	RDEKGERVDV	SKYLIKKGLA	LRERRINNLD	NSHSLSEKSL	EVPLEQEDSV
1050	1060	1070	1080	1090	1100	1110	1120
VTNCIKTNFD	PDKKTADIIS	EQKVSEFQEK	ILEPRTTRGY	KPPAIPNMNV	FEATVSCVGD	DGTIFVVPKL	SEFELIKMTN
1130	1140	1150	1160	1170	1180	1190	1200
EIQSNLKCLG	LLEPYFWKKG	EACAVRGSDT	LWYRGKVMEV	VGGAVRVQYL	DHGFTEKIPQ	CHLYPILLYP	DIPQFCIPCQ
1210	1220	1230	1240	1250	1260	1270	1280
LHNTTPVGNV	WQPDAIEVLQ	QLLSKRQVDI	HIMELPKNPW	EKLSIHLYFD	GMSLSYFMAY	YKYCTSEHTE	EMLKEKPRSD
1290	1300	1310	1320	1330	1340	1350	1360
HDKKYEEEQW	EIRFEELLSA	ETDTPLLPPY	LSSSLPSPGE	LYAVQVKHVV	SPNEVYICLD	SIETSNQSNQ	HSDTDDSGVS
1370	1380	1390	1400	1410	1420	1430	1440
GESESESLDE	ALQRVNKKVE	ALPPLTDFRT	EMPCLAEYDD	GLWYRAKIVA	IKEFNPLSIL	VQFVDYGSTA	KLTLNRLCQI
1450	1460	1470	1480	1490	1500	1510	1520
PSHLMRYPAR	AIKVLLAGFK	PPLRDLGETR	IPYCPKWSME	ALWAMIDCLQ	GKQLYAVSMA	PAPEQIVTLY	DDEQHPVHMP
1530	1540						
LVEMGLADKD	E						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2739	1	698.3923	-31.29	4	63.2	12.7	0	628-652	K.LIIQKPVNSSLMLTVCLSHAILIVK.V	Carbamidomethyl: 16
2279	4	863.8727	-142.91	2	57.0	17.3	2	1375-1389	R.VNKKVEALPPLTDFR.T	

Detailed Protein Report

Protein 424: homeobox protein cut-like 2 [Homo sapiens]

Accession: gi|116517292
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 29.9
MW [kDa]: 161.6
pI: 5.3
Sequence Coverage [%]: 1.5
No. of unique Peptides: 1

Quantitation

mdown:qdown	**Median:**	0.45	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	1.05	**CV:**	0.00 %	**No. of Peptides:**	1

```
        10         20         30         40         50         60         70         80
MAANVGSMFQ YWKRFDLRRL QKELNSVASE LSARQEESEH SHKHLIELRR EFKKNVPEEI REMVAPVLKS FQAEVVALSK
        90        100        110        120        130        140        150        160
RSQEAEAAFL SVYKQLIEAP DPVPVFEAAR SLDDRLQPPS FDPSGQPRRD LHTSWKRNPE LLSPKEQREG TSPAGPTLTE
       170        180        190        200        210        220        230        240
GSRLPGIPGK ALLTETLLQR NEAEKQKGLQ EVQITLAARL GEAEEKIKVL HSALKATQAE LLELRRKYDE EAASKADEVG
       250        260        270        280        290        300        310        320
LIMTNLEKAN QRAEAAQREV ESLREQLASV NSSIRLACCS PQGPSGDKVN FTLCSGPRLE AALASKDREI LRLLKDVQHL
       330        340        350        360        370        380        390        400
QSSLQELEEA SANQIADLER QLTAKSEAIE KLEEKLQAQS DYEEIKTELS ILKAMKLASS TCSLPQGMAK PEDSLLIAKE
       410        420        430        440        450        460        470        480
AFFPTQKFLL EKPSLLASPE EDPSEDDSIK DSLGTEQSYP SPQQLPPPPG PEDPLSPSPG QPLLGPSLGP DGTRTFSLSP
       490        500        510        520        530        540        550        560
FPSLASGERL MMPPAAFKGE AGGLLVFPPA FYGAKPPTAP ATPAPGPEPL GGPEPADGGG GGAAGPGAEE EQLDTAEIAF
       570        580        590        600        610        620        630        640
QVKEQLLKHN IGQRVFGHYV LGLSQGSVSE ILARPKPWRK LTVKGKEPFI KMKQFLSDEQ NVLALRTIQV RQRGSITPRI
       650        660        670        680        690        700        710        720
RTPETGSDDA IKSILEQAKK EIESQKGGEP KTSVAPLSIA NGTTPASTSE DAIKSILEQA RREMQAQQQA LLEMEVAPRG
       730        740        750        760        770        780        790        800
RSVPPSPPER PSLATASQNG APALVKQEEG SGGPAQAPLP VLSPAAFVQS IIRKVKSEIG DAGYFDHHWA SDRGLLSRPY
       810        820        830        840        850        860        870        880
ASVSPSLSSS SSSGYSGQPN GRAWPRGDEA PVPPEDEAAA GAEDEPPRTG ELKAEGATAE AGARLPYYPA YVPRTLKPTV
       890        900        910        920        930        940        950        960
PPLTPEQYEL YMYREVDTLE LTRQVKEKLA KNGICQRIFG EKVLGLSQGS VSDMLSRPKP WSKLTQKGRE PFIRMQLWLS
       970        980        990       1000       1010       1020       1030       1040
DQLGQAVGQQ PGASQASPTE PRSSPSPPPS PTEPEKSSQE PLSLSLESSK ENQQPEGRSS SSLSGKMYSG SQAPGGIQEI
      1050       1060       1070       1080       1090       1100       1110       1120
VAMSPELDTY SITKRVKEVL TDNNLGQRLF GESILGLTQG SVSDLLSRPK PWHKLSLKGR EPFVRMQLWL NDPHNVEKLR
      1130       1140       1150       1160       1170       1180       1190       1200
DMKKLEKKAY LKRRYGLIST GSDSESPATR SECPSPCLQP QDLSLLQIKK PRVVLAPEEK EALRKAYQLE PYPSQQTIEL
      1210       1220       1230       1240       1250       1260       1270       1280
LSFQLNLKTN TVINWFHNYR SRMRREMLVE GTQDEPDLDP SGGPGILPPG HSHPDPTPQS PDSETEDQKP TVKELELQEG
      1290       1300       1310       1320       1330       1340       1350       1360
PEENSTPLTT QDKAQVRIKQ EQMEEDAEEE AGSQPQDSGE LDKGQGPPKE EHPDPPGNDG LPKVAPGPLL PGGSTPDCPS
      1370       1380       1390       1400       1410       1420       1430       1440
LHPQQESEAG ERLHPDPLSF KSASESSRCS LEVSLNSPSA ASSPGLMMSV SPVPSSSAPI SPSPPGAPPA KVPSASPTAD
      1450       1460       1470       1480       1490
MAGALHPSAK VNPNLQRRHE KMANLNNIIY RVERAANREE ALEWEF
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
561	2	661.2196	-178.61	2	35.9	14.0	1	912-922	K.NGICQRIFGEK.V	Carbamidomethyl: 4	Wdown:Qdown 1.05 mdown:qdown 0.45

Detailed Protein Report

Protein 425: treslin [Homo sapiens]

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

Score: 29.9
MW [kDa]: 210.7
pI: 9.8
Sequence Coverage [%]: 1.0
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MACCHKVMLL	LDTAGGAARH	SRVRRAALRL	LTYLSCRFGL	ARVHWAFKFF	DSQGARSRPS	RVSDFRELGS	RSWEDFEEEL
90	100	110	120	130	140	150	160
EARLEDRAHL	PGPAPRATHT	HGALMETLLD	YQWDRPEITS	PTKPILRSSG	RRLLDVESEA	KEAEAALGGL	VNAVFLLAPC
170	180	190	200	210	220	230	240
PHSQRELLQF	VSGCEAQAQR	LPPTPKQVME	KLLPKRVREV	MVARKITFYW	VDTTEWSKLW	ESPDHLGYWT	VCELLHHGGG
250	260	270	280	290	300	310	320
TVLPSESFSW	DFAQAGEMLL	RSGIKLSSEP	HLSPWISMLP	TDATLNRLLY	NSPEYEASFP	RMEGMLFLPV	EAGKEIQETW
330	340	350	360	370	380	390	400
TVTLEPLAMH	QRHFQKPVRI	FLKGSVAQWS	LPTSSTLGTD	SWMLGSPEES	TATQRLLFQQ	LVSRLTAEEL	HLVADVDPGE
410	420	430	440	450	460	470	480
GRPPITGVIS	PLSASAMILT	VCRTKEAEFQ	RHVLQTAVAD	SPRDTASLFS	DVVDSILNQT	HDSLADTASA	ASPVPEWAQQ
490	500	510	520	530	540	550	560
ELGHTTPWSP	AVVEKWFPFC	NISGASSDLM	ESFGLLQAAS	ANKEESSKTE	GELIHCLAEL	YQRKSREEST	IAHQEDSKKK
570	580	590	600	610	620	630	640
RGVPRTPVRQ	KMNTMCRSLK	MLNVARLNVK	AQKLHPDGSP	DVAGEKGIQK	IPSGRTVDKL	EDRGRTLRSS	KPKDFKTEEE
650	660	670	680	690	700	710	720
LLSYIRENYQ	KTVATGEIML	YACARNMIST	VKMFLKSKGT	KELEVNCLNQ	VKSSLLKTSK	SLRQNLGKKL	DKEDKVRECQ
730	740	750	760	770	780	790	800
LQVFLRLEMC	LQCPSINEST	DDMEQVVEEV	TDLLRMVCLT	EDSAYLAEFL	EEILRLYIDS	IPKTLGNLYN	SLGFVIPQKL
810	820	830	840	850	860	870	880
AGVLPTDFFS	DDSMTQENKS	PLLSVPFLSS	ARRSVSGSPE	SDELQELRTR	SAKKRRKNAL	IRHKSIAEVS	QNLRQIEIPK
890	900	910	920	930	940	950	960
VSKRATKKEN	SHPAPQQPSQ	PVKDTVQEVT	KVRRNLFNQE	LLSPSKRSLK	RGLPRSHSVS	AVDGLEDKLD	NFKKNKGYHK
970	980	990	1000	1010	1020	1030	1040
LLTKSVAETP	VHKQISKRLL	HRQIKGRSSD	PGPDIGVVEE	SPEKGDEISL	RRSPRIKQLS	FSRTHSASFY	SVSQPKSRSV
1050	1060	1070	1080	1090	1100	1110	1120
QRVHSFQQDK	SDQRENSPVQ	SIRSPKSLLF	GAMSEMISPS	EKGSARMKKR	SRNTLDSEVP	AAYQTPKKSH	QKSLSFSKTT
1130	1140	1150	1160	1170	1180	1190	1200
PRRISHTPQT	PLYTPERLQK	SPAKMTPTKQ	AAFKESLKDS	SSPGHDSPLD	SKITPQKRHT	QAGEGTSLET	KTPRTPKRQG
1210	1220	1230	1240	1250	1260	1270	1280
TQPPGFLPNC	TWPHSVNSSP	ESPSCPAPPT	SSTAQPRREC	LTPIRDPLRT	PPRAAAFMGT	PQNQTHQQPH	VLRAARAEEP
1290	1300	1310	1320	1330	1340	1350	1360
AQKLKDKAIK	TPKRPGNSTV	TSSPPVTPKK	LFTSPLCDVS	KKSPFRKSKI	ECPSPGELDQ	KEPQMSPSVA	ASLSCPVPST
1370	1380	1390	1400	1410	1420	1430	1440
PPELSQRATL	DTVPPPPPSK	VGKRCRKTSD	PRRSIVECQP	DASATPGVGT	ADSPAAPTDS	RDDQKGLSLS	PQSPPERRGY
1450	1460	1470	1480	1490	1500	1510	1520
PGPGLRSDWH	ASSPLLITSD	TEHVTLLSEA	EHHGIGDLKS	NVLSVEEGEG	LRTADAEKSS	LSHPGIPPSP	PSCGPGSPLM
1530	1540	1550	1560	1570	1580	1590	1600
PSRDVHCTTD	GRQCQASAQL	DNLPASAWHS	TDSASPQTYE	VELEMQASGL	PKLRIKKIDP	SSSLEAEPLS	KEESSLGEES
1610	1620	1630	1640	1650	1660	1670	1680
FLPALSMPRA	SRSLSKPEPT	YVSPPCPRLS	HSTPGKSRGQ	TYICQACTPT	HGPSSTPSPF	QTDGVPWTPS	PKHSGKTTPD
1690	1700	1710	1720	1730	1740	1750	1760
IIKDWPRRKR	AVGCGAGSSS	GRGEVGADLP	GSLSLLESEG	KDHGLELSIH	RTPILEDFEL	EGVCQLPDQS	PPRNSMPKAE
1770	1780	1790	1800	1810	1820	1830	1840
EASSWGQFGL	SSRKRVLLAK	EEADRGAKRI	CDLREDSEVS	KSKEGSPSWS	AWQLPSTGDE	EVFVSGSTPP	PSCAVRSCLS
1850	1860	1870	1880	1890	1900	1910	1920
ASALQALTQS	PLLFQGKTPS	SQSKDPRDED	VDVLPSTVED	SPFSRAFSRR	RPISRTYTRK	KLMGTWLEDL	

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
949	1	473.1120	-311.20	2	41.4	19.1	1	1005-1012	K.GDEISLRR.S	

Detailed Protein Report

Protein 426: **caspase recruitment domain-containing protein 9 isoform 2 [Homo sapiens]**

Accession:	gi|16554562	**Score:**	29.8
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
1767	1	627.2880	-179.52	2	50.6	12.0	1	60-70	R.KVGVLLDILQR.T	

Detailed Protein Report

Protein 427: zinc finger protein ZIC 5 [Homo sapiens]

Accession:	gi|118766337	**Score:**	29.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	68.4
Database Date:	2015-11-30	**pI:**	9.9
Modification(s):	Oxidation	**Sequence Coverage [%]:**	4.5
		No. of unique Peptides:	2

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
2925	1	1018.9798	-14.49	2	65.7	18.1	0	202-222	R.DLSATAPAAAMHGAPLGGEQR.S	Oxidation: 11
2142	1	1052.3280	-209.35	1	57.0	11.7	2	531-539	R.KFANSSDRK.K	

Detailed Protein Report

Protein 428: rho GTPase-activating protein 11A isoform 3 [Homo sapiens]

Accession:	gi|557128992	**Score:**	29.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	92.6
Database Date:	2015-11-30	**pI:**	9.9
		Sequence Coverage [%]:	5.4
		No. of unique Peptides:	2

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
2089	3	682.6083	-53.17	3	54.7	11.6	0	386-404	K.HNSNITSSPLSGDENNMTK.E	
2804	1	698.3677	40.53	4	64.2	18.2	2	716-741	K.SMSCEESNIGAISKSSMELPSKSFLK.M	

Detailed Protein Report

Protein 429: pyruvate carboxylase, mitochondrial precursor [Homo sapiens]

Accession:	gi|106049292	**Score:**	29.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	129.6
Database Date:	2015-11-30	**pI:**	6.4
		Sequence Coverage [%]:	2.1
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578821479	refseq_human (refseq_human_20140103.fasta)	PREDICTED: pyruvate carboxylase, mitochondrial isoform X5 [Homo sapiens]
gi|578821475	refseq_human (refseq_human_20140103.fasta)	PREDICTED: pyruvate carboxylase, mitochondrial isoform X4 [Homo sapiens]
gi|530396856	refseq_human (refseq_human_20140103.fasta)	PREDICTED: pyruvate carboxylase, mitochondrial isoform X3 [Homo sapiens]
gi|530396854	refseq_human (refseq_human_20140103.fasta)	PREDICTED: pyruvate carboxylase, mitochondrial isoform X2 [Homo sapiens]
gi|106049528	refseq_human (refseq_human_20140103.fasta)	pyruvate carboxylase, mitochondrial precursor [Homo sapiens]
gi|106049295	refseq_human (refseq_human_20140103.fasta)	pyruvate carboxylase, mitochondrial precursor [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MLKFRTVHGG LRLLGIRRTS TAPAASPNVR RLEYKPIKKV MVANRGEIAI RVFRACTELG IRTVAIYSEQ DTGQMHRQKA

        90        100        110        120        130        140        150        160
DEAYLIGRGL APVQAYLHIP DIIKVAKENN VDAVHPGYGF LSERADFAQA CQDAGVRFIG PSPEVVRKMG DKVEARAIAI

       170        180        190        200        210        220        230        240
AAGVPVVPGT DAPITSLHEA HEFSNTYGFP IIFKAAYGGG GRGMRVVHSY EELEENYTRA YSEALAAFGN GALFVEKFIE

       250        260        270        280        290        300        310        320
KPRHIEVQIL GDQYGNILHL YERDCSIQRR HQKVVEIAPA AHLDPQLRTR LTSDSVKLAK QVGYENAGTV EFLVDRHGKH

       330        340        350        360        370        380        390        400
YFIEVNSRLQ VEHTVTEEIT DVDLVHAQIH VAEGRSLPDL GLRQENIRIN GCAIQCRVTT EDPARSFQPD TGRIEVFRSG

       410        420        430        440        450        460        470        480
EGMGIRLDNA SAFQGAVISP HYDSLLVKVI AHGKDHPTAA TKMSRALAEF RVRGVKTNIA FLQNVLNNQQ FLAGTVDTQF

       490        500        510        520        530        540        550        560
IDENPELFQL RPAQNRAQKL LHYLGHVMVN GPTTPIPVKA SPSPTDPVVP AVPIGPPPAG FRDILLREGP EGFARAVRNH

       570        580        590        600        610        620        630        640
PGLLLMDTTF RDAHQSLLAT RVRTHDLKKI APYVAHNFSK LFSMENWGGA TFDVAMRFLY ECPWRRLQEL RELIPNIPFQ

       650        660        670        680        690        700        710        720
MLLRGANAVG YTNYPDNVVF KFCEVAKENG MDVFRVFDSL NYLPNMLLGM EAAGSAGGVV EAAISYTGDV ADPSRTKYSL

       730        740        750        760        770        780        790        800
QYYMGLAEEL VRAGTHILCI KDMAGLLKPT ACTMLVSSLR DRFPDLPLHI HTHDTSGAGV AAMLACAQAG ADVVDVAADS

       810        820        830        840        850        860        870        880
MSGMTSQPSM GALVACTRGT PLDTEVPMER VFDYSEYWEG ARGLYAAFDC TATMKSGNSD VYENEIPGGQ YTNLHFQAHS

       890        900        910        920        930        940        950        960
MGLGSKFKEV KKAYVEANQM LGDLIKVTPS SKIVGDLAQF MVQNGLSRAE AEAQAEELSF PRSVVEFLQG YIGVPHGGFP

       970        980        990       1000       1010       1020       1030       1040
EPFRSKVLKD LPRVEGRPGA SLPPLDLQAL EKELVDRHGE EVTPEDVLSA AMYPDVFAHF KDFTATFGPL DSLNTRLFLQ

      1050       1060       1070       1080       1090       1100       1110       1120
GPKIAEEFEV ELERGKTLHI KALAVSDLNR AGQRQVFFEL NGQLRSILVK DTQAMKEMHF HPKALKDVKG QIGAPMPGKV

      1130       1140       1150       1160       1170       1180
IDIKVVAGAK VAKGQPLCVL SAMKMETVVT SPMEGTVRKV HVTKDMTLEG DDLILEIE
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
511	1	706.0223	94.27	2	35.3	14.9	2	1120-1133	K.VIDIKVVAGAKVAK.G	

Detailed Protein Report

Protein 430: **basement membrane-specific heparan sulfate proteoglycan core protein precursor [Homo sapiens]**

Accession:	gi|126012571	**Score:**	29.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	468.5
Database Date:	2015-11-30	**pI:**	6.1
		Sequence Coverage [%]:	0.4
		No. of unique Peptides:	1

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
362	1	457.1238	-295.03	2	33.9	17.6	0	4004-4012	R.SAEPLALGR.W	

Detailed Protein Report

Protein 431: **PREDICTED: thrombospondin type-1 domain-containing protein 7A isoform X4 [Homo sapiens]**

Accession:	gi|578813343	**Score:**	29.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	169.7
Database Date:	2015-11-30	**pI:**	9.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.4
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MGLQARRWAS	GSRGAAGPRR	GVLQLLPLPL	PLPLLLLLLL	RPGAGRAAAQ	GEAEAPTLYL	WKTGPWGRCM	GDECGPGGIQ
90	100	110	120	130	140	150	160
TRAVWCAHVE	GWTTLHTNCK	QAERPNNQQN	CFKVCDWHKE	LYDWRLGPWN	QCQPVISKSL	EKPLECIKGE	EGIQVREIAC
170	180	190	200	210	220	230	240
IQKDKDIPAE	DIICEYFEPK	PLLEQACLIP	CQQDCIVSEF	SAWSECSKTC	GSGLQHRTRH	VVAPPQFGGS	GCPNLTEFQV
250	260	270	280	290	300	310	320
CQSSPCEAEE	LRYSLHVGPW	STCSMPHSRQ	VRQARRRGKN	KEREKDRSKG	VKDPEARELI	KKKRNRNRQN	RQENKYWDIQ
330	340	350	360	370	380	390	400
IGYQTREVMC	INKTGKAADL	SFCQQEKLPM	TFQSCVITKE	CQVSEWSEWS	PCSKTCHDMV	SPAGTRVRTR	TIRQFPIGSE
410	420	430	440	450	460	470	480
KECPEFEEKE	PCLSQGDGVV	PCATYGWRTT	EWTECRVDPL	LSQQDKRRGN	QTALCGGGIQ	TREVYCVQAN	ENLLSQLSTH
490	500	510	520	530	540	550	560
KNKEASKPMD	LKLCTGPIPN	TTQLCHIPCP	TECEVSPWSA	WGPCTYENCN	DQQGKKGFKL	RKRRITNEPT	GGSGVTGNCP
570	580	590	600	610	620	630	640
HLLEAIPCEE	PACYDWKAVR	LGNCEPDNGK	ECGPGTQVQE	VVCINSDGEE	VDRQLCRDAI	FPIPVACDAP	CPKDCVLSTW
650	660	670	680	690	700	710	720
STWSSCSHTC	SGKTTEGKQI	RARSILAYAG	EEGGIRCPNS	SALQEVRSCN	EHPCTVYHWQ	TGPWGQCIED	TSVSSFNTTT
730	740	750	760	770	780	790	800
TWNGEASCSV	GMQTRKVICV	RVNVGQVGPK	KCPESLRPET	VRPCLLPCKK	DCIVTPYSDW	TSCPSSCKEG	DSSIRKQSRH
810	820	830	840	850	860	870	880
RVIIQLPANG	GRDCTDPLYE	EKACEAPQAC	QSYRWKTHKW	RRCQLVPWSV	QQDSPGAQEG	CGPGRQARAI	TCRKQDGGQA
890	900	910	920	930	940	950	960
GIHECLQYAG	PVPALTQACQ	IPCQDDCQLT	SWSKFSSCNG	DCGAVRTRKR	TLVGKSKKKE	KCKNSHLYPL	IETQYCPCDK
970	980	990	1000	1010	1020	1030	1040
YNAQPVGNWS	DCILPEGKVE	VLLGMKVQGD	IKECGQGYRY	QAMACYDQNG	RLVETSRCNS	HGYIEEACII	PCPSDCKLSE
1050	1060	1070	1080	1090	1100	1110	1120
WSNWSRCSKS	CGSGVKVRSK	WLREKPYNGG	RPCPKLDHVN	QAQVYEVVPC	HSDCNQYLWV	TEPWSICKVT	FVNMRENCGE
1130	1140	1150	1160	1170	1180	1190	1200
GVQTRKVRCM	QNTADGPSEH	VEDYLCDPEE	MPLGSRVCKL	PCPEDCVISE	WGPWTQCVLP	CNQSSFRQRS	ADPIRQPADE
1210	1220	1230	1240	1250	1260	1270	1280
GRSCPNAVEK	EPCNLNKNCY	HYDYNVTDWS	TCQLSEKAVC	GNGIKTRMLD	CVRSDGKSVD	LKYCEALGLE	KNWQMNTSCM
1290	1300	1310	1320	1330	1340	1350	1360
VECPVNCQLS	DWSPWSECSQ	TCGLTGKMIR	RRTVTQPFQG	DGRPCPSLMD	QSKPCPVKPC	YRWQYGQWSP	CQVQEAQCGE
1370	1380	1390	1400	1410	1420	1430	1440
GTRTRNISCV	VSDGSADDFS	KVVDEEFCAD	IELIIDGNKN	MVLEESCSQP	CPGDCYLKDW	SSWSLCQLTC	VNGEDLGFGG
1450	1460	1470	1480	1490	1500	1510	1520
IQVRSRPVII	QELENQHLCP	EQMLETKSCY	DGQCYEYKWM	ASAWKGSSRT	VWCQRSDGIN	VTAKSQRNPK	EGKTTD

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2861	1	795.7251	11.18	3	64.4	16.9	1	253-272	R.YSLHVGPWSTCSMPHSRQVR.Q	Carbamidomethyl: 11
1536	2	977.3535	-97.31	2	47.7	12.7	1	394-409	R.QFPIGSEKECPEFEEK.E	Carbamidomethyl: 10

Detailed Protein Report

Protein 432: PREDICTED: zinc finger protein 33B isoform X3 [Homo sapiens]

Accession:	gi|578819760	**Score:**	29.5
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 433: PREDICTED: integrin alpha-11 isoform X2 [Homo sapiens]

Accession: gi|530405525
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 29.5
MW [kDa]: 122.0
pI: 6.0
Sequence Coverage [%]: 2.5
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 434: kinesin light chain 4 isoform c [Homo sapiens]

Accession:	gi|19923891	**Score:**	29.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	35.1
Database Date:	2015-11-30	**pI:**	5.3
		Sequence Coverage [%]:	12.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSGLVLGQRD	EPAGHRLSQE	EILGSTRLVS	QGLEALRSEH	QAVLQSLSQT	IECLQQGGHE	EGLVHEKARQ	LRRSMENIEL
90	100	110	120	130	140	150	160
GLSEAQVMLA	LASHLSTVES	EKQKLRAQVR	RLCQENQWLR	DELAGTQQRL	QRSEQAVAQL	EEEKKHLEFL	GQLRQYDEDG
170	180	190	200	210	220	230	240
HTSEEKEGDA	TKDSLDDLFP	NEEEEDPSNG	LSRGQGATAA	QQGGYEIPAR	LRTLHNLVIQ	YAAQGRYEVA	VPLCKQALED
250	260	270	280	290	300	310	320
LERTSGRGHP	DVATMLNILA	LVYRDQNKYK	EAAHLLNDAL	SIRESTLGPD	HPAVSIPCPP	HPTPRTPHHC	CFGLS

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1691	1	1293.5862	-85.42	2	49.8	17.1	1	213-235	R.TLHNLVIQYAAQGRYEVAVPLCK.Q	

Detailed Protein Report

Protein 435: matrix metalloproteinase-27 precursor [Homo sapiens]

Accession:	gi|73808268	**Score:**	29.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	59.0
Database Date:	2015-11-30	**pI:**	9.4
		Sequence Coverage [%]:	5.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MKRLLLLFLF	FITFSSAFPL	VRMTENEENM	QLAQAYLNQF	YSLEIEGNHL	VQSKNRSLID	DKIREMQAFF	GLTVTGKLDS
90	100	110	120	130	140	150	160
NTLEIMKTPR	CGVPDVGQYG	YTLPGWRKYN	LTYRIINYTP	DMARAAVDEA	IQEGLEVWSK	VTPLKFTKIS	KGIADIMIAF
170	180	190	200	210	220	230	240
RTRVHGRCPR	YFDGPLGVLG	HAFPPGPGLG	GDTHFDEDEN	WTKDGAGFNL	FLVAAHEFGH	ALGLSHSNDQ	TALMFPNYVS
250	260	270	280	290	300	310	320
LDPRKYPLSQ	DDINGIQSIY	GGLPKEPAKP	KEPTIPHACD	PDLTFDAITT	FRREVMFFKG	RHLWRIYYDI	TDVEFELIAS
330	340	350	360	370	380	390	400
FWPSLPADLQ	AAYENPRDKI	LVFKDENFWM	IRGYAVLPDY	PKSIHTLGFP	GRVKKIDAAV	CDKTTRKTYF	FVGIWCWRFD
410	420	430	440	450	460	470	480
EMTQTMDKGF	PQRVVKHFPG	ISIRVDAAFQ	YKGFFFFSRG	SKQFEYDIKT	KNITRIMRTN	TWFQCKEPKN	SSFGFDINKE
490	500	510	520				
KAHSGGIKIL	YHKSLSLFIF	GIVHLLKNTS	IYQ				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2773	1	1051.5696	39.22	2	66.0	16.6	2	425-442	R.VDAAFQYKGFFFFSRGSK.Q	

Detailed Protein Report

Protein 436: PREDICTED: sp110 nuclear body protein isoform X3 [Homo sapiens]

Accession:	gi|530370295	**Score:**	29.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	58.5
Database Date:	2015-11-30	**pI:**	10.2
		Sequence Coverage [%]:	4.5
		No. of unique Peptides:	1

Quantitation

mdown:qdown **Median:** 1.30 **CV:** 0.00 % **No. of Peptides:** 1

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2672	1	484.7588	30.75	2	61.7	13.8	1	460-466	R.DMRLMFR.N		mdown:qdown 1.30

Detailed Protein Report

Protein 437: **PREDICTED: janus kinase and microtubule-interacting protein 3 isoform X5 [Homo sapiens]**

Accession:	gi|530394820	**Score:**	29.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	105.7
Database Date:	2015-11-30	**pI:**	6.1
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	3.9
		No. of unique 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
1669	1	1045.0250	19.09	2	50.8	18.3	0	860-879	R.TAAPIPFPGMCSIPCQAGVR.T	Carbamidomethyl: 15; Oxidation: 10

Detailed Protein Report

Protein 438: **interferon-induced guanylate-binding protein 2 [Homo sapiens]**

Accession:	gi|38327558	**Score:**	29.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	67.2
Database Date:	2015-11-30	**pI:**	5.4
Modification(s):	Oxidation	**Sequence Coverage [%]:**	5.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAPEINLPGP	MSLIDNTKGQ	LVVNPEALKI	LSAITQPVVV	VAIVGLYRTG	KSYLMNKLAG	KKNGFSLGST	VKSHTKGIWM
90	100	110	120	130	140	150	160
WCVPHPKKPE	HTLVLLDTEG	LGDIEKGDNE	NDSWIFALAI	LLSSTFVYNS	MGTINQQAMD	QLHYVTELTD	RIKANSSPGN
170	180	190	200	210	220	230	240
NSVDDSADFV	SFFPAFVWTL	RDFTLELEVD	GEPITADDYL	ELSLKLRKGT	DKKSKSFNDP	RLCIRKFFPK	RKCFVFDWPA
250	260	270	280	290	300	310	320
PKKYLAHLEQ	LKEEELNPDF	IEQVAEFCSY	ILSHSNVKTL	SGGIPVNGPR	LESLVLTYVN	AISSGDLPCM	ENAVLALAQI
330	340	350	360	370	380	390	400
ENSAAVEKAI	AHYEQQMGQK	VQLPTETLQE	LLDLHRDSER	EAIEVFMKNS	FKDVDQMFQR	KLGAQLEARR	DDFCKQNSKA
410	420	430	440	450	460	470	480
SSDCCMALLQ	DIFGPLEEDV	KQGTFSKPGG	YRLFTQKLQE	LKNKYYQVPR	KGIQAKEVLK	KYLESKEDVA	DALLQTDQSL
490	500	510	520	530	540	550	560
SEKEKAIEVE	RIKAESAEAA	KKMLEEIQKK	NEEMMEQKEK	SYQEHVKQLT	EKMERDRAQL	MAEQEKTLAL	KLQEQERLLK
570	580	590	600				
EGFENESKRL	QKDIWDIQMR	SKSLEPICNI	L				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2870	1	1027.5482	62.66	2	65.0	11.1	2	503-518	K.MLEEIQKKNEEMMEQK.E	Oxidation: 12

Detailed Protein Report

Protein 439: zinc finger and SCAN domain-containing protein 29 [Homo sapiens]

Accession:	gi|109715825	**Score:**	29.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	96.7
Database Date:	2015-11-30	**pI:**	6.6
		Sequence Coverage [%]:	4.0
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578826641	refseq_human (refseq_human_20140103.fasta)	PREDICTED: zinc finger and SCAN domain-containing protein 29 isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MMAKSALREN	GTNSETFRQR	FRRFHYQEVA	GPREAFSQLW	ELCCRWLRPE	VRTKEQIVEL	LVLEQFLTVL	PGEIQNWVQE
90	100	110	120	130	140	150	160
QCPENGEEAV	TLVEDLEREP	GRPRSSVTVS	VKGQEVRLEK	MTPPKSSQEL	LSVRQESVEP	QPRGVPKKER	ARSPDLGPQE
170	180	190	200	210	220	230	240
QMNPKEKLKP	FQRSGLPFPK	SGVVSRLEQG	EPWIPDLLGS	KEKELPSGSH	IGDRRVHADL	LPSKKDRRSW	VEQDHWSFED
250	260	270	280	290	300	310	320
EKVAGVHWGY	EETRTLLAIL	SQTEFYEALR	NCHRNSQVYG	AVAERLREYG	FLRTLEQCRT	KFKGLQKSYR	KVKSGHPPET
330	340	350	360	370	380	390	400
CPFFEEMEAL	MSAQVIALPS	NGLEAAASHS	GLVGSDAETE	EPGQRGWQHE	EGAEEAVAQE	SDSDDMDLEA	TPQDPNSAAP
410	420	430	440	450	460	470	480
VVFRSPGGVH	WGYEETKTYL	AILSETQFYE	ALRNCHRNSQ	LYGAVAERLW	EYGFLRTPEQ	CRTKFKSLQT	SYRKVKNGQA
490	500	510	520	530	540	550	560
PETCPFFEEM	DALVSVRVAA	PPNDGQEETA	SCPVQGTSEA	EAQKQAEEAD	EATEEDSDDD	EEDTEIPPGA	VITRAPVLFQ
570	580	590	600	610	620	630	640
SPRGFEAGFE	NEDNSKRDIS	EEVQLHRTLL	ARSERKIPRY	LHQGKGNESD	CRSGRQWAKT	SGEKRGKLTL	PEKSLSEVLS
650	660	670	680	690	700	710	720
QQRPCLGERP	YKYLKYSKSF	GPNSLLMHQV	SHQVENPYKC	ADCGKSFSRS	ARLIRHRRIH	TGEKPYKCLD	CGKSFRDSSN
730	740	750	760	770	780	790	800
FITHRRIHTG	EKPYQCGECG	KCFNQSSSLI	IHQRTHTGEK	PYQCEECGKS	FNNSSHFSAH	RRIHTGERPH	VCPDCGKSFS
810	820	830	840	850	860		
KSSDLRAHHR	THTGEKPYGC	HDCGKCFSKS	SALNKHGEIH	AREKLLTQSA	PK		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1688	1	1136.5634	-13.85	2	49.6	11.2	1	438-456	R.NSQLYGAVAERLWEYGFLR.T	

Detailed Protein Report

Protein 440: **CDK5 regulatory subunit-associated protein 2 isoform c [Homo sapiens]**

Accession:	gi|440309853	**Score:**	29.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	189.5
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
MMDLVLEEDV	TVPGTLSGCS	GLVPSVPDDL	DGINPNAGLG	NGLLPNVSEE	TVSPTRARNM	KDFENQITEL	KKENFNLKLR
90	100	110	120	130	140	150	160
IYFLEERMQQ	EFHGPTEHIY	KTNIELKVEV	ESLKRELQER	EQLLIKASKA	VESLAEAGGS	EIQRVKEDAR	KKVQQVEDLL
170	180	190	200	210	220	230	240
TKRILLLEKD	VTAAQAELEK	AFAGTETEKA	LRLRLESKLS	EMKKMHEGDL	AMALVLDEKD	RLIEELKLSL	KSKEALIQCL
250	260	270	280	290	300	310	320
KEEKSQMACP	DENVSSGELR	GLCAAPREEK	ERETEAAQME	HQKERNSFEE	RIQALEEDLR	EKEREIATEK	KNSLKRDKAI
330	340	350	360	370	380	390	400
QGLTMALKSK	EKKVEELNSE	IEKLSAAFAK	AREALQKAQT	QEFQGSEDYE	TALSGKEALS	AALRSQNLTK	STENHRLRRS
410	420	430	440	450	460	470	480
IKKITQELSD	LQQERERLEK	DLEEAHREKS	KGDCTIRDLR	NEVEKLRNEV	NEREKAMENR	YKSLLSESNK	KLHNQEQVIK
490	500	510	520	530	540	550	560
HLTESTNQKD	VLLQKFNEKD	LEVIQQNCYL	MAAEDLELRS	EGLITEKCSS	QQPPGSKTIF	SKEKKQSSDY	EELIQVLKKE
570	580	590	600	610	620	630	640
QDIYTHLVKS	LQESDSINNL	QAELNKIFAL	RKQLEQDVLS	YQNLRKTLEE	QISEIRRREE	SFSLYSDQTS	YLSICLEENN
650	660	670	680	690	700	710	720
RFQVEHFSQE	ELKKKVSDLI	QLVKELYTDN	QHLKKTIFDL	SCMGFQGNGF	PDRLASTEQT	EEAKKSRLPI	LIKPSRSLGN
730	740	750	760	770	780	790	800
MYRLPATQEV	VTQLQSQILE	LQGELKEFKT	CNKQLHQKLI	LAEAVMEGRP	TPDKTLLNAQ	PPVGAAYQDS	PGEQKGIKTT
810	820	830	840	850	860	870	880
SSVWRDKEMD	SDQQRSYEID	SEICPPDDLA	SLPSCKENPE	DVLSPTSVAT	YLSSKSQPSA	KVSVMGTDQS	ESINTSNETE
890	900	910	920	930	940	950	960
YLKQKIHDLE	TELEGYQNFI	FQLQKHSQCS	EAIITVLCGT	EGAQDGLSKP	KNGSDGEEMT	FSSLHQVRYV	KHVKILGPLA
970	980	990	1000	1010	1020	1030	1040
PEMIDSRVLE	NLKQQLEEQE	YKLQKEQNLN	MQLFSEIHNL	QNKFRDLSPP	RYDSLVQSQA	RELSLQRQQI	KDGHGICVIS
1050	1060	1070	1080	1090	1100	1110	1120
RQHMNTMIKA	FEELLQASDV	DYCVAEGFQE	QLNQCAELLE	KLEKLFLNGK	SVGVEMNTQN	ELMERIEEDN	LTYQHLLPES
1130	1140	1150	1160	1170	1180	1190	1200
PEPSASHALS	DYETSEKSFF	SRDQKQDNET	EKTSVMVNSF	SQDLLMEHIQ	EIRTLRKRLE	ESIKTNEKLR	KQLERQGSEF
1210	1220	1230	1240	1250	1260	1270	1280
VQGSTSIFAS	GSELHSSLTS	EIHFLRKQNQ	ALNAMLIKGS	RDKQKENDKL	RESLSRKTVS	LEHLQREYAS	VKEENERLQK
1290	1300	1310	1320	1330	1340	1350	1360
EGSEKERHNQ	QLIQEVRCSG	QELSRVQEEV	KLRQQLLSQN	DKLLQSLRVE	LKAYEKLDEE	HRRLREASGE	GWKGQDPFRD
1370	1380	1390	1400	1410	1420	1430	1440
LHSLLMEIQA	LRLQLERSIE	TSSTLQSRLK	EQLARGAEKA	QEGALTLAVQ	AVSIPEVPLQ	PDKHDGDKYP	MESDNSFDLF
1450	1460	1470	1480	1490	1500	1510	1520
DSSQAVTPKS	VSETPPLSGN	DTDSLSCDSG	SSATSTPCVS	RLVTGHHLWA	SKNGRHVLGL	IEDYEALLKQ	ISQGQRLLAE
1530	1540	1550	1560	1570	1580	1590	1600
MDIQTQEAPS	STSQELGTKG	PHPAPLSKFV	SSVSTAKLTL	EEAYRRLKLL	WRVSLPEDGQ	CPLHCEQIGE	MKAEVTKLHK
1610	1620	1630	1640	1650	1660	1670	
KLFEQEKKLQ	NTMKLLQLSK	RQEKVIFDQL	VVTHKILRKA	RGNLELRPGG	AHPGTCSPSR	PGS	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
578	1	575.8071	-12.69	2	36.1	15.6	1	1558-1566	K.LTLEEAYRR.L	

Detailed Protein Report

Protein 441: adenylate cyclase type 9 [Homo sapiens]

Accession:	gi|50959205	**Score:**	29.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	150.6
Database Date:	2015-11-30	**pI:**	7.3
		Sequence Coverage [%]:	2.0
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MASPPHQQLL HHHSTEVSCD SSGDSNSVRV KINPKQLSSN SHPKHCKYSI SSSCSSSGDS GGVPRRVGGG GRLRRQKKLP

        90        100        110        120        130        140        150        160
QLFERASSRW WDPKFDSVNL EEACLERCFP QTQRRFRYAL FYIGFACLLW SIYFAVHMRS RLIVMVAPAL CFLLVCVGFF

       170        180        190        200        210        220        230        240
LFTFTKLYAR HYAWTSLALT LLVFALTLAA QFQVLTPVSG RGDSSNLTAT ARPTDTCLSQ VGSFSMCIEV LFLLYTVMHL

       250        260        270        280        290        300        310        320
PLYLSLCLGV AYSVLFETFG YHFRDEACFP SPGAGALHWE LLSRGLLHGC IHAIGVHLFV MSQVRSRSTF LKVGQSIMHG

       330        340        350        360        370        380        390        400
KDLEVEKALK ERMIHSVMPR IIADDLMKQG DEESENSVKR HATSSPKNRK KKSSIQKAPI AFRPFKMQQI EEVSILFADI

       410        420        430        440        450        460        470        480
VGFTKMSANK SAHALVGLLN DLFGRFDRLC EETKCEKIST LGDCYYCVAG CPEPRADHAY CCIEMGLGMI KAIEQFCQEK

       490        500        510        520        530        540        550        560
KEMVNMRVGV HTGTVLCGIL GMRRFKFDVW SNDVNLANLM EQLGVAGKVH ISEATAKYLD DRYEMEDGKV IERLGQSVVA

       570        580        590        600        610        620        630        640
DQLKGLKTYL ISGQRAKESR CSCAEALLSG FEVIDGSQVS SGPRGQGTAS SGNVSDLAQT VKTFDNLKTC PSCGITFAPK

       650        660        670        680        690        700        710        720
SEAGAEGGAP QNGCQDEHKN STKASGGPNP KTQNGLLSPP QEEKLTNSQT SLCEILQEKG RWAGVSLDQS ALLPLRFKNI

       730        740        750        760        770        780        790        800
REKTDAHFVD VIKEDSLMKD YFFKPPINQF SLNFLDQELE RSYRTSYQEE VIKNSPVKTF ASPTFSSLLD VFLSTTVFLT

       810        820        830        840        850        860        870        880
LSTTCFLKYE AATVPPPPAA LAVFSAALLL EVLSLAVSIR MVFFLEDVMA CTKRLLEWIA GWLPRHCIGA ILVSLPALAV

       890        900        910        920        930        940        950        960
YSHVTSEYET NIHFPVFTGS AALIAVVHYC NFCQLSSWMR SSLATVVGAG PLLLLYVSLC PDSSVLTSPL DAVQNFSSER

       970        980        990       1000       1010       1020       1030       1040
NPCNSSVPRD LRRPASLIGQ EVVLVFFLLL LLVWFLNREF EVSYRLHYHG DVEADLHRTK IQSMRDQADW LLRNIIPYHV

      1050       1060       1070       1080       1090       1100       1110       1120
AEQLKVSQTY SKNHDSGGVI FASIVNFSEF YEENYEGGKE CYRVLNELIG DFDELLSKPD YSSIEKIKTI GATYMAASGL

      1130       1140       1150       1160       1170       1180       1190       1200
NTAQAQDGSH PQEHLQILFE FAKEMMRVVD DFNNNMLWFN FKLRVGFNHG PLTAGVIGTT KLLYDIWGDT VNIASRMDTT

      1210       1220       1230       1240       1250       1260       1270       1280
GVECRIQVSE ESYRVLSKMG YDFDYRGTVN VKGKGQMKTY LYPKCTDHRV IPQHQLSISP DIRVQVDGSI GRSPTDEIAN

      1290       1300       1310       1320       1330       1340       1350       1360
LVPSVQYVDK TSLGSDSSTQ AKDAHLSPKR PWKEPVKAEE RGRFGKAIEK DDCDETGIEE ANELTKLNVS KSV
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1840	1	920.8515	-101.83	2	53.0	12.7	2	1235-1249	K.GQMKTYLYPKCTDHR.V	

Detailed Protein Report

Protein 442: **zinc finger protein 740 [Homo sapiens]**

Accession:	gi|51972182	**Score:**	29.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	21.8
Database Date:	2015-11-30	**pI:**	10.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	5.2
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MAQASLLACE	GLAGVSLVPT	AASKKMMLSQ	IASKQAENGE	RAGSPDVLRC	SSQGHRKDSD	KSRSRKDDDS	LSEASHSKKT
90	100	110	120	130	140	150	160
VKKVVVVEQN	GSFQVKIPKN	FVCEHCFGAF	RSSYHLKRHI	LIHTGEKPFE	CDICDMRFIQ	KYHLERHKRV	HSGEKPYQCE
170	180	190	200				
RCHQCFSRTD	RLLRHKRMCQ	GCQSKTSDGQ	FSL				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1915	2	655.2467	-50.69	2	52.6	13.1	1	162-171	R.CHQCFSRTDR.L	Carbamidomethyl: 4
1903	2	655.2746	-8.02	2	52.5	16.0	1	162-171	R.CHQCFSRTDR.L	Carbamidomethyl: 1

Detailed Protein Report

Protein 443: **PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X3 [Homo sapiens]**

Accession:	gi|530381810	**Score:**	29.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	73.7
Database Date:	2015-11-30	**pI:**	5.7
		Sequence Coverage [%]:	2.5
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	0.80	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.71	**CV:**	0.00 %	**No. of Peptides:**	1

```
        10         20         30         40         50         60         70         80
MSAGIVWALN KDSLGPWELY VPVKDLLGIY EKLYGRKVIT ENVIVDCSHI QFLEMYGEML AVSKLYPTYS TKSPFLVEQF
        90        100        110        120        130        140        150        160
QEYFLGGLDD MAFWSTNIYH LTSFMLENGT SDCNLPENPL FIACGGQQNH TQGSKMQKND FHRNLTTSLT ESVDRNINYT
       170        180        190        200        210        220        230        240
ERGVFFSVNS WTPDSMSFIY KALERNIRTM FIGGSQLSQK HVSSPLASYF LSFPYARLGW AMTSADLNQD GHGDLVVGAP
       250        260        270        280        290        300        310        320
GYSRPGHIHI GRVYLIYGND LGLPPVDLDL DKEAHRILEG FQPSGRFGSA LAVLDFNVDG VPDLAVGAPS VGSEQLTYKG
       330        340        350        360        370        380        390        400
AVYVYFGSKQ GGMSSSPNIT ISCQDIYCNL GWTLLAADVN GDSEPDLVIG SPFAPGGGKQ KGIVAAFYSG PSLSDKEKLN
       410        420        430        440        450        460        470        480
VEAANWTVRG EEDFSWFGYS LHGVTVDNRT LLLVGSPTWK NASRLGHLLH IRDEKKSLGR VYGYFPPNGQ SWFTISGDKA
       490        500        510        520        530        540        550        560
MGKLGTSLSS GHVLMNGTLK QVLLVGAPTY DDVSKVAFLT VTLHQGGATR MYALTSDAQP LLLSTFSGDR RFSRFGGVLH
       570        580        590        600        610        620        630        640
LSDLDDDGLD EIIMAAPLRI ADVTSGLIGG EDGRVYVYNG KETTLGDMTG KCKSWITPCP EEKAQYVLIS PEASSRFGSS
       650        660        670        680
LITVRSKAKN QVVIAAGRSS LGARLSGALH VYSLGSD
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
257	1	625.9672	-15.19	3	32.4	29.2	1	595-611	R.VYVYNGKETTLGDMTGK.C		Wdown:Qdown 0.71 mdown:qdown 0.80

Detailed Protein Report

Protein 444: 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 445: 5'-nucleotidase isoform 1 preproprotein [Homo sapiens]

Accession:	gi|4505467	**Score:**	29.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	63.3
Database Date:	2015-11-30	**pI:**	6.6
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	3.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MCPRAARAPA	TLLLALGAVL	WPAAGAWELT	ILHTNDVHSR	LEQTSEDSSK	CVNASRCMGG	VARLFTKVQQ	IRRAEPNVLL
90	100	110	120	130	140	150	160
LDAGDQYQGT	IWFTVYKGAE	VAHFMNALRY	DAMALGNHEF	DNGVEGLIEP	LLKEAKFPIL	SANIKAKGPL	ASQISGLYLP
170	180	190	200	210	220	230	240
YKVLPVGDEV	VGIVGYTSKE	TPFLSNPGTN	LVFEDEITAL	QPEVDKLKTL	NVNKIIALGH	SGFEMDKLIA	QKVRGVDVVV
250	260	270	280	290	300	310	320
GGHSNTFLYT	GNPPSKEVPA	GKYPFIVTSD	DGRKVPVVQA	YAFGKYLGYL	KIEFDERGNV	ISSHGNPILL	NSSIPEDPSI
330	340	350	360	370	380	390	400
KADINKWRIK	LDNYSTQELG	KTIVYLDGSS	QSCRFRECNM	GNLICDAMIN	NNLRHTDEMF	WNHVSMCILN	GGGIRSPIDE
410	420	430	440	450	460	470	480
RNNGTITWEN	LAAVLPFGGT	FDLVQLKGST	LKKAFEHSVH	RYGQSTGEFL	QVGGIHVVYD	LSRKPGDRVV	KLDVLCTKCR
490	500	510	520	530	540	550	560
VPSYDPLKMD	EVYKVILPNF	LANGGDGFQM	IKDELLRHDS	GDQDINVVST	YISKMKVIYP	AVEGRIKFST	GSHCHGSFSL
570	580						
IFLSLWAVIF	VLYQ						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1850	1	727.3153	-15.31	2	51.6	13.1	1	51-63	K.CVNASRCMGGVAR.L	Carbamidomethyl: 1, 7; Oxidation: 8

Detailed Protein Report

Protein 446: putative Polycomb group protein ASXL3 [Homo sapiens]

Accession:	gi|149944526	**Score:**	29.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	241.8
Database Date:	2015-11-30	**pI:**	5.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.7
		No. of unique Peptides:	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MKDKRKKKDR	TWAEAARLAL	EKHPNSPMTA	KQILEVIQKE	GLKETSGTSP	LACLNAMLHT	NTRIGDGTFF	KIPGKSGLYA
90	100	110	120	130	140	150	160
LKKEESSCPA	DGTLDLVCES	ELDGTDMAEA	NAHGEENGVC	SKQVTDEASS	TRDSSLTNTA	VQSKLVSSFQ	QHTKKALKQA
170	180	190	200	210	220	230	240
LRQQQKRRNG	VSMMVNKTVP	RVVLTPLKVS	DEQSDSPSGS	ESKNGEADSS	DKEMKHGQKS	PTGKQTSQHL	KRLKKSGLGH
250	260	270	280	290	300	310	320
LKWTKAEDID	IETPGSILVN	TNLRALINKH	TFASLPQHFQ	QYLLLLLPEV	DRQMGSDGIL	RLSTSALNNE	FFAYAAQGWK
330	340	350	360	370	380	390	400
QRLAEGEFTP	EMQLRIRQEI	EKEKKTEPWK	EKFFERFYGE	KLGMSREESV	KLTTGPNNAG	AQSSSSCGTS	GLPVSAQTAL
410	420	430	440	450	460	470	480
AEQQPKSMKS	PASPEPGFCA	TLCPMVEIPP	KDIMAELESE	DILIPEESVI	QEEIAEEVET	SICECQDENH	KTIPEFSEEA
490	500	510	520	530	540	550	560
ESLTNSHEEP	QIAPPEDNLE	SCVMMNDVLE	TLPHIEVKIE	GKSESPQEEM	TVVIDQLEVC	DSLIPSTSSM	THVSDTEHKE
570	580	590	600	610	620	630	640
SETAVETSTP	KIKTGSSSLE	GQFPNEGIAI	DMELQSDPEE	QLSENACISE	TSFSSESPEG	ACTSLPSPGG	ETQSTSEESC
650	660	670	680	690	700	710	720
TPASLETTFC	SEVSSTENTD	KYNQRNSTDE	NFHASLMSEI	SPISTSPEIS	EASLMSNLPL	TSEASPVSNL	PLTSETSPMS
730	740	750	760	770	780	790	800
DLPLTSETSS	VSSMLLTSET	TFVSSLPLPS	ETSPISNSSI	NERMAHQQRK	SPSVSEEPLS	PQKDESSATA	KPLGENLTSQ
810	820	830	840	850	860	870	880
QKNLSNTPEP	IIMSSSSIAP	EAFPSEDLHN	KTLSQQTCKS	HVDTEKPYPA	SIPELASTEM	IKVKNHSVLQ	RTEKKVLPSP
890	900	910	920	930	940	950	960
LELSVFSEGT	DNKGNELPSA	KLQDKQYISS	VDKAPFSEGS	RNKTHKQGST	QSRLETSHTS	KSSEPSKSPD	GIRNESRDSE
970	980	990	1000	1010	1020	1030	1040
ISKRKTAEQH	SFGICKEKRA	RIEDDQSTRN	ISSSSPPEKE	QPPREEPRVP	PLKIQLSKIG	PPFIIKSQPV	SKPESRASTS
1050	1060	1070	1080	1090	1100	1110	1120
TSVSGGRNTG	ARTLADIKAR	AQQARAQREA	AAAAAVAAAA	SIVSGAMGSP	GEGGKTRTLA	HIKEQTKAKL	FAKHQARAHL
1130	1140	1150	1160	1170	1180	1190	1200
FQTSKETRLP	PPLSSKEGPP	NLEVSSTPET	KMEGSTGVII	VNPNCRSPSN	KSAHLRETTT	VLQQSLNPSK	LPETATDLSV
1210	1220	1230	1240	1250	1260	1270	1280
HSSDENIPVS	HLSEKIVSST	SSENSSVPML	FNKNSVPVSV	CSTAISGAIK	EHPFVSSVDK	SSVLMSVDSA	NTTISACNIS
1290	1300	1310	1320	1330	1340	1350	1360
MLKTIQGTDT	PCIAIIPKCI	ESTPISATTE	GSSISSSMDD	KQLLISSSSA	SNLVSTQYTS	VPTPSIGNNL	PNLSTSSVLI
1370	1380	1390	1400	1410	1420	1430	1440
PPMGINNRFP	SEKIAIPGSE	EQATVSMGTT	VRAALSCSDS	VAVTDSLVAH	PTVAMFTGNM	LTINSYDSPP	KLSAESLDKN
1450	1460	1470	1480	1490	1500	1510	1520
SGPRNRADNS	GKPQQPPGGF	APAAINRSIP	CKVIVDHSTT	LTSSLSLTVS	VESSEASLDL	QGRPVRTEAS	VQPVACPQVS
1530	1540	1550	1560	1570	1580	1590	1600
VISRPEPVAN	EGIDHSSTFI	AASAAKQDSK	TLPATCTSLR	ELPLVPDKLN	EPTAPSHNFA	EQARGPAPFK	SEADTTCSNQ
1610	1620	1630	1640	1650	1660	1670	1680
YNPSNRICWN	DDGMRSTGQP	LVTHSGSSKQ	KEYLEQSCPK	AIKTEHANYL	NVSELHPRNL	VTNVALPVKS	ELHEADKGFR
1690	1700	1710	1720	1730	1740	1750	1760
MDTEDFPGPE	LPPPAAEGAS	SVQQTQNMKA	STSSPMEEAI	SLATDALKRV	PGAGSSGCRL	SSVEANNPLV	TQLLQGNLPL
1770	1780	1790	1800	1810	1820	1830	1840
EKVLPQPRLG	AKLEINRLPL	PLQTTSVGKT	APERNVEIPP	SSPNPDGKGY	LAGTLAPLQM	RKRENHPKKR	VARTVGEHTQ
1850	1860	1870	1880	1890	1900	1910	1920
VKCEPGKLLV	EPDVKGVPCV	ISSGISQLGH	SQPFKQEWLN	KHSMQNRIVH	SPEVKQQKRL	LPSCSFQQNL	FHVDKNGGFH
1930	1940	1950	1960	1970	1980	1990	2000
TDAGTSHRQQ	FYQMPVAARG	PIPTAALLQA	SSKTPVGCNA	FAFNRHLEQK	GLGEVSLSSA	PHQLRLANML	SPNMPMKEGD
2010	2020	2030	2040	2050	2060	2070	2080
EVGGTAHTMP	NKALVHPPPP	PPPPPPPPLA	LPPPPPPPPP	LPPPLPNAEV	PSDQKQPPVT	METTKRLSWP	QSTGICSNIK
2090	2100	2110	2120	2130	2140	2150	2160
SEPLSFEEGL	SSSCELGMKQ	VSYDQNEMKE	QLKAFALKSA	DFSSYLLSEP	QKPFTQLAAQ	KMQVQQQQQL	CGNYPTIHFG
2170	2180	2190	2200	2210	2220	2230	2240
STSFKRAASA	IEKSIGILGS	GSNPATGLSG	QNAQMPVQNF	ADSSNADELE	LKCSCRLKAM	IVCKGCGAFC	HDDCIGPSKL
2250							
CVACLVVR							

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1390	1	1030.1245	-9.16	3	47.1	12.9	0	1681-1709	R.MDTEDFPGPELPPPAAEGASSVQQTQNMK.A	Oxidation: 1

Detailed Protein Report

Protein 447: PREDICTED: histone-lysine N-methyltransferase SETD2 isoform X3 [Homo sapiens]

Accession:	gi|578806017	**Score:**	29.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	253.1
Database Date:	2015-11-30	**pI:**	6.6
		Sequence Coverage [%]:	1.1
		No. of unique Peptides:	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MKQLQPQPPP	KMGDFYDPEH	PTPEEEENEA	KIENVQKTGF	IKGPMFKGVA	SSRFLPKGTK	TKVNLEEQGR	QKVSFSFSLT
90	100	110	120	130	140	150	160
KKTLQNRFLT	ALGNEKQSDT	PNPPAVPLQV	DSTPKMKMEI	GDTLSTAEES	SPPKSRVELG	KIHFKKHLLH	VTSRPLLATT
170	180	190	200	210	220	230	240
TAVASPPTHA	APLPAVIAES	TTVDSPPSSP	PPPPPPAQAT	TLSSPAPVTE	PVALPHTPIT	VLMAAPVPLP	VDVAVRSLKE
250	260	270	280	290	300	310	320
PPIIIVPESL	EADTKQDTIS	NSLEEHVTQI	LNEQADISSK	KEDSHIGKDE	EIPDSSKISL	SCKKTGSKKK	SSQSEGIFLG
330	340	350	360	370	380	390	400
SESDEDSVRT	SSSQRSHDLK	FSASIEKERD	FKKSSAPLKS	EDLGKPSRSK	TDRDDKYFSY	SKLERDTRYV	SSRCRSERER
410	420	430	440	450	460	470	480
RRSRSHSRSE	RGSRTNLSYS	RSERSHYYDS	DRRYHRSSPY	RERTRYSRPY	TDNRARESSD	SEEEYKKTYS	RRTSSHSSSY
490	500	510	520	530	540	550	560
RDLRTSSYSK	SDRDCKTETS	YLEMERRGKY	SSKLERESKR	TSENEAIKRC	CSPPNELGFR	RGSSYSKHDS	SASRYKSTLS
570	580	590	600	610	620	630	640
KPIPKSDKFK	NSFCCTELNE	EIKQSHSFSL	QTPCSKGSEL	RMINKNPERE	KAGSPAPSNR	LNDSPTLKKL	DELPIFKSEF
650	660	670	680	690	700	710	720
ITHDSHDSIK	ELDSLSKVKN	DQLRSFCPIE	LNINGSPGAE	SDLATFCTSK	TDAVLMTSDD	SVTGSELSPL	VKACMLSSNG
730	740	750	760	770	780	790	800
FQNISRCKEK	DLDDTCMLHK	KSESPFRETE	PLVSPHQDKL	MSMPVMTVDY	SKTVVKEPVD	TRVSCCKTKD	SDIYCTLNDS
810	820	830	840	850	860	870	880
NPSLCNSEAE	NIEPSVMKIS	SNSFMNVHLE	SKPVICDSRN	LTDHSKFACE	EYKQSIGSTS	SASVNHFDDL	YQPIGSSGIA
890	900	910	920	930	940	950	960
SSLQSLPPGI	KVDSLTLLKC	GENTSPVLDA	VLKSKKSSEF	LKHAGKETIV	EVGSDLPDSG	KGFASRENRR	NNGLSGKCLQ
970	980	990	1000	1010	1020	1030	1040
EAQEEGNSIL	PERRGRPEIS	LDERGEGGHV	HTSDDSEVVF	SSCDLNLTME	DSDGVTYALK	CDSSGHAPEI	VSTVHEDYSG
1050	1060	1070	1080	1090	1100	1110	1120
SSESSNDESD	SEDTDSDDSS	IPRNRLQSVV	VVPKNSTLPM	EETSPCSSRS	SQSYRHYSDH	WEDERLESRR	HLYEEKFESI
1130	1140	1150	1160	1170	1180	1190	1200
ASKACPQTDK	FFLHKGTEKN	PEISFTQSSR	KQIDNRLPEL	SHPQSDGVDS	TSHTDVKSDP	LGHPNSEETV	KAKIPSRQQE
1210	1220	1230	1240	1250	1260	1270	1280
ELPIYSSDFE	DVPNKSWQQT	TFQNRPDSRL	GKTELSFSSS	CEIPHVDGLH	SSEELRNLGW	DFSQEKPSTT	YQQPDSSYGA
1290	1300	1310	1320	1330	1340	1350	1360
CGGHKYQQNA	EQYGGTRDYW	QGNGYWDPRS	GRPPGTGVVY	DRTQGQVPDS	LTDDREEEEN	WDQQDGSHFS	DQSDKFLLSL
1370	1380	1390	1400	1410	1420	1430	1440
QKDKGSVQAP	EISSNSIKDT	LAVNEKKDFS	KNLEKNDIKD	RGPLKKRRQE	IESDSESDGE	LQDRKKVRVE	VEQGETSVPP
1450	1460	1470	1480	1490	1500	1510	1520
GSALVGPSCV	MDDFRDPQRW	KECAKQGKMP	CYFDLIEENV	YLTERKKNKS	HRDIKRMQCE	CTPLSKDERA	QGEIACGEDC
1530	1540	1550	1560	1570	1580	1590	1600
LNRLLMIECS	SRCPNGDYCS	NRRFQRKQHA	DVEVILTEKK	GWGLRAAKDL	PSNTFVLEYC	GEVLDHKEFK	ARVKEYARNK
1610	1620	1630	1640	1650	1660	1670	1680
NIHYYFMALK	NDEIIDATQK	GNCSRFMNHS	CEPNCETQKW	TVNGQLRVGF	FTTKLVPSGS	ELTFDYQFQR	YGKEAQKCFC
1690	1700	1710	1720	1730	1740	1750	1760
GSANCRGYLG	GENRVSIRAA	GGKMKKERSR	KKDSEVYRIP	KKSQTEKENT	TTERGRDAVG	FRDQTPAPKT	PNRSRERDPD
1770	1780	1790	1800	1810	1820	1830	1840
KQTQNKEKRK	RRSSLSPPSS	AYERGTKRPD	DRYDTPTSKK	KVRIKDRNKL	STEERRKLFE	QEVAQREAQK	QQQQMQNLGM
1850	1860	1870	1880	1890	1900	1910	1920
TSPLPYDSLG	YNAPHHPFAG	YPPGYPMQAY	VDPSNPNAGK	VLLPTPSMDP	VCSPAPYDHA	QPLVGHSTEP	LSAPPPVPVV
1930	1940	1950	1960	1970	1980	1990	2000
PHVAAPVEVS	SSQYVAQSDG	VVHQDSSVAV	LPVPAPGPVQ	GQNYSVWDSN	QQSVSVQQQY	SPAQSQATIY	YQGQTCPTVY
2010	2020	2030	2040	2050	2060	2070	2080
GVTSPYSQTT	PPIVQSYAQP	SLQYIQGQQI	FTAHPQGVVV	QPAAAVTTIV	APGQPQPLQP	SEMVVTNNLL	DLPPPSPPKP
2090	2100	2110	2120	2130	2140	2150	2160
KTIVLPPNWK	TARDPEGKIY	YYHVITRQTQ	WDPPTWESPG	DDASLEHEAE	MDLGTPTYDE	NPMKASKKPK	TAEADTSSEL
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
2100	1	707.7227	-113.09	2	54.8	14.1	1	422-432	R.SERSHYYDSDR.R	

Detailed Protein Report

Protein 448: PREDICTED: putative Polycomb group protein ASXL1 isoform X6 [Homo sapiens]

Accession:	gi|578835836	**Score:**	28.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	159.1
Database Date:	2015-11-30	**pI:**	5.6
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	2.4
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MLSFPNLNQV	LENYSDAPMT	PKQILQVIEA	EGLKEMRSGT	SPLACLNAML	HSNSRGGEGL	FYKLPGRISL	FTLKKDALQW
90	100	110	120	130	140	150	160
SRHPATVEGE	EPEDTADVES	CGSNEASTVS	GENDVSLDET	SSNASCSTES	QSRPLSNPRD	SYRASSQANK	QKKKTGVMLP
170	180	190	200	210	220	230	240
RVVLTPLKVN	GAHVESASGQ	MKRNRGEEID	FETPGSILVN	TNLRALINSR	TFHALPSHFQ	QQLLFLLPEV	DRQVGTDGLL
250	260	270	280	290	300	310	320
RLSSSALNNE	FFTHAAQSWR	ERLADGEFTH	EMQVRIRQEM	EKEKKVEQWK	EKFFEDYYGQ	KLGLTKEESL	QQNVGQEEAE
330	340	350	360	370	380	390	400
IKSGLCVPGE	SVRIQRGPAT	RQRDGHFKKR	SRPDLRTRAR	RNLYKKQESE	QAGVAKDAKS	VASDVPLYKD	GEAKTDPAGL
410	420	430	440	450	460	470	480
SSPHLPGTSS	AAPDLEGPEF	PVESVASRIQ	AEPDNLARAS	ASPDRIPSLP	QETVDQEPKD	QKRKSFEQAA	SASFPEKKPR
490	500	510	520	530	540	550	560
LEDRQSFRNT	IESVHTEKPQ	PTKEEPKVPP	IRIQLSRIKP	PWVVKGQPTY	QICPRIIPTT	ESSCRGWTGA	RTLADIKARA
570	580	590	600	610	620	630	640
LQVRGARGHH	CHREAATTAI	GGGGGPGGGG	GGATDEGGGR	GSSSGDGGEA	CGHPEPRGGP	STPGKCTSDL	QRTQLLPPYP
650	660	670	680	690	700	710	720
LNGEHTQAGT	AMSRARREDL	PSLRKEESCL	LQRATVGLTD	GLGDASQLPV	APTGDQPCQA	LPLLSSQTSV	AERLVEQPQL
730	740	750	760	770	780	790	800
HPDVRTECES	GTTSWESDDE	EQGPTVPADN	GPIPSLVGDD	TLEKGTGQAL	DSHPTMKDPV	NVTPSSTPES	SPTDCLQNRA
810	820	830	840	850	860	870	880
FDDELGLGGS	CPPMRESDTR	QENLKTKALV	SNSSLHWIPI	PSNDEVVKQP	KPESREHIPS	VEPQVGEEWE	KAAPTPPALP
890	900	910	920	930	940	950	960
GDLTAEEGLD	PLDSLTSLWT	VPSRGGSDSN	GSYCQQVDIE	KLKINGDSEA	LSPHGESTDT	ASDFEGHLTE	DSSEADTREA
970	980	990	1000	1010	1020	1030	1040
AVTKGSSVDK	DEKPNWNQSA	PLSKVNGDMR	LVTRTDGMVA	PQSWVSRVCA	VRQKIPDSLL	LASTEYQPRA	VCLSMPGSSV
1050	1060	1070	1080	1090	1100	1110	1120
EATNPLVMQL	LQGSLPLEKV	LPPAHDDSMS	ESPQVPLTKD	QSHGSLRMGS	LHGLGKNSGM	VDGSSPSSLR	ALKEPLLPDS
1130	1140	1150	1160	1170	1180	1190	1200
CETGTGLARI	EATQAPGAPQ	KNCKAVPSFD	SLHPVTNPIT	SSRKLEEMDS	KEQFSSFSCE	DQKEVRAMSQ	DSNSNAAPGK
1210	1220	1230	1240	1250	1260	1270	1280
SPGDLTTSRT	PRFSSPNVIS	FGPEQTGRAL	GDQSNVTGQG	KKLFGSGNVA	ATLQRPRPAD	PMPLPAEIPP	VFPSGKLGPS
1290	1300	1310	1320	1330	1340	1350	1360
TNSMSGGVQT	PREDWAPKPH	AFVGSVKNEK	TFVGGPLKAN	AENRKATGHS	PLELVGHLEG	MPFVMDLPFW	KLPREPGKGL
1370	1380	1390	1400	1410	1420	1430	1440
SEPLEPSSLP	SQLSIKQAFY	GKLSKLQLSS	TSFNYSSSSP	TFPKGLAGSV	VQLSHKANFG	ASHSASLSLQ	MFTDSSTVES
1450	1460	1470	1480	1490			
ISLQCACSLK	AMIMCQGCGA	FCHDDCIGPS	KLCVLCLVVR				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2381	1	937.9548	9.34	2	58.5	11.6	0	38-55	R.SGTSPLACLNAMLHSNSR.G	Oxidation: 12
2764	2	922.4660	80.47	2	65.9	17.3	0	905-921	R.GGSDSNGSYCQQVDIEK.L	Carbamidomethyl: 10

Detailed Protein Report

Protein 449: PREDICTED: notchless protein homolog 1 isoform X5 [Homo sapiens]

Accession:	gi|578831085	**Score:**	28.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	42.7
Database Date:	2015-11-30	**pI:**	10.1
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.1
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MRAGSCWVPR STCPWTSPRT GCSSCATRYW PRYLASGSGD TTVRFWDLST ETPHFTCKGH RHWVLSISWS PDGRKLASGC
        90        100        110        120        130        140        150        160
KNGQILLWDP STGKQVGRTL AGHSKWITGL SWEPLHANPE CRYVASSSKD GSVRIWDTTA GRCERILTGH TQSVTCLRWG
       170        180        190        200        210        220        230        240
GDGLLYSASQ DRTIKVWRAH DGVLCRTLQG HGHWVNTMAL STDYALRTGA FEPAEASVNP QDLQGSLQEL KERALSRYNL
       250        260        270        280        290        300        310        320
VRGQGPERLV SGSDDFTLFL WSPAEDKKPL TRMTGHQALI NQVLFSPDSR IVASASFDKS IKLWDGRTGK YLASLRGHVA
       330        340        350        360        370        380        390
AVYQIAWSAD SRLLVSGSSD STLKVWDVKA QKLAMDLPGH ADEVYAVDWS PDGQRVASGG KDKCLRM
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2764	1	937.4600	-13.04	2	63.6	12.4	1	143-158	R.CERILTGHTQSVTCLR.W	Carbamidomethyl: 1

Detailed Protein Report

Protein 450: PREDICTED: ryanodine receptor 1 isoform X3 [Homo sapiens]

Accession:	gi|578834746	**Score:**	28.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	563.6
Database Date:	2015-11-30	**pI:**	5.1
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	0.6
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MGDAEGEDEV QFLRTDDEVV LQCSATVLKE QLKLCLAAEG FGNRLCFLEP TSNAQNVPPD LAICCFVLEQ SLSVRALQEM

        90        100        110        120        130        140        150        160
LANTVEAGVE SSQGGGHRTL LYGHAILLRH AHSRMYLSCL TTSRSMTDKL AFDVGLQEDA TGEACWWTMH PASKQRSEGE

       170        180        190        200        210        220        230        240
KVRVGDDIIL VSVSSERYLH LSTASGELQV DASFMQTLWN MNPICSRCEE GFVTGGHVLR LFHGHMDECL TISPADSDDQ

       250        260        270        280        290        300        310        320
RRLVYYEGGA VCTHARSLWR LEPLRISWSG SHLRWGQPLR VRHVTTGQYL ALTEDQGLVV VDASKAHTKA TSFCFRISKE

       330        340        350        360        370        380        390        400
KLDVAPKRDV EGMGPPEIKY GESLCFVQHV ASGLWLTYAA PDPKALRLGV LKKKAMLHQE GHMDDALSLT RCQQEESQAA

       410        420        430        440        450        460        470        480
RMIHSTNGLY NQFIKSLDSF SGKPRGSGPP AGTALPIEGV ILSLQDLIIY FEPPSEDLQH EEKQSKLRSL RNRQSLFQEE

       490        500        510        520        530        540        550        560
GMLSMVLNCI DRLNVYTTAA HFAEFAGEEA AESWKEIVNL LYELLASLIR GNRSNCALFS TNLDWLVSKL DRLEASSGIL

       570        580        590        600        610        620        630        640
EVLYCVLIES PEVLNIIQEN HIKSIISLLD KHGRNHKVLD VLCSLCVCNG VAVRSNQDLI TENLLPGREL LLQTNLINYV

       650        660        670        680        690        700        710        720
TSIRPNIFVG RAEGTTQYSK WYFEVMVDEV TPFLTAQATH LRVGWALTEG YTPYPGAGEG WGGNGVGDDL YSYGFDGLHL

       730        740        750        760        770        780        790        800
WTGHVARPVT SPGQHLLAPE DVISCCLDLS VPSISFRING CPVQGVFESF NLDGLFFPVV SFSAGVKVRF LLGGRHGEFK

       810        820        830        840        850        860        870        880
FLPPPGYAPC HEAVLPRERL HLEPIKEYRR EGPRGPHLVG PSRCLSHTDF VPCPVDTVQI VLPPHLERIR EKLAENIHEL

       890        900        910        920        930        940        950        960
WALTRIEQGW TYGPVRDDNK RLHPCLVDFH SLPEPERNYN LQMSGETLKT LLALGCHVGM ADEKAEDNLK KTKLPKTYMM

       970        980        990       1000       1010       1020       1030       1040
SNGYKPAPLD LSHVRLTPAQ TTLVDRLAEN GHNVWARDRV GQGWSYSAVQ DIPARRNPRL VPYRLLDEAT KRSNRDSLCQ

      1050       1060       1070       1080       1090       1100       1110       1120
AVRTLLGYGY NIEPPDQEPS QVENQSRCDR VRIFRAEKSY TVQSGRWYFE FEAVTTGEMR VGWARPELRP DVELGADELA

      1130       1140       1150       1160       1170       1180       1190       1200
YVFNGHRGQR WHLGSEPFGR PWQPGDVVGC MIDLTENTII FTLNGEVLMS DSGSETAFRE IEIGDGFLPV CSLGPGQVGH

      1210       1220       1230       1240       1250       1260       1270       1280
LNLGQDVSSL RFFAICGLQE GFEPFAINMQ RPVTTWFSKG LPQFEPVPLE HPHYEVSRVD GTVDTPPCLR LTHRTWGSQN

      1290       1300       1310       1320       1330       1340       1350       1360
SLVEMLFLRL SLPVQFHQHF RCTAGATPLA PPGLQPPAED EARAAEPDPD YENLRRSAGG WSEAENGKEG TAKEGAPGGT

      1370       1380       1390       1400       1410       1420       1430       1440
PQAGGEAQPA RAENEKDATT EKNKKRGFLF KAKKVAMMTQ PPATPTLPRL PHDVVPADNR DDPEIILNTT TYYYSVRVFA

      1450       1460       1470       1480       1490       1500       1510       1520
GQEPSCVWAG WVTPDYHQHD MSFDLSKVRV VTVTMGDEQG NVHSSLKCSN CYMVWGGDFV SPGQQGRISH TDLVIGCLVD

      1530       1540       1550       1560       1570       1580       1590       1600
LATGLMTFTA NGKESNTFFQ VEPNTKLFPA VFVLPTHQNV IQFELGKQKN IMPLSAAMFQ SERKNPAPQC PPRLEMQMLM

      1610       1620       1630       1640       1650       1660       1670       1680
PVSWSRMPNH FLQVETRRAG ERLGWAVQCQ EPLTMMALHI PEENRCMDIL ELSERLDLQR FHSHTLRLYR AVCALGNNRV

      1690       1700       1710       1720       1730       1740       1750       1760
AHALCSHVDQ AQLLHALEDA HLPGPLRAGY YDLLISIHLE SACRSRRSML SEYIVPLTPE TRAITLFPPG RSTENGHPRH

      1770       1780       1790       1800       1810       1820       1830       1840
GLPGVGVTTS LRPPHHFSPP CFVAALPAAG AAEAPARLSP AIPLEALRDK ALRMLGEAVR DGGQHARDPV GGSVEFQFVP

      1850       1860       1870       1880       1890       1900       1910       1920
VLKLVSTLLV MGIFGDEDVK QILKMIEPEV FTEEEEEEDE EEEGEEEDEE EKEEDEEETA QEKEDEEKEE EEAAEGEKEE

      1930       1940       1950       1960       1970       1980       1990       2000
GLEEGLLQMK LPESVKLQMC HLLEYFCDQE LQHRVESLAA FAERYVDKLQ ANQRSRYGLL IKAFSMTAAE TARRTREFRS

      2010       2020       2030       2040       2050       2060       2070       2080
PPQEQINMLL QFKDGTDEED CPLPEEIRQD LLDFHQDLLA HCGIQLDGEE EEPEEETTLG SRLMSLLEKV RLVKKKEEKP

      2090       2100       2110       2120       2130       2140       2150       2160
EEERSAEESK PRSLQELVSH MVVRWAQEDF VQSPELVRAM FSLLHRQYDG LGELLRALPR AYTISPSSVE DTMSLLECLG

      2170       2180       2190       2200       2210       2220       2230       2240
```

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2128	1	1051.4436	-85.59	2	55.2	12.7	1	901-917	K.RLHPCLVDFHSLPEPER.N	Carbamidomethyl: 5

Detailed Protein Report

Protein 451: PREDICTED: protein TBATA isoform X13 [Homo sapiens]

Accession:	gi|578819092	**Score:**	28.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	35.1
Database Date:	2015-11-30	**pI:**	6.4
		Sequence Coverage [%]:	9.2
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MGIPTISVPI GDPQSNRNPQ LSSAWKKELK ELASRVAFLT KEDELKKKED TTSLNWNCKS RRPQAPGLSG TDLGAAELGI
        90        100        110        120        130        140        150        160
KKEQKEEPLR EQGAKYSAET GRLIPASTRA VGRRSHQGQ QSQSSSRHEG VQAFLLQDQE LLVLELLCRI LETDLLSAIQ
       170        180        190        200        210        220        230        240
FWLLYAPPKE KDLALGLLQT AVAQLLPQPL VSIPTEKLLS QLPEVHEPPQ EKQEPPCRWA PHPALPFCSL LSSQSIPEEN
       250        260        270        280        290        300        310        320
EDITFYKKRK TRVHWRSSSP PDAFKPEHRE EDIEAEGREL RGPNTCTCLA QEQPQGFRGV SVSTTFTAVP DSLP
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2340	2	953.1627	151.14	2	57.7	17.7	2	96-113	K.YSAETGRLIPASTRAVGR.R	

Detailed Protein Report

Protein 452: PREDICTED: eukaryotic translation initiation factor 5B isoform X1 [Homo sapiens]

Accession:	gi|530368915	**Score:**	28.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	138.6
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
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 453: zinc finger protein 581 [Homo sapiens]

Accession:	gi|7705495	**Score:**	28.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	22.0
Database Date:	2015-11-30	**pI:**	10.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	13.7
		No. of unique Peptides:	2

Alias proteins:

Accession	Name	Description
gi|578834534	refseq_human (refseq_human_20140103.fasta)	PREDICTED: zinc finger protein 581 isoform X1 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MLVLPSPCPQ PLAFSSVETM EGPPRRTCRS PEPGPSSSIG SPQASSPPRP NHYLLIDTQG VPYTVLVDEE SQREPGASGA
        90        100        110        120        130        140        150        160
PGQKKCYSCP VCSRVFEYMS YLQRHSITHS EVKPFECDIC GKAFKRASHL ARHHSIHLAG GGRPHGCPLC PRRFRDAGEL
       170        180        190        200
AQHSRVHSGE RPFQCPHCPR RFMEQNTLQK HTRWKHP
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1072	2	984.1823	6.75	3	42.1	11.2	2	127-153	R.ASHLARHHSIHLAGGGRPHGCPLCPRR.F	Carbamidomethyl: 24
1056	2	984.2136	38.53	3	41.9	17.6	2	127-153	R.ASHLARHHSIHLAGGGRPHGCPLCPRR.F	Carbamidomethyl: 21

Detailed Protein Report

Protein 454: follistatin-related protein 1 precursor [Homo sapiens]

Accession:	gi|5901956	**Score:**	28.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	35.0
Database Date:	2015-11-30	**pI:**	5.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	8.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MWKRWLALAL	ALVAVAWVRA	EEELRSKSKI	CANVFCGAGR	ECAVTEKGEP	TCLCIEQCKP	HKRPVCGSNG	KTYLNHCELH
90	100	110	120	130	140	150	160
RDACLTGSKI	QVDYDGHCKE	KKSVSPSASP	VVCYQSNRDE	LRRRIIQWLE	AEIIPDGWFS	KGSNYSEILD	KYFKNFDNGD
170	180	190	200	210	220	230	240
SRLDSSEFLK	FVEQNETAIN	ITTYPDQENN	KLLRGLCVDA	LIELSDENAD	WKLSFQEFLK	CLNPSFNPPE	KKCALEDETY
250	260	270	280	290	300	310	
ADGAETEVDC	NRCVCACGNW	VCTAMTCDGK	NQKGAQTQTE	EEMTRYVQEL	QKHQETAEKT	KRVSTKEI	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2625	1	671.8235	5.72	2	61.5	11.9	0	72-81	K.TYLNHCELHR.D	Carbamidomethyl: 6

Detailed Protein Report

Protein 455: tyrosine-protein kinase TXK [Homo sapiens]

Accession:	gi|148596974	**Score:**	28.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	61.2
Database Date:	2015-11-30	**pI:**	9.1
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	6.5
		No. of unique Peptides:	2

Quantitation

mdown:qdown	**Median:**	0.34	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	1.88	**CV:**	171.26 %	**No. of Peptides:**	2

10	20	30	40	50	60	70	80
MILSSYNTIQ	SVFCCCCCCS	VQKRQMRTQI	SLSTDEELPE	KYTQRRRPWL	SQLSNKKQSN	TGRVQPSKRK	PLPPLPPSEV
90	100	110	120	130	140	150	160
AEEKIQVKAL	YDFLPREPCN	LALRRAEEYL	ILEKYNPHWW	KARDRLGNEG	LIPSNYVTEN	KITNLEIYEW	YHRNITRNQA
170	180	190	200	210	220	230	240
EHLLRQESKE	GAFIVRDSRH	LGSYTISVFM	GARRSTEAAI	KHYQIKKNDS	GQWYVAERHA	FQSIPELIWY	HQHNAAGLMT
250	260	270	280	290	300	310	320
RLRYPVGLMG	SCLPATAGFS	YEKWEIDPSE	LAFIKEIGSG	QFGVVHLGEW	RSHIQVAIKA	INEGSMSEED	FIEEAKVMMK
330	340	350	360	370	380	390	400
LSHSKLVQLY	GVCIQRKPLY	IVTEFMENGC	LLNYLRENKG	KLRKEMLLSV	CQDICEGMEY	LERNGYIHRD	LAARNCLVSS
410	420	430	440	450	460	470	480
TCIVKISDFG	MTRYVLDDEY	VSSFGAKFPI	KWSPPEVFLF	NKYSSKSDVW	SFGVLMWEVF	TEGKMPFENK	SNLQVVEAIS
490	500	510	520	530			
EGFRLYRPHL	APMSIYEVMY	SCWHEKPEGR	PTFAELLRAV	TEIAETW			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
169	1	898.4349	69.51	3	31.3	11.6	0	1-23	-.MILSSYNTIQSVFCCCCCCSVQK.R	Carbamidomethyl: 14, 15; Oxidation: 1	Wdown:Qdown 0.58
866	2	583.6973	-174.23	2	40.3	17.2	0	395-405	R.NCLVSSTCIVK.I		Wdown:Qdown 6.04 mdown:qdown 0.34

Detailed Protein Report

Protein 456: ATP-sensitive inward rectifier potassium channel 1 isoform a [Homo sapiens]

Accession:	gi|4504837	**Score:**	28.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	44.8
Database Date:	2015-11-30	**pI:**	9.9
Modification(s):	Oxidation	**Sequence Coverage [%]:**	9.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MNASSRNVFD	TLIRVLTESM	FKHLRKWVVT	RFFGHSRQRA	RLVSKDGRCN	IEFGNVEAQS	RFIFFVDIWT	TVLDLKWRYK
90	100	110	120	130	140	150	160
MTIFITAFLG	SWFFFGLLWY	AVAYIHKDLP	EFHPSANHTP	CVENINGLTS	AFLFSLETQV	TIGYGFRCVT	EQCATAIFLL
170	180	190	200	210	220	230	240
IFQSILGVII	NSFMCGAILA	KISRPKKRAK	TITFSKNAVI	SKRGGKLCLL	IRVANLRKSL	LIGSHIYGKL	LKTTVTPEGE
250	260	270	280	290	300	310	320
TIILDQININ	FVVDAGNENL	FFISPLTIYH	VIDHNSPFFH	MAAETLLQQD	FELVVFLDGT	VESTSATCQV	RTSYVPEEVL
330	340	350	360	370	380	390	400
WGYRFAPIVS	KTKEGKYRVD	FHNFSKTVEV	ETPHCAMCLY	NEKDVRARMK	RGYDNPNFIL	SEVNETDDTK	M

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2895	1	859.1037	-1.61	3	65.4	17.8	2	1-22	-.MNASSRNVFDTLIRVLTESMFK.H	Oxidation: 20

Detailed Protein Report

Protein 457: 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

Quantitation

mdown:qdown **Median:** 0.60 **CV:** 0.00 % **No. of 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						

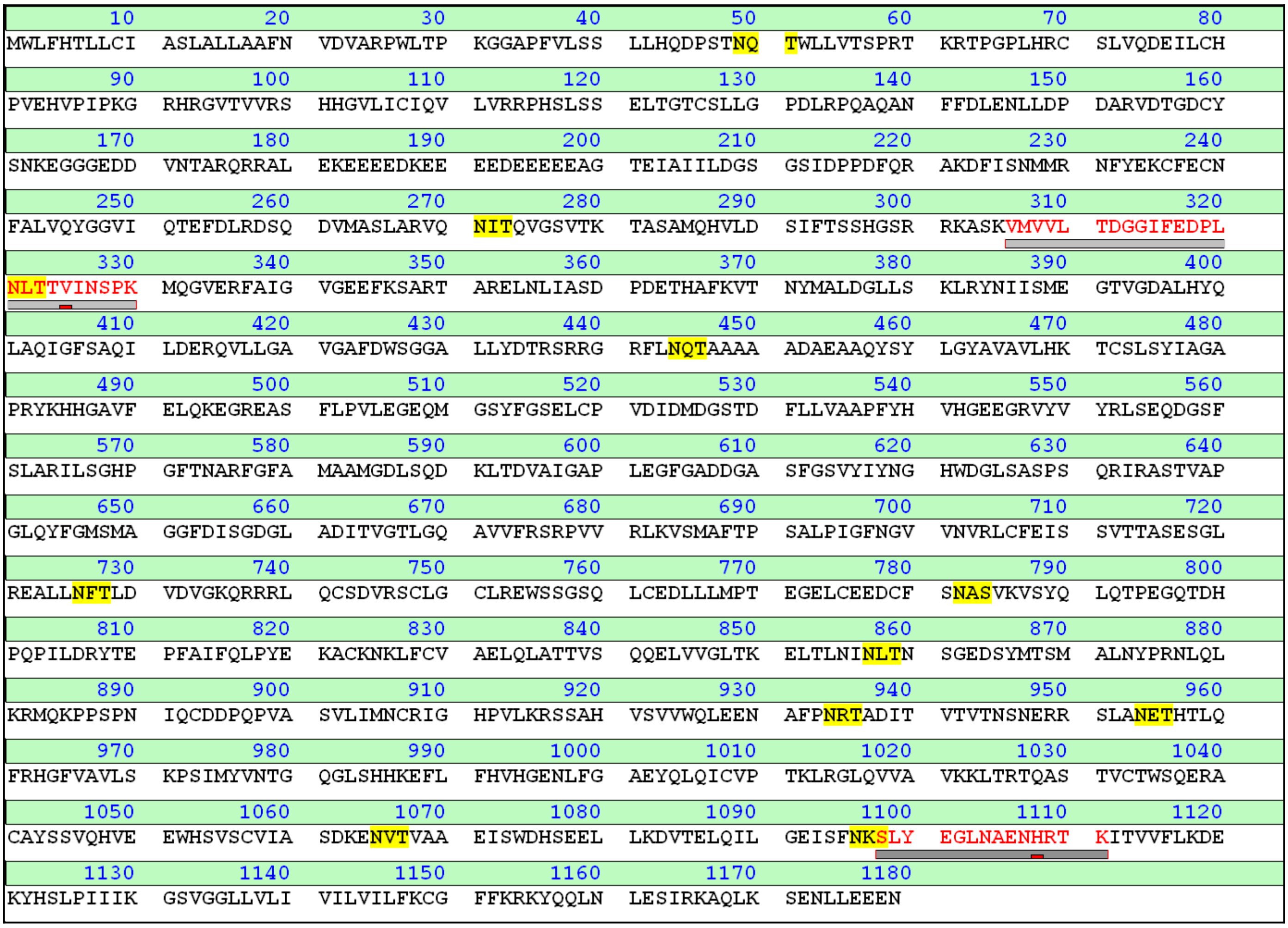
Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1490	1	977.1102	85.91	2	48.4	10.9	1	774-789	K.DWLQDGNHLFRILGLR.G		mdown:qdown 0.60

Detailed Protein Report

Protein 458: integrin alpha-E precursor [Homo sapiens]

Accession: gi|148728188
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 28.6
MW [kDa]: 130.1
pI: 5.4
Sequence Coverage [%]: 3.3
No. of unique Peptides: 2



10	20	30	40	50	60	70	80
MWLFHTLLCI	ASLALLAAFN	VDVARPWLTP	KGGAPFVLSS	LLHQDPSTNQ	TWLLVTSPRT	KRTPGPLHRC	SLVQDEILCH
90	100	110	120	130	140	150	160
PVEHVPIPKG	RHRGVTVVRS	HHGVLICIQV	LVRRPHSLSS	ELTGTCSLLG	PDLRPQAQAN	FFDLENLLDP	DARVDTGDCY
170	180	190	200	210	220	230	240
SNKEGGGEDD	VNTARQRRAL	EKEEEEDKEE	EEDEEEEEAG	TEIAIILDGS	GSIDPPDFQR	AKDFISNMMR	NFYEKCFECN
250	260	270	280	290	300	310	320
FALVQYGGVI	QTEFDLRDSQ	DVMASLARVQ	NITQVGSVTK	TASAMQHVLD	SIFTSSHGSR	RKASKVMVVL	TDGGIFEDPL
330	340	350	360	370	380	390	400
NLTTVINSPK	MQGVERFAIG	VGEEFKSART	ARELNLIASD	PDETHAFKVT	NYMALDGLLS	KLRYNIISME	GTVGDALHYQ
410	420	430	440	450	460	470	480
LAQIGFSAQI	LDERQVLLGA	VGAFDWSGGA	LLYDTRSRRG	RFLNQTAAAA	ADAEAAQYSY	LGYAVAVLHK	TCSLSYIAGA
490	500	510	520	530	540	550	560
PRYKHHGAVF	ELQKEGREAS	FLPVLEGEQM	GSYFGSELCP	VDIDMDGSTD	FLLVAAPFYH	VHGEEGRVYV	YRLSEQDGSF
570	580	590	600	610	620	630	640
SLARILSGHP	GFTNARFGFA	MAAMGDLSQD	KLTDVAIGAP	LEGFGADDGA	SFGSVYIYNG	HWDGLSASPS	QRIRASTVAP
650	660	670	680	690	700	710	720
GLQYFGMSMA	GGFDISGDGL	ADITVGTLGQ	AVVFRSRPVV	RLKVSMAFTP	SALPIGFNGV	VNVRLCFEIS	SVTTASESGL
730	740	750	760	770	780	790	800
REALLNFTLD	VDVGKQRRRL	QCSDVRSCLG	CLREWSSGSQ	LCEDLLLMPT	EGELCEEDCF	SNASVKVSYQ	LQTPEGQTDH
810	820	830	840	850	860	870	880
PQPILDRYTE	PFAIFQLPYE	KACKNKLFCV	AELQLATTVS	QQELVVGLTK	ELTLNINLTN	SGEDSYMTSM	ALNYPRNLQL
890	900	910	920	930	940	950	960
KRMQKPPSPN	IQCDDPQPVA	SVLIMNCRIG	HPVLKRSSAH	VSVVWQLEEN	AFPNRTADIT	VTVTNSNERR	SLANETHTLQ
970	980	990	1000	1010	1020	1030	1040
FRHGFVAVLS	KPSIMYVNTG	QGLSHHKEFL	FHVHGENLFG	AEYQLQICVP	TKLRGLQVVA	VKKLTRTQAS	TVCTWSQERA
1050	1060	1070	1080	1090	1100	1110	1120
CAYSSVQHVE	EWHSVSCVIA	SDKENVTVAA	EISWDHSEEL	LKDVTELQIL	GEISFNKSLY	EGLNAENHRT	KITVVFLKDE
1130	1140	1150	1160	1170	1180		
KYHSLPIIIK	GSVGGLLVLI	VILVILFKCG	FFKRKYQQLN	LESIRKAQLK	SENLLEEEN		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1655	1	896.8887	87.41	3	49.2	13.3	0	306-330	K.VMVVLTDGGIFEDPLNLTTVINSPK.M	Oxidation: 2
2277	1	816.2926	-144.34	2	58.7	15.3	1	1098-1111	K.SLYEGLNAENHRTK.I	

Detailed Protein Report

Protein 459: 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	

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Detailed Protein Report

Protein 460: LIM domain only protein 3 isoform 1 [Homo sapiens]

Accession:	gi|21361802	**Score:**	28.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	16.6
Database Date:	2015-11-30	**pI:**	9.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	26.2
		No. of unique Peptides:	2

Quantitation

Wdown:Qdown	**Median:**	1.61	**CV:**	0.00 %	**No. of Peptides:**	1

Alias proteins:

Accession	Name	Description
gi|578822949	refseq_human(refseq_human_20140103.fasta)	PREDICTED: LIM domain only protein 3 isoform X2 [Homo sapiens]
gi|578822947	refseq_human(refseq_human_20140103.fasta)	PREDICTED: LIM domain only protein 3 isoform X1 [Homo sapiens]
gi|343790979	refseq_human(refseq_human_20140103.fasta)	LIM domain only protein 3 isoform 1 [Homo sapiens]
gi|343790975	refseq_human(refseq_human_20140103.fasta)	LIM domain only protein 3 isoform 1 [Homo sapiens]
gi|47778935	refseq_human(refseq_human_20140103.fasta)	LIM domain only protein 3 isoform 1 [Homo sapiens]

10	20	30	40	50	60	70	80
MLSVQPDTKP	KGCAGCNRKI	KDRYLLKALD	KYWHEDCLKC	ACCDCRLGEV	GSTLYTKANL	ILCRRDYLRL	FGVTGNCAAC
90	100	110	120	130	140	150	
SKLIPAFEMV	MRAKDNVYHL	DCFACQLCNQ	RFCVGDKFFL	KNNMILCQTD	YEEGLMKEGY	APQVR	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2251	1	952.9306	80.50	2	56.8	15.2	1	32-46	K.YWHEDCLKCACCDCR.L	Carbamidomethyl: 14	
459	1	820.1336	71.06	3	35.1	13.3	1	70-92	R.LFGVTGNCAACSKLIPAFEMVMR.A		Wdown:Qdown 1.61

Detailed Protein Report

Protein 461: PREDICTED: protein ELYS isoform X2 [Homo sapiens]

Accession:	gi|578802192	**Score:**	28.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	252.3
Database Date:	2015-11-30	**pI:**	6.2
		Sequence Coverage [%]:	1.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
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					

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2789	1	735.0657	-23.60	3	66.4	12.6	2	1010-1028	R.KLAIERAKPYHLSTSSVFR.L	

Detailed Protein Report

Protein 462: ephrin type-A receptor 6 isoform a [Homo sapiens]

Accession:	gi|145312251	**Score:**	28.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	126.5
Database Date:	2015-11-30	**pI:**	6.5
		Sequence Coverage [%]:	2.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MQFPSPPAAR	SSPAPQAASS	SEAAAPATGQ	PGPSCPVPGT	SRRGRPGTPP	AGRVEEEEEE	EEEDVDKDPH	PTQNTCLRCR
90	100	110	120	130	140	150	160
HFSLRERKRE	PRRTMGGCEV	REFLLQFGFF	LPLLTAWPGD	CSHVSNNQVV	LLDTTTVLGE	LGWKTYPLNG	WDAITEMDEH
170	180	190	200	210	220	230	240
NRPIHTYQVC	NVMEPNQNNW	LRTNWISRDA	AQKIYVEMKF	TLRDCNSIPW	VLGTCKETFN	LFYMESDESH	GIKFKPNQYT
250	260	270	280	290	300	310	320
KIDTIAADES	FTQMDLGDRI	LKLNTEIREV	GPIERKGFYL	AFQDIGACIA	LVSVRVFYKK	CPFTVRNLAM	FPDTIPRVDS
330	340	350	360	370	380	390	400
SSLVEVRGSC	VKSAEERDTP	KLYCGADGDW	LVPLGRCICS	TGYEEIEGSC	HACRPGFYKA	FAGNTKCSKC	PPHSLTYMEA
410	420	430	440	450	460	470	480
TSVCQCEKGY	FRAEKDPPSM	ACTRPPSAPR	NVVFNINETA	LILEWSPPSD	TGGRKDLTYS	VICKKCGLDT	SQCEDCGGGL
490	500	510	520	530	540	550	560
RFIPRHTGLI	NNSVIVLDFV	SHVNYTFEIE	AMNGVSELSF	SPKPFTAITV	TTDQDAPSLI	GVVRKDWASQ	NSIALSWQAP
570	580	590	600	610	620	630	640
AFSNGAILDY	EIKYYEKEHE	QLTYSSTRSK	APSVIITGLK	PATKYVFHIR	VRTATGYSGY	SQKFEFETGD	ETSDMAAEQG
650	660	670	680	690	700	710	720
QILVIATAAV	GGFTLLVILT	LFFLITGRCQ	WYIKAKMKSE	EKRRNHLQNG	HLRFPGIKTY	IDPDTYEDPS	LAVHEFAKEI
730	740	750	760	770	780	790	800
DPSRIRIERV	IGAGEFGEVC	SGRLKTPGKR	EIPVAIKTLK	GGHMDRQRRD	FLREASIMGQ	FDHPNIIRLE	GVVTKRSFPA
810	820	830	840	850	860	870	880
IGVEAFCPSF	LRAGFLNSIQ	APHPVPGGGS	LPPRIPAGRP	VMIVVEYMEN	GSLDSFLRKH	DGHFTVIQLV	GMLRGIASGM
890	900	910	920	930	940	950	960
KYLSDMGYVH	RDLAARNILV	NSNLVCKVSD	FGLSRVLEDD	PEAAYTTTGG	KIPIRWTAPE	AIAYRKFSSA	SDAWSYGIVM
970	980	990	1000	1010	1020	1030	1040
WEVMSYGERP	YWEMSNQDVI	LSIEEGYRLP	APMGCPASLH	QLMLHCWQKE	RNHRPKFTDI	VSFLDKLIRN	PSALHTLVED
1050	1060	1070	1080	1090	1100	1110	1120
ILVMPESPGE	VPEYPLFVTV	GDWLDSIKMG	QYKNNFVAAG	FTTFDLISRM	SIDDIRRIGV	ILIGHQRRIV	SSIQTLRLHM
1130	1140						
MHIQEKGFHV							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2727	2	698.3840	-68.94	2	63.0	12.0	0	591-604	K.APSVIITGLKPATK.Y	

Detailed Protein Report

Protein 463: PREDICTED: ankyrin repeat domain-containing protein 24 isoform X6 [Homo sapiens]

Accession:	gi|578833058	**Score:**	28.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	121.1
Database Date:	2015-11-30	**pI:**	4.8
		Sequence Coverage [%]:	2.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MKTLRARFKK	TESQDWGKSD	ERLLQAVENN	DAPRVAALIA	RKGLVPTKLD	PEGKSAFHLA	AMRGAASCLE	VMIAHGSNVM
90	100	110	120	130	140	150	160
SADGAGYNAL	HLAAKYGHPQ	CLKQLLQASC	VVDVVDSSGW	TALHHAAAGG	CLSCSEVLCS	FKAHLNPQDR	SGATPLIIAA
170	180	190	200	210	220	230	240
QMCHTDLCRL	LLQQGAAAND	QDLQGRTALM	LACEGASPET	VEVLLQGGAQ	PGITDALGQD	AAHYGALAGD	KLILHLLQEA
250	260	270	280	290	300	310	320
AQRPSPPSAL	TEDDSGEASS	QNSMSSHGKQ	GAPKKRKAPP	PPASIPMPDD	RDAYEEIVRL	RQERGRLLQK	IRGLEQHKER
330	340	350	360	370	380	390	400
RQQESPEASS	LHILERQVQE	LQQLLVERQE	EKESLGREVE	SLQSRLSLLE	NERENTSYDV	TTLQDEEGEL	PDLPGAEVLL
410	420	430	440	450	460	470	480
SRQLSPSAQE	HLASLQEQVA	VLTRQNQELM	EKVQILENFE	KDETQMEVEA	LAEVIPLALY	DSLRAEFDQL	RRQHAEALQA
490	500	510	520	530	540	550	560
LRQQETREVP	REEGAACGES	EVAGATATKN	GPTHMELNGS	VAPETKVNGA	ETIDEEAAGD	ETMEARTMEA	EATGAEATGA
570	580	590	600	610	620	630	640
EATGAKVTET	KPTGAEVREM	ETTEEEANME	TKPTGAQATD	TETTGVEAMG	VEATKTKAEE	AEMQAYGVGA	GQAEPPVTGT
650	660	670	680	690	700	710	720
TNMEATGSRA	TGMESTGVSA	TGVENPGVEA	TVPGISAGPI	LHPGAAEASE	KLQVELETRI	RGLEEALRQR	EREAAAELEA
730	740	750	760	770	780	790	800
ALGKCEAAEA	EAGRLRERVR	EAEGSGASGG	GGGDTTQLRA	ALEQAREDLR	DRDSRLRELE	AASACLDEAR	ASRLLAEEEA
810	820	830	840	850	860	870	880
RGLRAELAQR	EEARLEQSRE	LEVLREQLAT	ARATGEQQRT	AAAELGRARD	AAEARVAELP	AACEEARQGL	AELREASEAL
890	900	910	920	930	940	950	960
RQSVVPASEH	RRLQEEALEL	RGRAASLEQE	VVATGKEAAR	LRAELERERV	CSVALSEHER	IVGTLQANVA	QLEGQLEELG
970	980	990	1000	1010	1020	1030	1040
RRHEKTSAEV	FQVQREALFM	KSERHAAEAQ	LATAEQQLRG	LRTEAERARQ	AQSRAQEALD	KAKEKDKKIT	ELSKEVFNLK
1050	1060	1070	1080	1090	1100	1110	1120
EALKEQPAAL	ATPEVEALRD	QVKDLQQQLQ	EAARDHSSVV	ALYRSHLLYA	IQGQMDEDVQ	RILSQILQMQ	RLQAQGR

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1938	1	780.7925	-113.31	2	52.9	10.6	2	725-738	K.CEAAEAEAGRLRER.V	

Detailed Protein Report

Protein 464: **PREDICTED: contactin-associated protein-like 3B isoform X6 [Homo sapiens]**

Accession:	gi|578816699	**Score:**	28.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	127.3
Database Date:	2015-11-30	**pI:**	9.3
		Sequence Coverage [%]:	3.0
		No. of unique Peptides:	2

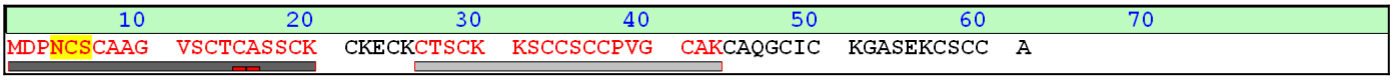
10	20	30	40	50	60	70	80
MASVAWAVLK	VLLLLPTQTW	SPVGAGNPPD	CDSPLASALP	RSSFSSSSEL	SSSHGPGFSR	LNRRDGAGGW	TPLVSNKYQW
90	100	110	120	130	140	150	160
LQIDLGERME	VTAVATQGGY	GSSDWVTSYL	LMFSDGGRNW	KQYRREESIW	GFPGNTNADS	VVHYRLQPPF	EARFLRFLPL
170	180	190	200	210	220	230	240
AWNPRGRIGM	RIEVYGCAYK	SEVVYFDGQS	ALLYTLDKKP	LKPIRDVISL	KFKAMQSNGI	LLHREGQHGN	HITLELIKGK
250	260	270	280	290	300	310	320
LVFFLNSGNA	KLPSTIAPVT	LTLGSLLDDQ	HWHSVLIELL	DTQVNFTVDK	HTHHFQAKGD	SSNLDLNFEI	SFGGILSPGR
330	340	350	360	370	380	390	400
SRAFTRKSFH	GCLENLYYNG	VDVTELAKKH	KPQILMMGNV	SFSCPQPQTV	PVTFLSSRSY	LALPGNSGED	KVSVTFQFRT
410	420	430	440	450	460	470	480
WNRAGHLLFG	ELQRGSGSFV	LFLKDGKLKL	SLFQAGQSPR	NVTAGAGLND	GQWHSVSFSA	KWSHMNVVVD	DDTAVQPLVA
490	500	510	520	530	540	550	560
VLIDSGDTYY	FGDSAWTVVR	HGGPDAVTLR	GAPSGHPLSA	VSFAYAAGAG	QLRAAVNLAE	RCEQRLALRC	GTARRPDSRD
570	580	590	600	610	620	630	640
GTPLSWWVGR	TNETHTSWGG	SLPDAQKCTC	GLEGNCIDSQ	YYCNCDAGQN	EWTSDTIVLS	QKEHLPVTQI	VMTDTGQPHS
650	660	670	680	690	700	710	720
EADYTLGPLL	CRGDKSFWNS	ASFNTETSYL	HFPAFHGELT	ADVCFFFKTT	VSSGVFMENL	GITDFIRIEL	RGRLATLDKS
730	740	750	760	770	780	790	800
QAPTEVTFSF	DVGNGPCEVT	VQSPTPFNDN	QWHHVRAERN	VKGASLQVDQ	LPQKMQPAPA	DGHVRLQLNS	QLFIGGTATR
810	820	830	840	850	860	870	880
QRGFLGCIRS	LQLNGVALDL	EERATVTPGV	EPGCAGHCST	YGHLCRNGGR	CREKRRGVTC	DCAFSAYDGP	FCSNEISAYF
890	900	910	920	930	940	950	960
ATGSSMTYHF	QEHYTLSENS	SSLVSSLHRD	VTLTREMITL	SFRTTRTPSL	LLYVSSFYEE	YLSVILANNG	SLQIRYKLDR
970	980	990	1000	1010	1020	1030	1040
HQNPDAFTFD	FKNMADGQLH	QVKINREEAV	VMVEVNQSAK	KQVILSSGTE	FNAVKSLILG	KVLEAAGADP	DTRRAATSGF
1050	1060	1070	1080	1090	1100	1110	1120
TGCLSAVRFG	CAAPLKAALR	PSGPSRVTVR	GHVAPMARCA	AGAASGSPAR	ELAPRLAGGA	GRSGPVDEGE	PLVNADRRDS
1130	1140	1150	1160	1170			
AVIGGVIAVE	IFILLCITAI	AIRIYQQRKL	RKENESKVSK	KEEC			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1888	1	899.4768	-2.42	2	52.3	14.7	1	400-414	R.TWNRAGHLLFGELQR.G	
1567	1	919.5953	159.08	2	49.4	13.7	1	1071-1090	R.GHVAPMARCAAGAASGSPAR.E	

Detailed Protein Report

Protein 465: metallothionein-1G [Homo sapiens]

Accession:	gi|10835230	**Score:**	28.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	6.1
Database Date:	2015-11-30	**pI:**	10.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	62.3
		No. of unique Peptides:	2



```
         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

Detailed Protein Report

Protein 466: mediator of RNA polymerase II transcription subunit 24 isoform 2 [Homo sapiens]

Accession: gi|119220575
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 28.3
MW [kDa]: 108.9
pI: 6.5
Sequence Coverage [%]: 2.3
No. of unique Peptides: 1

Alias proteins:

Accession	Name	Description
gi|392583926	refseq_huma (refseq_human_20140103.fasta)	mediator of RNA polymerase II transcription subunit 24 isoform 2 [Homo sapiens]

10	20	30	40	50	60	70	80
MKVVNLKQAI	LQAWKERWSD	YQWAINMKKF	FPKGATWDIL	NLADALLEQA	MIGPSPNPLI	LSYLKYAISS	QFDDFSRDLC
90	100	110	120	130	140	150	160
VQALLDIMDM	FCDRLSCHGK	AEECIGLCRA	LLSALHWLLR	CTAASAERLR	EGLEAGTPAA	GEKQLAMCLQ	RLEKTLSSTK
170	180	190	200	210	220	230	240
NRALLHIAKL	EEASSWTAIE	HSLLKLGEIL	ANLSNPQLRS	QAEQCGTLIR	SIPTMLSVHA	EQMHKTGFPT	VHAVILLEGT
250	260	270	280	290	300	310	320
MNLTGETQSL	VEQLTMVKRM	QHIPTPLFVL	EIWKACFVGL	IESPEGTEEL	KWTAFTFLKI	PQVLVKLKKY	SHGDKDFTED
330	340	350	360	370	380	390	400
VNCAFEFLLK	LTPLLDKADQ	RCNCDCTNFL	LQECGKQGLL	SEASVNNLMA	KRKADREHAP	QQKSGENANI	QPNIQLILRA
410	420	430	440	450	460	470	480
EPTVTNILKT	MDADHSKSPE	GLLGVLGHML	SGKSLDLLLA	AAAATGKLKS	FARKFINLNE	FTTYGSEEST	KPASVRALLF
490	500	510	520	530	540	550	560
DISFLMLCHV	AQTYGSEVIL	SESRTGAEVP	FFETWMQTCM	PEEGKILNPD	HPCFRPDSTK	VESLVALLNN	SSEMKLVQMK
570	580	590	600	610	620	630	640
WHEACLSISA	AILEILNAWE	NGVLAFESIQ	KITDNIKGKV	CSLAVCAVAW	LVAHVRMLGL	DEREKSLQMI	RQLAGPLFSE
650	660	670	680	690	700	710	720
NTLQFYNERV	VIMNSILERM	CADVLQQTAT	QIKFPSTGVD	TMPYWNLLPP	KRPIKEVLTD	IFAKVLEKGW	VDSRSIHIFD
730	740	750	760	770	780	790	800
TLLHMGGVYW	FCNNLIKELL	KETRKEHTLR	AVELLYSIFC	LDMQQVTLVL	LGHILPGLLT	DSSKWHSLMD	PPGTALAKLA
810	820	830	840	850	860	870	880
VWCALSSYSS	HKGQASTRQK	KRHREDIEDY	ISLFPLDDVQ	PSKLMRLLSS	NEDDANILSS	PTDRSMSSSL	SASQLHTVNM
890	900	910	920	930	940	950	960
RDPLNRVLAN	LFLLISSILG	SRTAGPHTQF	VQWFMEECVD	CLEQGGRGSV	LQFMPFTTVS	ELVKVSAMSS	PKVVLAITDL
970	980						
SLPLGRQVAA	KAIAAL						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1772	1	793.3983	26.85	2	50.8	14.1	1	18-29	R.WSDYQWAINMKK.F	Oxidation: 10

Detailed Protein Report

Protein 467: lysine-specific demethylase 3A [Homo sapiens]

Accession:	gi|20357522	**Score:**	28.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	147.2
Database Date:	2015-11-30	**pI:**	9.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.8
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|226442779	refseq_huma (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

Detailed Protein Report

Protein 468: zinc finger protein 441 [Homo sapiens]

Accession:	gi|193083160	**Score:**	28.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	80.1
Database Date:	2015-11-30	**pI:**	9.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.6
		No. of unique Peptides:	2

Quantitation

mdown:qdown **Median:** 1.65 **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
2763	1	1022.5215	80.04	2	63.0	13.2	1	256-272	K.QCGKAFSCSCYTQLYER.T	Carbamidomethyl: 2	
864	1	893.3321	-112.97	2	40.2	15.1	1	464-478	R.VHEKTHTGEKPYECK.Q		mdown:qdown 1.65

Detailed Protein Report

Protein 469: PREDICTED: ubiquitin carboxyl-terminal hydrolase 24 isoform X1 [Homo sapiens]

Accession:	gi|530362258	**Score:**	28.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	275.5
Database Date:	2015-11-30	**pI:**	6.1
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	1.0
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	1.09	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	1.24	**CV:**	0.00 %	**No. of Peptides:**	1

10	20	30	40	50	60	70	80
MDRCMPEAFK	KLLTSSAVHK	WGTEIHEGIY	NMLMLLIELV	AERIKQDPIP	TGLLGVLTMA	FNPDNEYHFK	NRMKVSQRNW
90	100	110	120	130	140	150	160
AEVFGEGNMF	AVSPVSTFQK	EPHGWVVDLV	NKFGELGGFA	AIQAKLHSED	IELGAVSALI	QPLGVCAEYL	NSSVVQPMLD
170	180	190	200	210	220	230	240
PVILTTIQDV	RSVEEKDLKD	KRLVSIPELL	SAVKLLCMRF	QPDLVTIVDD	LRLDILLRML	KSPHFSAKMN	SLKEVTKLIE
250	260	270	280	290	300	310	320
DSTLSKSVKN	AIDTDRLLDW	LVENSVLSIA	LEGNIDQAQY	CDRIKGIIEL	LGSKLSLDEL	TKIWKIQSGQ	SSTVIENIHT
330	340	350	360	370	380	390	400
IIAAAAVKFN	SDQLNHLFVL	IQKSWETESD	RVRQKLLSLI	GRIGREARFE	TTSGKVLDVL	WELAHLPTLP	SSLIQQALEE
410	420	430	440	450	460	470	480
HLTILSDAYA	VKEAIKRSYI	IKCIEDIKRP	GEWSGLEKNK	KDGFKSSQLN	NPQFVWVVPA	LRQLHEITRS	FIKQTYQKQD
490	500	510	520	530	540	550	560
KSIIQDLKKN	FEIVKLVTGS	LIACHRLAAA	VAGPGGLSGS	TLVDGRYTYR	EYLEAHLKFL	AFFLQEATLY	LGWNRAKEIW
570	580	590	600	610	620	630	640
ECLVTGQDVC	ELDREMCFEW	FTKGQHDLES	DVQQQLFKEK	ILKLESYEIT	MNGFNLFKTF	FENVNLCDHR	LKRQGAQLYV
650	660	670	680	690	700	710	720
EKLELIGMDF	IWKIAMESPD	EEIANEAIQL	IINYSYINLN	PRLKKDSVSL	HKKFIADCYT	RLEAASSALG	GPTLTHAVTR
730	740	750	760	770	780	790	800
ATKMLTATAM	PTVATSVQSP	YRSTKLVIIE	RLLLLAERYV	ITIEDFYSVP	RTILPHGASF	HGHLLTLNVT	YESTKDTFTV
810	820	830	840	850	860	870	880
EAHSNETIGS	VRWKIAKQLC	SPVDNIQIFT	NDSLLTVNKD	QKLLHQLGFS	DEQILTVKTS	GSGTPSGSSA	DSSTSSSSSS
890	900	910	920	930	940	950	960
SGVFSSSYAM	EQEKSLPGVV	MALVCNVFDM	LYQLANLEEP	RITLRVRKLL	LLIPTDPAIQ	EALDQLDSLG	RKKTLLSESS
970	980	990	1000	1010	1020	1030	1040
SQSSKSPSLS	SKQQHQPSAS	SILESLFRSF	APGMSTFRVL	YNLEVLSSKL	MPTADDDMAR	SCAKSFCENF	LKAGGLSLVV
1050	1060	1070	1080	1090	1100	1110	1120
NVMQRDSIPS	EVDYETRQGV	YSICLQLARF	LLVGQTMPTL	LDEDLTKDGI	EALSSRPFRN	VSRQTSRQMS	LCGTPEKSSY
1130	1140	1150	1160	1170	1180	1190	1200
RQLSVSDRSS	IRVEEIIPAA	RVAIQTMEVS	DFTSTVACFM	RLSWAAAAGR	LDLVGSSQPI	KESNSLCPAG	IRNRLSSSGS
1210	1220	1230	1240	1250	1260	1270	1280
NCSSGSEGEP	VALHAGICVR	QQSVSTKDSL	IAGEALSLLV	TCLQLRSQQL	ASFYNLPCVA	DFIIDILLGS	PSAEIRRVAC
1290	1300	1310	1320	1330	1340	1350	1360
DQLYTLSQTD	TSAHPDVQKP	NQFLLGVILT	AQLPLWSPTS	IMRGVNQRLL	SQCMEYFDLR	CQLLDDLTTS	EMEQLRISPA
1370	1380	1390	1400	1410	1420	1430	1440
TMLEDEITWL	DNFEPNRTAE	CETSEADNIL	LAGHLRLIKT	LLSLCGAEKE	MLGSSLIKPL	LDDFLFRASR	IILNSHSPAG
1450	1460	1470	1480	1490	1500	1510	1520
SAAISQQDFH	PKCSTANSRL	AAYEVLVMLA	DSSPSNLQII	IKELLSMHHQ	PDPALTKEFD	YLPPVDSRSS	SGFVGLRNGG
1530	1540	1550	1560	1570	1580	1590	1600
ATCYMNAVFQ	QLYMQPGLPE	SLLSVDDDTD	NPDDSVFYQV	QSLFGHLMES	KLQYYVPENF	WKIFKMWNKE	LYVREQQDAY
1610	1620	1630	1640	1650	1660	1670	1680
EFFTSLIDQM	DEYLKKMGRD	QIFKNTFQGI	YSDQKICKDC	PHRYEREEAF	MALNLGVTSC	QSLEISLDQF	VRGEVLEGSN
1690	1700	1710	1720	1730	1740	1750	1760
AYYCEKCKEK	RITVKRTCIK	SLPSVLVIHL	MRFGFDWESG	RSIKYDEQIR	FPWMLNMEPY	TVSGMARQDS	SSEVGENGRS
1770	1780	1790	1800	1810	1820	1830	1840
VDQGGGGSPR	KKVALTENYE	LVGVIVHSGQ	AHAGHYYSFI	KDRRGCGKGK	WYKFNDTVIE	EFDLNDETLE	YECFGGEYRP
1850	1860	1870	1880	1890	1900	1910	1920
KVYDQTNPYT	DVRRRYWNAY	MLFYQRVSDQ	NSPVLPKKSR	VSVVRQEAED	LSLSAPSSPE	ISPQSSPRPH	RPNNDRLSIL
1930	1940	1950	1960	1970	1980	1990	2000
TKLVKKGEKK	GLFVEKMPAR	IYQMVRDENL	KFMKNRDVYS	SDYFSFVLSL	ASLNATKLKH	PYYPCMAKVS	LQLAIQFLFQ
2010	2020	2030	2040	2050	2060	2070	2080
TYLRTKKKLR	VDTEEWIATI	EALLSKSFDA	CQWLVEYFIS	SEGRELIKIF	LLECNVREVR	VAVATILEKT	LDSALFYQDK
2090	2100	2110	2120	2130	2140	2150	2160
LKSLHQLLEV	LLALLDKDVP	ENCKNCAQYF	FLFNTFVQKQ	GIRAGDLLLR	HSALRHMISF	LLGASRQNNQ	IRRWSSAQAR
2170	2180	2190	2200	2210	2220	2230	2240
EFGNLHNTVA	LLVLHSDVSS	QRNVAPGIFK	QRPPISIAPS	SPLLPLHEEV	EALLFMSEGK	PYLLEVMFAL	RELTGSLLAL
2250	2260	2270	2280	2290	2300	2310	2320
IEMVVYCCFC	NEHFSFTMLH	FIKNQLETAP	PHELKNTFQL	LHEILVIEDP	IQVERVKFVF	ETENGLLALM	HHSNHVDSSR
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
143	2	849.3662	-2.35	2	31.0	11.7	1	1010-1024	K.LMPTADDDMARSCAK.S	Carbamidomethyl: 13; Oxidation: 2	Wdown:Qdown 1.24 mdown:qdown 1.09

Detailed Protein Report

Protein 470: 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 471: AP-3 complex subunit delta-1 isoform 2 [Homo sapiens]

Accession:	gi|117553580	**Score:**	28.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	130.1
Database Date:	2015-11-30	**pI:**	9.4
		Sequence Coverage [%]:	2.3
		No. of unique Peptides:	2

Quantitation

mdown:qdown **Median:** 0.50 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MALKMVKGSI	DRMFDKNLQD	LVRGIRNHKE	DEAKYISQCI	DEIKQELKQD	NIAVKANAVC	KLTYLQMLGY	DISWAAFNII
90	100	110	120	130	140	150	160
EVMSASKFTF	KRIGYLAASQ	SFHEGTDVIM	LTTNQIRKDL	SSPSQYDTGV	ALTGLSCFVT	PDLARDLAND	IMTLMSHTKP
170	180	190	200	210	220	230	240
YIRKKAVLIM	YKVFLKYPES	LRPAFPRLKE	KLEDPDPGVQ	SAAVNVICEL	ARRNPKNYLS	LAPLFFKLMT	SSTNNWVLIK
250	260	270	280	290	300	310	320
IIKLFGALTP	LEPRLGKKLI	EPLTNLIHST	SAMSLLYECV	NTVIAVLISL	SSGMPNHSAS	IQLCVQKLRI	LIEDSDQNLK
330	340	350	360	370	380	390	400
YLGLLAMSKI	LKTHPKSVQS	HKDLILQCLD	DKDESIRLRA	LDLLYGMVSK	KNLMEIVKKL	MTHVDKAEGT	TYRDELLTKI
410	420	430	440	450	460	470	480
IDICSQSNYQ	YITNFEWYIS	ILVELTRLEG	TRHGHLIAAQ	MLDVAIRVKA	IRKFAVSQMS	ALLDSAHLLA	SSTQRNGICE
490	500	510	520	530	540	550	560
VLYAAAWICG	EFSEHLQEPH	HTLEAMLRPR	VTTLPGHIQA	VYVQNVVKLY	ASILQQKEQA	GEAEGAQAVT	QLMVDRLPQF
570	580	590	600	610	620	630	640
VQSADLEVQE	RASCILQLVK	HIQKLQAKDV	PVAEEVSALF	AGELNPVAPK	AQKKVPVPEG	LDLDAWINEP	LSDSESEDER
650	660	670	680	690	700	710	720
PRAVFHEEEQ	RRPKHRPSEA	DEEELARRRE	ARKQEQANNP	FYIKSSPSPQ	KRYQDTPGVE	HIPVVQIDLS	VPLKVPGLPM
730	740	750	760	770	780	790	800
SDQYVKLEEE	RRHRQKLEKD	KRRKKRKEKE	KKGKRRHSSL	PTESDEDIAP	AQQVDIVTEE	MPENALPSDE	DDKDPNDPYR
810	820	830	840	850	860	870	880
ALDIDLDKPL	ADSEKLPIQK	HRNTETSKSP	EKDVPMVEKK	SKKPKKKEKK	HKEKERDKEK	KKEKEKKKSP	KPKKKKHRKE
890	900	910	920	930	940	950	960
KEERTKGKKK	SKKQPPGSEE	AAGEPVQNGA	PEEEQLPPES	SYSLLAENSY	VKMTCDIRGS	LQEDSQVTVA	IVLENRSSSI
970	980	990	1000	1010	1020	1030	1040
LKGMELSVLD	SLNARMARPQ	GSSVHDGVPV	PFQLPPGVSN	EAQYVFTIQS	IVMAQKLKGT	LSFIAKNDEG	ATHEKLDFRL
1050	1060	1070	1080	1090	1100	1110	1120
HFSCSSYLIT	TPCYSDAFAK	LLESGDLSMS	SIKVDGIRMS	FQNLLAKICF	HHHFSVVERV	DSCASMYSRS	IQGHHVCLLV
1130	1140	1150	1160				
KKGENSVSVD	GKCSDSTLLS	NLLEEMKATL	AKC				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
545	1	592.3161	-55.37	2	35.4	15.2	1	17-26	K.NLQDLVRGIR.N		mdown:qdown 0.50
1829	1	682.2682	-136.57	3	52.9	13.0	2	343-359	K.DLILQCLDDKDESIRLR.A		

Detailed Protein Report

Protein 472: von Willebrand factor D and EGF domain-containing protein precursor [Homo sapiens]

Accession:	gi|209571555	**Score:**	28.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	176.7
Database Date:	2015-11-30	**pI:**	5.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.4
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MPGGACVLVI	ALMFLAWGEA	QECSPGGHQF	LRSPYRSVRF	DSWHLQQSAV	QDLICDHSLS	PGWYRFLILD	RPAEMPTKCV
90	100	110	120	130	140	150	160
EMNHCGTQAP	IWLSLRDSET	LPSPGEIKQL	TACATWQFLF	STTKDCCLFQ	IPVSVRNCGN	FSVYLLQPTQ	GCMGYCAEAI
170	180	190	200	210	220	230	240
SDARLHPCGS	DETETGGDCV	RQLAASLPPP	PAGRPEVLVE	LIESRLFCRC	SFDVPATKNS	VGFHIAWSRL	SSQEVKEELT
250	260	270	280	290	300	310	320
QETTVQAFSL	LELDGINLRL	GDRIFCSASV	FFLENPHVQS	VAIESQEFFA	GFKLQPELST	ISEDGKEYYL	RIESTVPIIC
330	340	350	360	370	380	390	400
SEFSELDQEC	KISLKLKTIG	QGREHLGLNL	ALSSCHVDLL	QTSSCANGTC	SHTFVYYTAV	TDFSRDGDRV	SNIVVQPIVN
410	420	430	440	450	460	470	480
EDFLWNNYIP	DSIQIKVKDV	PTAYCYTFTD	PHIITFDGRV	YDNFKTGTFV	LYKSMSRDFE	VHVRQWDCRS	LHYPVSCNCG
490	500	510	520	530	540	550	560
FVAQEGGDIV	TFDMCNGQLR	ESQPYLFIKS	QDVTRNIKIS	ESYLGRKVTI	WFSSGAFIRA	DLGEWGMSLT	IRAPSVDYRN
570	580	590	600	610	620	630	640
TLGLCGTFDE	NPENDFHDKN	GMQIDQNFNN	YVAFINEWRI	LPGKSMSDTL	PVSMTSPGKP	SYCSCSLDTA	AYPSSEDLDS
650	660	670	680	690	700	710	720
VSRSEIALGC	KDLNHVSLSS	LIPELDVTSE	YINSDTLVRE	INKHTSPEEY	NLNLFLQEKK	HINLTKLGLN	VQKHPGNEKE
730	740	750	760	770	780	790	800
DSLQYLANKK	YTQGRGSHSQ	EMRYNRQNRW	KRQNFHEFPP	LFAFPSLSQT	DLEELTYFFP	EDHAEDVQQE	FFPSWPTPSG
810	820	830	840	850	860	870	880
LTEYSTLTLC	QETLANSSIG	RLCLAFLGKR	LDSVIEMCVK	DVLLKDDLSW	AEAGVALLEN	ECEKRIVEEG	KYNTEEYGTS
890	900	910	920	930	940	950	960
IEDILSVLKC	PNLCSGNGQC	MEWGCACSPS	FSSYDCSDSY	DKAPEITELG	NAGFCDVQKY	NCMMVRVFGK	GFKELPSIKC
970	980	990	1000	1010	1020	1030	1040
EVTKLQYNSS	EWMPGEPIYT	QTVFHNSRAV	DCQLPTDVQQ	FDTMDLVGGK	PTGKWQLKVS	NDGYKFSNPK	ITVIYDGACQ
1050	1060	1070	1080	1090	1100	1110	1120
VCGLYKNDSC	TIKENVCIID	GLCYVEGDKN	PTSPCLICRP	KISRFTWSFL	ENNQPPVIQA	LQDKLQTFYG	ENFEYQFVAF
1130	1140	1150	1160	1170	1180	1190	1200
DPEGSDIHFT	LDSGPEGASV	SSAGLFMWKT	DLLTTQQITV	RLNDDCDAET	RVTIEVTVKS	CDCLNGGSCV	SDRNFSPGSG
1210	1220	1230	1240	1250	1260	1270	1280
VYLCVCLPGF	HGSLCEVDIS	GCQSNPCGLG	SYISGFHSYS	CDCPPELKVE	TQFVNQFTTQ	TVVLTRSDKS	VNKEEDDKNA
1290	1300	1310	1320	1330	1340	1350	1360
QGRKRHVKPT	SGNAFTICKY	PCGKSRECVA	PNICKCKPGY	IGSNCQTALC	DPDCKNHGKC	IKPNICQCLP	GHGGATCDEE
1370	1380	1390	1400	1410	1420	1430	1440
HCNPPCQHGG	TCLAGNLCTC	PYGFVGPRCE	TMVCNRHCEN	GGQCLTPDIC	QCKPGWYGPT	CSTALCDPVC	LNGGSCNKPN
1450	1460	1470	1480	1490	1500	1510	1520
TCLCPNGFFG	EHCQNAFCHP	PCKNGGHCMR	NNVCVCREGY	TGRRFQKSIC	DPTCMNGGKC	VGPSTCSCPS	GWSGKRCNTP
1530	1540	1550	1560	1570	1580	1590	1600
ICLQKCKNGG	ECIAPSICHC	PSSWEGVRCQ	IPICNPKCLY	GGRCIFPNVC	SCRTEYSGVK	CEKKIQIRRH	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2213	1	916.8887	8.94	2	56.3	16.8	0	165-181	R.LHPCGSDETETGGDCVR.Q	Carbamidomethyl: 15
2186	1	1159.9541	-107.87	2	55.8	11.4	1	1026-1046	K.FSNPKITVIYDGACQVCGLYK.N	

Detailed Protein Report

Protein 473: eyes absent homolog 1 isoform 5 [Homo sapiens]

Accession:	gi|568384804	**Score:**	28.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	51.8
Database Date:	2015-11-30	**pI:**	5.7
		Sequence Coverage [%]:	5.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MQQATAYATY	PQPGQPYGIS	SYGIKTEGGL	SQSQSPGQTG	FLSYGTSFST	PQPGQAPYSY	QMQGSSFTTS	SGIYTGNNSL
90	100	110	120	130	140	150	160
TNSSGFNSSQ	QDYPSYPSFG	QGQYAQYYNS	SPYPAHYMTS	SNTSPTTPST	NATYQLQEPP	SGITSQAVTD	PTAEYSTIHS
170	180	190	200	210	220	230	240
PSTPIKDSDS	DRLRRGSDGK	SRGRGRRNNN	PSPPPDSDLE	RVFIWDLDET	IIVFHSLLTG	SYANRYGRDP	PTSVSLGLRM
250	260	270	280	290	300	310	320
EEMIFNLADT	HLFFNDLEEC	DQVHIDDVSS	DDNGQDLSTY	NFGTDGFPAA	ATSANLCLAT	GVRGGVDWMR	KLAFRYRRVK
330	340	350	360	370	380	390	400
EIYNTYKNNV	GGLLGPAKRE	AWLQLRAEIE	ALTDSWLTLA	LKALSLIHSR	TNCVNILVTT	TQLIPALAKV	LLYGLGIVFP
410	420	430	440	450	460	470	480
IENIYSATKI	GKESCFERII	QRFGRKVVYV	VIGDGVEEEQ	GAKKHAMPFW	RISSHSDLMA	LHHALELEYL	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2746	1	683.0052	-51.66	3	65.6	13.5	2	426-444	R.KVVYVVIGDGVEEEQGAKK.H	

Detailed Protein Report

Protein 474: **SCO-spondin precursor [Homo sapiens]**

Accession:	gi|134031945	**Score:**	28.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	547.1
Database Date:	2015-11-30	**pI:**	5.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	0.7
		No. of unique Peptides:	2

Detailed Protein Report

10	20	30	40	50	60	70	80
MLLPALLFGM	AWALADGRWC	EWTETIRVEE	EVAPRQEDLV	PCASLDHYSR	LGWRLDLPWS	GRSGLTRSPA	PGLCPIYKPP
90	100	110	120	130	140	150	160
ETRPAKWNRT	VRTCCPGWGG	AHCTEALAKA	SPEGHCFAMW	QCQLQAGSAN	ASAGSLEECC	ARPWGQSWWD	GSSQACRSCS
170	180	190	200	210	220	230	240
SRHLPGSASS	PALLQPLAGA	VGQLWSQHQR	PSATCASWSG	FHYRTFDGRH	YHFLGRCTYL	LAGAADSTWA	VHLTPGDRCP
250	260	270	280	290	300	310	320
QPGHCQRVTM	GPEEVLIQAG	NVSVKGQLVP	EGQSWLLHGL	SLQWLGDWLV	LSGGLGVVVR	LDRTGSISIS	VDHELWGQTQ
330	340	350	360	370	380	390	400
GLCGLYNGWP	EDDFMEPGGG	LAMLAATFGN	SWRLPGSESG	CLDAVEVAQG	CDPLGLIDAD	VEPGHLRAEA	QDVCHQLLEG
410	420	430	440	450	460	470	480
PFGQCHAQVS	PAEYHEACLF	AYCAGAMAGS	GQEGRQQAVC	ATFASYVQAC	ARRHIHIRWR	KPGFCERLCP	GGQLYSDCVS
490	500	510	520	530	540	550	560
LCPPSCEAVG	QGEEESCREE	CVSGCECPRG	LFWNGTLCVP	AAHCPCYYCR	QRYVPGDTVR	QLCNPCVCRD	GRWHCAQALC
570	580	590	600	610	620	630	640
PAECAVGGDG	HYLTFDGRSY	SFWGGQGCRY	SLVQDYVKGQ	LLILLEHGAC	DAGSCLHAIS	VSLEDTHIQL	RDSGAVLVNG
650	660	670	680	690	700	710	720
QDVGLPWIGA	EGLSVRRASS	AFLLLRWPGA	QVLWGLSDPV	AYITLDPRHA	HQVQGLCGTF	TQNQQDDFLT	PAGDVETSIA
730	740	750	760	770	780	790	800
AFASKFQVAG	KGRCPSEDSA	LLSPCTTHSQ	RHAFAEAACA	ILHSSVFQEC	HRLVDKEPFY	LRCLAAVCGC	DPGSDCLCPV
810	820	830	840	850	860	870	880
LSAYARRCAQ	EGASPPWRNQ	TLCPVMCPGG	QEYRECAPAC	GQHCGKPEDC	GELGSCVAGC	NCPLGLLWDP	EGQCVPPSLC
890	900	910	920	930	940	950	960
PCQLGARRYA	PGSATMKECN	RCICQERGLW	NCTARHCPSQ	AFCPRELVYA	PGACLLTCDS	PSANHSCPAG	STDGCVCPPG
970	980	990	1000	1010	1020	1030	1040
TVLLDERCVP	PDLCPCRHSG	QWYLPNATIQ	EDCNVCVCRG	RQWHCTGQRR	SGRCQASGAP	HYVTFDGLAF	TYPGACEYLL
1050	1060	1070	1080	1090	1100	1110	1120
VREASGLFTV	SAQNLPCGAS	GLTCTKALAV	RLEGTVVHML	RGRAVTVNGV	SVTPPKVYTG	PGLSLRRAGL	FLLLSTHLGL
1130	1140	1150	1160	1170	1180	1190	1200
TLLWDGGTRV	LVQLSPQFRG	RVAGLCGDFD	GDASNDLRSR	QGVLEPTAEL	AAHSWRLSPL	CPEPGDLPHP	CTMNTHRAGW
1210	1220	1230	1240	1250	1260	1270	1280
ARARCGALLQ	PLFTLCHAEV	PPQQHYEWCL	YDACGCDSGG	DCECLCSAIA	TYADECARHG	HHVRWRSQEL	CSLQCEGGQV
1290	1300	1310	1320	1330	1340	1350	1360
YEACGPTCPP	TCHEQHPEPG	WHCQVVACVE	GCFCPEGTLL	HGGACLEPAS	CPCEWGRNSF	PPGSVLQKDC	GNCTCQEGQW
1370	1380	1390	1400	1410	1420	1430	1440
HCGGDGGHCE	ELVPACAEGE	ALCQENGHCV	PHGWLCDNQD	DCGDGSDEEG	CAAPGCGEGQ	MTCSSGHCLP	LALLCDRQDD
1450	1460	1470	1480	1490	1500	1510	1520
CGDGTDEPSY	PCPQGLLACA	DGRCLPPALL	CDGHPDCLDA	ADEESCLGQV	TCVPGEVSCV	DGTCLGAIQL	CDGVWDCPDG
1530	1540	1550	1560	1570	1580	1590	1600
ADEGPGHCPL	PSLPTPPAST	LPGPSPGSLD	TASSPLASAS	PAPPCGPFEF	RCGSGECTPR	GWRCDQEEDC	ADGSDERGCG
1610	1620	1630	1640	1650	1660	1670	1680
GPCAPHHAPC	ARGPHCVSPE	QLCDGVRQCP	DGSDEGPDAC	GGLPALGGPN	RTGLPCPEYT	CPNGTCIGFQ	LVCDGQPDCG
1690	1700	1710	1720	1730	1740	1750	1760
RPGQVGPSPE	EQGCGAWGPW	SPWGPCSRTC	GPWGQGRSRR	CSPLGLLVLQ	NCPGPEHQSQ	ACFTAACPVD	GEWSTWSPWS
1770	1780	1790	1800	1810	1820	1830	1840
VCSEPCRGTM	TRQRQCHSPQ	NGGRTCAALP	GGLHSTRQTK	PCPQDGCPNA	TCSGELMFQP	CAPCPLTCDD	ISGQVTCPPD
1850	1860	1870	1880	1890	1900	1910	1920
WPCGSPGCWC	PEGQVLGSEG	WCVWPRQCPC	LVDGARYWPG	QRIKADCQLC	ICQDGRPRRC	RLNPDCAVDC	GWSSWSPWAK
1930	1940	1950	1960	1970	1980	1990	2000
CLGPCGSQSI	QWSFRSSNNP	RPSGRGRQCR	GIHRKARRCQ	TEPCEGCEHQ	GQVHRVGERW	HGGPCRVCQC	LHNLTAHCSP
2010	2020	2030	2040	2050	2060	2070	2080
YCPLGSCPQG	WVLVEGTGES	CCHCALPGEN	QTVQPMATPA	AAPAPSPQIR	FPLATYILPP	SGDPCYSPLG	LAGLAEGSLH
2090	2100	2110	2120	2130	2140	2150	2160
ASSQQLEHPT	QAALLGAPTQ	GPSPQGWHAG	GDAYAKWHTR	PHYLQLDLLQ	PRNLTGILVP	ETGSSNAYAS	SFSLQFSSNG
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1675	2	1136.5319	16.36	2	49.5	14.8	1	2854-2875	R.GRSCSSLAPGDTTCPGPHSQTR.D	Carbamidomethyl: 4
1364	1	669.3350	-3.76	2	45.8	13.3	1	3671-3682	R.RCARPPCPGPAR.Q	Carbamidomethyl: 2

Detailed Protein Report

Protein 475: growth arrest-specific protein 7 isoform a [Homo sapiens]

Accession:	gi|41406076	**Score:**	28.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	39.2
Database Date:	2015-11-30	**pI:**	6.3
		Sequence Coverage [%]:	8.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSNMENSFDD	VSCLSPQNLG	SSSPSKKQSK	ENTITINCVT	FPHPDTMPEQ	QLLKPTEWSY	CDYFWADKKD	PQGNGTVAGF
90	100	110	120	130	140	150	160
ELLLQKQLKG	KQMQKEMSEF	IRERIKIEED	YAKNLAKLSQ	NSLASQEEGS	LGEAWAQVKK	SLADEAEVHL	KFSAKLHSEV
170	180	190	200	210	220	230	240
EKPLMNFREN	FKKDMKKCDH	HIADLRKQLA	SRYASVEKAR	KALTERQRDL	EMKTQQLEIK	LSNKTEEDIK	KARRKSTQAG
250	260	270	280	290	300	310	320
DDLMRCVDLY	NQAQSKWFEE	MVTTTLELER	LEVERVEMIR	QHLCQYTQLR	HETDMFNQST	VEPVDQLLRK	VDPAKDRELW
330	340						
VREHKTGNIR	PVDMEI						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2697	1	596.2791	-61.86	3	62.6	14.1	0	70-86	K.DPQGNGTVAGFELLLQK.Q	

Detailed Protein Report

Protein 476: transmembrane protein 151A [Homo sapiens]

Accession:	gi|23397566	**Score:**	28.0
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:	2

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
1863	1	864.4736	-15.26	2	52.0	17.8	2	414-430	R.ATPGVFRSLSGGPLGRR.G	

Detailed Protein Report

Protein 477: SWI/SNF complex subunit SMARCC2 isoform b [Homo sapiens]

Accession:	gi|21237808	**Score:**	28.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	124.8
Database Date:	2015-11-30	**pI:**	5.3
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	2.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAVRKKDGGP	NVKYYEAADT	VTQFDNVRLW	LGKNYKKYIQ	AEPPTNKSLS	SLVVQLLQFQ	EEVFGKHVSN	APLTKLPIKC
90	100	110	120	130	140	150	160
FLDFKAGGSL	CHILAAAYKF	KSDQGWRRYD	FQNPSRMDRN	VEMFMTIEKS	LVQNNCLSRP	NIFLCPEIEP	KLLGKLKDII
170	180	190	200	210	220	230	240
KRHQGTVTED	KNNASHVVYP	VPGNLEEEEW	VRPVMKRDKQ	VLLHWGYYPD	SYDTWIPASE	IEASVEDAPT	PEKPRKVHAK
250	260	270	280	290	300	310	320
WILDTDTFNE	WMNEEDYEVN	DDKNPVSRRK	KISAKTLTDE	VNSPDSDRRD	KKGGNYKKRK	RSPSPSPTPE	AKKKNAKKGP
330	340	350	360	370	380	390	400
STPYTKSKRG	HREEEQEDLT	KDMDEPSPVP	NVEEVTLPKT	VNTKKDSESA	PVKGGTMTDL	DEQEDESMET	TGKDEDENST
410	420	430	440	450	460	470	480
GNKGEQTKNP	DLHEDNVTEQ	THHIIIPSYA	AWFDYNSVHA	IERRALPEFF	NGKNKSKTPE	IYLAYRNFMI	DTYRLNPQEY
490	500	510	520	530	540	550	560
LTSTACRRNL	AGDVCAIMRV	HAFLEQWGLI	NYQVDAESRP	TPMGPPPTSH	FHVLADTPSG	LVPLQPKTPQ	GRQVDADTKA
570	580	590	600	610	620	630	640
GRKGKELDDL	VPETAKGKPE	LQTSASQQML	NFPDKGKEKP	TDMQNFGLRT	DMYTKKNVPS	KSKAAASATR	EWTEQETLLL
650	660	670	680	690	700	710	720
LEALEMYKDD	WNKVSEHVGS	RTQDECILHF	LRLPIEDPYL	EDSEASLGPL	AYQPIPFSQS	GNPVMSTVAF	LASVVDPRVA
730	740	750	760	770	780	790	800
SAAAKSALEE	FSKMKEEVPT	ALVEAHVRKV	EEAAKVTGKA	DPAFGLESSG	IAGTTSDEPE	RIEESGNDEA	RVEGQATDEK
810	820	830	840	850	860	870	880
KEPKEPREGG	GAIEEEAKEK	TSEAPKKDEE	KGKEGDSEKE	SEKSDGDPIV	DPEKEKEPKE	GQEEVLKEVV	ESEGERKTKV
890	900	910	920	930	940	950	960
ERDIGEGNLS	TAAAAALAAA	AVKAKHLAAV	EERKIKSLVA	LLVETQMKKL	EIKLRHFEEL	ETIMDREREA	LEYQRQQLLA
970	980	990	1000	1010	1020	1030	1040
DRQAFHMEQL	KYAEMRARQQ	HFQQMHQQQQ	QPPPALPPGS	QPIPPTGAAG	PPAVHGLAVA	PASVVPAPAG	SGAPPGSLGP
1050	1060	1070	1080	1090	1100	1110	1120
SEQIGQAGST	AGPQQQQPAG	APQPGAVPPG	VPPPGPHGPS	PFPNQQTPPS	MMPGAVPGSG	HPGVADPGTP	LPPDPTAPSP
1130	1140						
GTVTPVPPPQ							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1963	2	696.2530	-136.00	2	54.6	12.3	1	488-499	R.RNLAGDVCAIMR.V	Carbamidomethyl: 8; Oxidation: 11

Detailed Protein Report

Protein 478: 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 479: **PREDICTED: putative dehydrogenase/reductase SDR family member 4-like 2 isoform X1 [Homo sapiens]**

Accession:	gi|578826096	**Score:**	28.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	26.3
Database Date:	2015-11-30	**pI:**	10.7
		Sequence Coverage [%]:	10.2
		No. of unique Peptides:	1

Quantitation

Wdown:Qdown **Median:** 3.09 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MHKARLRGHC	ARAGKSVRLA	SSGMTRRDPL	TNKVALVTAS	TDWIGFAVAQ	RLAQDGAHVV	VSRRKQQNVD	QAVATLQGEG
90	100	110	120	130	140	150	160
LSMTGTVCHV	GKMKDWERLV	ATNLDINGKA	LALMIKAVVP	EMEKRGGGSV	GFLASVAAFR	PLPGFSPYNV	SKTALLGLNK
170	180	190	200	210	220	230	240
TLAIELAPRN	IRVNCLAPGL	IKTSFSRMLW	MDKEKEESMK	ETLRIRRLGE	PEDSLGIVSF	LCSEDASYLT	GETVMVGGGT
250							
PSRL							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
36	1	660.7253	-206.67	2	29.1	13.6	2	16-27	K.SVRLASSGMTRR.D		Wdown:Qdown 3.09

Detailed Protein Report

Protein 480: **PREDICTED: egl nine homolog 1 isoform X1 [Homo sapiens]**

Accession:	gi|530366273	**Score:**	28.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	41.1
Database Date:	2015-11-30	**pI:**	9.8
		Sequence Coverage [%]:	11.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MANDSGGPGG	PSPSERDRQY	CELCGKMENL	LRCSRCRSSF	YCCKEHQRQD	WKKHKLVCQG	SEGALGHGVG	PHQHSGPAPP
90	100	110	120	130	140	150	160
AAVPPPRAGA	REPRKAAARR	DNASGDAAKG	KVKAKPPADP	AAAASPCRAA	AGGQGSAVAA	EAEPGKEEPP	ARSSLFQEKA
170	180	190	200	210	220	230	240
NLYPPSNTPG	DALSPGGGLR	PNGQTKPLPA	LKLALEYIVP	CMNKHGICVV	DDFLGKETGQ	QIGDEVRALH	DTGKFTDGQL
250	260	270	280	290	300	310	320
VSQKSDSSKD	IRGDKITWIE	GKEPGCETIG	LLMSSMDDLI	RHCNGKLGSY	KINGRTKAMV	ACYPGNGTGY	VRHVDNPNGD
330	340	350	360	370	380	390	
GRCVTCIYYL	NKDWDAKVSG	GILRIFPEGK	AQFADIEPKF	DRLLFFWSDR	RNPHEVQPAY	ATR	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1622	1	1100.2202	-32.79	3	50.2	17.8	0	160-192	K.ANLYPPSNTPGDALSPGGGLRPNGQTKPLPALK.L	

Detailed Protein Report

Protein 481: **PREDICTED: RANBP2-like and GRIP domain-containing protein 2 isoform X2 [Homo sapiens]**

Accession:	gi|530368052	**Score:**	27.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	185.5
Database Date:	2015-11-30	**pI:**	5.8
		Sequence Coverage [%]:	1.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MRRSKAYGER	YLASVQGSAP	SPGKKLRGFY	FAKLYYEAKE	YDLAKKYVCT	YLSVQERDPR	AHRFLGLLYE	LEENTEKAVE
90	100	110	120	130	140	150	160
CYRRSLELNP	PQKDLVLKIA	ELLCKNDVTD	GRAKYWVERA	AKLFPGSPAI	YKLKEHLLDC	EGEDGWNKLF	DWIQSELYVR
170	180	190	200	210	220	230	240
PDDVHMNIRL	VELYRSNKRL	KDAVARCHEA	ERNIALRSSL	EWNSCVVQTL	KEYLESLQCL	ESDKSDWRAT	NTDLLLAYAN
250	260	270	280	290	300	310	320
LMLLTLSTRD	VQESRELLES	FDSALQSAKS	SLGGNDELSA	TFLEMKGHFY	MHAGSLLLKM	GQHGNNVQWQ	ALSELAALCY
330	340	350	360	370	380	390	400
VIAFQVPRPK	IKLIKGEAGQ	NLLEMMACDR	LSQSGHMLLN	LSRGKQDFLK	EVVETFANKS	GQSVLYNALF	SSQSSKDTSF
410	420	430	440	450	460	470	480
LGSDDIGNID	VQEPELEDLA	RYDVGAIQAH	NGSLQHLTWL	GLQWNSLPAL	PGIRKWLKQL	FHHLPQETSR	LETNAPESIC
490	500	510	520	530	540	550	560
ILDLEVFLLG	VVYTSHLQLK	EKCNSHHSSY	QPLCLPLPVC	KRLCTERQKS	WWDAVCTLIH	RKAVPGNSAE	LRLVVQHEIN
570	580	590	600	610	620	630	640
TLRAQEKHGL	QPALLVHWAK	CLQKMGRGLN	SSYDQQEYIG	RSVHYWKKVL	PLLKIIKKNS	IPEPIDPLFK	HFHSVDIQAS
650	660	670	680	690	700	710	720
EIVEYEEDAH	ITFAILDAVH	GNIEDAVTAF	ESIKSVVSYW	NLALIFHRKA	EDIENDAVFP	EEQEECKNYL	RKTRDYLIKI
730	740	750	760	770	780	790	800
IDDSDSNLSV	VKKLPVPLES	VKEMLKSVMQ	ELEDYSEGGP	LYKNGSLRNA	DSEIKHSTPS	PTKYSLSPSK	SYKYSPKTPP
810	820	830	840	850	860	870	880
RWAEDQNSLR	KMICQEVKAI	TKLNSSKSAS	RHRWPTENYG	PDSVPDGYQG	SQTFHGAPLT	VATTGPSVYY	SQSPAYNSQY
890	900	910	920	930	940	950	960
LLRPAANVTP	TKGSSNTEFK	STKEGFSIAV	SADGFKFGIS	EPGNQEKKSE	KPLENDTGFQ	AQDISGQKNG	RGVIFGQTSS
970	980	990	1000	1010	1020	1030	1040
TFTFADVAKS	TSGEGFQFGK	KDPNFKGFSG	AGEKLFSSQC	GKMANKANTS	GDFEKDDDAC	KTEDSDDIHF	EPVVQMPEKV
1050	1060	1070	1080	1090	1100	1110	1120
ELVTGEEGEK	VLYSQGVKLF	RFDAEISQWK	ERGLGNLKIL	KNEVNGKPRM	LMRRDQVLKV	CANHWITTTM	NLKPLSGSDR
1130	1140	1150	1160	1170	1180	1190	1200
AWMWLASDFS	DGDAKLERLA	AQFKTPELAE	EFKQKFEECQ	RLLLDIPLQT	PHKLVDTGRA	AKLIQRAEEM	KSGLKDFKTF
1210	1220	1230	1240	1250	1260	1270	1280
LTNDQTKVTE	EENKGSGTGA	AGASDTTIKP	NPENTGPTLE	WDNYDLREDA	LDDNVSSSSV	HDSPLASSPV	RKNIFRFDES
1290	1300	1310	1320	1330	1340	1350	1360
TTGFNFSFKS	ALSLSKSPAK	LNQSGTSVGT	DEESDVTQEE	ERDGQYFEPV	VPLPDLVEVS	SGEENEQVVF	SHMAELYRYD
1370	1380	1390	1400	1410	1420	1430	1440
KDVGQWKERG	IGDIKILQNY	DNKQVRIVMR	RDQVLKLCAN	HRITPDMSLQ	NMKGTERVWV	WTACDFADGE	RKVEHLAVRF
1450	1460	1470	1480	1490	1500	1510	1520
KLQDVADSFK	KIFDEAKTAQ	EKDSLITPHV	SRSSTPRESP	CGKIAVAVLE	ETTRERTDVI	QGDDVADAAS	EVEVSSTSET
1530	1540	1550	1560	1570	1580	1590	1600
TTKAVVSPPK	FVFGSESVKR	IFSSEKSNPF	AFGNSSATGS	LFGFSFNAPL	KSNDSETSSV	AQSGSESKVE	PKKCELSKNS
1610	1620	1630	1640	1650	1660		
DIEQSSDSKV	KNLSASFPME	ESSINYTFKT	PEKAKEKKKP	EDSPSDSLGL	LTS		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2905	1	1023.0342	20.17	2	65.1	16.6	2	794-810	K.YSPKTPPRWAEDQNSLR.K	

Detailed Protein Report

Protein 482: **PREDICTED: membrane-associated guanylate kinase, WW and PDZ domain-containing protein 2 isoform X1 [Homo sapiens]**

Accession:	gi|530386693	**Score:**	27.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	157.1
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
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
1930	1	643.2948	-156.54	2	54.2	17.3	1	980-991	K.LIKDAGLSVTLR.I	

Detailed Protein Report

Protein 483: uncharacterized protein KIAA0408 [Homo sapiens]

Accession:	gi|59806363	**Score:**	27.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	79.1
Database Date:	2015-11-30	**pI:**	9.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.7
		No. of unique Peptides:	1

Quantitation

Wdown:Qdown **Median:** 2.32 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MDLHKQWENT	ETNWHKEKME	LLDQFDNERK	EWESQWKIMQ	KKIEELCREV	KLWRKININE	SAKIIDLYHE	KTIPEKVIES
90	100	110	120	130	140	150	160
SPNYPDLGQS	EFIRTNHKDG	LRKENKREQS	LVSGGNQMCK	EQKATKKSKV	GFLDPLATDN	QKECEAWPDL	RTSEEDSKSC
170	180	190	200	210	220	230	240
SGALSTALEE	LAKVSEELCS	FQEEIRKRSN	HRRMKSDSFL	QEMPNVTNIP	HGDPMINNDQ	CILPISLEKE	KQKNRKNLSC
250	260	270	280	290	300	310	320
TNVLQSNSTK	KCGIDTIDLK	RNETPPVPPP	RSTSRNFPSS	DSEQAYERWK	ERLDHNSWVP	HEGRSKRNYN	PHFPLRQQEM
330	340	350	360	370	380	390	400
SMLYPNEGKT	SKDGIIFSSL	VPEVKIDSKP	PSNEDVGLSM	WSCDIGIGAK	RSPSTSWFQK	TCSTPSNPKY	EMVIPDHPAK
410	420	430	440	450	460	470	480
SHPDLHVSND	CSSSVAESSS	PLRNFSCGFE	RTTRNEKLAA	KTDEFNRTVF	RTDRNCQAIQ	QNHSCSKSSE	DLKPCDTSST
490	500	510	520	530	540	550	560
HTGSISQSND	VSGIWKTNAH	MPVPMENVPD	NPTKKSTTGL	VRQMQGHLSP	RSYRNMLHEH	DWRPSNLSGR	PRSADPRSNY
570	580	590	600	610	620	630	640
GVVEKLLKTY	ETATESALQN	SKCFQDNWTK	CNSDVSGGAT	LSQHLEMLQM	EQQFQQKTAV	WGGQEVKQGI	DPKKITEESM
650	660	670	680	690	700		
SVNASHGKGF	SRPARPANRR	LPSRWASRSP	SAPPALRRTT	HNYTISLRSE	ALMV		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2682	2	841.8664	-25.81	2	61.9	15.5	1	17-29	K.EKMELLDQFDNER.K	Oxidation: 3	Wdown:Qdown 2.32

Detailed Protein Report

Protein 484: **transmembrane protein 2 isoform b [Homo sapiens]**

Accession: gi|209447096
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 27.9
MW [kDa]: 147.3
pI: 9.4
Sequence Coverage [%]: 1.4
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MYATDSRGHS	PAFLQPQNGN	SRHPSGYVPG	KVVPLRPPPP	PKSQASAKFT	SIRREDRATF	AFSPEEQQAQ	RESQKQKRHK
90	100	110	120	130	140	150	160
NTFICFAITS	FSFFIALAII	LGISSKYAPD	ENCPDQNPRL	RNWDPGQDSA	KQVVIKEGDM	LRLTSDATVH	SIVIQDGGLL
170	180	190	200	210	220	230	240
VFGDNKDGSR	NITLRTHYIL	IQDGGALHIG	AEKCRYKSKA	TITLYGKSDE	GESMPTFGKK	FIGVEAGGTL	ELHGARKASW
250	260	270	280	290	300	310	320
TLLARTLNSS	GLPFGSYTFE	KDFSRGLNVR	VIDQDTAKIL	ESERFDTHEY	RNESRRLQEF	LRFQDPGRIV	AIAVGDSAAK
330	340	350	360	370	380	390	400
SLLQGTIQMI	QERLGSELIQ	GLGYRQAWAL	VGVIDGGSTS	CNESVRNYEN	HSSGGKALAQ	REFYTVDGQK	FSVTAYSEWI
410	420	430	440	450	460	470	480
EETPQFLHMG	EIIDGVDMRA	EVGILTRNIV	IQGEVEDSCY	AENQCQFFDY	DTFGGHIMIM	KNFTSVHLSY	VELKHMGQQQ
490	500	510	520	530	540	550	560
MGRYPVHFHL	CGDVDYKGGY	RHATFVDGLS	IHHSFSRCIT	VHGTNGLLIK	DTIGFDTLGH	CFFLEDGIEQ	RNTLFHNLGL
570	580	590	600	610	620	630	640
LTKPGTLLPT	DRNNSMCTTM	RDKVFGNYIP	VPATDCMAVS	TFWIAHPNNN	LINNAAAGSQ	DAGIWYLFHK	EPTGESSGLQ
650	660	670	680	690	700	710	720
LLAKPELTPL	GIFYNNRVHS	NFKAGLFIDK	GVKTTNSSAA	DPREYLCLDN	SARFRPHQDA	NPEKPRVAAL	IDRLIAFKNN
730	740	750	760	770	780	790	800
DNGAWVRGGD	IIVQNSAFAD	NGIGLTFASD	GSFPSDEGSS	QEVSESLFVG	ESRNYGFQGG	QNKYVGTGGI	DQKPRTLPRN
810	820	830	840	850	860	870	880
RTFPIRGFQI	YDGPIHLTRS	TFKKYVPTPD	RYSSAIGFLM	KNSWQITPRN	NISLVKFGPH	VSLNVFFGKP	GPWFEDCEMD
890	900	910	920	930	940	950	960
GDKNSIFHDI	DGSVTGYKDA	YVGRMDNYLI	RHPSCVNVSK	WNAVICSGTY	AQVYVQTWST	QNLSMTITRD	EYPSNPMVLR
970	980	990	1000	1010	1020	1030	1040
GINQKAAFPQ	YQPVVMLEKG	YTIHWNGPAP	RTTFLYLVNF	NKNDWIRVGL	CYPSNTSFQV	TFGYLQRQNG	SLSKIEEYEP
1050	1060	1070	1080	1090	1100	1110	1120
VHSLEELQRK	QSERKFYFDS	STGLLFLYLK	AKSHRHGHSY	CSSQGCERVK	IQAATDSKDI	SNCMAKAYPQ	YYRKPSVVKR
1130	1140	1150	1160	1170	1180	1190	1200
MPAMLTGLCQ	GCGTRQVVFT	SDPHKSYLPV	QFQSPDKAET	QRGDPSVISV	NGTDFTFRSA	GVLLLVVDPC	SVPFRLTEKT
1210	1220	1230	1240	1250	1260	1270	1280
VFPLADVSRI	EEYLKTGIPP	RSIVLLSTRG	EIKQLNISHL	LVPLGLAKPA	HLYDKGSTIF	LGFSGNFKPS	WTKLFTSPAG
1290	1300	1310	1320	1330			
QGLGVLEQFI	PLQLDEYGCP	RATTVRRRDL	ELLKQASKAH				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2384	1	841.6330	235.44	1	58.2	16.4	2	194-199	K.CRYKSK.A	Carbamidomethyl: 1

Detailed Protein Report

Protein 485: zinc finger protein 182 isoform 2 [Homo sapiens]

Accession:	gi|55769561	**Score:**	27.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	71.5
Database Date:	2015-11-30	**pI:**	10.0
		Sequence Coverage [%]:	3.7
		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	2	820.1114	178.53	2	58.3	14.6	2	223-235	K.TFSKKSHLIVHWR.T	

Detailed Protein Report

Protein 486: 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 487: kinesin-like protein KIF1C [Homo sapiens]

Accession:	gi|40254834	**Score:**	27.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	122.9
Database Date:	2015-11-30	**pI:**	6.5
		Sequence Coverage [%]:	2.8
		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 488: trafficking protein particle complex subunit 9 isoform a [Homo sapiens]

Accession:	gi|238624122	**Score:**	27.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	139.3
Database Date:	2015-11-30	**pI:**	6.9
		Sequence Coverage [%]:	2.7
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	2.97	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	1.74	**CV:**	0.00 %	**No. of Peptides:**	1

```
        10         20         30         40         50         60         70         80
MVPAGDQDRA PHRGKPAQAG ARTSRASRAL RSWRRSQAAR ATVTHPRGGH DRGSHGGYRE GHRGCRRDPQ WASAGPPPLS
        90        100        110        120        130        140        150        160
FTEEVKFELR ALKDWDFKMS VPDYMQCAED HQTLLVVVQP VGIVSEENFF RIYKRICSVS QISVRDSQRV LYIRYRHHYP
       170        180        190        200        210        220        230        240
PENNEWGDFQ THRKVVGLIT ITDCFSAKDW PQTFEKFHVQ KEIYGSTLYD SRLFVFGLQG EIVEQPRTDV AFYPNYEDCQ
       250        260        270        280        290        300        310        320
TVEKRIEDFI ESLFIVLESK RLDRATDKSG DKIPLLCVPF EKKDFVGLDT DSRHYKKRCQ GRMRKHVGDL CLQAGMLQDS
       330        340        350        360        370        380        390        400
LVHYHMSVEL LRSVNDFLWL GAALEGLCSA SVIYHYPGGT GGKSGARRFQ GSTLPAEAAN RHRPGAQEVL IDPGALTTNG
       410        420        430        440        450        460        470        480
INPDTSTEIG RAKNCLSPED IIDKYKEAIS YYSKYKNAGV IELEACIKAV RVLAIQKRSM EASEFLQNAV YINLRQLSEE
       490        500        510        520        530        540        550        560
EKIQRYSILS ELYELIGFHR KSAFFKRVAA MQCVAPSIAE PGWRACYKLL LETLPGYSLS LDPKDFSRGT HRGWAAVQMR
       570        580        590        600        610        620        630        640
LLHELVYASR RMGNPALSVR HLSFLLQTML DFLSDQEKKD VAQSLENYTS KCPGTMEPIA LPGGLTLPPV PFTKLPIVRH
       650        660        670        680        690        700        710        720
VKLLNLPASL RPHKMKSLLG QNVSTKSPFI YSPIIAHNRG EERNKKIDFQ WVQGDVCEVQ LMVYNPMPFE LRVENMGLLT
       730        740        750        760        770        780        790        800
SGVEFESLPA ALSLPAESGL YPVTLVGVPQ TTGTITVNGY HTTVFGVFSD CLLDNLPGIK TSGSTVEVIP ALPRLQISTS
       810        820        830        840        850        860        870        880
LPRSAHSLQP SSGDEISTNV SVQLYNGESQ QLIIKLENIG MEPLEKLEVT SKVLTTKEKL YGDFLSWKLE ETLAQFPLQP
       890        900        910        920        930        940        950        960
GKVATFTINI KVKLDFSCQE NLLQDLSDDG ISVSGFPLSS PFRQVVRPRV EGKPVNPPES NKAGDYSHVK TLEAVLNFKY
       970        980        990       1000       1010       1020       1030       1040
SGGPGHTEGY YRNLSLGLHV EVEPSVFFTR VSTLPATSTR QCHLLLDVFN STEHELTVST RSSEALILHA GECQRMAIQV
      1050       1060       1070       1080       1090       1100       1110       1120
DKFNFESFPE SPGEKGQFAN PKQLEEERRE ARGLEIHSKL GICWRIPSLK RSGEASVEGL LNQLVLEHLQ LAPLQWDVLV
      1130       1140       1150       1160       1170       1180       1190       1200
DGQPCDREAV AACQVGDPVR LEVRLTNRSP RSVGPFALTV VPFQDHQNGV HNYDLHDTVS FVGSSTFYLD AVQPSGQSAC
      1210       1220       1230       1240       1250
LGALLFLYTG DFFLHIRFHE DSTSKELPPS WFCLPSVHVC ALEAQA
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
69	1	820.3460	-71.39	3	30.1	12.0	1	951-972	K.TLEAVLNFKYSGGPGHTEGYYR.N		Wdown:Qdown 1.74 mdown:qdown 2.97

Detailed Protein Report

Protein 489: 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 490: **putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16 isoform 1 [Homo sapiens]**

Accession:	gi|255982614	**Score:**	27.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	119.2
Database Date:	2015-11-30	**pI:**	6.4
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	3.0
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MATPAGLERW VQDELHSVLG LSERHVAQFL IGTAQRCTSA EEFVQRLRDT DTLDLSGPAR DFALRLWNKV PRKAVVEKPA
        90        100        110        120        130        140        150        160
RAAEREARAL LEKNRSYRLL EDSEESSEET VSRAGSSLQK KRKKRKHLRK KREEEEEEEA SEKGKKKTGG SKQQTEKPES
       170        180        190        200        210        220        230        240
EDEWERTERE RLQDLEERDA FAERVRQRDK DRTRNVLERS DKKAYEEAQK RLKMAEEDRK AMVPELRKKS RREYLAKRER
       250        260        270        280        290        300        310        320
EKLEDLEAEL ADEEFLFGDV ELSRHERQEL KYKRRVRDLA REYRAAGEQE KLEATNRYHM PKETRGQPAR AVDLVEEESG
       330        340        350        360        370        380        390        400
APGEEQRRWE EARLGAASLK FGARDAASQE PKYQLVLEEE ETIEFVRATQ LQGDEEPSAP PTSTQAQQKE SIQAVRRSLP
       410        420        430        440        450        460        470        480
VFPFREELLA AIANHQVLII EGETGSGKTT QIPQYLFEEG YTNKGMKIAC TQPRRVAAMS VAARVAREMG VKLGNEVGYS
       490        500        510        520        530        540        550        560
IRFEDCTSER TVLRYMTDGM LLREFLSEPD LASYSVVMVD EAHERTLHTD ILFGLIKDVA RFRPELKVLV ASATMDTARF
       570        580        590        600        610        620        630        640
STFFDDAPVF RIPGRRFPVD IFYTKAPEAD YLEACVVSVL QIHVTQPPGD ILVFLTGQEE IEAACEMLQD RCRRLGSKIR
       650        660        670        680        690        700        710        720
ELLVLPIYAN LPSDMQARIF QPTPPGARKV VVATNIAETS LTIEGIIYVL DPGFCKQKSY NPRTGMESLT VTPCSKASAN
       730        740        750        760        770        780        790        800
QRAGRAGRVA AGKCFRLYTA WAYQHELEET TVPEIQRTSL GNVVLLLKSL GIHDLMHFDF LDPPPYETLL LALEQLYALG
       810        820        830        840        850        860        870        880
ALNHLGELTT SGRKMAELPV DPMLSKMILA SEKYSCSEEI LTVAAMLSVN NSIFYRPKDK VVHADNARVN FFLPGGDHLV
       890        900        910        920        930        940        950        960
LLNVYTQWAE SGYSSQWCYE NFVQFRSMRR ARDVREQLEG LLERVEVGLS SCQGDYIRVR KAITAGYFYH TARLTRSGYR
       970        980        990       1000       1010       1020       1030       1040
TVKQQQTVFI HPNSSLFEQQ PRWLLYHELV LTTKEFMRQV LEIESSWLLE VAPHYYKAKE LEDPHAKKMP KKIGKTREEL
      1050
G
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2134	1	937.3539	-151.57	2	55.3	12.3	2	448-464	K.IACTQPRRVAAMSVAAR.V	Carbamidomethyl: 3; Oxidation: 12

Detailed Protein Report

Protein 491: PREDICTED: zinc finger protein 778 isoform X4 [Homo sapiens]

Accession:	gi|578828903	**Score:**	27.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	66.5
Database Date:	2015-11-30	**pI:**	9.6
		Sequence Coverage [%]:	4.1
		No. of unique Peptides:	1

Quantitation

mdown:qdown **Median:** 0.60 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MAAPDLAHGG	HVSRDSVCLH	EEQTQAAGMV	AGWLINCYQD	AVTFDDVAVD	FTQEEWTLLD	PSQRDLYRDV	MLENYENLAS
90	100	110	120	130	140	150	160
VGHHLFQPSV	IYWLEQEEEL	RAGRRAVLQE	WRLKTKGPAL	RQDRSWFRAS	NETQTARSHN	GGQLCDRTQC	GEAFSEHSGL
170	180	190	200	210	220	230	240
STHVRTQNTG	DSCVSNHYER	DFFIPCQKTL	FKIGEQFSVL	GQCGKAFSST	PNVVSQQACT	RDRSLDYSSC	GEVFLNQSYL
250	260	270	280	290	300	310	320
QARAGSHNGE	ETWKWKPCGK	ALTHSMGCAT	PVEMHAVRNP	HVCRECGKAF	RYTAYLTGRV	QVHPGEKPCE	LEECGKASPV
330	340	350	360	370	380	390	400
SSSLTQHVRI	HAAEKPCECK	ECGKAFTGLS	GLSKHVQTDP	GQKPYECKDC	GKAYNRVYLL	NEHVKTHTEE	KPFICTVCRK
410	420	430	440	450	460	470	480
SFRNSSCLNK	HIQIHTGIKP	YECKDCGKTF	TVSSSLTEHI	RTHTGEKPYE	CKVCGKAFTT	SSHLIVHIRT	HTGEKPYICK
490	500	510	520	530	540	550	560
ECGKAFASSS	HLIEHRRTHT	GEKPYICNEC	GKAFRASSHL	HKHGRIHTGQ	KPYKCKECGK	AYNRFYLLKE	HLKTYTEEQV
570	580	590					
FVCKDCGKSF	KNSSCLNHHT	QIHTDEKPF					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1559	1	977.1043	137.72	2	48.2	11.4	2	122-137	R.QDRSWFRASNETQTAR.S		mdown:qdown 0.60

Detailed Protein Report

Protein 492: PREDICTED: cullin-9 isoform X3 [Homo sapiens]

Accession:	gi|578811520	**Score:**	27.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	268.2
Database Date:	2015-11-30	**pI:**	5.3
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.3
		No. of unique Peptides:	2

Detailed Protein Report

10	20	30	40	50	60	70	80
MVGERHAGDL	MVPLGPRLQA	YPEELIRQRP	GHDGHPEYLI	RWSVLKCGEV	GKVGVEEGKA	EHILMWLSAP	EVYANCPGLL
90	100	110	120	130	140	150	160
GERALSKGLQ	HEPAGVSGSF	PRDPGGLDEV	AMGEMEADVQ	ALVRRAARQL	AESGTPSLTA	AVLHTIHVLS	AYASIGPLTG
170	180	190	200	210	220	230	240
VFRETGALDL	LMHMLCNPEP	QIRRSAGKML	QALAAHDAGS	RAHVLLSLSQ	QDGIEQHMDF	DSRYTLLELF	AETTSSEEHC
250	260	270	280	290	300	310	320
MAFEGIHLPQ	IPGKLLFSLV	KRYLCVTSLL	DQLNSSPELG	AGDQSSPCAT	REKSRGQREL	EFSMAVGNLI	SELVRSMGWA
330	340	350	360	370	380	390	400
RNLSEQGMSP	PRPTRSIFQP	YISGPSLLLP	TIVTTPRRQG	WVFRQRSEFS	SRSGYGEYVQ	QTLQPGMRVR	MLDDYEEISA
410	420	430	440	450	460	470	480
GDEGEFRQSN	NGIPPVQTLG	EKALGEISVS	VEMAESLLQV	LSSRFEGSTL	NDLLNSQIYT	KYGLLSNEPS	SSSTSRNHSC
490	500	510	520	530	540	550	560
TPDPEEESKS	EASFSEEETE	SLKAKAEAPK	TEAEPTKTRT	ETPMAQSDSQ	LFNQLLVTEG	MTLPTEMKEA	ASEMARALRG
570	580	590	600	610	620	630	640
PGPRSSLDQH	VAAVVATVQI	SSLDTNLQLS	GLSALSQAVE	EVTERDHPLV	RPDRSLREKL	VKMLVELLTN	QVGEKMVVVQ
650	660	670	680	690	700	710	720
ALRLLYLLMT	KHEWRPLFAR	EGGIYAVLVC	MQEYKTSVLV	QQAGLAALKM	LAVASSSEIP	TFVTGRDSIH	SLFDAQMTRE
730	740	750	760	770	780	790	800
IFASIDSATR	PGSESLLLTV	PAAVILMLNT	EGCSSAARNG	LLLLNLLLCN	HHTLGDQIIT	QELRDTLFRH	SGIAPRTEPM
810	820	830	840	850	860	870	880
PTTRTILMML	LNRYSEPPGS	PERAALETPI	IQGQDGSPEL	LIRSLVGGPS	AELLLDLERV	LCREGSPGGA	VRPLLKRLQQ
890	900	910	920	930	940	950	960
ETQPFLLLLR	TLDAPGPNKT	LLLSVLRVIT	RLLDFPEAMV	LPWHEVLEPC	LNCLSGPSSD	SEIVQELTCF	LHRLASMHKD
970	980	990	1000	1010	1020	1030	1040
YAVVLCCLGA	KEILSKVLDK	HSAQLLLGCE	LRDLVTECEK	YAQLYSNLTS	SILAGCIQMV	LGQIEDHRRT	HQPINIPFFD
1050	1060	1070	1080	1090	1100	1110	1120
VFLRHLCQGS	SVEVKEDKCW	EKVEVSSNPH	RASKLTDHNP	KTYWESNGST	GSHYITLHMH	RGVLVRQLTL	LVASEDSSYM
1130	1140	1150	1160	1170	1180	1190	1200
PARVVVFGGD	STSCIGTELN	TVNVMPSASR	VILLENLNRF	WPIIQIRIKR	CQQGGIDTRV	RGVEVLGPKP	TFWPLFREQL
1210	1220	1230	1240	1250	1260	1270	1280
CRRTCLFYTI	RAQAWSRDIA	EDHRRLLQLC	PRLNRVLRHE	QNFADRFLPD	DEAAQALGKT	CWEALVSPLV	QNITSPDAEG
1290	1300	1310	1320	1330	1340	1350	1360
VSALGWLLDQ	YLEQRETSRN	PLSRAASFAS	RVRRLCHLLV	HVEPPPGPSP	EPSTRPFSKN	SKGRDRSPAP	SPVLPSSSLR
1370	1380	1390	1400	1410	1420	1430	1440
NITQCWLSVV	QEQVSRFLAA	AWRAPDFVPR	YCKLYEHLQR	AGSELFGPRA	AFMLALRSGF	SGALLQQSFL	TAAHMSEQFA
1450	1460	1470	1480	1490	1500	1510	1520
RYIDQQIQGG	LIGGAPGVEM	LGQLQRHLEP	IMVLSGLELA	TTFEHFYQHY	MADRLLSFGS	SWLEGAVLEQ	IGLCFPNRLP
1530	1540	1550	1560	1570	1580	1590	1600
QLMLQSLSTS	EELQRQFHLF	QLQRLDKLFL	EQEDEEEKRL	EEEEEEEEEE	EAEKELFIED	PSPAISILVL	SPRCWPVSPL
1610	1620	1630	1640	1650	1660	1670	1680
CYLYHPRKCL	PTEFCDALDR	FSSFYSQSQN	HPVLDMGPHR	RLQWTWLGRA	ELQFGKQILH	VSTVQMWLLL	KFNQTEEVSV
1690	1700	1710	1720	1730	1740	1750	1760
ETLLKDSDLS	PELLLQALVP	LTSGNGPLTL	HEGQDFPHGG	VLRLHEPGPQ	RSGEALWLIP	PQAYLNVEKD	EGRTLEQKRN
1770	1780	1790	1800	1810	1820	1830	1840
LLSCLLVRIL	KAHGEKGLHI	DQLVCLVLEA	WQKGPNPPGT	LGHTVAGGVA	CTSTDVLSCI	LHLLGQGYVK	RRDDRPQILM
1850	1860	1870	1880	1890	1900	1910	1920
YAAPEPMGPC	RGQADVPFCG	SQSETSKPSP	EAVATLASLQ	LPAGRTMSPQ	EVEGLMKQTV	RQVQETLNLE	PDVAQHLLAH
1930	1940	1950	1960	1970	1980	1990	2000
SHWGAEQLLQ	SYSEDPEPLL	LAAGLCVHQA	QAVPVRPDHC	PVCVSPLGCD	DDLPSLCCMH	YCCKSCWNEY	LTTRIEQNLV
2010	2020	2030	2040	2050	2060	2070	2080
LNCTCPIADC	PAQPTGAFIR	AIVSSPEVIS	KYEKALLRGY	VESCSNLTWC	TNPQGCDRIL	CRQGLGCGTT	CSKCGWASCF
2090	2100	2110	2120	2130	2140	2150	2160
NCSFPEAHYP	ASCGHMSQWV	DDGGYYDGMS	VEAQSKHLAK	LISKRCPSCQ	APIEKNEGCL	HMTCAKCNHG	FCWRCLKSWK
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2528	1	938.1784	46.28	3	60.3	13.1	2	164-188	R.ETGALDLLMHMLCNPEPQIRRSAGK.M	Oxidation: 9, 11
949	1	737.3420	-85.80	1	40.4	14.7	0	790-796	R.HSGIAPR.T	

Detailed Protein Report

Protein 493: probable guanine nucleotide exchange factor MCF2L2 [Homo sapiens]

Accession:	gi|540344580	**Score:**	27.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	126.9
Database Date:	2015-11-30	**pI:**	6.0
		Sequence Coverage [%]:	3.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLSCLKEEMP	PQELTRRLAT	VITHVDEIMQ	QEVRPLMAVE	IIEQLHRQFA	ILSGGRGEDG	APIITFPEFS	GFKHIPDEDF
90	100	110	120	130	140	150	160
LNVMTYLTSI	PSVEAASIGF	IVVIDRRRDK	WSSVKASLTR	IAVAFPGNLQ	LIFILRPSRF	IQRTFTDIGI	KYYRNEFKTK
170	180	190	200	210	220	230	240
VPIIMVNSVS	DLHGYIDKSQ	LTRELGGTLE	YRHGQWVNHR	TAIENFALTL	KTTAQMLQTF	GSCLATAELP	RSMLSTEDLL
250	260	270	280	290	300	310	320
MSHTRQRDKL	QDELKLLGKQ	GTTLLSCIQE	PATKCPNSKL	NLNQLENVTT	MERLLVQLDE	TEKAFSHFWS	EHHLKLNQCL
330	340	350	360	370	380	390	400
QLQHFEHDFC	KAKLALDNLL	EEQAEFTGIG	DSVMHVEQIL	KEHKKLEEKS	QEPLEKAQLL	ALVGDQLIQS	HHYAADAIRP
410	420	430	440	450	460	470	480
RCVELRHLCD	DFINGNKKKW	DILGKSLEFH	RQLDKVSQWC	EAGIYLLASQ	AVDKCQSREG	VDIALNDIAT	FLGTVKEYPL
490	500	510	520	530	540	550	560
LSPKEFYNEF	ELLLTLDAKA	KAQKVLQRLD	DVQEIFHKRQ	VSLMKLAAKQ	TRPVQPVAPH	PESSPKWVSS	KTSQPSTSVP
570	580	590	600	610	620	630	640
LARPLRTSEE	PYTETELNSR	GKEDDETKFE	VKSEEIFESH	HERGNPELEQ	QARLGDLSPR	RRIIRDLLET	EEIYIKEIKS
650	660	670	680	690	700	710	720
IIDGYITPMD	FIWLKHLIPD	VLQNNKDFLF	GNIRELYEFH	NRTFLKELEK	CAENPELLAH	CFLKRKEDLQ	IYFKYHKNLP
730	740	750	760	770	780	790	800
RARAIWQECQ	DCAYFGVCQR	QLDHNLPLFK	YLKGPSQRLI	KYQMLLKGLL	DFESPEDMEI	DPGELGGSAK	DGPKRTKDSA
810	820	830	840	850	860	870	880
FSTELQQALA	VIEDLIKSCE	LAVDLAAVTE	CPDDIGKLGK	LLLHGPFSVW	TIHKDRYKMK	DLIRFKPSQR	QIYLFERGIV
890	900	910	920	930	940	950	960
FCKIRMEPGD	QGLSPHYSFK	KAMKLMTLSI	RQLGRGSHRK	FEIASRNGLE	KYILQAASKE	IRDCWFSEIS	KLLMEQQNNI
970	980	990	1000	1010	1020	1030	1040
KDQGNPQFEM	STSKGSGAGS	GPWIKNMERA	TTSKEDPASS	TGGIKGCSSR	EFSSMDTFED	CEGAEDMEKE	SSALSLAGLF
1050	1060	1070	1080	1090	1100	1110	1120
QSDDSHETCS	SKSAFLERGE	SSQGEKEERD	EEETATRSTE	EERAGASTGR	LAPAGATAGF	QARALRPRTS	AQES

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2845	1	938.5013	-5.79	2	64.1	16.3	0	459-476	R.EGVDIALNDIATFLGTVK.E	

Detailed Protein Report

Protein 494: PREDICTED: uncharacterized protein LOC101928647 [Homo sapiens]

Accession:	gi|530368444	**Score:**	27.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	25.5
Database Date:	2015-11-30	**pI:**	12.1
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	13.3
		No. of unique Peptides:	2

```
        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
593	1	690.2064	-214.88	2	36.3	15.6	0	1-13	-.MEISLAGISACLR.G	Oxidation: 1
27	1	1182.5709	-22.85	2	29.6	12.2	1	84-103	R.IWVSSCFPCLVTRPVCRGQR.R	Carbamidomethyl: 9

Detailed Protein Report

Protein 495: PREDICTED: nephronectin isoform X3 [Homo sapiens]

Accession:	gi|530377475	**Score:**	27.8
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 496: mitochondrial dynamic protein MID49 isoform 3 [Homo sapiens]

Accession:	gi|222080060	**Score:**	27.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	20.5
Database Date:	2015-11-30	**pI:**	10.7
		Sequence Coverage [%]:	17.6
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:** 1.43	**CV:** 0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:** 0.30	**CV:** 0.00 %	**No. of Peptides:**	1

10	20	30	40	50	60	70	80
MAEFSQKRGK	RRSDEGLGSM	VDFLLANARL	VLGVGGAAVL	GIATLAVKRF	IDRATSPRDE	DDTKADSWKE	LSLLKATPHL
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
QPRPPPAALS	QPVLPLAPSS	SAPGEAAGLR	AGPCDHPSSP	GGFGQTAGWR	HRPGAAGLLS	EQVPGTALWG	IRAWGAALRR
170	**180**	**190**	**200**	**210**			
AAGGGCGPCA	SPGATGAGAG	PVEPGAGRGH	CGEGPSLLGR	AQDAA			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
773	1	450.7679	13.60	2	38.5	10.8	1	153-160	R.AWGAALRR.A		mdown:qdown 1.43 Wdown:Qdown 0.30

Detailed Protein Report

Protein 497: PREDICTED: T-lymphoma invasion and metastasis-inducing protein 1 isoform X4 [Homo sapiens]

Accession:	gi|530419050	**Score:**	27.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	161.7
Database Date:	2015-11-30	**pI:**	6.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.4
		No. of unique Peptides:	1

Quantitation

Wdown:Qdown **Median:** 1.24 **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
1363	1	942.5111	16.59	2	45.8	11.1	2	1139-1154	R.FKLYSAFCASHTKVPK.V	Carbamidomethyl: 8	Wdown:Qdown 1.24

Detailed Protein Report

Protein 498: PREDICTED: serine/threonine-protein kinase Nek4 isoform X1 [Homo sapiens]

Accession:	gi|578806508	**Score:**	27.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	89.9
Database Date:	2015-11-30	**pI:**	8.7
		Sequence Coverage [%]:	4.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPLAAYCYLR	VVGKGSYGEV	TLVKHRRDGK	QYVIKKLNLR	NASSRERRAA	EQEAQLLSQL	KHPNIVTYKE	SWEGGDGLLY
90	100	110	120	130	140	150	160
IVMGFCEGGD	LYRKLKEQKG	QLLPENQVVE	WFVQIAMALQ	YLHEKHILHR	DLKTQNVFLT	RTNIIKVGDL	GIARVLENHC
170	180	190	200	210	220	230	240
DMASTLIGTP	YYMSPELFSN	KPYNYKSDVW	ALGCCVYEMA	TLKHAFNAKD	MNSLVYRIIE	GKLPPMPRDY	SPELAELIRT
250	260	270	280	290	300	310	320
MLSKRPEERP	SVRSILRQPY	IKRQISFFLE	ATKIKTSKNN	IKNGDSQSKP	FATVVSGEAE	SNHEVIHPQP	LSSEGSQTYI
330	340	350	360	370	380	390	400
MGEGKCLSQE	KPRASGLLKS	PASLKAHTCK	QDLSNTTELA	TISSVNIDIL	PAKGRDSVSD	GFVQENQPRY	LDASNELGGI
410	420	430	440	450	460	470	480
CSISQVEEEM	LQDNTKSSAQ	PENLIPMWSS	DIVTGEKNEP	VKPLQPLIKE	QKPKDQDQVA	GECIIEKQGR	IHPDLQPHNS
490	500	510	520	530	540	550	560
GSEPSLSRQR	RQKRREQTEH	RGEKRQVRRD	LFAFQESPPR	FLPSHPIVGK	VDVTSTQKEA	ENQRRVVTGS	VSSSRSSEMS
570	580	590	600	610	620	630	640
SSKDRPLSAR	ERRRLKQSQE	EMSSSGPSVR	KASLSVAGPG	KPQEEDQPLP	ARRLSSDCSV	TQERKQIHCL	SEDELSSSTS
650	660	670	680	690	700	710	720
STDKSDGDYG	EGKGQTNEIN	ALVQLMTQTL	KLDSKESCED	VPVANPVSEF	KLHRKYRDTL	ILHGKVAEEA	EEIHFKELPS
730	740	750	760	770	780	790	800
AIMPGSEKIR	RLVEVLRTDV	IRGLGVQLLE	QVYDLLEEED	EFDREVRLRE	HMGEKYTTYS	VKARQLKFFE	ENMNF

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1866	1	716.4002	35.77	3	52.0	13.8	0	592-612	K.ASLSVAGPGKPQEEDQPLPAR.R	

Detailed Protein Report

Protein 499: PREDICTED: histone acetyltransferase KAT2A isoform X2 [Homo sapiens]

Accession:	gi|578830713	**Score:**	27.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	54.1
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
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 500: 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 501: dynein heavy chain 9, axonemal isoform 2 [Homo sapiens]

Accession:	gi|114155133	**Score:**	27.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	511.6
Database Date:	2015-11-30	**pI:**	5.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	0.7
		No. of unique Peptides:	1

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

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
106	1	1068.1367	75.32	2	30.1	13.8	2	182-201	K.GKTLLPLPAGSEKMEFADSK.S	Oxidation: 14

Detailed Protein Report

Protein 502: **PERQ amino acid-rich with GYF domain-containing protein 2 isoform c [Homo sapiens]**

Accession:	gi|156766047	**Score:**	27.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	149.4
Database Date:	2015-11-30	**pI:**	5.3
		Sequence Coverage [%]:	1.6
		No. of unique Peptides:	2

Quantitation

mdown:qdown **Median:** 2.00 **CV:** 94.41 % **No. of Peptides:** 2

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
1628	1	1071.6266	33.70	1	50.2	10.0	1	758-765	R.QQEEILRR.Q		mdown:qdown 4.44
175	2	838.3909	-15.70	2	31.6	17.6	0	1010-1022	K.QQQQQQQHQQPNR.A		mdown:qdown 0.90

Detailed Protein Report

Protein 503: **dnaJ homolog subfamily A member 3, mitochondrial isoform 3 [Homo sapiens]**

Accession:	gi|557357763	**Score:**	27.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	33.1
Database Date:	2015-11-30	**pI:**	10.1
Modification(s):	Oxidation	**Sequence Coverage [%]:**	9.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAEPQAERPR	LCVFPDLLRP	PSAADIETWC	QPYRKIFGEF	SSSSFGDFQT	VFDQPQEYFM	ELTFNQAAKG	VNKEFTVNIM
90	100	110	120	130	140	150	160
DTCERCNGKG	NEPGTKVQHC	HYCGGSGMET	INTGPFVMRS	TCRRCGGRGS	IIISPCVVCR	GAGQAKQKKR	VMIPVPAGVE
170	180	190	200	210	220	230	240
DGQTVRMPVG	KREIFITFRV	QKSPVFRRDG	ADIHSDLFIS	IAQALLGGTA	RAQGLYETIN	VTIPPGTQTD	QKIRMGGKGI
250	260	270	280	290	300	310	
PRINSYGYGD	HYIHIKIRVP	KRLTSRQQSL	ILSYAEDETD	VEGTVNGVTL	TSSGKRSTGN		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2705	1	842.5419	120.53	2	62.2	10.1	0	151-166	R.VMIPVPAGVEDGQTVR.M	Oxidation: 2

Detailed Protein Report

Protein 504: laminin subunit gamma-1 precursor [Homo sapiens]

Accession: gi|145309326
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 27.6
MW [kDa]: 177.5
pI: 4.9
Sequence Coverage [%]: 1.6
No. of unique Peptides: 2

Quantitation

mdown:qdown **Median:** 1.02 **CV:** 0.00 % **No. of Peptides:** 1
Wdown:Qdown **Median:** 1.63 **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
2687	2	941.9781	66.10	2	62.0	14.3	1	303-318	K.LVCNCKHNTYGVDCEK.C	Carbamidomethyl: 14	
1858	1	590.7710	-122.60	2	53.3	13.3	2	1037-1046	R.LVKDKVADHR.V		Wdown:Qdown 1.63 mdown:qdown 1.02

Detailed Protein Report

Protein 505: PREDICTED: calpastatin isoform X10 [Homo sapiens]

Accession:	gi|578810591	**Score:**	27.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	80.1
Database Date:	2015-11-30	**pI:**	4.9
		Sequence Coverage [%]:	4.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSQPGQKPAA	SPRPRRAAAA	RRTHEHVSEK	TSESPSKPGE	KKGSDEKKAA	SLGSSQSSRT	YAGGTASATK	VSASSGATSK
90	100	110	120	130	140	150	160
SSSMNPTETK	AVKTEPEKKS	QSTKPKSLPK	QASDTGSNDA	HNKKAVSRSA	EQQPSEKSTE	PKTKPQDMIS	AGGESVAGIT
170	180	190	200	210	220	230	240
AISGKPGDKK	KEKKSLTPAV	PVESKPDKPS	GKSGMDAALD	DLIDTLGGPE	ETEEENTTYT	GPEVSDPMSS	TYIEELGKRE
250	260	270	280	290	300	310	320
VTIPPKYREL	LAKKEGITGP	PADSSKPIGP	DDAIDALSSD	FTCGSPTAAG	KKTEKEESTE	VLKAQSAGTV	RSAAPPQEKK
330	340	350	360	370	380	390	400
RKVEKDTMSD	QALEALSASL	GTRQAEPELD	LRSIKEVDEA	KAKEEKLEKC	GEDDETIPSE	YRLKPATDKD	GKPLLPEPEE
410	420	430	440	450	460	470	480
KPKPRSESEL	IDELSEDFDR	SECKEKPSKP	TEKTEESKAA	APAPVSEAVC	RTSMCSIQSA	PPEPATLKGT	VPDDAVEALA
490	500	510	520	530	540	550	560
DSLGKKEADP	EDGKPVMDKV	KEKAKEEDRE	KLGEKEETIP	PDYRLEEVKD	KDGKPLLPKE	SKEQLPPMSE	DFLLDALSED
570	580	590	600	610	620	630	640
FSGPQNASSL	KFEDAKLAAA	ISEVVSQTPA	STTQAGAPPR	DTSSDKDLDD	ALDKLSDSLG	QRQPDPDENK	PMEDKVKEKA
650	660	670	680	690	700	710	720
KAEHRDKLGE	RDDTIPPEYR	HLLDDNGQDK	PVKPPTKKSE	DSKKPADDQD	PIDALSGDLD	SCPSTTETSQ	NTAKDKCKKA
730	740	750					
ASSSKAPKNG	GKAKDSAKTT	EETSKPKDD					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2971	1	816.9085	-57.77	2	65.9	16.1	1	2-16	M.SQPGQKPAASPRPRR.A	

Detailed Protein Report

Protein 506: TRAF-type zinc finger domain-containing protein 1 [Homo sapiens]

Accession:	gi|5729828	**Score:**	27.5
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 507: beta-defensin 119 isoform a precursor [Homo sapiens]

Accession:	gi|37704382	**Score:**	27.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	9.8
Database Date:	2015-11-30	**pI:**	10.1
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	20.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MKLLYLFLAI	LLAIEEPVIS	GKRHILRCMG	NSGICRASCK	KNEQPYLYCR	NCQSCCLQSY	MRISISGKEE	NTDWSYEKQW
90							
PRLP							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1509	1	981.9713	5.72	2	47.6	13.7	2	24-40	R.HILRCMGNSGICRASCK.K	Carbamidomethyl: 12, 16

Detailed Protein Report

Protein 508: **retinitis pigmentosa 9 protein [Homo sapiens]**

Accession:	gi|42718020	**Score:**	27.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	26.1
Database Date:	2015-11-30	**pI:**	10.4
		Sequence Coverage [%]:	9.5
		No. of unique Peptides:	2

Quantitation

Wdown:Qdown **Median:** 0.61 **CV:** 0.00 % **No. of Peptides:** 1

```
         10         20         30         40         50         60         70         80
MSSRPGREDV GAAGARRPRE PPEQELQRRR EQKRRRHDAQ QLQQLKHLES FYEKPPPGLI KEDETKPEDC IPDVPGNEHA
         90        100        110        120        130        140        150        160
REFLAHAPTK GLWMPLGKEV KVMQCWRCKR YGHRTGDKEC PFFIKGNQKL EQFRVAHEDP MYDIIRDNKR HEKDVRIQQL
        170        180        190        200        210        220        230
KQLLEDSTSD EDRSSSSSSE GKEKHKKKKK KEKHKKRKKE KKKKKKRKHK SSKSNEGSDS E
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1338	1	845.6519	284.75	1	46.4	14.4	0	8-16	R.EDVGAAGAR.R		Wdown:Qdown 0.61
2386	1	704.1871	-182.11	2	58.5	13.1	0	162-173	K.QLLEDSTSDEDR.S		

Detailed Protein Report

Protein 509: **dehydrogenase/reductase SDR family member on chromosome X precursor [Homo sapiens]**

Accession: gi|193804850
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 27.5
MW [kDa]: 36.4
pI: 9.7
Sequence Coverage [%]: 11.2
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MSPLSAARAA	LRVYAVGAAV	ILAQLLRRCR	GGFLEPVFPP	RPDRVAIVTG	GTDGIGYSTA	KHLARLGMHV	IIAGNNDSKA
90	100	110	120	130	140	150	160
KQVVSKIKEE	TLNDKVEFLY	CDLASMTSIR	QFVQKFKMKK	IPLHVLINNA	GVMMVPQRKT	RDGFEEHFGL	NYLGHFLLTN
170	180	190	200	210	220	230	240
LLLDTLKESG	SPGHSARVVT	VSSATHYVAE	LNMDDLQSSA	CYSPHAAYAQ	SKLALVLFTY	HLQRLLAAEG	SHVTANVVDP
250	260	270	280	290	300	310	320
GVVNTDVYKH	VFWATRLAKK	LLGWLLFKTP	DEGAWTSIYA	AVTPELEGVG	GHYLYNEKET	KSLHVTYNQK	LQQQLWSKSC
330	340						
EMTGVLDVTL							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1586	1	1073.1340	41.86	2	48.5	14.7	2	62-81	K.HLARLGMHVIIAGNNDSKAK.Q	

Detailed Protein Report

Protein 510: PREDICTED: coiled-coil domain-containing protein 125 isoform X5 [Homo sapiens]

Accession:	gi|530379210	**Score:**	27.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	48.2
Database Date:	2015-11-30	**pI:**	9.5
		Sequence Coverage [%]:	5.5
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530430737	refseq_human (refseq_human_20140103.fasta)	PREDICTED: coiled-coil domain-containing protein 125 isoform X5 [Homo sapiens]

10	20	30	40	50	60	70	80
MKRVFSIPSI	RASKIHSLKC	PEFPITDDKV	ALEVEMLKTE	LEASQRQLRG	KEEALKILQS	MAILGKATSH	TQAVLQKTME
90	100	110	120	130	140	150	160
QNRSLEKEIN	ALQWEIEFDH	NRFKNIEESW	IQKYDRLNCE	NAVLKENLKV	KTEEIKMLKS	DNAVLNQRYL	EALAMLDIKQ
170	180	190	200	210	220	230	240
QKMAQENMCC	DKSGFAEASG	LELAVLGACL	CHGPGGNPCS	CARMAASTRK	LLLQLKQELE	ILQKSKEEAY	VMADAFRIAF
250	260	270	280	290	300	310	320
EQQLMRKNDQ	ALQLTQMDKM	HKKATKWMNW	KHLKEDGFPS	PRSKKTFGQR	LLGMLPSENS	SKRMEDQDSP	QEVLKMLIDL
330	340	350	360	370	380	390	400
LNDKEEALAH	QRKVSYMLAR	ALEDKDTASN	ENKEKNPIKE	NFPFNNPWRK	TSEFSVLGDP	IHSSVCILNS	VGCICSIQHS
410	420	430					
QIDPNYRTLK	RSHSLPSSII	F					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2803	1	973.5138	-3.08	2	64.1	15.5	1	30-46	K.VALEVEMLKTELEASQR.Q	

Detailed Protein Report

Protein 511: PREDICTED: Hermansky-Pudlak syndrome 3 protein isoform X3 [Homo sapiens]

Accession:	gi|578807815	**Score:**	27.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	106.3
Database Date:	2015-11-30	**pI:**	5.8
		Sequence Coverage [%]:	3.5
		No. of unique Peptides:	1

Quantitation

mdown:qdown **Median:** 1.76 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MVQLYNLHPF	GSQQVVPCKL	EPDRFCGGGR	DALFVAAGCK	VEAFAVAGQE	LCQPRCAFST	LGRVLRLAYS	EAGDYLVAIE
90	100	110	120	130	140	150	160
EKNKATFLRA	YVNWRNKRTE	NSRVCIRMIG	HNVEGPFSKA	FRDQMYIIEM	PLSEAPLCIS	CCPVKGDLLV	GCTNKLVLFS
170	180	190	200	210	220	230	240
LKYQIINEEF	SLLDFERSLI	IHIDNITPVE	VSFCVGYVAV	MSDLEVLIVK	LESGPKNGER	VHHHPHKTNN	RIRRTEEGIS
250	260	270	280	290	300	310	320
NEISQLESDD	FVICQKPLEL	LGEKSEQSGL	SVTLESTGLA	DEKRKYSHFQ	HLLYRRFAPD	ISSYVLSDDI	KLHSLQLLPI
330	340	350	360	370	380	390	400
YQTGSLTSDG	KNLSQEKELL	SLFCFFSLPH	VGYLYMVVKS	VELMSVYQYP	EKSQQAVLTP	QFLHVITSNN	LQCFTVRCSA
410	420	430	440	450	460	470	480
AAAREEDPYM	DTTLKACPPV	SMDVCALRIQ	LFIGLKAICH	FKNHIILLTK	AEPEAIPERR	QSPKRLLSRK	DTSVKIKIPP
490	500	510	520	530	540	550	560
VAEAGWNLYI	VNTISPVQLY	KEMVDYSNTY	KTVKTQSCIH	LLSEAHLLVR	AALMDASQLE	PGEKAELLEA	FKESCGHLGD
570	580	590	600	610	620	630	640
CYSRLDSQHS	HLTLPYYKMS	GLSMAEVLAR	TDWTVEDGLQ	KYERGLIFYI	NHSLYENLDE	ELNEELAAKV	VQMFYVAEPK
650	660	670	680	690	700	710	720
QVPHILCSPS	MKNINPLTAM	SYLRKLDTSG	FSSILVTLTK	AAVALKMGDL	DMHRNEMKSH	SEMKLVCGFI	LEPRLLIQQR
730	740	750	760	770	780	790	800
KGQIVPTELA	LHLKETQPGL	LVASVLGLQK	NNKIGIEEAD	SFFKVLCAKD	EDTIPQLLVD	FWEAQLVACL	PDVVLQELFF
810	820	830	840	850	860	870	880
KLTSQYIWRL	SKRQPPDTTP	LRTSEDLINA	CSHYGLIYPW	VHVVISSDSL	ADKNYTEDLS	KLQSLICGPS	FDIASIIPFL
890	900	910	920	930	940	950	
EPLSEDTIAG	LSVHVLCRTR	LKEYEQCIDI	LLERCPEAVI	PYANHELKEE	NRIDSVVEKT	VA	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2610	1	449.6838	-247.84	2	60.9	14.6	1	715-721	R.LLIQQRK.G		mdown:qdown 1.76

Detailed Protein Report

Protein 512: calcium/calmodulin-dependent protein kinase kinase 2 isoform 6 [Homo sapiens]

Accession:	gi|27437023	**Score:**	27.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	54.1
Database Date:	2015-11-30	**pI:**	7.0
		Sequence Coverage [%]:	8.4
		No. of unique Peptides:	2

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	
1288	2	917.4243	-149.73	2	44.9	16.6	2	430-445	K.NPESRIVVPEIKILVK.T	

Detailed Protein Report

Protein 513: **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

mdown:qdown **Median:** 0.21 **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	mdown:qdown 0.21
1747	1	851.2332	-164.00	2	51.8	12.2	0	812-827	K.SAEMEPEDSGGIHSQK.Q		

Detailed Protein Report

Protein 514: aspartyl aminopeptidase [Homo sapiens]

Accession:	gi|156416028	**Score:**	27.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	53.4
Database Date:	2015-11-30	**pI:**	8.0
		Sequence Coverage [%]:	7.6
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MSGHSPTRGA MQVAMNGKAR KEAVQTAAKE LLKFVNRSPS PFHAVAECRN RLLQAGFSEL KETEKWNIKP ESKYFMTRNS
        90        100        110        120        130        140        150        160
STIIAFAVGG QYVPGNGFSL IGAHTDSPCL RVKRRSRRSQ VGFQQVGVET YGGGIWSTWF DRDLTLAGRV IVKCPTSGRL
       170        180        190        200        210        220        230        240
EQQLVHVERP ILRIPHLAIH LQRNINENFG PNTEMHLVPI LATAIQEELE KGTPEPGPLN AVDERHHSVL MSLLCAHLGL
       250        260        270        280        290        300        310        320
SPKDIVEMEL CLADTQPAVL GGAYDEFIFA PRLDNLHSCF CALQALIDSC AGPGSLATEP HVRMVTLYDN EEVGSESAQG
       330        340        350        360        370        380        390        400
AQSLLTELVL RRISASCQHP TAFEEAIPKS FMISADMAHA VHPNYLDKHE ENHRPLFHKG PVIKVNSKQR YASNAVSEAL
       410        420        430        440        450        460        470        480
IREVANKVKV PLQDLMVRND TPCGTTIGPI LASRLGLRVL DLGSPQLAMH SIREMACTTG VLQTLTLFKG FFELFPSLSH
       490
NLLVD
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2198	1	1031.5929	23.90	2	56.1	12.4	2	391-409	R.YASNAVSEALIREVANKVK.V	

Detailed Protein Report

Protein 515: **PREDICTED: suppressor of tumorigenicity 7 protein-like isoform X10 [Homo sapiens]**

Accession:	gi|530362849	**Score:**	27.4
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
2047	1	625.2681	-128.78	2	54.2	13.8	1	259-269	K.QALKAGETIYR.Q	
2581	2	836.1729	-298.97	1	60.5	13.6	1	298-304	R.RLAMCAR.K	Oxidation: 4

Detailed Protein Report

Protein 516: voltage-dependent R-type calcium channel subunit alpha-1E isoform 2 [Homo sapiens]

Accession:	gi|329663531	**Score:**	27.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	254.4
Database Date:	2015-11-30	**pI:**	9.3
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.3
		No. of unique Peptides:	2

Quantitation

Wdown:Qdown	**Median:** 1.28	**CV:** 0.00 %	**No. of Peptides:** 1

Detailed Protein Report

10	20	30	40	50	60	70	80
MARFGEAVVA	RPGSGDGDSD	QSRNRQGTPV	PASGQAAAYK	QTKAQRARTM	ALYNPIPVRQ	NCFTVNRSLF	IFGEDNIVRK
90	100	110	120	130	140	150	160
YAKKLIDWPP	FEYMILATII	ANCIVLALEQ	HLPEDDKTPM	SRRLEKTEPY	FIGIFCFEAG	IKIVALGFIF	HKGSYLRNGW
170	180	190	200	210	220	230	240
NVMDFIVVLS	GILATAGTHF	NTHVDLRTLR	AVRVLRPLKL	VSGIPSLQIV	LKSIMKAMVP	LLQIGLLLFF	AILMFAIIGL
250	260	270	280	290	300	310	320
EFYSGKLHRA	CFMNNSGILE	GFDPPHPCGV	QGCPAGYECK	DWIGPNDGIT	QFDNILFAVL	TVFQCITMEG	WTTVLYNTND
330	340	350	360	370	380	390	400
ALGATWNWLY	FIPLIIIGSF	FVLNLVLGVL	SGEFAKERER	VENRRAFMKL	RRQQQIEREL	NGYRAWIDKA	EEVMLAEENK
410	420	430	440	450	460	470	480
NAGTSALEVL	RRATIKRSRT	EAMTRDSSDE	HCVDISSVGT	PLARASIKSA	KVDGVSYFRH	KERLLRISIR	HMVKSQVFYW
490	500	510	520	530	540	550	560
IVLSLVALNT	ACVAIVHHNQ	PQWLTHLLYY	AEFLFLGLFL	LEMSLKMYGM	GPRLYFHSSF	NCFDFGVTVG	SIFEVVWAIF
570	580	590	600	610	620	630	640
RPGTSFGISV	LRALRLLRIF	KITKYWASLR	NLVVSLMSSM	KSIISLLFLL	FLFIVVFALL	GMQLFGGRFN	FNDGTPSANF
650	660	670	680	690	700	710	720
DTFPAAIMTV	FQILTGEDWN	EVMYNGIRSQ	GGVSSGMWSA	IYFIVLTLFG	NYTLLNVFLA	IAVDNLANAQ	ELTKDEQEEE
730	740	750	760	770	780	790	800
EAFNQKHALQ	KAKEVSPMSA	PNMPSIERER	RRRHHMSVWE	QRTSQLRKHM	QMSSQEALNR	EEAPTMNPLN	PLNPLSSLNP
810	820	830	840	850	860	870	880
LNAHPSLYRR	PRAIEGLALG	LALEKFEEER	ISRGGSLKGD	GGDRSSALDN	QRTPLSLGQR	EPPWLARPCH	GNCDPTQQEA
890	900	910	920	930	940	950	960
GGGEAVVTFE	DRARHRQSQR	RSRHRRVRTE	GKESSSASRS	RSASQERSLD	EAMPTEGEKD	HELRGNHGAK	EPTIQEERAQ
970	980	990	1000	1010	1020	1030	1040
DLRRTNSLMV	SRGSGLAGGL	DEADTPLVLP	HPELEVGKHV	VLTEQEPEGS	SEQALLGNVQ	LDMGRVISQS	EPDLSCITAN
1050	1060	1070	1080	1090	1100	1110	1120
TDKATTESTS	VTVAIPDVDP	LVDSTVVHIS	NKTDGEASPL	KEAEIREDEE	EVEKKKQKKE	KRETGKAMVP	HSSMFIFSTT
1130	1140	1150	1160	1170	1180	1190	1200
NPIRRACHYI	VNLRYFEMCI	LLVIAASSIA	LAAEDPVLTN	SERNKVLRYF	DYVFTGVFTF	EMVIKMIDQG	LILQDGSYFR
1210	1220	1230	1240	1250	1260	1270	1280
DLWNILDFVV	VVGALVAFAL	ANALGTNKGR	DIKTIKSLRV	LRVLRPLKTI	KRLPKLKAVF	DCVVTSLKNV	FNILIVYKLF
1290	1300	1310	1320	1330	1340	1350	1360
MFIFAVIAVQ	LFKGKFFYCT	DSSKDTEKEC	IGNYVDHEKN	KMEVKGREWK	RHEFHYDNII	WALLTLFTVS	TGEGWPQVLQ
1370	1380	1390	1400	1410	1420	1430	1440
HSVDVTEEDR	GPSRSNRMEM	SIFYVVYFVV	FPFFFVNIFV	ALIIITFQEQ	GDKMMEECSL	EKNERACIDF	AISAKPLTRY
1450	1460	1470	1480	1490	1500	1510	1520
MPQNRHTFQY	RVWHFVVSPS	FEYTIMAMIA	LNTVVLMMKY	YSAPCTYELA	LKYLNIAFTM	VFSLECVLKV	IAFGFLNYFR
1530	1540	1550	1560	1570	1580	1590	1600
DTWNIFDFIT	VIGSITEIIL	TDSKLVNTSG	FNMSFLKLFR	AARLIKLLRQ	GYTIRILLWT	FVQSFKALPY	VCLLIAMLFF
1610	1620	1630	1640	1650	1660	1670	1680
IYAIIGMQVF	GNIKLDEESH	INRHNNFRSF	FGSLMLLFRS	ATGEAWQEIM	LSCLGEKGCE	PDTTAPSGQN	ENERCGTDLA
1690	1700	1710	1720	1730	1740	1750	1760
YVYFVSFIFF	CSFLMLNLFV	AVIMDNFEYL	TRDSSILGPH	HLDEFVRVWA	EYDRAACGRI	HYTEMYEMLT	LMSPPLGLGK
1770	1780	1790	1800	1810	1820	1830	1840
RCPSKVAYKR	LVLMNMPVAE	DMTVHFTSTL	MALIRTALDI	KIAKGGADRQ	QLDSELQKET	LAIWPHLSQK	MLDLLVPMPK
1850	1860	1870	1880	1890	1900	1910	1920
ASDLTVGKIY	AAMMIMDYYK	QSKVKKQRQQ	LEEQKNAPMF	QRMEPSSLPQ	EIIANAKALP	YLQQDPVSGL	SGRSGYPSMS
1930	1940	1950	1960	1970	1980	1990	2000
PLSPQDIFQL	ACMDPADDGQ	FQERQSLVVT	DPSSMRRSFS	TIRDKRSNSS	WLEEFSMERS	SENTYKSRRR	SYHSSLRLSA
2010	2020	2030	2040	2050	2060	2070	2080
HRLNSDSGHK	SDTHRSGGRE	RGRSKERKHL	LSPDVSRCNS	EERGTQADWE	SPERRQSRSP	SEGRSQTPNR	QGTGSLSESS
2090	2100	2110	2120	2130	2140	2150	2160
IPSVSDTSTP	RRSRRQLPPV	PPKPRPLLSY	SSLIRHAGSI	SPPADGSEEG	SPLTSQALES	NNACLTESSN	SPHPQQSQHA
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2194	1	973.4542	-4.91	2	57.6	16.3	1	734-750	K.EVSPMSAPNMPSIERER.R	Oxidation: 10	Wdown:Qdown 1.28
1976	1	698.7954	-42.34	2	53.2	11.0	1	1728-1739	R.VWAEYDRAACGR.I		

Detailed Protein Report

Protein 517: unconventional myosin-IXb isoform 2 [Homo sapiens]

Accession:	gi|194272142	**Score:**	27.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	229.0
Database Date:	2015-11-30	**pI:**	9.4
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	1.3
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MSVKEAGSSG RREQAAYHLH IYPQLSTTES QASCRVTATK DSTTSDVIKD AIASLRLDGT KCYVLVEVKE SGGEEWVLDA
        90        100        110        120        130        140        150        160
NDSPVHRVLL WPRRAQDEHP QEDGYYFLLQ ERNADGTIKY VHMQLVAQAT ATRRLVERGL LPRQQADFDD LCNLPELTEG
       170        180        190        200        210        220        230        240
NLLKNLKHRF LQQKIYTYAG SILVAINPFK FLPIYNPKYV KMYENQQLGK LEPHVFALAD VAYYTMLRKR VNQCIVISGE
       250        260        270        280        290        300        310        320
SGSGKTQSTN FLIHCLTALS QKGYASGVER TILGAGPVLE AFGNAKTAHN NNSSRFGKFI QVSYLESGIV RGAVVEKYLL
       330        340        350        360        370        380        390        400
EKSRLVSQEK DERNYHVFYY LLLGVSEEER QEFQLKQPED YFYLNQHNLK IEDGEDLKHD FERLKQAMEM VGFLPATKKQ
       410        420        430        440        450        460        470        480
IFAVLSAILY LGNVTYKKRA TGREEGLEVG PPEVLDTLSQ LLKVKREILV EVLTKRKTVT VNDKLILPYS LSEAITARDS
       490        500        510        520        530        540        550        560
MAKSLYSALF DWIVLRINHA LLNKKDVEEA VSCLSIGVLD IFGFEDFERN SFEQFCINYA NEQLQYYFNQ HIFKLEQEEY
       570        580        590        600        610        620        630        640
QGEGITWHNI GYTDNVGCIH LISKKPTGLF YLLDEESNFP HATSQTLLAK FKQQHEDNKY FLGTPVMEPA FIIQHFAGKV
       650        660        670        680        690        700        710        720
KYQIKDFREK NMDYMRPDIV ALLRGSDSSY VRELIGMDPV AVFRWAVLRA AIRAMAVLRE AGRLRAERAE KAAGMSSPGA
       730        740        750        760        770        780        790        800
QSHPEELPRG ASTPSEKLYR DLHNQMIKSI KGLPWQGEDP RSLLQSLSRL QKPRAFILKS KGIKQKQIIP KNLLDSKSLK
       810        820        830        840        850        860        870        880
LIISMTLHDR TTKSLLHLHK KKKPPSISAQ FQTSLNKLLE ALGKAEPFFI RCIRSNAEKK ELCFDDELVL QQLRYTGMLE
       890        900        910        920        930        940        950        960
TVRIRRSGYS AKYTFQDFTE QFQVLLPKDA QPCREVISTL LEKMKIDKRN YQIGKTKVFL KETERQALQE TLHREVVRKI
       970        980        990       1000       1010       1020       1030       1040
LLLQSWFRMV LERRHFLQMK RAAVTIQACW RSYRVRRALE RTQAAVYLQA SWRGYWQRKL YRHQKQSIIR LQSLCRGHLQ
      1050       1060       1070       1080       1090       1100       1110       1120
RKSFSQMISE KQKAEEKERE ALEAARAGAE EGGQGQAAGG QQVAEQGPEP AEDGGHLASE PEVQPSDRSP LEHSSPEKEA
      1130       1140       1150       1160       1170       1180       1190       1200
PSPEKTLPPQ KTVAAESHEK VPSSREKRES RRQRGLEHVK FQNKHIQSCK EESALREPSR RVTQEQGVSL LEDKKESRED
      1210       1220       1230       1240       1250       1260       1270       1280
ETLLVVETEA ENTSQKQPTE QPQAMAVGKV SEETEKTLPS GSPRPGQLER PTSLALDSRV SPPAPGSAPE TPEDKSKPCG
      1290       1300       1310       1320       1330       1340       1350       1360
SPRVQEKPDS PGGSTQIQRY LDAERLASAV ELWRGKKLVA AASPSAMLSQ SLDLSDRHRA TGAALTPTEE RRTSFSTSDV
      1370       1380       1390       1400       1410       1420       1430       1440
SKLLPSLAKA QPAAETTDGE RSAKKPAVQK KKPGDASSLP DAGLSPGSQV DSKSTFKRLF LHKTKDKKYS LEGAEELENA
      1450       1460       1470       1480       1490       1500       1510       1520
VSGHVVLEAT TMKKGLEAPS GQQHRHAAGE KRTKEPGGKG KKNRNVKIGK ITVSEKWRES VFRQITNANE LKYLDEFLLN
      1530       1540       1550       1560       1570       1580       1590       1600
KINDLRSQKT PIESLFIEAT EKFRSNIKTM YSVPNGKIHV GYKDLMENYQ IVVSNLATER GQKDTNLVLN LFQSLLDEFT
      1610       1620       1630       1640       1650       1660       1670       1680
RGYTKNDFEP VKQSKAQKKK RKQERAVQEH NGHVFASYQV SIPQSCEQCL SYIWLMDKAL LCSVCKMTCH KKCVHKIQSH
      1690       1700       1710       1720       1730       1740       1750       1760
CSYTYGRKGE PGVEPGHFGV CVDSLTSDKA SVPIVLEKLL EHVEMHGLYT EGLYRKSGAA NRTRELRQAL QTDPAAVKLE
      1770       1780       1790       1800       1810       1820       1830       1840
NFPIHAITGV LKQWLRELPE PLMTFAQYGD FLRAVELPEK QEQLAAIYAV LEHLPEANHN SLERLIFHLV KVALLEDVNR
      1850       1860       1870       1880       1890       1900       1910       1920
MSPGALAIIF APCLLRCPDN SDPLTSMKDV LKITTCVEML IKEQMRKYKV KMEEISQLEA AESIAFRRLS LLRQNAPWPL
      1930       1940       1950       1960       1970       1980       1990       2000
KLGFSSPYEG VLNKSPKTRD IQEEELEVLL EEEAAGGDED REKEILIERI QSIKEEKEDI TYRLPELDPR GSDEENLDSE
      2010       2020       2030
TSASTESLLE ERAGRGASEG QY
```

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
1951	1	918.3471	-89.50	2	53.1	10.7	1	1857-1872	R.CPDNSDPLTSMKDVLK.I	Carbamidomethyl: 1; Oxidation: 11

Detailed Protein Report

Protein 518: **PREDICTED: iron-sulfur cluster assembly enzyme ISCU, mitochondrial isoform X1 [Homo sapiens]**

Accession:	gi|530400013	**Score:**	27.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	16.9
Database Date:	2015-11-30	**pI:**	10.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	16.0
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MAAAGAFRLR	RAASALLLRS	PRLPARELSA	PARLYHKKVV	DHYENPRNVG	SLDKTSKNVG	TGLVGAPACG	DVMKLQIQVD
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
EKGKIVDARF	KTFGCGSAIA	SSSLATEWVK	GKTVEEALTI	KNTDIAKELC	LPPVKLHCSR	KEGMRNISLN	ASMEVY

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2838	1	485.7928	-38.39	2	64.0	10.4	1	11-19	R.RAASALLLR.S	
2964	1	619.9693	5.46	3	66.2	16.9	2	141-156	R.KEGMRNISLNASMEVY.-	Oxidation: 4

Detailed Protein Report

Protein 519: **PREDICTED: DNA (cytosine-5)-methyltransferase 3A isoform X4 [Homo sapiens]**

Accession:	gi|578802756	**Score:**	27.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	89.3
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
MPAMPSSGPG	DTSSSAAERE	EDRKDGEEQE	EPRGKEERQE	PSTTARKVGR	PGRKRKHPPV	ESGDTPKDPA	VISKSPSMAQ
90	100	110	120	130	140	150	160
DSGASELLPN	GDLEKRSEPQ	PEEGSPAGGQ	KGGAPAEGEG	AAETLPEASR	AVENGCCTPK	EGRGAPAEAG	KEQKETNIES
170	180	190	200	210	220	230	240
MKMEGSRGRL	RGGLGWESSL	RQRPMPRLTF	QAGDPYYISK	RKRDEWLARW	KREAEKKAKV	IAGMNAVEEN	QGPGESQKVE
250	260	270	280	290	300	310	320
EASPPAVQQP	TDPASPTVAT	TPEPVGSDAG	DKNATKAGDD	EPEYEDGRGF	GIGELVWGKL	RGFSWWPGRI	VSWWMTGRSR
330	340	350	360	370	380	390	400
AAEGTRWVMW	FGDGKFSVVC	VEKLMPLSSF	CSAFHQATYN	KQPMYRKAIY	EVLQVASSRA	GKLFPVCHDS	DESDTAKAVE
410	420	430	440	450	460	470	480
VQNKPMIEWA	LGGFQPSGPK	GLEPPEEEKN	PYKEVYTDMW	VEPEAAAYAP	PPPAKKPRKS	TAEKPKVKEI	IDERTRERLV
490	500	510	520	530	540	550	560
YEVRQKCRNI	EDICISCGSL	NVTLEHPLFV	GGMCQNCKNC	FLECAYQYDD	DGYQSYCTIC	CGGREVLMCG	NNNCCRCFCV
570	580	590	600	610	620	630	640
ECVDLLVGPG	AAQAAIKEDP	WNCYMCGHKG	TYGLLRRRED	WPSRLQMFFA	NNHDQEFDPP	KVYPPVPAEK	RKPIRVLSLF
650	660	670	680	690	700	710	720
DGIATGLLVL	KDLGIQVDRY	IASEVCEDSI	TVGMVRHQGK	IMYVGDVRSV	TQKHIQEWGP	FDLVIGGSPC	NDLSIVNPAR
730	740	750	760	770	780	790	800
KGLYEGTGRL	FFEFYRLLHD	ARPKEGDDRP	FFWLFENVVA	MGVSDKRDIS	RFLESNPVMI	DAKEVSAAHR	ARYFWGNLPG
810							
MNSSAK							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2336	1	873.3793	-3.43	2	57.6	10.1	2	20-33	R.EEDRKDGEEQEEPR.G	

Detailed Protein Report

Protein 520: G protein-regulated inducer of neurite outgrowth 1 [Homo sapiens]

Accession:	gi|112821681	**Score:**	27.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	102.3
Database Date:	2015-11-30	**pI:**	9.3
		Sequence Coverage [%]:	3.4
		No. of unique Peptides:	2

Alias proteins:

Accession	Name	Description
gi|530380833	refseq_human (refseq_human_20140103.fasta)	PREDICTED: G protein-regulated inducer of neurite outgrowth 1 isoform X1 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MDTAEDPAWL QLLQKDSSPP GPRPTAFFCP QDGSLGAGSS AMRDYCPSQQ KASPAPPRHT PDQSPGMESR HRSPSGAGEG

        90        100        110        120        130        140        150        160
ASCSDGPRGS LACPSPTCFS PQESPSKETL EAHGASISGT PEATTSGKPE PVSSVKTEPK SSDDRNPMFL EKMDFKSSKQ

       170        180        190        200        210        220        230        240
ADSTSIGKED PGSSRKADPM FTGKAEPEIL GKGDPVAPGR MDPMTVRKED LGSLGKVDPL CSSKTYTVSP RKEDPGSLRK

       250        260        270        280        290        300        310        320
VDPVSSDKVD PVFPRKEEPR YSGKEHPVSS EKVAPTSAEK VDLVLSGKRD PGPSGKADPM PLESMDSAST GKTEPGLLGK

       330        340        350        360        370        380        390        400
LIPGSSGKNG PVSSGTGAPG SLGRLDPTCL GMADPASVGN VETVPATKED SRFLGKMDPA SSGEGRPVSG HTDTTASAKT

       410        420        430        440        450        460        470        480
DLTSLKNVDP MSSGKVDPVS LGKMDPMCSG KPELLSPGQA ERVSVGKAGT VSPGKEDPVS SRREDPISAG SRKTSSEKVN

       490        500        510        520        530        540        550        560
PESSGKTNPV SSGPGDPRSL GTAGPPSAVK AEPATGGKGD PLSSEKAGLV ASGKAAPTAS GKAEPLAVGK EDPVSKGKAD

       570        580        590        600        610        620        630        640
AGPSGQGDSV SIGKVVSTPG KTVPVPSGKV DPVSLGKAEA IPEGKVGSLP LEKGSPVTTT KADPRASGKA QPQSGGKAET

       650        660        670        680        690        700        710        720
KLPGQEGAAA PGEAGAVCLK KETPQASEKV DPGSCRKAEP LASGKGEPVS LGKADSAPSR KTESPSLGKV VPLSLEKTKP

       730        740        750        760        770        780        790        800
SSSSRQLDRK ALGSARSPEG ARGSEGRVEP KAEPVSSTEA SSLGQKDLEA AGAERSPCPE AAAPPPGPRT RDNFTKAPSW

       810        820        830        840        850        860        870        880
EASAPPPPRE DAGTQAGAQA CVSVAVSPMS PQDGAGGSAF SFQAAPRAPS PPSRRDAGLQ VSLGAAETRS VATGPMTPQA

       890        900        910        920        930        940        950        960
AAPPAFPEVR VRPGSALAAA VAPPEPAEPV RDVSWDEKGM TWEVYGAAME VEVLGMAIQK HLERQIEEHG RQGAPAPPPA

       970        980        990       1000       1010
ARAGPGRSGS VRTAPPDGAA KRPPGLFRAL LQSVRRPRCC SRAGPTAE
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2305	1	853.3930	-63.26	2	57.5	15.6	2	225-239	K.TYTVSPRKEDPGSLR.K	
2330	1	682.5941	-86.77	3	57.6	11.6	0	424-442	K.MDPMCSGKPELLSPGQAER.V	

Detailed Protein Report

Protein 521: PREDICTED: sodium/hydrogen exchanger 10 isoform X2 [Homo sapiens]

Accession:	gi|578807311	**Score:**	27.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	126.9
Database Date:	2015-11-30	**pI:**	7.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSPDLFFRIF	TPVVFFTTAF	DMDTYMLQKL	FWQILLISIP	GFLVNYILVL	WHLASVNQLL	LKPTQWLLFS	AILVSSDPML
90	100	110	120	130	140	150	160
TAAAIRDLGL	SRSLISLING	ESLMTSVISL	ITFTSIMDFD	QRLQSKRNHT	LAEEIVGGIC	SYIIASFLFG	ILSSKLIQFW
170	180	190	200	210	220	230	240
MSTVFGDDVN	HISLIFSILY	LIFYICELVG	MSGIFTLAIV	GLLLNSTSFK	AAIEETLLLE	FWTFLSRIAF	LMVFTFFGLL
250	260	270	280	290	300	310	320
IPAHTYLYIE	FVDIYYSLNI	YLTLIVLRFL	TLLLISPVLS	RVGHEFSWRW	IFIMVCSEMK	GMPNINMALL	LAYSDLYFGS
330	340	350	360	370	380	390	400
DKEKSQILFH	GVLVCLITLV	VNRFILPVAV	TILGLRDATS	TKYKSVCCTF	QHFQELTKSA	ASALKFDKDL	ANADWNMIEK
410	420	430	440	450	460	470	480
AITLENPYML	NEEETTEHQK	VKCPHCNKEI	DEIFNTEAME	LANRRLLSAQ	IASYQRQYRN	EILSQSAVQV	LVGAAESFGE
490	500	510	520	530	540	550	560
KKGKCMSLDT	IKNYSESQKT	VTFARKLLLN	WVYNTRKEKE	GPSKYFFFRI	CHTIVFTEEF	EHVGYLVILM	NIFPFIISWI
570	580	590	600	610	620	630	640
SQLNVIYHSE	LKHTNYCFLT	LYILEALLKI	AAMRKDFFSH	AWNIFELAIT	LIGILHVILI	EIDTIKYIFN	ETEVIVFIKV
650	660	670	680	690	700	710	720
VQFFRILRIF	KLIAPKLLQI	IDKRMSHQKT	FWYGILKGYV	QGEADIMTII	DQITSSKQIK	QMLLKQVIRN	MEHAIKELGY
730	740	750	760	770	780	790	800
LEYDHPEIAV	TVKTKEEINV	MLNMATEILK	AFGLKGIISK	TEGAGINKLI	MAKKKEVLDS	QSIIRPLTVE	EVLYHIPWLD
810	820	830	840	850	860	870	880
KNKDYINFIQ	EKAKVVTFDC	GNDIFEEGDE	PKGIYIIISG	MVKLEKSKPG	LGIDQMVESK	EKDFPIIDTD	YMLSGEIIGE
890	900	910	920	930	940	950	960
INCLTNEPMK	YSATCKTVVE	TCFIPKTHLY	DAFEQCSPLI	KQKMWLKLGL	AITARKIREH	LSYEDWNYNM	QLKLSNIYVV
970	980	990	1000	1010	1020	1030	1040
DIPMSTKTDI	YDENLIYVIL	IHGAVEDCLL	RKTYRAPFLI	PITCHQIQSI	EDFTKVVIIQ	TPINMKTFRR	NIRKFVPKHK
1050	1060	1070	1080	1090	1100	1110	
SYLTPGLIGS	VGTLEEGIQE	ERNVKEDGAH	SAATARSPQP	CSLLGTKFNC	KESPRINLRK	VRKE	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1365	1	817.1004	44.43	3	46.8	12.7	0	301-322	K.GMPNINMALLLAYSDLYFGSDK.E	Oxidation: 2

Detailed Protein Report

Protein 522: coiled-coil domain-containing protein 38 [Homo sapiens]

Accession:	gi|226491199	**Score:**	27.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	65.3
Database Date:	2015-11-30	**pI:**	9.4
		Sequence Coverage [%]:	5.9
		No. of unique Peptides:	2

Quantitation

mdown:qdown **Median:** 1.82 **CV:** 0.00 % **No. of 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	390	400
LLDDEMDVDL	EPALYFKEPE	ELLQVLRELE	EQNLTLFQYS	QDVDENLEEV	NKREKVIQDK	TNSNIEFLLE	QEKMLKANCV
410	420	430	440	450	460	470	480
REEEKAAELQ	LKSKLFSFGE	FNSDAQEILI	DSLSKKITQV	YKVCIGDAED	DGLNPIQKLV	KVESRLVELC	DLIESIPKEN
490	500	510	520	530	540	550	560
VEAIERMKQK	EWRQKFRDEK	MKEKQRHQQE	RLKAALEKAV	AQPKKKLGRR	LVFHSKPPSG	NKQQLPLVNE	TKTKSQEEEY
570							
FFT							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
39	1	750.3346	-92.35	2	29.8	15.7	1	85-98	R.SFEKFGPGPAPIPR.L		
353	1	676.4443	133.31	3	33.1	11.6	1	443-461	K.VCIGDAEDDGLNPIQKLVK.V		mdown:qdown 1.82

Detailed Protein Report

Protein 523: PREDICTED: histone-lysine N-methyltransferase ASH1L isoform X3 [Homo sapiens]

Accession:	gi|530365072	**Score:**	27.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	191.3
Database Date:	2015-11-30	**pI:**	10.4
		Sequence Coverage [%]:	1.8
		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 524: ral GTPase-activating protein subunit alpha-2 [Homo sapiens]

Accession:	gi|118600961	**Score:**	27.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	210.6
Database Date:	2015-11-30	**pI:**	5.7
Modification(s):	Oxidation	**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				

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
2782	2	1024.0405	20.51	2	66.1	16.6	1	433-448	K.WILQDKPVFMEEPDRK.D	Oxidation: 10
1722	1	1273.4940	-96.18	2	51.5	10.6	0	1341-1363	K.SSEPVQYHSSAELGNLLTVEEEK.K	

Detailed Protein Report

Protein 525: tumor necrosis factor receptor superfamily member 21 precursor [Homo sapiens]

Accession:	gi|7657039	**Score:**	27.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	71.8
Database Date:	2015-11-30	**pI:**	9.3
		Sequence Coverage [%]:	4.6
		No. of unique Peptides:	1

Quantitation

Wdown:Qdown **Median:** 0.67 **CV:** 0.00 % **No. of 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	Ratios
2722	1	941.9859	28.38	2	62.4	13.6	1	1-19	-.MGTSPSSSTALASCSRIAR.R		Wdown:Qdown 0.67

Detailed Protein Report

Protein 526: PREDICTED: neuroligin-2 isoform X1 [Homo sapiens]

Accession:	gi|530410532	**Score:**	27.1
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:	1

```
        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
1419	1	981.9479	-37.80	2	47.5	11.8	0	17-40	R.GGGGPGGGAPGGPGLGLGSLGEER.F	

Detailed Protein Report

Protein 527: **PREDICTED: U2 snRNP-associated SURP motif-containing protein isoform X3 [Homo sapiens]**

Accession: gi|530374190
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 27.1
MW [kDa]: 111.5
pI: 6.5
Sequence Coverage [%]: 2.1
No. of unique Peptides: 2

10	20	30	40	50	60	70	80
MADKTPGGSQ	KASSKTRSSD	VHSSGSSDAH	MDASGPSDSD	MPSRTRPKSP	RKHNYRNESA	RESLCDSPHQ	NLSRPLLENK
90	100	110	120	130	140	150	160
LKAFSIGKMS	TAKRTLSKKE	QEELKKKEDE	KAAAEIYEEF	LAAFEGSDGN	KVKTFVRGGV	VNAAKEEHET	DEKRGKIYKP
170	180	190	200	210	220	230	240
SSRFADQKNP	PNQSSNERPP	SLLVIETKKP	PLKKGEKEKK	KSNLELFKEE	LKQIQEERDE	RHKTKGRLSR	FEPPQSDSDG
250	260	270	280	290	300	310	320
QRRSMDAPSR	RNRSSGVLDD	YAPGSHDVGD	PSTTNLYLGN	INPQMNEEML	CQEFGRFGPL	ASVKIMWPRT	DEERARERNC
330	340	350	360	370	380	390	400
GFVAFMNRRD	AERALKNLNG	KMIMSFEMKL	GWGKAVPIPP	HPIYIPPSMM	EHTLPPPPSG	LPFNAQPRER	LKNPNAPMLP
410	420	430	440	450	460	470	480
PPKNKEDFEK	TLSQAIVKVV	IPTERNLLAL	IHRMIEFVVR	EGPMFEAMIM	NREINNPMFR	FLFENQTPAH	VYYRWKLYSI
490	500	510	520	530	540	550	560
LQGDSPTKWR	TEDFRMFKNG	SFWRPPPLNP	YLHGMSEEQE	TEAFVEEPSK	KGALKEEQRD	KLEEILRGLT	PRKNDIGDAM
570	580	590	600	610	620	630	640
VFCLNNAEAA	EEIVDCITES	LSILKTPLPK	KIARLYLVSD	VLYNSSAKVA	NASYYRKFFE	TKLCQIFSDL	NATYRTIQGH
650	660	670	680	690	700	710	720
LQSENFKQRV	MTCFRAWEDW	AIYPEPFLIK	LQNIFLGLVN	IIEEKETEDV	PDDLDGAPIE	EELDGAPLED	VDGIPIDATP
730	740	750	760	770	780	790	800
IDDLDGVPIK	SLDDDLDGVP	LDATEDSKKN	EPIFKVAPSK	WEAVDESELE	AQAVTTSKWE	LFDQHEESEE	EENQNQEEES
810	820	830	840	850	860	870	880
EDEEDTQSSK	SEEHHLYSNP	IKEEMTESKF	SKYSEMSEEK	RAKLREIELK	VMKFQDELES	GKRPKKPGQS	FQEQVEHYRD
890	900	910	920	930	940	950	960
KLLQREKEKE	LERERERDKK	DKEKLESRSK	DKKEKDECTP	TRKERSPSGS	RTPKRSRRSR	SRSPKKSGKK	SRSQSRSPHR
970	980						
SHKKSKKNKH							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
662	1	460.1225	-221.33	2	37.1	12.9	1	244-251	R.SMDAPSRR.N	
2921	1	729.3717	78.12	2	65.3	14.3	0	441-452	R.EGPMFEAMIMNR.E	Oxidation: 4, 10

Detailed Protein Report

Protein 528: PREDICTED: gametocyte-specific factor 1-like isoform X1 [Homo sapiens]

Accession:	gi|530417873	**Score:**	27.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	11.9
Database Date:	2015-11-30	**pI:**	9.1
		Sequence Coverage [%]:	20.4
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	0.79	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	2.92	**CV:**	0.00 %	**No. of Peptides:**	1

```
        10         20         30         40         50         60         70         80
MEPEAFEICP YDPHHRIPLS RFQYHLASCR RKNPKKAKKM ATCKYNACHV VPIKNLEEHE AVCVNRSAVE EEDTENPLKV
        90        100        110
VCENDTKESA RETSPQKILR PGQ
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
675	1	562.6665	-181.99	2	37.0	16.1	0	22-30	R.FQYHLASCR.R		mdown:qdown 0.79 Wdown:Qdown 2.92

Detailed Protein Report

Protein 529: **PREDICTED: gamma-aminobutyric acid type B receptor subunit 2 isoform X1 [Homo sapiens]**

Accession:	gi|530391788	**Score:**	27.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	77.5
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
MAAKVFCCAY	EENMYGSKYQ	WIIPGWYEPS	WWEQVHTEAN	SSRCLRKNLL	AAMEGYIGVD	FEPLSSKQIK	TISGKTPQQY
90	100	110	120	130	140	150	160
EREYNNKRSG	VGPSKFHGYA	YDGIWVIAKT	LQRAMETLHA	SSRHQRIQDF	NYTDHTLGRI	ILNAMNETNF	FGVTGQVVFR
170	180	190	200	210	220	230	240
NGERMGTIKF	TQFQDSREVK	VGEYNAVADT	LEIINDTIRF	QGSEPPKDKT	IILEQLRKIS	LPLYSILSAL	TILGMIMASA
250	260	270	280	290	300	310	320
FLFFNIKNRN	QKLIKMSSPY	MNNLIILGGM	LSYASIFLFG	LDGSFVSEKT	FETLCTVRTW	ILTVGYTTAF	GAMFAKTWRV
330	340	350	360	370	380	390	400
HAIFKNVKMK	KKIIKDQKLL	VIVGGMLLID	LCILICWQAV	DPLRRTVEKY	SMEPDPAGRD	ISIRPLLEHC	ENTHMTIWLG
410	420	430	440	450	460	470	480
IVYAYKGLLM	LFGCFLAWET	RNVSIPALND	SKYIGMSVYN	VGIMCIIGAA	VSFLTRDQPN	VQFCIVALVI	IFCSTITLCL
490	500	510	520	530	540	550	560
VFVPKLITLR	TNPDAATQNR	RFQFTQNQKK	EDSKTSTSVT	SVNQASTSRL	EGLQSENHRL	RMKITELDKD	LEEVTMQLQD
570	580	590	600	610	620	630	640
TPEKTTYIKQ	NHYQELNDIL	NLGNFTESTD	GGKAILKNHL	DQNPQLQWNT	TEPSRTCKDP	IEDINSPEHI	QRRLSLQLPI
650	660	670	680	690			
LHHAYLPSIG	GVDASCVSPC	VSPTASPRHR	HVPPSFRVMV	SGL			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
814	1	965.4561	44.99	2	39.0	10.5	1	2-18	M.AAKVFCCAYEENMYGSK.Y	Oxidation: 13

Detailed Protein Report

Protein 530: **PREDICTED: TBC domain-containing protein kinase-like protein isoform X1 [Homo sapiens]**

Accession:	gi|578809649	**Score:**	27.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	84.9
Database Date:	2015-11-30	**pI:**	5.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MFPLKDAEMG	AFTFFASALP	HDVCGSNGLP	LTPNSIKILG	RFQILKTITH	PRLCQYVDIS	RGKHERLVVV	AEHCERSLED
90	100	110	120	130	140	150	160
LLRERKPVSC	STVLCIAFEV	LQGLQYMNKH	GIVHRALSPH	NILLDRKGHI	KLAKFGLYHM	TAHGDDVDFP	IGYPSYLAPE
170	180	190	200	210	220	230	240
VIAQGIFKTT	DHMPSKKPLP	SGPKSDVWSL	GIILFELCVG	RKLFQSLDIS	ERLKFLLTLD	CVDDTLIVLA	EEHGCLDIIK
250	260	270	280	290	300	310	320
ELPETVIDLL	NKCLTFHPSK	RPTPDQLMKD	KVFSEVSPLY	TPFTKPASLF	SSSLRCADLT	LPEDISQLCK	DINNDYLAER
330	340	350	360	370	380	390	400
SIEEVYYLWC	LAGGDLEKEL	VNKEIIRSKP	PICTLPNFLF	EDGESFGQGR	DRSSLLDDTT	VTLSLCQLRN	RLKDVGGEAF
410	420	430	440	450	460	470	480
YPLLEDDQSN	LPHSNSNNEL	SAAATLPLII	REKDTEYQLN	RIILFDRLLK	AYPYKKNQIW	KEARVDIPPL	MRGLTWAALL
490	500	510	520	530	540	550	560
GVEGAIHAKY	DAIDKDTPIP	TDRQIEVDIP	RCHQYDELLS	SPEGHAKFRR	VLKAWVVSHP	DLVYWQGLDS	LCAPFLYLNF
570	580	590	600	610	620	630	640
NNEALAYACM	SAFIPKYLYN	FFLKDNSHVI	QEYLTVFSQM	IAFHDPELSN	HLNEIGFIPD	LYAIPWFLTM	FTHVFPLHKI
650	660	670	680	690	700	710	720
FHLWDTLLLG	NSSFPFCIGV	AILQQLRDRL	LANGFNECIL	LFSDLPEIDI	ERCVRESINL	FCWTPKSATY	RQHAQPPKPS
730	740	750					
SDSSGGRSSA	PYFSAECPDP	PKTDLKIH					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1977	3	876.8617	-79.82	2	53.4	16.4	1	693-706	R.CVRESINLFCWTPK.S	Carbamidomethyl: 10

Detailed Protein Report

Protein 531: PREDICTED: inhibitor of Bruton tyrosine kinase isoform X3 [Homo sapiens]

Accession: gi|578812678
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 27.1
MW [kDa]: 148.9
pI: 8.5
Sequence Coverage [%]: 2.2
No. of unique Peptides: 2

10	20	30	40	50	60	70	80
MSSPMPDCTS	KCRSLKHALD	VLSVVTKGSE	NQIKAFLSSH	CYNAATIKDV	FGRNALHLVS	SCGKKGVLDW	LIQKGVDLLV
90	100	110	120	130	140	150	160
KDKESGWTAL	HRSIFYGHID	CVWSLLKHGV	SLYIQDKEGL	SALDLVMKDR	PTHVVFKNTD	PTDVYTWGDN	TNFTLGHGSQ
170	180	190	200	210	220	230	240
NSKHHPELVD	LFSRSGIYIK	QVVLCKFHSV	FLSQKGQVYT	CGHGPGGRLG	HGDEQTCLVP	RLVEGLNGHN	CSQVAAAKDH
250	260	270	280	290	300	310	320
TVVLTEDGCV	YTFGLNIFHQ	LGIIPPPSSC	NVPRQIQAKY	LKGRTIIGVA	AGRFHTVLWT	REAVYTMGLN	GGQLGCLLDP
330	340	350	360	370	380	390	400
NGEKCVTAPR	QVSALHHKDI	ALSLVAASDG	ATVCVTTRGD	IYLLADYQCK	KMASKQLNLK	KVLVSGGHME	YKVDPEHLKE
410	420	430	440	450	460	470	480
NGGQKICILA	MDGAGRVFCW	RSVNSSLKQC	RWAYPRQVFI	SDIALNRNEI	LFVTQDGEGF	RGRWFEEKRK	SSEKKEILSN
490	500	510	520	530	540	550	560
LHNSSSDVSY	VSDINSVYER	IRLEKLTFAH	RAVSVSTDPS	GCNFAILQSD	PKTSLYEIPA	VSSSSFFEEF	GKLLREADEM
570	580	590	600	610	620	630	640
DSIHDVTFQV	GNRLFPAHKY	ILAVHSDFFQ	KLFLSDGNTS	EFTDIYQKDE	DSAGCHLFVV	EKVHPDMFEY	LLQFIYTDTC
650	660	670	680	690	700	710	720
DFLTHGFKPR	IHLNKNPEEY	QGTLNSHLNK	VNFHEDDNQK	SAFEVYKSNQ	AQTVSERQKS	KPKSCKKGKN	IREDDPVRML
730	740	750	760	770	780	790	800
QTVAKKFDFS	NLSSRLDGVR	FENEKINVIA	KNTGNKLKLS	QKKCSFLCDV	TMKSVDGKEF	PCHKCVLCAR	LEYFHSMLSS
810	820	830	840	850	860	870	880
SWIEASSCAA	LEMPIHSDIL	KVILDYLYTD	EAVVIKESQN	VDFICSVLVV	ADQLLITRLK	EICEVALTEK	LTLKNAAMLL
890	900	910	920	930	940	950	960
EFAAMYSAKQ	LKLSCLQFIG	LNMAALLEAR	SLDVLSDGVL	KDLSEFYRKM	IPAMDRRVIT	PYQDGPDISY	LEVEDGDIFL
970	980	990	1000	1010	1020	1030	1040
KEEINMEQNH	SETMFKKAKT	KAKKKPRKRS	DSSGGYNLSD	IIQSPSSTEL	LTSDSEGSYA	GVGSPRDLQS	PDFTTGFHSD
1050	1060	1070	1080	1090	1100	1110	1120
KIEAKVKPYV	NGTSPVYSRE	DLKPWEKSPI	LKISAPQPIP	SNRIDTTSSA	SWVAGSFSPV	SPPVVDLRTI	MEIEESRQKC
1130	1140	1150	1160	1170	1180	1190	1200
GATPKSHLGK	TVSHGVKLSQ	KQRKMIALTT	KENNSGMNSM	ETVLFTPSKA	PKPVNAWASS	LHSVSSKSFR	DFLLEEKKSV
1210	1220	1230	1240	1250	1260	1270	1280
TSHSSGDHVK	KVSFKGIENS	QAPKIVRCST	HGTPGPEGNH	ISDLPLLDSP	NPWLSSSVTA	PSMVAPVTFA	SIVEEELQQE
1290	1300	1310	1320	1330	1340		
AALIRSREKP	LALIQIEEHA	IQDLLVFYEA	FGNPEEFVIV	ERTPQGPLAV	PMWNKHGC		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1342	1	388.0955	-190.68	3	45.3	14.3	0	764-773	K.CSFLCDVTMK.S	Oxidation: 9
2082	1	701.2889	-119.01	3	54.6	12.7	1	871-889	K.LTLKNAAMLLEFAAMYSAK.Q	Oxidation: 15

Detailed Protein Report

Protein 532: spermatogenesis-associated protein 31E1 [Homo sapiens]

Accession: gi|155029550
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 27.1
MW [kDa]: 157.0
pI: 10.3
Sequence Coverage [%]: 1.7
No. of unique Peptides: 2

10	20	30	40	50	60	70	80
MGNLVIPLGK	GRAGRVESGQ	RIPPPAPRPS	VECTGDDIAL	QMEKMLFPLK	SPSATWLSPS	STPWMMDFIL	TSVCGLVLLF
90	100	110	120	130	140	150	160
LLLLYVHSDP	PSPPPGRKRS	SREPQRERSG	RSRSRKISAL	KACRILLREL	EETRDLNYLL	ESHLRKLAGE	GSSHLPLGGD
170	180	190	200	210	220	230	240
PLGDVCKPVP	AKAHQPHGKC	MQDPSPASLS	PPAPPAPLAS	TLSPGPMTFS	EPFGPHSTLS	ASGPPEPLLP	LKCPATQPHV
250	260	270	280	290	300	310	320
VFPPSPQPHG	PLASSPPPPD	SSLAGLQCGS	TTCPVPQSSP	LHNQVLPPPT	RVISGLGCSS	DPIWDLYCWR	EAATTWGLST
330	340	350	360	370	380	390	400
YSHGKSQPRH	LPDHTSEASF	WGDPTPKHME	VGGCTFIHPD	VQKLLETLIA	KRALMKMWQE	KERKRADHPH	MTSLGKEWDI
410	420	430	440	450	460	470	480
TTLNPFWNVS	TQPQQLPRPQ	QVSDATTVGN	HLQQKRSQLF	WDLPSLNSES	LATTVWVSRN	PSSQNAHSVP	LDKASTSLPG
490	500	510	520	530	540	550	560
EPEVEASSQL	SQAPPQPHHM	AQPQHFTPAW	PQSQPPPLAE	IQTQAHLSPP	VPSLGCSSPP	QIRGCGASYP	TSQERTQSVI
570	580	590	600	610	620	630	640
PTGKEYLEWP	LKKRPKWKRV	LPSLLKKSQA	VLSQPTAHLP	QERPASWSPK	SAPILPGVVT	SPELPEHWWQ	GRNAIHQEQS
650	660	670	680	690	700	710	720
CGPPSRLQAS	GDLLQPDGEF	PGRPQSQAED	TQQALLPSQP	SDFAGKGRKD	VQKTGFRSSG	RFSDKGCLGS	KLGPDPSRDQ
730	740	750	760	770	780	790	800
GSGRTSVKAL	DEDKEAEGDL	RRSWKYQSVS	STPRDPDKEH	LENKLQIHLA	RKVGEIKEGW	IPMPVRRSWL	MAKCAVPKSD
810	820	830	840	850	860	870	880
THRKPGKLAS	WRGGKAHVNT	SQELSFLHPC	TQQILEVHLV	RFCVRHSWGT	DLQSLEPINV	WSGEAQAPPF	PQSTFTPWAS
890	900	910	920	930	940	950	960
WVSRVESVPK	VPIFLGKRPQ	NGPGDNRTTS	KSVPTVSGPL	AAPPPEQEGV	QRPPRGSQSA	DTHGRSEAFP	TGHKGRGCSQ
970	980	990	1000	1010	1020	1030	1040
PPTCSLVGRT	WQSRTVLESG	KPKPRLEGSM	GSEMAGNEAW	LESESMSPGD	PCSSRALQVL	SIGSQWARAE	DALQALKVGE
1050	1060	1070	1080	1090	1100	1110	1120
KPPTWEVTLG	ASVRASSGSV	QEDLRSTGAL	GTTGNPSASS	VCVAQDPEQL	HLKAQVVSEI	ALIVQVDSEE	QLPGRAPGIL
1130	1140	1150	1160	1170	1180	1190	1200
LQDGATGLCL	PGRHMDMLTA	ADRLPTQAPL	STSQSVSGKN	MTASQGPCAL	LWKGGDSPGQ	QEPGSPKAKA	PQKSQKTLGC
1210	1220	1230	1240	1250	1260	1270	1280
ADKGEAHRRP	RTGEQGHRSK	GPRTSEASGR	SHPAQAREIG	DKQERKYNQL	QLEKGQTPPE	SHFQRKISHH	PQGLHPRKGG
1290	1300	1310	1320	1330	1340	1350	1360
TRWEDVLQKG	KPGADAFQSW	GSGPPRQFMD	CMADKAWTIS	RVVGQILVDK	LGLQWGRGPS	EVNRHKGDFR	AQENVPSCCH
1370	1380	1390	1400	1410	1420	1430	1440
RGHCHQERSR	EMRALACSPK	ATPKGHHCPV	KNRGIRDRDS	SWAPPPREPV	SPAGPHHHRP	RMASTSGGPH	PQLQELMSAQ
1450							
RCLAS							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2526	1	574.6432	-239.26	2	60.3	12.8	0	1055-1065	R.ASSGSVQEDLR.S	
1848	1	805.3101	-128.16	2	53.1	14.3	2	1394-1407	R.GIRDRDSSWAPPPR.E	

Detailed Protein Report

Protein 533: SH3 and multiple ankyrin repeat domains protein 3 [Homo sapiens]

Accession:	gi|380748963	**Score:**	27.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	184.6
Database Date:	2015-11-30	**pI:**	9.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.4
		No. of unique Peptides:	2

```
        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
498	1	546.2697	-47.83	2	34.8	13.2	0	853-862	R.SSFKPGLEAR.L	

Detailed Protein Report

Protein 534: spatacsin isoform 2 [Homo sapiens]

Accession:	gi|237681069	**Score:**	27.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	266.5
Database Date:	2015-11-30	**pI:**	5.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAAEEGVASA	ASAGGSWGTA	AMGRVLPMLL	VPVPAEAMGQ	LGSRAQLRTQ	PEALGSLTAA	GSLQVLSLTP	GSRGGGRCCL
90	100	110	120	130	140	150	160
EGPFWHFLWE	DSRNSSTPTE	KPKLLALGEN	YELLIYEFNL	KDGRCDATIL	YSCSREALQK	LIDDQDISIS	LLSLRILSFH
170	180	190	200	210	220	230	240
NNTSLLFINK	CVILHIIFPE	RDAAIRVLNC	FTLPLPAQAV	DMIIDTQLCR	GILFVLSSLG	WIYIFDVVDG	TYVAHVDLAL
250	260	270	280	290	300	310	320
HKEDMCNEQQ	QEPAKISSFT	SLKVSQDLDV	AVIVSSSNSA	VALNLNLYFR	QHPGHLLCER	ILEDLPIQGP	KGVDEDDPVN
330	340	350	360	370	380	390	400
SAYNMKLAKF	SFQIDRSWKA	QLSSLNETIK	NSKLEVSCCA	PWFQDILHLE	SPESGNHSTS	VQSWAFIPQD	IMHGQYNVLQ
410	420	430	440	450	460	470	480
KDHAKTSDPG	RSWKIMHISE	QEEPIELKCV	SVTGFTALFT	WEVERMGYTI	TLWDLETQGM	QCFSLGTKCI	PVDSSGDQQL
490	500	510	520	530	540	550	560
CFVLTENGLS	LILFGLTQEE	FLNRLMIHGS	ASTVDTLCHL	NGWGRCSIPI	HALEAGIENR	QLDTVNFFLK	SKENLFNPSS
570	580	590	600	610	620	630	640
KSSVSDQFDH	LSSHLYLRNV	EELIPALDLL	CSAIRESYSE	PQSKHFSEQL	LNLTLSFLNN	QIKELFIHTE	ELDEHLQKGV
650	660	670	680	690	700	710	720
NILTSYINEL	RTFMIKFPWK	LTDAIDEYDV	HENVPKVKES	NIWKKLSFEE	VIASAILNNK	IPEAQTFFRI	DSHSAQKLEE
730	740	750	760	770	780	790	800
LIGIGLNLVF	DNLKKNNIKE	ASELLKNMGF	DVKGQLLKIC	FYTTNKNIRD	FLVEILKEKN	YFSEKEKRTI	DFVHQVEKLY
810	820	830	840	850	860	870	880
LGHFQENMQI	QSFPRYWIKE	QDFFKHKSVL	DSFLKYDCKD	EFNKQDHRIV	LNWALWWDQL	TQESILLPRI	SPEEYKSYSP
890	900	910	920	930	940	950	960
EALWRYLTAR	HDWLNIILWI	GEFQTQHSYA	SLQQNKWPLL	TVDVINQNTS	CNNYMRNEIL	DKLARNGVFL	ASELEDFECF
970	980	990	1000	1010	1020	1030	1040
LLRLSRIGGV	IQDTLPVQNY	KTKEGWDFHS	QFILYCLEHS	LQHLLYVYLD	CYKLSPENCP	FLEKKELHEA	HPWFEFLVQC
1050	1060	1070	1080	1090	1100	1110	1120
RQVASNLTDP	KLIFQASLAN	AQILIPTNQA	SVSSMLLEGH	TLLALATTMY	SPGGVSQVVQ	NEENENCLKK	VDPQLLKMAL
1130	1140	1150	1160	1170	1180	1190	1200
TPYPKLKTAL	FPQCTPPSVL	PSDITIYHLI	QSLSPFDPSR	LFGWQSANTL	AIGDAWSHLP	HFSSPDLVNK	YAIVERLNFA
1210	1220	1230	1240	1250	1260	1270	1280
YYLHNGRPSF	AFGTFLVQEL	IKSKTPKQLI	QQVGNEAYVI	GLSSFHIPSI	GAACVCFLEL	LGLDSLKLRV	DMKVANIILS
1290	1300	1310	1320	1330	1340	1350	1360
YKCRNEDAQY	SFIRESVAEK	LSKLADGEKT	TTEELLVLLE	EGTWNSIQQQ	EIKRLSSESS	SQWALVVQFC	RLHNMKLSIS
1370	1380	1390	1400	1410	1420	1430	1440
YLRECAKAND	WLQFIIHSQL	HNYHPAEVKS	LIQYFSPVIQ	DHLRLAFENL	PSVPTSKMDS	DQVCNKCPQE	LQGSKQEMTD
1450	1460	1470	1480	1490	1500	1510	1520
LFEILLQCSE	EPDSWHWLLV	EAVKQQAPIL	SVLASCLQGA	SAISCLCVWI	ITSVEDNVAT	EAMGHIQDST	EDHTWNLEDL
1530	1540	1550	1560	1570	1580	1590	1600
SVIWRTLLTR	QKSKTLIRGF	QLFFKDSPLL	LVMEMYELCM	FFRNYKEAEA	KLLEFQKSLE	TLNTAATKVH	PVIPAMWLED
1610	1620	1630	1640	1650	1660	1670	1680
QVCFLLKLML	QQCKTQYELG	KLLQLFVERE	HLFSDGPDVK	KLCILCQILK	DTSIAINHTI	ITSYSIENLQ	HECRSILERL
1690	1700	1710	1720	1730	1740	1750	1760
QTDGQFALAR	RVAELAELPV	DNLVIKEITQ	EMQTLKHIEQ	WSLKQARIDF	WKKCHENFKK	NSISSKAASS	FFSTQAHVAC
1770	1780	1790	1800	1810	1820	1830	1840
EHPTGWSSME	ERHLLLTLAG	HWLAQEDVVP	LDKLEELEKQ	IWLCRITQHT	LGRNQEETEP	RFSRQISTSG	ELSFDSLASE
1850	1860	1870	1880	1890	1900	1910	1920
FSFSKLAALN	TSKYLELNSL	PSKETCENRL	DWKEQESLNF	LIGRLLDDGC	VHEASRVCRY	FHFYNPDVAL	VLHCRALASG
1930	1940	1950	1960	1970	1980	1990	2000
EASMEDLHPE	IHALLQSAEL	LEEEAPDIPL	RRVHSRHKQM	FNPTEESQTF	LQLTTLCQDR	TLVGMKLLDK	ISSVPHGELS
2010	2020	2030	2040	2050	2060	2070	2080
CTTELLILAH	HCFTLTCHME	GIIRVLQAAH	MLTDNHLAPS	EEYGLVVRLL	TGIGRYNEMT	YIFDLLHKKH	YFEVLMRKKL
2090	2100	2110	2120	2130	2140	2150	2160
DPSGTLKTAL	LDYIKRCRPG	DSEKHNMIAL	CFSMCREIGE	NHEAAARIQL	KLIESQPWED	SLKDGHQLKQ	LLLKALTLML
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
1898	1	686.2375	-119.80	2	52.2	12.6	0	1885-1896	R.LLDDGCVHEASR.V	Carbamidomethyl: 6

Detailed Protein Report

Protein 535: PREDICTED: ubiquitin thioesterase ZRANB1 isoform X3 [Homo sapiens]

Accession:	gi|530393888	**Score:**	27.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	44.2
Database Date:	2015-11-30	**pI:**	4.7
		Sequence Coverage [%]:	5.5
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MLAILLTEVS	QQAAKCIPAM	VCPELTEQIR	REIAASLHQR	KGDFACYFLT	DLVTFTLPAD	IEDLPPTVQE	KLFDEVLDRD
90	100	110	120	130	140	150	160
VQKELEEESP	IINWSLELAT	RLDSRLYALW	NRTAGDCLLD	SVLQATWGIY	DKDSVLRKAL	HDSLHDCSHW	FYTRWKDWES
170	180	190	200	210	220	230	240
WYSQSFGLHF	SLREEQWQED	WAFILSLASQ	PGASLEQTHI	FVLAHILRRP	IIVYGVKYYK	SFRGETLGYT	RFQGVYLPLL
250	260	270	280	290	300	310	320
WEQSFCWKSP	IALGYTRGHF	SALVAMENDG	YGNRGAGANL	NTDDDVTITF	LPLVDSERKL	LHVHFLSAQE	LGNEEQQEKL
330	340	350	360	370	380	390	
LREWLDCCVT	EGGVLVAMQK	SSRRRNHPLV	TQMVEKWLDR	YRQIRPCTSL	SDGEEDEDDE	DE	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1033	2	590.8060	-42.13	2	41.7	16.3	1	31-40	R.REIAASLHQR.K	
2725	1	648.3400	-3.80	2	62.5	10.7	0	346-356	R.NHPLVTQMVEK.W	

Detailed Protein Report

Protein 536: probable ATP-dependent RNA helicase DDX20 [Homo sapiens]

Accession:	gi|256223453	**Score:**	27.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	92.2
Database Date:	2015-11-30	**pI:**	6.5
		Sequence Coverage [%]:	1.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAAAFEASGA	LAAVATAMPA	EHVAVQVPAP	EPTPGPVRIL	RTAQDLSSPR	TRTGDVLLAE	PADFESLLLS	RPVLEGLRAA
90	100	110	120	130	140	150	160
GFERPSPVQL	KAIPLGRCGL	DLIVQAKSGT	GKTCVFSTIA	LDSLVLENLS	TQILILAPTR	EIAVQIHSVI	TAIGIKMEGL
170	180	190	200	210	220	230	240
ECHVFIGGTP	LSQDKTRLKK	CHIAVGSPGR	IKQLIELDYL	NPGSIRLFIL	DEADKLLEEG	SFQEQINWIY	SSLPASKQML
250	260	270	280	290	300	310	320
AVSATYPEFL	ANALTKYMRD	PTFVRLNSSD	PSLIGLKQYY	KVVNSYPLAH	KVFEEKTQHL	QELFSRIPFN	QALVFSNLHS
330	340	350	360	370	380	390	400
RAQHLADILS	SKGFPAECIS	GNMNQNQRLD	AMAKLKHFHC	RVLISTDLTS	RGIDAEKVNL	VVNLDVPLDW	ETYMHRIGRA
410	420	430	440	450	460	470	480
GRFGTLGLTV	TYCCRGEEEN	MMMRIAQKCN	INLLPLPDPI	PSGLMEECVD	WDVEVKAAVH	TYGIASVPNQ	PLKKQIQKIE
490	500	510	520	530	540	550	560
RTLQIQKAHG	DHMASSRNNS	VSGLSVKSKN	NTKQKLPVKS	HSECGIIEKA	TSPKELGCDR	QSEEQMKNSV	QTPVENSTNS
570	580	590	600	610	620	630	640
QHQVKEALPV	SLPQIPCLSS	FKIHQPYTLT	FAELVEDYEH	YIKEGLEKPV	EIIRHYTGPG	DQTVNPQNGF	VRNKVIEQRV
650	660	670	680	690	700	710	720
PVLASSSQSG	DSESDSDSYS	SRTSSQSKGN	KSYLEGSSDN	QLKDSESTPV	DDRISLEQPP	NGSDTPNPEK	YQESPGIQMK
730	740	750	760	770	780	790	800
TRLKEGASQR	AKQSRRNLPR	RSSFRLQTEA	QEDDWYDCHR	EIRLSFSDTY	QDYEEYWRAY	YRAWQEYYAA	ASHSYYWNAQ
810	820	830					
RHPSWMAAYH	MNTIYLQEMM	HSNQ					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
827	1	683.3392	-78.48	2	39.2	27.0	2	178-190	R.LKKCHIAVGSPGR.I	

Detailed Protein Report

Protein 537: **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 538: **zinc finger protein 610 isoform b [Homo sapiens]**

Accession:	gi|239787106	**Score:**	27.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	48.6
Database Date:	2015-11-30	**pI:**	10.2
		Sequence Coverage [%]:	7.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLCDEEAQKR	KAKESGMALP	QGRLTFMDVA	IEFSQEEWKS	LDPGQRALYR	DVMLENYRNL	VFLGRSCVLG	SNAENKPIKN
90	100	110	120	130	140	150	160
QLGLTLEAHL	SELQLFQAGR	KIYRSNQVEK	FTNHRSSVSP	LQKISSSFTT	HIFNKYRNDL	IDFPLLPQEE	KAYIRGKSYE
170	180	190	200	210	220	230	240
YECSEDGEVF	RVRASLTNHQ	VIHTAEKPYK	CTECGKVFSR	NSHLVEHWRI	HTGQKPYKCS	ECDKVFNRNS	NLARHQRIHT
250	260	270	280	290	300	310	320
GEKPHKCNEC	GKAFRECSGL	TTHLVIHTGE	KPYKCNECGK	NFRHKFSLTN	HQRSHTAEKP	YKCNECGKVF	SLLSYLARHQ
330	340	350	360	370	380	390	400
IIHSTEKPYK	CNECGRAFHK	RPGLMAHLLI	HTGEKPYKCN	ECDKVFGRKL	YLTNHQRIHT	GERPYKCNAC	GKVFNQNPHL
410	420						
SRHRKIHAGE	NSLRTLQME						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1493	1	949.3248	-78.23	2	48.5	12.6	1	156-171	R.GKSYEYECSEDGEVFR.V	

Detailed Protein Report

Protein 539: zinc finger protein 177 isoform b [Homo sapiens]

Accession:	gi|289547607	**Score:**	27.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	36.4
Database Date:	2015-11-30	**pI:**	9.8
		Sequence Coverage [%]:	5.3
		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
977	1	512.1767	-143.10	2	41.0	10.1	0	41-48	K.DVMLENFR.N	
1517	1	1008.6274	90.62	1	48.8	16.8	0	216-224	K.AFIDQSSLK.K	

Detailed Protein Report

Protein 540: poly [ADP-ribose] polymerase 10 [Homo sapiens]

Accession: gi|157738665
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 26.9
MW [kDa]: 109.9
pI: 4.8
Sequence Coverage [%]: 3.8
No. of unique Peptides: 2

Quantitation

mdown:qdown	**Median:**	0.70	**CV:**	29.92 %	**No. of Peptides:**	2
Wdown:Qdown	**Median:**	0.74	**CV:**	0.00 %	**No. of Peptides:**	1

10	20	30	40	50	60	70	80
MVAMAEAEAG	VAVEVRGLPP	AVPDELLTLY	FENRRRSGGG	PVLSWQRLGC	GGVLTFREPA	DAERVLAQAD	HELHGAQLSL
90	100	110	120	130	140	150	160
RPAPPRAPAR	LLLQGLPPGT	TPQRLEQHVQ	ALLRASGLPV	QPCCALASPR	PDRALVQLPK	PLSEADVRVL	EEQAQNLGLE
170	180	190	200	210	220	230	240
GTLVSLARVP	QARAVRVVGD	GASVDLLLLE	LYLENERRSG	GGPLEDLQRL	PGPLGTVASF	QQWQVAERVL	QQEHRLQGSE
250	260	270	280	290	300	310	320
LSLVPHYDIL	EPEELAENTS	GGDHPSTQGP	RATKHALLRT	GGLVTALQGA	GTVTMGSGEE	PGQSGASLRT	GPMVQGRGIM
330	340	350	360	370	380	390	400
TTGSGQEPGQ	SGTSLRTGPM	GSLGQAEQVS	SMPMGSLEHE	GLVSLRPVGL	QEQEGPMSLG	PVGSAGPVET	SKGLLGQEGL
410	420	430	440	450	460	470	480
VEIAMDSPEQ	EGLVGPMEIT	MGSLEKAGPV	SPGCVKLAGQ	EGLVEMVLLM	EPGAMRFLQL	YHEDLLAGLG	DVALLPLEGP
490	500	510	520	530	540	550	560
DMTGFRLCGA	QASCQAAEEF	LRSLLGSISC	HVLCLEHPGS	ARFLLGPEGQ	HLLQGLEAQF	QCVFGTERLA	TATLDTGLEE
570	580	590	600	610	620	630	640
VDPTEALPVL	PGNAHTLWTP	DSTGGDQEDV	SLEEVRELLA	TLEGLDLDGE	DWLPRELEEE	GPQEQPEEEV	TPGHEEEEPV
650	660	670	680	690	700	710	720
APSTVAPRWL	EEEAALQLAL	HRSLEPQGQV	AEQEEAAALR	QALTLSLLEQ	PPLEAEEPPD	GGTDGKAQLV	VHSAFEQDVE
730	740	750	760	770	780	790	800
ELDRALRAAL	EVHVQEETVG	PWRRTLPAEL	RARLERCHGV	SVALRGDCTI	LRGFGAHPAR	AARHLVALLA	GPWDQSLAFP
810	820	830	840	850	860	870	880
LAASGPTLAG	QTLKGPWNNL	ERLAENTGEF	QEVVRAFYDT	LDAARSSIRV	VRVERVSHPL	LQQQYELYRE	RLLQRCERRP
890	900	910	920	930	940	950	960
VEQVLYHGTT	APAVPDICAH	GFNRSFCGRN	ATVYGKGVYF	ARRASLSVQD	RYSPPNADGH	KAVFVARVLT	GDYGQGRRGL
970	980	990	1000	1010	1020	1030	
RAPPLRGPGH	VLLRYDSAVD	CICQPSIFVI	FHDTQALPTH	LITCEHVPRA	SPDDPSGLPG	RSPDT	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1670	1	932.4465	-0.39	2	49.6	13.6	0	318-336	R.GIMTTGSGQEPGQSGTSLR.T		mdown:qdown 0.94 Wdown:Qdown 0.74
45	1	1096.9782	-64.39	2	29.9	13.4	0	503-522	R.SLLGSISCHVLCLEHPGSAR.F	Carbamidomethyl: 8, 12	mdown:qdown 0.52

Detailed Protein Report

Protein 541: **PREDICTED: MAM domain-containing glycosylphosphatidylinositol anchor protein 1 isoform X2 [Homo sapiens]**

Accession:	gi|578811587	**Score:**	26.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	59.5
Database Date:	2015-11-30	**pI:**	9.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	7.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEVTCLLLLA	LIPFHCRGQG	VYAPAQAQIV	HAGQACVVKE	DNISERVYTI	REGDTLMLQC	LVTGHPRPQV	RWTKTAGSAS
90	100	110	120	130	140	150	160
DKFQETSVFN	ETLRIERIAR	TQGGRYYCKA	ENGVGVPAIK	SIRVDVQYLD	EPMLTVHQTV	SDVRGNFYQE	KTVFLRCTVN
170	180	190	200	210	220	230	240
SNPPARFIWK	RGSDTLSHSQ	DNGVDIYEPL	YTQGETKVLK	LKNLRPQDYA	SYTCQVSVRN	VCGIPDKAIT	FRLTNTTAPP
250	260	270	280	290	300	310	320
ALKLSVNETL	VVNPGENVTV	QCLLTGGDPL	PQLQWSHGPG	PLPLGALAQG	GTLSIPSVQA	RDSGYYNCTA	TNNVGNPAKK
330	340	350	360	370	380	390	400
TVNLLVRSMK	NATFQITPDV	IKESENIQLG	QDLKLSCHVD	AVPQEKVTYQ	WFKNGKPARM	SKRLLVTRND	PELPAVTSSL
410	420	430	440	450	460	470	480
ELIDLHFSDY	GTYLCMASFP	GAPVPDLSVE	VNISSETVPP	TISVPKGRAV	VTVREGSPAE	LQCEVRGKPR	PPVLWSRVDK
490	500	510	520	530	540		
EAALLPSGLP	LEETPDGKLR	LERVSRDMSG	TYRCQTARYN	GFNVRPREAQ	VQLNVQWTR		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1451	1	652.4568	150.96	3	46.7	16.5	0	2-17	M.EVTCLLLLALIPFHCR.G	Carbamidomethyl: 4, 15

Detailed Protein Report

Protein 542: **PREDICTED: beta/gamma crystallin domain-containing protein 3 isoform X1 [Homo sapiens]**

Accession:	gi|530373918	**Score:**	26.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	298.2
Database Date:	2015-11-30	**pI:**	5.0
		Sequence Coverage [%]:	0.7
		No. of unique Peptides:	1

Detailed Protein Report

```
        10         20         30         40         50         60         70         80
MKGNLLEGPL EDSDCSKTSF NKENSLTNNP ELQNIASSNN LLNKNAWGSI ERNRSSPSSV TNSSYDGESD SQHHLSCEPV

        90        100        110        120        130        140        150        160
SQTNRNLVCS ALLTGSNHRK VPCSPDFQRV TTTENTIKEN STVMSNRTLV QREELVEPQG PAISDFSCSK SDGSDTTEQE

       170        180        190        200        210        220        230        240
STNLPSPNKS IRHEHLQLPE SECSDKQTID SSSKQAATHT NIIALQRHAV TDTEFVNEGK RLSAQDSQKN VAVREIRRET

       250        260        270        280        290        300        310        320
ESASAGESIA SSHVKAPEDK IESLPKDTDQ YFETKAKKLD FRSHDKIPHI RMNKKDLASL NYISESAVVA SLGNENAPEL

       330        340        350        360        370        380        390        400
KFELNRSHIS ETPLDSESPQ QAEVSPDAKT SLSLDCKKLN FSISPPTFVS GVGMLSKLDI PDLMNEGSPV PIETGNVNIV

       410        420        430        440        450        460        470        480
GISYQPRKCK EENVKNHVEA AGRKSPPPSF CLEYTSAIFE FKEVLSNSEK CQVLPGSEAS GPHLTGLELL SFDSGNLSKD

       490        500        510        520        530        540        550        560
CSSILSQDPN RVELVSSNTK ANMSIIEKSD SLSLEAKTAN IVSKAEIDGQ NNVLVESHSG RGKTISLSKV SLSKVEPRNI

       570        580        590        600        610        620        630        640
SQDKMSSFPL KITHVPEKPI LSELTFLEVE QGKRFQSINH NEIGEKCSDA GLKENCQAEL SPAASKYEDK PEPEVDALGS

       650        660        670        680        690        700        710        720
PPALLKSNIS WILPPIHDEK ISRQMAQNCE AHTCVFHQSL DICGTKKISG HSEMAELSLT NISPKFQETG SMKVNSPFLD

       730        740        750        760        770        780        790        800
SDSSLEKNSS ASEDSSFLKV PSVLKLEKKS SSYRKKENIH FLNGGIDSVS SSSSYPEEVS MIVNSHKPQN NLDSIQVTKD

       810        820        830        840        850        860        870        880
LTHEGTSVTN LLYPTTSYLE FETSVSIGTE VTPFQEHFGI YTGKISIDFP TAAQFDNLVE AETGAVAGPA ASVNSSGQQC

       890        900        910        920        930        940        950        960
SEASAEHIEA RRRAHDQLLD LKSSLLKKAD TLIGEIFNSV REELKFKHTV STCQEHIAIE GIMNLGTLKE DISEKNPSEV

       970        980        990       1000       1010       1020       1030       1040
TLTEIQQTEG LEEQGMENMS EVKEKPCVSP TVGEKNLLVD PNSMNVSCLL EDKARELVNE IIYVAQEKLR NDTFEDTEDT

      1050       1060       1070       1080       1090       1100       1110       1120
WDSELQANTS KILNSDSVKP HDVVREFLVS EQPVNQSTQI SENKVLNEFF SLSNLASGTE SIKGGEIVLY QKSLFSGNGS

      1130       1140       1150       1160       1170       1180       1190       1200
GLSDSINLQE SDTVLLAEDM SHKRLDDRVK THLFRSEDCN ETMEIENVDN NKTETEDRRT LVLNFKWPPL VNDDIHAPGT

      1210       1220       1230       1240       1250       1260       1270       1280
SKSSLSDSLV CISEKNLPGH SKNTPLAMSD VGKVHKKDNE INIGKIELIP SMLETGKTNK KDAELNILKY EAVPPMIEMG

      1290       1300       1310       1320       1330       1340       1350       1360
RIHKMDAELN VTKTEPKANV FKMGEVYQMD AESCIEKTEG SAVILGMEKA YKMKDTEGDI GKIEVIPMMP EVKNIHQKDA

      1370       1380       1390       1400       1410       1420       1430       1440
EGDIVKTEMT PVTVDMENIY QTHAEGDIGK TGTIALSEVE NIHQKGGEGI SEKAEVIPVT LAMENTYQKD AEGDIGKAEV

      1450       1460       1470       1480       1490       1500       1510       1520
MPVRLEMENT YPKDTERDGG KTEVMPLALE VVNTYQKNAK GFTGNTEGSV LKMEATYRKT AEEVIKNTEI VPCVLKVKEA

      1530       1540       1550       1560       1570       1580       1590       1600
HETAPAPLEM EKACKRDVKE TIGATVSTPS VIEMEKISPE DRGENIGKHK VLPAVVDIEK IHGTGLELTT KQGEAMLPAF

      1610       1620       1630       1640       1650       1660       1670       1680
ESKTPQEYAE GSVEETKEEP TEIKEGLIAH ENRLPTYFRG YESPTLSKDY EGYPAPAMPD FQPGDTTVRL DKRMSLTAIY

      1690       1700       1710       1720       1730       1740       1750       1760
DKRRETDYSD KGYNLAFVSQ DEQENSSFTI LYEEPLQEED KYASAEARQT QSVLFHDTSA DSMPVLACER SESRTDLVHH

      1770       1780       1790       1800       1810       1820       1830       1840
FEKGTKLGET FDSDSSEMFL SVEAKRYKIY PLALSPIYED DSSQEDILSS EVSPGHHGPR KSRDSENQSS SVLSLLQSVS

      1850       1860       1870       1880       1890       1900       1910       1920
ERLKMNFDED DREAADEEEE EEEAAVLHKG DLRAGSGERV TFQLPDPSIT FYPDDQESVG ISKNSYVMPN EPTTSNLQVG

      1930       1940       1950       1960       1970       1980       1990       2000
LWPEKTSFLQ KSDLTSKLHS SLKSAYHQYL QTSQSHSSEK GARFGGIFQE PVSKYFRVQD SPGRLSPFIE NVDKQTLRCN

      2010       2020       2030       2040       2050       2060       2070       2080
PRPGKMVIYD LHESTYKQEV YCNIPDATSW SFPNGVLIKV VRGCWILYEK PHFRGQKCVL EEGEKVLNRD WILQNRRHPQ

      2090       2100       2110       2120       2130       2140       2150       2160
RNFILGSLKR VLKDCSIPEI ELFPQSDPAC CPVYIQRAVP NLEELNISKS VSFTVKSGVW LAYPDINFKG QATVLEEDHG

      2170       2180       2190       2200       2210       2220       2230       2240
```

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2896	1	1012.4872	-151.04	1	65.4	13.7	1	740-748	K.VPSVLKLEK.K	

Detailed Protein Report

Protein 543: **PREDICTED: tubulin polymerization-promoting protein family member 3 isoform X1 [Homo sapiens]**

Accession:	gi|530423965	**Score:**	26.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	28.3
Database Date:	2015-11-30	**pI:**	10.1
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	6.8
		No. of unique Peptides:	1

Quantitation

mdown:qdown **Median:** 0.59 **CV:** 0.00 % **No. of Peptides:** 1

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	Ratios
396	1	595.2630	-86.70	2	34.3	12.8	2	11-20	R.RSRLGCSPTR.E	Carbamidomethyl: 6	mdown:qdown 0.59

Detailed Protein Report

Protein 544: FERM domain-containing protein 6 isoform 1 [Homo sapiens]

Accession:	gi|22748721	**Score:**	26.9
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:	1

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
1818	1	731.8030	-66.05	2	52.7	13.2	0	512-524	R.GQSTDSLPQTICR.K	Carbamidomethyl: 12

Detailed Protein Report

Protein 545: PREDICTED: SNW domain-containing protein 1 isoform X2 [Homo sapiens]

Accession:	gi|530403266	**Score:**	26.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	65.4
Database Date:	2015-11-30	**pI:**	10.2
Modification(s):	Oxidation	**Sequence Coverage [%]:**	5.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MALTSFLPAP	TQLSQDQLEA	EEKARSQRSR	QTSLVSSRRE	PPPYGYRKGW	IPRLLEDFGD	GGAFPEIHVA	QYPLDMGRKK
90	100	110	120	130	140	150	160
KMSNALAIQV	DSEGKIKYDA	IARQGQSKDK	VIYSKYTDLV	PKEVMNADDP	DLQRPDEEAI	KEITEKTRVA	LEKSVSQKVA
170	180	190	200	210	220	230	240
AAMPVRAADK	LAPAQYIRYT	PSQQGVAFNS	GAKQRVIRMV	EMQKDPMEPP	RFKINKKIPR	GPPSPPAPVM	HSPSRKMTVK
250	260	270	280	290	300	310	320
EQQEWKIPPC	ISNWKNAKGY	TIPLDKRLAA	DGRGLQTVHI	NENFAKLAEA	LYIADRKARE	AVEMRAQVER	KMAQKEKEKH
330	340	350	360	370	380	390	400
EEKLREMAQK	ARERRAGIKT	HVEKEDGEAR	ERDEIRHDRR	KERQHDRNLS	RAAPDKRSKL	QRNENRDISE	VIALGVPNPR
410	420	430	440	450	460	470	480
TSNEVQYDQR	LFNQSKGMDS	GFAGGEDEIY	NVYDQAWRGG	KDMAQSIYRP	SKNLDKDMYG	DDLEARIKTN	RCQAIQLNFS
490	500	510	520	530	540	550	560
VYTGESKVVH	SFFSFSLDLF	PTRSFLVQTV	DREAEKDQCS	LRKILLVWTS	FWKKPNSMVA	LKDPQIAAAP	RNTSMKARRG
570	580						
GRNRHRSLQS	E						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1677	1	956.4573	-2.25	2	49.5	13.3	2	453-468	K.NLDKDMYGDDLEARIK.T	Oxidation: 6

Detailed Protein Report

Protein 546: 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

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
1676	1	916.3092	-152.23	2	50.9	15.0	1	174-190	R.RSTCQAQGSCTGLPPLR.G	Carbamidomethyl: 10

Detailed Protein Report

Protein 547: proteoglycan 4 isoform D precursor [Homo sapiens]

Accession: gi|189181724
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 26.8
MW [kDa]: 136.5
pI: 10.1
Sequence Coverage [%]: 1.4
No. of unique Peptides: 2

Quantitation

mdown:qdown **Median:** 1.04 **CV:** 0.00 % **No. of Peptides:** 1
Wdown:Qdown **Median:** 1.77 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MAWKTLPIYL	LLLLSVFVIQ	QVSSQELSCK	GRCFESFERG	RECDCDAQCK	KYDKCCPDYE	SFCAEVKDNK	KNRTKKKPTP
90	100	110	120	130	140	150	160
KPPVVDEAGS	GLDNGDFKVT	TPDTSTTQHN	KVSTSPKITT	AKPINPRPSL	PPNSDTSKET	SLTVNKETTV	ETKETTTTNK
170	180	190	200	210	220	230	240
QTSTDGKEKT	TSAKETQSIE	KTSAKDLAPT	SKVLAKPTPK	AETTTKGPAL	TTPKEPTPTT	PKEPASTTPK	EPTPTTIKSA
250	260	270	280	290	300	310	320
PTTPKEPAPT	TTKSAPTTPK	EPAPTTTKEP	APTTPKEPAP	TTTKEPAPTT	TKSAPTTPKE	PAPTTPKKPA	PTTPKEPAPT
330	340	350	360	370	380	390	400
TPKEPTPTTP	KEPAPTTKEP	APTTPKEPAP	TAPKKPAPTT	PKEPAPTTPK	EPAPTTTKEP	SPTTPKEPAP	TTTKSAPTTT
410	420	430	440	450	460	470	480
KEPAPTTTKS	APTTPKEPSP	TTTKEPAPTT	PKEPAPTTPK	KPAPTTPKEP	APTTPKEPAP	TTTKKPAPTT	PKEPAPTTPK
490	500	510	520	530	540	550	560
ETAPTTPKKL	TPTTPEKLAP	TTPEKPAPTT	PEELAPTTPE	EPTPTTPEEP	APTTPKAAAP	NTPKEPAPTT	PKEPAPTTPK
570	580	590	600	610	620	630	640
EPAPTTPKET	APTTPKGTAP	TTLKEPAPTT	PKKPAPKELA	PTTTKEPTST	TCDKPAPTTP	KGTAPTTPKE	PAPTTPKEPA
650	660	670	680	690	700	710	720
PTTPKGTAPT	TLKEPAPTTP	KKPAPKELAP	TTTKGPTSTT	SDKPAPTTPK	ETAPTTPKEP	APTTPKKPAP	TTPETPPPTT
730	740	750	760	770	780	790	800
SEVSTPTTTK	EPTTIHKSPD	ESTPELSAEP	TPKALENSPK	EPGVPTTKTP	AATKPEMTTT	AKDKTTERDL	RTTPETTTAA
810	820	830	840	850	860	870	880
PKMTKETATT	TEKTTESKIT	ATTTQVTSTT	TQDTTPFKIT	TLKTTTLAPK	VTTTKKTITT	TEIMNKPEET	AKPKDRATNS
890	900	910	920	930	940	950	960
KATTPKPQKP	TKAPKKPTST	KKPKTMPRVR	KPKTTPTPRK	MTSTMPELNP	TSRIAEAMLQ	TTTRPNQTPN	SKLVEVNPKS
970	980	990	1000	1010	1020	1030	1040
EDAGGAEGET	PHMLLRPHVF	MPEVTPDMDY	LPRVPNQGII	INPMLSDETN	ICNGKPVDGL	TTLRNGTLVA	FRGHYFWMLS
1050	1060	1070	1080	1090	1100	1110	1120
PFSPPSPARR	ITEVWGIPSP	IDTVFTRCNC	EGKTFFFKDS	QYWRFTNDIK	DAGYPKPIFK	GFGGLTGQIV	AALSTAKYKN
1130	1140	1150	1160	1170	1180	1190	1200
WPESVYFFKR	GGSIQQYIYK	QEPVQKCPGR	RPALNYPVYG	ETTQVRRRRF	ERAIGPSQTH	TIRIQYSPAR	LAYQDKGVLH
1210	1220	1230	1240	1250	1260	1270	1280
NEVKVSILWR	GLPNVVTSAI	SLPNIRKPDG	YDYYAFSKDQ	YYNIDVPSRT	ARAITTRSGQ	TLSKVWYNCP	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2386	1	994.9816	-34.55	2	58.2	14.8	2	785-802	K.TTERDLRTTPETTTAAPK.M		Wdown:Qdown 1.77
285	1	559.1440	-261.71	2	32.7	12.0	0	792-802	R.TTPETTTAAPK.M		mdown:qdown 1.04

Detailed Protein Report

Protein 548: PREDICTED: autophagy-related protein 2 homolog B isoform X1 [Homo sapiens]

Accession:	gi|578825925	**Score:**	26.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	232.5
Database Date:	2015-11-30	**pI:**	5.4
		Sequence Coverage [%]:	1.2
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	0.87	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.18	**CV:**	0.00 %	**No. of Peptides:**	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MPWPFSESIK	KRACRYLLQR	YLGHFLQEKL	SLEQLSLDLY	QGTGSLAQVP	LDKWCLNEIL	ESADAPLEVT	EGFIQSISLS
90	100	110	120	130	140	150	160
VPWGSLLQDN	CALEVRGLEM	VFRPRPRPAT	GSEPMYWSSF	MTSSMQLAKE	CLSQKLTDEQ	GEGSQPFEGL	EKFAETIETV
170	180	190	200	210	220	230	240
LRRVKVTFID	TVLRIEHVPE	NSKTGTALEI	RIERTVYCDE	TADESSGINV	HQPTAFAHKL	LQLSGVSLFW	DEFSASAKSS
250	260	270	280	290	300	310	320
PVCSTAPVET	EPKLSPSWNP	KIIYEPHPQL	TRNLPEIAPS	DPVQIGRLIG	RLELSLTLKQ	NEVLPGAKLD	VDGQIDSIHL
330	340	350	360	370	380	390	400
LLSPRQVHLL	LDMLAAIAGP	ENSSKIGLAN	KDRKNRPMQQ	EDEYRIQMEL	NRYYLRKDSL	SVGVSSEQSF	YETETARTPS
410	420	430	440	450	460	470	480
SREEVFFSMA	DMDMSHSLSS	LPPLGDPPNM	DLELSLTSTY	TNTPAGSPLS	ATVLQPTWGE	FLDHHKEQPV	RGSTFPSNLV
490	500	510	520	530	540	550	560
HPTPLQKTSL	PSRSVSVDES	RPELIFRLAV	GTFSISVLHI	DPLSPPETSQ	NLNPLTPMAV	AFFTCIEKID	PARFSTEDFK
570	580	590	600	610	620	630	640
SFRAVFAEAC	SHDHLRFIGT	GIKVSYEQRQ	RSASRYFSTD	MSIGQMEFLE	CLFPTDFHSV	PPHYTELLTF	HSKEETGSHS
650	660	670	680	690	700	710	720
PVCLQLHYKH	SENRGPQGNQ	ARLSSVPHKA	ELQIKLNPVC	CELDISIVDR	LNSLLQPQKL	ATVEMMASHM	YTSYNKHISL
730	740	750	760	770	780	790	800
HKAFTEVFLD	DSHSPANCRI	SVQVATPALN	LSVRFPIPDL	RSDQERGPWF	KKSLQKEILY	LAFTDLEFKT	EFIGGSTPEQ
810	820	830	840	850	860	870	880
IKLELTFREL	IGSFQEEKGD	PSIKFFHVSS	GVDGDTTSSD	DFDWPRIVLK	INPPAMHSIL	ERIAAEEEEE	NDGHYQEEEE
890	900	910	920	930	940	950	960
GGAHSLKDVC	DLRRPAPSPF	SSRRVMFENE	QMVMPGDPVE	MTEFQDKAIS	NSHYVLELTL	PNIYVTLPNK	SFYEKLYNRI
970	980	990	1000	1010	1020	1030	1040
FNDLLLWEPT	APSPVETFEN	ISYGIGLSVA	SQLINTFNKD	SFSAFKSAVH	YDEESGSEEE	TLQYFSTVDP	NYRSRRKKKL
1050	1060	1070	1080	1090	1100	1110	1120
DSQNKNSQSF	LSVLLNINHG	LIAVFTDVKQ	DNGDLLENKH	GEFWLEFNSG	SLFCVTKYEG	FDDKHYICLH	SSSFSLYHKG
1130	1140	1150	1160	1170	1180	1190	1200
IVNGVILPTE	TRLPSSTRPH	WLEPTIYSSE	EDGLSKTSSD	GVGGDSLNML	SVAVKILSDK	SESNTKEFLI	AVGLKGATLQ
1210	1220	1230	1240	1250	1260	1270	1280
HRMLPSGLSW	HEQILYFLNI	ADEPVLGYNP	PTSFTTFHVH	LWSCALDYRP	LYLPIRSLLT	VETFSVSSSV	ALDKSSSTLR
1290	1300	1310	1320	1330	1340	1350	1360
IILDEAALHL	SDKCNTVTIN	LSRDYVRVMD	MGLLELTITA	VKSDSDGEQT	EPRFELHCSS	DVVHIRTCSD	SCAALMNLIQ
1370	1380	1390	1400	1410	1420	1430	1440
YIASYGDLQT	PNKADMKPGA	FQRRSKVDSS	GRSSSRGPVL	PEADQQMLRD	LMSDAMEEID	MQQGTSSVKP	QANGVLDEKS
1450	1460	1470	1480	1490	1500	1510	1520
QIQEPCCSDL	FLFPDESGNV	SQESGPTYAS	FSHHFISDAM	TGVPTENDDF	CILFAPKAAM	QEKEEEPVIK	IMVDDAIVIR
1530	1540	1550	1560	1570	1580	1590	1600
DNYFSLPVNK	TDTSKAPLHF	PIPVIRYVVK	EVSLVWHLYG	GKDFGIVPPT	SPAKSYISPH	SSPSHTPTRH	GRNTVCGGKG
1610	1620	1630	1640	1650	1660	1670	1680
RNHDFLMEIQ	LSKVKFQHEV	YPPCKPDCDS	SLSEHPVSRQ	VFIVQDLEIR	DRLATSQMNK	FLYLYCSKEM	PRKAHSNMLT
1690	1700	1710	1720	1730	1740	1750	1760
VKALHVCPES	GRSPQECCLR	VSLMPLRLNI	DQDALFFLKD	FFTSLSAEVE	LQMTPDPEVK	KSPGADVTCS	LPRHLSTSKE
1770	1780	1790	1800	1810	1820	1830	1840
PNLVISFSGP	KQPSQNDSAN	SVEVVNGMEE	KNFSAEEASF	RDQPVFFREF	RFTSEVPIRL	DYHGKHVSMD	QGTLAGILIG
1850	1860	1870	1880	1890	1900	1910	1920
LAQLNCSELK	LKRLSYRHGL	LGVDKLFSYA	ITEWLNDIKK	NQLPGILGGV	GPMHSLVQLV	QGLKDLVWLP	IEQYRKDGRI
1930	1940	1950	1960	1970	1980	1990	2000
VRGFQRGAAS	FGTSTAMAAL	ELTNRMVQTI	QAAAETAYDM	VSPGTLSIEP	KKTKRFPHHR	LAHQPVDLRE	GVAKAYSVVK
2010	2020	2030	2040	2050	2060	2070	2080
EGITDTAQTI	YETAAREHES	RGVTGAVGEV	LRQIPPAVVK	PLIVATEATS	NVLGGMRNQI	RPDVRQDESQ	KWRHGDD

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

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2179	1	766.3372	-41.60	2	55.9	12.0	0	239-253	K.SSPVCSTAPVETEPK.L		Wdown:Qdown 0.18 mdown:qdown 0.87

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Detailed Protein Report

Protein 549: PREDICTED: peripheral plasma membrane protein CASK isoform X4 [Homo sapiens]

Accession:	gi|578838134	**Score:**	26.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	100.7
Database Date:	2015-11-30	**pI:**	5.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MADDDVLFED	VYELCEVIGK	GPFSVVRRCI	NRETGQQFAV	KIVDVAKFTS	SPGLSTEDLK	REASICHMLK	HPHIVELLET
90	100	110	120	130	140	150	160
YSSDGMLYMV	FEFMDGADLC	FEIVKRADAG	FVYSEAVASH	YMRQILEALR	YCHDNNIIHR	DVKPHCVLLA	SKENSAPVKL
170	180	190	200	210	220	230	240
GGFGVAIQLG	ESGLVAGGRV	GTPHFMAPEV	VKREPYGKPV	DVWGCGVILF	ILLSGCLPFY	GTKERLFEGI	IKGKYKMNPR
250	260	270	280	290	300	310	320
QWSHISESAK	DLVRRMLMLD	PAERITVYEA	LNHPWLKERD	RYAYKIHLPE	TVEQLRKFNA	RRKLKGAVLA	AVSSHKFNSF
330	340	350	360	370	380	390	400
YGDPPEELPD	FSEDPTSSGA	VSQVLDSLEE	IHALTDCSEK	DLDFLHSVFQ	DQHLHTLLDL	YDKINTKSSP	QIRNPPSDAV
410	420	430	440	450	460	470	480
QRAKEVLEEI	SCYPENNDAK	ELKRILTQPH	FMALLQTHDV	VAHEVYSDEA	LRVTPPPTSP	YLNGDSPESA	NGDMDMENVT
490	500	510	520	530	540	550	560
RVRLVQFQKN	TDEPMGITLK	MNELNHCIVA	RIMHGGMIHR	QGTLHVGDEI	REINGISVAN	QTVEQLQKML	REMRGSITFK
570	580	590	600	610	620	630	640
IVPSYRTQSS	SCEIYVRAQF	EYDPAKDDLI	PCKEAGIRFR	VGDIIQIISK	DDHNWWQGKL	ENSKNGTAGL	IPSPELQEWR
650	660	670	680	690	700	710	720
VACIAMEKTK	QEQQASCTWF	GKKKKQYKDK	YLAKHNAVFD	QLDLVTYEEV	VKLPAFKRKT	LVLLGAHGVG	RRHIKNTLIT
730	740	750	760	770	780	790	800
KHPDRFAYPI	PHTTRPPKKD	EENGKNYYFV	SHDQMMQDIS	NNEYLEYGSH	EDAMYGTKLE	TIRKIHEQGL	IAILDVEPQA
810	820	830	840	850	860	870	880
LKVLRTAEFA	PFVVFIAAPT	ITPGLNEDES	LQRLQKESDI	LQRTYAHYFD	LTIINNEIDE	TIRHLEEAVE	LVCTAPQWVP
890							
VSWVY							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2304	1	1022.8910	-115.95	2	59.1	14.3	1	561-577	K.IVPSYRTQSSSCEIYVR.A	Carbamidomethyl: 12

Detailed Protein Report

Protein 550: **RNA polymerase-associated protein RTF1 homolog [Homo sapiens]**

Accession: gi|195976782
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 26.8
MW [kDa]: 80.3
pI: 8.9
Sequence Coverage [%]: 4.4
No. of unique Peptides: 2

```
        10         20         30         40         50         60         70         80
MRGRLCVGRA AAAAAAVAVP LAGGQEGSPG GGRRGSRGTT MVKKRKGRVV IDSDTEDSGS DENLDQELLS LAKRKRSDSE
        90        100        110        120        130        140        150        160
EKEPPVSQPA ASSDSETSDS DDEWTFGSNK NKKKGKARKI EKKGTMKKQA NKTASSGSSD KDSSAESSAP EEGEVSDSDS
       170        180        190        200        210        220        230        240
NSSSSSSDSD SSSEDEEFHD GYGEDLMGDE EDRARLEQMT EKEREQELFN RIEKREVLKR RFEIKKKLKT AKKKEKKEKK
       250        260        270        280        290        300        310        320
KKQEEEQEKK KLTQIQESQV TSHNKERRSK RDEKLDKKSQ AMEELKAERE KRKNRTAELL AKKQPLKTSE VYSDDEEEEE
       330        340        350        360        370        380        390        400
DDKSSEKSDR SSRTSSSDEE EEKEEIPPKS QPVSLPEELN RVRLSRHKLE RWCHMPFFAK TVTGCFVRIG IGNHNSKPVY
       410        420        430        440        450        460        470        480
RVAEITGVVE TAKVYQLGGT RTNKGLQLRH GNDQRVFRLE FVSNQEFTES EFMKWKEAMF SAGMQLPTLD EINKKELSIK
       490        500        510        520        530        540        550        560
EALNYKFNDQ DIEEIVKEKE RFRKAPPNYA MKKTQLLKEK AMAEDLGDQD KAKQIQDQLN ELEERAEALD RQRTKNISAI
       570        580        590        600        610        620        630        640
SYINQRNREW NIVESEKALV AESHNMKNQQ MDPFTRRQCK PTIVSNSRDP AVQAAILAQL NAKYGSGVLP DAPKEMSKGQ
       650        660        670        680        690        700        710        720
GKDKDLNSKS ASDLSEDLFK VHDFDVKIDL QVPSSESKAL AITSKAPPAK DGAPRRSLNL EDYKKRRGLI
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
255	1	530.8805	-123.29	3	32.6	11.9	2	203-214	K.EREQELFNRIEK.R	
90	1	650.3247	-10.31	3	29.8	14.9	2	624-642	K.YGSGVLPDAPKEMSKGQGK.D	

Detailed Protein Report

Protein 551: **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:	1

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

Detailed Protein Report

Protein 552: PREDICTED: RAS guanyl-releasing protein 2 isoform X5 [Homo sapiens]

Accession: gi|578821082
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 26.8
MW [kDa]: 52.4
pI: 7.0
Sequence Coverage [%]: 8.8
No. of unique Peptides: 2

Alias proteins:

Accession	Name	Description
gi|578821084	refseq_human(refseq_human_20140103.fasta)	PREDICTED: RAS guanyl-releasing protein 2 isoform X6 [Homo sapiens]

10	20	30	40	50	60	70	80
MSLLFDHLEP	MELAEHLTYL	EYRSFCKILF	QDYHSFVTHG	CTVDNPVLER	FISLFNSVSQ	WVQLMILSKP	TAPQRALVIT
90	100	110	120	130	140	150	160
HFVHVAEKLL	QLQNFNTLMA	VVGGLSHSSI	SRLKETHSHV	SPETIKLWEG	LTELVTATGN	YGNYRRRLAA	CVGFRFPILG
170	180	190	200	210	220	230	240
VHLKDLVALQ	LALPDWLDPA	RTRLNGAKMK	QLFSILEELA	MVTSLRPPVQ	ANPDLLSLLT	VSLDQYQTED	ELYQLSLQRE
250	260	270	280	290	300	310	320
PRSKSSPTSP	TSCTPPPRPP	VLEEWTSAAK	PKLDQALVVE	HIEKMVESVF	RNFDVDGDGH	ISQEEFQIIR	GNFPYLSAFG
330	340	350	360	370	380	390	400
DLDQNQDGCI	SREEMVSYFL	RSSSVLGGRM	GFVHNFQESN	SLRPVACRHC	KALILGIYKQ	GLKCRACGVN	CHKQCKDRLS
410	420	430	440	450	460	470	
VECRRRAQSV	SLEGSAPSPS	PMHSHHHRAF	SFSLPRPGRR	GSRPPEIREE	EVQTVEDGVF	DIHL	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1804	1	1056.6673	56.24	3	52.5	10.2	2	156-183	R.FPILGVHLKDLVALQLALPDWLDPARTR.L	
2600	1	731.3793	68.68	2	63.1	16.6	2	386-398	R.ACGVNCHKQCKDR.L	

Detailed Protein Report

Protein 553: **PREDICTED: double zinc ribbon and ankyrin repeat-containing protein 1 isoform X7 [Homo sapiens]**

Accession:	gi|578835454	**Score:**	26.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	76.5
Database Date:	2015-11-30	**pI:**	9.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.4
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	7.99	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.15	**CV:**	0.00 %	**No. of Peptides:**	1

10	20	30	40	50	60	70	80
MTAGSVCVPQ	IIPLRVPQPG	KANHEIDNNT	LLEMKSDTPD	VNIYYTLDGS	KPEFLKRIGY	GENNTFKYIK	PITLPDGKIQ
90	100	110	120	130	140	150	160
VKAIAVSKDC	RQSGIVTKVF	HVDYEPPNIV	SPEDNVENVL	KDSSRQEFKN	GFVGSKLKKK	YKNSENQRSW	NVNLRKFPVP
170	180	190	200	210	220	230	240
RFCTRKRSEV	FDKHGDNENS	KGDRLSQMGL	CAECRSLVPM	NTPICVVCEA	PLALQLQPQA	SLHLKEKVIC	RACGTGNPAH
250	260	270	280	290	300	310	320
LRYCVTCEGA	LPSSQESMCS	GDKAPPPPTQ	KGGTISCYRC	GRWNLWEASF	CGWCGAMLGI	PAGCSVCPKC	GASNHLSARF
330	340	350	360	370	380	390	400
CGSCGICVKS	LVKLSLDRSL	ALAAEEPRPF	SEPRCAWQSL	NIPLPRSDVG	TKRDIGTQTV	GLFYPSGKLL	AKKEQELASQ
410	420	430	440	450	460	470	480
KQRQEKMSDH	KPLLTAISPG	RGYWRRQLDH	ISAHLRCYAQ	NNPEFRALIA	EPRMGKLISA	TVHEDGCEVS	IRLNYSQVSN
490	500	510	520	530	540	550	560
KNLYLNKAVN	FSDHLLSSAA	EGDGGLCGSR	SSWVSDYSQS	TSDTIEKIKR	IKNFKTKTFQ	EKKEQLIPEN	RLLLKEVGPT
570	580	590	600	610	620	630	640
GEGRVSVIEQ	LLDEGADPNC	CDEDNRPVIT	VAVMNKHHEA	IPVLVQRGAD	IDQQWGPLRN	TALHEATLLG	LAGRESTATL
650	660	670	680	690	700		
LGCNASIQKK	NAGGQTAYDL	ALNTGDDLVT	SLFAAKFGQG	LEDQLAQTRS	LSLDDC		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1524	2	829.3909	-6.37	2	47.8	13.0	0	22-35	K.ANHEIDNNTLLEMK.S	Oxidation: 13	Wdown:Qdown 0.15

Detailed Protein Report

Protein 554: ubiquitin carboxyl-terminal hydrolase 32 [Homo sapiens]

Accession:	gi|22550104	**Score:**	26.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	181.5
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
MGAKESRIGF	LSYEEALRRV	TDVELKRLKD	AFKRTCGLSY	YMGQHCFIRE	VLGDGVPPKV	AEVIYCSFGG	TSKGLHFNNL
90	100	110	120	130	140	150	160
IVGLVLLTRG	KDEEKAKYIF	SLFSSESGNY	VIREEMERML	HVVDGKVPDT	LRKCFSEGEK	VNYEKFRNWL	FLNKDAFTFS
170	180	190	200	210	220	230	240
RWLLSGGVYV	TLTDDSDTPT	FYQTLAGVTH	LEESDIIDLE	KRYWLLKAQS	RTGRFDLETF	GPLVSPPIRP	SLSEGLFNAF
250	260	270	280	290	300	310	320
DENRDNHIDF	KEISCGLSAC	CRGPLAERQK	FCFKVFDVDR	DGVLSRVELR	DMVVALLEVW	KDNRTDDIPE	LHMDLSDIVE
330	340	350	360	370	380	390	400
GILNAHDTTK	MGHLTLEDYQ	IWSVKNVLAN	EFLNLLFQVC	HIVLGLRPAT	PEEEGQIIRG	WLERESRYGL	QAGHNWFIIS
410	420	430	440	450	460	470	480
MQWWQQWKEY	VKYDANPVVI	EPSSVLNGGK	YSFGTAAHPM	EQVEDRIGSS	LSYVNTTEEK	FSDNISTASE	ASETAGSGFL
490	500	510	520	530	540	550	560
YSATPGADVC	FARQHNTSDN	NNQCLLGANG	NILLHLNPQK	PGAIDNQPLV	TQEPVKATSL	TLEGGRLKRT	PQLIHGRDYE
570	580	590	600	610	620	630	640
MVPEPVWRAL	YHWYGANLAL	PRPVIKNSKT	DIPELELFPR	YLLFLRQQPA	TRTQQSNIWV	NMGNVPSPNA	PLKRVLAYTG
650	660	670	680	690	700	710	720
CFSRMQTIKE	IHEYLSQRLR	IKEEDMRLWL	YNSENYLTLL	DDEDHKLEYL	KIQDEQHLVI	EVRNKDMSWP	EEMSFIANSS
730	740	750	760	770	780	790	800
KIDRHKVPTE	KGATGLSNLG	NTCFMNSSIQ	CVSNTQPLTQ	YFISGRHLYE	LNRTNPIGMK	GHMAKCYGDL	VQELWSGTQK
810	820	830	840	850	860	870	880
NVAPLKLRWT	IAKYAPRFNG	FQQQDSQELL	AFLLDGLHED	LNRVHEKPYV	ELKDSDGRPD	WEVAAEAWDN	HLRRNRSIVV
890	900	910	920	930	940	950	960
DLFHGQLRSQ	VKCKTCGHIS	VRFDPFNFLS	LPLPMDSYMH	LEITVIKLDG	TTPVRYGLRL	NMDEKYTGLK	KQLSDLCGLN
970	980	990	1000	1010	1020	1030	1040
SEQILLAEVH	GSNIKNFPQD	NQKVRLSVSG	FLCAFEIPVP	VSPISASSPT	QTDFSSSPST	NEMFTLTTNG	DLPRPIFIPN
1050	1060	1070	1080	1090	1100	1110	1120
GMPNTVVPCG	TEKNFTNGMV	NGHMPSLPDS	PFTGYIIAVH	RKMMRTELYF	LSSQKNRPSL	FGMPLIVPCT	VHTRKKDLYD
1130	1140	1150	1160	1170	1180	1190	1200
AVWIQVSRLA	SPLPPQEASN	HAQDCDDSMG	YQYPFTLRVV	QKDGNSCAWC	PWYRFCRGCK	IDCGEDRAFI	GNAYIAVDWD
1210	1220	1230	1240	1250	1260	1270	1280
PTALHLRYQT	SQERVVDEHE	SVEQSRRAQA	EPINLDSCLR	AFTSEEELGE	NEMYYCSKCK	THCLATKKLD	LWRLPPILII
1290	1300	1310	1320	1330	1340	1350	1360
HLKRFQFVNG	RWIKSQKIVK	FPRESFDPSA	FLVPRDPALC	QHKPLTPQGD	ELSEPRILAR	EVKKVDAQSS	AGEEDVLLSK
1370	1380	1390	1400	1410	1420	1430	1440
SPSSLSANII	SSPKGSPSSS	RKSGTSCPSS	KNSSPNSSPR	TLGRSKGRLR	LPQIGSKNKL	SSSKENLDAS	KENGAGQICE
1450	1460	1470	1480	1490	1500	1510	1520
LADALSRGHV	LGGSQPELVT	PQDHEVALAN	GFLYEHEACG	NGYSNGQLGN	HSEEDSTDDQ	REDTRIKPIY	NLYAISCHSG
1530	1540	1550	1560	1570	1580	1590	1600
ILGGGHYVTY	AKNPNCKWYC	YNDSSCKELH	PDEIDTDSAY	ILFYEQQGID	YAQFLPKTDG	KKMADTSSMD	EDFESDYKKY
1610							
CVLQ							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2778	1	1023.5416	14.56	2	63.2	11.2	1	1361- 1381	K.SPSSLSANIISSPKGSPSSSR.K	

Detailed Protein Report

Protein 555: PREDICTED: zinc finger protein 124 isoform X3 [Homo sapiens]

Accession:	gi|578802322	**Score:**	26.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	35.5
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
MQETFRNLAS	IGNKGEDQSI	EDQYKNSSRN	LRHIISHSGN	NPYGCEECGK	KPCTCKQCQK	TSLSVTRVHR	DTVMHTGNGH
90	100	110	120	130	140	150	160
YGCTICEKVF	NIPSSFQIHQ	RNHTGEKPYE	CMECGKALGF	SRSLNRHKRI	HTGEKRYECK	QCGKAFSRSS	HLRDHERTHT
170	180	190	200	210	220	230	240
GEKPYECKHC	GKAFRYSNCL	HYHERTHTGE	KPYVCMECGK	AFSCLSSLQG	HIKAHAGEEP	YPCKQCGKAF	RYASSLQKHE
250	260	270	280	290	300	310	320
KTHIAQKPYV	CNNCGKGFRC	SSSLRDHERT	HTGEKPYECQ	KCGKAFSRAS	TLWKHKKTHT	GEKPYKCKKM	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2539	1	787.0551	174.57	2	60.0	14.7	0	89-101	K.VFNIPSSFQIHQR.N	

Detailed Protein Report

Protein 556: **PREDICTED: probable global transcription activator SNF2L1 isoform X5 [Homo sapiens]**

Accession:	gi|578838748	**Score:**	26.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	121.1
Database Date:	2015-11-30	**pI:**	9.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.2
		No. of unique Peptides:	2

Quantitation

Wdown:Qdown **Median:** 8.01 **CV:** 0.00 % **No. of 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	Ratios
1545	1	765.2820	-48.68	2	49.2	16.1	1	75-86	K.SEKEMDPEYEEK.M	Oxidation: 5	
2348	1	646.6880	-199.21	2	58.0	10.6	2	684-694	R.GEKKTAEMNER.L		Wdown:Qdown 8.01

Detailed Protein Report

Protein 557: DNA polymerase zeta catalytic subunit isoform b [Homo sapiens]

Accession: gi|556695361
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 26.7
MW [kDa]: 343.9
pI: 9.5
Sequence Coverage [%]: 1.1
No. of unique Peptides: 2

Alias proteins:

Accession	Name	Description
gi|578812913	refseq_human (refseq_human_20140103.fasta)	PREDICTED: DNA polymerase zeta catalytic subunit isoform X6 [Homo sapiens]
gi|556695404	refseq_human (refseq_human_20140103.fasta)	DNA polymerase zeta catalytic subunit isoform b [Homo sapiens]

10	20	30	40	50	60	70	80
MAFSIDRALN	VALGNPSSTA	QHVFKVSLVS	GMPFYGYHEK	ERHFMKIYLY	NPTMVKRICE	LLQSGAIMNK	FYQPHEAHIP
90	100	110	120	130	140	150	160
YLLQLFIDYN	LYGMNLINLA	AVKFRKARRK	SNTLHATGSC	KNHLSGNSLA	DTLFRWEQDE	IPSSLILEGV	EPQSTCELEV
170	180	190	200	210	220	230	240
DAVAADILNR	LDIEAQIGGN	PGLQAIWEDE	KQRRRNRNET	SQMSQPESQD	HRFVPATESE	KKFQKRLQEI	LKQNDFSVTL
250	260	270	280	290	300	310	320
SGSVDYSDGS	QEFSAELTLH	SEVLSPEMLQ	CTPANMVEVH	KDKESSKGHT	RHKVEEALIN	EEAILNLMEN	SQTFQPLTQR
330	340	350	360	370	380	390	400
LSESPVFMDS	SPDEALVHLL	AGLESDGYRG	ERNRMPSPCR	SFGNNKYPQN	SDDEENEPQI	EKEEMELSLV	MSQRWDSNIE
410	420	430	440	450	460	470	480
EHCAKKRSLC	RNTHRSSTED	DDSSSGEEME	WSDNSLLLAS	LSIPQLDGTA	DENSDNPLNN	ENSRTHSSVI	ATSKLSVKPS
490	500	510	520	530	540	550	560
IFHKDAATLE	PSSSAKITFQ	CKHTSALSSH	VLNKEDLIED	LSQTNKNTEK	GLDNSVTSFT	NESTYSMKYP	GSLSSTVHSE
570	580	590	600	610	620	630	640
NSHKENSKKE	ILPVSSCESS	IFDYEEDIPS	VTRQVPSRKY	TNIRKIEKDS	PFIHMHRHPN	ENTLGKNSFN	FSDLNHSKNK
650	660	670	680	690	700	710	720
VSSEGNEKGN	STALSSLFPS	SFTENCELLS	CSGENRTMVH	SLNSTADESG	LNKLKIRYEE	FQEHKTEKPS	LSQQAAHYMF
730	740	750	760	770	780	790	800
FPSVVLSNCL	TRPQKLSPVT	YKLQPGNKPS	RLKLNKRKLA	GHQETSTKSS	ETGSTKDNFI	QNNPCNSNPE	KDNALASDLT
810	820	830	840	850	860	870	880
KTTRGAFENK	TPTDGFIDCH	FGDGTLETEQ	SFGLYGNKYT	LRAKRKVNYE	TEDSESSFVT	HNSKISLPHP	MEIGESLDGT
890	900	910	920	930	940	950	960
LKSRKRRKMS	KKLPPVIIKY	IIINRFRGRK	NMLVKLGKID	SKEKQVILTE	EKMELYKKLA	PLKDFWPKVP	DSPATKYPIY
970	980	990	1000	1010	1020	1030	1040
PLTPKKSHRR	KSKHKSAKKK	TGKQQRTNNE	NIKRTLSFRK	KRSHAILSPP	SPSYNAETED	CDLNYSDVMS	KLGFLSERST
1050	1060	1070	1080	1090	1100	1110	1120
SPINSSPPRC	WSPTDPRAEE	IMAAAEKEAM	LFKGPNVYKK	TVNSRIGKTS	RARAQIKKSK	AKLANPSIVT	KKRNKRNQTN
1130	1140	1150	1160	1170	1180	1190	1200
KLVDDGKKKP	RAKQKTNEKG	TSRKHTTLKD	EKIKSQSGAE	VKFVLKHQNV	SEFASSSGGS	QLLFKQKDMP	LMGSAVDHPL
1210	1220	1230	1240	1250	1260	1270	1280
SASLPTGINA	QQKLSGCFSS	FLESKKSVDL	QTFPSSRDDL	HPSVVCNSIG	PGVSKINVQR	PHNQSAMFTL	KESTLIQKNI
1290	1300	1310	1320	1330	1340	1350	1360
FDLSNHLSQV	AQNTQISSGM	SSKIEDNANN	IQRNYLSSIG	KLSEYRNSLE	SKLDQAYTPN	FLHCKDSQQQ	IVCIAEQSKH
1370	1380	1390	1400	1410	1420	1430	1440
SETCSPGNTA	SEESQMPNNC	FVTSLRSPIK	QIAWEQKQRG	FILDMSNFKP	ERVKPRSLSE	AISQTKALSQ	CKNRNVSTPS
1450	1460	1470	1480	1490	1500	1510	1520
AFGEGQSGLA	VLKELLQKRQ	QKAQNANTTQ	DPLSNKHQPN	KNISGSLEHN	KANKRTRSVT	SPRKPRTPRS	TKQKEKIPKL
1530	1540	1550	1560	1570	1580	1590	1600
LKVDSLNLQN	SSQLDNSVSD	DSPIFFSDPG	FESCYSLEDS	LSPEHNYNFD	INTIGQTGFC	SFYSGSQFVP	ADQNLPQKFL
1610	1620	1630	1640	1650	1660	1670	1680
SDAVQDLFPG	QAIEKNEFLS	HDNQKCDEDK	HHTTDSASWI	RSGTLSPEIF	EKSTIDSNEN	RRHNQWKNSF	HPLTTRSNSI
1690	1700	1710	1720	1730	1740	1750	1760
MDSFCVQQAE	DCLSEKSRLN	RSSVSKEVFL	SLPQPNNSDW	IQGHTRKEMG	QSLDSANTSF	TAILSSPDGE	LVDVACEDLE
1770	1780	1790	1800	1810	1820	1830	1840
LYVSRNNDML	TPTPDSSPRS	TSSPSQSKNG	SFTPRTANIL	KPLMSPPSRE	EIMATLLDHD	LSETIYQEPF	CSNPSDVPEK
1850	1860	1870	1880	1890	1900	1910	1920
PREIGGRLLM	VETRLANDLA	EFEGDFSLEG	LRLWKTAFSA	MTQNPRPGSP	LRSGQGVVNK	GSSNSPKMVE	DKKIVIMPCK
1930	1940	1950	1960	1970	1980	1990	2000
CAPSRQLVQV	WLQAKEEYER	SKKLPKTKPT	GVVKSAENFS	SSVNPDDKPV	VPPKMDVSPC	ILPTTAHTKE	DVDNSQIALQ
2010	2020	2030	2040	2050	2060	2070	2080
APTTGCSQTA	SESQMLPPVA	SASDPEKDED	DDDNYYISYS	SPDSPVIPPW	QQPISPDSKA	LNGDDRPSSP	VEELPSLAFE
2090	2100	2110	2120	2130	2140	2150	2160
NFLKPIKDGI	QKSPCSEPQE	PLVISPINTR	ARTGKCESLC	FHSTPIIQRK	LLERLPEAPG	LSPLSTEPKT	QKLSNKKGSN
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
2757	1	710.3801	13.75	2	63.5	13.2	0	58-70	R.ICELLQSGAIMNK.F	
1743	1	786.4023	-29.21	3	50.5	13.6	1	2643-2664	R.QLGLKLIANVTFGYTSANFSGR.M	

Detailed Protein Report

Protein 558: **pleckstrin homology domain-containing family N member 1 isoform b [Homo sapiens]**

Accession:	gi|237820624	**Score:**	26.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	62.6
Database Date:	2015-11-30	**pI:**	9.4
		Sequence Coverage [%]:	5.0
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	0.67	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	1.36	**CV:**	0.00 %	**No. of Peptides:**	1

10	20	30	40	50	60	70	80
MGNSHCVPQA	PRRLRASFSR	KPSLKGNRED	SARMSAGLPG	PEAARSGDAA	ANKLFHYIPG	TDILDLENQR	ENLEQPFLSV
90	100	110	120	130	140	150	160
FKKGRRRVPV	RNLGKVVHYA	KVQLRFQHSQ	DVSDCYLELF	PAHLYFQAHG	SEGLTFQGLL	PLTELSVCPL	EGSREHAFQI
170	180	190	200	210	220	230	240
TGPLPAPLLV	LCPSRAELDR	WLYHLEKQTA	LLGGPRRCHS	APPQGSCGDE	LPWTLQRRLT	RLRTASGHEP	GGSAVCASRV
250	260	270	280	290	300	310	320
KLQHLPAQEQ	WDRLLVLYPT	SLAIFSEELD	GLCFKGELPL	RAVHINLEEK	EKQIRSFLIE	GPLINTIRVV	CASYEDYGHW
330	340	350	360	370	380	390	400
LLCLRAVTHR	EGAPPLPGAE	SFPGSQVMGS	GRGSLSSGGQ	TSWDSGCLAP	PSTRTSHSLP	ESSVPSTVGC	SSQHTPLHRL
410	420	430	440	450	460	470	480
SLESSPDAPD	HTSETSHSPL	YADPYTPPAT	SHRRVTDVRG	LEEFLSAMQS	ARGPTPSSPL	PSVPVSVPAS	DPRSCSSGPA
490	500	510	520	530	540	550	560
GPYLLSKKGA	LQSRAAQRHR	GSAKDGGPQP	PDAPQLVSSA	REGSPEPWLP	LTDGRSPRRS	RDPGYDHLWD	ETLSSSHQKC
570	580						
PQLGGPEASG	GLVQWI						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
94	1	846.3548	-78.26	2	30.6	15.7	0	505-521	K.DGGPQPPDAPQLVSSAR.E		Wdown:Qdown 1.36 mdown:qdown 0.67

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Detailed Protein Report

Protein 559: protein-glutamine gamma-glutamyltransferase 2 isoform a [Homo sapiens]

Accession:	gi|39777597	**Score:**	26.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	77.3
Database Date:	2015-11-30	**pI:**	5.0
		Sequence Coverage [%]:	4.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAEELVLERC	DLELETNGRD	HHTADLCREK	LVVRRGQPFW	LTLHFEGRNY	EASVDSLTFS	VVTGPAPSQE	AGTKARFPLR
90	100	110	120	130	140	150	160
DAVEEGDWTA	TVVDQQDCTL	SLQLTTPANA	PIGLYRLSLE	ASTGYQGSSF	VLGHFILLFN	AWCPADAVYL	DSEEERQEYV
170	180	190	200	210	220	230	240
LTQQGFIYQG	SAKFIKNIPW	NFGQFEDGIL	DICLILLDVN	PKFLKNAGRD	CSRRSSPVYV	GRVVSGMVNC	NDDQGVLLGR
250	260	270	280	290	300	310	320
WDNNYGDGVS	PMSWIGSVDI	LRRWKNHGCQ	RVKYGQCWVF	AAVACTVLRC	LGIPTRVVTN	YNSAHDQNSN	LLIEYFRNEF
330	340	350	360	370	380	390	400
GEIQGDKSEM	IWNFHCWVES	WMTRPDLQPG	YEGWQALDPT	PQEKSEGTYC	CGPVPVRAIK	EGDLSTKYDA	PFVFAEVNAD
410	420	430	440	450	460	470	480
VVDWIQQDDG	SVHKSINRSL	IVGLKISTKS	VGRDEREDIT	HTYKYPEGSS	EEREAFTRAN	HLNKLAEKEE	TGMAMRIRVG
490	500	510	520	530	540	550	560
QSMNMGSDFD	VFAHITNNTA	EEYVCRLLLC	ARTVSYNGIL	GPECGTKYLL	NLNLEPFSEK	SVPLCILYEK	YRDCLTESNL
570	580	590	600	610	620	630	640
IKVRALLVEP	VINSYLLAER	DLYLENPEIK	IRILGEPKQK	RKLVAEVSLQ	NPLPVALEGC	TFTVEGAGLT	EEQKTVEIPD
650	660	670	680	690			
PVEAGEEVKV	RMDLLPLHMG	LHKLVVNFES	DKLKAVKGFR	NVIIGPA			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2534	1	742.5453	192.31	2	62.1	11.8	1	541-552	K.SVPLCILYEKYR.D	

Detailed Protein Report

Protein 560: general transcription factor 3C polypeptide 1 isoform 2 [Homo sapiens]

Accession:	gi|555943794	**Score:**	26.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	236.1
Database Date:	2015-11-30	**pI:**	8.2
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	1.6
		No. of unique Peptides:	2

Detailed Protein Report

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        10         20         30         40         50         60         70         80
MDALESLLDE VALEGLDGLC LPALWSRLET RVPPFPLPLE PCTQEFLWRA LATHPGISFY EEPRERPDLQ LQDRYEEIDL
        90        100        110        120        130        140        150        160
ETGILESRRD PVALEDVYPI HMILENKDGI QGSCRYFKER KNITNDIRTK SLQPRCTMVE AFDRWGKKLI IVASQAMRYR
       170        180        190        200        210        220        230        240
ALIGQEGDPD LKLPDFSYCI LERLGRSRWQ GELQRDLHTT AFKVDAGKLH YHRKILNKNG LITMQSHVIR LPTGAQQHSI
       250        260        270        280        290        300        310        320
LLLLNRFHVD RRSKYDILME KLSVMLSTRT NHIETLGKLR EELGLCERTF KRLYQYMLNA GLAKVVSLRL QEIHPECGPC
       330        340        350        360        370        380        390        400
KTKKGTDVMV RCLKLLKEFK RNDHDDDEDE EVISKTVPPV DIVFERDMLT QTYDLIERRG TKGISQAEIR VAMNVGKLEA
       410        420        430        440        450        460        470        480
RMLCRLLQRF KVVKGFMEDE GRQRTTKYIS CVFAEESDLS RQYQREKARS ELLTTVSLAS MQEESLLPEG EDTFLSESDS
       490        500        510        520        530        540        550        560
EEERSSSKRR GRGSQKDTRA SANLRPKTQP HHSTPTKGGW KVVNLHPLKK QPPSFPGAAE ERACQSLASR DSLLDTSSVS
       570        580        590        600        610        620        630        640
EPNVSFVSHC ADSNSGDIAV IEEVRMENPK ESSSSLKTGR HSSGQDKPHE TYRLLKRRNL IIEAVTNLRL IESLFTIQKM
       650        660        670        680        690        700        710        720
IMDQEKQEGV STKCCKKSIV RLVRNLSEEG LLRLYRTTVI QDGIKKKVDL VVHPSMDQND PLVRSAIEQV RFRISNSSTA
       730        740        750        760        770        780        790        800
NRVKTSQPPV PQGEAEEDSQ GKEGPSGSGD SQLSASSRSE SGRMKKSDNK MGITPLRNYH PIVVPGLGRS LGFLPKMPRL
       810        820        830        840        850        860        870        880
RVVHMFLWYL IYGHPASNTV EKPSFISERR TIKQESGRAG VRPSSSGSAW EACSEAPSKG SQDGVTWEAE VELATETVYV
       890        900        910        920        930        940        950        960
DDASWMRYIP PIPVHRDFGF GWALVSDILL CLPLSIFIQI VQVSYKVDNL EEFLNDPLKK HTLIRFLPRP IRQQLLYKRR
       970        980        990       1000       1010       1020       1030       1040
YIFSVVENLQ RLCYMGLLQF GPTEKFQDKD QVFIFLKKNA VIVDTTICDP HYNLARSSRP FERRLYVLNS MQDVENYWFD
      1050       1060       1070       1080       1090       1100       1110       1120
LQCVCLNTPL GVVRCPRVRK NSSTDQGSDE EGSLQKEQES AMDKHNLERK CAMLEYTTGS REVVDEGLIP GDGLGAAGLD
      1130       1140       1150       1160       1170       1180       1190       1200
SSFYGHLKRN WIWTSYIINQ AKKENTAAEN GLTVRLQTFL SKRPMPLSAR GNSRLNIWGE ARVGSELCAG WEEQFEVDRE
      1210       1220       1230       1240       1250       1260       1270       1280
PSLDRNRRVR GGKSQKRKRL KKDPGKKIKR KKKGEFPGEK SKRLRYHDEA DQSALQRMTR LRVTWSMQED GLLVLCRIAS
      1290       1300       1310       1320       1330       1340       1350       1360
NVLNTKVKGP FVTWQVVRDI LHATFEESLD KTSHSVGRRA RYIVKNPQAY LNYKVCLAEV YQDKALVGDF MNRRGDYDDP
      1370       1380       1390       1400       1410       1420       1430       1440
KVCANEFKEF VEKLKEKFSS ALRNSNLEIP DTLQELFARY RVLAIGDEKD QTRKEDELNS VDDIHFLVLQ NLIQSTLALS
      1450       1460       1470       1480       1490       1500       1510       1520
DSQMKSYQSF QTFRLYREYK DHVLVKAFME CQKRSLVNRR RVNHTLGPKK NRALPFVPMS YQLSQTYYRI FTWRFPSTIC
      1530       1540       1550       1560       1570       1580       1590       1600
TESFQFLDRM RAAGKLDQPD RFSFKDQDNN EPTNDMVAFS LDGPGGNCVA VLTLFSLGLI SVDVRIPEQI IVVDSSMVEN
      1610       1620       1630       1640       1650       1660       1670       1680
EVIKSLGKDG SLEDDEDEED DLDEGVGGKR RSMEVKPAQA SHTNYLLMRG YYSPGIVSTR NLNPNDSIVV NSCQMKFQLR
      1690       1700       1710       1720       1730       1740       1750       1760
CTPVPARLRP AAAPLEELTM GTSCLPDTFT KLINPQENTC SLEEFVLQLE LSGYSPEDLT AALEILEAII ATGCFGIDKE
      1770       1780       1790       1800       1810       1820       1830       1840
ELRRRFSALE KAGGGRTRTF ADCIQALLEQ HQVLEVGGNT ARLVAMGSAW PWLLHSVRLK DREDADIQRE DPQARPLEGS
      1850       1860       1870       1880       1890       1900       1910       1920
SSEDSPPEGQ APPSHSPRGT KRRASWASEN GETDAEGTQM TPAKRPALQD SNLAPSLGPG AEDGAEAQAP SPPPALEDTA
      1930       1940       1950       1960       1970       1980       1990       2000
AAGAAQEDQE GVGFTESFGA ANISQAARER DCESVCFIGR PWRVVDGHLN LPVCKGMMEA MLYHIMTRPG IPESSLLRHY
      2010       2020       2030       2040       2050       2060       2070       2080
QGVLQPVAVL ELLQGLESLG CIRKRWLRKP RPVSLFSTPV VEEVEVPSSL DESPMAFYEP TLDCTLRLGR VFPHEVNWNK
      2090
WIHL
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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
2192	1	1052.3938	-65.32	2	55.9	13.3	2	640-656	K.MIMDQEKQEGVSTKCCK.K	Carbamidomethyl: 15, 16; Oxidation: 1, 3
1476	1	977.4972	62.60	2	47.0	13.3	0	1183-1199	R.VGSELCAGWEEQFEVDR.E	

Detailed Protein Report

Protein 561: NF-X1-type zinc finger protein NFXL1 [Homo sapiens]

Accession:	gi|89363020	**Score:**	26.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	101.3
Database Date:	2015-11-30	**pI:**	10.5
		Sequence Coverage [%]:	3.2
		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]

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        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 562: protein phosphatase 1A isoform 3 [Homo sapiens]

Accession:	gi|193211600	**Score:**	26.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	51.3
Database Date:	2015-11-30	**pI:**	6.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	8.1
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MFCSGRKWVA	EATICTKLMK	REKRRMGKRR	AKKAKREEKK	KGGERRRNEK	RGNQMKRMCE	RKKYETDLED	QDIMGAFLDK
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
PKMEKHNAQG	QGNGLRYGLS	SMQGWRVEME	DAHTAVIGLP	SGLESWSFFA	VYDGHAGSQV	AKYCCEHLLD	HITNNQDFKG
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
SAGAPSVENV	KNGIRTGFLE	IDEHMRVMSE	KKHGADRSGS	TAVGVLISPQ	HTYFINCGDS	RGLLCRNRKV	HFFTQDHKPS
250	**260**	**270**	**280**	**290**	**300**	**310**	**320**
NPLEKERIQN	AGGSVMIQRV	NGSLAVSRAL	GDFDYKCVHG	KGPTEQLVSP	EPEVHDIERS	EEDDQFIILA	CDGIWDVMGN
330	**340**	**350**	**360**	**370**	**380**	**390**	**400**
EELCDFVRSR	LEVTDDLEKV	CNEVVDTCLY	KGSRDNMSVI	LICFPNAPKV	SPEAVKKEAE	LDKYLECRVE	EIIKKQGEGV
410	**420**	**430**	**440**	**450**	**460**		
PDLVHVMRTL	ASENIPSLPP	GGELASKRNV	IEAVYNRLNP	YKNDDTDSTS	TDDMW		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2669	1	974.0887	123.98	2	62.2	10.6	2	1-17	-.MFCSGRKWVAEATICTK.L	Oxidation: 1
2937	1	1018.9845	-66.59	2	65.9	15.9	1	409-428	R.TLASENIPSLPPGGELASKR.N	

Detailed Protein Report

Protein 563: PREDICTED: immunoglobulin-like domain-containing receptor 2 isoform X6 [Homo sapiens]

Accession:	gi|578800910	**Score:**	26.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	65.5
Database Date:	2015-11-30	**pI:**	9.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.8
		No. of unique Peptides:	2

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

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

Detailed Protein Report

Protein 564: 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

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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 565: **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 566:	**protein sidekick-2 precursor [Homo sapiens]**		
Accession:	gi|222352127	**Score:**	26.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	239.2
Database Date:	2015-11-30	**pI:**	6.6
		Sequence Coverage [%]:	1.5
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:** 2.45	**CV:** 0.00 %	**No. of Peptides:** 1

Detailed Protein Report

```
        10         20         30         40         50         60         70         80
MWGLLIWTLL ALHQIRAARA QDDVSPYFKT EPVRTQVHLE GNRLVLTCMA EGSWPLEFKW LHNNRELTKF SLEYRYMITS
        90        100        110        120        130        140        150        160
LDRTHAGFYR CIVRNRMGAL LQRQTEVQVA YMGSFEEGEK HQSVSHGEAA VIRAPRIASF PQPQVTWFRD GRKIPPSSRI
       170        180        190        200        210        220        230        240
AITLENTLVI LSTVAPDAGR YYVQAVNDKN GDNKTSQPIT LTVENVGGPA DPIAPTIIIP PKNTSVVAGT SEVTLECVAN
       250        260        270        280        290        300        310        320
ARPLIKLHII WKKDGVLLSG GISDHNRRLT IPNPTGSDAG YYECEAVLRS SSVPSVVRGA YLSVLEPPQF VKEPERHITA
       330        340        350        360        370        380        390        400
EMEKVVDIPC QAKGVPPPSI TWYKDAAVVE VEKLTRFRQR NDGGLQISGL VPDDTGMFQC FARNAAGEVQ TSTYLAVTSI
       410        420        430        440        450        460        470        480
APNITRGPLD STVIDGMSVV LACETSGAPR PAITWQKGER ILASGSVQLP RFTPLESGSL LISPTHISDA GTYTCLATNS
       490        500        510        520        530        540        550        560
RGVDEASADL VVWARTRITK PPQDQSVIKG TQASMVCGVT HDPRVTIRYI WEKDGATLGT ESHPRIRLDR NGSLHISQTW
       570        580        590        600        610        620        630        640
SGDIGTYTCR VISAGGNDSR SAHLRVRQLP HAPEHPVATL STVERRAINL TWTKPFDGNS PLIRYILEMS ENNAPWTVLL
       650        660        670        680        690        700        710        720
ASVDPKATSV TVKGLVPARS YQFRLCAVND VGKGQFSKDT ERVSLPEEPP TAPPQNVIAS GRTNQSIMIQ WQPPPESHQN
       730        740        750        760        770        780        790        800
GILKGYIIRY CLAGLPVGYQ FKNITDADVN NLLLEDLIIW TNYEIEVAAY NSAGLGVYSS KVTEWTLQGV PTVPPGNVHA
       810        820        830        840        850        860        870        880
EATNSTTIRF TWNAPSPQFI NGINQGYKLI AWEPEQEEEV TMVTARPNFQ DSIHVGFVSG LKKFTEYFTS VLCFTTPGDG
       890        900        910        920        930        940        950        960
PRSTPQLVRT HEDVPGPVGH LSFSEILDTS LKVSWQEPGE KNGILTGYRI SWEEYNRTNT RVTHYLPNVT LEYRVTGLTA
       970        980        990       1000       1010       1020       1030       1040
LTTYTIEVAA MTSKGQGQVS ASTISSGVPP ELPGPPTNLG ISNIGPRSVT LQFRPGYDGK TSISRWLVEA QVGVVGEGEE
      1050       1060       1070       1080       1090       1100       1110       1120
WLLIHQLSNE PDARSMEVPD LNPFTCYSFR MRQVNIVGTS PPSQPSRKIQ TLQAPPDMAP ANVSLRTASE TSLWLRWMPL
      1130       1140       1150       1160       1170       1180       1190       1200
PEMEYNGNPE SVGYKIKYSR SDGHGKTLSH VVQDRVERDY TIEDLEEWTE YRVQVQAFNA IGSGPWSQTV VGRTRESVPS
      1210       1220       1230       1240       1250       1260       1270       1280
SGPTNVSALA TTSSSMLVRW SEVPEADRNG LVLGYKVMYK EKDSDTQPRF WLVEGNSSRS AQLTGLGKYV LYEVQVLAFT
      1290       1300       1310       1320       1330       1340       1350       1360
RIGDGSPSHP PILERTLDDV PGPPMGILFP EVRTTSVRLI WQPPAAPNGI ILAYQITHRL NTTTANTATV EVLAPSARQY
      1370       1380       1390       1400       1410       1420       1430       1440
TATGLKPESV YLFRITAQTR KGWGEAAEAL VVTTEKRDRP QPPSRPMVQQ EDVRARSVLL SWEPGSDGLS PVRYYTIQTR
      1450       1460       1470       1480       1490       1500       1510       1520
ELPSGRWALH SASVSHNASS FIVDRLKPFT SYKFRVKATN DIGDSEFSEE SESLTTLQAA PDEAPTILSV TPHTTTSVLI
      1530       1540       1550       1560       1570       1580       1590       1600
RWQPPAEDKI NGILLGFRIR YRELLYEGLR GFTLRGINNP GATWAELTSM YSMRNLSRPS LTQYELDNLN KHRRYEIRMS
      1610       1620       1630       1640       1650       1660       1670       1680
VYNAVGEGPS SPPQEVFVGE AVPTAAPRNV VVHGATATQL DVTWEPPPLD SQNGDIQGYK IYFWEAQRGN LTERVKTLFL
      1690       1700       1710       1720       1730       1740       1750       1760
AENSVKLKNL TGYTAYMVSV AAFNAAGDGP RSTPTQGQTQ QAAPSAPSSV KFSELTTTSV NVSWEAPQFP NGILEGYRLV
      1770       1780       1790       1800       1810       1820       1830       1840
YEPCSPVDGV SKIVTVDVKG NSPLWLKVKD LAEGVTYRFR IRAKTFTYGP EIEANVTTGP GEGAPGPPGV PIIVRYSSAI
      1850       1860       1870       1880       1890       1900       1910       1920
AIHWSSGDPG KGPITRYVIE ARPSDEGLWD ILIKDIPKEV SSYTFSMDIL KPGVSYDFRV IAVNDYGFGT PSSPSQSVPA
      1930       1940       1950       1960       1970       1980       1990       2000
QKANPFYEEW WFLVVIALVG LIFILLLVFV LIIRGQSKKY AKKTDSGNSA KSGALGHSEM MSLDESSFPA LELNNRRLSV
      2010       2020       2030       2040       2050       2060       2070       2080
KNSFCRKNGL YTRSPPRPSP GSLHYSDEDV TKYNDLIPAE SSSLTEKPSE ISDSQGSDSE YEVDSNHQKA HSFVNHYISD
      2090       2100       2110       2120       2130       2140       2150       2160
PTYYNSWRRQ QKGISRAQAY SYTESDSGEP DHTTVTNSTS TQQGSLFRPK ASRTPTPQNP PNPPSQQSTL YRPPSSLAPG
      2170       2180
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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
2022	1	1134.9008	-126.03	2	53.8	15.1	0	269-289	R.LTIPNPTGSDAGYYECEAVLR.S		mdown:qdown 2.45

Detailed Protein Report

Protein 567: origin recognition complex subunit 1 isoform 2 [Homo sapiens]

Accession: gi|299890795
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 26.4
MW [kDa]: 96.7
pI: 10.1
Sequence Coverage [%]: 2.5
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MAHYPTRLKT	RKTYSWVGRP	LLDRKLHYQT	YREMCVKTEG	CSTEIHIQIG	QFVLIEGDDD	ENPYVAKLLE	LFEDDSDPPP
90	100	110	120	130	140	150	160
KKRARVQWFV	RFCEVPACKR	HLLGRKPGAQ	EIFWYDYPAC	DSNINAETII	GLVRVIPLAP	KDVVPTNLKN	EKTLFVKLSW
170	180	190	200	210	220	230	240
NEKKFRPLSS	ELFAELNKPQ	ESAAKCQKPV	RAKSKSAESP	SWTPAEHVAK	RIESRHSASK	SRQTPTHPLT	PRARKRLELG
250	260	270	280	290	300	310	320
NLGNPQMSQQ	TSCASLDSPG	RIKRKVAFSE	ITSPSKRSQP	DKLQTLSPAL	KAPEKTRETG	LSYTEDDKKA	SPEHRIILRT
330	340	350	360	370	380	390	400
RIAASKTIDI	REERTLTPIS	GGQRSSVVPS	VILKPENIKK	RDAKEAKAQN	EATSTPHRIR	RKSSVLTMNR	IRQQLRFLGN
410	420	430	440	450	460	470	480
SKSDQEEKEI	LPAAEISDSS	SDEEEASTPP	LPRRAPRTVS	RNLRSSLKSS	LHTLTKLKPR	TPRCAAPQIR	SRSLAAQEPA
490	500	510	520	530	540	550	560
SVLEEARLRL	HVSAVPESLP	CREQEFQDIY	NFVESKLLDH	TGGCMYISGV	PGTGKTATVH	EVIRCLQQAA	QANDVPPFQY
570	580	590	600	610	620	630	640
IEVNGMKLTE	PHQVYVQILQ	KLTGQKATAN	HAAELLAKQF	CTRGSPQETT	VLLVDELDLL	WTHKQDIMYN	LFDWPTHKEA
650	660	670	680	690	700	710	720
RLVVLAIANT	MDLPERIMMN	RVSSRLGLTR	MCFQPYTYSQ	LQQILRSRLK	HLKAFEDDAI	QLVARKVAAL	SGDARRCLDI
730	740	750	760	770	780	790	800
CRRATEICEF	SQQKPDSPGL	VTIAHSMEAV	DEMFSSSYIT	AIKNSSVLEQ	SFLRAILAEF	RRSGLEEATF	QQIYSQHVAL
810	820	830	840	850	860		
CRMEGLPYPT	MSETMAVCSH	LGSCRLLLVE	PSRNDLLLRV	RLNVSQDDVL	YALKDE		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1039	1	516.1512	-244.92	2	41.5	10.2	1	327-334	K.TIDIREER.T	

Detailed Protein Report

Protein 568: **X-ray repair cross-complementing protein 6 isoform 3 [Homo sapiens]**

Accession:	gi|573014819	**Score:**	26.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	64.2
Database Date:	2015-11-30	**pI:**	9.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	7.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MKKQRKNKKR	TLKQVCIQSV	YISKIISSDR	DLLAVVFYGT	EKDKNSVNFK	NIYVLQELDN	PGAKRILELD	QFKGQQGQKR
90	100	110	120	130	140	150	160
FQDMMGHGSD	YSLSEVLWVC	ANLFSDVQFK	MSHKRIMLFT	NEDNPHGNDS	AKASRARTKA	GDLRDTGIFL	DLMHLKKPGG
170	180	190	200	210	220	230	240
FDISLFYRDI	ISIAEDEDLR	VHFEESSKLE	DLLRKVRAKE	TRKRALSRLK	LKLNKDIVIS	VGIYNLVQKA	LKPPPIKLYR
250	260	270	280	290	300	310	320
ETNEPVKTKT	RTFNTSTGGL	LLPSDTKRSQ	IYGSRQIILE	KEETEELKRF	DDPGLMLMGF	KPLVLLKKHH	YLRPSLFVYP
330	340	350	360	370	380	390	400
EESLVIGSST	LFSALLIKCL	EKEVAALCRY	TPRRNIPPYF	VALVPQEEEL	DDQKIQVTPP	GFQLVFLPFA	DDKRKMPFTE
410	420	430	440	450	460	470	480
KIMATPEQVG	KMKAIVEKLR	FTYRSDSFEN	PVLQQHFRNL	EALALDLMEP	EQAVDLTLPK	VEAMNKRLGS	LVDEFKELVY
490	500	510	520	530	540	550	560
PPDYNPEGKV	TKRKHDNEGS	GSKRPKVEYS	EEELKTHISK	GTLGKFTVPM	LKEACRAYGL	KSGLKKQELL	EALTKHFQD

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
50	1	813.6863	-91.93	3	30.0	12.2	0	439-460	R.NLEALALDLMEPEQAVDLTLPK.V	Oxidation: 10

Detailed Protein Report

Protein 569: serine/threonine-protein kinase TAO3 [Homo sapiens]

Accession:	gi|148746218	**Score:**	26.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	105.3
Database Date:	2015-11-30	**pI:**	6.9
		Sequence Coverage [%]:	2.8
		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	SSSVVHKKDH
410	420	430	440	450	460	470	480
VFIRDEAGHG	DPRPEPRPTQ	SVQSQALHYR	NRERFATIKS	ASLVTRQIHE	HEQENELREQ	MSGYKRMRRQ	HQKQLIALEN
490	500	510	520	530	540	550	560
KLKAEMDEHR	LKLQKEVETH	ANNSSIELEK	LAKKQVAIIE	KEAKVAAADE	KKFQQQILAQ	QKKDLTTFLE	SQKKQYKICK
570	580	590	600	610	620	630	640
EKIKEEMNED	HSTPKKEKQE	RISKHKENLQ	HTQAEEEAHL	LTQQRLYYDK	NCRFFKRKIM	IKRHEVEQQN	IREELNKKRT
650	660	670	680	690	700	710	720
QKEMEHAMLI	RHDESTRELE	YRQLHTLQKL	RMDLIRLQHQ	TELENQLEYN	KRRERELHRK	HVMELRQQPK	NLKAMEMQIK
730	740	750	760	770	780	790	800
KQFQDTCKVQ	TKQYKALKNH	QLEVTPKNEH	KTILKTLKDE	QTRKLAILAE	QYEQSINEMM	ASQALRLDEA	QEAECQALRL
810	820	830	840	850	860	870	880
QLQQEMELLN	AYQSKIKMQT	EAQHERELQK	LEQRVSLRRA	HLEQKIEEEL	AALQKERSER	IKNLLERQER	EIETFDMESL
890	900						
RMGFGNLVTL	DFPKEDYR						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2240	1	927.9733	43.59	2	56.5	10.8	1	643-657	K.EMEHAMLIRHDESTR.E	

Detailed Protein Report

Protein 570: protein-glutamine gamma-glutamyltransferase 5 isoform 2 [Homo sapiens]

Accession:	gi|4759230	**Score:**	26.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	71.9
Database Date:	2015-11-30	**pI:**	5.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	6.7
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MAQGLEVALT	DLQSSRNNVR	HHTEEITVDH	LLVRRGQAFN	LTLYFRNRSF	QPGLDNIIFV	VETEDAVYLD	SEPQRQEYVM
90	100	110	120	130	140	150	160
NDYGFIYQGS	KNWIRPCPWN	YGQFEDKIID	ICLKLLDKSL	HFQTDPATDC	ALRGSPVYVS	RVVCAMINSN	DDNGVLNGNW
170	180	190	200	210	220	230	240
SENYTDGANP	AEWTGSVAIL	KQWNATGCQP	VRYGQCWVFA	AVMCTVMRCL	GIPTRVITNF	DSGHDTDGNL	IIDEYYDNTG
250	260	270	280	290	300	310	320
RILGNKKKDT	IWNFHVWNEC	WMARKDLPPA	YGGWQVLDAT	PQEMSNGVYC	CGPASVRAIK	EGEVDLNYDT	PFVFSMVNAD
330	340	350	360	370	380	390	400
CMSWLVQGGK	EQKLHQDTSS	VGNFISTKSI	QSDERDDITE	NYKYEEGSLQ	ERQVFLKALQ	KLKARSFHGS	QRGAELQPSR
410	420	430	440	450	460	470	480
PTSLSQDSPR	SLHTPSLRPS	DVVQVSLKFK	LLDPPNMGQD	ICFVLLALNM	SSQFKDLKVN	LSAQSLLHDG	SPLSPFWQDT
490	500	510	520	530	540	550	560
AFITLSPKEA	KTYPCKISYS	QYSQYLSTDK	LIRISALGEE	KSSPEKILVN	KIITLSYPSI	TINVLGAAVV	NQPLSIQVIF
570	580	590	600	610	620	630	640
SNPLSEQVED	CVLTVEGSGL	FKKQQKVFLG	VLKPQHQASI	ILETVPFKSG	QRQIQANMRS	NKFKDIKGYR	NVYVDFAL

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2196	1	961.3531	-82.76	2	56.1	16.4	0	193-208	R.YGQCWVFAAVMCTVMR.C	Carbamidomethyl: 4
1787	1	1023.8570	-1.46	3	52.3	10.0	1	429-455	K.FKLLDPPNMGQDICFVLLALNMSSQFK.D	

Detailed Protein Report

Protein 571: PREDICTED: histone-lysine N-methyltransferase EHMT1 isoform X7 [Homo sapiens]

Accession:	gi|530426806	**Score:**	26.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	99.7
Database Date:	2015-11-30	**pI:**	5.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAAADAEAVP	ARGEPQQDCC	VKTELLGEET	PMAADEGSAE	KQAGEAHMAA	DGETNGSCEN	SDASSHANAA	KHTQDSARVN
90	100	110	120	130	140	150	160
PQDGTNTLTR	IAENGVSERD	SEAAKQNHVT	ADDFVQTSVI	GSNGYILNKP	ALQAQPLRTT	STLASSLPGH	AAKTLPGGAG
170	180	190	200	210	220	230	240
KGRTPSAFPQ	TPAAPPATLG	EGSADTEDRK	LPAPGADVKV	HRARKTMPKS	VVGLHAASKD	PREVREARDH	KEPKEEINKN
250	260	270	280	290	300	310	320
ISDFGRQQLL	PPFPSLHQSL	PQNQCYMATT	KSQTACLPFV	LAAAVSRKKK	RRMGTYSLVP	KKKTKVLKQR	TVIEMFKSIT
330	340	350	360	370	380	390	400
HSTVGSKGEK	DLGASSLHVN	GESLEMDSDE	DDSEELEEDD	GHGAEQAAAF	PTEDSRTSKE	SMSEADRAQK	MDGESEEEQE
410	420	430	440	450	460	470	480
SVDTGEEEEG	GDESDLSSES	SIKKKFLKRK	GKTDSPWIKP	ARKRRRRSRK	KPSGALGSES	YKSSAGSAEQ	TAPGDSTGYM
490	500	510	520	530	540	550	560
EVSLDSLDLR	VKGILSSQAE	GLANGPDVLE	TDGLQEVPLC	SCRMETPKSR	EITTLANNQC	MATESVDHEL	GRCTNSVVKY
570	580	590	600	610	620	630	640
ELMRPSNKAP	LLVLCEDHRG	RMVKHQCCPG	CGYFCTAGNF	MECQPESSIS	HRFHKDCASR	VNNASYCPHC	GEESSKAKEV
650	660	670	680	690	700	710	720
TIAKADTTST	VTPVPGQEKG	SALEGRADTT	TGSAAGPPLS	EDDKLQGAAS	HVPEGFDPTG	PAGLGRPTPG	LSQGPGKETL
730	740	750	760	770	780	790	800
ESALIALDSE	KPKKLRFHPK	QLYFSARQGE	LQKVLLMLVD	GIDPNFKMEH	QNKRSPLHAA	AEAGHVDICH	MLVQAGANID
810	820	830	840	850	860	870	880
TCSEDQRTPL	MEAAENNHLE	AVKYLIKAGA	LVDPKDAEGS	TCLHLAAKKG	HYEVVQYLLS	NGQMDVNCQD	DGGWTPMIWA
890	900	910	920	930			
TEYKHVDLVK	LLLSKGSDIN	IRDNDDGTMK	RGALSRQKEE	KREAEEP			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1764	1	990.9536	23.24	2	50.6	10.5	1	621-638	R.VNNASYCPHCGEESSKAK.E	Carbamidomethyl: 7

Detailed Protein Report

Protein 572: mitochondrial inner membrane protein OXA1L [Homo sapiens]

Accession:	gi|223718097	**Score:**	26.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	55.2
Database Date:	2015-11-30	**pI:**	10.6
		Sequence Coverage [%]:	3.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
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
1726	1	546.7057	-111.00	2	51.5	15.2	1	428-436	K.GWKNAEMTR.Q	

Detailed Protein Report

Protein 573: helicase SRCAP [Homo sapiens]

Accession:	gi|146219843	**Score:**	26.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	343.3
Database Date:	2015-11-30	**pI:**	5.6
		Sequence Coverage [%]:	1.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
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
1437	1	1087.6372	55.64	2	46.7	13.2	0	880-898	K.ETLATGHFMSVINILMQLR.K	

Detailed Protein Report

Protein 574: nucleolar RNA helicase 2 isoform 2 [Homo sapiens]

Accession:	gi|379317177	**Score:**	26.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	79.6
Database Date:	2015-11-30	**pI:**	10.0
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	2.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MNSPKSKKAK	KKEEPSQNDI	SPKTKSLRKK	KEPIEKKVVS	SKTKKVTKNE	EPSEEEIDAP	KPKKMKKEKE	MNGETREKSP
90	100	110	120	130	140	150	160
KLKNGFPHPE	PDCNPSEAAS	EESNSEIEQE	IPVEQKEGAF	SNFPISEETI	KLLKGRGVTF	LFPIQAKTFH	HVYSGKDLIA
170	180	190	200	210	220	230	240
QARTGTGKTF	SFAIPLIEKL	HGELQDRKRG	RAPQVLVLAP	TRELANQVSK	DFSDITKKLS	VACFYGGTPY	GGQFERMRNG
250	260	270	280	290	300	310	320
IDILVGTPGR	IKDHIQNGKL	DLTKLKHVVL	DEVDQMLDMG	FADQVEEILS	VAYKKDSEDN	PQTLLFSATC	PHWVFNVAKK
330	340	350	360	370	380	390	400
YMKSTYEQVD	LIGKKTQKTA	ITVEHLAIKC	HWTQRAAVIG	DVIRVYSGHQ	GRTIIFCETK	KEAQELSQNS	AIKQDAQSLH
410	420	430	440	450	460	470	480
GDIPQKQREI	TLKGFRNGSF	GVLVATNVAA	RGLDIPEVDL	VIQSSPPKDV	ESYIHRSGRT	GRAGRTGVCI	CFYQHKEEYQ
490	500	510	520	530	540	550	560
LVQVEQKAGI	KFKRIGVPSA	TEIIKASSKD	AIRLLDSVPP	TAISHFKQSA	EKLIEEKGAV	EALAAALAHI	SGATSVDQRS
570	580	590	600	610	620	630	640
LINSNVGFVT	MILQCSIEMP	NISYAWKELK	EQLGEEIDSK	VKGMVFLKGK	LGVCFDVPTA	SVTEIQEKWH	DSRRWQLSVA
650	660	670	680	690	700	710	720
TEQPELEGPR	EGYGGFRGQR	EGSRGFRGQR	DGNRRFRGQR	EGSRGPRGQR	SGGGNKSNRS	QNKGQKRSFS	KAFGQ

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
63	1	814.0267	-36.10	3	30.1	14.9	2	218-238	K.KLSVACFYGGTPYGGQFERMR.N	Carbamidomethyl: 6; Oxidation: 20

Detailed Protein Report

Protein 575: queuine tRNA-ribosyltransferase [Homo sapiens]

Accession:	gi|13654276	**Score:**	26.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	44.0
Database Date:	2015-11-30	**pI:**	7.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	6.5
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	0.33	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	1.10	**CV:**	0.00 %	**No. of Peptides:**	1

10	20	30	40	50	60	70	80
MAGAATQASL	ESAPRIMRLV	AECSRSRARA	GELWLPHGTV	ATPVFMPVGT	QATMKGITTE	QLDALGCRIC	LGNTYHLGLR
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
PGPELIQKAN	GLHGFMNWPH	NLLTDSGGFQ	MVSLVSLSEV	TEEGVRFRSP	YDGNETLLSP	EKSVQIQNAL	GSDIIMQLDD
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
VVSSTVTGPR	VEEAMYRSIR	WLDRCIAAHQ	RPDKQNLFAI	IQGGLDADLR	ATCLEEMTKR	DVPGFAIGGL	SGGESKSQFW
250	**260**	**270**	**280**	**290**	**300**	**310**	**320**
RMVALSTSRL	PKDKPRYLMG	VGYATDLVVC	VALGCDMFDC	VFPTRTARFG	SALVPTGNLQ	LRKKVFEKDF	GPIDPECTCP
330	**340**	**350**	**360**	**370**	**380**	**390**	**400**
TCQKHSRAFL	HALLHSDNTA	ALHHLTVHNI	AYQLQLMSAV	RTSIVEKRFP	DFVRDFMGAM	YGDPTLCPTW	ATDALASVGI
410							
TLG							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
512	1	719.0204	199.94	2	35.3	10.4	2	16-27	R.IMRLVAECSRSR.A	Oxidation: 2	Wdown:Qdown 1.10 mdown:qdown 0.33

BRUKER

Detailed Protein Report

Protein 576: 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

mdown:qdown	**Median:**	0.43	**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		mdown:qdown 0.43

Detailed Protein Report

Protein 577: PREDICTED: death ligand signal enhancer isoform X6 [Homo sapiens]

Accession:	gi|530380768	**Score:**	26.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	42.7
Database Date:	2015-11-30	**pI:**	10.1
		Sequence Coverage [%]:	6.2
		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 578: **PREDICTED: dehydrogenase/reductase SDR family member 11 isoform X3 [Homo sapiens]**

Accession:	gi|578831391	**Score:**	26.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	14.1
Database Date:	2015-11-30	**pI:**	10.1
		Sequence Coverage [%]:	32.3
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578840409	refseq_human (refseq_human_20140103.fasta)	PREDICTED: dehydrogenase/reductase SDR family member 11 isoform X3 [Homo sapiens]

10	20	30	40	50	60	70	80
MARPGMERWR	DRLALVTGAS	GGIGAAVARA	LVQQGLKVVG	CARTVGNIEE	LAAECKSAGY	PGTLIPYRCD	LSNEEDILSM
90	**100**	**110**	**120**	**130**	**140**		
FSAIRSQHSG	VDICINNAGL	ARPDTLLSGS	TSGWKDMFNG	LSSLPHKPTL	PRR		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2671	1	1079.8373	-43.87	3	64.6	12.8	2	38-68	K.VVGCARTVGNIEELAAECKSAGYPGTLIPYR.C	

Detailed Protein Report

Protein 579: PREDICTED: protein CASP isoform X6 [Homo sapiens]

Accession:	gi|578813926	**Score:**	26.2
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:	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
1855	1	738.7765	-167.06	2	53.2	12.2	2	100-111	R.WMLCVAGARLKR.E	Carbamidomethyl: 4; Oxidation: 2

Detailed Protein Report

Protein 580: **sperm-specific antigen 2 isoform 4 [Homo sapiens]**

Accession:	gi|566559898	**Score:**	26.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	119.1
Database Date:	2015-11-30	**pI:**	5.1
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.7
		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

Detailed Protein Report

Protein 581: **1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase eta-1 isoform c [Homo sapiens]**

Accession:	gi|195972873	**Score:**	26.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	114.4
Database Date:	2015-11-30	**pI:**	8.3
		Sequence Coverage [%]:	3.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MADLEVYKNL	SPEKVERCMS	VMQSGTQMIK	LKRGTKGLVR	LFYLDEHRTR	LRWRPSRKSE	KAKILIDSIY	KVTEGRQSEI
90	100	110	120	130	140	150	160
FHRQAEGNFD	PSCCFTIYHG	NHMESLDLIT	SNPEEARTWI	TGLKYLMAGI	SDEDSLAKRQ	RTHDQWVKQT	FEEADKNGDG
170	180	190	200	210	220	230	240
LLNIEEIHQL	MHKLNVNLPR	RKVRQMFQEA	DTDENQGTLT	FEEFCVFYKM	MSLRRDLYLL	LLSYSDKKDH	LTVEELAQFL
250	260	270	280	290	300	310	320
KVEQKMNNVT	TDYCLDIIKK	FEVSEENKVK	NVLGIEGFTN	FMRSPACDIF	NPLHHEVYQD	MDQPLCNYYI	ASSHNTYLTG
330	340	350	360	370	380	390	400
DQLLSQSKVD	MYARVLQEGC	RCVEVDCWDG	PDGEPVVHHG	YTLTSKILFR	DVVETINKHA	FVKNEFPVIL	SIENHCSIQQ
410	420	430	440	450	460	470	480
QRKIAQYLKG	IFGDKLDLSS	VDTGECKQLP	SPQSLKGKIL	VKGKKLPYHL	GDDAEEGEVS	DEDSADEIED	ECKFKLHYSN
490	500	510	520	530	540	550	560
GTTEHQVESF	IRKKLESLLK	ESQIRDKEDP	DSFTVRALLK	ATHEGLNAHL	KQSPDVKESG	KKSHGRSLMT	NFGKHKKTTK
570	580	590	600	610	620	630	640
SRSKSYSTDD	EEDTQQSTGK	EGGQLYRLGR	RRKTMKLCRE	LSDLVVYTNS	VAAQDIVDDG	TTGNVLSFSE	TRAHQVVQQK
650	660	670	680	690	700	710	720
SEQFMIYNQK	QLTRIYPSAY	RIDSSNFNPL	PYWNAGCQLV	ALNYQSEGRM	MQLNRAKFKA	NGNCGYVLKP	QQMCKGTFNP
730	740	750	760	770	780	790	800
FSGDPLPANP	KKQLILKVIS	GQQLPKPPDS	MFGDRGEIID	PFVEVEIIGL	PVDCCKDQTR	VVDDNGFNPV	WEETLTFTVH
810	820	830	840	850	860	870	880
MPEIALVRFL	VWDHDPIGRD	FVGQRTVTFS	SLVPGYRHVY	LEGLTEASIF	VHITINEIYG	KWSPLILNPS	YTILHFLGAT
890	900	910	920	930	940	950	960
KNRQLQGLKG	LFNKNPRHSS	SENNSHYVRK	RSIGDRILRR	TASAPAKGRK	KSKMGFQEMV	EIKDSVSEAT	RDQDGVLRRT
970	980	990	1000	1010			
TRSLQARPVS	MPVDRNLLGA	LSLPVSETAK	DIEGKENSLV	QI			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
845	1	1419.3283	69.70	2	39.4	12.2	1	379-402	K.HAFVKNEFPVILSIENHCSIQQQR.K	

Detailed Protein Report

Protein 582: AP-1 complex subunit mu-1 isoform 2 [Homo sapiens]

Accession:	gi|14210504	**Score:**	26.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	48.6
Database Date:	2015-11-30	**pI:**	7.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	6.4
		No. of unique Peptides:	2

Quantitation

Wdown:Qdown **Median:** 1.64 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MSASAVYVLD	LKGKVLICRN	YRGDVDMSEV	EHFMPILMEK	EEEGMLSPIL	AHGGVRFMWI	KHNNLYLVAT	SKKNACVSLV
90	100	110	120	130	140	150	160
FSFLYKVVQV	FSEYFKELEE	ESIRDNFVII	YELLDELMDF	GYPQTTDSKI	LQEYITQEGH	KLETGAPRPP	ATVTNAVSWR
170	180	190	200	210	220	230	240
SEGIKYRKNE	VFLDVIESVN	LLVSANGNVL	RSEIVGSIKM	RVFLSGMPEL	RLGLNDKVLF	DNTGRGKSKS	VELEDVKFHQ
250	260	270	280	290	300	310	320
CVRLSRFEND	RTISFIPPDG	EFELMSYRLN	THVKPLIWIE	SVIEKHSHSR	IEYMIKAKSQ	FKRRSTANNV	EIHIPVPNDA
330	340	350	360	370	380	390	400
DSPKFKTTVG	SVKWVPENSE	IVWSIKSFPG	GKEYLMRAHF	GLPSVEAEDK	EGKPPISVKF	EIPYFTTSGI	QVRYLKIIEK
410	420	430					
SGYQALPWVR	YITQNGDYQL	RTQ					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1641	1	873.4079	-31.68	2	49.0	15.9	1	230-243	K.SVELEDVKFHQCVR.L	Carbamidomethyl: 12	Wdown:Qdown 1.64
1957	1	700.2365	-156.66	2	54.6	10.2	0	358-370	R.AHFGLPSVEAEDK.E		

Detailed Protein Report

Protein 583: nuclear receptor subfamily 1 group D member 1 [Homo sapiens]

Accession:	gi|13430848	**Score:**	26.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	66.8
Database Date:	2015-11-30	**pI:**	9.9
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	2.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MTTLDSNNNT	GGVITYIGSS	GSSPSRTSPE	SLYSDNSNGS	FQSLTQGCPT	YFPPSPTGSL	TQDPARSFGS	IPPSLSDDGS
90	100	110	120	130	140	150	160
PSSSSSSSSS	SSSFYNGSPP	GSLQVAMEDS	SRVSPSKSTS	NITKLNGMVL	LCKVCGDVAS	GFHYGVHACE	GCKGFFRRSI
170	180	190	200	210	220	230	240
QQNIQYKRCL	KNENCSIVRI	NRNRCQQCRF	KKCLSVGMSR	DAVRFGRIPK	REKQRMLAEM	QSAMNLANNQ	LSSQCPLETS
250	260	270	280	290	300	310	320
PTQHPTPGPM	GPSPPPAPVP	SPLVGFSQFP	QQLTPPRSPS	PEPTVEDVIS	QVARAHREIF	TYAHDKLGSS	PGNFNANHAS
330	340	350	360	370	380	390	400
GSPPATTPHR	WENQGCPPAP	NDNNTLAAQR	HNEALNGLRQ	APSSYPPTWP	PGPAHHSCHQ	SNSNGHRLCP	THVYAAPEGK
410	420	430	440	450	460	470	480
APANSPRQGN	SKNVLLACPM	NMYPHGRSGR	TVQEIWEDFS	MSFTPAVREV	VEFAKHIPGF	RDLSQHDQVT	LLKAGTFEVL
490	500	510	520	530	540	550	560
MVRFASLFNV	KDQTVMFLSR	TTYSLQELGA	MGMGDLLSAM	FDFSEKLNSL	ALTEEELGLF	TAVVLVSADR	SGMENSASVE
570	580	590	600	610	620		
QLQETLLRAL	RALVLKNRPL	ETSRFTKLLL	KLPDLRTLNN	MHSEKLLSFR	VDAQ		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
116	1	1044.8604	-131.76	2	30.7	26.1	1	413-430	K.NVLLACPMNMYPHGRSGR.T	Carbamidomethyl: 6; Oxidation: 10

Detailed Protein Report

Protein 584: nucleolar transcription factor 1 isoform b [Homo sapiens]

Accession:	gi|115529449	**Score:**	26.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	84.9
Database Date:	2015-11-30	**pI:**	5.3
		Sequence Coverage [%]:	3.9
		No. of unique Peptides:	1

Alias proteins:

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

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1966	1	871.8504	-139.97	2	54.7	11.1	1	108-121	K.HPDFPKKPLTPYFR.F	

Detailed Protein Report

Protein 585: **PREDICTED: 6-phosphofructokinase, liver type isoform X4 [Homo sapiens]**

Accession: gi|530419271
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 26.1
MW [kDa]: 82.2
pI: 7.9
Sequence Coverage [%]: 4.3
No. of unique Peptides: 2

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	TRTRLSMDKG	F				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1744	1	647.3021	-75.58	4	50.5	11.6	1	38-61	K.QANWLSVSNIIQLGGTIIGSARCK.A	Carbamidomethyl: 23
156	1	584.6910	-183.35	2	31.3	14.4	2	60-69	R.CKAFTTREGR.R	

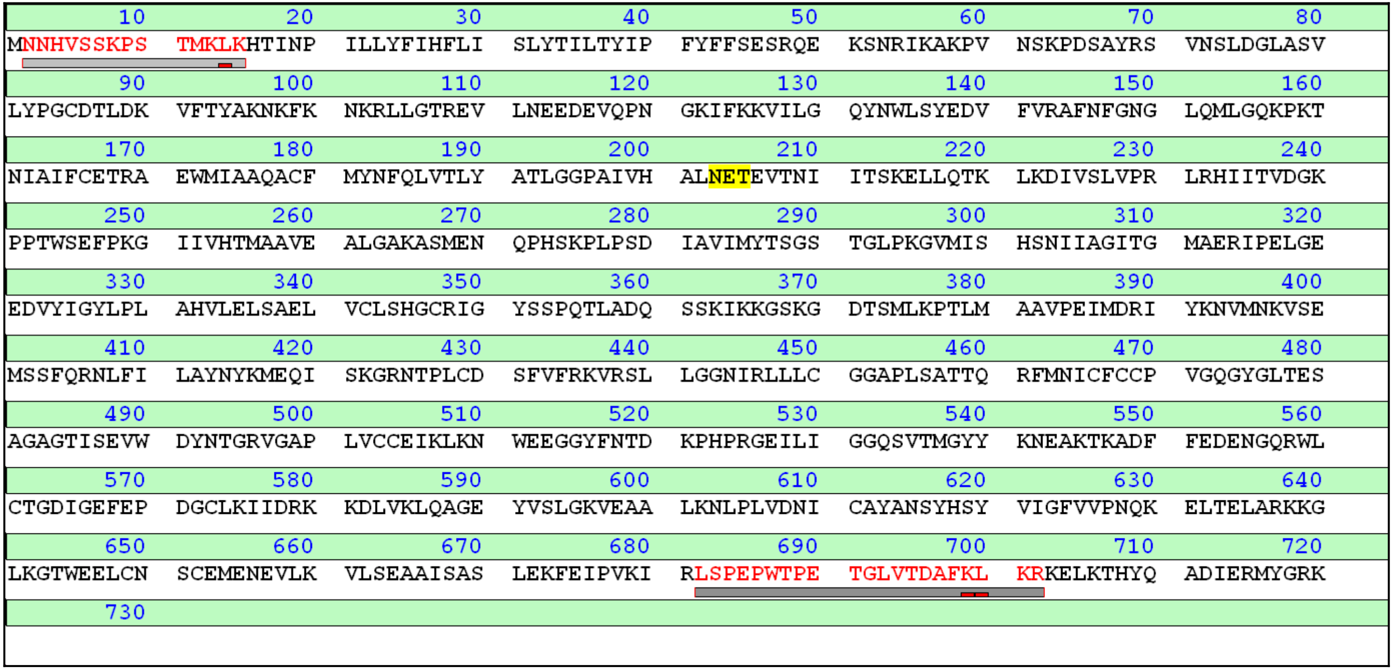
Detailed Protein Report

Protein 586: long-chain-fatty-acid--CoA ligase 3 [Homo sapiens]

Accession:	gi|42794752	**Score:**	26.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	80.4
Database Date:	2015-11-30	**pI:**	9.4
		Sequence Coverage [%]:	4.9
		No. of unique Peptides:	2

Alias proteins:

Accession	Name	Description
gi|42794754	refseq_human (refseq_human_20140103.fasta)	long-chain-fatty-acid--CoA ligase 3 [Homo sapiens]



```
        10         20         30         40         50         60         70         80
MNNHVSSKPS TMKLKHTINP ILLYFIHFLI SLYTILTYIP FYFFSESRQE KSNRIKAKPV NSKPDSAYRS VNSLDGLASV
        90        100        110        120        130        140        150        160
LYPGCDTLDK VFTYAKNKFK NKRLLGTREV LNEEDEVQPN GKIFKKVILG QYNWLSYEDV FVRAFNFGNG LQMLGQKPKT
       170        180        190        200        210        220        230        240
NIAIFCETRA EWMIAAQACF MYNFQLVTLY ATLGGPAIVH ALNETEVTNI ITSKELLQTK LKDIVSLVPR LRHIITVDGK
       250        260        270        280        290        300        310        320
PPTWSEFPKG IIVHTMAAVE ALGAKASMEN QPHSKPLPSD IAVIMYTSGS TGLPKGVMIS HSNIIAGITG MAERIPELGE
       330        340        350        360        370        380        390        400
EDVYIGYLPL AHVLELSAEL VCLSHGCRIG YSSPQTLADQ SSKIKKGSKG DTSMLKPTLM AAVPEIMDRI YKNVMNKVSE
       410        420        430        440        450        460        470        480
MSSFQRNLFI LAYNYKMEQI SKGRNTPLCD SFVFRKVRSL LGGNIRLLLC GGAPLSATTQ RFMNICFCCP VGQGYGLTES
       490        500        510        520        530        540        550        560
AGAGTISEVW DYNTGRVGAP LVCCEIKLKN WEEGGYFNTD KPHPRGEILI GGQSVTMGYY KNEAKTKADF FEDENGQRWL
       570        580        590        600        610        620        630        640
CTGDIGEFEP DGCLKIIDRK KDLVKLQAGE YVSLGKVEAA LKNLPLVDNI CAYANSYHSY VIGFVVPNQK ELTELARKKG
       650        660        670        680        690        700        710        720
LKGTWEELCN SCEMENEVLK VLSEAAISAS LEKFEIPVKI RLSPEPWTPE TGLVTDAFKL KRKELKTHYQ ADIERMYGRK
       730
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1801	1	785.8979	-30.88	2	51.2	15.7	1	2-15	M.NNHVSSKPSTMKLK.H	
2875	1	1193.0834	-51.05	2	64.7	10.4	2	682-702	R.LSPEPWTPETGLVTDAFKLKR.K	

Detailed Protein Report

Protein 587: vacuolar protein sorting-associated protein 13B isoform 1 [Homo sapiens]

Accession:	gi|35493701	**Score:**	26.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	445.7
Database Date:	2015-11-30	**pI:**	6.0
		Sequence Coverage [%]:	0.9
		No. of unique Peptides:	1

Detailed Protein Report

```
        10         20         30         40         50         60         70         80
MLESYVTPIL MSYVNRYIKN LKPSDLQLSL WGGDVVLSKL ELKLDVLEQE LKLPFTFLSG HIHELRIHVP WTKLGSEPVV
        90        100        110        120        130        140        150        160
ITINTMECIL KLKDGIQDDH ESCGSNSTNR STAESTKSSI KPRRMQQAAP TDPDLPPGYV QSLIRRVVNN VNIVINNLIL
       170        180        190        200        210        220        230        240
KYVEDDIVLS VNITSAECYT VGELWDRAFM DISATDLVLR KVINFSDCTV CLDKRNASGK IEFYQDPLLY KCSFRTRLHF
       250        260        270        280        290        300        310        320
TYENLNSKMP SVIKIHTLVE SLKLSITDQQ LPMFIRIMQL GIALYYGEIG NFKEGEIEDL TCHNKDMLGN ITGSEDETRI
       330        340        350        360        370        380        390        400
DMQYPAQHKG QELYSQQDEE QPQGWVSWAW SFVPAIVSYD DGEEDFVGND PASTMHQQKA QTLKDPIVSI GFYCTKATVT
       410        420        430        440        450        460        470        480
FKLTEMQVES SYYSPQKVKS KEVLCWEQEG TTVEALMMGE PFFDCQIGFV GCRAMCLKGI MGVKDFEENM NRSETEACFF
       490        500        510        520        530        540        550        560
ICGDNLSTKG FTYLTNSLFD YRSPENNGTR AEFILDSTHH KETYTEIAGM QRFGAFYMDY LYTMENTSGK GSTNQQDFSS
       570        580        590        600        610        620        630        640
GKSEDLGTVQ EKSTKSLVIG PLDFRLDSSA VHRILKMIVC ALEHEYEPYS RLKSDIKDEN ETILNPEEVA LLEEYIPTRH
       650        660        670        680        690        700        710        720
TSVTLLKCTC TISMAEFNLL DHLLPVIMGE KNSSNFMNTT NFQSLRPLPS IRILVDKINL EHSVPMYAEQ LVHVVSSLTQ
       730        740        750        760        770        780        790        800
PSDNLLHYCY VHCYLKIFGF QAGLTSLDCS GSYCLPVPVI PSFSTALYGK LLKLPTCWTK RSQIAITEGI FELPNLTIQA
       810        820        830        840        850        860        870        880
TRAQTLLLQA IYQSWSHLGN VSSSAVIEAL INEIFLSIGV KSKNPLPTLE GSIQNVELKY CSTSLVKCAS GTMGSIKICA
       890        900        910        920        930        940        950        960
KAPVDSGKEK LIPLLQGPSD TKDLHSTKWL NESRKPESLL APDLMAFTIQ VPQYIDYCHN SGAVLLCSIQ GLAVNIDPIL
       970        980        990       1000       1010       1020       1030       1040
YTWLIYQPQK RTSRHMQQQP VVAVPLVMPV CRRKEDEVSI GSAPLAKQQS YQASEYASSP VKTKTVTESR PLSVPVKAML
      1050       1060       1070       1080       1090       1100       1110       1120
NISESCRSPE ERMKEFIGIV WNAVKHLTLQ LEVQSCCVFI PNDSLPSPST IVSGDIPGTV RSWYHGQTSM PGTLVLCLPQ
      1130       1140       1150       1160       1170       1180       1190       1200
IKIISAGHKY MEPLQEIPFV IPRPILEEGD AFPWTISLHN FSIYTLLGKQ VTLCLVEPMG CTSTLAVTSQ KLLATGPDTR
      1210       1220       1230       1240       1250       1260       1270       1280
HSFVVCLHVD LESLEIKCSN PQVQLFYELT DIMNKVWNKI QKRGNLNLSP TSPETMAGPV PTSPVRSSIG TAPPDTSTCS
      1290       1300       1310       1320       1330       1340       1350       1360
PSADIGTTTE GDSIQAGEES PFSDSVTLEQ TTSNIGGTSG RVSLWMQWVL PKITIKLFAP DPENKGTEVC MVSELEDLSA
      1370       1380       1390       1400       1410       1420       1430       1440
SIDVQDVYTK VKCKIESFNI DHYRSRPGEG WQSGHFEGVF LQCKEKSVTT TKLLDGTHQQ HGFLSLTYTK AVTKNVRHKL
      1450       1460       1470       1480       1490       1500       1510       1520
TSRNERRSFH KLSEGLMDGS PHFLHEILLS AQAFDIVLYF PLLNAIASIF QAKLPKTQKE KRKSPGQPMR THTLTSRNLP
      1530       1540       1550       1560       1570       1580       1590       1600
LIYVNTSVIR IFIPKTEEMQ PTVEANQAAK EDTVVLKIGS VAMAPQADNP LGRSVLRKDI YQRALNLGIL RDPGSEIEDR
      1610       1620       1630       1640       1650       1660       1670       1680
QYQIDLQSIN IGTAQWHQLK PEKESVSGGV VTETERNSQN PALEWNMASS IRRHQERRAI LTPVLTDFSV RITGAPAVIF
      1690       1700       1710       1720       1730       1740       1750       1760
TKVVSPENLH TEEILVCGHS LEVNITTNLD FFLSVAQVQL LHQLIVANMT GLEPSNKAAE ISKQEQKKVD IFDGGMAETS
      1770       1780       1790       1800       1810       1820       1830       1840
SRYSGAQDSG IGSDSVKIRI VQIEQHSGAS QHRIARPSRQ SSIVKNLNFI PFDIFITASR ISLMTYSCMA LSKSKSQEQK
      1850       1860       1870       1880       1890       1900       1910       1920
NNEKTDKSSL NLPEVDSDVA KPNQACISTV TAEDLLRSSI SFPSGKKIGV LSLESLHAST RSSARQALGI TIVRQPGRRG
      1930       1940       1950       1960       1970       1980       1990       2000
TGDLQLEPFL YFIVSQPSLL LSCHHRKQRV EVSIFDAVLK GVASDYKCID PGKTLPEALD YCTVWLQTVP GEIDSKSGIP
      2010       2020       2030       2040       2050       2060       2070       2080
PSFITLQIKD FLNGPADVNL DISKPLKANL SFTKLDQINL FLKKIKNAHS LAHSEETSAM SNTMVNKDDL PVSKYYRGKL
      2090       2100       2110       2120       2130       2140       2150       2160
SKPKIHGDGV QKISAQENMW RAVSCFQKIS VQTTQIVISM ETVPHTSKPC LLASLSNLNG SLSVKATQKV PGIILGSSFL
      2170       2180       2190       2200       2210       2220       2230       2240
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
```

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1721	1	682.3288	-51.59	3	51.5	13.2	1	2196-2214	K.HSGNPGPEQSIPKISIDLR.G	

Detailed Protein Report

Protein 588: 2-oxoglutarate dehydrogenase-like, mitochondrial isoform c [Homo sapiens]

Accession:	gi|221316669	**Score:**	26.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	91.2
Database Date:	2015-11-30	**pI:**	6.4
		Sequence Coverage [%]:	3.1
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MFINDVEQCQ WIRQKFETPG VMQFSSEEKR TLLARLVRSM RFEDFLARKW SSEKRFGLEG CEVMIPALKT IIDKSSEMGI
        90        100        110        120        130        140        150        160
ENVILGMPHR GRLNVLANVI RKDLEQIFCQ FDPKLEAADE GSGDVKYHLG MYHERINRVT NRNITLSLVA NPSHLEAVDP
       170        180        190        200        210        220        230        240
VVQGKTKAEQ FYRGDAQGKK VMSILVHGDA AFAGQGVVYE TFHLSDLPSY TTNGTVHVVV NNQIGFTTDP RMARSSPYPT
       250        260        270        280        290        300        310        320
DVARVVNAPI FHVNADDPEA VIYVCSVAAE WRNTFNKDVV VDLVCYRRRG HNEMDEPMFT QPLMYKQIHR QVPVLKKYAD
       330        340        350        360        370        380        390        400
KLIAEGTVTL QEFEEEIAKY DRICEEAYGR SKDKKILHIK HWLDSPWPGF FNVDGEPKSM TCPATGIPED MLTHIGSVAS
       410        420        430        440        450        460        470        480
SVPLEDFKIH TGLSRILRGR ADMTKNRTVD WALAEYMAFG SLLKEGIHVR LSGQDVERGT FSHRHHVLHD QEVDRRTCVP
       490        500        510        520        530        540        550        560
MNHLWPDQAP YTVCNSSLSE YGVLGFELGY AMASPNALVL WEAQFGDFHN TAQCIIDQFI STGQAKWVRH NGIVLLLPHG
       570        580        590        600        610        620        630        640
MEGMGPEHSS ARPERFLQMS NDDSDAYPAF TKDFEVSQLY DCNWIVVNCS TPANYFHVLR RQILLPFRKP LIIFTPKSLL
       650        660        670        680        690        700        710        720
RHPEAKSSFD QMVSGTSFQR VIPEDGAAAR APEQVQRLIF CTGKVYYDLV KERSSQDLEE KVAITRLEQI SPFPFDLIKQ
       730        740        750        760        770        780        790        800
EAEKYPGAEL AWCQEEHKNM GYYDYISPRF MTILRRARPI WYVGRDPAAA PATGNRNTHL VSLKKFLDTA FNLQAFEGKT
       810
F
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
865	1	676.8710	-83.95	2	39.3	10.8	2	91-102	R.GRLNVLANVIRK.D	

Detailed Protein Report

Protein 589: speckle-type POZ protein [Homo sapiens]

Accession:	gi|4507183	**Score:**	26.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	42.1
Database Date:	2015-11-30	**pI:**	5.5
		Sequence Coverage [%]:	7.8
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	1.45	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	1.52	**CV:**	0.00 %	**No. of Peptides:**	1

Alias proteins:

Accession	Name	Description
gi|530412967	refseq_human (refseq_human_20140103.fasta)	PREDICTED: speckle-type POZ protein isoform X3 [Homo sapiens]
gi|530412965	refseq_human (refseq_human_20140103.fasta)	PREDICTED: speckle-type POZ protein isoform X2 [Homo sapiens]
gi|56117836	refseq_human (refseq_human_20140103.fasta)	speckle-type POZ protein [Homo sapiens]
gi|56117834	refseq_human (refseq_human_20140103.fasta)	speckle-type POZ protein [Homo sapiens]
gi|56117832	refseq_human (refseq_human_20140103.fasta)	speckle-type POZ protein [Homo sapiens]
gi|56117830	refseq_human (refseq_human_20140103.fasta)	speckle-type POZ protein [Homo sapiens]
gi|56117828	refseq_human (refseq_human_20140103.fasta)	speckle-type POZ protein [Homo sapiens]

10	20	30	40	50	60	70	80
MSRVPSPPPP	AEMSSGPVAE	SWCYTQIKVV	KFSYMWTINN	FSFCREEMGE	VIKSSTFSSG	ANDKLKWCLR	VNPKGLDEES
90	100	110	120	130	140	150	160
KDYLSLYLLL	VSCPKSEVRA	KFKFSILNAK	GEETKAMESQ	RAYRFVQGKD	WGFKKFIRRD	FLLDEANGLL	PDDKLTLFCE
170	180	190	200	210	220	230	240
VSVVQDSVNI	SGQNTMNMVK	VPECRLADEL	GGLWENSRFT	DCCLCVAGQE	FQAHKAILAA	RSPVFSAMFE	HEMEESKKNR
250	260	270	280	290	300	310	320
VEINDVEPEV	FKEMMCFIYT	GKAPNLDKMA	DDLLAAADKY	ALERLKVMCE	DALCSNLSVE	NAAEILILAD	LHSADQLKTQ
330	340	350	360	370	380		
AVDFINYHAS	DVLETSGWKS	MVVSHPHLVA	EAYRSLASAQ	CPFLGPPRKR	LKQS		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1325	1	508.1630	-228.12	2	45.1	14.8	1	67-74	K.WCLRVNPK.G		mdown:qdown 1.45 Wdown:Qdown 1.52

Detailed Protein Report

Protein 590: **methylcytosine dioxygenase TET1 [Homo sapiens]**

Accession:	gi|156139122	**Score:**	26.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	235.2
Database Date:	2015-11-30	**pI:**	9.4
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.5
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	1.06	**CV:**	0.00 %	**No. of Peptides:**	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MSRSRHARPS	RLVRKEDVNK	KKKNSQLRKT	TKGANKNVAS	VKTLSPGKLK	QLIQERDVKK	KTEPKPPVPV	RSLLTRAGAA
90	100	110	120	130	140	150	160
RMNLDRTEVL	FQNPESLTCN	GFTMALRSTS	LSRRLSQPPL	VVAKSKKVPL	SKGLEKQHDC	DYKILPALGV	KHSENDSVPM
170	180	190	200	210	220	230	240
QDTQVLPDIE	TLIGVQNPSL	LKGKSQETTQ	FWSQRVEDSK	INIPTHSGPA	AEILPGPLEG	TRCGEGLFSE	ETLNDTSGSP
250	260	270	280	290	300	310	320
KMFAQDTVCA	PFPQRATPKV	TSQGNPSIQL	EELGSRVESL	KLSDSYLDPI	KSEHDCYPTS	SLNKVIPDLN	LRNCLALGGS
330	340	350	360	370	380	390	400
TSPTSVIKFL	LAGSKQATLG	AKPDHQEAFE	ATANQQEVSD	TTSFLGQAFG	AIPHQWELPG	ADPVHGEALG	ETPDLPEIPG
410	420	430	440	450	460	470	480
AIPVQGEVFG	TILDQQETLG	MSGSVVPDLP	VFLPVPPNPI	ATFNAPSKWP	EPQSTVSYGL	AVQGAIQILP	LGSGHTPQSS
490	500	510	520	530	540	550	560
SNSEKNSLPP	VMAISNVENE	KQVHISFLPA	NTQGFPLAPE	RGLFHASLGI	AQLSQAGPSK	SDRGSSQVSV	TSTVHVVNTT
570	580	590	600	610	620	630	640
VVTMPVPMVS	TSSSSYTTLL	PTLEKKKRKR	CGVCEPCQQK	TNCGECTYCK	NRKNSHQICK	KRKCEELKKK	PSVVVPLEVI
650	660	670	680	690	700	710	720
KENKRPQREK	KPKVLKADFD	NKPVNGPKSE	SMDYSRCGHG	EEQKLELNPH	TVENVTKNED	SMTGIEVEKW	TQNKKSQLTD
730	740	750	760	770	780	790	800
HVKGDFSANV	PEAEKSKNSE	VDKKRTKSPK	LFVQTVRNGI	KHVHCLPAET	NVSFKKFNIE	EFGKTLENNS	YKFLKDTANH
810	820	830	840	850	860	870	880
KNAMSSVATD	MSCDHLKGRS	NVLVFQQPGF	NCSSIPHSSH	SIINHHASIH	NEGDQPKTPE	NIPSKEPKDG	SPVQPSLLSL
890	900	910	920	930	940	950	960
MKDRRLTLEQ	VVAIEALTQL	SEAPSENSSP	SKSEKDEESE	QRTASLLNSC	KAILYTVRKD	LQDPNLQGEP	PKLNHCPSLE
970	980	990	1000	1010	1020	1030	1040
KQSSCNTVVF	NGQTTTLSNS	HINSATNQAS	TKSHEYSKVT	NSLSLFIPKS	NSSKIDTNKS	IAQGIITLDN	CSNDLHQLPP
1050	1060	1070	1080	1090	1100	1110	1120
RNNEVEYCNQ	LLDSSKKLDS	DDLSCQDATH	TQIEEDVATQ	LTQLASIIKI	NYIKPEDKKV	ESTPTSLVTC	NVQQKYNQEK
1130	1140	1150	1160	1170	1180	1190	1200
GTIQQKPPSS	VHNNHGSSLT	KQKNPTQKKT	KSTPSRDRRK	KKPTVVSYQE	NDRQKWEKLS	YMYGTICDIW	IASKFQNFGQ
1210	1220	1230	1240	1250	1260	1270	1280
FCPHDFPTVF	GKISSSTKIW	KPLAQTRSIM	QPKTVFPPLT	QIKLQRYPES	AEEKVKVEPL	DSLSLFHLKT	ESNGKAFTDK
1290	1300	1310	1320	1330	1340	1350	1360
AYNSQVQLTV	NANQKAHPLT	QPSSPPNQCA	NVMAGDDQIR	FQQVVKEQLM	HQRLPTLPGI	SHETPLPESA	LTLRNVNVVC
1370	1380	1390	1400	1410	1420	1430	1440
SGGITVVSTK	SEEEVCSSSF	GTSEFSTVDS	AQKNFNDYAM	NFFTNPTKNL	VSITKDSELP	TCSCLDRVIQ	KDKGPYYTHL
1450	1460	1470	1480	1490	1500	1510	1520
GAGPSVAAVR	EIMENRYGQK	GNAIRIEIVV	YTGKEGKSSH	GCPIAKWVLR	RSSDEEKVLC	LVRQRTGHHC	PTAVMVVLIM
1530	1540	1550	1560	1570	1580	1590	1600
VWDGIPLPMA	DRLYTELTEN	LKSYNGHPTD	RRCTLNENRT	CTCQGIDPET	CGASFSFGCS	WSMYFNGCKF	GRSPSPRRFR
1610	1620	1630	1640	1650	1660	1670	1680
IDPSSPLHEK	NLEDNLQSLA	TRLAPIYKQY	APVAYQNQVE	YENVARECRL	GSKEGRPFSG	VTACLDFCAH	PHRDIHNMNN
1690	1700	1710	1720	1730	1740	1750	1760
GSTVVCTLTR	EDNRSLGVIP	QDEQLHVLPL	YKLSDTDEFG	SKEGMEAKIK	SGAIEVLAPR	RKKRTCFTQP	VPRSGKKRAA
1770	1780	1790	1800	1810	1820	1830	1840
MMTEVLAHKI	RAVEKKPIPR	IKRKNNSTTT	NNSKPSSLPT	LGSNTETVQP	EVKSETEPHF	ILKSSDNTKT	YSLMPSAPHP
1850	1860	1870	1880	1890	1900	1910	1920
VKEASPGFSW	SPKTASATPA	PLKNDATASC	GFSERSSTPH	CTMPSGRLSG	ANAAAADGPG	ISQLGEVAPL	PTLSAPVMEP
1930	1940	1950	1960	1970	1980	1990	2000
LINSEPSTGV	TEPLTPHQPN	HQPSFLTSPQ	DLASSPMEED	EQHSEADEPP	SDEPLSDDPL	SPAEEKLPHI	DEYWSDSEHI
2010	2020	2030	2040	2050	2060	2070	2080
FLDANIGGVA	IAPAHGSVLI	ECARRELHAT	TPVEHPNRNH	PTRLSLVFYQ	HKNLNKPQHG	FELNKIKFEA	KEAKNKKMKA
2090	2100	2110	2120	2130	2140		
SEQKDQAANE	GPEQSSEVNE	LNQIPSHKAL	TLTHDNVVTV	SPYALTHVAG	PYNHWV		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1153	1	945.9628	20.41	2	43.1	13.0	0	1674-1690	R.DIHNMNNGSTVVCTLTR.E	Oxidation: 5	mdown:qdown 1.06

Detailed Protein Report

Protein 591: PREDICTED: MORC family CW-type zinc finger protein 4 isoform X2 [Homo sapiens]

Accession:	gi|578838478	**Score:**	26.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	92.9
Database Date:	2015-11-30	**pI:**	6.4
		Sequence Coverage [%]:	3.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLLYRGAPAG	PGAPGCGLAR	PGGGPQAFGI	RLSTMSPRYL	QSNSSSHTRP	FSAIAELLDN	AVDPDVSART	VFIDVEEVKN
90	100	110	120	130	140	150	160
KSCLTFTDDG	CGMTPHKLHR	MLRNKNGKSE	LDFDTDQYDI	LVSDFDTEEK	MTGGVTSELP	ETEYSLRAFC	GILYMKPRMK
170	180	190	200	210	220	230	240
IFLRQKKVTT	QMIAKSLANV	EYDTYKPTFT	NKQVRITFGF	SCKNSNQFGI	MMYHNNRLIK	SFEKVGCQVK	PTRGEGVGVI
250	260	270	280	290	300	310	320
GVIECNFLKP	AYNKQDFEYT	KEYRLTINAL	AQKLNAYWKE	KTSQDNFETS	TVARPIPKVP	DQTWVQCDEC	LKWRKLPGKI
330	340	350	360	370	380	390	400
DPSMLPARWF	CYYNSHPKYR	RCSVPEEQEL	TDEDLCLSKA	KKQEQTVEEK	KKMPMENENH	QVFSNPPKIL	TVQEMAGLNN
410	420	430	440	450	460	470	480
KTIGYEGIHS	PSVLPSGGEE	SRSPSLQLKP	LDSSVLQFSS	KYKWILGEEP	VEKRRRLQNE	MTTPSLDYSM	PAPYRRVEAP
490	500	510	520	530	540	550	560
VAYPEGENSH	DKSSSERSTP	PYLFPEYPEA	SKNTGQNREV	SILYPGAKDQ	RQGSLLPEEL	EDQMPRLVAE	ESNRGSTTIN
570	580	590	600	610	620	630	640
KEEVNKGPFV	AVVGVAKGVR	DSGAPIQLIP	FNREELAERR	KAVESWNPVP	YSVASAAIPA	AAIGEKARGY	EESEGHNTPK
650	660	670	680	690	700	710	720
LKNQRELEEL	KRTTEKLERV	LAERNLFQQK	VEELEQERNH	WQSEFKKVQH	ELVIYSTQEA	EGLYWSKKHM	GYRQAEFQIL
730	740	750	760	770	780	790	800
KAELERTKEE	KQELKEKLKE	TETHLEMLQK	AQVSYRTPEG	DDLERALAKL	TRLRIHVSYL	LTSVLPHLEL	REIGYDSEQV
810	820						
DGILYTVLEA	NHILD						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2715	1	856.8870	34.41	2	65.2	15.1	0	82-97	K.SCLTFTDDGCGMTPHK.L	

Detailed Protein Report

Protein 592: **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 593: TNF receptor-associated factor 6 [Homo sapiens]

Accession:	gi|4759254	**Score:**	25.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	59.5
Database Date:	2015-11-30	**pI:**	6.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.8
		No. of unique Peptides:	2

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
2891	1	713.3518	19.27	2	64.9	11.3	0	68-78	K.YECPICLMALR.E	Carbamidomethyl: 3, 6
1778	1	1057.3158	-132.00	1	52.2	14.7	0	134-142	K.CPNEGCLHK.M	Carbamidomethyl: 1

Detailed Protein Report

Protein 594: **PREDICTED: zinc finger protein with KRAB and SCAN domains 4 isoform X3 [Homo sapiens]**

Accession:	gi|530381975	**Score:**	25.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	49.6
Database Date:	2015-11-30	**pI:**	9.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	7.5
		No. of unique Peptides:	2

Alias proteins:

Accession	Name	Description
gi|530381977	refseq_human (refseq_human_20140103.fasta)	PREDICTED: zinc finger protein with KRAB and SCAN domains 4 isoform X4 [Homo sapiens]

10	20	30	40	50	60	70	80
MAREPRKNAA	LDAQSAEDQT	GLLTVKVEKE	EASALTAEVP	VGDQGQELLC	CKMALLTQTQ	GSQSSQCQPM	KALFKHESLG
90	100	110	120	130	140	150	160
SQPLHDRVLQ	VPGLAQGGCC	REDAMVASRL	TPGSQGLLKM	EDVALTLTPG	WTQLDSSQVN	LYRDEKQENH	SSLVSLGGEI
170	180	190	200	210	220	230	240
QTKSRDLPPV	KKLPEKEHGK	ICHLREDIAQ	IPTHAEAGEQ	EGRLQRKQKN	AIGSRRHYCH	ECGKSFAQSS	GLTKHRRIHT
250	260	270	280	290	300	310	320
GEKPYECEDC	GKTFIGSSAL	VIHQRVHTGE	KPYECEECGK	VFSHSSNLIK	HQRTHTGEKP	YECDDCGKTF	SQSCSLLEHH
330	340	350	360	370	380	390	400
KIHTGEKPYQ	CNMCGKAFRR	NSHLLRHQRI	HGDKNVQNPE	HGESWESQGR	TESQWENTEA	PVSYKCNECE	RSFTRNRSLI
410	420	430	440	450			
EHQKIHTGEK	PYQCDTCGKG	FTRTSYLVQH	QRSHVGKKTL	SQ			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2714	1	973.1242	130.42	2	62.3	15.6	0	8-26	K.NAALDAQSAEDQTGLLTVK.V	
2444	1	729.3737	3.44	2	58.9	10.3	0	88-101	R.VLQVPGLAQGGCCR.E	Carbamidomethyl: 12

Detailed Protein Report

Protein 595: **kinesin-like protein KIF3B [Homo sapiens]**

Accession:	gi|4758646	**Score:**	25.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	85.1
Database Date:	2015-11-30	**pI:**	7.8
		Sequence Coverage [%]:	4.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSKLKSSESV	RVVVRCRPMN	GKEKAASYDK	VVDVDVKLGQ	VSVKNPKGTA	HEMPKTFTFD	AVYDWNAKQF	ELYDETFRPL
90	100	110	120	130	140	150	160
VDSVLQGFNG	TIFAYGQTGT	GKTYTMEGIR	GDPEKRGVIP	NSFDHIFTHI	SRSQNQQYLV	RASYLEIYQE	EIRDLLSKDQ
170	180	190	200	210	220	230	240
TKRLELKERP	DTGVYVKDLS	SFVTKSVKEI	EHVMNVGNQN	RSVGATNMNE	HSSRSHAIFV	ITIECSEVGL	DGENHIRVGK
250	260	270	280	290	300	310	320
LNLVDLAGSE	RQAKTGAQGE	RLKEATKINL	SLSALGNVIS	ALVDGKSTHI	PYRDSKLTRL	LQDSLGGNAK	TVMVANVGPA
330	340	350	360	370	380	390	400
SYNVEETLTT	LRYANRAKNI	KNKPRVNEDP	KDALLREFQE	EIARLKAQLE	KRSIGRRKRR	EKRREGGGSG	GGGEEEEEEG
410	420	430	440	450	460	470	480
EEGEEEGDDK	DDYWREQQEK	LEIEKRAIVE	DHSLVAEEKM	RLLKEKEKKM	EDLRREKDAA	EMLGAKIKAM	ESKLLVGGKN
490	500	510	520	530	540	550	560
IVDHTNEQQK	ILEQKRQEIA	EQKRREREIQ	QQMESRDEET	LELKETYSSL	QQEVDIKTKK	LKKLFSKLQA	VKAEIHDLQE
570	580	590	600	610	620	630	640
EHIKERQELE	QTQNELTREL	KLKHLIIENF	IPLEEKSKIM	NRAFFDEEED	HWKLHPITRL	ENQQMMKRPV	SAVGYKRPLS
650	660	670	680	690	700	710	720
QHARMSMMIR	PEARYRAENI	VLLELDMPSR	TTRDYEGPAI	APKVQAALDA	ALQDEDEIQV	DASSFESTAN	KKSKARPKSG
730	740	750					
RKSGSSSSSS	GTPASQLYPQ	SRGLVPK					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
850	1	911.1296	-3.32	3	39.4	14.3	2	178-201	K.DLSSFVTKSVKEIEHVMNVGNQNR.S	

Detailed Protein Report

Protein 596: **PREDICTED: ryanodine receptor 2 isoform X7 [Homo sapiens]**

Accession:	gi|578802309	**Score:**	25.9
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

Detailed Protein Report

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
1437	1	946.4677	46.36	2	46.5	13.9	2	4372- 4388	K.EETKSEPEKAEGEDGEK.E	

Detailed Protein Report

Protein 597: protein AKNAD1 [Homo sapiens]

Accession:	gi|91754185	**Score:**	25.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	92.8
Database Date:	2015-11-30	**pI:**	6.4
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	4.7
		No. of unique Peptides:	2

```
        10         20         30         40         50         60         70         80
MDEADFSEHT TYKQEDLPYD GDLSQIKIGN DYSFTSKKDG LEVLNQIIFI ADDPQEKAMH SETCGNTAVT IPLGKITENA
        90        100        110        120        130        140        150        160
ANKKDEKEKQ CTAALHIPAN EGDASKSSIS DILLHHLSKE PFLRGQGIDC ETLPEISNAD SFEEEAIIKS IISCYNKNSW
       170        180        190        200        210        220        230        240
PKEQTPELTD QLNPKRDGEN SNKPGSATTT EENTSDLEGP VAAGDSSHQE NVNVLTKTKG PGDKQKSYQG QSPQKQQTEK
       250        260        270        280        290        300        310        320
ANSGNTFKYG QGQVHYQLPD FSKIAPKVKI PKNKIINKPL AIAKQASFSS KSRDKPTLVQ DSLETTPESN CVEKQHQEQK
       330        340        350        360        370        380        390        400
GKITEPSQQI QMEPIVHIHQ ELLTGIESEA SLSKLSPTSQ KGTSSSSSYI FQKISQGKQM CQKLKEQTDQ LKTKVQEFSK
       410        420        430        440        450        460        470        480
RIKQDSPYHL QDKKLVLEKL QGHLELLEQN FLATKDKHLT LQQQVHKHES TIVGDFDPER KVEGEIFKLE MLLEDVKEKM
       490        500        510        520        530        540        550        560
DESKYTSAPS LPVSSPVTLD DLASTFSSLS NEIPKEHPGH PSGPRGSGGS EVTGTPQGGP QEAPNEELCE LAPQTYLNGH
       570        580        590        600        610        620        630        640
YGDAAAQNKP DQVAMRLSSN SGEDPNGTPR RQDCAEMTAP SPSCAFCRRL LEWKQNVEKK GHGRINCGRF SIVLHEKAPH
       650        660        670        680        690        700        710        720
SDSTPNSDTG HSFCSDSGTE MQSNKCQDCG TKIPTSRRAC RKEPTKEFHY RYNTPGQNYS NHSKRGAFVQ PHSLDESKNS
       730        740        750        760        770        780        790        800
SPSFLKPKRI CSQRVNSKSF KGEHEPTPGK KKLQAFMTYS SDPATPSPHF YSCRISGSKS LCDFDSTEEI KSEILNSALD
       810        820        830        840
HALRTATILK ETTDQMIKTI AEDLAKAQRW RNRLKY
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2577	1	1202.2445	83.07	2	60.9	12.0	2	249-269	K.YGQGQVHYQLPDFSKIAPKVK.I	
2161	1	1023.4064	-11.81	2	55.6	13.9	1	592-609	R.QDCAEMTAPSPSCAFCRR.L	Carbamidomethyl: 16; Oxidation: 6

Detailed Protein Report

Protein 598: tetratricopeptide repeat protein 40 [Homo sapiens]

Accession:	gi|359385708	**Score:**	25.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	303.3
Database Date:	2015-11-30	**pI:**	7.2
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.3
		No. of unique Peptides:	2

Quantitation

Wdown:Qdown	**Median:** 1.22	**CV:** 0.00 %	**No. of 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	Ratios
2308	1	841.6632	-116.58	3	57.3	10.2	2	972-994	K.KFGPEESRLVAEMLCTATAIQGR.S	Oxidation: 13	
114	1	793.3810	-31.26	2	30.8	15.7	1	1161-1173	K.LGQNFSMEIQKFK.A	Oxidation: 7	Wdown:Qdown 1.22

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Detailed Protein Report

Protein 599: E3 ubiquitin-protein ligase RNF103 isoform 2 [Homo sapiens]

Accession:	gi|312147324	**Score:**	25.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	78.6
Database Date:	2015-11-30	**pI:**	5.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	4.6
		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
2911	1	840.9107	-41.30	2	65.2	10.8	1	167-182	R.STLIMSVPQTSTSKGK.V	Oxidation: 5

Detailed Protein Report

Protein 600: 1-phosphatidylinositol 3-phosphate 5-kinase isoform 2 [Homo sapiens]

Accession:	gi|121583483	**Score:**	25.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	237.0
Database Date:	2015-11-30	**pI:**	6.2
		Sequence Coverage [%]:	1.2
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	1.96	**CV:**	0.00 %	**No. of Peptides:**	1

```
        10         20         30         40         50         60         70         80
MATDDKTSPT LDSANDLPRS PTSPSHLTHF KPLTPDQDEP PFKSAYSSFV NLFRFNKERA EGGQGEQQPL SGSWTSPQLP

        90        100        110        120        130        140        150        160
SRTQSVRSPT PYKKQLNEEL QRRSSALDTR RKAEPTFGGH DPRTAVQLRS LSTVLKRLKE IMEGKSQDSD LKQYWMPDSQ

       170        180        190        200        210        220        230        240
CKECYDCSEK FTTFRRRHHC RLCGQIFCSR CCNQEIPGKF MGYTGDLRAC TYCRKIALSY AHSTDSNSIG EDLNALSDSA

       250        260        270        280        290        300        310        320
CSVSVLDPSE PRTPVGSRKA SRNIFLEDDL AWQSLIHPDS SNTPLSTRLV SVQEDAGKSP ARNRSASITN LSLDRSGSPM

       330        340        350        360        370        380        390        400
VPSYETSVSP QANRTYVRTE TTEDERKILL DSVQLKDLWK KICHHSSGME FQDHRYWLRT HPNCIVGKEL VNWLIRNGHI

       410        420        430        440        450        460        470        480
ATRAQAIAIG QAMVDGRWLD CVSHHDQLFR DEYALYRPLQ STEFSETPSP DSDSVNSVEG HSEPSWFKDI KFDDSDTEQI

       490        500        510        520        530        540        550        560
AEEGDDNLAN SASPSKRTSV SSFQSTVDSD SAASISLNVE LDNVNFHIKK PSKYPHVPPH PADQKEYLIS DTGGQQLSIS

       570        580        590        600        610        620        630        640
DAFIKESLFN RRVEEKSKEL PFTPLGWHHN NLELLREENG EKQAMERLLS ANHNHMMALL QQLLHSDSLS SSWRDIIVSL

       650        660        670        680        690        700        710        720
VCQVVQTVRP DVKNQDDDMD IRQFVHIKKI PGGKKFDSVV VNGFVCTKNI AHKKMSSCIK NPKILLLKCS IEYLYREETK

       730        740        750        760        770        780        790        800
FTCIDPIVLQ EREFLKNYVQ RIVDVRPTLV LVEKTVSRIA QDMLLEHGIT LVINVKSQVL ERISRMTQGD LVMSMDQLLT

       810        820        830        840        850        860        870        880
KPHLGTCHKF YMQIFQLPNE QTKTLMFFEG CPQHLGCTIK LRGGSDYELA RVKEILIFMI CVAYHSQLEI SFLMDEFAMP

       890        900        910        920        930        940        950        960
PTLMQNPSFH SLIEGRGHEG AVQEQYGGGS IPWDPDIPPE SLPCDDSSLL ELRIVFEKGE QENKNLPQAV ASVKHQEHST

       970        980        990       1000       1010       1020       1030       1040
TACPAGLPCA FFAPVPESLL PLPVDDQQDA LGSEQPETLQ QTVVLQDPKS QIRAFRDPLQ DDTGLYVTEE VTSSEDKRKT

      1050       1060       1070       1080       1090       1100       1110       1120
YSLAFKQELK DVILCISPVI TFREPFLLTE KGMRCSTRDY FAEQVYWSPL LNKEFKEMEN RRKKQLLRDL SGLQGMNGSI

      1130       1140       1150       1160       1170       1180       1190       1200
QAKSIQVLPS HELVSTRIAE HLGDSQSLGR MLADYRARGG RIQPKNSDPF AHSKDASSTS SGQSGSKNEG DEERGLILSD

      1210       1220       1230       1240       1250       1260       1270       1280
AVWSTKVDCL NPINHQRLCV LFSSSSAQSS NAPSACVSPW IVTMEFYGKN DLTLGIFLER YCFRPSYQCP SMFCDTPMVH

      1290       1300       1310       1320       1330       1340       1350       1360
HIRRFVHGQG CVQIILKELD SPVPGYQHTI LTYSWCRICK QVTPVVALSN ESWSMSFAKY LELRFYGHQY TRRANAEPCG

      1370       1380       1390       1400       1410       1420       1430       1440
HSIHHDYHQY FSYNQMVASF SYSPIRLLEV CVPLPKIFIK RQAPLKVSLL QDLKDFFQKV SQVYVAIDER LASLKTDTFS

      1450       1460       1470       1480       1490       1500       1510       1520
KTREEKMEDI FAQKEMEEGE FKNWIEKMQA RLMSSSVDTP QQLQSVFESL IAKKQSLCEV LQAWNNRLQD LFQQEKGRKR

      1530       1540       1550       1560       1570       1580       1590       1600
PSVPPSPGRL RQGEESKISA MDASPRNISP GLQNGEKEDR FLTTLSSQSS TSSTHLQLPT PPEVMSEQSV GGPPELDTAS

      1610       1620       1630       1640       1650       1660       1670       1680
SSEDVFDGHL LGSTDSQVKE KSTMKAIFAN LLPGNSYNPI PFPFDPDKHY LMYEHERVPI AVCEKEPSSI IAFALSCKEY

      1690       1700       1710       1720       1730       1740       1750       1760
RNALEELSKA TQWNSAEEGL PTNSTSDSRP KSSSPIRLPE MSGGQTNRTT ETEPQPTKKA SGMLSFFRGT AGKSPDLSSQ

      1770       1780       1790       1800       1810       1820       1830       1840
KRETLRGADS AYYQVGQTGK EGTENQGVEP QDEVDGGDTQ KKQLINPHVE LQFSDANAKF YCRLYYAGEF HKMREVILDS

      1850       1860       1870       1880       1890       1900       1910       1920
SEEDFIRSLS HSSPWQARGG KSGAAFYATE DDRFILKQMP RLEVQSFLDF APHYFNYITN AVQQKRPTAL AKILGVYRIG

      1930       1940       1950       1960       1970       1980       1990       2000
YKNSQNNTEK KLDLLVMENL FYGRKMAQVF DLKGSLRNRN VKTDTGKESC DVVLLDENLL KMVRDNPLYI RSHSKAVLRT

      2010       2020       2030       2040       2050       2060       2070       2080
SIHSDSHFLS SHLIIDYSLL VGRDDTSNEL VVGIIDYIRT FTWDKKLEMV VKSTGILGGQ GKMPTVVSPE LYRTRFCEAM

      2090       2100
DKYFLMVPDH WTGLGLNC
```

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
596	1	656.3887	96.05	2	36.0	14.0	1	112-123	R.KAEPTFGGHDPR.T		mdown:qdown 1.96

Detailed Protein Report

Protein 601: zinc finger protein 268 isoform c [Homo sapiens]

Accession: gi|259490323
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 25.9
MW [kDa]: 98.7
pI: 10.1
Sequence Coverage [%]: 3.5
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MDVFVDFTWE	EWQLLDPAQK	CLYRSVMLEN	YSNLVSLGYQ	HTKPDIIFKL	EQGEELCMVQ	AQVPNQTCPN	TVWKIDDLMD
90	100	110	120	130	140	150	160
WHQENKDKLG	STAKSFECTT	FGKLCLLSTK	YLSRQKPHKC	GTHGKSLKYI	DFTSDYARNN	PNGFQVHGKS	FFHSKHEQTV
170	180	190	200	210	220	230	240
IGIKYCESIE	SGKTVNKKSQ	LMCQQMYMGE	KPFGCSCCEK	AFSSKSYLLV	HQQTHAEEKP	YGCNECGKDF	SSKSYLIVHQ
250	260	270	280	290	300	310	320
RIHTGEKLHE	CSECRKTFSF	HSQLVIHQRI	HTGENPYECC	ECGKVFSRKD	QLVSHQKTHS	GQKPYVCNEC	GKAFGLKSQL
330	340	350	360	370	380	390	400
IIHERIHTGE	KPYECNECQK	AFNTKSNLMV	HQRTHTGEKP	YVCSDCGKAF	TFKSQLIVHQ	GIHTGVKPYG	CIQCGKGFSL
410	420	430	440	450	460	470	480
KSQLIVHQRS	HTGMKPYVCN	ECGKAFRSKS	YLIIHTRTHT	GEKLHECNNC	GKAFSFKSQL	IIHQRIHTGE	NPYECHECGK
490	500	510	520	530	540	550	560
AFSRKYQLIS	HQRTHAGEKP	YECTDCGKAF	GLKSQLIIHQ	RTHTGEKPFE	CSECQKAFNT	KSNLIVHQRT	HTGEKPYSCN
570	580	590	600	610	620	630	640
ECGKAFTFKS	QLIVHKGVHT	GVKPYGCSQC	AKTFSLKSQL	IVHQRSHTGV	KPYGCSECGK	AFRSKSYLII	HMRTHTGEKP
650	660	670	680	690	700	710	720
HECRECGKSF	SFNSQLIVHQ	RIHTGENPYE	CSECGKAFNR	KDQLISHQRT	HAGEKPYGCS	ECGKAFSSKS	YLIIHMRTHS
730	740	750	760	770	780	790	800
GEKPYECNEC	GKAFIWKSLL	IVHERTHAGV	NPYKCSQCEK	SFSGKLRLLV	HQRMHTREKP	YECSECGKAF	IRNSQLIVHQ
810	820	830	840	850	860	870	
RTHSGEKPYG	CNECGKTFSQ	KSILSAHQRT	HTGEKPCKCT	ECGKAFCWKS	QLIMHQRTHV	DDKH	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2187	1	618.9601	39.18	3	55.8	10.5	1	774-788	R.MHTREKPYECSECGK.A	Carbamidomethyl: 13

Detailed Protein Report

Protein 602: ubiquitin carboxyl-terminal hydrolase 35 [Homo sapiens]

Accession:	gi|148746183	**Score:**	25.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	113.3
Database Date:	2015-11-30	**pI:**	5.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.1
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	0.20	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.22	**CV:**	0.00 %	**No. of Peptides:**	1

```
        10         20         30         40         50         60         70         80
MDKILEAVVT SSYPVSVKQG LVRRVLEAAR QPLEREQCLA LLALGARLYV GGAEELPRRV GCQLLHVAGR HHPDVFAEFF

        90        100        110        120        130        140        150        160
SARRVLRLLQ GGAGPPGPRA LACVQLGLQL LPEGPAADEV FALLRREVLR TVCERPGPAA CAQVARLLAR HPRCVPDGPH

       170        180        190        200        210        220        230        240
RLLFCQQLVR CLGRFRCPAE GEEGAVEFLE QAQQVSGLLA QLWRAQPAAI LPCLKELFAV ISCAEEEPPS SALASVVQHL

       250        260        270        280        290        300        310        320
PLELMDGVVR NLSNDDSVTD SQMLTAISRM IDWVSWPLGK NIDKWIIALL KGLAAVKKFS ILIEVSLTKI EKVFSKLLYP

       330        340        350        360        370        380        390        400
IVRGAALSVL KYMLLTFQHS HEAFHLLLPH IPPMVASLVK EDSNSGTSCL EQLAELVHCM VFRFPGFPDL YEPVMEAIKD

       410        420        430        440        450        460        470        480
LHVPNEDRIK QLLGQDAWTS QKSELAGFYP RLMAKSDTGK IGLINLGNTC YVNSILQALF MASDFRHCVL RLTENNSQPL

       490        500        510        520        530        540        550        560
MTKLQWLFGF LEHSQRPAIS PENFLSASWT PWFSPGTQQD CSEYLKYLLD RLHEEEKTGT RICQKLKQSS SPSPPEEPPA

       570        580        590        600        610        620        630        640
PSSTSVEKMF GGKIVTRICC LCCLNVSSRE EAFTDLSLAF PPPERCRRRR LGSVMRPTED ITARELPPPT SAQGPGRVGP

       650        660        670        680        690        700        710        720
RRQRKHCITE DTPPTSLYIE GLDSKEAGGQ SSQEERIERE EEGKEERTEK EEVGEEEEST RGEGEREKEE EVEEEEEKVE

       730        740        750        760        770        780        790        800
KETEKEAEQE KEEDSLGAGT HPDAAIPSGE RTCGSEGSRS VLDLVNYFLS PEKLTAENRY YCESCASLQD AEKVVELSQG

       810        820        830        840        850        860        870        880
PCYLILTLLR FSFDLRTMRR RKILDDVSIP LLLRLPLAGG RGQAYDLCSV VVHSGVSSES GHYYCYAREG AARPAASLGT

       890        900        910        920        930        940        950        960
ADRPEPENQW YLFNDTRVSF SSFESVSNVT SFFPKDTAYV LFYRQRPREG PEAELGSSRV RTEPTLHKDL MEAISKDNIL

       970        980        990       1000       1010       1020
YLQEQEKEAR SRAAYISALP TSPHWGRGFD EDKDEDEGSP GGCNPAGGNG GDFHRLVF
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
574	1	469.1409	-166.57	2	36.0	10.2	0	154-161	R.CVPDGPHR.L	Carbamidomethyl: 1	mdown:qdown 0.20 Wdown:Qdown 0.22

Detailed Protein Report

Protein 603: **tumor necrosis factor receptor superfamily member 10B isoform 2 precursor [Homo sapiens]**

Accession: gi|224494026
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 25.8
MW [kDa]: 45.1
pI: 5.4
Sequence Coverage [%]: 4.6
No. of unique Peptides: 2

10	20	30	40	50	60	70	80
MEQRGQNAPA	ASGARKRHGP	GPREARGARP	GPRVPKTLVL	VVAAVLLLVS	AESALITQQD	LAPQQRAAPQ	QKRSSPSEGL
90	100	110	120	130	140	150	160
CPPGHHISED	GRDCISCKYG	QDYSTHWNDL	LFCLRCTRCD	SGEVELSPCT	TTRNTVCQCE	EGTFREEDSP	EMCRKCRTGC
170	180	190	200	210	220	230	240
PRGMVKVGDC	TPWSDIECVH	KESGIIIGVT	VAAVVLIVAV	FVCKSLLWKK	VLPYLKGICS	GGGGDPERVD	RSSQRPGAED
250	260	270	280	290	300	310	320
NVLNEIVSIL	QPTQVPEQEM	EVQEPAEPTG	VNMLSPGESE	HLLEPAEAER	SQRRRLLVPA	NEGDPTETLR	QCFDDFADLV
330	340	350	360	370	380	390	400
PFDSWEPLMR	KLGLMDNEIK	VAKAEAAGHR	DTLYTMLIKW	VNKTGRDASV	HTLLDALETL	GERLAKQKIE	DHLLSSGKFM
410	420						
YLEGNADSAM	S						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2928	1	973.4951	-17.22	2	65.4	11.7	2	210-228	K.KVLPYLKGICSGGGGDPER.V	
2235	1	937.9180	-60.88	2	56.4	14.1	1	211-228	K.VLPYLKGICSGGGGDPER.V	Carbamidomethyl: 9

Detailed Protein Report

Protein 604: zinc finger protein 688 isoform b [Homo sapiens]

Accession:	gi|67010013	**Score:**	25.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	28.9
Database Date:	2015-11-30	**pI:**	11.6
		Sequence Coverage [%]:	6.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPRSPLRSSL	STEASGPRGP	FKCPASPRPI	TAQLLPGSSP	IIGRCVLRVQ	RGFPGPKPAL	ISWMEQESEA	WSPAAQDPEK
90	100	110	120	130	140	150	160
GERLGGARRG	DVPNRKEEEP	EEVPRAKGPR	KAPVKESPEV	LVERNPDPAI	SVAPARAQPP	KNAAWDPTTG	AQPPAPIPSM
170	180	190	200	210	220	230	240
DAQAGQRRHV	CTDCGRRFTY	PSLLVSHRRM	HSGERPFPCP	ECGMRFKRKF	AVEAHQWIHR	SCSGGRRGRR	PGIRAVPRAP
250	260	270					
VRGDRDPPVL	FRHYPDIFEE	CG					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1884	1	600.0016	18.70	3	52.2	14.1	2	2-18	M.PRSPLRSSLSTEASGPR.G	

Detailed Protein Report

Protein 605: lysine-specific demethylase 4C isoform 3 [Homo sapiens]

Accession:	gi|226442893	**Score:**	25.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	91.8
Database Date:	2015-11-30	**pI:**	5.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.2
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
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
149	1	855.2460	-164.97	2	31.1	10.1	1	748-761	K.RNAWTAECCLCNLR.G	Carbamidomethyl: 8

Detailed Protein Report

Protein 606: 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 607: PREDICTED: centromere protein T isoform X3 [Homo sapiens]

Accession:	gi|578829227	**Score:**	25.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	34.4
Database Date:	2015-11-30	**pI:**	5.0
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	4.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSWCCLWLCL	SSVGRTGSAG	PSLPFSELCS	LGLLRLRPVF	SPLHSGPGKP	AQFLAGEAEE	VNAFALGFLS	TSSGVSGEDE
90	100	110	120	130	140	150	160
VEPLHDGVEE	AEKKMEEEGV	SVSEMEATGA	QGPSRVEEAE	GHTEVTEAEG	SQGTAEADGP	GASSGDEDAS	GRAASPESAS
170	180	190	200	210	220	230	240
STPESLQARR	HHQFLEPAPA	PGAAVLSSEP	AEPLLVRHPP	RPRTTGPRPR	QDPHKAGLSH	YVKLFSFYAK	MPMERKALEM
250	260	270	280	290	300	310	320
VEKCLDKYFQ	HLCDDLEVFA	AHAGRKTVKP	EDLELLMRRQ	GLVTDQVSLH	VLVERHLPLE	YRQLLIPCAY	SGNSVFPAQ

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2474	1	965.7758	-154.68	2	59.6	14.1	0	1-15	-.MSWCCLWLCLSSVGR.T	Carbamidomethyl: 4, 5, 9; Oxidation: 1

Detailed Protein Report

Protein 608: sushi domain-containing protein 1 isoform 3 precursor [Homo sapiens]

Accession:	gi|544063419	**Score:**	25.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	80.4
Database Date:	2015-11-30	**pI:**	6.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.0
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MGRGPWDAGP SRRLLPLLLL LGLARGAAGA PGPDGLDVCA TCHEHATCQQ REGKKICICN YGFVGNGRTQ CVDKNECQFG

        90        100        110        120        130        140        150        160
ATLVCGNHTS CHNTPGGFYC ICLEGYRATN NNKTFIPNDG TFCTDIDECE VSGLCRHGGR CVNTHGSFEC YCMDGYLPRN

       170        180        190        200        210        220        230        240
GPEPFHPTTD ATSCTEIDCG TPPEVPDGYI IGNYTSSLGS QVRYACREGF FSVPEDTVSS CTGLGTWESP KLHCQEINCG

       250        260        270        280        290        300        310        320
NPPEMRHAIL VGNHSSRLGG VARYVCQEGF ESPGGKITSV CTEKGTWRES TLTCTEILTK INDVSLFNDT CVRWQINSRR

       330        340        350        360        370        380        390        400
INPKISYVIS IKGQRLDPME SVREETVNLT TDSRTPEVCL ALYPGTNYTV NISTAPPRRS MPAVIGFQTA EVDLLEDDGS

       410        420        430        440        450        460        470        480
FNISIFNETC LKLNRRSRKV GSEHMYQFTV LGQRWYLANF SHATSFNFTT REQVPVVCLD LYPTTDYTVN VTLLRSPKRH

       490        500        510        520        530        540        550        560
SVQITIATPP AVKQTISNIS GFNETCLRWR SIKTADMEEM YLFHIWGQRW YQKEFAQEMT FNISSSSRDP EVCLDLRPGT

       570        580        590        600        610        620        630        640
NYNVSLRALS SELPVVISLT TQITEPPLPE VEFFTVHRGP LPRLRLRKAK EKNGPISSYQ VLVLPLALQS TFSCDSEGAS

       650        660        670        680        690        700        710        720
SFFSNASDAD GYVAAELLAK DVPDDAMEIP IGDRLYYGEY YNAPLKRGSD YCIILRITSE WNKIRHSCCC RWRVLDWVPW

       730
LL
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
844	1	776.9364	79.23	2	39.3	10.6	0	301-313	K.INDVSLFNDTCVR.W	Carbamidomethyl: 11

Detailed Protein Report

Protein 609: PREDICTED: kinesin-like protein KIF21A isoform X9 [Homo sapiens]

Accession:	gi|530400550	**Score:**	25.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	179.8
Database Date:	2015-11-30	**pI:**	6.1
		Sequence Coverage [%]:	1.5
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	0.95	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	1.95	**CV:**	0.00 %	**No. of 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	Ratios

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
770	1	839.4295	-37.29	2	38.4	14.8	2	731-744	K.ELQRLQAAQKEHAR.L		Wdown:Qdown 1.95 mdown:qdown 0.95

Detailed Protein Report

Protein 610: 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 611: zinc finger and BTB domain-containing protein 5 [Homo sapiens]

Accession:	gi|7662074	**Score:**	25.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	74.2
Database Date:	2015-11-30	**pI:**	5.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	5.2
		No. of unique Peptides:	2

Alias proteins:

Accession	Name	Description
gi|530390257	refseq_human (refseq_human_20140103.fasta)	PREDICTED: zinc finger and BTB domain-containing protein 5 isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MDFPGHFEQI	FQQLNYQRLH	GQLCDCVIVV	GNRHFKAHRS	VLAACSTHFR	ALFSVAEGDQ	TMNMIQLDSE	VVTAEAFAAL
90	100	110	120	130	140	150	160
IDMMYTSTLM	LGESNVMDVL	LAASHLHLNS	VVKACKHYLT	TRTLPMSPPS	ERVQEQSARM	QRSFMLQQLG	LSIVSSALNS
170	180	190	200	210	220	230	240
SQNGEEQPAP	MSSSMRSNLD	QRTPFPMRRL	HKRKQSAEER	ARQRLRPSID	ESAISDVTPE	NGPSGVHSRE	EFFSPDSLKI
250	260	270	280	290	300	310	320
VDNPKADGMT	DNQEDSAIMF	DQSFGTQEDA	QVPSQSDNSA	GNMAQLSMAS	RATQVETSFD	QEAAPEKSSF	QCENPEVGLG
330	340	350	360	370	380	390	400
EKEHMRVVVK	SEPLSSPEPQ	DEVSDVTSQA	EGSESVEVEG	VVVSAEKIDL	SPESSDRSFS	DPQSSTDRVG	DIHILEVTNN
410	420	430	440	450	460	470	480
LEHKSTFSIS	NFLNKSRGNN	FTANQNNDDN	IPNTTSDCRL	ESEAPYLLSP	EAGPAGGPSS	APGSHVENPF	SEPADSHFVR
490	500	510	520	530	540	550	560
PMQEVMGLPC	VQTSGYQGGE	QFGMDFSRSG	LGLHSSFSRV	MIGSPRGGAS	NFPYYRRIAP	KMPVVTSVRS	SQIPENSTSS
570	580	590	600	610	620	630	640
QLMMNGATSS	FENGHPSQPG	PPQLTRASAD	VLSKCKKALS	EHNVLVVEGA	RKYACKICCK	TFLTLTDCKK	HIRVHTGEKP
650	660	670	680				
YACLKCGKRF	SQSSHLYKHS	KTTCLRWQSS	NLPSTLL				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2671	1	699.0932	93.54	3	62.2	11.2	1	19-36	R.LHGQLCDCVIVVGNRHFK.A	Carbamidomethyl: 6
1742	1	689.9841	-17.31	3	50.5	14.5	2	613-629	K.YACKICCKTFLTLTDCK.K	Carbamidomethyl: 6, 7

Detailed Protein Report

Protein 612: prosaposin receptor GPR37 precursor [Homo sapiens]

Accession:	gi|4885323	**Score:**	25.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	67.1
Database Date:	2015-11-30	**pI:**	9.9
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.8
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	1.22	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	5.84	**CV:**	0.00 %	**No. of 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	Ratios
2128	2	721.2347	-109.30	2	56.8	13.5	1	601-613	R.REMSTFASVGTHC.-	Oxidation: 3	Wdown:Qdown 5.84 mdown:qdown 1.22

Detailed Protein Report

Protein 613: 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

Quantitation

mdown:qdown **Median:** 0.47 **CV:** 0.00 % **No. of 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	Ratios
402	1	711.3339	-88.13	2	34.3	14.6	2	178-189	K.TFSVSQKVDRVR.S		mdown:qdown 0.47

Detailed Protein Report

Protein 614: PREDICTED: leucine-rich repeat and coiled-coil domain-containing protein 1 isoform X6 [Homo sapiens]

Accession:	gi|530388606	**Score:**	25.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	77.0
Database Date:	2015-11-30	**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 615: PREDICTED: collagen alpha-1(XXII) chain isoform X2 [Homo sapiens]

Accession: gi|578815852

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Modification(s): Oxidation

Score: 25.6

MW [kDa]: 129.6

pI: 7.8

Sequence Coverage [%]: 3.7

No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MAGLRGNAVA	GLLWMLLLWS	GGGGCQAQRA	GCKSVHYDLV	FLLDTSSSVG	KEDFEKVRQW	VANLVDTFEV	GPDRTRVGVV
90	100	110	120	130	140	150	160
RYSDRPTTAF	ELGLFGSQEE	VKAAARRLAY	HGGNTNTGDA	LRYITARSFS	PHAGGRPRDR	AYKQVAILLT	DGRSQDLVLD
170	180	190	200	210	220	230	240
AAAAAHRAGI	RIFAVGVGEA	LKEELEEIAS	EPKSAHVFHV	SDFNAIDKIR	GKLRRRLCEN	VLCPSVRVEG	DRFKHTNGGT
250	260	270	280	290	300	310	320
KEITGFDLMD	LFSVKEILGK	RENGAQSSYV	RMGSFPVVQS	TEDVFPQGLP	DEYAFVTTFR	FRKTSRKEDW	YIWQVIDQYS
330	340	350	360	370	380	390	400
IPQVSIRLDG	ENKAVEYNAV	AGPQGEKGDV	GPAGPPGVPG	SVVQQEGLKG	EQGAPGPRGH	QGAPGPPGAR	GPIGPEGRDG
410	420	430	440	450	460	470	480
PPGLQGLRGK	KGDMGPPGIP	GLLGLQGPPG	PPGVPGPPGP	GGSPGLPGEI	GFPGKPGPPG	PTGPPGKDGP	NGPPGPPGTK
490	500	510	520	530	540	550	560
GEPGERGEDG	LPGKPGLRGE	IGEQGLAGRP	GEKGEAGLPG	APGFPGVRGE	KGDQGEKGEL	GLPGLKGDRG	EKGEAGPAGP
570	580	590	600	610	620	630	640
PGLPGTTSLF	TPHPRMPGEQ	GPKGEKGDPG	LPGEPGLQGR	PGELGPQGPT	GPPGAKGQEG	AHGAPGAAGN	PGAPGHVGAP
650	660	670	680	690	700	710	720
GPSGPPGSVG	APGLRGTPGK	DGERGEKGAA	GEEGSPGPVG	PRGDPGAPGL	PGPPGKGKDG	EPGLRGSPGL	PGPLGTKGDR
730	740	750	760	770	780	790	800
GAPGIPGSPG	SRGDPGIGVA	GPPGPSGPPG	DKGSPGSRGL	PGFPGPQGPA	GRDGAPGNPG	ERGPPGKPGL	SSLLSPGDIN
810	820	830	840	850	860	870	880
LLAKDVCNDC	PPGPPGLPGL	PGFKGDKGVP	GKPGREGTEG	KKGEAGPPGL	PGPPGIAGPQ	GSQGERGADG	EVGQKGDQGH
890	900	910	920	930	940	950	960
PGVPGFMGPP	GNPGPPGADG	IAGAAGPPGI	QGSPGKEGPP	GPQGPSGLPG	IPGEEGKEGR	DGKPGPPGEP	GKAGEPGLPG
970	980	990	1000	1010	1020	1030	1040
PEGARGPPGF	KGHTGDSGAP	GPRGESGAMG	LPGQEGLPGK	DGDTGPTGPQ	GPQGPRGPPG	KNGSPGSPGE	PGPSGTPGQK
1050	1060	1070	1080	1090	1100	1110	1120
GSKGENGSPG	LPGFLGPRGP	PGEPGEKGVP	GKEGVPGKPG	EPGFKGERGD	PGIKGDKGPP	GGKGQPGDPG	IPGHKGHTGL
1130	1140	1150	1160	1170	1180	1190	1200
MGPQGLPGEN	GPVGPPGPPG	QPGFPGLRGE	SPSMETLRRL	IQEELGKQLE	TRLAYLLAQM	PPAYMKSSQG	RPGPPGPPGK
1210	1220	1230	1240	1250	1260	1270	1280
DGLPGRAGPM	GEPGRPGQGG	LEGPSGPIGP	KGERGAKGDP	GAPGVGLRGE	MGPPGIPGQP	GEPGYAKDGL	PGIPGPQGET
1290	1300	1310	1320				
GPAGHPGLPG	PPGPPGQCDP	SQCAYFASLA	ARPGNVKGP				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1945	1	927.8884	-53.65	2	53.0	13.2	0	1249-1267	R.GEMGPPGIPGQPGEPGYAK.D	Oxidation: 3

Detailed Protein Report

Protein 616: PREDICTED: alpha-tectorin isoform X1 [Homo sapiens]

Accession:	gi|530398338	**Score:**	25.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	238.8
Database Date:	2015-11-30	**pI:**	5.1
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.3
		No. of unique Peptides:	1

Quantitation

Wdown:Qdown	**Median:** 1.63	**CV:** 0.00 %	**No. of Peptides:**	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MNYSSFLRIW	VSFIFALVQH	QAQPRELMYP	FWQNDTKTPK	VDDGSSSEIK	LAIPVFFFGV	PYRTVYVNNN	GVVSFNVLVS
90	100	110	120	130	140	150	160
QFTPESFPLT	DGRAFVAPFW	ADVHNGIRGE	IYYRETMEPA	ILKRATKDIR	KYFKDMATFS	ATWVFIVTWE	EVTFYGGSST
170	180	190	200	210	220	230	240
TPVNTFQAVL	VSDGSYTFTL	FNYYEINWTT	GTASGGDPLT	GLGGVMAQAG	FNGGNLTNFF	SLPGSRTPEI	VNIQETTNVN
250	260	270	280	290	300	310	320
VPGRWAFKVD	GKEIDPANGC	TSRGQFLRRG	EVFWDDLNCT	VKCRCLDFNN	EIYCQEASCS	PYEVCEPKGK	FFYCSAVETS
330	340	350	360	370	380	390	400
TCVVFGEPHY	HTFDGFLFHF	QGSCAYLLAR	QCLQTSSLPF	FSVEAKNEHR	RGSAVSWVKE	LSVEVNGYKI	LIPKGSYGRV
410	420	430	440	450	460	470	480
KVNDLVTSLP	VTLDLGTVKI	YQSGISTAVE	TDFGLLVTFD	GQHYASISVP	GSYINSTCGL	CGNYNKNPLD	DFLRPDGRPA
490	500	510	520	530	540	550	560
MSVLDLGESW	RVYHADWKCD	SGCVDNCTQC	DAATEALYFG	SDYCGFLNKT	DGPLWECGTV	VDPTAFVHSC	VYDLCSVRDN
570	580	590	600	610	620	630	640
GTLLCQAIQA	YALVCQALGI	PIGDWRTQTG	CVSTVQCPSF	SHYSVCTSSC	PDTCSDLTAS	RNCATPCTEG	CECNQGFVLS
650	660	670	680	690	700	710	720
TSQCVPLHKC	GCDFDGHYYT	MGEFFWATAN	CTVQCLCEEG	GDVYCFNKTC	GSGEVCAVED	GYQGCFPKRE	TVCLLSQNQV
730	740	750	760	770	780	790	800
LHTFDGASYA	FPSEFSYTLL	KTCPERPEYL	EIDINKKKPD	AGPAWLRGLR	ILVADQEVKI	GGIGASEVKL	NGQEVELPFF
810	820	830	840	850	860	870	880
HPSGKLEIYR	NKNSTTVESK	GVVTVQYSDI	GLLYIRLSTT	YFNCTGGLCG	FYNANASDEF	CLPNGKCTDN	LAVFLESWTT
890	900	910	920	930	940	950	960
FEEICNGECG	DLLKACNNDS	ELLKFYRSRS	RCGIINDPSN	SSFLECHGVV	NVTAYYRTCL	FRLCQSGGNE	SELCDSVARY
970	980	990	1000	1010	1020	1030	1040
ASACKNADVE	VGPWRTYDFC	PLECPENSHF	EECITCTETC	ETLTLGPICV	DSCSEGCQCD	EGYALLGSQC	VTRSECGCNF
1050	1060	1070	1080	1090	1100	1110	1120
EGHQLATNET	FWVDLDCQIF	CYCSGTDNRV	HCETIPCKDD	EYCMEEGGLY	YCQARTDASC	IVSGYGHYLT	FDGFPFDFQT
1130	1140	1150	1160	1170	1180	1190	1200
SCPLILCTTG	SRPSSDSFPK	FVVTAKNEDR	DPSLALWVKQ	VDVTVFGYSI	VIHRAYKHTV	LVNSERLYLP	LKLGQGKINI
1210	1220	1230	1240	1250	1260	1270	1280
FSFGFHVVVE	TDFGLKVVYD	WKTFLSITVP	RSMQNSTYGL	CGRYNGNPDD	DLEMPMGLLA	SSVNEFGQSW	VKRDTFCQVG
1290	1300	1310	1320	1330	1340	1350	1360
CGDRCPSCAK	VEGFSKVQQL	CSLIPNQNAA	FSKCHSKVNP	TFFYKNCLFD	SCIDGGAVQT	ACSWLQNYAS	TCQTQGITVT
1370	1380	1390	1400	1410	1420	1430	1440
GWRNYTSCTV	TCPPNSHYES	CVSVCQPRCA	AIRLKSDCSH	YCVEGCHCDA	GYVLNGKSCI	LPHSCGCYSD	GKYYEPKQLF
1450	1460	1470	1480	1490	1500	1510	1520
WNSDCTRRCR	CFRRNVIQCD	PRQCKSDEEC	ALRNGVRGCF	STKTSYCLAA	GGGVFRTFDG	AFLRFPANCA	FVLSTICQKL
1530	1540	1550	1560	1570	1580	1590	1600
PDISFQLIIN	FDKWSAPNLT	IISPVYFYIN	EEQILINDRN	TVKVNGTQVN	VPFITGLATK	IYSSEGFLVI	DTSPDIQIYY
1610	1620	1630	1640	1650	1660	1670	1680
NGFNVIKISI	SERLQNKVCG	LCGNFNGDLT	DDYVTLRGKP	VVSSVVLAQS	WKTNGMQKSC	NELQFSQYAA	MCDNVHIQKM
1690	1700	1710	1720	1730	1740	1750	1760
QGDGYCLKLT	DMKGFFQPCY	GLLDPLPFYE	SCYLDGCYSH	KKFQLCGSLA	AYGEACRSFG	ILSTEWIEKE	NCSGVVEDPC
1770	1780	1790	1800	1810	1820	1830	1840
VGADCPNRTC	ELGNGRELCG	CIEPPPYGNN	SHDIIDAEVT	CKAAQMEVSI	SKCKLFQLGF	EREGVRINDR	QCTGIEGEDF
1850	1860	1870	1880	1890	1900	1910	1920
ISFQINNTKG	NCGNIVQSNG	THIMYKNTLW	IESANNTGNI	ITRDRTINVE	FSCAYELDIK	ISLDSVVKPM	LSVINLTVPT
1930	1940	1950	1960	1970	1980	1990	2000
QEGSFITKMA	LYKNASYKHP	YRQGEVVLTT	RDVLYVGVFV	VGADATHLIL	TLNKCYATPT	RDSNDKLRYF	IIEGGCQNLK
2010	2020	2030	2040	2050	2060	2070	2080
DNTIGIEENA	VSLTCRFHVT	VFKFIGDYDE	VHLHCAVSLC	DSEKYSCKIT	CPHNSRIATD	YTKEPKEQII	SVGPIRRKRL
2090	2100	2110	2120	2130	2140	2150	2160
DWCEDNGGCE	QICTSRVDGP	LCSCVTGTLQ	EDGKSCRASN	SSMELQVWTL	LLIMIQISLW	HFVYKSGTTS	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
132	1	673.3206	73.69	3	30.4	10.7	1	1274-1290	R.DTFCQVGCGDRCPSCAK.V	Carbamidomethyl: 4, 8, 12, 15	Wdown:Qdown 1.63

Detailed Protein Report

Protein 617: PREDICTED: protein TANC2 isoform X9 [Homo sapiens]

Accession:	gi|578830697	**Score:**	25.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	154.7
Database Date:	2015-11-30	**pI:**	8.9
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MFRNSLKMLL	TGGKSSRKNR	SSDGGSEEPP	DRRQSSVDSR	QSRSGQGGIS	TESDCAFEPD	YAVPPLPVSE	GMQHIRIMEG
90	100	110	120	130	140	150	160
MSRSLPSSPL	LTHQSISVRL	QPVKKLTAPL	RKAKFVESPR	IPESELGSPT	LTSAQKLDVD	AYCPGDAEQE	LGPPPSVDEA
170	180	190	200	210	220	230	240
ANTLMTRLGF	LLGEKVTEVQ	PGDQYSMEVQ	DENQTSAITQ	RISPCSTLTS	STASPPASSP	CSTLPPISTN	ATAKDCSYGA
250	260	270	280	290	300	310	320
VTSPTSTLES	RDSGIIATLT	SYSENVERTK	YAGESSKELG	SGGNIKPWQS	QKSSMDSCLY	RVDENMTAST	YSLNKIPERN
330	340	350	360	370	380	390	400
LETVLSQSVQ	SIPLYLMPRP	NSVAATSSAH	LEDLAYLDEQ	RHTPLRTSLR	MPRQSMGGAR	TQQDLRVRFA	PYRPPDISLK
410	420	430	440	450	460	470	480
PLLFEVPSIT	TESVFVGRDW	VFHEIDAQLQ	SSNASVNQGV	VIVGNIGFGK	TAIISRLVAL	SCHGTRMRQI	ASDSPHASPK
490	500	510	520	530	540	550	560
HVDANRELPL	TQPPSAHSSI	TSGSCPGTPE	MRRRQEEAMR	RLASQVVAYH	YCQADNAYTC	LVPEFVHNVA	ALLCRSPQLT
570	580	590	600	610	620	630	640
AYREQLLREP	HLQSMLSLRS	CVQDPMASFR	RGVLEPLENL	HKERKIPDED	FIILIDGLNE	AEFHKPDYGD	TIVSFLSKMI
650	660	670	680	690	700	710	720
GKFPSWLKLI	VTVRTSLQEI	TKLLPFHRIF	LDRLEENEAI	DQDLQAYILH	RIHSSSEIQN	NISLNGKMDN	TTFGKLSSHL
730	740	750	760	770	780	790	800
KTLSQGSYLY	LKLTFDLIEK	GYLVLKSSSY	KVVPVSLSEV	YLLQCNMKFP	TQSSFDRVMP	LLNVAVASLH	PLTDEHIFQA
810	820	830	840	850	860	870	880
INAGSIEGTL	EWEDFQQRME	NLSMFLIKRR	DMTRMFVHPS	FREWLIWREE	GEKTKFLCDP	RSGHTLLAFW	FSRQEGKLNR
890	900	910	920	930	940	950	960
QQTIELGHHI	LKAHIFKGLS	KKVGVSSSIL	QGLWISYSTE	GLSMALASLR	NLYTPNIKVS	RLLILGGANI	NYRTEVLNNA
970	980	990	1000	1010	1020	1030	1040
PILCVQSHLG	YTEMVALLLE	FGANVDASSE	SGLTPLGYAA	AAGYLSIVVL	LCKKRAKVDH	LDKNGQCALV	HAALRGHLEV
1050	1060	1070	1080	1090	1100	1110	1120
VKFLIQCDWT	MAGQQQGVFK	KSHAIQQALI	AAASMGYTEI	VSYLLDLPEK	DEEEVERAQI	NSFDSLWGET	ALTAAAGRGK
1130	1140	1150	1160	1170	1180	1190	1200
LEVCRLLLEQ	GAAVAQPNRR	GAVPLFSTVR	QGHWQIVDLL	LTHGADVNMA	DKQGRTPLMM	AASEGHLGTV	DFLLAQGASI
1210	1220	1230	1240	1250	1260	1270	1280
ALMDKEGLTA	LSWACLKGHL	SVVRSLVDNG	AATDHADKNG	RTPLDLAAFY	GDAEVVQFLV	DHGAMIEHVD	YSGMRPLDRA
1290	1300	1310	1320	1330	1340	1350	1360
VGCRNTSVVV	TLLKKGAKIG	PATWAMATSK	PDIMIILLSK	LMEEGDMFYK	KGKVKEAAQR	YQYALKKFPR	EGFGEDLKTF
1370	1380	1390	1400				
RELKVSLLLN	LSRCRRKMNT	VRSSLRGPER	GHQAVSQQP				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1044	1	983.4577	-74.07	2	41.8	11.9	1	564-579	R.EQLLREPHLQSMLSLR.S	Oxidation: 12

Detailed Protein Report

Protein 618: kinase D-interacting substrate of 220 kDa [Homo sapiens]

Accession:	gi|55741641	**Score:**	25.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	196.4
Database Date:	2015-11-30	**pI:**	6.2
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSVLISQSVI	NYVEEENIPA	LKALLEKCKD	VDERNECGQT	PLMIAAEQGN	LEIVKELIKN	GANCNLEDLD	NWTALISASK
90	100	110	120	130	140	150	160
EGHVHIVEEL	LKCGVNLEHR	DMGGWTALMW	ACYKGRTDVV	ELLLSHGANP	SVTGLYSVYP	IIWAAGRGHA	DIVHLLLQNG
170	180	190	200	210	220	230	240
AKVNCSDKYG	TTPLVWAARK	GHLECVKHLL	AMGADVDQEG	ANSMTALIVA	VKGGYTQSVK	EILKRNPNVN	LTDKDGNTAL
250	260	270	280	290	300	310	320
MIASKEGHTE	IVQDLLDAGT	YVNIPDRSGD	TVLIGAVRGG	HVEIVRALLQ	KYADIDIRGQ	DNKTALYWAV	EKGNATMVRD
330	340	350	360	370	380	390	400
ILQCNPDTEI	CTKDGETPLI	KATKMRNIEV	VELLLDKGAK	VSAVDKKGDT	PLHIAIRGRS	RKLAELLLRN	PKDGRLLYRP
410	420	430	440	450	460	470	480
NKAGETPYNI	DCSHQKSILT	QIFGARHLSP	TETDGDMLGY	DLYSSALADI	LSEPTMQPPI	CVGLYAQWGS	GKSFLLKKLE
490	500	510	520	530	540	550	560
DEMKTFAGQQ	IEPLFQFSWL	IVFLTLLLCG	GLGLLFAFTV	HPNLGIAVSL	SFLALLYIFF	IVIYFGGRRE	GESWNWAWVL
570	580	590	600	610	620	630	640
STRLARHIGY	LELLLKLMFV	NPPELPEQTT	KALPVRFLFT	DYNRLSSVGG	ETSLAEMIAT	LSDACEREFG	FLATRLFRVF
650	660	670	680	690	700	710	720
KTEDTQGKKK	WKKTCCLPSF	VIFLFIIGCI	ISGITLLAIF	RVDPKHLTVN	AVLISIASVV	GLAFVLNCRT	WWQVLDSLLN
730	740	750	760	770	780	790	800
SQRKRLHNAA	SKLHKLKSEG	FMKVLKCEVE	LMARMAKTID	SFTQNQTRLV	VIIDGLDACE	QDKVLQMLDT	VRVLFSKGPF
810	820	830	840	850	860	870	880
IAIFASDPHI	IIKAINQNLN	SVLRDSNING	HDYMRNIVHL	PVFLNSRGLS	NARKFLVTSA	TNGDVPCSDT	TGIQEDADRR
890	900	910	920	930	940	950	960
VSQNSLGEMT	KLGSKTALNR	RDTYRRRQMQ	RTITRQMSFD	LTKLLVTEDW	FSDISPQTMR	RLLNIVSVTG	RLLRANQISF
970	980	990	1000	1010	1020	1030	1040
NWDRLASWIN	LTEQWPYRTS	WLILYLEETE	GIPDQMTLKT	IYERISKNIP	TTKDVEPLLE	IDGDIRNFEV	FLSSRTPVLV
1050	1060	1070	1080	1090	1100	1110	1120
ARDVKVFLPC	TVNLDPKLRE	IIADVRAARE	QISIGGLAYP	PLPLHEGPPR	APSGYSQPPS	VCSSTSFNGP	FAGGVVSPQP
1130	1140	1150	1160	1170	1180	1190	1200
HSSYYSGMTG	PQHPFYNRPF	FAPYLYTPRY	YPGGSQHLIS	RPSVKTSLPR	DQNNGLEVIK	EDAAEGLSSP	TDSSRGSGPA
1210	1220	1230	1240	1250	1260	1270	1280
PGPVVLLNSL	NVDAVCEKLK	QIEGLDQSML	PQYCTTIKKA	NINGRVLAQC	NIDELKKEMN	MNFGDWHLFR	STVLEMRNAE
1290	1300	1310	1320	1330	1340	1350	1360
SHVVPEDPRF	LSESSSGPAP	HGEPARRASH	NELPHTELSS	QTPYTLNFSF	EELNTLGLDE	GAPRHSNLSW	QSQTRRTPSL
1370	1380	1390	1400	1410	1420	1430	1440
SSLNSQDSSI	EISKLTDKVQ	AEYRDAYREY	IAQMSQLEGG	PGSTTISGRS	SPHSTYYMGQ	SSSGGSIHSN	LEQEKGKDSE
1450	1460	1470	1480	1490	1500	1510	1520
PKPDDGRKSF	LMKRGDVIDY	SSSGVSTNDA	SPLDPITEED	EKSDQSGSKL	LPGKKSSERS	SLFQTDLKLK	GSGLRYQKLP
1530	1540	1550	1560	1570	1580	1590	1600
SDEDESGTEE	SDNTPLLKDD	KDRKAEGKVE	RVPKSPEHSA	EPIRTFIKAK	EYLSDALLDK	KDSSDSGVRS	SESSPNHSLH
1610	1620	1630	1640	1650	1660	1670	1680
NEVADDSQLE	KANLIELEDD	SHSGKRGIPH	SLSGLQDPII	ARMSICSEDK	KSPSECSLIA	SSPEENWPAC	QKAYNLNRTP
1690	1700	1710	1720	1730	1740	1750	1760
STVTLNNNSA	PANRANQNFD	EMEGIRETSQ	VILRPSSSPN	PTTIQNENLK	SMTHKRSQRS	SYTRLSKDPP	ELHAAASSES
1770	1780						
TGFGEERESI	L						

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

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 619: sterile alpha motif domain-containing protein 9 [Homo sapiens]

Accession:	gi|38201706	**Score:**	25.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	184.2
Database Date:	2015-11-30	**pI:**	8.7
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	2.1
		No. of unique Peptides:	2

Quantitation

mdown:qdown	**Median:**	1.09	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	1.76	**CV:**	0.00 %	**No. of 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
```

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2028	2	840.7762	-104.20	2	55.5	13.9	0	118-133	K.ENPDMANPSAMSTTAK.G	Oxidation: 5	
1785	1	660.9025	-122.86	3	50.8	11.7	0	714-731	R.LEAMIQNCADSSKPTSTK.I	Carbamidomethyl: 8	Wdown:Qdown 1.76 mdown:qdown 1.09

Detailed Protein Report

Protein 620: **regulator of G-protein signaling 12 isoform 2 [Homo sapiens]**

Accession:	gi|4506509	**Score:**	25.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	149.5
Database Date:	2015-11-30	**pI:**	8.0
		Sequence Coverage [%]:	2.3
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	1.47	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	1.74	**CV:**	0.00 %	**No. of Peptides:**	1

10	20	30	40	50	60	70	80
MFRAGEASKR	PLPGPSPPRV	RSVEVARGRA	GYGFTLSGQA	PCVLSCVMRG	SPADFVGLRA	GDQILAVNEI	NVKKASHEDV
90	100	110	120	130	140	150	160
VKLIGKCSGV	LHMVIAEGVG	RFESCSSDEE	GGLYEGKGWL	KPKLDSKALG	INRAERVVEE	MQSGGIFNMI	FENPSLCASN
170	180	190	200	210	220	230	240
SEPLKLKQRS	LSESAATRFD	VGHESINNPN	PNMLSKEEIS	KVIHDDSVFS	IGLESHDDFA	LDASILNVAM	IVGYLGSIEL
250	260	270	280	290	300	310	320
PSTSSNLESD	SLQAIRGCMR	RLRAEQKIHS	LVTMKIMHDC	VQLSTDKAGV	VAEYPAEKLA	FSAVCPDDRR	FFGLVTMQTN
330	340	350	360	370	380	390	400
DDGSLAQEEE	GALRTSCHVF	MVDPDLFNHK	IHQGIARRFG	FECTADPDTN	GCLEFPASSL	PVLQFISVLY	RDMGELIEGM
410	420	430	440	450	460	470	480
RARAFLDGDA	DAHQNNSTSS	NSDSGIGNFH	QEEKSNRVLV	VDLGGSSSRH	GPGGSAWDGV	GGRGAQPWGA	PWTGPFCPDP
490	500	510	520	530	540	550	560
EGSPPFEAAH	QTDRFWDLNK	HLGPASPVEV	PPASLRSSVP	PSKRGTVGAG	CGFNQRWLPV	HVLREWQCGH	TSDQDSYTDS
570	580	590	600	610	620	630	640
TDGWSSINCG	TLPPPMSKIP	ADRYRVEGSF	AQPPLNAPKR	EWSRKAFGMQ	SIFGPHRNVR	KTKEDKKGSK	FGRGTGLTQP
650	660	670	680	690	700	710	720
SQRTSARRSF	GRSKRFSITR	SLDDLESATV	SDGELTGADL	KDCVSNNSLS	SNASLPSVQS	CRRLRERRVA	SWAVSFERLL
730	740	750	760	770	780	790	800
QDPVGVRYFS	DFLRKEFSEE	NILFWQACEY	FNHVPAHDKK	ELSYRAREIF	SKFLCSKATT	PVNIDSQAQL	ADDVLRAPHP
810	820	830	840	850	860	870	880
DMFKEQQLQI	FNLMKFDSYT	RFLKSPLYQE	CILAEVEGRA	LPDSQQVPSS	PASKHSLGSD	HSSVSTPKKL	SGKSKSGRSL
890	900	910	920	930	940	950	960
NEELGDEDSE	KKRKGAFFSW	SRTRSTGRSQ	KKREHGDHAD	DALHANGGLC	RRESQGSVSS	AGSLDLSEAC	RTLAPEKDKA
970	980	990	1000	1010	1020	1030	1040
TKHCCIHLPD	GTSCVVAVKA	GFSIKDILSG	LCERHGINGA	AADLFLVGGD	KPLVLHQDSS	ILESRDLRLE	KRTLFRLDLV
1050	1060	1070	1080	1090	1100	1110	1120
PINRSVGLKA	KPTKPVTEVL	RPVVARYGLD	LSGLLVRLSG	EKEPLDLGAP	ISSLDGQRVV	LEEKDPSRGK	ASADKQKGVP
1130	1140	1150	1160	1170	1180	1190	1200
VKQNTAVNSS	SRNHSATGEE	RTLGKSNSIK	IKGENGKNAR	DPRLSKREES	IAKIGKKKYQ	KINLDEAEEF	FELISKAQSN
1210	1220	1230	1240	1250	1260	1270	1280
RADDQRGLLR	KEDLVLPEFL	RLPPGSTELT	LPTPAAVAKG	FSKRSATGNG	RESASQPGEQ	WEPVQESSDS	PSTSPGSASS
1290	1300	1310	1320	1330	1340	1350	1360
PPGPPGTTPP	GQKSPSGPFC	TPQSPVSLAQ	EGTAQIWKRQ	SQEVEAGGIQ	TVEDEHVAEL	TLMGEGDISS	PNSTLLPPPS
1370	1380						
TPQEVPGPSR	PGTSRF						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
592	1	607.1554	-246.73	2	36.0	14.3	2	1153-1163	K.GENGKNARDPR.L		mdown:qdown 1.47 Wdown:Qdown 1.74

Detailed Protein Report

Protein 621: PREDICTED: protein MAATS1 isoform X2 [Homo sapiens]

Accession:	gi|578807867	**Score:**	25.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	62.4
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
MIERAREKRA	WEASLPALSD	TSQFEKRRKM	MNEMERKEWA	FREQEIEKLQ	EIRLEVLKEL	LRKREENQNE	VNMKHLNARW
90	100	110	120	130	140	150	160
SKLQEGKEAK	MAKIQRTHVS	SNAIRKLVGK	RKNIEGKLER	RNIIKDYSDY	ASQVYGPLSR	LGCFPDNNSE	DFVVKNYYLN
170	180	190	200	210	220	230	240
TYEGLVELES	CLPDFVTQPQ	IRAPKPKVIT	TKAGFLKRAA	RLDYELAEVH	KALLDKKNKV	LEVKKPPRFL	QRNPIPQPRL
250	260	270	280	290	300	310	320
PTPTLEMTSN	EEEEMEMAVI	YLQKLLRGRV	VQNMMFEGKE	KRLELIQELR	TCHALQEDEK	LVKKAEKQVT	LALQRQRNLH
330	340	350	360	370	380	390	400
EHKVSLVENH	LAGLEGRALA	DMFDFLSKEL	VRLQEERRIH	AFVMLAERQR	RVREAEESGR	RQVEKQRLRE	EDEIFKEVVK
410	420	430	440	450	460	470	480
VHHSTISSYL	EDIILNTEAN	TAEEQARAEI	EKMAEKINDI	AYEMESRRTY	LQSEEIVAEL	VYSFLIPEVQ	KYFVKEKVRN
490	500	510	520	530	540		
AQRKHILAAH	QIIHSYTESM	VQKKLTEGEQ	DEASNAAMLL	EKETQNENNS			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2124	1	652.6392	-14.46	3	55.1	11.1	2	433-448	K.MAEKINDIAYEMESRR.T	

Detailed Protein Report

Protein 622: **catenin delta-2 isoform 4 [Homo sapiens]**

Accession:	gi|570359551	**Score:**	25.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	87.2
Database Date:	2015-11-30	**pI:**	9.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	5.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MRSLSQSQGD	PLPPAHTGTY	RTSTAPSSPG	VDSVPLQRTG	SQHGPQNAAA	ATFQRASYAA	GPASNYADPY	RQLQYCPSVE
90	100	110	120	130	140	150	160
SPYSKSGPAL	PPEGTLARSP	SIDSIQKDPR	EFGWRDPELP	EVIQMLQHQF	PSVQSNAAAY	LQHLCFGDNK	IKAEIRRQGG
170	180	190	200	210	220	230	240
IQLLVDLLDH	RMTEVHRSAC	GALRNLVYGK	ANDDNKIALK	NCGGIPALVR	LLRKTTDLEI	RELVTGVLWN	LSSCDALKMP
250	260	270	280	290	300	310	320
IIQDALAVLT	NAVIIPHSGW	ENSPLQDDRK	IQLHSSQVLR	NATGCLRNVS	SAGEEARRRM	RECDGLTDAL	LYVIQSALGS
330	340	350	360	370	380	390	400
SEIDSKTVEN	CVCILRNLSY	RLAAETSQGQ	HMGTDELDGL	LCGEANGKDA	ESSGCWGKKK	KKKKSQDQWD	GVGPLPDCAE
410	420	430	440	450	460	470	480
PPKGIQMLWH	PSIVKPYLTL	LSECSNPDTL	EGAAGALQNL	AAGSWKWSVY	IRAAVRKEKG	LPILVELLRI	DNDRVVCAVA
490	500	510	520	530	540	550	560
TALRNMALDV	RNKELIGKYA	MRDLVHRLPG	GNNSNNTASK	AMSDDTVTAV	CCTLHEVITK	NMENAKALRD	AGGIEKLVGI
570	580	590	600	610	620	630	640
SKSKGDKHSP	KVVKAASQVL	NSMWQYRDLR	SLYKKDGWSQ	YHFVASSSTI	ERDRQRPYSS	SRTPSISPVR	VSPNNRSASA
650	660	670	680	690	700	710	720
PASPREMISL	KERKTDYECT	GSNATYHGAK	GEHTSRKDAM	TAQNTGISTL	YRNSYGAPAE	DIKHNQVSAQ	PVPQEPSRKD
730	740	750	760	770	780	790	800
YETYQPFQNS	TRNYDESFFE	DQVHHRPPAS	EYTMHLGLKS	TGNYVDFYSA	ARPYSELNYE	TSHYPASPDS	WV

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
292	1	1293.8398	-46.50	3	32.8	12.9	1	342-378	R.LAAETSQGQHMGTDELDGLLCGEANGKDAESSGCWGK.K	Carbamidomethyl: 21, 34

Detailed Protein Report

Protein 623: vacuole membrane protein 1 [Homo sapiens]

Accession:	gi|20070349	**Score:**	25.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	46.2
Database Date:	2015-11-30	**pI:**	6.5
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	7.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAENGKNCDQ	RRVAMNKEHH	NGNFTDPSSV	NEKKRREREE	RQNIVLWRQP	LITLQYFSLE	ILVILKEWTS	KLWHRQSIVV
90	100	110	120	130	140	150	160
SFLLLLAVLI	ATYYVEGVHQ	QYVQRIEKQF	LLYAYWIGLG	ILSSVGLGTG	LHTFLLYLGP	HIASVTLAAY	ECNSVNFPEP
170	180	190	200	210	220	230	240
PYPDQIICPD	EEGTEGTISL	WSIISKVRIE	ACMWGIGTAI	GELPPYFMAR	AARLSGAEPD	DEEYQEFEEM	LEHAESAQDF
250	260	270	280	290	300	310	320
ASRAKLAVQK	LVQKVGFFGI	LACASIPNPL	FDLAGITCGH	FLVPFWTFFG	ATLIGKAIIK	MHIQKIFVII	TFSKHIVEQM
330	340	350	360	370	380	390	400
VAFIGAVPGI	GPSLQKPFQE	YLEAQRQKLH	HKSEMGTPQG	ENWLSWMFEK	LVVVMVCYFI	LSIINSMAQS	YAKRIQQRLN
410							
SEEKTK							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2411	1	669.6353	-215.87	2	58.5	12.4	1	1-11	-.MAENGKNCDQR.R	Carbamidomethyl: 8; Oxidation: 1

Detailed Protein Report

Protein 624: ubiquitin-like-conjugating enzyme ATG10 [Homo sapiens]

Accession:	gi|18594496	**Score:**	25.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	25.3
Database Date:	2015-11-30	**pI:**	5.3
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	6.8
		No. of unique Peptides:	2

Quantitation

Wdown:Qdown	**Median:** 0.93	**CV:** 0.00 %	**No. of Peptides:** 1

Alias proteins:

Accession	Name	Description
gi|530379522	refseq_human (refseq_human_20140103.fasta)	PREDICTED: ubiquitin-like-conjugating enzyme ATG10 isoform X2 [Homo sapiens]
gi|530379520	refseq_human (refseq_human_20140103.fasta)	PREDICTED: ubiquitin-like-conjugating enzyme ATG10 isoform X1 [Homo sapiens]
gi|196162717	refseq_human (refseq_human_20140103.fasta)	ubiquitin-like-conjugating enzyme ATG10 [Homo sapiens]

10	20	30	40	50	60	70	80
MEEDEFIGEK	TFQRYCAEFI	KHSQQIGDSW	EWRPSKDCSD	GYMCKIHFQI	KNGSVMSHLG	ASTHGQTCLP	MEEAFELPLD
90	100	110	120	130	140	150	160
DCEVIETAAA	SEVIKYEYHV	LYSCSYQVPV	LYFRASFLDG	RPLTLKDIWE	GVHECYKMRL	LQGPWDTITQ	QEHPILGQPF
170	180	190	200	210	220	230	
FVLHPCKTNE	FMTPVLKNSQ	KININKNVNYIT	SWLSIVGPVV	GLNLPLSYAK	ATSQDERNVP		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1635	1	576.3013	186.62	2	49.0	10.1	0	37-45	K.DCSDGYMCK.I	Carbamidomethyl: 2, 8; Oxidation: 7	
2921	2	922.9870	83.40	2	65.7	15.3	1	37-51	K.DCSDGYMCKIHFQIK.N	Carbamidomethyl: 2	Wdown:Qdown 0.93

Detailed Protein Report

Protein 625: anaphase-promoting complex subunit 2 [Homo sapiens]

Accession:	gi|7019327	**Score:**	25.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	93.8
Database Date:	2015-11-30	**pI:**	5.0
		Sequence Coverage [%]:	3.2
		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 626: multiple epidermal growth factor-like domains protein 8 isoform 2 precursor [Homo sapiens]

Accession:	gi|145701025	**Score:**	25.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	295.7
Database Date:	2015-11-30	**pI:**	6.5
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	1.6
		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
1779	1	820.8211	-36.25	2	50.8	10.3	1	1000-1012	R.WAYARCPDVDECR.L	Carbamidomethyl: 12

Detailed Protein Report

Protein 627: PREDICTED: protein FAM65C isoform X2 [Homo sapiens]

Accession:	gi|578835791	**Score:**	25.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	105.1
Database Date:	2015-11-30	**pI:**	7.0
		Sequence Coverage [%]:	2.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MVTTMSVRLR	FLSPGDTGAV	GVVGRSASFA	GFSSAQSRRI	ANSVRSRMPA	KSSKMYGTLR	KGSVCADPKP	QQVKKIFEAL
90	100	110	120	130	140	150	160
KRGLKEYLCV	QQAELDHLSG	RHKDTRRNSR	LAFYYDLDKQ	TRCVERHIRK	MEFHISKVDE	LYEDYCIQCR	LRDGASSMQR
170	180	190	200	210	220	230	240
AFARCPPSRA	ARESLQELGR	SLHECAEDMW	LIEGALEVHL	GEFHIRMKGL	VGYARLCPGD	HYEVLMRLGR	QRWKLKGRIE
250	260	270	280	290	300	310	320
SDDSQTWDEE	EKAFIPTLHE	NLDIKVTELR	GLGSLAVGAV	TCDIADFFTT	RPQVIVVDIT	ELGTIKLQLE	VQWNPFDTES
330	340	350	360	370	380	390	400
FLVSPSPTGK	FSMGSRKGSL	YNWTPPSTPS	FRERYYLSVL	QQPTQQALLL	GGPRATSILS	YLSDSDLRGP	SLRSQSQELP
410	420	430	440	450	460	470	480
EMDSFSSEDP	RDTETSTSAS	TSDVGFLPLT	FGPHASIEEE	AREDPLPPGL	LPEMAHLSGG	PFAEQPGWRN	LGGESPSLPQ
490	500	510	520	530	540	550	560
GSLFHSGTAS	SSQNGHEEGA	TGDREDGPGV	ALEGPLQEVL	ELLRPTDSTQ	PQLRELEYQV	LGFRDRLKPC	RARQEHTSAE
570	580	590	600	610	620	630	640
SLMECILESF	AFLNADFALD	ELSLFGGSQG	LRKDRPLPPP	SSLKASSREL	TAGAPELDVL	LMVHLQVCKA	LLQKLASPNL
650	660	670	680	690	700	710	720
SRLVQECLLE	EVAQQKHVLE	TLSVLDFEKV	GKATSIEEII	PQASRTKGCL	KLWRGCTGPG	RVLSCPATTL	LNQLKKTFQH
730	740	750	760	770	780	790	800
RVRGKYPGQL	EIACRRLLEQ	VVSCGGLLPG	AGLPEEQIIT	WFQFHSYLQR	QSVSDLEKHF	TQLTKEVTLI	EELHCAGQAK
810	820	830	840	850	860	870	880
VVRKLQGKRL	GQLQPLPQTL	RAWALLQLDG	TPRVCRAASA	RLAGAVRNRS	FREKALLFYT	NALAENDARL	QQAACLALKH
890	900	910	920	930	940	950	
LKGIESIDQT	ASLCQSDLEA	VRAAARETTL	SFGEKGRLAF	EKMDKLCSEQ	REVFCQEADV	EITIF	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2833	1	651.8526	69.50	2	63.9	12.0	0	26-38	R.SASFAGFSSAQSR.R	

Detailed Protein Report

Protein 628: **type 2 lactosamine alpha-2,3-sialyltransferase isoform 3 [Homo sapiens]**

Accession:	gi|403225032	**Score:**	25.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	43.4
Database Date:	2015-11-30	**pI:**	9.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	8.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MWQAPRERQQ	PAGAAAPQVS	EPGAPLRSSL	LGLGGSLLPA	GFAAGLHCPG	EPAMRGYLVA	IFLSAVFLYY	VLHCILWGTN
90	100	110	120	130	140	150	160
VYWVAPVEMK	RRNKIQPCLS	KPAFASLLRF	HQFHPFLCAA	DFRKIASLYG	SDKFDLPYGM	RTSAEYFRLA	LSKLQSCDLF
170	180	190	200	210	220	230	240
DEFDNIPCKK	CVVVGNGGVL	KNKTLGEKID	SYDVIIRMNN	GPVLGHEEEV	GRRTTFRLFY	PESVFSDPIH	NDPNTTVILT
250	260	270	280	290	300	310	320
AFKPHDLRWL	LELLMGDKIN	TNGFWKKPAL	NLIYKPYQIR	ILDPFIIRTA	AYELLHFPKV	FPKNQKPKHP	TTGIIAITLA
330	340	350	360	370	380	390	
FYICHEVHLA	GFKYNFSDLK	SPLHYYGNAT	MSLMNKNAYH	NVTAEQLFLK	DIIEKNLVIN	LTQD	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
426	1	672.4157	57.87	2	34.6	11.5	1	171-183	K.CVVVGNGGVLKNK.T	Carbamidomethyl: 1

Detailed Protein Report

Protein 629: **G-protein coupled receptor 98 precursor [Homo sapiens]**

Accession:	gi|113722120	**Score:**	25.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	692.6
Database Date:	2015-11-30	**pI:**	4.4
Modification(s):	Oxidation	**Sequence Coverage [%]:**	0.4
		No. of unique Peptides:	2

Detailed Protein Report

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        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
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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
112	2	793.8850	-70.56	2	30.7	12.9	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 630: undifferentiated embryonic cell transcription factor 1 [Homo sapiens]

Accession:	gi|71043876	**Score:**	25.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	36.4
Database Date:	2015-11-30	**pI:**	11.8
		Sequence Coverage [%]:	10.3
		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 631: PREDICTED: DDB1- and CUL4-associated factor 6 isoform X1 [Homo sapiens]

Accession:	gi|530365060	**Score:**	25.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	104.8
Database Date:	2015-11-30	**pI:**	5.1
		Sequence Coverage [%]:	2.0
		No. of unique Peptides:	1

Quantitation

Wdown:Qdown **Median:** 0.46 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MSRGGSYPHL	LWDVRKRSLG	LEDPSRLRSR	YLGRREFIQR	LKLEATLNVH	DGCVNTICWN	DTGEYILSGS	DDTKLVISNP
90	100	110	120	130	140	150	160
YSRKVLTTIR	SGHRANIFSA	KFLPCTNDKQ	IVSCSGDGVI	FYTNVEQDAE	TNRQCQFTCH	YGTTYEIMTV	PNDPYTFLSC
170	180	190	200	210	220	230	240
GEDGTVRWFD	TRIKTSCTKE	DCKDDILINC	RRAATSVAIC	PPIPYYLAVG	CSDSSVRIYD	RRMLGTRATG	NYAGRGTTGM
250	260	270	280	290	300	310	320
VARFIPSHLN	NKSCRVTSLC	YSEDGQEILV	SYSSDYIYLF	DPKDDTAREL	KTPSAEERRE	ELRQPPVKRL	RLRGDWSDTG
330	340	350	360	370	380	390	400
PRARPESERE	RDGEQSPNVS	LMQRMSDMLS	RWFEEASEVA	QSNRGRGRSR	PRGGTSQSDI	STLPTVPSSP	DLEVSETAME
410	420	430	440	450	460	470	480
VDTPAEQFLQ	PSTSSTMSAQ	AHSTSSPTES	PHSTPLLSSP	DSEQRQSVEA	SGHHTHHQSE	FLRGPEIALL	RKRLQQLRLK
490	500	510	520	530	540	550	560
KAEQQRQQEL	AAHTQQQPST	SDQSSHEGSS	QDPHASDSPS	SVVNKQLGSM	SLDEQQDNNN	EKLSPKPGTG	EPVLSLHYST
570	580	590	600	610	620	630	640
EGTTTSTIKL	NFTDEWSSIA	SSSRGIGSHC	KSEGQEESFV	PQSSVQPPEG	DSETKAPEES	SEDVTKYQEG	VSAENPVENH
650	660	670	680	690	700	710	720
INITQSDKFT	AKPLDSNSGE	RNDLNLDRSC	GVPEESASSE	KAKEPETSDQ	TSTESATNEN	NTNPEPQFQT	EATGPSAHEE
730	740	750	760	770	780	790	800
TSTRDSALQD	TDDSDDDPVL	IPGARYRAGP	GDRRSAVARI	QEFFRRRKER	KEMEELDTLN	IRRPLVKMVY	KGHRNSRTMI
810	820	830	840	850	860	870	880
KEANFWGANF	VMSGSDCGHI	FIWDRHTAEH	LMLLEADNHV	VNCLQPHPFD	PILASSGIDY	DIKIWSPLEE	SRIFNRKLAD
890	900	910	920	930	940		
EVITRNELML	EETRNTITVP	ASFMLRMLAS	LNHIRADRLE	GDRSEGSGQE	NENEDEE		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1173	1	500.6606	-275.48	2	43.3	13.4	2	479-486	R.LKKAEQQR.Q		Wdown:Qdown 0.46

Detailed Protein Report

Protein 632: PREDICTED: enhancer of polycomb homolog 2 isoform X1 [Homo sapiens]

Accession:	gi|578804049	**Score:**	25.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	77.3
Database Date:	2015-11-30	**pI:**	9.9
		Sequence Coverage [%]:	4.8
		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 633: **treacle protein isoform b [Homo sapiens]**

Accession: gi|57164975
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 25.3
MW [kDa]: 144.2
pI: 9.6
Sequence Coverage [%]: 1.9
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MAEARKRREL	LPLIYHHLLR	AGYVRAAREV	KEQSGQKCFL	AQPVTLLDIY	THWQQTSELG	RKRKAEEDAA	LQAKKTRVSD
90	100	110	120	130	140	150	160
PISTSESSEE	EEEAEAETAK	ATPRLASTNS	SVLGADLPSS	MKEKAKAETE	KAGKTGNSMP	HPATGKTVAN	LLSGKSPRKS
170	180	190	200	210	220	230	240
AEPSANTTLV	SETEEEGSVP	AFGAAAKPGM	VSAGQADSSS	EDTSSSSDET	DVEVKASEKI	LQVRAASAPA	KGTPGKGATP
250	260	270	280	290	300	310	320
APPGKAGAVA	SQTKAGKPEE	DSESSSEESS	DSEEETPAAK	ALLQAKASGK	TSQVGAASAP	AKESPRKGAA	PAPPGKTGPA
330	340	350	360	370	380	390	400
VAKAQAGKRE	EDSQSSSEES	DSEEEAPAQA	KPSGKAPQVR	AASAPAKESP	RKGAAPAPPR	KTGPAAAQVQ	VGKQEEDSRS
410	420	430	440	450	460	470	480
SSEESDSDRE	ALAAMNAAQV	KPLGKSPQVK	PASTMGMGPL	GKGAGPVPPG	KVGPATPSAQ	VGKWEEDSES	SSEESSDSSD
490	500	510	520	530	540	550	560
GEVPTAVAPA	QEKSLGNILQ	AKPTSSPAKG	PPQKAGPVAV	QVKAEKPMDN	SESSEESSDS	ADSEEAPAAM	TAAQAKPALK
570	580	590	600	610	620	630	640
IPQTKACPKK	TNTTASAKVA	PVRVGTQAPR	KAGTATSPAG	SSPAVAGGTQ	RPAEDSSSSE	ESDSEEEKTG	LAVTVGQAKS
650	660	670	680	690	700	710	720
VGKGLQVKAA	SVPVKGSLGQ	GTAPVLPGKT	GPTVTQVKAE	KQEDSESSEE	ESDSEEAAAS	PAQVKTSVKK	TQAKANPAAA
730	740	750	760	770	780	790	800
RAPSAKGTIS	APGKVVTAAA	QAKQRSPSKV	KPPVRNPQNS	TVLARGPASV	PSVGKAVATA	AQAQTGPEED	SGSSEEESDS
810	820	830	840	850	860	870	880
EEEAETLAQV	KPSGKTHQIR	AALAPAKESP	RKGAAPTPPG	KTGPSAAQAG	KQDDSGSSSE	ESDSDGEAPA	AVTSAQVIKP
890	900	910	920	930	940	950	960
PLIFVDPNRS	PAGPAATPAQ	AQAASTPRKA	RASESTARSS	SSESEDEDVI	PATQCLTPGI	RTNVVTMPTA	HPRIAPKASM
970	980	990	1000	1010	1020	1030	1040
AGASSSKESS	RISDGKKQEG	PATQVSKKNP	ASLPLTQAAL	KVLAQKASEA	QPPVARTQPS	SGVDSAVGTL	PATSPQSTSV
1050	1060	1070	1080	1090	1100	1110	1120
QAKGTNKLRK	PKLPEVQQAT	KAPESSDDSE	DSSDSSSGSE	EDGEGPQGAK	SAHTLGPTPS	RTETLVEETA	AESSEDDVVA
1130	1140	1150	1160	1170	1180	1190	1200
PSQSLLSGYM	TPGLTPANSQ	ASKATPKLDS	SPSVSSTLAA	KDDPDGKQEA	KPQQAAGMLS	PKTGGKEAAS	GTTPQKSRKP
1210	1220	1230	1240	1250	1260	1270	1280
KKGAGNPQAS	TLALQSNITQ	CLLGQPWPLN	EAQVQASVVK	VLTELLEQER	KKVVDTTKES	SRKGWESRKR	KLSGDQPAAR
1290	1300	1310	1320	1330	1340	1350	1360
TPRSKKKKKL	GAGEGGEASV	SPEKTSTTSK	GKAKRDKASG	DVKEKKGKGS	LGSQGAKDEP	EEELQKGMGT	VEGGDQSNPK
1370	1380	1390	1400	1410	1420		
SKKEKKKSDK	RKKDKEKKEK	KKKAKKASTK	DSESPSQKKK	KKKKKTAEQT	V		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2600	1	625.2017	-222.77	2	60.8	10.7	2	1252-1262	K.KVVDTTKESSR.K	

Detailed Protein Report

Protein 634: **PREDICTED: G protein-coupled receptor kinase 4 isoform X4 [Homo sapiens]**

Accession:	gi|530376052	**Score:**	25.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	50.8
Database Date:	2015-11-30	**pI:**	9.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	8.0
		No. of unique Peptides:	1

Quantitation

mdown:qdown **Median:** 0.52 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MELENIVANS	LLLKARQGGY	GKKSGRSKKW	KEILTLPPVS	QCSELRHSIE	KDYSSLCDKQ	PIGRRLFRQF	CDTKPTLKRH
90	100	110	120	130	140	150	160
IEFLDAVAEY	EVADDEDRSD	CGLSILDRFF	NDKLAAPLPE	IPPDVVTECR	LGLKEENPSK	KAFEECTRVA	HNYLRGEPFE
170	180	190	200	210	220	230	240
EYQESSYFSQ	FLQWKWLERQ	PVTKNTFRHY	RVLGKGGFGE	VCACQVRATG	KMYACKKLQK	KRIKKRKGEA	MALNEKRILE
250	260	270	280	290	300	310	320
KVQSRFVVSL	AYAYETKDAL	CLVLTIMNGG	DLKFHIYNLG	NPGFDEQRAV	FYAAELCCGL	EDLQRERIVY	RDLKPENILL
330	340	350	360	370	380	390	400
DDRGHIRISD	LGLATEIPEG	QRVRGRVGTV	GYMAPEVVNN	EKYTFSPDWW	GLGCLIYEMI	QGHSPFKKYK	EKVKWEEVDQ
410	420	430	440	450			
RIKNDTEEYS	EKFSEDAKSI	CRMGCLTMVP	SEKEVEPKQC				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
117	1	1096.9944	-45.10	2	30.2	14.2	2	189-207	R.HYRVLGKGGFGEVCACQVR.A	Carbamidomethyl: 14, 16	mdown:qdown 0.52

Detailed Protein Report

Protein 635: **PREDICTED: steroidogenic acute regulatory protein, mitochondrial isoform X4 [Homo sapiens]**

Accession:	gi|578815478	**Score:**	25.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	19.5
Database Date:	2015-11-30	**pI:**	9.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	15.0
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MLLATFKLCA GSSYRHMRNM KGLRQQAVMA ISQELNRRAL GGPTPSTWIN QVRRRSSLLG SRLEETLYSD QELAYLQQGE
        90        100        110        120        130        140        150        160
EAMQKALGIL SNQEGWKKES QQDNGDKVMS KVVPDVGKVF RLEVVVDQPM ERLYEELVER MEAMGEWNPN VKEIKGGARS
       170        180
HLHGASPVGW KSL
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1893	1	719.2685	-58.42	2	52.2	10.1	0	141-152	R.MEAMGEWNPNVK.E	Oxidation: 1, 4

Detailed Protein Report

Protein 636: 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

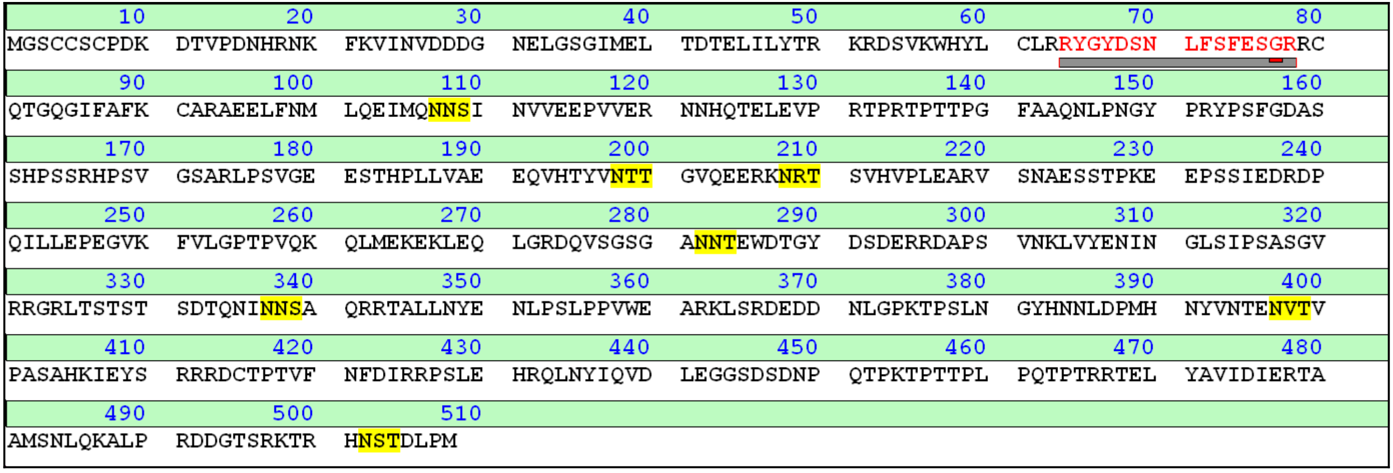
Protein 637: fibroblast growth factor receptor substrate 2 [Homo sapiens]

Accession: gi|110347408
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 25.2
MW [kDa]: 57.0
pI: 5.6
Sequence Coverage [%]: 4.3
No. of unique Peptides: 1

Alias proteins:

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



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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2113	1	899.3324	-89.81	2	56.6	12.8	1	64-78	R.RYGYDSNLFSFESGR.R	

Detailed Protein Report

Protein 638: PREDICTED: zinc finger protein 493 isoform X2 [Homo sapiens]

Accession:	gi|530414758	**Score:**	25.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	81.4
Database Date:	2015-11-30	**pI:**	10.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	5.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MKGHSTVVKP	PVICSHFAED	FCPGPGIKDS	FQKVILREYV	KCGHKDLQLR	KGCKSMNECN	VHKEGYNELN	QYLTTTQSKI
90	100	110	120	130	140	150	160
FQCDKYVKVF	HKLLNSNRHN	TKHTGKKPFK	CKKCGKSFCM	LLHLCQHKRI	HIRENSYRCE	ECGKAFIWFS	TLTRHRRVHT
170	180	190	200	210	220	230	240
GEKSYKYECG	KSFNQDSNLT	THKRIHTGQK	PYKCEECGTS	FYQFSYLTRH	KLIHTREKPY	KCEQYGKTFN	QSSTLTGHKI
250	260	270	280	290	300	310	320
IHNGEKPYKC	EECGKAFSIF	STPTKHKIIH	TEEKSHRCEE	YCKAYKESSH	LTTHKRIHTG	EKPYKCEECG	KAFSIFSTLT
330	340	350	360	370	380	390	400
KHKIIHTEEK	SHRCEECGKA	YKESSHLTTH	KRIHTGEKPY	KCEECGKTFS	VFSILTKHKI	IHTEEKPYKC	EECGKAFKRS
410	420	430	440	450	460	470	480
STLTKHRIIH	TEEKPYKCEE	CGKAFNQSST	LSIHKIIHTG	EKPYKCEECG	KAFKRSSTLT	IHKMIHTGEK	PYKCEECGKA
490	500	510	520	530	540	550	560
FNRSSHLTTH	KRIHTGHKPY	KCKECGKSFS	VFSTLTKHKI	IHTDKKPYKC	EECGKAFNRS	SILSIHKKIH	TGEKPYKCEE
570	580	590	600	610	620	630	640
CGKAFKRSSH	LAGHKQIHSV	QKPYKCEECG	KAFSIFSTLT	KHKIIHTEEK	PYKCEKCGKT	FYRFSNLNTH	KIIHTGEKPC
650	660	670	680	690	700	710	
KCEECGKAFN	HSSNLIKHKL	IHTGDKPYKC	EACGKAFRRS	SHLSRHKIIH	IGIHTEETVQ	K	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1622	1	927.1215	-7.05	3	49.0	11.9	0	3-28	K.GHSTVVKPPVICSHFAEDFCPGPGIK.D	Carbamidomethyl: 12

Detailed Protein Report

Protein 639: **PREDICTED: zinc finger SWIM domain-containing protein 6 isoform X1 [Homo sapiens]**

Accession:	gi|578810477	**Score:**	25.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	68.8
Database Date:	2015-11-30	**pI:**	8.9
		Sequence Coverage [%]:	5.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MFRTQKKELP	HKNITSITNL	EGWVGHPLDP	VGTLFSSLME	ACRIDDENLS	GFSDFTENMG	QCKSLEYQHL	PAHKFLEEGE
90	100	110	120	130	140	150	160
SYLTLAVEVA	LIGLGQQRIM	PDGLYTQEKV	CRNEEQLISK	LQEIELDDTL	VKIFRKQAVF	LLEAGPYSGL	GEIIHRESVP
170	180	190	200	210	220	230	240
MHTFAKYLFT	SLLPHDAELA	YKIALRAMRL	LVLESTAPSG	DLTRPHHIAS	VVPNRYPRWF	TLSHIESQQC	ELASTMLTAA
250	260	270	280	290	300	310	320
KGDVRRLETV	LESIQKNIHS	SSHIFKLAQD	AFKIATLMDS	LPDITLLKVS	LELGLQVMRM	TLSTLNWRRR	EMVRWLVTCA
330	340	350	360	370	380	390	400
TEVGVYALDS	IMQTWFTLFT	PTEATSIVAT	TVMSNSTIVR	LHLDCHQQEK	LASSARTLAL	QCAMKDPQNC	ALSALTLCEK
410	420	430	440	450	460	470	480
DHIAFETAYQ	IVLDAATTGM	SYTQLFTIAR	YMEHRGYPMR	AYKLATLAMT	HLNLSYNQDT	HPAINDVLWA	CALSHSLGKN
490	500	510	520	530	540	550	560
ELAAIIPLVV	KSVKCATVLS	DILRRCTLTT	PGMVGLHGRR	NSGKLMSLDK	APLRQLLDAT	IGAYINTTHS	RLTHISPRHY
570	580	590	600	610	620		
SEFIEFLSKA	RETFLMAHDG	HIQFTQFIDN	LKQIYKGKKK	LMMLVRERFG			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1688	1	916.3971	-125.22	2	51.0	10.9	1	121-135	K.LQEIELDDTLVKIFR.K	

Detailed Protein Report

Protein 640: epidermal growth factor receptor kinase substrate 8-like protein 1 isoform b [Homo sapiens]

Accession:	gi|148539855	**Score:**	25.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	66.4
Database Date:	2015-11-30	**pI:**	5.9
		Sequence Coverage [%]:	4.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MNRTWPRRIW	GSSQDEAELI	REDIQGALHN	YRSGRGERRA	AALRATQEEL	QRDRSPAAET	PPLQRRPSVR	AVISTVERGA
90	100	110	120	130	140	150	160
GRGRPQAKPI	PEAEEAQRPE	PVGTSSNADS	ASPDLGPRGP	DLAVLQAERE	VDILNHVFDD	VESFVSRLQK	SAEAARVLEH
170	180	190	200	210	220	230	240
RERGRRSRRR	AAGEGLLTLR	AKPPSEAEYT	DVLQKIKYAF	SLLARLRGNI	ADPSSPELLH	FLFGPLQMIV	NTSGGPEFAS
250	260	270	280	290	300	310	320
SVRRPHLTSD	AVALLRDNVT	PRENELWTSL	GDSWTRPGLE	LSPEEGPPYR	PEFFSGWEPP	VTDPQSRAWE	DPVEKQLQHE
330	340	350	360	370	380	390	400
RRRRQQSAPQ	VAVNGHRDLE	PESEPQLESE	TAGKWVLCNY	DFQARNSSEL	SVKQRDVLEV	LDDSRKWWKV	RDPAGQEGYV
410	420	430	440	450	460	470	480
PYNILTPYPG	PRLHHSQSPA	RSLNSTPPPP	PAPAPAPPPA	LARPRWDRPR	WDSCDSLNGL	DPSEKEKFSQ	MLIVNEELQA
490	500	510	520	530	540	550	560
RLAQGRSGPS	RAVPGPRAPE	PQLSPGSDAS	EVRAWLQAKG	FSSGTVDALG	VLTGAQLFSL	QKEELRAVSP	EEGARVYSQV
570	580	590	600				
TVQRSLLEDK	EKVSELEAVM	EKQKKKVEGE	VEMEVI				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2109	1	696.2869	-105.74	2	54.9	11.9	0	325-337	R.QQSAPQVAVNGHR.D	

Detailed Protein Report

Protein 641: PREDICTED: kazrin isoform X2 [Homo sapiens]

Accession:	gi|530360946	**Score:**	25.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	51.7
Database Date:	2015-11-30	**pI:**	6.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	4.5
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MTNTKDPKRA	MESTLATSNS	ATGPVTFSHV	FGQQCQLMQA	AVQSLHTLND	QISHFIVTKS	KALEEDKDPF	LPTEKETLKS
90	100	110	120	130	140	150	160
SMILMRHLLM	DAQAKILSMM	EDNKQLALRI	DGAVQSASQE	VTNLRAELTA	TNRRLAELSG	GGGPGPGPGA	AASASAAGDS
170	180	190	200	210	220	230	240
AATNMENPQL	GAQVLLREEV	SRLQEEVHLL	RQMKEMLAKD	LEESQGGKSS	EVLSATELRV	QLAQKEQELA	RAKEALQAMK
250	260	270	280	290	300	310	320
ADRKRLKGEK	TDLVSQMQQL	YATLESREEQ	LRDFIRNYEQ	HRKESEDAVK	ALAKEKDLLE	REKWELRRQA	KEATDHATAL
330	340	350	360	370	380	390	400
RSQLDLKDNR	MKELEAELAM	AKQSLATLTK	DVPKRHSLAM	PGETVLNGNQ	EWVVQADLPL	TAAIRQSQQT	LYHSHPPHPA
410	420	430	440	450	460	470	
DRQAVRVSPC	HSRQPSVISD	ASAAEGDRSS	TPSDINSPRH	RTHSLWRQSR	PSSEEPAQPY	CTVTRGS	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1080	1	540.6535	-191.17	2	42.2	13.5	0	96-104	K.ILSMMEDNK.Q	
2651	1	698.3866	57.31	2	61.9	11.6	1	331-342	R.MKELEAELAMAK.Q	Oxidation: 1, 10

Detailed Protein Report

Protein 642: zinc finger protein 567 [Homo sapiens]

Accession:	gi|34303941	**Score:**	25.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	71.5
Database Date:	2015-11-30	**pI:**	10.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.5
		No. of unique Peptides:	1

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
1247	1	873.9372	79.81	2	45.3	12.8	0	172-186	K.TETPAQSFGYNDCEK.S	Carbamidomethyl: 13

Detailed Protein Report

Protein 643: **zinc finger and SCAN domain-containing protein 26 isoform b [Homo sapiens]**

Accession:	gi|161353483	**Score:**	25.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	55.2
Database Date:	2015-11-30	**pI:**	9.5
		Sequence Coverage [%]:	10.3
		No. of unique Peptides:	2

```
        10         20         30         40         50         60         70         80
MATALVSAHS LAPLNLKKEG LRVVREDHYS TWEQGFKLQG NSKGLGQEPL CKQFRQLRYE ETTGPREALS RLRELCQQWL
        90        100        110        120        130        140        150        160
QPETHTKEQI LELLVLEQFL IILPKELQAR VQEHHPESRE DVVVVLEDLQ LDLGETGQQD PDQPKKQKIL VEEMAPLKGV
       170        180        190        200        210        220        230        240
QEQQVRHECE VTKPEKEKGE ETRIENGKLI VVTDSCGRVE SSGKISEPME AHNEGSNLER HQAKPKEKIE YKCSEREQRF
       250        260        270        280        290        300        310        320
IQHLDLIEHA STHTGKKLCE SDVCQSSSLT GHKKVLSREK GHQCHECGKA FQRSSHLVRH QKIHLGEKPY QCNECGKVFS
       330        340        350        360        370        380        390        400
QNAGLLEHLR IHTGEKPYLC IHCGKNFRRS SHLNRHQRIH SQEEPCECKE CGKTFSQALL LTHHQRIHSH SKSHQCNECG
       410        420        430        440        450        460        470        480
KAFSLTSDLI RHHRIHTGEK PFKCNICQKA FRLNSHLAQH VRIHNEEKPY QCSECGEAFR QRSGLFQHQR YHHKDKLA
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2927	1	1254.6046	-9.85	2	65.7	14.6	2	23-43	R.VVREDHYSTWEQGFKLQGNSK.G	
2244	1	1061.7676	-92.40	3	58.3	10.4	1	303-330	K.IHLGEKPYQCNECGKVFSQNAGLLEHLR.I	

Detailed Protein Report

Protein 644: PREDICTED: telomerase-binding protein EST1A isoform X2 [Homo sapiens]

Accession:	gi|530410168	**Score:**	25.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	101.9
Database Date:	2015-11-30	**pI:**	9.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.3
		No. of unique Peptides:	1

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
1746	1	916.9097	-83.20	2	50.5	10.0	2	1-16	-.MAEGLERVRISASELR.G	Oxidation: 1

Detailed Protein Report

Protein 645: ret finger protein-like 4A [Homo sapiens]

Accession:	gi|222446629	**Score:**	24.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	32.2
Database Date:	2015-11-30	**pI:**	9.2
		Sequence Coverage [%]:	12.9
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MAEHFKQIIR	CPVCLKDLEE	AVQLKCGYAC	CLQCLNSLQK	EPDGEGLLCR	FCSVVSQKDD	IKPKYKLRAL	VSIIKELEPK
90	100	110	120	130	140	150	160
LKSVLTMNPR	MRKFQVDMTF	DVDTANNYLI	ISEDLRSFRS	GDLSQNRKEQ	AERFDTALCV	LGTPRFTSGR	HYWEVDVGTS
170	180	190	200	210	220	230	240
QVWDVGVCKE	SVNRQGKIVL	SSEHGFLTVG	CREGKVFAAS	TVPMTPLWVS	PQLHRVGIFL	DVGMRSIAFY	NVSDGCHIYT
250	260	270	280	290			
FIEIPVCEPW	RPFFAHKRGS	QDDQSILSIC	SVINPSAASA	PVSSEGK			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2944	1	953.4516	-27.66	2	66.0	13.0	1	129-145	K.EQAERFDTALCVLGTPR.F	
1612	1	746.4374	48.07	3	48.9	11.9	0	196-215	K.VFAASTVPMTPLWVSPQLHR.V	

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Detailed Protein Report

Protein 646: PREDICTED: probable E3 ubiquitin-protein ligase TRIML1 isoform X2 [Homo sapiens]

Accession:	gi|578809099	**Score:**	24.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	32.2
Database Date:	2015-11-30	**pI:**	5.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	10.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MKMHQFLKEE	EQLQLQLLEQ	EEKENMRKLR	NNEIKLTQQI	RSLSKMIAQI	ESSSQSSAFE	SLEEVRGALE	RSEPLLLQCP
90	100	110	120	130	140	150	160
EATTTELSLC	RITGMKEMLR	KFSTEITLDP	ATANAYLVLS	EDLKSVKYGG	SRQQLPDNPE	RFDQSATVLG	TQIFTSGRHY
170	180	190	200	210	220	230	240
WEVEVGNKTE	WEVGICKDSV	SRKGNLPKPP	GDLFSLIGLK	IGDDYSLWVS	SPLKGQHVRE	PVCKVGVFLD	YESGHIAFYN
250	260	270	280	290			
GTDESLIYSF	PQASFQEALR	PIFSPCLPNE	GTNTDPLTIC	SLNSHV			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2309	1	1131.1776	102.92	2	57.3	10.8	0	72-91	R.SEPLLLQCPEATTTELSLCR.I	Carbamidomethyl: 8

Detailed Protein Report

Protein 647: PREDICTED: MDS1 and EVI1 complex locus protein EVI1 isoform X14 [Homo sapiens]

Accession: gi|530374146
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 24.8
MW [kDa]: 102.8
pI: 5.8
Sequence Coverage [%]: 3.1
No. of unique Peptides: 1

```
        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
CENCAKVFTD PSNLQRHIRS QHVGARAHAC PECGKTFATS SGLKQHKHIH SSVKPFISFS QSMYPFPDRD LRSLPLKMEP
       410        420        430        440        450        460        470        480
QSPGEVKKLQ KGSSESPFDL TTKRKDEKPL TPVPSKPPVT PATSQDQPLD LSMGSRSRAS GTKLTEPRKN HVFGGKKGSN
       490        500        510        520        530        540        550        560
VESRPASDGS LQHARPTPFF MDPIYRVEKR KLTDPLEALK EKYLRPSPGF LFHPQMSAIE NMAEKLESFS ALKPEASELL
       570        580        590        600        610        620        630        640
QSVPSMFNFR APPNALPENL LRKGKERYTC RYCGKIFPRS ANLTRHLRTH TGEQPYRCKY CDRSFSISSN LQRHVRNIHN
       650        660        670        680        690        700        710        720
KEKPFKCHLC DRCFGQQTNL DRHLKKHENG NMSGTATSSP HSELESTGAI LDDKEDAYFT EIRNFIGNSN HGSQSPRNVE
       730        740        750        760        770        780        790        800
ERMNGSHFKD EKALVTSQNS DLLDDEEVED EVLLDEEDED NDITGKTGKE PVTSNLHEGN PEDDYEETSA LEMSCKTSPV
       810        820        830        840        850        860        870        880
RYKEEEYKSG LSALDHIRHF TDSLKMRKME DNQYSEAELS SFSTSHVPEE LKQPLHRKSK SQAYAMMLSL SDKESLHSTS
       890        900        910
HSSSNVWHSM ARAAAESSAI QSISHV
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2083	1	1052.4215	-3.40	2	56.2	11.1	1	309-326	R.HQMSHDSGKHYECENCAK.V	

Detailed Protein Report

Protein 648: 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

mdown:qdown	**Median:**	1.88	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.51	**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		Wdown:Qdown 0.51 mdown:qdown 1.88

Detailed Protein Report

Protein 649: leucine-rich repeat neuronal protein 2 precursor [Homo sapiens]

Accession:	gi|42544231	**Score:**	24.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	78.8
Database Date:	2015-11-30	**pI:**	7.3
		Sequence Coverage [%]:	4.6
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578800423	refseq_human (refseq_human_20140103.fasta)	PREDICTED: leucine-rich repeat neuronal protein 2 isoform X3 [Homo sapiens]
gi|578800421	refseq_human (refseq_human_20140103.fasta)	PREDICTED: leucine-rich repeat neuronal protein 2 isoform X2 [Homo sapiens]
gi|530364022	refseq_human (refseq_human_20140103.fasta)	PREDICTED: leucine-rich repeat neuronal protein 2 isoform X1 [Homo sapiens]
gi|42544233	refseq_human (refseq_human_20140103.fasta)	leucine-rich repeat neuronal protein 2 precursor [Homo sapiens]

10	20	30	40	50	60	70	80
MRLLVAPLLL	AWVAGATAAV	PVVPWHVPCP	PQCACQIRPW	YTPRSSYREA	TTVDCNDLFL	TAVPPALPAG	TQTLLLQSNS
90	100	110	120	130	140	150	160
IVRVDQSELG	YLANLTELDL	SQNSFSDARD	CDFHALPQLL	SLHLEENQLT	RLEDHSFAGL	ASLQELYLNH	NQLYRIAPRA
170	180	190	200	210	220	230	240
FSGLSNLLRL	HLNSNLLRAI	DSRWFEMLPN	LEILMIGGNK	VDAILDMNFR	PLANLRSLVL	AGMNLREISD	YALEGLQSLE
250	260	270	280	290	300	310	320
SLSFYDNQLA	RVPRRALEQV	PGLKFLDLNK	NPLQRVGPGD	FANMLHLKEL	GLNNMEELVS	IDKFALVNLP	ELTKLDITNN
330	340	350	360	370	380	390	400
PRLSFIHPRA	FHHLPQMETL	MLNNNALSAL	HQQTVESLPN	LQEVGLHGNP	IRCDCVIRWA	NATGTRVRFI	EPQSTLCAEP
410	420	430	440	450	460	470	480
PDLQRLPVRE	VPFREMTDHC	LPLISPRSFP	PSLQVASGES	MVLHCRALAE	PEPEIYWVTP	AGLRLTPAHA	GRRYRVYPEG
490	500	510	520	530	540	550	560
TLELRRVTAE	EAGLYTCVAQ	NLVGADTKTV	SVVVGRALLQ	PGRDEGQGLE	LRVQETHPYH	ILLSWVTPPN	TVSTNLTWSS
570	580	590	600	610	620	630	640
ASSLRGQGAT	ALARLPRGTH	SYNITRLLQA	TEYWACLQVA	FADAHTQLAC	VWARTKEATS	CHRALGDRPG	LIAILALAVL
650	660	670	680	690	700	710	720
LLAAGLAAHL	GTGQPRKGVG	GRRPLPPAWA	FWGWSAPSVR	VVSAPLVLPW	NPGRKLPRSS	EGETLLPPLS	QNS

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
753	1	541.2892	-37.06	3	38.3	12.1	1	170-183	R.LHLNSNLLRAIDSR.W	

Detailed Protein Report

Protein 650: **myosin-4 [Homo sapiens]**

Accession:	gi|110611903	**Score:**	24.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	222.9
Database Date:	2015-11-30	**pI:**	5.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.4
		No. of unique Peptides:	1

Detailed Protein Report

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
202	1	561.6237	-229.75	2	31.3	12.3	0	947-955	K.LEDECSELK.K	Carbamidomethyl: 5

Detailed Protein Report

Protein 651: transcription factor HES-4 isoform 1 [Homo sapiens]

Accession:	gi|216548627	**Score:**	24.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	26.1
Database Date:	2015-11-30	**pI:**	12.0
		Sequence Coverage [%]:	14.2
		No. of unique Peptides:	2

```
        10         20         30         40         50         60         70         80
MAADTPGKPS ASPMAGAPAS ASRTPDKPRS AAEHRKVGSR PGVRGATGGR EGRGTQPVPD PQSSKPVMEK RRRARINESL
        90        100        110        120        130        140        150        160
AQLKTLILDA LRKESSRHSK LEKADILEMT VRHLRSLRRV QVTAALSADP AVLGKYRAGF HECLAEVNRF LAGCEGVPAD
       170        180        190        200        210        220        230        240
VRSRLLGHLA ACLRQLGPSR RPASLSPAAP AEAPAPEVYA GRPLLPSLGG PFPLLAPPLL PGLTRALPAA PRAGPQGPGG
       250
PWRPWLR
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2708	1	835.0993	174.40	2	62.3	10.6	2	37-53	K.VGSRPGVRGATGGREGR.G	
1118	1	974.4533	-104.11	2	42.7	14.1	2	163-180	R.SRLLGHLAACLRQLGPSR.R	

Detailed Protein Report

Protein 652: PREDICTED: basic proline-rich protein-like [Homo sapiens]

Accession:	gi|578837749	**Score:**	24.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	40.4
Database Date:	2015-11-30	**pI:**	13.1
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	8.7
		No. of unique Peptides:	2

Alias proteins:

Accession	Name	Description
gi|578847054	refseq_human (refseq_human_20140103.fasta)	PREDICTED: basic proline-rich protein-like [Homo sapiens]

10	20	30	40	50	60	70	80
MPGPCPASAP	PALLQVHLQG	KCPAPAQHPS	PGPPPGSPPE	QMPGPCPASA	PPALLQVHLQ	GKCPAPAQHP	CPRPSSRFTS
90	100	110	120	130	140	150	160
RANARPLPSI	HAPGPPPGSP	PGQVPGPCPA	SMPPALLQVH	LQSKCPAPAQ	HPCPRPSSRF	TSRANARPLP	SVRAPGPPPG
170	180	190	200	210	220	230	240
SPPEQMPGPC	PASMPPALLQ	VHLQSKCPAP	AQRLRPRPSS	RFTSRANARP	LPSIHAPGPP	PGSPPGQMPG	PCPASMPPAL
250	260	270	280	290	300	310	320
LQVHLQGKCL	APAQRPRPRP	SSRFTSRANA	RPLPSIHAPG	PPPGSPPEQM	PGPCPASMPP	ALLQVHLQSK	CPAPAQRPRP
330	340	350	360	370	380	390	400
QPSSRFTSRA	NARPLPSIHA	PGPPPGSPPE	QMPGPCPASA	PPALLQVHLQ	SKCPAPAQCP	RPLPSSRTLL	FE

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
407	1	717.9592	-76.97	3	34.1	11.6	1	63-81	K.CPAPAQHPCPRPSSRFTSR.A	Carbamidomethyl: 1
2994	1	846.4470	-21.67	2	66.2	13.1	1	187-201	K.CPAPAQRLRPRPSSR.F	

Detailed Protein Report

Protein 653: **PREDICTED: sushi, nidogen and EGF-like domain-containing protein 1 isoform X4 [Homo sapiens]**

Accession:	gi|578804038	**Score:**	24.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	142.7
Database Date:	2015-11-30	**pI:**	6.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.0
		No. of unique Peptides:	1

```
        10          20          30          40          50          60          70          80
MRHGVAWALL  VAAALGLGAR  GVRGAVALAD  FYPFGAERGD  AVTPKQDDGG  SGLRPLSVPF  PFFGAEHSGL  YVNNNGIISF

        90         100         110         120         130         140         150         160
LKEVSQFTPV  AFPIAKDRCV  VAAFWADVDN  RRAGDVYYRE  ATDPAMLRRA  TEDVRHYFPE  LLDFNATWVF  VATWYRVTFF

       170         180         190         200         210         220         230         240
GGSSSSPVNT  FQTVLITDGK  LSFTIFNYES  IVWTTGTHAS  SGGNATGLGG  IAAQAGFNAG  DGQRYFSIPG  SRTADMAEVE

       250         260         270         280         290         300         310         320
TTTNVGVPGR  WAFRIDDAQV  RVGGCGHTTS  VCLALRPCLN  GGKCIDDCVT  GNPSYTCSCL  SGFTGRRCHL  DVNECASQPC

       330         340         350         360         370         380         390         400
QNGGTCTHGI  NSFRCQCPAG  FGGPTCETAQ  SPCDTKECQH  GGQCQVENGS  AVCVCQAGYT  GAACEMDVDD  CSPDPCLNGG

       410         420         430         440         450         460         470         480
SCVDLVGNYT  CLCAEPFKGL  RCETGDHPVP  DACLSAPCHN  GGTCVDADQG  YVCECPEGFM  GLDCRERVPD  DCECRNGGRC

       490         500         510         520         530         540         550         560
LGANTTLCQC  PLGFFGLLCE  FEITAMPCNM  NTQCPDGGYC  MEHGGSYLCV  CHTDHNASHS  LPSPCDSDPC  FNGGSCDAHD

       570         580         590         600         610         620         630         640
DSYTCECPRG  FHGKHCEKAR  PHLCSSGPCR  NGGTCKEAGG  EYHCSCPYRF  TGRHCEIGKP  DSCASGPCHN  GGTCFHYIGK

       650         660         670         680         690         700         710         720
YKCDCPPGFS  GRHCEIAPSP  CFRSPCVNGG  TCEDRDTDFF  CHCQAGYMGR  RCQAEVDCGP  PEEVKHATLR  FNGTRLGAVA

       730         740         750         760         770         780         790         800
LYACDRGYSL  SAPSRIRVCQ  PHGVWSEPPQ  CLEIDECRSQ  PCLHGGSCQD  RVAGYLCLCS  TGYEGAHCEL  ERDECRAHPC

       810         820         830         840         850         860         870         880
RNGGSCRNLP  GAYVCRCPAG  FVGVHCETEV  DACDSSPCQH  GGRCESGGGA  YLCVCPESFF  GYHCETVSDP  CFSSPCGGRG

       890         900         910         920         930         940         950         960
YCLASNGSHS  CTCKVGYTGE  DCAKELFPPT  ALKMERVEES  GVSISWNPPN  GPAARQMLDG  YAVTYVSSDG  SYRRTDFVDR

       970         980         990        1000        1010        1020        1030        1040
TRSSHQLQAL  AAGRAYNISV  FSVKRNSNNK  NDISRPAVLL  ARTRPRPVEG  FEVTNVTAST  ISVQWALHRI  RHATVSGVRV

      1050        1060        1070        1080        1090        1100        1110        1120
SIRHPEALRD  QATDVDRSVD  RFTFRALLPG  KRYTIQLTTL  SGLRGEEHPT  ESLATAPTHV  WTRPLPPANL  TAARVTATSA

      1130        1140        1150        1160        1170        1180        1190        1200
HVVWDAPTPG  SLLEAYVINV  TTSQSTKSRY  VPNGKLASYT  VRDLLPGRRY  QLSVIAVQST  ELGPQHSEPA  HLYIITSPRD

      1210        1220        1230        1240        1250        1260        1270        1280
GADRRWHQGG  HHPRVLKNRP  PPARLPELRL  LNDHSAPETP  TQPPRFSELV  DGRGRVSARF  GGSPSKAATV  RSQPTASAQL

      1290        1300        1310        1320        1330
ENMEEAPKRV  SLALQLPEHG  SKDIGSLDLL  LAPVSTRRTG  LCIRRRE
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1017	1	788.6695	-45.57	3	41.2	10.3	2	570-590	R.GFHGKHCEKARPHLCSSGPCR.N	Carbamidomethyl: 15

Detailed Protein Report

Protein 654: **probable E3 ubiquitin-protein ligase HERC6 isoform 2 [Homo sapiens]**

Accession:	gi|259089405	**Score:**	24.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	111.0
Database Date:	2015-11-30	**pI:**	9.2
		Sequence Coverage [%]:	4.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MYFCWGADSR	ELQRRRTAGS	PGAELLQAAS	GERHSLLLLT	NHRVLSCGDN	SRGQLGRRGA	QRGELPEPIQ	ALETLIVDLV
90	100	110	120	130	140	150	160
SCGKEHSLAV	CHKGRVFAWG	AGSEGQLGIG	EFKEISFTPK	KIMTLNDIKI	IQVSCGHYHS	LALSKDSQVF	SWGKNSHGQL
170	180	190	200	210	220	230	240
GLGKEFPSQA	SPQRVRSLEG	IPLAQVAAGG	AHSFALSLCG	TSFGWGSNSA	GQLALSGRNV	PVQSNKPLSV	GALKNLGVVY
250	260	270	280	290	300	310	320
ISCGDAHTAV	LTQDGKVFTF	GDNRSGQLGY	SPTPEKRGPQ	LVERIDGLVS	QIDCGSYHTL	AYVHTTGQVV	SFGHGPSDTS
330	340	350	360	370	380	390	400
KPTHPEALTE	NFDISCLISA	EDFVDVQVKH	IFAGTYANFV	TTHQDTSSTR	APGKTLPEIS	RISQSMAEKW	IAVKRRSTEH
410	420	430	440	450	460	470	480
EMAKSEIRMI	FSSPACLTAS	FLKKRGTGET	TSIDVDLEMA	RDTFKKLTKK	EWISSMITTC	LEDDLLRALP	CHSPHQEALS
490	500	510	520	530	540	550	560
VFLLLPECPV	MHDSKNWKNL	VVPFAKAVCE	MSKQSLQVLK	KCWAFLQESS	LNPLIQMLKA	AIISQLLHQT	KTEQDHCNVK
570	580	590	600	610	620	630	640
ALLGMMKELH	KVNKANCRLP	ENTFNINELS	NLLNFYIDRG	RQLFRDNHLM	SEKKAYMLMH	ETILQKKDEF	PPSPRFILRV
650	660	670	680	690	700	710	720
RRSRLVKDAL	RQLSQAEATD	FCKVLVVEFI	NEICPESGGV	SSEFFHCMFE	EMTKPEYGMF	MYPEMGSCMW	FPAKPKPEKK
730	740	750	760	770	780	790	800
RYFLFGMLCG	LSLFNLNVAN	LPFPLALYKK	LLDQKPSLED	LKELSPRLGK	SLQEVLDDAA	DDIGDALCIR	FSIHWDQNDV
810	820	830	840	850	860	870	880
DLIPNGISIP	VDQTNKRDYV	SKYIDYIFNV	SVKAVYEEFQ	RGFYRVCEKE	ILRHFYPEEL	MTAIIGNTDY	DWKQFEQNSK
890	900	910	920	930	940	950	960
YEQGYQKSHP	TIQLFWKAFH	KLTLDEKKKF	LFFLTGRDRL	HARGIQKMEI	VFRCPETFSE	RDHPTSITCH	NILSLPKYST
970	980	990					
MERMEEALQV	AINNNRGFVS	PMLTQS					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2078	1	882.8691	72.62	3	54.5	13.8	2	34-57	R.HSLLLLTNHRVLSCGDNSRGQLGR.R	

Detailed Protein Report

Protein 655: 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

Protein 656: endogenous Bornavirus-like nucleoprotein 2 [Homo sapiens]

Accession:	gi|40538806	**Score:**	24.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	30.4
Database Date:	2015-11-30	**pI:**	10.0
		Sequence Coverage [%]:	11.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGYFLKLYAY	VNSHSLFVWV	CDRSYKRSFR	PMILNKIKEL	SRNQFSTMSH	LRKDSQPSSP	GDDAMDRSGL	PDLQGRFELS
90	100	110	120	130	140	150	160
GKNRQYPLDA	LEPQPSIGDI	KDIKKAAKSM	LDPAHKSHFH	PVTPSLVFLC	FIFDGLHQAL	LSVGVSKRSN	TVVGNENEER
170	180	190	200	210	220	230	240
GTPYASRFKD	MPNFIALEKS	SVLRHCCDLL	IGIAAGSSDK	ICTSSLQVQR	RFKAMMASIG	RLSHGESADL	LISCNAESAI
250	260	270	280				
GWISSRPWVG	ELMFTLLFGD	FESPLHKLRK	SS				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
737	1	729.1287	119.14	3	38.0	10.5	2	161-179	R.GTPYASRFKDMPNFIALEK.S	

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Detailed Protein Report

Protein 657: PREDICTED: DBIRD complex subunit ZNF326 isoform X1 [Homo sapiens]

Accession:	gi|530362445	**Score:**	24.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	43.1
Database Date:	2015-11-30	**pI:**	4.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	6.9
		No. of unique Peptides:	1

Quantitation

Wdown:Qdown **Median:** 10.84 **CV:** 0.00 % **No. of Peptides:** 1

Alias proteins:

Accession	Name	Description
gi|530362447	refseq_human (refseq_human_20140103.fasta)	PREDICTED: DBIRD complex subunit ZNF326 isoform X2 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MGDFGSIHRP GIVVDYQNKS TNVTVAAARG IKRKMMQPFN KPSGTFIKKP KLAKPMEKIS LSKSPTKTDP KNEEEEKRRI
        90        100        110        120        130        140        150        160
EARREKQRRR REKNSEKYGD GYRMAFTCSF CKFRTFEEKD IELHLESSSH QETLDHIQKQ TKFDKVVMEF LHECMVNKFK
       170        180        190        200        210        220        230        240
KTSIRKQQTN NQTEVVKIIE KDVMEGVTVD DHMMKVETVH CSACSVYIPA LHSSVQQHLK SPDHIKGKQA YKEQIKRESV
       250        260        270        280        290        300        310        320
LTATSILNNP IVKARYERFV KGENPFEIQD HSQDQQIEGD EEDEEKIDEP IEEEEDEDEE EEAEEVGEVE EVEEVEEVRE
       330        340        350        360        370        380
GGIEGEGNIQ GVGEGGEVGV VGEVEGVGEV EEVEELEEET AKEEPADFPV EQPEEN
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2131	1	955.8582	-116.90	2	55.2	10.3	1	146-160	K.VVMEFLHECMVNKFK.K	Carbamidomethyl: 9	Wdown:Qdown 10.84

Detailed Protein Report

Protein 658: **differentially expressed in FDCP 6 homolog [Homo sapiens]**

Accession:	gi|145312241	**Score:**	24.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	73.9
Database Date:	2015-11-30	**pI:**	5.7
		Sequence Coverage [%]:	2.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MALRKELLKS	IWYAFTALDV	EKSGKVSKSQ	LKVLSHNLYT	VLHIPHDPVA	LEEHFRDDDD	GPVSSQGYMP	YLNKYILDKV
90	100	110	120	130	140	150	160
EEGAFVKEHF	DELCWTLTAK	KNYRADSNGN	SMLSNQDAFR	LWCLFNFLSE	DKYPLIMVPD	EVEYLLKKVL	SSMSLEVSLG
170	180	190	200	210	220	230	240
ELEELLAQEA	QVAQTTGGLS	VWQFLELFNS	GRCLRGVGRD	TLSMAIHEVY	QELIQDVLKQ	GYLWKRGHLR	RNWAERWFQL
250	260	270	280	290	300	310	320
QPSCLCYFGS	EECKEKRGII	PLDAHCCVEV	LPDRDGKRCM	FCVKTANRTY	EMSASDTRQR	QEWTAAIQMA	IRLQAEGKTS
330	340	350	360	370	380	390	400
LHKDLKQKRR	EQREQRERRR	AAKEEELLRL	QQLQEEKERK	LQELELLQEA	QRQAERLLQE	EEERRRSQHR	ELQQALEGQL
410	420	430	440	450	460	470	480
REAEQARASM	QAEMELKEEE	AARQRQRIKE	LEEMQQRLQE	ALQLEVKARR	DEESVRIAQT	RLLEEEEEKL	KQLMQLKEEQ
490	500	510	520	530	540	550	560
ERYIERAQQE	KEELQQEMAQ	QSRSLQQAQQ	QLEEVRQNRQ	RADEDVEAAQ	RKLRQASTNV	KHWNVQMNRL	MHPIEPGDKR
570	580	590	600	610	620	630	640
PVTSSSFSGF	QPPLLAHRDS	SLKRLTRWGS	QGNRTPSPNS	NEQQKSLNGG	DEAPAPASTP	QEDKLDPAPE	N

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1011	1	645.1242	-360.14	1	42.2	11.0	0	313-318	R.LQAEGK.T	

Detailed Protein Report

Protein 659: PREDICTED: uncharacterized protein KIAA1109 isoform X12 [Homo sapiens]

Accession:	gi|578809467	**Score:**	24.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	451.7
Database Date:	2015-11-30	**pI:**	6.4
		Sequence Coverage [%]:	0.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MFINCLYKLA	CLLEWGQTFV	FHVVCREYEL	ERPKSVIICQ	HGIDRRFCES	KLSCIPGPCP	TSDDLKYTMI	RLAVDGADIY
90	100	110	120	130	140	150	160
IVEHGCATNI	KMGAIRVANC	NLHNQSVGEG	ISAAIQDFQV	RQYIEQLNNC	RIGLQPAVLR	RAYWLEAGSA	NLGLITVDIA
170	180	190	200	210	220	230	240
LAADHHSKHE	AQRHFLETHD	ARTKRLWFLW	PDDILKNKRC	RNKCGCLGGC	RFFGGTVTGL	DFFKLEELTP	SSSSAFSSTS
250	260	270	280	290	300	310	320
AESDMYYGQS	LLQPGEWIIT	KEIPKIIDGN	VNGMKRKEWE	NKSVGIEVER	KTQHLSLQVP	LRSHSSSSSS	EENSSSSAAQ
330	340	350	360	370	380	390	400
PLLAGEKESP	SSVADDHLVQ	KEFLHGTKRD	DGQASIPTEI	SGNSPVSPNT	QDKSVGQSPL	RSPLKRQASV	CSTRLGSTKS
410	420	430	440	450	460	470	480
LTAAFYGDKQ	PVTVGVQFSS	DVSRSDENVL	DSPKQRRSFG	SFPYTPSADS	NSFHQYRSMD	SSMSMADSEA	YFSAAEEFEP
490	500	510	520	530	540	550	560
ISSDEGPGTY	PGRKKKKKQT	QQIDYSRGSI	YHSVEGPLTG	HGESIQDSRT	LPFKTHPSQA	SFVSALGGED	DVIEHLYIVE
570	580	590	600	610	620	630	640
GEKTVESEQI	TPQQPVMNCY	QTYLTQFQVI	NWSVKHPTNK	RTSKSSLHRP	LDLDTPTSEE	SSSSFEQLSV	PTFKVIKQGL
650	660	670	680	690	700	710	720
TANSLLDRGM	QLSGSTSNTP	YTPLEKKLAD	NTDDETLTEE	WTLDQPVSQT	RTTAIVEVKG	TVDIVLTPLV	AEALDRYIEA
730	740	750	760	770	780	790	800
MVHCASTRHP	AAIVDDLHAK	VLREAVQNSK	TTFSENLSSK	QDIRGTKTEQ	STIGTTNQGQ	AQTNLTMKQD	NVTIKGLQTN
810	820	830	840	850	860	870	880
VSIPKVNLCL	LQASVEESPT	TAPSRSVTHV	SLVALCFDRI	ATQVRMNRGV	VEETSNNAEP	GRTSNFDRYV	HATKMQPQSS
890	900	910	920	930	940	950	960
GSLRSNAGAE	KGKEIAAKLN	IHRVHGQLRG	LDTTDIGTCA	ITAIPFEKSK	VLFTLEELDE	FTFVDETDQQ	AVPDVTRIGP
970	980	990	1000	1010	1020	1030	1040
SQEKWGWIMF	ECGLENLTIK	GGRQSGAVLY	NSFGIMGKAS	DTERGGVLTS	NNSSDSPTGS	GYNTDVSDDN	LPCDRTSPSS
1050	1060	1070	1080	1090	1100	1110	1120
DLNGNSVSDE	QDEGVESDDL	KKDLPLMPPP	PDSCSMKLTI	KEIWFSFAAP	TNVRSHTHAF	SRQLNLLSTA	TPAVGAWLVP
1130	1140	1150	1160	1170	1180	1190	1200
IDQLKSSLNK	LETEGTLRIC	AVMGCIMTEA	LENKSVHFPL	RSKYNRLTKV	ARFLQENPSC	LLCNILHHYL	HQANYSIIDD
1210	1220	1230	1240	1250	1260	1270	1280
ATMSDGLPAL	VTLKKGLVAL	ARQWMKFIVV	TPAFKGVSLH	RPAQPLKPQI	AMDHEHEDGL	GLDNGGGLQS	DTSADGAEFE
1290	1300	1310	1320	1330	1340	1350	1360
FDAATVSEHT	MLLEGTANRP	PPGSSGPVTG	AEIMRKLSKT	HTHSDSALKI	KGIHPYHSLS	YTSGDTATDS	PVHVGRAGMP
1370	1380	1390	1400	1410	1420	1430	1440
VKDSPRKESL	LSYLTGSFPS	LHNLLEGTPQ	RSSAAVKSSS	LTRTGNTVAT	DMLSEHPLLS	EPSSVSFYNW	MSNAVGNRGS
1450	1460	1470	1480	1490	1500	1510	1520
VLQESPVTKS	GHNSLPTGVA	PNLPTIPSAS	DFNTVLSSDQ	NTLDGTHSQH	STSQDDVAGV	EEANQGFPAV	QLADAQVVFK
1530	1540	1550	1560	1570	1580	1590	1600
PLLSHTGIQS	QDTMPFCYRM	YFGEHLSFSG	TLDCLRADIV	DSDTAKERKG	KRARRQGHVN	LPPLEFKPAL	MLGTFSISAV
1610	1620	1630	1640	1650	1660	1670	1680
VMEKSVCTPQ	NSTSALSFHD	LSKRYYNTFH	CNFTISCQSI	SQHVDMALVR	LIHQFSTMID	DIKATQTDIK	LSRYTAGSAS
1690	1700	1710	1720	1730	1740	1750	1760
PTPTFKTRKH	RDFRSSDFSR	SSRGSLNGGN	RVNNAKNKRT	NNENNKKESR	NKNSLGRSER	RTSKVSRKGS	KDVVDHMTIH
1770	1780	1790	1800	1810	1820	1830	1840
MDDSDSITVS	EQSEPSAECW	QNMYKLLNFY	SLISDPTGIL	EKSSETFGPA	GVRSPTEPTC	KVVFENEQDN	SSLTKTQRKR
1850	1860	1870	1880	1890	1900	1910	1920
SLVTSEPQHV	TLIVFGIGMV	NRTHLEADIG	GLTMESELKR	IHGSFTLKEK	MKDVLHQKMT	ETCATAHIGG	VNIVLLEGIT
1930	1940	1950	1960	1970	1980	1990	2000
PNIQLEDFPT	SPTSTAKQEF	LTVVKCSIAK	SQALYSAQRG	LKTNNAAVFK	VGAISINIPQ	HPATLHSMMV	RSSHQLSKQI
2010	2020	2030	2040	2050	2060	2070	2080
SDLIRQPSTA	PQPVKEDIAT	PLPSEKTPTS	VNQTPVETNE	FPQLPEGLEK	KPIVLKFSAM	LDGIAIGAAL	LPSLKAEYKM
2090	2100	2110	2120	2130	2140	2150	2160
GRMRSHGMTG	AQTRFTFELP	NHRLRFTSKV	SATDMSTIPP	SASLNLPPVT	MSGKYIMEEH	DSYSDQVWSI	DELPSKQGYY
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
2265	1	618.9864	-97.88	3	56.8	10.2	2	4077-4093	K.VLSVLIKKLGTALQDEK.E	

Detailed Protein Report

Protein 660: protein scribble homolog isoform b [Homo sapiens]

Accession:	gi|355390315	**Score:**	24.5
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
92	1	696.1357	141.31	3	30.4	24.5	2	861-880	R.HVACLARSERGLGFSIAGGK.G	Carbamidomethyl: 4

Detailed Protein Report

Protein 661: metallothionein-1B [Homo sapiens]

Accession:	gi|27414495	**Score:**	24.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	6.1
Database Date:	2015-11-30	**pI:**	10.7
		Sequence Coverage [%]:	34.4
		No. of unique Peptides:	1

```
         10         20         30         40         50         60         70
MDPNCSCTTG GSCACAGSCK CKECKCTSCK KCCCSCCPVG CAKCAQGCVC KGSSEKCRCC A
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
319	1	699.6539	78.39	3	33.1	12.9	2	31-51	K.KCCCSCCPVGCAKCAQGCVCK.G	

Detailed Protein Report

Protein 662: PREDICTED: disks large homolog 2 isoform X10 [Homo sapiens]

Accession:	gi|578821149	**Score:**	24.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	73.1
Database Date:	2015-11-30	**pI:**	6.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	5.1
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	0.77	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.99	**CV:**	0.00 %	**No. of Peptides:**	1

```
        10         20         30         40         50         60         70         80
MNAYLTKQHS CSRGSDGMDA VRSAPTLIRD AHCACGWQRN CQGLGYSSQT MPSSGPGGPA SNRTGGSSFN RTLWDSVRKS
        90        100        110        120        130        140        150        160
PHKTSTKGKG TCGEHCTCPH GWFSPAQASP APIIVNTDTL DTIPYVNGTE IEYEFEEITL ERGNSGLGFS IAGGTDNPHI
       170        180        190        200        210        220        230        240
GDDPGIFITK IIPGGAAAED GRLRVNDCIL RVNEVDVSEV SHSKAVEALK EAGSIVRLYV RRRRPILETV VEIKLFKGPK
       250        260        270        280        290        300        310        320
GLGFSIAGGV GNQHIPGDNS IYVTKIIDGG AAQKDGRLQV GDRLLMVNNY SLEEVTHEEA VAILKNTSEV VYLKVGKPTT
       330        340        350        360        370        380        390        400
IYMTDPYGPP DITHSYSPPM ENHLLSGNNG TLEYKTSLPP ISPGRYSPIP KHMLVDDDYT RPPEPVYSTV NKLCDKPASP
       410        420        430        440        450        460        470        480
RHYSPVECDK SFLLSAPYSH YHLGLLPDSE MTSHSQHSTA TRQPSMTLQR AVSLEGEPRK VVLHKGSTGL GFNIVGGEDG
       490        500        510        520        530        540        550        560
EGIFVSFILA GGPADLSGEL QRGDQILSVN GIDLRGASHE QAAAALKGAG QTVTIIAQYQ PEDYARFEAK IHDLREQMMN
       570        580        590        600        610        620        630        640
HSMSSGSGSL RTNQKRSLYV RAMFDYDKSK DSGLPSQGLS FKYGDILHVI NASDDEWWQA RRVMLEGDSE EMGVIPSKRR
       650        660        670        680
VERKERARLK TVKFNAKPGV IDSKGLLEFK YA
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
56	1	877.9030	41.74	2	29.9	12.3	0	556-571	R.EQMMNHSMSSGSGSLR.T	Oxidation: 8	mdown:qdown 0.77 Wdown:Qdown 0.99

BRUKER

Detailed Protein Report

Protein 663: protein canopy homolog 4 precursor [Homo sapiens]

Accession:	gi|22749479	**Score:**	24.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	28.3
Database Date:	2015-11-30	**pI:**	4.4
		Sequence Coverage [%]:	9.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGPVRLGILL	FLFLAVHEAW	AGMLKEEDDD	TERLPSKCEV	CKLLSTELQA	ELSRTGRSRE	VLELGQVLDT	GKRKRHVPYS
90	100	110	120	130	140	150	160
VSETRLEEAL	ENLCERILDY	SVHAERKGSL	RYAKGQSQTM	ATLKGLVQKG	VKVDLGIPLE	LWDEPSVEVT	YLKKQCETML
170	180	190	200	210	220	230	240
EEFEDIVGDW	YFHHQEQPLQ	NFLCEGHVLP	AAETACLQET	WTGKEITDGE	EKTEGEEEQE	EEEEEEEEEG	GDKMTKTGSH
250							
PKLDREDL							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2741	1	922.4990	-51.89	1	63.2	10.1	2	107-114	R.KGSLRYAK.G	

Detailed Protein Report

Protein 664: PREDICTED: RING finger protein 32 isoform X5 [Homo sapiens]

Accession:	gi|578813915	**Score:**	24.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	27.1
Database Date:	2015-11-30	**pI:**	10.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	9.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLKNKGHSSK	KDNLAVNAVA	LQDHILHDLQ	LRNLSVADHS	KTQVQKKENK	SLKRDTKAII	DTGLKKTTQC	PKLEDSEKEY
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
VLDPKPPPLT	LAQKLGLIGP	PPPPLSSDEW	EKVKQRSLLQ	GDSVQPCPIC	KEEFELRPQV	LLSCSHVFHK	ACLQAFEKFT
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
NKKTCPLCRK	NQYQTRVIHD	GARLFRIKCV	TRIQAYWRGC	VVRKWYRNLR	KTVPPTDAKL	RKKFFEKKTQ	DWKPA

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2582	1	834.4528	52.62	2	62.8	12.0	2	164-176	K.TCPLCRKNQYQTR.V	Carbamidomethyl: 2

Detailed Protein Report

Protein 665: PREDICTED: sal-like protein 4 isoform X1 [Homo sapiens]

Accession:	gi|530418220	**Score:**	24.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	100.9
Database Date:	2015-11-30	**pI:**	9.3
		Sequence Coverage [%]:	3.3
		No. of unique Peptides:	2

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	
811	1	848.9801	1.28	2	39.0	11.3	2	321-334	K.GNLKVHFHRHPQVK.A	

Detailed Protein Report

Protein 666: histone deacetylase complex subunit SAP18 [Homo sapiens]

Accession: gi|215490089
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 24.4
MW [kDa]: 19.5
pI: 10.3
Sequence Coverage [%]: 7.0
No. of unique Peptides: 1

```
        10         20         30         40         50         60         70         80
MLAAGVGGQG ERLAGRRRKM AVESRVTQEE IKKEPEKPID REKTCPLLLR VFTTNNGRHH RMDEFSRGNV PSSELQIYTW
        90        100        110        120        130        140        150        160
MDATLKELTS LVKEVYPEAR KKGTHFNFAI VFTDVKRPGY RVKEIGSTMS GRKGTDDSMT LQSQKFQIGD YLDIAITPPN
       170        180
RAPPPSGRMR PY
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2664	1	541.3186	91.64	2	61.6	14.2	1	124-133	K.EIGSTMSGRK.G	Oxidation: 6

Detailed Protein Report

Protein 667: **PREDICTED: ligand-dependent nuclear receptor-interacting factor 1 isoform X2 [Homo sapiens]**

Accession:	gi|578799447	**Score:**	24.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	69.2
Database Date:	2015-11-30	**pI:**	10.3
Modification(s):	Oxidation	**Sequence Coverage [%]:**	4.2
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	0.79	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	2.92	**CV:**	0.00 %	**No. of 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	Ratios
451	1	562.6268	-261.41	2	35.0	12.9	0	354-363	K.DNALVMFNGK.V	Oxidation: 6	mdown:qdown 0.79 Wdown:Qdown 2.92

Detailed Protein Report

Protein 668: BTB/POZ domain-containing protein 7 isoform 3 [Homo sapiens]

Accession:	gi|574284911	**Score:**	24.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	85.5
Database Date:	2015-11-30	**pI:**	8.0
		Sequence Coverage [%]:	4.7
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	6.56	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	9.19	**CV:**	0.00 %	**No. of Peptides:**	1

```
        10         20         30         40         50         60         70         80
MAGGAGAGAD GGAGGGGGGG DGSGPSGSSS GGRSLRGCED IIAESISLDT LIAILKWSSH PYGSKWVHRQ ALHFLCEEFS
        90        100        110        120        130        140        150        160
QVMTSDVFYE LSKDHLLTAI QSDYLQASEQ DILKYLIKWG EHQLMKRIAD REPNLLSGTA HSVNKRGVKR RDLDMEELRE
       170        180        190        200        210        220        230        240
ILSSLLPFVR IEHILPINSE VLSDAMKRGL ISTPPSDMLP TTEGGKSNAW LRQKNAGIYV RPRLFSPYVE EAKSVLDEMM
       250        260        270        280        290        300        310        320
VEQTDLVRLR MVRMSNVPDT LYMVNNAVPQ CCHMISHQQI SSNQSSPPSV VANEIPVPRL LIMKDMVRRL QELRHTEQVQ
       330        340        350        360        370        380        390        400
RAYALNCGEG ATVSYEIQIR VLREFGLADA AAELLQNPHK FFPDERFGDE SPLLTMRQPG RCRVNSTPPA ETMFTDLDSF
       410        420        430        440        450        460        470        480
VAFHPPLPPP PPPYHPPATP IHNQLKAGWK QRPPSQHPSR SFSYPCNHSL FHSRTAPKAG PPPVYLPSVK AAPPDCTSTA
       490        500        510        520        530        540        550        560
GLGRQTVAAA AATTTSTATA AAAAASEKQV RTQPVLNDLM PDIAVGVSTL SLKDRRLPEL AVDTELSQSV SEAGPGPPQH
       570        580        590        600        610        620        630        640
LSCIPQRHTH TSRKKHTLEQ KTDTRENPQE YPDFYDFSNA ACRPSTPALS RRTPSPSQGG YFGPDLYSHN KASPSGLKSA
       650        660        670        680        690        700        710        720
YLPGQTSPKK QEEARREYPL SPDGHLHRQK NEPIHLDVVE QPPQRSDFPL AAPENASTGP AHVRGRTAVE TDLTFGLTPN
       730        740        750        760        770        780        790
RPSLSACSSE APEERSGRRL ADSESLGHGA QRNTDLERED SISRGRRSPS KPDFLYKKSA L
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1042	1	670.8061	-37.58	2	41.8	11.1	0	740-752	R.LADSESLGHGAQR.N		Wdown:Qdown 9.19 mdown:qdown 6.56

Detailed Protein Report

Protein 669: 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:	2

Quantitation

mdown:qdown	**Median:**	1.70	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	1.00	**CV:**	0.00 %	**No. of 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	Ratios
1739	1	1023.8681	-109.14	2	51.7	12.0	1	71-87	K.ECKHCNIVAYFGSYLSR.E	Carbamidomethyl: 2	
710	1	676.9374	111.28	2	38.2	12.4	0	143-155	K.GANILLTDHGDVK.L		Wdown:Qdown 1.00 mdown:qdown 1.70

Detailed Protein Report

Protein 670: myosin phosphatase Rho-interacting protein isoform 2 [Homo sapiens]

Accession:	gi|50980301	**Score:**	24.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	116.5
Database Date:	2015-11-30	**pI:**	5.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.6
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MSAAKENPCR KFQANIFNKS KCQNCFKPRE SHLLNDEDLT QAKPIYGGWL LLAPDGTDFD NPVHRSRKWQ RRFFILYEHG

        90        100        110        120        130        140        150        160
LLRYALDEMP TTLPQGTINM NQCTDVVDGE GRTGQKFSLC ILTPEKEHFI RAETKEIVSG WLEMLMVYPR TNKQNQKKKR

       170        180        190        200        210        220        230        240
KVEPPTPQEP GPAKVAVTSS SSSSSSSSSI PSAEKVPTTK STLWQEEMRT KDQPDGSSLS PAQSPSQSQP PAASSLREPG

       250        260        270        280        290        300        310        320
LESKEEESAM SSDRMDCGRK VRVESGYFSL EKTKQDLKAE EQQLPPPLSP PSPSTPNHRR SQVIEKFEAL DIEKAEHMET

       330        340        350        360        370        380        390        400
NAVGPSPSSD TRQGRSEKRA FPRKRDFTNE APPAPLPDAS ASPLSPHRRA KSLDRRSTEP SVTPDLLNFK KGWLTKQYED

       410        420        430        440        450        460        470        480
GQWKKHWFVL ADQSLRYYRD SVAEEAADLD GEIDLSACYD VTEYPVQRNY GFQIHTKEGE FTLSAMTSGI RRNWIQTIMK

       490        500        510        520        530        540        550        560
HVHPTTAPDV TSSLPEEKNK SSCSFETCPR PTEKQEAELG EPDPEQKRSR ARERRREGRS KTFDWAEFRP IQQALAQERV

       570        580        590        600        610        620        630        640
GGVGPADTHE PLRPEAEPGE LERERARRRE ERRKRFGMLD ATDGPGTEDA ALRMEVDRSP GLPMSDLKTH NVHVEIEQRW

       650        660        670        680        690        700        710        720
HQVETTPLRE EKQVPIAPVH LSSEDGGDRL STHELTSLLE KELEQSQKEA SDLLEQNRLL QDQLRVALGR EQSAREGYVL

       730        740        750        760        770        780        790        800
QATCERGFAA MEETHQKKIE DLQRQHQREL EKLREEKDRL LAEETAATIS AIEAMKNAHR EEMERELEKS QRSQISSVNS

       810        820        830        840        850        860        870        880
DVEALRRQYL EELQSVQREL EVLSEQYSQK CLENAHLAQA LEAERQALRQ CQRENQELNA HNQELNNRLA AEITRLRTLL

       890        900        910        920        930        940        950        960
TGDGGGEATG SPLAQGKDAY ELEVLLRVKE SEIQYLKQEI SSLKDELQTA LRDKKYASDK YKDIYTELSI AKAKADCDIS

       970        980        990       1000       1010       1020       1030
RLKEQLKAAT EALGEKSPDS ATVSGYDIMK SKSNPDFLKK DRSCVTRQLR NIRSKSVIEQ VSWDT
```

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	614-639	R.MEVDRSPGLPMSDLKTHNVHVEIEQR.W	Oxidation: 11

Detailed Protein Report

Protein 671: **actin-binding Rho-activating protein [Homo sapiens]**

Accession: gi|21040251
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 24.4
MW [kDa]: 43.1
pI: 9.4
Sequence Coverage [%]: 7.9
No. of unique Peptides: 1

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

Detailed Protein Report

Protein 672: F-box only protein 32 isoform 2 [Homo sapiens]

Accession:	gi|22547144	**Score:**	24.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	24.7
Database Date:	2015-11-30	**pI:**	10.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	5.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MNILEKVVLK	VLEDQQNIRL	IRELLQTLYT	SLCTLVQRVG	KSVLVGNINM	WVYRMETILH	WQQQLNNIQI	TRPAFKGLTF
90	100	110	120	130	140	150	160
TDLPLCLQLN	IMQRLSDGRD	LVSLGQAAPD	LHVLSEDRLL	WKKLCQYHFS	ERQIRKRLIL	SDKGQLDWKK	MYFKLVRCYP
170	180	190	200	210	220		
RKEQYGDTLQ	LCKHCHILSW	KGTDHPCTAN	NPESCSVSLS	PQDFINLFKF			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2617	2	741.8602	-8.51	2	63.4	24.4	1	162-173	R.KEQYGDTLQLCK.H	Carbamidomethyl: 11

Detailed Protein Report

Protein 673: **amyloid beta A4 precursor protein-binding family B member 1-interacting protein [Homo sapiens]**

Accession:	gi|56118221	**Score:**	24.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	73.1
Database Date:	2015-11-30	**pI:**	5.3
		Sequence Coverage [%]:	3.3
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|578818421	refseq_human (refseq_human_20140103.fasta)	PREDICTED: amyloid beta A4 precursor protein-binding family B member 1-interacting protein isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MGESSEDIDQ	MFSTLLGEMD	LLTQSLGVDT	LPPPDPNPPR	AEFNYSVGFK	DLNESLNALE	DQDLDALMAD	LVADISEAEQ
90	100	110	120	130	140	150	160
RTIQAQKESL	QNQHHSASLQ	ASIFSGAASL	GYGTNVAATG	ISQYEDDLPP	PPADPVLDLP	LPPPPPEPLS	QEEEEAQAKA
170	180	190	200	210	220	230	240
DKIKLALEKL	KEAKVKKLVV	KVHMNDNSTK	SLMVDERQLA	RDVLDNLFEK	THCDCNVDWC	LYEIYPELQI	ERFFEDHENV
250	260	270	280	290	300	310	320
VEVLSDWTRD	TENKILFLEK	EEKYAVFKNP	QNFYLDNRGK	KESKETNEKM	NAKNKESLLE	ESFCGTSIIV	PELEGALYLK
330	340	350	360	370	380	390	400
EDGKKSWKRR	YFLLRASGIY	YVPKGKTKTS	RDLACFIQFE	NVNIYYGTQH	KMKYKAPTDY	CFVLKHPQIQ	KESQYIKYLC
410	420	430	440	450	460	470	480
CDDTRTLNQW	VMGIRIAKYG	KTLYDNYQRA	VAKAGLASRW	TNLGTVNAAA	PAQPSTGPKT	GTTQPNGQIP	QATHSVSAVL
490	500	510	520	530	540	550	560
QEAQRHAETS	KDKKPALGNH	HDPAVPRAPH	APKSSLPPPP	PVRRSSDTSG	SPATPLKAKG	TGGGGLPAPP	DDFLPPPPPP
570	580	590	600	610	620	630	640
PPLDDPELPP	PPPDFMEPPP	DFVPPPPPSY	AGIAGSELPP	PPPPPPAPAP	APVPDSARPP	PAVAKRPPVP	PKRQENPGHP
650	660	670					
GGAGGGEQDF	MSDLMKALQK	KRGNVS					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
587	1	472.2712	-35.10	2	36.2	12.5	1	430-439	R.AVAKAGLASR.W	

Detailed Protein Report

Protein 674: **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

Detailed Protein Report

Protein 675: PREDICTED: nuclear receptor coactivator 1 isoform X5 [Homo sapiens]

Accession: gi|578803237
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 24.3
MW [kDa]: 151.3
pI: 5.7
Sequence Coverage [%]: 2.2
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MSGLGDSSSD	PANPDSHKRK	GSPCDTLASS	TEKRRREQEN	KYLEELAELL	SANISDIDSL	SVKPDKCKIL	KKTVDQIQLM
90	100	110	120	130	140	150	160
KRMEQEKSTT	DDDVQKSDIS	SSSQGVIEKE	SLGPLLLEAL	DGFFFVVNCE	GRIVFVSENV	TSYLGYNQEE	LMNTSVYSIL
170	180	190	200	210	220	230	240
HVGDHAEFVK	NLLPKSLVNG	VPWPQEATRR	NSHTFNCRML	IHPPDEPGTE	NQEACQRYEV	MQCFTVSQPK	SIQEDGEDFQ
250	260	270	280	290	300	310	320
SCLICIARRL	PRPPAITGVE	SFMTKQDTTV	MTRGTASSPS	YRFILNDGTM	LSAHTKCKLC	YPQSPDMQPF	IMGIHIIDRE
330	340	350	360	370	380	390	400
HSGLSPQDDT	NSGMSIPRVN	PSVNPSISPA	HGVARSSTLP	PSNSNMVSTR	INRQQSSDLH	SSSHSNSSNS	QGSFGCSPGS
410	420	430	440	450	460	470	480
QIVANVALNQ	GQASSQSSNP	SLNLNNSPME	GTGISLAQFM	SPRRQVTSGL	ATRPRMPNNS	FPPNISTLSS	PVGMTSSACN
490	500	510	520	530	540	550	560
NNNRSYSNIP	VTSLQGMNEG	PNNSVGFSAS	SPVLRQMSSQ	NSPSRLNIQP	AKAESKDNKE	IASILNEMIQ	SDNSSSDGKP
570	580	590	600	610	620	630	640
LDSGLLHNND	RLSDGDSKYS	QTSHKLVQLL	TTTAEQQLRH	ADIDTSCKDV	LSCTGTSNSA	SANSSGGSCP	SSHSSLTERH
650	660	670	680	690	700	710	720
KILHRLLQEG	SPSDITTLSV	EPDKKDSAST	SVSVTGQVQG	NSSIKLELDA	SKKKESKDHQ	LLRYLLDKDE	KDLRSTPNLS
730	740	750	760	770	780	790	800
LDDVKVKVEK	KEQMDPCNTN	PTPMTKPTPE	EIKLEAQSQF	TADLDQFDQL	LPTLEKAAQL	PGLCETDRMD	GAVTSVTIKS
810	820	830	840	850	860	870	880
EILPASLQSA	TARPTSRLNR	LPELELEAID	NQFGQPGTGD	QIPWTNNTVT	AINQSKSEDQ	CISSQLDELL	CPPTTVEGRN
890	900	910	920	930	940	950	960
DEKALLEQLV	SFLSGKDETE	LAELDRALGI	DKLVQGGGLD	VLSERFPPQQ	ATPPLIMEER	PNLYSQPYSS	PSPTANLPSP
970	980	990	1000	1010	1020	1030	1040
FQGMVRQKPS	LGTMPVQVTP	PRGAFSPGMG	MQPRQTLNRP	PAAPNQLRLQ	LQQRLQGQQQ	LIHQNRQAIL	NQFAATAPVG
1050	1060	1070	1080	1090	1100	1110	1120
INMRSGMQQQ	ITPQPPLNAQ	MLAQRQRELY	SQQHRQRQLI	QQQRAMLMRQ	QSFGNNLPPS	SGLPVQMGNP	RLPQGAPQQF
1130	1140	1150	1160	1170	1180	1190	1200
PYPPNYGTNP	GTPPASTSPF	SQLAANPEAS	LANRNSMVSR	GMTGNIGGQF	GTGINPQMQQ	NVFQYPGAGM	VPQGEANFAP
1210	1220	1230	1240	1250	1260	1270	1280
SLSPGSSMVP	MPIPPPQSSL	LQQTPPASGY	QSPDMKAWQQ	GAIGNNNVFS	QAVQNQPTPA	QPGVYNNMSI	TVSMAGGNTN
1290	1300	1310	1320	1330	1340	1350	1360
VQNMNPMMAQ	MQMSSLQMPG	MNTVCPEQIN	DPALRHTGLY	CNQLSSTDLL	KTEADGTQQV	QQVQVFADVQ	CTVNLVGGDP
1370	1380	1390	1400				
YLNQPGPLGT	QKPTSGPQTP	QAQQKSLLQQ	LLTE				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2435	1	648.2013	-141.21	2	60.8	10.5	0	21-33	K.GSPCDTLASSTEK.R	

Detailed Protein Report

Protein 676: **PREDICTED: kinesin-like protein KIF3C isoform X1 [Homo sapiens]**

Accession:	gi|578802893	**Score:**	24.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	89.3
Database Date:	2015-11-30	**pI:**	9.0
		Sequence Coverage [%]:	2.4
		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 677: 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
1710	1	1273.4767	-125.38	1	51.3	11.0	0	151-160	R.IWSPWSPWSK.C	

Detailed Protein Report

Protein 678: 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 679: 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 680: chitotriosidase-1 isoform 3 precursor [Homo sapiens]

Accession:	gi|395393999	**Score:**	24.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	46.7
Database Date:	2015-11-30	**pI:**	8.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	5.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MVRSVAWAGF	MVLLMIPWGS	AAKLVCYFTN	WAQYRQGEAR	FLPKDLDPSL	CTHLIYAFAG	MTNHQLSTTE	WNDETLYQEF
90	100	110	120	130	140	150	160
NGLKKMNPKL	KTLLAIGGWN	FGTQKFTDMV	ATANNRQTFV	NSAIRFLRKY	SFDGLDLDWE	YPGSQGSPAF	QQEAQTSGKE
170	180	190	200	210	220	230	240
RLLLSAAVPA	GQTYVDAGYE	VDKIAQNLDF	VNLMAYDFHG	SWEKVTGHNS	PLYKRQEESG	AAASLNVDAA	VQQWLQKGTP
250	260	270	280	290	300	310	320
ASKLILGMPT	YGRSFTLASS	SDTRVGAPAT	GSGTPGPFTK	EGGMLAYYEV	CSWKGATKQR	IQDQKVPYIF	RDNQWVGFDD
330	340	350	360	370	380	390	400
VESFKTKGRY	PLIQTLRQEL	SLPYLPSGTP	ELEVPKPGQP	SEPEHGPSPG	QDTFCQGKAD	GLYPNPRERS	SFYSCAAGRL
410	420	430					
FQQSCPTGLV	FSNSCKCCTW	N					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2659	1	826.4139	65.06	2	64.4	13.9	0	281-294	K.EGGMLAYYEVCSWK.G	Oxidation: 4

Detailed Protein Report

Protein 681: transcription factor LBX2 isoform 2 [Homo sapiens]

Accession:	gi|57528437	**Score:**	24.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	21.3
Database Date:	2015-11-30	**pI:**	11.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	9.8
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MGKRTSLEVS LGELGGEKCR GGRRSFPPLA ASRPARPGGW RWARRDLCKT ASRAENNSQA CRPQRRAGPD ALGPGPFGRK
        90        100        110        120        130        140        150        160
RRKSRTAFTA QQVLELERRF VFQKYLAPSE RDGLATRLGL ANAQVVTWFQ NRRAKLKRDV EEMRADVASL RALSPEVLCS
       170        180        190        200
LALPEGAPDP GLCLGPAGPD SRPHLSDEEI QVDD
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
86	1	1003.1478	137.21	2	29.8	12.4	2	5-23	R.TSLEVSLGELGGEKCRGGR.R	Carbamidomethyl: 15

Detailed Protein Report

Protein 682: 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 683: 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 684: **conserved oligomeric Golgi complex subunit 5 isoform 2 [Homo sapiens]**

Accession:	gi|240849537	**Score:**	24.1
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 685: PREDICTED: germinal-center associated nuclear protein isoform X6 [Homo sapiens]

Accession:	gi|578836729	**Score:**	24.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	165.4
Database Date:	2015-11-30	**pI:**	5.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.4
		No. of unique Peptides:	2

Quantitation

Wdown:Qdown **Median:** 1.69 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MAIFWHRKKI	SPNKKPFSLK	EKKPGDGEVS	PSTEDAPFQH	SPLGKAAGRT	GASSLLNKSS	PVKKPSLLKA	HQFEGDSFDS
90	100	110	120	130	140	150	160
ASEGSEGLGP	CVLSLSTLIG	TVAETSKEKY	RLLDQRDRIM	RQARVKRTDL	DKARTFVGTC	LDMCPEKERY	MRETRSQLSV
170	180	190	200	210	220	230	240
FEVVPGTDQV	DHAAAVKEYS	RSSADQEEPL	PHELRPLPVL	SRTMDYLVTQ	IMDQKEGSLR	DWYDFVWNRT	RGIRKDITQQ
250	260	270	280	290	300	310	320
HLCDPLTVSL	IEKCTRFHIH	CAHFMCEEPM	SSFDAKINNE	NMTKCLQSLK	EMYQDLRNKG	VFCASEAEFQ	GYNVLLSLNK
330	340	350	360	370	380	390	400
GDILREVQQF	HPAVRNSSEV	KFAVQAFAAL	NSNNFVRFFK	LVQSASYLNA	CLLHCYFSQI	RKDALRALNF	AYTVSTQRST
410	420	430	440	450	460	470	480
IFPLDGVVRM	LLFRDCEEAT	DFLTCHGLTV	SDGCVELNRS	AFLEPEGLSK	TRKSVFITRK	LTVSVGEIVN	GGPLPPVPRH
490	500	510	520	530	540	550	560
TPVCSFNSQN	KYIGESLAAE	LPVSTQRPGS	DTVGGGRGEE	CGVEPDAPLS	SLPQSLPAPA	PSPVPLPPVL	ALTPSVAPSL
570	580	590	600	610	620	630	640
FQLSVQPEPP	PPEPVPMYSD	EDLAQVVDEL	IQEALQRDCE	EVGSAGAAYA	AAALGVSNAA	MEDLLTAATT	GILRHIAAEE
650	660	670	680	690	700	710	720
VSKERERREQ	ERQRAEEERL	KQERELVLSE	LSQGLAVELM	ERVMMEFVRE	TCSQELKNAV	ETDQRVRVAR	CCEDVCAHLV
730	740	750	760	770	780	790	800
DLFLVEEIFQ	TAKETLQELQ	CFCKYLQRWR	EAVTARKKLR	RQMRAFPAAP	CCVDVSDRLR	ALAPSAECPI	AEENLARGLL
810	820	830	840	850	860	870	880
DLGHAGRLGI	SCTRLRRLRN	KTAHQMKVQH	FYQQLLSDVA	WASLDLPSLV	AEHLPGRQEH	VFWKLVLVLP	DVEEQSPESC
890	900	910	920	930	940	950	960
GRILANWLKV	KFMGDEGSVD	DTSSDAGGIQ	TLSLFNSLSS	KGDQMISVNV	CIKVAHGALS	DGAIDAVETQ	KDLLGASGLM
970	980	990	1000	1010	1020	1030	1040
LLLPPKMKSE	DMAEEDVYWL	SALLQLKQLL	QAKPFQPALP	LVVLVPSPGG	DAVEKEVEDG	LMLQDLVSAK	LISDYTVTEI
1050	1060	1070	1080	1090	1100	1110	1120
PDTINDLQGS	TKVLQAVQWL	VSHCPHSLDL	CCQTLIQYVE	DGIGHEFSGR	FFHDRRERRL	GGLASQEPGA	IIELFNSVLQ
1130	1140	1150	1160	1170	1180	1190	1200
FLASVVSSEQ	LCDLSWPVTE	FAEAGGSRLL	PHLHWNAPEH	LAWLKQAVLG	FQLPQMDLPP	LGAPWLPVCS	MVVQYASQIP
1210	1220	1230	1240	1250	1260	1270	1280
SSRQTQPVLQ	SQVENLLHRT	YCRWKSKSPS	PVHGAGPSVM	EIPWDDLIAL	CINHKLRDWT	PPRLPVTSEA	LSEDGQICVY
1290	1300	1310	1320	1330	1340	1350	1360
FFKNDLKKYD	VPLSWEQARL	QTQKELQLRE	GRLAIKPFHP	SANNFPIPLL	HMHRNWKRST	ECAQEGRIPS	TEDLMRGASA
1370	1380	1390	1400	1410	1420	1430	1440
EELLAQCLSS	SLLLEKEENK	RFEDQLQQWL	SEDSGAFTDL	TSLPLYLPQT	LVSLSHTIEP	VMKTSVTTSP	QSDMMREQLQ
1450	1460	1470	1480	1490			
LSEATGTCLG	ERLKHLERLI	RSSREEEVAS	ELHLSALLDM	VDI			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2547	1	885.0863	142.56	2	62.3	12.8	0	342-357	K.FAVQAFAALNSNNFVR.F		Wdown:Qdown 1.69
101	1	707.1277	128.95	3	30.0	11.3	0	1357-1376	R.GASAEELLAQCLSSSLLLEK.E	Carbamidomethyl: 11	

Detailed Protein Report

Protein 686: PREDICTED: leucine-rich repeat-containing protein 49 isoform X3 [Homo sapiens]

Accession:	gi|530406077	**Score:**	24.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	45.4
Database Date:	2015-11-30	**pI:**	9.0
		Sequence Coverage [%]:	4.6
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MMQLRQLDMK RITEEERRMA SVLAKKEEEK KRESHKQSLL KEKKRLTINN VARQWDLQQQ RVANIATNED RKDSDSPQDP
        90        100        110        120        130        140        150        160
CQIDGSTLSA FPEETGPLDS GLNNALQGLS VIDTYLVEVD GDTLSLYGSG ALESLDRNWS VQTAGMITTV SFTFIEFDEI
       170        180        190        200        210        220        230        240
VQVLPKLKIK FPNSLHLKFK ETNLVMLQQF NALAQLRRID QLTIDPQGNP VVNFTLWKYY VLFRLSHFSM QKINGTEVTQ
       250        260        270        280        290        300        310        320
NDMIMAERLF GILAHVASSE LPQYRLISIL GDARKKQFRY LLESKGKKPG IINEENNDSK RLVGENTNRA TLNYTTRDFY
       330        340        350        360        370        380        390        400
NEKLEEIKEK KKFCKTYIED LVKEATEINM KNEALQKLWP QMFIELVRDA VIEIRNKNSY MKLCLQQITD QK
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
784	1	450.7564	-22.94	2	38.6	10.3	0	46-53	R.LTINNVAR.Q	

Detailed Protein Report

Protein 687: **DDB1- and CUL4-associated factor 13 [Homo sapiens]**

Accession:	gi|229892270	**Score:**	24.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	67.5
Database Date:	2015-11-30	**pI:**	10.2
		Sequence Coverage [%]:	4.0
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MQWPPPWRRS PLVSATPPPG PTRGLLCPRR VSEAGDSSTE GARTGHRHYV TPAESAMEGR SQPLPSLRPA SPTNAPAHGR
        90        100        110        120        130        140        150        160
GSDCTAKEPP LANVCRQNYG AAQDPVEPAG RRSASHVTGS SLGKAEVACG RRWRWAELLA DTSWSPAGRA TEMKVKMLSR
       170        180        190        200        210        220        230        240
NPDNYVRETK LDLQRVPRNY DPALHPFEVP REYIRALNAT KLERVFAKPF LASLDGHRDG VNCLAKHPEK LATVLSGACD
       250        260        270        280        290        300        310        320
GEVRIWNLTQ RNCIRTIQAH EGFVRGICTR FCGTSFFTVG DDKTVKQWKM DGPGYGDEEE PLHTILGKTV YTGIDHHWKE
       330        340        350        360        370        380        390        400
AVFATCGQQV DIWDEQRTNP ICSMTWGFDS ISSVKFNPIE TFLLGSCASD RNIVLYDMRQ ATPLKKVILD MRTNTICWNP
       410        420        430        440        450        460        470        480
MEAFIFTAAN EDYNLYTFDM RALDTPVMVH MDHVSAVLDV DYSPTGKEFV SASFDKSIRI FPVDKSRSRE VYHTKRMQHV
       490        500        510        520        530        540        550        560
ICVKWTSDSK YIMCGSDEMN IRLWKANASE KLGVLTSREK AAKDYNQKLK EKFQHYPHIK RIARHRHLPK SIYSQIQEQR
       570        580        590        600
IMKEARRRKE VNRIKHSKPG SVPLVSEKKK HVVAVVK
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1462	1	706.0794	76.84	3	47.1	12.4	1	179-195	R.NYDPALHPFEVPREYIR.A	

Detailed Protein Report

Protein 688: **PREDICTED: V(D)J recombination-activating protein 1 isoform X1 [Homo sapiens]**

Accession:	gi|530395605	**Score:**	24.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	119.0
Database Date:	2015-11-30	**pI:**	9.8
		Sequence Coverage [%]:	3.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAASFPPTLG	LSSAPDEIQH	PHIKFSEWKF	KLFRVRSFEK	TPEEAQKEKK	DSFEGKPSLE	QSPAVLDKAD	GQKPVPTQPL
90	100	110	120	130	140	150	160
LKAHPKFSKK	FHDNEKARGK	AIHQANLRHL	CRICGNSFRA	DEHNRRYPVH	GPVDGKTLGL	LRKKEKRATS	WPDLIAKVFR
170	180	190	200	210	220	230	240
IDVKADVDSI	HPTEFCHNCW	SIMHRKFSSA	PCEVYFPRNV	TMEWHPHTPS	CDICNTARRG	LKRKSLQPNL	QLSKKLKTVL
250	260	270	280	290	300	310	320
DQARQARQHK	RRAQARISSK	DVMKKIANCS	KIHLSTKLLA	VDFPEHFVKS	ISCQICEHIL	ADPVETNCKH	VFCRVCILRC
330	340	350	360	370	380	390	400
LKVMGSYCPS	CRYPCFPTDL	ESPVKSFLSV	LNSLMVKCPA	KECNEEVSLE	KYNHHISSHK	ESKEIFVHIN	KGGRPRQHLL
410	420	430	440	450	460	470	480
SLTRRAQKHR	LRELKLQVKA	FADKEEGGDV	KSVCMTLFLL	ALRARNEHRQ	ADELEAIMQG	KGSGLQPAVC	LAIRVNTFLS
490	500	510	520	530	540	550	560
CSQYHKMYRT	VKAITGRQIF	QPLHALRNAE	KVLLPGYHHF	EWQPPLKNVS	SSTDVGIIDG	LSGLSSSVDD	YPVDTIAKRF
570	580	590	600	610	620	630	640
RYDSALVSAL	MDMEEDILEG	MRSQDLDDYL	NGPFTVVVKE	SCDGMGDVSE	KHGSGPVVPE	KAVRFSFTIM	KITIAHSSQN
650	660	670	680	690	700	710	720
VKVFEEAKPN	SELCCKPLCL	MLADESDHET	LTAILSPLIA	EREAMKSSEL	MLELGGILRT	FKFIFRGTGY	DEKLVREVEG
730	740	750	760	770	780	790	800
LEASGSVYIC	TLCDATRLEA	SQNLVFHSIT	RSHAENLERY	EVWRSNPYHE	SVEELRDRVK	GVSAKPFIET	VPSIDALHCD
810	820	830	840	850	860	870	880
IGNAAEFYKI	FQLEIGEVYK	NPNASKEERK	RWQATLDKHL	RKKMNLKPIM	RMNGNFARKL	MTKETVDAVC	ELIPSEERHE
890	900	910	920	930	940	950	960
ALRELMDLYL	KMKPVWRSSC	PAKECPESLC	QYSFNSQRFA	ELLSTKFKYR	YEGKITNYFH	KTLAHVPEII	ERDGSIGAWA
970	980	990	1000	1010	1020	1030	1040
SEGNESGNKL	FRRFRKMNAR	QSKCYEMEDV	LKHHWLYTSK	YLQKFMNAHN	ALKTSGFTMN	PQASLGDPLG	IEDSLESQDS
1050							
MEF							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
692	1	648.3377	-44.07	2	37.5	11.1	2	487-497	K.MYRTVKAITGR.Q	

Detailed Protein Report

Protein 689: **zinc finger protein 93 [Homo sapiens]**

Accession:	gi|38708324	**Score:**	24.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	70.9
Database Date:	2015-11-30	**pI:**	10.3
		Sequence Coverage [%]:	3.2
		No. of unique Peptides:	1

Quantitation

Wdown:Qdown **Median:** 0.97 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MGPLQFRDVA	IEFSLEEWHC	LDTAQRNLYR	NVMLENYSNL	VFLGIVVSKP	DLIAHLEQGK	KPLTMKRHEM	VANPSVICSH
90	100	110	120	130	140	150	160
FAQDLWPEQN	IKDSFQKVIL	RRYEKRGHGN	LQLIKRCESV	DECKVHTGGY	NGLNQCSTTT	QSKVFQCDKY	GKVFHKFSNS
170	180	190	200	210	220	230	240
NRHNIRHTEK	KPFKCIECGK	AFNQFSTLIT	HKKIHTGEKP	YICEECGKAF	KYSSALNTHK	RIHTGEKPYK	CDKCDKAFIA
250	260	270	280	290	300	310	320
SSTLSKHEII	HTGKKPYKCE	ECGKAFNQSS	TLTKHKKIHT	GEKPYKCEEC	GKAFNQSSTL	TKHKKIHTGE	KPYVCEECGK
330	340	350	360	370	380	390	400
AFKYSRILTT	HKRIHTGEKP	YKCNKCGKAF	IASSTLSRHE	FIHMGKKHYK	CEECGKAFIW	SSVLTRHKRV	HTGEKPYKCE
410	420	430	440	450	460	470	480
ECGKAFKYSS	TLSSHKRSHT	GEKPYKCEEC	GKAFVASSTL	SKHEIIHTGK	KPYKCEECGK	AFNQSSSLTK	HKKIHTGEKP
490	500	510	520	530	540	550	560
YKCEECGKAF	NQSSSLTKHK	KIHTGEKPYK	CEECGKAFNQ	SSTLIKHKKI	HTREKPYKCE	ECGKAFHLST	HLTTHKILHT
570	580	590	600	610	620	630	
GEKPYRCREC	GKAFNHSATL	SSHKKIHSGE	KPYECDKCGK	AFISPSSLSR	HEIIHTGEKP		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
645	1	512.6921	-185.63	2	36.9	10.7	0	237-246	K.AFIASSTLSK.H		Wdown:Qdown 0.97

Detailed Protein Report

Protein 690: **stAR-related lipid transfer protein 8 isoform a [Homo sapiens]**

Accession:	gi|215820650	**Score:**	24.0
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:	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
2225	1	916.3247	-127.33	2	56.5	11.6	1	63-78	K.KNHGFLDEDSLGALCR.R	Carbamidomethyl: 15

Detailed Protein Report

Protein 691: PREDICTED: caspase-10 isoform X6 [Homo sapiens]

Accession:	gi|578805020	**Score:**	23.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	30.8
Database Date:	2015-11-30	**pI:**	9.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	13.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLRHSWKPYR	SPGKISMQVV	MRAAVYRMNR	NHRGLCVIVN	NHSFTSLKDR	QGTHKDAEIL	SHVFQWLGFT	VHIHNNVTKV
90	100	110	120	130	140	150	160
EMEMVLQKQK	CNPAHADGDC	FVFCILTHGR	FGAVYSSDEA	LIPIREIMSH	FTALQCPRLA	EKPKLFFIQA	CQGEEIQPSV
170	180	190	200	210	220	230	240
SIEADALNPE	QAPTSLQDSI	PAEADFLLGL	ATVPGYVSFR	HVEEGSWYIQ	SLCNHLKKLV	PRHEDILSIL	TAVNDDVSRR
250	260	270	280				
VDKQGTKKQM	PQPAFTLRKK	LVFPVPLDAL	SL				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1119	1	954.9584	-55.00	2	42.7	12.3	2	11-27	R.SPGKISMQVVMRAAVYR.M	Oxidation: 11

Detailed Protein Report

Protein 692: 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: 23.9
MW [kDa]: 111.2
pI: 6.4
Sequence Coverage [%]: 2.9
No. of unique Peptides: 2

Quantitation

Wdown:Qdown **Median:** 0.13 **CV:** 0.00 % **No. of 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	Ratios
2745	1	917.4783	88.58	2	63.3	10.8	0	644-660	K.HQCVCGNSTTHPEHAGR.I		
819	1	706.2304	-210.02	2	39.7	13.1	1	1000-1011	K.IIEIQSMSLKFS.-	Oxidation: 7	Wdown:Qdown 0.13

Detailed Protein Report

Protein 693: PREDICTED: tubulin-specific chaperone D isoform X12 [Homo sapiens]

Accession:	gi|578832042	**Score:**	23.9
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 694:	**PREDICTED: transforming acidic coiled-coil-containing protein 2 isoform X20 [Homo sapiens]**		
Accession:	gi|578818751	**Score:**	23.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	296.6
Database Date:	2015-11-30	**pI:**	4.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	0.9
		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

Detailed Protein Report

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 695: phosphoglycolate phosphatase [Homo sapiens]

Accession:	gi|108796653	**Score:**	23.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	34.0
Database Date:	2015-11-30	**pI:**	5.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	13.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAAAEAGGDD	ARCVRLSAER	AQALLADVDT	LLFDCDGVLW	RGETAVPGAP	EALRALRARG	KRLGFITNNS	SKTRAAYAEK
90	100	110	120	130	140	150	160
LRRLGFGGPA	GPGASLEVFG	TAYCTALYLR	QRLAGAPAPK	AYVLGSPALA	AELEAVGVAS	VGVGPEPLQG	EGPGDWLHAP
170	180	190	200	210	220	230	240
LEPDVRAVVV	GFDPHFSYMK	LTKALRYLQQ	PGCLLVGTNM	DNRLPLENGR	FIAGTGCLVR	AVEMAAQRQA	DIIGKPSRFI
250	260	270	280	290	300	310	320
FDCVSQEYGI	NPERTVMVGD	RLDTDILLGA	TCGLKTILTL	TGVSTLGDVK	NNQESDCVSK	KKMVPDFYVD	SIADLLPALQ
330							
G							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2202	1	1057.5324	-23.37	3	56.1	10.7	2	81-110	K.LRRLGFGGPAGPGASLEVFGTAYCTALYLR.Q	Carbamidomethyl: 24

Detailed Protein Report

Protein 696: FYVE, RhoGEF and PH domain-containing protein 4 [Homo sapiens]

Accession:	gi|198041928	**Score:**	23.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	86.6
Database Date:	2015-11-30	**pI:**	5.7
		Sequence Coverage [%]:	2.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
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 697: 60S ribosomal protein L35a [Homo sapiens]

Accession:	gi|16117791	**Score:**	23.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	12.5
Database Date:	2015-11-30	**pI:**	11.7
		Sequence Coverage [%]:	22.7
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|530375914	refseq_human (refseq_human_20140103.fasta)	PREDICTED: 60S ribosomal protein L35a isoform X2 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MSGRLWSKAI FAGYKRGLRN QREHTALLKI EGVYARDETE FYLGKRCAYV YKAKNNTVTP GGKPNKTRVI WGKVTRAHGN
        90        100        110        120
SGMVRAKFRS NLPAKAIGHR IRVMLYPSRI
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2762	1	733.8633	-77.98	2	63.6	11.8	2	88-100	K.FRSNLPAKAIGHR.I	

Protein 698: GTPase HRas isoform 2 [Homo sapiens]

Accession:	gi|34222246	**Score:**	23.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	18.9
Database Date:	2015-11-30	**pI:**	4.7
		Sequence Coverage [%]:	10.6
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	1.46	**CV:**	0.00 %	**No. of Peptides:**	1

Alias proteins:

Accession	Name	Description
gi|578839846	refseq_human (refseq_human_20140103.fasta)	PREDICTED: GTPase HRas isoform X1 [Homo sapiens]
gi|578820498	refseq_human (refseq_human_20140103.fasta)	PREDICTED: GTPase HRas isoform X3 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MTEYKLVVVG AGGVGKSALT IQLIQNHFVD EYDPTIEDSY RKQVVIDGET CLLDILDTAG QEEYSAMRDQ YMRTGEGFLC
        90        100        110        120        130        140        150        160
VFAINNTKSF EDIHQYREQI KRVKDSDDVP MVLVGNKCDL AARTVESRQA QDLARSYGIP YIETSAKTRQ GSRSGSSSSS
       170        180
GTLWDPPGPM
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2770	1	1002.0175	9.51	2	63.1	10.3	2	118-135	K.CDLAARTVESRQAQDLAR.S		mdown:qdown 1.46

Detailed Protein Report

Protein 699: **SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1-related [Homo sapiens]**

Accession:	gi|83715964	**Score:**	23.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	35.8
Database Date:	2015-11-30	**pI:**	9.9
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	6.9
		No. of unique Peptides:	2

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
318	1	591.7318	-78.66	2	33.1	10.4	1	145-153	K.MCTEKIQEK.K	Carbamidomethyl: 2; Oxidation: 1
132	1	725.9894	99.94	2	31.0	13.4	1	305-317	R.IKEILAQVASEHL.-	

Detailed Protein Report

Protein 700: E3 ubiquitin-protein ligase PDZRN3 [Homo sapiens]

Accession:	gi|57529737	**Score:**	23.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	119.5
Database Date:	2015-11-30	**pI:**	5.6
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	3.5
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MGFELDRFDG	DVDPDLKCAL	CHKVLEDPLT	TPCGHVFCAG	CVLPWVVQEG	SCPARCRGRL	SAKELNHVLP	LKRLILKLDI
90	100	110	120	130	140	150	160
KCAYATRGCG	RVVKLQQLPE	HLERCDFAPA	RCRHAGCGQV	LLRRDVEAHM	RDACDARPVG	RCQEGCGLPL	THGEQRAGGH
170	180	190	200	210	220	230	240
CCARALRAHN	GALQARLGAL	HKALKKEALR	AGKREKSLVA	QLAAAQLELQ	MTALRYQKKF	TEYSARLDSL	SRCVAAPPGG
250	260	270	280	290	300	310	320
KGEETKSLTL	VLHRDSGSLG	FNIIGGRPSV	DNHDGSSSEG	IFVSKIVDSG	PAAKEGGLQI	HDRIIEVNGR	DLSRATHDQA
330	340	350	360	370	380	390	400
VEAFKTAKEP	IVVQVLRRTP	RTKMFTPPSE	SQLVDTGTQT	DITFEHIMAL	TKMSSPSPPV	LDPYLLPEEH	PSAHEYYDPN
410	420	430	440	450	460	470	480
DYIGDIHQEM	DREELELEEV	DLYRMNSQDK	LGLTVCYRTD	DEDDIGIYIS	EIDPNSIAAK	DGRIREGDRI	IQINGIEVQN
490	500	510	520	530	540	550	560
REEAVALLTS	EENKNFSLLI	ARPELQLDEG	WMDDDRNDFL	DDLHMDMLEE	QHHQAMQFTA	SVLQQKKHDE	DGGTTDTATI
570	580	590	600	610	620	630	640
LSNQHEKDSG	VGRTDESTRN	DESSEQENNG	DDATASSNPL	AGQRKLTCSQ	DTLGSGDLPF	SNESFISADC	TDADYLGIPV
650	660	670	680	690	700	710	720
DECERFRELL	ELKCQVKSAT	PYGLYYPSGP	LDAGKSDPES	VDKELELLNE	ELRSIELECL	SIVRAHKMQQ	LKEQYRESWM
730	740	750	760	770	780	790	800
LHNSGFRNYN	TSIDVRRHEL	SDITELPEKS	DKDSSSAYNT	GESCRSTPLT	LEISPDNSLR	RAAEGISCPS	SEGAVGTTEA
810	820	830	840	850	860	870	880
YGPASKNLLS	ITEDPEVGTP	TYSPSLKELD	PNQPLESKER	RASDGSRSPT	PSQKLGSAYL	PSYHHSPYKH	AHIPAHAQHY
890	900	910	920	930	940	950	960
QSYMQLIQQK	SAVEYAQSQM	SLVSMCKDLS	SPTPSEPRME	WKVKIRSDGT	RYITKRPVRD	RLLRERALKI	REERSGMTTD
970	980	990	1000	1010	1020	1030	1040
DDAVSEMKMG	RYWSKEERKQ	HLVKAKEQRR	RREFMMQSRL	DCLKEQQAAD	DRKEMNILEL	SHKKMMKKRN	KKIFDNWMTI
1050	1060	1070					
QELLTHGTKS	PDGTRVYNSF	LSVTTV					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1837	1	716.3485	-12.08	3	51.6	12.4	2	157-176	R.AGGHCCARALRAHNGALQAR.L	Carbamidomethyl: 5, 6
2035	1	939.3035	-130.12	2	55.6	11.3	0	891-907	K.SAVEYAQSQMSLVSMCK.D	Oxidation: 10

Detailed Protein Report

Protein 701: myotubularin-related protein 8 [Homo sapiens]

Accession:	gi|21361759	**Score:**	23.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	78.9
Database Date:	2015-11-30	**pI:**	6.2
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDHITVPKVE	NVKLVDRYVS	KKPANGILYL	TATHLIYVEA	SGAARKETWI	ALHHIATVEK	LPITSLGCPL	TLRCKNFRVA
90	100	110	120	130	140	150	160
HFVLDSDLVC	HEVYISLLKL	SQPALPEDLY	AFSYNPKSSK	EMRESGWKLI	DPISDFGRMG	IPNRNWTITD	ANRNYEICST
170	180	190	200	210	220	230	240
YPPEIVVPKS	VTLGTVVGSS	KFRSKERVPV	LSYLYKENNA	AICRCSQPLS	GFYTRCVDDE	LLLEAISQTN	PGSQFMYVVD
250	260	270	280	290	300	310	320
TRPKLNAMAN	RAAGKGYENE	DNYANIRFRF	MGIENIHVMR	SSLQKLLEVC	ELKTPTMSEF	LSGLESSGWL	RHIKAIMDAG
330	340	350	360	370	380	390	400
IFITKAVKVE	KASVLVHCSD	GWDRTAQVCS	VASILLDPFY	RTFKGLMILI	EKEWISMGHK	FSQRCGHLDG	DSKEVSPIFT
410	420	430	440	450	460	470	480
QFLDCIWQLM	EQFPCAFEFN	ENFLLEIHDH	VFSCQFGNFL	GNCQKDREDL	RVYEKTHSVW	PFLVQRKPDF	RNPLYKGFTM
490	500	510	520	530	540	550	560
YGVLNPSTVP	YNIQFWCGMY	NRFDKGLQPK	QSMLESLLEI	KKQRAMLETD	VHELEKKLKV	RDEPPEEICT	CSQLGNILSQ
570	580	590	600	610	620	630	640
HLGSPLTNPL	GFMGINGDLN	TLMENGTLSR	EGGLRAQMDQ	VKSQGADLHH	NCCEIVGSLR	AINISGDVGI	SEAMGISGDM
650	660	670	680	690	700	710	
CTFEATGFSK	DLGICGAMDI	SEATGISGNL	GISEARGFSG	DMGILGDTGI	SKASTKEADY	SKHQ	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1061	1	956.7040	226.87	1	42.9	13.2	0	1-8	-.MDHITVPK.V	Oxidation: 1

Detailed Protein Report

Protein 702: **PREDICTED: ankyrin repeat domain-containing protein SOWAHC-like [Homo sapiens]**

Accession:	gi|341914886	**Score:**	23.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	25.7
Database Date:	2015-11-30	**pI:**	12.2
		Sequence Coverage [%]:	7.8
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	3.18	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	1.10	**CV:**	0.00 %	**No. of Peptides:**	1

10	20	30	40	50	60	70	80
MRSAAFTIPS	LKQWSPRCST	GRAELGKGEP	SPCTGRPEQR	GRRKSSLAPP	APTPDAGPQT	SKDLEPPPHG	CQEADRGGSW
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
GATTSRPFRQ	NLSDLGRHSV	LPLKRNLCPG	GSSLGAPPLR	TPQRRVTLAA	QRWLSRPQRR	AVGLGELDQG	AQLAALGLRW
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
GVDSLGGCPR	ASQPAGHSGL	HHTLTCLRRH	LALQAGASGH	AGQLPQRASA	AWEQQGQSYT	ALHLAAMYLG	DGEAASGNIG
250							
RRC							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1819	1	719.7489	-178.16	2	51.3	10.6	0	106-120	R.NLCPGGSSLGAPPLR.T		mdown:qdown 3.18 Wdown:Qdown 1.10

Detailed Protein Report

Protein 703: **PREDICTED: coiled-coil domain-containing protein 13 isoform X2 [Homo sapiens]**

Accession:	gi|530371957	**Score:**	23.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	52.8
Database Date:	2015-11-30	**pI:**	9.0
		Sequence Coverage [%]:	5.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAADESSQNT	LRLQFKAMQE	MQHKRLQKQM	EKKREKELSL	KSRADDQEEP	LEVSDGLSLL	HAGEPNSKNS	FEKRVLEDEI
90	100	110	120	130	140	150	160
EHLRNELRET	VDENGRLYKL	LKERDFEIKH	LKKKIEEDRF	AFTGTAGVAG	DVVATKIVEL	SKKNRLLMAE	SEGAKTRVKQ
170	180	190	200	210	220	230	240
LTNRIQELER	ELQTALTRLS	AKGATDAGAK	PPRAQMGDRA	LLETPEVKAL	QDRLVATNLK	MSDLRNQIQS	VKQELRMAQK
250	260	270	280	290	300	310	320
VLAREVGEDI	NVQQLLSSPG	TWRGRAQQIL	VLQSKVQELE	KQLGQARSQS	AGTASDELSV	YPDPRKLSAQ	EKNLLRIRSL
330	340	350	360	370	380	390	400
EREKQEGLEK	LASERDVLQR	ELEELKKKFE	GMRSRNKLLS	SEMKTLKSQM	GTLVEKGRHD	DELIDALMDQ	LKQLQEILGS
410	420	430	440	450	460	470	
LSLQEEKTRV	SQHHLDQQLN	SEAQRSNSLV	AQLQAMVAER	EAKVRQLEME	IGQLNVHASE	PKP	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1302	1	857.8300	-157.01	2	45.0	11.4	0	393-407	K.QLQEILGSLSLQEEK.T	

Detailed Protein Report

Protein 704: calcium-activated chloride channel regulator 1 precursor [Homo sapiens]

Accession:	gi|110611231	**Score:**	23.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	100.2
Database Date:	2015-11-30	**pI:**	5.9
		Sequence Coverage [%]:	4.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGPFKSSVFI	LILHLLEGAL	SNSLIQLNNN	GYEGIVVAID	PNVPEDETLI	QQIKDMVTQA	SLYLFEATGK	RFYFKNVAIL
90	100	110	120	130	140	150	160
IPETWKTKAD	YVRPKLETYK	NADVLVAEST	PPGNDEPYTE	QMGNCGEKGE	RIHLTPDFIA	GKKLAEYGPQ	GRAFVHEWAH
170	180	190	200	210	220	230	240
LRWGVFDEYN	NDEKFYLSNG	RIQAVRCSAG	ITGTNVVKKC	QGGSCYTKRC	TFNKVTGLYE	KGCEFVLQSR	QTEKASIMFA
250	260	270	280	290	300	310	320
QHVDSIVEFC	TEQNHNKEAP	NKQNQKCNLR	STWEVIRDSE	DFKKTTPMTT	QPPNPTFSLL	QIGQRIVCLV	LDKSGSMATG
330	340	350	360	370	380	390	400
NRLNRLNQAG	QLFLLQTVEL	GSWVGMVTFD	SAAHVQNELI	QINSGSDRDT	LAKRLPAAAS	GGTSICSGLR	SAFTVIRKKY
410	420	430	440	450	460	470	480
PTDGSEIVLL	TDGEDNTISG	CFNEVKQSGA	IIHTVALGPS	AAQELEELSK	MTGGLQTYAS	DQVQNNGLID	AFGALSSGNG
490	500	510	520	530	540	550	560
AVSQRSIQLE	SKGLTLQNSQ	WMNGTVIVDS	TVGKDTLFLI	TWTMQPPQIL	LWDPSGQKQG	GFVVDKNTKM	AYLQIPGIAK
570	580	590	600	610	620	630	640
VGTWKYSLQA	SSQTLTLTVT	SRASNATLPP	ITVTSKTNKD	TSKFPSPLVV	YANIRQGASP	ILRASVTALI	ESVNGKTVTL
650	660	670	680	690	700	710	720
ELLDNGAGAD	ATKDDGVYSR	YFTTYDTNGR	YSVKVRALGG	VNAARRRVIP	QQSGALYIPG	WIENDEIQWN	PPRPEINKDD
730	740	750	760	770	780	790	800
VQHKQVCFSR	TSSGGSFVAS	DVPNAPIPDL	FPPGQITDLK	AEIHGGSLIN	LTWTAPGDDY	DHGTAHKYII	RISTSILDLR
810	820	830	840	850	860	870	880
DKFNESLQVN	TTALIPKEAN	SEEVFLFKPE	NITFENGTDL	FIAIQAVDKV	DLKSEISNIA	RVSLFIPPQT	PPETPSPDET
890	900	910	920				
SAPCPNIHIN	STIPGIHILK	IMWKWIGELQ	LSIA				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2143	1	797.8056	45.88	3	57.0	11.8	2	374-397	K.RLPAAASGGTSICSGLRSAFTVIR.K	

Detailed Protein Report

Protein 705: PREDICTED: transcription elongation regulator 1 isoform X3 [Homo sapiens]

Accession:	gi|530380386	**Score:**	23.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	118.5
Database Date:	2015-11-30	**pI:**	9.6
		Sequence Coverage [%]:	1.9
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MAERGGDGGE	SERFNPGELR	MAQQQALRFR	GPAPPPNAVM	RGPPPLMRPP	PPFGMMRGPP	PPPRPPFGRP	PFDPNMPPMP
90	100	110	120	130	140	150	160
PPGGIPPPMG	PPHLQRPPFM	PPPMSSMPPP	PGMMFPPGMP	PVTAPGTPAL	PPTEEIWVEN	KTPDGKVYYY	NARTRESAWT
170	180	190	200	210	220	230	240
KPDGVKVIQQ	SELTPMLAAQ	AQVQAQAQAQ	AQAQAQAQAQ	AQAQAQAQAQ	AQAQAQAQAQ	AQAQAQAQAQ	AQAQAQAQAQ
250	260	270	280	290	300	310	320
AQVQAQVQAQ	VQAQAVGAST	PTTSSPAPAV	STSTSSSTPS	STTSTTTTAT	SVAQTVSTPT	TQDQTPSSAV	SVATPTVSVS
330	340	350	360	370	380	390	400
TPAPTATPVQ	TVPQPHPQTL	PPAVPHSVPQ	PTTAIPAFPP	VMVPPFRVPL	PGMPIPLPGV	AMMQIVSCPY	VKTVATTKTG
410	420	430	440	450	460	470	480
VLPGMAPPIV	PMIHPQVAIA	ASPATLAGAT	AVSEWTEYKT	ADGKTYYYNN	RTLESTWEKP	QELKEKEKLE	EKIKEPIKEP
490	500	510	520	530	540	550	560
SEEPLPMETE	EEDPKEEPIK	EIKEEPKEEE	MTEEEKAAQK	AKPVATAPIP	GTPWCVVWTG	DERVFFYNPT	TRLSMWDRPD
570	580	590	600	610	620	630	640
DLIGRADVDK	IIQEPPHKKG	MEELKKLRHP	TPTMLSIQKW	QFSMSAIKEE	QELMEEINED	EPVKAKKRKR	MSKKSFMWIA
650	660	670	680	690	700	710	720
RASLFRRDDN	KDIDSEKEAA	MEAEIKAARE	RAIVPLEARM	KQFKDMLLER	GVSAFSTWEK	ELHKIVFDPR	YLLLNPKERK
730	740	750	760	770	780	790	800
QVFDQYVKTR	AEEERREKKN	KIMQAKEDFK	KMMEEAKFNP	RATFSEFAAK	HAKDSRFKAI	EKMKDREALF	NEFVAAARKK
810	820	830	840	850	860	870	880
EKEDSKTRGE	KIKSDFFELL	SNHHLDSQSR	WSKVKDKVES	DPRYKAVDSS	SMREDLFKQY	IEKIAKVRSS	DVSWSDTRRT
890	900	910	920	930	940	950	960
LRKDHRWESG	SLLEREEKEK	LFNEHIEALT	KKKREHFRQL	LDETSAITLT	STWKEVKKII	KEDPRCIKFS	SSDRKKQREF
970	980	990	1000	1010	1020	1030	1040
EEYIRDKYIT	AKADFRTLLK	ETKFITYRSK	KLIQESDQHL	KDVEKILQND	KRYLVLDCVP	EERRKLIVAY	VDDLDRRGPP
1050	1060						
PPPTASEPTR	RSTK						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1365	3	473.0897	-307.94	2	45.6	13.1	1	836-843	K.DKVESDPR.Y	
809	1	697.8381	2.18	2	38.9	10.5	1	867-878	K.VRSSDVSWSDTR.R	

Detailed Protein Report

Protein 706: PREDICTED: hemicentin-2 isoform X1 [Homo sapiens]

Accession:	gi|578796176	**Score:**	23.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	139.5
Database Date:	2015-11-30	**pI:**	7.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPPTTGDATL	AFVFDVTGSM	WDELMQVIDG	ASRILERSLS	RRSQAIANYA	LVPFHDPDIG	PVTLTADPTV	FQRELRELYV
90	100	110	120	130	140	150	160
QGGGDCPEMS	VGAIKAAVEV	ANPGSFIYVF	SDARAKDYHK	KEELLRLLQL	KQSQVVFVLT	GDCGDHTHPG	YLAYEEIAAT
170	180	190	200	210	220	230	240
SSGQVFHLDK	QQVTEVLKWV	ESAIQASKVH	LLSTDHEEEG	EHTWRLPFDP	SLKEVTISLS	GPGPEIEVQD	PLGRILQEDE
250	260	270	280	290	300	310	320
GLNVLLNIPD	SAKVVAFKPE	HPGLWSIKVY	SSGRHSVRIT	GVSNIDFRAG	FSTQPLLDLN	HTLEWPLQGV	PISLVINSTG
330	340	350	360	370	380	390	400
LKAPGRLDSV	ELAQSSGKPL	LTLPTKPLSN	GSTHQLWGGP	PFHTPKERFY	LKVKGKDHEG	NPLLRVSGVS	YSGVAPGAPL
410	420	430	440	450	460	470	480
VSMAPRIHGY	LHQPLLVSCS	VHSALPFRLQ	LRRGEARLGE	ERHFQESGNS	SWEILRASKA	EEGTYECTAV	SRAGTGRAKA
490	500	510	520	530	540	550	560
QIVVTDPPPQ	LVPAPNVTVS	PGETAVLSCR	VLGEAPYNLT	WVRDWRVLPA	STGRVAQLAD	LSLEISGIIP	TDGGRYQCVA
570	580	590	600	610	620	630	640
SNANGVTRAS	VWLLVREAPQ	VSIHTSSQHF	SQGVEVKVSC	SASGYPTPHI	SWSRESQALQ	EDSRIHVDAQ	GTLIIQGVAP
650	660	670	680	690	700	710	720
EDAGNYSCQA	TNEVGTDQET	VTLYYTDPPS	VSAVNAVVLV	AVGEEAVLVC	EASGVPPPRV	IWYRGGLEMI	LAPEGSSSGK
730	740	750	760	770	780	790	800
LRIPAAQERD	AGTYTCRAVN	ELGDASAEIQ	LAVGHAPQLT	ELPRDVTVEL	GRSALLACRA	TGRPPPTVTW	RRGDGQPLGL
810	820	830	840	850	860	870	880
RLGAGRGSRS	RQPDSGVLFF	ESVAPEDQAP	YVCEARNVFG	KVQAEARLIV	TGHAPPQIAS	SAPTVRVLEG	QPVSLPCIVL
890	900	910	920	930	940	950	960
AGRPLPERHW	LKDGRPLPPG	SRHSIRADGS	LHLDRALQEH	AGRYSCVATN	TAGSQHRDVE	LVVQVPPRIH	PTATHHITNE
970	980	990	1000	1010	1020	1030	1040
GVPASLPCVA	SGVPAPTITW	TKETNALTSR	GPHYNVSKEG	TLLIAQPSAQ	DAGAYVCTAT	NTVGFSSQEM	RLSVNTKPRI
1050	1060	1070	1080	1090	1100	1110	1120
HMNGSRNANV	PLQVTAKAGE	EVTLDCEAKG	SPPPLVTWTK	DSRPVPPITN	RYGLLPSGSL	RLAQVQVGDS	GHYECTASNP
1130	1140	1150	1160	1170	1180	1190	1200
AGSASHRYVL	GVQGRTSWQP	QSLPVPHHPA	CLSGLSVPLL	QPTPRSVRLC	HLSLRAPLPP	PFATPTSCLS	QACLSSSTLS
1210	1220	1230	1240	1250	1260	1270	1280
LHLSPYPLRG	PGDAVQRPPT	TQGRAQWGPG	FGRTGVRGEP	MKVGLRGSLP	GTRGPAGSPG	CGDGKRPVRC	HRAPPAGSIL
1290	1300	1310					
MPPRGPSEPL	LPPLPSTRHF	VHL					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
423	1	718.2901	-107.80	3	34.3	11.0	2	1243-1265	K.VGLRGSLPGTRGPAGSPGCGDGK.R	Carbamidomethyl: 19

Detailed Protein Report

Protein 707: transcriptional regulator ERG isoform 5 [Homo sapiens]

Accession: gi|343478178
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 23.5
MW [kDa]: 41.4
pI: 7.9
Sequence Coverage [%]: 6.1
No. of unique Peptides: 1

```
        10         20         30         40         50         60         70         80
MVGSPDTVGM NYGSYMEEKH MPPPNMTTNE RRVIVPADPT LWSTDHVRQW LEWAVKEYGL PDVNILLFQN IDGKELCKMT
        90        100        110        120        130        140        150        160
KDDFQRLTPS YNADILLSHL HYLRETPLPH LTSDDVDKAL QNSPRLMHAR NTDLPYEPPR RSAWTGHGHP TPQSKAAQPS
       170        180        190        200        210        220        230        240
PSTVPKTEDQ RPQLDPYQIL GPTSSRLANP GSGQIQLWQF LLELLSDSSN SSCITWEGTN GEFKMTDPDE VARRWGERKS
       250        260        270        280        290        300        310        320
KPNMNYDKLS RALRYYYDKN IMTKVHGKRY AYKFDFHGIA QALQPHPPES SLYKYPSDLP YMGSYHAHPQ KMNFVAPHPP
       330        340        350        360        370
ALPVTSSSFF AAPNPYWNSP TGGIYPNTRL PTSHMPSHLG TYY
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2099	1	720.7086	-156.70	2	54.8	12.8	0	20-31	K.HMPPPNMTTNER.R	Oxidation: 2

Detailed Protein Report

Protein 708: dual specificity protein kinase TTK isoform 2 [Homo sapiens]

Accession:	gi|262399361	**Score:**	23.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	96.9
Database Date:	2015-11-30	**pI:**	9.2
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	4.1
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MESEDLSGRE	LTIDSIMNKV	RDIKNKFKNE	DLTDELSLNK	ISADTTDNSG	TVNQIMMMAN	NPEDWLSLLL	KLEKNSVPLS
90	100	110	120	130	140	150	160
DALLNKLIGR	YSQAIEALPP	DKYGQNESFA	RIQVRFAELK	AIQEPDDARD	YFQMARANCK	KFAFVHISFA	QFELSQGNVK
170	180	190	200	210	220	230	240
KSKQLLQKAV	ERGAVPLEML	EIALRNLNLQ	KKQLLSEEEK	KNLSASTVLT	AQESFSGSLG	HLQNRNNSCD	SRGQTTKARF
250	260	270	280	290	300	310	320
LYGENMPPQD	AEIGYRNSLR	QTNKTKQSCP	FGRVPVNLLN	SPDCDVKTDD	SVVPCFMKRQ	TSRSECRDLV	VPGSKPSGND
330	340	350	360	370	380	390	400
SCELRNLKSV	QNSHFKEPLV	SDEKSSELII	TDSITLKNKT	ESSLLAKLEE	TKEYQEPEVP	ESNQKQWQSK	RKSECINQNP
410	420	430	440	450	460	470	480
AASSNHWQIP	ELARKVNTEK	HTTFEQPVFS	VSKQSPPIST	SKWFDPKSIC	KTPSSNTLDD	YMSCFRTPVV	KNDFPPACQL
490	500	510	520	530	540	550	560
STPYGQPACF	QQQQHQILAT	PLQNLQVLAS	SSANECISVK	GRIYSILKQI	GSGGSSKVFQ	VLNEKKQIYA	IKYVNLEEAD
570	580	590	600	610	620	630	640
NQTLDSYRNE	IAYLNKLQQH	SDKIIRLYDY	EITDQYIYMV	MECGNIDLNS	WLKKKKSIDP	WERKSYWKNM	LEAVHTIHQH
650	660	670	680	690	700	710	720
GIVHSDLKPA	NFLIVDGMLK	LIDFGIANQM	QPDTTSVVKD	SQVGTVNYMP	PEAIKDMSSS	RENGKSKSKI	SPKSDVWSLG
730	740	750	760	770	780	790	800
CILYYMTYGK	TPFQQIINQI	SKLHAIIDPN	HEIEFPDIPE	KDLQDVLKCC	LKRDPKQRIS	IPELLAHPYV	QIQTHPVNQM
810	820	830	840	850	860		
AKGTTEEMKY	VLGQLVGLNS	PNSILKAAKT	LYEHYSGGES	HNSSSSKTFE	KKRGKK		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2620	1	710.3519	57.75	2	61.4	12.5	1	130-140	R.DYFQMARANCK.K	Carbamidomethyl: 10; Oxidation: 5
309	1	936.1804	52.20	3	32.6	11.1	2	391-414	K.RKSECINQNPAASSNHWQIPELAR.K	Carbamidomethyl: 5

Detailed Protein Report

Protein 709: ankyrin repeat and zinc finger domain-containing protein 1 isoform 1 [Homo sapiens]

Accession:	gi|109150425	**Score:**	23.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	80.9
Database Date:	2015-11-30	**pI:**	9.6
		Sequence Coverage [%]:	2.9
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|109150435	refseq_human (refseq_human_20140103.fasta)	ankyrin repeat and zinc finger domain-containing protein 1 isoform 1 [Homo sapiens]

10	20	30	40	50	60	70	80
MSPAPDAAPA	PASISLFDLS	ADAPVFQGLS	LVSHAPGEAL	ARAPRTSCSG	SGERESPERK	LLQGPMDISE	KLFCSTCDQT
90	100	110	120	130	140	150	160
FQNHQEQREH	YKLDWHRFNL	KQRLKDKPLL	SALDFEKQSS	TGDLSSISGS	EDSDSASEED	LQTLDRERAT	FEKLSRPPGF
170	180	190	200	210	220	230	240
YPHRVLFQNA	QGQFLYAYRC	VLGPHQDPPE	EAELLLQNLQ	SRGPRDCVVL	MAAAGHFAGA	IFQGREVVTH	KTFHRYTVRA
250	260	270	280	290	300	310	320
KRGTAQGLRD	ARGGPSHSAG	ANLRRYNEAT	LYKDVRDLLA	GPSWAKALEE	AGTILLRAPR	SGRSLFFGGK	GAPLQRGDPR
330	340	350	360	370	380	390	400
LWDIPLATRR	PTFQELQRVL	HKLTTLHVYE	EDPREAVRLH	SPQTHWKTVR	EERKKPTEEE	IRKICRDEKE	ALGQNEESPK
410	420	430	440	450	460	470	480
QGSGSEGEDG	FQVELELVEL	TVGTLDLCES	EVLPKRRRRK	RNKKEKSRDQ	EAGAHRTLLQ	QTQEEEPSTQ	SSQAVAAPLG
490	500	510	520	530	540	550	560
PLLDEAKAPG	QPELWNALLA	ACRAGDVGVL	KLQLAPSPAD	PRVLSLLSAP	LGSGGFTLLH	AAAAAGRGSV	VRLLLEAGAD
570	580	590	600	610	620	630	640
PTVQDSRARP	PYTVAADKST	RNEFRRFMEK	NPDAYDYNKA	QVPGPLTPEM	EARQATRKRE	QKAARRQREE	QQQRQQEQEE
650	660	670	680	690	700	710	720
REREEQRRFA	ALSDREKRAL	AAERRLAAQL	GAPTSPIPDS	AIVNTRRCWS	CGASLQGLTP	FHYLDFSFCS	TRCLQDHRRQ
730							
AGRPSS							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
939	2	529.3080	38.86	2	40.5	12.1	0	277-286	R.DLLAGPSWAK.A	

Detailed Protein Report

Protein 710: **leucine-rich repeat and calponin homology domain-containing protein 1 isoform 3 [Homo sapiens]**

Accession:	gi|256017180	**Score:**	23.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	77.2
Database Date:	2015-11-30	**pI:**	5.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.6
		No. of unique Peptides:	1

Quantitation

mdown:qdown **Median:** 0.72 **CV:** 0.00 % **No. of 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	Ratios
599	1	690.3992	85.05	2	36.8	23.5	1	645-655	R.NVENFLEACRK.L	Carbamidomethyl: 9	mdown:qdown 0.72

Protein 711: 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
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	6.4
		No. of unique Peptides:	2

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
1681	1	1044.8573	-98.83	2	50.9	12.1	1	92-111	K.GLNGCDSPDPDADDSALNKK.E	Carbamidomethyl: 5
672	1	676.1898	-213.65	2	37.7	11.3	1	418-428	R.YPQHTRHEAGR.S	

Detailed Protein Report

Protein 712: 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

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
1776	1	806.7498	-172.60	2	52.2	23.4	0	157-170	K.ASECMQVIFGIDVK.E	Carbamidomethyl: 4; Oxidation: 5

Detailed Protein Report

Protein 713: PREDICTED: condensin-2 complex subunit H2 isoform X1 [Homo sapiens]

Accession:	gi|530420802	**Score:**	23.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	65.2
Database Date:	2015-11-30	**pI:**	4.6
		Sequence Coverage [%]:	4.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSQRWGRCWL	DQICISFDEG	KTTMNFIEAA	LLIQGSACVY	SKKVEYLYSL	VYQALDFISG	KRRAKQLSSV	QEDRANGVAS
90	100	110	120	130	140	150	160
SGVPQEAENE	FLSLDDFPDS	RTNVDLKNDQ	TPSEVLIIPL	LPMALVAPDE	MEKNNNPLYS	RQGEVLASRK	DFRMNTCVPH
170	180	190	200	210	220	230	240
PRGAFMLEPE	GMSPMEPAGV	SPMPGTQKDT	GRTEEQPMEV	SVCRSPVPAL	GFSQEPGPSP	EGPMPLGGGE	DEDAEEAVEL
250	260	270	280	290	300	310	320
PEASAPKAAL	EPKESRSPQQ	SAALPRRYML	REREGAPEPA	SCVKETPDPW	QSLDPFDSLE	SKPFKKGRPY	SVPPCVEEAL
330	340	350	360	370	380	390	400
GQKRKRKGAA	KLQDFHQWYL	AAYADHADSR	RLRRKGPSFA	DMEVLYWTHV	KEQLETLRKL	QRREVAEQWL	RPAEEDHLED
410	420	430	440	450	460	470	480
SLEDLGAAAD	DFLEPEEYME	PEGADPREAA	DLDAVPMSLS	YEELVRRNVE	LFIATSQKFV	QETELSQRIR	DWEDTVQPLL
490	500	510	520	530	540	550	560
QEQEQHVPFD	IHTYGDQLVS	RFPQLNEWCP	FAELVAGQPA	FEVCRSMLAS	LQLANDYTVE	ITQQPGLEMA	VDTMSLRLLT
570	580						
HQRAHKRFQT	YAAPSMAQP						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1785	1	734.4108	74.56	2	51.0	11.4	1	567-579	K.RFQTYAAPSMAQP.-	

Detailed Protein Report

Protein 714: PREDICTED: E3 ubiquitin-protein ligase LRSAM1 isoform X2 [Homo sapiens]

Accession:	gi|578817973	**Score:**	23.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	79.5
Database Date:	2015-11-30	**pI:**	5.5
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	2.6
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MPLFFRKRKP	SEEARKRLEY	QMCLAKEAGA	DDILDISKCE	LSEIPFGAFA	TCKVLQKKVL	IVHTNHLTSL	LPKSCSLLSL
90	100	110	120	130	140	150	160
ATIKVLDLHD	NQLTALPDDL	GQLTALQVLN	VERNQLMQLP	RSIGNLTQLQ	TLNVKDNKLK	ELPDTVGELR	SLRTLNISGN
170	180	190	200	210	220	230	240
EIQRLPQMLA	HVRTLEMLSL	DASAMVYPPR	EVCGAGTAAI	LQFLCKESGL	EYYPPSQYLL	PILEQDGIEN	SRDSPDGPTD
250	260	270	280	290	300	310	320
RFSREELEWQ	NRFSDYEKRK	EQKMLEKLEF	ERRLELGQRE	HTQLLQQSSS	QKDEILQTVK	EEQSRLEQGL	SEHQRHLNAE
330	340	350	360	370	380	390	400
RQRLQEQLKQ	TEQNISSRIQ	KLLQDNQRQK	KSSEILKSLE	NERIRMEQLM	SITQEETESL	RRRDVASAMQ	QMLTESCKNR
410	420	430	440	450	460	470	480
LIQMAYESQR	QNLVQQACSS	MAEMDERFQQ	ILSWQQMDQN	KAISQILQES	AMQKAAFEAL	QVKKDLMHRQ	IRSQIKLIET
490	500	510	520	530	540	550	560
ELLQLTQLEL	KRKSLDTESL	QEMISEQRWA	LSSLLQQLLK	EKQQREEELR	EILEEGMERQ	LVALLEELSA	EHYLPIFAHH
570	580	590	600	610	620	630	640
RLSLDLLSQM	SPGDLAKVGV	SEAGLQHEIL	RRVQELLDAA	RIQPELKPPM	GEVVTPTAPQ	EPPESVRPSA	PPAELEVQAS
650	660	670	680	690	700		
ECVVCLEREA	QMIFLNCGHV	CCCQQCCQPL	RTCPLCRQDI	AQRLRIYHSS			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1755	1	689.9840	-17.28	3	50.6	11.1	2	383-400	R.RDVASAMQQMLTESCKNR.L	
2902	1	992.7980	-150.93	2	65.0	12.3	1	384-400	R.DVASAMQQMLTESCKNR.L	Carbamidomethyl: 14; Oxidation: 6

Detailed Protein Report

Protein 715: zinc finger and BTB domain-containing protein 21 isoform L [Homo sapiens]

Accession:	gi|50345873	**Score:**	23.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	118.8
Database Date:	2015-11-30	**pI:**	9.6
		Sequence Coverage [%]:	1.9
		No. of unique Peptides:	2

Alias proteins:

Accession	Name	Description
gi|530419238	refseq_human (refseq_human_20140103.fasta)	PREDICTED: zinc finger and BTB domain-containing protein 21 isoform X1 [Homo sapiens]
gi|148491088	refseq_human (refseq_human_20140103.fasta)	zinc finger and BTB domain-containing protein 21 isoform L [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MEGLLHYINP AHAISLLSAL NEERLKGQLC DVLLIVGDQK FRAHKNVLAA SSEYFQSLFT NKENESQTVF QLDFCEPDAF
        90        100        110        120        130        140        150        160
DNVLNYIYSS SLFVEKSSLA AVQELGYSLG ISFLTNIVSK TPQAPFPTCP NRKKVFVEDD ENSSQKRSVI VCQSRNEAQG
       170        180        190        200        210        220        230        240
KTVSQNQPDV SHTSRPSPSI AVKANTNKPH VPKPIEPLHN LSLTEKSWPK DSSVVYAKSL EHSGSLDDPN RISLVKRNAV
       250        260        270        280        290        300        310        320
LPSKPLQDRE AMDDKPGVSG QLPKGKALEL ALKRPRPPVL SVCSSSETPY LLKETNKGNG QGEDRNLLYY SKLGLVIPSS
       330        340        350        360        370        380        390        400
GSGSGNQSID RSGPLVKSLL RRSLSMDSQV PVYSPSIDLK SSQGSSSVSS DAPGNVLCAL SQKSSLKDCS EKTALDDRPQ
       410        420        430        440        450        460        470        480
VLQPHRLRSF SASQSTDREG ASPVTEVRIK TEPSSPLSDP SDIIRVTVGD AATTAAASSS SVTRDLSLKT EDDQKDMSRL
       490        500        510        520        530        540        550        560
PAKRRFQADR RLPFKKLKVN EHGSPVSEDN FEEGSSPTLL DADFPDSDLN KDEFGELEGT RPNKKFKCKH CLKIFRSTAG
       570        580        590        600        610        620        630        640
LHRHVNMYHN PEKPYACDIC HKRFHTNFKV WTHCQTQHGI VKNPSPASSS HAVLDEKFQR KLIDIVRERE IKKALIIKLR
       650        660        670        680        690        700        710        720
RGKPGFQGQS SSQAQQVIKR NLRSRAKGAY ICTYCGKAYR FLSQFKQHIK MHPGEKPLGV NKVAKPKEHA PLASPVENKE
       730        740        750        760        770        780        790        800
VYQCRLCNAK LSSLLEQGSH ERLCRNAAVC PYCSLRFFSP ELKQEHESKC EYKKLTCLEC MRTFKSSFSI WRHQVEVHNQ
       810        820        830        840        850        860        870        880
NNMAPTENFS LPVLDHNGDV TGSSRPQSQP EPNKVNHIVT TKDDNVFSDS SEQVNFDSED SSCLPEDLSL SKQLKIQVKE
       890        900        910        920        930        940        950        960
EPVEEAEEEA PEASTAPKEA GPSKEASLWP CEKCGKMFTV HKQLERHQEL LCSVKPFICH VCNKAFRTNF RLWSHFQSHM
       970        980        990       1000       1010       1020       1030       1040
SQASEESAHK ESEVCPVPTN SPSPPPLPPP PPLPKIQPLE PDSPTGLSEN PTPATEKLFV PQESDTLFYH APPLSAITFK
      1050       1060       1070
RQFMCKLCHR TFKTAFSLWS HEQTHN
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1333	4	698.8883	104.97	2	45.4	12.8	0	135-146	K.VFVEDDENSSQK.R	
861	1	491.8136	-69.69	2	39.6	10.6	2	634-641	K.ALIIKLRR.G	

Detailed Protein Report

Protein 716: collagen alpha-3(VI) chain isoform 4 precursor [Homo sapiens]

Accession:	gi|240255535	**Score:**	23.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	278.0
Database Date:	2015-11-30	**pI:**	9.1
		Sequence Coverage [%]:	1.1
		No. of unique Peptides:	1

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
FFVVLGIGRK	VNIKEVYTFA	SEPNDVFFKL	VDKSTELNEE	PLMRFGRLLP	SFVSSENAFY	LSPDIRKQCD	WFQGDQPTKN
2250	2260	2270	2280	2290	2300	2310	2320
LVKFGHKQVN	VPNNVTSSPT	SNPVTTTKPV	TTTKPVTTTT	KPVTTTTKPV	TIINQPSVKP	AAAKPAPAKP	VAAKPVATKM
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
1827	1	1056.0066	84.56	3	52.9	23.4	2	2131-2158	K.IVVLMLTGEVPEQQLEEAQRVILQAKCK.G	

Detailed Protein Report

Protein 717: 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

mdown:qdown	**Median:**	0.48	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.93	**CV:**	0.00 %	**No. of Peptides:**	1

```
        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		mdown:qdown 0.48 Wdown:Qdown 0.93
298	1	535.7922	-16.95	2	33.1	12.4	2	2027-2035	K.QKQPQEKGK.V		

Detailed Protein Report

Protein 718: valine--tRNA ligase, mitochondrial isoform 3 [Homo sapiens]

Accession:	gi|268370295	**Score:**	23.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	102.4
Database Date:	2015-11-30	**pI:**	6.1
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MCIPPPNVTG	SLHIGHALTV	AIQDALVRWH	RMRGDQVLWV	PGSDHAGIAT	QAVVEKQLWK	ERGVRRHELS	REAFLREVWQ
90	100	110	120	130	140	150	160
WKEAKGGEIC	EQLRALGASL	DWDRECFTMD	VGSSVAVTEA	FVRLYKAGLL	YRNHQLVNWS	CALRSAISDI	EVENRPLPGH
170	180	190	200	210	220	230	240
TQLRLPGCPT	PVSFGLLFSV	AFPVDGEPDA	EVVVGTTRPE	TLPGDVAVAV	HPDDSRYTHL	HGRQLRHPLM	GQPLPLITDY
250	260	270	280	290	300	310	320
AVQPHVGTGA	VKVTPAHSPA	DAEMGARHGL	SPLNVIAEDG	TMTSLCGDWL	QGLHRFVARE	KIMSVLSEWG	LFRGLQNHPM
330	340	350	360	370	380	390	400
VLPICSRSGD	VIEYLLKNQW	FVRCQEMGAR	AAKAVESGAL	ELSPSFHQKN	WQHWFSHIGD	WCVSRQLWWG	HQIPAYLVVE
410	420	430	440	450	460	470	480
DHAQGEEDCW	VVGRSEAEAR	EVAAELTGRP	GAELTLERDP	DVLDTWFSSA	LFPFSALGWP	QETPDLARFY	PLSLLETGSD
490	500	510	520	530	540	550	560
LLLFWVGRMV	MLGTQLTGQL	PFSKVLLHPM	VRDRQGRKMS	KSLGNVLDPR	DIISGVEMQV	LQEKLRSGNL	DPAELAIVAA
570	580	590	600	610	620	630	640
AQKKDFPHGI	PECGTDALRF	TLCSHGVQAG	DLHLSVSEVQ	SCRHFCNKIW	NALRFILNAL	GEKFVPQPAE	ELSPSSPMDA
650	660	670	680	690	700	710	720
WILSRLALAA	QECERGFLTR	ELSLVTHALH	HFWLHNLCDV	YLEAVKPVLW	HSPRPLGPPQ	VLFSCADLGL	RLLAPLMPFL
730	740	750	760	770	780	790	800
AEELWQRLPP	RPGCPPAPSI	SVAPYPSACS	LEHWRQPELE	RRFSRVQEVV	QVLRALRATY	QLTKARPRVL	LQSSEPGDQG
810	820	830	840	850	860	870	880
LFEAFLEPLG	TLGYCGAVGL	LPPGAAAPSG	WAQAPLSDTA	QVYMELQGLV	DPQIQLPLLA	ARRYKLQKQL	DSLTARTPSE
890	900	910	920	930			
GEAGTQRQQK	LSSLQLELSK	LDKAASHLRQ	LMDEPPAPGS	PEL			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
124	1	896.3913	-39.84	3	30.9	11.1	0	580-603	R.FTLCSHGVQAGDLHLSVSEVQSCR.H	Carbamidomethyl: 4, 23

Detailed Protein Report

Protein 719: zinc finger protein 329 [Homo sapiens]

Accession:	gi|71037407	**Score:**	23.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	61.7
Database Date:	2015-11-30	**pI:**	10.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	5.5
		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 720: **PREDICTED: zinc finger and BTB domain-containing protein 38 isoform X2 [Homo sapiens]**

Accession:	gi|530374206	**Score:**	23.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	134.3
Database Date:	2015-11-30	**pI:**	9.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.1
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MMTVMSLSRD LKDDFHSDTV LSILNEQRIR GILCDVTIIV EDTKFKAHSN VLAASSLYFK NIFWSHTICI SSHVLELDDL
        90        100        110        120        130        140        150        160
KAEVFTEILN YIYSSTVVVK RQETVTDLAA AGKKLGISFL EDLTDRNFSN SPGPYVFCIT EKGVVKEEKN EKRHEEPAIT
       170        180        190        200        210        220        230        240
NGPRITNAFS IIETENSNNM FSPLDLRASF KKVSDSMRTA SLCLERTDVC HEAEPVRTLA EHSYAVSSVA EAYRSQPVRE
       250        260        270        280        290        300        310        320
HDGSSPGNTG KENCEALAAK PKTCRKPKTF SIPQDSDSAT ENIPPPPVSN LEVNQERSPQ PAAVLTRSKS PNNEGDVHFS
       330        340        350        360        370        380        390        400
REDENQSSDV PGPPAAEVPP LVYNCSCCSK AFDSSTLLSA HMQLHKPTQE PLVCKYCNKQ FTTLNRLDRH EQICMRSSHM
       410        420        430        440        450        460        470        480
PIPGGNQRFL ENYPTIGQNG GSFTGPEPLL SENRIGEFSS TGSTLPDTDH MVKFVNGQML YSCVVCKRSY VTLSSLRRHA
       490        500        510        520        530        540        550        560
NVHSWRRTYP CHYCNKVFAL AEYRTRHEIW HTGERRYQCI FCLETFMTYY ILKNHQKSFH AIDHRLSISK KTANGGLKPS
       570        580        590        600        610        620        630        640
VYPYKLYRLL PMKCKRAPYK SYRNSSYENA RENSQMNESA PGTYVVQNPH SSELPTLNFQ DTVNTLTNSP AIPLETSACQ
       650        660        670        680        690        700        710        720
DIPTSANVQN AEGTKWGEEA LKMDLDNNFY STEVSVSSTE NAVSSDLRAG DVPVLSLSNS SENAASVISY SGSAPSVIVH
       730        740        750        760        770        780        790        800
SSQFSSVIMH SNAIAAMTSS NHRAFSDPAV SQSLKDDSKP EPDKVGRFAS RPKSIKEKKK TTSHTRGEIP EESNYVADPG
       810        820        830        840        850        860        870        880
GSLSKTTNIA EETSKIETYI AKPALPGTST NSNVAPLCQI TVKIGNEAIV KRHILGSKLF YKRGRRPKYQ MQEEPLPQGN
       890        900        910        920        930        940        950        960
DPEPSGDSPL GLCQSECMEM SEVFDDASDQ DSTDKPWRPY YNYKPKKKSR QLKKMRKVNW RKEHGNRSPS HKCKYPAELD
       970        980        990       1000       1010       1020       1030       1040
CAVGKAPQDK PFEEEETKEM PKLQCELCDG DKAVGAGNQG RPHRHLTSRP YACELCAKQF QSPSTLKMHM RCHTGEKPYQ
      1050       1060       1070       1080       1090       1100       1110       1120
CKTCGRCFSV QGNLQKHERI HLGLKEFVCQ YCNKAFTLNE TLKIHERIHT GEKRYHCQFC FQRFLYLSTK RNHEQRHIRE
      1130       1140       1150       1160       1170       1180       1190       1200
HNGKGYACFQ CPKICKTAAA LGMHQKKHLF KSPSQQEKIG DVCHENSNPL ENQHFIGSED NDQKDNIQTG VENVVL
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2863	1	922.9727	-41.66	2	65.0	11.0	1	29-44	R.IRGILCDVTIIVEDTK.F	Carbamidomethyl: 6

Detailed Protein Report

Protein 721: protocadherin Fat 1 precursor [Homo sapiens]

Accession:	gi|66346693	**Score:**	23.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	506.0
Database Date:	2015-11-30	**pI:**	4.7
		Sequence Coverage [%]:	0.7
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578808907	refseq_human (refseq_human_20140103.fasta)	PREDICTED: protocadherin Fat 1 isoform X3 [Homo sapiens]

Detailed Protein Report

10	20	30	40	50	60	70	80
MGRHLALLLL	LLLLFQHFGD	SDGSQRLEQT	PLQFTHLEYN	VTVQENSAAK	TYVGHPVKMG	VYITHPAWEV	RYKIVSGDSE
90	100	110	120	130	140	150	160
NLFKAEEYIL	GDFCFLRIRT	KGGNTAILNR	EVKDHYTLIV	KALEKNTNVE	ARTKVRVQVL	DTNDLRPLFS	PTSYSVSLPE
170	180	190	200	210	220	230	240
NTAIRTSIAR	VSATDADIGT	NGEFYYSFKD	RTDMFAIHPT	SGVIVLTGRL	DYLETKLYEM	EILAADRGMK	LYGSSGISSM
250	260	270	280	290	300	310	320
AKLTVHIEQA	NECAPVITAV	TLSPSELDRD	PAYAIVTVDD	CDQGANGDIA	SLSIVAGDLL	QQFRTVRSFP	GSKEYKVKAI
330	340	350	360	370	380	390	400
GGIDWDSHPF	GYNLTLQAKD	KGTPPQFSSV	KVIHVTSPQF	KAGPVKFEKD	VYRAEISEFA	PPNTPVVMVK	AIPAYSHLRY
410	420	430	440	450	460	470	480
VFKSTPGKAK	FSLNYNTGLI	SILEPVKRQQ	AAHFELEVTT	SDRKASTKVL	VKVLGANSNP	PEFTQTAYKA	AFDENVPIGT
490	500	510	520	530	540	550	560
TVMSLSAVDP	DEGENGYVTY	SIANLNHVPF	AIDHFTGAVS	TSENLDYELM	PRVYTLRIRA	SDWGLPYRRE	VEVLATITLN
570	580	590	600	610	620	630	640
NLNDNTPLFE	KINCEGTIPR	DLGVGEQITT	VSAIDADELQ	LVQYQIEAGN	ELDFFSLNPN	SGVLSLKRSL	MDGLGAKVSF
650	660	670	680	690	700	710	720
HSLRITATDG	ENFATPLYIN	ITVAASHKLV	NLQCEETGVA	KMLAEKLLQA	NKLHNQGEVE	DIFFDSHSVN	AHIPQFRSTL
730	740	750	760	770	780	790	800
PTGIQVKENQ	PVGSSVIFMN	STDLDTGFNG	KLVYAVSGGN	EDSCFMIDME	TGMLKILSPL	DRETTDKYTL	NITVYDLGIP
810	820	830	840	850	860	870	880
QKAAWRLLHV	VVVDANDNPP	EFLQESYFVE	VSEDKEVHSE	IIQVEATDKD	LGPNGHVTYS	IVTDTDTFSI	DSVTGVVNIA
890	900	910	920	930	940	950	960
RPLDRELQHE	HSLKIEARDQ	AREEPQLFST	VVVKVSLEDV	NDNPPTFIPP	NYRVKVREDL	PEGTVIMWLE	AHDPDLGQSG
970	980	990	1000	1010	1020	1030	1040
QVRYSLLDHG	EGNFDVDKLS	GAVRIVQQLD	FEKKQVYNLT	VRAKDKGKPV	SLSSTCYVEV	EVVDVNENLH	PPVFSSFVEK
1050	1060	1070	1080	1090	1100	1110	1120
GTVKEDAPVG	SLVMTVSAHD	EDARRDGEIR	YSIRDGSGVG	VFKIGEETGV	IETSDRLDRE	STSHYWLTVF	ATDQGVVPLS
1130	1140	1150	1160	1170	1180	1190	1200
SFIEIYIEVE	DVNDNAPQTS	EPVYYPEIME	NSPKDVSVVQ	IEAFDPDSSS	NDKLMYKITS	GNPQGFFSIH	PKTGLITTTS
1210	1220	1230	1240	1250	1260	1270	1280
RKLDREQQDE	HILEVTVTDN	GSPPKSTIAR	VIVKILDEND	NKPQFLQKFY	KIRLPEREKP	DRERNARREP	LYHVIATDKD
1290	1300	1310	1320	1330	1340	1350	1360
EGPNAEISYS	IEDGNEHGKF	FIEPKTGVVS	SKRFSAAGEY	DILSIKAVDN	GRPQKSSTTR	LHIEWISKPK	PSLEPISFEE
1370	1380	1390	1400	1410	1420	1430	1440
SFFTFTVMES	DPVAHMIGVI	SVEPPGIPLW	FDITGGNYDS	HFDVDKGTGT	IIVAKPLDAE	QKSNYNLTVE	ATDGTTTILT
1450	1460	1470	1480	1490	1500	1510	1520
QVFIKVIDTN	DHRPQFSTSK	YEVVIPEDTA	PETEILQISA	VDQDEKNKLI	YTLQSSRDPL	SLKKFRLDPA	TGSLYTSEKL
1530	1540	1550	1560	1570	1580	1590	1600
DHEAVHQHTL	TVMVRDQDVP	VKRNFARIVV	NVSDTNDHAP	WFTASSYKGR	VYESAAVGSV	VLQVTALDKD	KGKNAEVLYS
1610	1620	1630	1640	1650	1660	1670	1680
IESGNIGNSF	MIDPVLGSIK	TAKELDRSNQ	AEYDLMVKAT	DKGSPPMSEI	TSVRIFVTIA	DNASPKFTSK	EYSVELSETV
1690	1700	1710	1720	1730	1740	1750	1760
SIGSFVGMVT	AHSQSSVVYE	IKDGNTGDAF	DINPHSGTII	TQKALDFETL	PIYTLIIQGT	NMAGLSTNTT	VLVHLQDEND
1770	1780	1790	1800	1810	1820	1830	1840
NAPVFMQAEY	TGLISESASI	NSVVLTDRNV	PLVIRAADAD	KDSNALLVYH	IVEPSVHTYF	AIDSSTGAIH	TVLSLDYEET
1850	1860	1870	1880	1890	1900	1910	1920
SIFHFTVQVH	DMGTPRLFAE	YAANVTVHVI	DINDCPPVFA	KPLYEASLLL	PTYKGVKVIT	VNATDADSSA	FSQLIYSITE
1930	1940	1950	1960	1970	1980	1990	2000
GNIGEKFSMD	YKTGALTVQN	TTQLRSRYEL	TVRASDGRFA	GLTSVKINVK	ESKESHLKFT	QDVYSAVVKE	NSTEAETLAV
2010	2020	2030	2040	2050	2060	2070	2080
ITAIGNPINE	PLFYHILNPD	RRFKISRTSG	VLSTTGTPFD	REQQEAFDVV	VEVTEEHKPS	AVAHVVVKVI	VEDQNDNAPV
2090	2100	2110	2120	2130	2140	2150	2160
FVNLPYYAVV	KVDTEVGHVI	RYVTAVDRDS	GRNGEVHYYL	KEHHEHFQIG	PLGEISLKKQ	FELDTLNKEY	LVTVVAKDGG
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2147	1	719.8600	-56.51	2	55.4	10.9	1	1300-1312	K.FFIEPKTGVVSSK.R	

Detailed Protein Report

Protein 722: putative protein FAM47C [Homo sapiens]

Accession: gi|61966919
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl, Oxidation

Score: 23.3
MW [kDa]: 115.3
pI: 6.8
Sequence Coverage [%]: 4.0
No. of unique Peptides: 2

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
2667	1	1057.0851	36.44	2	62.2	11.9	1	368-386	R.QLPPEAGVSHLCPEPPKTR.V	Carbamidomethyl: 12
2436	1	822.6843	-57.00	3	60.8	11.4	0	567-588	R.MYSLRPEPPDTGVSHLCPEPPK.T	Oxidation: 1

Detailed Protein Report

Protein 723: PREDICTED: serine/threonine-protein kinase N3 isoform X4 [Homo sapiens]

Accession: gi|578817399
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 23.3
MW [kDa]: 92.9
pI: 10.0
Sequence Coverage [%]: 3.5
No. of unique Peptides: 1

Quantitation

mdown:qdown **Median:** 1.09 **CV:** 0.00 % **No. of Peptides:** 1
Wdown:Qdown **Median:** 1.24 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MEEGAPRQPG	PSQWPPEDEK	EVIRRAIQKE	LKIKEGVENL	RRVATDRRHL	GHVQQLLRSS	NRRLEQLHGE	LRELHARILL
90	100	110	120	130	140	150	160
PGPGPGPAEP	VASGPRPWAE	QLRARHLEAL	RRQLHVELKV	KQGAENMTHT	CASGTPKERK	LLAAAQQMLR	DSQLKVALLR
170	180	190	200	210	220	230	240
MKISSLEASG	SPEPGPELLA	EELQHRLHVE	AAVAEGAKNV	VKLLSSRRTQ	DRKALAEAQA	QLQESSQKLD	LLRLALEQLL
250	260	270	280	290	300	310	320
EQLPPAHPLR	SRVTRELRAA	VPGYPQPSGT	PVKPTALTGT	LQVRLLGCEQ	LLTAVPGRSP	AAALASSPSE	GWLRTKAKHQ
330	340	350	360	370	380	390	400
RGRGELASEV	LAVLKVDNRV	VGQTGWGQVA	EQSWDQTFVI	PLERARELEI	GVHWRDWRQL	CGVAFLRLED	FLDNACHQLS
410	420	430	440	450	460	470	480
LSLVPQGLLF	AQVTFCDPVI	ERRPRLQRQE	RIFSKRRGQD	FLRASQMNLG	MAAWGRLVMN	LLPPCSSPST	ISPPKGCPRT
490	500	510	520	530	540	550	560
PTTLREASDP	ATPSNFLPKK	TPLGEEMTPP	PKPPRLYLPQ	EPTSEETPRT	KRPHMEPRTR	RGPSPPASPT	RKPPRLQDFR
570	580	590	600	610	620	630	640
CLAVLGRGHF	GKVLLVQFKG	TGKYYAIKAL	KKQEVLSRDE	IESLYCEKRI	LEAVGCTGHP	FLLSLLACFQ	TSSHACFVTE
650	660	670	680	690	700	710	720
FVPGGDLMMQ	IHEDVFPEPQ	ARFYVACVVL	GLQFLHEKKI	IYRDLKLDNL	LLDAQGFLKI	ADFGLCKEGI	GFGDRTSTFC
730	740	750	760	770	780	790	800
GTPEFLAPEV	LTQEAYTRAV	DWWGLGVLLY	EMLVGECPFP	GDTEEEVFDC	IVNMDAPYPG	FLSVQGLEFI	QKLLQKCPEK
810	820	830	840				
RLGADHQLAS	PARPHHPAPL	RAYPVWPCGP	ALL				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
242	1	566.5934	-38.74	3	31.8	10.9	1	700-715	K.IADFGLCKEGIGFGDR.T		Wdown:Qdown 1.24 mdown:qdown 1.09

Detailed Protein Report

Protein 724: E3 ubiquitin-protein ligase UBR2 isoform 1 [Homo sapiens]

Accession: gi|27597061
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 23.3
MW [kDa]: 200.4
pI: 5.8
Sequence Coverage [%]: 1.7
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MASELEPEVQ	AIDRSLLECS	AEEIAGKWLQ	ATDLTREVYQ	HLAHYVPKIY	CRGPNPFPQK	EDMLAQHVLL	GPMEWYLCGE
90	100	110	120	130	140	150	160
DPAFGFPKLE	QANKPSHLCG	RVFKVGEPTY	SCRDCAVDPT	CVLCMECFLG	SIHRDHRYRM	TTSGGGGFCD	CGDTEAWKEG
170	180	190	200	210	220	230	240
PYCQKHELNT	SEIEEEEDPL	VHLSEDVIAR	TYNIFAITFR	YAVEILTWEK	ESELPADLEM	VEKSDTYYCM	LFNDEVHTYE
250	260	270	280	290	300	310	320
QVIYTLQKAV	NCTQKEAIGF	ATTVDRDGRR	SVRYGDFQYC	EQAKSVIVRN	TSRQTKPLKV	QVMHSSIVAH	QNFGLKLLSW
330	340	350	360	370	380	390	400
LGSIIGYSDG	LRRILCQVGL	QEGPDGENSS	LVDRLMLSDS	KLWKGARSVY	HQLFMSSLLM	DLKYKKLFAV	RFAKNYQQLQ
410	420	430	440	450	460	470	480
RDFMEDDHER	AVSVTALSVQ	FFTAPTLARM	LITEENLMSI	IIKTFMDHLR	HRDAQGRFQF	ERYTALQAFK	FRRVQSLILD
490	500	510	520	530	540	550	560
LKYVLISKPT	EWSDELRQKF	LEGFDAFLEL	LKCMQGMDPI	TRQVGQHIEM	EPEWEAAFTL	QMKLTHVISM	MQDWCASDEK
570	580	590	600	610	620	630	640
VLIEAYKKCL	AVLMQCHGGY	TDGEQPITLS	ICGHSVETIR	YCVSQEKVSI	HLPVSRLLAG	LHVLLSKSEV	AYKFPELLPL
650	660	670	680	690	700	710	720
SELSPPMLIE	HPLRCLVLCA	QVHAGMWRRN	GFSLVNQIYY	YHNVKCRREM	FDKDVVMLQT	GVSMMDPNHF	LMIMLSRFEL
730	740	750	760	770	780	790	800
YQIFSTPDYG	KRFSSEITHK	DVVQQNNTLI	EEMLYLIIML	VGERFSPGVG	QVNATDEIKR	EIIHQLSIKP	MAHSELVKSL
810	820	830	840	850	860	870	880
PEDENKETGM	ESVIEAVAHF	KKPGLTGRGM	YELKPECAKE	FNLYFYHFSR	AEQSKAEEAQ	RKLKRQNRED	TALPPPVLPP
890	900	910	920	930	940	950	960
FCPLFASLVN	ILQSDVMLCI	MGTILQWAVE	HNGYAWSESM	LQRVLHLIGM	ALQEEKQHLE	NVTEEHVVTF	TFTQKISKPG
970	980	990	1000	1010	1020	1030	1040
EAPKNSPSIL	AMLETLQNAP	YLEVHKDMIR	WILKTFNAVK	KMRESSPTSP	VAETEGTIME	ESSRDKDKAE	RKRKAEIARL
1050	1060	1070	1080	1090	1100	1110	1120
RREKIMAQMS	EMQRHFIDEN	KELFQQTLEL	DASTSAVLDH	SPVASDMTLT	ALGPAQTQVP	EQRQFVTCIL	CQEEQEVKVE
1130	1140	1150	1160	1170	1180	1190	1200
SRAMVLAAFV	QRSTVLSKNR	SKFIQDPEKY	DPLFMHPDLS	CGTHTSSCGH	IMHAHCWQRY	FDSVQAKEQR	RQQRLRLHTS
1210	1220	1230	1240	1250	1260	1270	1280
YDVENGEFLC	PLCECLSNTV	IPLLLPPRNI	FNNRLNFSDQ	PNLTQWIRTI	SQQIKALQFL	RKEESTPNNA	STKNSENVDE
1290	1300	1310	1320	1330	1340	1350	1360
LQLPEGFRPD	FRPKIPYSES	IKEMLTTFGT	ATYKVGLKVH	PNEEDPRVPI	MCWGSCAYTI	QSIERILSDE	DKPLFGPLPC
1370	1380	1390	1400	1410	1420	1430	1440
RLDDCLRSLT	RFAAAHWTVA	SVSVVQGHFC	KLFASLVPND	SHEELPCILD	IDMFHLLVGL	VLAFPALQCQ	DFSGISLGTG
1450	1460	1470	1480	1490	1500	1510	1520
DLHIFHLVTM	AHIIQILLTS	CTEENGMDQE	NPPCEEESAV	LALYKTLHQY	TGSALKEIPS	GWHLWRSVRA	GIMPFLKCSA
1530	1540	1550	1560	1570	1580	1590	1600
LFFHYLNGVP	SPPDIQVPGT	SHFEHLCSYL	SLPNNLICLF	QENSEIMNSL	IESWCRNSEV	KRYLEGERDA	IRYPRESNKL
1610	1620	1630	1640	1650	1660	1670	1680
INLPEDYSSL	INQASNFSCP	KSGGDKSRAP	TLCLVCGSLL	CSQSYCCQTE	LEGEDVGACT	AHTYSCGSGV	GIFLRVRECQ
1690	1700	1710	1720	1730	1740	1750	1760
VLFLAGKTKG	CFYSPPYLDD	YGETDQGLRR	GNPLHLCKER	FKKIQKLWHQ	HSVTEEIGHA	QEANQTLVGI	DWQHL

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
170	1	793.8952	4.91	2	31.4	10.8	0	655-668	R.CLVLCAQVHAGMWR.R	

Detailed Protein Report

Protein 725: granulysin isoform 519 [Homo sapiens]

Accession:	gi|157502222	**Score:**	23.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	14.8
Database Date:	2015-11-30	**pI:**	10.5
Modification(s):	Carbamidomethyl	**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 726: PNMA-like protein 2 [Homo sapiens]

Accession:	gi|146219841	**Score:**	23.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	68.6
Database Date:	2015-11-30	**pI:**	5.2
		Sequence Coverage [%]:	4.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAMSLLQDWC	RSLDVDAHRA	LLVTGIPEGL	EQADVEAVLQ	PTLLPLGTFR	LRHMKALMNE	KAQAALVEFV	EDVNHAAIPR
90	100	110	120	130	140	150	160
EIPGKDGVWR	VLWKDRAQDT	RVLRQMRRLL	LDDGPTQAAE	AGTPGEAPTP	PASETQAQDS	GEVTGQAGSL	LGAARNPRRG
170	180	190	200	210	220	230	240
RRGRRNRTRR	NRLTQKGKKR	SRGGRPSAPA	RSEAEDSSDE	SLGIVIEEID	QGDLSGEEDQ	SALYATLQAA	ARELVRQWAP
250	260	270	280	290	300	310	320
CNSEGEEDGP	REFLALVTVT	DKSKKEEAEK	EPAGAESIRL	NTKEDKNGVP	DLVALLAVRD	TPDEEPVDSD	TSESDSQESG
330	340	350	360	370	380	390	400
DQETEELDNP	EFVAIVAYTD	PSDPWAREEM	LKIASVIESL	GWSDEKDKRD	PLRQVLSVMS	KDTNGTRVKV	EEAGREVDAV
410	420	430	440	450	460	470	480
VLRKAGDDGD	LRECISTLAQ	PDLPPQAKKA	GRGLFGGWSE	HREDEGGLLE	LVALLAAQDM	AEVMKEEKEN	AWEGGKYKYP
490	500	510	520	530	540	550	560
KGKLGEVLAL	LAARENMGSN	EGSEEASDEQ	SEEESEDTES	EASEPEDRAS	RKPRAKRART	APRGLTPAGA	PPTASGARKT
570	580	590	600	610	620	630	640
RAGGRGRGRG	VTPEKKAGSR	GSAQDDAAGS	RKKKGSAGAG	AHARAGEAKG	QAPTGSKAAR	GKKARRGRRL	PPKCR

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1644	1	662.3238	-46.15	2	49.1	11.9	0	544-558	R.GLTPAGAPPTASGAR.K	

Detailed Protein Report

Protein 727: **voltage-dependent T-type calcium channel subunit alpha-1G isoform 14 [Homo sapiens]**

Accession:	gi|38505268	**Score:**	23.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	240.8
Database Date:	2015-11-30	**pI:**	6.7
		Sequence Coverage [%]:	1.6
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	0.81	**CV:**	0.00 %	**No. of Peptides:**	1

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		mdown:qdown 0.81

Detailed Protein Report

Protein 728: laminin subunit alpha-2 isoform b precursor [Homo sapiens]

Accession:	gi|119466532	**Score:**	23.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	343.3
Database Date:	2015-11-30	**pI:**	6.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPGAAGVLLL	LLLSGGLGGV	QAQRPQQQRQ	SQAHQQRGLF	PAVLNLASNA	LITTNATCGE	KGPEMYCKLV	EHVPGQPVRN
90	100	110	120	130	140	150	160
PQCRICNQNS	SNPNQRHPIT	NAIDGKNTWW	QSPSIKNGIE	YHYVTITLDL	QQVFQIAYVI	VKAANSPRPG	NWILERSLDD
170	180	190	200	210	220	230	240
VEYKPWQYHA	VTDTECLTLY	NIYPRTGPPS	YAKDDEVICT	SFYSKIHPLE	NGEIHISLIN	GRPSADDPSP	ELLEFTSARY
250	260	270	280	290	300	310	320
IRLRFQRIRT	LNADLMMFAH	KDPREIDPIV	TRRYYYSVKD	ISVGGMCICY	GHARACPLDP	ATNKSRCECE	HNTCGDSCDQ
330	340	350	360	370	380	390	400
CCPGFHQKPW	RAGTFLTKTE	CEACNCHGKA	EECYYDENVA	RRNLSLNIRG	KYIGGGVCIN	CTQNTAGINC	ETCTDGFFRP
410	420	430	440	450	460	470	480
KGVSPNYPRP	CQPCHCDPIG	SLNEVCVKDE	KHARRGLAPG	SCHCKTGFGG	VSCDRCARGY	TGYPDCKACN	CSGLGSKNED
490	500	510	520	530	540	550	560
PCFGPCICKE	NVEGGDCSRC	KSGFFNLQED	NWKGCDECFC	SGVSNRCQSS	YWTYGKIQDM	SGWYLTDLPG	RIRVAPQQDD
570	580	590	600	610	620	630	640
LDSPQQISIS	NAEARQALPH	SYYWSAPAPY	LGNKLPAVGG	QLTFTISYDL	EEEEEDTERV	LQLMIILEGN	DLSISTAQDE
650	660	670	680	690	700	710	720
VYLHPSEEHT	NVLLLKEESF	TIHGTHFPVR	RKEFMTVLAN	LKRVLLQITY	SFGMDAIFRL	SSVNLESAVS	YPTDGSIAAA
730	740	750	760	770	780	790	800
VEVCQCPPGY	TGSSCESCWP	RHRRVNGTIF	GGICEPCQCF	GHAESCDDVT	GECLNCKDHT	GGPYCDKCLP	GFYGEPTKGT
810	820	830	840	850	860	870	880
SEDCQPCACP	LNIPSNNFSP	TCHLDRSLGL	ICDGCPVGYT	GPRCERCAEG	YFGQPSVPGG	SCQPCQCNDN	LDFSIPGSCD
890	900	910	920	930	940	950	960
SLSGSCLICK	PGTTGRYCEL	CADGYFGDAV	DAKNCQPCRC	NAGGSFSEVC	HSQTGQCECR	ANVQGQRCDK	CKAGTFGLQS
970	980	990	1000	1010	1020	1030	1040
ARGCVPCNCN	SFGSKSFDCE	ESGQCWCQPG	VTGKKCDRCA	HGYFNFQEGG	CTACECSHLG	NNCDPKTGRC	ICPPNTIGEK
1050	1060	1070	1080	1090	1100	1110	1120
CSKCAPNTWG	HSITTGCKAC	NCSTVGSLDF	QCNVNTGQCN	CHPKFSGAKC	TECSRGHWNY	PRCNLCDCFL	PGTDATTCDS
1130	1140	1150	1160	1170	1180	1190	1200
ETKKCSCSDQ	TGQCTCKVNV	EGIHCDRCRP	GKFGLDAKNP	LGCSSCYCFG	TTTQCSEAKG	LIRTWVTLKA	EQTILPLVDE
1210	1220	1230	1240	1250	1260	1270	1280
ALQHTTTKGI	VFQHPEIVAH	MDLMREDLHL	EPFYWKLPEQ	FEGKKLMAYG	GKLKYAIYFE	AREETGFSTY	NPQVIIRGGT
1290	1300	1310	1320	1330	1340	1350	1360
PTHARIIVRH	MAAPLIGQLT	RHEIEMTEKE	WKYYGDDPRV	HRTVTREDFL	DILYDIHYIL	IKATYGNFMR	QSRISEISME
1370	1380	1390	1400	1410	1420	1430	1440
VAEQGRGTTM	TPPADLIEKC	DCPLGYSGLS	CEACLPGFYR	LRSQPGGRTP	GPTLGTCVPC	QCNGHSSLCD	PETSICQNCQ
1450	1460	1470	1480	1490	1500	1510	1520
HHTAGDFCER	CALGYYGIVK	GLPNDCQQCA	CPLISSSNNF	SPSCVAEGLD	DYRCTACPRG	YEGQYCERCA	PGYTGSPGNP
1530	1540	1550	1560	1570	1580	1590	1600
GGSCQECECD	PYGSLPVPCD	PVTGFCTCRP	GATGRKCDGC	KHWHAREGWE	CVFCGDECTG	LLLGDLARLE	QMVMSINLTG
1610	1620	1630	1640	1650	1660	1670	1680
PLPAPYKMLY	GLENMTQELK	HLLSPQRAPE	RLIQLAEGNL	NTLVTEMNEL	LTRATKVTAD	GEQTGQDAER	TNTRAKSLGE
1690	1700	1710	1720	1730	1740	1750	1760
FIKELARDAE	AVNEKAIKLN	ETLGTRDEAF	ERNLEGLQKE	IDQMIKELRR	KNLETQKEIA	EDELVAAEAL	LKKVKKLFGE
1770	1780	1790	1800	1810	1820	1830	1840
SRGENEEMEK	DLREKLADYK	NKVDDAWDLL	REATDKIREA	NRLFAVNQKN	MTALEKKKEA	VESGKRQIEN	TLKEGNDILD
1850	1860	1870	1880	1890	1900	1910	1920
EANRLADEIN	SIIDYVEDIQ	TKLPPMSEEL	NDKIDDLSQE	IKDRKLAEKV	SQAESHAAQL	NDSSAVLDGI	LDEAKNISFN
1930	1940	1950	1960	1970	1980	1990	2000
ATAAFKAYSN	IKDYIDEAEK	VAKEAKDLAH	EATKLATGPR	GLLKEDAKGC	LQKSFRILNE	AKKLANDVKE	NEDHLNGLKT
2010	2020	2030	2040	2050	2060	2070	2080
RIENADARNG	DLLRTLNDTL	GKLSAIPNDT	AAKLQAVKDK	ARQANDTAKD	VLAQITELHQ	NLDGLKKNYN	KLADSVAKTN
2090	2100	2110	2120	2130	2140	2150	2160
AVVKDPSKNK	IIADADATVK	NLEQEADRLI	DKLKPIKELE	DNLKKNISEI	KELINQARKQ	ANSIKVSVSS	GGDCIRTYKP
2170	2180	2190	2200	2210	2220	2230	2240
EIKKGSYNNI	VVNVKTAVAD	NLLFYLGSAK	FIDFLAIEMR	KGKVSFLWDV	GSGVGRVEYP	DLTIDDSYWY	RIVASRTGRN
2250	2260	2270	2280	2290	2300	2310	2320
GTISVRALDG	PKASIVPSTH	HSTSPPGYTI	LDVDANAMLF	VGGLTGKLKK	ADAVRVITFT	GCMGETYFDN	KPIGLWNFRE
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
1220	1	1018.6209	-90.98	3	44.9	11.4	0	307-331	R.CECEHNTCGDSCDQCCPGFHQKPWR.A	Carbamidomethyl: 12, 15, 16

Detailed Protein Report

Protein 729: PREDICTED: radial spoke head 10 homolog B isoform X5 [Homo sapiens]

Accession: gi|530384952
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 23.2
MW [kDa]: 59.8
pI: 6.8
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

Detailed Protein Report

Protein 730: PREDICTED: mitochondrial Rho GTPase 1 isoform X3 [Homo sapiens]

Accession:	gi|578831127	**Score:**	23.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	76.8
Database Date:	2015-11-30	**pI:**	6.2
		Sequence Coverage [%]:	3.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MKKDVRILLV	GEPRVGKTSL	IMSLVSEEFP	EEVPPRAEEI	TIPADVTPER	VPTHIVDYSE	AEQSDEQLHQ	EISQANVICI
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
VYAVNNKHSI	DKVTSRWIPL	INERTDKDSR	LPLILVGNKS	DLVEYSSMET	ILPIMNQYTE	IETCVECSAK	NLKNISELFY
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
YAQKAVLHPT	GPLYCPEEKE	MKPACIKALT	RIFKISDQDN	DGTLNDAELN	FFQRICFNTP	LAPQALEDVK	NVVRKHISDG
250	**260**	**270**	**280**	**290**	**300**	**310**	**320**
VADSGLTLKG	FLFLHTLFIQ	RGRHETTWTV	LRRFGYDDDL	DLTPEYLFPL	LKIPPDCTTE	LNHHAYLFLQ	STFDKHDLDR
330	**340**	**350**	**360**	**370**	**380**	**390**	**400**
DCALSPDELK	DLFKVFPYIP	WGPDVNNTVC	TNERGWITYQ	GFLSQWTLTT	YLDVQRCLEY	LGYLGYSILT	EQESQASAVT
410	**420**	**430**	**440**	**450**	**460**	**470**	**480**
VTRDKKIDLQ	KKQTQRNVFR	CNVIGVKNCG	KSGVLQALLG	RNLMRQKKIR	EDHKSYYAIN	TVYVYGQEKY	LLLHDISESE
490	**500**	**510**	**520**	**530**	**540**	**550**	**560**
FLTEAEIICD	VVCLVYDVSN	PKSFEYCARI	FKQHFMDSRI	PCLIVAAKSD	LHEVKQEYSI	SPTDFCRKHK	MPPPQAFTCN
570	**580**	**590**	**600**	**610**	**620**	**630**	**640**
TADAPSKDIF	VKLTTMAMYP	EDHYRDRLSR	DMGHTDRIEN	LRKIWVFLKT	AFHARLRCMC	TCNRCTFCIC	QNFLNSDLLQ
650	**660**	**670**					
SVKNKIFTAV	LNRHENSPGS	LPWRLH					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2821	1	914.4775	-32.72	2	64.4	10.3	2	93-107	K.VTSRWIPLINERTDK.D	

Detailed Protein Report

Protein 731: tripartite motif-containing protein 46 isoform 4 [Homo sapiens]

Accession:	gi|375298680	**Score:**	23.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	81.8
Database Date:	2015-11-30	**pI:**	9.6
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	3.2
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MGAKGNGLTS	MKNMEKELLC	PVCQEMYKQP	LVLPCTHNVC	QACAREVLGQ	QGYIGHGGDP	SSEPTSPAST	PSTRSPRLSR
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
RTLPKPDRLD	RLLKSGFGTY	PGRKRGALHP	QVIMFPCPAC	QGDVELGERG	LAGLFRNLTL	ERVVERYRQS	VSVGGAILCQ
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
LCKPPPLEAT	KGCTECRATF	CNECFKLFHP	WGTQKAQHEP	TLPTLSFRPK	GLMCPDHKEE	VTHYCKTCQR	LVCQLCRVRR
250	**260**	**270**	**280**	**290**	**300**	**310**	**320**
THSGHKITPV	LSAYQALKDK	LTKSLTYILG	NQDTVQTQIC	ELEEAVRHTE	VSGQQAKEEV	SQLVRGLGAV	LEEKRASLLQ
330	**340**	**350**	**360**	**370**	**380**	**390**	**400**
AIEECQQERL	ARLSAQIQEH	RSLLDGSGLV	GYAQEVLKET	DQPCFVQAAK	QLHNRIARAT	EALQTFRPAA	SSSFRHCQLD
410	**420**	**430**	**440**	**450**	**460**	**470**	**480**
VGREMKLLTE	LNFLRVPEAP	VIDTQRTFAY	DQIFLCWRLP	PHSPPAWHYT	VEFRRTDVPA	QPGPTRWQRR	EEVRGTSALL
490	**500**	**510**	**520**	**530**	**540**	**550**	**560**
ENPDTGSVYV	LRVRGCNKAG	YGEYSEDVHL	HTPPAPVLHF	FLDSRWGASR	ERLAISKDQR	AVRSVPGLPL	LLAADRLLTG
570	**580**	**590**	**600**	**610**	**620**	**630**	**640**
CHLSVDVVLG	DVAVTQGRSY	WACAVDPASY	LVKVGVGLES	KLQESFQGAP	DVISPRYDPD	SGHDSGAEDA	TVEASPPFAF
650	**660**	**670**	**680**	**690**	**700**	**710**	**720**
LTIGMGKILL	GSGASSNAGL	TGRDGPTAGC	TVPLPPRLGI	CLDYERGRVS	FLDAVSFRGL	LECPLDCSGP	VCPAFCFIGG
730	**740**	**750**					
GAVQLQEPVG	TKPERKVTIG	GFAKLD					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1373	1	926.7345	-26.95	3	45.9	10.5	2	5-28	K.GNGLTSMKNMEKELLCPVCQEMYK.Q	Oxidation: 10, 22
1590	1	945.6946	-76.21	3	48.4	12.7	2	5-28	K.GNGLTSMKNMEKELLCPVCQEMYK.Q	Carbamidomethyl: 16; Oxidation: 7, 22

Detailed Protein Report

Protein 732: PREDICTED: focadhesin isoform X1 [Homo sapiens]

Accession:	gi|578816557	**Score:**	23.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	199.9
Database Date:	2015-11-30	**pI:**	6.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSDDIRKRFE	FPNSLIQSQA	VGHLIAAVLK	ENGFSEKIHQ	STNQTPALNL	LWEKCCSDNV	VVRTACCEGL	VALVAQDHAE
90	100	110	120	130	140	150	160
FSYVLNGILN	LIPSTRNTHG	LIKAIMHLLQ	MQALKEGQGG	EKNIQSIYTI	RNHPHPLITV	LEHRPDCWPV	FLQQLTAFFQ
170	180	190	200	210	220	230	240
QCPERLEVSC	IQIMAPFLWY	LYCEPSQLQE	YAKLRLALLK	VLLQPQVLCD	KDQPSILEQQ	ILQLCCDIVP	CLQVKDLIQT
250	260	270	280	290	300	310	320
TEAMMFIEEV	CLSLLRHPVF	WKIQLTQMSL	QLLCVSEVSL	KITGECSSSI	HLLEHSVELL	KEDFPVELVI	IGIALLLLQT
330	340	350	360	370	380	390	400
PASQQKPILN	LALKLLSVTE	DQKIPKSSLL	LVMPILQILS	STALEDCISV	DEEGPSRQQL	ALNLLEMIQQ	ECYRDDHQKL
410	420	430	440	450	460	470	480
SYKLVCPVTS	MYGTIFTAWR	ILEVMTDSSA	ASDWLASVES	LLPITAVIPA	PAFLLLAHLL	VEDKGQNLHQ	ILKVTTELAQ
490	500	510	520	530	540	550	560
ADSSQVPNLI	PVLMFKLGRP	LEPILYNDIL	YTLPKLGVHK	VCIGQILRII	QLLGTTPRLR	AVTLRLLTSL	WEKQDRVYPE
570	580	590	600	610	620	630	640
LQRFMAVSDV	PSLSVGKEVQ	WEKLIAKAAS	IRDICKQRPY	QHGADMLAAI	SQVLNECTKP	DQATPAALVL	QGLHALCQAE
650	660	670	680	690	700	710	720
VVCIRSTWNA	LSPKLSCDTR	PLILKTLSEL	FSLVPSLTVN	TTEYENFKVQ	VLSFLWTHTQ	NKDPIVANAA	YRSLANFSAG
730	740	750	760	770	780	790	800
EHTILHLPEK	IRPEIPIPEE	LDDDEDVEDV	DLSVPGSCYL	KLLSLTPPLV	LPALEEFFTS	LVKQEMVNMP	RGIYHSALKG
810	820	830	840	850	860	870	880
GARSDQGKTV	AGIPNFILKM	YETNKQPGLK	PGLAGGMLFC	YDVSMYQSKD	GKPLNRLMAS	RGRSFKQTSL	ALVHEVHIQL
890	900	910	920	930	940	950	960
SEWHRAIFLP	QAWLAYMNRA	YHAILQGRLG	ELELQLKHGK	EEPEEVQYKK	STAWLWVRDM	LTDEITKAAA	KESPVVKGNA
970	980	990	1000	1010	1020	1030	1040
LLALSSLAVV	VSRHEASLSS	DSDGLLEVQP	NFLSMKEWVS	MVLDTLLVIV	DSHYQPRGQL	LSWFYYKSYS	GENTASAIAR
1050	1060	1070	1080	1090	1100	1110	1120
SAAATALSLL	VPVFIISCKE	KVEEILNMLT	ARLPGKPSAD	ESQAVQIHMG	LALGMFLSRL	CEEKLSDISG	QEMNLLLMKS
1130	1140	1150	1160	1170	1180	1190	1200
LDALENCCFD	TSLEYNTGCI	LGVGLVLSLM	SHSSQMQSRV	HVAALLRKLS	AHVDDSGSQS	RTFQEVLAYT	LSCVCTSAFS
1210	1220	1230	1240	1250	1260	1270	1280
AGIIEATEAE	DVMNKLRLLV	ENSQQTSGFA	LALGNIVHGL	SVCGHGKAED	LGSKLLPAWI	RIVLTEGTPT	MLCLAALHGM
1290	1300	1310	1320	1330	1340	1350	1360
VALVGSEGDV	MQLKSEAIQT	SHFQGRLNEV	IRTLTQVISV	SGVIGLQSNA	VWLLGHLHLS	TLSSSQSRAS	VPTDYSYLPE
1370	1380	1390	1400	1410	1420	1430	1440
SSFIGAAIGF	FITGGKKGPE	SVPPSLLKVV	MKPIATVGES	YQYPPVNWAA	LLSPLMRLNF	GEEIQQLCLE	IMVTQAQSSQ
1450	1460	1470	1480	1490	1500	1510	1520
NAAALLGLWV	TPPLIHSLSL	NTKRYLLISA	PLWIKHISDE	QILGFVENLM	VAVFKAASPL	GSPELCPSAL	HGLSQAMKLP
1530	1540	1550	1560	1570	1580	1590	1600
SPAHHLWSLL	SEATGKIFDL	LPNKIRRKDL	ELYISIAKCL	LEMTDDDANR	IAQVTKSNIE	KAAFVKLYLV	SQGRFPLVNL
1610	1620	1630	1640	1650	1660	1670	1680
TDMLSVAVQH	REKEVLAWMI	LHSLYQARIV	SHANTGVLKR	MEWLLELMGY	IRNVAYQSTS	FHNTALDKAL	DFFLLIFATA
1690	1700	1710	1720	1730	1740	1750	1760
VVAWADHTAP	LLLGLSASWL	PWHQENGPAG	PVPSFLGRSP	MHRVTLQEVL	TLLPNSMALL	LQKEPWKEQT	QKFIDWLFSI
1770	1780	1790	1800	1810			
MESPKEALSA	QSRDLLKATL	LSLRVLPEFK	KKAVWTRAYG	W			

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

Detailed Protein Report

	Cmpds.		[ppm]		[min]					
2532	1	729.9581	43.06	2	59.9	12.6	2	584-596	K.LIAKAASIRDICK.Q	Carbamidomethyl: 12

Detailed Protein Report

Protein 733: PREDICTED: HEAT repeat-containing protein 5B isoform X1 [Homo sapiens]

Accession:	gi|530367723	**Score:**	23.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	203.3
Database Date:	2015-11-30	**pI:**	6.7
		Sequence Coverage [%]:	1.4
		No. of unique Peptides:	1

Quantitation

Wdown:Qdown	**Median:** 4.04	**CV:** 0.00 %	**No. of Peptides:** 1

Detailed Protein Report

10	20	30	40	50	60	70	80
MELAHSLLLN	EEALAQITEA	KRPVFIFEWL	RFLDKVLVAA	NKTDVKEKQK	KLVEQLTGLI	SSSPGPPTRK	LLAKNLAALY
90	100	110	120	130	140	150	160
SIGDTFTVFQ	TLDKCNDIIR	NKDDTAAYLP	TKLAAVACVG	AFYEKMGRML	GSAFPETVNN	LLKSLKSAES	QGRSEILMSL
170	180	190	200	210	220	230	240
QKVLSGLGGA	AASSHRDIYK	NARSLLTDRS	MAVRCAVAKC	LLELQNEAVF	MWTAELENIA	TLCFKALENS	NYGVRVAVSK
250	260	270	280	290	300	310	320
LLGTVMATAL	MPKQATVMRQ	NVKRATFDEV	LELMATGFLR	GGSGFLKSGG	EMLKVGGSVN	REVRVGVTQA	YVVFVTTLGG
330	340	350	360	370	380	390	400
QWLERSFATF	LSHVLDLVSH	PRATQTHVEA	VYSRRCVSFI	LRATVGSLLG	EKAQIAAAKE	ICQAIGKQMK	AVEAVVNDTS
410	420	430	440	450	460	470	480
GENKSGAADI	AASQHVMVCA	LQELGSLVQS	LNATASPLIQ	EASIGLLEIV	TSVLLHPSMA	ARLAAAWCLR	CVAVALPFQL
490	500	510	520	530	540	550	560
TPFLDRCAER	LNNLKTSPEA	VSGYSFAMAA	LLGGVHQCPL	GIPHAKGKMV	VSIAEDLLRT	AAQNSRLSLQ	RTQAGWLLLG
570	580	590	600	610	620	630	640
ALMTLGPSVV	RYHLPKMLLL	WRNVFPRSLK	ELEAEKARGD	SFTWQVTLEG	RAGALCAMRS	FVAHCPELLT	EDVIRKLMTP
650	660	670	680	690	700	710	720
IECAMTMMSH	IPSVMKAHGA	HLKASAAMVR	LRLYDILALL	PPKTYEGSFN	ALLRELVAEF	TLTDNSANTT	TSLLRSLCHY
730	740	750	760	770	780	790	800
DDSVLLGSWL	QETDHKSIED	QLQPNSASGS	GALEHDPSSI	YLRIPAGEAV	PGPLPLGVSV	IDASVALFGV	VFPHVSYKHR
810	820	830	840	850	860	870	880
LQMLDHFAEC	VKQAKGVRQQ	AVQLNIFTAV	LSALKGLAEN	KSTLGPEEVR	KSALTLVMGP	LDNPNPILRC	AAGEALGRMA
890	900	910	920	930	940	950	960
QVVGEATFIA	RMAQYSFDKL	KSARDVVSRT	GHSLALGCLH	RYVGGIGSGQ	HLKTSVSILL	ALAQDGTSPE	VQTWSLHSLA
970	980	990	1000	1010	1020	1030	1040
LIVDSSGPMY	RGYVEPTLSL	VLTLLLTVPP	SHTEVHQCLG	RCLGAIITTV	GPELQGNGAT	TSTIRSSCLV	GCAITQDHSD
1050	1060	1070	1080	1090	1100	1110	1120
SLVQAAAISC	LQQLHMFAPR	HVNLSSLVPS	LCVHLCSSHL	LLRRAAVACL	RQLAQREAAE	VCEYAMSLAK	NTGDKESSSA
1130	1140	1150	1160	1170	1180	1190	1200
NVSPFAPGVS	SRTDIHCRHQ	GVNITETGLE	GLLFGMLDRE	TDRKLCSDIH	DTLGHMLSSL	AVEKLSHWLM	LCKDVLAASS
1210	1220	1230	1240	1250	1260	1270	1280
DMSTATLLSS	GKDEEAEKKD	EMDDDTMFTT	LGEEDKSKPF	VAPRWATRVF	AADCLCRIIN	LCENADQAHF	DLALARSAKL
1290	1300	1310	1320	1330	1340	1350	1360
RNPTNDLLVL	HLSDLIRMAF	MAATDHSNQL	RMAGLQALED	IIKKFASVPE	PEFPGHVILE	QYQANVGAAL	RPAFSQDTPS
1370	1380	1390	1400	1410	1420	1430	1440
DIIAKACQVC	STWIGSGVVS	DLNDLRRVHN	LLVSSLDKVQ	AGKGSSSQLY	RESATTMEKL	AVLKAWAEVY	VVAMNIKKEA
1450	1460	1470	1480	1490	1500	1510	1520
ESKPKRAIKN	TDDDDDDCGT	IDELPPDSLI	TLVQPELPTL	SRLWLAALKD	YALLTLPAEF	SSQLPPDGGA	FYTPETIDTA
1530	1540	1550	1560	1570	1580	1590	1600
RLHYRNSWAP	ILHAVALWLN	STGFTCSEST	EAAAISGLQK	RSTSVNLNQA	SGAVGSAKSL	PEINKDRMHL	ILGVSIQFLC
1610	1620	1630	1640	1650	1660	1670	1680
SPRPEEPIEH	VTACLQALHT	LLDSPYARVH	IAEDQLIGVE	LLSVLHRLLL	TWNPSSVQLL	VTGVVQQIVR	AAQDYLQEKR
1690	1700	1710	1720	1730	1740	1750	1760
NTLNEDDMEK	EACTVLGEGG	DSGGLIPGKS	LVFATMELLM	FILVRHMPHL	STKVSDSPSH	IATKTRLSEE	SARLVAATVT
1770	1780	1790	1800	1810	1820	1830	1840
ILSDLPSLCS	PAGCMTILPT	ILFLIARILK	DTAIKSADNQ	VPPPVSAALQ	GIKSIVTLSM	AKTEAGVQKQ	WTALIRSTLA
1850	1860	1870	1880	1890			
CILEYSQPGS	SQMLPASPLS	LPAFQSCPFN	SLYSFISSNS	G			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
284	1	635.8126	-19.46	2	32.3	12.1	0	684-694	K.TYEGSFNALLR.E		Wdown:Qdown 4.04

Detailed Protein Report

Protein 734: 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	1	937.8811	-22.59	2	56.3	23.1	0	21-36	K.CHASENEEDSPAYLPR.I	Carbamidomethyl: 1

Detailed Protein Report

Protein 735: PREDICTED: adenylate cyclase type 8 isoform X1 [Homo sapiens]

Accession:	gi|530388711	**Score:**	23.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	136.6
Database Date:	2015-11-30	**pI:**	6.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.4
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MELSDVRCLT	GSEELYTIHP	TPPAGDGRSA	SRPQRLLWQT	AVRHITEQRF	IHGHRGGSGS	GSGGSGKASD	PAGGGPNHHA
90	100	110	120	130	140	150	160
PQLSGDSALP	LYSLGPGERA	HSTCGTKVFP	ERSGSGSASG	SGGGGDLGFL	HLDCAPSNSD	FFLNGGYSYR	GVIFPTLRNS
170	180	190	200	210	220	230	240
FKSRDLERLY	QRYFLGQRRK	SEVVMNVLDV	LTKLTLLVLH	LSLASAPMDP	LKGILLGFFT	GIEVVICALV	VVRKDTTSHT
250	260	270	280	290	300	310	320
YLQYSGVVTW	VAMTTQILAA	GLGYGLLGDG	IGYVLFTLFA	TYSMLPLPLT	WAILAGLGTS	LLQVILQVVI	PRLAVISINQ
330	340	350	360	370	380	390	400
VVAQAVLFMC	MNTAGIFISY	LSDRAQRQAF	LETRRCVEAR	LRLETENQRQ	ERLVLSVLPR	FVVLEMINDM	TNVEDEHLQH
410	420	430	440	450	460	470	480
QFHRIYIHRY	ENVSILFADV	KGFTNLSTTL	SAQELVRMLN	ELFARFDRLA	HEHHCLRIKI	LGDCYYCVSG	LPEPRQDHAH
490	500	510	520	530	540	550	560
CCVEMGLSMI	KTIRYVRSRT	KHDVDMRIGI	HSGSVLCGVL	GLRKWQFDVW	SWDVDIANKL	ESGGIPGRIH	ISKATLDCLN
570	580	590	600	610	620	630	640
GDYNVEEGHG	KERNEFLRKH	NIETYLIKQP	EDSLLSLPED	IVKESVSSSD	RRNSGATFTE	GSWSPELPFD	NIVGKQNTLA
650	660	670	680	690	700	710	720
ALTRNSINLL	PNHLAQALHV	QSGPEEINKR	IEHTIDLRSG	DKLRREHIKP	FSLMFKDSSL	EHKYSQMRDE	VFKSNLVCAF
730	740	750	760	770	780	790	800
IVLLFITAIQ	SLLPSSRVMP	MTIQFSILIM	LHSALVLITT	AEDYKCLPLI	LRKTCCWINE	TYLARNVIIF	ASILINFLGA
810	820	830	840	850	860	870	880
ILNIYFVFTG	VLAMVTCAVF	LRLNSVLKLA	VLLIMIAIYA	LLTETVYAGL	FLRYDNLNHS	GEDFLGTKEV	SLLLMAMFLL
890	900	910	920	930	940	950	960
AVFYHGQQLE	YTARLDFLWR	VQAKEEINEM	KELREHNENM	LRNILPSHVA	RHFLEKDRDN	EELYSQSYDA	VGVMFASIPG
970	980	990	1000	1010	1020	1030	1040
FADFYSQTEM	NNQGVECLRL	LNEIIADFDE	LLGEDRFQDI	EKIKTIGSTY	MAVSGLSPEK	QQCEDKWGHL	CALADFSLAL
1050	1060	1070	1080	1090	1100	1110	1120
TESIQEINKH	SFNNFELRIG	ISHGSVVAGV	IGAKKPQYDI	WGKTVNLASR	MDSTGVSGRI	QVPEETYLIL	KDQGFAFDYR
1130	1140	1150	1160	1170	1180	1190	1200
GEIYVKGISE	QEGKIKTYFL	LGRVQPNPFI	LPPRRLPGQY	SLAAVVLGLV	QSLNRQRQKQ	LLNENNNTGI	IKGHYNRRTL
1210	1220	1230					
LSPSGTEPGA	QAEGTDKSDL	P					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2777	1	735.3766	48.62	3	66.0	11.8	1	476-494	R.QDHAHCCVEMGLSMIKTIR.Y	Oxidation: 10, 14
158	1	659.9157	162.56	2	31.2	11.3	1	704-713	K.YSQMRDEVFK.S	Oxidation: 4

Detailed Protein Report

Protein 736: 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 737: PREDICTED: tudor domain-containing protein 7 isoform X1 [Homo sapiens]

Accession: gi|578817238
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 23.1
MW [kDa]: 115.3
pI: 6.7
Sequence Coverage [%]: 2.8
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MACTETARIA	QLVARQRSSK	RKTGRQVNCQ	MRVKKTMPFF	LEGKPKATLR	QPGFASNFSV	GKKPNPAPLR	DKGNSVGVKP
90	100	110	120	130	140	150	160
DAEMSPYMLH	TTLGNEAFKD	IPVQRHVTMS	TNNRFSPKAS	LQPPLQMHLS	RTSTKEMSDN	LNQTVEKPNV	KPPASYTYKM
170	180	190	200	210	220	230	240
DEVQNRIKEI	LNKHNNGIWI	SKLPHFYKEL	YKEDLNQGIL	QQFEHWPHIC	TVEKPCSGGQ	DLLLYPAKRK	QLLRSELDTE
250	260	270	280	290	300	310	320
KVPLSPLPGP	KQTPPLKGCP	TVMAGDFKEK	VADLLVKYTS	GLWASALPKA	FEEMYKVKFP	EDALKNLASL	SDVCSIDYIS
330	340	350	360	370	380	390	400
GNPQKAILYA	KLPLPTDKIQ	KDAGQAHGDN	DIKAMVEQEY	LQVEESIAES	ANTFMEDITV	PPLMIPTEAS	PSVLVVELSN
410	420	430	440	450	460	470	480
TNEVVIRYVG	KDYSAAQELM	EDEMKEYYSK	NPKITPVQAV	NVGQLLAVNA	EEDAWLRAQV	ISTEENKIKV	CYVDYGFSEN
490	500	510	520	530	540	550	560
VEKSKAYKLN	PKFCSLSFQA	TKCKLAGLEV	LSDDPDLVKV	VESLTCGKIF	AVEILDKADI	PLVVLYDTSG	EDDININATC
570	580	590	600	610	620	630	640
LKAICDKSLE	VHLQVDAMYT	NVKVTNICSD	GTLYCQVPCK	GLNKLSDLLR	KIEDYFHCKH	MTSECFVSLP	FCGKICLFHC
650	660	670	680	690	700	710	720
KGKWLRVEIT	NVHSSRALDV	QFLDSGTVTS	VKVSELREIP	PRFLQEMIAI	PPQAIKCCLA	DLPQSIGMWT	PDAVLWLRDS
730	740	750	760	770	780	790	800
VLNCSDCSIK	VTKVDETRGI	AHVYLFTPKN	FPDPHRSINR	QITNADLWKH	QKDVFLSAIS	SGADSPNSKN	GNMPMSGNTG
810	820	830	840	850	860	870	880
ENFRKNLTDV	IKKSMVDHTS	AFSTEELPPP	VHLSKPGEHM	DVYVPVACHP	GYFVIQPWQE	IHKLEVLMEE	MILYYSVSEE
890	900	910	920	930	940	950	960
RHIAVEKDQV	YAAKVENKWH	RVLLKGILTN	GLVSVYELDY	GKHELVNIRK	VQPLVDMFRK	LPFQAVTAQL	AGVKCNQWSE
970	980	990	1000	1010	1020	1030	
EASMVFRNHV	EKKPLVALVQ	TVIENANPWD	RKVVVYLVDT	SLPDTDTWIH	DFMSEYLIEL	SKVN	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2184	1	955.9047	-109.56	2	55.9	11.2	1	119-135	K.ASLQPPLQMHLSRTSTK.E	Oxidation: 9

Detailed Protein Report

Protein 738: pannexin-2 isoform 2 [Homo sapiens]

Accession:	gi|237757297	**Score:**	23.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	70.6
Database Date:	2015-11-30	**pI:**	9.7
		Sequence Coverage [%]:	5.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MHHLLEQSAD	MATALLAGEK	LRELILPGAQ	DDKAGALAAL	LLQLKLELPF	DRVVTIGTVL	VPILLVTLVF	TKNFAEEPIY
90	100	110	120	130	140	150	160
CYTPHNFTRD	QALYARGYCW	TELRDALPGV	DASLWPSLFE	HKFLPYALLA	FAAIMYVPAL	GWEFLASTRL	TSELNFLLQE
170	180	190	200	210	220	230	240
IDNCYHRAAE	GRAPKIEKQI	QSKGPGITER	EKREIIENAE	KEKSPEQNLF	EKYLERRGRS	NFLAKLYLAR	HVLILLLSAV
250	260	270	280	290	300	310	320
PISYLCTYYA	TQKQNEFTCA	LGASPDGAAG	AGPAVRVSCK	LPSVQLQRII	AGVDIVLLCV	MNLIILVNLI	HLFIFRKSNF
330	340	350	360	370	380	390	400
IFDKLHKVGI	KTRRQWRRSQ	FCDINILAMF	CNENRDHIKS	LNRLDFITNE	SDLMYDNVVR	QLLAALAQSN	HDATPTVRDS
410	420	430	440	450	460	470	480
GVQTVDPSAN	PAEPDGAAEP	PVVKRPRKKM	KWIPTSNPLP	QPFKEPLAIM	RVENSKAEKP	KPARRKTATD	TLIAPLLDRS
490	500	510	520	530	540	550	560
AHHYKGGGGD	PGPGPAPAPA	PPPAPDKKHA	RHFSLDVHPY	ILGTKKAKAE	AVPAALPASR	SQEGGFLSQA	EDCGLGLAPA
570	580	590	600	610	620	630	640
PIKDAPLPEK	EIPYPTEPAR	AGLPSGGPFH	VRSPPAAPAV	APLTPASLGK	AEPLTILSRN	ATHPLLHINT	LSSSPPSTSR
650							
ERS							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1970	1	1051.4242	-48.76	2	53.3	11.9	0	73-89	K.NFAEEPIYCYTPHNFTR.D	

Detailed Protein Report

Protein 739: **metallothionein-1A [Homo sapiens]**

Accession:	gi|71274113	**Score:**	23.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	6.1
Database Date:	2015-11-30	**pI:**	10.5
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	32.8
		No. of unique Peptides:	2

```
         10          20          30          40          50          60          70
MDPNCSCATG  GSCTCTGSCK  CKECKCTSCK  KSCCSCCPMS  CAKCAQGCIC  KGASEKCSCC  A
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2067	2	701.2708	34.48	3	54.4	11.5	1	32-51	K.SCCSCCPMSCAKCAQGCICK.G	Carbamidomethyl: 6; Oxidation: 8
2158	1	701.2771	43.49	3	55.5	11.5	1	32-51	K.SCCSCCPMSCAKCAQGCICK.G	Carbamidomethyl: 19; Oxidation: 8

Detailed Protein Report

Protein 740: **unconventional myosin-VIIa isoform 2 [Homo sapiens]**

Accession:	gi|189083802	**Score:**	23.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	250.1
Database Date:	2015-11-30	**pI:**	9.4
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.8
		No. of unique Peptides:	2

Detailed Protein Report

```
        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
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2700	1	869.0838	124.35	2	62.1	12.0	1	528-542	K.LNSQHKLNANYIPPK.N	
1136	1	985.2085	56.47	3	43.8	11.0	1	1959-1983	K.LWTTTVPGKDPMADSIFHYYQELPK.Y	Oxidation: 12

Detailed Protein Report

Protein 741: **PREDICTED: immunoglobulin-like and fibronectin type III domain-containing protein 1 isoform X3 [Homo sapiens]**

Accession:	gi|578801693	**Score:**	23.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	355.2
Database Date:	2015-11-30	**pI:**	5.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.1
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MAGKLRKSHI	PGVSIWQLVE	EIPEGCSTPD	FEQKPVTSAL	PEGKNAVFRA	VVCGEPRPEV	RWQNSKGDLS	DSSKYKISSS
90	100	110	120	130	140	150	160
PGSKEHVLQI	NKLTGEDTDL	YRCTAVNAYG	EAACSVRLTV	IEVGFRKNRK	RHREPQEDLR	KELMDFRKLL	KKRAPPAPKK
170	180	190	200	210	220	230	240
KMDLEQIWQL	LMTADRKDYE	KICLKYGIVD	YRGMLRRLQE	MKKEQEDKMA	QYINTISSLR	HIRVTKDGNA	KFDLELDLKD
250	260	270	280	290	300	310	320
SQSKIYLYKD	GEMIPYGFNN	QTKHCLRRLG	KRYEFQIQDL	RPEDSGIYQV	KVEDAVVFST	ELEASAIPPR	VVVPLAETHC
330	340	350	360	370	380	390	400
EEQGDAVFEC	TLSSPCPSAA	WHFRHRLLHP	SDKYEVYVSP	DGLTHRLVVR	GARFSDMGPY	SLGTGLYTSS	AWLVVEAGKD
410	420	430	440	450	460	470	480
KDLQSTSADH	KLQRQGAQAS	GAEESGSIES	QGEKSREQGP	RGGSLEGAGP	ASGLQHIASP	DRDGLGRHGY	SLMGDKGTAD
490	500	510	520	530	540	550	560
SAWGPGQEGE	GFPVAEGSRA	TLPRENQSHR	EGGWARSLAE	RPHLQGESSE	SGLGLPEKQQ	QDRGRDSNSD	ECWRKAGGWE
570	580	590	600	610	620	630	640
AGSSRLQAGG	LGSSREGKEH	RGDSGRQLDR	HAPEQLWDAR	LGPGRGKSDL	QGCQSDPVGS	WPRGKQIEIS	QDDSLAEMDR
650	660	670	680	690	700	710	720
GDAPSRERGR	GIVVWGGGTG	LGEAGDSNGA	GGPGTLELTG	GRGSGSKVGM	APESWGSQGG	RDADYGEARG	YWGSGELLEQ
730	740	750	760	770	780	790	800
IPGGKDFQEP	SISGGRKFLL	GDGSPEIKAE	DSLQEADGIC	RGESVVTGSA	YKTGPGGPGD	PRGCEGVLQE	LRGRDGQETA
810	820	830	840	850	860	870	880
WASGEVEYDP	RSFQSSQGWT	AGHRAAGGIG	RIESKGTSPW	DDTPSSLRKT	GAHHGPGVLG	PSGGQEGMGG	IWVAGLTESG
890	900	910	920	930	940	950	960
QGVDARSHWL	SRAPGLGAQG	SGGTLGDKKG	LRGPGSIGSE	PDFWNGSGSS	RVKGPRGETG	YKDGLEGPGR	MESRYEGGLG
970	980	990	1000	1010	1020	1030	1040
YSREISSKSG	AGYSYGSGVP	GEMGSGHGAG	CRVSPRAPAG	VESEEGGGYR	HGSGAPGGVW	SGNEDSGPAG	GGSGRVASLK
1050	1060	1070	1080	1090	1100	1110	1120
NGSGGPDGAP	MNDTRNWASA	CQAGMDPRGG	HHSDGGLGSP	GVTGSAGRGG	LKAPGVVETV	GMGCVEAEPE	SSGRIRPWGQ
1130	1140	1150	1160	1170	1180	1190	1200
TGNYGGFRAS	EALGAFGEGG	YEDGSGGPGA	MGPGSLRAGS	KVGEGDGTRC	PGAKASGAGA	GYRDDTRHPE	SLAPHNGAAS
1210	1220	1230	1240	1250	1260	1270	1280
GSQWAYGAGN	VLGYEDGSEL	PGPQGTGVRT	AYGERSRGLG	PRSTGPGGEA	GFRDGSGGLQ	GMGSADGPGC	RKGIGSSGEM
1290	1300	1310	1320	1330	1340	1350	1360
GSVDKEGYKK	DLGAPENMGS	GSKADYRDGV	GGSGAMGSMD	EAGYRKDLGA	PEGISSGSKA	DYRGGLQDSR	EAGSGSKADY
1370	1380	1390	1400	1410	1420	1430	1440
SGGLKGSREI	GSMDETDNRK	DLGVPEGMGA	GYRAGLRGPG	EMGSLDESGH	RNGIGGYGEM	GSGYREDLGA	PEGMGTGSKA
1450	1460	1470	1480	1490	1500	1510	1520
GYRDGLRGSG	EMRSMDEAGY	RKNLGAPERM	DSGSKAGYRG	GLRGSGEMGL	IEAGYRKDLG	VSEGGGSGSK	AGYRGGLGSG
1530	1540	1550	1560	1570	1580	1590	1600
EMGSVDKAGY	RKDLGASEAI	GSGSKAGFTD	GLGGSEEMGS	VNKAGYRKDL	GAPKGMGSGS	KASFRDGLGG	SGEMGSVNEA
1610	1620	1630	1640	1650	1660	1670	1680
GYRKDLGVPE	GIGSGSKAGF	RDGLGGSEEM	GSVNKAGYRK	DLGAPKGIGS	GSKAGFRDGL	GSSGEMGSMD	EAGYRKNLGA
1690	1700	1710	1720	1730	1740	1750	1760
PEGIGSGSKA	GFRDGLGSSV	EMGSVNEAGY	RKDLGAPEGM	GSGSKAGFRD	GLGGSGEMGS	VNEAGYRKDL	GAPKGIGSGS
1770	1780	1790	1800	1810	1820	1830	1840
KADFRDALGS	SGEMGSMDEA	GYRKDLWAPE	GIGSGSKAGF	RDGLGSSVEM	GSVNEAGYRK	DLGAPEGMGS	GSKAGFRDGL
1850	1860	1870	1880	1890	1900	1910	1920
GGSGEMGSVN	EAGYRKDLGA	PKGIGSGSKA	DFRDALGSSG	EMGSMDEAGY	RKDLWAPEGI	GSGSKAGFRD	GLGSSVEMGS
1930	1940	1950	1960	1970	1980	1990	2000
VNEAGYRKDL	GAPEGMGSGS	KEGFRDGLGG	SEEMGSVNKA	GYRKDLGAPK	GMGSGSKEGF	RDGLGGSEEM	GSMDEAGYRK
2010	2020	2030	2040	2050	2060	2070	2080
DLGAPEGIGS	GSKAGFRDGL	GGSEEMRSMD	EAGYRKDLGA	PERIGSGSKA	GFRDGLGSSV	EMGSVNEAGY	RKDLGAPKGM
2090	2100	2110	2120	2130	2140	2150	2160
GSGSKTGFRD	GLGGSEEMES	MDEAGYRKDL	GAPEGIGSGS	KAGFRDGLGS	STEMGSVNEA	GYRKDLGAPK	GMGSESKAGF
2170	2180	2190	2200	2210	2220	2230	2240

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
548	1	512.1851	-91.29	2	35.5	10.1	0	468-476	R.HGYSLMGDK.G	Oxidation: 6
765	1	937.7156	-58.56	3	38.1	12.9	1	2411-2439	R.ETRLVDGAGPGVEPGMAGMPGTAGGMAHR.D	Oxidation: 16, 19

Detailed Protein Report

Protein 742: **PREDICTED: protein-methionine sulfoxide oxidase MICAL3 isoform X15 [Homo sapiens]**

Accession:	gi|578836826	**Score:**	22.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	153.9
Database Date:	2015-11-30	**pI:**	5.0
		Sequence Coverage [%]:	2.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MELKFLLCCQ	QTYRDLDADN	RGKQSPHHER	KYIKMYTGGV	SSLAEQIANQ	LQRKEQPKAL	LDKKELGSMK	KEFPQNLGGS
90	100	110	120	130	140	150	160
DTCYFCQKRV	YVMERLSAEG	KFFHRSCFKC	EYCATTLRLS	AYAYDIEDGK	FYCKPHYCYR	LSGYAQRKRP	AVAPLSGKEA
170	180	190	200	210	220	230	240
KGPLQDGATT	DANGRANAVA	SSTERTPGSG	VNGLEEPSIA	KRLRGTPERI	ELENYRLSLR	QAEALQEVPE	ETQAEHNLSS
250	260	270	280	290	300	310	320
VLDTGAEEDV	ASSSSESEME	EEGEEEEEEP	RLPPSDLGGV	PWKEAVRIHA	LLKGKSEEEL	EASKSFGPGN	EEEEEEEEEY
330	340	350	360	370	380	390	400
EEEEEEDYDE	EEEESSEAGN	QRLQQVMHAA	DPLEIQADVH	WTHIREREEE	ERMAPASESS	ASGVPDLPSI	RHAAVQAWLE
410	420	430	440	450	460	470	480
TVSGGTPLDE	NDLEEDVDSE	PAEIEGEAAE	DGDPGDTGAE	LDDDQHWSDS	PSDADRELRL	PCPAEGEAEL	ELRVSEDEEK
490	500	510	520	530	540	550	560
LPASPKHQER	GPSQATSPIR	SPQESALLFI	PVHSPSTEGP	QLPPVPAATQ	EKSPEERLFP	EPLLPKEKPK	ADAPSDLKAV
570	580	590	600	610	620	630	640
HSPIRSQPVT	LPEARTPVSP	GSPQPQPPVA	ASTPPPSPLP	ICSQPQPSTE	ATVPSPTQSP	IRFQPAPAKT	STPLAPLPVQ
650	660	670	680	690	700	710	720
SQSDTKDRLG	SPLAVDEALR	RSDLVEEFWM	KSAEIRRSLG	LTPVDRSKGP	EPSFPTPAFR	PVSLKSYSVE	KSPQDEGLHL
730	740	750	760	770	780	790	800
LKPLSIPKRL	GLPKPEGEPL	SLPTPRSPSD	RELRSAQEER	RELSSSSGLG	LHGSSSNMKT	LGSQSFNTSD	SAMLTPPSSP
810	820	830	840	850	860	870	880
PPPPPPGEEP	ATLRRKLREA	EPNASVVPPP	LPATWMRPPR	EPAQPPREEV	RKSFVESVEE	IPFADDVEDT	YDDKTEDSSL
890	900	910	920	930	940	950	960
QEKFFTPPSC	WPRPEKPRHP	PLAKENGRLP	ALEGTLQPQK	RGLPLVSAEA	KELAEERMRA	REKSVKSQAL	RDAMARQLSR
970	980	990	1000	1010	1020	1030	1040
MQQMELASGA	PRPRKASSAP	SQGKERRPDS	PTRPTLRGSE	EPTLKHEATS	EEVLSPPSDS	GGPDGSFTSS	EGSSGKSKKR
1050	1060	1070	1080	1090	1100	1110	1120
SSLFSPRRNK	KEKKSKGEGR	PPEKPSSNLL	EEAAAKPKSL	WKSVFSGYKK	DKKKKADDKS	CPSTPSSGAT	VDSGKHRVLP
1130	1140	1150	1160	1170	1180	1190	1200
VVRAELQLRR	QLSFSEDSDL	SSDDVLEKSS	QKSRRESIYV	PHALAFRRSC	ASKPRTYTEE	ELNAKLTRRV	QKAARRQAKQ
1210	1220	1230	1240	1250	1260	1270	1280
EELKRLHRAQ	IIQRQLQQVE	ERQRRLEERG	VAVEKALRGE	AVEPSGGTPR	RRPLSFCPCC	VQEGMGKKDD	PKLMQEWFKL
1290	1300	1310	1320	1330	1340	1350	1360
VQEKNAMVRY	ESELMIFARE	LELEDRQSRL	QQELRERMAV	EDHLKTEEEL	SEEKQILNEM	LEVVEQRDSL	VALLEEQRLR
1370	1380	1390					
EREEDKDLEA	AMLSKGFSLN	WS					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2512	1	834.4289	-40.88	2	61.8	10.6	2	647-661	K.DRLGSPLAVDEALRR.S	

Detailed Protein Report

Protein 743: PREDICTED: PH and SEC7 domain-containing protein 3 isoform X5 [Homo sapiens]

Accession:	gi|578815265	**Score:**	22.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	57.9
Database Date:	2015-11-30	**pI:**	9.6
		Sequence Coverage [%]:	4.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MILLYSRTSN	AGVKTTRLEA	HSEMGSTEIL	EKETPENLSN	GTSSNVEAAK	RLAKRLYQLD	RFKRSDVAKH	LGKNNEFSKL
90	100	110	120	130	140	150	160
VAEEYLKFFD	FTGMTLDQSL	RYFFKAFSLV	GETQERERVL	IHFSNRYFYC	NPDTIASQDG	VHCLTCAIML	LNTDLHGHNI
170	180	190	200	210	220	230	240
GKKMTCQEFI	ANLQGVNEGV	DFSKDLLKAL	YNSIKNEKLE	WAVDDEEKKK	SPSESTEEKA	NGTHPKTISR	IGSTTNPFLD
250	260	270	280	290	300	310	320
IPHDPNAAVY	KSGFLARKIH	ADMDGKKTPR	GKRGWKTFYA	VLKGTVLYLQ	KDEYKPEKAL	SEEDLKNAVS	VHHALASKAT
330	340	350	360	370	380	390	400
DYEKKPNVFK	LKTADWRVLL	FQTQSPEEMQ	GWINKINCVA	AVFSAPPFPA	AIGSQKKFSR	PLLPATTTKL	SQEEQLKSHE
410	420	430	440	450	460	470	480
SKLKQITTEL	AEHRSYPPDK	KVKAKDVDEY	KLKDHYLEFE	KTRYEMYVSI	LKEGGKELLS	NDESEAAGLK	KSHSSPSLNP
490	500	510	520				
DTSPITAKVK	RNVSERKDHR	PETPSIKQKV	T				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
249	1	561.2240	-81.38	2	31.8	12.9	1	210-219	K.KSPSESTEEK.A	

Detailed Protein Report

Protein 744: **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 745: putative RNA polymerase II subunit B1 CTD phosphatase RPAP2 [Homo sapiens]

Accession:	gi|226246608	**Score:**	22.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	69.5
Database Date:	2015-11-30	**pI:**	8.8
		Sequence Coverage [%]:	3.9
		No. of unique Peptides:	2

Quantitation

mdown:qdown	**Median:**	1.51	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	6.04	**CV:**	0.00 %	**No. of Peptides:**	1

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1581	1	583.8284	105.83	2	48.3	11.8	0	1-12	-.MADFAGPSSAGR.K		mdown:qdown 1.51 Wdown:Qdown 6.04
1728	1	725.3276	-76.17	2	50.1	11.1	0	595-606	K.NEDLESLTIIFR.T		

Detailed Protein Report

Protein 746: pumilio domain-containing protein KIAA0020 [Homo sapiens]

Accession:	gi|109948283	**Score:**	22.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	73.5
Database Date:	2015-11-30	**pI:**	10.2
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.2
		No. of unique Peptides:	1

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2240	1	569.1603	-210.52	2	56.7	10.9	0	302-310	K.LELIMDEMK.Q	Oxidation: 8

Detailed Protein Report

Protein 747: guanylate-binding protein 7 [Homo sapiens]

Accession:	gi|148234215	**Score:**	22.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	72.5
Database Date:	2015-11-30	**pI:**	5.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MASEIHMPGP	VCLTENTKGH	LVVNSEALEI	LSAITQPVVV	VAIVGLYRTG	KSYLMNKLAG	KNKGFPLGCT	VKSETKGIWM
90	100	110	120	130	140	150	160
WCVPHPSKPN	HTLILLDTEG	LGDMEKSDPK	SDSWIFALAV	LLSSSFVYNS	MGTINHQALE	QLHYVTELTE	LIRAKSCPRP
170	180	190	200	210	220	230	240
DEVEDSSEFV	SFFPDFIWTV	RDFTLELKLD	GHPITEDEYL	ENALKLISGK	NPQIQNSNKP	REWIRHFFPK	QKCFVFDRPI
250	260	270	280	290	300	310	320
NDKKLLLHVE	EVREDQLDSN	FQMQSENFCS	YIFTHAKTKT	LREGILVTGN	RLGMLVETYL	DAINSGATPC	LENAMAVLAQ
330	340	350	360	370	380	390	400
CENSAAVQRA	ANHYSQQMAQ	QVRFPTDTLQ	ELLDVHAVCE	REAIAVFMEY	SFKDKSQEFQ	KKLVDTMEKK	KEDFVLQNEE
410	420	430	440	450	460	470	480
ASAKYCQAEL	KRLSELLTES	ISRGTFFVPG	GHNIYLEAKK	KIEQDYTLVP	RKGVKADEVL	QSFLQSQVVI	EESILQSDKA
490	500	510	520	530	540	550	560
LTAGEKAIAA	KQAKKEAAEK	EQELLRQKQK	EQQQMMEAQE	RSFQENIAQL	KKKMEREREN	YMRELRKMLS	HKMKVLEELL
570	580	590	600	610	620	630	640
TEGFKEIFES	LNEEINRLKE	QIEAAENEEP	SVFSQILDVA	GSIFIAALPG	AAKLVDLGMK	ILSSLCNRLR	NPGKKIIS

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
838	1	712.3324	-47.27	2	39.0	11.9	1	64-76	K.GFPLGCTVKSETK.G	Carbamidomethyl: 6

Detailed Protein Report

Protein 748: **PREDICTED: asparagine synthetase domain-containing protein 1 isoform X1 [Homo sapiens]**

Accession:	gi|530370551	**Score:**	22.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	72.0
Database Date:	2015-11-30	**pI:**	6.4
		Sequence Coverage [%]:	5.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MCGICCSVNF	SAEHFSQDLK	EDLLYNLKQR	GPNSSKQLLK	SDVNYQCLFS	AHVLHLRGVL	TTQPVEDERG	NVFLWNGEIF
90	100	110	120	130	140	150	160
SGIKVEAEEN	DTQILFNYLS	SCKNESEILS	LFSEVQGPWS	FIYYQASSHY	LWFGRDFFGR	RSLLWHFSNL	GKSFCLSSVG
170	180	190	200	210	220	230	240
TQTSGLANQW	QEVPASGLFR	IDLKSTVISG	CIILQLYPWK	YISRENIIEE	NVNSLSQISA	DLPAFVSVVA	NEAKLYLEKP
250	260	270	280	290	300	310	320
VVPLNMMLPQ	AALETHCSNI	SNVPPTREIL	QVFLTDVHMK	EVIQQFIDVL	SVAVKKRVLC	LPRDENLTAN	EVLKTCDRKA
330	340	350	360	370	380	390	400
NVAILFSGGI	DSMVIATLAD	RHIPLDEPID	LLNVAFIAEE	KTMPTTFNRE	GNKQKNKCEI	PSEEFSKDVA	AAAADSPNKH
410	420	430	440	450	460	470	480
VSVPDRITGR	AGLKELQAVS	PSRIWNFVEI	NVSMEELQKL	RRTRICHLIR	PLDTVLDDSI	GCAVWFASRG	IGWLVAQEGV
490	500	510	520	530	540	550	560
KSYQSNAKVV	LTGIGADEQL	AGYSRHRVRF	QSHGLEGLNK	EIMMELGRIS	SRNLGRDDRV	IGDHGKEARF	PFLDENVVSF
570	580	590	600	610	620	630	640
LNSLPIWEKA	NLTLPRGIGE	KLLLRLAAVE	LGLTASALLP	KRAMQFGSRI	AKMEKINEKA	SDKCGRLQIM	SLENLSIEKE
650							
TKL							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1674	1	882.4076	-157.19	2	49.6	12.4	2	570-585	K.ANLTLPRGIGEKLLLR.L	

Detailed Protein Report

Protein 749: **MAM and LDL-receptor class A domain-containing protein C10orf112 precursor [Homo sapiens]**

Accession:	gi|565671710	**Score:**	22.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	240.9
Database Date:	2015-11-30	**pI:**	4.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.4
		No. of unique Peptides:	2

Quantitation

mdown:qdown	**Median:**	3.18	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.98	**CV:**	0.00 %	**No. of Peptides:**	1

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

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2517	1	913.4615	10.45	2	61.9	10.8	1	1425-1439	R.REELSLFGDEDFQLK.F		Wdown:Qdown 0.98 mdown:qdown 3.18
777	1	541.1764	-129.12	3	38.5	12.0	1	2032-2046	R.NGGTCVVEKNGPMCR.C	Carbamidomethyl: 5	

Detailed Protein Report

Protein 750: hepatoma-derived growth factor isoform a [Homo sapiens]

Accession: gi|4758516
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 22.9
MW [kDa]: 26.8
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 751: otogelin precursor [Homo sapiens]

Accession:	gi|471270262	**Score:**	22.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	314.6
Database Date:	2015-11-30	**pI:**	5.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGVLASALCW	LLCVWLPWGE	QAAESLRVQR	LGERVVDSGR	SGARGMRNVK	GMRNGPAQTR	VSSSSSHQEA	TLAMGDKATV
90	100	110	120	130	140	150	160
VGGQQAEAPD	SVAMSSWERR	LHRAKCAPSY	LFSCFNGGEC	VHPAFCDCRR	FNATGPRCQM	VYNAGPERDS	ICRAWGQHHV
170	180	190	200	210	220	230	240
ETFDGLYYYL	SGKGSYTLVG	RHEPEGQSFS	IQVHNDPQCG	SSPYTCSRAV	SLFFVGEQEI	HLAKEVTHGG	MRVQLPHVMG
250	260	270	280	290	300	310	320
SARLQQLAGY	VIVRHQSAFT	LAWDGASAVY	IKMSPELLGW	THGLCGNNNA	DPKDDLVTSS	GKLTDDVVEF	VHSWQEQAPN
330	340	350	360	370	380	390	400
QPPGPTTSSL	PRPPCLQQNP	GTMQGVYEQC	EALLRPPFDA	CHAYVSPLPF	TASCTSDLCQ	SMGDVATWCR	ALAEYARACA
410	420	430	440	450	460	470	480
QAGRPLQGWR	TQLRQCTVHC	KEKAFTYNEC	IACCPASCHP	RASCVDSEIA	CVDGCYCPNG	LIFEDGGCVA	PAECPCEFHG
490	500	510	520	530	540	550	560
TLYPPGSVVK	EDCNTCTCTS	GKWECSTAVC	PAECSVTGDI	HFTTFDGRRY	TFPATCQYIL	AKSRSSGTFT	VTLQNAPCGL
570	580	590	600	610	620	630	640
NQDGACVQSV	SVILHQDPRR	QVTLTQAGDV	LLFDQYKIIP	PYTDDAFEIR	RLSSVFLRVR	TNVGVRVLYD	REGLRLYLQV
650	660	670	680	690	700	710	720
DQRWVEDTVG	LCGTFNGNTQ	DDFLSPVGVP	ESTPQLFGNS	WKTLSACSPL	VSGSPLDPCD	VHLQAASYSV	QACSVLTGEM
730	740	750	760	770	780	790	800
FAPCSAFLSP	VPYFEQCRRD	ACRCGQPCLC	ATLAHYAHLC	RRHGLPVDFR	ARLPACALSC	EASKEYSPCV	APCGRTCQDL
810	820	830	840	850	860	870	880
ASPEACGVDG	GDDLSRDECV	EGCACPPDTY	LDTQADLCVP	RNQCSCHFQG	VDYPPGDSDI	PSLGHCHCKD	GVMSCDSRAP
890	900	910	920	930	940	950	960
AAACPAGQVF	VNCSDLHTDL	ELSRERTCEQ	QLLNLSVSAR	GPCLSGCACP	QGLLRHGDAC	FLPEECPCTW	KGKEYFPGDQ
970	980	990	1000	1010	1020	1030	1040
VMSPCHTCVC	QRGSFQCTLH	PCASTCTAYG	DRHYRTFDGL	PFDFVGACKV	HLVKSTSDVS	FSVIVENVNC	YSSGMICRKF
1050	1060	1070	1080	1090	1100	1110	1120
ISINVGNSLI	VFDDDSGNPS	PESFLDDKQE	VHTWRVGFFT	LVHFPQEHIT	LLWDQRTTVH	VQAGPQWQGQ	LAGLCGNFDL
1130	1140	1150	1160	1170	1180	1190	1200
KTINEMRTPE	NLELTNPQEF	GSSWAAVECP	DTLDPRDMCV	LNPLREPFAK	KECSILLSEV	FEICHPVVDV	TWFYSNCLTD
1210	1220	1230	1240	1250	1260	1270	1280
TCGCSQGGDC	ECFCASVSAY	AHQCCQHGVA	VDWRTPRLCP	YDCDFFNKVL	GKGPYQLSSL	AAGGALVGMK	AVGDDIVLVR
1290	1300	1310	1320	1330	1340	1350	1360
TEDVAPADIV	SFLLTAALYK	AKAHDPDVVS	LEAADRPNFF	LHVTANGSLE	LAKWQGRDTF	QQHASFLLHR	GTRQAGLVAL
1370	1380	1390	1400	1410	1420	1430	1440
ESLAKPSSFL	YVSGAVLALR	LYEHTEVFRR	GTLFRLLDAK	PSGAAYPICE	WRYDACASPC	FQTCRDPRAA	SCRDVPRVEG
1450	1460	1470	1480	1490	1500	1510	1520
CVPVCPTPQV	LDEVTQRCVY	LEDCVEPAVW	VPTEALGNET	LPPSQGLPTP	SDEEPQLSQE	SPRTPTHRPA	LTPAAPLTTA
1530	1540	1550	1560	1570	1580	1590	1600
LNPPVTATEE	PVVSPGPTQT	TLQQPLELTA	SQLPAGPTES	PASKGVTASL	LAIPHTPESS	SLPVALQTPT	PGMVSGAMET
1610	1620	1630	1640	1650	1660	1670	1680
TRVTVIFAGS	PNITVSSRSP	PAPRFPLMTK	AVTVRGHGSL	PVRTTPPQPS	LTASPSSRPV	ASPGAISRSP	TSSGSHKAVL
1690	1700	1710	1720	1730	1740	1750	1760
TPAVTKVISR	TGVPQPTQAQ	SASSPSTPLT	VAGTAAEQVP	VSPLATRSLE	IVLSTEKGEA	GHSQPMGSPA	SPQPHPLPSA
1770	1780	1790	1800	1810	1820	1830	1840
PPRPAQHTTM	ATRSPALPPE	TPAAASLSTA	TDGLAATPFM	SLESTRPSQL	LSGLPPDTSL	PLAKVGTSAP	VATPGPKASV
1850	1860	1870	1880	1890	1900	1910	1920
ITTPLQPQAT	TLPAQTLSPV	LPFTPAAMTQ	AHPPTHIAPP	AAGTAPGLLL	GATLPTSGVL	PVAEGTASMV	SVVPRKSTTG
1930	1940	1950	1960	1970	1980	1990	2000
KVAILSKQVS	LPTSMYGSAE	GGPTELTPAT	SHPLTPLVAE	PEGAQAGTAL	PVPTSYALSR	VSARTAPQDS	MLVLLPQLAE
2010	2020	2030	2040	2050	2060	2070	2080
AHGTSAGPHL	AAEPVDEATT	EPSGRSAPAL	SIVEGLAEAL	ATTTEANTST	TCVPIAEQDC	VRHICLEGQL	IRVNQSQHCP
2090	2100	2110	2120	2130	2140	2150	2160
QGAAPPRCGI	LGLAVRVGGD	RCCPLWECAC	RCSIFPDLSF	VTFDGSHVAL	FKEAIYILSQ	SPDEMLTVHV	LDCKSANLGH
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2044	1	1135.9200	78.97	3	54.1	22.8	1	921-951	R.GPCLSGCACPQGLLRHGDACFLPEECPCTWK.G	Carbamidomethyl: 7, 9

Detailed Protein Report

Protein 752: serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform [Homo sapiens]

Accession:	gi|21361399	**Score:**	22.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	65.3
Database Date:	2015-11-30	**pI:**	4.9
		Sequence Coverage [%]:	5.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAAADGDDSL	YPIAVLIDEL	RNEDVQLRLN	SIKKLSTIAL	ALGVERTRSE	LLPFLTDTIY	DEDEVLLALA	EQLGTFTTLV
90	100	110	120	130	140	150	160
GGPEYVHCLL	PPLESLATVE	ETVVRDKAVE	SLRAISHEHS	PSDLEAHFVP	LVKRLAGGDW	FTSRTSACGL	FSVCYPRVSS
170	180	190	200	210	220	230	240
AVKAELRQYF	RNLCSDDTPM	VRRAAASKLG	EFAKVLELDN	VKSEIIPMFS	NLASDEQDSV	RLLAVEACVN	IAQLLPQEDL
250	260	270	280	290	300	310	320
EALVMPTLRQ	AAEDKSWRVR	YMVADKFTEL	QKAVGPEITK	TDLVPAFQNL	MKDCEAEVRA	AASHKVKEFC	ENLSADCREN
330	340	350	360	370	380	390	400
VIMSQILPCI	KELVSDANQH	VKSALASVIM	GLSPILGKDN	TIEHLLPLFL	AQLKDECPEV	RLNIISNLDC	VNEVIGIRQL
410	420	430	440	450	460	470	480
SQSLLPAIVE	LAEDAKWRVR	LAIIEYMPLL	AGQLGVEFFD	EKLNSLCMAW	LVDHVYAIRE	AATSNLKKLV	EKFGKEWAHA
490	500	510	520	530	540	550	560
TIIPKVLAMS	GDPNYLHRMT	TLFCINVLSE	VCGQDITTKH	MLPTVLRMAG	DPVANVRFNV	AKSLQKIGPI	LDNSTLQSEV
570	580	590					
KPILEKLTQD	QDVDVKYFAQ	EALTVLSLA					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2800	1	942.9802	-36.08	2	64.1	10.2	0	382-398	R.LNIISNLDCVNEVIGIR.Q	

Detailed Protein Report

Protein 753: PREDICTED: zinc finger protein 155 isoform X1 [Homo sapiens]

Accession:	gi|530417166	**Score:**	22.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	62.0
Database Date:	2015-11-30	**pI:**	9.9
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	5.8
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MTTFKEAVTF KDVAVVFTEE ELGLLDPAQR KLYRDVMLEN FRNLLSVGHQ PFHQDTCHFL REEKFWMMGT ATQREGNSGG

        90        100        110        120        130        140        150        160
KIQTELESVP EAGAHEEWSC QQIWEQIAKD LTRSQDSIIN NSQFFENGDV PSQVEAGLPT IHTGQKPSQG GKCKQSISDV

       170        180        190        200        210        220        230        240
PIFDLPQQLY SEEKSYTCDE CGKSICYISA LHVHQRVHVG EKLFMCDVCG KEFSQSSHLQ THQRVHTGEK PFKCEQCGKG

       250        260        270        280        290        300        310        320
FSRRSALNVH RKLHTGEKPY ICEACGKAFI HDSQLKEHKR IHTGEKPFKC DICGKTFYFR SRLKSHSMVH TGEKPFRCDT

       330        340        350        360        370        380        390        400
CDKSFHQRSA LNRHCMVHTG EKPYRCEQCG KGFIGRLDFY KHQVVHTGEK PYNCKECGKS FRWSSCLLNH QRVHSGEKSF

       410        420        430        440        450        460        470        480
KCEECGKGFY TNSQLSSHQR SHSGEKPYKC EECGKGYVTK FNLDLHQRVH TGERPYNCKE CGKNFSRASS ILNHKRLHCQ

       490        500        510        520        530        540
KKPFKCEDCG KRLVHRTYRK DQPRDYSGEN PSKCEDCGRR YKRRLNLDIL LSLFLNDT
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1111	1	903.7510	4.42	3	42.6	12.7	2	334-356	R.HCMVHTGEKPYRCEQCGKGFIGR.L	Carbamidomethyl: 16; Oxidation: 3

Detailed Protein Report

Protein 754: DNA helicase MCM8 isoform 4 [Homo sapiens]

Accession: gi|528078341
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 22.8
MW [kDa]: 88.7
pI: 7.8
Sequence Coverage [%]: 2.8
No. of unique Peptides: 1

Quantitation

Wdown:Qdown **Median:** 0.57 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MNGEYRGRGF	GRGRFQSWKR	GRGGGNFSGK	WREREHRPDL	SKTTGKRTSE	QTPQFLLSTK	TPQSMQSTLD	RFIPYKGWKL
90	100	110	120	130	140	150	160
YFSEVYSDSS	PLIEKIQAFE	KFFTRHIDLY	DKDEIERKGS	ILVDFKELTE	GGEVTNLIPD	IATELRDAPE	KTLACMGLAI
170	180	190	200	210	220	230	240
HQVLTKDLER	HAAELQAQEG	LSNDGETMVN	VPHIHARVYN	YEPLTQLKNV	RANYYGKYIA	LRGTVVRVSN	IKPLCTKMAF
250	260	270	280	290	300	310	320
LCAACGEIQS	FPLPDGKYSL	PTKCPVPVCR	GRSFTALRSS	PLTVTMDWQS	IKIQELMSDD	QREAGRIPRT	IECELVHDLV
330	340	350	360	370	380	390	400
DSCVPGDTVT	ITGIVKVSNA	EEGSRNKNDK	CMFLLYIEAN	SISNSKGQKT	KSSEDGCKHG	MLMEFSLKDL	YAIQEIQAEE
410	420	430	440	450	460	470	480
NLFKLIVNSL	CPVIFGHEAA	CNVAPRGVYV	CGNTTTTSGL	TVTLSKDSSS	GDFALEAGAL	VLGDQGICGI	DEFDKMGNQH
490	500	510	520	530	540	550	560
QALLEAMEQQ	SISLAKAGVV	CSLPARTSII	AAANPVGGHY	NKAKTVSENL	KMGSALLSRF	DLVFILLDTP	NEHHDHLLSE
570	580	590	600	610	620	630	640
HVIAIRAGKQ	RTISSATVAR	MNSQDSNTSV	LEVVSEKPLS	ERLKVVPGET	IDPIPHQLLR	KYIGYARQYV	YPRLSTEAAR
650	660	670	680	690	700	710	720
VLQDFYLELR	KQSQRLNSSP	ITTRQLESLI	RLTEARARLE	LREEATKEDA	EDIVEIMKYS	MLGTYSDEFG	NLDFERSQHG
730	740	750	760	770	780	790	800
SGMSNRSTAK	RFISALNNVA	ERTYNNIFQF	HQLRQIAKEL	NIQVADFENF	IGSLNDQGYL	LKKGPKVYQL	QTM

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
527	1	882.7095	306.55	1	35.2	11.9	0	787-793	K.VYQLQTM.-		Wdown:Qdown 0.57

Detailed Protein Report

Protein 755: **PREDICTED: tumor necrosis factor receptor superfamily member 3 isoform X3 [Homo sapiens]**

Accession:	gi|578822606	**Score:**	22.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	27.6
Database Date:	2015-11-30	**pI:**	5.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	7.1
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MLLPWATSAP GLAWGPLVLG LFGLLAASQP QAVPPYASEN QTCRDQEKEY YEPQHRICCS RCPPGTYVSA KCSRIRDTVC
        90        100        110        120        130        140        150        160
ATCAENSYNE HWNYLTICQL CRPCDPVMGL EEIAPCTSKR KTQCRCQPGM FCAAWALECT HCELLSDCPP GTEAELKDEV
       170        180        190        200        210        220        230        240
GKGNNHCVPC KAGHFQNTSS PSARCQPHTR CENQGLVEAA PGTAQSDTTC KNPLEPLPPE MSEPALSKGV ENLQALLYQA
       250        260
ATGSSEASFP TLSPL
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2006	1	701.2886	-42.08	3	53.7	10.9	2	57-74	R.ICCSRCPPGTYVSAKCSR.I	Carbamidomethyl: 2, 3, 6

Detailed Protein Report

Protein 756: serine/threonine-protein kinase ATR [Homo sapiens]

Accession:	gi|157266317	**Score:**	22.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	301.2
Database Date:	2015-11-30	**pI:**	7.3
		Sequence Coverage [%]:	1.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGEHGLELAS	MIPALRELGS	ATPEEYNTVV	QKPRQILCQF	IDRILTDVNV	VAVELVKKTD	SQPTSVMLLD	FIQHIMKSSP
90	100	110	120	130	140	150	160
LMFVNVSGSH	EAKGSCIEFS	NWIITRLLRI	AATPSCHLLH	KKICEVICSL	LFLFKSKSPA	IFGVLTKELL	QLFEDLVYLH
170	180	190	200	210	220	230	240
RRNVMGHAVE	WPVVMSRFLS	QLDEHMGYLQ	SAPLQLMSMQ	NLEFIEVTLL	MVLTRIIAIV	FFRRQELLLW	QIGCVLLEYG
250	260	270	280	290	300	310	320
SPKIKSLAIS	FLTELFQLGG	LPAQPASTFF	SSFLELLKHL	VEMDTDQLKL	YEEPLSKLIK	TLFPFEAEAY	RNIEPVYLNM
330	340	350	360	370	380	390	400
LLEKLCVMFE	DGVLMRLKSD	LLKAALCHLL	QYFLKFVPAG	YESALQVRKV	YVRNICKALL	DVLGIEVDAE	YLLGPLYAAL
410	420	430	440	450	460	470	480
KMESMEIIEE	IQCQTQQENL	SSNSDGISPK	RRRLSSSLNP	SKRAPKQTEE	IKHVDMNQKS	ILWSALKQKA	ESLQISLEYS
490	500	510	520	530	540	550	560
GLKNPVIEML	EGIAVVLQLT	ALCTVHCSHQ	NMNCRTFKDC	QHKSKKKPSV	VITWMSLDFY	TKVLKSCRSL	LESVQKLDLE
570	580	590	600	610	620	630	640
ATIDKVVKIY	DALIYMQVNS	SFEDHILEDL	CGMLSLPWIY	SHSDDGCLKL	TTFAANLLTL	SCRISDSYSP	QAQSRCVFLL
650	660	670	680	690	700	710	720
TLFPRRIFLE	WRTAVYNWAL	QSSHEVIRAS	CVSGFFILLQ	QQNSCNRVPK	ILIDKVKDDS	DIVKKEFASI	LGQLVCTLHG
730	740	750	760	770	780	790	800
MFYLTSSLTE	PFSEHGHVDL	FCRNLKATSQ	HECSSSQLKA	SVCKPFLFLL	KKKIPSPVKL	AFIDNLHHLC	KHLDFREDET
810	820	830	840	850	860	870	880
DVKAVLGTLL	NLMEDPDKDV	RVAFSGNIKH	ILESLDSEDG	FIKELFVLRM	KEAYTHAQIS	RNNELKDTLI	LTTGDIGRAA
890	900	910	920	930	940	950	960
KGDLVPFALL	HLLHCLLSKS	ASVSGAAYTE	IRALVAAKSV	KLQSFFSQYK	KPICQFLVES	LHSSQMTALP	NTPCQNADVR
970	980	990	1000	1010	1020	1030	1040
KQDVAHQREM	ALNTLSEIAN	VFDFPDLNRF	LTRTLQVLLP	DLAAKASPAA	SALIRTLGKQ	LNVNRREILI	NNFKYIFSHL
1050	1060	1070	1080	1090	1100	1110	1120
VCSCSKDELE	RALHYLKNET	EIELGSLLRQ	DFQGLHNELL	LRIGEHYQQV	FNGLSILASF	ASSDDPYQGP	RDIISPELMA
1130	1140	1150	1160	1170	1180	1190	1200
DYLQPKLLGI	LAFFNMQLLS	SSVGIEDKKM	ALNSLMSLMK	LMGPKHVSSV	RVKMMTTLRT	GLRFKDDFPE	LCCRAWDCFV
1210	1220	1230	1240	1250	1260	1270	1280
RCLDHACLGS	LLSHVIVALL	PLIHIQPKET	AAIFHYLIIE	NRDAVQDFLH	EIYFLPDHPE	LKKIKAVLQE	YRKETSESTD
1290	1300	1310	1320	1330	1340	1350	1360
LQTTLQLSMK	AIQHENVDVR	IHALTSLKET	LYKNQEKLIK	YATDSETVEP	IISQLVTVLL	KGCQDANSQA	RLLCGECLGE
1370	1380	1390	1400	1410	1420	1430	1440
LGAIDPGRLD	FSTTETQGKD	FTFVTGVEDS	SFAYGLLMEL	TRAYLAYADN	SRAQDSAAYA	IQELLSIYDC	REMETNGPGH
1450	1460	1470	1480	1490	1500	1510	1520
QLWRRFPEHV	REILEPHLNT	RYKSSQKSTD	WSGVKKPIYL	SKLGSNFAEW	SASWAGYLIT	KVRHDLASKI	FTCCSIMMKH
1530	1540	1550	1560	1570	1580	1590	1600
DFKVTIYLLP	HILVYVLLGC	NQEDQQEVYA	EIMAVLKHDD	QHTINTQDIA	SDLCQLSTQT	VFSMLDHLTQ	WARHKFQALK
1610	1620	1630	1640	1650	1660	1670	1680
AEKCPHSKSN	RNKVDSMVST	VDYEDYQSVT	RFLDLIPQDT	LAVASFRSKA	YTRAVMHFES	FITEKKQNIQ	EHLGFLQKLY
1690	1700	1710	1720	1730	1740	1750	1760
AAMHEPDGVA	GVSAIRKAEP	SLKEQILEHE	SLGLLRDATA	CYDRAIQLEP	DQIIHYHGVV	KSMLGLGQLS	TVITQVNGVH
1770	1780	1790	1800	1810	1820	1830	1840
ANRSEWTDEL	NTYRVEAAWK	LSQWDLVENY	LAADGKSTTW	SVRLGQLLLS	AKKRDITAFY	DSLKLVRAEQ	IVPLSAASFE
1850	1860	1870	1880	1890	1900	1910	1920
RGSYQRGYEY	IVRLHMLCEL	EHSIKPLFQH	SPGDSSQEDS	LNWVARLEMT	QNSYRAKEPI	LALRRALLSL	NKRPDYNEMV
1930	1940	1950	1960	1970	1980	1990	2000
GECWLQSARV	ARKAGHHQTA	YNALLNAGES	RLAELYVERA	KWLWSKGDVH	QALIVLQKGV	ELCFPENETP	PEGKNMLIHG
2010	2020	2030	2040	2050	2060	2070	2080
RAMLLVGRFM	EETANFESNA	IMKKYKDVTA	CLPEWEDGHF	YLAKYYDKLM	PMVTDNKMEK	QGDLIRYIVL	HFGRSLQYGN
2090	2100	2110	2120	2130	2140	2150	2160
QFIYQSMPRM	LTLWLDYGTK	AYEWEKAGRS	DRVQMRNDLG	KINKVITEHT	NYLAPYQFLT	AFSQLISRIC	HSHDEVFVVL
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
828	1	965.4657	-14.77	2	39.2	12.7	1	1650-1665	K.AYTRAVMHFESFITEK.K	

Detailed Protein Report

Protein 757: **PREDICTED: arf-GAP with GTPase, ANK repeat and PH domain-containing protein 1 isoform X8 [Homo sapiens]**

Accession:	gi|578803598	**Score:**	22.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	85.9
Database Date:	2015-11-30	**pI:**	9.8
		Sequence Coverage [%]:	3.7
		No. of unique Peptides:	1

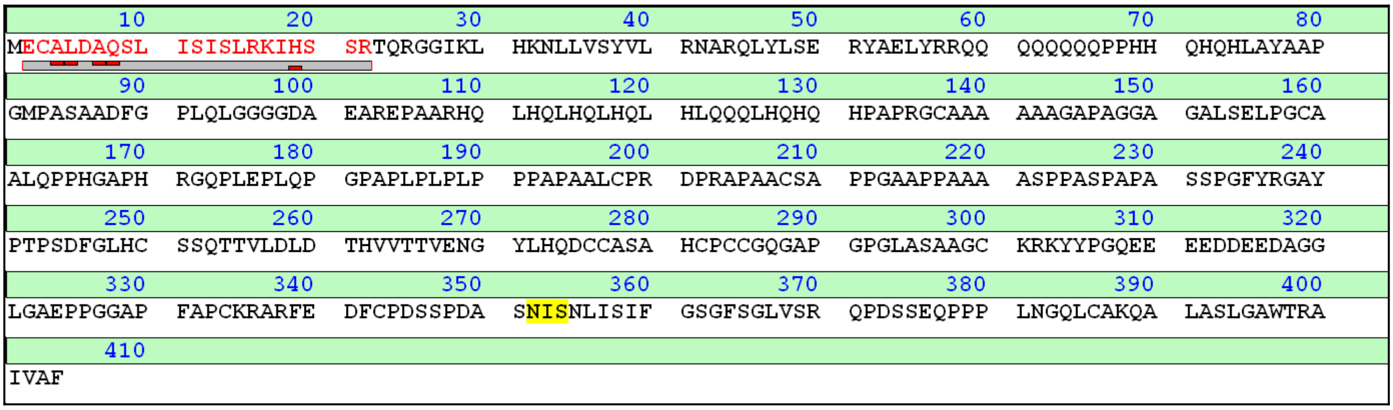
10	20	30	40	50	60	70	80
MDAGGRFKKE	IVVDGQSYLL	LIRDEGGPPE	AQFAMWVDAV	IFVFSLEDEI	SFQTVYHYYS	RMANYRNTSE	IPLVLVGTQD
90	100	110	120	130	140	150	160
AISSANPRVI	DDARARKLSN	DLKRCTYYET	CATYGLNVER	VFQDVAQKIV	ATRKKQQLSI	GPCKSLPNSP	SHSSVCSAQV
170	180	190	200	210	220	230	240
SAVHISQTSN	GGGSLSDYSS	SVPSTPSTSQ	KELRIDVPPT	ANTPTPVRKQ	SKRRSNLFTS	RKGSDPDKEK	KGLESRADSI
250	260	270	280	290	300	310	320
GSGRAIPIKQ	GMLLKRSGKS	LNKEWKKKYV	TLCDNGVLTY	HPSLHDYMQN	VHGKEIDLLR	TTVKVPGKRP	PRATSACAPI
330	340	350	360	370	380	390	400
SSPKTNGLSK	DMSSLHISPN	SGNVTSASGS	QMASGISLVS	FNSRPDGMHQ	RSYSVSSADQ	WSEATVIANS	AISSDTGLGD
410	420	430	440	450	460	470	480
SVCSSPSISS	TTSPKLDPPP	SPHANRKKHR	RKKSTSNFKA	DGLSGTAEAK	RKAWKLNRVG	SLRNIYSSST	NTEEQEENFE
490	500	510	520	530	540	550	560
FIIVSLTGQT	WHFEATTYEE	RDAWVQAIES	QILASLQSCE	SSKNKSRLTS	QSEAMALQSI	RNMRGNSHCV	DCETQNPNWA
570	580	590	600	610	620	630	640
SLNLGALMCI	ECSGIHRNLG	THLSRVRSLD	LDDWPVELIK	VMSSIGNELA	NSVWEESSQG	RTKPSVDSTR	EEKERWIRAK
650	660	670	680	690	700	710	720
YEQKLFLAPL	PCTELSLGQH	LLRATADEDL	RTAILLLAHG	SRDEVNETCG	EGDGRTALHL	ACRKGNVVLA	QLLIWYGVDV
730	740	750	760	770	780	790	
TARDAHGNTA	LAYARQASSQ	ECIDVLLQYG	CPDERFVLMA	TPNLSRRNNN	RNNSSGRVPT	II	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
139	1	768.0380	181.88	2	30.5	12.7	0	528-541	R.LTSQSEAMALQSIR.N	

Detailed Protein Report

Protein 758: immediate early response gene 5-like protein [Homo sapiens]

Accession:	gi|148727370	**Score:**	22.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	42.1
Database Date:	2015-11-30	**pI:**	6.5
		Sequence Coverage [%]:	8.2
		No. of unique Peptides:	1



10	20	30	40	50	60	70	80
MECALDAQSL	ISISLRKIHS	SRTQRGGIKL	HKNLLVSYVL	RNARQLYLSE	RYAELYRRQQ	QQQQQQPPHH	QHQHLAYAAP
90	100	110	120	130	140	150	160
GMPASAADFG	PLQLGGGGDA	EAREPAARHQ	LHQLHQLHQL	HLQQQLHQHQ	HPAPRGCAAA	AAAGAPAGGA	GALSELPGCA
170	180	190	200	210	220	230	240
ALQPPHGAPH	RGQPLEPLQP	GPAPLPLPLP	PPAPAALCPR	DPRAPAACSA	PPGAAPPAAA	ASPPASPAPA	SSPGFYRGAY
250	260	270	280	290	300	310	320
PTPSDFGLHC	SSQTTVLDLD	THVVTTVENG	YLHQDCCASA	HCPCCGQGAP	GPGLASAAGC	KRKYYPGQEE	EEDDEEDAGG
330	340	350	360	370	380	390	400
LGAEPPGGAP	FAPCKRARFE	DFCPDSSPDA	SNISNLISIF	GSGFSGLVSR	QPDSSEQPPP	LNGQLCAKQA	LASLGAWTRA
410							
IVAF							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1295	1	1164.2240	81.89	2	44.7	10.5	2	2-22	M.ECALDAQSLISISLRKIHSSR.T	

Detailed Protein Report

Protein 759: **PREDICTED: formin-binding protein 1 isoform X20 [Homo sapiens]**

Accession:	gi|530390795	**Score:**	22.7
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

Wdown:Qdown **Median:** 0.78 **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
819	2	603.8114	-24.03	2	39.1	11.7	2	223-232	R.RIVRMGESMK.T		Wdown:Qdown 0.78

Detailed Protein Report

Protein 760: U4/U6 small nuclear ribonucleoprotein Prp3 [Homo sapiens]

Accession:	gi|4758556	**Score:**	22.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	77.5
Database Date:	2015-11-30	**pI:**	10.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	5.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MALSKRELDE	LKPWIEKTVK	RVLGFSEPTV	VTAALNCVGK	GMDKKKAADH	LKPFLDDSTL	RFVDKLFEAV	EEGRSSRHSK
90	100	110	120	130	140	150	160
SSSDRSRKRE	LKEVFGDDSE	ISKESSGVKK	RRIPRFEEVE	EEPEVIPGPP	SESPGMLTKL	QIKQMMEAAT	RQIEERKKQL
170	180	190	200	210	220	230	240
SFISPPTPQP	KTPSSSQPER	LPIGNTIQPS	QAATFMNDAI	EKARKAAELQ	ARIQAQLALK	PGLIGNANMV	GLANLHAMGI
250	260	270	280	290	300	310	320
APPKVELKDQ	TKPTPLILDE	QGRTVDATGK	EIELTHRMPT	LKANIRAVKR	EQFKQQLKEK	PSEDMESNTF	FDPRVSIAPS
330	340	350	360	370	380	390	400
QRQRRTFKFH	DKGKFEKIAQ	RLRTKAQLEK	LQAEISQAAR	KTGIHTSTRL	ALIAPKKELK	EGDIPEIEWW	DSYIIPNGFD
410	420	430	440	450	460	470	480
LTEENPKRED	YFGITNLVEH	PAQLNPPVDN	DTPVTLGVYL	TKKEQKKLRR	QTRREAQKEL	QEKVRLGLMP	PPEPKVRISN
490	500	510	520	530	540	550	560
LMRVLGTEAV	QDPTKVEAHV	RAQMAKRQKA	HEEANAARKL	TAEQRKVKKI	KKLKEDISQG	VHISVYRVRN	LSNPAKKFKI
570	580	590	600	610	620	630	640
EANAGQLYLT	GVVVLHKDVN	VVVVEGGPKA	QKKFKRLMLH	RIKWDEQTSN	TKGDDDEESD	EEAVKKTNKC	VLVWEGTAKD
650	660	670	680	690			
RSFGEMKFKQ	CPTENMAREH	FKKHGAEHYW	DLALSESVLE	STD			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2051	1	1051.4305	-132.06	2	54.3	10.5	2	1-17	-.MALSKRELDELKPWIEK.T	Oxidation: 1

Detailed Protein Report

Protein 761: zinc finger protein 471 [Homo sapiens]

Accession:	gi|150170667	**Score:**	22.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	73.0
Database Date:	2015-11-30	**pI:**	9.9
		Sequence Coverage [%]:	4.6
		No. of unique Peptides:	1

Quantitation

mdown:qdown **Median:** 0.72 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MNVEVVKVMP	QDLVTFKDVA	IDFSQEEWQW	MNPAQKRLYR	SMMLENYQSL	VSLGLCISKP	YVISLLEQGR	EPWEMTSEMT
90	100	110	120	130	140	150	160
RSPFSDWESI	YVTQELPLKQ	FMYDDACMEG	ITSYGLECST	FEENWKWEDL	FEKQMGSHEM	FSKKEIITHK	ETITKETEFK
170	180	190	200	210	220	230	240
YTKFGKCIHL	ENIEESIYNH	TSDKKSFSKN	SMVIKHKKVY	VGKKLFKCNE	CDKTFTHSSS	LTVHFRIHTG	EKPYACEECG
250	260	270	280	290	300	310	320
KAFKQRQHLA	QHHRTHTGEK	LFECKECRKA	FKQSEHLIQH	QRIHTGEKPY	KCKECRKAFR	QPAHLAQHQR	IHTGEKPYEC
330	340	350	360	370	380	390	400
KECGKAFSDG	SSFARHQRCH	TGKRPYECIE	CGKAFRYNTS	FIRHWRSYHT	GEKPFNCIDC	GKAFSVHIGL	ILHRRIHTGE
410	420	430	440	450	460	470	480
KPYKCGVCGK	TFSSGSSRTV	HQRIHTGEKP	YECDICGKDF	SHHASLTQHQ	RVHSGEKPYE	CKECGKAFRQ	NVHLVSHLRI
490	500	510	520	530	540	550	560
HTGEKPYECK	ECGKAFRISS	QLATHQRIHT	GEKPYECIEC	GNAFKQRSHL	AQHQKTHTGE	KPYECNECGK	AFSQTSNLTQ
570	580	590	600	610	620	630	
HQRIHTGEKP	YKCTECGKAF	SDSSSCAQHQ	RLHTGQRPYQ	CFECGKAFRR	KLSLICHQRS	HTGEEP	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
653	2	690.4099	83.82	2	37.0	10.7	1	357-366	R.YNTSFIRHWR.S		mdown:qdown 0.72

Detailed Protein Report

Protein 762: PREDICTED: brain-specific angiogenesis inhibitor 3 isoform X3 [Homo sapiens]

Accession:	gi|578812890	**Score:**	22.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	168.1
Database Date:	2015-11-30	**pI:**	6.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MKAVRNLLIY	IFSTYLLVMF	GFNAAQDFWC	STLVKGVIYG	SYSVSEMFPK	NFTNCTWTLE	NPDPTKYSIY	LKFSKKDLSC
90	100	110	120	130	140	150	160
SNFSLLAYQF	DHFSHEKIKD	LLRKNHSIMQ	LCNSKNAFVF	LQYDKNFIQI	RRVFPTNFPG	LQKKGEEDQK	SFFEFLVLNK
170	180	190	200	210	220	230	240
VSPSQFGCHV	LCTWLESCLK	SENGRTESCG	IMYTKCTCPQ	HLGEWGIDDQ	SLILLNNVVL	PLNEQTEGCL	TQELQTTQVC
250	260	270	280	290	300	310	320
NLTREAKRPP	KEEFGMMGDH	TIKSQRPRSV	HEKRVPQEQA	DAAKFMAQTG	ESGVEEWSQW	STCSVTCGQG	SQVRTRTCVS
330	340	350	360	370	380	390	400
PYGTHCSGPL	RESRVCNNTA	LCPVHGVWEE	WSPWSLCSFT	CGRGQRTRTR	SCTPPQYGGR	PCEGPETHHK	PCNIALCPVD
410	420	430	440	450	460	470	480
GQWQEWSSWS	QCSVTCSNGT	QQRSRQCTAA	AHGGSECRGP	WAESRECYNP	ECTANGQWNQ	WGHWSGCSKS	CDGGWERRIR
490	500	510	520	530	540	550	560
TCQGAVITGQ	QCEGTGEEVR	RCNEQRCPAP	YEICPEDYLM	SMVWKRTPAG	DLAFNQCPLN	ATGTTSRRCS	LSLHGVAFWE
570	580	590	600	610	620	630	640
QPSFARCISN	EYRHLQHSIK	EHLAKGQRML	AGDGMSQVTK	TLLDLTQRKN	FYAGDLLMSV	EILRNVTDTF	KRASYIPASD
650	660	670	680	690	700	710	720
GVQNFFQIVS	NLLDEENKEK	WEDAQQIYPG	SIELMQVIED	FIHIVGMGMM	DFQNSYLMTG	NVVASIQKLP	AASVLTDINF
730	740	750	760	770	780	790	800
PMKGRKGMVD	WARNSEDRVV	IPKSIFTPVS	SKELDESSVF	VLGAVLYKNL	DLILPTLRNY	TVINSKIIVV	TIRPEPKTTD
810	820	830	840	850	860	870	880
SFLEIELAHL	ANGTLNPYCV	LWDDSKTNES	LGTWSTQGCK	TVLTDASHTK	CLCDRLSTFA	ILAQQPREII	MESSGTPSVT
890	900	910	920	930	940	950	960
LIVGSGLSCL	ALITLAVVYA	ALWRYIRSER	SIILINFCLS	IISSNILILV	GQTQTHNKSI	CTTTTAFLHF	FFLASFCWVL
970	980	990	1000	1010	1020	1030	1040
TEAWQSYMAV	TGKIRTRLIR	KRFLCLGWGL	PALVVATSVG	FTRTKGYGTD	HYCWLSLEGG	LLYAFVGPAA	AVVLVNMVIG
1050	1060	1070	1080	1090	1100	1110	1120
ILVFNKLVSR	DGILDKKLKH	RAGASLWSSC	VVLPLLALTW	MSAVLAMTDK	RSILFQILFA	VFDSLQGFVI	VMVHCILRRE
1130	1140	1150	1160	1170	1180	1190	1200
VQDAFRCRLR	NCQDPINADS	SSSFPNGHAQ	IMTDFEKDVD	IACRSVLHKD	IGPCRAATIT	GTLSRISLND	DEEEKGTNPE
1210	1220	1230	1240	1250	1260	1270	1280
GLSYSTLPGN	VISKVIIQQP	TGLHMPMSMN	ELSNPCLKKE	NSELRRTVYL	CTDDNLRGAD	MDIVHPQERM	MESDYIVMPR
1290	1300	1310	1320	1330	1340	1350	1360
SSVNNQPSMK	EESKMNIGME	TLPHERLLHY	KVNPEFNMNP	PVMDQFNMNL	EQHLAPQEHM	QNLPFEPRTA	VKNFMASELD
1370	1380	1390	1400	1410	1420	1430	1440
DNAGLSRSET	GSTISMSSLE	RRKSRYSDLD	FEKVMHTRKR	HMELFQELNQ	KFQTLDRFRD	IPNTSSMENP	APNKNPWDTF
1450	1460	1470	1480	1490			
KNPSEYPHYT	TINVLDTEAK	DALELRPAEW	EKCLNLPLDV	QEGDFQTEV			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
205	1	850.2148	81.42	3	31.8	11.2	2	981-1003	R.KRFLCLGWGLPALVVATSVGFTR.T	Carbamidomethyl: 5

Detailed Protein Report

Protein 763: putative ankyrin repeat domain-containing protein 31 [Homo sapiens]

Accession:	gi|256574792	**Score:**	22.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	210.7
Database Date:	2015-11-30	**pI:**	5.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEEGVQAPDW	DSDETVIEGS	VTESDLEEKE	LPWRRLLFDQ	DASLKSEFSL	HPDTRGMCKG	MPSPEIQLGF	KLREDLQEQM
90	100	110	120	130	140	150	160
NKNKMMPVLS	EDTILQSQDE	TERNQALLQT	RKNCSMFIGS	FRQSGLSLNH	QNIEGPEAES	PEVLPHIEKE	LSEGRDSPEV
170	180	190	200	210	220	230	240
SLLSGTAITV	SDTVAVKETS	LVEPEKILAA	PNTFFEPRKE	VTMTMTSEET	KDEESSLETF	VSALESLLTS	PESTQEERLF
250	260	270	280	290	300	310	320
ELVSDFDRKE	LMNPLSDSLS	SISIPLNSWS	ACHRDLLEDA	KDDALPAELL	EALNTLSEAK	VETICHRKEG	GSSLIARNEC
330	340	350	360	370	380	390	400
LEVEFNTSQT	NEDCTQIAET	LQDPNPSGLQ	TLAHQNITSC	EPLSNKRNSN	SVTNSSDQET	ACVLRRSSRL	EKLKVSRDAK
410	420	430	440	450	460	470	480
YSDHMYKMPE	KILPKILGCE	DLTNNNSSAQ	NFRMQDPALM	IDGKEKNMHS	ARFKNGKQIR	KNEQFSGKKE	KMKVNKISLH
490	500	510	520	530	540	550	560
SINRRNIFGE	NLVYKAALHD	DADLVHHCIK	KGGNVNQPSY	AGWTALHEAS	VGGFYRTASE	LLKGGADVNI	KGLYQITPLH
570	580	590	600	610	620	630	640
DAVMNGHYKV	AELLLLNGAD	PLFRNDDGKC	ALDEAKDLCM	KRLLERYIPK	HQKCLTSAQR	SSIDPLDIED	VYQHKKPKFS
650	660	670	680	690	700	710	720
SKSHIWHVYN	ENSNRQKLEH	VKVNKGSKAS	LFINKEDVYE	YYQKDPKNTK	FGKSKHKQST	LDQIYSTGLR	KGNLHNVKDP
730	740	750	760	770	780	790	800
NTNVPKGIGR	RKTQHKRTQV	DDVDCNPRKI	LAVSPSRRIN	RLVTYQQHIP	ETHNDLPEEL	CEPSSLTLSS	LRNGLDSSTE
810	820	830	840	850	860	870	880
ACSVSKEKHI	QNLDLSDSQE	VQCLELESVD	QTEAVSFPGL	LLHKEIKLPV	VTTDKQPHTL	QEQHHVLYKS	HENSNLVPKD
890	900	910	920	930	940	950	960
ERFNKWENSF	LSFVKENSDN	DDDDDCSTSE	KAITSKKVLC	STGGKKHYNF	KENLTNKKEM	GFQQFLLSED	HLSQENELKA
970	980	990	1000	1010	1020	1030	1040
VSLTTLPEQE	AVNFSYSDNA	VISEHVANYE	QCIFGPSFDH	SNGNPEQNSL	ACMRTLLTHE	ASKLTNHVEL	FKKPQDYIPR
1050	1060	1070	1080	1090	1100	1110	1120
APTFLMNQTD	THIVEKMAKN	CDTERNYIDR	DQKIIYSNEP	LSIVAHSQVI	ETTKVEKRRQ	NHLESETIHN	IDSHSTDNMS
1130	1140	1150	1160	1170	1180	1190	1200
KELANISKLS	QREKKEISHK	PGMKAGRINK	RNARGESQLH	LAVRRGNLPL	VKALIESGAD	VNLNDNAGWT	PLHEASNEGS
1210	1220	1230	1240	1250	1260	1270	1280
IDIIVELLKA	GAKVNCENID	GILPLHDAVA	NNHLKAAEIL	LQNGANPNQK	DQKQKSALDE	ADDEKMKELL	RSYGAIETVN
1290	1300	1310	1320	1330	1340	1350	1360
RDESDAIVNE	KIPAVRSKRH	KQCFCDDGKT	IDSSSLSHQE	RSRESLSVHQ	TLSAILQDIE	EKQEYLLEFE	IRNPEDAEQY
1370	1380	1390	1400	1410	1420	1430	1440
IEKMLKIKKI	MDNVLAKQKA	ERDDLAKKYR	VSIESFKHGA	LREQLANLAA	RQKSLLVVAK	KQKKISLKIQ	NCRNVTSLPC
1450	1460	1470	1480	1490	1500	1510	1520
LSLRKLPPRS	EISSEKDSQE	LTSLENLEHP	QSGSLSPVSG	SMQETQLSLE	TWNYSQNTNI	CLNSEAVRRG	EFSGNDMNSK
1530	1540	1550	1560	1570	1580	1590	1600
QNGSDCTLDG	FPKSRHSDGT	EKNKLPSQPV	AFIGQTEYSQ	KENDLTEATD	KDHEFYVSSP	VIGKLNISET	ASVLAENAAH
1610	1620	1630	1640	1650	1660	1670	1680
PSNIICDQDL	SNYDPKRGNR	KTSSQQSPTG	ASESLAHQGI	AVLGSDTVHQ	MKPYLKKSVS	VVPCADDSQI	SSSSGSGQQD
1690	1700	1710	1720	1730	1740	1750	1760
TIKKALNYST	APKKKCIQIK	DLILLGRINP	GNNILEFKTQ	ETTHKASILL	NGKLKVESGQ	IYKNPVTWLK	DLLGGNSYVT
1770	1780	1790	1800	1810	1820	1830	1840
WNYAWSKVTY	LGKELLRYVS	EDAPILPEPN	SVPQQYQPCL	PEVACLDDPV	QEPNKSMFEK	TKFGQGTSRE	SMQSSPRYLQ
1850	1860	1870	1880				
INEILLISDQ	EFLPCHIMDQ	HWKFCVECEE	LTP				

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2612	1	812.4151	42.97	2	61.3	12.1	2	1254-1267	K.QKSALDEADDEKMK.E	Oxidation: 13

Detailed Protein Report

Protein 764: PREDICTED: E3 ubiquitin-protein ligase HECW2 isoform X4 [Homo sapiens]

Accession:	gi|578804640	**Score:**	22.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	157.7
Database Date:	2015-11-30	**pI:**	5.1
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGAEGMEGGA	SGNLHSRKLV	SFTLSDLRAV	GLKKGMFFNP	DPYLKMSIQP	GKKSSFPTCA	HHGQERRSTI	ISNTTNPIWH
90	100	110	120	130	140	150	160
REKYSFFALL	TDVLEIEIKD	KFAKSRPIIK	RFLGKLTIPV	QRLLERQAIG	DQMLSYNLGR	RLPADHVSGY	LQFKVEVTSS
170	180	190	200	210	220	230	240
VHEEMLFSHS	DASPEAVGTI	LGVNSVNGDL	GSPSDDEDMP	GSHHDSQVCS	NGPVSEDSAA	DGTPKHSFRT	SSTLEIDTEE
250	260	270	280	290	300	310	320
LTSTSSRTSP	PRGRQDSLND	YLDAIEHNGH	SRPGTATCSE	RSMGASPKLR	SSFPTDTRLN	AMLHIDSDEE	DHEFQQDLGY
330	340	350	360	370	380	390	400
PSSLEEEGGL	IMFSRASRAD	DGSLTSQTKL	EDNPVENEEA	STHEAASFED	KPENLPELAE	SSLPAGPAPE	EGEGGPEPQP
410	420	430	440	450	460	470	480
SADQGSAELC	GSQEVDQPTS	GADTGTSDAS	GGSRRAVSET	ESLDQGSEPS	QVSSETEPSD	PARTESVSEA	STRPEGESDL
490	500	510	520	530	540	550	560
ECADSSCNES	VTTQLSSVDT	RCSSLESARF	PETPAFSSQE	EEDGACAAEP	TSSGPAEGSQ	ESVCTAGSLP	VVQVPSGEDE
570	580	590	600	610	620	630	640
GPGAESATVP	DQEELGEVWQ	RRGSLEGAAA	AAESPPQEEG	SAGEAQGTCE	GATAQEEGAT	GGSQANGHQP	LRSLPSVRQD
650	660	670	680	690	700	710	720
VSRYQRVDEA	LPPNWEARID	SHGRIFYVDH	VNRTTTWQRP	TAPPAPQVLQ	RSNSIQQMEQ	LNRRYQSIRR	TMTNERPEEN
730	740	750	760	770	780	790	800
TNAIDGAGEE	ADFHQASADF	RRENILPHST	SRSRITLLLQ	SPPVKFLISP	EFFTVLHSNP	SAYRMFTNNT	CLKHMITKVR
810	820	830	840	850	860	870	880
RDTHHFERYQ	HNRDLVGFLN	MFANKQLELP	RGWEMKHDHQ	GKAFFVDHNS	RTTTFIDPRL	PLQSSRPTSA	LVHRQHLTRQ
890	900	910	920	930	940	950	960
RSHSAGEVGE	DSRHAGPPVL	PRPSSTFNTV	SRPQYQDMVP	VAYNDKIVAF	LRQPNIFEIL	QERQPDLTRN	HSLREKIQFI
970	980	990	1000	1010	1020	1030	1040
RTEGTPGLVR	LSSDADLVML	LSLFEEEIMS	YVPPHALLHP	SYCQSPRGSP	VSSPQNSPGT	QRANARAPAP	YKRDFEAKLR
1050	1060	1070	1080	1090	1100	1110	1120
NFYRKLETKG	YGQGPGKLKL	IIRRDHLLED	AFNQIMGYSR	KDLQRNKLYV	TFVGEEGLDY	SGPSREFFFL	VSRELFNPYY
1130	1140	1150	1160	1170	1180	1190	1200
GLFEYSANDT	YTVQISPMSA	FVDNHHEWFR	FSGRILGLAL	IHQYLLDAFF	TRPFYKALLR	ILCDLSDLEY	LDEEFHQSLQ
1210	1220	1230	1240	1250	1260	1270	1280
WMKDNDIHDI	LDLTFTVNEE	VFGQITEREL	KPGGANIPVT	EKNKKEYIER	MVKWRIERGV	VQQTESLVRG	FYEVVDARLV
1290	1300	1310	1320	1330	1340	1350	1360
SVFDARELEL	VIAGTAEIDL	SDWRNNTEYR	GGYHDNHIVI	RWFWAAVERF	NNEQRLRLLQ	FVTGTSSIPY	EGFASLRGSN
1370	1380	1390	1400	1410	1420		
GPRRFCVEKW	GKITALPRAH	TCFNRLDLPP	YPSFSMLYEK	LLTAVEETST	FGLE		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1753	1	835.2741	-131.88	2	51.9	11.7	1	54-67	K.SSFPTCAHHGQERR.S	Carbamidomethyl: 6

Detailed Protein Report

Protein 765: PREDICTED: anoctamin-2 isoform X1 [Homo sapiens]

Accession: gi|578822628
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 22.5
MW [kDa]: 113.3
pI: 6.2
Sequence Coverage [%]: 2.4
No. of unique Peptides: 2

Quantitation

Wdown:Qdown **Median:** 1.02 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MATPGPRDIP	LLPGSPRRLS	PQAGSRGGQG	PKHGQQCLKM	PGPRAPGLQG	GSNRDPGQPC	GGESTRSSSV	INNYLDANEP
90	100	110	120	130	140	150	160
VSLEARLSRM	HFHDSQRKVD	YVLAYHYRKR	GVHLAQGFPG	HSLAIVSNGE	TGKEPHAGGP	GDIELGPLDA	LEEERKEQRE
170	180	190	200	210	220	230	240
EFEHNLMEAG	LELEKDLENK	SQGSIFVRIH	APWQVLAREA	EFLKIKVPTK	KMYEIKAGGS	IAKKFSAALQ	KLSSHLQPRV
250	260	270	280	290	300	310	320
PEHSNNKMKN	LSYPFSREKM	YLYNIQEKDT	FFDNATRSRI	VHEILKRTAC	SRANNTMGIN	SLIANNIYEA	AYPLHDGEYD
330	340	350	360	370	380	390	400
SPEDDMNDRK	LLYQEWARYG	VFYKFQPIDL	IRKYFGEKIG	LYFAWLGLYT	SFLIPSSVIG	VIVFLYGCAT	IEEDIPSREM
410	420	430	440	450	460	470	480
CDQQNAFTMC	PLCDKSCDYW	NLSSACGTAQ	ASHLFDNPAT	VFFSIFMALW	ATMFLENWKR	LQMRLGYFWD	LTGIEEEEEH
490	500	510	520	530	540	550	560
SRPEYETKVR	EKMLKESNQS	AVQKLETNTT	ECGDEDDEDK	LTWKDRFPGY	LMNFASILFM	IALTFSIVFG	VIVYRITTAA
570	580	590	600	610	620	630	640
ALSLNKATRS	NVRVTVTATA	VIINLVVILI	LDEIYGAVAK	WLTKIEVPKT	EQTFEERLIL	KAFLLKFVNA	YSPIFYVAFF
650	660	670	680	690	700	710	720
KGRFVGRPGS	YVYVFDGYRM	EECAPGGCLM	ELCIQLSIIM	LGKQLIQNNI	FEIGVPKLKK	LFRKLKDETE	AGETDSAHSK
730	740	750	760	770	780	790	800
HPEQWDLDYS	LEPYTGLTPE	YMEMIIQFGF	VTLFVASFPL	APVFALLNNV	IEVRLDAKKF	VTELRRPDAV	RTKDIGIWFD
810	820	830	840	850	860	870	880
ILSGIGKFSV	ISNAFVIAIT	SDFIPRLVYQ	YSYSHNGTLH	GFVNHTLSFF	NVSQLKEGTQ	PENSQFDQEV	QFCRFKDYRE
890	900	910	920	930	940	950	960
PPWAPNPYEF	SKQYWFILSA	RLAFVIIFQN	LVMFLSVLVD	WMIPDIPTDI	SDQIKKEKSL	LVDFFLKEEH	EKLKLMDEPA
970	980	990	1000				
LRSPGGGDRS	RSRAASSAPS	GQSQLGSMMS	SGSQHTNV				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2771	1	698.3681	-26.85	2	63.7	10.4	2	212-224	K.MYEIKAGGSIAKK.F		Wdown:Qdown 1.02
2163	1	1131.2917	-238.27	1	57.2	12.1	2	963-973	R.SPGGGDRSRSR.A		

Detailed Protein Report

Protein 766: PREDICTED: double homeobox protein 4-like protein 4-like [Homo sapiens]

Accession:	gi|530359602	**Score:**	22.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	41.8
Database Date:	2015-11-30	**pI:**	9.2
		Sequence Coverage [%]:	6.3
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MALLTPSEGT	LPEEVRGRGW	LKRFIWTPSQ	SEALRACFER	NPYPGIAIRE	WLAQAISIPE	PWIQIWFQNE	RSCQLRQHQQ
90	100	110	120	130	140	150	160
QSQPWPRRSG	LQEGRQKWTA	VTGFQTTLLL	LAFEKDSFPG	ITAKEELSRE	RGLPESRIQM	CFQNQRARHP	GQAGRVPTQA
170	180	190	200	210	220	230	240
GGLSNAAPGG	CHPARSCVAF	AHTCVWGTGL	PLPHVPCAPG	ALPLGAFMSQ	GATAVPILQP	SQGALAEGIS	EPAPAHGNFV
250	260	270	280	290	300	310	320
RATTAPPEGR	SPTLRLLGRL	RTRAKAGRTG	TRSTTACRAL	AGWDSLRPLK	RGHRANPEPT	EASAWQGQMQ	GLPVPSKALQ
330	340	350	360	370	380	390	
EPRGSPARPF	DLLLDELLAS	PEILQQAQPF	IETEAPGELE	ALEDAASLEA	PLNEEEYGAL	LEEI	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
263	1	795.8251	-122.95	2	32.7	11.2	1	23-35	K.RFIWTPSQSEALR.A	
2734	1	710.3788	44.12	2	63.1	11.3	0	77-87	R.QHQQQSQPWPR.R	

Detailed Protein Report

Protein 767: 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 768: transmembrane channel-like protein 1 [Homo sapiens]

Accession:	gi|21071070	**Score:**	22.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	87.7
Database Date:	2015-11-30	**pI:**	6.2
		Sequence Coverage [%]:	4.9
		No. of unique Peptides:	2

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	
962	1	529.1944	-206.45	2	40.8	10.6	1	722-731	K.GQKAANLDLK.K	

Detailed Protein Report

Protein 769: PREDICTED: cyclin-dependent kinase-like 5 isoform X2 [Homo sapiens]

Accession: gi|530421243
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 22.4
MW [kDa]: 110.0
pI: 10.1
Sequence Coverage [%]: 3.0
No. of unique Peptides: 1

Quantitation

mdown:qdown **Median:** 0.82 **CV:** 0.00 % **No. of Peptides:** 1
Wdown:Qdown **Median:** 1.35 **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		Wdown:Qdown 1.35 mdown:qdown 0.82

Detailed Protein Report

Protein 770: C-type mannose receptor 2 precursor [Homo sapiens]

Accession:	gi|110624774	**Score:**	22.4
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:	1

Quantitation

Wdown:Qdown **Median:** 0.59 **CV:** 0.00 % **No. of Peptides:** 1

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	Wdown:Qdown 0.59

Detailed Protein Report

Protein 771: 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

Quantitation

mdown:qdown	**Median:**	0.57	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	1.08	**CV:**	0.00 %	**No. of 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	Ratios
12	1	803.7126	-4.89	3	29.3	12.4	2	651-670	R.REVEHQETAYETSVKENTMK.Y		mdown:qdown 0.57 Wdown:Qdown 1.08

Detailed Protein Report

Protein 772: PREDICTED: RAD51-associated protein 2 isoform X1 [Homo sapiens]

Accession:	gi|530367071	**Score:**	22.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	132.8
Database Date:	2015-11-30	**pI:**	7.1
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.7
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	1.08	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.55	**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
147	1	492.5609	-86.58	3	31.1	10.7	1	629-640	R.LLEDNMKPMLKK.R	Oxidation: 9	Wdown:Qdown 0.55 mdown:qdown 1.08

Protein 773: neuropathy target esterase isoform c [Homo sapiens]

Accession:	gi|260656039	**Score:**	22.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	143.3
Database Date:	2015-11-30	**pI:**	8.8
		Sequence Coverage [%]:	2.5
		No. of unique Peptides:	1

```
        10          20          30          40          50          60          70          80
MEAPLQTGMV  LGVMIGAGVA  VVVTAVLILL  VVRRLRVPKT  PAPDGPRYRF  RKRDKVLFYG  RKIMRKVSQS  TSSLVDTSVS

        90         100         110         120         130         140         150         160
ATSRPRMRKK  LKMLNIAKKI  LRIQKETPTL  QRKEPPPAVL  EADLTEGDLA  NSHLPSEVLY  MLKNVRVLGH  FEKPLFLELC

       170         180         190         200         210         220         230         240
RHMVFQRLGQ  GDYVFRPGQP  DASIYVVQDG  LLELCLPGPD  GKECVVKEVV  PGDSVNSLLS  ILDVITGHQH  PQRTVSARAA

       250         260         270         280         290         300         310         320
RDSTVLRLPV  EAFSAVFTKY  PESLVRVVQI  IMVRLQRVTF  LALHNYLGLT  NELFSHEIQP  LRLFPSPGLP  TRTSPVRGSK

       330         340         350         360         370         380         390         400
RMVSTSATDE  PRETPGRPPD  PTGAPLPGPT  GDPVKPTSLE  TPSAPLLSRC  VSMPGDISGL  QGGPRSDFDM  AYERGRISVS

       410         420         430         440         450         460         470         480
LQEEASGGSL  AAPARTPTQE  PREQPAGACE  YSYCEDESAT  GGCPFGPYQG  RQTSSIFEAA  KQELAKLMRI  EDVSLHFVLW

       490         500         510         520         530         540         550         560
GCLHVYQRMI  DKAEDVCLFV  AQPGELVGQL  AVLTGEPLIF  TLRAQRDCTF  LRISKSDFYE  IMRAQPSVVL  SAAHTVAARM

       570         580         590         600         610         620         630         640
SPFVRQMDFA  IDWTAVEAGR  ALYRQGDRSD  CTYIVLNGRL  RSVIQRGSGK  KELVGEYGRG  DLIGVVEALT  RQPRATTVHA

       650         660         670         680         690         700         710         720
VRDTELAKLP  EGTLGHIKRR  YPQVVTRLIH  LLSQKILGNL  QQLQGPFPGS  GLGVPPHSEL  TNPASNLATV  AILPVCAEVP

       730         740         750         760         770         780         790         800
MVAFTLELQH  ALQAIGPTLL  LNSDIIRARL  GASALDSIQE  FRLSGWLAQQ  EDAHRIVLYQ  TDASLTPWTV  RCLRQADCIL

       810         820         830         840         850         860         870         880
IVGLGDQEPT  LGQLEQMLEN  TAVRALKQLV  LLHREEGAGP  TRTVEWLNMR  SWCSGHLHLR  CPRRLFSRRS  PAKLHELYEK

       890         900         910         920         930         940         950         960
VFSRRADRHS  DFSRLARVLT  GNTIALVLGG  GGARGCSHIG  VLKALEEAGV  PVDLVGGTSI  GSFIGALYAE  ERSASRTKQR

       970         980         990        1000        1010        1020        1030        1040
AREWAKSMTS  VLEPVLDLTY  PVTSMFTGSA  FNRSIHRVFQ  DKQIEDLWLP  YFNVTTDITA  SAMRVHKDGS  LWRYVRASMT

      1050        1060        1070        1080        1090        1100        1110        1120
LSGYLPPLCD  PKDGHLLMDG  GYINNLPADI  ARSMGAKTVI  AIDVGSQDET  DLSTYGDSLS  GWWLLWKRLN  PWADKVKVPD

      1130        1140        1150        1160        1170        1180        1190        1200
MAEIQSRLAY  VSCVRQLEVV  KSSSYCEYLR  PPIDCFKTMD  FGKFDQIYDV  GYQYGKAVFG  GWSRGNVIEK  MLTDRRSTDL

      1210        1220        1230        1240        1250        1260        1270        1280
NESRRADVLA  FPSSGFTDLA  EIVSRIEPPT  SYVSDGCADG  EESDCLTEYE  EDAGPDCSRD  EGGSPEGASP  STASEMEEEK

      1290        1300        1310
SILRQRRCLP  QEPPGSATDA
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
55	1	699.0697	59.10	3	29.4	10.8	0	1206-1225	R.ADVLAFPSSGFTDLAEIVSR.I	

Detailed Protein Report

Protein 774: puratrophin-1 isoform 2 [Homo sapiens]

Accession:	gi|193211603	**Score:**	22.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	122.8
Database Date:	2015-11-30	**pI:**	5.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.4
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MERPLENGDE	SPDSQGHATD	WRFAVCSFRD	AWEEEEPASQ	MHVKDPGPPR	PPAGATQDEE	LQGSPLSRKF	QLPPAADESG
90	100	110	120	130	140	150	160
DAQRGTVESS	SVLSEGPGPS	GVESLLCPMS	SHLSLAQGTR	DVQGRAVLLL	CAHSPAWLQS	ECSSQELIRL	LLYLRSIPRP
170	180	190	200	210	220	230	240
EVQALGLTVL	VDARICAPSS	SLFSGLSQLQ	EAAPGAVYQV	LLVGSTLLKE	VPSGLQLEQL	PSQSLLTHIP	TAGLPTSLGG
250	260	270	280	290	300	310	320
GLPYCHQAWL	DFRRRLEALL	QNCQAACALL	QGAIESVKAV	PQPMEPGEVG	QLLQQTEVLM	QQVLDSPWLA	WLQCQGGREL
330	340	350	360	370	380	390	400
TWLKQEVPEV	TLSPDYRTAM	DKADELYDRV	DGLLHQLTLQ	SNQRIQALEL	VQTLEARESG	LHQIEVWLQQ	VGWPALEEAG
410	420	430	440	450	460	470	480
EPSLDMLLQA	QGSFQELYQV	AQEQVRQGEK	FLQPLTGWEA	AELDPPGARF	LALRAQLTEF	SRALAQRCQR	LADAERLFQL
490	500	510	520	530	540	550	560
FREALTWAEE	GQRVLAELEQ	ERPGVVLQQL	QLHWTRHPDL	PPAHFRKMWA	LATGLGSEAI	RQECRWAWAR	CQDTWLALDQ
570	580	590	600	610	620	630	640
KLEASLKLPP	VGSTASLCVS	QVPAAPAHPP	LRKAYSFDRN	LGQSLSEPAC	HCHHAATIAA	CRRPEAGGGA	LPQASPTVPP
650	660	670	680	690	700	710	720
PGSSDPRSLN	RLQLVLAEMV	ATEREYVRAL	EYTMENYFPE	LDRPDVPQGL	RGQRAHLFGN	LEKLRDFHCH	FFLRELEACT
730	740	750	760	770	780	790	800
RHPPRVAYAF	LRHRVQFGMY	ALYSKNKPRS	DALMSSYGHT	FFKDKQQALG	DHLDLASYLL	KPIQRMGKYA	LLLQELARAC
810	820	830	840	850	860	870	880
GGPTQELSAL	REAQSLVHFQ	LRHGNDLLAM	DAIQGCDVNL	KEQGQLVRQD	EFVVRTGRHK	SVRRIFLFEE	LLLFSKPRHG
890	900	910	920	930	940	950	960
PTGVDTFAYK	RSFKMADLGL	TECCGNSNLR	FEIWFRRRKA	RDTFVLQASS	LAIKQAWTAD	ISHLLWRQAV	HNKEVRMAEM
970	980	990	1000	1010	1020	1030	1040
VSMGVGNKAF	RDIAPSEEAI	NDRTVNYVLK	CREVRSRASI	AVAPFDHDSL	YLGASNSLPG	DPASCSVLGS	LNLHLYRDPA
1050	1060	1070	1080	1090	1100	1110	1120
LLGLRCPLYP	SFPEEAALEA	EAELGGQPSL	TAEDSEISSQ	CPSASGSSGS	DSSCVSGQAL	GRGLEDLPCV	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1533	1	835.4469	69.38	2	47.9	10.1	1	954-968	K.EVRMAEMVSMGVGNK.A	Oxidation: 4, 7
2818	2	665.3626	67.46	2	63.7	12.3	0	972-983	R.DIAPSEEAINDR.T	

Detailed Protein Report

Protein 775: dehydrogenase/reductase SDR family member 1 [Homo sapiens]

Accession:	gi|19923983	**Score:**	22.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	33.9
Database Date:	2015-11-30	**pI:**	9.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.8
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|209862901	refseq_huma (refseq_human_20140103.fasta)	dehydrogenase/reductase SDR family member 1 [Homo sapiens]

10	20	30	40	50	60	70	80
MAAPMNGQVC	VVTGASRGIG	RGIALQLCKA	GATVYITGRH	LDTLRVVAQE	AQSLGGQCVP	VVCDSSQESE	VRSLFEQVDR
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
EQQGRLDVLV	NNAYAGVQTI	LNTRNKAFWE	TPASMWDDIN	NVGLRGHYFC	SVYGARLMVP	AGQGLIVVIS	SPGSLQYMFN
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
VPYGVGKAAC	DKLAADCAHE	LRRHGVSCVS	LWPGIVQTEL	LKEHMAKEEV	LQDPVLKQFK	SAFSSAETTE	LSGKCVVALA
250	**260**	**270**	**280**	**290**	**300**	**310**	**320**
TDPNILSLSG	KVLPSCDLAR	RYGLRDVDGR	PVQDYLSLSS	VLSHVSGLGW	LASYLPSFLR	VPKWIIALYT	SKF

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
141	1	822.3919	8.30	2	31.0	10.4	1	168-182	K.AACDKLAADCAHELR.R	Carbamidomethyl: 3

Detailed Protein Report

Protein 776: low-density lipoprotein receptor-related protein 1B precursor [Homo sapiens]

Accession:	gi|93102379	**Score:**	22.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	515.2
Database Date:	2015-11-30	**pI:**	5.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	0.7
		No. of unique Peptides:	1

Quantitation

Wdown:Qdown	**Median:**	1.97	**CV:**	0.00 %	**No. of Peptides:**	1

10	20	30	40	50	60	70	80
MSEFLLALLT	LSGLLPIARV	LTVGADRDQQ	LCDPGEFLCH	DHVTCVSQSW	LCDGDPDCPD	DSDESLDTCP	EEVEIKCPLN
90	100	110	120	130	140	150	160
HIACLGTNKC	VHLSQLCNGV	LDCPDGYDEG	VHCQELLSNC	QQLNCQYKCT	MVRNSTRCYC	EDGFEITEDG	RSCKDQDECA
170	180	190	200	210	220	230	240
VYGTCSQTCR	NTHGSYTCSC	VEGYLMQPDN	RSCKAKIEPT	DRPPILLIAN	FETIEVFYLN	GSKMATLSSV	NGNEIHTLDF
250	260	270	280	290	300	310	320
IYNEDMICWI	ESRESSNQLK	CIQITKAGGL	TDEWTINILQ	SFHNVQQMAI	DWLTRNLYFV	DHVGDRIFVC	NSNGSVCVTL
330	340	350	360	370	380	390	400
IDLELHNPKA	IAVDPIAGKL	FFTDYGNVAK	VERCDMDGMN	RTRIIDSKTE	QPAALALDLV	NKLVYWVDLY	LDYVGVVDYQ
410	420	430	440	450	460	470	480
GKNRHTVIQG	RQVRHLYGIT	VFEDYLYATN	SDNYNIVRIN	RFNGTDIHSL	IKIENAWGIR	IYQKRTQPTV	RSHACEVDPY
490	500	510	520	530	540	550	560
GMPGGCSHIC	LLSSSYKTRT	CRCRTGFNLG	SDGRSCKRPK	NELFLFYGKG	RPGIVRGMDL	NTKIADEYMI	PIENLVNPRA
570	580	590	600	610	620	630	640
LDFHAETNYI	YFADTTSFLI	GRQKIDGTER	ETILKDDLDN	VEGIAVDWIG	NNLYWTNDGH	RKTINVARLE	KASQSRKTLL
650	660	670	680	690	700	710	720
EGEMSHPRGI	VVDPVNGWMY	WTDWEEDEID	DSVGRIEKAW	MDGFNRQIFV	TSKMLWPNGL	TLDFHTNTLY	WCDAYYDHIE
730	740	750	760	770	780	790	800
KVFLNGTHRK	IVYSGRELNH	PFGLSHHGNY	VFWTDYMNGS	IFQLDLITSE	VTLLRHERPP	LFGLQIYDPR	KQQGDNMCRV
810	820	830	840	850	860	870	880
NNGGCSTLCL	AIPGGRVCAC	ADNQLLDENG	TTCTFNPGEA	LPHICKAGEF	RCKNRHCIQA	RWKCDGDDDC	LDGSDEDSVN
890	900	910	920	930	940	950	960
CFNHSCPDDQ	FKCQNNRCIP	KRWLCDGAND	CGSNEDESNQ	TCTARTCQVD	QFSCGNGRCI	PRAWLCDRED	DCGDQTDEMA
970	980	990	1000	1010	1020	1030	1040
SCEFPTCEPL	TQFVCKSGRC	ISSKWHCDSD	DDCGDGSDEV	GCVHSCFDNQ	FRCSSGRCIP	GHWACDGDND	CGDFSDEAQI
1050	1060	1070	1080	1090	1100	1110	1120
NCTKEEIHSP	AGCNGNEFQC	HPDGNCVPDL	WRCDGEKDCE	DGSDEKGCNG	TIRLCDHKTK	FSCWSTGRCI	NKAWVCDGDI
1130	1140	1150	1160	1170	1180	1190	1200
DCEDQSDEDD	CDSFLCGPPK	HPCANDTSVC	LQPEKLCNGK	KDCPDGSDEG	YLCDECSLNN	GGCSNHCSVV	PGRGIVCSCP
1210	1220	1230	1240	1250	1260	1270	1280
EGLQLNKDNK	TCEIVDYCSN	HLKCSQVCEQ	HKHTVKCSCY	EGWKLDVDGE	SCTSVDPFEA	FIIFSIRHEI	RRIDLHKRDY
1290	1300	1310	1320	1330	1340	1350	1360
SLLVPGLRNT	IALDFHFNQS	LLYWTDVVED	RIYRGKLSES	GGVSAIEVVV	EHGLATPEGL	TVDWIAGNIY	WIDSNLDQIE
1370	1380	1390	1400	1410	1420	1430	1440
VAKLDGSLRT	TLIAGAMEHP	RAIALDPRYG	ILFWTDWDAN	FPRIESASMS	GAGRKTIYKD	MKTGAWPNGL	TVDHFEKRIV
1450	1460	1470	1480	1490	1500	1510	1520
WTDARSDAIY	SALYDGTNMI	EIIRGHEYLS	HPFAVSLYGS	EVYWTDWRTN	TLSKANKWTG	QNVSVIQKTS	AQPFDLQIYH
1530	1540	1550	1560	1570	1580	1590	1600
PSRQPQAPNP	CAANDGKGPC	SHMCLINHNR	SAACACPHLM	KLSSDKKTCY	EMKKFLLYAR	RSEIRGVDID	NPYFNFITAF
1610	1620	1630	1640	1650	1660	1670	1680
TVPDIDDVTV	IDFDASEERL	YWTDIKTQTI	KRAFINGTGL	ETVISRDIQS	IRGLAVDWVS	RNLYWISSEF	DETQINVARL
1690	1700	1710	1720	1730	1740	1750	1760
DGSLKTSIIH	GIDKPQCLAA	HPVRGKLYWT	DGNTINMANM	DGSNSKILFQ	NQKEPVGLSI	DYVENKLYWI	SSGNGTINRC
1770	1780	1790	1800	1810	1820	1830	1840
NLDGGNLEVI	ESMKEELTKA	TALTIMDKKL	WWADQNLAQL	GTCSKRDGRN	PTILRNKTSG	VVHMKVYDKE	AQQGSNSCQL
1850	1860	1870	1880	1890	1900	1910	1920
NNGGCSQLCL	PTSETTRTCM	CTVGYYLQKN	RMSCQGIESF	LMYSVHEGIR	GIPLEPSDKM	DALMPISGTS	FAVGIDFHAE
1930	1940	1950	1960	1970	1980	1990	2000
NDTIYWTDMG	FNKISRAKRD	QTWKEDIITN	GLGRVEGIAV	DWIAGNIYWT	DHGFNLIEVA	RLNGSFRYVI	ISQGLDQPRS
2010	2020	2030	2040	2050	2060	2070	2080
IAVHPEKGLL	FWTEWGQMPC	IGKARLDGSE	KVVLVSMGIA	WPNGISIDYE	ENKLYWCDAR	TDKIERIDLE	TGGNREMVLS
2090	2100	2110	2120	2130	2140	2150	2160
GSNVDMFSVA	VFGAYIYWSD	RAHANGSVRR	GHKNDATETI	TMRTGLGVNL	KEVKIFNRVR	EKGTNVCARD	NGGCKQLCLY
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2037	2	977.3860	-129.29	2	54.0	11.5	1	1364-1381	K.LDGSLRTTLIAGAMEHPR.A	Oxidation: 14	Wdown:Qdown 1.97

Detailed Protein Report

Protein 777: protocadherin beta-15 precursor [Homo sapiens]

Accession:	gi|9256610	**Score:**	22.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	86.3
Database Date:	2015-11-30	**pI:**	4.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.8
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MEPAGERFPE QRQVLILLLL LEVTLAGWEP RRYSVMEETE RGSFVANLAN DLGLGVGELA ERGARVVSED NEQGLQLDLQ
        90        100        110        120        130        140        150        160
TGQLILNEKL DREKLCGPTE PCIMHFQVLL KKPLEVFRAE LLVTDINDHS PEFPEREMTL KIPETSSLGT VFPLKKARDL
       170        180        190        200        210        220        230        240
DVGSNNVQNY NISPNSHFHV STRTRGDGRK YPELVLDTEL DREEQAELRL TLTAVDGGSP PRSGTVQILI LVLDANDNAP
       250        260        270        280        290        300        310        320
EFVQALYEVQ VPENSPVGSL VVKVSARDLD TGTNGEISYS LYYSSQEIDK PFELSSLSGE IRLIKKLDFE TMSSYDLDIE
       330        340        350        360        370        380        390        400
ASDGGGLSGK CSVSVKVLDV NDNFPELSIS SLTSPIPENS PETEVALFRI RDRDSGENGK MICSIQDDVP FKLKPSVENF
       410        420        430        440        450        460        470        480
YRLVTEGALD RETRAEYNIT ITITDLGTPR LKTEQSITVL VSDVNDNAPA FTQTSYTLFV RENNSPALHI GSVSATDRDS
       490        500        510        520        530        540        550        560
GTNAQVTYSL LPPRDPHLPL TSLVSINTDN GHLFALQSLD YEALQAFEFR VGATDRGFPA LSSEALVRVL VLDANDNSPF
       570        580        590        600        610        620        630        640
VLYPLQNGSA PCTELVPRAA EPGYLVTKVV AVDGDSGQNA WLSYQLLKAT EPGLFGVWAH NGEVRTARLL SERDVAKHRL
       650        660        670        680        690        700        710        720
VVLVKDNGEP PRSATATLQV LLVDGFSQPY LPLPEAAPAQ AQADSLTVYL VVALASVSSL FLFSVFLFVA VRLCRRSRAA
       730        740        750        760        770        780        790
SVGRCSVPEG PFPGHLVDVS GTGTLSQSYQ YEVCLTGGSE SNDFKFLKPI FPNIVSQDSR RKSEFLE
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
270	1	862.8505	82.24	3	32.5	22.3	2	90-111	K.LDREKLCGPTEPCIMHFQVLLK.K	Oxidation: 15

Detailed Protein Report

Protein 778: elongation factor G, mitochondrial [Homo sapiens]

Accession: gi|18390331
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 22.3
MW [kDa]: 83.4
pI: 6.6
Sequence Coverage [%]: 3.9
No. of unique Peptides: 1

Quantitation

mdown:qdown	**Median:**	2.74	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.67	**CV:**	0.00 %	**No. of Peptides:**	1

10	20	30	40	50	60	70	80
MRLLGAAAVA	ALGRGRAPAS	LGWQRKQVNW	KACRWSSSGV	IPNEKIRNIG	ISAHIDSGKT	TLTERVLYYT	GRIAKMHEVK
90	100	110	120	130	140	150	160
GKDGVGAVMD	SMELERQRGI	TIQSAATYTM	WKDVNINIID	TPGHVDFTIE	VERALRVLDG	AVLVLCAVGG	VQCQTMTVNR
170	180	190	200	210	220	230	240
QMKRYNVPFL	TFINKLDRMG	SNPARALQQM	RSKLNHNAAF	MQIPMGLEGN	FKGIVDLIEE	RAIYFDGDFG	QIVRYGEIPA
250	260	270	280	290	300	310	320
ELRAAATDHR	QELIECVANS	DEQLGEMFLE	EKIPSISDLK	LAIRRATLKR	SFTPVFLGSA	LKNKGVQPLL	DAVLEYLPNP
330	340	350	360	370	380	390	400
SEVQNYAILN	KEDDSKEKTK	ILMNSSRDNS	HPFVGLAFKL	EVGRFGQLTY	VRSYQGELKK	GDTIYNTRTR	KKVRLQRLAR
410	420	430	440	450	460	470	480
MHADMMEDVE	EVYAGDICAL	FGIDCASGDT	FTDKANSGLS	MESIHVPDPV	ISIAMKPSNK	NDLEKFSKGI	GRFTREDPTF
490	500	510	520	530	540	550	560
KVYFDTENKE	TVISGMGELH	LEIYAQRLER	EYGCPCITGK	PKVAFRETIT	APVPFDFTHK	KQSGGAGQYG	KVIGVLEPLD
570	580	590	600	610	620	630	640
PEDYTKLEFS	DETFGSNIPK	QFVPAVEKGF	LDACEKGPLS	GHKLSGLRFV	LQDGAHHMVD	SNEISFIRAG	EGALKQALAN
650	660	670	680	690	700	710	720
ATLCILEPIM	AVEVVAPNEF	QGQVIAGINR	RHGVITGQDG	VEDYFTLYAD	VPLNDMFGYS	TELRSCTEGK	GEYTMEYSRY
730	740	750	760				
QPCLPSTQED	VINKYLEATG	QLPVKKGKAK	N				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
24	1	750.8366	-54.77	2	29.5	11.7	0	222-234	R.AIYFDGDFGQIVR.Y		Wdown:Qdown 0.67 mdown:qdown 2.74

Detailed Protein Report

Protein 779: **glycosyltransferase-like domain-containing protein 1 isoform d [Homo sapiens]**

Accession:	gi|545746399	**Score:**	22.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	37.7
Database Date:	2015-11-30	**pI:**	6.6
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	9.1
		No. of unique Peptides:	2

```
        10         20         30         40         50         60         70         80
MESFLTSMGK FMKLIPDHRP KDLESIIRPK CQVIYFPIRF PDVSRFMPKH KTTHLKKMLG LKGNGGAVLS MALPFQPEQR
        90        100        110        120        130        140        150        160
DSEDLLKNFN SECDTHCGLD TARQEYLGNS LRQESDLKKS TSSDNSSSHH GENKQNLTVD PCDILGGVDN QQRLLHIVWP
       170        180        190        200        210        220        230        240
HRWEHDKDPE SFFKVLMHLK DLGLNFHVSV LGETFTDVPD IFSEAKKALG SSVLHWGYLP SKDDYFQVLC MADVVISTAK
       250        260        270        280        290        300        310        320
HEFFGVAMLE AVYCGCYPLC PKDLVYPEIF PAEYLYSTPE QLSKRLQNFC KRPDIIRKHL YKGEIAPFSW AALHGKFRSL
       330
LTTEPREDL
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2624	1	488.2210	-141.97	2	61.5	11.7	0	14-21	K.LIPDHRPK.D	
2608	1	869.7489	29.96	3	60.9	10.6	0	241-262	K.HEFFGVAMLEAVYCGCYPLCPK.D	Carbamidomethyl: 14, 20; Oxidation: 8

Detailed Protein Report

Protein 780: liprin-beta-2 isoform 3 [Homo sapiens]

Accession:	gi|375151575	**Score:**	22.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	83.1
Database Date:	2015-11-30	**pI:**	9.3
Modification(s):	Oxidation	**Sequence Coverage [%]:**	4.4
		No. of unique Peptides:	2

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	
2166	1	977.4261	-10.11	2	55.7	11.7	0	367-383	R.TQSGNFYTDTLGMAEFR.R	Oxidation: 13

Detailed Protein Report

Protein 781: PREDICTED: uncharacterized protein C11orf85 isoform X7 [Homo sapiens]

Accession:	gi|578821305	**Score:**	22.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	24.4
Database Date:	2015-11-30	**pI:**	10.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	7.9
		No. of unique Peptides:	1

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2875	1	922.9828	-58.69	2	65.1	22.3	2	78-94	K.GGVTGICFLLKVPVEKK.A	Carbamidomethyl: 7

Detailed Protein Report

Protein 782: PREDICTED: apoptosis-stimulating of p53 protein 2 isoform X1 [Homo sapiens]

Accession:	gi|530366444	**Score:**	22.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	125.2
Database Date:	2015-11-30	**pI:**	5.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.0
		No. of unique Peptides:	2

```
        10         20         30         40         50         60         70         80
MFLTVYLSNN EQHFTEVPVT PETICRDVVD LCKEPGESDC HLAEVWCGSE RPVADNERMF DVLQRFGSQR NEVRFFLRHE
        90        100        110        120        130        140        150        160
RPPGRDIVSG PRSQDPSLKR NGVKVPGEYR RKENGVNSPR MDLTLAELQE MASRQQQQIE AQQQLLATKE QRLKFLKQQD
       170        180        190        200        210        220        230        240
QRQQQQVAEQ EKLKRLKEIA ENQEAKLKKV RALKGHVEQK RLSNGKLVEE IEQMNNLFQQ KQRELVLAVS KVEELTRQLE
       250        260        270        280        290        300        310        320
MLKNGRIDSH HDNQSAVAEL DRLYKELQLR NKLNQEQNAK LQQQRECLNK RNSEVAVMDK RVNELRDRLW KKKAALQQKE
       330        340        350        360        370        380        390        400
NLPVSSDGNL PQQAASAPSR VAAVGPYIQS STMPRMPSRP ELLVKPALPD GSLVIQASEG PMKIQTLPNM RSGAASQTKG
       410        420        430        440        450        460        470        480
SKIHPVGPDW SPSNADLFPS QGSASVPQST GNALDQVDDG EVPLREKEKK VRPFSMFDAV DQSNAPPSFG TLRKNQSSED
       490        500        510        520        530        540        550        560
ILRDAQVANK NVAKVPPPVP TKPKQINLPY FGQTNQPPSD IKPDGSSQQL STVVPSMGTK PKPAGQQPRV LLSPSIPSVG
       570        580        590        600        610        620        630        640
QDQTLSPGSK QESPPAAAVR PFTPQPSKDT LLPPFRKPQT VAASSIYSMY TQQQAPGKNF QQAVQSALTK THTRGPHFSS
       650        660        670        680        690        700        710        720
VYGKPVIAAA QNQQQHPENI YSNSQGKPGS PEPETEPVSS VQENHENERI PRPLSPTKLL PFLSNPYRNQ SDADLEALRK
       730        740        750        760        770        780        790        800
KLSNAPRPLK KRSSITEPEG PNGPNIQKLL YQRTTIAAME TISVPSYPSK SASVTASSES PVEIQNPYLH VEPEKEVVSL
       810        820        830        840        850        860        870        880
VPESLSPEDV GNASTENSDM PAPSPGLDYE PEGVPDNSPN LQNNPEEPNP EAPHVLDVYL EEYPPYPPPP YPSGEPEGPG
       890        900        910        920        930        940        950        960
EDSVSMRPPE ITGQVSLPPG KRTNLRKTGS ERIAHGMRVK FNPLALLLDS SLEGEFDLVQ RIIYEVDDPS LPNDEGITAL
       970        980        990       1000       1010       1020       1030       1040
HNAVCAGHTE IVKFLVQFGV NVNAADSDGW TPLHCAASCN NVQVCKFLVE SGAAVFAMTY SDMQTAADKC EEMEEGYTQC
      1050       1060       1070       1080       1090       1100       1110       1120
SQFLYGVQEK MGIMNKGVIY ALWDYEPQND DELPMKEGDC MTIIHREDED EIEWWWARLN DKEGYVPRNL LGLYPRIKPR
      1130
QRSLA
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1220	1	500.6481	-227.72	2	43.8	12.1	1	112-120	R.KENGVNSPR.M	
2874	1	964.7996	-6.06	3	64.7	10.2	2	238-262	R.QLEMLKNGRIDSHHDNQSAVAELDR.L	Oxidation: 4

Detailed Protein Report

Protein 783: laminin subunit beta-3 precursor [Homo sapiens]

Accession:	gi|62868215	**Score:**	22.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	129.5
Database Date:	2015-11-30	**pI:**	7.9
		Sequence Coverage [%]:	2.7
		No. of unique Peptides:	2

Alias proteins:

Accession	Name	Description
gi|530366188	refseq_human (refseq_human_20140103.fasta)	PREDICTED: laminin subunit beta-3 isoform X1 [Homo sapiens]
gi|189083719	refseq_human (refseq_human_20140103.fasta)	laminin subunit beta-3 precursor [Homo sapiens]
gi|62868217	refseq_human (refseq_human_20140103.fasta)	laminin subunit beta-3 precursor [Homo sapiens]

10	20	30	40	50	60	70	80
MRPFFLLCFA	LPGLLHAQQA	CSRGACYPPV	GDLLVGRTRF	LRASSTCGLT	KPETYCTQYG	EWQMKCCKCD	SRQPHNYYSH
90	100	110	120	130	140	150	160
RVENVASSSG	PMRWWQSQND	VNPVSLQLDL	DRRFQLQEVM	MEFQGPMPAG	MLIERSSDFG	KTWRVYQYLA	ADCTSTFPRV
170	180	190	200	210	220	230	240
RQGRPQSWQD	VRCQSLPQRP	NARLNGGKVQ	LNLMDLVSGI	PATQSQKIQE	VGEITNLRVN	FTRLAPVPQR	GYHPPSAYYA
250	260	270	280	290	300	310	320
VSQLRLQGSC	FCHGHADRCA	PKPGASAGPS	TAVQVHDVCV	CQHNTAGPNC	ERCAPFYNNR	PWRPAEGQDA	HECQRCDCNG
330	340	350	360	370	380	390	400
HSETCHFDPA	VFAASQGAYG	GVCDNCRDHT	EGKNCERCQL	HYFRNRRPGA	SIQETCISCE	CDPDGAVPGA	PCDPVTGQCV
410	420	430	440	450	460	470	480
CKEHVQGERC	DLCKPGFTGL	TYANPQGCHR	CDCNILGSRR	DMPCDEESGR	CLCLPNVVGP	KCDQCAPYHW	KLASGQGCEP
490	500	510	520	530	540	550	560
CACDPHNSLS	PQCNQFTGQC	PCREGFGGLM	CSAAAIRQCP	DRTYGDVATG	CRACDCDFRG	TEGPGCDKAS	GRCLCRPGLT
570	580	590	600	610	620	630	640
GPRCDQCQRG	YCNRYPVCVA	CHPCFQTYDA	DLREQALRFG	RLRNATASLW	SGPGLEDRGL	ASRILDAKSK	IEQIRAVLSS
650	660	670	680	690	700	710	720
PAVTEQEVAQ	VASAILSLRR	TLQGLQLDLP	LEEETLSLPR	DLESLDRSFN	GLLTMYQRKR	EQFEKISSAD	PSGAFRMLST
730	740	750	760	770	780	790	800
AYEQSAQAAQ	QVSDSSRLLD	QLRDSRREAE	RLVRQAGGGG	GTGSPKLVAL	RLEMSSLPDL	TPTFNKLCGN	SRQMACTPIS
810	820	830	840	850	860	870	880
CPGELCPQDN	GTACGSRCRG	VLPRAGGAFL	MAGQVAEQLR	GFNAQLQRTR	QMIRAAEESA	SQIQSSAQRL	ETQVSASRSQ
890	900	910	920	930	940	950	960
MEEDVRRTRL	LIQQVRDFLT	DPDTDAATIQ	EVSEAVLALW	LPTDSATVLQ	KMNEIQAIAA	RLPNVDLVLS	QTKQDIARAR
970	980	990	1000	1010	1020	1030	1040
RLQAEAEEAR	SRAHAVEGQV	EDVVGNLRQG	TVALQEAQDT	MQGTSRSLRL	IQDRVAEVQQ	VLRPAEKLVT	SMTKQLGDFW
1050	1060	1070	1080	1090	1100	1110	1120
TRMEELRHQA	RQQGAEAVQA	QQLAEGASEQ	ALSAQEGFER	IKQKYAELKD	RLGQSSMLGE	QGARIQSVKT	EAEELFGETM
1130	1140	1150	1160	1170	1180		
EMMDRMKDME	LELLRGSQAI	MLRSADLTGL	EKRVEQIRDH	INGRVLYYAT	CK		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2105	1	926.8168	-61.93	2	54.9	12.0	1	523-539	R.TYGDVATGCRACDCDFR.G	
569	1	671.4345	103.14	2	36.4	10.2	1	752-766	R.LVRQAGGGGGTGSPK.L	

Detailed Protein Report

Protein 784: destrin isoform a [Homo sapiens]

Accession:	gi|5802966	**Score:**	22.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	18.5
Database Date:	2015-11-30	**pI:**	9.2
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	14.5
		No. of unique Peptides:	2

```
        10         20         30         40         50         60         70         80
MASGVQVADE VCRIFYDMKV RKCSTPEEIK KRKKAVIFCL SADKKCIIVE EGKEILVGDV GVTITDPFKH FVGMLPEKDC
        90        100        110        120        130        140        150        160
RYALYDASFE TKESRKEELM FFLWAPELAP LKSKMIYASS KDAIKKKFQG IKHECQANGP EDLNRACIAE KLGGSLIVAF
       170
EGCPV
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1879	1	719.2624	-89.30	2	53.5	11.7	0	1-13	-.MASGVQVADEVCR.I	Carbamidomethyl: 12; Oxidation: 1
237	1	613.7692	-92.64	2	31.7	10.5	1	115-125	K.MIYASSKDAIK.K	

Detailed Protein Report

Protein 785: PREDICTED: ubiquitin carboxyl-terminal hydrolase 45 isoform X4 [Homo sapiens]

Accession:	gi|530384120	**Score:**	22.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	81.3
Database Date:	2015-11-30	**pI:**	9.1
		Sequence Coverage [%]:	5.1
		No. of unique Peptides:	2

Quantitation

mdown:qdown **Median:** 0.74 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MRVKDPTKAL PEKAKRSKRP TVPHDEDSSD DIAVGLTCQH VSHAISVNHV KRAIAENLWS VCSECLKERR FYDGQLVLTS

        90        100        110        120        130        140        150        160
DIWLCLKCGF QGCGKNSESQ HSLKHFKSSR TEPHCIIINL STWIIWCYEC DEKLSTHCNK KVLAQIVDFL QKHASKTQTS

       170        180        190        200        210        220        230        240
AFSRIMKLCE EKCETDEIQK GGKCRNLSVR GITNLGNTCF FNAVMQNLAQ TYTLTDLMNE IKESSTKLKI FPSSDSQLDP

       250        260        270        280        290        300        310        320
LVVELSRPGP LTSALFLFLH SMKETEKGPL SPKVLFNQLC QKAPRFKDFQ QQDSQELLHY LLDAVRTEET KRIQASILKA

       330        340        350        360        370        380        390        400
FNNPTTKTAD DETRKKVKAY GKEGVKMNFI DRIFIGELTS TVMCEECANI STVKDPFIDI SLPIIEERVS KPLLWGRMNK

       410        420        430        440        450        460        470        480
YRSLRETDHD RYSGNVTIEN IHQPRAAKKH SSSKDKSQLI HDRKCIRKLS SGETVTYQKN ENLEMNGDSL MFASLMNSES

       490        500        510        520        530        540        550        560
RLNESPTDDS EKEASHSESN VDADSEPSES ESASKQTGLF RSSSGSGVQP DGPLYPLSAG KLLYTKETDS GDKEMAEAIS

       570        580        590        600        610        620        630        640
ELRLSSTVTG DQDFDRENQP LNISNNLCFL EGKHLRSYSP QNAFQTLSQS YITTSKECSI QSCLYQFTSM ELLMGNNKLL

       650        660        670        680        690        700        710        720
CENCTKNKQK YQEETSFAEK KVEGVYTNAR KQLLISAVPA VLILHLKRFH QAGLSLRKVN RHVDFPLMLD LAPFCSATCK

       730
V
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
825	3	848.9721	-22.06	2	39.1	11.5	1	142-156	K.VLAQIVDFLQKHASK.T		mdown:qdown 0.74
331	1	847.0323	-20.10	3	33.5	10.7	0	617-638	K.ECSIQSCLYQFTSMELLMGNNK.L		

Detailed Protein Report

Protein 786: oxygen-regulated protein 1 [Homo sapiens]

Accession:	gi|5454016	**Score:**	22.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	240.5
Database Date:	2015-11-30	**pI:**	5.5
		Sequence Coverage [%]:	0.9
		No. of unique Peptides:	2

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
```

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	
2984	1	729.3744	-46.74	2	66.1	10.0	0	1731-1743	R.ILTDIEEGVLIDK.G	

Detailed Protein Report

Protein 787: PREDICTED: myotubularin-related protein 13 isoform X2 [Homo sapiens]

Accession:	gi|530395847	**Score:**	22.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	207.1
Database Date:	2015-11-30	**pI:**	6.9
		Sequence Coverage [%]:	0.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MARLADYFIV	VGYDHEKPGS	GEGLGKIIQR	FPQKDWDDTP	FPQGIELFCQ	PGGWQLSRER	KQPTFFVVVL	TDIDSDRHYC
90	100	110	120	130	140	150	160
SCLTFYEAEI	NLQGTKKEEI	EGEAKVSGLI	QPAEVFAPKS	LVLVSRLYYP	EIFRACLGLI	YTVYVDSLNV	SLESLIANLC
170	180	190	200	210	220	230	240
ACLVPAAGGS	QKLFSLGAGD	RQLIQTPLHD	SLPITGTSVA	LLFQQLGIQN	VLSLFCAVLT	ENKVLFHSAS	FQRLSDACRA
250	260	270	280	290	300	310	320
LESLMFPLKY	SYPYIPILPA	QLLEVLSSPT	PFIIGVHSVF	KTDVHELLDV	IIADLDGGTI	KIPECIHLSS	LPEPLLHQTQ
330	340	350	360	370	380	390	400
SALSLILHPD	LEVADHAFPP	PRTALSHSKM	LDKEVRAVFL	RLFAQLFQGY	RSCLQLIRIH	AEPVIHFHKL	VAFEVERIKV
410	420	430	440	450	460	470	480
EENNPVKMIK	HVRELAEQLF	KNENPNPHMA	FQKVPRPTEG	SHLRVHILPF	PEINEARVQE	LIQENVAKNQ	NAPPATRIEK
490	500	510	520	530	540	550	560
KCVVPAGPPV	VSIMDKVTTV	FNSAQRLEVV	RNCISFIFEN	KILETEKTLP	AALRALKGKA	ARQCLTDELG	LHVQQNRAIL
570	580	590	600	610	620	630	640
DHQQFDYIIR	MMNCTLQDCS	SLEEYNIAAA	LLPLTSAFYR	KLAPGVSQFA	YTCVQDHPIW	TNQQFWETTF	YNAVQEQVRS
650	660	670	680	690	700	710	720
LYLSAKEDNH	APHLKQKDKL	PDDHYQEKTA	MDLAAEQLRL	WPTLSKSTQQ	ELVQHEESTV	FSQAIHFANL	MVNLLVPLDT
730	740	750	760	770	780	790	800
SKNKLLRTSA	PGDWESGSNS	IVTNSIAGSV	AESYDTESGF	EDSENTDIAN	SVVRFITRFI	DKVCTESGVT	QDHIKSLHCM
810	820	830	840	850	860	870	880
IPGIVAMHIE	TLEAVHRESR	RLPPIQKPKI	LRPALLPGEE	IVCEGLRVLL	DPDGREEATG	GLLGGPQLLP	AEGALFLTTY
890	900	910	920	930	940	950	960
RILFRGTPHD	QLVGEQTVVR	SFPIASITKE	KKITMQNQLQ	QNMQEGLQIT	SASFQLIKVA	FDEEVSPEVV	EIFKKQLMKF
970	980	990	1000	1010	1020	1030	1040
RYPQSIFSTF	AFAAGQTTPQ	IILPKQKEKN	TSFRTFSKTI	VKGAKRAGKM	TIGRQYLLKK	KTGTIVEERV	NRPGWNEDDD
1050	1060	1070	1080	1090	1100	1110	1120
VSVSDESELP	TSTTLKASEK	STMEQLVEKA	CFRDYQRLGL	GTISGSSSRS	RPEYFRITAS	NRMYSLCRSY	PGLLVVPQAV
1130	1140	1150	1160	1170	1180	1190	1200
QDSSLPRVAR	CYRHNRLPVV	CWKNSRSGTL	LLRSGGFHGK	GVVGLFKSQN	SPQAAPTSSL	ESSSSIEQEK	YLQALLNAVS
1210	1220	1230	1240	1250	1260	1270	1280
VHQKLRGNST	LTVRPAFALS	PGTERRTSRM	STVLKQVVPG	HLDVNPSNSF	AQGGVWASLR	SSTRLISSPT	SFIDVGARLA
1290	1300	1310	1320	1330	1340	1350	1360
GKDHSASFSN	SSYLQNQLLK	RQAALYIFGE	KSQLRNFKVE	FALNCEFVPV	EFHEIRQVKA	SFKKLMRACI	PSTIPTDSEV
1370	1380	1390	1400	1410	1420	1430	1440
TFLKALGDSE	WFPQLHRIMQ	LAVVVSEVLE	NGSSVLVCLE	EGWDITAQVT	SLVQLLSDPF	YRTLEGFQML	VEKEWLSFGH
1450	1460	1470	1480	1490	1500	1510	1520
KFSQRSSLTL	NCQGSGFAPV	FLQFLDCVHQ	VHNQYPTEFE	FNLYYLKFLA	FHYVSNRFKT	FLLDSDYERL	EHGTLFDDKG
1530	1540	1550	1560	1570	1580	1590	1600
EKHAKKGVCI	WECIDRMHKR	SPIFFNYLYS	PLEIEALKPN	VNVSSLKKWD	YYIEETLSTG	PSYDWMMLTP	KHFPSEDSDL
1610	1620	1630	1640	1650	1660	1670	1680
AGEAGPRSQR	RTVWPCYDDV	SCTQPDALTS	LFSEIEKLEH	KLNQAPEKWQ	QLWERVTVDL	KEEPRTDRSQ	RHLSRSPGIV
1690	1700	1710	1720	1730	1740	1750	1760
STNLPSYQKR	SLLHLPDSSM	GEEQNSSISP	SNGVERRAAT	LYSQYTSKND	ENRSFEGTLY	KRGALLKGWK	PRWFVLDVTK
1770	1780	1790	1800	1810	1820	1830	1840
HQLRYYDSGE	DTSCKGHIDL	AEVEMVIPAG	PSMGAPKHTS	DKAFFDLKTS	KRVYNFCAQD	GQSAQQWMDK	IQSCISDA

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

	Cmpds.		[ppm]		[min]					
246	1	530.5813	-5.79	3	32.2	10.0	1	1527-1539	K.GVCIWECIDRMHK.R	

Detailed Protein Report

Protein 788: **germ cell-less protein-like 1 [Homo sapiens]**

Accession: gi|30410765
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 22.2
MW [kDa]: 58.6
pI: 8.5
Sequence Coverage [%]: 3.1
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MGSLSSRVLR	QPRPALAQQA	QGARAGGSAR	RPDTGDDAAG	HGFCYCAGSH	KRKRSSGSFC	YCHPDSETDE	DEEEGDEQQR
90	100	110	120	130	140	150	160
LLNTPRRKKL	KSTSKYIYQT	LFLNGENSDI	KICALGEEWS	LHKIYLCQSG	YFSSMFSGSW	KESSMNIIEL	EIPDQNIDVE
170	180	190	200	210	220	230	240
ALQVAFGSLY	RDDVLIKPSR	VVAILAAACL	LQLDGLIQQC	GETMKETVNV	KTVCGYYTSA	GTYGLDSVKK	KCLEWLLNNL
250	260	270	280	290	300	310	320
MTHQNVELFK	ELSINVMKQL	IGSSNLFVMQ	VEMDIYTALK	KWMFLQLVPS	WNGSLKQLLT	ETDVWFSKQR	KDFEGMAFLE
330	340	350	360	370	380	390	400
TEQGKPFVSV	FRHLRLQYII	SDLASARIIE	QDAVVPSEWL	SSVYKQQWFA	MLRAEQDSEV	GPQEINKEEL	EGNSMRCGRK
410	420	430	440	450	460	470	480
LAKDGEYCWR	WTGFNFGFDL	LVTYTNRYII	FKRNTLNQPC	SGSVSLQPRR	SIAFRLRLAS	FDSSGKLICS	RTTGYQILTL
490	500	510	520				
EKDQEQVVMN	LDSRLLIFPL	YICCNFLYIS	PEKKN				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1992	1	584.9082	-132.40	3	53.5	10.2	2	456-471	R.LRLASFDSSGKLICSR.T	

Detailed Protein Report

Protein 789: transcriptional repressor CTCF isoform 2 [Homo sapiens]

Accession:	gi|300388142	**Score:**	22.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	46.0
Database Date:	2015-11-30	**pI:**	9.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	7.3
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	1.41	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	1.20	**CV:**	0.00 %	**No. of Peptides:**	1

```
        10         20         30         40         50         60         70         80
MAFVTSGELV RHRRYKHTHE KPFKCSMCDY ASVEVSKLKR HIRSHTGERP FQCSLCSYAS RDTYKLKRHM RTHSGEKPYE
        90        100        110        120        130        140        150        160
CYICHARFTQ SGTMKMHILQ KHTENVAKFH CPHCDTVIAR KSDLGVHLRK QHSYIEQGKK CRYCDAVFHE RYALIQHQKS
       170        180        190        200        210        220        230        240
HKNEKRFKCD QCDYACRQER HMIMHKRTHT GEKPYACSHC DKTFRQKQLL DMHFKRYHDP NFVPAAFVCS KCGKTFTRRN
       250        260        270        280        290        300        310        320
TMARHADNCA GPDGVEGENG GETKKSKRGR KRKMRSKKED SSDSENAEPD LDDNEDEEEP AVEIEPEPEP QPVTPAPPPA
       330        340        350        360        370        380        390        400
KKRRGRPPGR TNQPKQNQPT AIIQVEDQNT GAIENIIVEV KKEPDAEPAE GEEEEAQPAA TDAPNGDLTP EMILSMMDR
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1114	1	612.2788	-15.06	3	42.6	11.3	2	25-40	K.CSMCDYASVEVSKLKR.H	Oxidation: 3	Wdown:Qdown 1.20 mdown:qdown 1.41

Detailed Protein Report

Protein 790: methylthioribose-1-phosphate isomerase isoform 2 [Homo sapiens]

Accession: gi|23943880
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 22.2
MW [kDa]: 34.5
pI: 5.4
Sequence Coverage [%]: 1.9
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MTLEAIRYSR	GSLQILDQLL	LPKQSRYEAV	GSVHQAWEAI	RAMKVRGAPA	IALVGCLSLA	VELQAGAGGP	GLAALVAFVR
90	100	110	120	130	140	150	160
DKLSFLVTAR	PTAVNMARAA	RDLADVAARE	AEREGATEEA	VRERRETELC	EHWEEHTRQR	ELPLRGPLGG	TVLETRPYNQ
170	180	190	200	210	220	230	240
GARLTAFELV	YEQIPATLIT	DSMVAAAMAH	RGVSAVVVGA	DRVVANGDTA	NKVGTYQLAI	VAKHHGIPFY	VAAPSSSCDL
250	260	270	280	290	300	310	320
RLETGKEIII	EERPGQELTD	VNGVRIAAPG	IGVWNPAFDV	TPHDLITGGI	ITELGVFAPE	ELRTALTTTI	SSRDGTLDGP
330							
QM							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2639	1	702.1743	-341.86	1	61.3	22.2	0	2-7	M.TLEAIR.Y	

Detailed Protein Report

Protein 791: **PREDICTED: regulator of G-protein signaling 7-binding protein isoform X2 [Homo sapiens]**

Accession:	gi|578810352	**Score:**	22.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	22.7
Database Date:	2015-11-30	**pI:**	7.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	13.2
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:** 2.56	**CV:** 0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:** 4.25	**CV:** 0.00 %	**No. of Peptides:**	1

```
        10         20         30         40         50         60         70         80
MSSAPNGRKK RPSRSTRSSI FQISKPPLQS GDWERRGSGS ESAHKTQRAL DDCKMLVQEF NTQVALYREL VISIGDVSVS
        90        100        110        120        130        140        150        160
CPSLRAEMHK TRTKGCEMAR QAHQKLAAIS GPEDGEIHPE ICRLYIQLQC CLEMYTTEML KSICLLGSLQ FHRKGKEPGG
       170        180        190        200        210
GTKSLDCKIE ESAETPALED SSSSPVDSQQ HSWQVSTDIE NTER
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1047	1	973.9236	-30.05	2	41.6	11.7	2	37-54	R.GSGSESAHKTQRALDDCK.M	Carbamidomethyl: 17	mdown:qdown 2.56 Wdown:Qdown 4.25

Detailed Protein Report

Protein 792: PDZ and LIM domain protein 4 isoform 1 [Homo sapiens]

Accession:	gi|19923181	**Score:**	22.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	35.4
Database Date:	2015-11-30	**pI:**	9.2
		Sequence Coverage [%]:	13.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPHSVTLRGP	SPWGFRLVGG	RDFSAPLTIS	RVHAGSKAAL	AALCPGDLIQ	AINGESTELM	THLEAQNRIK	GCHDHLTLSV
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
SRPEGRSWPS	APDDSKAQAH	RIHIDPEIQD	GSPTTSRRPS	GTGTGPEDGR	PSLGSPYGQP	PRFPVPHNGS	SEATLPAQMS
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
TLHVSPPPSA	DPARGLPRSR	DCRVDLGSEV	YRMLREPAEP	VAAEPKQSGS	FRYLQGMLEA	GEGGDWPGPG	GPRNLKPTAS
250	**260**	**270**	**280**	**290**	**300**	**310**	**320**
KLGAPLSGLQ	GLPECTRCGH	GIVGTIVKAR	DKLYHPECFM	CSDCGLNLKQ	RGYFFLDERL	YCESHAKARV	KPPEGYDVVA
330	**340**						
VYPNAKVELV							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1594	1	715.4238	125.91	3	48.6	10.0	0	213-233	R.YLQGMLEAGEGGDWPGPGGPR.N	

Detailed Protein Report

Protein 793: PREDICTED: anoctamin-9 isoform X8 [Homo sapiens]

Accession:	gi|578820507	**Score:**	22.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	68.7
Database Date:	2015-11-30	**pI:**	7.5
		Sequence Coverage [%]:	4.3
		No. of unique Peptides:	1

Quantitation

Wdown:Qdown **Median:** 0.35 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MQGEESLRIL	VEPEGDSFPL	MEISTCETEA	SEQWDYVLVA	QRHTQRDPRQ	ARQQQFLEEL	RRKGFHIKVI	RDQKQVFFGI
90	100	110	120	130	140	150	160
RADNSVFGLY	RTLLLEPEGP	APHAELAAPT	TIPVTTSLRI	RIVNFVVMNN	KTSAGETFED	LMKDGVFEAR	FPLHKGEGRL
170	180	190	200	210	220	230	240
KKTWARWRHM	FREQPVDEIR	NYFGEKVALY	FVWLGWYTYM	LVPAALTGLL	VFLSGFSLFE	ASQISKEICE	AHDILMCPLG
250	260	270	280	290	300	310	320
DHSRRYQRLS	ETCTFAKLTH	LFDNDGTVVF	AIFMALWATV	FLEIWKRQRA	RVVLHWDLYV	WDEEQEEMAL	QLINCPDYKL
330	340	350	360	370	380	390	400
RPYQHSYLRS	TVILVLTLLM	ICLMIGMAHV	LVVYRVLASA	LFSSSAVPFL	EEQVTTAVVV	TGALVHYVTI	IIMTKINRDA
410	420	430	440	450	460	470	480
QDLLGAREQV	HHPLLHTAVL	HPFLVSHLHR	LHPGQDQRPP	REVHAPGGLV	EAGRVPRQRL	HDGPLRADGH	HHGPEADAQQ
490	500	510	520	530	540	550	560
LRRVPGPVGD	PQVPLSAGLR	VRAPAPGPRA	QGLAAQLPSE	PGQHLQPVRR	VHGDDDPVRL	HHHLRGRLPA	GAAARALQQP
570	580	590	600	610	620		
RGDPPGRHQD	GLVAAAPGAA	QGQGHRDLAA	GAGDHRCAGG	HCQWDGHCLH	I		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
729	1	866.9494	-59.21	2	37.9	10.1	2	540-555	R.LHHHLRGRLPAGAAAR.A		Wdown:Qdown 0.35

Detailed Protein Report

Protein 794: protocadherin-20 precursor [Homo sapiens]

Accession:	gi|190194360	**Score:**	22.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	104.9
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
MRGRGNARSS	QALGVSWCPA	TWHPRLDMGR	LHRPRSSTSY	RNLPHLFLFF	LFVGPFSCLG	SYSRATELLY	SLNEGLPAGV
90	100	110	120	130	140	150	160
LIGSLAEDLR	LLPRSAGRPD	PQSQLPERTG	AEWNPPLSFS	LASRGLSGQY	VTLDNRSGEL	HTSAQEIDRE	ALCVEGGGGT
170	180	190	200	210	220	230	240
AWSGSVSISS	SPSDSCLLLL	DVLVLPQEYF	RFVKVKIAIR	DINDNAPQFP	VSQISVWVPE	NAPVNTRLAI	EHPAVDPDVG
250	260	270	280	290	300	310	320
INGVQTYRLL	DYHGMFTLDV	EENENGERTP	YLIVMGALDR	ETQDQYVSII	IAEDGGSPPL	LGSATLTIGI	SDINDNCPLF
330	340	350	360	370	380	390	400
TDSQINVTVY	GNATVGTPIA	AVQAVDKDLG	TNAQITYSYS	QKVPQASKDL	FHLDENTGVI	KLFSKIGGSV	LESHKLTILA
410	420	430	440	450	460	470	480
NGPGCIPAVI	TALVSIIKVI	FRPPEIVPRY	IANEIDGVVY	LKELEPVNTP	IAFFTIRDPE	GKYKVNCYLD	GEGPFRLSPY
490	500	510	520	530	540	550	560
KPYNNEYLLE	TTKPMDYELQ	QFYEVAVVAW	NSEGFHVKRV	IKVQLLDDND	NAPIFLQPLI	ELTIEENNSP	NAFLTKLYAT
570	580	590	600	610	620	630	640
DADSEERGQV	SYFLGPDAPS	YFSLDSVTGI	LTVSTQLDRE	EKEKYRYTVR	AVDCGKPPRE	SVATVALTVL	DKNDNSPRFI
650	660	670	680	690	700	710	720
NKDFSFFVPE	NFPGYGEIGV	ISVTDADAGR	NGWVALSVVN	QSDIFVIDTG	KGMLRAKVSL	DREQQSSYTL	WVEAVDGGEP
730	740	750	760	770	780	790	800
ALSSTAKITI	LLLDINDNPP	LVLFPQSNMS	YLLVLPSTLP	GSPVTEVYAV	DKDTGMNAVI	AYSIIGRRGP	RPESFRIDPK
810	820	830	840	850	860	870	880
TGNITLEEAL	LQTDYGLHRL	LVKVSDHGYP	EPLHSTVMVN	LFVNDTVSNE	SYIESLLRKE	PEINIEEKEP	QISIEPTHRK
890	900	910	920	930	940	950	960
VESVSCMPTL	VALSVISLGS	ITLVTGMGIY	ICLRKGEKHP	REDENLEVQI	PLKGKIDLHM	RERKPMDISN	I

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1727	1	1293.5590	-108.94	2	50.3	22.1	2	363-385	K.VPQASKDLFHLDENTGVIKLFSK.I	

Detailed Protein Report

Protein 795: tubulin polyglutamylase TTLL5 [Homo sapiens]

Accession:	gi|50658079	**Score:**	22.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	143.5
Database Date:	2015-11-30	**pI:**	9.5
		Sequence Coverage [%]:	1.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPIVMARDLE	ETASSSEDEE	VISQEDHPCI	MWTGGCRRIP	VLVFHADAIL	TKDNNIRVIG	ERYHLSYKIV	RTDSRLVRSI
90	100	110	120	130	140	150	160
LTAHGFHEVH	PSSTDYNLMW	TGSHLKPFLL	RTLSEAQKVN	HFPRSYELTR	KDRLYKNIIR	MQHTHGFKAF	HILPQTFLLP
170	180	190	200	210	220	230	240
AEYAEFCNSY	SKDRGPWIVK	PVASSRGRGV	YLINNPNQIS	LEENILVSRY	INNPLLIDDF	KFDVRLYVLV	TSYDPLVIYL
250	260	270	280	290	300	310	320
YEEGLARFAT	VRYDQGAKNI	RNQFMHLTNY	SVNKKSGDYV	SCDDPEVEDY	GNKWSMSAML	RYLKQEGRDT	TALMAHVEDL
330	340	350	360	370	380	390	400
IIKTIISAEL	AIATACKTFV	PHRSSCFELY	GFDVLIDSTL	KPWLLEVNLS	PSLACDAPLD	LKIKASMISD	MFTVVGFVCQ
410	420	430	440	450	460	470	480
DPAQRASTRP	IYPTFESSRR	NPFQKPQRCR	PLSASDAEMK	NLVGSAREKG	PGKLGGSVLG	LSMEEIKVLR	RVKEENDRRG
490	500	510	520	530	540	550	560
GFIRIFPTSE	TWEIYGSYLE	HKTSMNYMLA	TRLFQDRMTA	DGAPELKIES	LNSKAKLHAA	LYERKLLSLE	VRKRRRRSSR
570	580	590	600	610	620	630	640
LRAMRPKYPV	ITQPAEMNVK	TETESEEEEE	VALDNEDEEQ	EASQEESAGF	LRENQAKYTP	SLTALVENTP	KENSMKVREW
650	660	670	680	690	700	710	720
NNKGGHCCKL	ETQELEPKFN	LMQILQDNGN	LSKMQARIAF	SAYLQHVQIR	LMKDSGGQTF	SASWAAKEDE	QMELVVRFLK
730	740	750	760	770	780	790	800
RASNNLQHSL	RMVLPSRRLA	LLERRRILAH	QLGDFIIVYN	KETEQMAEKK	SKKKVEEEEE	DGVNMENFQE	FIRQASEAEL
810	820	830	840	850	860	870	880
EEVLTFYTQK	NKSASVFLGT	HSKISKNNNN	YSDSGAKGDH	PETIMEEVKI	KPPKQQQTTE	IHSDKLSRFT	TSAEKEAKLV
890	900	910	920	930	940	950	960
YSNSSSGPTA	TLQKIPNTHL	SSVTTSDLSP	GPCHHSSLSQ	IPSAIPSMPH	QPTILLNTVS	ASASPCLHPG	AQNIPSPTGL
970	980	990	1000	1010	1020	1030	1040
PRCRSGSHTI	GPFSSFQSAA	HIYSQKLSRP	SSAKAGSCYL	NKHHSGIAKT	QKEGEDASLY	SKRYNQSMVT	AELQRLAEKQ
1050	1060	1070	1080	1090	1100	1110	1120
AARQYSPSSH	INLLTQQVTN	LNLATGIINR	SSASAPPTLR	PIISPSGPTW	STQSDPQAPE	NHSSSPGSRS	LQTGGFAWEG
1130	1140	1150	1160	1170	1180	1190	1200
EVENNVYSQA	TGVVPQHKYH	PTAGSYQLQF	ALQQLEQQKL	QSRQLLDQSR	ARHQAIFGSQ	TLPNSNLWTM	NNGAGCRISS
1210	1220	1230	1240	1250	1260	1270	1280
ATASGQKPTT	LPQKVVPPPS	SCASLVPKPP	PNHEQVLRRA	TSQKASKGSS	AEGQLNGLQS	SLNPAAFVPI	TSSTDPAHTK
1290							
I							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2086	1	720.2523	-137.01	2	54.7	11.9	0	1024-1035	R.YNQSMVTAELQR.L	

Detailed Protein Report

Protein 796: matrix-remodeling-associated protein 5 precursor [Homo sapiens]

Accession:	gi|139948432	**Score:**	22.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	312.0
Database Date:	2015-11-30	**pI:**	9.3
		Sequence Coverage [%]:	1.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPKRAHWGAL	SVVLILLWGH	PRVALACPHP	CACYVPSEVH	CTFRSLASVP	AGIAKHVERI	NLGFNSIQAL	SETSFAGLTK
90	100	110	120	130	140	150	160
LELLMIHGNE	IPSIPDGALR	DLSSLQVFKF	SYNKLRVITG	QTLQGLSNLM	RLHIDHNKIE	FIHPQAFNGL	TSLRLLHLEG
170	180	190	200	210	220	230	240
NLLHQLHPST	FSTFTFLDYF	RLSTIRHLYL	AENMVRTLPA	SMLRNMPLLE	NLYLQGNPWT	CDCEMRWFLE	WDAKSRGILK
250	260	270	280	290	300	310	320
CKKDKAYEGG	QLCAMCFSPK	KLYKHEIHKL	KDMTCLKPSI	ESPLRQNRSR	SIEEEQEQEE	DGGSQLILEK	FQLPQWSISL
330	340	350	360	370	380	390	400
NMTDEHGNMV	NLVCDIKKPM	DVYKIHLNQT	DPPDIDINAT	VALDFECPMT	RENYEKLWKL	IAYYSEVPVK	LHRELMLSKD
410	420	430	440	450	460	470	480
PRVSYQYRQD	ADEEALYYTG	VRAQILAEPE	WVMQPSIDIQ	LNRRQSTAKK	VLLSYYTQYS	QTISTKDTRQ	ARGRSWVMIE
490	500	510	520	530	540	550	560
PSGAVQRDQT	VLEGGPCQLS	CNVKASESPS	IFWVLPDGSI	LKAPMDDPDS	KFSILSSGWL	RIKSMEPSDS	GLYQCIAQVR
570	580	590	600	610	620	630	640
DEMDRMVYRV	LVQSPSTQPA	EKDTVTIGKN	PGESVTLPCN	ALAIPEAHLS	WILPNRRIIN	DLANTSHVYM	LPNGTLSIPK
650	660	670	680	690	700	710	720
VQVSDSGYYR	CVAVNQQGAD	HFTVGITVTK	KGSGLPSKRG	RRPGAKALSR	VREDIVEDEG	GSGMGDEENT	SRRLLHPKDQ
730	740	750	760	770	780	790	800
EVFLKTKDDA	INGDKKAKKG	RRKLKLWKHS	EKEPETNVAE	GRRVFESRRR	INMANKQINP	ERWADILAKV	RGKNLPKGTE
810	820	830	840	850	860	870	880
VPPLIKTTSP	PSLSLEVTPP	FPAISPPSAS	PVQTVTSAEE	SSADVPLLGE	EEHVLGTISS	ASMGLEHNHN	GVILVEPEVT
890	900	910	920	930	940	950	960
STPLEEVVDD	LSEKTEEITS	TEGDLKGTAA	PTLISEPYEP	SPTLHTLDTV	YEKPTHEETA	TEGWSAADVG	SSPEPTSSEY
970	980	990	1000	1010	1020	1030	1040
EPPLDAVSLA	ESEPMQYFDP	DLETKSQPDE	DKMKEDTFAH	LTPTPTIWVN	DSSTSQLFED	STIGEPGVPG	QSHLQGLTDN
1050	1060	1070	1080	1090	1100	1110	1120
IHLVKSSLST	QDTLLIKKGM	KEMSQTLQGG	NMLEGDPTHS	RSSESEGQES	KSITLPDSTL	GIMSSMSPVK	KPAETTVGTL
1130	1140	1150	1160	1170	1180	1190	1200
LDKDTTTATT	TPRQKVAPSS	TMSTHPSRRR	PNGRRRLRPN	KFRHRHKQTP	PTTFAPSETF	STQPTQAPDI	KISSQVESSL
1210	1220	1230	1240	1250	1260	1270	1280
VPTAWVDNTV	NTPKQLEMEK	NAEPTSKGTP	RRKHGKRPNK	HRYTPSTVSS	RASGSKPSPS	PENKHRNIVT	PSSETILLPR
1290	1300	1310	1320	1330	1340	1350	1360
TVSLKTEGPY	DSLDYMTTTR	KIYSSYPKVQ	ETLPVTYKPT	SDGKEIKDDV	ATNVDKHKSD	ILVTGESITN	AIPTSRSLVS
1370	1380	1390	1400	1410	1420	1430	1440
TMGEFKEESS	PVGFPGTPTW	NPSRTAQPGR	LQTGIPVTTS	GENLTDPPLL	KELEDVDFTS	EFLSSLTVST	PFHQEEAGSS
1450	1460	1470	1480	1490	1500	1510	1520
TTLSSIKVEV	ASSQAETTTL	DQDHLETTVA	ILLSETRPQN	HTPTAARMKE	PASSSPSTIL	MSLGQTTTTK	PALPSPRISQ
1530	1540	1550	1560	1570	1580	1590	1600
ASRDSKENVF	LNYVGNPETE	ATPVNNEGTQ	HMSGPNELST	PSSDQDAFNL	STKLELEKQV	FGSRSLPRGP	DSQRQDGRVH
1610	1620	1630	1640	1650	1660	1670	1680
ASHQLTRVPA	KPILPTATVR	LPEMSTQSAS	RYFVTSQSPR	HWTNKPEITT	YPSGALPENK	QFTTPRLSST	TIPLPLHMSK
1690	1700	1710	1720	1730	1740	1750	1760
PSIPSKFTDR	RTDQFNGYSK	VFGNNNIPEA	RNPVGKPPSP	RIPHYSNGRL	PFFTNKTLSF	PQLGVTRRPQ	IPTSPAPVMR
1770	1780	1790	1800	1810	1820	1830	1840
ERKVIPGSYN	RIHSHSTFHL	DFGPPAPPLL	HTPQTTGSPS	TNLQNIPMVS	STQSSISFIT	SSVQSSGSFH	QSSSKFFAGG
1850	1860	1870	1880	1890	1900	1910	1920
PPASKFWSLG	EKPQILTKSP	QTVSVTAETD	TVFPCEATGK	PKPFVTWTKV	STGALMTPNT	RIQRFEVLKN	GTLVIRKVQV
1930	1940	1950	1960	1970	1980	1990	2000
QDRGQYMCTA	SNLHGLDRMV	VLLSVTVQQP	QILASHYQDV	TVYLGDTIAM	ECLAKGTPAP	QISWIFPDRR	VWQTVSPVEG
2010	2020	2030	2040	2050	2060	2070	2080
RITLHENRTL	SIKEASFSDR	GVYKCVASNA	AGADSLAIRL	HVAALPPVIH	QEKLENISLP	PGLSIHIHCT	AKAAPLPSVR
2090	2100	2110	2120	2130	2140	2150	2160
WVLGDGTQIR	PSQFLHGNLF	VFPNGTLYIR	NLAPKDSGRY	ECVAANLVGS	ARRTVQLNVQ	RAAANARITG	TSPRRTDVRY
2170	2180	2190	2200	2210	2220	2230	2240
GGTLKLDCSA	SGDPWPRILW	RLPSKRMIDA	LFSFDSRIKV	FANGTLVVKS	VTDKDAGDYL	CVARNKVGDD	YVVLKVDVVM
2250	2260	2270	2280	2290	2300	2310	2320
KPAKIEHKEE	NDHKVFYGGD	LKVDCVATGL	PNPEISWSLP	DGSLVNSFMQ	SDDSGGRTKR	YVVFNNGTLY	FNEVGMREEG
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
2644	1	1175.1326	48.53	2	61.3	10.5	1	2597-2619	K.ADGMLHISGLSSVDAGAYRCVAR.N	

Detailed Protein Report

Protein 797: 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: 22.0
MW [kDa]: 197.3
pI: 5.8
Sequence Coverage [%]: 1.5
No. of unique Peptides: 2

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
607	1	766.5212	180.82	2	36.2	10.1	0	1343-1355	K.WNFSSGFIEAVFK.H	

Detailed Protein Report

Protein 798: 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 799: **neuronal acetylcholine receptor subunit alpha-4 isoform 1 precursor [Homo sapiens]**

Accession:	gi|4502827	**Score:**	21.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	69.9
Database Date:	2015-11-30	**pI:**	6.9
		Sequence Coverage [%]:	4.0
		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 800: microtubule-associated tumor suppressor candidate 2 isoform a [Homo sapiens]

Accession:	gi|140161498	**Score:**	21.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	151.1
Database Date:	2015-11-30	**pI:**	6.3
		Sequence Coverage [%]:	1.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MASSPTKGLT	MSVPVAPKKS	CYTQLRDNRN	AARNNNESIL	SLGDTNANQI	MLEVSSSHDE	SKTCDLGDEI	GNTNSSEPEN
90	100	110	120	130	140	150	160
RTHFHKEFHQ	LQGFGKGSQA	GSASLKDFRL	SSTIQRELNE	EHTVERGTDS	LQTTRSIQGP	SLSSWRNVMS	EASLDVLAKR
170	180	190	200	210	220	230	240
DAEIPRHVPK	DKLAKTLDNE	ELRRHSLERA	SSSVAAVGSL	TPQHPQPLSL	DSREARGQIP	GGGEGPQKTL	PDHAVPAAFP
250	260	270	280	290	300	310	320
ATDSTSEGKS	VRHPKPSTSE	SKQSTPSETQ	TVGAHVLQVC	SEHTSHSAHP	EPALNLTLAS	KEIPSKLEAQ	LGQGKGEAKL
330	340	350	360	370	380	390	400
DLKYVPPRRV	EQEGKAAQEG	YLGCHKEENL	SALEGRDPCG	EAHPEATDAL	GHLLNSDLHH	LGVGRGNCEE	KRGVNPGEQD
410	420	430	440	450	460	470	480
SLHTTPKQGS	ASLGGADNQP	TGKISPCAGE	KLGERTSSSF	SPGDSHVAFI	PNNLTDSKPL	DVIEEERRLG	SGNKDSVMVL
490	500	510	520	530	540	550	560
VFNPSVGENK	TEVPEPLDPQ	SGRSEARESK	EVTTSVAENR	NLLENADKIE	STSARADSVL	NIPAPLHPET	TVNMTYQPTT
570	580	590	600	610	620	630	640
PSSSFQDVSV	FGMDAGSPLV	VPPPTDSARL	LNTSPKVPDK	NTCPSGIPKP	VFTHSKDTPS	SQEGMENYQV	EKTEERTETK
650	660	670	680	690	700	710	720
PIIMPKPKHV	RPKIITYIRR	NPQALGQVDA	SLVPVGLPYA	PPTCTMPLPH	EEKAAGGDLK	PSANLYEKFK	PDLQKPRVFS
730	740	750	760	770	780	790	800
SGLMVSGIKP	PGHPFSQMSE	KFLQEVTDHP	GKEEFCSPPY	AHYEVPPTFY	RSAMLLKPQL	GLGAMSRLPS	AKSRILIASQ
810	820	830	840	850	860	870	880
RSSASAIHPP	GPITTATSLY	SSDPSADLKK	ASSSNAAKSN	LPKSGLRPPG	YSRLPAAKLA	AFGFVRSSSV	SSVSSTQSGD
890	900	910	920	930	940	950	960
SAQPEQGRPA	TRSTFGNEEQ	PVLKASLPSK	DTPKGAGRVA	PPASSSVTAP	RRSLLPAPKS	TSTPAGTKKD	AQKDQDTNKP
970	980	990	1000	1010	1020	1030	1040
AVSSPKRVAA	STTKLHSPGY	PKQRTAAARN	GFPPKPDPQA	REAERQLVLR	LKERCEQQTR	QLGVAQGELK	RAICGFDALA
1050	1060	1070	1080	1090	1100	1110	1120
VATQHFFRKN	ESALVKEKEL	SIELANIRDE	VAFHTAKCEK	LQKEKEELER	RFEDEVKRLG	WQQQAELQEL	EERLQLQFEA
1130	1140	1150	1160	1170	1180	1190	1200
EMARLQEEHG	DQLLSIRCQH	QEQVEDLTAS	HDAALLEMEN	NHTVAITILQ	DDHDHKVQEL	MSTHELEKKE	LEENFEKLRL
1210	1220	1230	1240	1250	1260	1270	1280
SLQDQVDTLT	FQSQSLRDRA	RRFEEALRKN	TEEQLEIALA	PYQHLEEDMK	SLKQVLEMKN	QQIHEQEKKI	LELEKLAEKN
1290	1300	1310	1320	1330	1340	1350	1360
IILEEKIQVL	QQQNEDLKAR	IDQNTVVTRQ	LSEENANLQE	YVEKETQEKK	RLSRTNEELL	WKLQTGDPTS	PIKLSPTSPV
1370	1380						
YRGSSSGPSS	PARVSTTPR						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1804	1	899.4822	-27.71	2	51.2	11.6	2	307-323	K.LEAQLGQGKGEAKLDLK.Y	

Detailed Protein Report

Protein 801: PREDICTED: protein PRRC2C isoform X16 [Homo sapiens]

Accession:	gi|530364444	**Score:**	21.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	296.8
Database Date:	2015-11-30	**pI:**	9.4
		Sequence Coverage [%]:	1.2
		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 802: serine/threonine-protein kinase MRCK alpha isoform A [Homo sapiens]

Accession:	gi|30089960	**Score:**	21.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	186.0
Database Date:	2015-11-30	**pI:**	5.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.1
		No. of unique Peptides:	2

Quantitation

mdown:qdown	**Median:**	0.37	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	1.53	**CV:**	0.17 %	**No. of Peptides:**	2

10	20	30	40	50	60	70	80
MSGEVRLRQL	EQFILDGPAQ	TNGQCFSVET	LLDILICLYD	ECNNSPLRRE	KNILEYLEWA	KPFTSKVKQM	RLHREDFEIL
90	100	110	120	130	140	150	160
KVIGRGAFGE	VAVVKLKNAD	KVFAMKILNK	WEMLKRAETA	CFREERDVLV	NGDNKWITTL	HYAFQDDNNL	YLVMDYYVGG
170	180	190	200	210	220	230	240
DLLTLLSKFE	DRLPEDMARF	YLAEMVIAID	SVHQLHYVHR	DIKPDNILMD	MNGHIRLADF	GSCLKLMEDG	TVQSSVAVGT
250	260	270	280	290	300	310	320
PDYISPEILQ	AMEDGKGRYG	PECDWWSLGV	CMYEMLYGET	PFYAESLVET	YGKIMNHKER	FQFPAQVTDV	SENAKDLIRR
330	340	350	360	370	380	390	400
LICSREHRLG	QNGIEDFKKH	PFFSGIDWDN	IRNCEAPYIP	EVSSPTDTSN	FDVDDDCLKN	SETMPPPTHT	AFSGHHLPFV
410	420	430	440	450	460	470	480
GFTYTSSCVL	SDRSCLRVTA	GPTSLDLDVN	VQRTLDNNLA	TEAYERRIKR	LEQEKLELSR	KLQESTQTVQ	ALQYSTVDGP
490	500	510	520	530	540	550	560
LTASKDLEIK	NLKEEIEKLR	KQVTESSHLE	QQLEEANAVR	QELDDAFRQI	KAYEKQIKTL	QQEREDLNKL	EVHTEALAAE
570	580	590	600	610	620	630	640
ASKDRKLREQ	SEHYSKQLEN	ELEGLKQKQI	SYSPGVCSIE	HQQEITKLKT	DLEKKSIFYE	EELSKREGIH	ANEIKNLKKE
650	660	670	680	690	700	710	720
LHDSEGQQLA	LNKEIMILKD	KLEKTRRESQ	SEREEFESEF	KQQYEREKVL	LTEENKKLTS	ELDKLTTLYE	NLSIHNQQLE
730	740	750	760	770	780	790	800
EEVKDLADKK	ESVAHWEAQI	TEIIQWVSDE	KDARGYLQAL	ASKMTEELEA	LRNSSLGTRA	TDMPWKMRRF	AKLDMSARLE
810	820	830	840	850	860	870	880
LQSALDAEIR	AKQAIQEELN	KVKASNIITE	CKLKDSEKKN	LELLSEIEQL	IKDTEELRSE	KGIEHQDSQH	SFLAFLNTPT
890	900	910	920	930	940	950	960
DALDQFETVD	STPLSVHTPT	LRKKGCPGST	GFPPKRKTHQ	FFVKSFTTPT	KCHQCTSLMV	GLIRQGCSCE	VCGFSCHITC
970	980	990	1000	1010	1020	1030	1040
VNKAPTTCPV	PPEQTKGPLG	IDPQKGIGTA	YEGHVRIPKP	AGVKKGWQRA	LAIVCDFKLF	LYDIAEGKAS	QPSVVISQVI
1050	1060	1070	1080	1090	1100	1110	1120
DMRDEEFSVS	SVLASDVIHA	SRKDIPCIFR	VTASQLSASN	NKCSILMLAD	TENEKNKWVG	VLSELHKILK	KNKFRDRSVY
1130	1140	1150	1160	1170	1180	1190	1200
VPKEAYDSTL	PLIKTTQAAA	IIDHERIALG	NEEGLFVVHV	TKDEIIRVGD	NKKIHQIELI	PNDQLVAVIS	GRNRHVRLFP
1210	1220	1230	1240	1250	1260	1270	1280
MSALDGRETD	FYKLSETKGC	QTVTSGKVRH	GALTCLCVAM	KRQVLCYELF	QSKTRHRKFK	EIQVPYNVQW	MAIFSEQLCV
1290	1300	1310	1320	1330	1340	1350	1360
GFQSGFLRYP	LNGEGNPYSM	LHSNDHTLSF	IAHQPMDAIC	AVEISSKEYL	LCFNSIGIYT	DCQGRRSRQQ	ELMWPANPSS
1370	1380	1390	1400	1410	1420	1430	1440
CCYNAPYLSV	YSENAVDIFD	VNSMEWIQTL	PLKKVRPLNN	EGSLNLLGLE	TIRLIYFKNK	MAEGDELVVP	ETSDNSRKQM
1450	1460	1470	1480	1490	1500	1510	1520
VRNINNKRRY	SFRVPEEERM	QQRREMLRDP	EMRNKLISNP	TNFNHIAHMG	PGDGIQILKD	LPMNPRPQES	RTVFSGSVSI
1530	1540	1550	1560	1570	1580	1590	1600
PSITKSRPEP	GRSMSASSGL	SARSSAQNGS	ALKREFSGGS	YSAKRQPMPS	PSEGSLSSGG	MDQGSDAPAR	DFDGEDSDSP
1610	1620	1630	1640				
RHSTASNSSN	LSSPPSPASP	RKTKSLSLES	TDRGSWDP				

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
249	2	679.3367	-48.57	2	32.5	11.4	0	799-810	R.LELQSALDAEIR.A		Wdown:Qdown 1.53
55	1	826.3683	-54.04	3	29.9	10.5	2	1219-1241	K.GCQTVTSGKVRHGALTCLCVAMKR	Carbamidomethyl: 2, 17	mdown:qdown 0.37 Wdown:Qdown 1.53

Detailed Protein Report

Protein 803: amiloride-sensitive sodium channel subunit beta [Homo sapiens]

Accession: gi|124301196
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 21.8
MW [kDa]: 72.6
pI: 5.9
Sequence Coverage [%]: 3.3
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 804: janus kinase and microtubule-interacting protein 2 isoform 4 [Homo sapiens]

Accession:	gi|533112496	**Score:**	21.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	91.5
Database Date:	2015-11-30	**pI:**	5.5
		Sequence Coverage [%]:	4.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MVSKLEREKT	QEAKRIRELE	QRKHTVLVTE	LKAKLHEEKM	KELQAVRENL	IKQHEQEMSR	TVKVRDGEIQ	RLKSALCALR
90	100	110	120	130	140	150	160
DGSSDKVRTA	LTIEAREEAR	KLFDTERLKL	LQEIADLKTA	KKQVDEALSN	MIQADKIKAG	DLRSEHQSHQ	EAISKIKWES
170	180	190	200	210	220	230	240
ERDIRRLMDE	IKAKDRIIFS	LEKELETQTG	YVQKLQLQKE	ALDEQLFLVK	EAECNMSSPK	REIPGRAGDG	SEHCSSPDLR
250	260	270	280	290	300	310	320
RNQKRIAELN	ATIRKLEDRN	TLLGDERNEL	LKRVRETEKQ	CKPLLERNKC	LAKRNDELMV	SLQRMEEKLK	AVTKENSEMR
330	340	350	360	370	380	390	400
EKITSHPPLK	KLKSLNDLDQ	ANEEQETEFL	KLQVIEQQNI	IDELTRDREK	LIRRRKHRRS	SKPIKRPVLD	PFIGYDEDSM
410	420	430	440	450	460	470	480
DSETSSMASF	RTDRTPATPD	DDLDESLAAE	ESELRFRQLT	KEYQALQRAY	ALLQEQTGGI	IDAEREAKAQ	EQLQAEVLRY
490	500	510	520	530	540	550	560
KAKIEDLEAT	LAQKGQDSHW	VEDKQLFIKR	NQELLEKIEK	QEAENHRLQQ	ELQDARDQNE	LLEFRNLELE	ERERRSPPFN
570	580	590	600	610	620	630	640
LQIHPFSDGV	SALQIYCMKE	GVKDVNIPDL	IKQLDILGDN	GNLRNEEQVA	IIQASTVLSL	AEKWIQQIEG	AEAALHQKMM
650	660	670	680	690	700	710	720
ELESDMEQFC	KIKGYLEEEL	DYRKQALDQA	YMRIQELEAT	LYNALQQETV	IKFGELLSEK	QQEELRTAVE	KLRRQMLRKS
730	740	750	760	770	780		
REYDCQILQE	RMELLQQAHQ	RIRDLEDKTD	IQKRQIKDLE	EKFLFLFLFF	SLAFILWP		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1632	1	713.6458	-35.90	3	48.9	10.3	2	222-241	R.EIPGRAGDGSEHCSSPDLRR.N	

Detailed Protein Report

Protein 805: PREDICTED: protein eva-1 homolog C isoform X3 [Homo sapiens]

Accession:	gi|530419006	**Score:**	21.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	37.5
Database Date:	2015-11-30	**pI:**	5.9
		Sequence Coverage [%]:	5.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLLPGRARQP	PTPQPVQHPG	LRRQVEPPGQ	LLRLFYCTVL	VCSKEISALT	DFSDELKNKT	VCEDQELKLH	CHESKFLNIY
90	100	110	120	130	140	150	160
SATYGRRTQE	RDICSSKAER	LPPFDCLSYS	ALQVLSRRCY	GKQRCKIIVN	NHHFGSPCLP	GVKKYLTVTY	ACVPKNILTA
170	180	190	200	210	220	230	240
IDPAIANLKP	SLKQKDGEYG	INFDPSGSKV	LRKDGILVSN	SLAAFAYIRA	HPERAALLFV	SSVCIGLALT	LCALVIRESC
250	260	270	280	290	300	310	320
AKDFRDLQLG	REQLVPGSDK	VEEDSEDEEE	EEDPSESDFP	GELSGFCRTS	YPIYSSIEAA	ELAERIERRE	QIIQEIWMNS
330	340						
GLDTSLPRNM	GQFY						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1516	1	927.4902	37.95	2	47.7	21.8	1	176-192	K.DGEYGINFDPSGSKVLR.K	

Detailed Protein Report

Protein 806: PREDICTED: PHD finger protein 20-like protein 1 isoform X14 [Homo sapiens]

Accession:	gi|578816001	**Score:**	21.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	63.4
Database Date:	2015-11-30	**pI:**	9.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	5.8
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MSKKPPNRPG ITFEIGARLE ALDYLQKWYP SRIEKIDYEE GKMLVHFERW SHRYDEWIYW DSNRLRPLER PALRKEGLKD
        90        100        110        120        130        140        150        160
EEDFFDFKAG EEVLARWTDC RYYPAKIEAI NKEGTFTVQF YDGVIRCLKR MHIKAMPEDA KGQVKSQHPL SWCCPIDPAG
       170        180        190        200        210        220        230        240
SCNQSMGSED WIALVKAAAA AAAKNKTGSK PRTSANSNKD KDKDERKWFK VPSKKEETST CIATPDVEKK EDLPTSSETF
       250        260        270        280        290        300        310        320
GLHVENVPKM VFPQPESTLS NKRKNNQGNS FQAKRARLNK ITGLLASKAV GVDGAEKKED YNETAPMLEQ AISPKPQSQK
       330        340        350        360        370        380        390        400
KNEADISSSA NTQKPALLSS TLSSGKARSK KCKHESGDSS GCIKPPKSPL SPELIQVEDL TLVSQLSSSV INKTSPPQPV
       410        420        430        440        450        460        470        480
NPPRPFKHSE RRRRSQRLAT LPMPDDSVEK VSSPSPATDG KVFSISSQNQ QESSVPEVPD VAHLPLEKLG PCLPLDLSRG
       490        500        510        520        530        540        550        560
SEVTAPVASD SSYRNECPRA EKEDTQMLPN PSSKAIADGR GAPAAAGISK TEKKVKLEDK SSTAFGIRSW DFSALLMKIP
       570        580
SYSPISLSGL PES
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1939	1	918.3463	-119.86	2	52.9	10.8	2	215-230	K.KEETSTCIATPDVEKK.E	Carbamidomethyl: 7

Detailed Protein Report

Protein 807: transcription factor SOX-6 isoform 3 [Homo sapiens]

Accession:	gi|224967050	**Score:**	21.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	88.9
Database Date:	2015-11-30	**pI:**	6.9
		Sequence Coverage [%]:	3.5
		No. of unique Peptides:	2

```
        10         20         30         40         50         60         70         80
MSSKQATSPF ACAADGEDAM TQDLTSREKE EGSDQHVASH LPLHPIMHNK PHSEELPTLV STIQQDADWD SVLSSQQRME
        90        100        110        120        130        140        150        160
SENNKLCSLY SFRNTSTSPH KPDEGSRDRE IMTSVTFGTP ERRKGSLADV VDTLKQKKLE EMTRTEQEDS SCMEKLLSKD
       170        180        190        200        210        220        230        240
WKEKMERLNT SELLGEIKGT PESLAEKERQ LSTMITQLIS LREQLLAAHD EQKKLAASQI EKQRQQMDLA RQQQEQIARQ
       250        260        270        280        290        300        310        320
QQQLLQQQHK INLLQQQIQV QGHMPPLMIP IFPHDQRTLA AAAAAQQGFL FPPGITYKPG DNYPVQFIPS TMAAAAASGL
       330        340        350        360        370        380        390        400
SPLQLQQLYA AQLASMQVSP GAKMPSTPQP PNTAGTVSPT GIKNEKRGTS PVTQVKDEAA AQPLNLSSRP KTAEPVKSPT
       410        420        430        440        450        460        470        480
SPTQNLFPAS KTSPVNLPNK SSIPSPIGGS LGRGSSLGKW KSQHQEETYE LDILSSLNSP ALFGDQDTVM KAIQEARKMR
       490        500        510        520        530        540        550        560
EQIQREQQQQ QPHGVDGKLS SINNMGLNSC RNEKERTRFE NLGPQLTGKS NEDGKLGPGV IDLTRPEDAE GSKAMNGSAA
       570        580        590        600        610        620        630        640
KLQQYYCWPT GGATVAEARV YRDARGRASS EPHIKRPMNA FMVWAKDERR KILQAFPDMH NSNISKILGS RWKSMSNQEK
       650        660        670        680        690        700        710        720
QPYYEEQARL SKIHLEKYPN YKYKPRPKRT CIVDGKKLRI GEYKQLMRSR RQEMRQFFTV GQQPQIPITT GTGVVYPGAI
       730        740        750        760        770        780        790        800
TMATTTPSPQ MTSDCSSTSA SPEPSLPVIQ STYGMKTDGG SLAGNEMING EDEMEMYDDY EDDPKSDYSS ENEAPEAVSA
       810
N
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1137	10	500.6373	-249.35	2	42.7	11.7	0	232-239	R.QQQEQIAR.Q	
1752	1	990.9543	-52.79	2	50.4	10.0	0	344-363	K.MPSTPQPPNTAGTVSPTGIK.N	

Detailed Protein Report

Protein 808: hephaestin-like protein 1 precursor [Homo sapiens]

Accession:	gi|148886707	**Score:**	21.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	131.5
Database Date:	2015-11-30	**pI:**	6.3
		Sequence Coverage [%]:	0.9
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MPRKQPAGCI FLLTFLGLSG LVGTVTRTYY IGIVEEYWNY VPQGKNVITG KSFTEDKLAT LFLERGPNRI GSIYKKAVYR
        90        100        110        120        130        140        150        160
RFTDGTYSIE IPKPPWLGFL GPILRAEVGD VIVIHLKNFA SRPYSLHPHG VFYNKDSEGA LYPDGTSGRN KNDDMVPPGK
       170        180        190        200        210        220        230        240
NYTYVWPVRE EYAPTPADAN CLTWVYHSHI DAPKDICSGL IGPLLVCKEG ILNRYSGTRN DVDREFVIMF TLVDENQSWY
       250        260        270        280        290        300        310        320
LNENIKHFCT NPDSVDKKDA VFQRSNKMHA LNGYLFGNFP EPDMCVGESV SWHLFGMGNE IDIHSIYFYG NTFISRGHRT
       330        340        350        360        370        380        390        400
DVVNLFPATF LTTEMIAENP GKWMITCQVS DHLQAGMLGQ YNVDNCKSDI FYPKMKGQQR RYFIAAEKIL WDYAPQGYNK
       410        420        430        440        450        460        470        480
FSGLPLNASG SDSDLYFTQG DNRIGGKYWK VRYTEFVDAT FTKRKRLSAE EAHLGILGPV IKAEVGDTLL VTFANKADKV
       490        500        510        520        530        540        550        560
YSILPHGVIY DKASDAAPNL DGFVKPGAHV KPGETFTYKW TVPESVSPTA GDPPCLTYLY FSAVDPIKDT SSGLVGPLLV
       570        580        590        600        610        620        630        640
CKKGVLNADG TQKGIDKEFY LLFTVFDENL SRYFDENIQK FIWHPFSIDK EDKEFVKSNR MHAVNGYMYG NQPGLNMCKR
       650        660        670        680        690        700        710        720
DRVSWHLIGL GTDTDMHGIV FQGNTIHLRG THRDSLALFP HMATTAFMQP DHAGIFRVFC ATMPHLSRGM GQIYEVSSCD
       730        740        750        760        770        780        790        800
NRDPSEQRYG MIRTFYIAAE EVEWDYAPNK NWEFEKQHVD ARGERHGDIF MNRTENWIGS QYKKVVYREY TDGEFVEIKA
       810        820        830        840        850        860        870        880
RPPREEHLEL LGPMIHAEVG NTVLIIFKNK ASRPYSISAQ GVEEMDSGKQ FQVPMTKPGE VKTYRWNIPK RSGPGPSDPN
       890        900        910        920        930        940        950        960
CIPWVYYSTV NFVKDTYSGL MGPLITCRKG VLNEKGRRSD VDYEFALLFL VFNENESWYL DDNIKKYLNK DPRDFKRTDD
       970        980        990       1000       1010       1020       1030       1040
FEESNRMHAI NGKIFGNLHG LIMNEDTMTN WYLLGIGSEV DIHTIHYHAE SFLFKIDKSY REDVYDLFPG TFQTIELFAD
      1050       1060       1070       1080       1090       1100       1110       1120
HPGTWLLHCH VSDHIHAGME TTYTVLRNID NRIPYSTTSP GVASHPATVP SNERPGKEQL YFFGKNLGPT GAKAALVILF
      1130       1140       1150       1160
IIGLLLLITT VILSLRLCSA MKQTDYQQVQ SCALPTDAL
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2243	1	666.2803	-55.46	2	56.5	21.7	1	763-773	R.GERHGDIFMNR.T	

Detailed Protein Report

Protein 809: probable ATP-dependent RNA helicase DDX46 [Homo sapiens]

Accession: gi|41327773
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl, Oxidation

Score: 21.7
MW [kDa]: 117.3
pI: 9.9
Sequence Coverage [%]: 3.4
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
1720	1	863.0927	-49.60	3	50.2	11.0	2	366-388	K.GCPKPIKSWVQCGISMKILNSLK.K	Carbamidomethyl: 2
1054	1	752.4550	172.69	2	42.8	10.7	0	534-545	R.MFDMGFEPQVMR.I	Oxidation: 1

Detailed Protein Report

Protein 810: PREDICTED: uncharacterized protein LOC285556 isoform X1 [Homo sapiens]

Accession:	gi|578809699	**Score:**	21.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	190.0
Database Date:	2015-11-30	**pI:**	9.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.0
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578809701	refseq_human (refseq_human_20140103.fasta)	PREDICTED: uncharacterized protein LOC285556 isoform X2 [Homo sapiens]

Detailed Protein Report

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1275	1	874.2865	-135.51	2	45.6	10.1	1	334-352	K.GGGGGGAGDGTECRDIIAK.S	Carbamidomethyl: 13

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Detailed Protein Report

Protein 811: PREDICTED: homeobox protein Hox-A6 isoform X1 [Homo sapiens]

Accession:	gi|578813472	**Score:**	21.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	23.6
Database Date:	2015-11-30	**pI:**	12.3
		Sequence Coverage [%]:	16.2
		No. of unique Peptides:	1

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	

Detailed Protein Report

Protein 812: PREDICTED: sister chromatid cohesion protein PDS5 homolog B isoform X3 [Homo sapiens]

Accession: gi|530402178
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 21.7
MW [kDa]: 160.7
pI: 9.2
Sequence Coverage [%]: 1.9
No. of unique Peptides: 2

10	20	30	40	50	60	70	80
MAHSKTRTND	GKITYPPGVK	EISDKISKEE	MVRRLKMVVK	TFMDMDQDSE	EEKELYLNLA	LHLASDFFLK	HPDKDVRLLV
90	100	110	120	130	140	150	160
ACCLADIFRI	YAPEAPYTSP	DKLKDIFMFI	TRQLKGLEDT	KSPQFNRYFY	LLENIAWVKS	YNICFELEDS	NEIFTQLYRT
170	180	190	200	210	220	230	240
LFSVINNGHN	QKVHMHMVDL	MSSIICEGDT	VSQELLDTVL	VNLVPAHKNL	NKQAYDLAKA	LLKRTAQAIE	PYITNFFNQV
250	260	270	280	290	300	310	320
LMLGKTSISD	LSEHVFDLIL	ELYNIDSHLL	LSVLPQLEFK	LKSNDNEERL	QVVKLLAKMF	GAKDSELASQ	NKPLWQCYLG
330	340	350	360	370	380	390	400
RFNDIHVPIR	LECVKFASHC	LMNHPDLAKD	LTEYLKVRSH	DPEEAIRHDV	IVSIVTAAKK	DILLVNDHLL	NFVRERTLDK
410	420	430	440	450	460	470	480
RWRVRKEAMM	GLAQIYKKYA	LQSAAGKDAA	KQIAWIKDKL	LHIYYQNSID	DRLLVERIFA	QYMVPHNLET	TERMKCLYYL
490	500	510	520	530	540	550	560
YATLDLNAVK	ALNEMWKCQN	LLRHQVKDLL	DLIKQPKTDA	SVKAIFSKVM	VITRNLPDPG	KAQDFMKKFT	QVLEDDEKIR
570	580	590	600	610	620	630	640
KQLEVLVSPT	CSCKQAEGCV	REITKKLGNP	KQPTNPFLEM	IKFLLERIAP	VHIDTESISA	LIKQVNKSID	GTADDEDEGV
650	660	670	680	690	700	710	720
PTDQAIRAGL	ELLKVLSFTH	PISFHSAETF	ESLLACLKMD	DEKVAEAALQ	IFKNTGSKIE	EDFPHIRSAL	LPVLHHKSKK
730	740	750	760	770	780	790	800
GPPRQAKYAI	HCIHAIFSSK	ETQFAQIFEP	LHKSLDPSNL	EHLITPLVTI	GHIALLAPDQ	FAAPLKSLVA	TFIVKDLLMN
810	820	830	840	850	860	870	880
DRLPGKKTTK	LWVPDEEVSP	ETMVKIQAIK	MMVRWLLGMK	NNHSKSGTST	LRLLTTILHS	DGDLTEQGKI	SKPDMSRLRL
890	900	910	920	930	940	950	960
AAGSAIVKLA	QEPCYHEIIT	LEQYQLCALA	INDECYQVRQ	VFAQKLHKGL	SRLRLPLEYM	AICALCAKDP	VKERRAHARQ
970	980	990	1000	1010	1020	1030	1040
CLVKNINVRR	EYLKQHAAVS	EKLLSLLPEY	VVPYTIHLLA	HDPDYVKVQD	IEQLKDVKEC	LWFVLEILMA	KNENNSHAFI
1050	1060	1070	1080	1090	1100	1110	1120
RKMVENIKQT	KDAQGPDDAK	MNEKLYTVCD	VAMNIIMSKS	TTYSLESPKD	PVLPARFFTQ	PDKNFSNTKN	YLPPEMKSFF
1130	1140	1150	1160	1170	1180	1190	1200
TPGKPKTTNV	LGAVNKPLSS	AGKQSQTKSS	RMETVSNASS	SSNPSSPGRI	KGRLDSSEMD	HSENEDYTMS	SPLPGKKSDK
1210	1220	1230	1240	1250	1260	1270	1280
RDDSDLVRSE	LEKPRGRKKT	PVTEQEEKLG	MDDLTKLVQE	QKPKGSQRSR	KRGHTASESD	EQQWPEEKRL	KEDILENEDE
1290	1300	1310	1320	1330	1340	1350	1360
QNSPPKKGKR	GRPPKPLGGG	TPKEEPTMKT	SKKGSKKKSG	PPAPEEEEEE	ERQSGNTEQK	SKSKQHRVSR	RAQQSRVGRS
1370	1380	1390	1400	1410	1420		
KQAATKENDS	SEEVDVFQGS	SPVDDIPQEE	TEEEEVSTVN	VRRRSAKRER	R		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
504	1	699.9329	104.76	2	34.9	11.3	1	406-417	R.KEAMMGLAQIYK.K	Oxidation: 4
1604	1	882.0680	124.94	2	48.8	10.4	0	476-490	K.CLYYLYATLDLNAVK.A	

Detailed Protein Report

Protein 813: OTU domain-containing protein 7A [Homo sapiens]

Accession:	gi|18702331	**Score:**	21.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	100.6
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
MVSSVLPNPT	SAECWAALLH	DPMTLDMDAV	LSDFVRSTGA	EPGLARDLLE	GKNWDLTAAL	SDYEQLRQVH	TANLPHVFNE
90	100	110	120	130	140	150	160
GRGPKQPERE	PQPGHKVERP	CLQRQDDIAQ	EKRLSRGISH	ASSAIVSLAR	SHVASECNNE	QFPLEMPIYT	FQLPDLSVYS
170	180	190	200	210	220	230	240
EDFRSFIERD	LIEQATMVAL	EQAGRLNWWS	TVCTSCKRLL	PLATTGDGNC	LLHAASLGMW	GFHDRDLVLR	KALYTMMRTG
250	260	270	280	290	300	310	320
AEREALKRRW	RWQQTQQNKE	EEWEREWTEL	LKLASSEPRT	HFSKNGGTGG	GVDNSEDPVY	ESLEEFHVFV	LAHILRRPIV
330	340	350	360	370	380	390	400
VVADTMLRDS	GGEAFAPIPF	GGIYLPLEVP	PNRCHCSPLV	LAYDQAHFSA	LVSMEQRDQQ	REQAVIPLTD	SEHKLLPLHF
410	420	430	440	450	460	470	480
AVDPGKDWEW	GKDDNDNARL	AHLILSLEAK	LNLLHSYMNV	TWIRIPSETR	APLAQPESPT	ASAGEDVQSL	ADSLDSDRDS
490	500	510	520	530	540	550	560
VCSNSNSNNG	KNGKDKEKEK	QRKEKDKTRA	DSVANKLGSF	SKTLGIKLKK	NMGGLGGLVH	GKMGRANSAN	GKNGDSAERG
570	580	590	600	610	620	630	640
KEKKAKSRKG	SKEESGASAS	TSPSEKTTPS	PTDKAAGASP	AEKGGGPRGD	AWKYSTDVKL	SLNILRAAMQ	GERKFIFAGL
650	660	670	680	690	700	710	720
LLTSHRHQFH	EEMIGYYLTS	AQERFSAEQE	QRRRDAATAA	AAAAAAAAAT	AKRPPRRPET	EGVPVPERAS	PGPPTQLVLK
730	740	750	760	770	780	790	800
LKERPSPGPA	AGRAARAAAG	GTASPGGGAR	RASASGPVPG	RSPPAPARQS	VIHVQASGAR	DEACAPAVGA	LRPCATYPQQ
810	820	830	840	850	860	870	880
NRSLSSQSYS	PARAAALRTV	NTVESLARAV	PGALPGAAGT	AGAAEHKSQT	YTNGFGALRD	GLEFADADAP	TARSNGECGR
890	900	910	920	930			
GGPGPVQRRC	QRENCAFYGR	AETEHYCSYC	YREELRRRRE	ARGARP			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2849	1	1001.0230	-1.34	2	64.2	10.3	1	68-85	R.QVHTANLPHVFNEGRGPK.Q	

Detailed Protein Report

Protein 814: 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
		Sequence Coverage [%]:	0.7
		No. of unique Peptides:	1

Detailed Protein Report

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2089	1	925.3261	-72.47	1	56.3	10.1	0	1269-1276	K.NMSTEDTK.K	

Detailed Protein Report

Protein 815: protein FAM83F [Homo sapiens]

Accession:	gi|156564372	**Score:**	21.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	55.5
Database Date:	2015-11-30	**pI:**	9.2
		Sequence Coverage [%]:	7.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAESQLNCLD	EAHVNEKVTE	AQAAFYYCER	RRAALEALLG	GGEQAYRERL	KEEQLRDFLS	SPERQALRAA	WSPYEDAVPA
90	100	110	120	130	140	150	160
ANARGKSKAK	AKAPAPAPAE	SGESLAYWPD	RSDTEVPPLD	LGWTDTGFYR	GVSRVTLFTH	PPKDEKAPHL	KQVVRQMIQQ
170	180	190	200	210	220	230	240
AQKVIAVVMD	LFTDGDIFQD	IVDAACKRRV	PVYIILDEAG	VKYFLEMCQD	LQLTDFRIRN	IRVRSVTGVG	FYMPMGRIKG
250	260	270	280	290	300	310	320
TLSSRFLMVD	GDKVATGSYR	FTWSSSHVDR	NLLLLLTGQN	VEPFDTEFRE	LYAISEEVDL	YRQLSLAGRV	GLHYSSTVAR
330	340	350	360	370	380	390	400
KLINPKYALV	SGCRHPPGEM	MRWAARQQRE	AGGNPEGQEE	GASGGESAWR	LESFLKDLVT	VEQVLPPVEP	IPLGELSQKD
410	420	430	440	450	460	470	480
GRMVSHMHRD	LKPKSREAPS	RNGMGEAARG	EAAPARRFSS	RLFSRRAKRP	AAPNGMASSV	STETSEVEFL	TGKRPNENSS
490	500	510					
ADISGKTSPS	SAKPSNCVIS						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1194	1	628.4650	156.14	3	43.4	11.0	2	310-326	R.VGLHYSSTVARKLINPK.Y	

Detailed Protein Report

Protein 816: **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 817: **PREDICTED: mediator of RNA polymerase II transcription subunit 19 isoform X1 [Homo sapiens]**

Accession:	gi|530396419	**Score:**	21.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	28.0
Database Date:	2015-11-30	**pI:**	10.4
		Sequence Coverage [%]:	7.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MKITNGRHGD	SAGAEGTMEN	FTALFGAQAD	PPPPPTALGF	GPGKPPPPPP	PPAGGGPGTA	PPPTAATAPP	GADKSGAGCG
90	100	110	120	130	140	150	160
PFYLMRELPG	STELTGSTNL	ITHYNLEQAY	NKFCGKKVKE	KLSNFLPDLP	GMIDLPGSHD	NSSLRSLIEK	PPILSSSFNP
170	180	190	200	210	220	230	240
ITGTMLAGFR	LHTGPLPEQC	RLMHIQPPKK	KNKHKHKQSR	TQDPVPPETP	SDSDHKKKKK	KKEEDPERKR	KKKEKKKKKN
250	260	270					
RHSPDHPGMG	SSQASSSSSL	R					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1493	1	671.3930	137.00	3	47.4	21.4	0	242-261	R.HSPDHPGMGSSQASSSSSLR.-	

Detailed Protein Report

Protein 818: spectrin beta chain, non-erythrocytic 5 [Homo sapiens]

Accession:	gi|485837026	**Score:**	21.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	416.5
Database Date:	2015-11-30	**pI:**	6.2
		Sequence Coverage [%]:	0.5
		No. of unique Peptides:	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MAGQPHSPRE	LLGAAGHRSR	RPSTELRVPP	SPSLTMDSQY	ETGHIRKLQA	RHMQMQEKTF	TKWINNVFQC	GQAGIKIRNL
90	100	110	120	130	140	150	160
YTELADGIHL	LRLLELISGE	ALPPPSRGRL	RVHFLENSSR	ALAFLRAKVP	VPLIGPENIV	DGDQTLILGL	IWVIILRFQI
170	180	190	200	210	220	230	240
SHISLDKEEF	GASAALLSTK	EALLVWCQRK	TASYTNVNIT	DFSRSWSDGL	GFNALIHAHR	PDLLDYGSLR	PDRPLHNLAF
250	260	270	280	290	300	310	320
AFLVAEQELG	IAQLLDPEDV	AAAQPDERSI	MTYVSLYYHY	CSRLHQGQTV	QRRLTKILLQ	LQETELLQTQ	YEQLVADLLR
330	340	350	360	370	380	390	400
WIAEKQMQLE	ARDFPDSLPA	MRQLLAAFTI	FRTQEKPPRL	QQRGAAEALL	FRLQTALQAQ	NRRPFLPHEG	LGLAELSQCW
410	420	430	440	450	460	470	480
AGLEWAEAAR	SQALQQRLLQ	LQRLETLARR	FQHKAALRES	FLKDAEQVLD	QARAPPASLA	TVEAAVQRLG	MLEAGILPQE
490	500	510	520	530	540	550	560
GRFQALAEIA	DILRQEQYHS	WADVARRQEE	VTVRWQRLLQ	HLQGQRKQVA	DMQAVLSLLQ	EVEAASHQLE	ELQEPARSTA
570	580	590	600	610	620	630	640
CGQQLAEVVE	LLQRHDLLEA	QVSAHGAHVS	HLAQQTAELD	SSLGTSVEVL	QAKARTLAQL	QQSLVALVRA	RRALLEQTLQ
650	660	670	680	690	700	710	720
RAEFLRNCEE	EEAWLKECGQ	RVGNAALGRD	LSQIAGALQK	HKALEAEVHR	HQAVCVDLVR	RGRDLSARRP	PTQPDPGERA
730	740	750	760	770	780	790	800
EAVQGGWQLL	QTRVVGRGAR	LQTALLVLQY	FADAAEAASW	LRERRSSLER	ASCGQDQAAA	ETLLRRHVRL	ERVLRAFAAE
810	820	830	840	850	860	870	880
LRRLEEQGRA	ASARASLFTV	NSALSPPGES	LRNPGPWSEA	SCHPGPGDAW	KMALPAEPDP	DFDPNTILQT	QDHLSQDYES
890	900	910	920	930	940	950	960
LRALAQLRRA	RLEEAMALFG	FCSSCGELQL	WLEKQTVLLQ	RVQPQADTLE	VMQLKYENFL	TALAVGKGLW	AEVSSSAEQL
970	980	990	1000	1010	1020	1030	1040
RQRYPGNSTQ	IQRQQEELSQ	RWGQLEALKR	EKAVQLAHSV	EVCSFLQECG	PTQVQLRDVL	LQLEALQPGS	SEDTCHALQL
1050	1060	1070	1080	1090	1100	1110	1120
AQKKTLVLER	RVHFLQSVVV	KVEEPGYAES	QPLQGQVETL	QGLLKQVQEQ	VAQRARRQAE	TQARQSFLQE	SQQLLLWAES
1130	1140	1150	1160	1170	1180	1190	1200
VQAQLRSKEV	SVDVASAQRL	LREHQDLLEE	IHLWQERLQQ	LDAQSQPMAA	LDCPDSQEVP	NTLRVLGQQG	QELKVLWEQR
1210	1220	1230	1240	1250	1260	1270	1280
QQWLQEGLEL	QKFGREVDGF	TATCANHQAW	LHLDNLGEDV	REALSLLQQH	REFGRLLSTL	GPRAEALRAH	GEKLVQSQHP
1290	1300	1310	1320	1330	1340	1350	1360
AAHTVREQLQ	SIQAQWTRLQ	GRSEQRRRQL	LASLQLQEWK	QDVAELMQWM	EEKGLMAAHE	PSGARRNILQ	TLKRHEAAES
1370	1380	1390	1400	1410	1420	1430	1440
ELLATRRHVE	ALQQVGRELL	SRRPCGQEDI	QTRLQGLRSK	WEALNRKMTE	RGDELQQAGQ	QEQLLRQLQD	AKEQLEQLEG
1450	1460	1470	1480	1490	1500	1510	1520
ALQSSETGQD	LRSSQRLQKR	HQQLESESRT	LAAKMAALAS	MAHGMAASPA	ILEETQKHLR	RLELLQGHLA	IRGLQLQASV
1530	1540	1550	1560	1570	1580	1590	1600
ELHQFCHLSN	MELSWVAEHM	PHGSPTSYTE	CLNGAQSLHR	KHKELQVEVK	AHQGQVQRVL	SSGRSLAASG	HPQAQHIVEQ
1610	1620	1630	1640	1650	1660	1670	1680
CQELEGHWAE	LERACEARAQ	CLQQAVTFQQ	YFLDVSELEG	WVEEKRPLVS	SRDYGRDEAA	TLRLINKHQA	LQEELAIYWS
1690	1700	1710	1720	1730	1740	1750	1760
SMEELDQTAQ	TLTGPEVPEQ	QRVVQERLRE	QLRALQELAA	TRDRELEGTL	RLHEFLREAE	DLQGWLASQK	QAAKGGESLG
1770	1780	1790	1800	1810	1820	1830	1840
EDPEHALHLC	TKFAKFQHQV	EMGSQRVAAC	RLLAESLLER	GHSAGPMVRQ	RQQDLQTAWS	ELWELTQARG	HALRDTETTL
1850	1860	1870	1880	1890	1900	1910	1920
RVHRDLLEVL	TQVQEKATSL	PNNVARDLCG	LEAQLRSHQG	LERELVGTER	QLQELLETAG	RVQKLCPGPQ	AHAVQQRQQA
1930	1940	1950	1960	1970	1980	1990	2000
VTQAWAVLQR	RMEQRRAQLE	RARLLARFRT	AVRDYASWAA	RVRQDLQVEE	SSQEPSSGPL	KLSAHQWLRA	ELEAREKLWQ
2010	2020	2030	2040	2050	2060	2070	2080
QATQLGQQAL	LAAGTPTKEV	QEELRALQDQ	RDQVYQTWAR	KQERLQAEQQ	EQLFLRECGR	LEEILAAQEV	SLKTSALGSS
2090	2100	2110	2120	2130	2140	2150	2160
VEEVEQLIRK	HEVFLKVLTA	QDKKEAALRE	RLKTLRRPRV	RDRLPILLQR	RMRVKELAES	RGHALHASLL	MASFTQAATQ
2170	2180	2190	2200	2210	2220	2230	2240

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	

Detailed Protein Report

Protein 819: **nicotinate-nucleotide pyrophosphorylase [carboxylating] precursor [Homo sapiens]**

Accession:	gi|45269149	**Score:**	21.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	30.8
Database Date:	2015-11-30	**pI:**	5.8
		Sequence Coverage [%]:	10.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDAEGLALLL	PPVTLAALVD	SWLREDCPGL	NYAALVSGAG	PSQAALWAKS	PGVLAGQPFF	DAIFTQLNCQ	VSWFLPEGSK
90	100	110	120	130	140	150	160
LVPVARVAEV	RGPAHCLLLG	ERVALNTLAR	CSGIASAAAA	AVEAARGAGW	TGHVAGTRKT	TPGFRLVEKY	GLLVGGAASH
170	180	190	200	210	220	230	240
RYDLGGLVMV	KDNHVVAAGG	VEKAVRAARQ	AADFALKVEV	ECSSLQEAVQ	AAEAGADLVL	LDNFKPEELH	PTATVLKAQF
250	260	270	280	290	300		
PSVAVEASGG	ITLDNLPQFC	GPHIDVISMG	MLTQAAPALD	FSLKLFAKEV	APVPKIH		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2650	1	835.3977	-89.98	2	61.4	11.1	1	146-161	R.LVEKYGLLVGGAASHR.Y	

Detailed Protein Report

Protein 820: A disintegrin and metalloproteinase with thrombospondin motifs 2 isoform 1 preproprotein [Homo sapiens]

Accession:	gi|110825974	**Score:**	21.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	134.7
Database Date:	2015-11-30	**pI:**	6.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.3
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MDPPAGAARR	LLCPALLLLL	LLLPPPLLPP	PPPPANARLA	AAADPPGGPL	GHGAERILAV	PVRTDAQGRL	VSHVVSAATS
90	100	110	120	130	140	150	160
RAGVRARRAA	PVRTPSFPGG	NEEEPGSHLF	YNVTVFGRDL	HLRLRPNARL	VAPGATMEWQ	GEKGTTRVEP	LLGSCLYVGD
170	180	190	200	210	220	230	240
VAGLAEASSV	ALSNCDGLAG	LIRMEEEEFF	IEPLEKGLAA	QEAEQGRVHV	VYRRPPTSPP	LGGPQALDTG	ASLDSLDSLS
250	260	270	280	290	300	310	320
RALGVLEEHA	NSSRRRARRH	AADDDYNIEV	LLGVDDSVVQ	FHGKEHVQKY	LLTLMNIVNE	IYHDESLGAH	INVVLVRIIL
330	340	350	360	370	380	390	400
LSYGKSMSLI	EIGNPSQSLE	NVCRWAYLQQ	KPDTGHDEYH	DHAIFLTRQD	FGPSGMQGYA	PVTGMCHPVR	SCTLNHEDGF
410	420	430	440	450	460	470	480
SSAFVVAHET	GHVLGMEHDG	QGNRCGDEVR	LGSIMAPLVQ	AAFHRFHWSR	CSQQELSRYL	HSYDCLLDDP	FAHDWPALPQ
490	500	510	520	530	540	550	560
LPGLHYSMNE	QCRFDFGLGY	MMCTAFRTFD	PCKQLWCSHP	DNPYFCKTKK	GPPLDGTMCA	PGKHCFKGHC	IWLTPDILKR
570	580	590	600	610	620	630	640
DGSWGAWSPF	GSCSRTCGTG	VKFRTRQCDN	PHPANGGRTC	SGLAYDFQLC	SRQDCPDSLA	DFREEQCRQW	DLYFEHGDAQ
650	660	670	680	690	700	710	720
HHWLPHEHRD	AKERCHLYCE	SRETGEVVSM	KRMVHDGTRC	SYKDAFSLCV	RGDCRKVGCD	GVIGSSKQED	KCGVCGGDNS
730	740	750	760	770	780	790	800
HCKVVKGTFT	RSPKKHGYIK	MFEIPAGARH	LLIQEVDATS	HHLAVKNLET	GKFILNEEND	VDASSKTFIA	MGVEWEYRDE
810	820	830	840	850	860	870	880
DGRETLQTMG	PLHGTITVLV	IPVGDTRVSL	TYKYMIHEDS	LNVDDNNVLE	EDSVVYEWAL	KKWSPCSKPC	GGGSQFTKYG
890	900	910	920	930	940	950	960
CRRRLDHKMV	HRGFCAALSK	PKAIRRACNP	QECSQPVWVT	GEWEPCSQTC	GRTGMQVRSV	RCIQPLHDNT	TRSVHAKHCN
970	980	990	1000	1010	1020	1030	1040
DARPESRRAC	SRELCPGRWR	AGPWSQCSVT	CGNGTQERPV	LCRTADDSFG	ICQEERPETA	RTCRLGPCPR	NISDPSKKSY
1050	1060	1070	1080	1090	1100	1110	1120
VVQWLSRPDP	DSPIRKISSK	GHCQGDKSIF	CRMEVLSRYC	SIPGYNKLCC	KSCNLYNNLT	NVEGRIEPPP	GKHNDIDVFM
1130	1140	1150	1160	1170	1180	1190	1200
PTLPVPTVAM	EVRPSPSTPL	EVPLNASSTN	ATEDHPETNA	VDEPYKIHGL	EDEVQPPNLI	PRRPSPYEKT	RNQRIQELID
1210	1220						
EMRKKEMLGK	F						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1134	1	984.4501	-53.47	2	42.9	11.3	1	544-559	K.HCFKGHCIWLTPDILK.R	Carbamidomethyl: 2
2148	1	766.2823	-164.03	2	55.4	10.0	2	1183-1194	R.RPSPYEKTRNQR.I	

Detailed Protein Report

Protein 821: **PREDICTED: protocadherin Fat 3 isoform X1 [Homo sapiens]**

Accession:	gi|578821974	**Score:**	21.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	382.5
Database Date:	2015-11-30	**pI:**	4.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	0.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGSYWLTVYA	TDRGVVPLYS	TIEVYIEVED	VNDNAPLTSE	PIYYPVVMEN	SPKDVSVIQI	QAEDPDSSSN	EKLTYRITSG
90	100	110	120	130	140	150	160
NPQNFFAINI	KTGLITTTSR	KLDREQQAEH	FLEVTVTDGG	PSPKQSTIWV	VVQVLDENDN	KPQFPEKVYQ	IKLPERDRKK
170	180	190	200	210	220	230	240
RGEPIYRAFA	FDRDEGPNAE	ISYSIVDGND	DGKFFIDPKT	GMVSSRKQFT	AGSYDILTIK	AVDNGRPQKS	STARLHIEWI
250	260	270	280	290	300	310	320
KKPPPSPIPL	TFDEPFYNFT	VMESDRVTEI	VGVVSVQPAN	TPLWFDIVGG	NFDSAFDAEK	GVGTIVIAKP	LDAEQRSIYN
330	340	350	360	370	380	390	400
MSVEVTDGTN	VAVTQVFIKV	LDNNDNGPEF	SQPNYDVTIS	EDVLPDTEIL	QIEATDRDEK	HKLSYTVHSS	IDSISMRKFR
410	420	430	440	450	460	470	480
IDPSTGVLYT	AERLDHEAQD	KHILNIMVRD	QEFPYRRNLA	RVIVNVEDAN	DHSPYFTNPL	YEASVFESAA	LGSAVLQVTA
490	500	510	520	530	540	550	560
LDKDKGENAE	LIYTIEAGNT	GNMFKIEPVL	GIITICKEPD	MTTMGQFVLS	IKVTDQGSPP	MSATAIVRIS	VTMSDNSHPK
570	580	590	600	610	620	630	640
FIHKDYQAEV	NENVDIGTSV	ILISAISQST	LIYEVKDGDI	NGIFTINPYS	GVITTQKALD	YERTSSYQLI	IQATNMAGMA
650	660	670	680	690	700	710	720
SNATVNIQIV	DENDNAPVFL	FSQYSGSLSE	AAPINSIVRS	LDNSPLVIRA	TDADSNRNAL	LVYQIVESTA	KKFFTVDSST
730	740	750	760	770	780	790	800
GAIRTIANLD	HETIAHFHFH	VHVRDSGSPQ	LTAESPVEVN	IEVTDVNDNP	PVFTQAVFET	ILLLPTYVGV	EVLKVSATDP
810	820	830	840	850	860	870	880
DSEVPPELTY	SLMEGSLDHF	LIDSNSGVLT	IKNNNLSKDH	YMLIVKVSDG	KFYSTSMVTI	MVKEAMDSGL	HFTQSFYSTS
890	900	910	920	930	940	950	960
ISENNTNITK	VAIVNAVGNR	LNEPLKYSIL	NPGNKFKIKS	TSGVIQTTGV	PFDREEQELY	ELVVEASREL	DHLRVARVVV
970	980	990	1000	1010	1020	1030	1040
RVNIEDINDN	SPVFVGLPYY	AAVQVDAEPG	TLIYQVTAID	KDKGPNGEVT	YVLQDDYGHF	EINPNSGNVI	LKEAFNSDLS
1050	1060	1070	1080	1090	1100	1110	1120
NIEYGVTILA	KDGGKPSLST	SVELPITIVN	KAMPVFDKPF	YTASVNEDIR	MNTPILSINA	TSPEGQGIIY	IIIDGDPFKQ
1130	1140	1150	1160	1170	1180	1190	1200
FNIDFDTGVL	KVVSPLDYEV	TSAYKLTIRA	SDALTGARAE	VTVDLLVNDV	NDNPPIFDQP	TYNTTLSEAS	LIGTPVLQVV
1210	1220	1230	1240	1250	1260	1270	1280
SIDADSENNK	MVHYQIVQDT	YNSTDYFHID	SSSGLILTAR	MLDHELVQHC	TLKVRSIDSG	FPSLSSEVLV	HIYISDVNDN
1290	1300	1310	1320	1330	1340	1350	1360
PPVFNQLIYE	SYVSELAPRG	HFVTCVQASD	ADSSDFDRLE	YSILSGNDRT	SFLMDSKSGV	ITLSNHRKQR	MEPLYSLNVS
1370	1380	1390	1400	1410	1420	1430	1440
VSDGLFTSTA	QVHIRVLGAN	LYSPAFSQST	YVAEVRENVA	AGTKVIHVRA	TDGDPGTYGQ	ISYAIINDFA	KDRFLIDSNG
1450	1460	1470	1480	1490	1500	1510	1520
QVITTERLDR	ENPLEGDVSI	FVRALDGGGR	TTFCTVRVIV	VDENDNAPQF	MTVEYRASVR	ADVGRGHLVT	QVQAIDPDDG
1530	1540	1550	1560	1570	1580	1590	1600
ANSRITYSLY	SEASVSVADL	LEIDPDNGWM	VTKGNFNQLK	NTVLSFFVKA	VDGGIPVKHS	LIPVYIHVLP	PETFLPSFTQ
1610	1620	1630	1640	1650	1660	1670	1680
SQYSFTIAED	TAIGSTVDTL	RILPSQNVWF	STVNGERPEN	NKGGIFVIEQ	ETGTIKLDKR	LDRETSPAFH	FKVAATIPLD
1690	1700	1710	1720	1730	1740	1750	1760
KVDIVFTVDV	DIKVLDLNDN	KPVFETSSYD	TIIMEGMPVG	TKLTQVRAID	MDWGANGQVT	YSLHSDSQPE	KVMEAFNIDS
1770	1780	1790	1800	1810	1820	1830	1840
NTGWISTLKD	LDHETDPTFT	FSVVASDLGE	AFSLSSTALV	SVRVTDINDN	APVFAQEVYR	GNVKESDPPG	EVVAVLSTWD
1850	1860	1870	1880	1890	1900	1910	1920
RDTSDVNRQV	SYHITGGNPR	GRFALGLVQS	EWKVYVKRPL	DREEQDIYFL	NITATDGLFV	TQAMVEVSVS	DVNDNSPVCD
1930	1940	1950	1960	1970	1980	1990	2000
QVAYTALLPE	DIPSNKIILK	VSAKDADIGS	NGYIRYSLYG	SGNSEFFLDP	ESGELKTLAL	LDRERIPVYS	LMAKATDGGG
2010	2020	2030	2040	2050	2060	2070	2080
RFCQSNIHLI	LEDVNDNPPV	FSSDHYNTCV	YENTATKALL	TRVQAVDPDI	GINRKVVYSL	ADSAGGVFSI	DSSSGIIILE
2090	2100	2110	2120	2130	2140	2150	2160
QPLDREQQSS	YNISVRATDQ	SPGQSLSSLT	TVTITVLDIN	DNPPVFERRD	YLVTVPEDTS	PGTQVLAVFA	TSKDIGTNAE
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
1036	2	954.9665	-9.91	2	41.7	11.1	1	847-863	K.VSDGKFYSTSMVTIMVK.E	Oxidation: 15

BRUKER

Detailed Protein Report

Protein 822: **syntaphilin [Homo sapiens]**

Accession:	gi|38202246	**Score:**	21.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	53.5
Database Date:	2015-11-30	**pI:**	5.3
		Sequence Coverage [%]:	6.1
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MAMSLPGSRR	TSAGSRRRTS	PPVSVRDAYG	TSSLSSSSNS	GSYKGSDSSP	TPRRSMKYTL	CSDNHGIKPP	TPEQYLTPLQ
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
QKEVCIRHLK	ARLKDTQDRL	QDRDTEIDDL	KTQLSRMQED	WIEEECHRVE	AQLALKEARK	EIKQLKQVID	TVKNNLIDKD
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
KGLQKYFVDI	NIQNKKLETL	LHSMEVAQNG	MAKEDGTGES	AGGSPARSLT	RSSTYTKLSD	PAVCGDRQPG	DPSSGSAEDG
250	**260**	**270**	**280**	**290**	**300**	**310**	**320**
ADSGFAAADD	TLSRTDALEA	SSLLSSGVDC	GTEETSLHSS	FGLGPRFPAS	NTYEKLLCGM	EAGVQASCMQ	ERAIQTDFVQ
330	**340**	**350**	**360**	**370**	**380**	**390**	**400**
YQPDLDTILE	KVTQAQVCGT	DPESGDRCPE	LDAHPSGPRD	PNSAVVVTVG	DELEAPEPIT	RGPTPQRPGA	NPNPGQSVSV
410	**420**	**430**	**440**	**450**	**460**	**470**	**480**
VCPMEEEEEA	AVAEKEPKSY	WSRHYIVDLL	AVVVPAVPTV	AWLCRSQRRQ	GQPIYNISSL	LRGCCTVALH	SIRRISCRSL
490	**500**						
SQPSPSPAGG	GSQL						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1925	1	899.3727	-21.77	2	52.7	10.9	0	27-44	R.DAYGTSSLSSSSNSGSYK.G	
605	1	730.9957	178.78	2	36.2	10.4	1	100-111	R.LQDRDTEIDDLK.T	

Detailed Protein Report

Protein 823: 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

mdown:qdown	**Median:**	0.39	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	2.21	**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	mdown:qdown 0.39 Wdown:Qdown 2.21

Detailed Protein Report

Protein 824: 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 825: **ubiquitin-associated and SH3 domain-containing protein A isoform 3 [Homo sapiens]**

Accession:	gi|343478263	**Score:**	21.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	59.1
Database Date:	2015-11-30	**pI:**	9.3
Modification(s):	Oxidation	**Sequence Coverage [%]:**	8.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAAGETQLYA	KVSNKLKSRS	SPSLLEPLLA	MGFPVHTALK	ALAATGRKTA	EEALAWLHDH	CNDPSLDDPI	PQEYALFLCP
90	100	110	120	130	140	150	160
TGPLLEKLQE	FWRESKRQCA	KNRAHEVFPH	VTLCDFFTCE	DQKVECLYEA	LKRAGDRLLG	SFPTAVPLAL	HSSISYLGFF
170	180	190	200	210	220	230	240
VSGSPADVIR	EFAMTFATEA	SLLADCSVKP	CTKQLHLTLA	HKFYPHHQRT	LEQLARAIPL	GHSCQWTAAL	YSRDMRFVHY
250	260	270	280	290	300	310	320
QTLRALFQYK	PQNVDELTLS	PGDYIFVDPT	QQDEASEGWV	IGISQRTGCR	GFLPENYTDR	ASESDTWVKH	RMYTFSLATD
330	340	350	360	370	380	390	400
LNSRKDGEAS	SRCSGEFLPQ	TARSLSSLQA	LQATVARKSV	LVVRHGERVD	QIFGKAWLQQ	CSTPDGKYYR	PDLNFPCSLP
410	420	430	440	450	460	470	480
RRSRGIKDFE	NDPPLSSCGI	FQSRIAGDAL	LDSGIRISSV	FASPALRCVQ	TAKLILEELK	LEKKIKIRVE	PGIFEWTKWE
490	500	510	520	530			
AGKTTPTLMS	LEELKEANFN	IDTDYRSLPW	ACASVKKIKR	KENGSW			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
869	1	955.4602	-71.25	3	39.3	10.1	1	20-47	R.SSPSLLEPLLAMGFPVHTALKALAATGR.K	Oxidation: 12

Detailed Protein Report

Protein 826: sodium-dependent phosphate transport protein 2B isoform b [Homo sapiens]

Accession:	gi|295789158	**Score:**	21.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	75.5
Database Date:	2015-11-30	**pI:**	9.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.3
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|295789160	refseq_human (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 827: PREDICTED: probable helicase with zinc finger domain isoform X6 [Homo sapiens]

Accession:	gi|578831752	**Score:**	21.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	177.5
Database Date:	2015-11-30	**pI:**	9.0
		Sequence Coverage [%]:	1.4
		No. of unique Peptides:	1

Quantitation

Wdown:Qdown **Median:** 0.22 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MHAKQQLVTT	AKRWDSSSKT	IIDFEPNETT	DLEKSLLIRY	QIPLSADQLF	TQSVLDKSLT	KSNYQSRLHD	LLYIEEIAQY
90	100	110	120	130	140	150	160
KEISNTSGAS	TSRILLQDTT	NVTRGFSCCS	KLFNLKVQLQ	ILASFMLTGV	SGGAKYAQNG	QLFGRFKLTE	TLSEDTLAGR
170	180	190	200	210	220	230	240
LVMTKVNAVY	LLPVPKQKLV	QTQGTKEKVY	EATIEEKTKE	YIFLRLSREC	CEELNLRPDC	DTQVELQFQL	NRLPLCEMHY
250	260	270	280	290	300	310	320
ALDRIKDNGV	LFPDISMTPT	IPWSPNRQWD	EQLDPRLNAK	QKEAVLAITT	PLAIQLPPVL	IIGPYGTGKT	FTLAQAVKHI
330	340	350	360	370	380	390	400
LQQQETSRIL	ICTHSNSAAD	LYIKDYLHPY	VEAGNPQARP	LRVYFRNRWV	KTVHPVVHQY	CLISSAHSTF	QMPQKEDILK
410	420	430	440	450	460	470	480
HRVVVVTLNT	SQYLCQLDLE	PGFFTHILLD	EAAQAMECET	IMPLALATQN	TRIVLAGDHM	QLSPFVYSEF	ARERNLHVSL
490	500	510	520	530	540	550	560
LDRLYEHYPA	EFPCRILLCE	NYRSHEAIIN	YTSELFYEGK	LMASGKQPAH	KDFYPLTFFT	ARGEDVQEKN	STAFYNNAEV
570	580	590	600	610	620	630	640
FEVVERVEEL	RRKWPVAWGK	LDDGSIGVVT	PYADQVFRIR	AELRKKRLSD	VNVERVLNVQ	GKQFRVLFLS	TVRTRHTCKH
650	660	670	680	690	700	710	720
KQTPIKKKEQ	LLEDSTEDLD	YGFLSNYKLL	NTAITRAQSL	VAVVGDPIAL	CSIGRCRKFW	ERFIALCHEN	SSLHGITFEQ
730	740	750	760	770	780	790	800
IKAQLEALEL	KKTYVLNPLA	PEFIPRALRL	QHSGSTNKQQ	QSPPKGKSLH	HTQNDHFQND	GIVQPNPSVL	IGNPIRAYTP
810	820	830	840	850	860	870	880
PPPLGPHPNL	GKSPSPVQRI	DPHTGTSILY	VPAVYGGNVV	MSVPLPVPWT	GYQGRFAVDP	RIITHQAAMA	YNMNLLQTHG
890	900	910	920	930	940	950	960
RGSPIPYGLG	HHPPVTIGQP	QNQHQEKDQH	EQNRNGKSDT	NNSGPEINKI	RTPEKKPTEP	KQVDLESNPQ	NRSPESRPSV
970	980	990	1000	1010	1020	1030	1040
VYPSTKFPRK	DNLNPRHINL	PLPAPHAQYA	IPNRHFHPLP	QLPRPPFPIP	QQHTLLNQQQ	NNLPEQPNQI	PPQPNQVVQQ
1050	1060	1070	1080	1090	1100	1110	1120
QSQLNQQPQQ	PPPQLSPAYQ	AGPNNAFFNS	AVAHRPQSPP	AEAVIPEQQP	PPMLQEGHSP	LRAIAQPGPI	LPSHLNSFID
1130	1140	1150	1160	1170	1180	1190	1200
ENPSGLPIGE	ALDRIHGSVA	LETLRQQQAR	FQQWSEHHAF	LSQGSAPYPH	HHHPHLQHLP	QPPLGLHQPP	VRADWKLTSS
1210	1220	1230	1240	1250	1260	1270	1280
AEDEVETTYS	RFQDLIRELS	HRDQSETREL	AEMPPPQSRL	LQYRQVQSRS	PPAVPSPPSS	TDHSSHFSNF	NDNSRDIEVA
1290	1300	1310	1320	1330	1340	1350	1360
SNPAFPQRLP	PQIFNSPFSL	PSEHLAPPPL	KYLAPDGAWT	FANLQQNHLM	GPGFPYGLPP	LPHRPPQNPF	VQIQNHQHAI
1370	1380	1390	1400	1410	1420	1430	1440
GQEPFHPLSS	RTVSSSSLPS	LEEYEPRGPG	RPLYQRRISS	SSVQPCSEEV	STPQDSLAQC	KELQDHSNQS	SFNFSSPESW
1450	1460	1470	1480	1490	1500	1510	1520
VNTTSSTPYQ	NIPCNGSSRT	AQPRELIAPP	KTVKPPEDQL	KSENLEVSSS	FNYSVLQHLG	QFPPLMPNKQ	IAESANSSSP
1530	1540	1550	1560	1570	1580		
QSSAGGKPAM	SYASALRAPP	KPRPPPEQAK	KSSDPLSLFQ	ELSLGSSSGS	NGFYSYFK		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1212	1	533.7834	-38.28	2	43.8	10.2	0	475-483	R.NLHVSLLDR.L		Wdown:Qdown 0.22

Detailed Protein Report

Protein 828: retinal guanylyl cyclase 2 [Homo sapiens]

Accession:	gi|134152694	**Score:**	21.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	124.8
Database Date:	2015-11-30	**pI:**	7.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.5
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	1.00	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.78	**CV:**	0.00 %	**No. of Peptides:**	1

10	20	30	40	50	60	70	80
MFLGLGRFSR	LVLWFAAFRK	LLGHHGLASA	KFLWCLCLLS	VMSLPQQVWT	LPYKIGVVGP	WACDSLFSKA	LPEVAARLAI
90	100	110	120	130	140	150	160
ERINRDPSFD	LSYSFEYVIL	NEDCQTSRAL	SSFISHHQMA	SGFIGPTNPG	YCEAASLLGN	SWDKGIFSWA	CVNYELDNKI
170	180	190	200	210	220	230	240
SYPTFSRTLP	SPIRVLVTVM	KYFQWAHAGV	ISSDEDIWVH	TANRVASALR	SHGLPVGVVL	TTGQDSQSMR	KALQRIHQAD
250	260	270	280	290	300	310	320
RIRIIIMCMH	SALIGGETQM	HLLECAHDLK	MTDGTYVFVP	YDALLYSLPY	KHTPYRVLRN	NPKLREAYDA	VLTITVESQE
330	340	350	360	370	380	390	400
KTFYQAFTEA	AARGEIPEKL	EFDQVSPLFG	TIYNSIYFIA	QAMNNAMKEN	GQAGAASLVQ	HSRNMQFHGF	NQLMRTDSNG
410	420	430	440	450	460	470	480
NGISEYVILD	TNLKEWELHS	TYTVDMEMEL	LRFGGTPIHF	PGGRPPRADA	KCWFAEGKIC	HGGIDPAFAM	MVCLTLLIAL
490	500	510	520	530	540	550	560
LSINGFAYFI	RRRINKIQLI	KGPNRILLTL	EDVTFINPHF	GSKRGSRASV	SFQITSEVQS	GRSPRLSFSS	GSLTPATYEN
570	580	590	600	610	620	630	640
SNIAIYEGDW	VWLKKFSLGD	FGDLKSIKSR	ASDVFEMMKD	LRHENINPLL	GFFYDSGMFA	IVTEFCSRGS	LEDILTNQDV
650	660	670	680	690	700	710	720
KLDWMFKSSL	LLDLIKGMKY	LHHREFVHGR	LKSRNCVVDG	RFVLKVTDYG	FNDILEMLRL	SEEESSMEEL	LWTAPELLRA
730	740	750	760	770	780	790	800
PRGSRLGSFA	GDVYSFAIIM	QEVMVRGTPF	CMMDLPAQEI	INRLKKPPPV	YRPVVPPEHA	PPECLQLMKQ	CWAEAAEQRP
810	820	830	840	850	860	870	880
TFDEIFNQFK	TFNKGKKTNI	IDSMLRMLEQ	YSSNLEDLIR	ERTEELEIEK	QKTEKLLTQM	LPPSVAESLK	KGCTVEPEGF
890	900	910	920	930	940	950	960
DLVTLYFSDI	VGFTTISAMS	EPIEVVDLLN	DLYTLFDAII	GSHDVYKVET	IGDAYMVASG	LPKRNGSRHA	AEIANMSLDI
970	980	990	1000	1010	1020	1030	1040
LSSVGTFKMR	HMPEVPVRIR	IGLHSGPVVA	GVVGLTMPRY	CLFGDTVNTA	SRMESTGLPY	RIHVSLSTVT	ILQNLSEGYE
1050	1060	1070	1080	1090	1100	1110	
VELRGRTELK	GKGTEETFWL	IGKKGFMKPL	PVPPPVDKDG	QVGHGLQPVE	IAAFQRRKAE	RQLVRNKP	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
190	1	642.1902	-203.56	2	31.6	10.2	1	969-978	K.MRHMPEVPVR.I	Oxidation: 1, 4	mdown:qdown 1.00 Wdown:Qdown 0.78

Protein 829: AT-hook DNA-binding motif-containing protein 1 [Homo sapiens]

Accession:	gi|71274144	**Score:**	21.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	168.2
Database Date:	2015-11-30	**pI:**	10.0
		Sequence Coverage [%]:	1.9
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|530361060	refseq_human (refseq_human_20140103.fasta)	PREDICTED: AT-hook DNA-binding motif-containing protein 1 isoform X6 [Homo sapiens]
gi|530361058	refseq_human (refseq_human_20140103.fasta)	PREDICTED: AT-hook DNA-binding motif-containing protein 1 isoform X5 [Homo sapiens]
gi|530361056	refseq_human (refseq_human_20140103.fasta)	PREDICTED: AT-hook DNA-binding motif-containing protein 1 isoform X4 [Homo sapiens]
gi|530361054	refseq_human (refseq_human_20140103.fasta)	PREDICTED: AT-hook DNA-binding motif-containing protein 1 isoform X3 [Homo sapiens]
gi|530361052	refseq_human (refseq_human_20140103.fasta)	PREDICTED: AT-hook DNA-binding motif-containing protein 1 isoform X2 [Homo sapiens]
gi|530361050	refseq_human (refseq_human_20140103.fasta)	PREDICTED: AT-hook DNA-binding motif-containing protein 1 isoform X1 [Homo sapiens]

Detailed Protein Report

```
        10         20         30         40         50         60         70         80
MRVKPQGLVV TSSAVCSSPD YLREPKYYPG GPPTPRPLLP TRPPASPPDK AFSTHAFSEN PRPPPRRDPS TRRPPVLAKG
        90        100        110        120        130        140        150        160
DDPLPPRAAR PVSQARCPTP VGDGSSSRRC WDNGRVNLRP VVQLIDIMKD LTRLSQDLQH SGVHLDCGGL RLSRPPAPPP
       170        180        190        200        210        220        230        240
GDLQYSFFSS PSLANSIRSP EERATPHAKS ERPSHPLYEP EPEPRDSPQP GQGHSPGATA AATGLPPEPE PDSTDYSELA
       250        260        270        280        290        300        310        320
DADILSELAS LTCPEAQLLE AQALEPPSPE PEPQLLDPQP RFLDPQALEP LGEALELPPL QPLADPLGLP GLALQALDTL
       330        340        350        360        370        380        390        400
PDSLESQLLD PQALDPLPKL LDVPGRRLEP QQPLGHCPLA EPLRLDLCSP HGPPGPEGHP KYALRRTDRP KILCRRRKAG
       410        420        430        440        450        460        470        480
RGRKADAGPE GRLLPLPMPT GLVAALAEPP PPPPPPPPAL PGPGPVSVPE LKPESSQTPV VSTRKGKCRG VRRMVVKMAK
       490        500        510        520        530        540        550        560
IPVSLGRRNK TTYKVSSLSS SLSVEGKELG LRVSAEPTPL LKMKNNGRNV VVVFPPGEMP IILKRKRGRP PKNLLLGPGK
       570        580        590        600        610        620        630        640
PKEPAVVAAE AATVAAATMA MPEVKKRRRR KQKLASPQPS YAADANDSKA EYSDVLAKLA FLNRQSQCAG RCSPPRCWTP
       650        660        670        680        690        700        710        720
SEPESVHQAP DTQSISHFLH RVQGFRRRGG KAGGFGGRGG GHAAKSARCS FSDFFEGIGK KKKVVAVAAA GVGGPGLTEL
       730        740        750        760        770        780        790        800
GHPRKRGRGE VDAVTGKPKR KRRSRKNGTL FPEQVPSGPG FGEAGAEWAG DKGGGWAPHH GHPGGQAGRN CGFQGTEARA
       810        820        830        840        850        860        870        880
FASTGLESGA SGRGSYYSTG APSGQTELSQ ERQNLFTGYF RSLLDSDDSS DLLDFALSAS RPESRKASGT YAGPPTSALP
       890        900        910        920        930        940        950        960
AQRGLATFPS RGAKASPVAV GSSGAGADPS FQPVLSARQT FPPGRAASYG LTPAASDCRA AETFPKLVPP PSAMARSPTT
       970        980        990       1000       1010       1020       1030       1040
HPPANTYLPQ YGGYGAGQSV FAPTKPFTGQ DCANSKDCSF AYGSGNSLPA SPSSAHSAGY APPPTGGPCL PPSKASFFSS
      1050       1060       1070       1080       1090       1100       1110       1120
SEGAPFSGSA PTPLRCDSRA STVSPGGYMV PKGTTASATS AASAASSSSS SFQPSPENCR QFAGASQWPF RQGYGGLDWA
      1130       1140       1150       1160       1170       1180       1190       1200
SEAFSQLYNP SFDCHVSEPN VILDISNYTP QKVKQQTAVS ETFSESSSDS TQFNQPVGGG GFRRANSEAS SSEGQSSLSS
      1210       1220       1230       1240       1250       1260       1270       1280
LEKLMMDWNE ASSAPGYNWN QSVLFQSSSK PGRGRRKKVD LFEASHLGFP TSASAAASGY PSKRSTGPRQ PRGGRGGGAC
      1290       1300       1310       1320       1330       1340       1350       1360
SAKKERGGAA AKAKFIPKPQ PVNPLFQDSP DLGLDYYSGD SSMSPLPSQS RAFGVGERDP CDFIGPYSMN PSTPSDGTFG
      1370       1380       1390       1400       1410       1420       1430       1440
QGFHCDSPSL GAPELDGKHF PPLAHPPTVF DAGLQKAYSP TCSPTLGFKE ELRPPPTKLA ACEPLKHGLQ GASLGHAAAA
      1450       1460       1470       1480       1490       1500       1510       1520
QAHLSCRDLP LGQPHYDSPS CKGTAYWYPP GSAARSPPYE GKVGTGLLAD FLGRTEAACL SAPHLASPPA TPKADKEPLE
      1530       1540       1550       1560       1570       1580       1590       1600
MARPPGPPRG PAAAAAGYGC PLLSDLTLSP VPRDSLLPLQ DTAYRYPGFM PQAHPGLGGG PKSGFLGPMA EPHPEDTFTV
      1610
TSL
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1735	1	945.9132	-52.92	2	50.2	11.2	1	592-609	K.QKLASPQPSYAADANDSK.A	

Detailed Protein Report

Protein 830: PREDICTED: serine/threonine-protein kinase ULK4 isoform X4 [Homo sapiens]

Accession:	gi|530372727	**Score:**	21.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	100.6
Database Date:	2015-11-30	**pI:**	8.8
		Sequence Coverage [%]:	4.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MENFILYEEI	GRGSKTVVYK	GRRKGTINFV	AILCTDKCKR	PEITNWVRLT	REIKHKNIVT	FHEWYETSNH	LWLVVELCTG
90	100	110	120	130	140	150	160
GSLKTVIAQD	ENLPEDVVRE	FGIDLISGLH	HLHKLGILFC	DISPRKILLE	GPGTLKFSNF	CLAKVEGENL	EEFFALVAAE
170	180	190	200	210	220	230	240
EGGGDNGENV	LKKSMKSRVK	GSPVYTAPEV	VRGADFSISS	DLWSLGCLLY	EMFSGKPPFF	SESISELTEK	ILCEDPLPPI
250	260	270	280	290	300	310	320
PKDSSRPKAS	SDFINLLDGL	LQRDPQKRLT	WTRLLQHSFW	KKAFAGADQE	SSVEDLSLSR	NTMECSGPQD	SKELLQNSQS
330	340	350	360	370	380	390	400
RQAKGHKSGQ	PLGHSFRLEN	PTEFRPKSTL	EGQLNESMFL	LSSRPTPRTS	TAVEVSPGED	MTHCSPQKTS	PLTKITSGHL
410	420	430	440	450	460	470	480
SQQDLESQMR	ELIYTDSDLV	VTPIIDNPKI	MKQPPVKFDA	KILHLPTYSV	DKLLFLKDQD	WNDFLQQVCS	QIDSTEKSMG
490	500	510	520	530	540	550	560
ASRAKLNLLC	YLCVVAGHQE	VATRLLHSPL	FQLLIQHLRI	APNWDIRAKV	AHVIGLLASH	TAELQENTPV	VEAIVLLTEL
570	580	590	600	610	620	630	640
IRENFRNSKL	KQCLLPTLGE	LIYLVATQEE	KKKNPRECWA	VPLAAYTVLM	RCLREGEERV	VNHMAAKIIE	NVCTTFSAQS
650	660	670	680	690	700	710	720
QGFITGEIGP	ILWYLFRHST	ADSLRITAVS	ALCRITRHSP	TAFQNVIEKV	GLNSVINSLA	SAICKVQQYM	LTLFAAMLSC
730	740	750	760	770	780	790	800
GIHLQRLIQE	KGFVSTIIRL	LDSPSTCIRA	KAFLVLLYIL	IYNREMLLLS	CQARLVMYIE	RDSRKTTPGK	EQQSGNEYLS
810	820	830	840	850	860	870	880
KCLDLLICHI	VQELPRILGD	ILNSLANVSG	RKHPSTVQVK	QLKLCLPLMP	VVLHLVTSQV	FRPQVVTEEF	LFSYGTILSH
890	900						
IKSVDSGETN	IDGAIGC						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1551	1	715.7619	64.52	3	48.1	11.0	0	411-429	R.ELIYTDSDLVVTPIIDNPK.I	

Detailed Protein Report

Protein 831: 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
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	11.6
		No. of unique Peptides:	2

```
        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
2601	1	626.8465	80.54	2	63.1	10.2	1	145-154	R.ICEMGEVMRK.A	Carbamidomethyl: 2
1321	1	781.0677	172.15	2	46.2	10.9	1	182-195	R.ELLSISSESLQARK.E	

Detailed Protein Report

Protein 832: putative ATP-dependent RNA helicase DHX30 isoform 1 [Homo sapiens]

Accession:	gi|20336294	**Score:**	21.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	133.9
Database Date:	2015-11-30	**pI:**	9.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.4
		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 833: rho guanine nucleotide exchange factor 33 [Homo sapiens]

Accession:	gi|290463441	**Score:**	21.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	97.5
Database Date:	2015-11-30	**pI:**	6.4
		Sequence Coverage [%]:	3.7
		No. of unique Peptides:	2

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
2130	1	701.3007	-88.45	3	55.2	10.3	2	715-735	R.APPADGVAPRLYSTRSSSGGR.A	
856	1	647.8324	-5.87	2	39.5	10.7	1	758-768	R.GASRTFFPQQR.S	

Detailed Protein Report

Protein 834: 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
2638	2	673.3669	33.04	2	63.8	10.8	1	149-159	K.YFVNMKISTDK.S	

Detailed Protein Report

Protein 835: laminin subunit gamma-2 isoform b precursor [Homo sapiens]

Accession: gi|157419140
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 20.9
MW [kDa]: 121.5
pI: 6.0
Sequence Coverage [%]: 3.3
No. of unique Peptides: 2

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
170	1	1382.5832	-84.12	2	30.9	10.1	1	1-24	-.MPALWLGCCLCFSLLLPAARATSR.R	Carbamidomethyl: 8, 9, 11
2722	1	772.4355	47.96	2	65.3	10.8	0	653-665	R.MQQAEQALQDILR.D	

Detailed Protein Report

Protein 836: transmembrane protein 70, mitochondrial isoform a [Homo sapiens]

Accession:	gi|34147498	**Score:**	20.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	29.0
Database Date:	2015-11-30	**pI:**	9.6
		Sequence Coverage [%]:	10.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLFLALGSPW	AVELPLCGRR	TALCAAAALR	GPRASVSRAS	SSSGPSGPVA	GWSTGPSGAA	RLLRRPGRAQ	IPVYWEGYVR
90	100	110	120	130	140	150	160
FLNTPSDKSE	DGRLIYTGNM	ARAVFGVKCF	SYSTSLIGLT	FLPYIFTQNN	AISESVPLPI	QIIFYGIMGS	FTVITPVLLH
170	180	190	200	210	220	230	240
FITKGYVIRL	YHEATTDTYK	AITYNAMLAE	TSTVFHQNDV	KIPDAKHVFT	TFYAKTKSLL	VNPVLFPNRE	DYIHLMGYDK
250	260	270					
EEFILYMEET	SEEKRHKDDK						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1713	1	820.3878	-79.60	2	50.1	10.2	1	94-108	R.LIYTGNMARAVFGVK.C	

Detailed Protein Report

Protein 837: PREDICTED: uncharacterized protein LOC101928193 [Homo sapiens]

Accession:	gi|530427280	**Score:**	20.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	65.8
Database Date:	2015-11-30	**pI:**	10.1
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.8
		No. of unique Peptides:	2

Quantitation

Wdown:Qdown **Median:** 0.73 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MKVLVLGLAL AVSWELGLEL VPELILAVVL GQRLALPLEF VLELDLPPLM VLELFLELLV ALKLVLGPSV ALQLVRELLL
        90        100        110        120        130        140        150        160
ARALPLELMR EPVLPLALPL NLALGLAPCL VVEQREELWL QSPETENLKG LPLYSRFTGF TVIFQGPGVH HHIPGVWGSL
       170        180        190        200        210        220        230        240
SYSRCLGFIV VFQVSGVHHC IPGVWGSLSY SRCLGFTVIF QGPGVHHHIP EVWSSPSYSR CLAFTVVFQV SGVHHCIPGV
       250        260        270        280        290        300        310        320
WGSLSYSRCL GFTVVFQVSG VHCHIPGAWG SPSYSRCLGL TVVFQVSGVH CHILGAWGSP PYSRCLGFTV VFQVSGVHRH
       330        340        350        360        370        380        390        400
IPGAWVHCYI PGVWDSLSYS RCLGFTVIFQ GPGVHHHIPG VWGSLLYSRC LGFTVIFQGP GVHHHIPGVW RSLSYSRCLG
       410        420        430        440        450        460        470        480
FTIVFQVSGA HCCIPGVWGS LLYSRCLGFT VIFQGPGVHH HIPGVWRSLS YSRCRVHRCI PGVWGSLSYS RCLGFTVIFQ
       490        500        510        520        530        540        550        560
VPGFTVIFQV SGIHCHIPGV WGSLLYSRCL GFTLIFQVSG VHCCIPGVWA HHRIPGAWGS PSYSRGLGFI IVFQGSGIHH
       570        580        590        600
HIPGAWGSLL YSRCLRLTVI FQVSAYNREQ HTGAECMND
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2754	1	639.3520	54.35	2	62.8	10.3	0	265-276	H.IPGAWGSPSYSR.C		Wdown:Qdown 0.73
2636	1	625.6343	-143.74	2	61.2	10.5	0	589-599	R.EQHTGAECMND.-	Oxidation: 9	

Detailed Protein Report

Protein 838: **titin isoform novex-3 [Homo sapiens]**

Accession:	gi|110349721	**Score:**	20.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	631.2
Database Date:	2015-11-30	**pI:**	5.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	0.6
		No. of unique Peptides:	1

BRUKER

Detailed Protein Report

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

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2174	1	986.3858	-94.84	2	57.4	10.5	1	5586-5604	R.CVATNKSGMAESFAALTLT.-	Carbamidomethyl: 1

Detailed Protein Report

Protein 839: advillin [Homo sapiens]

Accession:	gi|295821173	**Score:**	20.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	92.0
Database Date:	2015-11-30	**pI:**	5.4
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.4
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|578823197	refseq_human (refseq_human_20140103.fasta)	PREDICTED: advillin isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MPLTSAFRAV	DNDPGIIVWR	IEKMELALVP	VSAHGNFYEG	DCYVILSTRR	VASLLSQDIH	FWIGKDSSQD	EQSCAAIYTT
90	100	110	120	130	140	150	160
QLDDYLGGSP	VQHREVQYHE	SDTFRGYFKQ	GIIYKQGGVA	SGMKHVETNT	YDVKRLLHVK	GKRNIRATEV	EMSWDSFNRG
170	180	190	200	210	220	230	240
DVFLLDLGKV	IIQWNGPESN	SGERLKAMLL	AKDIRDRERG	GRAKIGVIEG	DKEAASPELM	KVLQDTLGRR	SIIKPTVPDE
250	260	270	280	290	300	310	320
IIDQKQKSTI	MLYHISDSAG	QLAVTEVATR	PLVQDLLNHD	DCYILDQSGT	KIYVWKGKGA	TKAEKQAAMS	KALGFIKMKS
330	340	350	360	370	380	390	400
YPSSTNVETV	NDGAESAMFK	QLFQKWSVKD	QTMGLGKTFS	IGKIAKVFQD	KFDVTLLHTK	PEVAAQERMV	DDGNGKVEVW
410	420	430	440	450	460	470	480
RIENLELVPV	EYQWYGFFYG	GDCYLVLYTY	EVNGKPHHIL	YIWQGRHASQ	DELAASAYQA	VEVDRQFDGA	AVQVRVRMGT
490	500	510	520	530	540	550	560
EPRHFMAIFK	GKLVIFEGGT	SRKGNAEPDP	PVRLFQIHGN	DKSNTKAVEV	PAFASSLNSN	DVFLLRTQAE	HYLWYGKGSS
570	580	590	600	610	620	630	640
GDERAMAKEL	ASLLCDGSEN	TVAEGQEPAE	FWDLLGGKTP	YANDKRLQQE	ILDVQSRLFE	CSNKTGQFVV	TEITDFTQDD
650	660	670	680	690	700	710	720
LNPTDVMLLD	TWDQVFLWIG	AEANATEKES	ALATAQQYLH	THPSGRDPDT	PILIIKQGFE	PPIFTGWFLA	WDPNIWSAGK
730	740	750	760	770	780	790	800
TYEQLKEELG	DAAAIMRITA	DMKNATLSLN	SNDSEPKYYP	IAVLLKNQNQ	ELPEDVNPAK	KENYLSEQDF	VSVFGITRGQ
810	820						
FAALPGWKQL	QMKKEKGLF						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2968	1	937.4525	-37.87	2	66.3	10.1	1	213-229	K.EAASPELMKVLQDTLGR.R	Oxidation: 8

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Detailed Protein Report

Protein 840: limbin isoform 2 [Homo sapiens]

Accession:	gi|260763994	**Score:**	20.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	139.8
Database Date:	2015-11-30	**pI:**	6.2
		Sequence Coverage [%]:	2.7
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578808088	refseq_human (refseq_human_20140103.fasta)	PREDICTED: limbin isoform X2 [Homo sapiens]

10	20	30	40	50	60	70	80
MIWPKVECCH	FKTAVEAPLG	MKLDKKMEVF	IPLSTSAASS	GPWAHSLFAF	IPSWPKKNLF	KRESPITHRL	YGDISREVQG
90	100	110	120	130	140	150	160
TSENGVIFQK	CALVSGSSEA	QTARIWLLVN	NTKTTSSANL	SELLLLDSIA	GLTIWDSVGN	RTSEGFQAFS	KKFLQVGDAF
170	180	190	200	210	220	230	240
AVSYAATLQA	GDLGNGESLK	LPAQLTFQSS	SRNRTQLKVL	FSITAEENVT	VLPHHGLHAA	GFFIAFLLSL	VLTWAALFLM
250	260	270	280	290	300	310	320
VRYQCLKGNM	LTRHRVWQYE	SKLEPLPFTS	ADGVNEDLSL	NDQMIDILSS	EDPGSMLQAL	EELEIATLNR	ADADLEACRT
330	340	350	360	370	380	390	400
QISKDIIALL	LKNLTSSGHL	SPQVERKMSA	VFKKQFLLLE	NEIQEEYDRK	MVALTAECDL	ETRKKMENQY	QREMMAMEEA
410	420	430	440	450	460	470	480
EELLKRAGER	SAVECSNLLR	TLHGLEQEHL	RKSLALQQEE	DFAKAHRQLA	VFQRNELHSI	FFTQIKSAIF	KGELKPEAAK
490	500	510	520	530	540	550	560
MLLQNYSKIQ	ENVEELMDFF	QASKRYHLSK	RFGHREYLVQ	NLQSSETRVQ	GLLSTAAAQL	THLIQKHERA	GYLDEDQMEM
570	580	590	600	610	620	630	640
LLERAQTEVF	SIKQKLDNDL	KQEKKKLHQK	LITKRRRELL	QKHREQRREQ	ASVGEAFRTV	EDAGQYLHQK	RSLMEEHGAT
650	660	670	680	690	700	710	720
LEELQERLDQ	AALDDLRTLT	LSLFEKATDE	LRRLQNSAMT	QELLKRGVPW	LFLQQILEEH	GKEMAARAEQ	LEGEERDRDQ
730	740	750	760	770	780	790	800
EGVQSVRQRL	KDDAPEAVTE	EQAELRRWEH	LIFMKLCSSV	FSLSEEELLR	MRQEVHGCFA	QMDRSLALPK	IRARVLLQQF
810	820	830	840	850	860	870	880
QTAWREAEFV	KLDQAVAAPE	LQQQSKVRKS	RSKSKSKGEL	LKKCIEDKIH	LCEEQASEDL	VEKVRGELLR	ERVQRMEAQE
890	900	910	920	930	940	950	960
GGFAQSLVAL	QFQKASRVTE	TLSAYTALLS	IQDLLLEELS	ASEMLTKSAC	TQILESHSRE	LQELERKLED	QLVQQEAAQQ
970	980	990	1000	1010	1020	1030	1040
QQALASWQQW	VADGPGILNE	PGEVDSERQV	STVLHQALSK	SQTLLEQHQQ	CLREEQQNSV	VLEDLLENME	ADTFATLCSQ
1050	1060	1070	1080	1090	1100	1110	1120
ELRLASYLAR	MAMVPGATLR	RLLSVVLPTA	SQPQLLALLD	SATERHVDHA	AESDGGAEQA	DVGRRRKHQS	WWQALDGKLR
1130	1140	1150	1160	1170	1180	1190	1200
GDLISRGLEK	MLWARKRKQS	ILKKTCLPLR	ERMIFSGKGS	WPHLSLEPIG	ELAPVPIVGA	ETIDLLNTGE	KLFIFRNPKE
1210	1220	1230					
PEISLHVPPR	KKKNFLNAKK	AMRALGMD					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1920	1	600.5632	-153.22	3	52.7	10.1	2	62-76	K.RESPITHRLYGDISR.E	

Detailed Protein Report

Protein 841: 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 842: RNA-binding protein 12B [Homo sapiens]

Accession:	gi|118722349	**Score:**	20.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	118.0
Database Date:	2015-11-30	**pI:**	6.3
		Sequence Coverage [%]:	0.7
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578815970	refseq_human (refseq_human_20140103.fasta)	PREDICTED: RNA-binding protein 12B isoform X5 [Homo sapiens]
gi|578815966	refseq_human (refseq_human_20140103.fasta)	PREDICTED: RNA-binding protein 12B isoform X4 [Homo sapiens]
gi|578815964	refseq_human (refseq_human_20140103.fasta)	PREDICTED: RNA-binding protein 12B isoform X3 [Homo sapiens]
gi|530389016	refseq_human (refseq_human_20140103.fasta)	PREDICTED: RNA-binding protein 12B isoform X2 [Homo sapiens]
gi|530389014	refseq_human (refseq_human_20140103.fasta)	PREDICTED: RNA-binding protein 12B isoform X1 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MAVVIRLLGL PFIAGPVDIR HFFTGLTIPD GGVHIIGGEI GEAFIIFATD EDARRAISRS GGFIKDSSVE LFLSSKAEMQ
        90        100        110        120        130        140        150        160
KTIEMKRTDR VGRGRPGSGT SGVDSLSNFI ESVKEEASNS GYGSSINQDA GFHTNGTGHG NLRPRKTRPL KAENPYLFLR
       170        180        190        200        210        220        230        240
GLPYLVNEDD VRVFFSGLCV DGVIFLKHHD GRNNGDAIVK FASCVDASGG LKCHRSFMGS RFIEVMQGSE QQWIEFGGNA
       250        260        270        280        290        300        310        320
VKEGDVLRRS EEHSPPRGIN DRHFRKRSHS KSPRRTRSRS PLGFYVHLKN LSLSIDERDL RNFFRGTDLT DEQIRFLYKD
       330        340        350        360        370        380        390        400
ENRTRYAFVM FKTLKDYNTA LSLHKTVLQY RPVHIDPISR KQMLKFIARY EKKRSGSLER DRPGHVSQKY SQEGNSGQKL
       410        420        430        440        450        460        470        480
CIYIRNFPFD VTKVEVQKFF ADFLLAEDDI YLLYDDKGVG LGEALVKFKS EEQAMKAERL NRRRFLGTEV LLRLISEAQI
       490        500        510        520        530        540        550        560
QEFGVNFSVM SSEKMQARSQ SRERGDHSHL FDSKDPPIYS VGAFENFRHQ LEDLRQLDNF KHPQRDFRQP DRHPPEDFRH
       570        580        590        600        610        620        630        640
SSEDFRFPPE DFRHSPEDFR RPREEDFRRP SEEDFRRPWE EDFRRPPEDD FRHPREEDWR RPLEEDWRRP LEEDFRRSPT
       650        660        670        680        690        700        710        720
EDFRQLPEED FRQPPEEDLR WLPEEDFRRP PEEDWRRPPE EDFRRPLQGE WRRPPEDDFR RPPEEDFRHS PEEDFRQSPQ
       730        740        750        760        770        780        790        800
EHFRRPPQEH FRRPPPEHFR RPPPEHFRRP PPEHFRRPPP EHFRRPPPEH FRRPPPEHFR RPPQEHFRRP PQEHFRRSRE
       810        820        830        840        850        860        870        880
EDFRHPPDED FRGPPDEDFR HPPDEDFRSP QEEDFRCPSD EDFRQLPEED LREAPEEDPR LPDNFRPPGE DFRSPPDDFR
       890        900        910        920        930        940        950        960
SHRPFVNFGR PEGGKFDFGK HNMGSFPEGR FMPDPKINCG SGRVTPIKIM NLPFKANVNE ILDFFHGYRI IPDSVSIQYN
       970        980        990       1000       1010
EQGLPTGEAI VAMINYNEAM AAIKDLNDRP VGPRKVKLTL L
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2646	1	439.1044	-203.15	2	61.4	20.6	0	560-566	R.HSSEDFR.F	

Detailed Protein Report

Protein 843: PREDICTED: monocarboxylate transporter 8 isoform X1 [Homo sapiens]

Accession:	gi|530421807	**Score:**	20.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	45.8
Database Date:	2015-11-30	**pI:**	5.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.1
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MALQSQASEE AKGPWQEADQ EQQEPVGSPE PESEPEPEPE PEPVPVPPPE PQPEPQPLPD PAPLPELEFE SERVHEPEPT

        90        100        110        120        130        140        150        160
PTVETRGTAR GFQPPEGGFG WVVVFAATWC NGSIFGIHNS VGILYSMLLE EEKEKNRQVE FQAAWVGALA MGMIFFCSPI

       170        180        190        200        210        220        230        240
VSIFTDRLGC RITATAGAAV AFIGLHTSSF TSSLSLRYFT YGILFGCGCS FAFQPSLVIL GHYFQRRLGL ANGVVSAGSS

       250        260        270        280        290        300        310        320
IFSMSFPFLI RMLGDKIKLA QTFQVLSTFM FVLMLLSLTY RPLLPSSQDT PSKRGVRTLH QRFLAQLRKY FNMRVFRQRT

       330        340        350        360        370        380        390        400
YRIWAFGIAA AALGYFVPYV HLMKYVEEEF SEIKETWVLL VCIGATSGLG RLVSGHISDS IPGLKKIYLQ AYSATVLGTT

       410        420
MWPSTLPVCP PSSGL
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2201	1	916.4855	-5.38	2	56.1	20.5	0	355-371	K.ETWVLLVCIGATSGLGR.L	Carbamidomethyl: 8

Detailed Protein Report

Protein 844: long-chain fatty acid transport protein 3 [Homo sapiens]

Accession:	gi|13236579	**Score:**	20.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	78.6
Database Date:	2015-11-30	**pI:**	7.9
		Sequence Coverage [%]:	3.8
		No. of unique Peptides:	1

Quantitation

mdown:qdown **Median:** 0.95 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MGVCQRTRAP	WKEKSQLERA	ALGFRKGGSG	MFASGWNQTV	PIEEAGSMAA	LLLLPLLLLL	PLLLLKLHLW	PQLRWLPADL
90	100	110	120	130	140	150	160
AFAVRALCCK	RALRARALAA	AAADPEGPEG	GCSLAWRLAE	LAQQRAAHTF	LIHGSRRFSY	SEAERESNRA	ARAFLRALGW
170	180	190	200	210	220	230	240
DWGPDGGDSG	EGSAGEGERA	APGAGDAAAG	SGAEFAGGDG	AARGGGAAAP	LSPGATVALL	LPAGPEFLWL	WFGLAKAGLR
250	260	270	280	290	300	310	320
TAFVPTALRR	GPLLHCLRSC	GARALVLAPE	FLESLEPDLP	ALRAMGLHLW	AAGPGTHPAG	ISDLLAEVSA	EVDGPVPGYL
330	340	350	360	370	380	390	400
SSPQSITDTC	LYIFTSGTTG	LPKAARISHL	KILQCQGFYQ	LCGVHQEDVI	YLALPLYHMS	GSLLGIVGCM	GIGATVVLKS
410	420	430	440	450	460	470	480
KFSAGQFWED	CQQHRVTVFQ	YIGELCRYLV	NQPPSKAERG	HKVRLAVGSG	LRPDTWERFV	RRFGPLQVLE	TYGLTEGNVA
490	500	510	520	530	540	550	560
TINYTGQRGA	VGRASWLYKH	IFPFSLIRYD	VTTGEPIRDP	QGHCMATSPG	EPGLLVAPVS	QQSPFLGYAG	GPELAQGKLL
570	580	590	600	610	620	630	640
KDVFRPGDVF	FNTGDLLVCD	DQGFLRFHDR	TGDTFRWKGE	NVATTEVAEV	FEALDFLQEV	NVYGVTVPGH	EGRAGMAALV
650	660	670	680	690	700	710	720
LRPPHALDLM	QLYTHVSENL	PPYARPRFLR	LQESLATTET	FKQQKVRMAN	EGFDPSTLSD	PLYVLDQAVG	AYLPLTTARY
730	740						
SALLAGNLRI							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
852	1	683.3354	-63.10	2	39.4	10.5	1	126-137	R.AAHTFLIHGSRR.F		mdown:qdown 0.95

Detailed Protein Report

Protein 845: **PREDICTED: mitogen-activated protein kinase kinase kinase kinase 2 isoform X4 [Homo sapiens]**

Accession:	gi|578821648	**Score:**	20.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	71.1
Database Date:	2015-11-30	**pI:**	6.0
		Sequence Coverage [%]:	5.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLMSKSSFQP	PKLRDKTRWT	QNFHHFLKLA	LTKNPKKRPT	AEKLLQHPFT	TQQLPRALLT	QLLDKASDPH	LGTPSPEDCE
90	100	110	120	130	140	150	160
LETYDMFPDT	IHSRGQHGPA	ERTPSEIQFH	QVKFGAPRRK	ETDPLNEPWE	EEWTLLGKEE	LSGSLLQSVQ	EALEERSLTI
170	180	190	200	210	220	230	240
RSASEFQVPH	RGRLELGSRP	LQRVRLEWDV	VTGQPGNGRA	GPCPSYQELD	SPDDTMGTIK	RAPFLGPLPT	DPPAEEPLSS
250	260	270	280	290	300	310	320
PPGTLPPPPS	GPNSSPLLPT	AWATMKQRED	PERSSCHGLP	PTPKVHMGAC	FSKVFNGCPL	RIHAAVTWIH	PVTRDQFLVV
330	340	350	360	370	380	390	400
GAEEGIYTLN	LHELHEDTLE	KLISHRCSWL	YCVNNVLLSL	SGKSTHIWAH	DLPGLFEQRR	LQQQVPLSIP	TNRLTQRIIP
410	420	430	440	450	460	470	480
RRFALSTKIP	DTKGCLQCRV	VRNPYTGATF	LLAALPTSLL	LLQWYEPLQK	FLLLKNFSSP	LPSPAGMLEP	LVLDGKELPQ
490	500	510	520	530	540	550	560
VCVGAEGPEG	PGCRVLFHVL	PLEAGLTPDI	LIPPEGIPGS	AQQVIQVDRD	TILVSFERCV	RIVNMQGEPT	ATLAPELTFD
570	580	590	600	610	620	630	640
FPIETVVCLQ	DSVLAFWSHG	MQGRSLDTNE	VTQEITDETR	IFRVLGAHRD	IILESIPTDN	PEAHSNLYIL	TGHQSTY

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1876	1	899.5084	102.10	2	52.1	10.3	0	477-494	K.ELPQVCVGAEGPEGPGCR.V	

Detailed Protein Report

Protein 846: **PREDICTED: zinc finger protein 717 isoform X8 [Homo sapiens]**

Accession:	gi|578805503	**Score:**	20.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	73.9
Database Date:	2015-11-30	**pI:**	9.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	6.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MFPVFSGCFQ	ELQEKNKSLE	LVSFEEVAVH	FTWEEWQDLD	DAQRTLYRDV	MLETYSSLVS	LGHYITKPEM	IFKLEQGAEP
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
WIVEETPNLR	LSAVQIIDDL	IERSHESHDR	FFWQIVITNS	NTSTQERVEL	GKTFNLNSNH	VLNLIINNGN	SSGMKPGQFN
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
DCQNMLFPIK	PGETQSGEKP	HVCDITRRSH	RHHEHLTQHH	KIQTLLQTFQ	CNEQGKTFNT	EAMFFIHKRV	HIVQTFGKYN
250	**260**	**270**	**280**	**290**	**300**	**310**	**320**
EYEKACNNSA	VIVQVITQVG	QPTCCRKSDF	TKHQQTHTGE	KPYECVECEK	PSISKSDLML	QCKMPTEEKP	YACNWCEKLF
330	**340**	**350**	**360**	**370**	**380**	**390**	**400**
SYKSSLIIHQ	RIHTGEKPYG	CNECGKTFRR	KSFLTLHERT	HTGDKPYKCI	ECGKTFHCKS	LLTLHHRTHS	GEKPYQCSEC
410	**420**	**430**	**440**	**450**	**460**	**470**	**480**
GKTFSQKSYL	TIHHRTHTGE	KPYACDHCEE	AFSHKSRLTV	HQRTHTGEKP	YECNECGKPF	INKSNLRLHQ	RTHTGEKPYE
490	**500**	**510**	**520**	**530**	**540**	**550**	**560**
CNECGKTFHR	KSFLTIHQWT	HTGEKPYECN	ECGKTFRCKS	FLTVHQRTHA	GEKPYACNEC	GKTYSHKSYL	TVHHRTHTGE
570	**580**	**590**	**600**	**610**	**620**	**630**	**640**
KPFRCNECRK	TFSQKSGLSI	HQRTHTGEKP	YECKECGKTF	CQKSHLSRHQ	QTHIGEKSDV	AEAGYVFPQN	HSFFP

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1805	2	1273.5509	-66.38	2	51.2	10.2	1	245-267	K.ACNNSAVIVQVITQVGQPTCCRK.S	Carbamidomethyl: 2, 21

Detailed Protein Report

Protein 847: heat shock 70 kDa protein 1A/1B [Homo sapiens]

Accession:	gi|167466173	**Score:**	20.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	70.0
Database Date:	2015-11-30	**pI:**	5.4
		Sequence Coverage [%]:	1.9
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|194248072	refseq_human(refseq_human_20140103.fasta)	heat shock 70 kDa protein 1A/1B [Homo sapiens]

10	20	30	40	50	60	70	80
MAKAAAIGID	LGTTYSCVGV	FQHGKVEIIA	NDQGNRTTPS	YVAFTDTERL	IGDAAKNQVA	LNPQNTVFDA	KRLIGRKFGD
90	100	110	120	130	140	150	160
PVVQSDMKHW	PFQVINDGDK	PKVQVSYKGE	TKAFYPEEIS	SMVLTKMKEI	AEAYLGYPVT	NAVITVPAYF	NDSQRQATKD
170	180	190	200	210	220	230	240
AGVIAGLNVL	RIINEPTAAA	IAYGLDRTGK	GERNVLIFDL	GGGTFDVSIL	TIDDGIFEVK	ATAGDTHLGG	EDFDNRLVNH
250	260	270	280	290	300	310	320
FVEEFKRKHK	KDISQNKRAV	RRLRTACERA	KRTLSSSTQA	SLEIDSLFEG	IDFYTSITRA	RFEELCSDLF	RSTLEPVEKA
330	340	350	360	370	380	390	400
LRDAKLDKAQ	IHDLVLVGGS	TRIPKVQKLL	QDFFNGRDLN	KSINPDEAVA	YGAAVQAAIL	MGDKSENVQD	LLLLDVAPLS
410	420	430	440	450	460	470	480
LGLETAGGVM	TALIKRNSTI	PTKQTQIFTT	YSDNQPGVLI	QVYEGERAMT	KDNNLLGRFE	LSGIPPAPRG	VPQIEVTFDI
490	500	510	520	530	540	550	560
DANGILNVTA	TDKSTGKANK	ITITNDKGRL	SKEEIERMVQ	EAEKYKAEDE	VQRERVSAKN	ALESYAFNMK	SAVEDEGLKG
570	580	590	600	610	620	630	640
KISEADKKKV	LDKCQEVISW	LDANTLAEKD	EFEHKRKELE	QVCNPIISGL	YQGAGGPGPG	GFGAQGPKGG	SGSGPTIEEV
650							
D							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2298	1	599.2128	-230.78	2	57.4	20.4	0	160-171	K.DAGVIAGLNVLR.I	

Detailed Protein Report

Protein 848: Down syndrome cell adhesion molecule-like protein 1 [Homo sapiens]

Accession:	gi|21359935	**Score:**	20.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	230.5
Database Date:	2015-11-30	**pI:**	9.3
		Sequence Coverage [%]:	0.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MTGAGEPRRE	EPPPQPSAGL	RSRESGAPSA	GGWERAERGR	GAAARPATGP	PPRRIGPLYG	MWLVTFLLLL	DSLHKARPED
90	100	110	120	130	140	150	160
VGTSLYFVND	SLQQVTFSSS	VGVVVPCPAA	GSPSAALRWY	LATGDDIYDV	PHIRHVHANG	TLQLYPFSPS	AFNSFIHDND
170	180	190	200	210	220	230	240
YFCTAENAAG	KIRSPNIRVK	AVFREPYTVR	VEDQRSMRGN	VAVFKCLIPS	SVQEYVSVVS	WEKDTVSIIP	EHRFFITYHG
250	260	270	280	290	300	310	320
GLYISDVQKE	DALSTYRCIT	KHKYSGETRQ	SNGARLSVTD	PAESIPTILD	GFHSQEVWAG	HTVELPCTAS	GYPIPAIRWL
330	340	350	360	370	380	390	400
KDGRPLPADS	RWTKRITGLT	ISDLRTEDSG	TYICEVTNTF	GSAEATGILM	VIDPLHVTLT	PKKLKTGIGS	TVILSCALTG
410	420	430	440	450	460	470	480
SPEFTIRWYR	NTELVLPDEA	ISIRGLSNET	LLITSAQKSH	SGAYQCFATR	KAQTAQDFAI	IALEDGTPRI	VSSFSEKVVN
490	500	510	520	530	540	550	560
PGEQFSLMCA	AKGAPPPTVT	WALDDEPIVR	DGSHRTNQYT	MSDGTTISHM	NVTGPQIRDG	GVYRCTARNL	VGSAEYQARI
570	580	590	600	610	620	630	640
NVRGPPSIRA	MRNITAVAGR	DTLINCRVIG	YPYYSIKWYK	DALLLPDNHR	QVVFENGTLK	LTDVQKGMDE	GEYLCSVLIQ
650	660	670	680	690	700	710	720
PQLSISQSVH	VAVKVPPLIQ	PFEFPPASIG	QLLYIPCVVS	SGDMPIRITW	RKDGQVIISG	SGVTIESKEF	MSSLQISSVS
730	740	750	760	770	780	790	800
LKHNGNYTCI	ASNAAATVSR	ERQLIVRVPP	RFVVQPNNQD	GIYGKAGVLN	CSVDGYPPPK	VMWKHAKGSG	NPQQYHPVPL
810	820	830	840	850	860	870	880
TGRIQILPNS	SLLIRHVLEE	DIGYYLCQAS	NGVGTDISKS	MFLTVKIPAM	ITSHPNTTIA	IKGHAKELNC	TARGERPIII
890	900	910	920	930	940	950	960
RWEKGDTVID	PDRVMRYAIA	TKDNGDEVVS	TLKLKPADRG	DSVFFSCHAI	NSYGEDRGLI	QLTVQEPPDP	PELEIREVKA
970	980	990	1000	1010	1020	1030	1040
RSMNLRWTQR	FDGNSIITGF	DIEYKNKSDS	WDFKQSTRNI	SPTINQANIV	DLHPASVYSI	RMYSFNKIGR	SEPSKELTIS
1050	1060	1070	1080	1090	1100	1110	1120
TEEAAPDGPP	MDVTLQPVTS	QSIQVTWKAP	KKELQNGVIR	GYQIGYRENS	PGSNGQYSIV	EMKATGDSEV	YTLDNLKKFA
1130	1140	1150	1160	1170	1180	1190	1200
QYGVVVQAFN	RAGTGPSSSE	INATTLEDVP	SQPPENVRAL	SITSDVAVIS	WSEPPRSTLN	GVLKGYRVIF	WSLYVDGEWG
1210	1220	1230	1240	1250	1260	1270	1280
EMQNITTTRE	RVELRGMEKF	TNYSVQVLAY	TQAGDGVRSS	VLYIQTKEDV	PGPPAGIKAV	PSSASSVVVS	WLPPTKPNGV
1290	1300	1310	1320	1330	1340	1350	1360
IRKYTIFCSS	PGSGQPAPSE	YETSPEQLFY	RIAHLNRGQQ	YLLWVAAVTS	AGRGNSSEKV	TIEPAGKAPA	KIISFGGTVT
1370	1380	1390	1400	1410	1420	1430	1440
TPWMKDVRLP	CNSVGDPAPA	VKWTKDSEDS	AIPVSMDGHR	LIHTNGTLLL	RAVKAEDSGY	YTCTATNTGG	FDTIIVNLLV
1450	1460	1470	1480	1490	1500	1510	1520
QVPPDQPRLT	VSKTSASSIT	LTWIPGDNGG	SSIRGFVLQY	SVDNSEEWKD	VFISSSERSF	KLDSLKCGTW	YKVKLAAKNS
1530	1540	1550	1560	1570	1580	1590	1600
VGSGRISEII	EAKTHGREPS	FSKDQHLFTH	INSTHARLNL	QGWNNGGCPI	TAIVLEYRPK	GTWAWQGLRA	NSSGEVFLTE
1610	1620	1630	1640	1650	1660	1670	1680
LREATWYELR	MRACNSAGCG	NETAQFATLD	YDGSTIPPIK	SAQGEGDDVK	KLFTIGCPVI	LATLGVALLF	IVRKKRKEKR
1690	1700	1710	1720	1730	1740	1750	1760
LKRLRDAKSL	AEMLISKNNR	SFDTPVKGPP	QGPRLHIDIP	RVQLLIEDKE	GIKQLGDDKA	TIPVTDAEFS	QAVNPQSFCT
1770	1780	1790	1800	1810	1820	1830	1840
GVSLHHPTLI	QSTGPLIDMS	DIRPGTNPVS	RKNVKSAHST	RNRYSSQWTL	TKCQASTPAR	TLTSDWRTVG	SQHGVTVTES
1850	1860	1870	1880	1890	1900	1910	1920
DSYSASLSQD	TDKGRNSMVS	TESASSTYEE	LARAYEHAKL	EEQLQHAKFE	ITECFISDSS	SDQMTTGTNE	NADSMTSMST
1930	1940	1950	1960	1970	1980	1990	2000
PSEPGICRFT	ASPPKPQDAD	RGKNVAVPIP	HRANKSDYCN	LPLYAKSEAF	FRKADGREPC	PVVPPREASI	RNLARTYHTQ
2010	2020	2030	2040	2050	2060	2070	2080
ARHLTLDPAS	KSLGLPHPGA	PAAASTATLP	QRTLAMPAPP	AGTAPPAPGP	TPAEPPTAPS	AAPPAPSTEP	PRAGGPHTKM
2090	2100	2110	2120				
GGSRDSLLEM	STSGVGRSQK	QGAGAYSKSY	TLV				

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2598	1	728.7090	-26.65	3	61.1	20.2	2	867-884	K.ELNCTARGERPIIIRWEK.G	

Detailed Protein Report

Protein 849: menin isoform 2 [Homo sapiens]

Accession:	gi|18860847	**Score:**	20.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	67.4
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
MGLKAAQKTL	FPLRSIDDVV	RLFAAELGRE	EPDLVLLSLV	LGFVEHFLAV	NRVIPTNVPE	LTFQPSPAPD	PPGGLTYFPV
90	100	110	120	130	140	150	160
ADLSIIAALY	ARFTAQIRGA	VDLSLYPREG	GVSSRELVKK	VSDVIWNSLS	RSYFKDRAHI	QSLFSFITGT	KLDSSGVAFA
170	180	190	200	210	220	230	240
VVGACQALGL	RDVHLALSED	HAWVVFGPNG	EQTAEVTWHG	KGNEDRRGQT	VNAGVAERSW	LYLKGSYMRC	DRKMEVAFMV
250	260	270	280	290	300	310	320
CAINPSIDLH	TDSLELLQLQ	QKLLWLLYDL	GHLERYPMAL	GNLADLEELE	PTPGRPDPLT	LYHKGIASAK	TYYRDEHIYP
330	340	350	360	370	380	390	400
YMYLAGYHCR	NRNVREALQA	WADTATVIQD	YNYCREDEEI	YKEFFEVAND	VIPNLLKEAA	SLLEAGEERP	GEQSQGTQSQ
410	420	430	440	450	460	470	480
GSALQDPECF	AHLLRFYDGI	CKWEEGSPTP	VLHVGWATFL	VQSLGRFEGQ	VRQKVRIVSR	EAEAAEAEEP	WGEEAREGRR
490	500	510	520	530	540	550	560
RGPRRESKPE	EPPPPKKPAL	DKGLGTGQGA	VSGPPRKPPG	TVAGTARGPE	GGSTAQVPAP	AASPPPEGPV	LTFQSEKMKG
570	580	590	600	610	620		
MKELLVATKI	NSSAIKLQLT	AQSQVQMKKQ	KVSTPSDYTL	SFLKRQRKGL			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1413	2	1021.9933	-70.41	2	46.4	20.2	2	485-502	R.RESKPEEPPPPKKPALDK.G	

Detailed Protein Report

Protein 850: PREDICTED: serine/threonine-protein kinase ULK2 isoform X1 [Homo sapiens]

Accession:	gi|578830126	**Score:**	20.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	110.3
Database Date:	2015-11-30	**pI:**	9.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.2
		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
2716	1	913.4684	61.75	2	62.4	10.2	0	721-739	R.TTSVGPSNSGGSLCAMSGR.V	Carbamidomethyl: 14

Detailed Protein Report

Protein 851: PREDICTED: coiled-coil domain-containing protein 158 isoform X8 [Homo sapiens]

Accession:	gi|578809093	**Score:**	20.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	122.8
Database Date:	2015-11-30	**pI:**	6.4
		Sequence Coverage [%]:	3.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MESKAWESNN	EDLLSSSGVT	SNGGSSSSFF	VSSIRGTIIE	NTSSAGTLTQ	VPFFPKYEVE	LDSPRKIIPS	PGKEHFERVL
90	100	110	120	130	140	150	160
EEYSHQVKDL	QRRLNESNEL	HEKQKFYLRQ	SVIDLQTKLQ	EMQMERDAMA	DIRRRESQSQ	EDLRNQLQNT	VHELEAAKCL
170	180	190	200	210	220	230	240
KEDMLKDSNT	QIEQLRKMML	SHEGVLQEIR	SILVDFEEAS	GKKICEHDSM	STLHFRSLGS	AISKILRELD	TEISYLKGRI
250	260	270	280	290	300	310	320
FPVEDQLEAL	KSESQNKIEL	LLQQHQDRIE	QLISEHEVEI	TGLTEKASSA	RSQANSIQSQ	MEIIQEQARN	QNSMYMRQLS
330	340	350	360	370	380	390	400
DLESTVSQLR	SELREAKRMY	EDKTEELEKQ	LVLANSELTE	ARTERDQFSQ	ESGNLDDQLQ	KLLADLHKRE	KELSLEKEQN
410	420	430	440	450	460	470	480
KRLWDRDTGN	SITIDHLRRE	LDNRNMEVQR	LEALLKALKS	ECQGQMERQM	AAIQGKNESL	EKVSSLTAQL	ESTKEMLRKV
490	500	510	520	530	540	550	560
VEELTAKKMT	LESSERTISD	LTTSLQEKER	AIEATNAEIT	KLRSRVDLKL	QELQHLKNEG	DHLRNVQTEC	EALKLQMTEK
570	580	590	600	610	620	630	640
DKVIEILRQQ	IENMTQLVGQ	HGRTAGAMQV	EKAQLEKEIN	DRRMELKELK	ILKDKKDAKI	RELEARVSDL	ELEKVKLVNA
650	660	670	680	690	700	710	720
GSERLRAVKD	IKQERDQLLN	EVKTSRSELN	NLSAMKVAMG	MQKQITAKRG	QIDALQSKIQ	FLEEAMTNAN	KEKHFLKEEK
730	740	750	760	770	780	790	800
SKLSQELSTV	ATEKNKMAGE	LEVLRSQERR	LKEKVTNMEV	ALDKASLQFA	ECQDIIQRQE	QESVRLKLQH	TLDIKELQGP
810	820	830	840	850	860	870	880
GYTSNSSLKP	RLLQPASVTR	SHSNVPSSQS	TASFLSHHST	KANTLKEDPT	RDLKQLLQEL	RSVINEEPAV	SLSKTEEDGR
890	900	910	920	930	940	950	960
TSLGALYVAV	EDRVRDCITE	SSLRSDMCHR	SNNSLRDSTE	GSKSSETLSR	EPVTLHAGDR	EDPSGCFTFT	SAASPSVKNS
970	980	990	1000	1010	1020	1030	1040
ASRSFNSSPK	KSPVHSLLTS	SVEGSIGSTS	QYRSAKPIHS	SDSVKVSANR	NNRKNMQEAS	EQTRKLANSG	RRFTAEEPSN
1050	1060	1070	1080				
VFNDQKSRKE	DTESKRPGKN	VTKMTRCLPI	LYRGMRPN				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1460	1	982.5829	82.94	3	47.0	10.1	2	530-554	K.LQELQHLKNEGDHLRNVQTECEALK.L	

Detailed Protein Report

Protein 852: 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 853: inorganic pyrophosphatase [Homo sapiens]

Accession: gi|11056044
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl, Oxidation

Score: 19.8
MW [kDa]: 32.6
pI: 5.5
Sequence Coverage [%]: 6.6
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MSGFSTEERA	APFSLEYRVF	LKNEKGQYIS	PFHDIPIYAD	KDVFHMVVEV	PRWSNAKMEI	ATKDPLNPIK	QDVKKGKLRY
90	100	110	120	130	140	150	160
VANLFPYKGY	IWNYGAIPQT	WEDPGHNDKH	TGCCGDNDPI	DVCEIGSKVC	ARGEIIGVKV	LGILAMIDEG	ETDWKVIAIN
170	180	190	200	210	220	230	240
VDDPDAANYN	DINDVKRLKP	GYLEATVDWF	RRYKVPDGKP	ENEFAFNAEF	KDKDFAIDII	KSTHDHWKAL	VTKKTNGKGI
250	260	270	280	290			
SCMNTTLSES	PFKCDPDAAR	AIVDALPPPC	ESACTVPTDV	DKWFHHQKN			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1596	1	696.7599	139.50	3	48.7	19.8	1	235-253	K.TNGKGISCMNTTLSESPFK.C	Carbamidomethyl: 8; Oxidation: 9

Detailed Protein Report

Protein 854: **PREDICTED: mediator of RNA polymerase II transcription subunit 13-like isoform X3 [Homo sapiens]**

Accession:	gi|578823481	**Score:**	19.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	227.2
Database Date:	2015-11-30	**pI:**	5.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	0.7
		No. of unique Peptides:	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MDKNFVRIGK	WFVRPYEKDE	KPVNKSEHLS	CAFTFFLHGE	SNVCTSVEIA	QHQPIYLINE	EHIHMAQSSP	APFQVLVSPY
90	100	110	120	130	140	150	160
GLNGTLTGQA	YKMSDPATRK	LIEEWQYFYP	MVLKKKEESK	EEDELGYDDD	FPVAVEVIVG	GVRMVYPSAF	VLISQNDIPV
170	180	190	200	210	220	230	240
PQSVASAGGH	IAVGQQGLGS	VKDPSNCGMP	LTPPTSPEQA	ILGESGGMQS	AASHLVSQDG	GMITMHSPKR	SGKIPPKLHN
250	260	270	280	290	300	310	320
HMVHRVWKEC	ILNRTQSKRS	QMSTPTLEEE	PASNPATWDF	VDPTQRVSCS	CSRHKLLKRC	AVGPNRPPTV	SQPGFSAGPS
330	340	350	360	370	380	390	400
SSSSLPPPAS	SKHKTAERQE	KGDKLQKRPL	IPFHHRPSVA	EELCMEQDTP	GQKLGLAGID	SSLEVSSSRK	YDKQMAVPSR
410	420	430	440	450	460	470	480
NTSKQMNLNP	MDSPHSPISP	LPPTLSPQPR	GQETESLDPP	SVPVNPALYG	NGLELQQLST	LDDRTVLVGQ	RLPLMAEVSE
490	500	510	520	530	540	550	560
TALYCGIRPS	NPESSEKWWH	SYRLPPSDDA	EFRPPELQGE	RCDAKMEVNS	ESTALQRLLA	QPNKRFKIWQ	DKQPQLQPLH
570	580	590	600	610	620	630	640
FLDPLPLSQQ	PGDSLGEVND	PYTFEDGDIK	YIFTANKKCK	QGTEKDSLKK	NKSEDGFGTK	DVTTPGHSTP	VPDGKNAMSI
650	660	670	680	690	700	710	720
FSSATKTDVR	QDNAAGRAGS	SSLTQVTDLA	PSLHDLDNIF	DNSDDDELGA	VSPALRSSKM	PAVGTEDRPL	GKDGRAAVPY
730	740	750	760	770	780	790	800
PPTVADLQRM	FPTPPSLEQH	PAFSPVMNYK	DGISSETVTA	LGMMESPMVS	MVSTQLTEFK	MEVEDGLGSP	KPEEIKDFSY
810	820	830	840	850	860	870	880
VHKVPSFQPF	VGSSMFAPLK	MLPSHCLLPL	KIPDACLFRP	SWAIPPKIEQ	LPMPPAATFI	RDGYNNVPSV	GSLADPDYLN
890	900	910	920	930	940	950	960
TPQMNTPVTL	NSAAPASNSG	AGVLPSPATP	RFSVPTPRTP	RTPRTPRGGG	TASGQGSVKY	DSTDQGSPAS	TPSTTRPLNS
970	980	990	1000	1010	1020	1030	1040
VEPATMQPIP	EAHSLYVTLI	LSDSVMNIFK	DRNFDSCCIC	ACNMNIKGAD	VGLYIPDSSN	EDQYRCTCGF	SAIMNRKLGY
1050	1060	1070	1080	1090	1100	1110	1120
NSGLFLEDEL	DIFGKNSDIG	QAAERRLMMC	QSTFLPQVEG	TKKPQEPPIS	LLLLLQNQHT	QPFASLNFLD	YISSNNRQTL
1130	1140	1150	1160	1170	1180	1190	1200
PCVSWSYDRV	QADNNDYWTE	CFNALEQGRQ	YVDNPTGGKV	DEALVRSATV	HSWPHSNVLD	ISMLSSQDVV	RMLLSLQPFL
1210	1220	1230	1240	1250	1260	1270	1280
QDAIQKKRTG	RTWENIQHVQ	GPLTWQQFHK	MAGRGTYGSE	ESPEPLPIPT	LLVGYDKDFL	TISPFSLPFW	ERLLLDPYGG
1290	1300	1310	1320	1330	1340	1350	1360
HRDVAYIVVC	PENEALLEGA	KTFFRDLSAV	YEMCRLGQHK	PICKVLRDGI	MRVGKTVAQK	LTDELVSEWF	NQPWSGEEND
1370	1380	1390	1400	1410	1420	1430	1440
NHSRLKLYAQ	VCRHHLAPYL	ATLQLDSSLL	IPPKYQTPPA	AAQGQATPGN	AGPLAPNGSA	APPAGSAFNP	TSNSSSTNPA
1450	1460	1470	1480	1490	1500	1510	1520
ASSSASGSSV	PPVSSSASAP	GISQISTTSS	SGFSGSVGGQ	NPSTGGISAD	RTQGNIGCGG	DTDPGQSSSQ	PSQDGQESVT
1530	1540	1550	1560	1570	1580	1590	1600
ERERIGIPTE	PDSADSHAHP	PAVVIYMVDP	FTYAAEEDST	SGNFWLLSLM	RCYTEMLDNL	PEHMRNSFIL	QIVPCQYMLQ
1610	1620	1630	1640	1650	1660	1670	1680
TMKDEQVFYI	QYLKSMAFSV	YCQCRRPLPT	QIHIKSLTGF	GPAASIEMTL	KNPERPSPIQ	LYSPPFILAP	IKDKQTELGE
1690	1700	1710	1720	1730	1740	1750	1760
TFGEASQKYN	VLFVGYCLSH	DQRWLLASCT	DLHGELLETC	VVNIALPNRS	RRSKVSARKI	GLQKLWEWCI	GIVQMTSLPW
1770	1780	1790	1800	1810	1820	1830	1840
RVVIGRLGRL	GHGELKDWSI	LLGECSLQTI	SKKLKDVCRM	CGISAADSPS	ILSACLVAME	PQGSFVVMPD	AVTMGSVFGR
1850	1860	1870	1880	1890	1900	1910	1920
STALNMQSSQ	LNTPQDASCT	HILVFPTSST	IQVAPANYPN	EDGFSPNNDD	MFVDLPFPDD	MDNDIGILMT	GNLHSSPNSS
1930	1940	1950	1960	1970	1980	1990	2000
PVPSPGSPSG	IGVGSHFQHS	RSQGERLLSR	EAPEELKQQP	LALGYFVSTA	KAENLPQWFW	SSCPQAQNQC	PLFLKASLHH
2010	2020	2030	2040	2050	2060	2070	2080
HISVAQTDEL	LPARNSQRVP	HPLDSKTTSD	VLRFVLEQYN	ALSWLTCNPA	TQDRTSCLPV	HFVVLTQLYN	AIMNIL

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
2308	1	892.3159	-67.35	2	57.5	19.8	0	1572-1585	R.CYTEMLDNLPEHMR.N	Oxidation: 5, 13

Detailed Protein Report

Protein 855: **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 856: PREDICTED: 39S ribosomal protein L28, mitochondrial isoform X1 [Homo sapiens]

Accession:	gi|530407456	**Score:**	19.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	33.8
Database Date:	2015-11-30	**pI:**	9.4
Modification(s):	Oxidation	**Sequence Coverage [%]:**	4.9
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MAFTASQRWE EGQARQIGFR FRWALNPERL AMPLHKYPVW LWKRLQLREG ICSRLPGHYL RSLEEERTPT PVHYRPHGAK
        90        100        110        120        130        140        150        160
FKINPKNGQR ERVEDVPIPI YFPPESQRGL WGGEGWILGQ IYANNDKLSK RLKKVWKPQL FEREFYSEIL DKKFTVTVTM
       170        180        190        200        210        220        230        240
RTLDLIDEAY GLDFYILKTP KEDLCSKFGM DLKRGMLLRL ARQDPQLHPE DPERRAAIYD KYKEFAIPEE EAEWVGLTLE
       250        260        270        280        290
EAIEKQRLLE EKDPVPLFKI YVAELIQQLQ QQALSEPAVV QKRASGQ
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2394	1	899.3523	-161.20	2	58.3	19.6	1	30-43	R.LAMPLHKYPVWLWK.R	Oxidation: 3

Detailed Protein Report

Protein 857: coilin [Homo sapiens]

Accession:	gi|4758024	**Score:**	19.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	62.6
Database Date:	2015-11-30	**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
1827	1	835.3577	-42.45	2	51.5	19.5	2	132-144	K.HWKSRENNNNNEK.V	

Detailed Protein Report

Protein 858: protein maestro isoform b [Homo sapiens]

Accession:	gi|187761377	**Score:**	19.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	23.0
Database Date:	2015-11-30	**pI:**	10.3
		Sequence Coverage [%]:	8.7
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530413995	refseq_human (refseq_human_20140103.fasta)	PREDICTED: protein maestro isoform X4 [Homo sapiens]

```
         10         20         30         40         50         60         70         80
MDQRQRRILG QPLSIPTSQP KQKRTSMISF FSKVSWKLRF QKREPLKNVF FILAERARDP SAKKRHMAMR NLGTMAYEAP
         90        100        110        120        130        140        150        160
DKVRKYKKIV LDLLVYGLYD PVNLEVIHES MKTLTVVLGK IQGKGLGSFF IDITLQTRTL LDDACKTTFQ ACSPYLKLKE
        170        180        190        200
EYSFQSEEDQ RNTKLYQQLS HYHPEILQFF YANKIL
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1043	1	630.9810	-97.07	3	41.8	19.5	2	8-24	R.ILGQPLSIPTSQPKQKR.T	

Detailed Protein Report

Protein 859: **PREDICTED: alpha-(1,3)-fucosyltransferase 11 isoform X4 [Homo sapiens]**

Accession:	gi|578819000	**Score:**	19.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	51.4
Database Date:	2015-11-30	**pI:**	5.7
		Sequence Coverage [%]:	1.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAAGPIRVVL	VLLGVLSVCA	ASGHGSVAER	EAGGEAEWAE	PWDGAVFRPP	SALGAVGVTR	SSGTPRPGRE	EAGDLPVLLW
90	100	110	120	130	140	150	160
WSPGLFPHFP	GDSERIECAR	GACVASRNRR	ALRDSRTRAL	LFYGTDFRAS	AAPLPRLAHQ	SWALLHEESP	LNNFLLSHGP
170	180	190	200	210	220	230	240
GIRLFNLTST	FSRHSDYPLS	LQWLPGTAYL	RRPVPPPMER	AEWRRRGYAP	LLYLQSHCDV	PADRDRYVRE	LMRHIPVDSY
250	260	270	280	290	300	310	320
GKCLQNRELP	TARLQDTATA	TTEDPELLAF	LSRYKFHLAL	ENAICNDYMT	EKLWRPMHLG	AVPVYRGSPS	VRDWMPNNHS
330	340	350	360	370	380	390	400
VILIDDFESP	QKLAEFIDFL	DKNDEEYMKY	LAYKQPGGIT	NQFLLDSLKH	REWGVNDPLL	PNYLNGFECF	VCDYELARLD
410	420	430	440	450	460		
AEKAHAASPG	DSPVFEPHIA	QPSHMDCPVP	TPGFGNVEEI	PENDRYWMLL	HFDAPSF		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
508	2	464.6701	-41.63	2	35.0	19.5	0	343-349	K.NDEEYMK.Y	

Detailed Protein Report

Protein 860: **neuroendocrine convertase 1 isoform 3 [Homo sapiens]**

Accession:	gi|295424145	**Score:**	19.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	49.3
Database Date:	2015-11-30	**pI:**	5.3
		Sequence Coverage [%]:	5.2
		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
1185	1	956.7150	-62.95	3	43.5	19.5	1	405-427	K.DSEDSLYNDYVDVFYNTKPYKHR.D	

Detailed Protein Report

Protein 861: **PREDICTED: alpha-L-iduronidase isoform X1 [Homo sapiens]**

Accession:	gi|578808149	**Score:**	19.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	78.7
Database Date:	2015-11-30	**pI:**	10.4
		Sequence Coverage [%]:	3.7
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MRPLRPRAAL LALLASLLAA PPVAPAEAPH LVHVDAARAL WPLRRFWRST GFCPPLPHSQ ADQYVLSWDQ QLNLAYVGAV
        90        100        110        120        130        140        150        160
PHRGIKQVRT HWLLELVTTR GSTGRGLSYN FTHLDGYLDL LRENQLLPGF ELMGSASGHF TDFEDKQQVF EWKDLVSSLA
       170        180        190        200        210        220        230        240
RRYIGRYGLA HVSKWNFETW NEPDHHDFDN VSMTMQGFLN YYDACSEGLR AASPALRLGG PGDSFHTPPR SPLSWGLLRH
       250        260        270        280        290        300        310        320
CHDGTNFFTG EAGVRLDYIS LHRKVRPAPP SAPVFCALSR CAPGRADPGG AEAAPPAGCA QLHLHPGAGE GRRAADPAAL
       330        340        350        360        370        380        390        400
PQVRGHPHLQ RRGGPAGGLV PATAVEGGRD LRGHGGEGGP AQRPARPPAT FLPRRDRRAV AAPPGPSCPG HPQVIAQHQN
       410        420        430        440        450        460        470        480
LLLANTTSAF PYALLSNDNA FLSYHPHPFA QRTLTARFQV NNTRPPHVQL LRKPVLTAMG LLALLDEEQL WAEVSQAGTV
       490        500        510        520        530        540        550        560
LDSNHTVGVL ASAHRPQGPA DAWRAAVLIY ASDDTRAHPN RSVAVTLRLR GVPPGPGLVY VTRYLDNGLC SPDGEWRRLG
       570        580        590        600        610        620        630        640
RPVFPTAEQF RRMRAAEDPV AAAPRPLPAG GRLTLRPALR LPSLLLVHVC ARPEKPPGQV TRLRALPLTQ GQLVLVWSDE
       650        660        670        680        690        700        710        720
HVGSKCLWTY EIQFSQDGKA YTPVSRKPST FNLFVFSPDT GAVSGSYRVR ALDYWARPGP FSDPVPYLEV PVPRGPPSPG
       730
NP
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1856	1	836.3130	-103.64	3	51.9	19.4	0	286-312	R.ADPGGAEAAPPAGCAQLHLHPGAGEGR.R	

Detailed Protein Report

Protein 862: 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 863: prostaglandin E2 receptor EP3 subtype isoform 8 [Homo sapiens]

Accession: gi|38505186
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 19.4
MW [kDa]: 46.7
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 864: 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 865: PREDICTED: zinc finger transcription factor Trps1 isoform X4 [Homo sapiens]

Accession: gi|530389293
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl, Oxidation

Score: 19.3
MW [kDa]: 141.4
pI: 8.3
Sequence Coverage [%]: 1.9
No. of unique Peptides: 1

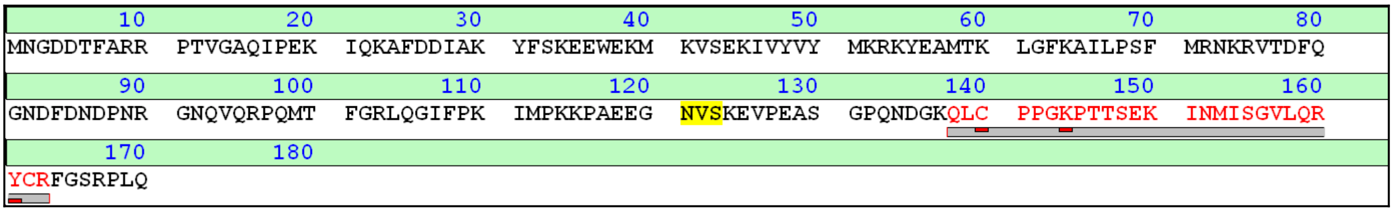
10	20	30	40	50	60	70	80
MVRKKNPPLR	NVASEGEGQI	LEPIGTESKV	SGKNKEFSAD	QMSENTDQSD	AAELNHKEEH	SLHVQDPSSS	SKKDLKSAVL
90	100	110	120	130	140	150	160
SEKAGFNYES	PSKGGNFPSF	PHDEVTDRNM	LAFSSPAAGG	VCEPLKSPQR	AEADDPQDMA	CTPSGDSLET	KEDQKMSPKA
170	180	190	200	210	220	230	240
TEETGQAQSG	QANCQGLSPV	SVASKNPQVP	SDGGVRLNKS	KTDLLVNDNP	DPAPLSPELQ	DFKCNICGYG	YYGNDPTDLI
250	260	270	280	290	300	310	320
KHFRKYHLGL	HNRTRQDAEL	DSKILALHNM	VQFSHSKDFQ	KVNRSVFSGV	LQDINSSRPV	LLNGTYDVQV	TSGGTFIGIG
330	340	350	360	370	380	390	400
RKTPDCQGNT	KYFRCKFCNF	TYMGNSSTEL	EQHFLQTHPN	KIKASLPSSE	VAKPSEKNSN	KSIPALQSSD	SGDLGKWQDK
410	420	430	440	450	460	470	480
ITVKAGDDTP	VGYSVPIKPL	DSSRQNGTEA	TSYYWCKFCS	FSCESSSSLK	LLEHYGKQHG	AVQSGGLNPE	LNDKLSRGSV
490	500	510	520	530	540	550	560
INQNDLAKSS	EGETMTKTDK	SSSGAKKKDF	SSKGAEDNMV	TSYNCQFCDF	RYSKSHGPDV	IVVGPLLRHY	QQLHNIHKCT
570	580	590	600	610	620	630	640
IKHCPFCPRG	LCSPEKHLGE	ITYPFACRKS	NCSHCALLLL	HLSPGAAGSS	RVKHQCHQCS	FTTPDVDVLL	FHYESVHESQ
650	660	670	680	690	700	710	720
ASDVKQEANH	LQGSDGQQSV	KESKEHSCTK	CDFITQVEEE	ISRHYRRAHS	CYKCRQCSFT	AADTQSLLEH	FNTVHCQEQD
730	740	750	760	770	780	790	800
ITTANGEEDG	HAISTIKEEP	KIDFRVYNLL	TPDSKMGEPV	SESVVKREKL	EEKDGLKEKV	WTESSSDDLR	NVTWRGADIL
810	820	830	840	850	860	870	880
RGSPSYTQAS	LGLLTPVSGT	QEQTKTLRDS	PNVEAAHLAR	PIYGLAVETK	GFLQGAPAGG	EKSGALPQQY	PASGENKSKD
890	900	910	920	930	940	950	960
ESQSLLRRRR	GSGVFCANCL	TTKTSLWRKN	ANGGYVCNAC	GLYQKLHSTP	RPLNIIKQNN	GEQIIRRRTR	KRLNPEALQA
970	980	990	1000	1010	1020	1030	1040
EQLNKQQRGS	NEEQVNGSPL	ERRSEDHLTE	SHQREIPLPS	LSKYEAQGSL	TKSHSAQQPV	LVSQTLDIHK	RMQPLHIQIK
1050	1060	1070	1080	1090	1100	1110	1120
SPQESTGDPG	NSSSVSEGKG	SSERGSPIEK	YMRPAKHPNY	SPPGSPIEKY	QYPLFGLPFV	HNDFQSEADW	LRFWSKYKLS
1130	1140	1150	1160	1170	1180	1190	1200
VPGNPHYLSH	VPGLPNPCQN	YVPYPTFNLP	PHFSAVGSDN	DIPLDLAIKH	SRPGPTANGA	SKEKTKAPPN	VKNEGPLNVV
1210	1220	1230	1240	1250	1260	1270	1280
KTEKVDRSTQ	DELSTKCVHC	GIVFLDEVMY	ALHMSCHGDS	GPFQCSICQH	LCTDKYDFTT	HIQRGLHRNN	AQVEKNGKPK
1290							
E							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1488	1	955.7431	8.20	3	47.1	19.3	2	508-531	K.KDFSSKGAEDNMVTSYNCQFCDFR.Y	Carbamidomethyl: 21; Oxidation: 12

Detailed Protein Report

Protein 866: PREDICTED: protein SSX3 isoform X3 [Homo sapiens]

Accession:	gi|530421398	**Score:**	19.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	19.4
Database Date:	2015-11-30	**pI:**	10.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	15.3
		No. of unique Peptides:	1



```
        10         20         30         40         50         60         70         80
MNGDDTFARR PTVGAQIPEK IQKAFDDIAK YFSKEEWEKM KVSEKIVYVY MKRKYEAMTK LGFKAILPSF MRNKRVTDFQ
        90        100        110        120        130        140        150        160
GNDFDNDPNR GNQVQRPQMT FGRLQGIFPK IMPKKPAEEG NVSKEVPEAS GPQNDGKQLC PPGKPTTSEK INMISGVLQR
       170        180
YCRFGSRPLQ
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2926	4	992.7825	-63.37	3	65.3	19.3	2	138-163	K.QLCPPGKPTTSEKINMISGVLQRYCR.F	Carbamidomethyl: 25

Detailed Protein Report

Protein 867: **PREDICTED: ras-GEF domain-containing family member 1B isoform X2 [Homo sapiens]**

Accession:	gi|530377246	**Score:**	19.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	50.3
Database Date:	2015-11-30	**pI:**	9.0
		Sequence Coverage [%]:	3.2
		No. of unique Peptides:	1

Quantitation

Wdown:Qdown **Median:** 0.98 **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
2776	3	913.4592	-12.74	2	63.1	19.1	2	209-222	K.KTRNLEAYVEWFNR.L		Wdown:Qdown 0.98

Detailed Protein Report

Protein 868: pantothenate kinase 4 [Homo sapiens]

Accession:	gi|8922665	**Score:**	19.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	85.9
Database Date:	2015-11-30	**pI:**	5.8
		Sequence Coverage [%]:	2.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAECGASGSG	SSGDSLDKSI	TLPPDEIFRN	LENAKRFAID	IGGSLTKLAY	YSTVQHKVAK	VRSFDHSGKD	TEREHEPPYE
90	100	110	120	130	140	150	160
ISVQEEITAR	LHFIKFENTY	IEACLDFIKD	HLVNTETKVI	QATGGGAYKF	KDLIEEKLRL	KVDKEDVMTC	LIKGCNFVLK
170	180	190	200	210	220	230	240
NIPHEAFVYQ	KDSDPEFRFQ	TNHPHIFPYL	LVNIGSGVSI	VKVETEDRFE	WVGGSSIGGG	TFWGLGALLT	KTKKFDELLH
250	260	270	280	290	300	310	320
LASRGQHSNV	DMLVRDVYGG	AHQTLGLSGN	LIASSFGKSA	TADQEFSKED	MAKSLLHMIS	NDIGQLACLH	ARLHSLDRVY
330	340	350	360	370	380	390	400
FGGFFIRGHP	VTMRTITYSI	NFFSKGEVQA	LFLRHEGYLG	AIGAFLKGAE	QDNPNQYSWG	ENYAGSSGLM	SASPELGPAQ
410	420	430	440	450	460	470	480
RARSGTFDLL	EMDRLERPLV	DLPLLLDPPS	YVPDTVDLTD	DALARKYWLT	CFEEALDGVV	KRAVASQPDS	VDAAERAEKF
490	500	510	520	530	540	550	560
RQKYWNKLQT	LRQQPFAYGT	LTVRSLLDTR	EHCLNEFNFP	DPYSKVKQRE	NGVALRCFPG	VVRSLDALGW	EERQLALVKG
570	580	590	600	610	620	630	640
LLAGNVFDWG	AKAVSAVLES	DPYFGFEEAK	RKLQERPWLV	DSYSEWLQRL	KGPPHKCALI	FADNSGIDII	LGVFPFVREL
650	660	670	680	690	700	710	720
LLRGTEVILA	CNSGPALNDV	THSESLIVAE	RIAGMDPVVH	SALQEERLLL	VQTGSSSPCL	DLSRLDKGLA	ALVRERGADL
730	740	750	760	770	780		
VVIEGMGRAV	HTNYHAALRC	ESLKLAVIKN	AWLAERLGGR	LFSVIFKYEV	PAE		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2133	1	701.2686	-140.84	3	56.8	19.1	1	110-129	K.DHLVNTETKVIQATGGGAYK.F	

Detailed Protein Report

Protein 869: **PREDICTED: nucleolar complex protein 3 homolog isoform X1 [Homo sapiens]**

Accession:	gi|530394138	**Score:**	19.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	58.7
Database Date:	2015-11-30	**pI:**	10.1
		Sequence Coverage [%]:	4.2
		No. of unique Peptides:	1

Quantitation

Wdown:Qdown **Median:** 0.83 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MKARRNKKQI	PSFRKLIKTS	KVKLENKLKN	KQFKQQSTLK	KYRKEQRKLR	QAVKDAVSKK	PIPLENPKEK	RPGKRIEREE
90	100	110	120	130	140	150	160
EEEEEALPLD	MMDEDDLQLM	KDLGQRVSFL	TRDLSSSEPV	HAKKRKHERI	IDKYEKIPRT	LQTAPEKELI	HLLPIKDKSG
170	180	190	200	210	220	230	240
IIPQTREKPV	TDSNKDEEDQ	EEERELEEEI	IEDPIQELTI	EEHLIERKKK	LQEKKMHIAA	LASAILSDPE	NNIKKLKELR
250	260	270	280	290	300	310	320
SMLMEQDPDV	AVTVRKLVIV	SLMELFKDIT	PSYKIRPLTE	AEKSTKTRKE	TQKLREFEEG	LVSQYKFYLE	NLEQMVKDWK
330	340	350	360	370	380	390	400
QRKLKKSNVV	SLKAYKGLAE	VAVKSLCELL	VALPHFNFHN	NIIVLIVPLM	NDMSKLISEM	CCEAVKKLFK	QDKLGQASLG
410	420	430	440	450	460	470	480
VIKVISGFVK	GRNYEVRPEM	LKTFLCLRIK	EVEVKKDTED	INKPKKFMTF	KEKRKSLSRM	QRKWKKAEEK	LERELREAEA
490	500	510					
SESTEKKLKL	VCSPYKCGIF						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2876	1	1132.6192	-5.27	2	65.1	19.1	2	215-235	K.KMHIAALASAILSDPENNIKK.L		Wdown:Qdown 0.83

Detailed Protein Report

Protein 870: protein S100-A9 [Homo sapiens]

Accession:	gi|4506773	**Score:**	19.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	13.2
Database Date:	2015-11-30	**pI:**	5.7
		Sequence Coverage [%]:	11.4
		No. of unique Peptides:	1

```
         10         20         30         40         50         60         70         80
MTCKMSQLER NIETIINTFH QYSVKLGHPD TLNQGEFKEL VRKDLQNFLK KENKNEKVIE HIMEDLDTNA DKQLSFEEFI
         90        100        110        120
MLMARLTWAS HEKMHEGDEG PGHHHKPGLG EGTP
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
253	1	728.3359	-39.98	2	31.9	19.1	0	26-38	K.LGHPDTLNQGEFK.E	

Detailed Protein Report

Protein 871: thyroid peroxidase isoform e precursor [Homo sapiens]

Accession:	gi|28558990	**Score:**	18.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	84.5
Database Date:	2015-11-30	**pI:**	5.9
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MRALAVLSVT	LVMACTEAFF	PFISRGKELL	WGKPEESRVS	SVLEESKRLV	DTAMYATMQR	NLKKRGILSP	AQLLSFSKLP
90	100	110	120	130	140	150	160
EPTSGVIARA	AEIMETSIQA	MKRKVNLKTQ	QSQHPTDALS	EDLLSIIANM	SGCLPYMLPP	KCPNTCLANK	YRPITGACNN
170	180	190	200	210	220	230	240
RDHPRWGASN	TALARWLPPV	YEDGFSQPRG	WNPGFLYNGF	PLPPVREVTR	HVIQVSNEVV	TDDDRYSDLL	MAWGQYIDHD
250	260	270	280	290	300	310	320
IAFTPQSTSK	AAFGGGADCQ	MTCENQNPCF	PIQIITLRDY	IPRILGPEAF	QQYVGPYEGY	DSTANPTVSN	VFSTAAFRFG
330	340	350	360	370	380	390	400
HATIHPLVRR	LDASFQEHPD	LPGLWLHQAF	FSPWTLLRGG	GLDPLIRGLL	ARPAKLQVQD	QLMNEELTER	LFVLSNSSTL
410	420	430	440	450	460	470	480
DLASINLQRG	RDHGLPGYNE	WREFCGLPRL	ETPADLSTAI	ASRSVADKIL	DLYKHPDNID	VWLGGLAENF	LPRARTGPLF
490	500	510	520	530	540	550	560
ACLIGKQMKA	LRDGDWFWWE	NSHVFTDAQR	RELEKHSLSR	VICDNTGLTR	VPMDAFQVGK	FPEDFESCDS	ITGMNLEAWR
570	580	590	600	610	620	630	640
ETFPQDDKCG	FPESVENGDF	VHCEESGRRV	LVYSCRHGYE	LQGREQLTCT	QEGWDFQPPL	CKDVNECADG	AHPPCHASAR
650	660	670	680	690	700	710	720
CRNTKGGFQC	LCADPYELGD	DGRTCVDSGR	LPRVTWISMS	LAALLIGGFA	GLTSTVICRW	TRTGTKSTLP	ISETGGGTPE
730	740	750	760	770			
LRCGKHQAVG	TSPQRAAAQD	SEQESAGMEG	RDTHRLPRAL				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2490	1	826.6956	-180.11	2	59.4	18.9	0	736-751	R.AAAQDSEQESAGMEGR.D	Oxidation: 13

Detailed Protein Report

Protein 872: 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 873: **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

Detailed Protein Report

Protein 874: T-complex protein 1 subunit gamma isoform c [Homo sapiens]

Accession:	gi|58761484	**Score:**	18.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	56.4
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
MMGHRPVLVL	SQNTKRESGR	KVQSGNINAA	KIQVQHPAAK	SMIEISRTQD	EEVGDGTTSV	IILAGEMLSV	AEHFLEQQMH
90	100	110	120	130	140	150	160
PTVVISAYRK	ALDDMISTLK	KISIPVDISD	SDMMLNIINS	SITTKAISRW	SSLACNIALD	AVKMVQFEEN	GRKEIDIKKY
170	180	190	200	210	220	230	240
ARVEKIPGGI	IEDSCVLRGV	MINKDVTHPR	MRRYIKNPRI	VLLDSSLEYK	KGESQTDIEI	TREEDFTRIL	QMEEEYIQQL
250	260	270	280	290	300	310	320
CEDIIQLKPD	VVITEKGISD	LAQHYLMRAN	ITAIRRVRKT	DNNRIARACG	ARIVSRPEEL	REDDVGTGAG	LLEIKKIGDE
330	340	350	360	370	380	390	400
YFTFITDCKD	PKACTILLRG	ASKEILSEVE	RNLQDAMQVC	RNVLLDPQLV	PGGGASEMAV	AHALTEKSKA	MTGVEQWPYR
410	420	430	440	450	460	470	480
AVAQALEVIP	RTLIQNCGAS	TIRLLTSLRA	KHTQENCETW	GVNGETGTLV	DMKELGIWEP	LAVKLQTYKT	AVETAVLLLR
490	500	510					
IDDIVSGHKK	KGDDQSRQGG	APDAGQE					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
93	1	1044.7083	124.99	2	30.4	18.8	2	333-351	K.ACTILLRGASKEILSEVER.N	

Detailed Protein Report

Protein 875: **polycystic kidney disease protein 1-like 3 precursor [Homo sapiens]**

Accession: gi|31559825
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 18.7
MW [kDa]: 195.8
pI: 9.6
Sequence Coverage [%]: 1.5
No. of unique Peptides: 1

Quantitation

mdown:qdown **Median:** 6.32 **CV:** 0.00 % **No. of 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
```

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
146	1	896.8772	102.59	3	31.2	18.7	2	1242-1267	K. CSSSVPGSRDKNNPVYVAPAINS H		mdown:qdown 6.32

Detailed Protein Report

Protein 876: PREDICTED: protein Shroom3 isoform X5 [Homo sapiens]

Accession:	gi|578809297	**Score:**	18.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	212.8
Database Date:	2015-11-30	**pI:**	8.5
		Sequence Coverage [%]:	1.6
		No. of unique Peptides:	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MLSHEARGLL	SLSNGGDLSQ	MVEEGGKADT	LSSKLQAGDE	VVHINEVTLS	SSRKEAVSLV	KGSYKTLRLV	VRRDVCTDPG
90	100	110	120	130	140	150	160
HADTGASNFV	SPEHLTSGPQ	HRKAAWSGGV	KLRLKHRRSE	PAGRPHSWHT	TKSGEKQPDA	SMMQISQGMI	GPPWHQSYHS
170	180	190	200	210	220	230	240
SSSTSDLSNY	DHAYLRRSPD	QCSSQGSMES	LEPSGAYPPC	HLSPAKSTGS	IDQLSHFHNK	RDSAYSSFST	SSSILEYPHP
250	260	270	280	290	300	310	320
GISGRERSGS	MDNTSARGGL	LEGMRQADIR	YVKTVYDTRR	GVSAEYEVNS	SALLLQGREA	RASANGQGYD	KWSNIPRGKG
330	340	350	360	370	380	390	400
VPPPSWSQQC	PSSLETATDN	LPPKVGAPLP	PARSDSYAAF	RHRERPSSWS	SLDQKRLCRP	QANSLGSLKS	PFIEEQLHTV
410	420	430	440	450	460	470	480
LEKSPENSPP	VKPKHNYTQK	AQPGQPLLPT	SIYPVPSLEP	HFAQVPQPSV	SSNGMLYPAL	AKESGYIAPQ	GACNKMATID
490	500	510	520	530	540	550	560
ENGNQNGSGR	PGFAFCQPLE	HDLLSPVEKK	PEATAKYVPS	KVHFCSVPEN	EEDASLKRHL	TPPQGNSPHS	NERKSTHSNK
570	580	590	600	610	620	630	640
PSSHPHSLKC	PQAQAWQAGE	DKRSSRLSEP	WEGDFQEDHN	ANLWRRLERE	GLGQSLSGNF	GKTKSAFSSL	QNIPESLRRH
650	660	670	680	690	700	710	720
SSLELGRGTQ	EGYPGGRPTC	AVNTKAEDPG	RKAAPDLGSH	LDRQVSYPRP	EGRTGASASF	NSTDPSPEEP	PAPSHPHTSS
730	740	750	760	770	780	790	800
LGRRGPGPGS	ASALQGFQYG	KPHCSVLEKV	SKFEQREQGS	QRPSVGGSGF	GHNYRPHRTV	STSSTSGNDF	EETKAHIRFS
810	820	830	840	850	860	870	880
ESAEPLGNGE	QHFKNGELKL	EEASRQPCGQ	QLSGGASDSG	RGPQRPDARL	LRSQSTFQLS	SEPEREPEWR	DRPGSPESPL
890	900	910	920	930	940	950	960
LDAPFSRAYR	NSIKDAQSRV	LGATSFRRRD	LELGAPVASR	SWRPRPSSAH	VGLRSPEASA	SASPHTPRER	HSVTPAEGDL
970	980	990	1000	1010	1020	1030	1040
ARPVPPAARR	GARRRLTPEQ	KKRSYSEPEK	MNEVGIVEEA	EPAPLGPQRN	GMRFPESSVA	DRRRLFERDG	KACSTLSLSG
1050	1060	1070	1080	1090	1100	1110	1120
PELKQFQQSA	LADYIQRKTG	KRPTSAAGCS	LQEPGPLRER	AQSAYLQPGP	AALEGSGLAS	ASSLSSLREP	SLQPRREATL
1130	1140	1150	1160	1170	1180	1190	1200
LPATVAETQQ	APRDRSSSFA	GGRRLGERRR	GDLLSGANGG	TRGTQRGDET	PREPSSWGAR	AGKSMSAEDL	LERSDVLAGP
1210	1220	1230	1240	1250	1260	1270	1280
VHVRSRSSPA	TADKRQDVLL	GQDSGFGLVK	DPCYLAGPGS	RSLSCSERGQ	EEMLPLFHHL	TPRWGGSGCK	AIGDSSVPSE
1290	1300	1310	1320	1330	1340	1350	1360
CPGTLDHQRQ	ASRTPCPRPP	LAGTQGLVTD	TRAAPLTPIG	TPLPSAIPSG	YCSQDGQTGR	QPLPPYTPAM	MHRSNGHTLT
1370	1380	1390	1400	1410	1420	1430	1440
QPPGPRGCEG	DGPEHGVEEG	TRKRVSLPQW	PPPSRAKWAH	AAREDSLPEE	SSAPDFANLK	HYQKQQSLPS	LCSTSDPDTP
1450	1460	1470	1480	1490	1500	1510	1520
LGAPSTPGRI	SLRISESVLR	DSPPPHEDYE	DEVFVRDPHP	KATSSPTFEP	LPPPPPPPPS	QETPVYSMDD	FPPPPPHTVC
1530	1540	1550	1560	1570	1580	1590	1600
EAQLDSEDPE	GPRPSFNKLS	KVTIARERHM	PGAAHVVGSQ	TLASRLQTSI	KGSEAESTPP	SFMSVHAQLA	GSLGGQPAPI
1610	1620	1630	1640	1650	1660	1670	1680
QTQSLSHDPV	SGTQGLEKKV	SPDPQKSSED	IRTEALAKEI	VHQDKSLADI	LDPDSRLKTT	MDLMEGLFPR	DVNLLKENSV
1690	1700	1710	1720	1730	1740	1750	1760
KRKAIQRTVS	SSGCEGKRNE	DKEAVSMLVN	CPAYYSVSAP	KAELLNKIKE	MPAEVNEEEE	QADVNEKKAE	LIGSLTHKLE
1770	1780	1790	1800	1810	1820	1830	1840
TLQEAKGSLL	TDIKLNNALG	EEVEALISEL	CKPNEFDKYR	MFIGDLDKVV	NLLLSLSGRL	ARVENVLSGL	GEDASNEERS
1850	1860	1870	1880	1890	1900	1910	1920
SLYEKRKILA	GQHEDARELK	ENLDRRERVV	LGILANYLSE	EQLQDYQHFV	KMKSTLLIEQ	RKLDDKIKLG	QEQVKCLLES
1930	1940	1950	1960	1970			
LPSDFIPKAG	ALALPPNLTS	EPIPAGGCTF	SGIFPTLTSP	L			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
676	1	1106.2349	41.88	3	37.3	18.7	2	73-103	R.RDVCTDPGHADTGASNFVSPEHLTSGPQHRK.A	

Detailed Protein Report

Protein 877: PREDICTED: uncharacterized protein C4orf50 [Homo sapiens]

Accession:	gi|530358255	**Score:**	18.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	97.6
Database Date:	2015-11-30	**pI:**	5.4
		Sequence Coverage [%]:	1.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPLLQGEASV	SKEGPESLSR	RERVEGYVWG	LRGGLSSENE	EVAPPATFSR	AHETKEPWPT	DSQLLAGKVR	ATGRTARGKE
90	100	110	120	130	140	150	160
ENQVWLGNAL	LLQGGSLEDK	GLEEEDEMPH	QEASGLGCRG	APEEPDSQEH	ESKEMLFFAG	ETGLPLFPRF	ALSVEGAEPT
170	180	190	200	210	220	230	240
DHGHPQAVSK	GHDRCALTID	ELAQDVEACF	QQLSTLQPGS	RGWQCSASAC	RGENWSFAQK	WHSGWERAHS	QQVWGNWGIC
250	260	270	280	290	300	310	320
SNEEAKSKES	GEGDKPGKTT	ALGTSEVPGN	PGTLPHWDEA	SPNPPQGPAE	PWGALERVRS	RFHQLISGLK	KQRSQILHDN
330	340	350	360	370	380	390	400
TKLHGDQERF	HERVCALERE	REREVTKISR	LERDNHRLVG	DISQLKKELD	QYLQAISDLE	DCNGKSYCKI	LELEEENETL
410	420	430	440	450	460	470	480
KGNLGQLQKA	TSESVRKSKD	TMEQVTLENW	KLQTLISELG	VSYKELIKDI	VLGIEDMIRA	LSGENEHLLR	RVHVLEREVT
490	500	510	520	530	540	550	560
LQRSTDQGRL	VRGREHLQGK	AKMHALDKEV	QVTPLTGQLL	SRACGPPLEE	EMSLAAGQTG	PSTGTGNSRR	GADSPPPSLV
570	580	590	600	610	620	630	640
WRNTGVANAL	QGNVSGAEVK	EAHLEKEEKR	PRCSVAQGQA	LSSLSNGPML	RDSEAEVTEE	DPRLRAQQLH	HRVLTLQCQL
650	660	670	680	690	700	710	720
RDQGAAHQAS	LDEATRLQEE	LQAKLEELQK	KQHEAKLAVT	PLKAKIASLV	RKCRERNRLI	THLLQELHRH	GLGNLLLSEL
730	740	750	760	770	780	790	800
AQNMLNDVAL	AEYTATFLAP	GVPETSHHLD	VKSEMTAALR	AQTYLLNPEM	DSVLQSSLSS	ESWPVPEPEW	PAQTAQLDSL
810	820	830	840	850	860	870	880
KLPLSLVSTL	DPGTCLAAVT	VEPGLPAQRL	QEKGGMPCPA	LQVDNVPAPS	ELLSPARILA	FHQELRQSIC	SNSQVHKSPL
890							
ELEM							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2185	5	1273.3850	-233.24	1	55.9	18.7	0	449-459	K.DIVLGIEDMIR.A	

Detailed Protein Report

Protein 878: IQ domain-containing protein H isoform 4 [Homo sapiens]

Accession:	gi|547235270	**Score:**	18.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	71.2
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
MTKAMKVKTP	LRALKSLWDY	DFLIYDGVID	NTAPDFLAFK	EHFSLAWGGI	FSLLEHVEKF	LRNYAIPEVK	IKGNNLVALL
90	100	110	120	130	140	150	160
PEFELTNKLT	RYDLLSVLED	PAHVQMLINL	PGQRYKGQDG	NSEAAMKIQA	TWKCYKARKF	FLFYRQQKWA	SGVIAIAWLL
170	180	190	200	210	220	230	240
YCHKTRLKKI	LKESRQRHLE	NFRIRAKHLA	ANWNRIRTSR	RTIIHIPSLG	YSQPVREHIA	DFNTQQNMQL	GRLCDILDAN
250	260	270	280	290	300	310	320
VNVIYICSHH	MNDELVLYYK	KILSLHAAVK	SGNLEDRSDL	QDRFKIITPE	AVNIFPMIEQ	LSQLITDHLQ	IQRWLFKMDS
330	340	350	360	370	380	390	400
EFRGNGTAFC	DIPSYLKCYK	WVLKESSRYG	LEDWRKKWAQ	EPALVKISEE	LAGILAQHAQ	PVNEKRFPTW	RKFLQTFLSQ
410	420	430	440	450	460	470	480
GGVIEAFPPA	DNVTNLTVDM	LIEPNGKISV	LSTGDQLHAE	SPFISSGTTV	PQTSVDPQVL	TYLCLQIGKA	CRMRDVVGYF
490	500	510	520	530	540	550	560
SIDLVTFIDP	STLEQQVWAT	GLNLAYSDQL	ALTQLTLYLT	NGHLDCSLST	LEVPRFVPKE	RKKTKCMSAL	SMPMLATSRY
570	580	590	600	610	620	630	
AVMTTQLRHS	NLSLVFHYVF	LQICRAHGIG	YDLENNRRGS	PGGPHDLCSP	SLHHPSRNIS	T	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1719	1	882.4159	18.82	3	50.2	18.6	2	318-340	K.MDSEFRGNGTAFCDIPSYLKCYK.W	

Detailed Protein Report

Protein 879: 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 880: **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 881: spindle assembly abnormal protein 6 homolog [Homo sapiens]

Accession:	gi|35038601	**Score:**	18.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	74.4
Database Date:	2015-11-30	**pI:**	7.9
		Sequence Coverage [%]:	2.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSQVLFHQLV	PLQVKCKDCE	ERRVSIRMSI	ELQSVSNPVH	RKDLVIRLTD	DTDPFFLYNL	VISEEDFQSL	KFQQGLLVDF
90	100	110	120	130	140	150	160
LAFPQKFIDL	LQQCTQEHAK	EIPRFLLQLV	SPAAILDNSP	AFLNVVETNP	FKHLTHLSLK	LLPGNDVEIK	KFLAGCLKCS
170	180	190	200	210	220	230	240
KEEKLSLMQS	LDDATKQLDF	TRKTLAEKKQ	ELDKLRNEWA	SHTAALTNKH	SQELTNEKEK	ALQAQVQYQQ	QHEQQKKDLE
250	260	270	280	290	300	310	320
ILHQQNIHQL	QNRLSELEAA	NKDLTERKYK	GDSTIRELKA	KLSGVEEELQ	RTKQEVLSLR	RENSTLDVEC	HEKEKHVNQL
330	340	350	360	370	380	390	400
QTKVAVLEQE	IKDKDQLVLR	TKEAFDTIQE	QKVVLEENGE	KNQVQLGKLE	ATIKSLSAEL	LKANEIIKKL	QGDLKTLMGK
410	420	430	440	450	460	470	480
LKLKNTVTIQ	QEKLLAEKEE	KLQKEQKELQ	DVGQSLRIKE	QEVCKLQEQL	EATVKKLEES	KQLLKNNEKL	ITWLNKELNE
490	500	510	520	530	540	550	560
NQLVRKQDVL	GPSTTPPAHS	SSNTIRSGIS	PNLNVVDGRL	TYPTCGIGYP	VSSAFAFQNT	FPHSISAKNT	SHPGSGTKVQ
570	580	590	600	610	620	630	640
FNLQFTKPNA	SLGDVQSGAT	ISMPCSTDKE	NGENVGLESK	YLKKREDSIP	LRGLSQNLFS	NSDHQRDGTL	GALHTSSKPT
650	660						
ALPSASSAYF	PGQLPNS						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1496	1	829.1351	164.97	2	48.5	18.4	2	375-389	K.SLSAELLKANEIIKK.L	

Protein 882: PREDICTED: orofacial cleft 1 candidate gene 1 protein [Homo sapiens]

Accession: gi|530358739
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 18.3
MW [kDa]: 48.0
pI: 5.4
Sequence Coverage [%]: 2.9
No. of unique Peptides: 1

Alias proteins:

Accession	Name	Description
gi|530435542	refseq_human (refseq_human_20140103.fasta)	PREDICTED: orofacial cleft 1 candidate gene 1 protein [Homo sapiens]
gi|530382966	refseq_human (refseq_human_20140103.fasta)	PREDICTED: orofacial cleft 1 candidate gene 1 protein [Homo sapiens]

10	20	30	40	50	60	70	80
MRETGLKSVH	CQGQEAENME	REKFQQKALK	QTKQKKSKSA	EFLMVKEDRE	ATEGTGNPAF	NMSSPDLSAC	QTAEKKVIRH
90	100	110	120	130	140	150	160
DMPDRTLAAH	QQKFRLPASA	EPKGNEYGRN	YFDPLMDEEI	NPRQCATEVS	REGAPSKEKW	SIPKKIGPCS	MDYDPNLLEE
170	180	190	200	210	220	230	240
DDELHSQGDS	LTDHSVKGKS	TVWRIGEAED	YSQDISYLEE	LEEHRFSVCC	SSVADSRYGD	FFKHLHFVLV	SASSELQLSQ
250	260	270	280	290	300	310	320
WQSQGFWYII	LLMFFLWFLR	LYLHYLGQWL	FLQAISTPVT	KFHFSLHIVE	LCYPTSSLHI	GEELPVVVMG	PLMLNAILLL
330	340	350	360	370	380	390	400
LVLIRWGCQL	LFASCPDVLS	KLIITMGLWT	ILDPLAVFIL	DTLLGRLTDN	EETPVADAAK	LYWMFVRTVQ	PGILGVVITV
410	420	430					
LLYILLFVIS	SLILYLYCLR						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
48	1	630.8632	146.24	2	29.3	18.3	0	206-217	R.FSVCCSSVADSR.Y	

Protein 883: histone H1.2 [Homo sapiens]

Accession: gi|4885375
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 18.3
MW [kDa]: 21.4
pI: 11.4
Sequence Coverage [%]: 8.0
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MSETAPAAPA	AAPPAEKAPV	KKKAAKKAGG	TPRKASGPPV	SELITKAVAA	SKERSGVSLA	ALKKALAAAG	YDVEKNNSRI
90	100	110	120	130	140	150	160
KLGLKSLVSK	GTLVQTKGTG	ASGSFKLNKK	AASGEAKPKV	KKAGGTKPKK	PVGAAKKPKK	AAGGATPKKS	AKKTPKKAKK
170	180	190	200	210	220		
PAAATVTKKV	AKSPKKAKVA	KPKKAAKSAA	KAVKPKAAKP	KVVKPKKAAP	KKK		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1937	1	805.3055	-115.03	2	52.9	18.3	0	1-17	-.MSETAPAAPAAAPPAEK.A	

Detailed Protein Report

Protein 884: **PREDICTED: TGF-beta-activated kinase 1 and MAP3K7-binding protein 3 isoform X3 [Homo sapiens]**

Accession:	gi|578837866	**Score:**	18.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	75.0
Database Date:	2015-11-30	**pI:**	9.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAQSSPQLDI	QVLHDLRQRF	PEIPEGVVSQ	CMLQNNNNLE	ACCRALSQES	SKYLYMEYHS	PDDNRMNRNR	LLHINLGIHS
90	100	110	120	130	140	150	160
PSSYHPGDGA	QLNGGRTLVH	SSSDGHIDPQ	HAAGKQLICL	VQEPHSAPAV	VAATPNYNPF	FMNEQNRSAA	TPPSQPPQQP
170	180	190	200	210	220	230	240
SSMQTGMNPS	AMQGPSPPPP	PPSYMHIPRY	STNPITVTVS	QNLPSGQTVP	RALQILPQIP	SNLYGSPGSI	YIRQTSQSSS
250	260	270	280	290	300	310	320
GRQTPQSTPW	QSSPQGPVPH	YSQRPLPVYP	HQQNYQPSQY	SPKQQQIPQS	AYHSPPPSQC	PSPFSSPQHQ	VQPSQLGHIF
330	340	350	360	370	380	390	400
MPPSPSTTPP	HPYQQGPPSY	QKQGSHSVAY	LPYTASSLSK	GSMKKIEITV	EPSQRPGTAI	NRSPSPISNQ	PSPRNQHSLY
410	420	430	440	450	460	470	480
TATTPPSSSP	SRGISSQPKP	PFSVNPVYIT	YTQPTGPSCT	PSPSPRVIPN	PTTVFKITVG	RATTENLLNL	VDQEERSAAP
490	500	510	520	530	540	550	560
EPIQPISVIP	GSGGEKGSHK	YQRSSSSGSD	DYAYTQALLL	HQRARMERLA	KQLKLEKEEL	ERLKSEVNGM	EHDLMQRRLR
570	580	590	600	610	620	630	640
RVSCTTAIPT	PEEMTRLRSM	NRQLQINVDC	TLKEVDLLQS	RGNFDPKAMN	NFYDNIEPGP	VVPPKPSKKE	HRTGSTQSPR
650	660	670	680				
TQPRDEDYEG	APWNCDSCTF	LNHPALNRCE	QCEMPRYT				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1041	1	955.6888	-79.15	3	42.6	18.2	0	20-44	R.FPEIPEGVVSQCMLQNNNNLEACCR.A	Carbamidomethyl: 23

Detailed Protein Report

Protein 885: homeobox protein Hox-A6 [Homo sapiens]

Accession:	gi|13489077	**Score:**	18.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	26.3
Database Date:	2015-11-30	**pI:**	9.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	6.0
		No. of unique Peptides:	1

Quantitation

mdown:qdown **Median:** 0.21 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MSSYFVNPTF	PGSLPSGQDS	FLGQLPLYQA	GYDALRPFPA	SYGASSLPDK	TYTSPCFYQQ	SNSVLACNRA	SYEYGASCFY
90	100	110	120	130	140	150	160
SDKDLSGASP	SGSGKQRGPG	DYLHFSPEQQ	YKPDSSSGQG	KALHDEGADR	KYTSPVYPWM	QRMNSCAGAV	YGSHGRRGRQ
170	180	190	200	210	220	230	240
TYTRYQTLEL	EKEFHFNRYL	TRRRRIEIAN	ALCLTERQIK	IWFQNRRMKW	KKENKLINST	QPSGEDSEAK	AGE

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2030	1	713.2881	-21.57	2	53.9	18.2	0	143-156	R.MNSCAGAVYGSHGR.R	Oxidation: 1	mdown:qdown 0.21

Detailed Protein Report

Protein 886: 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 887: tetratricopeptide repeat protein 24 [Homo sapiens]

Accession: gi|282165719
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 18.2
MW [kDa]: 63.4
pI: 10.2
Sequence Coverage [%]: 2.7
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MSSPNPEDVP	RRPEPEPSSS	NKKKKKRKWL	RQEASIQALT	RAGHGALQAG	QNHEALNNFQ	RAFLLASKAP	QTRDTPVLQA
90	100	110	120	130	140	150	160
CAFNLGAAYV	ETGDPARGLE	LLLRAHPEEK	AQGRRHGDQC	FNVALAYHAL	GELPQALAWY	HRALGHYQPQ	GDQGEAWAKM
170	180	190	200	210	220	230	240
GACYQALGQP	ELAAHCLQEA	SQAYAQERQL	RAAALALGAA	AGCMLKSGRH	RVGEVVQVLE	KSRRLAERST	ERRLLGHLYN
250	260	270	280	290	300	310	320
DLGLGYSQLQ	LFPLAVEAFL	QALPLCWVPG	EQATVLRNLG	MAHNALGNYQ	EAREFHQKAA	DLHGSVGQRW	EQGRSFGSLA
330	340	350	360	370	380	390	400
FALSQLGDHK	AARDNYLHAL	QAARDSGDMK	GQWQACEGLG	AAAARLGQYD	QALKYYKEAL	AQCQKEPDSV	RERLVAKLAD
410	420	430	440	450	460	470	480
TVRTRLAQVG	LVQTHTLTSA	PGRLQAPGGA	SQAEGTPAKA	GSSTAGVQHR	SSSGWEDEEF	EEGHQKKKEE	RSANVPVRAG
490	500	510	520	530	540	550	560
PGRPELCFLP	GTVNHSHHLA	SSCPTFTKHT	PCRGTVLGKA	SIYSPGPRAH	LPFVGPGPPR	AEYPSILVPN	GPQANRSSRW
570	580	590					
PRESLSRSRQ	RRPMESGICT	IV					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1610	3	839.3850	-57.62	2	48.6	18.2	0	315-330	R.SFGSLAFALSQLGDHK.A	

Detailed Protein Report

Protein 888: **PREDICTED: transmembrane 7 superfamily member 3 isoform X1 [Homo sapiens]**

Accession:	gi|530399194	**Score:**	18.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	58.7
Database Date:	2015-11-30	**pI:**	6.4
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGFLQLLVVA	VLASEHRVAG	AAEVFGNSSE	GLIEFSVGKF	RYFELNRPFP	EEAILHDISS	NVTFLIFQIH	SQYQNTTVSF
90	100	110	120	130	140	150	160
SPTLLSNSSE	TGTASGLVFI	LRPEQSTCTW	YLGTSGIQPV	QNMAILLSYS	ERDPVPGGCN	LEFDLDIDPN	IYLEYNFFET
170	180	190	200	210	220	230	240
TIKFAPANLG	YARGVDPPPC	DAGTDQDSRW	RLQYDVYQYF	LPENDLTEEM	LLKHLQRMVS	VPQVKASALK	VVTLTANDKT
250	260	270	280	290	300	310	320
SVSFSSLPGQ	GVIYNVIVWD	PFLNTSAAYI	PAHTYACSFE	AGEGSCASLG	RVSSKVFFTL	FALLGFFICF	FGHRFWKTEL
330	340	350	360	370	380	390	400
FFIGFIIMGF	FFYILITRLT	PIKYDGNLKI	FHDDGVFWVT	FSCIAILIPV	VFMGCLRILN	ILTCGVIGSY	SVVLAIDSYW
410	420	430	440	450	460	470	480
STSLSYITLN	VLKRALNKDF	HRAFTNVPFQ	TNDFIILAVW	GMLAVSGITL	QIRRERGRPF	FPPHPYKLWK	QERERRVTNI
490	500	510	520				
LDPSYHIPPL	RERLYGRLTQ	IKGLFQKEQP	AGERTPLLL				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2409	1	954.4178	-134.28	2	58.8	18.1	2	214-230	K.HLQRMVSVPQVKASALK.V	Oxidation: 5

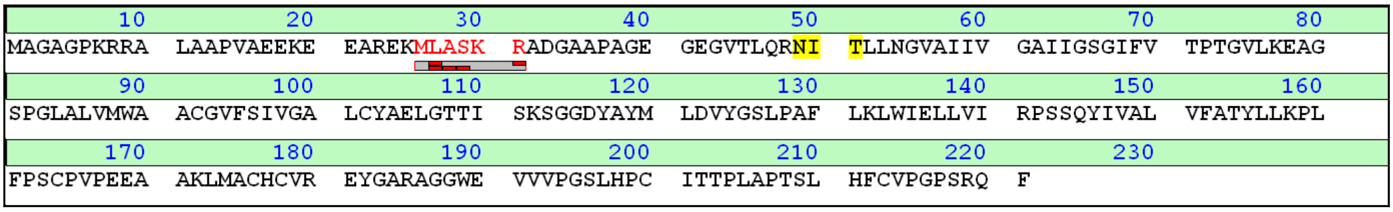
Detailed Protein Report

Protein 889: **PREDICTED: putative L-type amino acid transporter 1-like protein MLAS-like [Homo sapiens]**

Accession:	gi|578846041	**Score:**	18.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	23.1
Database Date:	2015-11-30	**pI:**	8.9
		Sequence Coverage [%]:	2.7
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	3.75	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	2.30	**CV:**	0.00 %	**No. of Peptides:**	1



```
        10         20         30         40         50         60         70         80
MAGAGPKRRA LAAPVAEEKE EAREKMLASK RADGAAPAGE GEGVTLQRNI TLLNGVAIIV GAIIGSGIFV TPTGVLKEAG
        90        100        110        120        130        140        150        160
SPGLALVMWA ACGVFSIVGA LCYAELGTTI SKSGGDYAYM LDVYGSLPAF LKLWIELLVI RPSSQYIVAL VFATYLLKPL
       170        180        190        200        210        220        230
FPSCPVPEEA AKLMACHCVR EYGARAGGWE VVVPGSLHPC ITTPLAPTSL HFCVPGPSRQ F
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1084	1	705.1875	-311.96	1	42.0	18.1	1	26-31	K.MLASKR.A		mdown:qdown 3.75 Wdown:Qdown 2.30

Detailed Protein Report

Protein 890: 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

Quantitation

mdown:qdown	**Median:**	2.84	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	2.08	**CV:**	0.00 %	**No. of 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	Ratios
1618	1	804.1891	-319.55	1	50.1	18.1	0	6-12	K.ETLSLNK.C		Wdown:Qdown 2.08 mdown:qdown 2.84

Detailed Protein Report

Protein 891: 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

BRUKER

Detailed Protein Report

Protein 892: 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

```
        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
550	1	679.2027	-190.28	2	36.2	17.9	1	137-152	R.GTAGPGGSGSGSPRGR.G	

Detailed Protein Report

Protein 893: 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 894: PREDICTED: unconventional myosin-XVIIIb isoform X5 [Homo sapiens]

Accession:	gi|578837447	**Score:**	17.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	157.5
Database Date:	2015-11-30	**pI:**	9.5
		Sequence Coverage [%]:	1.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAISSRLALW	EQKIREEDKS	PPPSSPPPLF	SVIPGGFIKQ	LVRGTEKEAK	EARQRKQLAV	ASPEREIPEI	SISQPNSKSS
90	100	110	120	130	140	150	160
SGTRSGSQQI	SQDDQSSSPG	SSDILGKESE	GSRSPDPEQM	TSINGEKAQE	LGSSATPTKK	TVPFKRGVRR	GDVLLMVAKL
170	180	190	200	210	220	230	240
DPDSAKPEKT	HPHDAPPCKT	SPPATDTGKE	KKGETSRTPC	GSQASTEILA	PKAEKTRTGG	LGDPGQGTVA	LKKGEEGQSI
250	260	270	280	290	300	310	320
VGKGLGTPKT	TELKEAEPQG	KDRQGTRPQA	QGPGEGVRPG	KAEKEGAEPT	NTVEKGNVSK	DVGSEGKHVR	PQIPGRKWGG
330	340	350	360	370	380	390	400
FLGRRSKWDG	PQNKKDKEGV	LLSKAEKTGE	PQTQMEKTSQ	VQGELGDDLR	MGEKAGELRS	TTGKAGESWD	KKEKMGQPQG
410	420	430	440	450	460	470	480
KSGNAGEARS	QTEKGCEAPK	EVSTMVESPA	APGKGGWPGS	RGQEAEEPCS	RAGDGAGALE	TELEGPSQPA	LEKDAERPRI
490	500	510	520	530	540	550	560
RKENQDGPAP	QEEGKGGQSR	DSDQAPEDRW	YEAEKVWLAQ	KDGFTLATVL	KPDEGTADLP	AGRVRLWIDA	DKTITEVDEE
570	580	590	600	610	620	630	640
HVHRANPPEL	DQVEDLASLI	SVNESSVLNT	LLQRYKAQLL	HTCTGPDLIV	LQPRGPSVPS	AGKVPKGRRD	GLPAHIGSMA
650	660	670	680	690	700	710	720
QRAYWALLNQ	RRDQSIVALG	WSGAGKTTCC	EQVLEHLVGM	AGSVDGRVSV	EKIRATFTVL	RAFGSVSMAH	SRSATRFSMV
730	740	750	760	770	780	790	800
MSLDFNATGR	ITAAQLQTML	LEKSRVARQP	EGESNFLVFS	QMLAGLDLDL	RTELNLHQMA	DSSSFGMGVW	SKPEDKQKAA
810	820	830	840	850	860	870	880
AAFAQLQGAM	EMLGISESEQ	RAVWRVLAAI	YHLGAAGACK	VGRKQFMRFE	WANYAAEALG	CEYEELNTAT	FKHHLRQIIQ
890	900	910	920	930	940	950	960
QMTFGPSRWG	LEDEETSSGL	KMTGVDCVEG	MASGLYQELF	AAVVSLINRS	FSSHHLSMAS	IMVVDSPGFQ	NPRHQGKDRA
970	980	990	1000	1010	1020	1030	1040
ATFEELCHNY	AHERLQLLFY	QRTFVSTLQR	YQEEGVPVQF	DLPDPSPGTT	VAVVDQNPSQ	QVRLPAGGGA	QDARGLFWVL
1050	1060	1070	1080	1090	1100	1110	1120
DEEVHVEGSS	DSVVLERLCA	AFEKKGAGTE	GSSALRTCEQ	PLQCEIFHQL	GWDPVRYDLT	GWLHRAKPNL	SALDAPQVLH
1130	1140	1150	1160	1170	1180	1190	1200
QSKREELRSL	FQARAKLPPV	CRAVAGLEGT	SQQALQRSRM	VRRTFASSLA	AVRRKAPCSQ	IKLQMDALTS	MIKRSRLHFI
1210	1220	1230	1240	1250	1260	1270	1280
HCLVPNPVVE	SRSGQESPPP	PQPGRDKPGA	GGPLALDIPA	LRVQLAGFHI	LEALRLHRTG	YADHMGLTRF	RRQFQVLDAP
1290	1300	1310	1320	1330	1340	1350	1360
LLKKLMSTSE	GIDERKAVEE	LLETLDLEKK	AVAVGHSQVF	LKAGVISRLE	KQREKLVSQS	IVLFQAACKG	FLSRQEFKKL
1370	1380	1390	1400	1410	1420	1430	1440
KIRRLAAQCI	QKNVAVFLAV	KDWPWWQLLG	SLQPLLSATI	GTEQLRAKEE	ELTTLRRKLE	KSEKLRNELR	QNTDLLESKG
1450							
IK							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2500	1	937.1908	150.69	2	60.0	17.9	1	1243-1258	R.VQLAGFHILEALRLHR.T	

Detailed Protein Report

Protein 895: **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 896: PREDICTED: epidermal growth factor-like protein 7 isoform X3 [Homo sapiens]

Accession:	gi|578817547	**Score:**	17.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	23.9
Database Date:	2015-11-30	**pI:**	10.4
		Sequence Coverage [%]:	8.2
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578817549	refseq_human (refseq_human_20140103.fasta)	PREDICTED: epidermal growth factor-like protein 7 isoform X4 [Homo sapiens]

10	20	30	40	50	60	70	80
MRGSQEVLLM	WLLVLAVGGT	EHAYRPGRRV	CAVRAHGDPV	SESFVQRVYQ	PFLTTCDGHR	ACSTYRTIYR	TAYRRSPGLA
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
PARPRYACCP	GWKRTSGLPG	ACGAAICQPP	CRNGGSCVQP	GRCRCPAGWR	GDTCQSGVDS	AMKEEVQRLQ	SRVDLLEEKL
170	**180**	**190**	**200**	**210**	**220**		
QLVLAPLHSL	ASQALEHGLP	DPGSLLVHSF	QQLGRIDSLS	EQISFLEEQL	GSCSCKKDS		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1851	2	851.2954	-119.49	2	51.8	17.8	0	95-112	R.TSGLPGACGAAICQPPCR.N	

Detailed Protein Report

Protein 897: ankyrin repeat domain-containing protein 40 [Homo sapiens]

Accession:	gi|16418357	**Score:**	17.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	41.1
Database Date:	2015-11-30	**pI:**	4.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.7
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	0.73	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	1.96	**CV:**	0.00 %	**No. of Peptides:**	1

```
        10         20         30         40         50         60         70         80
MNALLEQKEQ QERLREAAAL GDIREVQKLV ESGVDVNSQN EVNGWTCLHW ACKRNHGQVV SYLLKSGADK EILTTKGEMP
        90        100        110        120        130        140        150        160
VQLTSRREIR KIMGVEEEDD DDDDDDNLPQ LKKESELPFV PNYLANPAFP FIYTPTAEDS AQMQNGGPST PPASPPADGS
       170        180        190        200        210        220        230        240
PPLLPPGEPP LLGTFPRDHT SLALVQNGDV SAPSAILRTP ESTKPGPVCQ PPVSQSRSLF SSVPSKPPMS LEPQNGTYAG
       250        260        270        280        290        300        310        320
PAPAFQPFFF TGAFPFNMQE LVLKVRIQNP SLRENDFIEI ELDRQELTYQ ELLRVCCCEL GVNPDQVEKI RKLPNTLLRK
       330        340        350        360        370
DKDVARLQDF QELELVLMIS ENNFLFRNAA STLTERPCYN RRASKLTY
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
940	1	567.1435	-248.79	2	40.6	17.8	0	77-86	K.GEMPVQLTSR.R	Oxidation: 3	Wdown:Qdown 1.96 mdown:qdown 0.73

Detailed Protein Report

Protein 898: PREDICTED: 5-hydroxytryptamine receptor 2B isoform X1 [Homo sapiens]

Accession:	gi|530370281	**Score:**	17.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	41.1
Database Date:	2015-11-30	**pI:**	10.3
		Sequence Coverage [%]:	5.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MWPLPLVLCP	AWLFLDVLFS	TASIMHLCAI	SVDRYIAIKK	PIQANQYNSR	ATAFIKITVV	WLISIGIAIP	VPIKGIETDV
90	100	110	120	130	140	150	160
DNPNNITCVL	TKERFGDFML	FGSLAAFFTP	LAIMIVTYFL	TIHALQKKAY	LVKNKPPQRL	TWLTVSTVFQ	RDETPCSSPE
170	180	190	200	210	220	230	240
KVAMLDGSRK	DKALPNSGDE	TLMRRTSTIG	KKSVQTISNE	QRASKVLGIV	FFLFLLMWCP	FFITNITLVL	CDSCNQTTLQ
250	260	270	280	290	300	310	320
MLLEIFVWIG	YVSSGVNPLV	YTLFNKTFRD	AFGRYITCNY	RATKSVKTLR	KRSSKIYFRN	PMAENSKFFK	KHGIRNGINP
330	340	350	360	370			
AMYQSPMRLR	SSTIQSSSII	LLDTLLLTEN	EGDKTEEQVS	YV			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2657	1	973.4534	-27.78	2	61.5	17.7	0	75-92	K.GIETDVDNPNNITCVLTK.E	

Detailed Protein Report

Protein 899: **PREDICTED: sprouty-related, EVH1 domain-containing protein 2 isoform X2 [Homo sapiens]**

Accession:	gi|530367354	**Score:**	17.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	25.4
Database Date:	2015-11-30	**pI:**	7.8
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	7.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPRPYRQVSF	PDDDEEIVRI	NPREKIWMTG	YEDYRHAPVR	GKYPDPSEDA	DSSYVRFAKG	EVPKHDYNYP	YVDSSDFGLG
90	100	110	120	130	140	150	160
EDPKGRGGSV	IKTQPSRGKS	RRRKEDGERS	RCVYCRDMFN	HEENRRGHCQ	DAPDSVRTCI	RRVSCMWCAD	SMLYHCMSDP
170	180	190	200	210	220	230	
EGDYTDPCSC	DTSDEKFCLR	WMALIALSFL	APCMCCYLPL	RACYHCGVMC	RCCGGKHKAA	A	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1522	2	993.5046	109.60	2	47.7	17.6	2	202-218	R.ACYHCGVMCRCCGGKHK.A	Carbamidomethyl: 2, 5; Oxidation: 8

Detailed Protein Report

Protein 900: PREDICTED: exosome complex component RRP4 isoform X6 [Homo sapiens]

Accession:	gi|578817232	**Score:**	17.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	21.9
Database Date:	2015-11-30	**pI:**	10.0
		Sequence Coverage [%]:	11.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAMEMRLPVA	RKPLSERLGR	DTKKHLVVPG	DTITTDTGFM	RGHGTYMGEE	KLIASVAGSV	ERVNKLICVK	ALKTRYIGEV
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
GDIVVGRITE	VQQKRWKVET	NSRLDSVLLL	SSMNLPGGEL	RRRSAEDELA	MRGFLQEGDL	ISAEVQAVFS	DGAVSLHTRS
170	**180**	**190**	**200**				
LKYGKDVDLS	CPARTRHGFA	PSSTHLLTYP	EAHISQAR				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1784	1	807.3967	-14.46	3	51.0	17.5	0	177-198	R.HGFAPSSTHLLTYPEAHISQAR.-	

Detailed Protein Report

Protein 901: PREDICTED: ras association domain-containing protein 3 isoform X1 [Homo sapiens]

Accession:	gi|578823589	**Score:**	17.5
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
675	2	676.1711	-187.18	2	37.3	17.5	1	137-147	R.CHREDQVYACK.L	

Detailed Protein Report

Protein 902: **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 903: PREDICTED: GTP-binding nuclear protein Ran isoform X1 [Homo sapiens]

Accession:	gi|530401711	**Score:**	17.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	14.7
Database Date:	2015-11-30	**pI:**	5.9
		Sequence Coverage [%]:	8.6
		No. of unique Peptides:	1

```
         10         20         30         40         50         60         70         80
MFDVTSRVTY KNVPNWHRDL VRVCENIPIV LCGNKVDIKD RKVKAKSIVF HRKKNLQYYD ISAKSNYNFE KPFLWLARKL
         90        100        110        120        130
IGDPNLEFVA MPALAPPEVV MDPALAAQYE HDLEVAQTTA LPDEDDDL
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2729	1	671.8236	-44.80	2	63.1	17.4	1	54-64	K.KNLQYYDISAK.S	

Detailed Protein Report

Protein 904: peptidyl-prolyl cis-trans isomerase A-like 4G [Homo sapiens]

Accession: gi|178057341
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 17.3
MW [kDa]: 18.2
pI: 10.0
Sequence Coverage [%]: 12.8
No. of unique Peptides: 1

```
        10         20         30         40         50         60         70         80
MVNSVIFFDI TVDGKPLGRI SIKQFADKIP KTAENFRALS TGEKGFRYKG SCFHRIIPGF MCQGGDFTHP NGTGDKSIYG
        90        100        110        120        130        140        150        160
EKFDDENLIR KHTGSGILSM ANAGPNTNGS QFFICTAKTE WLDGKHVAFG KVKERVNIVE AMEHFGYRNS KTSKKITIAD
       170
CGQF
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
23	1	1104.5165	18.54	2	29.5	17.3	0	56-76	R.IIPGFMCQGGDFTHPNGTGDK.S	Oxidation: 6

Detailed Protein Report

Protein 905: 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

mdown:qdown	**Median:**	1.84	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.94	**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	2	607.3093	-2.65	2	61.4	17.3	1	373-383	R.CFSGPPPRAPK.Q	Carbamidomethyl: 1	Wdown:Qdown 0.94 mdown:qdown 1.84

Detailed Protein Report

Protein 906: 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 907: arachidonate 15-lipoxygenase [Homo sapiens]

Accession:	gi|40316937	**Score:**	17.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	74.8
Database Date:	2015-11-30	**pI:**	6.1
Modification(s):	Oxidation	**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

Protein 908: ceramide-1-phosphate transfer protein [Homo sapiens]

Accession:	gi|71274150	**Score:**	17.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	24.3
Database Date:	2015-11-30	**pI:**	6.9
Modification(s):	Oxidation	**Sequence Coverage [%]:**	8.4
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530360427	refseq_human (refseq_human_20140103.fasta)	PREDICTED: ceramide-1-phosphate transfer protein isoform X1 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MDDSETGFNL KVVLVSFKQC LDEKEEVLLD PYIASWKGLV RFLNSLGTIF SFISKDVVSK LRIMERLRGG PQSEHYRSLQ
        90        100        110        120        130        140        150        160
AMVAHELSNR LVDLERRSHH PESGCRTVLR LHRALHWLQL FLEGLRTSPE DARTSALCAD SYNASLAAYH PWVVRRAVTV
       170        180        190        200        210        220
AFCTLPTREV FLEAMNVGPP EQAVQMLGEA LPFIQRVYNV SQKLYAEHSL LDLP
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1745	4	682.2498	-142.26	3	51.8	17.2	1	1-18	-.MDDSETGFNLKVVLVSFK.Q	Oxidation: 1

Detailed Protein Report

Protein 909: **myeloperoxidase precursor [Homo sapiens]**

Accession:	gi|4557759	**Score:**	17.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	83.8
Database Date:	2015-11-30	**pI:**	10.1
		Sequence Coverage [%]:	1.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGVPFFSSLR	CMVDLGPCWA	GGLTAEMKLL	LALAGLLAIL	ATPQPSEGAA	PAVLGEVDTS	LVLSSMEEAK	QLVDKAYKER
90	100	110	120	130	140	150	160
RESIKQRLRS	GSASPMELLS	YFKQPVAATR	TAVRAADYLH	VALDLLERKL	RSLWRRPFNV	TDVLTPAQLN	VLSKSSGCAY
170	180	190	200	210	220	230	240
QDVGVTCPEQ	DKYRTITGMC	NNRRSPTLGA	SNRAFVRWLP	AEYEDGFSLP	YGWTPGVKRN	GFPVALARAV	SNEIVRFPTD
250	260	270	280	290	300	310	320
QLTPDQERSL	MFMQWGQLLD	HDLDFTPEPA	ARASFVTGVN	CETSCVQQPP	CFPLKIPPND	PRIKNQADCI	PFFRSCPACP
330	340	350	360	370	380	390	400
GSNITIRNQI	NALTSFVDAS	MVYGSEEPLA	RNLRNMSNQL	GLLAVNQRFQ	DNGRALLPFD	NLHDDPCLLT	NRSARIPCFL
410	420	430	440	450	460	470	480
AGDTRSSEMP	ELTSMHTLLL	REHNRLATEL	KSLNPRWDGE	RLYQEARKIV	GAMVQIITYR	DYLPLVLGPT	AMRKYLPTYR
490	500	510	520	530	540	550	560
SYNDSVDPRI	ANVFTNAFRY	GHTLIQPFMF	RLDNRYQPME	PNPRVPLSRV	FFASWRVVLE	GGIDPILRGL	MATPAKLNRQ
570	580	590	600	610	620	630	640
NQIAVDEIRE	RLFEQVMRIG	LDLPALNMQR	SRDHGLPGYN	AWRRFCGLPQ	PETVGQLGTV	LRNLKLARKL	MEQYGTPNNI
650	660	670	680	690	700	710	720
DIWMGGVSEP	LKRKGRVGPL	LACIIGTQFR	KLRDGDRFWW	ENEGVFSMQQ	RQALAQISLP	RIICDNTGIT	TVSKNNIFMS
730	740	750					
NSYPRDFVNC	STLPALNLAS	WREAS					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1741	1	640.7565	-196.31	2	51.7	17.2	0	537-548	R.VVLEGGIDPILR.G	

Detailed Protein Report

Protein 910: ankyrin repeat domain-containing protein SOWAHB [Homo sapiens]

Accession:	gi|71274172	**Score:**	17.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	85.7
Database Date:	2015-11-30	**pI:**	10.4
		Sequence Coverage [%]:	2.6
		No. of unique Peptides:	1

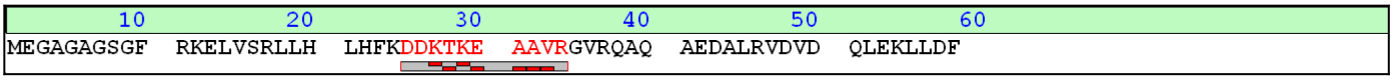
10	20	30	40	50	60	70	80
MARELSQEAL	LDFLCQAGGR	VTNAALLSHF	KSFLRDPDAS	PSQHQHRREL	FKGFVNSVAA	VRQDPDGTKY	VVLKRRYRDL
90	100	110	120	130	140	150	160
LGEEGLQRPR	EPPAAAPSAG	GAAPCSPRGA	RRGEPPQQQP	RRRRREKEPE	EEPAGAAARA	ADAACNGLPG	SDSRRAPGKG
170	180	190	200	210	220	230	240
GGSKGSPGQR	PPVPAAAAAG	AQARASCAAA	KTQGRCCWEC	LQNNLAVLPG	ELGALPHSAT	AEEKPARALP	AQDDRGASRE
250	260	270	280	290	300	310	320
REEGALAEPA	PVPAVAHSPP	ATVEAATSRA	SPPALLPGPA	PRGDRPELLT	PSSLHYSTLQ	QQQQRTREWV	ARHPQVPEAR
330	340	350	360	370	380	390	400
DQGPIRAWSV	LPDNFLQLPL	EPGSTEPNSE	PPDPCLSSHS	LFPVVPDESW	ESWAGNPSLT	VFRSIRCQLS	LQDLDDFVDQ
410	420	430	440	450	460	470	480
ESDGSEESSS	GPKDSPGASE	EGLQVVLGTP	DRGKLRNPAG	GLSVSRKEGS	PSRSPQGLRN	RGDGHISQQV	PAGANGLAGH
490	500	510	520	530	540	550	560
PLKPLPWPVP	KLRRSLRRSS	LAGRAKLSSS	DEEYLDEGLL	KRSRRPPRSR	KPSKAGTAPS	PRVDAGLSLK	LAEVKAVVAE
570	580	590	600	610	620	630	640
RGWRHSLWVP	SGEGSAALAP	HRTSEHKSSL	VPLDAREHEW	IVKLASGSWI	QVWTLFWEDP	QLALHKDFLT	GYTALHWIAK
650	660	670	680	690	700	710	720
HGDLRALQDL	VSGAKKAGIV	LDVNVRSSCG	YTPLHLAAIH	GHQGVIKLLV	QRLASRVNVR	DSSGKKPWQY	LTSNTSGEIW
730	740	750	760	770	780	790	800
QLLGAPRGKP	IFPVYPLVGS	SSPTRKAKSK	EISRSVTRKT	SFAALLKSQH	NKWKLANQYE	KFHSPREREE	YSD

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1748	1	945.9280	-39.73	2	50.4	17.1	1	91-111	R.EPPAAAPSAGGAAPCSPRGAR.R	

Detailed Protein Report

Protein 911: centromere protein X isoform 3 [Homo sapiens]

Accession:	gi|401871068	**Score:**	17.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	6.5
Database Date:	2015-11-30	**pI:**	6.1
		Sequence Coverage [%]:	17.2
		No. of unique Peptides:	1



```
         10         20         30         40         50         60
MEGAGAGSGF RKELVSRLLH LHFKDDKTKE AAVRGVRQAQ AEDALRVDVD QLEKLLDF
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
685	1	566.7912	-18.08	2	37.1	17.0	2	25-34	K.DDKTKEAAVR.G	

Detailed Protein Report

Protein 912: probable G-protein coupled receptor 179 precursor [Homo sapiens]

Accession:	gi|93352554	**Score:**	17.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	257.2
Database Date:	2015-11-30	**pI:**	5.4
		Sequence Coverage [%]:	0.4
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	0.62	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	1.33	**CV:**	0.00 %	**No. of Peptides:**	1

10	20	30	40	50	60	70	80
MGTRGAVMPP	PMWGLLGCCF	VCAWALGGPR	PIRSLPPLSS	QVKPGSVPMQ	VPLEGAEAAL	AYLYSGDAQQ	LSQVNCSERY
90	100	110	120	130	140	150	160
EARGAGAMPG	LPPSLQGAAG	TLAQAANFLN	MLLQANDIRE	SSVEEDVEWY	QALVRSVAEG	DPRVYRALLT	FNPPPGASHL
170	180	190	200	210	220	230	240
QLALQATRTG	EETILQDLSG	NWVQEENPPG	DLDTPALKKR	VLTNDLGSLG	SPKWPQADGY	VGDTQQVRLS	PPFLECQEGR
250	260	270	280	290	300	310	320
LRPGWLITLS	ATFYGLKPDL	SPEVRGQVQM	DVDLQSVDIN	QCASGPGWYS	NTHLCDLNST	QCVPLESQGF	VLGRYLCRCR
330	340	350	360	370	380	390	400
PGFYGASPSG	GLEESDFQTT	GQFGFPEGRS	GRLLQCLPCP	EGCTSCMDAT	PCLVEEAAVL	RAAVLACQAC	CMLAIFLSML
410	420	430	440	450	460	470	480
VSYRCRRNKR	IWASGVVLLE	TVLFGFLLLY	FPVFILYFKP	SVFRCIALRW	VRLLGFAIVY	GTIILKLYRV	LQLFLSRTAQ
490	500	510	520	530	540	550	560
RSALLSSGRL	LRRLGLLLLP	VLGFLAVWTV	GALERGIQHA	PLVIRGHTPS	GRHFYLCHHD	RWDYIMVVAE	LLLLCWGSFL
570	580	590	600	610	620	630	640
CYATRAVLSA	FHEPRYMGIA	LHNELLLSAA	FHTARFVLVP	SLHPDWTLLL	FFFHTHSTVT	TTLALIFIPK	FWKLGAPPRE
650	660	670	680	690	700	710	720
EMVDEVCEDE	LDLQHSGSYL	GSSIASAWSE	HSLDPGDIRD	ELKKLYAQLE	VHKTKEMAAN	NPHLPKKRGS	SCQGLGRSFM
730	740	750	760	770	780	790	800
RYLAEFPEAL	ARQHSRDSGS	PGHGSLPGSS	RRRLLSSSLQ	EPEGTPALHK	SRSTYDQRRE	QDPPLLDSLL	RRKLAKKASR
810	820	830	840	850	860	870	880
TESRESVEGP	PALGFRSASA	HNLTVGERLP	RARPASLQKS	LSVASSREKA	LLMASQAYLE	ETYRQAKERE	ERKKAKAAMA
890	900	910	920	930	940	950	960
SLVRRPSARR	LERPRGAPLS	APPSPAKSSS	VDSSHTSGRL	HEEARRRLPH	PPIRHQVSTP	ILALSGGLGE	PRMLSPTSTL
970	980	990	1000	1010	1020	1030	1040
APALLPALAP	TPAPALAPVP	VSPQSPNLLT	YICPWENAEL	PAKQENVPQE	GPSGPERGHH	SPAPARARLW	RALSVAVEKS
1050	1060	1070	1080	1090	1100	1110	1120
RAGENEMDAE	DAHHQREAND	VDEDRPKIFP	KSHSLKAPVQ	QGSMRSLGLA	IKALTRSRST	YREKESVEES	PEGQNSGTAG
1130	1140	1150	1160	1170	1180	1190	1200
ESMGAPSRSP	RLGRPKAVSK	QAALIPSDDK	ESLQNQQNAH	TSRMLQVCQR	EGSREQEDRG	RRMTQGLGER	KAERAGKTGL
1210	1220	1230	1240	1250	1260	1270	1280
AMLRQVSRDK	NIKQSKETPV	GWQELPKAGL	QSLGSADHRV	AEVCPWEVTE	SETRQPDSGN	KAEICPWETS	EGAPESRALR
1290	1300	1310	1320	1330	1340	1350	1360
QDPGDSQKKR	GEARGKSEPI	DVVPMMRKKP	ERLVREQEAV	CPWESADRGG	LSPGSAPQDP	GRIRDKSEAG	DSVEARKVEK
1370	1380	1390	1400	1410	1420	1430	1440
PGWEAAGPEA	HTPDITKAEP	CPWEASEGGE	DGKPAQEAVK	DLPQEKQKTR	KATFWKEQKP	GGDLESLCPW	ESTDFRGPSA
1450	1460	1470	1480	1490	1500	1510	1520
VSIQAPGSSE	CSGSLGSGIA	EVCLWEAGDA	PAIQKAEICP	WELDDNVMGQ	EMLSLGTGRE	SLQEKEKASR	KGSFGEMGEQ
1530	1540	1550	1560	1570	1580	1590	1600
TVKAVQKLSQ	QQESVCPRES	TVPGHSSPCL	DNSSSKAGSQ	FLCNGGSRAT	QVCPQEDLRP	EAQEATPAKT	EICPWEVNER
1610	1620	1630	1640	1650	1660	1670	1680
TREEWTSAQV	PRGGESQKDK	EKMPGKSEIE	DVTAWEKPEG	QIQKQEAVGP	WESVDPGSFS	PQPRPQDTER	PQTLLQMSGS
1690	1700	1710	1720	1730	1740	1750	1760
VGSKAADICP	LDVEENLTAG	KAEICPWEVG	AGAGEERALG	AEAIRKSPND	TGKVSADLGP	RERAVTAPEK	PQKPTPEWEV
1770	1780	1790	1800	1810	1820	1830	1840
ACPWGSVGPG	ACSQHPGTLD	ADGPKAGFQE	LDHMGCRPGE	VCPWEAQEAA	TSEKAKICPW	EVSEGTTGKG	LDQKAGSESA
1850	1860	1870	1880	1890	1900	1910	1920
EQREKALEKG	RLTSLGEDVS	KGMAKLCQQQ	ETICIWENKD	LRESPAQAPK	ISDLPSSMSS	EVAEGHSLEA	TEKGDLRQDP
1930	1940	1950	1960	1970	1980	1990	2000
KTGSFPEHIT	QEKAPAADTE	EFTTEDGEKT	SHELQSVCPW	ETTAPADSVS	HLDRQRPDQP	KASSQRLVST	GGRAADVCPW
2010	2020	2030	2040	2050	2060	2070	2080
DVPDAGVYKS	DSSAKAETCP	WEVTERIPVK	GVSRQDGKGD	SQEEKGRAPE	KSEPKGVPVQ	KKPEMADFRQ	QEAVCPWESQ
2090	2100	2110	2120	2130	2140	2150	2160
DGKGLSPQPA	PDASDRSRGS	SEAAGSVETR	VAEVCLWEVV	EAPSAKKAEI	CPWEAGGGAA	EEGEQERESQ	GQGEMFLQKA
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
966	4	509.2745	-44.80	2	40.6	17.0	1	1195-1204	R.AGKTGLAMLR.Q		Wdown:Qdown 1.33 mdown:qdown 0.62

Detailed Protein Report

Protein 913: probable G-protein coupled receptor 116 precursor [Homo sapiens]

Accession:	gi|148719671	**Score:**	16.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	149.4
Database Date:	2015-11-30	**pI:**	6.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	0.7
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|148719673	refseq_human (refseq_human_20140103.fasta)	probable G-protein coupled receptor 116 precursor [Homo sapiens]

10	20	30	40	50	60	70	80
MKSPRRTTLC	LMFIVIYSSK	AALNWNYEST	IHPLSLHEHE	PAGEEALRQK	RAVATKSPTA	EEYTVNIEIS	FENASFLDPI
90	100	110	120	130	140	150	160
KAYLNSLSFP	IHGNNTDQIT	DILSINVTTV	CRPAGNEIWC	SCETGYGWPR	ERCLHNLICQ	ERDVFLPGHH	CSCLKELPPN
170	180	190	200	210	220	230	240
GPFCLLQEDV	TLNMRVRLNV	GFQEDLMNTS	SALYRSYKTD	LETAFRKGYG	ILPGFKGVTV	TGFKSGSVVV	TYEVKTTPPS
250	260	270	280	290	300	310	320
LELIHKANEQ	VVQSLNQTYK	MDYNSFQAVT	INESNFFVTP	EIIFEGDTVS	LVCEKEVLSS	NVSWRYEEQQ	LEIQNSSRFS
330	340	350	360	370	380	390	400
IYTALFNNMT	SVSKLTIHNI	TPGDAGEYVC	KLILDIFEYE	CKKKIDVMPI	QILANEEMKV	MCDNNPVSLN	CCSQGNVNWS
410	420	430	440	450	460	470	480
KVEWKQEGKI	NIPGTPETDI	DSSCSRYTLK	ADGTQCPSGS	SGTTVIYTCE	FISAYGARGS	ANIKVTFISV	ANLTITPDPI
490	500	510	520	530	540	550	560
SVSEGQNFSI	KCISDVSNYD	EVYWNTSAGI	KIYQRFYTTR	RYLDGAESVL	TVKTSTREWN	GTYHCIFRYK	NSYSIATKDV
570	580	590	600	610	620	630	640
IVHPLPLKLN	IMVDPLEATV	SCSGSHHIKC	CIEEDGDYKV	TFHTGSSSLP	AAKEVNKKQV	CYKHNFNASS	VSWCSKTVDV
650	660	670	680	690	700	710	720
CCHFTNAANN	SVWSPSMKLN	LVPGENITCQ	DPVIGVGEPG	KVIQKLCRFS	NVPSSPESPI	GGTITYKCVG	SQWEEKRNDC
730	740	750	760	770	780	790	800
ISAPINSLLQ	MAKALIKSPS	QDEMLPTYLK	DLSISIDKAE	HEISSSPGSL	GAIINILDLL	STVPTQVNSE	MMTHVLSTVN
810	820	830	840	850	860	870	880
VILGKPVLNT	WKVLQQQWTN	QSSQLLHSVE	RFSQALQSGD	SPPLSFSQTN	VQMSSMVIKS	SHPETYQQRF	VFPYFDLWGN
890	900	910	920	930	940	950	960
VVIDKSYLEN	LQSDSSIVTM	AFPTLQAILA	QDIQENNFAE	SLVMTTTVSH	NTTMPFRISM	TFKNNSPSGG	ETKCVFWNFR
970	980	990	1000	1010	1020	1030	1040
LANNTGGWDS	SGCYVEEGDG	DNVTCICDHL	TSFSILMSPD	SPDPSSLLGI	LLDIISYVGV	GFSILSLAAC	LVVEAVVWKS
1050	1060	1070	1080	1090	1100	1110	1120
VTKNRTSYMR	HTCIVNIAAS	LLVANTWFIV	VAAIQDNRYI	LCKTACVAAT	FFIHFFYLSV	FFWMLTLGLM	LFYRLVFILH
1130	1140	1150	1160	1170	1180	1190	1200
ETSRSTQKAI	AFCLGYGCPL	AISVITLGAT	QPREVYTRKN	VCWLNWEDTK	ALLAFAIPAL	IIVVVNITIT	IVVITKILRP
1210	1220	1230	1240	1250	1260	1270	1280
SIGDKPCKQE	KSSLFQISKS	IGVLTPLLGL	TWGFGLTTVF	PGTNLVFHII	FAILNVFQGL	FILLFGCLWD	LKVQEALLNK
1290	1300	1310	1320	1330	1340	1350	
FSLSRWSSQH	SKSTSLGSST	PVFSMSSPIS	RRFNNLFGKT	GTYNVSTPEA	TSSSLENSSS	ASSLLN	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2911	1	671.8322	16.14	2	65.6	16.9	0	133-142	R.CLHNLICQER.D	Carbamidomethyl: 1, 7

Detailed Protein Report

Protein 914: protein FAM65B isoform 2 [Homo sapiens]

Accession:	gi|14277690	**Score:**	16.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	65.7
Database Date:	2015-11-30	**pI:**	5.1
		Sequence Coverage [%]:	2.5
		No. of unique Peptides:	1

```
        10          20          30          40          50          60          70          80
MLVGSQSFSP  GGPNGIIRSQ  SFAGFSGLQE  RRSRCNSFIE  NSSALKKPQA  KLKKMHNLGH  KNNNPPKEPQ  PKRVEEVYRA

        90         100         110         120         130         140         150         160
LKNGLDEYLE  VHQTELDKLT  AQLKDMKRNS  RLGVLYDLDK  QIKTIERYMR  RLEFHISKVD  ELYEAYCIQR  RLQDGASKMK

       170         180         190         200         210         220         230         240
QAFATSPASK  AARESLTEIN  RSFKEYTENM  CTIEVELENL  LGEFSIKMKG  LAGFARLCPG  DQYEIFMKYG  RQRWKLKGKI

       250         260         270         280         290         300         310         320
EVNGKQSWDG  EETVFLPLIV  GFISIKVTEL  KGLATHILVG  SVTCETKELF  AARPQVVAVD  INDLGTIKLN  LEITWYPFDV

       330         340         350         360         370         380         390         400
EDMTASSGAG  NKAAALQRRM  SMYSQGTPET  PTFKDHSFFS  NLPDDIFENG  KAAEEKMPLS  LSFSDLPNGD  CALTSHSTGS

       410         420         430         440         450         460         470         480
PSNSTNPEIT  ITPAEFNLSS  LASQNEGMDD  TSSASSRNSL  GEGQEPKSHL  KEEDPEEPRK  PASAPSEACR  RQSSGAGAEH

       490         500         510         520         530         540         550         560
LFLENDVAEA  LLQESEEASE  LKPVELDTSE  GNITKQLVKR  LTSAEVPMAT  DRLLSEGSVG  GESEGCRSFL  DGSLEDAFNG

       570         580         590         600
LLLALEPHKE  QYKEFQDLNQ  EVMNLDDILK  K
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
625	1	740.4433	138.33	2	36.7	16.9	0	533-547	R.LLSEGSVGGESEGCR.S	

Detailed Protein Report

Protein 915: PREDICTED: dedicator of cytokinesis protein 3 isoform X8 [Homo sapiens]

Accession:	gi|578805738	**Score:**	16.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	215.9
Database Date:	2015-11-30	**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 916: transmembrane protein 110 [Homo sapiens]

Accession: gi|38348402

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Score: 16.9

MW [kDa]: 33.2

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 917: 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 918: PREDICTED: M-phase phosphoprotein 8 isoform X2 [Homo sapiens]

Accession:	gi|530402464	**Score:**	16.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	68.4
Database Date:	2015-11-30	**pI:**	5.3
		Sequence Coverage [%]:	1.5
		No. of unique Peptides:	1

Quantitation

mdown:qdown **Median:** 1.41 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MEQVAEGARV	TAVPVSAADS	TEELAEVEEG	VGVVGEDNDA	AARGAEAFGD	SEEDGEDVFE	VEKILDMKTE	GGKVLYKVRW
90	100	110	120	130	140	150	160
KGYTSDDDTW	EPEIHLEDCK	EVLLEFRKKI	AENKAKAVRK	DIQRLSLNND	IFEANSDSDQ	QSETKEDTSP	KKKKKKLRQR
170	180	190	200	210	220	230	240
EEKSPDDLKK	KKAKAGKLKD	KSKPDLESSL	ESLVFDLRTK	KRISEAKEEL	KESKKPKKDE	VKETKELKKV	KKGEIRDLKT
250	260	270	280	290	300	310	320
KTREDPKENR	KTKKEKFVES	QVESESSVLN	DSPFPEDDSE	GLHSDSREEK	QNTKSARERA	GQDMGLEHGF	EKPLDSAMSA
330	340	350	360	370	380	390	400
EEDTDVRGRR	KKKTPRKAED	TRENRKLENK	NAFLEKKTVP	KKQRNQDRSK	SAAELEKLMP	VSAQTPKGRR	LSGEERGLWS
410	420	430	440	450	460	470	480
TDSAEEDKET	KRNESKEKYQ	KRHDSDKEEK	GRKEPKGLKT	LKEIRNAFDL	FKLTPEEKND	VSENNRKREE	IPLDFKTIDD
490	500	510	520	530	540	550	560
HKTKENKQSL	KERRNTRDET	DTWAYIAAEG	DQEVLDSVCQ	ADENSDGRQQ	ILSLGMDLQL	EWMKLEDFQK	HLDGKDENFA
570	580	590	600				
ATDAIPSNVL	RDAVKNGDYI	TVKVALNSNE	EYNLDQE				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
236	1	495.7647	55.25	2	32.1	16.8	0	1-9	-.MEQVAEGAR.V		mdown:qdown 1.41

Detailed Protein Report

Protein 919: E3 ubiquitin-protein ligase RNF128 isoform 2 precursor [Homo sapiens]

Accession:	gi|37588871	**Score:**	16.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	44.6
Database Date:	2015-11-30	**pI:**	5.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	5.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MNQENRSSFF	WLLVIFTFLL	KITASFSMSA	YVTVTYYNET	SNYTAIETCE	CGVYGLASPV	ANAMGVVGIP	KNNNYQACDH
90	100	110	120	130	140	150	160
NTEFSNTKKP	WIALIERGNC	TFSEKIQTAG	RRNADAVVIY	NAPETGNQTI	QMANFGAVDI	VAIMIGNLKG	TKILQSIQRG
170	180	190	200	210	220	230	240
IQVTMVIEVG	KKHGPWVNHY	SIFFVSVSFF	IITAATVGYF	IFYSARRLRN	ARAQSRKQRQ	LKADAKKAIG	RLQLRTLKQG
250	260	270	280	290	300	310	320
DKEIGPDGDS	CAVCIELYKP	NDLVRILTCN	HIFHKTCVDP	WLLEHRTCPM	CKCDILKALG	IEVDVEDGSV	SLQVPVSNEI
330	340	350	360	370	380	390	400
SNSASSHEED	NRSETASSGY	ASVQGTDEPP	LEEHVQSTNE	SLQLVNHEAN	SVAVDVIPHV	DNPTFEEDET	PNQETAVREI
410							
KS							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1366	1	1207.8238	107.80	2	45.6	16.8	2	150-171	K.GTKILQSIQRGIQVTMVIEVGK.K	Oxidation: 16

Detailed Protein Report

Protein 920: **PREDICTED: LOW QUALITY PROTEIN: uncharacterized protein LOC100129528 [Homo sapiens]**

Accession:	gi|530401977	**Score:**	16.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	37.6
Database Date:	2015-11-30	**pI:**	12.2
		Sequence Coverage [%]:	5.4
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|530437161	refseq_human (refseq_human_20140103.fasta)	PREDICTED: LOW QUALITY PROTEIN: uncharacterized protein LOC100129528 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MPALTEPVHV HHELPTSSPG RDPGPRAAHV LSRKGPGSTS CPRPLQEGTP GSRAAHALSR RGHRVHELPT SSPGGDTGFM
        90        100        110        120        130        140        150        160
SCPRPFQEGT PGSRAAHVLS RRGHRGPRVH ELPTSSPGRD PGSTSCPRPL QEGTRVTNCP RPLQEGTPGS RAAHVLSRRG
       170        180        190        200        210        220        230        240
HRVHELPTPS PGRDPGFMSC PRPLQEGTRV TNCPRPLQEG TRVTSCPRRL QEGTRVTSCP RPLQEGTRVT NCPRALQEGT
       250        260        270        280        290        300        310        320
PGSRAAHALS RKGPRVHELP TSSPGGDTGF TSCPRPLQEG TPGSRAAHAL SRRGHRVHEL PTSSPGRDPG HELPTSSPGG
       330        340        350        360
DTGFTSCPRT FQEGTPGSGL LPAHIVPLCK SEER
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2039	1	942.3107	-153.18	2	54.0	16.7	0	35-53	K.GPGSTSCPRPLQEGTPGSR.A	

Detailed Protein Report

Protein 921: 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 922: 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 923: **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	

Detailed Protein Report

Protein 924: **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 925: 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 926: olfactory receptor 51A2 [Homo sapiens]

Accession:	gi|52317146	**Score:**	16.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	35.1
Database Date:	2015-11-30	**pI:**	10.0
		Sequence Coverage [%]:	3.5
		No. of unique Peptides:	1

Quantitation

mdown:qdown **Median:** 0.80 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MSIINTSYVE	ITTFFLVGMP	GLEYAHIWIS	IPICSMYLIA	ILGNGTILFI	IKTEPSLHGP	MYYFLSMLAM	SDLGLSLSSL
90	100	110	120	130	140	150	160
PTVLSIFLFN	APETSSSACF	AQEFFIHGFS	VLESSVLLIM	SFDRFLAIHN	PLRYTSILTT	VRVAQIGIVF	SFKSMLLVLP
170	180	190	200	210	220	230	240
FPFTLRSLRY	CKKNQLSHSY	CLHQDVMKLA	CSDNRIDVIY	GFFGALCLMV	DFILIAVSYT	LILKTVPGIA	SKKEELKALN
250	260	270	280	290	300	310	320
TCVSHICAVI	IFYLPIINLA	VVHRFAGHVS	PLINVLMANV	LLLVPPLMKP	IVYCVKTKQI	RVRVVAKLCQ	WKI

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2802	1	665.3571	-56.63	2	64.1	16.5	2	302-312	R.VRVVAKLCQWK.I		mdown:qdown 0.80

Detailed Protein Report

Protein 927: **interferon-related developmental regulator 2 [Homo sapiens]**

Accession:	gi|197333755	**Score:**	16.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	54.8
Database Date:	2015-11-30	**pI:**	9.3
		Sequence Coverage [%]:	5.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAWNSPSRRP	VWQGGAPRED	GGARGVWLPS	SGQVSAQRTG	RRLVGLEPTP	TGSLTPRPPR	PVPGMPRARK	GNTLRKGGQR
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
RGGGARSSAQ	ADSGSSDDEA	ASEARSTASE	CPSLLSTTAE	DSLGGDVVDE	QGQQEDLEEK	LKEYVDCLTD	KSAKTRQGAL
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
ESLRLALASR	LLPDFLLERR	LTLADALEKC	LKKGKGEEQA	LAAAVLGLLC	VQLGPGPKGE	ELFHSLQPLL	VSVLSDSTAS
250	**260**	**270**	**280**	**290**	**300**	**310**	**320**
PAARLHCASA	LGLGCYVAAA	DIQDLVSCLA	CLESVFSRFY	GLGGSSTSPV	VPASLHGLLS	AALQAWALLL	TICPSTQISH
330	**340**	**350**	**360**	**370**	**380**	**390**	**400**
ILDRQLPRLP	QLLSSESVNL	RIAAGETIAL	LFELARDLEE	EFVYEDMEAL	CSVLRTLATD	SNKYRAKADR	RRQRSTFRAV
410	**420**	**430**	**440**	**450**	**460**	**470**	**480**
LHSVEGGECE	EEIVRFGFEV	LYMDSWARHR	IYAAFKEVLG	SGMHHHLQNN	ELLRDIFGLG	PVLLLDATAL	KACKVPRFEK
490	**500**	**510**					
HLYNAAAFKA	RTKARSRVRD	KRADIL					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1054	1	849.7307	-100.08	3	41.7	16.5	2	193-218	K.KGKGEEQALAAAVLGLLCVQLGPGPK.G	

Detailed Protein Report

Protein 928: **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 929: PREDICTED: HAUS augmin-like complex subunit 5 isoform X2 [Homo sapiens]

Accession:	gi|578834213	**Score:**	16.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	62.7
Database Date:	2015-11-30	**pI:**	10.1
		Sequence Coverage [%]:	4.5
		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
2816	1	964.8042	-49.50	3	63.7	16.5	2	33-57	R.RLCLGQGADIWAYILQHVHSQRTVK.K	

Detailed Protein Report

Protein 930: **PREDICTED: transmembrane emp24 domain-containing protein 3 isoform X1 [Homo sapiens]**

Accession:	gi|530405599	**Score:**	16.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	17.4
Database Date:	2015-11-30	**pI:**	4.7
		Sequence Coverage [%]:	12.3
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MGSTVPRSAS VLLLLLLLRR AEQPCGAELT FELPDNAKQC FHEEVEQGVK FSLDYQVITG GHYDVDCYVE DPQGNTIYRE
        90        100        110        120        130        140        150        160
TKKQYDSFTY RAEVKGVYQF CFSNEFSTFS HKTVYFDFQV GDEPPILPDM GNRVTALTQG PSASPTPTPP LRVPV
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1761	3	945.9383	-84.01	2	50.5	16.5	0	134-152	R.VTALTQGPSASPTPTPPLR.V	

Detailed Protein Report

Protein 931: zinc finger protein 469 [Homo sapiens]

Accession:	gi|188536004	**Score:**	16.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	409.9
Database Date:	2015-11-30	**pI:**	8.9
		Sequence Coverage [%]:	0.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPGERPRGAP	PPTMTGDLQP	RQVASSPGHP	SQPPLEDNTP	ATRTTKGARE	AGGQAQAMEL	PEAQPRQARD	GELKPPSLRG
90	100	110	120	130	140	150	160
QAPSSTPGKR	GSPQTPPGRS	PLQAPSRLAG	RAEGSPPQRY	ILGIASSRTK	PTLDETPENP	QLEAAQLPEV	DTPQGPGTGA
170	180	190	200	210	220	230	240
PLRPGLPRTE	AQPAAEELGF	HRCFQEPPSS	FTSTNYTSPS	ATPRPPAPGP	PQSRGTSPLQ	PGSYPEYQAS	GADSWPPAAE
250	260	270	280	290	300	310	320
NSFPGANFGV	PPAEPEPIPK	GSRPGGSPRG	VSFQFPFPAL	HGASTKPFPA	DVAGHAFTNG	PLVFAFHQPQ	GAWPEEAVGT
330	340	350	360	370	380	390	400
GPAYPLPTQP	APSPLPCYQG	QPGGLNRHSD	LSGALSSPGA	AHSAPRPFSD	SLHKSLTKIL	PERPPSAQDG	LGSTRGPPSS
410	420	430	440	450	460	470	480
LPQRHFPGQA	YRASGVDTSP	GPPDTELAAP	GPPPARLPQL	WDPTAAPYPT	PPGGPLAATR	SMFFNGQPSP	GQRLCLPQSA
490	500	510	520	530	540	550	560
PLPWPQVLPT	ARPSPHGMEM	LSRLPFPAGG	PEWQGGSQGA	LGTAGKTPGP	REKLPAVRSS	QGGSPALFTY	NGMTDPGAQP
570	580	590	600	610	620	630	640
LFFGVAQPQV	SPHGTPSLPP	PRVVGASPSE	SPLPSPATNT	AGSTCSSLSP	MSSSPANPSS	EESQLPGPLG	PSAFFHPPTH
650	660	670	680	690	700	710	720
PQETGSPFPS	PEPPHSLPTH	YQPEPAKAFP	FPADGLGAEG	AFQCLEETPF	PHEGPEVGRG	GLQGFPRAPP	PYPTHHFSLS
730	740	750	760	770	780	790	800
SASLDQLDVL	LTCRQCDRNY	SSLAAFLAHR	QFCGLLLARA	KDGHQRSPGP	PGLPSPPAAP	RVPADAHAGL	LSHAKTFLLA
810	820	830	840	850	860	870	880
GDAQAEGKDD	PLRTGFLPSL	AATPFPLPAS	DLDMEDDAKL	DSLITEALNG	MEYQSDNPEI	DSSFIDVFAD	EEPSGPRGPS
890	900	910	920	930	940	950	960
SGHPLKSKAG	VTPESKAPPP	LPAATPDPQT	PRPGDRGCPA	RGRPKTRSLG	LAPTEADAPS	QGRQQRRGKQ	LKLFRKDLDS
970	980	990	1000	1010	1020	1030	1040
GGAAEGSGSG	GGGRASGLRP	RRNDGLGERP	PPRPRRPRTQ	APGSRADPAP	RVPRAAALPE	ETRSSRRRRL	PPRKDPRKRK
1050	1060	1070	1080	1090	1100	1110	1120
ARGGAWGKEL	ILKIVQQKNR	LREYDFASES	EEDEQPPPRG	PGFRGRRGRG	EKRKEVELTQ	GPREDEPQKP	RKAARQEAGG
1130	1140	1150	1160	1170	1180	1190	1200
DGAPANPEEP	GGSRPGPGRS	PQARGPSRSL	ETGAAAREGG	PKCADRPSVA	PKDPLQVPTN	TETSEETRPS	LDFPQEAKEP
1210	1220	1230	1240	1250	1260	1270	1280
ETAEESAPDS	TEFTEALRSP	PAACAGEMGA	SPGLLIPEQP	PPSRHDTGTP	KPSGSLANTA	PHGSSPTPGV	GSLLGGPGGT
1290	1300	1310	1320	1330	1340	1350	1360
QAPVSHNSKD	PPARQPGEFL	APVANPSSTA	CPKPSVLSSK	ISSFGCDPAG	FNRDPLGVPV	AKKGPQPYSS	PHSELFLGPK
1370	1380	1390	1400	1410	1420	1430	1440
DLAGCFLEEL	HPKPSARDAP	PASSSCLCQD	GEDAGSLEPQ	LPRSPPGTAE	TEPGRAASPP	TLESSSLFPD	LPVDRFDPPL
1450	1460	1470	1480	1490	1500	1510	1520
YGSLSANRDS	GLPFACADPP	QKTVPSDPPY	PSFLLLEEVS	PMLPSHFPDL	SGGKVLSKTC	PPERTVVPGA	APSLPGKGSG
1530	1540	1550	1560	1570	1580	1590	1600
CSVALMSHLS	EDELEIQKLV	TELESQLQRS	KDTRGAPREL	AEAESVGRVE	LGTGTEPPSQ	RRTCQATVPH	EDTFSAADLT
1610	1620	1630	1640	1650	1660	1670	1680
RVGESTAHRE	GAESAVATVE	AVQGRPGGTW	PCPASFHPGH	AALLPCAQED	LVSGAPFSPR	GANFHFQPVQ	KAGASKTGLC
1690	1700	1710	1720	1730	1740	1750	1760
QAEGDSRPPQ	DVCLPEPSKQ	PGPQLDAGSL	AKCSPDQELS	FPKNKEAASS	QESEDSLRLL	PCEQRGGFLP	EPGTADQPHR
1770	1780	1790	1800	1810	1820	1830	1840
GAPAPEAFGS	PAVHLAPDLA	FQGDGAPPLD	ATWPFGASPS	HAAQGHSAGR	AGGHLHPTAG	RPGFEGNEFA	PAGASSLTAP
1850	1860	1870	1880	1890	1900	1910	1920
RGREAWLVPV	PSPACVSNTH	PSRRSQDPAL	SPPIRQLQLP	GPGVAKSKDG	ILGLQELTPA	AQSPPRVNPS	GLEGGTVEGG
1930	1940	1950	1960	1970	1980	1990	2000
KVACGPAQGS	PGGVQVTTLP	AVAGHQLGLE	ADGHWGLLGQ	AEKTQGQGTA	NQLQPENGVS	PGGTDNHASV	NASPKTALTG
2010	2020	2030	2040	2050	2060	2070	2080
PTEGAVLLEK	CKGSRAAMSL	QEEAEPTPSP	PSPNRESLAL	ALTAAHSRSG	SEGRTPERAS	SPGLNKPLLA	TGDSPAPSVG
2090	2100	2110	2120	2130	2140	2150	2160
DLAACAPSPT	SAAHMPCSLG	PLPREDPLTS	PSRAQGGLGG	QLPASPSCRD	PPGPQQLLAC	SPAWAPLEEA	DGVQATTDTG
2170	2180	2190	2200	2210	2220	2230	2240
AEDSPVAPPS	LTTSPCDPKE	ALAGCLLQGE	GSPLEDPSSW	PPGSVSAVTC	THSGDTPKDS	TLRIPEDSRK	EKLWESPGRA
2250	2260	2270	2280	2290	2300	2310	2320
TSPPLAGAVS	PSVAVRATGL	SSTPTGDEAQ	AGRGLPGPDP	QSRGAPPHTN	PDRMPRGHSS	YSPSNTARLG	HREGQAVTAV
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
2684	1	715.3525	-19.33	2	61.9	16.5	2	3063-3076	R.RTEEAAGAGRAQGR.G	

Detailed Protein Report

Protein 932: activating signal cointegrator 1 complex subunit 3 isoform c [Homo sapiens]

Accession:	gi|546232111	**Score:**	16.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	83.6
Database Date:	2015-11-30	**pI:**	6.1
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	2.3
		No. of unique Peptides:	1

Quantitation

mdown:qdown **Median:** 0.74 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MALPRLTGAL	RSFSNVTKQD	NYNEEVADLK	IKRSKLHEQV	LDLGLTWKKI	IKFLNEKLEK	SKMQSINEDL	KDILHAAKQI
90	100	110	120	130	140	150	160
VGTDNGREAI	ESGAAFLFMT	FHLKDSVGHK	ETKAIKQMFG	PFPSSSATAA	CNATNRIISH	FSQDDLTALV	QMTEKEHGDR
170	180	190	200	210	220	230	240
VFFGKNLAFS	FDMHDLDHFD	ELPINGETQK	TISLDYKKFL	NEHLQEACTP	ELKPVEKTNG	SFLWCEVEKY	LNSTLKEMTE
250	260	270	280	290	300	310	320
VPRVEDLCCT	LYDMLASIKS	GDELQDELFE	LLGPEGLELI	EKLLQNRITI	VDRFLNSSND	HRFQALQDNC	KKILGENAKP
330	340	350	360	370	380	390	400
NYGCQVTIQS	EQEKQLMKQY	RREEKRIARR	EKKAGEDLEV	SEGLMCFDPK	ELRIQREQAL	LNARSVPILS	RQRDADVEKI
410	420	430	440	450	460	470	480
HYPHVYDSQA	EAMKTSAFIA	GAKMILPEGI	QRENNKLYEE	VRIPYSEPMP	LSFEEKPVYI	QDLDEIGQLA	FKGMKRLNRI
490	500	510	520	530	540	550	560
QSIVFETAYN	TNENMLICAP	TGAGKTNIAM	LTVLHEIRQH	FQQGVIKKNE	FKIVYVAPMK	ALAAEMTDYF	SRRLEPLGII
570	580	590	600	610	620	630	640
VKELTGDMQL	SKSEILRTQM	LVTTPEKWDV	VTRKSVGDVA	LSQIVRLLIL	DEVHLLHEDR	GPVLESIVAR	TLRQVESTQS
650	660	670	680	690	700	710	720
MIRILGLSAT	LPNYLDVATF	LHVNPYIGLF	FFDGRFRPVP	LGQTFLGIKC	ANKMQQLNNM	DEVCYENVLK	QVKAGHQVHL
730	740						
FYLLLHLFIC	F						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
106	1	715.2726	-66.45	3	30.6	16.5	0	694-710	K.MQQLNNMDEVCYENVLK.Q	Carbamidomethyl: 11; Oxidation: 7	mdown:qdown 0.74

Detailed Protein Report

Protein 933: coiled-coil domain-containing protein 90B, mitochondrial isoform e [Homo sapiens]

Accession:	gi|554790349	**Score:**	16.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	16.2
Database Date:	2015-11-30	**pI:**	6.2
		Sequence Coverage [%]:	5.8
		No. of unique Peptides:	1

```
         10         20         30         40         50         60         70         80
MAHLDAIRKD MVILEKSEFA NLRAENEKMK IELDQVKQQL MHETSRIRAD NKLDINLERS RVTDMFTDQE KQLMETTTEF
         90        100        110        120        130        140
TKKDTQTKSI ISETSNKIDA EIASLKTLME SNKLETIRYL AASVFTCLAI ALGFYRFWK
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1075	1	463.6184	-278.22	2	43.0	16.4	0	1-8	-.MAHLDAIR.K	

Detailed Protein Report

Protein 934: proto-oncogene Mas [Homo sapiens]

Accession:	gi|4505105	**Score:**	16.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	37.4
Database Date:	2015-11-30	**pI:**	9.7
		Sequence Coverage [%]:	4.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDGSNVTSFV	VEEPTNISTG	RNASVGNAHR	QIPIVHWVIM	SISPVGFVEN	GILLWFLCFR	MRRNPFTVYI	THLSIADISL
90	100	110	120	130	140	150	160
LFCIFILSID	YALDYELSSG	HYYTIVTLSV	TFLFGYNTGL	YLLTAISVER	CLSVLYPIWY	RCHRPKYQSA	LVCALLWALS
170	180	190	200	210	220	230	240
CLVTTMEYVM	CIDREEESHS	RNDCRAVIIF	IAILSFLVFT	PLMLVSSTIL	VVKIRKNTWA	SHSSKLYIVI	MVTIIIFLIF
250	260	270	280	290	300	310	320
AMPMRLLYLL	YYEYWSTFGN	LHHISLLFST	INSSANPFIY	FFVGSSKKKR	FKESLKVVLT	RAFKDEMQPR	RQKDNCNTVT
330							
VETVV							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1615	1	853.4020	-33.46	2	48.9	16.4	2	311-325	R.RQKDNCNTVTVETVV.-	

Detailed Protein Report

Protein 935: PREDICTED: centrosomal protein CEP57L1 isoform X5 [Homo sapiens]

Accession:	gi|578812699	**Score:**	16.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	55.5
Database Date:	2015-11-30	**pI:**	9.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	5.2
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578812701	refseq_human(refseq_human_20140103.fasta)	PREDICTED: centrosomal protein CEP57L1 isoform X6 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MDSELMHSIV GSYHKPPERV FVPSFTQNEP SQNCHPANLE VTSPKILHSP NSQALILALK TLQEKIHRLE LERTQAEDNL
        90        100        110        120        130        140        150        160
NILSREAAQY KKALENETNE RNLAHQELIK QKKDISIQLS SAQSRCTLLE KQLEYTKRMV LNVEREKNMI LEQQAQLQRE
       170        180        190        200        210        220        230        240
KEQDQMKLYA KLEKLDVLEK ECFRLTTTQK TAEDKIKHLE EKLKEEEHQR KLFQDKASEL QTGLEISKII MSSVSNLKHS
       250        260        270        280        290        300        310        320
KEKKKSSKKT KCIKRRPPWQ ICSKFGALPF VAEKVRGDKM KIVVQKNSCF VMRQHRDPHI LQKPFNVTET RCLPKPSRTT
       330        340        350        360        370        380        390        400
SWCKAIPPDS EKSISICDNL SELLMAMQDE LDQMSMEHQE LLKQMKETES HSVCDDIECE LECLLKKMEI KGEQISKLKK
       410        420        430        440        450        460        470        480
HQDSVCKLQQ KVQNSKMSEA SGIQQEDSYP KGSKNIKNSP RKCLTDTNLF QKNSSFHPIR VHNLQMKLRR DDIMWEQ
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1822	1	1023.8932	45.34	3	51.5	16.4	2	287-311	K.NSCFVMRQHRDPHILQKPFNVTETR.C	Oxidation: 6

Detailed Protein Report

Protein 936: protein-methionine sulfoxide oxidase MICAL2 isoform e [Homo sapiens]

Accession:	gi|544063447	**Score:**	16.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	109.1
Database Date:	2015-11-30	**pI:**	9.2
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGENEDEKQA	QAGQVFENFV	QASTCKGTLQ	AFNILTRHLD	LDPLDHRNFY	SKLKSKVTTW	KAKALWYKLD	KRGSHKEYKR
90	100	110	120	130	140	150	160
GKSCTNTKCL	IVGGGPCGLR	TAIELAYLGA	KVVVVEKRDS	FSRNNVLHLW	PFTIHDLRGL	GAKKFYGKFC	AGSIDHISIR
170	180	190	200	210	220	230	240
QLQLILFKVA	LMLGVEIHVN	VEFVKVLEPP	EDQENQKIGW	RAEFLPTDHS	LSEFEFDVII	GADGRRNTLE	GFRRKEFRGK
250	260	270	280	290	300	310	320
LAIAITANFI	NRNSTAEAKV	EEISGVAFIF	NQKFFQDLKE	ETGIDLENIV	YYKDCTHYFV	MTAKKQSLLD	KGVIINDYID
330	340	350	360	370	380	390	400
TEMLLCAENV	NQDNLLSYAR	EAADFATNYQ	LPSLDFAMNH	YGQPDVAMFD	FTCMYASENA	ALVRERQAHQ	LLVALVGDSL
410	420	430	440	450	460	470	480
LEPFWPMGTG	CARGFLAAFD	TAWMVKSWNQ	GTPPLELLAE	RESLYRLLPQ	TTPENINKNF	EQYTLDPGTR	YPNLNSHCVR
490	500	510	520	530	540	550	560
PHQVKHLYIT	KELEHYPLER	LGSVRRSVNL	SRKESDIRPS	KLLTWCQQQT	EGYQHVNVTD	LTTSWRSGLA	LCAIIHRFRP
570	580	590	600	610	620	630	640
ELINFDSLNE	DDAVENNQLA	FDVAEREFGI	PPVTTGKEMA	SAQEPDKLSM	VMYLSKFYEL	FRGTPLRPVD	SWRKNYGENA
650	660	670	680	690	700	710	720
DLSLAKSSIS	NNYLNLTFPR	KRTPRVDGQT	GENDMNKRRR	KGFTNLDEPS	NFSSRSLGSN	QECGSSKEGG	NQNKVKSMAN
730	740	750	760	770	780	790	800
QLLAKFEEST	RNPSLMKQES	MRKSFPLNLG	GSDTCYFCKK	RVYVMERLSA	EGHFFHRECF	RCSICATTLR	LAAYTFDCDE
810	820	830	840	850	860	870	880
GKFYCKPHFI	HCKTNSKQRK	RRAELKQQRE	EEATWQEQEA	PRRDTPTESS	CAVAAIGTLE	GSPPGISTSF	FRKVLGWPLR
890	900	910	920	930	940	950	960
LPRDLCNWMQ	GLLQAAGLHI	RDNAYNYCYM	YELLSLGLPL	LWAFSEVLAA	MYRESEGSLE	SICNWVLRCF	PVKLR

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2008	2	1051.4154	-66.88	2	53.8	16.4	2	726-742	K.FEESTRNPSLMKQESMR.K	Oxidation: 11, 16

Detailed Protein Report

Protein 937: contactin-2 precursor [Homo sapiens]

Accession:	gi|4827022	**Score:**	16.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	113.3
Database Date:	2015-11-30	**pI:**	8.9
		Sequence Coverage [%]:	1.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGTATRRKPH	LLLVAAVALV	SSSAWSSALG	SQTTFGPVFE	DQPLSVLFPE	ESTEEQVLLA	CRARASPPAT	YRWKMNGTEM
90	100	110	120	130	140	150	160
KLEPGSRHQL	VGGNLVIMNP	TKAQDAGVYQ	CLASNPVGTV	VSREAILRFG	FLQEFSKEER	DPVKAHEGWG	VMLPCNPPAH
170	180	190	200	210	220	230	240
YPGLSYRWLL	NEFPNFIPTD	GRHFVSQTTG	NLYIARTNAS	DLGNYSCLAT	SHMDFSTKSV	FSKFAQLNLA	AEDTRLFAPS
250	260	270	280	290	300	310	320
IKARFPAETY	ALVGQQVTLE	CFAFGNPVPR	IKWRKVDGSL	SPQWTTAEPT	LQIPSVSFED	EGTYECEAEN	SKGRDTVQGR
330	340	350	360	370	380	390	400
IIVQAQPEWL	KVISDTEADI	GSNLRWGCAA	AGKPRPTVRW	LRNGEPLASQ	NRVEVLAGDL	RFSKLSLEDS	GMYQCVAENK
410	420	430	440	450	460	470	480
HGTIYASAEL	AVQALAPDFR	LNPVRRLIPA	ARGGEILIPC	QPRAAPKAVV	LWSKGTEILV	NSSRVTVTPD	GTLIIRNISR
490	500	510	520	530	540	550	560
SDEGKYTCFA	ENFMGKANST	GILSVRDATK	ITLAPSSADI	NLGDNLTLQC	HASHDPTMDL	TFTWTLDDFP	IDFDKPGGHY
570	580	590	600	610	620	630	640
RRTNVKETIG	DLTILNAQLR	HGGKYTCMAQ	TVVDSASKEA	TVLVRGPPGP	PGGVVVRDIG	DTTIQLSWSR	GFDNHSPIAK
650	660	670	680	690	700	710	720
YTLQARTPPA	GKWKQVRTNP	ANIEGNAETA	QVLGLTPWMD	YEFRVIASNI	LGTGEPSGPS	SKIRTREAAP	SVAPSGLSGG
730	740	750	760	770	780	790	800
GGAPGELIVN	WTPMSREYQN	GDGFGYLLSF	RRQGSTHWQT	ARVPGADAQY	FVYSNESVRP	YTPFEVKIRS	YNRRGDGPES
810	820	830	840	850	860	870	880
LTALVYSAEE	EPRVAPTKVW	AKGVSSSEMN	VTWEPVQQDM	NGILLGYEIR	YWKAGDKEAA	ADRVRTAGLD	TSARVSGLHP
890	900	910	920	930	940	950	960
NTKYHVTVRA	YNRAGTGPAS	PSANATTMKP	PPRRPPGNIS	WTFSSSSLSI	KWDPVVPFRN	ESAVTGYKML	YQNDLHLTPT
970	980	990	1000	1010	1020	1030	1040
LHLTGKNWIE	IPVPEDIGHA	LVQIRTTGPG	GDGIPAEVHI	VRNGGTSMMV	ENMAVRPAPH	PGTVISHSVA	MLILIGSLEL
1050							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1718	1	857.4054	-57.25	2	51.4	16.3	0	685-702	R.VIASNILGTGEPSGPSSK.I	

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Detailed Protein Report

Protein 938: 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 939: **zinc finger C3H1 domain-containing protein [Homo sapiens]**

Accession:	gi|87116683	**Score:**	16.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	226.2
Database Date:	2015-11-30	**pI:**	9.1
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MATADTPAPA	SSGLSPKEEG	ELEDGEISDD	DNNSQIRSRS	SSSSSGGGLL	PYPRRRPPHS	ARGGGSGGGG	GSSSSSSSSQ
90	100	110	120	130	140	150	160
QQLRNFSRSR	HASERGHLRG	PSSYRPKEPF	RSHPPSVRMP	SSSLSESSPR	PSFWERSHLA	LDRFRFRGRP	YRGGSRWSRG
170	180	190	200	210	220	230	240
RGVGERGGKP	GCRPPLGGGA	GSGFSSSQSW	REPSPPRKSS	KSFGRSPSRK	QNYSSKNENC	VEETFEDLLL	KYKQIQLELE
250	260	270	280	290	300	310	320
CINKDEKLAL	SSKEENVQED	PKTLNFEDQT	STDNVSITKD	SSKEVAPEEK	TQVKTFQAFE	LKPLRQKLTL	PGDKNRLKKV
330	340	350	360	370	380	390	400
KDGAKPLSLK	SDTTDSSQGL	QDKEQNLTRR	ISTSDILSEK	KLGEDEEELS	ELQLRLLALQ	SASKKWQQKE	QQVMKESKEK
410	420	430	440	450	460	470	480
LTKTKTVQQK	VKTSTKTHSA	KKVSTTAKQA	LRKQQTKAWK	KLQQQKEQER	QKEEDQRKQA	EEEERRKREE	EIRKIRDLSN
490	500	510	520	530	540	550	560
QEEQYNRFMK	LVGGKRRSRS	KSSDPDLRRS	LDKQPTDSGG	GIYQYDNYEE	VAMDTDSETS	SPAPSPVQPP	FFSECSLGYF
570	580	590	600	610	620	630	640
SPAPSLSLPP	PPQVSSLPPL	SQPYVEGLCV	SLEPLPPLPP	LPPLPPEDPE	QPPKPPFADE	EEEEEMLLRE	ELLKSLANKR
650	660	670	680	690	700	710	720
AFKPEETSSN	SDPPSPPVLN	NSHPVPRSNL	SIVSINTVSQ	PRIQNPKFHR	GPRLPRTVIS	LPKHKSVVVT	LNDSDDSESD
730	740	750	760	770	780	790	800
GEASKSTNSV	FGGLESMIKE	ARRTAEQASK	PKVPPKSEKE	NDPLRTPEAL	PEEKKIEYRL	LKEEIANREK	QRLIKSDQLK
810	820	830	840	850	860	870	880
TSSSSPANSD	VEIDGIGRIA	MVTKQVTDAE	SKLKKHRILL	MKDESVLKNL	VQQEAKKKES	VRNAEAKITK	LTEQLQATEK
890	900	910	920	930	940	950	960
ILNVNRMFLK	KLQEQIHRVQ	QRVTIKKALT	LKYGEELARA	KAVASKEIGK	RKLEQDRFGP	NKMMRLDSSP	VSSPRKHSAE
970	980	990	1000	1010	1020	1030	1040
LIAMEKRRLQ	KLEYEYALKI	QKLKEARALK	AKEQQNISPV	VEEEPEFSLP	QPSLHDLTQD	KLTLDTEEND	VDDEILSGSS
1050	1060	1070	1080	1090	1100	1110	1120
RERRRSFLES	NYFTKPNLKH	TDTANKECIN	KLNKNTVEKP	ELFLGLKIGE	LQKLYSKADS	LKQLILKTTT	GITEKVLHGQ
1130	1140	1150	1160	1170	1180	1190	1200
EISVDVDFVT	AQSKTMEVKP	CPFRPYHSPL	LVFKSYRFSP	YYRTKEKLPL	SSVSYSNMIE	PDQCFCRFDL	TGTCNDDDCQ
1210	1220	1230	1240	1250	1260	1270	1280
WQHIQDYTLS	RKQLFQDILS	YNLSLIGCAE	TSTNEEITAS	AEKYVEKLFG	VNKDRMSMDQ	MAVLLVSNIN	ESKGHTPPFT
1290	1300	1310	1320	1330	1340	1350	1360
TYKDKRKWKP	KFWRKPISDN	SFSSDEEQST	GPIKYAFQPE	NQINVPALDT	VVTPDDVRYF	TNETDDIANL	EASVLENPSH
1370	1380	1390	1400	1410	1420	1430	1440
VQLWLKLAYK	YLNQNEGECS	ESLDSALNVL	ARALENNKDN	PEIWCHYLRL	FSKRGTKDEV	QEMCETAVEY	APDYQSFWTF
1450	1460	1470	1480	1490	1500	1510	1520
LHLESTFEEK	DYVCERMLEF	LMGAAKQETS	NILSFQLLEA	LLFRVQLHIF	TGRCQSALAI	LQNALKSAND	GIVAEYLKTS
1530	1540	1550	1560	1570	1580	1590	1600
DRCLAWLAYI	HLIEFNILPS	KFYDPSNDNP	SRIVNTESFV	MPWQAVQDVK	TNPDMLLAVF	EDAVKACTDE	SLAVEERIEA
1610	1620	1630	1640	1650	1660	1670	1680
CLPLYTNMIA	LHQLLERYEA	AMELCKSLLE	SCPINCQLLE	ALVALYLQTN	QHDKARAVWL	TAFEKNPQNA	EVFYHMCKFF
1690	1700	1710	1720	1730	1740	1750	1760
ILQNRGDNLL	PFLRKFIASF	FKPGFEKYNN	LDLFRYLLNI	PGPIDIPSRL	CKGNFDDDMF	NHQVPYLWLI	YCLCHPLQSS
1770	1780	1790	1800	1810	1820	1830	1840
IKETVEAYEA	ALGVAMRCDI	VQKIWMDYLV	FANNRAAGSR	NKVQEFKFFT	DLVNRCLVTV	PARYPIPFSS	ADYWSNYEFH
1850	1860	1870	1880	1890	1900	1910	1920
NRVIFFYLSC	VPKTQHSKTL	ERFCSVMPAN	SGLALRLLQH	EWEESNVQIL	KLQAKMFTYN	IPTCLATWKI	AIAAEIVLKG
1930	1940	1950	1960	1970	1980	1990	
QREVHRLYQR	ALQKLPLCAS	LWKDQLLFEA	SEGGKTDNLR	KLVSKCQEIG	VSLNELLNLN	SNKTESKNH	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
750	1	937.7415	-84.31	3	37.9	16.3	1	1135-1157	K.TMEVKPCPFRPYHSPLLVFKSYR.F	Oxidation: 2

Protein 940: cathepsin Z preproprotein [Homo sapiens]

Accession: gi|22538442
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl, Oxidation

Score: 16.2
MW [kDa]: 33.8
pI: 6.9
Sequence Coverage [%]: 7.3
No. of unique Peptides: 1

```
        10         20         30         40         50         60         70         80
MARRGPGWRP LLLLVLLAGA AQGGLYFRRG QTCYRPLRGD GLAPLGRSTY PRPHEYLSPA DLPKSWDWRN VDGVNYASIT

        90        100        110        120        130        140        150        160
RNQHIPQYCG SCWAHASTSA MADRINIKRK GAWPSTLLSV QNVIDCGNAG SCEGGNDLSV WDYAHQHGIP DETCNNYQAK

       170        180        190        200        210        220        230        240
DQECDKFNQC GTCNEFKECH AIRNYTLWRV GDYGSLSGRE KMMAEIYANG PISCGIMATE RLANYTGGIY AEYQDTTYIN

       250        260        270        280        290        300        310
HVVSVAGWGI SDGTEYWIVR NSWGEPWGER GWLRIVTSTY KDGKGARYNL AIEEHCTFGD PIV
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2	1	1244.4788	-73.78	2	28.9	16.2	1	200-221	R.EKMMAEIYANGPISCGIMATER.L	Carbamidomethyl: 15; Oxidation: 18

Detailed Protein Report

Protein 941: peptidyl-prolyl cis-trans isomerase D [Homo sapiens]

Accession:	gi|4826932	**Score:**	16.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	40.7
Database Date:	2015-11-30	**pI:**	6.9
		Sequence Coverage [%]:	3.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSHPSPQAKP	SNPSNPRVFF	DVDIGGERVG	RIVLELFADI	VPKTAENFRA	LCTGEKGIGH	TTGKPLHFKG	CPFHRIIKKF
90	100	110	120	130	140	150	160
MIQGGDFSNQ	NGTGGESIYG	EKFEDENFHY	KHDREGLLSM	ANAGRNTNGS	QFFITTVPTP	HLDGKHVVFG	QVIKGIGVAR
170	180	190	200	210	220	230	240
ILENVEVKGE	KPAKLCVIAE	CGELKEGDDG	GIFPKDGSGD	SHPDFPEDAD	IDLKDVDKIL	LITEDLKNIG	NTFFKSQNWE
250	260	270	280	290	300	310	320
MAIKKYAEVL	RYVDSSKAVI	ETADRAKLQP	IALSCVLNIG	ACKLKMSNWQ	GAIDSCLEAL	ELDPSNTKAL	YRRAQGWQGL
330	340	350	360	370	380		
KEYDQALADL	KKAQGIAPED	KAIQAELLKV	KQKIKAQKDK	EKAVYAKMFA			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
920	1	678.9535	63.37	2	40.0	16.2	0	32-43	R.IVLELFADIVPK.T	

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Detailed Protein Report

Protein 942: PREDICTED: tyrosine-protein kinase BAZ1B isoform X1 [Homo sapiens]

Accession:	gi|530386606	**Score:**	16.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	121.5
Database Date:	2015-11-30	**pI:**	9.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.7
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MAPLLGRKPF PLVKPLPGEE PLFTIPHTQE AFRTREEYEA RLERYSERIW TCKSTGSSQL THKEAWEEEQ EVAELLKEEF
        90        100        110        120        130        140        150        160
PAWYEKLVLE MVHHNTASLE KLVDTAWLEI MTKYAVGEEC DFEVGKEKML KVKIVKIHPL EKVDEEATEK KSDGACDSPS
       170        180        190        200        210        220        230        240
SDKENSSQIA QDHQKKETVV KEDEGRRESI NDRARRSPRK LPTSLKKGER KWAPPKFLPH KYDVKLQNED KIISNVPADS
       250        260        270        280        290        300        310        320
LIRTERPPNK EIVRYFIRHN ALRAGTGENA PWVVEDELVK KYSLPSKFSD FLLDPYKYMT LNPSTKRKNT GSPDRKPSKK
       330        340        350        360        370        380        390        400
SKTDNSSLSS PLNPKLWCHV HLKKSLSGSP LKVKNSKNSK SPEEHLEEMM KMMSPNKLHT NFHIPKKGPP AKKPGKHSDK
       410        420        430        440        450        460        470        480
PLKAKGRSKG ILNGQKSTGN SKSPKKGLKT PKTKMKQMTL LDMAKGTQKM TRAPRNSGGT PRTSSKPHKH LPPAALHLIA
       490        500        510        520        530        540        550        560
YYKENKDRED KRSALSCVIS KTARLLSSED RARLPEELRS LVQKRYELLE HKKRWASMSE EQRKEYLKKK REELKKKLKE
       570        580        590        600        610        620        630        640
KAKERREKEM LERLEKQKRY EDQELTGKNL PAFRLVDTPE GLPNTLFGDV AMVVEFLSCY SGLLLPDAQY PITAVSLMEA
       650        660        670        680        690        700        710        720
LSADKGGFLY LNRVLVILLQ TLLQDEIAED YGELGMKLSE IPLTLHSVSE LVRLCLRRSD VQEESEGSDT DDNKDSAAFE
       730        740        750        760        770        780        790        800
DNEVQDEFLE KLETSEFFEL TSEEKLQILT ALCHRILMTY SVQDHMETRQ QMSAELWKER LAVLKEENDK KRAEKQKRKE
       810        820        830        840        850        860        870        880
MEAKNKENGK VENGLGKTDR KKEIVKFEPQ VDTEAEDMIS AVKSRRLLAI QAKKEREIQE REMKVKLERQ AEEERIRKHK
       890        900        910        920        930        940        950        960
AAAEKAFQEG IAKAKLVMRR TPIGTDRNHN RYWLFSDEVP GLFIEKGWVH DSIDYRFNHH CKDHTVSGDE DYCPRSKKAN
       970        980        990       1000       1010       1020       1030       1040
LGKNASMNTQ HGTATEVAVE TTTPKQGQNL WFLCDSQKEL DELLNCLHPQ GIRESQLKER LEKRFDGREK ENMIQYILYT
      1050       1060
IARLLRRTIG TLY
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1692	1	711.3527	18.60	3	49.8	16.2	2	114-131	K.YAVGEECDFEVGKEKMLK.V	Carbamidomethyl: 7

Detailed Protein Report

Protein 943: otogelin-like protein precursor [Homo sapiens]

Accession:	gi|294774585	**Score:**	16.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	263.4
Database Date:	2015-11-30	**pI:**	4.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	0.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MIPWSIFLLH	VLLFSLQEYI	CASSILMGTS	KNGFNENRQK	RALLAAQFEA	TSPRYFFHDA	INWGESKIKG	SCPYECLNGA
90	100	110	120	130	140	150	160
FCSKTGTCDC	QIFQALGTRC	QIIPNMGNGR	DGICKTWGQY	HFETFDGIYY	YFPGNCSYIF	AKDCGDLEPR	YTVWVHNSPK
170	180	190	200	210	220	230	240
CLGSVYSCYR	SISLFFSNQE	EIRIYGHEIK	KNGISLTLPQ	TIGQIFIEKL	ADYILVKTTF	GFSLAWDGIS	GIYLKLSEDH
250	260	270	280	290	300	310	320
KGKSCGLCGN	YNDIQSDDFI	ILQEDYTEDI	AMFANSWSVQ	TPDDTKCVLT	PSDFPNPCSS	GMPAFEAIFF	KCQILLQFPF
330	340	350	360	370	380	390	400
LSCHEYIDPY	LYIASCVNDL	CKTDDDETYC	RAATEYARAC	SHAGYPIQDW	RDDFPACTDK	CDDSFVHRDC	ISCCPPTCTF
410	420	430	440	450	460	470	480
EKQCLGSNLH	CLDGCYCPDG	LVMDNGTCIS	LENCPCGFHG	LAYSVGSKIE	QECTECVCVG	GVWNCTEQDC	PVQCSVVGDS
490	500	510	520	530	540	550	560
HFTTFDGRHY	SFIGMCQYIL	VKGTGKDKFT	ITLQKAPCEQ	NLGLVCLQSI	TLILEDDFNK	QVTLGRGGQI	LTSPNQGFNL
570	580	590	600	610	620	630	640
NGIVEIQTLS	SLFILLKTTF	GLKILFAIDG	ERIYIQLTSA	WKRRTLGLCG	TFNGNIRDDF	LSPSGMIEGT	PQLHANAWRV
650	660	670	680	690	700	710	720
SSTCFAPVHV	PVVDPCNINQ	QNIGYAAHCD	VIHQELFAPC	HIYISPGLYY	QLCRHDACKC	GSSCLCNALA	HYAYLCGQHG
730	740	750	760	770	780	790	800
VPIDFRTQIS	FCAVVCQKGM	LYHHCSSFCL	HSCISLSSPE	QCSDDCAEGC	NCPEGKFYED	TLNFCVPIFH	CRCHYRGSVY
810	820	830	840	850	860	870	880
QPGELIPTPS	GLCQCSNGTV	KCDELATPSA	VHICPEGKEY	FDCRFPDPEL	PAGGVNCETT	CANLAMNFTC	TPSSPCISGC
890	900	910	920	930	940	950	960
VCAPGMAEHR	GKCYVPESCP	CIWKDWEYLS	GEVIATPCYT	CVCRRGMFNC	TYYPCPAVCT	IYGDRHYYSF	DGLEYDYISD
970	980	990	1000	1010	1020	1030	1040
CQVFLIKSAD	DSDISVIAQN	KKCFDNDIVC	SKSVLISVGD	TEIYLNDTPY	KQKQSGFFLE	NKSTYQLWKA	GYYIVVYFPE
1050	1060	1070	1080	1090	1100	1110	1120
KDITILWDRK	TTIHIKVGPQ	WKNKLSGLCG	NFDKCTSNDM	TTSNNLEVRN	ARVFGDSWAL	GQCESPDETI	KPCEAHQNKF
1130	1140	1150	1160	1170	1180	1190	1200
PYAKKECSIL	YSDIFASCRN	VIDVTSFAKN	CHEDTCNCNL	GGDCECLCTS	IAAYAYKCCQ	EGISIHWRSS	TVCSLDCEYY
1210	1220	1230	1240	1250	1260	1270	1280
NEGLGEGPYM	LASYGQSGLV	LGANMTSRSV	FCLPRSSVHT	SLFFYFMITP	GLFKEKVSSL	ALVSLESAER	PNYFLYVHDN
1290	1300	1310	1320	1330	1340	1350	1360
DTLSLELWEA	NSAFHRRATF	FHHQGLWIPG	YSAFELYSKK	GFFIIFTDSS	VKASKYDDSE	EFKHSSSFSI	EEIQAAVPYR
1370	1380	1390	1400	1410	1420	1430	1440
KMCEWRYEPC	ATPCFKTCSD	PEALACKFLP	PVEGCLPYCP	KNMILDEVTL	KCVYPRDCIP	VIPTEPTLMP	PAKPTVPMFT
1450	1460	1470	1480	1490	1500	1510	1520
VWEMITPSDI	TVFDMLTPTT	GLECEPQKFD	PVYDCSQYIC	LNMEWQLYNW	SLNCPKDVEM	PDCGFRGRPV	QVNSDICCPE
1530	1540	1550	1560	1570	1580	1590	1600
WECPCRCSML	SELSIITFDG	NNAALYSMAS	YILVRIPGEI	IVAHIEKCSM	NQNGNSLKKL	APSGRISGLC	FKKLNVTTPI
1610	1620	1630	1640	1650	1660	1670	1680
HKIIVNRLAR	KVEVDSIVVP	LPFSSQELSI	EDSGSMYVIT	TPAGLIIKWS	HLTGIIDIHF	GFRFNLSSYT	EGLCGICNED
1690	1700	1710	1720	1730	1740	1750	1760
PDDDLRMQNG	TIITNMEDIG	LFIESWEIEK	SFEVTMRRPV	RNCTEHDCSQ	CIDLLNRRIF	IPCHDKVSPE	DFCEKMWINY
1770	1780	1790	1800	1810	1820	1830	1840
TYFWNYECDA	LSAYVALCNK	FDICIQWRTP	DYCSLSCPEG	KEYQPCVRPC	EARTCLNQWF	YGHTSCLNLR	EDCVCKVGTI
1850	1860	1870	1880	1890	1900	1910	1920
LHRPHSAQCI	PEKECACTDS	EDQPRTAGEI	WNGGIDECTL	YKCLENGSII	PIEPDCDEEP	TPVCEREAEV	VMGIIDKWTC
1930	1940	1950	1960	1970	1980	1990	2000
CSKEVCGCDT	TLCETSIPTC	TNSQKLIVGH	SPLSCCPQYK	CECDPLKCPS	ISTPECREDQ	FMIQVRQEEP	CCFSPFCVCE
2010	2020	2030	2040	2050	2060	2070	2080
SCTKPVPLCH	DGEFLTVDLN	STHFCCPQYY	CVCEPNLCPM	PLLNCAEDMN	LVKENVSGQC	CPTWHCECNC	ENLIMPTCEV
2090	2100	2110	2120	2130	2140	2150	2160
GEFTAIDHNF	QSDCGCIQYL	CEKDDVCVFQ	EVSVLNPGQS	MIKYLEEDFC	YAIECLEEKD	NHTGFHTLNF	TLVNCSKKCD
2170	2180	2190	2200	2210	2220	2230	2240
VHQVYTPSPS	DYGCCGTCKN	VSCKFHMENG	TSVVYAVGST	WHYNCTTYEC	VKTDEGAIIL	NYTMVCPPFN	ETECKMNEGI
2250	2260	2270	2280	2290	2300	2310	2320
VKLYNEGCCK	ICKREERICQ	KVIIKSVIRK	QDCMSQSPIN	VASCDGKCPS	ATIYNINIES	HLRFCKCCRE	NGVRNLSVPL
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
2111	1	1051.4432	-84.15	2	55.0	16.2	1	489-506	R.HYSFIGMCQYILVKGTGK.D	Carbamidomethyl: 8

Detailed Protein Report

Protein 944: PREDICTED: keratin, type I cuticular Ha4-like [Homo sapiens]

Accession:	gi|341916344	**Score:**	16.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	49.4
Database Date:	2015-11-30	**pI:**	4.9
Modification(s):	Carbamidomethyl	**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 945: 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 946: phosphatidylethanolamine N-methyltransferase isoform 4 [Homo sapiens]

Accession:	gi|388890235	**Score:**	16.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	23.7
Database Date:	2015-11-30	**pI:**	9.4
Modification(s):	Oxidation	**Sequence Coverage [%]:**	8.4
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MKRSGNPGAE ADFCVMTRLL GYVDPLDPSF VAAVITITFN PLYWNVVARW EHKTRKLSRA FGSPYLACYS LSVTILLLNF
        90        100        110        120        130        140        150        160
LRSHCFTQAM LSQPRMESLD TPAAYSLGLA LLGLGVVLVL SSFFALGFAG TFLGDYFGIL KEARVTVFPF NILDNPMYWG
       170        180        190        200        210        220
STANYLGWAI MHASPTGLLL TVLVALTYIV ALLYEEPFTA EIYRQKASGS HKRS
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1867	3	993.3614	-92.34	2	51.9	16.1	2	1-18	-.MKRSGNPGAEADFCVMTR.L	Oxidation: 1

Detailed Protein Report

Protein 947: **interferon-inducible GTPase 5 [Homo sapiens]**

Accession:	gi|10257429	**Score:**	16.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	50.3
Database Date:	2015-11-30	**pI:**	5.1
		Sequence Coverage [%]:	3.0
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578834645	refseq_human (refseq_human_20140103.fasta)	PREDICTED: interferon-inducible GTPase 5 isoform X2 [Homo sapiens]

10	20	30	40	50	60	70	80
MATSKLPVVP	GEEENTILMA	KERLEALRTA	FESGDLPQAA	SHLQELLAST	ESIRLEVGVT	GESGAGKSSL	INALRGLEAE
90	100	110	120	130	140	150	160
DPGAALTGVM	ETTMQPSPYP	HPQFPDVTLW	DLPGAGSPGC	PADKYLKQVD	FSRYDFFLLV	SPRRCGAVET	RLAAEILCQG
170	180	190	200	210	220	230	240
KKFYFVRTKV	DEDLAATRTQ	RPSGFREAAV	LQEIRDHCAE	RLREAGVADP	RIFLVSNLSP	ARYDFPTLVS	TWEHDLPSHR
250	260	270	280	290	300	310	320
RHAGLLSLPD	ISLEALQKKK	AMLQEQVLKT	ALVLGVIQAL	PVPGLAAAYD	DALLIHSLRG	YHRSFGLDDD	SLAKLAEQVG
330	340	350	360	370	380	390	400
KQAGDLRSVI	RSPLANEVSP	ETVLRLYSQS	SDGAMRVARA	FERGIPVFGT	LVAGGISFGA	VYTMLQGCLN	EMAEDAQRVR
410	420	430	440	450	460	470	
IKALEDDEPQ	PEVSLEVASD	NGVEKGGSGE	GGGEEAPLST	CRKLGLLLKY	ILDSWKKHDS	EEK	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
123	1	504.5745	-64.47	3	30.8	16.1	0	332-345	R.SPLANEVSPETVLR.L	

Detailed Protein Report

Protein 948: PREDICTED: terminal uridylyltransferase 4 isoform X7 [Homo sapiens]

Accession:	gi|530362244	**Score:**	16.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	173.2
Database Date:	2015-11-30	**pI:**	9.3
		Sequence Coverage [%]:	1.0
		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	RYWAKSPLAL	ETPNRVSLGQ	LWLELLKFYT	LDFALEEYVI	CVRIQDILTR	ENKNWPKRRI
570	580	590	600	610	620	630	640
AIEDPFSVKR	NVARSLNSQL	VYEYVVERFR	AAYRYFACPQ	TKGGNKSTVD	FKKREKGKIS	NKKPVKSNNM	ATNGCILLGE
650	660	670	680	690	700	710	720
TTEKINAERE	QPVQCDEMDC	TSQRCIIDNN	NLLVNELDFA	DHGQDSSSLS	TSKSSEIEPK	LDKKQDDLAP	SETCLKKELS
730	740	750	760	770	780	790	800
QCNCIDLSKS	PDPDKSTGTD	CRSNLETESS	HQSVCTDTSA	TSCNCKATED	ASDLNDDDNL	PTQELYYVFD	KFILTSGKPP
810	820	830	840	850	860	870	880
TIVCSICKKD	GHSKNDCPED	FRKIDLKPLP	PMTNRFREIL	DLVCKRCFDE	LSPPCSEQHN	REQILIGLEK	FIQKEYDEKA
890	900	910	920	930	940	950	960
RLCLFGSSKN	GFGFRDSDLD	ICMTLEGHEN	AEKLNCKEII	ENLAKILKRH	PGLRNILPIT	TAKVPIVKFE	HRRSGLEGDI
970	980	990	1000	1010	1020	1030	1040
SLYNTLAQHN	TRMLATYAAI	DPRVQYLGYT	MKVFAKRCDI	GDASRGSLSS	YAYILMVLYF	LQQRKPPVIP	VLQEIFDGKQ
1050	1060	1070	1080	1090	1100	1110	1120
IPQRMVDGWN	AFFFDKTEEL	KKRLPSLGKN	TESLGELWLG	LLRFYTEEFD	FKEYVISIRQ	KKLLTTFEKQ	WTSKCIAIED
1130	1140	1150	1160	1170	1180	1190	1200
PFDLNHNLGA	GVSRKMTNFI	MKAFINGRKL	FGTPFYPLIG	REAEYFFDSR	VLTDGELAPN	DRCCRVCGKI	GHYMKDCPKR
1210	1220	1230	1240	1250	1260	1270	1280
KSSLLFRLKK	KDSEEEKEGN	EEEKDSRDVL	DPRDLHDTRD	FRDPRDLRCF	ICGDAGHVRR	ECPEVKLARQ	RNSSVAAAQL
1290	1300	1310	1320	1330	1340	1350	1360
VRNLVNAQQV	AGSAQQQGDQ	SIRTRQSSEC	SESPSYSPQP	QPFPQNSSQS	AAITQPSSQP	GSQPKLGPPQ	QGAQPPHQVQ
1370	1380	1390	1400	1410	1420	1430	1440
MPLYNFPQSP	PAQYSPMHNM	GLLPMHPLQI	PAPSWPIHGP	VIHSAPGSAP	SNIGLNDPSI	IFAQPAARPV	AIPNTSHDGH
1450	1460	1470	1480	1490	1500	1510	1520
WPRTVAPNSL	VNSGAVGNSE	PGFRGLTPPI	PWEHAPRPHF	PLVPASWPYG	LHQNFMHQGN	ARFQPNKPFY	TQAGLPMHSN
1530	1540	1550					
QPILLSQGYP	YLNVSYIQQK	K					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2583	2	840.6326	169.50	2	60.5	16.0	0	1025-1039	R.KPPVIPVLQEIFDGK.Q	

BRUKER

Detailed Protein Report

Protein 949: 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 950: transcription intermediary factor 1-alpha isoform b [Homo sapiens]

Accession:	gi|47419909	**Score:**	16.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	112.9
Database Date:	2015-11-30	**pI:**	6.4
		Sequence Coverage [%]:	1.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEVAVEKAVA	AAAAASAAAS	GGPSAAPSGE	NEAESRQGPD	SERGGEAARL	NLLDTCAVCH	QNIQSRAPKL	LPCLHSFCQR
90	100	110	120	130	140	150	160
CLPAPQRYLM	LPAPMLGSAE	TPPPVPAPGS	PVSGSSPFAT	QVGVIRCPVC	SQECAERHII	DNFFVKDTTE	VPSSTVEKSN
170	180	190	200	210	220	230	240
QVCTSCEDNA	EANGFCVECV	EWLCKTCIRA	HQRVKFTKDH	TVRQKEEVSP	EAVGVTSQRP	VFCPFHKKEQ	LKLYCETCDK
250	260	270	280	290	300	310	320
LTCRDCQLLE	HKEHRYQFIE	EAFQNQKVII	DTLITKLMEK	TKYIKFTGNQ	IQNRIIEVNQ	NQKQVEQDIK	VAIFTLMVEI
330	340	350	360	370	380	390	400
NKKGKALLHQ	LESLAKDHRM	KLMQQQEVA	GLSKQLEHVM	HFSKWAVSSG	SSTALLYSKR	LITYRLRHLL	RARCDASPVT
410	420	430	440	450	460	470	480
NNTIQFHCDP	SFWAQNIINL	GSLVIEDKES	QPQMPKQNPV	VEQNSQPPSG	LSSNQLSKFP	TQISLAQLRL	QHMQQQPPP
490	500	510	520	530	540	550	560
RLINFQNHSP	KPNGPVLPPH	PQQLRYPPNQ	NIPRQAIKPN	PLQMAFLAQQ	AIKQWQISSG	QGTPSTTNST	SSTPSSPTIT
570	580	590	600	610	620	630	640
SAAGYDGKAF	GSPMIDLSSP	VGGSYNLPSL	PDIDCSSTIM	LDNIVRKDTN	IDHGQPRPPS	NRTVQSPNSS	VPSPGLAGPV
650	660	670	680	690	700	710	720
TMTSVHPPIR	SPSASSVGSR	GSSGSSSKPA	GADSTHKVPV	VMLEPIRIKQ	ENSGPPENYD	FPVVIVKQES	DEESRPQNAN
730	740	750	760	770	780	790	800
YPRSILTSLL	LNSSQSSTSE	ETVLRSDAPD	STGDQPGLHQ	DNSSNGKSEW	LDPSQKSPLH	VGETRKEDDP	NEDWCAVCQN
810	820	830	840	850	860	870	880
GGELLCCEKC	PKVFHLSCHV	PTLTNFPSGE	WICTFCRDLS	KPEVEYDCDA	PSHNSEKKKT	EGLVKLTPID	KRKCERLLLF
890	900	910	920	930	940	950	960
LYCHEMSLAF	QDPVPLTVPD	YYKIIKNPMD	LSTIKKRLQE	DYSMYSKPED	FVADFRLIFQ	NCAEFNEPDS	EVANAGIKLE
970	980	990	1000	1010	1020		
NYFEELLKNL	YPEKRFPKPE	FRNESEDNKF	SDDSDDDFVQ	PRKKRLKSIE	ERQLLK		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1407	1	637.4446	122.09	2	46.1	16.0	0	459-469	K.FPTQISLAQLR.L	

Detailed Protein Report

Protein 951: cadherin-related family member 4 precursor [Homo sapiens]

Accession:	gi|203097724	**Score:**	15.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	85.8
Database Date:	2015-11-30	**pI:**	5.1
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.3
		No. of unique Peptides:	1

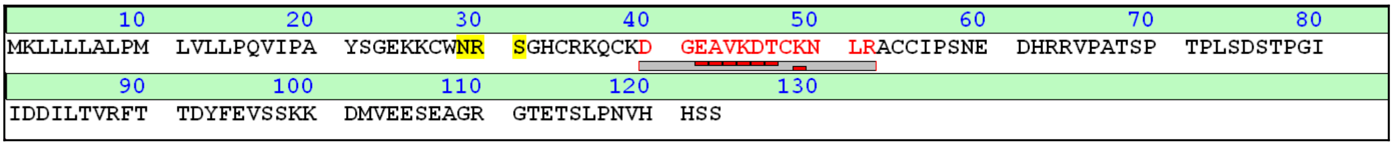
10	20	30	40	50	60	70	80
MVLLRLLVFL	FAPVVSDLCS	LPCFINVSES	QGPGTVLQFL	SFNCSSYTPT	PTLELLNVQP	PTTFFNPPSL	ARWQGTYVGK
90	100	110	120	130	140	150	160
LTLSSSAQLD	ALMVNHYKVQ	LKFTCGNHVM	EGSLSVDVQR	DLSHIQCAGQ	FASPAGEMIQ	VPETVTPGAR	LYTLLLPGLE
170	180	190	200	210	220	230	240
LHGAQMSIIS	AQDLPHFPGP	FSINEQGWLQ	APSQGLLGQA	QKVFQLQISV	SFGQRQSCQG	MVIVKVLPVP	SSQVSFLEQA
250	260	270	280	290	300	310	320
QNITIPENLA	PGSEVVQVQA	RGVDLRYEIL	SPVPSPLFSI	GRADGVVRTT	TPLELARTSG	TAVSRLQVKA	FEQGQLWASA
330	340	350	360	370	380	390	400
KLNLTMNVQL	VNLWPPRCLP	ALLVSQIPET	APVGTVLNTL	TCEDPDSVGA	TLDYKLWFRS	SSNPASLCLY	DRVLEVNATL
410	420	430	440	450	460	470	480
DCDTPGACFQ	HAASILVLDG	GQPQMTTEVP	VLVMVTPINE	FSPACAPRTF	RVQEDAAPHT	LLGSVVGTDM	DYPHDNIEYY
490	500	510	520	530	540	550	560
TSGGPTTFAV	DRLSGEVHLL	GPLDYEQQRL	YRLTVLVIDH	GQDQNPNHHL	SGSCTITIEV	EDVNDHAPEC	EPPFQELTIY
570	580	590	600	610	620	630	640
APLGRSVEVT	KMSCQIPQEP	QRLIYSYSIV	GGNSQNRFIL	QGAILVHSDL	VLGPFWPEQP	RTYELLICVA	DAGPSTPHLS
650	660	670	680	690	700	710	720
TTATIIVHLV	PRRASTVATS	THRTTVPSTM	TPMLVTDTEA	FWQPQPWFVV	VLTATGALLL	LALGWLLGRL	LQGLAQLLQA
730	740	750	760	770	780	790	
PSKPAQALLL	NSIQGTEGSI	EGFLEAPKME	MSQAPSSVMS	LHFDGRAQDS	RTGRDYLFNT	HTGARRWL	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1960	1	1029.3192	-117.25	2	53.0	15.9	0	749-766	K.MEMSQAPSSVMSLHFDGR.A	Oxidation: 1, 3, 11

Detailed Protein Report

Protein 952: **beta-defensin 118 precursor [Homo sapiens]**

Accession:	gi|16905373	**Score:**	15.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	13.6
Database Date:	2015-11-30	**pI:**	7.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	10.6
		No. of unique Peptides:	1



```
        10         20         30         40         50         60         70         80
MKLLLLALPM LVLLPQVIPA YSGEKKCWNR SGHCRKQCKD GEAVKDTCKN LRACCIPSNE DHRRVPATSP TPLSDSTPGI
        90        100        110        120        130
IDDILTVRFT TDYFEVSSKK DMVEESEAGR GTETSLPNVH HSS
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2473	1	753.2385	-177.83	2	59.6	15.9	2	40-52	K.DGEAVKDTCKNLR.A	Carbamidomethyl: 9

Detailed Protein Report

Protein 953: cyclic AMP-dependent transcription factor ATF-5 [Homo sapiens]

Accession:	gi|12597625	**Score:**	15.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	30.7
Database Date:	2015-11-30	**pI:**	4.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	6.4
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|302370956	refseq_human(refseq_human_20140103.fasta)	cyclic AMP-dependent transcription factor ATF-5 [Homo sapiens]

10	20	30	40	50	60	70	80
MSLLATLGLE	LDRALLPASG	LGWLVDYGKL	PPAPAPLAPY	EVLGGALEGG	LPVGGEPLAG	DGFSDWMTER	VDFTALLPLE
90	100	110	120	130	140	150	160
PPLPPGTLPQ	PSPTPPDLEA	MASLLKKELE	QMEDFFLDAP	PLPPPSPPPL	PPPPLPPAPS	LPLSLPSFDL	PQPPVLDTLD
170	180	190	200	210	220	230	240
LLAIYCRNEA	GQEEVGMPPL	PPPQQPPPPS	PPQPSRLAPY	PHPATTRGDR	KQKKRDQNKS	AALRYRQRKR	AEGEALEGEC
250	260	270	280	290			
QGLEARNREL	KERAESVERE	IQYVKDLLIE	VYKARSQRTR	SC			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2748	1	1002.0026	18.34	2	62.8	15.8	2	229-246	R.KRAEGEALEGECQGLEAR.N	Carbamidomethyl: 12

Detailed Protein Report

Protein 954: G-protein coupled receptor 55 [Homo sapiens]

Accession:	gi|33695107	**Score:**	15.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	36.6
Database Date:	2015-11-30	**pI:**	10.0
		Sequence Coverage [%]:	6.3
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530371161	refseq_human (refseq_human_20140103.fasta)	PREDICTED: G-protein coupled receptor 55 isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MSQQNTSGDC	LFDGVNELMK	TLQFAVHIPT	FVLGLLLNLL	AIHGFSTFLK	NRWPDYAATS	IYMINLAVFD	LLLVLSLPFK
90	100	110	120	130	140	150	160
MVLSQVQSPF	PSLCTLVECL	YFVSMYGSVF	TICFISMDRF	LAIRYPLLVS	HLRSPRKIFG	ICCTIWVLVW	TGSIPIYSFH
170	180	190	200	210	220	230	240
GKVEKYMCFH	NMSDDTWSAK	VFFPLEVFGF	LLPMGIMGFC	CSRSIHILLG	RRDHTQDWVQ	QKACIYSIAA	SLAVFVVSFL
250	260	270	280	290	300	310	320
PVHLGFFLQF	LVRNSFIVEC	RAKQSISFFL	QLSMCFSNVN	CCLDVFCYYF	VIKEFRMNIR	AHRPSRVQLV	LQDTTISRG

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2405	1	739.6886	40.20	3	58.8	15.8	0	1-20	-.MSQQNTSGDCLFDGVNELMK.T	

Detailed Protein Report

Protein 955: **MAM domain-containing glycosylphosphatidylinositol anchor protein 2 isoform 2 [Homo sapiens]**

Accession:	gi|38158013	**Score:**	15.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	81.3
Database Date:	2015-11-30	**pI:**	6.6
		Sequence Coverage [%]:	2.1
		No. of unique Peptides:	1

Quantitation

mdown:qdown **Median:** 0.69 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MVSFRLSNKT	ASPSIKLLVD	DPIVVNPGEA	ITLVCVTTGG	EPAPSLTWVR	SFGTLPEKTV	LNGGTLTIPA	ITSDDAGTYS
90	100	110	120	130	140	150	160
CIANNNVGNP	AKKSTNIIVR	ALKKGRFWIT	PDPYHKDDNI	QIGREVKISC	QVEAVPSEEL	TFSWFKNGRP	LRSSERMVIT
170	180	190	200	210	220	230	240
QTDPDVSPGT	TNLDIIDLKF	TDFGTYTCVA	SLKGGGISDI	SIDVNISSST	VPPNLTVPQE	KSPLVTREGD	TIELQCQVTG
250	260	270	280	290	300	310	320
KPKPIILWSR	ADKEVAMPDG	SMQMESYDGT	LRIVNVSREM	SGMYRCQTSQ	YNGFNVKPRE	ALVQLIVQYP	PAVEPAFLEI
330	340	350	360	370	380	390	400
RQGQDRSVTM	SCRVLRAYPI	RVLTYEWRLG	NKLLRTGQFD	SQEYTEYAVK	SLSNENYGVY	NCSIINEAGA	GRCSFLVTGK
410	420	430	440	450	460	470	480
AYAPEFYYDT	YNPVWQNRHR	VYSYSLQWTQ	MNPDAVDRIV	AYRLGIRQAG	QQRWWEQEIK	INGNIQKGEL	ITYNLTELIK
490	500	510	520	530	540	550	560
PEAYEVRLTP	LTKFGEGDST	IRVIKYSAPV	NPHLREFHCG	FEDGNICLFT	QDDTDNFDWT	KQSTATRNTK	YTPNTGPNAD
570	580	590	600	610	620	630	640
RSGSKEGFYM	YIETSRPRLE	GEKARLLSPV	FSIAPKNPYG	PTNTAYCFSF	FYHMYGQHIG	VLNVYLRLKG	QTTIENPLWS
650	660	670	680	690	700	710	720
SSGNKGQRWN	EAHVNIYPIT	SFQLIFEGIR	GPGIEGDIAI	DDVSIAEGEC	AKQDLATKNS	VDGAVGILVH	IWLFPIIVLI
730							
SILSPRR							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
134	1	876.6061	150.69	2	30.4	15.8	2	327-341	R.SVTMSCRVLRAYPIR.V		mdown:qdown 0.69

Detailed Protein Report

Protein 956: 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	

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Detailed Protein Report

Protein 957: protein FAM154A isoform b [Homo sapiens]

Accession:	gi|559098458	**Score:**	15.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	46.8
Database Date:	2015-11-30	**pI:**	9.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEGLTTSRRD	FGPHKVAPVK	VHQYDQFVPS	EENMDLLTTY	KKDYNPYPVC	RVDPIKPRDS	KYPCSDKMEC	LPTYKADYLP
90	100	110	120	130	140	150	160
WNQPRREPLR	LEHKYQPASV	RFDNRTTHQD	DYPIKGLVKT	ISCKPLAMPK	LCNIPLEDVT	NYKMSYVAHP	VEKRFVHEAE
170	180	190	200	210	220	230	240
KFRPCEIPFE	SLTTQKQSYR	GLMGEPAKSL	KPLARPPGLD	MPFCNTTEFR	DKYQAWPMPR	MFSKAPITYV	PPEDRMDLLT
250	260	270	280	290	300	310	320
TVQAHYTCPK	GAPAQSCRPA	LQIKKCGRFE	GSSTTKDDYK	QWSSMRTEPV	KPVPQLDLPT	EPLDCLTTTR	AHYVPHLPIN
330	340	350	360	370	380	390	400
TKSCKPHWSG	PRGNVPVESQ	TTYTISFTPK	EMGRCLASYP	EPPGYTFEEV	DALGHRIYKP	VSQAGSQQSS	HLSVDDSENP
410							
NQRELEVLA							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2413	1	1160.1933	96.65	2	58.9	15.7	2	43-61	K.DYNPYPVCRVDPIKPRDSK.Y	Carbamidomethyl: 8

Detailed Protein Report

Protein 958: DNA damage-inducible transcript 4-like protein [Homo sapiens]

Accession: gi|21687001
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl, Oxidation

Score: 15.7
MW [kDa]: 21.7
pI: 9.0
Sequence Coverage [%]: 7.8
No. of unique Peptides: 1

Alias proteins:

Accession	Name	Description
gi|530377132	refseq_human(refseq_human_20140103.fasta)	PREDICTED: DNA damage-inducible transcript 4-like protein isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MVATGSLSSK	NPASISELLD	CGYHPESLLS	DFDYWDYVVP	EPNLNEVIFE	ESTCQNLVKM	LENCLSKSKQ	TKLGCSKVLV
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
PEKLTQRIAQ	DVLRLSSTEP	CGLRGCVMHV	NLEIENVCKK	LDRIVCDSSV	VPTFELTLVF	KQENCSWTSF	RDFFFSRGRF
170	**180**	**190**	**200**				
SSGFRRTLIL	SSGFRLVKKK	LYSLIGTTVI	EGS				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1701	1	606.5258	-149.20	3	51.2	15.7	0	105-119	R.GCVMHVNLEIENVCK.K	Carbamidomethyl: 2, 14; Oxidation: 4

Detailed Protein Report

Protein 959: 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 960: **PREDICTED: high affinity cGMP-specific 3',5'-cyclic phosphodiesterase 9A isoform X2 [Homo sapiens]**

Accession:	gi|530419261	**Score:**	15.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	61.1
Database Date:	2015-11-30	**pI:**	6.1
		Sequence Coverage [%]:	2.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGSGSSSYRP	KAIYLDIDGR	IQKVIFSKYC	NSSDIMDLFC	IATGLPRNTT	ISLLTTDDAM	VSIDPTMPAN	SERTPYKVRP
90	100	110	120	130	140	150	160
VAIKQLSAGV	EDKRTTSRGQ	SAERPLRDRR	VVGLEQPRRE	GAFESGQVEP	RPREPQGCYQ	EGQRIPPERE	ELIQSVLAQV
170	180	190	200	210	220	230	240
AEQFSRAFKI	NELKAEVANH	LAVLEKRVEL	EGLKVVEIEK	CKSDIKKMRE	ELAARSSRTN	CPCKYSFLDN	HKKLTPRRDV
250	260	270	280	290	300	310	320
PTYPKYLLSP	ETIEALRKPT	FDVWLWEPNE	MLSCLEHMYH	DLGLVRDFSI	NPVTLRRWLF	CVHDNYRNNP	FHNFRHCFCV
330	340	350	360	370	380	390	400
AQMMYSMVWL	CSLQEKFSQT	DILILMTAAI	CHDLDHPGYN	NTYQINARTE	LAVRYNDISP	LENHHCAVAF	QILAEPECNI
410	420	430	440	450	460	470	480
FSNIPPDGFK	QIRQGMITLI	LATDMARHAE	IMDSFKEKME	NFDYSNEEHM	TLLKMILIKC	CDISNEVRPM	EVAEPWVDCL
490	500	510	520	530	540		
LEEYFMQPCQ	TNCLKVKKQG	LQKQEGAQEG	RDPAGQLTQM	ATGKVGDIEN	QAS		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
756	1	647.6373	-216.64	2	38.3	15.7	0	134-144	R.EPQGCYQEGQR.I	

Detailed Protein Report

Protein 961: CMT1A duplicated region transcript 15 protein-like protein [Homo sapiens]

Accession: gi|299782604
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 15.7
MW [kDa]: 30.1
pI: 10.9
Sequence Coverage [%]: 6.0
No. of unique Peptides: 1

```
        10         20         30         40         50         60         70         80
MFSCCFPTSR GCCFRNGGSE SLFRQCRRRL IPHPRRLWPF VRRRTQVPQD SPGQALAGQA TPEIPSGLPL HIVLVQEEIR

        90        100        110        120        130        140        150        160
EPMEAQTHAP GPYADIAALA APAVEPKPAW EEPPPERALE VEGAPAKDQP SQELPEIMAP TVATGLNAGA ENVAGERSGR

       170        180        190        200        210        220        230        240
EGVTSTAPAS RSHAAPSPGH GGKHGGGDQG IQTGLLYLAG ERLLSFAGTT ALLLQGLFIV LILVGYISVK VMLKSIKTRL

       250        260        270        280        290
GRRVPAAPPA LRRNLLLQAW KCVCNWASRL FAPNVLPRTG S
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2963	2	973.5100	12.30	2	66.2	15.7	1	262-278	K.CVCNWASRLFAPNVLPR.T	

Detailed Protein Report

Protein 962: cytochrome P450 26C1 [Homo sapiens]

Accession:	gi|62952502	**Score:**	15.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	57.1
Database Date:	2015-11-30	**pI:**	10.3
		Sequence Coverage [%]:	3.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MFPWGLSCLS	VLGAAGTALL	CAGLLLSLAQ	HLWTLRWMLS	RDRASTLPLP	KGSMGWPFFG	ETLHWLVQGS	RFHSSRRERY
90	100	110	120	130	140	150	160
GTVFKTHLLG	RPVIRVSGAE	NVRTILLGEH	RLVRSQWPQS	AHILLGSHTL	LGAVGEPHRR	RRKVLARVFS	RAALERYVPR
170	180	190	200	210	220	230	240
LQGALRHEVR	SWCAAGGPVS	VYDASKALTF	RMAARILLGL	RLDEAQCATL	ARTFEQLVEN	LFSLPLDVPF	SGLRKGIRAR
250	260	270	280	290	300	310	320
DQLHRHLEGA	ISEKLHEDKA	AEPGDALDLI	IHSARELGHE	PSMQELKESA	VELLFAAFFT	TASASTSLVL	LLLQHPAAIA
330	340	350	360	370	380	390	400
KIREELVAQG	LGRACGCAPG	AAGGSEGPPP	DCGCEPDLSL	AALGRLRYVD	CVVKEVLRLL	PPVSGGYRTA	LRTFELDGYQ
410	420	430	440	450	460	470	480
IPKGWSVMYS	IRDTHETAAV	YRSPPEGFDP	ERFGAAREDS	RGASSRFHYI	PFGGGARSCL	GQELAQAVLQ	LLAVELVRTA
490	500	510	520	530			
RWELATPAFP	AMQTVPIVHP	VDGLRLFFHP	LTPSVAGNGL	CL			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2715	1	928.5944	75.04	2	62.3	15.7	1	196-212	R.ILLGLRLDEAQCATLAR.T	

Detailed Protein Report

Protein 963: vacuolar protein sorting-associated protein 33A [Homo sapiens]

Accession:	gi|18105056	**Score:**	15.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	67.6
Database Date:	2015-11-30	**pI:**	6.5
		Sequence Coverage [%]:	2.2
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	0.31	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.06	**CV:**	0.00 %	**No. of Peptides:**	1

10	20	30	40	50	60	70	80
MAAHLSYGRV	NLNVLREAVR	RELREFLDKC	AGSKAIVWDE	YLTGPFGLIA	QYSLLKEHEV	EKMFTLKGNR	LPAADVKNII
90	100	110	120	130	140	150	160
FFVRPRLELM	DIIAENVLSE	DRRGPTRDFH	ILFVPRRSLL	CEQRLKDLGV	LGSFIHREEY	SLDLIPFDGD	LLSMESEGAF
170	180	190	200	210	220	230	240
KECYLEGDQT	SLYHAAKGLM	TLQALYGTIP	QIFGKGECAR	QVANMMIRMK	REFTGSQNSI	FPVFDNLLLL	DRNVDLLTPL
250	260	270	280	290	300	310	320
ATQLTYEGLI	DEIYGIQNSY	VKLPPEKFAP	KKQGDGGKDL	PTEAKKLQLN	SAEELYAEIR	DKNFNAVGSV	LSKKAKIISA
330	340	350	360	370	380	390	400
AFEERHNAKT	VGEIKQFVSQ	LPHMQAARGS	LANHTSIAEL	IKDVTTSEDF	FDKLTVEQEF	MSGIDTDKVN	NYIEDCIAQK
410	420	430	440	450	460	470	480
HSLIKVLRLV	CLQSVCNSGL	KQKVLDYYKR	EILQTYGYEH	ILTLHNLEKA	GLLKPQTGGR	NNYPTIRKTL	RLWMDDVNEQ
490	500	510	520	530	540	550	560
NPTDISYVYS	GYAPLSVRLA	QLLSRPGWRS	IEEVLRILPG	PHFEERQPLP	TGLQKKRQPG	ENRVTLIFFL	GGVTFAEIAA
570	580	590	600				
LRFLSQLEDG	GTEYVIATTK	LMNGTSWIEA	LMEKPF				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
770	1	689.8846	21.29	2	38.1	15.7	1	301-313	R.DKNFNAVGSVLSK.K		Wdown:Qdown 0.06 mdown:qdown 0.31

Detailed Protein Report

Protein 964: potassium voltage-gated channel subfamily KQT member 5 isoform 5 [Homo sapiens]

Accession:	gi|236462242	**Score:**	15.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	89.9
Database Date:	2015-11-30	**pI:**	10.2
		Sequence Coverage [%]:	1.6
		No. of unique Peptides:	1

Quantitation

Wdown:Qdown **Median:** 0.66 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MPRHHAGGEE	GGAAGLWVKS	GAAAAAAGGG	RLGSGMKDVE	SGRGRVLLNS	AAARGDGLLL	LGTRAATLGG	GGGGLRESRR
90	100	110	120	130	140	150	160
GKQGARMSLL	GKPLSYTSSQ	SCRRNVKYRR	VQNYLYNVLE	RPRGWAFIYH	AFVFLLVFGC	LILSVFSTIP	EHTKLASSCL
170	180	190	200	210	220	230	240
LILEFVMIVV	FGLEFIIRIW	SAGCCCRYRG	WQGRLRFARK	PFCVIDTIVL	IASIAVVSAK	TQGNIFATSA	LRSLRFLQIL
250	260	270	280	290	300	310	320
RMVRMDRRGG	TWKLLGSVVY	AHSKELITAW	YIGFLVLIFS	SFLVYLVEKD	ANKEFSTYAD	ALWWGTITLT	TIGYGDKTPL
330	340	350	360	370	380	390	400
TWLGRLLSAG	FALLGISFFA	LPAGILGSGF	ALKVQEQHRQ	KHFEKRRNPA	ANLIQCVWRS	YAADEKSVSI	ATWKPHLKAL
410	420	430	440	450	460	470	480
HTCSPTKKEQ	GEASSRIMKF	HVAKRKFKET	LRPYDVKDVI	EQYSAGHLDM	LCRIKSLQTR	VDQILGKGQI	TSDKKSREKI
490	500	510	520	530	540	550	560
TAEHETTDDL	SMLGRVVKVE	KQVQSIESKL	DCLLDIYQQV	LRKGSASALA	LASFQIPPFE	CEQTSDYQSP	VDSKDLSGSA
570	580	590	600	610	620	630	640
QNSGCLSRST	SANISRGLQF	ILTPNEFSAQ	TFYALSPTMH	SQATQVPISQ	SDGSAVAATN	TIANQINTAP	KPAAPTTLQI
650	660	670	680	690	700	710	720
PPPLPAIKHL	PRPETLHPNP	AGLQESISDV	TTCLVASKEN	VQVAQSNLTK	DRSMRKSFDM	GGETLLSVCP	MVPKDLGKSL
730	740	750	760	770	780	790	800
SVQNLIRSTE	ELNIQLSGSE	SSGSRGSQDF	YPKWRESKLF	ITDEEVGPEE	TETDTFDAAP	QPAREAAFAS	DSLRTGRSRS
810	820	830					
SQSICKAGES	TDALSLPHVK	LK					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
316	1	690.7007	-211.65	2	33.0	15.6	1	785-797	R.EAAFASDSLRTGR.S		Wdown:Qdown 0.66

Detailed Protein Report

Protein 965: PREDICTED: myotubularin-related protein 10 isoform X2 [Homo sapiens]

Accession:	gi|530406109	**Score:**	15.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	64.0
Database Date:	2015-11-30	**pI:**	9.3
		Sequence Coverage [%]:	2.3
		No. of unique Peptides:	1

Alias proteins:

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

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2250	1	752.7461	-190.38	2	56.8	15.6	0	75-87	K.ISFITDDPMPLQK.F	

Detailed Protein Report

Protein 966: 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 967: **extended synaptotagmin-1 isoform 2 [Homo sapiens]**

Accession:	gi|14149680	**Score:**	15.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	122.8
Database Date:	2015-11-30	**pI:**	5.5
		Sequence Coverage [%]:	1.1
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MERSPGEGPS PSPMDQPSAP SDPTDQPPAA HAKPDPGSGG QPAGPGAAGE ALAVLTSFGR RLLVLIPVYL AGAVGLSVGF
        90        100        110        120        130        140        150        160
VLFGLALYLG WRRVRDEKER SLRAARQLLD DEEQLTAKTL YMSHRELPAW VSFPDVEKAE WLNKIVAQVW PFLGQYMEKL
       170        180        190        200        210        220        230        240
LAETVAPAVR GSNPHLQTFT FTRVELGEKP LRIIGVKVHP GQRKEQILLD LNISYVGDVQ IDVEVKKYFC KAGVKGMQLH
       250        260        270        280        290        300        310        320
GVLRVILEPL IGDLPFVGAV SMFFIRRPTL DINWTGMTNL LDIPGLSSLS DTMIMDSIAA FLVLPNRLLV PLVPDLQDVA
       330        340        350        360        370        380        390        400
QLRSPLPRGI IRIHLLAARG LSSKDKYVKG LIEGKSDPYA LVRLGTQTFC SRVIDEELNP QWGETYEVMV HEVPGQEIEV
       410        420        430        440        450        460        470        480
EVFDKDPDKD DFLGRMKLDV GKVLQASVLD DWFPLQGGQG QVHLRLEWLS LLSDAEKLEQ VLQWNWGVSS RPDPPSAAIL
       490        500        510        520        530        540        550        560
VVYLDRAQDL PLKKGNKEPN PMVQLSIQDV TQESKAVYST NCPVWEEAFR FFLQDPQSQE LDVQVKDDSR ALTLGALTLP
       570        580        590        600        610        620        630        640
LARLLTAPEL ILDQWFQLSS SGPNSRLYMK LVMRILYLDS SEICFPTVPG CPGAWDVDSE NPQRGSSVDA PPRPCHTTPD
       650        660        670        680        690        700        710        720
SQFGTEHVLR IHVLEAQDLI AKDRFLGGLV KGKSDPYVKL KLAGRSFRSH VVREDLNPRW NEVFEVIVTS VPGQELEVEV
       730        740        750        760        770        780        790        800
FDKDLDKDDF LGRCKVRLTT VLNSGFLDEW LTLEDVPSGR LHLRLERLTP RPTAAELEEV LQVNSLIQTQ KSAELAAALL
       810        820        830        840        850        860        870        880
SIYMERAEDL PLRKGTKHLS PYATLTVGDS SHKTKTISQT SAPVWDESAS FLIRKPHTES LELQVRGEGT GVLGSLSLPL
       890        900        910        920        930        940        950        960
SELLVADQLC LDRWFTLSSG QGQVLLRAQL GILVSQHSGV EAHSHSYSHS SSSLSEEPEL SGGPPHITSS APELRQRLTH
       970        980        990       1000       1010       1020       1030       1040
VDSPLEAPAG PLGQVKLTLW YYSEERKLVS IVHGCRSLRQ NGRDPPDPYV SLLLLPDKNR GTKRRTSQKK RTLSPEFNER
      1050       1060       1070       1080       1090       1100       1110
FEWELPLDEA QRRKLDVSVK SNSSFMSRER ELLGKVQLDL AETDLSQGVA RWYDLMDNKD KGSS
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2291	2	666.2683	-223.38	2	57.1	15.5	2	193-204	R.IIGVKVHPGQRK.E	

Detailed Protein Report

Protein 968: twist-related protein 1 [Homo sapiens]

Accession:	gi|4507741	**Score:**	15.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	20.9
Database Date:	2015-11-30	**pI:**	10.1
		Sequence Coverage [%]:	9.9
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578813613	refseq_human (refseq_human_20140103.fasta)	PREDICTED: twist-related protein 1 isoform X1 [Homo sapiens]

```
         10         20         30         40         50         60         70         80
MMQDVSSSPV SPADDSLSNS EEEPDRQQPP SGKRGGRKRR SSRRSAGGGA GPGGAAGGGV GGGDEPGSPA QGKRGKKSAG

         90        100        110        120        130        140        150        160
CGGGGGAGGG GGSSSGGGSP QSYEELQTQR VMANVRERQR TQSLNEAFAA LRKIIPTLPS DKLSKIQTLK LAARYIDFLY

        170        180        190        200        210
QVLQSDELDS KMASCSYVAH ERLSYAFSVW RMEGAWSMSA SH
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
14	1	788.3704	-3.92	3	29.4	15.5	1	172-191	K.MASCSYVAHERLSYAFSVWR.M	

Protein 969: protein fem-1 homolog C [Homo sapiens]

Accession:	gi|17864094	**Score:**	15.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	68.6
Database Date:	2015-11-30	**pI:**	8.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.6
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530380049	refseq_human (refseq_human_20140103.fasta)	PREDICTED: protein fem-1 homolog C isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MDLKTAVFNA	ARDGKLRLLT	KLLASKSKEE	VSSLISEKTN	GATPLLMAAR	YGHLDMVEFL	LEQCSASIEV	GGSVNFDGET
90	100	110	120	130	140	150	160
IEGAPPLWAA	SAAGHLKVVQ	SLLNHGASVN	NTTLTNSTPL	RAACFDGHLE	IVKYLVEHKA	DLEVSNRHGH	TCLMISCYKG
170	180	190	200	210	220	230	240
HKEIAQYLLE	KGADVNRKSV	KGNTALHDCA	ESGSLDIMKM	LLMYCAKMEK	DGYGMTPLLS	ASVTGHTNIV	DFLTHHAQTS
250	260	270	280	290	300	310	320
KTERINALEL	LGATFVDKKR	DLLGALKYWK	KAMNMRYSDR	TNIISKPVPQ	TLIMAYDYAK	EVNSAEELEG	LIADPDEMRM
330	340	350	360	370	380	390	400
QALLIRERIL	GPSHPDTSYY	IRYRGAVYAD	SGNFKRCINL	WKYALDMQQS	NLDPLSPMTA	SSLLSFAELF	SFMLQDRAKG
410	420	430	440	450	460	470	480
LLGTTVTFDD	LMGILCKSVL	EIERAIKQTQ	CPADPLQLNK	ALSIILHLIC	LLEKVPCTLE	QDHFKKQTIY	RFLKLHPRGK
490	500	510	520	530	540	550	560
NNFSPLHLAV	DKNTTCVGRY	PVCKFPSLQV	TAILIECGAD	VNVRDSDDNS	PLHIAALNNH	PDIMNLLIKS	GAHFDATNLH
570	580	590	600	610	620		
KQTASDLLDE	KEIAKNLIQP	INHTTLQCLA	ARVIVNHRIY	YKGHIPEKLE	TFVSLHR		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2824	1	912.9573	-30.84	2	63.8	15.5	1	425-440	R.AIKQTQCPADPLQLNK.A	Carbamidomethyl: 7

Detailed Protein Report

Protein 970: PREDICTED: zinc finger protein 347 isoform X2 [Homo sapiens]

Accession: gi|530417417
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 15.5
MW [kDa]: 89.1
pI: 10.4
Sequence Coverage [%]: 1.2
No. of unique Peptides: 1

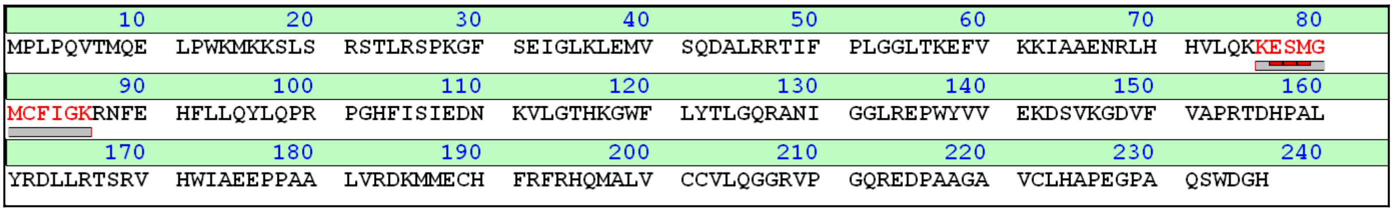
10	20	30	40	50	60	70	80
MLEQGKEPFT	LESQVQIAGN	PDGWEWIKAV	ITALSSEFVM	KDLLHKGKSN	TGEVFQTVML	ERQESQDIEG	CSFREVQKNT
90	100	110	120	130	140	150	160
HGLEYQCRDA	EGNYKGVLLT	QEGNLTHGRD	EHDKRDARNK	LIKNQLGLSL	QSHLPELQLF	QYEGKIYECN	QVEKSFNNNS
170	180	190	200	210	220	230	240
SVSPPQQMPY	NVKTHISKKY	LKDFISSLLL	TQGQKANNWG	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

Detailed Protein Report

Protein 971: mitochondrial tRNA-specific 2-thiouridylase 1 isoform f [Homo sapiens]

Accession:	gi|544346335	**Score:**	15.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	26.9
Database Date:	2015-11-30	**pI:**	10.3
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	4.7
		No. of unique Peptides:	1



```
        10         20         30         40         50         60         70         80
MPLPQVTMQE LPWKMKKSLS RSTLRSPKGF SEIGLKLEMV SQDALRRTIF PLGGLTKEFV KKIAAENRLH HVLQKKESMG
        90        100        110        120        130        140        150        160
MCFIGKRNFE HFLLQYLQPR PGHFISIEDN KVLGTHKGWF LYTLGQRANI GGLREPWYVV EKDSVKGDVF VAPRTDHPAL
       170        180        190        200        210        220        230        240
YRDLLRTSRV HWIAEEPPAA LVRDKMMECH FRFRHQMALV CCVLQGGRVP GQREDPAAGA VCLHAPEGPA QSWDGH
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2031	1	652.2575	-58.70	2	54.0	15.4	1	76-86	K.KESMGMCFIGK.R	Carbamidomethyl: 7; Oxidation: 6

Detailed Protein Report

Protein 972: zinc finger protein 560 [Homo sapiens]

Accession: gi|124517687
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl, Oxidation

Score: 15.4
MW [kDa]: 91.1
pI: 10.0
Sequence Coverage [%]: 2.5
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MAYCLTNCYQ	YSVTFEDTAV	DFTQEEWILL	DPVQRNLYRD	VMLENYENVA	KVGFQLFKPS	VISWLEEEEL	RTLQQGVLQD
90	100	110	120	130	140	150	160
WAIKHQTSVS	ALQQEFWKIQ	TSNGIQMDLV	TFDSVAVEFT	QEEWTLLDPA	QRNLYSDVML	ENYKNLSSVG	YQLFKPSLIS
170	180	190	200	210	220	230	240
WLEEEEELST	LPRVLQEWKM	CLKTKGPALW	QDNFCLKTLN	GIQLARNQNG	EELYDCKQCE	DVFCKHPCLK	TNMSTQNRGN
250	260	270	280	290	300	310	320
TSECIQYAKD	LLSLYNKTST	IRKVSVFSKH	GKSFRLILNV	QVQRKCTQDK	SFEGTDYGKA	FIYQSYLEAH	RKTQSGEKLN
330	340	350	360	370	380	390	400
EWKQCGEAFT	HSTSHAVNVE	THIIKNPYEC	KECGKDFRYP	THLNNHMQTH	IGIKPYKCKH	CGKTFTVPSG	FLEHVRTHTG
410	420	430	440	450	460	470	480
EKPYGCKECG	KAFGTSAGLI	EHIRCHAREK	TFKCDHCGKA	FISYPSLFGH	LRVHNGEKPY	EHKEYGKAFG	TSSGVIEDRR
490	500	510	520	530	540	550	560
SNTGQKRFDC	DQCGKVFVSF	SSLFAHLRTH	TGEKPFKCYK	CGKPFTSSAC	LRIHMRTHTE	ERLYQCKKCG	KAFTKCSYLT
570	580	590	600	610	620	630	640
KHLRTHAGEK	PYECMKCGKA	FTERSYLTKH	LRRHSGEKPY	ECKKCGKAFT	ERSDLTKHLR	RHTGDKPYEY	KDCGKAFVVS
650	660	670	680	690	700	710	720
SSLVDHLRTH	TGYKPYKCNA	CEKAYSRSCV	LTQHLKTHAA	EKTSECNACG	NSFRNSMCFH	DRLKTLTKIK	PYKCKDCGKA
730	740	750	760	770	780	790	800
FTCHSDLTNH	VRIHTGEKPY	KCKECGKAFR	TSSGRIQHLR	THMGEKPFEC	DQCGKAFASF	SARIAHLKTH	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
26	2	803.7093	79.22	3	29.6	15.4	1	683-702	K.TSECNACGNSFRNSMCFHDR.L	Carbamidomethyl: 4, 7; Oxidation: 15

Detailed Protein Report

Protein 973: **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

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 974: PREDICTED: proline-rich protein PRCC isoform X2 [Homo sapiens]

Accession:	gi|530365026	**Score:**	15.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	48.9
Database Date:	2015-11-30	**pI:**	5.3
		Sequence Coverage [%]:	2.6
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	3.49	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.57	**CV:**	0.00 %	**No. of Peptides:**	1

10	20	30	40	50	60	70	80
MSLVAYASSD	ESEPDEAEPE	PEEEEAVAPT	SGPALGGLFA	SLPAPKGPAL	LPPPPQMLAP	AFPPPLLLPP	PTGDPRLQPP
90	100	110	120	130	140	150	160
PPLPFGLGGF	PPPPGVSPAE	AAGVGEGLGL	GLPSPRGPGL	NLPPPIGGAG	PPLGLPKPKK	RKEPVKIAAP	ELHKGDSDSE
170	180	190	200	210	220	230	240
EDEPTKKKTI	LQGSSEGTGL	SALLPQPKNL	TVKETNRLLL	PHAFSRKPSD	GSPDTKPSRL	ASKTKTSSLA	PVVGTTTTTP
250	260	270	280	290	300	310	320
SPSAIKAAAK	SAALQVTKQI	TQEEDDSDEE	VAPENFFSLP	EKAEPPGVEP	YPYPIPTVPE	ELPPGTEPEP	AFQDDAANAP
330	340	350	360	370	380	390	400
LEFKMAAGSS	GAPWMPKPGD	DYSYNQFSTY	GDANAAGAYY	QFKRLQGKRN	RGREEINFVE	IKGDDQLSGA	QQWMTKSLTE
410	420	430	440	450	460		
EKTMKSFSKK	KGEQPTGQQR	RKHQITYLIH	QAKERELELK	NTWSENKLSR	RQTQAKYGF		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2175	1	666.2454	-213.60	2	55.7	15.4	1	143-154	K.EPVKIAAPELHK.G		Wdown:Qdown 0.57 mdown:qdown 3.49

Detailed Protein Report

Protein 975: **rap guanine nucleotide exchange factor 4 isoform e [Homo sapiens]**

Accession: gi|544583481
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl, Oxidation

Score: 15.4
MW [kDa]: 90.9
pI: 6.3
Sequence Coverage [%]: 2.9
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MIRDRKYHLK	TYRQCCVGTE	LVDWMMQQTP	CVHSRTQAVG	MWQVLLEDGV	LNHVDQEHHF	QDKYLFYRFL	DDEHEDAPLP
90	100	110	120	130	140	150	160
TEEEKKECDE	ELQDTMLLLS	QMGPDAHMRM	ILRKPPGQRT	VDDLEIIYEE	LLHIKALSHL	STTVKRELAG	VLIFESHAKG
170	180	190	200	210	220	230	240
GTVLFNQGEE	GTSWYIILKG	SVNVVIYGKG	VVCTLHEGDD	FGKLALVNDA	PRAASIVLRE	DNCHFLRVDK	EDFNRILRDV
250	260	270	280	290	300	310	320
EANTVRLKEH	DQDVLVLEKV	PAGNRASNQG	NSQPQQKYTV	MSGTPEKILE	HFLETIRLEA	TLNEATDSVL	NDFIMMHCVF
330	340	350	360	370	380	390	400
MPNTQLCPAL	VAHYHAQPSQ	GTEQEKMDYA	LNNKRRVIRL	VLQWAAMYGD	LLQEDDVSMA	FLEEFYVSVS	DDARMIAALK
410	420	430	440	450	460	470	480
EQLPELEKIV	KQISEDAKAP	QKKHKVLLQQ	FNTGDERAQK	RQPIRGSDEV	LFKVYCMDHT	YTTIRVPVAT	SVKEVISAVA
490	500	510	520	530	540	550	560
DKLGSGEGLI	IVKMSSGGEK	VVLKPNDVSV	FTTLTINGRL	FACPREQFDS	LTPLPEQEGP	TVGTVGTFEL	MSSKDLAYQM
570	580	590	600	610	620	630	640
TIYDWELFNC	VHELELIYHT	FGRHNFKKTT	ANLDLFLRRF	NEIQFWVVTE	ICLCSQLSKR	VQLLKKFIKI	AAHCKEYKNL
650	660	670	680	690	700	710	720
NSFFAIVMGL	SNVAVSRLAL	TWEKLPSKFK	KFYAEFESLM	DPSRNHRAYR	LTVAKLEPPL	IPFMPLLIKD	MTFTHEGNKT
730	740	750	760	770	780	790	800
FIDNLVNFEK	MRMIANTART	VRYYRSQPFN	PDAAQANKNH	QDVRSYVRQL	NVIDNQRTLS	QMSHRLEPRR	P

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2090	2	917.8279	107.57	3	54.7	15.4	0	87-109	K.ECDEELQDTMLLLSQMGPDAHMR.M	Carbamidomethyl: 2; Oxidation: 10, 22

Detailed Protein Report

Protein 976: PREDICTED: roundabout homolog 2 isoform X3 [Homo sapiens]

Accession:	gi|578806427	**Score:**	15.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	132.9
Database Date:	2015-11-30	**pI:**	6.9
		Sequence Coverage [%]:	0.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MARRHERVTR	RMWTWAPGLL	MMTVVFWGHQ	GNGQGQGSRL	RQEDFPPRIV	EHPSDVIVSK	GEPTTLNCKA	EGRPTPTIEW
90	100	110	120	130	140	150	160
YKDGERVETD	KDDPRSHRML	LPSGSLFFLR	IVHGRRSKPD	EGSYVCVARN	YLGEAVSRNA	SLEVALLRDD	FRQNPTDVVV
170	180	190	200	210	220	230	240
AAGEPAILEC	QPPRGHPEPT	IYWKKDKVRI	DDKEERISIR	GGKLMISNTR	KSDAGMYTCV	GTNMVGERDS	DPAELTVFER
250	260	270	280	290	300	310	320
PTFLRRPINQ	VVLEEEAVEF	RCQVQGDPQP	TVRWKKDDAD	LPRGRYDIKD	DYTLRIKKTM	STDEGTYMCI	AENRVGKMEA
330	340	350	360	370	380	390	400
SATLTVRARP	VAPPQFVVRP	RDQIVAQGRT	VTFPCETKGN	PQPAVFWQKE	GSQNLLFPNQ	PQQPNSRCSV	SPTGDLTITN
410	420	430	440	450	460	470	480
IQRSDAGYYI	CQALTVAGSI	LAKAQLEVTD	VLTDRPPPII	LQGPANQTLA	VDGTALLKCK	ATGDPLPVIS	WLKEGFTFPG
490	500	510	520	530	540	550	560
RDPRATIQEQ	GTLQIKNLRI	SDTGTYTCVA	TSSSGETSWS	AVLDVTESGA	TISKNYDLSD	LPGPPSKPQV	TDVTKNSVTL
570	580	590	600	610	620	630	640
SWQPGTPGTL	PASAYIIEAF	SQSVSNSWQT	VANHVKTTLY	TVRGLRPNTI	YLFMVRAINP	QGLSDPSPMS	DPVRTQDISP
650	660	670	680	690	700	710	720
PAQGVDHRQV	QKELGDVLVR	LHNPVVLTPT	TVQVTWTVDR	QPQFIQGYRV	MYRQTSGLQA	TSSWQNLDAK	VPTERSAVLV
730	740	750	760	770	780	790	800
NLKKGVTYEI	KVRPYFNEFQ	GMDSESKTVR	TTEEAPSAPP	QSVTVLTVGS	YNSTSISVSW	DPPPPDHQNG	IIQEYKIWCL
810	820	830	840	850	860	870	880
GNETRFHINK	TVDAAIRSVI	IGGLFPGIQY	RVEVAASTSA	GVGVKSEPQP	IIIGRRNEVV	ITENNNSITE	QITDVVKQPA
890	900	910	920	930	940	950	960
FIAGIGGACW	VILMGFSIWL	YWRRKKRKGL	SNYAVTFQRG	DGGLMSNGSR	PGLLNAGDPS	YPWLADSWPA	TSLPVNNSNS
970	980	990	1000	1010	1020	1030	1040
GPNEIGNFGR	GDVLPPVPGQ	GDKTATMLSD	GAIYSSIDFT	TKTSYNSSSQ	ITQATPYATT	QILHSNSIHE	LAVDLPDPQW
1050	1060	1070	1080	1090	1100	1110	1120
KSSIQQKTDL	MGFGYSLPDQ	NKGNNGGKGG	KKKKNKNSSK	PQKNNGSTWA	NVPLPPPPVQ	PLPGTELEHY	AVEQQENGYD
1130	1140	1150	1160	1170	1180	1190	1200
SDSWCPPLPV	QTYLHQGLED	ELEEDDDRVP	TPPVRGVASS	PAISFGQQST	ATLTPSPREE	MQPMLQAHLD	ELTRAYQFDI
1210							
AKQTW							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
588	1	469.2361	-75.04	2	36.2	15.4	1	724-731	K.KGVTYEIK.V	

Detailed Protein Report

Protein 977: interleukin-21 isoform 1 precursor [Homo sapiens]

Accession:	gi|11141875	**Score:**	15.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	18.6
Database Date:	2015-11-30	**pI:**	10.4
		Sequence Coverage [%]:	9.9
		No. of unique Peptides:	1

Quantitation

mdown:qdown **Median:** 0.60 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MRSSPGNMER	IVICLMVIFL	GTLVHKSSSQ	GQDRHMIRMR	QLIDIVDQLK	NYVNDLVPEF	LPAPEDVETN	CEWSAFSCFQ
90	100	110	120	130	140	150	160
KAQLKSANTG	NNERIINVSI	KKLKRKPPST	NAGRRQKHRL	TCPSCDSYEK	KPPKEFLERF	KSLLQKMIHQ	HLSSRTHGSE
170							
DS							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1445	1	977.1765	133.34	2	46.6	15.4	2	140-155	R.FKSLLQKMIHQHLSSR.T		mdown:qdown 0.60

Detailed Protein Report

Protein 978: **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 979: 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

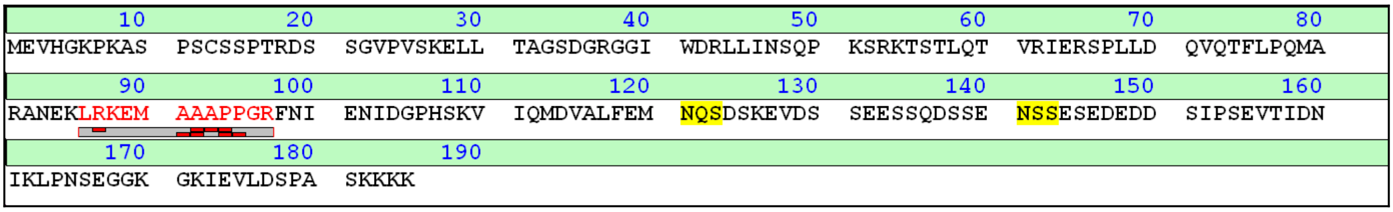
10	20	30	40	50	60	70	80
MSRSVLQPSQ	QKLAEKLTIL	NDRGVGMLTR	LYNIKKACGD	PKAKPSYLID	KNLESAVKFI	VRKFPAVETR	NNNLAQLQKE
90	100	110	120	130	140	150	160
KSEILKNLAL	YYFTFVDVME	FKDHVCELLN	TIDVCQVFFD	ITVNFDLTKN	YLDLIITYTT	LMILLSRIEE	RKAIIGLYNY
170	180	190	200	210	220	230	240
AHEMTHGASD	REYPRLGQMI	VDYENPLKKM	MEEFVPHSKS	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 980: uncharacterized protein C12orf45 [Homo sapiens]

Accession:	gi|116256458	**Score:**	15.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	20.1
Database Date:	2015-11-30	**pI:**	5.0
		Sequence Coverage [%]:	6.5
		No. of unique Peptides:	1



```
         10         20         30         40         50         60         70         80
MEVHGKPKAS PSCSSPTRDS SGVPVSKELL TAGSDGRGGI WDRLLINSQP KSRKTSTLQT VRIERSPLLD QVQTFLPQMA
         90        100        110        120        130        140        150        160
RANEKLRKEM AAAPPGRFNI ENIDGPHSKV IQMDVALFEM NQSDSKEVDS SEESSQDSSE NSSESEDEDD SIPSEVTIDN
        170        180        190
IKLPNSEGGK GKIEVLDSPA SKKKK
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1974	1	648.7898	-114.18	2	53.2	15.3	2	86-97	K.LRKEMAAAPPGR.F	

Detailed Protein Report

Protein 981: PREDICTED: nischarin isoform X2 [Homo sapiens]

Accession:	gi|578805595	**Score:**	15.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	110.7
Database Date:	2015-11-30	**pI:**	4.7
		Sequence Coverage [%]:	1.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MKCGIMFVQE	EALASSLSST	DSLTPEHQPI	AQGCSDSLES	IPAGQAASDD	LRDVPGAVGG	ASPEHAEPEV	QVVPGSGQII
90	100	110	120	130	140	150	160
FLPFTCIGYT	ATNQDFIQRL	STLIRQAIER	QLPAWIEAAN	QREEGQGEQG	EEEDEEEEEE	EDVAENRYFE	MGPPDVEEEE
170	180	190	200	210	220	230	240
GGGQGEEEEE	EEEDEEAEEE	RLALEWALGA	DEDFLLEHIR	ILKVLWCFLI	HVQGSIRQFA	ACLVLTDFGI	AVFEIPHQES
250	260	270	280	290	300	310	320
RGSSQHILSS	LRFVFCFPHG	DLTEFGFLMP	ELCLVLKVRH	SENTLFIISD	AANLHEFHAD	LRSCFAPQHM	AMLCSPILYG
330	340	350	360	370	380	390	400
SHTSLQEFLR	QLLTFYKVAG	GCQERSQGCF	PVYLVYSDKR	MVQTAAGDYS	GNIEWASCTL	CSAVRRSCCA	PSEAVKSAAI
410	420	430	440	450	460	470	480
PYWLLLTPQH	LNVIKADFNP	MPNRGTHNCR	NRNSFKLSRV	PLSTVLLDPT	RSCTQPRGAF	ADGHVLELLV	GYRFVTAIFV
490	500	510	520	530	540	550	560
LPHEKFHFLR	VYNQLRASLQ	DLKTVVIAKT	PGTGGSPQGS	FADGQPAERR	ASNDQRPQEV	PAEALAPAPA	EVPAPAPAAA
570	580	590	600	610	620	630	640
SASGPAKTPA	PAEASTSALV	PEETPVEAPA	PPPAEAPAQY	PSEHLIQATS	EENQIPSHLP	ACPSLRHVAS	LRGSAIIELF
650	660	670	680	690	700	710	720
HSSIAEVENE	ELRHLMWSSV	VFYQTPGLEV	TACVLLSTKA	VYFVLHDGLR	RYFSEPLQDF	WHQKNTDYNN	SPFHISQCFV
730	740	750	760	770	780	790	800
LKLSDLQSVN	VGLFDQHFRL	TGSTPMQVVT	CLTRDSYLTH	CFLQHLMVVL	SSLERTPSPE	PVDKDFYSEF	GNKTTGKMEN
810	820	830	840	850	860	870	880
YELIHSSRVK	FTYPSEEEIG	DLTFTVAQKM	AEPEKAPALS	ILLYVQAFQV	GMPPPGCCRG	PLRPKTLLLT	SSEIFLLDED
890	900	910	920	930	940	950	960
CVHYPLPEFA	KEPPQRDRYR	LDDGRRVRDL	DRVLMGYQTY	PQALTLVFDD	VQGHDLMGSV	TLDHFGEVPG	GPARASQGRE
970	980	990	1000				
VQWQVFVPSA	ESREKLISLL	ARQWEALCGR	ELPVELTG				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1738	1	1087.9436	-77.77	2	50.4	15.3	0	811-829	K.FTYPSEEEIGDLTFTVAQK.M	

Protein 982: PREDICTED: phosphoenolpyruvate carboxykinase [GTP], mitochondrial isoform X2 [Homo sapiens]

Accession:	gi|578825848	**Score:**	15.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	55.9
Database Date:	2015-11-30	**pI:**	6.7
		Sequence Coverage [%]:	3.6
		No. of unique Peptides:	1

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
972	1	984.1646	135.28	2	41.7	15.3	2	427-444	R.RLEGEDSARETPIGLVPK.E	

Detailed Protein Report

Protein 983: CUB and sushi domain-containing protein 1 precursor [Homo sapiens]

Accession:	gi|259013213	**Score:**	15.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	388.5
Database Date:	2015-11-30	**pI:**	5.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	0.3
		No. of unique Peptides:	1

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
714	1	512.2777	86.29	2	37.7	15.3	0	1100-1109	R.CVAECGASVK.G	Carbamidomethyl: 1

Detailed Protein Report

Protein 984: 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 985: bromodomain adjacent to zinc finger domain protein 1A isoform b [Homo sapiens]

Accession: gi|32967605
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 15.2
MW [kDa]: 175.3
pI: 6.4
Sequence Coverage [%]: 1.0
No. of unique Peptides: 1

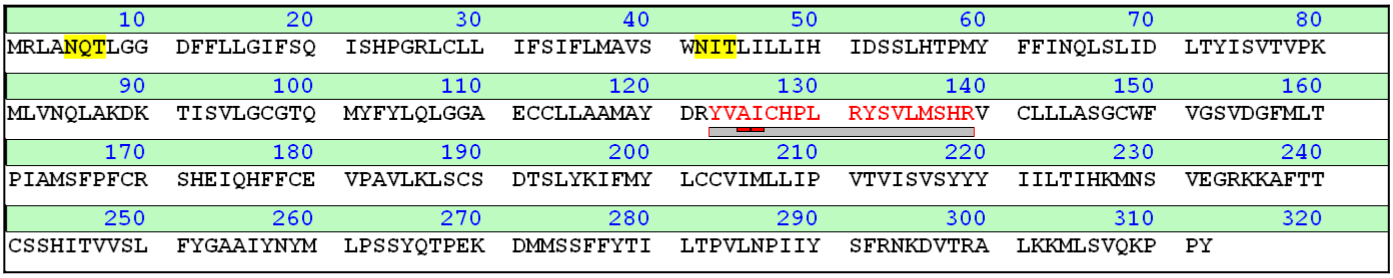
10	20	30	40	50	60	70	80
MPLLHRKPFV	RQKPPADLRP	DEEVFYCKVT	NEIFRHYDDF	FERTILCNSL	VWSCAVTGRP	GLTYQEALES	EKKARQNLQS
90	100	110	120	130	140	150	160
FPEPLIIPVL	YLTSLTHRSR	LHEICDDIFA	YVKDRYFVEE	TVEVIRNNGA	RLQCRILEVL	PPSHQNGFAN	GHVNSVDGET
170	180	190	200	210	220	230	240
IIISDSDDSE	TQSCSFQNGK	KKDAIDPLLF	KYKVQPTKKE	LHESAIVKAT	QISRRKHLFS	RDKLKLFLKQ	HCEPQDGVIK
250	260	270	280	290	300	310	320
IKASSLSTYK	IAEQDFSYFF	PDDPPTFIFS	PANRRRGRPP	KRIHISQEDN	VANKQTLASY	RSKATKERDK	LLKQEEMKSL
330	340	350	360	370	380	390	400
AFEKAKLKRE	KADALEAKKK	EKEDKEKKRE	ELKKIVEEER	LKKKEEKERL	KVEREKEREK	LREEKRKYVE	YLKQWSKPRE
410	420	430	440	450	460	470	480
DMECDDLKEL	PEPTPVKTRL	PPEIFGDALM	VLEFLNAFGE	LFDLQDEFPD	GVTLEVLEEA	LVGNDSEGPL	CELLFFFLTA
490	500	510	520	530	540	550	560
IFQAIAEEEE	EVAKEQLTDA	DTKGCSLKSL	DLDSCTLSEI	LRLHILASGA	DVTSANAKYR	YQKRGGFDAT	DDACMELRLS
570	580	590	600	610	620	630	640
NPSLVKKLSS	TSVYDLTPGE	KMKILHALCG	KLLTLVSTRD	FIEDYVDILR	QAKQEFRELK	AEQHRKEREE	AAARIRKRKE
650	660	670	680	690	700	710	720
EKLKEQEQKM	KEKQEKLKED	EQRNSTADIS	IGEEEREDFD	TSIESKDTEQ	KELDQDMVTE	DEDDPGSHKR	GRRGKRGQNG
730	740	750	760	770	780	790	800
FKEFTRQEQI	NCVTREPLTA	DEEEALKQEH	QRKEKELLEK	IQSAIACTNI	FPLGRDRMYR	RYWIFPSIPG	LFIEEDYSGL
810	820	830	840	850	860	870	880
TEDMLLPRPS	SFQNNVQSQD	PQVSTKTGEP	LMSESTSNID	QGPRDHSVQL	PKPVHKPNRW	CFYSSCEQLD	QLIEALNSRG
890	900	910	920	930	940	950	960
HRESALKETL	LQEKSRICAQ	LARFSEEKFH	FSDKPQPDSK	PTYSRGRSSN	AYDPSQMCAE	KQLELRLRDF	LLDIEDRIYQ
970	980	990	1000	1010	1020	1030	1040
GTLGAIKVTD	RHIWRSALES	GRYELLSEEN	KENGIIKTVN	EDVEEMEIDE	QTKVIVKDRL	LGIKTETPST	VSTNASTPQS
1050	1060	1070	1080	1090	1100	1110	1120
VSSVVHYLAM	ALFQIEQGIE	RRFLKAPLDA	SDSGRSYKTV	LDRWRESLLS	SASLSQVFLH	LSTLDRSVIW	SKSILNARCK
1130	1140	1150	1160	1170	1180	1190	1200
ICRKKGDAEN	MVLCDGCDRG	HHTYCVRPKL	KTVPEGDWFC	PECRPKQRSR	RLSSRQRPSL	ESDEDVEDSM	GGEDDEVDGD
1210	1220	1230	1240	1250	1260	1270	1280
EEEGQSEEEE	YEVEQDEDDS	QEEEEVSLPK	RGRPQVRLPV	KTRGKLSSSF	SSRGQQQEPG	RYPSRSQQST	PKTTVSSKTG
1290	1300	1310	1320	1330	1340	1350	1360
RSLRKINSAP	PTETKSLRIA	SRSTRHSHGP	LQADVFVELL	SPRRKRRGRK	SANNTPENSP	NFPNFRVIAT	KSSEQSRSVN
1370	1380	1390	1400	1410	1420	1430	1440
IASKLSLQES	ESKRRCRKRQ	SPEPSPVTLG	RRSSGRQGGV	HELSAFEQLV	VELVRHDDSW	PFLKLVSKIQ	VPDYYDIIKK
1450	1460	1470	1480	1490	1500	1510	1520
PIALNIIREK	VNKCEYKLAS	EFIDDIELMF	SNCFEYNPRN	TSEAKAGTRL	QAFFHIQAQK	LGLHVTPSNV	DQVSTPPAAK
1530							
KSRI							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1095	1	877.2623	-142.07	2	42.2	15.2	2	1124-1139	R.KKGDAENMVLCDGCDR.G	

Detailed Protein Report

Protein 986: **olfactory receptor 2T10 [Homo sapiens]**

Accession:	gi|52317215	**Score:**	15.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	35.4
Database Date:	2015-11-30	**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 987: **PREDICTED: dmX-like protein 1 isoform X5 [Homo sapiens]**

Accession:	gi|530379749	**Score:**	15.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	327.5
Database Date:	2015-11-30	**pI:**	6.0
		Sequence Coverage [%]:	0.5
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:** 1.50	**CV:** 0.00 %	**No. of Peptides:** 1

10	20	30	40	50	60	70	80
MNLHQVLTGA	VNPGDHCFSV	GSIGDQRFTA	YASGCDIVIL	GSDFERLQII	PGAKHGNIQV	GCVDCSMQQG	KIAASYGNVI
90	100	110	120	130	140	150	160
SIFEPVNLPK	QKKNLELYSQ	WQKSGQFFLE	SIAHNITWDP	TGSRLLTGSS	YLQLWSNTNL	EKPTEDENLN	KTDLNFGDWK
170	180	190	200	210	220	230	240
CIWHCKTASQ	VHLMKFSPDG	EFFATAGKDD	CLLKVWYNVE	NWRTAVTSPD	GSSEKQSQGE	IDFSFVYLAH	PRAVNGFSWR
250	260	270	280	290	300	310	320
KTSKYMPRAS	VCNVLLTCCK	DNVCRLWVET	FLPNDCLLYG	GDCSHWTESI	NLTNNFKRNA	SSKERVQNAL	EVNLRHFRRG
330	340	350	360	370	380	390	400
RRRSLALVAH	TGYLPHQQDP	HHVHRNTPLH	ANALCHFHIA	ASINPATDIP	LLPSITSLSL	NENEEKTGPF	VVHWLNNKEL
410	420	430	440	450	460	470	480
HFTLSMEVFL	QQLRKSFEQP	SSEASVEDSN	QADVKSDEET	DDGVDDLKIN	PEKKELGCDK	MVPNSSFTSL	SSAAIDHQIE
490	500	510	520	530	540	550	560
VLLSEWSKNA	DMLFSIHPMD	GSLLVWHVDW	LDEYQPGMFR	QVQVSFVSRI	PVAFPTGDAN	SLCKSIMMYA	CTKNVDLAIQ
570	580	590	600	610	620	630	640
QGKQKPSGLT	RSTSMLISSG	HNKSSNSLKL	SIFTPNVMMI	SKHADGSLNQ	WLVSFAEESA	FSTVLSISHK	SRYCGHRFHL
650	660	670	680	690	700	710	720
NDLACHSVLP	LLLTTSHHNA	LRTPDVDNPE	QPFDALNIEE	CSLTQQNKST	VDVAFQDPSA	VYSELILWRV	DPVGPLSFSG
730	740	750	760	770	780	790	800
GVSELARINS	LHVSAFSNVA	WLPTLIPSYC	LGAYCNSPSA	CFVASDGQYL	RLYEAVIDAK	KLLSELSNPE	ISKYVGEVFN
810	820	830	840	850	860	870	880
IVSQQSTARP	GCIIALDPIT	KLHGRKTQLL	HVFEEDFILN	NLEKKSLGKD	SILSNAGSSP	NGFSEKFYLI	VIECTQDNRS
890	900	910	920	930	940	950	960
LLHMWNLHLK	SIPVSLDEKV	DTKLSEAVWQ	PEEHYSSSPE	KILSPFSQKY	QACRANLQST	SRLTLFSEMV	YSQELHLPEG
970	980	990	1000	1010	1020	1030	1040
VEIISIKPSA	GHLSSSSIYP	ACSAPYLLAT	SCSDEKVRFW	RCRVTDGESA	TSKNGKIDLA	YIWEEWPLLI	EDGLQSNSSI
1050	1060	1070	1080	1090	1100	1110	1120
TVPGRPVEVS	CAHTNRLAVA	YKQPASNSRS	SQDFVMHVSI	FECESTGGSC	WVLEQTIHLD	ELSTVLDSGI	SVDSNLVAYN
1130	1140	1150	1160	1170	1180	1190	1200
KQDMYLSSKE	NITSNTKHLV	HLDWMSREDG	SHILTVGIGS	KLFMYGPLAG	KVQDQTGKET	LAFPLWESTK	VVPLSKFVLL
1210	1220	1230	1240	1250	1260	1270	1280
RSVDLVSSVD	GSPPFPVSLS	WVRDGILVVG	MDCEMHVYCQ	WQPSSKQEPV	ITDSYSGSTP	SITSLIKQSN	SSSGLHPPKK
1290	1300	1310	1320	1330	1340	1350	1360
TLTRSMTSLA	QKICGKKTAF	DPSVDMEDSG	LFEAAHVLSP	TLPQYHPLQL	LELMDLGKVR	RAKAILSHLV	KCIAGEVVAL
1370	1380	1390	1400	1410	1420	1430	1440
NEAESNHERR	LRSLTISASG	STTRDPQAFN	KAENTDYTEI	DSVPPLPLYA	LLAADDDSCY	SSLEKSSNES	TLSKSNQLSK
1450	1460	1470	1480	1490	1500	1510	1520
ESYDELFQTQ	LLMTDTHMLE	TDEENTKPRV	IDLSQYSPTY	FGPEHAQVLS	GHLLHSSLPG	LSRMEQMSLM	ALADTIATTS
1530	1540	1550	1560	1570	1580	1590	1600
TDIGESRDRS	QGGETLDECG	LKFLLAVRLH	TFLTTSLPAY	RAQLLHQGLS	TSHFAWAFHS	VAEEELLNML	PAMQKDDPTW
1610	1620	1630	1640	1650	1660	1670	1680
SELRAMGVGW	WVRNTRILRK	CIEKVAKAAF	YRKNDPLDAA	IFYLAMKKKA	VIWGLYRAEK	NTRMTQFFGH	NFEDERWRKA
1690	1700	1710	1720	1730	1740	1750	1760
ALKNAFSLLG	KQRFEHSAAF	FLLAGCLRDA	IEVCLEKLND	IQLALVIARL	YESEFDTSAA	YKSILRKKVL	GIDSPVSELC
1770	1780	1790	1800	1810	1820	1830	1840
SLNINMHHDP	FLRSMAYWIL	EDYSGALETL	IKQPIRENDD	QVLSASNPTV	FNFYNYLRTH	PLLLRRHFGS	SDTFSTHMSL
1850	1860	1870	1880	1890	1900	1910	1920
TGKSGLAGTI	NLSERRLFFT	TASAHLKAGC	PMLALEVLSK	MPKVIKKTRP	FYRASSFLDT	SKDCSPSSPL	KLDAREDKSS
1930	1940	1950	1960	1970	1980	1990	2000
AVDWSQSLIN	GFGSSSEGSS	EKQSNSTLSF	DWSQPSVVFQ	DDSLELKWDS	DNDEENEDVP	ISMKELKPLQ	RKTDKKLDDI
2010	2020	2030	2040	2050	2060	2070	2080
SSNYTESFST	LDENDLLNPS	EDIIAVQLKF	RACLKILTVE	LRTLSTGYEI	DGGKLRYQLY	HWLEKEVIAL	QRTCDFCSDA
2090	2100	2110	2120	2130	2140	2150	2160
EELQSAFGRN	EDEFGLNEDA	EDLPHQTKVK	QLRENFQEKR	QWLLKYQSLL	RMFLSYCILH	GSHGGGLASV	RMELILLLQE
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
751	1	765.8890	12.07	2	37.9	15.2	0	2355-2369	K.MWSAVFGGGAHVPSK.E		mdown:qdown 1.50

Detailed Protein Report

Protein 988: eukaryotic translation initiation factor 3 subunit H [Homo sapiens]

Accession:	gi|4503515	**Score:**	15.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	39.9
Database Date:	2015-11-30	**pI:**	6.1
		Sequence Coverage [%]:	5.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MASRKEGTGS	TATSSSSTAG	AAGKGKGKGG	SGDSAVKQVQ	IDGLVVLKII	KHYQEEGQGT	EVVQGVLLGL	VVEDRLEITN
90	100	110	120	130	140	150	160
CFPFPQHTED	DADFDEVQYQ	MEMMRSLRHV	NIDHLHVGWY	QSTYYGSFVT	RALLDSQFSY	QHAIEESVVL	IYDPIKTAQG
170	180	190	200	210	220	230	240
SLSLKAYRLT	PKLMEVCKEK	DFSPEALKKA	NITFEYMFEE	VPIVIKNSHL	INVLMWELEK	KSAVADKHEL	LSLASSNHLG
250	260	270	280	290	300	310	320
KNLQLLMDRV	DEMSQDIVKY	NTYMRNTSKQ	QQQKHQYQQR	RQQENMQRQS	RGEPPLPEED	LSKLFKPPQP	PARMDSLLIA
330	340	350	360				
GQINTYCQNI	KEFTAQNLGK	LFMAQALQEY	NN				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1815	1	716.3448	-29.65	3	51.4	15.2	1	242-259	K.NLQLLMDRVDEMSQDIVK.Y	

Detailed Protein Report

Protein 989: **PREDICTED: N(alpha)-acetyltransferase 38, NatC auxiliary subunit isoform X2 [Homo sapiens]**

Accession:	gi|530410697	**Score:**	15.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	13.5
Database Date:	2015-11-30	**pI:**	5.3
Modification(s):	Oxidation	**Sequence Coverage [%]:**	15.2
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MAGAGPTMLL REENGCCSRR QSSSSAGDSD GEREDSAAER ARQQLEALLN KTMRIRMTDG RTLVGCFLCT DRDCNVILGS
        90        100        110        120        130
AQEFLKPSDS FSAGEPRVLG LAMVPGHHIV SIEVQRESLT GPPYL
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
67	2	1018.8972	-76.15	2	29.5	15.2	2	2-20	M.AGAGPTMLLREENGCCSRR.Q	Oxidation: 7

Detailed Protein Report

Protein 990: **GLIPR1-like protein 2 isoform 1 [Homo sapiens]**

Accession: gi|394025727
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 15.1
MW [kDa]: 40.2
pI: 4.7
Sequence Coverage [%]: 4.7
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MEAARPFARE	WRAQSLPLAV	GGVLKLRLCE	LWLLLLGSSL	NARFLPDEED	VDFINEYVNL	HNELRGDVIP	RGSNLRFMTW
90	100	110	120	130	140	150	160
DVALSRTARA	WGKKCLFTHN	IYLQDVQMVH	PKFYGIGENM	WVGPENEFTA	SIAIRSWHAE	KKMYNFENGS	CSGDCSNYIQ
170	180	190	200	210	220	230	240
LVWDHSYKVG	CAVTPCSKIG	HIIHAAIFIC	NYAPGGTLTR	RPYEPGIFCT	RCGRRDKCTD	FLCSNADRDQ	ATYYRFWYPK
250	260	270	280	290	300	310	320
WEMPRPVVCD	PLCTFILLLR	ILCFILCVIT	VLIVQSQFPN	ILLEQQMIFT	PEESEAGNEE	EEKEEEKKEK	EEMEMEIMEM
330	340	350					
EEEKEEREEE	EEETQKEKME	EEEK					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2538	1	1045.4188	-0.85	2	60.0	15.1	1	309-324	K.EKEEMEMEIMEMEEEK.E	Oxidation: 12

Detailed Protein Report

Protein 991: **membrane-associated phosphatidylinositol transfer protein 1 isoform b [Homo sapiens]**

Accession:	gi|195927017	**Score:**	15.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	134.7
Database Date:	2015-11-30	**pI:**	5.6
		Sequence Coverage [%]:	1.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLIKEYHILL	PMSLDEYQVA	QLYMIQKKSR	EESSGEGSGV	EILANRPYTD	GPGGSGQYTH	KVYHVGSHIP	GWFRALLPKA
90	100	110	120	130	140	150	160
ALQVEEESWN	AYPYTRTRYT	CPFVEKFSIE	IETYYLPDGG	QQPNVFNLSG	AERRQRILDT	IDIVRDAVAP	GEYKAEEDPR
170	180	190	200	210	220	230	240
LYHSVKTGRG	PLSDDWARTA	AQTGPLMCAY	KLCKVEFRYW	GMQAKIEQFI	HDVGLRRVML	RAHRQAWCWQ	DEWTELSMAD
250	260	270	280	290	300	310	320
IRALEEETAR	MLAQRMAKCN	TGSEGSEAQP	PGKPSTEARS	AASNTGTPDG	PEAPPGPDAS	PDASFGKQWS	SSSRSSYSSQ
330	340	350	360	370	380	390	400
HGGAVSPQSL	SEWRMQNIAR	DSENSSEEEF	FDAHEGFSDS	EEVFPKEMTK	WNSNDFIDAF	ASPVEAEGTP	EPGAEAAKGI
410	420	430	440	450	460	470	480
EDGAQAPRDS	EGLDGAGELG	AEACAVHALF	LILHSGNILD	SGPGDANSKQ	ADVQTLSSAF	EAVTRIHFPE	ALGHVALRLV
490	500	510	520	530	540	550	560
PCPPICAAAY	ALVSNLSPYS	HDGDSLSRSQ	DHIPLAALPL	LATSSSRYQG	AVATVIARTN	QAYSAFLRSP	EGAGFCGQVA
570	580	590	600	610	620	630	640
LIGDGVGGIL	GFDALCHSAN	AGTGSRGSSR	RGSMNNELLS	PEFGPVRDPL	ADGVEGLGRG	SPEPSALPPQ	RIPSDMASPE
650	660	670	680	690	700	710	720
PEGSQNSLQA	APATTSSWEP	RRASTAFCPP	AASSEAPDGP	SSTARLDFKV	SGFFLFGSPL	GLVLALRKTV	MPALEAQMRP
730	740	750	760	770	780	790	800
ACEQIYNLFH	AADPCASRLE	PLLAPKFQAI	APLTVPRYQK	FPLGDGSSLL	LADTLQTHSS	LFLEELEMLV	PSTPTSTSGA
810	820	830	840	850	860	870	880
FWKGSELATD	PPAQPAAPST	TSEVVKILER	WWGTKRIDYS	LYCPEALTAF	PTVTLPHLFH	ASYWESADVV	AFILRQVIEK
890	900	910	920	930	940	950	960
ERPQLAECEE	PSIYSPAFPR	EKWQRKRTQV	KIRNVTSNHR	ASDTVVCEGR	PQVLSGRFMY	GPLDVVTLTG	EKVDVYIMTQ
970	980	990	1000	1010	1020	1030	1040
PLSGKWIHFG	TEVTNSSGRL	TFPVPPERAL	GIGVYPVRMV	VRGDHTYAEC	CLTVVARGTE	AVVFSIDGSF	TASVSIMGSD
1050	1060	1070	1080	1090	1100	1110	1120
PKVRAGAVDV	VRHWQDSGYL	IVYVTGRPDM	QKHRVVAWLS	QHNFPHGVVS	FCDGLTHDPL	RQKAMFLQSL	VQEVELNIVA
1130	1140	1150	1160	1170	1180	1190	1200
GYGSPKDVAV	YAALGLSPSQ	TYIVGRAVRK	LQAQCQFLSD	GYVAHLGQLE	AGSHSHASSG	PPRAALGKSS	YGVAAPVDFL
1210	1220	1230	1240	1250			
RKQSQLLRSR	GPSQAEREGP	GTPPTTLARG	KARSISLKLD	SEE			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1596	1	598.6726	-241.40	2	48.5	15.1	0	1218-1229	R.EGPGTPPTTLAR.G	

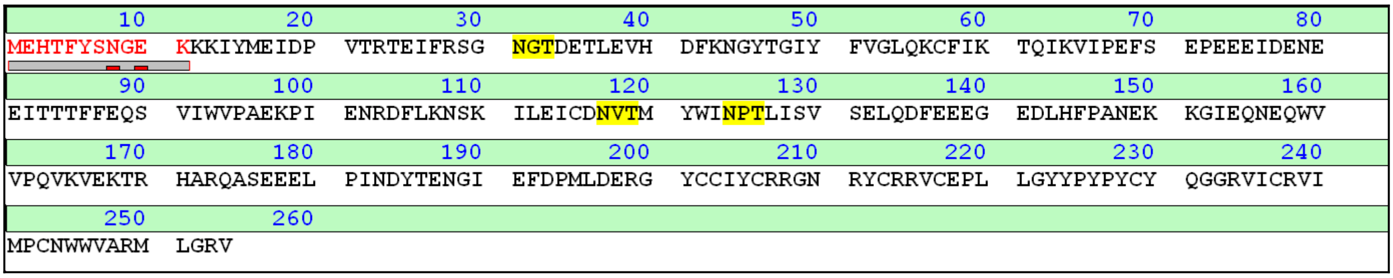
Detailed Protein Report

Protein 992: PREDICTED: tenomodulin isoform X1 [Homo sapiens]

Accession:	gi|530422140	**Score:**	15.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	30.0
Database Date:	2015-11-30	**pI:**	4.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	4.3
		No. of unique Peptides:	1

Quantitation

mdown:qdown **Median:** 0.40 **CV:** 0.00 % **No. of Peptides:** 1



```
        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	Ratios
1182	1	679.6416	-214.99	2	44.4	15.1	0	1-11	-.MEHTFYSNGEK.K	Oxidation: 1	mdown:qdown 0.40

Detailed Protein Report

Protein 993: procollagen-lysine,2-oxoglutarate 5-dioxygenase 1 precursor [Homo sapiens]

Accession:	gi|32307144	**Score:**	15.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	83.5
Database Date:	2015-11-30	**pI:**	6.5
		Sequence Coverage [%]:	1.9
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	0.94	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.74	**CV:**	0.00 %	**No. of Peptides:**	1

10	20	30	40	50	60	70	80
MRPLLLLALL	GWLLLAEAKG	DAKPEDNLLV	LTVATKETEG	FRRFKRSAQF	FNYKIQALGL	GEDWNVEKGT	SAGGGQKVRL
90	100	110	120	130	140	150	160
LKKALEKHAD	KEDLVILFAD	SYDVLFASGP	RELLKKFRQA	RSQVVFSAEE	LIYPDRRLET	KYPVVSDGKR	FLGSGGFIGY
170	180	190	200	210	220	230	240
APNLSKLVAE	WEGQDSDSDQ	LFYTKIFLDP	EKREQINITL	DHRCRIFQNL	DGALDEVVLK	FEMGHVRARN	LAYDTLPVLI
250	260	270	280	290	300	310	320
HGNGPTKLQL	NYLGNYIPRF	WTFETGCTVC	DEGLRSLKGI	GDEALPTVLV	GVFIEQPTPF	VSLFFQRLLR	LHYPQKHMRL
330	340	350	360	370	380	390	400
FIHNHEQHHK	AQVEEFLAQH	GSEYQSVKLV	GPEVRMANAD	ARNMGADLCR	QDRSCTYYFS	VDADVALTEP	NSLRLLIQQN
410	420	430	440	450	460	470	480
KNVIAPLMTR	HGRLWSNFWG	ALSADGYYAR	SEDYVDIVQG	RRVGVWNVPY	ISNIYLIKGS	ALRGELQSSD	LFHHSKLDPD
490	500	510	520	530	540	550	560
MAFCANIRQQ	DVFMFLTNRH	TLGHLLSLDS	YRTTHLHNDL	WEVFSNPEDW	KEKYIHQNYT	KALAGKLVET	PCPDVYWFPI
570	580	590	600	610	620	630	640
FTEVACDELV	EEMEHFGQWS	LGNNKDNRIQ	GGYENVPTID	IHMNQIGFER	EWHKFLLEYI	APMTEKLYPG	YYTRAQFDLA
650	660	670	680	690	700	710	720
FVVRYKPDEQ	PSLMPHHDAS	TFTINIALNR	VGVDYEGGGC	RFLRYNCSIR	APRKGWTLMH	PGRLTHYHEG	LPTTRGTRYI
730							
AVSFVDP							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1527	1	932.4083	-64.53	2	48.9	15.1	1	317-330	K.HMRLFIHNHEQHHK.A		mdown:qdown 0.94 Wdown:Qdown 0.74

Detailed Protein Report

Protein 994: class E basic helix-loop-helix protein 41 [Homo sapiens]

Accession:	gi|13540521	**Score:**	15.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	50.5
Database Date:	2015-11-30	**pI:**	7.2
		Sequence Coverage [%]:	3.7
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	0.65	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.13	**CV:**	0.00 %	**No. of Peptides:**	1

```
        10         20         30         40         50         60         70         80
MDEGIPHLQE RQLLEHRDFI GLDYSSLYMC KPKRSMKRDD TKDTYKLPHR LIEKKRRDRI NECIAQLKDL LPEHLKLTTL
        90        100        110        120        130        140        150        160
GHLEKAVVLE LTLKHLKALT ALTEQQHQKI IALQNGERSL KSPIQSDLDA FHSGFQTCAK EVLQYLSRFE SWTPREPRCV
       170        180        190        200        210        220        230        240
QLINHLHAVA TQFLPTPQLL TQQVPLSKGT GAPSAAGSAA APCLERAGQK LEPLAYCVPV IQRTQPSAEL AAENDTDTDS
       250        260        270        280        290        300        310        320
GYGGEAEARP DREKGKGAGA SRVTIKQEPP GEDSPAPKRM KLDSRGGGSG GGPGGGAAAA AAALLGPDPA AAAALLRPDA
       330        340        350        360        370        380        390        400
ALLSSLVAFG GGGGAPFPQP AAAAAPFCLP FCFLSPSAAA AYVQPFLDKS GLEKYLYPAA AAAPFPLLYP GIPAPAAAAA
       410        420        430        440        450        460        470        480
AAAAAAAAAA AFPCLSSVLS PPPEKAGAAA ATLLPHEVAP LGAPHPQHPH GRTHLPFAGP REPGNPESSA QEDPSQPGKE
       490
AP
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
119	1	529.4932	-185.08	3	30.8	15.1	0	189-206	K.GTGAPSAAGSAAAPCLER.A		mdown:qdown 0.65 Wdown:Qdown 0.13

BRUKER

Detailed Protein Report

Protein 995: PREDICTED: ubiquitin-associated and SH3 domain-containing protein B isoform X1 [Homo sapiens]

Accession:	gi|530398460	**Score:**	15.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	75.5
Database Date:	2015-11-30	**pI:**	6.1
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	2.2
		No. of unique Peptides:	1

Quantitation

mdown:qdown **Median:** 3.18 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MICVVLCIHG	FCTEKKKARC	VASDCLVSRE	ETDKAATQQQ	LSTLSKCGNE	RVWVSVLPAF	SAPAVPSGAE	GSVLLLRNFI
90	100	110	120	130	140	150	160
NLQKALASTG	GRSVQAACDW	LFSHVGDPFL	DDPLPREYVL	YLRPTGPLAQ	KLSDFWQQSK	QICGKNKAHN	IFPHITLCQF
170	180	190	200	210	220	230	240
FMCEDSKVDA	LGEALQTTVS	RWKCKFSAPL	PLELYTSSNF	IGLFVKEDSA	EVLKKFAADF	AAEAASKTEV	HVEPHKKQLH
250	260	270	280	290	300	310	320
VTLAYHFQAS	HLPTLEKLAQ	NIDVKLGCDW	VATIFSRDIR	FANHETLQVI	YPYTPQNDDE	LELVPGDFIF	MSPMEQTSTS
330	340	350	360	370	380	390	400
EGWIYGTSLT	TGCSGLLPEN	YITKADECST	WIFHGSYSIL	NTSSSNSLTF	GDGVLERRPY	EDQGLGETTP	LTIICQPMQP
410	420	430	440	450	460	470	480
LRVNSQPGPQ	KRCLFVCRHG	ERMDVVFGKY	WLSQCFDAKG	RYIRTNLNMP	HSLPQRSGGF	RDYEKDAPIT	VFGCMQARLV
490	500	510	520	530	540	550	560
GEALLESNTI	IDHVYCSPSL	RCVQTAHNIL	KGLQQENHLK	IRVEPGLFEW	TKWVAGSTLP	AWIPPSELAA	ANLSVDTTYR
570	580	590	600	610	620	630	640
PHIPISKLVV	SESYDTYISR	SFQVTKEIIS	ECKSKGNNIL	IVAHASSLEA	CTCQLQGLSP	QNSKDFVQMV	RKIPYLGFCS
650	660	670	680				
CEELGETGIW	QLTDPPILPL	THGPTGGFNW	RETLLQE				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2812	1	913.4675	44.29	2	63.6	15.1	0	1-15	-.MICVVLCIHGFCTEK.K	Carbamidomethyl: 7, 12; Oxidation: 1	mdown:qdown 3.18

Detailed Protein Report

Protein 996: uncharacterized protein C6orf136 isoform 2 [Homo sapiens]

Accession:	gi|238624193	**Score:**	15.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	21.3
Database Date:	2015-11-30	**pI:**	10.3
		Sequence Coverage [%]:	11.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MYQPSRGAAR	RLGPCLRAYQ	ARPQLPKLFL	QSHDYSLYSL	DVEFINEILN	IRTKGRTWYI	LSLTLCRFLA	WNYFAHLRLE
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
VLQLTRHPEN	WTLQARWRLV	GLPVHLLFLR	FYKRDKDEHY	RTYDAYSTFY	LNSSGLICRH	RLDKLMPSHS	PPTPVKKLLV
170	**180**	**190**					
GALVALGLSE	PEPDLNLCSK	P					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1541	1	789.6495	-77.98	3	49.1	15.0	1	122-141	R.TYDAYSTFYLNSSGLICRHR.L	

Detailed Protein Report

Protein 997: zinc finger protein 786 [Homo sapiens]

Accession: gi|170932473
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 15.0
MW [kDa]: 89.8
pI: 10.9
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

Detailed Protein Report

Protein 998: PREDICTED: microtubule-associated tumor suppressor 1 isoform X7 [Homo sapiens]

Accession:	gi|530387935	**Score:**	15.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	106.1
Database Date:	2015-11-30	**pI:**	9.1
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MTDDNSDDKI	EDELQTFFTS	DKDGNTHAYN	PKSPPTQNSS	ASSVNWNSAN	PDDMVVDYET	DPAVVTGENI	SLSLQGVEVF
90	100	110	120	130	140	150	160
GHEKSSSDFI	SKQVLDMHKD	SICQCPALVG	TEKPKYLQHS	CHSLEAVEGQ	SVEPSLPFVW	KPNDNLNCAG	YCDALELNQT
170	180	190	200	210	220	230	240
FDMTVDKVNC	TFISHHAIGK	SQSFHTAGSL	PPTGRRSGST	SSLSYSTWTS	SHSDKTHARE	TTYDRESFEN	PQVTPSEAQD
250	260	270	280	290	300	310	320
MTYTAFSDVV	MQSEVFVSDI	GNQCACSSGK	VTSEYTDGSQ	QRLVGEKETQ	ALTPVSDGME	VPNDSALQEF	FCLSHDESNS
330	340	350	360	370	380	390	400
EPHSQSSYRH	KEMGQNLRET	VSYCLIDDEC	PLMVPAFDKS	EAQVLNPEHK	VTETEDTQMV	SKGKDLGTQN	HTSELILSSP
410	420	430	440	450	460	470	480
PGQKVGSSFG	LTWDANDMVI	STDKTMCMST	PVLEPTKVTF	SVSPIEATEK	CKKVEKGNRG	LKNIPDSKEA	PVNLCKPSLG
490	500	510	520	530	540	550	560
KSTIKTNTPI	GCKVRKTEII	SYPRPNFKNV	KAKVMSRAVL	QPKDAALSKV	TPRPQQTSAS	SPSSVNSRQQ	TVLSRTPRSD
570	580	590	600	610	620	630	640
LNADKKAEIL	INKTHKQQFN	KLITSQAVHV	TTHSKNASHR	VPRTTSAVKS	NQEDVDKASS	SNSACETGSV	SALFQKIKGI
650	660	670	680	690	700	710	720
LPVKMESAEC	LEMTYVPNID	RISPEKKGEK	ENGTSMEKQE	LKQEIMNETF	EYGSLFLGSA	SKTTTTSGRN	ISKPDSCGLR
730	740	750	760	770	780	790	800
QIAAPKAKVG	PPVSCLRRNS	DNRNPSADRA	VSPQRIRRVS	SSGKPTSLKT	AQSSWVNLPR	PLPKSKASLK	SPALRRTGST
810	820	830	840	850	860	870	880
PSIASTHSEL	STYSNNSGNA	AVIKYEEKPP	KPAFQNGSSG	SFYLKPLVSR	AHVHLMKTPP	KGPSRKNLFT	ALNAVEKSRQ
890	900	910	920	930	940	950	960
KNPRSLCIQP	QTAPDALPPE	KTLELTQYKT	KCENQSGFIL	QLKQLLACGN	TKFEALTVVI	QHLLSEREEA	LKQHKTLSQE
970							
LVNLRGELA							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2237	1	869.3795	-55.11	2	56.4	15.0	1	85-99	K.SSSDFISKQVLDMHK.D	Oxidation: 13

Detailed Protein Report

Protein 999: PREDICTED: transcription elongation factor A protein 3 isoform X4 [Homo sapiens]

Accession:	gi|578799689	**Score:**	15.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	35.0
Database Date:	2015-11-30	**pI:**	10.2
		Sequence Coverage [%]:	4.5
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	0.68	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	1.92	**CV:**	0.00 %	**No. of Peptides:**	1

```
        10         20         30         40         50         60         70         80
MSIQLLQTTR IGVAVNGVRK HCSDKEVVSL AKVLIKNWKR LLDSPGPPKG EKGEEREKAK KKEKGLECSD WKPEAGLSPP
        90        100        110        120        130        140        150        160
RKKREDPKTR RDSVDSKSSA SSSPKRPSVE RSNSSKSKAE SPKTPSSPLT PTFASSMCLL APCYLTGDSV RDKCVEMLSA
       170        180        190        200        210        220        230        240
ALKADDDYKD YGVNCDKMAS EIEDHIYQEL KSTDMKYRNR VRSRISNLKD PRNPGLRRNV LSGAISAGLI AKMTAEEMAS
       250        260        270        280        290        300        310        320
DELRELRNAM TQEAIREHQM AKTGGTTTDL FQCSKCKKKN CTYNQVQTRS ADEPMTTFVL CNECGNRWKM ESAS
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
291	1	657.3457	-71.91	2	32.4	15.0	0	219-232	R.NVLSGAISAGLIAK.M		mdown:qdown 0.68 Wdown:Qdown 1.92

Detailed Protein Report

Protein 1000: PREDICTED: RNA-binding protein EWS isoform X3 [Homo sapiens]

Accession:	gi|578837005	**Score:**	14.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	68.1
Database Date:	2015-11-30	**pI:**	9.7
		Sequence Coverage [%]:	3.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MASTDYSTYS	QAAAQQGYSA	YTAQPTQGYA	QTTQAYGQQS	YGTYGQPTDV	SYTQAQTTAT	YGQTAYATSY	GQPPTGYTTP
90	100	110	120	130	140	150	160
TAPQAYSQPV	QGYGTGAYDT	TTATVTTTQA	SYAAQSAYGT	QPAYPAYGQQ	PAATAPTRPQ	DGNKPTETSQ	PQSSTGGYNQ
170	180	190	200	210	220	230	240
PSLGYGQSNY	SYPQVPGSYP	MQPVTAPPSY	PPTSYSSTQP	TSYDQSSYSQ	QNTYGQPSSY	GQQSSYGQQS	SYGQQPPTSY
250	260	270	280	290	300	310	320
PPQTGSYSQA	PSQYSQQSSS	YGQQSSFRQD	HPSSMGVYGQ	ESGGFSGPGE	NRSMSGPDNR	GRGRGGFDRG	GMSRGGRGGG
330	340	350	360	370	380	390	400
RGGMGSAGER	GGFNKPGGPM	DEGPDLDLGP	PVDPDEDSDN	SAIYVQGLND	SVTLDDLADF	FKQCGVVKMN	KRTGQPMIHI
410	420	430	440	450	460	470	480
YLDKETGKPK	GDATVSYEDP	PTAKAAVEWF	DGKDFQGSKL	KVSLARKKPP	MNSMRGGLPP	REGRGMPPPL	RGGPGGPGGP
490	500	510	520	530	540	550	560
GGPMGRMGGR	GGDRGGFPPR	GPRGSRGNPS	GGGNVQHRAG	DWQCPNPSIG	DFCCDVIVCR	GCGNQNFAWR	TECNQCGDRG
570	580	590	600	610	620	630	640
RGGPGGMRGG	RGGLMDRGGP	GGMFRGGRGG	DRGGFRGGRG	MDRGGFGGGR	RGGPGGPPGP	LMEQMGGRRG	GRGGPGKMDK
650	660						
GEHRQERRDR	PY						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
6	1	1186.3900	-88.40	2	28.4	14.9	2	541-561	R.GCGNQNFAWRTECNQCGDRGR.G	

Detailed Protein Report

Protein 1001: PREDICTED: metal transporter CNNM4 isoform X2 [Homo sapiens]

Accession:	gi|530368586	**Score:**	14.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	86.4
Database Date:	2015-11-30	**pI:**	6.2
		Sequence Coverage [%]:	0.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAPVGGGGRP	VGGPARGRLL	LAAPVLLVLL	WALGARGQGS	PQQGTIVGMR	LASCNKSCGT	NPDGIIFVSE	GSTVNLRLYG
90	100	110	120	130	140	150	160
YSLGNISSNL	ISFTEVDDAE	TLHKSTSCLE	LTKDLVVQQL	VNVSRGNTSG	VLVVLTKFLR	RSESMKLYAL	CTRAQPDGPW
170	180	190	200	210	220	230	240
LKWTDKDSLL	FMVEEPGRFL	PLWLHILLIT	VLLVLSGIFS	GLNLGLMALD	PMELRIVQNC	GTEKERRYAR	KIEPIRRKGN
250	260	270	280	290	300	310	320
YLLCSLLLGN	VLVNTSLTIL	LDNLIGSGLM	AVASSTIGIV	IFGEILPQAL	CSRHGLAVGA	NTILLTKFFM	LLTFPLSFPI
330	340	350	360	370	380	390	400
SKLLDFFLGQ	EIRTVYNREK	LMEMLKVTEP	YNDLVKEELN	MIQGALELRT	KTVEDIMTQL	QDCFMIRSDA	ILDFNTMSEI
410	420	430	440	450	460	470	480
MESGYTRIPV	FEDEQSNIVD	ILYVKDLAFV	DPDDCTPLKT	ITRFYNHPVH	FVFHDTKLDA	MLEEFKKGKS	HLAIVQKVNN
490	500	510	520	530	540	550	560
EGEGDPFYEV	LGLVTLEDVI	EEIIKSEILD	ESDMYTDNRS	RKRVSEKNKR	DFSAFKDADN	ELKVKISPQL	LLAAHRFLAT
570	580	590	600	610	620	630	640
EVSQFSPSLI	SEKILLRLLK	YPDVIQELKF	DEHNKYYARH	YLYTRNKPAD	YFILILQGKV	EVEAGKENMK	FETGAFSYYG
650	660	670	680	690	700	710	720
TMALTSVPSD	RSPAHPTPLS	RSASLSYPDR	TDVSTAATLA	GSSNQFGSSV	LGQYISDFSV	RALVDLQYIK	PQSWPCFSRP
730	740	750	760	770	780		
GDRVCLPAPP	SMNSSLPHAD	HSAAVPERAA	GFSHGEQPSV	SHRRVHHPHG	ELGREV		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2779	1	870.4221	-28.45	1	63.2	14.9	1	530-536	K.RDFSAFK.D	

Detailed Protein Report

Protein 1002: PREDICTED: sterol regulatory element-binding protein cleavage-activating protein isoform X2 [Homo sapiens]

Accession:	gi|530372098	**Score:**	14.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	139.5
Database Date:	2015-11-30	**pI:**	6.4
		Sequence Coverage [%]:	0.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MTLTERLREK	ISRAFYNHGL	LCASYPIPII	LFTGFCILAC	CYPLLKLPLP	GTGPVEFTTP	VKDYSPPPVD	SDRKQGEPTE
90	100	110	120	130	140	150	160
QPEWYVGAPV	AYVQQIFVKS	SVFPWHKNLL	AVDVFRSPLS	RAFQLVEEIR	NHVLRDSSGI	RSLEELCLQV	TDLLPGLRKL
170	180	190	200	210	220	230	240
RNLLPEHGCL	LLSPGNFWQN	DWERFHADPD	IIGTIHQHEP	KTLQTSATLK	DLLFGVPGKY	SGVSLYTRKR	MVSYTITLVF
250	260	270	280	290	300	310	320
QHYHAKFLGS	LRARLMLLHP	SPNCSLRAES	LVHVHFKEEI	GVAELIPLVT	TYIILFAYIY	FSTRKIDMVK	SKWGLALAAV
330	340	350	360	370	380	390	400
VTVLSSLLMS	VGLCTLFGLT	PTLNGGEIFP	YLVVVIGLEN	VLVLTKSVVS	TPVDLEVKLR	IAQGLSSESW	SIMKNMATEL
410	420	430	440	450	460	470	480
GIILIGYFTL	VPAIQEFCLF	AVVGLVSDFF	LQMLFFTTVL	SIDIRRMELA	DLNKRLPPEA	CLPSAKPVGQ	PTRYERQLAV
490	500	510	520	530	540	550	560
RPSTPHTITL	QPSSFRNLRL	PKRLRVVYFL	ARTRLAQRLI	MAGTVVWIGI	LVYTDPAGLR	NYLAAQVTEQ	SPLGEGALAP
570	580	590	600	610	620	630	640
MPVPSGMLPP	SHPDPAFSIF	PPDAPKLPEN	QTSPGESPER	GGPAEVVHDS	PVPEVTWGPE	DEELWRKLSF	RHWPTLFSYY
650	660	670	680	690	700	710	720
NITLAKRYIS	LLPVIPVTLR	LNPREALEGR	HPQDGRSAWP	PPGPIPAGHW	EAGPKGPGGV	QAHGDVTLYK	VAALGLATGI
730	740	750	760	770	780	790	800
VLVLLLLCLY	RVLCPRNYGQ	LGGGPGRRRR	GELPCDDYGY	APPETEIVPL	VLRGHLMDIE	CLASDGMLLV	SCCLAGHVCV
810	820	830	840	850	860	870	880
WDAQTGDCLT	RIPRPGQRRD	SGVGSGLEAQ	ESWERLSDGG	KAGPEEPGDS	PPLRHRPRGP	PPPSLFGDQP	DLTCLIDTNF
890	900	910	920	930	940	950	960
SAQPRSSQPT	QPEPRHRAVC	GRSRDSPGYD	FSCLVQRVYQ	EEGLAAVCTP	ALRPPSPGPV	LSQAPEDEGG	SPEKGSPSLA
970	980	990	1000	1010	1020	1030	1040
WAPSAEGSIW	SLELQGNLIV	VGRSSGRLEV	WDAIEGVLCC	SSEEVSSGIT	ALVFLDKRIV	AARLNGSLDF	FSLETHTALS
1050	1060	1070	1080	1090	1100	1110	1120
PLQFRGTPGR	GSSPASPVYS	SSDTVACHLT	HTVPCAHQKP	ITALKAAAGR	LVTGSQDHTL	RVFRLEDSCC	LFTLQGHSGA
1130	1140	1150	1160	1170	1180	1190	1200
ITTVYIDQTM	VLASGGQDGA	ICLWDVLTGS	RVSHVFAHRG	DVTSLTCTTS	CVISSGLDDL	ISIWDRSTGI	KFYSIQQDLG
1210	1220	1230	1240	1250	1260	1270	1280
CGASLGVISD	NLLVTGGQGC	VSFWDLNYGD	LLQTVYLGKN	SEAQPARQIL	VLDNAAIVCN	FGSELSLVYV	PSVLEKLD

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1688	1	1045.6717	134.35	1	49.8	14.9	0	220-228	K.YSGVSLYTR.K	

Detailed Protein Report

Protein 1003: DNA-binding protein RFX6 [Homo sapiens]

Accession: gi|258547126
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 14.9
MW [kDa]: 102.4
pI: 6.1
Sequence Coverage [%]: 1.0
No. of unique Peptides: 1

```
        10         20         30         40         50         60         70         80
MAKVPELEDT FLQAQPAPQL SPGIQEDCCV QLLGKGLLVY PEETVYLAAE GQPGGEQGGG EKGEDPELPG AVKSEMHLNN

        90        100        110        120        130        140        150        160
GNFSSEEEDA DNHDSKTKAA DQYLSQKKTI TQIVKDKKKQ TQLTLQWLEE NYIVCEGVCL PRCILYAHYL DFCRKEKLEP

       170        180        190        200        210        220        230        240
ACAATFGKTI RQKFPLLTTR RLGTRGHSKY HYYGIGIKES SAYYHSVYSG KGLTRFSGSK LKNEGGFTRK YSLSSKTGTL

       250        260        270        280        290        300        310        320
LPEFPSAQHL VYQGCISKDK VDTLIMMYKT HCQCILDNAI NGNFEEIQHF LLHFWQGMPD HLLPLLENPV IIDIFCVCDS

       330        340        350        360        370        380        390        400
ILYKVLTDVL IPATMQEMPE SLLADIRNFA KNWEQWVVSS LENLPEALTD KKIPIVRRFV SSLKRQTSFL HLAQIARPAL

       410        420        430        440        450        460        470        480
FDQHVVNSMV SDIERVDLNS IGSQALLTIS GSTDTESGIY TEHDSITVFQ ELKDLLKKNA TVEAFIEWLD TVVEQRVIKT

       490        500        510        520        530        540        550        560
SKQNGRSLKK RAQDFLLKWS FFGARVMHNL TLNNASSFGS FHLIRMLLDE YILLAMETQF NNDKEQELQN LLDKYMKNSD

       570        580        590        600        610        620        630        640
ASKAAFTASP SSCFLANRNK GSMVSSDAVK NESHVETTYL PLPSSQPGGL GPALHQFPAG NTDNMPLTGQ MELSQIAGHL

       650        660        670        680        690        700        710        720
MTPPISPAMA SRGSVINQGP MAGRPPSVGP VLSAPSHCST YPEPIYPTLP QANHDFYSTS SNYQTVFRAQ PHSTSGLYPH

       730        740        750        760        770        780        790        800
HTEHGRCMAW TEQQLSRDFF SGSCAGSPYN SRPPSSYGPS LQAQDSHNMQ FLNTGSFNFL SNTGAASCQG ATLPPNSPNG

       810        820        830        840        850        860        870        880
YYGSNINYPE SHRLGSMVNQ HVSVISSIRS LPPYSDIHDP LNILDDSGRK QTSSFYTDTS SPVACRTPVL ASSLQTPIPS

       890        900        910        920        930
SSSQCMYGTS NQYPAQETLD SHGTSSREMV SSLPPINTVF MGTAAGGT
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1798	1	1023.7921	275.12	1	51.2	14.9	0	99-107	K.AADQYLSQK.K	

Detailed Protein Report

Protein 1004: bisphosphoglycerate mutase [Homo sapiens]

Accession:	gi|4502445	**Score:**	14.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	30.0
Database Date:	2015-11-30	**pI:**	6.1
		Sequence Coverage [%]:	5.0
		No. of unique Peptides:	1

Quantitation

Wdown:Qdown **Median:** 0.98 **CV:** 0.00 % **No. of Peptides:** 1

Alias proteins:

Accession	Name	Description
gi|578814542	refseq_human (refseq_human_20140103.fasta)	PREDICTED: bisphosphoglycerate mutase isoform X1 [Homo sapiens]
gi|40353764	refseq_human (refseq_human_20140103.fasta)	bisphosphoglycerate mutase [Homo sapiens]

10	20	30	40	50	60	70	80
MSKYKLIMLR	HGEGAWNKEN	RFCSWVDQKL	NSEGMEEARN	CGKQLKALNF	EFDLVFTSVL	NRSIHTAWLI	LEELGQEWVP
90	100	110	120	130	140	150	160
VESSWRLNER	HYGALIGLNR	EQMALNHGEE	QVRLWRRSYN	VTPPPIEESH	PYYQEIYNDR	RYKVCDVPLD	QLPRSESLKD
170	180	190	200	210	220	230	240
VLERLLPYWN	ERIAPEVLRG	KTILISAHGN	SSRALLKHLE	GISDEDIINI	TLPTGVPILL	ELDENLRAVG	PHQFLGDQEA
250	260						
IQAAIKKVED	QGKVKQAKK						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
937	2	770.8595	-3.57	2	40.5	14.9	0	101-113	R.EQMALNHGEEQVR.L		Wdown:Qdown 0.98

Detailed Protein Report

Protein 1005: 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 1006: melanoma-associated antigen B6 [Homo sapiens]

Accession: gi|29337290

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Score: 14.9

MW [kDa]: 44.0

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 1007: ubiquinone biosynthesis protein COQ9, mitochondrial precursor [Homo sapiens]

Accession:	gi|40789233	**Score:**	14.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	35.5
Database Date:	2015-11-30	**pI:**	5.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	5.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAAAAVSGAL	GRAGWRLLQL	RCLPVARCRQ	ALVPRAFHAS	AVGLRSSDEQ	KQQPPNSFSQ	QHSETQGAEK	PDPESSHSPP
90	100	110	120	130	140	150	160
RYTDQGGEEE	EDYESEEQLQ	HRILTAALEF	VPAHGWTAEA	IAEGAQSLGL	SSAAASMFGK	DGSELILHFV	TQCNTRLTRV
170	180	190	200	210	220	230	240
LEEEQKLVQL	GQAEKRKTDQ	FLRDAVETRL	RMLIPYIEHW	PRALSILMLP	HNIPSSLSLL	TSMVDDMWHY	AGDQSTDFNW
250	260	270	280	290	300	310	320
YTRRAMLAAI	YNTTELVMMQ	DSSPDFEDTW	RFLENRVNDA	MNMGHTAKQV	KSTGEALVQG	LMGAAVTLKN	LTGLNQRR

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1422	1	982.5936	136.72	2	47.5	14.9	1	272-288	R.FLENRVNDAMNMGHTAK.Q	Oxidation: 12

Detailed Protein Report

Protein 1008: cbp/p300-interacting transactivator 4 [Homo sapiens]

Accession: gi|19263349
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 14.9
MW [kDa]: 18.6
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 1009: hippocalcin-like protein 4 isoform 1 [Homo sapiens]

Accession:	gi|7705419	**Score:**	14.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	22.2
Database Date:	2015-11-30	**pI:**	4.6
		Sequence Coverage [%]:	11.0
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|538918345	refseq_human (refseq_human_20140103.fasta)	hippocalcin-like protein 4 isoform 1 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MGKTNSKLAP EVLEDLVQNT EFSEQELKQW YKGFLKDCPS GILNLEEFQQ LYIKFFPYGD ASKFAQHAFR TFDKNGDGTI
        90        100        110        120        130        140        150        160
DFREFICALS VTSRGSFEQK LNWAFEMYDL DGDGRITRLE MLEIIEAIYK MVGTVIMMRM NQDGLTPQQR VDKIFKKMDQ
       170        180        190        200
DKDDQITLEE FKEAAKSDPS IVLLLQCDMQ K
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
70	1	826.6853	-24.83	3	30.3	14.8	1	95-115	R.GSFEQKLNWAFEMYDLDGDGR.I	

Detailed Protein Report

Protein 1010: fibrous sheath-interacting protein 2 [Homo sapiens]

Accession:	gi|297206791	**Score:**	14.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	789.4
Database Date:	2015-11-30	**pI:**	6.2
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	0.3
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MKFQLWSSQI RPLGPIFPAL RALYALARAA PQEATALLGP LPLEAWNAGG GAEVVGLWPF LVRSGQRDNG VLEKESGAGE
        90        100        110        120        130        140        150        160
EGAEGAVPAM ELYLGACSKP AKVAVTKTVA SVLAADTQQC RDGVHKTHFA GVGPAQLLDL PLGVKLPVIP GSNAVFYTTN
       170        180        190        200        210        220        230        240
FGEKLFRPSY GFNLTDPYCR LLENQYKSLH DPHLKAYYKR KDILKRLKKG GYITSNNKVV CTLRELNKYR QYLTSLKLDF
       250        260        270        280        290        300        310        320
ERNYIKEQRI LAKQLHNIPE NNQIPQHCDV AQVQNWLLKE GTESIKDQER LMRHRYLDMI SRKLEQLERT AEEQRLFLMD
       330        340        350        360        370        380        390        400
REERRQREHT RRKLTLRRKI EEEWKTKEML LLTRMAEDVK REERIEEQQH RNREESDRKK QDLLEKKMAY HLQKMQDTGF
       410        420        430        440        450        460        470        480
NGEDIGKNTF KYRGQDGTHA SPKNKKKTSE DIMLVYPAGD QNTYKETHGH TANAAHQRQN SSNNFTKKNS ASVVYQADVQ
       490        500        510        520        530        540        550        560
DNGINQKRDG MVSKNSSIFD DRGGINISGQ GSIISAQVSP TRNFSRVSQA FLDPSKEEKE TNADWDGRPT KRSSYLCESG
       570        580        590        600        610        620        630        640
PQAHATDPGI FSSPVYTNMQ QNLLQNCLQE KVTSEELNII IQNVMTWVVA TVTSILYPAI TKYEKRLQNN TYPVSDDSIL
       650        660        670        680        690        700        710        720
SSDSSSFCST CSEDFTYRSY TSATTKTFQA EPCAFVVDTS VRRPTTPIKP PPAHVEKTVV GKTCHIKGQS IISKHKYNKT
       730        740        750        760        770        780        790        800
NLLYSYPKLR SCKSDSHLLA SFETGTKKSK DATTETDSLG SSLHCDKTAK AMDEMKNLKN VFVNFKCYLK GETEVILESI
       810        820        830        840        850        860        870        880
LREIMSDLTQ AIPSLSSVTA EVFVEQCERE KEILLSNAHI PSVASEIVEN MLEKLESAVE KKCVEMFSQD LSVDIKPSLA
       890        900        910        920        930        940        950        960
ASDELLTSSN GKPLKNSMPH TLDPMCDIAE DMVHAILEKL MTLVSFKQNE FLHLKDTNKL SCQQHKTDPI CMFLQRAGKN
       970        980        990       1000       1010       1020       1030       1040
KSSLESDEAS LIVNEEVQNL ISNIFSQSSL VAYIEEAINA ILGYIQTELN NERIIASEET VVLLQLLEDI LFQLHQEPVN
      1050       1060       1070       1080       1090       1100       1110       1120
ESFQKSRQPR ISSPSDTKEK YRLTGTRLSN SPRSGRPFPP INVPGMVLYS DDENEEIDNI VKNVLDSTFK DEKVKSQEQI
      1130       1140       1150       1160       1170       1180       1190       1200
PNHWFTKGNT CFECKRNIKP PTKPGSRSKA AFHDWELKTE PPSTNHEDIL KKKLSSNKDI STFSQDQKHQ IEKASENIVT
      1210       1220       1230       1240       1250       1260       1270       1280
SILKEMLKDI SSVPFGHLDS KTGSEASVLV SEKPQGLSHQ EWIDQMFSVS EISTVAQEIT DSVLNILHKA SNYISNTTKS
      1290       1300       1310       1320       1330       1340       1350       1360
SISSSVHQIS LHNSDTEHIV KEAPNKYPLK TWFDSEKKMK YLSLFDVDPE KPPWLKSGKS EPKPVDDIND KIIRTIFKRL
      1370       1380       1390       1400       1410       1420       1430       1440
KSFICPKLHM GFKSSLRSQL SKYTAKIVNI VLCAIQNELE LHKENLNLRE IDHTKSLTDK GFFANTDKKL ESLVTSIDDD
      1450       1460       1470       1480       1490       1500       1510       1520
ILASPLLTCI YDMLLSSENA HQRSISLSSR KPKSATDSVD VQSILPNRQD KKSFHKYLAT PCTHHSVNGG NHIKENAKLQ
      1530       1540       1550       1560       1570       1580       1590       1600
VLERIGETLH EMLSKLLGTH LHSQLSCSQQ SREMTNKNQK MAAALQSNIQ LISKAILDYI LAKLCGVDMD TSFASCGLKA
      1610       1620       1630       1640       1650       1660       1670       1680
ISESLDIDNP SFASIIEKMA KSTKIISSIV SRRVQEDNKE ETKSKAKPVA PVSSKTPSTK EMHPNKLKAV ASDILNMVFA
      1690       1700       1710       1720       1730       1740       1750       1760
KLEGFANGHL EILGAINDGN KKSNKIGWEY ESTNISRDTH EASFLSALYM HAKKVSSAIL KVIQTELNVT SSDLKTSVEN
      1770       1780       1790       1800       1810       1820       1830       1840
PPPETQILKY VVKLILDAVS SDMFNEMESE GGGIETYRYR PTYGSLPGGA ESDSFLEDDA YTAKKIIDER SPQREEVKTR
      1850       1860       1870       1880       1890       1900       1910       1920
SLKQWALEKT LNKIEVKLKE PHISPIAPII RNILNEIFQS TLINQLNVLS LSHSNFNGMP HNVDEPTPQT SVQFMDKMMD
      1930       1940       1950       1960       1970       1980       1990       2000
PLLSEADITI VTDNIVRTVF HKLYSAAMTE RNVRENRYKT ITFSANVSSH EHTYKGKSSV TALDENPCTF QSRFSVADKE
      2010       2020       2030       2040       2050       2060       2070       2080
TKVNLAEDIV QAILTNLETF ATSKVKSLFY SQVNFTVPVA LPIQQDHSTL SKALSAKDSY SDEQFSCCSV DHTKSGKTNL
      2090       2100       2110       2120       2130       2140       2150       2160
CQLSLSKLNT YALQVARRNL QGIKQELDKE RENPFLTHDI GISESIASQI VNALLDIISR KGKCDKNSSD KEIDLDQQKG
      2170       2180       2190       2200       2210       2220       2230       2240
VIEKLLNETK YRKVLQLQIQ DTIEGILCDI YEKTLFQNNL SFATPTLKCS IADKHSEENS EMFMEGANKI IPKLSVPKSD
      2250       2260       2270       2280       2290       2300       2310       2320
VILISNDIVN IVLHNLSSAA TLVINAKNPT SARLPLTFCD TFPKIDCQQP LKGSKTERKT ERFSYSRNQK SAYADDNQIT
      2330       2340       2350       2360       2370       2380       2390       2400
```

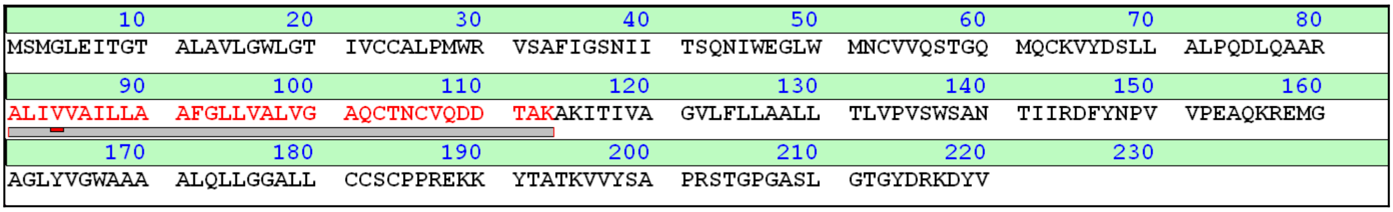
Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2211	1	933.6966	-60.77	3	56.3	14.8	0	896-919	K.NSMPHTLDPMCDIAEDMVHAILEK.L	Carbamidomethyl: 11; Oxidation: 3, 10

Detailed Protein Report

Protein 1011: 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	

Detailed Protein Report

Protein 1012: MOSC domain-containing protein 1, mitochondrial precursor [Homo sapiens]

Accession:	gi|224600454	**Score:**	14.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	37.5
Database Date:	2015-11-30	**pI:**	10.0
		Sequence Coverage [%]:	2.7
		No. of unique Peptides:	1

Quantitation

mdown:qdown **Median:** 0.65 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MGAAGSSALA	RFVLLAQSRP	GWLGVAALGL	TAVALGAVAW	RRAWPTRRRR	LLQQVGTVAQ	LWIYPVKSCK	GVPVSEAECT
90	100	110	120	130	140	150	160
AMGLRSGNLR	DRFWLVINQE	GNMVTARQEP	RLVLISLTCD	GDTLTLSAAY	TKDLLLPIKT	PTTNAVHKCR	VHGLEIEGRD
170	180	190	200	210	220	230	240
CGEATAQWIT	SFLKSQPYRL	VHFEPHMRPR	RPHQIADLFR	PKDQIAYSDT	SPFLILSEAS	LADLNSRLEK	KVKATNFRPN
250	260	270	280	290	300	310	320
IVISGCDVYA	EDSWDELLIG	DVELKRVMAC	SRCILTTVDP	DTGVMSRKEP	LETLKSYRQC	DPSERKLYGK	SPLFGQYFVL
330	340						
ENPGTIKVGD	PVYLLGQ						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
48	1	505.2491	-51.14	2	29.8	14.8	0	151-159	R.VHGLEIEGR.D		mdown:qdown 0.65

Detailed Protein Report

Protein 1013: inhibitor of growth protein 3 isoform 3 [Homo sapiens]

Accession:	gi|38201659	**Score:**	14.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	11.3
Database Date:	2015-11-30	**pI:**	4.3
Modification(s):	Oxidation	**Sequence Coverage [%]:**	16.3
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MLYLEDYLEM IEQLPMDLRD RFTEMREMDL QVQNAMDQLE QRVSEFFMNA KKNKPEWREE QMASIKKDYY KALEDADEKV
        90        100
QLANQIYDLQ HF
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
541	1	945.4099	-74.72	2	35.4	14.8	2	53-67	K.NKPEWREEQMASIKK.D	Oxidation: 10

Detailed Protein Report

Protein 1014: transcription factor ETV7 isoform 8 [Homo sapiens]

Accession:	gi|333470747	**Score:**	14.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	22.2
Database Date:	2015-11-30	**pI:**	9.6
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	9.5
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MDTRRGHLLQ PPDPGLTSNF GHLDDPGLAR WTPGKEESLN LCHCAELGCR TQGVCSFPAM PQAPIDGRIA DCRLLWDYVY
        90        100        110        120        130        140        150        160
QLLLDTRYEP YIKWEDKDAK IFRVVDPNGL ARLWGNHKNR VNMTYEKMSR ALRHYYKLNI IKKEPGQKLL FRFLKTPGKM
       170        180        190        200
VQDKHSHLEP LESQEQDRIE FKDKRPEISP
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
930	1	974.4715	15.67	2	40.4	14.7	0	51-68	R.TQGVCSFPAMPQAPIDGR.I	Carbamidomethyl: 5; Oxidation: 10

Detailed Protein Report

Protein 1015: DEP domain-containing protein 1B isoform 2 [Homo sapiens]

Accession:	gi|223633997	**Score:**	14.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	54.7
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
MEHRIVGPGP	YRATRLWNET	VELFRAKMPL	RKHRCRFKSY	EHCFTAAEAV	DWLHELLRCS	QNFGPEVTRK	QTVQLLKKFL
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
KNHVIEDIKG	KWGEEDFEDN	RHLYRFPPSS	PLKPYPKKPP	NQKDVIKFPE	WNDLPPGTSQ	ENIPVRPVVM	NSEMWYKRHS
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
IAIGEVPACR	LVHRRQLTEA	NVEEIWKSMT	LSYLQKILGL	DSLEEVLDVK	LVNSKFIIHN	VYSVSKQGVV	ILDDKSKELP
250	**260**	**270**	**280**	**290**	**300**	**310**	**320**
HWVLSAMKCL	ANWPNCSDLK	QPMYLGFEKD	VFKTIADYYG	HLKEPLLTFH	LFDAFVSVLG	LLQKEKVAVE	AFQICCLLLP
330	**340**	**350**	**360**	**370**	**380**	**390**	**400**
PENRRKLQLL	MRMMARICLN	KEMPPLCDGF	GTRTLMVQTF	SRCILCSKDE	VDLDELLAAR	LVTFLMDNYQ	EILKVPLALQ
410	**420**	**430**	**440**	**450**	**460**	**470**	
TSIEERVAHL	RRVQFQKSYP	EVYQERFPTP	ESAALLFPEK	PKPKPQLLMW	ALKKPFQPFQ	RTRSFRM	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2797	2	626.8488	34.86	2	63.4	14.7	0	159-170	R.HSIAIGEVPACR.L	

Detailed Protein Report

Protein 1016: secretogranin-3 isoform 2 [Homo sapiens]

Accession:	gi|259089433	**Score:**	14.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	26.9
Database Date:	2015-11-30	**pI:**	4.8
		Sequence Coverage [%]:	8.1
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MAAIQDGLAK GENDETVSNT LTLTNGLERR TKTYSEDNFE ELQYFPNFYA LLKSIDSEKE AKEKETLITI MKTLIDFVKM
        90        100        110        120        130        140        150        160
MVKYGTISPE EGVSYLENLD EMIALQTKNK LEKNATDNIS KLFPAPSEKS HEETDSTKEE AAKMEKEYGS LKDSTKDDNS
       170        180        190        200        210        220        230        240
NPGGKTDEPK GKTEAYLEAI RKNIEWLKKH DKKGNKEDYD LSKMRDFINK QADAYVEKGI LDKEEAEAIK RIYSSL
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1548	1	671.4028	135.82	3	48.0	14.7	2	147-165	K.EYGSLKDSTKDDNSNPGGK.T	

Detailed Protein Report

Protein 1017: 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

mdown:qdown	**Median:**	3.18	**CV:**	0.00 %	**No. of Peptides:**	1

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							

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	mdown:qdown 3.18

Protein 1018: 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 1019: 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

Quantitation

Wdown:Qdown **Median:** 0.88 **CV:** 0.00 % **No. of 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	Ratios
1386	1	896.6123	140.58	2	47.1	14.7	1	67-81	R.FLNGQVVFEAWGRLR.L		Wdown:Qdown 0.88

Detailed Protein Report

Protein 1020: 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 1021: 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

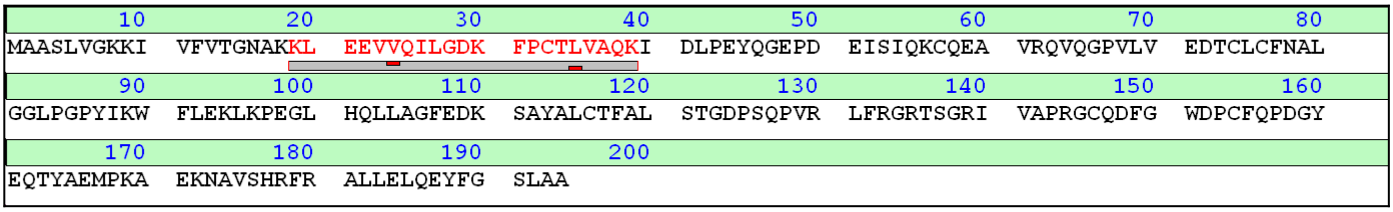
10	20	30	40	50	60	70	80
MWHFAVSVFL	VELYGNSLLL	TAVYGLVVAG	SVLVLGAIIG	DWVDKNARLK	VAQTSLVVQN	VSVILCGIIL	MMVFLHKHEL
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
LTMYHGWVLT	SCYILIITIA	NIANLASTAT	AITIQRDWIV	VVAGEDRSKL	ANMNATIRRI	DQLTNILAPM	AVGQIMTFGS
170	**180**	**190**	**200**	**210**	**220**	**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 1022: inosine triphosphate pyrophosphatase isoform a [Homo sapiens]

Accession:	gi|15626999	**Score:**	14.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	21.4
Database Date:	2015-11-30	**pI:**	5.4
		Sequence Coverage [%]:	10.8
		No. of unique Peptides:	1



10	20	30	40	50	60	70	80
MAASLVGKKI	VFVTGNAKKL	EEVVQILGDK	FPCTLVAQKI	DLPEYQGEPD	EISIQKCQEA	VRQVQGPVLV	EDTCLCFNAL
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
GGLPGPYIKW	FLEKLKPEGL	HQLLAGFEDK	SAYALCTFAL	STGDPSQPVR	LFRGRTSGRI	VAPRGCQDFG	WDPCFQPDGY
170	**180**	**190**	**200**				
EQTYAEMPKA	EKNAVSHRFR	ALLELQEYFG	SLAA				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1227	1	786.7216	-67.73	3	43.9	14.6	2	19-39	K.KLEEVVQILGDKFPCTLVAQK.I	

Detailed Protein Report

Protein 1023: **PREDICTED: conserved oligomeric Golgi complex subunit 3 isoform X9 [Homo sapiens]**

Accession:	gi|578825042	**Score:**	14.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	79.6
Database Date:	2015-11-30	**pI:**	6.0
		Sequence Coverage [%]:	2.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MRDYLSGFQE	QCDAILNDVN	SALQHLESLQ	KQYLFVSNKT	GTLHEACEQL	LKEQSELVDL	AENIQQKLSY	FNELETINTK
90	100	110	120	130	140	150	160
LNSPTLSVNS	DGFIPMLAKL	DDCITYISSH	PNFKDYPIYL	LKFKQCLSKA	LHLMKTYTVN	TLQTLTSQLL	KRDPSSVPNA
170	180	190	200	210	220	230	240
DNAFTLFYVK	FRAAAPKVRT	LIEQIELRSE	KIPEYQQLLN	DIHQCYLDQR	ELLLGPSIAC	TVAELTSQNN	RDHCALVRSG
250	260	270	280	290	300	310	320
CAFMVHVCQD	EHQLYNEFFT	KPTSKLDELL	EKLCVSLYDV	FRPLIIHVIH	LETLSELCGI	LKNEVLEDHV	QNNAEQLGAF
330	340	350	360	370	380	390	400
AAGVKQMLED	VQERLVYRTH	IYIQTDITGY	KPAPGDLAYP	DKLVMMEQIA	QSLKDEQKKV	PSEASFSDVH	LEEGESNSLT
410	420	430	440	450	460	470	480
KSGSTESLNP	RPQTTISPAD	LHGMWYPTVR	RTLVCLSKLY	RCIDRAVFQG	LSQEALSACI	QSLLGASESI	SKNKTQIDGQ
490	500	510	520	530	540	550	560
LFLIKHLLIL	REQIAPFHTE	FTIKEISLDL	KKTRDAAFKI	LNPMTVPRFF	RLNSNNALIE	FLLEGTPEIR	EHYLDSKKDV
570	580	590	600	610	620	630	640
DRHLKSACEQ	FIQQQTKLFV	EQLEEFMTKV	SALKTMASQG	GPKYTLSQQP	WAQPAKVNDL	AATAYKTIKT	KLPVTLRSMS
650	660	670	680	690	700		
LYLSNKDTEF	ILFKPVRNNI	QQVFQKFHAL	LKEEFSPEDI	QIIACPSMEQ	LSLLLLVSK		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1254	1	990.6132	53.89	2	44.3	14.6	1	136-152	K.TYTVNTLQTLTSQLLKR.D	

Detailed Protein Report

Protein 1024: fatty acid synthase [Homo sapiens]

Accession:	gi|41872631	**Score:**	14.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	273.3
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
MEEVVIAGMS	GKLPESENLQ	EFWDNLIGGV	DMVTDDDRRW	KAGLYGLPRR	SGKLKDLSRF	DASFFGVHPK	QAHTMDPQLR
90	100	110	120	130	140	150	160
LLLEVTYEAI	VDGGINPDSL	RGTHTGVWVG	VSGSETSEAL	SRDPETLVGY	SMVGCQRAMM	ANRLSFFFDF	RGPSIALDTA
170	180	190	200	210	220	230	240
CSSSLMALQN	AYQAIHSGQC	PAAIVGGINV	LLKPNTSVQF	LRLGMLSPEG	TCKAFDTAGN	GYCRSEGVVA	VLLTKKSLAR
250	260	270	280	290	300	310	320
RVYATILNAG	TNTDGFKEQG	VTFPSGDIQE	QLIRSLYQSA	GVAPESFEYI	EAHGTGTKVG	DPQELNGITR	ALCATRQEPL
330	340	350	360	370	380	390	400
LIGSTKSNMG	HPEPASGLAA	LAKVLLSLEH	GLWAPNLHFH	SPNPEIPALL	DGRLQVVDQP	LPVRGGNVGI	NSFGFGGSNV
410	420	430	440	450	460	470	480
HIILRPNTQP	PPAPAPHATL	PRLLRASGRT	PEAVQKLLEQ	GLRHSQDLAF	LSMLNDIAAV	PATAMPFRGY	AVLGGERGGP
490	500	510	520	530	540	550	560
EVQQVPAGER	PLWFICSGMG	TQWRGMGLSL	MRLDRFRDSI	LRSDEAVKPF	GLKVSQLLLS	TDESTFDDIV	HSFVSLTAIQ
570	580	590	600	610	620	630	640
IGLIDLLSCM	GLRPDGIVGH	SLGEVACGYA	DGCLSQEEAV	LAAYWRGQCI	KEAHLPPGAM	AAVGLSWEEC	KQRCPPGVVP
650	660	670	680	690	700	710	720
ACHNSKDTVT	ISGPQAPVFE	FVEQLRKEGV	FAKEVRTGGM	AFHSYFMEAI	APPLLQELKK	VIREPKPRSA	RWLSTSIPEA
730	740	750	760	770	780	790	800
QWHSSLARTS	SAEYNVNNLV	SPVLFQEALW	HVPEHAVVLE	IAPHALLQAV	LKRGLKPSCT	IIPLMKKDHR	DNLEFFLAGI
810	820	830	840	850	860	870	880
GRLHLSGIDA	NPNALFPPVE	FPAPRGTPLI	SPLIKWDHSL	AWDVPAAEDF	PNGSGSPSAA	IYNIDTSSES	PDHYLVDHTL
890	900	910	920	930	940	950	960
DGRVLFPATG	YLSIVWKTLA	RALGLGVEQL	PVVFEDVVLH	QATILPKTGT	VSLEVRLLEA	SRAFEVSENG	NLVVSGKVYQ
970	980	990	1000	1010	1020	1030	1040
WDDPDPRLFD	HPESPTPNPT	EPLFLAQAEV	YKELRLRGYD	YGPHFQGILE	ASLEGDSGRL	LWKDNWVSFM	DTMLQMSILG
1050	1060	1070	1080	1090	1100	1110	1120
SAKHGLYLPT	RVTAIHIDPA	THRQKLYTLQ	DKAQVADVVV	SRWLRVTVAG	GVHISGLHTE	SAPRRQQEQQ	VPILEKFCFT
1130	1140	1150	1160	1170	1180	1190	1200
PHTEEGCLSE	RAALQEELQL	CKGLVQALQT	KVTQQGLKMV	VPGLDGAQIP	RDPSQQELPR	LLSAACRLQL	NGNLQLELAQ
1210	1220	1230	1240	1250	1260	1270	1280
VLAQERPKLP	EDPLLSGLLD	SPALKACLDT	AVENMPSLKM	KVVEVLAGHG	HLYSRIPGLL	SPHPLLQLSY	TATDRHPQAL
1290	1300	1310	1320	1330	1340	1350	1360
EAAQAELQQH	DVAQGQWDPA	DPAPSALGSA	DLLVCNCAVA	ALGDPASALS	NMVAALREGG	FLLLHTLLRG	HPLGDIVAFL
1370	1380	1390	1400	1410	1420	1430	1440
TSTEPQYGQG	ILSQDAWESL	FSRVSLRLVG	LKKSFYGSTL	FLCRRPTPQD	SPIFLPVDDT	SFRWVESLKG	ILADEDSSRP
1450	1460	1470	1480	1490	1500	1510	1520
VWLKAINCAT	SGVVGLVNCL	RREPGGNRLR	CVLLSNLSST	SHVPEVDPGS	AELQKVLQGD	LVMNVYRDGA	WGAFRHFLLE
1530	1540	1550	1560	1570	1580	1590	1600
EDKPEEPTAH	AFVSTLTRGD	LSSIRWVCSS	LRHAQPTCPG	AQLCTVYYAS	LNFRDIMLAT	GKLSPDAIPG	KWTSQDSLLG
1610	1620	1630	1640	1650	1660	1670	1680
MEFSGRDASG	KRVMGLVPAK	GLATSVLLSP	DFLWDVPSNW	TLEEAASVPV	VYSTAYYALV	VRGRVRPGET	LLIHSGSGGV
1690	1700	1710	1720	1730	1740	1750	1760
GQAAIAIALS	LGCRVFTTVG	SAEKRAYLQA	RFPQLDSTSF	ANSRDTSFEQ	HVLWHTGGKG	VDLVLNSLAE	EKLQASVRCL
1770	1780	1790	1800	1810	1820	1830	1840
ATHGRFLEIG	KFDLSQNHPL	GMAIFLKNVT	FHGVLLDAFF	NESSADWREV	WALVQAGIRD	GVVRPLKCTV	FHGAQVEDAF
1850	1860	1870	1880	1890	1900	1910	1920
RYMAQGKHIG	KVVVQVLAEE	PEAVLKGAKP	KLMSAISKTF	CPAHKSYIIA	GGLGGFGLEL	AQWLIQRGVQ	KLVLTSRSGI
1930	1940	1950	1960	1970	1980	1990	2000
RTGYQAKQVR	RWRRQGVQVQ	VSTSNISSLE	GARGLIAEAA	QLGPVGGVFN	LAVVLRDGLL	ENQTPEFFQD	VCKPKYSGTL
2010	2020	2030	2040	2050	2060	2070	2080
NLDRVTREAC	PELDYFVVFS	SVSCGRGNAG	QSNYGFANSA	MERICEKRRH	EGLPGLAVQW	GAIGDVGILV	ETMSTNDTIV
2090	2100	2110	2120	2130	2140	2150	2160
SGTLPQRMAS	CLEVLDLFLN	QPHMVLSSFV	LAEKAAAYRD	RDSQRDLVEA	VAHILGIRDL	AAVNLDSSLA	DLGLDSLMSV
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
431	1	699.2762	-85.70	3	34.4	14.6	0	612-631	K.EAHLPPGAMAAVGLSWEECK.Q	

Detailed Protein Report

Protein 1025: **PREDICTED: signal-induced proliferation-associated 1-like protein 3 isoform X3 [Homo sapiens]**

Accession:	gi|578834186	**Score:**	14.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	120.1
Database Date:	2015-11-30	**pI:**	9.7
		Sequence Coverage [%]:	1.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MYQDYEIMFH	VSTLLPYTPN	NRQQLLRKRH	IGNDIVTIIF	QEPGALPFTP	KNIRSHFQHV	FIIVRVHNPC	TDNVCYSMAV
90	100	110	120	130	140	150	160
TRSKDAPPFG	PPIPSGTTFR	KSDVFRDFLL	AKVINAENAA	HKSDKFHTMA	TRTRQEYLKD	LAENCVSNTP	IDSTGKFNLI
170	180	190	200	210	220	230	240
SLTSKKKEKT	KARAGAEQHS	AGAIAWRVVA	QDYAQGVEID	CILGISNEFV	VLLDLRTKEV	VFNCYCGDVI	GWTPDSSTLK
250	260	270	280	290	300	310	320
IFYGRGDHIF	LQATEGSVED	IREIVQRLKV	MTSGWETVDM	TLRRNGLGQL	GFHVKYDGTV	AEVEDYGFAW	QAGLRQGSRL
330	340	350	360	370	380	390	400
VEICKVAVVT	LTHDQMIDLL	RTSVTVKVVI	IPPFEDGTPR	RGWPETYDMN	TSEPKTEQES	ITPGGRPPYR	SNAPWQWSGP
410	420	430	440	450	460	470	480
ASHNSLPASK	WATPTTPGHA	QSLSRPLKQT	PIVPFRESQP	LHSKRPVSFP	ETPYTVSPAG	ADRVPPYRQP	SGSFSTPGSA
490	500	510	520	530	540	550	560
TYVRYKPSPE	RYTAAPHPLL	SLDPHFSHDG	TSSGDSSSGG	LTSQESTMER	QKPEPLWHVP	AQARLSAIAG	SSGNKHPSRQ
570	580	590	600	610	620	630	640
DAAGKDSPNR	HSKGEPQYSS	HSSSNTLSSN	ASSSHSDDRW	FDPLDPLEPE	QDPLSKGGSS	DSGIDTTLYT	SSPSCMSLAK
650	660	670	680	690	700	710	720
APRPAKPHKP	PGSMGLCGGG	REAAGRSHHA	DRRREVSPAP	AVAGQSKGYR	PKLYSSGSST	PTGLAGGSRD	PPRQPSDMGS
730	740	750	760	770	780	790	800
RVGYPAQVYK	TASAETPRPS	QLAQPSPFQL	SASVPKSFFS	KQPVRNKHPT	GWKRTEEPPP	RPLPFSDPKK	QVDTNTKNVF
810	820	830	840	850	860	870	880
GQPRLRASLR	DLRSPRKNYK	STIEDDLKKL	IIMDNLGPEQ	ERDTGQSPQK	GLQRTLSDES	LCSGRREPSF	ASPAGLEPGL
890	900	910	920	930	940	950	960
PSDVLFTSTC	AFPSSTLPAR	RQHQHPHPPV	GPGATPAAGS	GFPEKKSTIS	ASELSLADGR	DRPLRRLDPG	LMPLPDTAAG
970	980	990	1000	1010	1020	1030	1040
LEWSSLVNAA	KAYEVQRAVS	LFSLNDPALS	PDIPPAHSPV	HSHLSLERGP	PTPRTTPTMS	EEPPLDLTGK	VYQLEVMLKQ
1050	1060	1070	1080	1090	1100		
LHTDLQKEKQ	DKVVLQSEVA	SLRQNNQRLQ	EESQAASEQL	RKFAEIFCRE	KKEL		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2765	1	671.8356	35.13	2	63.6	14.6	1	710-721	R.DPPRQPSDMGSR.V	

Detailed Protein Report

Protein 1026: kelch-like protein 23 [Homo sapiens]

Accession:	gi|40255071	**Score:**	14.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	63.9
Database Date:	2015-11-30	**pI:**	5.3
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	4.1
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|313151204	refseq_human (refseq_human_20140103.fasta)	kelch-like protein 23 [Homo sapiens]

10	20	30	40	50	60	70	80
MALKGQEDYI	YLFKDSTHPV	DFLDAFRTFY	LDGLFTDITL	QCPSGIIFHC	HRAVLAACSN	YFKAMFTADM	KEKFKNKIKL
90	100	110	120	130	140	150	160
SGIHHDILEG	LVNYAYTSQI	EITKRNVQSL	LEAADLLQFL	SVKKACERFL	VRHLDIDNCI	GMHSFAEFHV	CPELEKESRR
170	180	190	200	210	220	230	240
ILCSKFKEVW	QQEEFLEISL	EKFLFILSRK	NLSVWKEEAI	IEPVIKWTAH	DVENRIECLY	NLLSYINIDI	DPVYLKTALG
250	260	270	280	290	300	310	320
LQRSCLLTEN	KIRSLIYNAL	NPMHKEISQR	STATMYIIGG	YYWHPLSEVH	IWDPLTNVWI	QGAEIPDYTR	ESYGVTCLGP
330	340	350	360	370	380	390	400
NIYVTGGYRT	DNIEALDTVW	IYNSESDEWT	EGLPMLNARY	YHCAVTLGGC	VYALGGYRKG	APAEEAEFYD	PLKEKWIPIA
410	420	430	440	450	460	470	480
NMIKGVGNAT	ACVLHDVIYV	IGGHCGYRGS	CTYDKVQSYN	SDINEWSLIT	SSPHPEYGLC	SVPFENKLYL	VGGQTTITEC
490	500	510	520	530	540	550	560
YDPEQNEWRE	IAPMMERRME	CGAVIMNGCI	YVTGGYSYSK	GTYLQSIEKY	DPDLNKWEIV	GNLPSAMRSH	GCVCVYNV

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2946	1	859.1210	79.00	3	66.0	14.6	1	498-520	R.RMECGAVIMNGCIYVTGGYSYSK.G	Carbamidomethyl: 4; Oxidation: 2

Detailed Protein Report

Protein 1027: 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

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 1028: PREDICTED: transcription factor MafG isoform X1 [Homo sapiens]

Accession:	gi|578832019	**Score:**	14.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	21.2
Database Date:	2015-11-30	**pI:**	10.5
		Sequence Coverage [%]:	7.2
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MRGQGGQEAA QPSLGEAKGC LLSESACSLC PRVMTTPNKG NKALKVKREP GENGTSLTDE ELVTMSVREL NQHLRGLSKE
        90        100        110        120        130        140        150        160
EIVQLKQRRR TLKNRGYAAS CRVKRVTQKE ELEKQKAELQ QEVEKLASEN ASMKLELDAL RSKYEALQTF ARTVARSPVA
       170        180        190        200
PARGPLAAGL GPLVPGKVAA TSVITIVKSK TDARS
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2135	1	719.8043	-32.98	2	55.3	14.5	0	19-32	K.GCLLSESACSLCPR.V	

Detailed Protein Report

Protein 1029: acetyl-CoA acetyltransferase, cytosolic [Homo sapiens]

Accession:	gi|148539872	**Score:**	14.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	41.3
Database Date:	2015-11-30	**pI:**	6.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MNAGSDPVVI	VSAARTIIGS	FNGALAAVPV	QDLGSTVIKE	VLKRATVAPE	DVSEVIFGHV	LAAGCGQNPV	RQASVGAGIP
90	100	110	120	130	140	150	160
YSVPAWSCQM	ICGSGLKAVC	LAVQSIGIGD	SSIVVAGGME	NMSKAPHLAY	LRTGVKIGEM	PLTDSILCDG	LTDAFHNCHM
170	180	190	200	210	220	230	240
GITAENVAKK	WQVSREDQDK	VAVLSQNRTE	NAQKAGHFDK	EIVPVLVSTR	KGLIEVKTDE	FPRHGSNIEA	MSKLKPYFLT
250	260	270	280	290	300	310	320
DGTGTVTPAN	ASGINDGAAA	VVLMKKSEAD	KRGLTPLARI	VSWSQVGVEP	SIMGIGPIPA	IKQAVTKAGW	SLEDVDIFEI
330	340	350	360	370	380	390	400
NEAFAAVSAA	IVKELGLNPE	KVNIEGGAIA	LGHPLGASGC	RILVTLLHTL	ERMGRSRGVA	ALCIGGGMGI	AMCVQRE

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1725	1	932.4706	14.92	2	50.1	14.5	0	378-396	R.GVAALCIGGGMGIAMCVQR.E	Carbamidomethyl: 16

Detailed Protein Report

Protein 1030: 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 1031: neurogenic locus notch homolog protein 4 preproprotein [Homo sapiens]

Accession:	gi|55770876	**Score:**	14.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	209.5
Database Date:	2015-11-30	**pI:**	5.4
		Sequence Coverage [%]:	1.4
		No. of unique Peptides:	1

Detailed Protein Report

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        10         20         30         40         50         60         70         80
MQPPSLLLLL LLLLLLCVSV VRPRGLLCGS FPEPCANGGT CLSLSLGQGT CQCAPGFLGE TCQFPDPCQN AQLCQNGGSC
        90        100        110        120        130        140        150        160
QALLPAPLGL PSSPSPLTPS FLCTCLPGFT GERCQAKLED PCPPSFCSKR GRCHIQASGR PQCSCMPGWT GEQCQLRDFC
       170        180        190        200        210        220        230        240
SANPCVNGGV CLATYPQIQC HCPPGFEGHA CERDVNECFQ DPGPCPKGTS CHNTLGSFQC LCPVGQEGPR CELRAGPCPP
       250        260        270        280        290        300        310        320
RGCSNGGTCQ LMPEKDSTFH LCLCPPGFIG PDCEVNPDNC VSHQCQNGGT CQDGLDTYTC LCPETWTGWD CSEDVDECET
       330        340        350        360        370        380        390        400
QGPPHCRNGG TCQNSAGSFH CVCVSGWGGT SCEENLDDCI AATCAPGSTC IDRVGSFSCL CPPGRTGLLC HLEDMCLSQP
       410        420        430        440        450        460        470        480
CHGDAQCSTN PLTGSTLCLC QPGYSGPTCH QDLDECLMAQ QGPSPCEHGG SCLNTPGSFN CLCPPGYTGS RCEADHNECL
       490        500        510        520        530        540        550        560
SQPCHPGSTC LDLLATFHCL CPPGLEGQLC EVETNECASA PCLNHADCHD LLNGFQCICL PGFSGTRCEE DIDECRSSPC
       570        580        590        600        610        620        630        640
ANGGQCQDQP GAFHCKCLPG FEGPRCQTEV DECLSDPCPV GASCLDLPGA FFCLCPSGFT GQLCEVPLCA PNLCQPKQIC
       650        660        670        680        690        700        710        720
KDQKDKANCL CPDGSPGCAP PEDNCTCHHG HCQRSSCVCD VGWTGPECEA ELGGCISAPC AHGGTCYPQP SGYNCTCPTG
       730        740        750        760        770        780        790        800
YTGPTCSEEM TACHSGPCLN GGSCNPSPGG YYCTCPPSHT GPQCQTSTDY CVSAPCFNGG TCVNRPGTFS CLCAMGFQGP
       810        820        830        840        850        860        870        880
RCEGKLRPSC ADSPCRNRAT CQDSPQGPRC LCPTGYTGGS CQTLMDLCAQ KPCPRNSHCL QTGPSFHCLC LQGWTGPLCN
       890        900        910        920        930        940        950        960
LPLSSCQKAA LSQGIDVSSL CHNGGLCVDS GPSYFCHCPP GFQGSLCQDH VNPCESRPCQ NGATCMAQPS GYLCQCAPGY
       970        980        990       1000       1010       1020       1030       1040
DGQNCSKELD ACQSQPCHNH GTCTPKPGGF HCACPPGFVG LRCEGDVDEC LDQPCHPTGT AACHSLANAF YCQCLPGHTG
      1050       1060       1070       1080       1090       1100       1110       1120
QWCEVEIDPC HSQPCFHGGT CEATAGSPLG FICHCPKGFE GPTCSHRAPS CGFHHCHHGG LCLPSPKPGF PPRCACLSGY
      1130       1140       1150       1160       1170       1180       1190       1200
GGPDCLTPPA PKGCGPPSPC LYNGSCSETT GLGGPGFRCS CPHSSPGPRC QKPGAKGCEG RSGDGACDAG CSGPGGNWDG
      1210       1220       1230       1240       1250       1260       1270       1280
GDCSLGVPDP WKGCPSHSRC WLLFRDGQCH PQCDSEECLF DGYDCETPPA CTPAYDQYCH DHFHNGHCEK GCNTAECGWD
      1290       1300       1310       1320       1330       1340       1350       1360
GGDCRPEDGD PEWGPSLALL VVLSPPALDQ QLFALARVLS LTLRVGLWVR KDRDGRDMVY PYPGARAEEK LGGTRDPTYQ
      1370       1380       1390       1400       1410       1420       1430       1440
ERAAPQTQPL GKETDSLSAG FVVVMGVDLS RCGPDHPASR CPWDPGLLLR FLAAMAAVGA LEPLLPGPLL AVHPHAGTAP
      1450       1460       1470       1480       1490       1500       1510       1520
PANQLPWPVL CSPVAGVILL ALGALLVLQL IRRRRREHGA LWLPPGFTRR PRTQSAPHRR RPPLGEDSIG LKALKPKAEV
      1530       1540       1550       1560       1570       1580       1590       1600
DEDGVVMCSG PEEGEEVGQA EETGPPSTCQ LWSLSGGCGA LPQAAMLTPP QESEMEAPDL DTRGPDGVTP LMSAVCCGEV
      1610       1620       1630       1640       1650       1660       1670       1680
QSGTFQGAWL GCPEPWEPLL DGGACPQAHT VGTGETPLHL AARFSRPTAA RRLLEAGANP NQPDRAGRTP LHAAVAADAR
      1690       1700       1710       1720       1730       1740       1750       1760
EVCQLLLRSR QTAVDARTED GTTPLMLAAR LAVEDLVEEL IAAQADVGAR DKWGKTALHW AAAVNNARAA RSLLQAGADK
      1770       1780       1790       1800       1810       1820       1830       1840
DAQDNREQTP LFLAAREGAV EVAQLLLGLG AARELRDQAG LAPADVAHQR NHWDLLTLLE GAGPPEARHK ATPGREAGPF
      1850       1860       1870       1880       1890       1900       1910       1920
PRARTVSVSV PPHGGGALPR CRTLSAGAGP RGGGACLQAR TWSVDLAARG GGAYSHCRSL SGVGAGGGPT PRGRRFSAGM
      1930       1940       1950       1960       1970       1980       1990       2000
RGPRPNPAIM RGRYGVAAGR GGRVSTDDWP CDWVALGACG SASNIPIPPP CLTPSPERGS PQLDCGPPAL QEMPINQGGE
      2010
GKK
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1028	1	974.6819	-25.27	3	41.4	14.5	0	647-674	K.ANCLCPDGSPGCAPPEDNCTCHHGHCQR.S	

Detailed Protein Report

Protein 1032: PREDICTED: rab-3A-interacting protein isoform X3 [Homo sapiens]

Accession:	gi|578823282	**Score:**	14.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	42.2
Database Date:	2015-11-30	**pI:**	6.1
Modification(s):	Oxidation	**Sequence Coverage [%]:**	4.7
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MTFSNALAVA GMMGSGFYRI PPLPSPATHT HVVRCIWPRS LRLSYDEAFA MANDPLEGFH EVNLASPTSP DLLGVYESGT
        90        100        110        120        130        140        150        160
QEQTTSPSVI YRPHPSALSS VPIQANALDV SELPTQPVYS SPRRLNCAEI SSISFHVTDP APCSTSGVTA GLTKLTTRKD
       170        180        190        200        210        220        230        240
NYNAEREFLQ GATITEACDG SDDIFGLSTD SLSRLRSPSV LEVREKGYER LKEELAKAQR ELKLKDEECE RLSKVRDQLG
       250        260        270        280        290        300        310        320
QELEELTASL FEEAHKMVRE ANIKQATAEK QLKEAQGKID VLQAEVAALK TLVLSSSPTS PTQEPLPGGK TPFKKGHTRN
       330        340        350        360        370        380        390
KSTSSAMSGS HQDLSVIQPI VKDCKEKPSF TLLNSSPSLI LKKCVCLLNF CMEARSLLNG ITNVNLF
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1716	1	637.9569	-8.71	3	50.0	14.4	0	2-19	M.TFSNALAVAGMMGSGFYR.I	Oxidation: 11, 12

Detailed Protein Report

Protein 1033: F-box only protein 31 isoform 1 [Homo sapiens]

Accession:	gi|83035136	**Score:**	14.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	60.6
Database Date:	2015-11-30	**pI:**	6.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAVCARLCGV	GPSRGCRRRQ	QRRGPAETAA	ADSEPDTDPE	EERIEASAGV	GGGLCAGPSP	PPPRCSLLEL	PPELLVEIFA
90	100	110	120	130	140	150	160
SLPGTDLPSL	AQVCTKFRRI	LHTDTIWRRR	CREEYGVCEN	LRKLEITGVS	CRDVYAKLLH	RYRHILGLWQ	PDIGPYGGLL
170	180	190	200	210	220	230	240
NVVVDGLFII	GWMYLPPHDP	HVDDPMRFKP	LFRIHLMERK	AATVECMYGH	KGPHHGHIQI	VKKDEFSTKC	NQTDHHRMSG
250	260	270	280	290	300	310	320
GRQEEFRTWL	REEWGRTLED	IFHEHMQELI	LMKFIYTSQY	DNCLTYRRIY	LPPSRPDDLI	KPGLFKGTYG	SHGLEIVMLS
330	340	350	360	370	380	390	400
FHGRRARGTK	ITGDPNIPAG	QQTVEIDLRH	RIQLPDLENQ	RNFNELSRIV	LEVRERVRQE	QQEGGHEAGE	GRGRQGPRES
410	420	430	440	450	460	470	480
QPSPAQPRAE	APSKGPDGTP	GEDGGEPGDA	VAAAEQPAQC	GQGQPFVLPV	GVSSRNEDYP	RTCRMCFYGT	GLIAGHGFTS
490	500	510	520	530	540		
PERTPGVFIL	FDEDRFGFVW	LELKSFSLYS	RVQATFRNAD	APSPQAFDEM	LKNIQSLTS		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2660	1	974.0954	106.87	2	62.0	14.4	0	44-64	R.IEASAGVGGGLCAGPSPPPPR.C	Carbamidomethyl: 12

Detailed Protein Report

Protein 1034: spliceosome RNA helicase DDX39B [Homo sapiens]

Accession:	gi|4758112	**Score:**	14.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	49.0
Database Date:	2015-11-30	**pI:**	5.3
		Sequence Coverage [%]:	2.8
		No. of unique Peptides:	1

Quantitation

Wdown:Qdown	**Median:**	0.33	**CV:**	0.00 %	**No. of Peptides:**	1

Alias proteins:

Accession	Name	Description
gi|18375623	refseq_human (refseq_human_20140103.fasta)	spliceosome RNA helicase DDX39B [Homo sapiens]

10	20	30	40	50	60	70	80
MAENDVDNEL	LDYEDDEVET	AAGGDGAEAP	AKKDVKGSYV	SIHSSGFRDF	LLKPELLRAI	VDCGFEHPSE	VQHECIPQAI
90	100	110	120	130	140	150	160
LGMDVLCQAK	SGMGKTAVFV	LATLQQLEPV	TGQVSVLVMC	HTRELAFQIS	KEYERFSKYM	PNVKVAVFFG	GLSIKKDEEV
170	180	190	200	210	220	230	240
LKKNCPHIVV	GTPGRILALA	RNKSLNLKHI	KHFILDECDK	MLEQLDMRRD	VQEIFRMTPH	EKQVMMFSAT	LSKEIRPVCR
250	260	270	280	290	300	310	320
KFMQDPMEIF	VDDETKLTLH	GLQQYYVKLK	DNEKNRKLFD	LLDVLEFNQV	VIFVKSVQRC	IALAQLLVEQ	NFPAIAIHRG
330	340	350	360	370	380	390	400
MPQEERLSRY	QQFKDFQRRI	LVATNLFGRG	MDIERVNIAF	NYDMPEDSDT	YLHRVARAGR	FGTKGLAITF	VSDENDAKIL
410	420	430					
NDVQDRFEVN	ISELPDEIDI	SSYIEQTR					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
39	1	625.3631	57.54	2	29.2	14.4	0	164-175	K.NCPHIVVGTPGR.I		Wdown:Qdown 0.33

Detailed Protein Report

Protein 1035: PREDICTED: target of Nesh-SH3 isoform X33 [Homo sapiens]

Accession: gi|530374326
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 14.4
MW [kDa]: 148.7
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
955	1	955.6374	133.87	1	41.5	14.4	0	628-636	K.TTPSPEVPK.S	

Detailed Protein Report

Protein 1036: 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 1037: 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 1038: **PREDICTED: glyceraldehyde-3-phosphate dehydrogenase, testis-specific isoform X1 [Homo sapiens]**

Accession:	gi|530416161	**Score:**	14.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	44.4
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
MSKRDIVLTN	VTVVQLLRQP	CPVTRAPPPP	EPKAEVEPQP	QPEPTPVREE	IKPPPPPLPP	HPATPPPKMV	SVARELTVGI
90	100	110	120	130	140	150	160
NGFGRIGRLV	LRACMEKGVK	VVAVNDPFID	PEYMVYMFKY	DSTHGRYKGS	VEFRNGQLVV	DNHEISVYQC	KEPKQIPWRA
170	180	190	200	210	220	230	240
VGSPYVVEST	GVYLSIQAAS	DHISAGAQRV	VISAPSPDAP	MFVMGVNEND	YNPGSMNIVS	NASCTTNCLA	PLAKVIHERF
250	260	270	280	290	300	310	320
GIVEGLMTTV	HSYTATQKTV	DGPSRKAWRD	GRGAHQNIIP	ASTGAAKAVT	KVIPELKGKL	TGMAFRVPTP	DVSVVDLTCR
330	340	350	360	370	380	390	400
LAQPAPYSAI	KEAVKAAAKG	PMAGILAYTE	DEVGAEERRP	WEEPSGKGHD	FHLPGSCSQC	AKSETAGQEG	RSPCLRAFAL
410	420						
AVPLVWNASL	AR						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
588	1	581.7946	-33.98	2	35.9	14.3	0	75-85	R.ELTVGINGFGR.I	

Detailed Protein Report

Protein 1039: 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 1040: phosphatidylinositol 4-phosphate 5-kinase type-1 alpha isoform 4 [Homo sapiens]

Accession:	gi|208431776	**Score:**	14.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	56.0
Database Date:	2015-11-30	**pI:**	7.8
		Sequence Coverage [%]:	3.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MASASSGPSS	SVGFSSFDPA	VPSCTLSSAS	GIKRPMASEV	PYASGMPIKK	IGHRSVDSSG	ETTYKKTTSS	ALKGAIQLGI
90	100	110	120	130	140	150	160
THTVGSLSTK	PERDVLMQDF	YVVESIFFPS	EGSNLTPAHH	YNDFRFKTYA	PVAFRYFREL	FGIRPDDYLY	SLCSEPLIEL
170	180	190	200	210	220	230	240
CSSGASGSLF	YVSSDDEFII	KTVQHKEAEF	LQKLLPGYYM	NLNQNPRTLL	PKFYGLYCVQ	AGGKNIRIVV	MNNLLPRSVK
250	260	270	280	290	300	310	320
MHIKYDLKGS	TYKRRASQKE	REKPLPTFKD	LDFLQDIPDG	LFLDADMYNA	LCKTLQRDCL	VLQSFKIMDY	SLLMSIHNID
330	340	350	360	370	380	390	400
HAQREPLSSE	TQYSVDTRRP	APQKALYSTA	MESIQGEARR	GGTMETDDHM	GGIPARNSKG	ERLLLYIGII	DILQSYRFVK
410	420	430	440	450	460	470	480
KLEHSWKALV	HDGDTVSVHR	PGFYAERFQR	FMCNTVFKKI	PCVHLGRPDV	LPQTPPLEEI	SEGSPIPDPS	FSPLVGETLQ
490	500	510					
MLTTSTTLEK	LEVAESEFTH						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2199	1	933.6289	74.91	2	56.1	14.3	2	225-240	K.NIRIVVMNNLLPRSVK.M	

Detailed Protein Report

Protein 1041: long-chain-fatty-acid--CoA ligase 1 isoform d [Homo sapiens]

Accession:	gi|557878742	**Score:**	14.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	58.5
Database Date:	2015-11-30	**pI:**	8.6
		Sequence Coverage [%]:	2.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MVIVPLYDTL	GNEAITYIVN	KAELSLVFVD	KPEKAKLLLE	GVENKLIPGL	KIIVVMDAYG	SELVERGQRC	GVEVTSMKAM
90	100	110	120	130	140	150	160
EDLGRANRRK	PKPPAPEDLA	VICFTSGTTG	NPKGAMVTHR	NIVSDCSAFV	KATENTVNPC	PDDTLISFLP	LAHMFERVVE
170	180	190	200	210	220	230	240
CVMLCHGAKI	GFFQGDIRLL	MDDLKVLQPT	VFPVVPRLLN	RMFDRIFGQA	NTTLKRWLLD	FASKRKEAEL	RSGIIRNNSL
250	260	270	280	290	300	310	320
WDRLIFHKVQ	SSLGGRVRLM	VTGAAPVSAT	VLTFLRAALG	CQFYEGYGQT	ECTAGCCLTM	PGDWTAGHVG	APMPCNLIKL
330	340	350	360	370	380	390	400
VDVEEMNYMA	AEGEGEVCVK	GPNVFQGYLK	DPAKTAEALD	KDGWLHTGDI	GKWLPNGTLK	IIDRKKHIFK	LAQGEYIAPE
410	420	430	440	450	460	470	480
KIENIYMRSE	PVAQVFVHGE	SLQAFLIAIV	VPDVETLCSW	AQKRGFEGSF	EELCRNKDVK	KAILEDMVRL	GKDSGLKPFE
490	500	510	520	530			
QVKGITLHPE	LFSIDNGLLT	PTMKAKRPEL	RNYFRSQIDD	LYSTIKV			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
707	1	647.7728	-66.33	2	37.7	14.3	1	67-78	R.GQRCGVEVTSMK.A	

Protein 1042: PREDICTED: uncharacterized protein LOC646670 [Homo sapiens]

Accession: gi|578797043
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 14.3
MW [kDa]: 34.5
pI: 10.6
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 1043: PREDICTED: lisH domain and HEAT repeat-containing protein KIAA1468 isoform X4 [Homo sapiens]

Accession:	gi|530414274	**Score:**	14.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	110.2
Database Date:	2015-11-30	**pI:**	5.0
		Sequence Coverage [%]:	1.1
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MAAMAPGGSG SGGGVNPFLS DSDEDDDEVA ATEERRAVLR LGAGSGLDPG SAGSLSPQDP VALGSSARPG LPGEASAAAV
        90        100        110        120        130        140        150        160
ALGGTGETPA RLSIDAIAAQ LLRDQYLLTA LELHTELLES GRELPRLRDY FSNPGNFERQ SGTPPGMGAP GVPGAAGVGG
       170        180        190        200        210        220        230        240
AGGREPSTAS GGGQLNRAGS ISTLDSLDFA RYSDDGNRET DEKVAVLEFE LRKAKETIQA LRANLTKAAE HEVPLQERKN
       250        260        270        280        290        300        310        320
YKSSPEIQEP IKPLEKRALN FLVNEFLLKN NYKLTSITFS DENDDQDFEL WDDVGLNIPK PPDLLQLYRD FGNHQVTGKD
       330        340        350        360        370        380        390        400
LVDVASGVEE DELEALTPII SNLPPTLETP QPAENSMLVQ KLEDKISLLN SEKWSLMEQI RRLKSEMDFL KNEHFAIPAV
       410        420        430        440        450        460        470        480
CDSVQPPLDQ LPHKDSEDSG QHPDVNSSDK GKNTDIHLSI SDEADSTIPK ENSPNSFPRR EREGMPPSSL SSKKTVHFDK
       490        500        510        520        530        540        550        560
PNRKLSPAFH QALLSFCRMS ADSRLGYEVS RIADSEKSVM LMLGRCLPHI VPNVLLAKRE ELIPLILCTA CLHPEPKERD
       570        580        590        600        610        620        630        640
QLLHILFNLI KRPDDEQRQM ILTGCVAFAR HVGPTRVEAE LLPQCWEQIN HKYPERRLLV AESCGALAPY LPKEIRSSLV
       650        660        670        680        690        700        710        720
LSMLQQMLME DKADLVREAV IKSLGIIMGY IDDPDKYHQG FELLLSALGD PSERVVSATH QVFLPAYAAW TTELGNLQSH
       730        740        750        760        770        780        790        800
LILTLLNKIE KLLREGEHGL DEHKLHMYLS ALQSLIPSLF ALVLQNAPFS SKAKLHGEVP QIEVTRFPRP MSPLQDVSTI
       810        820        830        840        850        860        870        880
IGSREQLAVL LQLYDYQLEQ EGTTGWESLL WVVNQLLPQL IEIVGKINVT STACVHEFSR FFWRLCRTFG KIFTNTKVKP
       890        900        910        920        930        940        950        960
QFQEILRLSE ENIDSSAGNG VLTKATVPIY ATGVLTCYIQ EEDRKLLVGF LEDVMTLLSL SHAPLDSLKA SFVELGANPA
       970        980        990       1000
YHELLLTVLW YGVVHTSALV RCTAARMFEV RPERKENEK
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1816	1	673.2645	-43.90	2	52.7	14.3	0	129-139	R.DYFSNPGNFER.Q	

Detailed Protein Report

Protein 1044: putative RNA-binding protein 15B [Homo sapiens]

Accession:	gi|54607124	**Score:**	14.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	97.1
Database Date:	2015-11-30	**pI:**	10.3
		Sequence Coverage [%]:	1.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MKRQSERDSS	PSGRGSSSSA	KRPREREREA	EAGGRRAAHK	ASGGAKHPVP	ARARDKPRGS	GSGGGGHRDG	RGTGDANHRA
90	100	110	120	130	140	150	160
SSGRSSGSGA	GGGGRGGKAS	GDPGASGMSP	RASPLPPPPP	PPGAEPACPG	SSAAAPEYKT	LLISSLSPAL	PAEHLEDRLF
170	180	190	200	210	220	230	240
HQFKRFGEIS	LRLSHTPELG	RVAYVNFRHP	QDAREARQHA	LARQLLLYDR	PLKVEPVYLR	GGGGSSRRSS	SSSAAASTPP
250	260	270	280	290	300	310	320
PGPPAPADPL	GYLPLHGGYQ	YKQRSLSPVA	APPLREPRAR	HAAAAFALDA	AAAAAVGLSR	ERALDYYGLY	DDRGRPYGYP
330	340	350	360	370	380	390	400
AVCEEDLMPE	DDQRATRNLF	IGNLDHSVSE	VELRRAFEKY	GIIEEVVIKR	PARGQGGAYA	FLKFQNLDMA	HRAKVAMSGR
410	420	430	440	450	460	470	480
VIGRNPIKIG	YGKANPTTRL	WVGGLGPNTS	LAALAREFDR	FGSIRTIDHV	KGDSFAYIQY	ESLDAAQAAC	AKMRGFPLGG
490	500	510	520	530	540	550	560
PDRRLRVDFA	KAEETRYPQQ	YQPSPLPVHY	ELLTDGYTRH	RNLDADLVRD	RTPPHLLYSD	RDRTFLEGDW	TSPSKSSDRR
570	580	590	600	610	620	630	640
NSLEGYSRSV	RSRSGERWGA	DGDRGLPKPW	EERRKRRSLS	SDRGRTTHSP	YEERSRTKGS	GQQSERGSDR	TPERSRKENH
650	660	670	680	690	700	710	720
SSEGTKESSS	NSLSNSRHGA	EERGHHHHHH	EAADSSHGKK	ARDSERNHRT	TEAEPKPLEE	PKHETKKLKN	LSEYAQTLQL
730	740	750	760	770	780	790	800
GWNGLLVLKN	SCFPTSMHIL	EGDQGVISSL	LKDHTSGSKL	TQLKIAQRLR	LDQPKLDEVT	RRIKQGSPNG	YAVLLATQAT
810	820	830	840	850	860	870	880
PSGLGTEGMP	TVEPGLQRRL	LRNLVSYLKQ	KQAAGVISLP	VGGSKGRDGT	GMLYAFPPCD	FSQQYLQSAL	RTLGKLEEEH
890	900						
MVIVIVRDTA							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
609	1	666.9243	159.05	2	36.2	14.3	1	604-614	R.GRTTHSPYEER.S	

Detailed Protein Report

Protein 1045: 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 1046: PREDICTED: uncharacterized protein C12orf42 isoform X5 [Homo sapiens]

Accession:	gi|578823684	**Score:**	14.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	25.8
Database Date:	2015-11-30	**pI:**	11.7
		Sequence Coverage [%]:	6.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSTVICMKQR	EEEFLLTIRP	FANRMQKSPC	YIPIVSSATL	WDRSTPSAKH	IPCYERTSVP	CSRFINHMKN	FSESPKFRSL
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
HFLNFPGSAA	RPSTAIGLCR	RSQTPGALQS	TGPSNTELEP	EERMAVPAGA	QAHPDDIQSR	LLGASGNPVG	KGAVAMAPEM
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
LPKHPHTPRD	RRPQADTSLH	GNLAGAPLPL	LAGASTHFPS	KRLIKVCSSA	PPRPTRRFHT	VCSQALSRPV	VNAHLH

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2634	1	841.1201	156.92	2	61.2	14.2	2	202-216	K.RLIKVCSSAPPRPTR.R	

Detailed Protein Report

Protein 1047: heat shock 70 kDa protein 13 precursor [Homo sapiens]

Accession:	gi|48928056	**Score:**	14.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	51.9
Database Date:	2015-11-30	**pI:**	5.4
		Sequence Coverage [%]:	3.6
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MAREMTILGS AVLTLLLAGY LAQQYLPLPT PKVIGIDLGT TYCSVGVFFP GTGKVKVIPD ENGHISIPSM VSFTDNDVYV
        90        100        110        120        130        140        150        160
GYESVELADS NPQNTIYDAK RFIGKIFTAE ELEAEIGRYP FKVLNKNGMV EFSVTSNETI TVSPEYVGSR LLLKLKEMAE
       170        180        190        200        210        220        230        240
AYLGMPVANA VISVPAEFDL KQRNSTIEAA NLAGLKILRV INEPTAAAMA YGLHKADVFH VLVIDLGGGT LDVSLLNKQG
       250        260        270        280        290        300        310        320
GMFLTRAMSG NNKLGGQDFN QRLLQYLYKQ IYQTYGFVPS RKEEIHRLRQ AVEMVKLNLT LHQSAQLSVL LTVEEQDRKE
       330        340        350        360        370        380        390        400
PHSSDTELPK DKLSSADDHR VNSGFGRGLS DKKSGESQVL FETEISRKLF DTLNEDLFQK ILVPIQQVLK EGHLEKTEID
       410        420        430        440        450        460        470        480
EVVLVGGSTR IPRIRQVIQE FFGKDPNTSV DPDLAVVTGV AIQAGIDGGS WPLQVSALEI PNKHLQKTNF N
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1869	1	920.9474	-68.00	2	52.0	14.2	1	397-413	K.TEIDEVVLVGGSTRIPR.I	

Detailed Protein Report

Protein 1048: mitogen-activated protein kinase kinase kinase 11 [Homo sapiens]

Accession: gi|4505195
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 14.1
MW [kDa]: 92.6
pI: 9.4
Sequence Coverage [%]: 2.6
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MEPLKSLFLK	SPLGSWNGSG	SGGGGGGGGG	RPEGSPKAAG	YANPVWTALF	DYEPSGQDEL	ALRKGDRVEV	LSRDAAISGD
90	100	110	120	130	140	150	160
EGWWAGQVGG	QVGIFPSNYV	SRGGGPPPCE	VASFQELRLE	EVIGIGGFGK	VYRGSWRGEL	VAVKAARQDP	DEDISVTAES
170	180	190	200	210	220	230	240
VRQEARLFAM	LAHPNIIALK	AVCLEEPNLC	LVMEYAAGGP	LSRALAGRRV	PPHVLVNWAV	QIARGMHYLH	CEALVPVIHR
250	260	270	280	290	300	310	320
DLKSNNILLL	QPIESDDMEH	KTLKITDFGL	AREWHKTTQM	SAAGTYAWMA	PEVIKASTFS	KGSDVWSFGV	LLWELLTGEV
330	340	350	360	370	380	390	400
PYRGIDCLAV	AYGVAVNKLT	LPIPSTCPEP	FAQLMADCWA	QDPHRRPDFA	SILQQLEALE	AQVLREMPRD	SFHSMQEGWK
410	420	430	440	450	460	470	480
REIQGLFDEL	RAKEKELLSR	EEELTRAARE	QRSQAEQLRR	REHLLAQWEL	EVFERELTLL	LQQVDRERPH	VRRRRGTFKR
490	500	510	520	530	540	550	560
SKLRARDGGE	RISMPLDFKH	RITVQASPGL	DRRRNVFEVG	PGDSPTFPRF	RAIQLEPAEP	GQAWGRQSPR	RLEDSSNGER
570	580	590	600	610	620	630	640
RACWAWGPSS	PKPGEAQNGR	RRSRMDEATW	YLDSDDSSPL	GSPSTPPALN	GNPPRPSLEP	EEPKRPVPAE	RGSSSGTPKL
650	660	670	680	690	700	710	720
IQRALLRGTA	LLASLGLGRD	LQPPGGPGRE	RGESPTTPPT	PTPAPCPTEP	PPSPLICFSL	KTPDSPPTPA	PLLLDLGIPV
730	740	750	760	770	780	790	800
GQRSAKSPRR	EEEPRGGTVS	PPPGTSRSAP	GTPGTPRSPP	LGLISRPRPS	PLRSRIDPWS	FVSAGPRPSP	LPSPQPAPRR
810	820	830	840	850			
APWTLFPDSD	PFWDSPPANP	FQGGPQDCRA	QTKDMGAQAP	WVPEAGP			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1232	1	752.1726	114.82	3	44.0	14.1	0	702-723	K.TPDSPPTPAPLLLDLGIPVGQR.S	

Detailed Protein Report

Protein 1049: 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 1050: **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 1051: conserved oligomeric Golgi complex subunit 2 isoform 2 [Homo sapiens]

Accession:	gi|223029519	**Score:**	14.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	83.1
Database Date:	2015-11-30	**pI:**	6.2
		Sequence Coverage [%]:	2.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEKSRMNLPK	GPDTLCFDKD	EFMKEDFDVD	HFVSDCRKRV	QLEELRDDLE	LYYKLLKTAM	VELINKDYAD	FVNLSTNLVG
90	100	110	120	130	140	150	160
MDKALNQLSV	PLGQLREEVL	SLRSSVSEGI	RAVDERMSKQ	EDIRKKKMCV	LRLIQVIRSV	EKIEKILNSQ	SSKETSALEA
170	180	190	200	210	220	230	240
SSPLLTGQIL	ERIATEFNQL	QFHAVQSKGM	PLLDKVRPRI	AGITAMLQQS	LEGLLLEGLQ	TSDVDIIRHC	LRTYATIDKT
250	260	270	280	290	300	310	320
RDAEALVGQV	LVKPYIDEVI	IEQFVESHPN	GLQVMYNKLL	EFVPHHCRLL	REVTGGAISS	EKGNTVPGYD	FLVNSVWPQI
330	340	350	360	370	380	390	400
VQGLEEKLPS	LFNPGNPDAF	HEKYTISMDF	VRRLERQCGS	QASVKRLRAH	PAYHSFNKKW	NLPVYFQIRF	REIAGSLEAA
410	420	430	440	450	460	470	480
LTDVLEDAPA	ESPYCLLASH	RTWSSLRRCW	SDEMFLPLLV	HRLWRLTLQI	LARYSVFVNE	LSLRPISNES	PKEIKKPLVT
490	500	510	520	530	540	550	560
GSKEPSITQG	NTEDQGSGPS	ETKPVVSISR	TQLVYVVADL	DKLQEQLPEL	LEIIKPKLEM	IGFKNFSSIS	ALEDSQSSFS
570	580	590	600	610	620	630	640
ACVPSLSSKI	IQDLSDSCFG	FLKSALEVPR	LYRRTNKEVP	TTASSYVDSA	LKPLFQLQSG	HKDKLKQAII	QQWLEGTLSE
650	660	670	680	690	700	710	720
STHKYYETVS	DVLNSVKKME	ESLKRLKQAR	KTTPANPVGP	SGGMSDDDKI	RLQLALDVEY	LGEQIQKLGL	QASDIKSFSA
730	740						
LAELVAAAKD	QATAEQP						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
103	1	672.4409	120.25	3	30.0	14.1	0	154-172	K.ETSALEASSPLLTGQILER.I	

Detailed Protein Report

Protein 1052: 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

Quantitation

mdown:qdown	**Median:**	1.20	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.79	**CV:**	0.00 %	**No. of 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	Ratios
675	1	529.7280	-18.04	2	37.8	14.1	0	1-9	-.MTTCTTICK.R	Carbamidomethyl: 4	Wdown:Qdown 0.79 mdown:qdown 1.20

Detailed Protein Report

Protein 1053: PREDICTED: SH3-containing GRB2-like protein 3-interacting protein 1 isoform X9 [Homo sapiens]

Accession: gi|530363468
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 14.0
MW [kDa]: 68.2
pI: 9.4
Sequence Coverage [%]: 1.7
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MMEGLKKRTR	KAFGIRKKEK	DTDSTGSPDR	DGIKKSNGAP	NGFYAEIDWE	RYNSPELDEE	GYSIRPEEPG	STKGKHFYSS
90	100	110	120	130	140	150	160
SESEEEEESH	KKFNIKIKPL	QSKDILKNAA	TVDELKASIG	NIALSPSPVG	AIKRNLSSEE	VARPRRSTPT	PELISKKPPD
170	180	190	200	210	220	230	240
DTTALAPLFG	PPLESAFDEQ	KTEVLLDQPE	IWGSGQPINP	SMESPKLTRP	FPTGTPPPLP	PKNVPATPPR	TGSPLTIGPG
250	260	270	280	290	300	310	320
ASSPARPATP	LVPCRSTTPP	PPPPRPPSRP	KLPPGKPGVG	DVSRPFSPPI	HSSSPPPIAP	LARAESTSSI	SSTNSLSAAT
330	340	350	360	370	380	390	400
TPTVENEQPS	LVWFDRGKFY	LTFEGSSRGP	SPLTMGAQDT	LPVAAAFTET	VNAYFKGADP	SKCIVKITGE	MVLSFPAGIT
410	420	430	440	450	460	470	480
RHFANNPSPA	ALTFRVINFS	RLEHVLPNPQ	LLCCDNTQND	ANTKEFWVNM	PNLMTHLKKV	SEQKPQATYY	NVDMLKYQVS
490	500	510	520	530	540	550	560
AQGIQSTPLN	LAVNWRCEPS	STDLRIDYKY	NTDAMTTAVA	LNNVQFLVPI	DGGVTKLQAV	LPPAVWNAEQ	QRILWKIPDI
570	580	590	600	610	620	630	
SQKSENGGVG	SLLARFQLSE	GPSKPSPLVV	QFTSEGSTLS	GCDIELVGAG	YRFSLIKKRF	AAGKYLADN	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
419	2	629.3626	50.32	2	34.3	14.0	0	135-145	R.NLSSEEVARPR.R	

Detailed Protein Report

Protein 1054: sortilin-related receptor preproprotein [Homo sapiens]

Accession:	gi|4507157	**Score:**	14.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	248.3
Database Date:	2015-11-30	**pI:**	5.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	0.5
		No. of unique Peptides:	1

Detailed Protein Report

```
        10          20          30          40          50          60          70          80
MATRSSRRES  RLPFLFTLVA  LLPPGALCEV  WTQRLHGGSA  PLPQDRGFLV  VQGDPRELRL  WARGDARGAS  RADEKPLRRK
        90         100         110         120         130         140         150         160
RSAALQPEPI  KVYGQVSLND  SHNQMVVHWA  GEKSNVIVAL  ARDSLALARP  KSSDVYVSYD  YGKSFKKISD  KLNFGLGNRS
       170         180         190         200         210         220         230         240
EAVIAQFYHS  PADNKRYIFA  DAYAQYLWIT  FDFCNTLQGF  SIPFRAADLL  LHSKASNLLL  GFDRSHPNKQ  LWKSDDFGQT
       250         260         270         280         290         300         310         320
WIMIQEHVKS  FSWGIDPYDK  PNTIYIERHE  PSGYSTVFRS  TDFFQSRENQ  EVILEEVRDF  QLRDKYMFAT  KVVHLLGSEQ
       330         340         350         360         370         380         390         400
QSSVQLWVSF  GRKPMRAAQF  VTRHPINEYY  IADASEDQVF  VCVSHSNNRT  NLYISEAEGL  KFSLSLENVL  YYSPGGAGSD
       410         420         430         440         450         460         470         480
TLVRYFANEP  FADFHRVEGL  QGVYIATLIN  GSMNEENMRS  VITFDKGGTW  EFLQAPAFTG  YGEKINCELS  QGCSLHLAQR
       490         500         510         520         530         540         550         560
LSQLLNLQLR  RMPILSKESA  PGLIIATGSV  GKNLASKTNV  YISSSAGARW  REALPGPHYY  TWGDHGGIIT  AIAQGMETNE
       570         580         590         600         610         620         630         640
LKYSTNEGET  WKTFIFSEKP  VFVYGLLTEP  GEKSTVFTIF  GSNKENVHSW  LILQVNATDA  LGVPCTENDY  KLWSPSDERG
       650         660         670         680         690         700         710         720
NECLLGHKTV  FKRRTPHATC  FNGEDFDRPV  VVSNCSCTRE  DYECDFGFKM  SEDLSLEVCV  PDPEFSGKSY  SPPVPCPVGS
       730         740         750         760         770         780         790         800
TYRRTRGYRK  ISGDTCSGGD  VEARLEGELV  PCPLAEENEF  ILYAVRKSIY  RYDLASGATE  QLPLTGLRAA  VALDFDYEHN
       810         820         830         840         850         860         870         880
CLYWSDLALD  VIQRLCLNGS  TGQEVIINSG  LETVEALAFE  PLSQLLYWVD  AGFKKIEVAN  PDGDFRLTIV  NSSVLDRPRA
       890         900         910         920         930         940         950         960
LVLVPQEGVM  FWTDWGDLKP  GIYRSNMDGS  AAYHLVSEDV  KWPNGISVDD  QWIYWTDAYL  ECIERITFSG  QQRSVILDNL
       970         980         990        1000        1010        1020        1030        1040
PHPYAIAVFK  NEIYWDDWSQ  LSIFRASKYS  GSQMEILANQ  LTGLMDMKIF  YKGKNTGSNA  CVPRPCSLLC  LPKANNSRSC
      1050        1060        1070        1080        1090        1100        1110        1120
RCPEDVSSSV  LPSGDLMCDC  PQGYQLKNNT  CVKEENTCLR  NQYRCSNGNC  INSIWWCDFD  NDCGDMSDER  NCPTTICDLD
      1130        1140        1150        1160        1170        1180        1190        1200
TQFRCQESGT  CIPLSYKCDL  EDDCGDNSDE  SHCEMHQCRS  DEYNCSSGMC  IRSSWVCDGD  NDCRDWSDEA  NCTAIYHTCE
      1210        1220        1230        1240        1250        1260        1270        1280
ASNFQCRNGH  CIPQRWACDG  DTDCQDGSDE  DPVNCEKKCN  GFRCPNGTCI  PSSKHCDGLR  DCSDGSDEQH  CEPLCTHFMD
      1290        1300        1310        1320        1330        1340        1350        1360
FVCKNRQQCL  FHSMVCDGII  QCRDGSDEDA  AFAGCSQDPE  FHKVCDEFGF  QCQNGVCISL  IWKCDGMDDC  GDYSDEANCE
      1370        1380        1390        1400        1410        1420        1430        1440
NPTEAPNCSR  YFQFRCENGH  CIPNRWKCDR  ENDCGDWSDE  KDCGDSHILP  FSTPGPSTCL  PNYYRCSSGT  CVMDTWVCDG
      1450        1460        1470        1480        1490        1500        1510        1520
YRDCADGSDE  EACPLLANVT  AASTPTQLGR  CDRFEFECHQ  PKTCIPNWKR  CDGHQDCQDG  RDEANCPTHS  TLTCMSREFQ
      1530        1540        1550        1560        1570        1580        1590        1600
CEDGEACIVL  SERCDGFLDC  SDESDEKACS  DELTVYKVQN  LQWTADFSGD  VTLTWMRPKK  MPSASCVYNV  YYRVVGESIW
      1610        1620        1630        1640        1650        1660        1670        1680
KTLETHSNKT  NTVLKVLKPD  TTYQVKVQVQ  CLSKAHNTND  FVTLRTPEGL  PDAPRNLQLS  LPREAEGVIV  GHWAPPIHTH
      1690        1700        1710        1720        1730        1740        1750        1760
GLIREYIVEY  SRSGSKMWAS  QRAASNFTEI  KNLLVNTLYT  VRVAAVTSRG  IGNWSDSKSI  TTIKGKVIPP  PDIHIDSYGE
      1770        1780        1790        1800        1810        1820        1830        1840
NYLSFTLTME  SDIKVNGYVV  NLFWAFDTHK  QERRTLNFRG  SILSHKVGNL  TAHTSYEISA  WAKTDLGDSP  LAFEHVMTRG
      1850        1860        1870        1880        1890        1900        1910        1920
VRPPAPSLKA  KAINQTAVEC  TWTGPRNVVY  GIFYATSFLD  LYRNPKSLTT  SLHNKTVIVS  KDEQYLFLVR  VVVPYQGPSS
      1930        1940        1950        1960        1970        1980        1990        2000
DYVVVKMIPD  SRLPPRHLHV  VHTGKTSVVI  KWESPYDSPD  QDLLYAIAVK  DLIRKTDRSY  KVKSRNSTVE  YTLNKLEPGG
      2010        2020        2030        2040        2050        2060        2070        2080
KYHIIVQLGN  MSKDSSIKIT  TVSLSAPDAL  KIITENDHVL  LFWKSLALKE  KHFNESRGYE  IHMFDSAMNI  TAYLGNTTDN
      2090        2100        2110        2120        2130        2140        2150        2160
FFKISNLKMG  HNYTFTVQAR  CLFGNQICGE  PAILLYDELG  SGADASATQA  ARSTDVAAVV  VPILFLILLS  LGVGFAILYT
      2170        2180        2190        2200        2210        2220
```

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1162	1	610.6492	-203.57	2	44.2	14.0	0	1244-1254	R.CPNGTCIPSSK.H	Carbamidomethyl: 1, 6

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Detailed Protein Report

Protein 1055: 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

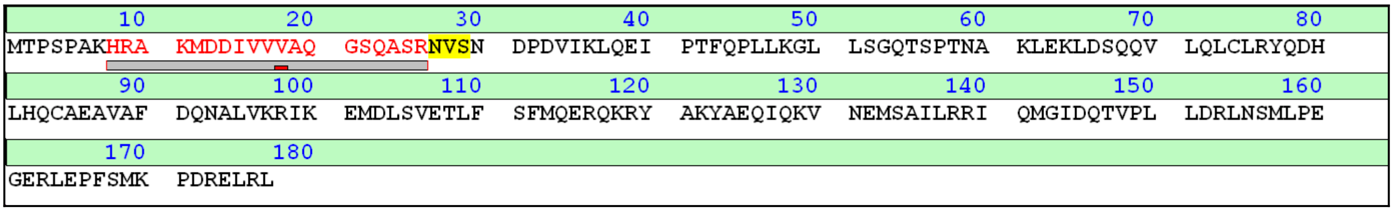
10	20	30	40	50	60	70	80
MRPGGERPVE	GGACNGRSEL	ELLKLRSAEC	IDEAAERLGA	LSRAIWSQPE	LAYEEHHAHR	VLTHFFEREP	PAASWAVQPH
90	100	110	120	130	140	150	160
YQLPTAFRAE	WEPPEARAPS	ATPRPLHLGF	LCEYDALPGI	GHACGHNLIA	EVGAAAALGV	RGALEGLPRP	PPPVKVVVLG
170	180	190	200	210	220	230	240
TPAEEDGGGK	IDLIEAGAFT	NLDVVFMAHP	SQENAAYLPD	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 1056: PREDICTED: loss of heterozygosity 12 chromosomal region 1 protein isoform X1 [Homo sapiens]

Accession:	gi|530398989	**Score:**	14.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	20.2
Database Date:	2015-11-30	**pI:**	9.0
		Sequence Coverage [%]:	10.7
		No. of unique Peptides:	1



```
        10         20         30         40         50         60         70         80
MTPSPAKHRA KMDDIVVVAQ GSQASRNVSN DPDVIKLQEI PTFQPLLKGL LSGQTSPTNA KLEKLDSQQV LQLCLRYQDH
        90        100        110        120        130        140        150        160
LHQCAEAVAF DQNALVKRIK EMDLSVETLF SFMQERQKRY AKYAEQIQKV NEMSAILRRI QMGIDQTVPL LDRLNSMLPE
       170        180
GERLEPFSMK PDRELRL
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1730	1	690.1247	139.16	3	50.3	14.0	2	8-26	K.HRAKMDDIVVVAQGSQASR.N	

Detailed Protein Report

Protein 1057: acyl-coenzyme A thioesterase 13 isoform 2 [Homo sapiens]

Accession:	gi|231567183	**Score:**	14.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	12.4
Database Date:	2015-11-30	**pI:**	9.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	15.4
		No. of unique Peptides:	1

```
         10          20          30          40          50          60          70          80
MVRKITLVSA  APGKVICEMK  VEEEHTNAIG  TLHGGLTATL  VDNISTMALL  CTERGAPGVS  VDMNITYMSP  AKLGEDIVIT
         90         100         110         120
AHVLKQGKTL  AFTSVDLTNK  ATGKLIAQGR  HTKHLGN
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1761	1	927.4490	7.27	2	50.7	14.0	0	55-72	R.GAPGVSVDMNITYMSPAK.L	Oxidation: 9

Detailed Protein Report

Protein 1058: uncharacterized protein CXorf22 [Homo sapiens]

Accession:	gi|90963001	**Score:**	14.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	110.3
Database Date:	2015-11-30	**pI:**	9.3
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MNTQKGSLTI	NVHRGSLAMS	IQRGSLVPRD	MDSSGRDMQL	RVIPAEVKFL	DTMAGRVYRL	PITVHNICRW	NQKIRFKEPV
90	100	110	120	130	140	150	160
KPQFKLMLTS	LDKELASGLQ	MTAMVEYHPD	KDEDTFDRLL	ISIENKTTEI	PLIGLIPSCQ	LEIESVVNFG	TLVANSKVYS
170	180	190	200	210	220	230	240
KEITITNHGK	APGIFKAEYH	GQLPILIFPT	SGIVDAKSSM	VIKVDFCADQ	PRIVDEEAIV	ILQGQPEMLL	SIKAHVVEQI
250	260	270	280	290	300	310	320
IELLSMSSDR	RLECIHFGPV	FFGSSKIKHA	RVYNNSPEPI	NWVAIIQDDA	VGEELGTDIQ	QRTDIALNNL	TYIRKIKNID
330	340	350	360	370	380	390	400
TTIIISCLPN	EGTLQPYQKT	VITFCFTPKL	MAVGKKDIGP	SYRQDYALFL	RFESVGSKDG	FLRDDDYKTI	KSERFQKVEL
410	420	430	440	450	460	470	480
ALTGTGLPVL	LQFDPGPVLN	FKPCFMGERS	EIQCIIKNQC	ELLPVTYHFK	KTANFEIDPE	KGKITGGGMV	DVMCSFVPHQ
490	500	510	520	530	540	550	560
LGVFKVKQMI	EIIGLVAEED	LQSLSVKSFH	HVYLAFNSIC	KASTKKVVMK	FDPGILPSIR	NPTGKFVVKD	LAKRKNYAPV
570	580	590	600	610	620	630	640
AMLQSAMTRT	HNHRSCEEPV	KDMLLAFPND	RAATIRSKDH	HKHFRPIFTK	VPRFNYVNHD	FAYTTFEKQQ	KKLHENYYAM
650	660	670	680	690	700	710	720
YLKYLRSVRL	QKKQAERERM	YSYDDTDIGL	EPGSGLKSPS	LSEAEIEEEL	SSAANSIRAN	RLLTTRGIAS	QEEESVRRKV
730	740	750	760	770	780	790	800
LKGLKSEPST	PQEKHDCSLM	LTPKQIHQVI	VGPSVLNFGN	ICVNSPNTHL	LHVINMLPMH	VLLQLDTDLE	ELQKTNQFSY
810	820	830	840	850	860	870	880
VILPTSSTYI	SMVFDSPTIG	KFWKSFTFTV	NNVPSGHILV	VAVVQPVTLE	LSSNELVLRP	RGFFMKTCFR	GTVRLYNRQN
890	900	910	920	930	940	950	960
CCAQFQWQPV	NTGRGIAFSI	CPAKGTVEAY	SSLECEVTWQ	QGFSSPEEGE	FILHVFQGNA	LKLKCVAHVI	IFLEHGFCFE
970	980						
GYEFVGYTLV	YIVTYI						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2562	1	1221.7289	102.41	2	60.3	14.0	2	723-744	K.GLKSEPSTPQEKHDCSLMLTPK.Q	Oxidation: 18

Detailed Protein Report

Protein 1059: PREDICTED: A-kinase anchor protein 7 isoform gamma isoform X2 [Homo sapiens]

Accession:	gi|530384237	**Score:**	14.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	37.7
Database Date:	2015-11-30	**pI:**	8.7
		Sequence Coverage [%]:	7.0
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MSEEFEANTM DSLVDMPFAT VDIQDDCGIT DEPQINLKRS QENEWVKSDQ VKKRKKKRKD YQPNYFLSIP ITNKEIIKGI
        90        100        110        120        130        140        150        160
KILQNAIIQQ DERLAKAMVS DGSFHITLLV MQLLNEDEVN IGIDALLELK PFIEELLQGK HLTLPFQGIG TFGNQVGFVK
       170        180        190        200        210        220        230        240
LAEGDHVNSL LEIAETANRT FQEKGILVGE SRSFKPHLTF MKLSKSPWLR KNGVKKIDPD LYEKFISHRF GEEILYRIDL
       250        260        270        280        290        300        310        320
CSMLKKKQSN GYYHCESSIV IGKKPIGIRD LINEALHRET MGLKSKVKQI KELLLKPETQ ARIRRELFEG RLINNSNSAN
       330
DVDFSTTLT
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
766	1	859.6992	-107.64	3	39.0	14.0	2	247-269	K.KQSNGYYHCESSIVIGKKPIGIR.D	

Detailed Protein Report

Protein 1060: 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 1061: phosphatidylinositol phosphatase PTPRQ precursor [Homo sapiens]

Accession:	gi|222537743	**Score:**	13.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	257.1
Database Date:	2015-11-30	**pI:**	5.4
Modification(s):	Oxidation	**Sequence Coverage [%]:**	0.4
		No. of unique Peptides:	1

Quantitation

Wdown:Qdown	**Median:** 0.83	**CV:** 0.00 %	**No. of Peptides:** 1

10	20	30	40	50	60	70	80
MDFLIIFLLL	FIGTSETQVD	VSNVVPGTRY	DITISSISTT	YTSPVTRIVT	TNVTKPGPPV	FLAGERVGSA	GILLSWNTPP
90	100	110	120	130	140	150	160
NPNGRIISYI	VKYKEVCPWM	QTVYTQVRSK	PDSLEVLLTN	LNPGTTYEIK	VAAENSAGIG	VFSDPFLFQT	AESAPGKVVN
170	180	190	200	210	220	230	240
LTVEAYNASA	VKLIWYLPRQ	PNGKITSFKI	SVKHARSGIV	VKDVSIRVED	ILTGKLPECN	ENSESFLWST	ASPSPTLGRV
250	260	270	280	290	300	310	320
TPPSRTTHSS	STLTQNEISS	VWKEPISFVV	THLRPYTTYL	FEVSAATTEA	GYIDSTIVRT	PESVPEGPPQ	NCVTGNITGK
330	340	350	360	370	380	390	400
SFSILWDPPT	IVTGKFSYRV	ELYGPSGRIL	DNSTKDLKFA	FTNLTPFTMY	DVYIAAETSA	GTGPKSNISV	FTPPDVPGAV
410	420	430	440	450	460	470	480
FDLQLAEVES	TQVRITWKKP	RQPNGIINQY	RVKVLVPETG	IILENTLLTG	NNEYINDPMA	PEIVNIVEPM	VGLYEGSAEM
490	500	510	520	530	540	550	560
SSDLHSLATF	IYNSHPDKNF	PARNRAEDQT	SPVVTTRNQY	ITDIAAEQLS	YVIRRLVPFT	EHMISVSAFT	IMGEGPPTVL
570	580	590	600	610	620	630	640
SVRTRQQVPS	SIKIINYKNI	SSSSILLYWD	PPEYPNGKIT	HYTIYAMELD	TNRAFQITTI	DNSFLITGLK	KYTKYKMRVA
650	660	670	680	690	700	710	720
ASTHVGESSL	SEENDIFVRT	SEDEPESSPQ	DVEVIDVTAD	EIRLKWSPPE	KPNGIIIAYE	VLYKNIDTLY	MKNTSTTDII
730	740	750	760	770	780	790	800
LRNLRPHTLY	NISVRSYTRF	GHGNQVSSLL	SVRTSETVPD	SAPENITYKN	ISSGEIELSF	LPPSSPNGII	QKYTIYLKRS
810	820	830	840	850	860	870	880
NGNEERTINT	TSLTQNIKVL	KKYTQYIIEV	SASTLKGEGV	RSAPISILTE	EDAPDSPPQD	FSVKQLSGVT	VKLSWQPPLE
890	900	910	920	930	940	950	960
PNGIILYYTV	YVWNRSSLKT	INVTETSLEL	SDLDYNVEYS	AYVTASTRFG	DGKTRSNIIS	FQTPEGAPSD	PPKDVYYANL
970	980	990	1000	1010	1020	1030	1040
SSSSIILFWT	PPSKPNGIIQ	YYSVYYRNTS	GTFMQNFTLH	EVTNDFDNMT	VSTIIDKLTI	FSYYTFWLTA	STSVGNGNKS
1050	1060	1070	1080	1090	1100	1110	1120
SDIIEVYTDQ	DIPEGFVGNL	TYESISSTAI	NVSWVPPAQP	NGLVFYYVSL	ILQQTPRHVR	PPLVTYERSI	YFDNLEKYTD
1130	1140	1150	1160	1170	1180	1190	1200
YILKITPSTE	KGFSDTYTAQ	LYIKTEEDVP	ETSPIINTFK	NLSSTSVLLS	WDPPVKPNGA	IISYDLTLQG	PNENYSFITS
1210	1220	1230	1240	1250	1260	1270	1280
DNYIILEELS	PFTLYSFFAA	ARTRKGLGPS	SILFFYTDES	VPLAPPQNLT	LINCTSDFVW	LKWSPSPLPG	GIVKVYSFKI
1290	1300	1310	1320	1330	1340	1350	1360
HEHETDTIYY	KNISGFKTEA	KLVGLEPVST	YSIRVSAFTK	VGNGNQFSNV	VKFTTQESVP	DVVQNMQCMA	TSWQSVLVKW
1370	1380	1390	1400	1410	1420	1430	1440
DPPKKANGII	TQYMVTVERN	STKVSPQDHM	YTFIKLLANT	SYVFKVRAST	SAGEGDESTC	HVSTLPETVP	SVPTNIAFSD
1450	1460	1470	1480	1490	1500	1510	1520
VQSTSATLTW	IRPDTILGYF	QNYKITTQLR	AQKCKEWESE	ECVEYQKIQY	LYEAHLTEET	VYGLKKFRWY	RFQVAASTNA
1530	1540	1550	1560	1570	1580	1590	1600
GYGNASNWIS	TKTLPGPPDG	PPENVHVVAT	SPFSISISWS	EPAVITGPTC	YLIDVKSVDN	DEFNISFIKS	NEENKTIEIK
1610	1620	1630	1640	1650	1660	1670	1680
DLEIFTRYSV	VITAFTGNIS	AAYVEGKSSA	EMIVTTLESA	PKDPPNNMTF	QKIPDEVTKF	QLTFLPPSQP	NGNIQVYQAL
1690	1700	1710	1720	1730	1740	1750	1760
VYREDDPTAV	QIHNLSIIQK	TNTFVIAMLE	GLKGGHTYNI	SVYAVNSAGA	GPKVPMRITM	DIKAPARPKT	KPTPIYDATG
1770	1780	1790	1800	1810	1820	1830	1840
KLLVTSTTIT	IRMPICYYSD	DHGPIKNVQV	LVTETGAQHD	GNVTKWYDAY	FNKARPYFTN	EGFPNPPCTE	GKTKFSGNEE
1850	1860	1870	1880	1890	1900	1910	1920
IYIIGADNAC	MIPGNEDKIC	NGPLKPKKQY	LFKFRATNIM	GQFTDSDYSD	PVKTLGEGLS	ERTVEIILSV	TLCILSIILL
1930	1940	1950	1960	1970	1980	1990	2000
GTAIFAFARI	RQKQKEGGTY	SPQDAEIIDT	KLKLDQLITV	ADLELKDERL	TRLLSYRKSI	KPISKKSFLQ	HVEELCTNNN
2010	2020	2030	2040	2050	2060	2070	2080
LKFQEEFSEL	PKFLQDLSST	DADLPWNRAK	NRFPNIKPYN	NNRVKLIADA	SVPGSDYINA	SYISGYLCPN	EFIATQGPLP
2090	2100	2110	2120	2130	2140	2150	2160
GTVGDFWRMV	WETRAKTLVM	LTQCFEKGRI	RCHQYWPEDN	KPVTVFGDIV	ITKLMEDVQI	DWTIRDLKIE	RHGDCMTVRQ
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
627	1	604.2948	34.08	2	36.7	13.9	0	1643-1652	K.DPPNNMTFQK.I	Oxidation: 6	Wdown:Qdown 0.83

Detailed Protein Report

Protein 1062: testis anion transporter 1 isoform b [Homo sapiens]

Accession:	gi|301601602	**Score:**	13.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	97.3
Database Date:	2015-11-30	**pI:**	5.7
		Sequence Coverage [%]:	1.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAQLERSAIS	GFSSKSRRNS	FAYDVKREVY	NEETFQQEHK	RKASSSGNMN	INITTFRHHV	QCRCSWHRFL	RCVLTIFPFL
90	100	110	120	130	140	150	160
EWMCMYRLKD	WLLGDLLAGI	SVGLVQVPQG	LTLSLLARQL	IPPLNIAYAA	FCSSVIYVIF	GSCHQMSIGS	FFLVSALLIN
170	180	190	200	210	220	230	240
VLKVSPFNNG	QLVMGSFVKN	EFSAPSYLMG	YNKSLSVVAT	TTFLTGIIQI	IGFTVIANKI	SMATETSQTL	IDMIPYSFLL
250	260	270	280	290	300	310	320
PVTPDFSLLP	KIILQAFSLS	LVSSFLLIFL	GKKIASLHNY	SVNSNQDLIA	IGLCNVVSSF	FRSCVFTGAI	ARTIIQDKSG
330	340	350	360	370	380	390	400
GRQQFASLVG	AGVMLLLMVK	MGHFFYTLPN	AVLAGIILSN	VIPYLETISN	LPSLWRQDQY	DCALWMMTFS	SSIFLGLDIG
410	420	430	440	450	460	470	480
LIISVVSAFF	ITTVRSHRAK	ILLLGQIPNT	NIYRSINDYR	EIITIPGVKI	FQCCSSITFV	NVYYLKHKLL	KEVDMVKVPL
490	500	510	520	530	540	550	560
KEEEIFSLFN	SSDTNLQGGK	ICRCFCNCDD	LEPLPRILYT	ERFENKLDPE	ASSINLIHCS	HFESMNTSQT	ASEDQVPYTV
570	580	590	600	610	620	630	640
SSVSQKNQGQ	QYEEVEEVWL	PNNSSRNSSP	GLPDVAESQG	RRSLIPYSDA	SLLPSVHTII	LDFSMVHYVD	SRGLVVLRQI
650	660	670	680	690	700	710	720
CNAFQNANIL	ILIAGCHSSI	VRAFERNDFF	DAGITKTQLF	LSVHDAVLFA	LSRKVIGSSE	LSIDESETVI	RETYSETDKN
730	740	750	760	770	780	790	800
DNSRYKMSSS	FLGSQKNVSP	GFIKIQQPVE	EESELDLELE	SEQEAGLGLD	LDLDRELEPE	MEPKAETETK	TQTEMEPQPE
810	820	830	840	850	860	870	
TEPEMEPNPK	SRPRAHTFPQ	QRYWPMYHPS	MASTQSQTQT	RTWSVERRRH	PMDSYSPEGN	SNEDV	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2795	1	835.4427	31.63	2	63.4	13.9	1	587-602	R.NSSPGLPDVAESQGRR.S	

Detailed Protein Report

Protein 1063: OTU domain-containing protein 4 isoform 3 [Homo sapiens]

Accession:	gi|156630992	**Score:**	13.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	117.0
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
MACIHYLREN	REKFEAFIEG	SFEEYLKRLE	NPQEWVGQVE	ISALSLMYRK	DFIIYREPNV	SPSQVTENNF	PEKVLLCFSN
90	100	110	120	130	140	150	160
GNHYDIVYPI	KYKESSAMCQ	SLLYELLYEK	VFKTDVSKIV	MELDTLEVAD	EDNSEISDSE	DDSCKSKTAA	AAADVNGFKP
170	180	190	200	210	220	230	240
LSGNEQLKNN	GNSTSLPLSR	KVLKSLNPAV	YRNVEYEIWL	KSKQAQQKRD	YSIAAGLQYE	VGDKCQVRLD	HNGKFLNADV
250	260	270	280	290	300	310	320
QGIHSENGPV	LVEELGKKHT	SKNLKAPPPE	SWNTVSGKKM	KKPSTSGQNF	HSDVDYRGPK	NPSKPIKAPS	ALPPRLQHPS
330	340	350	360	370	380	390	400
GVRQHAFSSH	SSGSQSQKFS	SEHKNLSRTP	SQIIRKPDRE	RVEDFDHTSR	ESNYFGLSPE	ERREKQAIEE	SRLLYEIQNR
410	420	430	440	450	460	470	480
DEQAFPALSS	SSVNQSASQS	SNPCVQRKSS	HVGDRKGSRR	RMDTEERKDK	DSIHGHSQLD	KRPEPSTLEN	ITDDKYATVS
490	500	510	520	530	540	550	560
SPSKSKKLEC	PSPAEQKPAE	HVSLSNPAPL	LVSPEVHLTP	AVPSLPATVP	AWPSEPTTFG	PTGVPAPIPV	LSVTQTLTTG
570	580	590	600	610	620	630	640
PDSAVSQAHL	TPSPVPVSIQ	AVNQPLMPLP	QTLSLYQDPL	YPGFPCNEKG	DRAIVPPYSL	CQTGEDLPKD	KNILRFFFNL
650	660	670	680	690	700	710	720
GVKAYSCPMW	APHSYLYPLH	QAYLAACRMY	PKVPVPVYPH	NPWFQEAPAA	QNESDCTCTD	AHFPMQTEAS	VNGQMPQPEI
730	740	750	760	770	780	790	800
GPPTFSSPLV	IPPSQVSESH	GQLSYQADLE	SETPGQLLHA	DYEESLSGKN	MFPQPSFGPN	PFLGPVPIAP	PFFPHVWYGY
810	820	830	840	850	860	870	880
PFQGFIENPV	MRQNIVLPSD	EKGELDLSLE	NLDLSKDCGS	VSTVDEFPEA	RGEHVHSLPE	ASVSSKPDEG	RTEQSSQTRK
890	900	910	920	930	940	950	960
ADTALASIPP	VAEGKAHPPT	QILNRERETV	PVELEPKRTI	QSLKEKTEKV	KDPKTAADVV	SPGANSVDSR	VQRPKEESSE
970	980	990	1000	1010	1020	1030	1040
DENEVSNILR	SGRSKQFYNQ	TYGSRKYKSD	WGYSGRGGYQ	HVRSEESWKG	QPSRSRDEGY	QYHRNVRGRP	FRGDRRRSGM
1050							
GDGHRGQHT							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2038	1	701.2778	-127.81	3	54.1	13.9	0	148-168	K.TAAAAADVNGFKPLSGNEQLK.N	

Detailed Protein Report

Protein 1064: PREDICTED: deleted in lung and esophageal cancer protein 1 isoform X6 [Homo sapiens]

Accession:	gi|578806835	**Score:**	13.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	160.3
Database Date:	2015-11-30	**pI:**	6.1
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
METRSSKTRR	SLASRTNECQ	GTMWAPTSPP	AGSSSPSQPT	WKSSLYSSLA	YSEAFHYSFA	ARPRRLTQLA	LAQRPEPQLL
90	100	110	120	130	140	150	160
RLRPSSLRTQ	DISHLLTGVF	RNLYSAEVIG	DEVSASLIKA	RGSENERHEE	FVDQLQQIRE	LYKQRLDEFE	MLERHITQAQ
170	180	190	200	210	220	230	240
ARAIAENERV	MSQAGVQDLE	SLVRLPPVKS	VSRWCIDSEL	LRKHHLISPE	DYYTDTVPFH	SAPKGISLPG	CSKLTFSCEK
250	260	270	280	290	300	310	320
RSVQKKELNK	KLEDSCRKKL	AEFEDELDHT	VDSLTWNLTP	KAKERTREPL	KKASQPRNKN	WMNHLRVPQR	ELDRLLLARM
330	340	350	360	370	380	390	400
ESRNHFLKNP	RFFPPNTRYG	GKSLVFPPKK	PAPIGEFQST	EPEQSCADTP	VFLAKPPIGF	FTDYEIGPVY	EMVIALQNTT
410	420	430	440	450	460	470	480
TTSRYLRVLP	PSTPYFALGL	GMFPGKGGMV	APGMTCQYIV	QFFPDCLGDF	DDFILVETQS	AHTLLIPLQA	RRPPPVLTLS
490	500	510	520	530	540	550	560
PVLDCGYCLI	GGVKMTRFIC	KNVGFSVGRF	CIMPKTSWPP	LSFKAIATVG	FVEQPPFGIL	PSVFELAPGH	AILVEVLFSP
570	580	590	600	610	620	630	640
KSLGKAEQTF	IIMCDNCQIK	ELVTIGIGQL	IALDLIYISG	EKSQPDPGEL	TDLTAQHFIR	FEPENLRSTA	RKQLIIRNAT
650	660	670	680	690	700	710	720
HVELAFYWQI	MKPNLQPLMP	GETFSMDSIK	CYPDKETAFS	IMPRKGVLSP	HTDHEFILSF	SPHELRDFHS	VLQMVLEEVP
730	740	750	760	770	780	790	800
EPVSSEAESL	GHSSYSVDDV	IVLEIEVKGS	VEPFQVLLEP	YALIIPGENY	IGINVKKAFK	MWNNSKSPIR	YLWGKISDCH
810	820	830	840	850	860	870	880
IIEVEPGTGV	IEPSEVGDFE	LNFTGGVPGP	TSQDLLCEIE	DSPSPVVLHI	EAVFKGPALI	INVSALQFGL	LRLGQKATNS
890	900	910	920	930	940	950	960
IQIRNVSQLP	ATWRMKESPV	SLQERPEDVS	PFDIEPSSGQ	LHSLGECRVD	ITLEALHCQH	LETVLELEVE	NGAWSYLPVY
970	980	990	1000	1010	1020	1030	1040
AEVQKPHVYL	QSSQVEVRNL	YLGVPTKTTI	TLINGTLLPT	QFHWGKLLGH	QAEFCMVTVS	PKHGLLGPSE	ECQLKLELTA
1050	1060	1070	1080	1090	1100	1110	1120
HTQEELTHLA	LPCHVSGMKK	PLVLGISGKP	QGLQVAITIS	KESSDCSVFS	TEQWPGHPKE	LRLDFGSAVP	LRTRVTRQLI
1130	1140	1150	1160	1170	1180	1190	1200
LTNRSPIRTR	FSLKFEYFGS	PQNSLSKKTS	LPNMPPALLK	TVRMQEHLAK	REQLDFMESM	LSHGKGAAFF	PHFSQGMLGP
1210	1220	1230	1240	1250	1260	1270	1280
YQQLCIDITG	CANMWGEYWD	NLICTVGDLL	PEVIPVHMAA	VGCPISSLRT	TSYTIDQAQK	EPAMRFGTQV	SGGDTVTRTL
1290	1300	1310	1320	1330	1340	1350	1360
RLNNSSPCDI	RLDWETYVPE	DKEDRLVELL	VFYGPPFPLR	DQAGNELVCP	DTPEGGCLLW	SPGPSSSSEF	SHETDSSVEG
1370	1380	1390	1400	1410	1420	1430	1440
SSSASNRVAQ	KLISVILQAH	EGVPSGHLYC	ISPKQVVVPA	GGSSTIYISF	TPMVLSPEIL	HKVECTGYAL	GFMSLDSK

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
34	1	628.3634	65.98	3	29.1	13.9	2	225-241	K.GISLPGCSKLTFSCEKR.S	Carbamidomethyl: 14

Detailed Protein Report

Protein 1065: PREDICTED: SH3 and PX domain-containing protein 2A isoform X5 [Homo sapiens]

Accession:	gi|530394650	**Score:**	13.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	106.0
Database Date:	2015-11-30	**pI:**	9.5
		Sequence Coverage [%]:	1.3
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	0.80	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	1.64	**CV:**	0.00 %	**No. of 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	Ratios
2667	1	665.3404	-37.39	2	61.7	13.9	2	858-870	R.SAAAEAKGRLAER.A		Wdown:Qdown 1.64 mdown:qdown 0.80

Detailed Protein Report

Protein 1066: transmembrane and coiled-coil domain-containing protein 5A [Homo sapiens]

Accession: gi|34303932
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 13.9
MW [kDa]: 34.2
pI: 5.8
Sequence Coverage [%]: 8.3
No. of unique Peptides: 1

Alias proteins:

Accession	**Name**	**Description**
gi|530405403	refseq_human (refseq_human_20140103.fasta)	PREDICTED: transmembrane and coiled-coil domain-containing protein 5A isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MEISRLAQSK	RNIISLNMDL	ERDTQRIDEA	NQKLLLKIQE	REDKIQRLES	EIIQTRGLVE	DEEWEKENRT	TMERERALQE
90	100	110	120	130	140	150	160
LEEETARLER	KNKTLVHSIT	ELQQKLTRKS	QKITNCEQSS	PDGALEETKV	KLQQLEASYA	CQEKELLKVM	KEYAFVTQLC
170	180	190	200	210	220	230	240
EDQALYIKKY	QETLKKIEEE	LEALFLEREV	SKLVSMNPVE	KEHTSQNNEG	TPTQKTARLF	SKKIFCCLFF	ITLFFIRLLS
250	260	270	280	290			
YMFFHVRFIN	PDLLVNVLPK	VLGRSTLWKL	RCFFFPSLTL	ETEDMLPH			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1410	1	978.1800	1.91	3	46.2	13.9	2	145-168	K.ELLKVMKEYAFVTQLCEDQALYIK.K	Carbamidomethyl: 16

Detailed Protein Report

Protein 1067: PREDICTED: WD repeat-containing protein 62 isoform X1 [Homo sapiens]

Accession:	gi|530416321	**Score:**	13.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	162.6
Database Date:	2015-11-30	**pI:**	5.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAAVGSGGYA	RNDAGEKLPS	VMAGVPARRG	QSSPPPAPPI	CLRRRTRLST	ASEETVQNRV	SLEKVLGITA	QNSSGLTCDP
90	100	110	120	130	140	150	160
GTGHVAYLAG	CVVVILDPKE	NKQQHIFNTA	RKSLSALAFS	PDGKYIVTGE	NGHRPAVRIW	DVEEKNQVAE	MLGHKYGVAC
170	180	190	200	210	220	230	240
VAFSPNMKHI	VSMGYQHDMV	LNVWDWKKDI	VVASNKVSCR	VIALSFSEDS	SYFVTVGNRH	VRFWFLEVST	ETKVTSTVPL
250	260	270	280	290	300	310	320
VGRSGILGEL	HNNIFCGVAC	GRGRMAGSTF	CVSYSGLLCQ	FNEKRVLEKW	INLKVSLSSC	LCVSQELIFC	GCTDGIVRIF
330	340	350	360	370	380	390	400
QAHSLHYLAN	LPKPHYLGVD	VAQGLEPSFL	FHRKAEAVYP	DTVALTFDPI	HQWLSCVYKD	HSIYIWDVKD	INRVGKVWSE
410	420	430	440	450	460	470	480
LFHSSYVWNV	EVYPEFEDQR	ACLPSGSFLT	CSSDNTIRFW	NLDSSPDSHW	QKNIFSNTLL	KVVYVENDIQ	HLQDMSHFPD
490	500	510	520	530	540	550	560
RGSENGTPMD	VKAGVRVMQV	SPDGQHLASG	DRSGNLRIHE	LHFMDELVKV	EAHDAEVLCL	EYSKPETGLT	LLASASRDRL
570	580	590	600	610	620	630	640
IHVLNVEKNY	NLEQTLDDHS	SSITAIKFAG	NRDIQMISCG	ADKSIYFRSA	QQGSDGLHFV	RTHHVAEKTT	LYDMDIDITQ
650	660	670	680	690	700	710	720
KYVAVACQDR	NVRVYNTVNG	KQKKCYKGSQ	GDEGSLLKVH	VDPSGTFLAT	SCSDKSISVI	DFYSGECIAK	MFGHSEIITS
730	740	750	760	770	780	790	800
MKFTYDCHHL	ITVSGDSCVF	IWHLGPEITN	CMKQHLLEID	HRQQQQHTND	KKRSGHPRQD	TYVSTPSEIH	SLSPGEQTED
810	820	830	840	850	860	870	880
DLEEECEPEE	MLKTPSKDSL	DPDPRCLLTN	GKLPLWAKRL	LGDDDVADGL	AFHAKRSYQP	HGRWAERAGQ	EPLKTILDAQ
890	900	910	920	930	940	950	960
DLDCYFTPMK	PESLENSILD	SLEPQSLASL	LSESESPQEA	GRGHPSFLPQ	QKESSEASEL	ILYSLEAEVT	VTGTDSQYCR
970	980	990	1000	1010	1020	1030	1040
KEVEAGPGDQ	QGDSYLRVSS	DSPKDQSPPE	GCAGPTEDEL	SLPEGPSVPS	SSLPQTPEQE	KFLRHHFETL	TESPCRELFP
1050	1060	1070	1080	1090	1100	1110	1120
AALGDVEASE	AEDHFFNPRL	SISTQFLSSL	QKASRFTHTF	PPRATQCLVK	SPEVKLMDRG	GSQPRAGTGY	ASPDRTHVLA
1130	1140	1150	1160	1170	1180	1190	1200
AGKAEETLEA	WRPPPPCLTS	LASCVPASSV	LPTDRNLPTP	TSAPTPGLAQ	GVHAPSTCSY	MEATASSRAR	ISRSISLGDS
1210	1220	1230	1240	1250	1260	1270	1280
EGPIVATLAQ	PLRRPSSVGE	LASLGQELQA	ITTATTPSLD	SEGQEPALRS	WGNHEARANL	RLTLSSACDG	LLQPPVDTQP
1290	1300	1310	1320	1330	1340	1350	1360
GVTVPAVSFP	APSPVEESAL	RLHGSAFRPS	LPAPESPGLP	AHPSNPQLPE	ARPGIPGGTA	SLLEPTSGAL	GLLQGSPARW
1370	1380	1390	1400	1410	1420	1430	1440
SEPWVPVEAL	PPSPLELSRV	GNILHRLQTT	FQEALDLYRV	LVSSGQVDTG	QQQARTELVS	TFLWIHSQLE	AECLVGTSVA
1450	1460	1470	1480	1490			
PAQALPSPGP	PSPPTLYPLA	SPDLQALLEH	YSELLVQAVR	RKARGH			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2816	1	842.6820	-64.26	3	64.3	13.9	1	146-168	K.NQVAEMLGHKYGVACVAFSPNMK.H	Oxidation: 6, 22

Detailed Protein Report

Protein 1068: **PREDICTED: zinc finger and BTB domain-containing protein 2 isoform X3 [Homo sapiens]**

Accession:	gi|530383922	**Score:**	13.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	48.3
Database Date:	2015-11-30	**pI:**	5.5
		Sequence Coverage [%]:	3.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MYTGKMAPQL	IDPVRLEQGI	KFLHAYPLIQ	EASLASQGAF	SHPDQVFPLA	SSLYGIQIAD	HQLRQATKIA	SAPEKLGRDP
90	100	110	120	130	140	150	160
RPQTSRISQE	QVPEASQLSQ	LTSNLAQVNR	TNMTPSDPLQ	TSLSPELVST	PVPPPPPGEE	TNLEASSSDE	QPASLTIAHV
170	180	190	200	210	220	230	240
KPSIMKRNGS	FPKYYACHLC	GRRFTLRSSL	REHLQIHTGV	PFTSSQQGES	RVPLTLCSNA	ADLGKDAMEV	PEAGMISDSE
250	260	270	280	290	300	310	320
LQHISDSPII	DGQQQSETPP	PSDIADIDNL	EQADQEREVK	RRKYECTICG	RKFIQKSHWR	EHMYIHTGKP	FKCSTCDKSF
330	340	350	360	370	380	390	400
CRANQAARHV	CLNQSIDTYT	MVDKQTLELC	TFEEGSQMDN	MLVQTNKPYK	CNLCDKTFST	PNEVVKHSCQ	NQNSDVFALD
410	420	430	440				
EGRSILLGSG	DSEVTEPDHP	VLASIKKEQE	TVLLD				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1963	1	899.3605	-76.28	2	53.2	13.9	1	371-386	K.CNLCDKTFSTPNEVVK.H	

Detailed Protein Report

Protein 1069: 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

Protein 1070: probable G-protein coupled receptor 173 [Homo sapiens]

Accession:	gi|9507143	**Score:**	13.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	41.5
Database Date:	2015-11-30	**pI:**	10.4
		Sequence Coverage [%]:	4.0
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	0.48	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.06	**CV:**	0.00 %	**No. of Peptides:**	1

10	20	30	40	50	60	70	80
MANTTGEPEE	VSGALSPPSA	SAYVKLVLLG	LIMCVSLAGN	AILSLLVLKE	RALHKAPYYF	LLDLCLADGI	RSAVCFPFVL
90	100	110	120	130	140	150	160
ASVRHGSSWT	FSALSCKIVA	FMAVLFCFHA	AFMLFCISVT	RYMAIAHHRF	YAKRMTLWTC	AAVICMAWTL	SVAMAFPPVF
170	180	190	200	210	220	230	240
DVGTYKFIRE	EDQCIFEHRY	FKANDTLGFM	LMLAVLMAAT	HAVYGKLLLF	EYRHRKMKPV	QMVPAISQNW	TFHGPGATGQ
250	260	270	280	290	300	310	320
AAANWIAGFG	RGPMPPTLLG	IRQNGHAASR	RLLGMDEVKG	EKQLGRMFYA	ITLLFLLLWS	PYIVACYWRV	FVKACAVPHR
330	340	350	360	370	380		
YLATAVWMSF	AQAAVNPIVC	FLLNKDLKKC	LRTHAPCWGT	GGAPAPREPY	CVM		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
276	1	493.4767	-189.31	3	32.2	13.8	0	353-367	R.THAPCWGTGGAPAPR.E		Wdown:Qdown 0.06 mdown:qdown 0.48

Detailed Protein Report

Protein 1071: 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 1072: 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 1073: oxysterol-binding protein-related protein 11 [Homo sapiens]

Accession: gi|19923592
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 13.8
MW [kDa]: 83.6
pI: 6.6
Sequence Coverage [%]: 2.4
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MQGGEPVSTM	KVSESEGKLE	GQATAVTPNK	NSSCGGGISS	SSSSRGGSAK	GWQYSDHMEN	VYGYLMKYTN	LVTGWQYRFF
90	100	110	120	130	140	150	160
VLNNEAGLLE	YFVNEQSRNQ	KPRGTLQLAG	AVISPSDEDS	HTFTVNAASG	EQYKLRATDA	KERQHWVSRL	QICTQHHTEA
170	180	190	200	210	220	230	240
IGKNNPPLKS	RSFSLASSSN	SPISQRRPSQ	NAISFFNVGH	SKLQSLSKRT	NLPPDHLVEV	REMMSHAEGQ	QRDLIRRIEC
250	260	270	280	290	300	310	320
LPTSGHLSSL	DQDLLMLKAT	SMATMNCLND	CFHILQLQHA	SHQKGSLPSG	TTIEWLEPKI	SLSNHYKNGA	DQPFATDQSK
330	340	350	360	370	380	390	400
PVAVPEEQPV	AESGLLAREP	EEINADDEIE	DTCDHKEDDL	GAVEEQRSVI	LHLLSQLKLG	MDLTRVVLPT	FILEKRSLLE
410	420	430	440	450	460	470	480
MYADFMSHPD	LFIAITNGAT	AEDRMIRFVE	YYLTSFHEGR	KGAIAKKPYN	PIIGETFHCS	WKMPKSEVAS	SVFSSSSTQG
490	500	510	520	530	540	550	560
VTNHAPLSGE	SLTQVGSDCY	TVRFVAEQVS	HHPPVSGFYA	ECTERKMCVN	AHVWTKSKFL	GMSIGVTMVG	EGILSLLEHG
570	580	590	600	610	620	630	640
EEYTFSLPCA	YARSILTVPW	VELGGKVSVN	CAKTGYSASI	TFHTKPFYGG	KLHRVTAEVK	HNITNTVVCR	VQGEWNSVLE
650	660	670	680	690	700	710	720
FTYSNGETKY	VDLTKLAVTK	KRVRPLEKQD	PFESRRLWKN	VTDSLRESEI	DKATEHKHTL	EERQRTEERH	RTETGTPWKT
730	740	750					
KYFIKEGDGW	VYHKPLWKII	PTTQPAE					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2097	2	701.2818	-9.24	3	54.8	13.8	0	339-356	R.EPEEINADDEIEDTCDHK.E	

Detailed Protein Report

Protein 1074: ankyrin repeat and SOCS box protein 3 isoform b [Homo sapiens]

Accession:	gi|22208951	**Score:**	13.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	49.6
Database Date:	2015-11-30	**pI:**	5.8
		Sequence Coverage [%]:	4.3
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|320202950	refseq_human (refseq_human_20140103.fasta)	ankyrin repeat and SOCS box protein 3 isoform b [Homo sapiens]

10	20	30	40	50	60	70	80
MKTFEGFCAL	HLAASQGHWK	IVQILLEAGA	DPNATTLEET	TPLFLAVENG	QIDVLRLLLQ	HGANVNGSHS	MCGWNSLHQA
90	100	110	120	130	140	150	160
SFQENAEIIK	LLLRKGANKE	CQDDFGITPL	FVAAQYGKLE	SLSILISSGA	NVNCQALDKA	TPLFIAAQEG	HTKCVELLLS
170	180	190	200	210	220	230	240
SGADPDLYCN	EDSWQLPIHA	AAQMGHTKIL	DLLIPLTNRA	CDTGLNKVSP	VYSAVFGGHE	DCLEILLRNG	YSPDAQACLV
250	260	270	280	290	300	310	320
FGFSSPVCMA	FQKDCEFFGI	VNILLKYGAQ	INELHLAYCL	KYEKFSIFRY	FLRKGCSLGP	WNHIYEFVNH	AIKAQAKYKE
330	340	350	360	370	380	390	400
WLPHLLVAGF	DPLILLCNSW	IDSVSIDTLI	FTLEFTNWKT	LAPAVERMLS	ARASNAWILQ	QHIATVPSLT	HLCRLEIRSS
410	420	430	440	450			
LKSERLRSDS	YISQLPLPRS	LHNYLLYEDV	LRMYEVPELA	AIQDG			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2058	1	1051.3794	-113.33	2	55.9	13.8	0	100-118	K.ECQDDFGITPLFVAAQYGK.L	

Detailed Protein Report

Protein 1075: phosphatidylinositol 3-kinase regulatory subunit beta [Homo sapiens]

Accession: gi|4826908

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Modification(s): Oxidation

Score: 13.8

MW [kDa]: 81.6

pI: 6.1

Sequence Coverage [%]: 1.9

No. of unique Peptides: 1

```
        10         20         30         40         50         60         70         80
MAGPEGFQYR ALYPFRRERP EDLELLPGDV LVVSRAALQA LGVAEGGERC PQSVGWMPGL NERTRQRGDF PGTYVEFLGP
        90        100        110        120        130        140        150        160
VALARPGPRP RGPRPLPARP RDGAPEPGLT LPDLPEQFSP PDVAPPLLVK LVEAIERTGL DSESHYRPEL PAPRTDWSLS
       170        180        190        200        210        220        230        240
DVDQWDTAAL ADGIKSFLLA LPAPLVTPEA SAEARRALRE AAGPVGPALE PPTLPLHRAL TLRFLLQHLG RVARRAPALG
       250        260        270        280        290        300        310        320
PAVRALGATF GPLLLRAPPP PSSPPPGGAP DGSEPSPDFP ALLVEKLLQE HLEEQEVAPP ALPPKPPKAK PAPTVLANGG
       330        340        350        360        370        380        390        400
SPPSLQDAEW YWGDISREEV NEKLRDTPDG TFLVRDASSK IQGEYTLTLR KGGNNKLIKV FHRDGHYGFS EPLTFCSVVD
       410        420        430        440        450        460        470        480
LINHYRHESL AQYNAKLDTR LLYPVSKYQQ DQIVKEDSVE AVGAQLKVYH QQYQDKSREY DQLYEEYTRT SQELQMKRTA
       490        500        510        520        530        540        550        560
IEAFNETIKI FEEQGQTQEK CSKEYLERFR REGNEKEMQR ILLNSERLKS RIAEIHESRT KLEQQLRAQA SDNREIDKRM
       570        580        590        600        610        620        630        640
NSLKPDLMQL RKIRDQYLVW LTQKGARQKK INEWLGIKNE TEDQYALMED EDDLPHHEER TWYVGKINRT QAEEMLSGKR
       650        660        670        680        690        700        710        720
DGTFLIRESS QRGCYACSVV VDGDTKHCVI YRTATGFGFA EPYNLYGSLK ELVLHYQHAS LVQHNDALTV TLAHPVRAPG
       730
PGPPPAAR
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
261	1	530.4911	-164.00	3	32.4	13.8	0	50-63	R.CPQSVGWMPGLNER.T	Oxidation: 8

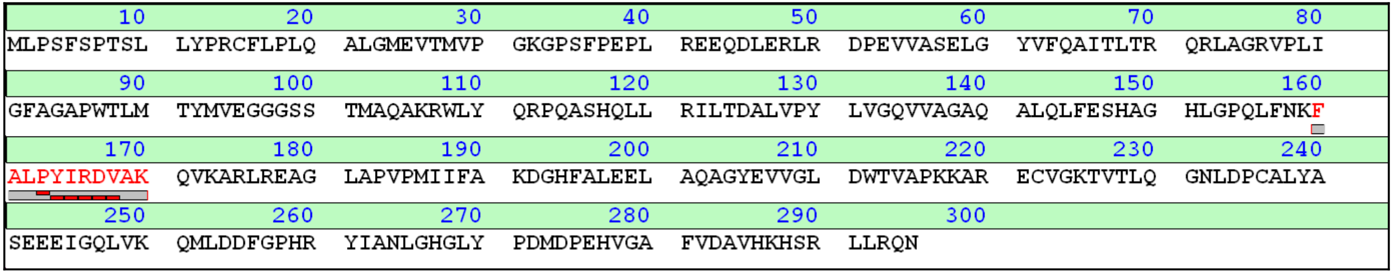
Detailed Protein Report

Protein 1076: PREDICTED: uroporphyrinogen decarboxylase isoform X2 [Homo sapiens]

Accession:	gi|530363258	**Score:**	13.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	32.6
Database Date:	2015-11-30	**pI:**	6.6
		Sequence Coverage [%]:	3.7
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530363260	refseq_human(refseq_human_20140103.fasta)	PREDICTED: uroporphyrinogen decarboxylase isoform X3 [Homo sapiens]



10	20	30	40	50	60	70	80
MLPSFSPTSL	LYPRCFLPLQ	ALGMEVTMVP	GKGPSFPEPL	REEQDLERLR	DPEVVASELG	YVFQAITLTR	QRLAGRVPLI
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
GFAGAPWTLM	TYMVEGGGSS	TMAQAKRWLY	QRPQASHQLL	RILTDALVPY	LVGQVVAGAQ	ALQLFESHAG	HLGPQLFNKF
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
ALPYIRDVAK	QVKARLREAG	LAPVPMIIFA	KDGHFALEEL	AQAGYEVVGL	DWTVAPKKAR	ECVGKTVTLQ	GNLDPCALYA
250	**260**	**270**	**280**	**290**	**300**		
SEEEIGQLVK	QMLDDFGPHR	YIANLGHGLY	PDMDPEHVGA	FVDAVHKHSR	LLRQN		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1090	1	646.7958	-117.34	2	42.3	13.8	1	160-170	K.FALPYIRDVAK.Q	

Detailed Protein Report

Protein 1077: PREDICTED: zinc finger protein 789 isoform X1 [Homo sapiens]

Accession:	gi|530385765	**Score:**	13.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	49.2
Database Date:	2015-11-30	**pI:**	10.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MELLSFEDVA	MYFTREEWGH	LNWGQKDLYR	DVMLENYRNM	VLLGFQFPKP	EMICQLENWD	EQWILDLPRT	GNRKASGSAC
90	100	110	120	130	140	150	160
PGSEARHKMK	KLTPKQKFSE	DLESYKISVV	MQESAEKLSE	KLHKCKEFVD	SCRLTFPTSG	DEYSRGFLQN	LNLIQDQNAQ
170	180	190	200	210	220	230	240
TRWKQGRYDE	DGKPFNQRSL	LLGHERILTR	AKSYECSECG	KVIRRKAWFD	QHQRIHFLEN	PFECKVCGQA	FRQRSALTVH
250	260	270	280	290	300	310	320
KQCHLQNKPY	RCHDCGKCFR	QLAYLVEHKR	IHTKEKPYKC	SKCEKTFSQN	STLIRHQVIH	SGEKRHKCLE	CGKAFGRHST
330	340	350	360	370	380	390	400
LLCHQQIHSK	PNTHKCSECG	QSFGRNVDLI	QHQRIHTKEE	FFQCGECGKT	FSFKRNLFRH	QVIHTGSQPY	QCVICGKSFK
410	420						
WHTSFIKHQG	THKGQIST						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2129	1	707.7420	-121.78	2	55.2	13.8	1	75-88	K.ASGSACPGSEARHK.M	Carbamidomethyl: 6

Detailed Protein Report

Protein 1078: 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 1079: tumor necrosis factor receptor superfamily member 1A precursor [Homo sapiens]

Accession:	gi|4507575	**Score:**	13.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	50.5
Database Date:	2015-11-30	**pI:**	6.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.0
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MGLSTVPDLL LPLVLLELLV GIYPSGVIGL VPHLGDREKR DSVCPQGKYI HPQNNSICCT KCHKGTYLYN DCPGPGQDTD
        90        100        110        120        130        140        150        160
CRECESGSFT ASENHLRHCL SCSKCRKEMG QVEISSCTVD RDTVCGCRKN QYRHYWSENL FQCFNCSLCL NGTVHLSCQE
       170        180        190        200        210        220        230        240
KQNTVCTCHA GFFLRENECV SCSNCKKSLE CTKLCLPQIE NVKGTEDSGT TVLLPLVIFF GLCLLSLLFI GLMYRYQRWK
       250        260        270        280        290        300        310        320
SKLYSIVCGK STPEKEGELE GTTTKPLAPN PSFSPTPGFT PTLGFSPVPS STFTSSSTYT PGDCPNFAAP RREVAPPYQG
       330        340        350        360        370        380        390        400
ADPILATALA SDPIPNPLQK WEDSAHKPQS LDTDDPATLY AVVENVPPLR WKEFVRRLGL SDHEIDRLEL QNGRCLREAQ
       410        420        430        440        450        460
YSMLATWRRR TPRREATLEL LGRVLRDMDL LGCLEDIEEA LCGPAALPPA PSLLR
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1608	1	1045.0366	108.79	2	48.8	13.8	0	65-82	K.GTYLYNDCPGPGQDTDCR.E	Carbamidomethyl: 8, 17

Detailed Protein Report

Protein 1080: **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 1081: protein FAM117B [Homo sapiens]

Accession:	gi|254910983	**Score:**	13.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	61.9
Database Date:	2015-11-30	**pI:**	10.8
		Sequence Coverage [%]:	5.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSQRVRRNGS	PTPAGSLGGG	AVATAGGPGS	RLQPMRATVP	FQLKQQQQQQ	HGSPTRSGGG	GGGNNNGGCC	GGASGPAGGG
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
GGGGPRTASR	STSPTRGGGN	AAARTSPTVA	TQTGASATST	RGTSPTRSAA	PGARGSPPRP	PPPPPLLGTV	SSPSSSPTHL
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
WTGEVSAAPP	PARVRHRRRS	PEQSRSSPEK	RSPSAPVCKA	GDKTRQPSSS	PSSIIRRTSS	LDTLAAPYLA	GHWPRDSHGQ
250	**260**	**270**	**280**	**290**	**300**	**310**	**320**
AAPCMRDKAT	QTESAWAEEY	SEKKKGSHKR	SASWGSTDQL	KEIAKLRQQL	QRSKHSSRHH	RDKERQSPFH	GNHAAINQCQ
330	**340**	**350**	**360**	**370**	**380**	**390**	**400**
APVPKSALIP	VIPITKSTGS	RFRNSVEGLN	QEIEIIIKET	GEKEEQLIPQ	DIPDGHRAPP	PLVQRSSSTR	SIDTQTPGGA
410	**420**	**430**	**440**	**450**	**460**	**470**	**480**
DRGSNNSSRS	QSVSPTSFLT	ISNEGSEESP	CSADDLLVDP	RDKENGNNSP	LPKYATSPKP	NNSYMFKREP	PEGCERVKVF
490	**500**	**510**	**520**	**530**	**540**	**550**	**560**
EECSPKQLHE	IPAFYCPDKN	KVNFIPKSGS	AFCLVSILKP	LLPTPDLTLK	GSGHSLTVTT	GMTTTLLQPI	AVASLSTNTE
570	**580**	**590**					
QDRVSRGTST	VMPSASLLPP	PEPIEEAEG					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2286	2	753.8859	-111.92	3	57.0	13.8	0	57-86	R.SGGGGGGNNNGGCCGGASGPAGGGGGGGPR.T	

Detailed Protein Report

Protein 1082: 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 1083: 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

mdown:qdown	**Median:**	7.99	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.15	**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		Wdown:Qdown 0.15

Detailed Protein Report

Protein 1084: 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 1085: unconventional myosin-Ie [Homo sapiens]

Accession:	gi|55956916	**Score:**	13.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	127.0
Database Date:	2015-11-30	**pI:**	9.5
		Sequence Coverage [%]:	0.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGSKGVYQYH	WQSHNVKHSG	VDDMVLLSKI	TENSIVENLK	KRYMDDYIFT	YIGSVLISVN	PFKQMPYFGE	KEIEMYQGAA
90	100	110	120	130	140	150	160
QYENPPHIYA	LADNMYRNMI	IDRENQCVII	SGESGAGKTV	AAKYIMSYIS	RVSGGGTKVQ	HVKDIILQSN	PLLEAFGNAK
170	180	190	200	210	220	230	240
TVRNNNSSRF	GKYFEIQFSP	GGEPDGGKIS	NFLLEKSRVV	MRNPGERSFH	IFYQLIEGAS	AEQKHSLGIT	SMDYYYYLSL
250	260	270	280	290	300	310	320
SGSYKVDDID	DRREFQETLH	AMNVIGIFAE	EQTLVLQIVA	GILHLGNISF	KEVGNYAAVE	SEEFLAFPAY	LLGINQDRLK
330	340	350	360	370	380	390	400
EKLTSRQMDS	KWGGKSESIH	VTLNVEQACY	TRDALAKALH	ARVFDFLVDS	INKAMEKDHE	EYNIGVLDIY	GFEIFQKNGF
410	420	430	440	450	460	470	480
EQFCINFVNE	KLQQIFIELT	LKAEQEEYVQ	EGIRWTPIEY	FNNKIVCDLI	ENKVNPPGIM	SILDDVCATM	HAVGEGADQT
490	500	510	520	530	540	550	560
LLQKLQMQIG	SHEHFNSWNQ	GFIIHHYAGK	VSYDMDGFCE	RNRDVLFMDL	IELMQSSELP	FIKSLFPENL	QADKKGRPTT
570	580	590	600	610	620	630	640
AGSKIKKQAN	DLVSTLMKCT	PHYIRCIKPN	ETKKPRDWEE	SRVKHQVEYL	GLKENIRVRR	AGYAYRRIFQ	KFLQRYAILT
650	660	670	680	690	700	710	720
KATWPSWQGE	EKQGVLHLLQ	SVNMDSDQFQ	LGRSKVFIKA	PESLFLLEEM	RERKYDGYAR	VIQKSWRKFV	ARKKYVQMRE
730	740	750	760	770	780	790	800
EASDLLLNKK	ERRRNSINRN	FIGDYIGMEE	HPELQQFVGK	REKIDFADTV	TKYDRRFKGV	KRDLLLTPKC	LYLIGREKVK
810	820	830	840	850	860	870	880
QGPDKGLVKE	VLKRKIEIER	ILSVSLSTMQ	DDIFILHEQE	YDSLLESVFK	TEFLSLLAKR	YEEKTQKQLP	LKFSNTLELK
890	900	910	920	930	940	950	960
LKKENWGPWS	AGGSRQVQFH	QGFGDLAVLK	PSNKVLQVSI	GPGLPKNSRP	TRRNTTQNTG	YSSGTQNANY	PVRAAPPPPG
970	980	990	1000	1010	1020	1030	1040
YHQNGVIRNQ	YVPYPHAPGS	QRSNQKSLYT	SMARPPLPRQ	QSTSSDRVSQ	TPESLDFLKV	PDQGAAGVRR	QTTSRPPPAG
1050	1060	1070	1080	1090	1100	1110	
GRPKPQPKPK	PQVPQCKALY	AYDAQDTDEL	SFNANDIIDI	IKEDPSGWWT	GRLRGKQGLF	PNNYVTKI	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2732	1	626.8302	-70.22	2	62.6	13.7	1	632-641	K.FLQRYAILTK.A	

Detailed Protein Report

Protein 1086: **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 1087: **PREDICTED: nuclear receptor subfamily 2 group C member 2 isoform X1 [Homo sapiens]**

Accession:	gi|530373071	**Score:**	13.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	65.4
Database Date:	2015-11-30	**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
1400	2	695.9396	-46.71	2	46.3	13.7	2	540-551	R.LARILVRLPALR.L	

Detailed Protein Report

Protein 1088: pappalysin-2 isoform 2 precursor [Homo sapiens]

Accession:	gi|116174734	**Score:**	13.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	92.1
Database Date:	2015-11-30	**pI:**	5.9
		Sequence Coverage [%]:	1.5
		No. of unique Peptides:	1

Quantitation

Wdown:Qdown **Median:** 1.00 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MMCLKILRIS	LAILAGWALC	SANSELGWTR	KKSLVEREHL	NQVLLEGERC	WLGAKVRRPR	ASPQHHLFGV	YPSRAGNYLR
90	100	110	120	130	140	150	160
PYPVGEQEIH	HTGRSKPDTE	GNAVSLVPPD	LTENPAGLRG	AVEEPAAPWV	GDSPIGQSEL	LGDDDAYLGN	QRSKESLGEA
170	180	190	200	210	220	230	240
GIQKGSAMAA	TTTTAIFTTL	NEPKPETQRR	GWAKSRQRRQ	VWKRRAEDGQ	GDSGISSHFQ	PWPKHSLKHR	VKKSPPEESN
250	260	270	280	290	300	310	320
QNGGEGSYRE	AETFNSQVGL	PILYFSGRRE	RLLLRPEVLA	EIPREAFTVE	AWVKPEGGQN	NPAIIAGVFD	NCSHTVSDKG
330	340	350	360	370	380	390	400
WALGIRSGKD	KGKRDARFFF	SLCTDRVKKA	TILISHSRYQ	PGTWTHVAAT	YDGRHMALYV	DGTQVASSLD	QSGPLNSPFM
410	420	430	440	450	460	470	480
ASCRSLLLGG	DSSEDGHYFR	GHLGTLVFWS	TALPQSHFQH	SSQHSSGEEE	ATDLVLTASF	EPVNTEWVPF	RDEKYPRLEV
490	500	510	520	530	540	550	560
LQGFEPEPEI	LSPLQPPLCG	QTVCDNVELI	SQYNGYWPLR	GEKVIRYQVV	NICDDEGLNP	IVSEEQIRLQ	HEALNEAFSR
570	580	590	600	610	620	630	640
YNISWQLSVH	QVHNSTLRHR	VVLVNCEPSK	IGNDHCDPEC	EHPLTGYDGG	DCRLQGRCYS	WNRRDGLCHV	ECNNMLNDFD
650	660	670	680	690	700	710	720
DGDCCDPQVA	DVRKTCFDPD	SPKRAYMSVK	ELKEALQLNS	THFLNIYFAS	SVREDLAGAA	TWPWDKDAVT	HLGGIVLSPA
730	740	750	760	770	780	790	800
YYGMPGHTDT	MIHEVGHVLG	LYHVFKGVSE	RESCNDPCKE	TVPSMETGDL	CADTAPTPKS	ELCREPEPTS	DTCGFTRFPG
810	820	830					
APFTNYMSYT	GITTVLFCFL	LRIHGGL					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
817	2	676.8688	-78.92	2	38.7	13.7	2	347-358	R.VKKATILISHSR.Y		Wdown:Qdown 1.00

Detailed Protein Report

Protein 1089: chromobox protein homolog 5 [Homo sapiens]

Accession:	gi|6912292	**Score:**	13.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	22.2
Database Date:	2015-11-30	**pI:**	5.6
		Sequence Coverage [%]:	4.7
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|188035910	refseq_human(refseq_human_20140103.fasta)	chromobox protein homolog 5 [Homo sapiens]
gi|188035908	refseq_human(refseq_human_20140103.fasta)	chromobox protein homolog 5 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MGKKTKRTAD SSSSEDEEEY VVEKVLDRRV VKGQVEYLLK WKGFSEEHNT WEPEKNLDCP ELISEFMKKY KKMKEGENNK
        90        100        110        120        130        140        150        160
PREKSESNKR KSNFSNSADD IKSKKKREQS NDIARGFERG LEPEKIIGAT DSCGDLMFLM KWKDTDEADL VLAKEANVKC
       170        180        190        200
PQIVIAFYEE RLTWHAYPED AENKEKETAK S
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
403	1	544.7625	-24.48	2	34.1	13.7	1	107-115	K.REQSNDIAR.G	

Detailed Protein Report

Protein 1090: PREDICTED: transcription factor SPT20 homolog isoform X22 [Homo sapiens]

Accession:	gi|530402530	**Score:**	13.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	60.2
Database Date:	2015-11-30	**pI:**	9.1
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.7
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	0.43	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.88	**CV:**	0.00 %	**No. of Peptides:**	1

10	20	30	40	50	60	70	80
MQQALELALD	RAEYVIESAR	QRPPKRKYLS	SGRKSVFQKL	YDLYIEECEK	EPEVKQKLRR	NVNLLEKLVM	QETLSCLVVN
90	100	110	120	130	140	150	160
LYPGNEGYSL	MLRGKNGSDS	ETIRLPYEEG	ELLEYLDAEE	LPPILVDLLE	KSQVNIFHCG	CVIAEIRDYR	QSSNMKSPGY
170	180	190	200	210	220	230	240
QSRHILLRPT	MQTLICDVHS	ITSDNHKWTQ	EDKLLLESQL	ILATAEPLCL	DPSIAVTCTA	NRLLYNKQKM	NTRPMKRCFK
250	260	270	280	290	300	310	320
RYSRSSLNRQ	QDLSHCPPPP	QLRLLDFLQK	RKERKAGQHY	DLKISKAGNC	VDMWKRSPCN	LAIPSEVDVE	KYAKVEKSIK
330	340	350	360	370	380	390	400
SDDSQPTVWP	AHDVKDDYVF	ECEAGTQYQK	TKLTILQSLG	DPLYYGKIQP	CKADEESDSQ	MSPSHSSTDD	HSNWFIIGSK
410	420	430	440	450	460	470	480
TDAERVVNQY	QELVQNEAKC	PVKMSHSSSG	SASLSQVSPG	KETDQTETVS	VQSSVLGKGV	KHRPPPIKLP	SSSGNSSSGN
490	500	510	520	530	540		
YFTPQQTSSF	LKSPTPPPSS	KPSSIPRKSS	VDLNQVSMLS	PAALSPASSS	QRHES		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
394	1	572.8091	92.30	2	34.0	13.7	1	148-156	R.DYRQSSNMK.S	Oxidation: 8	Wdown:Qdown 0.88 mdown:qdown 0.43

Detailed Protein Report

Protein 1091: PREDICTED: zinc finger protein 831 isoform X4 [Homo sapiens]

Accession:	gi|530417824	**Score:**	13.7
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
1918	3	1023.8682	-115.79	2	52.7	13.7	1	258-276	K.NLDVRTEAAPCPGSAFADR.E	Carbamidomethyl: 11

Detailed Protein Report

Protein 1092: zinc finger protein 624 [Homo sapiens]

Accession:	gi|172072608	**Score:**	13.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	99.9
Database Date:	2015-11-30	**pI:**	10.1
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.3
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578830001	refseq_human (refseq_human_20140103.fasta)	PREDICTED: zinc finger protein 624 isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MSLQDSTLSR	EGKPEGEIMA	AVFFSVGRLS	PEVTQPDEDL	HLQAEETQLV	KESVTFKDVA	IDFTLEEWRL	MDPTQRNLHK
90	100	110	120	130	140	150	160
DVMLENYRNL	VSLGLAVSKP	DMISHLENGK	GPWVTVREIS	RIPYPDMEPK	PATKKATRTK	AISEDLSQEA	ILEKLTENGL
170	180	190	200	210	220	230	240
WDSRMEGLWK	WNDRILRLQN	NQENHLSQRI	IPLKKTPTSQ	RGFRFESILI	PEPGIATEEL	HSRCQTQEEN	FTENLNLITD
250	260	270	280	290	300	310	320
THLGKIICKE	MKGSKAIRQT	SELTLGKKSN	NKEKPYKCST	CEKAFHYRSL	LIQHQRTHTK	EKPYECNECG	KTFSQPSYLS
330	340	350	360	370	380	390	400
QHKKIHTGEK	PYKCNECGKA	FIASSSLMVH	QRIHTKEKPY	QCNVCGKSFS	QCARLNQHQR	IQTGEKPYKC	SECGKAFSDK
410	420	430	440	450	460	470	480
SKLARHQETH	NGEKPYKCDD	CGKAFRNKSY	LSVHQKTHTE	EKPYQCNECG	KSFKNTTIFN	VHQRIHTGEK	PFRCNECGKA
490	500	510	520	530	540	550	560
YRSNSSLIVH	IRTHTGEKPY	ECNECGKAFN	RIANFTEHQR	IHTGEKPYKC	NECGKAFINY	SCLTVHHRMH	TGEKPYKCTE
570	580	590	600	610	620	630	640
CGKAFMRSSS	LIIHQRIHTE	EKPYLCNECG	ESFRIKSHLT	VHQRIHTGEK	PYKCTDCERA	FTKMVNLKEH	QKIHTGVKPY
650	660	670	680	690	700	710	720
KCYDCGKSFR	TKSYLIVHQR	THTGEKPYKC	NECEKAFTNT	SQLTVHQRRH	TGEKPYKCNE	CGKVFTSNSG	FNTHQRTHTG
730	740	750	760	770	780	790	800
EKPFKCNDCG	KAFSQMVHVT	EHQKIHSGEK	PYKCDVCGKA	FRRGSYLTVH	WRTHTGEKPY	TCKECGKGCI	TLSQLTLHQR
810	820	830	840	850	860	870	
IHTGERPYKC	EECGKAFRTN	SDFTVHLRMH	TGEKPYKCNE	CGKAFRSSSS	LTVHQRIHQR	ETQLI	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2758	1	701.4193	162.16	2	62.9	13.7	1	278-288	K.CSTCEKAFHYR.S	Carbamidomethyl: 1

Detailed Protein Report

Protein 1093: 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 1094: electroneutral sodium bicarbonate exchanger 1 isoform c [Homo sapiens]

Accession: gi|385719213
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 13.6
MW [kDa]: 117.1
pI: 6.5
Sequence Coverage [%]: 1.5
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MPLGRQSHRH	HRTHGQKHRR	RGRGKGASQG	EEGLEALAHD	TPSQRVQFIL	GTEEDEEHVP	HELFTELDEI	CMKEGEDAEW
90	100	110	120	130	140	150	160
KETARWLKFE	EDVEDGGERW	SKPYVATLSL	HSLFELRSCL	INGTVLLDMH	ANSIEEISDL	ILDQQELSSD	LNDSMRVKVR
170	180	190	200	210	220	230	240
EALLKKHHHQ	NEKKRNNLIP	IVRSFAEVGK	KQSDPHLMDK	HGQTVSPQSV	PTTNLEVKNG	VNCEHSPVDL	SKVDLHFMKK
250	260	270	280	290	300	310	320
IPTGAEASNV	LVGEVDILDR	PIVAFVRLSP	AVLLSGLTEV	PIPTRFLFIL	LGPVGKGQQY	HEIGRSMATI	MTDEIFHDVA
330	340	350	360	370	380	390	400
YKAKERDDLL	AGIDEFLDQV	TVLPPGEWDP	SIRIEPPKNV	PSQEKRKMPG	VPNGNVCHIE	QEPHGGHSGP	ELQRTGRLFG
410	420	430	440	450	460	470	480
GLVLDIKRKA	PWYWSDYRDA	LSLQCLASFL	FLYCACMSPV	ITFGGLLGEA	TEGRISAIES	LFGASMTGIA	YSLFAGQALT
490	500	510	520	530	540	550	560
ILGSTGPVLV	FEKILFKFCK	DYALSYLSLR	ACIGLWTAFL	CIVLVATDAS	SLVCYITRFT	EEAFASLICI	IFIYEAIEKL
570	580	590	600	610	620	630	640
IHLAETYPIH	MHSQLDHLSL	YYCRCTLPEN	PNNHTLQYWK	DHNIVTAEVH	WANLTVSECQ	EMHGEFMGSA	CGHHGPYTPD
650	660	670	680	690	700	710	720
VLFWSCILFF	TTFILSSTLK	TFKTSRYFPT	RVRSMVSDFA	VFLTIFTMVI	IDFLIGVPSP	KLQVPSVFKP	TRDDRGWIIN
730	740	750	760	770	780	790	800
PIGPNPWWTV	IAAIIPALLC	TILIFMDQQI	TAVIINRKEH	KLKKGCGYHL	DLLMVAIMLG	VCSIMGLPWF	VAATVLSITH
810	820	830	840	850	860	870	880
VNSLKLESEC	SAPGEQPKFL	GIREQRVTGL	MIFVLMGCSV	FMTAILKFIP	MPVLYGVFLY	MGVSSLQGIQ	FFDRLKLFGM
890	900	910	920	930	940	950	960
PAKHQPDFIY	LRHVPLRKVH	LFTLIQLTCL	VLLWVIKASP	AAIVFPMMVL	ALVFVRKVMD	LCFSKRELSW	LDDLMPESKK
970	980	990	1000	1010	1020	1030	1040
KKLDDAKKKA	KEEEEAEKML	EIGGDKFPLE	SRKLLSSPGK	NISCRCDPSE	INISDEMPKT	TVWKALSMNS	GNAKEKSLFN
1050							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2993	1	863.9668	48.28	2	66.2	13.6	2	1025-1040	K.ALSMNSGNAKEKSLFN.-	Oxidation: 4

Detailed Protein Report

Protein 1095: leucine-rich repeat transmembrane neuronal protein 2 precursor [Homo sapiens]

Accession:	gi|7662102	**Score:**	13.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	59.0
Database Date:	2015-11-30	**pI:**	9.4
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	3.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGLHFKWPLG	APMLAAIYAM	SMVLKMLPAL	GMACPPKCRC	EKLLFYCDSQ	GFHSVPNATD	KGSLGLSLRH	NHITELERDQ
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
FASFSQLTWL	HLDHNQISTV	KEDAFQGLYK	LKELILSSNK	IFYLPNTTFT	QLINLQNLDL	SFNQLSSLHP	ELFYGLRKLQ
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
TLHLRSNSLR	TIPVRLFWDC	RSLEFLDLST	NRLRSLARNG	FAGLIKLREL	HLEHNQLTKI	NFAHFLRLSS	LHTLFLQWNK
250	**260**	**270**	**280**	**290**	**300**	**310**	**320**
ISNLTCGMEW	TWGTLEKLDL	TGNEIKAIDL	TVFETMPNLK	ILLMDNNKLN	SLDSKILNSL	RSLTTVGLSG	NLWECSARIC
330	**340**	**350**	**360**	**370**	**380**	**390**	**400**
ALASWLGSFQ	GRWEHSILCH	SPDHTQGEDI	LDAVHGFQLC	WNLSTTVTVM	ATTYRDPTTE	YTKRISSSSY	HVGDKEIPTT
410	**420**	**430**	**440**	**450**	**460**	**470**	**480**
AGIAVTTEEH	FPEPDNAIFT	QRVITGTMAL	LFSFFFIIFI	VFISRKCCPP	TLRRIRQCSM	VQNHRQLRSQ	TRLHMSNMSD
490	**500**	**510**	**520**				
QGPYNEYEPT	HEGPFIIING	YGQCKCQQLP	YKECEV				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1679	1	1022.9863	-10.91	2	49.7	13.6	2	457-472	R.QCSMVQNHRQLRSQTR.L	Carbamidomethyl: 2; Oxidation: 4

Detailed Protein Report

Protein 1096: beta-1,3-galactosyltransferase 5 isoform a [Homo sapiens]

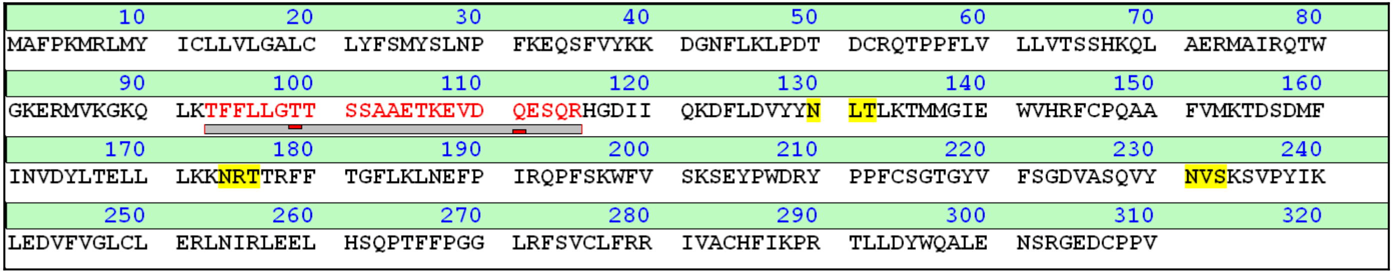
Accession:	gi|5174397	**Score:**	13.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	36.2
Database Date:	2015-11-30	**pI:**	9.8
		Sequence Coverage [%]:	7.4
		No. of unique Peptides:	1

Quantitation

mdown:qdown **Median:** 0.86 **CV:** 0.00 % **No. of Peptides:** 1

Alias proteins:

Accession	**Name**	**Description**
gi|530418764	refseq_human (refseq_human_20140103.fasta)	PREDICTED: beta-1,3-galactosyltransferase 5 isoform X1 [Homo sapiens]
gi|520975380	refseq_human (refseq_human_20140103.fasta)	beta-1,3-galactosyltransferase 5 isoform a [Homo sapiens]
gi|15451883	refseq_human (refseq_human_20140103.fasta)	beta-1,3-galactosyltransferase 5 isoform a [Homo sapiens]
gi|15451881	refseq_human (refseq_human_20140103.fasta)	beta-1,3-galactosyltransferase 5 isoform a [Homo sapiens]



10	20	30	40	50	60	70	80
MAFPKMRLMY	ICLLVLGALC	LYFSMYSLNP	FKEQSFVYKK	DGNFLKLPDT	DCRQTPPFLV	LLVTSSHKQL	AERMAIRQTW
90	100	110	120	130	140	150	160
GKERMVKGKQ	LKTFFLLGTT	SSAAETKEVD	QESQRHGDII	QKDFLDVYYN	LTLKTMMGIE	WVHRFCPQAA	FVMKTDSDMF
170	180	190	200	210	220	230	240
INVDYLTELL	LKKNRTTRFF	TGFLKLNEFP	IRQPFSKWFV	SKSEYPWDRY	PPFCSGTGYV	FSGDVASQVY	NVSKSVPYIK
250	260	270	280	290	300	310	320
LEDVFVGLCL	ERLNIRLEEL	HSQPTFFPGG	LRFSVCLFRR	IVACHFIKPR	TLLDYWQALE	NSRGEDCPPV	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2183	1	848.9946	-106.93	3	55.9	13.6	1	93-115	K. TFFLLGTTSSAAETKEVDQESQR. H		mdown:qdown 0.86

Detailed Protein Report

Protein 1097: PREDICTED: cysteine and glycine-rich protein 2 isoform X2 [Homo sapiens]

Accession:	gi|578823362	**Score:**	13.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	26.7
Database Date:	2015-11-30	**pI:**	10.1
		Sequence Coverage [%]:	7.8
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578823364	refseq_human (refseq_human_20140103.fasta)	PREDICTED: cysteine and glycine-rich protein 2 isoform X3 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MPVWGGGNKC GACGRTVYHA EEVQCDGRSF HRCCFLCMVC RKNLDSTTVA IHDEEIYCKS CYGKKYGPKG YGYGQGAGTL
        90        100        110        120        130        140        150        160
NMDRGERLGI KPESIPSCIK ESCSQKQVIC IYFNFTAPWR PDVMKLNGRE MCCVNHERCF SCAIVQPHRP TTNPNTSKFA
       170        180        190        200        210        220        230        240
QKYGGAEKCS RCGDSVYAAE KIIGAGKPWH KNCFRCAKCG KSLESTTLTE KEGEIYCKGC YAKNFGPKGF GYGQGAGALV
       250
HAQ
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1763	1	1023.8887	-139.71	2	52.0	13.6	1	88-106	R.LGIKPESIPSCIKESCSQK.Q	

Detailed Protein Report

Protein 1098: **PREDICTED: uncharacterized aarF domain-containing protein kinase 1 isoform X2 [Homo sapiens]**

Accession:	gi|530404248	**Score:**	13.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	52.0
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
MARKALKLAS	WTSMALAASG	IYFYSNKYLD	PNDFGAVRVG	RAVATTAVIS	YDYLTSLKSV	PYGSEEYLQL	RSKVHLRSAR
90	100	110	120	130	140	150	160
RLCELCCANR	GTFIKVGQHL	GALDYLLPEE	YTSTLKVLHS	QAPQSSMQEI	RQVIREDLGK	EIHDLFQSFD	DTPLGTASLA
170	180	190	200	210	220	230	240
QVHKAVLHDG	RTVAVKVQHP	KVRAQSSKDI	LLMEVLVLAV	KQLFPEFEFM	WLVDEAKKNL	PLELDFLNEG	RNAEKVSQML
250	260	270	280	290	300	310	320
RHFDFLKVPR	IHWDLSTERV	LLMEFVDGGQ	VNDRDYMERN	KIDVNEISRH	LGKMYSEMIF	VNGFVHCDPH	PGNVLVRKHP
330	340	350	360	370	380	390	400
GTGKAEIVLL	DHGLYQDLEI	RNNAANYLPQ	ISHLLNHVPR	QMLLILKTND	LLRGIEAALG	TRASASSFLN	MSRCCIRALA
410	420	430	440	450	460		
EHKKKNTCSF	FRRTQISFSE	AFNLWQINLH	ELILRVKGLK	LADRVLALIC	WLFPAPL		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2197	1	863.8529	-90.52	2	56.0	13.6	2	81-95	R.RLCELCCANRGTFIK.V	

Detailed Protein Report

Protein 1099: **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 1100: PREDICTED: F-box only protein 4 isoform X1 [Homo sapiens]

Accession:	gi|530378774	**Score:**	13.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	34.6
Database Date:	2015-11-30	**pI:**	6.5
		Sequence Coverage [%]:	2.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAGSEPRSGT	NSPPPPFSDW	GRLEAAILSG	WKTFWQSVSK	ERVARTTSRE	EVDEAASTLT	RLPIDVQLYI	LSFLSPHDLC
90	100	110	120	130	140	150	160
QLGSTNHYWN	ETVRDPILWR	YFLLRDLPSW	SSVDWKSLPD	LEILKKPISE	VTDGAFFDYM	AVYRMCCPYT	RRASKSSRPM
170	180	190	200	210	220	230	240
YGAVTSFLHS	LIIQNEPRFA	MFGPGLEELN	TSLVLSLMSS	EELCPTAGLP	QRQIDGIGSG	VNFQLNNQHK	FNILILYSTT
250	260	270	280	290	300	310	
RKERDRAREE	HTSAVNKMFS	RHNEGDDQQG	SRYSVIPQIQ	KVCEVVDGFI	YVANAEAHKS	PGYRG	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1192	1	491.6248	-261.20	2	43.4	13.6	0	33-40	K.TFWQSVSK.E	

Detailed Protein Report

Protein 1101: uncharacterized protein C2orf54 isoform 2 [Homo sapiens]

Accession:	gi|544710097	**Score:**	13.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	30.9
Database Date:	2015-11-30	**pI:**	9.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	4.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDTGSLNAAS	LREEQLHLSL	LVSSGWRTIS	FHVVPVVRRK	LGAPALEGVQ	QMPGFPEGSL	RRILSQGVDL	VPASAQLWRT
90	100	110	120	130	140	150	160
STDYLLTRLL	GELGSLQGHR	LDSLSILDRV	NHESWRDSGQ	TDGLTFGHLK	MVLLWASVLF	PAPEDWAELQ	GAVYRLLVVL
170	180	190	200	210	220	230	240
LCCLATRKLP	HFLHPQRNLL	QGSGLDLGAI	YQRVEGFASQ	PEAALRIHAT	HLGRSPPPRI	GSGLKALLQL	PASDPTYWAT
250	260	270	280				
AYFDVLLDKF	QVFNIQDKDR	ISAMQSIFQK	TRTLGGEES				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
914	1	626.3206	27.28	2	40.2	13.5	0	1-12	-.MDTGSLNAASLR.E	Oxidation: 1

Detailed Protein Report

Protein 1102: multiple epidermal growth factor-like domains protein 11 precursor [Homo sapiens]

Accession:	gi|181336739	**Score:**	13.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	110.8
Database Date:	2015-11-30	**pI:**	5.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MVLSLTGLIA	FSFLQATLAL	NPEDPNVCSH	WESYAVTVQE	SYAHPFDQIY	YTRCTDILNW	FKCTRHRISY	KTAYRRGLRT
90	100	110	120	130	140	150	160
MYRRRSQCCP	GYYESGDFCI	PLCTEECVHG	RCVSPDTCHC	EPGWGGPDCS	SGCDSDHWGP	HCSNRCQCQN	GALCNPITGA
170	180	190	200	210	220	230	240
CVCAAGFRGW	RCEELCAPGT	HGKGCQLPCQ	CRHGASCDPR	AGECLCAPGY	TGVYCEELCP	PGSHGAHCEL	RCPCQNGGTC
250	260	270	280	290	300	310	320
HHITGECACP	PGWTGAVCAQ	PCPPGTFGQN	CSQDCPCHHG	GQCDHVTGQC	HCTAGYMGDR	CQEECPFGSF	GFQCSQHCDC
330	340	350	360	370	380	390	400
HNGGQCSPTT	GACECEPGYK	GPRCQERLCP	EGLHGPGCTL	PCPCDADNTI	SCHPVTGACT	CQPGWSGHHC	NESCPVGYYG
410	420	430	440	450	460	470	480
DGCQLPCTCQ	NGADCHSITG	GCTCAPGFMG	EVCAVSCAAG	TYGPNCSSIC	SCNNGGTCSP	VDGSCTCKEG	WQGLDCTLPC
490	500	510	520	530	540	550	560
PSGTWGLNCN	ESCTCANGAA	CSPIDGSCSC	TPGWLGDTCE	LPCPDGTFGL	NCSEHCDCSH	ADGCDPVTGH	CCCLAGWTGI
570	580	590	600	610	620	630	640
RCDSTCPPGR	WGPNCSVSCS	CENGGSCSPE	DGSCECAPGF	RGPLCQRICP	PGFYGHGCAQ	PCPLCVHSSR	PCHHISGICE
650	660	670	680	690	700	710	720
CLPGFSGALC	NQVCAGGYFG	QDCAQLCSCA	NNGTCSPIDG	SCQCFPGWIG	KDCSQACPPG	FWGPACFHAC	SCHNGASCSA
730	740	750	760	770	780	790	800
EDGACHCTPG	WTGLFCTQRC	PAAFFGKDCG	RVCQCQNGAS	CDHISGKCTC	RTGFTGQHCE	QRCAPGTFGY	GCQQLCECMN
810	820	830	840	850	860	870	880
NSTCDHVTGT	CYCSPGFKGI	RCDQAALMME	ELNPYTKISP	ALGAERHSVG	AVTGIMLLLF	LIVVLLGLFA	WHRRRQKEKG
890	900	910	920	930	940	950	960
RDLAPRVSYT	PAMRMTSTDY	SLSGACGMDR	RQNTYIMDKG	FKDYMKESVC	SSSTCSLNSS	ENPYATIKDP	PILTCKLPES
970	980	990	1000	1010	1020	1030	1040
SYVEMKSPVH	MGSPYTDVPS	LSTSNKNIYE	VEPTVSVVQE	GCGHNSSYIQ	NAYDLPRNSH	IPGHYDLLPV	RQSPANGPSQ
1050							
DKQS							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2524	1	821.0832	83.31	3	59.8	13.5	1	172-192	R.CEELCAPGTHGKGCQLPCQCR.H	Carbamidomethyl: 5, 14, 18, 20

Protein 1103: V-type proton ATPase subunit G 2 isoform c [Homo sapiens]

Accession:	gi|323276655	**Score:**	13.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	8.9
Database Date:	2015-11-30	**pI:**	12.4
Modification(s):	Oxidation	**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 1104: 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

Detailed Protein Report

Protein 1105: 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 1106: 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 1107: methyl-CpG-binding domain protein 4 isoform 4 [Homo sapiens]

Accession:	gi|442796454	**Score:**	13.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	60.9
Database Date:	2015-11-30	**pI:**	9.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.2
		No. of unique Peptides:	1

Quantitation

mdown:qdown **Median:** 4.45 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MGTTGLESLS	LGDRGAAPTV	TSSERLVPDP	PNDLRKEDVA	MELERVGEDE	EQMMIKRSSE	CNPLLQEPIA	SAQFGATAGT
90	100	110	120	130	140	150	160
ECRKSVPCGW	ERVVKQRLFG	KTAGRFDVYF	ISPQGLKFRS	KSSLANYLHK	NGETSLKPED	FDFTVLSKRG	IKSRYKDCSM
170	180	190	200	210	220	230	240
AALTSHLQNQ	SNNSNWNLRT	RSKCKKDVFM	PPSSSSELQE	SRGLSNFTST	HLLLKEDEGV	DDVNFRKVRK	PKGKVTILKG
250	260	270	280	290	300	310	320
IPIKKTKKGC	RKSCSGFVQS	DSKRESVCNK	ADAESEPVAQ	KSQLDRTVCI	SDAGACGETL	SVTSEENSLV	KKKERSLSSG
330	340	350	360	370	380	390	400
SNFCSEQKTS	GIINKFCSAK	DSEHNEKYED	TFLESEEIGT	KVEVVERKEH	LHTDILKRGS	EMDNNCSPTR	KDFTGEKIFQ
410	420	430	440	450	460	470	480
EDTIPRTQIE	RRKTSLYFSS	KYNKEALSPP	RRKAFKKWTP	PRSPFNLVQE	TLFHDPWKLL	IATIFLNRTS	GKMAIPVLWK
490	500	510	520	530	540	550	
FLEKYPSAEV	ARTADWRDVS	ELLKPLGLYD	LRAKTIVKFS	DEYLTKQWKY	PIELHGIGAP		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
711	1	665.1654	-215.52	2	37.7	13.5	1	252-263	R.KSCSGFVQSDSK.R	Carbamidomethyl: 3	mdown:qdown 4.45

Detailed Protein Report

Protein 1108: galactose-3-O-sulfotransferase 3 [Homo sapiens]

Accession: gi|14719426
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 13.5
MW [kDa]: 48.9
pI: 10.7
Sequence Coverage [%]: 3.9
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MPPILQRLQQ	ATKMMSRRKI	LLLVLGCSTV	SLLIHQGAQL	SWYPKLFPLS	CPPLRNSPPR	PKHMTVAFLK	THKTAGTTVQ
90	100	110	120	130	140	150	160
NILFRFAERH	NLTVALPHPS	CEHQFCYPRN	FSAHFVHPAT	RPPHVLASHL	RFDRAELERL	MPPSTVYVTI	LREPAAMFES
170	180	190	200	210	220	230	240
LFSYYNQYCP	AFRRVPNASL	EAFLRAPEAY	YRAGEHFAMF	AHNTLAYDLG	GDNERSPRDD	AAYLAGLIRQ	VEEVFSLVMI
250	260	270	280	290	300	310	320
AEYFDESLVL	LRRLLAWDLD	DVLYAKLNAR	AASSRLAAIP	AALARAARTW	NALDAGLYDH	FNATFWRHVA	RAGRACVERE
330	340	350	360	370	380	390	400
ARELREARQR	LLRRCFGDEP	LLRPAAQIRT	KQLQPWQPSR	KVDIMGYDLP	GGGAGPATEA	CLKLAMPEVQ	YSNYLLRKQK
410	420	430	440				
RRGGARARPE	PVLDNPPPRP	IRVLPRGPQG	P				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2917	1	1023.0409	-3.50	2	65.2	13.5	2	1-17	-.MPPILQRLQQATKMMSR.R	Oxidation: 14

Detailed Protein Report

Protein 1109: PREDICTED: rho GTPase-activating protein 21 isoform X5 [Homo sapiens]

Accession:	gi|530392351	**Score:**	13.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	163.4
Database Date:	2015-11-30	**pI:**	9.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	0.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MMATRRTGLS	EGDGDKLKAC	EVSKNKDGKE	QSETVSLSED	ETFSWPGPKT	VTLKRTSQGF	GFTLRHFIVY	PPESAIQFSY
90	100	110	120	130	140	150	160
KDEENGNRGG	KQRNRLEPMD	TIFVKQVKEG	GPAFEAGLCT	GDRIIKVNGE	SVIGKTYSQV	IALIQNSDTT	LELSVMPKDE
170	180	190	200	210	220	230	240
DILQVLQFTK	DVTALAYSQD	AYLKGNEAYS	GNARNIPEPP	PICYPWLPSA	PSAMAQPVEI	SPPDSSLSKQ	QTSTPVLTQP
250	260	270	280	290	300	310	320
GRAYRMEIQV	PPSPTDVAKS	NTAVCVCNES	VRTVIVPSEK	VVDLLSNRNN	HTGPSHRTEE	VRYGVSEQTS	LKTVSRTTSP
330	340	350	360	370	380	390	400
PLSIPTTHLI	HQPAGSRSLE	PSGILLKSGN	YSGHSDGISS	SRSQAVEAPS	VSVNHYSPNS	HQHIDWKNYK	TYKEYIDNRR
410	420	430	440	450	460	470	480
LHIGCRTIQE	RLDSLRAASQ	STTDYNQVVP	NRTTLQGRRR	STSHDRVPQS	VQIRQRSVSQ	ERLEDSVLMK	YCPRSASQGA
490	500	510	520	530	540	550	560
LTSPSVSFSN	HRTRSWDYIE	GQDETLENVN	SGTPIPDSNG	EKKQTYKWSG	FTEQDDRRGI	CERPRQQEIH	KSFRGSNFTV
570	580	590	600	610	620	630	640
APSVVNSDNR	RMSGRGVGSV	SQFKKIPPDL	KTLQSNRNFQ	TTCGMSLPRG	ISQDRSPLVK	VRSNSLKAPS	THVTKPSFSQ
650	660	670	680	690	700	710	720
KSFVSIKDQR	PVNHLHQNSL	LNQQTWVRTD	SAPDQQVETG	KSPSLSGASA	KPAPQSSENA	GTSDLELPVS	QRNQDLSLQE
730	740	750	760	770	780	790	800
AETEQSDTLD	NKEAVILREK	PPSGRQTPQP	LRHQSYILAV	NDQETGSDTT	CWLPNDARRE	VHIKRMEERK	ASSTSPPGDS
810	820	830	840	850	860	870	880
LASIPFIDEP	TSPSIDHDIA	HIPASAVISA	STSQVPSIAT	VPPCLTTSAP	LIRRQLSHDH	ESVGPPSLDA	QPNSKTERSK
890	900	910	920	930	940	950	960
SYDEGLDDYR	EDAKLSFKHV	SSLKGIKIAD	SQKSSEDSGS	RKDSSSEVFS	DAAKEGWLHF	RPLVTDKGKR	VGGSIRPWKQ
970	980	990	1000	1010	1020	1030	1040
MYVVLRGHSL	YLYKDKREQT	TPSEEEQPIS	VNACLIDISY	SETKRKNVFR	LTTSDCECLF	QAEDRDDMLA	WIKTIQESSN
1050	1060	1070	1080	1090	1100	1110	1120
LNEEDTGVTN	RDLISRRIKE	YNNLMSKAEQ	LPKTPRQSLS	IRQTLLGAKS	EPKTQSPHSP	KEESERKLLS	KDDTSPPKDK
1130	1140	1150	1160	1170	1180	1190	1200
GTWRKGIPSI	MRKTFEKKPT	ATGTFGVRLD	DCPPAHTNRY	IPLIVDICCK	LVEERGLEYT	GIYRVPGNNA	AISSMQEELN
1210	1220	1230	1240	1250	1260	1270	1280
KGMADIDIQD	DKWRDLNVIS	SLLKSFFRKL	PEPLFTNDKY	ADFIEANRKE	DPLDRLKTLK	RLIHDLPEHH	YETLKFLSAH
1290	1300	1310	1320	1330	1340	1350	1360
LKTVAENSEK	NKMEPRNLAI	VFGPTLVRTS	EDNMTHMVTH	MPDQYKIVET	LIQHHDWFFT	EEGAEEPLIQ	LLVTQQNLRV
1370	1380	1390	1400	1410	1420	1430	1440
LGDLERISIA	GNCLCPPSLQ	LLVARGRSRK	KKHSLAAQKM	NWTMYFLRKK	MWNSVTMILK	RSPKKKVRHW	AENRRSSLPK
1450	1460						
KTALGKTPAR	QKMKRYH						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
160	1	619.8184	1.97	2	30.7	13.5	0	1411-1420	K.MWNSVTMILK.R	Oxidation: 7

Detailed Protein Report

Protein 1110: 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

Wdown:Qdown **Median:** 2.64 **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		Wdown:Qdown 2.64

Detailed Protein Report

Protein 1111: PREDICTED: retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma isoform X1 [Homo sapiens]

Accession:	gi|578831043	**Score:**	13.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	15.1
Database Date:	2015-11-30	**pI:**	10.8
		Sequence Coverage [%]:	20.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MKQRDKGRGW	HPAEGGPALT	AQPPETRPAL	DRSRRESRSQ	GCRGVSVSLT	MNLEPPKAEF	RSATRVAGGP	VTPRKGPPKF
90	**100**	**110**	**120**	**130**	**140**		
KQRQTRQFKS	KPPKKGVQGF	GDDIPGMEGL	GTDITVICPW	EAFNHLELHE	LAQYGII		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1451	1	994.1693	-10.60	3	46.9	13.5	2	7-34	K.GRGWHPAEGGPALTAQPPETRPALDRSR.R	

Detailed Protein Report

Protein 1112: PREDICTED: centrosomal protein of 68 kDa isoform X2 [Homo sapiens]

Accession:	gi|530367390	**Score:**	13.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	77.3
Database Date:	2015-11-30	**pI:**	5.1
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.1
		No. of unique Peptides:	1

Quantitation

mdown:qdown **Median:** 1.51 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MALGEEKAEA	EASEDTKAQS	YGRGSCRERE	LDIPGPMSGE	QPPRLEAEGG	LISPVWGAEG	IPAPTCWIGT	DPGGPSRAHQ
90	100	110	120	130	140	150	160
PQASDANREP	VAERSEPALS	GLPPATMGSG	DLLLSGESQV	EKTKLSSSEE	FPQTLSLPRT	TTICSGHDAD	TEDDPSLADL
170	180	190	200	210	220	230	240
PQALDLSQQP	HSSGLSCLSQ	WKSVLSPGSA	AQPSSCSISA	SSTGSSLQGH	QERAEPRGGS	LAKVSSSLEP	VVPQEPSSVV
250	260	270	280	290	300	310	320
GLGPRPQWSP	QPVFSGGDAS	GLGRRRLSFQ	AEYWACVLPD	SLPPSPDRHS	PLWNPNKEYE	DLLDYTYPLR	PGPQLPKHLD
330	340	350	360	370	380	390	400
SRVPADPVLQ	DSGVDLDSFS	VSPASTLKSP	TNVSPNCPPA	EATALPFSGP	REPSLKQWPS	RVPQKQGGMG	LASWSQLAST
410	420	430	440	450	460	470	480
PRAPGSRDAR	WERREPALRG	AKDRLTIGKH	LDMGSPQLRT	RDRGWPSPRP	EREKRTSQSA	RRPTCTESRW	KSEEEVESDD
490	500	510	520	530	540	550	560
EYLALPARLT	QVSSLVSYLG	SISTLVTLPT	GDIKGQSPLE	VSDSDGPASF	PSSSSQSQLP	PGAALQGSGD	PEGQNPCFLR
570	580	590	600	610	620	630	640
SFVRAHDSAG	EGSLGSSQAL	GVSSGLLKTR	PSLPARLDRW	PFSDPDVEGQ	LPRKGGEQGK	ESLVQCVKTF	CCQLEELICW
650	660	670	680	690	700	710	720
LYNVADVTDH	GTAARSNLTS	LKSSLQLYRQ	FKKDIDEHQS	LTESVLQKGE	ILLQCLLENT	PDMYPGSFRL	THSPSPSICL
730							
K							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
58	1	819.8353	-70.68	2	29.4	13.4	0	30-44	R.ELDIPGPMSGEQPPR.L	Oxidation: 8	mdown:qdown 1.51

Detailed Protein Report

Protein 1113: **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

Quantitation

mdown:qdown **Median:** 1.04 **CV:** 0.00 % **No. of 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	Ratios
2168	1	953.2792	-151.74	2	57.3	13.4	1	303-318	R.ADDCPFLMPICSHRER.R	Oxidation: 8	mdown:qdown 1.04

Detailed Protein Report

Protein 1114: 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

mdown:qdown	**Median:**	0.60	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.46	**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		mdown:qdown 0.60 Wdown:Qdown 0.46

Detailed Protein Report

Protein 1115: erythroid membrane-associated protein precursor [Homo sapiens]

Accession:	gi|19923536	**Score:**	13.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	52.6
Database Date:	2015-11-30	**pI:**	9.7
		Sequence Coverage [%]:	4.0
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|578798289	refseq_human (refseq_human_20140103.fasta)	PREDICTED: erythroid membrane-associated protein isoform X2 [Homo sapiens]
gi|63054855	refseq_human (refseq_human_20140103.fasta)	erythroid membrane-associated protein precursor [Homo sapiens]

10	20	30	40	50	60	70	80
MEMASSAGSW	LSGCLIPLVF	LRLSVHVSGH	AGDAGKFHVA	LLGGTAELLC	PLSLWPGTVP	KEVRWLRSPF	PQRSQAVHIF
90	100	110	120	130	140	150	160
RDGKDQDEDL	MPEYKGRTVL	VRDAQEGSVT	LQILDVRLED	QGSYRCLIQV	GNLSKEDTVI	LQVAAPSVGS	LSPSAVALAV
170	180	190	200	210	220	230	240
ILPVLVLLIM	VCLCLIWKQR	RAKEKLLYEH	VTEVDNLLSD	HAKEKGKLHK	AVKKLRSELK	LKRAAANSGW	RRARLHFVAV
250	260	270	280	290	300	310	320
TLDPDTAHPK	LILSEDQRCV	RLGDRRQPVP	DNPQRFDFVV	SILGSEYFTT	GCHYWEVYVG	DKTKWILGVC	SESVSRKGKV
330	340	350	360	370	380	390	400
TASPANGHWL	LRQSRGNEYE	ALTSPQTSFR	LKEPPRCVGI	FLDYEAGVIS	FYNVTNKSHI	FTFTHNFSGP	LRPFFEPCLH
410	420	430	440	450	460	470	480
DGGKNTAPLV	ICSELHKSEE	SIVPRPEGKG	HANGDVSLKV	NSSLLPPKAP	ELKDIILSLP	PDLGPALQEL	KAPSF

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1582	2	715.4259	42.30	3	48.5	13.4	2	232-250	R.RARLHFVAVTLDPDTAHPK.L	

Detailed Protein Report

Protein 1116: 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 1117: 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

BRUKER

Detailed Protein Report

Protein 1118: pyridoxal phosphate phosphatase PHOSPHO2 [Homo sapiens]

Accession:	gi|56606064	**Score:**	13.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	27.8
Database Date:	2015-11-30	**pI:**	6.4
		Sequence Coverage [%]:	4.6
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	0.93	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.32	**CV:**	0.00 %	**No. of Peptides:**	1

Alias proteins:

Accession	**Name**	**Description**
gi|313151197	refseq_huma (refseq_human_20140103.fasta)	pyridoxal phosphate phosphatase PHOSPHO2 [Homo sapiens]
gi|313151195	refseq_huma (refseq_human_20140103.fasta)	pyridoxal phosphate phosphatase PHOSPHO2 [Homo sapiens]
gi|313151193	refseq_huma (refseq_human_20140103.fasta)	pyridoxal phosphate phosphatase PHOSPHO2 [Homo sapiens]
gi|313151191	refseq_huma (refseq_human_20140103.fasta)	pyridoxal phosphate phosphatase PHOSPHO2 [Homo sapiens]

10	20	30	40	50	60	70	80
MKILLVFDFD	NTIIDDNSDT	WIVQCAPNKK	LPIELRDSYR	KGFWTEFMGR	VFKYLGDKGV	REHEMKRAVT	SLPFTPGMVE
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
LFNFIRKNKD	KFDCIIISDS	NSVFIDWVLE	AASFHDIFDK	VFTNPAAFNS	NGHLTVENYH	THSCNRCPKN	LCKKVVLIEF
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
VDKQLQQGVN	YTQIVYIGDG	GNDVCPVTFL	KNDDVAMPRK	GYTLQKTLSR	MSQNLEPMEY	SVVVWSSGVD	IISHLQFLIK
250							
D							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1387	1	695.3741	-31.67	2	46.1	13.4	2	30-40	K.KLPIELRDSYR.K		Wdown:Qdown 0.32 mdown:qdown 0.93

Detailed Protein Report

Protein 1119: PREDICTED: ankyrin repeat domain-containing protein 17 isoform X7 [Homo sapiens]

Accession:	gi|530376947	**Score:**	13.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	156.1
Database Date:	2015-11-30	**pI:**	4.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEKATVPVAA	ATAAEGEGSP	PAVAAVAGPP	AAAEVGGGVG	GSSRARSASS	PRGMVRVCDL	LLKKKPPQQQ	HHKAKRNRTC
90	100	110	120	130	140	150	160
RPPSSSESSS	DSDNSGGGGG	GGGGGGGGGG	TSSNNSEEEE	DDDDEEEEVS	EVESFILDQD	DLENPMLETA	SKLLLSGTAD
170	180	190	200	210	220	230	240
GADLRTVDPE	TQARLEALLE	AAGIGKLSTA	DGKAFADPEV	LRRLTSSVSC	ALDEAAAALT	RMRAESTANA	GQSDNRSLAE
250	260	270	280	290	300	310	320
ACSEGDVNAV	RKLLIEGRSV	NEHTEEGESL	LCLACSAGYY	ELAQVLLAMH	ANVEDRGIKG	DITPLMAAAN	GGHVKIVKLL
330	340	350	360	370	380	390	400
LAHKADVNAQ	SSTGNTALTY	ACAGGYVDVV	KVLLESGASI	EDHNENGHTP	LMEAGSAGHV	EVARLLLENG	AGINTHSNEF
410	420	430	440	450	460	470	480
KESALTLACY	KGHLEMVRFL	LEAGADQEHK	TDEMHTALME	ACMDGHVEVA	RLLLDSGAQV	NMPADSFESP	LTLAACGGHV
490	500	510	520	530	540	550	560
ELAALLIERG	ASLEEVNDEG	YTPLMEAARE	GHEEMVALLL	GQGANINAQT	EETQETALTL	ACCGGFLEVA	DFLIKAGADI
570	580	590	600	610	620	630	640
ELGCSTPLME	AAQEGHLELV	KYLLAAGANV	HATTATGDTA	LTYACENGHT	DVADVLLQAG	ADLEHESEGG	RTPLMKAARA
650	660	670	680	690	700	710	720
GHVCTVQFLI	SKGANVNRTT	ANNDHTVLSL	ACAGGHLAVV	ELLLAHGADP	THRLKDGSTM	LIEAAKGGHT	SVVCYLLDYP
730	740	750	760	770	780	790	800
NNLLSAPPPD	VTQLTPPSHD	LNRAPRVPVQ	ALPMVVPPQE	PDKPPANVAT	TLPIRNKAAS	KQKSSSHLPA	NSQDVQGYIT
810	820	830	840	850	860	870	880
NQSPESIVEE	AQGKLTELEQ	RIKEAIEKNA	QLQSLELAHA	DQLTKEKIEE	LNKTREEQIQ	KKQKILEELQ	KVERELQLKT
890	900	910	920	930	940	950	960
QQQLKKQYLE	VKAQRIQLQQ	QQQQSCQHLG	LLTPVGVGEQ	LSEGDYARLQ	QVDPVLLKDE	PQQTAAQMGF	APIQPLAMPQ
970	980	990	1000	1010	1020	1030	1040
ALPLAAGPLP	PGSIANLTEL	QGVIVGQPVL	GQAQLAGLGQ	GILTETQQGL	MVASPAQTLN	DTLDDIMAAV	SGRASAMSNT
1050	1060	1070	1080	1090	1100	1110	1120
PTHSIAASIS	QPQTPTPSPI	ISPSAMLPIY	PAIDIDAQTE	SNHDTALTLA	CAGGHEELVQ	TLLERGASIE	HRDKKGFTPL
1130	1140	1150	1160	1170	1180	1190	1200
ILAATAGHVG	VVEILLDNGA	DIEAQSERTK	DTPLSLACSG	GRQEVVELLL	ARGANKEHRN	VSDYTPLSLA	ASGGYVNIIK
1210	1220	1230	1240	1250	1260	1270	1280
ILLNAGAEIN	SRTGSKLGIS	PLMLAAMNGH	TAAVKLLLDM	GSDINAQIET	NRNTALTLAC	FQGRTEVVSL	LLDRKANVEH
1290	1300	1310	1320	1330	1340	1350	1360
RAKTGLTPLM	EAASGGYAEV	GRVLLDKGAD	VNAPPVPSSR	DTALTIAADK	GHYKFCELLI	GRGAHIDVRN	KKGNTPLWLA
1370	1380	1390	1400	1410	1420	1430	1440
ANGGHLDVVQ	LLVQAGADVD	AADNRKITPL	MAAFRKGHVK	VVRYLVKEVN	QFPSDSECMR	YIATITDKEM	LKKCHLCMES
1450	1460	1470	1480	1490			
IVQAKDRQAA	EANKNASILL	EELDLEKADY	NIIPIYSHGE				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2659	1	938.0625	114.26	2	62.0	13.4	2	1433-1447	K.KCHLCMESIVQAKDR.Q	Carbamidomethyl: 2, 5

Detailed Protein Report

Protein 1120: beta-defensin 123 precursor [Homo sapiens]

Accession:	gi|23503331	**Score:**	13.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	8.1
Database Date:	2015-11-30	**pI:**	10.9
Modification(s):	Oxidation	**Sequence Coverage [%]:**	26.9
		No. of unique Peptides:	1

```
         10         20         30         40         50         60         70
MKLLLLTLTV LLLLSQLTPG GTQRCWNLYG KCRYRCSKKE RVYVYCINNK MCCVKPKYQP KERWWPF
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
31	1	735.9836	-57.79	3	29.7	13.4	2	40-57	K.ERVYVYCINNKMCCVKPK.Y	Oxidation: 12

Detailed Protein Report

Protein 1121: 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

Quantitation

Wdown:Qdown **Median:** 4.96 **CV:** 0.00 % **No. of 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	Ratios
1096	1	737.2178	-190.33	2	43.3	13.3	0	338-350	R.GHAICVYHMSSIR.A		Wdown:Qdown 4.96

Detailed Protein Report

Protein 1122: 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_human (refseq_human_20140103.fasta)	inactive ribonuclease-like protein 9 isoform 1 precursor [Homo sapiens]
gi|160333420	refseq_human (refseq_human_20140103.fasta)	inactive ribonuclease-like protein 9 isoform 1 precursor [Homo sapiens]
gi|160333415	refseq_human (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 1123: PREDICTED: BAG family molecular chaperone regulator 3 isoform X1 [Homo sapiens]

Accession:	gi|530394628	**Score:**	13.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	61.4
Database Date:	2015-11-30	**pI:**	6.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSAATHSPMM	QVASGNGDRD	PLPPGWEIKI	DPQTGWPFFV	DHNSRTTTWN	DPRVPSEGPK	ETPSSANGPS	REGSRLPPAR
90	100	110	120	130	140	150	160
EGHPVYPQLR	PGYIPIPVLH	EGAENRQVHP	FHVYPQPGMQ	RFRTEAAAAA	PQRSQSPLRG	MPETTQPDKQ	CGQVAAAAAA
170	180	190	200	210	220	230	240
QPPASHGPER	SQSPAASDCS	SSSSSASLPS	SGRSSLGSHQ	LPRGYISIPV	IHEQNVTRPA	AQPSFHQAQK	THYPAQQGEY
250	260	270	280	290	300	310	320
QTHQPVYHKI	QGDDWEPRPL	RAASPFRSSV	QGASSREGSP	ARSSTPLHSP	SPIRVHTVVD	RPQPMTHRET	APVSQPENKP
330	340	350	360	370	380	390	400
ESKPGPVGPE	LPPGHIPIQV	IRKEVDSKPV	SQKPPPPSEK	VEVKVPPAPV	PCPPPSPGPS	AVPSSPKSVA	TEERAAPSTA
410	420	430	440	450	460	470	480
PAEATPPKPG	EAEAPPKHPG	VLKVEAILEK	VQGLEQAVDN	FEGKKTDKKY	LMIEEYLTKE	LLALDSVDPE	GRADVRQARR
490	500	510	520	530	540	550	560
DGVRKVQTIL	EKLEQKAIDV	PGQVQVYELQ	PSNLEADQPL	QAIMEMGAVA	ADKGKKNAGN	AEDPHTETQQ	PEATAAATSN
570	580						
PSSMTDTPGN	PAAP						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2079	1	916.9082	4.24	2	54.5	13.3	0	2-19	M.SAATHSPMMQVASGNGDR.D	Oxidation: 8

Detailed Protein Report

Protein 1124: **PREDICTED: serine/threonine-protein phosphatase 2A regulatory subunit B'' subunit gamma isoform X7 [Homo sapiens]**

Accession:	gi|578825918	**Score:**	13.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	33.3
Database Date:	2015-11-30	**pI:**	7.6
		Sequence Coverage [%]:	8.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDWKEVLRRR	LATPNTCPNK	KKSEQELKDE	EMDLFTKYYS	EWKGGRKNTN	EFYKTIPRFY	YRLPAEDEVL	LQKLREESRA
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
VFLQRKSREL	LDNEELQNLW	FLLDKHQTPP	MIGEEAMINY	ENFLKVGEKA	GAKCKQFFTA	KVFAKLLHTD	SYGRISIMQF
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
FNYVMRKVWL	HQTRIGLSLY	DVAGQGYLRE	SDLENYILEL	IPTLPQLDGL	EKSFYSFYVC	TAVRKFFFFL	DPLRTGKIKI
250	**260**	**270**	**280**	**290**			
QDILACSFLD	DLLELRDEEL	SKESQETNWF	SAPSALRVYG	L			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2954	1	891.7382	-98.03	3	66.1	13.3	2	167-189	R.KVWLHQTRIGLSLYDVAGQGYLR.E	

Detailed Protein Report

Protein 1125: 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	3	955.6427	92.95	2	41.9	13.3	1	149-169	R.INMVGLGLVGGAGAGLVRGAK.W	

Detailed Protein Report

Protein 1126: tubulin-specific chaperone E isoform c [Homo sapiens]

Accession:	gi|568215738	**Score:**	13.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	46.8
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
MYPCELCFSC	SQLSKLQEVS	LRNCAVSCAG	EKGGVAEACP	NIRKVDLSKN	LLSSWDEVIH	IADQLRHLEV	LNVSENKLKF
90	100	110	120	130	140	150	160
PSGSVLTGTL	SVLKVLVLNQ	TGITWAEVLR	CVAGCPGLEE	LYLESNNIFI	SERPTDVLQT	VKLLDLSSNQ	LIDENQLYLI
170	180	190	200	210	220	230	240
AHLPRLEQLI	LSDTGISSLH	FPDAGIGCKT	SMFPSLKYLV	VNDNQISQWS	FFNELEKLPS	LRALSCLRNP	LTKEDKEAET
250	260	270	280	290	300	310	320
ARLLIIASIG	QLKTLNKCEI	LPEERRRAEL	DYRKAFGNEW	KQAGGHKDPE	KNRLSEEFLT	AHPRYQFLCL	KYGAPEDWEL
330	340	350	360	370	380	390	400
KTQQPLMLKN	QLLTLKIKYP	HQLDQKVLEK	QLPGSMTIQK	VKGLLSRLLK	VPVSDLLLSY	ESPKKPGREI	ELENDLKSLQ
410	420						
FYSVENGDCL	LVRW						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
486	1	535.7503	-186.51	2	34.7	13.3	1	330-338	K.NQLLTLKIK.Y	

Detailed Protein Report

Protein 1127: PREDICTED: probable ATP-dependent RNA helicase DDX60-like isoform X7 [Homo sapiens]

Accession:	gi|578809624	**Score:**	13.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	152.1
Database Date:	2015-11-30	**pI:**	7.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	0.8
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578809626	refseq_human (refseq_human_20140103.fasta)	PREDICTED: probable ATP-dependent RNA helicase DDX60-like isoform X8 [Homo sapiens]

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					
LGIHMPCKSV	VFAQDSVYLD	ALNYRQIM					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1104	1	586.3508	80.45	2	42.5	13.3	2	639-648	K.HCRGEGKISK.D	Carbamidomethyl: 2

Detailed Protein Report

Protein 1128: centrin-2 [Homo sapiens]

Accession:	gi|4757902	**Score:**	13.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	19.7
Database Date:	2015-11-30	**pI:**	4.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	9.9
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MASNFKKANM ASSSQRKRMS PKPELTEEQK QEIREAFDLF DADGTGTIDV KELKVAMRAL GFEPKKEEIK KMISEIDKEG
        90        100        110        120        130        140        150        160
TGKMNFGDFL TVMTQKMSEK DTKEEILKAF KLFDDDETGK ISFKNLKRVA KELGENLTDE ELQEMIDEAD RDGDGEVSEQ
       170        180
EFLRIMKKTS LY
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2724	1	1028.0424	75.06	2	63.0	13.3	1	84-100	K.MNFGDFLTVMTQKMSEK.D	Oxidation: 1, 10, 14

Protein 1129: vitamin K epoxide reductase complex subunit 1 isoform 2 precursor [Homo sapiens]

Accession:	gi|45827739	**Score:**	13.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	9.9
Database Date:	2015-11-30	**pI:**	10.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	14.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGSTWGSPGW	VRLALCLTGL	VLSLYALHVK	AARARDRDYR	ALCDVGTAIS	CSRVFSSRLP	ADTLGLCPDA	AELPGVSRWF
90	100						
CLPGLDPVLR	AL						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1852	1	676.7559	-92.47	2	51.7	13.3	0	41-53	R.ALCDVGTAISCSR.V	Carbamidomethyl: 3

Detailed Protein Report

Protein 1130: BH3-interacting domain death agonist isoform 1 [Homo sapiens]

Accession:	gi|37574726	**Score:**	13.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	26.8
Database Date:	2015-11-30	**pI:**	6.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.6
		No. of unique Peptides:	1

Quantitation

mdown:qdown **Median:** 0.88 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MCSGAGVMMA	RWAARGRAGW	RSTVRILSPL	GHCEPGVSRS	CRAAQAMDCE	VNNGSSLRDE	CITNLLVFGF	LQSCSDNSFR
90	100	110	120	130	140	150	160
RELDALGHEL	PVLAPQWEGY	DELQTDGNRS	SHSRLGRIEA	DSESQEDIIR	NIARHLAQVG	DSMDRSIPPG	LVNGLALQLR
170	180	190	200	210	220	230	240
NTSRSEEDRN	RDLATALEQL	LQAYPRDMEK	EKTMLVLALL	LAKKVASHTP	SLLRDVFHTT	VNFINQNLRT	YVRSLARNGM
250							
D							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
836	1	585.7806	55.65	2	39.3	13.3	0	1-11	-.MCSGAGVMMAR.W	Carbamidomethyl: 2	mdown:qdown 0.88

Detailed Protein Report

Protein 1131: ras-GEF domain-containing family member 1C [Homo sapiens]

Accession:	gi|40255197	**Score:**	13.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	52.8
Database Date:	2015-11-30	**pI:**	8.6
		Sequence Coverage [%]:	3.9
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578811061	refseq_human (refseq_human_20140103.fasta)	PREDICTED: ras-GEF domain-containing family member 1C isoform X1 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MPQTLSASDM VTPGSLSPPP TEPTDGEQAG QPLLDGAPSS ASLETLIQHL VPTADYYPEK AYIFTFLLSS RLFIEPRELL
        90        100        110        120        130        140        150        160
ARVCHLCIEQ QQLDKPVLDK ARVRKFGPKL LQLLAEWTET FPRDFQEEST IGHLKDVVGR IAPCDEAYRK RMHQLLQALH
       170        180        190        200        210        220        230        240
QKLAALRQGP EGLVGADKPI SYRTKPPASI HRELLGVCSD PYTLAQQLTH VELERLRHIG PEEFVQAFVN KDPLASTKPC
       250        260        270        280        290        300        310        320
FSDKTSNLEA YVKWFNRLCY LVATEICMPA KKKQRAQVIE FFIDVARECF NIGNFNSLMA IISGMNMSPV SRLKKTWAKV
       330        340        350        360        370        380        390        400
RTAKFFILEH QMDPTGNFCN YRTALRGAAH RSLTAHSSRE KIVIPFFSLL IKDIYFLNEG CANRLPNGHV NFEKFLELAK
       410        420        430        440        450        460        470
QVGEFITWKQ VECPFEQDAS ITHYLYTAPI FSEDGLYLAS YESESPENQT EKERWKALRS SILGKT
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1850	1	715.9797	-114.03	3	51.8	13.2	1	106-123	K.FGPKLLQLLAEWTETFPR.D	

Detailed Protein Report

Protein 1132: 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

Quantitation

mdown:qdown **Median:** 0.67 **CV:** 0.00 % **No. of 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	Ratios
1640	1	1044.2554	-244.56	1	50.4	13.2	0	774-783	K.FGAPDGPQQK.T		mdown:qdown 0.67

Detailed Protein Report

Protein 1133: multivesicular body subunit 12A [Homo sapiens]

Accession: gi|24308440
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 13.2
MW [kDa]: 28.8
pI: 9.9
Sequence Coverage [%]: 8.4
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MDPVPGTDSA	PLAGLAWSSA	SAPPPRGFSA	ISCTVEGAPA	SFGKSFAQKS	GYFLCLSSLG	SLENPQENVV	ADIQIVVDKS
90	100	110	120	130	140	150	160
PLPLGFSPVC	DPMDSKASVS	KKKRMCVKLL	PLGATDTAVF	DVRLSGKTKT	VPGYLRIGDM	GGFAIWCKKA	KAPRPVPKPR
170	180	190	200	210	220	230	240
GLSRDMQGLS	LDAASQPSKG	GLLERTASRL	GSRASTLRRN	DSIYEASSLY	GISAMDGVPF	TLHPRFEGKS	CSPLAFSAFG
250	260	270	280				
DLTIKSLADI	EEEYNYGFVV	EKTAAARLPP	SVS				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2637	1	1145.5118	-44.07	2	61.7	13.2	1	27-49	R.GFSAISCTVEGAPASFGKSFAQK.S	

Detailed Protein Report

Protein 1134: 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 1135: **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 1136: 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

Quantitation

mdown:qdown	**Median:**	0.88	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.82	**CV:**	0.00 %	**No. of 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	Ratios
861	1	736.2893	-94.91	2	40.2	13.2	1	21-34	R.LFTRGGSGGMGYPR.L	Oxidation: 10	Wdown:Qdown 0.82 mdown:qdown 0.88

Detailed Protein Report

Protein 1137: nuclear pore complex protein Nup155 isoform 3 [Homo sapiens]

Accession:	gi|509155837	**Score:**	13.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	148.0
Database Date:	2015-11-30	**pI:**	5.9
		Sequence Coverage [%]:	1.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPSSLLGAAM	PASTSAAALQ	EALENAGRLI	DRQLQEDRMY	PDLSELLMVS	APNNPTVSGM	SDMDYPLQGP	GLLSVPNLPE
90	100	110	120	130	140	150	160
ISSIRRVPLP	PELVEQFGHM	QCNCMMGVFP	PISRAWLTID	SDIFMWNYED	GGDLAYFDGL	SETILAVGLV	KPKAGIFQPH
170	180	190	200	210	220	230	240
VRHLLVLATP	VDIVILGLSY	ANLQTGSGVL	NDSLSGGMQL	LPDPLYSLPT	DNTYLLTITS	TDNGRIFLAG	KDGCLYEVAY
250	260	270	280	290	300	310	320
QAEAGWFSQR	CRKINHSKSS	LSFLVPSLLQ	FTFSEDDPIL	QIAIDNSRNI	LYTRSEKGVI	QVYDLGQDGQ	GMSRVASVSQ
330	340	350	360	370	380	390	400
NAIVSAAGNI	ARTIDRSVFK	PIVQIAVIEN	SESLDCQLLA	VTHAGVRLYF	STCPFRQPLA	RPNTLTLVHV	RLPPGFSASS
410	420	430	440	450	460	470	480
TVEKPSKVHR	ALYSKGILLM	AASENEDNDI	LWCVNHDTFP	FQKPMMETQM	TAGVDGHSWA	LSAIDELKVD	KIITPLNKDH
490	500	510	520	530	540	550	560
IPITDSPVVV	QQHMLPPKKF	VLLSAQGSLM	FHKLRPVDQL	RHLLVSNVGG	DGEEIERFFK	LHQEDQACAT	CLILACSTAA
570	580	590	600	610	620	630	640
CDREVSAWAT	RAFFRYGGEA	QMRFPTTLPP	PSNVGPILGS	PVYSSSPVPS	GSPYPNPSFL	GTPSHGIQPP	AMSTPVCALG
650	660	670	680	690	700	710	720
NPATQATNMS	CVTGPEIVYS	GKHNGICIYF	SRIMGNIWDA	SLVVERIFKS	GNREITAIES	SVPCQLLESV	LQELKGLQEF
730	740	750	760	770	780	790	800
LDRNSQFAGG	PLGNPNTTAK	VQQRLIGFMR	PENGNPQQMQ	QELQRKFHEA	QLSEKISLQA	IQQLVRKSYQ	ALALWKLLCE
810	820	830	840	850	860	870	880
HQFTIIVAEL	QKANELLQRS	RQVQNKTEKE	RMLRESLKEY	QKISNQVDLS	NVCAQYRQVR	FYEGVVELSL	TAAEKKDPQG
890	900	910	920	930	940	950	960
LGLHFYKHGE	PEEDIVGLQA	FQERLNSYKC	ITDTLQELVN	QSKAAPQSPS	VPKKPGPPVL	SSDPNMLSNE	EAGHHFEQML
970	980	990	1000	1010	1020	1030	1040
KLSQRSKDEL	FSIALYNWLI	QVDLADKLLQ	VASPFLEPHL	VRMAKVDQNR	VRYMDLLWRY	YEKNRSFSNA	ARVLSRLADM
1050	1060	1070	1080	1090	1100	1110	1120
HSTEISLQQR	LEYIARAILS	AKSSTAISSI	AADGEFLHEL	EEKMEVARIQ	LQIQETLQRQ	YSHHSSVQDA	VSQLDSELMD
1130	1140	1150	1160	1170	1180	1190	1200
ITKLYGEFAD	PFKLAECKLA	IIHCAGYSDP	ILVQTLWQDI	IEKELSDSVT	LSSSDRMHAL	SLKIVLLGKI	YAGTPRFFPL
1210	1220	1230	1240	1250	1260	1270	1280
DFIVQFLEQQ	VCTLNWDVGF	VIQTMNEIGV	PLPRLLEVYD	QLFKSRDPFW	NRMKKPLHLL	DCIHVLLIRY	VENPSQVLNC
1290	1300	1310	1320	1330			
ERRRFTNLCL	DAVCGYLVEL	QSMSSSVAVQ	AITGNFKSLQ	AKLERLH			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2252	1	569.2585	-108.17	3	56.8	13.2	1	499-513	K.KFVLLSAQGSLMFHK.L	

Detailed Protein Report

Protein 1138: testis-expressed sequence 35 protein isoform 4 [Homo sapiens]

Accession: gi|282398137
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 13.2
MW [kDa]: 24.0
pI: 10.0
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 1139: CD9 antigen [Homo sapiens]

Accession:	gi|4502693	**Score:**	13.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	25.4
Database Date:	2015-11-30	**pI:**	7.7
		Sequence Coverage [%]:	3.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPVKGGTKCI	KYLLFGFNFI	FWLAGIAVLA	IGLWLRFDSQ	TKSIFEQETN	NNNSSFYTGV	YILIGAGALM	MLVGFLGCCG
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
AVQESQCMLG	LFFGFLLVIF	AIEIAAAIWG	YSHKDEVIKE	VQEFYKDTYN	KLKTKDEPQR	ETLKAIHYAL	NCCGLAGGVE
170	**180**	**190**	**200**	**210**	**220**	**230**	
QFISDICPKK	DVLETFTVKS	CPDAIKEVFD	NKFHIIGAVG	IGIAVVMIFG	MIFSMILCCA	IRRNREMV	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1067	1	942.2514	-217.87	1	42.9	13.2	0	120-126	K.EVQEFYK.D	

Detailed Protein Report

Protein 1140: WD repeat and FYVE domain-containing protein 1 [Homo sapiens]

Accession:	gi|18482373	**Score:**	13.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	46.3
Database Date:	2015-11-30	**pI:**	7.2
		Sequence Coverage [%]:	4.6
		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 1141: peptidyl-prolyl cis-trans isomerase FKBP7 isoform b precursor [Homo sapiens]

Accession:	gi|206725547	**Score:**	13.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	25.7
Database Date:	2015-11-30	**pI:**	5.9
		Sequence Coverage [%]:	5.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPKTMHFLFR	FIVFFYLWGL	FTAQRQKKEE	STEEVKIEVL	HRPENCSKTS	KKGDLLNAHY	DGYLAKDGSK	FYCSRTQNEG
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
HPKWFVLGVG	QVIKGLDIAM	TDMCPGEKRK	VVIPPSFAYG	KEGYEGKIPP	DATLIFEIEL	YAVTKGPRSI	ETFKQIDMDN
170	**180**	**190**	**200**	**210**	**220**	**230**	
DRQLSKAEIN	LYLQREFEKD	EKPRDKSYQD	AVLEDIFKKN	DHDGDGFISP	KEYNVYQHDE	L	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2564	1	731.7179	-182.33	2	60.7	13.1	1	155-166	K.QIDMDNDRQLSK.A	

Detailed Protein Report

Protein 1142: melanoregulin [Homo sapiens]

Accession: gi|124487399
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 13.1
MW [kDa]: 24.9
pI: 5.4
Sequence Coverage [%]: 7.5
No. of unique Peptides: 1

```
         10         20         30         40         50         60         70         80
MGLRDWLRTV CCCCGCECLE ERALPEKEPL VSDNNPYSSF GATLVRDDEK NLWSMPHDVS HTEADDDRTL YNLIVIRNQQ
         90        100        110        120        130        140        150        160
AKDSEEWQKL NYDIHTLRQV RREVRNRWKC ILEDLGFQKE ADSLLSVTKL STISDSKNTR KAREMLLKLA EETNIFPTSW
        170        180        190        200        210        220
ELSERYLFVV DRLIALDAAE EFFKLARRTY PKKPGVPCLA DGQKELHYLP FPSP
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2237	1	851.3609	-108.43	2	56.6	13.1	1	189-204	R.TYPKKPGVPCLADGQK.E	

Detailed Protein Report

Protein 1143: carcinoembryonic antigen-related cell adhesion molecule 20 isoform 4S precursor [Homo sapiens]

Accession:	gi|156564388	**Score:**	13.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	54.1
Database Date:	2015-11-30	**pI:**	5.9
		Sequence Coverage [%]:	4.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGPADSWGHH	WMGILLSASL	CTVWSPPAAA	QLTLNANPLD	ATQSEDVVLP	VFGTPRTPQI	HGRSRELAKP	SIAVSPGTAI
90	100	110	120	130	140	150	160
EQKDMVTFYC	TTKDVNITIH	WVSNNLSVVF	HERMQLSKDG	KILTILIVQR	EDSGTYQCEA	RDALLSQRSD	PIFLDVKYGP
170	180	190	200	210	220	230	240
DPVEIKLESG	VASGEVVEVM	EGSSMTFLAE	TKSHPPCAYT	WFLLDSILSH	TTRTFTIHAV	SREHEGLYRC	LVSNSATHLS
250	260	270	280	290	300	310	320
SLGTLKVRVL	ETLTMPQVVP	SSLNLVENAR	SVDLTCQTVN	QSVNVQWFLS	GQPLLPSEHL	QLSADNRTLI	IHGLQRNDTG
330	340	350	360	370	380	390	400
PYACEVWNWG	SRARSEPLEL	TINCPQSSSL	SSGAIAGIVI	GILAVIAVAS	ELGYFLYIRN	ARRPSRKTTE	DPSHETSQPI
410	420	430	440	450	460	470	480
PKEEHPTEPS	SESLSPEYCN	ISQLQGRIRV	ELTKLPSASR	RGNSFSPWKP	PPKPLMPPLR	LVSTVPKNME	SIYEELVNPE
490	500						
PNTYIQINPS	V						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
810	1	770.1691	128.26	3	38.6	13.1	1	122-141	K.ILTILIVQREDSGTYQCEAR.D	

Detailed Protein Report

Protein 1144: ectodysplasin-A isoform 2 [Homo sapiens]

Accession:	gi|54112101	**Score:**	13.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	41.0
Database Date:	2015-11-30	**pI:**	9.6
		Sequence Coverage [%]:	4.9
		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
1562	1	1059.0865	57.30	2	48.2	13.1	1	264-282	K.NDLSGGVLNDWSRITMNPK.V	

Detailed Protein Report

Protein 1145: E3 ubiquitin-protein ligase MSL2 isoform 2 [Homo sapiens]

Accession:	gi|224028284	**Score:**	13.1
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
341	2	635.5460	-95.49	3	33.3	13.1	2	407-422	R.CPCYSNRKACLDCICR.G	Carbamidomethyl: 1

Detailed Protein Report

Protein 1146: PREDICTED: peptidyl-prolyl cis-trans isomerase A isoform X1 [Homo sapiens]

Accession:	gi|530384859	**Score:**	13.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	11.4
Database Date:	2015-11-30	**pI:**	9.2
		Sequence Coverage [%]:	13.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MCQGGDFTRH	NGTGGKSIYG	EKFEDENFIL	KHTGPGILSM	ANAGPNTNGS	QFFICTAKTE	WLDGKHVVFG	KVKEGMNIVE
90	100	110					
AMERFGSRNG	KTSKKITIAD	CGQLE					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2048	2	753.7914	-137.80	2	55.7	13.1	2	92-105	K.TSKKITIADCGQLE.-	

Detailed Protein Report

Protein 1147: matrix metalloproteinase-25 preproprotein [Homo sapiens]

Accession:	gi|11968059	**Score:**	13.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	62.5
Database Date:	2015-11-30	**pI:**	9.5
		Sequence Coverage [%]:	2.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MRLRLRLLAL	LLLLLAPPAR	APKPSAQDVS	LGVDWLTRYG	YLPPPHPAQA	QLQSPEKLRD	AIKVMQRFAG	LPETGRMDPG
90	100	110	120	130	140	150	160
TVATMRKPRC	SLPDVLGVAG	LVRRRRRYAL	SGSVWKKRTL	TWRVRSFPQS	SQLSQETVRV	LMSYALMAWG	MESGLTFHEV
170	180	190	200	210	220	230	240
DSPQGQEPDI	LIDFARAFHQ	DSYPFDGLGG	TLAHAFFPGE	HPISGDTHFD	DEETWTFGSK	DGEGTDLFAV	AVHEFGHALG
250	260	270	280	290	300	310	320
LGHSSAPNSI	MRPFYQGPVG	DPDKYRLSQD	DRDGLQQLYG	KAPQTPYDKP	TRKPLAPPPQ	PPASPTHSPS	FPIPDRCEGN
330	340	350	360	370	380	390	400
FDAIANIRGE	TFFFKGPWFW	RLQPSGQLVS	PRPARLHRFW	EGLPAQVRVV	QAAYARHRDG	RILLFSGPQF	WVFQDRQLEG
410	420	430	440	450	460	470	480
GARPLTELGL	PPGEEVDAVF	SWPQNGKTYL	VRGRQYWRYD	EAAARPDPGY	PRDLSLWEGA	PPSPDDVTVS	NAGDTYFFKG
490	500	510	520	530	540	550	560
AHYWRFPKNS	IKTEPDAPQP	MGPNWLDCPA	PSSGPRAPRP	PKATPVSETC	DCQCELNQAA	GRWPAPIPLL	LLPLLVGGVA
570							
SR							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
869	1	647.8024	-99.59	2	39.7	13.1	2	108-118	R.YALSGSVWKKR.T	

Detailed Protein Report

Protein 1148: peroxisomal acyl-coenzyme A oxidase 1 isoform c [Homo sapiens]

Accession:	gi|297206874	**Score:**	13.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	70.1
Database Date:	2015-11-30	**pI:**	7.9
		Sequence Coverage [%]:	1.4
		No. of unique Peptides:	1

Quantitation

mdown:qdown **Median:** 0.63 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MILNDPDFQH	EDLNFLTRSQ	RYEVAVRKSA	IMVKKMREFG	IADPDEIMWF	KNFVHRGRPE	PLDLHLGMFL	PTLLHQATAE
90	100	110	120	130	140	150	160
QQERFFMPAW	NLEIIGTYAQ	TEMGHGTHLR	GLETTATYDP	ETQEFILNSP	TVTSIKWWPG	GLGKTSNHAI	VLAQLITKGK
170	180	190	200	210	220	230	240
CYGLHAFIVP	IREIGTHKPL	PGITVGDIGP	KFGYDEIDNG	YLKMDNHRIP	RENMLMKYAQ	VKPDGTYVKP	LSNKLTYGTM
250	260	270	280	290	300	310	320
VFVRSFLVGE	AARALSKACT	IAIRYSAVRH	QSEIKPGEPE	PQILDFQTQQ	YKLFPLLATA	YAFQFVGAYM	KETYHRINEG
330	340	350	360	370	380	390	400
IGQGDLSELP	ELHALTAGLK	AFTSWTANTG	IEACRMACGG	HGYSHCSGLP	NIYVNFTPSC	TFEGENTVMM	LQTARFLMKS
410	420	430	440	450	460	470	480
YDQVHSGKLV	CGMVSYLNDL	PSQRIQPQQV	AVWPTMVDIN	SPESLTEAYK	LRAARLVEIA	AKNLQKEVIH	RKSKEVAWNL
490	500	510	520	530	540	550	560
TSVDLVRASE	AHCHYVVVKL	FSEKLLKIQD	KAIQAVLRSL	CLLYSLYGIS	QNAGDFLQGS	IMTEPQITQV	NQRVKELLTL
570	580	590	600	610	620	630	
IRSDAVALVD	AFDFQDVTLG	SVLGRYDGNV	YENLFEWAKN	SPLNKAEVHE	SYKHLKSLQS	KL	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1782	1	568.7446	-150.72	2	52.3	13.1	1	463-471	K.NLQKEVIHR.K		mdown:qdown 0.63

Detailed Protein Report

Protein 1149: selenium-binding protein 1 isoform 2 [Homo sapiens]

Accession:	gi|385137128	**Score:**	13.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	45.4
Database Date:	2015-11-30	**pI:**	5.2
		Sequence Coverage [%]:	7.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MATKCGNCGP	GYSTPLEAMK	GPREEIVYLP	CIYRNTGTEA	PDYLATVDVD	PKSPQYCQVI	EPKDIHAKCE	LAFLHTSHCL
90	100	110	120	130	140	150	160
ASGEVMISSL	GDVKGNGKGG	FVLLDGETFE	VKGTWERPGG	AAPLGYDFWY	QPRHNVMIST	EWAAPNVLRD	GFNPADVEAG
170	180	190	200	210	220	230	240
LYGSHLYVWD	WQRHEIVQTL	SLKDGLIPLE	IRFLHNPDAA	QGFVGCALSS	TIQRFYKNEG	GTWSVEKVIQ	VPPKKVKGWL
250	260	270	280	290	300	310	320
LPEMPGLITD	ILLSLDDRFL	YFSNWLHGDL	RQYDISDPQR	PRLTGQLFLG	GSIVKGGPVQ	VLEDEELKSQ	PEPLVVKGKR
330	340	350	360	370	380	390	400
VAGGPQMIQL	SLDGKRLYIT	TSLYSAWDKQ	FYPDLIREGS	VMLQVDVDTV	KGGLKLNPNF	LVDFGKEPLG	PALAHELRYP
410	420						
GGDCSSDIWI							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
827	1	1106.2441	46.85	3	38.8	13.1	2	5-34	K.CGNCGPGYSTPLEAMKGPREEIVYLPCIYR.N	

Detailed Protein Report

Protein 1150: PREDICTED: nuclear pore complex protein Nup214 isoform X4 [Homo sapiens]

Accession:	gi|530427224	**Score:**	13.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	209.0
Database Date:	2015-11-30	**pI:**	9.0
		Sequence Coverage [%]:	0.9
		No. of unique Peptides:	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MRGQLRAAGA	EGRKFAVERP	GFRGQGRGRQ	RWLLRHTEGG	AMGDEMDAMI	PEREMKDFQF	RALKKVRIFD	SPEELPKERS
90	100	110	120	130	140	150	160
SLLAVSNKYG	LVFAGGASGL	QIFPTKNLLI	QNKPGDDPNK	IVDKVQGLLV	PMKFPIHHLA	LSCDNLTLSA	CMMSSEYGSI
170	180	190	200	210	220	230	240
IAFFDVRTFS	NEAKQQKRPF	AYHKLLKDAG	GMVIDMKWNP	TVPSMVAVCL	ADGSIAVLQV	TETVKVCATL	PSTVAVTSVC
250	260	270	280	290	300	310	320
WSPKGKQLAV	GKQNGTVVQY	LPTLQEKKVI	PCPPFYESDH	PVRVLDVLWI	GTYVFAIVYA	AADGTLETSP	DVVMALLPKK
330	340	350	360	370	380	390	400
EEKHPEIFVN	FMEPCYGSCT	ERQHHYYLSY	IEEWDLVLAA	SAASTEVSIL	ARQSDQINWE	SWLLEDSSRA	ELPVTDKSDD
410	420	430	440	450	460	470	480
SLPMGVVVDY	TNQVEITISD	EKTLPPAPVL	MLLSTDGVLC	PFYMINQNPG	VKSLIKTPER	LSLEGERQPK	SPASLAPTPA
490	500	510	520	530	540	550	560
ASPVAPSAAS	FSFGSSGFKP	TLESTPVPSV	SAPNIAMKPS	FPPSTSAVKV	NLSEKFTAAA	TSTPVSSSQS	APPMSPFSSA
570	580	590	600	610	620	630	640
SKPAASGPLS	HPTPLSAPPS	SVPLKSSVLP	SPSAGRSAQG	SSSPVPSMVQ	KSPRITPPAA	KPGSPQAKSL	QPAVAEKQGH
650	660	670	680	690	700	710	720
QWKDSDPVMA	GIGEEIAHFQ	KELEELKART	SKACFQVGTS	EEMKMLRTES	DDLHTFLLEI	KETTESLHGD	ISSLKTTLLE
730	740	750	760	770	780	790	800
GFAGVEEARE	QNERNRDSGY	LHLLYKRPLD	PKSEAQLQEI	RRLHQYVKFA	VQDVNDVLDL	EWDQHLEQKK	KQRHLLVPER
810	820	830	840	850	860	870	880
ETLFNTLANN	REIINQQRKR	LNHLVDSLQQ	LRLYKQTSLW	SLSSAVPSQS	SIHSFDSDLE	SLCNALLKTT	IESHTKSLPK
890	900	910	920	930	940	950	960
VPAKLSPMKQ	AQLRNFLAKR	KTPPVRSTAP	ASLSRSAFLS	QRYYEDLDEV	SSTSSVSQSL	ESEDARTSCK	DDEAVVQAPR
970	980	990	1000	1010	1020	1030	1040
HAPVVRTPSI	QPSLLPHAAP	FAKSHLVHGS	SPGVMGTSVA	TSASKIIPQG	ADSTMLATKT	VKHGAPSPSH	PISAPQAAAA
1050	1060	1070	1080	1090	1100	1110	1120
AALRRQMASQ	APAVNTLTES	TLKNVPQVVN	VQELKNNPAT	PSTAMGSSVP	YSTAKTPHPV	LTPVAANQAK	QGSLINSLKP
1130	1140	1150	1160	1170	1180	1190	1200
SGPTPASGQL	SSGDKASGTA	KIETAVTSTP	SASGQFSKPF	SFSPSGTGFN	FGIITPTPSS	NFTAAQGATP	STKESSQPDA
1210	1220	1230	1240	1250	1260	1270	1280
FSSGGGSKPS	YEAIPESSPP	SGITSASNTT	PGEPAASSSR	PVAPSGTALS	TTSSKLETPP	SKLGELLFPS	SLAGETLGSF
1290	1300	1310	1320	1330	1340	1350	1360
SGLRVGQADD	STKPTNKASS	TSLTSTQPTK	TSGVPSGFNF	TAPPVLGKHT	EPPVTSSATT	TSVAPPAATS	TSSTAVFGSL
1370	1380	1390	1400	1410	1420	1430	1440
PVTSAGSSGV	ISFGGTSLSA	GKTSFSFGSQ	QTNSTVPPSA	PPPTTAATPL	PTSFPTLSFG	SLLSSATTPS	LPMSAGRSTE
1450	1460	1470	1480	1490	1500	1510	1520
EATSSALPEK	PGDSEVSASA	ASLLEEQQSA	QLPQAPPQTS	DSVKKEPVLA	QPAVSNSGTA	ASSTSLVALS	AEATPATTGV
1530	1540	1550	1560	1570	1580	1590	1600
PDARTEAVPP	ASSFSVPGQT	AVTAAAISSA	GPVAVETSST	PIASSTTSIV	APGPSAEAAA	FGTVTSGSSV	FAQPPAASSS
1610	1620	1630	1640	1650	1660	1670	1680
SAFNQLTNNT	ATAPSATPVF	GQVAASTAPS	LFGQQTGSTA	STAAATPQVS	SSGFSSPAFG	TTAPGVFGQT	TFGQASVFGQ
1690	1700	1710	1720	1730	1740	1750	1760
SASSAASVFS	FSQPGFSSVP	AFGQPASSTP	TSTSGSVFGA	ASSTSSSSSF	SFGQSSPNTG	GGLFGQSNAP	AFGQSPGFGQ
1770	1780	1790	1800	1810	1820	1830	1840
GGSVFGGTSA	ATTTAATSGF	SFCQASGFGS	SNTGSVFGQA	ASTGGIVFGQ	QSSSSSGSVF	GSGNTGRGGG	FFSGLGGKPS
1850	1860	1870	1880	1890	1900	1910	1920
QDAANKNPFS	SASGGFGSTA	TSNTSNLFGN	SGAKTFGGFA	SSSFGEQKPT	GTFSSGGGSV	ASQGFGFSSP	NKTGGFGAAP
1930	1940	1950	1960	1970	1980	1990	2000
VFGSPPTFGG	SPGFGGVPAF	GSAPAFTSPL	GSTGGKVFGE	GTAAASAGGF	GFGSSSNTTS	FGTLASQNAP	TFGSLSQQTS
2010	2020	2030	2040				
GFGTQSSGFS	GFGSGTGGFS	FGSNNSSVQG	FGGWRS				

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

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2086	1	1023.4014	-90.92	2	54.7	13.0	2	670-687	R.TSKACFQVGTSEEMKMLR.T	

Detailed Protein Report

Protein 1151: excitatory amino acid transporter 5 isoform 3 [Homo sapiens]

Accession:	gi|567316040	**Score:**	13.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	51.2
Database Date:	2015-11-30	**pI:**	9.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	4.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MVPHAILARG	RDVCRRNGLL	ILSVLSVIVG	CLLGFFLRTR	RLSPQEISYF	QFPGELLMRM	LKMMILPLVV	SRNMFPANLV
90	100	110	120	130	140	150	160
EATFKQYRTK	TTPVVKSPKV	APEEAPPRRI	LIYGVQEENG	SHVQNFALDL	TPPPEVVYKS	EPGTSDGMNV	LGIVFFSATM
170	180	190	200	210	220	230	240
GIMLGRMGDS	GAPLVSFCQC	LNESVMKIVA	VAVWYFPFGI	VFLIAGKILE	MDDPRAVGKK	LGFYSVTVVC	GLVLHGLFIL
250	260	270	280	290	300	310	320
PLLYFFITKK	NPIVFIRGIL	QALLIALATS	SSSATLPITF	KCLLENNHID	RRIARFVLPV	GATINMDGTA	LYEAVAAIFI
330	340	350	360	370	380	390	400
AQVNNYELDF	GQIITISITA	TAASIGAAGI	PQAGLVTMVI	VLTSVGLPTD	DITLIIAVDW	ALDRFRTMIN	VLGDALAAGI
410	420	430	440	450	460	470	480
MAHICRKDFA	RDTGTETCFP	SPETAALRDQ	ASEPPGDRGS	PAEWLCEECS	RGLRAHPGPH	LPPPRPRSSG	AG

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1964	1	701.2760	-115.08	3	53.2	13.0	0	387-406	R.TMINVLGDALAAGIMAHICR.K	Oxidation: 2, 15

Detailed Protein Report

Protein 1152: PREDICTED: coiled-coil domain-containing protein 9 isoform X4 [Homo sapiens]

Accession:	gi|578834259	**Score:**	13.0
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

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
774	1	848.7818	-149.75	2	38.5	13.0	1	243-259	R.RAGLGSAGDMTLSMTGR.E	Oxidation: 10

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Detailed Protein Report

Protein 1153: PREDICTED: uncharacterized protein LOC101929108 [Homo sapiens]

Accession:	gi|578795301	**Score:**	13.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	23.1
Database Date:	2015-11-30	**pI:**	12.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	8.7
		No. of unique Peptides:	1

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2912	1	1012.4649	-62.98	2	65.6	13.0	2	137-155	R.CCGRGGSVAVRAVSVRPHR.L	Carbamidomethyl: 1

Detailed Protein Report

Protein 1154: zinc finger protein 92 homolog [Homo sapiens]

Accession:	gi|210147475	**Score:**	13.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	45.8
Database Date:	2015-11-30	**pI:**	11.6
		Sequence Coverage [%]:	4.3
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530422737	refseq_human (refseq_human_20140103.fasta)	PREDICTED: zinc finger protein 92 homolog isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MAAILLTTRP	KVPVSFEDVS	VYFTKTEWKL	LDLRQKVLYK	RVMLENYSHL	VSLGFSFSKP	HLISQLERGE	GPWVADIPRT
90	100	110	120	130	140	150	160
WATAGLHIGD	RTQSKTSTST	QKHSGRQLPG	ADPQGGKEGQ	AARSSVLQRG	AQGLGQSSAA	GPQGPKGAEK	RYLCQQCGKA
170	180	190	200	210	220	230	240
FSRSSNLIKH	RIIHSGEKPY	ACPECGKLFR	RSFALLEHQR	IHSGEKPYAC	PECSKTFTRS	SNLIKHQVIH	SGERPFACGD
250	260	270	280	290	300	310	320
CGKLFRRSFA	LLEHARVHSG	ERPYACPECG	KAFSRSSNLI	EHQRTHRGEK	PYACGQCAKA	FKGVSQLIHH	QRSHSGERPF
330	340	350	360	370	380	390	400
ACRECGKAFR	GRSGLSQHRR	VHSGEKPYEC	SDCGKAFGRR	ANLFKHQAVH	GARRPAKAET	ARRLAGPGST	GPGSAVAATS
410	420						
PPRPSTAARP	SRPSRR						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1499	1	682.7065	38.52	3	47.5	13.0	2	152-169	R.YLCQQCGKAFSRSSNLIK.H	

Detailed Protein Report

Protein 1155: 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 1156: PREDICTED: ATPase WRNIP1 isoform X3 [Homo sapiens]

Accession:	gi|530382259	**Score:**	13.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	38.9
Database Date:	2015-11-30	**pI:**	11.0
		Sequence Coverage [%]:	2.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MATGTRTRTA	RTTRGTGTRT	LPKPPPPSGP	VAGAARTPGR	WLPRRSDRCY	RASRWPTRCV	LTRCRITSGR	ARPWARIPCC
90	100	110	120	130	140	150	160
ARSWRPTKSP	RLSCGGRRAA	ARPAMFIEDK	AVDTLAYLSD	GDARAGLNGL	QLAVLARLSS	RKMFCKKSGQ	SYSPSRVLIT
170	180	190	200	210	220	230	240
ENDVKEGLQR	SHILYDRAGE	EHYNCISALH	KSMRGSDQNA	SLYWLARMLE	GGEDPLYVAR	RLVRFASEDI	GLADPSALTQ
250	260	270	280	290	300	310	320
AVAAYQGCHF	IGMPECEVLL	AQCVVYFARA	PKSIEVYSAY	NNVKACLRNH	QGPLPPVPLH	LRNAPTRLMK	DLGYGKGYKY
330	340	350					
NPMYSEPVDQ	EYLPEELRGV	DFFKQRRC					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2702	1	648.3522	42.11	2	62.2	13.0	2	49-58	R.CYRASRWPTR.C	

Detailed Protein Report

Protein 1157: centromere protein J [Homo sapiens]

Accession: gi|130980075
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 13.0
MW [kDa]: 152.9
pI: 6.2
Sequence Coverage [%]: 1.3
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MFLMPTSSEL	NSGQNFLTQW	MTNPSRAGVI	LNRGFPILEA	DKEKRAAVDI	STSFPIKGTH	FSDSFSFINE	EDSLLEEQKL
90	100	110	120	130	140	150	160
ESNNPYKPQS	DKSETHTAFP	CIKKGPQVAA	CHSAPGHQEE	NKNDFIPDLA	SEFKEGAYKD	PLFKKLEQLK	EVQQKKQEQL
170	180	190	200	210	220	230	240
KRQQLEQLQR	LMEEQEKLLT	MVSGQCTLPG	LSLLPDDQSQ	KHRSPGNTTT	GERATCCFPS	YVYPDPTQEE	TYPSNILSHE
250	260	270	280	290	300	310	320
QSNFCRTAHG	DFVLTSKRAS	PNLFSEAQYQ	EAPVEKNNLK	EENRNHPTGE	SILCWEKVTE	QIQEANDKNL	QKHDDSSEVA
330	340	350	360	370	380	390	400
NIEERPIKAA	IGERKQTFED	YLEEQIQLEE	QELKQKQLKE	AEGPLPIKAK	PKQPFLKRGE	GLARFTNAKS	KFQKGKESKL
410	420	430	440	450	460	470	480
VTNQSTSEDQ	PLFKMDRQQL	QRKTALKNKE	LCADNPILKK	DSKARTKSGS	VTLSQKPKML	KCSNRKSLSP	SGLKIQTGKK
490	500	510	520	530	540	550	560
CDGQFRDQIK	FENKVTSNNK	ENVTECPKPC	DTGCTGWNKT	QGKDRLPLST	GPASRLAAKS	PIRETMKESE	SSLDVSLQKK
570	580	590	600	610	620	630	640
LETWEREKEK	ENLELDEFLF	LEQAADEISF	SSNSSFVLKI	LERDQQICKG	HRMSSTPVKA	VPQKTNPADP	ISHCNRSEDL
650	660	670	680	690	700	710	720
DHTAREKESE	CEVAPKQLHS	LSSADELREQ	PCKIRKAVQK	STSENQTEWN	ARDDEGVPNS	DSSTDSEEQL	DVTIKPSTED
730	740	750	760	770	780	790	800
RERGISSRED	SPQVCDDKGP	FKDTRTQEDK	RRDVDLDLSD	KDYSSDESIM	ESIKHKVSEP	SRSSSLSLSK	MDFDDERTWT
810	820	830	840	850	860	870	880
DLEENLCNHD	VVLGNESTYG	TPQTCYPNNE	IGILDKTIKR	KIAPVKRGED	LSKSRRSRSP	PTSELMMKFF	PSLKPKPKSD
890	900	910	920	930	940	950	960
SHLGNELKLN	ISQDQPPGDN	ARSQVLREKI	IELETEIEKF	KAENASLAKL	RIERESALEK	LRKEIADFEQ	QKAKELARIE
970	980	990	1000	1010	1020	1030	1040
EFKKEEMRKL	QKERKVFEKY	TTAARTFPDK	KEREEIQTLK	QQIADLREDL	KRKETKWSST	HSRLRSQIQM	LVRENTDLRE
1050	1060	1070	1080	1090	1100	1110	1120
EIKVMERFRL	DAWKRAEAIE	SSLEVEKKDK	LANTSVRFQN	SQISSGTQVE	KYKKNYLPMQ	GNPPRRSKSA	PPRDLGNLDK
1130	1140	1150	1160	1170	1180	1190	1200
GQAASPREPL	EPLNFPDPEY	KEEEEDQDIQ	GEISHPDGKV	EKVYKNGCRV	ILFPNGTRKE	VSADGKTITV	TFFNGDVKQV
1210	1220	1230	1240	1250	1260	1270	1280
MPDQRVIYYY	AAAQTTHTTY	PEGLEVLHFS	SGQIEKHYPD	GRKEITFPDQ	TVKNLFPDGQ	EESIFPDGTI	VRVQRDGNKL
1290	1300	1310	1320	1330	1340		
IEFNNGQREL	HTAQFKRREY	PDGTVKTVYA	NGHQETKYRS	GRIRVKDKEG	NVLMDTEL		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1097	1	612.4614	154.39	3	42.4	13.0	2	526-543	R.LPLSTGPASRLAAKSPIR.E	

Detailed Protein Report

Protein 1158: PREDICTED: ran-binding protein 10 isoform X5 [Homo sapiens]

Accession:	gi|578829104	**Score:**	13.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	42.6
Database Date:	2015-11-30	**pI:**	6.1
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	4.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MVSSYLVHHG	YCATATAFAR	MTETPIQEEQ	ASIKNRQKIQ	KLVLEGRVGE	AIETTQRFYP	GLLEHNPNLL	FMLKCRQFVE
90	100	110	120	130	140	150	160
MVNGTDSEVR	SLSSRSPKSQ	DSYPGSPSLS	PRHGPSSSHM	HNTGADSPSC	SNGVASTKSK	QNHSKYPAPS	SSSSSSSSSS
170	180	190	200	210	220	230	240
SSSPSSVNYS	ESNSTDSTKS	QHHSSTSNQE	TSNPWLQLER	RPNQAAPTTP	PGPTPTSTPP	HSDSEMEMEA	EHYPNGVLGS
250	260	270	280	290	300	310	320
MSTRIVNGAY	KHEDLQTDES	SMDDRHPRRQ	LCGGNQAATE	RIILFGRELQ	ALSEQLGREY	GKNLAHTEML	QDAFSLLAYS
330	340	350	360	370	380	390	400
DPWSCPVGQQ	LDPIQREPVC	AALNSAILES	QNLPKQPPLM	LALGQASECL	RLMARAGLGS	CSFARVDDYL	H

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1769	1	900.4638	3.38	2	50.8	13.0	0	356-371	K.QPPLMLALGQASECLR.L	Carbamidomethyl: 14; Oxidation: 5

Detailed Protein Report

Protein 1159: 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 1160: PREDICTED: centrosomal protein of 57 kDa isoform X1 [Homo sapiens]

Accession:	gi|578822479	**Score:**	13.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	52.4
Database Date:	2015-11-30	**pI:**	10.1
		Sequence Coverage [%]:	2.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAAASVSAAS	GSHLSNSFAE	PSRSNGSMVR	HSSSPYVVYP	SDKPFLNSDL	RRSPSKPTLA	YPESNSRAIF	SALKNLQDKI
90	100	110	120	130	140	150	160
RRLELERIQA	EESVKTLSRE	TIEYKKVLDE	QIQERENSKN	EESKHNQELT	SQLLAAENKC	NLLEKQLEYM	RNMIKHAEME
170	180	190	200	210	220	230	240
RTSVLEKQKK	MQELEAKLHE	EEQERKRMQA	KAAELQTGLE	TNRLIFEDKA	TPCVPNARRI	KKKKSKPPEK	KSSRNYFGAQ
250	260	270	280	290	300	310	320
PHYRLCLGDM	PFVAGKSTSP	SHAVVANVQL	VLHLMKQHSK	ALCNDRVINS	IPLAKQVSSR	GGKSKKLSVT	PPSSNGINEE
330	340	350	360	370	380	390	400
LSEVLQTLQD	EFGQMSFDHQ	QLAKLIQESP	TVELKDKLEC	ELEALVGRME	AKANQITKVR	KYQAQLEKQK	LEKQKKELKA
410	420	430	440	450	460	470	
TKKTLDEERN	SSSRSGITGT	TNKKDFMKLR	PGEKRRKNLQ	LLKDMQSIQN	SLQSSSLCWD	Y	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2651	1	651.8176	-28.29	2	61.4	13.0	0	192-203	K.AAELQTGLETNR.L	

Detailed Protein Report

Protein 1161: PREDICTED: piwi-like protein 2 isoform X2 [Homo sapiens]

Accession:	gi|530387871	**Score:**	12.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	90.5
Database Date:	2015-11-30	**pI:**	10.1
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDPFRPSFRG	QSPIHPSQCQ	AVRMPGCWPQ	ASKPLDPALG	RGAPAGRGHV	FGKPEEPSTQ	RGPAQRESVG	LVSMFRGLGI
90	100	110	120	130	140	150	160
ETVSKTPLKR	EMLPSGRGIL	GRGLSANLVR	KDREELSPTF	WDPKVLAAGD	SKMAETSVGW	SRTLGRGSSD	ASLLPLGRAA
170	180	190	200	210	220	230	240
GGISREVDKP	PCTFSTPSRG	PPQLSSPPAL	PQSPLHSPDR	PLVLTVEHKE	KELIVKQGSK	GTPQSLGLNL	VKIQCHNEAV
250	260	270	280	290	300	310	320
YQYHVTFSPN	VECKSMRFGM	LKDHQAVTGN	VTAFDGSILY	LPVKLQQVLE	LKSQRKTDSA	EISIKIQMTK	ILEPCSDLCI
330	340	350	360	370	380	390	400
PFYNVVFRRV	MKLLDMKLVG	RNFYDPTSAM	VLQQHRLQIW	PGYAASIRRT	DGGLFLLADV	SHKVIRNDCV	LDVMHAIYQQ
410	420	430	440	450	460	470	480
NKEHFQDECT	KLLVGNIVIT	RYNNRTYRID	DVDWNKTPKD	SFTMSDGKEI	TFLEYYSKNY	GITVKEEDQP	LLIHRPSERQ
490	500	510	520	530	540	550	560
DNHGMLLKGE	ILLLPELSFM	TGIPEKMKKD	FRAMKDLAQQ	INLSPKQHHS	ALECLLQRIA	KNEAATNELM	RWGLRLQKDV
570	580	590	600	610	620	630	640
HKIEGRVLPM	ERINLKNTSF	ITSQELNWVK	EVTRDPSILT	IPMHFWALFY	PKRAMDQARE	LVNMLEKIAG	PIGMRMSPPA
650	660	670	680	690	700	710	720
WVELKDDRIE	TYVRTIQSTL	GAEGKIQMVV	CIIMGPRDDL	YGAIKKLCCV	QSPVPSQVVN	VRTIGQPTRL	RSVAQKILLQ
730	740	750	760	770	780	790	800
INCKLGGELW	GVDIPLKQLM	VIGMDVYHDP	SRGMRSVVGF	VASINLTLTK	WYSRVVFQMP	HQEIVDSLKL	CLVGSLKKFY
810							
EEWQ							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1983	1	665.3085	7.93	2	54.9	12.9	1	437-448	K.TPKDSFTMSDGK.E	Oxidation: 8

Detailed Protein Report

Protein 1162: protein dispatched homolog 2 [Homo sapiens]

Accession:	gi|25121980	**Score:**	12.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	151.9
Database Date:	2015-11-30	**pI:**	9.3
		Sequence Coverage [%]:	0.6
		No. of unique Peptides:	1

Quantitation

Wdown:Qdown **Median:** 4.13 **CV:** 0.00 % **No. of 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	Ratios
1845	2	1011.8041	245.60	1	51.7	12.9	0	811-818	R.WLLALCHR.A		Wdown:Qdown 4.13

Detailed Protein Report

Protein 1163: **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 DAILAAADKW 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 1164: **GDP-fucose protein O-fucosyltransferase 2 isoform A precursor [Homo sapiens]**

Accession:	gi|13273311	**Score:**	12.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	48.9
Database Date:	2015-11-30	**pI:**	6.3
		Sequence Coverage [%]:	5.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MATLSFVFLL	LGAVSWPPAS	ASGQEFWPGQ	SAADILSGAA	SRRRYLLYDV	NPPEGFNLRR	DVYIRIASLL	KTLLKTEEWV
90	100	110	120	130	140	150	160
LVLPPWGRLY	HWQSPDIHQV	RIPWSEFFDL	PSLNKNIPVI	EYEQFIAESG	GPFIDQVYVL	QSYAEGWKEG	TWEEKVDERP
170	180	190	200	210	220	230	240
CIDQLLYSQD	KHEYYRGWFW	GYEETRGLNV	SCLSVQGSAS	IVAPLLLRNT	SARSVMLDRA	ENLLHDHYGG	KEYWDTRRSM
250	260	270	280	290	300	310	320
VFARHLREVG	DEFRSRHLNS	TDDADRIPFQ	EDWMKMKVKL	GSALGGPYLG	VHLRRKDFIW	GHRQDVPSLE	GAVRKIRSLM
330	340	350	360	370	380	390	400
KTHRLDKVFV	ATDAVRKEYE	ELKKLLPEMV	RFEPTWEELE	LYKDGGVAII	DQWICAHARC	LPTSLSAESG	SGGFQRFFCP
410	420	430					
KYSVSEQMVA	CVHSGHFHTV	CLLV					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2161	1	1273.4685	-105.69	2	55.6	12.9	0	402-424	K.YSVSEQMVACVHSGHFHTVCLLV.-	

Detailed Protein Report

Protein 1165: PREDICTED: arrestin domain-containing protein 5 isoform X1 [Homo sapiens]

Accession:	gi|530425368	**Score:**	12.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	23.0
Database Date:	2015-11-30	**pI:**	7.9
		Sequence Coverage [%]:	8.3
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578833485	refseq_human(refseq_human_20140103.fasta)	PREDICTED: arrestin domain-containing protein 5 isoform X2 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MGREHILAKK RMYLLVQGTS TFHKETPFQN PLFVEAEEKV SYNCCRQGTV CLQIQMERNT FTPGEKVVFT TEINNQTSKC
        90        100        110        120        130        140        150        160
IKTVVFALYA HIQYEGFTPS AERRSRLDSS ELLRQEANTP VTRFNTTKVV STFNLPLLLS VSSSTQDGEI MHTRYELVTT
       170        180        190        200        210
VHLPWSLTSL KAKVPIIITS ASVDSAICQL SEDGVLPVNP DHQN
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2805	1	965.1168	115.45	2	63.5	12.9	1	107-123	R.LDSSELLRQEANTPVTR.F	

Detailed Protein Report

Protein 1166: PREDICTED: vinexin isoform X5 [Homo sapiens]

Accession:	gi|578815141	**Score:**	12.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	73.7
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
MQGPPRSLRA	GLSLDDFIPG	HLQSHIGSSS	RGTRFHDPAP	RTVCNGGYTP	RRDASQHPDP	AWYQTWPGPG	SKPSASTKIP
90	100	110	120	130	140	150	160
ASQHTQNWSA	TWTKDSKRRD	KRWVKYEGIG	PVDESGMPIA	PRSSVDRPRD	WYRRMFQQIH	RKMPDLQLDW	TFEEPPRDPR
170	180	190	200	210	220	230	240
HLGAQQRPAH	RPGPATSSSG	RSWDHSEELP	RSTFNYRPGA	FSTVLQPSNQ	VLRRREKVDN	VWTEESWNQF	LQELETGQRP
250	260	270	280	290	300	310	320
KKPLVDDPGE	KPSQPIEVLL	ERELAELSAE	LDKDLRAIET	RLPSPKSSPA	PRRAPEQRPP	AGPASAWSSS	YPHAPYLGSA
330	340	350	360	370	380	390	400
RSLSPHKMAD	GGSPFLGRRD	FVYPSSTRDP	SASNGGGSPA	RREEKKRKAA	RLKFDFQAQS	PKELTLQKGD	IVYIHKEVDK
410	420	430	440	450	460	470	480
NWLEGEHHGR	LGIFPANYVE	VLPADEIPKP	IKPPTYQVLE	YGEAVAQYTF	KGDLEVELSF	RKGEHICLIR	KVNENWYEGR
490	500	510	520	530	540	550	560
ITGTGRQGIF	PASYVQVSRE	PRLRLCDDGP	QLPTSPRLTA	AARSARHPSS	PSALRSPADP	IDLGGQTSPR	RTGFSFPTQE
570	580	590	600	610	620	630	640
PRPQTQNLGT	PGPALSHSRG	PSHPLDLGTS	SPNTSQIHWT	PYRAMYQYRP	QNEDELELRE	GDRVDVMQQC	DDGWFVGVSR
650	660						
RTQKFGTFPG	NYVAPV						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2813	1	944.5069	60.70	2	63.6	12.9	1	35-51	R.FHDPAPRTVCNGGYTPR.R	

Detailed Protein Report

Protein 1167: 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

mdown:qdown	**Median:**	0.47	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	1.73	**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.-		Wdown:Qdown 1.73 mdown:qdown 0.47

Detailed Protein Report

Protein 1168: 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

Protein 1169: 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 1170: PREDICTED: post-GPI attachment to proteins factor 2 isoform X12 [Homo sapiens]

Accession:	gi|578820443	**Score:**	12.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	23.1
Database Date:	2015-11-30	**pI:**	11.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	13.3
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578820445	refseq_human (refseq_human_20140103.fasta)	PREDICTED: post-GPI attachment to proteins factor 2 isoform X13 [Homo sapiens]

```
         10         20         30         40         50         60         70         80
MVEMHKNMVI SLDYPRQVPV CGGDGEGATM LLHKSQDSWG MRIQHFGPRT WKERSFGRGA QLPALGELSH RRGGAPALRV
         90        100        110        120        130        140        150        160
AFLHRPALGA SLLGGLRLLE PLPQLHLPVF LLSPALPPQL RPQCRGEPRV ASAHLCLLLR GLHHPRKCFH CVHCLIPRAH
        170        180        190        200        210        220
APHLHSLAVD QEAHSKSGGS QVLQLETAAL HHQLHLLLLG AGCLLSAQHV L
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1723	1	1011.4144	-77.48	3	51.5	12.9	1	7-34	K.NMVISLDYPRQVPVCGGDGEGATMLLHK.S	Oxidation: 2, 24

Detailed Protein Report

Protein 1171: heterogeneous nuclear ribonucleoprotein U isoform b [Homo sapiens]

Accession:	gi|14141161	**Score:**	12.9
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
441	1	658.3873	-11.97	2	34.5	12.9	2	11-21	K.LKVSELKEELK.K	

Detailed Protein Report

Protein 1172: perforin-1 precursor [Homo sapiens]

Accession:	gi|40254808	**Score:**	12.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	61.3
Database Date:	2015-11-30	**pI:**	9.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.2
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|133908621	refseq_human (refseq_human_20140103.fasta)	perforin-1 precursor [Homo sapiens]

10	20	30	40	50	60	70	80
MAARLLLLGI	LLLLLPLPVP	APCHTAARSE	CKRSHKFVPG	AWLAGEGVDV	TSLRRSGSFP	VDTQRFLRPD	GTCTLCENAL
90	100	110	120	130	140	150	160
QEGTLQRLPL	ALTNWRAQGS	GCQRHVTRAK	VSSTEAVARD	AARSIRNDWK	VGLDVTPKPT	SNVHVSVAGS	HSQAANFAAQ
170	180	190	200	210	220	230	240
KTHQDQYSFS	TDTVECRFYS	FHVVHTPPLH	PDFKRALGDL	PHHFNASTQP	AYLRLISNYG	THFIRAVELG	GRISALTALR
250	260	270	280	290	300	310	320
TCELALEGLT	DNEVEDCLTV	EAQVNIGIHG	SISAEAKACE	EKKKKHKMTA	SFHQTYRERH	SEVVGGHHTS	INDLLFGIQA
330	340	350	360	370	380	390	400
GPEQYSAWVN	SLPGSPGLVD	YTLEPLHVLL	DSQDPRREAL	RRALSQYLTD	RARWRDCSRP	CPPGRQKSPR	DPCQCVCHGS
410	420	430	440	450	460	470	480
AVTTQDCCPR	QRGLAQLEVT	FIQAWGLWGD	WFTATDAYVK	LFFGGQELRT	STVWDNNNPI	WSVRLDFGDV	LLATGGPLRL
490	500	510	520	530	540	550	560
QVWDQDSGRD	DDLLGTCDQA	PKSGSHEVRC	NLNHGHLKFR	YHARCLPHLG	GGTCLDYVPQ	MLLGEPPGNR	SGAVW

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1214	1	729.3686	38.59	2	43.8	12.9	1	376-387	R.DCSRPCPPGRQK.S	Carbamidomethyl: 2, 6

Detailed Protein Report

Protein 1173: PREDICTED: KN motif and ankyrin repeat domain-containing protein 3 isoform X2 [Homo sapiens]

Accession:	gi|530427478	**Score:**	12.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	91.0
Database Date:	2015-11-30	**pI:**	4.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MCGGRWLGGG	ELLGPVCLDS	KAGPRGSSQR	DSAQPHLHPF	CRVPLTAAAG	NMAKFALNQN	LPDLGGPRLC	PVPAAGGARS
90	100	110	120	130	140	150	160
PSSPYSVETP	YGFHLDLDFL	KYIEELERGP	AARRAPGPPT	SRRPRAPRPG	LAGARSPGAW	TSSESLASDD	GGAPGILSQG
170	180	190	200	210	220	230	240
APSGLLMQPL	SPRAPVRNPR	VEHTLRETSR	RLELAQTHER	APSPGRGVPR	SPRGSGRSSP	APNLAPASPG	PAQLQLVREQ
250	260	270	280	290	300	310	320
MAAALRRLRE	LEDQARTLPE	LQEQVRALRA	EKARLLAGRA	QPEPDGEAET	RPDKLAQLRR	LTERLATSER	GGRARASPRA
330	340	350	360	370	380	390	400
DSPDGLAAGR	SEGALQVLDG	EVGSLDGTPQ	TREVAAEAVP	ETREAGAQAV	PETREAGVEA	APETVEADAW	VTEALLGLPA
410	420	430	440	450	460	470	480
AAERELELLR	ASLEHQRGVS	ELLRGRLREL	EEAREAAEEA	AAGARAQLRE	ATTQTPWSCA	EKAAQTESPA	EAPSLTQESS
490	500	510	520	530	540	550	560
PGSMDGDRAV	APAGILKSIM	KKRDGTPGAQ	PSSGPKSLQF	VGVLNGEYES	SSSEDASDSD	GDSENGGAEP	PGSSSGSGDD
570	580	590	600	610	620	630	640
SGGGSDSGTP	GPPSGGDIRD	PEPEAEAEPQ	QVAQGRCELS	PRLREACVAL	QRQLSRPRGV	ASDGGAVRLV	AQEWFRVSSQ
650	660	670	680	690	700	710	720
RRSQAEPVAR	MLEGVRRLGP	ELLAHVVNLA	DGNGNTALHY	SVSHGNLAIA	SLLLDTGACE	VNRQNRAGYS	ALMLAALTSV
730	740	750	760	770	780	790	800
RQEEEDMAVV	QRLFCMGDVN	AKASQTGQTA	LMLAISHGRQ	DMVATLLACG	ADVNAQDADG	ATALMCASEY	GRLDTVRLLL
810	820	830	840	850	860	870	880
TQPGCDPAIL	DNEGTSALAI	ALEAEQDEVA	ALLHAHLSSG	QPDTQSESPP	GSQTATPGEG	ECGDNGENPQ	VQ

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
428	1	1293.7593	91.80	2	34.0	12.9	2	1-25	-.MCGGRWLGGGELLGPVCLDSKAGPR.G	Carbamidomethyl: 17

Detailed Protein Report

Protein 1174: 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 1175: DNA annealing helicase and endonuclease ZRANB3 isoform 3 [Homo sapiens]

Accession:	gi|557440858	**Score:**	12.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	71.5
Database Date:	2015-11-30	**pI:**	9.1
		Sequence Coverage [%]:	2.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MWGMLNRKAQ	VTGSTLNGRK	EKIQAEEGDK	EKWDFLQFAE	AWTPNDSSEE	LRKEALFTHF	EKEKQHDIRS	FFVPQPKKRQ
90	100	110	120	130	140	150	160
LMTSCDESKR	FREENTVVSS	DPTKTAARDI	IDYESDVEPE	TKRLKLAASE	DHCSPSEETP	SQSKQIRTPL	VESVQEAKAQ
170	180	190	200	210	220	230	240
LTTPAFPVEG	WQCSLCTYIN	NSELPYCEMC	ETPQGSAVMQ	IDSLNHIQDK	NEKDDSQKDT	SKKVQTISDC	EKQALAQSEP
250	260	270	280	290	300	310	320
GQLADSKEET	PKIEKEDGLT	SQPGNEQWKS	SDTLPVYDTL	MFCASRNTDR	IHIYTKDGKQ	MSCNFIPLDI	KLDLWEDLPA
330	340	350	360	370	380	390	400
SFQLKQYRSL	ILRFVREWSS	LTAMKQRIIR	KSGQLFCSPI	LALEEITKQQ	TKQNCTKRYI	TKEDVAVASM	DKVKNVGGHV
410	420	430	440	450	460	470	480
RLITKESRPR	DPFTKKLLED	GACVPFLNPY	TVQADLTVKP	STSKGYLQAV	DNEGNPLCLR	CQQPTCQTKQ	ACKANSWDSR
490	500	510	520	530	540	550	560
FCSLKCQEEF	WIRSNNSYLR	AKVFETEHGV	CQLCNVNAQE	LFLRLRDAPK	SQRKNLLYAT	WTSKLPLEQL	NEMIRNPGEG
570	580	590	600	610	620	630	
HFWQVDHIKP	VYGGGGQCSL	DNLQTLCTVC	HKERTARQAK	ERSQVRRQSL	ASKHGSDITR	FLVKK	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1603	1	853.0728	174.90	2	48.8	12.9	1	93-108	R.EENTVVSSDPTKTAAR.D	

Detailed Protein Report

Protein 1176: PREDICTED: alpha-tubulin N-acetyltransferase isoform X9 [Homo sapiens]

Accession:	gi|530382649	**Score:**	12.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	25.8
Database Date:	2015-11-30	**pI:**	9.6
		Sequence Coverage [%]:	9.3
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530429736	refseq_human(refseq_human_20140103.fasta)	PREDICTED: alpha-tubulin N-acetyltransferase isoform X9 [Homo sapiens]
gi|530429452	refseq_human(refseq_human_20140103.fasta)	PREDICTED: alpha-tubulin N-acetyltransferase isoform X9 [Homo sapiens]
gi|530429087	refseq_human(refseq_human_20140103.fasta)	PREDICTED: alpha-tubulin N-acetyltransferase isoform X9 [Homo sapiens]
gi|530428827	refseq_human(refseq_human_20140103.fasta)	PREDICTED: alpha-tubulin N-acetyltransferase isoform X9 [Homo sapiens]
gi|530428535	refseq_human(refseq_human_20140103.fasta)	PREDICTED: alpha-tubulin N-acetyltransferase isoform X9 [Homo sapiens]
gi|530428190	refseq_human(refseq_human_20140103.fasta)	PREDICTED: alpha-tubulin N-acetyltransferase isoform X9 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MEFPFDVDAL FPERITVLDQ HLRPPARRPG TTTPARVDLQ QQIMTIIDEL GKASAKAQNL SAPITSASRM QSNRHVVYIL
        90        100        110        120        130        140        150        160
KDSSARPAGK GAIIGFIKVG YKKLFVLDDR EAHNEVEPLC ILDFYIHESV QRHGHGRELF QYMLQKERVE PHQLAIDRPS
       170        180        190        200        210        220        230
QKLLKFLNKH YNLETTVPQV NNFVIFEGFF AHQHPPARKL PPKRAEGDIK PYSSSDREWG LPQVW
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
109	1	712.4379	47.78	3	30.1	12.9	2	82-102	K.DSSARPAGKGAIIGFIKVGYK.K	

Detailed Protein Report

Protein 1177: mucin-13 precursor [Homo sapiens]

Accession:	gi|308736985	**Score:**	12.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	54.6
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
MKAIIHLTLL ALLSVNTATN QGNSADAVTT TETATSGPTV AAADTTETNF PETASTTANT PSFPTATSPA PPIISTHSSS

        90        100        110        120        130        140        150        160
TIPTPAPPII STHSSSTIPI PTAADSESTT NVNSLATSDI ITASSPNDGL ITMVPSETQS NNEMSPTTED NQSSGPPTGT

       170        180        190        200        210        220        230        240
ALLETSTLNS TGPSNPCQDD PCADNSLCVK LHNTSFCLCL EGYYYNSSTC KKGKVFPGKI SVTVSETFDP EEKHSMAYQD

       250        260        270        280        290        300        310        320
LHSEITSLFK DVFGTSVYGQ TVILTVSTSL SPRSEMRADD KFVNVTIVTI LAETTSDNEK TVTEKINKAI RSSSSNFLNY

       330        340        350        360        370        380        390        400
DLTLRCDYYG CNQTADDCLN GLACDCKSDL QRPNPQSPFC VASSLKCPDA CNAQHKQCLI KKSGGAPECA CVPGYQEDAN

       410        420        430        440        450        460        470        480
GNCQKCAFGY SGLDCKDKFQ LILTIVGTIA GIVILSMIIA LIVTARSNNK TKHIEEENLI DEDFQNLKLR STGFTNLGAE

       490        500        510        520
GSVFPKVRIT ASRDSQMQNP YSRHSSMPRP DY
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1875	1	806.3633	-50.77	2	52.1	12.9	0	471-486	R.STGFTNLGAEGSVFPK.V	

Detailed Protein Report

Protein 1178: PNMA-like protein 1 isoform b [Homo sapiens]

Accession:	gi|156766054	**Score:**	12.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	41.8
Database Date:	2015-11-30	**pI:**	6.8
		Sequence Coverage [%]:	7.9
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MSKTMAMNLL EDWCRGMEVD IHRSLLVTGI PEDCGQAEIE ETLNGVLSPL GPYRVLNKIF VREENVKAAL IEVGEGVNLS
        90        100        110        120        130        140        150        160
TIPREFPGRG GVWRVVCRDP TQDAEFLKNL NEFLDAEGRT WEDVVRLLQL NHPTLSQNQH QPPENWAEAL GVLLGAVVQI
       170        180        190        200        210        220        230        240
IFCMDAEIRS REEARAQEAA EFEEMAAWAL AAGRKVKKEP GLAAEVGSAL KAETPNNWNA TEDQHEPTKP LVRRAGAKSR
       250        260        270        280        290        300        310        320
SRRKKQKKNS RQEAVPWKKP KGINSNSTAN LEDPEVGDAE SMAISEPIKG SRKPCVNKEE LALKKPMAKC AWKGPREPPQ
       330        340        350        360        370        380
DARAEAESPG GASESDQDGG HESPPKKKAV AWVSAKNPAP MRKKKKNPER FDLGDHPY
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1867	1	1011.4210	-20.28	3	52.0	12.9	1	317-346	R.EPPQDARAEAESPGGASESDQDGGHESPPK.K	

Detailed Protein Report

Protein 1179: protein FAM72B [Homo sapiens]

Accession:	gi|155029537	**Score:**	12.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	16.6
Database Date:	2015-11-30	**pI:**	5.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	5.4
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	2.10	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.88	**CV:**	0.00 %	**No. of Peptides:**	1

```
        10         20         30         40         50         60         70         80
MSTNICSFKD RCVSILCCKF CKQVLSSRGM KAVLLADTEI DLFSTDIPPT NAVDFTGRCY FTKICKCKLK DIACLKCGNI
        90        100        110        120        130        140        150
VGYHVIVPCS SCLPSCNNGH FWMFHSQAVY DINRLDSTGV NILLWGNLPE IEESTDEDVL NISAEECIR
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
223	1	491.6240	-214.74	2	31.5	12.8	0	12-19	R.CVSILCCK.F	Carbamidomethyl: 1, 6	Wdown:Qdown 0.88 mdown:qdown 2.10

Detailed Protein Report

Protein 1180: zinc finger SWIM domain-containing protein 3 [Homo sapiens]

Accession: gi|57863255
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 12.8
MW [kDa]: 79.4
pI: 7.9
Sequence Coverage [%]: 1.1
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MELGSCFKTY	EDFKECFSAY	KRENRCSFIL	RDCVSVRFHN	LNHGTSIRED	ILYVQVKFVC	IRTQSNRKRT	READMCPAYL
90	100	110	120	130	140	150	160
LLRYNERLDR	LFISELNTQH	IHGDSKVASP	GGDTTGKSQK	TMCLQRLQPV	QPTTKKDLDT	AEKSLVEPSF	CLDKVQVSSK
170	180	190	200	210	220	230	240
PEQEGITPSD	LAKIAKVMKN	FLKVDEGSMA	SFSVGDSQHL	DRLSFQSSKM	TDLFIRFPEN	LLLHRVENTQ	GHILYAFLVE
250	260	270	280	290	300	310	320
NKERESRVVH	FAVLKAETVT	SVAKMLSIFT	EFNSDWPKVK	VVFVDPSFHY	RAILQEIFPA	ARILLSIYHT	TRLLEKKLHR
330	340	350	360	370	380	390	400
SSANPSFKRL	MKEALREAVF	VTSEASLKNL	CQMSQAVLDE	DLFNFLQAHW	FTCELLWYMH	VRKGLLACNT	YMDSLDIVTS
410	420	430	440	450	460	470	480
KVSSLFREQQ	SLLDCILCFV	DYIDFFNTKG	LKNLPTPPPK	LKRARPASMP	LKSKKAFGIC	GESLTSLPAE	ETKPDAQQVQ
490	500	510	520	530	540	550	560
VQQQSQVPPS	QVGMLDTLHQ	SGSELAYKLC	HNEWEVVQNS	THLVDMAGSS	VDVQLLEDSH	QVSKDGCSCS	CSFQQWYHLP
570	580	590	600	610	620	630	640
CRHILALLHT	SQQPVGEAMV	CRRWQKKYQY	LLGPNGELQD	RGMVPNTGQP	EKQGRNDMIQ	DLSRELANLL	MQTEGPELEE
650	660	670	680	690	700		
RYSTLRKIVD	IWAGPSQPSE	LFQQPGDFKD	VGRLPFLWGK	QEEGEGFPPA	TAVMHY		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
974	1	530.6195	-241.54	2	41.0	12.8	1	15-22	K.ECFSAYKR.E	Carbamidomethyl: 2

Detailed Protein Report

Protein 1181: 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 1182: 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 1183: rab GTPase-binding effector protein 1 isoform 2 [Homo sapiens]

Accession:	gi|134152674	**Score:**	12.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	95.4
Database Date:	2015-11-30	**pI:**	4.8
		Sequence Coverage [%]:	3.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAQPGPASQP	DVSLQQRVAE	LEKINAEFLR	AQQQLEQEFN	QKRAKFKELY	LAKEEDLKRQ	NAVLQAAQDD	LGHLRTQLWE
90	100	110	120	130	140	150	160
AQAEMENIKA	IATVSENTKQ	EAIDEVKRQW	REEVASLQAV	MKETVRDYEH	QFHLRLEQER	TQWAQYRESA	EREIADLRRR
170	180	190	200	210	220	230	240
LSEGQEEENL	ENEMKKAQED	AEKLRSVVMP	MEKEIAALKD	KLTEAEDKIK	ELEASKVKEL	NHYLEAEKSC	RTDLEMYVAV
250	260	270	280	290	300	310	320
LNTQKSVLQE	DAEKLRKELH	EVCHLLEQER	QQHNQLKHTW	QKANDQFLES	QRLLMRDMQR	MEIVLTSEQL	RQVEELKKKD
330	340	350	360	370	380	390	400
QEDDEQQRLN	KRKDHKKADV	EEEIKIPVVC	ALTQEESSAQ	LSNEEEHLDS	TRGSVHSLDA	GLLLPSGDPF	SKSDNDMFKD
410	420	430	440	450	460	470	480
GLRRAQSTDS	LGTSGSLQSK	ALGYNYKAKS	AGNLDESDFG	PLVGADSVSE	NFDTASLGSL	QMPSGFMLTK	DQERAIKAMT
490	500	510	520	530	540	550	560
PEQEETASLL	SSVTQGMESA	YVSPSGYRLV	SETEWNLLQK	EVHNAGNKLG	RRCDMCSNYE	KQLQGIQIQE	AETRDQVKKL
570	580	590	600	610	620	630	640
QLMLRQANDQ	LEKTMKDKQE	LEDFIKQSSE	DSSHQISALV	LRAQASEILL	EELQQGLSQA	KRDVQEQMAV	LMQSREQVSE
650	660	670	680	690	700	710	720
ELVRLQKDND	SLQGKHSLHV	SLQQAEDFIL	PDTTEALREL	VLKYREDIIN	VRTAADHVEE	KLKAEILFLK	EQIQAEQCLK
730	740	750	760	770	780	790	800
ENLEETLQLE	IENCKEEIAS	ISSLKAELER	IKVEKGQATV	EQLMFEEKNK	AQRLQTELDV	SEQVQRDFVK	LSQTLQVQLE
810	820	830					
RIRQADSLER	IRAILNDTKL	TDINQLPET					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1654	1	954.7334	-84.91	3	49.4	12.8	1	721-745	K.ENLEETLQLEIENCKEEIASISSLK.A	

Detailed Protein Report

Protein 1184: PREDICTED: protein CBFA2T3 isoform X1 [Homo sapiens]

Accession:	gi|530424752	**Score:**	12.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	68.3
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
MPASRLRDRA	ASSASGSTCG	SMSQTHPVLE	SGLLASAGCS	APRGPRKGGP	APVDRKAKAS	AMPDSPAEVK	TQPRSTPPSM
90	100	110	120	130	140	150	160
PPPPPAASQG	ATRPPSFTPH	TLMNGSSHSP	TAINGAPCTP	NGFSNGPATS	STASLSTQHL	PPACGARQLS	KLKRFLTTLQ
170	180	190	200	210	220	230	240
QFGSDISPEI	GERVRTLVLG	LVNSTLTIEE	FHSKLQEATN	FPLRPFVIPF	LKANLPLLQR	ELLHCARLAK	QTPAQYLAQH
250	260	270	280	290	300	310	320
EQLLLDASAS	SPIDSSELLL	EVNENGKRRT	PDRTKENGSD	RDPLHPEHLS	KRPCTLNPAQ	RYSPSNGPPQ	PTPPPHYRLE
330	340	350	360	370	380	390	400
DIAMAHHFRD	AYRHPDPREL	RERHRPLVVP	GSRQEEVIDH	KLTEREWAEE	WKHLNNLLNC	IMDMVEKTRR	SLTVLRRCQE
410	420	430	440	450	460	470	480
ADREELNHWA	RRYSDAEDTK	KGPAPAAARP	RSSSAGPEGP	QLDVPREFLP	RTLTGYVPED	IWRKAEEAVN	EVKRQAMSEL
490	500	510	520	530	540	550	560
QKAVSDAERK	AHELITTERA	KMERALAEAK	RQASEDALTV	INQQEDSSES	CWNCGRKASE	TCSGCNAARY	CGSFCQHRDW
570	580	590	600	610	620	630	
EKHHHVCGQS	LQGPTAVVAD	PVPGPPEAAH	SLGPSLPVGA	ASPSEAGSAG	PSRPGSPSPP	GPLDTVPR	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2602	1	701.2274	-183.09	2	60.8	12.8	1	57-70	K.AKASAMPDSPAEVK.T	

Detailed Protein Report

Protein 1185: PREDICTED: dynamin-1 isoform X14 [Homo sapiens]

Accession:	gi|578817148	**Score:**	12.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	56.5
Database Date:	2015-11-30	**pI:**	6.4
		Sequence Coverage [%]:	3.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGNRGMEDLI	PLVNRLQDAF	SAIGQNADLD	LPQIAVVGGQ	SAGKSSVLEN	FVGRDFLPRG	SGIVTRRPLV	LQLVNATTEY
90	100	110	120	130	140	150	160
AEFLHCKGKK	FTDFEEVRLE	IEAETDRVTG	TNKGISPVPI	NLRVYSPHVL	NLTLVDLPGM	TKVPVGDQPP	DIEFQIRDML
170	180	190	200	210	220	230	240
MQFVTKENCL	ILAVSPANSD	LANSDALKVA	KEVDPQGQRT	IGVITKLDLM	DEGTDARDVL	ENKLLPLRRG	YIGVVNRSQK
250	260	270	280	290	300	310	320
DIDGKKDITA	ALAAERKFFL	SHPSYRHLAD	RMGTPYLQKV	LNQQLTNHIR	DTLPGLRNKL	QSQLLSIEKE	VEEYKNFRPD
330	340	350	360	370	380	390	400
DPARKTKALL	QMVQQFAVDF	EKRIEGSGDQ	IDTYELSGGA	RINRIFHERF	PFELVKMEFD	EKELRREISY	AIKNIHGIRT
410	420	430	440	450	460	470	480
GLFTPDLAFE	ATVKKQVQKL	KEPSIKCVDM	VVSELTATIR	KCSEKLQQYP	RLREEMERIV	TTHIREREGR	TKEQVMLLID
490	500						
IELAYMNTNH	EDFIGFAK						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2901	3	869.4256	-56.48	2	65.0	12.8	1	400-415	R.TGLFTPDLAFEATVKK.Q	

Detailed Protein Report

Protein 1186: reticulon-2 isoform B [Homo sapiens]

Accession:	gi|46255005	**Score:**	12.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	51.4
Database Date:	2015-11-30	**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 1187: PREDICTED: splicing regulator RBM11 isoform X4 [Homo sapiens]

Accession:	gi|578836581	**Score:**	12.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	12.7
Database Date:	2015-11-30	**pI:**	9.5
		Sequence Coverage [%]:	17.0
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MFPAQEEADR TVFVGNLEAR VREEILYELF LQAGPLTKVT ICKDREGKPK SFGFVCFKHP ESVSYAIALL NGIRLYGRPI
        90        100        110        120
NVQYRFGSSR SSEPANQSFE SCVKINSHNY SL
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2767	1	683.0222	65.19	3	65.9	12.8	1	86-104	R.FGSSRSSEPANQSFESCVK.I	

Detailed Protein Report

Protein 1188: PREDICTED: phosphatidylinositide phosphatase SAC2 isoform X2 [Homo sapiens]

Accession:	gi|578819140	**Score:**	12.8
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

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
1334	1	727.3902	-51.85	2	45.4	12.8	1	371-383	K.KQVIINLVDQAGR.E	

Detailed Protein Report

Protein 1189: zinc phosphodiesterase ELAC protein 1 [Homo sapiens]

Accession:	gi|8922122	**Score:**	12.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	40.0
Database Date:	2015-11-30	**pI:**	6.4
Modification(s):	Carbamidomethyl	**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 1190: myb-related transcription factor, partner of profilin [Homo sapiens]

Accession:	gi|60460889	**Score:**	12.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	42.5
Database Date:	2015-11-30	**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	

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Detailed Protein Report

Protein 1191: E3 ubiquitin-protein ligase RNF138 isoform 1 [Homo sapiens]

Accession:	gi|21361539	**Score:**	12.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	28.2
Database Date:	2015-11-30	**pI:**	6.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	6.9
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|395455059	refseq_human (refseq_human_20140103.fasta)	E3 ubiquitin-protein ligase RNF138 isoform 1 [Homo sapiens]

10	20	30	40	50	60	70	80
MAEDLSAATS	YTEDDFYCPV	CQEVLKTPVR	TTACQHVFCR	KCFLTAMRES	GAHCPLCRGN	VTRRERACPE	RALDLENIMR
90	100	110	120	130	140	150	160
KFSGSCRCCA	KQIKFYRMRH	HYKSCKKYQD	EYGVSSIIPN	FQISQDSVGN	SNRSETSTSD	NTETYQENTS	SSGHPTFKCP
170	180	190	200	210	220	230	240
LCQESNFTRQ	RLLDHCNSNH	LFQIVPVTCP	ICVSLPWGDP	SQITRNFVSH	LNQRHQFDYG	EFVNLQLDEE	TQYQTAVEES
250							
FQVNI							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2120	2	955.8719	-58.90	2	55.1	12.8	1	42-58	K.CFLTAMRESGAHCPLCR.G	Oxidation: 6

Detailed Protein Report

Protein 1192: neuroblastoma-amplified sequence [Homo sapiens]

Accession:	gi|41393547	**Score:**	12.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	268.4
Database Date:	2015-11-30	**pI:**	5.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	0.8
		No. of unique 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
MELLESSHHE	AEFQHLVLLL	QAWPPMKSEY	VITNNPWVRL	ATVMLTRCTM	ENKEGLGNEV	LKMCRSLYNT	KQMLPAEGVK
2250	2260	2270	2280	2290	2300	2310	2320
ELCLLLLNQS	LLLPSLKLLL	ESRDEHLHEM	ALEQITAVTT	VNDSNCDQEL	LSLLLDAKLL	VKCVSTPFYP	RIVDHLLASL
2330	2340	2350	2360	2370	2380		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2796	1	1045.0564	42.27	2	63.4	12.7	1	266-284	K.ASSCGLSAWRVLSGSPYYK.Q	Carbamidomethyl: 4

Detailed Protein Report

Protein 1193: galactose-3-O-sulfotransferase 2 [Homo sapiens]

Accession: gi|124256491
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 12.7
MW [kDa]: 46.1
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 1194: PREDICTED: zinc finger protein 44 isoform X1 [Homo sapiens]

Accession:	gi|530414905	**Score:**	12.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	58.4
Database Date:	2015-11-30	**pI:**	10.3
		Sequence Coverage [%]:	4.8
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578833313	refseq_human (refseq_human_20140103.fasta)	PREDICTED: zinc finger protein 44 isoform X3 [Homo sapiens]
gi|530414907	refseq_human (refseq_human_20140103.fasta)	PREDICTED: zinc finger protein 44 isoform X2 [Homo sapiens]

10	20	30	40	50	60	70	80
MGHSSLNCYI	RVDTGHKHRE	CHEYAEKSYT	HKQCGKGLSY	RHSFQTCERP	HTGKKPYDCK	ECGKTFSSPG	NLRRHMVVKG
90	100	110	120	130	140	150	160
GDGPYKCELC	GKAFFWPSLL	RMHERTHTGE	KPYECKQCSK	AFPVYSSYLR	HEKIHTGEKP	YECKQCSKAF	PDYSSYLRHE
170	180	190	200	210	220	230	240
RTHTGEKPYK	CKQCGKAFSV	SGSLRVHERI	HTGEKPYTCK	QCGKAFCHLG	SFQRHMIMHS	GDGPHKCKIC	GKGFDFPGSA
250	260	270	280	290	300	310	320
RIHEGTHTLE	KPYECKQCGK	LLSHRSSFRR	HMMAHTGDGP	HKCTVCGKAF	DSPSVFQRHE	RTHTGEKPYE	CKQCGKAFRT
330	340	350	360	370	380	390	400
SSSLRKHETT	HTGEQPYKCK	CGKAFSDLFS	FQSHETTHSE	EEPYECKECG	KAFSSFKYFC	RHERTHSEEK	SYECQICGKA
410	420	430	440	450	460	470	480
FSRFSYLKTH	ERTHTAEKPY	ECKQCRKAFF	WPSFLLRHER	THTGERPYEC	KHCGKAFSRS	SFCREHERTH	TGEKPYECKE
490	500	510					
CGKAFSSLSS	FNRHKRTHWK	DIL					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
958	1	946.6989	-96.52	3	40.8	12.7	2	37-60	K.GLSYRHSFQTCERPHTGKKPYDCK.E	

Detailed Protein Report

Protein 1195: plasminogen isoform 1 precursor [Homo sapiens]

Accession:	gi|4505881	**Score:**	12.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	90.5
Database Date:	2015-11-30	**pI:**	7.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEHKEVVLLL	LLFLKSGQGE	PLDDYVNTQG	ASLFSVTKKQ	LGAGSIEECA	AKCEEDEEFT	CRAFQYHSKE	QQCVIMAENR
90	100	110	120	130	140	150	160
KSSIIIRMRD	VVLFEKKVYL	SECKTGNGKN	YRGTMSKTKN	GITCQKWSST	SPHRPRFSPA	THPSEGLEEN	YCRNPDNDPQ
170	180	190	200	210	220	230	240
GPWCYTTDPE	KRYDYCDILE	CEEECMHCSG	ENYDGKISKT	MSGLECQAWD	SQSPHAHGYI	PSKFPNKNLK	KNYCRNPDRE
250	260	270	280	290	300	310	320
LRPWCFTTDP	NKRWELCDIP	RCTTPPPSSG	PTYQCLKGTG	ENYRGNVAVT	VSGHTCQHWS	AQTPHTHNRT	PENFPCKNLD
330	340	350	360	370	380	390	400
ENYCRNPDGK	RAPWCHTTNS	QVRWEYCKIP	SCDSSPVSTE	QLAPTAPPEL	TPVVQDCYHG	DGQSYRGTSS	TTTTGKKCQS
410	420	430	440	450	460	470	480
WSSMTPHRHQ	KTPENYPNAG	LTMNYCRNPD	ADKGPWCFTT	DPSVRWEYCN	LKKCSGTEAS	VVAPPPVVLL	PDVETPSEED
490	500	510	520	530	540	550	560
CMFGNGKGYR	GKRATTVTGT	PCQDWAAQEP	HRHSIFTPET	NPRAGLEKNY	CRNPDGDVGG	PWCYTTNPRK	LYDYCDVPQC
570	580	590	600	610	620	630	640
AAPSFDCGKP	QVEPKKCPGR	VVGGCVAHPH	SWPWQVSLRT	RFGMHFCGGT	LISPEWVLTA	AHCLEKSPRP	SSYKVILGAH
650	660	670	680	690	700	710	720
QEVNLEPHVQ	EIEVSRLFLE	PTRKDIALLK	LSSPAVITDK	VIPACLPSPN	YVVADRTECF	ITGWGETQGT	FGAGLLKEAQ
730	740	750	760	770	780	790	800
LPVIENKVCN	RYEFLNGRVQ	STELCAGHLA	GGTDSCQGDS	GGPLVCFEKD	KYILQGVTSW	GLGCARPNKP	GVYVRVSRFV
810	820						
TWIEGVMRNN							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1599	1	1073.5631	49.12	2	48.7	12.7	1	236-252	R.NPDRELRPWCFTTDPNK.R	Carbamidomethyl: 10

Detailed Protein Report

Protein 1196: 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

Quantitation

mdown:qdown	**Median:**	2.97	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	1.74	**CV:**	0.00 %	**No. of 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	Ratios
447	1	820.3791	-11.73	3	34.9	12.7	1	276-296	R. EKPYECNECGKAFIQMSNLVR.H		Wdown:Qdown 1.74 mdown:qdown 2.97

Detailed Protein Report

Protein 1197: 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 1198: 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

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 1199: clathrin heavy chain 1 isoform 1 [Homo sapiens]

Accession:	gi|4758012	**Score:**	12.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	191.5
Database Date:	2015-11-30	**pI:**	5.4
		Sequence Coverage [%]:	0.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAQILPIRFQ	EHLQLQNLGI	NPANIGFSTL	TMESDKFICI	REKVGEQAQV	VIIDMNDPSN	PIRRPISADS	AIMNPASKVI
90	100	110	120	130	140	150	160
ALKAGKTLQI	FNIEMKSKMK	AHTMTDDVTF	WKWISLNTVA	LVTDNAVYHW	SMEGESQPVK	MFDRHSSLAG	CQIINYRTDA
170	180	190	200	210	220	230	240
KQKWLLLTGI	SAQQNRVVGA	MQLYSVDRKV	SQPIEGHAAS	FAQFKMEGNA	EESTLFCFAV	RGQAGGKLHI	IEVGTPPTGN
250	260	270	280	290	300	310	320
QPFPKKAVDV	FFPPEAQNDF	PVAMQISEKH	DVVFLITKYG	YIHLYDLETG	TCIYMNRISG	ETIFVTAPHE	ATAGIIGVNR
330	340	350	360	370	380	390	400
KGQVLSVCVE	EENIIPYITN	VLQNPDLALR	MAVRNNLAGA	EELFARKFNA	LFAQGNYSEA	AKVAANAPKG	ILRTPDTIRR
410	420	430	440	450	460	470	480
FQSVPAQPGQ	TSPLLQYFGI	LLDQGQLNKY	ESLELCRPVL	QQGRKQLLEK	WLKEDKLECS	EELGDLVKSV	DPTLALSVYL
490	500	510	520	530	540	550	560
RANVPNKVIQ	CFAETGQVQK	IVLYAKKVGY	TPDWIFLLRN	VMRISPDQGQ	QFAQMLVQDE	EPLADITQIV	DVFMEYNLIQ
570	580	590	600	610	620	630	640
QCTAFLLDAL	KNNRPSEGPL	QTRLLEMNLM	HAPQVADAIL	GNQMFTHYDR	AHIAQLCEKA	GLLQRALEHF	TDLYDIKRAV
650	660	670	680	690	700	710	720
VHTHLLNPEW	LVNYFGSLSV	EDSLECLRAM	LSANIRQNLQ	ICVQVASKYH	EQLSTQSLIE	LFESFKSFEG	LFYFLGSIVN
730	740	750	760	770	780	790	800
FSQDPDVHFK	YIQAACKTGQ	IKEVERICRE	SNCYDPERVK	NFLKEAKLTD	QLPLIIVCDR	FDFVHDLVLY	LYRNNLQKYI
810	820	830	840	850	860	870	880
EIYVQKVNPS	RLPVVIGGLL	DVDCSEDVIK	NLILVVRGQF	STDELVAEVE	KRNRLKLLLP	WLEARIHEGC	EEPATHNALA
890	900	910	920	930	940	950	960
KIYIDSNNNP	ERFLRENPYY	DSRVVGKYCE	KRDPHLACVA	YERGQCDLEL	INVCNENSLF	KSLSRYLVRR	KDPELWGSVL
970	980	990	1000	1010	1020	1030	1040
LESNPYRRPL	IDQVVQTALS	ETQDPEEVSV	TVKAFMTADL	PNELIELLEK	IVLDNSVFSE	HRNLQNLLIL	TAIKADRTRV
1050	1060	1070	1080	1090	1100	1110	1120
MEYINRLDNY	DAPDIANIAI	SNELFEEAFA	IFRKFDVNTS	AVQVLIEHIG	NLDRAYEFAE	RCNEPAVWSQ	LAKAQLQKGM
1130	1140	1150	1160	1170	1180	1190	1200
VKEAIDSYIK	ADDPSSYMEV	VQAANTSGNW	EELVKYLQMA	RKKARESYVE	TELIFALAKT	NRLAELEEFI	NGPNNAHIQQ
1210	1220	1230	1240	1250	1260	1270	1280
VGDRCYDEKM	YDAAKLLYNN	VSNFGRLAST	LVHLGEYQAA	VDGARKANST	RTWKEVCFAC	VDGKEFRLAQ	MCGLHIVVHA
1290	1300	1310	1320	1330	1340	1350	1360
DELEELINYY	QDRGYFEELI	TMLEAALGLE	RAHMGMFTEL	AILYSKFKPQ	KMREHLELFW	SRVNIPKVLR	AAEQAHLWAE
1370	1380	1390	1400	1410	1420	1430	1440
LVFLYDKYEE	YDNAIITMMN	HPTDAWKEGQ	FKDIITKVAN	VELYYRAIQF	YLEFKPLLLN	DLLMVLSPRL	DHTRAVNYFS
1450	1460	1470	1480	1490	1500	1510	1520
KVKQLPLVKP	YLRSVQNHNN	KSVNESLNNL	FITEEDYQAL	RTSIDAYDNF	DNISLAQRLE	KHELIEFRRI	AAYLFKGNNR
1530	1540	1550	1560	1570	1580	1590	1600
WKQSVELCKK	DSLYKDAMQY	ASESKDTELA	EELLQWFLQE	EKRECFGACL	FTCYDLLRPD	VVLETAWRHN	IMDFAMPYFI
1610	1620	1630	1640	1650	1660	1670	1680
QVMKEYLTKV	DKLDASESLR	KEEEQATETQ	PIVYGQPQLM	LTAGPSVAVP	PQAPFGYGYT	APPYGQPQPG	FGYSM

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2257	2	925.3580	-133.04	1	56.7	12.7	1	904-911	R.VVGKYCEK.R	

Detailed Protein Report

Protein 1200: ladinin-1 [Homo sapiens]

Accession:	gi|20070205	**Score:**	12.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	57.1
Database Date:	2015-11-30	**pI:**	10.2
		Sequence Coverage [%]:	2.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAVSRKDWSA	LSSLARQRTL	EDEEEQERER	RRRHRNLSST	TDDEAPRLSQ	NGDRQASASE	RLPSVEEAEV	PKPLPPASKD
90	100	110	120	130	140	150	160
EDEDIQSILR	TRQERRQRRQ	VVEAAQAPIQ	ERLEAEEGRN	SLSPVQATQK	PLVSKKELEI	PPRRRLSREQ	RGPWALEEES
170	180	190	200	210	220	230	240
LVGREPEERK	KGVPEKSPVL	EKSSMPKKTA	PEKSLVSDKT	SISEKVLASE	KTSLSEKIAV	SEKRNSSEKK	SVLEKTSVSE
250	260	270	280	290	300	310	320
KSLAPGMALG	SGRRLVSEKA	SIFEKALASE	KSPTADAKPA	PKRATASEQP	LAQEPPASGG	SPATTKEQRG	RALPGKNLPS
330	340	350	360	370	380	390	400
LAKQGASDPP	TVASRLPPVT	LQVKIPSKEE	EADMSSPTQR	TYSSSLKRSS	PRTISFRMKP	KKENSETTLT	RSASMKLPDN
410	420	430	440	450	460	470	480
TVKLGEKLER	YHTAIRRSES	VKSRGLPCTE	LFVAPVGVAS	KRHLFEKELA	GQSRAEPASS	RKENLRLSGV	VTSRLNLWIS
490	500	510	520				
RTQESGDQDP	QEAQKASSAT	ERTQWGQKSD	SSLDAEV				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
775	1	585.7012	134.39	3	39.1	12.7	2	33-47	R.RHRNLSSTTDDEAPR.L	

Detailed Protein Report

Protein 1201: 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 1202: 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 1203: 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 1204: 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 1205: PREDICTED: killer cell immunoglobulin-like receptor 2DS5 [Homo sapiens]

Accession:	gi|578847295	**Score:**	12.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	33.6
Database Date:	2015-11-30	**pI:**	6.4
Modification(s):	Oxidation	**Sequence Coverage [%]:**	8.6
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MSLMVISMAC VAFFLLQGAW PHEGFRRKPS LLAHPGPLVK SEETVILQCW SDVMFEHFLL HREGTFNHTL RLIGEHIDGV
        90        100        110        120        130        140        150        160
SKGNFSIGRM TQDLAGTYRC YGSVTHSPYQ LSAPSDPLDI VITGLYEKPS LSAQPGPTVL AGESVTLSCS SRSSYDMYHL
       170        180        190        200        210        220        230        240
SREGEAHERR LPAGPKVNGT FQADFPLDPA THGGTYRCFG SFRDSPYEWS KSSDPLLVSV TGNSSNSWPS PTEPSSKTGN
       250        260        270        280        290        300        310
PRHLHVLIGT SVVKLPFTIL LFFLLHRWCS NKKNASVMDQ GPAGNRTVNR EDSDEQDHQE VSYA
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1791	1	991.8058	-8.57	3	50.9	12.6	0	1-26	-.MSLMVISMACVAFFLLQGAWPHEGFR.R	Oxidation: 1, 4

Detailed Protein Report

Protein 1206: 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 1207: prokineticin-1 precursor [Homo sapiens]

Accession: gi|14165282
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl, Oxidation

Score: 12.6
MW [kDa]: 11.7
pI: 11.6
Sequence Coverage [%]: 25.7
No. of unique Peptides: 1

```
        10         20         30         40         50         60         70         80
MRGATRVSIM LLLVTVSDCA VITGACERDV QCGAGTCCAI SLWLRGLRMC TPLGREGEEC HPGSHKVPFF RKRKHHTCPC
        90        100        110
LPNLLCSRFP DGRYRCSMDL KNINF
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1222	1	985.1748	34.31	3	43.9	12.6	2	29-55	R.DVQCGAGTCCAISLWLRGLRMCTPLGR.E	Carbamidomethyl: 10; Oxidation: 21

Detailed Protein Report

Protein 1208: 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 1209: coiled-coil domain-containing protein 7 isoform a [Homo sapiens]

Accession:	gi|37059792	**Score:**	12.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	55.7
Database Date:	2015-11-30	**pI:**	8.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.5
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|530392451	refseq_human (refseq_human_20140103.fasta)	PREDICTED: uncharacterized protein C10orf68 isoform X4 [Homo sapiens]
gi|71051596	refseq_human (refseq_human_20140103.fasta)	coiled-coil domain-containing protein 7 isoform a [Homo sapiens]

10	20	30	40	50	60	70	80
MKPVKHLLTT	SNKSANVPAL	TTKKGLHNLP	LSPELKEKHN	AKLIHDKIEP	MVLRSPPTGE	SILRYALPIP	SSKTKNLLPE
90	100	110	120	130	140	150	160
DEMIGKIIKH	LKMVVSTLEE	TYGHCDQNGE	EPFVKHEHEE	LSLSVGDDMN	SFLTYCSQFA	AQLEEALKEE	QNILESLFKW
170	180	190	200	210	220	230	240
FQWQVNQMEE	ISKDQTLLQA	EPPKPDKTVI	LNIAEIVRLV	QRFEELKNRL	KQRSKSSVKV	MLSKTMDKEN	RPEAVKSCEA
250	260	270	280	290	300	310	320
LAQKIEEFLE	AHSTDEFKDV	SATEPQTAHS	MTNRFNAMLK	VFENQANMLE	RAVNDQVLLD	AEYKQMQCDF	QLLSEEKLVL
330	340	350	360	370	380	390	400
ENELQKLKDK	EKTKPTNNRT	KKAVKTVKKK	DKGKSEDSEK	KMSPEKEFKI	KEDLDQVQKV	ARLEIENKVL	QEQLKQALQE
410	420	430	440	450	460	470	480
AEKAKHQLNY	FLNQEKLLKS	EGKTETTMQV	GNSQTKVKGE	DSKNIPLEKE	TRKSLVSDSG	GQRTSDKIQE	YPQITAQSGR
490							
LIEKRC							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2169	1	955.8950	-132.83	2	55.7	12.6	1	48-64	K.IEPMVLRSPPTGESILR.Y	Oxidation: 4

Detailed Protein Report

Protein 1210: 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 1211: PREDICTED: creatine kinase U-type, mitochondrial isoform X3 [Homo sapiens]

Accession:	gi|530405365	**Score:**	12.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	29.4
Database Date:	2015-11-30	**pI:**	9.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	4.7
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530406090	refseq_human (refseq_human_20140103.fasta)	PREDICTED: creatine kinase U-type, mitochondrial isoform X2 [Homo sapiens]

10	20	30	40	50	60	70	80
MPVKVRTGRS	IRGLSLPPAC	TRAERREVER	VVVDALSGLK	GDLAGRYYRL	SEMTEAEQQQ	LIDDHFLFDK	PVSPLLTAAG
90	100	110	120	130	140	150	160
MARDWPDARG	IWHNNEKSFL	IWVNEEDHTR	VISMEKGGNM	KRVFERFCRG	LKEVERLIQE	RGWEFMWNER	LGYILTCPSN
170	180	190	200	210	220	230	240
LGTGLRAGVH	IKLPLLSKDS	RFPKILENLR	LQKRGTGGVD	TAATGGVFDI	SNLDRLGKSE	VELVQLVIDG	VNYLIDCERR
250	260						
LERGQDIRIP	TPVIHTKH						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2616	1	683.2178	-197.10	2	61.0	12.6	2	111-122	R.VISMEKGGNMKR.V	Oxidation: 10

Detailed Protein Report

Protein 1212: PREDICTED: serine/threonine-protein kinase 38-like isoform X2 [Homo sapiens]

Accession:	gi|530399087	**Score:**	12.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	48.0
Database Date:	2015-11-30	**pI:**	8.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	4.1
		No. of unique Peptides:	1

Quantitation

Wdown:Qdown **Median:** 0.48 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MAMTAGTTTT	FPMSNHTRER	VTVAKLTLEN	FYSNLILQHE	ERETRQKKLE	VAMEEEGLAD	EEKKLRRSQH	ARKETEFLRL
90	100	110	120	130	140	150	160
KRTRLGLDDF	ESLKVIGRGA	FGEVRLVQKK	DTGHIYAMKI	LRKSDMLEKE	QVAHIRAERD	ILVEADGAWV	VKMFYSFQDK
170	180	190	200	210	220	230	240
RNLYLIMEFL	PGGDMMTLLM	KKDTLTEEET	QFYISETVLA	IDAIHQLGFI	HRDIKPDNLL	LDAKGHVKLS	DFGLCTGLKK
250	260	270	280	290	300	310	320
AHRTEFYRNL	THNPPSDFSF	QNMNSKRKAE	TWKKNRRQLA	YSTVGTPDYI	APEVFMQTGY	NKLCDWWSLG	VIMYEMLIGY
330	340	350	360	370	380	390	400
PPFCSETPQE	TYRKVMNWKE	TLVFPPEVPI	SEKAKDLILR	FCIDSENRIG	NSGVEEIKGH	PFFEGVDWEH	ISAKYHRTGL
410	420						
QIQRLGFSQL	YL						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
260	1	619.6380	39.26	3	32.0	12.5	0	2-18	M.AMTAGTTTTFPMSNHTR.E	Oxidation: 2, 12	Wdown:Qdown 0.48

Detailed Protein Report

Protein 1213: PREDICTED: uncharacterized protein LOC102725453 [Homo sapiens]

Accession:	gi|578794661	**Score:**	12.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	161.8
Database Date:	2015-11-30	**pI:**	0.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.1
		No. of unique Peptides:	1

Quantitation

mdown:qdown **Median:** 1.54 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MGNLCYCIQG	DSKNSSKKRV	KREPYSTTKV	TSGSTFNENT	RRYAVHTNQC	RRPHGFPVKK	KMYPQEDDFH	HTIFSNLERL
90	100	110	120	130	140	150	160
DKLQPTLEAS	EESLVHKDRG	DGERPVNVRV	VQVAPLRRES	TPHGDTIHDI	TNEDAVHDTT	DEDAVHGTAD	EDAVQGIADE
170	180	190	200	210	220	230	240
DAVHGIADWD	AIQGLADRDA	VHGFADGDAV	KGIADGDATQ	GIAEGDDVHG	IADGVAVQGI	ADEDAVQLIA	DEDPVHGITK
250	260	270	280	290	300	310	320
EDATQGFANK	DAAQGIANEQ	AIHGIPNEVA	IQGVANDDAV	QGVTLDDAVH	GVADGVAGIA	NEDATEGIAN	DDAIHGITNE
330	340	350	360	370	380	390	400
DTAQGIANWD	AVQDIANWDA	VHCIANEDGF	HGIDNEDAVQ	GIADWDAAQG	IADGVAAQGI	ALDDAVHGIA	NKDAAQGIAN
410	420	430	440	450	460	470	480
WDAVQDIANE	DGFHGIDNED	AVQGITNWDV	VQGIANWDTV	HSFADGVAFH	GIADGDAVQG	IALDDAVHGI	ANEDAAQGIA
490	500	510	520	530	540	550	560
NWDAVQDIAN	EDGFHGIDIE	DAAQGIDNED	AFQGIANREA	FHGIADGDAV	QGIADGVAVH	GIADGVVVHG	IADWDAAQGI
570	580	590	600	610	620	630	640
ADGDAVHGIA	DEEAAQGIAN	WDAVQDINNE	DGFHGIANED	ATQGIADGDA	AQGIADGDAV	QGIADWDTVH	GFANRVAIHG
650	660	670	680	690	700	710	720
FANRVAFHSI	ANGVPSRASL	TRRPSTASLM	RSPSRASLTR	TPSRASLTKM	ESTASITRTP	SRASPTWTPS	TASPTGSPST
730	740	750	760	770	780	790	800
ASATGSPSRA	ALTRTPSRAS	LTRTPSRASL	TTPSRASLTR	TPSTVSPTGM	PSSALLTKMD	STASITRTPP	RASPTGTPPR
810	820	830	840	850	860	870	880
ASPTGTPPRA	SPTGTPPRAS	PTGTPSRDSP	TGTPSRASLT	GTPSTDSLTG	TPSMASLTGT	PTGTPSRDSL	TGTPSRASLT
890	900	910	920	930	940	950	960
GMPSTDSLTG	TPSMASLTGT	PSRASLTGTP	PRASLTGMPS	TASLMVSPSR	ASLTTPSRAS	LMRTPSRASL	TTPSRASLMR
970	980	990	1000	1010	1020	1030	1040
TPSRASLTRT	MSMASLTRMP	PRALLTRTPP	RASLMRTPPR	ASLTRRPSTA	SLTRTPSRAS	LTKMESMALI	TRTPSRDIAN
1050	1060	1070	1080	1090	1100	1110	1120
EDGFHGIDNE	DAVQCIAEDA	VQGIATWHAV	QGIATWHAVQ	GIANWDAVQG	IADRDAVHGF	ADGDAVHDFA	SGDAVKGIAD
1130	1140	1150	1160	1170	1180	1190	1200
GNAAQGIADG	DVLHGIADGV	AIQGIANKDA	TQGIANEEAV	HSVTNADAVQ	GIANEDAIQG	IAKDDTVQGI	ANKDGVYGIA
1210	1220	1230	1240	1250	1260	1270	1280
EDAAQGIANE	DADQGIANED	TTQGIANEEA	AQGIAEDAIQ	GIANEEVAQG	IANGVAAQGI	ANEDATQGIA	NWDAVHGFAN
1290	1300	1310	1320	1330	1340	1350	1360
GDAVLSFANG	DAAQGIANGD	ATKGMGNEVT	IHGIANEDAV	QGIANEVAAQ	GIANEDAAQG	IAEDVAQGIA	NEDAAQGIAN
1370	1380	1390	1400	1410	1420	1430	1440
KEAAQGIANE	DAAQGIAEDV	AQGIANEDAA	QGIANEEAAQ	GIANRVAAQG	IANDATQGIA	EDTAQGFAND	DAVQGIANED
1450	1460	1470	1480	1490	1500	1510	1520
AVLGIANDDA	VQGIANEDGV	HGIDNEDTAQ	GIANWDSVQG	LADGDAVQGL	ADWVAVQGLA	DGDAVKGIAD	RDAVKGIADR
1530	1540	1550	1560	1570	1580	1590	
DAVKGIADGD	AAQGIPDGDV	VHGIADEDTI	QGIADEDAVQ	LIADEDPVHG	ITNEDAAQGI	TN	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
344	1	952.8297	-93.31	2	33.4	12.5	1	1-17	-.MGNLCYCIQGDSKNSSK.K	Carbamidomethyl: 5	mdown:qdown 1.54

Detailed Protein Report

Protein 1214: 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

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
919	1	662.1519	-199.14	2	40.9	12.5	0	2-15	M.PSCGACTCGAAAVR.L	Carbamidomethyl: 3

Detailed Protein Report

Protein 1215: 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 1216: TBC1 domain family member 2A isoform 2 [Homo sapiens]

Accession:	gi|222352143	**Score:**	12.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	104.0
Database Date:	2015-11-30	**pI:**	6.0
		Sequence Coverage [%]:	1.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEGAGENAPE	SSSSAPGSEE	SARDPQVPPP	EEESGDCARS	LEAVPKKLCG	YLSKFGGKGP	IRGWKSRWFF	YDERKCQLYY
90	100	110	120	130	140	150	160
SRTAQDANPL	DSIDLSSAVF	DCKADAEEGI	FEIKTPSRVI	TLKAATKQAM	LYWLQQLQMK	RWEFHNSPPA	PPATPDAALA
170	180	190	200	210	220	230	240
GNGPVLHLEL	GQEEAELEEF	LCPVKTPPGL	VGVAAALQPF	PALQNISLKH	LGTEIQNTMH	NIRGNKQAQG	TGHEPPGEDS
250	260	270	280	290	300	310	320
PQSGEPQREE	QPLASDASTP	GREPEDSPKP	APKPSLTISF	AQKAKRQNNT	FPFFSEGITR	NRTAQEKVAA	LEQQVLMLTK
330	340	350	360	370	380	390	400
ELKSQKELVK	ILHKALEAAQ	QEKRASSAYL	AAAEDKDRLE	LVRHKVRQIA	ELGRRVEALE	QERESLAHTA	SLREQQVQEL
410	420	430	440	450	460	470	480
QQHVQLLMDK	NHAKQQVICK	LSEKVTQDFT	HPPDQSPLRP	DAANRDFLSQ	QGKIEHLKDD	MEAYRTQNCF	LNSEIHQVTK
490	500	510	520	530	540	550	560
IWRKVAEKEK	ALLTKCAYLQ	ARNCQVESKY	LAGLRRLQEA	LGDEASECSE	LLRQLVQEAL	QWEAGEASSD	SIELSPISKY
570	580	590	600	610	620	630	640
DEYGFLTVPD	YEVEDLKLLA	KIQALESRSH	HLLGLEAVDR	PLRERWAALG	DLVPSAELKQ	LLRAGVPREH	RPRVWRWLVH
650	660	670	680	690	700	710	720
LRVQHLHTPG	CYQELLSRGQ	AREHPAARQI	ELDLNRTFPN	NKHFTCPTSS	FPDKLRRVLL	AFSWQNPTIG	YCQGLNRLAA
730	740	750	760	770	780	790	800
IALLVLEEEE	SAFWCLVAIV	ETIMPADYYC	NTLTASQVDQ	RVLQDLLSEK	LPRLMAHLGQ	HHVDLSLVTF	NWFLVVFADS
810	820	830	840	850	860	870	880
LISNILLRVW	DAFLYEGTKY	NEKEILRLQN	GLEIYQYLRF	FTKTISNSRK	LMNIAFNDMN	PFRMKQLRQL	RMVHRERLEA
890	900	910	920				
ELRELEQLKA	EYLERRASRR	RAVSEGCASE	DEVEGEA				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2337	1	729.3160	-42.50	2	57.6	12.5	0	249-262	R.EEQPLASDASTPGR.E	

Detailed Protein Report

Protein 1217: PREDICTED: orexin receptor type 1 isoform X2 [Homo sapiens]

Accession: gi|530362467

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Modification(s): Oxidation

Score: 12.5

MW [kDa]: 32.0

pI: 10.8

Sequence Coverage [%]: 8.5

No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MKMSFSAICG	AIICTQNSMS	GSSSQPMWLC	SSWPWWATRW	AVSVSVAVLT	LSFIALDRWY	AICHPLLFKS	TARRARGSIL
90	100	110	120	130	140	150	160
GIWAVSLAIM	VPQAAVMECS	SVLPELANRT	RLFSVCDERW	ADDLYPKIYH	SCFFIVTYLA	PLGLMAMAYF	QIFRKLWGRQ
170	180	190	200	210	220	230	240
IPGTTSALVR	NWKRPSDQLG	DLEQGLSGEP	QPRARAFLAE	VKQMRARRKT	AKMLMVVLLV	FALCYLPISV	LNVLKRVFGM
250	260	270	280	290			
FRQASDREAV	YACFTFSHWL	VYANSAANPI	IYNFLSGLPW	SLL			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1410	1	927.1430	-68.55	3	46.4	12.5	1	213-236	K.MLMVVLLVFALCYLPISVLNVLKR.V	Oxidation: 1, 3

Detailed Protein Report

Protein 1218: U8 snoRNA-decapping enzyme isoform 2 [Homo sapiens]

Accession:	gi|285026434	**Score:**	12.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	21.3
Database Date:	2015-11-30	**pI:**	6.4
		Sequence Coverage [%]:	10.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAGARRLELG	EALALGSGWR	HACHALLYAP	DPGMLFGRIP	LRYAILMQMR	FDGRLGFPGG	FVDTQDRSLE	DGLNRELREE
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
LGEAAAAFRV	ERTDYRSSHV	GSGPRVVAHF	YAKRLTLEEL	LAVEAGATRA	KDHGLEVLGL	VRVPLYTLRD	GVGGLPTFLE
170	**180**	**190**	**200**				
NSFIGSAREQ	LLEALQDLGL	LQSGSISGLK	IPAHH				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2174	1	1057.4538	-108.03	2	55.8	12.5	2	1-20	-.MAGARRLELGEALALGSGWR.H	

Detailed Protein Report

Protein 1219: PREDICTED: ankyrin repeat domain-containing protein 54 isoform X2 [Homo sapiens]

Accession:	gi|578836933	**Score:**	12.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	23.6
Database Date:	2015-11-30	**pI:**	9.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	6.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPMMWKQCSS	CWKMARIPVQ	LMTRAAQLYT	LPHAMAMTRL	CSCSWTMVLI	LTSEMGWGTR	HCTWRPAPTT	FLSSPHCYEE
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
VCGFFPSLSS	FSPSPPECSP	QLVPAGARVD	ALDRAGRTPL	HLAKSKLNIL	QEGHAQCLEA	VRLEVKQIIH	MLREYLERLG
170	**180**	**190**	**200**	**210**			
QHEQRERLDD	LCTRLQMTST	KEQVDEVTDL	LASFTSLSLQ	MQSMEKR			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1060	1	839.1982	-168.17	2	41.8	12.5	1	1-13	-.MPMMWKQCSSCWK.M	Oxidation: 3, 4

Detailed Protein Report

Protein 1220: methyltransferase-like protein 7B precursor [Homo sapiens]

Accession:	gi|164663805	**Score:**	12.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	27.8
Database Date:	2015-11-30	**pI:**	9.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	6.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDILVPLLQL	LVLLLTLPLH	LMALLGCWQP	LCKSYFPYLM	AVLTPKSNRK	MESKKRELFS	QIKGLTGASG	KVALLELGCG
90	100	110	120	130	140	150	160
TGANFQFYPP	GCRVTCLDPN	PHFEKFLTKS	MAENRHLQYE	RFVVAPGEDM	RQLADGSMDV	VVCTLVLCSV	QSPRKVLQEV
170	180	190	200	210	220	230	240
RRVLRPGGVL	FFWEHVAEPY	GSWAFMWQQV	FEPTWKHIGD	GCCLTRETWK	DLENAQFSEI	QMERQPPPLK	WLPVGPHIMG
250							
KAVK							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2769	1	973.5258	30.96	2	63.7	12.5	1	94-109	R.VTCLDPNPHFEKFLTK.S	Carbamidomethyl: 3

Detailed Protein Report

Protein 1221: PREDICTED: F-box/WD repeat-containing protein 1A isoform X1 [Homo sapiens]

Accession:	gi|530394581	**Score:**	12.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	37.0
Database Date:	2015-11-30	**pI:**	9.2
		Sequence Coverage [%]:	3.4
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	0.52	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.62	**CV:**	0.00 %	**No. of 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	Ratios
2332	3	596.6903	-176.88	2	57.8	12.5	0	148-158	R.AAVNVVDFDDK.Y		mdown:qdown 0.52 Wdown:Qdown 0.62

Detailed Protein Report

Protein 1222: 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

Quantitation

mdown:qdown	**Median:**	0.39	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	3.15	**CV:**	0.00 %	**No. of 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	Ratios
476	1	599.1470	-198.93	2	35.3	12.5	1	92-102	R.YCAGSCPRGAR.T	Carbamidomethyl: 6	Wdown:Qdown 3.15 mdown:qdown 0.39

Detailed Protein Report

Protein 1223: **PREDICTED: hydroxyacylglutathione hydrolase-like protein isoform X3 [Homo sapiens]**

Accession:	gi|530409265	**Score:**	12.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	31.5
Database Date:	2015-11-30	**pI:**	10.0
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	3.8
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MKVKVIPVLE DNYMYLVIEE LTREAVAVDV AVPKRLLEIV GREGVSLTAV LTTHHHWDHA RGNPELARLR PGLAVLGADE
        90        100        110        120        130        140        150        160
RIFSLTRRLA HGEELRFGAI HVRCLLTPGH TAGHMSYFLW EDDCPDPPAL FSGDALSVAG CGSCLEGSAQ QMYQSLAELG
       170        180        190        200        210        220        230        240
TLPPETKVFC GHEHTLSNLE FAQKVEPCND HVRAKLSWAK ARPLSRRGKR VGGEGTGFGV GGALRQGLMV TGACGHSRRG
       250        260        270        280        290        300
MRMTCPLCRR LWARSASTTP SCGWREYGCC PGASTVTWTL RKASGDCVLG
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2023	1	698.7910	-48.75	2	53.8	12.5	2	239-249	R.RGMRMTCPLCR.R	Carbamidomethyl: 10; Oxidation: 5

Detailed Protein Report

Protein 1224: transcriptional protein SWT1 [Homo sapiens]

Accession:	gi|157502207	**Score:**	12.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	103.2
Database Date:	2015-11-30	**pI:**	9.7
		Sequence Coverage [%]:	1.4
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|157502209	refseq_huma (refseq_human_20140103.fasta)	transcriptional protein SWT1 [Homo sapiens]

10	20	30	40	50	60	70	80
MSSKESCGKK	ETSQRKDTTT	SSPNFGEKDK	KERKTPASST	SSSSIRSVSS	EKRKLKSDHT	DVLYYNIKRR	QGLKRLSVEI
90	100	110	120	130	140	150	160
DTLRRRPKIG	SSSQRPIKLK	EASYSNDNQI	ILQSPSSNGT	KKDIHKCVDF	KPKDIKLTNA	GSKLDHGIKS	LSSPKIASDV
170	180	190	200	210	220	230	240
KPKAEGQASE	NKWSHLLVQR	EKMKELKKGR	NSKFRDNSEK	CVLEKWKRNQ	FSQDYNSNKI	IKEPLGSRRQ	KISFKIPIKS
250	260	270	280	290	300	310	320
RDTLQKLVEE	NVFNIDSNNS	KTKQEEREYL	ESSQVSLNVT	RQKTEHLLSD	FTYKRTVHEW	KRKHHYDHQE	SNDSHSRENL
330	340	350	360	370	380	390	400
TQSFEAPCCS	VSSESIQDAD	QEMQIVEELH	AARVGKSVDL	PGELMSMEID	LEDDVHSSSA	NNTSDRKLLI	VIDTNILMNH
410	420	430	440	450	460	470	480
LKFVRILKTT	EVPGFDKLVL	IIPWVVMQEL	DRMKEGKLLK	RAQHKAIPAV	HFINDSLKNQ	DRKLWGQSIQ	LASQKHYGLS
490	500	510	520	530	540	550	560
DENNDDRVLK	CCLQHQELFP	CSFVILCTDD	RNLRNKGLIS	GVKSLSKEEL	SAELLHLSLN	TDVCHQPCIP	KQQLKAETTP
570	580	590	600	610	620	630	640
LKESYKEEST	NSGLSILLES	IVSDLEKSLG	TGLSSILETE	MKIAFGNLWM	EILYLKPPWT	LLHLLQCFKK	HWLAVFGLVM
650	660	670	680	690	700	710	720
EKNLLLTIES	LYKNLRKANK	AVDFTTVKFL	LQDSRSLLHA	FSTRSNYDGI	LPQTFAQVNN	LLQTFAEVKT	KLKPNSSENT
730	740	750	760	770	780	790	800
VTKKQEGTSL	KNSHNQEITV	FSSSHLPQPS	RHQEIWSILE	SVWITIYQNS	TDVFQRLGSN	SALTTSNIAS	FEEAFICLQK
810	820	830	840	850	860	870	880
LMAAVRDILE	GIQRILAPNS	NYQDVETLYN	FLIKYEVNKN	VKFTAQEIYD	CVSQTEYREK	LTIGCRQLVE	MEYTMQQCNA
890	900	910					
SVYMEAKNRG	WCEDMLNYRI						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
69	1	665.8831	-34.85	2	29.6	12.5	2	515-527	R.NKGLISGVKSLSK.E	

Detailed Protein Report

Protein 1225: PREDICTED: exportin-4 isoform X3 [Homo sapiens]

Accession:	gi|530402602	**Score:**	12.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	97.1
Database Date:	2015-11-30	**pI:**	4.5
		Sequence Coverage [%]:	2.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAQDSLQCLA	QLASLHGPIF	PDEGSQVDYL	AHFIEGLLNT	INGIEIEDSE	AVGISSIISN	LITVFPRNVL	TAIPSELFSS
90	100	110	120	130	140	150	160
FVNCLTHLTC	SFGRSAALEE	VLDKDDMVYM	EAYDKLLESW	LTLVQDDKHF	HKGFFTQHAV	QVFNSYIQCH	LAAPDGTRNL
170	180	190	200	210	220	230	240
TANGVASREE	EEISELQEDD	RDQFSDQLAS	VGMLGRIAAE	HCIPLLTSLL	EERVTRLHGQ	LQRHQQQLLA	SPGSSTVDNK
250	260	270	280	290	300	310	320
MLDDLYEDIH	WLILVTGYLL	ADDTQGETPL	IPPEIMEYSI	KHSSEVDINT	TLQILGSPGE	KASSIPGYNR	TDSVIRLLSA
330	340	350	360	370	380	390	400
ILRVSEVESR	AIRADLTHLL	SPQMGKDIVW	FLKRWAKTYL	LVDEKLYDQI	SLPFSTAFGA	DTEGSQWIIG	YLLQKVISNL
410	420	430	440	450	460	470	480
SVWSSEQDLA	NDTVQLLVTL	VERRERANLV	IQCENWWNLA	KQFASRSPPL	NFLSSPVQRT	LMKALVLGGF	AHMDTETKQQ
490	500	510	520	530	540	550	560
YWTEVLQPLQ	QRFLRVINQE	NFQQMCQQEE	VKQEITATLE	ALCGIAEATQ	IDNVAILFNF	LMDFLTNCIG	LMEVYKNTPE
570	580	590	600	610	620	630	640
TVNLIIEVFV	EVAHKQICYL	GESKAMNLYE	ACLTLLQVYS	KNNLGRQRID	VTAEEEQYQD	LLLIMELLTN	LLSKEFIDFS
650	660	670	680	690	700	710	720
DTDEVFRGHE	PGQAANRSVS	AADVVLYGVN	LILPLMSQDL	LKFPTLCNQY	YKLITFICEI	FPEKIPQLPE	DLFKSLMYSL
730	740	750	760	770	780	790	800
ELGMTSMSSE	VCQLCLEALT	PLAEQCAKAQ	ETDSPLFLAT	RHFLKLVFDM	LVLQKHNTEM	TTAAGEAFYT	LVCLHQAEYS
810	820	830	840	850	860	870	
ELVETLLSSQ	QDPVIYQRLA	DAFNKLTASS	TPPTLDRKQK	MAFLKSLEEF	MANVGGLLCV	K	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2864	1	1132.6268	1.42	2	65.0	12.5	1	197-216	R.IAAEHCIPLLTSLLEERVTR.L	

Detailed Protein Report

Protein 1226: late cornified envelope protein 3E [Homo sapiens]

Accession:	gi|30410033	**Score:**	12.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	9.5
Database Date:	2015-11-30	**pI:**	12.6
		Sequence Coverage [%]:	17.4
		No. of unique Peptides:	1

```
         10         20         30         40         50         60         70         80
MSCQQNQKQC QPPPKCPSPK CPPKNPVQCL PPASSGCAPS SGGCGPSSEG GCFLNHHRRH HRCRRQRSNS CDRGSGQQGG
         90        100
GSGCCHGSGG CC
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1680	1	867.8636	-74.29	2	49.5	12.5	2	9-24	K.QCQPPPKCPSPKCPPK.N	

Detailed Protein Report

Protein 1227: CREB/ATF bZIP transcription factor [Homo sapiens]

Accession:	gi|88900495	**Score:**	12.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	37.1
Database Date:	2015-11-30	**pI:**	5.0
		Sequence Coverage [%]:	6.5
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578821635	refseq_human (refseq_human_20140103.fasta)	PREDICTED: CREB/ATF bZIP transcription factor isoform X8 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MRHSLTKLLA ASGSNSPTRS ESPEPAATCS LPSDLTRAAA GEEETAAAGS PGRKQQFGDE GELEAGRGSR GGVAVRAPSP

        90        100        110        120        130        140        150        160
EEMEEEAIAS LPGEETEDMD FLSGLELADL LDPRQPDWHL DPGLSSPGPL SSSGGGSDSG GLWRGDDDDE AAAAEMQRFS

       170        180        190        200        210        220        230        240
DLLQRLLNGI GGCSSSSDSG SAEKRRRKSP GGGGGGGSGN DNNQAATKSP RKAAAAAARL NRLKKKEYVM GLESRVRGLA

       250        260        270        280        290        300        310        320
AENQELRAEN RELGKRVQAL QEESRYLRAV LANETGLARL LSRLSGVGLR LTTSLFRDSP AGDHDYALPV GKQKQDLLEE

       330        340        350        360
DDSAGGVCLH VDKDKVSVEF CSACARKASS SLKM
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1905	1	1021.8816	-81.96	2	52.3	12.5	1	189-211	K.SPGGGGGGGSGNDNNQAATKSPR.K	

Detailed Protein Report

Protein 1228: coiled-coil domain-containing protein 167 [Homo sapiens]

Accession: gi|63003894
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 12.5
MW [kDa]: 11.5
pI: 10.1
Sequence Coverage [%]: 11.3
No. of unique Peptides: 1

```
         10         20         30         40         50         60         70         80
MTKKKRENLG VALEIDGLEE KLSQCRRDLE AVNSRLHSRE LSPEARRSLE KEKNSLMNKA SNYEKELKFL RQENRKNMLL
         90        100
SVAIFILLTL VYAYWTM
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
681	1	647.8148	-49.32	2	37.3	12.5	1	36-46	R.LHSRELSPEAR.R	

Detailed Protein Report

Protein 1229: 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 1230: transient receptor potential cation channel subfamily M member 4 isoform 2 [Homo sapiens]

Accession: gi|304766677
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 12.4
MW [kDa]: 118.6
pI: 9.1
Sequence Coverage [%]: 1.5
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MVVPEKEQSW	IPKIFKKKTC	TTFIVDSTDP	GGTLCQCGRP	RTAHPAVAME	DAFGAAVVTV	WDSDAHTTEK	PTDAYGELDF
90	100	110	120	130	140	150	160
TGAGRKHSNF	LRLSDRTDPA	AVYSLVTRTW	GFRAPNLVVS	VLGGSGGPVL	QTWLQDLLRR	GLVRAAQSTG	AWIVTGGLHT
170	180	190	200	210	220	230	240
GIGRHVGVAV	RDHQMASTGG	TKVVAMGVAP	WGVVRNRDTL	INPKGSFPAR	YRWRGDPEDG	VQFPLDYNYS	AFFLVDDGTH
250	260	270	280	290	300	310	320
GCLGGENRFR	LRLESYISQQ	KTGVGGTGID	IPVLLLLIDG	DEKMLTRIEN	ATQAQLPCLL	VAGSGGAADC	LAETLEDTLA
330	340	350	360	370	380	390	400
PGSGGARQGE	ARDRIRRFFP	KGDLEVLQAQ	VERIMTRKEL	LTVYSSEDGS	EEFETIVLKA	LVKACGSSEA	SAYLDELRLA
410	420	430	440	450	460	470	480
VAWNRVDIAQ	SELFRGDIQW	RSFHLEASLM	DALLNDRPEF	VRLLISHGLS	LGHFLTPMRL	AQLYSAAPSN	SLIRNLLDQA
490	500	510	520	530	540	550	560
SHSAGTKAPA	LKGGAAELRP	PDVGHVLRML	LGKMCAPRYP	SGGAWDPHPG	QGFGESMYLL	SDKATSPLSL	DAGLGQAPWS
570	580	590	600	610	620	630	640
DLLLWALLLN	RAQMAMYFWE	MGSNAVSSAL	GACLLLRVMA	RLEPDAEEAA	RRKDLAFKFE	GMGVDLFGEC	YRSSEVRAAR
650	660	670	680	690	700	710	720
LLLRRCPLWG	DATCLQLAMQ	ADARAFFAQD	GVQSLLTQKW	WGDMASTTPI	WALVLAFFCP	PLIYTRLITF	RKSEEEPTRE
730	740	750	760	770	780	790	800
ELEFDMDSVI	NGEGPVGLTP	GLYHLGRTVL	CIDFMVFTVR	LLHIFTVNKQ	LGPKIVIVSK	MMKDVFFFLF	FLGVWLVAYG
810	820	830	840	850	860	870	880
VATEGLLRPR	DSDFPSILRR	VFYRPYLQIF	GQIPQEDMDV	ALMEHSNCSS	EPGFWAHPPG	AQAGTCVSQY	ANWLVVLLLV
890	900	910	920	930	940	950	960
IFLLVANILL	VNLLIAMFSY	TFGKVQGNSD	LYWKAQRYRL	IREFHSRPAL	APPFIVISHL	RLLLRQLCRR	PRSPQPSSPA
970	980	990	1000	1010	1020	1030	1040
LEHFRVYLSK	EAERKLLTWE	SVHKENFLLA	RARDKRESDS	ERLKRTSQKV	DLALKQLGHI	REYEQRLKVL	EREVQQCSRV
1050	1060	1070					
LGWVAEALSR	SALLPPGGPP	PPDLPGSKD					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2774	1	937.4636	-32.07	2	63.8	12.4	1	342-357	K.GDLEVLQAQVERIMTR.K	Oxidation: 14

Detailed Protein Report

Protein 1231: 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 1232: cullin-7 isoform 2 [Homo sapiens]

Accession:	gi|41872646	**Score:**	12.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	191.0
Database Date:	2015-11-30	**pI:**	5.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	0.9
		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 1233: macrophage scavenger receptor types I and II isoform type 2 [Homo sapiens]

Accession:	gi|4505259	**Score:**	12.4
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
2764	1	913.4687	-65.26	2	63.0	12.4	2	242-257	K.GEVKVLNNITNDLRLK.D	

Detailed Protein Report

Protein 1234: PREDICTED: proline-rich transmembrane protein 1 isoform X2 [Homo sapiens]

Accession:	gi|578811995	**Score:**	12.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	16.2
Database Date:	2015-11-30	**pI:**	7.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	11.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPGTQTPAPA	EDPHSGCRDP	VPARPQACHP	KSQPYAGGTP	GGTGVTSTLP	PPPQGPGLAL	LEPRRPPHDY	MPIAVLTTIC
90	100	110	120	130	140	150	160
CFWPTGIIAI	FKAVQVRTAL	ARGDMVSAEI	ASREARNFSF	ISLAVGIAAM	VLCTILTVVI	IIAAQHHENY	WDP

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1066	1	954.8994	-21.56	2	42.0	12.4	0	1-18	-.MPGTQTPAPAEDPHSGCR.D	Carbamidomethyl: 17

Detailed Protein Report

Protein 1235: **PREDICTED: LOW QUALITY PROTEIN: uncharacterized protein LOC440292 [Homo sapiens]**

Accession:	gi|578845792	**Score:**	12.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	30.0
Database Date:	2015-11-30	**pI:**	10.3
		Sequence Coverage [%]:	7.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
METELVAEDW	NAKQVPPAFW	LRDILCFQAQ	TYTCCHKPLR	LFRGPMGSHT	HAGPACWAHL	HPGDSSLISP	WAKYPKQRPG
90	100	110	120	130	140	150	160
QGVFIRVPKK	HMQKGSACPL	WPVRGKDSGR	RRRRRQHFAP	GTSSGLRSAS	GLTRAGPALP	EARFWFCGDL	DCPDWVLAEI
170	180	190	200	210	220	230	240
STLAKMSSVK	LRLLCSQVLK	ELLGQGIDYK	KILKLTADAK	FGEHPTEFTG	PRQPWDLGLV	PGTEPAPTPH	PPPTHTPSSI
250	260	270	280				
LNLPSLVEEH	EGKKDIQSHL	PVLCQLLVEQ					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2742	1	1043.5474	-1.20	2	62.7	12.4	2	115-134	R.RQHFAPGTSSGLRSASGLTR.A	

Detailed Protein Report

Protein 1236: furin preproprotein [Homo sapiens]

Accession: gi|4505579
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 12.4
MW [kDa]: 86.6
pI: 6.0
Sequence Coverage [%]: 1.5
No. of unique Peptides: 1

Alias proteins:

Accession	Name	Description
gi|530407177	refseq_human (refseq_human_20140103.fasta)	PREDICTED: furin isoform X2 [Homo sapiens]
gi|530407175	refseq_human (refseq_human_20140103.fasta)	PREDICTED: furin isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MELRPWLLWV	VAATGTLVLL	AADAQGQKVF	TNTWAVRIPG	GPAVANSVAR	KHGFLNLGQI	FGDYYHFWHR	GVTKRSLSPH
90	100	110	120	130	140	150	160
RPRHSRLQRE	PQVQWLEQQV	AKRRTKRDVY	QEPTDPKFPQ	QWYLSGVTQR	DLNVKAAWAQ	GYTGHGIVVS	ILDDGIEKNH
170	180	190	200	210	220	230	240
PDLAGNYDPG	ASFDVNDQDP	DPQPRYTQMN	DNRHGTRCAG	EVAAVANNGV	CGVGVAYNAR	IGGVRMLDGE	VTDAVEARSL
250	260	270	280	290	300	310	320
GLNPNHIHIY	SASWGPEDDG	KTVDGPARLA	EEAFFRGVSQ	GRGGLGSIFV	WASGNGGREH	DSCNCDGYTN	SIYTLSISSA
330	340	350	360	370	380	390	400
TQFGNVPWYS	EACSSTLATT	YSSGNQNEKQ	IVTTDLRQKC	TESHTGTSAS	APLAAGIIAL	TLEANKNLTW	RDMQHLVVQT
410	420	430	440	450	460	470	480
SKPAHLNAND	WATNGVGRKV	SHSYGYGLLD	AGAMVALAQN	WTTVAPQRKC	IIDILTEPKD	IGKRLEVRKT	VTACLGEPNH
490	500	510	520	530	540	550	560
ITRLEHAQAR	LTLSYNRRGD	LAIHLVSPMG	TRSTLLAARP	HDYSADGFND	WAFMTTHSWD	EDPSGEWVLE	IENTSEANNY
570	580	590	600	610	620	630	640
GTLTKFTLVL	YGTAPEGLPV	PPESSGCKTL	TSSQACVVCE	EGFSLHQKSC	VQHCPPGFAP	QVLDTHYSTE	NDVETIRASV
650	660	670	680	690	700	710	720
CAPCHASCAT	CQGPALTDCL	SCPSHASLDP	VEQTCSRQSQ	SSRESPPQQQ	PPRLPPEVEA	GQRLRAGLLP	SHLPEVVAGL
730	740	750	760	770	780	790	800
SCAFIVLVFV	TVFLVLQLRS	GFSFRGVKVY	TMDRGLISYK	GLPPEAWQEE	CPSDSEEDEG	RGERTAFIKD	QSAL

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
554	1	731.2311	-195.37	2	35.8	12.4	1	749-760	K.VYTMDRGLISYK.G	Oxidation: 4

Detailed Protein Report

Protein 1237: PREDICTED: mitochondrial Rho GTPase 2 isoform X9 [Homo sapiens]

Accession:	gi|578828338	**Score:**	12.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	52.3
Database Date:	2015-11-30	**pI:**	6.7
		Sequence Coverage [%]:	1.5
		No. of unique Peptides:	1

Quantitation

mdown:qdown **Median:** 1.63 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MGGPRRGPVG	NKSDLRSGSS	MEAVLPIMSQ	FPEIETCVEC	SAKNLRNISE	LFYYAQKAVL	HPTAPLYDPE	AKQKSCFGHP
90	100	110	120	130	140	150	160
LAPQALEDVK	TVVCRNVAGG	VREDRLTLDG	FLFLNTLFIQ	RGRHETTWTI	LRRFGYSDAL	ELTADYLSPL	IHVPPGCSTE
170	180	190	200	210	220	230	240
LNHLGYQFVQ	RVFEKHDQDR	DGALSPVELQ	SLFSVFPAAP	WGPELPRTVR	TEAGRLPLHG	YLCQWTLVTY	LDVRSCLGHL
250	260	270	280	290	300	310	320
GYLGYPTLCE	QDQAHAITVT	REKRLDQEKG	QTQRSVLLCK	VVGARGVGKS	AFLQAFLGRG	LGHQDTREQP	PGYAIDTVQV
330	340	350	360	370	380	390	400
NGQEKYLILC	EVGTDGLLAT	SLDATCDVAC	LMFDGSDPKS	FAHCASVYKH	HYMDGQTPCL	FVSSKADLPE	GVAVSGPSPA
410	420	430	440	450	460	470	480
EFCRKHRLPA	PVPFSCAGPA	EPSTTIFTQL	ATMAAFPHLV	HAELHPSSFW	LRGLLGVVGA	AVAAVLSFSL	YRVLVKSQ

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2627	2	727.3858	-48.33	1	63.6	12.4	1	6-12	R.RGPVGNK.S		mdown:qdown 1.63

Detailed Protein Report

Protein 1238: PREDICTED: ezrin isoform X1 [Homo sapiens]

Accession: gi|578812963
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 12.4
MW [kDa]: 64.0
pI: 5.7
Sequence Coverage [%]: 1.5
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MPKPINVRVT	TMDAELEFAI	QPNTTGKQLF	DQVVKTIGLR	EVWYFGLHYV	DNKGFPTWLK	LDKKVSAQEV	RKENPLQFKF
90	100	110	120	130	140	150	160
RAKFYPEDVA	EELIQDITQK	LFFLQVKEGI	LSDEIYCPPE	TAVLLGSYAV	QAKFGDYNKE	VHKSGYLSSE	RLIPQRVMDQ
170	180	190	200	210	220	230	240
HKLTRDQWED	RIQVWHAEHR	GMLKDNAMLE	YLKIAQDLEM	YGINYFEIKN	KKGTDLWLGV	DALGLNIYEK	DDKLTPKIGF
250	260	270	280	290	300	310	320
PWSEIRNISF	NDKKFVIKPI	DKKAPDFVFY	APRLRINKRI	LQLCMGNHEL	YMRRRKPDTI	EVQQMKAQAR	EEKHQKQLER
330	340	350	360	370	380	390	400
QQLETEKKRR	ETVEREKEQM	MREKEELMLR	LQDYEEKTKK	AERELSEQIQ	RALQLEEERK	RAQEEAERLE	ADRMAALRAK
410	420	430	440	450	460	470	480
EELERQAVDQ	IKSQEQLAAE	LAEYTAKIAL	LEEARRRKED	EVEEWQHRAK	EAQDDLVKTK	EELHLVMTAP	PPPPPPVYEP
490	500	510	520	530	540	550	
VSYHVQESLQ	DEGAEPTGYS	AELSSEGIRD	DRNEEKRITE	AEKNERVQRQ	LLGTGRAIWG	GRD	

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	428-435	K.IALLEEAR.R	

Detailed Protein Report

Protein 1239: 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

Quantitation

mdown:qdown **Median:** 0.56 **CV:** 0.00 % **No. of 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	Ratios
890	1	622.8509	51.55	2	40.6	12.4	0	1-11	-.MQAAALPEEIR.W	Oxidation: 1	mdown:qdown 0.56

Detailed Protein Report

Protein 1240: 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

Quantitation

mdown:qdown	**Median:**	0.86	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	2.58	**CV:**	0.00 %	**No. of 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	Ratios
411	4	537.6424	-263.75	2	34.5	12.4	0	19-28	R.SSMSGLHLVK.Q	Oxidation: 3	mdown:qdown 0.86 Wdown:Qdown 2.58

Detailed Protein Report

Protein 1241: PREDICTED: mediator of DNA damage checkpoint protein 1 isoform X4 [Homo sapiens]

Accession:	gi|530428840	**Score:**	12.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	205.7
Database Date:	2015-11-30	**pI:**	5.3
Modification(s):	Oxidation	**Sequence Coverage [%]:**	0.9
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	0.49	**CV:**	0.00 %	**No. of Peptides:**	1	

Detailed Protein Report

10	20	30	40	50	60	70	80
MEDTQAIDWD	VEEEEETEQS	SESLRCNVEP	VGRLHIFSGA	HGPEKDFPLH	LGKNVVGRMP	DCSVALPFPS	ISKQHAEIEI
90	100	110	120	130	140	150	160
LAWDKAPILR	DCGSLNGTQI	LRPPKVLSPG	VSHRLRDQEL	ILFADLLCQY	HRLDVSLPFV	SRGPLTVEET	PRVQGETQPQ
170	180	190	200	210	220	230	240
RLLLAEDSEE	EVDFLSERRM	VKKSRTTSSS	VIVPESDEEG	HSPVLGGLGP	PFAFNLNSDT	DVEEGQQPAT	EEASSAARRG
250	260	270	280	290	300	310	320
ATVEAKQSEA	EVVTEIQLEK	DQPLVKERDN	DTKVKRGAGN	GVVPAGVILE	RSQPPGEDSD	TDVDDDSRPP	GRPAEVHLER
330	340	350	360	370	380	390	400
AQPFGFIDSD	TDAEEERIPA	TPVVIPMKKR	KIFHGVGTRG	PGAPGLAHLQ	ESQAGSDTDV	EEGKAPQAVP	LEKSQASMVI
410	420	430	440	450	460	470	480
NSDTDDEEEV	SAALTLAHLK	ESQPAIWNRD	AEEDMPQRVV	LLQRSQTTTE	RDSDTDVEEE	ELPVENREAV	LKDHTKIRAL
490	500	510	520	530	540	550	560
VRAHSEKDQP	PFGDSDDSVE	ADKSSPGIHL	ERSQASTTVD	INTQVEKEVP	PGSAIIHIKK	HQVSVEGTNQ	TDVKAVGGPA
570	580	590	600	610	620	630	640
KLLVVSLEEA	WPLHGDCETD	AEEGTSLTAS	VVADVRKSQL	PAEGDAGAEW	AAAVLKQERA	HEVGAQGGPP	VAQVEQDLPI
650	660	670	680	690	700	710	720
SRENLTDLVV	DTDTLGESTQ	PQREGAQVPT	GREREQHVGG	TKDSEDNYGD	SEDLDLQATQ	CFLENQGLEA	VQSMEDEPTQ
730	740	750	760	770	780	790	800
AFMLTPPQEL	GPSHCSFQTT	GTLDEPWEVL	ATQPFCLRES	EDSETQPFDT	HLEAYGPCLS	PPRAIPGDQH	PESPVHTEPM
810	820	830	840	850	860	870	880
GIQGRGRQTV	DKVMGLLNCK	MPPAEKASRI	RAAEKVSRGD	QESPDACLPP	TVPEAPAPPQ	KPLNSQSQKH	LAPPPLLSPL
890	900	910	920	930	940	950	960
LPSIKPTVRK	TRQDGSQEAP	EAPLSSELEP	FHPKPKIRTR	KSSRMTPFPA	TSAAPEPHPS	TSTAQPVTPK	PTSQATRSRT
970	980	990	1000	1010	1020	1030	1040
NRSSVKTPEP	VVPTAPELQP	STSTDQPVTS	EPTSQVTRGR	KSRSSVKTPE	TVVPTALELQ	PSTSTDRPVT	SEPTSQATRG
1050	1060	1070	1080	1090	1100	1110	1120
RKNRSSVKTP	EPVVPTAPEL	QPSTSTDQPV	TSEPTYQATR	GRKNRSSVKT	PEPVVPTAPE	LRPSTSTDRP	VTPKPTSRTT
1130	1140	1150	1160	1170	1180	1190	1200
RSRTNMSSVK	TPETVVPTAP	ELQISTSTDQ	PVTPKPTSRT	TRSRTNMSSV	KNPESTVPIA	PELPPSTSTE	QPVTPEPTSR
1210	1220	1230	1240	1250	1260	1270	1280
ATRGRKNRSS	GKTPETLVPT	APKLEPSTST	DQPVTPEPTS	QATRGRTNRS	SVKTPETVVP	TAPELQPSTS	TDQPVTPEPT
1290	1300	1310	1320	1330	1340	1350	1360
SQATRGRTDR	SSVKTPETVV	PTAPELQASA	STDQPVTSEP	TSRTTRGRKN	RSSVKTPETV	VPAAPELQPS	TSTDQPVTPE
1370	1380	1390	1400	1410	1420	1430	1440
PTSRATRGRT	NRSSVKTPES	IVPIAPELQP	STSRNQLVTP	EPTSRATRCR	TNRSSVKTPE	PVVPTAPEPH	PTTSTDQPVT
1450	1460	1470	1480	1490	1500	1510	1520
PKLTSRATRR	KTNRSSVKTP	KPVEPAASDL	EPFTPTDQSV	TPEAIAQGGQ	SKTLRSSTVR	AMPVPTTPEF	QSPVTTDQPI
1530	1540	1550	1560	1570	1580	1590	1600
SPEPITQPSC	IKRQRAAGNP	GSLAAPIDHK	PCSAPLEPKS	QASRNQRWGA	VRAAESLTAI	PEPASPQLLE	TPIHASQIQK
1610	1620	1630	1640	1650	1660	1670	1680
VEPAGRSRFT	PELQPKASQS	RKRSLATMDS	PPHQKQPQRG	EVSQKTVIIK	EEEEDTAEKP	GKEEDVVTPK	PGKRKRDQAE
1690	1700	1710	1720	1730	1740	1750	1760
EEPNRIPSRS	LRRTKLNQES	TAPKVLFTGV	VDARGERAVL	ALGGSLAGSA	AEASHLVTDR	IRRTVKFLCA	LGRGIPILSL
1770	1780	1790	1800	1810	1820	1830	1840
DWLHQSRKAG	FFLPPDEYVV	TDPEQEKNFG	FSLQDALSRA	RERRLLEGYE	IYVTPGVQPP	PPQMGEIISC	CGGTYLPSMP
1850	1860	1870	1880	1890	1900		
RSYKPQRVVI	TCPQDFPHCS	IPLRVGLPLL	SPEFLLTGVL	KQEAKPEAFV	LSPLEMSST		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1647	1	938.9364	-41.92	2	49.3	12.4	2	813-829	K.VMGLLNCKMPPAEKASR.I	Oxidation: 2, 9	mdown:qdown 0.49

Detailed Protein Report

Protein 1242: **PREDICTED: phosphorylase b kinase regulatory subunit alpha, liver isoform isoform X6 [Homo sapiens]**

Accession:	gi|578837920	**Score:**	12.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	118.7
Database Date:	2015-11-30	**pI:**	5.8
		Sequence Coverage [%]:	1.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MWERGDKTNQ	GIPELNASSV	GMAKAALEAI	DELDLFGAHG	GRKSVIHVLP	DEVEHCQSIL	FSMLPRASTS	KEIDAGLLSI
90	100	110	120	130	140	150	160
ISFPAFAVED	VNLVNVTKNE	IISKLQGRYG	CCRFLRDGYK	TPREDPNRLH	YDPAELKLFE	NIECEWPVFW	TYFIIDGVFS
170	180	190	200	210	220	230	240
GDAVQVQEYR	EALEGILIRG	KNGIRLVPEL	YAVPPNKVDE	EYKNPHTVDR	VPMGKVPHLW	GQSLYILSSL	LAEGFLAAGE
250	260	270	280	290	300	310	320
IDPLNRRFST	SVKPDVVVQV	TVLAENNHIK	DLLRKHGVNV	QSIADIHPIQ	VQPGRILSHI	YAKLGRNKNM	NLSGRPYRHI
330	340	350	360	370	380	390	400
GVLGTSKLYV	IRNQIFTFTP	QFTDQHHFYL	ALDNEMIVEM	LRIELAYLCT	CWRMTGRPTL	TFPISRTMLT	NDGSDIHSAV
410	420	430	440	450	460	470	480
LSTIRKLEDG	YFGGARVKLG	NLSEFLTTSF	YTYLTFLDPD	CDEKLFDNAS	EGTFSPDSDS	DLVGYLEDTC	NQESQDELDH
490	500	510	520	530	540	550	560
YINHLLQSTS	LRSYLPPLCK	NTEDRHVFSA	IHSTRDILSV	MAKAKGLEVP	FVPMTLPTKV	LSAHRKSLNL	VDSPQPLLEK
570	580	590	600	610	620	630	640
VPESDFQWPR	DDHGDVDCEK	LVEQLKDCSN	LQDQADILYI	LYVIKGPSWD	TNLSGQHGVT	VQNLLGELYG	KAGLNQEWGL
650	660	670	680	690	700	710	720
IRYISGLLRK	KVEVLAEACT	DLLSHQKQLT	VGLPPEPREK	IISAPLPPEE	LTKLIYEASG	QDISIAVLTQ	EIVVYLAMYV
730	740	750	760	770	780	790	800
RAQPSLFVEM	LRLRIGLIIQ	VMATELARSL	NCSGEEASES	LMNLSPFDMK	NLLHHILSGK	EFGVERSVRP	IHSSTSSPTI
810	820	830	840	850	860	870	880
SIHEVGHTGV	TKTERSGINR	LRSEMKQMTR	RFSADEQFFS	VGQAASSSAH	SSKSAVTVPR	DYCRSSTPSS	PTGTSSSDSG
890	900	910	920	930	940	950	960
GHHIGWGERQ	GQWLRRRRLD	GAINRVPVGF	YQRVWKILQK	CHGLSIDGYV	LPSSTTREMT	PHEIKFAVHV	ESVLNRVPQP
970	980	990	1000	1010	1020	1030	1040
EYRQLLVEAI	MVLTLLSDTE	MTSIGGIIHV	DQIVQMASQL	FLQDQVSIGA	MDTLEKDQAT	GICHFFYDSA	PSGAYGTMTY
1050	1060	1070					
LTRAVASYLQ	ELLPNSGCQM	Q					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
70	1	518.2613	-57.00	3	30.1	12.4	0	547-560	K.SLNLVDSPQPLLEK.V	

Detailed Protein Report

Protein 1243: ataxin-7-like protein 1 isoform 3 [Homo sapiens]

Accession:	gi|211971080	**Score:**	12.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	77.8
Database Date:	2015-11-30	**pI:**	10.8
		Sequence Coverage [%]:	2.0
		No. of unique Peptides:	1

Quantitation

mdown:qdown **Median:** 1.24 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MCRPSPSPVS	PASNPRTSLV	QVKTKACLSG	HHSASSTSKP	FKTPKDNLLT	SSSKQHTVFP	AKGSRDKPCV	PVPVVSLEKI
90	100	110	120	130	140	150	160
PNLVKADGAN	VKMNSTTTTA	VSASSTSSSA	VSTPPLIKPV	LMSKSVPPSP	EKILNGKGIL	PTTIDKKHQN	GTKNSNKPYR
170	180	190	200	210	220	230	240
RLSEREFDPN	KHCGVLDPET	KKPCTRSLTC	KTHSLSHRRA	VPGRKKQFDL	LLAEHKAKSR	EKEVKDKEHL	LTSTREILPS
250	260	270	280	290	300	310	320
QSGPAQDSLL	GSSGSSGPEP	KVASPAKSRP	PNSVLPRPSS	ANSISSSTSS	NHSGHTPEPP	LPPVGGDLAS	RLSSDEGEMD
330	340	350	360	370	380	390	400
GADESEKLDC	QFSTHHPRPL	AFCSFGSRLM	GRGYYVFDRR	WDRFRFALNS	MVEKHLNSQM	WKKIPPAADS	PLPSPAAHIT
410	420	430	440	450	460	470	480
TPVPASVLQP	FSNPSAVYLP	SAPISSRLTS	SYIMTSAMLS	NAAFVTSPDP	SALMSHTTAF	PHVAATLSIM	DSTFKAPSAV
490	500	510	520	530	540	550	560
SPIPAVIPSP	SHKPSKTKTS	KSSKVKDLST	RSDESPSNKK	RKPQSSTSSS	SSSSSSSLQT	SLSSPLSGPH	KKNCVLNASS
570	580	590	600	610	620	630	640
ALNSYQAAPP	YNSLSVHNSN	NGVSPLSAKL	EPSGRTSLPG	GPADIVRQVG	AVGGSSDSCP	LSVPSLALHA	GDLSLASHNA
650	660	670	680	690	700	710	720
VSSLPLSFDK	SEGKKRKNSS	SSSKACKITK	MPGMNSVHKK	NPPSLLAPVP	DPVNSTSSRQ	VGKNSSLALS	QSSPSSISSP
730	740						
GHSRQKNTNR	TGRIRTLP						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
638	1	776.3466	-53.90	2	36.6	12.4	0	2-16	M.CRPSPSPVSPASNPR.T		mdown:qdown 1.24

Detailed Protein Report

Protein 1244: PREDICTED: contactin-3 isoform X3 [Homo sapiens]

Accession:	gi|530373715	**Score:**	12.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	70.2
Database Date:	2015-11-30	**pI:**	5.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.9
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MQGKRQAQAF LPMAEKWSSP GARASAPDFS KNPMKKLVQV QVGSLVSLDC KPRASPRALS SWKKGDVSVQ EHERISLLND
        90        100        110        120        130        140        150        160
GGLKIANVTK ADAGTYTCMA ENQFGKANGT THLVVTEPTR ITLAPSNMDV SVGESVILPC QVQHDPLLDI IFTWYFNGAL
       170        180        190        200        210        220        230        240
ADFKKDGSHF EKVGGSSSGD LMIRNIQLKH SGKYVCMVQT GVDSVSSAAD LIVRGSPGPP ENVKVDEITD TTAQLSWKEG
       250        260        270        280        290        300        310        320
KDNHSPVISY SIQARTPFSV GWQTVTTVPE VIDGKTHTAT VVELNPWVEY EFRVVASNKI GGGEPSLPSE KVRTEEAVPE
       330        340        350        360        370        380        390        400
VPPSEVNGGG GSRSELVITW DPVPEELQNG EGFGYVVAFR PLGVTTWIQT VVTSPDTPRY VFRNESIVPY SPYEVKVGVY
       410        420        430        440        450        460        470        480
NNKGEGPFSP VTTVFSAEEE PTVAPSQVSA NSLSSSEIEV SWNTIPWKLS NGHLLGYEVR YWNGGGKEES SSKMKVAGNE
       490        500        510        520        530        540        550        560
TSARLRGLKS NLAYYTAVRA YNSAGAGPFS ATVNVTTKKT PPSQPPGNVV WNATDTKVLL NWEQVKAMEN ESEVTGYKVF
       570        580        590        600        610        620        630        640
YRTSSQNNVQ VLNTNKTSAE LVLPIKEDYI IEVKATTDGG DGTSSEQIRI PRITSMDARG STSAISNVHP MSSYMPIVLF
       650
LIVYVLW
```

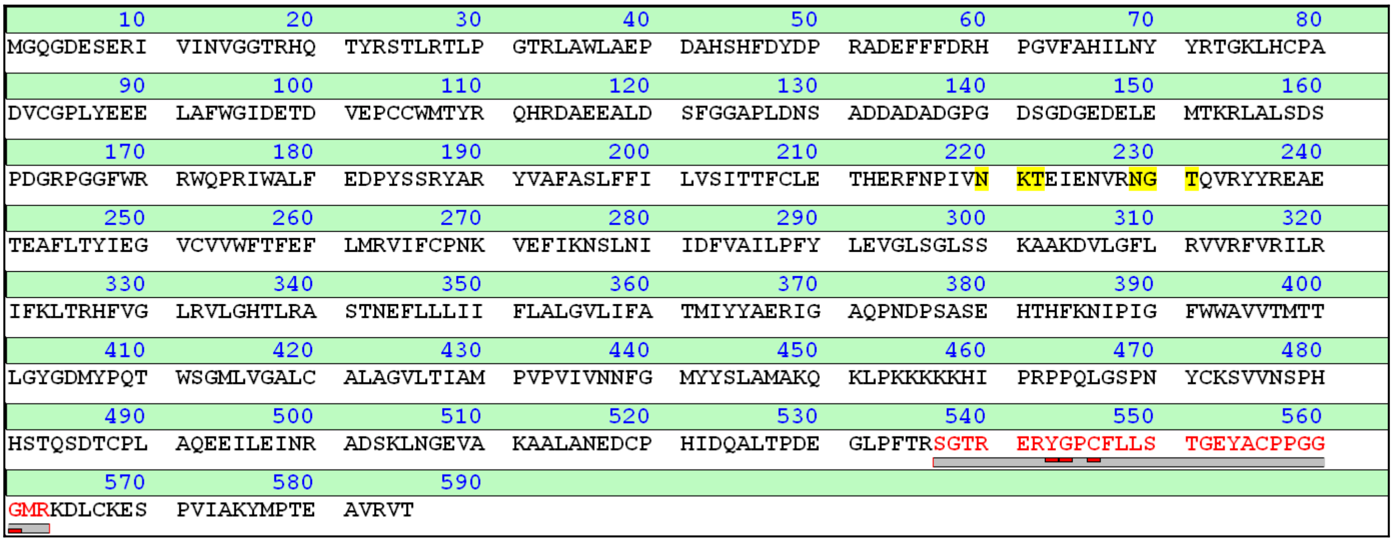
Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
897	1	703.2174	-211.87	2	40.0	12.4	1	5-16	K.RQAQAFLPMAEK.W	Oxidation: 9

Detailed Protein Report

Protein 1245: potassium voltage-gated channel subfamily C member 1 isoform A [Homo sapiens]

Accession: gi|163792201
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 12.4
MW [kDa]: 65.8
pI: 5.8
Sequence Coverage [%]: 4.6
No. of unique Peptides: 1



```
        10         20         30         40         50         60         70         80
MGQGDESERI VINVGGTRHQ TYRSTLRTLP GTRLAWLAEP DAHSHFDYDP RADEFFFDRH PGVFAHILNY YRTGKLHCPA
        90        100        110        120        130        140        150        160
DVCGPLYEEE LAFWGIDETD VEPCCWMTYR QHRDAEEALD SFGGAPLDNS ADDADADGPG DSGDGEDELE MTKRLALSDS
       170        180        190        200        210        220        230        240
PDGRPGGFWR RWQPRIWALF EDPYSSRYAR YVAFASLFFI LVSITTFCLE THERFNPIVN KTEIENVRNG TQVRYYREAE
       250        260        270        280        290        300        310        320
TEAFLTYIEG VCVVWFTFEF LMRVIFCPNK VEFIKNSLNI IDFVAILPFY LEVGLSGLSS KAAKDVLGFL RVVRFVRILR
       330        340        350        360        370        380        390        400
IFKLTRHFVG LRVLGHTLRA STNEFLLLII FLALGVLIFA TMIYYAERIG AQPNDPSASE HTHFKNIPIG FWWAVVTMTT
       410        420        430        440        450        460        470        480
LGYGDMYPQT WSGMLVGALC ALAGVLTIAM PVPVIVNNFG MYYSLAMAKQ KLPKKKKKHI PRPPQLGSPN YCKSVVNSPH
       490        500        510        520        530        540        550        560
HSTQSDTCPL AQEEILEINR ADSKLNGEVA KAALANEDCP HIDQALTPDE GLPFTRSGTR ERYGPCFLLS TGEYACPPGG
       570        580        590
GMRKDLCKES PVIAKYMPTE AVRVT
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2976	1	992.7804	-9.50	3	66.0	12.4	2	537-563	R.SGTRERYGPCFLLSTGEYACPPGGGMR.K	Carbamidomethyl: 10, 20

Detailed Protein Report

Protein 1246: telomerase reverse transcriptase isoform 2 [Homo sapiens]

Accession: gi|301129200
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 12.4
MW [kDa]: 120.0
pI: 11.9
Sequence Coverage [%]: 0.9
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MPRAPRCRAV	RSLLRSHYRE	VLPLATFVRR	LGPQGWRLVQ	RGDPAAFRAL	VAQCLVCVPW	DARPPPAAPS	FRQVSCLKEL
90	100	110	120	130	140	150	160
VARVLQRLCE	RGAKNVLAFG	FALLDGARGG	PPEAFTTSVR	SYLPNTVTDA	LRGSGAWGLL	LRRVGDDVLV	HLLARCALFV
170	180	190	200	210	220	230	240
LVAPSCAYQV	CGPPLYQLGA	ATQARPPPHA	SGPRRRLGCE	RAWNHSVREA	GVPLGLPAPG	ARRRGGSASR	SLPLPKRPRR
250	260	270	280	290	300	310	320
GAAPEPERTP	VGQGSWAHPG	RTRGPSDRGF	CVVSPARPAE	EATSLEGALS	GTRHSHPSVG	RQHHAGPPST	SRPPRPWDTP
330	340	350	360	370	380	390	400
CPPVYAETKH	FLYSSGDKEQ	LRPSFLLSSL	RPSLTGARRL	VETIFLGSRP	WMPGTPRRLP	RLPQRYWQMR	PLFLELLGNH
410	420	430	440	450	460	470	480
AQCPYGVLLK	THCPLRAAVT	PAAGVCAREK	PQGSVAAPEE	EDTDPRRLVQ	LLRQHSSPWQ	VYGFVRACLR	RLVPPGLWGS
490	500	510	520	530	540	550	560
RHNERRFLRN	TKKFISLGKH	AKLSLQELTW	KMSVRDCAWL	RRSPGVGCVP	AAEHRLREEI	LAKFLHWLMS	VYVVELLRSF
570	580	590	600	610	620	630	640
FYVTETTFQK	NRLFFYRKSV	WSKLQSIGIR	QHLKRVQLRE	LSEAEVRQHR	EARPALLTSR	LRFIPKPDGL	RPIVNMDYVV
650	660	670	680	690	700	710	720
GARTFRREKR	AERLTSRVKA	LFSVLNYERA	RRPGLLGASV	LGLDDIHRAW	RTFVLRVRAQ	DPPPELYFVK	VDVTGAYDTI
730	740	750	760	770	780	790	800
PQDRLTEVIA	SIIKPQNTYC	VRRYAVVQKA	AHGHVRKAFK	SHVSTLTDLQ	PYMRQFVAHL	QETSPLRDAV	VIEQSSSLNE
810	820	830	840	850	860	870	880
ASSGLFDVFL	RFMCHHAVRI	RGKSYVQCQG	IPQGSILSTL	LCSLCYGDME	NKLFAGIRRD	GLLLRLVDDF	LLVTPHLTHA
890	900	910	920	930	940	950	960
KTFLSYARTS	IRASLTFNRG	FKAGRNMRRK	LFGVLRLKCH	SLFLDLQVNS	LQTVCTNIYK	ILLLQAYRFH	ACVLQLPFHQ
970	980	990	1000	1010	1020	1030	1040
QVWKNPTFFL	RVISDTASLC	YSILKAKNAG	MSLGAKGAAG	PLPSEAVQWL	CHQAFLLKLT	RHRVTYVPLL	GSLRTAQTQL
1050	1060	1070					
SRKLPGTTLT	ALEAAANPAL	PSDFKTILD					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2746	1	626.8425	68.04	2	62.7	12.4	1	512-521	K.MSVRDCAWLR.R	Oxidation: 1

Detailed Protein Report

Protein 1247: teneurin-1 isoform 3 [Homo sapiens]

Accession:	gi|110347400	**Score:**	12.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	304.8
Database Date:	2015-11-30	**pI:**	6.0
		Sequence Coverage [%]:	0.8
		No. of unique Peptides:	1

Detailed Protein Report

```
        10         20         30         40         50         60         70         80
MEQTDCKPYQ PLPKVKHEMD LAYTSSSDES EDGRKPRQSY NSRETLHEYN QELRMNYNSQ SRKRKEVEKS TQEMEFCETS
        90        100        110        120        130        140        150        160
HTLCSGYQTD MHSVSRHGYQ LEMGSDVDTE TEGAASPDHA LRMWIRGMKS EHSSCLSSRA NSALSLTDTD HERKSDGENG
       170        180        190        200        210        220        230        240
FKFSPVCCDM EAQAGSTQDV QSSPHNQFTF RPLPPPPPPP HACTCARKPP PAADSLQRRS MTTRSQPSPA APAPPTSTQD
       250        260        270        280        290        300        310        320
SVHLHNSWVL NSNIPLETRH FLFKHGSGSS AIFSAASQNY PLTSNTVYSP PPRPLPRSTF SRPAFTFNKP YRCCNWKCTA
       330        340        350        360        370        380        390        400
LSATAITVTL ALLLAYVIAV HLFGLTWQLQ PVEGELYANG VSKGNRGTES MDTTYSPIGG KVSDKSEKKV FQKGRAIDTG
       410        420        430        440        450        460        470        480
EVDIGAQVMQ TIPPGLFWRF QITIHHPIYL KFNISLAKDS LLGIYGRRNI PPTHTQFDFV KLMDGKQLVK QDSKGSDDTQ
       490        500        510        520        530        540        550        560
HSPRNLILTS LQETGFIEYM DQGPWYLAFY NDGKKMEQVF VLTTAIEIMD DCSTNCNGNG ECISGHCHCF PGFLGPDCAR
       570        580        590        600        610        620        630        640
DSCPVLCGGN GEYEKGHCVC RHGWKGPECD VPEEQCIDPT CFGHGTCIMG VCICVPGYKG EICEEEDCLD PMCSNHGICV
       650        660        670        680        690        700        710        720
KGECHCSTGW GGVNCETPLP VCQEQCSGHG TFLLDAGVCS CDPKWTGSDC STELCTMECG SHGVCSRGIC QCEEGWVGPT
       730        740        750        760        770        780        790        800
CEERSCHSHC TEHGQCKDGK CECSPGWEGD HCTIAHYLDA VRDGCPGLCF GNGRCTLDQN GWHCVCQVGW SGTGCNVVME
       810        820        830        840        850        860        870        880
MLCGDNLDND GDGLTDCVDP DCCQQSNCYI SPLCQGSPDP LDLIQQSQTL FSQHTSRLFY DRIKFLIGKD STHVIPPEVS
       890        900        910        920        930        940        950        960
FDSRRACVIR GQVVAIDGTP LVGVNVSFLH HSDYGFTISR QDGSFDLVAI GGISVILIFD RSPFLPEKRT LWLPWNQFIV
       970        980        990       1000       1010       1020       1030       1040
VEKVTMQRVV SDPPSCDISN FISPNPIVLP SPLTSFGGSC PERGTIVPEL QVVQEEIPIP SSFVRLSYLS SRTPGYKTLL
      1050       1060       1070       1080       1090       1100       1110       1120
RILLTHSTIP VGMIKVHLTV AVEGRLTQKW FPAAINLVYT FAWNKTDIYG QKVWGLAEAL VSVGYEYETC PDFILWEQRT
      1130       1140       1150       1160       1170       1180       1190       1200
VVLQGFEMDA SNLGGWSLNK HHILNPQSGI IHKGNGENMF ISQQPPVIST IMGNGHQRSV ACTNCNGPAH NNKLFAPVAL
      1210       1220       1230       1240       1250       1260       1270       1280
ASGPDGSVYV GDFNFVRRIF PSGNSVSILE LSTSPAHKYY LAMDPVSESL YLSDTNTRKV YKLKSLVETK DLSKNFEVVA
      1290       1300       1310       1320       1330       1340       1350       1360
GTGDQCLPFD QSHCGDGGRA SEASLNSPRG ITVDRHGFIY FVDGTMIRKI DENAVITTVI GSNGLTSTQP LSCDSGMDIT
      1370       1380       1390       1400       1410       1420       1430       1440
QVRLEWPTDL AVNPMDNSLY VLDNNIVLQI SENRRVRIIA GRPIHCQVPG IDHFLVSKVA IHSTLESARA ISVSHSGLLF
      1450       1460       1470       1480       1490       1500       1510       1520
IAETDERKVN RIQQVTTNGE IYIIAGAPTD CDCKIDPNCD CFSGDGGYAK DAKMKAPSSL AVSPDGTLYV ADLGNVRIRT
      1530       1540       1550       1560       1570       1580       1590       1600
ISRNQAHLND MNIYEIASPA DQELYQFTVN GTHLHTLNLI TRDYVYNFTY NSEGDLGAIT SSNGNSVHIR RDAGGMPLWL
      1610       1620       1630       1640       1650       1660       1670       1680
VVPGGQVYWL TISSNGVLKR VSAQGYNLAL MTYPGNTGLL ATKSNENGWT TVYEYDPEGH LTNATFPTGE VSSFHSDLEK
      1690       1700       1710       1720       1730       1740       1750       1760
LTKVELDTSN RENVLMSTNL TATSTIYILK QENTQSTYRV NPDGSLRVTF ASGMEIGLSS EPHILAGAVN PTLGKCNISL
      1770       1780       1790       1800       1810       1820       1830       1840
PGEHNANLIE WRQRKEQNKG NVSAFERRLR AHNRNLLSID FDHITRTGKI YDDHRKFTLR ILYDQTGRPI LWSPVSRYNE
      1850       1860       1870       1880       1890       1900       1910       1920
VNITYSPSGL VTFIQRGTWN EKMEYDQSGK IISRTWADGK IWSYTYLEKS VMLLLHSQRR YIFEYDQPDC LLSVTMPSMV
      1930       1940       1950       1960       1970       1980       1990       2000
RHSLQTMLSV GYYRNIYTPP DSSTSFIQDY SRDGRLLQTL HLGTGRRVLY KYTKQARLSE VLYDTTQVTL TYEESSGVIK
      2010       2020       2030       2040       2050       2060       2070       2080
TIHLMHDGFI CTIRYRQTGP LIGRQIFRFS EEGLVNARFD YSYNNFRVTS MQAVINETPL PIDLYRYVDV SGRTEQFGKF
      2090       2100       2110       2120       2130       2140       2150       2160
SVINYDLNQV ITTTVMKHTK IFSANGQVIE VQYEILKAIA YWMTIQYDNV GRMVICDIRV GVDANITRYF YEYDADGQLQ
      2170       2180       2190       2200       2210       2220       2230       2240
```

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
286	1	879.7298	-17.42	3	32.3	12.4	2	15-37	K.VKHEMDLAYTSSSDESEDGRKPR.Q	

Detailed Protein Report

Protein 1248: insulin receptor substrate 1 [Homo sapiens]

Accession: gi|5031805
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 12.3
MW [kDa]: 131.5
pI: 9.6
Sequence Coverage [%]: 1.0
No. of unique Peptides: 1

Quantitation

Wdown:Qdown **Median:** 0.67 **CV:** 0.00 % **No. of Peptides:** 1

Alias proteins:

Accession	Name	Description
gi|578804290	refseq_human (refseq_human_20140103.fasta)	PREDICTED: insulin receptor substrate 1 isoform X2 [Homo sapiens]
gi|530370309	refseq_human (refseq_human_20140103.fasta)	PREDICTED: insulin receptor substrate 1 isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MASPPESDGF	SDVRKVGYLR	KPKSMHKRFF	VLRAASEAGG	PARLEYYENE	KKWRHKSSAP	KRSIPLESCF	NINKRADSKN
90	100	110	120	130	140	150	160
KHLVALYTRD	EHFAIAADSE	AEQDSWYQAL	LQLHNRAKGH	HDGAAALGAG	GGGGSCSGSS	GLGEAGEDLS	YGDVPPGPAF
170	180	190	200	210	220	230	240
KEVWQVILKP	KGLGQTKNLI	GIYRLCLTSK	TISFVKLNSE	AAAVVLQLMN	IRRCGHSENF	FFIEVGRSAV	TGPGEFWMQV
250	260	270	280	290	300	310	320
DDSVVAQNMH	ETILEAMRAM	SDEFRPRSKS	QSSSNCSNPI	SVPLRRHHLN	NPPPSQVGLT	RRSRTESITA	TSPASMVGGK
330	340	350	360	370	380	390	400
PGSFRVRASS	DGEGTMSRPA	SVDGSPVSPS	TNRTHAHRHR	GSARLHPPLN	HSRSIPMPAS	RCSPSATSPV	SLSSSSTSGH
410	420	430	440	450	460	470	480
GSTSDCLFPR	RSSASVSGSP	SDGGFISSDE	YGSSPCDFRS	SFRSVTPDSL	GHTPPARGEE	ELSNYICMGG	KGPSTLTAPN
490	500	510	520	530	540	550	560
GHYILSRGGN	GHRCTPGTGL	GTSPALAGDE	AASAADLDNR	FRKRTHSAGT	SPTITHQKTP	SQSSVASIEE	YTEMMPAYPP
570	580	590	600	610	620	630	640
GGGSGGRLPG	HRHSAFVPTR	SYPEEGLEMH	PLERRGGHHR	PDSSTLHTDD	GYMPMSPGVA	PVPSGRKGSG	DYMPMSPKSV
650	660	670	680	690	700	710	720
SAPQQIINPI	RRHPQRVDPN	GYMMMSPSGG	CSPDIGGGPS	SSSSSSNAVP	SGTSYGKLWT	NGVGGHHSHV	LPHPKPPVES
730	740	750	760	770	780	790	800
SGGKLLPCTG	DYMNMSPVGD	SNTSSPSDCY	YGPEDPQHKP	VLSYYSLPRS	FKHTQRPGEP	EEGARHQHLR	LSTSSGRLLY
810	820	830	840	850	860	870	880
AATADDSSSS	TSSDSLGGGY	CGARLEPSLP	HPHHQVLQPH	LPRKVDTAAQ	TNSRLARPTR	LSLGDPKAST	LPRAREQQQQ
890	900	910	920	930	940	950	960
QQPLLHPPEP	KSPGEYVNIE	FGSDQSGYLS	GPVAFHSSPS	VRCPSQLQPA	PREEETGTEE	YMKMDLGPGR	RAAWQESTGV
970	980	990	1000	1010	1020	1030	1040
EMGRLGPAPP	GAASICRPTR	AVPSSRGDYM	TMQMSCPRQS	YVDTSPAAPV	SYADMRTGIA	AEEVSLPRAT	MAAASSSSAA
1050	1060	1070	1080	1090	1100	1110	1120
SASPTGPQGA	AELAAHSSLL	GGPQGPGGMS	AFTRVNLSPN	RNQSAKVIRA	DPQGCRRRHS	SETFSSTPSA	TRVGNTVPFG
1130	1140	1150	1160	1170	1180	1190	1200
AGAAVGGGGG	SSSSSEDVKR	HSSASFENVW	LRPGELGGAP	KEPAKLCGAA	GGLENGLNYI	DLDLVKDFKQ	CPQECTPEPQ
1210	1220	1230	1240	1250			
PPPPPPPHQP	LGSGESSSTR	RSSEDLSAYA	SISFQKQPED	RQ			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1995	1	719.2866	-53.40	2	53.6	12.3	0	952-964	R.AAWQESTGVEMGR.L	Oxidation: 11	Wdown:Qdown 0.67

Detailed Protein Report

Protein 1249: complexin-4 [Homo sapiens]

Accession:	gi|31795561	**Score:**	12.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	18.3
Database Date:	2015-11-30	**pI:**	4.4
Modification(s):	Oxidation	**Sequence Coverage [%]:**	8.1
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MAFLMKSMIS NQVKNLGFGG GSEENKEEGG ASDPAAAQGM TREEYEEYQK QMIEEKMERD AAFTQKKAER ACLRVHLREK
        90        100        110        120        130        140        150        160
YRLPKSEMDE NQIQMAGDDV DLPEDLRKMV DEDQEEEEDK DSILGQIQNL QNMDLDTIKE KAQATFTEIK QTAEQKCSVM
       170
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1078	1	820.2655	-85.51	2	42.0	12.3	1	108-120	R.KMVDEDQEEEEDK.D	Oxidation: 2

Detailed Protein Report

Protein 1250: 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 1251: 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

Quantitation

Wdown:Qdown **Median:** 4.13 **CV:** 0.00 % **No. of 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	Ratios
1426	1	1011.7261	221.55	1	47.6	12.3	1	44-50	R.WGHRHYR.S		Wdown:Qdown 4.13

Detailed Protein Report

Protein 1252: tigger transposable element-derived protein 1 [Homo sapiens]

Accession:	gi|22209001	**Score:**	12.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	67.3
Database Date:	2015-11-30	**pI:**	9.1
		Sequence Coverage [%]:	2.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MASKCSSERK	SRTSLTLNQK	LEMIKLSEEG	MSKAEIGRRL	GLLRQTVSQV	VNAKEKFLKE	VKSATPMNTR	MIRKRNSLIA
90	100	110	120	130	140	150	160
DMEKVLVVWI	EDQTSRNIPL	SQSLIQNKAL	TLFNSMKAER	GVEAAEEKFE	ASRGWFMRFK	ERSHFHNIKA	QGEAASADVE
170	180	190	200	210	220	230	240
AAASYPEALA	KIIDEGGYTK	QQIFNVDETA	FYWKKMPSRT	FIAREEKSVP	GFKASKDRLT	LLLGANAAGD	FKLKPMLIYH
250	260	270	280	290	300	310	320
SENPRALKNY	TKSTLPVLYK	WNSKARMTAH	LFTAWFTEYF	KPTVETYCSE	KKIPFKILLL	IDNAPSHPRA	LMEIYEEINV
330	340	350	360	370	380	390	400
IFMPANTTSI	LQPMDQGVIS	TFKSYYLRNT	FHKALAAMDS	DVSDGSGQSK	LKTFWKGFTI	LDAIKNIRDS	WEEVKLSTLT
410	420	430	440	450	460	470	480
GVWKKLIPTL	IDDYEGFKTS	VEEVSADVVE	IAKELELEVE	PEDVTELLQS	HDKTLTDEEL	FLMDAQRKWF	LEMESTPGED
490	500	510	520	530	540	550	560
AVNIVEMTTK	DLEYYINLVD	KAAAGFERID	SNFERSSTVG	KMLSNSIACY	REIFHERKSQ	LMRKASPMSY	FRKLPQPPQP
570	580	590	600				
SAATTLTSQQ	PSTSRQDPPP	AKRVRLTEGS	D				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2487	1	729.9818	77.79	2	59.4	12.3	0	297-309	K.ILLLIDNAPSHPR.A	

Detailed Protein Report

Protein 1253: PREDICTED: calpain-7 isoform X2 [Homo sapiens]

Accession:	gi|530372183	**Score:**	12.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	82.2
Database Date:	2015-11-30	**pI:**	8.7
		Sequence Coverage [%]:	2.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDATALERDA	VQFARLAVQR	DHEGRYSEAV	FYYKEAAQAL	IYAEMAGSSL	ENIQEKITEY	LERVQALHSA	VQSKSADPLK
90	100	110	120	130	140	150	160
SKHQLDLERA	HFLVTQAFDE	DEKENVEDAI	ELYTEAVDLC	LKTSYETADK	VLQNKLKQLA	RQALDRAEAL	SEPLTKPVGK
170	180	190	200	210	220	230	240
ISSTSVKPKP	PPVRAHFPLG	ANPFLERPQS	FISPQSCDAQ	GQRYTAEEIE	VLRTTSKING	IEYVPFMNVD	LRERFAYPMP
250	260	270	280	290	300	310	320
FCDRWGKLPL	SPKQKTTFSK	WVRPEDLTNN	PTMIYTVSSF	SIKQTIVSDC	SFVASLAISA	AYERRFNKKL	ITGIIYPQNK
330	340	350	360	370	380	390	400
DGEPEYNPCG	KYMVKLHLNG	VPRKVIIDDQ	LPVDHKGELL	CSYSNNKSEL	WVSLIEKAYM	KVMGGYDFPG	SNSNIDLHAL
410	420	430	440	450	460	470	480
TGWIPERIAM	HSDSQTFSKD	NSFRMLYQRF	HKGDVLITAS	TGMMTEAEGE	KWGLVPTHAY	AVLDIREFKG	LRFIQLKNPW
490	500	510	520	530	540	550	560
SHLRWKGRYS	ENDVKNWTPE	LQKYLNFDPR	TAQKIDNGIF	WISWDDLCQY	YDVIYLSWNP	GLFKESTCIH	RMILRIIENL
570	580	590	600	610	620	630	640
SQWLYTRLMG	KKFITQVYSA	CSFTFSKIPS	PYTLSKRING	KWSGQSAGGC	GNFQETHKNN	PIYQFHIEKT	GPLLIELRGP
650	660	670	680	690	700	710	720
RQYSVGFEVV	TVSTLGDPGP	HGFLRKSSGD	YRCGFCYLEL	ENIPSGIFNI	IPSTFLPKQE	GPFFLDFNSI	IPIKITQLQ

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1269	1	1032.5931	79.63	2	44.6	12.3	2	487-503	K.GRYSENDVKNWTPELQK.Y	

Detailed Protein Report

Protein 1254: 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 1255: 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 1256: probable ATP-dependent RNA helicase DHX36 isoform 2 [Homo sapiens]

Accession:	gi|167830436	**Score:**	12.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	113.1
Database Date:	2015-11-30	**pI:**	8.3
		Sequence Coverage [%]:	1.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSYDYHQNWG	RDGGPRSSGG	GYGGGPAGGH	GGNRGSGGGG	GGGGGGRGGR	GRHPGHLKGR	EIGMWYAKKQ	GQKNKEAERQ
90	100	110	120	130	140	150	160
ERAVVHMDER	REEQIVQLLN	SVQAKNDKES	EAQISWFAPE	DHGYGTEVST	KNTPCSENKL	DIQEKKLINQ	EKKMFRIRNR
170	180	190	200	210	220	230	240
SYIDRDSEYL	LQENEPDGTL	DQKLLEDLQK	KKNDLRYIEM	QHFREKLPSY	GMQKELVNLI	DNHQVTVISG	ETGCGKTTQV
250	260	270	280	290	300	310	320
TQFILDNYIE	RGKGSACRIV	CTQPRRISAI	SVAERVAAER	AESCGSGNST	GYQIRLQSRL	PRKQGSILYC	TTGIILQWLQ
330	340	350	360	370	380	390	400
SDPYLSSVSH	IVLDEIHERN	LQSDVLMTVV	KDLLNFRSDL	KVILMSATLN	AEKFSEYFGN	CPMIHIPGFT	FPVVEYLLED
410	420	430	440	450	460	470	480
VIEKIRYVPE	QKEHRSQFKR	GFMQGHVNRQ	EKEEKEAIYK	ERWPDYVREL	RRRYSASTVD	VIEMMEDDKV	DLNLIVALIR
490	500	510	520	530	540	550	560
YIVLEEEDGA	ILVFLPGWDN	ISTLHDLLMS	QVMFKSVNQT	QVFKRTPPGV	RKIVIATNIA	ETSITIDDVV	YVIDGGKIKE
570	580	590	600	610	620	630	640
THFDTQNNIS	TMSAEWVSKA	NAKQRKGRAG	RVQPGHCYHL	YNGLRASLLD	DYQLPEILRT	PLEELCLQIK	ILRLGGIAYF
650	660	670	680	690	700	710	720
LSRLMDPPSN	EAVLLSIRHL	MELNALDKQE	ELTPLGVHLA	RLPVEPHIGK	MILFGALFCC	LDPVLTIAAS	LSFKDPFVIP
730	740	750	760	770	780	790	800
LGKEKIADAR	RKELAKDTRS	DHLTVVNAFE	GWEEARRRGF	RYEKDYCWEY	FLSSNTLQML	HNMKGQFAEH	LLGAGFVSSR
810	820	830	840	850	860	870	880
NPKDPESNIN	SDNEKIIKAV	ICAGLYPKVA	KIRLNLGKKR	KMVKVYTKTD	GLVAVHPKSV	NVEQTDFHYN	WLIYHLKMRT
890	900	910	920	930	940	950	960
SSIYLYDCTE	VSPYCLLFFG	GDISIQKDND	QETIAVDEWI	VFQSPARIAH	LVKELRKELD	ILLQEKIESP	HPVDWNDTKS
970	980	990	1000				
RDCAVLSAII	DLIKTQEKAT	PRNFPPRFQD	GYYS				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
416	1	686.9203	130.84	2	34.2	12.3	2	35-52	R.GSGGGGGGGGGGRGGRGR.H	

Detailed Protein Report

Protein 1257: zinc finger protein 568 isoform 6 [Homo sapiens]

Accession:	gi|325651964	**Score:**	12.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	66.6
Database Date:	2015-11-30	**pI:**	9.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MKPAQRNLYR	DVMLENYSNL	VTVGCQVTKP	DVIFKLEQEE	EPWVMEEEMF	GRHCPEPRRG	ENCCASEVMA	EGLKFKDVVI
90	100	110	120	130	140	150	160
YFSQKEWECL	HSAQKDLYRD	VMLENYGNLV	LLGLSDTKPN	VISLLEQKKE	PWMVKRKETK	EWCPDWEFGR	ETKNLSPKEN
170	180	190	200	210	220	230	240
IYEIRSPQQE	KARVIREIRC	QVERQQGHQE	GHFRPAVIPF	TSMQCTAHRE	YQWLHTGEKS	CECRKCKNAF	RYQSCPIQHE
250	260	270	280	290	300	310	320
IIHNKEKEPE	CGECRKIFNS	GSDLIKHQTL	HESKKHSENN	KCAFNHDSGI	TQPQSINTGE	KPHKCKECGK	AFRSSSQISQ
330	340	350	360	370	380	390	400
HQRMHLGEKP	YKCRECGKAF	PSTAQLNLHQ	RIHTDEKYYE	SKACGKAFTR	PSHLFRHQRI	HTGEKPHKCK	ECGKAFRYDT
410	420	430	440	450	460	470	480
QLSLHQIIHT	GERRYECREC	GKVYSCASQL	SLHQRIHTGE	KPHECKECGK	AFISDSHLIR	HQSVHTGEKP	CKCKECGKSF
490	500	510	520	530	540	550	560
RRGSELTRHQ	RAHTGEKPYE	CKECEKAFTC	STELVRHQKV	HTGERPHKCK	ECGKAFIRRS	ELTHHERSHT	GEKPYECKEC
570	580						
GKPFGGGSEL	S						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1887	1	918.4473	8.72	2	52.3	12.3	2	324-338	R.MHLGEKPYKCRECGK.A	Carbamidomethyl: 10

Detailed Protein Report

Protein 1258: ubiquitin-like protein 4A [Homo sapiens]

Accession:	gi|7657667	**Score:**	12.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	17.8
Database Date:	2015-11-30	**pI:**	9.5
		Sequence Coverage [%]:	5.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MQLTVKALQG	RECSLQVPED	ELVSTLKQLV	SEKLNVPVRQ	QRLLFKGKAL	ADGKRLSDYS	IGPNSKLNLV	VKPLEKVLLE
90	100	110	120	130	140	150	160
EGEAQRLADS	PPPQVWQLIS	KVLARHFSAA	DASRVLEQLQ	RDYERSLSRL	TLDDIERLAS	RFLHPEVTET	MEKGFSK

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1860	1	915.3255	-231.02	1	53.3	12.3	2	47-55	K.GKALADGKR.L	

Detailed Protein Report

Protein 1259: PREDICTED: exophilin-5 isoform X3 [Homo sapiens]

Accession:	gi|578822067	**Score:**	12.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	201.0
Database Date:	2015-11-30	**pI:**	6.8
		Sequence Coverage [%]:	0.8
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:** 0.70	**CV:** 0.00 %	**No. of Peptides:** 1

Detailed Protein Report

10	20	30	40	50	60	70	80
MREESGMPPP	WDASLLENEF	FQVLDDLDSK	LAQEQSASSV	NTRTPLNYGS	RTQFGHFYSS	GNRHGNITER	HKKHYNETSN
90	100	110	120	130	140	150	160
MSIYDILRPG	TPREGFKTFS	PRTSTIYDMY	RTREPRVFKE	DYVQKNTFGS	TSLCFDSRQR	SALPATGHFT	ARSLHFPATT
170	180	190	200	210	220	230	240
QSKSGFIPPR	HQQSPKRTPL	SSIIWNRSDS	SRDRENQEEF	LRAPSPMEID	PADKYVYPRG	FQENKRYESY	HSQNVYQRVS
250	260	270	280	290	300	310	320
LNAPMENAMS	PDTFENSENM	PFYHQSNTFT	RSFFSNTFGR	SGEQRRFGQG	PFWGQEKGHS	FWSDFHRSRK	SFSSSDRDFE
330	340	350	360	370	380	390	400
MISMEANSVS	AIHGHNVSSE	HWESFSSGYG	TDVSRGQEEP	HPWQFDFQRS	TLDSMVVSHG	NETQLTPHFG	TPNVCSMTGS
410	420	430	440	450	460	470	480
SYHVKSSELV	SQQDSSPVEV	HINKEASSFG	IAQTLASSFK	TSFSQISDDR	RNPQSPNLQN	PTVTLQKIFP	NKPASHPMRS
490	500	510	520	530	540	550	560
HTEVTVTSSN	SVDSLPLAKS	QPNILVTEVN	NEKDLNESIS	EEDKQLSKMD	QTNKAGEIPQ	PVSQTGISNS	LPDFQNPLSQ
570	580	590	600	610	620	630	640
DSAKSNGFGF	NASTIISSKK	SPRVFSRKDT	SKMYIPHTDK	SNDIKQDKRF	TENRKLGSTA	SLPFIQEHRT	PPSFPRTDQG
650	660	670	680	690	700	710	720
CHQELTVNNE	DISRIITNNH	WSSALTDTQN	AQYSKCKLTP	GHKTSCDSLD	LSSAALPDSS	PSKNSSLDAP	VVPSTTVFSR
730	740	750	760	770	780	790	800
RSPSDKDPSL	GEREEKDNAG	KNQKNQFIVS	HSENQERNDS	PVPTHDEVVD	VKCHSHSPFR	NERGKGKIRH	HISCIEKLSK
810	820	830	840	850	860	870	880
TESISVPTSD	HRSLIEANQS	NSKVSELDTI	YCTLPRKSSS	FLIHGRQSGS	KIMAASLRNG	PPPFQIKNNV	EDAMGNYMLN
890	900	910	920	930	940	950	960
KFSPSSPESA	NECSKVLSDS	ALEAPEATER	MTNVKSSGST	SVRKGPLPFL	INRAMSCPSG	EPHASTGREG	RKKPLTSGMD
970	980	990	1000	1010	1020	1030	1040
ASELTPRAWE	RIISPVESDS	SVRDCSLTKR	QHQKENFQEY	TEKEGKMAAS	RRSVFALSNE	DPLPFCSDLS	GKERGKTLHK
1050	1060	1070	1080	1090	1100	1110	1120
VKTTSTFSVS	GDEDNVKCLE	VVSIYYTLPR	KPSKKFCNLL	QQYTQNTNLL	IESPQVETET	FPNALEKDKQ	NYSTREQSGT
1130	1140	1150	1160	1170	1180	1190	1200
PSCENLKMSV	NSDQTLTTEN	MTAFRLSNRG	PLAPTLQEMA	SVEAAVSLPE	EESKAREIFS	DNLAKTPLGD	SENKKERGKK
1210	1220	1230	1240	1250	1260	1270	1280
LQSETLHTSL	MLQRKNVSEE	KSENCQQSIN	SSNSGPSSLP	ALSEVNIGNS	QTRRSSWECT	GSGRAIPFTG	SGKCPQKDHT
1290	1300	1310	1320	1330	1340	1350	1360
STAVGDGSSG	SQPREGRGDI	GTNCQKMTNK	TLSHSESQVF	ALTPALHKLQ	LGEETQSDEP	NLESLQSEPR	ELPQRSQEAN
1370	1380	1390	1400	1410	1420	1430	1440
MTESRKAEDE	MQKSAWDQPS	LPEGNKNKTN	LDDLVKGENR	SSVKHRLAAM	SKASRKFPAK	DVSPRRHVAT	IFPQSGSRSG
1450	1460	1470	1480	1490	1500	1510	1520
FDHLSLGTVE	CNPLFPEPTP	KSAESIGESR	LSENGKHVKK	SENLLPITVL	PNREPSTHVS	NQKSNSISQR	HQNEFKNVSE
1530	1540	1550	1560	1570	1580	1590	1600
SPSKHENSKD	VTAAQNLVRE	SGAPSPITFT	SLREAEFSDN	QRRLSPPFPL	EPAQKSRVSS	PLASFLQQQR	SASSLEWEPE
1610	1620	1630	1640	1650	1660	1670	1680
PHLYRSKSLK	SINVHGDLLR	KSHPPKVRER	HFSESTSIDN	ALSRLTLGNE	FSVNNGYSRR	FRSFSELPSC	DGNESWAYRS
1690	1700	1710	1720	1730	1740	1750	1760
GTKTGPRSAI	SIYRPIDYGI	FGKEQQLAFL	ENVKRSLTQG	RLWKPSFLKN	PGFLKDDLRN	PPNPSESLSS	NSPSSQVPED
1770	1780	1790	1800	1810			
GLSPSEPLNI	YEDDPVDSDC	DTDTTTDDEY	YLDENDKESE	L			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
309	1	558.5767	-48.96	3	33.2	12.3	2	722-736	R.SPSDKDPSLGEREEK.D		mdown:qdown 0.70

Detailed Protein Report

Protein 1260: PREDICTED: E3 SUMO-protein ligase PIAS1 isoform X2 [Homo sapiens]

Accession:	gi|530406586	**Score:**	12.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	70.8
Database Date:	2015-11-30	**pI:**	7.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.2
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MVMSLRVSEL QVLLGYAGRN KHGRKHELLT KALHLLKAGC SPAVQMKIKE LYRRRFPQKI MTPADLSIPN VHSSPMPATL

        90        100        110        120        130        140        150        160
SPSTIPQLTY DGHPASSPLL PVSLLGPKHE LELPHLTSAL HPVHPDIKLQ KLPFYDLLDE LIKPTSLASD NSQRFRETCF

       170        180        190        200        210        220        230        240
AFALTPQQVQ QISSSMDISG TKCDFTVQVQ LRFCLSETSC PQEDHFPPNL CVKVNTKPCS LPGYLPPTKN GVEPKRPSRP

       250        260        270        280        290        300        310        320
INITSLVRLS TTVPNTIVVS WTAEIGRNYS MAVYLVKQLS STVLLQRLRA KGIRNPDHSR ALIKEKLTAD PDSEIATTSL

       330        340        350        360        370        380        390        400
RVSLLCPLGK MRLTIPCRAL TCSHLQCFDA TLYIQMNEKK PTWVCPVCDK KAPYEHLIID GLFMEILKYC TDCDEIQFKE

       410        420        430        440        450        460        470        480
DGTWAPMRSK KEVQEVSASY NGVDGCLSST LEHQVASHHQ SSNKNKKVEV IDLTIDSSSD EEEEEPSAKR TCPSLSPTSP

       490        500        510        520        530        540        550        560
LNNKGILSLP HQASPVSRTP SLPAVDTSYI NTSLIQDYRH PFHMTPMPYD LQGLDFFPFL SGDNQHYNTS LLAAAAAAVS

       570        580        590        600        610        620        630        640
DDQDLLHSSR FFPYTSSQMF LDQLSAGGST SLPTTNGSSS GSNSSLVSSN SLRESHSHTV TNRSSTDTAS IFGIIPDIIS

       650
LD
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2137	1	1057.0868	-89.61	3	55.3	12.3	1	333-359	R.LTIPCRALTCSHLQCFDATLYIQMNEK.K	Carbamidomethyl: 10

Detailed Protein Report

Protein 1261: 60 kDa SS-A/Ro ribonucleoprotein isoform 4 [Homo sapiens]

Accession:	gi|291084635	**Score:**	12.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	58.4
Database Date:	2015-11-30	**pI:**	9.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.7
		No. of unique Peptides:	1

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

Detailed Protein Report

Protein 1262: PREDICTED: 5'-AMP-activated protein kinase catalytic subunit alpha-1 isoform X1 [Homo sapiens]

Accession:	gi|578809939	**Score:**	12.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	52.4
Database Date:	2015-11-30	**pI:**	5.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.2
		No. of unique Peptides:	1

Quantitation

Wdown:Qdown **Median:** 1.34 **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
274	2	424.1315	-203.85	3	32.2	12.3	1	157-166	K.HMLQVDPMKR.A	Oxidation: 8	Wdown:Qdown 1.34

Detailed Protein Report

Protein 1263: angiotensinogen preproprotein [Homo sapiens]

Accession:	gi|4557287	**Score:**	12.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	53.1
Database Date:	2015-11-30	**pI:**	5.9
		Sequence Coverage [%]:	2.9
		No. of unique Peptides:	1

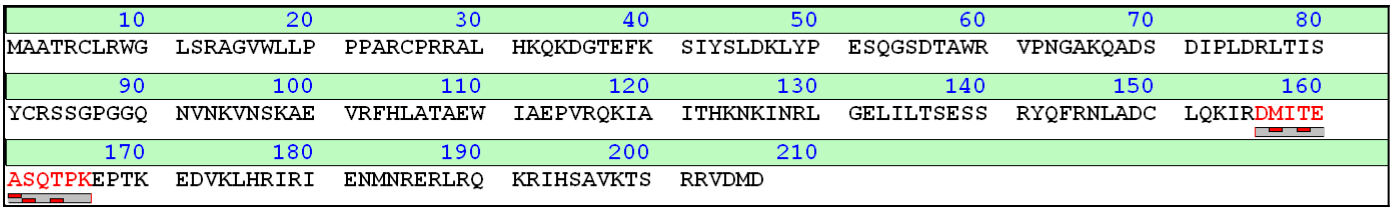
10	20	30	40	50	60	70	80
MRKRAPQSEM	APAGVSLRAT	ILCLLAWAGL	AAGDRVYIHP	FHLVIHNEST	CEQLAKANAG	KPKDPTFIPA	PIQAKTSPVD
90	100	110	120	130	140	150	160
EKALQDQLVL	VAAKLDTEDK	LRAAMVGMLA	NFLGFRIYGM	HSELWGVVHG	ATVLSPTAVF	GTLASLYLGA	LDHTADRLQA
170	180	190	200	210	220	230	240
ILGVPWKDKN	CTSRLDAHKV	LSALQAVQGL	LVAQGRADSQ	AQLLLSTVVG	VFTAPGLHLK	QPFVQGLALY	TPVVLPRSLD
250	260	270	280	290	300	310	320
FTELDVAAEK	IDRFMQAVTG	WKTGCSLMGA	SVDSTLAFNT	YVHFQGKMKG	FSLLAEPQEF	WVDNSTSVSV	PMLSGMGTFQ
330	340	350	360	370	380	390	400
HWSDIQDNFS	VTQVPFTESA	CLLLIQPHYA	SDLDKVEGLT	FQQNSLNWMK	KLSPRTIHLT	MPQLVLQGSY	DLQDLLAQAE
410	420	430	440	450	460	470	480
LPAILHTELN	LQKLSNDRIR	VGEVLNSIFF	ELEADEREPT	ESTQQLNKPE	VLEVTLNRPF	LFAVYDQSAT	ALHFLGRVAN
490							
PLSTA							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
557	1	707.4501	125.44	2	35.8	12.3	0	5-18	R.APQSEMAPAGVSLR.A	

Detailed Protein Report

Protein 1264: peptidyl-tRNA hydrolase ICT1, mitochondrial precursor [Homo sapiens]

Accession:	gi|4557657	**Score:**	12.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	23.6
Database Date:	2015-11-30	**pI:**	10.9
Modification(s):	Oxidation	**Sequence Coverage [%]:**	5.3
		No. of unique Peptides:	1



```
        10         20         30         40         50         60         70         80
MAATRCLRWG LSRAGVWLLP PPARCPRRAL HKQKDGTEFK SIYSLDKLYP ESQGSDTAWR VPNGAKQADS DIPLDRLTIS
        90        100        110        120        130        140        150        160
YCRSSGPGGQ NVNKVNSKAE VRFHLATAEW IAEPVRQKIA ITHKNKINRL GELILTSESS RYQFRNLADC LQKIRDMITE
       170        180        190        200        210
ASQTPKEPTK EDVKLHRIRI ENMNRERLRQ KRIHSAVKTS RRVDMD
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2107	1	618.7806	-19.22	2	54.9	12.2	0	156-166	R.DMITEASQTPK.E	Oxidation: 2

Detailed Protein Report

Protein 1265: **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 1266: 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 1267: PREDICTED: proton-coupled amino acid transporter 4 isoform X4 [Homo sapiens]

Accession:	gi|578821970	**Score:**	12.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	44.7
Database Date:	2015-11-30	**pI:**	9.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MHILVRCSHF	LCLRFKKSTL	GYSDTVSFAM	EVSPWSCLQK	QAAWGRSVVD	FFLVITQLGF	CSVYIVFLAE	NVKQVHEGFL
90	100	110	120	130	140	150	160
ESKVFISNST	NSSNPCERRS	VDLRIYMLCF	LPFIILLVFI	RELKNLFVLS	FLANVSMAVS	LVIIYQYVVR	NMPDPHNLPI
170	180	190	200	210	220	230	240
VAGWKKYPLF	FGTAVFAFEG	IGVVLPLENQ	MKESKRFPQA	LNIGMGIVTT	LYVTLATLGY	MCFHDEIKGS	ITLNLPQDVW
250	260	270	280	290	300	310	320
LYQSVKILYS	FGIFVTYSIQ	FYVPAEIIIP	GITSKFHTKW	KQICEFGIRS	FLVSITCAGA	ILIPRLDIVI	SFVGAVSSST
330	340	350	360	370	380	390	400
LALILPPLVE	ILTFSKEHYN	IWMVLKNISI	AFTGVVGFLL	GTYITVEEII	YPTPKVVAGT	PQSPFLNLNS	TCLTSGLK

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2948	1	965.1376	114.87	2	66.0	12.2	2	2-16	M.HILVRCSHFLCLRFK.K	Carbamidomethyl: 6

Detailed Protein Report

Protein 1268: B-cell CLL/lymphoma 7 protein family member C isoform 2 [Homo sapiens]

Accession:	gi|20336477	**Score:**	12.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	23.5
Database Date:	2015-11-30	**pI:**	5.0
		Sequence Coverage [%]:	4.1
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MAGRTVRAET RSRAKDDIKK VMATIEKVRR WEKRWVTVGD TSLRIFKWVP VVDPQEEERR RAGGGAERSR GRERRGRGAS
        90        100        110        120        130        140        150        160
PRGGGPLILL DLNDENSNQS FHSEGSLQKG TEPSPGGTPQ PSRPVSPAGP PEGVPEEAQP PRLGQERDPG GITAGSTDEP
       170        180        190        200        210        220
PMLTKEEPVP ELLEAEAPEA YPVFEPVPPV PEAAQGDTED SEGAPPLKRI CPNAPDP
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1204	1	491.6325	-223.38	2	43.6	12.2	1	209-217	K.RICPNAPDP.-	

Protein 1269: 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

BRUKER

Detailed Protein Report

Protein 1270: 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 1271: structural maintenance of chromosomes protein 3 [Homo sapiens]

Accession:	gi|4885399	**Score:**	12.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	141.5
Database Date:	2015-11-30	**pI:**	6.8
		Sequence Coverage [%]:	0.9
		No. of unique Peptides:	1

Quantitation

Wdown:Qdown **Median:** 7.90 **CV:** 0.00 % **No. of Peptides:** 1

```
        10           20           30           40           50           60           70           80
MYIKQVIIQG   FRSYRDQTIV   DPFSSKHNVI   VGRNGSGKSN   FFYAIQFVLS   DEFSHLRPEQ   RLALLHEGTG   PRVISAFVEI

        90          100          110          120          130          140          150          160
IFDNSDNRLP   IDKEEVSLRR   VIGAKKDQYF   LDKKMVTKND   VMNLLESAGF   SRSNPYYIVK   QGKINQMATA   PDSQRLKLLR

       170          180          190          200          210          220          230          240
EVAGTRVYDE   RKEESISLMK   ETEGKREKIN   ELLKYIEERL   HTLEEEKEEL   AQYQKWDKMR   RALEYTIYNQ   ELNETRAKLD

       250          260          270          280          290          300          310          320
ELSAKRETSG   EKSRQLRDAQ   QDARDKMEDI   ERQVRELKTK   ISAMKEEKEQ   LSAERQEQIK   QRTKLELKAK   DLQDELAGNS

       330          340          350          360          370          380          390          400
EQRKRLLKER   QKLLEKIEEK   QKELAETEPK   FNSVKEKEER   GIARLAQATQ   ERTDLYAKQG   RGSQFTSKEE   RDKWIKKELK

       410          420          430          440          450          460          470          480
SLDQAINDKK   RQIAAIHKDL   EDTEANKEKN   LEQYNKLDQD   LNEVKARVEE   LDRKYYEVKN   KKDELQSERN   YLWREENAEQ

       490          500          510          520          530          540          550          560
QALAAKREDL   EKKQQLLRAA   TGKAILNGID   SINKVLDHFR   RKGINQHVQN   GYHGIVMNNF   ECEPAFYTCV   EVTAGNRLFY

       570          580          590          600          610          620          630          640
HIVDSDEVST   KILMEFNKMN   LPGEVTFLPL   NKLDVRDTAY   PETNDAIPMI   SKLRYNPRFD   KAFKHVFGKT   LICRSMEVST

       650          660          670          680          690          700          710          720
QLARAFTMDC   ITLEGDQVSH   RGALTGGYYD   TRKSRLELQK   DVRKAEEELG   ELEAKLNENL   RRNIERINNE   IDQLMNQMQQ

       730          740          750          760          770          780          790          800
IETQQRKFKA   SRDSILSEMK   MLKEKRQQSE   KTFMPKQRSL   QSLEASLHAM   ESTRESLKAE   LGTDLLSQLS   LEDQKRVDAL

       810          820          830          840          850          860          870          880
NDEIRQLQQE   NRQLLNERIK   LEGIITRVET   YLNENLRKRL   DQVEQELNEL   RETEGGTVLT   ATTSELEAIN   KRVKDTMARS

       890          900          910          920          930          940          950          960
EDLDNSIDKT   EAGIKELQKS   MERWKNMEKE   HMDAINHDTK   ELEKMTNRQG   MLLKKKEECM   KKIRELGSLP   QEAFEKYQTL

       970          980          990         1000         1010         1020         1030         1040
SLKQLFRKLE   QCNTELKKYS   HVNKKALDQF   VNFSEQKEKL   IKRQEELDRG   YKSIMELMNV   LELRKYEAIQ   LTFKQVSKNF

      1050         1060         1070         1080         1090         1100         1110         1120
SEVFQKLVPG   GKATLVMKKG   DVEGSQSQDE   GEGSGESERG   SGSQSSVPSV   DQFTGVGIRV   SFTGKQGEMR   EMQQLSGGQK

      1130         1140         1150         1160         1170         1180         1190         1200
SLVALALIFA   IQKCDPAPFY   LFDEIDQALD   AQHRKAVSDM   IMELAVHAQF   ITTTFRPELL   ESADKFYGVK   FRNKVSHIDV

      1210         1220
ITAEMAKDFV   EDDTTHG
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
772	1	647.8341	17.27	2	38.5	12.2	1	161-171	R.EVAGTRVYDER.K		Wdown:Qdown 7.90

Detailed Protein Report

Protein 1272: angiogenin precursor [Homo sapiens]

Accession:	gi|4557313	**Score:**	12.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	16.5
Database Date:	2015-11-30	**pI:**	10.9
		Sequence Coverage [%]:	6.1
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	1.84	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.94	**CV:**	0.00 %	**No. of Peptides:**	1

Alias proteins:

Accession	Name	Description
gi|148277046	refseq_human (refseq_human_20140103.fasta)	angiogenin precursor [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MVMGLGVLLL VFVLGLGLTP PTLAQDNSRY THFLTQHYDA KPQGRDDRYC ESIMRRRGLT SPCKDINTFI HGNKRSIKAI
        90        100        110        120        130        140        150
CENKNGNPHR ENLRISKSSF QVTTCKLHGG SPWPPCQYRA TAGFRNVVVA CENGLPVHLD QSIFRRP
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2833	5	607.3303	49.85	2	64.6	12.2	2	49-57	R.YCESIMRRR.G		Wdown:Qdown 0.94 mdown:qdown 1.84

Detailed Protein Report

Protein 1273: PREDICTED: uncharacterized protein LOC144535 [Homo sapiens]

Accession:	gi|578796689	**Score:**	12.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	322.3
Database Date:	2015-11-30	**pI:**	9.5
		Sequence Coverage [%]:	0.6
		No. of unique Peptides:	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MAAQGSPSSS	PSDDSTTSGS	LPELPPTSTA	TSRSPPESKG	SSRSSLLQWT	CPEDSLPLAV	FYGPLDAKNP	LLASCEKEIQ
90	100	110	120	130	140	150	160
ELLGFMRKKK	ALATTEEEKH	EFRRRCATSL	FNIWTKYAPR	LPADYYNEKL	LKVGDSLCQM	KEYKLALLQC	YGRYLQQFNT
170	180	190	200	210	220	230	240
NFDENKVDVT	QFKATFFPKG	FKDKTAGLTF	HALSGKNMCN	YQLVCDSDEN	LKNKESVVQC	LHILSSLRLI	MQVALPQEHL
250	260	270	280	290	300	310	320
CWIIFNGTIY	IYTICRKLMV	IGQSSKALEY	LLWASMCMES	LVPLLSLRYL	TWRATLYTAV	CQCCYDCHAG	IHGEAFARRA
330	340	350	360	370	380	390	400
LAKIDELRQL	ELMSSSKSQE	ESRRYFREAT	MKMAVMIFKR	GVFESRRKNK	AVFRPKIRIN	LREVQTLSWP	RTVTERLLDE
410	420	430	440	450	460	470	480
MFDSTASQFL	AVLEALSDSN	RRILQTGPIV	TDEVEIHDVV	SELFMAGKEL	LIMSNIGADG	MLDFPKTSLL	ELMIGRKDVI
490	500	510	520	530	540	550	560
SVDAAVKFIK	LAFTYEEWSL	FESSAVHLIY	FLQRQDDPES	KKAEKDLTLL	IAMEPLINVK	RNKGLIFPLE	NYKEGQSAQI
570	580	590	600	610	620	630	640
YFKKIAVHDT	CLKTCGYSED	IFHLAATLYV	CVCTAPQDVQ	PDKEIVVDTI	MFLWQKCKLG	IQRLNISRND	YAKFTQKIST
650	660	670	680	690	700	710	720
NKWIYLLWQI	NEVIHCYKME	DIDIVVVAEV	TLRLSEILES	LGSPGRKFKQ	SLDVPLREGT	NKFPGAPKGI	TEILPILQKN
730	740	750	760	770	780	790	800
PVEQLLFAYK	LLDRAIGGIN	LNCMLTSLPN	GSSVIDHCYA	KRTHHIDGDT	YKPLASNSFM	MDLHLELIQA	QHRIAVVLLD
810	820	830	840	850	860	870	880
KLQVLQTPTV	SKDISTKGPE	KLKQSGSTDC	FTELNIMNKI	KKNTLSKAIY	LMQKALLIFE	KDATSTSSWE	LLMEAYSLIQ
890	900	910	920	930	940	950	960
RIEAEQNALY	SYQKYLESSK	RKKSRVPPPP	ILLSRTHCSV	TLKPAPFTSE	VKVSWYCILG	CKAEGSYGKV	RLNNNHLPNS
970	980	990	1000	1010	1020	1030	1040
GEAIPADGKS	VFEVKGLETN	EKYVFAVAAY	SNNGKLVGGA	IGETTKPILV	YPPLSTITAR	MFLTQVAYQV	GNYELAKKVF
1050	1060	1070	1080	1090	1100	1110	1120
SPVWDYFVAS	PLQDEQSVIC	LSNIITITQR	RLHSDILAET	SSILLYLFLR	NIFVTSDIKI	KEENLFCDNI	KGNEIFPSQQ
1130	1140	1150	1160	1170	1180	1190	1200
IARLIECERV	LVALELSNFL	NDSSYALQAV	TQCYGLLAPI	IYHNIVLVPV	VQILIKCIVV	LQGLPSIVCS	KKHTASFESI
1210	1220	1230	1240	1250	1260	1270	1280
QHMIACCIFY	ITKILRSWRE	YDLAVMIINY	GKKMLDITPG	CKSLFDGSNE	QEEMPEEDSS	KKSLKTKKPQ	QILLPEKINE
1290	1300	1310	1320	1330	1340	1350	1360
QLALLETHLL	KLTKQYVTSE	LSGGEDPIFL	YPVVLNWSVK	GAVKEVMKFK	QKPRFLEFFT	QVMLKCMNEE	KFHLMVEVTT
1370	1380	1390	1400	1410	1420	1430	1440
PVHDFLKRRN	ESLLGLIKVK	YKDSALNKKA	NKSLKFKAAV	MEIGRSAEMQ	QRIRSKKKET	LRDFIFKNPA	ISEMVAHERN
1450	1460	1470	1480	1490	1500	1510	1520
RRTSVRKAAQ	RYLMDYLNPL	ILSYVKRKRF	HRLSLEEMPW	RAQMNLYLAG	AHFNLVLQKL	WECTKMKFGT	SHMMVSFRSC
1530	1540	1550	1560	1570	1580	1590	1600
DPNMFSLYNS	GTVLPTRKLT	VENYKAMLDF	LLTAKKRKAN	LPSDAEEFST	FINSIMSDEN	MSKTQTVYDS	DSQSGSSAKE
1610	1620	1630	1640	1650	1660	1670	1680
KDRGANLCVM	DHFMKIFLYC	RRAMVLAHRG	GYWTLLQNCC	RALWNFTQEL	QILLKQAVDL	DKTFPISQDG	FLCTSVLPFY
1690	1700	1710	1720	1730	1740	1750	1760
LGAELLIDML	IQLQNTSSIK	PIEDKGEFSV	PSCYGNIKND	NGGSSLTFEH	PLDDVNVVDL	KWIHDFVLKS	LEVLYQVEKW
1770	1780	1790	1800	1810	1820	1830	1840
ETLVSLAIQF	NTVSHERYTE	QVTPLLVYAQ	RQLLLRIQKF	KGPDITQQPC	ARYEAEYGEK	ITCRNFIGKQ	LKINSSTIEA
1850	1860	1870	1880	1890	1900	1910	1920
TSNCTDLLKM	LISSEYSRAK	ALVCVPVDVT	DTLRCFRETL	EKSKYHNRSI	RHSRKLLSLF	LAQTQGEKGE	INDSKCTSGK
1930	1940	1950	1960	1970	1980	1990	2000
VEFCLGTEEM	HMSIPPDLSQ	EHFRVFSSVE	KSKLPYSQLG	LVISSYHQTI	DVLQASNQRS	LKVQALHSLG	SLLIFAEKKR
2010	2020	2030	2040	2050	2060	2070	2080
AAFKCWCQAL	DDIFRKPDVL	HTWKEFGPSL	TNVTNSHSPP	GFKDYSEEFL	SRVGIWGCLQ	GAVISAKIAQ	FIKSLNVEKK
2090	2100	2110	2120	2130	2140	2150	2160
TDCCILSALL	FQGLLRTTLP	HPKAERCYAQ	YEITQLLPGI	ELFSDRYRAD	ICSVIASLYY	IIRELHFVRQ	NLIVLPLLAL
2170	2180	2190	2200	2210	2220	2230	2240
YQYFVSGICQ	DITRNLEARI	LKIEVLIDLR	FFSEAFYEIS	QIFYGKNMPC	PIPAGYKATG	KMKIFQSFDS	GKPLTSKENI
2250	2260	2270	2280	2290	2300	2310	2320
QAIDELRNKG	LPAVLVTIGQ	PHLLNKFNFV	KAYFFLSVAA	TINCVPENKF	KTVITNKSKP	NLPNLKEIYS	KDDGSSFYNL
2330	2340	2350	2360	2370	2380	2390	2400

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2780	1	973.5049	-1.76	2	63.8	12.2	2	1398-1414	K.AAVMEIGRSAEMQQRIR.S	

Detailed Protein Report

Protein 1274: 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 1275: 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 1276: PREDICTED: nuclear factor erythroid 2-related factor 1 isoform X6 [Homo sapiens]

Accession: gi|530412326
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 12.2
MW [kDa]: 80.1
pI: 4.4
Sequence Coverage [%]: 1.2
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MLSLKKYLTE	GLLQFTILLS	LIGVRVDVDT	YLTSQLPPLR	EIILGPSSAY	TQTQFHNLRN	TLDGYGIHPK	SIDLDNYFTA
90	100	110	120	130	140	150	160
RRLLSQVRAL	DRFQVPTTEV	NAWLVHRDPE	GSVSGSQPNS	GLALESSSGL	QDVTGPDNGV	RESETEQGFG	EDLEDLGAVA
170	180	190	200	210	220	230	240
PPVSGDLTKE	DIDLGAGREV	FDYSHRQKEQ	DVEKELRDGG	EQDTWAGEGA	EALARNLLVD	GETGESFPAQ	FPADISSITE
250	260	270	280	290	300	310	320
AVPSESEPPA	LQNNLLSPLL	TGTESPFDLE	QQWQDLMSIM	EMQAMEVNTS	ASEILYSAPP	GDPLSTNYSL	APNTPINQNV
330	340	350	360	370	380	390	400
SLHQASLGGC	SQDFLLFSPE	VESLPVASSS	TLLPLAPSNS	TSLNSTFGST	NLTGLFFPPQ	LNGTANDTAG	PELPDPLGGL
410	420	430	440	450	460	470	480
LDEAMLDEIS	LMDLAIEEGF	NPVQASQLEE	EFDSDSGLSL	DSSHSPSSLS	SSEGSSSSSS	SSSSSSSSAS	SSASSSFSEE
490	500	510	520	530	540	550	560
GAVGYSSDSE	TLDLEEAEGA	VGYQPEYSKF	CRMSYQDPAQ	LSCLPYLEHV	GHNHTYNMAP	SALDSADLPP	PSALKKGSKE
570	580	590	600	610	620	630	640
KQADFLDKQM	SRDEHRARAM	KIPFTNDKII	NLPVEEFNEL	LSKYQLSEAQ	LSLIRDIRRR	GKNKMAAQNC	RKRKLDTILN
650	660	670	680	690	700	710	720
LERDVEDLQR	DKARLLREKV	EFLRSLRQMK	QKVQSLYQEV	FGRLRDENGR	PYSPSQYALQ	YAGDGSVLLI	PRTMADQQAR
730	740						
RQERKPKDRR	K						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1364	1	945.1721	-308.27	1	45.6	12.2	0	170-178	K.EDIDLGAGR.E	

Detailed Protein Report

Protein 1277: dedicator of cytokinesis protein 8 isoform 2 [Homo sapiens]

Accession:	gi|299473744	**Score:**	12.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	227.3
Database Date:	2015-11-30	**pI:**	6.3
		Sequence Coverage [%]:	0.6
		No. of unique Peptides:	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MTHLNSLDVQ	LAQELGDFTD	DDLDVVFTPK	ECRTLQPSLP	EEGVELDPHV	RDCVQTYIRE	WLIVNRKNQG	SPEICGFKKT
90	100	110	120	130	140	150	160
GSRKDFHKTL	PKQTFESETL	ECSEPAAQAG	PRHLNVLCDV	SGKGPVTACD	FDLRSLQPDK	RLENLLQQVS	AEDFEKQNEE
170	180	190	200	210	220	230	240
ARRTNRQAEL	FALYPSVDEE	DAVEIRPVPE	CPKEHLGNRI	LVKLLTLKFE	IEIEPLFASI	ALYDVKERKK	ISENFHCDLN
250	260	270	280	290	300	310	320
SDQFKGFLRA	HTPSVAASSQ	ARSAVFSVTY	PSSDIYLVVK	IEKVLQQGEI	GDCAEPYTVI	KESDGGKSKE	KIEKLKLQAE
330	340	350	360	370	380	390	400
SFCQRLGKYR	MPFAWAPISL	SSFFNVSTLE	REVTDVDSVV	GRSSVGERRT	LAQSRRLSER	ALSLEENGVG	SNFKTSTLSV
410	420	430	440	450	460	470	480
SSFFKQEGDR	LSDEDLFKFL	ADYKRSSSLQ	RRVKSIPGLL	RLEISTAPEI	INCCLTPEML	PVKPFPENRT	RPHKEILEFP
490	500	510	520	530	540	550	560
TREVYVPHTV	YRNLLYVYPQ	RLNFVNKLAS	ARNITIKIQF	MCGEDASNAM	PVIFGKSSGP	EFLQEVYTAV	TYHNKSPDFY
570	580	590	600	610	620	630	640
EEVKIKLPAK	LTVNHHLLFT	FYHISCQQKQ	GASVETLLGY	SWLPILLNER	LQTGSYCLPV	ALEKLPPNYS	MHSAEKVPLQ
650	660	670	680	690	700	710	720
NPPIKWAEGH	KGVFNIEVQA	VSSVHTQDNH	LEKFFTLCHS	LESQVTFPIR	VLDQKISEMA	LEHELKLSII	CLNSSRLEPL
730	740	750	760	770	780	790	800
VLFLHLVLDK	LFQLSVQPMV	IAGQTANFSQ	FAFESVVAIA	NSLHNSKDLS	KDQHGRNCLL	ASYVHYVFRL	PEVQRDVPKS
810	820	830	840	850	860	870	880
GAPTALLDPR	SYHTYGRTSA	AAVSSKLLQA	RVMSSSNPDL	AGTHSAADEE	VKNIMSSKHF	HEELALQMVV	STGMVRETVF
890	900	910	920	930	940	950	960
KYAWFFFELL	VKSMAQHVHN	MDKRDSFRRT	RFSDRFMDDI	TTIVNVVTSE	IAALLVKPQK	ENEQAEKMNI	SLAFFLYDLL
970	980	990	1000	1010	1020	1030	1040
SLMDRGFVFN	LIRHYCSQLS	AKLSNLPTLI	SMRLEFLRIL	CSHEHYLNLN	LFFMNADTAP	TSPCPSISSQ	NSSSCSSFQD
1050	1060	1070	1080	1090	1100	1110	1120
QKIASMFDLT	SEYRQQHFLT	GLLFTELAAA	LDAEGEGISK	VQRKAVSAIH	SLLSSHDLDP	RCVKPEVKVK	IAALYLPLVG
1130	1140	1150	1160	1170	1180	1190	1200
IILDALPQLC	DFTVADTRRY	RTSGSDEEQE	GAGAINQNVA	LAIAGNNFNL	KTSGIVLSSL	PYKQYNMLNA	DTTRNLMICF
1210	1220	1230	1240	1250	1260	1270	1280
LWIMKNADQS	LIRKWIADLP	STQLNRILDL	LFICVLCFEY	KGKQSSDKVS	TQVLQKSRDV	KARLEEALLR	GEGARGEMMR
1290	1300	1310	1320	1330	1340	1350	1360
RRAPGNDRFP	GLNENLRWKK	EQTHWRQANE	KLDKTKAELD	QEALISGNLA	TEAHLIILDM	QENIIQASSA	LDCKDSLLGG
1370	1380	1390	1400	1410	1420	1430	1440
VLRVLVNSLN	CDQSTTYLTH	CFATLRALIA	KFGDLLFEEE	VEQCFDLCHQ	VLHHCSSSMD	VTRSQACATL	YLLMRFSFGA
1450	1460	1470	1480	1490	1500	1510	1520
TSNFARVKMQ	VTMSLASLVG	RAPDFNEEHL	RRSLRTILAY	SEEDTAMQMT	PFPTQVEELL	CNLNSILYDT	VKMREFQEDP
1530	1540	1550	1560	1570	1580	1590	1600
EMLMDLMYRI	AKSYQASPDL	RLTWLQNMAE	KHTKKKCYTE	AAMCLVHAAA	LVAEYLSMLE	DHSYLPVGSV	SFQNISSNVL
1610	1620	1630	1640	1650	1660	1670	1680
EESVVSEDTL	SPDEDGVCAG	QYFTESGLVG	LLEQAAELFS	TGGLYETVNE	VYKLVIPILE	AHREFRKLTL	THSKLQRAFD
1690	1700	1710	1720	1730	1740	1750	1760
SIVNKDHKRM	FGTYFRVGFF	GSKFGDLDEQ	EFVYKEPAIT	KLPEISHRLE	AFYGQCFGAE	FVEVIKDSTP	VDKTKLDPNK
1770	1780	1790	1800	1810	1820	1830	1840
AYIQITFVEP	YFDEYEMKDR	VTYFEKNFNL	RRFMYTTPFT	LEGRPRGELH	EQYRRNTVLT	TMHAFPYIKT	RISVIQKEEF
1850	1860	1870	1880	1890	1900	1910	1920
VLTPIEVAIE	DMKKKTLQLA	VAINQEPPDA	KMLQMVLQGS	VGATVNQGPL	EVAQVFLAEI	PADPKLYRHH	NKLRLCFKEF
1930	1940	1950	1960	1970	1980	1990	2000
IMRCGEAVEK	NKRLITADQR	EYQQELKKNY	NKLKENLRPM	IERKIPELYK	PIFRVESQKR	DSFHRSSFRK	CETQLSQGS

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
130	2	1097.5160	-71.95	1	30.3	12.2	0	800-810	K.SGAPTALLDPR.S	

Detailed Protein Report

Protein 1278: 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

Quantitation

mdown:qdown	**Median:**	1.02	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	1.16	**CV:**	0.00 %	**No. of 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	Ratios
1826	1	740.3072	-124.40	2	52.9	12.2	1	312-325	R.LDPGLALGPGERER.L		Wdown:Qdown 1.16 mdown:qdown 1.02

Detailed Protein Report

Protein 1279: 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 1280: PREDICTED: DNA (cytosine-5)-methyltransferase 1 isoform X1 [Homo sapiens]

Accession:	gi|578833065	**Score:**	12.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	169.3
Database Date:	2015-11-30	**pI:**	8.8
		Sequence Coverage [%]:	0.7
		No. of unique Peptides:	1

Quantitation

mdown:qdown **Median:** 1.35 **CV:** 0.00 % **No. of 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	Ratios
273	1	685.7423	-204.14	2	32.8	12.1	2	778-788	R.LAEMRQKEIPR.V		mdown:qdown 1.35

Detailed Protein Report

Protein 1281: keratinocyte-associated protein 3 [Homo sapiens]

Accession:	gi|270265801	**Score:**	12.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	25.6
Database Date:	2015-11-30	**pI:**	9.7
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	5.4
		No. of unique 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
558	1	786.7320	-166.72	2	36.3	12.1	2	1-13	-.MRRCSLCAFDAAR.G	Carbamidomethyl: 4; Oxidation: 1

Detailed Protein Report

Protein 1282: PREDICTED: membrane protein FAM159A isoform X2 [Homo sapiens]

Accession:	gi|530362541	**Score:**	12.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	11.8
Database Date:	2015-11-30	**pI:**	6.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	15.5
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	0.79	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.88	**CV:**	0.00 %	**No. of Peptides:**	1

```
        10         20         30         40         50         60         70         80
MSGACTSYVS AEQEVVRGFS CPRPGGEAAA VFCCGFRDHK YCCDDPHSFF PYEHSYMWWL SIGALIGLSV AAVVLLAFIV
        90        100        110        120
TACVLCYLFI SSKPHTKLDL GLSLQTAGGS
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2304	1	937.3088	-123.46	2	57.2	12.1	0	1-17	-.MSGACTSYVSAEQEVVR.G	Carbamidomethyl: 5	mdown:qdown 0.79 Wdown:Qdown 0.88

Detailed Protein Report

Protein 1283: semaphorin-4F isoform 2 precursor [Homo sapiens]

Accession:	gi|410651493	**Score:**	12.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	66.4
Database Date:	2015-11-30	**pI:**	8.8
		Sequence Coverage [%]:	1.8
		No. of unique Peptides:	1

Quantitation

Wdown:Qdown **Median:** 0.11 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MPASAARPRP GPGQPTASPF PLLLLAVLSG PVSGRVPRSV PRTSLPISEA DSCLTRFAVP HTYNYSVLLV DPASHTLYVG
        90        100        110        120        130        140        150        160
ARDTIFALSL PFSGERPRRI DWMVPEAHRQ NCRKKGKKEG DLGGRKTLQQ RWTTFLKADL LCPGPEHGRA SSVLQDVAVL
       170        180        190        200        210        220        230        240
RPELGAGTPI FYGIFSSQWE GATISAVCAF RPQDIRTVLN GPFRELKHDC NRGLPVVDND VPQPRPGECI TNNMKLRHFG
       250        260        270        280        290        300        310        320
SSLSLPDRVL TFIRDHPLMD RPVFPADGHP LLVTTDTAYL RVVAHRVTSL SGKEYDVLYL GTEDGHLHRA VRIGAQLSVL
       330        340        350        360        370        380        390        400
EDLALFPEPQ PVENMKLYHS WLLVGSRTEV TQVNTTNCGR LQSCSECILA QDPVCAWSFR LDECVAHAGE HRGLVQDIES
       410        420        430        440        450        460        470        480
ADVSSLCPKE PGERPVVFEV PVATAAHVVL PCSPSSAWAS CVWHQPSGVT ALTPRRDGLE VVVTPGAMGA YACECQEGGA
       490        500        510        520        530        540        550        560
AHVVAAYSLV WGSQRDAPSR AHTVGAGLAG FFLGILAASL TLILIGRRQQ RRRQRELLAR DKVGLDLGAP PSGTTSYSQD
       570        580        590        600        610        620
PPSPSPEDER LPLALAKRGS GFGGFSPPFL LDPCPSPAHI RLTGAPLATC DETSI
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
804	1	705.3763	24.50	2	38.9	12.1	1	99-109	R.RIDWMVPEAHR.Q		Wdown:Qdown 0.11

Detailed Protein Report

Protein 1284: 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 1285: uncharacterized protein C14orf93 isoform c [Homo sapiens]

Accession:	gi|545479143	**Score:**	12.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	54.1
Database Date:	2015-11-30	**pI:**	5.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSFSATILFS	PPSGSEARCC	CCACKSETNG	GNTGSQGGNP	PPSTPITVTG	HGLAVQSSEQ	LLHVIYQRVD	KAVGLAEAAL
90	100	110	120	130	140	150	160
GLARANNELL	KRLQEEVGDL	RQGKVSIPDE	DGESRAHSSP	PEEPGPLKES	PGEAFKALSA	VEEECDSVGS	GVQVVIEELR
170	180	190	200	210	220	230	240
QLGAASVGPG	PLGFPATQRD	MRLPGCTLAA	SEAAPLLNPL	VDDYVASEGA	VQRVLVPAYA	KQLSPATQLA	IQRATPETGP
250	260	270	280	290	300	310	320
ENGTKLPPPR	PEDMLNAAAA	LDSALEESGP	GSTGELRHSL	GLTVSPCRTR	GSGQKNSRRK	RDLVLSKLVH	NVHNHITNDK
330	340	350	360	370	380	390	400
RFNGSESIKS	SWNISVVKFL	LEKLKQELVT	SPHNYTDKEL	KGACVAYFLT	KRREYRNSLN	PFKGLKEKEE	KKLRSRRYRL
410	420	430	440	450	460	470	480
FANRSSIMRH	FGPEDQRLWN	DVTEELMSDE	EDSLNEPDRL	PSAEAQLLPP	ELYNPNFQEE	EDEGGDENAP	GSPSFDQPHK
490	500						
TCCPDLNSFI	EIKVEKDE						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
438	1	847.2141	-29.18	1	34.1	12.1	0	19-25	R.CCCCACK.S	Carbamidomethyl: 1, 3

Detailed Protein Report

Protein 1286: 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

Quantitation

mdown:qdown	**Median:**	0.80	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.71	**CV:**	0.00 %	**No. of 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	Ratios
244	1	938.4223	1.97	2	32.4	12.1	1	912-926	R.MLRGYNHQQMSEGHR.Q	Oxidation: 1, 10	Wdown:Qdown 0.71 mdown:qdown 0.80

Detailed Protein Report

Protein 1287: endophilin-A3 [Homo sapiens]

Accession: gi|223468657
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 12.1
MW [kDa]: 39.3
pI: 5.1
Sequence Coverage [%]: 2.6
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MSVAGLKKQF	HKASQLFSEK	ISGAEGTKLD	DEFLDMERKI	DVTNKVVAEI	LSKTTEYLQP	NPAYRAKLGM	LNTVSKIRGQ
90	100	110	120	130	140	150	160
VKTTGYPQTE	GLLGDCMLKY	GKELGEDSTF	GNALIEVGES	MKLMAEVKDS	LDINVKQTFI	DPLQLLQDKD	LKEIGHHLKK
170	180	190	200	210	220	230	240
LEGRRLDYDY	KKKRVGKIPD	EEVRQAVEKF	EESKELAERS	MFNFLENDVE	QVSQLAVFIE	AALDYHRQST	EILQELQSKL
250	260	270	280	290	300	310	320
QMRISAASSV	PRREYKPRPV	KRSSSELNGV	STTSVVKTTG	SNIPMDQPCC	RGLYDFEPEN	QGELGFKEGD	IITLTNQIDE
330	340	350					
NWYEGMIHGE	SGFFPINYVE	VIVPLPQ					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2663	1	887.4811	-15.08	1	61.6	12.1	0	244-252	R.ISAASSVPR.R	

Detailed Protein Report

Protein 1288: **endonuclease/exonuclease/phosphatase family domain-containing protein 1 [Homo sapiens]**

Accession:	gi|71043966	**Score:**	12.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	62.4
Database Date:	2015-11-30	**pI:**	9.5
		Sequence Coverage [%]:	3.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
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 1289: **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 1290: glutathione reductase, mitochondrial isoform 4 precursor [Homo sapiens]

Accession:	gi|305410793	**Score:**	12.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	47.2
Database Date:	2015-11-30	**pI:**	9.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MALLPRALSA	GAGPSWRRAA	RAFRGFLLLL	PEPAALTRAL	SRAMACRQEP	QPQGPPPAAG	AVASYDYLVI	GGGSGGLASA
90	100	110	120	130	140	150	160
RRAAELGARA	AVVESHKLGG	TCVNVGCVPK	KVMWNTAVHS	EFMHDHADYG	FPSCEGKFNW	RVIKEKRDAY	VSRLNAIYQN
170	180	190	200	210	220	230	240
NLTKSHIEII	RGHAAFTSDP	KPTIEVSGKK	YTAPHILIAT	GGMPSTPHES	QIPGASLGIT	SDGFFQLEEL	PGRSVIVGAG
250	260	270	280	290	300	310	320
YIAVEMAGIL	SALGSKTSLM	IRHDKGIQTD	DKGHIIVDEF	QNTNVKGIYA	VGDVCGKALL	TPVAIAAGRK	LAHRLFEYKE
330	340	350	360	370	380	390	400
DSKLDYNNIP	TVVFSHPPIG	TVGLTEDEAI	HKYGIENVKT	YSTSFTPMYH	AVTKRKTKCV	MKMVCANKEE	KVVGIHMQGL
410	420	430	440	450			
GCDEMLQGFA	VAVKMGATKA	DFDNTVAIHP	TSSEELVTLR				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2535	1	686.2933	-59.83	2	60.4	12.1	2	377-388	K.TKCVMKMVCANK.E	Oxidation: 5

Detailed Protein Report

Protein 1291: zinc finger protein 77 [Homo sapiens]

Accession:	gi|33438586	**Score:**	12.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	61.9
Database Date:	2015-11-30	**pI:**	10.2
		Sequence Coverage [%]:	3.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDCVIFEEVA	VNFTPEEWAL	LDHAQRSLYR	DVMLETCRNL	ASLDCYIYVR	TSGSSSQRDV	FGNGISNDEE	IVKFTGSDSW
90	100	110	120	130	140	150	160
SIFGENWRFD	NTGDQHQIPQ	RHLRSQLGRL	CESNEGHQCG	ETLSQTANLL	VHKSYPTEAK	PSECTKCGKA	FENRQRSHTG
170	180	190	200	210	220	230	240
QRPCKECGQA	CSCLSCQSPP	MKTQTVEKPC	NCQDSRTASV	TYVKSLSSKK	SYECQKCGKA	FICPSSFRGH	VNSHHGQKTH
250	260	270	280	290	300	310	320
ACKVCGKTFM	YYSYLTRHVR	THTGEKPYEC	KECGKAFSCP	SYFREHVRTH	TGEKPYECKH	CGKSFSCYSS	FRDHVRTHTG
330	340	350	360	370	380	390	400
EKPCQCKHCG	KAFTCYSSLR	EHGRTHSGEK	PYECKECGKA	FRYPSSLRAH	MRMHTGEKPY	VCKQCGKAFG	CPTYFRRHVK
410	420	430	440	450	460	470	480
THSGVKPYQC	KECGKAYSFS	SSLRIHVRTH	TGEKPFECKH	CGKAFSCHSS	LREHVRTHSG	EKPYECNQCG	KAFSHAQYFQ
490	500	510	520	530	540	550	
KHVRSHSGVK	PYECTECGKA	YSCSSSLRVH	VRTHTGERPY	ECKQCGKTFR	YLASLQAHVR	THAGA	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1703	1	1070.9798	-22.91	2	49.8	12.1	2	513-530	R.THTGERPYECKQCGKTFR.Y	

Detailed Protein Report

Protein 1292: probable G-protein coupled receptor 27 [Homo sapiens]

Accession:	gi|9506747	**Score:**	12.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	39.8
Database Date:	2015-11-30	**pI:**	10.7
		Sequence Coverage [%]:	5.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MANASEPGGS	GGGEAAALGL	KLATLSLLLC	VSLAGNVLFA	LLIVRERSLH	RAPYYLLLDL	CLADGLRALA	CLPAVMLAAR
90	100	110	120	130	140	150	160
RAAAAAGAPP	GALGCKLLAF	LAALFCFHAA	FLLLGVGVTR	YLAIAHHRFY	AERLAGWPCA	AMLVCAAWAL	ALAAAFPPVL
170	180	190	200	210	220	230	240
DGGGDDEDAP	CALEQRPDGA	PGALGFLLLL	AVVVGATHLV	YLRLLFFIHD	RRKMRPARLV	PAVSHDWTFH	GPGATGQAAA
250	260	270	280	290	300	310	320
NWTAGFGRGP	TPPALVGIRP	AGPGRGARRL	LVLEEFKTEK	RLCKMFYAVT	LLFLLLWGPY	VVASYLRVLV	RPGAVPQAYL
330	340	350	360	370	380		
TASVWLTFAQ	AGINPVVCFL	FNRELRDCFR	AQFPCCQSPR	TTQATHPCDL	KGIGL		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1926	1	857.3073	-135.85	2	54.2	12.0	0	2-21	M.ANASEPGGSGGGEAAALGLK.L	

Detailed Protein Report

Protein 1293: 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 1294: tRNA pseudouridine synthase A, mitochondrial isoform 2 [Homo sapiens]

Accession:	gi|70166599	**Score:**	12.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	44.3
Database Date:	2015-11-30	**pI:**	8.7
		Sequence Coverage [%]:	2.5
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|70166634	refseq_huma (refseq_human_20140103.fasta)	tRNA pseudouridine synthase A, mitochondrial isoform 2 [Homo sapiens]

10	20	30	40	50	60	70	80
MAGNAEPPPA	GAACPQDRRS	CSGRAGGDRV	WEDGEHPAKK	LKSGGDEERR	EKPPKRKIVL	LMAYSGKGYH	GMQRNVGSSQ
90	100	110	120	130	140	150	160
FKTIEDDLVS	ALVRSGCIPE	NHGEDMRKMS	FQRCARTDKG	VSAAGQVVSL	KVWLIDDILE	KINSHLPSHI	RILGLKRVTG
170	180	190	200	210	220	230	240
GFNSKNRCDA	RTYCYLLPTF	AFAHKDRDVQ	DETYRLSAET	LQQVNRLLAC	YKGTHNFHNF	TSQKGPQDPS	ACRYILEMYC
250	260	270	280	290	300	310	320
EEPFVREGLE	FAVIRVKGQS	FMMHQIRKMV	GLVVAIVKGY	APESVLERSW	GTEKVDVPKA	PGLGLVLERV	HFEKYNQRFG
330	340	350	360	370	380	390	400
NDGLHEPLDW	AQEEGKVAAF	KEEHIYPTII	GTERDERSMA	QWLSTLPIHN	FSATALTAGG	TGAKVPSPLE	GSEGDGDTD

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
574	1	512.7132	-190.86	2	35.8	12.0	0	300-309	K.APGLGLVLER.V	

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Detailed Protein Report

Protein 1295: ATP-dependent RNA helicase DDX42 [Homo sapiens]

Accession:	gi|45446743	**Score:**	12.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	102.9
Database Date:	2015-11-30	**pI:**	6.6
		Sequence Coverage [%]:	2.1
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578830314	refseq_human (refseq_human_20140103.fasta)	PREDICTED: ATP-dependent RNA helicase DDX42 isoform X1 [Homo sapiens]
gi|45446747	refseq_human (refseq_human_20140103.fasta)	ATP-dependent RNA helicase DDX42 [Homo sapiens]

10	20	30	40	50	60	70	80
MNWNKGGPGT	KRGFGFGGFA	ISAGKKEEPK	LPQQSHSAFG	ATSSSSGFGK	SAPPQLPSFY	KIGSKRANFD	EENAYFEDEE
90	100	110	120	130	140	150	160
EDSSNVDLPY	IPAENSPTRQ	QFHSKPVDSD	SDDDPLEAFM	AEVEDQAARD	MKRLEEKDKE	RKNVKGIRDD	IEEEDDQEAY
170	180	190	200	210	220	230	240
FRYMAENPTA	GVVQEEEEDN	LEYDSDGNPI	APTKKIIDPL	PPIDHSEIDY	PPFEKNFYNE	HEEITNLTPQ	QLIDLRHKLN
250	260	270	280	290	300	310	320
LRVSGAAPPR	PGSSFAHFGF	DEQLMHQIRK	SEYTQPTPIQ	CQGVPVALSG	RDMIGIAKTG	SGKTAAFIWP	MLIHIMDQKE
330	340	350	360	370	380	390	400
LEPGDGPIAV	IVCPTRELCQ	QIHAECKRFG	KAYNLRSVAV	YGGGSMWEQA	KALQEGAEIV	VCTPGRLIDH	VKKKATNLQR
410	420	430	440	450	460	470	480
VSYLVFDEAD	RMFDMGFEYQ	VRSIASHVRP	DRQTLLFSAT	FRKKIEKLAR	DILIDPIRVV	QGDIGEANED	VTQIVEILHS
490	500	510	520	530	540	550	560
GPSKWNWLTR	RLVEFTSSGS	VLLFVTKKAN	AEELANNLKQ	EGHNLGLLHG	DMDQSERNKV	ISDFKKKDIP	VLVATDVAAR
570	580	590	600	610	620	630	640
GLDIPSIKTV	INYDVARDID	THTHRIGRTG	RAGEKGVAYT	LLTPKDSNFA	GDLVRNLEGA	NQHVSKELLD	LAMQNAWFRK
650	660	670	680	690	700	710	720
SRFKGGKGKK	LNIGGGGLGY	RERPGLGSEN	MDRGNNNVMS	NYEAYKPSTG	AMGDRLTAMK	AAFQSQYKSH	FVAASLSNQK
730	740	750	760	770	780	790	800
AGSSAAGASG	WTSAGSLNSV	PTNSAQQGHN	SPDSPVTSAA	KGIPGFGNTG	NISGAPVTYP	SAGAQGVNNT	ASGNNSREGT
810	820	830	840	850	860	870	880
GGSNGKRERY	TENRGSSRHS	HGETGNRHSD	SPRHGDGGRH	GDGYRHPESS	SRHTDGHRHG	ENRHGGSAGR	HGENRGANDG
890	900	910	920	930	940		
RNGESRKEAF	NRESKMEPKM	EPKVDSSKMD	KVDSKTDKTA	DGFAVPEPPK	RKKSRWDS		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1875	1	990.8378	-137.62	2	51.9	12.0	0	31-50	K.LPQQSHSAFGATSSSSGFGK.S	

Detailed Protein Report

Protein 1296: spermatid maturation protein 1 [Homo sapiens]

Accession:	gi|116268095	**Score:**	12.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	34.8
Database Date:	2015-11-30	**pI:**	9.2
Modification(s):	Oxidation	**Sequence Coverage [%]:**	9.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAMVERPRPE	WASYHNCNSN	SCQDLGNSVL	LLLGLIICIN	ISINIVTLLW	SRFRGVLYQV	FHDTICEKEA	PKSSLLRKQT
90	100	110	120	130	140	150	160
QPPKKQSSPA	VHLRCTMDPV	MMTVSPPPAH	RHRRRGSPTR	CAHCPVAWAP	DTDDEKPHQY	PAICSYHWDV	PEDWEGFQHT
170	180	190	200	210	220	230	240
QGTWVPWSQD	APESPPQTIR	FQPTVEERPL	KTGIWSELGL	RAYVYPVNPP	PPSPEAPSHK	NGGEGAVPEA	EAAQYQPVPA
250	260	270	280	290	300	310	
PTLGPAVIPE	FSRHRSSGRI	VYDARDMRRR	LRELTREVEA	LSGCYPLASG	SSTAEETSKN	WVYRSLTGR	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2077	1	1057.4596	-49.95	3	54.5	12.0	2	86-113	K.QSSPAVHLRCTMDPVMMTVSPPPAHRHR.R	Oxidation: 12, 17

Detailed Protein Report

Protein 1297: pyruvate dehydrogenase kinase, isozyme 2 isoform 3 precursor [Homo sapiens]

Accession:	gi|315630393	**Score:**	12.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	22.4
Database Date:	2015-11-30	**pI:**	9.4
		Sequence Coverage [%]:	7.5
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MRWVWALLKN ASLAGAPKYI EHFSKFSPSP LSMKQFLDFG SSNACEKTSF TFLRQELPVR LANIMKEINL LPDRVLSTPS
        90        100        110        120        130        140        150        160
VQLVQSWYVQ SLLDIMEFLD KDPEDHRTLS QFTDALVTIR NRHNDVVPTM AQGVLEYKDT YGDDPVSNQN IQYFLDRFYL
       170        180        190        200
SRISIRMLIN QHSGCRPQRR GAGGGGGGAG AQGRAAEGT
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
455	1	593.1800	-194.20	2	34.7	12.0	1	180-194	R.RGAGGGGGGAGAQGR.A	

Detailed Protein Report

Protein 1298: **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 1299: 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

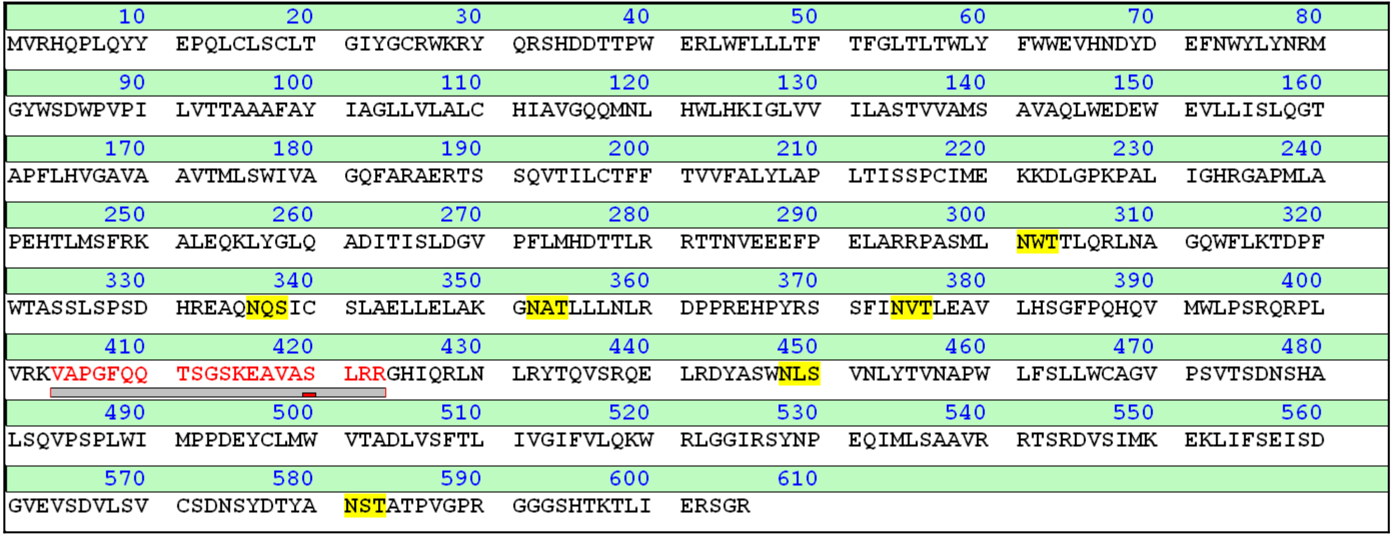
Detailed Protein Report

Protein 1300: **glycerophosphodiester phosphodiesterase domain-containing protein 5 [Homo sapiens]**

Accession:	gi|189571657	**Score:**	12.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	68.5
Database Date:	2015-11-30	**pI:**	8.6
		Sequence Coverage [%]:	3.3
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578821761	refseq_human (refseq_human_20140103.fasta)	PREDICTED: glycerophosphodiester phosphodiesterase domain-containing protein 5 isoform X4 [Homo sapiens]



```
        10         20         30         40         50         60         70         80
MVRHQPLQYY EPQLCLSCLT GIYGCRWKRY QRSHDDTTPW ERLWFLLLTF TFGLTLTWLY FWWEVHNDYD EFNWYLYNRM
        90        100        110        120        130        140        150        160
GYWSDWPVPI LVTTAAAFAY IAGLLVLALC HIAVGQQMNL HWLHKIGLVV ILASTVVAMS AVAQLWEDEW EVLLISLQGT
       170        180        190        200        210        220        230        240
APFLHVGAVA AVTMLSWIVA GQFARAERTS SQVTILCTFF TVVFALYLAP LTISSPCIME KKDLGPKPAL IGHRGAPMLA
       250        260        270        280        290        300        310        320
PEHTLMSFRK ALEQKLYGLQ ADITISLDGV PFLMHDTTLR RTTNVEEEFP ELARRPASML NWTTLQRLNA GQWFLKTDPF
       330        340        350        360        370        380        390        400
WTASSLSPSD HREAQNQSIC SLAELLELAK GNATLLLNLR DPPREHPYRS SFINVTLEAV LHSGFPQHQV MWLPSRQRPL
       410        420        430        440        450        460        470        480
VRKVAPGFQQ TSGSKEAVAS LRRGHIQRLN LRYTQVSRQE LRDYASWNLS VNLYTVNAPW LFSLLWCAGV PSVTSDNSHA
       490        500        510        520        530        540        550        560
LSQVPSPLWI MPPDEYCLMW VTADLVSFTL IVGIFVLQKW RLGGIRSYNP EQIMLSAAVR RTSRDVSIMK EKLIFSEISD
       570        580        590        600        610
GVEVSDVLSV CSDNSYDTYA NSTATPVGPR GGGSHTKTLI ERSGR
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2619	1	1045.1934	126.67	2	61.0	12.0	2	404-423	K.VAPGFQQTSGSKEAVASLRR.G	

Detailed Protein Report

Protein 1301: cytohesin-1 isoform 2 [Homo sapiens]

Accession:	gi|110349763	**Score:**	12.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	46.3
Database Date:	2015-11-30	**pI:**	5.3
		Sequence Coverage [%]:	4.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEEDDSYVPS	DLTAEERQEL	ENIRRRKQEL	LADIQRLKDE	IAEVANEIEN	LGSTEERKNM	QRNKQVAMGR	KKFNMDPKKG
90	100	110	120	130	140	150	160
IQFLIENDLL	KNTCEDIAQF	LYKGEGLNKT	AIGDYLGERD	EFNIQVLHAF	VELHEFTDLN	LVQALRQFLW	SFRLPGEAQK
170	180	190	200	210	220	230	240
IDRMMEAFAQ	RYCQCNNGVF	QSTDTCYVLS	FAIIMLNTSL	HNPNVKDKPT	VERFIAMNRG	INDGGDLPEE	LLRNLYESIK
250	260	270	280	290	300	310	320
NEPFKIPEDD	GNDLTHTFFN	PDREGWLLKL	GGRVKTWKRR	WFILTDNCLY	YFEYTTDKEP	RGIIPLENLS	IREVEDSKKP
330	340	350	360	370	380	390	400
NCFELYIPDN	KDQVIKACKT	EADGRVVEGN	HTVYRISAPT	PEEKEEWIKC	IKAAISRDPF	YEMLAARKKK	VSSTKRH

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1979	1	618.9233	-17.42	3	53.4	12.0	0	2-17	M.EEDDSYVPSDLTAEER.Q	

Detailed Protein Report

Protein 1302: PREDICTED: WD repeat-containing protein 20 isoform X13 [Homo sapiens]

Accession:	gi|578826296	**Score:**	12.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	16.6
Database Date:	2015-11-30	**pI:**	9.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	8.8
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MATEGGGKEM NEIKTQFTTR EGLYKLLPHS EYSRPNRVPF NSQGSNPVRV SFVNLNDQSG NGDRLCFNVG RELYFYIYKG
        90        100        110        120        130        140        150
VRKAADLSKP IDKRIYKGTQ PTCHDFNHLT ATAESVSLLV GFSAGQVQLI DPIKKETSKL FNEEMASS
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
188	1	744.8750	60.79	2	31.6	12.0	1	136-148	K.ETSKLFNEEMASS.-	Oxidation: 10

Detailed Protein Report

Protein 1303: TLR4 interactor with leucine rich repeats precursor [Homo sapiens]

Accession:	gi|76880480	**Score:**	11.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	88.7
Database Date:	2015-11-30	**pI:**	10.9
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEAARALRLL	LVVCGCLALP	PLAEPVCPER	CDCQHPQHLL	CTNRGLRVVP	KTSSLPSPHD	VLTYSLGGNF	ITNITAFDFH
90	100	110	120	130	140	150	160
RLGQLRRLDL	QYNQIRSLHP	KTFEKLSRLE	ELYLGNNLLQ	ALAPGTLAPL	RKLRILYANG	NEISRLSRGS	FEGLESLVKL
170	180	190	200	210	220	230	240
RLDGNALGAL	PDAVFAPLGN	LLYLHLESNR	IRFLGKNAFA	QLGKLRFLNL	SANELQPSLR	HAATFAPLRS	LSSLILSANN
250	260	270	280	290	300	310	320
LQHLGPRIFQ	HLPRLGLLSL	RGNQLTHLAP	EAFWGLEALR	ELRLEGNRLS	QLPTALLEPL	HSLEALDLSG	NELSALHPAT
330	340	350	360	370	380	390	400
FGHLGRLREL	SLRNNALSAL	SGDIFAASPA	LYRLDLDGNG	WTCDCRLRGL	KRWMGDWHSQ	GRLLTVFVQC	RHPPALRGKY
410	420	430	440	450	460	470	480
LDYLDDQQLQ	NGSCADPSPS	ASLTADRRRQ	PLPTAAGEEM	TPPAGLAEEL	PPQPQLQQQG	RFLAGVAWDG	AARELVGNRS
490	500	510	520	530	540	550	560
ALRLSRRGPG	LQQPSPSVAA	AAGPAPQSLD	LHKKPQRGRP	TRADPALAEP	TPTASPGSAP	SPAGDPWQRA	TKHRLGTEHQ
570	580	590	600	610	620	630	640
ERAAQSDGGA	GLPPLVSDPC	DFNKFILCNL	TVEAVGADSA	SVRWAVREHR	SPRPLGGARF	RLLFDRFGQQ	PKFHRFVYLP
650	660	670	680	690	700	710	720
ESSDSATLRE	LRGDTPYLVC	VEGVLGGRVC	PVAPRDHCAG	LVTLPEAGSR	GGVDYQLLTL	ALLTVNALLV	LLALAAWASR
730	740	750	760	770	780	790	800
WLRRKLRARR	KGGAPVHVRH	MYSTRRPLRS	MGTGVSADFS	GFQSHRPRTT	VCALSEADLI	EFPCDRFMDS	AGGGAGGSLR
810	820						
REDRLLQRFA	D						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1954	1	618.9203	-56.42	3	53.1	11.9	2	787-804	R.FMDSAGGGAGGSLRREDR.L	Oxidation: 2

Protein 1304: PREDICTED: cyclic nucleotide-gated cation channel beta-3 isoform X1 [Homo sapiens]

Accession: gi|578816058
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 11.9
MW [kDa]: 76.5
pI: 9.2
Sequence Coverage [%]: 5.0
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MRQRTALYKK	KLVEGDLSSP	EASPQTAKPT	AVPPVKESDD	KPTEHYYRLL	WFKVKKMPLT	EYLKRIKLPN	SIDSYTDRLY
90	100	110	120	130	140	150	160
LLWLLLVTLA	YNWNCCFIPL	RLVFPYQTAD	NIHYWLIADI	ICDIIYLYDM	LFIQPRLQFV	RGGDIIVDSN	ELRKHYRTST
170	180	190	200	210	220	230	240
KFQLDVASII	PFDICYLFFG	FNPMFRANRM	LKYTSFFEFN	HHLESIMDKA	YIYRVIRTTG	YLLFILHINA	CVYYWASNYE
250	260	270	280	290	300	310	320
GIGTTRWVYD	GEGNEYLRCY	YWAVRTLITI	GGLPEPQTLF	EIVFQLLNFF	SGVFVFSSLI	GQMRDVIGAA	TANQNYFRAC
330	340	350	360	370	380	390	400
MDDTIAYMNN	YSIPKLVQKR	VRTWYEYTWD	SQRMLDESDL	LKTLPTTVQL	ALAIDVNFSI	ISKVDLFKGC	DTQMIYDMLL
410	420	430	440	450	460	470	480
RLKSVLYLPG	DFVCKKGEIG	KEMYIIKHGE	VQVLGGPDGT	KVLVTLKAGS	VLLAAGGGNR	RTANVVAHGF	ANLLTLDKKT
490	500	510	520	530	540	550	560
LQEILVHYPD	SERILMKKAR	VLLKQKAKTA	EATPPRKDLA	LLFPPKEETP	KLFKTLLGGT	GKASLARLLK	LKREQAAQKK
570	580	590	600	610	620	630	640
ENSEGGEEEG	KENEDKQKEN	EDKQKENEDK	GKENEDKDKG	REPEEKPLDR	PECTASPIAV	EEEPHSVRRT	VLPRGTSRQS
650	660	670					
LIISMAPSAE	GGEEVLTIEV	KEKAKQ					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1889	1	1057.4942	-93.37	3	52.3	11.9	2	428-460	K.HGEVQVLGGPDGTKVLVTLKAGSVLLAAGGGNR.R	

Detailed Protein Report

Protein 1305: something about silencing protein 10 [Homo sapiens]

Accession:	gi|9966799	**Score:**	11.9
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

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
1806	2	697.0294	-33.06	3	51.2	11.9	0	242-260	K.DELEPLLELVEQGIIPPGK.G	

Protein 1306: 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 1307: dynactin subunit 5 isoform 2 [Homo sapiens]

Accession:	gi|312261189	**Score:**	11.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	9.7
Database Date:	2015-11-30	**pI:**	10.2
		Sequence Coverage [%]:	15.5
		No. of unique Peptides:	1

```
         10         20         30         40         50         60         70         80
MELGELLYNK SEYIETASGN KVSRQSVLCG SQNIVLNGKN FVISVFLSPY IRCHSACRDR KRSDESVRLS VNNREWWGLV
         90
NWRM
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2116	1	766.2591	-184.33	2	55.0	11.9	2	62-74	K.RSDESVRLSVNNR.E	

Detailed Protein Report

Protein 1308: melanoma-associated antigen D1 isoform b [Homo sapiens]

Accession: gi|52632377

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Score: 11.9

MW [kDa]: 86.1

pI: 5.5

Sequence Coverage [%]: 1.5

No. of unique Peptides: 1

Alias proteins:

Accession	Name	Description
gi|52632379	refseq_huma (refseq_human_20140103.fasta)	melanoma-associated antigen D1 isoform b [Homo sapiens]

10	20	30	40	50	60	70	80
MAQKMDCGAG	LLGFQAEASV	EDSALLMQTL	MEAIQISEAP	PTNQATAAAS	PQSSQPPTAN	EMADIQVSAA	AARPKSAFKV
90	100	110	120	130	140	150	160
QNATTKGPNG	VYDFSQAHNA	KDVPNTQPKA	AFKSQNATPK	GPNAAYDFSQ	AATTGELAAN	KSEMAFKAQN	ATTKVGPNAT
170	180	190	200	210	220	230	240
YNFSQSLNAN	DLANSRPKTP	FKAWNDTTKA	PTADTQTQNV	NQAKMATSQA	DIETDPGISE	PDGATAQTSA	DGSQAQNLES
250	260	270	280	290	300	310	320
RTIIRGKRTR	KINNLNVEEN	SSGDQRRAPL	AAGTWRSAPV	PVTTQNPPGA	PPNVLWQTPL	AWQNPSGWQN	QTARQTPPAR
330	340	350	360	370	380	390	400
QSPPARQTPP	AWQNPVAWQN	PVIWPNPVIW	QNPVIWPNPI	VWPGPVVWPN	PLAWQNPPGW	QTPPGWQTPP	GWQGPPDWQG
410	420	430	440	450	460	470	480
PPDWPLPPDW	PLPPDWPLPT	DWPLPPDWIP	ADWPIPPDWQ	NLRPSPNLRP	SPNSRASQNP	GAAQPRDVAL	LQERANKLVK
490	500	510	520	530	540	550	560
YLMLKDYTKV	PIKRSEMLRD	IIREYTDVYP	EIIERACFVL	EKKFGIQLKE	IDKEEHLYIL	ISTPESLAGI	LGTTKDTPKL
570	580	590	600	610	620	630	640
GLLLVILGVI	FMNGNRASEA	VLWEALRKMG	LRPGVRHPLL	GDLRKLLTYE	FVKQKYLDYR	RVPNSNPPEY	EFLWGLRSYH
650	660	670	680	690	700	710	720
ETSKMKVLRF	IAEVQKRDPR	DWTAQFMEAA	DEALDALDAA	AAEAEARAEA	RTRMGIGDEA	VSGPWSWDDI	EFELLTWDEE
730	740	750	760	770	780		
GDFGDPWSRI	PFTFWARYHQ	NARSRFPQTF	AGPIIGPGGT	ASANFAANFG	AIGFFWVE		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2048	1	731.3036	-178.47	2	54.2	11.9	2	645-656	K.MKVLRFIAEVQK.R	

Detailed Protein Report

Protein 1309: chondrosarcoma-associated gene 2/3 protein isoform b [Homo sapiens]

Accession:	gi|193788726	**Score:**	11.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	12.7
Database Date:	2015-11-30	**pI:**	10.9
		Sequence Coverage [%]:	16.4
		No. of unique Peptides:	1

Quantitation

Wdown:Qdown **Median:** 0.68 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MWMGLIQLVE	GVKRKDQGFL	EKEFYHKTNI	KMRCEFLACW	PAFTVLGEAW	RDQVDWSRLL	RDAGLVKMSR	KPRASSPLSN
90	100	110	120				
NHPPTPKRFP	RQPGREKGPI	KEVPGTKGSP					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2558	1	1002.0267	-5.40	2	60.2	11.9	2	74-91	R.ASSPLSNNHPPTPKRFPR.Q		Wdown:Qdown 0.68

Detailed Protein Report

Protein 1310: 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 1311: PREDICTED: zinc finger CCCH domain-containing protein 6 isoform X2 [Homo sapiens]

Accession:	gi|578804313	**Score:**	11.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	101.5
Database Date:	2015-11-30	**pI:**	6.4
		Sequence Coverage [%]:	1.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MTQEFINQHT	VEHKGKQICK	YFLEGRCIKG	DQCKFDHDAE	LEKRKEICKF	YLQGYCTKGE	NCIYMHNEFP	CKFYHSGAKC
90	100	110	120	130	140	150	160
YQGDNCKFSH	DDLTKETKKL	LDKVLNTDEE	LINEDERELE	ELRKRGITPL	PKPPPGVGLL	PTPPEHFPFS	DPEDDFQTDF
170	180	190	200	210	220	230	240
SDDFRKIPSL	FEIVVKPTVD	LAHKIGRKPP	AFYTSASPPG	PQFQGSSPHP	QHIYSSGSSP	GPGPNMSQGH	SSPVMHPGSP
250	260	270	280	290	300	310	320
GHHPCAGPPG	LPVPQSPPLP	PGPPEIVGPQ	NQAGVLVQPD	TSLTPPSMGG	AYHSPGFPGH	VMKVPRENHC	SPGSSYQQSP
330	340	350	360	370	380	390	400
GEMQLNTNYE	SLQNPAEFYD	NYYAQHSIHN	FQPPNNSGDG	MWHGEFAQQQ	PPVVQDSPNH	GSGSDGSSTR	TGHGPLPVPG
410	420	430	440	450	460	470	480
LLPAVQRALF	VRLTQRYQED	EEQTSTQPHR	APSKEEDDTV	NWYSSSEEEE	GSSVKSILKT	LQKQTETLRN	QQQPSTELST
490	500	510	520	530	540	550	560
PTDPRLAKEK	SKGNQVVDPR	LRTIPRQDIR	KPSESAPLDL	RLAWDPRKLR	GNGSGHIGSS	VGGAKFDLHH	ANAGTNVKHK
570	580	590	600	610	620	630	640
RGDDDDEDTE	RELREKAFLI	PLDASPGIML	QDPRSQLRQF	SHIKMDITLT	KPNFAKHIVW	APEDLLPVPL	PKPDPVSSIN
650	660	670	680	690	700	710	720
LPLPPLIADQ	RLNRLWNTKS	DLHQNTVSID	PKLAAKAKIN	TTNREGYLEQ	FGDSHGSGAK	LGDPRLQKNF	DPRLHRLPNT
730	740	750	760	770	780	790	800
ESHQVVMKDS	HASKGAPHLP	RSNPGSSQPS	GAGTSNSGSG	ALPPYAPKLS	SSAGLPLGTS	TSVLSGISLY	DPRDHGSSST
810	820	830	840	850	860	870	880
SELATASSGE	NSKNQKKSGG	LKSSDKTEPS	PGEAILPQKP	SPNVGVTLEG	PADPQADVPR	SSGKVQVPAV	HSLPVQALTG
890	900	910	920	930	940		
LIRPQYSDPR	QARQPGQGSP	TPDNDPGRET	DDKSLKEVFK	TFDPTASPFC			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1257	1	830.0861	111.46	2	44.4	11.9	2	456-469	K.SILKTLQKQTETLR.N	

Detailed Protein Report

Protein 1312: **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 1313: rho guanine nucleotide exchange factor 1 isoform 3 [Homo sapiens]

Accession: gi|39777604
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 11.9
MW [kDa]: 98.7
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	

Protein 1314: PREDICTED: clathrin heavy chain 2 isoform X7 [Homo sapiens]

Accession:	gi|578837411	**Score:**	11.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	177.9
Database Date:	2015-11-30	**pI:**	5.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAQILPVRFQ	EHFQLQNLGI	NPANIGFSTL	TMESDKFICI	REKVGEQAQV	TIIDMSDPMA	PIRRPISAES	AIMNPASKVI
90	100	110	120	130	140	150	160
ALKGAPGFCS	PASNSQSPGS	SLCPAGKTLQ	IFNIEMKSKM	KAHTMAEEVI	FWKWVSVNTV	ALVTETAVYH	WSMEGDSQPM
170	180	190	200	210	220	230	240
KMFDRHTSLV	GCQVIHYRTD	EYQKWLLLVG	ISAQQNRVVG	AMQLYSVDRK	VSQPIEGHAA	AFAEFKMEGN	AKPATLFCFA
250	260	270	280	290	300	310	320
VRNPTGGKLH	IIEVGQPAAG	NQPFVKKAVD	VFFPPEAQND	FPVAMQIGAK	HGVIYLITKY	GYLHLYDLES	GVCICMNRIS
330	340	350	360	370	380	390	400
ADTIFVTAPH	KPTSGIIGVN	KKGQVLSVCV	EEDNIVNYAT	NVLQNPDLGL	RLAVRSNLAG	AEKLFVRKFN	TLFAQGSYAE
410	420	430	440	450	460	470	480
AAKVAASAPK	GILRTRETVQ	KFQSIPAQSG	QASPLLQYFG	ILLDQGQLNK	LESLELCHLV	LQQGRKQLLE	KWLKEDKLEC
490	500	510	520	530	540	550	560
SEELGDLVKT	TDPMLALSVY	LRANVPSKVI	QCFAETGQFQ	KIVLYAKKVG	YTPDWIFLLR	GVMKISPEQG	LQFSRMLVQD
570	580	590	600	610	620	630	640
EEPLANISQI	VDIFMENSLI	QQCTSFLLDA	LKNNRPAEGL	LQTWLLEMNL	VHAPQVADAI	LGNKMFTHYD	RAHIAQLCEK
650	660	670	680	690	700	710	720
AGLLQQALEH	YTDLYDIKRA	VVHTHLLNPE	WLVNFFGSLS	VEDSVECLHA	MLSANIRQNL	QLCVQVASKY	HEQLGTQALV
730	740	750	760	770	780	790	800
ELFESFKSYK	GLFYFLGSIV	NFSQDPDVHL	KYIQAACKTG	QIKEVERICR	ESSCYNPERV	KNFLKEAKLT	DQLPLIIVCD
810	820	830	840	850	860	870	880
RFGFVHDLVL	YLYRNNLQRY	IEIYVQKVNP	SRTPAVIGGL	LDVDCSEEVI	KHLIMAVRGQ	FSTDELVAEV	EKRNRLKLLL
890	900	910	920	930	940	950	960
PWLESQIQEG	CEEPATHNAL	AKIYIDSNNS	PECFLRENAY	YDSSVVGRYC	EKRDPHLACV	AYERGQCDLE	LIKVCNENSL
970	980	990	1000	1010	1020	1030	1040
FKSEARYLVC	RKDPELWAHV	LEETNPSRRQ	LIDQVVQTAL	SETRDPEEIS	VTVKAFMTAD	LPNELIELLE	KIVLDNSVFS
1050	1060	1070	1080	1090	1100	1110	1120
EHRNLQNLLI	LTAIKADRTR	VMEYISRLDN	YDALDIASIA	VSSALYEEAF	TVFHKFDMNA	SAIQVLIEHI	GNLDRAYEFA
1130	1140	1150	1160	1170	1180	1190	1200
ERCNEPAVWS	QLAQAQLQKD	LVKEAINSYI	RGDDPSSYLE	VVQSASRSNN	WEDLVKFLQM	ARKKGRESYI	ETELIFALAK
1210	1220	1230	1240	1250	1260	1270	1280
TSRVSELEDF	INGPNNAHIQ	QVGDRCYEEG	MYEAAKLLYS	NVSNFARLAS	TLVHLGEYQA	AVDNSRKASS	TRTWKEVCFA
1290	1300	1310	1320	1330	1340	1350	1360
CMDGQEFRFA	QLCGLHIVIH	ADELEELMCY	YQDRGYFEEL	ILLLEAALGL	ERAHMGMFTE	LAILYSKFKP	QKMLEHLELF
1370	1380	1390	1400	1410	1420	1430	1440
WSRVNIPKVL	RAAEQAHLWA	ELVFLYDKYE	EYDNAVLTMM	SHPTEAWKEG	QFKDIITKVA	NVELCYRALQ	FYLDYKPLLI
1450	1460	1470	1480	1490	1500	1510	1520
NDLLLVLSPR	LDHTWTVSFF	SKDAMQHAAE	SRDAELAQKL	LQWFLEEGKR	ECFAACLFTC	YDLLRPDMVL	ELAWRHNLVD
1530	1540	1550	1560	1570			
LAMPYFIQVM	REYLSKVDKL	DALESLRKQE	EHVTEPAPLV	FDFDGHE			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
178	1	820.7984	68.97	3	31.0	11.9	1	42-63	R.EKVGEQAQVTIIDMSDPMAPIR.R	Oxidation: 14, 18

Detailed Protein Report

Protein 1315: NADP-dependent malic enzyme [Homo sapiens]

Accession:	gi|4505143	**Score:**	11.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	64.1
Database Date:	2015-11-30	**pI:**	5.7
		Sequence Coverage [%]:	1.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEPEAPRRRH	THQRGYLLTR	NPHLNKDLAF	TLEERQQLNI	HGLLPPSFNS	QEIQVLRVVK	NFEHLNSDFD	RYLLLMDLQD
90	100	110	120	130	140	150	160
RNEKLFYRVL	TSDIEKFMPI	VYTPTVGLAC	QQYSLVFRKP	RGLFITIHDR	GHIASVLNAW	PEDVIKAIVV	TDGERILGLG
170	180	190	200	210	220	230	240
DLGCNGMGIP	VGKLALYTAC	GGMNPQECLP	VILDVGTENE	ELLKDPLYIG	LRQRRVRGSE	YDDFLDEFME	AVSSKYGMNC
250	260	270	280	290	300	310	320
LIQFEDFANV	NAFRLLNKYR	NQYCTFNDDI	QGTASVAVAG	LLAALRITKN	KLSDQTILFQ	GAGEAALGIA	HLIVMALEKE
330	340	350	360	370	380	390	400
GLPKEKAIKK	IWLVDSKGLI	VKGRASLTQE	KEKFAHEHEE	MKNLEAIVQE	IKPTALIGVA	AIGGAFSEQI	LKDMAAFNER
410	420	430	440	450	460	470	480
PIIFALSNPT	SKAECSAEQC	YKITKGRAIF	ASGSPFDPVT	LPNGQTLYPG	QGNNSYVFPG	VALGVVACGL	RQITDNIFLT
490	500	510	520	530	540	550	560
TAEVIAQQVS	DKHLEEGRLY	PPLNTIRDVS	LKIAEKIVKD	AYQEKTATVY	PEPQNKEAFV	RSQMYSTDYD	QILPDCYSWP
570	580						
EEVQKIQTKV	DQ						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2267	1	1131.3787	-58.22	1	56.8	11.9	0	413-422	K.AECSAEQCYK.I	

Detailed Protein Report

Protein 1316: double-stranded RNA-specific adenosine deaminase isoform d [Homo sapiens]

Accession:	gi|70167113	**Score:**	11.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	103.6
Database Date:	2015-11-30	**pI:**	9.7
		Sequence Coverage [%]:	1.7
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|578800414	refseq_human (refseq_human_20140103.fasta)	PREDICTED: double-stranded RNA-specific adenosine deaminase isoform X5 [Homo sapiens]
gi|578800412	refseq_human (refseq_human_20140103.fasta)	PREDICTED: double-stranded RNA-specific adenosine deaminase isoform X4 [Homo sapiens]
gi|578800410	refseq_human (refseq_human_20140103.fasta)	PREDICTED: double-stranded RNA-specific adenosine deaminase isoform X3 [Homo sapiens]
gi|301601658	refseq_human (refseq_human_20140103.fasta)	double-stranded RNA-specific adenosine deaminase isoform d [Homo sapiens]

10	20	30	40	50	60	70	80
MAEIKEKICD	YLFNVSDSSA	LNLAKNIGLT	KARDINAVLI	DMERQGDVYR	QGTTPPIWHL	TDKKRERMQI	KRNTNSVPET
90	100	110	120	130	140	150	160
APAAIPETKR	NAEFLTCNIP	TSNASNNMVT	TEKVENGQEP	VIKLENRQEA	RPEPARLKPP	VHYNGPSKAG	YVDFENGQWA
170	180	190	200	210	220	230	240
TDDIPDDLNS	IRAAPGEFRA	IMEMPSFYSH	GLPRCSPYKK	LTECQLKNPI	SGLLEYAQFA	SQTCEFNMIE	QSGPPHEPRF
250	260	270	280	290	300	310	320
KFQVVINGRE	FPPAEAGSKK	VAKQDAAMKA	MTILLEEAKA	KDSGKSEESS	HYSTEKESEK	TAESQTPTPS	ATSFFSGKSP
330	340	350	360	370	380	390	400
VTTLLECMHK	LGNSCEFRLL	SKEGPAHEPK	FQYCVAVGAQ	TFPSVSAPSK	KVAKQMAAEE	AMKALHGEAT	NSMASDNQPE
410	420	430	440	450	460	470	480
GMISESLDNL	ESMMPNKVRK	IGELVRYLNT	NPVGGLLEYA	RSHGFAAEFK	LVDQSGPPHE	PKFVYQAKVG	GRWFPAVCAH
490	500	510	520	530	540	550	560
SKKQGKQEAA	DAALRVLIGE	NEKAERMGFT	EVTPVTGASL	RRTMLLLSRS	PEAQPKTLPL	TGSTFHDQIA	MLSHRCFNTL
570	580	590	600	610	620	630	640
TNSFQPSLLG	RKILAAIIMK	KDSEDMGVVV	SLGTGNRCVK	GDSLSLKGET	VNDCHAEIIS	RRGFIRFLYS	ELMKYNSQTA
650	660	670	680	690	700	710	720
KDSIFEPAKG	GEKLQIKKTV	SFHLYISTAP	CGDGALFDKS	CSDRAMESTE	SRHYPVFENP	KQGKLRTKVE	NGEGTIPVES
730	740	750	760	770	780	790	800
SDIVPTWDGI	RLGERLRTMS	CSDKILRWNV	LGLQGALLTH	FLQPIYLKSV	TLGYLFSQGH	LTRAICCRVT	RDGSAFEDGL
810	820	830	840	850	860	870	880
RHPFIVNHPK	VGRVSIYDSK	RQSGKTKETS	VNWCLADGYD	LEILDGTRGT	VDGPRNELSR	VSKKNIFLLF	KKLCSFRYRR
890	900	910	920	930	940		
DLLRLSYGEA	KKAARDYETA	KNYFKKGLKD	MGYGNWISKP	QEEKNFYLCP	V		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1852	1	899.4901	43.18	2	51.8	11.9	0	556-571	R.CFNTLTNSFQPSLLGR.K	

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Detailed Protein Report

Protein 1317: PREDICTED: zinc finger protein 621 isoform X2 [Homo sapiens]

Accession: gi|530372341
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 11.9
MW [kDa]: 45.1
pI: 10.4
Sequence Coverage [%]: 5.9
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MKPGDIRHAP	NNLASVAFPF	PKPALISHLE	RGEAPWGPDP	WDTEILRGIS	QGGESWIKNE	GLVIKQEASE	ETELHRMPVG
90	100	110	120	130	140	150	160
GLLRNVSQHF	DFKRKALKQT	FNLNPNLILR	GGMKFYECKE	CGKIFRYNSK	LIRHQMSHTG	EKPFKCKECG	KAFKSSYDCI
170	180	190	200	210	220	230	240
VHEKNHIGEG	PYECKECGKG	LSSNTALTQH	QRIHTGEKPY	ECKECGKAFR	RSAAYLQHQR	LHTGEKLYKC	KECWKAFGCR
250	260	270	280	290	300	310	320
SLFIVHQRIH	TGEKPYQCKE	CGKAFTQKIA	SIQHQRVHTG	EKPYECKVCG	KAFKWYGSFV	QHQKLHPVEK	KPVKVLGPSL
330	340	350	360	370	380	390	400
VSPQCSSPAI	PPVLLQGSCS	ASAVAVPSLT	FPHAVLIPTS	GNFFMLLPTS	GIPSSSAQIV	RVFQGLTPTV	KPSPVILTPS
410							
SHSS							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1346	1	956.6771	-101.46	3	45.4	11.9	2	152-175	K.AFKSSYDCIVHEKNHIGEGPYECK.E	Carbamidomethyl: 8, 23

Detailed Protein Report

Protein 1318: PREDICTED: zinc finger protein 749 isoform X2 [Homo sapiens]

Accession:	gi|578834454	**Score:**	11.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	80.6
Database Date:	2015-11-30	**pI:**	10.2
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	2.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MCSSILKDIL	HLAEHDGTHP	EQGLYTCAAE	HDLHQKEQIR	EKLTRSDEWR	PSFVNHSAHV	GERNFTCTQG	GKDFTASSDL
90	100	110	120	130	140	150	160
LQQQVLNSGW	KLYRDTQDGE	AFQGEQNDFN	SSQGGKDFCH	QHGLFEHQKT	HNGERPYEFS	ECGELFRYNS	NLIKYQQNHA
170	180	190	200	210	220	230	240
GERPYEGTEY	GKTFIRKSNL	VQHQKIHSEG	FLSKRSDPIE	HQEILSRPTP	YECTQCGKAF	LTQAHLVGHQ	KTHTGEQPYE
250	260	270	280	290	300	310	320
CNKCGKFFMY	NSKLIRHQKV	HTGERRYECS	ECGKLFMDSF	TLGRHQRVHT	GERPFECSIC	GKFFSHRSTL	NMHQRVHAGK
330	340	350	360	370	380	390	400
RLYKCSECGK	AFSLKHNVVQ	HLKIHTGERP	YECTECEKAF	VRKSHLVQHQ	KIHTDAFSKR	SDLIQHKRID	IRPRPYTCSE
410	420	430	440	450	460	470	480
CGKAFLTQAH	LVGHQKIHTG	ERPYECTQCA	KAFVRKSHLV	QHEKIHTDAF	SKRSDLIQHK	RIDLRPRPYV	CSECGKAFLT
490	500	510	520	530	540	550	560
QAHLDGHQKI	QTGERRYECN	ECGKFFLDSY	KLVIHQRIHT	GEKPYKCSKC	GKFFRYRCTL	SRHQKVHTGE	RPYECSECGK
570	580	590	600	610	620	630	640
FFRDSYKLII	HQRVHTGEKP	YECSNCGKFL	RYRSTFIKHH	KVCTGEKPHE	CSKCRELFRT	KSSLIIHQQS	HTGESPFKLR
650	660	670	680	690	700		
ECGKDFNKCN	TGQRQKTHTG	ERSYECGESS	KVFKYNSSLI	KHQIIHTGKR	P		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1936	1	1079.8471	-109.85	2	52.9	11.9	1	267-284	R.YECSECGKLFMDSFTLGR.H	Carbamidomethyl: 3; Oxidation: 11

Detailed Protein Report

Protein 1319: PREDICTED: ATP-binding cassette sub-family A member 1 isoform X8 [Homo sapiens]

Accession:	gi|530390682	**Score:**	11.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	186.5
Database Date:	2015-11-30	**pI:**	6.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MACWPQLRLL	LWKNLTFRRR	QTCQLLLEVA	WPLFIFLILI	SVRLSYPPYE	QHECHFPNKA	MPSAGTLPWV	QGIICNANNP
90	100	110	120	130	140	150	160
CFRYPTPGEA	PGVVGNFNKS	IVARLFSDAR	RLLLYSQKDT	SMKDMRKVLR	TLQQIKKSSS	NLKLQDFLVD	NETFSGFLYH
170	180	190	200	210	220	230	240
NLSLPKSTVD	KMLRADVILH	KVFLQGYQLH	LTSLCNGSKS	EEMIQLGDQE	VSELCGLPRE	KLAAAERVLR	SNMDILKPIL
250	260	270	280	290	300	310	320
RTLNSTSPFP	SKELAEATKT	LLHSLGTLAQ	ELFSMRSWSD	MRQEVMFLTN	VNSSSSSTQI	YQAVSRIVCG	HPEGGGLKIK
330	340	350	360	370	380	390	400
SLNWYEDNNY	KALFGGNGTE	EDAETFYDNS	TTPYCNDLMK	NLESSPLSRI	IWKALKPLLV	GKILYTPDTP	ATRQVMAEVN
410	420	430	440	450	460	470	480
KTFQELAVFH	DLEGMWEELS	PKIWTFMENS	QEMDLVRMLL	DSRDNDHFWE	QQLDGLDWTA	QDIVAFLAKH	PEDVQSSNGS
490	500	510	520	530	540	550	560
VYTWREAFNE	TNQAIRTISR	FMECVNLNKL	EPIATEVWLI	NKSMELLDER	KFWAGIVFTG	ITPGSIELPH	HVKYKIRMDI
570	580	590	600	610	620	630	640
DNVERTNKIK	DGYWDPGPRA	DPFEDMRYVW	GGFAYLQDVV	EQAIIRVLTG	TEKKTGVYMQ	QMPYPCYVDD	IFLRVMSRSM
650	660	670	680	690	700	710	720
PLFMTLAWIY	SVAVIIKGIV	YEKEARLKET	MRIMGLDNSI	LWFSWFISSL	IPLLVSAGLL	VVILKLGNLL	PYSDPSVVFV
730	740	750	760	770	780	790	800
FLSVFAVVTI	LQCFLISTLF	SRANLAAACG	GIIYFTLYLP	YVLCVAWQDY	VGFTLKIFAS	LLSPVAFGFG	CEYFALFEEQ
810	820	830	840	850	860	870	880
GIGVQWDNLF	ESPVEEDGFN	LTTSVSMMLF	DTFLYGVMTW	YIEAVFPGQY	GIPRPWYFPC	TKSYWFGEES	DEKSHPGSNQ
890	900	910	920	930	940	950	960
KRISEICMEE	EPTHLKLGVS	IQNLVKVYRD	GMKVAVDGLA	LNFYEGQITS	FLGHNGAGKT	TTMSILTGLF	PPTSGTAYIL
970	980	990	1000	1010	1020	1030	1040
GKDIRSEMST	IRQNLGVCPQ	HNVLFDMLTV	EEHIWFYARL	KGLSEKHVKA	EMEQMALDVG	LPSSKLKSKT	SQLSGGMQRK
1050	1060	1070	1080	1090	1100	1110	1120
LSVALAFVGG	SKVVILDEPT	AGVDPYSRRG	IWELLLKYRQ	GRTIILSTHH	MDEADVLGDR	IAIISHGKLC	CVGSSLFLKN
1130	1140	1150	1160	1170	1180	1190	1200
QLGTGYYLTL	VKKDVESSLS	SCRNSSSTVS	YLKKVVPELP	PAGQSGGRGG	EVQRLVALTQ	DVSAISNLIR	KHVSEARLVE
1210	1220	1230	1240	1250	1260	1270	1280
DIGHELTYVL	PYEAAKEGAF	VELFHEIDDR	LSDLGISSYG	ISETTLEEIF	LKVAEESGVD	AETSDGTLPA	RRNRRAFGDK
1290	1300	1310	1320	1330	1340	1350	1360
QSCLRPFTED	DAADPNDSDI	DPESRETDLL	SGMDGKGSYQ	VKGWKLTQQQ	FVALLWKRLL	IARRSRKGFF	AQIVLPAVFV
1370	1380	1390	1400	1410	1420	1430	1440
CIALVFSLIV	PPFGKYPSLE	LQPWMYNEQY	TFVSNDAPED	TGTLELLNAL	TKDPGFGTRC	MEGNPIPDTP	CQAGEEEWTT
1450	1460	1470	1480	1490	1500	1510	1520
APVPQTIMDL	FQNGNWTMQN	PSPACQCSSD	KIKKMLPVCP	PGAGGLPPPQ	RKQNTADILQ	DLTGRNISDY	LVKTYVQIIA
1530	1540	1550	1560	1570	1580	1590	1600
KSLKNKIWVN	EFRYGGFSLG	VSNTQALPPS	QEVNDAIKQM	KKHLKLAKDS	SADRFLNSLG	RFMTGLDTKN	NVKVWFNNKG
1610	1620	1630	1640	1650	1660		
WHAISSFLNV	INNAILRANL	QKGENPSHYG	ITAFNHPLNL	TKQQLSEVAL	GTAAETVIL		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1993	1	1051.4220	-89.87	2	53.6	11.9	1	1007-1025	K.HVKAEMEQMALDVGLPSSK.L	Oxidation: 6, 9

Detailed Protein Report

Protein 1320: beta-galactosidase-1-like protein 2 precursor [Homo sapiens]

Accession:	gi|31543093	**Score:**	11.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	72.0
Database Date:	2015-11-30	**pI:**	7.8
		Sequence Coverage [%]:	2.7
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578822458	refseq_human (refseq_human_20140103.fasta)	PREDICTED: beta-galactosidase-1-like protein 2 isoform X1 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MTTWSLRRRP ARTLGLLLLV VLGFLVLRRL DWSTLVPLRL RHRQLGLQAK GWNFMLEDST FWIFGGSIHY FRVPREYWRD
        90        100        110        120        130        140        150        160
RLLKMKACGL NTLTTYVPWN LHEPERGKFD FSGNLDLEAF VLMAAEIGLW VILRPGPYIC SEMDLGGLPS WLLQDPGMRL
       170        180        190        200        210        220        230        240
RTTYKGFTEA VDLYFDHLMS RVVPLQYKRG GPIIAVQVEN EYGSYNKDPA YMPYVKKALE DRGIVELLLT SDNKDGLSKG
       250        260        270        280        290        300        310        320
IVQGVLATIN LQSTHELQLL TTFLFNVQGT QPKMVMEYWT GWFDSWGGPH NILDSSEVLK TVSAIVDAGS SINLYMFHGG
       330        340        350        360        370        380        390        400
TNFGFMNGAM HFHDYKSDVT SYDYDAVLTE AGDYTAKYMK LRDFFGSISG IPLPPPPDLL PKMPYEPLTP VLYLSLWDAL
       410        420        430        440        450        460        470        480
KYLGEPIKSE KPINMENLPV NGGNGQSFGY ILYETSITSS GILSGHVHDR GQVFVNTVSI GFLDYKTTKI AVPLIQGYTV
       490        500        510        520        530        540        550        560
LRILVENRGR VNYGENIDDQ RKGLIGNLYL NDSPLKNFRI YSLDMKKSFF QRFGLDKWSS LPETPTLPAF FLGSLSISST
       570        580        590        600        610        620        630        640
PCDTFLKLEG WEKGVVFING QNLGRYWNIG PQKTLYLPGP WLSSGINQVI VFEETMAGPA LQFTETPHLG RNQYIK
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1578	2	948.1212	-11.41	2	48.4	11.9	1	13-29	R.TLGLLLLVVLGFLVLRR.L	

Detailed Protein Report

Protein 1321: pyroglutamyl-peptidase 1 [Homo sapiens]

Accession:	gi|8923198	**Score:**	11.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	23.1
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
MEQPRKAVVV TGFGPFGEHT VNASWIAVQE LEKLGLGDSV DLHVYEIPVE YQTVQRLIPA LWEKHSPQLV VHVGVSGMAT
         90        100        110        120        130        140        150        160
TVTLEKCGHN KGYKGLDNCR FCPGSQCCVE DGPESIDSII DMDAVCKRVT TLGLDVSVTI SQDAGRYLCD FTYYTSLYQS
        170        180        190        200        210
HGRSAFVHVP PLGKPYNADQ LGRALRAIIE EMLDLLEQSE GKINYCHKH
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
803	1	541.1573	-169.31	3	38.9	11.9	2	87-100	K.CGHNKGYKGLDNCR.F	Carbamidomethyl: 1

Detailed Protein Report

Protein 1322: regulator of G-protein signaling 16 [Homo sapiens]

Accession:	gi|156416009	**Score:**	11.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	22.7
Database Date:	2015-11-30	**pI:**	6.2
		Sequence Coverage [%]:	9.4
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MCRTLAAFPT TCLERAKEFK TRLGIFLHKS ELGCDTGSTG KFEWGSKHSK ENRNFSEDVL GWRESFDLLL SSKNGVAAFH
        90        100        110        120        130        140        150        160
AFLKTEFSEE NLEFWLACEE FKKIRSATKL ASRAHQIFEE FICSEAPKEV NIDHETHELT RMNLQTATAT CFDAAQGKTR
       170        180        190        200        210
TLMEKDSYPR FLKSPAYRDL AAQASAASAT LSSCSLDEPS HT
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
435	1	1014.5179	31.94	2	34.1	11.9	1	142-160	R.MNLQTATATCFDAAQGKTR.T	

Detailed Protein Report

Protein 1323: interferon-induced transmembrane protein 10 [Homo sapiens]

Accession:	gi|334848153	**Score:**	11.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	24.6
Database Date:	2015-11-30	**pI:**	7.5
		Sequence Coverage [%]:	5.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MREGKRGPPC	ILSFRGTLER	VEAQWELEAQ	GPGQCPAPLG	DPASTTDGAQ	EARVPLDGAF	WIPRPPAGSP	KGCFACVSKP
90	100	110	120	130	140	150	160
PALQAPAAPA	PEPSASPPMA	PTLFPMESKS	SKTDSVRAAG	APPACKHLAE	KKTMTNPTTV	IEVYPDTTEV	NDYYLWSIFN
170	180	190	200	210	220	230	
FVYLNFCCLG	FIALAYSLKV	RDKKLLNDLN	GAVEDAKTAR	LFNITSSALA	ASCIILVFIF	LRYPLTDY	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1913	1	686.2353	-180.69	2	52.4	11.9	0	185-197	K.LLNDLNGAVEDAK.T	

Detailed Protein Report

Protein 1324: armadillo repeat-containing protein 7 [Homo sapiens]

Accession:	gi|13375770	**Score:**	11.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	21.9
Database Date:	2015-11-30	**pI:**	5.7
		Sequence Coverage [%]:	10.1
		No. of unique Peptides:	1

```
         10         20         30         40         50         60         70         80
MAQKPKVDPH VGRLGYLQAL VTEFQETQSQ DAKEQVLANL ANFAYDPSNY EYLRQLQVLD LFLDSLSEEN ETLVEFAIGG
         90        100        110        120        130        140        150        160
LCNLCPDRAN KEHILHAGGV PLIINCLSSP NEETVLSAIT TLMHLSPPGR SFLPELTATP VVQCMLRFSL SASARLRNLA
        170        180        190        200
QIFLEDFCSP RQVAEARSRQ AHSALGIPLP RSVAPRQR
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1187	1	757.1449	125.66	3	43.4	11.9	0	14-33	R.LGYLQALVTEFQETQSQDAK.E	

Detailed Protein Report

Protein 1325: 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 1326: C4b-binding protein alpha chain precursor [Homo sapiens]

Accession:	gi|4502503	**Score:**	11.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	67.0
Database Date:	2015-11-30	**pI:**	7.9
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.2
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|530366456	refseq_human (refseq_human_20140103.fasta)	PREDICTED: C4b-binding protein alpha chain isoform X2 [Homo sapiens]
gi|530366454	refseq_human (refseq_human_20140103.fasta)	PREDICTED: C4b-binding protein alpha chain isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MHPPKTPSGA	LHRKRKMAAW	PFSRLWKVSD	PILFQMTLIA	ALLPAVLGNC	GPPPTLSFAA	PMDITLTETR	FKTGTTLKYT
90	100	110	120	130	140	150	160
CLPGYVRSHS	TQTLTCNSDG	EWVYNTFCIY	KRCRHPGELR	NGQVEIKTDL	SFGSQIEFSC	SEGFFLIGST	TSRCEVQDRG
170	180	190	200	210	220	230	240
VGWSHPLPQC	EIVKCKPPPD	IRNGRHSGEE	NFYAYGFSVT	YSCDPRFSLL	GHASISCTVE	NETIGVWRPS	PPTCEKITCR
250	260	270	280	290	300	310	320
KPDVSHGEMV	SGFGPIYNYK	DTIVFKCQKG	FVLRGSSVIH	CDADSKWNPS	PPACEPNSCI	NLPDIPHASW	ETYPRPTKED
330	340	350	360	370	380	390	400
VYVVGTVLRY	RCHPGYKPTT	DEPTTVICQK	NLRWTPYQGC	EALCCPEPKL	NNGEITQHRK	SRPANHCVYF	YGDEISFSCH
410	420	430	440	450	460	470	480
ETSRFSAICQ	GDGTWSPRTP	SCGDICNFPP	KIAHGHYKQS	SSYSFFKEEI	IYECDKGYIL	VGQAKLSCSY	SHWSAPAPQC
490	500	510	520	530	540	550	560
KALCRKPELV	NGRLSVDKDQ	YVEPENVTIQ	CDSGYGVVGP	QSITCSGNRT	WYPEVPKCEW	ETPEGCEQVL	TGKRLMQCLP
570	580	590	600				
NPEDVKMALE	VYKLSLEIEQ	LELQRDSARQ	STLDKEL				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
59	1	722.7955	-113.42	2	30.0	11.9	1	1-13	-.MHPPKTPSGALHR.K	Oxidation: 1

Detailed Protein Report

Protein 1327: PREDICTED: AP-4 complex subunit mu-1 isoform X3 [Homo sapiens]

Accession:	gi|530386622	**Score:**	11.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	25.3
Database Date:	2015-11-30	**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 1328: PREDICTED: transketolase isoform X1 [Homo sapiens]

Accession:	gi|578806532	**Score:**	11.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	68.8
Database Date:	2015-11-30	**pI:**	9.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MESYHKPDQQ	KLQALKDTAN	RLRISSIQAT	TAAGSGHPTS	CCSAAEIMAV	LFFHTMRYKS	QDPRNPHNDR	FVLSKGHAAP
90	100	110	120	130	140	150	160
ILYAVWAEAG	FLAEAELLNL	RKISSDLDGH	PVPKQAFTDV	ATGSLGQGLG	AACGMAYTGK	YFDKASYRVY	CLLGDGELSE
170	180	190	200	210	220	230	240
GSVWEAMAFA	SIYKLDNLVA	ILDINRLGQS	DPAPLQHQMD	IYQKRCEAFG	WHAIIVDGHS	VEELCKAFGQ	AKHQPTAIIA
250	260	270	280	290	300	310	320
KTFKGRGITG	VEDKESWHGK	PLPKNMAEQI	IQEIYSQIQS	KKKILATPPQ	EDAPSVDIAN	IRMPSLPSYK	VGDKIATRKA
330	340	350	360	370	380	390	400
YGQALAKLGH	ASDRIIALDG	DTKNSTFSEI	FKKEHPDRFI	ECYIAEQNMV	SIAVGCATRN	RTVPFCSTFA	AFFTRAFDQI
410	420	430	440	450	460	470	480
RMAAISESNI	NLCGSHCGVS	IGEDGPSQMA	LEDLAMFRSV	PTSTVFYPSD	GVATEKAVEL	AANTKGICFI	RTSRPENAII
490	500	510	520	530	540	550	560
YNNNEDFQVG	QAKVVLKSKD	DQVTVIGAGV	TLHEALAAAE	LLKKGEEKGP	PKSSTERPLH	ARSWGSFFRS	FCSFLKSSQL
570	580	590	600	610	620	630	640
ERKHFISLNN	DSNYSHPLST	CSVWHVAKSW	GCSAHSPYPM	TLKSRPPQHG	GQISGLEPAS	WAGITQPGTS	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2369	1	840.8066	-86.15	2	58.0	11.8	0	589-603	K.SWGCSAHSPYPMTLK.S	Oxidation: 12

Detailed Protein Report

Protein 1329: **PREDICTED: connector enhancer of kinase suppressor of ras 2 isoform X2 [Homo sapiens]**

Accession:	gi|530421010	**Score:**	11.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	98.2
Database Date:	2015-11-30	**pI:**	6.4
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MALIMEPVSK	WSPSQVVDWM	KGLDDCLQQY	IKNFEREKIS	GDQLLRITHQ	ELEDLGVSRI	GHQELILEAV	DLLCALNYGL
90	100	110	120	130	140	150	160
ETENLKTLSH	KLNASAKNLQ	NFITGRRRSG	HYDGRTSRKL	PNDFLTSVVD	LIGAAKSLLA	WLDRSPFAAV	TDYSVTRNNV
170	180	190	200	210	220	230	240
IQLCLELTTI	VQQDCTVYET	ENKILHVCKT	LSGVCDHIIS	LSSDPLVSQS	AHLEVIQLAN	IKPSEGLGMY	IKSTYDGLHV
250	260	270	280	290	300	310	320
ITGTTENSPA	DRCKKIHAGD	EVIQVNHQTV	VGWQLKNLVN	ALREDPSGVI	LTLKKRPQSM	LTSAPALLKN	MRWKPLALQP
330	340	350	360	370	380	390	400
LIPRSPTSSV	ATPSSTISTP	TKRDSSALQD	LYIPPPPAEP	YIPRDEKGNL	PCEDLRGHMV	GKPVHKGSES	PNSFLDQEYR
410	420	430	440	450	460	470	480
KRFNIVEEDT	VLYCYEYEKG	RSSSQGRRES	TPTYENSLLR	YMSNEKIAQE	EYMFQRNSKK	DTGKKSKKKG	DKSNSPTHYS
490	500	510	520	530	540	550	560
LLPSLQMDAL	RQDIMGTPVP	ETTLYHTFQQ	SSLQHKSKKK	NKGPIAGKSK	RRISCKDLGR	GDCEGWLWKK	KDAKSYFSQK
570	580	590	600	610	620	630	640
WKKYWFVLKD	ASLYWYINEE	DEKAEGFISL	PEFKIDRASE	CRKKYAFKAC	HPKIKSFYFA	AEHLDDMNRW	LNRINMLTAG
650	660	670	680	690	700	710	720
YAERERIKQE	QDYWSESDKE	EADTPSTPKQ	DSPPPPYDTY	PRPPSMSCAS	PYVEAKHSRL	SSTETSQSQS	SHEEFRQEVT
730	740	750	760	770	780	790	800
GSSAVSPIRK	TASQRRSWQD	LIETPLTSSG	LHYLQTLPLE	DSVFSDSAAI	SPEHRRQSTL	PTQKCHLQDH	YGPYPLAESE
810	820	830	840	850	860	870	
RMQVLNGNGG	KPRSFTLPRD	SGFNHCCLNA	PVSACDPQDD	VQPPEVEEEE	EEEEEEGEAA	GENIGEKS	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2618	1	973.4719	-48.48	2	61.4	11.8	1	296-312	K.RPQSMLTSAPALLKNMR.W	Oxidation: 5, 16

Detailed Protein Report

Protein 1330: inactive serine protease 35 precursor [Homo sapiens]

Accession:	gi|281427284	**Score:**	11.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	47.1
Database Date:	2015-11-30	**pI:**	10.3
		Sequence Coverage [%]:	7.3
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|281427286	refseq_huma (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
1626	1	1135.9599	6.52	3	50.2	11.8	2	366-395	K.IIAVYSGHQWVDVHGVQKDYNVAVRITPLK.Y	

Detailed Protein Report

Protein 1331: leucine-rich repeat-containing protein 24 precursor [Homo sapiens]

Accession:	gi|229089140	**Score:**	11.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	55.2
Database Date:	2015-11-30	**pI:**	10.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.3
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MALRAPALLP LLLLLLPLRA AGCPAACRCY SATVECGALR LRVVPLGIPP GTQTLFLQDN NIARLEPGAL APLAALRRLY
        90        100        110        120        130        140        150        160
LHNNSLRALE AGAFRAQPRL LELALTSNRL RGLRSGAFVG LAQLRVLYLA GNQLARLLDF TFLHLPRLQE LHLQENSIEL
       170        180        190        200        210        220        230        240
LEDQALAGLS SLALLDLSRN QLGTISREAL QPLASLQVLR LTENPWRCDC ALHWLGAWIK EGGQRLLTSR DRKIMCAEPP
       250        260        270        280        290        300        310        320
RLALQSLLDV SHSSLICIPP SVHVQPLELT ANLGEDLRVA CQASGYPQPL VTWRKVPQPR EGRPRAQAQL EGGLLGLGGH
       330        340        350        360        370        380        390        400
SASDTGSGML FLSNITLAHA GKYECEASNA GGAARVPFRL LVNASRQQPQ QPAQPPPPAA RPAGSEPRPE AGSMAFRALG
       410        420        430        440        450        460        470        480
VATQTAIAAA IALLALTALL LVAMICRRRR RRKKARGPPG EGALFVNDYL DGPCTFAQLE ELRDERGHEM FVINRSKPLF
       490        500        510        520
AEGPAEAPAD CGPEQGAGPG LRVPPPVAYE IHC
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2253	1	927.9306	-0.70	2	56.6	11.8	1	343-359	K.YECEASNAGGAARVPFR.L	Carbamidomethyl: 3

Detailed Protein Report

Protein 1332: dehydrogenase/reductase SDR family member 2, mitochondrial isoform 1 [Homo sapiens]

Accession:	gi|33667109	**Score:**	11.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	31.5
Database Date:	2015-11-30	**pI:**	11.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	4.7
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	2.01	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	2.67	**CV:**	0.00 %	**No. of Peptides:**	1

10	20	30	40	50	60	70	80
MLSAVARGYQ	GWFHPCARLS	VRMSSTGIDR	KGVLANRVAV	VTGSTSGIGF	AIARRLARDG	AHVVISSRKQ	QNVDRAMAKL
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
QGEGLSVAGI	VCHVGKAEDR	EQLVAKALEH	CGGVDFLVCS	AGVNPLVGST	LGTSEQIWDK	ILSVNVKSPA	LLLSQLLPYM
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
ENRRGAVILV	SSIAAYNPVV	ALGVYNVSKT	ALLGLTRTLA	LELAPKDIRV	NCVVPGIIKT	DFSKVVRIGF	MGMSLSGRTS
250	**260**	**270**	**280**	**290**	**300**	**310**	
RNIISCRGLG	SQRTVQESCP	SCALQMPATS	TGRTLRWQAT	PLGSERSGGG	CVAVVPGPGA		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
767	1	766.4829	145.43	2	38.1	11.8	1	228-241	R.IGFMGMSLSGRTSR.N	Oxidation: 4, 6	Wdown:Qdown 2.67 mdown:qdown 2.01

Detailed Protein Report

Protein 1333: potassium voltage-gated channel subfamily H member 4 [Homo sapiens]

Accession:	gi|6912446	**Score:**	11.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	111.6
Database Date:	2015-11-30	**pI:**	9.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPVMKGLLAP	QNTFLDTIAT	RFDGTHSNFL	LANAQGTRGF	PIVYCSDGFC	ELTGYGRTEV	MQKTCSCRFL	YGPETSEPAL
90	100	110	120	130	140	150	160
QRLHKALEGH	QEHRAEICFY	RKDGSAFWCL	LDMMPIKNEM	GEVVLFLFSF	KDITQSGSPG	LGPQGGRGDS	NHENSLGRRG
170	180	190	200	210	220	230	240
ATWKFRSARR	RSRTVLHRLT	GHFGRRGQGG	MKANNNVFEP	KPSVPEYKVA	SVGGSRCLLL	HYSVSKAIWD	GLILLATFYV
250	260	270	280	290	300	310	320
AVTVPYNVCF	SGDDDTPITS	RHTLVSDIAV	EMLFILDIIL	NFRTTYVSQS	GQVISAPRSI	GLHYLATWFF	IDLIAALPFD
330	340	350	360	370	380	390	400
LLYIFNITVT	SLVHLLKTVR	LLRLLRLLQK	LERYSQCSAV	VLTLLMSVFA	LLAHWMACIW	YVIGRREMEA	NDPLLWDIGW
410	420	430	440	450	460	470	480
LHELGKRLEV	PYVNGSVGGP	SRRSAYIAAL	YFTLSSLTSV	GFGNVCANTD	AEKIFSICTM	LIGALMHAVV	FGNVTAIIQR
490	500	510	520	530	540	550	560
MYSRRSLYHS	RMKDLKDFIR	VHRLPRPLKQ	RMLEYFQTTW	AVNSGIDANE	LLRDFPDELR	ADIAMHLNRE	ILQLPLFGAA
570	580	590	600	610	620	630	640
SRGCLRALSL	HIKTSFCAPG	EYLLRRGDAL	QAHYYVCSGS	LEVLRDNMVL	AILGKGDLIG	ADIPEPGQEP	GLGADPNFVL
650	660	670	680	690	700	710	720
KTSADVKALT	YCGLQQLSSR	GLAEVLRLYP	EYGAAFRAGL	PRDLTFNLRQ	GSDTSGLSRF	SRSPRLSQPR	SESLGSSSDK
730	740	750	760	770	780	790	800
TLPSITEAES	GAEPGGGPRP	RRPLLLPNLS	PARPRGSLVS	LLGEELPPFS	ALVSSPSLSP	SLSPALAGQG	HSASPHGPPR
810	820	830	840	850	860	870	880
CSAAWKPPQL	LIPPLGTFGP	PDLSPRIVDG	IEDSGSTAEA	PSFRFSRRPE	LPRPRSQAPP	TGTRPSPELA	SEAEEVKEKV
890	900	910	920	930	940	950	960
CRLNQEISRL	NQEVSQLSRE	LRHIMGLLQA	RLGPPGHPAG	SAWTPDPPCP	QLRPPCLSPC	ASRPPPSLQD	TTLAEVHCPA
970	980	990	1000	1010	1020		
SVGTMETGTA	LLDLRPSILP	PYPSEPDPLG	PSPVPEASPP	TPSLLRHSFQ	SRSDTFH		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2599	1	610.2335	-156.17	2	61.2	11.8	0	217-226	R.CLLLHYSVSK.A	Carbamidomethyl: 1

Detailed Protein Report

Protein 1334: 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 1335: PREDICTED: BTB/POZ domain-containing protein 16 isoform X2 [Homo sapiens]

Accession:	gi|530392993	**Score:**	11.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	50.8
Database Date:	2015-11-30	**pI:**	9.9
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MIMSNTHKAR	LERRVTGSTN	RWRLPKQPFS	GDLLSLSQMC	KALSIDFEEA	LRNPDRLCIS	QIQKFFFENF	KNKDIQSGEA
90	100	110	120	130	140	150	160
DVILECLGFK	WELHQPQLFQ	SETLAKLYLK	ALAQGTTHPL	RELEELLRAQ	SPKKTKEKSP	AKRIIISLKI	NDPLVTKVAF
170	180	190	200	210	220	230	240
ATALKNLYMS	EVEINLEDLL	GVLASAHILQ	FSGLFQRLFT	FSEFHLLKTM	LLWVFLQLNY	KIQAIPTYET	VMTFFKSFPE
250	260	270	280	290	300	310	320
NCCFLDRDIG	RSLRPLFLCL	RLHGITKGKD	LEVLRHLNFF	PESWLDQVTV	NHYHALENGG	DMVHLKDLNT	QAVRFGLLFN
330	340	350	360	370	380	390	400
QENTTYSKTI	ALYGFFFKIK	GLKHDTTSYS	FYMQRIKHTD	LESPSAVYEH	NHVSLRAARL	VKYEIRAEAL	VDGKWQEFRT
410	420	430	440				
NQIKQKFGLT	TSSCKSHTLK	IQTVGIPIYV	SFAFIFPAS				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2605	1	835.2606	-166.64	2	60.8	11.8	0	27-41	K.QPFSGDLLSLSQMCK.A	Oxidation: 13

Detailed Protein Report

Protein 1336: 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 1337: ovochymase-2 precursor [Homo sapiens]

Accession:	gi|373838920	**Score:**	11.8
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
1469	1	850.5817	148.95	2	48.2	11.8	0	290-303	K.VLPWIHEHIQTGNR.R	

Detailed Protein Report

Protein 1338: 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

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
1525	1	648.1346	-228.79	2	48.9	11.8	0	457-466	R.SFCHPEPHER.D	Carbamidomethyl: 3

Protein 1339: 60S ribosomal protein L35 [Homo sapiens]

Accession:	gi|6005860	**Score:**	11.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	14.5
Database Date:	2015-11-30	**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	

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Detailed Protein Report

Protein 1340: PREDICTED: phospholipase D2 isoform X1 [Homo sapiens]

Accession:	gi|530410430	**Score:**	11.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	76.6
Database Date:	2015-11-30	**pI:**	9.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MTATPESLFP	TGDELDSSQL	QMESDEVDTL	KEGEDPADRM	HPFLAIYELQ	SLKVHPLVFA	PGVPVTAQVV	GTERYTSGSK
90	100	110	120	130	140	150	160
VGTCTLYSVR	LTHGDFSWTT	KKKYRHFQEL	HRDLLRHKVL	MSLLPLARFA	VAYSPARDAG	NREMPSLPRA	GPEGSTRHAA
170	180	190	200	210	220	230	240
SKQKYLENYL	NRLLTMSFYR	NYHAMTEFLE	VSQLSFIPDL	GRKGLEGMIR	KRSGGHRVPG	LTCCGRDQVC	YRWSKRWLVV
250	260	270	280	290	300	310	320
KDSFLLYMCL	ETGAISFVQL	FDPGFEVQVG	KRSTEARHGV	RIDTSHRSLI	LKCSSYRQAR	WWAQEITELA	QGPGRDFLQL
330	340	350	360	370	380	390	400
HRHDSYAPPR	PGTLARWFVN	GAGYFAAVAD	AILRAQEEIF	ITDWWLSPEV	YLKRPAHSDD	WRLDIMLKRK	AEEGVRVSIL
410	420	430	440	450	460	470	480
LFKEVELALG	INSGYSKRAL	MLLHPNIKVM	RHPDQVTLWA	HHEKLLVVDQ	VVAFLGGLDL	AYGRWDDLHY	RLTDLGDSSE
490	500	510	520	530	540	550	560
SAASQPPTPR	PDSPATPDLS	HNQFFWLGKD	YSNLITKDWV	QLDRPFEDFI	DRETTPRMPW	RDVGVVVHGL	PARDLARHFI
570	580	590	600	610	620	630	640
QRWNFTKTTK	AKYKTPTYPY	LLPKSTSTAN	QLPFTLPGGQ	CTTVQVLRSV	DRWSAGTLEN	SILNAYLHTI	RESQHFLYIE
650	660	670	680				
NQFFISCSDG	RTVLNKVGDE	IVDRILKAHK					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2983	1	863.9596	75.03	2	66.1	11.8	1	218-232	R.VPGLTCCGRDQVCYR.W	Carbamidomethyl: 13

Detailed Protein Report

Protein 1341: 39S ribosomal protein L52, mitochondrial isoform e [Homo sapiens]

Accession:	gi|31083085	**Score:**	11.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	9.1
Database Date:	2015-11-30	**pI:**	9.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	17.2
		No. of unique Peptides:	1

```
         10         20         30         40         50         60         70         80
MAALGTVLFT GVRRLHCSVA AWAGGQWRLQ QGLAANPSGY GPLTELPDWS YAETSCTAVT GNGRWITSMA AQAAEVAGRT
         90
KEAGKCS
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2730	1	877.9630	30.30	2	63.1	11.8	1	14-28	R.RLHCSVAAWAGGQWR.L	Carbamidomethyl: 4

Detailed Protein Report

Protein 1342: signal-regulatory protein beta-2 isoform 1 precursor [Homo sapiens]

Accession:	gi|171906611	**Score:**	11.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	36.9
Database Date:	2015-11-30	**pI:**	5.4
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	3.8
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	1.08	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	1.76	**CV:**	0.00 %	**No. of Peptides:**	1

```
        10         20         30         40         50         60         70         80
MCSTMSAPTC LAHLPPCFLL LALVLVPSDA SGQSSRNDWQ VLQPEGPMLV AEGETLLLRC MVVGSCTDGM IKWVKVSTQD
        90        100        110        120        130        140        150        160
QQEIYNFKRG SFPGVMPMIQ RTSEPLNCDY SIYIHNVTRE HTGTYHCVRF DGLSEHSEMK SDEGTSVLVK GAGDPEPDLW
       170        180        190        200        210        220        230        240
IIQPQELVLG TTGDTVFLNC TVLGDGPPGP IRWFQGAGLS REAIYNFGGI SHPKETAVQA SNNDFSILLQ NVSSEDAGTY
       250        260        270        280        290        300        310        320
YCVKFQRKPN RQYLSGQGTS LKVKAKSTSS KEAEFTSEPA TEMSPTGLLV VFAPVVLGLK AITLAALLLA LATSRRSPGQ
       330        340        350
EDVKTTGPAG AMNTLAWSKG QE
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
555	1	708.8400	52.03	2	35.5	11.8	0	60-72	R.CMVVGSCTDGMIK.W	Carbamidomethyl: 7; Oxidation: 2	mdown:qdown 1.08 Wdown:Qdown 1.76

Detailed Protein Report

Protein 1343: PREDICTED: rho guanine nucleotide exchange factor 16 isoform X1 [Homo sapiens]

Accession:	gi|530360293	**Score:**	11.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	47.2
Database Date:	2015-11-30	**pI:**	7.9
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	4.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MFASDLLRAL	DCCPGAGSSG	LLPQLGPRQL	LAFTVNCLGN	HRYLGFFEDL	EQRHKAQVLV	EDISDILEEH	AEKHFHPYIA
90	100	110	120	130	140	150	160
YCSNEVYQQR	TLQKLISSNA	AFREALREIE	RRPACGGLPM	LSFLILPMQR	VTRLPLLMDT	LCLKTQGHSE	RYKAASRALK
170	180	190	200	210	220	230	240
AISKLVRQCN	EGAHRMERME	QMYTLHTQLD	FSKVKSLPLI	SASRWLLKRG	ELFLVEETGL	FRKIASRPTC	YLFLFNDVLV
250	260	270	280	290	300	310	320
VTKKKSEESY	MVQDYAQMNH	IQVEKIEPSE	LPLPGGGNRS	SSVPHPFQVT	LLRNSEGRQE	QLLLSSDSAS	DRARWIVALT
330	340	350	360	370	380	390	400
HSERQWQGLS	SKGDLPQVEI	TKAFFAKQAD	EVTLQQADVV	LVLQQEDGWL	YGERLRDGET	GWFPEDFARF	ITSRVAVEGN
410	420						
VRRMERLRVE	TDV						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2873	1	1087.0534	-20.59	2	64.6	11.8	0	112-130	R.RPACGGLPMLSFLILPMQR.V	Carbamidomethyl: 4; Oxidation: 9

Detailed Protein Report

Protein 1344: striatin-interacting protein 1 isoform 2 [Homo sapiens]

Accession: gi|399154157
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 11.8
MW [kDa]: 85.4
pI: 6.3
Sequence Coverage [%]: 1.5
No. of unique Peptides: 1

Quantitation

mdown:qdown **Median:** 0.87 **CV:** 0.00 % **No. of Peptides:** 1
Wdown:Qdown **Median:** 0.18 **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	Wdown:Qdown 0.18 mdown:qdown 0.87

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Detailed Protein Report

Protein 1345: PREDICTED: collagen alpha-1(III) chain-like [Homo sapiens]

Accession:	gi|530361513	**Score:**	11.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	26.3
Database Date:	2015-11-30	**pI:**	12.5
		Sequence Coverage [%]:	7.2
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	0.77	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.13	**CV:**	0.00 %	**No. of Peptides:**	1

10	20	30	40	50	60	70	80
MIPAVSSAER	PGPVFVFSPP	PTPPRGGPGT	GGLEGARQQP	GRREPESERG	PSPAPCLPSP	AAAWVEAAAR	QRAGEQAVGR
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
TERLERPTLL	RVPLTPTRGS	ALPFYPAPSR	PPGKPGVESG	AGAGRGTDSL	PSLHKGGGER	TSRGGGRPSA	AFARQRRRRR
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
LRRKPGPEPA	HLWSLRRLPP	GVPIQVCPLP	AVPRGAGSVN	FTRGCKIGQS	LRPRPPRPSP	DPLAAGPVRW	LLLSTSTALF
250							
VFKAFYGPR							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
953	2	637.0944	77.56	3	41.4	11.8	1	177-194	R.RLPPGVPIQVCPLPAVPR.G		mdown:qdown 0.77 Wdown:Qdown 0.13

Detailed Protein Report

Protein 1346: **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 1347: 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 1348: protein Tob2 [Homo sapiens]

Accession:	gi|7706739	**Score:**	11.7
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
2339	1	841.6560	-116.68	3	57.7	11.7	2	191-218	K.MKKGGGAASGGGVASSGAGGQQPPQQPR.M	

Protein 1349: PREDICTED: ephrin type-B receptor 2 isoform X2 [Homo sapiens]

Accession:	gi|578798608	**Score:**	11.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	106.7
Database Date:	2015-11-30	**pI:**	5.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MALRRLGAAL	LLLPLLAAVE	ETLMDSTTAT	AELGWMVHPP	SGWEEVSGYD	ENMNTIRTYQ	VCNVFESSQN	NWLRTKFIRR
90	100	110	120	130	140	150	160
RGAHRIHVEM	KFSVRDCSSI	PSVPGSCKET	FNLYYYEADF	DSATKTFPNW	MENPWVKVDT	IAADESFSQV	DLGGRVMKIN
170	180	190	200	210	220	230	240
TEVRSFGPVS	RSGFYLAFQD	YGGCMSLIAV	RVFYRKCPRI	IQNGAIFQET	LSGAESTSLV	AARGSCIANA	EEVDVPIKLY
250	260	270	280	290	300	310	320
CNGDGEWLVP	IGRCMCKAGF	EAVENGTVCR	GCPSGTFKAN	QGDEACTHCP	INSRTTSEGA	TNCVCRNGYY	RADLDPLDMP
330	340	350	360	370	380	390	400
CTTIPSAPQA	VISSVNETSL	MLEWTPPRDS	GGREDLVYNI	ICKSCGSGRG	ACTRCGDNVQ	YAPRQLGLTE	PRIYISDLLA
410	420	430	440	450	460	470	480
HTQYTFEIQA	VNGVTDQSPF	SPQFASVNIT	TNQAAPSAVS	IMHQVSRTVD	SITLSWSQPD	QPNGVILDYE	LQYYEKVRAR
490	500	510	520	530	540	550	560
TVAGYGRYSG	KMYFQTMTEA	EYQTSIQEKL	PLIIGSSAAG	LVFLIAVVVI	AIVCNRRRGF	ERADSEYTDK	LQHYTSGHMT
570	580	590	600	610	620	630	640
PGMKIYIDPF	TYEDPNEAVR	EFAKEIDISC	VKIEQVIGAG	EFGEVCSGHL	KLPGKREIFV	AIKTLKSGYT	EKQRRDFLSE
650	660	670	680	690	700	710	720
ASIMGQFDHP	NVIHLEGVVT	KSTPVMIITE	FMENGSLDSF	LRQNDGQFTV	IQLVGMLRGI	AAGMKYLADM	NYVHRDLAAR
730	740	750	760	770	780	790	800
NILVNSNLVC	KVSDFGLSRF	LEDDTSDPTY	TSALGGKIPI	RWTAPEAIQY	RKFTSASDVW	SYGIVMWEVM	SYGERPYWDM
810	820	830	840	850	860	870	880
TNQDVINAIE	QDYRLPPPMD	CPSALHQLML	DCWQKDRNHR	PKFGQIVNTL	DKMIRNPNSL	KAMAPLSSGI	NLPLLDRTIP
890	900	910	920	930	940	950	960
DYTSFNTVDE	WLEAIKMGQY	KESFANAGFT	SFDVVSQMMM	EDILRVGVTL	AGHQKKILNS	IQVMRAQMNQ	IQSVEV

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
927	1	625.5184	-139.00	3	40.4	11.7	1	254-270	R.CMCKAGFEAVENGTVCR.G	Carbamidomethyl: 16

Detailed Protein Report

Protein 1350: pancreatic lipase-related protein 2 precursor [Homo sapiens]

Accession:	gi|106507261	**Score:**	11.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	52.0
Database Date:	2015-11-30	**pI:**	5.2
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	2.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MMLPPWTLGL	LLLATVRGKE	VCYGQLGCFS	DEKPWAGTLQ	RPVKLLPWSP	EDIDTRFLLY	TNENPNNFQL	ITGTEPDTIE
90	100	110	120	130	140	150	160
ASNFQLDRKT	RFIIHGFLDK	AEDSWPSDMC	KKMFEVEKVN	CICVDWRHGS	RAMYTQAVQN	IRVVGAETAF	LIQALSTQLG
170	180	190	200	210	220	230	240
YSLEDVHVIG	HSLGAHTAAE	AGRRLGGRVG	RITGLDPAGP	CFQDEPEEVR	LDPSDAVFVD	VIHTDSSPIV	PSLGFGMSQK
250	260	270	280	290	300	310	320
VGHLDFFPNG	GKEMPGCKKN	VLSTITDIDG	IWEGIGGFVS	CNHLRSFEYY	SSSVLNPDGF	LGYPCASYDE	FQESKCFPCP
330	340	350	360	370	380	390	400
AEGCPKMGHY	ADQFKGKTSA	VEQTFFLNTG	ESGNFTSWRY	KVSVTLSGKE	KVNGYIRIAL	YGSNENSKQY	EIFKGSLKPD
410	420	430	440	450	460	470	480
ASHTCAIDVD	FNVGKIQKVK	FLWNKRGINL	SEPKLGASQI	TVQSGEDGTE	YNFCSSDTVE	ENVLQSLYPC	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1225	1	671.3731	171.64	2	43.8	11.7	0	101-111	K.AEDSWPSDMCK.K	Carbamidomethyl: 10; Oxidation: 9

Detailed Protein Report

Protein 1351: uncharacterized protein C8orf58 isoform 2 [Homo sapiens]

Accession:	gi|311771785	**Score:**	11.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	38.6
Database Date:	2015-11-30	**pI:**	9.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MMGRRRAFAV	DGRDGAGEGL	ARGCIVPGVT	STYRRIPDAA	HGCSSWERGD	KFRGVGREAL	FLKLASRDSG	VEMAVGDSPL
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
AALPGLSQDS	LDFESSGSSE	PPAQVGRLLA	SQKLGEVLER	SRRLPTAPTS	LSGQHRSLRL	ASKPEREVPL	GAGQQESMEA
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
DTDLEAGLEE	EAVGGLGPGA	WACLPGQGLR	YLEHLCLVLE	QMARLQQLYL	QLRIQRPPGD	PGEEESTRAP	LPSPLHTPGN
250	**260**	**270**	**280**	**290**	**300**	**310**	**320**
RGQGPWELLS	QTEHTGAKAA	SPPKVEVPSA	NPPRLPETPV	EPTYHLPSSQ	GHKVKVLLNR	ICRRSHHHPE	PPAPPDGSDP
330	**340**	**350**	**360**				
RIESRDLPER	PQCRPHRKTF	MPSLVVKKQR	AKNLSVG				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1696	1	647.5157	204.05	2	49.9	11.7	2	338-348	R.KTFMPSLVVKK.Q	Oxidation: 4

Detailed Protein Report

Protein 1352: **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 1353: membrane-spanning 4-domains subfamily A member 14 isoform 2 [Homo sapiens]

Accession:	gi|119226220	**Score:**	11.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	74.6
Database Date:	2015-11-30	**pI:**	5.2
		Sequence Coverage [%]:	1.4
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MESTSQDRRA THVITIKPNE TVLTAFPYRP HSSLLDFLKG EPRVLGATQI LLALIIVGFG TIFALNYIGF SQRLPLVVLT
        90        100        110        120        130        140        150        160
GYPFWGALIG QGVTGMNVIS SLVAITGITF TILSYRHQDK YCQMPSFEEI CVFSRTLFIV LFFLPSDVTQ NSEQPAPEEN
       170        180        190        200        210        220        230        240
DQLQFVLQEE FSSDDSTTNA QSVIFGGYAF FKLTLSRSPL VSQPGNKGRE FVPDEQKQSI LPSPKFSEEE IEPLPPTLEK
       250        260        270        280        290        300        310        320
KPSENMSIQL DSTFKQMKDE DLQSAIVQPS QMQTKLLQDQ AASLQVFPSH SALKLEDISP EDLPSQALPV EGLSEQTMPS
       330        340        350        360        370        380        390        400
KSTSSHVKQS SNLTANDLPP QGILSQDTSS QDMLFHDMTS QDMQSLDMLS QDTPSHAMPP QDIPSQDMLS QALSAHAILP
       410        420        430        440        450        460        470        480
EASTSHIVQF PEIQHLLQQP PDLQPENTEP QNQQILQMSY QDIRSEVMEE TKEWKSEEEL HRRKSSRRHS LNQQTKALQY
       490        500        510        520        530        540        550        560
LRRHSLDVQA KGQKSSKRHS LDQQSKGWQS PKQKSLDQQI KDWLSPKRHS VDKQAQLNQT KEQLPDQQAE DQQAKGEQYP
       570        580        590        600        610        620        630        640
EGQSKDGQVK DQQTDKEQNS KKQTQDQQTE DQPAQEKKSP KGQFQNVQAE GQQAQVEKVP KLLCQDSESQ IQQYQFWQFH
       650        660        670
KGNLQAGQPR TVNLLAKNPL TG
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
974	1	555.2031	-91.32	2	40.7	11.7	1	1-9	-.MESTSQDRR.A	

Detailed Protein Report

Protein 1354: zinc finger protein 26 isoform 3 [Homo sapiens]

Accession: gi|372266178

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Modification(s): Carbamidomethyl

Score: 11.7

MW [kDa]: 57.6

pI: 10.2

Sequence Coverage [%]: 3.2

No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MATSFRTASC	WGLLSFKDIS	MEFTWDEWQL	LDSTQKYLYR	DVILENYHNL	ISVDGWEEWY	QNNQDELESI	ERSYACSVLG
90	100	110	120	130	140	150	160
RLNLSKTHDS	SRQRLYNTRG	KSLTQNSAPS	RSYLRKNPDK	FHGYEEPYFL	KHQRAHSIEK	NCVCSECGKA	FRCKSQLIVH
170	180	190	200	210	220	230	240
LRIHTGERPY	ECSKCERAFS	AKSNLNAHQR	VHTGEKPYSC	SECEKVFSFR	SQLIVHQEIH	TGGKPYGCSE	CGKAYSWKSQ
250	260	270	280	290	300	310	320
LLLHQRSHTG	VKPYECSECG	KAFSLKSPFV	VHQRTHTGVK	PHKCSECGKA	FRSKSYLLVH	IRMHTGEKPY	QCSDCGKAFN
330	340	350	360	370	380	390	400
MKTQLIVHQG	VHTGNNPYQC	GECGKAFGRK	EQLTAHLRAH	AGEKPYGCSE	CGKAFSSKSY	LVIHRRTHTG	ERPYECSLCE
410	420	430	440	450	460	470	480
RAFCGKSQLI	IHQRTHSTEK	PYECNECEKA	YPRKASLQIH	QKTHSGEKPF	KCSECGKAFT	QKSSLSEHQR	VHTGEKPWKC
490	500	510					
SECGKSFCWN	SGLRIHRKTH	K					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2652	1	665.3901	129.73	3	61.9	11.7	1	386-401	R.RTHTGERPYECSLCER.A	Carbamidomethyl: 14

Detailed Protein Report

Protein 1355: metastasis-associated protein MTA2 [Homo sapiens]

Accession:	gi|14141170	**Score:**	11.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	75.0
Database Date:	2015-11-30	**pI:**	10.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAANMYRVGD	YVYFENSSSN	PYLVRRIEEL	NKTANGNVEA	KVVCLFRRRD	ISSSLNSLAD	SNAREFEEES	KQPGVSEQQR
90	100	110	120	130	140	150	160
HQLKHRELFL	SRQFESLPAT	HIRGKCSVTL	LNETDILSQY	LEKEDCFFYS	LVFDPVQKTL	LADQGEIRVG	CKYQAEIPDR
170	180	190	200	210	220	230	240
LVEGESDNRN	QQKMEMKVWD	PDNPLTDRQI	DQFLVVARAV	GTFARALDCS	SSIRQPSLHM	SAAAASRDIT	LFHAMDTLQR
250	260	270	280	290	300	310	320
NGYDLAKAMS	TLVPQGGPVL	CRDEMEEWSA	SEAMLFEEAL	EKYGKDFNDI	RQDFLPWKSL	ASIVQFYYMW	KTTDRYIQQK
330	340	350	360	370	380	390	400
RLKAAEADSK	LKQVYIPTYT	KPNPNQIISV	GSKPGMNGAG	FQKGLTCESC	HTTQSAQWYA	WGPPNMQCRL	CASCWIYWKK
410	420	430	440	450	460	470	480
YGGLKTPTQL	EGATRGTTEP	HSRGHLSRPE	AQSLSPYTTS	ANRAKLLAKN	RQTFLLQTTK	LTRLARRMCR	DLLQPRRAAR
490	500	510	520	530	540	550	560
RPYAPINANA	IKAECSIRLP	KAAKTPLKIH	PLVRLPLATI	VKDLVAQAPL	KPKTPRGTKT	PINRNQLSQN	RGLGGIMVKR
570	580	590	600	610	620	630	640
AYETMAGAGV	PFSANGRPLA	SGIRSSSQPA	AKRQKLNPAD	APNPVVFVAT	KDTRALRKAL	THLEMRRAAR	RPNLPLKVKP
650	660	670					
TLIAVRPPVP	LPAPSHPAST	NEPIVLED					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1808	1	780.2935	-154.53	2	51.1	11.7	1	139-152	K.TLLADQGEIRVGCK.Y	Carbamidomethyl: 13

Detailed Protein Report

Protein 1356: PREDICTED: methyltransferase-like protein 16 isoform X1 [Homo sapiens]

Accession:	gi|530410652	**Score:**	11.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	38.9
Database Date:	2015-11-30	**pI:**	9.3
		Sequence Coverage [%]:	2.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAEGGELEFV	KRIIHDSLQL	KKRLRWYSCM	LGKKCSLAPL	KEELRIQGVP	KVTYTEFCQG	RTMRWALAWS	FYDDVTVPSP
90	100	110	120	130	140	150	160
PSKRRKLEKP	RKPITFVVLA	SVMKELSLKA	SPLRSETAEG	IVVVTTWIEK	ILTDLKVQHK	RVPCGKEEVS	LFLTAIENSW
170	180	190	200	210	220	230	240
IHLRRKKRER	VRQLREVPRA	PEDVIQALEE	KKPTPKESGN	SQELARGPQE	RTPCGPALRE	GEAAAVEGPC	PSQESLSQEE
250	260	270	280	290	300	310	320
NPEPTEDERS	EEKGGVEVLE	SCQGSSNGAQ	DQEASEQFGS	PVAERGKRLP	GVAGQYLFKC	LINVKKEVDD	ALVEMHWVEG
330	340	350					
QNRDLMNQLC	TYIRNQIFRL	VAVN					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
866	1	859.6854	207.59	1	39.6	11.7	1	34-41	K.KCSLAPLK.E	

Detailed Protein Report

Protein 1357: **PREDICTED: arf-GAP domain and FG repeat-containing protein 2 isoform X2 [Homo sapiens]**

Accession:	gi|578814185	**Score:**	11.7
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

Quantitation

Wdown:Qdown **Median:** 1.28 **CV:** 0.00 % **No. of 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	Ratios
2691	1	973.5107	-18.13	2	62.0	11.7	1	110-126	K.IWLGLFDARTSLVPDSR.D		Wdown:Qdown 1.28

Detailed Protein Report

Protein 1358: 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

Detailed Protein Report

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

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 1359: 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 1360: PREDICTED: acyl-CoA synthetase short-chain family member 3, mitochondrial isoform X2 [Homo sapiens]

Accession:	gi|530400836	**Score:**	11.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	49.7
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
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 1361: PREDICTED: sperm-associated antigen 8 isoform X4 [Homo sapiens]

Accession:	gi|578816456	**Score:**	11.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	31.4
Database Date:	2015-11-30	**pI:**	7.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	5.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MTVPGFRNLV	ADRVPNYTSW	SQHCPWEPQK	QPPWEFLQVL	EPGARGLWKP	PDIKGKLMVC	YETLPRGQCL	LYNWEEERAT
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
NHLDQVPSMQ	DGSESFFFRH	GHRGLLTMQL	KSPMPSSTTQ	KDSYQPPGNV	YWPLRGKREA	MLEMLLQHQI	CKEVQAEQEP
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
TRKLFEVESV	THHDYRMELA	QAGTPAPTKP	HDYRQEQPET	FWIQRAPQLP	GVSNIRTLDT	PFRKNCSFST	PVPLSLGKLL
250	**260**	**270**	**280**				
PYEPENYPYQ	LGEISSLPCP	GGRLGGGGGR	MTPF				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2737	1	753.8991	19.19	2	63.2	11.7	0	225-238	K.NCSFSTPVPLSLGK.L	Carbamidomethyl: 2

Detailed Protein Report

Protein 1362: 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-4 isoform b [Homo sapiens]

Accession:	gi|289547591	**Score:**	11.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	134.4
Database Date:	2015-11-30	**pI:**	6.5
		Sequence Coverage [%]:	1.5
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|578835425	refseq_human (refseq_human_20140103.fasta)	PREDICTED: 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-4 isoform X12 [Homo sapiens]

10	20	30	40	50	60	70	80
MAKPYEFNWQ	KEVPSFLQEG	AVFDRYEEES	FVFEPNCLFK	VDEFGFFLTW	RSEGKEGQVL	ECSLINSIRS	GAIPKDPKIL
90	100	110	120	130	140	150	160
AALEAVGKSE	NDLEGRIVCV	CSGTDLVNIS	FTYMVAENPE	VTKQWVEGLR	SIIHNFRANN	VSPMTCLKKH	WMKLAFMTNT
170	180	190	200	210	220	230	240
NGKIPVRSIT	RTFASGKTEK	VIFQALKELG	LPSGKNDEIE	PTAFSYEKFY	ELTQKICPRT	DIEDLFKKIN	GDKTDYLTVD
250	260	270	280	290	300	310	320
QLVSFLNEHQ	RDPRLNEILF	PFYDAKRAMQ	IIEMYEPDED	LKKKGLISSD	GFCRYLMSDE	NAPVFLDRLE	LYQEMDHPLA
330	340	350	360	370	380	390	400
HYFISSSHNT	YLTGRQFGGK	SSVEMYRQVL	LAGCRCVELD	CWDGKGEDQE	PIITHGKAMC	TDILFKDVIQ	AIKETAFVTS
410	420	430	440	450	460	470	480
EYPVILSFEN	HCSKYQQYKM	SKYCEDLFGD	LLLKQALESH	PLEPGRALPS	PNDLKRKILI	KNKRLKPEVE	KKQLEALRSM
490	500	510	520	530	540	550	560
MEAGESASPA	NILEDDNEEE	IESADQEEEA	HPEFKFGNEL	SADDLGHKEA	VANSVKKGLV	TVEDEQAWMA	SYKYVGATTN
570	580	590	600	610	620	630	640
IHPYLSTMIN	YAQPVKFQGF	HVAEERNIHY	NMSSFNESVG	LGYLKTHAIE	FVNYNKRQMS	RIYPKGGRVD	SSNYMPQIFW
650	660	670	680	690	700	710	720
NAGCQMVSLN	YQTPDLAMQL	NQGKFEYNGS	CGYLLKPDFM	RRPDRTFDPF	SETPVDGVIA	ATCSVQVISG	QFLSDKKIGT
730	740	750	760	770	780	790	800
YVEVDMYGLP	TDTIRKEFRT	RMVMNNGLNP	VYNEESFVFR	KVILPDLAVL	RIAVYDDNNK	LIGQRILPLD	GLQAGYRHIS
810	820	830	840	850	860	870	880
LRNEGNKPLS	LPTIFCNIVL	KTYVPDGFGD	IVDALSDPKK	FLSITEKRAD	QMRAMGIETS	DIADVPSDTS	KNDKKGKANT
890	900	910	920	930	940	950	960
AKANVTPQSS	SELRPTTTAA	LASGVEAKKG	IELIPQVRIE	DLKQMKAYLK	HLKKQQKELN	SLKKKHAKEH	STMQKLHCTQ
970	980	990	1000	1010	1020	1030	1040
VDKIVAQYDK	EKSTHEKILE	KAMKKKGGSN	CLEMKKETEI	KIQTLTSDHK	SKVKEIVAQH	TKEWSEMINT	HSAEEQEIRD
1050	1060	1070	1080	1090	1100	1110	1120
LHLSQQCELL	KKLLINAHEQ	QTQQLKLSHD	RESKEMRAHQ	AKISMENSKA	ISQDKSIKNK	AERERRVREL	NSSNTKKFLE
1130	1140	1150	1160	1170	1180		
ERKRLAMKQS	KEMDQLKKVQ	LEHLEFLEKQ	NEQAKEMQQM	VKLEAEMDRR	PATVV		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1890	1	682.2697	-120.90	3	53.7	11.7	1	131-148	R.SIIHNFRANNVSPMTCLK.K	

Detailed Protein Report

Protein 1363: protein orai-3 [Homo sapiens]

Accession:	gi|22748651	**Score:**	11.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	31.5
Database Date:	2015-11-30	**pI:**	8.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	6.4
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MKGGEGDAGE QAPLNPEGES PAGSATYREF VHRGYLDLMG ASQHSLRALS WRRLYLSRAK LKASSRTSAL LSGFAMVAMV
        90        100        110        120        130        140        150        160
EVQLESDHEY PPGLLVAFSA CTTVLVAVHL FALMVSTCLL PHIEAVSNIH NLNSVHQSPH QRLHRYVELA WGFSTALGTF
       170        180        190        200        210        220        230        240
LFLAEVVLVG WVKFVPIGAP LDTPTPMVPT SRVPGTLAPV ATSLSPASNL PRSSASAAPS QAEPACPPRQ ACGGGGAHGP
       250        260        270        280        290        300
GWQAAMASTA IMVPVGLVFV AFALHFYRSL VAHKTDRYKQ ELEELNRLQG ELQAV
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1484	1	1006.5855	55.41	2	47.3	11.6	0	174-192	K.FVPIGAPLDTPTPMVPTSR.V	Oxidation: 14

Detailed Protein Report

Protein 1364: 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 1365: PREDICTED: progesterone-induced-blocking factor 1 isoform X1 [Homo sapiens]

Accession:	gi|530402040	**Score:**	11.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	52.9
Database Date:	2015-11-30	**pI:**	5.2
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSRKISKESK	KVNISSSLES	EDISLETTVP	TDDISSSEER	EGKVRITRQL	IERKELLHNI	QLLKIELSQK	TMMIDNLKVD
90	100	110	120	130	140	150	160
YLTKIEELEE	KLNDALHQKQ	LLTLRLDNQL	AFQQKDASKY	QELMKQEMET	ILLRQKQLEE	TNLQLREKAG	DVRRNLRDFE
170	180	190	200	210	220	230	240
LTEEQYIKLK	AFPEDQLSIP	EYVSVRFYEL	VNPLRKEICE	LQVKKNILAE	ELSTNKNQLK	QLTETYEEDR	KNYSEVQIRC
250	260	270	280	290	300	310	320
QRLALELADT	KQLIQQGDYR	QENYDKVKSE	RDALEQEVIE	LRRKHEILEA	SHMIQTKERS	ELSKEVVTLE	QTVTLLQKDK
330	340	350	360	370	380	390	400
EYLNRQNMEL	SVRCAHEEDR	LERLQAQLEE	SKKAREEMYE	KYVASRDHYK	TEYENKLHDE	LEQIRLKTNQ	EIDQLRNASR
410	420	430	440	450			
EMYERENRNL	REARDNAVAE	KERAVMAEKD	ALEKHDQLLD	RF			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2214	1	753.3333	-68.66	2	56.3	11.6	2	422-434	K.ERAVMAEKDALEK.H	Oxidation: 5

Detailed Protein Report

Protein 1366: neuronal pentraxin-2 precursor [Homo sapiens]

Accession:	gi|28195384	**Score:**	11.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	47.0
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
MLALLAASVA	LAVAAGAQDS	PAPGSRFVCT	ALPPEAVHAG	CPLPAMPMQG	GAQSPEEELR	AAVLQLRETV	VQQKETLGAQ
90	100	110	120	130	140	150	160
REAIRELTGK	LARCEGLAGG	KARGAGATGK	DTMGDLPRDP	GHVVEQLSRS	LQTLKDRLES	LEHQLRANVS	NAGLPGDFRE
170	180	190	200	210	220	230	240
VLQQRLGELE	RQLLRKVAEL	EDEKSLLHNE	TSAHRQKTES	TLNALLQRVT	ELERGNSAFK	SPDAFKVSLP	LRTNYLYGKI
250	260	270	280	290	300	310	320
KKTLPELYAF	TICLWLRSSA	SPGIGTPFSY	AVPGQANEIV	LIEWGNNPIE	LLINDKVAQL	PLFVSDGKWH	HICVTWTTRD
330	340	350	360	370	380	390	400
GMWEAFQDGE	KLGTGENLAP	WHPIKPGGVL	ILGQEQDTVG	GRFDATQAFV	GELSQFNIWD	RVLRAQEIVN	IANCSTNMPG
410	420	430	440				
NIIPWVDNNV	DVFGGASKWP	VETCEERLLD	L				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1754	1	785.8976	-58.56	2	50.6	11.6	2	172-184	R.QLLRKVAELEDEK.S	

Detailed Protein Report

Protein 1367: 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 1368: nuclear receptor coactivator 7 isoform 3 [Homo sapiens]

Accession:	gi|313850978	**Score:**	11.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	92.4
Database Date:	2015-11-30	**pI:**	4.9
		Sequence Coverage [%]:	1.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MVVQKPHGTM	EYTAGNQDTL	NSIALKFNIT	PNKLVELNKL	FTHTIVPGQV	LFVPDANSPS	STLRLSSSSP	GATVSPSSSD
90	100	110	120	130	140	150	160
AEYDKLPDAD	LARKALKPIE	RVLSSTSEED	EPGVVKFLKM	NCRYFTDGKG	VVGGVMIVTP	NNIMFDPHKS	DPLVIENGCE
170	180	190	200	210	220	230	240
EYGLICPMEE	VVSIALYNDI	SHMKIKDALP	SPGEWEDLAS	EKDINPFSKF	KSINKEKRQQ	NGEKIMTSDS	RPIVPLEKST
250	260	270	280	290	300	310	320
GHTPTKPSGS	SVSEKLKKLD	SSRETSHGSP	TVTKLSKEPS	DTSSAFESTA	KENFLGEDDD	FVDLEELSSQ	TGGGMHKKDT
330	340	350	360	370	380	390	400
LKECLSLDPE	ERKKAESQIN	NSAVEMQVQS	ALAFLGTEND	VELKGALDLE	TCEKQDIMPE	VDKQSGSPES	RVENTLNIHE
410	420	430	440	450	460	470	480
DLDKVKLIEY	YLTKNKEGPQ	VSENLQKTEL	SDGKSIEPGG	IDITLSSSLS	QAGDPITEGN	KEPDKTWVKK	GEPLPVKLNS
490	500	510	520	530	540	550	560
STEANVIKEA	LDSSLESTLD	NSCQGAQMDN	KSEVQLWLLK	RIQVPIEDIL	PSKEEKSKTP	PMFLCIKVGK	PMRKSFATHT
570	580	590	600	610	620	630	640
AAMVQQYGKR	RKQPEYWFAV	PRERVDHLYT	FFVQWSPDVY	GKDAKEQGFV	VVEKEELNMI	DNFFSEPTTK	SWEIITVEEA
650	660	670	680	690	700	710	720
KRRKSTCSYY	EDEDEEVLPV	LRPHSALLEN	MHIEQLARRL	PARVQGYPWR	LAYSTLEHGT	SLKTLYRKSA	SLDSPVLLVI
730	740	750	760	770	780	790	800
KDMDNQIFGA	YATHPFKFSD	HYYGTGETFL	YTFSPHFKVF	KWSGENSYFI	NGDISSLELG	GGGGRFGLWL	DADLYHGRSN
810	820	830					
SCSTFNNDIL	SKKEDFIVQD	LEVWAFD					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2346	1	788.3203	-89.68	2	57.7	11.6	0	102-116	R.VLSSTSEEDEPGVVK.F	

Detailed Protein Report

Protein 1369: 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 1370: beta-1,4 N-acetylgalactosaminyltransferase 1 isoform 3 precursor [Homo sapiens]

Accession:	gi|451172103	**Score:**	11.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	35.4
Database Date:	2015-11-30	**pI:**	10.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	8.2
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MWLGRRALCA LVLLLACASL GLLYASTRDA PGLRLPLAPW APPQSPRRPE LPDLAPEPRY AHIPVRIKEQ VVGLLAWNNC
        90        100        110        120        130        140        150        160
SCESSGGGLP LPFQKQVRAI DLTKAFDPAE LRAASATREQ EFQAFLSRSQ SPADQLLIAP ANSPLQYPLQ GVEVQPLRSI
       170        180        190        200        210        220        230        240
LVPGLSLQAA SGQEVYQVNL TASLGTWDVA GEVTGVTLTG EGQADLTLVS PGLDQLNRQL QLVTYSSRSY QTNTADTGAR
       250        260        270        280        290        300        310        320
PGWRDGQAGQ TEKNQKGWSG QMAEGMGGIW AMARAVQPHN GCFNWTSRAR GRKGAFVHLG LEQARGKPEP WVCLPFRPTV
       330
GGPRKRLV
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1470	1	1006.5955	27.03	3	47.1	11.6	2	2-28	M.WLGRRALCALVLLLACASLGLLYASTR.D	Carbamidomethyl: 8, 16

Detailed Protein Report

Protein 1371: globoside alpha-1,3-N-acetylgalactosaminyltransferase 1 isoform 5 [Homo sapiens]

Accession:	gi|568384828	**Score:**	11.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	24.3
Database Date:	2015-11-30	**pI:**	9.4
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	9.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MRGYRVHYYI	FTDNPAAVPG	VPLGPHRLLS	SIPIQGHSHW	EETSMRRMET	ISQHIAKRAH	REVDYLFCLD	VDMVFRNPWG
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
PETLGDLVAA	IHPSYYAVPR	QQFPYERRRV	STAFVADSEG	DFYYGGAVFG	GQVARVYEFT	RGCHMAILAD	KANGIMAAWR
170	**180**	**190**	**200**	**210**	**220**		
EESHLNRHFI	SNKPSKVLSP	EYLWDDRKPQ	PPSLKLIRFS	TLDKDISCLR	S		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2044	1	701.2711	-100.00	3	55.7	11.6	1	142-160	R.GCHMAILADKANGIMAAWR.E	Carbamidomethyl: 2; Oxidation: 15

Detailed Protein Report

Protein 1372: 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

mdown:qdown	**Median:**	0.20	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.22	**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		mdown:qdown 0.20 Wdown:Qdown 0.22

Detailed Protein Report

Protein 1373: serine/arginine repetitive matrix protein 4 [Homo sapiens]

Accession:	gi|50083281	**Score:**	11.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	68.5
Database Date:	2015-11-30	**pI:**	12.4
		Sequence Coverage [%]:	3.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MASVQQGEKQ	LFEKFWRGTF	KAVATPRPES	IIVASITARK	PLPRTEPQNN	PVVPAQDGPS	EKLGQHLATE	PLGTNSWERD
90	100	110	120	130	140	150	160
KTCRELGATR	GHSASHDKDL	TPPPSSRGKK	KKKKSTRKKR	RRSSSYSPSP	VKKKKKKSSK	KHKRRRSFSK	KRRHSSSSPK
170	180	190	200	210	220	230	240
SKRRDEKRHK	KQSRSRPRKS	HRHRHHRCPS	RSQSSESRPS	SCESRHRGRS	PEEGQKSRRR	HSRRCSKTLC	KDSPEAQSSR
250	260	270	280	290	300	310	320
PPSQPLQMLG	YLSARGVITG	SGSAADLFTK	TASPLTTSRG	RSQEYDSGND	TSSPPSTQTS	SARSRGQEKG	SPSGGLSKSR
330	340	350	360	370	380	390	400
ELNSGNTSDS	GNSFTTSSPQ	NKGAMLENLS	PTSRGRESRG	FQSPCLECAE	VKKSSLVPST	ARSSPMKGCS	RSSSYASTRS
410	420	430	440	450	460	470	480
SSHSSRSPNP	RASPRYTQSR	STSSEKRSYS	RSPSYSSKSG	KRSPPSRSSR	SRRSPSYSRY	SPSRERDPKY	SEKDSQQRER
490	500	510	520	530	540	550	560
ERARRRRRSY	SPMRKRRRDS	PSHLEARRIT	SARKRPIPYY	RPSPSSSGSL	SSTSSWYSSS	SSRSASRSYS	RSRSRSRSRR
570	580	590	600	610	620		
RSRTRTSSSS	SSRSPSPGSR	SRSRSRSRSR	SRSRSQSRSY	SSADSYSSTR	R		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
22	1	713.2871	-70.21	3	29.5	11.6	2	392-411	R.SSSYASTRSSSHSSRSPNPR.A	

Detailed Protein Report

Protein 1374: 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

Quantitation

mdown:qdown	**Median:** 0.59	**CV:** 0.00 %	**No. of Peptides:** 1

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	Ratios
1404	1	816.5863	183.79	1	47.3	11.6	0	1984-1990	K.VFTHQGK.V		mdown:qdown 0.59

Detailed Protein Report

Protein 1375: **PREDICTED: transmembrane and coiled-coil domains protein 3 isoform X1 [Homo sapiens]**

Accession:	gi|530400601	**Score:**	11.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	50.1
Database Date:	2015-11-30	**pI:**	9.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.0
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|530400605	refseq_human (refseq_human_20140103.fasta)	PREDICTED: transmembrane and coiled-coil domains protein 3 isoform X3 [Homo sapiens]
gi|530400603	refseq_human (refseq_human_20140103.fasta)	PREDICTED: transmembrane and coiled-coil domains protein 3 isoform X2 [Homo sapiens]

10	20	30	40	50	60	70	80
MNTLSLPLNI	RRGGSDTNLN	FDVPDGILDF	HKVKLTADSL	KQKILKVTEQ	IKIEQTSRDG	NVAEYLKLVN	NADKQQAGRI
90	100	110	120	130	140	150	160
KQVFEKKNQK	SAHSIAQLQK	KLEQYHRKLR	EIEQNGASRS	SKDISKDHLK	DIHRSLKDAH	VKSRTAPHCM	ESSKSGMPGV
170	180	190	200	210	220	230	240
SLTPPVFVFN	KSREFANLIR	NKFGSADNIA	HLKNSLEEFR	PEASARAYGG	SATIVNKPKY	GSDDECSSGT	SGSADSNGNQ
250	260	270	280	290	300	310	320
SFGAGGASTL	DSQGKLAVIL	EELREIKDTQ	AQLAEDIEAL	KVQFKREYGF	ISQTLQEERY	RYERLEDQLH	DLTDLHQHET
330	340	350	360	370	380	390	400
ANLKQELASI	EEKVAYQAYE	RSRDIQEALE	SCQTRISKLE	LHQQEQQALQ	TDTVNAKVLL	GRCINVILAF	MTVILVCVST
410	420	430	440	450			
IAKFVSPMMK	SRCHILGTFF	AVTLLAIFCK	NWDHILCAIE	RMIIPR			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2855	1	1027.5252	-26.05	2	64.9	11.5	0	413-430	R.CHILGTFFAVTLLAIFCK.N	Carbamidomethyl: 1

Detailed Protein Report

Protein 1376: PREDICTED: serine racemase isoform X3 [Homo sapiens]

Accession:	gi|578830012	**Score:**	11.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	20.3
Database Date:	2015-11-30	**pI:**	4.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	8.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MVHPNQEPAV	IAGQGTIALE	VLNQVPLVDA	LVVPVGGGGM	LAGIAITVKA	LKPSVKVYAA	EPSNADDCYQ	SKLKGKLMPN
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
LYPPETIADG	VKSSIGLNTW	PIIRDLVDDI	FTVTEDEIKC	ATQLVWERMK	LLIEPTAGVG	VAAVLSQHFQ	TVSPEVKNIC
170	**180**	**190**	**200**				
IVLSGGNVDL	TSSITWVKQA	ERPASYQSVS	V				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2683	1	887.4745	18.38	2	61.9	11.5	0	77-92	K.LMPNLYPPETIADGVK.S	Oxidation: 2

Detailed Protein Report

Protein 1377: melanotransferrin isoform 2 precursor [Homo sapiens]

Accession:	gi|16163666	**Score:**	11.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	32.7
Database Date:	2015-11-30	**pI:**	5.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	6.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MRGPSGALWL	LLALRTVLGG	MEVRWCATSD	PEQHKCGNMS	EAFREAGIQP	SLLCVRGTSA	DHCVQLIAAQ	EADAITLDGG
90	100	110	120	130	140	150	160
AIYEAGKEHG	LKPVVGEVYD	QEVGTSYYAV	AVVRRSSHVT	IDTLKGVKSC	HTGINRTVGW	NVPVGYLVES	GRLSVMGCDV
170	180	190	200	210	220	230	240
LKAVSDYFGG	SCVPGAGETS	YSESLCRLCR	GDSSGEGVCD	KSPLERYYDY	SGAFRCLAEG	AGDVAFVKHS	TVLENTDESP
250	260	270	280	290	300	310	
SRRQTWTRSE	EEEGECPAHE	EARRTMRSSA	GQAWKWAPVH	RPQDESDKGE	FGKRAKSRDM	LG	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2850	1	754.6730	23.67	3	64.8	11.5	2	249-267	R.SEEEEGECPAHEEARRTMR.S	Oxidation: 18

Detailed Protein Report

Protein 1378: **PREDICTED: cleavage and polyadenylation specificity factor subunit 7 isoform X5 [Homo sapiens]**

Accession:	gi|530397403	**Score:**	11.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	41.9
Database Date:	2015-11-30	**pI:**	10.1
		Sequence Coverage [%]:	3.1
		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
2417	1	572.6438	-211.80	2	58.9	11.5	0	317-328	K.SYSVGASGSSSR.K	

Detailed Protein Report

Protein 1379: 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 1380: protein argonaute-2 isoform 2 [Homo sapiens]

Accession:	gi|257467482	**Score:**	11.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	93.6
Database Date:	2015-11-30	**pI:**	10.1
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MYSGAGPALA	PPAPPPPIQG	YAFKPPPRPD	FGTSGRTIKL	QANFFEMDIP	KIDIYHYELD	IKPEKCPRRV	NREIVEHMVQ
90	100	110	120	130	140	150	160
HFKTQIFGDR	KPVFDGRKNL	YTAMPLPIGR	DKVELEVTLP	GEGKDRIFKV	SIKWVSCVSL	QALHDALSGR	LPSVPFETIQ
170	180	190	200	210	220	230	240
ALDVVMRHLP	SMRYTPVGRS	FFTASEGCSN	PLGGGREVWF	GFHQSVRPSL	WKMMLNIDVS	ATAFYKAQPV	IEFVCEVLDF
250	260	270	280	290	300	310	320
KSIEEQQKPL	TDSQRVKFTK	EIKGLKVEIT	HCGQMKRKYR	VCNVTRRPAS	HQTFPLQQES	GQTVECTVAQ	YFKDRHKLVL
330	340	350	360	370	380	390	400
RYPHLPCLQV	GQEQKHTYLP	LEVCNIVAGQ	RCIKKLTDNQ	TSTMIRATAR	SAPDRQEEIS	KLMRSASFNT	DPYVREFGIM
410	420	430	440	450	460	470	480
VKDEMTDVTG	RVLQPPSILY	GGRNKAIATP	VQGVWDMRNK	QFHTGIEIKV	WAIACFAPQR	QCTEVHLKSF	TEQLRKISRD
490	500	510	520	530	540	550	560
AGMPIQGQPC	FCKYAQGADS	VEPMFRHLKN	TYAGLQLVVV	ILPGKTPVYA	EVKRVGDTVL	GMATQCVQMK	NVQRTTPQTL
570	580	590	600	610	620	630	640
SNLCLKINVK	LGGVNNILLP	QGRPPVFQQP	VIFLGADVTH	PPAGDGKKPS	IAAVVGSMDA	HPNRYCATVR	VQQHRQEIIQ
650	660	670	680	690	700	710	720
DLAAMVRELL	IQFYKSTRFK	PTRIIFYRDG	VSEGQFQQVL	HHELLAIREA	CIKLEKDYQP	GITFIVVQKR	HHTRLFCTDK
730	740	750	760	770	780	790	800
NERGTSRPSH	YHVLWDDNRF	SSDELQILTY	QLCHTYVRCT	RSVSIPAPAY	YAHLVAFRAR	YHLVDKEHDS	AEGSHTSGQS
810	820	830					
NGRDHQALAK	AVQVHQDTLR	TMYFA					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2829	1	869.4101	-11.64	2	63.9	11.5	0	535-550	R.VGDTVLGMATQCVQMK.N	Carbamidomethyl: 12

Detailed Protein Report

Protein 1381: chloride intracellular channel protein 5 isoform a [Homo sapiens]

Accession:	gi|166197662	**Score:**	11.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	46.5
Database Date:	2015-11-30	**pI:**	4.6
Modification(s):	Oxidation	**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 1382: myeloid leukemia factor 2 [Homo sapiens]

Accession: gi|4885487
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 11.5
MW [kDa]: 28.1
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	

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Detailed Protein Report

Protein 1383: rap1 GTPase-activating protein 1 isoform c [Homo sapiens]

Accession:	gi|224809582	**Score:**	11.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	73.3
Database Date:	2015-11-30	**pI:**	5.5
		Sequence Coverage [%]:	2.7
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MIEKMQGSRM DEQRCSFPPP LKTEEDYIPY PSVHEVLGRE GPFPLILLPQ FGGYWIEGTN HEITSIPETE PLQSPTTKVK
        90        100        110        120        130        140        150        160
LECNPTARIY RKHFLGKEHF NYYSLDAALG HLVFSLKYDV IGDQEHLRLL LRTKCRTYHD VIPISCLTEF PNVVQMAKLV
       170        180        190        200        210        220        230        240
CEDVNVDRFY PVLYPKASRL IVTFDEHVIS NNFKFGVIYQ KLGQTSEEEL FSTNEESPAF VEFLEFLGQK VKLQDFKGFR
       250        260        270        280        290        300        310        320
GGLDVTHGQT GTESVYCNFR NKEIMFHVST KLPYTEGDAQ QLQRKRHIGN DIVAVVFQDE NTPFVPDMIA SNFLHAYVVV
       330        340        350        360        370        380        390        400
QAEGGGPDGP LYKVSVTARD DVPFFGPPLP DPAVFRKGPE FQEFLLTKLI NAEYACYKAE KFAKLEERTR AALLETLYEE
       410        420        430        440        450        460        470        480
LHIHSQSMMG LGGDEDKMEN GSGGGGFFES FKRVIRSRSQ SMDAMGLSNK KPNTVSTSHS GSFAPNNPDL AKAAGISLIV
       490        500        510        520        530        540        550        560
PGKSPTRKKS GPFGSRRSSA IGIENIQEVQ EKRESPPAGQ KTPDSGHVSQ EPKSENSSTQ SSPEMPTTKN RAETAAQRAE
       570        580        590        600        610        620        630        640
ALKDFSRSSS SASSFASVVE ETEGVDGEDT GLESVSSSGT PHKRDSFIYS TWLEDSVSTT SGGSSPGPSR SPHPDAGKLG
       650        660        670
DPACPEIKIQ LEASEQHMPQ LGC
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2007	1	660.8874	-123.62	3	53.6	11.5	1	534-551	K.SENSSTQSSPEMPTTKNR.A	

BRUKER

Detailed Protein Report

Protein 1384: 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 1385: WAP four-disulfide core domain protein 2 precursor [Homo sapiens]

Accession:	gi|56699495	**Score:**	11.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	13.0
Database Date:	2015-11-30	**pI:**	4.5
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	17.7
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MPACRLGPLA AALLLSLLLF GFTLVSGTGA EKTGVCPELQ ADQNCTQECV SDSECADNLK CCSAGCATFC SLPNDKEGSC
        90        100        110        120        130
PQVNINFPQL GLCRDQCQVD SQCPGQMKCC RNGCGKVSCV TPNF
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2885	1	1287.8628	-110.66	2	65.2	11.5	2	95-116	R.DQCQVDSQCPGQMKCCRNGCGK.V	Carbamidomethyl: 9, 15, 16; Oxidation: 13

Detailed Protein Report

Protein 1386: lethal(3)malignant brain tumor-like protein 2 [Homo sapiens]

Accession:	gi|20149698	**Score:**	11.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	79.1
Database Date:	2015-11-30	**pI:**	6.4
		Sequence Coverage [%]:	3.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEKPRSIEET	PSSEPMEEEE	DDDLELFGGY	DSFRSYNSSV	GSESSSYLEE	SSEAENEDRE	AGELPTSPLH	LLSPGTPRSL
90	100	110	120	130	140	150	160
DGSGSEPAVC	EMCGIVGTRE	AFFSKTKRFC	SVSCSRSYSS	NSKKASILAR	LQGKPPTKKA	KVLHKAAWSA	KIGAFLHSQG
170	180	190	200	210	220	230	240
TGQLADGTPT	GQDALVLGFD	WGKFLKDHSY	KAAPVSCFKH	VPLYDQWEDV	MKGMKVEVLN	SDAVLPSRVY	WIASVIQTAG
250	260	270	280	290	300	310	320
YRVLLRYEGF	ENDASHDFWC	NLGTVDVHPI	GWCAINSKIL	VPPRTIHAKF	TDWKGYLMKR	LVGSRTLPVD	FHIKMVESMK
330	340	350	360	370	380	390	400
YPFRQGMRLE	VVDKSQVSRT	RMAVVDTVIG	GRLRLLYEDG	DSDDDFWCHM	WSPLIHPVGW	SRRVGHGIKM	SERRSDMAHH
410	420	430	440	450	460	470	480
PTFRKIYCDA	VPYLFKKVRA	VYTEGGWFEE	GMKLEAIDPL	NLGNICVATV	CKVLLDGYLM	ICVDGGPSTD	GLDWFCYHAS
490	500	510	520	530	540	550	560
SHAIFPATFC	QKNDIELTPP	KGYEAQTFNW	ENYLEKTKSK	AAPSRLFNMD	CPNHGFKVGM	KLEAVDLMEP	RLICVATVKR
570	580	590	600	610	620	630	640
VVHRLLSIHF	DGWDSEYDQW	VDCESPDIYP	VGWCELTGYQ	LQPPVAAEPA	TPLKAKEATK	KKKKQFGKKR	KRIPPTKTRP
650	660	670	680	690	700	710	
LRQGSKKPLL	EDDPQGARKI	SSEPVPGEII	AVRVKEEHLD	VASPDKASSP	ELPVSVENIK	QETDD	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1773	1	689.9786	3.24	3	50.8	11.5	0	79-99	R.SLDGSGSEPAVCEMCGIVGTR.E	

Detailed Protein Report

Protein 1387: 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 1388: 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

Quantitation

mdown:qdown **Median:** 0.95 **CV:** 0.00 % **No. of 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	Ratios
730	1	683.3948	125.77	2	38.5	11.5	0	233-244	K.SHVYSLEGQDCK.Y		mdown:qdown 0.95

Detailed Protein Report

Protein 1389: **cyclin-dependent kinase 14 isoform a [Homo sapiens]**

Accession:	gi|560231615	**Score:**	11.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	53.0
Database Date:	2015-11-30	**pI:**	9.7
		Sequence Coverage [%]:	2.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MCDLIEPQPA	EKIGKMKKLR	RTLSESFSRI	ALKKDDTTFD	EICVTKMSTR	NCQGMDSVIK	PLDTIPEDKK	VRVQRTQSTF
90	100	110	120	130	140	150	160
DPFEKPANQV	KRVHSENNAC	INFKTSSTGK	ESPKVRRHSS	PSSPTSPKFG	KADSYEKLEK	LGEGSYATVY	KGKSKVNGKL
170	180	190	200	210	220	230	240
VALKVIRLQE	EEGTPFTAIR	EASLLKGLKH	ANIVLLHDII	HTKETLTLVF	EYVHTDLCQY	MDKHPGGLHP	DNVKLFLFQL
250	260	270	280	290	300	310	320
LRGLSYIHQR	YILHRDLKPQ	NLLISDTGEL	KLADFGLARA	KSVPSHTYSN	EVVTLWYRPP	DVLLGSTEYS	TCLDMWGVGC
330	340	350	360	370	380	390	400
IFVEMIQGVA	AFPGMKDIQD	QLERIFLVLG	TPNEDTWPGV	HSLPHFKPER	FTLYSSKNLR	QAWNKLSYVN	HAEDLASKLL
410	420	430	440	450	460	470	
QCSPKNRLSA	QAALSHEYFS	DLPPRLWELT	DMSSIFTVPN	VRLQPEAGES	MRAFGKNNSY	GKSLSNSKH	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1903	1	676.2591	-182.65	2	52.3	11.4	1	22-33	R.TLSESFSRIALK.K	

Detailed Protein Report

Protein 1390: putative polypeptide N-acetylgalactosaminyltransferase-like protein 3 [Homo sapiens]

Accession:	gi|22538495	**Score:**	11.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	67.7
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
MASLRRVKVL	LVLNLIAVAG	FVLFLAKCRP	IAVRSGDAFH	EIRPRAEVAN	LSAHSASPIQ	DAVLKRLSLL	EDIVYRQLNG
90	100	110	120	130	140	150	160
LSKSLGLIEG	YGGRGKGGLP	ATLSPAEEEK	AKGPHEKYGY	NSYLSEKISL	DRSIPDYRPT	KCKELKYSKD	LPQISIIFIF
170	180	190	200	210	220	230	240
VNEALSVILR	SVHSAVNHTP	THLLKEIILV	DDNSDEEELK	VPLEEYVHKR	YPGLVKVVRN	QKREGLIRAR	IEGWKVATGQ
250	260	270	280	290	300	310	320
VTGFFDAHVE	FTAGWAEPVL	SRIQENRKRV	ILPSIDNIKQ	DNFEVQRYEN	SAHGYSWELW	CMYISPPKDW	WDAGDPSLPI
330	340	350	360	370	380	390	400
RTPAMIGCSF	VVNRKFFGEI	GLLDPGMDVY	GGENIELGIK	VWLCGGSMEV	LPCSRVAHIE	RKKKPYNSNI	GFYTKRNALR
410	420	430	440	450	460	470	480
VAEVWMDDYK	SHVYIAWNLP	LENPGIDIGD	VSERRALRKS	LKCKNFQWYL	DHVYPEMRRY	NNTVAYGELR	NNKAKDVCLD
490	500	510	520	530	540	550	560
QGPLENHTAI	LYPCHGWGPQ	LARYTKEGFL	HLGALGTTTL	LPDTRCLVDN	SKSRLPQLLD	CDKVKSSLYK	RWNFIQNGAI
570	580	590	600				
MNKGTGRCLE	VENRGLAGID	LILRSCTGQR	WTIKNSIK				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2906	1	981.9571	-51.41	2	65.5	11.4	2	551-567	K.RWNFIQNGAIMNKGTGR.C	

Detailed Protein Report

Protein 1391: PREDICTED: echinoderm microtubule-associated protein-like 5 isoform X4 [Homo sapiens]

Accession:	gi|578825576	**Score:**	11.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	176.2
Database Date:	2015-11-30	**pI:**	8.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	0.8
		No. of unique Peptides:	1

Quantitation

Wdown:Qdown **Median:** 0.15 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MAARSAPSCH LRLEWVYGYR GHQCRNNLYY TAAKEIVYFV AGVGVVYSPR EHRQKFYRGH SDDIISLALH PERVLVATGQ

        90        100        110        120        130        140        150        160
VGKEPYICIW DSYTVQTISV LKDVHTHGIA CLAFDLDGQR LVSVGLDSKN AVCVWDWKRG KMLSMAPGHT DRIFDISWDL

       170        180        190        200        210        220        230        240
YQPNKLVSCG VKHIKFWSLC GNALTPKRGV FGKTGDLQTI LCLACARDEL TYSGALNGDI YVWKGINLIR TIQGAHAAGI

       250        260        270        280        290        300        310        320
FSMNACEEGF ATGGRDGCIR LWDLTFKPIT VIDLRETDQG YKGLSVRSVC WRGDHILVGT QDSEIFEIVV QERNKPFLIM

       330        340        350        360        370        380        390        400
QGHCEGELWA LAVHPTKPLA VTGSDDRSVR IWSLVDHALI ARCNMEEPIR CAAVNADGIH LALGMKDGSF TVLRVRDMTE

       410        420        430        440        450        460        470        480
VVHIKDRKEA IHELKYSPDG TYLAVGCNDS SVDIYGVAQR YKKVGECLGS LSFITHLDWS SDSRYLQTND GNGKRLFYRM

       490        500        510        520        530        540        550        560
PGGKEVTSTE EIKGVHWASW TCVSGLEVNG IWPKYSDIND INSVDGNYIG QVLVTADDYG IIKLFRYPCL RKGAKFRKYI

       570        580        590        600        610        620        630        640
GHSAHVTNVR WSHDYQWVIS IGGADHSVFQ WKFIPERKLK DAVHIAPQES LADSHSDESD SDLSDVPELD SEIEQETQLT

       650        660        670        680        690        700        710        720
YRRQVYKEDL PQLKEQCKEK QKSATSKRRE RAPGNSIRLH FVHGYRGYDC RSNLFYTQIG EIVYHVAAVG VIYNRQQNTQ

       730        740        750        760        770        780        790        800
RFYLGHDDDI LCLTIHPLKD YVATGQVGRD PSIHIWDTET IKPLSILKGH HQYGVSAVDF SADGKRLASV GIDDSHTVVL

       810        820        830        840        850        860        870        880
WDWKKGEKLS IARGSKDKIF VVKMNPYVPD KLITAGIKHM KFWRKAGGGL IGRKGYIGTL GKNDTMMCAV YGWTEEMAFS

       890        900        910        920        930        940        950        960
GTSTGDVCIW RDIFLVKTVK AHDGPVFSMH ALEKGFVTGG KDGIVALWDD SFERCLKTYA IKRAALAPGS KGLLLEDNPS

       970        980        990       1000       1010       1020       1030       1040
IRAISLGHGH ILVGTKNGEI LEVDKSGPIT LLVQGHMEGE VWGLATHPYL PICATVSDDK TLRIWDLSPS HCMLAVRKLK

      1050       1060       1070       1080       1090       1100       1110       1120
KGGRCCCFSP DGKALAVGLN DGSFLMANAD TLEDLVSFHH RKDMISDIRF SPGSGKYLAV ASHDSFIDIY NVMSSKRVGI

      1130       1140       1150       1160       1170       1180       1190       1200
CKGATSYITH IDWDIRGKLL QVNTGAKEQL FFEAPRGKKQ TIPSVEVEKI AWASWTSVLG LCCEGIWPVI GEVTDVTASC

      1210       1220       1230       1240       1250       1260       1270       1280
LTSDKMVLAT GDDLGFVKLF RYPTKGKFGK FKRYVAHSTH VTNVRWTYDD SMLVTLGGTD MSLMVWTNEM EGYREKRPCD

      1290       1300       1310       1320       1330       1340       1350       1360
SEESDIDSEE DGGYDSDVTR ENEISYTIRA LSTNIRPMLG IKPHLQQKEP SIDERPPVSR APPQPEKLQT NNVGKKKRPI

      1370       1380       1390       1400       1410       1420       1430       1440
EDLVLELIFG YRGRDCRNNV HYLNDGDDII YHTASVGILH NVATGSQSFY QEHNDDILCL TVNQHPKFIN IVATGQVGDS

      1450       1460       1470       1480       1490       1500       1510       1520
ADMSATAPSI HIWDAMNKQT LSILRCYHSK GVCSVSFSAT GKLLLSVGLD PEHTITIWRW QEGAKIASRA GHNQRIFVAE

      1530       1540       1550       1560       1570       1580
FRPDSDTQFV SVGVKHVKFW TLAGRALLSK KGLLSTLEDA RMQTMLAIAF GAVKRRRSG
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1357	1	698.8708	1.22	2	45.7	11.4	0	1562-1574	R.MQTMLAIAFGAVK.R	Oxidation: 4	Wdown:Qdown 0.15

Detailed Protein Report

Protein 1392: PREDICTED: protein LAP2 isoform X4 [Homo sapiens]

Accession: gi|578810464
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl, Oxidation

Score: 11.4
MW [kDa]: 139.9
pI: 5.1
Sequence Coverage [%]: 1.4
No. of unique Peptides: 1

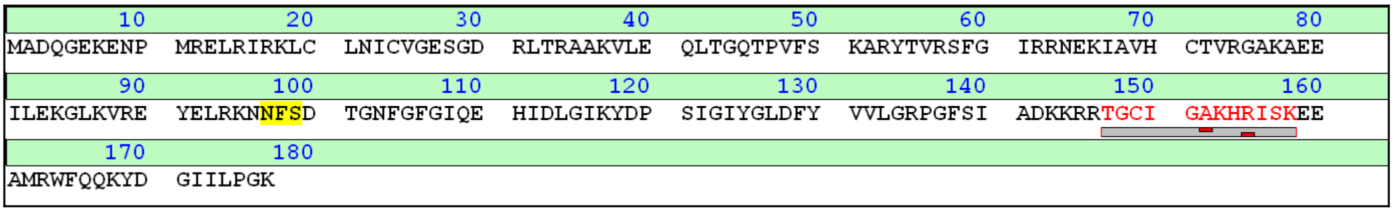
10	20	30	40	50	60	70	80
MTTKRSLFVR	LVPCRCLRGE	EETVTTLDYS	HCSLEQVPKE	IFTFEKTLEE	LYLDANQIEE	LPKQLFNCQS	LHKLSLPDND
90	100	110	120	130	140	150	160
LTTLPASIAN	LINLRELDVS	KNGIQEFPEN	IKNCKVLTIV	EASVNPISKL	PDGFSQLLNL	TQLYLNDAFL	EFLPANFGRL
170	180	190	200	210	220	230	240
TKLQILELRE	NQLKMLPKTM	NRLTQLERLD	LGSNEFTEVP	EVLEQLSGLK	EFWMDANRLT	FIPGFIGSLK	QLTYLDVSKN
250	260	270	280	290	300	310	320
NIEMVEEGIS	TCENLQDLLL	SSNSLQQLPE	TIGSLKNITT	LKIDENQLMY	LPDSIGGLIS	VEELDCSFNE	VEALPSSIGQ
330	340	350	360	370	380	390	400
LTNLRTFAAD	HNYLQQLPPE	IGSWKNITVL	FLHSNKLETL	PEEMGDMQKL	KVINLSDNRL	KNLPFSFTKL	QQLTAMWLSD
410	420	430	440	450	460	470	480
NQSKPLIPLQ	KETDSETQKM	VLTNYMFPQQ	PRTEDVMFIS	DNESFNPSLW	EEQRKQRAQV	AFECDEDKDE	REAPPREGNL
490	500	510	520	530	540	550	560
KRYPTPYPDE	LKNMVKTVQT	IVHRLKDEET	NEDSGRDLKP	HEDQQDINKD	VGVKTSESTT	TVKSKVDERE	KYMIGNSVQK
570	580	590	600	610	620	630	640
ISEPEAEISP	GSLPVTANMK	ASENLKHIVN	HDDVFEESEE	LSSDEEMKMA	EMRPPLIETS	INQPKVVALS	NNKKDDTKET
650	660	670	680	690	700	710	720
DSLSDEVTHN	SNQNNSNCSS	PSRMSDSVSL	NTDSSQDTSL	CSPVKQTHID	INSKIRQEDE	NFNSLLQNGD	ILNSSTEEKF
730	740	750	760	770	780	790	800
KAHDKKDFNL	PEYDLNVEER	LVLIEKSVDS	TATADDTHKL	DHINMNLNKL	ITNDTFQPEI	MERSKTQDIV	LGTSFLSINS
810	820	830	840	850	860	870	880
KEETEHLENG	NKYPNLESVN	KVNGHSEETS	QSPNRTEPHD	SDCSVDLGIS	KSTEDLSPQK	SGPVGSVVKS	HSITNMEIGG
890	900	910	920	930	940	950	960
LKIYDILSDN	GPQQPSTTVK	ITSAVDGKNI	VRSKSATLLY	DQPLQVFTGS	SSSSDLISGT	KAIFKFDSNH	NPEEPNIIRG
970	980	990	1000	1010	1020	1030	1040
PTSGPQSAPQ	IYGPPQYNIQ	YSSSAAVKDT	LWHSKQNPQI	DHASFPPQLL	PRSESTENQS	YAKHSANMNF	SNHNNVRANT
1050	1060	1070	1080	1090	1100	1110	1120
AYHLHQRLGP	ARHGEMWAIS	PNDRLIPAVT	RSTIQRQSSV	SSTASVNLGD	PGSTRRAQIP	EGDYLSYREF	HSAGRTPPMM
1130	1140	1150	1160	1170	1180	1190	1200
PGSQRPLSAR	TYSIDGPNAS	RPQSARPSIN	EIPERTMSVS	DFNYSRTSPS	KRPNARVGSE	HSLLDPPGKS	KVPRDWREQV
1210	1220	1230	1240	1250			
LRHIEAKKLE	KVFFSGTGNR	VPNLNSARTI	GMIMCVSILS	FTPHCF			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1657	1	697.0355	61.97	3	49.4	11.4	0	1229-1246	R.TIGMIMCVSILSFTPHCF.-	Carbamidomethyl: 7; Oxidation: 4, 6

Detailed Protein Report

Protein 1393: 60S ribosomal protein L11 isoform 2 [Homo sapiens]

Accession:	gi|315221152	**Score:**	11.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	20.1
Database Date:	2015-11-30	**pI:**	10.3
		Sequence Coverage [%]:	6.8
		No. of unique Peptides:	1



```
        10         20         30         40         50         60         70         80
MADQGEKENP MRELRIRKLC LNICVGESGD RLTRAAKVLE QLTGQTPVFS KARYTVRSFG IRRNEKIAVH CTVRGAKAEE
        90        100        110        120        130        140        150        160
ILEKGLKVRE YELRKNNFSD TGNFGFGIQE HIDLGIKYDP SIGIYGLDFY VVLGRPGFSI ADKKRRTGCI GAKHRISKEE
       170        180
AMRWFQQKYD GIILPGK
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
173	1	424.2196	-47.66	3	31.4	11.4	2	147-158	R.TGCIGAKHRISK.E	

Detailed Protein Report

Protein 1394: 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

Quantitation

Wdown:Qdown **Median:** 0.93 **CV:** 0.00 % **No. of 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	Ratios
507	1	809.7240	-171.17	2	35.7	11.4	1	307-320	R.QTWSRFHCPGQGSQ.-		Wdown:Qdown 0.93

Detailed Protein Report

Protein 1395: PREDICTED: uncharacterized protein LOC102723902 [Homo sapiens]

Accession:	gi|578824635	**Score:**	11.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	12.5
Database Date:	2015-11-30	**pI:**	12.7
		Sequence Coverage [%]:	15.5
		No. of unique Peptides:	1

Quantitation

Wdown:Qdown **Median:** 0.33 **CV:** 0.00 % **No. of Peptides:** 1

```
         10         20         30         40         50         60         70         80
MRAAPAPPGL PRPRACARAL SPGGVWVCGA RARAARRRTC EVSLRRGRAP CVRQRRRASR SGDEEPLAHP AQKAAAAGRL
         90        100        110        120
HCLTTTRAGF SPRPANPRDT SLEDKRASSR PKKETA
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2347	1	899.4199	-73.85	2	57.8	11.4	2	19-36	R.ALSPGGVWVCGARARAAR.R		Wdown:Qdown 0.33

Detailed Protein Report

Protein 1396: 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 1397: chloride transport protein 6 isoform 2 [Homo sapiens]

Accession:	gi|379698826	**Score:**	11.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	94.5
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
MAGCRGSLCC	CCRWCCCCGE	RETRTPEELT	ILGETQEEED	EILPRKDYEK	GRRYEAVKWM	VVFAIGVCTG	LVGLFVDFFV
90	100	110	120	130	140	150	160
RLFTQLKFGV	VQTSVEECSQ	KGCLALSLLE	LLGFNLTFVF	LASLLVLIEP	VAAGSGIPEV	KCYLNGVKVP	GIVRLRTLLC
170	180	190	200	210	220	230	240
KVLGVLFSVA	GGLFVGKEGP	MIHSGSVVGA	GLPQFQSISL	RKIQFNFPYF	RSDRDKRDFV	SAGAAAGVAA	AFGAPIGGTL
250	260	270	280	290	300	310	320
FSLEEGSSFW	NQGLTWKVLF	CSMSATFTLN	FFRSGIQFGS	WGSFQLPGLL	NFGEFKCSDS	DKKCHLWTAM	DLGFFVVMGV
330	340	350	360	370	380	390	400
IGGLLGATFN	CLNKRLAKYR	MRNVHPKPKL	VRVLESLLVS	LVTTVVVFVA	SMVLGECRQM	SSSSQIGNDS	FQLQVTEDVN
410	420	430	440	450	460	470	480
SSIKTFFCPN	DTYNDMATLF	FNPQESAILQ	LFHQDGTFSP	VTLALFFVLY	FLLACWTYGI	SVPSGLFVPS	LLCGAAFGRL
490	500	510	520	530	540	550	560
VANVLKSYIG	LGHIYSGTFA	LIGAAAFLGG	VVRMTISLTV	ILIESTNEIT	YGLPIMVTLM	VAKWTGDFFN	KGIYDIHVGL
570	580	590	600	610	620	630	640
RGVPLLEWET	EVEMDKLRAS	DIMEPNLTYV	YPHTRIQSLV	SILRTTVHHA	FPVVTENRGN	EKEFMKGNQL	ISNNIKFKKS
650	660	670	680	690	700	710	720
SILTRAGEQR	KRSQSMKSYP	SSELRNMCDE	HIASEEPAEK	EDLLQQMLER	RYTPYPNLYP	DQSPSEDWTM	EERFRPLTFH
730	740	750	760	770	780	790	800
GLILRSQLVT	LLVRGVCYSE	SQSSASQPRL	SYAEMAEDYP	RYPDIHDLDL	TLLNPRMIVD	VTPYMNPSPF	TVSPNTHVSQ
810	820	830	840	850			
VFNLFRTMGL	RHLPVVNAVG	EIVGIITRHN	LTYEFLQARL	RQHYQTI			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
535	1	689.6644	-127.65	2	35.6	11.4	1	1-13	-.MAGCRGSLCCCCR.W	Oxidation: 1

Detailed Protein Report

Protein 1398: PREDICTED: voltage-dependent T-type calcium channel subunit alpha-1H isoform X8 [Homo sapiens]

Accession:	gi|578828330	**Score:**	11.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	172.6
Database Date:	2015-11-30	**pI:**	9.4
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	1.3
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MTEGARAADE VRVPLGAPPP GPAALVGASP ESPGAPGREA ERGSELGVSP SESPAAERGA ELGADEEQRV PYPALAATVF
        90        100        110        120        130        140        150        160
FCLGQTTRPR SWCLRLVCNP WFEHVSMLVI MLNCVTLGMF RPCEDVECGS ERCNILEAFD AFIFAFFAVE MVIKMVALGL
       170        180        190        200        210        220        230        240
FGQKCYLGDT WNRLDFFIVV AGMMEYSLDG HNVSLSAIRT VRVLRPLRAI NRVPSMRILV TLLLDTLPML GNVLLLCFFV
       250        260        270        280        290        300        310        320
FFIFGIVGVQ LWAGLLRNRC FLDSAFVRNN NLTFLRPYYQ TEEGEENPFI CSSRRDNGMQ KCSHIPGRRE LRMPCTLGWE
       330        340        350        360        370        380        390        400
AYTQPQAEGV GAARNACINW NQYYNVCRSG DSNPHNGAIN FDNIGYAWIA IFQVITLEGW VDIMYYVMDA HSFYNFIYFI
       410        420        430        440        450        460        470        480
LLIIVGSFFM INLCLVVIAT QFSETKQRES QLMREQRARH LSNDSTLASF SEPGSCYEEL LKYVGHIFRK VKRRSLRLYA
       490        500        510        520        530        540        550        560
RWQSRWRKKV DPSAVQGQGP GHRQRRAGRH TASVHHLVYH HHHHHHHHYH FSHGSPRRPG PEPGACDTRL VRAGAPPSPP
       570        580        590        600        610        620        630        640
SPGRGPPDAE SVHSIYHADC HIEGPQERAR VAHAAATAAA SLRLATGLGT MNYPTILPSG VGSGKGSTSP GPKGKWAGGP
       650        660        670        680        690        700        710        720
PGTGGHGPLS LNSPDPYEKI PHVVGEHGLG QAPGHLSGLS VPCPLPSPPA GTLTCELKSC PYCTRALEDP EGELSGSESG
       730        740        750        760        770        780        790        800
DSDGRGVYEF TQDVRHGDRW DPTRPPRATD TPGPGPGSPQ RRAQQRAAPG EPGWMGRLWV TFSGKLRRIV DSKYFSRGIM
       810        820        830        840        850        860        870        880
MAILVNTLSM GVEYHEQPEE LTNALEISNI VFTSMFALEM LLKLLACGPL GYIRNPYNIF DGIIVVISVW EIVGQADGGL
       890        900        910        920        930        940        950        960
SVLRTFRLLR VLKLVRFLPA LRRQLVVLVK TMDNVATFCT LLMLFIFIFS ILGMHLFGCK FSLKTDTGDT VPDRKNFDSL
       970        980        990       1000       1010       1020       1030       1040
LWAIVTVFQI LTQEDWNVVL YNGMASTSSW AALYFVALMT FGNYVLFNLL VAILVEGFQA EGDANRSDTD EDKTSVHFEE
      1050       1060       1070       1080       1090       1100       1110       1120
DFHKLRELQT TELKMCSLAV TPNGHLEGRG SLSPPLIMCT AATPMPTPKS SPFLDAAPSL PDSRRGSSSS GDPPLGDQKP
      1130       1140       1150       1160       1170       1180       1190       1200
PASLRSSPCA PWGPSGAWSS RRSSWSSLGR APSLKRRGQC GERESLLSGE GKGSTDDEAE DGRAAPGPRA TPLRRAESLD
      1210       1220       1230       1240       1250       1260       1270       1280
PRPLRPAALP PTKCRDRDGQ VVALPSDFFL RIDSHREDAA ELDDDSEDSC CLRLHKVLEP YKPQWCRSRE AWALYLFSPQ
      1290       1300       1310       1320       1330       1340       1350       1360
NRFRVSCQKV ITHKMFDHVV LVFIFLNCVT IALERPDIDP GSTERVFLSV SNYIFTAIFV AEMMVKVVAL GLLSGEHAYL
      1370       1380       1390       1400       1410       1420       1430       1440
QSSWNLLDGL LVLVSLVDIV VAMASAGGAK ILGVLRVLRL LRTLRPLRVI SRAPGLKLVV ETLISSLRPI GNIVLICCAF
      1450       1460       1470       1480       1490       1500       1510       1520
FIIFGILGVQ LFKGKFYYCE GPDTRNISTK AQCRAAHYRW VRRKYNFDNL GQALMSLFVL SSKDGWVNIM YDGLDAVGVD
      1530       1540       1550       1560       1570
QQLLRAQHVR GRRGRELPQV PAAPGGGGGA AARGEAAAAP REEAQE
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2023	1	701.2793	-99.62	3	53.9	11.4	0	1070-1089	R.GSLSPPLIMCTAATPMPTPK.S	Carbamidomethyl: 10; Oxidation: 9, 16

Detailed Protein Report

Protein 1399: PREDICTED: RNA-binding protein 44 isoform X1 [Homo sapiens]

Accession:	gi|530371379	**Score:**	11.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	117.5
Database Date:	2015-11-30	**pI:**	5.4
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.0
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578804309	refseq_human (refseq_human_20140103.fasta)	PREDICTED: RNA-binding protein 44 isoform X2 [Homo sapiens]

10	20	30	40	50	60	70	80
MMQATAVVET	ASGKGYHSNG	GNLQKDKPSN	PKKENLLLSS	NGCDEVKLTF	PDDDWNSSTL	EQRANNKEIS	NIDKMDLLEP
90	100	110	120	130	140	150	160
FFSVSQDTNT	ESTQFQSSEL	EDSTDYAFLN	KTYSIPYSES	KLKKESLTPL	SSELDPEVQK	KEEVFFNILE	HQDKTVGLER
170	180	190	200	210	220	230	240
IYNISDANYR	ESAEDTQKHD	TDEDSQQEYH	SAEEQEYISN	HLSFDQTKAL	DISNPEVVEL	GNSGYEVKCA	SNVEDNRVNS
250	260	270	280	290	300	310	320
GSGSIISFDS	LDVYGQEESL	HVSKFQNSVM	LREYHDLKHE	KYKEQETNSM	YHTVFDGSVL	RSNSPGNQES	QSKSGSLSPQ
330	340	350	360	370	380	390	400
KVLKMKIYTE	NMKSQINEGK	DFCGNKIVEN	KILLHLENPS	TLPQDKALET	LLQPCKDCQT	SWTSVFDDSI	ISACGYYESL
410	420	430	440	450	460	470	480
QNTADSALDF	SAMLPKIAVR	DNQAIEDNTS	LKVAHSSTTK	KTCFHNIGEM	CTKSLTDAAS	CTVTINQTVD	VSTDFRACFT
490	500	510	520	530	540	550	560
TSRATSARPS	VVSTSSNTEI	TMMNKKRPDE	WQNEKQKSVA	CSTDWSYSED	CIDTQMAITK	GSGKSLSVDS	LKPNGNFLNK
570	580	590	600	610	620	630	640
DFLELRKACG	ITDLKKHPER	EFQLFKDTEK	DLPSMCCQKI	MQRAIKAELH	LLNVHYQMCR	RHCCDIYKLV	MENRNLSSNS
650	660	670	680	690	700	710	720
AKKELGSALL	SLLGDLKVRY	VTLKEKIHKG	IPLEELPPLS	LESKLLSTFS	TFASRLMKKE	THVFSEADAE	QDNQRAHDVD
730	740	750	760	770	780	790	800
VSSNLKKTLS	QMSLSSDNSH	ATQNISPKKD	DFKNGDINAD	FSQLKLGDKD	CRHYQETSED	WSDAKESLTG	VDVSGTQGNQ
810	820	830	840	850	860	870	880
VEQDTWNLDL	TGEMKNVEPS	QRDKGYLIHV	GGLCPSVSEA	DLRSHFQKYQ	VSEISIYDST	NYRYASLAFT	KNSDAKIAVK
890	900	910	920	930	940	950	960
EMNGIEINGK	SVNVWPVKIL	GEYTSPLSSK	NGNRISSNNL	EKSTNKQIHS	EFSISRLPRT	RPRQLGSEQD	SEVFPSDQGV
970	980	990	1000	1010	1020	1030	1040
KKNCKQIESA	KLLPDTPVQF	IPPNTLNLRS	FTKIIKRLAE	LHPEVSRDHI	INALQEVRIR	HKGFLNGLSI	TTIVEMTSSL
1050							
LKNSASS							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2324	1	1131.4711	-58.20	2	57.5	11.4	0	728-748	K.TLSQMSLSSDNSHATQNISPK.K	Oxidation: 5

Detailed Protein Report

Protein 1400: E3 ubiquitin-protein ligase MIB2 isoform 5 [Homo sapiens]

Accession:	gi|282394038	**Score:**	11.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	82.1
Database Date:	2015-11-30	**pI:**	8.1
		Sequence Coverage [%]:	0.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDPDPQAGVQ	VGMRVVRGVD	WKWGQQDGGE	GGVGTVVELG	RHGSPSTPDR	TVVVQWDQGT	RTNYRAGYQG	AHDLLLYDNA
90	100	110	120	130	140	150	160
QIGVRHPNII	CDCCKKHGLR	GMRWKCRVCL	DYDLCTQCYM	HNKHELAHAF	DRYETAHSRP	VTLSPRQGLP	RIPLRGIFQG
170	180	190	200	210	220	230	240
AKVVRGPDWE	WGSQDGKPAE	LQRRVSADSQ	PFQHGDKVKC	LLDTDVLREM	QEGHGGWNPR	MAEFIGQTGT	VHRITDRGDV
250	260	270	280	290	300	310	320
RVQFNHETRW	TFHPGALTKH	HSFWVGDVVR	VIGDLDTVKR	LQAGHGEWTD	DMAPALGRVG	KVVKVFGDGN	LRVAVAGQRW
330	340	350	360	370	380	390	400
TFSPSCLVAY	RPEEDANLDV	AERARENKSS	LSVALDKLRA	QKSDPEHPGR	LVVEVALGNA	ARALDLLRRR	PEQVDTKNQG
410	420	430	440	450	460	470	480
RTALQVAAYL	GQVELIRLLL	QARAGVDLPD	DEGNTALHYA	ALGNQPEATR	VLLSAGCRAD	AINSTQSTAL	HVAVQRGFLE
490	500	510	520	530	540	550	560
VVRALCERGC	DVNLPDAHSD	TPLHSAISAG	TGASGIVEVL	TEVPNIDVTA	TNSQGFTLLH	HASLKGHALA	VRKILARARQ
570	580	590	600	610	620	630	640
LVDAKKEDGF	TALHLAALNN	HREVAQILIR	EGRCDVNVRN	RKLQSPLHLA	VQQAHVGLVP	LLVDAGCSVN	AEDEEGDTAL
650	660	670	680	690	700	710	720
HVALQRHQLL	PLVADGAGGD	PGPLQLLSRL	QASGLPGSAE	LTVGAAVACF	LALEGADVSY	TNHRGRSPLD	LAAEGRVLKA
730	740	750	760				
LQGCAQRFRV	RAQDEEVHQV	PGGRQQETAP	RRL				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1170	1	713.1709	-414.81	1	43.1	11.4	0	418-423	R.LLLQAR.A	

Detailed Protein Report

Protein 1401: nucleolar protein 11 [Homo sapiens]

Accession:	gi|21361468	**Score:**	11.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	81.1
Database Date:	2015-11-30	**pI:**	5.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.5
		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 1402: guanine nucleotide-binding protein subunit beta-5 isoform a [Homo sapiens]

Accession:	gi|5729852	**Score:**	11.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	38.7
Database Date:	2015-11-30	**pI:**	5.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MATEGLHENE	TLASLKSEAE	SLKGKLEEER	AKLHDVELHQ	VAERVEALGQ	FVMKTRRTLK	GHGNKVLCMD	WCKDKRRIVS
90	100	110	120	130	140	150	160
SSQDGKVIVW	DSFTTNKEHA	VTMPCTWVMA	CAYAPSGCAI	ACGGLDNKCS	VYPLTFDKNE	NMAAKKKSVA	MHTNYLSACS
170	180	190	200	210	220	230	240
FTNSDMQILT	ASGDGTCALW	DVESGQLLQS	FHGHGADVLC	LDLAPSETGN	TFVSGGCDKK	AMVWDMRSGQ	CVQAFETHES
250	260	270	280	290	300	310	320
DINSVRYYPS	GDAFASGSDD	ATCRLYDLRA	DREVAIYSKE	SIIFGASSVD	FSLSGRLLFA	GYNDYTINVW	DVLKGSRVSI
330	340	350	360				
LFGHENRVST	LRVSPDGTAF	CSGSWDHTLR	VWA				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2176	1	994.3487	-118.16	2	55.8	11.4	1	129-145	K.CSVYPLTFDKNENMAAK.K	Carbamidomethyl: 1

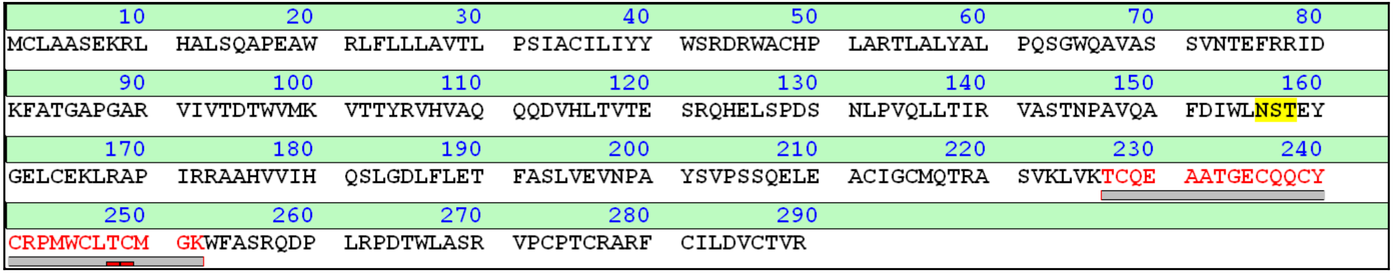
Detailed Protein Report

Protein 1403: 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 1404: PREDICTED: interferon regulatory factor 2 isoform X2 [Homo sapiens]

Accession:	gi|530377663	**Score:**	11.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	39.1
Database Date:	2015-11-30	**pI:**	7.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.9
		No. of unique Peptides:	1

Quantitation

mdown:qdown **Median:** 0.08 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MPVERMRMRP	WLEEQINSNT	IPGLKWLNKE	KKIFQIPWMH	AARHGWDVEK	DAPLFRNWAI	HTGKHQPGVD	KPDPKTWKAN
90	100	110	120	130	140	150	160
FRCAMNSLPD	IEEVKDKSIK	KGNNAFRVYR	MLPLSERPSK	KGKKPKTEKE	DKVKHIKQEP	VESSLGLSNG	VSDLSPEYAV
170	180	190	200	210	220	230	240
LTSTIKNEVD	STVNIIGQSH	LDSNIENQEI	VTNPPDICQV	VEVTTESDEQ	PVSMSELYPL	QISPVSSYAE	SETTDSVPSD
250	260	270	280	290	300	310	320
EESAEGRPHW	RKRNIEGKQY	LSNMGTRGSY	LLPGMASFVT	SNKPDLQVTI	KEESNPVPYN	SSWPPFQDLP	LSSSMTPASS
330	340	350					
SSRPDRETRA	SVIKKTSDIT	QARVKSC					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
513	1	587.1711	-250.83	2	35.0	11.4	0	111-120	R.MLPLSERPSK.K	Oxidation: 1	mdown:qdown 0.08

Detailed Protein Report

Protein 1405: paired box protein Pax-8 isoform PAX8E [Homo sapiens]

Accession:	gi|7669542	**Score:**	11.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	31.0
Database Date:	2015-11-30	**pI:**	9.8
		Sequence Coverage [%]:	6.3
		No. of unique Peptides:	1

Quantitation

Wdown:Qdown **Median:** 0.13 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MPHNSIRSGH GGLNQLGGAF VNGRPLPEVV RQRIVDLAHQ GVRPCDISRQ LRVSHGCVSK ILGRYYETGS IRPGVIGGSK
        90        100        110        120        130        140        150        160
PKVATPKVVE KIGDYKRQNP TMFAWEIRDR LLAEGVCDND TVPSVSSINR IIRTKVQQPF NLPMDSCVAT KSLSPGHTLI
       170        180        190        200        210        220        230        240
PSSAVTPPES PQSDSLGSTY SINGLLGIAQ PGSDKRKMDD SDQDSCRLSI DSQSSSSGPR KHLRTDAFSQ HHLEPLECPF
       250        260        270        280        290
ERQHYPEAYA SPSHTKGEQE VNTLAMPMAT PPTPPTARPG ASPTPAC
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1475	1	954.9298	-86.64	2	47.0	11.4	0	65-82	R.YYETGSIRPGVIGGSKPK.V		Wdown:Qdown 0.13

Detailed Protein Report

Protein 1406: PREDICTED: formin-like protein 1 isoform X8 [Homo sapiens]

Accession:	gi|578831370	**Score:**	11.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	119.1
Database Date:	2015-11-30	**pI:**	5.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGNAAGSAEQ	PAGPAAPPPK	QPAPPKQPMP	AAGELEERFN	RALNCMNLPP	DKVQLLSQYD	NEKKWELICD	QERFQVKNPP
90	100	110	120	130	140	150	160
AAYIQKLKSY	VDTGGVSRKV	AADWMSNLGF	KRRVQESTQV	LRELETSLRT	NHIGWVQEFL	NEENRGLDVL	LEYLAFAQCS
170	180	190	200	210	220	230	240
VTYDMESTDN	GASNSEKNKP	LEQSVEDLSK	GPPSSVPKSR	HLTIKCPPSP	RLTPAHSRKA	LRNSRIVSQK	DDVHVCIMCL
250	260	270	280	290	300	310	320
RAIMNYQSGF	SLVMNHPACV	NEIALSLNNK	NPRTKALVLE	LLAAVCLVRG	GHDIILAAFD	NFKEVCGEQH	RFEKLMEYFR
330	340	350	360	370	380	390	400
NEDSNIDFMV	ACMQFINIVV	HSVENMNFRV	FLQYEFTHLG	LDLYLERLRL	TESDKLQVQI	QAYLDNIFDV	GALLEDTETK
410	420	430	440	450	460	470	480
NAVLEHMEEL	QEQVALLTER	LRDAENESMA	KIAELEKQLS	QARKELETLR	ERFSESTAMG	PSRRPPEPEK	APPAAPTRPS
490	500	510	520	530	540	550	560
ALELKVEELE	EKGLIRILRG	PGDAVSIEIL	PVAVATPSGG	DAPTPGVPTG	SPSPDLAPAA	EPAPGAAPPP	PPPLPGLPSP
570	580	590	600	610	620	630	640
QEAPPSAPPQ	APPLPGSPEP	PPAPPLPGDL	PPPPPPPPPP	PGTDGPVPPP	PPPPPPPPGG	PPDALGRRDS	ELGPGVKAKK
650	660	670	680	690	700	710	720
PIQTKFRMPL	LNWVALKPSQ	ITGTVFTELN	DEKVLQELDM	SDFEEQFKTK	SQGPSLDLSA	LKSKAAQKAP	SKATLIEANR
730	740	750	760	770	780	790	800
AKNLAITLRK	GNLGAERICQ	AIEAYDLQAL	GLDFLELLMR	FLPTEYERSL	ITRFEREQRP	MEELSEEDRF	MLCFSRIPRL
810	820	830	840	850	860	870	880
PERMTTLTFL	GNFPDTAQLL	MPQLNAIIAA	SMSIKSSDKL	RQILEIVLAF	GNYMNSSKRG	AAYGFRLQSL	DALLEMKSTD
890	900	910	920	930	940	950	960
RKQTLLHYLV	KVIAEKYPQL	TGFHSDLHFL	DKAGSVSLDS	VLADVRSLQR	GLELTQREFV	RQDDCMVLKE	FLRANSPTMD
970	980	990	1000	1010	1020	1030	1040
KLLADSKTAQ	KAEQEVEQWK	KEAAAQEAGA	DTPGKGEPPA	PKSPPKARRP	QMDLISELKR	RQQKEPLIYE	SDRDGAIEDI
1050	1060	1070	1080				
ITDLRNQPYI	RADTGRRSAR	RRPPGPPLQV	TSDLSL				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2052	1	937.3073	-130.77	2	54.2	11.4	0	674-688	K.VLQELDMSDFEEQFK.T	Oxidation: 7

Detailed Protein Report

Protein 1407: PREDICTED: transcription factor E2F3 isoform X4 [Homo sapiens]

Accession:	gi|530381501	**Score:**	11.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	24.6
Database Date:	2015-11-30	**pI:**	4.1
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	8.9
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MGCSLSEDGG MLAQCQGLSK EVTELSQEEK KLDELIQSCT LDLKLLTEDS ENQRLAYVTY QDIRKISGLK DQTVIVVKAP
        90        100        110        120        130        140        150        160
PETRLEVPDS IESLQIHLAS TQGPIEVYLC PEETETHSPM KTNNQDHNGN IPKPASKDLA STNSGHSDCS VSMGNLSPLA
       170        180        190        200        210        220        230
SPANLLQQTE DQIPSNLEGP FVNLLPPLLQ EDYLLSLGEE EGISDLFDAY DLEKLPLVED FMCS
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1607	1	715.6762	49.39	3	48.8	11.4	0	1-20	-.MGCSLSEDGGMLAQCQGLSK.E	Carbamidomethyl: 3, 15; Oxidation: 11

Detailed Protein Report

Protein 1408: 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 1409: PREDICTED: spindle and kinetochore-associated protein 3 isoform X1 [Homo sapiens]

Accession:	gi|530402160	**Score:**	11.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	36.9
Database Date:	2015-11-30	**pI:**	5.0
		Sequence Coverage [%]:	4.8
		No. of unique Peptides:	1

Quantitation

Wdown:Qdown **Median:** 28.15 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MEKNSMDIMK	IREYFQKYGY	SPRVKKNSVH	EQEAINSDPE	LSNCENFQKT	DVKDDLSDPP	VASSCISEKS	PRSPQLSDFG
90	100	110	120	130	140	150	160
LERYIVSQVL	PNPPQAVNNY	KEEPVIVTPP	TKQSLVKVLK	TPKCALKMDD	FECVTPKLEH	FGISEYTMCL	NEDYTMGLKN
170	180	190	200	210	220	230	240
ARNNKSEEAI	DTESRLNDNV	FATPSPIIQQ	LEKSDAEYTN	SPLVPTFCTP	GLKIPSTKNS	IALVSTNYPL	SKTNSSSNDL
250	260	270	280	290	300	310	320
EVEDRTSLVL	NSDTCFENLT	DPSSPTISSY	ENLLRTPTPP	EVTKIPEDIL	QLLSKYNSNL	ATPIAIKAVP	PSKRFLKHGQ
330	340						
NIRDVSNKEN							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1765	1	917.4139	-26.15	2	50.6	11.4	2	160-175	K.NARNNKSEEAIDTESR.L		Wdown:Qdown 28.15

Detailed Protein Report

Protein 1410: ataxin-7-like protein 2 [Homo sapiens]

Accession: gi|93277115
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 11.4
MW [kDa]: 77.1
pI: 10.5
Sequence Coverage [%]: 1.2
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MAVRERAAAA	MAALERRVPS	LDDFAGQSWS	SWVERADLPA	ADGAELEESS	KNTKKLDAMT	LIKEDMSIFG	HCPAHDDFYL
90	100	110	120	130	140	150	160
VVCNHCSQVV	KPQAFQKHCE	RRHGPLSKLY	GRAPPPPPAP	ASSQKCHVVN	GQGPACRAPG	STKTSSREKG	QGSRSRGHQP
170	180	190	200	210	220	230	240
PEKTQKDNLC	QPGGLTKDSP	GKPPMAPPSK	EPPGRENIEI	IPSEGSSHWA	EGSPPEKEPS	GTRLPPKTHR	KMARKECDLN
250	260	270	280	290	300	310	320
RQCGVINPET	KKICTRLLTC	KIHSVHQRRE	VQGRAKDFDV	LVAELKANSR	KGESPKEKSP	GRKEQVLERP	SQELPSSVQV
330	340	350	360	370	380	390	400
VAAVAAPSST	FSVRAKQTYP	YCALPRSRAS	SESELDDEGP	CGGDGDPGLF	PFPMPRGGTQ	ASSEESEEEG	TSDDLHPPPD
410	420	430	440	450	460	470	480
CHYATRPPRP	QAFCTFGSRL	VSPGCYVFSR	RLDRFCSALS	SMLERHLSTH	MWKKIPPAAE	PPAHLVNSPL	SAPLSPSSTG
490	500	510	520	530	540	550	560
TCPRLPGPTL	RPACPASMPP	TKDNLVPSYP	AGSPSVAAAC	SQAECMGGSQ	AITSPLPANT	PSPSFSKLPP	SKASKSSKGK
570	580	590	600	610	620	630	640
DGVEVEAPSR	KRKLSPGPTT	LKRTCILEPT	GKGKPSGCRG	LSAKTKTALS	MGLNGTMGPR	VKRAGPLDCR	GSPHQLPTPV
650	660	670	680	690	700	710	720
KASQLENRGA	AGHPAKALPT	NCLSEEEVAK	KRKNLATYCR	PVKAKHCQAG	APADVACSVR	RKKPGPALAF	EEKCSTLKSK
730							
AH							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
796	2	509.7026	-123.40	2	38.5	11.4	0	584-592	R.TCILEPTGK.G	Carbamidomethyl: 2

Detailed Protein Report

Protein 1411: 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

Quantitation

mdown:qdown	**Median:**	1.82	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	1.02	**CV:**	0.00 %	**No. of 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	Ratios
1627	1	698.3584	-25.47	2	50.2	11.4	1	372-383	K.SRELNNVHTAVR.S		Wdown:Qdown 1.02 mdown:qdown 1.82

Detailed Protein Report

Protein 1412: 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 1413: 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

Quantitation

mdown:qdown	**Median:**	0.46	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	7.90	**CV:**	0.00 %	**No. of 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	Ratios
758	1	647.6599	-226.81	2	38.8	11.4	0	820-830	K.AAMCKPLMQNR.G	Oxidation: 3, 8	Wdown:Qdown 7.90 mdown:qdown 0.46

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Detailed Protein Report

Protein 1414: prostaglandin E2 receptor EP2 subtype [Homo sapiens]

Accession:	gi|31881630	**Score:**	11.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	39.7
Database Date:	2015-11-30	**pI:**	10.7
		Sequence Coverage [%]:	4.7
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MGNASNDSQS EDCETRQWLP PGESPAISSV MFSAGVLGNL IALALLARRW RGDVGCSAGR RSSLSLFHVL VTELVFTDLL
        90        100        110        120        130        140        150        160
GTCLISPVVL ASYARNQTLV ALAPESRACT YFAFAMTFFS LATMLMLFAM ALERYLSIGH PYFYQRRVSR SGGLAVLPVI
       170        180        190        200        210        220        230        240
YAVSLLFCSL PLLDYGQYVQ YCPGTWCFIR HGRTAYLQLY ATLLLLLIVS VLACNFSVIL NLIRMHRRSR RSRCGPSLGS
       250        260        270        280        290        300        310        320
GRGGPGARRR GERVSMAEET DHLILLAIMT ITFAVCSLPF TIFAYMNETS SRKEKWDLQA LRFLSINSII DPWVFAILRP
       330        340        350        360
PVLRLMRSVL CCRISLRTQD ATQTSCSTQS DASKQADL
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
183	1	879.8364	-45.02	2	31.5	11.3	0	338-354	R.TQDATQTSCSTQSDASK.Q	

Detailed Protein Report

Protein 1415: repressor of RNA polymerase III transcription MAF1 homolog [Homo sapiens]

Accession:	gi|110349740	**Score:**	11.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	28.8
Database Date:	2015-11-30	**pI:**	4.3
Modification(s):	Oxidation	**Sequence Coverage [%]:**	5.1
		No. of unique Peptides:	1

Quantitation

Wdown:Qdown **Median:** 0.74 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MKLLENSSFE AINSQLTVET GDAHIIGRIE SYSCKMAGDD KHMFKQFCQE GQPHVLEALS PPQTSGLSPS RLSKSQGGEE
        90        100        110        120        130        140        150        160
EGPLSDKCSR KTLFYLIATL NESFRPDYDF STARSHEFSR EPSLSWVVNA VNCSLFSAVR EDFKDLKPQL WNAVDEEICL
       170        180        190        200        210        220        230        240
AECDIYSYNP DLDSDPFGED GSLWSFNYFF YNKRLKRIVF FSCRSISGST YTPSEAGNEL DMELGEEEVE EESRSGGSGA
       250        260
EETSTMEEDR VPVICI
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
418	1	731.6703	-195.14	2	33.9	11.3	1	29-41	R.IESYSCKMAGDDK.H	Oxidation: 8	Wdown:Qdown 0.74

Detailed Protein Report

Protein 1416: regulator of G-protein signaling 9-binding protein [Homo sapiens]

Accession:	gi|115496700	**Score:**	11.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	25.1
Database Date:	2015-11-30	**pI:**	7.8
		Sequence Coverage [%]:	8.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAREECKALL	DGLNKTTACY	HHLVLTVGGS	ADSQNLRQEL	QKTRQKAQEL	AVSTCARLTA	VLRDRGLAAD	ERAEFERLWV
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
AFSGCLDLLE	ADMRRALELG	AAFPLHAPRR	PLVRTGVAGA	SSGVAARALS	TRSLRLEAEG	DFDVADLREL	EREVLQVGEM
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
IDNMEMKVNV	PRWTVQARQA	AGAELLSTVS	AGPSSVVSLQ	ERGGGCDPRK	ALAAILFGAV	LLAAVALAVC	VAKLS

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2371	1	994.7007	148.11	2	58.0	11.3	2	115-135	R.TGVAGASSGVAARALSTRSLR.L	

Detailed Protein Report

Protein 1417: 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 1418: eukaryotic peptide chain release factor subunit 1 isoform 3 [Homo sapiens]

Accession:	gi|532164728	**Score:**	11.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	47.4
Database Date:	2015-11-30	**pI:**	5.3
Modification(s):	Oxidation	**Sequence Coverage [%]:**	6.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MKQDVLNCTE	GPIHSNGTSM	ISLIIPPKDQ	ISRVAKMLAD	EFGTASNIKS	RVNRLSVLGA	ITSVQQRLKL	YNKVPPNGLV
90	100	110	120	130	140	150	160
VYCGTIVTEE	GKEKKVNIDF	EPFKPINTSL	YLCDNKFHTE	ALTALLSDDS	KFGFIVIDGS	GALFGTLQGN	TREVLHKFTV
170	180	190	200	210	220	230	240
DLPKKHGRGG	QSALRFARLR	MEKRHNYVRK	VAETAVQLFI	SGDKVNVAGL	VLAGSADFKT	ELSQSDMFDQ	RLQSKVLKLV
250	260	270	280	290	300	310	320
DISYGGENGF	NQAIELSTEV	LSNVKFIQEK	KLIGRYFDEI	SQDTGKYCFG	VEDTLKALEM	GAVEILIVYE	NLDIMRYVLH
330	340	350	360	370	380	390	400
CQGTEEEKIL	YLTPEQEKDK	SHFTDKETGQ	EHELIESMPL	LEWFANNYKK	FGATLEIVTD	KSQEGSQFVK	GFGGIGGILR
410	420	430					
YRVDFQGMEY	QGGDDEFFDL	DDY					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1675	1	927.3870	-89.60	3	49.6	11.3	0	3-28	K.QDVLNCTEGPIHSNGTSMISLIIPPK.D	Oxidation: 18

Detailed Protein Report

Protein 1419: probable G-protein coupled receptor 150 [Homo sapiens]

Accession:	gi|40385873	**Score:**	11.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	46.3
Database Date:	2015-11-30	**pI:**	11.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEDLFSPSIL	PPAPNISVPI	LLGWGLNLTL	GQGAPASGPP	SRRVRLVFLG	VILVVAVAGN	TTVLCRLCGG	GGPWAGPKRR
90	100	110	120	130	140	150	160
KMDFLLVQLA	LADLYACGGT	ALSQLAWELL	GEPRAATGDL	ACRFLQLLQA	SGRGASAHLV	VLIALERRRA	VRLPHGRPLP
170	180	190	200	210	220	230	240
ARALAALGWL	LALLLALPPA	FVVRGDSPSP	LPPPPPPTSL	QPGAPPAARA	WPGERRCHGI	FAPLPRWHLQ	VYAFYEAVAG
250	260	270	280	290	300	310	320
FVAPVTVLGV	ACGHLLSVWW	RHRPQAPAAA	APWSASPGRA	PAPSALPRAK	VQSLKMSLLL	ALLFVGCELP	YFAARLAAAW
330	340	350	360	370	380	390	400
SSGPAGDWEG	EGLSAALRVV	AMANSALNPF	VYLFFQAGDC	RLRRQLRKRL	GSLCCAPQGG	AEDEEGPRGH	QALYRQRWPH
410	420	430	440				
PHYHHARREP	LDEGGLRPPP	PRPRPLPCSC	ESAF				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2711	1	973.5265	106.80	2	62.8	11.3	0	370-388	R.LGSLCCAPQGGAEDEEGPR.G	Carbamidomethyl: 6

Detailed Protein Report

Protein 1420: heterogeneous nuclear ribonucleoprotein L isoform a [Homo sapiens]

Accession: gi|52632383
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 11.3
MW [kDa]: 64.1
pI: 9.2
Sequence Coverage [%]: 3.7
No. of unique Peptides: 1

Quantitation

mdown:qdown **Median:** 1.52 **CV:** 0.00 % **No. of Peptides:** 1
Wdown:Qdown **Median:** 0.46 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MSRRLLPRAE	KRRRRLEQRQ	QPDEQRRRSG	AMVKMAAAGG	GGGGGRYYGG	GSEGGRAPKR	LKTDNAGDQH	GGGGGGGGGA
90	100	110	120	130	140	150	160
GAAGGGGGGE	NYDDPHKTPA	SPVVHIRGLI	DGVVEADLVE	ALQEFGPISY	VVVMPKKRQA	LVEFEDVLGA	CNAVNYAADN
170	180	190	200	210	220	230	240
QIYIAGHPAF	VNYSTSQKIS	RPGDSDDSRS	VNSVLLFTIL	NPIYSITTDV	LYTICNPCGP	VQRIVIFRKN	GVQAMVEFDS
250	260	270	280	290	300	310	320
VQSAQRAKAS	LNGADIYSGC	CTLKIEYAKP	TRLNVFKNDQ	DTWDYTNPNL	SGQGDPGSNP	NKRQRQPPLL	GDHPAEYGGP
330	340	350	360	370	380	390	400
HGGYHSHYHD	EGYGPPPPHY	EGRRMGPPVG	GHRRGPSRYG	PQYGHPPPPP	PPPEYGPHAD	SPVLMVYGLD	QSKMNCDRVF
410	420	430	440	450	460	470	480
NVFCLYGNVE	KVKFMKSKPG	AAMVEMADGY	AVDRAITHLN	NNFMFGQKLN	VCVSKQPAIM	PGQSYGLEDG	SCSYKDFSES
490	500	510	520	530	540	550	560
RNNRFSTPEQ	AAKNRIQHPS	NVLHFFNAPL	EVTEENFFEI	CDELGVKRPS	SVKVFSGKSE	RSSSGLLEWE	SKSDALETLG
570	580	590					
FLNHYQMKNP	NGPYPYTLKL	CFSTAQHAS					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2243	1	951.4429	25.12	2	56.7	11.3	1	35-56	K. MAAAGGGGGGGRYYGGGSEGG A		Wdown:Qdown 0.46 mdown:qdown 1.52

Detailed Protein Report

Protein 1421: PREDICTED: tudor domain-containing protein 1 isoform X3 [Homo sapiens]

Accession:	gi|578819639	**Score:**	11.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	123.7
Database Date:	2015-11-30	**pI:**	5.8
		Sequence Coverage [%]:	1.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSVKSPFNVM	SRNNLEAPPC	KMTEPFNFEK	NENKLPPHES	LRSPGTLPNH	PNFRLKSSEN	GNKKNNFLLC	EQTKQYLASQ
90	100	110	120	130	140	150	160
EDNSVSSNPN	GINGEVVGSK	GDRKKLPAGN	SVSPPSAESN	SPPKEVNIKP	GNNVRPAKSK	KLNKLVENSL	SISNPGLFTS
170	180	190	200	210	220	230	240
LGPPLRSTTC	HRCGLFGSLR	CSQCKQTYYC	STACQRRDWS	AHSIVCRPVQ	PNFHKLENKS	SIETKDVEVN	NKSDCPLGVT
250	260	270	280	290	300	310	320
KEIAIWAERI	MFSDLRSLQL	KKTMEIKGTV	TEFKHPGDFY	VQLYSSEVLE	YMNQLSASLK	ETYANVHEKD	YIPVKGEVCI
330	340	350	360	370	380	390	400
AKYTVDQTWN	RAIIQNVDVQ	QKKAHVLYID	YGNEEIIPLN	RIYHLNRNID	LFPPCAIKCF	VANVIPAEGN	WSSDCIKATK
410	420	430	440	450	460	470	480
PLLMEQYCSI	KIVDILEEEV	VTFAVEVELP	NSGKLLDHVL	IEMGYGLKPS	GQDSKKENAD	QSDPEDVGKM	TTENNIVVDK
490	500	510	520	530	540	550	560
SDLIPKVLTL	NVGDEFCGVV	AHIQTPEDFF	CQQLQSGRKL	AELQASLSKY	CDQLPPRSDF	YPAIGDICCA	QFSEDDQWYR
570	580	590	600	610	620	630	640
ASVLAYASEE	SVLVGYVDYG	NFEILSLMRL	CPIIPKLLEL	PMQAIKCVLA	GVKPSLGIWT	PEAICLMKKL	VQNKIITVKV
650	660	670	680	690	700	710	720
VDKLENSSLV	ELIDKSETPH	VSVSKVLLDA	GFAVGEQSMV	TDKPSDVKET	SVPLGVEGKV	NPLEWTWVEL	GVDQTVDVVV
730	740	750	760	770	780	790	800
CVIYSPGEFY	CHVLKEDALK	KLNDLNKSLA	EHCQQKLPNG	FKAEIGQPCC	AFFAGDGSWY	RALVKEILPN	GHVKVHFVDY
810	820	830	840	850	860	870	880
GNIEEVTADE	LRMISSTFLN	LPFQGIRCQL	ADIQSRNKHW	SEEAITRFQM	CVAGIKLQAR	VVEVTENGIG	VELTDLSTCY
890	900	910	920	930	940	950	960
PRIISDVLID	EHLVLKSASP	HKDLPNDRLV	NKHELQVHVQ	GLQATSSAEQ	WKTIELPVDK	TIQANVLEII	SPNLFYALPK
970	980	990	1000	1010	1020	1030	1040
GMPENQEKLC	MLTAELLEYC	NAPKSRPPYR	PRIGDACCAK	YTSDDFWYRA	VVLGTSDTDV	EVLYADYGNI	ETLPLCRVQP
1050	1060	1070	1080	1090	1100	1110	
ITSSHLALPF	QIIRCSLEEK	MYRMNCCCTE	LQKQVEKHEH	ILLFLLNNST	NQNKFIEMKK	LLKS	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2870	1	795.7257	-4.35	3	64.6	11.3	2	828-847	R.CQLADIQSRNKHWSEEAITR.F	

Detailed Protein Report

Protein 1422: APC membrane recruitment protein 1 [Homo sapiens]

Accession: gi|124244056

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Score: 11.3

MW [kDa]: 124.0

pI: 4.6

Sequence Coverage [%]: 1.4

No. of unique Peptides: 1

10	20	30	40	50	60	70	80
METQKDEAAQ	AKGAAASGST	REQTAEKGAK	NKAAEATEGP	TSEPSSSGPG	RLKKTAMKLF	GGKKGICTLP	SFFGGGRSKG
90	100	110	120	130	140	150	160
SGKGSSKKGL	SKSKTHDGLS	EAAHGPEDVV	SEGTGFSLPL	PELPCQFPSS	QSAHGALETG	SRCKTSVAGA	TEKAVAEKFP
170	180	190	200	210	220	230	240
SMPKPKKGLK	GFFSSIRRHR	KSKVTGAEQS	EPGAKGPERV	RARPHEHVSS	APQVPCFEET	FQAPRKENAN	PQDAPGPKVS
250	260	270	280	290	300	310	320
PTPEPSPPAT	EKMACKDPEK	PMEACASAHV	QPKPAPEASS	LEEPHSPETG	EKVVAGEVNP	PNGPVGDPLS	LLFGDVTSLK
330	340	350	360	370	380	390	400
SFDSLTGCGD	IIAEQDMDSM	TDSMASGGQR	ANRDGTKRSS	CLVTYQGGGE	EMALPDDDDE	EEEEEEEVEL	EEEEEEVKEE
410	420	430	440	450	460	470	480
EEDDDLEYLW	ETAQMYPRPN	MNLGYHPTTS	PGHHGYMLLD	PVRSYPGLAP	GELLTPQSDQ	QESAPNSDEG	YYDSTTPGFE
490	500	510	520	530	540	550	560
DDSGEALGLV	RRDCLPRDSY	SGDALYEFYE	PDDSLENSPP	GDDCLYDLHG	RSSEMFDPFL	NFEPFLSSRP	PGAMETEEER
570	580	590	600	610	620	630	640
LVTIQKQLLY	WELRREQLEA	QEARAREAHA	REAHAREAYT	REAYGREAYA	REAHTWEAHG	REARTREAQA	REVRCRETQV
650	660	670	680	690	700	710	720
RETQARQEKP	VLEYQMRPLG	PSVMGLAAGV	SGTSQISHRG	ITSAFPTTAS	SEPDWRDFRP	LEKRYEGTCS	KKDQSTCLMQ
730	740	750	760	770	780	790	800
LFQSDAMFEP	DMQEANFGGS	PRRAYPTYSP	PEDPEEEEVE	KEGNATVSFS	QALVEFTSNG	NLFSSMSCSS	DSDSSFTQNL
810	820	830	840	850	860	870	880
PELPPMVTFD	IADVERDGEG	KCEENPEFHN	DEDLAASLEA	FELGYYHKHA	FNNYHSRFYQ	GLPWGVSSLP	RYLGLPGLHP
890	900	910	920	930	940	950	960
RPPPAAMALN	RRSRSLDTAE	TLEMELSNSH	LVQGYLESDE	LQAQQEDSDE	EDEEEEEGEW	SRDSPLSLYT	EPPGAYDWPA
970	980	990	1000	1010	1020	1030	1040
WAPCPLPVGP	GPAWISPNQL	DRPSSQSPYR	QATCCIPPMT	MSISLSVPES	RAPGESGPQL	ARPSHLHLPM	GPCYNLQPQA
1050	1060	1070	1080	1090	1100	1110	1120
SQSMRARPRD	VLLPVDEPSC	SSSSGGFSPS	PLPQAKPVGI	THGIPQLPRV	RPEHPQPQPT	HYGPSSLDLS	KERAEQGASL
1130	1140						
ATSYSSTAMN	GNLAK						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
50	1	796.8030	-145.92	2	29.8	11.3	2	143-158	R.CKTSVAGATEKAVAEK.F	

Protein 1423: zinc finger RNA-binding protein [Homo sapiens]

Accession:	gi|34101286	**Score:**	11.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	116.9
Database Date:	2015-11-30	**pI:**	9.8
		Sequence Coverage [%]:	1.4
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	0.95	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	1.95	**CV:**	0.00 %	**No. of Peptides:**	1

10	20	30	40	50	60	70	80
MIPICPVVSF	TYVPSRLGED	AKMATGNYFG	FTHSGAAAAA	AAAQYSQQPA	SGVAYSHPTT	VASYTVHQAP	VAAHTVTAAY
90	100	110	120	130	140	150	160
APAAATVAVA	RPAPVAVAAA	ATAAAYGGYP	TAHTATDYGY	TQRQQEAPPP	PPPATTQNYQ	DSYSYVRSTA	PAVAYDSKQY
170	180	190	200	210	220	230	240
YQQPTATAAA	VAAAAQPQPS	VAETYYQTAP	KAGYSQGATQ	YTQAQQTRQV	TAIKPATPSP	ATTTFSIYPV	SSTVQPVAAA
250	260	270	280	290	300	310	320
ATVVPSYTQS	ATYSTTAVTY	SGTSYSGYEA	AVYSAASSYY	QQQQQQQKQA	AAAAAAAAAT	AAWTGTTFTK	KAPFQNKQLK
330	340	350	360	370	380	390	400
PKQPPKPPQI	HYCDVCKISC	AGPQTYKEHL	EGQKHKKKEA	ALKASQNTSS	SNSSTRGTQN	QLRCELCDVS	CTGADAYAAH
410	420	430	440	450	460	470	480
IRGAKHQKVV	KLHTKLGKPI	PSTEPNVVSQ	ATSSTAVSAS	KPTASPSSIA	ANNCTVNTSS	VATSSMKGLT	TTGNSSLNST
490	500	510	520	530	540	550	560
SNTKVSAVPT	NMAAKKTSTP	KINFVGGNKL	QSTGNKAEDI	KGTECVKSTP	VTSAVQIPEV	KQDTVSEPVT	PASLAALQSD
570	580	590	600	610	620	630	640
VQPVGHDYVE	EVRNDEGKVI	RFHCKLCECS	FNDPNAKEMH	LKGRRHRLQY	KKKVNPDLQV	EVKPSIRARK	IQEEKMRKQM
650	660	670	680	690	700	710	720
QKEEYWRRRE	EEERWRMEMR	RYEEDMYWRR	MEEEQHHWDD	RRRMPDGGYP	HGPPGPLGLL	GVRPGMPPQP	QGPAPLRRPD
730	740	750	760	770	780	790	800
SSDDRYVMTK	HATIYPTEEE	LQAVQKIVSI	TERALKLVSD	SLSEHEKNKN	KEGDDKKEGG	KDRALKGVLR	VGVLAKGLLL
810	820	830	840	850	860	870	880
RGDRNVNLVL	LCSEKPSKTL	LSRIAENLPK	QLAVISPEKY	DIKCAVSEAA	IILNSCVEPK	MQVTITLTSP	IIREENMREG
890	900	910	920	930	940	950	960
DVTSGMVKDP	PDVLDRQKCL	DALAALRHAK	WFQARANGLQ	SCVIIIRILR	DLCQRVPTWS	DFPSWAMELL	VEKAISSASS
970	980	990	1000	1010	1020	1030	1040
PQSPGDALRR	VFECISSGII	LKGSPGLLDP	CEKDPFDTLA	TMTDQQREDI	TSSAQFALRL	LAFRQIHKVL	GMDPLPQMSQ
1050	1060	1070	1080				
RFNIHNNRKR	RRDSDGVDGF	EAEGKKDKKD	YDNF				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1045	1	839.3856	-82.99	2	41.6	11.3	0	2-16	M.IPICPVVSFTYVPSR.L		Wdown:Qdown 1.95 mdown:qdown 0.95

Detailed Protein Report

Protein 1424: RNA-binding protein 33 [Homo sapiens]

Accession:	gi|151301053	**Score:**	11.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	129.9
Database Date:	2015-11-30	**pI:**	6.5
		Sequence Coverage [%]:	1.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAAALGASGG	AGAGDDDFDQ	FDKPGAERSW	RRRAADEDWD	SELEDDLLGE	DLLSGKKNQS	DLSDEELNDD	LLQSDNEDEE
90	100	110	120	130	140	150	160
NFSSQGVTIS	LNATSGMVTS	FELSDNTNDQ	SGEQESEYEQ	EQGEDELVYH	KSDGSELYTQ	EYPEEGQYEG	HEAELTEDQI
170	180	190	200	210	220	230	240
EYVEEPEEEQ	LYTDEVLDIE	INEPLDEFTG	GMETLELQKD	IKEESDEEEE	DDEESGRLRF	KTERKEGTII	RLSDVTRERR
250	260	270	280	290	300	310	320
NIPETLELSA	EAKAALLEFE	ERERQHKQGR	YSSRRGGRRG	GPLMCRGVGD	QRRESTERGR	MKDHRPALLP	TQPPVVPQAP
330	340	350	360	370	380	390	400
PPPPPPPQQQ	PIRSLFQPQP	LQPLLPVQHP	HHPSPPQGMH	MPPQLETPRM	MMTPPPVTPQ	QPKNIHINPH	FKGTVVTPVQ
410	420	430	440	450	460	470	480
VPLLPVPSQP	RPAVGPQRFP	GPPEFPQHTP	GPVPNSFSQP	PRLPLQDQWR	APPPPQDRDP	FFLGVSGEPR	FPSHLFLEQR
490	500	510	520	530	540	550	560
SPPPPPPPPT	LLNSSHPVPT	QSPLPFTQPG	PAFNQQGQQP	VFPRERPVRP	ALQPPGPVGI	LHFSQPGSAT	TRPFIPPRQP
570	580	590	600	610	620	630	640
FLPGPGQPFL	PTHTQPNLQG	PLHPPLPPPH	QPQPQQPQQQ	PPPQHQPPHQ	PPHQPPPQHQ	PPPQHPPQHP	PQHQHHHHHH
650	660	670	680	690	700	710	720
HLSVPPPPLM	PMSQPQFRPH	VQTAQPQASS	SRMQCPQRQG	LRHNTTSQNV	SKRPMQQMQP	TAPRNSNLRE	LPIAPSHVIE
730	740	750	760	770	780	790	800
MSSSRCSATP	SAQVKPIVSA	SPPSRAVAGS	RSSQGKTEVK	VKPASPVAQP	KEEAKTETEF	PDEDEETRLY	RLKIEEQKRL
810	820	830	840	850	860	870	880
REEILKQKEL	RRQQQAGARK	KELLERLAQQ	QQQLYAPPPP	AEQEEQALSP	SPTNGNPLLP	FPGAQVRQNV	KNRLLVKNQD
890	900	910	920	930	940	950	960
VSISNVQPKT	SNFVPSSANM	QYQGQQMKAL	KHLRQTRTVP	QSQTQPLHKV	LPIKPADVEE	PAVPQTPRVA	SIQGRPQDTK
970	980	990	1000	1010	1020	1030	1040
PGVKRTVTHR	TNSGGGDGPH	ISSKVRVIKL	SGGGGESDGF	FHPEGQPQRL	PQPPEVGPQP	ARKVTLTRGG	LQQPPHLPAG
1050	1060	1070	1080	1090	1100	1110	1120
PHAHSPVPPG	IKSIQGIHPA	KKAIMHGRGR	GVAGPMGRGR	LMPNKQNLRV	VECKPQPCVV	SVEGLSSSTT	DAQLKSLLMS
1130	1140	1150	1160	1170	1180		
VGPIQSLQML	PQQRKAIAKF	KEPAHALAFQ	QKFHRHMIDL	SHINVALIVE			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2699	1	928.6057	116.79	2	62.1	11.3	2	238-253	R.ERRNIPETLELSAEAK.A	

Detailed Protein Report

Protein 1425: 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 1426: cullin-4A isoform 2 [Homo sapiens]

Accession:	gi|11140811	**Score:**	11.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	76.8
Database Date:	2015-11-30	**pI:**	6.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.8
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|511772961	refseq_human (refseq_human_20140103.fasta)	cullin-4A isoform 2 [Homo sapiens]

10	20	30	40	50	60	70	80
MLYKQLRQAC	EDHVQAQILP	FREDSLDSVL	FLKKINTCWQ	DHCRQMIMIR	SIFLFLDRTY	VLQNSTLPSI	WDMGLELFRT
90	100	110	120	130	140	150	160
HIISDKMVQS	KTIDGILLLI	ERERSGEAVD	RSLLRSLLGM	LSDLQVYKDS	FELKFLEETN	CLYAAEGQRL	MQEREVPEYL
170	180	190	200	210	220	230	240
NHVSKRLEEE	GDRVITYLDH	STQKPLIACV	EKQLLGEHLT	AILQKGLDHL	LDENRVPDLA	QMYQLFSRVR	GGQQALLQHW
250	260	270	280	290	300	310	320
SEYIKTFGTA	IVINPEKDKD	MVQDLLDFKD	KVDHVIEVCF	QKNERFVNLM	KESFETFINK	RPNKPAELIA	KHVDSKLRAG
330	340	350	360	370	380	390	400
NKEATDEELE	RTLDKIMILF	RFIHGKDVFE	AFYKKDLAKR	LLVGKSASVD	AEKSMLSKLK	HECGAAFTSK	LEGMFKDMEL
410	420	430	440	450	460	470	480
SKDIMVHFKQ	HMQNQSDSGP	IDLTVNILTM	GYWPTYTPME	VHLTPEMIKL	QEVFKAFYLG	KHSGRKLQWQ	TTLGHAVLKA
490	500	510	520	530	540	550	560
EFKEGKKEFQ	VSLFQTLVLL	MFNEGDGFSF	EEIKMATGIE	DSELRRTLQS	LACGKARVLI	KSPKGKEVED	GDKFIFNGEF
570	580	590	600	610	620	630	640
KHKLFRIKIN	QIQMKETVEE	QVSTTERVFQ	DRQYQIDAAI	VRIMKMRKTL	GHNLLVSELY	NQLKFPVKPG	DLKKRIESLI
650	660						
DRDYMERDKD	NPNQYHYVA						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2723	1	774.4242	-43.85	2	63.0	11.3	2	564-575	K.LFRIKINQIQMK.E	Oxidation: 11

Detailed Protein Report

Protein 1427: diphthamide biosynthesis protein 7 [Homo sapiens]

Accession:	gi|24308452	**Score:**	11.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	50.5
Database Date:	2015-11-30	**pI:**	6.1
Modification(s):	Oxidation	**Sequence Coverage [%]:**	4.0
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MMGCFALQTV DTELTADSVE WCPLQGCRHL LACGTYQLRR PEDRPAGPQN KGGMEVKEPQ VRLGRLFLYS FNDNNSIHPL
        90        100        110        120        130        140        150        160
VEVQRKDTSA ILDMKWCHIP VAGHALLGLA DASGSIQLLR LVESEKSHVL EPLSSLALEE QCLALSLDWS TGKTGRAGDQ
       170        180        190        200        210        220        230        240
PLKIISSDST GQLHLLMVNE TRPRLQKVAS WQAHQFEAWI AAFNYWHPEI VYSGGDDGLL RGWDTRVPGK FLFTSKRHTM
       250        260        270        280        290        300        310        320
GVCSIQSSPH REHILATGSY DEHILLWDTR NMKQPLADTP VQGGVWRIKW HPFHHHLLLA ACMHSGFKIL NCQKAMEERQ
       330        340        350        360        370        380        390        400
EATVLTSHTL PDSLVYGADW SWLLFRSLQR APSWSFPSNL GTKTADLKGA SELPTPCHEC REDNDGEGHA RPQSGMKPLT
       410        420        430        440        450        460
EGMRKNGTWL QATAATTRDC GVNPEEADSA FSLLATCSFY DHALHLWEWE GN
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1360	1	991.6333	137.20	2	45.5	11.3	1	40-57	R.RPEDRPAGPQNKGGMEVK.E	Oxidation: 15

Detailed Protein Report

Protein 1428: PREDICTED: sorting nexin-13 isoform X3 [Homo sapiens]

Accession:	gi|530384600	**Score:**	11.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	62.1
Database Date:	2015-11-30	**pI:**	4.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLTEASLSIW	GWGSLGIVLF	LITFGPFVIF	YLTFYILCFV	GGGLVVTLLF	GKTNSEKYLE	QCEHSFLPPT	SPGVPKCLEE
90	100	110	120	130	140	150	160
MKREARTIKI	DRRLTGANII	DEPLQQVIQF	SLRDYVQYWY	YTLSDDESFL	LEIRQTLQNA	LIQFATRSKE	IDWQPYFTTR
170	180	190	200	210	220	230	240
IVDDFGTHLR	VFRKAQQKIT	EKDDQVKGTA	EDLVDTFFEV	EVEMEKEVCR	DLVCTSPKDE	EGFLRDLCEV	LLYLLLPPGD
250	260	270	280	290	300	310	320
FQNKIMRYFV	REILARGILL	PLINQLSDPD	YINQYVIWMI	RDSNCNYEAF	MNIIKLSDNI	GELEAVRDKA	AEELQYLRSL
330	340	350	360	370	380	390	400
DTAGDDINTI	KNQINSLLFV	KKVCDSRIQR	LQSGKEINTV	KLAANFGKLC	TVPLDSILVD	NVALQFFMDY	MQQTGGQAHL
410	420	430	440	450	460	470	480
FFWMTVEGYR	VTAQQQLEVL	LSRQRDGKHQ	TNQTKGLLRA	AAVGIYEQYL	SEKASPRVTV	DDYLVAKLAD	TLNHEDPTPE
490	500	510	520	530	540		
IFDDIQRKVY	ELMLRDERFY	PSFRQNALYV	RMLAELDMLK	DPSFRGSDDG	DGEISSYL		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2929	1	1155.5370	-8.04	2	65.4	11.3	2	207-225	K.EVCRDLVCTSPKDEEGFLR.D	Carbamidomethyl: 3, 8

Detailed Protein Report

Protein 1429: 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

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
1556	1	853.3369	-142.17	2	49.3	11.3	1	205-222	R.GGALNRALAAANAAPDPR.A	

Detailed Protein Report

Protein 1430: PREDICTED: rho GTPase-activating protein 32 isoform X2 [Homo sapiens]

Accession:	gi|578822484	**Score:**	11.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	156.7
Database Date:	2015-11-30	**pI:**	6.2
		Sequence Coverage [%]:	0.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MKKSPVGSWR	SFFNLGKSSS	VSKRKLQRNE	SEPSEMKAMA	LKGGRAEGTL	RSAKSEESLT	SLHAVDGDSK	LFRPRRPRSS
90	100	110	120	130	140	150	160
SDALSASFNG	EMLGNRCNSY	DNLPHDNESE	EEGGLLHIPA	LMSPHSAEDV	DLSPPDIGVA	SLDFDPMSFQ	CSPPKAESEC
170	180	190	200	210	220	230	240
LESGASFLDS	PGYSKDKPSA	NKKDAETGSS	QCQTPGSTAS	SEPVSPLQEK	LSPFFTLDLS	PTEDKSSKPS	SFTEKVVYAF
250	260	270	280	290	300	310	320
SPKIGRKLSK	SPSMSISEPI	SVTLPPRVSE	VIGTVSNTTA	QNASSSTWDK	CVEERDATNR	SPTQIVKMKT	NETVAQEAYE
330	340	350	360	370	380	390	400
SEVQPLDQVA	AEEVELPGKE	DQSVSSSQSK	AVASGQTQTG	AVTHDPPQDS	VPVSSVSLIP	PPPPPKNVAR	MLALALAESA
410	420	430	440	450	460	470	480
QQASTQSLKR	PGTSQAGYTN	YGDIAVATTE	DNLSSSYSAV	ALDKAYFQTD	RPAEQFHLQN	NAPGNCDHPL	PETTATGDPT
490	500	510	520	530	540	550	560
HSNTTESGEQ	HHQVDLTGNQ	PHQAYLSGDP	EKARITSVPL	DSEKSDDHVS	FPEDQSGKNS	MPTVSFLDQD	QSPPRFYSGD
570	580	590	600	610	620	630	640
QPPSYLGASV	DKLHHPLEFA	DKSPTPPNLP	SDKIYPPSGS	PEENTSTATM	TYMTTTPATA	QMSTKEASWD	VAEQPTTADF
650	660	670	680	690	700	710	720
AAATLQRTHR	TNRPLPPPPS	QRSAEQPPVV	GQVQAATNIG	LNNSHKVQGV	VPVPERPPEP	RAMDDPASAF	ISDSGAAAAQ
730	740	750	760	770	780	790	800
CPMATAVQPG	LPEKVRDGAR	VPLLHLRAES	VPAHPCGFPA	PLPPTRMMES	KMIAAIHSSS	ADATSSSNYH	SFVTASSTSV
810	820	830	840	850	860	870	880
DDALPLPLPV	PQPKHASQKT	VYSSFARPDV	TTEPFGPDNC	LHFNMTPNCQ	YRPQSVPPHH	NKLEQHQVYG	ARSEPPASMG
890	900	910	920	930	940	950	960
LRYNTYVAPG	RNASGHHSKP	CSRVEYVSSL	SSSVRNTCYP	EDIPPYPTIR	RVQSLHAPPS	SMIRSVPISR	TEVPPDDEPA
970	980	990	1000	1010	1020	1030	1040
YCPRPLYQYK	PYQSSQARSD	YHVTQLQPYF	ENGRVHYRYS	PYSSSSSSYY	SPDGALCDVD	AYGTVQLRPL	HRLPNRDFAF
1050	1060	1070	1080	1090	1100	1110	1120
YNPRLQGKSL	YSYAGLAPRP	RANVTGYFSP	NDHNVVSMPP	AADVKHTYTS	WDLEDMEKYR	MQSIRRESRA	RQKVKGPVMS
1130	1140	1150	1160	1170	1180	1190	1200
QYDNMTPAVQ	DDLGGIYVIH	LRSKSDPGKT	GLLSVAEGKE	SRHAAKAISP	EGEDRFYRRH	PEAEMDRAHH	HGGHGSTQPE
1210	1220	1230	1240	1250	1260	1270	1280
KPSLPQKQSS	LRSRKLPDMG	CSLPEHRAHQ	EASHRQFCES	KNGPPYPQGA	GQLDYGSKGI	PDTSEPVSYH	NSGVKYAASG
1290	1300	1310	1320	1330	1340	1350	1360
QESLRLNHKE	VRLSKEMERP	WVRQPSAPEK	HSRDCYKEEE	HLTQSIVPPP	KPERSHSLKL	HHTQNVERDP	SVLYQYQPHG
1370	1380	1390	1400	1410	1420	1430	1440
KRQSSVTVVS	QYDNLEDYHS	LPQHQRGVFG	GGGMGTYVPP	GFPHPQSRTY	ATALGQGAFL	PAELSLQHPE	TQIHAE

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2733	1	656.8584	26.75	2	62.6	11.3	0	904-915	R.VEYVSSLSSSVR.N	

Detailed Protein Report

Protein 1431: PREDICTED: hypoxia-inducible factor 3-alpha isoform X4 [Homo sapiens]

Accession:	gi|530417039	**Score:**	11.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	63.4
Database Date:	2015-11-30	**pI:**	7.2
		Sequence Coverage [%]:	2.4
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530417041	refseq_human (refseq_human_20140103.fasta)	PREDICTED: hypoxia-inducible factor 3-alpha isoform X5 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MALGLQRARP ALSCGVISPP CAPTRNSHPG PGCTASPPAP PGWPFSQRGP GRWSTTELRK EKSRDAARSR RSQETEVLYQ
        90        100        110        120        130        140        150        160
LAHTLPFARG VSAHLDKASI MRLTISYLRM HRLCAAGEWN QVGAGGEPLD ACYLKALEGF VMVLTAEGDM AYLSENVSKH
       170        180        190        200        210        220        230        240
LGLSQLELIG HSIFDFIHPC DQEELQDALT PQQTLSRRKV EAPTERCFSL RMKSTLTSRG RTLNLKAATW KVLNCSGHMR
       250        260        270        280        290        300        310        320
AYKPPAQTSP AGSPDSEPPL QCLVLICEAI PHPGSLEPPL GRGAFLSRHS LDMKFTYCDD RIAEVAGYSP DDLIGCSAYE
       330        340        350        360        370        380        390        400
YIHALDSDAV SKSIHTLLSK GQAVTGQYRF LARSGGYLWT QTQATVVSGG RGPQSESIVC VHFLISQVEE TGVVLSLEQT
       410        420        430        440        450        460        470        480
EQHSRRPIQR GAPSQKDTPN PGDSLDTPGP RILAFLHPPS LSEAALAADP RRFCSPDLRR LLGPILDGAS VAATPSTPLA
       490        500        510        520        530        540        550        560
TRHPQSPLSA DLPDELPVGT ENVHRLFTSG KDTEAVETDL DIAQDPGPEL RGRGRGSGAA GSETSQKVPQ PRTRKLSALS
       570        580        590
SQPEFPSDRR TSPREPAGPQ HPTPEPE
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2337	1	646.6647	-229.39	2	57.9	11.3	1	534-547	R.GRGSGAAGSETSQK.V	

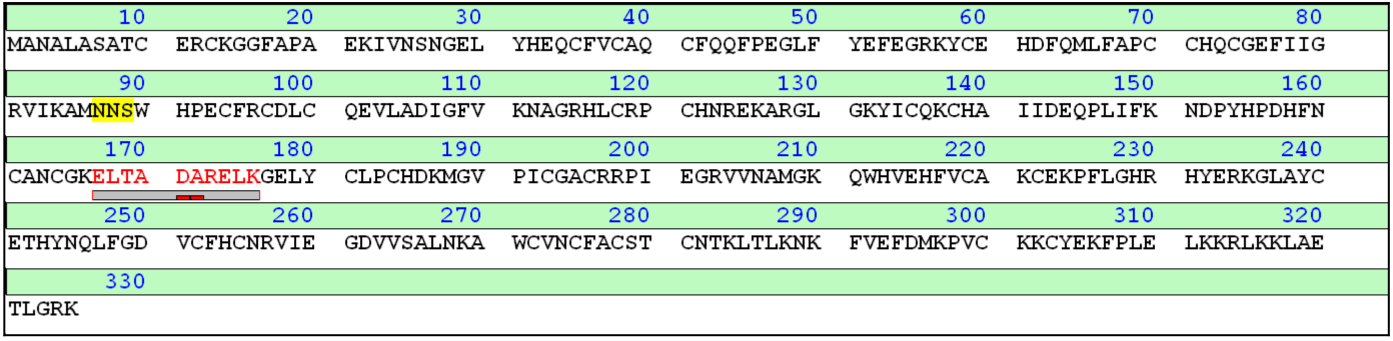
Detailed Protein Report

Protein 1432: LIM and senescent cell antigen-like-containing domain protein 1 isoform b [Homo sapiens]

Accession:	gi|13518026	**Score:**	11.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	37.2
Database Date:	2015-11-30	**pI:**	9.8
		Sequence Coverage [%]:	3.1
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|301601630	refseq_human (refseq_human_20140103.fasta)	LIM and senescent cell antigen-like-containing domain protein 1 isoform b [Homo sapiens]



10	20	30	40	50	60	70	80
MANALASATC	ERCKGGFAPA	EKIVNSNGEL	YHEQCFVCAQ	CFQQFPEGLF	YEFEGRKYCE	HDFQMLFAPC	CHQCGEFIIG
90	100	110	120	130	140	150	160
RVIKAMNNSW	HPECFRCDLC	QEVLADIGFV	KNAGRHLCRP	CHNREKARGL	GKYICQKCHA	IIDEQPLIFK	NDPYHPDHFN
170	180	190	200	210	220	230	240
CANCGKELTA	DARELKGELY	CLPCHDKMGV	PICGACRRPI	EGRVVNAMGK	QWHVEHFVCA	KCEKPFLGHR	HYERKGLAYC
250	260	270	280	290	300	310	320
ETHYNQLFGD	VCFHCNRVIE	GDVVSALNKA	WCVNCFACST	CNTKLTLKNK	FVEFDMKPVC	KKCYEKFPLE	LKKRLKKLAE
330							
TLGRK							

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	167-176	K.ELTADARELK.G	

Detailed Protein Report

Protein 1433: 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 1434: **phosphatidylinositol N-acetylglucosaminyltransferase subunit A isoform 3 [Homo sapiens]**

Accession:	gi|299782546	**Score:**	11.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	28.0
Database Date:	2015-11-30	**pI:**	5.7
		Sequence Coverage [%]:	4.4
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MELTGIDLLS GIIPELCQKY PDLNFIIGGE GPKRIILEEV RERYQLHDRV RLLGALEHKD VRNVLVQGHI FLNTSLTEAF
        90        100        110        120        130        140        150        160
CMAIVEAASC GLQVVSTRVG GIPEVLPENL IILCEPSVKS LCEGLEKAIF QLKSGTLPAP ENIHNIVKTF YTWRNVAERT
       170        180        190        200        210        220        230        240
EKVYDRVSVE AVLPMDKRLD RLISHCGPVT GYIFALLAVF NFLFLIFLRW MTPDSIIDVA IDATGPRGAW TNNYSHSKRG
       250        260
GENNEISETR
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2751	1	625.8294	-55.99	2	62.8	11.3	1	52-62	R.LLGALEHKDVR.N	

Detailed Protein Report

Protein 1435: RIMS-binding protein 3A [Homo sapiens]

Accession:	gi|153792195	**Score:**	11.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	180.6
Database Date:	2015-11-30	**pI:**	6.5
		Sequence Coverage [%]:	0.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAKDSPSPLG	ASPKKPGCSS	PAAAVLENQR	RELEKLRAEL	EAERAGWRAE	RRRFAARERQ	LREEAERERR	QLADRLRSKW
90	100	110	120	130	140	150	160
EAQRSRELRQ	LQEEMQRERE	AEIRQLLRWK	EAEQRQLQQL	LHRERDGVVR	QARELQRQLA	EELVNRGHCS	RPGASEVSAA
170	180	190	200	210	220	230	240
QCRCRLQEVL	AQLRWQTDGE	QAARIRYLQA	ALEVERQLFL	KYILAHFRGH	PALSGSPDPQ	AVHSLEEPLP	QTSSGSCHAP
250	260	270	280	290	300	310	320
KPACQLGSLD	SLSAEVGVRS	RSLGLVSSAC	SSSPDGLLST	HASSLDCFAP	ACSRSLDSTR	SLPKASKSEE	RPSSPDTSTP
330	340	350	360	370	380	390	400
GSRRLSPPPS	PLPPPPPPSA	HRKLSNPRGG	EGSESQPCEV	LTPSPPGLGH	HELIKLNWLL	AKALWVLARR	CYTLQAENKQ
410	420	430	440	450	460	470	480
LRRAGCPYQA	DEKVKRLKVK	RAELTGLARR	LADRARKLQE	TNLRAVSAPI	PGESCAGLEL	CQVFARQRAR	DLSEQASAPL
490	500	510	520	530	540	550	560
AKDKQIEELR	QECHLLQARV	ASGPCSDLHT	GRGGPCTQWL	NVRDLDRLQR	ESQREVLRLQ	RQLMLQQGNG	GAWPEAGGQS
570	580	590	600	610	620	630	640
ATCEEVRRQM	LALERELDQR	RRECQELGAQ	AAPARRRGEE	AETQLQAALL	KNAWLAEENG	RLQAKTDWVR	KVEAENSEVR
650	660	670	680	690	700	710	720
GHLGRACQER	DASGLIAEQL	LQQAARGQDR	QQQLQRDPQK	ALCDLHPSWK	EIQALQCRPG	HPPEQPWETS	QMPESQVKGS
730	740	750	760	770	780	790	800
RRPKFHARPE	DYAVSQPNRD	IQEKREASLE	ESPVALGESA	SVPQVSETVP	ASQPLSKKTS	SQSNSSSEGS	MWATVPSSPT
810	820	830	840	850	860	870	880
LDRDTASEVD	DLEPDSVSLA	LEMGGSAAPA	APKLKIFMAQ	YNYNPFEGPN	DHPEGELPLT	AGDYIYIFGD	MDEDGFYEGE
890	900	910	920	930	940	950	960
LEDGRRGLVP	SNFVEQIPDS	YIPGCLPAKS	PDLGPSQLPA	GQDEALEEDS	LLSGKAQGVV	DRGLCQMVRV	GSKTEVATEI
970	980	990	1000	1010	1020	1030	1040
LDTKTEACQL	GLLQSMGKQG	LSRPLLGTKG	VLRMAPMQLH	LQNVTATSAN	ITWVYSSHRH	PHVVYLDDRE	HALTPAGVSC
1050	1060	1070	1080	1090	1100	1110	1120
YTFQGLCPGT	HYRARVEVRL	PRDLLQVYWG	TMSSTVTFDT	LLAGPPYPPL	DVLVERHASP	GVLVVSWLPV	TIDSAGSSNG
1130	1140	1150	1160	1170	1180	1190	1200
VQVTGYAVYA	DGLKVCEVAD	ATAGSTLLEF	SQLQVPLTWQ	KVSVRTMSLC	GESLDSVPAQ	IPEDFFMCHR	WPETPPFSYT
1210	1220	1230	1240	1250	1260	1270	1280
CGDPSTYRVT	FPVCPQKLSL	APPSAKASPH	NPGSCGEPQA	KFLEAFFEEP	PRRQSPVSNL	GSEGECPSSG	AGSQAQELAE
1290	1300	1310	1320	1330	1340	1350	1360
AWEGCRKDLL	FQKSPQNHRP	PSVSDQPGEK	ENCSQHMGTS	KSPAPGFIHL	RTECGPRKEP	CQEKAALERV	LRQKQDAQGF
1370	1380	1390	1400	1410	1420	1430	1440
TPPQLGASQQ	YASDFHNVLK	EEQEALCLDL	WGTERREERR	EPEPHSRQGQ	ALGVKRGCQL	HEPSSALCPA	PSAKVIKMPR
1450	1460	1470	1480	1490	1500	1510	1520
GGPQQLGTGA	NTPARVFVAL	SDYNPLVMSA	NLKAAEEELV	FQKRQLLRVW	GSQDTHDFYL	SECNRQVGNI	PGRLVAEMEV
1530	1540	1550	1560	1570	1580	1590	1600
GTEQTDRRWR	SPAQGNLPSV	AHLEDFQGLT	IPQGSSLVLQ	GNSKRLPLWT	PKIMIAALDY	DPGDGQMGGQ	GKGRLALRAG
1610	1620	1630	1640				
DVVMVYGPMD	DQGFYYGELG	GHRGLVPAHL	LDHMSLHGH				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2660	1	733.8590	-21.34	2	61.6	11.3	1	391-402	R.CYTLQAENKQLR.R	

Detailed Protein Report

Protein 1436: schwannomin-interacting protein 1 isoform 4 [Homo sapiens]

Accession:	gi|308193348	**Score:**	11.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	27.5
Database Date:	2015-11-30	**pI:**	4.9
Modification(s):	Oxidation	**Sequence Coverage [%]:**	7.0
		No. of unique Peptides:	1

Quantitation

Wdown:Qdown **Median:** 0.47 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MVHQDNCSYQ AQKNERESIR QKLALGSFFD DGPGIYTSCS KSGKPSLSSR LQSGMNLQIC FVNDSGSDKD SDADDSKTET
        90        100        110        120        130        140        150        160
SLDTPLSPMS KQSSSYSDRD TTEEESESLD DMDFLTRQKK LQAEAKMALA MAKPMAKMQV EVEKQNRKKS PVADLLPHMP
       170        180        190        200        210        220        230        240
HISECLMKRS LKPTDLRDMT IGQLQVIVND LHSQIESLNE ELVQLLLIRD ELHTEQDAML VDIEDLTRHA ESQQKHMAEK
       250
MPAK
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2015	1	909.8448	-154.70	2	53.8	11.3	1	121-137	K.LQAEAKMALAMAKPMAK.M	Oxidation: 15	Wdown:Qdown 0.47

Detailed Protein Report

Protein 1437: PREDICTED: PR domain zinc finger protein 15 isoform X2 [Homo sapiens]

Accession:	gi|578836645	**Score:**	11.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	128.4
Database Date:	2015-11-30	**pI:**	9.2
		Sequence Coverage [%]:	1.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPRRRPPASG	AAQFPERIAT	RSPDPIPLCT	FQRQVSEMAE	DGSEEIMFIW	CEDCSQYHDS	ECPELGPVVM	VKDSFVLSRA
90	100	110	120	130	140	150	160
RSSLPPNLEI	RRLEDGAEGV	FAITQLVKRT	QFGPFESRRV	AKWEKESAFP	LKVFQKDGHP	VCFDTSNEDD	CNWMMLVRPA
170	180	190	200	210	220	230	240
AEAEHQNLTA	YQHGSDVYFT	TSRDIPPGTE	LRVWYAAFYA	KKMDKPMLKQ	AGSGVHAAGT	PENSAPVESE	PSQWACKVCS
250	260	270	280	290	300	310	320
ATFLELQLLN	EHLLGHLEQA	KSLPPGSQSE	AAAPEKEQDT	PRGEPPAVPE	SENVATKEQK	KKPRRGRKPK	VSKAEQPLVI
330	340	350	360	370	380	390	400
VEDKEPTEQV	AEIITEVPPD	EPVSATPDER	IMELVLGKLA	TTTTDTSSVP	KFTHHQNNTI	TLKRSLILSS	RHGIRRKLIK
410	420	430	440	450	460	470	480
QLGEHKRVYQ	CNICSKIFQN	SSNLSRHVRS	HGDKLFKCEE	CAKLFSRKES	LKQHVSYKHS	RNEVDGEYRY	RCGTCEKTFR
490	500	510	520	530	540	550	560
IESALEFHNC	RTDDKTFQCE	MCFRFFSTNS	NLSKHKKKHG	DKKFACEVCS	KMFYRKDVML	DHQRRHLEGV	RRVKREDLEA
570	580	590	600	610	620	630	640
GGENLVRYKK	EPSGCPVCGK	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
1448	1	699.6392	-84.48	3	47.9	11.3	1	184-201	R.DIPPGTELRVWYAAFYAK.K	

Detailed Protein Report

Protein 1438: 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 1439: cystathionine gamma-lyase isoform 2 [Homo sapiens]

Accession:	gi|25453487	**Score:**	11.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	39.5
Database Date:	2015-11-30	**pI:**	6.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	6.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MQEKDASSQG	FLPHFQHFAT	QAIHVGQDPE	QWTSRAVVPP	ISLSTTFKQG	APGQHSGFEY	SRSGNPTRNC	LEKAVAALDG
90	100	110	120	130	140	150	160
AKYCLAFASG	LAATVTITHL	LKAGDQIICM	DDVYGGTNRY	FRQVASEFGL	KISFVDCSKI	KLLEAAITPE	TKRPLALGAD
170	180	190	200	210	220	230	240
ISMYSATKYM	NGHSDVVMGL	VSVNCESLHN	RLRFLQNSLG	AVPSPIDCYL	CNRGLKTLHV	RMEKHFKNGM	AVAQFLESNP
250	260	270	280	290	300	310	320
WVEKVIYPGL	PSHPQHELVK	RQCTGCTGMV	TFYIKGTLQH	AEIFLKNLKL	FTLAESLGGF	ESLAELPAIM	THASVLKNDR
330	340	350	360	370			
DVLGISDTLI	RLSVGLEDEE	DLLEDLDQAL	KAAHPPSGSH	S			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1446	1	695.0851	13.55	4	46.9	11.2	2	49-73	K.QGAPGQHSGFEYSRSGNPTRNCLEK.A	Carbamidomethyl: 22

Detailed Protein Report

Protein 1440: 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 1441: transcription factor AP-2 gamma [Homo sapiens]

Accession:	gi|4507445	**Score:**	11.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	49.1
Database Date:	2015-11-30	**pI:**	8.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	6.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLWKITDNVK	YEEDCEDRHD	GSSNGNPRVP	HLSSAGQHLY	SPAPPLSHTG	VAEYQPPPYF	PPPYQQLAYS	QSADPYSHLG
90	100	110	120	130	140	150	160
EAYAAAINPL	HQPAPTGSQQ	QAWPGRQSQE	GAGLPSHHGR	PAGLLPHLSG	LEAGAVSARR	DAYRRSDLLL	PHAHALDAAG
170	180	190	200	210	220	230	240
LAENLGLHDM	PHQMDEVQNV	DDQHLLLHDQ	TVIRKGPISM	TKNPLNLPCQ	KELVGAVMNP	TEVFCSVPGR	LSLLSSTSKY
250	260	270	280	290	300	310	320
KVTVAEVQRR	LSPPECLNAS	LLGGVLRRAK	SKNGGRSLRE	KLDKIGLNLP	AGRRKAAHVT	LLTSLVEGEA	VHLARDFAYV
330	340	350	360	370	380	390	400
CEAEFPSKPV	AEYLTRPHLG	GRNEMAARKN	MLLAAQQLCK	EFTELLSQDR	TPHGTSRLAP	VLETNIQNCL	SHFSLITHGF
410	420	430	440	450	460		
GSQAICAAVS	ALQNYIKEAL	IVIDKSYMNP	GDQSPADSNK	TLEKMEKHRK			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2528	1	1023.7905	-56.96	3	59.9	11.2	1	203-230	K.NPLNLPCQKELVGAVMNPTEVFCSVPGR.L	Carbamidomethyl: 23

Detailed Protein Report

Protein 1442: UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 6 [Homo sapiens]

Accession:	gi|118918426	**Score:**	11.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	42.7
Database Date:	2015-11-30	**pI:**	8.9
		Sequence Coverage [%]:	2.9
		No. of unique Peptides:	1

Quantitation

mdown:qdown **Median:** 0.47 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MAFPCRRSLT	AKTLACLLVG	VSFLALQQWF	LQAPRSPREE	RSPQEETPEG	PTDAPAADEP	PSELVPGPPC	VANASANATA
90	100	110	120	130	140	150	160
DFEQLPARIQ	DFLRYRHCRH	FPLLWDAPAK	CAGGRGVFLL	LAVKSAPEHY	ERRELIRRTW	GQERSYGGRP	VRRLFLLGTP
170	180	190	200	210	220	230	240
GPEDEARAER	LAELVALEAR	EHGDVLQWAF	ADTFLNLTLK	HLHLLDWLAA	RCPHARFLLS	GDDDVFVHTA	NVVRFLQAQP
250	260	270	280	290	300	310	320
PGRHLFSGQL	MEGSVPIRDS	WSKYFVPPQL	FPGSAYPVYC	SGGGFLLSGP	TARALRAAAR	HTPLFPIDDA	YMGMCLERAG
330	340	350	360	370	380	390	
LAPSGHEGIR	PFGVQLPGAQ	QSSFDPCMYR	ELLLVHRFAP	YEMLLMWKAL	HSPALSCDRG	HRVS	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
820	1	585.2809	-15.94	2	39.1	11.2	0	369-379	K.ALHSPALSCDR.G		mdown:qdown 0.47

Detailed Protein Report

Protein 1443: adrenodoxin-like protein, mitochondrial precursor [Homo sapiens]

Accession:	gi|72534754	**Score:**	11.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	19.5
Database Date:	2015-11-30	**pI:**	5.1
Modification(s):	Oxidation	**Sequence Coverage [%]:**	8.7
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MAASMARGGV SARVLLQAAR GTWWNRPGGT SGSGEGVALG TTRKFQATGS RPAGEEDAGG PERPGDVVNV VFVDRSGQRI
        90        100        110        120        130        140        150        160
PVSGRVGDNV LHLAQRHGVD LEGACEASLA CSTCHVYVSE DHLDLLPPPE EREDDMLDMA PLLQENSRLG CQIVLTPELE
       170        180        190
GAEFTLPKIT RNFYVDGHVP KPH
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1025	1	954.9501	32.22	2	41.6	11.2	0	133-148	R.EDDMLDMAPLLQENSR.L	Oxidation: 4, 7

Detailed Protein Report

Protein 1444: 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 1445: PREDICTED: uncharacterized protein LOC101929393 [Homo sapiens]

Accession: gi|530356822
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl, Oxidation

Score: 11.2
MW [kDa]: 20.3
pI: 11.1
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 1446: 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	

Detailed Protein Report

Protein 1447: epithelial-stromal interaction protein 1 isoform 2 [Homo sapiens]

Accession:	gi|15147248	**Score:**	11.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	35.4
Database Date:	2015-11-30	**pI:**	10.5
		Sequence Coverage [%]:	4.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MNTRNRVVNS	GLGASPASRP	TRDPQDPSGR	QGELSPVEDQ	REGLEAAPKG	PSRESVVHAG	QRRTSAYTLI	APNINRRNEI
90	100	110	120	130	140	150	160
QRIAEQELAN	LEKWKEQNRA	KPVHLVPRRL	GGSQSETEVR	QKQQLQLMQS	KYKQKLKREE	SVRIKKEAEE	AELQKMKAIQ
170	180	190	200	210	220	230	240
REKSNKLEEK	KRLQENLRRE	AFREHQQYKT	AEFLSKLNTE	SPDRSACQSA	VCGPQSSTWA	RSWAYRDSLK	AEENRKLQKM
250	260	270	280	290	300	310	
KDEQHQKSEL	LELKRQQQEQ	ERAKIHQTEH	RRVNNAFLDR	LQGKSQPGGL	EQSGGCWNMN	SGNSWGI	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1468	1	620.0709	76.55	3	47.1	11.2	2	94-108	K.WKEQNRAKPVHLVPR.R	

Detailed Protein Report

Protein 1448: **PREDICTED: methylglutaconyl-CoA hydratase, mitochondrial isoform X7 [Homo sapiens]**

Accession:	gi|530391285	**Score:**	11.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	26.3
Database Date:	2015-11-30	**pI:**	10.4
		Sequence Coverage [%]:	7.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAAAVAAAPG	ALGSLHAGGA	RLVAACSAWL	CPGLRLPGSL	AGRRAGPAIW	AQGWVPAAGG	PAPKRGYSSE	MKTEDELRVR
90	100	110	120	130	140	150	160
HLEEENRGIV	VLGINRAYGK	NSLSKNLIKM	LSKAVDALKS	DKKVRTIIIR	SEVPGIFCAG	ADLKERAKMS	SSEVGPFVSK
170	180	190	200	210	220	230	240
IRAVINDIAN	LPVPTIAAID	GLALGGGLEL	ALACDIRVAA	SSAKMGLVET	KLAIIPGGVT	SSTEVLNPSK	SSMKIGIIIF
250	260						
QTPVNIDILA	SSHES						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2735	1	941.9591	-73.03	2	62.6	11.2	0	212-230	K.LAIIPGGVTSSTEVLNPSK.S	

Detailed Protein Report

Protein 1449: minor histocompatibility protein HA-1 isoform 3 [Homo sapiens]

Accession:	gi|537361054	**Score:**	11.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	84.6
Database Date:	2015-11-30	**pI:**	5.5
Modification(s):	Oxidation	**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 1450: acetylcholine receptor subunit delta isoform 2 precursor [Homo sapiens]

Accession:	gi|375331911	**Score:**	11.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	57.0
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
MEGPVLTLGL	LAALAVCGSW	GLNEEERLIR	HLFQEKGYNK	ELRPVAHKEE	SVDVALALTL	SNLISLGWTD	NRLKWNAEEF
90	100	110	120	130	140	150	160
GNISVLRLPP	DMVWLPEIVL	ENNNDGSFQI	SYSCNVLVYH	YGFVYWLPPA	IFRSSCPISV	TYFPFDWQNC	SLKFSSLKYT
170	180	190	200	210	220	230	240
AKEITLSLKQ	DAKENRTYPV	EWIIIDPEGF	TENGEWEIVH	RPARVNVDPR	APLDSPSRQD	ITFYLIIRRK	PLFYIINILV
250	260	270	280	290	300	310	320
PCVLISFMVN	LVFYLPADSG	EKTSVAISVL	LAQSVFLLLI	SKRLPATSMA	IPLIGKFLLF	GMVLVTMVVV	ICVIVLNIHF
330	340	350	360	370	380	390	400
RTPSTHVLSE	GVKKLFLETL	PELLHMSRPA	EDGPSPGALV	RRSSSLGYIS	KAEEYFLLKS	RSDLMFEKQS	ERHGLARRLT
410	420	430	440	450	460	470	480
TARRPPASSE	QAQQELFNEL	KPAVDGANFI	VNHMRDQNNY	NEEKDSWNRV	ARTVDRLCLF	VVTPVMVVGT	AWIFLQGVYN
490	500	510					
QPPPQPFPGD	PYSYNVQDKR	FI					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1637	1	823.4275	-42.26	2	49.2	11.2	2	28-40	R.LIRHLFQEKGYNK.E	

Detailed Protein Report

Protein 1451: D-3-phosphoglycerate dehydrogenase [Homo sapiens]

Accession:	gi|23308577	**Score:**	11.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	56.6
Database Date:	2015-11-30	**pI:**	6.3
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.1
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	0.86	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	1.19	**CV:**	0.00 %	**No. of Peptides:**	1

10	20	30	40	50	60	70	80
MAFANLRKVL	ISDSLDPCCR	KILQDGGLQV	VEKQNLSKEE	LIAELQDCEG	LIVRSATKVT	ADVINAAEKL	QVVGRAGTGV
90	100	110	120	130	140	150	160
DNVDLEAATR	KGILVMNTPN	GNSLSAAELT	CGMIMCLARQ	IPQATASMKD	GKWERKKFMG	TELNGKTLGI	LGLGRIGREV
170	180	190	200	210	220	230	240
ATRMQSFGMK	TIGYDPIISP	EVSASFGVQQ	LPLEEIWPLC	DFITVHTPLL	PSTTGLLNDN	TFAQCKKGVR	VVNCARGGIV
250	260	270	280	290	300	310	320
DEGALLRALQ	SGQCAGAALD	VFTEEPPRDR	ALVDHENVIS	CPHLGASTKE	AQSRCGEEIA	VQFVDMVKGK	SLTGVVNAQA
330	340	350	360	370	380	390	400
LTSAFSPHTK	PWIGLAEALG	TLMRAWAGSP	KGTIQVITQG	TSLKNAGNCL	SPAVIVGLLK	EASKQADVNL	VNAKLLVKEA
410	420	430	440	450	460	470	480
GLNVTTSHSP	AAPGEQGFGE	CLLAVALAGA	PYQAVGLVQG	TTPVLQGLNG	AVFRPEVPLR	RDLPLLLFRT	QTSDPAMLPT
490	500	510	520	530	540		
MIGLLAEAGV	RLLSYQTSLV	SDGETWHVMG	ISSLLPSLEA	WKQHVTEAFQ	FHF		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1642	1	634.8441	11.21	2	49.1	11.2	2	136-146	R.KKFMGTELNGK.T	Oxidation: 4	Wdown:Qdown 1.19 mdown:qdown 0.86

Detailed Protein Report

Protein 1452: PREDICTED: unconventional myosin-X isoform X2 [Homo sapiens]

Accession:	gi|530378821	**Score:**	11.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	163.5
Database Date:	2015-11-30	**pI:**	5.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPDQFDQAVV	LNQLRYSGML	ETVRIRKAGY	AVRRPFQDFY	KRYKVLMRNL	ALPEDVRGKC	TSLLQLYDAS	NSEWQLGKTK
90	100	110	120	130	140	150	160
VFLRESLEQK	LEKRREEEVS	HAAMVIRAHV	LGFLARKQYR	KVLYCVVIIQ	KNYRAFLLRR	RFLHLKKAAI	VFQKQLRGQI
170	180	190	200	210	220	230	240
ARRVYRQLLA	EKREQEEKKK	QEEEEKKKRE	EEERERERER	REAELRAQQE	EETRKQQELE	ALQKSQKEAE	LTRELEKQKE
250	260	270	280	290	300	310	320
NKQVEEILRL	EKEIEDLQRM	KEQQELSLTE	ASLQKLQERR	DQELRRLEEE	ACRAAQEFLE	SLNFDEIDEC	VRNIERSLSV
330	340	350	360	370	380	390	400
GSEFSSELAE	SACEEKPNFN	FSQPYPEEEV	DEGFEADDDA	FKDSPNPSEH	GHSDQRTSGI	RTSDDSSEED	PYMNDTVVPT
410	420	430	440	450	460	470	480
SPSADSTVLL	APSVQDSGSL	HNSSSGESTY	CMPQNAGDLP	SPDGDYDYDQ	DDYEDGAITS	GSSVTFSNSY	GSQWSPDYRC
490	500	510	520	530	540	550	560
SVGTYNSSGA	YRFSSEGAQS	SFEDSEEDFD	SRFDTDDELS	YRRDSVYSCV	TLPYFHSFLY	MKGGLMNSWK	RRWCVLKDET
570	580	590	600	610	620	630	640
FLWFRSKQEA	LKQGWLHKKG	GGSSTLSRRN	WKKRWFVLRQ	SKLMYFENDS	EEKLKGTVEV	RTAKEIIDNT	TKENGIDIIM
650	660	670	680	690	700	710	720
ADRTFHLIAE	SPEDASQWFS	VLSQVHASTD	QEIQEMHDEQ	ANPQNAVGTL	DVGLIDSVCA	SDSPDRPNSF	VIITANRVLH
730	740	750	760	770	780	790	800
CNADTPEEMH	HWITLLQRSK	GDTRVEGQEF	IVRGWLHKEV	KNSPKMSSLK	LKKRWFVLTH	NSLDYYKSSE	KNALKLGTLV
810	820	830	840	850	860	870	880
LNSLCSVVPP	DEKIFKETGY	WNVTVYGRKH	CYRLYTKLLN	EATRWSSAIQ	NVTDTKAPID	TPTQQLIQDI	KENCLNSDVV
890	900	910	920	930	940	950	960
EQIYKRNPIL	RYTHHPLHSP	LLPLPYGDIN	LNLLKDKGYT	TLQDEAIKIF	NSLQQLESMS	DPIPIIQGIL	QTGHDLRPLR
970	980	990	1000	1010	1020	1030	1040
DELYCQLIKQ	TNKVPHPGSV	GNLYSWQILT	CLSCTFLPSR	GILKYLKFHL	KRIREQFPGS	EMEKYALFTY	ESLKKTKCRE
1050	1060	1070	1080	1090	1100	1110	1120
FVPSRDEIEA	LIHRQEMTST	VYCHGGGSCK	ITINSHTTAG	EVVEKLIRGL	AMEDSRNMFA	LFEYNGHVDK	AIESRTVVAD
1130	1140	1150	1160	1170	1180	1190	1200
VLAKFEKLAA	TSEVGDLPWK	FYFKLYCFLD	TDNVPKDSVE	FAFMFEQAHE	AVIHGHHPAP	EENLQVLAAL	RLQYLQGDYT
1210	1220	1230	1240	1250	1260	1270	1280
LHAAIPPLEE	VYSLQRLKAR	ISQSTKTFTP	CERLEKRRTS	FLEGTLRRSF	RTGSVVRQKV	EEEQMLDMWI	KEEVSSARAS
1290	1300	1310	1320	1330	1340	1350	1360
IIDKWRKFQG	MNQEQAMAKY	MALIKEWPGY	GSTLFDVECK	EGGFPQELWL	GVSADAVSVY	KRGEGRPLEV	FQYEHILSFG
1370	1380	1390	1400	1410	1420		
APLANTYKIV	VDERELLFET	SEVVDVAKLM	KAYISMIVKK	RYSTTRSASS	QGSSR		

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	1055-1085	R.QEMTSTVYCHGGGSCKITINSHTTAGEVVEK.L	Carbamidomethyl: 15

Detailed Protein Report

Protein 1453: PREDICTED: ubiquitin carboxyl-terminal hydrolase 31 isoform X1 [Homo sapiens]

Accession:	gi|530408620	**Score:**	11.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	119.3
Database Date:	2015-11-30	**pI:**	10.2
		Sequence Coverage [%]:	1.3
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578828616	refseq_human (refseq_human_20140103.fasta)	PREDICTED: ubiquitin carboxyl-terminal hydrolase 31 isoform X2 [Homo sapiens]

10	20	30	40	50	60	70	80
MMPEGPSFPV	CSTFVQELFQ	AQYRSSLTCP	HCQKQSNTFD	PFLCISLPIP	LPHTRPLYVT	VVYQGKCSHC	MRIGVAVPLS
90	100	110	120	130	140	150	160
GTVARLREAV	SMETKIPTDQ	IVLTEMYYDG	FHRSFCDTDD	LETVHESDCI	FAFETPEIFR	PEGILSQRGI	HLNNNLNHLK
170	180	190	200	210	220	230	240
FGLDYHRLSS	PTQTAAKQGK	MDSPTSRAGS	DKIVLLVCNR	ACTGQQGKRF	GLPFVLHLEK	TIAWDLLQKE	ILEKMKYFLR
250	260	270	280	290	300	310	320
PTVCIQVCPF	SLRVVSVVGI	TYLLPQEEQP	LCHPIVERAL	KSCGPGGTAH	VKLVVEWDKE	TRDFLFVNTE	DEYIPDAESV
330	340	350	360	370	380	390	400
RLQRERHHQP	QTCTLSQCFQ	LYTKEERLAP	DDAWRCPHCK	QLQQGSITLS	LWTLPDVLII	HLKRFRQEGD	RRMKLQNMVK
410	420	430	440	450	460	470	480
FPLTGLDMTP	HVVKRSQSSW	SLPSHWSPWR	RPYGLGRDPE	DYIYDLYAVC	NHHGTMQGGH	YTAYCKNSVD	GLWYCFDDSD
490	500	510	520	530	540	550	560
VQQLSEDEVC	TQTAYILFYQ	RRTAIPSWSA	NSSVAGSTSS	SLCEHWVSRL	PGSKPASVTS	AASSRRTSLA	SLSESVEMTG
570	580	590	600	610	620	630	640
ERSEDDGGFS	TRPFVRSVQR	QSLSSRSSVT	SPLAVNENCM	RPSWSLSAKL	QMRSNSPSRF	SGDSPIHSSA	STLEKIGEAA
650	660	670	680	690	700	710	720
DDKVSISCFG	SLRNLSSSYQ	EPSDSHSRRE	HKAVGRAPLA	VMEGVFKDES	DTRRLNSSVV	DTQSKHSAQG	DRLPPLSGPF
730	740	750	760	770	780	790	800
DNNNQIAYVD	QSDSVDSSPV	KEVKAPSHPG	SLAKKPESTT	KRSPSSKGTS	EPEKSLRKGR	PALASQESSL	SSTSPSSPLP
810	820	830	840	850	860	870	880
VKVSLKPSRS	RSKADSSSRG	SGRHSSPAPA	QPKKESSPKS	QDSVSSPSPQ	KQKSASALTY	TASSTSAKKA	SGPATRSPFP
890	900	910	920	930	940	950	960
PGKSRTSDHS	LSREGSRQSL	GSDRASATST	SKPNSPRVSQ	ARAGEGRGAG	KHVRSSSMAS	LRSPSTSIKS	GLKRDSKSED
970	980	990	1000	1010	1020	1030	1040
KGLSFFKSAL	RQKETRRSTD	LGKTALLSKK	AGGSSVKSVC	KNTGDDEAER	GHQPPASQQP	NANTTGKEQL	VTKDPASAKH
1050	1060	1070	1080	1090			
SLLSARKSKS	SQLDSGVPSS	PGGRQSAEKS	SKKLSSSMQT	SARPSQKPQ			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2244	1	792.8941	-36.04	2	56.7	11.2	2	958-971	K.SEDKGLSFFKSALR.Q	

Detailed Protein Report

Protein 1454: PREDICTED: pre-mRNA 3'-end-processing factor FIP1 isoform X13 [Homo sapiens]

Accession:	gi|530376863	**Score:**	11.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	61.3
Database Date:	2015-11-30	**pI:**	5.3
		Sequence Coverage [%]:	2.7
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MSAGEVERLV SELSGGTGGD EEEEWLYGGP WDVHVHSDLA KDLDENEVER PEEENASANP PSGIEDETAE NGVPKPKVTE
        90        100        110        120        130        140        150        160
TEDDSDSDSD DDEDDVHVTI GDIKTGAPQY GSYGTAPVNL NIKTGGRVYG TTGTKVKGVD LDAPGSINGV PLLEVDLDSF
       170        180        190        200        210        220        230        240
EDKPWRKPGA DLSDYFNYGF NEDTWKAYCE KQKRIRMGLE VIPVTSTTNK ITVQQGRTGN SEKETALPST KAEFTSPPSL
       250        260        270        280        290        300        310        320
FKTGLPPSRR LPGAIDVIGQ TITISRVEGR RRANENSNIQ VLSERSATEV DNNFSKPPPF FPPGAPPTHL PPPPFLPPPP
       330        340        350        360        370        380        390        400
TVSTAPPLIP PPGIPITVPP PGFPPPPGAP PPSLIPTIES GHSSGYDSRS ARAFPYGNVA FPHLPGSAPS WPSLVDTSKQ
       410        420        430        440        450        460        470        480
WDYYARREKD RDRERDRDRE RDRDRDRERE RTRERERERD HSPTPSVFNR FVGDEERYRY REYAERGYER HRASREKEER
       490        500        510        520        530        540        550
HRERRHREKE ETRHKSSRSN SRRRHESEEG DSHRRHKHKK SKRSKEGKEA GSEPAPEQES TEATPAE
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2704	1	914.0851	149.67	2	62.2	11.2	2	436-450	R.ERERDHSPTPSVFNR.F	

Detailed Protein Report

Protein 1455: putative uncharacterized protein ENSP00000383407 [Homo sapiens]

Accession:	gi|375151595	**Score:**	11.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	15.5
Database Date:	2015-11-30	**pI:**	9.1
		Sequence Coverage [%]:	8.3
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MSSRTDSPIP PFGESEQTPN NLFVGVSNLE NAKPKKRKLF RRFMSENKIF EGKTVNDKIW QEHSKHKNDS HIRRPCQLKD
        90        100        110        120        130        140
LNENDFLSNN IHTYQGKTLQ GTSYQVTSEC WSPFHYQRHV ETTVDELAQE FM
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2759	1	665.3721	64.79	2	63.5	11.2	1	43-53	R.FMSENKIFEGK.T	

Detailed Protein Report

Protein 1456: 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 1457: 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 1458: PREDICTED: C-type lectin domain family 18 member C isoform X3 [Homo sapiens]

Accession:	gi|530423816	**Score:**	11.2
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
2562	1	856.9435	-20.66	2	62.5	11.2	0	86-102	R.AALCGIPTPSLASGLWR.T	

Detailed Protein Report

Protein 1459: **PREDICTED: probable phospholipid-transporting ATPase IM isoform X2 [Homo sapiens]**

Accession:	gi|578827423	**Score:**	11.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	114.6
Database Date:	2015-11-30	**pI:**	7.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MVSVMLKLLS	LMGIVVCEVP	NNKLDKFMGI	LSWKDSKHSL	NNEKIILRGC	ILRNTSWCFG	MVIFAGPDTK	LMQNSGKTKF
90	100	110	120	130	140	150	160
KRTSIDRLMN	TLVLWIFGFL	ICLGIILAIG	NSIWESQTGD	QFRTFLFWNE	GEKSSVFSGF	LTFWSYIIIL	NTVVPISLYV
170	180	190	200	210	220	230	240
SVEVIRLGHS	YFINWDRKMY	YSRKAIPAVA	RTTTLNEELG	QIEYIFSDKT	GTLTQNIMTF	KRCSINGRIY	GEVHDDLDQK
250	260	270	280	290	300	310	320
TEITQEKEPV	DFSVKSQADR	EFQFFDHHLM	ESIKMGDPKV	HEFLRLLALC	HTVMSEENSA	GELIYQVQSP	DEGALVTAAR
330	340	350	360	370	380	390	400
NFGFIFKSRT	PETITIEELG	TLVTYQLLAF	LDFNNTRKRM	SVIVRNPEGQ	IKLYSKGADT	ILFEKLHPSN	EVLLSLTSDH
410	420	430	440	450	460	470	480
LSEFAGEGLR	TLAIAYRDLD	DKYFKEWHKM	LEDANAATEE	RDERIAGLYE	EIERDLMLLG	ATAVEDKLQE	GVIETVTSLS
490	500	510	520	530	540	550	560
LANIKIWVLT	GDKQETAINI	GYACNMLTDD	MNDVFVIAGN	NAVEVREELR	KAKQNLFGQN	RNFSNGHVVC	EKKQQLELDS
570	580	590	600	610	620	630	640
IVEETITGDY	ALIINGHSLA	HALESDVKND	LLELACMCKT	VICCRVTPLQ	KAQVVELVKK	YRNAVTLAIG	DGANDVSMIK
650	660	670	680	690	700	710	720
SAHIGVGISG	QEGLQAVLAS	DYSFAQFRYL	QRLLLVHGRW	SYFRMCKFLC	YFFYKNFAFT	LVHFWFGFFC	GFSAQTVYDQ
730	740	750	760	770	780	790	800
WFITLFNIVY	TSLPVLAMGI	FDQDVSDQNS	VDCPQLYKPG	QLNLLFNKRK	FFICVLHGIY	TSLVLFFIPY	GAFYNVAGED
810	820	830	840	850	860	870	880
GQHIADYQSF	AVTMATSLVI	VVSVQIALDT	SYWTFINHVF	IWGSIAIYFS	ILFTMHSNGI	FGIFPNQFPF	VGNARHSLTQ
890	900	910	920	930	940	950	960
KCIWLVILLT	TVASVMPVVA	FRFLKVDLYP	TLSDQIRRWQ	KAQKKARPPS	SRRPRTRRSS	SRRSGYAFAH	QEGYGELITS
970	980	990	1000	1010			
GKNMRAKNPP	PTSGLEKTHY	NSTSWIENLC	KKTTDTVSSF	SQDKTVKL			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1681	1	863.3176	-113.07	3	49.7	11.2	2	943-965	R.RSGYAFAHQEGYGELITSGKNMR.A	Oxidation: 22

Detailed Protein Report

Protein 1460: keratin-associated protein 5-1 [Homo sapiens]

Accession: gi|54400749

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Modification(s): Carbamidomethyl

Score: 11.2

MW [kDa]: 24.2

pI: 12.2

Sequence Coverage [%]: 7.2

No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MGCCGCSGGC	GSSCGGCGSG	CGGCGSGCGG	CGSGCGGSGS	SCCVPVCCCK	PVCCRVPTCS	CSSCGKGGCG	SSGGSKGGCG
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
SCGGCKGGCG	SCGGSKGGCG	SCGGSKGGCG	SCGGSKGGCG	SGCGGCGSSC	CVPVCCCKPM	CCCVPACSCS	SCGKGGCGSC
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
GCSKGACGSC	GGSKGGCGSC	GGCKGGCGSC	GGSKGGCGSG	CGGCGSGCGV	PVCCCSCSSC	GSCAGSKGGC	GSSCSQCSCC
250	**260**	**270**	**280**				
KPCCCSSGCG	SSCCQSSCCK	PCCSQSSCCV	PVCCQCKI				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1917	1	890.3320	13.02	2	52.6	11.2	1	155-174	K.GGCGSCGCSKGACGSCGGSK.G	Carbamidomethyl: 6, 8

Detailed Protein Report

Protein 1461: PREDICTED: monocarboxylate transporter 10 isoform X1 [Homo sapiens]

Accession:	gi|530383357	**Score:**	11.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	49.9
Database Date:	2015-11-30	**pI:**	9.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.3
		No. of unique Peptides:	1

Quantitation

mdown:qdown **Median:** 1.06 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MVLSQEEPDS	ARGTSEAQPL	GPAPTGAAPP	PGPGPSDSPE	AAVEKVEVEL	AGPATAEPHE	PPEPPEGGWG	WLVMLAAMWC
90	100	110	120	130	140	150	160
NGSVFGIQNA	CGVLFVSMLE	TFGSKDDDKM	VFKTAWVGSL	SMGMIFFCCP	IVSVFTDLFG	CRKTAVVGAA	VGFVGLMSSS
170	180	190	200	210	220	230	240
FVSSIEPLYL	TYGIIFACGC	SFAYQPSLVI	LGHYFKKRLG	LVNGIVTAGS	SVFTILLPLL	LRVLIDSVGL	FYTLRVLCIF
250	260	270	280	290	300	310	320
MFVLFLAGFT	YRPLATSTKD	KESGGSGSSL	FSRKKFSPPK	KIFNFAIFKV	TAYAVWAVGI	PLALFGYFVP	YVHLMKHVNE
330	340	350	360	370	380	390	400
RFQDEKNKEV	VLMCIGVTSG	VGRLLFGRIA	DYVPGVKKVY	LQGYFVTNWA	PMMWHSTSLE	SLPLLEVLCF	VLSRGSIVRS
410	420	430	440	450	460		
KERSVKPLEK	KRWRKCWKTR	TLCCQVHLEC	SRKNLTLLFN	ILHTSTRLDL	LFEF		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1828	1	945.8179	-148.57	2	51.4	11.2	2	419-433	K.TRTLCCQVHLECSRK.N	Carbamidomethyl: 5, 6	mdown:qdown 1.06

Detailed Protein Report

Protein 1462: probable palmitoyltransferase ZDHHC8 isoform 2 [Homo sapiens]

Accession: gi|32698692
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 11.2
MW [kDa]: 81.4
pI: 10.2
Sequence Coverage [%]: 1.8
No. of unique Peptides: 1

Quantitation

Wdown:Qdown **Median:** 0.59 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MPRSPGTRLK	PAKYIPVATA	AALLVGSSTL	FFVFTCPWLT	RAVSPAVPVY	NGIIFLFVLA	NFSMATFMDP	GVFPRADEDE
90	100	110	120	130	140	150	160
DKEDDFRAPL	YKNVDVRGIQ	VRMKWCATCH	FYRPPRCSHC	SVCDNCVEDF	DHHCPWVNNC	IGRRNYRYFF	LFLLSLSAHM
170	180	190	200	210	220	230	240
VGVVAFGLVY	VLNHAEGLGA	AHTTITMAVM	CVAGLFFIPV	IGLTGFHVVL	VTRGRTTNEQ	VTGKFRGGVN	PFTRGCCGNV
250	260	270	280	290	300	310	320
EHVLCSPLAP	RYVVEPPRLP	LAVSLKPPFL	RPELLDRAAP	LKVKLSDNGL	KAGLGRSKSK	GSLDRLDEKP	LDLGPPLPPK
330	340	350	360	370	380	390	400
IEAGTFSSDL	QTPRPGSAES	ALSVQRTSPP	TPAMYKFRPA	FPTGPKVPFC	GPGEQVPGPD	SLTLGDDSIR	SLDFVSEPSL
410	420	430	440	450	460	470	480
DLPDYGPGGL	HAAYPPSPPL	SASDAFSGAL	RSLSLKASSR	RGGDHVALQP	LRSEGGPPTP	HRSIFAPHAL	PNRNGSLSYD
490	500	510	520	530	540	550	560
SLLNPGSPGG	HACPAHPAVG	VAGYHSPYLH	PGATGDPPRP	LPRSFSPVLG	PRPREPSPVR	YDNLSRTIMA	SIQERKDREE
570	580	590	600	610	620	630	640
RERLLRSQAD	SLFGDSGVYD	APSSYSLQQA	SVLSEGPRGP	ALRYGSRDDL	VAGPGFGGAR	NPALQTSLSS	LSSSVSRAPR
650	660	670	680	690	700	710	720
TSSSSLQADQ	ASSNAPGPRP	SSGSHRSPAR	QGLPSPPGTP	HSPSYAGPKA	VAFIHTDLPE	PPPSLTVQRD	HPQLKTPPSK
730	740	750	760	770			
LNGQSPGLAR	LGPATGPPGP	SASPTRHTLV	KKVSGVGGTT	YEISV			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1760	1	727.3946	-63.07	2	50.5	11.2	2	278-291	R.AAPLKVKLSDNGLK.A		Wdown:Qdown 0.59

BRUKER

Detailed Protein Report

Protein 1463: 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 1464: CD109 antigen isoform 2 precursor [Homo sapiens]

Accession:	gi|227430301	**Score:**	11.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	159.6
Database Date:	2015-11-30	**pI:**	5.5
		Sequence Coverage [%]:	1.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MQGPPLLTAA	HLLCVCTAAL	AVAPGPRFLV	TAPGIIRPGG	NVTIGVELLE	HCPSQVTVKA	ELLKTASNLT	VSVLEAEGVF
90	100	110	120	130	140	150	160
EKGSFKTLTL	PSLPLNSADE	IYELRVTGRT	QDEILFSNST	RLSFETKRIS	VFIQTDKALY	KPKQEVKFRI	VTLFSDFKPY
170	180	190	200	210	220	230	240
KTSLNILIKD	PKSNLIQQWL	SQQSDLGVIS	KTFQLSSHPI	LGDWSIQVQV	NDQTYYQSFQ	VSEYVLPKFE	VTLQTPLYCS
250	260	270	280	290	300	310	320
MNSKHLNGTI	TAKYTYGKPV	KGDVTLTFLP	LSFWGKKKNI	TKTFKINGSA	NFSFNDEEMK	NVMDSSNGLS	EYLDLSSPGP
330	340	350	360	370	380	390	400
VEILTTVTES	VTGISRNVST	NVFFKQHDYI	IEFFDYTTVL	KPSLNFTATV	KVTRADGNQL	TLEERRNNVV	ITVTQRNYTE
410	420	430	440	450	460	470	480
YWSGSNSGNQ	KMEAVQKINY	TVPQSGTFKI	EFPILEDSSE	LQLKAYFLGS	KSSMAVHSLF	KSPSKTYIQL	KTRDENIKVG
490	500	510	520	530	540	550	560
SPFELVVSGN	KRLKELSYMV	VSRGQLVAVG	KQNSTMFSLT	PENSWTPKAC	VIVYYIEDDG	EIISDVLKIP	VQLVFKNKIK
570	580	590	600	610	620	630	640
LYWSKVKAEP	SEKVSLRISV	TQPDSIVGIV	AVDKSVNLMN	ASNDITMENV	VHELELYNTG	YYLGMFMNSF	AVFQECGLWV
650	660	670	680	690	700	710	720
LTDANLTKDY	IDGVYDNAEY	AERFMEENEG	HIVDIHDFSL	GSSPHVRKHF	PETWIWLDTN	MGYRIYQEFE	VTVPDSITSW
730	740	750	760	770	780	790	800
VATGFVISED	LGLGLTTTPV	ELQAFQPFFI	FLNLPYSVIR	GEEFALEITI	FNYLKDATEV	KVIIEKSDKF	DILMTSNEIN
810	820	830	840	850	860	870	880
ATGHQQTLLV	PSEDGATVLF	PIRPTHLGEI	PITVTALSPT	ASDAVTQMIL	VKAEGIEKSY	SQSILLDLTD	NRLQSTLKTL
890	900	910	920	930	940	950	960
SFSFPPNTVT	GSERVQITAI	GDVLGPSING	LASLIRMPYG	CGEQNMINFA	PNIYILDYLT	KKKQLTDNLK	EKALSFMRQG
970	980	990	1000	1010	1020	1030	1040
YQRELLYQRE	DGSFSAFGNY	DPSGSTWLSA	FVLRCFLEAD	PYIDIDQNVL	HRTYTWLKGH	QKSNGEFWDP	GRVIHSELQG
1050	1060	1070	1080	1090	1100	1110	1120
GNKSPVTLTA	YIVTSLLGYR	KYQPNIDVQE	SIHFLESEFS	RGISDNYTLA	LITYALSSVG	SPKAKEALNM	LTWRAEQEGG
1130	1140	1150	1160	1170	1180	1190	1200
MQFWVSSESK	LSDSWQPRSL	DIEVAAYALL	SHFLQFQTSE	GIPIMRWLSR	QRNSLGGFAS	TQDTTVALKA	LSEFAALMNT
1210	1220	1230	1240	1250	1260	1270	1280
ERTNIQVTVT	GPSSPSPLAV	VQPTAVNISA	NGFGFAICQL	NVVYNVKASG	SSRRRRSIQN	QEAFDLDVAV	KENKDDLNHV
1290	1300	1310	1320	1330	1340	1350	1360
DLNVCTSFSG	PGRSGMALME	VNLLSGFMVP	SEAISLSETV	KKVEYDHGKL	NLYLDSVNET	QFCVNIPAVR	NFKVSNTQDA
1370	1380	1390	1400	1410	1420	1430	
SVSIVDYYEP	RRQAVRSYNS	EVKLSSCDLC	SDVQGCRPCE	DGASGSHHHS	SVIFIFCFKL	LYFMELWL	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1523	1	705.9891	-48.60	3	47.8	11.1	1	110-127	R.TQDEILFSNSTRLSFETK.R	

Detailed Protein Report

Protein 1465: **calcium/calmodulin-dependent protein kinase type II subunit alpha isoform 2 [Homo sapiens]**

Accession:	gi|25952118	**Score:**	11.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	54.1
Database Date:	2015-11-30	**pI:**	6.7
		Sequence Coverage [%]:	2.9
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	0.40	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.34	**CV:**	0.00 %	**No. of Peptides:**	1

10	20	30	40	50	60	70	80
MATITCTRFT	EEYQLFEELG	KGAFSVVRRC	VKVLAGQEYA	AKIINTKKLS	ARDHQKLERE	ARICRLLKHP	NIVRLHDSIS
90	100	110	120	130	140	150	160
EEGHHYLIFD	LVTGGELFED	IVAREYYSEA	DASHCIQQIL	EAVLHCHQMG	VVHRDLKPEN	LLLASKLKGA	AVKLADFGLA
170	180	190	200	210	220	230	240
IEVEGEQQAW	FGFAGTPGYL	SPEVLRKDPY	GKPVDLWACG	VILYILLVGY	PPFWDEDQHR	LYQQIKAGAY	DFPSPEWDTV
250	260	270	280	290	300	310	320
TPEAKDLINK	MLTINPSKRI	TAAEALKHPW	ISHRSTVASC	MHRQETVDCL	KKFNARRKLK	GAILTTMLAT	RNFSGGKSGG
330	340	350	360	370	380	390	400
NKKSDGVKES	SESTNTTIED	EDTKVRKQEI	IKVTEQLIEA	ISNGDFESYT	KMCDPGMTAF	EPEALGNLVE	GLDFHRFYFE
410	420	430	440	450	460	470	480
NLWSRNSKPV	HTTILNPHIH	LMGDESACIA	YIRITQYLDA	GGIPRTAQSE	ETRVWHRRDG	KWQIVHFHRS	GAPSVLPH

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
66	1	768.2839	-179.38	2	30.0	11.1	2	29-42	R.RCVKVLAGQEYAAK.I		mdown:qdown 0.40 Wdown:Qdown 0.34

Detailed Protein Report

Protein 1466: **thrombospondin-type laminin G domain and EAR repeat-containing protein isoform 1 precursor [Homo sapiens]**

Accession: gi|22001420
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 11.1
MW [kDa]: 74.9
pI: 6.0
Sequence Coverage [%]: 1.5
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MSALLSLCFV	LPLAAPGHGT	QGWEPCTDLR	PLDILAEVVP	SDGATSGIRI	VQVHGARGLQ	LSVAAPRTMS	FPASRIFSQC
90	100	110	120	130	140	150	160
DLFPEEFSIV	VTLRVPNLPP	KRNEYLLTVV	AEESDLLLLG	LRLSPAQLHF	LFLREDTAGA	WQTRVSFRSP	ALVDGRWHTL
170	180	190	200	210	220	230	240
VLAVSAGVFS	LTTDCGLPVD	IMADVPFPAT	LSVKGARFFV	GSRRRAKGLF	MGLVRQLVLL	PGSDATPRLC	PSRNAPLAVL
250	260	270	280	290	300	310	320
SIPRVLQALT	GKPEDNEVLK	YPYETNIRVT	LGPQPPCTEV	EDAQFWFDAS	RKGLYLCVGN	EWVSVLAAKE	RLDYVEEHQN
330	340	350	360	370	380	390	400
LSTNSETLGI	EVFRIPQVGL	FVATANRKAT	SAVYKWTEEK	FVSYQNIPTH	QAQAWRHFTI	GKKIFLAVAN	FEPDEKGQEF
410	420	430	440	450	460	470	480
SVIYKWSHRK	LKFTPYQSIA	THSARDWEAF	EVDGEHFLAV	ANHREGDNHN	IDSVIYKWNP	ATRLFEANQT	IATSGAYDWE
490	500	510	520	530	540	550	560
FFSVGPYSFL	VVANTFNGTS	TKVHSHLYIR	LLGSFQLFQS	FPTFGAADWE	VFQIGERIFL	AVANSHSYDV	EMQVQNDSYV
570	580	590	600	610	620	630	640
INSVIYELNV	TAQAFVKFQD	ILTCSALDWE	FFSVGEDYFL	VVANSFDGRT	FSVNSIIYRW	QGYEGFVAVH	SLPTVGCRDW
650	660	670					
EAFSTTAGAY	LIYSSAKEPL	SRVLRLRTR					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1797	1	1011.7680	171.47	1	51.1	11.1	0	58-67	R.GLQLSVAAPR.T	

Detailed Protein Report

Protein 1467: PREDICTED: sentrin-specific protease 1 isoform X2 [Homo sapiens]

Accession:	gi|578823630	**Score:**	11.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	51.2
Database Date:	2015-11-30	**pI:**	9.2
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	6.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MVTGKQFTIA	KPTTHFPLHL	SRCLSSSKNT	LKDSLFKNGN	SCASQIIGSD	TSSSGSASIL	TNQEQLSHSV	YSLSSYTPDV
90	100	110	120	130	140	150	160
AFGSKDSGTL	HHPHHHHSVP	HQPDNLAASN	TQSEGSDSVI	LLKVKDSQTP	TPSSTFFQAE	LWIKELTSVY	DSRARERLRQ
170	180	190	200	210	220	230	240
IEEQKALALQ	LQNQRLQERE	HSVHDSVELH	LRVPLEKEIP	VTVVQETQKK	GHKLTDSEDE	FPEITEEMEK	EIKNVFRNGN
250	260	270	280	290	300	310	320
QDEVLSEAFR	LTITRKDIQT	LNHLNWLNDE	IINFYMNMLM	ERSKEKGLPS	VHAFNTFFFT	KLKTAGYQAV	KRWTKKVDVF
330	340	350	360	370	380	390	400
SVDILLVPIH	LGVHWCLAVV	DFRKKNITYY	DSMGGINNEA	CRILLQYLKQ	ESIDKKRKEF	DTNGWQLFSK	KSQEIPQQMN
410	420	430	440	450			
GSDCGMFACK	YADCITKDRP	INFTQQHMPY	FRKRMVWEIL	HRKLL			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2416	1	1023.7717	-7.71	3	58.6	11.1	2	391-417	K.KSQEIPQQMNGSDCGMFACKYADCITK.D	Carbamidomethyl: 24; Oxidation: 16

Detailed Protein Report

Protein 1468: **epidermal growth factor receptor kinase substrate 8-like protein 3 isoform c [Homo sapiens]**

Accession:	gi|21071014	**Score:**	11.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	63.5
Database Date:	2015-11-30	**pI:**	8.7
		Sequence Coverage [%]:	3.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSRPSSRAIY	LHRKEYSQNL	TSEPTLLQHR	VEHLMTCKQG	SQRVQGPEDA	LQKLFEMDAQ	GRVWSQDLIL	QVRDGWLQLL
90	100	110	120	130	140	150	160
DIETKEELDS	YRLDSIQAMN	VALNTCSYNS	ILSITVQEPG	LPGTSTLLFQ	CQEVGAERLK	TSLQKALEEE	LEQRPRLGGL
170	180	190	200	210	220	230	240
QPGQDRWRGP	AMERPLPMEQ	ARYLEPGIPP	EQPHQRTLEH	SLPPSPRPLP	RHTSAREPSA	FTLPPPRRSS	SPEDPERDEE
250	260	270	280	290	300	310	320
VLNHVLRDIE	LFMGKLEKAQ	AKTSRKKKFG	KKNKDQGGLT	QAQYIDCFQK	IKHSFNLLGR	LATWLKETSA	PELVHILFKS
330	340	350	360	370	380	390	400
LNFILARCPE	AGLAAQVISP	LLTPKAINLL	QSCLSPPESN	LWMGLGPAWT	TSRADWTGDE	PLPYQPTFSD	DWQLPEPSSQ
410	420	430	440	450	460	470	480
APLGYQDPVS	LRPSSPKPAQ	PALKMQVLYE	FEARNPRELT	VVQGEKLEVL	DHSKRWWLVK	NEAGRSGYIP	SNILEPLQPG
490	500	510	520	530	540	550	560
TPGTQGQSPS	RVPMLRLSSR	PEEVTDWLQA	ENFSTATVRT	LGSLTGSQLL	RIRPGELQML	CPQEAPRILS	RLEAVRRMLG
570							
ISP							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1644	1	711.3358	-24.02	3	49.3	11.1	1	44-62	R.VQGPEDALQKLFEMDAQGR.V	

Detailed Protein Report

Protein 1469: 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 1470: tyrosine 3-monooxygenase isoform b [Homo sapiens]

Accession:	gi|88900503	**Score:**	11.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	55.6
Database Date:	2015-11-30	**pI:**	5.7
		Sequence Coverage [%]:	5.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPTPDATTPQ	AKGFRRAVSE	LDAKQAEAIM	SPRFIGRRQS	LIEDARKERE	AAVAAAAAAV	PSEPGDPLEA	VAFEEKEGKA
90	100	110	120	130	140	150	160
VLNLLFSPRA	TKPSALSRAV	KVFETFEAKI	HHLETRPAQR	PRAGGPHLEY	FVRLEVRRGD	LAALLSGVRQ	VSEDVRSPAG
170	180	190	200	210	220	230	240
PKVPWFPRKV	SELDKCHHLV	TKFDPDLDLD	HPGFSDQVYR	QRRKLIAEIA	FQYRHGDPIP	RVEYTAEEIA	TWKEVYTTLK
250	260	270	280	290	300	310	320
GLYATHACGE	HLEAFALLER	FSGYREDNIP	QLEDVSRFLK	ERTGFQLRPV	AGLLSARDFL	ASLAFRVFQC	TQYIRHASSP
330	340	350	360	370	380	390	400
MHSPEPDCCH	ELLGHVPMLA	DRTFAQFSQD	IGLASLGASD	EEIEKLSTLY	WFTVEFGLCK	QNGEVKAYGA	GLLSSYGELL
410	420	430	440	450	460	470	480
HCLSEEPEIR	AFDPEAAAVQ	PYQDQTYQSV	YFVSESFSDA	KDKLRSYASR	IQRPFSVKFD	PYTLAIDVLD	SPQAVRRSLE
490	500						
GVQDELDTLA	HALSAIG						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2777	1	964.4641	-76.93	3	63.1	11.1	2	281-306	K.ERTGFQLRPVAGLLSARDFLASLAFR.V	

Detailed Protein Report

Protein 1471: 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 1472: epidermal growth factor receptor substrate 15-like 1 isoform 4 [Homo sapiens]

Accession: gi|385648259

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Score: 11.1

MW [kDa]: 66.4

pI: 5.0

Sequence Coverage [%]: 1.3

No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MAAPLIPLSQ	QIPTGNSLYE	SYYKQVDPAY	TGRVGASEAA	LFLKKSGLSD	IILGKIWDLA	DPEGKGFLDK	QGFYVALRLV
90	100	110	120	130	140	150	160
ACAQSGHEVT	LSNLNLSMPP	PKFHDTSSPL	MVTPPSAEAH	WAVRVEEKAK	FDGIFESLLP	INGLLSGDKV	KPVLMNSKLP
170	180	190	200	210	220	230	240
LDVLGRVWDL	SDIDKDGHLD	RDEFAVAMHL	VYRALEKEPV	PSALPPSLIP	PSKRKKTVFP	GAVPVLPASP	PPKDSLRSTP
250	260	270	280	290	300	310	320
SHGSVSSLNS	TGSLSPKHSL	KQTQPTVNWV	VPVADKMRFD	EIFLKTDLDL	DGYVSGQEVK	EIFMHSGLTQ	NLLAHIWALA
330	340	350	360	370	380	390	400
DTRQTGKLSK	DQFALAMYFI	QQKVSKGIDP	PQVLSPDMVP	PSERGTPGPD	SSGSLGSGEF	TGVKELDDIS	QEIAQLQREK
410	420	430	440	450	460	470	480
YSLEQDIREK	EEAIRQKTSE	VQELQNDLDR	ETSSLQELEA	QKQDAQDRLD	EMDQQKAKLR	DMLSDVRQKC	QDETQMISSL
490	500	510	520	530	540	550	560
KTQIQSQESD	LKSQEDDLNR	AKSELNRLQQ	EETQLEQSIQ	AGRVQLETII	KSLKSTQDEI	NQARSKLSQL	HESRQEAHRS
570	580	590	600	610			
LEQYDQVLDG	AHGASLTDLA	NLSEGVSLAE	RGSFGAMVKV	E			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
604	1	472.2410	-113.78	2	36.4	11.1	0	524-531	R.VQLETIIK.S	

Detailed Protein Report

Protein 1473: PREDICTED: rotatin isoform X1 [Homo sapiens]

Accession:	gi|530414157	**Score:**	11.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	146.0
Database Date:	2015-11-30	**pI:**	6.5
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	1.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MRVSLSQQSS	LLTVLFRVSL	IFHEDCSVVT	EVGALFCLLL	FDEVSRMDMW	SVNPSNKPSL	PSVFSLPVSV	FRRYHLPVHV
90	100	110	120	130	140	150	160
IGHHAVSPYS	IVLPLSADCL	ALKPVSDMLR	IAWNLSWYHG	SDNLLKQMNS	ETKTQEILDA	LKLSTEDILT	LKITHMASGL
170	180	190	200	210	220	230	240
QDCLHSIVQA	ATHREVRAAV	TRMSFYLLND	RLSLKGCPGP	CGVTLKSLAW	HTALNRFLQV	LPACTEDEKL	LIDIIHFLNK
250	260	270	280	290	300	310	320
LIKEQRKNSS	LELLNWILEL	LLRHSANPLL	DLLVLTESQA	REETDDIRTA	VRQQLQKELI	ALFDTLLLNF	MEVTDRKCSE
330	340	350	360	370	380	390	400
LLYVFQTQLA	LKLLQCLKVT	DAPHFYGLPS	LERTLRGMAN	LTAFPGWSSH	SPLTKPLDIC	VKYLSGLLEV	ITSFYVERGG
410	420	430	440	450	460	470	480
NAMSFMGKGV	TKSTILCLLH	LSHEMMAQAG	SLEWMSLWFL	PLGSHSEEHI	PTQQGLAWLI	PLWVDRDPEV	RFTSLGLGSA
490	500	510	520	530	540	550	560
LTTLETGCVA	LANSCQNISG	GLWGTVVNIL	LDQSECSMVR	REAAFILQNL	LVIPMPTEII	KDYTWQGPCV	HDEDSGLSLI
570	580	590	600	610	620	630	640
GKPALQALLY	HCHFYEHLNQ	MVKHCYLGRC	MFDLNFSAFD	RNSESNDLNG	LDDSFKFWRA	PSRTSQDRDP	SSLSTSETTV
650	660	670	680	690	700	710	720
APSLGSTEFQ	PLVQSTTLLP	EASHDQFVAQ	GHQESTSPRP	PHDSSLSAPL	PKLCVFVTPS	LLSAMCSLLD	NLLTIAPRDT
730	740	750	760	770	780	790	800
AKAFRQAHLI	ELLCSIADAT	LIQTCVQELR	ALLPSSPPAE	HTQAQVSFLL	EYLSSLSRLL	QSCLLVEPDL	VIQDELVKPL
810	820	830	840	850	860	870	880
ITNIIGILTI	CTKDVLDKEL	ISAFYHTWTH	LFNLLAMLLR	KAGAITLPFV	TVALAKHWTA	AIDMFCTCAG	LSATCPALYT
890	900	910	920	930	940	950	960
ASLQFLSVLL	TEEAKGHLQA	KSKTHLCCSP	TVASLLDDSQ	ENQKSLEQLS	DVILQCYEGK	SSKDILKRVA	ANALMSLLAV
970	980	990	1000	1010	1020	1030	1040
SRRAQKHALK	ANLIDNCMEQ	MKHINAQLNL	DSLRPGKAAL	KKKEDGVIKE	LSIAMQLLRN	CLYQNEECKE	AALEAHLVPV
1050	1060	1070	1080	1090	1100	1110	1120
LHSLWPWILM	DDSLMQISLQ	LLCVYTANFP	NGCSSLCWSS	CGQHPVQATH	RGAVSNSLML	CILKLASQMP	LENTTVQQMV
1130	1140	1150	1160	1170	1180	1190	1200
FMLLSNLALS	HDCKGVIQKS	NFLQNFLSLA	LPKGGNKHLS	NLTILWLKLL	LNISSGEDGQ	QMILRLDGCL	DLLTEMSKYK
1210	1220	1230	1240	1250	1260	1270	1280
HKSSPLLPLL	IFHNVCFSPA	NKPKILANEK	VITVLAACLE	SENQNAQRIG	AAALWALIYN	YQKAKTALKS	PSVKRRVDEA
1290	1300	1310	1320				
YSLAKKTFPN	SEANPLNAYY	LKCLENLVQL	LNSS				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2647	1	753.6332	-97.01	3	61.9	11.1	2	964-982	R.AQKHALKANLIDNCMEQMK.H	Carbamidomethyl: 14; Oxidation: 15

Detailed Protein Report

Protein 1474: PREDICTED: uncharacterized protein LOC100996273 [Homo sapiens]

Accession:	gi|397137819	**Score:**	11.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	23.1
Database Date:	2015-11-30	**pI:**	12.1
		Sequence Coverage [%]:	8.0
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|410173446	refseq_human (refseq_human_20140103.fasta)	PREDICTED: uncharacterized protein LOC100996273 [Homo sapiens]
gi|397139660	refseq_human (refseq_human_20140103.fasta)	PREDICTED: uncharacterized protein LOC100996273 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MSPKCAETAQ QLRCLTENVQ RPLCPTMPAW GRPSLGLLRV SPACQPKGGR SCGCSQPLLK VGLWVEMWAA SGRHSYKCIP
        90        100        110        120        130        140        150        160
ALRTTFLLPS PFLRTPMQKR GRQLTKDREG YCSWHLMGSI CCIPLGCCPG WIGKELAGRL SSVLTTWLGG GRGAWQEQSA
       170        180        190        200        210        220
GPGNWGLVHV CTHVCVCVRA CWVGREEAVK PHPLLSAAVL LCVSAARGCH HTS
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2595	1	973.1975	143.11	2	61.1	11.1	1	78-94	K.CIPALRTTFLLPSPFLR.T	

Detailed Protein Report

Protein 1475: PREDICTED: zinc finger protein 541 isoform X3 [Homo sapiens]

Accession:	gi|530417371	**Score:**	11.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	99.9
Database Date:	2015-11-30	**pI:**	8.6
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	3.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDQYSLGDEG	ALPSEMHLPS	FSESQGLNCS	DTLNRDLGPN	TRGFLYAGLS	GLDPDPSLPT	PDMSSEVLED	NLDTLSLYSG
90	100	110	120	130	140	150	160
KDSDSVKLLE	EYADSESQAS	LQDLGLGVLK	AKEADEGGRA	TSGSARKGKR	QHSSPQNPLL	DCSLCGKVFS	SASSLSKHYL
170	180	190	200	210	220	230	240
THSQERKHVC	KICSKAFKRQ	DHLTGHMLTH	QKTKPFVCIE	QGCSKSYCDY	RSLRRHYEVH	HGLCILKEAP	PEEEACGDSP
250	260	270	280	290	300	310	320
HAHESAGQPP	PSSLRSLVPP	EARSPGSLLP	HRDLLRRIVS	SIVHQKTPSP	GPAPAGASDS	EGRNTACPCP	ASSGSSSCTP
330	340	350	360	370	380	390	400
AGPHAAPAAL	DTELPEEPCL	PQKEPATDVF	TAPNSRAAEN	GAPDPPEPEP	DTALLQARST	AECWPEGGSV	PACLPLFRGQ
410	420	430	440	450	460	470	480
TVPASSQPSS	HSFQWLRNLP	GCPKSKGNNV	FVVHKPSAVP	SREGSESGPG	PSSGSPSEES	PPGPGGGLED	ALPFPAALLR
490	500	510	520	530	540	550	560
VPAEAPSDPR	SASGEDDPCA	PKKVKVDCDS	FLCQNPGEPG	LQEAQKAGGL	PADASPLFRQ	LFLKSQEPLV	SHEQMQVFQM
570	580	590	600	610	620	630	640
ITKSQRIFSH	AQVAAVSSQL	PAPEGKPAAL	RPLQGPWPQQ	PPPLAPAVDS	LHAGPGNPEA	EGSPARRRKT	TPGVPREASP
650	660	670	680	690	700	710	720
GSTRRDAKGG	LKVAAVPTPL	AAPSLDPSRN	PDISSLAKQL	RSSKGTLDLE	DIFPSTGQRQ	TQLGGEEPPG	ASLPGKQAPA
730	740	750	760	770	780	790	800
ENGAASRITK	GEKGPACSRG	GGYRLLGNPR	APRFSGFRKE	KAKMDMCCAA	SPSQVAMASF	SSAGPPADPS	KSKLTIFSRI
810	820	830	840	850	860	870	880
QGGNIYRLPH	PVKEENVAGR	GNQQNGSPTD	WTKPRSTFVC	KNCSQMFYTE	KGLSSHMCFH	SDQWPSPRGK	QEPQVFGTEF
890	900	910	920	930	940	950	
CKPLRQVLRP	EGDRHSPPGT	KKPLDPTAAA	PLVVPQSIPV	VPVTRHIGSM	AMIKWMGPLA	SVW	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2278	1	1011.3645	-70.43	3	56.9	11.1	1	764-793	K.MDMCCAASPSQVAMASFSSAGPPADPSKSK.L	Carbamidomethyl: 4; Oxidation: 14

Detailed Protein Report

Protein 1476: PREDICTED: tRNA-splicing endonuclease subunit Sen2 isoform X5 [Homo sapiens]

Accession:	gi|530373218	**Score:**	11.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	42.4
Database Date:	2015-11-30	**pI:**	8.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	7.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAEAVFHAPK	RKRRVYETYE	SPLPIPFGQD	HGPLKEFKIF	RAEMINNNVI	VRNAEDIEQL	YGKGYFGKGI	LSRSRPSFTI
90	100	110	120	130	140	150	160
SDPKLVAKWK	DMKTNMPIIT	SKRYQHSVEW	AAELMRRQGQ	DESTVRRILK	DYTKPLEHPP	VKRNEEAQVH	DKLNSGMVSN
170	180	190	200	210	220	230	240
MEGTAGGERP	SVVNGDSGKS	GGVGDPREPL	GCLQEGSGCH	PTTESFEKSV	REDASPLPHV	CCCKQDALIL	QRGLHHEDGS
250	260	270	280	290	300	310	320
QHIGLLHPGD	RGPDHEYVLV	EEAECAMSER	EAAPNEELVQ	RNRLICRRNP	YRIFEYLQLS	LEEAFFLVYA	LGCLSIYYEK
330	340	350	360	370	380		
EPLTIVKLWK	AFTVVQPTFR	TTYMAYHYFR	SKGWVPKVGL	KYGTDLLILS	LSS		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2156	1	1030.0351	-91.45	3	55.5	11.0	1	180-208	K.SGGVGDPREPLGCLQEGSGCHPTTESFEK.S	Carbamidomethyl: 13, 20

Detailed Protein Report

Protein 1477: nucleolar protein of 40 kDa isoform f [Homo sapiens]

Accession:	gi|543173125	**Score:**	11.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	20.4
Database Date:	2015-11-30	**pI:**	10.5
		Sequence Coverage [%]:	6.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGPLSKSQAV	GSKMKNDRIK	VSLSMKVVNQ	GTGKDLDPNN	VIIEQEERRR	RSFQDYTGQK	ITLEAVLNTT	CKKCGCKGHF
90	100	110	120	130	140	150	160
AKDCFMQPGG	TKYSLIPDEE	EEKEEAKSAE	FEKPDPTRNP	SRKRKKEKKK	KKHRDRKSSD	SDSSDSESDT	GKRARHTSKD
170	180						
SKAAKKKKKK	KKHKKKHKE						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1952	1	676.2626	-80.17	2	52.9	11.0	0	93-103	K.YSLIPDEEEEK.E	

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Detailed Protein Report

Protein 1478: 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

Alias proteins:

Accession	Name	Description
gi|511772972	refseq_huma (refseq_human_20140103.fasta)	adenosine receptor A2a [Homo sapiens]
gi|511772970	refseq_huma (refseq_human_20140103.fasta)	adenosine receptor A2a [Homo sapiens]
gi|511772967	refseq_huma (refseq_human_20140103.fasta)	adenosine receptor A2a [Homo sapiens]
gi|511772965	refseq_huma (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
1218	1	695.7632	-135.29	2	44.9	11.0	1	310-322	R.QQEPFKAAGTSAR.V	

Detailed Protein Report

Protein 1479: **phosphatidylinositol 3,4,5-trisphosphate 3-phosphatase TPTE2 isoform delta [Homo sapiens]**

Accession:	gi|213972593	**Score:**	11.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	48.4
Database Date:	2015-11-30	**pI:**	9.5
		Sequence Coverage [%]:	3.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MNESPQTNEF	KGTTEEAPAK	ESPHTSEFKG	AALVSPISKS	MLERLSKFEV	EDAENVASYE	WTHLVRLLRL	IILIRIFHLL
90	100	110	120	130	140	150	160
HQKRQLEKLM	RRLVSENKRR	YTRDGFDLDL	TYVTERIIAM	SFPSSGRQSF	YRNPIEEVVR	FLDKKHRNHY	RVYNLCSERA
170	180	190	200	210	220	230	240
YDPKHFHNRV	SRIMIDDHNV	PTLHEMVVFT	KEVNEWMAQD	LENIVAIHCK	GGKGRTGTMV	CALLIASEIF	LTAEESLYYF
250	260	270	280	290	300	310	320
GERRTNKTHS	NKFQGVETPS	QNRYVGYFAQ	VKHLYNWNLP	PRRILFIKRF	IIYSIRGDVC	DLKVQVVMEK	KVVFSSTSLG
330	340	350	360	370	380	390	400
NCSILHDIET	DKILINVYDG	PPLYDDVKVQ	FFSSNLPKYY	DNCPFFFWFN	TSFIQNNRLC	LPRNELDNPH	KQKAWKIYPP
410	420						
EFAVEILFGE	K						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
89	1	879.2188	170.15	2	30.3	11.0	1	70-83	R.LIILIRIFHLLHQK.R	

Detailed Protein Report

Protein 1480: PREDICTED: uridine-cytidine kinase 1 isoform X2 [Homo sapiens]

Accession:	gi|530427236	**Score:**	11.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	28.8
Database Date:	2015-11-30	**pI:**	8.9
		Sequence Coverage [%]:	4.3
		No. of unique Peptides:	1

Quantitation

Wdown:Qdown **Median:** 0.87 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MASAGGEDCE	SPAPEADRPH	QRPFLIGVSG	GTASGKSTVC	EKIMELLGQN	EVEQRQRKVV	ILSQDRFYKV	LTAEQKAKAL
90	100	110	120	130	140	150	160
KGQYNFDHPD	AFDNDLMHRT	LKNIVEGKTV	EVPTYDFVTH	SSQEIRDMFH	LRLFVDTDSD	VRLSRRVLRD	VRRGRDLEQI
170	180	190	200	210	220	230	240
LTQYTTFVKP	AFEEFCLPTK	KYADVIIPRG	VDNMVAINLI	VQHIQDILNG	DICKWHRGGS	NGRSYKRTFS	EPGDHPGMLT
250	260						
SGKRSHLESS	SRPH						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
309	1	646.7814	-69.45	2	33.0	11.0	1	244-254	K.RSHLESSSRPH.-		Wdown:Qdown 0.87

Detailed Protein Report

Protein 1481: PREDICTED: NADPH oxidase 4 isoform X5 [Homo sapiens]

Accession: gi|578822233
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 11.0
MW [kDa]: 59.9
pI: 10.0
Sequence Coverage [%]: 1.0
No. of unique Peptides: 1

Quantitation

mdown:qdown **Median:** 1.49 **CV:** 0.00 % **No. of Peptides:** 1
Wdown:Qdown **Median:** 4.69 **CV:** 0.00 % **No. of 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	Ratios
1019	1	700.1280	-288.50	1	42.3	11.0	0	506-510	R.FEYNK.E		mdown:qdown 1.49 Wdown:Qdown 4.69

Detailed Protein Report

Protein 1482: **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 1483: lutropin-choriogonadotropic hormone receptor precursor [Homo sapiens]

Accession:	gi|106067657	**Score:**	11.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	78.6
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
MKQRFSALQL	LKLLLLLQPP	LPRALREALC	PEPCNCVPDG	ALRCPGPTAG	LTRLSLAYLP	VKVIPSQAFR	GLNEVIKIEI
90	100	110	120	130	140	150	160
SQIDSLERIE	ANAFDNLLNL	SEILIQNTKN	LRYIEPGAFI	NLPRLKYLSI	CNTGIRKFPD	VTKVFSSESN	FILEICDNLH
170	180	190	200	210	220	230	240
ITTIPGNAFQ	GMNNESVTLK	LYGNGFEEVQ	SHAFNGTTLT	SLELKENVHL	EKMHNGAFRG	ATGPKTLDIS	STKLQALPSY
250	260	270	280	290	300	310	320
GLESIQRLIA	TSSYSLKKLP	SRETFVNLLE	ATLTYPSHCC	AFRNLPTKEQ	NFSHSISENF	SKQCESTVRK	VNNKTLYSSM
330	340	350	360	370	380	390	400
LAESELSGWD	YEYGFCLPKT	PRCAPEPDAF	NPCEDIMGYD	FLRVLIWLIN	ILAIMGNMTV	LFVLLTSRYK	LTVPRFLMCN
410	420	430	440	450	460	470	480
LSFADFCMGL	YLLLIASVDS	QTKGQYYNHA	IDWQTGSGCS	TAGFFTVFAS	ELSVYTLTVI	TLERWHTITY	AIHLDQKLRL
490	500	510	520	530	540	550	560
RHAILIMLGG	WLFSSLIAML	PLVGVSNYMK	VSICFPMDVE	TTLSQVYILT	ILILNVVAFF	IICACYIKIY	FAVRNPELMA
570	580	590	600	610	620	630	640
TNKDTKIAKK	MAILIFTDFT	CMAPISFFAI	SAAFKVPLIT	VTNSKVLLVL	FYPINSCANP	FLYAIFTKTF	QRDFFLLLSK
650	660	670	680	690	700		
FGCCKRRAEL	YRRKDFSAYT	SNCKNGFTGS	NKPSQSTLKL	STLHCQGTAL	LDKTRYTEC		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2554	1	836.1315	177.64	2	60.2	11.0	1	63-77	K.VIPSQAFRGLNEVIK.I	

Detailed Protein Report

Protein 1484: **microtubule-associated protein 1S [Homo sapiens]**

Accession:	gi|50428935	**Score:**	11.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	112.1
Database Date:	2015-11-30	**pI:**	7.1
		Sequence Coverage [%]:	1.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAAVAGSGAA	AAPSSLLLVV	GSEFGSPGLL	TYVLEELERG	IRSWDVDPGV	CNLDEQLKVF	VSRHSATFSS	IVKGQRSLHH
90	100	110	120	130	140	150	160
RGDNLETLVL	LNPSDKSLYD	ELRNLLLDPA	SHKLLVLAGP	CLEETGELLL	QTGGFSPHHF	LQVLKDREIR	DILATTPPPV
170	180	190	200	210	220	230	240
QPPILTITCP	TFGDWAQLAP	AVPGLQGALR	LQLRLNPPAQ	LPNSEGLCEF	LEYVAESLEP	PSPFELLEPP	TSGGFLRLGR
250	260	270	280	290	300	310	320
PCCYIFPGGL	GDAAFFAVNG	FTVLVNGGSN	PKSSFWKLVR	HLDRVDAVLV	THPGADSLPG	LNSLLRRKLA	ERSEVAAGGG
330	340	350	360	370	380	390	400
SWDDRLRRLI	SPNLGVVFFN	ACEAASRLAR	GEDEAELALS	LLAQLGITPL	PLSRGPVPAK	PTVLFEKMGV	GRLDMYVLHP
410	420	430	440	450	460	470	480
PSAGAERTLA	SVCALLVWHP	AGPGEKVVRV	LFPGCTPPAC	LLDGLVRLQH	LRFLREPVVT	PQDLEGPGRA	ESKESVGSRD
490	500	510	520	530	540	550	560
SSKREGLLAT	HPRPGQERPG	VARKEPARAE	APRKTEKEAK	TPRELKKDPK	PSVSRTQPRE	VRRAASSVPN	LKKTNAQAAP
570	580	590	600	610	620	630	640
KPRKAPSTSH	SGFPPVANGP	RSPPSLRCGE	ASPPSAACGS	PASQLVATPS	LELGPIPAGE	EKALELPLAA	SSIPRPRTPS
650	660	670	680	690	700	710	720
PESHRSPAEG	SERLSLSPLR	GGEAGPDASP	TVTTPTVTTP	SLPAEVGSPH	STEVDESLSV	SFEQVLPPSA	PTSEAGLSLP
730	740	750	760	770	780	790	800
LRGPRARRSA	SPHDVDLCLV	SPCEFEHRKA	VPMAPAPASP	GSSNDSSARS	QERAGGLGAE	ETPPTSVSES	LPTLSDSDPV
810	820	830	840	850	860	870	880
PLAPGAADSD	EDTEGFGVPR	HDPLPDPLKV	PPPLPDPSSI	CMVDPEMLPP	KTARQTENVS	RTRKPLARPN	SRAAAPKATP
890	900	910	920	930	940	950	960
VAAAKTKGLA	GGDRASRPLS	ARSEPSEKGG	RAPLSRKSST	PKTATRGPSG	SASSRPGVSA	TPPKSPVYLD	LAYLPSGSSA
970	980	990	1000	1010	1020	1030	1040
HLVDEEFFQR	VRALCYVISG	QDQRKEEGMR	AVLDALLASK	QHWDRDLQVT	LIPTFDSVAM	HTWYAETHAR	HQALGITVLG
1050	1060						
SNSMVSMQDD	AFPACKVEF						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2793	1	698.3606	-84.41	2	64.0	11.0	2	873-887	R.AAAPKATPVAAAKTK.G	

Detailed Protein Report

Protein 1485: potassium voltage-gated channel subfamily H member 5 isoform 1 [Homo sapiens]

Accession:	gi|22024390	**Score:**	11.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	111.8
Database Date:	2015-11-30	**pI:**	8.3
		Sequence Coverage [%]:	1.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPGGKRGLVA	PQNTFLENIV	RRSSESSFLL	GNAQIVDWPV	VYSNDGFCKL	SGYHRADVMQ	KSSTCSFMYG	ELTDKKTIEK
90	100	110	120	130	140	150	160
VRQTFDNYES	NCFEVLLYKK	NRTPVWFYMQ	IAPIRNEHEK	VVLFLCTFKD	ITLFKQPIED	DSTKGWTKFA	RLTRALTNSR
170	180	190	200	210	220	230	240
SVLQQLTPMN	KTEVVHKHSR	LAEVLQLGSD	ILPQYKQEAP	KTPPHIILHY	CAFKTTWDWV	ILILTFYTAI	MVPYNVSFKT
250	260	270	280	290	300	310	320
KQNNIAWLVL	DSVVDVIFLV	DIVLNFHTTF	VGPGGEVISD	PKLIRMNYLK	TWFVIDLLSC	LPYDIINAFE	NVDEGISSLF
330	340	350	360	370	380	390	400
SSLKVVRLLR	LGRVARKLDH	YLEYGAAVLV	LLVCVFGLVA	HWLACIWYSI	GDYEVIDEVT	NTIQIDSWLY	QLALSIGTPY
410	420	430	440	450	460	470	480
RYNTSAGIWE	GGPSKDSLYV	SSLYFTMTSL	TTIGFGNIAP	TTDVEKMFSV	AMMMVGSLLY	ATIFGNVTTI	FQQMYANTNR
490	500	510	520	530	540	550	560
YHEMLNNVRD	FLKLYQVPKG	LSERVMDYIV	STWSMSKGID	TEKVLSICPK	DMRADICVHL	NRKVFNEHPA	FRLASDGCLR
570	580	590	600	610	620	630	640
ALAVEFQTIH	CAPGDLIYHA	GESVDALCFV	VSGSLEVIQD	DEVVAILGKG	DVFGDIFWKE	TTLAHACANV	RALTYCDLHI
650	660	670	680	690	700	710	720
IKREALLKVL	DFYTAFANSF	SRNLTLTCNL	RKRIIFRKIS	DVKKEEEERL	RQKNEVTLSI	PVDHPVRKLF	QKFKQQKELR
730	740	750	760	770	780	790	800
NQGSTQGDPE	RNQLQVESRS	LQNGASITGT	SVVTVSQITP	IQTSLAYVKT	SESLKQNNRD	AMELKPNGGA	DQKCLKVNSP
810	820	830	840	850	860	870	880
IRMKNGNGKG	WLRLKNNMGA	HEEKKEDWNN	VTKAESMGLL	SEDPKSSDSE	NSVTKNPLRK	TDSCDSGITK	SDLRLDKAGE
890	900	910	920	930	940	950	960
ARSPLEHSPI	QADAKHPFYP	IPEQALQTTL	QEVKHELKED	IQLLSCRMTA	LEKQVAEILK	ILSEKSVPQA	SSPKSQMPLQ
970	980	990					
VPPQIPCQDI	FSVSRPESPE	SDKDEIHF					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2333	1	788.3805	-60.37	2	57.6	11.0	0	694-707	K.NEVTLSIPVDHPVR.K	

Detailed Protein Report

Protein 1486: **PREDICTED: solute carrier organic anion transporter family member 2B1 isoform X1 [Homo sapiens]**

Accession:	gi|578821116	**Score:**	11.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	68.1
Database Date:	2015-11-30	**pI:**	9.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGPRIGPAGE	VPQVPDKETK	ATMGTENTPG	GKASPDPQDV	RPSVFHNIKL	FVLCHSLLQL	AQLMISGYLK	SSISTVEKRF
90	100	110	120	130	140	150	160
GLSSQTSGLL	ASFNEVGNTA	LIVFVSYFGS	RVHRPRMIGY	GAILVALAGL	LMTLPHFISE	PYRYDNTSPE	DMPQDFKASL
170	180	190	200	210	220	230	240
CLPTTSAPAS	APSNGNCSSY	TETQHLSVVG	IMFVAQTLLG	VGGVPIQPFG	ISYIDDFAHN	SNSPLYLGIL	FAVTMMGPGL
250	260	270	280	290	300	310	320
AFGLGSLMLR	LYVDINQMPE	GGISLTIKDP	RWVGAWWLGF	LIAAGAVALA	AIPYFFFPKE	MPKEKRELQF	RRKVLAVTDS
330	340	350	360	370	380	390	400
PARKGKDSPS	KQSPGESTKK	QDGLVQIAPN	LTVIQFIKVF	PRVLLQTLRH	PIFLLVVLSQ	VCLSSMAAGM	ATFLPKFLER
410	420	430	440	450	460	470	480
QFSITASYAN	LLIGCLSFPS	VIVGIVVGGV	LVKRLHLGPV	GCGALCLLGM	LLCLFFSLPL	FFIGCSSHQI	AGITHQTSAH
490	500	510	520	530	540	550	560
PGLELSPSCM	EACSCPLDGF	NPVCDPSTRV	EYITPCHAGC	SSWVVQDALD	NSQVFYTNCS	CVVEGNPVLA	GSCDSTCSHL
570	580	590	600	610	620	630	640
VVPFLLLVSL	GSALACLTHT	PSFMLILRGV	KKEDKTLAVG	IQFMFLRILD	PILRAAVPWP	GGGLSQLLPA	TRSNK

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1287	1	882.4630	4.40	2	44.9	11.0	1	1-17	-.MGPRIGPAGEVPQVPDK.E	Oxidation: 1

Detailed Protein Report

Protein 1487: ephrin-B1 precursor [Homo sapiens]

Accession:	gi|4758248	**Score:**	11.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	38.0
Database Date:	2015-11-30	**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 1488: arf-GAP domain and FG repeat-containing protein 1 isoform 4 [Homo sapiens]

Accession:	gi|206597509	**Score:**	11.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	54.1
Database Date:	2015-11-30	**pI:**	9.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.3
		No. of unique Peptides:	1

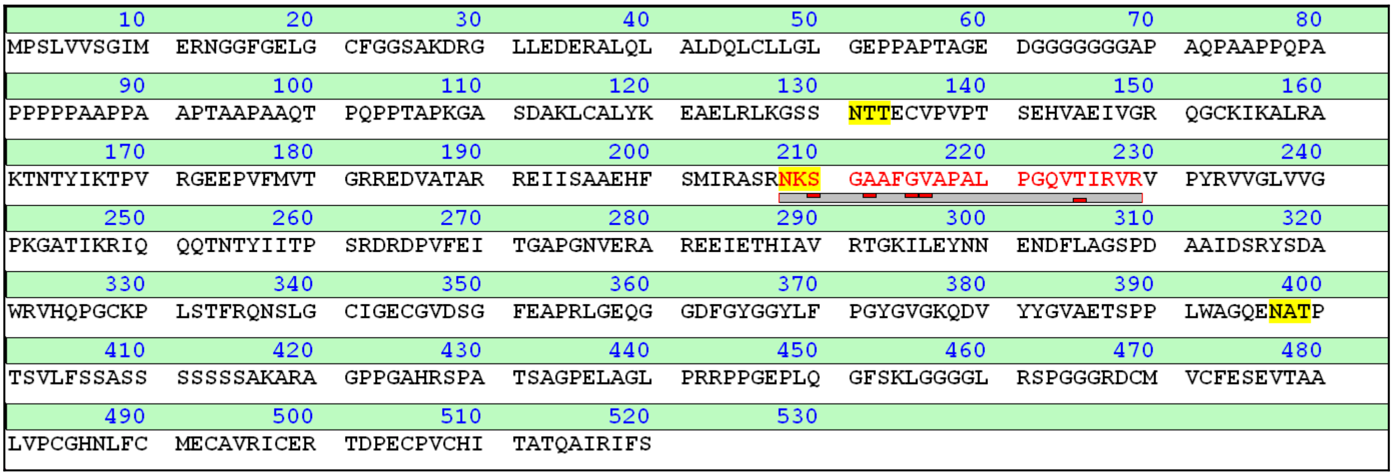
10	20	30	40	50	60	70	80
MAASAKRKQE	EKHLKMLRDM	TGLPHNRKCF	DCDQRGPTYV	NMTVGSFVCT	SCSGSLRGLN	PPHRVKSISM	TTFTQQEIEF
90	100	110	120	130	140	150	160
LQKHGNEVCK	QIWLGLFDDR	SSAIPDFRDP	QKVKEFLQEK	YEKKRWYVPP	EQAKVVASVH	ASISGSSASS	TSSTPEVKPL
170	180	190	200	210	220	230	240
KSLLGDSAPT	LHLNKGTPSQ	SPVVGRSQGQ	QQEKKQFDLL	SDLGSDIFAA	PAPQSTATAN	FANFAHFNSH	AGGSAASVNA
250	260	270	280	290	300	310	320
NFAHFDNFPK	SSSADFGTFN	TSQSHQTASA	VSKVSTNKAG	LQTADKYAAL	ANLDNIFSAG	QGGDQGSGFG	TTGKAPVGSV
330	340	350	360	370	380	390	400
VSVPSQSSAS	SDKYAALAEL	DSVFSSAATS	SNAYTSTSNA	SSNVFGTVPV	VASAQTQPAS	SSVPAPFGAT	PSTNPFVAAA
410	420	430	440	450	460	470	480
GPSVASSTNP	FQTNARGATA	ATFGTASMSM	PTGFGTPAPY	SLPTSFSGSF	QQPAFPAQAA	FPQQTAFSQQ	PNGAGFAAFG
490	500	510	520	530			
QTKPVVTPFG	QVAAAGVSSN	PFMTGAPTGQ	FPTGSSSTNP	FL			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2525	1	1044.1469	131.14	2	59.8	11.0	1	84-100	K.HGNEVCKQIWLGLFDDR.S	Carbamidomethyl: 6

Detailed Protein Report

Protein 1489: RNA-binding protein MEX3A [Homo sapiens]

Accession:	gi|147902746	**Score:**	11.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	54.1
Database Date:	2015-11-30	**pI:**	7.8
		Sequence Coverage [%]:	4.2
		No. of unique Peptides:	1



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        10         20         30         40         50         60         70         80
MPSLVVSGIM ERNGGFGELG CFGGSAKDRG LLEDERALQL ALDQLCLLGL GEPPAPTAGE DGGGGGGGAP AQPAAPPQPA
        90        100        110        120        130        140        150        160
PPPPPAAPPA APTAAPAAQT PQPPTAPKGA SDAKLCALYK EAELRLKGSS NTTECVPVPT SEHVAEIVGR QGCKIKALRA
       170        180        190        200        210        220        230        240
KTNTYIKTPV RGEEPVFMVT GRREDVATAR REIISAAEHF SMIRASRNKS GAAFGVAPAL PGQVTIRVRV PYRVVGLVVG
       250        260        270        280        290        300        310        320
PKGATIKRIQ QQTNTYIITP SRDRDPVFEI TGAPGNVERA REEIETHIAV RTGKILEYNN ENDFLAGSPD AAIDSRYSDA
       330        340        350        360        370        380        390        400
WRVHQPGCKP LSTFRQNSLG CIGECGVDSG FEAPRLGEQG GDFGYGGYLF PGYGVGKQDV YYGVAETSPP LWAGQENATP
       410        420        430        440        450        460        470        480
TSVLFSSASS SSSSSAKARA GPPGAHRSPA TSAGPELAGL PRRPPGEPLQ GFSKLGGGGL RSPGGGRDCM VCFESEVTAA
       490        500        510        520        530
LVPCGHNLFC MECAVRICER TDPECPVCHI TATQAIRIFS
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
977	1	737.1785	119.61	3	40.7	11.0	2	208-229	R.NKSGAAFGVAPALPGQVTIRVR.V	

Detailed Protein Report

Protein 1490: olfactory receptor 1L6 [Homo sapiens]

Accession:	gi|256773201	**Score:**	11.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	35.2
Database Date:	2015-11-30	**pI:**	10.2
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	5.1
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MEIKNYSSST SGFILLGLSS NPQLQKPLFA IFLIMYLLAA VGNVLIIPAI YSDPRLHTPM YFFLSNLSFM DICFTTVIVP
        90        100        110        120        130        140        150        160
KMLVNFLSET KVISYVGCLA QMYFFMAFGN TDSYLLASMA IDRLVAICNP LHYDVVMKPR HCLLMLLGSC SISHLHSLFR
       170        180        190        200        210        220        230        240
VLLMSRLSFC ASHIIKHFFC DTQPVLKLSC SDTSSSQMVV MTETLAVIVT PFLCIIFSYL RIMVTVLRIP SAAGKWKAFS
       250        260        270        280        290        300        310        320
TCGSHLTAVA LFYGSIIYVY FRPLSMYSVV RDRVATVMYT VVTPMLNPFI YSLRNKDMKR GLKKLQDRIY R
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
970	1	945.9344	-88.68	2	40.9	11.0	1	161-176	R.VLLMSRLSFCASHIIK.H	Carbamidomethyl: 10; Oxidation: 4

Detailed Protein Report

Protein 1491: PREDICTED: anamorsin isoform X3 [Homo sapiens]

Accession:	gi|530424142	**Score:**	11.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	27.5
Database Date:	2015-11-30	**pI:**	7.8
		Sequence Coverage [%]:	5.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MADFGISAGQ	FVAVVWDKSS	PVEALKGLVD	KLQALTGNEG	RVSVENIKQL	LQCLVPGSTT	LHSAEILAEI	ARILRPGGCL
90	100	110	120	130	140	150	160
FLKEPVETAV	DNNSKVKTAS	KLCSALTLSG	LVEVKELQRE	PLTPEEVQSV	REHLGHESDN	LLFVQITGKK	PNFEVGSSRQ
170	180	190	200	210	220	230	240
LKLSITKKSS	PSVKPAVDPA	AAKLWTLSAN	DMEDDSMHLW	PCRRTGKREV	KGTDELPTQV	SLWKLLPGRC	LPLCQLPLPW
250	260						
DASLQTWGKG	ASE						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1766	1	785.8755	-70.66	2	50.8	11.0	1	27-41	K.GLVDKLQALTGNEGR.V	

Detailed Protein Report

Protein 1492: 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

mdown:qdown	**Median:**	1.98	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.75	**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	Wdown:Qdown 0.75 mdown:qdown 1.98

Detailed Protein Report

Protein 1493: transmembrane protein 121 [Homo sapiens]

Accession:	gi|13376888	**Score:**	11.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	35.8
Database Date:	2015-11-30	**pI:**	10.2
		Sequence Coverage [%]:	8.5
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|578826154	refseq_human (refseq_human_20140103.fasta)	PREDICTED: transmembrane protein 121 isoform X2 [Homo sapiens]
gi|530404697	refseq_human (refseq_human_20140103.fasta)	PREDICTED: transmembrane protein 121 isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MVLPPPDRRH	VCLTTLVIMG	SMAVMDAYLV	EQNQGPRKIG	VCIIVLVGDV	CFLLVLRYVA	VWVGAEVRTA	KRGYAMILWF
90	100	110	120	130	140	150	160
LYIFVLEIKL	YFIFQNYKAA	RRGAADPVAR	KALTLLLSVC	VPGLFLLLVA	LDRMEYVRTF	RKREDLRGRL	FWVALDLLDL
170	180	190	200	210	220	230	240
LDMQASLWEP	PRSGLPLWAE	GLTFFYCYML	LLVLPCVALS	EVSMQGEHIA	PQKMMLYPVL	SLATVNVVAV	LARAANMALF
250	260	270	280	290	300	310	320
RDSRVSAIFV	GKNVVALATK	ACTFLEYRRQ	VRDFPPPALS	LELQPPPPQR	NSVPPPPPPL	HGPPGRPHMS	SPTRDPLDT

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1526	1	1006.6420	60.28	3	47.8	11.0	1	112-138	K.ALTLLLSVCVPGLFLLLVALDRMEYVR.T	

Detailed Protein Report

Protein 1494: **PREDICTED: proline synthase co-transcribed bacterial homolog protein isoform X1 [Homo sapiens]**

Accession:	gi|530387555	**Score:**	11.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	17.6
Database Date:	2015-11-30	**pI:**	11.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	9.5
		No. of unique Peptides:	1

Quantitation

Wdown:Qdown **Median:** 0.67 **CV:** 0.00 % **No. of Peptides:** 1

```
         10         20         30         40         50         60         70         80
MMSNDWFTRR KLGGTGRWCE PRAAGGLGLG VGPRGMWRAG SMSAELGVGC ALRAVNERVQ QAVARRPRDL PAIQPRLVAV
         90        100        110        120        130        140        150        160
SKTKPADMVI EAYGHGQRTF GENYVQELLE KASNPKILSL CPEIKWHFIG HLQKQNVNKL MGKSEFLIKR ENIMPRTE
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1926	1	719.2731	-99.81	2	52.6	11.0	0	39-53	R.AGSMSAELGVGCALR.A	Oxidation: 4	Wdown:Qdown 0.67

Detailed Protein Report

Protein 1495: **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 1496: late cornified envelope protein 1D [Homo sapiens]

Accession:	gi|30387648	**Score:**	11.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	11.2
Database Date:	2015-11-30	**pI:**	12.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	26.3
		No. of unique Peptides:	1

```
         10          20          30          40          50          60          70          80
MSCQQSQQQC  QPPPKCTPKC  TPKCPAPKCP  PKCPPVSSCC  SVSSGGCCGS  SSGGGCGSNS  GGCCSSGGGG  CCLSHHRRHR
         90         100         110         120
SHRRRPQSSD  CCSQPSGGSS  CCGGGSSQHS  GGCC
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2178	1	1011.9998	-26.60	3	55.7	11.0	0	85-114	R.RPQSSDCCSQPSGGSSCCGGGSSQHSGGCC.-	Carbamidomethyl: 7, 8, 17, 18

Detailed Protein Report

Protein 1497: N-acylneuraminate cytidylyltransferase [Homo sapiens]

Accession:	gi|8923900	**Score:**	11.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	48.3
Database Date:	2015-11-30	**pI:**	9.1
		Sequence Coverage [%]:	3.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDSVEKGAAT	SVSNPRGRPS	RGRPPKLQRN	SRGGQGRGVE	KPPHLAALIL	ARGGSKGIPL	KNIKHLAGVP	LIGWVLRAAL
90	100	110	120	130	140	150	160
DSGAFQSVWV	STDHDEIENV	AKQFGAQVHR	RSSEVSKDSS	TSLDAIIEFL	NYHNEVDIVG	NIQATSPCLH	PTDLQKVAEM
170	180	190	200	210	220	230	240
IREEGYDSVF	SVVRRHQFRW	SEIQKGVREV	TEPLNLNPAK	RPRRQDWDGE	LYENGSFYFA	KRHLIEMGYL	QGGKMAYYEM
250	260	270	280	290	300	310	320
RAEHSVDIDV	DIDWPIAEQR	VLRYGYFGKE	KLKEIKLLVC	NIDGCLTNGH	IYVSGDQKEI	ISYDVKDAIG	ISLLKKSGIE
330	340	350	360	370	380	390	400
VRLISERACS	KQTLSSLKLD	CKMEVSVSDK	LAVVDEWRKE	MGLCWKEVAY	LGNEVSDEEC	LKRVGLSGAP	ADACSTAQKA
410	420	430	440				
VGYICKCNGG	RGAIREFAEH	ICLLMEKVNN	SCQK				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1229	1	945.6711	141.77	2	44.0	11.0	2	189-204	R.EVTEPLNLNPAKRPRR.Q	

Detailed Protein Report

Protein 1498: microfibrillar-associated protein 2 isoform b precursor [Homo sapiens]

Accession:	gi|207028905	**Score:**	11.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	20.7
Database Date:	2015-11-30	**pI:**	4.7
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	10.4
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|207028935	refseq_human (refseq_human_20140103.fasta)	microfibrillar-associated protein 2 isoform b precursor [Homo sapiens]

10	20	30	40	50	60	70	80
MRAAYLFLLF	LPGLLAQGQY	DLDPLPPFPD	HVQYTHYSDQ	IDNPDYYDYQ	EVTPRPSEEQ	FQFQSQQQVQ	QEVIPAPTPE
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
PGNAELEPTE	PGPLDCREEQ	YPCTRLYSIH	RPCKQCLNEV	CFYSLRRVYV	INKEICVRTV	CAHEELLRAD	LCRDKFSKCG
170	**180**	**190**					
VMASSGLCQS	VAASCARSCG	SC					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2288	1	937.3710	-36.11	2	57.1	11.0	0	159-177	K.CGVMASSGLCQSVAASCAR.S	Carbamidomethyl: 10; Oxidation: 4

Detailed Protein Report

Protein 1499: PREDICTED: polypyrimidine tract-binding protein 3 isoform X5 [Homo sapiens]

Accession: gi|578818044
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 11.0
MW [kDa]: 56.5
pI: 9.9
Sequence Coverage [%]: 5.2
No. of unique Peptides: 1

Quantitation

mdown:qdown **Median:** 0.68 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MNSSTPSTAN GNDSKKFKRD RPPCSPSRVL HLRKIPCDVT EAEIISLGLP FGKVTNLLML KGKSQAFLEM ASEEAAVTMV
        90        100        110        120        130        140        150        160
NYYTPITPHL RSQPVYIQYS NHRELKTDNL PNQARAQAAL QAVSAVQSGS LALSGGPSNE GTVLPGQSPV LRIIIENLFY
       170        180        190        200        210        220        230        240
PVTLEVLHQI FSKFGTVLKI ITFTKNNQFQ ALLQYADPVN AHYAKMALDG QNIYNACCTL RIDFSKLTSL NVKYNNDKSR
       250        260        270        280        290        300        310        320
DFTRLDLPTG DGQPSLEPPM AAAFGAPGII SSPYAGAAGF APAIGFPQAT GLSVPAVPGA LGPLTITSSA VTGRMAIPGA
       330        340        350        360        370        380        390        400
SGIPGNSVLL VTNLNPDLIT PHGLFILFGV YGDVHRVKIM FNKKENALVQ MADANQAQLA MNHLSGQRLY GKVLRATLSK
       410        420        430        440        450        460        470        480
HQAVQLPREG QEDQGLTKDF SNSPLHRFKK PGSKNFQNIF PPSATLHLSN IPPSVTVDDL KNLFIEAGCS VKAFKFFQKD
       490        500        510        520        530
RKMALIQLGS VEEAIQALIE LHNHDLGENH HLRVSFSKST I
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
266	1	977.4418	-97.99	3	32.1	11.0	1	35-61	K. IPCDVTEAEIISLGLPFGKVTNLLMI G	Oxidation: 25	mdown:qdown 0.68

Protein 1500: **PREDICTED: 26S proteasome non-ATPase regulatory subunit 6 isoform X2 [Homo sapiens]**

Accession:	gi|530373467	**Score:**	11.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	40.0
Database Date:	2015-11-30	**pI:**	5.7
		Sequence Coverage [%]:	2.9
		No. of unique Peptides:	1

Quantitation

mdown:qdown **Median:** 2.27 **CV:** 0.00 % **No. of Peptides:** 1

Alias proteins:

Accession	**Name**	**Description**
gi|578806816	refseq_human (refseq_human_20140103.fasta)	PREDICTED: 26S proteasome non-ATPase regulatory subunit 6 isoform X3 [Homo sapiens]

10	20	30	40	50	60	70	80
MAPYYEALCK	SLDWQIDVDL	LNKMKKANED	ELKRLDEELE	DAEKNLGESE	IRDAMMAKAE	YLCRIGDKEG	ALTAFRKTYD
90	100	110	120	130	140	150	160
KTVALGHRLD	IVFYLLRIGL	FYMDNDLITR	NTEKAKSLIE	EGGDWDRRNR	LKVYQGLYCV	AIRDFKQAAE	LFLDTVSTFT
170	180	190	200	210	220	230	240
SYELMDYKTF	VTYTVYVSMI	ALERPDLREK	VIKGAEILEV	LHSLPAVRQY	LFSLYECRYS	VFFQSLAVVE	QEMKKDWLFA
250	260	270	280	290	300	310	320
PHYRYYVREM	RIHAYSQLLE	SYRSLTLGYM	AEAFGVGVEF	IDQELSRFIA	AGRLHCKIDK	VNEIVETNRP	DSKNWQYQET
330	340	350					
IKKGDLLLNR	VQKLSRVINM						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1145	1	666.8366	-14.10	2	43.0	11.0	1	235-244	K.KDWLFAPHYR.Y		mdown:qdown 2.27

Detailed Protein Report

Protein 1501: PREDICTED: tyrosine-protein phosphatase non-receptor type 11 isoform X2 [Homo sapiens]

Accession:	gi|578824047	**Score:**	10.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	64.0
Database Date:	2015-11-30	**pI:**	7.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.8
		No. of unique Peptides:	1

Quantitation

mdown:qdown **Median:** 0.23 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MTSRRWFHPN	ITGVEAENLL	LTRGVDGSFL	ARPSKSNPGD	FTLSVRRNGA	VTHIKIQNTG	DYYDLYGGEK	FATLAELVQY
90	100	110	120	130	140	150	160
YMEHHGQLKE	KNGDVIELKY	PLNCADPTSE	RWFHGHLSGK	EAEKLLTEKG	KHGSFLVRES	QSHPGDFVLS	VRTGDDKGES
170	180	190	200	210	220	230	240
NDGKSKVTHV	MIRCQELKYD	VGGGERFDSL	TDLVEHYKKN	PMVETLGTVL	QLKQTLQQQE	CKLLYSRKEG	QRQENKNKNR
250	260	270	280	290	300	310	320
YKNILPFDHT	RVVLHDGDPN	EPVSDYINAN	IIMPEFETKC	NNSKPKKSYI	ATQGCLQNTV	NDFWRMVFQE	NSRVIVMTTK
330	340	350	360	370	380	390	400
EVERGKSKCV	KYWPDEYALK	EYGVMRVRNV	KESAAHDYTL	RELKLSKVGQ	ALLQGNTERT	VWQYHFRTWP	DHGVPSDPGG
410	420	430	440	450	460	470	480
VLDFLEEVHH	KQESIMDAGP	VVVHCSAGIG	RTGTFIVIDI	LIDIIREKGV	DCDIDVPKTI	QMVRSQRSGM	VQTEAQYRFI
490	500	510	520	530	540	550	560
YMAVQHYIET	LQRRIEEEQK	SKRKGHEYTN	IKYSLADQTS	GDQSPLPPCT	PTPPCAEMRE	DSARVYENVG	LMQQQKSFR

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
360	1	559.1189	-258.27	2	33.2	10.9	0	449-458	K.GVDCDIDVPK.T	Carbamidomethyl: 4	mdown:qdown 0.23

Detailed Protein Report

Protein 1502: neurensin-1 [Homo sapiens]

Accession:	gi|189217874	**Score:**	10.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	21.5
Database Date:	2015-11-30	**pI:**	8.9
		Sequence Coverage [%]:	6.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSSCSNVCGS	RQAQAAAEGG	YQRYGVRSYL	HQFYEDCTAS	IWEYEDDFQI	QRSPNRWSSV	FWKVGLISGT	VFVILGLTVL
90	100	110	120	130	140	150	160
AVGFLVPPKI	EAFGEADFVV	VDTHAVQFNS	ALDMYKLAGA	VLFCIGGTSM	AGCLLMSVFV	KSYSKEEKFL	QQKFKERIAD
170	180	190	200				
IKAHTQPVTK	APGPGETKIP	VTLSRVQNVQ	PLLAT				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2762	1	625.3101	16.69	2	62.9	10.9	0	12-23	R.QAQAAAEGGYQR.Y	

Detailed Protein Report

Protein 1503: 28S ribosomal protein S35, mitochondrial isoform 2 precursor [Homo sapiens]

Accession:	gi|300068923	**Score:**	10.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	21.4
Database Date:	2015-11-30	**pI:**	10.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	9.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAAAALPAWL	SLQSRARTLR	AFSTAVYSAT	PVPTPSLPER	TPGNERPPRR	KALPPRTEKM	AVDQDWPSVY	PVAAPFKPSA
90	100	110	120	130	140	150	160
VPLPVRMGYP	VKKGVPMAKE	GNLELLKIPN	FLHLTPVAIK	KHCEALKDFC	TEWPAALDSD	EKCEKHFPIE	IDSTDYVSSG
170	180	190	200				
PSVRNPRARV	VVLRVPFKEA	ELRLCSVSTN	SVIP				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1620	1	715.3707	94.57	3	49.0	10.9	1	128-145	K.DFCTEWPAALDSDEKCEK.H	Carbamidomethyl: 16

Detailed Protein Report

Protein 1504: PREDICTED: protein ECT2 isoform X6 [Homo sapiens]

Accession:	gi|530374050	**Score:**	10.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	85.9
Database Date:	2015-11-30	**pI:**	9.7
		Sequence Coverage [%]:	1.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGGVIRKDFN	SKVTHLVANC	TQGEKFRVAV	SLGTPIMKPE	WIYKAWERRN	EQDFYAAVDD	FRNEFKVPPF	QDCILSFLGF
90	100	110	120	130	140	150	160
SDEEKTNMEE	MTEMQGGKYL	PLGDERCTHL	VVEENIVKDL	PFEPSKKLYV	VKQEWFWGSI	QMDARAGETM	YLYEKANTPE
170	180	190	200	210	220	230	240
LKKSVSMLSL	NTPNSNRKRR	RLKETLAQLS	RETDVSPFPP	RKRPSAEHSL	SIGSLLDISN	TPESSINYGD	TPKSCTKSSK
250	260	270	280	290	300	310	320
SSTPVPSKQS	ARWQVAKELY	QTESNYVNIL	ATIIQLFQVP	LEEEGQRGGP	ILAPEEIKTI	FGSIPDIFDV	HTKIKDDLED
330	340	350	360	370	380	390	400
LIVNWDESKS	IGDIFLKYSK	DLVKTYPPFV	NFFEMSKETI	IKCEKQKPRF	HAFLKINQAK	PECGRQSLVE	LLIRPVQRLP
410	420	430	440	450	460	470	480
SVALLLNDLK	KHTADENPDK	STLEKAIGSL	KEVMTHINED	KRKTEAQKQI	FDVVYEVDGC	PANLLSSHRS	LVQRVETISL
490	500	510	520	530	540	550	560
GEHPCDRGEQ	VTLFLFNDCL	EIARKRHKVI	GTFRSPHGQT	RPPASLKHIH	LMPLSQIKKV	LDIRETEDCH	NAFALLVRPP
570	580	590	600	610	620	630	640
TEQANVLLSF	QMTSDELPKE	NWLKMLCRHV	ANTICKADAE	NLIYTADPES	FEVNTKDMDS	TLSRASRAIK	KTSKKVTRAF
650	660	670	680	690	700	710	720
SFSKTPKRAL	RRALMTSHGS	VEGRSPSSND	KHVMSRLSST	SSLAITHSVS	TSNVIGFTKH	VYVQRLNSTG	GRSQYSWFQS
730	740	750	760				
VRHSAFRASF	SEILEGNTDF	SNFKKVLSKS	SLTFVKN				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1030	2	700.2304	-175.90	2	41.4	10.9	0	13-25	K.VTHLVANCTQGEK.F	

Detailed Protein Report

Protein 1505: 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 1506: PREDICTED: E3 ubiquitin-protein ligase TRAF7 isoform X1 [Homo sapiens]

Accession:	gi|530409257	**Score:**	10.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	74.3
Database Date:	2015-11-30	**pI:**	6.9
		Sequence Coverage [%]:	1.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSSGKSARYN	RFSGGPSNLP	TPDVTTGTRM	ETTFGPAFSA	VTTITKADGT	STYKQHCRTP	SSSSTLAYSP	RDEEDSMPPI
90	100	110	120	130	140	150	160
STPRRSDSAI	SVRSLHSESS	MSLRSTFSLP	EEEEEPEPLV	FAEQPSVKLC	CQLCCSVFKD	PVITTCGHTF	CRRCALKSEK
170	180	190	200	210	220	230	240
CPVDNVKLTV	VVNNIAVAEQ	IGELFIHCRH	GCRVAGSGKP	PIFEVDPRGC	PFTIKLSARK	DHEGSCDYRP	VRCPNNPSCP
250	260	270	280	290	300	310	320
PLLRMNLEAH	LKECEHIKCP	HSKCTFIGNQ	DTYETHLETC	RFEGLKEFLQ	QTDDRFHEMH	VALAQKDQEI	AFLRSMLGKL
330	340	350	360	370	380	390	400
SEKIDQLEKS	LELKFDVLDE	NQSKLSEDLM	EFRRDASMLN	DELSHINARL	NMGILGSYDP	QQIFKCKGTF	VGHQGPVWCL
410	420	430	440	450	460	470	480
CVYSMGDLLF	SGSSDKTIKV	WDTCTTYKCQ	KTLEGHDGIV	LALCIQGCKL	YSGSADCTII	VWDIQNLQKV	NTIRAHDNPV
490	500	510	520	530	540	550	560
CTLVSSHNVL	FSGSLKAIKV	WDIVGTELKL	KKELTGLNHW	VRALVAAQSY	LYSGSYQTIK	IWDIRTLDCI	HVLQTSGGSV
570	580	590	600	610	620	630	640
YSIAVTNHHI	VCGTYENLIH	VWDIESKEQV	RTLTGHVGTV	YALAVISTPD	QTKVFSASYD	RSLRVWSMDN	MICTQTLLRH
650	660	670					
QGSVTALAVS	RGRLFSGAVD	STVKVWTC					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1965	1	676.7537	-179.62	2	53.1	10.9	1	512-522	K.KELTGLNHWVR.A	

Detailed Protein Report

Protein 1507: BEN domain-containing protein 4 isoform a [Homo sapiens]

Accession: gi|148762950
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 10.9
MW [kDa]: 58.3
pI: 5.7
Sequence Coverage [%]: 2.2
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MEEEMQPAEE	GPSVPKIYKQ	RSPYSVLKTF	PSKRPALAKR	YERPTLVELP	HVRAPPPPPP	PFAPHAAVSI	SSSEPPPQQF
90	100	110	120	130	140	150	160
QAQSSYPPGP	GRAAAAASSS	SPSCTPATSQ	GHLRTPAQPP	PASPAASSSS	SFAAVVRYGP	GAAAAAGTGG	TGSDSASLEL
170	180	190	200	210	220	230	240
SAESRMILDA	FAQQCSRVLS	LLNCGGKLLD	SNHSQSMISC	VKQEGSSYNE	RQEHCHIGKG	VHSQTSDNVD	IEMQYMQRKQ
250	260	270	280	290	300	310	320
QTSAFLRVFT	DSLQNYLLSG	SFPTPNPSSA	SEYGHLADVD	PLSTSPVHTL	GGWTSPATSE	SHGHPSSSTL	PEEEEEEDEE
330	340	350	360	370	380	390	400
GYCPRCQELE	QEVISLQQEN	EELRRKLESI	PVPCQTVLDY	LKMVLQHHNQ	LLIPQPADQP	TEGSKQLLNN	YPVYITSKQW
410	420	430	440	450	460	470	480
DEAVNSSKKD	GRRLLRYLIR	FVFTTDELKY	SCGLGKRKRS	VQSGETGPER	RPLDPVKVTC	LREFIRMHCT	SNPDWWMPSE
490	500	510	520	530	540		
EQINKVFSDA	VGHARQGRAV	GTFLHNGGSF	YEGIDHQASQ	DEVFNKSSQD	GSGD		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2807	1	651.8564	50.52	2	63.5	10.9	1	439-450	K.RSVQSGETGPER.R	

Detailed Protein Report

Protein 1508: peroxisome proliferator-activated receptor delta isoform 2 [Homo sapiens]

Accession:	gi|29171750	**Score:**	10.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	40.4
Database Date:	2015-11-30	**pI:**	8.7
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	3.3
		No. of unique Peptides:	1

Quantitation

Wdown:Qdown **Median:** 1.20 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MEQPQEEAPE	VREEEEKEEV	AEAEGAPELN	GGPQHALPSS	SYTDLSRSSS	PPSLLDQLQM	GCDGASCGSL	NMECRVCGDK
90	100	110	120	130	140	150	160
ASGFHYGVHA	CEGCKGFFRR	TIRMKLEYEK	CERSCKIQKK	NRNKCQYCRF	QKCLALGMSH	NAIRFGRMPE	AEKRKLVAGL
170	180	190	200	210	220	230	240
TANEGSQYNP	QVADLKAFSK	HIYNAYLKNF	NMTKKKARSI	LTGKASHTAP	FVIHDIETLW	QAEKGLVWKQ	LVNGLPPYKE
250	260	270	280	290	300	310	320
ISVHVFYRCQ	CTTVETVREL	TEFAKSIPSF	SSLFLNDQVT	LLKYGVHEAI	FAMLASIVNK	DGLLVANGSG	FVTREFLRSL
330	340	350	360	370			
RKPFSDIIEP	KFEFAVKFNA	LELDDSDLAL	FIAAIILCGG	E			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
217	1	679.7025	-197.92	2	31.5	10.9	0	133-144	K.CLALGMSHNAIR.F	Carbamidomethyl: 1; Oxidation: 6	Wdown:Qdown 1.20

Detailed Protein Report

Protein 1509: PREDICTED: monoacylglycerol lipase ABHD12 isoform X3 [Homo sapiens]

Accession:	gi|530425689	**Score:**	10.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	29.5
Database Date:	2015-11-30	**pI:**	6.5
		Sequence Coverage [%]:	3.0
		No. of unique Peptides:	1

Quantitation

Wdown:Qdown **Median:** 1.58 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MWYEDALASS	HPIILYLHGN	AGTRGGDHRV	ELYKVLSSLG	YHVVTFDYRG	WGDSVGTPSE	RGMTYDALHV	FDWIKARSGD
90	100	110	120	130	140	150	160
NPVYIWGHSL	GTGVATNLVR	RLCERETPPD	ALILESPFTN	IREEAKSHPF	SVIYRYFPGF	DWFFLDPITS	SGIKFANDEN
170	180	190	200	210	220	230	240
VKHISCPLLI	LHAEDDPVVP	FQLGRKVGPG	LCLWCSWHLA	HSASVGGPGW	EWAGGKAAPA	CCITGCAPAT	SGSGGHLILP
250	260	270					
ASPPGCFGRT	WEVWCKGWGR	GPLMLSPRI					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
450	1	435.6288	-270.98	2	34.3	10.9	0	261-268	R.GPLMLSPR.I		Wdown:Qdown 1.58

Detailed Protein Report

Protein 1510: zinc finger protein 211 isoform 6 [Homo sapiens]

Accession: gi|388240796
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 10.9
MW [kDa]: 57.5
pI: 10.3
Sequence Coverage [%]: 2.0
No. of unique Peptides: 1

Quantitation

mdown:qdown **Median:** 0.50 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MLENFALTSS	LGCWCGVEHE	ETPSEQRISG	ERVPQFRTSK	EGSSSQNADS	CEICCLVLRD	ILHLAEHQGT	NCGQKLHTCG
90	100	110	120	130	140	150	160
KQFYISANLQ	QHQRQHITEA	PFRSYVDTAS	FTQSCIVHVS	EKPFTCREIR	KDFLANMRFL	HQDATQTGEK	PNNSNKCAVA
170	180	190	200	210	220	230	240
FYSGKSHHNW	GKCSKAFSHI	DTLVQDQRIL	TREGLFECSK	CGKACTRRCN	LIQHQKVHSE	ERPYECNECG	KFFTYYSSFI
250	260	270	280	290	300	310	320
IHQRVHTGER	PYACPECGKS	FSQIYSLNSH	RKVHTGERPY	ECGECGKSFS	QRSNLMQHRR	VHTGERPYEC	SECGKSFSQN
330	340	350	360	370	380	390	400
FSLIYHQRVH	TGERPHECNE	CGKSFSRSSS	LIHHRRLHTG	ERPYECSKCG	KSFKQSSSFS	SHRKVHTGER	PYVCGECGKS
410	420	430	440	450	460	470	480
FSHSSNLKNH	QRVHTGERPV	ECSECSKSFS	CKSNLIKHLR	VHTGERPYEC	SECGKSFSQS	SSLIQHRRVH	TGKRPYQCSQ
490	500	510					
CGKSFGCKSV	LIQHQRVHIG	EKP					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
221	1	592.1368	-233.25	2	31.9	10.9	1	166-175	K.SHHNWGKCSK.A		mdown:qdown 0.50

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Detailed Protein Report

Protein 1511: retinoic acid receptor responder protein 3 [Homo sapiens]

Accession:	gi|149588791	**Score:**	10.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	18.2
Database Date:	2015-11-30	**pI:**	9.6
		Sequence Coverage [%]:	6.7
		No. of unique Peptides:	1

```
        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
826	1	607.1581	-185.27	2	38.8	10.9	0	65-75	R.LEDVVGGCCYR.V	

Protein 1512: BTB/POZ domain-containing protein KCTD17 isoform 4 [Homo sapiens]

Accession:	gi|544186114	**Score:**	10.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	24.8
Database Date:	2015-11-30	**pI:**	5.5
		Sequence Coverage [%]:	5.5
		No. of unique Peptides:	1

Quantitation

mdown:qdown **Median:** 0.54 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MQTPRPAMRM	EAGEAAPPAG	AGGRAAGGWG	KWVRLNVGGT	VFLTTRQTLC	REQKSFLSRL	CQGEELQSDR	DETGAYLIDR
90	100	110	120	130	140	150	160
DPTYFGPILN	FLRHGKLVLD	KDMAEEGVLE	EAEFYNIGPL	IRIIKDRMEE	KDYTVTQVPP	KHVYRVLQCQ	EEELTQMVST
170	180	190	200	210	220	230	
MSDGWRFEQL	VNIGSSYNYG	SEDQAEFLCV	VSKELHSTPN	GLSSESSRKT	KLLQARGTRM		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
637	1	639.3279	-56.84	2	36.8	10.9	0	35-46	R.LNVGGTVFLTTR.Q		mdown:qdown 0.54

Detailed Protein Report

Protein 1513: mitochondrial 10-formyltetrahydrofolate dehydrogenase precursor [Homo sapiens]

Accession:	gi|238814322	**Score:**	10.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	101.7
Database Date:	2015-11-30	**pI:**	6.1
		Sequence Coverage [%]:	2.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLRRGSQALR	RFSTGRVYFK	NKLKLALIGQ	SLFGQEVYSH	LRKEGHRVVG	VFTVPDKDGK	ADPLALAAEK	DGTPVFKLPK
90	100	110	120	130	140	150	160
WRVKGKTIKE	VAEAYRSVGA	ELNVLPFCTQ	FIPMDIIDSP	KHGSIIYHPS	ILPRHRGASA	INWTLIMGDK	KAGFSVFWAD
170	180	190	200	210	220	230	240
DGLDTGPILL	QRSCDVEPND	TVDALYNRFL	FPEGIKAMVE	AVQLIADGKA	PRIPQPEEGA	TYEGIQKKEN	AEISWDQSAE
250	260	270	280	290	300	310	320
VLHNWIRGHD	KVPGAWTEIN	GQMVTFYGST	LLNSSVPPGE	PLEIKGAKKP	GLVTKNGLVL	FGNDGKALTV	RNLQFEDGKM
330	340	350	360	370	380	390	400
IPASQYFSTG	ETSVVELTAE	EVKVAETIKV	IWAGILSNVP	IIEDSTDFFK	SGASSMDVAR	LVEEIRQKCG	GLQLQNEDVY
410	420	430	440	450	460	470	480
MATKFEGFIQ	KVVRKLRGED	QEVELVVDYI	SKEVNEIMVK	MPYQCFINGQ	FTDADDGKTY	DTINPTDGST	ICKVSYASLA
490	500	510	520	530	540	550	560
DVDKAVAAAK	DAFENGEWGR	MNARERGRLM	YRLADLLEEN	QEELATIEAL	DSGAVYTLAL	KTHIGMSVQT	FRYFAGWCDK
570	580	590	600	610	620	630	640
IQGSTIPINQ	ARPNRNLTFT	KKEPLGVCAI	IIPWNYPLMM	LAWKSAACLA	AGNTLVLKPA	QVTPLTALKF	AELSVKAGFP
650	660	670	680	690	700	710	720
KGVINIIPGS	GGIAGQRLSE	HPDIRKLGFT	GSTPIGKQIM	KSCAVSNLKK	VSLELGGKSP	LIIFNDCELD	KAVRMGMGAV
730	740	750	760	770	780	790	800
FFNKGENCIA	AGRLFVEESI	HDEFVTRVVE	EIKKMKIGDP	LDRSTDHGPQ	NHKAHLEKLL	QYCETGVKEG	ATLVYGGRQV
810	820	830	840	850	860	870	880
QRPGFFMEPT	VFTDVEDYMY	LAKEESFGPI	MVISKFQNGD	IDGVLQRANS	TEYGLASGVF	TRDINKAMYV	SEKLEAGTVF
890	900	910	920	930			
INTYNKTDVA	APFGGVKQSG	FGKDLGEEAL	NEYLKTKTVT	LEY			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
935	1	838.8802	82.27	3	40.2	10.9	2	21-42	K.NKLKLALIGQSLFGQEVYSHLR.K	

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Detailed Protein Report

Protein 1514: PREDICTED: arf-GAP with GTPase, ANK repeat and PH domain-containing protein 2-like [Homo sapiens]

Accession: gi|578805484
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 10.9
MW [kDa]: 31.5
pI: 12.7
Sequence Coverage [%]: 6.4
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MTGFSFENLN	TEKKSGENEP	PAHNPFRSAA	RLRCLLALRA	FPAPPNMPKL	LAALGPLPLP	RISSGTRAPG	LRTAGDPRSG
90	100	110	120	130	140	150	160
RSLLWLAVRA	RLERRDLRQR	CCGRLCSVNE	PPNGSASFPL	CVPRKSLLSK	PSQLRRARVA	LARPNPGVLG	QARGAGVRRG
170	180	190	200	210	220	230	240
RAGPGAPSGL	RAHAPHLGEA	RCAGAQRGGS	GRALKPGAGK	SWTVQGPRRA	ELSPAPPPPP	PLLPPPPPPG	LQQIAGERLR
250	260	270	280	290	300		
EAPVQPWRDR	SNHRSVSNSF	PAGGATAPRA	RGPRAELLRC	SQPPELPTAS	FVGGNPTV		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2203	1	956.9064	-68.85	2	56.2	10.9	1	251-269	R.SNHRSVSNSFPAGGATAPR.A	

Detailed Protein Report

Protein 1515: GRAM domain-containing protein 1B isoform 3 [Homo sapiens]

Accession:	gi|557440793	**Score:**	10.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	81.0
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
MVEKGSDHSS	DKSPSTPEQG	VQRSCSSQSG	RSGGKNSKKS	QSWYNVLSPT	YKQRNEDFRK	LFKQLPDTER	LIVDYSCALQ
90	100	110	120	130	140	150	160
RDILLQGRLY	LSENWICFYS	NIFRWETLLT	VRLKDICSMT	KEKTARLIPN	AIQVCTDSEK	HFFTSFGARD	RTYMMMFRLW
170	180	190	200	210	220	230	240
QNALLEKPLC	PKELWHFVHQ	CYGNELGLTS	DDEDYVPPDD	DFNTMGYCEE	IPVEENEVND	SSSKSSIETK	PDASPQLPKK
250	260	270	280	290	300	310	320
SITNSTLTST	GSSEAPVSFD	GLPLEEEALE	GDGSLEKELA	IDNIMGEKIE	MIAPVNSPSL	DFNDNEDIPT	ELSDSSDTHD
330	340	350	360	370	380	390	400
EGEVQAFYED	LSGRQYVNEV	FNFSVDKLYD	LLFTNSPFQR	DFMEQRRFSD	IIFHPWKKEE	NGNQSRVILY	TITLTNPLAP
410	420	430	440	450	460	470	480
KTATVRETQT	MYKASQESEC	YVIDAEVLTH	DVPYHDYFYT	INRYTLTRVA	RNKSRLRVST	ELRYRKQPWG	LVKTFIEKNF
490	500	510	520	530	540	550	560
WSGLEDYFRH	LESELAKTES	TYLAEMHRQS	PKEKASKTTT	VRRRKRPHAH	LRVPHLEEVM	SPVTTPTDED	VGHRIKHVAG
570	580	590	600	610	620	630	640
STQTRHIPED	TPNGFHLQSV	SKLLLVISCV	ICFSLVLLVI	LNMMLFYKLW	MLEYTTQTLT	AWQGLRLQER	LPQSQTEWAQ
650	660	670	680	690	700		
LLESQQKYHD	TELQKWREII	KSSVMLLDQM	KDSLINLQNG	IRSRDYTSES	EEKRNRYH		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
838	1	788.6916	-14.93	3	39.3	10.9	2	13-35	K.SPSTPEQGVQRSCSSQSGRSGGK.N	Carbamidomethyl: 13

Detailed Protein Report

Protein 1516: PREDICTED: dyslexia-associated protein KIAA0319-like protein isoform X6 [Homo sapiens]

Accession:	gi|578799795	**Score:**	10.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	76.2
Database Date:	2015-11-30	**pI:**	5.4
		Sequence Coverage [%]:	2.6
		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
2406	1	701.3175	-124.95	3	58.4	10.9	2	5-22	K.HSQILKLSKLTPGLYEFK.V	

Detailed Protein Report

Protein 1517: 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 1518: ubiquitin carboxyl-terminal hydrolase 48 isoform b [Homo sapiens]

Accession:	gi|76257392	**Score:**	10.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	56.1
Database Date:	2015-11-30	**pI:**	6.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.5
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	0.91	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	1.20	**CV:**	0.00 %	**No. of Peptides:**	1

10	20	30	40	50	60	70	80
MAPRLQLEKA	AWRWAETVRP	EEVSQEHIET	AYRIWLEPCI	RGVCRRNCKG	NPNCLVGIGE	HIWLGEIDEN	SFHNIDDPNC
90	100	110	120	130	140	150	160
ERRKKNSFVG	LTNLGATCYV	NTFLQVWFLN	LELRQALYLC	PSTCSDYMLG	DGIQEEKDYE	PQTICEHLQY	LFALLQNSNR
170	180	190	200	210	220	230	240
RYIDPSGFVK	ALGLDTGQQQ	DAQEFSKLFM	SLLEDTLSKQ	KNPDVRNIVQ	QQFCGEYAYV	TVCNQCGRES	KLLSKFYELE
250	260	270	280	290	300	310	320
LNIQGHKQLT	DCISEFLKEE	KLEGDNRYFC	ENCQSKQNAT	RKIRLLSLPC	TLNLQLMRFV	FDRQTGHKKK	LNTYIGFSEI
330	340	350	360	370	380	390	400
LDMEPYVEHK	GGSYVYELSA	VLIHRGVSAY	SGHYIAHVKD	PQSGEWYKFN	DEDIEKMEGK	KLQLGIEEDL	AEPSKSQTRK
410	420	430	440	450	460	470	480
PKCGKGTHCS	RNAYMLVYRL	QTQEKPNTTV	QVPAFLQELV	DRDNSKFEEW	CIEMAEMRKQ	SVDKGKAKHE	EVKELYQRLP
490							
AGAGL							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
120	1	679.7199	-180.53	2	30.8	10.9	2	400-411	R.KPKCGKGTHCSR.N	Carbamidomethyl: 4	Wdown:Qdown 1.20 mdown:qdown 0.91

Detailed Protein Report

Protein 1519: **deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial isoform 2 [Homo sapiens]**

Accession:	gi|4503423	**Score:**	10.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	17.7
Database Date:	2015-11-30	**pI:**	6.2
		Sequence Coverage [%]:	9.1
		No. of unique Peptides:	1

Quantitation

Wdown:Qdown **Median:** 0.76 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MPCSEETPAI	SPSKRARPAE	VGGMQLRFAR	LSEHATAPTR	GSARAAGYDL	YSAYDYTIPP	MEKAVVKTDI	QIALPSGCYG
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
RVAPRSGLAA	KHFIDVGAGV	IDEDYRGNVG	VVLFNFGKEK	FEVKKGDRIA	QLICERIFYP	EIEEVQALDD	TERGSGGFGS
170							
TGKN							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1060	1	816.8541	-43.54	2	42.0	10.9	1	1-15	-.MPCSEETPAISPSKR.A		Wdown:Qdown 0.76

Detailed Protein Report

Protein 1520: E3 ubiquitin-protein ligase HECW1 isoform b [Homo sapiens]

Accession:	gi|559098413	**Score:**	10.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	175.6
Database Date:	2015-11-30	**pI:**	5.2
		Sequence Coverage [%]:	1.1
		No. of unique Peptides:	1

Quantitation

Wdown:Qdown **Median:** 0.30 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MLLHLCSVKN	LYQNRFLGLA	AMASPSRNSQ	SRRRCKEPLR	YSYNPDQFHN	MDLRGGPHDG	VTIPRSTSDT	DLVTSDSRST
90	100	110	120	130	140	150	160
LMVSSSYYSI	GHSQDLVIHW	DIKEEVDAGD	WIGMYLIDEV	LSENFLDYKN	RGVNGSHRGQ	IIWKIDASSY	FVEPETKICF
170	180	190	200	210	220	230	240
KYYHGVSGAL	RATTPSVTVK	NSAAPIFKSI	GADETVQGQG	SRRLISFSLS	DFQAMGLKKG	MFFNPDPYLK	ISIQPGKHSI
250	260	270	280	290	300	310	320
FPALPHHGQE	RRSKIIGNTV	NPIWQAEQFS	FVSLPTDVLE	IEVKDKFAKS	RPIIKRFLGK	LSMPVQRLLE	RHAIGDRVVS
330	340	350	360	370	380	390	400
YTLGRRLPTD	HVSGQLQFRF	EITSSIHPDD	EEISLSTEPE	SAQIQDSPMN	NLMESGSGEP	RSEAPESSES	WKPEQLGEGS
410	420	430	440	450	460	470	480
VPDGPGNQSI	ELSRPAEEAA	VITEAGDQGM	VSVGPEGAGE	LLAQVQKDIQ	PAPSAEELAE	QLDLGEEASA	LLLEDGEAPA
490	500	510	520	530	540	550	560
STKEEPLEEE	ATTQSRAGRE	EEEKEQEEEG	DVSTLEQGEG	RLQLRASVKR	KSRPCSLPVS	ELETVIASAC	GDPETPRTHY
570	580	590	600	610	620	630	640
IRIHTLLHSM	PSAQGGSAAE	EEDGAEEEST	LKDSSEKDGL	SEVDTVAADP	SALEEDREEP	EGATPGTAHP	GHSGGHFPSL
650	660	670	680	690	700	710	720
ANGAAQDGDT	HPSTGSESDS	SPRQGGDHSC	EGCDASCCSP	SCYSSSCYST	SCYSSSCYSA	SCYSPSCYNG	NRFASHTRFS
730	740	750	760	770	780	790	800
SVDSAKISES	TVFSSQDDEE	EENSAFESVP	DSMQSPELDP	ESTNGAGPWQ	DELAAPSGHV	ERSPEGLESP	VAGPSNRRED
810	820	830	840	850	860	870	880
WEARIDSHGR	VFYVDHVNRT	TTWQRPTAAA	TPDGMRRSGS	IQQMEQLNRR	YQNIQRTIAT	ERSEEDSGSQ	SCEQAPAGGG
890	900	910	920	930	940	950	960
GGGGSDSEAE	SSQSSLDLRR	EGSLSPVNSQ	KITLLLQSPA	VKFITNPEFF	TVLHANYSAY	RVFTSSTCLK	HMILKVRRDA
970	980	990	1000	1010	1020	1030	1040
RNFERYQHNR	DLVNFINMFA	DTRLELPRGW	EIKTDQQGKS	FFVDHNSRAT	TFIDPRIPLQ	NGRLPNHLTH	RQHLQRLRSY
1050	1060	1070	1080	1090	1100	1110	1120
SAGEASEVSR	NRGASLLARP	GHSLVAAIRS	QHQHESLPLA	YNDKIVAFLR	QPNIFEMLQE	RQPSLARNHT	LREKIHYIRT
1130	1140	1150	1160	1170	1180	1190	1200
EGNHGLEKLS	CDADLVILLS	LFEEEIMSYV	PLQAAFHPGY	SFSPRCSPCS	SPQNSPGLQR	ASARAPSPYR	RDFEAKLRNF
1210	1220	1230	1240	1250	1260	1270	1280
YRKLEAKGFG	QGPGKIKLII	RRDHLLEGTF	NQVMAYSRKE	LQRNKLYVTF	VGEEGLDYSG	PSREFFFLLS	QELFNPYYGL
1290	1300	1310	1320	1330	1340	1350	1360
FEYSANDTYT	VQISPMSAFV	ENHLEWFRFS	GRILGLALIH	QYLLDAFFTR	PFYKALLRLP	CDLSDLEYLD	EEFHQSLQWM
1370	1380	1390	1400	1410	1420	1430	1440
KDNNITDILD	LTFTVNEEVF	GQVTERELKS	GGANTQVTEK	NKKEYIERMV	KWRVERGVVQ	QTEALVRGFY	EVVDSRLVSV
1450	1460	1470	1480	1490	1500	1510	1520
FDARELELVI	AGTAEIDLND	WRNNTEYRGG	YHDGHLVIRW	FWAAVERFNN	EQRLRLLQFV	TGTSSVPYEG	FAALRGSNGL
1530	1540	1550	1560	1570	1580		
RRFCIEKWGK	ITSLPRAHTC	FNRLDLPPYP	SYSMLYEKLL	TAVEETSTFG	LE		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
405	1	631.2089	-107.18	3	34.4	10.9	0	505-521	K.EQEEEGDVSTLEQGEGR.L		Wdown:Qdown 0.30

Detailed Protein Report

Protein 1521: 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 1522: 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 1523: PREDICTED: cell adhesion molecule 4 isoform X1 [Homo sapiens]

Accession:	gi|530415930	**Score:**	10.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	38.3
Database Date:	2015-11-30	**pI:**	5.9
		Sequence Coverage [%]:	4.6
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MGRARRFQWP LLLLWAAAAG PGAGQEVQTE NVTVAEGGVA EITCRLHQYD GSIVVIQNPA RQTLFFNGTR ALKDERFQLE
        90        100        110        120        130        140        150        160
EFSPRRVRIR LSDARLEDEG GYFCQLYTED THHQIATLTV LVAPENPVVE VREQAVEGGE VELSCLVPRS RPAATLRWYR
       170        180        190        200        210        220        230        240
DRKELKGVSS SQENGKVWSV ASTVRFRVDR KDDGGIIICE AQNQALPSGH SKQTQYVLDV QYSPTARIHA SQAVVREGDT
       250        260        270        280        290        300        310        320
LVLTCAVTGN PRPNQIRWNR GNESLPERAE AVGETLTLPG LVSADNGTYT CEASNKHGHA RALYVLVVYG SYLTHEASGL
       330        340        350
DEQGEAREAF LNGSDGHKRK EEFFI
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1674	1	905.3397	-159.27	2	49.4	10.9	0	46-61	R.LHQYDGSIVVIQNPAR.Q	

Detailed Protein Report

Protein 1524: homeobox protein Nkx-2.6 [Homo sapiens]

Accession:	gi|343183350	**Score:**	10.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	32.1
Database Date:	2015-11-30	**pI:**	10.7
		Sequence Coverage [%]:	5.0
		No. of unique Peptides:	1

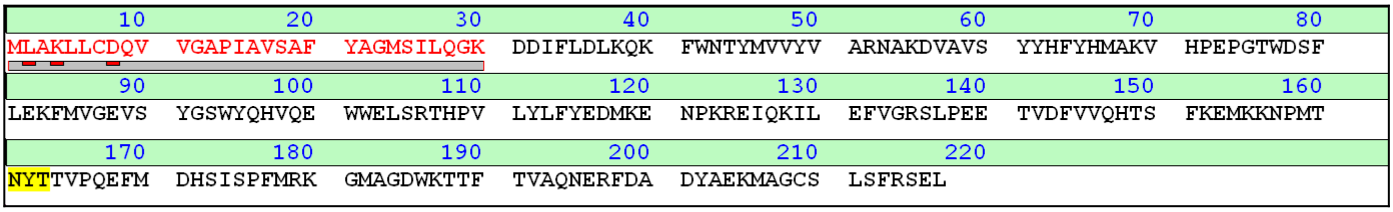
10	20	30	40	50	60	70	80
MLLSPVTSTP	FSVKDILRLE	RERSCPAASP	HPRVRKSPEN	FQYLRMDAEP	RGSEVHNAGG	GGGDRKLDGS	EPPGGPCEAV
90	100	110	120	130	140	150	160
LEMDAERMGE	PQPGLNAASP	LGGGTRVPER	GVGNSGDSVR	GGRSEQPKAR	QRRKPRVLFS	QAQVLALERR	FKQQRYLSAP
170	180	190	200	210	220	230	240
EREHLASALQ	LTSTQVKIWF	QNRRYKCKRQ	RQDKSLELAG	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 1525: 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 1526: polymerase delta-interacting protein 3 isoform 2 [Homo sapiens]

Accession:	gi|30089919	**Score:**	10.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	42.9
Database Date:	2015-11-30	**pI:**	10.5
		Sequence Coverage [%]:	5.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MADISLDELI	RKRGAAAKGR	LNARPGVGGV	RSRVGIQQGL	LSQSTRTATF	QQRFDARQKI	GLSDARLKLG	VKDAREKLLQ
90	100	110	120	130	140	150	160
KDARFRIKGK	VQDAREMLNS	RKQQTTVPQK	PRQVADAREK	ISLKRSSPAA	FINPPIGTVT	PALKLTKTIQ	NLYDLDEDDD
170	180	190	200	210	220	230	240
GIASVPTKQM	KFAASGGFLH	HMAGLSSSKL	SMSKALPLTK	VVQNDAYTAP	ALPSSIRTKA	LTNMSRTLVN	KEEPPKELPA
250	260	270	280	290	300	310	320
AEPVLSPLEG	TKMTVNNLHP	RVTEEDIVEL	FCVCGALKRA	RLVHPGVAEV	VFVKKDDAIT	AYKKYNNRCL	DGQPMKCNLH
330	340	350	360	370	380	390	400
MNGNVITSDQ	PILLRLSDSP	SMKKESELPR	RVNSASSSNP	PAEVDPDTIL	KALFKSSGAS	VTTQPTEFKI	KL

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
119	1	731.4478	116.11	3	30.2	10.8	1	169-189	K.QMKFAASGGFLHHMAGLSSSK.L	

Detailed Protein Report

Protein 1527: 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

mdown:qdown	**Median:**	1.06	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.50	**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	Wdown:Qdown 0.50 mdown:qdown 1.06

Detailed Protein Report

Protein 1528: LIM/homeobox protein Lhx4 [Homo sapiens]

Accession:	gi|15375314	**Score:**	10.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	43.1
Database Date:	2015-11-30	**pI:**	8.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MMQSATVPAE	GAVKGLPEML	GVPMQQIPQC	AGCNQHILDK	FILKVLDRHW	HSSCLKCADC	QMQLADRCFS	RAGSVYCKED
90	100	110	120	130	140	150	160
FFKRFGTKCT	ACQQGIPPTQ	VVRKAQDFVY	HLHCFACIIC	NRQLATGDEF	YLMEDGRLVC	KEDYETAKQN	DDSEAGAKRP
170	180	190	200	210	220	230	240
RTTITAKQLE	TLKNAYKNSP	KPARHVREQL	SSETGLDMRV	VQVWFQNRRA	KEKRLKKDAG	RHRWGQFYKS	VKRSRGSSKQ
250	260	270	280	290	300	310	320
EKESSAEDCG	VSDSELSFRE	DQILSELGHT	NRIYGNVGDV	TGGQLMNGSF	SMDGTGQSYQ	DLRDGSPYGI	PQSPSSISSL
330	340	350	360	370	380	390	400
PSHAPLLNGL	DYTVDSNLGI	IAHAGQGVSQ	TLRAMAGGPT	SDISTGSSVG	YPDFPTSPGS	WLDEMDHPPF	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2734	1	639.3382	72.41	2	62.6	10.8	1	68-78	R.CFSRAGSVYCK.E	Carbamidomethyl: 1

Detailed Protein Report

Protein 1529: PREDICTED: cysteine-rich with EGF-like domain protein 1 isoform X2 [Homo sapiens]

Accession:	gi|578806578	**Score:**	10.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	42.9
Database Date:	2015-11-30	**pI:**	6.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAPWPPKGLV	PAMLWGLSLF	LNLPGPIWLQ	PSPPPQSSPP	PQPHPCHTCR	GLVDSFNKGL	ERTIRDNFGG	GNTAWEEENL
90	100	110	120	130	140	150	160
SKYKDSETRL	VEVLEGVCSK	SDFECHRLLE	LSEELVESWW	FHKQQEAPDL	FQWLCSDSLK	LCCPAGTFGP	SCLPCPGGTE
170	180	190	200	210	220	230	240
RPCGGYGQCE	GEGTRGGSGH	CDCQAGYGGE	ACGQCGLGYF	EAERNASHLV	CSACFGPCAR	CSGPEESNCL	QCKKGWALHH
250	260	270	280	290	300	310	320
LKCVDCAKAC	LGCMGAGPGR	CKKCSPGYQQ	VGSKCLDVDE	CETEVCPGEN	KQCENTEGGY	RCICAEGYKQ	MEGICVKEQI
330	340	350	360	370	380	390	400
PGAFPILTDL	TPETTRRWKL	GSHPHSTYVK	MKMQRDEATF	PGLYGKQVAK	LGSQSRQSDR	GTRLIHSQQA	SSQR

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2830	1	913.4702	92.84	2	64.5	10.8	1	243-260	K.CVDCAKACLGCMGAGPGR.C	Carbamidomethyl: 4, 8

Detailed Protein Report

Protein 1530: protein FAM196B [Homo sapiens]

Accession:	gi|193788653	**Score:**	10.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	59.2
Database Date:	2015-11-30	**pI:**	9.4
		Sequence Coverage [%]:	2.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAQQNMKVRP	VLLKRNSLES	VEFVKQPHHR	RSKSQQVRFK	EDGTTKNPTG	LAEVDVQTPE	DPAVMGKTQA	TRHHLPPTYS
90	100	110	120	130	140	150	160
LSFPRSQKAG	GFRNIAIQTS	PSLRKHFPVF	KRKRLTASKS	LVEMPTASQS	AIQVNGNLSE	QDIVSSDLAY	LRLAQHLEDG
170	180	190	200	210	220	230	240
PRRVKVSHAF	LPRVPKVQSN	GPVSICLEAG	TWRSLEKATA	AIQVPDDIYH	SPSWEARESA	LSPDRSAEVS	NSIHPLDDTR
250	260	270	280	290	300	310	320
PGDGRRVTPL	DSEKSTSCLN	ATSVASHTPG	TEELKPELLL	PKDNSDDKDL	GSLSSQSKET	CVPSSPRTHS	SPSQGSHSQP
330	340	350	360	370	380	390	400
AHPGRASDCP	SSSNNHQNLV	SLKTNSASKS	APGCQEQTAN	NPTESDTLEF	PNCPGSNHLP	SSLSRSETKL	QSNREISDIN
410	420	430	440	450	460	470	480
QIHLARGELC	DLQGRLQSVE	ESLHSNQEKI	KVLLNVIQDL	EKARALTEGR	NFYRTGQDLN	NCSTCQNTAC	IIYSVEYDFR
490	500	510	520	530	540		
QQEGRFHEVL	QSLEEAEPVE	EASPPPKSPA	EPPAPEKQDL	RRKTKKVKKK	CFWWI		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
290	1	642.3243	-89.90	2	32.3	10.8	0	432-442	K.VLLNVIQDLEK.A	

Detailed Protein Report

Protein 1531: protein GUCD1 isoform d [Homo sapiens]

Accession:	gi|50845407	**Score:**	10.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	27.2
Database Date:	2015-11-30	**pI:**	6.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	5.8
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:** 2.02	**CV:** 0.00 %	**No. of Peptides:** 1

10	20	30	40	50	60	70	80
MRTEAEAAGP	PLEPGDFVQL	PVPVIQQLYH	WDCGLACSRM	VLRYLGQLDD	SEFERALQKL	QLTRSIWTID	LAYLMHHFGV
90	100	110	120	130	140	150	160
RHRFCTQTLG	VDKGYKNQSF	YRKHFDTEET	RVNQLFAQAK	ACKVLVEKCT	VSVKDIQAHL	AQGHVAIVLV	NSGVLHCDLC
170	180	190	200	210	220	230	240
SSPVKYCCFT	PSGHHCFCRT	PDYQGHFIVL	RGYNRATGCI	FYNNPAYADP	GMCSTSISNF	EEARTSYGTD	EDILFVYLDS
250							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
227	1	782.3496	-107.19	2	32.0	10.8	2	121-134	K.ACKVLVEKCTVSVK.D	Carbamidomethyl: 9	mdown:qdown 2.02

Detailed Protein Report

Protein 1532: tripartite motif-containing protein 47 [Homo sapiens]

Accession:	gi|54792146	**Score:**	10.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	69.5
Database Date:	2015-11-30	**pI:**	6.0
		Sequence Coverage [%]:	3.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDGSGPFSCP	ICLEPLREPV	TLPCGHNFCL	ACLGALWPHR	GASGAGGPGG	AARCPLCQEP	FPDGLQLRKN	HTLSELLQLR
90	100	110	120	130	140	150	160
QGSGPGSGPG	PAPALAPEPS	APSALPSVPE	PSAPCAPEPW	PAGEEPVRCD	ACPEGAALPA	ALSCLSCLAS	FCPAHLGPHE
170	180	190	200	210	220	230	240
RSPALRGHRL	VPPLRRLEES	LCPRHLRPLE	RYCRAERVCL	CEACAAQEHR	GHELVPLEQE	RALQEAEQSK	VLSAVEDRMD
250	260	270	280	290	300	310	320
ELGAGIAQSR	RTVALIKSAA	VAERERVSRL	FADAAAALQG	FQTQVLGFIE	EGEAAMLGRS	QGDLRRQEEQ	RSRLSRARQN
330	340	350	360	370	380	390	400
LSQVPEADSV	SFLQELLALR	LALEDGCGPG	PGPPRELSFT	KSSQAVRAVR	DMLAVACVNQ	WEQLRGPGGN	EDGPQKLDSE
410	420	430	440	450	460	470	480
ADAEPQDLES	TNLLESEAPR	DYFLKFAYIV	DLDSDTADKF	LQLFGTKGVK	RVLCPINYPL	SPTRFTHCEQ	VLGEGALDRG
490	500	510	520	530	540	550	560
TYYWEVEIIE	GWVSMGVMAE	DFSPQEPYDR	GRLGRNAHSC	CLQWNGRSFS	VWFHGLEAPL	PHPFSPTVGV	CLEYADRALA
570	580	590	600	610	620	630	640
FYAVRDGKMS	LLRRLKASRP	RRGGIPASPI	DPFQSRLDSH	FAGLFTHRLK	PAFFLESVDA	HLQIGPLKKS	CISVLKRR

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
669	1	706.3289	-44.12	3	36.9	10.8	1	231-250	K.VLSAVEDRMDELGAGIAQSR.R	

Detailed Protein Report

Protein 1533: **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 1534: 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

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 1535: PREDICTED: methionine synthase isoform X7 [Homo sapiens]

Accession:	gi|578802222	**Score:**	10.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	126.1
Database Date:	2015-11-30	**pI:**	5.2
Modification(s):	Oxidation	**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 1536: forkhead box protein D4-like 1 [Homo sapiens]

Accession:	gi|18959276	**Score:**	10.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	43.6
Database Date:	2015-11-30	**pI:**	10.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MNLPRAERPR	STPQRSLRDS	DGEDGKIDVL	GEEEDEDEVE	DEEEEASQKF	LEQSLQPGLQ	VARWGGVALP	REHIEGGGPS
90	100	110	120	130	140	150	160
DPSEFGTEFR	APPRSAAASE	DARQPAKPPY	SYIALITMAI	LQSPHKRLTL	SGICAFISGR	FPYYRRKFPA	WQNSIRHNLS
170	180	190	200	210	220	230	240
LNDCFVKIPR	EPGHPGKGTY	WSLDPASQDM	FDNGSFLRRR	KRFKRHQLTP	GAHLPHPFPL	PAAHAALHNP	RPGPLLGAPA
250	260	270	280	290	300	310	320
LPQPVPGAYP	NTAPGRRPYA	LLHPHPPRYL	LLSAPAYAGA	PKKAEGADLA	TPGTLPVLQP	SLGPQPWEEG	KGLASPPGGG
330	340	350	360	370	380	390	400
CISFSIESIM	QGVRGAGTGA	AQSLSPTAWS	YCPLLQRPSS	LSDNFAATAA	ASGGGLRQRL	RSHQGRGAGR	APVGRVGAAA
410							
VSGGGRGL							

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	157-170	R.HNLSLNDCFVKIPR.E	Carbamidomethyl: 8

Detailed Protein Report

Protein 1537: PREDICTED: uncharacterized protein LOC102724921 [Homo sapiens]

Accession:	gi|578803401	**Score:**	10.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	90.1
Database Date:	2015-11-30	**pI:**	9.5
		Sequence Coverage [%]:	1.9
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578843117	refseq_human (refseq_human_20140103.fasta)	PREDICTED: uncharacterized protein LOC102724921 [Homo sapiens]

10	20	30	40	50	60	70	80
MAPIWGMDVP	LPSDISLLLL	FVFFIWRLWT	LFSRNRSWKQ	VAAKINSETS	KQHRLKKIQK	LTDPQWEENL	RMACTEANLT
90	100	110	120	130	140	150	160
CVSELPVGWT	QEYILWSMER	SLQQIFRYLE	SARSRLVEQD	LPESQDMISS	STTSVLVAQK	TVLCCCDYKK	AKHSTDHSIS
170	180	190	200	210	220	230	240
FSSSCNDSSL	SHLPVFSEGT	TWEFRSHSLP	ISHKKQSSVF	RNQGRTLPLF	QLSEPQKSKI	FQNLADLSPL	QPQSSFINSI
250	260	270	280	290	300	310	320
SEPLNICKQK	RKKNDERMSK	SHLTSDHEPN	SVSKERPRLP	RWATFKLSPS	VRRELEGHMS	QKVFALRQQT	APLPLRKSWA
330	340	350	360	370	380	390	400
MLNYITEVQG	GVAESEKPQT	QLSMPIHQNT	EQNINNKSSD	LPSFQLHVNA	GVGSGSNSTE	TKLSQSLISD	KQLQPGDGPQ
410	420	430	440	450	460	470	480
ILGFKPLVTS	MGSLPPRSLE	LNVIQEETPL	LKNDPKHVLE	LSIEERVIGF	PEKRIQQHKT	QVTNVELTPR	LSYQVKDSLK
490	500	510	520	530	540	550	560
VTPLALLRVM	DSMGMIPESH	SEFAGLFSQL	PSQVVKPMET	METVSITPKP	PNQVIQSMEA	APRSQHQVME	SERVATRLLN
570	580	590	600	610	620	630	640
QVTDNKKVTP	VALLQVMDSM	GMINKSHPCI	ESVGMTPTPR	YQVIESVKMN	TLLNHQDTKP	EKMNLRPQHA	VTETVEMMPG
650	660	670	680	690	700	710	720
PQHKVMESAG	MTSGSQSQVM	EQGKATPGLI	CQDTKSLEMI	SAPLHQVMGY	VKGIPVALLQ	AMDFREIIPP	AQPHVIESGG
730	740	750	760	770	780	790	800
LTPSSQLQGR	RSVHLVLPPE	FQDINTVELT	LRPPTEDTKS	AELAPKPWLH	DVRSEKGHSC	QVSDFQRYFQ	DHFFKAKNL

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1540	1	949.6512	148.55	2	48.0	10.8	2	57-71	K.KIQKLTDPQWEENLR.M	

Detailed Protein Report

Protein 1538: coiled-coil domain-containing protein 171 [Homo sapiens]

Accession: gi|38348729
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 10.8
MW [kDa]: 152.7
pI: 6.4
Sequence Coverage [%]: 0.6
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MNLNTSSNTG	DTQRLKIASL	DVKQILKNET	ELDITDNLRK	KLHWAKKEKL	EITTKHNAEL	ASYESQIAKL	RSEVEKGEAL
90	100	110	120	130	140	150	160
RQSLEYDLAV	ARKEAGLGRR	AAEERLAEAH	RIQEKLCAQN	SELQAKTNET	EKAFQTSQQK	WKEECRRFEH	DLEERDNMIQ
170	180	190	200	210	220	230	240
NCNREYDLLM	KEKSRLEKTL	QEALEKHQRE	KNEMESHIRE	TALEEFRLQE	EQWEAERREL	QFIVQEQDTA	VQNMHKKVEK
250	260	270	280	290	300	310	320
LETEHMDCSD	LLRRQTSELE	FSTQREERLR	KEFEATTLRV	RKLEENIEAE	RAAHLESKFN	SEIIQLRIRD	LEGALQVEKA
330	340	350	360	370	380	390	400
SQAEAVADLE	IIKNEFKEVE	SAYEREKHNA	QESFAKLNLL	EKEYFSKNKK	LNEDIEEQKK	VIIDLSKRLQ	YNEKSCSELQ
410	420	430	440	450	460	470	480
EELVMAKKHQ	AFLVETCENN	VKELESILDS	FTVSGQWTSG	IHKDKDKPPS	FSVVLERLRR	TLTDYQNKLE	DASNEEKACN
490	500	510	520	530	540	550	560
ELDSTKQKID	SHTKNIKELQ	DKLADVNKEL	SHLHTKCADR	EALISTLKVE	LQNVLHCWEK	EKAQAAQSES	ELQKLSQAFH
570	580	590	600	610	620	630	640
KDAEEKLTFL	HTLYQHLVAG	CVLIKQPEGM	LDKFSWSELC	AVLQENVDAL	IADLNRANEK	IRHLEYICKN	KSDTMRELQQ
650	660	670	680	690	700	710	720
TQEDTFTKVA	EQIKAQESCW	HRQKKELELQ	YSELFLEVQK	RAQKFQEIAE	KNMEKLNHIE	KSHEQLVLEN	SHFKKLLSQT
730	740	750	760	770	780	790	800
QREQMSLLAA	CALMAGALYP	LYSRSCALST	QRDFLQEQVN	TFELFKLEIR	TLAQALSTVE	EKKQEEAKMK	KKTFKGLIRI
810	820	830	840	850	860	870	880
FRKGVIAVLA	ANRLKILGQS	CASLFTWMES	FKEGIGMLVC	TGEPQDKHKF	PKHQKEQLRC	LQALSWLTSS	DLLAAIISSM
890	900	910	920	930	940	950	960
AELQDVIGKA	DPNSRICGHL	LIGAAKNSFA	KLMDKISLVM	ECIPLHSSRS	ITYVEKDSLV	QRLAHGLHKV	NTLALKYGLR
970	980	990	1000	1010	1020	1030	1040
GHVPITKSTA	SLQKQILGFT	QRLHAAEVER	RSLRLEVTEF	KRSVNEMKKE	LDKAQGLQMQ	LNEFKQSKLI	THEKFESACE
1050	1060	1070	1080	1090	1100	1110	1120
ELNNALLREE	QAQMLLNEQA	QQLQELNYKL	ELHSSEEADK	NQTLGEAVKS	LSEAKMELRR	KDQSLRQLNR	HLTQLEQDKR
1130	1140	1150	1160	1170	1180	1190	1200
RLEENIHDAE	SALRMAAKDK	ECVANHMRAV	ENTLHKVRDQ	ISLSWSAASR	NDFTLQLPKL	HLETFAMEGL	KGGPEVVACQ
1210	1220	1230	1240	1250	1260	1270	1280
AMIKSFMDVY	QLASTRIMTL	EKEMTSHRSH	IAALKSELHT	ACLRENASLQ	SIGSRDHSNL	SIPSRAPLPA	DTTGIGDFLP
1290	1300	1310	1320	1330			
LKAELDTTYT	FLKETFINTV	PHALTSSHSS	PVTMSANANR	PTQIGL			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
945	1	491.8025	115.71	2	40.6	10.8	0	461-468	R.TLTDYQNK.L	

Detailed Protein Report

Protein 1539: 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 1540: DNA-binding protein RFX5 [Homo sapiens]

Accession:	gi|4557843	**Score:**	10.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	65.3
Database Date:	2015-11-30	**pI:**	10.0
		Sequence Coverage [%]:	2.1
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530365212	refseq_human (refseq_human_20140103.fasta)	PREDICTED: DNA-binding protein RFX5 isoform X2 [Homo sapiens]
gi|530365210	refseq_human (refseq_human_20140103.fasta)	PREDICTED: DNA-binding protein RFX5 isoform X1 [Homo sapiens]
gi|71040090	refseq_human (refseq_human_20140103.fasta)	DNA-binding protein RFX5 [Homo sapiens]

10	20	30	40	50	60	70	80
MAEDEPDAKS	PKTGGRAPPG	GAEAGEPTTL	LQRLRGTISK	AVQNKVEGIL	QDVQKFSDND	KLYLYLQLPS	GPTTGDKSSE
90	100	110	120	130	140	150	160
PSTLSNEEYM	YAYRWIRNHL	EEHTDTCLPK	QSVYDAYRKY	CESLACCRPL	STANFGKIIR	EIFPDIKARR	LGGRGQSKYC
170	180	190	200	210	220	230	240
YSGIRRKTLV	SMPPLPGLDL	KGSESPEMGP	EVTPAPRDEL	VEAACALTCD	WAERILKRSF	SSIVEVARFL	LQQHLISARS
250	260	270	280	290	300	310	320
AHAHVLKAMG	LAEEDEHAPR	ERSSKPKNGL	ENPEGGAHKK	PERLAQPPKD	LEARTGAGPL	ARGERKKSVV	ESSAPGANNL
330	340	350	360	370	380	390	400
QVNALVARLP	LLLPRAPRSL	IPPIPVSPPI	LAPRLSSGAL	KVATLPLSSR	AGAPPAAVPI	INMILPTVPA	LPGPGPGPGR
410	420	430	440	450	460	470	480
APPGGLTQPR	GTENREVGIG	GDQGPHDKGV	KRTAEVPVSE	ASGQAPPAKA	AKQDIEDTAS	DAKRKRGRPR	KKSGGSGERN
490	500	510	520	530	540	550	560
STPLKSAAAM	ESAQSSRLPW	ETWGSGGEGN	SAGGAERPGP	MGEAEKGAVL	AQGQGDGTVS	KGGRGPGSQH	TKEAEDKIPL
570	580	590	600	610	620		
VPSKVSVIKG	SRSQKEAFPL	AKGEVDTAPQ	GNKDLKEHVL	QSSLSQEHKD	PKATPP		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
905	1	654.8549	64.59	2	40.1	10.7	0	416-428	R.EVGIGGDQGPHDK.G	

Detailed Protein Report

Protein 1541: PREDICTED: cardiolipin synthase isoform X2 [Homo sapiens]

Accession:	gi|530425765	**Score:**	10.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	21.1
Database Date:	2015-11-30	**pI:**	9.5
		Sequence Coverage [%]:	6.3
		No. of unique Peptides:	1

Quantitation

Wdown:Qdown **Median:** 0.15 **CV:** 0.00 % **No. of Peptides:** 1

Alias proteins:

Accession	**Name**	**Description**
gi|578835443	refseq_human (refseq_human_20140103.fasta)	PREDICTED: cardiolipin synthase isoform X5 [Homo sapiens]
gi|530425767	refseq_human (refseq_human_20140103.fasta)	PREDICTED: cardiolipin synthase isoform X3 [Homo sapiens]

10	20	30	40	50	60	70	80
MLSMTRIGLA	PVLGYLIIEE	DFNIALGVFA	LAGLTDLLDG	FIARNWANQR	SALGSALDPL	ADKILISILY	VSLTYADLIP
90	100	110	120	130	140	150	160
VPLTYMIISR	DVMLIAAVFY	VRYRTLPTPR	TLAKYFNPCY	ATARLKPTFI	SKVNTAVQLI	LVAASLAAPV	FNYADSIYLQ
170	180	190	200				
ILWCFTAFTT	AASAYSYYHY	GRKTVQVIKD					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1256	1	698.8457	-58.32	2	45.4	10.7	0	91-102	R.DVMLIAAVFYVR.Y		Wdown:Qdown 0.15

Detailed Protein Report

Protein 1542: thymidine kinase 2, mitochondrial isoform 3 precursor [Homo sapiens]

Accession:	gi|290657146	**Score:**	10.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	28.4
Database Date:	2015-11-30	**pI:**	10.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	7.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLLWPLRGWA	ARALRCFGPG	SRGSPASGPG	PRRVQRRAWP	PDKEQEKEKK	SVVLTEPVSK	WRNVRGHNPL	GLMYHDASRW
90	100	110	120	130	140	150	160
GLTLQTYVQL	TMLDRHTRPQ	VSSVRLMERS	IHSARYIFVE	NLYRSGKMPE	VDYVVLSEWF	DWILRNMDVS	VDLIVYLRTN
170	180	190	200	210	220	230	240
PETCYQRLKK	RCREEEKVIP	LEYLEAIHHL	HEEWLIKGSL	FPMAAPVLVI	EADHHMERML	ELFEQNRDRI	LTPENRKHCP
250							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2172	1	900.3349	-116.17	2	55.8	10.7	2	16-33	R.CFGPGSRGSPASGPGPRR.V	Carbamidomethyl: 1

Detailed Protein Report

Protein 1543: PREDICTED: AT-rich interactive domain-containing protein 2 isoform X2 [Homo sapiens]

Accession:	gi|578823400	**Score:**	10.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	191.1
Database Date:	2015-11-30	**pI:**	7.1
		Sequence Coverage [%]:	0.4
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	1.75	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.95	**CV:**	0.00 %	**No. of Peptides:**	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MANSTGKAPP	DERRKGLAFL	DELRQFHHSR	GSPFKKIPAV	GGKELDLHGL	YTRVTTLGGF	AKVSEKNQWG	EIVEEFNFPR
90	100	110	120	130	140	150	160
SCSNAAFALK	QYYLRYLEKY	EKVHHFGEDD	DEVPPGNPKP	QLPIGAIPSS	YNYQQHSVSD	YLRQSYGLSM	DFNSPNDYNK
170	180	190	200	210	220	230	240
LVLSLLSGLP	NEVDFAINVC	TLLSNESKHV	MQLEKDPKII	TLLLANAGVF	DDTLGSFSTV	FGEEWKEKTD	RDFVKFWKDI
250	260	270	280	290	300	310	320
VDDNEVRDLI	SDRNKSHEGT	SGEWIWESLF	HPPRKLGIND	IEGQRLLLDP	VDFKTTHLMF	HTVTKCLMSR	DRFLKMRGME
330	340	350	360	370	380	390	400
ILGNLCKAED	NGVLICEYVD	QDSYREIICH	LTLPDVLLVI	STLEVLYMLT	EMGDVACTKI	AKVEKSIDML	VCLVSMDIQM
410	420	430	440	450	460	470	480
FGPDALAAVK	LIEHPSSSHQ	MLSEIRPQAI	EQVQTQTHVA	SAPASRAVVA	QHVAPPPGIV	EIDSEKFACQ	WLNAHFEVNP
490	500	510	520	530	540	550	560
DCSVSRAEMY	SEYLSTCSKL	ARGGILTSTG	FYKCLRTVFP	NHTVKRVEDS	SSNGQAHIHV	VGVKRRAIPL	PIQMYYQQQP
570	580	590	600	610	620	630	640
VSTSVVRVDS	VPDVSPAPSP	AGIPHGSQTI	GNHFQRTPVA	NQSSNLTATQ	MSFPVQGVHT	VAQTVSRIPQ	NPSPHTHQQQ
650	660	670	680	690	700	710	720
NAPVTVIQSK	APIPCEVVKA	TVIQNSIPQT	GVPVSIAVGG	GPPQSSVVQN	HSTGPQPVTV	VNSQTLLHHP	SVIPQQSPLH
730	740	750	760	770	780	790	800
TVVPGQIPSG	TPVTVIQQAV	PQSHMFGRVQ	NIPACTSTVS	QGQQLITTSP	QPVQTSSQQT	SAGSQSQDTV	IIAPPQYVTT
810	820	830	840	850	860	870	880
SASNIVSATS	VQNFQVATGQ	MVTIAGVPSP	QASRVGFQNI	APKPLPSQQV	SSTVVQQPIQ	QPQQPTQQSV	VIVSQPAQQG
890	900	910	920	930	940	950	960
QTYAPAIHQI	VLANPAALPA	GQTVQLTGQP	NITPSSSPSP	VPATNNQVPT	AMSSSSTPQS	QGPPPTVSQM	LSVKRQQQQQ
970	980	990	1000	1010	1020	1030	1040
HSPAPPPQQV	QVQVQQPQQV	QMQVQPQQSN	AGVGQPASGE	SSLIKQLLLP	KRGPSTPGGK	LILPAPQIPP	PNNARAPSPQ
1050	1060	1070	1080	1090	1100	1110	1120
VVYQVASNQA	AGFGVQGQTP	AQQLLVGQQN	VQLVPSAMPP	SGGVQTVPIS	NLQILPGPLI	SNSPATIFQG	TSGNQVTITV
1130	1140	1150	1160	1170	1180	1190	1200
VPNTSFAPAT	VSQGNATQLI	APAGITMSGT	QTGVGLPVQT	LPATQASPAG	QSSCTTATPP	FKGDKIICQK	EEEAKEATGL
1210	1220	1230	1240	1250	1260	1270	1280
HVHERKIEVM	ENPSCRRGAT	NTSNGDTKEN	EMHVGSLLNG	RKYSDSSLPP	SNSGKIQSET	NQCSLISNGP	SLELGENGAS
1290	1300	1310	1320	1330	1340	1350	1360
GKQNSEQIDM	QDIKSDLRKP	LVNGICDFDK	GDGSHLSKNI	PNHKTSNHVG	NGEISPMEPQ	GTLDITQQDT	AKGDQLERIS
1370	1380	1390	1400	1410	1420	1430	1440
NGPVLTLGGS	SVSSIQEASN	AATQQFSGTD	LLNGPLASSL	NSDVPQQRPS	VVVSPHSTTS	VIQGHQIIAV	PDSGSKVSHS
1450	1460	1470	1480	1490	1500	1510	1520
PALSSDVRST	NGTAECKTVK	RPAEDTDRET	VAGIPNKVGV	RIVTISDPNN	AGCSATMVAV	PAGADPSTVA	KVAIESAVQQ
1530	1540	1550	1560	1570	1580	1590	1600
KQQHPPTYVQ	NVVPQNTPMP	PSPAVQVQGQ	PNSSQPSPFS	GSSQPGDPMR	KPGQNFMCLW	QSCKKWFQTP	SQVFYHAATE
1610	1620	1630	1640	1650	1660	1670	1680
HGGKDVYPGQ	CLWEGCEPFQ	RQRFSFITHL	QDKHCSKDAL	LAGLKQDEPG	QAGSQKSSTK	QPTVGGTSST	PRAQKAIVNH
1690	1700	1710	1720	1730	1740	1750	1760
PSAALMALRR	GSRNLVFRDF	TDEKEGPITK	HIRLTAALIL	KNIGKYSECG	RRLLKRHENN	LSVLAISNME	ASSTLAKCLY
1770	1780						
ELNFTVQSKE	QEKDSEMLQ						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
198	1	486.6257	-266.72	2	31.2	10.7	1	96-102	R.YLEKYEK.V		Wdown:Qdown 0.95 mdown:qdown 1.75

Detailed Protein Report

Protein 1544: PREDICTED: cytochrome P450 4A22 isoform X2 [Homo sapiens]

Accession:	gi|530362418	**Score:**	10.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	40.1
Database Date:	2015-11-30	**pI:**	9.2
Modification(s):	Oxidation	**Sequence Coverage [%]:**	7.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSVSVLSPSR	RLGGVSGILQ	VTSLLILLLL	LIKAAQLYLH	RQWLLKALQQ	FPCPPSHWLF	GHIQEFQHDQ	ELQRIQERVK
90	100	110	120	130	140	150	160
TFPSACPYWI	WGGKVRVQLY	DPDYMKVILG	RSDPKSHGSY	KFLAPRIGYG	LLLLNGQTWF	QHRRMLTPAF	HNDILKPYVG
170	180	190	200	210	220	230	240
LMADSVRVML	DKWEELLGQD	SPLEVFQHVS	LMTLDTIMKS	AFSHQGSIQV	DRPSDPTEEG	STTEGGGAGE	DQEEEALGFS
250	260	270	280	290	300	310	320
GHPPLGQRAP	GLPRPCWCSG	WNCFRNHLDQ	MPYTTMCIKE	ALRLYPPVPG	IGRELSTPVT	FPDGRSLPKG	IMVLLSIYGL
330	340	350	360				
HHNPKVWPNL	EVFDPSRFAP	GSAQHSHAFL	PFSGGSR				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
9	1	1083.3275	79.88	3	28.6	10.7	1	310-337	K.GIMVLLSIYGLHHNPKVWPNLEVFDPSR.F	Oxidation: 3

Detailed Protein Report

Protein 1545: 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 1546: PREDICTED: LOW QUALITY PROTEIN: putative speedy protein E8-like [Homo sapiens]

Accession:	gi|578844233	**Score:**	10.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	21.6
Database Date:	2015-11-30	**pI:**	6.5
		Sequence Coverage [%]:	9.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MKAKRRRVSL	VLPEYYEAFN	RLLEDPVIKR	LLAWDKDLRV	SDKYLLAMVI	AYFSRAGLPS	WQYQRIHFFL	ALYLANDMEE
90	100	110	120	130	140	150	160
DDEAEDDEAP	KQNIFYFLYE	ETRSHIPLLS	ELWFQLCRYM	NPRARKNCSQ	IALFRKYRFH	FFCSMRCRAW	VSLEELEEIQ
170	180						
AYDPEPWVWA	RDRAHLS						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1521	1	671.4152	79.35	3	47.7	10.7	2	6-21	R.RRVSLVLPEYYEAFNR.L	

Detailed Protein Report

Protein 1547: **disintegrin and metalloproteinase domain-containing protein 19 preproprotein [Homo sapiens]**

Accession:	gi|15451844	**Score:**	10.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	100.8
Database Date:	2015-11-30	**pI:**	9.9
		Sequence Coverage [%]:	1.5
		No. of unique Peptides:	1

Quantitation

Wdown:Qdown **Median:** 1.20 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MPGGAGAARL	CLLAFALQPL	RPRAAREPGW	TRGSEEGSPK	LQHELIIPQW	KTSESPVREK	HPLKAELRVM	AEGRELILDL
90	100	110	120	130	140	150	160
EKNEQLFAPS	YTETHYTSSG	NPQTTTRKLE	DHCFYHGTVR	ETELSSVTLS	TCRGIRGLIT	VSSNLSYVIE	PLPDSKGQHL
170	180	190	200	210	220	230	240
IYRSEHLKPP	PGNCGFEHSK	PTTRDWALQF	TQQTKKRPRR	MKREDLNSMK	YVELYLVADY	LEFQKNRRDQ	DATKHKLIEI
250	260	270	280	290	300	310	320
ANYVDKFYRS	LNIRIALVGL	EVWTHGNMCE	VSENPYSTLW	SFLSWRRKLL	AQKYHDNAQL	ITGMSFHGTT	IGLAPLMAMC
330	340	350	360	370	380	390	400
SVYQSGGVNM	DHSENAIGVA	ATMAHEMGHN	FGMTHDSADC	CSASAADGGC	IMAAATGHPF	PKVFNGCNRR	ELDRYLQSGG
410	420	430	440	450	460	470	480
GMCLSNMPDT	RMLYGGRRCG	NGYLEDGEEC	DCGEEEECNN	PCCNASNCTL	RPGAECAHGS	CCHQCKLLAP	GTLCREQARQ
490	500	510	520	530	540	550	560
CDLPEFCTGK	SPHCPTNFYQ	MDGTPCEGGQ	AYCYNGMCLT	YQEQCQQLWG	PGARPAPDLC	FEKVNVAGDT	FGNCGKDMNG
570	580	590	600	610	620	630	640
EHRKCNMRDA	KCGKIQCQSS	EARPLESNAV	PIDTTIIMNG	RQIQCRGTHV	YRGPEEEGDM	LDPGLVMTGT	KCGYNHICFE
650	660	670	680	690	700	710	720
GQCRNTSFFE	TEGCGKKCNG	HGVCNNNQNC	HCLPGWAPPF	CNTPGHGGSI	DSGPMPPESV	GPVVAGVLVA	ILVLAVLMLM
730	740	750	760	770	780	790	800
YYCCRQNNKL	GQLKPSALPS	KLRQQFSCPF	RVSQNSGTGH	ANPTFKLQTP	QGKRKVINTP	EILRKPSQPP	PRPPPDYLRG
810	820	830	840	850	860	870	880
GSPPAPLPAH	LSRAARNSPG	PGSQIERTES	SRRPPPSRPI	PPAPNCIVSQ	DFSRPRPPQK	ALPANPVPGR	RSLPRPGGAS
890	900	910	920				
PLRPPGAGPQ	QSRPLAALAP	KFPEYRSQRA	GGMISSKI				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2074	1	720.2852	-119.33	2	54.5	10.7	1	814-827	R.AARNSPGPGSQIER.T		Wdown:Qdown 1.20

Detailed Protein Report

Protein 1548: protein ERGIC-53 precursor [Homo sapiens]

Accession:	gi|5031873	**Score:**	10.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	57.5
Database Date:	2015-11-30	**pI:**	6.3
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.8
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	0.80	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.94	**CV:**	0.00 %	**No. of Peptides:**	1

10	20	30	40	50	60	70	80
MAGSRQRGLR	ARVRPLFCAL	LLSLGRFVRG	DGVGGDPAVA	LPHRRFEYKY	SFKGPHLVQS	DGTVPFWAHA	GNAIPSSDQI
90	100	110	120	130	140	150	160
RVAPSLKSQR	GSVWTKTKAA	FENWEVEVTF	RVTGRGRIGA	DGLAIWYAEN	QGLEGPVFGS	ADLWNGVGIF	FDSFDNDGKK
170	180	190	200	210	220	230	240
NNPAIVIIGN	NGQIHYDHQN	DGASQALASC	QRDFRNKPYP	VRAKITYYQN	TLTVMINNGF	TPDKNDYEFC	AKVENMIIPA
250	260	270	280	290	300	310	320
QGHFGISAAT	GGLADDHDVL	SFLTFQLTEP	GKEPPTPDKE	ISEKEKEKYQ	EEFEHFQQEL	DKKKEEFQKG	HPDLQGQPAE
330	340	350	360	370	380	390	400
EIFESVGDRE	LRQVFEGQNR	IHLEIKQLNR	QLDMILDEQR	RYVSSLTEEI	SKRGAGMPGQ	HGQITQQELD	TVVKTQHEIL
410	420	430	440	450	460	470	480
RQVNEMKNSM	SETVRLVSGM	QHPGSAGGVY	ETTQHFIDIK	EHLHIVKRDI	DNLVQRNMPS	NEKPKCPELP	PFPSCLSTVH
490	500	510	520				
FIIFVVVQTV	LFIGYIMYRS	QQEAAAKKFF					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1282	1	530.6426	-217.90	2	44.5	10.7	0	457-465	R.NMPSNEKPK.C	Oxidation: 2	Wdown:Qdown 0.94 mdown:qdown 0.80

Detailed Protein Report

Protein 1549: PREDICTED: collagen alpha-1(III) chain-like [Homo sapiens]

Accession:	gi|530356951	**Score:**	10.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	22.6
Database Date:	2015-11-30	**pI:**	12.4
		Sequence Coverage [%]:	7.3
		No. of unique Peptides:	1

Quantitation

Wdown:Qdown **Median:** 0.98 **CV:** 0.00 % **No. of Peptides:** 1

Alias proteins:

Accession	**Name**	**Description**
gi|530434069	refseq_human (refseq_human_20140103.fasta)	PREDICTED: collagen alpha-1(III) chain-like [Homo sapiens]
gi|530365851	refseq_human (refseq_human_20140103.fasta)	PREDICTED: collagen alpha-1(III) chain-like [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MEAPLGCTIA QKGCQGQPRP PSCSNHKVRR QGSAEPPRKL RALSRLAARQ RRQQPEPELV AATTTERCGE GEQGPDETLR
        90        100        110        120        130        140        150        160
LKTGGGRGTR LTTAPREWKG SSPLAAAHTS SPRGGSARPG CRTVPSRAVE PPRRGAREPK AHPGGPGSPG AGAGAPGRPG
       170        180        190        200        210        220
SRLDPPGASP LCGHDIPMGT VARNAPLCRT QTLQTPSFPG RPRPPASPSA AEGPRRTQ
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2841	1	913.4679	-6.42	2	64.7	10.7	1	52-67	R.RQQPEPELVAATTTER.C		Wdown:Qdown 0.98

Detailed Protein Report

Protein 1550: zinc finger protein 506 isoform 2 [Homo sapiens]

Accession:	gi|224028219	**Score:**	10.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	48.0
Database Date:	2015-11-30	**pI:**	10.2
		Sequence Coverage [%]:	2.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGPLQFRDVA	IEFSLEEWHC	LDAAQRNLYR	DVMLENYRNL	IFLVMYSHFA	QDLWSEQSIK	DSFQKVILRR	YEKCRHDNLQ
90	100	110	120	130	140	150	160
LKKGCESVDE	CPVHKRGYNG	LKQCLATTQR	KIFQCDEYVK	FLHKFSNSNK	HKIRDTGKKS	FKCIEYGKTF	NQSSTRTTYK
170	180	190	200	210	220	230	240
KIDAGEKRYK	CEECGKAYKQ	SSHLTTHKKI	HTGEKPYKCE	ECGKAYKQSC	NLTTHKIIHT	GEKPYRCREC	GKAFNHPATL
250	260	270	280	290	300	310	320
FSHKKIHTGE	KPYKCDKCGK	AFISSSTLTK	HEIIHTGEKP	YKCEECGKAF	NRSSNLTKHK	RIHTGDVPYK	CDECGKTFTW
330	340	350	360	370	380	390	400
YSSLSKHKRA	HTGEKPYKCE	ECGKAFTAFS	TLTEHKIIHT	GEKPYKCEEC	GKAFNWSSAL	NKHKKIHIRQ	KPCIVKNVEN
410	420						
LLNVPQPLIS	IR						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2642	1	685.3766	32.71	2	61.3	10.7	0	233-244	K.AFNHPATLFSHK.K	

Detailed Protein Report

Protein 1551: PREDICTED: uncharacterized protein LOC388210 [Homo sapiens]

Accession:	gi|578846031	**Score:**	10.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	81.1
Database Date:	2015-11-30	**pI:**	6.7
		Sequence Coverage [%]:	2.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MRQNLTYERH	WPSQPDKIIM	EATLEHVLGA	SCTRQSFWGE	VQTDYARWLR	HSLHLGLCDL	PRALLVVGEH	TLGQGGLLLR
90	100	110	120	130	140	150	160
SRCHLGLAPD	PDHGLHLSLT	LQNHSRPRSA	DFSGALELRG	SKAQRVGLLG	RVSTSTSQSL	VRLEGSVDNR	EEKVRLSVFR
170	180	190	200	210	220	230	240
APSCLQASVA	HEEGGREESV	VLRACAHGRT	AEAEVLFRDG	RQPSQPLGRL	TLQAANQSLL	LAARGCQGGL	LGHVESRIAA
250	260	270	280	290	300	310	320
VGSQVQARLE	EKVQGLGASV	RRFQQLVQPA	GTLDGVAGLL	LQLSQAGREA	MQASGWAVAT	LWARSQALTQ	HLPLYLEWLQ
330	340	350	360	370	380	390	400
VGLEQLREEL	EWPLATLKDA	YLEVTLRPLE	EVWRERAEEA	MRRLQAWVPG	MPGNGGPRPI	RAALGAMKGA	LELAAHQMLS
410	420	430	440	450	460	470	480
WAEATFSRAL	KRLCKPLLDL	YSLSARNRSV	VVMLPLLPAG	DEPLDVARVT	SYLMEEKLLR	PLRELSGANV	LAEYYWLRRR
490	500	510	520	530	540	550	560
LLAGPWEYHA	LVAGAQHVVT	FDGRVWDLST	QCGSILLAQD	FAHNTFSLTL	SRTGSGLTAL	FVELNHKTLI	LYPSLQAYRL
570	580	590	600	610	620	630	640
YNSSLPGDSC	PDLKLHPATT	RKDVSRIELA	SEDGVSVSCD	VPTGLCSLTL	GLWQHGISAG	LLGTNDNEAG	NELMLPDGSM
650	660	670	680	690	700	710	720
ARSLEELSLA	WQVGGDCRAT	EKPQQEQACP	GQLPACWAFF	EGPHSSLRDC	FRVVDPTPFL	SLCVQVPCGT	QELQPACNLA
730	740	750					
AAYIHLCARG	FVPLAPPPQC	V					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2653	1	1058.0400	-59.79	2	61.9	10.7	2	123-142	K.AQRVGLLGRVSTSTSQSLVR.L	

Detailed Protein Report

Protein 1552: PREDICTED: calcium-responsive transcription factor isoform X7 [Homo sapiens]

Accession:	gi|530370982	**Score:**	10.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	49.5
Database Date:	2015-11-30	**pI:**	5.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MECQYGPRRK	GFQLKKVSEQ	ESRSCQLYKA	TCPARIYIKK	VQKFPEYRVP	TDPKIDKKII	RMEQEKAFNM	LKKNLVDAGG
90	100	110	120	130	140	150	160
VLRWYVQLPT	QQAHQYHELE	TPCLTLSPSP	FPVSSLEEEE	TAVRDENCAL	PSRLHPQVAH	KIQELVSQGI	EQVYAVRKQL
170	180	190	200	210	220	230	240
RKFVERELFK	PDEVPERHNL	SFFPTVNDIK	NHIHEVQKSL	RNGDTVYNSE	IIPATLQWTT	DSGNILKETM	TVTFAEGNSP
250	260	270	280	290	300	310	320
GESITTKVET	NQTRGSLSPE	PTHLLSSLSS	FQPKIFTQLQ	GLQLQPRYTS	PDESPAVVSV	NNQPSSSPSG	LLDTIGSAVM
330	340	350	360	370	380	390	400
NNNSLLLGQS	HSLQRDTCLT	QNNSTASTMG	NLPEPDQNLV	AMDELVEVGD	VEDTGNLEGT	VHRILLGDVQ	TIPIQIIDNH
410	420	430	440	450			
SALIEENPES	TISVSQVKQE	PKEPALSMEA	KKTVDYKKLS	AT			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1348	1	991.6617	186.83	1	45.4	10.7	0	423-431	K.EPALSMEAK.K	Oxidation: 6

Detailed Protein Report

Protein 1553: kanadaptin [Homo sapiens]

Accession: gi|155722990
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 10.7
MW [kDa]: 88.8
pI: 5.0
Sequence Coverage [%]: 2.0
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MLAPLRNAPG	REGATSPSPP	TDATGSLGEW	DVDRNVKTEG	WVSKERISKL	HRLRMADILS	QSETLASQDL	SGDFKKPALP
90	100	110	120	130	140	150	160
VSPAARSKAP	ASSSSNPEEV	QKEGPTALQD	SNSGEPDIPP	PQPDCGDFRS	LQEEQSRPPT	AVSSPGGPAR	APPYQEPPWG
170	180	190	200	210	220	230	240
GPATAPYSLE	TLKGGTILGT	RSLKGTSYCL	FGRLSGCDVC	LEHPSVSRYH	AVLQHRASGP	DGECDSNGPG	FYLYDLGSTH
250	260	270	280	290	300	310	320
GTFLNKTRIP	PRTYCRVHVG	HVVRFGGSTR	LFILQGPEED	REAESELTVT	QLKELRKQQQ	ILLEKKMLGE	DSDEEEEMDT
330	340	350	360	370	380	390	400
SERKINAGSQ	DDEMGCTWGM	GEDAVEDDAE	ENPIVLEFQQ	EREAFYIKDP	KKALQGFFDR	EGEELEYEFD	EQGHSTWLCR
410	420	430	440	450	460	470	480
VRLPVDDSTG	KQLVAEAIHS	GKKKEAMIQC	SLEACRILDT	LGLLRQEAVS	RKRKAKNWED	EDFYDSDDDT	FLDRTGLIEK
490	500	510	520	530	540	550	560
KRLNRMKKAG	KIDEKPETFE	SLVAKLNDAE	RELSEISERL	KASSQVLSES	PSQDSLDAFM	SEMKSGSTLD	GVSRKKLHLR
570	580	590	600	610	620	630	640
TFELRKEQQR	LKGLIKIVKP	AEIPELKKTE	TQTTGAENKA	KKLTLPLFGA	MKGGSKFKLK	TGTVGKLPPK	RPELPPTLMR
650	660	670	680	690	700	710	720
MKDEPEVEEE	EEEEEEEEKE	KEEHEKKKLE	DGSLSRPQPE	IEPEAAVQEM	RPPTDLTHFK	ETQTHENMSQ	LSEEEQNKDY
730	740	750	760	770	780	790	800
QDCSKTTSLC	AGPSASKNEY	EKSRGELKKK	KTPGPGKLPP	TLSSKYPEDD	PDYCVWVPPE	GQSGDGRTHL	NDKYGY

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2813	1	973.4922	-45.30	2	64.3	10.7	2	249-264	R.IPPRTYCRVHVGHVVR.F	Carbamidomethyl: 7

Detailed Protein Report

Protein 1554: sodium-dependent multivitamin transporter [Homo sapiens]

Accession:	gi|256985183	**Score:**	10.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	68.6
Database Date:	2015-11-30	**pI:**	9.5
		Sequence Coverage [%]:	2.4
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578803248	refseq_human (refseq_human_20140103.fasta)	PREDICTED: sodium-dependent multivitamin transporter isoform X3 [Homo sapiens]
gi|578803246	refseq_human (refseq_human_20140103.fasta)	PREDICTED: sodium-dependent multivitamin transporter isoform X2 [Homo sapiens]
gi|578803244	refseq_human (refseq_human_20140103.fasta)	PREDICTED: sodium-dependent multivitamin transporter isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MSVGVSTSAP	LSPTSGTSVG	MSTFSIMDYV	VFVLLLVLSL	AIGLYHACRG	WGRHTVGELL	MADRKMGCLP	VALSLLATFQ
90	100	110	120	130	140	150	160
SAVAILGVPS	EIYRFGTQYW	FLGCCYFLGL	LIPAHIFIPV	FYRLHLTSAY	EYLELRFNKT	VRVCGTVTFI	FQMVIYMGVV
170	180	190	200	210	220	230	240
LYAPSLALNA	VTGFDLWLSV	LALGIVCTVY	TALGGLKAVI	WTDVFQTLVM	FLGQLAVIIV	GSAKVGGLGR	VWAVASQHGR
250	260	270	280	290	300	310	320
ISGFELDPDP	FVRHTFWTLA	FGGVFMMLSL	YGVNQAQVQR	YLSSRTEKAA	VLSCYAVFPF	QQVSLCVGCL	IGLVMFAYYQ
330	340	350	360	370	380	390	400
EYPMSIQQAQ	AAPDQFVLYF	VMDLLKGLPG	LPGLFIACLF	SGSLSTISSA	FNSLATVTME	DLIRPWFPEF	SEARAIMLSR
410	420	430	440	450	460	470	480
GLAFGYGLLC	LGMAYISSQM	GPVLQAAISI	FGMVGGPLLG	LFCLGMFFPC	ANPPGAVVGL	LAGLVMAFWI	GIGSIVTSMG
490	500	510	520	530	540	550	560
SSMPPSPSNG	SSFSLPTNLT	VATVTTLMPL	TTFSKPTGLQ	RFYSLSYLWY	SAHNSTTVIV	VGLIVSLLTG	RMRGRSLNPA
570	580	590	600	610	620	630	640
TIYPVLPKLL	SLLPLSCQKR	LHCRSYGQDH	LDTGLFPEKP	RNGVLGDSRD	KEAMALDGTA	YQGSSSTCIL	QETSL

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2810	1	813.4027	-85.59	2	64.3	10.7	1	554-568	R.GRSLNPATIYPVLPK.L	

Detailed Protein Report

Protein 1555: 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

Quantitation

Wdown:Qdown **Median:** 1.27 **CV:** 0.00 % **No. of 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	Ratios
872	1	736.7983	-61.16	2	40.4	10.7	2	318-329	R.KEMEIMADSKMK.A	Oxidation: 6, 11	Wdown:Qdown 1.27

Detailed Protein Report

Protein 1556: 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 1557: A-kinase anchor protein 6 [Homo sapiens]

Accession:	gi|21493045	**Score:**	10.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	256.6
Database Date:	2015-11-30	**pI:**	4.8
		Sequence Coverage [%]:	0.4
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	1.44	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	1.82	**CV:**	0.00 %	**No. of Peptides:**	1

10	20	30	40	50	60	70	80
MLTMSVTLSP	LRSQDLDPMA	TDASPMAINM	TPTVEQGEGE	EAMKDMDSDQ	QYEKPPPLHT	GADWKIVLHL	PEIETWLRMT
90	100	110	120	130	140	150	160
SERVRDLTYS	VQQDSDSKHV	DVHLVQLKDI	CEDISDHVEQ	IHALLETEFS	LKLLSYSVNV	IVDIHAVQLL	WHQLRVSVLV
170	180	190	200	210	220	230	240
LRERILQGLQ	DANGNYTRQT	DILQAFSEET	KEGRLDSLTE	VDDSGQLTIK	CSQNYLSLDC	GITAFELSDY	SPSEDLLSGL
250	260	270	280	290	300	310	320
GDMTSSQVKT	KPFDSWSYSE	MEKEFPELIR	SVGLLTVAAD	SISTNGSEAV	TEEVSQVSLS	VDDKGGCEED	NASAVEEQPG
330	340	350	360	370	380	390	400
LTLGVSSSSG	EALTNAAQPS	SETVQQESSS	SSHHDAKNQQ	PVPCENATPK	RTIRDCFNYN	EDSPTQPTLP	KRGLFLKEET
410	420	430	440	450	460	470	480
FKNDLKGNGG	KRQMVDLKPE	MSRSTPSLVD	PPDRSKLCLV	LQSSYPNSPS	AASQSYECLH	KVGNGNLENT	VKFHIKEISS
490	500	510	520	530	540	550	560
SLGRLNDCYK	EKSRLKKPHK	TSEEVPPCRT	PKRGTGSGKQ	AKNTKSSAVP	NGELSYTSKA	IEGPQTNSAS	TSSLEPCNQR
570	580	590	600	610	620	630	640
SWNAKLQLQS	ETSSSPAFTQ	SSESSVGSDN	IMSPVPLLSK	HKSKKGQASS	PSHVTRNGEV	VEAWYGSDEY	LALPSHLKQT
650	660	670	680	690	700	710	720
EVLALKLENL	TKLLPQKPRG	ETIQNIDDWE	LSEMNSDSEI	YPTYHVKKKH	TRLGRVSPSS	SSDIASSLGE	SIESGPLSDI
730	740	750	760	770	780	790	800
LSDEESSMPL	AGMKKYADEK	SERASSSEKN	ESHSATKSAL	IQKLMQDIQH	QDNYEAIWEK	IEGFVNKLDE	FIQWLNEAME
810	820	830	840	850	860	870	880
TTENWTPPKA	EMDDLKLYLE	THLSFKLNVD	SHCALKEAVE	EEGHQLLELI	ASHKAGLKDM	LRMIASQWKE	LQRQIKRQHS
890	900	910	920	930	940	950	960
WILRALDTIK	AEILATDVSV	EDEEGTGSPK	AEVQLCYLEA	QRDAVEQMSL	KLYSEQYTSS	SKRKEEFADM	SKVHSVGSNG
970	980	990	1000	1010	1020	1030	1040
LLDFDSEYQE	LWDWLIDMES	LVMDSHDLMM	SEEQQQHLYK	RYSVEMSIRH	LKKTELLSKV	EALKKGGVLL	PNDLLEKVDS
1050	1060	1070	1080	1090	1100	1110	1120
INEKWELLGK	TLGEKIQDTM	AGHSGSSPRD	LLSPESGSLV	RQLEVRIKEL	KGWLRDTELF	IFNSCLRQEK	EGTMNTEKQL
1130	1140	1150	1160	1170	1180	1190	1200
QYFKSLCREI	KQRRRGVASI	LRLCQHLLDD	RETCNLNADH	QPMQLIIVNL	ERRWEAIVMQ	AVQWQTRLQK	KMGKESETLN
1210	1220	1230	1240	1250	1260	1270	1280
VIDPGLMDLN	GMSEDALEWD	EMDISNKLIS	LNEESNDLDQ	ELQPVIPSLK	LGETSNEDPG	YDEEADNHGG	SQYASNITAP
1290	1300	1310	1320	1330	1340	1350	1360
SSPHIYQVYS	LHNVELYEDN	HMPFLKNNPK	VTGMTQPNVL	TKSLSKDSSF	SSTKSLPDLL	GGSNLVKPCA	CHGGDMSQNS
1370	1380	1390	1400	1410	1420	1430	1440
GSESGIVSEG	DTETTTNSEM	CLLNAVDGSP	SNLETEHLDP	QMGDAVNVLK	QKFTDEGESI	KLPNSSQSSI	SPVGCVNGKV
1450	1460	1470	1480	1490	1500	1510	1520
GDLNSITKHT	PDCLGEELQG	KHDVFTFYDY	SYLQGSKLKL	PMIMKQSQSE	KAHVEDPLLR	GFYFDKKSCK	SKHQTTELQP
1530	1540	1550	1560	1570	1580	1590	1600
DVPPHERILA	SASHEMDRIS	YKSGNIEKTF	TGMQNAKQLS	LLSHSSSIES	LSPGGDLFGL	GIFKNGSDSL	QRSTSLESWL
1610	1620	1630	1640	1650	1660	1670	1680
TSYKSNEDLF	SCHSSGDISV	SSGSVGELSK	RTLDLLNRLE	NIQSPSEQKI	KRSVSDITLQ	SSSQKMSFTG	QMSLDIASSI
1690	1700	1710	1720	1730	1740	1750	1760
NEDSAASLTE	LSSSDELSLC	SEDIVLHKNK	IPESNASFRK	RLTRSVADES	DVNVSMIVNV	SCTSACTDDE	DDSDLLSSST
1770	1780	1790	1800	1810	1820	1830	1840
LTLTEEELCI	KDEDDDSSIA	TDDEIYEDCT	LMSGLDYIKN	ELQTWIRPKL	SLTRDKKRCN	VSDEMKGSKD	ISSSEMTNPS
1850	1860	1870	1880	1890	1900	1910	1920
DTLNIETLLN	GSVKRVSENN	GNGKNSSHTH	ELGTKRENKK	TIFKVNKDPY	VADMENGNIE	GIPERQKGKP	NVTSKVSENL
1930	1940	1950	1960	1970	1980	1990	2000
GSHGKEISES	EHCKCKALMD	SLDDSNTAGK	EFVSQDVRHL	PKKCPNHHHF	ENQSTASTPT	EKSFSELALE	TRFNNRQDSD
2010	2020	2030	2040	2050	2060	2070	2080
ALKSSDDAPS	MAGKSAGCCL	ALEQNGTEEN	ASISNISCCN	CEPDVFHQKD	AEDCSVHNFV	KEIIDMASTA	LKSKSQPENE
2090	2100	2110	2120	2130	2140	2150	2160
VAAPTSLTQI	KEKVLEHSHR	PIQLRKGDFY	SYLSLSSHDS	DCGEVTNYIE	EKSSTPLPLD	TTDSGLDDKE	DIECFFEACV
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
1101	1	628.3123	5.90	2	42.5	10.7	2	485-494	R.LNDCYKEKSR.L		Wdown:Qdown 1.82 mdown:qdown 1.44

Detailed Protein Report

Protein 1558: cell division cycle-associated protein 2 [Homo sapiens]

Accession:	gi|44681484	**Score:**	10.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	112.6
Database Date:	2015-11-30	**pI:**	9.7
		Sequence Coverage [%]:	0.8
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	0.54	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.36	**CV:**	0.00 %	**No. of Peptides:**	1

10	20	30	40	50	60	70	80
MDANSKDKPP	ETKESAMNNA	GNASFILGTG	KIVTPQKHAE	LPPNPCTPDT	FKSPLNFSTV	TVEQLGITPE	SFVRNSAGKS
90	100	110	120	130	140	150	160
SSYLKKCRRR	SAVGARGSPE	TNHLIRFIAR	QQNIKNARKS	PLAQDSPSQG	SPALYRNVNT	LRERISAFQS	AFHSIKENEK
170	180	190	200	210	220	230	240
MTGCLEFSEA	GKESEMTDLT	RKEGLSACQQ	SGFPAVLSSK	RRRISYQRDS	DENLTDAEGK	VIGLQIFNID	TDRACAVETS
250	260	270	280	290	300	310	320
VDLSEISSKL	GSTQSGFLVE	ESLPLSELTE	TSNALKVADC	VVGKGSSDAV	SPDTFTAEVS	SDAVPDVRSP	ATPACRRDLP
330	340	350	360	370	380	390	400
TPKTFVLRSV	LKKPSVKMCL	ESLQEHCNNL	YDDDGTHPSL	ISNLPNCCKE	KEAEDEENFE	APAFLNMRKR	KRVTFGEDLS
410	420	430	440	450	460	470	480
PEVFDESLPA	NTPLRKGGTP	VCKKDFSGLS	SLLLEQSPVP	EPLPQPDFDD	KGENLENIEP	LQVSFAVLSS	PNKSSISETL
490	500	510	520	530	540	550	560
SGTDTFSSSN	NHEKISSPKV	GRITRTSNRR	NQLVSVVEES	VCNLLNTEVQ	PCKEKKINRR	KSQETKCTKR	ALPKKSQVLK
570	580	590	600	610	620	630	640
SCRKKKGKGK	KSVQKSLYGE	RDIASKKPLL	SPIPELPEVP	EMTPSIPSIR	RLGSGYFSSN	GKLEEVKTPK	NPVKRKDLLR
650	660	670	680	690	700	710	720
HDPDLHMHQG	YDKYDVSEFC	SYIKSSSSLG	NATSDEDPNT	NIMNINENKN	IPKAKNKSES	ENEPKAGTDS	PVSCASVTEE
730	740	750	760	770	780	790	800
RVASDSPKPA	LTLQQGQEFS	AGGQNAENLC	QFFKISPDLN	IKCERKDDFL	GAAEGKLQCN	RLMPNSQKDC	HCLGDVLIEN
810	820	830	840	850	860	870	880
TKESKSQSED	LGRKPMESSS	VVSCRDRKDR	RRSMCYSDGR	SLHLEKNGNH	TPSSSVGSSV	EISLENSELF	KDLSDAIEQT
890	900	910	920	930	940	950	960
FQRRNSETKV	RRSTRLQKDL	ENEGLVWISL	PLPSTSQKAK	RRTICTFDSS	GFESMSPIKE	TVSSRQKPQM	APPVSDPENS
970	980	990	1000	1010	1020	1030	
QGPAAGSSDE	PGKRRKSFCI	STLANTKATS	QFKGYRRRSS	LNGKGESSLT	ALERIEHNGE	RKQ	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1156	1	491.6232	-271.81	2	43.0	10.7	1	1015-1022	R.IEHNGERK.Q		Wdown:Qdown 0.36 mdown:qdown 0.54

Detailed Protein Report

Protein 1559: protein FAM216B [Homo sapiens]

Accession:	gi|32698855	**Score:**	10.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	16.4
Database Date:	2015-11-30	**pI:**	12.1
		Sequence Coverage [%]:	8.6
		No. of unique Peptides:	1

Quantitation

mdown:qdown **Median:** 2.46 **CV:** 0.00 % **No. of Peptides:** 1

Alias proteins:

Accession	Name	Description
gi|530402103	refseq_human (refseq_human_20140103.fasta)	PREDICTED: protein FAM216B isoform X1 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MGQNWKRQQK LWNVPQLPFI RVPPSIYDTS LLKALNQGQQ RYFYSIMRIY NSRPQWEALQ TRYIHSLQHQ QLLGYITQRE
        90        100        110        120        130        140
ALSYALVLRD STKRASAKVA PQRTIPRKTS AMTRRCPSVL PVSVVLPRAQ SKRRQVLRN
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
421	1	666.9204	69.47	2	34.3	10.7	0	22-33	R.VPPSIYDTSLLK.A		mdown:qdown 2.46

Detailed Protein Report

Protein 1560: cyclin-I2 isoform 2 [Homo sapiens]

Accession:	gi|89886237	**Score:**	10.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	40.6
Database Date:	2015-11-30	**pI:**	9.3
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	4.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MASGAQLPPQ	PSSSEVSAVQ	SPGGRPGAGL	EETALGVPLP	PSPGEAPLPR	SNRSRCPGTR	QPGAASLHAA	SAAVPVRPRR
90	100	110	120	130	140	150	160
GTAPAGKTAD	AVPAAAPEQA	PRPAPQSRKP	RNLEGDLDER	RLLCHLQLAQ	DREARLWRGG	KPQDEICDAF	EEVVLWLLRL
170	180	190	200	210	220	230	240
QNTFYFSQST	FNLALTIFGR	LLISVKVKEK	YLHCATITSL	RLAAKVNEEE	EFIPQVKDFT	KHYGSDYSPN	ELLRMELAIL
250	260	270	280	290	300	310	320
DRLHWDLYIG	TPLDFLTIFH	ALVVLSWPHV	LELLPQRNPS	LHVASLTRQL	QHCMAGHQLL	QFKGSTLALV	IITLELERLM
330	340	350	360	370			
PGWCAPISDL	LKKAQVGDMQ	YSCCKELVMQ	QLRSLQSSSC	TDNFVSPAN			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2391	1	872.9472	-14.49	2	58.3	10.7	1	319-333	R.LMPGWCAPISDLLKK.A	Carbamidomethyl: 6; Oxidation: 2

Detailed Protein Report

Protein 1561: **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 1562: ankyrin repeat and SOCS box protein 16 [Homo sapiens]

Accession:	gi|24586688	**Score:**	10.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	49.6
Database Date:	2015-11-30	**pI:**	9.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.3
		No. of unique 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
1199	1	874.6540	165.48	2	44.7	10.7	2	427-441	R.CRQGATRLPLPPLLR.D	Carbamidomethyl: 1

Detailed Protein Report

Protein 1563: 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 1564: 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 1565: PREDICTED: collagen alpha-5(IV) chain isoform X3 [Homo sapiens]

Accession:	gi|530421929	**Score:**	10.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	103.2
Database Date:	2015-11-30	**pI:**	8.9
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.5
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	0.35	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.30	**CV:**	0.00 %	**No. of Peptides:**	1

```
        10         20         30         40         50         60         70         80
MKLRGVSLAA GLFLLALSLW GQPAEAAACY GCSPGSKCDC SGIKGEKGER GFPGLEGHPG LPGFPGPEGP PGPRGQKGDD
        90        100        110        120        130        140        150        160
GIPGPPGPKG IRGPPGLPGF PGTPGLPGMP GHDGAPGPQG IPGCNGTKGE RGFPGSPGFP GLQGPPGPPG IPGMKGEPGS
       170        180        190        200        210        220        230        240
IIMSSLPGPK GNPGYPGPPG IQGLPGPTGI PGPIGPPGPP GLMGPPGPPG LPGPKGNMGL NFQGPKGEKG EQGLQGPPGP
       250        260        270        280        290        300        310        320
PGQISEQKRP IDVEFQKGDQ GLPGDRGPPG PPGIRGPPGP PGGEKGEKGE QGEPGKRGKP GKDGENGQPG IPGLPGDPGY
       330        340        350        360        370        380        390        400
PGEPGRDGEK GQKGDTGPPG PPGLVIPRPG TGITIGEKGN IGLPGLPGEK GERGFPGIQG PPGLPGPPGA AVMGPPGPPG
       410        420        430        440        450        460        470        480
FPGERGQKGD EGPPGISIPG PPGLDGQPGA PGLPGPPGPA GPHIPPSDEI CEPGPPGPPG SPGDKGLQGE QGVKGDKGDT
       490        500        510        520        530        540        550        560
CFNCIGTGIS GPPGQPGLPG LPGPPGSLGF PGQKGEKGQA GATGPKGLPG IPGAPGAPGF PGSKGEPGDI LTFPGMKGDK
       570        580        590        600        610        620        630        640
GELGSPGAPG LPGLPGTPGQ DGLPGLPGPK GEPGGITFKG ERGPPGNPGL PGLPGNIGPM GPPGFGPPGP VGEKGIQGVA
       650        660        670        680        690        700        710        720
GNPGQPGIPG PKGDPGQTIT QPGKPGLPGN PGRDGDVGLP GDPGLPGQPG LPGIPGSKGE PGIPGIGLPG PPGPKGFPGI
       730        740        750        760        770        780        790        800
PGPPGAPGTP GRIGLEGPPG PPGFPGPKGE PGFALPGPPG PPGLPGFKGA LGPKGDRGFP GPPGPPGRTG LDGLPGPKGD
       810        820        830        840        850        860        870        880
VGPNGQPGPM GPPGLPGIGV QGPPGPPGIP GPIGQPGLHG IPGEKGDPGP PGLDVPGPPG ERGSPGIPGA PGPIGPPGSP
       890        900        910        920        930        940        950        960
GLPGKAGASG FPGTKGEMGM MGPPGPPGPL GIPGRSGVPG LKGDDGLQGQ PGLPGPTGEK GSKGEPGLPG PPGPMDPNLL
       970        980        990       1000       1010       1020       1030       1040
GSKGEKGEPG LPGIPGVSGP KGYQGLPGDP GQPGLSGQPG LPGPPGPKGN PGLPGQPGLI GPPGLKGTIG DMGFPGPQGV
      1050       1060       1070       1080       1090       1100
EGPPGPSGVP GQPGSPGLPG QKGDKGDPGI SSIGLPGLPG PKMIRRYVLG FVASPK
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1051	1	839.4103	-1.09	2	41.9	10.7	1	545-560	K.GEPGDILTFPGMKGDK.G	Oxidation: 12	Wdown:Qdown 0.30 mdown:qdown 0.35

Detailed Protein Report

Protein 1566: proline-rich protein 15 [Homo sapiens]

Accession:	gi|28557711	**Score:**	10.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	13.7
Database Date:	2015-11-30	**pI:**	10.1
		Sequence Coverage [%]:	12.4
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:** 0.88	**CV:** 0.00 %	**No. of Peptides:** 1

Alias proteins:

Accession	Name	Description
gi|530384560	refseq_human (refseq_human_20140103.fasta)	PREDICTED: proline-rich protein 15 isoform X2 [Homo sapiens]
gi|530384558	refseq_human (refseq_human_20140103.fasta)	PREDICTED: proline-rich protein 15 isoform X1 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MADSGDAGSS GPWWKSLTNS RKKSKEAAVG VPPPAQPAPG EPTPPAPPSP DWTSSSRENQ HPNLLGGAGE PPKPDKLYGD
        90        100        110        120        130
KSGSSRRNLK ISRSGRFKEK RKVRATLLPE AGRSPEEAGF PGDPHEDKQ
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
351	1	870.3997	23.73	2	33.1	10.6	1	114-129	R.SPEEAGFPGDPHEDKQ.-		mdown:qdown 0.88

Detailed Protein Report

Protein 1567: 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

Protein 1568: programmed cell death 6-interacting protein isoform 1 [Homo sapiens]

Accession:	gi|22027538	**Score:**	10.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	96.0
Database Date:	2015-11-30	**pI:**	6.1
		Sequence Coverage [%]:	1.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MATFISVQLK	KTSEVDLAKP	LVKFIQQTYP	SGGEEQAQYC	RAAEELSKLR	RAAVGRPLDK	HEGALETLLR	YYDQICSIEP
90	100	110	120	130	140	150	160
KFPFSENQIC	LTFTWKDAFD	KGSLFGGSVK	LALASLGYEK	SCVLFNCAAL	ASQIAAEQNL	DNDEGLKIAA	KHYQFASGAF
170	180	190	200	210	220	230	240
LHIKETVLSA	LSREPTVDIS	PDTVGTLSLI	MLAQAQEVFF	LKATRDKMKD	AIIAKLANQA	ADYFGDAFKQ	CQYKDTLPKE
250	260	270	280	290	300	310	320
VFPVLAAKHC	IMQANAEYHQ	SILAKQQKKF	GEEIARLQHA	AELIKTVASR	YDEYVNVKDF	SDKINRALAA	AKKDNDFIYH
330	340	350	360	370	380	390	400
DRVPDLKDLD	PIGKATLVKS	TPVNVPISQK	FTDLFEKMVP	VSVQQSLAAY	NQRKADLVNR	SIAQMREATT	LANGVLASLN
410	420	430	440	450	460	470	480
LPAAIEDVSG	DTVPQSILTK	SRSVIEQGGI	QTVDQLIKEL	PELLQRNREI	LDESLRLLDE	EEATDNDLRA	KFKERWQRTP
490	500	510	520	530	540	550	560
SNELYKPLRA	EGTNFRTVLD	KAVQADGQVK	ECYQSHRDTI	VLLCKPEPEL	NAAIPSANPA	KTMQGSEVVN	VLKSLLSNLD
570	580	590	600	610	620	630	640
EVKKEREGLE	NDLKSVNFDM	TSKFLTALAQ	DGVINEEALS	VTELDRVYGG	LTTKVQESLK	KQEGLLKNIQ	VSHQEFSKMK
650	660	670	680	690	700	710	720
QSNNEANLRE	EVLKNLATAY	DNFVELVANL	KEGTKFYNEL	TEILVRFQNK	CSDIVFARKT	ERDELLKDLQ	QSIAREPSAP
730	740	750	760	770	780	790	800
SIPTPAYQSS	PAGGHAPTPP	TPAPRTMPPT	KPQPPARPPP	PVLPANRAPS	ATAPSPVGAG	TAAPAPSQTP	GSAPPPQAQG
810	820	830	840	850	860	870	
PPYPTYPGYP	GYCQMPMPMG	YNPYAYGQYN	MPYPPVYHQS	PGQAPYPGPQ	QPSYPFPQPP	QQSYYPQQ	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
636	1	712.9230	75.22	2	36.8	10.6	2	691-702	K.CSDIVFARKTER.D	

Detailed Protein Report

Protein 1569: 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 1570: antileukoproteinase precursor [Homo sapiens]

Accession:	gi|4507065	**Score:**	10.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	14.3
Database Date:	2015-11-30	**pI:**	10.7
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	8.3
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MKSSGLFPFL VLLALGTLAP WAVEGSGKSF KAGVCPPKKS AQCLRYKKPE CQSDWQCPGK KRCCPDTCGI KCLDPVDTPN
        90        100        110        120        130        140
PTRRKPGKCP VTYGQCLMLN PPNFCEMDGQ CKRDLKCCMG MCGKSCVSPV KA
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2384	1	696.1781	-126.02	2	58.5	10.6	1	114-124	R.DLKCCMGMCGK.S	Carbamidomethyl: 4, 5, 9; Oxidation: 6, 8

Detailed Protein Report

Protein 1571: 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 1572: 72 kDa type IV collagenase isoform b [Homo sapiens]

Accession:	gi|189217853	**Score:**	10.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	68.8
Database Date:	2015-11-30	**pI:**	5.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MQYLNTFYGC	PKESCNLFVL	KDTLKKMQKF	FGLPQTGDLD	QNTIETMRKP	RCGNPDVANY	NFFPRKPKWD	KNQITYRIIG
90	100	110	120	130	140	150	160
YTPDLDPETV	DDAFARAFQV	WSDVTPLRFS	RIHDGEADIM	INFGRWEHGD	GYPFDGKDGL	LAHAFAPGTG	VGGDSHFDDD
170	180	190	200	210	220	230	240
ELWTLGEGQV	VRVKYGNADG	EYCKFPFLFN	GKEYNSCTDT	GRSDGFLWCS	TTYNFEKDGK	YGFCPHEALF	TMGGNAEGQP
250	260	270	280	290	300	310	320
CKFPFRFQGT	SYDSCTTEGR	TDGYRWCGTT	EDYDRDKKYG	FCPETAMSTV	GGNSEGAPCV	FPFTFLGNKY	ESCTSAGRSD
330	340	350	360	370	380	390	400
GKMWCATTAN	YDDDRKWGFC	PDQGYSLFLV	AAHEFGHAMG	LEHSQDPGAL	MAPIYTYTKN	FRLSQDDIKG	IQELYGASPD
410	420	430	440	450	460	470	480
IDLGTGPTPT	LGPVTPEICK	QDIVFDGIAQ	IRGEIFFFKD	RFIWRTVTPR	DKPMGPLLVA	TFWPELPEKI	DAVYEAPQEE
490	500	510	520	530	540	550	560
KAVFFAGNEY	WIYSASTLER	GYPKPLTSLG	LPPDVQRVDA	AFNWSKNKKT	YIFAGDKFWR	YNEVKKKMDP	GFPKLIADAW
570	580	590	600	610	620		
NAIPDNLDAV	VDLQGGGHSY	FFKGAYYLKL	ENQSLKSVKF	GSIKSDWLGC			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
928	1	824.4253	82.38	3	40.1	10.6	0	221-242	K.YGFCPHEALFTMGGNAEGQPCK.F	Carbamidomethyl: 4, 21

Detailed Protein Report

Protein 1573: PREDICTED: heterogeneous nuclear ribonucleoprotein K isoform X7 [Homo sapiens]

Accession:	gi|530391071	**Score:**	10.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	48.5
Database Date:	2015-11-30	**pI:**	5.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	5.2
		No. of unique Peptides:	1

Quantitation

Wdown:Qdown **Median:** 2.24 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
METEQPEETF	PNTETNGEFG	KRPAEDMEEE	QAFKRSRNTD	EMVELRILLQ	SKNAGAVIGK	GGKNIKALRT	DYNASVSVPD
90	100	110	120	130	140	150	160
SSGPERILSI	SADIETIGEI	LKKIIPTLEE	YQHYKGSDFD	CELRLLIHQS	LAGGIIGVKG	AKIKELRENT	QTTIKLFQEC
170	180	190	200	210	220	230	240
CPHSTDRVVL	IGGKPDRVVE	CIKIILDLIS	ESPIKGRAQP	YDPNFYDETY	DYGGFTMMFD	DRRGRPVGFP	MRGRGGFDRM
250	260	270	280	290	300	310	320
PPGRGGRPMP	PSRRDYDDMS	PRRGPPPPPP	GRGGRGGSRA	RNLPLPPPPP	PRGGDLMAYD	RRGRPGDRYD	GMVGFSADET
330	340	350	360	370	380	390	400
WDSAIDTWSP	SEWQMAYEPQ	GGSGYDYSYA	GGRGSYGDLG	GPIITTQVTI	PKDLAGSIIG	KGGQRIKQIR	HESGASIKID
410	420	430	440				
EPLEGSEDRI	ITITGTQDQI	QNAQYLLQNS	VKQYSGKFF				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
294	1	936.0541	-63.02	3	32.4	10.6	2	145-167	K. ELRENTQTTIKLFQECCPHSTDR. V	Carbamidomethyl: 16	Wdown:Qdown 2.24

Detailed Protein Report

Protein 1574: **PREDICTED: mitogen-activated protein kinase kinase kinase 10 isoform X2 [Homo sapiens]**

Accession:	gi|530416611	**Score:**	10.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	78.9
Database Date:	2015-11-30	**pI:**	9.9
		Sequence Coverage [%]:	2.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEEEEGAVAK	EWGTTPAGPV	WTAVFDYEAA	GDEELTLRRG	DRVQVLSQDC	AVSGDEGWWT	GQLPSGRVGV	FPSNYVAPGA
90	100	110	120	130	140	150	160
PAAPAGLQLP	QEIPFHELQL	EEIIGVGGFG	KVYRALWRGE	EVAVKAARLD	PEKDPAVTAE	QVCQEARLFG	ALQHPNIIAL
170	180	190	200	210	220	230	240
RGACLNPPHL	CLVMEYARGG	ALSRVLAGRR	VPPHVLVNWA	VQVARGMNYL	HNDAPVPIIH	RDLKSINILI	LEAIENHNLA
250	260	270	280	290	300	310	320
DTVLKITDFG	LAREWHKTTK	MSAAGTYAWM	APEVIRLSLF	SKSSDVWSFG	VLLWELLTGE	VPYREIDALA	VAYGVAMNKL
330	340	350	360	370	380	390	400
TLPIPSTCPE	PFARLLEECW	DPDPHGRPDF	GSILKRLEVI	EQSALFQMPL	ESFHSLQEDW	KLEIQHMFDD	LRTKEKELRS
410	420	430	440	450	460	470	480
REEELLRAAQ	EQRFQEEQLR	RREQELAERE	MDIVERELHL	LMCQLSQEKP	RVRKRKGNFK	RSRLLKLREG	GSHISLPSGF
490	500	510	520	530	540	550	560
EHKITVQASP	TLDKRKGSDG	ASPPASPSII	PRLRAIRLTP	VDCGGSSSGS	SSGGSGTWSR	GGPPKKEELV	GGKKKGRTWG
570	580	590	600	610	620	630	640
PSSTLQKERV	GGEERLKGLG	EGSKQWSSSA	PNLGKSPKHT	PIAPGFASLN	EMDSRTMLVG	LGLAVGGVIG	GCPLAQVPVG
650	660	670	680	690	700	710	720
PWPALQRSDG	PLRLQRSSRR	QRMEAAACPL	PPTRPRPTSQ	CHCLPSPPRG	RGRRGSRRRP	RPPLGGDTAP	GGAATWRC

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2664	1	731.3710	-12.27	3	62.1	10.6	2	698-718	R.RRPRPPLGGDTAPGGAATWRC.-	

Detailed Protein Report

Protein 1575: ras-like protein family member 10A precursor [Homo sapiens]

Accession: gi|5454030
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 10.6
MW [kDa]: 22.5
pI: 10.7
Sequence Coverage [%]: 10.8
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MGGSLRVAVL	GAPGVGKTAI	IRQFLFGDYP	ERHRPTDGPR	LYRPAVLLDG	AVYDLSIRDG	DVAGPGSSPG	GPEEWPDAKD
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
WSLQDTDAFV	LVYDICSPDS	FDYVKALRQR	IAETRPAGAP	EAPILVVGNK	RDRQRLRFGP	RRALAALVRR	GWRCGYLECS
170	**180**	**190**	**200**	**210**			
AKYNWHVLRL	FRELLRCALV	RARPAHPALR	LQGALHPARC	SLM			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1650	1	1070.0254	-93.20	2	49.1	10.6	2	1-22	-.MGGSLRVAVLGAPGVGKTAIIR.Q	Oxidation: 1

Detailed Protein Report

Protein 1576: interferon alpha responsive protein isoform a [Homo sapiens]

Accession:	gi|11641255	**Score:**	10.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	15.3
Database Date:	2015-11-30	**pI:**	7.8
		Sequence Coverage [%]:	13.0
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MFSDNSHCPD CGQQWFPSLE LGHWLYQTEL VENECYQVFL DRINRADYCP ECYPDNPANR SLVLPWSFPL EWAPQNLTRW
        90        100        110        120        130        140
TFEKACHPFL LGPPLVRKRI HDSRVAGFNP ALQLILTRTD KTLNKKLGQN K
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
248	1	619.6295	-99.62	3	31.8	10.6	1	105-121	R.VAGFNPALQLILTRTDK.T	

Detailed Protein Report

Protein 1577: **PREDICTED: N-alpha-acetyltransferase 35, NatC auxiliary subunit isoform X4 [Homo sapiens]**

Accession: gi|530391404
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 10.6
MW [kDa]: 66.0
pI: 9.7
Sequence Coverage [%]: 4.6
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MNIILKMKMF	NVGRNAEDFQ	SMTYGFKMAN	SVTDLRVTGM	LKDVEDDMQR	RVKSTRSRQG	EERDPEVELE	HQQCLAVFSR
90	100	110	120	130	140	150	160
VKFTRVLLTV	LIAFTKKETS	AVAEAQKLMV	QAADLLSAIH	NSLHHGIQAQ	NDTTKGDHPI	MMGFEPLVNQ	RLLPPTFPRY
170	180	190	200	210	220	230	240
AKIIKREEMV	NYFARLIDRI	KTVCEVVNLT	NLHCILDFFC	EFSEQSPCVL	SRSLLQTTFL	VDNKKVFGTH	LMQDMVKDAL
250	260	270	280	290	300	310	320
RSFVSPPVLS	PKCYLYNNHQ	AKDCIDSFVT	HCVRPFCSLI	QIHGHNRARQ	RDKLGHILEE	FATLQDEAEK	VDAALHTMLL
330	340	350	360	370	380	390	400
KQEPQRQHLA	CLGTWVLYHN	LRIMIQYLLS	GFELELYSMH	EYYYIYWYLS	EFLYAWLMST	LSRADGSQMA	EERIMEEQQK
410	420	430	440	450	460	470	480
GRSSKKTKKK	KKVRPLSREI	TMSQAYQNMC	AGMFKTMVAF	DMDGKVRKPK	FELDSEQVRY	EHRFAPFNSV	MTPPPVHYLQ
490	500	510	520	530	540	550	560
FKEMSDLNKY	SPPPQSPELY	VAASKHFQQA	KMILENIPNP	DHEVNRILKV	AKPNFVVMKL	LAGGHKKESK	VPPEFDFSAH
570							
KYFPVVKLV							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2314	1	1023.8450	11.53	3	57.4	10.6	1	464-489	R.FAPFNSVMTPPPVHYLQFKEMSDLNK.Y	Oxidation: 8, 21

Detailed Protein Report

Protein 1578: **PREDICTED: brefeldin A-inhibited guanine nucleotide-exchange protein 3 isoform X1 [Homo sapiens]**

Accession:	gi|578812850	**Score:**	10.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	232.7
Database Date:	2015-11-30	**pI:**	5.4
		Sequence Coverage [%]:	0.6
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	0.51	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	1.89	**CV:**	0.00 %	**No. of Peptides:**	1

Detailed Protein Report

```
        10         20         30         40         50         60         70         80
MQKLLSEERF VSMETDSDEK QLLNQILNAV KVTPSLNEDL QVEVMKVLLC ITYTPTFDLN GSAVLKIAEV CIETYISSCH
        90        100        110        120        130        140        150        160
QRSINTAVRA TLSQMLSDLT LQLRQRQENT IIENPDVPQD FGNQGSTVES LCDDVVSVLT VLCEKLQAAI NDSQQLQLLY
       170        180        190        200        210        220        230        240
LECILSVLSS SSSSMHLHRR FTDLIWKNLC PALIVILGNP IHDKTITSAH TSSTSTSLES DSASPGVSDH GRGSGCSCTA
       250        260        270        280        290        300        310        320
PALSGPVART IYYIAAELVR LVGSVDSMKP VLQSLYHRVL LYPPPQHRVE AIKIMKEILG SPQRLCDLAG PSSTESESRK
       330        340        350        360        370        380        390        400
RSISKRKSHL DLLKLIMDGM TEACIKGGIE ACYAAVSCVC TLLGALDELS QGKGLSEGQV QLLLLRLEEL KDGAEWSRDS
       410        420        430        440        450        460        470        480
MEINEADFRW QRRVLSSEHT PWESGNERSL DISISVTTDT GQTTLEGELG QTTPEDHSGN HKNSLKSPAI PEGKETLSKV
       490        500        510        520        530        540        550        560
LETEAVDQPD VVQRSHTVPY PDITNFLSVD CRTRSYGSRY SESNFSVDDQ DLSRTEFDSC DQYSMAAEKD SGRSDVSDIG
       570        580        590        600        610        620        630        640
SDNCSLADEE QTPRDCLGHR SLRTAALSLK LLKNQEADQH SARLFIQSLE GLLPRLLSLS NVEEVDTALQ NFASTFCSGM
       650        660        670        680        690        700        710        720
MHSPGFDGNS SLSFQMLMNA DSLYTAAHCA LLLNLKLSHG DYYRKRPTLA PGVMKDFMKQ VQTSGVLMVF SQAWIEELYH
       730        740        750        760        770        780        790        800
QVLDRNMLGE AGYWGSPEDN SLPLITMLTD IDGLESSAIG GQLMASAATE SPFAQSRRID DSTVAGVAFA RYILVGCWKN
       810        820        830        840        850        860        870        880
LIDTLSTPLT GRMAGSSKGL AFILGAEGIK EQNQKERDAI CMSLDGLRKA ARLSCALGVA ANCASALAQM AAASCVQEEK
       890        900        910        920        930        940        950        960
EEREAQEPSD AITQVKLKVE QKLEQIGKVQ GVWLHTAHVL CMEAILSVGL EMGSHNPDCW PHVFRVCEYV GTLEHNHFSD
       970        980        990       1000       1010       1020       1030       1040
GASQPPLTIS QPQKATGSAG LLGDPECEGS PPEHSPEQGR SLSTAPVVQP LSIQDLVREG SRGRASDFRG GSLMSGSSAA
      1050       1060       1070       1080       1090       1100       1110       1120
KVVLTLSTQA DRLFEDATDK LNLMALGGFL YQLKKASQSQ LFHSVTDTVD YSLAMPGEVK STQDRKSALH LFRLGNAMLR
      1130       1140       1150       1160       1170       1180       1190       1200
IVRSKARPLL HVMRCWSLVA PHLVEAACHK ERHVSQKAVS FIHDILTEVL TDWNEPPHFH FNEALFRPFE RIMQLELCDE
      1210       1220       1230       1240       1250       1260       1270       1280
DVQDQVVTSI GELVEVCSTQ IQSGWRPLFS ALETVHGGNK SEMKEYLVGD YSMGKGQAPV FDVFEAFLNT DNIQVFANAA
      1290       1300       1310       1320       1330       1340       1350       1360
TSYIMCLMKF VKGLGEVDCK EIGDCAPAPG APSTDLCLPA LDYLRRCSQL LAKIYKMPLK PIFLSGRLAG LPRRLQEQSA
      1370       1380       1390       1400       1410       1420       1430       1440
SSEDGIESVL SDFDDDTGLI EVWIILLEQL TAAVSNCPRQ HQPPTLDLLF ELLRDVTKTP GPGFGIYAVV HLLLPVMSVW
      1450       1460       1470       1480       1490       1500       1510       1520
LRRSHKDHSY WDMASANFKH AIGLSCELVV EHIQSFLHSD IRYESMINTM LKDLFELLVA CVAKPTETIS RVGCSCIRYV
      1530       1540       1550       1560       1570       1580       1590       1600
LVTAGPVFTE EMWRLACCAL QDAFSATLKP VKDLLGCFHS GTESFSGEGC QVRVAAPSSS PSAEAEYWRI RAMAQQVFML
      1610       1620       1630       1640       1650       1660       1670       1680
DTQCSPKTPN NFDHAQSCQL IIELPPDEKP NGHTKKSVSF REIVVSLLSH QVLLQNLYDI LLEEFVKGPS PGEEKTIQVP
      1690       1700       1710       1720       1730       1740       1750       1760
EAKLAGFLRY ISMQNLAVIF DLLLDSYRTA REFDTSPGLK CLLKKVSGIG GAANLYRQSA MSFNIYFHAL VCAVLTNQET
      1770       1780       1790       1800       1810       1820       1830       1840
ITAEQVKKVL FEDDERSTDS SQQCSSEDED IFEETAQVSP PRGKEKRQWR ARMPLLSVQP VSNADWVWLV KRLHKLCMEL
      1850       1860       1870       1880       1890       1900       1910       1920
CNNYIQMHLD LENCMEEPPI FKGDPFFILP SFQSESSTPS TGGFSGKETP SEDDRSQSRE HMGESLSLKA GGGDLLLPPS
      1930       1940       1950       1960       1970       1980       1990       2000
PKVEKKDPSR KKEWWENAGN KIYTMAADKT ISKLMTEYKK RKQQHNLSAF PKEVKVEKKG EPLGPRGQDS PLLQRPQHLM
      2010       2020       2030       2040       2050       2060       2070       2080
DQGQMRHSFS AGPELLRQDK RPRSGSTGSS LSVSVRDAEA QIQAWTNMVL TVLNQIQILP DQTFTALQPA VFPCISQLTC
      2090       2100       2110
HVTDIRVRQA VREWLGRVGR VYDIIV
```

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
912	1	679.3350	-108.10	2	40.2	10.6	2	1114-1125	R.LGNAMLRIVRSK.A		Wdown:Qdown 1.89 mdown:qdown 0.51

Detailed Protein Report

Protein 1579: 39S ribosomal protein L12, mitochondrial [Homo sapiens]

Accession:	gi|27436901	**Score:**	10.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	21.3
Database Date:	2015-11-30	**pI:**	9.9
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	6.1
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	0.88	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.82	**CV:**	0.00 %	**No. of Peptides:**	1

10	20	30	40	50	60	70	80
MLPAAARPLW	GPCLGLRAAA	FRLARRQVPC	VCAVRHMRSS	GHQRCEALAG	APLDNAPKEY	PPKIQQLVQD	IASLTLLEIS
90	100	110	120	130	140	150	160
DLNELLKKTL	KIQDVGLVPM	GGVMSGAVPA	AAAQEAVEED	IPIAKERTHF	TVRLTEAKPV	DKVKLIKEIK	NYIQGINLVQ
170	180	190	200				
AKKLVESLPQ	EIKANVAKAE	AEKIKAALEA	VGGTVVLE				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1189	1	736.3734	21.42	2	43.5	10.6	1	27-38	R.QVPCVCAVRHMR.S	Carbamidomethyl: 4; Oxidation: 11	Wdown:Qdown 0.82 mdown:qdown 0.88

Detailed Protein Report

Protein 1580: kinesin-like protein KIF2B [Homo sapiens]

Accession:	gi|145275216	**Score:**	10.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	76.2
Database Date:	2015-11-30	**pI:**	9.7
		Sequence Coverage [%]:	1.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MASQFCLPES	PCLSPLKPLK	PHFGDIQEGI	YVAIQRSDKR	IHLAVVTEIN	RENYWVTVEW	VEKAVKKGKK	IDLETILLLN
90	100	110	120	130	140	150	160
PALDSAEHPM	PPPPLSPLAL	APSSAIRDQR	TATKWVAMIP	QKNQTASGDS	LDVRVPSKPC	LMKQKKSPCL	WEIQKLQEQR
170	180	190	200	210	220	230	240
EKRRRLQQEI	RARRALDVNT	RNPNYEIMHM	IEEYRRHLDS	SKISVLEPPQ	EHRICVCVRK	RPLNQRETTL	KDLDIITVPS
250	260	270	280	290	300	310	320
DNVVMVHESK	QKVDLTRYLQ	NQTFCFDHAF	DDKASNELVY	QFTAQPLVES	IFRKGMATCF	AYGQTGSGKT	YTMGGDFSGT
330	340	350	360	370	380	390	400
AQDCSKGIYA	LVAQDVFLLL	RNSTYEKLDL	KVYGTFFEIY	GGKVYDLLNW	KKKLQVLEDG	NQQIQVVGLQ	EKEVCCVEEV
410	420	430	440	450	460	470	480
LNLVEIGNSC	RTSRQTPVNA	HSSRSHAVFQ	IILKSGRIMH	GKFSLVDLAG	NERGADTTKA	SRKRQLEGAE	INKSLLALKE
490	500	510	520	530	540	550	560
CILALGQNKP	HTPFRASKLT	LVLRDSFIGQ	NSSTCMIATI	SPGMTSCENT	LNTLRYANRV	KKLNVDVRPY	HRGHYPIGHE
570	580	590	600	610	620	630	640
APRMLKSHIG	NSEMSLQRDE	FIKIPYVQSE	EQKEIEEVET	LPTLLGKDTT	ISGKGSSQWL	ENIQERAGGV	HHDIDFCIAR
650	660	670	680				
SLSILEQKID	ALTEIQKKLK	LLLADLHVKS	KVE				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
167	1	579.2618	-95.79	2	31.3	10.6	1	464-473	K.RQLEGAEINK.S	

Detailed Protein Report

Protein 1581: PREDICTED: exonuclease GOR-like [Homo sapiens]

Accession: gi|578844508
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 10.6
MW [kDa]: 73.8
pI: 10.3
Sequence Coverage [%]: 2.7
No. of unique Peptides: 1

Quantitation

mdown:qdown	**Median:**	0.94	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.74	**CV:**	0.00 %	**No. of Peptides:**	1

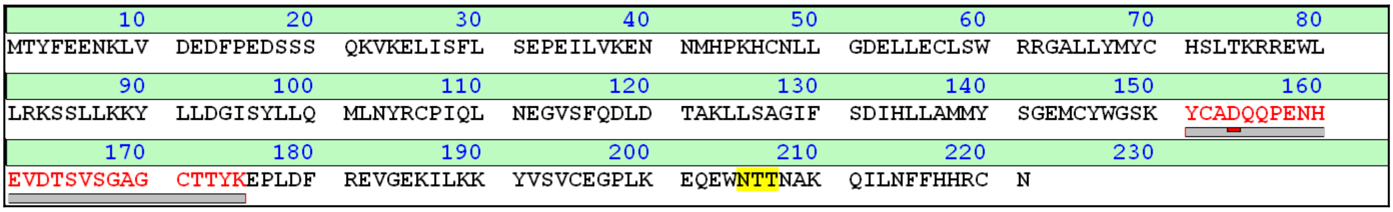
10	20	30	40	50	60	70	80
MLRATAPCWF	PPGYPEAKKV	AEEAALEASR	HLGGEQSQAG	APEGSKMLRA	TAPCWFRPGY	PEAKKVAKEA	APEASRHLGA
90	100	110	120	130	140	150	160
GQSPAGAPEG	SKMLRATAPC	WFPPGYPEAK	KVAEEAALEA	PEFPLPSHQP	AQSFGLWVPQ	MHKQASAFVD	IQAEPQNRGP
170	180	190	200	210	220	230	240
AVPPAWPKMV	TESCYFPAQR	GSACRLPAAP	RLTERPSGVR	ISAPRKRKTI	AHSSSPCLVT	GYTDAKRTRV	ASSSQRSRVS
250	260	270	280	290	300	310	320
KVGRQPGKTR	NRSGMACKTT	ATTSSKRIVR	RASLPSLSLK	KPIILRSSGC	QVPTVLRRGY	LQLFTEECLK	FCASKQEAEE
330	340	350	360	370	380	390	400
KALNEEKVAY	DCSPNKNRYL	NVVLNTLKRL	KGLTPSSMPG	LSRAALYSRL	QEFLLTQDQL	KENGYPFPHP	ERPGGAVLFT
410	420	430	440	450	460	470	480
GQGKGPGDSS	CRVCCRCGTE	YLVSSSGRCV	RDQLCYYHWG	RVRSSQVAGG	RVSQYTCCAA	APGSVGCQVA	KQHVRDGRKE
490	500	510	520	530	540	550	560
SLDGFVETFK	KELSRDAYPG	IYALDCEMCY	TTHGLELTRV	TVVDADMRVV	YDTFVKPDNE	IVDYNTRFSG	VTEADVAKTS
570	580	590	600	610	620	630	640
ITLPQVQAIL	LSFFSAQTIL	IGHSLESDLL	ALKLIHSTVV	DTAVLFPHYL	GFPYKRSLRN	LAADYLAQII	QDSQDGHNSS
650	660	670	680				
EDANACLQLV	MWKVRQRAQI	QPRHRSASPA	ALACP				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1968	1	932.3760	-123.26	2	53.1	10.6	1	352-369	K.GLTPSSMPGLSRAALYSR.L		mdown:qdown 0.94 Wdown:Qdown 0.74

Detailed Protein Report

Protein 1582: PREDICTED: UPF0600 protein C5orf51 isoform X2 [Homo sapiens]

Accession:	gi|578809912	**Score:**	10.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	25.7
Database Date:	2015-11-30	**pI:**	5.5
Modification(s):	Carbamidomethyl	**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 1583: collagen alpha-1(XIX) chain precursor [Homo sapiens]

Accession:	gi|47778921	**Score:**	10.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	115.1
Database Date:	2015-11-30	**pI:**	9.3
		Sequence Coverage [%]:	2.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MRLTGPWKLW	LWMSIFLLPA	STSVTVRDKT	EESCPILRIE	GHQLTYDNIN	KLEVSGFDLG	DSFSLRRAFC	ESDKTCFKLG
90	100	110	120	130	140	150	160
SALLIRDTIK	IFPKGLPEEY	SVAAMFRVRR	NAKKERWFLW	QVLNQQNIPQ	ISIVVDGGKK	VVEFMFQATE	GDVLNYIFRN
170	180	190	200	210	220	230	240
RELRPLFDRQ	WHKLGISIQS	QVISLYMDCN	LIARRQTDEK	DTVDFHGRTV	IATRASDGKP	VDIELHQLKI	YCSANLIAQE
250	260	270	280	290	300	310	320
TCCEISDTKC	PEQDGFGNIA	SSWVTAHASK	MSSYLPAKQE	LKDQCQCIPN	KGEAGLPGAP	GSPGQKGHKG	EPGENGLHGA
330	340	350	360	370	380	390	400
PGFPGQKGEQ	GFEGSKGETG	EKGEQGEKGD	PALAGLNGEN	GLKGDLGPHG	PPGPKGEKGD	TGPPGPPALP	GSLGIQGPQG
410	420	430	440	450	460	470	480
PPGKEGQRGR	RGKTGPPGKP	GPPGPPGPPG	IQGIHQTLGG	YYNKDNKGND	EHEAGGLKGD	KGETGLPGFP	GSVGPKGQKG
490	500	510	520	530	540	550	560
EPGEPFTKGE	KGDRGEPGVI	GSQGVKGEPG	DPGPPGLIGS	PGLKGQQGSA	GSMGPRGPPG	DVGLPGEHGI	PGKQGIKGEK
570	580	590	600	610	620	630	640
GDPGGIIGPP	GLPGPKGEAG	PPGKSLPGEP	GLDGNPGAPG	PRGPKGERGL	PGVHGSPGDI	GPQGIGIPGR	TGAQGPAGEP
650	660	670	680	690	700	710	720
GIQGPRGLPG	LPGTPGTPGN	DGVPGRDGKP	GLPGPPGDPI	ALPLLGDIGA	LLKNFCGNCQ	ASVPGLKSNK	GEEGGAGEPG
730	740	750	760	770	780	790	800
KYDSMARKGD	IGPRGPPGIP	GREGPKGSKG	ERGYPGIPGE	KGDEGLQGIP	GIPGAPGPTG	PPGLMGRTGH	PGPTGAKGEK
810	820	830	840	850	860	870	880
GSDGPPGKPG	PPGPPGIPFN	ERNGMSSLYK	IKGGVNVPSY	PGPPGPPGPK	GDPGPVGEPG	AMGLPGLEGF	PGVKGDRGPA
890	900	910	920	930	940	950	960
GPPGIAGMSG	KPGAPGPPGV	PGEPGERGPV	GDIGFPGPEG	PSGKPGINGK	DGIPGAQGIM	GKPGDRGPKG	ERGDQGIPGD
970	980	990	1000	1010	1020	1030	1040
RGSQGERGKP	GLTGMKGAIG	PMGPPGNKGS	MGSPGHQGPP	GSPGIPGIPA	DAVSFEEIKK	YINQEVLRIF	EERMAVFLSQ
1050	1060	1070	1080	1090	1100	1110	1120
LKLPAAMLAA	QAYGRPGPPG	KDGLPGPPGD	PGPQGYRGQK	GERGEPGIGL	PGSPGLPGTS	ALGLPGSPGA	PGPQGPPGPS
1130	1140	1150					
GRCNPEDCLY	PVSHAHQRTG	GN					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1829	1	1074.5529	-12.84	3	51.5	10.6	1	412-444	R.GKTGPPGKPGPPGPPGPPGIQGIHQTLGGYYNK.D	

Detailed Protein Report

Protein 1584: C-type lectin domain family 2 member L [Homo sapiens]

Accession:	gi|168229214	**Score:**	10.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	23.9
Database Date:	2015-11-30	**pI:**	7.7
		Sequence Coverage [%]:	6.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEPAREPPSR	ARPPPPLAAR	PAPAPAAPRP	RSPAEAEARG	PEGLLRRSGS	GYEGSTSWKA	ALEDTTTRLL	LGAIAVLLFA
90	100	110	120	130	140	150	160
ILVVMSILAS	KGCIKCEAPC	PEDWLLYGRK	CYFFSEEPRD	WNTGRQYCHT	HEAVLAVIQS	QKELEFMFKF	TRREPWIGLR
170	180	190	200	210	220		
RVGDEFHWVN	GDPFDPDTFT	IAGPGECVFV	EPTRLVSTEC	LMTRPWVCSK	MAYT		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2753	1	701.4057	117.54	2	62.8	10.6	1	47-59	R.RSGSGYEGSTSWK.A	

Detailed Protein Report

Protein 1585: 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 1586: PREDICTED: zinc finger protein 181 isoform X5 [Homo sapiens]

Accession:	gi|578834388	**Score:**	10.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	65.3
Database Date:	2015-11-30	**pI:**	10.0
		Sequence Coverage [%]:	3.4
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MPQVTFNDVA IDFTHEEWGW LSSAQRDLYK DVMVQNYENL VSVGLSVTKP YVITLLEDGK EPWMMEKKLS KDWESRWENK
        90        100        110        120        130        140        150        160
ELSTKKDNYD EDSPQTVIIE KVVKQSYEFS NSKKNLEYIE KLEGKHGSQV DHFRPAILTS RESPTADSVY KYNIFRSTFH
       170        180        190        200        210        220        230        240
SKSTLSEPQK ISAEGNSHKY DILKKNLPKK SVIKNEKVNG GKKLLNSNKS GAAFSQGKSL TLPQTCNREK IYTCSECGKA
       250        260        270        280        290        300        310        320
FGKQSILNRH WRIHTGEKPY ECRECGKTFS HGSSLTRHLI SHSGEKPYKC IECGKAFSHV SSLTNHQSTH TGEKPYECMN
       330        340        350        360        370        380        390        400
CGKSFSRVSH LIEHLRIHTQ EKLYECRICG KAFIHRSSLI HHQKIHTGEK PYECRECGKA FCCSSHLTRH QRIHTMEKQY
       410        420        430        440        450        460        470        480
ECNKCLKVFS SLSFLVQHQS IHTEEKPFEC QKCRKSFNQL ESLNMHLRNH IRLKPYECSI CGKAFSHRSS LLQHHRIHTG
       490        500        510        520        530        540        550        560
EKPYECIKCG KTFSCSSNLT VHQRIHTGEK PYKCNECGKA FSKGSNLTAH QRVHNGEKPN SVVSVEKPLD YMNHYTCEKS
       570
YRRETV
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1323	1	740.7826	87.27	3	45.1	10.5	2	86-104	K.KDNYDEDSPQTVIIEKVVK.Q	

Detailed Protein Report

Protein 1587: lysine-specific demethylase 5A [Homo sapiens]

Accession:	gi|110618244	**Score:**	10.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	192.0
Database Date:	2015-11-30	**pI:**	6.1
		Sequence Coverage [%]:	0.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAGVGPGGYA	AEFVPPPECP	VFEPSWEEFT	DPLSFIGRIR	PLAEKTGICK	IRPPKDWQPP	FACEVKSFRF	TPRVQRLNEL
90	100	110	120	130	140	150	160
EAMTRVRLDF	LDQLAKFWEL	QGSTLKIPVV	ERKILDLYAL	SKIVASKGGF	EMVTKEKKWS	KVGSRLGYLP	GKGTGSLLKS
170	180	190	200	210	220	230	240
HYERILYPYE	LFQSGVSLMG	VQMPNLDLKE	KVEPEVLSTD	TQTSPEPGTR	MNILPKRTRR	VKTQSESGDV	SRNTELKKLQ
250	260	270	280	290	300	310	320
IFGAGPKVVG	LAMGTKDKED	EVTRRRKVTN	RSDAFNMQMR	QRKGTLSVNF	VDLYVCMFCG	RGNNEDKLLL	CDGCDDSYHT
330	340	350	360	370	380	390	400
FCLIPPLPDV	PKGDWRCPKC	VAEECSKPRE	AFGFEQAVRE	YTLQSFGEMA	DNFKSDYFNM	PVHMVPTELV	EKEFWRLVSS
410	420	430	440	450	460	470	480
IEEDVIVEYG	ADISSKDFGS	GFPVKDGRRK	ILPEEEEYAL	SGWNLNNMPV	LEQSVLAHIN	VDISGMKVPW	LYVGMCFSSF
490	500	510	520	530	540	550	560
CWHIEDHWSY	SINYLHWGEP	KTWYGVPSHA	AEQLEEVMRE	LAPELFESQP	DLLHQLVTIM	NPNVLMEHGV	PVYRTNQCAG
570	580	590	600	610	620	630	640
EFVVTFPRAY	HSGFNQGYNF	AEAVNFCTAD	WLPIGRQCVN	HYRRLRRHCV	FSHEELIFKM	AADPECLDVG	LAAMVCKELT
650	660	670	680	690	700	710	720
LMTEEETRLR	ESVVQMGVLM	SEEEVFELVP	DDERQCSACR	TTCFLSALTC	SCNPERLVCL	YHPTDLCPCP	MQKKCLRYRY
730	740	750	760	770	780	790	800
PLEDLPSLLY	GVKVRAQSYD	TWVSRVTEAL	SANFNHKKDL	IELRVMLEDA	EDRKYPENDL	FRKLRDAVKE	AETCASVAQL
810	820	830	840	850	860	870	880
LLSKKQKHRQ	SPDSGRTRTK	LTVEELKAFV	QQLFSLPCVI	SQARQVKNLL	DDVEEFHERA	QEAMMDETPD	SSKLQMLIDM
890	900	910	920	930	940	950	960
GSSLYVELPE	LPRLKQELQQ	ARWLDEVRLT	LSDPQQVTLD	VMKKLIDSGV	GLAPHHAVEK	AMAELQELLT	VSERWEEKAK
970	980	990	1000	1010	1020	1030	1040
VCLQARPRHS	VASLESIVNE	AKNIPAFLPN	VLSLKEALQK	AREWTAKVEA	IQSGSNYAYL	EQLESLSAKG	RPIPVRLEAL
1050	1060	1070	1080	1090	1100	1110	1120
PQVESQVAAA	RAWRERTGRT	FLKKNSSHTL	LQVLSPRTDI	GVYGSGKNRR	KKVKELIEKE	KEKDLDLEPL	SDLEEGLEET
1130	1140	1150	1160	1170	1180	1190	1200
RDTAMVVAVF	KEREQKEIEA	MHSLRAANLA	KMTMVDRIEE	VKFCICRKTA	SGFMLQCELC	KDWFHNSCVP	LPKSSSQKKG
1210	1220	1230	1240	1250	1260	1270	1280
SSWQAKEVKF	LCPLCMRSRR	PRLETILSLL	VSLQKLPVRL	PEGEALQCLT	ERAMSWQDRA	RQALATDELS	SALAKLSVLS
1290	1300	1310	1320	1330	1340	1350	1360
QRMVEQAARE	KTEKIISAEL	QKAAANPDLQ	GHLPSFQQSA	FNRVVSSVSS	SPRQTMDYDD	EETDSDEDIR	ETYGYDMKDT
1370	1380	1390	1400	1410	1420	1430	1440
ASVKSSSSLE	PNLFCDEEIP	IKSEEVVTHM	WTAPSFCAEH	AYSSASKSCS	QGSSTPRKQP	RKSPLVPRSL	EPPVLELSPG
1450	1460	1470	1480	1490	1500	1510	1520
AKAQLEELMM	VGDLLEVSLD	ETQHIWRILQ	ATHPPSEDRF	LHIMEDDSME	EKPLKVKGKD	SSEKKRKRKL	EKVEQLFGEG
1530	1540	1550	1560	1570	1580	1590	1600
KQKSKELKKM	DKPRKKKLKL	GADKSKELNK	LAKKLAKEEE	RKKKKEKAAA	AKVELVKEST	EKKREKKVLD	IPSKYDWSGA
1610	1620	1630	1640	1650	1660	1670	1680
EESDDENAVC	AAQNCQRPCK	DKVDWVQCDG	GCDEWFHQVC	VGVSPEMAEN	EDYICINCAK	KQGPVSPGPA	PPPSFIMSYK
1690	1700						
LPMEDLKETS							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1038	1	530.7671	-21.17	2	41.7	10.5	2	259-266	K.EDEVTRRR.K	

Detailed Protein Report

Protein 1588: 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					

Detailed Protein Report

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 1589: 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 1590: cytochrome P450 2S1 precursor [Homo sapiens]

Accession:	gi|13449277	**Score:**	10.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	55.8
Database Date:	2015-11-30	**pI:**	9.5
		Sequence Coverage [%]:	2.6
		No. of unique Peptides:	1

Quantitation

mdown:qdown **Median:** 1.36 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MEATGTWALL	LALALLLLLT	LALSGTRARG	HLPPGPTPLP	LLGNLLQLRP	GALYSGLMRL	SKKYGPVFTI	YLGPWRPVVV
90	100	110	120	130	140	150	160
LVGQEAVREA	LGGQAEEFSG	RGTVAMLEGT	FDGHGVFFSN	GERWRQLRKF	TMLALRDLGM	GKREGEELIQ	AEARCLVETF
170	180	190	200	210	220	230	240
QGTEGRPFDP	SLLLAQATSN	VVCSLLFGLR	FSYEDKEFQA	VVRAAGGTLL	GVSSQGGQTY	EMFSWFLRPL	PGPHKQLLHH
250	260	270	280	290	300	310	320
VSTLAAFTVR	QVQQHQGNLD	ASGPARDLVD	AFLLKMAQEE	QNPGTEFTNK	NMLMTVIYLL	FAGTMTVSTT	VGYTLLLLMK
330	340	350	360	370	380	390	400
YPHVQKWVRE	ELNRELGAGQ	APSLGDRTRL	PYTDAVLHEA	QRLLALVPMG	IPRTLMRTTR	FRGYTLPQGT	EVFPLLGSIL
410	420	430	440	450	460	470	480
HDPNIFKHPE	EFNPDRFLDA	DGRFRKHEAF	LPFSLGKRVC	LGEGLAKAEL	FLFFTTILQA	FSLESPCPPD	TLSLKPTVSG
490	500	510					
LFNIPPAFQL	QVRPTDLHST	TQTR					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
263	1	424.1265	-215.05	3	32.0	10.5	0	335-347	R.ELGAGQAPSLGDR.T		mdown:qdown 1.36

Detailed Protein Report

Protein 1591: 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

Detailed Protein Report

10	20	30	40	50	60	70	80
MATLEKLMKA	FESLKSFQQQ	QQQQQQQQQQ	QQQQQQQQQQ	PPPPPPPPPP	PQLPQPPPQA	QPLLPQPQPP	PPPPPPPPGP
90	100	110	120	130	140	150	160
AVAEEPLHRP	KKELSATKKD	RVNHCLTICE	NIVAQSVRNS	PEFQKLLGIA	MELFLLCSDD	AESDVRMVAD	ECLNKVIKAL
170	180	190	200	210	220	230	240
MDSNLPRLQL	ELYKEIKKNG	APRSLRAALW	RFAELAHLVR	PQKCRPYLVN	LLPCLTRTSK	RPEESVQETL	AAAVPKIMAS
250	260	270	280	290	300	310	320
FGNFANDNEI	KVLLKAFIAN	LKSSSPTIRR	TAAGSAVSIC	QHSRRTQYFY	SWLLNVLLGL	LVPVEDEHST	LLILGVLLTL
330	340	350	360	370	380	390	400
RYLVPLLQQQ	VKDTSLKGSF	GVTRKEMEVS	PSAEQLVQVY	ELTLHHTQHQ	DHNVVTGALE	LLQQLFRTPP	PELLQTLTAV
410	420	430	440	450	460	470	480
GGIGQLTAAK	EESGGRSRSG	SIVELIAGGG	SSCSPVLSRK	QKGKVLLGEE	EALEDDSESR	SDVSSSALTA	SVKDEISGEL
490	500	510	520	530	540	550	560
AASSGVSTPG	SAGHDIITEQ	PRSQHTLQAD	SVDLASCDLT	SSATDGDEED	ILSHSSSQVS	AVPSDPAMDL	NDGTQASSPI
570	580	590	600	610	620	630	640
SDSSQTTTEG	PDSAVTPSDS	SEIVLDGTDN	QYLGLQIGQP	QDEDEEATGI	LPDEASEAFR	NSSMALQQAH	LLKNMSHCRQ
650	660	670	680	690	700	710	720
PSDSSVDKFV	LRDEATEPGD	QENKPCRIKG	DIGQSTDDDS	APLVHCVRLL	SASFLLTGGK	NVLVPDRDVR	VSVKALALSC
730	740	750	760	770	780	790	800
VGAAVALHPE	SFFSKLYKVP	LDTTEYPEEQ	YVSDILNYID	HGDPQVRGAT	AILCGTLICS	ILSRSRFHVG	DWMGTIRTLT
810	820	830	840	850	860	870	880
GNTFSLADCI	PLLRKTLKDE	SSVTCKLACT	AVRNCVMSLC	SSSYSELGLQ	LIIDVLTLRN	SSYWLVRTEL	LETLAEIDFR
890	900	910	920	930	940	950	960
LVSFLEAKAE	NLHRGAHHYT	GLLKLQERVL	NNVVIHLLGD	EDPRVRHVAA	ASLIRLVPKL	FYKCDQGQAD	PVVAVARDQS
970	980	990	1000	1010	1020	1030	1040
SVYLKLLMHE	TQPPSHFSVS	TITRIYRGYN	LLPSITDVTM	ENNLSRVIAA	VSHELITSTT	RALTFGCCEA	LCLLSTAFPV
1050	1060	1070	1080	1090	1100	1110	1120
CIWSLGWHCG	VPPLSASDES	RKSCTVGMAT	MILTLLSSAW	FPLDLSAHQD	ALILAGNLLA	ASAPKSLRSS	WASEEEANPA
1130	1140	1150	1160	1170	1180	1190	1200
ATKQEEVWPA	LGDRALVPMV	EQLFSHLLKV	INICAHVLDD	VAPGPAIKAA	LPSLTNPPSL	SPIRRKGKEK	EPGEQASVPL
1210	1220	1230	1240	1250	1260	1270	1280
SPKKGSEASA	ASRQSDTSGP	VTTSKSSSLG	SFYHLPSYLK	LHDVLKATHA	NYKVTLDLQN	STEKFGGFLR	SALDVLSQIL
1290	1300	1310	1320	1330	1340	1350	1360
ELATLQDIGK	CVEEILGYLK	SCFSREPMMA	TVCVQQLLKT	LFGTNLASQF	DGLSSNPSKS	QGRAQRLGSS	SVRPGLYHYC
1370	1380	1390	1400	1410	1420	1430	1440
FMAPYTHFTQ	ALADASLRNM	VQAEQENDTS	GWFDVLQKVS	TQLKTNLTSV	TKNRADKNAI	HNHIRLFEPL	VIKALKQYTT
1450	1460	1470	1480	1490	1500	1510	1520
TTCVQLQKQV	LDLLAQLVQL	RVNYCLLDSD	QVFIGFVLKQ	FEYIEVGQFR	ESEAIIPNIF	FFLVLLSYER	YHSKQIIGIP
1530	1540	1550	1560	1570	1580	1590	1600
KIIQLCDGIM	ASGRKAVTHA	IPALQPIVHD	LFVLRGTNKA	DAGKELETQK	EVVVSMLLRL	IQYHQVLEMF	ILVLQQCHKE
1610	1620	1630	1640	1650	1660	1670	1680
NEDKWKRLSR	QIADIILPML	AKQQMHIDSH	EALGVLNTLF	EILAPSSLRP	VDMLLRSMFV	TPNTMASVST	VQLWISGILA
1690	1700	1710	1720	1730	1740	1750	1760
ILRVLISQST	EDIVLSRIQE	LSFSPYLISC	TVINRLRDGD	STSTLEEHSE	GKQIKNLPEE	TFSRFLLQLV	GILLEDIVTK
1770	1780	1790	1800	1810	1820	1830	1840
QLKVEMSEQQ	HTFYCQELGT	LLMCLIHIFK	SGMFRRITAA	ATRLFRSDGC	GGSFYTLDSL	NLRARSMITT	HPALVLLWCQ
1850	1860	1870	1880	1890	1900	1910	1920
ILLLVNHTDY	RWWAEVQQTP	KRHSLSSTKL	LSPQMSGEEE	DSDLAAKLGM	CNREIVRRGA	LILFCDYVCQ	NLHDSEHLTW
1930	1940	1950	1960	1970	1980	1990	2000
LIVNHIQDLI	SLSHEPPVQD	FISAVHRNSA	ASGLFIQAIQ	SRCENLSTPT	MLKKTLQCLE	GIHLSQSGAV	LTLYVDRLLC
2010	2020	2030	2040	2050	2060	2070	2080
TPFRVLARMV	DILACRRVEM	LLAANLQSSM	AQLPMEELNR	IQEYLQSSGL	AQRHQRLYSL	LDRFRLSTMQ	DSLSPSPPVS
2090	2100	2110	2120	2130	2140	2150	2160
SHPLDGDGHV	SLETVSPDKD	WYVHLVKSQC	WTRSDSALLE	GAELVNRIPA	EDMNAFMMNS	EFNLSLLAPC	LSLGMSEISG
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2586	1	836.2590	-135.02	1	62.8	10.5	0	2970-2976	K.GFPCEAR.V	Carbamidomethyl: 4

Detailed Protein Report

Protein 1592: PREDICTED: zinc finger protein basonuclin-1 isoform X2 [Homo sapiens]

Accession:	gi|578827289	**Score:**	10.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	110.6
Database Date:	2015-11-30	**pI:**	6.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MCYCIGPQSR	CSNNFFKNIF	FSSKRQDFGL	TAISCTLNCS	CQSFKPGKIN	HRQCDQCKHG	WVAHALSKLR	IPPMYPTSQV
90	100	110	120	130	140	150	160
EIVQSNVVFD	ISSLMLYGTQ	AIPVRLKILL	DRLFSVLKQD	EVLQILHALD	WTLQDYIRGY	VLQDASGKVL	DHWSIMTSEE
170	180	190	200	210	220	230	240
EVATLQQFLR	FGETKSIVEL	MAIQEKEEQS	IIIPPSTANV	DIRAFIESCS	HRSSSLPTPV	DKGNPSSIHP	FENLISNMTF
250	260	270	280	290	300	310	320
MLPFQFFNPL	PPALIGSLPE	QYMLEQGHDQ	SQDPKQEVHG	PFPDSSFLTS	SSTPFQVEKD	QCLNCPDAIT	KKEDSTHLSD
330	340	350	360	370	380	390	400
SSSYNIVTKF	ERTQLSPEAK	VKPERNSLGT	KKGRVFCTAC	EKTFYDKGTL	KIHYNAVHLK	IKHKCTIEGC	NMVFSSLRSR
410	420	430	440	450	460	470	480
NRHSANPNPR	LHMPMNRNNR	DKDLRNSLNL	ASSENYKCPG	FTVTSPDCRP	PPSYPGSGED	SKGQPAFPNI	GQNGVLFPNL
490	500	510	520	530	540	550	560
KTVQPVLPFY	RSPATPAEVA	NTPGILPSLP	LLSSSIPEQL	ISNEMPFDAL	PKKKSRKSSM	PIKIEKEAVE	IANEKRHNLS
570	580	590	600	610	620	630	640
SDEDMPLQVV	SEDEQEACSP	QSHRVSEEQH	VQSGGLGKPF	PEGERPCHRE	SVIESSGAIS	QTPEQATHNS	ERETEQTPAL
650	660	670	680	690	700	710	720
IMVPREVEDG	GHEHYFTPGM	EPQVPFSDYM	ELQQRLLAGG	LFSALSNRGM	AFPCLEDSKE	LEHVGQHALA	RQIEENRFQC
730	740	750	760	770	780	790	800
DICKKTFKNA	CSVKIHHKNM	HVKEMHTCTV	EGCNATFPSR	RSRDRHSSNL	NLHQKALSQE	ALESSEDHFR	AAYLLKDVAK
810	820	830	840	850	860	870	880
EAYQDVAFTQ	QASQTSVIFK	GTSRMGSLVY	PITQVHSASL	ESYNSGPLSE	GTILDLSTTS	SMKSESSSHS	SWDSDGVSEE
890	900	910	920	930	940	950	960
GTVLMEDSDG	NCEGSSLVPG	EDEYPICVLM	EKADQSLASL	PSGLPITCHL	CQKTYSNKGT	FRAHYKTVHL	RQLHKCKVPG
970	980	990	1000				
CNTMFSSVRS	RNRHSQNPNL	HKSLASSPSH	LQ				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1802	1	990.7899	-140.63	2	51.0	10.5	1	2-17	M.CYCIGPQSRCSNNFFK.N	Carbamidomethyl: 1, 10

Detailed Protein Report

Protein 1593: POU domain, class 4, transcription factor 2 [Homo sapiens]

Accession:	gi|110347455	**Score:**	10.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	43.1
Database Date:	2015-11-30	**pI:**	10.1
Modification(s):	Oxidation	**Sequence Coverage [%]:**	4.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MMMMSLNSKQ	AFSMPHGGSL	HVEPKYSALH	STSPGSSAPI	APSASSPSSS	SNAGGGGGGG	GGGGGGGGRS	SSSSSSGSSG
90	100	110	120	130	140	150	160
GGGSEAMRRA	CLPTPPSNIF	GGLDESLLAR	AEALAAVDIV	SQSKSHHHHP	PHHSPFKPDA	TYHTMNTIPC	TSAASSSSVP
170	180	190	200	210	220	230	240
ISHPSALAGT	HHHHHHHHHH	HHQPHQALEG	ELLEHLSPGL	ALGAMAGPDG	AVVSTPAHAP	HMATMNPMHQ	AALSMAHAHG
250	260	270	280	290	300	310	320
LPSHMGCMSD	VDADPRDLEA	FAERFKQRRI	KLGVTQADVG	SALANLKIPG	VGSLSQSTIC	RFESLTLSHN	NMIALKPILQ
330	340	350	360	370	380	390	400
AWLEEAEKSH	REKLTKPELF	NGAEKKRKRT	SIAAPEKRSL	EAYFAIQPRP	SSEKIAAIAE	KLDLKKNVVR	VWFCNQRQKQ
410							
KRMKYSAGI							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1598	1	839.3261	-9.94	2	48.5	10.5	0	70-88	R.SSSSSSSGSSGGGGSEAMR.R	Oxidation: 18

Detailed Protein Report

Protein 1594: cyclic nucleotide-gated olfactory channel [Homo sapiens]

Accession: gi|42718011
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 10.5
MW [kDa]: 76.0
pI: 5.8
Sequence Coverage [%]: 2.1
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MTEKTNGVKS	SPANNHNHHA	PPAIKANGKD	DHRTSSRPHS	AADDDTSSEL	QRLADVDAPQ	QGRSGFRRIV	RLVGIIREWA
90	100	110	120	130	140	150	160
NKNFREEEPR	PDSFLERFRG	PELQTVTTQE	GDGKGDKDGE	DKGTKKKFEL	FVLDPAGDWY	YCWLFVIAMP	VLYNWCLLVA
170	180	190	200	210	220	230	240
RACFSDLQKG	YYLVWLVLDY	VSDVVYIADL	FIRLRTGFLE	QGLLVKDTKK	LRDNYIHTLQ	FKLDVASIIP	TDLIYFAVDI
250	260	270	280	290	300	310	320
HSPEVRFNRL	LHFARMFEFF	DRTETRTNYP	NIFRISNLVL	YILVIIHWNA	CIYYAISKSI	GFGVDTWVYP	NITDPEYGYL
330	340	350	360	370	380	390	400
AREYIYCLYW	STLTLTTIGE	TPPPVKDEEY	LFVIFDFLIG	VLIFATIVGN	VGSMISNMNA	TRAEFQAKID	AVKHYMQFRK
410	420	430	440	450	460	470	480
VSKGMEAKVI	RWFDYLWTNK	KTVDEREILK	NLPAKLRAEI	AINVHLSTLK	KVRIFHDCEA	GLLVELVLKL	RPQVFSPGDY
490	500	510	520	530	540	550	560
ICRKGDIGKE	MYIIKEGKLA	VVADDGVTQY	ALLSAGSCFG	EISILNIKGS	KMGNRRTANI	RSLGYSDLFC	LSKDDLMEAV
570	580	590	600	610	620	630	640
TEYPDAKKVL	EERGREILMK	EGLLDENEVA	TSMEVDVQEK	LGQLETNMET	LYTRFGRLLA	EYTGAQQKLK	QRITVLETKM
650	660	670					
KQNNEDDYLS	DGMNSPELAA	ADEP					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1498	1	798.9215	3.49	2	47.5	10.5	2	485-498	K.GDIGKEMYIIKEGK.L	Oxidation: 7

Detailed Protein Report

Protein 1595: fatty acid-binding protein 9 [Homo sapiens]

Accession:	gi|122937490	**Score:**	10.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	15.1
Database Date:	2015-11-30	**pI:**	9.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	10.6
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MVEPFLGTWK LVSSENFEDY MKELGVNFAA RNMAGLVKPT VTISVDGKMM TIRTESSFQD TKISFKLGEE FDETTADNRK
        90        100        110        120        130        140
VKSTITLENG SMIHVQKWLG KETTIKRKIV DEKMVVECKM NNIVSTRIYE KV
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
643	1	820.5020	122.11	2	36.9	10.5	1	114-127	K.MVVECKMNNIVSTR.I	Oxidation: 1

Detailed Protein Report

Protein 1596: amyloid protein-binding protein 2 isoform 2 [Homo sapiens]

Accession: gi|541862246
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 10.5
MW [kDa]: 58.5
pI: 6.6
Sequence Coverage [%]: 3.5
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MFTTRHLLHH	CFQALMDHGV	KVASVLAYSF	SRRCSYIAES	DAAVKEKAIQ	VGFVLGGFLS	DAGWYSDAEK	VFLSCLQLCT
90	100	110	120	130	140	150	160
LHDEMLHWFR	AVECCVRLLH	VRNGNCKYHL	GEETFKLAQT	YMDKLSKHGQ	QANKAALYGE	LCALLFAKSH	YDEAYKWCIE
170	180	190	200	210	220	230	240
AMKEITAGLP	VKVVVDVLRQ	ASKACVVKRE	FKKAEQLIKH	AVYLARDHFG	SKHPKYSDTL	LDYGFYLLNV	DNICQSVAIY
250	260	270	280	290	300	310	320
QAALDIRQSV	FGGKNIHVAT	AHEDLAYSSY	VHQYSSGKFD	NALFHAERAI	GIITHILPED	HLLLASSKRV	KALILEEIAI
330	340	350	360	370	380	390	400
DCHNKETEQR	LLQEAHDLHL	SSLQLAKKAF	GEFNVQTAKH	YGNLGRLYQS	MRKFKEAEEM	HIKAIQIKEQ	LLGQEDYEVA
410	420	430	440	450	460	470	480
LSVGHLASLY	NYDMNQYENA	EKLYLRSIAI	GKKLFGEGYS	GLEYDYRGLI	KLYNSIGNYE	KVFEYHNVLS	NWNRLRDRQY
490	500	510	520				
SVTDALEDVS	TSPQSTEEVV	QSFLISQNVE	GPSC				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1368	1	1022.5418	-38.43	2	45.9	10.5	1	331-348	R.LLQEAHDLHLSSLQLAKK.A	

Detailed Protein Report

Protein 1597: kinesin-like protein KIF18A [Homo sapiens]

Accession:	gi|148612831	**Score:**	10.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	102.2
Database Date:	2015-11-30	**pI:**	9.9
		Sequence Coverage [%]:	1.9
		No. of unique Peptides:	1

```
         10         20         30         40         50         60         70         80
MSVTEEDLCH HMKVVVRVRP ENTKEKAAGF HKVVHVVDKH ILVFDPKQEE VSFFHGKKTT NQNVIKKQNK DLKFVFDAVF
         90        100        110        120        130        140        150        160
DETSTQSEVF EHTTKPILRS FLNGYNCTVL AYGATGAGKT HTMLGSADEP GVMYLTMLHL YKCMDEIKEE KICSTAVSYL
        170        180        190        200        210        220        230        240
EVYNEQIRDL LVNSGPLAVR EDTQKGVVVH GLTLHQPKSS EEILHLLDNG NKNRTQHPTD MNATSSRSHA VFQIYLRQQD
        250        260        270        280        290        300        310        320
KTASINQNVR IAKMSLIDLA GSERASTSGA KGTRFVEGTN INRSLLALGN VINALADSKR KNQHIPYRNS KLTRLLKDSL
        330        340        350        360        370        380        390        400
GGNCQTIMIA AVSPSSVFYD DTYNTLKYAN RAKDIKSSLK SNVLNVNNHI TQYVKICNEQ KAEILLLKEK LKAYEEQKAF
        410        420        430        440        450        460        470        480
TNENDQAKLM ISNPQEKEIE RFQEILNCLF QNREEIRQEY LKLEMLLKEN ELKSFYQQQC HKQIEMMCSE DKVEKATGKR
        490        500        510        520        530        540        550        560
DHRLAMLKTR RSYLEKRREE ELKQFDENTN WLHRVEKEMG LLSQNGHIPK ELKKDLHCHH LHLQNKDLKA QIRHMMDLAC
        570        580        590        600        610        620        630        640
LQEQQHRQTE AVLNALLPTL RKQYCTLKEA GLSNAAFESD FKEIEHLVER KKVVVWADQT AEQPKQNDLP GISVLMTFPQ
        650        660        670        680        690        700        710        720
LGPVQPIPCC SSSGGTNLVK IPTEKRTRRK LMPSPLKGQH TLKSPPSQSV QLNDSLSKEL QPIVYTPEDC RKAFQNPSTV
        730        740        750        760        770        780        790        800
TLMKPSSFTT SFQAISSNIN SDNCLKMLCE VAIPHNRRKE CGQEDLDSTF TICEDIKSSK CKLPEQESLP NDNKDILQRL
        810        820        830        840        850        860        870        880
DPSSFSTKHS MPVPSMVPSY MAMTTAAKRK RKLTSSTSNS SLTADVNSGF AKRVRQDNSS EKHLQENKPT MEHKRNICKI
        890        900
NPSMVRKFGR NISKGNLR
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1967	1	618.9198	-133.11	3	53.3	10.5	1	169-185	R.DLLVNSGPLAVREDTQK.G	

Detailed Protein Report

Protein 1598: PREDICTED: kallikrein-2 isoform X2 [Homo sapiens]

Accession: gi|578834440
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl, Oxidation

Score: 10.5
MW [kDa]: 29.6
pI: 6.5
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 1599: 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	

Detailed Protein Report

Protein 1600: 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

Quantitation

mdown:qdown **Median:** 0.08 **CV:** 0.00 % **No. of 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	Ratios
386	1	587.1707	-251.58	2	34.2	10.5	0	1-12	-.MSVSVLAPAGNK.L		mdown:qdown 0.08

Detailed Protein Report

Protein 1601: PREDICTED: semaphorin-3C isoform X2 [Homo sapiens]

Accession:	gi|530385421	**Score:**	10.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	78.5
Database Date:	2015-11-30	**pI:**	9.8
		Sequence Coverage [%]:	1.2
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MDEDQDRIYV GSKDHILSLN INNISQEALS VFWPASTIKV EECKMAGKDP THGCGNFVRV IQTFNRTHLY VCGSGAFSPV
        90        100        110        120        130        140        150        160
CTYLNRGRRS EDQVFMIDSK CESGKGRCSF NPNVNTVSVM INEELFSGMY IDFMGTDAAI FRSLTKRNAV RTDQHNSKWL
       170        180        190        200        210        220        230        240
SEPMFVDAHV IPDGTDPNDA KVYFFFKEKL TDNNRSTKQI HSMIARICPN DTGGLRSLVN KWTTFLKARL VCSVTDEDGP
       250        260        270        280        290        300        310        320
ETHFDELEDV FLLETDNPRT TLVYGIFTTS SSVFKGSAVC VYHLSDIQTV FNGPFAHKEG PNHQLISYQG RIPYPRPGTC
       330        340        350        360        370        380        390        400
PGGAFTPNMR TTKEFPDDVV TFIRNHPLMY NSIYPIHKRP LIVRIGTDYK YTKIAVDRVN AADGRYHVLF LGTDRGTVQK
       410        420        430        440        450        460        470        480
VVVLPTNNSV SGELILEELE VFKNHAPITT MKISSKKQQL YVSSNEGVSQ VSLHRCHIYG TACADCCLAR DPYCAWDGHS
       490        500        510        520        530        540        550        560
CSRFYPTGKR RSRRQDVRHG NPLTQCRGFN LKAYRNAAEI VQYGVKNNTT FLECAPKSPQ ASIKWLLQKD KDRRKEVKLN
       570        580        590        600        610        620        630        640
ERIIATSQGL LIRSVQGSDQ GLYHCIATEN SFKQTIAKIN FKVLDSEMVA VVTDKWSPWT WASSVRALPF HPKDIMGAFS
       650        660        670        680        690        700
HSEMQMINQY CKDTRQQHQQ GDESQKMRGD YGKLKALINS RKSRNRRNQL PES
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1085	1	508.1558	-280.39	2	42.3	10.5	2	555-562	R.KEVKLNER.I	

Detailed Protein Report

Protein 1602: 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 1603: PREDICTED: nuclear distribution protein nudE homolog 1 isoform X9 [Homo sapiens]

Accession:	gi|578828131	**Score:**	10.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	39.7
Database Date:	2015-11-30	**pI:**	5.2
		Sequence Coverage [%]:	4.8
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578840026	refseq_human (refseq_human_20140103.fasta)	PREDICTED: nuclear distribution protein nudE homolog 1 isoform X3 [Homo sapiens]

10	20	30	40	50	60	70	80
MNTAFPVTGW	ASRKEILRHH	ATRRVISSPV	FTMEDSGKTF	SSEEEEANYW	KDLAMTYKQR	AENTQEELRE	FQEGSREYEA
90	100	110	120	130	140	150	160
ELETQLQQIE	TRNRDLLSEN	NRLRMELETI	KEKFEVQHSE	GYRQISALED	DLAQTKAIKD	QLQKYIRELE	QANDDLERAK
170	180	190	200	210	220	230	240
RATIMSLEDF	EQRLNQAIER	NAFLESELDE	KENLLESVQR	LKDEARDLRQ	ELAVQQKQEK	PRTPMPSSVE	AERTDTAVQA
250	260	270	280	290	300	310	320
TGSVPSTPIA	HRGPSSSLNT	PGSFRRGLDD	STGGTPLTPA	ARISALNIVG	DLLRKVGALE	SKLASCRNLV	YDQSPNRTGG
330	340	350	360				
PASGRSSKNR	DGGERRPSST	SVPLGDKGRE	N				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2463	1	973.4886	-46.60	2	59.1	10.5	2	2-18	M.NTAFPVTGWASRKEILR.H	

Detailed Protein Report

Protein 1604: RAD52 motif-containing protein 1 isoform 2 [Homo sapiens]

Accession:	gi|77873934	**Score:**	10.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	26.4
Database Date:	2015-11-30	**pI:**	9.8
		Sequence Coverage [%]:	3.8
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	0.90	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.46	**CV:**	0.00 %	**No. of Peptides:**	1

10	20	30	40	50	60	70	80
MAELVPFAVP	IESDKTLLVW	ELSSGPTAEA	LHHSLFTAFS	QFGLLYSVRV	FPNAAVAHPG	FYAVIKFYSA	RAAHRAQKAC
90	100	110	120	130	140	150	160
DRKQLFQKSP	VKVRLGTRHK	AVQHQALALN	SSKCQELANY	YFGFNGCSKR	IIKLQELSDL	EERENEDSMV	PLPKQSLKFF
170	180	190	200	210	220	230	240
CALEVVLPSC	DCRSPGIGLV	EEPMDKVEEG	PLSFLMKRKT	AQKLAIQKAL	SDAFQKLLIV	VLGKTVLIIL	EVLQFQ

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1615	1	500.6665	-288.74	2	48.7	10.5	1	200-208	K.TAQKLAIQK.A		Wdown:Qdown 0.46 mdown:qdown 0.90

Detailed Protein Report

Protein 1605: 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	SPVQKEKKKD	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 1606: PREDICTED: coiled-coil domain-containing protein 57 isoform X3 [Homo sapiens]

Accession:	gi|530413473	**Score:**	10.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	85.4
Database Date:	2015-11-30	**pI:**	5.5
		Sequence Coverage [%]:	2.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLPLGSEPAL	NELLLRKEEE	WRALQAHRTQ	LQEAALQDTR	SQLEEAQGKL	RCLQEDFVYN	LQVLEERDLE	LERYDAAFAQ
90	100	110	120	130	140	150	160
AREWEEARRA	EVSELKIEAA	KLRQALAREA	RKVEELQQQQ	QLAFQEHRLE	LERVHSDKNG	EIDHHREQYE	NLKWTLERKL
170	180	190	200	210	220	230	240
EELDGELALQ	RQELLLEFES	KMRKREHEFR	LQADNMSNTA	LSRELKVKLL	HKELEALKEA	GAKAAESLQR	AEATNAELER
250	260	270	280	290	300	310	320
KLQSRAGELQ	DLEAMSRARV	KDLEDKLHSV	QLTRKKEEET	FKRKHEELDR	LAREKDAVLV	AVKGAHVEQL	QELQTRVLEL
330	340	350	360	370	380	390	400
QAHCETLEAQ	LRRAEWRQAD	TAKEKDAAID	QLREDASTVK	SAWDAQIAQL	SKEMVSRDLQ	IQTLQEEEVK	LKAQVARSQQ
410	420	430	440	450	460	470	480
DIERYKQQLS	LAVERERSLE	RDQVQLGLDW	QRRCDDIERD	QIQKSEALIQ	GLSMAKSQVA	AKLQETEQAL	QEQEVVLKAV
490	500	510	520	530	540	550	560
TLERDQAVQA	LRMHGLPRPG	AQMLLRQHEE	EISKDFPSSE	IQRLREQNTS	LRNAIAQMRK	EMEALSHQIP	PPIQTAAEST
570	580	590	600	610	620	630	640
DANQPDPEAG	GDAATPDYVL	ALEAEIRTLK	HKFKTLEKHL	EDVLDPLKMS	SPHAESQPSV	RTSTETTGGS	AQAGQAGGSV
650	660	670	680	690	700	710	720
QAGQAGGSVQ	AGPVSSGLAL	RKLGDRVQLL	NLLVTRLRQK	VLREPLEPAA	LQRELPREVD	QVHLEVLELR	KQVAELGKHL
730	740	750	760				
RIAQHGGAEP	SGRKQPPASD	AVALGREVGA	R				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1662	1	857.6109	168.48	2	49.3	10.5	2	719-734	K.HLRIAQHGGAEPSGRK.Q	

Detailed Protein Report

Protein 1607: **PREDICTED: caspase recruitment domain-containing protein 8 isoform X17 [Homo sapiens]**

Accession:	gi|578834172	**Score:**	10.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	39.4
Database Date:	2015-11-30	**pI:**	4.4
		Sequence Coverage [%]:	5.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEKKECPEKS	SSSEEELPRR	DSGSSRNIDA	SKLIRLQGSR	KLLVDNSIRE	LQYTKTGIFF	QAEACVTNDT	VYRELPCVSE
90	100	110	120	130	140	150	160
TLCDISHFFQ	EDDETEAEPL	LFRAVPECQL	SGGDIPSVSE	EQESSEGQDS	GDICSEENQI	VSSYASKVCF	EIEEDYKNRQ
170	180	190	200	210	220	230	240
FLGPEGNVDV	ELIDKSTNRY	SVWFPTAGWY	LWSATGLGFL	VRDEVTVTIA	FGSWSQHLAL	DLQHHEQWLV	GGPLFDVTAE
250	260	270	280	290	300	310	320
PEEAVAEIHL	PHFISLQAGE	VDVSWFLVAH	FKNEGMVLEH	PARVEPFYAV	LESPSFSLMG	ILLRIASGTR	LSIPITSNTL
330	340	350	360				
IYYHPHPEDI	KFHLYLVPSD	ALLTKWISSL					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1515	1	735.1472	95.61	3	47.7	10.5	1	332-350	K.FHLYLVPSDALLTKWISSL.-	

Detailed Protein Report

Protein 1608: PREDICTED: spectrin beta chain, non-erythrocytic 4 isoform X1 [Homo sapiens]

Accession:	gi|578834710	**Score:**	10.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	270.1
Database Date:	2015-11-30	**pI:**	5.4
		Sequence Coverage [%]:	0.4
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	0.80	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.94	**CV:**	0.00 %	**No. of 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	Ratios
1005	2	530.6211	-272.57	2	41.3	10.5	2	2383-2392	R.EGGDRRASGR.R		Wdown:Qdown 0.94 mdown:qdown 0.80

Detailed Protein Report

Protein 1609: protein Wnt-2b isoform WNT-2B2 [Homo sapiens]

Accession:	gi|13518021	**Score:**	10.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	43.7
Database Date:	2015-11-30	**pI:**	11.0
Modification(s):	Oxidation	**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 1610: 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 1611: PREDICTED: probable E3 ubiquitin-protein ligase HERC4 isoform X2 [Homo sapiens]

Accession:	gi|578819226	**Score:**	10.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	104.8
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
MLCWGNASFG	QLGLGGIDEE	IVLEPRKSDF	FINKRVRDVG	CGLRHTVFVL	DDGTVYTCGC	NDLGQLGHEK	SRKKPEQVVA
90	100	110	120	130	140	150	160
LDAQNIVAVS	CGEAHTLALN	DKGQVYAWGL	DSDGQLGLVG	SEECIRVPRN	IKSLSDIQIV	QVACGYYHSL	ALSKASEVFC
170	180	190	200	210	220	230	240
WGQNKYGQLG	LGTDCKKQTS	PQLLKSLLGI	PFMQVAAGGA	HSFVLTLSGA	IFGWGRNKFG	QLGLNDENDR	YVPNLLKSLR
250	260	270	280	290	300	310	320
SQKIVYICCG	EDHTAALTKE	GGVFTFGAGG	YGQLGHNSTS	HEINPRKVFE	LMGSIVTEIA	CGRQHTSAFV	PSSGRIYSFG
330	340	350	360	370	380	390	400
LGGNGQLGTG	STSNRKSPFT	VKGNWYPYNG	QCLPDIDSEE	YFCVKRIFSG	GDQSFSHYSS	PQNCGPPDDF	RCPNPTKQIW
410	420	430	440	450	460	470	480
TVNEALIQKW	LSYPSGRFPV	EIANEIDGTF	SSSGCLNGSF	LAVSNDDHYR	TGTRFSGVDM	NAARLLFHKL	IQPDHPQISQ
490	500	510	520	530	540	550	560
QVNEKMGQII	QYDKFYIHEV	QELIDIRNDY	INWVQQQAYG	MDVNHGLTEL	ADIPVTICTY	PFVFDAQAKT	TLLQTDAVLQ
570	580	590	600	610	620	630	640
MQMAIDQAHR	QNVSSLFLPV	IESVNPCLIL	VVRRENIVGD	AMEVLRKTKN	IDYKKPLKVI	FVGEDAVDAG	GVRKEFFLLI
650	660	670	680	690	700	710	720
MRELLDPKYG	MFRYYEDSRL	IWFSDKTFED	SDLFHLIGVI	CGLAIYNCTI	VDLHFPLALY	KKLLKKKPSL	DDLKELMPDV
730	740	750	760	770	780	790	800
GRSMQQLLDY	PEDDIEETFC	LNFTITVENF	GATEVKELVL	NGADTAVNKQ	NRQEFVDAYV	DYIFNKSVAS	LFDAFHAGFH
810	820	830	840	850	860	870	880
KVCGGKVLLL	FQPNELQAMV	IGNTNYDWKE	LEKNTEYKGE	YWAEHPTIKI	FWEVFHELPL	EKKKQFLLFL	TGSDRIPILG
890	900	910	920	930	940		
MKSLKLVIQS	TGGGEEYLPV	SHTCFNLLDL	PKYTEKETLR	SKLIQAIDHN	EGFSLI		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
605	1	625.2922	-61.03	3	36.4	10.4	0	470-485	K.LIQPDHPQISQQVNEK.M	

Detailed Protein Report

Protein 1612: 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 1613: spermatogenesis-associated protein 2 [Homo sapiens]

Accession:	gi|5174487	**Score:**	10.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	58.4
Database Date:	2015-11-30	**pI:**	9.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.7
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578836253	refseq_human (refseq_human_20140103.fasta)	PREDICTED: spermatogenesis-associated protein 2 isoform X1 [Homo sapiens]
gi|209413749	refseq_human (refseq_human_20140103.fasta)	spermatogenesis-associated protein 2 [Homo sapiens]

10	20	30	40	50	60	70	80
MGKPSSMDTK	FKDDLFRKYV	QFHESKVDTT	TSRQRPGSDE	CLRVAASTLL	SLHKVDPFYR	FRLIQFYEVV	ESSLRSLSSS
90	100	110	120	130	140	150	160
SLRALHGAFS	MLETVGINLF	LYPWKKEFRS	IKTYTGPFVY	YVKSTLLEED	IRAILSCMGY	TPELGTAYKL	RELVETLQVK
170	180	190	200	210	220	230	240
MVSFELFLAK	VECEQMLEIH	SQVKDKGYSE	LDIVSERKSS	AEDVRGCSDA	LRRRAEGREH	LTASMSRVAL	QKSASERAAK
250	260	270	280	290	300	310	320
DYYKPRVTKP	SRSVDAYDSY	WESRKPPLKA	SLSLRKEPVA	TDVGDDLKDE	IIRPSPSLLT	MASSPHGSPD	VLPPASPSNG
330	340	350	360	370	380	390	400
PALLRGTYFS	TQDDVDLYTD	SEPRATYRRQ	DALRPDVWLL	RNDAHSLYHK	RSPPAKESAL	SKCQSCGLSC	SSSLCQRCDS
410	420	430	440	450	460	470	480
LLTCPPASKP	SAFPSKASTH	DSLAHGASLR	EKYPGQTQGL	DRLPHLHSKS	KPSTTPTSRC	GFCNRPGATN	TCTQCSKVSC
490	500	510	520	530			
DACLSAYHYD	PCYKKSELHK	FMPNNQLNYK	STQLSHLVYR				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1652	1	865.4599	50.67	2	49.4	10.4	0	171-184	K.VECEQMLEIHSQVK.D	Carbamidomethyl: 3

Detailed Protein Report

Protein 1614: T-box transcription factor TBX4 [Homo sapiens]

Accession:	gi|18129690	**Score:**	10.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	60.2
Database Date:	2015-11-30	**pI:**	7.9
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLQDKGLSES	EEAFRAPGPA	LGEASAANAP	EPALAAPGLS	GAALGSPPGP	GADVVAAAAA	EQTIENIKVG	LHEKELWKKF
90	100	110	120	130	140	150	160
HEAGTEMIIT	KAGRRMFPSY	KVKVTGMNPK	TKYILLIDIV	PADDHRYKFC	DNKWMVAGKA	EPAMPGRLYV	HPDSPATGAH
170	180	190	200	210	220	230	240
WMRQLVSFQK	LKLTNNHLDP	FGHIILNSMH	KYQPRLHIVK	ADENNAFGSK	NTAFCTHVFP	ETSFISVTSY	QNHKITQLKI
250	260	270	280	290	300	310	320
ENNPFAKGFR	GSDDSDLRVA	RLQSKEYPVI	SKSIMRQRLI	SPQLSATPDV	GPLLGTHQAL	QHYQHENGAH	SQLAEPQDLP
330	340	350	360	370	380	390	400
LSTFPTQRDS	SLFYHCLKRR	DGTRHLDLPC	KRSYLEAPSS	VGEDHYFRSP	PPYDQQMLSP	SYCSEVTPRE	ACMYSGSGPE
410	420	430	440	450	460	470	480
IAGVSGVDDL	PPPPLSCNMW	TSVSPYTSYS	VQTMETVPYQ	PFPTHFTATT	MMPRLPTLSA	QSSQPPGNAH	FSVYNQLSQS
490	500	510	520	530	540	550	
QVRERGPSAS	FPRERGLPQG	CERKPPSPHL	NAANEFLYSQ	TFSLSRESSL	QYHSGMGTVE	NWTDG	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1587	1	902.9302	-46.68	2	48.3	10.4	2	79-94	K.KFHEAGTEMIITKAGR.R	Oxidation: 9

Detailed Protein Report

Protein 1615: mastermind-like protein 2 [Homo sapiens]

Accession:	gi|33286444	**Score:**	10.4
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
1853	1	1057.5056	-4.32	2	51.8	10.4	2	44-60	R.IAVCRQHHLSCEGRYER.G	Carbamidomethyl: 11

Detailed Protein Report

Protein 1616: long-chain-fatty-acid--CoA ligase ACSBG2 isoform c [Homo sapiens]

Accession:	gi|574584663	**Score:**	10.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	53.5
Database Date:	2015-11-30	**pI:**	9.3
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MKKNNNLYSW	DDFMELGRSI	PDTQLEQVIE	SQKANQCAVL	IYTSGTTGIP	KGVMLSHDNI	TWIAGAVTKD	FKLTDKHETV
90	100	110	120	130	140	150	160
VSYLPLSHIA	AQMMDIWVPI	KIGALTYFAQ	ADALKGTLVS	TLKEVKPTVF	IGVPQIWEKI	HEMVKKNSAK	SMGLKKKAFV
170	180	190	200	210	220	230	240
WARNIGFKVN	SKKMLGKYNT	PVSYRMAKTL	VFSKVKTSLG	LDHCHSFISG	TAPLNQETAE	FFLSLDIPIG	ELYGLSESSG
250	260	270	280	290	300	310	320
PHTISNQNNY	RLLSCGKILT	GCKNMLFQQN	KDGIGEICLW	GRHIFMGYLE	SETETTEAID	DEGWLHSGDL	GQLDGLGFLY
330	340	350	360	370	380	390	400
VTGHIKEILI	TAGGENVPPI	PVETLVKKKI	PIISNAMLVG	DKLKFLSMLL	TLKCEMNQMS	GEPLDKLNFE	AINFCRGLGS
410	420	430	440	450	460	470	480
QASTVTEIVK	QQDPLVYKAI	QQGINAVNQE	AMNNAQRIEK	WVILEKDFSI	YGGELGPMMK	LKRHFVAQKY	KKQIDHMYH

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2122	1	757.2736	-37.46	2	55.1	10.4	0	374-386	K.CEMNQMSGEPLDK.L	Oxidation: 3, 6

Detailed Protein Report

Protein 1617: sulfiredoxin-1 [Homo sapiens]

Accession:	gi|22129778	**Score:**	10.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	14.3
Database Date:	2015-11-30	**pI:**	9.1
		Sequence Coverage [%]:	4.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGLRAGGTLG	RAGAGRGAPE	GPGPSGGAQG	GSIHSGRIAA	VHNVPLSVLI	RPLPSVLDPA	KVQSLVDTIR	EDPDSVPPID
90	**100**	**110**	**120**	**130**	**140**		
VLWIKGAQGG	DYFYSFGGCH	RYAAYQQLQR	ETIPAKLVQS	TLSDLRVYLG	ASTPDLQ		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
486	1	658.1368	-364.79	1	35.0	10.4	0	111-116	R.ETIPAK.L	

Detailed Protein Report

Protein 1618: segment polarity protein dishevelled homolog DVL-3 [Homo sapiens]

Accession:	gi|41406097	**Score:**	10.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	78.0
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
MGETKIIYHL	DGQETPYLVK	LPLPAERVTL	ADFKGVLQRP	SYKFFFKSMD	DDFGVVKEEI	SDDNAKLPCF	NGRVVSWLVS
90	100	110	120	130	140	150	160
AEGSHPDPAP	FCADNPSELP	PPMERTGGIG	DSRPPSFHPH	AGGGSQENLD	NDTETDSLVS	AQRERPRRRD	GPEHATRLNG
170	180	190	200	210	220	230	240
TAKGERRREP	GGYDSSSTLM	SSELETTSFF	DSDEDDSTSR	FSSSTEQSSA	SRLMRRHKRR	RRKQKVSRIE	RSSSFSSITD
250	260	270	280	290	300	310	320
STMSLNIITV	TLNMEKYNFL	GISIVGQSNE	RGDGGIYIGS	IMKGGAVAAD	GRIEPGDMLL	QVNEINFENM	SNDDAVRVLR
330	340	350	360	370	380	390	400
EIVHKPGPIT	LTVAKCWDPS	PRGCFTLPRS	EPIRPIDPAA	WVSHTAAMTG	TFPAYGMSPS	LSTITSTSSS	ITSSIPDTER
410	420	430	440	450	460	470	480
LDDFHLSIHS	DMAAIVKAMA	SPESGLEVRD	RMWLKITIPN	AFIGSDVVDW	LYHNVEGFTD	RREARKYASN	LLKAGFIRHT
490	500	510	520	530	540	550	560
VNKITFSEQC	YYIFGDLCGN	MANLSLHDHD	GSSGASDQDT	LAPLPHPGAA	PWPMAFPYQY	PPPPHPYNPH	PGFPELGYSY
570	580	590	600	610	620	630	640
GGGSASSQHS	EGSRSSGSNR	SGSDRRKEKD	PKAGDSKSGG	SGSESDHTTR	SSLRGPRERA	PSERSGPAAS	EHSHRSHHSL
650	660	670	680	690	700	710	720
ASSLRSHHTH	PSYGPPGVPP	LYGPPMLMMP	PPPAAMGPPG	APPGRDLASV	PPELTASRQS	FRMAMGNPSE	FFVDVM

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2710	1	937.4704	-22.97	2	62.8	10.4	1	686-702	R.DLASVPPELTASRQSFR.M	

BRUKER

Detailed Protein Report

Protein 1619: protein FAM214B [Homo sapiens]

Accession:	gi|33636717	**Score:**	10.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	56.7
Database Date:	2015-11-30	**pI:**	10.0
		Sequence Coverage [%]:	2.8
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578816745	refseq_human (refseq_human_20140103.fasta)	PREDICTED: protein FAM214B isoform X12 [Homo sapiens]
gi|530390168	refseq_human (refseq_human_20140103.fasta)	PREDICTED: protein FAM214B isoform X4 [Homo sapiens]
gi|530390166	refseq_human (refseq_human_20140103.fasta)	PREDICTED: protein FAM214B isoform X3 [Homo sapiens]
gi|530390164	refseq_human (refseq_human_20140103.fasta)	PREDICTED: protein FAM214B isoform X2 [Homo sapiens]
gi|530390162	refseq_human (refseq_human_20140103.fasta)	PREDICTED: protein FAM214B isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MRHVQAEPSP	SSEPEAGPSQ	PPVRQGALQG	GLLMGYSPAG	GATSPGVYQV	SIFSPPAGTS	EPHRALKRQA	PSTEGPRELK
90	100	110	120	130	140	150	160
RGPGLGAREG	LPPEEPSTVG	LLGPEGPGLG	LGVASQHFSH	RGLCVVEQRS	SVTSSWTSGA	WSPPCPPSNA	SCNTLHTRDW
170	180	190	200	210	220	230	240
ASPDPGGQGS	LGESPGPAPP	GQLHTLDTDL	HSLAQIGGKS	PVAGVGNGGS	LWPRESPGTA	NGHSPEHTPP	GPGPPGPCPT
250	260	270	280	290	300	310	320
KRRLLPAGEA	PDVSSEEEGP	APRRRRGSLG	HPTAANSSDA	KATPFWSHLL	PGPKEPVLDP	TDCGPMGRRL	KGARRLKLSP
330	340	350	360	370	380	390	400
LRSLRKGPGL	LSPPSASPVP	TPAVSRTLLG	NFEESLLRGR	FAPSGHIEGF	TAEIGASGSY	CPQHVTLPVT	VTFFDVSEQN
410	420	430	440	450	460	470	480
APAPFLGIVD	LNPLGRKGYS	VPKVGTVQVT	LFNPNQTVVK	MFLVTFDFSD	MPAAHMTFLR	HRLFLVPVGE	EGNANPTHRL
490	500	510	520	530	540		
LCYLLHLRFR	SSRSGRLSLH	GDIRLLFSRR	SLELDTGLPY	ELQAVTEAPH	NPRYSPLP		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1734	1	727.3981	23.60	2	50.2	10.4	0	200-214	K.SPVAGVGNGGSLWPR.E	

Detailed Protein Report

Protein 1620: 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 1621: 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

Quantitation

mdown:qdown	**Median:**	0.64	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	9.17	**CV:**	0.00 %	**No. of 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	Ratios
390	1	704.6907	-199.27	2	34.2	10.4	0	336-350	K.DGNGTTSGIGSSVEK.Y		mdown:qdown 0.64 Wdown:Qdown 9.17

Detailed Protein Report

Protein 1622: PREDICTED: zinc finger protein 558 isoform X2 [Homo sapiens]

Accession:	gi|530414534	**Score:**	10.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	37.9
Database Date:	2015-11-30	**pI:**	10.5
		Sequence Coverage [%]:	4.5
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MLENCRNLAS LGCRVNKPSL ISQLEQDKKV VTEERGILPS TCPDLETLLK AKWLTPKKNV FRKEQSKGVK TERSHRGVKL
        90        100        110        120        130        140        150        160
NECNQCFKVF STKSNLTQHK RIHTGEKPYD CSQCGKSFSS RSYLTIHKRI HNGEKPYECN HCGKAFSDPS SLRLHLRIHT
       170        180        190        200        210        220        230        240
GEKPYECNQC FHVFRTSCNL KSHKRIHTGE NHHECNQCGK AFSTRSSLTG HNSIHTGEKP YECHDCGKTF RKSSYLTQHV
       250        260        270        280        290        300        310        320
RTHTGEKPYE CNECGKSFSS SFSLTVHKRI HTGEKPYECS DCGKAFNNLS AVKKHLRTHT GEKPYECNHC GKSFTSNSYL
       330        340
SVHKRIHNRW I
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2266	1	863.8501	-160.21	2	56.8	10.4	1	15-29	R.VNKPSLISQLEQDKK.V	

Detailed Protein Report

Protein 1623: dickkopf-related protein 2 precursor [Homo sapiens]

Accession:	gi|7657023	**Score:**	10.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	28.4
Database Date:	2015-11-30	**pI:**	10.9
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	4.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAALMRSKDS	SCCLLLLAAV	LMVESSQIGS	SRAKLNSIKS	SLGGETPGQA	ANRSAGMYQG	LAFGGSKKGK	NLGQAYPCSS
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
DKECEVGRYC	HSPHQGSSAC	MVCRRKKKRC	HRDGMCCPST	RCNNGICIPV	TESILTPHIP	ALDGTRHRDR	NHGHYSNHDL
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
GWQNLGRPHT	KMSHIKGHEG	DPCLRSSDCI	EGFCCARHFW	TKICKPVLHQ	GEVCTKQRKK	GSHGLEIFQR	CDCAKGLSCK
250	**260**						
VWKDATYSSK	ARLHVCQKI						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2021	1	719.7845	12.19	2	53.9	10.4	1	110-121	R.CHRDGMCCPSTR.C	Carbamidomethyl: 7; Oxidation: 6

Detailed Protein Report

Protein 1624: PREDICTED: sodium/hydrogen exchanger 7 isoform X6 [Homo sapiens]

Accession:	gi|578838129	**Score:**	10.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	77.7
Database Date:	2015-11-30	**pI:**	6.3
		Sequence Coverage [%]:	2.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEPGDAARPG	SGRATGAPPP	RLLLLPLLLG	WGLRVAAAAS	ASSSGAAAED	SSAMEELATE	KEAEESHRQD	SVSLLTFILL
90	100	110	120	130	140	150	160
LTLTILTIWL	FKHRRVRFLH	ETGLAMIYGL	IVGVILRYGT	PATSGRDKSL	SCTQEDRAFS	TLLVNVSGKF	FEYTLKGEIS
170	180	190	200	210	220	230	240
PGKINSVEQN	DMLRKVTFDP	EVFFNILLPP	IIFHAGYSLK	KRHFFRNLGS	ILAYAFLGTA	VSCFIIGNLM	YGVVKLMKIM
250	260	270	280	290	300	310	320
GQLSDKFYYT	DCLFFGAIIS	ATDPVTVLAI	FNELHADVDL	YALLFGESVL	NDAVAIVLSS	SIVAYQPAGL	NTHAFDAAAF
330	340	350	360	370	380	390	400
FKSVGIFLGI	FSGSFTMGAV	TGVVTALVTK	FTKLHCFPLL	ETALFFLMSW	STFLLAEACG	FTGVVAVLFC	GITQAHYTYN
410	420	430	440	450	460	470	480
NLSVESRSRT	KQLFEVLHFL	AENFIFSYMG	LALFTFQKHV	FSPIFIIGAF	VAIFLGRAAH	IYPLSFFLNL	GRRHKIGWNF
490	500	510	520	530	540	550	560
QHMMMFSGLR	GAMAFALAIR	DTASYARQMM	FTTTLLIVFF	TVWIIGGGTT	PMLSWLNIRV	GVDPDQDPPP	NNDSFQVLQG
570	580	590	600	610	620	630	640
DGPDSARGNR	TKQESAWIFR	LWYSFDHNYL	KPILTHSGPP	LTTTLPAWCG	LLARCLTSPQ	VYDNQEPLRE	EDSDFILTEG
650	660	670	680	690	700	710	
DLTLTYGDST	VTANGSSSSH	TASTSLEGSR	RTKSSSEEVL	ERDLGMGDQK	VSSRGTRLVF	PLEDNA	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
919	1	937.9706	-55.89	2	40.3	10.4	1	458-473	R.AAHIYPLSFFLNLGRR.H	

Detailed Protein Report

Protein 1625: TCR gamma alternate reading frame protein isoform 2 [Homo sapiens]

Accession:	gi|51702238	**Score:**	10.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	12.8
Database Date:	2015-11-30	**pI:**	9.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	12.6
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	1.32	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	1.09	**CV:**	0.00 %	**No. of Peptides:**	1

Alias proteins:

Accession	**Name**	**Description**
gi|578813513	refseq_human (refseq_human_20140103.fasta)	PREDICTED: TCR gamma alternate reading frame protein isoform X1 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MKTNDTYMKF SWLTVPEKSL DKEHRCIVRH ENNKNGVDQE IIFPPIKTDV ITMDPKDNCS KDANDTLLLQ LTNTSAYYMY
        90        100        110        120
LLLLLKSVVY FAIITCCLLR RTAFCCNGEK S
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
71	1	857.9091	-53.04	2	30.1	10.4	0	87-100	K.SVVYFAIITCCLLR.R	Carbamidomethyl: 10, 11	Wdown:Qdown 1.09 mdown:qdown 1.32

Detailed Protein Report

Protein 1626: PREDICTED: zinc finger CCHC domain-containing protein 9-like [Homo sapiens]

Accession:	gi|530410856	**Score:**	10.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	21.5
Database Date:	2015-11-30	**pI:**	9.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	6.2
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MRLALSFGSF TPHPPISFTT CRPPLSTQPF LQEDSQWEVR RFKRQGAKKN AMVCFHCRKP GRGIADCPAA LENQDMGTRR
        90        100        110        120        130        140        150        160
CYKCGSTDHE ITKCKAKVDP PLGECPFAEC FVCGEMGHLS RSCPDNPKGL YADGSGCQLH GSVEHLKKDC PESENSDRMA
       170        180        190        200
TVGLWAKGIS ADYEDIVDAP KPQKPKTKIP KGVNF
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
492	1	689.6601	-214.61	2	35.1	10.4	1	84-95	K.CGSTDHEITKCK.A	Carbamidomethyl: 1

Detailed Protein Report

Protein 1627: PREDICTED: uncharacterized protein C9orf173 isoform X2 [Homo sapiens]

Accession:	gi|578817480	**Score:**	10.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	38.0
Database Date:	2015-11-30	**pI:**	12.0
		Sequence Coverage [%]:	3.4
		No. of unique Peptides:	1

Quantitation

mdown:qdown **Median:** 0.46 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MMNSDQKAVK	FLANFYINGG	KHWTHGHLRQ	TQPEPTQPKA	SVLLLGPEPG	MAWDETQPPK	MKEIPVGLRL	QTGTPQESLP
90	100	110	120	130	140	150	160
TYTQTLRELS	PPGTRCRARP	YESPPHTPTT	ASAASTRAER	AVAAGHGRLC	GSRAKAPSRR	KLTSTKSKSF	RGCHSASKTP
170	180	190	200	210	220	230	240
EGHTHLGLPG	ARGLGLRVQP	QSLLQASLQA	PGKRCPGPNT	YNILPGSRLQ	SPRSPAFSMS	RSPAFTSWLS	TSFSFGSPNP
250	260	270	280	290	300	310	320
WPSRLPRGGL	QLTLPFGAWR	GHPGCTQTQA	PRHRPLLHAL	EPAGHNLLGP	ATEWNHGLPR	GFPRPPLGLG	APAWPSDPLG
330	340	350	360				
TPMHPSGWPT	LLWAVDKAGP	AWIPHLPISP	LH				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
815	1	647.8146	-7.85	2	39.0	10.4	2	147-158	K.SKSFRGCHSASK.T		mdown:qdown 0.46

Detailed Protein Report

Protein 1628: upstream stimulatory factor 1 isoform 2 [Homo sapiens]

Accession:	gi|46877102	**Score:**	10.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	27.4
Database Date:	2015-11-30	**pI:**	5.9
		Sequence Coverage [%]:	4.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MYRVIQVSEG	QLDGQTEGTG	AISGYPATQS	MTQAVIQGAF	TSDDAVDTEG	TAAETHYTYF	PSTAVGDGAG	GTTSGSTAAV
90	100	110	120	130	140	150	160
VTTQGSEALL	GQATPPGTGQ	FFVMMSPQEV	LQGGSQRSIA	PRTHPYSPKS	EAPRTTRDEK	RRAQHNEVER	RRRDKINNWI
170	180	190	200	210	220	230	240
VQLSKIIPDC	SMESTKSGQS	KGGILSKACD	YIQELRQSNH	RLSEELQGLD	QLQLDNDVLR	QQVEDLKNKN	LLLRAQLRHH
250	260						
GLEVVIKNDS	N						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
829	1	647.8199	-30.73	2	39.2	10.4	2	142-151	R.RAQHNEVERR.R	

Detailed Protein Report

Protein 1629: PREDICTED: potassium channel subfamily T member 2 isoform X3 [Homo sapiens]

Accession:	gi|578800878	**Score:**	10.4
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

mdown:qdown	**Median:**	0.87	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.18	**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
2058	1	766.2651	-167.59	2	54.3	10.4	1	1-12	-.MFSRQDHQTILR.A		Wdown:Qdown 0.18 mdown:qdown 0.87

Protein 1630: PREDICTED: collagen alpha-3(IV) chain isoform X6 [Homo sapiens]

Accession:	gi|530369772	**Score:**	10.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	99.9
Database Date:	2015-11-30	**pI:**	9.9
		Sequence Coverage [%]:	2.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSARTAPRPQ	VLLLPLLLVL	LAAAPAASKG	CVCKDKGQCF	CDGAKGEKGE	KGFPGPPGSP	GQKGFTGPEG	LPGPQGPKGF
90	100	110	120	130	140	150	160
PGLPGLTGSK	GVRGISGLPG	FSGSPGLPGT	PGNTGPYGLV	GVPGCSGSKG	EQGFPGLPGT	LGYPGIPGAA	GLKGQKGAPA
170	180	190	200	210	220	230	240
KEEDIELDAK	GDPGLPGAPG	PQGLPGPPGF	PGPVGPPGPP	GFFGFPGAMG	PRGPKGHMGE	RVIGHKGERG	VKGLTGPPGP
250	260	270	280	290	300	310	320
PGTVIVTLTG	PDNRTDLKGE	KGDKGAMGEP	GPPGPSGLPG	ESYGSEKGAP	GDPGLQGKPG	KDGVPGFPGS	EGVKGNRGFP
330	340	350	360	370	380	390	400
GLMGEDGIKG	QKGDIGPPGF	RGPTEYYDTY	QEKGDEGTPG	PPGPRGARGP	QGPSGPPGVP	GSPGSSRPGL	RGAPGWPGLK
410	420	430	440	450	460	470	480
GSKGERGRPG	KDAMGTPGSP	GCAGSPGLPG	SPGPPGPPGD	IVFRKGPPGD	HGLPGYLGSP	GIPGVDGPKG	EPGLLCTQCP
490	500	510	520	530	540	550	560
YIPGPPGLPG	LPGLHGVKGI	PGRQGAAGLK	GSPGSPGNTG	LPGFPGFPGA	QGDPGLKGEK	GETLQPEGQV	GVPGDPGLRG
570	580	590	600	610	620	630	640
QPGRKGLDGI	PGTPGVKGLP	GPKGELALSG	EKGDQGPPGD	PGSPGSPGPA	GPAGPPGYGP	QGEPGLQGTQ	GVPGAPGPPG
650	660	670	680	690	700	710	720
EAGPRGELSV	STPVPGPPGP	PGPPGHPGPQ	GPPGIPGSLG	KCGDPGLPGP	DGEPGIPGIG	FPGPPGPKGD	QGFPGTKGSL
730	740	750	760	770	780	790	800
GCPGKMGEPG	LPGKPGLPGA	KGEPAVAMPG	GPGTPGFPGE	RGNSGEHGEI	GLPGLPGLPG	TPGNEGLDGP	RGDPGQPGPP
810	820	830	840	850	860	870	880
GEQGPPGRCI	EGPRGAQGLP	GLNGLKGQQG	RRGKTGPKGD	PGIPGLDRSG	FPGETGSPGI	PGHQGEMGPL	GQRGYPGNPG
890	900	910	920	930	940	950	960
ILGPPGEDGV	IGMMGFPGAI	GPPGPPGNPG	TPGQRGSPGI	PGVKGQRGTP	GAKGEQGDKG	NPGPSEISHV	IGDKGEPGLK
970	980	990	1000	1010	1020	1030	1040
GFAGNPGEKG	NRGVPGMPGL	KGLKGLPGPA	GPPGPRGDLG	STGNPGEPGL	RGIPGSMGNM	GMPGSKGKRG	TLGFPGRAGR
1050	1060						
PGLPGGSRTA	G						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1731	1	927.5221	67.52	3	50.3	10.4	1	511-540	K.GSPGSPGNTGLPGFPGFPGAQGDPGLKGEK.G	

Detailed Protein Report

Protein 1631: **disintegrin and metalloproteinase domain-containing protein 28 isoform 3 preproprotein [Homo sapiens]**

Accession: gi|54292117
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 10.4
MW [kDa]: 61.2
pI: 6.6
Sequence Coverage [%]: 1.3
No. of unique 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
1056	1	770.2315	-318.65	1	42.8	10.4	1	21-27	K.ELPGVKK.Y	

Protein 1632: rho guanine nucleotide exchange factor 18 isoform a [Homo sapiens]

Accession:	gi|41327769	**Score:**	10.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	114.0
Database Date:	2015-11-30	**pI:**	5.9
		Sequence Coverage [%]:	1.2
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|578833135	refseq_human (refseq_human_20140103.fasta)	PREDICTED: rho guanine nucleotide exchange factor 18 isoform X8 [Homo sapiens]
gi|578833133	refseq_human (refseq_human_20140103.fasta)	PREDICTED: rho guanine nucleotide exchange factor 18 isoform X7 [Homo sapiens]

10	20	30	40	50	60	70	80
MTVSQKGGPQ	PTPSPAGPGT	QLGPITGEMD	EADSAFLKFK	QTADDSLSLT	SPNTESIFVE	DPYTASLRSE	IESDGHEFEA
90	100	110	120	130	140	150	160
ESWSLAVDAA	YAKKQKREVV	KRQDVLYELM	QTEVHHVRTL	KIMLKVYSRA	LQEELQFSSK	AIGRLFPCAD	DLLETHSHFL
170	180	190	200	210	220	230	240
ARLKERRQES	LEEGSDRNYV	IQKIGDLLVQ	QFSGENGERM	KEKYGVFCSG	HNEAVSHYKL	LLQQNKKFQN	LIKKIGNFSI
250	260	270	280	290	300	310	320
VRRLGVQECI	LLVTQRITKY	PVLVERIIQN	TEAGTEDYED	LTQALNLIKD	IISQVDAKVS	ECEKGQRLRE	IAGKMDLKSS
330	340	350	360	370	380	390	400
SKLKNGLTFR	KEDMLQRQLH	LEGMLCWKTT	SGRLKDILAI	LLTDVLLLLQ	EKDQKYVFAS	VDSKPPVISL	QKLIVREVAN
410	420	430	440	450	460	470	480
EEKAMFLISA	SLQGPEMYEI	YTSSKEDRNA	WMAHIQRAVE	SCPDEEEGPF	SLPEEERKVV	EARATRLRDF	QERLSMKDQL
490	500	510	520	530	540	550	560
IAQSLLEKQQ	IYLEMAEMGG	LEDLPQPRGL	FRGGDPSETL	QGELILKSAM	SEIEGIQSLI	CRQLGSANGQ	AEDGGSSTGP
570	580	590	600	610	620	630	640
PRRAETFAGY	DCTNSPTKNG	SFKKKVSSTD	PRPRDWRGPP	NSPDLKLSDS	DIPGSSEESP	QVVEAPGTES	DPRLPTVLES
650	660	670	680	690	700	710	720
ELVQRIQTLS	QLLLNLQAVI	AHQDSYVETQ	RAAIQEREKQ	FRLQSTRGNL	LLEQERQRNF	EKQREERAAL	EKLQSQLRHE
730	740	750	760	770	780	790	800
QQRWERERQW	QHQELERAGA	RLQEREGEAR	QLRERLEQER	AELERQRQAY	QHDLERLREA	QRAVERERER	LELLRRLKKQ
810	820	830	840	850	860	870	880
NTAPGALPPD	TLAEAQPPSH	PPSFNGEGLE	GPRVSMLPSG	VGPEYAERPE	VARRDSAPTE	NRLAKSDVPI	QLLSATNQFQ
890	900	910	920	930	940	950	960
RQAAVQQQIP	TKLAASTKGG	KDKGGKSRGS	QRWESSASFD	LKQQLLLNKL	MGKDESTSRN	RRSLSPILPG	RHSPAPPPDP
970	980	990	1000	1010	1020		
GFPAPSPPPA	DSPSEGFSLK	AGGTALLPGP	PAPSPLPATP	LSAKEDASKE	DVIFF		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1380	1	683.3455	-90.52	2	45.8	10.4	2	940-951	R.NRRSLSPILPGR.H	

Detailed Protein Report

Protein 1633: 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 1634: PREDICTED: ankyrin repeat and SOCS box protein 15 isoform X7 [Homo sapiens]

Accession:	gi|578813924	**Score:**	10.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	54.7
Database Date:	2015-11-30	**pI:**	5.7
		Sequence Coverage [%]:	2.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDTNDDPDED	HLTSYDIQLS	IQESIEASKT	ALCPERFVPL	SAQNRKLVEA	IKQAVKKGSY	DMVSTLIKHN	TSLDQPCVKR
90	100	110	120	130	140	150	160
WSAMHEAAKQ	GRKDIVALLL	KHGGNVHLRD	GFGVTPLGVA	AEYGHCDVLE	HLIHKGGDVL	ALADDGASVL	FEAAGGGNPD
170	180	190	200	210	220	230	240
CISLLLEYGG	SGNVPNRAGH	LPIHRAAYEG	HYLALKYLIP	VTSKNAIRKS	GLTPIHSAAD	GQNAQCLELL	IENGFDVNTL
250	260	270	280	290	300	310	320
LADHISQSYD	DERKTALYFG	VSNNDVHCTE	VLLAAGADPN	LDPLNCLLVA	VRANNYEIVR	LLLSHGANVN	CYFMHVNDTR
330	340	350	360	370	380	390	400
FPSVIQYALN	DEVMLRLLLN	NGYQVEMCFD	CMHGDIFGNS	FVWSEIQEEV	LPGWTSCVIK	DNPFCEFITV	PWMKHLVGRV
410	420	430	440	450	460	470	480
TRVLIDYMDY	VPLCAKLKSA	LEVQREWPEI	RQILENPCSL	KHLCRLKIRR	LMGLQKLCQP	ASVEKLPLPP	AIQRYILFKE
490	500						
YDLYGQELKL	T						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1536	1	671.4430	126.89	2	47.9	10.3	1	57-68	K.KGSYDMVSTLIK.H	

Detailed Protein Report

Protein 1635: PREDICTED: calcyphosin-like protein isoform X2 [Homo sapiens]

Accession:	gi|578809847	**Score:**	10.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	23.1
Database Date:	2015-11-30	**pI:**	8.9
Modification(s):	Oxidation	**Sequence Coverage [%]:**	10.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MQETASIVSV	RSNWWQKMAG	TARHDREMAI	QAKKKLTTAT	DPIERLRLQC	LARGSAGIKG	LGRVFRIMDD	DNNRTLDFKE
90	100	110	120	130	140	150	160
FMKGLNDYAV	VMEKEEVEEL	FRRFDKDGNG	TIDFNEFLLT	LRPPMSRARK	EVIMQAFRKL	DKTGDGVITI	EDLREVYNAK
170	180	190	200				
HHPKYQNGEW	SEEQVFRKFL	DNFDSPYDKD	GLVHKVGAH				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
71	1	1205.0469	-41.61	2	29.6	10.3	0	107-127	K.DGNGTIDFNEFLLTLRPPMSR.A	Oxidation: 19

Detailed Protein Report

Protein 1636: 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 1637: E3 ubiquitin-protein ligase MARCH9 precursor [Homo sapiens]

Accession:	gi|40255016	**Score:**	10.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	37.7
Database Date:	2015-11-30	**pI:**	10.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	9.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLKSRLRMFL	NELKLLVLTG	GGRPRAEPQP	RGGRGGGCGW	APFAGCSTRD	GDGDEEEYYG	SEPRARGLAG	DKEPRAGPLP
90	100	110	120	130	140	150	160
PPAPPLPPPG	ALDALSLSSS	LDSGLRTPQC	RICFQGPEQG	ELLSPCRCDG	SVRCTHQPCL	IRWISERGSW	SCELCYFKYQ
170	180	190	200	210	220	230	240
VLAISTKNPL	QWQAISLTVI	EKVQIAAIVL	GSLFLVASIS	WLIWSSLSPS	AKWQRQDLLF	QICYGMYGFM	DVVCIGLIIH
250	260	270	280	290	300	310	320
EGSSVYRIFK	RWQAVNQQWK	VLNYDKTKDI	GGDAGGGTAG	KSGPRNSRTG	PTSGATSRPP	AAQRMRTLLP	QRCGYTILHL
330	340	350					
LGQLRPPDAR	SSSHSGREVV	MRVTTV					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1271	1	1137.1500	14.26	3	44.6	10.3	2	35-66	R.GGGCGWAPFAGCSTRDGDGDEEEYYGSEPRAR.G	Carbamidomethyl: 4

Detailed Protein Report

Protein 1638: transmembrane protein 165 precursor [Homo sapiens]

Accession:	gi|32189371	**Score:**	10.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	34.9
Database Date:	2015-11-30	**pI:**	6.7
		Sequence Coverage [%]:	5.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAAAAPGNGR	ASAPRLLLLF	LVPLLWAPAA	VRAGPDEDLS	HRNKEPPAPA	QQLQPQPVAV	QGPEPARVEK	IFTPAAPVHT
90	100	110	120	130	140	150	160
NKEDPATQTN	LGFIHAFVAA	ISVIIVSELG	DKTFFIAAIM	AMRYNRLTVL	AGAMLALGLM	TCLSVLFGYA	TTVIPRVYTY
170	180	190	200	210	220	230	240
YVSTVLFAIF	GIRMLREGLK	MSPDEGQEEL	EEVQAELKKK	DEEFQRTKLL	NGPGDVETGT	SITVPQKKWL	HFISPIFVQA
250	260	270	280	290	300	310	320
LTLTFLAEWG	DRSQLTTIVL	AAREDPYGVA	VGGTVGHCLC	TGLAVIGGRM	IAQKISVRTV	TIIGGIVFLA	FAFSALFISP
330							
DSGF							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2323	1	953.2249	122.58	2	57.7	10.3	0	16-32	R.LLLLFLVPLLWAPAAVR.A	

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Detailed Protein Report

Protein 1639: 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 1640: 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

mdown:qdown	**Median:**	4.15	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	1.18	**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	Wdown:Qdown 1.18 mdown:qdown 4.15

Detailed Protein Report

Protein 1641: 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

```
        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
2405	1	665.1991	-138.24	2	60.4	10.3	1	129-140	R.ERCGVPFSCCTK.D	

Detailed Protein Report

Protein 1642: 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 1643: ferritin, heavy polypeptide-like 18 [Homo sapiens]

Accession:	gi|410991933	**Score:**	10.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	25.1
Database Date:	2015-11-30	**pI:**	9.2
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	5.0
		No. of unique Peptides:	1

Quantitation

Wdown:Qdown **Median:** 0.15 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MVVLRGPHRC RHCPRRCRYP LRAPGKPTAF PLLPAPALPA LGPLSQVQRY HHPSCEAAIN THISLELHAS YVYLSMAFYF
        90        100        110        120        130        140        150        160
DQDDAALEHF DCYFLCQLQE KREHAQELMR LHNLRGGRIC LHDVGKPEGQ GWESGLKAME CAFHLEKNIN QSLLELHQLA
       170        180        190        200        210        220        230
KENGDPQLCD FLENHFLNQQ AKTIKELGGY LSNLRKMGSP EAGLAEYLFN KLTLGRSQKH T
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1720	1	698.9029	40.96	2	50.0	10.3	2	1-11	-.MVVLRGPHRCR.H	Carbamidomethyl: 10; Oxidation: 1	Wdown:Qdown 0.15

Detailed Protein Report

Protein 1644: **epithelial discoidin domain-containing receptor 1 isoform 4 precursor [Homo sapiens]**

Accession:	gi|321400059	**Score:**	10.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	56.1
Database Date:	2015-11-30	**pI:**	6.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	4.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGPEALSSLL	LLLLVASGDA	DMKGHFDPAK	CRYALGMQDR	TIPDSDISAS	SSWSDSTAAR	HSRLESSDGD	GAWCPAGSVF
90	100	110	120	130	140	150	160
PKEEEYLQVD	LQRLHLVALV	GTQGRHAGGL	GKEFSRSYRL	RYSRDGRRWM	GWKDRWGQEV	ISGNEDPEGV	VLKDLGPPMV
170	180	190	200	210	220	230	240
ARLVRFYPRA	DRVMSVCLRV	ELYGCLWRDG	LLSYTAPVGQ	TMYLSEAVYL	NDSTYDGHTV	GGLQYGGLGQ	LADGVVGLDD
250	260	270	280	290	300	310	320
FRKSQELRVW	PGYDYVGWSN	HSFSSGYVEM	EFEFDRLRAF	QAMQVHCNNM	HTLGARLPGG	VECRFRRGPA	MAWEGEPMRH
330	340	350	360	370	380	390	400
NLGGNLGDPR	ARAVSVPLGG	RVARFLQCRF	LFAGPWLLFS	EISFISDVVN	NSSPALGGTF	PPAPWWPPGP	PPTNFSSLEL
410	420	430	440	450	460	470	480
EPRGQQPVAK	AEGSPTAILI	GCLVAIILLL	LLIIALMLWR	LHWRRLLSKA	ERRVLEEELT	VHLSVPGDTI	LINNRPGPRE
490	500	510					
PPPYQEPRPR	GNPPHSAPCV	PNGSGAPV					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
165	1	1239.6313	46.44	2	30.8	10.3	1	308-330	R.GPAMAWEGEPMRHNLGGNLGDPR.A	Oxidation: 4

Detailed Protein Report

Protein 1645: PREDICTED: golgin subfamily A member 6-like protein 2 [Homo sapiens]

Accession: gi|578796967
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 10.3
MW [kDa]: 55.8
pI: 5.6
Sequence Coverage [%]: 2.0
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MREEERMRER	EKKMREEEEM	MREQEEKMQE	QEEKMQEQEE	KMWEQEEKMQ	EQEEKMWEQE	EKMWEQEEKM	WEQQRLPEQK
90	100	110	120	130	140	150	160
EKLWEHEKMQ	EQEKMQEQEE	KIWEQEKMRD	QEEKMWDQKE	RMWEQDERLR	EKEERMREQK	MWQQVEKMRE	EKKTQEQEKK
170	180	190	200	210	220	230	240
TWDQEKMREE	ESMREREKKM	REEEEMMREQ	EEKMQEQEEK	MQEQEEEMWE	QEEKMWEQEE	KMWEQQRLPE	QKEKLWEHEK
250	260	270	280	290	300	310	320
MQEQEKIWEQ	EEKMRDQEEK	MRGQEEKMRG	QEEKMRGQEE	KMWGQEEKMW	GQEEKMWGQE	EKMWGQEEKM	WGQEEKMRGA
330	340	350	360	370	380	390	400
GGEDAGAGGE	DAGPGGEDAG	AGGEDAGGRR	RRCGGQEEKM	RGTGGEDAGA	RRRRCGSRRR	RCGSRRRRCR	ARRRRCGSRR
410	420	430	440	450			
RRCGARRRRC	GSRRRRCGAR	RRRCGARRRR	CGGRRRRCGG	RRR			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
302	1	409.4394	-183.74	3	32.5	10.3	1	310-318	K.MWGQEEKMR.G	Oxidation: 1, 8

Detailed Protein Report

Protein 1646: PREDICTED: stabilin-2 isoform X1 [Homo sapiens]

Accession:	gi|578823928	**Score:**	10.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	243.6
Database Date:	2015-11-30	**pI:**	6.1
		Sequence Coverage [%]:	0.6
		No. of unique Peptides:	1

Quantitation

Wdown:Qdown	**Median:** 1.51	**CV:** 0.00 %	**No. of Peptides:** 1

Detailed Protein Report

10	20	30	40	50	60	70	80
MMLQHLVIFC	LGLVVQNFCS	PAETTGQARR	CDRKSLLTIR	TECRSCALNL	GVKCPDGYTM	ITSGSVGVRD	CRYTFEVRTY
90	100	110	120	130	140	150	160
SLSLPGCRHI	CRKDYLQPRC	CPGRWGPDCI	ECPGGAGSPC	NGRGSCAEGM	EGNGTCSCQE	GFGGTACETC	ADDNLFGPSC
170	180	190	200	210	220	230	240
SSVCNCVHGV	CNSGLDGDGT	CECYSAYTGP	KCDKPIPECA	ALLCPENSRC	SPSTEDENKL	ECKCLPNYRG	DGKYCDPINP
250	260	270	280	290	300	310	320
CLRKICHPHA	HCTYLGPNRH	SCTCQEGYRG	DGQVCLPVDP	CQINFGNCPT	KSTVCKYDGP	GQSHCECKEH	YQNFVPGVGC
330	340	350	360	370	380	390	400
SMTDICKSDN	PCHRNANCTT	VAPGRTECIC	QKGYVGDGLT	CYGNIMERLR	ELNTEPRGKW	QGRLTSFISL	LDKAYAWPLS
410	420	430	440	450	460	470	480
KLGPFTVLLP	TDKGLKGFNV	NELLVDNKAA	QYFVKLHIIA	GQMNIEYMNN	TDMFYTLTGK	SGEIFNSDKD	NQIKLKLHGG
490	500	510	520	530	540	550	560
KKKVKIIQGD	IIASNGLLHI	LDRAMDKLEP	TFESNNEQTI	MTMLQPRYSK	FRSLLEETNL	GHALDEDGVG	GPYTIFVPNN
570	580	590	600	610	620	630	640
EALNNMKDGT	LDYLLSPEGS	RKLLELVRYH	IVPFTQLEVA	TLISTPHIRS	MANQLIQFNT	TDNGQILAND	VAMEEIEITA
650	660	670	680	690	700	710	720
KNGRIYTLTG	VLIPPSIVPI	LPHRCDETKR	EMKLGTCVSC	SLVYWSRCPA	NSEPTALFTH	RCVYSGRFGS	LKSGCARYCN
730	740	750	760	770	780	790	800
ATVKIPKCCK	GFYGPDCNQC	PGGFSNPCSG	NGQCADSLGG	NGTCICEEGF	QGSQCQFCSD	PNKYGPRCNK	KCLCVHGTCN
810	820	830	840	850	860	870	880
NRIDSDGACL	TGTCRDGSAG	RLCDKQTSAC	GPYVQFCHIH	ATCEYSNGTA	SCICKAGYEG	DGTLCSEMDP	CTGLTPGGCS
890	900	910	920	930	940	950	960
RNAECIKTGT	GTHTCVCQQG	WTGNGRDCSE	INNCLLPSAG	GCHDNASCLY	VGPGQNECEC	KKGFRGNGID	CEPITSCLEQ
970	980	990	1000	1010	1020	1030	1040
TGKCHPLASC	QSTSSGVWSC	VCQEGYEGDG	FLCYGNAAVE	LSFLSEAAIF	NRWINNASLQ	PTLSATSNLT	VLVPSQQATE
1050	1060	1070	1080	1090	1100	1110	1120
DMDQDEKSFW	LSQSNIPALI	KYHMLLGTYR	VADLQTLSSS	DMLATSLQGN	FLHLAKVDGN	ITIEGASIVD	GDNAATNGVI
1130	1140	1150	1160	1170	1180	1190	1200
HIINKVLVPQ	RRLTGSLPNL	LMRLEQMPDY	SIFRGYIIQY	NLANAIEAAD	AYTVFAPNNN	AIENYIREKK	VLSLEEDVLR
1210	1220	1230	1240	1250	1260	1270	1280
YHVVLEEKLL	KNDLHNGMHR	ETMLGFSYFL	SFFLHNDQLY	VNEAPINYTN	VATDKGVIHG	LGKVLEIQKN	RCDNNDTTII
1290	1300	1310	1320	1330	1340	1350	1360
RGRCRTCSSE	LTCPFGTKSL	GNEKRRCIYT	SYFMGRRTLF	IGCQPKCVRT	VITRECCAGF	FGPQCQPCPG	NAQNVCFGNG
1370	1380	1390	1400	1410	1420	1430	1440
ICLDGVNGTG	VCECGEGFSG	TACETCTEGK	YGIHCDQACS	CVHGRCNQGP	LGDGSCDCDV	GWRGVHCDNA	TTEDNCNGTC
1450	1460	1470	1480	1490	1500	1510	1520
HTSANCLTNS	DGTASCKCAA	GFQGNGTICT	AINACEISNG	GCSAKADCKR	TTPGRRVCTC	KAGYTGDGIV	CLEINPCLEN
1530	1540	1550	1560	1570	1580	1590	1600
HGGCDKNAEC	TQTGPNQAAC	NCLPAYTGDG	KVCTLINVCL	TKNGGCSEFA	ICNHTGQVER	TCTCKPNYIG	DGFTCRGSIY
1610	1620	1630	1640	1650	1660	1670	1680
QELPKNPKTS	QYFFQLQEHF	VKDLVGPGPF	TVFAPLSAAF	DEEARVKDWD	KYGLMPQVLR	YHVVACHQLL	LENLKLISNA
1690	1700	1710	1720	1730	1740	1750	1760
TSLQGEPIVI	SVSQSTVYIN	NKAKIISSDI	ISTNGIVHII	DKLLSPKNLL	ITPKDNSGRI	LQNLTTLATN	NGYIKFSNLI
1770	1780	1790	1800	1810	1820	1830	1840
QDSGLLSVIT	DPIHTPVTLF	WPTDQALHAL	PAEQQDFLFN	QDNKDKLKEY	LKFHVIRDAK	VLAVDLPTST	AWKTLQGSEL
1850	1860	1870	1880	1890	1900	1910	1920
SVKCGAGRDI	GDLFLNGQTC	RIVQRELLFD	LGVAYGIDCL	LIDPTLGGRC	DTFTTFDASG	ECGSCVNTPS	CPRWSKPKGV
1930	1940	1950	1960	1970	1980	1990	2000
KQKCLYNLPF	KRNLEGCRER	CSLVIQIPRC	CKGYFGRDCQ	ACPGGPDAPC	NNRGVCLDQY	SATGECKCNT	GFNGTACEMC
2010	2020	2030	2040	2050	2060	2070	2080
WPGRFGPDCL	PCGCSDHGQC	DDGITGSGQC	LCETGWTGPS	CDTQAVLPAV	CTPPCSAHAT	CKENNTCECN	LDYEGDGITC
2090	2100	2110	2120	2130	2140	2150	2160
TVVDFCKQDN	GGCAKVARCS	QKGTKVSCSC	QKGYKGDGHS	CTEIDPCADG	LNGGCHEHAT	CKMTGPGKHK	CECKSHYVGD
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
424	1	761.9985	164.95	2	34.3	10.3	0	568-581	K.DGTLDYLLSPEGSR.K		Wdown:Qdown 1.51

Detailed Protein Report

Protein 1647: protein-tyrosine sulfotransferase 2 precursor [Homo sapiens]

Accession:	gi|56699463	**Score:**	10.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	41.9
Database Date:	2015-11-30	**pI:**	9.9
		Sequence Coverage [%]:	4.8
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|56699465	refseq_human (refseq_human_20140103.fasta)	protein-tyrosine sulfotransferase 2 precursor [Homo sapiens]

10	20	30	40	50	60	70	80
MRLSVRRVLL	AAGCALVLVL	AVQLGQQVLE	CRAVLAGLRS	PRGAMRPEQE	ELVMVGTNHV	EYRYGKAMPL	IFVGGVPRSG
90	100	110	120	130	140	150	160
TTLMRAMLDA	HPEVRCGEET	RIIPRVLAMR	QAWSKSGREK	LRLDEAGVTD	EVLDAAMQAF	ILEVIAKHGE	PARVLCNKDP
170	180	190	200	210	220	230	240
FTLKSSVYLS	RLFPNSKFLL	MVRDGRASVH	SMITRKVTIA	GFDLSSYRDC	LTKWNKAIEV	MYAQCMEVGK	EKCLPVYYEQ
250	260	270	280	290	300	310	320
LVLHPRRSLK	LILDFLGIAW	SDAVLHHEDL	IGKPGGVSLS	KIERSTDQVI	KPVNLEALSK	WTGHIPGDVV	RDMAQIAPML
330	340	350	360	370	380		
AQLGYDPYAN	PPNYGNPDPF	VINNTQRVLK	GDYKTPANLK	GYFQVNQNST	SSHLGSS		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1673	1	1045.0313	-28.88	2	49.6	10.3	2	178-195	K.FLLMVRDGRASVHSMITR.K	

Detailed Protein Report

Protein 1648: PREDICTED: zinc finger protein 451 isoform X2 [Homo sapiens]

Accession:	gi|530381758	**Score:**	10.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	111.8
Database Date:	2015-11-30	**pI:**	6.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGDPGSEIIE	SVPPAGPEAS	ESTTDENEDD	IQFVSEGPLR	PVLEYIDLVS	SDDEEPSTSY	TDENIKRKDH	IDYQKDKVAL
90	100	110	120	130	140	150	160
TLARLARHVE	VEKQQKEEKN	RAFREKIDFQ	HAHGLQELEF	IRGHSDTEAA	RLCVDQWLKM	PGLKTGTINC	GTKSSFRRGG
170	180	190	200	210	220	230	240
HTWVSGKPIL	CPIMHCNKEF	DNGHLLLGHL	KRFDHSPCDP	TITLHGPFFS	SFACVVCYKK	FVTQQQYRDH	LFDKEATDDG
250	260	270	280	290	300	310	320
HNNNLLPQII	QCFACPNCFL	LFSRKEECSK	HMSGKNHFHQ	SFKLGDNKGI	AHPISFPSFA	KKLLISLCKD	VPFQVKCVAC
330	340	350	360	370	380	390	400
HKTLRSHMEL	TAHFRVHCRN	AGPVAVAEKS	ITQVAEKFIL	RGYCPDCNQV	FVDETSTQNH	KQNSGHKVRV	INSVEESVLL
410	420	430	440	450	460	470	480
YCHSSEGNKD	PSSDLHLLLD	QSKFSSLKRT	MSIKESSSLE	CIAIPKKKMN	LKDKSHEGVA	CVQKEKSVVK	TWFCECNQRF
490	500	510	520	530	540	550	560
PSEDAVEKHV	FSANTMGYKC	VVCGKVCDDS	GVIRLHMSRI	HGGAHLNNFL	FWCRTCKKEL	TRKDTIMAHV	TEFHNGHRYF
570	580	590	600	610	620	630	640
YEMDEVEGET	LPSSSTTLDN	LTANKPSSAI	TVIDHSPANS	SPRGKWQCRI	CEDMFDSQEY	VKQHCMSLAS	HKFHRYSCAH
650	660	670	680	690	700	710	720
CRKPFHKIET	LYRHCQDEHD	NEIKIKYFCG	LCDLIFNVEE	AFLSHYEEHH	SIDYVFVSEK	TETSIKTEDD	FPVIETSNQL
730	740	750	760	770	780	790	800
TCGCRESYIC	KVNRKEDYSR	CLQIMLDKGK	LWFRCSLCSA	TAQNLTDMNT	HIHQVHKEKS	DEEEQQYVIK	CGTCTKAFHD
810	820	830	840	850	860	870	880
PESAQQHFHR	KHCFLQKPSV	AHFGSEKSNL	YKFTASASHT	ERKLKQAINY	SKSLDMEKGV	ENDLSYQNIE	EEIVELPDLD
890	900	910	920	930	940	950	960
YLRTMTHIVF	VDFDNWSNFF	GHLPGHLNQG	TFIWGFQGGN	TNWKPPLNCK	IYNYLNRIGC	FFLHPRCSKR	KDAADFAICM
970	980						
HNVTVMITWV	PKILQ						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2396	1	832.2427	-131.97	2	58.6	10.3	0	610-622	R.ICEDMFDSQEYVK.Q	Carbamidomethyl: 2

Detailed Protein Report

Protein 1649: 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 1650: schlafen family member 11 [Homo sapiens]

Accession:	gi|157388957	**Score:**	10.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	102.8
Database Date:	2015-11-30	**pI:**	9.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.2
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|578831629	refseq_human (refseq_human_20140103.fasta)	PREDICTED: schlafen family member 11 isoform X3 [Homo sapiens]
gi|530411217	refseq_human (refseq_human_20140103.fasta)	PREDICTED: schlafen family member 11 isoform X2 [Homo sapiens]
gi|157388965	refseq_human (refseq_human_20140103.fasta)	schlafen family member 11 [Homo sapiens]
gi|157388963	refseq_human (refseq_human_20140103.fasta)	schlafen family member 11 [Homo sapiens]
gi|157388961	refseq_human (refseq_human_20140103.fasta)	schlafen family member 11 [Homo sapiens]
gi|157388959	refseq_human (refseq_human_20140103.fasta)	schlafen family member 11 [Homo sapiens]

10	20	30	40	50	60	70	80
MEANQCPLVV	EPSYPDLVIN	VGEVTLGEEN	RKKLQKIQRD	QEKERVMRAA	CALLNSGGGV	IRMAKKVEHP	VEMGLDLEQS
90	100	110	120	130	140	150	160
LRELIQSSDL	QAFFETKQQG	RCFYIFVKSW	SSGPFPEDRS	VKPRLCSLSS	SLYRRSETSV	RSMDSREAFC	FLKTKRKPKI
170	180	190	200	210	220	230	240
LEEGPFHKIH	KGVYQELPNS	DPADPNSDPA	DLIFQKDYLE	YGEILPFPES	QLVEFKQFST	KHFQEYVKRT	IPEYVPAFAN
250	260	270	280	290	300	310	320
TGGGYLFIGV	DDKSREVLGC	AKENVDPDSL	RRKIEQAIYK	LPCVHFCQPQ	RPITFTLKIV	NVLKRGELYG	YACMIRVNPF
330	340	350	360	370	380	390	400
CCAVFSEAPN	SWIVEDKYVC	SLTTEKWVGM	MTDTDPDLLQ	LSEDFECQLS	LSSGPPLSRP	VYSKKGLEHK	KELQQLLFSV
410	420	430	440	450	460	470	480
PPGYLRYTPE	SLWRDLISEH	RGLEELINKQ	MQPFFRGILI	FSRSWAVDLN	LQEKPGVICD	ALLIAQNSTP	ILYTILREQD
490	500	510	520	530	540	550	560
AEGQDYCTRT	AFTLKQKLVN	MGGYTGKVCV	RAKVLCLSPE	SSAEALEAAV	SPMDYPASYS	LAGTQHMEAL	LQSLVIVLLG
570	580	590	600	610	620	630	640
FRSLLSDQLG	CEVLNLLTAQ	QYEIFSRSLR	KNRELFVHGL	PGSGKTIMAM	KIMEKIRNVF	HCEAHRILYV	CENQPLRNFI
650	660	670	680	690	700	710	720
SDRNICRAET	RKTFLRENFE	HIQHIVIDEA	QNFRTEDGDW	YGKAKSITRR	AKGGPGILWI	FLDYFQTSHL	DCSGLPPLSD
730	740	750	760	770	780	790	800
QYPREELTRI	VRNADPIAKY	LQKEMQVIRS	NPSFNIPTGC	LEVFPEAEWS	QGVQGTLRIK	KYLTVEQIMT	CVADTCRRFF
810	820	830	840	850	860	870	880
DRGYSPKDVA	VLVSTAKEVE	HYKYELLKAM	RKKRVVQLSD	ACDMLGDHIV	LDSVRRFSGL	ERSIVFGIHP	RTADPAILPN
890	900	910					
VLICLASRAK	QHLYIFPWGG	H					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1159	1	666.8476	60.36	2	43.2	10.3	0	306-316	R.GELYGYACMIR.V	Carbamidomethyl: 8

Detailed Protein Report

Protein 1651: 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

Quantitation

mdown:qdown	**Median:**	0.34	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	17.44	**CV:**	0.00 %	**No. of 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	Ratios
623	1	675.6771	-160.57	2	37.1	10.3	0	804-813	R.NMYCIDIYCR.S	Carbamidomethyl: 9	mdown:qdown 0.34 Wdown:Qdown 17.44

Detailed Protein Report

Protein 1652: delta-like protein 4 precursor [Homo sapiens]

Accession:	gi|9506545	**Score:**	10.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	74.6
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
MAAASRSASG	WALLLLVALW	QQRAAGSGVF	QLQLQEFINE	RGVLASGRPC	EPGCRTFFRV	CLKHFQAVVS	PGPCTFGTVS
90	100	110	120	130	140	150	160
TPVLGTNSFA	VRDDSSGGGR	NPLQLPFNFT	WPGTFSLIIE	AWHAPGDDLR	PEALPPDALI	SKIAIQGSLA	VGQNWLLDEQ
170	180	190	200	210	220	230	240
TSTLTRLRYS	YRVICSDNYY	GDNCSRLCKK	RNDHFGHYVC	QPDGNLSCLP	GWTGEYCQQP	ICLSGCHEQN	GYCSKPAECL
250	260	270	280	290	300	310	320
CRPGWQGRLC	NECIPHNGCR	HGTCSTPWQC	TCDEGWGGLF	CDQDLNYCTH	HSPCKNGATC	SNSGQRSYTC	TCRPGYTGVD
330	340	350	360	370	380	390	400
CELELSECDS	NPCRNGGSCK	DQEDGYHCLC	PPGYYGLHCE	HSTLSCADSP	CFNGGSCRER	NQGANYACEC	PPNFTGSNCE
410	420	430	440	450	460	470	480
KKVDRCTSNP	CANGGQCLNR	GPSRMCRCRP	GFTGTYCELH	VSDCARNPCA	HGGTCHDLEN	GLMCTCPAGF	SGRRCEVRTS
490	500	510	520	530	540	550	560
IDACASSPCF	NRATCYTDLS	TDTFVCNCPY	GFVGSRCEFP	VGLPPSFPWV	AVSLGVGLAV	LLVLLGMVAV	AVRQLRLRRP
570	580	590	600	610	620	630	640
DDGSREAMNN	LSDFQKDNLI	PAAQLKNTNQ	KKELEVDCGL	DKSNCGKQQN	HTLDYNLAPG	PLGRGTMPGK	FPHSDKSLGE
650	660	670	680	690			
KAPLRLHSEK	PECRISAICS	PRDSMYQSVC	LISEERNECV	IATEV			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2633	1	1175.1428	60.41	2	61.2	10.3	2	557-576	R.LRRPDDGSREAMNNLSDFQK.D	

Detailed Protein Report

Protein 1653: serine/threonine-protein phosphatase 6 regulatory ankyrin repeat subunit C [Homo sapiens]

Accession: gi|157743284
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 10.3
MW [kDa]: 115.0
pI: 6.0
Sequence Coverage [%]: 1.0
No. of unique Peptides: 1

Quantitation

mdown:qdown	**Median:**	0.64	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.25	**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		Wdown:Qdown 0.25 mdown:qdown 0.64

Detailed Protein Report

Protein 1654: 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

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Detailed Protein Report

Protein 1655: PREDICTED: pyruvate dehydrogenase phosphatase regulatory subunit, mitochondrial isoform X5 [Homo sapiens]

Accession:	gi|530424049	**Score:**	10.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	69.8
Database Date:	2015-11-30	**pI:**	5.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPVFCQLCWP	AIVDADGRIY	IRNWQGGILS	GGFEKNPKPI	FTEGKNQLEI	QNLQEDWDHF	EPLLSSLLRR	MPELETLEIM
90	100	110	120	130	140	150	160
KLVNCPETFT	PDMRCIMGES	PAVQGYFVLA	GMNSAGLSFG	GGAGKYLAEW	MVHGYPSENV	WELDLKRFGA	LQSSRTFLRH
170	180	190	200	210	220	230	240
RVMEVMPLMY	DLKVPRWDFQ	TGRQLRTSPL	YDRLDAQGAR	WMEKHGFERP	KYFVPPDKDL	LALEQSKTFY	KPDWFDIVES
250	260	270	280	290	300	310	320
EVKCCKEAVC	VIDMSSFTKF	EITSTGDQAL	EVLQYLFSND	LDVPVGHIVH	TGMLNEGGGY	ENDCSIARLN	KRSFFMISPT
330	340	350	360	370	380	390	400
DQQVHCWAWL	KKHMPKDSNL	LLEDVTWKYT	ALNLIGPRAV	DVLSELSYAP	MTPDHFPSLF	CKEMSVGYAN	GIRVMSMTHT
410	420	430	440	450	460	470	480
GEPGFMLYIP	IEYALHVYNE	VMSVGQKYGI	RNAGYYALRS	LRIEKFFAFW	GQDINNLTTP	LECGRESRVK	LEKGMDFIGR
490	500	510	520	530	540	550	560
DALLQQKQNG	VYKRLTMFIL	DDHDSDLDLW	PWWGEPIYRN	GQYVGKTTSS	AYSYSLERHV	CLGFVHNFSE	DTGEEQVVTA
570	580	590	600	610			
DFINRGEYEI	DIAGYRFQAK	AKLYPVASLF	TQKRRKDDME	LSDLHGK			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2226	1	753.2849	-137.90	2	56.5	10.3	1	70-81	R.RMPELETLEIMK.L	Oxidation: 2

Protein 1656: sodium channel protein type 3 subunit alpha isoform 3 [Homo sapiens]

Accession:	gi|126362955	**Score:**	10.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	221.3
Database Date:	2015-11-30	**pI:**	5.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAQALLVPPG	PESFRLFTRE	SLAAIEKRAA	EEKAKKPKKE	QDNDDENKPK	PNSDLEAGKN	LPFIYGDIPP	EMVSEPLEDL
90	100	110	120	130	140	150	160
DPYYINKKTF	IVMNKGKAIF	RFSATSALYI	LTPLNPVRKI	AIKILVHSLF	SMLIMCTILT	NCVFMTLSNP	PDWTKNVEYT
170	180	190	200	210	220	230	240
FTGIYTFESL	IKILARGFCL	EDFTFLRDPW	NWLDFSVIVM	AYVTEFVSLG	NVSALRTFRV	LRALKTISVI	PGLKTIVGAL
250	260	270	280	290	300	310	320
IQSVKKLSDV	MILTVFCLSV	FALIGLQLFM	GNLRNKCLQW	PPSDSAFETN	TTSYFNGTMD	SNGTFVNVTM	STFNWKDYIG
330	340	350	360	370	380	390	400
DDSHFYVLDG	QKDPLLCGNG	SDAGQCPEGY	ICVKAGRNPN	YGYTSFDTFS	WAFLSLFRLM	TQDYWENLYQ	LTLRAAGKTY
410	420	430	440	450	460	470	480
MIFFVLVIFL	GSFYLVNLIL	AVVAMAYEEQ	NQATLEEAEQ	KEAEFQQMLE	QLKKQQEEAQ	AVAAASAASR	DFSGIGGLGE
490	500	510	520	530	540	550	560
LLESSSEASK	LSSKSAKEWR	NRRKKRRQRE	HLEGNNKGER	DSFPKSESED	SVKRSSFLFS	MDGNRLTSDK	KFCSPHQSLL
570	580	590	600	610	620	630	640
SIRGSLFSPR	RNSKTSIFSF	RGRAKDVGSE	NDFADDEHST	FEDSESRRDS	LFVPHRHGER	RNSNGTTTET	EVRKRRLSSY
650	660	670	680	690	700	710	720
QISMEMLEDS	SGRQRAVSIA	SILTNTMEEL	EESRQKCPPC	WYRFANVFLI	WDCCDAWLKV	KHLVNLIVMD	PFVDLAITIC
730	740	750	760	770	780	790	800
IVLNTLFMAM	EHYPMTEQFS	SVLTVGNLVF	TGIFTAEMVL	KIIAMDPYYY	FQEGWNIFDG	IIVSLSLMEL	GLSNVEGLSV
810	820	830	840	850	860	870	880
LRSFRLLRVF	KLAKSWPTLN	MLIKIIGNSV	GALGNLTLVL	AIIVFIFAVV	GMQLFGKSYK	ECVCKINDDC	TLPRWHMNDF
890	900	910	920	930	940	950	960
FHSFLIVFRV	LCGEWIETMW	DCMEVAGQTM	CLIVFMLVMV	IGNLVVLNLF	LALLLSSFSS	DNLAATDDDN	EMNNLQIAVG
970	980	990	1000	1010	1020	1030	1040
RMQKGIDYVK	NKMRECFQKA	FFRKPKVIEI	HEGNKIDSCM	SNNTGIEISK	ELNYLRDGNG	TTSGVGTGSS	VEKYVIDEND
1050	1060	1070	1080	1090	1100	1110	1120
YMSFINNPSL	TVTVPIAVGE	SDFENLNTEE	FSSESELEES	KEKLNATSSS	EGSTVDVVLP	REGEQAETEP	EEDLKPEACF
1130	1140	1150	1160	1170	1180	1190	1200
TEGCIKKFPF	CQVSTEEGKG	KIWWNLRKTC	YSIVEHNWFE	TFIVFMILLS	SGALAFEDIY	IEQRKTIKTM	LEYADKVFTY
1210	1220	1230	1240	1250	1260	1270	1280
IFILEMLLKW	VAYGFQTYFT	NAWCWLDFLI	VDVSLVSLVA	NALGYSELGA	IKSLRTLRAL	RPLRALSRFE	GMRVVVNALV
1290	1300	1310	1320	1330	1340	1350	1360
GAIPSIMNVL	LVCLIFWLIF	SIMGVNLFAG	KFYHCVNMTT	GNMFDISDVN	NLSDCQALGK	QARWKNVKVN	FDNVGAGYLA
1370	1380	1390	1400	1410	1420	1430	1440
LLQVATFKGW	MDIMYAAVDS	RDVKLQPVYE	ENLYMYLYFV	IFIIFGSFFT	LNLFIGVIID	NFNQQKKKFG	GQDIFMTEEQ
1450	1460	1470	1480	1490	1500	1510	1520
KKYYNAMKKL	GSKKPQKPIP	RPANKFQGMV	FDFVTRQVFD	ISIMILICLN	MVTMMVETDD	QGKYMTLVLS	RINLVFIVLF
1530	1540	1550	1560	1570	1580	1590	1600
TGEFVLKLVS	LRHYYFTIGW	NIFDFVVVIL	SIVGMFLAEM	IEKYFVSPTL	FRVIRLARIG	RILRLIKGAK	GIRTLLFALM
1610	1620	1630	1640	1650	1660	1670	1680
MSLPALFNIG	LLLFLVMFIY	AIFGMSNFAY	VKKEAGIDDM	FNFETFGNSM	ICLFQITTSA	GWDGLLAPIL	NSAPPDCDPD
1690	1700	1710	1720	1730	1740	1750	1760
TIHPGSSVKG	DCGNPSVGIF	FFVSYIIISF	LVVVNMYIAV	ILENFSVATE	ESAEPLSEDD	FEMFYEVWEK	FDPDATQFIE
1770	1780	1790	1800	1810	1820	1830	1840
FSKLSDFAAA	LDPPLLIAKP	NKVQLIAMDL	PMVSGDRIHC	LDILFAFTKR	VLGESGEMDA	LRIQMEDRFM	ASNPSKVSYE
1850	1860	1870	1880	1890	1900	1910	1920
PITTTLKRKQ	EEVSAAIIQR	NFRCYLLKQR	LKNISSNYNK	EAIKGRIDLP	IKQDMIIDKL	NGNSTPEKTD	GSSSTTSPPS
1930	1940	1950	1960				
YDSVTKPDKE	KFEKDKPEKE	SKGKEVRENQ	K				

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2349	1	1073.7513	-75.47	3	59.7	10.2	2	675-699	R.QKCPPCWYRFANVFLIWDCCDAWLK.V	Carbamidomethyl: 6, 19

Detailed Protein Report

Protein 1657: protein lin-54 homolog isoform b [Homo sapiens]

Accession:	gi|169234721	**Score:**	10.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	56.2
Database Date:	2015-11-30	**pI:**	10.6
		Sequence Coverage [%]:	2.5
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|573014793	refseq_human (refseq_human_20140103.fasta)	protein lin-54 homolog isoform b [Homo sapiens]
gi|169234723	refseq_human (refseq_human_20140103.fasta)	protein lin-54 homolog isoform b [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MEVVPAEIAK KPRTPTSGPV ITKLIFAKPI NSKAVTGQTT QVSPPVIAGR VLSQSTPGTP SKTITISESG VIGSTLNSTT
        90        100        110        120        130        140        150        160
QTPNKIAISP LKSPNKAVKS TVQTITVGGV STSQFKTIIP LATAPNVQQI QVPGSKFHYV RLVTATSASS STQPVSQNPS
       170        180        190        200        210        220        230        240
TNTQPLQQAK PVVVNTTPVR MSVPIVSAQA VKQVVPKPIN PTSQIVTTSQ PQQRLIMPAT PLPQIQPNLT NLPPGTVLAP
       250        260        270        280        290        300        310        320
APGTGNVGYA VLPAQYVTQL QQSSYVSIAS NSTFTGTSGI QTQARLPFNG IIPSESASRP RKPCNCTKSL CLKLYCDCFA
       330        340        350        360        370        380        390        400
NGEFCNNCNC TNCYNNLEHE NERQKAIKAC LDRNPEAFKP KIGKGKEGES DRRHSKGCNC KRSGCLKNYC ECYEAKIMCS
       410        420        430        440        450        460        470        480
SICKCIGCKN FEESPERKTL MHLADAAEVR VQQQTAAKTK LSSQISDLLT RPTPALNSGG GKLPFTFVTK EVAEATCNCL
       490        500        510        520        530
LAQAEQADKK GKSKAAAERM ILEEFGRCLM SVINSAGKAK SDPCAMNC
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
107	1	504.5800	42.14	3	30.6	10.2	1	405-417	K.CIGCKNFEESPER.K	

Detailed Protein Report

Protein 1658: UPF0687 protein C20orf27 isoform 1 [Homo sapiens]

Accession:	gi|85362737	**Score:**	10.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	21.6
Database Date:	2015-11-30	**pI:**	7.1
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	10.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAAANKGKCL	PGVVGLAQAL	PVGPGRRAIA	AGNKPRVRSI	RFAAGHDAEG	SHSHVHFDEK	LHDSVVMVTQ	ESDSSFLVKV
90	100	110	120	130	140	150	160
GFLKILHRYE	ITFTLPPVHR	LSKDVREAPV	PSLHLKLLSV	VPVPEGYSVK	CEYSAHKEGV	LKEEILLACE	GGTGTCVRVT
170	180	190	200				
VQARVMDRHH	GTPMLLDGVK	CVGAELEYDS	EHSDWHGFD				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2677	1	973.4960	-59.36	2	62.4	10.2	1	7-26	K.GKCLPGVVGLAQALPVGPGR.R	Carbamidomethyl: 3

Detailed Protein Report

Protein 1659: mitochondrial import receptor subunit TOM70 [Homo sapiens]

Accession:	gi|54607135	**Score:**	10.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	67.4
Database Date:	2015-11-30	**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 1660: splicing factor 1 isoform 3 [Homo sapiens]

Accession:	gi|42544123	**Score:**	10.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	59.7
Database Date:	2015-11-30	**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 1661: PREDICTED: glyoxalase domain-containing protein 5 isoform X1 [Homo sapiens]

Accession:	gi|578838023	**Score:**	10.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	13.3
Database Date:	2015-11-30	**pI:**	5.2
		Sequence Coverage [%]:	11.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MTVKSIKDTT	MFYSKILGME	VMTFKEDRKA	LCFGDQKFNL	HEVGKEFEPK	AAHPVPGSLD	ICLITEVPLE	EMIQHLKACD
90	**100**	**110**	**120**				
VPIEEGPVPR	TGAKGPIMSI	YFRDPDRNLI	EVSNYISS				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
786	1	848.9729	36.84	2	38.7	10.2	2	16-29	K.ILGMEVMTFKEDRK.A	

Detailed Protein Report

Protein 1662: tripartite motif-containing protein 3 isoform 1 [Homo sapiens]

Accession:	gi|32454737	**Score:**	10.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	80.8
Database Date:	2015-11-30	**pI:**	9.1
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	3.2
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|351721563	refseq_human (refseq_human_20140103.fasta)	tripartite motif-containing protein 3 isoform 1 [Homo sapiens]
gi|32454739	refseq_human (refseq_human_20140103.fasta)	tripartite motif-containing protein 3 isoform 1 [Homo sapiens]

10	20	30	40	50	60	70	80
MAKREDSPGP	EVQPMDKQFL	VCSICLDRYQ	CPKVLPCLHT	FCERCLQNYI	PAQSLTLSCP	VCRQTSILPE	QGVSALQNNF
90	100	110	120	130	140	150	160
FISSLMEAMQ	QAPDGAHDPE	DPHPLSVVAG	RPLSCPNHEG	KTMEFYCEAC	ETAMCGECRA	GEHREHGTVL	LRDVVEQHKA
170	180	190	200	210	220	230	240
ALQRQLEAVR	GRLPQLSAAI	ALVGGISQQL	QERKAEALAQ	ISAAFEDLEQ	ALQQRKQALV	SDLETICGAK	QKVLQSQLDT
250	260	270	280	290	300	310	320
LRQGQEHIGS	SCSFAEQALR	LGSAPEVLLV	RKHMRERLAA	LAAQAFPERP	HENAQLELVL	EVDGLRRSVL	NLGALLTTSA
330	340	350	360	370	380	390	400
TAHETVATGE	GLRQALVGQP	ASLTVTTKDK	DGRLVRTGSA	ELRAEITGPD	GTRLPVPVVD	HKNGTYELVY	TARTEGELLL
410	420	430	440	450	460	470	480
SVLLYGQPVR	GSPFRVRALR	PGDLPPSPDD	VKRRVKSPGG	PGSHVRQKAV	RRPSSMYSTG	GKRKDNPIED	ELVFRVGSRG
490	500	510	520	530	540	550	560
REKGEFTNLQ	GVSAASSGRI	VVADSNNQCI	QVFSNEGQFK	FRFGVRGRSP	GQLQRPTGVA	VDTNGDIIVA	DYDNRWVSIF
570	580	590	600	610	620	630	640
SPEGKFKTKI	GAGRLMGPKG	VAVDRNGHII	VVDNKSCCVF	TFQPNGKLVG	RFGGRGATDR	HFAGPHFVAV	NNKNEIVVTD
650	660	670	680	690	700	710	720
FHNHSVKVYS	ADGEFLFKFG	SHGEGNGQFN	APTGVAVDSN	GNIIVADWGN	SRIQVFDSSG	SFLSYINTSA	EPLYGPQGLA
730	740	750					
LTSDGHVVVA	DAGNHCFKAY	RYLQ					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1313	1	946.1922	94.03	3	44.9	10.2	1	5-28	R.EDSPGPEVQPMDKQFLVCSICLDR.Y	Carbamidomethyl: 18, 21; Oxidation: 11

Detailed Protein Report

Protein 1663: PREDICTED: choriogonadotropin subunit beta variant 1 isoform X1 [Homo sapiens]

Accession:	gi|530415623	**Score:**	10.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	15.3
Database Date:	2015-11-30	**pI:**	10.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	16.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGGTWASKEP	LRPRCRPINA	TLAVEKEGCP	VCITVNTTIC	AGYCPTMTRV	LQGVLPALPQ	VVCNYRDVRF	ESIRLPGCPR
90	**100**	**110**	**120**	**130**	**140**	**150**	
GVNPVVSYAV	ALSCQCALCR	RSTTDCGGPK	DHPLTCDDPR	FQDSSSSKAP	PPSLPSPSRL	PGP	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
175	1	1302.5158	-43.75	2	30.9	10.2	0	27-49	K.EGCPVCITVNTTICAGYCPTMTR.V	Carbamidomethyl: 3, 14, 18

Detailed Protein Report

Protein 1664: ADNP homeobox protein 2 [Homo sapiens]

Accession:	gi|7662346	**Score:**	10.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	122.8
Database Date:	2015-11-30	**pI:**	10.1
		Sequence Coverage [%]:	1.3
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530414111	refseq_human (refseq_human_20140103.fasta)	PREDICTED: ADNP homeobox protein 2 isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MFQIPVENLD	NIRKVRKKVK	GILVDIGLDS	CKELLKDLKG	FDPGEKYFHN	TSWGDVSLWE	PSGKKVRYRT	KPYCCGLCKY
90	100	110	120	130	140	150	160
STKVLTSFKN	HLHRYHEDEI	DQELVIPCPN	CVFASQPKVV	GRHFRMFHAP	VRKVQNYTVN	ILGETKSSRS	DVISFTCLKC
170	180	190	200	210	220	230	240
NFSNTLYYSM	KKHVLVAHFH	YLINSYFGLR	TEEMGEQPKT	NDTVSIEKIP	PPDKYYCKKC	NANASSQDAL	MYHILTSDIH
250	260	270	280	290	300	310	320
RDLENKLRSV	ISEHIKRTGL	LKQTHIAPKP	AAHLAAPANG	SAPSAPAQPP	CFHLALPQNS	PSPAAGQPVT	VAQGAPGSLT
330	340	350	360	370	380	390	400
HSPPAAGQSH	MTLVSSPLPV	GQNSLTLQPP	APQPVFLSHG	VPLHQSVNPP	VLPLSQPVGP	VNKSVGTSVL	PINQTVRPGV
410	420	430	440	450	460	470	480
LPLTQPVGPI	NRPVGPGVLP	VSPSVTPGVL	QAVSPGVLSV	SRAVPSGVLP	AGQMTPAGQM	TPAGVIPGQT	ATSGVLPTGQ
490	500	510	520	530	540	550	560
MVQSGVLPVG	QTAPSRVLPP	GQTAPLRVIS	AGQVVPSGLL	SPNQTVSSSA	VVPVNQGVNS	GVLQLSQPVV	SGVLPVGQPV
570	580	590	600	610	620	630	640
RPGVLQLNQT	VGTNILPVNQ	PVRPGASQNT	TFLTSGSILR	QLIPTGKQVN	GIPTYTLAPV	SVTLPVPPGG	LATVAPPQMP
650	660	670	680	690	700	710	720
IQLLPSGAAA	PMAGSMPGMP	SPPVLVNAAQ	SVFVQASSSA	ADTNQVLKQA	KQWKTCPVCN	ELFPSNVYQV	HMEVAHKHSE
730	740	750	760	770	780	790	800
SKSGEKLEPE	KLAACAPFLK	WMREKTVRCL	SCKCLVSEEE	LIHHLLMHGL	GCLFCPCTFH	DIKGLSEHSR	NRHLGKKKLP
810	820	830	840	850	860	870	880
MDYSNRGFQL	DVDANGNLLF	PHLDFITILP	KEKLGEREVY	LAILAGIHSK	SLVPVYVKVR	PQAEGTPGST	GKRVSTCPFC
890	900	910	920	930	940	950	960
FGPFVTTEAY	ELHLKERHHI	MPTVHTVLKS	PAFKCIHCCG	VYTGNMTLAA	IAVHLVRCRS	APKDSSSDLQ	AQPGFIHNSE
970	980	990	1000	1010	1020	1030	1040
LLLVSGEVMH	DSSFSVKRKL	PDGHLGAEDQ	RHGEEQPPIL	NADAAPGPEK	VTSVVPFKRQ	RNESRTEGPI	VKDEALQILA
1050	1060	1070	1080	1090	1100	1110	1120
LDPKKYEGRS	YEEKKQFLKD	YFHKKPYPSK	KEIELLSSLF	WVWKIDVASF	FGKRRYICMK	AIKNHKPSVL	LGFDMSELKN
1130	1140						
VKHRLNFEYE	P						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
951	1	770.8434	-90.42	2	40.7	10.2	1	859-873	K.VRPQAEGTPGSTGKR.V	

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Detailed Protein Report

Protein 1665: 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

mdown:qdown	**Median:**	0.69	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	1.02	**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		Wdown:Qdown 1.02 mdown:qdown 0.69

Detailed Protein Report

Protein 1666: transcription initiation factor TFIID subunit 1-like [Homo sapiens]

Accession:	gi|24429572	**Score:**	10.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	207.2
Database Date:	2015-11-30	**pI:**	5.1
		Sequence Coverage [%]:	0.9
		No. of unique Peptides:	1

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

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

Detailed Protein Report

	Cmpds.		[ppm]		[min]					
1092	1	839.4008	43.81	2	42.4	10.2	0	1050- 1065	R.TMSTEQAHSGEGPMSK.F	

Detailed Protein Report

Protein 1667: kin of IRRE-like protein 1 isoform 2 precursor [Homo sapiens]

Accession:	gi|556503362	**Score:**	10.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	72.7
Database Date:	2015-11-30	**pI:**	5.4
		Sequence Coverage [%]:	2.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLSLLVWILT	LSDTFSQVPP	EDTRIDGGPV	ILLQAGTPHN	LTCRAFNAKP	AATIIWFRDG	TQQEGAVAST	ELLKDGKRET
90	100	110	120	130	140	150	160
TVSQLLINPT	DLDIGRVFTC	RSMNEAIPSG	KETSIELDVH	HPPTVTLSIE	PQTVQEGERV	VFTCQATANP	EILGYRWAKG
170	180	190	200	210	220	230	240
GFLIEDAHES	RYETNVDYSF	FTEPVSCEVH	NKVGSTNVST	LVNVHFAPRI	VVDPKPTTTD	IGSDVTLTCV	WVGNPPLTLT
250	260	270	280	290	300	310	320
WTKKDSNMVL	SNSNQLLLKS	VTQADAGTYT	CRAIVPRIGV	AEREVPLYVN	GPPIISSEAV	QYAVRGDGGK	VECFIGSTPP
330	340	350	360	370	380	390	400
PDRIAWAWKE	NFLEVGTLER	YTVERTNSGS	GVLSTLTINN	VMEADFQTHY	NCTAWNSFGP	GTAIIQLEER	EVLPVGIIAG
410	420	430	440	450	460	470	480
ATIGASILLI	FFFIALVFFL	YRRRKGSRKD	VTLRKLDIKV	ETVNREPLTM	HSDREDDTAS	VSTATRVMKA	IYSSFKDDVD
490	500	510	520	530	540	550	560
LKQDLRCDTI	DTREEYEMKD	PTNGYYNVRA	HEDRPSSRAV	LYADYRAPGP	ARFDGRPSSR	LSHSSGYAQL	NTYSRGPASD
570	580	590	600	610	620	630	640
YGPEPTPPGP	AAPAGTDTTS	QLSYENYEKF	NSHPFPGAAG	YPTYRLGYPQ	APPSGLERTP	YEAYDPIGKY	ATATRFSYTS
650	660						
QHSDYGQRFQ	QRMQTHV						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1905	1	891.3754	-53.76	2	52.5	10.2	0	590-605	K.FNSHPFPGAAGYPTYR.L	

Protein 1668: beta-defensin 108B precursor [Homo sapiens]

Accession:	gi|50344744	**Score:**	10.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	8.3
Database Date:	2015-11-30	**pI:**	10.5
		Sequence Coverage [%]:	28.8
		No. of unique Peptides:	1

```
         10         20         30         40         50         60         70         80
MRIAVLLFAI FFFMSQVLPA RGKFKEICER PNGSCRDFCL ETEIHVGRCL NSQPCCLPLG HQPRIESTTP KKD
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
713	1	824.1368	3.71	3	37.5	10.2	1	1-21	-.MRIAVLLFAIFFFMSQVLPAR.G	

Detailed Protein Report

Protein 1669: noggin precursor [Homo sapiens]

Accession:	gi|4885523	**Score:**	10.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	25.8
Database Date:	2015-11-30	**pI:**	10.2
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	6.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MERCPSLGVT	LYALVVVLGL	RATPAGGQHY	LHIRPAPSDN	LPLVDLIEHP	DPIFDPKEKD	LNETLLRSLL	GGHYDPGFMA
90	100	110	120	130	140	150	160
TSPPEDRPGG	GGGAAGGAED	LAELDQLLRQ	RPSGAMPSEI	KGLEFSEGLA	QGKKQRLSKK	LRRKLQMWLW	SQTFCPVLYA
170	180	190	200	210	220	230	240
WNDLGSRFWP	RYVKVGSCFS	KRSCSVPEGM	VCKPSKSVHL	TVLRWRCQRR	GGQRCGWIPI	QYPIISECKC	SC

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2199	1	869.3168	-104.52	2	56.0	10.2	1	182-196	K.RSCSVPEGMVCKPSK.S	Carbamidomethyl: 3, 11; Oxidation: 9

Detailed Protein Report

Protein 1670: **PREDICTED: dual specificity mitogen-activated protein kinase kinase 6 isoform X1 [Homo sapiens]**

Accession:	gi|530412539	**Score:**	10.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	31.3
Database Date:	2015-11-30	**pI:**	6.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	5.0
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578831139	refseq_human (refseq_human_20140103.fasta)	PREDICTED: dual specificity mitogen-activated protein kinase kinase 6 isoform X4 [Homo sapiens]
gi|530412543	refseq_human (refseq_human_20140103.fasta)	PREDICTED: dual specificity mitogen-activated protein kinase kinase 6 isoform X3 [Homo sapiens]
gi|530412541	refseq_human (refseq_human_20140103.fasta)	PREDICTED: dual specificity mitogen-activated protein kinase kinase 6 isoform X2 [Homo sapiens]

10	20	30	40	50	60	70	80
MELGRGAYGV	VEKMRHVPSG	QIMAVKRIRA	TVNSQEQKRL	LMDLDISMRT	VDCPFTVTFY	GALFREGDVW	ICMELMDTSL
90	100	110	120	130	140	150	160
DKFYKQVIDK	GQTIPEDILG	KIAVSIVKAL	EHLHSKLSVI	HRDVKPSNVL	INALGQVKMC	DFGISGYLVD	SVAKTIDAGC
170	180	190	200	210	220	230	240
KPYMAPERIN	PELNQKGYSV	KSDIWSLGIT	MIELAILRFP	YDSWGTPFQQ	LKQVVEEPSP	QLPADKFSAE	FVDFTSQCLK
250	260	270	280				
KNSKERPTYP	ELMQHPFFTL	HESKGTDVAS	FVKLILGD				

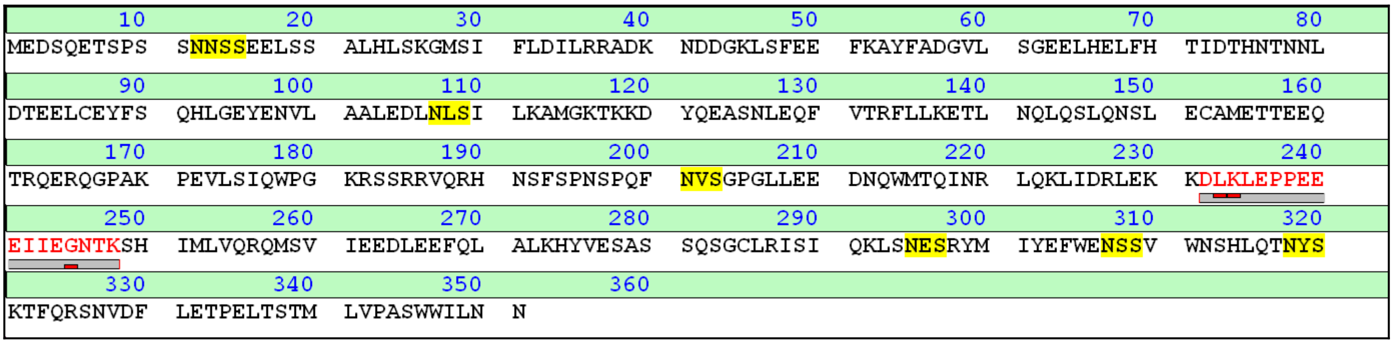
Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2791	1	813.3853	-67.23	2	64.0	10.2	2	14-27	K.MRHVPSGQIMAVKR.I	Oxidation: 10

Detailed Protein Report

Protein 1671: N-terminal EF-hand calcium-binding protein 1 [Homo sapiens]

Accession: gi|24308279
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 10.2
MW [kDa]: 40.5
pI: 4.7
Sequence Coverage [%]: 4.8
No. of unique Peptides: 1



10	20	30	40	50	60	70	80
MEDSQETSPS	SNNSSEELSS	ALHLSKGMSI	FLDILRRADK	NDDGKLSFEE	FKAYFADGVL	SGEELHELFH	TIDTHNTNNL
90	100	110	120	130	140	150	160
DTEELCEYFS	QHLGEYENVL	AALEDLNLSI	LKAMGKTKKD	YQEASNLEQF	VTRFLLKETL	NQLQSLQNSL	ECAMETTEEQ
170	180	190	200	210	220	230	240
TRQERQGPAK	PEVLSIQWPG	KRSSRRVQRH	NSFSPNSPQF	NVSGPGLLEE	DNQWMTQINR	LQKLIDRLEK	KDLKLEPPEE
250	260	270	280	290	300	310	320
EIIEGNTKSH	IMLVQRQMSV	IEEDLEEFQL	ALKHYVESAS	SQSGCLRISI	QKLSNESRYM	IYEFWENSSV	WNSHLQTNYS
330	340	350	360				
KTFQRSNVDF	LETPELTSTM	LVPASWWILN	N				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2070	1	977.3619	-145.82	2	54.4	10.2	1	232-248	K.DLKLEPPEEEIIEGNTK.S	

Detailed Protein Report

Protein 1672: ribonucleases P/MRP protein subunit POP1 [Homo sapiens]

Accession:	gi|225007648	**Score:**	10.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	114.6
Database Date:	2015-11-30	**pI:**	10.3
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	1.0
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|225007652	refseq_human (refseq_human_20140103.fasta)	ribonucleases P/MRP protein subunit POP1 [Homo sapiens]
gi|225007650	refseq_human (refseq_human_20140103.fasta)	ribonucleases P/MRP protein subunit POP1 [Homo sapiens]

10	20	30	40	50	60	70	80
MSNAKERKHA	KKMRNQPTNV	TLSSGFVADR	GVKHHSGGEK	PFQAQKQEPH	PGTSRQRQTR	VNPHSLPDPE	VNEQSSSKGM
90	100	110	120	130	140	150	160
FRKKGGWKAG	PEGTSQEIPK	YITASTFAQA	RAAEISAMLK	AVTQKSSNSL	VFQTLPRHMR	RRAMSHNVKR	LPRRLQEIAQ
170	180	190	200	210	220	230	240
KEAEKAVHQK	KEHSKNKCHK	ARRCHMNRTL	EFNRRQKKNI	WLETHIWHAK	RFHMVKKWGY	CLGERPTVKS	HRACYRAMTN
250	260	270	280	290	300	310	320
RCLLQDLSYY	CCLELKGKEE	EILKALSGMC	NIDTGLTFAA	VHCLSGKRQG	SLVLYRVNKY	PREMLGPVTF	IWKSQRTPGD
330	340	350	360	370	380	390	400
PSESRQLWIW	LHPTLKQDIL	EEIKAACQCV	EPIKSAVCIA	DPLPTPSQEK	SQTELPDEKI	GKKRKRKDDG	ENAKPIKKII
410	420	430	440	450	460	470	480
GDGTRDPCLP	YSWISPTTGI	IISDLTMEMN	RFRLIGPLSH	SILTEAIKAA	SVHTVGEDTE	ETPHRWWIET	CKKPDSVSLH
490	500	510	520	530	540	550	560
CRQEAIFELL	GGITSPAEIP	AGTILGLTVG	DPRINLPQKK	SKALPNPEKC	QDNEKVRQLL	LEGVPVECTH	SFIWNQDICK
570	580	590	600	610	620	630	640
SVTENKISDQ	DLNRMRSELL	VPGSQLILGP	HESKIPILLI	QQPGKVTGED	RLGWGSGWDV	LLPKGWGMAF	WIPFIYRGVR
650	660	670	680	690	700	710	720
VGGLKESAVH	SQYKRSPNVP	GDFPDCPAGM	LFAEEQAKNL	LEKYKRRPPA	KRPNYVKLGT	LAPFCCPWEQ	LTQDWESRVQ
730	740	750	760	770	780	790	800
AYEEPSVASS	PNGKESDLRR	SEVPCAPMPK	KTHQPSDEVG	TSIEHPREAE	EVMDAGCQES	AGPERITDQE	ASENHVAATG
810	820	830	840	850	860	870	880
SHLCVLRSRK	LLKQLSAWCG	PSSEDSRGGR	RAPGRGQQGL	TREACLSILG	HFPRALVWVS	LSLLSKGSPE	PHTMICVPAK
890	900	910	920	930	940	950	960
EDFLQLHEDW	HYCGPQESKH	SDPFRSKILK	QKEKKKREKR	QKPGRASSDG	PAGEEPVAGQ	EALTLGLWSG	PLPRVTLHCS
970	980	990	1000	1010	1020	1030	
RTLLGFVTQG	DFSMAVGCGE	ALGFVSLTGL	LDMLSSQPAA	QRGLVLLRPP	ASLQYRFARI	AIEV	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2209	1	1131.3087	-184.38	1	56.1	10.2	0	741-750	R.SEVPCAPMPK.K	Carbamidomethyl: 5; Oxidation: 8

Detailed Protein Report

Protein 1673: dual specificity protein phosphatase 3 [Homo sapiens]

Accession:	gi|4758208	**Score:**	10.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	20.5
Database Date:	2015-11-30	**pI:**	8.9
		Sequence Coverage [%]:	9.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSGSFELSVQ	DLNDLLSDGS	GCYSLPSQPC	NEVTPRIYVG	NASVAQDIPK	LQKLGITHVL	NAAEGRSFMH	VNTNANFYKD
90	100	110	120	130	140	150	160
SGITYLGIKA	NDTQEFNLSA	YFERAADFID	QALAQKNGRV	LVHCREGYSR	SPTLVIAYLM	MRQKMDVKSA	LSIVRQNREI
170	180	190					
GPNDGFLAQL	CQLNDRLAKE	GKLKP					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2739	1	922.4796	-41.08	2	65.5	10.2	1	37-53	R.IYVGNASVAQDIPKLQK.L	

Detailed Protein Report

Protein 1674: cullin-1 [Homo sapiens]

Accession:	gi|32307161	**Score:**	10.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	89.6
Database Date:	2015-11-30	**pI:**	8.9
		Sequence Coverage [%]:	1.4
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530387140	refseq_human (refseq_human_20140103.fasta)	PREDICTED: cullin-1 isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MSSTRSQNPH	GLKQIGLDQI	WDDLRAGIQQ	VYTRQSMAKS	RYMELYTHVY	NYCTSVHQSN	QARGAGVPPS	KSKKGQTPGG
90	100	110	120	130	140	150	160
AQFVGLELYK	RLKEFLKNYL	TNLLKDGEDL	MDESVLKFYT	QQWEDYRFSS	KVLNGICAYL	NRHWVRRECD	EGRKGIYEIY
170	180	190	200	210	220	230	240
SLALVTWRDC	LFRPLNKQVT	NAVLKLIEKE	RNGETINTRL	ISGVVQSYVE	LGLNEDDAFA	KGPTLTVYKE	SFESQFLADT
250	260	270	280	290	300	310	320
ERFYTRESTE	FLQQNPVTEY	MKKAEARLLE	EQRRVQVYLH	ESTQDELARK	CEQVLIEKHL	EIFHTEFQNL	LDADKNEDLG
330	340	350	360	370	380	390	400
RMYNLVSRIQ	DGLGELKKLL	ETHIHNQGLA	AIEKCGEAAL	NDPKMYVQTV	LDVHKKYNAL	VMSAFNNDAG	FVAALDKACG
410	420	430	440	450	460	470	480
RFINNNAVTK	MAQSSSKSPE	LLARYCDSLL	KKSSKNPEEA	ELEDTLNQVM	VVFKYIEDKD	VFQKFYAKML	AKRLVHQNSA
490	500	510	520	530	540	550	560
SDDAEASMIS	KLKQACGFEY	TSKLQRMFQD	IGVSKDLNEQ	FKKHLTNSEP	LDLDFSIQVL	SSGSWPFQQS	CTFALPSELE
570	580	590	600	610	620	630	640
RSYQRFTAFY	ASRHSGRKLT	WLYQLSKGEL	VTNCFKNRYT	LQASTFQMAI	LLQYNTEDAY	TVQQLTDSTQ	IKMDILAQVL
650	660	670	680	690	700	710	720
QILLKSKLLV	LEDENANVDE	VELKPDTLIK	LYLGYKNKKL	RVNINVPMKT	EQKQEQETTH	KNIEEDRKLL	IQAAIVRIMK
730	740	750	760	770	780		
MRKVLKHQQL	LGEVLTQLSS	RFKPRVPVIK	KCIDILIEKE	YLERVDGEKD	TYSYLA		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1171	1	666.8327	-29.92	2	43.3	10.2	0	365-375	K.MYVQTVLDVHK.K	

Protein 1675: 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

mdown:qdown	**Median:**	0.33	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	1.10	**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		Wdown:Qdown 1.10 mdown:qdown 0.33

Detailed Protein Report

Protein 1676: 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 1677: sodium/potassium/calcium exchanger 3 precursor [Homo sapiens]

Accession: gi|31563526

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Modification(s): Oxidation

Score: 10.1

MW [kDa]: 71.9

pI: 5.1

Sequence Coverage [%]: 1.6

No. of unique Peptides: 1

Quantitation

mdown:qdown	**Median:**	0.75	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	1.04	**CV:**	0.00 %	**No. of Peptides:**	1

10	20	30	40	50	60	70	80
MRPSGDEDRA	RRRRRRRRRR	DLLLSQLCFL	ASVALLLWSL	SSLREQKELD	LMDLVGEDRK	WMMARKLMQV	NDTLTSEDAG
90	100	110	120	130	140	150	160
LRNSKNCTEP	ALHEFPNDIF	TNEDRRQGAV	VLHVLCAIYM	FYALAIVCDD	FFVPSLEKIC	ERLHLSEDVA	GATFMAAGSS
170	180	190	200	210	220	230	240
APELFTSVIG	VFITKGDVGV	GTIVGSAVFN	ILCIIGVCGL	FAGQVVALSS	WCLLRDSIYY	TLSVIALIVF	IYDEKVSWWE
250	260	270	280	290	300	310	320
SLVLVLMYLI	YIVIMKYNAC	IHQCFERRTK	GAGNMVNGLA	NNAEIDDSSN	CDATVVLLKK	ANFHRKASVI	MVDELLSAYP
330	340	350	360	370	380	390	400
HQLSFSEAGL	RIMITSHFPP	KTRLSMASRM	LINERQRLIN	SRAYTNGESE	VAIKIPIKHT	VENGTGPSSA	PDRGVNGTRR
410	420	430	440	450	460	470	480
DDVVAEAGNE	TENENEDNEN	DEEEEEDEDD	DEGPYTPFDT	PSGKLETVKW	AFTWPLSFVL	YFTVPNCNKP	RWEKWFMVTF
490	500	510	520	530	540	550	560
ASSTLWIAAF	SYMMVWMVTI	IGYTLGIPDV	IMGITFLAAG	TSVPDCMASL	IVARQGMGDM	AVSNSIGSNV	FDILIGLGLP
570	580	590	600	610	620	630	640
WALQTLAVDY	GSYIRLNSRG	LIYSVGLLLA	SVFVTVFGVH	LNKWQLDKKL	GCGCLLLYGV	FLCFSIMTEF	NVFTFVNLPM
650							
CGDH							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1276	1	593.6730	-244.29	2	44.5	10.1	0	332-341	R.IMITSHFPPK.T	Oxidation: 2	mdown:qdown 0.75 Wdown:Qdown 1.04

Detailed Protein Report

Protein 1678: ranBP-type and C3HC4-type zinc finger-containing protein 1 isoform 1 [Homo sapiens]

Accession:	gi|5454168	**Score:**	10.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	52.9
Database Date:	2015-11-30	**pI:**	5.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGTATPDGRE	DQERLWVSVE	DAQMHTVTIW	LTVRPDMTVA	SLKDMVFLDY	GFPPVLQQWV	IGQRLARDQE	TLHSHGVRQN
90	100	110	120	130	140	150	160
GDSAYLYLLS	ARNTSLNPQE	LQRERQLRML	EDLGFKDLTL	QPRGPLEPGP	PKPGVPQEPG	RGQPDAVPEP	PPVGWQCPGC
170	180	190	200	210	220	230	240
TFINKPTRPG	CEMCCRARPE	AYQVPASYQP	DEEERARLAG	EEEALRQYQQ	RKQQQQEGNY	LQHVQLDQRS	LVLNTEPAEC
250	260	270	280	290	300	310	320
PVCYSVLAPG	EAVVLRECLH	TFCRECLQGT	IRNSQEAEVS	CPFIDNTYSC	SGKLLEREIK	ALLTPEDYQR	FLDLGISIAE
330	340	350	360	370	380	390	400
NRSAFSYHCK	TPDCKGWCFF	EDDVNEFTCP	VCFHVNCLLC	KAIHEQMNCK	EYQEDLALRA	QNDVAARQTT	EMLKVMLQQG
410	420	430	440	450	460	470	
EAMRCPQCQI	VVQKKDGCDW	IRCTVCHTEI	CWVTKGPRWG	PGGPGDTSGG	CRCRVNGIPC	HPSCQNCH	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1428	1	783.1753	-189.81	2	46.6	10.1	0	455-468	R.VNGIPCHPSCQNCH.-	Carbamidomethyl: 13

Detailed Protein Report

Protein 1679: 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

mdown:qdown	**Median:**	0.16	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.20	**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	Wdown:Qdown 0.20 mdown:qdown 0.16

Detailed Protein Report

Protein 1680: 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

Quantitation

mdown:qdown	**Median:** 0.32	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:** 0.30	**CV:**	0.00 %	**No. of 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	Ratios
315	1	881.3242	-98.81	3	33.3	10.1	1	1-24	-. MSGELAVCRVTEGASCMSELAVW V	Carbamidomethyl: 8	mdown:qdown 0.32 Wdown:Qdown 0.30

Detailed Protein Report

Protein 1681: cytochrome c oxidase assembly factor 5 [Homo sapiens]

Accession: gi|56118949
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 10.1
MW [kDa]: 8.4
pI: 10.0
Sequence Coverage [%]: 20.3
No. of unique Peptides: 1

```
         10         20         30         40         50         60         70         80
MPKYYEDKPQ GGACAGLKED LGACLLQSDC VVQEGKSPRQ CLKEGYCNSL KYAFFECKRS VLDNRARFRG RKGY
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2682	1	958.4638	44.34	2	62.4	10.1	1	44-58	K.EGYCNSLKYAFFECK.R	Carbamidomethyl: 4, 14

Detailed Protein Report

Protein 1682: PREDICTED: uncharacterized protein LOC101930265 [Homo sapiens]

Accession:	gi|530355909	**Score:**	10.1
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 [%]:**	3.6
		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 1683: **serpin A12 precursor [Homo sapiens]**

Accession:	gi|27777657	**Score:**	10.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	47.1
Database Date:	2015-11-30	**pI:**	9.8
		Sequence Coverage [%]:	1.9
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530403137	refseq_human (refseq_human_20140103.fasta)	PREDICTED: serpin A12 isoform X1 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MNPTLGLAIF LAVLLTVKGL LKPSFSPRNY KALSEVQGWK QRMAAKELAR QNMDLGFKLL KKLAFYNPGR NIFLSPLSIS

        90        100        110        120        130        140        150        160
TAFSMLCLGA QDSTLDEIKQ GFNFRKMPEK DLHEGFHYII HELTQKTQDL KLSIGNTLFI DQRLQPQRKF LEDAKNFYSA

       170        180        190        200        210        220        230        240
ETILTNFQNL EMAQKQINDF ISQKTHGKIN NLIENIDPGT VMLLANYIFF RARWKHEFDP NVTKEEDFFL EKNSSVKVPM

       250        260        270        280        290        300        310        320
MFRSGIYQVG YDDKLSCTIL EIPYQKNITA IFILPDEGKL KHLEKGLQVD TFSRWKTLLS RRVVDVSVPR LHMTGTFDLK

       330        340        350        360        370        380        390        400
KTLSYIGVSK IFEEHGDLTK IAPHRSLKVG EAVHKAELKM DERGTEGAAG TGAQTLPMET PLVVKIDKPY LLLIYSEKIP

       410        420
SVLFLGKIVN PIGK
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
462	1	435.6354	-276.28	2	34.4	10.1	0	303-310	R.VVDVSVPR.L	

Protein 1684: probable gluconokinase isoform 3 [Homo sapiens]

Accession: gi|379642551
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 10.1
MW [kDa]: 15.7
pI: 5.9
Sequence Coverage [%]: 5.0
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MGKGIPLNDQ	DRIPWLCNLH	DILLRDVASG	QRVVLACSAL	KKTYRDILTQ	GKDGVALKCE	ESGKEAKQAE	MQLLVVHLSG
90	**100**	**110**	**120**	**130**	**140**	**150**	
SFEVISGRLL	KREGHFMPPE	LLQSQFETLE	PPAAPENFIQ	ISVDKNVSEI	IATIMETLKM	K	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
702	1	387.7050	-42.29	2	37.6	10.1	0	46-52	R.DILTQGK.D	

Detailed Protein Report

Protein 1685: PREDICTED: outer dense fiber protein 3B isoform X8 [Homo sapiens]

Accession: gi|578837697

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Score: 10.1

MW [kDa]: 21.9

pI: 11.9

Sequence Coverage [%]: 8.8

No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MGSDAWVGLW	RPHRPRGPIA	AHYGGPGPKY	KLPPNTGRYF	PERAGNATYP	SAPRHTIAPR	NWGVQAEQQS	PGPAAYTVPS
90	100	110	120	130	140	150	160
LLGPRVIGKV	SAPTCSIYGR	RAAGSFFEDL	SKVGEGPGRT	QGVPGPRQWR	RQPAPSALSQ	TPGPCAYQVV	SPGVYKSRAP
170	180	190	200	210			
QFTILARTSL	PQDNTRKPGP	AAYNVDQVAW	SPGSRVRVRR	VGRA			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1116	1	645.3234	-28.32	3	42.6	10.1	2	113-130	K.VGEGPGRTQGVPGPRQWR.R	

Detailed Protein Report

Protein 1686: PREDICTED: zinc finger CCCH domain-containing protein 4 isoform X3 [Homo sapiens]

Accession:	gi|530416049	**Score:**	10.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	135.2
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
MLRGREDGEL	EEGELEDDGA	EETQDTSGGP	ERSRKEKGEK	HHSDSDEEKS	HRRLKRKRKK	EREKEKRRSK	KRRKSKHKRH
90	100	110	120	130	140	150	160
ASSSDDFSDF	SDDSDFSPSE	KGHRKYREYS	PPYAPSHQQY	PPSHATPLPK	KAYSKMDSKS	YGMYEDYENE	QYGEYEGDEE
170	180	190	200	210	220	230	240
EDMGKEDYDD	FTKELNQYRR	AKEGSSRGRG	SRGRGRGYRG	RGSRGGSRGR	GMGRGSRGRG	RGSMGGDHPE	DEEDFYEEEM
250	260	270	280	290	300	310	320
DYGESEEPMG	DDDYDEYSKE	LNQYRRSKDS	RGRGLSRGRG	RGSRGRGKGM	GRGRGRGGSR	GGMNKGGMND	DEDFYDEDMG
330	340	350	360	370	380	390	400
DGGGGSYRSR	DHDKPHQQSD	KKGKVICKYF	VEGRCTWGDH	CNFSHDIELP	KKRELCKFYI	TGFCARAENC	PYMHGDFPCK
410	420	430	440	450	460	470	480
LYHTTGNCIN	GDDCMFSHDP	LTEETRELLD	KMLADDAEAG	AEDEKEVEEL	KKQGINPLPK	PPPGVGLLPT	PPRPPGPQAP
490	500	510	520	530	540	550	560
TSPNGRPMQG	GPPPPPPPPP	PPPGPPQMPM	PVHEPLSPQQ	LQQQDMYNKK	IPSLFEIVVR	PTGQLAEKLG	VRFPGPGGPP
570	580	590	600	610	620	630	640
GPMGPGPNMG	PPGPMGGPMH	PDMHPDMHPD	MHPDMHADMH	ADMPMGPGMN	PGPPMGPGGP	PMMPYGPGDS	PHSGMMPPIP
650	660	670	680	690	700	710	720
PAQNFYENFY	QQQEGMEMEP	GLLGDAEDYG	HYEELPGEPG	EHLFPEHPLE	PDSFSEGGPP	GRPKPGAGVP	DFLPSAQRAL
730	740	750	760	770	780	790	800
YLRIQQKQQE	EEERARRLAE	SSKQDRENEE	GDTGNWYSSD	EDEGGSSVTS	ILKTLRQQTS	SRPPASVGEL	SSSGLGDPRL
810	820	830	840	850	860	870	880
QKGHPTGSRL	ADPRLSRDPR	LTRHVEASGG	SGPGDSGPSD	PRLARALPTS	KPEGSLHSSP	VGPSSSKGSG	PPPTEEEEGE
890	900	910	920	930	940	950	960
RALREKAVNI	PLDPLPGHPL	RDPRSQLQQF	SHIKKDVTLS	KPSFARTVLW	NPEDLIPLPI	PKQDAVPPVP	AALQSMPTLD
970	980	990	1000	1010	1020	1030	1040
PRLHRAATAG	PPNARQRPGA	STDSSTQGAN	LPDFELLSRI	LKTVNATGSS	AAPGSSDKPS	DPRVRKAPTD	PRLQKPTDST
1050	1060	1070	1080	1090	1100	1110	1120
ASSRAAKPGP	AEAPSPTASP	SGDASPPATA	PYDPRVLAAG	GLGQGGGGGQ	SSVLSGISLY	DPRTPNAGGK	ATEPAADTGA
1130	1140	1150	1160	1170	1180	1190	1200
QPKGAEGNGK	SSASKAKEPP	FVRKSALEQP	ETGKAGADGG	TPTDRYNSYN	RPRPKAAAAP	AATTATPPPE	GAPPQPGVHN
1210	1220	1230	1240	1250	1260		
LPVPTLFGTV	KQTPKTGSGS	PFAGNSPARE	GEQDAASLKD	VFKGFDPTAS	PFCQ		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
924	1	712.6415	-45.15	3	40.0	10.1	1	821-842	R.LTRHVEASGGSGPGDSGPSDPR.L	

Detailed Protein Report

Protein 1687: PREDICTED: nuclear factor NF-kappa-B p100 subunit isoform X3 [Homo sapiens]

Accession:	gi|578819504	**Score:**	10.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	92.6
Database Date:	2015-11-30	**pI:**	5.6
		Sequence Coverage [%]:	1.3
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
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 1688: growth arrest-specific protein 1 precursor [Homo sapiens]

Accession:	gi|167466169	**Score:**	10.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	35.7
Database Date:	2015-11-30	**pI:**	5.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MVAALLGGGG	EARGGTVPGA	WLCLMALLQL	LGSAPRGSGL	AHGRRLICWQ	ALLQCQGEPE	CSYAYNQYAE	ACAPVLAQHG
90	100	110	120	130	140	150	160
GGDAPGAAAA	AFPASAASFS	SRWRCPSHCI	SALIQLNHTR	RGPALEDCDC	AQDENCKSTK	RAIEPCLPRT	SGGGAGGPGA
170	180	190	200	210	220	230	240
GGVMGCTEAR	RRCDRDSRCN	LALSRYLTYC	GKVFNGLRCT	DECRTVIEDM	LAMPKAALLN	DCVCDGLERP	ICESVKENMA
250	260	270	280	290	300	310	320
RLCFGAELGN	GPGSSGSDGG	LDDYYDEDYD	DEQRTGGAGG	EQPLDDDDGV	PHPPRPGSGA	AASGGRGDLP	YGPGRRSSGG
330	340	350					
GGRLAPRGAW	TPLASILLLL	LGPLF					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1959	1	660.8945	-58.20	3	53.0	10.1	1	121-137	R.RGPALEDCDCAQDENCK.S	Carbamidomethyl: 8, 16

Detailed Protein Report

Protein 1689: **PREDICTED: splicing factor, suppressor of white-apricot homolog isoform X1 [Homo sapiens]**

Accession:	gi|578824119	**Score:**	10.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	96.4
Database Date:	2015-11-30	**pI:**	9.4
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MYGASGGRAK	PERKSGAKEE	AGPGGAGGGG	SRVELLVFGY	ACKLFRDDER	ALAQEQGQHL	IPWMGDHKIL	IDRYDGRGHL
90	100	110	120	130	140	150	160
HDLSEYDAEY	STWNRDYQLS	EEEARIEALC	DEERYLALHT	DLLEEEARQE	EEYKRLSEAL	AEDGSYNAVG	FTYGSDYYDP
170	180	190	200	210	220	230	240
SEPTEEEEPS	KQREKNEAEN	LEENEEPFVA	PLGLSVPSDV	ELPPTAKMHA	IIERTASFVC	RQGAQFEIML	KAKQARNSQF
250	260	270	280	290	300	310	320
DFLRFDHYLN	PYYKFIQKAM	KEGRYTVLAE	NKSDEKKKSG	VSSDNEDDDD	EEDGNYLHPS	LFASKKCNRL	EELMKPLKVV
330	340	350	360	370	380	390	400
DPDHPLAALV	RKAQADSSTP	TPHNADGAPV	QPSQVEYTAD	STVAAMYYSY	YMLPDGTYCL	APPPPGIDVT	TYYSTLPAGV
410	420	430	440	450	460	470	480
TVSNSPGVTT	TAPPPPGTTP	LPPPTTAETS	SGATSTTTTT	SALAPVAAII	PPPPDVQPVI	DKLAEYVARN	GLKFETSVRA
490	500	510	520	530	540	550	560
KNDQRFEFLQ	PWHQYNAYYE	FKKQFFLQKE	GGDSMQAVSA	PEEAPTDSAP	EKPSDAGEDG	APEDAAEVGA	RAGSGGKKEA
570	580	590	600	610	620	630	640
SSSKTVPDGK	LVKAKQKLED	RLAAAAREKL	AQASKESKEK	QLQAERKRKA	ALFLQTLKNP	LPEAEAGKIE	ESPFSVEESS
650	660	670	680	690	700	710	720
TTPCPLLTGG	RPLPTLEVKP	PDRPSSKSKD	PPREEEKEKK	KKKHKKRSRT	RSRSPKYHSS	SKSRSRSHSK	AKHSLPSAYR
730	740	750	760	770	780	790	800
TVRRSRSRSR	SPRRRAHSPE	RRREERSVPT	AYRVSRSPGA	SRKRTRSRSP	HEKKKKRRSR	SRTKSKARSQ	SVSPSKQAAP
810	820	830	840	850	860	870	880
RPAAPAAHSA	HSASVSPVES	RGSSQERSRG	VSQEKEAQIS	SAIVSSVQSK	ITQDLMAKVR	AMLAASKNLQ	TSAS

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2815	1	698.3601	23.69	2	64.3	10.1	1	1-13	-.MYGASGGRAKPER.K	Oxidation: 1

Detailed Protein Report

Protein 1690: PREDICTED: obscurin-like protein 1 isoform X8 [Homo sapiens]

Accession:	gi|530370081	**Score:**	10.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	188.3
Database Date:	2015-11-30	**pI:**	5.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	0.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MKASSGDQGS	PPCFLRFPRP	VRVVSGAEAE	LKCVVLGEPP	PVVVWEKGGQ	QLAASERLSF	PADGAEHGLL	LTAALPTDAG
90	100	110	120	130	140	150	160
VYVCRARNAA	GEAYAAAAVT	VLEPPASDPE	LQPAERPLPS	PGSGEGAPVF	LTGPRSQWVL	RGAEVVLTCR	AGGLPEPTLY
170	180	190	200	210	220	230	240
WEKDGMALDE	VWDSSHFALQ	PGRAEDGPGA	SLALRILAAR	LPDSGVYVCH	ARNAHGHAQA	GALLQVHQPP	ESPPADPDEA
250	260	270	280	290	300	310	320
PAPVVEPLKC	APKTFWVNEG	KHAKFRCYVM	GKPEPEIEWH	WEGRPLLPDR	RRLMYRDRDG	GFVLKVLYCQ	AKDRGLYVCA
330	340	350	360	370	380	390	400
ARNSAGQTLS	AVQLHVKEPR	LRFTRPLQDV	EGREHGIAVL	ECKVPNSRIP	TAWFREDQRL	LPCRKYEQIE	EGTVRRLIIH
410	420	430	440	450	460	470	480
RLKADDDGIY	LCEMRGRVRT	VANVTVKGPI	LKRLPRKLDV	LEGENAVLLV	ETLEAGVEGR	WSRDGEELPV	ICQSSSGHMH
490	500	510	520	530	540	550	560
ALVLPGVTRE	DAGEVTFSLG	NSRTTTLLRV	KCVKHSPPGP	PILAEMFKGH	KNTVLLTWKP	PEPAPETPFI	YRLERQEVGS
570	580	590	600	610	620	630	640
EDWIQCFSIE	KAGAVEVPGD	CVPSEGDYRF	RICTVSGHGR	SPHVVFHGSA	HLVPTARLVA	GLEDVQVYDG	EDAVFSLDLS
650	660	670	680	690	700	710	720
TIIQGTWFLN	GEELKSNEPE	GQVEPGALRY	RIEQKGLQHR	LILHAVKHQD	SGALVGFSCP	GVQDSAALTI	QESPVHILSP
730	740	750	760	770	780	790	800
QDRVSLTFTT	SERVVLTCEL	SRVDFPATWY	KDGQKVEESE	LLVVKMDGRK	HRLILPEAKV	QDSGEFECRT	EGVSAFFGVT
810	820	830	840	850	860	870	880
VQDPPVHIVD	PREHVFVHAI	TSECVMLACE	VDREDAPVRW	YKDGQEVEES	DFVVLENEGP	HRRLVLPATQ	PSDGGEFQCV
890	900	910	920	930	940	950	960
AGDECAYFTV	TITDVSSWIV	YPSGKVYVAA	VRLERVVLTC	ELCRPWAEVR	WTKDGEEVVE	SPALLLQKED	TVRRLVLPAV
970	980	990	1000	1010	1020	1030	1040
QLEDSGEYLC	EIDDESASFT	VTVTEPPVRI	IYPRDEVTLI	AVTLECVVLM	CELSREDAPV	RWYKDGLEVE	ESEALVLERD
1050	1060	1070	1080	1090	1100	1110	1120
GPRCRLVLPA	AQPEDGGEFV	CDAGDDSAFF	TVTVTEPPVQ	FLALETTPSP	LCVAPGEPVV	LSCELSRAGA	PVVWSHNGRP
1130	1140	1150	1160	1170	1180	1190	1200
VQEGEGLELH	AEGPRRVLCI	QAAGPAHAGL	YTCQSGAAPG	APSLSFTVQV	AEPLLVKLVS	ELTPLTVHEG	DDATFRCEVS
1210	1220	1230	1240	1250	1260	1270	1280
PPDADVTWLR	NGAVVTPGPQ	VEMAQNGSSR	ILTLRGCQLG	DAGTVTLRAG	STATSARLHV	RETELLFLRR	LQDVRAEEGQ
1290	1300	1310	1320	1330	1340	1350	1360
DVCLEVETGR	VGAAGAVRWV	RGGQPLPHDS	RLSMAQDGHI	HRLFIHGVIL	ADQGTYGCES	HHDRTLARLS	VRPRQLRVLR
1370	1380	1390	1400	1410	1420	1430	1440
PLEDVTISEG	GSATFQLELS	QEGVTGEWAR	GGVQLYPGPK	CHIHSDGHRH	RLVLNGLGLA	DSGCVSFTAD	SLRCAARLIV
1450	1460	1470	1480	1490	1500	1510	1520
REVPVTIVRG	PHDLEVTEGD	TATFECELSQ	ALADVTWEKD	GNALTPSPRL	RLQALGTRRL	LQLRRCGPSD	AGTYSCAVGT
1530	1540	1550	1560	1570	1580	1590	1600
ARAGPVRLTV	RERTVAVLSE	LRSVSAREGD	GATFECTVSE	VETTGRWELG	GRPLRPGARV	RIRQEGKKHI	LVLSELRAED
1610	1620	1630	1640	1650	1660	1670	1680
AGEVRFQAGP	AQSLALLEVE	ALPLQMCRHP	PREKTVLVGR	RAVLEVTVSR	SGGHVCWLRE	GAELCPGDKY	EMRSHGPTHS
1690	1700	1710	1720	1730			
LVIHDVRPED	QGTYCCQAGQ	DSTHTRLLVE	GFSSLLPLDH	VCLS			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
402	1	538.2257	-26.26	2	34.1	10.1	0	1660-1669	R.EGAELCPGDK.Y	Carbamidomethyl: 6

Detailed Protein Report

Protein 1691: PREDICTED: zinc finger MYM-type protein 2 isoform X7 [Homo sapiens]

Accession:	gi|578824999	**Score:**	10.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	129.3
Database Date:	2015-11-30	**pI:**	6.2
		Sequence Coverage [%]:	1.5
		No. of unique Peptides:	1

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
2179	1	966.3391	-135.18	2	57.4	10.1	2	720-736	R.LGLRCVTCNYCSQLCKK.G	

Detailed Protein Report

Protein 1692: PREDICTED: lon protease homolog 2, peroxisomal isoform X1 [Homo sapiens]

Accession:	gi|530424409	**Score:**	10.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	89.6
Database Date:	2015-11-30	**pI:**	6.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.5
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MSSVSPIQIP SRLPLLLTHE GVLLPGSTMR TSVDSARNLQ LVRSRLLKGT SLQSTILGVI PNTPDPASDA QDLPPLHRIG

        90        100        110        120        130        140        150        160
TAALAVQVVG SNWPKPHYTL LITGLCRFQI VQVLKEKPYP IAEVEQLDRL EEFPNTCKMR EELGELSEQF YKYAVQILDA

       170        180        190        200        210        220        230        240
VSLEERFKMT IPLLVRQIEG LKLLQKTRKP KQDDDKRVIA IRPIRRITHI SGTLEDEDED EDNDDIVMLE KKIRTSSMPE

       250        260        270        280        290        300        310        320
QAHKVCVKEI KRLKKMPQSM PEYALTRNYL ELMVELPWNK STTDRLDIRA ARILLDNDHY AMEKLKKRVL EYLAVRQLKN

       330        340        350        360        370        380        390        400
NLKGPILCFV GPPGVGKTSV GRSVAKTLGR EFHRIALGGV CDQSDIRGHR RTYVGSMPGR IINGLKTVGV NNPVFLLDEV

       410        420        430        440        450        460        470        480
DKLGKSLQGD PAAALLEVLD PEQNHNFTDH YLNVAFDLSQ VLFIATANTT ATIPAALLDR MEIIQVPGYT QEEKIEIAHR

       490        500        510        520        530        540        550        560
HLIPKQLEQH GLTPQQIQIP QVTTLDIITR YTREAGVRSL DRKLGAICRA VAVKVAEGQH KEAKLDRSDV TEREGCREHI

       570        580        590        600        610        620        630        640
LEDEKPESIS DTTDLALPPE MPILIDFHAL KDILGPPMYE MEVSQRLSQP GVAIGLAWTP LGGEIMFVEA SRMDGEGQLT

       650        660        670        680        690        700        710        720
LTGQLGDVMK ESAHLAISWL RSNAKKYQLT NAFGSFDLLD NTDIHLHFPA GAVTKDGPSA GVTIVTCLAS LFSGRLVRSD

       730        740        750        760        770        780        790        800
VAMTGEITLR GLVLPVGGIK DKVLAAHRAG LKQVIIPRRN EKDLEGIPGN VRQDLSFVTA SCLDEVLNAA FDGGFTVKTR

       810
PGLLNSKL
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2792	1	700.9125	87.47	2	63.3	10.1	1	233-244	K.IRTSSMPEQAHK.V	Oxidation: 6

Detailed Protein Report

Protein 1693: PREDICTED: prothymosin alpha-like [Homo sapiens]

Accession: gi|113420837
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 10.1
MW [kDa]: 11.9
pI: 3.7
Sequence Coverage [%]: 16.5
No. of unique Peptides: 1

Alias proteins:

Accession	Name	Description
gi|410172476	refseq_human (refseq_human_20140103.fasta)	PREDICTED: prothymosin alpha-like [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MSDAAVDTSS EIIAKDLKEK KEVVKDAENG RDAPANGNAN EENGEQEADN EVDEEGEESG EEEEEEKEGD GEEEDGDEEE
        90        100        110
AESATGKRAA EDDEDDDVDT KKQKTDKDD
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2007	1	947.3382	-146.89	2	53.7	10.1	1	1-18	-.MSDAAVDTSSEIIAKDLK.E	

Detailed Protein Report

Protein 1694: 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 1695: PREDICTED: EH domain-binding protein 1 isoform X4 [Homo sapiens]

Accession:	gi|530367409	**Score:**	10.1
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

mdown:qdown	**Median:**	4.15	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	1.18	**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
157	1	688.1811	-190.45	2	31.2	10.1	0	558-569	K.HNTNTATPFCNR.Q		Wdown:Qdown 1.18 mdown:qdown 4.15

Detailed Protein Report

Protein 1696: 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 1697: 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

Quantitation

mdown:qdown **Median:** 0.59 **CV:** 0.00 % **No. of 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	Ratios
692	1	454.6453	-240.71	2	38.0	10.1	0	812-818	K.IQTLMFR.N		mdown:qdown 0.59

Detailed Protein Report

Protein 1698: PREDICTED: zinc finger protein 532 isoform X14 [Homo sapiens]

Accession:	gi|578832581	**Score:**	10.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	114.0
Database Date:	2015-11-30	**pI:**	9.7
		Sequence Coverage [%]:	0.9
		No. of unique Peptides:	1

Quantitation

mdown:qdown **Median:** 0.86 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MTMGDMKTPD	FDDLLAAFDI	PDMVDPKAAI	ESGHDDHESH	MKQNAHGEDD	SHAPSSSDVG	VSVIVKNVRN	IDSSEGGEKD
90	100	110	120	130	140	150	160
GHNPTGNGLH	NGFLTASSLD	SYSKDGAKSL	KGDVPASEVT	LKDSTFSQFS	PISSAEEFDD	DEKIEVDDPP	DKEDMRSSFR
170	180	190	200	210	220	230	240
SNVLTGSAPQ	QDYDKLKALG	GENSSKTGLS	TSGNVEKNKA	VKRETEASSI	NLSVYEPFKV	RKAEDKLKES	SDKVLENRVL
250	260	270	280	290	300	310	320
DGKLSSEKND	TSLPSVAPSK	TKSSSKLSSC	IAAIAALSAK	KAASDSCKEP	VANSRESSPL	PKEVNDSPRA	ADKSPESQNL
330	340	350	360	370	380	390	400
IDGTKKPSLK	QPDSPRSISS	ENSSKGSPSS	PAGSTPAIPK	VRIKTIKTSS	GEIKRTVTRV	LPEVDLDSGK	KPSEQTASVM
410	420	430	440	450	460	470	480
ASVTSLLSSP	ASAAVLSSPP	RAPLQSAVVT	NAVSPAELTP	KQVTIKPVAT	AFLPVSAVKT	AGSQVINLKL	ANNTTVKATV
490	500	510	520	530	540	550	560
ISAASVQSAS	SAIIKAANAI	QQQTVVVPAS	SLANAKLVPK	TVHLANLNLL	PQGAQATSEL	RQVLTKPQQQ	IKQAIINAAA
570	580	590	600	610	620	630	640
SQPPKKVSRV	QVVSSLQSSV	VEAFNKVLSS	VNPVPVYIPN	LSPPANAGIT	LPTRGYKCLE	CGDSFALEKS	LTQHYDRRSV
650	660	670	680	690	700	710	720
RIEVTCNHCT	KNLVFYNKCS	LLSHARGHKE	KGVVMQCSHL	ILKPVPADQM	IVSPSSNTST	STSTLQSPVG	AGTHTVTKIQ
730	740	750	760	770	780	790	800
SGITGTVISA	PSSTPITPAM	PLDEDPSKLC	RHSLKCLECN	EVFQDETSLA	THFQQAADTS	GQKTCTICQM	LLPNQCSYAS
810	820	830	840	850	860	870	880
HQRIHQHKSP	YTCPECGAIC	RSVHFQTHVT	KNCLHYTRRV	GFRCVHCNVV	YSDVAALKSH	IQGSHCEVFY	KCPICPMAFK
890	900	910	920	930	940	950	960
SAPSTHSHAY	TQHPGIKIGE	PKIIYKCSMC	DTVFTLQTLL	YRHFDQHIEN	QKVSVFKCPD	CSLLYAQKQL	MMDHIKSMHG
970	980	990	1000	1010	1020	1030	1040
TLKSIEGPPN	LGINLPLSIK	PATQNSANQN	KEDTKSMNGK	EKLEKKSPSP	VKKSMETKKV	ASPGWTCWEC	DCLFMQRDVY
1050	1060	1070					
ISHVRKEHGK	FGSGKRNHIL						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
633	1	537.6446	-266.88	2	36.5	10.1	2	1046-1055	R.KEHGKFGSGK.R		mdown:qdown 0.86

Detailed Protein Report

Protein 1699: zinc finger protein 227 isoform d [Homo sapiens]

Accession: gi|574584777
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 10.1
MW [kDa]: 80.4
pI: 10.2
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 1700: PREDICTED: L-fucose kinase isoform X3 [Homo sapiens]

Accession:	gi|578828897	**Score:**	10.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	81.7
Database Date:	2015-11-30	**pI:**	6.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MTSSASEFLL	SLTLPGAPGA	QIVHSQVEEQ	QLLAAGSSVV	SCLLEGPVQL	GPGSVLQHCH	LQGPIHIGAG	CLVTGLDTAH
90	100	110	120	130	140	150	160
SKALHGRELR	DLVLQGHHTR	LHGSPGHAFT	LVGRLDSWER	QGAGTYLNVP	WSEFFKRTGV	RAWDLWDPET	LPAEYCLPSA
170	180	190	200	210	220	230	240
RLFPVLHPSR	ELGPQDLLWM	LDHQEDGGEA	LRAWRASWRL	SWEQLQPCLD	RAATLASRRD	LFFRQALHKA	RHVLEARQDL
250	260	270	280	290	300	310	320
SLRPLIWAAV	REGCPGPLLA	TLDQVAAGAG	DPGVAARALA	CVADVLGCMA	EGRGGLRSGP	AANPEWMRPF	SYLECGDLAA
330	340	350	360	370	380	390	400
GVEALAQERD	KWLSRPALLV	RAARHYEGAG	QILIRQAVMS	AQHFVSTEQV	ELPGPGQWVV	AECPARVDFS	GGWSDTPPLA
410	420	430	440	450	460	470	480
YELGGAVLGL	AVRVDGRRPI	GARARRIPEP	ELWLAVGPRQ	DEMTVKIVCR	CLADLRDYCQ	PHAPGALLKA	AFICAGIVHV
490	500	510	520	530	540	550	560
HSELQLSEQL	LRTFGGGFEL	HTWSELPHGS	GLGTSSILAG	TALAALQRAA	GRVVGTEALI	HAVLHLEQVL	TTGGGWQDQV
570	580	590	600	610	620	630	640
GGLMPGIKVG	RSRAQLPLKV	EVEEVTVPEG	FVQKLNDHLL	LVYTGKTRLA	RNLLQDVLRS	WYARLPAVVQ	NAHSLVRQTE
650	660	670	680	690	700	710	720
ECAEGFRQGS	LPLLGQCLTS	YWEQKKLMAP	GCEPLTVRRM	MDVLAPHVHG	QSLAGAGGGG	FLYLLTKEPQ	QKEALEAVLA
730	740	750	760				
KTEGLGNYSI	HLVEVDTQGL	SLKLLGTEAS	TCCPFP				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2561	1	698.1910	-181.61	2	60.7	10.1	0	744-756	K.LLGTEASTCCPFP.-	Carbamidomethyl: 9

Detailed Protein Report

Protein 1701: zinc finger protein 219 [Homo sapiens]

Accession: gi|156415996
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 10.1
MW [kDa]: 76.8
pI: 10.9
Sequence Coverage [%]: 2.2
No. of unique Peptides: 1

Alias proteins:

Accession	Name	Description
gi|578825867	refseq_human (refseq_human_20140103.fasta)	PREDICTED: zinc finger protein 219 isoform X4 [Homo sapiens]
gi|578825865	refseq_human (refseq_human_20140103.fasta)	PREDICTED: zinc finger protein 219 isoform X3 [Homo sapiens]
gi|156416026	refseq_human (refseq_human_20140103.fasta)	zinc finger protein 219 [Homo sapiens]
gi|156415998	refseq_human (refseq_human_20140103.fasta)	zinc finger protein 219 [Homo sapiens]

10	20	30	40	50	60	70	80
MEGSRPRAPS	GHLAPSPPAF	DGELDLQRYS	NGPAVSAGSL	GMGAVSWSES	RAGERRFPCP	VCGKRFRFNS	ILALHLRAHP
90	100	110	120	130	140	150	160
GAQAFQCPHC	GHRAAQRALL	RSHLRTHQPE	RPRSPAARLL	LELEERALLR	EARLGRARSS	GGMQATPATE	GLARPQAPSS
170	180	190	200	210	220	230	240
SAFRCPYCKG	KFRTSAERER	HLHILHRPWK	CGLCSFGSSQ	EEELLHHSLT	AHGAPERPLA	ATSAAPPPQP	QPQPPPQPEP
250	260	270	280	290	300	310	320
RSVPQPEPEP	EPEREATPTP	APAAPEEPPA	PPEFRCQVCG	QSFTQSWFLK	GHMRKHKASF	DHACPVCGRC	FKEPWFLKNH
330	340	350	360	370	380	390	400
MKVHASKLGP	LRAPGPASGP	ARAPQPPDLG	LLAYEPLGPA	LLLAPAPTPA	ERREPPSLLG	YLSLRAGEGR	PNGEGAEPGP
410	420	430	440	450	460	470	480
GRSFGGFRPL	SSALPARARR	HRAEEPEEEE	EVVEAEEETW	ARGRSLGSLA	SLHPRPGEGP	GHSASAAGAQ	ARSTATQEEN
490	500	510	520	530	540	550	560
GLLVGGTRPE	GGRGATGKDC	PFCGKSFRSA	HHLKVHLRVH	TGERPYKCPH	CDYAGTQSGS	LKYHLQRHHR	EQRSGAGPGP
570	580	590	600	610	620	630	640
PPEPPPPSQR	GSAPQSGAKP	SPQPATWVEG	ASSPRPPSSG	AGPGSRRKPA	SPGRTLRNGR	GGEAEPLDLS	LRAGPGGEAG
650	660	670	680	690	700	710	720
PGGALHRCLF	CPFATGAPEL	MALHLQVHHS	RRARGRRPPQ	ADASPPYARV	PSGETPPSPS	QEGEEGSGLS	RPGEAGLGGQ
730							
ER							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1199	1	591.8419	-151.95	3	43.6	10.1	0	78-93	R.AHPGAQAFQCPHCGHR.A	Carbamidomethyl: 13

Detailed Protein Report

Protein 1702: carbamoyl-phosphate synthase [ammonia], mitochondrial isoform c [Homo sapiens]

Accession: gi|170295797
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 10.0
MW [kDa]: 116.0
pI: 5.6
Sequence Coverage [%]: 1.6
No. of unique Peptides: 1

```
        10         20         30         40         50         60         70         80
MKEENVKTVL MNPNIASVQT NEVGLKQADT VYFLPITPQF VTEVIKAEQP DGLILGMGGQ TALNCGVELF KRGVLKEYGV

        90        100        110        120        130        140        150        160
KVLGTSVESI MATEDRQLFS DKLNEINEKI APSFAVESIE DALKAADTIG YPVMIRSAYA LGGLGSGICP NRETLMDLST

       170        180        190        200        210        220        230        240
KAFAMTNQIL VEKSVTGWKE IEYEVVRDAD DNCVTVCNME NVDAMGVHTG DSVVVAPAQT LSNAEFQMLR RTSINVVRHL

       250        260        270        280        290        300        310        320
GIVGECNIQF ALHPTSMEYC IIEVNARLSR SSALASKATG YPLAFIAAKI ALGIPLPEIK NVVSGKTSAC FEPSLDYMVT

       330        340        350        360        370        380        390        400
KIPRWDLDRF HGTSSRIGSS MKSVGEVMAI GRTFEESFQK ALRMCHPSIE GFTPRLPMNK EWPSNLDLRK ELSEPSSTRI

       410        420        430        440        450        460        470        480
YAIAKAIDDN MSLDEIEKLT YIDKWFLYKM RDILNMEKTL KGLNSESMTE ETLKRAKEIG FSDKQISKCL GLTEAQTREL

       490        500        510        520        530        540        550        560
RLKKNIHPWV KQIDTLAAEY PSVTNYLYVT YNGQEHDVNF DDHGMMVLGC GPYHIGSSVE FDWCAVSSIR TLRQLGKKTV

       570        580        590        600        610        620        630        640
VVNCNPETVS TDFDECDKLY FEELSLERIL DIYHQEACGG CIISVGGQIP NNLAVPLYKN GVKIMGTSPL QIDRAEDRSI

       650        660        670        680        690        700        710        720
FSAVLDELKV AQAPWKAVNT LNEALEFAKS VDYPCLLRPS YVLSGSAMNV VFSEDEMKKF LEEATRVSQE HPVVLTKFVE

       730        740        750        760        770        780        790        800
GAREVEMDAV GKDGRVISHA ISEHVEDAGV HSGDATLMLP TQTISQGAIE KVKDATRKIA KAFAISGPFN VQFLVKGNDV

       810        820        830        840        850        860        870        880
LVIECNLRAS RSFPFVSKTL GVDFIDVATK VMIGENVDEK HLPTLDHPII PADYVAIKAP MFSWPRLRDA DPILRCEMAS

       890        900        910        920        930        940        950        960
TGEVACFGEG IHTAFLKAML STGFKIPQKG ILIGIQQSFR PRFLGVAEQL HNEGFKLFAT EATSDWLNAN NVPATPVAWP

       970        980        990       1000       1010       1020       1030       1040
SQEGQNPSLS SIRKLIRDGS IDLVINLPNN NTKFVHDNYV IRRTAVDSGI PLLTNFQVTK LFAEAVQKSR KVDSKSLFHY

      1050
RQYSAGKAA
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2548	1	973.5400	12.35	2	60.1	10.0	2	465-481	K.QISKCLGLTEAQTRELR.L	

Detailed Protein Report

Protein 1703: 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 1704: protein aurora borealis isoform 3 [Homo sapiens]

Accession:	gi|557948052	**Score:**	10.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	53.4
Database Date:	2015-11-30	**pI:**	4.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.2
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	0.43	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	1.62	**CV:**	0.00 %	**No. of Peptides:**	1

```
        10          20          30          40          50          60          70          80
MNKLSPVLLF  LNQQNYQIDK  DVEDKRQKAI  EEFFTKDVIV  PSPWTDHEGK  QLSQCHSSKC  TNINSDSPVG  KKLTIHSEKS

        90         100         110         120         130         140         150         160
DAACQTLLSL  PVDFNLENIL  GDYFRADEFA  DQSPGNLSSS  SLRRKLFLDG  NGSISDSLPS  ASPGSPHSGV  QTSLEMFYSI

       170         180         190         200         210         220         230         240
DLSPVKCRSP  LQTPSSGQFS  SSPIQASAKK  YSLGSITSPS  PISSPTFSPI  EFQIGETPLS  EQRKFTVHSP  DASSGTNSNG

       250         260         270         280         290         300         310         320
ITNPCIRSPY  IDGCSPIKNW  SPMRLQMYSG  GTQYRTSVIQ  IPFTLETQGE  DEEDKENIPS  TDVSSPAMDA  AGIHLRQFSN

       330         340         350         360         370         380         390         400
EASTHGTHLV  VTAMSVTQNQ  SSASEKELAL  LQDVEREKDN  NTVDMVDPIE  IADETTWIKE  PVDNGSLPMT  DFVSGIAFSI

       410         420         430         440         450         460         470         480
ENSHMCMSPL  AESSVIPCES  SNIQMDSGYN  TQNCGSNIMD  TVGAESYCKE  SDAQTCEVES  KSQAFNMKQD  HTTQRCWMKT

       490
ASPFQCSSP
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1061	1	660.1801	-190.79	2	41.8	10.0	0	265-275	R.LQMYSGGTQYR.T	Oxidation: 3	Wdown:Qdown 1.62 mdown:qdown 0.43

Detailed Protein Report

Protein 1705: carnosine synthase 1 isoform 2 [Homo sapiens]

Accession:	gi|148839342	**Score:**	10.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	88.4
Database Date:	2015-11-30	**pI:**	5.8
		Sequence Coverage [%]:	2.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLLCLSPAWL	MKVPAPGQPG	EAALLVSKAV	SFHPGGLTFL	DDFVPPRRAT	YFLAGLGLGP	GRGREAAELA	RDLTCPTGAS
90	100	110	120	130	140	150	160
AELARLLEDR	LLTRQLLAQQ	GGVAVPATLA	FTYKPPGLLR	GGDASLGLRL	VELSGKEGQE	TLVKEEVEAF	LRSEALGDIL
170	180	190	200	210	220	230	240
QVAVKLSGWR	WRGRQAWRLH	PRAELGAVVD	TVLALLEKLE	EEESVLVEAV	YPPAQLPCSD	GPSPGPGLAV	RICAVVCRTQ
250	260	270	280	290	300	310	320
GDRPLLSKVV	CGVGRGDRPL	RHHNSLPRTL	EVALAQCGLG	EEAQVAAVRQ	RVKAAAEAAL	AAVLALEAGL	SAEQRGGRRA
330	340	350	360	370	380	390	400
HTDFLGVDFA	LTAAGGVLTP	VALELNGGLC	LEACGALEGL	WAAPRLGPAA	DEAVAAPLVE	TMLRRSARCL	MEGKQLLVVG
410	420	430	440	450	460	470	480
AGGVSKKFVW	EAARDYGLQL	HLVESDPNHF	ASQLVQTFIH	FDMTEHRRDE	ENARLLAELV	RARGLKLDGC	FSYWDDCLVL
490	500	510	520	530	540	550	560
TALLCQELGL	PCSSPAAMRL	AKQKSLTQLH	LLHHHGPPWP	APSLHAVPCC	PLESEADVER	AVHQVPLPGV	MKLEFGAGAV
570	580	590	600	610	620	630	640
GVRLVEDAPQ	CHEHFSRITR	DLQGEADHPG	IGLGWGNAML	LMEFVEGTEH	DVDLVLFGGR	LLAAFVSDNG	PTRLPGFTET
650	660	670	680	690	700	710	720
AACMPTGLAP	EQEAQMVQAA	FRCCLGCGLL	DGVFNVELKL	TGAGPRLIEI	NPRMGGFYLR	DWILELYGVD	LLLAAVMVAC
730	740	750	760	770	780	790	800
GLRPALPTRP	RARGHLVGVM	CLVSQHLQAL	SSTASRETLQ	ALHDRGLLRL	NLLEEALVPG	EYEEPYCSVA	CAGPSPTEAR
810	820	830					
LRLLGLCQGL	GIDGPSYPVA	HFLSHFK					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1575	1	1073.1550	112.90	2	48.4	10.0	1	65-85	R.EAAELARDLTCPTGASAELAR.L	

Detailed Protein Report

Protein 1706: coiled-coil domain-containing protein 108 isoform 4 [Homo sapiens]

Accession: gi|507144067
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 10.0
MW [kDa]: 81.3
pI: 9.1
Sequence Coverage [%]: 1.6
No. of unique Peptides: 1

Quantitation

Wdown:Qdown **Median:** 1.10 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MMLTQAPSSV	VRSRNSRNHT	VNSGGSCLSA	STVAIPAIND	SSAAMSACST	ISAQPASSMD	TQMHSPKKQE	RVNKRVIWGI
90	100	110	120	130	140	150	160
EVAEELHWKG	WELGKETTRN	LVLKNRSLKL	QKMKYRPPKT	KFFFTVIPQP	IFLSPGITLT	LPIVFRPLEA	KEYMDQLWFE
170	180	190	200	210	220	230	240
KAEGMFCVGL	RATLPCHRLI	CRPPSLQLPM	CAVGDTTEAF	FCLDNVGDLP	TFFTWEFSSP	FQMLPATGLL	EPGQASQIKV
250	260	270	280	290	300	310	320
TFQPLTAVIY	EVQATCWYGA	GSRQRSSIQL	QAVAKCAQLL	VSIKHKCPED	QDAEGFQKLL	YFGSVAVGCT	SERQIRLHNP
330	340	350	360	370	380	390	400
SAVNAPFRIE	ISPDELAEDQ	AFSCPTAHGI	VLPGEKKCVS	VFFHPKTLDT	RTVDYCSIMP	SGCASKTLLK	VVGFCRGPAV
410	420	430	440	450	460	470	480
SLQHYCVNFS	WVNLGERSEQ	PLWIENQSDC	TAHFQFAIDC	LESVFTIRPA	FGTLVGKARM	TLHCAFQPTH	PIICFRRVAC
490	500	510	520	530	540	550	560
LIHHQDPLFL	DLMGTCHSDS	TKPAILKPQH	LTWYRTHLAR	GLTLYPPDIL	DAMLKEKKLA	QDQNGALMIP	IQDLEDMPAP
570	580	590	600	610	620	630	640
QYPYIPPMTE	FFFDGTSDIT	IFPPPISVEP	VEVDFGACPG	PEAPNPVPLC	LMNHTKGKIM	VVWTRRSDCP	FWVTPESCDV
650	660	670	680	690	700	710	720
PPLKSMAMRL	HFQPPHPNCL	YTVELEAFAI	YKVCARNERE	ECGVSARSLS	GLVGWQEVTE	GSFRLHPLRA	RLSLGWTVTP
730	740						
MSLSPPKLLA							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
640	1	712.1825	-155.63	2	37.3	10.0	0	287-298	K.CPEDQDAEGFQK.L	Carbamidomethyl: 1	Wdown:Qdown 1.10

Detailed Protein Report

Protein 1707: **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 1708: NFX1-type zinc finger-containing protein 1 [Homo sapiens]

Accession:	gi|28626521	**Score:**	10.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	220.1
Database Date:	2015-11-30	**pI:**	7.2
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	0.5
		No. of unique Peptides:	1

Quantitation

mdown:qdown	**Median:**	0.64	**CV:**	0.00 %	**No. of Peptides:**	1
Wdown:Qdown	**Median:**	0.17	**CV:**	0.00 %	**No. of Peptides:**	1

Alias proteins:

Accession	Name	Description
gi|578836091	refseq_human (refseq_human_20140103.fasta)	PREDICTED: NFX1-type zinc finger-containing protein 1 isoform X1 [Homo sapiens]

Detailed Protein Report

10	20	30	40	50	60	70	80
MEERRPHLDA	RPRNSHTNHR	GPVDGELPPR	ARNQANNPPA	NALRGGASHP	GRHPRANNHP	AAYWQREERF	RAMGRNPHQG
90	100	110	120	130	140	150	160
RRNQEGHASD	EARDQRHDQE	NDTRWRNGNQ	DCRNRRPPWS	NDNFQQWRTP	HQKPTEQPQQ	AKKLGYKFLE	SLLQKDPSEV
170	180	190	200	210	220	230	240
VITLATSLGL	KELLSHSSMK	SNFLELICQV	LRKACSSKMD	RQSVLHVLGI	LKNSKFLKVC	LPAYVVGMIT	EPIPDIRNQY
250	260	270	280	290	300	310	320
PEHISNIISL	LQDLVSVFPA	SSVQETSMLV	SLLPTSLNAL	RASGVDIEEE	TEKNLEKVQT	IIEHLQEKRR	EGTLRVDTYT
330	340	350	360	370	380	390	400
LVQPEAEDHV	ESYRTMPIYP	TYNEVHLDER	PFLRPNIISG	KYDSTAIYLD	THFRLLREDF	VRPLREGILE	LLQSFEDQGL
410	420	430	440	450	460	470	480
RKRKFDDIRI	YFDTRIITPM	CSSSGIVYKV	QFDTKPLKFV	RWQNSKRLLY	GSLVCMSKDN	FETFLFATVS	NREQEDLCRG
490	500	510	520	530	540	550	560
IVQLCFNEQS	QQLLAEVQPS	DSFLMVETTA	YFEAYRHVLE	GLQEVQEEDV	PFQRNIVECN	SHVKEPRYLL	MGGRYDFTPL
570	580	590	600	610	620	630	640
IENPSATGEF	LRNVEGLRHP	RINVLDPGQW	PSKEALKLDD	SQMEALQFAL	TRELAIIQGP	PGTGKTYVGL	KIVQALLTNE
650	660	670	680	690	700	710	720
SVWQISLQKF	PILVVCYTNH	ALDQFLEGIY	NCQKTSIVRV	GGRSNSEILK	QFTLRELRNK	REFRRNLPMH	LRRAYMSIMT
730	740	750	760	770	780	790	800
QMKESEQELH	EGAKTLECTM	RGVLREQYLQ	KYISPQHWES	LMNGPVQDSE	WICFQHWKHS	MMLEWLGLGV	GSFTQSVSPA
810	820	830	840	850	860	870	880
GPENTAQAEG	DEEEEGEEES	SLIEIAEEAD	LIQADRVIEE	EEVVRPQRRK	KEESGADQEL	AKMLLAMRLD	HCGTGTAAGQ
890	900	910	920	930	940	950	960
EQATGEWQTQ	RNQKKKMKKR	VKDELRKLNT	MTAAEANEIE	DVWQLDLSSR	WQLYRLWLQL	YQADTRRKIL	SYERQYRTSA
970	980	990	1000	1010	1020	1030	1040
ERMAELRLQE	DLHILKDAQV	VGMTTTGAAK	YRQILQKVEP	RIVIVEEAAE	VLEAHTIATL	SKACQHLILI	GDHQQLRPSA
1050	1060	1070	1080	1090	1100	1110	1120
NVYDLAKNFN	LEVSLFERLV	KVNIPFVRLN	YQHRMCPEIA	RLLTPHIYQD	LENHPSVLKY	EKIKGVSSNL	FFVEHNFPEQ
1130	1140	1150	1160	1170	1180	1190	1200
EIQEGKSHQN	QHEAHFVVEL	CKYFLCQEYL	PSQITILTTY	TGQLFCLRKL	MPAKTFAGVR	VHVVDKYQGE	ENDIILLSLV
1210	1220	1230	1240	1250	1260	1270	1280
RSNQEGKVGF	LQISNRICVA	LSRAKKGMYC	IGNMQMLAKV	PLWSKIIHTL	RENNQIGPML	RLCCQNHPET	HTLVSKASDF
1290	1300	1310	1320	1330	1340	1350	1360
QKVPEGGCSL	PCEFRLGCGH	VCTRACHPYD	SSHKEFQCMK	PCQKVICQEG	HRCPLVCFQE	CQPCQVKVPK	TIPRCGHEQM
1370	1380	1390	1400	1410	1420	1430	1440
VPCSVPESDF	CCQEPCSKSL	RCGHRCSHPC	GEDCVQLCSE	MVTIKLKCGH	SQPVKCGHVE	GLLYGGLLVK	CTTKCGTILD
1450	1460	1470	1480	1490	1500	1510	1520
CGHPCPGSCH	SCFEGRFHER	CQQPCKRLLI	CSHKCQEPCI	GECPPCQRTC	QNRCVHSQCK	KKCGELCSPC	VEPCVWRCQH
1530	1540	1550	1560	1570	1580	1590	1600
YQCTKLCSEP	CNRPPCYVPC	TKLLVCGHPC	IGLCGEPCPK	KCRICHMDEV	TQIFFGFEDE	PDARFVQLED	CSHIFEVQAL
1610	1620	1630	1640	1650	1660	1670	1680
DRYMNEQKDD	EVAIRLKVCP	ICQVPIRKNL	RYGTSIKQRL	EEIEIIKEKI	QGSAGEIATS	QERLKALLER	KSLLHQLLPE
1690	1700	1710	1720	1730	1740	1750	1760
DFLMLKEKLA	QKNLSVKDLG	LVENYISFYD	HLASLWDSLK	KMHVLEEKRV	RTRLEQVHEW	LAKKRLSFTS	QELSDLRSEI
1770	1780	1790	1800	1810	1820	1830	1840
QRLTYLVNLL	TRYKIAEKKV	KDSIAVEVYS	VQNILEKTCK	FTQEDEQLVQ	EKMEALKATL	PCSGLGISEE	ERVQIVSAIG
1850	1860	1870	1880	1890	1900	1910	1920
YPRGHWFKCR	NGHIYVIGDC	GGAMERGTCP	DCKEVIGGTN	HTLERSNQLA	SEMDGAQHAA	WSDTANNLMN	FEEIQGMM

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
293	1	657.7265	-89.80	2	32.8	10.0	0	1315- 1324	K.EFQCMKPCQK.V	Carbamidomethyl: 4; Oxidation: 5	Wdown:Qdown 0.17 mdown:qdown 0.64

Detailed Protein Report

Protein 1709: 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 1710: interferon omega-1 precursor [Homo sapiens]

Accession:	gi|4504605	**Score:**	10.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	22.3
Database Date:	2015-11-30	**pI:**	10.1
Modification(s):	Carbamidomethyl	**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

Detailed Protein Report

Protein 1711: 2'-5'-oligoadenylate synthase-like protein isoform a [Homo sapiens]

Accession:	gi|11321577	**Score:**	10.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	59.2
Database Date:	2015-11-30	**pI:**	8.8
		Sequence Coverage [%]:	2.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MALMQELYST	PASRLDSFVA	QWLQPHREWK	EEVLDAVRTV	EEFLRQEHFQ	GKRGLDQDVR	VLKVVKVGSF	GNGTVLRSTR
90	100	110	120	130	140	150	160
EVELVAFLSC	FHSFQEAAKH	HKDVLRLIWK	TMWQSQDLLD	LGLEDLRMEQ	RVPDALVFTI	QTRGTAEPIT	VTIVPAYRAL
170	180	190	200	210	220	230	240
GPSLPNSQPP	PEVYVSLIKA	CGGPGNFCPS	FSELQRNFVK	HRPTKLKSLL	RLVKHWYQQY	VKARSPRANL	PPLYALELLT
250	260	270	280	290	300	310	320
IYAWEMGTEE	DENFMLDEGF	TTVMDLLLEY	EVICIYWTKY	YTLHNAIIED	CVRKQLKKER	PIILDPADPT	LNVAEGYRWD
330	340	350	360	370	380	390	400
IVAQRASQCL	KQDCCYDNRE	NPISSWNVKR	ARDIHLTVEQ	RGYPDFNLIV	NPYEPIRKVK	EKIRRTRGYS	GLQRLSFQVP
410	420	430	440	450	460	470	480
GSERQLLSSR	CSLAKYGIFS	HTHIYLLETI	PSEIQVFVKN	PDGGSYAYAI	NPNSFILGLK	QQIEDQQGLP	KKQQQLEFQG
490	500	510	520				
QVLQDWLGLG	IYGIQDSDTL	ILSKKKGEAL	FPAS				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2656	1	665.3226	-39.85	2	61.5	10.0	1	340-350	R.ENPISSWNVKR.A	