Detailed Protein Report

Project Info

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

Sample Info & Protocols

Name:	ID-W	**Date:**	Dec 8, 2015
Fraction:			
Volume:		**Concentration:**	
Note:			
Buffer:		**Organism:**	

Search Result Info

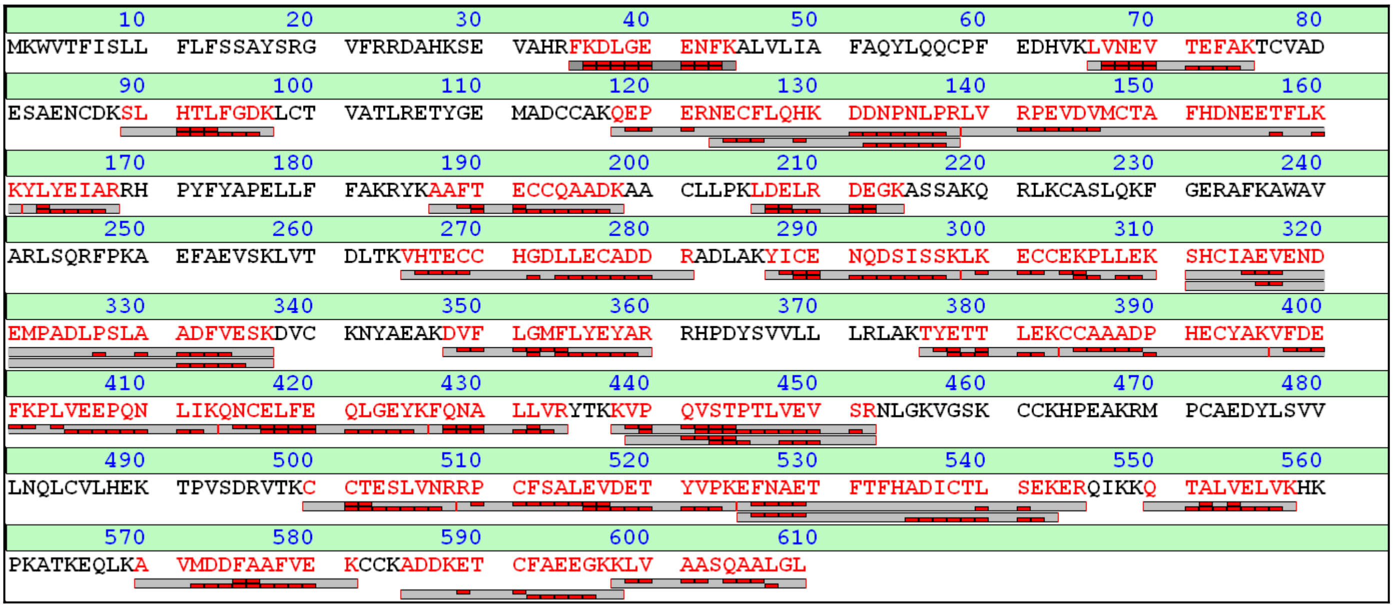
Search Result	Location	Search Engine	Database
ZT_human_PE_2015-12-08 22:06:17	/teeth-151208/ID-W/"Combined MS/MS spectra"	Mascot	refseq_human

Protein 1: serum albumin preproprotein [Homo sapiens]

Accession:	gi|4502027	**Score:**	1403.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	69.3
Database Date:	2015-11-30	**pI:**	5.9
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	57.1
		No. of unique Peptides:	30

Quantitation

WD:WU **Median:** 0.80 **CV:** 33.46 % **No. of Peptides:** 13



Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
151	7	613.6605	-237.38	2	30.8	67.2	1	35-44	R.FKDLGEENFK.A		
514	8	575.2390	-125.46	2	34.9	63.4	0	66-75	K.LVNEVTEFAK.T		WD:WU 0.89
345	3	509.1558	-227.88	2	33.4	45.7	0	89-97	K.SLHTLFGDK.L		WD:WU 0.61
171	1	659.8150	4.22	4	31.4	26.5	2	118-138	K.QEPERNECFLQHKDDNPNLPR.L	Carbamidomethyl: 8	
144	1	666.2970	-26.44	3	30.7	28.6	1	123-138	R.NECFLQHKDDNPNLPR.L	Carbamidomethyl: 3	WD:WU 0.65
1425	1	695.3249	-29.21	4	46.6	14.9	1	139-161	R.LVRPEVDVMCTAFHDNEETFLKK.Y	Carbamidomethyl: 10	
326	8	464.1239	-272.44	2	32.8	30.1	0	162-168	K.YLYEIAR.R		WD:WU 1.28

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
33	3	686.2794	-11.06	2	29.6	70.0	0	187-198	K.AAFTECCQAADK.A	Carbamidomethyl: 6, 7	
20	4	537.7465	-52.90	2	29.5	44.4	1	206-214	K.LDELRDEGK.A		WD:WU 0.60
102	2	696.2880	5.70	3	30.5	50.5	0	265-281	K.VHTECCHGDLLECADDR.A	Carbamidomethyl: 5, 6, 13	WD:WU 0.85
15	6	722.3161	-11.90	2	29.1	70.8	0	287-298	K.YICENQDSISSK.L	Carbamidomethyl: 3	WD:WU 0.63
75	1	773.8989	-4.03	2	30.2	28.9	1	299-310	K.LKECCEKPLLEK.S	Carbamidomethyl: 4, 5	WD:WU 0.62
2459	1	997.4538	2.48	3	59.0	27.7	0	311-337	K. SHCIAEVENDEMPADLPSLAADFV D	Carbamidomethyl: 3; Oxidation: 12	
2988	1	992.1219	2.21	3	66.1	32.9	0	311-337	K. SHCIAEVENDEMPADLPSLAADFV D	Carbamidomethyl: 3	
2516	5	820.4094	17.73	2	59.7	54.5	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		WD:WU 0.72
8	3	776.7890	-17.37	2	29.1	42.3	0	384-396	K.CCAAADPHECYAK.V	Carbamidomethyl: 1, 2, 10	
2246	54	682.3456	-35.78	3	56.6	62.3	0	397-413	K.VFDEFKPLVEEPQNLIK.Q		
1301	9	829.3216	-70.31	2	45.0	69.3	0	414-426	K.QNCELFEQLGEYK.F	Carbamidomethyl: 3	WD:WU 0.81
565	19	480.6987	-179.31	2	35.9	50.6	0	427-434	K.FQNALLVR.Y		
783	8	820.4638	-10.68	2	38.6	67.6	1	438-452	K.KVPQVSTPTLVEVSR.N		
1019	3	756.4151	-13.09	2	41.5	37.1	0	439-452	K.VPQVSTPTLVEVSR.N		WD:WU 0.54
33	3	569.7395	-23.07	2	29.3	55.6	0	500-508	K.CCTESLVNR.R	Carbamidomethyl: 1, 2	WD:WU 1.44
1168	2	637.6273	-33.66	3	43.3	58.3	0	509-524	R.RPCFSALEVDETYVPK.E	Carbamidomethyl: 3	
2419	14	753.9221	-119.82	3	58.5	64.2	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	
860	13	500.8124	13.72	2	39.6	52.8	0	550-558	K.QTALVELVK.H		
2105	11	671.7288	-137.21	2	54.9	98.5	0	570-581	K.AVMDDFAAFVEK.C		
15	1	543.2576	19.22	3	29.4	27.1	2	585-598	K.ADDKETCFAEEGKK.L	Carbamidomethyl: 7	
895	1	571.3207	-52.32	2	39.6	22.1	1	598-609	K.KLVAASQAALGL.-		WD:WU 1.39

Protein 2: hemoglobin subunit beta [Homo sapiens]

Accession: gi|4504349

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Modification(s): Carbamidomethyl, Oxidation

Score: 728.2

MW [kDa]: 16.0

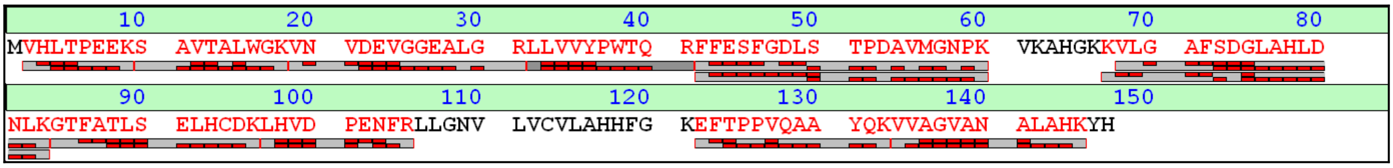
pI: 6.9

Sequence Coverage [%]: 83.0

No. of unique Peptides: 12

Quantitation

WD:WU **Median:** 0.67 **CV:** 60.02 % **No. of Peptides:** 8



Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
47	3	476.7443	-29.87	2	29.8	25.8	0	2-9	M.VHLTPEEK.S		WD:WU 0.85
629	11	466.7591	-9.74	2	36.3	58.8	0	10-18	K.SAVTALWGK.V		WD:WU 1.30
696	8	657.8312	-7.38	2	37.5	40.3	0	19-31	K.VNVDEVGGEALGR.L		WD:WU 0.90
2284	23	637.8143	-81.79	2	56.9	61.8	0	32-41	R.LLVVYPWTQR.F		
2307	8	1029.9789	1.35	2	57.1	52.0	0	42-60	R.FFESFGDLSTPDAVMGNPK.V		
1677	1	1037.9101	-62.48	2	49.6	60.1	0	42-60	R.FFESFGDLSTPDAVMGNPK.V	Oxidation: 15	
2072	35	599.9066	-155.81	3	54.5	102.5	1	67-83	K.KVLGAFSDGLAHLDNLK.G		WD:WU 0.18
2515	93	835.4601	13.21	2	59.7	95.3	0	68-83	K.VLGAFSDGLAHLDNLK.G		
595	4	739.7263	-168.37	2	36.3	53.2	0	84-96	K.GTFATLSELHCDK.L	Carbamidomethyl: 11	WD:WU 0.58
187	15	563.6579	-226.49	2	31.2	45.5	0	97-105	K.LHVDPENFR.L		WD:WU 0.82
563	2	689.7251	-186.44	2	35.9	45.0	0	122-133	K.EFTPPVQAAYQK.V		WD:WU 0.82
213	4	575.2065	-233.10	2	31.9	88.0	0	134-145	K.VVAGVANALAHK.Y		WD:WU 0.60

Detailed Protein Report

Protein 3: apolipoprotein A-I preproprotein [Homo sapiens]

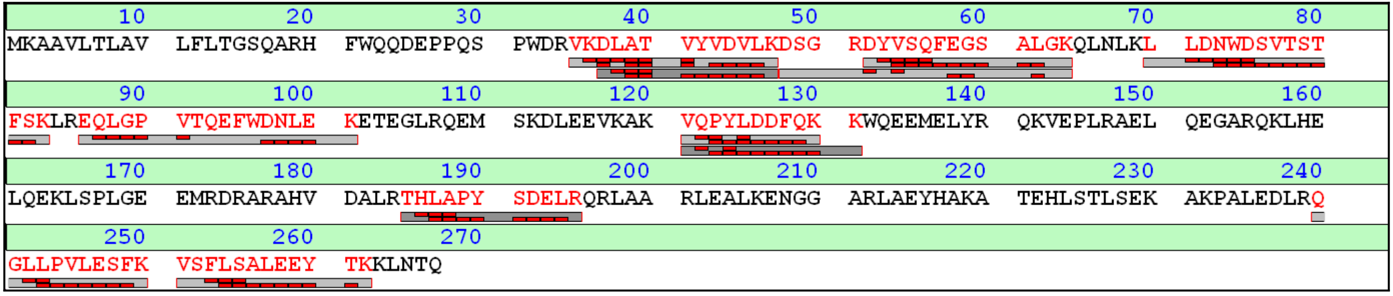
Accession:	gi|4557321	**Score:**	515.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	30.8
Database Date:	2015-11-30	**pI:**	5.5
		Sequence Coverage [%]:	39.3
		No. of unique Peptides:	11

Quantitation

WD:WU **Median:** 0.58 **CV:** 22.73 % **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	8	731.8942	-48.16	2	52.1	53.6	1	35-47	R.VKDLATVYVDVLK.D		
2093	4	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		
893	3	700.8159	-31.87	2	39.6	45.2	0	52-64	R.DYVSQFEGSALGK.Q		WD:WU 0.67
1807	11	806.8737	-27.99	2	51.3	94.1	0	70-83	K.LLDNWDSVTSTFSK.L		
2426	1	966.9435	-27.92	2	58.6	21.1	0	86-101	R.EQLGPVTQEFWDNLEK.E		
497	2	626.6875	-201.93	2	34.7	29.3	0	121-130	K.VQPYLDDFQK.K		WD:WU 0.43
257	1	690.8471	-20.89	2	32.0	53.5	1	121-131	K.VQPYLDDFQKK.W		WD:WU 0.76
182	2	651.3208	-10.84	2	31.5	40.3	0	185-195	R.THLAPYSDELR.Q		WD:WU 0.50
2876	20	615.8555	-4.42	2	64.7	47.2	0	240-250	R.QGLLPVLESFK.V		
2300	9	693.8302	-44.61	2	57.2	61.0	0	251-262	K.VSFLSALEEYTK.K		

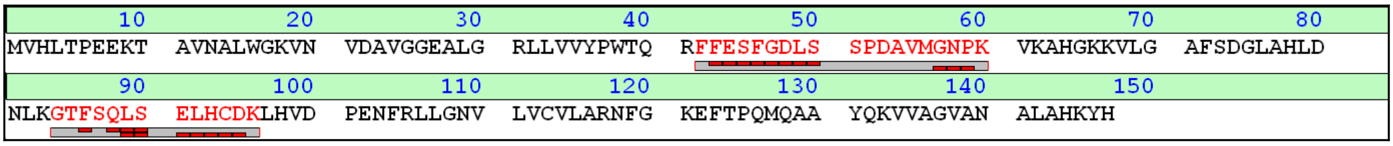
Detailed Protein Report

Protein 4: hemoglobin subunit delta [Homo sapiens]

Accession:	gi|4504351	**Score:**	483.6
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

Quantitation

WD:WU	**Median:**	3.02	**CV:**	0.00 %	**No. of Peptides:**	1	



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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
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	WD:WU 3.02

Detailed Protein Report

Protein 5: hemoglobin subunit alpha [Homo sapiens]

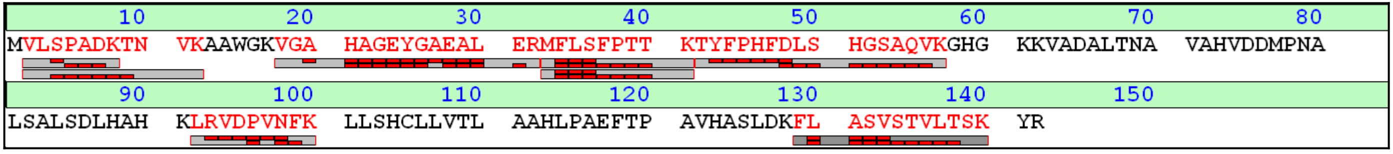
Accession:	gi|4504345	**Score:**	453.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	15.2
Database Date:	2015-11-30	**pI:**	9.4
Modification(s):	Oxidation	**Sequence Coverage [%]:**	50.7
		No. of unique Peptides:	8

Quantitation

WD:WU **Median:** 2.18 **CV:** 58.48 % **No. of Peptides:** 4

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
4	1	729.4098	-5.99	1	29.0	28.6	0	2-8	M.VLSPADK.T		
39	2	586.3399	3.78	2	29.7	55.0	1	2-12	M.VLSPADKTNVK.A		WD:WU 2.39
111	10	765.3757	6.39	2	30.7	80.1	0	18-32	K.VGAHAGEYGAEALER.M		
1126	3	544.1344	-264.30	2	42.3	39.7	0	33-41	R.MFLSFPTTK.T	Oxidation: 1	WD:WU 1.65
1845	35	536.1590	-227.09	2	51.4	57.9	0	33-41	R.MFLSFPTTK.T		
1032	5	917.4300	-21.34	2	41.7	79.5	0	42-57	K.TYFPHFDLSHGSAQVK.G		WD:WU 1.16
446	2	544.2062	-202.71	2	34.1	32.4	1	92-100	K.LRVDPVNFK.L		WD:WU 5.00
1648	44	626.8403	-33.03	2	48.9	80.4	0	129-140	K.FLASVSTVLTSK.Y		

Detailed Protein Report

Protein 6: alpha-2-macroglobulin precursor [Homo sapiens]

Accession:	gi|66932947	**Score:**	380.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	163.2
Database Date:	2015-11-30	**pI:**	6.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	11.9
		No. of unique Peptides:	13

Quantitation

WD:WU **Median:** 0.91 **CV:** 30.93 % **No. of Peptides:** 9

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	6	802.8311	-117.18	2	49.7	41.2	0	175-188	R.IAQWQSFQLEGGLK.Q		WD:WU	0.76
2299	2	924.9110	-35.46	2	57.0	20.1	0	189-204	K.QFSFPLSSEPFQGSYK.V			
2052	4	574.7391	-130.69	2	54.0	26.2	0	361-370	R.QGIPFFGQVR.L			
898	2	542.6752	-250.41	2	39.6	25.9	0	522-531	K.GHFSISIPVK.S		WD:WU	0.97
2454	1	922.9898	-34.93	2	59.0	33.4	0	540-557	R.LLIYAVLPTGDVIGDSAK.Y			
174	1	636.8164	-37.15	2	31.0	23.9	0	587-598	R.VTAAPQSVCALR.A	Carbamidomethyl: 9	WD:WU	0.62
											WD:WU	0.98

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Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
1177	1	509.7828	-34.15	2	43.4	37.2	0	812-820	K.ATVLNYLPK.C			
2461	2	942.5232	-4.52	2	59.1	21.9	0	824-841	R.VSVQLEASPAFLAVPVEK.E			
305	1	558.6600	-261.38	2	32.5	48.3	0	854-863	R.QTVSWAVTPK.S		WD:WU	1.34
189	1	605.6838	-232.96	2	31.2	17.9	0	935-945	K.LPPNVVEESAR.A		WD:WU	0.64
2462	1	669.8332	5.93	2	59.1	43.0	0	1123-1133	R.NALFCLESAWK.T	Carbamidomethyl: 5	WD:WU	1.62
1151	1	796.4102	8.78	3	43.1	23.4	0	1241-1263	K.QQNAQGGFSSTQDTVVALHALSK Y		WD:WU	0.78
891	2	809.4242	-4.39	2	39.9	18.3	0	1408-1421	R.TEVSSNHVLIYLDK.V		WD:WU	0.90

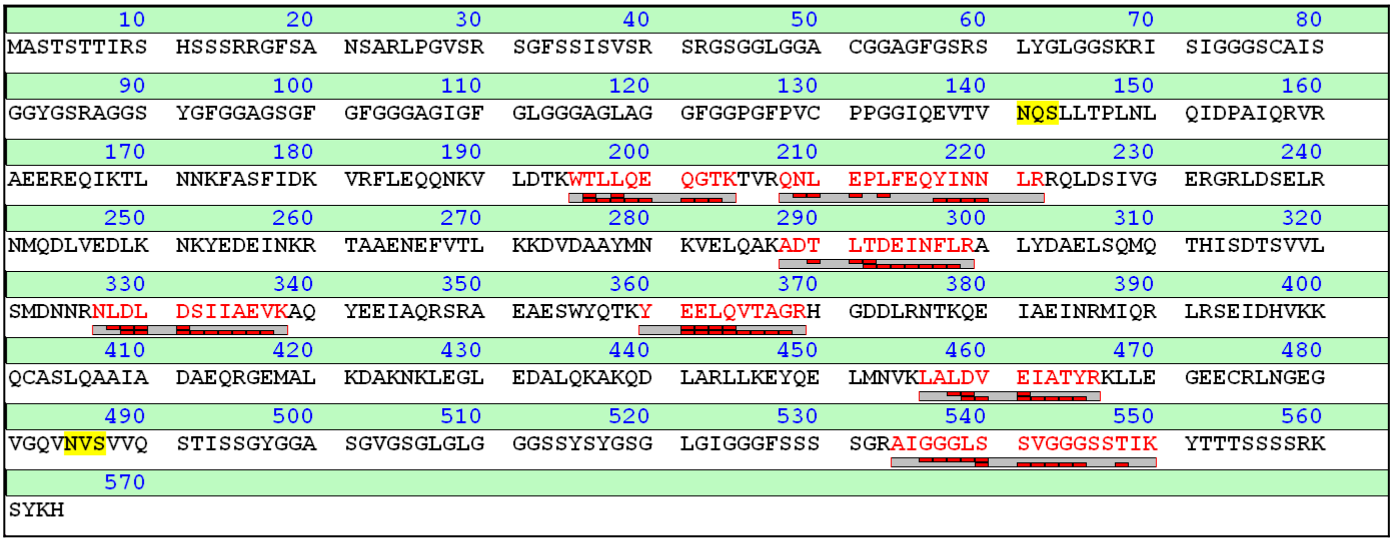
Detailed Protein Report

Protein 7: keratin, type II cytoskeletal 6C [Homo sapiens]

Accession:	gi|155969697	**Score:**	324.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	60.0
Database Date:	2015-11-30	**pI:**	8.9
		Sequence Coverage [%]:	15.4
		No. of unique Peptides:	7

Quantitation

WD:WU **Median:** 0.90 **CV:** 54.88 % **No. of Peptides:** 4



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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
709	1	602.2745	-78.87	2	37.7	32.3	0	195-204	K.WTLLQEQGTK.T		
2908	5	945.9990	10.55	2	65.1	35.8	0	208-222	R.QNLEPLFEQYINNLR.R		
1994	4	704.2662	-132.28	2	53.6	55.7	0	288-299	K.ADTLTDEINFLR.A		WD:WU 0.91
2923	16	665.3592	-11.18	2	65.3	86.6	0	327-338	R.NLDLDSIIAEVK.A		
145	2	583.2816	-24.68	2	31.1	63.8	0	360-369	K.YEELQVTAGR.H		WD:WU 0.49
1680	1	632.3373	-21.31	2	49.3	33.5	0	456-466	K.LALDVEIATYR.K		WD:WU 0.74
359	1	724.3637	-37.90	2	33.6	16.6	0	534-550	R.AIGGGLSSVGGGSSTIK.Y		WD:WU 2.01

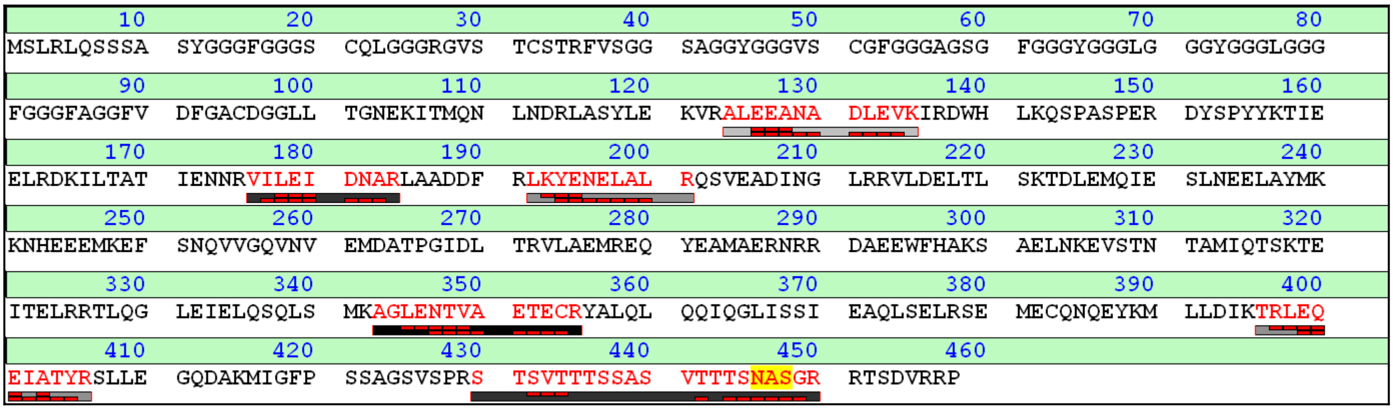
Detailed Protein Report

Protein 8: keratin, type I cytoskeletal 13 isoform a [Homo sapiens]

Accession:	gi|131412225	**Score:**	313.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	49.5
Database Date:	2015-11-30	**pI:**	4.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	16.6
		No. of unique Peptides:	6

Quantitation

WD:WU **Median:** 0.87 **CV:** 31.32 % **No. of Peptides:** 6



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
260	1	651.3006	-49.51	2	32.4	59.5	0	124-135	R.ALEEANADLEVK.I		WD:WU 0.89
539	1	521.6610	-263.02	2	35.6	53.1	0	176-184	R.VILEIDNAR.L		WD:WU 0.48
342	2	624.7261	-199.84	2	33.4	46.8	1	192-201	R.LKYENELALR.Q		WD:WU 0.86
101	1	725.3298	-7.92	2	30.2	62.2	0	343-355	K.AGLENTVAETECR.Y	Carbamidomethyl: 12	WD:WU 0.92
258	1	690.3402	-39.52	2	32.4	52.8	1	396-406	K.TRLEQEIATYR.S		WD:WU 0.90
17	1	1001.9627	-17.06	2	29.4	39.4	0	430-450	R.STSVTTTSSASVTTTSNASGR.R		WD:WU 1.38

Detailed Protein Report

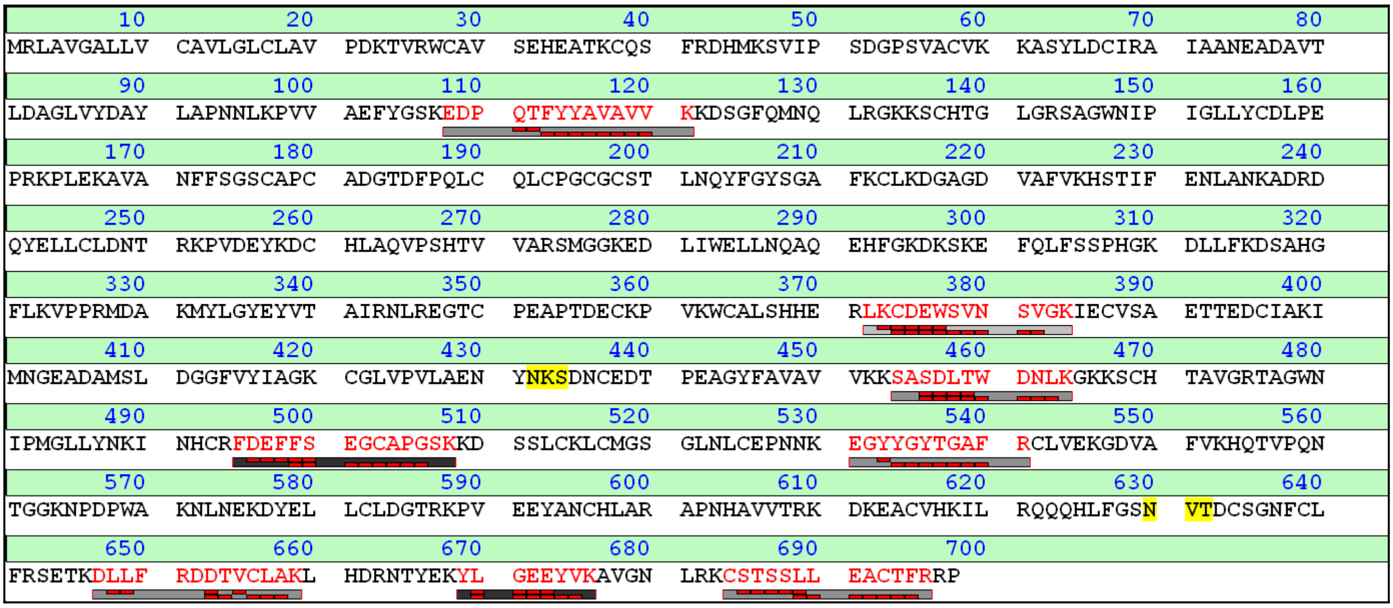
Protein 9: serotransferrin precursor [Homo sapiens]

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

Score: 308.3
MW [kDa]: 77.0
pI: 7.0
Sequence Coverage [%]: 13.9
No. of unique Peptides: 8

Quantitation

WD:WU **Median:** 0.65 **CV:** 59.99 % **No. of Peptides:** 6



```
        10         20         30         40         50         60         70         80
MRLAVGALLV CAVLGLCLAV PDKTVRWCAV SEHEATKCQS FRDHMKSVIP SDGPSVACVK KASYLDCIRA IAANEADAVT
        90        100        110        120        130        140        150        160
LDAGLVYDAY LAPNNLKPVV AEFYGSKEDP QTFYYAVAVV KKDSGFQMNQ LRGKKSCHTG LGRSAGWNIP IGLLYCDLPE
       170        180        190        200        210        220        230        240
PRKPLEKAVA NFFSGSCAPC ADGTDFPQLC QLCPGCGCST LNQYFGYSGA FKCLKDGAGD VAFVKHSTIF ENLANKADRD
       250        260        270        280        290        300        310        320
QYELLCLDNT RKPVDEYKDC HLAQVPSHTV VARSMGGKED LIWELLNQAQ EHFGKDKSKE FQLFSSPHGK DLLFKDSAHG
       330        340        350        360        370        380        390        400
FLKVPPRMDA KMYLGYEYVT AIRNLREGTC PEAPTDECKP VKWCALSHHE RLKCDEWSVN SVGKIECVSA ETTEDCIAKI
       410        420        430        440        450        460        470        480
MNGEADAMSL DGGFVYIAGK CGLVPVLAEN YNKSDNCEDT PEAGYFAVAV VKKSASDLTW DNLKGKKSCH TAVGRTAGWN
       490        500        510        520        530        540        550        560
IPMGLLYNKI NHCRFDEFFS EGCAPGSKKD SSLCKLCMGS GLNLCEPNNK EGYYGYTGAF RCLVEKGDVA FVKHQTVPQN
       570        580        590        600        610        620        630        640
TGGKNPDPWA KNLNEKDYEL LCLDGTRKPV EEYANCHLAR APNHAVVTRK DKEACVHKIL RQQHLFGSN 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
1759	1	815.3781	-41.02	2	50.7	25.1	0	108-121	K.EDPQTFYYAVAVVK.K		
172	2	761.3492	-29.85	2	31.0	78.7	1	372-384	R.LKCDEWSVNSVGK.I	Carbamidomethyl: 3	
708	2	625.2611	-72.75	2	37.7	48.9	0	454-464	K.SASDLTWDNLK.G		WD:WU 0.24
817	1	789.3225	-12.58	2	39.0	49.5	0	495-508	R.FDEFFSEGCAPGSK.K	Carbamidomethyl: 9	WD:WU 0.71
448	1	642.1562	-205.50	2	34.1	34.3	0	531-541	K.EGYYGYTGAFR.C		WD:WU 1.50
1439	1	783.3662	-47.33	2	46.8	10.9	1	647-659	K.DLLFRDDTVCLAK.L	Carbamidomethyl: 10	WD:WU 0.58
232	2	500.6172	-271.08	2	32.1	36.9	0	669-676	K.YLGEEYVK.A		WD:WU 0.58
915	2	766.3408	-8.88	2	40.2	24.0	0	684-696	K.CSTSSLLEACTFR.R	Carbamidomethyl: 1, 10	WD:WU 0.91

Detailed Protein Report

Protein 10: alpha-1-antitrypsin precursor [Homo sapiens]

Accession:	gi|50363217	**Score:**	228.4
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

WD:WU	**Median:**	0.95	**CV:**	65.16 %	**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
2391	1	1287.6505	-18.34	2	58.2	20.0	0	126-149	R. TLNQPDSQLQLTTGNGLFLSEGLK L		
722	1	729.3434	-11.09	3	37.9	16.3	1	161-179	K.LYHSEAFTVNFGDTEEAKK.Q		
762	1	601.9916	0.24	3	38.4	25.3	0	284-298	K.LQHLENELTHDIITK.F		WD:WU 0.63
725	2	555.8033	-4.33	2	37.9	69.3	0	315-324	K.LSITGTYDLK.S		WD:WU 0.61
1068	2	508.1796	-258.32	2	42.1	41.2	0	325-334	K.SVLGQLGITK.V		WD:WU 2.19

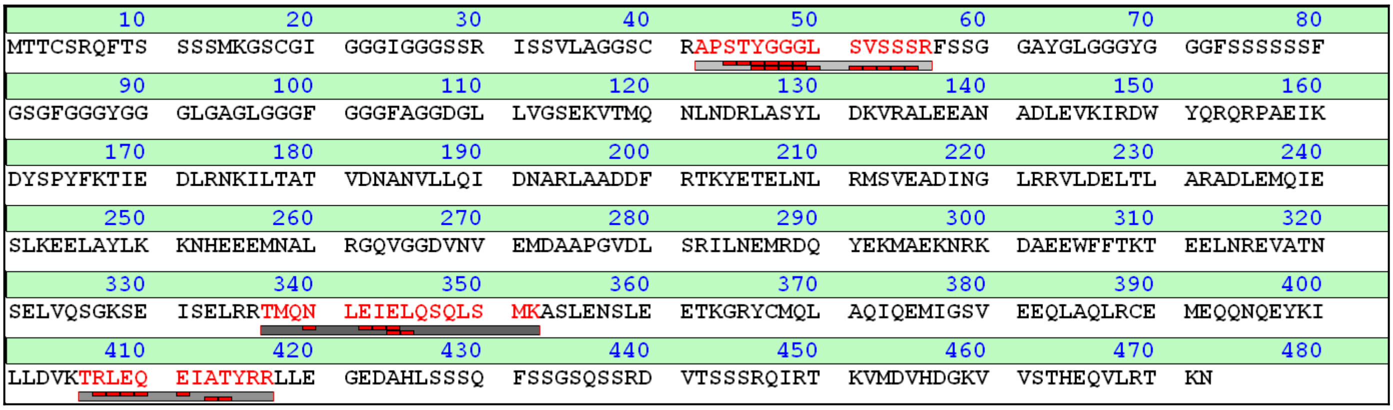
Detailed Protein Report

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

Accession:	gi|15431310	**Score:**	208.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	51.6
Database Date:	2015-11-30	**pI:**	4.9
Modification(s):	Oxidation	**Sequence Coverage [%]:**	11.7
		No. of unique Peptides:	3

Quantitation

WD:WU **Median:** 0.77 **CV:** 16.45 % **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		
1027	2	636.9803	-7.37	3	41.6	10.2	0	337-352	R.TMQNLEIELQSQLSMK.A	Oxidation: 15	WD:WU 0.65
134	1	512.5910	-45.89	3	30.6	20.2	2	406-417	K.TRLEQEIATYRR.L		WD:WU 0.90

Detailed Protein Report

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

Accession:	gi|153791158	**Score:**	195.3
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

Quantitation

WD:WU **Median:** 0.76 **CV:** 0.00 % **No. of 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	Ratios
300	1	678.9411	74.83	2	32.5	11.4	1	413-424	K.LVDLEEALQKAK.Q		WD:WU 0.76

Detailed Protein Report

Protein 13: haptoglobin isoform 2 preproprotein [Homo sapiens]

Accession:	gi|186910296	**Score:**	169.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	38.4
Database Date:	2015-11-30	**pI:**	6.1
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	12.7
		No. of unique Peptides:	3

Quantitation

WD:WU	**Median:** 0.91	**CV:** 32.14 %	**No. of Peptides:** 3

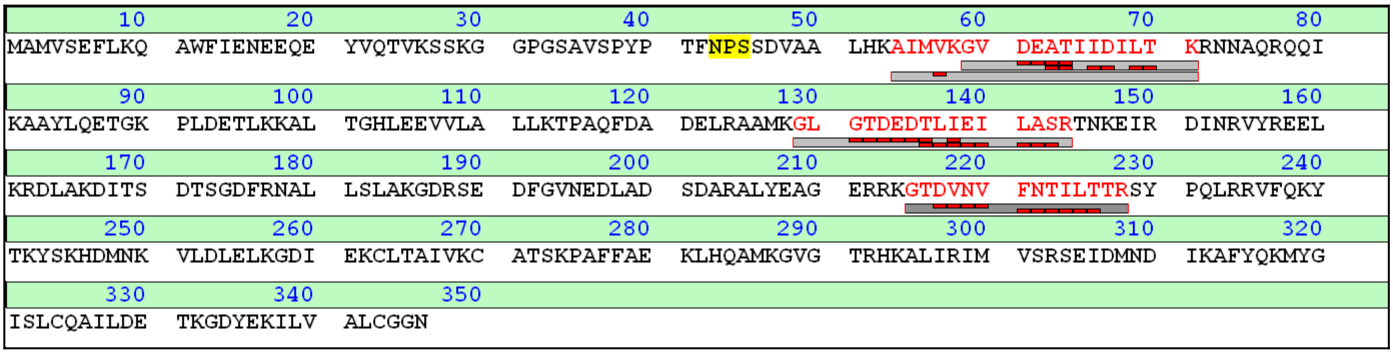
10	20	30	40	50	60	70	80
MSALGAVIAL	LLWGQLFAVD	SGNDVTDIAD	DGCPKPPEIA	HGYVEHSVRY	QCKNYYKLRT	EGDGVYTLNN	EKQWINKAVG
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
DKLPECEAVC	GKPKNPANPV	QRILGGHLDA	KGSFPWQAKM	VSHHNLTTGA	TLINEQWLLT	TAKNLFLNHS	ENATAKDIAP
170	**180**	**190**	**200**	**210**	**220**	**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		WD:WU	0.63
73	2	619.9745	-5.86	3	29.9	61.3	1	78-94	K.AVGDKLPECEAVCGKPK.N	Carbamidomethyl: 9, 13	WD:WU	1.35
1754	4	645.8334	-54.84	2	50.3	65.3	0	157-168	K.DIAPTLTLYVGK.K		WD:WU	0.87

Detailed Protein Report

Protein 14: **annexin A1 [Homo sapiens]**

Accession:	gi|4502101	**Score:**	145.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	38.7
Database Date:	2015-11-30	**pI:**	6.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	13.9
		No. of unique Peptides:	4



```
        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
2994	1	973.5095	-39.14	2	66.2	10.2	1	54-71	K.AIMVKGVDEATIIDILTK.R	Oxidation: 3
2228	1	694.3075	-115.27	2	56.3	17.4	0	59-71	K.GVDEATIIDILTK.R	
2959	5	851.9284	-21.25	2	65.8	81.3	0	129-144	K.GLGTDEDTLIEILASR.T	
2388	2	775.8834	-37.22	2	58.2	36.2	0	215-228	K.GTDVNVFNTILTTR.S	

Detailed Protein Report

Protein 15: **fibrinogen gamma chain isoform gamma-A precursor [Homo sapiens]**

Accession:	gi|70906437	**Score:**	139.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	49.5
Database Date:	2015-11-30	**pI:**	5.7
		Sequence Coverage [%]:	10.8
		No. of unique Peptides:	4

Quantitation

WD:WU **Median:** 0.89 **CV:** 12.14 % **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
127	2	757.2233	-190.62	2	30.5	61.4	0	135-146	R.YLQEIYNSNNQK.I		WD:WU 1.00
1191	1	647.3732	-13.52	2	43.1	26.2	0	189-199	K.QSGLYFIKPLK.A		
2104	2	841.8525	-155.05	2	54.7	23.4	0	259-273	K.IHLISTQSAIPYALR.V		
329	1	559.1487	-212.08	2	33.2	28.9	0	274-282	R.VELEDWNGR.T		WD:WU 0.79

Detailed Protein Report

Protein 16: titin isoform N2-A [Homo sapiens]

Accession:	gi|291045225	**Score:**	136.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	3711.3
Database Date:	2015-11-30	**pI:**	6.1
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	0.4
		No. of unique Peptides:	10

Quantitation

WD:WU	**Median:**	0.95	**CV:**	23.37 %	**No. of Peptides:**	3

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	Ratios	
1331	1	640.2131	-156.95	2	45.0	10.2	1	9719-9728	K.EVTIMEEKER.A	Oxidation: 5	WD:WU	0.85
881	2	555.3353	87.65	2	39.8	14.2	0	11321-11331	K.GTAIFACDIAK.D		WD:WU	1.31
627	8	481.1600	-205.16	2	36.2	13.1	0	13135-13142	K.TWVLATDR.A			
1108	1	540.7821	22.96	2	42.5	15.6	1	15065-15073	K.EIREGADYK.L			
2888	1	900.4707	-22.65	2	64.8	13.7	0	15435-15450	K.NETVIEKPTDALQITK.E			
2673	3	813.4051	24.69	2	61.8	13.6	0	17073-17085	R.VPDLLEGCQYEFR.V	Carbamidomethyl: 8		
2745	1	656.8669	67.42	2	62.7	10.9	0	28426-28437	K.YTLTVENNSGSK.S			
98	1	529.8207	-183.86	3	30.5	11.1	1	30355-30368	K.DDGGSRVTGYYIER.K			
2593	1	616.1731	-223.16	2	60.7	11.0	1	31970-31979	R.MPYDVPEPRK.Y			
27	2	731.6483	-99.39	3	29.3	11.9	2	32802-32820	K.TNLQFMGQAFKSIHEKVSK.I		WD:WU	0.77

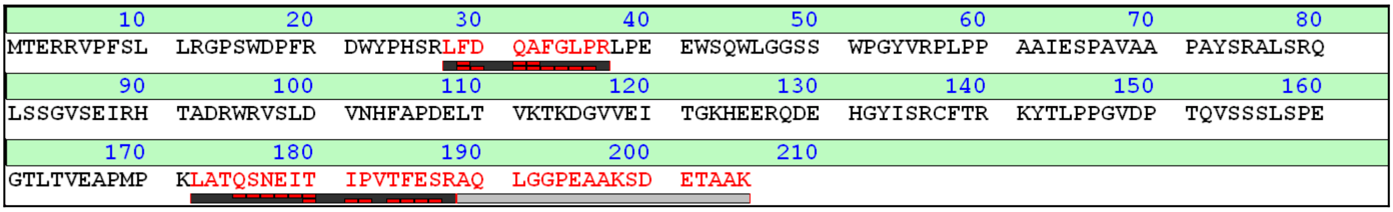
Detailed Protein Report

Protein 17: heat shock protein beta-1 [Homo sapiens]

Accession:	gi|4504517	**Score:**	113.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	22.8
Database Date:	2015-11-30	**pI:**	6.0
		Sequence Coverage [%]:	21.5
		No. of unique Peptides:	3

Quantitation

WD:WU **Median:** 0.49 **CV:** 0.00 % **No. of Peptides:** 1



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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1772	4	582.3088	-9.00	2	50.5	62.7	0	28-37	R.LFDQAFGLPR.L		
1666	1	953.4317	-71.06	2	49.5	35.6	0	172-188	K.LATQSNEITIPVTFESR.A		WD:WU 0.49
2886	2	822.4678	63.76	2	64.8	15.6	1	189-205	R.AQLGGPEAAKSDETAAK.-		

Detailed Protein Report

Protein 18: PREDICTED: POTE ankyrin domain family member E isoform X1 [Homo sapiens]

Accession:	gi|578804361	**Score:**	106.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	76.6
Database Date:	2015-11-30	**pI:**	4.9
		Sequence Coverage [%]:	7.0
		No. of unique Peptides:	3

Quantitation

WD:WU **Median:** 0.44 **CV:** 20.64 % **No. of Peptides:** 3

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	Ratios
1146	1	984.4853	-59.25	2	43.0	11.3	0	396-413	R.VAPEEHPILLTEAPLNPK.A		WD:WU 0.47
1411	4	895.9110	-43.08	2	46.4	42.4	0	539-554	K.SYELPDGQVITIGNER.F		WD:WU 0.54
74	2	758.8545	-0.57	2	30.1	53.0	0	660-672	K.QEYDESGPSIVHR.K		WD:WU 0.33

Detailed Protein Report

Protein 19: complement C3 precursor [Homo sapiens]

Accession:	gi|115298678	**Score:**	79.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	187.0
Database Date:	2015-11-30	**pI:**	6.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.5
		No. of unique Peptides:	4

Quantitation

WD:WU	**Median:** 4.52	**CV:** 0.00 %	**No. of Peptides:** 1

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2933	1	940.0026	13.02	2	65.4	22.8	0	226-241	K.EYVLPSFEVIVEPTEK.F		

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2727	4	701.3852	-51.38	2	62.5	16.6	0	892-904	K.SSLSVPYVIVPLK.T		
1782	5	1086.9427	-40.31	2	50.9	20.1	2	1505-1522	K.LCRDELCRCAEENCFIQK.S		WD:WU 4.52
192	1	650.8121	22.36	2	31.2	19.9	0	1536-1546	K.ACEPGVDYVYK.T	Carbamidomethyl: 2	

Detailed Protein Report

Protein 20: hemoglobin subunit epsilon [Homo sapiens]

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

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2297	8	596.8075	-111.81	2	57.0	16.1	0	134-145	K.LVSAVAIALAHK.Y	

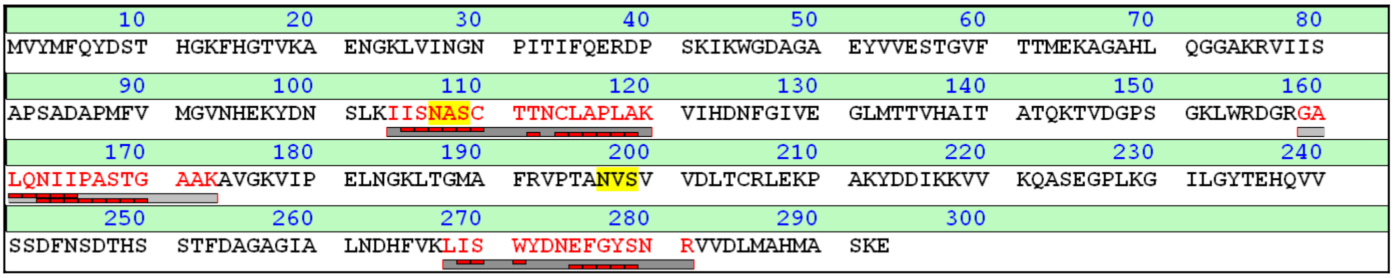
Detailed Protein Report

Protein 21: glyceraldehyde-3-phosphate dehydrogenase isoform 2 [Homo sapiens]

Accession:	gi|378404908	**Score:**	77.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	31.5
Database Date:	2015-11-30	**pI:**	7.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	15.7
		No. of unique Peptides:	3

Quantitation

WD:WU **Median:** 1.30 **CV:** 5.57 % **No. of Peptides:** 2



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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
703	1	917.4101	-58.22	2	37.6	39.4	0	104-120	K.IISNASCTTNCLAPLAK.V	Carbamidomethyl: 7, 11	WD:WU 1.23
904	2	706.3818	-24.09	2	40.1	26.3	0	159-173	R.GALQNIIPASTGAAK.A		WD:WU 1.37
1642	1	882.2784	-143.30	2	48.8	12.0	0	268-281	K.LISWYDNEFGYSNR.V		

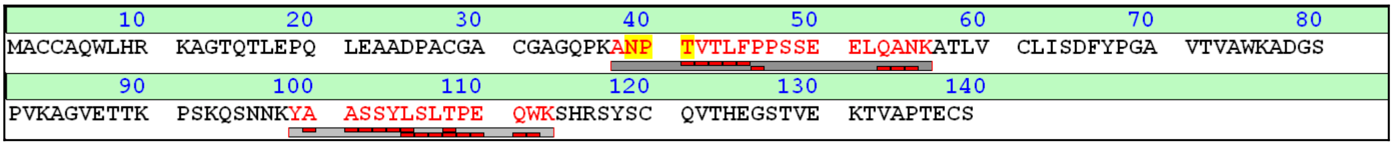
Detailed Protein Report

Protein 22: immunoglobulin lambda-like polypeptide 5 isoform 2 [Homo sapiens]

Accession:	gi|372466586	**Score:**	76.9
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

Quantitation

WD:WU **Median:** 0.70 **CV:** 7.71 % **No. of 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	Ratios
1500	1	1022.0151	-8.03	2	47.1	12.8	0	38-56	K.ANPTVTLFPPSSEELQANK.A		WD:WU 0.65
1789	11	872.4180	-17.25	2	50.7	64.0	0	99-113	K.YAASSYLSLTPEQWK.S		WD:WU 0.76

Detailed Protein Report

Protein 23: transthyretin precursor [Homo sapiens]

Accession:	gi|4507725	**Score:**	76.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	15.9
Database Date:	2015-11-30	**pI:**	5.4
		Sequence Coverage [%]:	8.8
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 1.69 **CV:** 0.00 % **No. of Peptides:** 1

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1401	2	683.8722	-15.95	2	45.9	76.1	0	42-54	R.GSPAINVAVHVFR.K		WD:WU 1.69

Detailed Protein Report

Protein 24: **c-myc promoter-binding protein-1 isoform MBP-1 [Homo sapiens]**

Accession: gi|319996655
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 71.8
MW [kDa]: 36.9
pI: 5.9
Sequence Coverage [%]: 7.9
No. of unique Peptides: 2

Quantitation

WD:WU **Median:** 0.81 **CV:** 20.36 % **No. of Peptides:** 2

10	20	30	40	50	60	70	80
MIEMDGTENK	SKFGANAILG	VSLAVCKAGA	VEKGVPLYRH	IADLAGNSEV	ILPVPAFNVI	NGGSHAGNKL	AMQEFMILPV
90	100	110	120	130	140	150	160
GAANFREAMR	IGAEVYHNLK	NVIKEKYGKD	ATNVGDEGGF	APNILENKEG	LELLKTAIGK	AGYTDKVVIG	MDVAASEFFR
170	180	190	200	210	220	230	240
SGKYDLDFKS	PDDPSRYISP	DQLADLYKSF	IKDYPVVSIE	DPFDQDDWGA	WQKFTASAGI	QVVGDDLTVT	NPKRIAKAVN
250	260	270	280	290	300	310	320
EKSCNCLLLK	VNQIGSVTES	LQACKLAQAN	GWGVMVSHRS	GETEDTFIAD	LVVGLCTGQI	KTGAPCRSER	LAKYNQLLRI
330	340	350					
EEELGSKAKF	AGRNFRNPLA	K					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1599	2	713.3423	-34.09	2	48.3	38.9	0	177-188	R.YISPDQLADLYK.S		WD:WU 0.67
584	1	817.3947	-24.01	2	36.2	33.0	0	251-265	K.VNQIGSVTESLQACK.L	Carbamidomethyl: 14	WD:WU 1.00

Detailed Protein Report

Protein 25: stAR-related lipid transfer protein 9 [Homo sapiens]

Accession:	gi|270265793	**Score:**	69.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	516.0
Database Date:	2015-11-30	**pI:**	5.9
		Sequence Coverage [%]:	1.3
		No. of unique Peptides:	4

Quantitation

WD:WU	**Median:**	0.73	**CV:**	0.00 %	**No. of Peptides:**	1

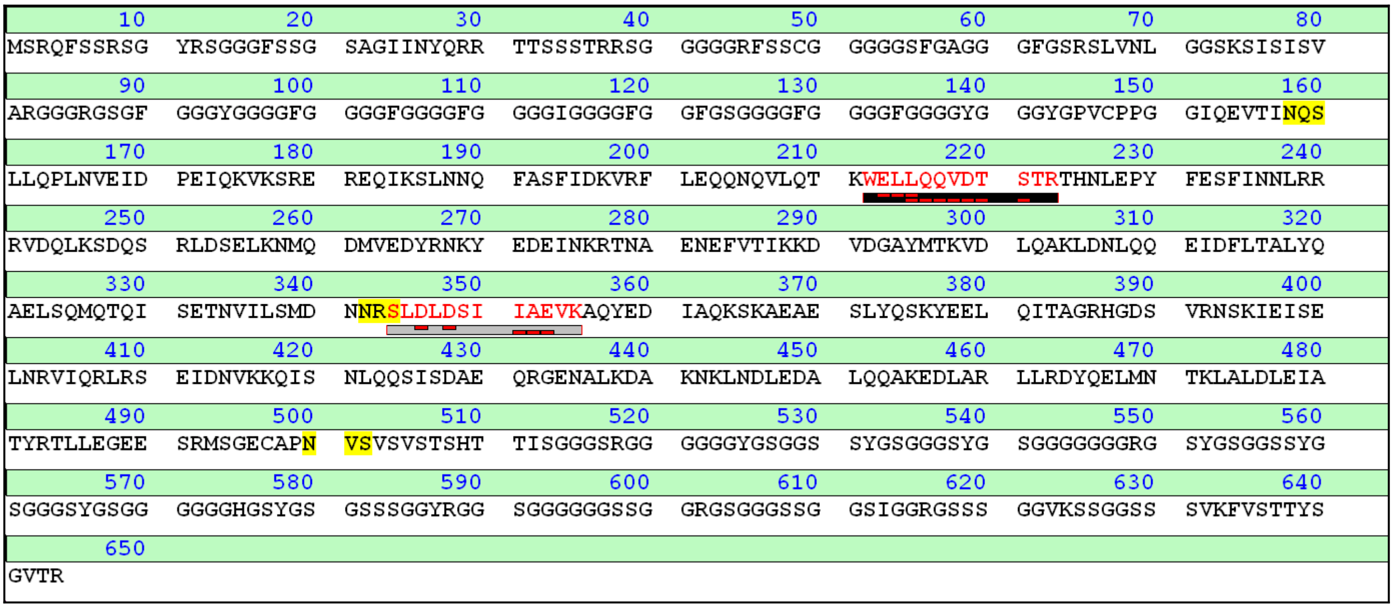
Detailed Protein Report

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2859	3	648.3692	122.78	2	64.5	15.6	1	134-145	R.EKDCASLPSSCR.I		
2847	1	665.3691	57.41	2	64.1	17.6	0	2192-2202	R.EFTNTSLHPQR.M		
405	1	565.3234	16.33	2	34.1	11.7	0	2310-2319	R.QETVSPLLSR.T		
1886	1	863.9273	-37.56	2	52.2	12.3	1	2739-2754	K.KVVAALPSQAPYDDPR.V		WD:WU 0.73

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

Accession:	gi|119395750	**Score:**	69.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	66.0
Database Date:	2015-11-30	**pI:**	8.8
		Sequence Coverage [%]:	3.7
		No. of unique Peptides:	2



```
        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	

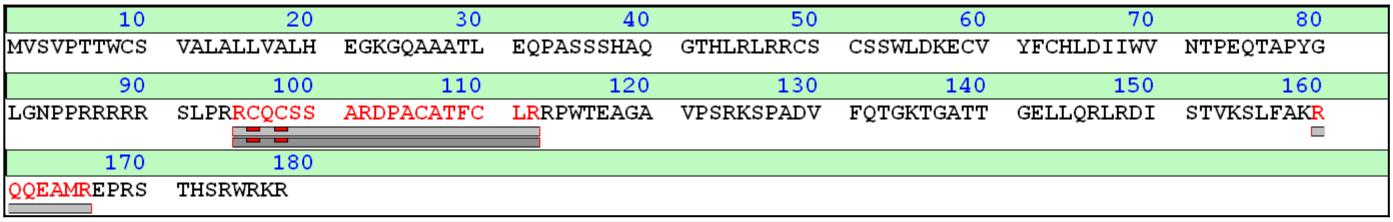
Detailed Protein Report

Protein 27: endothelin-2 preproprotein [Homo sapiens]

Accession:	gi|4503463	**Score:**	57.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	19.9
Database Date:	2015-11-30	**pI:**	12.1
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	14.0
		No. of unique Peptides:	3

Quantitation

WD:WU **Median:** 0.64 **CV:** 0.00 % **No. of 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	Ratios
2946	1	1051.5610	95.12	2	65.6	10.9	2	95-112	R.RCQCSSARDPACATFCLR.R	Carbamidomethyl: 4, 12	
2155	1	1051.4608	-0.17	2	55.5	16.2	2	95-112	R.RCQCSSARDPACATFCLR.R	Carbamidomethyl: 12, 16	
587	1	459.6056	-275.62	2	35.7	17.8	1	160-166	K.RQQEAMR.E		WD:WU 0.64

Detailed Protein Report

Protein 28: keratin, type II cytoskeletal 4 [Homo sapiens]

Accession:	gi|331999954	**Score:**	57.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	56.1
Database Date:	2015-11-30	**pI:**	6.2
		Sequence Coverage [%]:	3.3
		No. of unique Peptides:	2

Quantitation

WD:WU **Median:** 0.82 **CV:** 0.00 % **No. of Peptides:** 1

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

```
       490        500        510        520        530
GFGLSSGFGS GSGSGFGFGG SVSGSSSSKI ISTTTLNKRR
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
365	1	678.3483	-55.17	2	33.6	39.9	1	401-412	K.RVELEAALQQAK.E		WD:WU 0.82
1796	1	599.9815	-22.51	3	51.1	17.3	1	402-417	R.VELEAALQQAKEELAR.M		

Detailed Protein Report

Protein 29: centromere protein F [Homo sapiens]

Accession:	gi|55770834	**Score:**	56.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	357.3
Database Date:	2015-11-30	**pI:**	4.9
		Sequence Coverage [%]:	1.4
		No. of unique Peptides:	2

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
104	2	1043.8924	-98.05	2	30.5	15.3	0	128-147	R.SQQAAQSADVSLNPCNTPQK.I	
552	1	600.8199	-67.28	2	35.3	13.6	1	2316-2325	K.KQLCVLQQLK.E	

Detailed Protein Report

Protein 30: PREDICTED: nebulin isoform X22 [Homo sapiens]

Accession:	gi|530370465	**Score:**	56.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	961.5
Database Date:	2015-11-30	**pI:**	9.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	0.6
		No. of unique Peptides:	4

Quantitation

WD:WU	**Median:** 0.74	**CV:** 5.98 %	**No. of Peptides:** 2

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

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
415	4	544.7701	86.52	2	34.2	12.0	0	646-654	K.SMNYCETPK.Y	Oxidation: 2		
1176	2	729.3599	-9.93	2	43.4	18.3	1	3617-3628	R.KAYDLQSDNLYK.S		WD:WU	0.69
993	1	662.3199	-62.62	2	41.2	12.9	2	7204-7214	K.VKDEVSDLKYK.E		WD:WU	0.78
2801	1	994.5013	20.67	2	63.5	13.2	1	8000-8015	K.LNQENFSSVLYKENMR.K	Oxidation: 15		

Detailed Protein Report

Protein 31: PREDICTED: splicing factor, proline- and glutamine-rich isoform X5 [Homo sapiens]

Accession:	gi|530363148	**Score:**	54.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	72.2
Database Date:	2015-11-30	**pI:**	9.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	5.1
		No. of unique Peptides:	3

Quantitation

WD:WU	**Median:**	1.47	**CV:**	0.00 %	**No. of Peptides:**	1	

Alias proteins:

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

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
378	2	678.1836	-200.95	2	33.8	28.3	1	268-279	R.SEEKISDSEGFK.A		
18	2	736.0042	54.34	3	29.4	11.7	1	609-630	R. DMRMGGGGAMNMGDPYGSGGQ F	Oxidation: 2, 10	
8	2	736.0117	64.51	3	29.3	14.9	1	609-630	R. DMRMGGGGAMNMGDPYGSGGQ F	Oxidation: 4, 12	WD:WU 1.47

Detailed Protein Report

Protein 32: CDK5 regulatory subunit-associated protein 2 isoform c [Homo sapiens]

Accession:	gi|440309853	**Score:**	54.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	189.5
Database Date:	2015-11-30	**pI:**	5.4
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.8
		No. of unique Peptides:	4

Quantitation

WD:WU **Median:** 0.89 **CV:** 5.29 % **No. of Peptides:** 2

```
        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	Ratios
93	1	529.5810	3.65	3	30.1	13.6	1	271-283	K.ERETEAAQMEHQK.E		WD:WU 0.84

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2305	1	937.4652	-77.24	2	57.1	11.9	1	708-723	R.LPILIKPSRSLGNMYR.L	Oxidation: 14	
268	3	501.1673	-209.52	2	32.1	13.8	1	1391-1399	K.EQLARGAEK.A		WD:WU 0.94
578	1	575.8071	-12.69	2	36.1	15.6	1	1558-1566	K.LTLEEAYRR.L		

Detailed Protein Report

Protein 33: **PREDICTED: ceruloplasmin isoform X4 [Homo sapiens]**

Accession:	gi|578807068	**Score:**	54.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	103.1
Database Date:	2015-11-30	**pI:**	5.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.6
		No. of unique Peptides:	1

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

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

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

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

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

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

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

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

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

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

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

       890        900        910
STVDQVKDLY CKEGEKKWSR L
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2949	1	735.4039	-26.64	2	65.6	54.0	0	188-201	K.DIASGLIGPLIICK.K	Carbamidomethyl: 13

Detailed Protein Report

Protein 34: cadherin EGF LAG seven-pass G-type receptor 3 precursor [Homo sapiens]

Accession:	gi|145309304	**Score:**	53.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	358.0
Database Date:	2015-11-30	**pI:**	6.2
		Sequence Coverage [%]:	1.2
		No. of unique Peptides:	3

Detailed Protein Report

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

Detailed Protein Report

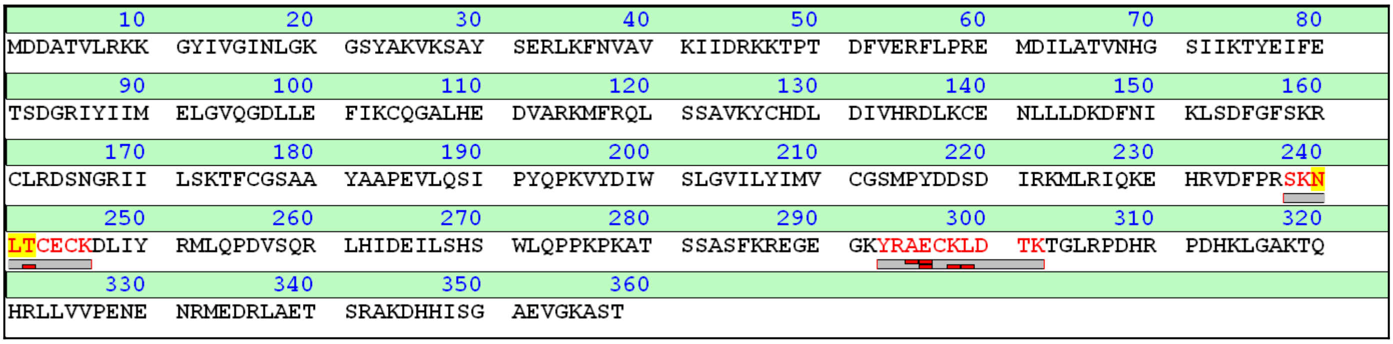
Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1390	1	942.4814	27.90	2	46.2	11.4	1	232-250	R.RNCLPGASGSGPELDSAPR.T	
2841	1	648.3701	87.56	1	64.1	13.5	0	1513-1518	R.CEVAAR.S	
942	1	470.6329	-182.64	2	40.6	10.3	0	2331-2338	R.MEHPSSPR.G	

Protein 35: testis-specific serine/threonine-protein kinase 2 [Homo sapiens]

Accession:	gi|194294513	**Score:**	52.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	40.9
Database Date:	2015-11-30	**pI:**	9.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	5.3
		No. of unique Peptides:	2

Quantitation

WD:WU **Median:** 0.95 **CV:** 0.00 % **No. of Peptides:** 1



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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1388	1	570.1598	-180.58	2	45.7	10.7	1	238-246	R.SKNLTCECK.D	Carbamidomethyl: 6, 8	
174	3	642.2924	-49.65	2	31.4	20.1	2	293-302	K.YRAECKLDTK.T	Carbamidomethyl: 5	WD:WU 0.95

Detailed Protein Report

Protein 36: glycerol-3-phosphate dehydrogenase, mitochondrial precursor [Homo sapiens]

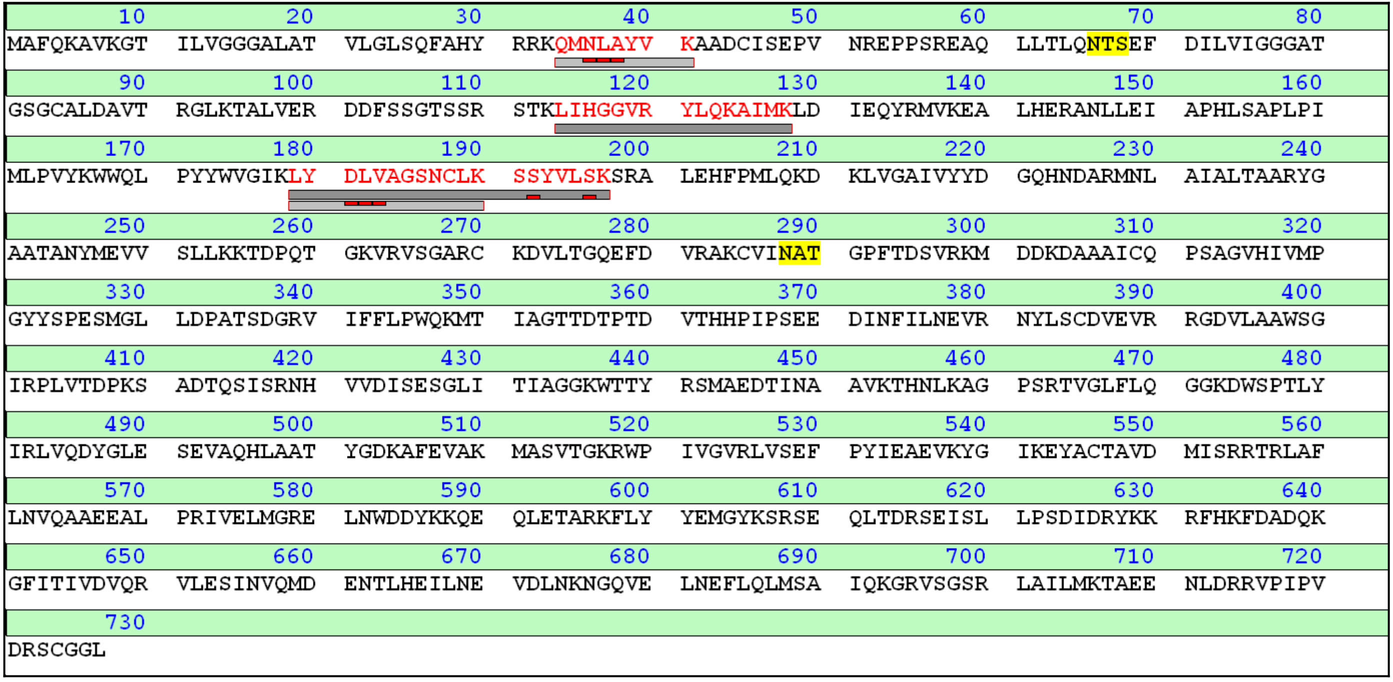
Accession:	gi|285002231	**Score:**	51.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	80.8
Database Date:	2015-11-30	**pI:**	8.4
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	5.8
		No. of unique Peptides:	4

Quantitation

WD:WU **Median:** 0.94 **CV:** 0.00 % **No. of Peptides:** 1

Alias proteins:

Accession	Name	Description
gi|530370176	refseq_human (refseq_human_20140103.fasta)	PREDICTED: glycerol-3-phosphate dehydrogenase, mitochondrial isoform X1 [Homo sapiens]
gi|285002233	refseq_human (refseq_human_20140103.fasta)	glycerol-3-phosphate dehydrogenase, mitochondrial precursor [Homo sapiens]



```
        10         20         30         40         50         60         70         80
MAFQKAVKGT ILVGGGALAT VLGLSQFAHY RRKQMNLAYV KAADCISEPV NREPPSREAQ LLTLQNTSEF DILVIGGGAT
        90        100        110        120        130        140        150        160
GSGCALDAVT RGLKTALVER DDFSSGTSSR STKLIHGGVR YLQKAIMKLD IEQYRMVKEA LHERANLLEI APHLSAPLPI
       170        180        190        200        210        220        230        240
MLPVYKWWQL PYYWVGIKLY DLVAGSNCLK SSYVLSKSRA LEHFPMLQKD KLVGAIVYYD GQHNDARMNL AIALTAARYG
       250        260        270        280        290        300        310        320
AATANYMEVV SLLKKTDPQT GKVRVSGARC KDVLTGQEFD VRAKCVINAT GPFTDSVRKM DDKDAAAICQ PSAGVHIVMP
       330        340        350        360        370        380        390        400
GYYSPESMGL LDPATSDGRV IFFLPWQKMT IAGTTDTPTD VTHHPIPSEE DINFILNEVR NYLSCDVEVR RGDVLAAWSG
       410        420        430        440        450        460        470        480
IRPLVTDPKS ADTQSISRNH VVDISESGLI TIAGGKWTTY RSMAEDTINA AVKTHNLKAG PSRTVGLFLQ GGKDWSPTLY
       490        500        510        520        530        540        550        560
IRLVQDYGLE SEVAQHLAAT YGDKAFEVAK MASVTGKRWP IVGVRLVSEF PYIEAEVKYG IKEYACTAVD MISRRTRLAF
       570        580        590        600        610        620        630        640
LNVQAAEEAL PRIVELMGRE LNWDDYKKQE QLETARKFLY YEMGYKSRSE QLTDRSEISL LPSDIDRYKK RFHKFDADQK
       650        660        670        680        690        700        710        720
GFITIVDVQR VLESINVQMD ENTLHEILNE VDLNKNGQVE LNEFLQLMSA IQKGRVSGSR LAILMKTAEE NLDRRVPIPV
       730
DRSCGGL
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
810	2	491.6440	-225.52	2	38.5	17.3	0	34-41	K.QMNLAYVK.A	Oxidation: 2	WD:WU 0.94
1028	1	863.9268	-97.49	2	41.6	10.0	2	114-128	K.LIHGGVRYLQKAIMK.L		
2820	1	676.8699	33.04	2	63.9	12.5	0	179-190	K.LYDLVAGSNCLK.S	Carbamidomethyl: 10	
29	1	706.3122	-81.53	3	29.6	11.9	1	179-197	K.LYDLVAGSNCLKSSYVLSK.S	Carbamidomethyl: 10	

Detailed Protein Report

Protein 37: **Fanconi anemia group I protein isoform 1 [Homo sapiens]**

Accession:	gi|164607124	**Score:**	51.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	149.2
Database Date:	2015-11-30	**pI:**	6.3
		Sequence Coverage [%]:	3.2
		No. of unique Peptides:	3

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	SSLLTALFRD	SIQSHQESLS	VLRSSNEFMR	YAVNVALQKV	QQLKETGHVS	GPDGQNPEKI	FQNLCDITRV
890	900	910	920	930	940	950	960
LLWRYTSIPT	SVEESGKKEK	GKSISLLCLE	GLQKIFSAVQ	QFYQPKIQQF	LRALDVTDKE	GEEREDADVS	VTQRTAFQIR
970	980	990	1000	1010	1020	1030	1040
QFQRSLLNLL	SSQEEDFNSK	EALLLVTVLT	SLSKLLEPSS	PQFVQMLSWT	SKICKENSRE	DALFCKSLMN	LLFSLHVSYK
1050	1060	1070	1080	1090	1100	1110	1120
SPVILLRDLS	QDIHGHLGDI	DQDVEVEKTN	HFAIVNLRTA	APTVCLLVLS	QAEKVLEEVD	WLITKLKGQV	SQETLSEEAS
1130	1140	1150	1160	1170	1180	1190	1200
SQATLPNQPV	EKAIIMQLGT	LLTFFHELVQ	TALPSGSCVD	TLLKDLCKMY	TTLTALVRYY	LQVCQSSGGI	PKNMEKLVKL
1210	1220	1230	1240	1250	1260	1270	1280
SGSHLTPLCY	SFISYVQNKS	KSLNYTGEKK	EKPAAVATAM	ARVLRETKPI	PNLIFAIEQY	EKFLIHLSKK	SKVNLMQHMK
1290	1300	1310	1320	1330			
LSTSRDFKIK	GNILDMVLRE	DGEDENEEGT	ASEHGGQNKE	PAKKKRKK			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
426	4	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	945-960	R.EDADVSVTQRTAFQIR.Q	
13	1	814.3623	-84.24	2	29.4	15.2	1	1165-1178	K.DLCKMYTTLTALVR.Y	

Detailed Protein Report

Protein 38: 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

Quantitation

WD:WU **Median:** 3.50 **CV:** 0.00 % **No. of 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	Ratios
766	1	606.3268	-23.04	2	38.4	50.1	0	140-150	R.QITVNDLPVGR.S		WD:WU 3.50

Detailed Protein Report

Protein 39: PREDICTED: serine/threonine-protein kinase 31 isoform X3 [Homo sapiens]

Accession:	gi|578813577	**Score:**	49.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	95.7
Database Date:	2015-11-30	**pI:**	4.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.8
		No. of unique Peptides:	3

Quantitation

WD:WU **Median:** 0.61 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MWVQGHSSRA	SATESVSFSG	IVQMDEDTHY	DKVEDVVGSH	IEDAVTFWAQ	SINRNKDIMK	IGCSLSEVCP	QASSVLGNLD
90	100	110	120	130	140	150	160
PNKIYGGLFS	EDQCWYRCKV	LKIISVEKCL	VRYIDYGNTE	ILNRSDIVEI	PLELQFSSVA	KKYKLWGLHI	PSDQEVTQFD
170	180	190	200	210	220	230	240
QQEKAAAVDL	TNHLEYTLKT	YIDTRMKNLA	AKMEILKEMR	HVDISVRFGK	DLSDAIQVLD	EGCFTTPASL	NGLEIIWAEY
250	260	270	280	290	300	310	320
SLAQENIKTC	EYVSEGNILI	AQRNEMQQKL	YMSVEDFILE	VDESSLNKRL	KTLQDLSVSL	EAVYGQAKEG	ANSDEILKKF
330	340	350	360	370	380	390	400
YDWKCDKREE	FTSVRSETDA	SLHRLVAWFQ	RTLKVFDLSV	EGSLISEDAM	DNIDEILEKT	ESSVCKELEI	ALVDQGDADK
410	420	430	440	450	460	470	480
EIISNTYSQV	LQKIHSEERL	IATVQAKYKD	SIEFKKQLIE	YLNKSPSVDH	LLSIKKTLKS	LKALLRWKLV	EKSNLEESDD
490	500	510	520	530	540	550	560
PDGSQIEKIK	EEITQLRNNV	FQEIYHEREE	YEMLTSLAQK	WFPELPLLHP	EIGLLKYMNS	GGLLTMSLER	DLLDAEPMKE
570	580	590	600	610	620	630	640
LSSKRPLVRS	EVNGQIILLK	GYSVDVDTEA	KVIERAATYH	RAWREAEGDS	GLLPLIFLFL	CKSDPMAYLM	VPYYPRANLN
650	660	670	680	690	700	710	720
AVQANMPLNS	EETLKVMKGV	AQGLHTLHKA	DIIHGSLHQN	NVFALNREQG	IVGDFDFTKS	VSQRASVNMM	VGDLSLMSPE
730	740	750	760	770	780	790	800
LKMGKPASPG	SDLYAYGCLL	LWLSVQNQEF	EINKDGIPKV	DQFHLDDKVK	SLLCSLICYR	SSMTAEQVLN	AECFLMPKEQ
810	820	830	840	850			
SVPNPEKDTE	YTLYKKEEEI	KTENLDKCME	KTRNGEANFD	C			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
452	1	524.1225	-252.65	2	34.6	17.8	0	551-559	R.DLLDAEPMK.E	Oxidation: 8	
181	7	592.2959	31.07	2	31.1	21.2	0	581-591	K.GYSVDVDTEAK.V		WD:WU 0.61
1907	1	734.2871	-85.93	2	52.2	10.5	2	822-833	K.TENLDKCMEKTR.N		

Detailed Protein Report

Protein 40: **fibrillin-1 precursor [Homo sapiens]**

Accession:	gi|281485550	**Score:**	49.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	312.1
Database Date:	2015-11-30	**pI:**	4.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.4
		No. of unique Peptides:	3

Quantitation

WD:WU	**Median:** 0.75	**CV:** 0.00 %	**No. of Peptides:**	1

10	20	30	40	50	60	70	80
MRRGRLLEIA	LGFTVLLASY	TSHGADANLE	AGNVKETRAS	RAKRRGGGGH	DALKGPNVCG	SRYNAYCCPG	WKTLPGGNQC
90	100	110	120	130	140	150	160
IVPICRHSCG	DGFCSRPNMC	TCPSGQIAPS	CGSRSIQHCN	IRCMNGGSCS	DDHCLCQKGY	IGTHCGQPVC	ESGCLNGGRC
170	180	190	200	210	220	230	240
VAPNRCACTY	GFTGPQCERD	YRTGPCFTVI	SNQMCQGQLS	GIVCTKTLCC	ATVGRAWGHP	CEMCPAQPHP	CRRGFIPNIR
250	260	270	280	290	300	310	320
TGACQDVDEC	QAIPGLCQGG	NCINTVGSFE	CKCPAGHKLN	EVSQKCEDID	ECSTIPGICE	GGECTNTVSS	YFCKCPPGFY
330	340	350	360	370	380	390	400
TSPDGTRCID	VRPGYCYTAL	TNGRCSNQLP	QSITKMQCCC	DAGRCWSPGV	TVAPEMCPIR	ATEDFNKLCS	VPMVIPGRPE
410	420	430	440	450	460	470	480
YPPPPLGPIP	PVLPVPPGFP	PGPQIPVPRP	PVEYLYPSRE	PPRVLPVNVT	DYCQLVRYLC	QNGRCIPTPG	SYRCECNKGF
490	500	510	520	530	540	550	560
QLDLRGECID	VDECEKNPCA	GGECINNQGS	YTCQCRAGYQ	STLTRTECRD	IDECLQNGRI	CNNGRCINTD	GSFHCVCNAG
570	580	590	600	610	620	630	640
FHVTRDGKNC	EDMDECSIRN	MCLNGMCINE	DGSFKCICKP	GFQLASDGRY	CKDINECETP	GICMNGRCVN	TDGSYRCECF
650	660	670	680	690	700	710	720
PGLAVGLDGR	VCVDTHMRST	CYGGYKRGQC	IKPLFGAVTK	SECCCASTEY	AFGEPCQPCP	AQNSAEYQAL	CSSGPGMTSA
730	740	750	760	770	780	790	800
GSDINECALD	PDICPNGICE	NLRGTYKCIC	NSGYEVDSTG	KNCVDINECV	LNSLLCDNGQ	CRNTPGSFVC	TCPKGFIYKP
810	820	830	840	850	860	870	880
DLKTCEDIDE	CESSPCINGV	CKNSPGSFIC	ECSSESTLDP	TKTICIETIK	GTCWQTVIDG	RCEININGAT	LKSQCCSSLG
890	900	910	920	930	940	950	960
AAWGSPCTLC	QVDPICGKGY	SRIKGTQCED	IDECEVFPGV	CKNGLCVNTR	GSFKCQCPSG	MTLDATGRIC	LDIRLETCFL
970	980	990	1000	1010	1020	1030	1040
RYEDEECTLP	IAGRHRMDAC	CCSVGAAWGT	EECEECPMRN	TPEYEELCPR	GPGFATKEIT	NGKPFFKDIN	ECKMIPSLCT
1050	1060	1070	1080	1090	1100	1110	1120
HGKCRNTIGS	FKCRCDSGFA	LDSEERNCTD	IDECRISPDL	CGRGQCVNTP	GDFECKCDEG	YESGFMMMKN	CMDIDECQRD
1130	1140	1150	1160	1170	1180	1190	1200
PLLCRGGVCH	NTEGSYRCEC	PPGHQLSPNI	SACIDINECE	LSAHLCPNGR	CVNLIGKYQC	ACNPGYHSTP	DRLFCVDIDE
1210	1220	1230	1240	1250	1260	1270	1280
CSIMNGGCET	FCTNSEGSYE	CSCQPGFALM	PDQRSCTDID	ECEDNPNICD	GGQCTNIPGE	YRCLCYDGFM	ASEDMKTCVD
1290	1300	1310	1320	1330	1340	1350	1360
VNECDLNPNI	CLSGTCENTK	GSFICHCDMG	YSGKKGKTGC	TDINECEIGA	HNCGKHAVCT	NTAGSFKCSC	SPGWIGDGIK
1370	1380	1390	1400	1410	1420	1430	1440
CTDLDECSNG	THMCSQHADC	KNTMGSYRCL	CKEGYTGDGF	TCTDLDECSE	NLNLCGNGQC	LNAPGGYRCE	CDMGFVPSAD
1450	1460	1470	1480	1490	1500	1510	1520
GKACEDIDEC	SLPNICVFGT	CHNLPGLFRC	ECEIGYELDR	SGGNCTDVNE	CLDPTTCISG	NCVNTPGSYI	CDCPPDFELN
1530	1540	1550	1560	1570	1580	1590	1600
PTRVGCVDTR	SGNCYLDIRP	RGDNGDTACS	NEIGVGVSKA	SCCCSLGKAW	GTPCEMCPAV	NTSEYKILCP	GGEGFRPNPI
1610	1620	1630	1640	1650	1660	1670	1680
TVILEDIDEC	QELPGLCQGG	KCINTFGSFQ	CRCPTGYYLN	EDTRVCDDVN	ECETPGICGP	GTCYNTVGNY	TCICPPDYMQ
1690	1700	1710	1720	1730	1740	1750	1760
VNGGNNCMDM	RRSLCYRNYY	ADNQTCDGEL	LFNMTKKMCC	CSYNIGRAWN	KPCEQCPIPS	TDEFATLCGS	QRPGFVIDIY
1770	1780	1790	1800	1810	1820	1830	1840
TGLPVDIDEC	REIPGVCENG	VCINMVGSFR	CECPVGFFYN	DKLLVCEDID	ECQNGPVCQR	NAECINTAGS	YRCDCKPGYR
1850	1860	1870	1880	1890	1900	1910	1920
FTSTGQCNDR	NECQEIPNIC	SHGQCIDTVG	SFYCLCHTGF	KTNDDQTMCL	DINECERDAC	GNGTCRNTIG	SFNCRCNHGF
1930	1940	1950	1960	1970	1980	1990	2000
ILSHNNDCID	VDECASGNGN	LCRNGQCINT	VGSFQCQCNE	GYEVAPDGRT	CVDINECLLE	PRKCAPGTCQ	NLDGSYRCIC
2010	2020	2030	2040	2050	2060	2070	2080
PPGYSLQNEK	CEDIDECVEE	PEICALGTCS	NTEGSFKCLC	PEGFSLSSSG	RRCQDLRMSY	CYAKFEGGKC	SSPKSRNHSK
2090	2100	2110	2120	2130	2140	2150	2160
QECCCALKGE	GWGDPCELCP	TEPDEAFRQI	CPYGSGIIVG	PDDSAVDMDE	CKEPDVCKHG	QCINTDGSYR	CECPFGYILA
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

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	WD:WU 0.75
2800	1	913.4636	99.50	2	63.5	13.3	0	1178-1192	K.YQCACNPGYHSTPDR.L	Carbamidomethyl: 3, 5	
748	6	635.3242	75.75	2	37.8	23.9	1	2482-2492	R.SCKDLDECATK.Q	Carbamidomethyl: 8	

Detailed Protein Report

Protein 41: PREDICTED: ankyrin repeat domain-containing protein 11 isoform X3 [Homo sapiens]

Accession:	gi|578828957	**Score:**	48.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	293.2
Database Date:	2015-11-30	**pI:**	6.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.1
		No. of unique Peptides:	3

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

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2918	1	1155.0468	-67.97	2	65.2	13.4	2	50-71	R.KAGLLFGMGLSGIRAGYPLSER.Q	Oxidation: 8
462	1	475.6124	-248.29	2	34.3	11.4	1	1227-1235	K.SSRSADAEK.S	
2267	1	937.3359	-108.02	2	56.7	10.6	1	1527-1542	R.EKLLGDGDLMMTSFER.M	Oxidation: 10, 11

Detailed Protein Report

Protein 42: neurogenic locus notch homolog protein 1 preproprotein [Homo sapiens]

Accession:	gi|148833508	**Score:**	48.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	272.3
Database Date:	2015-11-30	**pI:**	4.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.3
		No. of unique Peptides:	4

Detailed Protein Report

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        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
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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	
2039	1	698.2787	-136.84	2	54.1	11.8	0	1992-2004	R.MHDGTTPLILAAR.L	

Detailed Protein Report

Protein 43: PREDICTED: neurobeachin-like protein 1 isoform X8 [Homo sapiens]

Accession:	gi|578804777	**Score:**	48.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	305.4
Database Date:	2015-11-30	**pI:**	6.0
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	1.7
		No. of unique Peptides:	3

Quantitation

WD:WU	**Median:**	0.18	**CV:**	0.00 %	**No. of Peptides:**	1

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	Ratios
1799	1	1045.0496	94.89	2	50.8	15.5	0	672-690	R.FPAMNEPFTSCCIGSAGQR.T	Carbamidomethyl: 12; Oxidation: 4	
2060	1	899.3817	-81.00	2	54.1	19.6	0	713-730	R.TSFGGILSSASWGGTIEK.S		WD:WU 0.18
864	1	471.1407	-120.89	2	39.2	13.3	0	1269-1276	K.NMSTEDTK.K	Oxidation: 2	

Detailed Protein Report

Protein 44: **PREDICTED: pleckstrin homology domain-containing family A member 4 isoform X3 [Homo sapiens]**

Accession:	gi|530416942	**Score:**	47.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	65.5
Database Date:	2015-11-30	**pI:**	10.7
		Sequence Coverage [%]:	9.6
		No. of unique Peptides:	4

Quantitation

WD:WU **Median:** 0.98 **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	1	711.1755	-208.54	2	33.6	11.6	1	151-163	R.ASRAEGDDYGQPR.S		WD:WU 0.98
375	1	603.6767	-228.84	2	33.8	10.1	0	300-312	R.GPPSEAGGGKPPR.S		
20	1	706.3988	42.59	2	29.2	15.0	2	412-424	R.EAGAPGRAWGRQR.L		
1037	1	945.4829	-32.03	2	41.7	11.1	2	565-582	R.ASSPEGRHLPSPQLGTKK.Y		

Detailed Protein Report

Protein 45: protein FAM45A [Homo sapiens]

Accession:	gi|46275835	**Score:**	47.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	40.5
Database Date:	2015-11-30	**pI:**	6.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	10.4
		No. of unique Peptides:	4

10	20	30	40	50	60	70	80
MAAAEVADTQ	LMLGVGLIEK	DTNGEVLWVW	CYPSTTATLR	NLLLRKCCLT	DENKLLHPFV	FGQYRRTWFY	ITTIEVPDSS
90	100	110	120	130	140	150	160
ILKKVTHFSI	VLTAKDFNPE	KYAAFTRILC	RMYLKHGSPV	KMMESYIAVL	TKGICQSEEN	GSFLSKDFDA	RKAYLAGSIK
170	180	190	200	210	220	230	240
DIVSQFGMET	VILHTALMLK	KRIVVYHPKI	EAVQEFTRTL	PALVWHRQDW	TILHSYVHLN	ADELEALQMC	TGYVAGFVDL
250	260	270	280	290	300	310	320
EVSNRPDLYD	VFVNLAESEI	TIAPLAKEAM	AMGKLHKEMG	QLIVQSAEDP	EKSESHVIQD	IALKTREIFT	NLAPFSEVSA
330	340	350	360				
DGEKRVLNLE	ALKQKRFPPA	TENFLYHLAA	AEQMLKI				

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	46-65	R.KCCLTDENKLLHPFVFGQYR.R	
837	1	491.6643	-76.81	2	38.9	11.9	0	47-54	K.CCLTDENK.L	Carbamidomethyl: 1
917	2	491.6624	-80.76	2	40.3	12.6	0	47-54	K.CCLTDENK.L	Carbamidomethyl: 2
2881	2	973.5257	3.04	2	64.8	12.2	1	85-101	K.VTHFSIVLTAKDFNPEK.Y	

Detailed Protein Report

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

Accession:	gi|332164777	**Score:**	46.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	49.9
Database Date:	2015-11-30	**pI:**	9.0
		Sequence Coverage [%]:	5.3
		No. of unique Peptides:	2

Quantitation

WD:WU **Median:** 0.70 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MSKPHSEAGT	AFIQTQQLHA	AMADTFLEHM	CRLDIDSPPI	TARNTGIICT	IGPASRSVEL	KKGATLKITL	DNAYMEKCDE
90	100	110	120	130	140	150	160
NILWLDYKNI	CKVVEVGSKI	YVDDGLISLQ	VKQKGADFLV	TEVENGGSLG	SKKGVNLPGA	AVDLPAVSEK	DIQDLKFGVE
170	180	190	200	210	220	230	240
QDVDMVFASF	IRKASDVHEV	RKVLGEKGKN	IKIISKIENH	EGVRRFDEIL	EASDGIMVAR	GDLGIEIPAE	KVFLAQKMMI
250	260	270	280	290	300	310	320
GRCNRAGKPV	ICATQMLESM	IKKPRPTRAE	GSDVANAVLD	GADCIMLSGE	TAKGDYPLEA	VRMQHLIARE	AEAAIYHLQL
330	340	350	360	370	380	390	400
FEELRRLAPI	TSDPTEATAV	GAVEASFKCC	SGAIIVLTKS	GRSAHQVARY	RPRAPIIAVT	RNPQTARQAH	LYRGIFPVLC
410	420	430	440	450	460		
KDPVQEAWAE	DVDLRVNFAM	NVGKARGFFK	KGDVVIVLTG	WRPGSGFTNT	MRVVPVP		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
721	1	599.3228	-7.49	2	37.8	35.2	0	33-43	R.LDIDSPPITAR.N		WD:WU 0.70
2063	1	731.7933	-161.16	2	54.4	11.5	0	100-112	K.IYVDDGLISLQVK.Q		

Detailed Protein Report

Protein 47: **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

Quantitation

WD:WU **Median:** 1.59 **CV:** 0.00 % **No. of 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	Ratios
1023	3	617.8379	-30.01	2	41.5	46.2	0	114-123	R.EHVAHLLFLR.D		WD:WU 1.59

Detailed Protein Report

Protein 48: tetratricopeptide repeat protein 37 [Homo sapiens]

Accession:	gi|7662078	**Score:**	45.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	175.4
Database Date:	2015-11-30	**pI:**	8.1
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.4
		No. of unique Peptides:	2

Quantitation

WD:WU **Median:** 0.52 **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	WD:WU 0.52
728	1	705.9560	-25.50	2	37.6	14.3	1	1440-1452	K.LSSLLRLALLALK.V		

Detailed Protein Report

Protein 49: serine/threonine-protein kinase Nek1 isoform 5 [Homo sapiens]

Accession:	gi|313661434	**Score:**	45.8
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 50: transitional endoplasmic reticulum ATPase [Homo sapiens]

Accession:	gi|6005942	**Score:**	45.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	89.3
Database Date:	2015-11-30	**pI:**	5.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.8
		No. of unique Peptides:	2

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2051	4	1051.4305	-44.06	2	54.3	14.5	1	678-696	K.MTNGFSGADLTEICQRACK.L	Carbamidomethyl: 18
1970	4	1051.4242	-50.05	2	53.3	20.7	1	678-696	K.MTNGFSGADLTEICQRACK.L	Carbamidomethyl: 14

Detailed Protein Report

Protein 51: PREDICTED: zinc finger protein 665 isoform X5 [Homo sapiens]

Accession:	gi|578834915	**Score:**	45.3
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 [%]:**	6.9
		No. of unique Peptides:	3

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
2293	1	937.4457	-16.78	2	57.0	19.3	0	1-18	-.MVCPCSGLLLAVGGMPPR.C	Carbamidomethyl: 3; Oxidation: 15
1877	2	1057.5274	21.10	3	52.1	10.3	2	453-480	K.CNDCGKVFTQNSHLASHRGIHSGEKPYK.C	Carbamidomethyl: 4
1830	2	1057.5034	-1.56	3	51.5	15.7	2	453-480	K.CNDCGKVFTQNSHLASHRGIHSGEKPYK.C	Carbamidomethyl: 1

Detailed Protein Report

Protein 52: **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
Modification(s):	Oxidation	**Sequence Coverage [%]:**	8.6
		No. of unique Peptides:	3

```
        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	
2198	1	905.3670	-138.71	2	56.0	17.3	1	335-350	R.SKMVLSNTSPQITFLK.L	Oxidation: 3

Detailed Protein Report

Protein 53: PREDICTED: rootletin-like [Homo sapiens]

Accession:	gi|578805488	**Score:**	44.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	147.5
Database Date:	2015-11-30	**pI:**	5.5
		Sequence Coverage [%]:	4.9
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MRAAIERRWR	REQELCLQLK	SSQALVASLQ	EQLSESRREL	WAAQKLQQER	AREQAREREA	LRGQLEAQRL	EVQQCRASCK
90	100	110	120	130	140	150	160
LLGREKAALE	MVVEELKGKA	DAADAEKQGL	EAEAAELQRS	LLLQAERREE	LALRRERSCR	ALETSQGRLQ	QLEEKVSGLR
170	180	190	200	210	220	230	240
EELASVREAL	STAQLQRDVV	ESEREGLRSA	LARAECSNAD	LELLVRRLKS	EGVEQRDSLA	AMAALMEGLA	QDKSALNHLA
250	260	270	280	290	300	310	320
LQLEQERDQL	REQRKTLEQE	RARAGEQLAQ	AEQQLALERA	ERRGLQQACG	RLEQRQEQLE	GQAALLGREK	AQLQEQVGQV
330	340	350	360	370	380	390	400
TCQKQALEEQ	LAQSLQDQEA	QMGTLQQALQ	GKDALSEERA	QLLAKQEALE	RQGRLAAEEA	ADLRVERDSL	ESSLLEAQQL
410	420	430	440	450	460	470	480
ATKLQEQLEE	EARSAGLARQ	ALQVEMEQLQ	SDWEVQEMKL	RQDTVRLQRQ	VAQQEREAQR	ALESQALAHR	EALAQLQREK
490	500	510	520	530	540	550	560
ETLSLTLAEE	KEVARCQLEQ	EKELVTKSAA	EREALKGEIQ	SLKQERDESL	LQLEHKMQQA	LSLKETERSL	LSEELSRARR
570	580	590	600	610	620	630	640
TLERVQQEAQ	SQQEQAQATI	SATTEELKAL	QAQFEDAITA	HQRETTALRE	SLQDLAAERG	DVEREVRGRA	GGLLGMPEDR
650	660	670	680	690	700	710	720
RKQGRRKVSF	QQISKSGPVS	DHTGKQNEIA	KLGAAGGGGG	GGVERAERLR	AQLTVAQEGL	AALRQELQGV	EESREGLHRE
730	740	750	760	770	780	790	800
AQEARRALSD	EAREKDVLLL	FNSELRATIC	RAEQEKASFK	RSKEEKEQKL	LILEEAQAAL	QQEASALRAH	LWELEQAGGD
810	820	830	840	850	860	870	880
ARQELRELHR	QVLGLQRKLA	EVEAAGEAHG	QRLQEHLRES	RGAEQTLRAE	LHSVTRKLQE	ASGVADALQA	RLDQACHRIH
890	900	910	920	930	940	950	960
SLEQELAQAE	GARQDAEAQL	GRLCSTLRRG	LGLQRQSPWA	SPEQPGSPTK	GSDSSQALPG	QQGTSPPARP	HSPLRWPSPT
970	980	990	1000	1010	1020	1030	1040
PGGRSSELMD	VATVQDILRD	FVQKLREAQR	ERDDSRIQMA	TLSSRLSEAE	CRCARAQSRV	GQLQKALAEA	EEGQRRVEGA
1050	1060	1070	1080	1090	1100	1110	1120
LSSARAARAL	QKEALRRLEL	EHLASVRAAG	QEKRRLQEQL	ETLRQALEES	RRHSQGLAKQ	GKLLEEQLTN	LEHRCQKAEV
1130	1140	1150	1160	1170	1180	1190	1200
SLEPLRQVLC	RPQRLSGGQE	AAEAQAERRV	LQEQTAALRT	ERARLQGELA	ALRAQLAQME	QETLKREEDV	ARLGAEKEQL
1210	1220	1230	1240	1250	1260	1270	1280
DQSLNSLHQE	VDGALRQNQQ	LQAQMTEMEQ	AHTQRLQDLT	AQHQRDLATE	AERLHGARPQ	ATQALESQEW	THQQQVKVLE
1290	1300	1310	1320				
EQVASLKEQL	DQEVQWRQQA	HLGQAFQTGQ					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2904	4	973.5046	-21.62	2	65.1	13.6	2	479-495	R.EKETLSLTLAEEKEVAR.C	
1510	1	899.4718	8.92	2	47.2	10.7	1	666-685	K.QNEIAKLGAAGGGGGGGVER.A	

Detailed Protein Report

Protein 54:	PREDICTED: nesprin-2 isoform X6 [Homo sapiens]		
Accession:	gi|530403362	**Score:**	44.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	795.8
Database Date:	2015-11-30	**pI:**	5.1
		Sequence Coverage [%]:	0.5
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MASSPELPTE	DEQGSWGIDD	LHISLQAEQE	DTQKKAFTCW	INSQLARHTS	PSVISDLFTD	IKKGHVLLDL	LEVLSGQQLP
90	100	110	120	130	140	150	160
RDKGSNTFQC	RINIEHALTF	LRNRSIKLIN	IHVTDIIDGN	PSIILGLIWT	IILHFHIEKL	AQTLSCNYNQ	PSLDDVSVVD
170	180	190	200	210	220	230	240
SSPASSPPAK	KCSKVQARWQ	MSARKALLLW	AQEQCATYES	VNVTDFKSSW	RNGMAFLAII	HALRPDLIDM	KSVKHRSNKD
250	260	270	280	290	300	310	320
NLREAFRIAE	QELKIPRLLE	PEDVDVVDPD	EKSIMTYVAQ	FLQYSKDAPG	TGEEAQGKVK	DAMGWLTLQK	EKLQKLLKDS
330	340	350	360	370	380	390	400
ENDTYFKKYN	SLLSFMESFN	EEKKSFLDVL	SIKRDLDELD	KDHLQLREAW	DGLDHQINAW	KIKLNYALPP	PLHQTEAWLQ
410	420	430	440	450	460	470	480
EVEELMDEDL	SASQDHSQAV	TLIQEKMTLF	KSLMDRFEHH	SNILLTFENK	DENHLPLVPP	NKLEEMKRRI	NNILEKKFIL
490	500	510	520	530	540	550	560
LLEFHYYKCL	VLGLVDEVKS	KLDIWNIKYG	SRESVELLLE	DWHKFIEEKE	FLARLDTSFQ	KCGEIYKNLA	GECQNINKQY
570	580	590	600	610	620	630	640
MMVKSDVCMY	RKNIYNVKST	LQKVLACWAT	YVENLRLLRA	CFEETKKEEI	KEVPFETLAQ	WNLEHATLNE	AGNFLVEVSN
650	660	670	680	690	700	710	720
DVVGSSISKE	LRRLNKRWRK	LVSKTQLEMN	LPLMIKKQDQ	PTFDNSGNIL	SKEEKATVEF	STDMSVELPE	NYNQNIKAGE
730	740	750	760	770	780	790	800
KHEKENEEFT	GQLKVAKDVE	KLIGQVEIWE	AEAKSVLDQD	DVDTSMEESL	KHLIAKGSMF	DELMARSEDM	LQMDIQNISS
810	820	830	840	850	860	870	880
QESFQHVLTT	GLQAKIQEAK	EKVQINVVKL	IAALKNLTDV	SPDLDIRLKM	EESQKELESY	MMRAQQLLGQ	RESPGELISK
890	900	910	920	930	940	950	960
HKEALIISNT	KSLAKYLKAV	EELKNNVTED	IKMSLEEKSR	DVCAKWESLH	HELSLYVQQL	KIDIEKGKLS	DNILKLEKQI
970	980	990	1000	1010	1020	1030	1040
NKEKKLIRRG	RTKGLIKEHE	ACFSEEGCLY	QLNHHMEVLR	ELCEELPSQK	SQQEVKRLLK	DYEQKIERLL	KCASEIHMTL
1050	1060	1070	1080	1090	1100	1110	1120
QPTAGGTSKN	EGTITTSENR	GGDPHSEAPF	AKSDNQPSTE	KAMEPTMKFS	LASVLRPLQE	ESIMEKDYSA	SINSLLERYD
1130	1140	1150	1160	1170	1180	1190	1200
TYRDILEHHL	QNNKFRITSD	FSSEEDRSSS	CLQAKLTDLQ	VIKNETDARW	KEFEIISLKL	ENHVNDIKKP	FVIKERDTLK
1210	1220	1230	1240	1250	1260	1270	1280
ERERELQMTL	NTRMESLETA	LRLVLPVEKA	SLLLCGSDLP	LHKMAIQGFH	LIDADRIYQH	LRNIQDSIAK	QIEICNRLEE
1290	1300	1310	1320	1330	1340	1350	1360
PGNFVLKELH	PFDLHAMQNI	ILKYKTQFEG	MNHRVQRSED	TLKALEDFLA	SLRTAKLSAE	PVTDLSASDT	QVAQENTLTV
1370	1380	1390	1400	1410	1420	1430	1440
KNKEGEIHLM	KDKAKHLDKC	LKMLDMSFKD	AERGDDTSCE	NLLDAFSIKL	SETHGYGVQE	EFTEENKLLE	ACIFKNNELL
1450	1460	1470	1480	1490	1500	1510	1520
KNIQDVQSQI	SKIGLKDPTV	PAVKHRKKSL	IRLDKVLDEY	EEEKRHLQEM	ANSLPHFKDG	REKTVNQQCQ	NTVVLWENTK
1530	1540	1550	1560	1570	1580	1590	1600
ALVTECLEQC	GRVLELLKQY	QNFKSILTTL	IQKEESVISL	QASYMGKENL	KKRIAEIEIV	KEEFNEHLEV	VDKINQVCKN
1610	1620	1630	1640	1650	1660	1670	1680
LQFYLNKMKT	FEEPPFEKEA	NIIVDRWLDI	NEKTEDYYEN	LGRALALWDK	LFNLKNVIDE	WTEKALQKME	LHQLTEEDRE
1690	1700	1710	1720	1730	1740	1750	1760
RLKEELQVHE	QKTSEFSRRV	AEIQFLLQSS	EIPLELQVME	SSILNKMEHV	QKCLTGESNC	HALSGSTAEL	REDLDQAKTQ
1770	1780	1790	1800	1810	1820	1830	1840
IGMTESLLKA	LSPSDSLEIF	TKLEEIQQQI	LQQKHSMILL	ENQIGCLTPE	LSELKKQYES	VSDLFNTKKS	VLQDHFSKLL
1850	1860	1870	1880	1890	1900	1910	1920
NDQCKNFNDW	FSNIKVNLKE	CFESSETKKS	VEQKLQKLSD	FLTLEGRNSK	IKQVDSVLKH	VKKHLPKAHV	KELISWLVGQ
1930	1940	1950	1960	1970	1980	1990	2000
EFELEKMESI	CQARAKELED	SLQQLLRLQD	DHRNLRKWLT	NQEEKWKGME	EPGEKTELFC	QALARKREQF	ESVAQLNNSL
2010	2020	2030	2040	2050	2060	2070	2080
KEYGFTEEEE	IIMEATCLMD	RYQTLLRQLS	EIEEEDKLLP	TEDQSFNDLA	HDVIHWIKEI	KESLMVLNSS	EGKMPLEERI
2090	2100	2110	2120	2130	2140	2150	2160
QKIKEIILLK	PEGDARIETI	MKQAESSEAP	LVQKTLTDIS	NQWDNTLHLA	STYLSHQEKL	LLEGEKYLQS	KEDLRLMLIE
2170	2180	2190	2200	2210	2220	2230	2240
LKKKQEAGFA	LQHGLQEKKA	QLKIYKKFLK	KAQDLTSLLK	ELKSQGNYLL	ECTKNPSFSE	EPWLEIKHLH	ESLLQQLQDS
2250	2260	2270	2280	2290	2300	2310	2320
VQNLDGHVRE	HDSYQVCVTD	LNTTLDNFSK	EFVSFSDKPV	DQIAVEEKLQ	KLQELENRLS	LQDGTLKKIL	ALAKSVKQNT
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
2961	1	927.4882	-20.92	2	65.8	15.8	1	864-880	R.AQQLLGQRESPGELISK.H	
1911	1	568.7711	-62.35	2	52.2	11.0	1	4627-4636	K.SLKAGLDYNR.S	

Detailed Protein Report

Protein 55: **PREDICTED: chromodomain-helicase-DNA-binding protein 4 isoform X6 [Homo sapiens]**

Accession:	gi|578822562	**Score:**	44.0
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 56: **voltage-dependent P/Q-type calcium channel subunit alpha-1A isoform 3 [Homo sapiens]**

Accession:	gi|187828880	**Score:**	43.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	256.6
Database Date:	2015-11-30	**pI:**	9.3
		Sequence Coverage [%]:	1.9
		No. of unique Peptides:	3

Detailed Protein Report

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

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
35	1	796.7935	-124.10	2	29.4	12.9	0	12-31	R.YGGGGSGAAAGVVVGSGGGR.G	
2300	2	822.4329	20.49	2	57.1	15.3	1	1124-1139	R.RTPNNPGNPSNPGPPK.T	
2837	1	913.4693	21.67	1	64.1	15.5	1	1869-1876	K.CPHRVACK.R	

Detailed Protein Report

Protein 57: serine/arginine repetitive matrix protein 2 [Homo sapiens]

Accession:	gi|118572613	**Score:**	43.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	299.4
Database Date:	2015-11-30	**pI:**	12.6
		Sequence Coverage [%]:	1.4
		No. of unique Peptides:	3

Alias proteins:

Accession	Name	Description
gi|578828051	refseq_human (refseq_human_20140103.fasta)	PREDICTED: serine/arginine repetitive matrix protein 2 isoform X6 [Homo sapiens]
gi|530407855	refseq_human (refseq_human_20140103.fasta)	PREDICTED: serine/arginine repetitive matrix protein 2 isoform X1 [Homo sapiens]

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2951	7	703.3519	-15.42	2	65.6	16.8	1	833-845	R.QSHSSSSPHPKVK.S	
2324	1	841.5088	116.64	2	57.3	10.3	1	1614-1630	R.AQSGSDSSPEPKAPAPR.A	
873	1	491.7878	51.39	2	39.7	16.0	1	1866-1874	R.SRASPATHR.R	

Detailed Protein Report

Protein 58: fibrillin-2 precursor [Homo sapiens]

Accession:	gi|66346695	**Score:**	43.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	314.6
Database Date:	2015-11-30	**pI:**	4.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.5
		No. of unique Peptides:	3

Quantitation

WD:WU	**Median:**	1.22	**CV:**	20.64 %	**No. of Peptides:**	2	

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

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
186	1	806.9057	27.18	2	31.2	11.0	0	49-64	R.SATAGSEGGFLAPEYR.E		WD:WU 0.99
2112	1	600.2270	-134.67	3	54.8	15.6	2	77-92	R.RGQQDVLRGPNVCGSR.F	Carbamidomethyl: 13	
291	2	642.2098	-115.38	2	32.8	16.5	1	2529-2539	K.TCKDLDECQTK.Q		WD:WU 1.50

Detailed Protein Report

Protein 59: 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:	3

Quantitation

WD:WU **Median:** 1.35 **CV:** 0.00 % **No. of Peptides:** 1

Alias proteins:

Accession	**Name**	**Description**
gi|578827456	refseq_human(refseq_human_20140103.fasta)	PREDICTED: AP-3 complex subunit beta-2 isoform X3 [Homo sapiens]

10	20	30	40	50	60	70	80
MLDTNKDSLK	LEAMKRIVAM	IARGKNASDL	FPAVVKNVAC	KNIEVKKLVY	VYLVRYAEEQ	QDLALLSIST	FQRGLKDPNQ
90	100	110	120	130	140	150	160
LIRASALRVL	SSIRVPIIVP	IMMLAIKEAA	SDMSPYVRKT	AAHAIPKLYS	LDSDQKDQLI	EVIEKLLADK	TTLVAGSVVM
170	180	190	200	210	220	230	240
AFEEVCPERI	DLIHKNYRKL	CNLLIDVEEW	GQVVIISMLT	RYARTQFLSP	TQNESLLEEN	AEKAFYGSEE	DEAKGAGSEE
250	260	270	280	290	300	310	320
TAAAAAPSRK	PYVMDPDHRL	LLRNTKPLLQ	SRSAAVVMAV	AQLYFHLAPK	AEVGVIAKAL	VRLLRSHSEV	QYVVLQNVAT
330	340	350	360	370	380	390	400
MSIKRRGMFE	PYLKSFYIRS	TDPTQIKILK	LEVLTNLANE	TNIPTVLREF	QTYIRSMDKD	FVAATIQAIG	RCATNIGRVR
410	420	430	440	450	460	470	480
DTCLNGLVQL	LSNRDELVVA	ESVVVIKKLL	QMQPAQHGEI	IKHLAKLTDN	IQVPMARASI	LWLIGEYCEH	VPRIAPDVLR
490	500	510	520	530	540	550	560
KMAKSFTAEE	DIVKLQVINL	AAKLYLTNSK	QTKLLTQYVL	SLAKYDQNYD	IRDRARFTRQ	LIVPSEQGGA	LSRHAKKLFL
570	580	590	600	610	620	630	640
APKPAPVLES	SFKDRDHFQL	GSLSHLLNAK	ATGYQELPDW	PEEAPDPSVR	NVEVPEWTKC	SNREKRKEKE	KPFYSDSEGE
650	660	670	680	690	700	710	720
SGPTESADSD	PESESESDSK	SSSESGSGES	SSESDNEDQD	EDEEKGRGSE	SEQSEEDGKR	KTKKKVPERK	GEASSSDEGS
730	740	750	760	770	780	790	800
DSSSSSSESE	MTSESEEEQL	EPASWSRKTP	PSSKSAPATK	EISLLDLEDF	TPPSVQPVSP	PAIVSTSLAA	DLEGLTLTDS
810	820	830	840	850	860	870	880
TLVPSLLSPV	SGVGRQELLH	RVAGEGLAVD	YTFSRQPFSG	DPHMVSVHIH	FSNSSDTPIK	GLHVGTPKLP	AGISIQEFPE
890	900	910	920	930	940	950	960
IESLAPGESA	TAVMGINFCD	STQAANFQLC	TQTRQFYVSI	QPPVGELMAP	VFMSENEFKK	EQGKLMGMNE	ITEKLMLPDT
970	980	990	1000	1010	1020	1030	1040
CRSDHIVVQK	VTATANLGRV	PCGTSDEYRF	AGRTLTGGSL	VLLTLDARPA	GAAQLTVNSE	KMVIGTMLVK	DVIQALTQ

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2503	1	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		
768	2	495.2668	-4.57	2	38.4	20.2	1	392-400	R.CATNIGRVR.D		WD:WU 1.35

Detailed Protein Report

Protein 60: PREDICTED: methylcytosine dioxygenase TET3 isoform X1 [Homo sapiens]

Accession:	gi|530367326	**Score:**	43.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	193.6
Database Date:	2015-11-30	**pI:**	9.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.8
		No. of unique Peptides:	2

Alias proteins:

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

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2885	1	1129.0588	22.81	2	64.8	17.8	0	24-45	R.QVMVGSFPGSGLSMAGSESQLR.G	Oxidation: 3, 14
1833	2	697.0345	-7.09	3	51.3	12.9	2	1724-1742	R.QEEAARLGLGQQEAKLYGK.K	

Detailed Protein Report

Protein 61: ATP-binding cassette sub-family A member 3 [Homo sapiens]

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

Score: 42.8
MW [kDa]: 191.2
pI: 8.2
Sequence Coverage [%]: 1.5
No. of unique Peptides: 2

Quantitation

WD:WU **Median:** 1.60 **CV:** 0.00 % **No. of Peptides:** 1

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

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
32	1	877.8644	-76.86	2	29.3	10.4	1	739-753	K.GELQCCGSSLFLKQK.Y	Carbamidomethyl: 5, 6	
448	1	607.1484	-239.81	2	34.6	32.5	0	988-998	K.DALQAEGQEPR.E		WD:WU 1.60

Detailed Protein Report

Protein 62: 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

Quantitation

WD:WU **Median:** 0.72 **CV:** 0.00 % **No. of Peptides:** 1

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1632	2	942.4899	12.06	2	49.1	42.5	0	56-71	K.FQDGDLTLYQSNTILR.H		WD:WU 0.72

Protein 63: **serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B beta isoform isoform e [Homo sapiens]**

Accession: gi|430727947
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 42.5
MW [kDa]: 62.5
pI: 6.4
Sequence Coverage [%]: 6.6
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MHQPPPASCS	SSSSSSSSSC	ECARVGVRVS	ALAPAAAPCP	APRQLPYPRL	PEPPSRGTST	LIPARLGPWC	SPTGSPAPLS
90	100	110	120	130	140	150	160
CETGCGEGSW	ILVCRLLVPT	QVSLLSMEED	IDTRKINNSF	LRDHSYATEA	DIISTVEFNH	TGELLATGDK	GGRVVIFQRE
170	180	190	200	210	220	230	240
QESKNQVHRR	GEYNVYSTFQ	SHEPEFDYLK	SLEIEEKINK	IRWLPQQNAA	YFLLSTNDKT	VKLWKVSERD	KRPEGYNLKD
250	260	270	280	290	300	310	320
EEGRLRDPAT	ITTLRVPVLR	PMDLMVEATP	RRVFANAHTY	HINSISVNSD	YETYMSADDL	RINLWNFEIT	NQSFNIVDIK
330	340	350	360	370	380	390	400
PANMEELTEV	ITAAEFHPHH	CNTFVYSSSK	GTIRLCDMRA	SALCDRHTKF	FEEPEDPSNR	SFFSEIISSI	SDVKFSHSGR
410	420	430	440	450	460	470	480
YIMTRDYLTV	KVWDLNMENR	PIETYQVHDY	LRSKLCSLYE	NDCIFDKFEC	VWNGSDSVIM	TGSYNNFFRM	FDRNTKRDVT
490	500	510	520	530	540	550	
LEASRENSKP	RAILKPRKVC	VGGKRRKDEI	SVDSLDFSKK	ILHTAWHPSE	NIIAVAATNN	LYIFQDKVN	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1632	1	1073.5401	-40.07	2	48.7	20.8	1	29-49	R.VSALAPAAAPCPAPRQLPYPR.L	

Detailed Protein Report

Protein 64: E3 ubiquitin-protein ligase BRE1A [Homo sapiens]

Accession: gi|34878777
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl, Oxidation

Score: 42.3
MW [kDa]: 113.6
pI: 5.6
Sequence Coverage [%]: 5.5
No. of unique Peptides: 3

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
1337	1	926.7938	6.01	3	45.5	12.7	1	257-280	K.VETAESRVSVLESMIDDLQWDIDK.I	
2961	1	788.3914	-25.63	2	65.8	15.7	2	835-848	K.RKAMEAAQLADDLK.A	Oxidation: 4
1957	2	918.3405	-92.02	2	52.8	13.9	2	956-971	R.KCPKCNAAFGANDFHR.I	Carbamidomethyl: 5

Detailed Protein Report

Protein 65: **frizzled-10 precursor [Homo sapiens]**

Accession:	gi|6005762	**Score:**	42.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	65.3
Database Date:	2015-11-30	**pI:**	9.9
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	6.4
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MQRPGPRLWL	VLQVMGSCAA	ISSMDMERPG	DGKCQPIEIP	MCKDIGYNMT	RMPNLMGHEN	QREAAIQLHE	FAPLVEYGCH
90	100	110	120	130	140	150	160
GHLRFFLCSL	YAPMCTEQVS	TPIPACRVMC	EQARLKCSPI	MEQFNFKWPD	SLDCRKLPNK	NDPNYLCMEA	PNNGSDEPTR
170	180	190	200	210	220	230	240
GSGLFPPLFR	PQRPHSAQEH	PLKDGGPGRG	GCDNPGKFHH	VEKSASCAPL	CTPGVDVYWS	REDKRFAVVW	LAIWAVLCFF
250	260	270	280	290	300	310	320
SSAFTVLTFL	IDPARFRYPE	RPIIFLSMCY	CVYSVGYLIR	LFAGAESIAC	DRDSGQLYVI	QEGLESTGCT	LVFLVLYYFG
330	340	350	360	370	380	390	400
MASSLWWVVL	TLTWFLAAGK	KWGHEAIEAN	SSYFHLAAWA	IPAVKTILIL	VMRRVAGDEL	TGVCYVGSMD	VNALTGFVLI
410	420	430	440	450	460	470	480
PLACYLVIGT	SFILSGFVAL	FHIRRVMKTG	GENTDKLEKL	MVRIGLFSVL	YTVPATCVIA	CYFYERLNMD	YWKILAAQHK
490	500	510	520	530	540	550	560
CKMNNQTKTL	DCLMAASIPA	VEIFMVKIFM	LLVVGITSGM	WIWTSKTLQS	WQQVCSRRLK	KKSRRKPASV	ITSGGIYKKA
570	580	590					
QHPQKTHHGK	YEIPAQSPTC	V					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1958	2	655.2730	-62.48	2	52.8	10.4	0	281-292	R.LFAGAESIACDR.D	Carbamidomethyl: 10
2186	1	928.7350	-68.15	3	55.7	17.1	1	483-507	K.MNNQTKTLDCLMAASIPAVEIFMVK.I	Oxidation: 23

Detailed Protein Report

Protein 66: PREDICTED: dynein heavy chain 12, axonemal isoform X1 [Homo sapiens]

Accession:	gi|578805765	**Score:**	42.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	454.9
Database Date:	2015-11-30	**pI:**	5.5
		Sequence Coverage [%]:	1.1
		No. of unique Peptides:	2

Quantitation

WD:WU	**Median:** 0.56	**CV:** 15.68 %	**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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1482	1	681.7771	64.45	3	47.3	18.6	2	267-284	K.VINLFTKKEALEGVKPEK.L		WD:WU 0.65
1201	1	1070.0173	-20.70	2	43.7	12.3	1	583-600	K.INPIFDENDELIENAKHK.K		WD:WU 0.48

Detailed Protein Report

Protein 67: PREDICTED: tetratricopeptide repeat protein 13 isoform X7 [Homo sapiens]

Accession:	gi|578802328	**Score:**	41.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	57.4
Database Date:	2015-11-30	**pI:**	9.3
		Sequence Coverage [%]:	8.2
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MMLYHHGSLQ EALKNFKRCL QLEPYNEVCQ YMKGLSHVAM GQFYEGIKAQ TKVMLNDPLP GQKASPEYLK VKYLREYSRY

        90        100        110        120        130        140        150        160
LHAHLDTPLT EYNIDVDLPG SFKDHWAKNL PFLIEDYEEQ PGLQPHIKDV LHQNFESYKP EVQELICVAD RLGSLMQYET

       170        180        190        200        210        220        230        240
PGFLPNKRIH RAMGLAALEV MQAVQRTWTN SKVRMNGKTR LMQWRDMFDI AVKWRRIADP DQPVLWLDQM PARSLSRGFN

       250        260        270        280        290        300        310        320
NHINLIRGQV INMRYLEYFE KILHFIKDRI LVYHGANNPK GLLEVREALE KVHKVEDLLP IMKQFNTKTK DGFTVNTKVP

       330        340        350        360        370        380        390        400
SLKDQGKEYD GFTITITGDK VGNILFSVET QTTEERTQLY HAEIDALYKD LTAKGKVLIL SSEFGEADAV CNLILSLVYY

       410        420        430        440        450        460        470        480
FYNLMPLSRG SSVIAYSVIV GALMASGKEV AGKIPKGKLV DFEAMTAPGS EAFSKVAKSW MNLKSISPSY KTLPSVSETF

       490        500        510
PTLRSMIEVL NTDSSPRCLK KL
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1682	2	820.8728	-97.18	2	49.4	15.9	1	234-247	R.SLSRGFNNHINLIR.G	

Detailed Protein Report

Protein 68: DNA-directed RNA polymerase, mitochondrial precursor [Homo sapiens]

Accession: gi|110618253

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Modification(s): Carbamidomethyl

Score: 41.3

MW [kDa]: 138.5

pI: 10.1

Sequence Coverage [%]: 1.2

No. of unique Peptides: 1

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
125	2	793.8591	-42.14	2	30.8	18.8	1	107-121	K.VQMGAKDATPVPCGR.W	Carbamidomethyl: 13

Detailed Protein Report

Protein 69: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform a [Homo sapiens]

Accession: gi|4502285

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Modification(s): Oxidation

Score: 41.2

MW [kDa]: 109.6

pI: 5.1

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
1921	1	781.2702	-187.08	2	52.7	14.2	0	219-234	K.AMGVVVATGVNTEIGK.I	Oxidation: 2
1931	1	709.7683	-152.59	2	52.8	13.6	1	511-523	K.MFVKGAPEGVIDR.C	

Detailed Protein Report

Protein 70: dynein heavy chain 6, axonemal [Homo sapiens]

Accession:	gi|194353966	**Score:**	41.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	475.7
Database Date:	2015-11-30	**pI:**	5.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.1
		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]

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
2264	1	1011.7667	170.21	1	56.8	10.2	1	2148-2157	R.KNILGAPGNK.R	
1872	1	973.5013	-53.30	2	51.7	13.0	2	2694-2710	K.NGLTKLLETNILVDKMK.L	Oxidation: 16
2924	1	1015.5128	-43.32	2	65.3	18.0	2	2905-2922	K.LRAAQAELDITMATLREK.Q	

Detailed Protein Report

Protein 71: **PREDICTED: LOW QUALITY PROTEIN: ubiquitin carboxyl-terminal hydrolase 17-like protein 20 [Homo sapiens]**

Accession:	gi|578843530	**Score:**	41.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	38.1
Database Date:	2015-11-30	**pI:**	9.8
		Sequence Coverage [%]:	6.0
		No. of unique Peptides:	2

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	
1491	1	981.6005	60.92	2	47.4	15.8	1	264-279	R.ALLVCQISQWKYRPTR.T	

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Detailed Protein Report

Protein 72: PREDICTED: WD repeat-containing protein 88 isoform X1 [Homo sapiens]

Accession:	gi|578833944	**Score:**	41.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	31.0
Database Date:	2015-11-30	**pI:**	6.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	13.7
		No. of unique Peptides:	3

Quantitation

WD:WU **Median:** 0.74 **CV:** 25.19 % **No. of Peptides:** 2

10	20	30	40	50	60	70	80
MASPPRCSPT	AHDRECKLPP	PSAPASEYCP	GKLSWGTMAR	ALGRFKLSIP	HTHLLATLDP	LALDREPPPH	LLPEKHQVPE
90	100	110	120	130	140	150	160
KLIWGDQDPL	SKIPFKILSG	HEHAVSTCHF	CVDDTKLLSG	SYDCTVKLWD	PVDGSVVRDF	EHRPKAPVVE	CSITGDSSRV
170	180	190	200	210	220	230	240
IAASYDKTVR	AWDLETGKLL	WKVRYDTFIV	SCKFSPDGKY	VVSGFDVDHG	ICIMDAENIT	TVSVIKDHHT	RSITSCCFDP
250	260	270	280				
DSQRVASVSL	DRCIKIWDVT	SQATLLTITK	LFSHFWRV				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
573	1	472.1766	-62.66	2	36.0	10.2	0	7-14	R.CSPTAHDR.E	Carbamidomethyl: 1	
2091	1	757.2566	-151.54	2	54.7	16.0	0	18-32	K.LPPPSAPASEYCPGK.L		WD:WU 0.95
1628	1	882.4156	-3.95	2	48.7	14.8	1	185-199	R.YDTFIVSCKFSPDGK.Y	Carbamidomethyl: 8	WD:WU 0.58

Detailed Protein Report

Protein 73: protein scribble homolog isoform b [Homo sapiens]

Accession: gi|355390315
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 40.8
MW [kDa]: 174.8
pI: 4.9
Sequence Coverage [%]: 1.7
No. of unique Peptides: 2

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
707	1	450.6514	-240.33	2	37.3	16.3	2	838-845	R.ERRGGGLR.L	
92	2	696.1357	141.31	3	30.4	24.5	2	861-880	R.HVACLARSERGLGFSIAGGK.G	Carbamidomethyl: 4

Detailed Protein Report

Protein 74: Alstrom syndrome protein 1 [Homo sapiens]

Accession:	gi|110349786	**Score:**	40.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	460.9
Database Date:	2015-11-30	**pI:**	5.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.1
		No. of unique Peptides:	2

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

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 75: PREDICTED: ADAMTS-like protein 3 isoform X3 [Homo sapiens]

Accession:	gi|530406914	**Score:**	40.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	186.1
Database Date:	2015-11-30	**pI:**	9.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MASWTSPWWV	LIGMVFMHSP	LPQTTAEKSP	GAYFLPEFAL	SPQGSFLEDT	TGEQFLTYRY	DDQTSRNTRS	DEDKDGNWDA
90	100	110	120	130	140	150	160
WGDWSDCSRT	CGGGASYSLR	RCLTGRNCEG	QNIRYKTCSN	HDCPPDAEDF	RAQQCSAYND	VQYQGHYYEW	LPRYNDPAAP
170	180	190	200	210	220	230	240
CALKCHAQGQ	NLVVELAPKV	LDGTRCNTDS	LDMCISGICQ	AVGCDRQLGS	NAKEDNCGVC	AGDGSTCRLV	RGQSKSHVSP
250	260	270	280	290	300	310	320
EKREENVIAV	PLGSRSVRIT	VKGPAHLFIE	SKTLQGSKGE	HSFNSPGVFL	VENTTVEFQR	GSERQTFKIP	GPLMADFIFK
330	340	350	360	370	380	390	400
TRYTAAKDSV	VQFFFYQPIS	HQWRQTDFFP	CTVTCGGGYQ	LNSAECVDIR	LKRVVPDHYC	HYYPENVKPK	PKLKECSMDP
410	420	430	440	450	460	470	480
CPSSDGFKEI	MPYDHFQPLP	RWEHNPWTAC	SVSCGGGIQR	RSFVCVEESM	HGEILQVEEW	KCMYAPKPKV	MQTCNLFDCP
490	500	510	520	530	540	550	560
KWIAMEWSQC	TVTCGRGLRY	RVVLCINHRG	EHVGGCNPQL	KLHIKEECVI	PIPCYKPKEK	SPVEAKLPWL	KQAQELEETR
570	580	590	600	610	620	630	640
IATEEPTFIP	EPWSACSTTC	GPGVQVREVK	CRVLLTFTQT	ETELPEEECE	GPKLPTERPC	LLEACDESPA	SRELDIPLPE
650	660	670	680	690	700	710	720
DSETTYDWEY	AGFTPCTATC	VGGHQEAIAV	CLHIQTQQTV	NDSLCDMVHR	PPAMSQACNT	EPCPPRWHVG	SWGPCSATCG
730	740	750	760	770	780	790	800
VGIQTRDVYC	LHPGETPAPP	EECRDEKPHA	LQACNQFDCP	PGWHIEEWQQ	CSRTCGGGTQ	NRRVTCRQLL	TDGSFLNLSD
810	820	830	840	850	860	870	880
ELCQGPKASS	HKSCARTDCP	PHLAVGDWSK	CSVSCGVGIQ	RRKQVCQRLA	AKGRRIPLSE	MMCRDLPGLP	LVRSCQMPEC
890	900	910	920	930	940	950	960
SKIKSEMKTK	LGEQGPQILS	VQRVYIQTRE	EKRINLTIGS	RAYLLPNTSV	IIKCPVRRFQ	KSLIQWEKDG	RCLQNSKRLG
970	980	990	1000	1010	1020	1030	1040
ITKSGSLKIH	GLAAPDIGVY	RCIAGSAQET	VVLKLIGTDN	RLIARPALRE	PMREYPGMDH	SEANSLGVTW	HKMRQMWNNK
1050	1060	1070	1080	1090	1100	1110	1120
NDLYLDDDHI	SNQPFLRALL	GHCSNSAGST	NSWELKNKQF	EAAVKQGAYS	MDTAQFDELI	RNMSQLMETG	EVSDDLASQL
1130	1140	1150	1160	1170	1180	1190	1200
IYQLVAELAK	AQPTHMQWRG	IQEETPPAAQ	LRGETGSVSQ	SSHAKNSGKL	TFKPKGPVLM	RQSQPPSISF	NKTINSRIGN
1210	1220	1230	1240	1250	1260	1270	1280
TVYITKRTEV	INILCDLITP	SEATYTWTKD	GTLLQPSVKI	ILDGTGKIQI	QNPTRKEQGI	YECSVANHLG	SDVESSSVLY
1290	1300	1310	1320	1330	1340	1350	1360
AEAPVILSVE	RNITKPEHNH	LSVVVGGIVE	AALGANVTIR	CPVKGVPQPN	ITWLKRGGSL	SGNVSLLFNG	SLLLQNVSLE
1370	1380	1390	1400	1410	1420	1430	1440
NEGTYVCIAT	NALGKAVATS	VLHLLERRWP	ESRIVFLQGH	KKYILQATNT	RTNSNDPTGE	PPPQEPFWEP	GNWSHCSATC
1450	1460	1470	1480	1490	1500	1510	1520
GHLGARIQRP	QCVMANGQEV	SEALCDHLQK	PLAGFEPCNI	RDCPARWFTS	VWSQCSVSCG	EGYHSRQVTC	KRTKANGTVQ
1530	1540	1550	1560	1570	1580	1590	1600
VVSPRACAPK	DRPLGRKPCF	GHPCVQWEPG	NRCPGRCMGR	AVRMQQRHTA	CQHNSSDSNC	DDRKRPTLRR	NCTSGACDVC
1610	1620	1630	1640	1650	1660	1670	1680
WHTGPWKPCT	AACGRGFQSR	KVDCIHTRSC	KPVAKRHCVQ	KKKPISWRHC	LGPSCDNRYK	QRCCQSCQEG	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
445	1	475.6547	-114.30	2	34.1	10.8	0	774-782	R.TCGGGTQNR.R	Carbamidomethyl: 2

Detailed Protein Report

Protein 76: **kinesin-like protein KIF3B [Homo sapiens]**

Accession:	gi|4758646	**Score:**	40.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	85.1
Database Date:	2015-11-30	**pI:**	7.8
		Sequence Coverage [%]:	5.9
		No. of unique Peptides:	2

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	
182	2	795.4018	9.53	2	31.1	14.3	2	505-516	R.REREIQQQMESR.D	

Detailed Protein Report

Protein 77: DNA polymerase zeta catalytic subunit isoform b [Homo sapiens]

Accession:	gi|556695361	**Score:**	40.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	343.9
Database Date:	2015-11-30	**pI:**	9.5
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	1.4
		No. of unique Peptides:	3

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
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
727	2	517.1500	-168.10	2	37.5	14.5	1	353-360	R.NRMPSPCR.S	Carbamidomethyl: 7; Oxidation: 3
671	1	648.3571	-103.32	2	36.8	12.0	2	1943-1954	K.KLPKTKPTGVVK.S	
1743	1	786.4023	-29.21	3	50.5	13.6	1	2643-2664	R.QLGLKLIANVTFGYTSANFSGR.M	

Detailed Protein Report

Protein 78: von Willebrand factor preproprotein [Homo sapiens]

Accession:	gi|89191868	**Score:**	40.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	309.1
Database Date:	2015-11-30	**pI:**	5.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.0
		No. of unique Peptides:	3

Quantitation

WD:WU	**Median:**	0.69	**CV:**	0.00 %	**No. of Peptides:**	1

10	20	30	40	50	60	70	80
MIPARFAGVL	LALALILPGT	LCAEGTRGRS	STARCSLFGS	DFVNTFDGSM	YSFAGYCSYL	LAGGCQKRSF	SIIGDFQNGK
90	100	110	120	130	140	150	160
RVSLSVYLGE	FFDIHLFVNG	TVTQGDQRVS	MPYASKGLYL	ETEAGYYKLS	GEAYGFVARI	DGSGNFQVLL	SDRYFNKTCG
170	180	190	200	210	220	230	240
LCGNFNIFAE	DDFMTQEGTL	TSDPYDFANS	WALSSGEQWC	ERASPPSSSC	NISSGEMQKG	LWEQCQLLKS	TSVFARCHPL
250	260	270	280	290	300	310	320
VDPEPFVALC	EKTLCECAGG	LECACPALLE	YARTCAQEGM	VLYGWTDHSA	CSPVCPAGME	YRQCVSPCAR	TCQSLHINEM
330	340	350	360	370	380	390	400
CQERCVDGCS	CPEGQLLDEG	LCVESTECPC	VHSGKRYPPG	TSLSRDCNTC	ICRNSQWICS	NEECPGECLV	TGQSHFKSFD
410	420	430	440	450	460	470	480
NRYFTFSGIC	QYLLARDCQD	HSFSIVIETV	QCADDRDAVC	TRSVTVRLPG	LHNSLVKLKH	GAGVAMDGQD	VQLPLLKGDL
490	500	510	520	530	540	550	560
RIQHTVTASV	RLSYGEDLQM	DWDGRGRLLV	KLSPVYAGKT	CGLCGNYNGN	QGDDFLTPSG	LAEPRVEDFG	NAWKLHGDCQ
570	580	590	600	610	620	630	640
DLQKQHSDPC	ALNPRMTRFS	EEACAVLTSP	TFEACHRAVS	PLPYLRNCRY	DVCSCSDGRE	CLCGALASYA	AACAGRGVRV
650	660	670	680	690	700	710	720
AWREPGRCEL	NCPKGQVYLQ	CGTPCNLTCR	SLSYPDEECN	EACLEGCFCP	PGLYMDERGD	CVPKAQCPCY	YDGEIFQPED
730	740	750	760	770	780	790	800
IFSDHHTMCY	CEDGFMHCTM	SGVPGSLLPD	AVLSSPLSHR	SKRSLSCRPP	MVKLVCPADN	LRAEGLECTK	TCQNYDLECM
810	820	830	840	850	860	870	880
SMGCVSGCLC	PPGMVRHENR	CVALERCPCF	HQGKEYAPGE	TVKIGCNTCV	CRDRKWNCTD	HVCDATCSTI	GMAHYLTFDG
890	900	910	920	930	940	950	960
LKYLFPGECQ	YVLVQDYCGS	NPGTFRILVG	NKGCSHPSVK	CKKRVTILVE	GGEIELFDGE	VNVKRPMKDE	THFEVVESGR
970	980	990	1000	1010	1020	1030	1040
YIILLLGKAL	SVVWDRHLSI	SVVLKQTYQE	KVCGLCGNFD	GIQNNDLTSS	NLQVEEDPVD	FGNSWKVSSQ	CADTRKVPLD
1050	1060	1070	1080	1090	1100	1110	1120
SSPATCHNNI	MKQTMVDSSC	RILTSDVFQD	CNKLVDPEPY	LDVCIYDTCS	CESIGDCACF	CDTIAAYAHV	CAQHGKVVTW
1130	1140	1150	1160	1170	1180	1190	1200
RTATLCPQSC	EERNLRENGY	ECEWRYNSCA	PACQVTCQHP	EPLACPVQCV	EGCHAHCPPG	KILDELLQTC	VDPEDCPVCE
1210	1220	1230	1240	1250	1260	1270	1280
VAGRRFASGK	KVTLNPSDPE	HCQICHCDVV	NLTCEACQEP	GGLVVPPTDA	PVSPTTLYVE	DISEPPLHDF	YCSRLLDLVF
1290	1300	1310	1320	1330	1340	1350	1360
LLDGSSRLSE	AEFEVLKAFV	VDMMERLRIS	QKWVRVAVVE	YHDGSHAYIG	LKDRKRPSEL	RRIASQVKYA	GSQVASTSEV
1370	1380	1390	1400	1410	1420	1430	1440
LKYTLFQIFS	KIDRPEASRI	TLLLMASQEP	QRMSRNFVRY	VQGLKKKKVI	VIPVGIGPHA	NLKQIRLIEK	QAPENKAFVL
1450	1460	1470	1480	1490	1500	1510	1520
SSVDELEQQR	DEIVSYLCDL	APEAPPPTLP	PDMAQVTVGP	GLLGVSTLGP	KRNSMVLDVA	FVLEGSDKIG	EADFNRSKEF
1530	1540	1550	1560	1570	1580	1590	1600
MEEVIQRMDV	GQDSIHVTVL	QYSYMVTVEY	PFSEAQSKGD	ILQRVREIRY	QGGNRTNTGL	ALRYLSDHSF	LVSQGDREQA
1610	1620	1630	1640	1650	1660	1670	1680
PNLVYMVTGN	PASDEIKRLP	GDIQVVPIGV	GPNANVQELE	RIGWPNAPIL	IQDFETLPRE	APDLVLQRCC	SGEGLQIPTL
1690	1700	1710	1720	1730	1740	1750	1760
SPAPDCSQPL	DVILLLDGSS	SFPASYFDEM	KSFAKAFISK	ANIGPRLTQV	SVLQYGSITT	IDVPWNVVPE	KAHLLSLVDV
1770	1780	1790	1800	1810	1820	1830	1840
MQREGGPSQI	GDALGFAVRY	LTSEMHGARP	GASKAVVILV	TDVSVDSVDA	AADAARSNRV	TVFPIGIGDR	YDAAQLRILA
1850	1860	1870	1880	1890	1900	1910	1920
GPAGDSNVVK	LQRIEDLPTM	VTLGNSFLHK	LCSGFVRICM	DEDGNEKRPG	DVWTLPDQCH	TVTCQPDGQT	LLKSHRVNCD
1930	1940	1950	1960	1970	1980	1990	2000
RGLRPSCPNS	QSPVKVEETC	GCRWTCPCVC	TGSSTRHIVT	FDGQNFKLTG	SCSYVLFQNK	EQDLEVILHN	GACSPGARQG
2010	2020	2030	2040	2050	2060	2070	2080
CMKSIEVKHS	ALSVELHSDM	EVTVNGRLVS	VPYVGGNMEV	NVYGAIMHEV	RFNHLGHIFT	FTPQNNEFQL	QLSPKTFASK
2090	2100	2110	2120	2130	2140	2150	2160
TYGLCGICDE	NGANDFMLRD	GTVTTDWKTL	VQEWTVQRPG	QTCQPILEEQ	CLVPDSSHCQ	VLLLPLFAEC	HKVLAPATFY
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1145	4	729.1568	-199.23	2	42.6	14.5	0	1944-1956	R.WTCPCVCTGSSTR.H	Carbamidomethyl: 5	WD:WU 0.69
1133	2	729.1918	-151.33	2	42.4	15.1	0	1944-1956	R.WTCPCVCTGSSTR.H	Carbamidomethyl: 3	
1951	1	918.3471	-96.34	2	53.1	10.5	2	2365-2379	K.EECKRVSPPSCPPHR.L	Carbamidomethyl: 3, 11	

Detailed Protein Report

Protein 79: DNA-dependent protein kinase catalytic subunit isoform 2 [Homo sapiens]

Accession:	gi|126032350	**Score:**	40.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	465.2
Database Date:	2015-11-30	**pI:**	6.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.0
		No. of unique Peptides:	3

Quantitation

WD:WU	**Median:** 1.65	**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

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
9	1	798.7834	5.94	3	29.1	17.8	2	2314-2334	K.EVYAAAAEVLGLILRYVMERK.N			
698	1	512.2692	-22.73	2	37.6	10.8	0	2434-2441	K.VCLDIIYK.M	Carbamidomethyl: 2	WD:WU	1.65
2214	1	722.7106	-205.39	2	56.0	11.5	2	3236-3247	K.FSMKMKMIDSAR.K			

Detailed Protein Report

Protein 80: **PREDICTED: lethal(3)malignant brain tumor-like protein 4 isoform X7 [Homo sapiens]**

Accession:	gi|578832232	**Score:**	40.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	55.5
Database Date:	2015-11-30	**pI:**	7.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.1
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 0.55 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MKQPNRKRKL NMDSKERLDQ DGRLEQAEEE KKPKDSTTPL SHVPSAAAQG AWSWEWYLKE QKAVAAPVEL FSKDQSFPEH

        90        100        110        120        130        140        150        160
ENGFQIGMRL EGIDPRHPSV FCVLSVAEVC GYRLRLHFDG YLSCYDFWTN AGSPDIHPVG WCEKTKHELH IPKGYRKDKF

       170        180        190        200        210        220        230        240
VWMDYLKACK LQNAPKKLFR NRSPNGPMSK EFQVGMKLEA VDRKNPSLVC VATIADIVED RLLVHFDNWD DSYDYWCDVN

       250        260        270        280        290        300        310        320
SPYVQPVGWC QENGRTLIAP QGYPNPENFS WTEYLEATQT NAVPAKVFKM RLPHGFLPNM KLEVVDKRNP RLIRVATIVD

       330        340        350        360        370        380        390        400
VDDQRVKVHF DGWDHKYDYW VEADSPDIHP IGWCDVTGHP LEVPQRTNDL KILPGQAVCP TPGCRGIGHI RGPRYSGHHS

       410        420        430        440        450        460        470        480
AFGCPYSDMN LKKEATLHDR LREQTQANLE SDSSHSKSKS LCSLNFNGKH EKVNSQPRLV QQAKCLKIKG KEDIDLDNLF

       490
RDGTV
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2406	3	701.3175	-82.26	3	58.4	16.5	1	372-391	K.ILPGQAVCPTPGCRGIGHIR.G	Carbamidomethyl: 13	WD:WU 0.55

Detailed Protein Report

Protein 81: zinc finger protein 700 isoform 1 [Homo sapiens]

Accession:	gi|55742736	**Score:**	40.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	86.2
Database Date:	2015-11-30	**pI:**	10.1
Modification(s):	Oxidation	**Sequence Coverage [%]:**	6.1
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MPCCSHRSCR	EDPGTSESRE	MDPVAFEDVA	VNFTQEEWTL	LDISQKNLFR	EVMLETFRNL	TSIGKKWSDQ	NIEYEYQNPR
90	100	110	120	130	140	150	160
RSFRSLIEEK	VNEIKEDSHC	GETFTQVPDD	RLNFQEKKAS	PEVKSCDSFV	CAEVGIGNSS	FNMSIRGDTG	HKAYEYQEYG
170	180	190	200	210	220	230	240
PKPYKCQQPK	NKKAFRYRPS	IRTQERDHTG	EKPYACKVCG	KTFIFHSSIR	RHMVMHSGDG	TYKCKFCGKA	FHSFSLYLIH
250	260	270	280	290	300	310	320
ERTHTGEKPY	ECKQCGKSFT	YSATLQIHER	THTGEKPYEC	SKCDKAFHSS	SSYHRHERSH	MGEKPYQCKE	CGKAFAYTSS
330	340	350	360	370	380	390	400
LRRHERTHSG	KKPYECKQYG	EGLSYLISFQ	THIRMNSGER	PYKCKICGKG	FYSAKSFQTH	EKTHTGEKRY	KCKQCGKAFN
410	420	430	440	450	460	470	480
LSSSFRYHER	IHTGEKPYEC	KQCGKAFRSA	SQLRVHGGTH	TGEKPYECKE	CGKAFRSTSH	LRVHGRTHTG	EKPYECKECG
490	500	510	520	530	540	550	560
KAFRYVKHLQ	IHERTEKHIR	MPSGERPYKC	SICEKGFYSA	KSFQTHEKTH	TGEKPYECNQ	CGKAFRCCNS	LRYHERTHTG
570	580	590	600	610	620	630	640
EKPYECKQCG	KAFRSASHLR	MHERTHTGEK	PYECKQCGKA	FSCASNLRKH	GRTHTGEKPY	ECKQCGKAFR	SASNLQMHER
650	660	670	680	690	700	710	720
THTGEKPYEC	KECEKAFCKF	SSFQIHERKH	RGEKPYECKH	CGNGFTSAKI	LQIHARTHIG	EKHYECKECG	KAFNYFSSLH
730	740	750					
IHARTHMGEK	PYECKDCGKA	FS					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2885	1	1023.0269	78.47	2	64.8	13.1	2	212-229	R.HMVMHSGDGTYKCKFCGK.A	Oxidation: 2
2660	4	484.7692	71.54	2	61.6	15.8	0	600-608	K.AFSCASNLR.K	

Detailed Protein Report

Protein 82: **PREDICTED: sphingosine-1-phosphate phosphatase 1 isoform X1 [Homo sapiens]**

Accession:	gi|578826162	**Score:**	39.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	45.6
Database Date:	2015-11-30	**pI:**	9.9
		Sequence Coverage [%]:	7.5
		No. of unique Peptides:	2

```
        10         20         30         40         50         60         70         80
MSLRQRLAQL VGRLQDPQKV ARFQRLCGVE APPRRSADRR EDEKAEAPLA GDPRLRGRQP GAPGGPQPPG SDRNQCPAKP
        90        100        110        120        130        140        150        160
DGGGAPNGVR NGLAAELGPA SPRRAGALRR NSLTGEEGQL ARVSNWPLYC LFCFGTELGN ELFYILFFPF WIWNLDPLVG
       170        180        190        200        210        220        230        240
RRLVVIWVLV MYLGQCTKDI IRWPRPASPP VVKLEVFYNS EYSMPSTHAM SGTAIPISMV LLTYGRWQDI IAGFLYTILI
       250        260        270        280        290        300        310        320
LAVFYPFVDL IDNFNQTHKY APFIIIGLHL ALGIFSFTLD TWSTSRGDTA EILGSGAGIA CGSHVTYNMG LVLDPSLDTL
       330        340        350        360        370        380        390        400
PLAGPPITVT LFGKAILRIL IGMVFVLIIR DVMKKITIPL ACKIFNIPCD DIRKARQHME VELPYRYITY GMVGFSITFF
       410        420
VPYIFFFIGI S
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2846	1	626.8511	24.33	2	64.3	11.3	0	91-103	R.NGLAAELGPASPR.R	
2736	1	1023.0146	-34.37	2	62.6	14.4	1	356-373	K.ITIPLACKIFNIPCDDIR.K	

Detailed Protein Report

Protein 83: 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

Quantitation

WD:WU	**Median:**	1.94	**CV:**	0.00 %	**No. of Peptides:**		1

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	Ratios
687	1	512.1344	-204.56	2	37.4	13.3	1	251-259	R.EKSCGACLR.E	Carbamidomethyl: 4	WD:WU 1.94
436	1	734.3141	-70.58	3	34.5	10.6	2	422-440	R.ESWDSAKKLPPVQESQSER.L		

Detailed Protein Report

Protein 84: **peroxisome biogenesis factor 1 isoform 3 [Homo sapiens]**

Accession:	gi|544186104	**Score:**	39.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	119.5
Database Date:	2015-11-30	**pI:**	5.7
		Sequence Coverage [%]:	1.9
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MMKELQTKQL QSNTVGITES NENESEIPVD SSSVASLWTM IGSIFSFQSE KKQETSWGLT EINAFKNMQS KVVPLDNIFR

        90        100        110        120        130        140        150        160
VCKSQPPSIY NASATSVFHK HCAIHVFPWD QEYFDVEPSF TVTYGKLVKL LSPKQQQSKT KQNVLSPEKE KQMSEPLDQK

       170        180        190        200        210        220        230        240
KIRSDHNEED EKACVLQVVW NGLEELNNAI KYTKNVEVLH LGKVWIPDDL RKRLNIEMHA VVRITPVEVT PKIPRSLKLQ

       250        260        270        280        290        300        310        320
PRENLPKDIS EEDIKTVFYS WLQQSTTTML PLVISEEEFI KLETKDGLKE FSLSIVHSWE KEKDKNIFLL SPNLLQKTTI

       330        340        350        360        370        380        390        400
QVLLDPMVKE ENSEEIDFIL PFLKLSSLGG VNSLGVSSLE HITHSLLGRP LSRQLMSLVA GLRNGALLLT GGKGSGKSTL

       410        420        430        440        450        460        470        480
AKAICKEAFD KLDAHVERVD CKALRGKRLE NIQKTLEVAF SEAVWMQPSV VLLDDLDLIA GLPAVPEHEH SPDAVQSQRL

       490        500        510        520        530        540        550        560
AHALNDMIKE FISMGSLVAL IATSQSQQSL HPLLVSAQGV HIFQCVQHIQ PPNQEQRCEI LCNVIKNKLD CDINKFTDLD

       570        580        590        600        610        620        630        640
LQHVAKETGG FVARDFTVLV DRAIHSRLSR QSISTREKLV LTTLDFQKAL RGFLPASLRS VNLHKPRDLG WDKIGGLHEV

       650        660        670        680        690        700        710        720
RQILMDTIQL PAKYPELFAN LPIRQRTGIL LYGPPGTGKT LLAGVIARES RMNFISVKGP ELLSKYIGAS EQAVRDIFIR

       730        740        750        760        770        780        790        800
AQAAKPCILF FDEFESIAPR RGHDNTGVTD RVVNQLLTQL DGVEGLQGVY VLAATSRPDL IDPALLRPGR LDKCVYCPPP

       810        820        830        840        850        860        870        880
DQVSRLEILN VLSDSLPLAD DVDLQHVASV TDSFTGADLK ALLYNAQLEA LHGMLLSSGL QDGSSSSDSD LSLSSMVFLN

       890        900        910        920        930        940        950        960
HSSGSDDSAG DGECGLDQSL VSLEMSEILP DESKFNMYRL YFGSSYESEL GNGTSSDLSS QCLSAPSSMT QDLPGVPGKD

       970        980        990       1000       1010       1020       1030       1040
QLFSQPPVLR TASQEGCQEL TQEQRDQLRA DISIIKGRYR SQSGEDESMN QPGPIKTRLA ISQSHLMTAL GHTRPSISED

      1050       1060       1070       1080
DWKNFAELYE SFQNPKRRKN QSGTMFRPGQ KVTLA
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1127	4	1207.8838	99.74	1	42.8	28.3	2	233-242	K.IPRSLKLQPR.E	

Detailed Protein Report

Protein 85: E3 ubiquitin-protein ligase TRIP12 isoform c [Homo sapiens]

Accession:	gi|10863903	**Score:**	39.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	220.3
Database Date:	2015-11-30	**pI:**	9.6
		Sequence Coverage [%]:	2.5
		No. of unique Peptides:	2

Quantitation

WD:WU	**Median:**	0.74	**CV:**	0.00 %	**No. of Peptides:**	1	

```
        10         20         30         40         50         60         70         80
MSNRPNNNPG GSLRRSQRNT AGAQPQDDSI GGRSCSSSSA VIVPQPEDPD RANTSERQKT GQVPKKDNSR GVKRSASPDY
        90        100        110        120        130        140        150        160
NRTNSPSSAK KPKALQHTES PSETNKPHSK SKKRHLDQEQ QLKSAQSPST SKAHTRKSGA TGGSRSQKRK RTESSCVKSG
       170        180        190        200        210        220        230        240
SGSESTGAEE RSAKPTKLAS KSATSAKAGC STITDSSSAA STSSSSSAVA SASSTVPPGA RVKQGKDQNK ARRSRSASSP
       250        260        270        280        290        300        310        320
SPRRSSREKE QSKTGGSSKF DWAARFSPKV SLPKTKLSLP GSSKSETSKP GPSGLQAKLA SLRKSTKKRS ESPPAELPSL
       330        340        350        360        370        380        390        400
RRSTRQKTTG SCASTSRRGS GLGKRGAAEA RRQEKMADPE SNQEAVNSSA ARTDEAPQGA AGAVGMTTSG ESESDDSEMG
       410        420        430        440        450        460        470        480
RLQALLEARG LPPHLFGPLG PRMSQLFHRT IGSGASSKAQ QLLQGLQASD ESQQLQAVIE MCQLLVMGNE ETLGGFPVKS
       490        500        510        520        530        540        550        560
VVPALITLLQ MEHNFDIMNH ACRALTYMME ALPRSSAVVV DAIPVFLEKL QVIQCIDVAE QALTALEMLS RRHSKAILQA
       570        580        590        600        610        620        630        640
GGLADCLLYL EFFSINAQRN ALAIAANCCQ SITPDEFHFV ADSLPLLTQR LTHQDKKSVE STCLCFARLV DNFQHEENLL
       650        660        670        680        690        700        710        720
QQVASKDLLT NVQQLLVVTP PILSSGMFIM VVRMFSLMCS NCPTLAVQLM KQNIAETLHF LLCGASNGSC QEQIDLVPRS
       730        740        750        760        770        780        790        800
PQELYELTSL ICELMPCLPK EGIFAVDTML KKGNAQNTDG AIWQWRDDRG LWHPYNRIDS RIIEQINEDT GTARAIQRKP
       810        820        830        840        850        860        870        880
NPLANSNTSG YSESKKDDAR AQLMKEDPEL AKSFIKTLFG VLYEVYSSSA GPAVRHKCLR AILRIIYFAD AELLKDVLKN
       890        900        910        920        930        940        950        960
HAVSSHIASM LSSQDLKIVV GALQMAEILM QKLPDIFSVY FRREGVMHQV KHLAESESLL TSPPKACTNG SGSMGSTTSV
       970        980        990       1000       1010       1020       1030       1040
SSGTATAATH AAADLGSPSL QHSRDDSLDL SPQGRLSDVL KRKRLPKRGP RRPKYSPPRD DDKVDNQAKS PTTTQSPKSS
      1050       1060       1070       1080       1090       1100       1110       1120
FLASLNPKTW GRLSTQSNSN NIEPARTAGG SGLARAASKD TISNNREKIK GWIKEQAHKF VERYFSSENM DGSNPALNVL
      1130       1140       1150       1160       1170       1180       1190       1200
QRLCAATEQL NLQVDGGAEC LVEIRSIVSE SDVSSFEIQH SGFVKQLLLY LTSKSEKDAV SREIRLKRFL HVFFSSPLPG
      1210       1220       1230       1240       1250       1260       1270       1280
EEPIGRVEPV GNAPLLALVH KMNNCLSQME QFPVKVHDFP SGNGTGGSFS LNRGSQALKF FNTHQLKCQL QRHPDCANVK
      1290       1300       1310       1320       1330       1340       1350       1360
QWKGGPVKID PLALVQAIER YLVVRGYGRV REDDEDSDDD GSDEEIDESL AAQFLNSGNV RHRLQFYIGE HLLPYNMTVY
      1370       1380       1390       1400       1410       1420       1430       1440
QAVRQFSIQA EDERESTDDE SNPLGRAGIW TKTHTIWYKP VREDEESNKD CVGGKRGRAQ TAPTKTSPRN AKKHDELWHD
      1450       1460       1470       1480       1490       1500       1510       1520
GVCPSVSNPL EVYLIPTPPE NITFEDPSLD VILLLRVLHA ISRYWYYLYD NAMCKEIIPT SEFINSKLTA KANRQLQDPL
      1530       1540       1550       1560       1570       1580       1590       1600
VIMTGNIPTW LTELGKTCPF FFPFDTRQML FYVTAFDRDR AMQRLLDTNP EINQSDSQDS RVAPRLDRKK RTVNREELLK
      1610       1620       1630       1640       1650       1660       1670       1680
QAESVMQDLG SSRAMLEIQY ENEVGTGLGP TLEFYALVSQ ELQRADLGLW RGEEVTLSNP KGSQEGTKYI QNLQGLFALP
      1690       1700       1710       1720       1730       1740       1750       1760
FGRTAKPAHI AKVKMKFRFL GKLMAKAIMD FRLVDLPLGL PFYKWMLRQE TSLTSHDLFD IDPVVARSVY HLEDIVRQKK
      1770       1780       1790       1800       1810       1820       1830       1840
RLEQDKSQTK ESLQYALETL TMNGCSVEDL GLDFTLPGFP NIELKKGGKD IPVTIHNLEE YLRLVIFWAL NEGVSRQFDS
      1850       1860       1870       1880       1890       1900       1910       1920
FRDGFESVFP LSHLQYFYPE ELDQLLCGSK ADTWDAKTLM ECCRPDHGYT HDSRAVKFLF EILSSFDNEQ QRLFLQFVTG
      1930       1940       1950       1960       1970       1980       1990       2000
SPRLPVGGFR SLNPPLTIVR KTFESTENPD DFLPSVMTCV NYLKLPDYSS IEIMREKLLI AAREGQQSFH LS
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1453	1	929.4464	3.04	2	46.5	10.5	1	16-33	R.SQRNTAGAQPQDDSIGGR.S		WD:WU 0.74
2056	1	973.8963	-110.34	2	54.1	16.5	2	1067-1086	R.TAGGSGLARAASKDTISNNR.E		

Detailed Protein Report

Protein 86: relaxin receptor 1 isoform 7 [Homo sapiens]

Accession:	gi|359279881	**Score:**	38.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	69.5
Database Date:	2015-11-30	**pI:**	9.9
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	1.5
		No. of unique Peptides:	2

Quantitation

WD:WU	**Median:** 1.34	**CV:** 79.73 %	**No. of Peptides:** 2

10	20	30	40	50	60	70	80
MVTCTQNMKA	ALKSLLYHSR	NLGYLQNNKI	TSISIYAFRG	LNSLTKLYLS	HNRITFLKPG	VFEDLHRLEW	LIIEDNHLSR
90	100	110	120	130	140	150	160
ISPPTFYGLN	SLILLVLMNN	VLTRLPDKPL	CQHMPRLHWL	VMRKNKINHL	NENTFAPLQK	LDELDLGSNK	IENLPPLIFK
170	180	190	200	210	220	230	240
DLKELSQLNL	SYNPIQKIQA	NQFDYLVKLK	SLSLEGIEIS	NIQQRMFRPL	MNLSHIYFKK	FQYCGYAPHV	RSCKPNTDGI
250	260	270	280	290	300	310	320
SSLENLLASI	IQRVFVWVVS	AVTCFGNIFV	ICMRPYIRSE	NKLYAMSIIS	LCCADCLMGI	YLFVIGGFDL	KFRGEYNKHA
330	340	350	360	370	380	390	400
QLWMESTHCQ	LVGSLAILST	EVSVLLLTFL	TLEKYICIVY	PFRCVRPGKC	RTITVLILIW	ITGFIVAFIP	LSNKEFFKNY
410	420	430	440	450	460	470	480
YGTNGVCFPL	HSEDTESIGA	QIYSVAIFLG	INLAAFIIIV	FSYGSMFYSV	HQSAITATEI	RNQVKKEMIL	AKRFFFIVFT
490	500	510	520	530	540	550	560
DALCWIPIFV	VKFLSLLQVE	IPGTITSWVV	IFILPINSAL	NPILYTLTTR	PFKEMIHRFW	YNYRQRKSMD	SKGQKTYAPS
570	580	590	600	610			
FIWVEMWPLQ	EMPPELMKPD	LFTYPCEMSL	ISQSTRLNSY	S			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
386	6	544.1543	-144.04	2	33.4	14.3	0	1-9	-.MVTCTQNMK.A	Oxidation: 1, 8	WD:WU 2.71
468	2	572.6830	-105.55	2	34.3	24.6	0	1-9	-.MVTCTQNMK.A	Carbamidomethyl: 4; Oxidation: 1, 8	WD:WU 0.67

Detailed Protein Report

Protein 87: 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

WD:WU **Median:** 2.71 **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		
2723	1	639.3585	-37.42	2	62.4	12.0	2	348-358	K.KSLALQKTNFK.E		WD:WU 2.71
1809	2	1011.7628	-33.19	3	51.3	16.1	2	535-560	K. KKCTTQEMMSICPELLDFQDMIGE N		

Detailed Protein Report

Protein 88: **PREDICTED: N-alpha-acetyltransferase 15, NatA auxiliary subunit isoform X1 [Homo sapiens]**

Accession:	gi|530378196	**Score:**	38.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	101.1
Database Date:	2015-11-30	**pI:**	7.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.6
		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 89: probable ATP-dependent RNA helicase DDX20 [Homo sapiens]

Accession:	gi|256223453	**Score:**	38.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	92.2
Database Date:	2015-11-30	**pI:**	6.5
		Sequence Coverage [%]:	3.3
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MAAAFEASGA	LAAVATAMPA	EHVAVQVPAP	EPTPGPVRIL	RTAQDLSSPR	TRTGDVLLAE	PADFESLLLS	RPVLEGLRAA
90	100	110	120	130	140	150	160
GFERPSPVQL	KAIPLGRCGL	DLIVQAKSGT	GKTCVFSTIA	LDSLVLENLS	TQILILAPTR	EIAVQIHSVI	TAIGIKMEGL
170	180	190	200	210	220	230	240
ECHVFIGGTP	LSQDKTRLKK	CHIAVGSPGR	IKQLIELDYL	NPGSIRLFIL	DEADKLLEEG	SFQEQINWIY	SSLPASKQML
250	260	270	280	290	300	310	320
AVSATYPEFL	ANALTKYMRD	PTFVRLNSSD	PSLIGLKQYY	KVVNSYPLAH	KVFEEKTQHL	QELFSRIPFN	QALVFSNLHS
330	340	350	360	370	380	390	400
RAQHLADILS	SKGFPAECIS	GNMNQNQRLD	AMAKLKHFHC	RVLISTDLTS	RGIDAEKVNL	VVNLDVPLDW	ETYMHRIGRA
410	420	430	440	450	460	470	480
GRFGTLGLTV	TYCCRGEEEN	MMMRIAQKCN	INLLPLPDPI	PSGLMEECVD	WDVEVKAAVH	TYGIASVPNQ	PLKKQIQKIE
490	500	510	520	530	540	550	560
RTLQIQKAHG	DHMASSRNNS	VSGLSVKSKN	NTKQKLPVKS	HSECGIIEKA	TSPKELGCDR	QSEEQMKNSV	QTPVENSTNS
570	580	590	600	610	620	630	640
QHQVKEALPV	SLPQIPCLSS	FKIHQPYTLT	FAELVEDYEH	YIKEGLEKPV	EIIRHYTGPG	DQTVNPQNGF	VRNKVIEQRV
650	660	670	680	690	700	710	720
PVLASSSQSG	DSESDSDSYS	SRTSSQSKGN	KSYLEGSSDN	QLKDSESTPV	DDRISLEQPP	NGSDTPNPEK	YQESPGIQMK
730	740	750	760	770	780	790	800
TRLKEGASQR	AKQSRRNLPR	RSSFRLQTEA	QEDDWYDCHR	EIRLSFSDTY	QDYEEYWRAY	YRAWQEYYAA	ASHSYYWNAQ
810	820	830					
RHPSWMAAYH	MNTIYLQEMM	HSNQ					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1828	1	807.3949	-77.75	2	51.2	11.4	2	39-52	R.ILRTAQDLSSPRTR.T	
827	1	683.3392	-78.48	2	39.2	27.0	2	178-190	R.LKKCHIAVGSPGR.I	

Protein 90: protein FAM104A isoform 3 [Homo sapiens]

Accession: gi|574956994
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 38.3
MW [kDa]: 9.8
pI: 12.7
Sequence Coverage [%]: 40.8
No. of unique Peptides: 1

```
        10         20         30         40         50         60         70         80
MGGRGADAGS SGGTGPTEGY SPPAASTRAA ARAKARGGGR GGRRNTTPSV PSLRGAAPRS FHPPAAMSER LRPSLQAVTV
        90        100        110
VGAAAAAAAA SIARTGPAGR KAA
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2165	5	974.4048	-53.21	3	55.4	21.1	2	1-32	-.MGGRGADAGSSGGTGPTEGYSPPAASTRAAAR.A	

Detailed Protein Report

Protein 91: **small proline-rich protein 2E [Homo sapiens]**

Accession: gi|83582817
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 38.2
MW [kDa]: 7.8
pI: 10.6
Sequence Coverage [%]: 18.1
No. of unique Peptides: 2

Quantitation

WD:WU **Median:** 1.04 **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
2928	1	724.8814	36.56	2	65.4	11.5	0	10-22	K.QPCQPPPVCPTPK.C	Carbamidomethyl: 3	
68	2	753.3471	-24.59	2	30.1	26.7	0	10-22	K.QPCQPPPVCPTPK.C	Carbamidomethyl: 3, 9	WD:WU 1.04

Detailed Protein Report

Protein 92: **DNA repair and recombination protein RAD54B isoform 1 [Homo sapiens]**

Accession:	gi|6912622	**Score:**	38.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	102.9
Database Date:	2015-11-30	**pI:**	9.4
Modification(s):	Oxidation	**Sequence Coverage [%]:**	4.6
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MRRSAAPSQL	QGNSFKKPKF	IPPGRSNPGL	NEEITKLNPD	IKLFEGVAIN	NTFLPSQNDL	RICSLNLPSE	ESTREINNRD
90	100	110	120	130	140	150	160
NCSGKYCFEA	PTLATLDPPH	TVHSAPKEVA	VSKEQEEKSD	SLVKYFSVVW	CKPSKKKHKK	WEGDAVLIVK	GKSFILKNLE
170	180	190	200	210	220	230	240
GKDIGRGIGY	KFKELEKIEE	GQTLMICGKE	IEVMGVISPD	DFSSGRCFQL	GGGSTAISHS	SQVARKCFSN	PFKSVCKPSS
250	260	270	280	290	300	310	320
KENRQNDFQN	CKPRHDPYTP	NSLVMPRPDK	NHQWVFNKNC	FPLVDVVIDP	YLVYHLRPHQ	KEGIIFLYEC	VMGMRMNGRC
330	340	350	360	370	380	390	400
GAILADEMGL	GKTLQCISLI	WTLQCQGPYG	GKPVIKKTLI	VTPGSLVNNW	KKEFQKWLGS	ERIKIFTVDQ	DHKVEEFIKS
410	420	430	440	450	460	470	480
IFYSVLIISY	EMLLRSLDQI	KNIKFDLLIC	DEGHRLKNSA	IKTTTALISL	SCEKRIILTG	TPIQNDLQEF	FALIDFVNPG
490	500	510	520	530	540	550	560
ILGSLSSYRK	IYEEPIILSR	EPSASEEEKE	LGERRAAELT	CLTGLFILRR	TQEIINKYLP	PKIENVVFCR	PGALQIELYR
570	580	590	600	610	620	630	640
KLLNSQVVRF	CLQGLLENSP	HLICIGALKK	LCNHPCLLFN	SIKEKECSST	CDKNEEKSLY	KGLLSVFPAD	YNPLLFTEKE
650	660	670	680	690	700	710	720
SGKLQVLSKL	LAVIHELRPT	EKVVLVSNYT	QTLNILQEVC	KRHGYAYTRL	DGQTPISQRQ	QIVDGFNSQH	SSFFIFLLSS
730	740	750	760	770	780	790	800
KAGGVGLNLI	GGSHLILYDI	DWNPATDIQA	MSRVWRDGQK	YPVHIYRLLT	TGTIEEKIYQ	RQISKQGLCG	AVVDLTKTSE
810	820	830	840	850	860	870	880
HIQFSVEELK	NLFTLHESSD	CVTHDLLDCE	CTGEEVHTGD	SLEKFIVSRD	CQLGPHHQKS	NSLKPLSMSQ	LKQWKHFSGD
890	900	910	920				
HLNLTDPFLE	RITENVSFIF	QNITTQATGT					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1860	2	599.9988	-42.55	3	51.9	12.1	2	357-372	K.KTLIVTPGSLVNNWKK.E	
920	1	945.9532	-58.91	2	39.9	10.3	1	860-875	K.SNSLKPLSMSQLKQWK.H	Oxidation: 9

Detailed Protein Report

Protein 93: histone H4 [Homo sapiens]

Accession:	gi|4504301	**Score:**	37.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	11.4
Database Date:	2015-11-30	**pI:**	11.8
		Sequence Coverage [%]:	7.8
		No. of unique Peptides:	1

Quantitation

WD:WU	**Median:** 1.43	**CV:** 0.00 %	**No. of Peptides:** 1

Alias proteins:

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

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1347	4	495.2734	-38.66	2	45.6	37.9	0	61-68	K.VFLENVIR.D		WD:WU 1.43

Detailed Protein Report

Protein 94: **protein FAM115C isoform B [Homo sapiens]**

Accession:	gi|293651621	**Score:**	37.9
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:	3

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
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	1	705.1921	-194.39	2	35.1	10.8	1	636-646	K.EIINEMDMRSR.G	Oxidation: 6

Detailed Protein Report

Protein 95:	**PREDICTED: probable E3 ubiquitin-protein ligase MYCBP2 isoform X1 [Homo sapiens]**		
Accession:	gi|530402182	**Score:**	37.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	521.8
Database Date:	2015-11-30	**pI:**	6.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.2
		No. of unique Peptides:	1

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1748	3	697.3510	1.93	3	50.2	15.7	1	680-698	K.GHFVTQVAMGKAHTCVLMK.N	Oxidation: 9, 18

Detailed Protein Report

Protein 96:	unconventional myosin-IXb isoform 2 [Homo sapiens]		
Accession:	gi|194272142	**Score:**	37.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	229.0
Database Date:	2015-11-30	**pI:**	9.4
		Sequence Coverage [%]:	1.8
		No. of unique Peptides:	1

Detailed Protein Report

```
        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
1465	1	671.4099	1.89	2	47.1	16.6	1	1964-1974	K.EILIERIQSIK.E	

Detailed Protein Report

Protein 97: PREDICTED: NEDD8 ultimate buster 1 isoform X3 [Homo sapiens]

Accession: gi|530387034
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 37.1
MW [kDa]: 67.7
pI: 5.7
Sequence Coverage [%]: 1.7
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MKTNGGRCRI	RALCWSRREW	RGAGMAQKKY	LQAKLTQFLR	EDRIQLWKPP	YTDENKKVGL	ALKDLAKQYS	DRLECCENEV
90	100	110	120	130	140	150	160
EKVIEEIRCK	AIERGTGNDN	YRTTGIATIE	VFLPPRLKKD	RKNLLETRLH	ITGRELRSKI	AETFGLQENY	IKIVINKKQL
170	180	190	200	210	220	230	240
QLGKTLEEQG	VAHNVKAMVL	ELKQSEEDAR	KNFQLEEEEQ	NEAKLKEKQI	QRTKRGLEIL	AKRAAETVVD	PEMTPYLDIA
250	260	270	280	290	300	310	320
NQTGRSIRIP	PSERKALMLA	MGYHEKGRAF	LKRKEYGIAL	PCLLDADKYF	CECCRELLDT	VDNYAVLQLD	IVWCYFRLEQ
330	340	350	360	370	380	390	400
LECLDDAEKK	LNLAQKCFKN	CYGENHQRLV	HIKGNCGKEK	VLFLRLYLLQ	GIRNYHSGND	VEAYEYLNKA	RQLFKELYID
410	420	430	440	450	460	470	480
PSKVDNLLQL	GFTAQEARLG	LRACDGNVDH	AATHITNRRE	ILLSNPQMWW	LNDSNPETDN	RQESPSQENI	DRLVYMGFDA
490	500	510	520	530	540	550	560
LVAEAALRVF	RGNVQLAAQT	LAHNGGSLPP	ELPLSPEDSL	SPPATSPSDS	AGTSSASTDE	DMETEAVNEI	LEDIPEHEED
570	580	590	600				
YLDSTLEDEE	IIIAEYLSYV	ENRKSATKKN					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2062	2	625.2581	-159.60	2	54.4	16.1	2	330-339	K.KLNLAQKCFK.N	Carbamidomethyl: 8

Protein 98: **ubiquitin carboxyl-terminal hydrolase 32 [Homo sapiens]**

Accession:	gi|22550104	**Score:**	37.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	181.5
Database Date:	2015-11-30	**pI:**	6.0
		Sequence Coverage [%]:	2.4
		No. of unique Peptides:	3

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
362	1	539.2298	-162.41	2	33.2	10.4	1	549-557	K.RTPQLIHGR.D	
434	3	565.3154	-75.69	2	34.4	15.6	2	1292-1300	R.WIKSQKIVK.F	
2778	1	1023.5416	14.56	2	63.2	11.2	1	1361-1381	K.SPSSLSANIISSPKGSPSSSR.K	

Detailed Protein Report

Protein 99: probable ATP-dependent RNA helicase DDX10 [Homo sapiens]

Accession:	gi|13514831	**Score:**	37.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	100.8
Database Date:	2015-11-30	**pI:**	9.3
		Sequence Coverage [%]:	4.6
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MGKTANSPGS	GARPDPVRSF	NRWKKKHSHR	QNKKKQLRKQ	LKKPEWQVER	ESISRLMQNY	EKINVNEITR	FSDFPLSKKT
90	100	110	120	130	140	150	160
LKGLQEAQYR	LVTEIQKQTI	GLALQGKDVL	GAAKTGSGKT	LAFLVPVLEA	LYRLQWTSTD	GLGVLIISPT	RELAYQTFEV
170	180	190	200	210	220	230	240
LRKVGKNHDF	SAGLIIGGKD	LKHEAERINN	INILVCTPGR	LLQHMDETVS	FHATDLQMLV	LDEADRILDM	GFADTMNAVI
250	260	270	280	290	300	310	320
ENLPKKRQTL	LFSATQTKSV	KDLARLSLKN	PEYVWVHEKA	KYSTPATLEQ	NYIVCELQQK	ISVLYSFLRS	HLKKKSIVFF
330	340	350	360	370	380	390	400
SSCKEVQYLY	RVFCRLRPGV	SILALHGRQQ	QMRRMEVYNE	FVRKRAAVLF	ATDIAARGLD	FPAVNWVLQF	DCPEDANTYI
410	420	430	440	450	460	470	480
HRAGRTARYK	EDGEALLILL	PSEKAMVQQL	LQKKVPVKEI	KINPEKLIDV	QKKLESILAQ	DQDLKERAQR	CFVSYVRSVY
490	500	510	520	530	540	550	560
LMKDKEVFDV	SKLPIPEYAL	SLGLAVAPRV	RFLQKMQKQP	TKELVRSQAD	KVIEPRAPSL	TNDEVEEFRA	YFNEKMSILQ
570	580	590	600	610	620	630	640
KGGKRLEGTE	HRQDNDTGNE	EQEEEEDDEE	EMEEKLAKAK	GSQAPSLPNT	SEAQKIKEVP	TQFLDRDEEE	EDADFLKVKR
650	660	670	680	690	700	710	720
HNVFGLDLKD	EKTLQKKEPS	KSSIKKKMTK	VAEAKKVMKR	NFKVNKKITF	TDEGELVQQW	PQMQKSAIKD	AEEDDDTGGI
730	740	750	760	770	780	790	800
NLHKAKERLQ	EEDKFDKEEY	RKKIKAKHRE	KRLKEREARR	EANKRQAKAK	DEEEAFLDWS	DDDDDDDDGF	DPSTLPDPDK
810	820	830	840	850	860	870	880
YRSSEDSDSE	DMENKISDTK	KKQGMKKRSN	SEVEDVGPTS	HNRKKARWDT	LEPLDTGLSL	AEDEELVLHL	LRSQS

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1771	5	599.9726	0.40	3	50.8	16.0	1	1-18	-.MGKTANSPGSGARPDPVR.S	
2294	1	713.3369	-116.31	2	57.0	10.6	2	638-649	K.VKRHNVFGLDLK.D	

Detailed Protein Report

Protein 100: conserved oligomeric Golgi complex subunit 1 [Homo sapiens]

Accession:	gi|21237783	**Score:**	37.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	108.9
Database Date:	2015-11-30	**pI:**	7.1
Modification(s):	Oxidation	**Sequence Coverage [%]:**	4.5
		No. of unique Peptides:	2

Quantitation

WD:WU **Median:** 0.38 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MATAATSPAL KRLDLRDPAA LFETHGAEEI RGLERQVRAE IEHKKEELRQ MVGERYRDLI EAADTIGQMR RCAVGLVDAV
        90        100        110        120        130        140        150        160
KATDQYCARL RQAGSAAPRP PRAQQPQQPS QEKFYSMAAQ IKLLLEIPEK IWSSMEASQC LHATQLYLLC CHLHSLLQLD
       170        180        190        200        210        220        230        240
SSSSRYSPVL SRFPILIRQV AAASHFRSTI LHESKMLLKC QGVSDQAVAE ALCSIMLLEE SSPRQALTDF LLARKATIQK
       250        260        270        280        290        300        310        320
LLNQPHHGAG IKAQICSLVE LLATTLKQAH ALFYTLPEGL LPDPALPCGL LFSTLETITG QHPAGKGTGV LQEEMKLCSW
       330        340        350        360        370        380        390        400
FKHLPASIVE FQPTLRTLAH PISQEYLKDT LQKWIHMCNE DIKNGITNLL MYVKSMKGLA GIRDAMWELL TNESTNHSWD
       410        420        430        440        450        460        470        480
VLCRRLLEKP LLFWEDMMQQ LFLDRLQTLT KEGFDSISSS SKELLVSALQ ELESSTSNSP SNKHIHFEYN MSLFLWSESP
       490        500        510        520        530        540        550        560
NDLPSDAAWV SVANRGQFAS SGLSMKAQAI SPCVQNFCSA LDSKLKVKLD DLLAYLPSDD SSLPKDVSPT QAKSSAFDRY
       570        580        590        600        610        620        630        640
ADAGTVQEML RTQSVACIKH IVDCIRAELQ SIEEGVQGQQ DALNSAKLHS VLFMARLCQS LGELCPHLKQ CILGKSESSE
       650        660        670        680        690        700        710        720
KPAREFRALR KQGKVKTQEI IPTQAKWQEV KEVLLQQSVM GYQVWSSAVV KVLIHGFTQS LLLDDAGSVL ATATSWDELE
       730        740        750        760        770        780        790        800
IQEEAESGSS VTSKIRLPAQ PSWYVQSFLF SLCQEINRVG GHALPKVTLQ EMLKSCMVQV VAAYEKLSEE KQIKKEGAFP
       810        820        830        840        850        860        870        880
VTQNRALQLL YDLRYLNIVL TAKGDEVKSG RSKPDSRIEK VTDHLEALID PFDLDVFTPH LNSNLHRLVQ RTSVLFGLVT
       890        900        910        920        930        940        950        960
GTENQLAPRS STFNSQEPHN ILPLASSQIR FGLLPLSMTS TRKAKSTRNI ETKAQVVPPA RSTAGDPTVP GSLFRQLVSE
       970        980        990
EDNTSAPSLF KLGWLSSMTK
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2917	1	724.8590	4.01	2	65.2	12.8	0	58-70	R.DLIEAADTIGQMR.R	Oxidation: 12	
1712	1	1045.0032	-51.34	2	49.7	13.3	1	527-545	K.VKLDDLLAYLPSDDSSLPK.D		WD:WU 0.38

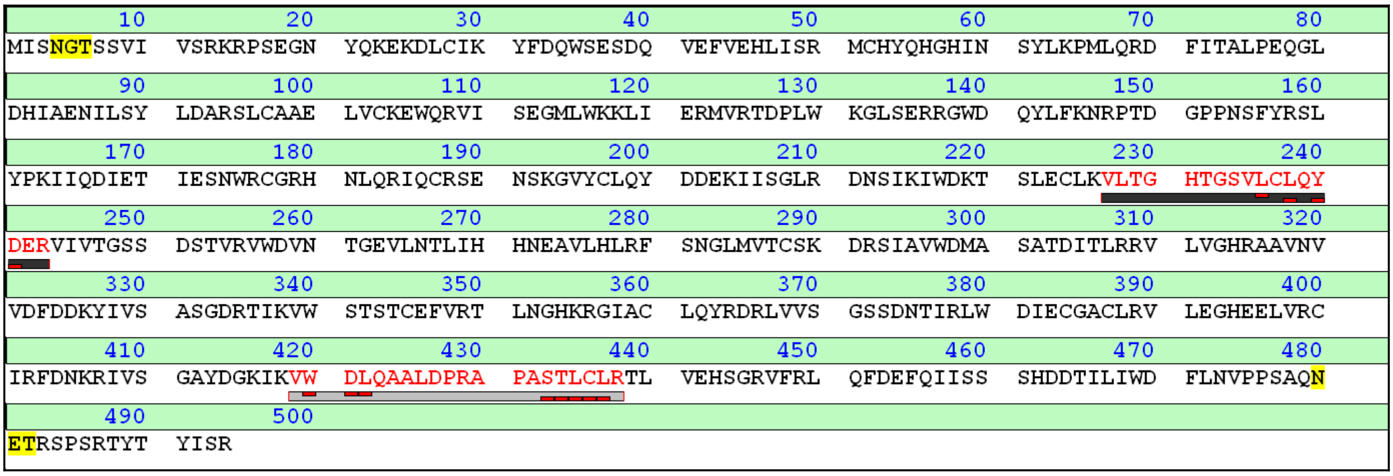
Detailed Protein Report

Protein 101: PREDICTED: F-box/WD repeat-containing protein 11 isoform X5 [Homo sapiens]

Accession:	gi|530380941	**Score:**	36.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	56.8
Database Date:	2015-11-30	**pI:**	8.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	9.7
		No. of unique Peptides:	2

Quantitation

WD:WU **Median:** 1.09 **CV:** 0.00 % **No. of Peptides:** 1



```
        10         20         30         40         50         60         70         80
MISNGTSSVI VSRKRPSEGN YQKEKDLCIK YFDQWSESDQ VEFVEHLISR MCHYQHGHIN SYLKPMLQRD FITALPEQGL
        90        100        110        120        130        140        150        160
DHIAENILSY LDARSLCAAE LVCKEWQRVI SEGMLWKKLI ERMVRTDPLW KGLSERRGWD QYLFKNRPTD GPPNSFYRSL
       170        180        190        200        210        220        230        240
YPKIIQDIET IESNWRCGRH NLQRIQCRSE NSKGVYCLQY DDEKIISGLR DNSIKIWDKT SLECLKVLTG HTGSVLCLQY
       250        260        270        280        290        300        310        320
DERVIVTGSS DSTVRVWDVN TGEVLNTLIH HNEAVLHLRF SNGLMVTCSK DRSIAVWDMA SATDITLRRV LVGHRAAVNV
       330        340        350        360        370        380        390        400
VDFDDKYIVS ASGDRTIKVW STSTCEFVRT LNGHKRGIAC LQYRDRLVVS GSSDNTIRLW DIECGACLRV LEGHEELVRC
       410        420        430        440        450        460        470        480
IRFDNKRIVS GAYDGKIKVW DLQAALDPRA PASTLCLRTL VEHSGRVFRL QFDEFQIISS SHDDTILIWD FLNVPPSAQN
       490        500
ETRSPSRTYT YISR
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
891	1	630.9500	-54.02	3	39.5	12.1	0	227-243	K.VLTGHTGSVLCLQYDER.V		WD:WU 1.09
1138	1	751.8302	130.90	3	42.5	11.7	1	419-438	K.VWDLQAALDPRAPASTLCLR.T	Carbamidomethyl: 18	

Detailed Protein Report

Protein 102: uncharacterized protein C4orf21 [Homo sapiens]

Accession:	gi|254826809	**Score:**	36.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	236.5
Database Date:	2015-11-30	**pI:**	5.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.1
		No. of unique Peptides:	3

Alias proteins:

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

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2940	1	973.5071	-8.25	2	65.5	10.8	1	167-183	K.KDVNNILADPENIVTYK.N	
2069	1	698.2854	-192.09	2	54.5	11.7	1	282-294	K.QPQGSLKIATKPK.Y	
2882	1	938.5029	-0.62	2	64.8	14.3	1	1419-1433	R.SQKIPLYEECQLLVR.K	Carbamidomethyl: 10

Detailed Protein Report

Protein 103: apolipoprotein A-II preproprotein [Homo sapiens]

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

Score: 36.7
MW [kDa]: 11.2
pI: 7.1
Sequence Coverage [%]: 22.0
No. of unique Peptides: 1

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2890	2	1193.0548	-39.81	2	64.9	36.7	0	79-100	K.AGTELVNFLSYFVELGTQPATQ.-	

Detailed Protein Report

Protein 104: regulator of G-protein signaling 9 isoform 3 [Homo sapiens]

Accession:	gi|260099635	**Score:**	36.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	56.7
Database Date:	2015-11-30	**pI:**	9.8
		Sequence Coverage [%]:	6.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MTIRHQGQQY	RPRMAFLQKI	EALVKDMQNP	ETGVRMQNQR	VLVTSVPHAM	TGSDVLQWIV	QRLWISSLEA	QNLGNFIVRY
90	100	110	120	130	140	150	160
GYIYPLQDPK	NLILKPDGSL	YRFQTPYFWP	TQQWPAEDTD	YAIYLAKRNI	KKKGILEEYE	KENYNFLNQK	MNYKWDFVIM
170	180	190	200	210	220	230	240
QAKEQYRAGK	ERNKADRYAL	DCQEKAYWLV	HRCPPGMDNV	LDYGLDRVTN	PNEVKKQTVV	AVKKEIMYYQ	QALMRSTVKS
250	260	270	280	290	300	310	320
SVSLGGIVKY	SEQFSSNDAI	MSGCLPSNPW	ITDDTQFWDL	NAKLVEIPTK	MRVERWAFNF	SELIRDPKGR	QSFQYFLKKE
330	340	350	360	370	380	390	400
FSGENLGFWE	ACEDLKYGDQ	SKVKEKAEEI	YKLFLAPGAR	RWINIDGKTM	DITVKGLKHP	HRYVLDAAQT	HIYMLMKKDS
410	420	430	440	450	460	470	480
YARYLKSPIY	KDMLAKAIEP	QETTKKSSTL	PFMRRHLRSS	PSPVILRQLE	EEAKAREAAN	TVDITQVMSK	LDRRSQLQKE
490							
LPPK							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2782	1	681.4961	134.76	2	63.3	19.3	1	436-447	R.HLRSSPSPVILR.Q	

Detailed Protein Report

Protein 105: biorientation of chromosomes in cell division protein 1-like 1 [Homo sapiens]

Accession:	gi|87299628	**Score:**	36.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	330.3
Database Date:	2015-11-30	**pI:**	4.9
Modification(s):	Oxidation	**Sequence Coverage [%]:**	0.8
		No. of unique Peptides:	1

Detailed Protein Report

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

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2965	1	557.6376	40.39	3	65.8	10.0	2	2881-2894	K.YPVETTLKMKDDSK.T	Oxidation: 9

Detailed Protein Report

Protein 106: PREDICTED: myotubularin-related protein 5 isoform X5 [Homo sapiens]

Accession:	gi|530420851	**Score:**	36.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	208.2
Database Date:	2015-11-30	**pI:**	6.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.0
		No. of unique Peptides:	2

Quantitation

WD:WU	**Median:** 0.65	**CV:** 0.00 %	**No. of Peptides:** 1

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	HMGSHGKWGS
1290	1300	1310	1320	1330	1340	1350	1360
VRTSGRSSGL	GTDVGSRLAG	RDALAPPQAN	GGPPDPGFLR	PQRAALYILG	DKAQLKGVRS	DPLQQWELVP	IEVFEARQVK
1370	1380	1390	1400	1410	1420	1430	1440
ASFKKLLKAC	VPGCPAAEPS	PASFLRSLED	SEWLIQIHKL	LQVSVLVVEL	LDSGSSVLVG	LEDGWDITTQ	VVSLVQLLSD
1450	1460	1470	1480	1490	1500	1510	1520
PFYRTLEGFR	LLVEKEWLSF	GHRFSHRGAH	TLAGQSSGFT	PVFLQFLDCV	HQVHLQFPME	FEFSQFYLKF	LGYHHVSRRF
1530	1540	1550	1560	1570	1580	1590	1600
RTFLLDSDYE	RIELGLLYEE	KGERRGQVPC	RSVWEYVDRL	SKRTPVFHNY	MYAPEDAEVL	RPYSNVSNLK	VWDFYTEETL
1610	1620	1630	1640	1650	1660	1670	1680
AEGPPYDWEL	AQGPPEPPEE	ERSDGGAPQS	RRRVVWPCYD	SCPRAQPDAI	SRLLEELQRL	ETELGQPAER	WKDTWDRVKA
1690	1700	1710	1720	1730	1740	1750	1760
AQRLEGRPDG	RGTPSSLLVS	TAPHHRRSLG	VYLQEGPVGS	TLSLSLDSDQ	SSGSTTSGSR	QAARRSTSTL	YSQFQTAESE
1770	1780	1790	1800	1810	1820	1830	1840
NRSYEGTLYK	KGAFMKPWKA	RWFVLDKTKH	QLRYYDHRVD	TECKGVIDLA	EVEAVAPGTP	TMGAPKTVDE	KAFFDVKTTR
1850	1860	1870					
RVYNFCAQDV	PSAQQWVDRI	QSCLSDA					

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		WD:WU 0.65
1064	3	751.8788	61.27	2	42.0	11.0	1	1116-1128	R.MTMSSLVERACCR.D	Oxidation: 3	

Detailed Protein Report

Protein 107: TRIO and F-actin-binding protein isoform 1 [Homo sapiens]

Accession:	gi|88501740	**Score:**	36.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	74.0
Database Date:	2015-11-30	**pI:**	6.5
		Sequence Coverage [%]:	6.1
		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
1361	1	711.8629	-0.75	2	45.3	11.9	1	22-38	R.AAERGGGGGGGGVPAPR.S	
2143	1	1051.3799	-114.76	2	55.3	12.5	1	276-294	K.WFEATDSRTPEVPAGEGPR.R	

Detailed Protein Report

Protein 108: plectin isoform 1d [Homo sapiens]

Accession:	gi|41322910	**Score:**	36.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	512.3
Database Date:	2015-11-30	**pI:**	5.5
		Sequence Coverage [%]:	1.0
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MKIVPDERDR	VQKKTFTKWV	NKHLIKAQRH	ISDLYEDLRD	GHNLISLLEV	LSGDSLPREK	GRMRFHKLQN	VQIALDYLRH
90	100	110	120	130	140	150	160
RQVKLVNIRN	DDIADGNPKL	TLGLIWTIIL	HFQISDIQVS	GQSEDMTAKE	KLLLWSQRMV	EGYQGLRCDN	FTSSWRDGRL
170	180	190	200	210	220	230	240
FNAIIHRHKP	LLIDMNKVYR	QTNLENLDQA	FSVAERDLGV	TRLLDPEDVD	VPQPDEKSII	TYVSSLYDAM	PRVPDVQDGV
250	260	270	280	290	300	310	320
RANELQLRWQ	EYRELVLLLL	QWMRHHTAAF	EERRFPSSFE	EIEILWSQFL	KFKEMELPAK	EADKNRSKGI	YQSLEGAVQA
330	340	350	360	370	380	390	400
GQLKVPPGYH	PLDVEKEWGK	LHVAILEREK	QLRSEFERLE	CLQRIVTKLQ	MEAGLCEEQL	NQADALLQSD	VRLLAAGKVP
410	420	430	440	450	460	470	480
QRAGEVERDL	DKADSMIRLL	FNDVQTLKDG	RHPQGEQMYR	RVYRLHERLV	AIRTEYNLRL	KAGVAAPATQ	VAQVTLQSVQ
490	500	510	520	530	540	550	560
RRPELEDSTL	RYLQDLLAWV	EENQHRVDGA	EWGVDLPSVE	AQLGSHRGLH	QSIEEFRAKI	ERARSDEGQL	SPATRGAYRD
570	580	590	600	610	620	630	640
CLGRLDLQYA	KLLNSSKARL	RSLESLHSFV	AAATKELMWL	NEKEEEEVGF	DWSDRNTNMT	AKKESYSALM	RELELKEKKI
650	660	670	680	690	700	710	720
KELQNAGDRL	LREDHPARPT	VESFQAALQT	QWSWMLQLCC	CIEAHLKENA	AYFQFFSDVR	EAEGQLQKLQ	EALRRKYSCD
730	740	750	760	770	780	790	800
RSATVTRLED	LLQDAQDEKE	QLNEYKGHLS	GLAKRAKAVV	QLKPRHPAHP	MRGRLPLLAV	CDYKQVEVTV	HKGDECQLVG
810	820	830	840	850	860	870	880
PAQPSHWKVL	SSSGSEAAVP	SVCFLVPPPN	QEAQEAVTRL	EAQHQALVTL	WHQLHVDMKS	LLAWQSLRRD	VQLIRSWSLA
890	900	910	920	930	940	950	960
TFRTLKPEEQ	RQALHSLELH	YQAFLRDSQD	AGGFGPEDRL	MAEREYGSCS	HHYQQLLQSL	EQGAQEESRC	QRCISELKDI
970	980	990	1000	1010	1020	1030	1040
RLQLEACETR	TVHRLRLPLD	KEPARECAQR	IAEQQKAQAE	VEGLGKGVAR	LSAEAEKVLA	LPEPSPAAPT	LRSELELTLG
1050	1060	1070	1080	1090	1100	1110	1120
KLEQVRSLSA	IYLEKLKTIS	LVIRGTQGAE	EVLRAHEEQL	KEAQAVPATL	PELEATKASL	KKLRAQAEAQ	QPTFDALRDE
1130	1140	1150	1160	1170	1180	1190	1200
LRGAQEVGER	LQQRHGERDV	EVERWRERVA	QLLERWQAVL	AQTDVRQREL	EQLGRQLRYY	RESADPLGAW	LQDARRRQEQ
1210	1220	1230	1240	1250	1260	1270	1280
IQAMPLADSQ	AVREQLRQEQ	ALLEEIERHG	EKVEECQRFA	KQYINAIKDY	ELQLVTYKAQ	LEPVASPAKK	PKVQSGSESV
1290	1300	1310	1320	1330	1340	1350	1360
IQEYVDLRTH	YSELTTLTSQ	YIKFISETLR	RMEEEERLAE	QQRAEERERL	AEVEAALEKQ	RQLAEAHAQA	KAQAEREAKE
1370	1380	1390	1400	1410	1420	1430	1440
LQQRMQEEVV	RREEAAVDAQ	QQKRSIQEEL	QQLRQSSEAE	IQAKARQAEA	AERSRLRIEE	EIRVVRLQLE	ATERQRGGAE
1450	1460	1470	1480	1490	1500	1510	1520
GELQALRARA	EEAEAQKRQA	QEEAERLRRQ	VQDESQRKRQ	AEVELASRVK	AEAEAAREKQ	RALQALEELR	LQAEEAERRL
1530	1540	1550	1560	1570	1580	1590	1600
RQAEVERARQ	VQVALETAQR	SAEAELQSKR	ASFAEKTAQL	ERSLQEEHVA	VAQLREEAER	RAQQQAEAER	AREEAERELE
1610	1620	1630	1640	1650	1660	1670	1680
RWQLKANEAL	RLRLQAEEVA	QQKSLAQAEA	EKQKEEAERE	ARRRGKAEEQ	AVRQRELAEQ	ELEKQRQLAE	GTAQQRLAAE
1690	1700	1710	1720	1730	1740	1750	1760
QELIRLRAET	EQGEQQRQLL	EEELARLQRE	AAAATQKRQE	LEAELAKVRA	EMEVLLASKA	RAEEESRSTS	EKSKQRLEAE
1770	1780	1790	1800	1810	1820	1830	1840
AGRFRELAEE	AARLRALAEE	AKRQRQLAEE	DAARQRAEAE	RVLAEKLAAI	GEATRLKTEA	EIALKEKEAE	NERLRRLAED
1850	1860	1870	1880	1890	1900	1910	1920
EAFQRRRLEE	QAAQHKADIE	ERLAQLRKAS	DSELERQKGL	VEDTLRQRRQ	VEEEILALKA	SFEKAAAGKA	ELELELGRIR
1930	1940	1950	1960	1970	1980	1990	2000
SNAEDTLRSK	EQAELEAARQ	RQLAAEEERR	RREAEERVQK	SLAAEEEAAR	QRKAALEEVE	RLKAKVEEAR	RLRERAEQES
2010	2020	2030	2040	2050	2060	2070	2080
ARQLQLAQEA	AQKRLQAEEK	AHAFAVQQKE	QELQQTLQQE	QSVLDQLRGE	AEAARRAAEE	AEEARVQAER	EAAQSRRQVE
2090	2100	2110	2120	2130	2140	2150	2160
EAERLKQSAE	EQAQARAQAQ	AAAEKLRKEA	EQEAARRAQA	EQAALRQKQA	ADAEMEKHKK	FAEQTLRQKA	QVEQELTTLR
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1213	1	713.6809	-62.89	3	43.8	10.9	2	2243-2262	K.QVAEEAARLSVAAQEAARLR.Q	
1785	2	582.1343	-236.00	2	50.7	11.8	0	2343-2352	R.QLEMSAEAER.L	

Detailed Protein Report

Protein 109: PDZ domain-containing RING finger protein 4 isoform 2 [Homo sapiens]

Accession:	gi|142976783	**Score:**	36.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	89.0
Database Date:	2015-11-30	**pI:**	5.0
		Sequence Coverage [%]:	3.2
		No. of unique Peptides:	2

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
652	2	639.3334	-62.76	2	37.0	25.9	2	369-378	R.FRQLLELKCK.I	
2536	1	821.0789	154.65	2	60.0	10.2	1	497-511	R.SPDSSLPRVINLTNK.K	

Detailed Protein Report

Protein 110: dynein heavy chain 5, axonemal [Homo sapiens]

Accession:	gi|19115954	**Score:**	36.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	528.7
Database Date:	2015-11-30	**pI:**	5.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	0.8
		No. of unique Peptides:	2

Detailed Protein Report

10	20	30	40	50	60	70	80
MFRIGRRQLW	KHSVTRVLTQ	RLKGEKEAKR	ALLDARHNYL	FAIVASCLDL	NKTEVEDAIL	EGNQIERIDQ	LFAVGGLRHL
90	100	110	120	130	140	150	160
MFYYQDVEEA	ETGQLGSLGG	VNLVSGKIKK	PKVFVTEGND	VALTGVCVFF	IRTDPSKAIT	PDNIHQEVSF	NMLDAADGGL
170	180	190	200	210	220	230	240
LNSVRRLLSD	IFIPALRATS	HGWGELEGLQ	DAANIRQEFL	SSLEGFVNVL	SGAQESLKEK	VNLRKCDILE	LKTLKEPTDY
250	260	270	280	290	300	310	320
LTLANNPETL	GKIEDCMKVW	IKQTEQVLAE	NNQLLKEADD	VGPRAELEHW	KKRLSKFNYL	LEQLKSPDVK	AVLAVLAAAK
330	340	350	360	370	380	390	400
SKLLKTWREM	DIRITDATNE	AKDNVKYLYT	LEKCCDPLYS	SDPLSMMDAI	PTLINAIKMI	YSISHYYNTS	EKITSLFVKV
410	420	430	440	450	460	470	480
TNQIISACKA	YITNNGTASI	WNQPQDVVEE	KILSAIKLKQ	EYQLCFHKTK	QKLKQNPNAK	QFDFSEMYIF	GKFETFHRRL
490	500	510	520	530	540	550	560
AKIIDIFTTL	KTYSVLQDST	IEGLEDMATK	YQGIVATIKK	KEYNFLDQRK	MDFDQDYEEF	CKQTNDLHNE	LRKFMDVTFA
570	580	590	600	610	620	630	640
KIQNTNQALR	MLKKFERLNI	PNLGIDDKYQ	LILENYGADI	DMISKLYTKQ	KYDPPLARNQ	PPIAGKILWA	RQLFHRIQQP
650	660	670	680	690	700	710	720
MQLFQQHPAV	LSTAEAKPII	RSYNRMAKVL	LEFEVLFHRA	WLRQIEEIHV	GLEASLLVKA	PGTGELFVNF	DPQILILFRE
730	740	750	760	770	780	790	800
TECMAQMGLE	VSPLATSLFQ	KRDRYKRNFS	NMKMMLAEYQ	RVKSKIPAAI	EQLIVPHLAK	VDEALQPGLA	ALTWTSLNIE
810	820	830	840	850	860	870	880
AYLENTFAKI	KDLELLLDRV	NDLIEFRIDA	ILEEMSSTPL	CQLPQEEPLT	CEEFLQMTKD	LCVNGAQILH	FKSSLVEEAV
890	900	910	920	930	940	950	960
NELVNMLLDV	EVLSEEESEK	ISNENSVNYK	NESSAKREEG	NFDTLTSSIN	ARANALLLTT	VTRKKKETEM	LGEEARELLS
970	980	990	1000	1010	1020	1030	1040
HFNHQNMDAL	LKVTRNTLEA	IRKRIHSSHT	INFRDSNSAS	NMKQNSLPIF	RASVTLAIPN	IVMAPALEDV	QQTLNKAVEC
1050	1060	1070	1080	1090	1100	1110	1120
IISVPKGVRQ	WSSELLSKKK	IQERKMAALQ	SNEDSDSDVE	MGENELQDTL	EIASVNLPIP	VQTKNYYKNV	SENKEIVKLV
1130	1140	1150	1160	1170	1180	1190	1200
SVLSTIINST	KKEVITSMDC	FKRYNHIWQK	GKEEAIKTFI	TQSPLLSEFE	SQILYFQNLE	QEINAEPEYV	CVGSIALYTA
1210	1220	1230	1240	1250	1260	1270	1280
DLKFALTAET	KAWMVVIGRH	CNKKYRSEME	NIFMLIEEFN	KKLNRPIKDL	DDIRIAMAAL	KEIREEQISI	DFQVGPIEES
1290	1300	1310	1320	1330	1340	1350	1360
YALLNRYGLL	IAREEIDKVD	TLHYAWEKLL	ARAGEVQNKL	VSLQPSFKKE	LISAVEVFLQ	DCHQFYLDYD	LNGPMASGLK
1370	1380	1390	1400	1410	1420	1430	1440
PQEASDRLIM	FQNQFDNIYR	KYITYTGGEE	LFGLPATQYP	QLLEIKKQLN	LLQKIYTLYN	SVIETVNSYY	DILWSEVNIE
1450	1460	1470	1480	1490	1500	1510	1520
KINNELLEFQ	NRCRKLPRAL	KDWQAFLDLK	KIIDDFSECC	PLLEYMASKA	MMERHWERIT	TLTGHSLDVG	NESFKLRNIM
1530	1540	1550	1560	1570	1580	1590	1600
EAPLLKYKEE	IEDICISAVK	ERDIEQKLKQ	VINEWDNKTF	TFGSFKTRGE	LLLRGDSTSE	IIANMEDSLM	LLGSLLSNRY
1610	1620	1630	1640	1650	1660	1670	1680
NMPFKAQIQK	WVQYLSNSTD	IIESWMTVQN	LWIYLEAVFV	GGDIAKQLPK	EAKRFSNIDK	SWVKIMTRAH	EVPSVVQCCV
1690	1700	1710	1720	1730	1740	1750	1760
GDETLGQLLP	HLLDQLEICQ	KSLTGYLEKK	RLCFPRFFFV	SDPALLEILG	QASDSHTIQA	HLLNVFDNIK	SVKFHEKIYD
1770	1780	1790	1800	1810	1820	1830	1840
RILSISSQEG	ETIELDKPVM	AEGNVEVWLN	SLLEESQSSL	HLVIRQAAAN	IQETGFQLTE	FLSSFPAQVG	LLGIQMIWTR
1850	1860	1870	1880	1890	1900	1910	1920
DSEEALRNAK	FDKKIMQKTN	QAFLELLNTL	IDVTTRDLSS	TERVKYETLI	TIHVHQRDIF	DDLCHMHIKS	PMDFEWLKQC
1930	1940	1950	1960	1970	1980	1990	2000
RFYFNEDSDK	MMIHITDVAF	IYQNEFLGCT	DRLVITPLTD	RCYITLAQAL	GMSMGGAPAG	PAGTGKTETT	KDMGRCLGKY
2010	2020	2030	2040	2050	2060	2070	2080
VVVFNCSDQM	DFRGLGRIFK	GLAQSGSWGC	FDEFNRIDLP	VLSVAAQQIS	IILTCKKEHK	KSFIFTDGDN	VTMNPEFGLF
2090	2100	2110	2120	2130	2140	2150	2160
LTMNPGYAGR	QELPENLKIN	FRSVAMMVPD	RQIIIRVKLA	SCGFIDNVVL	ARKFFTLYKL	CEEQLSKQVH	YDFGLRNILS
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
78	1	529.5845	-42.73	3	29.9	11.4	2	3744-3756	R.THLMEDVTANKRR.M	Oxidation: 4
1942	2	709.7806	-178.71	2	52.9	13.6	0	4137-4148	K.QFPITLLQMSIK.F	

Detailed Protein Report

Protein 111: transcription initiation factor TFIID subunit 1-like [Homo sapiens]

Accession:	gi|24429572	**Score:**	35.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	207.2
Database Date:	2015-11-30	**pI:**	5.1
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.6
		No. of unique Peptides:	3

Quantitation

WD:WU	**Median:**	0.80	**CV:**	0.00 %	**No. of Peptides:**	1

Detailed Protein Report

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2709	1	813.0615	149.49	2	62.3	13.8	0	227-241	K.LTLPLAGIMQHDATK.L	Oxidation: 9	
1092	1	839.4008	43.81	2	42.4	10.2	0	1050-1065	R.TMSTEQAHSGEGPMSK.F		WD:WU 0.80
2649	1	835.4339	3.24	2	61.4	11.7	1	1150-1165	R.RMLLVAGSAASGNNHR.D	Oxidation: 2	

Detailed Protein Report

Protein 112: **PREDICTED: cylicin-1 isoform X1 [Homo sapiens]**

Accession:	gi|530421958	**Score:**	35.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	74.1
Database Date:	2015-11-30	**pI:**	10.2
		Sequence Coverage [%]:	4.2
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MSLPRLKVNI RTYDNSIPIS ESSRKSWNQK HFALTFPKPL QRGTNDKSRP LKSQITVTRH DKRKLEEGQK PAHKWIRHSF

        90        100        110        120        130        140        150        160
RKILQWPPIY TAAREQTPFR HLYTSKTHLK KAEYKKSKDE KGGTPLKKDS KKKGGSYATN PESKQIVEEK TKRQNEADKT

       170        180        190        200        210        220        230        240
PLKSSHENEQ SKKSKSSSET NPESQNSKTV SKNCSQKDKK DSKNSKKTNT EFLHTKNNPK KDLKRSKTSN DPISEICSEN

       250        260        270        280        290        300        310        320
SLNVDFLMLV GQSDDESINF DAWLRNYSQN NSKNYSLKYT KYTKKDTKKN AKKSSDAESE DSKDAKKDSK KVKKNVKKDD

       330        340        350        360        370        380        390        400
KKKDVKKDTE STDAESGDSK DERKDTKKDK KKLKKDDKKK DTKKYPESTD TESGDAKDAR NDSRNLKKAS KNDDKKKDAK

       410        420        430        440        450        460        470        480
KITFSTDSES ELESKESQKD EKKDKKDSKT DNKKSVKNDE ESTDADSEPK GDSKKGKKDE KKGKKDSKKD DKKKDAKKNA

       490        500        510        520        530        540        550        560
ESTEMESDLE LKKDKKHSKE KKGSKKDIKK DARKDTESTD AEFDESSKTG FKTSTKIKGS DTESEESLYK PGAKKKIDES

       570        580        590        600        610        620        630        640
DGTSANSKME GLESKRGFRM SSKKTTFNEK GEKASTGRVP PSREKPPLPA CEPSLPSPKV RRLCWCKMPP PPPKPRYAPL

       650        660
PEAPWIHKLL
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
547	1	472.6490	-226.33	2	35.3	16.3	1	119-127	K.DEKGGTPLK.K	

Detailed Protein Report

Protein 113: SURP and G-patch domain-containing protein 2 [Homo sapiens]

Accession:	gi|224282117	**Score:**	35.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	120.1
Database Date:	2015-11-30	**pI:**	7.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.4
		No. of unique Peptides:	2

Quantitation

WD:WU **Median:** 0.67 **CV:** 0.00 % **No. of Peptides:** 1

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	DQLVKKRVIEG	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	Ratios
2696	1	835.4525	-15.26	2	62.1	11.4	1	213-228	R.GRALNIVDQEGSLLGK.G		
1571	1	948.4992	16.11	2	48.0	14.2	0	439-455	K.SVTPLLMACNAYELSVK.M	Carbamidomethyl: 9	WD:WU 0.67

Detailed Protein Report

Protein 114: zinc finger protein 540 isoform a [Homo sapiens]

Accession:	gi|22749241	**Score:**	35.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	77.0
Database Date:	2015-11-30	**pI:**	10.5
		Sequence Coverage [%]:	6.5
		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 115: laminin subunit alpha-2 isoform b precursor [Homo sapiens]

Accession:	gi|119466532	**Score:**	35.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	343.3
Database Date:	2015-11-30	**pI:**	6.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.2
		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
892	1	739.3524	121.81	2	39.5	10.1	0	1125-1137	K.CSCSDQTGQCTCK.V	Carbamidomethyl: 1, 10

Detailed Protein Report

Protein 116: transmembrane protein 169 [Homo sapiens]

Accession: gi|19923913
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 35.4
MW [kDa]: 33.6
pI: 4.6
Sequence Coverage [%]: 6.4
No. of unique Peptides: 1

Alias proteins:

Accession	Name	Description
gi|578805184	refseq_human (refseq_human_20140103.fasta)	PREDICTED: transmembrane protein 169 isoform X1 [Homo sapiens]
gi|214831834	refseq_human (refseq_human_20140103.fasta)	transmembrane protein 169 [Homo sapiens]
gi|214831799	refseq_human (refseq_human_20140103.fasta)	transmembrane protein 169 [Homo sapiens]
gi|214831780	refseq_human (refseq_human_20140103.fasta)	transmembrane protein 169 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MEEPTAVEGQ VQLPSPHQGS LRKAVAAALA LDGESTMGHR KKKRKESRPE SIIIYRSDNE KTDEEPGESE GGDQPKEEEG
        90        100        110        120        130        140        150        160
DDFLDYPVDD DMWNLPLDSR YVTLTGTITR GKKKGQMVDI HVTLTEKELQ ELTKPKESSR ETTPEGRMAC QMGADRGPHV
       170        180        190        200        210        220        230        240
VLWTLICLPV VFILSFVVSF YYGTITWYNI FLVYNEERTF WHKISYCPCL VLFYPVLIMA MASSLGLYAA VVQLSWSWEA
       250        260        270        280        290        300
WWQAARDMEK GFCGWLCSKL GLEDCSPYSI VELLESDNIS STLSNKDPIQ EVETSTV
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1888	1	899.4768	10.43	2	52.3	12.3	1	24-41	K.AVAAALALDGESTMGHRK.K	

Detailed Protein Report

Protein 117: keratin, type II cuticular Hb5 [Homo sapiens]

Accession:	gi|4504935	**Score:**	35.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	55.8
Database Date:	2015-11-30	**pI:**	6.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	6.5
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MSCRSYRISS GCGVTRNFSS CSAVAPKTGN RCCISAAPYR GVSCYRGLTG FGSRSLCNLG SCGPRIAVGG FRAGSCGRSF

        90        100        110        120        130        140        150        160
GYRSGGVCGP SPPCITTVSV NESLLTPLNL EIDPNAQCVK QEEKEQIKSL NSRFAAFIDK VRFLEQQNKL LETKWQFYQN

       170        180        190        200        210        220        230        240
QRCCESNLEP LFSGYIETLR REAECVEADS GRLASELNHV QEVLEGYKKK YEEEVALRAT AENEFVVLKK DVDCAYLRKS

       250        260        270        280        290        300        310        320
DLEANVEALV EESSFLRRLY EEEIRVLQAH ISDTSVIVKM DNSRDLNMDC IIAEIKAQYD DVASRSRAEA ESWYRSKCEE

       330        340        350        360        370        380        390        400
MKATVIRHGE TLRRTKEEIN ELNRMIQRLT AEIENAKCQR AKLEAAVAEA EQQGEAALSD ARCKLAELEG ALQKAKQDMA

       410        420        430        440        450        460        470        480
CLLKEYQEVM NSKLGLDIEI ATYRRLLEGE EHRLCEGVGS VNVCVSSSRG GVSCGGLSYS TTPGRQITSG PSAIGGSITV

       490        500        510
VAPDSCAPCQ PRSSSFSCGS SRSVRFA
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
953	1	531.2210	2.88	2	40.3	11.1	0	493-502	R.SSSFSCGSSR.S	Carbamidomethyl: 6

Detailed Protein Report

Protein 118: **PREDICTED: regulator of G-protein signaling 3 isoform X1 [Homo sapiens]**

Accession:	gi|578817731	**Score:**	35.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	120.9
Database Date:	2015-11-30	**pI:**	5.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.1
		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        630        640
IAKQQQLAAS PPDSKMFETE ADEKREMALE EGKGPGAEDS PPSKEPSPGQ ELPPGQDLPP NKDSPSGQEP APSQEPLSSK
       650        660        670        680        690        700        710        720
DSATSEGSPP GPDAPPSKDV PPCQEPPPAQ DLSPCQDLPA GQEPLPHQDP LLTKDLPAIQ ESPTRDLPPC QDLPPSQVSL
       730        740        750        760        770        780        790        800
PAKALTEDTM SSGDLLAATG DPPAAPRPAF VIPEVRLDST YSQKAGAEQG CSGDEEDAEE AEEVEEGEEG EEDEDEDTSD
       810        820        830        840        850        860        870        880
DNYGERSEAK RSSMIETGQG AEGGLSLRVQ NSLRRRTHSE GSLLQEPRGP CFASDTTLHC SDGEGAASTW GMPSPSTLKK
       890        900        910        920        930        940        950        960
ELGRNGGSMH HLSLFFTGHR KMSGADTVGD DDEASRKRKS KNLAKDMKNK LGIFRRRNES PGAPPAGKAD KMMKSFKPTS
       970        980        990       1000       1010       1020       1030       1040
EEALKWGESL EKLLVHKYGL AVFQAFLRTE FSEENLEFWL ACEDFKKVKS QSKMASKAKK IFAEYIAIQA CKEVNLDSYT
      1050       1060       1070       1080       1090       1100
REHTKDNLQS VTRGCFDLAQ KRIFGLMEKD SYPRFLRSDL YLDLINQKKM SPPL
```

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	
1	3	819.8417	-105.55	2	28.8	11.8	2	81-93	R.LRHQKTQTVPDCR.D	Carbamidomethyl: 12
1949	1	599.9043	-89.98	3	52.7	12.8	0	885-900	R.NGGSMHHLSLFFTGHR.K	

Detailed Protein Report

Protein 119: PREDICTED: CAS1 domain-containing protein 1 isoform X2 [Homo sapiens]

Accession:	gi|578814529	**Score:**	35.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	72.0
Database Date:	2015-11-30	**pI:**	9.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.2
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 0.75 **CV:** 0.00 % **No. of Peptides:** 1

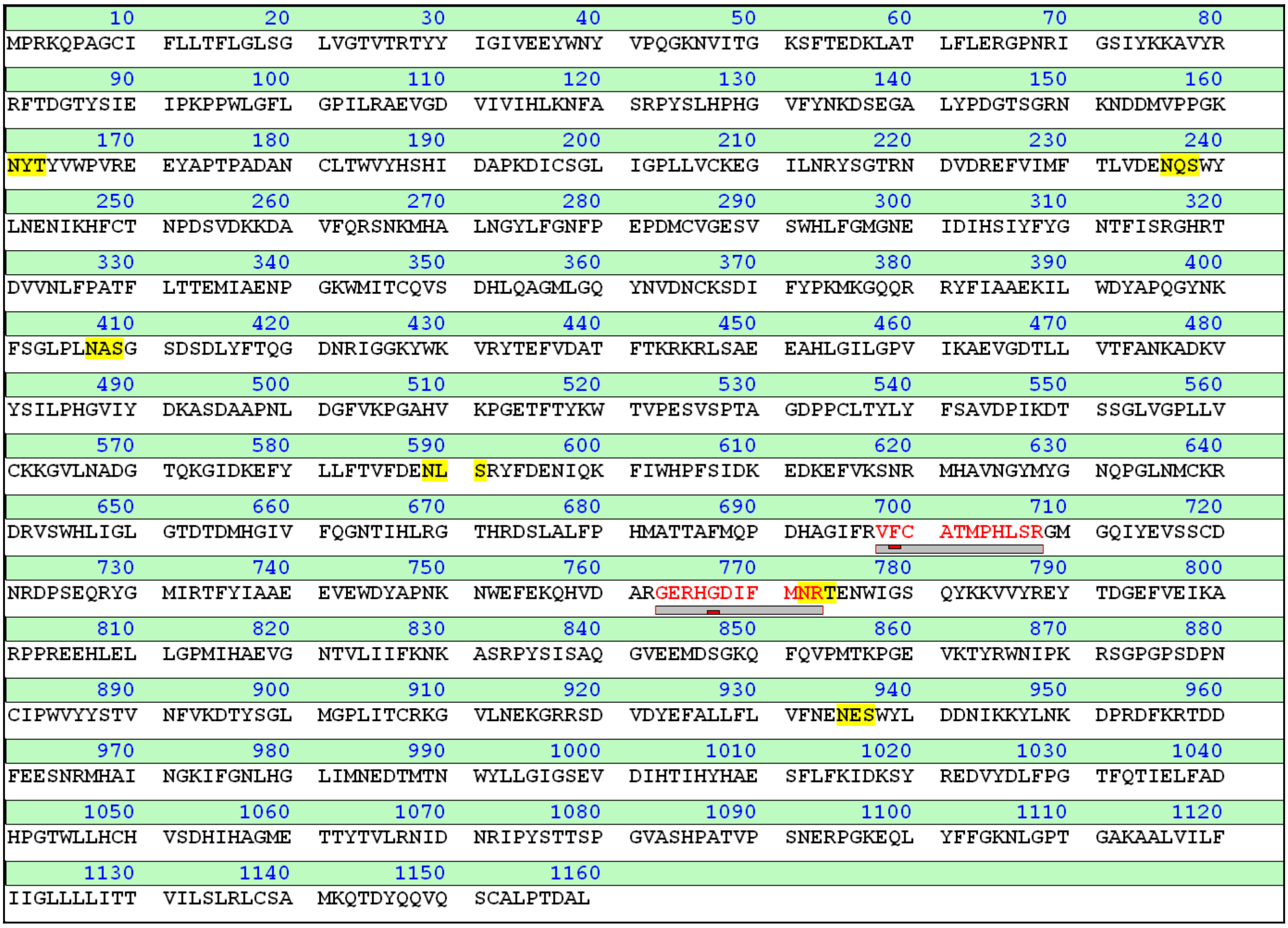
```
        10         20         30         40         50         60         70         80
MGRCVLFSRN CSSIAPTWAQ VAASKLGDSP KARVRARRVP LVLSPHTPMA LPQPPPPAGA RDPVTPEHWA SGPPSQAQPL

        90        100        110        120        130        140        150        160
LRQEAKEEEE GEETGVQGAW GTGTAEQRRR GWGEAAESAA AEEGQAEVGG AAAAGSGSPA GGAGGGLGSW RPLLAWLQRR

       170        180        190        200        210        220        230        240
QPQCCPCAAP LSRSAAHCCH GGTKMAALAY NLGKREINHY FSVRSAKVLA LVAVLLLAAC HLASRRYRGN DSCEYLLSSG

       250        260        270        280        290        300        310        320
RFLGEKVWQP HSCMMHKYKI SEAKNCLVDK HIAFIGDSRI RQLFYSFVKI INPQFKEEGN KHENIPFEDK TASVKVDFLW

       330        340        350        360        370        380        390        400
HPEVNGSMKQ CIKVWTEDSI AKPHVIVAGA ATWSIKIHNG SSEALSQYKM NITSIAPLLE KLAKTSDVYW VLQDPVYEDL

       410        420        430        440        450        460        470        480
LSENRKMITN EKIDAYNEAA VSILNSSTRN SKSNVKMFSV SKLIAQETIM ESLDGLHLPE SSRETTAMIL MNVYCNKILK

       490        500        510        520        530        540        550        560
PVDGSCCQPR PPVTLIQKLA ACFFTLSIIG YLIFYIIHRN AHRKNKPCTD LESGEEKKNI INTPVSSLEI LLQSFCKLGL

       570        580        590        600        610        620        630        640
IMAYFYMCDR ANLFMKENKF YTHSSFFIPI IYILVLGVFY NENTKETKVL NREQTDEWKG WMQLVILIYH ISGASTIVGA

       650        660
IGTQEGMTF  I
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
117	1	793.7232	-186.24	2	30.4	10.2	1	160-173	R.RQPQCCPCAAPLSR.S	Carbamidomethyl: 8	WD:WU 0.75

Detailed Protein Report

Protein 120: **hephaestin-like protein 1 precursor [Homo sapiens]**

Accession:	gi|148886707	**Score:**	35.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	131.5
Database Date:	2015-11-30	**pI:**	6.3
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.9
		No. of unique Peptides:	2



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
2733	1	639.3478	58.98	2	62.6	13.4	0	698-708	R.VFCATMPHLSR.G	Oxidation: 6
2243	1	666.2803	-55.46	2	56.5	21.7	1	763-773	R.GERHGDIFMNR.T	

Detailed Protein Report

Protein 121: **collagen alpha-2(XI) chain isoform 3 preproprotein [Homo sapiens]**

Accession:	gi|111118968	**Score:**	35.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	159.8
Database Date:	2015-11-30	**pI:**	9.5
		Sequence Coverage [%]:	1.7
		No. of unique Peptides:	1

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2871	4	645.8309	-41.94	2	64.6	23.7	1	158-169	K.GQSVTLIVDCKK.R	

Detailed Protein Report

Protein 122:	**PREDICTED: sacsin isoform X1 [Homo sapiens]**		
Accession:	gi|530402261	**Score:**	34.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	521.9
Database Date:	2015-11-30	**pI:**	6.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	0.9
		No. of unique Peptides:	2

Detailed Protein Report

10	20	30	40	50	60	70	80
METKENRWVP	VTVLPGCVGC	RTVAALASWT	VRDVKERIFA	ETGFPVSEQR	LWRGGRELSD	WIKIGDLTSK	NCHLFVNLQS
90	100	110	120	130	140	150	160
KGLKGGGRFG	QTTPPLVDFL	KDILRRYPEG	GQILKELIQN	AEDAGATEVK	FLYDETQYGT	ETLWSKDMAP	YQGPALYVYN
170	180	190	200	210	220	230	240
NAVFTPEDWH	GIQEIARSRK	KDDPLKVGRF	GIGFNSVYHI	TDVPCIFSGD	QIGMLDPHQT	LFGPHESGQC	WNLKDDSKEI
250	260	270	280	290	300	310	320
SELSDQFAPF	VGIFGSTKET	FINGNFPGTF	FRFPLRLQPS	QLSSNLYNKQ	KVLELFESFR	ADADTVLLFL	KSVQDVSLYV
330	340	350	360	370	380	390	400
READGTEKLV	FRVTSSESKA	LKHERPNSIK	ILGTAISNYC	KKTPSNNITC	VTYHVNIVLE	EESTKDAQKT	SWLVCNSVGG
410	420	430	440	450	460	470	480
RGISSKLDSL	ADELKFVPII	GIAMPLSSRD	DEAKGATSDF	SGKAFCFLPL	PPGEESSTGL	PVHISGFFGL	TDNRRSIKWR
490	500	510	520	530	540	550	560
ELDQWRDPAA	LWNEFLVMNV	VPKAYATLIL	DSIKRLEMEK	SSDFPLSVDV	IYKLWPEASK	VKVHWQPVLE	PLFSELLQNA
570	580	590	600	610	620	630	640
VIYSISCDWV	RLEQVYFSEL	DENLEYTKTV	LNYLQSSGKQ	IAKVPGNVDA	AVQLTAASGT	TPVRKVTPAW	VRQVLRKCAH
650	660	670	680	690	700	710	720
LGCAEEKLHL	LEFVLSDQAY	SELLGLELLP	LQNGNFVPFS	SSVSDQDVIY	ITSAEYPRSL	FPSLEGRFIL	DNLKPHLVAA
730	740	750	760	770	780	790	800
LKEAAQTRAQ	QQLWGYSGRP	CTQLQLLNPE	RFARLIKEVM	NTFWPGRELI	VQWYPFDENR	NHPSVSWLKM	VWKNLYIHFS
810	820	830	840	850	860	870	880
EDLTLFDEMP	LIPRTILEEG	QTCVELIRLR	IPSLVILDDE	SEAQLPEFLA	DIVQKLGGFV	LKKLDASIQH	PLIKKYIHSP
890	900	910	920	930	940	950	960
LPSAVLQIME	KMPLQKLCNQ	ITSLLPTHKD	ALRKFLASLT	DSSEKEKRII	QELAIFKRIN	HSSDQGISSY	TKLKGCKVLH
970	980	990	1000	1010	1020	1030	1040
HTAKLPADLR	LSISVIDSSD	EATIRLANML	KIEQLKTTSC	LKLVLKDIEN	AFYSHEEVTQ	LMLWVLENLS	SLKNENPNVL
1050	1060	1070	1080	1090	1100	1110	1120
EWLTPLKFIQ	ISQEQMVSAG	ELFDPDIEVL	KDLFCNEEGT	YFPPSVFTSP	DILHSLRQIG	LKNEASLKEK	DVVQVAKKIE
1130	1140	1150	1160	1170	1180	1190	1200
ALQVGACPDQ	DVLLKKAKTL	LLVLNKNHTL	LQSSEGKMTL	KKIKWVPACK	ERPPNYPGSL	VWKGDLCNLC	APPDMCDVGH
1210	1220	1230	1240	1250	1260	1270	1280
AILIGSSLPL	VESIHVNLEK	ALGIFTKPSL	SAVLKHFKIV	VDWYSSKTFS	DEDYYQFQHI	LLEIYGFMHD	HLNEGKDSFR
1290	1300	1310	1320	1330	1340	1350	1360
ALKFPWVWTG	KKFCPLAQAV	IKPIHDLDLQ	PYLHNVPKTM	AKFHQLFKVC	GSIEELTSDH	ISMVIQKIYL	KSDQDLSEQE
1370	1380	1390	1400	1410	1420	1430	1440
SKQNLHLMLN	IIRWLYSNQI	PASPNTPVPI	HHSKNPSKLI	MKPIHECCYC	DIKVDDLNDL	LEDSVEPIIL	VHEDIPMKTA
1450	1460	1470	1480	1490	1500	1510	1520
EWLKVPCLST	RLINPENMGF	EQSGQREPLT	VRIKNILEEY	PSVSDIFKEL	LQNADDANAT	ECSFLIDMRR	NMDIRENLLD
1530	1540	1550	1560	1570	1580	1590	1600
PGMAACHGPA	LWSFNNSQFS	DSDFVNITRL	GESLKRGEVD	KVGKFGLGFN	SVYHITDIPI	IMSREFMIMF	DPNINHISKH
1610	1620	1630	1640	1650	1660	1670	1680
IKDKSNPGIK	INWSKQQKRL	RKFPNQFKPF	IDVFGCQLPL	TVEAPYSYNG	TLFRLSFRTQ	QEAKVSEVSS	TCYNTADIYS
1690	1700	1710	1720	1730	1740	1750	1760
LVDEFSLCGH	RLIIFTQSVK	SMYLKYLKIE	ETNPSLAQDT	VIIKKKSCSS	KALNTPVLSV	LKEAAKLMKT	CSSSNKKLPS
1770	1780	1790	1800	1810	1820	1830	1840
DEPKSSCILQ	ITVEEFHHVF	RRIADLQSPL	FRGPDDDPAA	LFEMAKSGQS	KKPSDELSQK	TVECTTWLLC	TCMDTGEALK
1850	1860	1870	1880	1890	1900	1910	1920
FSLSESGRRL	GLVPCGAVGV	QLSEIQDQKW	TVKPHIGEVF	CYLPLRIKTG	LPVHINGCFA	VTSNRKEIWK	TDTKGRWNTT
1930	1940	1950	1960	1970	1980	1990	2000
FMRHVIVKAY	LQVLSVLRDL	ATSGELMDYT	YYAVWPDPDL	VHDDFSVICQ	GFYEDIAHGK	GKELTKVFSD	GSTWVSMKNV
2010	2020	2030	2040	2050	2060	2070	2080
RFLDDSILKR	RDVGSAAFKI	FLKYLKKTGS	KNLCAVELPS	SVKLGFEEAG	CKQILLENTF	SEKQFFSEVF	FPNIQEIAEE
2090	2100	2110	2120	2130	2140	2150	2160
LRDPLMIFVL	NEKVDEFSGV	LRVTPCIPCS	LEGHPLVLPS	RLIHPEGRVA	KLFDIKDGRF	PYGSTQDYLN	PIILIKLVQL
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1798	1	916.4469	-78.82	2	50.8	10.5	2	1726-1742	K.KSCSSKALNTPVLSVLK.E	Carbamidomethyl: 3
1779	1	516.2947	105.86	2	50.6	10.7	0	2492-2499	K.YCHADIPR.E	Carbamidomethyl: 2

Detailed Protein Report

Protein 123: niban-like protein 1 isoform 2 [Homo sapiens]

Accession:	gi|79750824	**Score:**	34.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	82.6
Database Date:	2015-11-30	**pI:**	5.8
		Sequence Coverage [%]:	2.5
		No. of unique Peptides:	1

Quantitation

WD:WU	**Median:** 1.73	**CV:** 0.00 %	**No. of Peptides:** 1

10	20	30	40	50	60	70	80
MGWMGEKTGK	ILTEFLQFYE	DQYGVALFNS	MRHEIEGTGL	PQAQLLWRKV	PLDERIVFSG	NLFQHQEDSK	KWRNRFSLVP
90	100	110	120	130	140	150	160
HNYGLVLYEN	KAAYERQVPP	RAVINSAGYK	ILTSVDQYLE	LIGNSLPGTT	AKSGSAPILK	CPTQFPLILW	HPYARHYYFC
170	180	190	200	210	220	230	240
MMTEAEQDKW	QAVLQDCIRH	CNNGIPEDSK	VEGPAFTDAI	RMYRQSKELY	GTWEMLCGNE	VQILSNLVME	ELGPELKAEL
250	260	270	280	290	300	310	320
GPRLKGKPQE	RQRQWIQISD	AVYHMVYEQA	KARFEEVLSK	VQQVQPAMQA	VIRTDMDQII	TSKEHLASKI	RAFILPKAEV
330	340	350	360	370	380	390	400
CVRNHVQPYI	PSILEALMVP	TSQGFTEVRD	VFFKEVTDMN	LNVINEGGID	KLGEYMEKLS	RLAYHPLKMQ	SCYEKMESLR
410	420	430	440	450	460	470	480
LDGLQQRFDV	SSTSVFKQRA	QIHMREQMDN	AVYTFETLLH	QELGKGPTKE	ELCKSIQRVL	ERVLKKYDYD	SSSVRKRFFR
490	500	510	520	530	540	550	560
EALLQISIPF	LLKKLAPTCK	SELPRFQELI	FEDFARFILV	ENTYEEVVLQ	TVMKDILQAV	KEAAVQRKHN	LYRDSMVMHN
570	580	590	600	610	620	630	640
SDPNLHLLAE	GAPIDWGEEY	SNSGGGGSPS	PSTPESATLS	EKRRRAKQVV	SVVQDEEVGL	PFEASPESPP	PASPDGVTEI
650	660	670	680	690	700	710	720
RGLLAQGLRP	ESPPPAGPLL	NGAPAGESPQ	PKAAPEASSP	PASPLQHLLP	GKAVDLGPPK	PSDQETGEQV	SSPSSHPALH
730	740						
TTTEDSAGVQ	TEF						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
367	3	607.8374	9.31	2	33.2	19.6	1	495-505	K.LAPTCKSELPR.F		WD:WU 1.73

Detailed Protein Report

Protein 124: PREDICTED: lysosomal-trafficking regulator isoform X4 [Homo sapiens]

Accession:	gi|530365992	**Score:**	34.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	313.5
Database Date:	2015-11-30	**pI:**	6.1
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.5
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MSTDSNSLAR	EFLTDVNRLC	NAVVQRVEAR	EEEEEETHMA	TLGQYLVHGR	GFLLLTKLNS	IIDQALTCRE	ELLTLLLSLL
90	100	110	120	130	140	150	160
PLVWKIPVQE	EKATDFNLPL	SADIILTKEK	NSSSQRSTQE	KLHLEGSALS	SQVSAKVNVF	RKSRRQRKIT	HRYSVRDARK
170	180	190	200	210	220	230	240
TQLSTSDSEA	NSDEKGIAMN	KHRRPHLLHH	FLTSFPKQDH	PKAKLDRLAT	KEQTPPDAMA	LENSREIIPR	QGSNTDILSE
250	260	270	280	290	300	310	320
PAALSVISNM	NNSPFDLCHV	LLSLLEKVCK	FDVTLNHNSP	LAASVVPTLT	EFLAGFGDCC	SLSDNLESRV	VSAGWTEEPV
330	340	350	360	370	380	390	400
ALIQRMLFRT	VLHLLSVDVS	TAEMMPENLR	KNLTELLRAA	LKIRICLEKQ	PDPFAPRQKK	TLQEVQEDFV	FSKYRHRALL
410	420	430	440	450	460	470	480
LPELLEGVLQ	ILICCLQSAA	SNPFYFSQAM	DLVQEFIQHH	GFNLFETAVL	QMEWLVLRDG	VPPEASEHLK	ALINSVMKIM
490	500	510	520	530	540	550	560
STVKKVKSEQ	LHHSMCTRKR	HRRCEYSHFM	HHHRDLSGLL	VSAFKNQVSK	NPFEETADGD	VYYPERCCCI	AVCAHQCLRL
570	580	590	600	610	620	630	640
LQQASLSSTC	VQILSGVHNI	GICCCMDPKS	VIIPLLHAFK	LPALKNFQQH	ILNILNKLIL	DQLGGAEISP	KIKKAACNIC
650	660	670	680	690	700	710	720
TVDSDQLAQL	EETLQGNLCD	AELSSSLSSP	SYRFQGILPS	SGSEDLLWKW	DALKAYQNFV	FEEDRLHSIQ	IANHICNLIQ
730	740	750	760	770	780	790	800
KGNIVVQWKL	YNYIFNPVLQ	RGVELAHHCQ	HLSVTSAQSH	VCSHHNQCLP	QDVLQIYVKT	LPILLKSRVI	RDLFLSCNGV
810	820	830	840	850	860	870	880
SQIIELNCLN	GIRSHSLKAF	ETLIISLGEQ	QKDASVPDID	GIDIEQKELS	SVHVGTSFHH	QQAYSDSPQS	LSKFYAGLKE
890	900	910	920	930	940	950	960
AYPKRRKTVN	QDVHINTINL	FLCVAFLCVS	KEAESDRESA	NDSEDTSGYD	STASEPLSHM	LPCISLESLV	LPSPEHMHQA
970	980	990	1000	1010	1020	1030	1040
ADIWSMCRWI	YMLSSVFQKQ	FYRLGGFRVC	HKLIFMIIQK	LFRSHKEEQG	KKEGDTSVNE	NQDLNRISQP	KRTMKEDLLS
1050	1060	1070	1080	1090	1100	1110	1120
LAIKSDPIPS	ELGSLKKSAD	SLGKLELQHI	SSINVEEVSA	TEAAPEEAKL	FTSQESETSL	QSIRLLEALL	AICLHGARTS
1130	1140	1150	1160	1170	1180	1190	1200
QQKMELELPN	QNLSVESILF	EMRDHLSQSK	VIETQLAKPL	FDALLRVALG	NYSADFEHND	AMTEKSHQSA	EELSSQPGDF
1210	1220	1230	1240	1250	1260	1270	1280
SEEAEDSQCC	SFKLLVEEEG	YEADSESNPE	DGETQDDGVD	LKSETEGFSA	SSSPNDLLEN	LTQGEIIYPE	ICMLELNLLS
1290	1300	1310	1320	1330	1340	1350	1360
ASKAKLDVLA	HVFESFLKII	RQKEKNVFLL	MQQGTVKNLL	GGFLSILTQD	DSDFQACQRV	LVDLLVSLMS	SRTCSEELTL
1370	1380	1390	1400	1410	1420	1430	1440
LLRIFLEKSP	CTKILLLGIL	KIIESDTTMS	PSQYLTFPLL	HAPNLSNGVS	SQKYPGILNS	KAMGLLRRAR	VSRSKKEADR
1450	1460	1470	1480	1490	1500	1510	1520
ESFPHRLLSS	WHIAPVHLPL	LGQNCWPHLS	EGFSVSLWFN	VECIHEAEST	TEKGKKIKKR	NKSLILPDSS	FDGTESDRPE
1530	1540	1550	1560	1570	1580	1590	1600
GAEYINPGER	LIEEGCIHII	SLGSKALMIQ	VWADPHNATL	IFRVCMDSND	DMKAVLLAQV	ESQENIFLPS	KWQHLVLTYL
1610	1620	1630	1640	1650	1660	1670	1680
QQPQGKRRIH	GKISIWVSGQ	RKPDVTLDFM	LPRKTSLSSD	SNKTFCMIGH	CLSSQEEFLQ	LAGKWDLGNL	LLFNGAKVGS
1690	1700	1710	1720	1730	1740	1750	1760
QEAFYLYACG	PNHTSVMPCK	YGKPVNDYSK	YINKEILRCE	QIRELFMTKK	DVDIGLLIES	LSVVYTTYCP	AQYTIYEPVI
1770	1780	1790	1800	1810	1820	1830	1840
RLKGQMKTQL	SQRPFSSKEV	QSILLEPHHL	KNLQPTEYKT	IQGILHEIGG	TGIFVFLFAR	VVELSSCEET	QALALRVILS
1850	1860	1870	1880	1890	1900	1910	1920
LIKYNQQRVH	ELENCNGLSM	IHQVLIKQKC	IVGFYILKTL	LEGCCGEDII	YMNENGEFKL	DVDSNAIIQD	VKLLEELLLD
1930	1940	1950	1960	1970	1980	1990	2000
WKIWSKAEQG	VWETLLAALE	VLIRADHHQQ	MFNIKQLLKA	QVVHHFLLTC	QVLQEYKEGQ	LTPMPREVCR	SFVKIIAEVL
2010	2020	2030	2040	2050	2060	2070	2080
GSPPDLELLT	IIFNFLLAVH	PPTNTYVCHN	PTNFYFSLHI	DGKIFQEKVR	SIMYLRHSSS	GGRSLMSPGF	MVISPSGFTA
2090	2100	2110	2120	2130	2140	2150	2160
SPYEGENSSN	IIPQQMAAHM	LRSRSLPAFP	TSSLLTQSQK	LTGSLGCSID	RLQNIADTYV	ATQSKKQNSL	GSSDTLKKGK
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1683	1	853.4016	-89.30	2	49.4	11.6	1	515-530	R.DLSGLLVSAFKNQVSK.N	
2340	1	953.1627	116.28	2	57.7	13.1	2	989-1003	R.VCHKLIFMIIQKLFR.S	Oxidation: 8

Detailed Protein Report

Protein 125: dystrophin Dp260-1 isoform [Homo sapiens]

Accession:	gi|150036268	**Score:**	34.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	271.2
Database Date:	2015-11-30	**pI:**	5.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.7
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MTEMILLIFF	PAYFLNAVRR	QKLLEQSIQS	AQETEKSLHL	IQESLTFIDK	QLAAYIADKV	DAAQMPQEAQ	KIQSDLTSHE
90	100	110	120	130	140	150	160
ISLEEMKKHN	QGKEAAQRVL	SQIDVAQKKL	QDVSMKFRLF	QKPANFEQRL	QESKMILDEV	KMHLPALETK	SVEQEVVQSQ
170	180	190	200	210	220	230	240
LNHCVNLYKS	LSEVKSEVEM	VIKTGRQIVQ	KKQTENPKEL	DERVTALKLH	YNELGAKVTE	RKQQLEKCLK	LSRKMRKEMN
250	260	270	280	290	300	310	320
VLTEWLAATD	MELTKRSAVE	GMPSNLDSEV	AWGKATQKEI	EKQKVHLKSI	TEVGEALKTV	LGKKETLVED	KLSLLNSNWI
330	340	350	360	370	380	390	400
AVTSRAEEWL	NLLLEYQKHM	ETFDQNVDHI	TKWIIQADTL	LDESEKKKPQ	QKEDVLKRLK	AELNDIRPKV	DSTRDQAANL
410	420	430	440	450	460	470	480
MANRGDHCRK	LVEPQISELN	HRFAAISHRI	KTGKASIPLK	ELEQFNSDIQ	KLLEPLEAEI	QQGVNLKEED	FNKDMNEDNE
490	500	510	520	530	540	550	560
GTVKELLQRG	DNLQQRITDE	RKREEIKIKQ	QLLQTKHNAL	KDLRSQRRKK	ALEISHQWYQ	YKRQADDLLK	CLDDIEKKLA
570	580	590	600	610	620	630	640
SLPEPRDERK	IKEIDRELQK	KKEELNAVRR	QAEGLSEDGA	AMAVEPTQIQ	LSKRWREIES	KFAQFRRLNF	AQIHTVREET
650	660	670	680	690	700	710	720
MMVMTEDMPL	EISYVPSTYL	TEITHVSQAL	LEVEQLLNAP	DLCAKDFEDL	FKQEESLKNI	KDSLQQSSGR	IDIIHSKKTA
730	740	750	760	770	780	790	800
ALQSATPVER	VKLQEALSQL	DFQWEKVNKM	YKDRQGRFDR	SVEKWRRFHY	DIKIFNQWLT	EAEQFLRKTQ	IPENWEHAKY
810	820	830	840	850	860	870	880
KWYLKELQDG	IGQRQTVVRT	LNATGEEIIQ	QSSKTDASIL	QEKLGSLNLR	WQEVCKQLSD	RKKRLEEQKN	ILSEFQRDLN
890	900	910	920	930	940	950	960
EFVLWLEEAD	NIASIPLEPG	KEQQLKEKLE	QVKLLVEELP	LRQGILKQLN	ETGGPVLVSA	PISPEEQDKL	ENKLKQTNLQ
970	980	990	1000	1010	1020	1030	1040
WIKVSRALPE	KQGEIEAQIK	DLGQLEKKLE	DLEEQLNHLL	LWLSPIRNQL	EIYNQPNQEG	PFDVQETEIA	VQAKQPDVEE
1050	1060	1070	1080	1090	1100	1110	1120
ILSKGQHLYK	EKPATQPVKR	KLEDLSSEWK	AVNRLLQELR	AKQPDLAPGL	TTIGASPTQT	VTLVTQPVVT	KETAISKLEM
1130	1140	1150	1160	1170	1180	1190	1200
PSSLMLEVPA	LADFNRAWTE	LTDWLSLLDQ	VIKSQRVMVG	DLEDINEMII	KQKATMQDLE	QRRPQLEELI	TAAQNLKNKT
1210	1220	1230	1240	1250	1260	1270	1280
SNQEARTIIT	DRIERIQNQW	DEVQEHLQNR	RQQLNEMLKD	STQWLEAKEE	AEQVLGQARA	KLESWKEGPY	TVDAIQKKIT
1290	1300	1310	1320	1330	1340	1350	1360
ETKQLAKDLR	QWQTNVDVAN	DLALKLLRDY	SADDTRKVHM	ITENINASWR	SIHKRVSERE	AALEETHRLL	QQFPLDLEKF
1370	1380	1390	1400	1410	1420	1430	1440
LAWLTEAETT	ANVLQDATRK	ERLLEDSKGV	KELMKQWQDL	QGEIEAHTDV	YHNLDENSQK	ILRSLEGSDD	AVLLQRRLDN
1450	1460	1470	1480	1490	1500	1510	1520
MNFKWSELRK	KSLNIRSHLE	ASSDQWKRLH	LSLQELLVWL	QLKDDELSRQ	APIGGDFPAV	QKQNDVHRAF	KRELKTKEPV
1530	1540	1550	1560	1570	1580	1590	1600
IMSTLETVRI	FLTEQPLEGL	EKLYQEPREL	PPEERAQNVT	RLLRKQAEEV	NTEWEKLNLH	SADWQRKIDE	TLERLQELQE
1610	1620	1630	1640	1650	1660	1670	1680
ATDELDLKLR	QAEVIKGSWQ	PVGDLLIDSL	QDHLEKVKAL	RGEIAPLKEN	VSHVNDLARQ	LTTLGIQLSP	YNLSTLEDLN
1690	1700	1710	1720	1730	1740	1750	1760
TRWKLLQVAV	EDRVRQLHEA	HRDFGPASQH	FLSTSVQGPW	ERAISPNKVP	YYINHETQTT	CWDHPKMTEL	YQSLADLNNV
1770	1780	1790	1800	1810	1820	1830	1840
RFSAYRTAMK	LRRLQKALCL	DLLSLSAACD	ALDQHNLKQN	DQPMDILQII	NCLTTIYDRL	EQEHNNLVNV	PLCVDMCLNW
1850	1860	1870	1880	1890	1900	1910	1920
LLNVYDTGRT	GRIRVLSFKT	GIISLCKAHL	EDKYRYLFKQ	VASSTGFCDQ	RRLGLLLHDS	IQIPRQLGEV	ASFGGSNIEP
1930	1940	1950	1960	1970	1980	1990	2000
SVRSCFQFAN	NKPEIEAALF	LDWMRLEPQS	MVWLPVLHRV	AAAETAKHQA	KCNICKECPI	IGFRYRSLKH	FNYDICQSCF
2010	2020	2030	2040	2050	2060	2070	2080
FSGRVAKGHK	MHYPMVEYCT	PTTSGEDVRD	FAKVLKNKFR	TKRYFAKHPR	MGYLPVQTVL	EGDNMETPVT	LINFWPVDSA
2090	2100	2110	2120	2130	2140	2150	2160
PASSPQLSHD	DTHSRIEHYA	SRLAEMENSN	GSYLNDSISP	NESIDDEHLL	IQHYCQSLNQ	DSPLSQPRSP	AQILISLESE
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
129	1	619.6434	29.86	3	30.9	11.2	2	395-410	R.DQAANLMANRGDHCRK.L	Carbamidomethyl: 14
1813	1	785.8684	-31.80	2	51.3	11.2	0	1318-1330	K.VHMITENINASWR.S	

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Detailed Protein Report

Protein 126: 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 127: PREDICTED: rho guanine nucleotide exchange factor 5-like, partial [Homo sapiens]

Accession:	gi|578844357	**Score:**	34.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	165.0
Database Date:	2015-11-30	**pI:**	5.4
		Sequence Coverage [%]:	2.3
		No. of unique Peptides:	1

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
1626	1	1058.4994	-29.00	2	49.0	12.0	2	933-951	K.DEAGVSEHPEAPAREPLRR.T	

Detailed Protein Report

Protein 128: 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

WD:WU	**Median:** 0.84	**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		WD:WU 0.84

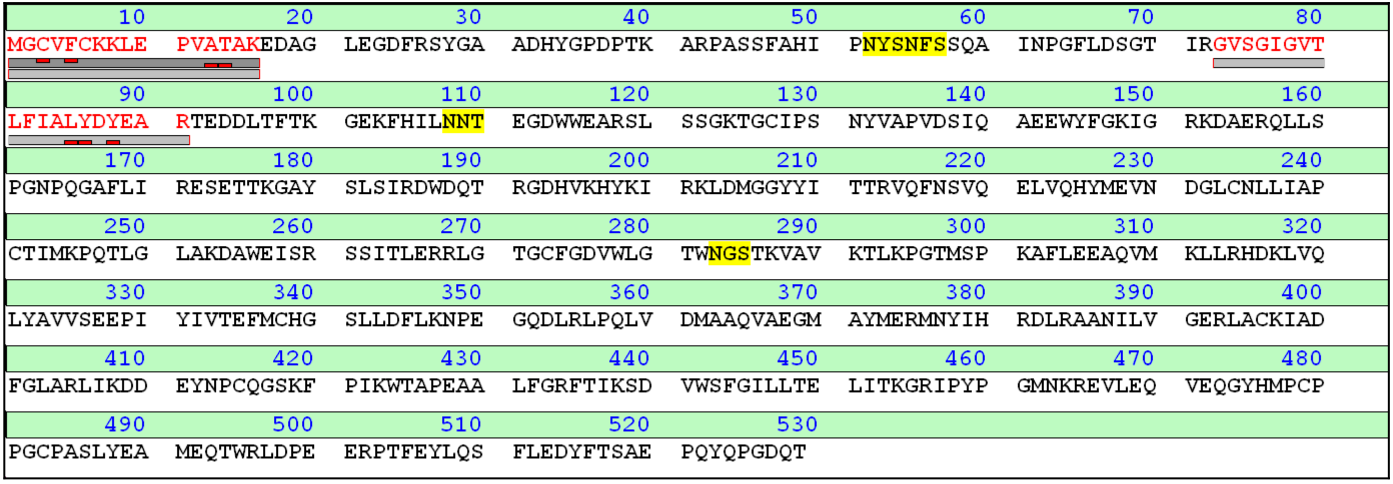
Detailed Protein Report

Protein 129: tyrosine-protein kinase Fgr [Homo sapiens]

Accession:	gi|4885235	**Score:**	34.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	59.4
Database Date:	2015-11-30	**pI:**	5.3
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	6.6
		No. of unique Peptides:	3

Alias proteins:

Accession	Name	Description
gi|578798632	refseq_human (refseq_human_20140103.fasta)	PREDICTED: tyrosine-protein kinase Fgr isoform X1 [Homo sapiens]
gi|112382244	refseq_human (refseq_human_20140103.fasta)	tyrosine-protein kinase Fgr [Homo sapiens]
gi|112382241	refseq_human (refseq_human_20140103.fasta)	tyrosine-protein kinase Fgr [Homo sapiens]



10	20	30	40	50	60	70	80
MGCVFCKKLE	PVATAKEDAG	LEGDFRSYGA	ADHYGPDPTK	ARPASSFAHI	PNYSNFSSQA	INPGFLDSGT	IRGVSGIGVT
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
LFIALYDYEA	RTEDDLTFTK	GEKFHILNNT	EGDWWEARSL	SSGKTGCIPS	NYVAPVDSIQ	AEEWYFGKIG	RKDAERQLLS
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
PGNPQGAFLI	RESETTKGAY	SLSIRDWDQT	RGDHVKHYKI	RKLDMGGYYI	TTRVQFNSVQ	ELVQHYMEVN	DGLCNLLIAP
250	**260**	**270**	**280**	**290**	**300**	**310**	**320**
CTIMKPQTLG	LAKDAWEISR	SSITLERRLG	TGCFGDVWLG	TWNGSTKVAV	KTLKPGTMSP	KAFLEEAQVM	KLLRHDKLVQ
330	**340**	**350**	**360**	**370**	**380**	**390**	**400**
LYAVVSEEPI	YIVTEFMCHG	SLLDFLKNPE	GQDLRLPQLV	DMAAQVAEGM	AYMERMNYIH	RDLRAANILV	GERLACKIAD
410	**420**	**430**	**440**	**450**	**460**	**470**	**480**
FGLARLIKDD	EYNPCQGSKF	PIKWTAPEAA	LFGRFTIKSD	VWSFGILLTE	LITKGRIPYP	GMNKREVLEQ	VEQGYHMPCP
490	**500**	**510**	**520**	**530**			
PGCPASLYEA	MEQTWRLDPE	ERPTFEYLQS	FLEDYFTSAE	PQYQPGDQT			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1840	1	899.4842	30.62	2	51.7	11.7	2	1-16	-.MGCVFCKKLEPVATAK.E	Carbamidomethyl: 3; Oxidation: 1
2000	2	899.3791	-86.20	2	53.4	11.8	2	1-16	-.MGCVFCKKLEPVATAK.E	Carbamidomethyl: 6; Oxidation: 1
1458	1	1022.6515	107.92	2	46.6	10.7	0	73-91	R.GVSGIGVTLFIALYDYEAR.T	

Detailed Protein Report

Protein 130: PREDICTED: exostosin-like 1 isoform X3 [Homo sapiens]

Accession:	gi|578798624	**Score:**	34.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	53.0
Database Date:	2015-11-30	**pI:**	9.6
		Sequence Coverage [%]:	6.0
		No. of unique Peptides:	2

Quantitation

WD:WU **Median:** 0.62 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MQSWRRRKSL	WLALSASWLL	LVLLGGFSLL	RLALPPRPRP	GASQGWPRWL	DAELLQSFSQ	PGELPEDAVS	PPQAPHGGSC
90	100	110	120	130	140	150	160
NWESCFDTSK	CRGDGLKVFV	YPAVGTISET	HRRILASIEG	SRFYTFSPAG	ACLLLLLSLD	AQTGECSSMP	LQWNRGRNHL
170	180	190	200	210	220	230	240
VLRLHPAPCP	RTFQLGQAMV	AEASPTVDSF	RPGFDVALPF	LPEAHPLRGG	APGQLRQHSP	QPGVALLALE	EERGGWRTAD
250	260	270	280	290	300	310	320
TGSSACPWDG	RCEQDPGPGQ	TQRQETLPNA	TFCLISGHRP	EAASRFLQAL	QAGCIPVLLS	PRWELPFSEV	IDWTKAAIVA
330	340	350	360	370	380	390	400
DERLPLQVLA	ALQEMSPARV	LALRQQTQFL	WDAYFSSVEK	VIHTTLEVIQ	DRIFGTSAHP	SLLWNSPPGA	LLALSTFSTS
410	420	430	440	450	460	470	480
PQDFPFYYLQ	QGSRPEGRFS	ALIWVGPPGQ	PPLKLIQAVA	GSQHCAQFTK	LTSQTSSTLR	KITPAPRNPP	SAPDPRLQEQ
490							
PPIL							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2276	1	937.4372	-58.45	2	56.9	14.5	0	217-233	R.QHSPQPGVALLALEEER.G		
933	1	712.4616	88.10	2	40.0	19.7	0	361-372	K.VIHTTLEVIQDR.I		WD:WU 0.62

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Detailed Protein Report

Protein 131: kinesin light chain 4 isoform d [Homo sapiens]

Accession:	gi|573459761	**Score:**	34.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	59.6
Database Date:	2015-11-30	**pI:**	5.8
		Sequence Coverage [%]:	8.5
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MSGLVLGQRD	EPAGHRLSQE	EILGSTRLVS	QGLEALRSEH	QAVLQSLSQT	IECLQQGGHE	EGLVHEKARQ	LRRSMENIEL
90	100	110	120	130	140	150	160
GLSEAQEEKE	GDATKDSLDD	LFPNEEEEDP	SNGLSRGQGA	TAAQQGGYEI	PARLRTLHNL	VIQYAAQGRY	EVAVPLCKQA
170	180	190	200	210	220	230	240
LEDLERTSGR	GHPDVATMLN	ILALVYRDQN	KYKEAAHLLN	DALSIRESTL	GPDHPAVAAT	LNNLAVLYGK	RGKYKEAEPL
250	260	270	280	290	300	310	320
CQRALEIREK	VLGTNHPDVA	KQLNNLALLC	QNQGKYEAVE	RYYQRALAIY	EGQLGPDNPN	VARTKNNLAS	CYLKQGKYAE
330	340	350	360	370	380	390	400
AETLYKEILT	RAHVQEFGSV	DDDHKPIWMH	AEEREEMSKS	RHHEGGTPYA	EYGGWYKACK	VSSPTVNTTL	RNLGALYRRQ
410	420	430	440	450	460	470	480
GKLEAAETLE	ECALRSRRQG	TDPISQTKVA	ELLGESDGRR	TSQEGPGDSV	KFEGGEDASV	AVEWSGDGSG	TLQRSGSLGK
490	500	510	520	530	540	550	
IRDVLRRSSE	LLVRKLQGTE	PRPSSSNMKR	AASLNYLNQP	SAAPLQVSRG	LSASTMDLSS	SS	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1691	1	1293.5862	-85.42	2	49.8	17.1	1	136-158	R.TLHNLVIQYAAQGRYEVAVPLCK.Q	
2084	1	900.3300	-81.09	3	54.4	16.9	2	355-377	R.EEMSKSRHHEGGTPYAEYGGWYK.A	

Detailed Protein Report

Protein 132: PREDICTED: TFIIH basal transcription factor complex helicase XPB subunit isoform X1 [Homo sapiens]

Accession:	gi|530369093	**Score:**	34.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	81.9
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
MPLKDDHTSR	PLWVAPDGHI	FLEAFSPVYK	YAQDFLVAIA	EPVCRPTHVH	EYKLTAYSLY	AAVSVGLQTS	DITEYLRKLS
90	100	110	120	130	140	150	160
KTGVPDGIMQ	FIKLCTVSYG	KVKLVLKHNR	YFVESCHPDV	IQHLLQDPVI	RECRLRNSEG	EATELITETF	TSKSAISKTA
170	180	190	200	210	220	230	240
ESSGGPSTSR	VTDPQGKSDI	PMDLFDFYEQ	MDKDEEEEEE	TQTVSFEVKQ	EMIEELQKRC	IHLEYPLLAE	YDFRNDSVNP
250	260	270	280	290	300	310	320
DINIDLKPTA	VLRPYQEKSL	RKMFGNGRAR	SGVIVLPCGA	GKSLVGVTAA	CTVRKRCLVL	GNSAVSVEQW	KAQFKMWSTI
330	340	350	360	370	380	390	400
DDSQICRFTS	DAKDKPIGCS	VAISTYSMLG	HTTKRSWEAE	RVMEWLKTQE	WGLMILDEVH	TIPAKMFRRV	LTIVQAHCKL
410	420	430	440	450	460	470	480
GLTATLVRED	DKIVDLNFLI	GPKLYEANWM	ELQNNGYIAK	VQCAEVWCPM	SPEFYREYVA	IKTKKRILLY	TMNPNKFRAC
490	500	510	520	530	540	550	560
QFLIKFHERR	NDKIIVFADN	VFALKEYAIR	LNKPYIYGPT	SQGERMQILQ	NFKHNPKINT	IFISKVGDTS	FDLPEANVLI
570	580	590	600	610	620	630	640
QISSHGGSRR	QEAQRLGRVL	RAKKGMVAEE	YNAFFYSLVS	QDTQEMAYST	KRQRFLVDQG	YSFKVITKLA	GMEEEDLAFS
650	660	670	680	690	700	710	720
TKEEQQQLLQ	KVLAATDLDA	EEEVVAGEFG	SRSSQASRRF	GTMSSMSGAD	DTVYMEYHSS	RSKAPSKHVH	PLFKRFRK

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
141	2	822.3919	-53.97	2	31.0	11.9	2	612-624	K.RQRFLVDQGYSFK.V	

Detailed Protein Report

Protein 133: PREDICTED: complement receptor type 1 isoform X4 [Homo sapiens]

Accession:	gi|578800553	**Score:**	34.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	224.1
Database Date:	2015-11-30	**pI:**	6.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.7
		No. of unique Peptides:	1

Quantitation

WD:WU	**Median:** 0.66	**CV:** 0.00 %	**No. of Peptides:** 1

Detailed Protein Report

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
39	2	826.3468	-30.22	3	29.4	21.7	1	339-361	R. GAASMRCTPQGDWSPAAPTCEV S	Carbamidomethyl: 7, 20	WD:WU 0.66

Detailed Protein Report

Protein 134: PREDICTED: histone-lysine N-methyltransferase ASH1L isoform X3 [Homo sapiens]

Accession:	gi|530365072	**Score:**	33.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	191.3
Database Date:	2015-11-30	**pI:**	10.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.9
		No. of unique Peptides:	2

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
1736	1	853.3885	-153.79	2	50.1	10.2	2	256-272	R.KAGVGSVAGIIHKDLIK.K	
1687	1	696.2420	-115.78	3	49.4	11.7	1	744-762	K.NVSCSSLSNSNSEPAKFMK.N	Carbamidomethyl: 4

Detailed Protein Report

Protein 135: **stromal interaction molecule 2 isoform 2 precursor [Homo sapiens]**

Accession:	gi|281182822	**Score:**	33.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	83.9
Database Date:	2015-11-30	**pI:**	6.3
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	3.8
		No. of unique Peptides:	2

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
2262	1	937.3682	-104.97	2	56.7	12.8	0	678-694	K.SCSMNQLSSGIPVPKPR.H	Carbamidomethyl: 2; Oxidation: 4
1467	1	619.9415	-65.11	3	46.7	10.7	0	678-694	K.SCSMNQLSSGIPVPKPR.H	Carbamidomethyl: 2

Detailed Protein Report

Protein 136: PREDICTED: ubiquitin thioesterase ZRANB1 isoform X3 [Homo sapiens]

Accession:	gi|530393888	**Score:**	33.7
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

Quantitation

WD:WU **Median:** 1.22 **CV:** 41.38 % **No. of 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	Ratios
1033	2	590.8060	-42.13	2	41.7	16.3	1	31-40	R.REIAASLHQR.K		WD:WU 0.82
2848	4	648.3529	16.16	2	64.3	17.3	0	346-356	R.NHPLVTQMVEK.W		WD:WU 1.81

Detailed Protein Report

Protein 137: replication factor C subunit 1 isoform 1 [Homo sapiens]

Accession:	gi|32528306	**Score:**	33.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	128.1
Database Date:	2015-11-30	**pI:**	9.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.6
		No. of unique Peptides:	3

Quantitation

WD:WU **Median:** 1.66 **CV:** 0.00 % **No. of Peptides:** 1

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
967	2	530.7788	-57.17	2	40.4	11.1	2	42-50	K.EIKVNSSRK.E		WD:WU 1.66
1884	1	974.4729	4.34	2	51.9	11.6	2	125-142	K.SKENGRSTNSHLGTSNMK.K		
2929	1	965.1417	7.65	3	65.4	10.9	1	657-682	K. TTTASLVCQELGYSYVELNASDTR S	Carbamidomethyl: 8	

Detailed Protein Report

Protein 138: PREDICTED: extracellular matrix protein FRAS1 isoform X2 [Homo sapiens]

Accession:	gi|578809381	**Score:**	33.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	438.5
Database Date:	2015-11-30	**pI:**	5.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.1
		No. of unique Peptides:	2

Detailed Protein Report

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

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 139: **PREDICTED: putative tripartite motif-containing protein 61 isoform X1 [Homo sapiens]**

Accession:	gi|578809113	**Score:**	33.5
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 140: wee1-like protein kinase 2 [Homo sapiens]

Accession:	gi|157738687	**Score:**	32.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	62.9
Database Date:	2015-11-30	**pI:**	6.1
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.9
		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
1865	1	785.9040	-18.42	2	51.7	15.7	1	218-231	K.IGVGEFGTVYKCIK.R	Carbamidomethyl: 12
135	1	725.9700	90.61	2	30.9	17.2	0	378-391	K.IGDLGHATSINKPK.V	

Detailed Protein Report

Protein 141: H/ACA ribonucleoprotein complex subunit 4 isoform 3 [Homo sapiens]

Accession:	gi|570700851	**Score:**	32.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	47.6
Database Date:	2015-11-30	**pI:**	10.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	6.7
		No. of unique Peptides:	2

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
2864	1	651.8581	-55.52	2	64.5	14.1	2	390-400	K.KLMIKQGLLDK.H	Oxidation: 3

Detailed Protein Report

Protein 142: protein unc-13 homolog C [Homo sapiens]

Accession:	gi|122937514	**Score:**	32.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	250.8
Database Date:	2015-11-30	**pI:**	5.6
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	1.5
		No. of unique Peptides:	2

Quantitation

WD:WU **Median:** 0.62 **CV:** 0.00 % **No. of Peptides:** 1

Alias proteins:

Accession	**Name**	**Description**
gi|530405876	refseq_human (refseq_human_20140103.fasta)	PREDICTED: protein unc-13 homolog C isoform X1 [Homo sapiens]

```
        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 ENVPCILMNN IQQLRVQLEK MFESMGGKEL DSEASTILKE LQVKLSGVLD
      1850       1860       1870       1880       1890       1900       1910       1920
ELSVTYGESF QVIIEECIKQ MSFELNQMRA NGNTTSNKNS AAMDAEIVLR SLMDFLDKTL SLSAKICEKT VLKRVLKELW
      1930       1940       1950       1960       1970       1980       1990       2000
KLVLNKIEKQ IVLPPLTDQT GPQMIFIAAK DLGQLSKLKE HMIREDARGL TPRQCAIMEV VLATIKQYFH AGGNGLKKNF
      2010       2020       2030       2040       2050       2060       2070       2080
LEKSPDLQSL RYALSLYTQT TDALIKKFID TQTSQSRSSK DAVGQISVHV DITATPGTGD HKVTVKVIAI NDLNWQTTAM
      2090       2100       2110       2120       2130       2140       2150       2160
FRPFVEVCIL GPNLGDKKRK QGTKTKSNTW SPKYNETFQF ILGKENRPGA YELHLSVKDY CFAREDRIIG MTVIQLQNIA
      2170       2180       2190       2200       2210       2220
```

Detailed Protein Report

Cmpd.	**No. of Cmpds.**	**m/z meas.**	**Δ m/z [ppm]**	**z**	**Rt [min]**	**Score**	**P**	**Range**	**Sequence**	**Modification**	**Ratios**
1046	1	742.4006	68.40	2	41.8	12.0	1	1497-1508	K.YRENFPASNTER.L		WD:WU 0.62
1482	1	619.9673	-23.43	3	46.9	10.7	0	1791-1805	K.ENVPCILMNNIQQLR.V	Carbamidomethyl: 5; Oxidation: 8	

Detailed Protein Report

Protein 143: **PREDICTED: MAGUK p55 subfamily member 6 isoform X2 [Homo sapiens]**

Accession:	gi|530384825	**Score:**	32.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	48.7
Database Date:	2015-11-30	**pI:**	9.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	10.0
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MNNSSINNQL	LPVDAIRILG	IHKRAGEPLG	VTFRVENNDL	VIARILHGGM	IDRQGLLHVG	DIIKEVNGHE	VGNNPKELQE
90	100	110	120	130	140	150	160
LLKNISGSVT	LKILPSYRDT	ITPQQVFVKC	HFDYNPYNDN	LIPCKEAGLK	FSKGEILQIV	NREDPNWWQA	SHVKEGGSAG
170	180	190	200	210	220	230	240
LIPSQFLEEK	RKAFVRRDWD	NSGPFCGTIS	SKKKKKMMYL	TTRNAEFDRH	EIQIYEEVAK	MPPFQRKTLV	LIGAQGVGRR
250	260	270	280	290	300	310	320
SLKNRFIVLN	PTRFGTTVPF	TSRKPREDEK	DGQAYKFVSR	SEMEADIKAG	KYLEHGEYEG	NLYGTKIDSI	LEVVQTGRTC
330	340	350	360	370	380	390	400
ILDVNPQALK	VLRTSEFMPY	VVFIAAPELE	TLRAMHKAVV	DAGITTKLLT	DSDLKKTVDE	SARIQRAYNH	YFDLIIINDN
410	420	430					
LDKAFEKLQT	AIEKLRMEPQ	WVPISWVY					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2335	1	938.2188	84.20	3	57.5	10.4	1	334-357	R.TSEFMPYVVFIAAPELETLRAMHK.A	Oxidation: 5, 22
2850	1	994.4934	-74.35	2	64.3	22.2	2	358-376	K.AVVDAGITTKLLTDSDLKK.T	

Detailed Protein Report

Protein 144: usherin isoform B [Homo sapiens]

Accession:	gi|219842266	**Score:**	32.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	575.2
Database Date:	2015-11-30	**pI:**	6.4
		Sequence Coverage [%]:	0.5
		No. of unique Peptides:	1

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

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2191	1	863.3484	-20.01	2	55.8	14.2	0	794-811	K.ACDCDTAGSLPGTVCNAK.T	

Detailed Protein Report

Protein 145: macrophage mannose receptor 1 precursor [Homo sapiens]

Accession:	gi|4505245	**Score:**	32.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	165.9
Database Date:	2015-11-30	**pI:**	6.1
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MRLPLLLVFA	SVIPGAVLLL	DTRQFLIYNE	DHKRCVDAVS	PSAVQTAACN	QDAESQKFRW	VSESQIMSVA	FKLCLGVPSK
90	100	110	120	130	140	150	160
TDWVAITLYA	CDSKSEFQKW	ECKNDTLLGI	KGEDLFFNYG	NRQEKNIMLY	KGSGLWSRWK	IYGTTDNLCS	RGYEAMYTLL
170	180	190	200	210	220	230	240
GNANGATCAF	PFKFENKWYA	DCTSAGRSDG	WLWCGTTTDY	DTDKLFGYCP	LKFEGSESLW	NKDPLTSVSY	QINSKSALTW
250	260	270	280	290	300	310	320
HQARKSCQQQ	NAELLSITEI	HEQTYLTGLT	SSLTSGLWIG	LNSLSFNSGW	QWSDRSPFRY	LNWLPGSPSA	EPGKSCVSLN
330	340	350	360	370	380	390	400
PGKNAKWENL	ECVQKLGYIC	KKGNTTLNSF	VIPSESDVPT	HCPSQWWPYA	GHCYKIHRDE	KKIQRDALTT	CRKEGGDLTS
410	420	430	440	450	460	470	480
IHTIEELDFI	ISQLGYEPND	ELWIGLNDIK	IQMYFEWSDG	TPVTFTKWLR	GEPSHENNRQ	EDCVVMKGKD	GYWADRGCEW
490	500	510	520	530	540	550	560
PLGYICKMKS	RSQGPEIVEV	EKGCRKGWKK	HHFYCYMIGH	TLSTFAEANQ	TCNNENAYLT	TIEDRYEQAF	LTSFVGLRPE
570	580	590	600	610	620	630	640
KYFWTGLSDI	QTKGTFQWTI	EEEVRFTHWN	SDMPGRKPGC	VAMRTGIAGG	LWDVLKCDEK	AKFVCKHWAE	GVTHPPKPTT
650	660	670	680	690	700	710	720
TPEPKCPEDW	GASSRTSLCF	KLYAKGKHEK	KTWFESRDFC	RALGGDLASI	NNKEEQQTIW	RLITASGSYH	KLFWLGLTYG
730	740	750	760	770	780	790	800
SPSEGFTWSD	GSPVSYENWA	YGEPNNYQNV	EYCGELKGDP	TMSWNDINCE	HLNNWICQIQ	KGQTPKPEPT	PAPQDNPPVT
810	820	830	840	850	860	870	880
EDGWVIYKDY	QYYFSKEKET	MDNARAFCKR	NFGDLVSIQS	ESEKKFLWKY	VNRNDAQSAY	FIGLLISLDK	KFAWMDGSKV
890	900	910	920	930	940	950	960
DYVSWATGEP	NFANEDENCV	TMYSNSGFWN	DINCGYPNAF	ICQRHNSSIN	ATTVMPTMPS	VPSGCKEGWN	FYSNKCFKIF
970	980	990	1000	1010	1020	1030	1040
GFMEEERKNW	QEARKACIGF	GGNLVSIQNE	KEQAFLTYHM	KDSTFSAWTG	LNDVNSEHTF	LWTDGRGVHY	TNWGKGYPGG
1050	1060	1070	1080	1090	1100	1110	1120
RRSSLSYEDA	DCVVIIGGAS	NEAGKWMDDT	CDSKRGYICQ	TRSDPSLTNP	PATIQTDGFV	KYGKSSYSLM	RQKFQWHEAE
1130	1140	1150	1160	1170	1180	1190	1200
TYCKLHNSLI	ASILDPYSNA	FAWLQMETSN	ERVWIALNSN	LTDNQYTWTD	KWRVRYTNWA	ADEPKLKSAC	VYLDLDGYWK
1210	1220	1230	1240	1250	1260	1270	1280
TAHCNESFYF	LCKRSDEIPA	TEPPQLPGRC	PESDHTAWIP	FHGHCYYIES	SYTRNWGQAS	LECLRMGSSL	VSIESAAESS
1290	1300	1310	1320	1330	1340	1350	1360
FLSYRVEPLK	SKTNFWIGLF	RNVEGTWLWI	NNSPVSFVNW	NTGDPSGERN	DCVALHASSG	FWSNIHCSSY	KGYICKRPKI
1370	1380	1390	1400	1410	1420	1430	1440
IDAKPTHELL	TTKADTRKMD	PSKPSSNVAG	VVIIVILLIL	TGAGLAAYFF	YKKRRVHLPQ	EGAFENTLYF	NSQSSPGTSD
1450	1460						
MKDLVGNIEQ	NEHSVI						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2976	1	928.0036	17.04	2	66.0	14.3	2	126-140	K.NIMLYKGSGLWSRWK.I	Oxidation: 3

Detailed Protein Report

Protein 146: **unconventional myosin-Ie [Homo sapiens]**

Accession:	gi|55956916	**Score:**	32.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	127.0
Database Date:	2015-11-30	**pI:**	9.5
		Sequence Coverage [%]:	1.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGSKGVYQYH	WQSHNVKHSG	VDDMVLLSKI	TENSIVENLK	KRYMDDYIFT	YIGSVLISVN	PFKQMPYFGE	KEIEMYQGAA
90	100	110	120	130	140	150	160
QYENPPHIYA	LADNMYRNMI	IDRENQCVII	SGESGAGKTV	AAKYIMSYIS	RVSGGGTKVQ	HVKDIILQSN	PLLEAFGNAK
170	180	190	200	210	220	230	240
TVRNNNSSRF	GKYFEIQFSP	GGEPDGGKIS	NFLLEKSRVV	MRNPGERSFH	IFYQLIEGAS	AEQKHSLGIT	SMDYYYYLSL
250	260	270	280	290	300	310	320
SGSYKVDDID	DRREFQETLH	AMNVIGIFAE	EQTLVLQIVA	GILHLGNISF	KEVGNYAAVE	SEEFLAFPAY	LLGINQDRLK
330	340	350	360	370	380	390	400
EKLTSRQMDS	KWGGKSESIH	VTLNVEQACY	TRDALAKALH	ARVFDFLVDS	INKAMEKDHE	EYNIGVLDIY	GFEIFQKNGF
410	420	430	440	450	460	470	480
EQFCINFVNE	KLQQIFIELT	LKAEQEEYVQ	EGIRWTPIEY	FNNKIVCDLI	ENKVNPPGIM	SILDDVCATM	HAVGEGADQT
490	500	510	520	530	540	550	560
LLQKLQMQIG	SHEHFNSWNQ	GFIIHHYAGK	VSYDMDGFCE	RNRDVLFMDL	IELMQSSELP	FIKSLFPENL	QADKKGRPTT
570	580	590	600	610	620	630	640
AGSKIKKQAN	DLVSTLMKCT	PHYIRCIKPN	ETKKPRDWEE	SRVKHQVEYL	GLKENIRVRR	AGYAYRRIFQ	KFLQRYAILT
650	660	670	680	690	700	710	720
KATWPSWQGE	EKQGVLHLLQ	SVNMDSDQFQ	LGRSKVFIKA	PESLFLLEEM	RERKYDGYAR	VIQKSWRKFV	ARKKYVQMRE
730	740	750	760	770	780	790	800
EASDLLLNKK	ERRRNSINRN	FIGDYIGMEE	HPELQQFVGK	REKIDFADTV	TKYDRRFKGV	KRDLLLTPKC	LYLIGREKVK
810	820	830	840	850	860	870	880
QGPDKGLVKE	VLKRKIEIER	ILSVSLSTMQ	DDIFILHEQE	YDSLLESVFK	TEFLSLLAKR	YEEKTQKQLP	LKFSNTLELK
890	900	910	920	930	940	950	960
LKKENWGPWS	AGGSRQVQFH	QGFGDLAVLK	PSNKVLQVSI	GPGLPKNSRP	TRRNTTQNTG	YSSGTQNANY	PVRAAPPPPG
970	980	990	1000	1010	1020	1030	1040
YHQNGVIRNQ	YVPYPHAPGS	QRSNQKSLYT	SMARPPLPRQ	QSTSSDRVSQ	TPESLDFLKV	PDQGAAGVRR	QTTSRPPPAG
1050	1060	1070	1080	1090	1100	1110	
GRPKPQPKPK	PQVPQCKALY	AYDAQDTDEL	SFNANDIIDI	IKEDPSGWWT	GRLRGKQGLF	PNNYVTKI	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1182	1	478.1928	-225.01	2	43.0	13.4	1	782-789	K.RDLLLTPK.C	

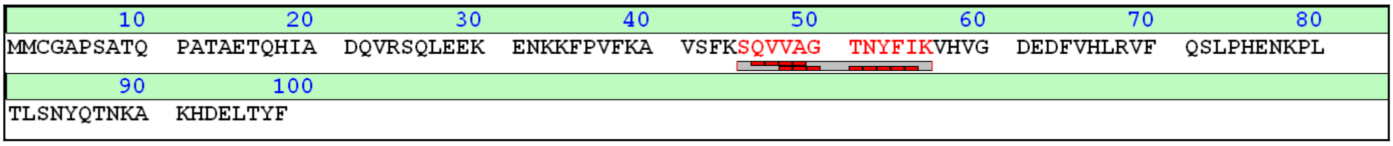
Detailed Protein Report

Protein 147: cystatin-B [Homo sapiens]

Accession:	gi|4503117	**Score:**	31.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	11.1
Database Date:	2015-11-30	**pI:**	7.9
		Sequence Coverage [%]:	12.2
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 0.65 **CV:** 0.00 % **No. of Peptides:** 1



```
        10        20        30        40        50        60        70        80
MMCGAPSATQ PATAETQHIA DQVRSQLEEK ENKKFPVFKA VSFKSQVVAG TNYFIKVHVG DEDFVHLRVF QSLPHENKPL
        90       100
TLSNYQTNKA KHDELTYF
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
695	1	663.8458	-15.71	2	37.1	31.9	0	45-56	K.SQVVAGTNYFIK.V		WD:WU 0.65

Detailed Protein Report

Protein 148: PREDICTED: uncharacterized protein C7orf63 isoform X1 [Homo sapiens]

Accession:	gi|530386429	**Score:**	31.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	101.8
Database Date:	2015-11-30	**pI:**	6.2
		Sequence Coverage [%]:	3.1
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 2.21 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MWTEEAGATA	EAQESGIRNK	SSSSSQIPVV	GVVTEDDEAQ	DVFKPMDLNR	VIKLLEETDK	DGLEEKQLKF	VKKLVQCYQN
90	100	110	120	130	140	150	160
GLPLRDLAQI	FKILNLCSGK	IKNQPRFIES	AYDIIKLCGL	PFLKKKVSDE	ITYAEDTANS	IALLGDLMKI	PSSELRIQIC
170	180	190	200	210	220	230	240
KCIVDFYHAE	PPKKHIPGYQ	QASSSYKIQM	AEVGGLAKTM	VQSMTLLENQ	LVEKLWVLKV	LQHLSTSEVN	CTIMMKAQAA
250	260	270	280	290	300	310	320
SGICTHLNDP	DPSGQLLFRS	SEILWNLLEK	SSKEEVIQQL	SNLECLLALK	EVFKNLFMRG	FSHYDRQLRN	DILVITTIIA
330	340	350	360	370	380	390	400
QNPEAPMIEC	GFTKDLILFA	TFNEVKSQNL	LVKGLKLSNS	YEDFELKKLL	FNVIVILCKD	LPTVQLLIDG	KVILALFTYV
410	420	430	440	450	460	470	480
KKPEKQKIID	WSAAQHEELQ	LHAIATLSSV	APLLIEEYMS	CQGNARVLAF	LEWCESEDPF	FSHGNSFHGT	GGRGNKFAQM
490	500	510	520	530	540	550	560
RYSLRLLRAV	VYLEDETVNK	DLCEKGTIQQ	MIGIFKNIIS	KPNEKEEAIV	LEIQSDILLI	LSGLCENHIQ	RKEIFGTEGV
570	580	590	600	610	620	630	640
DIVLHVMKTD	PRKLQSGLGY	NVLLFSTLDS	IWCCILGCYP	SEDYFLEKEG	IFLLLDLLAL	NQKKFCNLIL	GIMVEFCDNP
650	660	670	680	690	700	710	720
KTAAHVNAWQ	GKKDQTAASL	LIKLWRKEEK	ELGVKRDKNG	KIIDTKKPLF	TSFQEEQKII	PLPANCPSIA	VMDVSENIRA
730	740	750	760	770	780	790	800
KIYAILGKLD	FENLPGLSAE	DFVTLCIIHR	YLDFKIGEIW	NEIYEEIKLE	KLRPVTTDKK	ALEAITTASE	NIGKMVASLQ
810	820	830	840	850	860	870	880
SDIIESQACQ	DMQNEQKVYA	KIQATHKQRE	LANKSWEDFL	ARTSNAKTLK	VPSGGVVTVE	STPARLVGGP	LVDTDIALKK
890	900	910					
LPIRGGALQR	VKAVKIVDAP	KKSIPT					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1060	1	540.7960	-72.96	2	41.5	14.8	1	881-890	K.LPIRGGALQR.V		WD:WU 2.21

Detailed Protein Report

Protein 149: estrogen sulfotransferase [Homo sapiens]

Accession: gi|4885617

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Modification(s): Oxidation

Score: 31.5

MW [kDa]: 35.1

pI: 6.2

Sequence Coverage [%]: 7.8

No. of unique Peptides: 1

```
        10         20         30         40         50         60         70         80
MNSELDYYEK FEEVHGILMY KDFVKYWDNV EAFQARPDDL VIATYPKSGT TWVSEIVYMI YKEGDVEKCK EDVIFNRIPF
        90        100        110        120        130        140        150        160
LECRKENLMN GVKQLDEMNS PRIVKTHLPP ELLPASFWEK DCKIIYLCRN AKDVAVSFYY FFLMVAGHPN PGSFPEFVEK
       170        180        190        200        210        220        230        240
FMQGQVPYGS WYKHVKSWWE KGKSPRVLFL FYEDLKEDIR KEVIKLIHFL ERKPSEELVD RIIHHTSFQE MKNNPSTNYT
       250        260        270        280        290        300
TLPDEIMNQK LSPFMRKGIT GDWKNHFTVA LNEKFDKHYE QQMKESTLKF RTEI
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2974	1	826.4375	3.18	2	65.9	13.7	2	251-264	K.LSPFMRKGITGDWK.N	Oxidation: 5

Detailed Protein Report

Protein 150: **PREDICTED: sodium bicarbonate transporter-like protein 11 isoform X2 [Homo sapiens]**

Accession:	gi|530426013	**Score:**	31.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	96.0
Database Date:	2015-11-30	**pI:**	8.9
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSQNGYFEDS	SYYKCDTDDT	FEAREEILGD	EAFDTANSSI	VSGESIRFFV	NVNLEMQATN	TENEATSGGC	VLLHTSRKYL
90	100	110	120	130	140	150	160
KLKNFKEEIR	AHRDLDGFLA	QASIVLNETA	TSLDNVLRTM	LRRFARDPDN	NEPNCNLDLL	MAMLFTDAGA	PMRGKVHLLS
170	180	190	200	210	220	230	240
DTIQGVTATV	TGVRYQQSWL	CIICTMKALQ	KRHVCISRLV	RPQNWGENSC	EVRFVILVLA	PPKMKSTKTA	MEVARTFATM
250	260	270	280	290	300	310	320
FSDIAFRQKL	LETRTEEEFK	EALVHQRQLL	TMVSHGPVAP	RTKERSTVSL	PAHRHPEPPK	CKDFVPFGKG	IREDIARRFP
330	340	350	360	370	380	390	400
LYPLDFTDGI	IGKNKAVGKY	ITTTLFLYFA	CLLPTIAFGS	LNDENTDGAI	DVQKTIAGQS	IGGLLYALFS	GQPLVILLTT
410	420	430	440	450	460	470	480
APLALYIQVI	RVICDDYDLD	FNSFYAWTGL	WNSFFLALYA	FFNLSLVMSL	FKRSTEEIIA	LFISITFVLD	AVKGTVKIFW
490	500	510	520	530	540	550	560
KYYYGHYLDD	YHTKRTSSLV	SLSGLGASLN	ASLHTALNAS	FLASPTELPS	ATHSGQATAV	LSLLIMLGTL	WLGYTLYQFK
570	580	590	600	610	620	630	640
KSPYLHPCVR	EILSDCALPI	AVLAFSLISS	HGFREIEMSK	FRYNPSESPF	AMAQIQSLSL	RAVSGAMGLG	FLLSMLFFIE
650	660	670	680	690	700	710	720
QNLVAALVNA	PENRLVKGTA	YHWDLLLLAI	INTGLSLFGL	PWIHAAYPHS	PLHVRALALV	EERVENGHIY	DTIVNVKETR
730	740	750	760	770	780	790	800
LTSLGASVLV	GLSLLLLPVP	LQWIPKPVLY	GLFLYIALTS	LDGNQLVQRV	ALLLKEQTAY	PPTHYIRRVP	QRKIHYFTGL
810	820	830	840	850	860		
QVLQLLLLCA	FGMSSLPYMK	MIFPLIMIAM	IPIRYILLPR	IIEAKYLDVM	DAEHRP		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
823	1	711.9737	188.22	2	38.7	20.7	0	236-247	R.TFATMFSDIAFR.Q	Oxidation: 5

Detailed Protein Report

Protein 151: archaemetzincin-1 isoform 1 [Homo sapiens]

Accession:	gi|55741645	**Score:**	31.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	54.9
Database Date:	2015-11-30	**pI:**	5.6
		Sequence Coverage [%]:	4.4
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 0.54 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MLQCRPAQEF SFGPRALKDA LVSTDAALQQ LYVSAFSPAE RLFLAEAYNP QRTLFCTLLI RTGFDWLLSR PEAPEDFQTF

        90        100        110        120        130        140        150        160
HASLQHRKPR LARKHIYLQP IDLSEEPVGS SLLHQLCSCT EAFFLGLRVK CLPSVAAASI RCSSRPSRDS DRLQLHTDGI

       170        180        190        200        210        220        230        240
LSFLKNNKPG DALCVLGLTL SDLYPHEAWS FTFSKFLPGH EVGVCSFARF SGEFPKSGPS APDLALVEAA ADGPEAPLQD

       250        260        270        280        290        300        310        320
RGWALCFSAL GMVQCCKVTC HELCHLLGLG NCRWLRCLMQ GALSLDEALR RPLDLCPICL RKLQHVLGFR LIERYQRLYT

       330        340        350        360        370        380        390        400
WTQAVVGTWP SQEAGEPSVW EDTPPASADS GMCCESDSEP GTSVSEPLTP DAGSHTFASG PEEGLSYLAA SEAPLPPGGP

       410        420        430        440        450        460        470        480
AEAIKEHERW LAMCIQALQR EVAEEDLVQV DRAVDALDRW EMFTGQLPAT RQDPPSSRDS VGLRKVLGDK FSSLRRKLSA

       490        500
RKLARAESAP RPWDGEES
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
704	1	457.7465	-113.16	2	37.6	18.2	2	478-485	K.LSARKLAR.A		WD:WU 0.54

Detailed Protein Report

Protein 152: PREDICTED: kelch-like protein 17 isoform X1 [Homo sapiens]

Accession:	gi|530360301	**Score:**	31.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	66.6
Database Date:	2015-11-30	**pI:**	6.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEGAVQLLSR	EGHSVAHNSK	RHYHDAFVAM	SRMRQRGLLC	DIVLHVAAKE	IRAHKVVLAS	CSPYFHAMFT	NEMSESRQTH
90	100	110	120	130	140	150	160
VTLHDIDPQA	LDQLVQFAYT	AEIVVGEGNV	QTLLPAASLL	QLNGVRDACC	KFLLSQLDPS	NCLGIRGFAD	AHSCSDLLKA
170	180	190	200	210	220	230	240
AHRYVLQHFV	DVAKTEEFML	LPLKQASSGL	PGSTGPSPDL	RSEDPHSQVL	ELVSSDSLNV	PSEEEVYRAV	LSWVKHDVDA
250	260	270	280	290	300	310	320
RRQHVPRLMK	CVRLPLLSRD	FLLGHVDAES	LVRHHPDCKD	LLIEALKFHL	LPEQRGVLGT	SRTRPRRCEG	AGPVLFAVGG
330	340	350	360	370	380	390	400
GSLFAIHGDC	EAYDTRTDRW	HVVASMSTRR	ARVGVAAVGN	RLYAVGGYDG	TSDLATVESY	DPVTNTWQPE	VSMGTRRSCL
410	420	430	440	450	460	470	480
GVAALHGLLY	SAGGYDGASC	LNSAERYDPL	TGTWTSVAAM	STRRRYVRVA	TLDGNLYAVG	GYDSSSHLAT	VEKYEPQVNV
490	500	510	520	530	540	550	560
WSPVASMLSR	RSSAGVAVLE	GALYVAGGND	GTSCLNSVER	YSPKAGAWES	VAPMNIRRST	HDLVAMDGWL	YAVGGNDGSS
570	580	590	600	610	620		
SLNSIEKYNP	RTNKWVAASC	MFTRRSSVGV	AVLELLNFPP	PSSPTLSVSS	TSL		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2931	1	1051.5566	47.56	2	65.4	17.0	2	568-584	K.YNPRTNKWVAASCMFTR.R	Carbamidomethyl: 13

Detailed Protein Report

Protein 153: beta-crystallin B1 [Homo sapiens]

Accession:	gi|4503061	**Score:**	31.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	28.0
Database Date:	2015-11-30	**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 154: PREDICTED: pulmonary surfactant-associated protein C isoform X1 [Homo sapiens]

Accession:	gi|530387966	**Score:**	31.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	28.6
Database Date:	2015-11-30	**pI:**	10.8
		Sequence Coverage [%]:	14.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAPRDAHRDP	EMPAVLGSPA	GQLPTWLRPS	THPGHTWERR	RGEHSTCSKM	DVGSKEVLME	SPPDYSAAPR	GRFGIPCCPV
90	100	110	120	130	140	150	160
HLKRLLIVVV	VVVLIVVVIV	GALLMGLHMS	QKHTEMVLEM	SIGAPEAQQR	LALSEHLVTT	ATFSIGSTGL	VVYDYQQLLI
170	180	190	200	210	220	230	240
AYKPAPGTCC	YIMKIAPESI	PSLEALTRKV	HNFQGQWKPQ	RERKRPGQRV	FCSFCRRARS	CFCPHRRDKP	WRNGSLGRGW
250	260						
EWAEVAPRGP	GTPATTE						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1479	1	1006.6165	136.56	2	46.9	11.4	1	239-257	R.GWEWAEVAPRGPGTPATTE.-	

Detailed Protein Report

Protein 155: RNA polymerase II subunit A C-terminal domain phosphatase isoform 3 [Homo sapiens]

Accession:	gi|321267522	**Score:**	31.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	92.3
Database Date:	2015-11-30	**pI:**	4.9
		Sequence Coverage [%]:	4.9
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 0.82 **CV:** 0.00 % **No. of Peptides:** 1

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1965	2	899.3643	-116.81	2	52.9	16.3	2	779-797	R.TLGAPASSERSAAGGRGPR.G		WD:WU 0.82

Protein 156: PREDICTED: autoimmune regulator isoform X1 [Homo sapiens]

Accession: gi|530419216
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 31.1
MW [kDa]: 36.5
pI: 6.4
Sequence Coverage [%]: 6.9
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MWLVYSSGAP	GTQQPARNRV	FFPIGMAPGG	VCWRPDGWGT	GGQGRISGPG	SMGAGQRLGS	SGTQRCCWGS	CFGKEVALRR
90	100	110	120	130	140	150	160
VLHPSPVCMG	VSCLCQKNED	ECAVCRDGGE	LICCDGCPRA	FHLACLSPPL	REIPSGTWRC	SSCLQATVQE	VQPRAEEPRP
170	180	190	200	210	220	230	240
QEPPVETPLP	PGLRSAGEEV	RGPPGEPLAG	MDTTLVYKHL	PAPPSAAPLP	GLDSSALHPL	LCVGPEGQQN	LAPGARCGVC
250	260	270	280	290	300	310	320
GDGTDVLRCT	HCAAAFHWRC	HFPAGTSRPG	TGLRCRSCSG	DVTPAPVEGV	LAPSPARLAP	GPAKDDTASH	EPALHRDDLE
330	340	350					
SLLSEHTFDG	ILQWAIQSMA	RPAAPFPS					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1351	1	669.2815	20.48	2	45.7	14.6	0	107-119	R.DGGELICCDGCPR.A	

Detailed Protein Report

Protein 157: **PREDICTED: Golgin subfamily A member 8A isoform X1 [Homo sapiens]**

Accession:	gi|578826741	**Score:**	31.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	67.1
Database Date:	2015-11-30	**pI:**	6.4
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.2
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 0.66 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MAEETGQSKL	AAAKKKFKEY	WQRNRPGVPA	AAKRNTKANG	SSPETAASGG	CHSSEASSSA	SSSLHARQSP	CQEQAAVLNS
90	100	110	120	130	140	150	160
RSIKISRLND	TIKSLKQQKK	QVEHQLEEEK	KANNEKQKAE	RELEGQIQRL	NTEKKKLNTD	LYHMKHSLRY	FEEESKDLAG
170	180	190	200	210	220	230	240
RLQRSSQRIG	ELEWSLCAVA	ATQKKKPDGF	SSRSKALLKR	QLEQSIREQI	LLKGHVTQLK	ESLKEVQLER	DQYAEQIKGE
250	260	270	280	290	300	310	320
RAQWQQRMRK	MSQEVCTLKE	EKKHDTHRVE	ELERSLSRLK	NQMAEPLPPD	APAVSSEVEL	QDLRKELERV	AGELQAQVEN
330	340	350	360	370	380	390	400
NQCISLLNRG	QKERLREQEE	RLQEQQERLR	EREKRLQQLA	EPQSDLEELH	ENKSALQLEQ	QVKELQEKLG	QVMETLTSAE
410	420	430	440	450	460	470	480
KEPEAAVPAS	GTGGESSGLM	DLLEEKADLR	EHVEKLELGF	IQYRRERCHQ	KVHRLLTEPG	DSAKDASPGG	GHHQAGPGQG
490	500	510	520	530	540	550	560
GEEGEAAGAA	GDGVAACGSY	SEGHGKFLAA	ARNPAAEPSP	GAPAPQELGA	ADKHGDLCEA	SLTNSVEPAQ	GEAREGSSQD
570	580	590	600	610			
NPTAQPVVQL	LGEMQDHQEH	PGLGSNCCVP	CFCWAWLPRR	RR			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
103	1	822.3979	-26.54	2	30.5	11.3	1	137-149	K.LNTDLYHMKHSLR.Y	Oxidation: 8	WD:WU 0.66

Detailed Protein Report

Protein 158: **keratin, type II cytoskeletal 73 [Homo sapiens]**

Accession: gi|28173564
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 30.7
MW [kDa]: 58.9
pI: 7.6
Sequence Coverage [%]: 4.6
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MSRQFTYKSG	AAAKGGFSGC	SAVLSGGSSS	SYRAGGKGLS	GGFSSRSLYS	LGGARSISFN	VASGSGWAGG	YGFGRGRASG
90	100	110	120	130	140	150	160
FAGSMFGSVA	LGSVCPSLCP	PGGIHQVTIN	KSLLAPLNVE	LDPEIQKVRA	QEREQIKVLN	NKFASFIDKV	RFLEQQNQVL
170	180	190	200	210	220	230	240
ETKWELLQQL	DLNNCKNNLE	PILEGYISNL	RKQLETLSGD	RVRLDSELRS	VREVVEDYKK	RYEEEINKRT	TAENEFVVLK
250	260	270	280	290	300	310	320
KDVDAAYTSK	VELQAKVDAL	DGEIKFFKCL	YEGETAQIQS	HISDTSIILS	MDNNRNLDLD	SIIAEVRAQY	EEIARKSKAE
330	340	350	360	370	380	390	400
AEALYQTKFQ	ELQLAAGRHG	DDLKHTKNEI	SELTRLIQRL	RSEIESVKKQ	CANLETAIAD	AEQRGDCALK	DARAKLDELE
410	420	430	440	450	460	470	480
GALQQAKEEL	ARMLREYQEL	LSVKLSLDIE	IATYRKLLEG	EECRMSGEYT	NSVSISVINS	SMAGMAGTGA	GFGFSNAGTY
490	500	510	520	530	540	550	
GYWPSSVSGG	YSMLPGGCVT	GSGNCSPRGE	ARTRLGSASE	FRDSQGKTLA	LSSPTKKTMR		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2930	1	899.4860	22.51	2	65.4	12.0	1	329-344	K.FQELQLAAGRHGDDLK.H	

Detailed Protein Report

Protein 159: PREDICTED: kinesin-like protein KIF13B isoform X2 [Homo sapiens]

Accession:	gi|530387685	**Score:**	30.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	195.4
Database Date:	2015-11-30	**pI:**	5.4
Modification(s):	Oxidation	**Sequence Coverage [%]:**	0.9
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|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
1541	1	513.1056	-215.54	2	48.0	12.4	1	585-592	K.QNCRSMDR.F	Oxidation: 6

Detailed Protein Report

Protein 160:	**PREDICTED: beta/gamma crystallin domain-containing protein 3 isoform X1 [Homo sapiens]**		
Accession:	gi|530373918	**Score:**	30.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	298.2
Database Date:	2015-11-30	**pI:**	5.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.3
		No. of unique Peptides:	1

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
1726	1	900.4572	47.30	3	49.9	14.8	1	1649-1672	K.DYEGYPAPAMPDFQPGDTTVRLDK.R	Oxidation: 10

Detailed Protein Report

Protein 161: PREDICTED: OTU domain-containing protein 7B isoform X2 [Homo sapiens]

Accession:	gi|530432124	**Score:**	30.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	84.0
Database Date:	2015-11-30	**pI:**	7.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPPSVILNSY	VKSMLETYPH	PLVRGVVAPG	PLKKGFLTES	LLALPDPSSS	GRMTSFKLPD	LTVYNEDFRS	FIERDLIEQS
90	100	110	120	130	140	150	160
MLVALEQAGR	LNWWVSVDPT	SQRLLPLATT	GDGNCLLHAA	SLGMWGFHDR	DLMLRKALYA	LMEKGVEKEA	LKRRWRWQQT
170	180	190	200	210	220	230	240
QQNKESGLVY	TEDEWQKEWN	ELIKLASSEP	RMHLGTNGAN	CGGVESSEEP	VYESLEEFHV	FVLAHVLRRP	IVVVADTMLR
250	260	270	280	290	300	310	320
DSGGEAFAPI	PFGGIYLPLE	VPASQCHRSP	LVLAYDQAHF	SALVSMEQKE	NTKEQAVIPL	TDSEYKLLPL	HFAVDPGKGW
330	340	350	360	370	380	390	400
EWGKDDSDNV	RLASVILSLE	VKLHLLHSYM	NVKWIPLSSD	AQAPLAQPES	PTASAGDEPR	STPESGDSDK	ESVGSSSTSN
410	420	430	440	450	460	470	480
EGGRRKEKSK	RDREKDKKRA	DSVANKLGSF	GKTLGSKLKK	NMGGLMHSKG	SKPGGVGTGL	GGSSGTETLE	KKKKNSLKSW
490	500	510	520	530	540	550	560
KGGKEEAAGD	GPVSEKPPAE	SVGNGGSKYS	QEVMQSLSIL	RTAMQGEGKF	IFVGTLKMGH	RHQYQEEMIQ	RYLSDAEERF
570	580	590	600	610	620	630	640
LAEQKQKEAE	RKIMNGGIGG	GPPPAKKPEP	DAREEQPTGP	PAESRAMAFS	TGYPGDFTIP	RPSGGGVHCQ	EPRRQLAGGP
650	660	670	680	690	700	710	720
CVGGLPPYAT	FPRQCPPGRP	YPHQDSIPSL	EPGSHSKDGL	HRGALLPPPY	RVADSYSNGY	REPPEPDGWA	GGLRGLPPTQ
730	740	750	760	770			
TKCKQPNCSF	YGHPETNNFC	SCCYREELRR	REREPDGELL	VHRF			

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	269-289	R.SPLVLAYDQAHFSALVSMEQK.E	Oxidation: 18

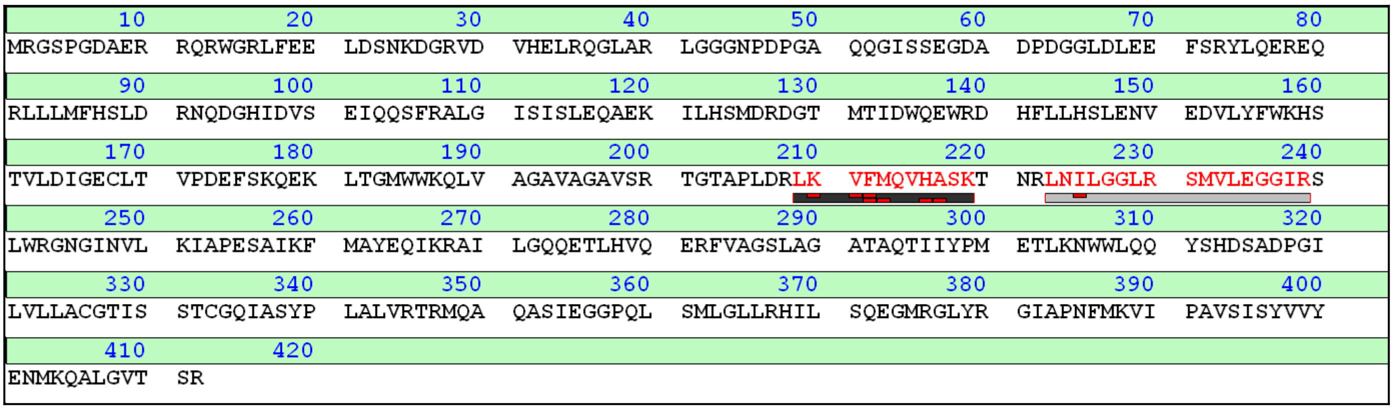
Detailed Protein Report

Protein 162: **PREDICTED: calcium-binding mitochondrial carrier protein SCaMC-3 isoform X1 [Homo sapiens]**

Accession:	gi|578833593	**Score:**	30.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	45.9
Database Date:	2015-11-30	**pI:**	6.0
		Sequence Coverage [%]:	6.8
		No. of unique Peptides:	2

Quantitation

WD:WU **Median:** 0.81 **CV:** 0.00 % **No. of Peptides:** 1



```
        10         20         30         40         50         60         70         80
MRGSPGDAER RQRWGRLFEE LDSNKDGRVD VHELRQGLAR LGGGNPDPGA QQGISSEGDA DPDGGLDLEE FSRYLQEREQ
        90        100        110        120        130        140        150        160
RLLLMFHSLD RNQDGHIDVS EIQQSFRALG ISISLEQAEK ILHSMDRDGT MTIDWQEWRD HFLLHSLENV EDVLYFWKHS
       170        180        190        200        210        220        230        240
TVLDIGECLT VPDEFSKQEK LTGMWWKQLV AGAVAGAVSR TGTAPLDRLK VFMQVHASKT NRLNILGGLR SMVLEGGIRS
       250        260        270        280        290        300        310        320
LWRGNGINVL KIAPESAIKF MAYEQIKRAI LGQQETLHVQ ERFVAGSLAG ATAQTIIYPM ETLKNWWLQQ YSHDSADPGI
       330        340        350        360        370        380        390        400
LVLLACGTIS STCGQIASYP LALVRTRMQA QASIEGGPQL SMLGLLRHIL SQEGMRGLYR GIAPNFMKVI PAVSISYVVY
       410        420
ENMKQALGVT SR
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1152	1	644.3310	-53.87	2	43.1	13.1	1	209-219	R.LKVFMQVHASK.T		WD:WU 0.81
1852	4	899.4901	-35.49	2	51.8	17.3	1	223-239	R.LNILGGLRSMVLEGGIR.S		

Detailed Protein Report

Protein 163: PREDICTED: nuclear pore complex protein Nup214 isoform X4 [Homo sapiens]

Accession:	gi|530427224	**Score:**	30.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	209.0
Database Date:	2015-11-30	**pI:**	9.0
		Sequence Coverage [%]:	1.5
		No. of unique Peptides:	2

Quantitation

WD:WU	**Median:** 1.48	**CV:** 0.00 %	**No. of Peptides:** 1

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	Ratios

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2741	1	715.3112	-107.27	2	62.7	17.4	1	66-77	K.VRIFDSPEELPK.E		WD:WU 1.48
2086	1	1023.4014	-90.92	2	54.7	13.0	2	670-687	R.TSKACFQVGTSEEMKMLR.T		

Detailed Protein Report

Protein 164: sortilin-related receptor preproprotein [Homo sapiens]

Accession:	gi|4507157	**Score:**	30.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	248.3
Database Date:	2015-11-30	**pI:**	5.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	0.7
		No. of unique Peptides:	1

Quantitation

WD:WU	**Median:** 1.02	**CV:** 0.00 %	**No. of Peptides:** 1

Detailed Protein Report

10	20	30	40	50	60	70	80
MATRSSRRES	RLPFLFTLVA	LLPPGALCEV	WTQRLHGGSA	PLPQDRGFLV	VQGDPRELRL	WARGDARGAS	RADEKPLRRK
90	100	110	120	130	140	150	160
RSAALQPEPI	KVYGQVSLND	SHNQMVVHWA	GEKSNVIVAL	ARDSLALARP	KSSDVYVSYD	YGKSFKKISD	KLNFGLGNRS
170	180	190	200	210	220	230	240
EAVIAQFYHS	PADNKRYIFA	DAYAQYLWIT	FDFCNTLQGF	SIPFRAADLL	LHSKASNLLL	GFDRSHPNKQ	LWKSDDFGQT
250	260	270	280	290	300	310	320
WIMIQEHVKS	FSWGIDPYDK	PNTIYIERHE	PSGYSTVFRS	TDFFQSRENQ	EVILEEVRDF	QLRDKYMFAT	KVVHLLGSEQ
330	340	350	360	370	380	390	400
QSSVQLWVSF	GRKPMRAAQF	VTRHPINEYY	IADASEDQVF	VCVSHSNNRT	NLYISEAEGL	KFSLSLENVL	YYSPGGAGSD
410	420	430	440	450	460	470	480
TLVRYFANEP	FADFHRVEGL	QGVYIATLIN	GSMNEENMRS	VITFDKGGTW	EFLQAPAFTG	YGEKINCELS	QGCSLHLAQR
490	500	510	520	530	540	550	560
LSQLLNLQLR	RMPILSKESA	PGLIIATGSV	GKNLASKTNV	YISSSAGARW	REALPGPHYY	TWGDHGGIIT	AIAQGMETNE
570	580	590	600	610	620	630	640
LKYSTNEGET	WKTFIFSEKP	VFVYGLLTEP	GEKSTVFTIF	GSNKENVHSW	LILQVNATDA	LGVPCTENDY	KLWSPSDERG
650	660	670	680	690	700	710	720
NECLLGHKTV	FKRRTPHATC	FNGEDFDRPV	VVSNCSCTRE	DYECDFGFKM	SEDLSLEVCV	PDPEFSGKSY	SPPVPCPVGS
730	740	750	760	770	780	790	800
TYRRTRGYRK	ISGDTCSGGD	VEARLEGELV	PCPLAEENEF	ILYAVRKSIY	RYDLASGATE	QLPLTGLRAA	VALDFDYEHN
810	820	830	840	850	860	870	880
CLYWSDLALD	VIQRLCLNGS	TGQEVIINSG	LETVEALAFE	PLSQLLYWVD	AGFKKIEVAN	PDGDFRLTIV	NSSVLDRPRA
890	900	910	920	930	940	950	960
LVLVPQEGVM	FWTDWGDLKP	GIYRSNMDGS	AAYHLVSEDV	KWPNGISVDD	QWIYWTDAYL	ECIERITFSG	QQRSVILDNL
970	980	990	1000	1010	1020	1030	1040
PHPYAIAVFK	NEIYWDDWSQ	LSIFRASKYS	GSQMEILANQ	LTGLMDMKIF	YKGKNTGSNA	CVPRPCSLLC	LPKANNSRSC
1050	1060	1070	1080	1090	1100	1110	1120
RCPEDVSSSV	LPSGDLMCDC	PQGYQLKNNT	CVKEENTCLR	NQYRCSNGNC	INSIWWCDFD	NDCGDMSDER	NCPTTICDLD
1130	1140	1150	1160	1170	1180	1190	1200
TQFRCQESGT	CIPLSYKCDL	EDDCGDNSDE	SHCEMHQCRS	DEYNCSSGMC	IRSSWVCDGD	NDCRDWSDEA	NCTAIYHTCE
1210	1220	1230	1240	1250	1260	1270	1280
ASNFQCRNGH	CIPQRWACDG	DTDCQDGSDE	DPVNCEKKCN	GFRCPNGTCI	PSSKHCDGLR	DCSDGSDEQH	CEPLCTHFMD
1290	1300	1310	1320	1330	1340	1350	1360
FVCKNRQQCL	FHSMVCDGII	QCRDGSDEDA	AFAGCSQDPE	FHKVCDEFGF	QCQNGVCISL	IWKCDGMDDC	GDYSDEANCE
1370	1380	1390	1400	1410	1420	1430	1440
NPTEAPNCSR	YFQFRCENGH	CIPNRWKCDR	ENDCGDWSDE	KDCGDSHILP	FSTPGPSTCL	PNYYRCSSGT	CVMDTWVCDG
1450	1460	1470	1480	1490	1500	1510	1520
YRDCADGSDE	EACPLLANVT	AASTPTQLGR	CDRFEFECHQ	PKTCIPNWKR	CDGHQDCQDG	RDEANCPTHS	TLTCMSREFQ
1530	1540	1550	1560	1570	1580	1590	1600
CEDGEACIVL	SERCDGFLDC	SDESDEKACS	DELTVYKVQN	LQWTADFSGD	VTLTWMRPKK	MPSASCVYNV	YYRVVGESIW
1610	1620	1630	1640	1650	1660	1670	1680
KTLETHSNKT	NTVLKVLKPD	TTYQVKVQVQ	CLSKAHNTND	FVTLRTPEGL	PDAPRNLQLS	LPREAEGVIV	GHWAPPIHTH
1690	1700	1710	1720	1730	1740	1750	1760
GLIREYIVEY	SRSGSKMWAS	QRAASNFTEI	KNLLVNTLYT	VRVAAVTSRG	IGNWSDSKSI	TTIKGKVIPP	PDIHIDSYGE
1770	1780	1790	1800	1810	1820	1830	1840
NYLSFTLTME	SDIKVNGYVV	NLFWAFDTHK	QERRTLNFRG	SILSHKVGNL	TAHTSYEISA	WAKTDLGDSP	LAFEHVMTRG
1850	1860	1870	1880	1890	1900	1910	1920
VRPPAPSLKA	KAINQTAVEC	TWTGPRNVVY	GIFYATSFLD	LYRNPKSLTT	SLHNKTVIVS	KDEQYLFLVR	VVVPYQGPSS
1930	1940	1950	1960	1970	1980	1990	2000
DYVVVKMIPD	SRLPPRHLHV	VHTGKTSVVI	KWESPYDSPD	QDLLYAIAVK	DLIRKTDRSY	KVKSRNSTVE	YTLNKLEPGG
2010	2020	2030	2040	2050	2060	2070	2080
KYHIIVQLGN	MSKDSSIKIT	TVSLSAPDAL	KIITENDHVL	LFWKSLALKE	KHFNESRGYE	IHMFDSAMNI	TAYLGNTTDN
2090	2100	2110	2120	2130	2140	2150	2160
FFKISNLKMG	HNYTFTVQAR	CLFGNQICGE	PAILLYDELG	SGADASATQA	ARSTDVAAVV	VPILFLILLS	LGVGFAILYT
2170	2180	2190	2200	2210	2220		

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1196	1	610.6448	-210.75	2	43.2	10.3	0	1244-1254	R.CPNGTCIPSSK.H	Carbamidomethyl: 1, 6	WD:WU 1.02

Detailed Protein Report

Protein 165: **CMP-N-acetylneuraminate-beta-1,4-galactoside alpha-2,3-sialyltransferase isoform n [Homo sapiens]**

Accession:	gi|394953753	**Score:**	30.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	26.7
Database Date:	2015-11-30	**pI:**	10.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	10.4
		No. of unique Peptides:	2

Quantitation

WD:WU **Median:** 0.77 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MGLLVFVRNL	LLALCLFLVL	GFLYYSAWKL	HLLQWEEDSK	YDRLGFLLNL	DSKLFSKPAP	MFLDDSFRKW	ARIREFVPPF
90	100	110	120	130	140	150	160
GIKGQDNLIK	AILSVTKEYR	LTPALDSLRC	RRCIIVGNGG	VLANKSLGSR	IDDYDIVVRL	NSAPVKGFEK	DVGSKTTLRI
170	180	190	200	210	220	230	240
TYPEGAMQRP	EQYERDSLFV	LAGFKWQDFK	WLKYIVYKER	VSWTHNIQRE	KEFLRKLVKA	RVITDLSSGI	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
146	1	657.8165	-71.56	2	31.1	10.8	0	113-125	R.CIIVGNGGVLANK.S	Carbamidomethyl: 1	WD:WU 0.77
2295	3	1131.4541	-161.50	1	57.1	19.5	1	220-230	K.ARVITDLSSGI.-		

Detailed Protein Report

Protein 166: protein FAM83G [Homo sapiens]

Accession:	gi|115392150	**Score:**	30.2
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

```
        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
1617	1	712.0414	-43.20	3	48.9	13.8	2	33-51	R.LALEALVARGRDAFYEVLK.R	
509	4	492.6651	-183.49	2	34.8	16.4	0	44-51	R.DAFYEVLK.R	

Detailed Protein Report

Protein 167: cGMP-specific 3',5'-cyclic phosphodiesterase isoform 2 [Homo sapiens]

Accession:	gi|61744430	**Score:**	30.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	94.7
Database Date:	2015-11-30	**pI:**	5.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLPFGDKTRE	MVNAWFAERV	HTIPVCKEGI	RGHTESCSCP	LQQSPRADNS	APGTPTRKIS	ASEFDRPLRP	IVVKDSEGTV
90	100	110	120	130	140	150	160
SFLSDSEKKE	QMPLTPPRFD	HDEGDQCSRL	LELVKDISSH	LDVTALCHKI	FLHIHGLISA	DRYSLFLVCE	DSSNDKFLIS
170	180	190	200	210	220	230	240
RLFDVAEGST	LEEVSNNCIR	LEWNKGIVGH	VAALGEPLNI	KDAYEDPRFN	AEVDQITGYK	TQSILCMPIK	NHREEVVGVA
250	260	270	280	290	300	310	320
QAINKKSGNG	GTFTEKDEKD	FAAYLAFCGI	VLHNAQLYET	SLLENKRNQV	LLDLASLIFE	EQQSLEVILK	KIAATIISFM
330	340	350	360	370	380	390	400
QVQKCTIFIV	DEDCSDSFSS	VFHMECEELE	KSSDTLTREH	DANKINYMYA	QYVKNTMEPL	NIPDVSKDKR	FPWTTENTGN
410	420	430	440	450	460	470	480
VNQQCIRSLL	CTPIKNGKKN	KVIGVCQLVN	KMEENTGKVK	PFNRNDEQFL	EAFVIFCGLG	IQNTQMYEAV	ERAMAKQMVT
490	500	510	520	530	540	550	560
LEVLSYHASA	AEEETRELQS	LAAAVVPSAQ	TLKITDFSFS	DFELSDLETA	LCTIRMFTDL	NLVQNFQMKH	EVLCRWILSV
570	580	590	600	610	620	630	640
KKNYRKNVAY	HNWRHAFNTA	QCMFAALKAG	KIQNKLTDLE	ILALLIAALS	HDLDHRGVNN	SYIQRSEHPL	AQLYCHSIME
650	660	670	680	690	700	710	720
HHHFDQCLMI	LNSPGNQILS	GLSIEEYKTT	LKIIKQAILA	TDLALYIKRR	GEFFELIRKN	QFNLEDPHQK	ELFLAMLMTA
730	740	750	760	770	780	790	800
CDLSAITKPW	PIQQRIAELV	ATEFFDQGDR	ERKELNIEPT	DLMNREKKNK	IPSMQVGFID	AICLQLYEAL	THVSEDCFPL
810	820	830	840				
LDGCRKNRQK	WQALAEQQEK	MLINGESGQA	KRN				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2288	1	937.3710	-111.47	2	57.1	12.3	2	751-765	R.ERKELNIEPTDLMNR.E	Oxidation: 13

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Detailed Protein Report

Protein 168: PREDICTED: dedicator of cytokinesis protein 7 isoform X2 [Homo sapiens]

Accession:	gi|530363514	**Score:**	30.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	209.0
Database Date:	2015-11-30	**pI:**	6.1
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAERRAFAQK	ISRTVAAEVR	KQISGQYSGS	PQLLKNLNIV	GNISHHTTVP	LTEAVDPVDL	EDYLITHPLA	VDSGPLRDLI
90	100	110	120	130	140	150	160
EFPPDDIEVV	YSPRDCRTLV	SAVPEESEMD	PHVRDCIRSY	TEDWAIVIRK	YHKLGTGFNP	NTLDKQKERQ	KGLPKQVFES
170	180	190	200	210	220	230	240
DEAPDGNSYQ	DDQDDLKRRS	MSIDDTPRGS	WACSIFDLKN	SLPDALLPNL	LDRTPNEEID	RQNDDQRKSN	RHKELFALHP
250	260	270	280	290	300	310	320
SPDEEEPIER	LSVPDIPKEH	FGQRLLVKCL	SLKFEIEIEP	IFASLALYDV	KEKKKISENF	YFDLNSEQMK	GLLRPHVPPA
330	340	350	360	370	380	390	400
AITTLARSAI	FSITYPSQDV	FLVIKLEKVL	QQGDIGECAE	PYMIFKEADA	TKNKEKLEKL	KSQADQFCQR	LGKYRMPFAW
410	420	430	440	450	460	470	480
TAIHLMNIVS	SAGSLERDST	EVEISTGERK	GSWSERRNSS	IVGRRSLERT	TSGDDACNLT	SFRPATLTVT	NFFKQEGDRL
490	500	510	520	530	540	550	560
SDEDLYKFLA	DMRRPSSVLR	RLRPITAQLK	IDISPAPENP	HYCLTPELLQ	VKLYPDSRVR	PTREILEFPA	RDVYVPNTTY
570	580	590	600	610	620	630	640
RNLLYIYPQS	LNFANRQGSA	RNITVKVQFM	YGEDPSNAMP	VIFGKSSCSE	FSKEAYTAVV	YHNRSPDFHE	EIKVKLPATL
650	660	670	680	690	700	710	720
TDHHHLLFTF	YHVSCQQKQN	TPLETPVGYT	WIPMLQNGRL	KTGQFCLPVS	LEKPPQAYSV	LSPEVPLPGM	KWVDNHKGVF
730	740	750	760	770	780	790	800
NVEVVAVSSI	HTQDPYLDKF	FALVNALDEH	LFPVRIGDMR	IMENNLENEL	KSSISALNSS	QLEPVVRFLH	LLLDKLILLV
810	820	830	840	850	860	870	880
IRPPVIAGQI	VNLGQASFEA	MASIINRLHK	NLEGNHDQHG	RNSLLASYIH	YVFRLPNTYP	NSSSPGPGGL	GGSVHYATMA
890	900	910	920	930	940	950	960
RSAVRPASLN	LNRSRSLSNS	NPDISGTPTS	PDDEVRSIIG	SKGLDRSNSW	VNTGGPKAAP	WGSNPSPSAE	STQAMDRSCN
970	980	990	1000	1010	1020	1030	1040
RMSSHTETSS	FLQTLTGRLP	TKKLFHEELA	LQWVVCSGSV	RESALQQAWF	FFELMVKSMV	HHLYFNDKLE	APRKSRFPER
1050	1060	1070	1080	1090	1100	1110	1120
FMDDIAALVS	TIASDIVSRF	QKDTEMVERL	NTSLAFFLND	LLSVMDRGFV	FSLIKSCYKQ	VSSKLYSLPN	PSVLVSLRLD
1130	1140	1150	1160	1170	1180	1190	1200
FLRIICSHEH	YVTLNLPCSL	LTPPASPSPS	VSSATSQSSG	FSTNVQDQKI	ANMFELSVPF	RQQHYLAGLV	LTELAVILDP
1210	1220	1230	1240	1250	1260	1270	1280
DAEGLFGLHK	KVINMVHNLL	SSHDSDPRYS	DPQIKARVAM	LYLPLIGIIM	ETVPQLYDFT	ETHNQRGRPI	CIATDDYESE
1290	1300	1310	1320	1330	1340	1350	1360
SGSMISQTVA	MAIAGTSVPQ	LTRPGSFLLT	STSGRQHTTF	SAESSRSLLI	CLLWVLKNAD	ETVLQKWFTD	LSVLQLNRLL
1370	1380	1390	1400	1410	1420	1430	1440
DLLYLCVSCF	EYKGKKVFER	MNSLTFKKSK	DMRAKLEEAI	LGSIGARQEM	VRRSRGQLER	SPSGSAFGSQ	ENLRWRKDMT
1450	1460	1470	1480	1490	1500	1510	1520
HWRQNTEKLD	KSRAEIEHEA	LIDGNLATEA	NLIILDTLEI	VVQTVSVTES	KESILGGVLK	VLLHSMACNQ	SAVYLQHCFA
1530	1540	1550	1560	1570	1580	1590	1600
TQRALVSKFP	ELLFEEETEQ	CADLCLRLLR	HCSSSIGTIR	SHASASLYLL	MRQNFEIGNN	FARVKMQVTM	SLSSLVGTSQ
1610	1620	1630	1640	1650	1660	1670	1680
NFNEEFLRRS	LKTILTYAEE	DLELRETTFP	DQVQDLVFNL	HMILSDTVKM	KEHQEDPEML	IDLMYRIAKG	YQTSPDLRLT
1690	1700	1710	1720	1730	1740	1750	1760
WLQNMAGKHS	ERSNHAEAAQ	CLVHSAALVA	EYLSMLEDRK	YLPVGCVTFQ	NISSNVLEES	AVSDDVVSPD	EEGICSGKYF
1770	1780	1790	1800	1810	1820	1830	1840
TESGLVGLLE	QAAASFSMAG	MYEAVNEVYK	VLIPIHEANR	DAKKLSTIHG	KLQEAFSKIV	HQSTGWEFYL	VYIFLFDSMK
1850	1860						
TSVILFFLKA	MFPS						

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

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
122	1	879.4101	-14.16	3	30.5	16.1	0	1501-1523	K.VLLHSMACNQSAVYLQHCFATQR.A	Oxidation: 6

Detailed Protein Report

Protein 169: kinesin-like protein KIF1C [Homo sapiens]

Accession: gi|40254834
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 29.7
MW [kDa]: 122.9
pI: 6.5
Sequence Coverage [%]: 2.7
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
1261	1	1044.6916	131.82	2	44.1	13.7	2	630-646	K.ELLEQQGIDIKLEMEKR.L	Oxidation: 14

Detailed Protein Report

Protein 170: **PREDICTED: putative uncharacterized protein LOC388900 isoform X1 [Homo sapiens]**

Accession: gi|530420293
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 29.7
MW [kDa]: 55.6
pI: 10.1
Sequence Coverage [%]: 4.8
No. of unique Peptides: 2

Quantitation

WD:WU **Median:** 0.04 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MLFSWVKRQR KSQYSCKGSE LRHARSSVIK RKTADKNLLA ELYQYSNFNS SKPNKLPNGV DFCDMVGNVV RAERDCLSGK
        90        100        110        120        130        140        150        160
HFCSGRELEK FLSSSSPRAI WLDSFWWIFH ERYQPNKELQ NNLFDRIAQH YALLLFRVPK SHSEEALLKR LPSLLSKAVY
       170        180        190        200        210        220        230        240
TSFCCCFPQS WFDTHEFKSD ICNTMSLWIS GTYPSPQSYD SWDYSELDPE RFRREELMLY RRRLTKGREF SLFAGKRAFS
       250        260        270        280        290        300        310        320
QKPAQSRKFY HPQSSSANSP SEKTSSAKQN SEKSLRMQNT AKEHHCQTLV LKKPTQEVKR ISEARECENM FPKKSCAACK
       330        340        350        360        370        380        390        400
SPELTSNLFN IYGKSPLIVY FLQNYASLQQ HGKNVLIVRR EKTTSTPDCT PTYTDVISET LCSMKKRKDN LNQLYQHHWT
       410        420        430        440        450        460        470        480
EWNYFDKHLK ELQDNFSREM KNIDPKAADT KKANHMFIPP SAVNEESPDK KTKEGKGGEG KRRETEVEHF FPLTSKP
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1201	2	507.1525	-225.20	2	43.3	10.5	0	141-149	K.SHSEEALLK.R		WD:WU 0.04
1811	4	863.4321	30.21	2	51.3	19.2	2	300-313	K.RISEARECENMFPK.K	Oxidation: 11	

Detailed Protein Report

Protein 171: **PREDICTED: sushi, nidogen and EGF-like domain-containing protein 1 isoform X4 [Homo sapiens]**

Accession: gi|578804038
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 29.7
MW [kDa]: 142.7
pI: 6.4
Sequence Coverage [%]: 1.4
No. of unique Peptides: 2

10	20	30	40	50	60	70	80
MRHGVAWALL	VAAALGLGAR	GVRGAVALAD	FYPFGAERGD	AVTPKQDDGG	SGLRPLSVPF	PFFGAEHSGL	YVNNNGIISF
90	100	110	120	130	140	150	160
LKEVSQFTPV	AFPIAKDRCV	VAAFWADVDN	RRAGDVYYRE	ATDPAMLRRA	TEDVRHYFPE	LLDFNATWVF	VATWYRVTFF
170	180	190	200	210	220	230	240
GGSSSSPVNT	FQTVLITDGK	LSFTIFNYES	IVWTTGTHAS	SGGNATGLGG	IAAQAGFNAG	DGQRYFSIPG	SRTADMAEVE
250	260	270	280	290	300	310	320
TTTNVGVPGR	WAFRIDDAQV	RVGGCGHTTS	VCLALRPCLN	GGKCIDDCVT	GNPSYTCSCL	SGFTGRRCHL	DVNECASQPC
330	340	350	360	370	380	390	400
QNGGTCTHGI	NSFRCQCPAG	FGGPTCETAQ	SPCDTKECQH	GGQCQVENGS	AVCVCQAGYT	GAACEMDVDD	CSPDPCLNGG
410	420	430	440	450	460	470	480
SCVDLVGNYT	CLCAEPFKGL	RCETGDHPVP	DACLSAPCHN	GGTCVDADQG	YVCECPEGFM	GLDCRERVPD	DCECRNGGRC
490	500	510	520	530	540	550	560
LGANTTLCQC	PLGFFGLLCE	FEITAMPCNM	NTQCPDGGYC	MEHGGSYLCV	CHTDHNASHS	LPSPCDSDPC	FNGGSCDAHD
570	580	590	600	610	620	630	640
DSYTCECPRG	FHGKHCEKAR	PHLCSSGPCR	NGGTCKEAGG	EYHCSCPYRF	TGRHCEIGKP	DSCASGPCHN	GGTCFHYIGK
650	660	670	680	690	700	710	720
YKCDCPPGFS	GRHCEIAPSP	CFRSPCVNGG	TCEDRDTDFF	CHCQAGYMGR	RCQAEVDCGP	PEEVKHATLR	FNGTRLGAVA
730	740	750	760	770	780	790	800
LYACDRGYSL	SAPSRIRVCQ	PHGVWSEPPQ	CLEIDECRSQ	PCLHGGSCQD	RVAGYLCLCS	TGYEGAHCEL	ERDECRAHPC
810	820	830	840	850	860	870	880
RNGGSCRNLP	GAYVCRCPAG	FVGVHCETEV	DACDSSPCQH	GGRCESGGGA	YLCVCPESFF	GYHCETVSDP	CFSSPCGGRG
890	900	910	920	930	940	950	960
YCLASNGSHS	CTCKVGYTGE	DCAKELFPPT	ALKMERVEES	GVSISWNPPN	GPAARQMLDG	YAVTYVSSDG	SYRRTDFVDR
970	980	990	1000	1010	1020	1030	1040
TRSSHQLQAL	AAGRAYNISV	FSVKRNSNNK	NDISRPAVLL	ARTRPRPVEG	FEVTNVTAST	ISVQWALHRI	RHATVSGVRV
1050	1060	1070	1080	1090	1100	1110	1120
SIRHPEALRD	QATDVDRSVD	RFTFRALLPG	KRYTIQLTTL	SGLRGEEHPT	ESLATAPTHV	WTRPLPPANL	TAARVTATSA
1130	1140	1150	1160	1170	1180	1190	1200
HVVWDAPTPG	SLLEAYVINV	TTSQSTKSRY	VPNGKLASYT	VRDLLPGRRY	QLSVIAVQST	ELGPQHSEPA	HLYIITSPRD
1210	1220	1230	1240	1250	1260	1270	1280
GADRRWHQGG	HHPRVLKNRP	PPARLPELRL	LNDHSAPETP	TQPPRFSELV	DGRGRVSARF	GGSPSKAATV	RSQPTASAQL
1290	1300	1310	1320	1330			
ENMEEAPKRV	SLALQLPEHG	SKDIGSLDLL	LAPVSTRRTG	LCIRRRE			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1667	1	1073.2934	-127.64	2	49.2	19.6	1	591-609	R.NGGTCKEAGGEYHCSCPYR.F	Carbamidomethyl: 5, 16
2019	1	715.9639	11.03	3	53.6	10.1	1	591-609	R.NGGTCKEAGGEYHCSCPYR.F	Carbamidomethyl: 14, 16

Detailed Protein Report

Protein 172: structural maintenance of chromosomes protein 4 isoform 2 [Homo sapiens]

Accession:	gi|570700827	**Score:**	29.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	144.4
Database Date:	2015-11-30	**pI:**	6.7
		Sequence Coverage [%]:	1.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPRKGTQPST	ARRREEGPPP	PSPDGASSDA	EPEPPSGRTE	SPATAAAMTN	EAGAPRLMIT	HIVNQNFKSY	AGEKILGPFH
90	100	110	120	130	140	150	160
KRFSCIIGPN	GSGKSNVIDS	MLFVFGYRAQ	KIRSKKLSVL	IHNSDEHKDI	QSCTVEVHFQ	KIIDKEGDDY	EVIPNSNFYV
170	180	190	200	210	220	230	240
SRTACRDNTS	VYHISGKKKT	FKDVGNLLRS	HGIDLDHNRF	LILQGEVEQI	AMMKPKGQTE	HDEGMLEYLE	DIIGCGRLNE
250	260	270	280	290	300	310	320
PIKVLCRRVE	ILNEHRGEKL	NRVKMVEKEK	DALEGEKNIA	IEFLTLENEI	FRKKNHVCQY	YIYELQKRIA	EMETQKEKIH
330	340	350	360	370	380	390	400
EDTKEINEKS	NILSNEMKAK	NKDVKDTEKK	LNKITKFIEE	NKEKFTQLDL	EDVQVREKLK	HATSKAKKLE	KQLQKDKEKV
410	420	430	440	450	460	470	480
EEFKSIPAKS	NNIINETTTR	NNALEKEKEK	EEKKLKEVMD	SLKQETQGLQ	KEKESREKEL	MGFSKSVNEA	RSKMDVAQSE
490	500	510	520	530	540	550	560
LDIYLSRHNT	AVSQLTKAKE	ALIAASETLK	ERKAAIRDIE	GKLPQTEQEL	KEKEKELQKL	TQEETNFKSL	VHDLFQKVEE
570	580	590	600	610	620	630	640
AKSSLAMNRS	RGKVLDAIIQ	EKKSGRIPGI	YGRLGDLGAI	DEKYDVAISS	CCHALDYIVV	DSIDIAQECV	NFLKRQNIGV
650	660	670	680	690	700	710	720
ATFIGLDKMA	VWAKKMTEIQ	TPENTPRLFD	LVKVKDEKIR	QAFYFALRDT	LVADNLDQAT	RVAYQKDRRW	RVVTLQGQII
730	740	750	760	770	780	790	800
EQSGTMTGGG	SKVMKGRMGS	SLVIEISEEE	VNKMESQLQN	DSKKAMQIQE	QKVQLEERVV	KLRHSEREMR	NTLEKFTASI
810	820	830	840	850	860	870	880
QRLIEQEEYL	NVQVKELEAN	VLATAPDKKK	QKLLEENVSA	FKTEYDAVAE	KAGKVEAEVK	RLHNTIVEIN	NHKLKAQQDK
890	900	910	920	930	940	950	960
LDKINKQLDE	CASAITKAQV	AIKTADRNLQ	KAQDSVLRTE	KEIKDTEKEV	DDLTAELKSL	EDKAAEVVKN	TNAAEESLPE
970	980	990	1000	1010	1020	1030	1040
IQKEHRNLLQ	ELKVIQENEH	ALQKDALSIK	LKLEQIDGHI	AEHNSKIKYW	HKEISKISLH	PIEDNPIEEI	SVLSPEDLEA
1050	1060	1070	1080	1090	1100	1110	1120
IKNPDSITNQ	IALLEARCHE	MKPNLGAIAE	YKKKEELYLQ	RVAELDKITY	ERDSFRQAYE	DLRKQRLNEF	MAGFYIITNK
1130	1140	1150	1160	1170	1180	1190	1200
LKENYQMLTL	GGDAELELVD	SLDPFSEGIM	FSVRPPKKSW	KKIFNLSGGE	KTLSSLALVF	ALHHYKPTPL	YFMDEIDAAL
1210	1220	1230	1240	1250	1260	1270	
DFKNVSIVAF	YIYEQTKNAQ	FIIISLRNNM	FEISDRLIGI	YKTYNITKSV	AVNPKEIASK	GLC	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
282	2	862.8833	-60.41	2	32.7	29.6	2	457-471	R.EKELMGFSKSVNEAR.S	

Detailed Protein Report

Protein 173: zinc finger protein 622 [Homo sapiens]

Accession:	gi|15529978	**Score:**	29.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	54.2
Database Date:	2015-11-30	**pI:**	5.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	6.3
		No. of unique Peptides:	2

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1830	3	938.9541	-36.71	2	51.2	19.3	2	34-50	R.RKVASMAPVTAEGFQER.V	
2237	1	753.3462	-49.90	2	56.3	10.4	1	299-311	K.VGVGKICLWCNEK.G	Carbamidomethyl: 7

Detailed Protein Report

Protein 174: polycystin-2 [Homo sapiens]

Accession:	gi|4505835	**Score:**	29.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	109.6
Database Date:	2015-11-30	**pI:**	5.4
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	3.9
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MVNSSRVQPQ	QPGDAKRPPA	PRAPDPGRLM	AGCAAVGASL	AAPGGLCEQR	GLEIEMQRIR	QAAARDPPAG	AAASPSPPLS
90	100	110	120	130	140	150	160
SCSRQAWSRD	NPGFEAEEEE	EEVEGEEGGM	VVEMDVEWRP	GSRRSAASSA	VSSVGARSRG	LGGYHGAGHP	SGRRRRREDQ
170	180	190	200	210	220	230	240
GPPCPSPVGG	GDPLHRHLPL	EGQPPRVAWA	ERLVRGLRGL	WGTRLMEESS	TNREKYLKSV	LRELVTYLLF	LIVLCILTYG
250	260	270	280	290	300	310	320
MMSSNVYYYT	RMMSQLFLDT	PVSKTEKTNF	KTLSSMEDFW	KFTEGSLLDG	LYWKMQPSNQ	TEADNRSFIF	YENLLLGVPR
330	340	350	360	370	380	390	400
IRQLRVRNGS	CSIPQDLRDE	IKECYDVYSV	SSEDRAPFGP	RNGTAWIYTS	EKDLNGSSHW	GIIATYSGAG	YYLDLSRTRE
410	420	430	440	450	460	470	480
ETAAQVASLK	KNVWLDRGTR	ATFIDFSVYN	ANINLFCVVR	LLVEFPATGG	VIPSWQFQPL	KLIRYVTTFD	FFLAACEIIF
490	500	510	520	530	540	550	560
CFFIFYYVVE	EILEIRIHKL	HYFRSFWNCL	DVVIVVLSVV	AIGINIYRTS	NVEVLLQFLE	DQNTFPNFEH	LAYWQIQFNN
570	580	590	600	610	620	630	640
IAAVTVFFVW	IKLFKFINFN	RTMSQLSTTM	SRCAKDLFGF	AIMFFIIFLA	YAQLAYLVFG	TQVDDFSTFQ	ECIFTQFRII
650	660	670	680	690	700	710	720
LGDINFAEIE	EANRVLGPIY	FTTFVFFMFF	ILLNMFLAII	NDTYSEVKSD	LAQQKAEMEL	SDLIRKGYHK	ALVKLKLKKN
730	740	750	760	770	780	790	800
TVDDISESLR	QGGGKLNFDE	LRQDLKGKGH	TDAEIEAIFT	KYDQDGDQEL	TEHEHQQMRD	DLEKEREDLD	LDHSSLPRPM
810	820	830	840	850	860	870	880
SSRSFPRSLD	DSEEDDDEDS	GHSSRRRGSI	SSGVSYEEFQ	VLVRRVDRME	HSIGSIVSKI	DAVIVKLEIM	ERAKLKRREV
890	900	910	920	930	940	950	960
LGRLLDGVAE	DERLGRDSEI	HREQMERLVR	EELERWESDD	AASQISHGLG	TPVGLNGQPR	PRSSRPSSSQ	STEGMEGAGG
970							
NGSSNVHV							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
418	1	686.6239	-116.77	3	33.8	12.4	2	400-417	R.EETAAQVASLKKNVWLDR.G	
5	1	1205.0356	-34.52	2	29.0	17.2	2	576-595	K.FINFNRTMSQLSTTMSRCAK.D	Carbamidomethyl: 18; Oxidation: 8

Detailed Protein Report

Protein 175: PREDICTED: protein FAM214A isoform X6 [Homo sapiens]

Accession:	gi|578827201	**Score:**	29.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	111.5
Database Date:	2015-11-30	**pI:**	9.2
		Sequence Coverage [%]:	2.3
		No. of unique Peptides:	2

Alias proteins:

Accession	Name	Description
gi|578827203	refseq_human (refseq_human_20140103.fasta)	PREDICTED: protein FAM214A isoform X7 [Homo sapiens]

```
        10          20          30          40          50          60          70          80
MVEMMLLPDC  CYSDDGPTTE  GIDLNDPAIK  QDALLLERWI  LEPVPRQNGD  RFIEEKTLLL  AVRSFVFFSQ  LSAWLSVSHG
        90         100         110         120         130         140         150         160
AIPRNILYRI  SAADVDLQWN  FSQTPIEHVF  PVPNVSHNVA  LKVSVQSLPR  QSNYPVLTCS  IHTNIGLYEK  RIQQHKLKTH
       170         180         190         200         210         220         230         240
QHHNPNEAEQ  CGTNSSQRLC  SKQTWTMAPE  SVLHAKSGPS  PEYTAAVKNI  KLYPGTGSKS  DHGTSQANIL  GFSGIGDIKS
       250         260         270         280         290         300         310         320
QETSVRTLKS  FSMVDSSISN  RQSFWQSAGE  TNPLIGSLIQ  ERQEIIARIA  QHLIHCDPST  SHVSGRPFNT  QESSSLHSKL
       330         340         350         360         370         380         390         400
FRVSQENENV  GKGKEAFSMT  FGSPEFSSPE  DTNEGKIRLK  PETPRSETCI  SNDFYSHMPV  GETNPLIGSL  LQERQDVIAR
       410         420         430         440         450         460         470         480
IAQHLEHIDP  TASHIPRQSF  NMHDSSSVAS  KVFRSSYEDK  NLLKKNKDES  SVSISHTKCS  LLGDISDGKN  LVPNKCFTSF
       490         500         510         520         530         540         550         560
KNNSKEKCSL  KHQTRNQCQN  NPSEIIQSTY  QETQNKSSSL  STSSILSQHK  ENNLDLTSRF  KEQEMSNGID  KQYSNCTTID
       570         580         590         600         610         620         630         640
KQICTNKYKE  KIINENYNPK  FFGNLQSDDS  KKNDSKIKVT  VLEMSEYLNK  YESMSSNKDS  KRPKTCEQNT  QLNSIENYLN
       650         660         670         680         690         700         710         720
KDNEGFKCKK  SDQLKNEQDK  QEDPTNEKSQ  NYSQRRSIKD  CLSTCEQPKN  TEVLRTTLKH  SNVWRKHNFH  SLDGTSTRAF
       730         740         750         760         770         780         790         800
HPQTGLPLLS  SPVPQRKTQS  GCFDLDSSLL  HLKSFSSRSP  RPCLNIEDDP  DIHEKPFLSS  SAPPITSLSL  LGNFEESVLN
       810         820         830         840         850         860         870         880
YRFDPLGIVD  GFTAEVGASG  AFCPTHLTLP  VEVSFYSVSD  DNAPSPYMGV  ITLESLGKRG  YRVPPSGTIQ  VTLFNPNKTV
       890         900         910         920         930         940         950         960
VKMFVVIYDL  RDMPANHQTF  LRQRTFSVPV  KQEVKRSVNK  ENIRHTEERL  LRYLIHLRFQ  SSKSGKIYLH  RDVRLLFSRK
       970         980         990
SMEVDSGAAY  ELKSYTESPT  NPQFSPRC
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2952	1	557.9715	37.67	3	65.7	10.1	1	247-261	R.TLKSFSMVDSSISNR.Q	
1649	3	480.7758	122.24	2	48.9	19.4	0	661-668	K.QEDPTNEK.S	

Detailed Protein Report

Protein 176: squalene monooxygenase [Homo sapiens]

Accession:	gi|62865635	**Score:**	29.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	63.9
Database Date:	2015-11-30	**pI:**	9.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.9
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 2.62 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MWTFLGIATF TYFYKKFGDF ITLANREVLL CVLVFLSLGL VLSYRCRHRN GGLLGRQQSG SQFALFSDIL SGLPFIGFFW
        90        100        110        120        130        140        150        160
AKSPPESENK EQLEARRRRK GTNISETSLI GTAACTSTSS QNDPEVIIVG AGVLGSALAA VLSRDGRKVT VIERDLKEPD
       170        180        190        200        210        220        230        240
RIVGEFLQPG GYHVLKDLGL GDTVEGLDAQ VVNGYMIHDQ ESKSEVQIPY PLSENNQVQS GRAFHHGRFI MSLRKAAMAE
       250        260        270        280        290        300        310        320
PNAKFIEGVV LQLLEEDDVV MGVQYKDKET GDIKELHAPL TVVADGLFSK FRKSLVSNKV SVSSHFVGFL MKNAPQFKAN
       330        340        350        360        370        380        390        400
HAELILANPS PVLIYQISSS ETRVLVDIRG EMPRNLREYM VEKIYPQIPD HLKEPFLEAT DNSHLRSMPA SFLPPSSVKK
       410        420        430        440        450        460        470        480
RGVLLLGDAY NMRHPLTGGG MTVAFKDIKL WRKLLKGIPD LYDDAAIFEA KKSFYWARKT SHSFVVNILA QALYELFSAT
       490        500        510        520        530        540        550        560
DDSLHQLRKA CFLYFKLGGE CVAGPVGLLS VLSPNPLVLI GHFFAVAIYA VYFCFKSEPW ITKPRALLSS GAVLYKACSV
       570        580
IFPLIYSEMK YMVH
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1572	3	648.3277	-29.30	2	48.0	29.4	2	46-56	R.CRHRNGGLLGR.Q	Carbamidomethyl: 1	WD:WU 2.62

Detailed Protein Report

Protein 177: tenascin-X isoform 1 precursor [Homo sapiens]

Accession:	gi|188528648	**Score:**	29.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	457.9
Database Date:	2015-11-30	**pI:**	4.9
		Sequence Coverage [%]:	0.8
		No. of unique Peptides:	2

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
1929	1	890.3591	-119.35	2	52.8	13.5	1	1418-1435	R.VGGKESEVTVGGLEPGHK.Y	
2906	2	557.9675	41.54	3	65.1	15.9	0	2141-2157	R.VGGEESEVTVGGLEPGR.K	

Detailed Protein Report

Protein 178: probable G-protein coupled receptor 179 precursor [Homo sapiens]

Accession:	gi|93352554	**Score:**	29.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	257.2
Database Date:	2015-11-30	**pI:**	5.4
		Sequence Coverage [%]:	0.9
		No. of unique Peptides:	1

Quantitation

WD:WU	**Median:** 1.45	**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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
813	6	509.1525	-284.31	2	38.6	17.2	1	1195-1204	R.AGKTGLAMLR.Q		WD:WU 1.45

Detailed Protein Report

Protein 179: cyclic AMP-dependent transcription factor ATF-5 [Homo sapiens]

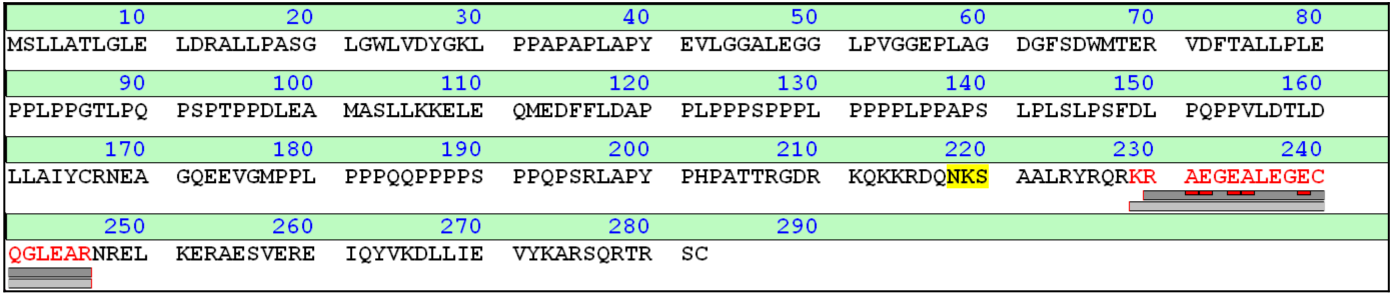
Accession:	gi|12597625	**Score:**	29.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	30.7
Database Date:	2015-11-30	**pI:**	4.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	6.4
		No. of unique Peptides:	2

Quantitation

WD:WU **Median:** 1.40 **CV:** 0.00 % **No. of 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	Ratios
2748	1	1002.0026	18.34	2	62.8	15.8	2	229-246	R.KRAEGEALEGECQGLEAR.N	Carbamidomethyl: 12	
533	1	625.6275	0.96	3	35.1	13.5	1	230-246	K.RAEGEALEGECQGLEAR.N	Carbamidomethyl: 11	WD:WU 1.40

Detailed Protein Report

Protein 180: multicilin [Homo sapiens]

Accession: gi|299782571
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl, Oxidation

Score: 29.2
MW [kDa]: 41.7
pI: 5.5
Sequence Coverage [%]: 2.9
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MQACGGGAAG	RRAFDSICPN	RMLALPGRAL	LCKPGKPERK	FAPPRKFFPG	CTGGSPVSVY	EDPPDAEPTA	LPALTTIDLQ
90	100	110	120	130	140	150	160
DLADCSSLLG	SDAPPGGDLA	ASQNHSHQTE	ADFNLQDFRD	TVDDLISDSS	SMMSPTLASG	DFPFSPCDIS	PFGPCLSPPL
170	180	190	200	210	220	230	240
DPRALQSPPL	RPPDVPPPEQ	YWKEVADQNQ	RALGDALVEN	NQLHVTLTQK	QEEIASLKER	NVQLKELASR	TRHLASVLDK
250	260	270	280	290	300	310	320
LMITQSRDCG	AAAEPFLLKA	KAKRSLEELV	SAAGQDCAEV	DAILREISER	CDEALQSRDP	KRPRLLPEPA	NTDTRPGNLH
330	340	350	360	370	380	390	
GAFRGLRTDC	SRSALNLSHS	ELEEGGSFST	RIRSHSTIRT	LAFPQGNAFT	IRTANGGYKF	RWVPS	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
809	1	526.2922	129.61	2	38.5	29.2	0	1-11	-.MQACGGGAAGR.R	Carbamidomethyl: 4; Oxidation: 1

Detailed Protein Report

Protein 181: **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

WD:WU **Median:** 0.78 **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		WD:WU 0.78

Detailed Protein Report

Protein 182: **PREDICTED: condensin-2 complex subunit H2 isoform X1 [Homo sapiens]**

Accession:	gi|530420802	**Score:**	29.2
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 183: unconventional myosin-Id [Homo sapiens]

Accession:	gi|51100974	**Score:**	29.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	116.1
Database Date:	2015-11-30	**pI:**	10.0
		Sequence Coverage [%]:	1.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAEQESLEFG	KADFVLMDTV	SMPEFMANLR	LRFEKGRIYT	FIGEVVVSVN	PYKLLNIYGR	DTIEQYKGRE	LYERPPHLFA
90	100	110	120	130	140	150	160
IADAAYKAMK	RRSKDTCIVI	SGESGAGKTE	ASKYIMQYIA	AITNPSQRAE	VERVKNMLLK	SNCVLEAFGN	AKTNRNDNSS
170	180	190	200	210	220	230	240
RFGKYMDINF	DFKGDPIGGH	INNYLLEKSR	VIVQQPGERS	FHSFYQLLQG	GSEQMLRSLH	LQKSLSSYNY	IHVGAQLKSS
250	260	270	280	290	300	310	320
INDAAEFRVV	ADAMKVIGFK	PEEIQTVYKI	LAAILHLGNL	KFVVDGDTPL	IENGKVVSII	AELLSTKTDM	VEKALLYRTV
330	340	350	360	370	380	390	400
ATGRDIIDKQ	HTEQEASYGR	DAFAKAIYER	LFCWIVTRIN	DIIEVKNYDT	TIHGKNTVIG	VLDIYGFEIF	DNNSFEQFCI
410	420	430	440	450	460	470	480
NYCNEKLQQL	FIQLVLKQEQ	EEYQREGIPW	KHIDYFNNQI	IVDLVEQQHK	GIIAILDDAC	MNVGKVTDEM	FLEALNSKLG
490	500	510	520	530	540	550	560
KHAHFSSRKL	CASDKILEFD	RDFRIRHYAG	DVVYSVIGFI	DKNKDTLFQD	FKRLMYNSSN	PVLKNMWPEG	KLSITEVTKR
570	580	590	600	610	620	630	640
PLTAATLFKN	SMIALVDNLA	SKEPYYVRCI	KPNDKKSPQI	FDDERCRHQV	EYLGLLENVR	VRRAGFAFRQ	TYEKFLHRYK
650	660	670	680	690	700	710	720
MISEFTWPNH	DLPSDKEAVK	KLIERCGFQD	DVAYGKTKIF	IRTPRTLFTL	EELRAQMLIR	IVLFLQKVWR	GTLARMRYKR
730	740	750	760	770	780	790	800
TKAALTIIRY	YRRYKVKSYI	HEVARRFHGV	KTMRDYGKHV	KWPSPPKVLR	RFEEALQTIF	NRWRASQLIK	SIPASDLPQV
810	820	830	840	850	860	870	880
RAKVAAVEML	KGQRADLGLQ	RAWEGNYLAS	KPDTPQTSGT	FVPVANELKR	KDKYMNVLFS	CHVRKVNRFS	KVEDRAIFVT
890	900	910	920	930	940	950	960
DRHLYKMDPT	KQYKVMKTIP	LYNLTGLSVS	NGKDQLVVFH	TKDNKDLIVC	LFSKQPTHES	RIGELVGVLV	NHFKSEKRHL
970	980	990	1000	1010			
QVNVTNPVQC	SLHGKKCTVS	VETRLNQPQP	DFTKNRSGFI	LSVPGN			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2982	3	729.3741	-5.85	2	66.0	18.2	1	985-996	R.LNQPQPDFTKNR.S	

Detailed Protein Report

Protein 184: **PREDICTED: forkhead box protein P3 isoform X2 [Homo sapiens]**

Accession:	gi|578838031	**Score:**	29.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	56.2
Database Date:	2015-11-30	**pI:**	10.7
		Sequence Coverage [%]:	7.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MTRKGQRKKP	KISKFPFKSH	NQEKEKHRER	EKKNYENPSP	PRDYQRTHSS	KKIWIIRRER	SAASTPYSVV	FLLGIKAKLF
90	100	110	120	130	140	150	160
LIRDSFPQAR	LILFCQSTSP	SLPLDKDPMP	NPRPGKPSAP	SLALGPSPGA	SPSWRAAPKA	SDLLGARGPG	GTFQGRDLRG
170	180	190	200	210	220	230	240
GAHASSSSLN	PMPPSQLQLS	TVDAHARTPV	LQVHPLESPA	MISLTPPTTA	TGVFSLKARP	GLPPGINVAS	LEWVSREPAL
250	260	270	280	290	300	310	320
LCTFPNPSAP	RKDSTLSAVP	QSSYPLLANG	VCKWPGCEKV	FEEPEDFLKH	CQADHLLDEK	GRAQCLLQRE	MVQSLEQQLV
330	340	350	360	370	380	390	400
LEKEKLSAMQ	AHLAGKMALT	KASSVASSDK	GSCCIVAAGS	QGPVVPAWSG	PREAPDSLFA	VRRHLWGSHG	NSTFPEFLHN
410	420	430	440	450	460	470	480
MDYFKFHNMR	PPFTYATLIR	WAILEAPEKQ	RTLNEIYHWF	TRMFAFFRNH	PATWKNAIRH	NLSLHKCFVR	VESEKGAVWT
490	500	510					
VDELEFRKKR	SQRPSRCSNP	TPGP					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
14	1	712.9876	-118.49	3	29.1	16.9	2	59-78	R.ERSAASTPYSVVFLLGIKAK.L	

Detailed Protein Report

Protein 185: PREDICTED: rap guanine nucleotide exchange factor 3 isoform X2 [Homo sapiens]

Accession:	gi|530399600	**Score:**	29.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	87.5
Database Date:	2015-11-30	**pI:**	7.2
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	3.3
		No. of unique Peptides:	2

Quantitation

WD:WU	**Median:**	2.90	**CV:**	0.00 %	**No. of Peptides:**	1

Alias proteins:

Accession	Name	Description
gi|530399602	refseq_human (refseq_human_20140103.fasta)	PREDICTED: rap guanine nucleotide exchange factor 3 isoform X3 [Homo sapiens]

10	20	30	40	50	60	70	80
MGSWPWDLGS	IPGAKLWESA	RCCWMKVPSA	MDRDAQFYRF	PGPEPEPVRT	HEMEEELAEA	VALLSQRGPD	ALLTVALRKP
90	100	110	120	130	140	150	160
PGQRTDEELD	LIFEELLHIK	AVAHLSNSVK	RELAAVLLFE	PHSKAGTVLF	SQGDKGTSWY	IIWKGSVNVV	THGKGLVTTL
170	180	190	200	210	220	230	240
HEGDDFGQLA	LVNDAPRAAT	IILREDNCHF	LRVDKQDFNR	IIKDVEAKTM	RLEEHGKVVL	VLERASQGAG	PSRPPTPGRN
250	260	270	280	290	300	310	320
RYTVMSGTPE	KILELLLEAM	GPDSSAHDPT	ETFLSDFLLT	HRVFMPSAQL	CAALLHHFHV	EPAGGSEQER	STYVCNKRQQ
330	340	350	360	370	380	390	400
ILRLVSQWVA	LYGSMLHTDP	VATSFLQKLS	DLVGRDTRLS	NLLREQWPER	RRCHRLENGC	GNASPQMKAR	NLPVWLPNQD
410	420	430	440	450	460	470	480
EPLPGSSCAI	QVGDKVPYDI	CRPDHSVLTL	QLPVTASVRE	VMAALAQEDG	WTKGQVLVKV	NSAGDAIGLQ	PDARGVATSL
490	500	510	520	530	540	550	560
GLNERLFVVN	PQEVHELIPH	PDQLGPTVGS	AEGLDLVSAK	DLAGQLTDHD	WSLFNSIHQV	ELIHYVLGPQ	HLRDVTTANL
570	580	590	600	610	620	630	640
ERFMRRFNEL	QYWVATELCL	CPVPGPRAQL	LRKFIKLAAH	LKEQKNLNSF	FAVMFGLSNS	AISRLAHTWE	RLPHKVRKLY
650	660	670	680	690	700	710	720
SALERLLDPS	WNHRVYRLAL	AKLSPPVIPF	MPLLLKDMTF	IHEGNHTLVE	NLINFEKMRM	MARAARMLHH	CRSHNPVPLS
730	740	750	760	770	780		
PLRSRVSHLH	EDSQVARIST	CSEQSLSTRS	PASTWAYVQQ	LKVIDNQREL	SRLSRELEP		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1402	1	727.3976	-11.71	2	45.9	15.2	0	112-124	R.ELAAVLLFEPHSK.A		
870	1	711.3337	31.93	2	39.7	13.9	0	376-388	R.LENGCGNASPQMK.A	Carbamidomethyl: 5; Oxidation: 12	WD:WU 2.90

Detailed Protein Report

Protein 186: deoxyribonuclease gamma isoform 2 precursor [Homo sapiens]

Accession:	gi|375151549	**Score:**	29.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	31.8
Database Date:	2015-11-30	**pI:**	9.7
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	9.1
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MSRELAPLLL	LLLSIHSALA	MRICSFNVRS	FGESKQEDKN	AMDVIVKVIK	RCDIILVMEI	KDSNNRICPI	LMEKLNREKL
90	100	110	120	130	140	150	160
VSVKRSYHYH	DYQDGDADVF	SREPFVVWFQ	SPHTAVKDFV	IIPLHTTPET	SVKEIDELVE	VYTDVKHRWK	AENFIFMGDF
170	180	190	200	210	220	230	240
NAGCSYVPKK	AWKNIRLRTD	PRFVWLIGDQ	EDTTVKKSTN	CAYDRIVLRG	QEIVSSVVPK	SNSVFDFQKA	YKLTEEEALD
250	260	270	280				
VSDHFPVEFK	LQSSRAFTNS	KKSVTLRKKT	KSKRS				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2460	2	873.4565	-23.34	2	59.0	11.5	2	36-50	K.QEDKNAMDVIVKVIK.R	Oxidation: 7
2658	1	625.2870	-69.08	2	61.5	17.6	0	52-61	R.CDIILVMEIK.D	Carbamidomethyl: 1; Oxidation: 7

Detailed Protein Report

Protein 187: poly [ADP-ribose] polymerase 4 [Homo sapiens]

Accession:	gi|112789550	**Score:**	29.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	192.5
Database Date:	2015-11-30	**pI:**	5.3
		Sequence Coverage [%]:	2.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MVMGIFANCI	FCLKVKYLPQ	QQKKKLQTDI	KENGGKFSFS	LNPQCTHIIL	DNADVLSQYQ	LNSIQKNHVH	IANPDFIWKS
90	100	110	120	130	140	150	160
IREKRLLDVK	NYDPYKPLDI	TPPPDQKASS	SEVKTEGLCP	DSATEEEDTV	ELTEFGMQNV	EIPHLPQDFE	VAKYNTLEKV
170	180	190	200	210	220	230	240
GMEGGQEAVV	VELQCSRDSR	DCPFLISSHF	LLDDGMETRR	QFAIKKTSED	ASEYFENYIE	ELKKQGFLLR	EHFTPEATQL
250	260	270	280	290	300	310	320
ASEQLQALLL	EEVMNSSTLS	QEVSDLVEMI	WAEALGHLEH	MLLKPVNRIS	LNDVSKAEGI	LLLVKAALKN	GETAEQLQKM
330	340	350	360	370	380	390	400
MTEFYRLIPH	KGTMPKEVNL	GLLAKKADLC	QLIRDMVNVC	ETNLSKPNPP	SLAKYRALRC	KIEHVEQNTE	EFLRVRKEVL
410	420	430	440	450	460	470	480
QNHHSKSPVD	VLQIFRVGRV	NETTEFLSKL	GNVRPLLHGS	PVQNIVGILC	RGLLLPKVVE	DRGVQRTDVG	NLGSGIYFSD
490	500	510	520	530	540	550	560
SLSTSIKYSH	PGETDGTRLL	LICDVALGKC	MDLHEKDFSL	TEAPPGYDSV	HGVSQTASVT	TDFEDDEFVV	YKTNQVKMKY
570	580	590	600	610	620	630	640
IIKFSMPGDQ	IKDFHPSDHT	ELEEYRPEFS	NFSKVEDYQL	PDAKTSSSTK	AGLQDASGNL	VPLEDVHIKG	RIIDTVAQVI
650	660	670	680	690	700	710	720
VFQTYTNKSH	VPIEAKYIFP	LDDKAAVCGF	EAFINGKHIV	GEIKEKEEAQ	QEYLEAVTQG	HGAYLMSQDA	PDVFTVSVGN
730	740	750	760	770	780	790	800
LPPKAKVLIK	ITYITELSIL	GTVGVFFMPA	TVAPWQQDKA	LNENLQDTVE	KICIKEIGTK	QSFSLTMSIE	MPYVIEFIFS
810	820	830	840	850	860	870	880
DTHELKQKRT	DCKAVISTME	GSSLDSSGFS	LHIGLSAAYL	PRMWVEKHPE	KESEACMLVF	QPDLDVDLPD	LASESEVIIC
890	900	910	920	930	940	950	960
LDCSSSMEGV	TFLQAKQIAL	HALSLVGEKQ	KVNIIQFGTG	YKELFSYPKH	ITSNTMAAEF	IMSATPTMGN	TDFWKTLRYL
970	980	990	1000	1010	1020	1030	1040
SLLYPARGSR	NILLVSDGHL	QDESLTLQLV	KRSRPHTRLF	ACGIGSTANR	HVLRILSQCG	AGVFEYFNAK	SKHSWRKQIE
1050	1060	1070	1080	1090	1100	1110	1120
DQMTRLCSPS	CHSVSVKWQQ	LNPDVPEALQ	APAQVPSLFL	NDRLLVYGFI	PHCTQATLCA	LIQEKEFRTM	VSTTELQKTT
1130	1140	1150	1160	1170	1180	1190	1200
GTMIHKLAAR	ALIRDYEDGI	LHENETSHEM	KKQTLKSLII	KLSKENSLIT	QFTSFVAVEK	RDENESPFPD	IPKVSELIAK
1210	1220	1230	1240	1250	1260	1270	1280
EDVDFLPYMS	WQGEPQEAVR	NQSLLASSEW	PELRLSKRKH	RKIPFSKRKM	ELSQPEVSED	FEEDGLGVLP	AFTSNLERGG
1290	1300	1310	1320	1330	1340	1350	1360
VEKLLDLSWT	ESCKPTATEP	LFKKVSPWET	STSSFFPILA	PAVGSYLPPT	ARAHSPASLS	FASYRQVASF	GSAAPPRQFD
1370	1380	1390	1400	1410	1420	1430	1440
ASQFSQGPVP	GTCADWIPQS	ASCPTGPPQN	PPSSPYCGIV	FSGSSLSSAQ	SAPLQHPGGF	TTRPSAGTFP	ELDSPQLHFS
1450	1460	1470	1480	1490	1500	1510	1520
LPTDPDPIRG	FGSYHPSASS	PFHFQPSAAS	LTANLRLPMA	SALPEALCSQ	SRTTPVDLCL	LEESVGSLEG	SRCPVFAFQS
1530	1540	1550	1560	1570	1580	1590	1600
SDTESDELSE	VLQDSCFLQI	KCDTKDDSIL	CFLEVKEEDE	IVCIQHWQDA	VPWTELLSLQ	TEDGFWKLTP	ELGLILNLNT
1610	1620	1630	1640	1650	1660	1670	1680
NGLHSFLKQK	GIQSLGVKGR	ECLLDLIATM	LVLQFIRTRL	EKEGIVFKSL	MKMDDASISR	NIPWAFEAIK	QASEWVRRTE
1690	1700	1710	1720	1730			
GQYPSICPRL	ELGNDWDSAT	KQLLGLQPIS	TVSPLHRVLH	YSQG			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
122	1	981.4639	-29.75	2	30.8	17.4	1	1015-1032	R.ILSQCGAGVFEYFNAKSK.H	

Detailed Protein Report

Protein 188: nucleolin [Homo sapiens]

Accession:	gi|55956788	**Score:**	28.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	76.6
Database Date:	2015-11-30	**pI:**	4.4
		Sequence Coverage [%]:	3.9
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 1.03 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MVKLAKAGKN	QGDPKKMAPP	PKEVEEDSED	EEMSEDEEDD	SSGEEVVIPQ	KKGKKAAATS	AKKVVVSPTK	KVAVATPAKK
90	100	110	120	130	140	150	160
AAVTPGKKAA	ATPAKKTVTP	AKAVTTPGKK	GATPGKALVA	TPGKKGAAIP	AKGAKNGKNA	KKEDSDEEED	DDSEEDEEDD
170	180	190	200	210	220	230	240
EDEDEDEDEI	EPAAMKAAAA	APASEDEDDE	DDEDDEDDDD	DEEDDSEEEA	METTPAKGKK	AAKVVPVKAK	NVAEDEDEEE
250	260	270	280	290	300	310	320
DDEDEDDDDD	EDDEDDDDED	DEEEEEEEEE	EPVKEAPGKR	KKEMAKQKAA	PEAKKQKVEG	TEPTTAFNLF	VGNLNFNKSA
330	340	350	360	370	380	390	400
PELKTGISDV	FAKNDLAVVD	VRIGMTRKFG	YVDFESAEDL	EKALELTGLK	VFGNEIKLEK	PKGKDSKKER	DARTLLAKNL
410	420	430	440	450	460	470	480
PYKVTQDELK	EVFEDAAEIR	LVSKDGKSKG	IAYIEFKTEA	DAEKTFEEKQ	GTEIDGRSIS	LYYTGEKGQN	QDYRGGKNST
490	500	510	520	530	540	550	560
WSGESKTLVL	SNLSYSATEE	TLQEVFEKAT	FIKVPQNQNG	KSKGYAFIEF	ASFEDAKEAL	NSCNKREIEG	RAIRLELQGP
570	580	590	600	610	620	630	640
RGSPNARSQP	SKTLFVKGLS	EDTTEETLKE	SFDGSVRARI	VTDRETGSSK	GFGFVDFNSE	EDAKAAKEAM	EDGEIDGNKV
650	660	670	680	690	700	710	720
TLDWAKPKGE	GGFGGRGGGR	GGFGGRGGGR	GGRGGFGGRG	RGGFGGRGGF	RGGRGGGGDH	KPQGKKTKFE	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
165	1	635.8027	-108.85	2	31.3	12.6	1	97-109	K.TVTPAKAVTTPGK.K		WD:WU 1.03

Detailed Protein Report

Protein 189: 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	VGRRRSHQGQ	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
2897	1	655.6487	-212.02	2	65.0	11.2	0	49-59	K.EDTTSLNWNCK.S	

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Detailed Protein Report

Protein 190: **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

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Detailed Protein Report

Protein 191: PREDICTED: focal adhesion kinase 1 isoform X12 [Homo sapiens]

Accession:	gi|530389222	**Score:**	28.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	108.1
Database Date:	2015-11-30	**pI:**	5.7
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	2.7
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MEMLLMSGYE	LRIRYLPKGF	LNQFTEDKPT	LNFFYQQVKS	DYMLEIADQV	DQEIALKLGC	LEIRRSYWEM	RGNALEKKSN
90	100	110	120	130	140	150	160
YEVLEKDVGL	KRFFPKSLLD	SVKAKTLRKL	IQQTFRQFAN	LNREESILKF	FEILSPVYRF	DKECFKCALG	SSWIISVELA
170	180	190	200	210	220	230	240
IGPEEGISYL	TDKGCNPTHL	ADFTQVQTIQ	YSNSEDKDRK	GMLQLKIAGA	PEPLTVTAPS	LTIAENMADL	IDGYCRLVNG
250	260	270	280	290	300	310	320
TSQSFIIRPQ	KEGERALPSI	PKLANSEKQG	MRTHAVSVSD	EISGDETDDY	AEIIDEEDTY	TMPSKSYGID	EARDYEIQRE
330	340	350	360	370	380	390	400
RIELGRCIGE	GQFGDVHQGI	YMSPENPALA	VAIKTCKNCT	SDSVREKFLQ	EALTMRQFDH	PHIVKLIGVI	TENPVWIIME
410	420	430	440	450	460	470	480
LCTLGELRSF	LQVRKYSLDL	ASLILYAYQL	STALAYLESK	RFVHRDIAAR	NVLVSSNDCV	KLGDFGLSRY	MEDSTYYKAS
490	500	510	520	530	540	550	560
KGKLPIKWMA	PESINFRRFT	SASDVWMFGV	CMWEILMHGV	KPFQGVKNND	VIGRIENGER	LPMPPNCPPT	LYSLMTKCWA
570	580	590	600	610	620	630	640
YDPSRRPRFT	ELKAQLSTIL	EEEKAQQEER	MRMESRRQAT	VSWDSGGSDE	APPKPSRPGY	PSPRSSEGFY	PSPQHMVQTN
650	660	670	680	690	700	710	720
HYQVSGYPGS	HGITAMAGSI	YPGQASLLDQ	TDSWNHRPQE	IAMWQPNVED	STVLDLRGIG	QVLPTHLMEE	RLIRQQQEME
730	740	750	760	770	780	790	800
EDQRWLEKEE	RFLKPDVRLS	RGSIDREDGS	LQGPIGNQHI	YQPVGKPDPA	APPKKPPRPG	APGHLGSLAS	LSSPADSYNE
810	820	830	840	850	860	870	880
GVKPWRLQPQ	EISPPPTANL	DRSNDKVYEN	VTGLVKAVIE	MSSKIQPAPP	EEYVPMVKEV	GLALRTLLAT	VDETIPLLPA
890	900	910	920	930	940	950	960
STHREIEMAQ	KLLNSDLGEL	INKMKLAQQY	VMTSLQQEYK	KQMLTAAHAL	AVDAKNLLDV	IDQARLKMLG	QTRPH

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
153	2	635.8187	61.87	2	31.1	14.9	1	355-365	K.TCKNCTSDSVR.E	Carbamidomethyl: 2
2249	1	937.4207	-94.13	2	56.6	13.7	2	484-498	K.LPIKWMAPESINFRR.F	Oxidation: 6

Detailed Protein Report

Protein 192: ankyrin repeat and zinc finger domain-containing protein 1 isoform 1 [Homo sapiens]

Accession:	gi|109150425	**Score:**	28.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	80.9
Database Date:	2015-11-30	**pI:**	9.6
		Sequence Coverage [%]:	2.9
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|109150435	refseq_human (refseq_human_20140103.fasta)	ankyrin repeat and zinc finger domain-containing protein 1 isoform 1 [Homo sapiens]

10	20	30	40	50	60	70	80
MSPAPDAAPA	PASISLFDLS	ADAPVFQGLS	LVSHAPGEAL	ARAPRTSCSG	SGERESPERK	LLQGPMDISE	KLFCSTCDQT
90	100	110	120	130	140	150	160
FQNHQEQREH	YKLDWHRFNL	KQRLKDKPLL	SALDFEKQSS	TGDLSSISGS	EDSDSASEED	LQTLDRERAT	FEKLSRPPGF
170	180	190	200	210	220	230	240
YPHRVLFQNA	QGQFLYAYRC	VLGPHQDPPE	EAELLLQNLQ	SRGPRDCVVL	MAAAGHFAGA	IFQGREVVTH	KTFHRYTVRA
250	260	270	280	290	300	310	320
KRGTAQGLRD	ARGGPSHSAG	ANLRRYNEAT	LYKDVRDLLA	GPSWAKALEE	AGTILLRAPR	SGRSLFFGGK	GAPLQRGDPR
330	340	350	360	370	380	390	400
LWDIPLATRR	PTFQELQRVL	HKLTTLHVYE	EDPREAVRLH	SPQTHWKTVR	EERKKPTEEE	IRKICRDEKE	ALGQNEESPK
410	420	430	440	450	460	470	480
QGSGSEGEDG	FQVELELVEL	TVGTLDLCES	EVLPKRRRRK	RNKKEKSRDQ	EAGAHRTLLQ	QTQEEEPSTQ	SSQAVAAPLG
490	500	510	520	530	540	550	560
PLLDEAKAPG	QPELWNALLA	ACRAGDVGVL	KLQLAPSPAD	PRVLSLLSAP	LGSGGFTLLH	AAAAAGRGSV	VRLLLEAGAD
570	580	590	600	610	620	630	640
PTVQDSRARP	PYTVAADKST	RNEFRRFMEK	NPDAYDYNKA	QVPGPLTPEM	EARQATRKRE	QKAARRQREE	QQQRQQEQEE
650	660	670	680	690	700	710	720
REREEQRRFA	ALSDREKRAL	AAERRLAAQL	GAPTSPIPDS	AIVNTRRCWS	CGASLQGLTP	FHYLDFSFCS	TRCLQDHRRQ
730							
AGRPSS							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
883	4	529.1891	-185.79	2	39.4	16.5	0	277-286	R.DLLAGPSWAK.A	

Detailed Protein Report

Protein 193: activating signal cointegrator 1 complex subunit 3 isoform c [Homo sapiens]

Accession:	gi|546232111	**Score:**	28.6
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 [%]:**	3.6
		No. of unique Peptides:	2

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
330	1	539.2345	-58.27	2	32.8	12.1	0	63-71	K.MQSINEDLK.D	
106	1	715.2726	-66.45	3	30.6	16.5	0	694-710	K.MQQLNNMDEVCYENVLK.Q	Carbamidomethyl: 11; Oxidation: 7

Detailed Protein Report

Protein 194: **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 195: PREDICTED: SNW domain-containing protein 1 isoform X2 [Homo sapiens]

Accession:	gi|530403266	**Score:**	28.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	65.4
Database Date:	2015-11-30	**pI:**	10.2
		Sequence Coverage [%]:	6.0
		No. of unique Peptides:	1

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
2279	3	863.8727	-94.70	2	57.0	13.5	2	543-558	K.DPQIAAAPRNTSMKAR.R	

Detailed Protein Report

Protein 196: **glycogenin-1 isoform 3 [Homo sapiens]**

Accession:	gi|296040507	**Score:**	28.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	31.4
Database Date:	2015-11-30	**pI:**	6.1
		Sequence Coverage [%]:	5.4
		No. of unique Peptides:	1

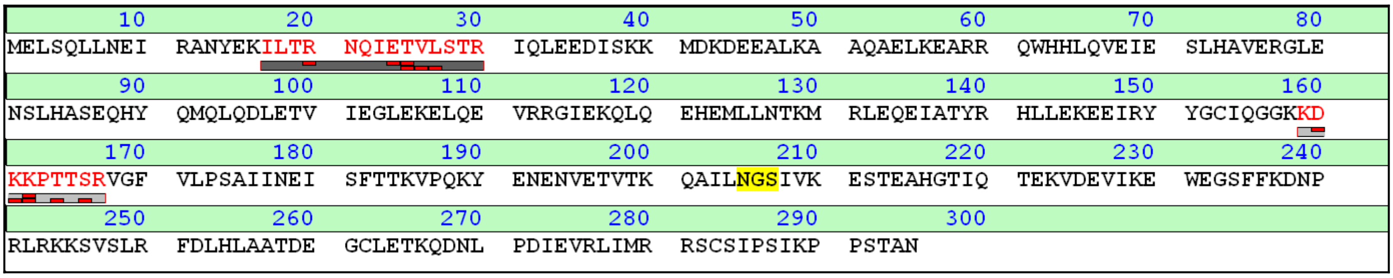
10	20	30	40	50	60	70	80
MTDQAFVTLT	TNDAYAKGAL	VLGSSLKQHR	TTRRLVVLAT	PQVSDSMRKV	LETVFDEVIM	VDVLDSGDSA	HLTLMKRPEL
90	100	110	120	130	140	150	160
GVTLTKLHCW	SLTQYSKCVF	MDADTLVLAN	IDDLFDREEL	SAAPDPGWPD	CFNSGVFVYQ	PSVETYNQLL	HLASEQGSFD
170	180	190	200	210	220	230	240
GGDQGILNTF	FSSWATTDIR	KHLPFIYNLS	SISIYSYLPA	FKVKMSQEPY	HICPLGRSQL	WHSRLYPRKN	GRNDGNRARL
250	260	270	280				
IIWEQIPLTT	SRGNLTLTSS	RNTAFFCEHI	HFTSLVSDT				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2959	2	822.4635	2.95	2	65.8	28.2	1	35-49	R.LVVLATPQVSDSMRK.V	

Detailed Protein Report

Protein 197: keratin-like protein KRT222 [Homo sapiens]

Accession:	gi|22748757	**Score:**	28.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	34.1
Database Date:	2015-11-30	**pI:**	5.6
		Sequence Coverage [%]:	7.8
		No. of unique Peptides:	2



```
        10         20         30         40         50         60         70         80
MELSQLLNEI RANYEKILTR NQIETVLSTR IQLEEDISKK MDKDEEALKA AQAELKEARR QWHHLQVEIE SLHAVERGLE
        90        100        110        120        130        140        150        160
NSLHASEQHY QMQLQDLETV IEGLEKELQE VRRGIEKQLQ EHEMLLNTKM RLEQEIATYR HLLEKEEIRY YGCIQGGKKD
       170        180        190        200        210        220        230        240
KKPTTSRVGF VLPSAIINEI SFTTKVPQKY ENENVETVTK QAILNGSIVK ESTEAHGTIQ TEKVDEVIKE WEGSFFKDNP
       250        260        270        280        290        300
RLRKKSVSLR FDLHLAATDE GCLETKQDNL PDIEVRLIMR RSCSIPSIKP PSTAN
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2910	1	822.4663	-11.24	2	65.1	15.1	1	17-30	K.ILTRNQIETVLSTR.I	
1053	2	530.7772	-60.09	2	41.4	13.2	2	159-167	K.KDKKPTTSR.V	

Detailed Protein Report

Protein 198: **PREDICTED: collagen alpha-2(I) chain-like [Homo sapiens]**

Accession:	gi|530375734	**Score:**	28.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	28.8
Database Date:	2015-11-30	**pI:**	12.9
		Sequence Coverage [%]:	12.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAPFHLSHAP	AGARKVKLRH	PRKWSPSGSP	QPPAQLQPLE	APRLPGEVRT	SGRLATWFCR	LLARRSAAQR	KSKSRKDLNR
90	100	110	120	130	140	150	160
RVQSPLTPHS	FHYFSSQGIG	GGGGGRDKFA	GRLAWSNPRG	WDRPRGSGGA	LPRPEGDCGG	ARPPAGGAGR	WASPGAAGRW
170	180	190	200	210	220	230	240
SLPGRVCGAF	AQPAPCPHLT	SSPPRPLGGP	LRCAAQARSV	AARAVRPRSL	GQGPGAQGVG	RAGRERGRPS	TASGSARAGA
250	260	270	280				
ALPAAVRPRE	GPRGPSACAL	GRRRLCVGRP	GGPRGTD				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1759	1	881.8978	-107.69	2	50.4	14.1	1	204-221	R.AVRPRSLGQGPGAQGVGR.A	

Detailed Protein Report

Protein 199: protein fem-1 homolog C [Homo sapiens]

Accession:	gi|17864094	**Score:**	28.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	68.6
Database Date:	2015-11-30	**pI:**	8.5
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	4.5
		No. of unique Peptides:	2

Alias proteins:

Accession	Name	Description
gi|530380049	refseq_human (refseq_human_20140103.fasta)	PREDICTED: protein fem-1 homolog C isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MDLKTAVFNA	ARDGKLRLLT	KLLASKSKEE	VSSLISEKTN	GATPLLMAAR	YGHLDMVEFL	LEQCSASIEV	GGSVNFDGET
90	100	110	120	130	140	150	160
IEGAPPLWAA	SAAGHLKVVQ	SLLNHGASVN	NTTLTNSTPL	RAACFDGHLE	IVKYLVEHKA	DLEVSNRHGH	TCLMISCYKG
170	180	190	200	210	220	230	240
HKEIAQYLLE	KGADVNRKSV	KGNTALHDCA	ESGSLDIMKM	LLMYCAKMEK	DGYGMTPLLS	ASVTGHTNIV	DFLTHHAQTS
250	260	270	280	290	300	310	320
KTERINALEL	LGATFVDKKR	DLLGALKYWK	KAMNMRYSDR	TNIISKPVPQ	TLIMAYDYAK	EVNSAEELEG	LIADPDEMRM
330	340	350	360	370	380	390	400
QALLIRERIL	GPSHPDTSYY	IRYRGAVYAD	SGNFKRCINL	WKYALDMQQS	NLDPLSPMTA	SSLLSFAELF	SFMLQDRAKG
410	420	430	440	450	460	470	480
LLGTTVTFDD	LMGILCKSVL	EIERAIKQTQ	CPADPLQLNK	ALSIILHLIC	LLEKVPCTLE	QDHFKKQTIY	RFLKLHPRGK
490	500	510	520	530	540	550	560
NNFSPLHLAV	DKNTTCVGRY	PVCKFPSLQV	TAILIECGAD	VNVRDSDDNS	PLHIAALNNH	PDIMNLLIKS	GAHFDATNLH
570	580	590	600	610	620		
KQTASDLLDE	KEIAKNLIQP	INHTTLQCLA	ARVIVNHRIY	YKGHIPEKLE	TFVSLHR		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2809	1	676.8768	34.84	2	63.7	12.6	1	1-12	-.MDLKTAVFNAAR.D	Oxidation: 1
2824	1	912.9573	-30.84	2	63.8	15.5	1	425-440	R.AIKQTQCPADPLQLNK.A	Carbamidomethyl: 7

Detailed Protein Report

Protein 200: PREDICTED: general transcription factor 3C polypeptide 1 isoform X1 [Homo sapiens]

Accession:	gi|578828542	**Score:**	27.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	231.4
Database Date:	2015-11-30	**pI:**	6.3
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	1.6
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MDALESLLDE	VALEGLDGLC	LPALWSRLET	RVPPFPLPLE	PCTQEFLWRA	LATHPGISFY	EEPRERPDLQ	LQDRYEEIDL
90	100	110	120	130	140	150	160
ETGILESRRD	PVALEDVYPI	HMILENKDGI	QGSCRYFKER	KNITNDIRTK	SLQPRCTMVE	AFDRWGKKLI	IVASQAMRYR
170	180	190	200	210	220	230	240
ALIGQEGDPD	LKLPDFSYCI	LERLGRSRWQ	GELQRDLHTT	AFKVDAGKLH	YHRKILNKNG	LITMQSHVIR	LPTGAQQHSI
250	260	270	280	290	300	310	320
LLLLNRFHVD	RRSKYDILME	KLSVMLSTRT	NHIETLGKLR	EELGLCERTF	KRLYQYMLNA	GLAKVVSLRL	QEIHPECGPC
330	340	350	360	370	380	390	400
KTKKGTDVMV	RCLKLLKEFK	RNDHDDDEDE	EVISKTVPPV	DIVFERDMLT	QTYDLIERRG	TKGISQAEIR	VAMNVGKLEA
410	420	430	440	450	460	470	480
RMLCRLLQRF	KVVKGFMEDE	GRQRTTKYIS	CVFAEESDLS	RQYQREKARS	ELLTTVSLAS	MQEESLLPEG	EDTFLSESDS
490	500	510	520	530	540	550	560
EEERSSSKRR	GRGSQKDTRA	SANLRPKTQP	HHSTPTKGGW	KVVNLHPLKK	QPPSFPGAAE	ERACQSLASR	DSLLDTSSVS
570	580	590	600	610	620	630	640
EPNVSFVSHC	ADSNSGDIAV	IEEVRMENPK	ESSSSLKTGR	HSSGQDKPHE	TYRLLKRRNL	IIEAVTNLRL	IESLFTIQKM
650	660	670	680	690	700	710	720
IMDQEKQEGV	STKCCKKSIV	RLVRNLSEEG	LLRLYRTTVI	QDGIKKKVDL	VVHPSMDQND	PLVRSAIEQV	RFRISNSSTA
730	740	750	760	770	780	790	800
NRVKTSQPPV	PQGEAEEDSQ	GKEGPSGSGD	SQLSASSRSE	SGRMKKSDNK	MGITPLRNYH	PIVVPGLGRS	LGFLPKMPRL
810	820	830	840	850	860	870	880
RVVHMFLWYL	IYGHPASNTV	EKPSFISERR	TIKQESGRAG	VRPSSSGSAW	EACSEAPSKG	SQDGVTWEAE	VELATETVYV
890	900	910	920	930	940	950	960
DDASWMRYIP	PIPVHRDFGF	GWALVSDILL	CLPLSIFIQI	VQVSYKVDNL	EEFLNDPLKK	HTLIRFLPRP	IRQQLLYKRR
970	980	990	1000	1010	1020	1030	1040
YIFSVVENLQ	RLCYMGLLQF	GPTEKFQDKD	QVFIFLKKNA	VIVDTTICDP	HYNLARSSRP	FERRLYVLNS	MQDVENYWFD
1050	1060	1070	1080	1090	1100	1110	1120
LQCVCLNTPL	GVVRCPRVRK	NSSTDQGSDE	EGSLQKEQES	AMDKHNLERK	CAMLEYTTGS	REVVDEGLIP	GDGLGAAGLD
1130	1140	1150	1160	1170	1180	1190	1200
SSFYGHLKRN	WIWTSYIINQ	AKKENTAAEN	GLTVRLQTFL	SKRPMPLSAR	GEFPGEKSKR	LRYHDEADQS	ALQRMTRLRV
1210	1220	1230	1240	1250	1260	1270	1280
TWSMQEDGLL	VLCRIASNVL	NTKVKGPFVT	WQVVRDILHA	TFEESLDKTS	HSVGRRARYI	VKNPQAYLNY	KVCLAEVYQD
1290	1300	1310	1320	1330	1340	1350	1360
KALVGDFMNR	RGDYDDPKVC	ANEFKEFVEK	LKEKFSSALR	NSNLEIPDTL	QELFARYRVL	AIGDEKDQTR	KEDELNSVDD
1370	1380	1390	1400	1410	1420	1430	1440
IHFLVLQNLI	QSTLALSDSQ	MKSYQSFQTF	RLYREYKDHV	LVKAFMECQK	RSLVNRRRVN	HTLGPKKNRA	LPFVPMSYQL
1450	1460	1470	1480	1490	1500	1510	1520
SQTYYRIFTW	RFPSTICTES	FQFLDRMRAA	GKLDQPDRFS	FKDQDNNEPT	NDMVAFSLDG	PGGNCVAVLT	LFSLGLISVD
1530	1540	1550	1560	1570	1580	1590	1600
VRIPEQIIVV	DSSMVENEVI	KSLGKDGSLE	DDEDEEDDLD	EGVGGKRRSM	EVKPAQASHT	NYLLMRGYYS	PGIVSTRNLN
1610	1620	1630	1640	1650	1660	1670	1680
PNDSIVVNSC	QMKFQLRCTP	VPARLRPAAA	PLEELTMGTS	CLPDTFTKLI	NPQENTCSLE	EFVLQLELSG	YSPEDLTAAL
1690	1700	1710	1720	1730	1740	1750	1760
EILEAIIATG	CFGIDKEELR	RRFSALEKAG	GGRTRTFADC	IQALLEQHQV	LEVGGNTARL	VAMGSAWPWL	LHSVRLKDRE
1770	1780	1790	1800	1810	1820	1830	1840
DADIQREDPQ	ARPLEGSSSE	DSPPEGQAPP	SHSPRGTKRR	ASWASENGET	DAEGTQMTPA	KRPALQDSNL	APSLGPGAED
1850	1860	1870	1880	1890	1900	1910	1920
GAEAQAPSPP	PALEDTAAAG	AAQEDQEGVG	EFSSPGQEQL	SGQAQPPEGS	EDPRGFTESF	GAANISQAAR	ERDCESVCFI
1930	1940	1950	1960	1970	1980	1990	2000
GRPWRVVDGH	LNLPVCKGMM	EAMLYHIMTR	PGIPESSLLR	HYQGVLQPVA	VLELLQGLES	LGCIRKRWLR	KPRPVSLFST
2010	2020	2030	2040	2050			
PVVEEVEVPS	SLDESPMAFY	EPTLDCTLRL	GRVFPHEVNW	NKWIHL			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2710	1	941.5667	103.70	2	62.3	14.6	2	129-144	R.TKSLQPRCTMVEAFDR.W	
2192	1	1052.3938	-65.32	2	55.9	13.3	2	640-656	K.MIMDQEKQEGVSTKCCK.K	Carbamidomethyl: 15, 16; Oxidation: 1, 3

Detailed Protein Report

Protein 201: Na(+)/H(+) exchange regulatory cofactor NHE-RF3 isoform 2 [Homo sapiens]

Accession:	gi|318037207	**Score:**	27.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	44.6
Database Date:	2015-11-30	**pI:**	4.9
		Sequence Coverage [%]:	7.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MTSTFNPREC	KLSKQEGQNY	GFFLRIEKDT	EGHLVRVVEK	CSPAEKAGLQ	DGDRVLRING	VFVDKEEHMQ	VVDLVRKSGN
90	100	110	120	130	140	150	160
SVTLLVLDGD	SYEKAVKTRV	DLKELGQSQK	EQGLSDNILS	PVMNGGVQTW	TQPRLCYLVK	EGGSYGFSLK	TVQGQIIKDI
170	180	190	200	210	220	230	240
DSGSPAEEAG	LKNNDLVVAV	NGESVETLDH	DSVVEMIRKG	GDQTSLLVVD	KETDNMYRLA	HFSPFLYYQS	QELPNGSVKE
250	260	270	280	290	300	310	320
APAPTPTSLE	VSSPPDTTEE	VDHKPKLCRL	AKGENGYGFH	LNAIRGLPGS	FIKEVQKGGP	ADLAGLEDED	VIIEVNGVNV
330	340	350	360	370	380	390	400
LDEPYEKVVD	RIQSSGKNVT	LLVCGKKAYD	YFQAKKIPIV	SSLADPLDTP	PDSKEGIVVE	SNHDSHMAKE	RAHSTASHSS
410							
SNSEDTEM							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2317	1	951.3323	-147.80	2	57.4	13.6	2	37-54	R.VVEKCSPAEKAGLQDGDR.V	

Detailed Protein Report

Protein 202: 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:	2

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
1485	1	600.4356	169.47	2	47.3	15.9	1	14-25	R.GKPAQAGARTSR.A	
69	1	820.3460	-71.39	3	30.1	12.0	1	951-972	K.TLEAVLNFKYSGGPGHTEGYYR.N	

Detailed Protein Report

Protein 203: **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:	2

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
1559	1	977.1043	137.72	2	48.2	11.4	2	122-137	R.QDRSWFRASNETQTAR.S	
559	1	472.6946	-107.46	2	35.8	16.4	0	292-299	R.YTAYLTGR.V	

Detailed Protein Report

Protein 204: **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:	2

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
2332	1	952.9342	-37.03	2	57.6	11.4	1	232-247	R.SMLSTEDLLMSHTRQR.D	
2845	1	938.5013	-5.79	2	64.1	16.3	0	459-476	R.EGVDIALNDIATFLGTVK.E	

Detailed Protein Report

Protein 205: chromosome-associated kinesin KIF4A [Homo sapiens]

Accession:	gi|116686122	**Score:**	27.7
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:	1

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

Detailed Protein Report

Protein 206: PREDICTED: leucine-rich repeat-containing protein 16C isoform X1 [Homo sapiens]

Accession:	gi|530423607	**Score:**	27.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	148.1
Database Date:	2015-11-30	**pI:**	6.1
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.9
		No. of unique Peptides:	1

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2909	1	682.3620	-10.00	3	65.1	17.7	2	1177-1196	R.VQVMLQRIGVSRGSGGAEGK.R	Oxidation: 4

Detailed Protein Report

Protein 207: PREDICTED: midasin isoform X3 [Homo sapiens]

Accession:	gi|578812559	**Score:**	27.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	627.0
Database Date:	2015-11-30	**pI:**	5.4
		Sequence Coverage [%]:	0.3
		No. of unique Peptides:	1

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

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
558	1	512.6910	-181.41	2	35.4	13.3	2	1688-1695	K.IYDRMKAK.E	

Detailed Protein Report

Protein 208: protein FAM65B isoform 2 [Homo sapiens]

Accession:	gi|14277690	**Score:**	27.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	65.7
Database Date:	2015-11-30	**pI:**	5.1
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	4.7
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MLVGSQSFSP	GGPNGIIRSQ	SFAGFSGLQE	RRSRCNSFIE	NSSALKKPQA	KLKKMHNLGH	KNNNPPKEPQ	PKRVEEVYRA
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
LKNGLDEYLE	VHQTELDKLT	AQLKDMKRNS	RLGVLYDLDK	QIKTIERYMR	RLEFHISKVD	ELYEAYCIQR	RLQDGASKMK
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
QAFATSPASK	AARESLTEIN	RSFKEYTENM	CTIEVELENL	LGEFSIKMKG	LAGFARLCPG	DQYEIFMKYG	RQRWKLKGKI
250	**260**	**270**	**280**	**290**	**300**	**310**	**320**
EVNGKQSWDG	EETVFLPLIV	GFISIKVTEL	KGLATHILVG	SVTCETKELF	AARPQVVAVD	INDLGTIKLN	LEITWYPFDV
330	**340**	**350**	**360**	**370**	**380**	**390**	**400**
EDMTASSGAG	NKAAALQRRM	SMYSQGTPET	PTFKDHSFFS	NLPDDIFENG	KAAEEKMPLS	LSFSDLPNGD	CALTSHSTGS
410	**420**	**430**	**440**	**450**	**460**	**470**	**480**
PSNSTNPEIT	ITPAEFNLSS	LASQNEGMDD	TSSASSRNSL	GEGQEPKSHL	KEEDPEEPRK	PASAPSEACR	RQSSGAGAEH
490	**500**	**510**	**520**	**530**	**540**	**550**	**560**
LFLENDVAEA	LLQESEEASE	LKPVELDTSE	GNITKQLVKR	LTSAEVPMAT	DRLLSEGSVG	GESEGCRSFL	DGSLEDAFNG
570	**580**	**590**	**600**				
LLLALEPHKE	QYKEFQDLNQ	EVMNLDDILK	K				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1567	1	994.1375	-4.03	3	47.9	10.8	2	520-547	K.RLTSAEVPMATDRLLSEGSVGGESEGCR.S	Carbamidomethyl: 27; Oxidation: 9
625	1	740.4433	138.33	2	36.7	16.9	0	533-547	R.LLSEGSVGGESEGCR.S	

Detailed Protein Report

Protein 209: **queuine tRNA-ribosyltransferase [Homo sapiens]**

Accession:	gi|13654276	**Score:**	27.7
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

WD:WU **Median:** 0.94 **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	WD:WU 0.94

Detailed Protein Report

Protein 210: glyoxalase domain-containing protein 4 [Homo sapiens]

Accession:	gi|217330598	**Score:**	27.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	33.2
Database Date:	2015-11-30	**pI:**	5.3
		Sequence Coverage [%]:	8.4
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 0.86 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MAARRALHFV	FKVGNRFQTA	RFYRDVLGMK	VLRHEEFEEG	CKAACNGPYD	GKWSKTMVGF	GPEDDHFVAE	LTYNYGVGDY
90	100	110	120	130	140	150	160
KLGNDFMGIT	LASSQAVSNA	RKLEWPLTEV	AEGVFETEAP	GGYKFYLQNR	SLPQSDPVLK	VTLAVSDLQK	SLNYWCNLLG
170	180	190	200	210	220	230	240
MKIYEKDEEK	QRALLGYADN	QCKLELQGVK	GGVDHAAAFG	RIAFSCPQKE	LPDLEDLMKR	ENQKILTPLV	SLDTPGKATV
250	260	270	280	290	300		
QVVILADPDG	HEICFVGDEA	FRELSKMDPE	GSKLLDDAMA	ADKSDEWFAK	HNKPKASG		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1097	3	631.1089	141.12	3	42.0	17.0	2	6-21	R.ALHFVFKVGNRFQTAR.F		WD:WU 0.86

Detailed Protein Report

Protein 211: 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 212: **PREDICTED: leucine-rich PPR motif-containing protein, mitochondrial isoform X2 [Homo sapiens]**

Accession:	gi|578802653	**Score:**	27.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	119.1
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
MAALLRSARW	LLRAGAAPRL	PLSLRLLPGG	PGRLHAASYL	PAARAGPVAG	GLLSPARLYA	IAAKEKDIQE	ESTFSSRKIS
90	100	110	120	130	140	150	160
NQFDWALMRL	DLSVRRTGRI	PKKLLQKVFN	DTCRSGGLGG	SHALLLLRSC	GSLLPELKLE	ERTEFAHRIW	DTLQKLGAVY
170	180	190	200	210	220	230	240
DVSHYNALLK	VYLQNEYKFS	PTDFLAKMEE	ANIQPNRVTY	QRLIASYCNV	GDIEGASKIL	GFMKTKDLPV	TEAVFSALVT
250	260	270	280	290	300	310	320
GHARAGDMEN	AENILTVMRD	AGIEPGPDTY	LALLNAYAEK	GDIDHVKQTL	EKVEKSELHL	MDRDLLQIIF	SFSKAGYPQY
330	340	350	360	370	380	390	400
VSEILEKVTC	ERRYIPDAMN	LILLLVTEKL	EDVALQILLA	CPVSKEDGPS	VFGSFFLQHC	VTMNTPVEKL	TDYCKKLKEV
410	420	430	440	450	460	470	480
QMHSFPLQFT	LHCALLANKT	DLAKALMKAV	KEEGFPIRPH	YFWPLLVGRR	KEKNVQGIIE	ILKGMQELGV	HPDQETYTDY
490	500	510	520	530	540	550	560
VIPCFDSVNS	ARAILQENGC	LSDSDMFSQA	GLRSEAANGN	LDFVLSFLKS	NTLPISLQSI	RSSLLLGFRR	SMNINLWSEI
570	580	590	600	610	620	630	640
TELLYKDGRY	CQEPRGPTEA	VGYFLYNLID	SMSDSEVQAK	EEHLRQYFHQ	LEKMNVKIPE	NIYRGIRNLL	ESYHVPELIK
650	660	670	680	690	700	710	720
DAHLLVESKN	LDFQKTVQLT	SSELESTLET	LKAENQPIRD	VLKQLILVLC	SEENMQKALE	LKAKYESDMV	TGGYAALINL
730	740	750	760	770	780	790	800
CCRHDKVEDA	LNLKEEFDRL	DSSAVLDTGK	YVGLVRVLAK	HGKLQDAINI	LKEMKEKDVL	IKDTTALSFF	HMLNGAALRG
810	820	830	840	850	860	870	880
EIETVKQLHE	AIVTLGLAEP	STNISFPLVT	VHLEKGDLST	ALEVAIDCYE	KYKVLPRIHD	VLCKLVEKGE	TDLIQKAMDF
890	900	910	920	930	940	950	960
VSQEQGEMVM	LYDLFFAFLQ	TGNYKEAKKI	IETPGIRARS	ARLQWFCDRC	VANNQVETLE	KLVELTQKLF	ECDRDQMYYN
970	980	990	1000	1010	1020	1030	1040
LLKLYKINGD	WQRADAVWNK	IQEENVIPRE	KTLRLLAEIL	REGNQEVPFD	VPELWYEDEK	HSLNSSSAST	TEPDFQKDIL
1050	1060						
IACRLNQKKR	GI						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
235	2	627.3257	-99.42	2	32.1	15.2	2	909-919	K.KIIETPGIRAR.S	

Detailed Protein Report

Protein 213: 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 214: dehydrogenase/reductase SDR family member on chromosome X precursor [Homo sapiens]

Accession:	gi|193804850	**Score:**	27.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	36.4
Database Date:	2015-11-30	**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 215: ephrin type-A receptor 3 isoform b precursor [Homo sapiens]

Accession:	gi|32967314	**Score:**	27.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	60.9
Database Date:	2015-11-30	**pI:**	5.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDCQLSILLL	LSCSVLDSFG	ELIPQPSNEV	NLLDSKTIQG	ELGWISYPSH	GWEEISGVDE	HYTPIRTYQV	CNVMDHSQNN
90	100	110	120	130	140	150	160
WLRTNWVPRN	SAQKIYVELK	FTLRDCNSIP	LVLGTCKETF	NLYYMESDDD	HGVKFREHQF	TKIDTIAADE	SFTQMDLGDR
170	180	190	200	210	220	230	240
ILKLNTEIRE	VGPVNKKGFY	LAFQDVGACV	ALVSVRVYFK	KCPFTVKNLA	MFPDTVPMDS	QSLVEVRGSC	VNNSKEEDPP
250	260	270	280	290	300	310	320
RMYCSTEGEW	LVPIGKCSCN	AGYEERGFMC	QACRPGFYKA	LDGNMKCAKC	PPHSSTQEDG	SMNCRCENNY	FRADKDPPSM
330	340	350	360	370	380	390	400
ACTRPPSSPR	NVISNINETS	VILDWSWPLD	TGGRKDVTFN	IICKKCGWNI	KQCEPCSPNV	RFLPRQFGLT	NTTVTVTDLL
410	420	430	440	450	460	470	480
AHTNYTFEID	AVNGVSELSS	PPRQFAAVSI	TTNQAAPSPV	LTIKKDRTSR	NSISLSWQEP	EHPNGIILDY	EVKYYEKQEQ
490	500	510	520	530	540		
ETSYTILRAR	GTNVTISSLK	PDTIYVFQIR	ARTAAGYGTN	SRKFEFETSP	DCMYYFNAV		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2832	2	945.9883	67.92	2	64.0	16.1	1	366-381	K.CGWNIKQCEPCSPNVR.F	Carbamidomethyl: 8

Detailed Protein Report

Protein 216: **PREDICTED: uncharacterized protein LOC101927628 [Homo sapiens]**

Accession:	gi|578827891	**Score:**	27.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	109.0
Database Date:	2015-11-30	**pI:**	12.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.8
		No. of unique Peptides:	1

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
2316	1	937.2798	-119.93	2	57.4	14.7	1	951-967	R.NSSSQSCCPTCTRVGMR.R	Carbamidomethyl: 7

Detailed Protein Report

Protein 217: PREDICTED: insulin-like growth factor 1 receptor isoform X2 [Homo sapiens]

Accession:	gi|530407102	**Score:**	27.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	141.1
Database Date:	2015-11-30	**pI:**	5.4
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	2.4
		No. of unique Peptides:	2

Quantitation

WD:WU **Median:** 0.98 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MTNLKDIGLY	NLRNITRGAI	RIEKNADLCY	LSTVDWSLIL	DAVSNNYIVG	NKPPKECGDL	CPGTMEEKPM	CEKTTINNEY
90	100	110	120	130	140	150	160
NYRCWTTNRC	QKMCPSTCGK	RACTENNECC	HPECLGSCSA	PDNDTACVAC	RHYYYAGVCV	PACPPNTYRF	EGWRCVDRDF
170	180	190	200	210	220	230	240
CANILSAESS	DSEGFVIHDG	ECMQECPSGF	IRNGSQSMYC	IPCEGPCPKV	CEEEKKTKTI	DSVTSAQMLQ	GCTIFKGNLL
250	260	270	280	290	300	310	320
INIRRGNNIA	SELENFMGLI	EVVTGYVKIR	HSHALVSLSF	LKNLRLILGE	EQLEGNYSFY	VLDNQNLQQL	WDWDHRNLTI
330	340	350	360	370	380	390	400
KAGKMYFAFN	PKLCVSEIYR	MEEVTGTKGR	QSKGDINTRN	NGERASCESD	VLHFTSTTTS	KNRIIITWHR	YRPPDYRDLI
410	420	430	440	450	460	470	480
SFTVYYKEAP	FKNVTEYDGQ	DACGSNSWNM	VDVDLPPNKD	VEPGILLHGL	KPWTQYAVYV	KAVTLTMVEN	DHIRGAKSEI
490	500	510	520	530	540	550	560
LYIRTNASVP	SIPLDVLSAS	NSSSQLIVKW	NPPSLPNGNL	SYYIVRWQRQ	PQDGYLYRHN	YCSKDKIPIR	KYADGTIDIE
570	580	590	600	610	620	630	640
EVTENPKTEV	CGGEKGPCCA	CPKTEAEKQA	EKEEAEYRKV	FENFLHNSIF	VPRPERKRRD	VMQVANTTMS	SRSRNTTAAD
650	660	670	680	690	700	710	720
TYNITDPEEL	ETEYPFFESR	VDNKERTVIS	NLRPFTLYRI	DIHSCNHEAE	KLGCSASNFV	FARTMPAEGA	DDIPGPVTWE
730	740	750	760	770	780	790	800
PRPENSIFLK	WPEPENPNGL	ILMYEIKYGS	QVEDQRECVS	RQEYRKYGGA	KLNRLNPGNY	TARIQATSLS	GNGSWTDPVF
810	820	830	840	850	860	870	880
FYVQAKTGYE	NFIHLIIALP	VAVLLIVGGL	VIMLYVFHRK	RNNSRLGNGV	LYASVNPEYF	SAADVYVPDE	WEVAREKITM
890	900	910	920	930	940	950	960
SRELGQGSFG	MVYEGVAKGV	VKDEPETRVA	IKTVNEAASM	RERIEFLNEA	SVMKEFNCHH	VVRLLGVVSQ	GQPTLVIMEL
970	980	990	1000	1010	1020	1030	1040
MTRGDLKSYL	RSLRPEMENN	PVLAPPSLSK	MIQMAGEIAD	GMAYLNANKF	VHRDLAARNC	MVAEDFTVKI	GDFGMTRDIY
1050	1060	1070	1080	1090	1100	1110	1120
ETDYYRKGGK	GLLPVRWMSP	ESLKDGVFTT	YSDVWSFGVV	LWEIATLAEQ	PYQGLSNEQV	LRFVMEGGLL	DKPDNCPDML
1130	1140	1150	1160	1170	1180	1190	1200
FELMRMCWQY	NPKMRPSFLE	IISSIKEEME	PGFREVSFYY	SEENKLPEPE	ELDLEPENME	SVPLDPSASS	SSLPLPDRHS
1210	1220	1230	1240	1250			
GHKAENGPGP	GVLVLRASFD	ERQPYAHMNG	GRKNERALPL	PQSSTC			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1849	2	1045.0301	118.60	2	51.5	16.2	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		WD:WU 0.98

Detailed Protein Report

Protein 218: **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

Quantitation

WD:WU **Median:** 3.90 **CV:** 0.00 % **No. of Peptides:** 1

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	Ratios
2047	4	625.2681	-128.78	2	54.2	13.8	1	259-269	K.QALKAGETIYR.Q		WD:WU 3.90
2581	2	836.1729	-298.97	1	60.5	13.6	1	298-304	R.RLAMCAR.K	Oxidation: 4	

Detailed Protein Report

Protein 219: PREDICTED: zinc finger protein 462 isoform X10 [Homo sapiens]

Accession:	gi|578817729	**Score:**	27.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	192.3
Database Date:	2015-11-30	**pI:**	6.4
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.9
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MEVLQCDGCD FRAPSYEDLK AHIQDVHTAF LQPTDVAEDN VNELRCGSVN ASNQTEVEFS SIKDEFAIAE DLSGQNATSL
        90        100        110        120        130        140        150        160
GTGGYYGHSP GYYGQHIAAN PKPTNKFFQC KFCVRYFRSK NLLIEHTRKV HGAQAEGSSS GPPVPGSLNY NIMMHEGFGK
       170        180        190        200        210        220        230        240
VFSCQFCTYK SPRRARIIKH QKMYHKNNLK ETTAPPPAPA PMPDPVVPPV SLQDPCKELP AEVVERSILE SMVKPLTKSR
       250        260        270        280        290        300        310        320
GNFCCEWCSY QTPRRERWCD HMMKKHRSMV KILSSLRQQQ EGTNLPDVPN KSAPSPTSNS TYLTMNAASR EIPNTTVSNF
       330        340        350        360        370        380        390        400
RGSMGNSIMR PNSSASKFSP MSYPQMKPKS PHNSGLVNLT ERSRYGMTDM TNSSADLETN SMLNDSSSDE ELNEIDSENG
       410        420        430        440        450        460        470        480
LSAMDHQTSG LSAEQLMGSD GNKLLETKGI PFRRFMNRFQ CPFCPFLTMH RRSISRHIEN IHLSGKTAVY KCDECPFTCK
       490        500        510        520        530        540        550        560
SSLKLGAHKQ CHTGTTSDWD AVNSQSESIS SSLNEGVVSY ESSSINGRKS GVMLDPLQQQ QPPQPPPPPP PPPPSQPQPL
       570        580        590        600        610        620        630        640
QQPQPPQLQP PHQVPPQPQT QPPPTQQPQP PTQAAPLHPY KCTMCNYSTT TLKGLRVHQQ HKHSFCDNLP KFEGQPSSLP
       650        660        670        680        690        700        710        720
LENETDSHPS SSNTVKKSQT SILGLSSKNN FVAKASRKLA NDFPLDLSPV KKRTRIDEIA SNLQSKINQT KQQEDAVINV
       730        740        750        760        770        780        790        800
EDDEEEEEDN EVEIEVELDR EEEPTEPIIE VPTSFSAQQI WVRDTSEPQK EPNFRNITHD YNATNGAEIE LTLSEDEEDY
       810        820        830        840        850        860        870        880
YGSSTNLKDH QVSNTALLNT QTPIYGTEHN SENTDFGDSG RLYYCKHCDF NNKSARSVST HYQRMHPYIK FSFRYILDPN
       890        900        910        920        930        940        950        960
DHSAVYRCLE CYIDYTNFED LQQHYGEHHP EAMNVLNFDH SDLIYRCRFC SYTSPNVRSL MPHYQRMHPT VKINNAMIFS
       970        980        990       1000       1010       1020       1030       1040
SYVVEQQEGL NTESQTLREI LNSAPKNMAT STPVARGGGL PATFNKNTPK TFTPECENQK DPLVNTVVVY DCDVCSFASP
      1050       1060       1070       1080       1090       1100       1110       1120
NMHSVLVHYQ KKHPEEKASY FRIQKTMRMV SVDRGSALSQ LSFEPFGHLE EVPKIKERKV VGYKCKFCVE VHPTLRAICN
      1130       1140       1150       1160       1170       1180       1190       1200
HLRKHVQYGN VPAVSAAVKQ EADDPAHLFL DGLEAAKDAS GALVGRVDGE HCLLDGMLED ETRPGGYHCS QCDRVLMSMQ
      1210       1220       1230       1240       1250       1260       1270       1280
GLRSHERSHL ALAMFTREDK YSCQYCSFVS AFRHNLDRHM QTHHGHHKPF RCKLCSFKSS YNSRLKTHIL KAHAGEHAYK
      1290       1300       1310       1320       1330       1340       1350       1360
CSWCSFSTMT ISQLKEHSLK VHGKALTLPR PRIVSLLSSH SHHSSQKATP AEEVEDSNDS SYSEPPDVQQ QLNHYQSAAL
      1370       1380       1390       1400       1410       1420       1430       1440
ARNNSRVSPV PLSGAAAGTE QKTEAVLHCE FCEFSSGYIQ SIRRHYRDKH GGKKLFKCKD CSFYTGFKSA FTMHVEAGHS
      1450       1460       1470       1480       1490       1500       1510       1520
AVPEEGPKDL RCPLCLYHTK YKRNMIDHIV LHREERVVPI EVCRSKLSKY LQGVVFRCDK CTFTCSSDES LQQHIEKHNE
      1530       1540       1550       1560       1570       1580       1590       1600
LKPYKCQLCY YETKHTEELD SHLRDEHKVS RNFELVGRVN LDQLEQMKEK MESSSSDDED KEEEMNSKAE DRELMRFSDH
      1610       1620       1630       1640       1650       1660       1670       1680
GAALNTEKRF PCEFCGRAFS QGSEWERHVL RHGMALNDTK QVSREEIHPK EIMENSVKMP SIEEKEDDEA IGIDFSLKNE
      1690       1700       1710
TVAICVVTAD KSLLENAEAK KE
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2878	1	869.4050	22.02	2	64.7	13.3	0	1281-1295	K.CSWCSFSTMTISQLK.E	Oxidation: 9

Detailed Protein Report

Protein 220: ankyrin repeat and fibronectin type-III domain-containing protein 1 [Homo sapiens]

Accession:	gi|114842396	**Score:**	27.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	87.5
Database Date:	2015-11-30	**pI:**	9.5
		Sequence Coverage [%]:	4.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEASLTRRLL	FKDRHFTCSK	IIGRRFACFA	QRLSHRRKQS	QCDLLNESTG	QLPTTCSSAA	SNSINWNCRV	KMTQQMQNLH
90	100	110	120	130	140	150	160
LCQSKKHSAP	SSPNAAKRLY	RNLSEKLKGS	HSSFDEAYFR	TRTDRLSLRK	TSVNFQGNEA	MFEAVEQQDM	DAVQILLYQY
170	180	190	200	210	220	230	240
TPEELDLNTP	NSEGLTPLDI	AIMTNNVPIA	RILLRTGARE	SPHFVSLESR	AMHLNTLVQE	AQERVSELSA	QVENEGFTLD
250	260	270	280	290	300	310	320
NTEKEKQLKA	WEWRYRLYRR	MKTGFEHARA	PEMPTNVCLM	VTSSTSLTVS	FQEPLSVNAA	VVTRYKVEWS	MSEDFSPLAG
330	340	350	360	370	380	390	400
EIIMDNLQTL	RCTITGLTMG	QQYFVQVSAY	NMKGWGPAQT	TTPACASPSN	WKDYDDREPR	HKGQSEVLEG	LLQQVRALHQ
410	420	430	440	450	460	470	480
HYSCRESTKL	QTTGRKQSVS	RSLKHLFHSS	NKFVKTLKRG	LYIAVIFYYK	DNILVTNEDQ	VPIVEIDDSH	TSSITQDFLW
490	500	510	520	530	540	550	560
FTKLSCMWED	IRWLRQSIPI	SSSSSTVLQT	RQKMLAATAQ	LQNLLGTHNL	GRVYYEPIKD	RHGNILIVTI	REVEMLYSFF
570	580	590	600	610	620	630	640
NGKWMQISKL	QSQRKSLSTP	EEPTALDILL	ITIQDILSYH	KRSHQRLFPG	LYLGYLKLCS	SVDQIKVLVT	QKLPNILCHV
650	660	670	680	690	700	710	720
KIRENNNISR	EEWEWIQKLS	GSESMESVDH	TSDCPMQLFF	YELQMAVKAL	LQQINIPLHQ	ARNFRLYTQE	VLEMGHNVSF
730	740	750	760	770			
LLLLPASDDV	CTAPGQNNPY	TPHSGFLNLP	LQMFELGIVA	CFT			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2705	1	716.0445	-19.86	3	62.3	12.3	1	493-511	R.WLRQSIPISSSSSTVLQTR.Q	

Detailed Protein Report

Protein 221: **PREDICTED: rho guanine nucleotide exchange factor 10-like protein isoform X17 [Homo sapiens]**

Accession:	gi|578799376	**Score:**	27.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	114.3
Database Date:	2015-11-30	**pI:**	6.5
		Sequence Coverage [%]:	1.5
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MSLSTFAQMT	QLMKAAKSGT	KDGLEKTRMA	VMRKVSFLHR	KDVLGDSEEE	DMGLLEVSVS	DIKPPAPELG	PMPEGLSPQQ
90	100	110	120	130	140	150	160
VVRRHILGSI	VQSEGSYVES	LKRILQDYRN	PLMEMEPKAL	SARKCQVVFF	RVKEILHCHS	MFQIALSSRV	AEWDSTEKIG
170	180	190	200	210	220	230	240
DLFVASFSKS	MVLDVYSDYV	NNFTSAMSII	KKACLTKPAF	LEFLKRRQVC	SPDRVTLYGL	MVKPIQRFPQ	FILLLQDMLK
250	260	270	280	290	300	310	320
NTPRGHPDRL	SLQLALTELE	TLAEKLNEQK	RLADQVAEIQ	QLTKSVSDRS	SLNKLLTSGQ	RQLLLCETLT	ETVYGDRGQL
330	340	350	360	370	380	390	400
IKSKERRVFL	LNDMLVCANI	NFKGQLEISS	LVPLGPKYVV	KWNTALPQVQ	VVEVGQDGGT	YDKDNVLIQH	SGAKKASASG
410	420	430	440	450	460	470	480
QAQNKVYLGP	PRLFQELQDL	QKDLAVVEQI	TLLISTLHGT	YQNLNMTVAQ	DWCLALQRLM	RVKEEEIHSA	NKCRLRLLLP
490	500	510	520	530	540	550	560
GKPDKSGRPI	SFMVVFITPN	PLSKISWVNR	LHLAKIGLRE	ENQPGWLCPD	EDKKSKAPFW	CPILACCIPA	FSSRALSLQL
570	580	590	600	610	620	630	640
GALVHSPVNC	PLLGFSAVST	SLPQGYLWVG	GGQEGAGGQV	EIFSLNRPSP	RTVKSFPLAA	PVLCMEYIPE	LEEEAESRDE
650	660	670	680	690	700	710	720
SPTVADPSAT	VHPTICLGLQ	DGSILLYSSV	DTGTQCLVSC	RSPGLQPVLC	LRHSPFHLLA	GLQDGTLAAY	PRTSGGVLWD
730	740	750	760	770	780	790	800
LESPPVCLTV	GPGPVRTLLS	LEDAVWASCG	PRVTVLEATT	LQPQQSFEAH	QDEAVSVTHM	VKAGSGVWMA	FSSGTSIRLF
810	820	830	840	850	860	870	880
HTETLEHLQE	INIATRTTFL	LPGQKHLCVT	SLLICQGLLW	VGTDQGVIVL	LPVPRLEGIP	KITGKGMVSL	NGHCGPVAFL
890	900	910	920	930	940	950	960
AVATSILAPD	ILRSDQEEAE	GPRAEEDKPD	GQAHEPMPDS	HVGRELTRKK	GILLQYRLRS	TAHLPGPLLS	MREPAPADGA
970	980	990	1000	1010	1020	1030	1040
ALEHSEEDGS	IYEMADDPDI	WVRSRPCARD	AHRKEICSVA	IISGGQGYRN	FGSALGSSGR	QAPCGETDST	LLIWQVPLML
1050							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2999	4	840.9055	-41.65	2	66.4	15.4	1	994-1009	R.KEICSVAIISGGQGYR.N	
63	1	518.2825	34.79	3	30.0	11.8	0	995-1009	K.EICSVAIISGGQGYR.N	

Detailed Protein Report

Protein 222: PREDICTED: putative GTP-binding protein 6 isoform X1 [Homo sapiens]

Accession:	gi|578837777	**Score:**	27.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	42.1
Database Date:	2015-11-30	**pI:**	10.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	7.2
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 0.84 **CV:** 0.00 % **No. of Peptides:** 1

Alias proteins:

Accession	**Name**	**Description**
gi|578838996	refseq_human (refseq_human_20140103.fasta)	PREDICTED: putative GTP-binding protein 6 isoform X2 [Homo sapiens]

10	20	30	40	50	60	70	80
MVVSTKTPDR	KLIFGKGNFE	HLTEKIRGSP	DITCVFLNVE	RMAAPTKKEL	EAAWGVEVFD	RFTVVLHIFR	CNARTKEARL
90	100	110	120	130	140	150	160
QVALAEMPLH	RSNLKRDVAH	LYRGVGSRYI	MGSGESFMQL	QQRLLREKEA	KIRKALDRLR	KKRHLLRRQR	TRREFPVISV
170	180	190	200	210	220	230	240
VGYTNCGKTT	LIKALTGDAA	IQPRDQLFAT	LDVTAHAGTL	PSRMTVLYVD	TIGFLSQLPH	GLIESFSATL	EDVAHSDLIL
250	260	270	280	290	300	310	320
HVRDVSHPEA	ELQKCSVLST	LRGLQLPAPL	LDSMVEVHNK	VDLVPGYSPT	EPNVVPVSAL	RGHGLQELKA	ELDAAVLKAT
330	340	350	360	370	380		
GRQILTLRVR	LAGAQLSWLY	KEATVQEVDV	IPEDGAADVR	VIISNSAYGK	FRKLFPG		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2802	1	913.4638	-3.45	2	63.6	10.3	1	153-168	R.REFPVISVVGYTNCGK.T	Carbamidomethyl: 14	WD:WU 0.84

Detailed Protein Report

Protein 223: poly [ADP-ribose] polymerase 8 isoform 2 [Homo sapiens]

Accession:	gi|295844832	**Score:**	27.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	91.1
Database Date:	2015-11-30	**pI:**	9.5
		Sequence Coverage [%]:	3.1
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 1.25 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MGMCSRQERI	QKDIDVVIQK	SRAEKDCLFA	DFRYSDSTFT	FTYVGGPRSV	SYSVHVSEDY	PDNTYVSSSE	NDEDVLVTTE
90	100	110	120	130	140	150	160
PIPVIFHRIA	TELRKTNDIN	CCLSIKSKLQ	KENGEESRQN	STVEEDSEGD	NDSEEFYYGG	QVNYDGELHK	HPQLEADLSA
170	180	190	200	210	220	230	240
VREIYGPHAV	SLREYGAIDD	VDIDLHIDVS	FLDEEIAVAW	EVIRTEPIIV	RLHCSLTQYL	NGPVPTVDVF	QISTKERFGL
250	260	270	280	290	300	310	320
GHQLKKIMQT	FVTQQWKQSK	EKSNCLHNKK	LSEKKVKSPL	HLFSTLRRSP	SYPPPGCGKS	KSKLKSEQDG	ISKTHKLLRR
330	340	350	360	370	380	390	400
TCSSTVKTDD	VCVTKSHRTF	GRSLSSDPRA	EQAMTAIKSH	KLLNRPCPAA	VKSEECLTLK	SHRLLTRSCS	GDPRCEHNTN
410	420	430	440	450	460	470	480
LKPHKLLSRS	YSSNLRMEEL	YGLKNHKLLS	KSYSSAPKSS	KTELFKEPNA	EGRRLSLTSG	LIGILTPSSS	SSSQLAPNGA
490	500	510	520	530	540	550	560
KCIPVRDRGF	LVQTIEFAEQ	RIPVLNEYCV	VCDEPHVFQN	GPMLRPTVCE	RELCVFAFQT	LGVMNEAADE	IATGAQKKNY
570	580	590	600	610	620	630	640
DRVMKALDSI	TSIREMTQAP	YLEIKKQMDK	QDPLAHPLLQ	WVISSNRSHI	VKLPVNRQLK	FMHTPHQFLL	LSSPPAKESN
650	660	670	680	690	700	710	720
FRAAKKLFGS	TFAFHGSHIE	NWHSILRNGL	VVASNTRLQL	HGAMYGSGIY	LSPMSSISFG	YSGMNKKQKV	SAKDEPASSS
730	740	750	760	770	780	790	800
KSSNTSQSQK	KGQQSQFLQS	RNLKCIALCE	VITSSDLHKH	GEIWVVPNTD	HVCTRFFFVY	EDGQVGDANI	NTQEGGIHKE
810	820						
ILRVIGNQTA	TG						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1355	1	719.8571	2.88	2	45.3	12.6	1	96-108	K.TNDINCCLSIKSK.L		WD:WU 1.25

Detailed Protein Report

Protein 224: **matrix metalloproteinase-27 precursor [Homo sapiens]**

Accession:	gi|73808268	**Score:**	27.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	59.0
Database Date:	2015-11-30	**pI:**	9.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.3
		No. of unique Peptides:	2

```
        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
2670	1	625.3045	-14.98	2	61.7	12.8	1	376-386	K.IDAAVCDKTTR.K	Carbamidomethyl: 6
2792	4	626.8670	-20.54	2	63.5	14.4	1	414-424	R.VVKHFPGISIR.V	

Detailed Protein Report

Protein 225: 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 226: nuclear receptor corepressor 1 isoform 1 [Homo sapiens]

Accession:	gi|22538461	**Score:**	27.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	270.0
Database Date:	2015-11-30	**pI:**	6.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.5
		No. of unique Peptides:	2

Quantitation

WD:WU	**Median:** 0.92	**CV:** 0.00 %	**No. of Peptides:** 1

Detailed Protein Report

10	20	30	40	50	60	70	80
MSSSGYPPNQ	GAFSTEQSRY	PPHSVQYTFP	NTRHQQEFAV	PDYRSSHLEV	SQASQLLQQQ	QQQQLRRRPS	LLSEFHPGSD
90	100	110	120	130	140	150	160
RPQERRTSYE	PFHPGPSPVD	HDSLESKRPR	LEQVSDSHFQ	RVSAAVLPLV	HPLPEGLRAS	ADAKKDPAFG	GKHEAPSSPI
170	180	190	200	210	220	230	240
SGQPCGDDQN	ASPSKLSKEE	LIQSMDRVDR	EIAKVEQQIL	KLKKKQQQLE	EEAAKPPEPE	KPVSPPPVEQ	KHRSIVQIIY
250	260	270	280	290	300	310	320
DENRKKAEEA	HKIFEGLGPK	VELPLYNQPS	DTKVYHENIK	TNQVMRKKLI	LFFKRRNHAR	KQREQKICQR	YDQLMEAWEK
330	340	350	360	370	380	390	400
KVDRIENNPR	RKAKESKTRE	YYEKQFPEIR	KQREQQERFQ	RVGQRGAGLS	ATIARSEHEI	SEIIDGLSEQ	ENNEKQMRQL
410	420	430	440	450	460	470	480
SVIPPMMFDA	EQRRVKFINM	NGLMEDPMKV	YKDRQFMNVW	TDHEKEIFKD	KFIQHPKNFG	LIASYLERKS	VPDCVLYYYL
490	500	510	520	530	540	550	560
TKKNENYKAL	VRRNYGKRRG	RNQQIARPSQ	EEKVEEKEED	KAEKTEKKEE	EKKDEEEKDE	KEDSKENTKE	KDKIDGTAEE
570	580	590	600	610	620	630	640
TEEREQATPR	GRKTANSQGR	RKGRITRSMT	NEAAAASAAA	AAATEEPPPP	LPPPPEPIST	EPVETSRWTE	EEMEVAKKGL
650	660	670	680	690	700	710	720
VEHGRNWAAI	AKMVGTKSEA	QCKNFYFNYK	RRHNLDNLLQ	QHKQKTSRKP	REERDVSQCE	SVASTVSAQE	DEDIEASNEE
730	740	750	760	770	780	790	800
ENPEDSEVEA	VKPSEDSPEN	ATSRGNTEPA	VELEPTTETA	PSTSPSLAVP	STKPAEDESV	ETQVNDSISA	ETAEQMDVDQ
810	820	830	840	850	860	870	880
QEHSAEEGSV	CDPPPATKAD	SVDVEVRVPE	NHASKVEGDN	TKERDLDRAS	EKVEPRDEDL	VVAQQINAQR	PEPQSDNDSS
890	900	910	920	930	940	950	960
ATCSADEDVD	GEPERQRMFP	MDSKPSLLNP	TGSILVSSPL	KPNPLDLPQL	QHRAAVIPPM	VSCTPCNIPI	GTPVSGYALY
970	980	990	1000	1010	1020	1030	1040
QRHIKAMHES	ALLEEQRQRQ	EQIDLECRSS	TSPCGTSKSP	NREWEVLQPA	PHQVITNLPE	GVRLPTTRPT	RPPPPLIPSS
1050	1060	1070	1080	1090	1100	1110	1120
KTTVASEKPS	FIMGGSISQG	TPGTYLTSHN	QASYTQETPK	PSVGSISLGL	PRQQESAKSA	TLPYIKQEEF	SPRSQNSQPE
1130	1140	1150	1160	1170	1180	1190	1200
GLLVRAQHEG	VVRGTAGAIQ	EGSITRGTPT	SKISVESIPS	LRGSITQGTP	ALPQTGIPTE	ALVKGSISRM	PIEDSSPEKG
1210	1220	1230	1240	1250	1260	1270	1280
REEAASKGHV	IYEGKSGHIL	SYDNIKNARE	GTRSPRTAHE	ISLKRSYESV	EGNIKQGMSM	RESPVSAPLE	GLICRALPRG
1290	1300	1310	1320	1330	1340	1350	1360
SPHSDLKERT	VLSGSIMQGT	PRATTESFED	GLKYPKQIKR	ESPPIRAFEG	AITKGKPYDG	ITTIKEMGRS	IHEIPRQDIL
1370	1380	1390	1400	1410	1420	1430	1440
TQESRKTPEV	VQSTRPIIEG	SISQGTPIKF	DNNSGQSAIK	HNVKSLITGP	SKLSRGMPPL	EIVPENIKVV	ERGKYEDVKA
1450	1460	1470	1480	1490	1500	1510	1520
GETVRSRHTS	VVSSGPSVLR	STLHEAPKAQ	LSPGIYDDTS	ARRTPVSYQN	TMSRGSPMMN	RTSDVTISSN	KSTNHERKST
1530	1540	1550	1560	1570	1580	1590	1600
LTPTQRESIP	AKSPVPGVDP	VVSHSPFDPH	HRGSTAGEVY	RSHLPTHLDP	AMPFHRALDP	AAAAYLFQRQ	LSPTPGYPSQ
1610	1620	1630	1640	1650	1660	1670	1680
YQLYAMENTR	QTILNDYITS	QQMQVNLRPD	VARGLSPREQ	PLGLPYPATR	GIIDLTNMPP	TILVPHPGGT	STPPMDRITY
1690	1700	1710	1720	1730	1740	1750	1760
IPGTQITFPP	RPYNSASMSP	GHPTHLAAAA	SAERERERER	EKERERERIA	AASSDLYLRP	GSEQPGRPGS	HGYVRSPSPS
1770	1780	1790	1800	1810	1820	1830	1840
VRTQETMLQQ	RPSVFQGTNG	TSVITPLDPT	AQLRIMPLPA	GGPSISQGLP	ASRYNTAADA	LAALVDAAAS	APQMDVSKTK
1850	1860	1870	1880	1890	1900	1910	1920
ESKHEAARLE	ENLRSRSAAV	SEQQQLEQKT	LEVEKRSVQC	LYTSSAFPSG	KPQPHSSVVY	SEAGKDKGPP	PKSRYEEELR
1930	1940	1950	1960	1970	1980	1990	2000
TRGKTTITAA	NFIDVIITRQ	IASDKDARER	GSQSSDSSSS	LSSHRYETPS	DAIEVISPAS	SPAPPQEKLQ	TYQPEVVKAN
2010	2020	2030	2040	2050	2060	2070	2080
QAENDPTRQY	EGPLHHYRPQ	QESPSPQQQL	PPSSQAEGMG	QVPRTHRLIT	LADHICQIIT	QDFARNQVSS	QTPQQPPTST
2090	2100	2110	2120	2130	2140	2150	2160
FQNSPSALVS	TPVRTKTSNR	YSPESQAQSV	HHQRPGSRVS	PENLVDKSRG	SRPGKSPERS	HVSSEPYEPI	SPPQVPVVHE
2170	2180	2190	2200	2210	2220	2230	2240

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2870	1	973.5098	46.41	2	64.6	11.5	1	417-432	K.FINMNGLMEDPMKVYK.D	Oxidation: 8	
41	3	1068.4648	-20.43	2	29.7	15.6	2	1946-1965	K.DARERGSQSSDSSSSLSSHR.Y		WD:WU 0.92

Detailed Protein Report

Protein 227: PREDICTED: thrombopoietin isoform X2 [Homo sapiens]

Accession:	gi|578807693	**Score:**	27.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	56.2
Database Date:	2015-11-30	**pI:**	10.3
		Sequence Coverage [%]:	1.5
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 1.07 **CV:** 0.00 % **No. of Peptides:** 1

Alias proteins:

Accession	Name	Description
gi|578807695	refseq_human (refseq_human_20140103.fasta)	PREDICTED: thrombopoietin isoform X3 [Homo sapiens]

10	20	30	40	50	60	70	80
MSCQIPPGKK	LLLLSPSRSQ	VAHVQEKMDP	PIQIFSVVCV	GGGVDPGPGR	GSREEKASLP	GAFTSVWWLP	SLIGQKWPRQ
90	100	110	120	130	140	150	160
AYDLLLWRGC	APPPHVFLPI	CSPEGCLLCT	WVLEPFSTRI	DSSPLARLCP	TLLCPEVQEP	KPPPWPQEGF	RGEAPNREPR
170	180	190	200	210	220	230	240
QPDTPARMEL	TELLLVVMLL	LTARLTLSSP	APPACDLRVL	SKLLRDSHVL	HSRLSQCPEV	HPLPTPVLLP	AVDFSLGEWK
250	260	270	280	290	300	310	320
TQMEETKAQD	ILGAVTLLLE	GVMAARGQLG	PTCLSSLLGQ	LSGQVRLLLG	ALQSLLGTQL	PPQGRTTAHK	DPNAIFLSFQ
330	340	350	360	370	380	390	400
HLLRGKVRFL	MLVGGSTLCV	RRAPPTTAVP	SRTSLVLTLN	ELPNRTSGLL	ETNFTASART	TGSGLLKWQQ	GFRAKIPGLL
410	420	430	440	450	460	470	480
NQTSRSLDQI	PGYLNRIHEL	LNGTRGLFPG	PSRRTLGAPD	ISSGTSDTGS	LPPNLQPGYS	PSPTHPPTGQ	YTLFPLPPTL
490	500	510	520	530			
PTPVVQLHPL	LPDPSAPTPT	PTSPLLNTSY	THSQNLSQEG				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2610	1	449.6838	-235.36	2	60.9	27.0	0	11-18	K.LLLLSPSR.S		WD:WU 1.07

Detailed Protein Report

Protein 228: hemicentin-1 precursor [Homo sapiens]

Accession:	gi|118572606	**Score:**	27.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	613.0
Database Date:	2015-11-30	**pI:**	6.1
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	0.6
		No. of unique 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
1984	1	883.9757	-72.13	3	53.5	15.0	1	5183-5205	R.RTSDGLSCQDINECQESSPCHQR.C	Carbamidomethyl: 8

Detailed Protein Report

Protein 229: **N-acetyl-D-glucosamine kinase [Homo sapiens]**

Accession:	gi|295844834	**Score:**	27.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	42.0
Database Date:	2015-11-30	**pI:**	6.2
		Sequence Coverage [%]:	6.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MRTRTGSQLA	AREVTGSGAV	PRQLEGRRCQ	AGRDANGGTS	SDGSSSMAAI	YGGVEGGGTR	SEVLLVSEDG	KILAEADGLS
90	100	110	120	130	140	150	160
TNHWLIGTDK	CVERINEMVN	RAKRKAGVDP	LVPLRSLGLS	LSGGDQEDAG	RILIEELRDR	FPYLSESYLI	TTDAAGSIAT
170	180	190	200	210	220	230	240
ATPDGGVVLI	SGTGSNCRLI	NPDGSESGCG	GWGHMMGDEG	SAYWIAHQAV	KIVFDSIDNL	EAAPHDIGYV	KQAMFHYFQV
250	260	270	280	290	300	310	320
PDRLGILTHL	YRDFDKCRFA	GFCRKIAEGA	QQGDPLSRYI	FRKAGEMLGR	HIVAVLPEID	PVLFQGKIGL	PILCVGSVWK
330	340	350	360	370	380	390	400
SWELLKEGFL	LALTQGREIQ	AQNFFSSFTL	MKLRHSSALG	GASLGARHIG	HLLPMDYSAN	AIAFYSYTFS	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1617	1	781.3954	24.46	2	48.5	14.0	0	116-131	R.SLGLSLSGGDQEDAGR.I	

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Detailed Protein Report

Protein 230: PREDICTED: UPF0501 protein KIAA1430 isoform X2 [Homo sapiens]

Accession:	gi|530378018	**Score:**	26.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	50.5
Database Date:	2015-11-30	**pI:**	7.9
		Sequence Coverage [%]:	4.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDQFGDILEG	EVDHSFFDSD	FEEGKKCETN	SVFDKQNDDP	KERIDKDTKN	VNSNTGMQTT	ENYLTEKGNE	RNVKFPPEHP
90	100	110	120	130	140	150	160
VENDVTQTVS	SFSLPASSRS	KKLCDVTTGL	KIHVSIPNRI	PKIVKEGEDD	YYTDGEESSD	DGKKYHVKSK	SAKPSTNVKK
170	180	190	200	210	220	230	240
SIRKKYCKVS	SSSSSSLSSS	SSGSGTDCLD	AGSDSHLSDS	SPSSKSSKKH	VSGITLLSPK	HKYKSGIKST	ETQPSSTTPK
250	260	270	280	290	300	310	320
CGHYPEESED	TVTDVSPLST	PDISPLQSFE	LGIANDQKVK	IKKQENVSQE	IYEDVEDLKN	NSKYLKAAKK	GKEKHEPDVS
330	340	350	360	370	380	390	400
SKSSSVLDSS	LDHRHKQKVL	HDTMDLNHLL	KAFLQLDKKG	PQKHHFDQPS	VAPGKNYSFT	REEVRQIDRE	NQRLLKELSR
410	420	430	440	450	460		
QAEKPGSKST	IPRSADHPPK	LYHSALNRQK	EQQRIERENL	TISLCHPGWS	AVT		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2833	1	651.8526	53.29	2	63.9	14.8	0	323-334	K.SSSVLDSSLDHR.H	

Detailed Protein Report

Protein 231: catenin alpha-2 isoform 2 [Homo sapiens]

Accession:	gi|259013216	**Score:**	26.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	95.5
Database Date:	2015-11-30	**pI:**	5.6
		Sequence Coverage [%]:	2.4
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 7.25 **CV:** 0.00 % **No. of Peptides:** 1

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        10         20         30         40         50         60         70         80
MTSATSPIIL KWDPKSLEIR TLTVERLLEP LVTQVTTLVN TSNKGPSGKK KGRSKKAHVL AASVEQATQN FLEKGEQIAK
        90        100        110        120        130        140        150        160
ESQDLKEELV AAVEDVRKQG ETMRIASSEF ADDPCSSVKR GTMVRAARAL LSAVTRLLIL ADMADVMRLL SHLKIVEEAL
       170        180        190        200        210        220        230        240
EAVKNATNEQ DLANRFKEFG KEMVKLNYVA ARRQQELKDP HCRDEMAAAR GALKKNATML YTASQAFLRH PDVAATRANR
       250        260        270        280        290        300        310        320
DYVFKQVQEA IAGISNAAQA TSPTDEAKGH TGIGELAAAL NEFDNKIILD PMTFSEARFR PSLEERLESI ISGAALMADS
       330        340        350        360        370        380        390        400
SCTRDDRRER IVAECNAVRQ ALQDLLSEYM NNTGRKEKGD PLNIAIDKMT KKTRDLRRQL RKAVMDHISD SFLETNVPLL
       410        420        430        440        450        460        470        480
VLIEAAKSGN EKEVKEYAQV FREHANKLVE VANLACSISN NEEGVKLVRM AATQIDSLCP QVINAALTLA ARPQSKVAQD
       490        500        510        520        530        540        550        560
NMDVFKDQWE KQVRVLTEAV DDITSVDDFL SVSENHILED VNKCVIALQE GDVDTLDRTA GAIRGRAARV IHIINAEMEN
       570        580        590        600        610        620        630        640
YEAGVYTEKV LEATKLLSET VMPRFAEQVE VAIEALSANV PQPFEENEFI DASRLVYDGV RDIRKAVLMI RTPEELEDDS
       650        660        670        680        690        700        710        720
DFEQEDYDVR SRTSVQTEDD QLIAGQSARA IMAQLPQEEK AKIAEQVEIF HQEKSKLDAE VAKWDDSGND IIVLAKQMCM
       730        740        750        760        770        780        790        800
IMMEMTDFTR GKGPLKNTSD VINAAKKIAE AGSRMDKLAR AVADQLDSAT SLIQAAKNLM NAVVLTVKAS YVASTKYQKV
       810        820        830        840        850        860        870
YGTAAVNSPV VSWKMKAPEK KPLVKREKPE EFQTRVRRGS QKKHISPVQA LSEFKAMDSF
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
747	1	516.6531	-225.60	2	37.8	14.1	0	737-746	K.NTSDVINAAK.K		WD:WU 7.25

Detailed Protein Report

Protein 232: protein diaphanous homolog 2 isoform 12C [Homo sapiens]

Accession:	gi|6382071	**Score:**	26.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	124.7
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
MEQPGAAASG	AGGGSEEPGG	GRSNKRSAGN	RAANEEETKN	KPKLNIQIKT	LADDVRDRIT	SFRKSTVKKE	KPLIQHPIDS
90	100	110	120	130	140	150	160
QVAMSEFPAA	QPLYDERSLN	LSEKEVLDLF	EKMMEDMNLN	EEKKAPLRNK	DFTTKREMVV	QYISATAKSG	GLKNSKHECT
170	180	190	200	210	220	230	240
LSSQEYVHEL	RSGISDEKLL	NCLESLRVSL	TSNPVSWVNN	FGHEGLGLLL	DELEKLLDKK	QQENIDKKNQ	YKLIQCLKAF
250	260	270	280	290	300	310	320
MNNKFGLQRI	LGDERSLLLL	ARAIDPKQPN	MMTEIVKILS	AICIVGEENI	LDKLLGAITT	AAERNNRERF	SPIVEGLENQ
330	340	350	360	370	380	390	400
EALQLQVACM	QFINALVTSP	YELDFRIHLR	NEFLRSGLKT	MLPDLKEKEN	DELDIQLKVF	DENKEDDLTE	LSHRLNDIRA
410	420	430	440	450	460	470	480
EMDDMNEVYH	LLYNMLKDTA	AENYFLSILQ	HFLLIRNDYY	IRPQYYKIIE	ECVSQIVLHC	SGMDPDFKYR	QRLDIDLTHL
490	500	510	520	530	540	550	560
IDSCVNKAKV	EESEQKAAEF	SKKFDEEFTA	RQEAQAELQK	RDEKIKELEA	EIQQLRTQAQ	VLSSSSGIPG	PPAAPPLPGV
570	580	590	600	610	620	630	640
GPPPPPPAPP	LPGGAPLPPP	PPPLPGMMGI	PPPPPPPLLF	GGPPPPPPLG	GVPPPPGISL	NLPYGMKQKK	MYKPEVSMKR
650	660	670	680	690	700	710	720
INWSKIEPTE	LSENCFWLRV	KEDKFENPDL	FAKLALNFAT	QIKVQKNAEA	LEEKKTGPTK	KKVKELRILD	PKTAQNLSIF
730	740	750	760	770	780	790	800
LGSYRMPYED	IRNVILEVNE	DMLSEALIQN	LVKHLPEQKI	LNELAELKNE	YDDLCEPEQF	GVVMSSVKML	QPRLSSILFK
810	820	830	840	850	860	870	880
LTFEEHINNI	KPSIIAVTLA	CEELKKSESF	NRLLELVLLV	GNYMNSGSRN	AQSLGFKINF	LCKIRDTKSA	DQKTTLLHFI
890	900	910	920	930	940	950	960
ADICEEKYRD	ILKFPEELEH	VESASKVSAQ	ILKSNLASME	QQIVHLERDI	KKFPQAENQH	DKFVEKMTSF	TKTAREQYEK
970	980	990	1000	1010	1020	1030	1040
LSTMHNNMMK	LYENLGEYFI	FDSKTVSIEE	FFGDLNNFRT	LFLEAVRENN	KRREMEEKTR	RAKLAKEKAE	QEKLERQKKK
1050	1060	1070	1080	1090	1100		
KQLIDINKEG	DETGVMDNLL	EALQSGAAFR	DRRKRIPRNP	VVNHPCATRA	NPRSAT		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2360	1	1151.7502	128.51	2	57.8	15.9	2	469-487	K.YRQRLDIDLTHLIDSCVNK.A	

Detailed Protein Report

Protein 233: proteoglycan 4 isoform D precursor [Homo sapiens]

Accession:	gi|189181724	**Score:**	26.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	136.5
Database Date:	2015-11-30	**pI:**	10.1
		Sequence Coverage [%]:	1.4
		No. of unique Peptides:	2

Quantitation

WD:WU **Median:** 2.06 **CV:** 9.19 % **No. of Peptides:** 2

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		WD:WU 1.88
285	2	559.1440	-261.71	2	32.7	12.0	0	792-802	R.TTPETTTAAPK.M		WD:WU 2.25

Detailed Protein Report

Protein 234: long-chain fatty acid transport protein 6 [Homo sapiens]

Accession:	gi|13325055	**Score:**	26.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	70.1
Database Date:	2015-11-30	**pI:**	9.5
		Sequence Coverage [%]:	3.6
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|530379865	refseq_human (refseq_human_20140103.fasta)	PREDICTED: long-chain fatty acid transport protein 6 isoform X5 [Homo sapiens]
gi|530379863	refseq_human (refseq_human_20140103.fasta)	PREDICTED: long-chain fatty acid transport protein 6 isoform X4 [Homo sapiens]
gi|530379861	refseq_human (refseq_human_20140103.fasta)	PREDICTED: long-chain fatty acid transport protein 6 isoform X3 [Homo sapiens]
gi|530379859	refseq_human (refseq_human_20140103.fasta)	PREDICTED: long-chain fatty acid transport protein 6 isoform X2 [Homo sapiens]
gi|530379857	refseq_human (refseq_human_20140103.fasta)	PREDICTED: long-chain fatty acid transport protein 6 isoform X1 [Homo sapiens]
gi|62865631	refseq_human (refseq_human_20140103.fasta)	long-chain fatty acid transport protein 6 [Homo sapiens]

10	20	30	40	50	60	70	80
MLLSWLTVLG	AGMVVLHFLQ	KLLFPYFWDD	FWFVLKVVLI	IIRLKKYEKR	GELVTVLDKF	LSHAKRQPRK	PFIIYEGDIY
90	100	110	120	130	140	150	160
TYQDVDKRSS	RVAHVFLNHS	SLKKGDTVAL	LMSNEPDFVH	VWFGLAKLGC	VVAFLNTNIR	SNSLLNCIRA	CGPRALVVGA
170	180	190	200	210	220	230	240
DLLGTVEEIL	PSLSENISVW	GMKDSVPQGV	ISLKEKLSTS	PDEPVPRSHH	VVSLLKSTCL	YIFTSGTTGL	PKAAVISQLQ
250	260	270	280	290	300	310	320
VLRGSAVLWA	FGCTAHDIVY	ITLPLYHSSA	AILGISGCVE	LGATCVLKKK	FSASQFWSDC	KKYDVTVFQY	IGELCRYLCK
330	340	350	360	370	380	390	400
QSKREGEKDH	KVRLAIGNGI	RSDVWREFLD	RFGNIKVCEL	YAATESSISF	MNYTGRIGAI	GRTNLFYKLL	STFDLIKYDF
410	420	430	440	450	460	470	480
QKDEPMRNEQ	GWCIHVKKGE	PGLLISRVNA	KNPFFGYAGP	YKHTKDKLLC	DVFKKGDVYL	NTGDLIVQDQ	DNFLYFWDRT
490	500	510	520	530	540	550	560
GDTFRWKGEN	VATTEVADVI	GMLDFIQEAN	VYGVAISGYE	GRAGMASIIL	KPNTSLDLEK	VYEQVVTFLP	AYACPRFLRI
570	580	590	600	610	620		
QEKMEATGTF	KLLKHQLVED	GFNPLKISEP	LYFMDNLKKS	YVLLTRELYD	QIMLGEIKL		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2869	1	724.8749	-70.28	2	64.6	15.4	2	329-341	K.DHKVRLAIGNGIR.S	

Detailed Protein Report

Protein 235: 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 236: IgGFc-binding protein precursor [Homo sapiens]

Accession:	gi|154146262	**Score:**	26.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	571.6
Database Date:	2015-11-30	**pI:**	5.0
		Sequence Coverage [%]:	0.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGALWSWWIL	WAGATLLWGL	TQEASVDLKN	TGREEFLTAF	LQNYQLAYSK	AYPRLLISSL	SESPASVSIL	SQADNTSKKV
90	100	110	120	130	140	150	160
TVRPGESVMV	NISAKAEMIG	SKIFQHAVVI	HSDYAISVQA	LNAKPDTAEL	TLLRPIQALG	TEYFVLTPPG	TSARNVKEFA
170	180	190	200	210	220	230	240
VVAGAAGASV	SVTLKGSVTF	NGKFYPAGDV	LRVTLQPYNV	AQLQSSVDLS	GSKVTASSPV	AVLSGHSCAQ	KHTTCNHVVE
250	260	270	280	290	300	310	320
QLLPTSAWGT	HYVVPTLASQ	SRYDLAFVVA	SQATKLTYNH	GGITGSRGLQ	AGDVVEFEVR	PSWPLYLSAN	VGIQVLLFGT
330	340	350	360	370	380	390	400
GAIRNEVTYD	PYLVLIPDVA	AYCPAYVVKS	VPGCEGVALV	VAQTKAISGL	TIDGHAVGAK	LTWEAVPGSE	FSYAEVELGT
410	420	430	440	450	460	470	480
ADMIHTAEAT	TNLGLLTFGL	AKAIGYATAA	DCGRTVLSPV	EPSCEGMQCA	AGQRCQVVGG	KAGCVAESTA	VCRAQGDPHY
490	500	510	520	530	540	550	560
TTFDGRRYDM	MGTCSYTMVE	LCSEDDTLPA	FSVEAKNEHR	GSRRVSYVGL	VTVRAYSHSV	SLTRGEVGFV	LVDNQRSRLP
570	580	590	600	610	620	630	640
VSLSEGRLRV	YQSGPRAVVE	LVFGLVVTYD	WDCQLALSLP	ARFQDQVCGL	CGNYNGDPAD	DFLTPDGALA	PDAVEFASSW
650	660	670	680	690	700	710	720
KLDDGDYLCE	DGCQNNCPAC	TPGQAQHYEG	DRLCGMLTKL	DGPFAVCHDT	LDPRPFLEQC	VYDLCVVGGE	RLSLCRGLSA
730	740	750	760	770	780	790	800
YAQACLELGI	SVGDWRSPAN	CPLSCPANSR	YELCGPACPT	SCNGAAAPSN	CSGRPCVEGC	VCLPGFVASG	GACVPASSCG
810	820	830	840	850	860	870	880
CTFQGLQLAP	GQEVWADELC	QRRCTCNGAT	HQVTCRDKQS	CPAGERCSVQ	NGLLGCYPDR	FGTCQGSGDP	HYVSFDGRRF
890	900	910	920	930	940	950	960
DFMGTCTYLL	VGSCGQNAAL	PAFRVLVENE	HRGSQTVSYT	RAVRVEARGV	KVAVRREYPG	QVLVDDVLQY	LPFQAADGQV
970	980	990	1000	1010	1020	1030	1040
QVFRQGRDAV	VRTDFGLTVT	YDWNARVTAK	VPSSYAEALC	GLCGNFNGDP	ADDLALRGGG	QAANALAFGN	SWQEETRPGC
1050	1060	1070	1080	1090	1100	1110	1120
GATEPGDCPK	LDSLVAQQLQ	SKNECGILAD	PKGPFRECHS	KLDPQGAVRD	CVYDRCLLPG	QSGPLCDALA	TYAAACQAAG
1130	1140	1150	1160	1170	1180	1190	1200
ATVHPWRSEE	LCPLSCPPHS	HYEACSYGCP	LSCGDLPVPG	GCGSECHEGC	VCDEGFALSG	ESCLPLASCG	CVHQGTYHPP
1210	1220	1230	1240	1250	1260	1270	1280
GQTFYPGPGC	DSLCHCQEGG	LVSCESSSCG	PHEACQPSGG	SLGCVAVGSS	TCQASGDPHY	TTFDGRRFDF	MGTCVYVLAQ
1290	1300	1310	1320	1330	1340	1350	1360
TCGTRPGLHR	FAVLQENVAW	GNGRVSVTRV	ITVQVANFTL	RLEQRQWKVT	VNGVDMKLPV	VLANGQIRAS	QHGSDVVIET
1370	1380	1390	1400	1410	1420	1430	1440
DFGLRVAYDL	VYYVRVTVPG	NYYQQMCGLC	GNYNGDPKDD	FQKPNGSQAG	NANEFGNSWE	EVVPDSPCLP	PTPCPPGSED
1450	1460	1470	1480	1490	1500	1510	1520
CIPSHKCPPE	LEKKYQKEEF	CGLLSSPTGP	LSSCHKLVDP	QGPLKDCIFD	LCLGGGNLSI	LCSNIHAYVS	ACQAAGGHVE
1530	1540	1550	1560	1570	1580	1590	1600
PWRTETFCPM	ECPPNSHYEL	CADTCSLGCS	ALSAPPQCQD	GCAEGCQCDS	GFLYNGQACV	PIQQCGCYHN	GVYYEPEQTV
1610	1620	1630	1640	1650	1660	1670	1680
LIDNCRQQCT	CHAGKGMVCQ	EHSCKPGQVC	QPSGGILSCV	TKDPCHGVTC	RPQETCKEQG	GQGVCLPNYE	ATCWLWGDPH
1690	1700	1710	1720	1730	1740	1750	1760
YHSFDGRKFD	FQGTCNYVLA	TTGCPGVSTQ	GLTPFTVTTK	NQNRGNPAVS	YVRVVTVAAL	GTNISIHKDE	IGKVRVNGVL
1770	1780	1790	1800	1810	1820	1830	1840
TALPVSVADG	RISVTQGASK	ALLVADFGLQ	VSYDWNWRVD	VTLPSSYHGA	VCGLCGNMDR	NPNNDQVFPN	GTLAPSIPIW
1850	1860	1870	1880	1890	1900	1910	1920
GGSWRAPGWD	PLCWDECRGS	CPTCPEDRLE	QYEGPGFCGP	LAPGTGGPFT	TCHAHVPPES	FFKGCVLDVC	MGGGDRDILC
1930	1940	1950	1960	1970	1980	1990	2000
KALASYVAAC	QAAGVVIEDW	RAQVGCEITC	PENSHYEVCG	SPCPASCPSP	APLTTPAVCE	GPCVEGCQCD	AGFVLSADRC
2010	2020	2030	2040	2050	2060	2070	2080
VPLNNGCGCW	ANGTYHEAGS	EFWADGTCSQ	WCRCGPGGGS	LVCTPASCGL	GEVCGLLPSG	QHGCQPVSTA	ECQAWGDPHY
2090	2100	2110	2120	2130	2140	2150	2160
VTLDGHRFNF	QGTCEYLLSA	PCHGPPLGAE	NFTVTVANEH	RGSQAVSYTR	SVTLQIYNHS	LTLSARWPRK	LQVDGVFVTL
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2667	1	665.3404	79.29	2	61.7	11.0	1	5395-5405	K.WRAQDFSPCYG.-	

Detailed Protein Report

Protein 237: **ectodysplasin-A isoform 2 [Homo sapiens]**

Accession:	gi|54112101	**Score:**	26.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	41.0
Database Date:	2015-11-30	**pI:**	9.6
		Sequence Coverage [%]:	8.7
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MGYPEVERRE	LLPAAAPRER	GSQGCGCGGA	PARAGEGNSC	LLFLGFFGLS	LALHLLTLCC	YLELRSELRR	ERGAESRLGG
90	100	110	120	130	140	150	160
SGTPGTSGTL	SSLGGLDPDS	PITSHLGQPS	PKQQPLEPGE	AALHSDSQDG	HQMALLNFFF	PDEKPYSEEE	SRRVRRNKRS
170	180	190	200	210	220	230	240
KSNEGADGPV	KNKKKGKKAG	PPGPNGPPGP	PGPPGPQGPP	GIPGIPGIPG	TTVMGPPGPP	GPPGPQGPPG	LQGPSGAADK
250	260	270	280	290	300	310	320
AGTRENQPAV	VHLQGQGSAI	QVKNDLSGGV	LNDWSRITMN	PKVFKLHPRS	GELEVLVDGT	YFIYSQVYYI	NFTDFASYEV
330	340	350	360	370	380	390	
VVDEKPFLQC	TRSIETGKTN	YNTCYTAGVC	LLKARQKIAV	KMVHADISIN	MSKHTTFFGA	IRLGEAPAS	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1964	4	703.2668	-56.59	2	52.9	13.6	1	19-33	R.ERGSQGCGCGGAPAR.A	
1562	2	1059.0865	57.30	2	48.2	13.1	1	264-282	K.NDLSGGVLNDWSRITMNPK.V	

Detailed Protein Report

Protein 238: copper-transporting ATPase 1 isoform 2 [Homo sapiens]

Accession: gi|532691752
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 26.7
MW [kDa]: 154.3
pI: 5.7
Sequence Coverage [%]: 2.3
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MDPSMGVNSV	TISVEGMTCN	SCVWTIEQQI	GKVNGVHHIK	VSLEEKNATI	IYDPKLQTPK	TLQEAIDDMG	FDAVIHNPDP
90	100	110	120	130	140	150	160
LPVLTDTLFL	TVTASLTLPW	DHIQSTLLKT	KGVTDIKIYP	QKRTVAVTII	PSIVNANQIK	ELVPELSLDT	GTLEKKSGAC
170	180	190	200	210	220	230	240
EDHSMAQAGE	VVLKMKVEGM	TCHSCTSTIE	GKIGKLQGVQ	RIKVSLDNQE	ATIVYQPHLI	SVEEMKKQIE	AMGFPAFVKK
250	260	270	280	290	300	310	320
QPKYLKLGAI	DVERLKNTPV	KSSEGSQQRS	PSYTNDSTAT	FIIDGMHCKS	CVSNIESTLS	ALQYVSSIVV	SLENRSAIVK
330	340	350	360	370	380	390	400
YNASSVTPES	LRKAIEAVSP	GLYRVSITSE	VESTSNSPSS	SSLQKIPLNV	VSQPLTQETV	INIDGMTCNS	CVQSIEGVIS
410	420	430	440	450	460	470	480
KKPGVKSIRV	SLANSNGTVE	YDPLLTSPET	LRGAIEDMGF	DATLSDTNEP	LVVIAQPSSE	MPLLTSTNEF	YTKGMTPVQD
490	500	510	520	530	540	550	560
KEEGKNSSKC	YIQVTGMTCA	SCVANIERNL	RREEGIYSIL	VALMAGKAEV	RYNPAVIQPP	MIAEFIRELG	FGATVIENAD
570	580	590	600	610	620	630	640
EGDGVLELVV	RGMTCASCVH	KIESSLTKHR	GILYCSVALA	TNKAHIKYDP	EIIGPRDIIH	TIESLGFEAS	LVKKDRSASH
650	660	670	680	690	700	710	720
LDHKREIRQW	RRSFLVSLFF	CIPVMGLMIY	MMVMDHHFAT	LHHNQNMSKE	EMINLHSSMF	LERQILPGLS	VMNLLSFLLC
730	740	750	760	770	780	790	800
VPVQGKTSEA	LAKLISLQAT	EATIVTLDSD	NILLSEEQVD	VELVQRGDII	KVVPGGKFPV	DGRVIEGHSM	VDESLITGEA
810	820	830	840	850	860	870	880
MPVAKKPGST	VIAGSINQNG	SLLICATHVG	ADTTLSQIVK	LVEEAQTSKA	PIQQFADKLS	GYFVPFIVFV	SIATLLVWIV
890	900	910	920	930	940	950	960
IGFLNFEIVE	TYFPGYNRSI	SRTETIIRFA	FQASITVLCI	ACPCSLGLAT	PTAVMVGTGV	GAQNGILIKG	GEPLEMAHKV
970	980	990	1000	1010	1020	1030	1040
KVVVFDKTGT	ITHGTPVVNQ	VKVLTESNRI	SHHKILAIVG	TAESNSEHPL	GTAITKYCKQ	ELDTETLGTC	IDFQVVPGCG
1050	1060	1070	1080	1090	1100	1110	1120
ISCKVTNIEG	LLHKNNWNIE	DNNIKNASLV	QIDASNEQSS	TSSSMIIDAQ	ISNALNAQQY	KVLIGNREWM	IRNGLVINND
1130	1140	1150	1160	1170	1180	1190	1200
VNDFMTEHER	KGRTAVLVAV	DDELCGLIAI	ADTVKPEAEL	AIHILKSMGL	EVVLMTGDNS	KTARSIASQV	GITKVFAEVL
1210	1220	1230	1240	1250	1260	1270	1280
PSHKVAKVKQ	LQEEGKRVAM	VGDGINDSPA	LAMANVGIAI	GTGTDVAIEA	ADVVLIRNDL	LDVVASIDLS	RKTVKRIRIN
1290	1300	1310	1320	1330	1340	1350	1360
FVFALIYNLV	GIPIAAGVFM	PIGLVLQPWM	GSAAMAASSV	SVVLSSLFLK	LYRKPTYESY	ELPARSQIGQ	KSPSEISVHV
1370	1380	1390	1400	1410	1420	1430	
GIDDTSRNSP	KLGLLDRIVN	YSRASINSLL	SDKRSLNSVV	TSEPDKHSLL	VGDFREDDDT	AL	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2946	1	822.4713	37.34	2	65.6	13.4	0	141-155	K.ELVPELSLDTGTLEK.K	

Detailed Protein Report

Protein 239: uncharacterized protein KIAA1751 [Homo sapiens]

Accession:	gi|122937416	**Score:**	26.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	86.9
Database Date:	2015-11-30	**pI:**	5.3
		Sequence Coverage [%]:	2.5
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MEDDGSLLPE DELLADALLL EDERDELEDP EFDIKCLLQE AEDDVDPGHS SSVKELDTDA DKLKKKTAED RTQAFHLRQN
        90        100        110        120        130        140        150        160
LSALDKMHEE QELFTEKMRG ELRACRQRRD LIDKQQEAVA AEIATEEEAG NMAAVGRLQA VSRRLFAELE NERDLQSRTE
       170        180        190        200        210        220        230        240
AVLKESENTM WHIEIQEGRL EAFRTADREE VEATGRRLQV RAAEQLCREQ EALGKVERNR LLRIRKSLNT QKELGLRHQK
       250        260        270        280        290        300        310        320
LLEDARKNHK VAVRFLKASL GRIREQEKKE EMECHEYMRR RMDAVVALKG SISANRDTLR KFQAWDRAKA ELAEQRVQAE
       330        340        350        360        370        380        390        400
KKAILAQGRD AFRHLVHQRR RQELEAQKRA FEEEQKLRKQ EIISRILKEE AEEEKRKKQH PPTSARHRLT LRDKTWNYIS
       410        420        430        440        450        460        470        480
DFCKKTTVPT NTYTLDYEAA AGPGPSRLLE VVSSELIQGD PGASSEEETL AEPEISGLWN EDYKPYQVPK EDVDRKPVGG
       490        500        510        520        530        540        550        560
TKMDKDILER TVERLRSRVV HKQVVWGREF QGRPFNSKPE LLHFQDFDIG KVYKKKITLV NTTYTINYCK LVGVEEHLRD
       570        580        590        600        610        620        630        640
FIHVDFDPPG PLSAGMSCEV LVTFKPMINK DLEGNISFLA QTGEFSVPLK CSTKKCSLSL DKELIDFGSY VVGETTSRTI
       650        660        670        680        690        700        710        720
TLTNVGGLGT TFKFLPASEP CEMDDSQSAL KLSSLLTYED KSLYDKAATS FSEQQLEGTE SSQADMQSRK ELEKLDKEQE
       730        740        750        760        770
EEQPAGEPGC QAKPGWAGGE GLRAAFQGAE GPRGGLESRE FS
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2144	1	687.4001	47.83	2	55.2	15.0	2	366-376	R.ILKEEAEEEKR.K	

Detailed Protein Report

Protein 240: **protein canopy homolog 4 precursor [Homo sapiens]**

Accession:	gi|22749479	**Score:**	26.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	28.3
Database Date:	2015-11-30	**pI:**	4.4
Modification(s):	Oxidation	**Sequence Coverage [%]:**	13.7
		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
2841	1	945.5312	3.89	2	64.2	12.2	2	115-132	K.GQSQTMATLKGLVQKGVK.V	Oxidation: 6

Detailed Protein Report

Protein 241: nuclear receptor coactivator 4 isoform 3 [Homo sapiens]

Accession: gi|14149617
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 26.6
MW [kDa]: 69.7
pI: 5.7
Sequence Coverage [%]: 3.1
No. of unique Peptides: 1

Alias proteins:

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

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
24	1	1103.4962	75.19	2	29.2	26.6	0	406-424	R.ANEPCTSFAECVCDENCEK.E	Carbamidomethyl: 5, 17

Protein 242: ubiquitin carboxyl-terminal hydrolase 12 [Homo sapiens]

Accession:	gi|301500675	**Score:**	26.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	42.8
Database Date:	2015-11-30	**pI:**	6.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	7.0
		No. of unique Peptides:	1

Quantitation

WD:WU	**Median:** 0.64	**CV:** 0.00 %	**No. of Peptides:** 1

10	20	30	40	50	60	70	80
MEILMTVSKF	ASICTMGANA	SALEKEIGPE	QFPVNEHYFG	LVNFGNTCYC	NSVLQALYFC	RPFREKVLAY	KSQPRKKESL
90	100	110	120	130	140	150	160
LTCLADLFHS	IATQKKKVGV	IPPKKFITRL	RKENELFDNY	MQQDAHEFLN	YLLNTIADIL	QEERKQEKQN	GRLPNGNIDN
170	180	190	200	210	220	230	240
ENNNSTPDPT	WVHEIFQGTL	TNETRCLTCE	TISSKDEDFL	DLSVDVEQNT	SITHCLRGFS	NTETLCSEYK	YYCEECRSKQ
250	260	270	280	290	300	310	320
EAHKRMKVKK	LPMILALHLK	RFKYMDQLHR	YTKLSYRVVF	PLELRLFNTS	GDATNPDRMY	DLVAVVVHCG	SGPNRGHYIA
330	340	350	360	370	380		
IVKSHDFWLL	FDDDIVEKID	AQAIEEFYGL	TSDISKNSES	GYILFYQSRD			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
620	1	647.6390	-191.68	2	36.2	14.2	1	231-239	K.YYCEECRSK.Q	Carbamidomethyl: 3, 6	WD:WU 0.64

Detailed Protein Report

Protein 243: PREDICTED: zinc finger protein 737 isoform X4 [Homo sapiens]

Accession:	gi|530414419	**Score:**	26.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	60.3
Database Date:	2015-11-30	**pI:**	10.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.4
		No. of unique Peptides:	1

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2022	1	1051.4074	-85.21	2	53.9	10.6	2	399-416	K.CEECGKAFKCFSILTTHK.R	Carbamidomethyl: 10

Detailed Protein Report

Protein 244: PREDICTED: hedgehog-interacting protein isoform X1 [Homo sapiens]

Accession:	gi|530378067	**Score:**	26.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	76.8
Database Date:	2015-11-30	**pI:**	9.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	5.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLKMLSFKLL	LLAVALGFFE	GDAKFGERNE	GSGARRRRCL	NGNPPKRLKR	RDRRMMSQLE	LLSGGEMLCG	GFYPRLSCCL
90	100	110	120	130	140	150	160
RSDSPGLGRL	ENKIFSVTNN	TECGKLLEEI	KCALCSPHSQ	SLFHSPEREV	LERDLVLPLL	CKDYCKEFFY	TCRGHIPGFL
170	180	190	200	210	220	230	240
QTTADEFCFY	YARKDGGLCF	PDFPRKQVRG	PASNYLDQME	EYDKVEEISR	KHKHNCFCIQ	EVVSGLRQPV	GALHSGDGSQ
250	260	270	280	290	300	310	320
RLFILEKEGY	VKILTPEGEI	FKEPYLDIHK	LVQSGIKGGD	ERGLLSLAFH	PNYKKNGKLY	VSYTTNQERW	AIGPHDHILR
330	340	350	360	370	380	390	400
VVEYTVSRKN	PHQVDLRTAR	VFLEVAELHR	KHLGGQLLFG	PDGFLYIILG	DGMITLDDME	EMDGLSDFTG	SVLRLDVDTD
410	420	430	440	450	460	470	480
MCNVPYSIPR	SNPHFNSTNQ	PPEVFAHGLH	DPGRCAVDRH	PTDININLTI	LCSDSNGKNR	SSARILQIIK	GKDYESEPSL
490	500	510	520	530	540	550	560
LEFKPFSNGP	LVGGFVYRGC	QSERLYGSYV	FGDRNGNFLT	LQQSPVTKQW	QEKPLCLGTS	GSCRGYFSGH	ILGFGEDELG
570	580	590	600	610	620	630	640
EVYILSSSKS	MTQTHNGKLY	KIVDPKRPLM	PEECRATVQP	AQTLTSECSR	LCRNGYCTPT	GKCCCSPGWE	GDFCRTAKCE
650	660	670	680	690			
PACRHGGVCV	RPNKCLCKKG	YLGPQCEQVD	RNIRRVTRAD	IT			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1709	1	938.7505	-122.25	2	49.7	10.2	1	623-638	K.CCCSPGWEGDFCRTAK.C	Carbamidomethyl: 3, 12

Detailed Protein Report

Protein 245: **tumor necrosis factor receptor superfamily member 10B isoform 2 precursor [Homo sapiens]**

Accession:	gi|224494026	**Score:**	26.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	45.1
Database Date:	2015-11-30	**pI:**	5.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.6
		No. of unique Peptides:	2

Quantitation

WD:WU **Median:** 0.58 **CV:** 0.00 % **No. of Peptides:** 1

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	Ratios
2927	3	973.5285	17.13	2	65.4	12.3	2	210-228	K.KVLPYLKGICSGGGGDPER.V		WD:WU 0.58
2235	1	937.9180	-60.88	2	56.4	14.1	1	211-228	K.VLPYLKGICSGGGGDPER.V	Carbamidomethyl: 9	

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Detailed Protein Report

Protein 246: cytoplasmic phosphatidylinositol transfer protein 1 isoform a [Homo sapiens]

Accession:	gi|32307140	**Score:**	26.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	38.4
Database Date:	2015-11-30	**pI:**	6.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	10.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLLKEYRICM	PLTVDEYKIG	QLYMISKHSH	EQSDRGEGVE	VVQNEPFEDP	HHGNGQFTEK	RVYLNSKLPS	WARAVVPKIF
90	100	110	120	130	140	150	160
YVTEKAWNYY	PYTITEYTCS	FLPKFSIHIE	TKYEDNKGSN	DTIFDNEAKD	VEREVCFIDI	ACDEIPERYY	KESEDPKHFK
170	180	190	200	210	220	230	240
SEKTGRGQLR	EGWRDSHQPI	MCSYKLVTVK	FEVWGLQTRV	EQFVHKVVRD	ILLIGHRQAF	AWVDEWYDMT	MDEVREFERA
250	260	270	280	290	300	310	320
TQEATNKKIG	IFPPAISISS	IPLLPSSVRS	APSSAPSTPL	STDAPEFLSV	PKDRPRKKSA	PETLTLPDPE	KKATLNLPGM
330	340						
HSSDKPCRPK	SE						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
26	1	712.9803	-81.39	3	29.3	11.2	1	312-330	K.KATLNLPGMHSSDKPCRPK.S	Carbamidomethyl: 16

Detailed Protein Report

Protein 247: PREDICTED: oleosin-B4-like [Homo sapiens]

Accession:	gi|410170263	**Score:**	26.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	49.8
Database Date:	2015-11-30	**pI:**	12.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	7.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSSPVLEPSP	GPRSPYLHGP	YLLLGEVLGH	SALGAQHAQP	ANGDADELLE	LPALLQHPTG	CDPCASLRDS	RVTPATALLL
90	100	110	120	130	140	150	160
LSHRGRAQRR	SIQAAAAQEQ	STGRGCLGKE	PPSQESWTRS	DPRRCLSQDA	VRSGSRVCRS	RPQTRGGGGK	QPRRQKAAVA
170	180	190	200	210	220	230	240
GAKSRGGEGK	KPQRRGQKAA	TAGAKSRGGG	VRSLGGKKMR	RGQKGAAGAK	RCGGGKQPRR	RGQKASKSGG	VRCQTPQKAA
250	260	270	280	290	300	310	320
AQGVKSRKKL	RQRGQKAAAA	GQEAAAGKTC	GGGGEKHRGG	GDKKPLRKNS	RWRGQKAAAA	GGKKPQKAAA	AGGERRKKLR
330	340	350	360	370	380	390	400
RQKAAVARAK	SPKKPRWRGQ	NSGNGVEGQR	SLAFLEFDVE	GKVQRKTKIP	GGVVKQFVPA	DQGPLWQKAA	NLHKMSLPHQ
410	420	430	440	450	460	470	
LALKMEWNGI	IIEWNRMELS	SNGINRDHHR	MEPNGVIIEW	NRKASSCNGI	EWHHQRMDSK	GIIIE	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1321	1	1045.0547	21.73	2	44.8	13.5	2	90-109	R.RSIQAAAAQEQSTGRGCLGK.E	Carbamidomethyl: 17

Detailed Protein Report

Protein 248: PREDICTED: ninein isoform X5 [Homo sapiens]

Accession:	gi|578825856	**Score:**	26.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	231.1
Database Date:	2015-11-30	**pI:**	4.8
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	1.4
		No. of unique Peptides:	2

Detailed Protein Report

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        10         20         30         40         50         60         70         80
MDEVEQDQHE ARLKELFDSF DTTGTGSLGQ EELTDLCHML SLEEVAPVLQ QTLLQDNLLG RVHFDQFKEA LILILSRTLS
        90        100        110        120        130        140        150        160
NEEHFQEPDC SLEAQPKYVR GGKRYGRRSL PEFQESVEEF PEVTVIEPLD EEARPSHIPA GDCSEHWKTQ RSEEYEAEGQ
       170        180        190        200        210        220        230        240
LRFWNPDDLN ASQSGSSPPQ DWIEEKLQEV CEDLGITRDG HLNRKKLVSI CEQYGLQNVD GEMLEEVFHN LDPDGTMSVE
       250        260        270        280        290        300        310        320
DFFYGLFKNG KSLTPSASTP YRQLKRHLSM QSFDESGRRT TTSSAMTSTI GFRVFSCLDD GMGHASVERI LDTWQEEGIE
       330        340        350        360        370        380        390        400
NSQEILKALD FSLDGNINLT ELTLALENEL LVTKNSIHQA ALASFKAEIR HLLERVDQVV REKEKLRSDL DKAEKLKSLM
       410        420        430        440        450        460        470        480
ASEVDDHHAA IERRNEYNLR KLDEEYKERI AALKNELRKE REQILQQAGK QRLELEQEIE KAKTEENYIR DRLALSLKEN
       490        500        510        520        530        540        550        560
SRLENELLEN AEKLAEYENL TNKLQRNLEN VLAEKFGDLD PSSAEFFLQE ERLTQMRNEY ERQCRVLQDQ VDELQSELEE
       570        580        590        600        610        620        630        640
YRAQGRVLRL PLKNSPSEEV EANSGGIEPE HGLGSEECNP LNMSIEAELV IEQMKEQHHR DICCLRLELE DKVRHYEKQL
       650        660        670        680        690        700        710        720
DETVVSCKKA QENMKQRHEN ETHTLEKQIS DLKNEIAELQ GQAAVLKEAH HEATCRHEEE KKQLQVKLEE EKTHLQEKLR
       730        740        750        760        770        780        790        800
LQHEMELKAR LTQAQASFER EREGLQSSAW TEEKVRGLTQ ELEQFHQEQL TSLVEKHTLE KEELRKELLE KHQRELQEGR
       810        820        830        840        850        860        870        880
EKMETECNRR TSQIEAQFQS DCQKVTERCE SALQSLEGRY RQELKDLQEQ QREEKSQWEF EKDELTQECA EAQELLKETL
       890        900        910        920        930        940        950        960
KREKTTSLVL TQEREMLEKT YKEHLNSMVV ERQQLLQDLE DLRNVSETQQ SLLSDQILEL KSSHKRELRE REEVLCQAGA
       970        980        990       1000       1010       1020       1030       1040
SEQLASQRLE RLEMEHDQER QEMMSKLLAM ENIHKATCET ADRERAEMST EISRLQSKIK EMQQATSPLS MLQSGCQVIG
      1050       1060       1070       1080       1090       1100       1110       1120
EEEVEGDGAL SLLQQGEQLL EENGDVLLSL QRAHEQAVKE NVKMATEISR LQQRLQKLEP GLVMSSCLDE PATEFFGNTA
      1130       1140       1150       1160       1170       1180       1190       1200
EQTEQFLQQN RTKQVEGVTR RHVLSDLEDD EVRDLGSTGT SSVQRQEVKI EESEASVEGF SELENSEETR TESWELKNQI
      1210       1220       1230       1240       1250       1260       1270       1280
SQLQEQLMML CADCDRASEK KQDLLFDVSV LKKKLKMLER IPEASPKYKL LYEDVSREND CLQEELRMME TRYDEALENN
      1290       1300       1310       1320       1330       1340       1350       1360
KELTAEVFRL QDELKKMEEV TETFLSLEKS YDEVKIENEG LNVLVLRLQG KIEKLQESVV QRCDCCLWEA SLENLEIEPD
      1370       1380       1390       1400       1410       1420       1430       1440
GNILQLNQTL EECVPRVRSV HHVIEECKQE NQYLEGNTQL LEKVKAHEIA WLHGTIQTHQ ERPRVQNQVI LEENTTLLGF
      1450       1460       1470       1480       1490       1500       1510       1520
QDKHFQHQAT IAELELEKTK LQELTRKLKE RVTILVKQKD VLSHGEKEEE LKAMMHDLQI TCSEMQQKVE LLRYESEKLQ
      1530       1540       1550       1560       1570       1580       1590       1600
QENSILRNEI TTLNEEDSIS NLKLGTLNGS QEEMWQKTET VKQENAAVQK MVENLKKQIS ELKIKNQQLD LENTELSQKN
      1610       1620       1630       1640       1650       1660       1670       1680
SQNQEKLQEL NQRLTEMLCQ KEKEPGNSAL EEREQEKFNL KEELERCKVQ SSTLVSSLEA ELSEVKIQTH IVQQENHLLK
      1690       1700       1710       1720       1730       1740       1750       1760
DELEKMKQLH RCPDLSDFQQ KISSVLSYNE KLLKEKEALS EELNSCVDKL AKSSLLEHRI ATMKQEQKSW EHQSASLKSQ
      1770       1780       1790       1800       1810       1820       1830       1840
LVASQEKVQN LEDTVQNVNL QMSRMKSDLR VTQQEKEALK QEVMSLHKQL QNAGGKSWAP EIATHPSGLH NQQKRLSWDK
      1850       1860       1870       1880       1890       1900       1910       1920
LDHLMNEEQQ LLWQENERLQ TMVQNTKAEL THSREKVRQL ESNLLPKHQK HLNPSGTMNP TEQEKLSLKR ECDQFQKEQS
      1930       1940       1950       1960       1970       1980       1990
PANRKVSQMN SLEQELETIH LENEGLKKKQ VKLDEQLMEN SVVGSSREGC SSLPEIVCEG RTFSFNELS
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1578	1	685.8860	27.18	2	48.0	10.3	0	913-923	R.QQLLQDLEDLR.N	
2071	5	1023.8928	-100.81	2	54.5	16.0	2	1686-1701	K.MKQLHRCPDLSDFQQK.I	Carbamidomethyl: 7; Oxidation: 1

Detailed Protein Report

Protein 249: huntingtin [Homo sapiens]

Accession:	gi|90903231	**Score:**	26.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	347.6
Database Date:	2015-11-30	**pI:**	5.8
		Sequence Coverage [%]:	0.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MATLEKLMKA	FESLKSFQQQ	QQQQQQQQQQ	QQQQQQQQQQ	PPPPPPPPPP	PQLPQPPPQA	QPLLPQPQPP	PPPPPPPPGP
90	100	110	120	130	140	150	160
AVAEEPLHRP	KKELSATKKD	RVNHCLTICE	NIVAQSVRNS	PEFQKLLGIA	MELFLLCSDD	AESDVRMVAD	ECLNKVIKAL
170	180	190	200	210	220	230	240
MDSNLPRLQL	ELYKEIKKNG	APRSLRAALW	RFAELAHLVR	PQKCRPYLVN	LLPCLTRTSK	RPEESVQETL	AAAVPKIMAS
250	260	270	280	290	300	310	320
FGNFANDNEI	KVLLKAFIAN	LKSSSPTIRR	TAAGSAVSIC	QHSRRTQYFY	SWLLNVLLGL	LVPVEDEHST	LLILGVLLTL
330	340	350	360	370	380	390	400
RYLVPLLQQQ	VKDTSLKGSF	GVTRKEMEVS	PSAEQLVQVY	ELTLHHTQHQ	DHNVVTGALE	LLQQLFRTPP	PELLQTLTAV
410	420	430	440	450	460	470	480
GGIGQLTAAK	EESGGRSRSG	SIVELIAGGG	SSCSPVLSRK	QKGKVLLGEE	EALEDDSESR	SDVSSSALTA	SVKDEISGEL
490	500	510	520	530	540	550	560
AASSGVSTPG	SAGHDIITEQ	PRSQHTLQAD	SVDLASCDLT	SSATDGDEED	ILSHSSSQVS	AVPSDPAMDL	NDGTQASSPI
570	580	590	600	610	620	630	640
SDSSQTTTEG	PDSAVTPSDS	SEIVLDGTDN	QYLGLQIGQP	QDEDEEATGI	LPDEASEAFR	NSSMALQQAH	LLKNMSHCRQ
650	660	670	680	690	700	710	720
PSDSSVDKFV	LRDEATEPGD	QENKPCRIKG	DIGQSTDDDS	APLVHCVRLL	SASFLLTGGK	NVLVPDRDVR	VSVKALALSC
730	740	750	760	770	780	790	800
VGAAVALHPE	SFFSKLYKVP	LDTTEYPEEQ	YVSDILNYID	HGDPQVRGAT	AILCGTLICS	ILSRSRFHVG	DWMGTIRTLT
810	820	830	840	850	860	870	880
GNTFSLADCI	PLLRKTLKDE	SSVTCKLACT	AVRNCVMSLC	SSSYSELGLQ	LIIDVLTLRN	SSYWLVRTEL	LETLAEIDFR
890	900	910	920	930	940	950	960
LVSFLEAKAE	NLHRGAHHYT	GLLKLQERVL	NNVVIHLLGD	EDPRVRHVAA	ASLIRLVPKL	FYKCDQGQAD	PVVAVARDQS
970	980	990	1000	1010	1020	1030	1040
SVYLKLLMHE	TQPPSHFSVS	TITRIYRGYN	LLPSITDVTM	ENNLSRVIAA	VSHELITSTT	RALTFGCCEA	LCLLSTAFPV
1050	1060	1070	1080	1090	1100	1110	1120
CIWSLGWHCG	VPPLSASDES	RKSCTVGMAT	MILTLLSSAW	FPLDLSAHQD	ALILAGNLLA	ASAPKSLRSS	WASEEEANPA
1130	1140	1150	1160	1170	1180	1190	1200
ATKQEEVWPA	LGDRALVPMV	EQLFSHLLKV	INICAHVLDD	VAPGPAIKAA	LPSLTNPPSL	SPIRRKGKEK	EPGEQASVPL
1210	1220	1230	1240	1250	1260	1270	1280
SPKKGSEASA	ASRQSDTSGP	VTTSKSSSLG	SFYHLPSYLK	LHDVLKATHA	NYKVTLDLQN	STEKFGGFLR	SALDVLSQIL
1290	1300	1310	1320	1330	1340	1350	1360
ELATLQDIGK	CVEEILGYLK	SCFSREPMMA	TVCVQQLLKT	LFGTNLASQF	DGLSSNPSKS	QGRAQRLGSS	SVRPGLYHYC
1370	1380	1390	1400	1410	1420	1430	1440
FMAPYTHFTQ	ALADASLRNM	VQAEQENDTS	GWFDVLQKVS	TQLKTNLTSV	TKNRADKNAI	HNHIRLFEPL	VIKALKQYTT
1450	1460	1470	1480	1490	1500	1510	1520
TTCVQLQKQV	LDLLAQLVQL	RVNYCLLDSD	QVFIGFVLKQ	FEYIEVGQFR	ESEAIIPNIF	FFLVLLSYER	YHSKQIIGIP
1530	1540	1550	1560	1570	1580	1590	1600
KIIQLCDGIM	ASGRKAVTHA	IPALQPIVHD	LFVLRGTNKA	DAGKELETQK	EVVVSMLLRL	IQYHQVLEMF	ILVLQQCHKE
1610	1620	1630	1640	1650	1660	1670	1680
NEDKWKRLSR	QIADIILPML	AKQQMHIDSH	EALGVLNTLF	EILAPSSLRP	VDMLLRSMFV	TPNTMASVST	VQLWISGILA
1690	1700	1710	1720	1730	1740	1750	1760
ILRVLISQST	EDIVLSRIQE	LSFSPYLISC	TVINRLRDGD	STSTLEEHSE	GKQIKNLPEE	TFSRFLLQLV	GILLEDIVTK
1770	1780	1790	1800	1810	1820	1830	1840
QLKVEMSEQQ	HTFYCQELGT	LLMCLIHIFK	SGMFRRITAA	ATRLFRSDGC	GGSFYTLDSL	NLRARSMITT	HPALVLLWCQ
1850	1860	1870	1880	1890	1900	1910	1920
ILLLVNHTDY	RWWAEVQQTP	KRHSLSSTKL	LSPQMSGEEE	DSDLAAKLGM	CNREIVRRGA	LILFCDYVCQ	NLHDSEHLTW
1930	1940	1950	1960	1970	1980	1990	2000
LIVNHIQDLI	SLSHEPPVQD	FISAVHRNSA	ASGLFIQAIQ	SRCENLSTPT	MLKKTLQCLE	GIHLSQSGAV	LTLYVDRLLC
2010	2020	2030	2040	2050	2060	2070	2080
TPFRVLARMV	DILACRRVEM	LLAANLQSSM	AQLPMEELNR	IQEYLQSSGL	AQRHQRLYSL	LDRFRLSTMQ	DSLSPSPPVS
2090	2100	2110	2120	2130	2140	2150	2160
SHPLDGDGHV	SLETVSPDKD	WYVHLVKSQC	WTRSDSALLE	GAELVNRIPA	EDMNAFMMNS	EFNLSLLAPC	LSLGMSEISG
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
347	1	524.3773	160.20	2	33.0	15.3	2	93-101	K.ELSATKKDR.V	

Detailed Protein Report

Protein 250: sodium-driven chloride bicarbonate exchanger isoform 2 [Homo sapiens]

Accession:	gi|155722998	**Score:**	26.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	122.6
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
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
63	1	724.6832	-193.81	2	29.7	11.3	1	128-139	R.EGEDAEWRETAR.W	

Detailed Protein Report

Protein 251: potassium voltage-gated channel subfamily KQT member 5 isoform 5 [Homo sapiens]

Accession:	gi|236462242	**Score:**	26.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	89.9
Database Date:	2015-11-30	**pI:**	10.2
		Sequence Coverage [%]:	3.8
		No. of unique Peptides:	2

```
        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
2983	1	965.4581	-18.53	2	66.1	10.6	2	399-416	K.ALHTCSPTKKEQGEASSR.I	
316	1	690.7007	-211.65	2	33.0	15.6	1	785-797	R.EAAFASDSLRTGR.S	

Detailed Protein Report

Protein 252: PREDICTED: spidroin-1-like [Homo sapiens]

Accession: gi|530356740
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 26.2
MW [kDa]: 27.8
pI: 12.6
Sequence Coverage [%]: 17.2
No. of unique Peptides: 2

10	20	30	40	50	60	70	80
MLRPRARADC	GVRGRGALGG	VPGRAASRGA	GSRGGRGPGE	GGVPGGRGGA	WGALSGGRVS	RGEGLRLLGA	TGGGCGAWGR
90	100	110	120	130	140	150	160
PGLPAAAPKG	LSGGSGGRGS	SQGLSYGRTR	GEAAKSRRAW	TGPRADRTVL	GELRGAAGDR	GVRLPRGDAQ	RPGQNLDGAE
170	180	190	200	210	220	230	240
SPARAPAAST	WEDTQGPGAR	SGRRAASAVS	TDGQKPQRVP	SCSRRGSITI	GPGLPGGASE	GSMLRQELGT	AGDEMRLFGQ
250	260	270	280				
GVCFRAMRQP	GSWATGGRPG	VRALQPVPAP	AFHGRRVLP				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1604	2	978.1044	-91.99	3	48.4	15.7	2	59-89	R.VSRGEGLRLLGATGGGCGAWGRPGLPAAAPK.G	
2694	1	913.4475	-91.49	2	62.1	10.6	2	263-279	R.ALQPVPAPAFHGRRVLP.-	

Detailed Protein Report

Protein 253: **interleukin-33 isoform 2 [Homo sapiens]**

Accession:	gi|313851030	**Score:**	26.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	25.9
Database Date:	2015-11-30	**pI:**	10.2
Modification(s):	Oxidation	**Sequence Coverage [%]:**	11.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MKPKMKYSTN	KISTAKWKNT	ASKALCFKLG	KSQQKAKEVC	PMYFMKLRSG	LMIKKEACYF	RRETTKRPSL	KTGRKHKRHL
90	100	110	120	130	140	150	160
VLAACQQQST	VECFAFGISG	VQKYTRALHD	SSITDKVLLS	YYESQHPSNE	SGDGVDGKML	MVTLSPTKDF	WLHANNKEHS
170	180	190	200	210	220	230	
VELHKCEKPL	PDQAFFVLHN	MHSNCVSFEC	KTDPGVFIGV	KDNHLALIKV	DSSENLCTEN	ILFKLSET	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1897	1	568.7721	-60.19	2	52.1	15.8	0	139-148	K.MLMVTLSPTK.D	Oxidation: 1

Detailed Protein Report

Protein 254: PREDICTED: sarcolemmal membrane-associated protein isoform X16 [Homo sapiens]

Accession:	gi|530373158	**Score:**	26.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	90.8
Database Date:	2015-11-30	**pI:**	5.1
		Sequence Coverage [%]:	3.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPSALAIFTC	RPNSHPFQER	HVYLDEPIKI	GRSVARCRPA	QNNATFDCKV	LSRNHALVWF	DHKTGKFYLQ	DTKSSNGTFI
90	100	110	120	130	140	150	160
NSQRLSRGSE	ESPPCEILSG	DIIQFGVDVT	ENTRKVTHGC	IVSTIKLFLP	DGMEARLRSD	VIHAPLPSPV	DKVAANTPSM
170	180	190	200	210	220	230	240
YSQELFQLSQ	YLQEALHREQ	MLEQKLATLQ	RLLAITQEAS	DTSWQALIDE	DRLLSRLEVM	GNQLQACSKN	QTEDSLRKEL
250	260	270	280	290	300	310	320
IALQEDKHNY	ETTAKESLRR	VLQEKIEVVR	KLSEVERSLS	NTEDECTHLK	EMNERTQEEL	RELANKYNGA	VNEIKDLSDK
330	340	350	360	370	380	390	400
LKVAEGKQEE	IQQKGQAEKK	ELQHKIDEME	EKEQELQAKI	EALQADNDFT	NERLTALQEK	LIVEGHLTKA	VEETKLSKEN
410	420	430	440	450	460	470	480
QTRAKESDFS	DTLSPSKEKS	SDDTTDAQMD	EQDLNEPLAK	VSLLKDDLQG	AQSEIEAKQE	IQHLRKELIE	AQELARTSKQ
490	500	510	520	530	540	550	560
KCFELQALLE	EERKAYRNQV	EESTKQIQVL	QAQLQRLHID	TENLREEKDS	EITSTRDELL	SARDEILLLH	QAAAKVASER
570	580	590	600	610	620	630	640
DTDIASLQEE	LKKVRAELER	WRKAASEYEK	EITSLQNSFQ	LRCQQCEDQQ	REEATRLQGE	LEKLRKEWNA	LETECHSLKR
650	660	670	680	690	700	710	720
ENVLLSSELQ	RQEKELHNSQ	KQSLELTSDL	SILQMSRKEL	ENQVGSLKEQ	HLRDSADLKT	LLSKAENQAK	DVQKEYEKTQ
730	740	750	760	770	780	790	800
TVLSELKLKF	EMTEQEKQSI	TDELKQCKNN	LKLLREKGNN	KPWPWMPMLA	ALVAVTAIVL	YVPGLARASP	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1042	1	586.1730	-249.89	2	41.3	10.5	0	467-476	K.ELIEAQELAR.T	

Detailed Protein Report

Protein 255: 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 256: PREDICTED: bromodomain-containing protein 1 isoform X12 [Homo sapiens]

Accession:	gi|578837129	**Score:**	26.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	110.4
Database Date:	2015-11-30	**pI:**	9.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.9
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 0.87 **CV:** 0.00 % **No. of Peptides:** 1

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	Ratios
832	1	902.3468	-117.98	2	39.2	13.7	1	303-319	R.ARPADCVLCPNKGGAFK.K	Carbamidomethyl: 6	WD:WU 0.87

Detailed Protein Report

Protein 257: 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:	1

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	

Detailed Protein Report

Protein 258: **PREDICTED: zinc finger protein 449 isoform X1 [Homo sapiens]**

Accession:	gi|530422388	**Score:**	26.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	32.2
Database Date:	2015-11-30	**pI:**	10.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	11.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
METMYPFIVT	LEGNALQGPI	LQKDYVQLEN	QWETPPEDLQ	TDLAKLVDQQ	NPTLGETPEN	SNLEEPLNPK	PHKKKSPGEK
90	100	110	120	130	140	150	160
PHRCPQCGKC	FARKSQLTGH	QRIHSGEEPH	KCPECGKRFL	RSSDLYRHQR	LHTGERPYEC	TVCKKRFTRR	SHLIGHQRTH
170	180	190	200	210	220	230	240
SEEETYKCLE	CGKSFCHGSS	LKRHLKTHTG	EKPHRCHNCG	KSFSRLTALT	LHQRTHTEER	PFKCNYCGKS	FRQRPSLVIH
250	260	270	280				
LRIHTGEKPY	KCTHCSKSFR	QRAGLIMHQV	THFRGLI				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2874	1	964.7996	7.38	3	64.7	11.1	2	122-144	R.SSDLYRHQRLHTGERPYECTVCK.K	Carbamidomethyl: 19, 22

Detailed Protein Report

Protein 259: treacle protein isoform b [Homo sapiens]

Accession:	gi|57164975	**Score:**	26.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	144.2
Database Date:	2015-11-30	**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 260: polyadenylate-binding protein 4-like [Homo sapiens]

Accession:	gi|291084655	**Score:**	26.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	48.1
Database Date:	2015-11-30	**pI:**	9.9
		Sequence Coverage [%]:	6.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MRVLPELGES	CLNSIAWPLC	GDPEASTLEP	GQSCDLVSPH	RDCSKNSRGQ	THSGKDKEMN	VAAKYRMASL	YVGDLHADVT
90	100	110	120	130	140	150	160
EDLLFRKFST	VGPVLSIRIC	RDQVTRRSLG	YAYVNFLQLA	DAQKALDTMN	FDIIKGKSIR	LMWSQRDAYL	RRSGIGNVFI
170	180	190	200	210	220	230	240
KNLDKSIDNK	TLYEHFSAFG	KILSSKVMSD	DQGSKGYAFV	HFQNQSAADR	AIEEMNGKLL	KGCKVFVGRF	KNRKDREAEL
250	260	270	280	290	300	310	320
RSKASEFTNV	YIKNFGGDMD	DERLKDVFSK	YGKTLSVKVM	TDSSGKSKGF	GFVSFDSHEA	AKKAVEEMNG	RDINGQLIFV
330	340	350	360	370	380	390	400
GRAQKKVERQ	AELKQMFEQL	KRERIRGCQG	VKLYIKNLDD	TIDDEKLRNE	FSSFGSISRV	KVMQEEGQSK	GFGLICFSSP
410	420	430					
EDATKAMTEM	NGRILGSKPL	SIALAQRH					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1937	1	847.8487	-93.34	2	52.6	15.3	1	353-366	K.LYIKNLDDTIDDEK.L	

Detailed Protein Report

Protein 261: **PREDICTED: mediator of RNA polymerase II transcription subunit 1 isoform X1 [Homo sapiens]**

Accession:	gi|530412429	**Score:**	26.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	149.1
Database Date:	2015-11-30	**pI:**	9.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.8
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MYLALQSLEQ	DLSKMAIMYW	KATNAGPLDK	ILHGSVGYLT	PRSGGHLMNL	KYYVSPSDLL	DDKTASPIIL	HENNVSRSLG
90	100	110	120	130	140	150	160
MNASVTIEGT	SAVYKLPIAP	LIMGSHPVDN	KWTPSFSSIT	SANSVDLPAC	FFLKFPQPIP	VSRAFVQKLQ	NCTGIPLFET
170	180	190	200	210	220	230	240
QPTYAPLYEL	ITQFELSKDP	DPIPLNHNMR	FYAALPGQQH	CYFLNKDAPL	PDGRSLQGTL	VSKITFQHPG	RVPLILNLIR
250	260	270	280	290	300	310	320
HQVAYNTLIG	SCVKRTILKE	DSPGLLQFEV	CPLSESRFSV	SFQHPVNDSL	VCVVMDVQDS	THVSCKLYKG	LSDALICTDD
330	340	350	360	370	380	390	400
FIAKVVQRCM	SIPVTMRAIR	RKAETIQADT	PALSLIAETV	EDMVKKNLPP	ASSPGYGMTT	GNNPMSGTTT	PTNTFPGGPI
410	420	430	440	450	460	470	480
TTLFNMSMSI	KDRHESVGHG	EDFSKVSQNP	ILTSLLQITG	NGGSTIGSSP	TPPHHTPPPV	SSMAGNTKNH	PMLMNLLKDN
490	500	510	520	530	540	550	560
PAQDFSTLYG	SSPLERQNSS	SGSPRMEICS	GSNKTKKKKS	SRLPPEKPKH	QTEDDFQREL	FSMDVDSQNP	IFDVNMTADT
570	580	590	600	610	620	630	640
LDTPHITPAP	SQCSTPPTTY	PQPVPHPQPS	IQRMVRLSSS	DSIGPDVTDI	LSDIAEEASK	LPSTSDDCPA	IGTPLRDSSS
650	660	670	680	690	700	710	720
SGHSQSTLFD	SDVFQTNNNE	NPYTDPADLI	ADAAGSPSSD	SPTNHFFHDG	VDFNPDLLNS	QSQSGFGEEY	FDESSQSGDN
730	740	750	760	770	780	790	800
DDFKGFASQA	LNTLGVPMLG	GDNGETKFKG	NNQADTVDFS	IISVAGKALA	PADLMEHHSG	SQGPLLTTGD	LGKEKTQKRV
810	820	830	840	850	860	870	880
KEGNGTSNST	LSGPGLDSKP	GKRSRTPSND	GKSKDKPPKR	KKADTEGKSP	SHSSSNRPFT	PPTSTGGSKS	PGSAGRSQTP
890	900	910	920	930	940	950	960
PGVATPPIPK	ITIQIPKGTV	MVGKPSSHSQ	YTSSGSVSSS	GSKSHHSHSS	SSSSSASTSG	KMKSSKSEGS	SSSKLSSSMY
970	980	990	1000	1010	1020	1030	1040
SSQGSSGSSQ	SKNSSQSGGK	PGSSPITKHG	LSSGSSSTKM	KPQGKPSSLM	NPSLSKPNIS	PSHSRPPGGS	DKLASPMKPV
1050	1060	1070	1080	1090	1100	1110	1120
PGTPPSSKAK	SPISSGSGGS	HMSGTSSSSG	MKSSSGLGSS	GSLSQKTPPS	SNSCTASSSS	FSSSGSSMSS	SQNQHGSSKG
1130	1140	1150	1160	1170	1180	1190	1200
KSPSRNKKPS	LTAVIDKLKH	GVVTSGPGGE	DPLDGQMGVS	TNSSSHPMSS	KHNMSGGEFQ	GKREKSDKDK	SKVSTSGSSV
1210	1220	1230	1240	1250	1260	1270	1280
DSSKKTSESK	NVGSTGVAKI	IISKHDGGSP	SIKAKVTLQK	PGESSGEGLR	PQMASSKNYG	SPLISGSTPK	HERGSPSHSK
1290	1300	1310	1320	1330	1340	1350	1360
SPAYTPQNLD	SESESGSSIA	EKSYQNSPSS	DDGIRPLPEY	STEKHKKHKK	EKKKVKDKDR	DRDRDKDRDK	KKSHSIKPES
1370	1380	1390	1400	1410			
WSKSPISSDQ	SLSMTSNTIL	SADRPSRLSP	DFMIGEEDDD	LMDVALIGN			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2702	1	842.5321	94.33	3	62.2	11.9	2	307-328	K.LYKGLSDALICTDDFIAKVVQR.C	Carbamidomethyl: 11
1993	1	918.3565	-113.08	2	53.3	14.1	0	750-767	K.GNNQADTVDFSIISVAGK.A	

Detailed Protein Report

Protein 262: putative hexokinase HKDC1 [Homo sapiens]

Accession:	gi|156151420	**Score:**	26.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	102.4
Database Date:	2015-11-30	**pI:**	7.2
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.3
		No. of unique Peptides:	2

```
        10         20         30         40         50         60         70         80
MFAVHLMAFY FSKLKEDQIK KVDRFLYHMR LSDDTLLDIM RRFRAEMEKG LAKDTNPTAA VKMLPTFVRA IPDGSENGEF
        90        100        110        120        130        140        150        160
LSLDLGGSKF RVLKVQVAEE GKRHVQMESQ FYPTPNEIIR GNGTELFEYV ADCLADFMKT KDLKHKKLPL GLTFSFPCRQ
       170        180        190        200        210        220        230        240
TKLEEGVLLS WTKKFKARGV QDTDVVSRLT KAMRRHKDMD VDILALVNDT VGTMMTCAYD DPYCEVGVII GTGTNACYME
       250        260        270        280        290        300        310        320
DMSNIDLVEG DEGRMCINTE WGAFGDDGAL EDIRTEFDRE LDLGSLNPGK QLFEKMISGL YLGELVRLIL LKMAKAGLLF
       330        340        350        360        370        380        390        400
GGEKSSALHT KGKIETRHVA AMEKYKEGLA NTREILVDLG LEPSEADCIA VQHVCTIVSF RSANLCAAAL AAILTRLREN
       410        420        430        440        450        460        470        480
KKVERLRTTV GMDGTLYKIH PQYPKRLHKV VRKLVPSCDV RFLLSESGST KGAAMVTAVA SRVQAQRKQI DRVLALFQLT
       490        500        510        520        530        540        550        560
REQLVDVQAK MRAELEYGLK KKSHGLATVR MLPTYVCGLP DGTEKGKFLA LDLGGTNFRV LLVKIRSGRR SVRMYNKIFA
       570        580        590        600        610        620        630        640
IPLEIMQGTG EELFDHIVQC IADFLDYMGL KGASLPLGFT FSFPCRQMSI DKGTLIGWTK GFKATDCEGE DVVDMLREAI
       650        660        670        680        690        700        710        720
KRRNEFDLDI VAVVNDTVGT MMTCGYEDPN CEIGLIAGTG SNMCYMEDMR NIEMVEGGEG KMCINTEWGG FGDNGCIDDI
       730        740        750        760        770        780        790        800
RTRYDTEVDE GSLNPGKQRY EKMTSGMYLG EIVRQILIDL TKQGLLFRGQ ISERLRTRGI FETKFLSQIE SDRLALLQVR
       810        820        830        840        850        860        870        880
RILQQLGLDS TCEDSIVVKE VCGAVSRRAA QLCGAGLAAI VEKRREDQGL EHLRITVGVD GTLYKLHPHF SRILQETVKE
       890        900        910        920
LAPRCDVTFM LSEDGSGKGA ALITAVAKRL QQAQKEN
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2718	1	648.3573	22.96	2	62.4	12.9	2	43-53	R.FRAEMEKGLAK.D	Oxidation: 5
2984	5	973.5068	-23.83	2	66.1	13.0	2	313-331	K.MAKAGLLFGGEKSSALHTK.G	

Detailed Protein Report

Protein 263: **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	2	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 264: PREDICTED: sp110 nuclear body protein isoform X3 [Homo sapiens]

Accession:	gi|530370295	**Score:**	25.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	58.5
Database Date:	2015-11-30	**pI:**	10.2
		Sequence Coverage [%]:	6.3
		No. of unique 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
1618	1	882.8999	95.52	3	48.5	11.3	2	171-195	R.VTQGAASPGHGIQEKLQVVDKVTQR.K	

Detailed Protein Report

Protein 265: phosphatidylinositol phosphatase PTPRQ precursor [Homo sapiens]

Accession:	gi|222537743	**Score:**	25.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	257.1
Database Date:	2015-11-30	**pI:**	5.4
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.2
		No. of unique Peptides:	2

Detailed Protein Report

10	20	30	40	50	60	70	80
MDFLIIFLLL	FIGTSETQVD	VSNVVPGTRY	DITISSISTT	YTSPVTRIVT	TNVTKPGPPV	FLAGERVGSA	GILLSWNTPP
90	100	110	120	130	140	150	160
NPNGRIISYI	VKYKEVCPWM	QTVYTQVRSK	PDSLEVLLTN	LNPGTTYEIK	VAAENSAGIG	VFSDPFLFQT	AESAPGKVVN
170	180	190	200	210	220	230	240
LTVEAYNASA	VKLIWYLPRQ	PNGKITSFKI	SVKHARSGIV	VKDVSIRVED	ILTGKLPECN	ENSESFLWST	ASPSPTLGRV
250	260	270	280	290	300	310	320
TPPSRTTHSS	STLTQNEISS	VWKEPISFVV	THLRPYTTYL	FEVSAATTEA	GYIDSTIVRT	PESVPEGPPQ	NCVTGNITGK
330	340	350	360	370	380	390	400
SFSILWDPPT	IVTGKFSYRV	ELYGPSGRIL	DNSTKDLKFA	FTNLTPFTMY	DVYIAAETSA	GTGPKSNISV	FTPPDVPGAV
410	420	430	440	450	460	470	480
FDLQLAEVES	TQVRITWKKP	RQPNGIINQY	RVKVLVPETG	IILENTLLTG	NNEYINDPMA	PEIVNIVEPM	VGLYEGSAEM
490	500	510	520	530	540	550	560
SSDLHSLATF	IYNSHPDKNF	PARNRAEDQT	SPVVTTRNQY	ITDIAAEQLS	YVIRRLVPFT	EHMISVSAFT	IMGEGPPTVL
570	580	590	600	610	620	630	640
SVRTRQQVPS	SIKIINYKNI	SSSSILLYWD	PPEYPNGKIT	HYTIYAMELD	TNRAFQITTI	DNSFLITGLK	KYTKYKMRVA
650	660	670	680	690	700	710	720
ASTHVGESSL	SEENDIFVRT	SEDEPESSPQ	DVEVIDVTAD	EIRLKWSPPE	KPNGIIIAYE	VLYKNIDTLY	MKNTSTTDII
730	740	750	760	770	780	790	800
LRNLRPHTLY	NISVRSYTRF	GHGNQVSSLL	SVRTSETVPD	SAPENITYKN	ISSGEIELSF	LPPSSPNGII	QKYTIYLKRS
810	820	830	840	850	860	870	880
NGNEERTINT	TSLTQNIKVL	KKYTQYIIEV	SASTLKGEGV	RSAPISILTE	EDAPDSPPQD	FSVKQLSGVT	VKLSWQPPLE
890	900	910	920	930	940	950	960
PNGIILYYTV	YVWNRSSLKT	INVTETSLEL	SDLDYNVEYS	AYVTASTRFG	DGKTRSNIIS	FQTPEGAPSD	PPKDVYYANL
970	980	990	1000	1010	1020	1030	1040
SSSSIILFWT	PPSKPNGIIQ	YYSVYYRNTS	GTFMQNFTLH	EVTNDFDNMT	VSTIIDKLTI	FSYYTFWLTA	STSVGNGNKS
1050	1060	1070	1080	1090	1100	1110	1120
SDIIEVYTDQ	DIPEGFVGNL	TYESISSTAI	NVSWVPPAQP	NGLVFYYVSL	ILQQTPRHVR	PPLVTYERSI	YFDNLEKYTD
1130	1140	1150	1160	1170	1180	1190	1200
YILKITPSTE	KGFSDTYTAQ	LYIKTEEDVP	ETSPIINTFK	NLSSTSVLLS	WDPPVKPNGA	IISYDLTLQG	PNENYSFITS
1210	1220	1230	1240	1250	1260	1270	1280
DNYIILEELS	PFTLYSFFAA	ARTRKGLGPS	SILFFYTDES	VPLAPPQNLT	LINCTSDFVW	LKWSPSPLPG	GIVKVYSFKI
1290	1300	1310	1320	1330	1340	1350	1360
HEHETDTIYY	KNISGFKTEA	KLVGLEPVST	YSIRVSAFTK	VGNGNQFSNV	VKFTTQESVP	DVVQNMQCMA	TSWQSVLVKW
1370	1380	1390	1400	1410	1420	1430	1440
DPPKKANGII	TQYMVTVERN	STKVSPQDHM	YTFIKLLANT	SYVFKVRAST	SAGEGDESTC	HVSTLPETVP	SVPTNIAFSD
1450	1460	1470	1480	1490	1500	1510	1520
VQSTSATLTW	IRPDTILGYF	QNYKITTQLR	AQKCKEWESE	ECVEYQKIQY	LYEAHLTEET	VYGLKKFRWY	RFQVAASTNA
1530	1540	1550	1560	1570	1580	1590	1600
GYGNASNWIS	TKTLPGPPDG	PPENVHVVAT	SPFSISISWS	EPAVITGPTC	YLIDVKSVDN	DEFNISFIKS	NEENKTIEIK
1610	1620	1630	1640	1650	1660	1670	1680
DLEIFTRYSV	VITAFTGNIS	AAYVEGKSSA	EMIVTTLESA	PKDPPNNMTF	QKIPDEVTKF	QLTFLPPSQP	NGNIQVYQAL
1690	1700	1710	1720	1730	1740	1750	1760
VYREDDPTAV	QIHNLSIIQK	TNTFVIAMLE	GLKGGHTYNI	SVYAVNSAGA	GPKVPMRITM	DIKAPARPKT	KPTPIYDATG
1770	1780	1790	1800	1810	1820	1830	1840
KLLVTSTTIT	IRMPICYYSD	DHGPIKNVQV	LVTETGAQHD	GNVTKWYDAY	FNKARPYFTN	EGFPNPPCTE	GKTKFSGNEE
1850	1860	1870	1880	1890	1900	1910	1920
IYIIGADNAC	MIPGNEDKIC	NGPLKPKKQY	LFKFRATNIM	GQFTDSDYSD	PVKTLGEGLS	ERTVEIILSV	TLCILSIILL
1930	1940	1950	1960	1970	1980	1990	2000
GTAIFAFARI	RQKQKEGGTY	SPQDAEIIDT	KLKLDQLITV	ADLELKDERL	TRLLSYRKSI	KPISKKSFLQ	HVEELCTNNN
2010	2020	2030	2040	2050	2060	2070	2080
LKFQEEFSEL	PKFLQDLSST	DADLPWNRAK	NRFPNIKPYN	NNRVKLIADA	SVPGSDYINA	SYISGYLCPN	EFIATQGPLP
2090	2100	2110	2120	2130	2140	2150	2160
GTVGDFWRMV	WETRAKTLVM	LTQCFEKGRI	RCHQYWPEDN	KPVTVFGDIV	ITKLMEDVQI	DWTIRDLKIE	RHGDCMTVRQ
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
13	1	1002.9641	-45.61	2	29.1	11.9	0	30-47	R.YDITISSISTTYTSPVTR.I	
627	1	604.2948	34.08	2	36.7	13.9	0	1643-1652	K.DPPNNMTFQK.I	Oxidation: 6

Detailed Protein Report

Protein 266: sushi domain-containing protein 1 isoform 3 precursor [Homo sapiens]

Accession:	gi|544063419	**Score:**	25.8
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

Quantitation

WD:WU **Median:** 1.11 **CV:** 0.00 % **No. of 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	Ratios	
844	1	776.9364	79.23	2	39.3	10.6	0	301-313	K.INDVSLFNDTCVR.W	Carbamidomethyl: 11	WD:WU	1.11

Detailed Protein Report

Protein 267: nucleus accumbens-associated protein 1 [Homo sapiens]

Accession:	gi|16418383	**Score:**	25.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	57.2
Database Date:	2015-11-30	**pI:**	5.4
		Sequence Coverage [%]:	4.9
		No. of unique Peptides:	1

Quantitation

WD:WU	**Median:**	1.11	**CV:**	0.00 %	**No. of Peptides:**	1

Alias proteins:

Accession	**Name**	**Description**
gi|578832952	refseq_human (refseq_human_20140103.fasta)	PREDICTED: nucleus accumbens-associated protein 1 isoform X2 [Homo sapiens]
gi|530414464	refseq_human (refseq_human_20140103.fasta)	PREDICTED: nucleus accumbens-associated protein 1 isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MAQTLQMEIP	NFGNSILECL	NEQRLQGLYC	DVSVVVKGHA	FKAHRAVLAA	SSSYFRDLFN	NSRSAVVELP	AAVQPQSFQQ
90	100	110	120	130	140	150	160
ILSFCYTGRL	SMNVGDQFLL	MYTAGFLQIQ	EIMEKGTEFF	LKVSSPSCDS	QGLHAEEAPS	SEPQSPVAQT	SGWPACSTPL
170	180	190	200	210	220	230	240
PLVSRVKTEQ	QESDSVQCMP	VAKRLWDSGQ	KEAGGGGNGS	RKMAKFSTPD	LAANRPHQPP	PPQQAPVVAA	AQPAVAAGAG
250	260	270	280	290	300	310	320
QPAGGVAAAG	GVVSGPSTSE	RTSPGTSSAY	TSDSPGSYHN	EEDEEEDGGE	EGMDEQYRQI	CNMYTMYSMM	NVGQTAEKVE
330	340	350	360	370	380	390	400
ALPEQVAPES	RNRIRVRQDL	ASLPAELINQ	IGNRCHPKLY	DEGDPSEKLE	LVTGTNVYIT	RAQLMNCHVS	AGTRHKVLLR
410	420	430	440	450	460	470	480
RLLASFFDRN	TLANSCGTGI	RSSTNDPRRK	PLDSRVLHAV	KYYCQNFAPN	FKESEMNAIA	ADMCTNARRV	VRKSWMPKVK
490	500	510	520	530			
VLKAEDDAYT	TFISETGKIE	PDMMGVEHGF	ETASHEGEAG	PSAEALQ			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1836	4	916.4485	5.61	2	51.3	14.2	2	184-201	K.RLWDSGQKEAGGGGNGSR.K		WD:WU 1.11

Detailed Protein Report

Protein 268: **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:	2

```
        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
1358	1	727.3750	-7.81	2	45.7	15.7	1	313-324	K.DMVKISMDIFVR.K	
149	1	855.2460	-164.97	2	31.1	10.1	1	748-761	K.RNAWTAECCLCNLR.G	Carbamidomethyl: 8

Detailed Protein Report

Protein 269: PREDICTED: ribonuclease 3 isoform X4 [Homo sapiens]

Accession:	gi|530378791	**Score:**	25.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	151.2
Database Date:	2015-11-30	**pI:**	8.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.2
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 0.82 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MMQGNTCHRM	SFHPGRGCPR	GRGGHGARPS	APSFRPQNLR	LLHPQQPPVQ	YQYEPPSAPS	TTFSNSPAPN	FLPPRPDFVP
90	100	110	120	130	140	150	160
FPPPMPPSAQ	GPLPPCPIRP	PFPNHQMRHP	FPVPPCFPPM	PPPMPCPNNP	PVPGAPPGQG	TFPFMMPPPS	MPHPPPPPVM
170	180	190	200	210	220	230	240
PQQVNYQYPP	GYSHHNFPPP	SFNSFQNNPS	SFLPSANNSS	SPHFRHLPPY	PLPKAPSERR	SPERLKHYDD	HRHRDHSHGR
250	260	270	280	290	300	310	320
GERHRSLDRR	ERGRSPDRRR	QDSRYRSDYD	RGRTPSRHRS	YERSSRSPSR	EKKRARWEEE	KDRWSDNQSS	GKDKNYTSIK
330	340	350	360	370	380	390	400
EKEPEETMPD	KNEEEEEELL	KPVWIRCTHS	ENYYSSDPMD	QVGDSTVVGT	SRLRDLYDKF	EEELGSRQEK	AKAARPPWEP
410	420	430	440	450	460	470	480
PKTKLDEDLE	SSSESECESD	EDSTCSSSSD	SEVFDVIAEI	KRKKAHPDRL	HDELWYNDPG	QMNDGPLCKC	SAKARRTGIR
490	500	510	520	530	540	550	560
HSIYPGEEAI	KPCRPMTNNA	GRLFHYRITV	SPPTNFLTDR	PTVIEYDDHE	YIFEGFSMFA	HAPLTNIPLC	KVIRFNIDYT
570	580	590	600	610	620	630	640
IHFIEEMMPE	NFCVKGLELF	SLFLFRDILE	LYDWNLKGPL	FEDSPPCCPR	FHFMPRFVRF	LPDGGKEVLS	MHQILLYLLR
650	660	670	680	690	700	710	720
CSKALVPEEE	IANMLQWEEL	EWQKYAEECK	GMIVTNPGTK	PSSVRIDQLD	REQFNPDVIT	FPIIVHFGIR	PAQLSYAGDP
730	740	750	760	770	780	790	800
QYQKLWKSYV	KLRHLLANSP	KVKQTDKQKL	AQREEALQKI	RQKNTMRREV	TVELSSQGFW	KTGIRSDVCQ	HAMMLPVLTH
810	820	830	840	850	860	870	880
HIRYHQCLMH	LDKLIGYTFQ	DRCLLQLAMT	HPSHHLNFGM	NPDHARNSLS	NCGIRQPKYG	DRKVHHMHMR	KKGINTLINI
890	900	910	920	930	940	950	960
MSRLGQDDPT	PSRINHNERL	EFLGDAVVEF	LTSVHLYYLF	PSLEEGGLAT	YRTAIVQNQH	LAMLAKKLEL	DRFMLYAHGP
970	980	990	1000	1010	1020	1030	1040
DLCRESDLRH	AMANCFEALI	GAVYLEGSLE	EAKQLFGRLL	FNDPDLREVW	LNYPLHPLQL	QEPNTDRQLI	ETSPVLQKLT
1050	1060	1070	1080	1090	1100	1110	1120
EFEEAIGVIF	THVRLLARAF	TLRTVGFNHL	TLGHNQRMEF	LGDSIMQLVA	TEYLFIHFPD	HHEGHLTLLR	SSLVNNRTQA
1130	1140	1150	1160	1170	1180	1190	1200
KVAEELGMQE	YAITNDKTKR	PVALRTKTLA	DLLESFIAAL	YIDKDLEYVH	TFMNVCFFPR	LKEFILNQDW	NDPKSQLQQC
1210	1220	1230	1240	1250	1260	1270	1280
CLTLRTEGKE	PDIPLYKTLQ	TVGPSHARTY	TVAVYFKGER	IGCGKGPSIQ	QAEMGAAMDA	LEKYNFPQMA	HQKRFIERKY
1290	1300	1310					
RQELKEMRWE	REHQEREPDE	TEDIKK					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
787	1	1115.0348	37.23	2	38.7	10.4	2	2-20	M.MQGNTCHRMSFHPGRGCPR.G	Carbamidomethyl: 6	WD:WU 0.82

Detailed Protein Report

Protein 270: protein strawberry notch homolog 2 isoform 2 [Homo sapiens]

Accession:	gi|154355004	**Score:**	25.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	144.1
Database Date:	2015-11-30	**pI:**	6.2
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MREPLPGSAS	WGTPGPPSAG	TMSQLQLWLQ	FEALNKDSSY	FEDFSNISIF	SSSVDSLSDI	VDTPDFLPAD	SLNQVSTIWD
90	100	110	120	130	140	150	160
DNPAPSTHDK	LFQLSRPFAG	FEDFLPSHST	PLLVSYQEQS	VQSQPEEEDE	AEEEEAEELG	HTETYADYVP	SKSKIGKQHP
170	180	190	200	210	220	230	240
DRVVETSTLS	SVPPPDITYT	LALPSDSGAL	SALQLEAITY	ACQQHEVLLP	SGQRAGFLIG	DGAGVGKGRT	VAGVILENHL
250	260	270	280	290	300	310	320
RGRKKALWFS	VSNDLKYDAE	RDLRDIEATG	IAVHALSKIK	YGDTTTSEGV	LFATYSALIG	ESQAGGQHRT	RLRQILDWCG
330	340	350	360	370	380	390	400
EAFEGVIVFD	ECHKAKNAGS	TKMGKAVLDL	QNKLPLARVV	YASATGASEP	RNMIYMSRLG	IWGEGTPFRN	FEEFLHAIEK
410	420	430	440	450	460	470	480
RGVGAMEIVA	MDMKVSGMYI	ARQLSFSGVT	FRIEEIPLAP	AFECVYNRAA	LLWAEALNVF	QQAADWIGLE	SRKSLWGQFW
490	500	510	520	530	540	550	560
SAHQRFFKYL	CIAAKVRRLV	ELAREELARD	KCVVIGLQST	GEARTREVLG	ENDGHLNCFV	SAAEGVFLSL	IQKHFPSTKR
570	580	590	600	610	620	630	640
KRDRGAGSKR	KRRPRGRGAK	APRLACETAG	VIRISDDSST	ESDPGLDSDF	NSSPESLVDD	DVVIVDAVGL	PSDDRGPLCL
650	660	670	680	690	700	710	720
LQRDPHGPGV	LERVERLKQD	LLDKVRRLGR	ELPVNTLDEL	IDQLGGPQRV	AEMTGRKGRV	VSRPDGTVAF	ESRAEQGLSI
730	740	750	760	770	780	790	800
DHVNLREKQR	FMSGEKLVAI	ISEASSSGVS	LQADRRVQNQ	RRRVHMTLEL	PWSADRAIQQ	FGRTHRSNQV	SAPEYVFLIS
810	820	830	840	850	860	870	880
ELAGERRFAS	IVAKRLESLG	ALTHGDRRAT	ESRDLSKYNF	ENKYGTRALH	CVLTTILSQT	ENKVPVPQGY	PGGVPTFFRD
890	900	910	920	930	940	950	960
MKQGLLSVGI	GGRESRNGCL	DVEKDCSITK	FLNRILGLEV	HKQNALFQYF	SDTFDHLIEM	DKREGKYDMG	ILDLAPGIEE
970	980	990	1000	1010	1020	1030	1040
IYEESQQVFL	APGHPQDGQV	VFYKISVDRG	LKWEDAFAKS	LALTGPYDGF	YLSYKVRGNK	PSCLLAEQNR	GQFFTVYKPN
1050	1060	1070	1080	1090	1100	1110	1120
IGRQSQLEAL	DSLRRKFHRV	TAEEAKEPWE	SGYALSLTHC	SHSAWNRHCR	LAQEGKDCLQ	GLRLRHHYML	CGALLRVWGR
1130	1140	1150	1160	1170	1180	1190	1200
IAAVMADVSS	SSYLQIVRLK	TKDRKKQVGI	KIPEGCVRRV	LQELRLMDAD	VKRRQAPALG	CPAPPAPRPL	ALPCGPGEVL
1210	1220	1230	1240	1250	1260	1270	1280
DLTYSPPAEA	FPPPPHFSFP	APLSLDAGPG	VVPLGTPDAQ	ADPAALAHQG	CDINFKEVLE	DMLRSLHAGP	PSEGALGEGA
1290	1300	1310					
GAGGAAGGGP	ERQSVIQFSP	PFPGAQAPL					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2599	1	665.2392	-138.50	2	60.7	12.3	0	1106-1116	R.HHYMLCGALLR.V	Oxidation: 4

Detailed Protein Report

Protein 271: prolow-density lipoprotein receptor-related protein 1 precursor [Homo sapiens]

Accession:	gi|126012562	**Score:**	25.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	504.3
Database Date:	2015-11-30	**pI:**	5.0
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	0.7
		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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
127	2	849.3809	-43.54	2	30.9	15.1	1	1560-1573	R.TVSCACPHLMKLHK.D	Carbamidomethyl: 4, 6; Oxidation: 10

Detailed Protein Report

Protein 272: **PREDICTED: tolloid-like protein 1 isoform X2 [Homo sapiens]**

Accession:	gi|530378097	**Score:**	25.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	82.0
Database Date:	2015-11-30	**pI:**	5.5
		Sequence Coverage [%]:	3.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MISTVSCTMP	GTPSQGWSLR	GMFLDTILPS	RDDNGIRPAI	GQRTRLSKGD	IAQARKLYRC	PACGETLQES	NGNLSSPGFP
90	100	110	120	130	140	150	160
NGYPSYTHCI	WRVSVTPGEK	IVLNFTTMDL	YKSSLCWYDY	IEVRDGYWRK	SPLLGRFCGD	KLPEVLTSTD	SRMWIEFRSS
170	180	190	200	210	220	230	240
SNWVGKGFAA	VYEAICGGEI	RKNEGQIQSP	NYPDDYRPMK	ECVWKITVSE	SYHVGLTFQS	FEIERHDNCA	YDYLEVRDGT
250	260	270	280	290	300	310	320
SENSPLIGRF	CGYDKPEDIR	STSNTLWMKF	VSDGTVNKAG	FAANFFKEED	ECAKPDRGGC	EQRCLNTLGS	YQCACEPGYE
330	340	350	360	370	380	390	400
LGPDRRSCEA	ACGGLLTKLN	GTITTPGWPK	EYPPNKNCVW	QVVAPTQYRI	SVKFEFFELE	GNEVCKYDYV	EIWSGLSSES
410	420	430	440	450	460	470	480
KLHGKFCGAE	VPEVITSQFN	NMRIEFKSDN	TVSKKGFKAH	FFSDKDECSK	DNGGCQHECV	NTMGSYMCQC	RNGFVLHDNK
490	500	510	520	530	540	550	560
HDCKEAECEQ	KIHSPSGLIT	SPNWPDKYPS	RKECTWEISA	TPGHRIKLAF	SEFEIEQHQE	CAYDHLEVFD	GETEKSPILG
570	580	590	600	610	620	630	640
RLCGNKIPDP	LVATGNKMFV	RFVSDASVQR	KGFQATHSTE	CGGRLKAESK	PRDLYSHAQF	GDNNYPGQVD	CEWLLVSERG
650	660	670	680	690	700	710	720
SRLELSFQTF	EVEEEADCGY	DYVELFDGLD	STAVGLGRFC	GSGPPEEIYS	IGDSVLIHFH	TDDTINKKGF	HIRYKSIRYP
730							
DTTHTKK							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
556	1	658.3907	22.79	2	35.8	11.5	2	44-55	R.TRLSKGDIAQAR.K	

Detailed Protein Report

Protein 273: PREDICTED: glucose-6-phosphate 1-dehydrogenase isoform X2 [Homo sapiens]

Accession: gi|530422749
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 25.5
MW [kDa]: 59.4
pI: 6.6
Sequence Coverage [%]: 4.8
No. of unique Peptides: 1

```
        10         20         30         40         50         60         70         80
MAEQVALSRT QVCGILREEL FQGDAFHQSD THIFIIMGAS GDLAKKKIYP TIWWLFRDGL LPENTFIVGY ARSRLTVADI
        90        100        110        120        130        140        150        160
RKQSEPFFKA TPEEKLKLED FFARNSYVAG QYDDAASYQR LNSHMNALHL GSQANRLFYL ALPPTVYEAV TKNIHESCMS
       170        180        190        200        210        220        230        240
QIRGWNRIIV EKPFGRDLQS SDRLSNHISS LFREDQIYRI DHYLGKEMVQ NLMVLRFANR IFGPIWNRDN IACVILTFKE
       250        260        270        280        290        300        310        320
PFGTEGRGGY FDEFGIIRDV MQNHLLQMLC LVAMEKPAST NSDDVRDEKV KVLKCISEVQ ANNVVLGQYV GNPDGEGEAT
       330        340        350        360        370        380        390        400
KGYLDDPTVP RGSTTATFAA VVLYVENERW DGVPFILRCG KALNERKAEV RLQFHDVAGD IFHQQCKRNE LVIRVQPNEA
       410        420        430        440        450        460        470        480
VYTKMMTKKP GMFFNPEESE LDLTYGNRYK NVKLPDAYER LILDVFCGSQ MHFVRSDELR EAWRIFTPLL HQIELEKPKP
       490        500        510        520
IPYIYGSRGP TEADELMKRV GFQYEGTYKW VNPHKL
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2614	1	659.1695	-206.35	2	61.0	15.2	0	153-163	K.NIHESCMSQIR.G	

Detailed Protein Report

Protein 274: scaffold attachment factor B1 isoform 4 [Homo sapiens]

Accession:	gi|321267473	**Score:**	25.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	95.1
Database Date:	2015-11-30	**pI:**	6.0
		Sequence Coverage [%]:	2.6
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 1.08 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MAETLSGLGD	SGAAGAAALS	SASSETGTRR	LSDLRVIDLR	AELRKRNVDS	SGNKSVLMER	LKKAIEDEGG	NPDEIEITSE
90	100	110	120	130	140	150	160
GNKKTSKRSS	KGRKPEEEGV	EDNGLEENSG	DGQIEDKETI	NNLDTSSSDF	TILQEIEEPS	LEPENEKILD	ILGETCKSEP
170	180	190	200	210	220	230	240
VKEESSELEQ	PFAQDTSSVG	PDRKLAEEED	LFDSAHPEEG	DLDLASESTA	HAQSSKADSL	LAVVKREPAE	QPGDGERTDC
250	260	270	280	290	300	310	320
EPVGLEPAVE	QSSAASELAE	ASSEELAEAP	TEAPSPEARD	SKEDGRKFDF	DACNEVPPAP	KESSTSEGAD	QKMSSPEDDS
330	340	350	360	370	380	390	400
DTKRLSKEEK	GRSSCGRNFW	VSGLSSTTRA	TDLKNLFSKY	GKVVGAKVVT	NARSPGARCY	GFVTMSTAEE	ATKCINHLHK
410	420	430	440	450	460	470	480
TELHGKMISV	EKAKNEPVGK	KTSDKRDSDG	KKEKSSNSDR	STNLKRDDKC	DRKDDAKKGD	DGSGEKSKDQ	DDQKPGPSER
490	500	510	520	530	540	550	560
SRATKSGSRG	TERTVVMDKS	KGVPVISVKT	SGSKERASKS	QDRKSASREK	RSVVSFDKVK	EPRKSRDSES	HSRVRERSER
570	580	590	600	610	620	630	640
EQRMQAQWER	EERERLEIAR	ERLAFQRQRL	ERERMERERL	ERERMHVEHE	RRREQERIHR	EREELRRQQE	LRYEQERRPA
650	660	670	680	690	700	710	720
VRRPYDLDRR	DDAYWPEAKR	AALDERYHSD	FNRQDRFHDF	DHRDRGRYPD	HSVDRREGSR	SMMGEREGQH	YPERHGGPER
730	740	750	760	770	780	790	800
HGRDSRDGWG	GYGSDKRMSE	GRGLPPPPRG	RRDWGDHGRR	EDDRSWQGTA	DGGMMDRDHK	RWQGGERSMS	GHSGPGHMMN
810	820	830	840	850			
RGGMSGRGSF	APGGASRGHP	IPHGGMQGGF	GGQSRGSRPS	DARFTRRY			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
980	2	530.6065	-255.21	2	40.6	14.1	1	545-553	K.SRDSESHSR.V		WD:WU 1.08

Detailed Protein Report

Protein 275: 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 276: **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:	2

Quantitation

WD:WU	**Median:** 1.62	**CV:** 0.00 %	**No. of Peptides:** 1

10	20	30	40	50	60	70	80
MAENGKNCDQ	RRVAMNKEHH	NGNFTDPSSV	NEKKREREE	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	Ratios
2411	1	669.6353	-215.87	2	58.5	12.4	1	1-11	-.MAENGKNCDQR.R	Carbamidomethyl: 8; Oxidation: 1	WD:WU 1.62
443	2	699.2695	-93.64	3	34.5	13.0	2	18-35	K.EHHNGNFTDPSSVNEKKR.R		

Detailed Protein Report

Protein 277: PREDICTED: peroxisomal acyl-coenzyme A oxidase 2 isoform X3 [Homo sapiens]

Accession:	gi|578806607	**Score:**	25.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	65.2
Database Date:	2015-11-30	**pI:**	7.3
Modification(s):	Oxidation	**Sequence Coverage [%]:**	5.5
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MKQVGEKISR	ALSGDVALNI	HRVFVRALRS	LGSEEQIAKW	DPLCKNIQII	ATYAQTELGH	GTYLQGLETE	ATYDAATQEF
90	100	110	120	130	140	150	160
VIHSPTLTAT	KWWPGDLGRS	ATHALVQAQL	ICSGARRGMH	AFIVPIRSLQ	DHTPLPGIII	GDIGPKMDFD	QTDNGFLQLN
170	180	190	200	210	220	230	240
HVRVPRENML	SRFAQVLPDG	TYVKLGTAQS	NYLPMVVVRV	ELLSGEILPI	LQKACVIAMR	YSVIRRQSRL	RPSDPEAKVL
250	260	270	280	290	300	310	320
DYQTQQQKLF	PQLAISYAFH	FLAVSLLEFF	QHSYTAILNQ	DFSFLPELHA	LSTGMKAMMS	EFCTQGAEMC	RRACGGHGYS
330	340	350	360	370	380	390	400
KLSGLPSLVT	KLSASCTYEG	ENTVLYLQVA	RFLVKSYLQT	QMSPGSTPQR	SLSPSVAYLT	APDLARCPAQ	RAADFLCPEL
410	420	430	440	450	460	470	480
YTTAWAHVAV	RLIKDSVQHL	QTLTQSGADQ	HEAWNQTTVI	HLQAAKVHCY	YVTVKGFTEA	LEKLENEPAI	QQVLKRLCDL
490	500	510	520	530	540	550	560
HAIHGILTNS	GDFLHDAFLS	GAQVDMARTA	YLDLLRLIRK	DAILLTDAFD	FTDQCLNSAL	GCYDGNVYER	LFQWAQKSPT
570	580	590					
NTQENPAYEE	YIRPLLQSWR	SKL					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2421	1	863.4315	-29.41	2	58.6	10.1	0	100-116	R.SATHALVQAQLICSGAR.R	
2448	1	863.7544	-77.93	2	58.9	15.3	0	297-311	K.AMMSEFCTQGAEMCR.R	Oxidation: 2, 13

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Detailed Protein Report

Protein 278: PREDICTED: uncharacterized protein C6orf201 isoform X6 [Homo sapiens]

Accession:	gi|578811686	**Score:**	25.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	15.9
Database Date:	2015-11-30	**pI:**	12.3
		Sequence Coverage [%]:	10.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MASGPLGPGA	RPTRLHPPFP	PPAHIKPGAP	PGENPELSGL	ERILARHQLP	KEINLTPKPN	RMPPWKRKII	NNVTDGWKKC
90	**100**	**110**	**120**	**130**	**140**	**150**	
HLLKRNTKEP	PMSTIVVRKL	IQKNVPRRHS	LRNTSRKLRN	LPTTAKGTQT	GKSQCLLGIS	EPT	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1772	1	793.3983	-70.98	2	50.8	25.4	2	118-132	K.LRNLPTTAKGTQTGK.S	

Detailed Protein Report

Protein 279: brain-specific angiogenesis inhibitor 1 precursor [Homo sapiens]

Accession:	gi|111118994	**Score:**	25.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	173.4
Database Date:	2015-11-30	**pI:**	9.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.8
		No. of unique Peptides:	2

Quantitation

WD:WU **Median:** 0.46 **CV:** 0.00 % **No. of Peptides:** 1

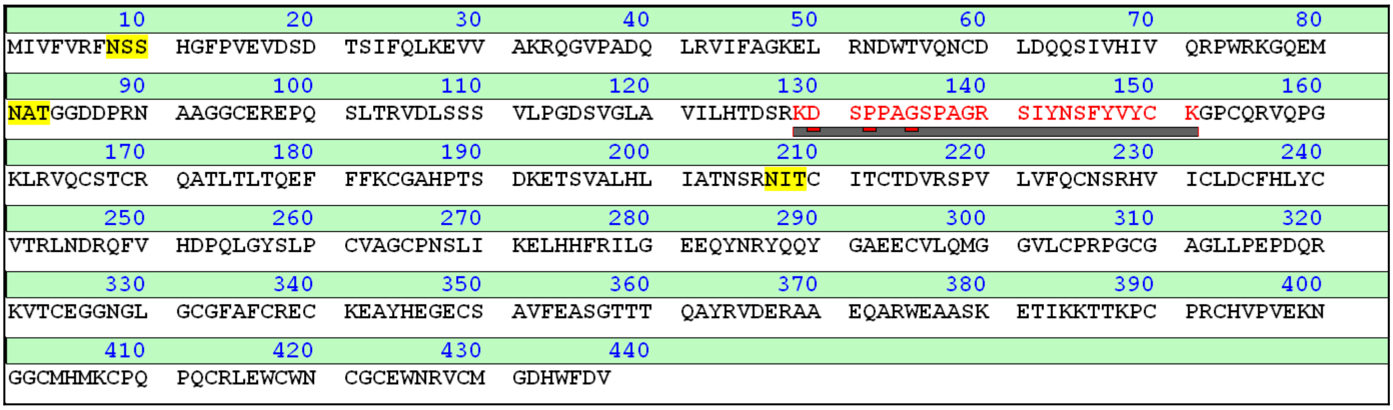
```
        10         20         30         40         50         60         70         80
MRGQAAAPGP VWILAPLLLL LLLLGRRARA AAGADAGPGP EPCATLVQGK FFGYFSAAAV FPANASRCSW TLRNPDPRRY
        90        100        110        120        130        140        150        160
TLYMKVAKAP VPCSGPGRVR TYQFDSFLES TRTYLGVESF DEVLRLCDPS APLAFLQASK QFLQMRRQQP PQHDGLRPRA
       170        180        190        200        210        220        230        240
GPPGPTDDFS VEYLVVGNRN PSRAACQMLC RWLDACLAGS RSSHPCGIMQ TPCACLGGEA GGPAAGPLAP RGDVCLRDAV
       250        260        270        280        290        300        310        320
AGGPENCLTS LTQDRGGHGA TGGWKLWSLW GECTRDCGGG LQTRTRTCLP APGVEGGGCE GVLEEGRQCN REACGPAGRT
       330        340        350        360        370        380        390        400
SSRSQSLRST DARRREELGD ELQQFGFPAP QTGDPAAEEW SPWSVCSSTC GEGWQTRTRF CVSSSYSTQC SGPLREQRLC
       410        420        430        440        450        460        470        480
NNSAVCPVHG AWDEWSPWSL CSSTCGRGFR DRTRTCRPPQ FGGNPCEGPE KQTKFCNIAL CPGRAVDGNW NEWSSWSACS
       490        500        510        520        530        540        550        560
ASCSQGRQQR TRECNGPSYG GAECQGHWVE TRDCFLQQCP VDGKWQAWAS WGSCSVTCGA GSQRRERVCS GPFFGGAACQ
       570        580        590        600        610        620        630        640
GPQDEYRQCG TQRCPEPHEI CDEDNFGAVI WKETPAGEVA AVRCPRNATG LILRRCELDE EGIAYWEPPT YIRCVSIDYR
       650        660        670        680        690        700        710        720
NIQMMTREHL AKAQRGLPGE GVSEVIQTLV EISQDGTSYS GDLLSTIDVL RNMTEIFRRA YYSPTPGDVQ NFVQILSNLL
       730        740        750        760        770        780        790        800
AEENRDKWEE AQLAGPNAKE LFRLVEDFVD VIGFRMKDLR DAYQVTDNLV LSIHKLPASG ATDISFPMKG WRATGDWAKV
       810        820        830        840        850        860        870        880
PEDRVTVSKS VFSTGLTEAD EASVFVVGTV LYRNLGSFLA LQRNTTVLNS KVISVTVKPP PRSLRTPLEI EFAHMYNGTT
       890        900        910        920        930        940        950        960
NQTCILWDET DVPSSSAPPQ LGPWSWRGCR TVPLDALRTR CLCDRLSTFA ILAQLSADAN MEKATLPSVT LIVGCGVSSL
       970        980        990       1000       1010       1020       1030       1040
TLLMLVIIYV SVWRYIRSER SVILINFCLS IISSNALILI GQTQTRNKVV CTLVAAFLHF FFLSSFCWVL TEAWQSYMAV
      1050       1060       1070       1080       1090       1100       1110       1120
TGHLRNRLIR KRFLCLGWGL PALVVAISVG FTKAKGYSTM NYCWLSLEGG LLYAFVGPAA AVVLVNMVIG ILVFNKLVSK
      1130       1140       1150       1160       1170       1180       1190       1200
DGITDKKLKE RAGASLWSSC VVLPLLALTW MSAVLAVTDR RSALFQILFA VFDSLEGFVI VMVHCILRRE VQDAVKCRVV
      1210       1220       1230       1240       1250       1260       1270       1280
DRQEEGNGDS GGSFQNGHAQ LMTDFEKDVD LACRSVLNKD IAACRTATIT GTLKRPSLPE EEKLKLAHAK GPPTNFNSLP
      1290       1300       1310       1320       1330       1340       1350       1360
ANVSKLHLHG SPRYPGGPLP DFPNHSLTLK RDKAPKSSFV GDGDIFKKLD SELSRAQEKA LDTSYVILPT ATATLRPKPK
      1370       1380       1390       1400       1410       1420       1430       1440
EEPKYSIHID QMPQTRLIHL STAPEASLPA RSPPSRQPPS GGPPEAPPAQ PPPPPPPPPP PPQQPLPPPP NLEPAPPSLG
      1450       1460       1470       1480       1490       1500       1510       1520
DPGEPAAHPG PSTGPSTKNE NVATLSVSSL ERRKSRYAEL DFEKIMHTRK RHQDMFQDLN RKLQHAAEKD KEVLGPDSKP
      1530       1540       1550       1560       1570       1580       1590
EKQQTPNKRP WESLRKAHGT PTWVKKELEP LQPSPLELRS VEWERSGATI PLVGQDIIDL QTEV
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
273	1	442.6382	-283.34	2	32.1	14.2	0	911-918	R.TVPLDALR.T		WD:WU 0.46
1629	1	711.6687	-83.42	3	49.1	11.1	2	1235-1254	R.SVLNKDIAACRTATITGTLK.R	Carbamidomethyl: 10	

Detailed Protein Report

Protein 280: **E3 ubiquitin-protein ligase parkin isoform 2 [Homo sapiens]**

Accession:	gi|169790971	**Score:**	25.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	48.7
Database Date:	2015-11-30	**pI:**	7.9
		Sequence Coverage [%]:	9.4
		No. of unique Peptides:	1



10	20	30	40	50	60	70	80
MIVFVRFNSS	HGFPVEVDSD	TSIFQLKEVV	AKRQGVPADQ	LRVIFAGKEL	RNDWTVQNCD	LDQQSIVHIV	QRPWRKGQEM
90	100	110	120	130	140	150	160
NATGGDDPRN	AAGGCEREPQ	SLTRVDLSSS	VLPGDSVGLA	VILHTDSRKD	SPPAGSPAGR	SIYNSFYVYC	KGPCQRVQPG
170	180	190	200	210	220	230	240
KLRVQCSTCR	QATLTLTQEF	FFKCGAHPTS	DKETSVALHL	IATNSRNITC	ITCTDVRSPV	LVFQCNSRHV	ICLDCFHLYC
250	260	270	280	290	300	310	320
VTRLNDRQFV	HDPQLGYSLP	CVAGCPNSLI	KELHHFRILG	EEQYNRYQQY	GAEECVLQMG	GVLCPRPGCG	AGLLPEPDQR
330	340	350	360	370	380	390	400
KVTCEGGNGL	GCGFAFCREC	KEAYHEGECS	AVFEASGTTT	QAYRVDERAA	EQARWEAASK	ETIKKTTKPC	PRCHVPVEKN
410	420	430	440				
GGCMHMKCPQ	PQCRLEWCWN	CGCEWNRVCM	GDHWFDV				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2156	1	836.3125	-111.36	3	55.3	11.7	2	129-151	R.KDSPPAGSPAGRSIYNSFYVYCK.G	

Detailed Protein Report

Protein 281: protein AKNAD1 [Homo sapiens]

Accession: gi|91754185
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl, Oxidation

Score: 25.3
MW [kDa]: 92.8
pI: 6.4
Sequence Coverage [%]: 3.7
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MDEADFSEHT	TYKQEDLPYD	GDLSQIKIGN	DYSFTSKKDG	LEVLNQIIFI	ADDPQEKAMH	SETCGNTAVT	IPLGKITENA
90	100	110	120	130	140	150	160
ANKKDEKEKQ	CTAALHIPAN	EGDASKSSIS	DILLHHLSKE	PFLRGQGIDC	ETLPEISNAD	SFEEEAIIKS	IISCYNKNSW
170	180	190	200	210	220	230	240
PKEQTPELTD	QLNPKRDGEN	SNKPGSATTT	EENTSDLEGP	VAAGDSSHQE	NVNVLTKTKG	PGDKQKSYQG	QSPQKQQTEK
250	260	270	280	290	300	310	320
ANSGNTFKYG	QGQVHYQLPD	FSKIAPKVKI	PKNKIINKPL	AIAKQASFSS	KSRDKPTLVQ	DSLETTPESN	CVEKQHQEQK
330	340	350	360	370	380	390	400
GKITEPSQQI	QMEPIVHIHQ	ELLTGIESEA	SLSKLSPTSQ	KGTSSSSSYI	FQKISQGKQM	CQKLKEQTDQ	LKTKVQEFSK
410	420	430	440	450	460	470	480
RIKQDSPYHL	QDKKLVLEKL	QGHLELLEQN	FLATKDKHLT	LQQQVHKHES	TIVGDFDPER	KVEGEIFKLE	MLLEDVKEKM
490	500	510	520	530	540	550	560
DESKYTSAPS	LPVSSPVTLD	DLASTFSSLS	NEIPKEHPGH	PSGPRGSGGS	EVTGTPQGGP	QEAPNEELCE	LAPQTYLNGH
570	580	590	600	610	620	630	640
YGDAAAQNKP	DQVAMRLSSN	SGEDPNGTPR	RQDCAEMTAP	SPSCAFCRRL	LEWKQNVEKK	GHGRINCGRF	SIVLHEKAPH
650	660	670	680	690	700	710	720
SDSTPNSDTG	HSFCSDSGTE	MQSNKCQDCG	TKIPTSRRAC	RKEPTKEFHY	RYNTPGQNYS	NHSKRGAFVQ	PHSLDESKNS
730	740	750	760	770	780	790	800
SPSFLKPKRI	CSQRVNSKSF	KGEHEPTPGK	KKLQAFMTYS	SDPATPSPHF	YSCRISGSKS	LCDFDSTEEI	KSEILNSALD
810	820	830	840				
HALRTATILK	ETTDQMIKTI	AEDLAKAQRW	RNRLKY				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
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 282: **PREDICTED: uncharacterized aarF domain-containing protein kinase 1 isoform X2 [Homo sapiens]**

Accession:	gi|530404248	**Score:**	25.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	52.0
Database Date:	2015-11-30	**pI:**	9.7
		Sequence Coverage [%]:	7.9
		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 283: **zinc finger protein 358 [Homo sapiens]**

Accession:	gi|133922582	**Score:**	25.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	59.2
Database Date:	2015-11-30	**pI:**	6.1
		Sequence Coverage [%]:	2.6
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|530427462	refseq_human (refseq_human_20140103.fasta)	PREDICTED: zinc finger protein 358 isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MRRSVLVRNP	GHKGLRPVYE	ELDSDSEDLD	PNPEDLDPVS	EDPEPDPEDL	NTVPEDVDPS	YEDLEPVSED	LDPDAEAPGS
90	100	110	120	130	140	150	160
EPQDPDPMSS	SFDLDPDVIG	PVPLILDPNS	DTLSPGDPKV	DPISSGLTAT	PQVLATSPAV	LPAPASPPRP	FSCPDCGRAF
170	180	190	200	210	220	230	240
RRSSGLSQHR	RTHSGEKPYR	CPDCGKSFSH	GATLAQHRGI	HTGARPYQCA	ACGKAFGWRS	TLLKHRSSHS	GEKPHHCPVC
250	260	270	280	290	300	310	320
GKAFGHGSLL	AQHLRTHGGP	RPHKCPVCAK	GFGQGSALLK	HLRTHTGERP	YPCPQCGKAF	GQSSALLQHQ	RTHTAERPYR
330	340	350	360	370	380	390	400
CPHCGKAFGQ	SSNLQHHLRI	HTGERPYACP	HCSKAFGQSS	ALLQHLHVHS	GERPYRCQLC	GKAFGQASSL	TKHKRVHEGA
410	420	430	440	450	460	470	480
AAAAAAAAAA	AAAAAAGLGL	GPGLSPASMM	RPGQVSLLGP	DAVSVLGSGL	GLSPGTSSGR	NPDPGSGPGT	LPDPSSKPLP
490	500	510	520	530	540	550	560
GSRSTPSPTP	VESSDPKAGH	DAGPDLVPSP	DLDPVPSPDP	DPVPSPDPNP	VSCPDPCSPT	RGTVSPALPT	GESPEWVQEQ
570							
GALLGPDG							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
770	1	839.4295	62.27	2	38.4	25.2	1	172-186	R.THSGEKPYRCPDCGK.S	

Detailed Protein Report

Protein 284: PREDICTED: fibrillin-3 isoform X1 [Homo sapiens]

Accession:	gi|578833689	**Score:**	25.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	301.1
Database Date:	2015-11-30	**pI:**	4.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.1
		No. of unique Peptides:	2

Quantitation

WD:WU	**Median:** 0.85	**CV:** 0.00 %	**No. of Peptides:** 1

10	20	30	40	50	60	70	80
MTLEGLYLAR	GPLARLLLAW	SALLCMAGGQ	GRWDGALEAA	GPGRVRRRGS	PGILQGPNVC	GSRFHAYCCP	GWRTFPGRSQ
90	100	110	120	130	140	150	160
CVVRSGCSVS	CMNGGTCRGA	SCLCQKGYTG	TVCGQPICDR	GCHNGGRCIG	PNRCACVYGF	MGPQCERDYR	TGPCFGQVGP
170	180	190	200	210	220	230	240
EGCQHQLTGL	VCTKALCCAT	VGRAWGLPCE	LCPAQPHPCR	RGFIPNIHTG	ACQDVDECQA	VPGLCQGGSC	VNMVGSFHCR
250	260	270	280	290	300	310	320
CPVGHRLSDS	SAACEDVNEC	LSLSGLCSGG	DCTNTVGSYV	CTCSQGFASS	LDGTHCLNYR	AGACFSVLFG	GRCAGDLAGH
330	340	350	360	370	380	390	400
YTRRQCCCDR	GRCWAAGPVP	ELCPPRGSNE	FQQLCAQRLP	LLPGHPGLFP	GLLGFGSNGM	GPPLGPARLN	PHGSDARGIP
410	420	430	440	450	460	470	480
SLGPGNSNIG	TATLNQTIDI	CRHFTNLCLN	GRCLPTPSSY	RCECNVGYTQ	DVRGECIDVD	ECTSSPCHHG	DCVNIPGTYH
490	500	510	520	530	540	550	560
CRCYPGFQAT	PTRQACVDVD	ECIVSGGLCH	LGRCVNTEGS	FQCVCNAGFE	LSPDGKNCVD	HNECATSTMC	VNGVCLNEDG
570	580	590	600	610	620	630	640
SFSCLCKPGF	LLAPGGHYCM	DIDECQTPGI	CVNGHCTNTE	GSFRCQCLGG	LAVGTDGRVC	VDTHVRSTCY	GAIEKGSCAR
650	660	670	680	690	700	710	720
PFPGTVTKSE	CCCANPDHGF	GEPCQLCPAK	DSAEFQALCS	SGLGITTDGR	DINECALDPE	VCANGVCENL	RGSYRCVCNL
730	740	750	760	770	780	790	800
GYEAGASGKD	CTDVDECALN	SLLCDNGWCQ	NSPGSYSCSC	PPGFHFWQDT	EICKDVDECL	SSPCVSGVCR	NLAGSYTCKC
810	820	830	840	850	860	870	880
GPGSRLDPSG	TFCLDSTKGT	CWLKIQESRC	EVNLQGASLR	SECCATLGAA	WGSPCERCEI	DPACARGFAR	MTGVTCDDVN
890	900	910	920	930	940	950	960
ECESFPGVCP	NGRCVNTAGS	FRCECPEGLM	LDASGRLCVD	VRLEPCFLRW	DEDECGVTLP	GKYRMDVCCC	SIGAVWGVEC
970	980	990	1000	1010	1020	1030	1040
EACPDPESLE	FASLCPRGLG	FASRDFLSGR	PFYKDVNECK	VFPGLCTHGT	CRNTVGSFHC	ACAGGFALDA	QERNCTDIDE
1050	1060	1070	1080	1090	1100	1110	1120
CRISPDLCGQ	GTCVNTPGSF	ECECFPGYES	GFMLMKNCMD	VDECARDPLL	CRGGTCTNTD	GSYKCQCPPG	HELTAKGTAC
1130	1140	1150	1160	1170	1180	1190	1200
EDIDECSLSD	GLCPHGQCVN	VIGAFQCSCH	AGFQSTPDRQ	GCVDINECRV	QNGGCDVHCI	NTEGSYRCSC	GQGYSLMPDG
1210	1220	1230	1240	1250	1260	1270	1280
RACADVDECE	ENPRVCDQGH	CTNMPGGHRC	LCYDGFMATP	DMRTCVDVDE	CDLNPHICLH	GDCENTKGSF	VCHCQLGYMV
1290	1300	1310	1320	1330	1340	1350	1360
RKGATGCSDV	DECEVGGHNC	DSHASCLNIP	GSFSCRCLPG	WVGDGFECHD	LDECVSQEHR	CSPRGDCLNV	PGSYRCTCRQ
1370	1380	1390	1400	1410	1420	1430	1440
GFAGDGFFCE	DRDECAENVD	LCDNGQCLNA	PGGYRCECEM	GFDPTEDHRA	CQDVDECAQG	NLCAFGSCEN	LPGMFRCICN
1450	1460	1470	1480	1490	1500	1510	1520
GGYELDRGGG	NCTDINECAD	PVNCINGVCI	NTPGSYLCSC	PQDFELNPSG	VGCVDTRAGN	CFLETHDRGD	SGISCSAEIG
1530	1540	1550	1560	1570	1580	1590	1600
VGVTRASCCC	SLGRAWGNPC	ELCPMANTTE	YRTLCPGGEG	FQPNRITVIL	EDIDECQELP	GLCQGGDCVN	TFGSFQCECP
1610	1620	1630	1640	1650	1660	1670	1680
PGYHLSEHTR	ICEDIDECST	HSGICGPGTC	YNTLGNYTCV	CPAEYLQVNG	GNNCMDMRKS	VCFRHYNGTC	QNELAFNVTR
1690	1700	1710	1720	1730	1740	1750	1760
KMCCCSYNIG	QAWNRPCEAC	PTPISPDYQI	LCGNQAPGFL	TDIHTGKPLD	IDECGEIPAI	CANGICINQI	GSFRCECPAG
1770	1780	1790	1800	1810	1820	1830	1840
FNYNSILLAC	EDVDECGSRE	SPCQQNADCI	NIPGSYRCKC	TRGYKLSPGG	ACVGRNECRE	IPNVCSHGDC	MDTEGSYMCL
1850	1860	1870	1880	1890	1900	1910	1920
CHRGFQASAD	QTLCMDIDEC	DRQPCGNGTC	KNIIGSYNCL	CFPGFVVTHN	GDCVDFDECT	TLVGQVCRFG	HCLNTAGSFH
1930	1940	1950	1960	1970	1980	1990	2000
CLCQDGFELT	ADGKNCVDTN	ECLSLAGTCL	PGTCQNLEGS	FRCICPPGFQ	VQSDHCIDID	ECSEEPNLCL	FGTCTNSPGS
2010	2020	2030	2040	2050	2060	2070	2080
FQCLCPPGFV	LSDNGHRCFD	TRQSFCFTRF	EAGKCSVPKA	FNTTKTRCCC	SKRPGEGWGD	PCELCPQEGS	AAFQELCPFG
2090	2100	2110	2120	2130	2140	2150	2160
HGAVPGPDDS	REDVNECAEN	PGVCTNGVCV	NTDGSFRCEC	PFGYSLDFTG	INCVDTDECS	VGHPCGQGTC	TNVIGGFECA
2170	2180	2190	2200	2210	2220	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
147	1	492.5609	80.32	3	31.1	13.5	0	85-98	R.SGCSVSCMNGGTCR.G	Carbamidomethyl: 3, 7	WD:WU 0.85
2042	1	733.5869	-72.63	3	53.9	11.7	2	313-330	R.CAGDLAGHYTRRQCCCDR.G	Carbamidomethyl: 14, 15, 16	

Detailed Protein Report

Protein 285: **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 286: zinc finger protein 92 isoform 4 [Homo sapiens]

Accession:	gi|566559828	**Score:**	25.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	59.4
Database Date:	2015-11-30	**pI:**	10.3
		Sequence Coverage [%]:	1.8
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 0.46 **CV:** 0.00 % **No. of Peptides:** 1

Alias proteins:

Accession	**Name**	**Description**
gi|566559924	refseq_human (refseq_human_20140103.fasta)	zinc finger protein 92 isoform 4 [Homo sapiens]

10	20	30	40	50	60	70	80
MCSHFAQDVW	PEHSIKDSFQ	KVILRTYGKY	GHENLQLRKD	HKSVDACKVY	KGGYNGLNQC	LTTTDSKIFQ	CDKYVKVFHK
90	100	110	120	130	140	150	160
FPNVNRNKIR	HTGKKPFKCK	NRGKSFCMLS	QLTQHKKIHT	REYSYKCEEC	GKAFNWSSTL	TKHKIIHTGE	KPYKCEECGK
170	180	190	200	210	220	230	240
AFNRSSNLTK	HKIIHTGEKP	YKCEECGKAF	NRSSTLTKHK	RIHTEEKPYK	CEECGKAFNQ	FSILNKHKRI	HMEDKPYKCE
250	260	270	280	290	300	310	320
ECGKAFRVFS	ILKKHKIIHT	GEKPYKCEEC	GKAFNQFSNL	TKHKIIHTGE	KPYKCDECGK	AFNQSSTLTK	HKRIHTGEKP
330	340	350	360	370	380	390	400
YKCEECGKAF	KQSSTLTEHK	IIHTGEKPYK	CEKCGKAFSW	SSAFTKHKRN	HMEDKPYKCE	ECGKAFSVFS	TLTKHKIIHT
410	420	430	440	450	460	470	480
REKPYKCEEC	GKAFNQSSIF	TKHKIIHTEG	KSYKCEKCGN	AFNQSSNLTA	RKIIYTGEKP	YKYEECDKAF	NKFSTLITHQ
490	500	510	520				
IIYTGEKPCK	HECGRAFNKS	SNYTKEKLQT					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1095	1	540.7909	-75.68	2	41.9	25.1	1	245-253	K.AFRVFSILK.K		WD:WU 0.46

Protein 287: GH3 domain-containing protein isoform 2 precursor [Homo sapiens]

Accession:	gi|217330592	**Score:**	25.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	53.5
Database Date:	2015-11-30	**pI:**	10.0
		Sequence Coverage [%]:	3.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLLWPLLLLL	LLLPTLALLR	QQRSQDARLS	WLAGLQHRVA	WGALVWAATW	QRRRLEQSTL	HVHQSQQQAL	RWCLQGAQRP
90	100	110	120	130	140	150	160
HCSLRRSTDI	STFRNHLPLT	KAYPEVLAQG	RTARVTLTSP	WPRPLPWPGN	TLGQVGTPGT	KDPRALLLDA	LRSPGLRALE
170	180	190	200	210	220	230	240
AGTAVELLDV	FLGLETDGEE	LAGAIAAGNP	GAPLRERAAE	LREALEQGPR	GLALRLWPKL	QVVVTLDAGG	QAEAVAALGA
250	260	270	280	290	300	310	320
LWCQGLAFFS	PAYAASGGVL	GLNLQPEQPH	GLYLLPPGAP	FIELLPVKEG	TQEEAASTLL	LAEAQQGKEY	ELVLTDRASL
330	340	350	360	370	380	390	400
TRCRLGDVVR	VVGAYNQCPV	VRFICRLDQT	LSVRGEDIGE	DLFSEALGRA	VGQWAGAKLL	DHGCVESSIL	DSSAGSAPHY
410	420	430	440	450	460	470	480
EVFVALRGLR	NLSEENRDKL	DHCLQEASPR	YKSLRFWGSV	GPARVHLVGQ	GAFRALRAAL	AACPSSPFPP	AMPRVLRHRH
490	500						
LAQCLQERVV	S						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2063	1	634.7944	-18.66	2	54.2	10.9	0	420-430	K.LDHCLQEASPR.Y	

Detailed Protein Report

Protein 288: PREDICTED: glutamine-rich protein 2 isoform X2 [Homo sapiens]

Accession:	gi|578831523	**Score:**	25.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	72.2
Database Date:	2015-11-30	**pI:**	9.9
Modification(s):	Oxidation	**Sequence Coverage [%]:**	5.5
		No. of unique Peptides:	1

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
592	1	1105.2058	124.92	2	35.8	10.7	1	151-169	R.YEQLQDMVNSLAVSRPSKK.A	Oxidation: 7

Detailed Protein Report

Protein 289: retinoblastoma-associated protein [Homo sapiens]

Accession:	gi|108773787	**Score:**	25.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	106.1
Database Date:	2015-11-30	**pI:**	8.9
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	1.8
		No. of unique Peptides:	2

Quantitation

WD:WU **Median:** 5.87 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MPPKTPRKTA	ATAAAAAAEP	PAPPPPPPPE	EDPEQDSGPE	DLPLVRLEFE	ETEEPDFTAL	CQKLKIPDHV	RERAWLTWEK
90	100	110	120	130	140	150	160
VSSVDGVLGG	YIQKKKELWG	ICIFIAAVDL	DEMSFTFTEL	QKNIEISVHK	FFNLLKEIDT	STKVDNAMSR	LLKKYDVLFA
170	180	190	200	210	220	230	240
LFSKLERTCE	LIYLTQPSSS	ISTEINSALV	LKVSWITFLL	AKGEVLQMED	DLVISFQLML	CVLDYFIKLS	PPMLLKEPYK
250	260	270	280	290	300	310	320
TAVIPINGSP	RTPRRGQNRS	ARIAKQLEND	TRIIEVLCKE	HECNIDEVKN	VYFKNFIPFM	NSLGLVTSNG	LPEVENLSKR
330	340	350	360	370	380	390	400
YEEIYLKNKD	LDARLFLDHD	KTLQTDSIDS	FETQRTPRKS	NLDEEVNVIP	PHTPVRTVMN	TIQQLMMILN	SASDQPSENL
410	420	430	440	450	460	470	480
ISYFNNCTVN	PKESILKRVK	DIGYIFKEKF	AKAVGQGCVE	IGSQRYKLGV	RLYYRVMESM	LKSEEERLSI	QNFSKLLNDN
490	500	510	520	530	540	550	560
IFHMSLLACA	LEVVMATYSR	STSQNLDSGT	DLSFPWILNV	LNLKAFDFYK	VIESFIKAEG	NLTREMIKHL	ERCEHRIMES
570	580	590	600	610	620	630	640
LAWLSDSPLF	DLIKQSKDRE	GPTDHLESAC	PLNLPLQNNH	TAADMYLSPV	RSPKKKGSTT	RVNSTANAET	QATSAFQTQK
650	660	670	680	690	700	710	720
PLKSTSLSLF	YKKVYRLAYL	RLNTLCERLL	SEHPELEHII	WTLFQHTLQN	EYELMRDRHL	DQIMMCSMYG	ICKVKNIDLK
730	740	750	760	770	780	790	800
FKIIVTAYKD	LPHAVQETFK	RVLIKEEEYD	SIIVFYNSVF	MQRLKTNILQ	YASTRPPTLS	PIPHIPRSPY	KFPSSPLRIP
810	820	830	840	850	860	870	880
GGNIYISPLK	SPYKISEGLP	TPTKMTPRSR	ILVSIGESFG	TSEKFQKINQ	MVCNSDRVLK	RSAEGSNPPK	PLKKLRFDIE
890	900	910	920	930			
GSDEADGSKH	LPGESKFQQK	LAEMTSTRTR	MQKQKMNDSM	DTSNKEEK			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1645	2	1045.0357	59.07	2	49.3	10.1	1	699-715	R.HLDQIMMCSMYGICKVK.N	Carbamidomethyl: 14; Oxidation: 6, 7	
1658	2	1045.0497	72.41	2	49.4	15.0	1	699-715	R.HLDQIMMCSMYGICKVK.N	Carbamidomethyl: 14; Oxidation: 6, 10	WD:WU 5.87

Detailed Protein Report

Protein 290: **PREDICTED: vinexin isoform X5 [Homo sapiens]**

Accession:	gi|578815141	**Score:**	25.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	73.7
Database Date:	2015-11-30	**pI:**	9.9
		Sequence Coverage [%]:	4.7
		No. of unique Peptides:	2

```
        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	
1731	1	803.8844	-67.43	2	50.0	12.1	2	369-382	K.AARLKFDFQAQSPK.E	

Detailed Protein Report

Protein 291: **PREDICTED: E3 ubiquitin-protein ligase RNF220 isoform X7 [Homo sapiens]**

Accession:	gi|578799381	**Score:**	25.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	35.4
Database Date:	2015-11-30	**pI:**	6.8
		Sequence Coverage [%]:	6.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDLHRAAFKM	ENSSYLPNPL	ASPALMVLAS	TAEASRDASI	PCQQPRPFGV	PVSVDKDVHI	PFTNGSYTFA	SMYHRQGGVP
90	100	110	120	130	140	150	160
GTFANRDFPP	SLLHLHPQFA	PPNLDCTPIS	MLNHSGVGAF	RPFASTEDRE	SYQSAFTPAK	RLKNCHDTES	PHLRFSDADG
170	180	190	200	210	220	230	240
KEYDFGTQLP	SSSPGSLKVD	DTGKKIFAVS	GLISDREASS	SPEDRNDRCK	KKAAALFDSQ	APICPICQVL	LRPSELQEHM
250	260	270	280	290	300	310	320
EQELEQLAQL	PSSKNSLLKD	AMAPGTPKSL	LLSASIKREG	ESPTASPHSS	ATDDLHHSDR	YQTFLRVRAN	RQTRLNEGRL
330							
LHG							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2277	1	775.3245	-72.44	2	56.8	11.4	1	142-154	R.LKNCHDTESPHLR.F	

Detailed Protein Report

Protein 292: beta-defensin 119 isoform a precursor [Homo sapiens]

Accession:	gi|37704382	**Score:**	24.9
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

Quantitation

WD:WU **Median:** 0.88 **CV:** 0.00 % **No. of 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	Ratios
1509	1	981.9713	5.72	2	47.6	13.7	2	24-40	R.HILRCMGNSGICRASCK.K	Carbamidomethyl: 12, 16	WD:WU 0.88

Detailed Protein Report

Protein 293: zinc finger protein with KRAB and SCAN domains 1 isoform c [Homo sapiens]

Accession:	gi|559098399	**Score:**	24.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	39.3
Database Date:	2015-11-30	**pI:**	10.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	8.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MASALFTADS	QAMVKIEDMA	VSLILEEWGC	QNLARRNLSR	DNRQENYGSA	FPQGGENRNE	NEESTSKAET	SEDSASRGET
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
TGRSQKEFGE	KRDQEGKTGE	RQQKNPEEKT	RKEKRDSGPA	IGKDKKTITG	ERGPREKGKG	LGRSFSLSSN	FTTPEEVPTG
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
TKSHRCDECG	KCFTRSSSLI	RHKIIHTGEK	PYECSECGKA	FSLNSNLVLH	QRIHTGEKPH	ECNECGKAFS	HSSNLILHQR
250	**260**	**270**	**280**	**290**	**300**	**310**	**320**
IHSGEKPYEC	NECGKAFSQS	SDLTKHQRIH	TGEKPYECSE	CGKAFNRNSY	LILHRRIHTR	EKPYKCTKCG	KAFTRSSTLT
330	**340**	**350**	**360**				
LHHRIHARER	ASEYSPASLD	AFGAFLKSCV					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1971	1	1079.8531	-128.17	2	53.3	10.5	1	266-283	K.HQRIHTGEKPYECSECGK.A	Carbamidomethyl: 16

Detailed Protein Report

Protein 294: **protein lin-7 homolog C [Homo sapiens]**

Accession:	gi|8922944	**Score:**	24.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	21.8
Database Date:	2015-11-30	**pI:**	9.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	11.2
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MAALGEPVRL ERDICRAIEL LEKLQRSGEV PPQKLQALQR VLQSEFCNAV REVYEHVYET VDISSSPEVR ANATAKATVA
        90        100        110        120        130        140        150        160
AFAASEGHSH PRVVELPKTE EGLGFNIMGG KEQNSPIYIS RIIPGGIADR HGGLKRGDQL LSVNGVSVEG EHHEKAVELL
       170        180        190        200
KAAQGKVKLV VRYTPKVLEE MESRFEKMRS AKRRQQT
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2712	1	878.0523	93.56	2	62.4	10.8	2	2-16	M.AALGEPVRLERDICR.A	Carbamidomethyl: 14

Detailed Protein Report

Protein 295: myosin-13 [Homo sapiens]

Accession:	gi|110624781	**Score:**	24.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	223.5
Database Date:	2015-11-30	**pI:**	5.4
		Sequence Coverage [%]:	1.4
		No. of unique Peptides:	1

Quantitation

WD:WU	**Median:** 0.84	**CV:** 0.00 %	**No. of Peptides:** 1

Detailed Protein Report

```
        10         20         30         40         50         60         70         80
MSSDAEMAIF GEAAPYLRKP EKERIEAQNR PFDSKKACFV ADNKEMYVKG MIQTRENDKV IVKTLDDRML TLNNDQVFPM
        90        100        110        120        130        140        150        160
NPPKFDKIED MAMMTHLHEP AVLYNLKERY AAWMIYTYSG LFCVTVNPYK WLPVYKPEVV AAYRGKKRQE APPHIFSISD
       170        180        190        200        210        220        230        240
NAYQFMLTDR DNQSILITGE SGAGKTVNTK RVIQYFATIA VTGDKKKETQ PGKMQGTLED QIIQANPLLE AFGNAKTVRN
       250        260        270        280        290        300        310        320
DNSSRFGKFI RIHFGATGKL ASADIETYLL EKSRVTFQLS SERSYHIFYQ IMSNKKPELI DLLLISTNPF DFPFVSQGEV
       330        340        350        360        370        380        390        400
TVASIDDSEE LLATDNAIDI LGFSSEEKVG IYKLTGAVMH YGNMKFKQKQ REEQAEPDGT EVADKAGYLM GLNSAEMLKG
       410        420        430        440        450        460        470        480
LCCPRVKVGN EYVTKGQNVQ QVTNSVGALA KAVYEKMFLW MVTRINQQLD TKQPRQYFIG VLDIAGFEIF DFNSLEQLCI
       490        500        510        520        530        540        550        560
NFTNEKLQQF FNHHMFVLEQ EEYKKEGIEW EFIDFGMDLA ACIELIEKPM GIFSILEEEC MFPKATDTSF KNKLYDQHLG
       570        580        590        600        610        620        630        640
KSNNFQKPKP AKGKAEAHFS LVHYAGTVDY NIAGWLDKNK DPLNETVVGL YQKSSLKLLS FLFSNYAGAE TGDSGGSKKG
       650        660        670        680        690        700        710        720
GKKKGSSFQT VSAVFRENLN KLMTNLRSTH PHFVRCLIPN ETKTPGVMDH YLVMHQLRCN GVLEGIRICR KGFPSRILYA
       730        740        750        760        770        780        790        800
DFKQRYRILN ASAIPEGQFI DSKNASEKLL NSIDVDREQF RFGNTKVFFK AGLLGLLEEM RDEKLVTLMT STQAVCRGYL
       810        820        830        840        850        860        870        880
MRVEFKKMME RRDSIFCIQY NIRSFMNVKH WPWMNLFFKI KPLLKSAEAE KEMATMKEDF ERTKEELARS EARRKELEEK
       890        900        910        920        930        940        950        960
MVSLLQEKND LQLQVQSETE NLMDAEERCE GLIKSKILLE AKVKELTERL EEEEEMNSEL VAKKRNLEDK CSSLKRDIDD
       970        980        990       1000       1010       1020       1030       1040
LELTLTKVEK EKHATENKVK NLSEEMTALE ENISKLTKEK KSLQEAHQQT LDDLQVEEDK VNGLIKINAK LEQQTDDLEG
      1050       1060       1070       1080       1090       1100       1110       1120
SLEQEKKLRA DLERAKRKLE GDLKMSQESI MDLENDKQQI EEKLKKKEFE LSQLQAKIDD EQVHSLQFQK KIKELQARIE
      1130       1140       1150       1160       1170       1180       1190       1200
ELEEEIEAEH TLRAKIEKQR SDLARELEEI SERLEEASGA TSAQIEMNKK REAEFQKMRR DLEEATLQHE ATAATLRKKQ
      1210       1220       1230       1240       1250       1260       1270       1280
ADSVAELGEQ IDNLQRVKQK LEKEKSELKM EIDDMASNIE ALSKSKSNIE RTCRTVEDQF SEIKAKDEQQ TQLIHDLNMQ
      1290       1300       1310       1320       1330       1340       1350       1360
KARLQTQNGE LSHRVEEKES LISQLTKSKQ ALTQQLEELK RQMEEETKAK NAMAHALQSS RHDCDLLREQ YEEEQEAKAE
      1370       1380       1390       1400       1410       1420       1430       1440
LQRALSKANS EVAQWRTKYE TDAIQRTEEL EEAKKKLAQR LQEAEENTET ANSKCASLEK TKQRLQGEVE DLMRDLERSH
      1450       1460       1470       1480       1490       1500       1510       1520
TACATLDKKQ RNFDKVLAEW KQKLDESQAE LEAAQKESRS LSTELFKMRN AYEEVVDQLE TLRRENKNLQ EEISDLTEQI
      1530       1540       1550       1560       1570       1580       1590       1600
AETGKNLQEA EKTKKLVEQE KSDLQVALEE VEGSLEHEES KILRVQLELS QVKSELDRKV IEKDEEIEQL KRNSQRAAEA
      1610       1620       1630       1640       1650       1660       1670       1680
LQSVLDAEIR SRNDALRLKK KMEGDLNEME IQLGHSNRQM AETQKHLRTV QGQLKDSQLH LDDALRSNED LKEQLAIVER
      1690       1700       1710       1720       1730       1740       1750       1760
RNGLLLEELE EMKVALEQTE RTRRLSEQEL LDASDRVQLL HSQNTSLINT KKKLEADIAQ CQAEVENSIQ ESRNAEEKAK
      1770       1780       1790       1800       1810       1820       1830       1840
KAITDAAMMA EELKKEQDTS AHLERMKKNL EQTVKDLQHR LDEAEQLALK GGKKQIQKLE NRVRELENEL DVEQKRGAEA
      1850       1860       1870       1880       1890       1900       1910       1920
LKGAHKYERK VKEMTYQAEE DHKNILRLQD LVDKLQAKVK SYKRQAEEAE EQANTQLSRC RRVQHELEEA AERADIAESQ
      1930       1940
VNKLRAKSRD VGSQKMEE
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
112	1	793.8850	-11.43	2	30.7	10.0	0	1098-1110	K.IDDEQVHSLQFQK.K		WD:WU 0.84

Detailed Protein Report

Protein 296: PREDICTED: autophagy-related protein 2 homolog B isoform X1 [Homo sapiens]

Accession:	gi|578825925	**Score:**	24.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	232.5
Database Date:	2015-11-30	**pI:**	5.4
		Sequence Coverage [%]:	1.0
		No. of unique Peptides:	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MPWPFSESIK	KRACRYLLQR	YLGHFLQEKL	SLEQLSLDLY	QGTGSLAQVP	LDKWCLNEIL	ESADAPLEVT	EGFIQSISLS
90	100	110	120	130	140	150	160
VPWGSLLQDN	CALEVRGLEM	VFRPRPRPAT	GSEPMYWSSF	MTSSMQLAKE	CLSQKLTDEQ	GEGSQPFEGL	EKFAETIETV
170	180	190	200	210	220	230	240
LRRVKVTFID	TVLRIEHVPE	NSKTGTALEI	RIERTVYCDE	TADESSGINV	HQPTAFAHKL	LQLSGVSLFW	DEFSASAKSS
250	260	270	280	290	300	310	320
PVCSTAPVET	EPKLSPSWNP	KIIYEPHPQL	TRNLPEIAPS	DPVQIGRLIG	RLELSLTLKQ	NEVLPGAKLD	VDGQIDSIHL
330	340	350	360	370	380	390	400
LLSPRQVHLL	LDMLAAIAGP	ENSSKIGLAN	KDRKNRPMQQ	EDEYRIQMEL	NRYYLRKDSL	SVGVSSEQSF	YETETARTPS
410	420	430	440	450	460	470	480
SREEVFFSMA	DMDMSHSLSS	LPPLGDPPNM	DLELSLTSTY	TNTPAGSPLS	ATVLQPTWGE	FLDHHKEQPV	RGSTFPSNLV
490	500	510	520	530	540	550	560
HPTPLQKTSL	PSRSVSVDES	RPELIFRLAV	GTFSISVLHI	DPLSPPETSQ	NLNPLTPMAV	AFFTCIEKID	PARFSTEDFK
570	580	590	600	610	620	630	640
SFRAVFAEAC	SHDHLRFIGT	GIKVSYEQRQ	RSASRYFSTD	MSIGQMEFLE	CLFPTDFHSV	PPHYTELLTF	HSKEETGSHS
650	660	670	680	690	700	710	720
PVCLQLHYKH	SENRGPQGNQ	ARLSSVPHKA	ELQIKLNPVC	CELDISIVDR	LNSLLQPQKL	ATVEMMASHM	YTSYNKHISL
730	740	750	760	770	780	790	800
HKAFTEVFLD	DSHSPANCRI	SVQVATPALN	LSVRFPIPDL	RSDQERGPWF	KKSLQKEILY	LAFTDLEFKT	EFIGGSTPEQ
810	820	830	840	850	860	870	880
IKLELTFREL	IGSFQEEKGD	PSIKFFHVSS	GVDGDTTSSD	DFDWPRIVLK	INPPAMHSIL	ERIAAEEEEE	NDGHYQEEEE
890	900	910	920	930	940	950	960
GGAHSLKDVC	DLRRPAPSPF	SSRRVMFENE	QMVMPGDPVE	MTEFQDKAIS	NSHYVLELTL	PNIYVTLPNK	SFYEKLYNRI
970	980	990	1000	1010	1020	1030	1040
FNDLLLWEPT	APSPVETFEN	ISYGIGLSVA	SQLINTFNKD	SFSAFKSAVH	YDEESGSEEE	TLQYFSTVDP	NYRSRRKKKL
1050	1060	1070	1080	1090	1100	1110	1120
DSQNKNSQSF	LSVLLNINHG	LIAVFTDVKQ	DNGDLLENKH	GEFWLEFNSG	SLFCVTKYEG	FDDKHYICLH	SSSFSLYHKG
1130	1140	1150	1160	1170	1180	1190	1200
IVNGVILPTE	TRLPSSTRPH	WLEPTIYSSE	EDGLSKTSSD	GVGGDSLNML	SVAVKILSDK	SESNTKEFLI	AVGLKGATLQ
1210	1220	1230	1240	1250	1260	1270	1280
HRMLPSGLSW	HEQILYFLNI	ADEPVLGYNP	PTSFTTFHVH	LWSCALDYRP	LYLPIRSLLT	VETFSVSSSV	ALDKSSSTLR
1290	1300	1310	1320	1330	1340	1350	1360
IILDEAALHL	SDKCNTVTIN	LSRDYVRVMD	MGLLELTITA	VKSDSDGEQT	EPRFELHCSS	DVVHIRTCSD	SCAALMNLIQ
1370	1380	1390	1400	1410	1420	1430	1440
YIASYGDLQT	PNKADMKPGA	FQRRSKVDSS	GRSSSRGPVL	PEADQQMLRD	LMSDAMEEID	MQQGTSSVKP	QANGVLDEKS
1450	1460	1470	1480	1490	1500	1510	1520
QIQEPCCSDL	FLFPDESGNV	SQESGPTYAS	FSHHFISDAM	TGVPTENDDF	CILFAPKAAM	QEKEEEPVIK	IMVDDAIVIR
1530	1540	1550	1560	1570	1580	1590	1600
DNYFSLPVNK	TDTSKAPLHF	PIPVIRYVVK	EVSLVWHLYG	GKDFGIVPPT	SPAKSYISPH	SSPSHTPTRH	GRNTVCGGKG
1610	1620	1630	1640	1650	1660	1670	1680
RNHDFLMEIQ	LSKVKFQHEV	YPPCKPDCDS	SLSEHPVSRQ	VFIVQDLEIR	DRLATSQMNK	FLYLYCSKEM	PRKAHSNMLT
1690	1700	1710	1720	1730	1740	1750	1760
VKALHVCPES	GRSPQECCLR	VSLMPLRLNI	DQDALFFLKD	FFTSLSAEVE	LQMTPDPEVK	KSPGADVTCS	LPRHLSTSKE
1770	1780	1790	1800	1810	1820	1830	1840
PNLVISFSGP	KQPSQNDSAN	SVEVVNGMEE	KNFSAEEASF	RDQPVFFREF	RFTSEVPIRL	DYHGKHVSMD	QGTLAGILIG
1850	1860	1870	1880	1890	1900	1910	1920
LAQLNCSELK	LKRLSYRHGL	LGVDKLFSYA	ITEWLNDIKK	NQLPGILGGV	GPMHSLVQLV	QGLKDLVWLP	IEQYRKDGRI
1930	1940	1950	1960	1970	1980	1990	2000
VRGFQRGAAS	FGTSTAMAAL	ELTNRMVQTI	QAAAETAYDM	VSPGTLSIEP	KKTKRFPHHR	LAHQPVDLRE	GVAKAYSVVK
2010	2020	2030	2040	2050	2060	2070	2080
EGITDTAQTI	YETAAREHES	RGVTGAVGEV	LRQIPPAVVK	PLIVATEATS	NVLGGMRNQI	RPDVRQDESQ	KWRHGDD

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

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2278	1	713.2212	-186.29	2	56.8	10.0	1	549-560	K.IDPARFSTEDFK.S	

Detailed Protein Report

Protein 297: 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

Quantitation

WD:WU	**Median:** 1.32	**CV:** 0.00 %	**No. of 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	Ratios
753	1	541.2892	-37.06	3	38.3	12.1	1	170-183	R.LHLNSNLLRAIDSR.W		WD:WU 1.32

Detailed Protein Report

Protein 298: PREDICTED: LOW QUALITY PROTEIN: spidroin-1-like [Homo sapiens]

Accession:	gi|578798093	**Score:**	24.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	23.4
Database Date:	2015-11-30	**pI:**	12.7
		Sequence Coverage [%]:	4.4
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MRGLDQMEIR	GGPYLLLGEV	VGHSALGAQP	AQAADEVLEL	PALLQRPAGR	RPCASHRGRR	ITPATALLLL	SHRGRAEXAA
90	100	110	120	130	140	150	160
AAKAGSPGRR	RVGKGPPIRE	SWTRSAPQRC	PSQDAGRAGS	RVCRSRPQSR	GGQKAAASGA	KRRGVGGKEL	WRRGQRAATA
170	180	190	200	210	220	230	
KTRGGGGKKP	RGQKPQKATA	AGAKSRGGGG	KKPRRQKTAA	AGAKSRGGGG	NKPQKAAAAG	ICCYQR	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2067	1	643.2889	-61.34	2	54.2	12.7	1	0-0	.AEEAAAAKAGSPGR.	
1162	2	500.6748	-221.98	2	43.2	12.1	2	74-83	R.GRAERAAAAK.A	

Detailed Protein Report

Protein 299:	**PREDICTED: lipopolysaccharide-responsive and beige-like anchor protein isoform X5 [Homo sapiens]**		
Accession:	gi|530378479	**Score:**	24.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	315.5
Database Date:	2015-11-30	**pI:**	5.3
		Sequence Coverage [%]:	1.1
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MASEDNRVPS	PPPTGDDGGG	GGREETPTEG	GALSLKPGLP	IRGIRMKFAV	LTGLVEVGEV	SNRDIVETVF	NLLVGGQFDL
90	100	110	120	130	140	150	160
EMNFIIQEGE	SINCMVDLLE	KCDITCQAEV	WSMFTAILKK	SIRNLQVCTE	VGLVEKVLGK	IEKVDNMIAD	LLVDMLGVLA
170	180	190	200	210	220	230	240
SYNLTVRELK	LFFSKLQGDK	GRWPPHAGKL	LSVLKHMPQK	YGPDAFFNFP	GKSAAAIALP	PIAKWPYQNG	FTFHTWLRMD
250	260	270	280	290	300	310	320
PVNNINVDKD	KPYLYCFRTS	KGLGYSAHFV	GGCLIVTSIK	SKGKGFQHCV	KFDFKPQKWY	MVTIVHIYNR	WKNSELRCYV
330	340	350	360	370	380	390	400
NGELASYGEI	TWFVNTSDTF	DKCFLGSSET	ADANRVFCGQ	MTAVYLFSEA	LNAAQIFAIY	QLGLGYKGTF	KFKAESDLFL
410	420	430	440	450	460	470	480
AEHHKLLLYD	GKLSSAIAFT	YNPRATDAQL	CLESSPKDNP	SIFVHSPHAL	MLQDVKAVLT	HSIQSAMHSI	GGVQVLFPLF
490	500	510	520	530	540	550	560
AQLDYRQYLS	DEIDLTICST	LLAFIMELLK	NSIAMQEQML	ACKGFLVIGY	SLEKSSKSHV	SRAVLELCLA	FSKYLSNLQN
570	580	590	600	610	620	630	640
GMPLLKQLCD	HVLLNPAIWI	HTPAKVQLML	YTYLSTEFIG	TVNIYNTIRR	VGTVLLIMHT	LKYYYWAVNP	QDRSGITPKG
650	660	670	680	690	700	710	720
LDGPRPNQKE	MLSLRAFLLM	FIKQLVMKDS	GVKEDELQAI	LNYLLTMHED	DNLMDVLQLL	VALMSEHPNS	MIPAFDQRNG
730	740	750	760	770	780	790	800
LRVIYKLLAS	KSEGIRVQAL	KAMGYFLKHL	APKRKAEVML	GHGLFSLLAE	RLMLQTNLIT	MTTYNVLFEI	LIEQIGTQVI
810	820	830	840	850	860	870	880
HKQHPDPDSS	VKIQNPQILK	VIATLLRNSP	QCPESMEVRR	AFLSDMIKLF	NNSRENRRSL	LQCSVWQEWM	LSLCYFNPKN
890	900	910	920	930	940	950	960
SDEQKITEMV	YAIFRILLYH	AVKYEWGGWR	VWVDTLSITH	SKVTFEIHKE	NLANIFREQQ	GKVDEEIGLC	SSTSVQAASG
970	980	990	1000	1010	1020	1030	1040
IRRDINVSVG	SQQPDTKDSP	VCPHFTTNGN	ENSSIEKTSS	LESASNIELQ	TTNTSYEEMK	AEQENQELPD	EGTLEETLTN
1050	1060	1070	1080	1090	1100	1110	1120
ETRNADDLEV	SSDIIEAVAI	SSNSFITTGK	DSMTVSEVTA	SISSPSEEDA	SEMPEFLDKS	IVEEEEDDDY	VELKVEGSPT
1130	1140	1150	1160	1170	1180	1190	1200
EEANLPTELQ	DNSLSPAASE	AGEKLDMFGN	DDKLIFQEGK	PVTEKQTDTE	TQDSKDSGIQ	TMTASGSSAM	SPETTVSQIA
1210	1220	1230	1240	1250	1260	1270	1280
VESDLGQMLE	EGKKATNLTR	ETKLINDCHG	SVSEASSEQK	IAKLDVSNVA	TDTERLELKA	SPNVEAPQPH	RHVLEISRQH
1290	1300	1310	1320	1330	1340	1350	1360
EQPGQGIAPD	AVNGQRRDSR	STVFRIPEFN	WSQMHQRLLT	DLLFSIETDI	QMWRSHSTKT	VMDFVNSSDN	VIFVHNTIHL
1370	1380	1390	1400	1410	1420	1430	1440
ISQVMDNMVM	ACGGILPLLS	AATSATHELE	NIEPTQGLSI	EASVTFLQRL	ISLVDVLIFA	SSLGFTEIEA	EKSMSSGGIL
1450	1460	1470	1480	1490	1500	1510	1520
RQCLRLVCAV	AVRNCLECQQ	HSQLKTRGDK	ALKPMHSLIP	LGKSAAKEDS	KQAQFLALAV	VYFISVLMVS	KYRDILEPQN
1530	1540	1550	1560	1570	1580	1590	1600
ERHSQSCTET	GSENENVSLS	EITPAAFSTL	TTASVEESES	TSSARRRDSG	IGEETATGLG	SHVEVTPHTA	PPGVSAGPDA
1610	1620	1630	1640	1650	1660	1670	1680
ISEVLSTLSL	EVNKSPETKN	DRGNDLDTKA	TPSVSVSKNV	NVKDILRSLV	NIPADGVTVD	PALLPPACLG	ALGDLSVEQP
1690	1700	1710	1720	1730	1740	1750	1760
VQFRSFDRSV	IVAAKKSAVS	PSTFNTSIPT	NAVSVVSSVD	SAQASDMGGE	SPGSRSSNAK	LPSVPTVDSV	SQDPVSNMSI
1770	1780	1790	1800	1810	1820	1830	1840
TERLEHALEK	AAPLLREIFV	DFAPFLSRTL	LGSHGQELLI	EGTSLVCMKS	SSSVVELVML	LCSQEWQNSI	QKNAGLAFIE
1850	1860	1870	1880	1890	1900	1910	1920
LVNEGRLLSQ	TMKDHLVRVA	NEAEFILSRQ	RAEDIHRHAE	FESLCAQYSA	DKREDEKMCD	HLIRAAKYRD	HVTATQLIQK
1930	1940	1950	1960	1970	1980	1990	2000
IINILTDKHG	AWGNSAVSRP	LEFWRLDYWE	DDLRRRRRFV	RNPLGSTHPE	ATLKTAVEHV	CIFKLRENSK	ATDEDILAKG
2010	2020	2030	2040	2050	2060	2070	2080
KQSIRSQALG	NQNSENEILL	EGDDDTLSSV	DEKDLENLAG	PVSLSTPAQL	VAPSVVVKGT	LSVTSSELYF	EVDEEDPNFK
2090	2100	2110	2120	2130	2140	2150	2160
KIDPKILAYT	EGLHGKWLFT	EIRSIFSRRY	LLQNTALEIF	MANRVAVMFN	FPDPATVKKV	VNYLPRVGVG	TSFGLPQTRR
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1230	1	715.1053	93.99	3	43.7	12.4	1	821-839	K.VIATLLRNSPQCPESMEVR.R	
2402	1	682.7983	-93.44	2	58.4	12.3	0	1962-1974	R.NPLGSTHPEATLK.T	

Detailed Protein Report

Protein 300: **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 301: rho GTPase-activating protein 11A isoform 3 [Homo sapiens]

Accession:	gi|557128992	**Score:**	24.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	92.6
Database Date:	2015-11-30	**pI:**	9.9
		Sequence Coverage [%]:	3.7
		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]

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        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	2	682.6083	-53.17	3	54.7	11.6	0	386-404	K.HNSNITSSPLSGDENNMTK.E	
2120	2	703.2439	-91.13	2	54.9	13.2	0	550-561	K.ENENMMEGNLPK.C	

Detailed Protein Report

Protein 302: 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 303: **PREDICTED: keratin, type II cuticular Hb3 isoform X1 [Homo sapiens]**

Accession: gi|530400232
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 24.7
MW [kDa]: 49.6
pI: 5.3
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 304: TPR and ankyrin repeat-containing protein 1 [Homo sapiens]

Accession:	gi|257467636	**Score:**	24.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	336.0
Database Date:	2015-11-30	**pI:**	6.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.1
		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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1592	1	919.4423	-40.82	2	48.6	13.0	2	913-928	K.AICNAYNRGLSCVLRK.K	Carbamidomethyl: 3

Detailed Protein Report

Protein 305: PREDICTED: protein FAM186A isoform X1 [Homo sapiens]

Accession:	gi|578823289	**Score:**	24.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	262.1
Database Date:	2015-11-30	**pI:**	9.1
		Sequence Coverage [%]:	0.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
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
82	1	724.8160	-30.23	2	30.3	10.0	0	308-319	R.DLSNENEMLQQK.L	

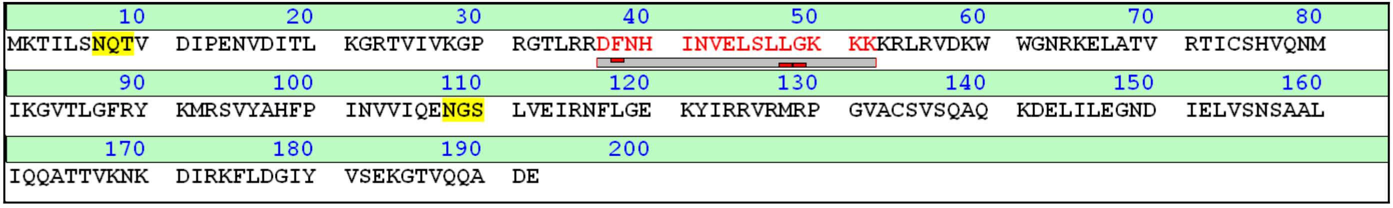
Detailed Protein Report

Protein 306: 60S ribosomal protein L9 [Homo sapiens]

Accession:	gi|15431303	**Score:**	24.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	21.8
Database Date:	2015-11-30	**pI:**	10.5
		Sequence Coverage [%]:	13.5
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530376503	refseq_human (refseq_human_20140103.fasta)	PREDICTED: 60S ribosomal protein L9 isoform X1 [Homo sapiens]
gi|67944630	refseq_human (refseq_human_20140103.fasta)	60S ribosomal protein L9 [Homo sapiens]



```
         10         20         30         40         50         60         70         80
MKTILSNQTV DIPENVDITL KGRTVIVKGP RGTLRRDFNH INVELSLLGK KKKRLRVDKW WGNRKELATV RTICSHVQNM
         90        100        110        120        130        140        150        160
IKGVTLGFRY KMRSVYAHFP INVVIQENGS LVEIRNFLGE KYIRRVRMRP GVACSVSQAQ KDELILEGND IELVSNSAAL
        170        180        190        200
IQQATTVKNK DIRKFLDGIY VSEKGTVQQA DE
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2187	1	618.9601	-95.70	3	55.8	10.7	2	37-52	R.DFNHINVELSLLGKKK.K	

Detailed Protein Report

Protein 307: laminin subunit gamma-1 precursor [Homo sapiens]

Accession:	gi|145309326	**Score:**	24.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	177.5
Database Date:	2015-11-30	**pI:**	4.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.9
		No. of unique 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
2687	1	941.9781	66.10	2	62.0	14.3	1	303-318	K.LVCNCKHNTYGVDCEK.C	Carbamidomethyl: 14

Detailed Protein Report

Protein 308: GDP-Man:Man(3)GlcNAc(2)-PP-Dol alpha-1,2-mannosyltransferase [Homo sapiens]

Accession:	gi|304434672	**Score:**	24.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	55.6
Database Date:	2015-11-30	**pI:**	9.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	4.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAAGERSWCL	CKLLRFFYSL	FFPGLIVCGT	LCVCLVIVLW	GIRLLLQRKK	KLVSTSKNGK	NQMVIAFFHP	YCNAGGGGER
90	100	110	120	130	140	150	160
VLWCALRALQ	KKYPEAVYVV	YTGDVNVNGQ	QILEGAFRRF	NIRLIHPVQF	VFLRKRYLVE	DSLYPHFTLL	GQSLGSIFLG
170	180	190	200	210	220	230	240
WEALMQCVPD	VYIDSMGYAF	TLPLFKYIGG	CQVGSYVHYP	TISTDMLSVV	KNQNIGFNNA	AFITRNPFLS	KVKLIYYYLF
250	260	270	280	290	300	310	320
AFIYGLVGSC	SDVVMVNSSW	TLNHILSLWK	VGNCTNIVYP	PCDVQTFLDI	PLHEKKMTPG	HLLVSVGQFR	PEKNHPLQIR
330	340	350	360	370	380	390	400
AFAKLLNKKM	VESPPSLKLV	LIGGCRNKDD	ELRVNQLRRL	SEDLGVQEYV	EFKINIPFDE	LKNYLSEATI	GLHTMWNEHF
410	420	430	440	450	460	470	480
GIGVVECMAA	GTIILAHNSG	GPKLDIVVPH	EGDITGFLAE	SEEDYAETIA	HILSMSAEKR	LQIRKSARAS	VSRFSDQEFE
490	500						
VTFLSSVEKL	FK						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2001	1	876.8626	-87.10	2	53.7	10.1	2	1-15	-.MAAGERSWCLCKLLR.F	Oxidation: 1

Detailed Protein Report

Protein 309: spectrin alpha chain, non-erythrocytic 1 isoform 3 [Homo sapiens]

Accession:	gi|306966132	**Score:**	24.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	282.1
Database Date:	2015-11-30	**pI:**	5.1
		Sequence Coverage [%]:	1.0
		No. of unique Peptides:	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MDPSGVKVLE	TAEDIQERRQ	QVLDRYHRFK	ELSTLRRQKL	EDSYRFQFFQ	RDAEELEKWI	QEKLQIASDE	NYKDPTNLQG
90	100	110	120	130	140	150	160
KLQKHQAFEA	EVQANSGAIV	KLDETGNLMI	SEGHFASETI	RTRLMELHRQ	WELLLEKMRE	KGIKLLQAQK	LVQYLRECED
170	180	190	200	210	220	230	240
VMDWINDKEA	IVTSEELGQD	LEHVEVLQKK	FEEFQTDMAA	HEERVNEVNQ	FAAKLIQEQH	PEEELIKTKQ	DEVNAAWQRL
250	260	270	280	290	300	310	320
KGLALQRQGK	LFGAAEVQRF	NRDVDETISW	IKEKEQLMAS	DDFGRDLASV	QALLRKHEGL	ERDLAALEDK	VKALCAEADR
330	340	350	360	370	380	390	400
LQQSHPLSAT	QIQVKREELI	TNWEQIRTLA	AERHARLNDS	YRLQRFLADF	RDLTSWVTEM	KALINADELA	SDVAGAEALL
410	420	430	440	450	460	470	480
DRHQEHKGEI	DAHEDSFKSA	DESGQALLAA	GHYASDEVRE	KLTVLSEERA	ALLELWELRR	QQYEQCMDLQ	LFYRDTEQVD
490	500	510	520	530	540	550	560
NWMSKQEAFL	LNEDLGDSLD	SVEALLKKHE	DFEKSLSAQE	EKITALDEFA	TKLIQNNHYA	MEDVATRRDA	LLSRRNALHE
570	580	590	600	610	620	630	640
RAMRRRAQLA	DSFHLQQFFR	DSDELKSWVN	EKMKTATDEA	YKDPSNLQGK	VQKHQAFEAE	LSANQSRIDA	LEKAGQKLID
650	660	670	680	690	700	710	720
VNHYAKDEVA	ARMNEVISLW	KKLLEATELK	GIKLREANQQ	QQFNRNVEDI	ELWLYEVEGH	LASDDYGKDL	TNVQNLQKKH
730	740	750	760	770	780	790	800
ALLEADVAAH	QDRIDGITIQ	ARQFQDAGHF	DAENIKKKQE	ALVARYEALK	EPMVARKQKL	ADSLRLQQLF	RDVEDEETWI
810	820	830	840	850	860	870	880
REKEPIAAST	NRGKDLIGVQ	NLLKKHQALQ	AEIAGHEPRI	KAVTQKGNAM	VEEGHFAAED	VKAKLHELNQ	KWEALKAKAS
890	900	910	920	930	940	950	960
QRRQDLEDSL	QAQQYFADAN	EAESWMREKE	PIVGSTDYGK	DEDSAEALLK	KHEALMSDLS	AYGSSIQALR	EQAQSCRQQV
970	980	990	1000	1010	1020	1030	1040
APTDDETGKE	LVLALYDYQE	KSPREVTMKK	GDILTLLNST	NKDWWKVEVN	DRQGFVPAAY	VKKLDPAQSA	SRENLLEEQG
1050	1060	1070	1080	1090	1100	1110	1120
SIALRQEQID	NQYHSLLELG	EKRKGMLEKS	CKKFMLFREA	NELQQWINEK	EAALTSEEVG	ADLEQVEVLQ	KKFDDFQKDL
1130	1140	1150	1160	1170	1180	1190	1200
KANESRLKDI	NKVAEDLESE	GLMAEEVQAV	QQQEVYGMMP	RDETDSKTAS	PWKSARLMVH	TVATFNSIKE	LNERWRSLQQ
1210	1220	1230	1240	1250	1260	1270	1280
LAEERSQLLG	SAHEVQRFHR	DADETKEWIE	EKNQALNTDN	YGHDLASVQA	LQRKHEGFER	DLAALGDKVN	SLGETAERLI
1290	1300	1310	1320	1330	1340	1350	1360
QSHPESAEDL	QEKCTELNQA	WSSLGKRADQ	RKAKLGDSHD	LQRFLSDFRD	LMSWINGIRG	LVSSDELAKD	VTGAEALLER
1370	1380	1390	1400	1410	1420	1430	1440
HQEHRTEIDA	RAGTFQAFEQ	FGQQLLAHGH	YASPEIKQKL	DILDQERADL	EKAWVQRRMM	LDQCLELQLF	HRDCEQAENW
1450	1460	1470	1480	1490	1500	1510	1520
MAAREAFLNT	EDKGDSLDSV	EALIKKHEDF	DKAINVQEEK	IAALQAFADQ	LIAAGHYAKG	DISSRRNEVL	DRWRRLKAQM
1530	1540	1550	1560	1570	1580	1590	1600
IEKRSKLGES	QTLQQFSRDV	DEIEAWISEK	LQTASDESYK	DPTNIQSKHQ	KHQAFEAELH	ANADRIRGVI	DMGNSLIERG
1610	1620	1630	1640	1650	1660	1670	1680
ACAGSEDAVK	ARLAALADQW	QFLVQKSAEK	SQKLKEANKQ	QNFNTGIKDF	DFWLSEVEAL	LASEDYGKDL	ASVNNLLKKH
1690	1700	1710	1720	1730	1740	1750	1760
QLLEADISAH	EDRLKDLNSQ	ADSLMTSSAF	DTSQVKDKRD	TINGRFQKIK	SMAASRRAKL	NESHRLHQFF	RDMDDEESWI
1770	1780	1790	1800	1810	1820	1830	1840
KEKKLLVGSE	DYGRDLTGVQ	NLRKKHKRLE	AELAAHEPAI	QGVLDTGKKL	SDDNTIGKEE	IQQRLAQFVE	HWKELKQLAA
1850	1860	1870	1880	1890	1900	1910	1920
ARGQRLEESL	EYQQFVANVE	EEEAWINEKM	TLVASEDYGD	TLAAIQGLLK	KHEAFETDFT	VHKDRVNDVC	TNGQDLIKKN
1930	1940	1950	1960	1970	1980	1990	2000
NHHEENISSK	MKGLNGKVSD	LEKAAAQRKA	KLDENSAFLQ	FNWKADVVES	WIGEKENSLK	TDDYGRDLSS	VQTLLTKQET
2010	2020	2030	2040	2050	2060	2070	2080
FDAGLQAFQQ	EGIANITALK	DQLLAAKHVQ	SKAIEARHAS	LMKRWSQLLA	NSAARKKKLL	EAQSHFRKVE	DLFLTFAKKA
2090	2100	2110	2120	2130	2140	2150	2160
SAFNSWFENA	EEDLTDPVRC	NSLEEIKALR	EAHDAFRSSL	SSAQADFNQL	AELDRQIKSF	RVASNPYTWF	TMEALEETWR
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2410	1	873.4266	-11.74	2	58.4	10.4	1	1810-1824	K.LSDDNTIGKEEIQQR.L	

Detailed Protein Report

Protein 310: 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

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Detailed Protein Report

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 311: protein CASP isoform a [Homo sapiens]

Accession:	gi|148277064	**Score:**	24.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	164.1
Database Date:	2015-11-30	**pI:**	5.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.4
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 1.11 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MLCVAGARLK	RELDATATVL	ANRQDESEQS	RKRLIEQSRE	FKKNTPEDLR	KQVAPLLKSF	QGEIDALSKR	SKEAEAAFLN
90	100	110	120	130	140	150	160
VYKRLIDVPD	PVPALDLGQQ	LQLKVQRLHD	IETENQKLRE	TLEEYNKEFA	EVKNQEVTIK	ALKEKIREYE	QTLKNQAETI
170	180	190	200	210	220	230	240
ALEKEQKLQN	DFAEKERKLQ	ETQMSTTSKL	EEAEHKVQSL	QTALEKTRTE	LFDLKTKYDE	ETTAKADEIE	MIMTDLERAN
250	260	270	280	290	300	310	320
QRAEVAQREA	ETLREQLSSA	NHSLQLASQI	QKAPDVEQAI	EVLTRSSLEV	ELAAKEREIA	QLVEDVQRLQ	ASLTKLRENS
330	340	350	360	370	380	390	400
ASQISQLEQQ	LSAKNSTLKQ	LEEKLKGQAD	YEEVKKELNI	LKSMEFAPSE	GAGTQDAAKP	LEVLLLEKNR	SLQSENAALR
410	420	430	440	450	460	470	480
ISNSDLSGSA	RRKGKDQPES	RRPGSLPAPP	PSQLPRNPGE	QASNTNGTHQ	FSPAGLSQDF	FSSSLASPSL	PLASTGKFAL
490	500	510	520	530	540	550	560
NSLLQRQLMQ	SFYSKAMQEA	GSTSMIFSTG	PYSTNSISSQ	SPLQQSPDVN	GMAPSPSQSE	SAGSVSEGEE	MDTAEIARQV
570	580	590	600	610	620	630	640
KEQLIKHNIG	QRIFGHYVLG	LSQGSVSEIL	ARPKPWNKLT	VRGKEPFHKM	KQFLSDEQNI	LALRSIQGRQ	RENPGQSLNR
650	660	670	680	690	700	710	720
LFQEVPKRRN	GSEGNITTRI	RASETGSDEA	IKSILEQAKR	ELQVQKTAEP	AQPSSASGSG	NSDDAIRSIL	QQARREMEAQ
730	740	750	760	770	780	790	800
QAALDPALKQ	APLSQSDITI	LTPKLLSTSP	MPTVSSYPPL	AISLKKPSAA	PEAGASALPN	PPALKKEAQD	APGLDPQGAA
810	820	830	840	850	860	870	880
DCAQGVLRQV	KNEVGRSGAW	KDHWWSAVQP	ERRNAASSEE	AKAEETGGGK	EKGSGGSGGG	SQPRAERSQL	QGPSSSEYWK
890	900	910	920	930	940	950	960
EWPSAESPYS	QSSELSLTGA	SRSETPQNSP	LPSSPIVPMS	KPTKPSVPPL	TPEQYEVYMY	QEVDTIELTR	QVKEKLAKNG
970	980	990	1000	1010	1020	1030	1040
ICQRIFGEKV	LGLSQGSVSD	MLSRPKPWSK	LTQKGREPFI	RMQLWLNGEL	GQGVLPVQGQ	QQGPVLHSVT	SLQDPLQQGC
1050	1060	1070	1080	1090	1100	1110	1120
VSSESTPKTS	ASCSPAPESP	MSSSESVKSL	TELVQQPCPP	IEASKDSKPP	EPSDPPASDS	QPTTPLPLSG	HSALSIQELV
1130	1140	1150	1160	1170	1180	1190	1200
AMSPELDTYG	ITKRVKEVLT	DNNLGQRLFG	ETILGLTQGS	VSDLLARPKP	WHKLSLKGRE	PFVRMQLWLN	DPNNVEKLMD
1210	1220	1230	1240	1250	1260	1270	1280
MKRMEKKAYM	KRRHSSVSDS	QPCEPPSVGT	EYSQGASPQP	QHQLKKPRVV	LAPEEKEALK	RAYQQKPYPS	PKTIEDLATQ
1290	1300	1310	1320	1330	1340	1350	1360
LNLKTSTVIN	WFHNYRSRIR	RELFIEEIQA	GSQGQAGASD	SPSARSGRAA	PSSEGDSCDG	VEATEGPGSA	DTEEPKSQGE
1370	1380	1390	1400	1410	1420	1430	1440
AEREEVPRPA	EQTEPPPSGT	PGPDDARDDD	HEGGPVEGPG	PLPSPASATA	TAAPAAPEDA	ATSAAAAPGE	GPAAPSSAPP
1450	1460	1470	1480	1490	1500	1510	
PSNSSSSSAP	RRPSSLQSLF	GLPEAAGARD	SRDNPLRKKK	AANLNSIIHR	LEKAASREEP	IEWEF	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
561	2	661.2196	-178.61	2	35.9	14.0	1	959-969	K.NGICQRIFGEK.V	Carbamidomethyl: 4	WD:WU 1.11

Detailed Protein Report

Protein 312: **PREDICTED: UDP-glucose:glycoprotein glucosyltransferase 1 isoform X3 [Homo sapiens]**

Accession:	gi|578804605	**Score:**	24.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	176.2
Database Date:	2015-11-30	**pI:**	5.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.1
		No. of unique Peptides:	1

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2009	1	599.9210	-67.30	3	53.5	11.7	1	1009-1023	R.VFMNCQSKLSDMPLK.S	Carbamidomethyl: 5

Detailed Protein Report

Protein 313: 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

WD:WU **Median:** 2.30 **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	WD:WU 2.30

Detailed Protein Report

Protein 314: inner centromere protein isoform 2 [Homo sapiens]

Accession:	gi|102467242	**Score:**	24.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	104.9
Database Date:	2015-11-30	**pI:**	10.0
		Sequence Coverage [%]:	2.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGTTAPGPIH	LLELCDQKLM	EFLCNMDNKD	LVWLEEIQEE	AERMFTREFS	KEPELMPKTP	SQKNRRKKRR	ISYVQDENRD
90	100	110	120	130	140	150	160
PIRRRLSRRK	SRSSQLSSRR	LRSKDSVEKL	ATVVGENGSV	LRRVTRAAAA	AAAATMALAA	PSSPTPESPT	MLTKKPEDNH
170	180	190	200	210	220	230	240
TQCQLVPVVE	IGISERQNAE	QHVTQLMSTE	PLPRTLSPTP	ASATAPTSQG	IPTSDEESTP	KKSKARILES	ITVSSLMATP
250	260	270	280	290	300	310	320
QDPKGQGVGT	GRSASKLRIA	QVSPGPRDSP	AFPDSPWRER	VLAPILPDNF	STPTGSRTDS	QSVRHSPIAP	SSPSPQVLAQ
330	340	350	360	370	380	390	400
KYSLVAKQES	VVRRASRRLA	KKTAEEPAAS	GRIICHSYLE	RLLNVEVPQK	VGSEQKEPPE	EAEPVAAAEP	EVPENNGNNS
410	420	430	440	450	460	470	480
WPHNDTEIAN	STPNPKPAAS	SPETPSAGQQ	EAKTDQADGP	REPPQSARRK	RSYKQAVSEL	DEEQHLEDEE	LQPPRSKTPS
490	500	510	520	530	540	550	560
SPCPASKVVR	PLRTFLHTVQ	RNQMLMTPTS	APRSVMKSFI	KRNTPLRMDP	KEKERQRLEN	LRRKEEAEQL	RRQKVEEDKR
570	580	590	600	610	620	630	640
RRLEEVKLKR	EERLRKVLQA	RERVEQMKEE	KKKQIEQKFA	QIDEKTEKAK	EERLAEEKAK	KKAAAKKMEE	VEARRKQEEE
650	660	670	680	690	700	710	720
ARRLRWLQQE	EEERRHQELL	QKKKEEEQER	LRKAAEAKRL	AEQREQERRE	QERREQERRE	QERREQERRE	QERQLAEQER
730	740	750	760	770	780	790	800
RREQERLQAE	RELQEREKAL	RLQKEQLQRE	LEEKKKKEEQ	QRLAERQLQE	EQEKKAKEAA	GASKALNVTV	DVQSPACTSY
810	820	830	840	850	860	870	880
QMTPQGHRAP	PKINPDNYGM	DLNSDDSTDD	EAHPRKPIPT	WARGTPLSQA	IIHQYYHPPN	LLELFGTILP	LDLEDIFKKS
890	900	910	920				
KPRYHKRTSS	AVWNSPPLQG	ARVPSSLAYS	LKKH				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1737	3	502.2720	31.12	2	50.1	13.7	1	611-618	K.EERLAEEK.A	

Detailed Protein Report

Protein 315: histone deacetylase complex subunit SAP18 [Homo sapiens]

Accession:	gi|215490089	**Score:**	24.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	19.5
Database Date:	2015-11-30	**pI:**	10.3
Modification(s):	Oxidation	**Sequence Coverage [%]:**	7.0
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 1.13 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MLAAGVGGQG ERLAGRRRKM AVESRVTQEE IKKEPEKPID REKTCPLLLR VFFTTNNGRHH 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	Ratios
2664	1	541.3186	91.64	2	61.6	14.2	1	124-133	K.EIGSTMSGRK.G	Oxidation: 6	WD:WU 1.13

Detailed Protein Report

Protein 316: **PREDICTED: neuroblast differentiation-associated protein AHNAK isoform X10 [Homo sapiens]**

Accession:	gi|578821732	**Score:**	24.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	368.2
Database Date:	2015-11-30	**pI:**	6.1
		Sequence Coverage [%]:	0.7
		No. of unique Peptides:	1

Quantitation

WD:WU	**Median:**	0.64	**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	VNLPKADLDV	SGPKVDVDVP	DVNIEGPDAK
810	820	830	840	850	860	870	880
LKGPKFKMPE	MNIKAPKISM	PDLDLNLKGP	KMKGEVDVSL	ANVEGDLKGP	ALDIKGPKID	VDAPDIDIHG	PDAKLKGPKL
890	900	910	920	930	940	950	960
KMPDMHVNMP	KISMPEIDLN	LKGSKLKGDV	DVSGPKLEGD	IKAPSLDIKG	PEVDVSGPKL	NIEGKSKKSR	FKLPKFNFSG
970	980	990	1000	1010	1020	1030	1040
SKVQTPEVDV	KGKKPDIDIT	GPKVDINAPD	VEVQGKVKGS	KFKMPFLSIS	SPKVSMPDVE	LNLKSPKVKG	DLDIAGPNLE
1050	1060	1070	1080	1090	1100	1110	1120
GDFKGPKVDI	KAPEVNLNAP	DVDVHGPDWN	LKMPKMKMPK	FSVSGLKAEG	PDVAVDLPKG	DINIEGPSMN	IEGPDLNVEG
1130	1140	1150	1160	1170	1180	1190	1200
PEGGLKGPKF	KMPDMNIKAP	KISMPDIDLN	LKGPKVKGDV	DISLPKLEGD	LKGPEVDIKG	PKVDINAPDV	DVHGPDWHLK
1210	1220	1230	1240	1250	1260	1270	1280
MPKVKMPKFS	MPGFKGEGPE	VDVTLPKADI	DISGPNVDVD	VPDVNIEGPD	AKLKGPKFKM	PEMNIKAPKI	SMPDFDLNLK
1290	1300	1310	1320	1330	1340	1350	1360
GPKMKGDVVV	SLPKVEGDLK	GPEVDIKGPK	VDIDTPDINI	EGSEGKFKGP	KFKIPEMHLK	APKISMPDID	LNLKGPKVKG
1370	1380	1390	1400	1410	1420	1430	1440
DVDVSLPKME	GDLKGPEVDI	KGPKVDINAP	DVDVQGPDWH	LKMPKVKMPK	FSMPGFKGEG	PDVDVNLPKA	DLDVSGPKVD
1450	1460	1470	1480	1490	1500	1510	1520
IDVPDVNIEG	PEGKLKGPKF	KMPEMNIKAP	KISMPDIDLN	LKGPKVKGDM	DVSLPKVEGD	MQVPDLDIKG	PKVDINAPDV
1530	1540	1550	1560	1570	1580	1590	1600
DVRGPDWHLK	MPKIKMPKIS	MPGFKGEGPE	VDVNLPKADL	DVSGPKVDVD	VPDVNIEGPD	AKLKGPKFKM	PEMNIKAPKI
1610	1620	1630	1640	1650	1660	1670	1680
SMPDFDLHLK	GPKVKGDVDV	SLPKMEGDLK	APEVDIKGPK	VDIDAPDVDV	HGPDWHLKMP	KVKMPKFSMP	GFKGEGPEVD
1690	1700	1710	1720	1730	1740	1750	1760
VNLPKADIDV	SGPKVDIDTP	DIDIHGPEGK	LKGPKFKMPD	LHLKAPKISM	PEVDLNLKGP	KMKGDVDVSL	PKVEGDLKGP
1770	1780	1790	1800	1810	1820	1830	1840
EVDIKGPKVD	IDVPDVDVQG	PDWHLKMPKV	KMPKFSMPGF	KGEGPDVDVN	LPKADLDVSG	PKVDIDVPDV	NIEGPDAKLK
1850	1860	1870	1880	1890	1900	1910	1920
GPKFKMPEMN	IKAPKISMPD	FDLHLKGPKV	KGDVDVSLPK	VEGDLKGPEV	DIKGPKVDID	APDVDVHGPD	WHLKMPKVKM
1930	1940	1950	1960	1970	1980	1990	2000
PKFSMPGFKG	EGPDVDVTLP	KADIEISGPK	VDIDAPDVSI	EGPDAKLKGP	KFKMPEMNIK	APKISMPDID	FNLKGPKVKG
2010	2020	2030	2040	2050	2060	2070	2080
DVDVSLPKVE	GDLKGPEIDI	KGPSLDIDTP	DVNIEGPEGK	LKGPKFKMPE	MNIKAPKISM	PDFDLHLKGP	KVKGDVDVSL
2090	2100	2110	2120	2130	2140	2150	2160
PKVESDLKGP	EVDIEGPEGK	LKGPKFKMPD	VHFKSPQISM	SDIDLNLKGP	KIKGDMDISV	PKLEGDLKGP	KVDVKGPKVG
2170	2180	2190	2200	2210	2220	2230	2240

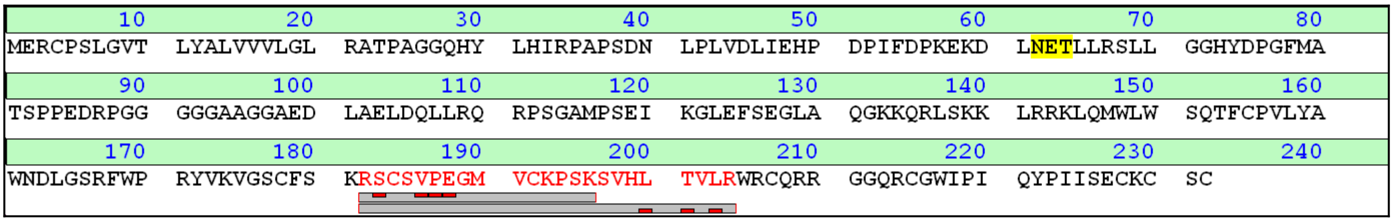
Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
1546	1	506.2878	21.02	2	47.6	11.8	1	2351-2360	K.GPEADIKGPK.V		WD:WU	0.64

Detailed Protein Report

Protein 317: noggin precursor [Homo sapiens]

Accession:	gi|4885523	**Score:**	24.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	25.8
Database Date:	2015-11-30	**pI:**	10.2
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	9.9
		No. of unique Peptides:	2



```
        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
1566	1	862.7593	-26.29	3	47.9	14.3	2	182-204	K.RSCSVPEGMVCKPSKSVHLTVLR.W	Carbamidomethyl: 11; Oxidation: 9

Detailed Protein Report

Protein 318: **catenin alpha-2 isoform 5 [Homo sapiens]**

Accession:	gi|543583701	**Score:**	24.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	65.1
Database Date:	2015-11-30	**pI:**	5.4
Modification(s):	Oxidation	**Sequence Coverage [%]:**	4.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDGWRRPLQS	VGKVCEKNMK	TSEMHTMSGA	QTGRKEKGDP	LNIAIDKMTK	KTRDLRRQLR	KAVMDHISDS	FLETNVPLLV
90	100	110	120	130	140	150	160
LIEAAKSGNE	KEVKEYAQVF	REHANKLVEV	ANLACSISNN	EEGVKLVRMA	ATQIDSLCPQ	VINAALTLAA	RPQSKVAQDN
170	180	190	200	210	220	230	240
MDVFKDQWEK	QVRVLTEAVD	DITSVDDFLS	VSENHILEDV	NKCVIALQEG	DVDTLDRTAG	AIRGRAARVI	HIINAEMENY
250	260	270	280	290	300	310	320
EAGVYTEKVL	EATKLLSETV	MPRFAEQVEV	AIEALSANVP	QPFEENEFID	ASRLVYDGVR	DIRKAVLMIR	TPEELEDDSD
330	340	350	360	370	380	390	400
FEQEDYDVRS	RTSVQTEDDQ	LIAGQSARAI	MAQLPQEEKA	KIAEQVEIFH	QEKSKLDAEV	AKWDDSGNDI	IVLAKQMCMI
410	420	430	440	450	460	470	480
MMEMTDFTRG	KGPLKNTSDV	INAAKKIAEA	GSRMDKLARA	VADQCPDSAC	KQDLLAYLQR	IALYCHQLNI	CSKVKAEVQN
490	500	510	520	530	540	550	560
LGGELIVSGL	DSATSLIQAA	KNLMNAVVLT	VKASYVASTK	YQKVYGTAAV	NSPVVSWKMK	APEKKPLVKR	EKPEEFQTRV
570	580	590					
RRGSQKKHIS	PVQALSEFKA	MDSF					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1343	1	1021.9669	10.42	2	45.6	10.3	2	18-35	K.NMKTSEMHTMSGAQTGRK.E	Oxidation: 2, 7, 10

Detailed Protein Report

Protein 319: PREDICTED: centrosome-associated protein CEP250 isoform X4 [Homo sapiens]

Accession:	gi|530417804	**Score:**	24.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	208.3
Database Date:	2015-11-30	**pI:**	4.9
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.2
		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 320: **PREDICTED: p21-activated protein kinase-interacting protein 1 isoform X2 [Homo sapiens]**

Accession:	gi|578811766	**Score:**	24.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	41.4
Database Date:	2015-11-30	**pI:**	10.1
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	7.3
		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

Detailed Protein Report

Protein 321: uncharacterized aarF domain-containing protein kinase 2 [Homo sapiens]

Accession:	gi|32261307	**Score:**	24.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	68.9
Database Date:	2015-11-30	**pI:**	10.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	4.8
		No. of unique Peptides:	2

```
        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
2782	2	835.4333	6.80	2	63.2	13.6	0	235-251	R.ASCLPPFSHTGAVGGLR.E	
2880	1	713.3447	-10.93	2	64.7	10.8	0	510-522	R.AVFMAVVMGQGQR.V	Oxidation: 4, 8

Detailed Protein Report

Protein 322: PREDICTED: exosome complex exonuclease RRP44 isoform X1 [Homo sapiens]

Accession:	gi|530402172	**Score:**	24.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	90.5
Database Date:	2015-11-30	**pI:**	6.5
		Sequence Coverage [%]:	3.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSADNQLQVI	FITNDRRNKE	KAIEEGIPAF	TCEEYVKSLT	ANPELIDRLA	CLSEEGNEIE	SGKIIFSEHL	PLSKLQQGIK
90	100	110	120	130	140	150	160
SGTYLQGTFR	ASRENYLEAT	VWIHGDNEEN	KEIILQGLKH	LNRAVHEDIV	AVELLPKSQW	VAPSSVVLHD	EGQNEEDVEK
170	180	190	200	210	220	230	240
EEETERMLKT	AVSEKMLKPT	GRVVGIIKRN	WRPYCGMLSK	SDIKESRRHL	FTPADKRIPR	IRIETRQAST	LEGRRIIVAI
250	260	270	280	290	300	310	320
DGWPRNSRYP	NGHFVRNLGD	VGEKETETEV	LLLEHDVPHQ	PFSQAVLSFL	PKMPWSITEK	DMKNREDLRH	LCICSVDPPG
330	340	350	360	370	380	390	400
CTDIDDALHC	RELENGNLEV	GVHIADVSHF	IRPGNALDQE	SARRGTTVYL	CEKRIDMVPE	LLSSNLCSLK	CDVDRLAFSC
410	420	430	440	450	460	470	480
IWEMNHNAEI	LKTKFTKSVI	NSKASLTYAE	AQLRIDSANM	NDDITTSLRG	LNKLAKILKK	RRIEKGALTL	SSPEVRFHMD
490	500	510	520	530	540	550	560
SETHDPIDLQ	TKELRETNSM	VEEFMLLANI	SVAKKIHEEF	SEHALLRKHP	APPPSNYEIL	VKAARSRNLE	IKTDTAKSLA
570	580	590	600	610	620	630	640
ESLDQAESPT	FPYLNTLLRI	LATRCMMQAV	YFCSGMDNDF	HHYGLASPIY	THFTSPIRRY	ADVIVHRLLA	VAIGADCTYP
650	660	670	680	690	700	710	720
ELTDKHKLAD	ICKNLNFRHK	MAQYAQRASV	AFHTQLFFKS	KGIVSEEAYI	LFVRKNAIVV	LIPKYGLEGT	VFFEEKDKPN
730	740	750	760	770	780	790	800
PQLIYDDEIP	SLKIEDTVFH	VFDKVKVKIM	LDSSNLQHQK	IRMSLVEPQI	PGISIPTDTS	NMDLNGPKKK	KMKLGK

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2612	1	588.6601	-226.00	2	60.9	13.0	2	301-309	K.DMKNREDLR.H	

Detailed Protein Report

Protein 323: fibrocystin isoform 2 precursor [Homo sapiens]

Accession:	gi|126131104	**Score:**	24.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	371.4
Database Date:	2015-11-30	**pI:**	5.9
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	0.9
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MTAWLISLMS	IEVLLLAVRH	LSLHIEPEEG	SLAGGTWITV	IFDGLELGVL	YPNNGSQLEI	HLVNVNMVVP	ALRSVPCDVF
90	100	110	120	130	140	150	160
PVFLDLPVVT	CRTRSVLSEA	HEGLYFLEAY	FGGQLVSSPN	PGPRDSCTFK	FSKAQTPIVH	QVYPPSGVPG	KLIHVYGWII
170	180	190	200	210	220	230	240
TGRLETFDFD	AEYIDSPVIL	EAQGDKWVTP	CSLINRQMGS	CYPIQEDHGL	GTLQCHVEGD	YIGSQNVSFS	VFNKGKSMVH
250	260	270	280	290	300	310	320
KKAWLISAKQ	DLFLYQTHSE	ILSVFPETGS	LGGRTNITIT	GDFFDNSAQV	TIAGIPCDIR	HVSPRKIECT	TRAPGKDVRL
330	340	350	360	370	380	390	400
TTPQPGNRGL	LFEVGDAVEG	LELTEATPGY	RWQIVPNASS	PFGFWSQEGQ	PFRARLSGFF	VAPETNNYTF	WIQADSQASL
410	420	430	440	450	460	470	480
HFSWSEEPRT	KVKVASISVG	TADWFDSWEQ	NRDEGTWQQK	TPKLELLGGA	MYYLEAEHHG	IAPSRGMRIG	VQIHNTWLNP
490	500	510	520	530	540	550	560
DVVTTYLREK	HQIRVRAQRL	PEVQVLNVSG	RGNFFLTWDN	VSSQPIPANA	TAHLIQTTIE	ELLAVKCKLE	PLWSNILLRL
570	580	590	600	610	620	630	640
GFERGPEVSN	SDGDLTSGTE	PFCGRFSLRQ	PRHLVLTPPA	AQKGYRLDQY	THLCLAYKGH	MNKILKMIVS	FTIGFQNMVK
650	660	670	680	690	700	710	720
NTTCDWSLTR	TSPESWQFDC	TDLWETCVRC	FGDLQPPPAN	SPVLVHQINL	LPLAQETGLF	YVDEIIIADT	NVTVSQADSG
730	740	750	760	770	780	790	800
TARPGGNLVE	SVSVVGSPPV	YSVTSWLAGC	GTELPLITAR	SVPTEGTEEG	SGLVLVTTQR	RQRTSPPLGG	HFRIQLPNTV
810	820	830	840	850	860	870	880
ISDVPVQISA	HHLHQLLQNN	ADDFTSRYLN	ASDFTVKEDL	YTCYEHVWTL	SWSTQIGDLP	NFIRVSDENL	TGVNPAAATR
890	900	910	920	930	940	950	960
VVYDGGVFLG	PIFGDMLATA	NQHTQVVVRV	NDVPAHCPGS	CSFQYLQGST	PCVHSVWYSI	DGDINLMIYI	TGTGFSGDSQ
970	980	990	1000	1010	1020	1030	1040
FLQVTVNKTS	CKVIFSNQTN	VVCQTDLLPV	GMHRILMLVR	PSGLAISATG	EDLFLNVKPR	LDMVEPSRAA	DIGGLWATIR
1050	1060	1070	1080	1090	1100	1110	1120
GSSLEGVSLI	LFGSYSCAIN	VATSNSSRIQ	CKVPPRGKDG	RIVNVTVIRG	DYSAVLPRAF	TYVSSLNPVI	VTLSRNISNI
1130	1140	1150	1160	1170	1180	1190	1200
AGGETLVIGV	ARLMNYTDLD	VEVHVQDALA	PVHTQSAWGL	EVALPPLPAG	LHRISVSING	VSIHSQGVDL	HIQYLTEVFS
1210	1220	1230	1240	1250	1260	1270	1280
IEPCCGSLLG	GTILSISGIG	FSRDPALVWV	LVGNRSCDIV	NLTEASIWCE	TLPAPQIPDA	GAPTVPAAVE	VWAGNRFFAR
1290	1300	1310	1320	1330	1340	1350	1360
GPSPSLVGKG	FTFMYEAAAT	PVVTAMQGEI	TNSSLSLHVG	GSNLSNSVIL	LGNLNCDVET	QSFQGNVSLS	GCSIPLHSLE
1370	1380	1390	1400	1410	1420	1430	1440
AGIYPLQVRQ	KQMGFANMSV	VLQQFAVMPR	IMAIFPSQGS	ACGGTILTVR	GLLLNSRRRS	VRVDLSGPFT	CVILSLGDHT
1450	1460	1470	1480	1490	1500	1510	1520
ILCQVSLEGD	PLPGASFSLN	VTVLVNGLTS	ECQGNCTLFI	REEASPVMDA	LSTNTSGSLT	TVLIRGQRLA	TTADEPMVFV
1530	1540	1550	1560	1570	1580	1590	1600
DDQLPCNVTF	FNASHVVCQT	RDLAPGPHYL	SVFYTRNGYA	CSGNVSRHFY	IMPQVFHYFP	KNFSLHGGSL	LTIEGTGLRG
1610	1620	1630	1640	1650	1660	1670	1680
QNTTSVYIDQ	QTCLTVNIGA	ELIRCIVPTG	NGSVALEIEV	DGLWYHIGVI	GYNKAFTPEL	ISISQSDDIL	TFAVAQISGA
1690	1700	1710	1720	1730	1740	1750	1760
ANIDIFIGMS	PCVGVSGNHT	VLQCVVPSLP	AGEYHVRGYD	CIRGWASSAL	VFTSRVIITA	VTENFGCLGG	RLVHVFGAGF
1770	1780	1790	1800	1810	1820	1830	1840
SPGNVSAAVC	GAPCRVLANA	TVSAFSCLVL	PLDVSLAFLC	GLKREEDSCE	AARHTYVQCD	LTVAMATEQL	LESWPYLYIC
1850	1860	1870	1880	1890	1900	1910	1920
EESSQCLFVP	DHWAESMFPS	FSGLFISPKL	ERDEVLIYNS	SCNITMETEA	EMECETPNQP	ITVKITEIRK	RWGQNTQGNF
1930	1940	1950	1960	1970	1980	1990	2000
SLQFCRRWSR	THSWFPERLP	QDGDNVTVEN	GQLLLLDTNT	SILNLLHIKG	GKLIFMAPGP	IELRAHAILV	SDGGELRIGS
2010	2020	2030	2040	2050	2060	2070	2080
EDKPFQGRAQ	ITLYGSSYST	PFFPYGVKFL	AVRNGTLSLH	GSLPEVIVTC	LRATAHALDT	VLALEDAVDW	NPGDEVVIIS
2090	2100	2110	2120	2130	2140	2150	2160
GTGVKGAKPM	EEIVTVETVQ	DTDLYLKSPL	RYSHNFTENW	VAGEHHILKA	TVALLSRSIT	IQGNLTNERE	KLLVSCQEAN
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2756	1	1023.5380	40.37	2	63.0	11.3	1	1718-1735	R.GYDCIRGWASSALVFTSR.V	Carbamidomethyl: 4
2847	1	686.8886	50.79	2	64.3	13.0	1	3263-3274	K.VRNDHSISGIMK.L	Oxidation: 11

Detailed Protein Report

Protein 324: **hematopoietic lineage cell-specific protein [Homo sapiens]**

Accession:	gi|167234422	**Score:**	24.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	54.0
Database Date:	2015-11-30	**pI:**	4.6
		Sequence Coverage [%]:	8.0
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MWKSVVGHDV	SVSVETQGDD	WDTDPDFVND	ISEKEQRWGA	KTIEGSGRTE	HINIHQLRNK	VSEEHDVLRK	KEMESGPKAS
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
HGYGGRFGVE	RDRMDKSAVG	HEYVAEVEKH	SSQTDAAKGF	GGKYGVERDR	ADKSAVGFDY	KGEVEKHTSQ	KDYSRGFGGR
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
YGVEKDKWDK	AALGYDYKGE	TEKHESQRDY	AKGFGGQYGI	QKDRVDKSAV	GFNEMEAPTT	AYKKTTPIEA	ASSGTRGLKA
250	**260**	**270**	**280**	**290**	**300**	**310**	**320**
KFESMAEEKR	KREEEEKAQQ	VARRQQERKA	VTKRSPEAPQ	PVIAMEEPAV	PAPLPKKISS	EAWPPVGTPP	SSESEPVRTS
330	**340**	**350**	**360**	**370**	**380**	**390**	**400**
REHPVPLLPI	RQTLPEDNEE	PPALPPRTLE	GLQVEEEPVY	EAEPEPEPEP	EPEPENDYED	VEEMDRHEQE	DEPEGDYEEV
410	**420**	**430**	**440**	**450**	**460**	**470**	**480**
LEPEDSSFSS	ALAGSSGCPA	GAGAGAVALG	ISAVALYDYQ	GEGSDELSFD	PDDVITDIEM	VDEGWWRGRC	HGHFGLFPAN
490							
YVKLLE							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2470	1	1131.1745	0.11	3	59.2	13.4	0	4-34	K.SVVGHDVSVSVETQGDDWDTDPDFVNDISEK.E	
2838	1	485.7928	164.40	2	64.0	10.8	0	242-249	K.FESMAEEK.R	

Detailed Protein Report

Protein 325: **PREDICTED: latent-transforming growth factor beta-binding protein 1 isoform X5 [Homo sapiens]**

Accession: gi|530367595
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 24.3
MW [kDa]: 134.0
pI: 9.1
Sequence Coverage [%]: 2.9
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
1842	1	1074.5505	92.79	2	51.7	12.2	1	578-596	K.QEDCCGTVGTSWGFNKCQK.C	Carbamidomethyl: 4

Detailed Protein Report

Protein 326: **PREDICTED: pleckstrin homology domain-containing family B member 2 isoform X1 [Homo sapiens]**

Accession:	gi|578804522	**Score:**	24.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	16.1
Database Date:	2015-11-30	**pI:**	10.3
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	23.9
		No. of unique Peptides:	1

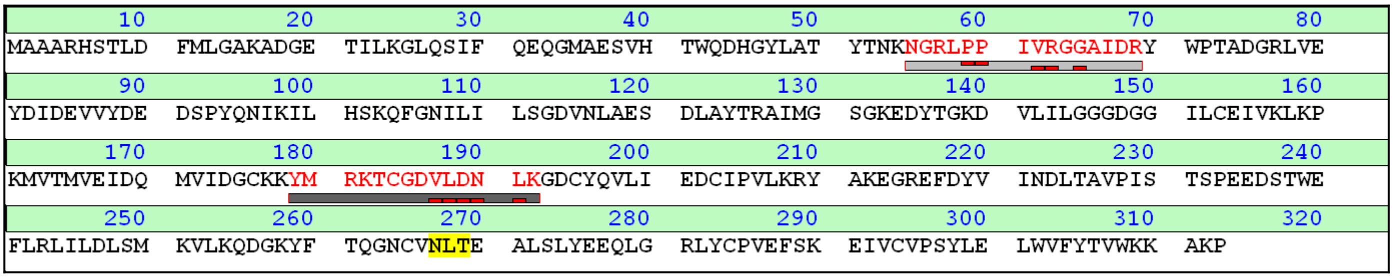
10	20	30	40	50	60	70	80
MAFVKSGWLL	RQSTILKRWK	KNWFDLWSDG	HLIYYDDQTR	QNIEDKVHMP	MDCINIRTGQ	ECRDTQPPDG	KSKDCMLQIV
90	100	110	120	130	140		
CRDGKTISLC	AESTDDCFRL	MAMGHTVVRT	RQELKLSTLR	MGRRMPCPTS	THMQRPSS		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2213	1	1103.9435	-65.96	2	56.2	14.1	2	64-82	R.DTQPPDGKSKDCMLQIVCR.D	Carbamidomethyl: 12; Oxidation: 13

Detailed Protein Report

Protein 327: spermine synthase isoform 2 [Homo sapiens]

Accession:	gi|386643030	**Score:**	24.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	35.3
Database Date:	2015-11-30	**pI:**	4.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	9.3
		No. of unique Peptides:	2



10	20	30	40	50	60	70	80
MAAARHSTLD	FMLGAKADGE	TILKGLQSIF	QEQGMAESVH	TWQDHGYLAT	YTNKNGRLPP	IVRGGAIDRY	WPTADGRLVE
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
YDIDEVVYDE	DSPYQNIKIL	HSKQFGNILI	LSGDVNLAES	DLAYTRAIMG	SGKEDYTGKD	VLILGGGDGG	ILCEIVKLKP
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
KMVTMVEIDQ	MVIDGCKKYM	RKTCGDVLDN	LKGDCYQVLI	EDCIPVLKRY	AKEGREFDYV	INDLTAVPIS	TSPEEDSTWE
250	**260**	**270**	**280**	**290**	**300**	**310**	**320**
FLRLILDLSM	KVLKQDGKYF	TQGNCVNLTE	ALSLYEEQLG	RLYCPVEFSK	EIVCVPSYLE	LWVFYTVWKK	AKP

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
143	1	796.0835	151.41	2	30.7	10.9	2	55-69	K.NGRLPPIVRGGAIDR.Y	
2926	5	557.9598	27.25	3	65.3	13.3	2	179-192	K.YMRKTCGDVLDNLK.G	Oxidation: 2

Detailed Protein Report

Protein 328: mis18-binding protein 1 [Homo sapiens]

Accession: gi|42415492
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 24.2
MW [kDa]: 129.0
pI: 9.9
Sequence Coverage [%]: 3.3
No. of unique Peptides: 2

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

Detailed Protein Report

Protein 329: AT-hook DNA-binding motif-containing protein 1 [Homo sapiens]

Accession:	gi|71274144	**Score:**	24.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	168.2
Database Date:	2015-11-30	**pI:**	10.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.2
		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
2595	1	665.2784	-146.69	2	60.7	10.1	1	513-524	R.VSAEPTPLLKMK.N	Oxidation: 11

Detailed Protein Report

Protein 330: zinc finger protein 568 isoform 3 [Homo sapiens]

Accession:	gi|325651958	**Score:**	24.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	67.0
Database Date:	2015-11-30	**pI:**	10.0
		Sequence Coverage [%]:	1.6
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|325651960	refseq_human(refseq_human_20140103.fasta)	zinc finger protein 568 isoform 3 [Homo sapiens]

10	20	30	40	50	60	70	80
MKPAQRNLYR	DVMLENYSNL	VTVGCQVTKP	DVIFKLEQEE	EPWVMEEEMF	GRHCPEVWEV	DEQIKKQQET	LVRKVTSISK
90	100	110	120	130	140	150	160
KILIKEKVIE	CKKVAKIFPL	SSDIVTSRQS	FYDCDSLDKG	LEHNLDLLRY	EKGCVREKQS	NEFGKPFYHC	ASYVVTPFKC
170	180	190	200	210	220	230	240
NQCGQDFSHK	FDLIRHERIH	AGEKPYECKE	CGKAFSRKEN	LITHQKIHTG	EKPYKCNECG	KAFIQMSNLI	RHHRIHTGEK
250	260	270	280	290	300	310	320
PYACKDCWKA	FSQKSNLIEH	ERIHTGEKPY	ECKECGKSFS	QKQNLIEHEK	IHTGEKPYAC	NECGRAFSRM	SSVTLHMRSH
330	340	350	360	370	380	390	400
TGEKPYKCNK	CGKAFSQCSV	FIIHMRSHTG	EKPYVCSECG	KAFSQSSSLT	VHMRNHTAEK	PYECKECGKA	FSRKENLITH
410	420	430	440	450	460	470	480
QKIHTGEKPY	ECSECGKAFI	QMSNLIRHQR	IHTGEKPYAC	TVCGKAFSQK	SNLTEHEKIH	TGEKPYHCNQ	CGKAFSQRQN
490	500	510	520	530	540	550	560
LLEHEKIHTG	EKPFKCNECG	KAFSRISSLT	LHVRSHTGEK	PYECNKCGKA	FSQCSLLIIH	MRSHTGEKPF	ECNECGKAFS
570	580	590					
QRASLSIHKR	GHTGERHQVY						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
858	1	501.2115	-157.63	2	39.1	12.8	1	66-73	K.KQQETLVR.K	

Detailed Protein Report

Protein 331: ribonucleoside-diphosphate reductase subunit M2 isoform 1 [Homo sapiens]

Accession:	gi|260064013	**Score:**	24.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	51.1
Database Date:	2015-11-30	**pI:**	6.1
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.9
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MGRVGGMAQP	MGRAGAPKPM	GRAGSARRGR	FKGCWSEGSP	VHPVPAVLSW	LLALLRCAST	MLSLRVPLAP	ITDPQQLQLS
90	100	110	120	130	140	150	160
PLKGLSLVDK	ENTPPALSGT	RVLASKTARR	IFQEPTEPKT	KAAAPGVEDE	PLLRENPRRF	VIFPIEYHDI	WQMYKKAEAS
170	180	190	200	210	220	230	240
FWTAEEVDLS	KDIQHWESLK	PEERYFISHV	LAFFAASDGI	VNENLVERFS	QEVQITEARC	FYGFQIAMEN	IHSEMYSLLI
250	260	270	280	290	300	310	320
DTYIKDPKER	EFLFNAIETM	PCVKKKADWA	LRWIGDKEAT	YGERVVAFAA	VEGIFFSGSF	ASIFWLKKRG	LMPGLTFSNE
330	340	350	360	370	380	390	400
LISRDEGLHC	DFACLMFKHL	VHKPSEERVR	EIIINAVRIE	QEFLTEALPV	KLIGMNCTLM	KQYIEFVADR	LMLELGFSKV
410	420	430	440	450			
FRVENPFDFM	ENISLEGKTN	FFEKRVGEYQ	RMGVMSSPTE	NSFTLDADF			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
517	8	690.2024	-171.27	2	34.9	11.7	1	1-13	-.MGRVGGMAQPMGR.A	Oxidation: 7, 11
653	5	690.4099	129.21	2	37.0	12.3	1	1-13	-.MGRVGGMAQPMGR.A	Oxidation: 1, 11

Detailed Protein Report

Protein 332: protein FAM216B [Homo sapiens]

Accession:	gi|32698855	**Score:**	24.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	16.4
Database Date:	2015-11-30	**pI:**	12.1
		Sequence Coverage [%]:	14.4
		No. of unique 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
421	1	666.9204	69.47	2	34.3	10.7	0	22-33	R.VPPSIYDTSLLK.A	

Detailed Protein Report

Protein 333: PREDICTED: serine/threonine-protein kinase MRCK alpha isoform X7 [Homo sapiens]

Accession:	gi|530366603	**Score:**	24.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	198.5
Database Date:	2015-11-30	**pI:**	5.8
		Sequence Coverage [%]:	2.1
		No. of unique Peptides:	1

Quantitation

WD:WU	**Median:**	0.47	**CV:**	0.00 %	**No. of Peptides:**		1

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
DALDQFEDSF	SSSSSSLIDF	LDDTDPVENT	YVWNPSVKFH	IQSRSTSPST	SSEAEPVKTV	DSTPLSVHTP	TLRKKGCPGS
970	980	990	1000	1010	1020	1030	1040
TGFPPKRKTH	QFFVKSFTTP	TKCHQCTSLM	VGLIRQGCSC	EVCGFSCHIT	CVNKAPTTCP	VPPEQTKGPL	GIDPQKGIGT
1050	1060	1070	1080	1090	1100	1110	1120
AYEGHVRIPK	PAGVKKGWQR	ALAIVCDFKL	FLYDIAEGKA	SQPSVVISQV	IDMRDEEFSV	SSVLASDVIH	ASRKDIPCIF
1130	1140	1150	1160	1170	1180	1190	1200
RVTASQLSAS	NNKCSILMLA	DTENEKNKWV	GVLSELHKIL	KKNKFRDRSV	YVPKEAYDST	LPLIKTTQAA	AIIDHERIAL
1210	1220	1230	1240	1250	1260	1270	1280
GNEEGLFVVH	VTKDEIIRVG	DNKKIHQIEL	IPNDQLVAVI	SGRNRHVRLF	PMSALDGRET	DFYKLSETKG	CQTVTSGKVR
1290	1300	1310	1320	1330	1340	1350	1360
HGALTCLCVA	MKRQVLCYEL	FQSKTRHRKF	KEIQVPYNVQ	WMAIFSEQLC	VGFQSGFLRY	PLNGEGNPYS	MLHSNDHTLS
1370	1380	1390	1400	1410	1420	1430	1440
FIAHQPMDAI	CAVEISSKEY	LLCFNSIGIY	TDCQGRRSRQ	QELMWPANPS	SCCYNAPYLS	VYSENAVDIF	DVNSMEWIQT
1450	1460	1470	1480	1490	1500	1510	1520
LPLKKVRPLN	NEGSLNLLGL	ETIRLIYFKN	KMAEGDELVV	PETSDNSRKQ	MVRNINNKRR	YSFRVPEEER	MQQRREMLRD
1530	1540	1550	1560	1570	1580	1590	1600
PEMRNKLISN	PTNFNHIAHM	GPGDGIQILK	DLPMPGFPYP	SPHHHSGLIS	SPINFEHIYH	MTVNSAEKFL	SPDSINPEYS
1610	1620	1630	1640	1650	1660	1670	1680
PSLRSVPGTP	SFMTLRNPRP	QESRTVFSGS	VSIPSITKSR	PEPGRSMSAS	SGLSARSSAQ	NGSALKREFS	GGSYSAKRQP
1690	1700	1710	1720	1730	1740	1750	1760
MPSPSEGSLS	SGGMDQGSDA	PARDFDGEDS	DSPRHSTASN	SSNLSSPPSP	ASPRKTKSLS	LESTDRGSWD	P

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
2023	3	703.7681	-96.27	2	53.7	13.5	0	925-938	R.STSPSTSSEAEPVK.T		WD:WU	0.47

Detailed Protein Report

Protein 334: ubiquitin carboxyl-terminal hydrolase 34 [Homo sapiens]

Accession:	gi|110347427	**Score:**	24.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	404.0
Database Date:	2015-11-30	**pI:**	5.4
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.0
		No. of unique Peptides:	1

Detailed Protein Report

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
1545	1	948.9999	79.00	2	47.6	10.2	0	647-664	K.LESQAGICLGDSQGMSER.N	Oxidation: 15

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Detailed Protein Report

Protein 335: regulator of G-protein signaling 22 isoform 2 [Homo sapiens]

Accession:	gi|557878614	**Score:**	23.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	145.7
Database Date:	2015-11-30	**pI:**	8.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.6
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MPEKRLTAEP	PTITEEEFED	SLATDDFLVD	YFNEFLSLPT	FSEAIRFNAD	YGVFEVANDA	PQFLEKQLKK	ILQNQQPRNP
90	100	110	120	130	140	150	160
IYDVVRKGKN	EVKPVQMNAP	DEDETINVNY	NIMCLSREEG	IKWIKKERLP	AFLESDCYFE	YRLAKLVSQV	RWSKSGMNFT
170	180	190	200	210	220	230	240
VGSNFSPWIV	KKPPSLPPPA	TEEDNLASYT	QTKDWFALAK	QSQQTVSTFS	LPCCVPYNKL	KSPAISSVSE	NFIFDDGVHP
250	260	270	280	290	300	310	320
RTKKDPSKTN	KLISEFEEEE	GEEEEVSVSL	QDTPSQALLR	VYLEKKQDVD	ESLTMHFSTC	EEFLSSYIYF	ILRGAIQQIV
330	340	350	360	370	380	390	400
GKPVGETPDY	INFNNITKVS	FDDCFESIHG	KNFLSELVQT	TKERSEEIEQ	TSLSSKNESA	GPESRADWCI	SHRTYDIGNR
410	420	430	440	450	460	470	480
KEFERFKKFI	KGTLGERYWW	LWMDIERLKV	LKDPGRHQRH	LEKMKKCYLV	SNGDYYLSAE	ILSKFKLLDG	SQWNEEHLRN
490	500	510	520	530	540	550	560
IQSEVLKPLL	LYWAPRFCVT	HSASTKYASA	ELKFWHLRQA	KPRKDIDPFP	QMATLLPLRP	KSCIPQIPEI	QKEEFSLSQP
570	580	590	600	610	620	630	640
PKSPNKSPEV	KTATQKPWKR	ELLYPGSSKD	DVIEKGSKYM	SESSKVIHLT	SFTDISECLK	PQLDRRYAYT	EEPRVKTVSD
650	660	670	680	690	700	710	720
VGALGGSDME	NLLQSLYVEN	RAGFFFTKFC	EHSGNKLWKN	SVYFWFDLQA	YHQLFYQETL	QPFKVCKQAQ	YLFATYVAPS
730	740	750	760	770	780	790	800
ATLDIGLQQE	KKKEIYMKIQ	PPFEDLFDTA	EEYILLLLLE	PWTKMVKSDQ	IAYKKVELVE	ETRQLDSTYF	RKLQALHKET
810	820	830	840	850	860	870	880
FSKKAEDTTC	EIGTGILSLS	NVSKRTEYWD	NVPAEYKHFK	FSDLLNNKLE	FEHFRQFLET	HSSSMDLMCW	TDIEQFRRIT
890	900	910	920	930	940	950	960
YRDRNQRKAK	SIYIKNKYLN	KKYFFGPNSP	ASLYQQNQVM	HLSGGWGKIL	HEQLDAPVLV	EIQKHVQNRL	ENVWLPLFLA
970	980	990	1000	1010	1020	1030	1040
SEQFAARQKI	KVQMKDIAEE	LLLQKAEKKI	GVWKPVESKW	ISSSCKIIAF	RKALLNPVTS	RQFQRFVALK	GDLLENGLLF
1050	1060	1070	1080	1090	1100	1110	1120
WQEVQKYKDL	CHSHCDESVI	QKKITTIINC	FINSSIPPAL	QIDIPVEQAQ	KIIEHRKELG	PYVFREAQMT	IFGVLFKFWP
1130	1140	1150	1160	1170	1180	1190	1200
QFCEFRKNLT	DENIMSVLER	RQEYNKQKKK	LAVLEDEKSG	KDGIKQYANT	SVPAIKTALL	SDSFLGLQPY	GRQPTWCYSK
1210	1220	1230	1240	1250	1260		
YIEALEQERI	LLKIQEELEK	KLFAGLQPLT	NFKASSSTMS	LKKNMSAHSS	QK		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2902	1	1192.7378	113.29	2	65.0	10.5	0	172-193	K.KPPSLPPPATEEDNLASYTQTK.D	
2013	1	703.2744	-90.02	2	53.5	13.4	1	669-679	K.FCEHSGNKLWK.N	Carbamidomethyl: 2

Detailed Protein Report

Protein 336: zinc finger and BTB domain-containing protein 21 isoform L [Homo sapiens]

Accession:	gi|50345873	**Score:**	23.9
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

Quantitation

WD:WU	**Median:**	0.61	**CV:**	0.00 %	**No. of Peptides:**	1	

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	Ratios
1308	3	698.8804	93.56	2	44.7	13.3	0	135-146	K.VFVEDDENSSQK.R		
861	1	491.8136	-69.69	2	39.6	10.6	2	634-641	K.ALIIKLRR.G		WD:WU 0.61

Detailed Protein Report

Protein 337: **A disintegrin and metalloproteinase with thrombospondin motifs 6 preproprotein [Homo sapiens]**

Accession:	gi|64276808	**Score:**	23.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	125.2
Database Date:	2015-11-30	**pI:**	6.3
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	3.8
		No. of unique Peptides:	2

Quantitation

WD:WU **Median:** 1.11 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MEILWKTLTW	ILSLIMASSE	FHSDHRLSYS	SQEEFLTYLE	HYQLTIPIRV	DQNGAFLSFT	VKNDKHSRRR	RSMDPIDPQQ
90	100	110	120	130	140	150	160
AVSKLFFKLS	AYGKHFHLNL	TLNTDFVSKH	FTVEYWGKDG	PQWKHDFLDN	CHYTGYLQDQ	RSTTKVALSN	CVGLHGVIAT
170	180	190	200	210	220	230	240
EDEEYFIEPL	KNTTEDSKHF	SYENGHPHVI	YKKSALQQRH	LYDHSHCGVS	DFTRSGKPWW	LNDTSTVSYS	LPINNTHIHH
250	260	270	280	290	300	310	320
RQKRSVSIER	FVETLVVADK	MMVGYHGRKD	IEHYILSVMN	IVAKLYRDSS	LGNVVNIIVA	RLIVLTEDQP	NLEINHHADK
330	340	350	360	370	380	390	400
SLDSFCKWQK	SILSHQSDGN	TIPENGIAHH	DNAVLITRYD	ICTYKNKPCG	TLGLASVAGM	CEPERSCSIN	EDIGLGSAFT
410	420	430	440	450	460	470	480
IAHEIGHNFG	MNHDGIGNSC	GTKGHEAAKL	MAAHITANTN	PFSWSACSRD	YITSFLDSGR	GTCLDNEPPK	RDFLYPAVAP
490	500	510	520	530	540	550	560
GQVYDADEQC	RFQYGATSRQ	CKYGEVCREL	WCLSKSNRCV	TNSIPAAEGT	LCQTGNIEKG	WCYQGDCVPF	GTWPQSIDGG
570	580	590	600	610	620	630	640
WGPWSLWGEC	SRTCGGGVSS	SLRHCDSPAP	SGGGKYCLGE	RKRYRSCNTD	PCPLGSRDFR	EKQCADFDNM	PFRGKYYNWK
650	660	670	680	690	700	710	720
PYTGGGVKPC	ALNCLAEGYN	FYTERAPAVI	DGTQCNADSL	DICINGECKH	VGCDNILGSD	AREDRCRVCG	GDGSTCDAIE
730	740	750	760	770	780	790	800
GFFNDSLPRG	GYMEVVQIPR	GSVHIEVREV	AMSKNYIALK	SEGDDYYING	AWTIDWPRKF	DVAGTAFHYK	RPTDEPESLE
810	820	830	840	850	860	870	880
ALGPTSENLI	VMVLLQEQNL	GIRYKFNVPI	TRTGSGDNEV	GFTWNHQPWS	ECSATCAGGV	QRQEVVCKRL	DDNSIVQNNY
890	900	910	920	930	940	950	960
CDPDSKPPEN	QRACNTEPCP	PEWFIGDWLE	CSKTCDGGMR	TRAVLCIRKI	GPSEEETLDY	SGCLTHRPVE	KEPCNNQSCP
970	980	990	1000	1010	1020	1030	1040
PQWVALDWSE	CTPKCGPGFK	HRIVLCKSSD	LSKTFPAAQC	PEESKPPVRI	RCSLGRCPPP	RWVTGDWGQC	SAQCGLGQQM
1050	1060	1070	1080	1090	1100	1110	1120
RTVQCLSYTG	QASSDCLETV	RPPSMQQCES	KCDSTPISNT	EECKDVNKVA	YCPLVLKFKF	CSRAYFRQMC	CKTCQGH

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
885	1	649.9950	65.11	3	39.5	10.1	1	584-601	R.HCDSPAPSGGGKYCLGER.K	Carbamidomethyl: 2, 14	WD:WU 1.11
2995	1	964.4577	34.33	3	66.2	13.8	1	1017-1041	R. CPPPRWVTGDWGQCSAQCGLG(T	Carbamidomethyl: 14, 18; Oxidation: 24	

Detailed Protein Report

Protein 338: prosaposin receptor GPR37 precursor [Homo sapiens]

Accession:	gi|4885323	**Score:**	23.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	67.1
Database Date:	2015-11-30	**pI:**	9.9
		Sequence Coverage [%]:	2.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MRAPGALLAR	MSRLLLLLLL	KVSASSALGV	APASRNETCL	GESCAPTVIQ	RRGRDAWGPG	NSARDVLRAR	APREEQGAAF
90	100	110	120	130	140	150	160
LAGPSWDLPA	APGRDPAAGR	GAEASAAGPP	GPPTRPPGPW	RWKGARGQEP	SETLGRGNPT	ALQLFLQISE	EEEKGPRGAG
170	180	190	200	210	220	230	240
ISGRSQEQSV	KTVPGASDLF	YWPRRAGKLQ	GSHHKPLSKT	ANGLAGHEGW	TIALPGRALA	QNGSLGEGIH	EPGGPRRGNS
250	260	270	280	290	300	310	320
TNRRVRLKNP	FYPLTQESYG	AYAVMCLSVV	IFGTGIIGNL	AVMCIVCHNY	YMRSISNSLL	ANLAFWDFLI	IFFCLPLVIF
330	340	350	360	370	380	390	400
HELTKKWLLE	DFSCKIVPYI	EVASLGVTTF	TLCALCIDRF	RAATNVQMYY	EMIENCSSTT	AKLAVIWVGA	LLLALPEVVL
410	420	430	440	450	460	470	480
RQLSKEDLGF	SGRAPAERCI	IKISPDLPDT	IYVLALTYDS	ARLWWYFGCY	FCLPTLFTIT	CSLVTARKIR	KAEKACTRGN
490	500	510	520	530	540	550	560
KRQIQLESQM	NCTVVALTIL	YGFCIIPENI	CNIVTAYMAT	GVSQQTMDLL	NIISQFLLFF	KSCVTPVLLF	CLCKPFSRAF
570	580	590	600	610	620		
MECCCCCCEE	CIQKSSTVTS	DDNDNEYTTE	LELSPFSTIR	REMSTFASVG	THC		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2716	2	715.3661	-44.05	2	62.4	11.7	2	1-13	-.MRAPGALLARMSR.L	

Detailed Protein Report

Protein 339: **telomerase reverse transcriptase isoform 2 [Homo sapiens]**

Accession:	gi|301129200	**Score:**	23.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	120.0
Database Date:	2015-11-30	**pI:**	11.9
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.8
		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 340: 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

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
2770	1	1002.0175	9.51	2	63.1	10.3	2	118-135	K.CDLAARTVESRQAQDLAR.S	

Detailed Protein Report

Protein 341: **PREDICTED: nascent polypeptide-associated complex subunit alpha isoform X6 [Homo sapiens]**

Accession:	gi|578823772	**Score:**	23.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	201.3
Database Date:	2015-11-30	**pI:**	10.2
		Sequence Coverage [%]:	1.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPGEATETVP	ATEQELPQPQ	AETAVLPMSS	ALSVTAALGQ	PGPTLPPPCS	PAPQQCPLSA	ANQASPFPSP	STIASTPLEV
90	100	110	120	130	140	150	160
PFPQSSSGTA	LPLGTAPEAP	TFLPNLIGPP	ISPAALALAS	PMIAPTLKGT	PSSSAPLALV	ALAPHSVQKS	SAFPPNLLTS
170	180	190	200	210	220	230	240
PPSVAVAESG	SVITLSAPIA	PSEPKTNLNK	VPSEVVPNPK	GTPSPPCIVS	TVPYHCVTPM	ASIQSGVASL	PQTTPTTTLA
250	260	270	280	290	300	310	320
IASPQVKDTT	ISSVLISPQN	PGSLSLKGPV	SPPAALSLST	QSLPVVTSSQ	KTAGPNTPPD	FPISLGSHLA	PLHQSSFGSV
330	340	350	360	370	380	390	400
QLLGQTGPSA	LSDPTVKTIS	VDHSSTGASY	PSQRSVIPPL	PSRNEVVPAT	VAAFPVVAPS	VDKGPSTISS	ITCSPSGSLN
410	420	430	440	450	460	470	480
VATSFSLSPT	TSLILKSSPN	ATYHYPLVAQ	MPVSSVGTTP	LVVTNPCTIA	AAPTTTFEVA	TCVSPPMSSG	PISNIEPTSP
490	500	510	520	530	540	550	560
AALVMAPVAP	KEPSTQVATT	LRIPVSPPLP	DPEDLKNLPS	SVLVKFPTQK	DLQTVPASLE	GAPFSPAQAG	LTTKKDPTVL
570	580	590	600	610	620	630	640
PLVQAAPKNS	PSFQSTSSSP	EIPLSPEATL	AKKSLGEPLP	IGKPASSMTS	PLGVNSSASV	IKTDSYAGPD	SAGPLLKSSL
650	660	670	680	690	700	710	720
ITPTVAAFPL	ESADPAGVAP	TTAKGTSTYT	TTASPFLEGT	VSLAPKNHPV	KEGTLTTLPL	VPTASENCPV	APSPQNTCAP
730	740	750	760	770	780	790	800
LATLVLAPEI	PKSVPSPSLP	PAGTPPGTKK	VDGISHTSAL	APVASSPKEC	PTEDSGASAT	ASSKGTLTYL	ADSPSPLGVS
810	820	830	840	850	860	870	880
VSPQTKRPPT	KKGSAGPDTP	IGNLSSPVSP	VEASFLPENS	LSFQGSKDSP	ATTHSPTPPS	PKGAPTPSAV	TPLSPKGVTL
890	900	910	920	930	940	950	960
PPKETPTPSV	VNLPFPKEGP	ATPAPKQAPA	LSMTSSSPKK	ARATPAPKGI	PASPSPKGAP	TPPAATPPSP	KGGPATPSPK
970	980	990	1000	1010	1020	1030	1040
WAPTPPAATP	PSPKGGPATP	SPKGAPTPPA	ATPPSPKGSP	AATPLPKGAP	TTPAATLPSP	KGGPATPSLK	GAPTPPAATP
1050	1060	1070	1080	1090	1100	1110	1120
PSPKGGPATP	SPKGAPMPPA	ATPPSPKGGL	ATPPHKGAPT	TPAATPPSPK	GGLATPPPKG	APTTPAATPP	SPKGGLATPP
1130	1140	1150	1160	1170	1180	1190	1200
PKGAPTTPAA	TPPSPKGGLA	TPSPKGAPTT	PAATPPSPKG	GLATPSPKGA	PTTPAATPPS	PKGGLATPSP	KGAPTTPAAT
1210	1220	1230	1240	1250	1260	1270	1280
PPSPKGGPAT	PPPKGAPTPP	AATPPSLKGG	LATPPHKGAP	NPAVVTPPSP	KGGPATSPPK	GAPTPPAATP	PSPKGSPGTP
1290	1300	1310	1320	1330	1340	1350	1360
PPKGAPTPPA	VTPPSPKGTP	TLPATTPSSK	GGPTTPSSKE	GPTPPAATPS	HKGGPAMTPP	SPKRGPAIPS	PKGDPTSPAV
1370	1380	1390	1400	1410	1420	1430	1440
IPLSPKKAPA	TPVTREGAAT	PSKGDLTPPA	VTPVSLKKAP	ATSAPKGGPA	TPSSKGDPTL	PAVTPPSPKE	PPAPKQVATS
1450	1460	1470	1480	1490	1500	1510	1520
SSPKKAPATP	APMGAPTLPA	VIPSSPKEVP	ATPSSRRDPI	APTATLLSKK	TPATLAPKEA	LIPPAMTVPS	PKKTPAIPTP
1530	1540	1550	1560	1570	1580	1590	1600
KEAPATPSSK	EASSPPAVTP	STYKGAPSPK	ELLIPPAVTS	PSPKEAPTPP	AVTPPSPEKG	PATPAPKGTP	TSPPVTPSSL
1610	1620	1630	1640	1650	1660	1670	1680
KDSPTSPASV	TCKMGATVPQ	ASKGLPAKKG	PTALKEVLVA	PAPESTPIIT	APTRKGPQTK	KSSATSPPIC	PDPSAKNGSK
1690	1700	1710	1720	1730	1740	1750	1760
GPLSTVAPAP	LLPVQKDSSK	TAKGKDASHS	PKGPLAPPES	KASTPLTAAA	FEKVLPKPES	ASVSAAPSPP	VSLPLAPSPV
1770	1780	1790	1800	1810	1820	1830	1840
PTLPPKQQFL	PSSPGLVLES	PSKPLAPADE	DELLPLIPPE	PISGGVPFQS	VLVNMPTPKS	AGIPVPTPSA	KQPVTKNNKG
1850	1860	1870	1880	1890	1900	1910	1920
SGTESDSDES	VPELEEQDST	QATTQQAQLA	AAAEIDEEPV	SKAKQSRSEK	KARKAMSKLG	LRQVTGVTRV	TIRKSKNILF
1930	1940	1950	1960	1970	1980	1990	2000
VITKPDVYKS	PASDTYIVFG	EAKIEDLSQQ	AQLAAAEKFK	VQGEAVSNIQ	ENTQTPTVQE	ESEEEEVDET	GVEVKDIELV
2010	2020	2030	2040				
MSQANVSRAK	AVRALKNNSN	DIVNAIMVSV	QAFVP				

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

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2894	2	724.8707	-70.24	2	64.9	11.4	0	1551-1564	K.ELLIPPAVTSPSPK.E	

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Detailed Protein Report

Protein 342: PREDICTED: multimerin-1 isoform X1 [Homo sapiens]

Accession:	gi|530377406	**Score:**	23.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	134.3
Database Date:	2015-11-30	**pI:**	9.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MKGARLFVLL	SSLWSGGIGL	NNSKHSWTIP	EDGNSQKTMP	SASVPPNKIQ	SLQILPTTRV	MSAEIATTPE	ARTSEDSLLK
90	100	110	120	130	140	150	160
STLPPSETSA	PAEGVRNQTL	TSTEKAEGVV	KLQNLTLPTN	ASIKFNPGAE	SVVLSNSTLK	FLQSFARKSN	EQATSLNTVG
170	180	190	200	210	220	230	240
GTGGIGGVGG	TGGVGNRAPR	ETYLSRGDSS	SSQRTDYQKS	NFETTRGKNW	CAYVHTRLSP	TVILDNQVTY	VPGGKGPCGW
250	260	270	280	290	300	310	320
TGGSCPQRSQ	KISNPVYRMQ	HKIVTSLDWR	CCPGYSGPKC	QLREVMQKMT	DQVNYQAMKL	TLLQKKIDNI	SLTVNDVRNT
330	340	350	360	370	380	390	400
YSSLEGKVSE	DKSREFQSLL	KGLKSKSINV	LIRDIVREQF	KIFQNDMQET	VAQLFKTVSS	LSEDLESTRQ	IIQKVNESVV
410	420	430	440	450	460	470	480
SIAAQQKFVL	VQENRPTLTD	IVELRNHIVN	VRQEMTLTCE	KPIKELEVKQ	THLEGALEQE	HSRSILYYES	LNKTLSKLKE
490	500	510	520	530	540	550	560
VHEQLLSTEQ	VSDQKNAPAA	ESVSNNVTEY	MSTLHENIKK	QSLMMLQMFE	DLHIQESKIN	NLTVSLEMEK	ESLRGECEDM
570	580	590	600	610	620	630	640
LSKCRNDFKF	QLKDTEENLH	VLNQTLAEVL	FPMDNKMDKM	SEQLNDLTYD	MEILQPLLEQ	GASLRQTMTY	EQPKEAIVIR
650	660	670	680	690	700	710	720
KKIENLTSAV	NSLNFIIKEL	TKRHNLLRNE	VQGRDDALER	RINEYALEME	DGLNKTMTII	NNAIDFIQDN	YALKETLSTI
730	740	750	760	770	780	790	800
KDNSEIHHKC	TSDMETILTF	IPQFHRLNDS	IQTLVNDNQR	YNFVLQVAKT	LAGIPRDEKL	NQSNFQKMYQ	MFNETTSQVR
810	820	830	840	850	860	870	880
KYQQNMSHLE	EKLLLTTKIS	KNFETRLQDI	ESKVTQTLIP	YYISVKKGSV	VTNERDQALQ	LQVLNSRFKA	LEAKSIHLSI
890	900	910	920	930	940	950	960
NFFSLNKTLH	EVLTMCHNAS	TSVSELNATI	PKWIKHSLPD	IQLLQKGLTE	FVEPIIQIKT	QAALSNLTCC	IDRSLPGSLA
970	980	990	1000	1010	1020	1030	1040
NVVKSQKQVK	SLPKKINALK	KPTVNLTTVL	IGRTQRNTDN	IIYPEEYSSC	SRHPCQNGGT	CINGRTSFTC	ACRHPFTGDN
1050	1060	1070	1080	1090	1100	1110	1120
CTIKLVEENA	LAPDFSKGSY	RYAPMVAFFA	SHTYGMTIPG	PILFNNLDVN	YGASYTPRTG	KFRIPYLGVY	VFKYTIESFS
1130	1140	1150	1160	1170	1180	1190	1200
AHISGFLVVD	GIDKLAFESE	NINSEIHCDR	VLTGDALLEL	NYGQEVWLRL	AKGTIPAKFP	PVTTFSGYLL	YRT

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1058	1	974.4611	39.05	2	41.5	12.5	0	997-1012	R.NTDNIIYPEEYSSCSR.H	Carbamidomethyl: 14

Detailed Protein Report

Protein 343: protein unc-45 homolog A isoform 3 [Homo sapiens]

Accession:	gi|89179321	**Score:**	23.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	101.6
Database Date:	2015-11-30	**pI:**	5.7
		Sequence Coverage [%]:	2.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MTASSVEQLR	KEGNELFKCG	DYGGALAAYT	QALGLDATPQ	DQAVLHRNRA	ACHLKLEDYD	KAETEASKAI	EKDGGDVKAL
90	100	110	120	130	140	150	160
YRRSQALEKL	GRLDQAVLDL	QRCVSLEPKN	KVFQEALRNI	GGQIQEKVRY	MSSTDAKVEQ	MFQILLDPEE	KGTEKKQKAS
170	180	190	200	210	220	230	240
QNLVVLARED	AGAEKIFRSN	GVQLLQRLLD	MGETDLMLAA	LRTLVGICSE	HQSRTVATLS	ILGTRRVVSI	LGVESQAVSL
250	260	270	280	290	300	310	320
AACHLLQVMF	DALKEGVKKG	FRGKEGAIIV	DPARELKVLI	SNLLDLLTEV	GVSGQGRDNA	LTLLIKAVPR	KSLKDPNNSL
330	340	350	360	370	380	390	400
TLWVIDQGLK	KILEVGGSLQ	DPPGELAVTA	NSRMSASILL	SKLFDDLKCD	AERENFHRLC	ENYIKSWFEG	QGLAGKLRAI
410	420	430	440	450	460	470	480
QTVSCLLQGP	CDAGNRALEL	SGVMESVIAL	CASEQEEEQL	VAVEALIHAA	GKAKRASFIT	ANGVSLLKDL	YKCSEKDSIR
490	500	510	520	530	540	550	560
IRALVGLCKL	GSAGGTDFSM	KQFAEGSTLK	LAKQCRKWLC	NDQIDAGTRR	WAVEGLAYLT	FDADVKEEFV	EDAAALKALF
570	580	590	600	610	620	630	640
QLSRLEERSV	LFAVASALVN	CTNSYDYEEP	DPKMVELAKY	AKQHVPEQHP	KDKPSFVRAR	VKKLLAAGVV	SAMVCMVKTE
650	660	670	680	690	700	710	720
SPVLTSSCRE	LLSRVFLALV	EEVEDRGTVV	AQGGGRALIP	LALEGTDVGQ	TKAAQALAKL	TITSNPEMTF	PGERIYEVVR
730	740	750	760	770	780	790	800
PLVSLLHLNC	SGLQNFEALM	ALTNLAGISE	RLRQKILKEK	AVPMIEGYMF	EEHEMIRRAA	TECMCNLAMS	KEVQDLFEAQ
810	820	830	840	850	860	870	880
GNDRLKLLVL	YSGEDDELLQ	RAAAGGLAML	TSMRPTLCSR	IPQVTTHWLE	ILQALLLSSN	QELQHRGAVV	VLNMVEASRE
890	900	910	920	930			
IASTLMESEM	MEILSVLAKG	DHSPVTRAAA	ACLDKAVEYG	LIQPNQDGE			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2777	1	703.4893	208.47	2	63.3	10.5	1	50-61	R.AACHLKLEDYDK.A	

Detailed Protein Report

Protein 344: PREDICTED: ubiquitin carboxyl-terminal hydrolase 24 isoform X1 [Homo sapiens]

Accession:	gi|530362258	**Score:**	23.7
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 [%]:**	1.1
		No. of unique Peptides:	2

Quantitation

WD:WU	**Median:** 0.78	**CV:** 0.00 %	**No. of Peptides:** 1

Detailed Protein Report

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

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2676	1	585.8808	7.47	2	61.8	11.9	1	284-294	R.IKGIIELLGSK.L		
143	1	849.3662	-2.35	2	31.0	11.7	1	1010-1024	K.LMPTADDDMARSCAK.S	Carbamidomethyl: 13; Oxidation: 2	WD:WU 0.78

Detailed Protein Report

Protein 345: PREDICTED: CAD protein isoform X4 [Homo sapiens]

Accession:	gi|530368098	**Score:**	23.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	235.9
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
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	

Detailed Protein Report

Protein 346: melanotransferrin isoform 1 precursor [Homo sapiens]

Accession:	gi|134244281	**Score:**	23.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	80.2
Database Date:	2015-11-30	**pI:**	5.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.8
		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	TVLENTDGKT
250	260	270	280	290	300	310	320
LPSWGQALLS	QDFELLCRDG	SRADVTEWRQ	CHLARVPAHA	VVVRADTDGG	LIFRLLNEGQ	RLFSHEGSSF	QMFSSEAYGQ
330	340	350	360	370	380	390	400
KDLLFKDSTS	ELVPIATQTY	EAWLGHEYLH	AMKGLLCDPN	RLPPYLRWCV	LSTPEIQKCG	DMAVAFRRQR	LKPEIQCVSA
410	420	430	440	450	460	470	480
KSPQHCMERI	QAEQVDAVTL	SGEDIYTAGK	TYGLVPAAGE	HYAPEDSSNS	YYVVAVVRRD	SSHAFTLDEL	RGKRSCHAGF
490	500	510	520	530	540	550	560
GSPAGWDVPV	GALIQRGFIR	PKDCDVLTAV	SEFFNASCVP	VNNPKNYPSS	LCALCVGDEQ	GRNKCVGNSQ	ERYYGYRGAF
570	580	590	600	610	620	630	640
RCLVENAGDV	AFVRHTTVFD	NTNGHNSEPW	AAELRSEDYE	LLCPNGARAE	VSQFAACNLA	QIPPHAVMVR	PDTNIFTVYG
650	660	670	680	690	700	710	720
LLDKAQDLFG	DDHNKNGFKM	FDSSNYHGQD	LLFKDATVRA	VPVGEKTTYR	GWLGLDYVAA	LEGMSSQQCS	GAAAPAPGAP
730	740						
LLPLLLPALA	ARLLPPAL						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2932	1	713.3656	28.08	2	65.4	11.9	2	379-390	K.CGDMAVAFRRQR.L	Oxidation: 4

Detailed Protein Report

Protein 347: vacuolar protein sorting-associated protein 13B isoform 1 [Homo sapiens]

Accession:	gi|35493701	**Score:**	23.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	445.7
Database Date:	2015-11-30	**pI:**	6.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.0
		No. of unique Peptides:	1

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
1842	1	1273.5438	-34.83	2	51.4	10.7	1	3110-3132	K.EYFRVPDSATFSICPGGEQPAMK.S	Oxidation: 22

Detailed Protein Report

Protein 348: obscurin isoform a [Homo sapiens]

Accession:	gi|403501448	**Score:**	23.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	721.1
Database Date:	2015-11-30	**pI:**	5.4
Modification(s):	Oxidation	**Sequence Coverage [%]:**	0.6
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MDQPQFSGAP	RFLTRPKAFV	VSVGKDATLS	CQIVGNPTPQ	VSWEKDQQPV	AAGARFRLAQ	DGDLYRLTIL	DLALGDSGQY
90	100	110	120	130	140	150	160
VCRARNAIGE	AFAAVGLQVD	AEAACAEQAP	HFLLRPTSIR	VREGSEATFR	CRVGGSPRPA	VSWSKDGRRL	GEPDGPRVRV
170	180	190	200	210	220	230	240
EELGEASALR	IRAARPRDGG	TYEVRAENPL	GAASAAAALV	VDSDAADTAS	RPGTSTAALL	AHLQRRREAM	RAEGAPASPP
250	260	270	280	290	300	310	320
STGTRTCTVT	EGKHARLSCY	VTGEPKPETV	WKKDGQLVTE	GRRHVVYEDA	QENFVLKILF	CKQSDRGLYT	CTASNLVGQT
330	340	350	360	370	380	390	400
YSSVLVVVRE	PAVPFKKRLQ	DLEVREKESA	TFLCEVPQPS	TEAAWFKEET	RLWASAKYGI	EEEGTERRLT	VRNVSADDDA
410	420	430	440	450	460	470	480
VYICETPEGS	RTVAELAVQG	NLLRKLPRKT	AVRVGDTAMF	CVELAVPVGP	VHWLRNQEEV	VAGGRVAISA	EGTRHTLTIS
490	500	510	520	530	540	550	560
QCCLEDVGQV	AFMAGDCQTS	TQFCVSAPRK	PPLQPPVDPV	VKARMESSVI	LSWSPPPHGE	RPVTIDGYLV	EKKKLGTYTW
570	580	590	600	610	620	630	640
IRCHEAEWVA	TPELTVADVA	EEGNFQFRVS	ALNSFGQSPY	LEFPGTVHLA	PKLAVRTPLK	AVQAVEGGEV	TFSVDLTVAS
650	660	670	680	690	700	710	720
AGEWFLDGQA	LKASSVYEIH	CDRTRHTLTI	REVPASLHGA	QLKFVANGIE	SSIRMEVRAA	PGLTANKPPA	AAAREVLARL
730	740	750	760	770	780	790	800
HEEAQLLAEL	SDQAAAVTWL	KDGRTLSPGP	KYEVQASAGR	RVLLVRDVAR	DDAGLYECVS	RGGRIAYQLS	VQGLARFLHK
810	820	830	840	850	860	870	880
DMAGSCVDAV	AGGPAQFECE	TSEAHVHVHW	YKDGMELGHS	GERFLQEDVG	TRHRLVAATV	TRQDEGTYSC	RVGEDSVDFR
890	900	910	920	930	940	950	960
LRVSEPKVVF	AKEQLARRKL	QAEAGASATL	SCEVAQAQTE	VTWYKDGKKL	SSSSKVCMEA	TGCTRRLVVQ	QAGQADAGEY
970	980	990	1000	1010	1020	1030	1040
SCEAGGQRLS	FHLDVKEPKV	VFAKDQVAHS	EVQAEAGASA	TLSCEVAQAQ	TEVMWYKDGK	KLSSSLKVHV	EAKGCRRRLV
1050	1060	1070	1080	1090	1100	1110	1120
VQQAGKTDAG	DYSCEARGQR	VSFRLHITEP	KMMFAKEQSV	HNEVQAEAGA	SAMLSCEVAQ	AQTEVTWYKD	GKKLSSSSKV
1130	1140	1150	1160	1170	1180	1190	1200
GMEVKGCTRR	LVLPQAGKAD	AGEYSCEAGG	QRVSFHLHIT	EPKGVFAKEQ	SVHNEVQAEA	GTTAMLSCEV	AQPQTEVTWY
1210	1220	1230	1240	1250	1260	1270	1280
KDGKKLSSSS	KVRMEVKGCT	RRLVVQQVGK	ADAGEYSCEA	GGQRVSFQLH	ITEPKAVFAK	EQLVHNEVRT	EAGASATLSC
1290	1300	1310	1320	1330	1340	1350	1360
EVAQAQTEVT	WYKDGKKLSS	SSKVRIEAAG	CMRQLVVQQA	GQADAGEYTC	EAGGQRLSFH	LDVSEPKAVF	AKEQLAHRKV
1370	1380	1390	1400	1410	1420	1430	1440
QAEAGAIATL	SCEVAQAQTE	VTWYKDGKKL	SSSSKVRMEA	VGCTRRLVVQ	QACQADTGEY	SCEAGGQRLS	FSLDVAEPKV
1450	1460	1470	1480	1490	1500	1510	1520
VFAKEQPVHR	EVQAQAGAST	TLSCEVAQAQ	TEVMWYKDGK	KLSFSSKVRM	EAVGCTRRLV	VQQAGQAVAG	EYSCEAGSQR
1530	1540	1550	1560	1570	1580	1590	1600
LSFHLHVAEP	KAVFAKEQPA	SREVQAEAGT	SATLSCEVAQ	AQTEVTWYKD	GKKLSSSSKV	RMEAVGCTRR	LVVQEAGQAD
1610	1620	1630	1640	1650	1660	1670	1680
AGEYSCKAGD	QRLSFHLHVA	EPKVVFAKEQ	PAHREVQAEA	GASATLSCEV	AQAQTEVTWY	KDGKKLSSSS	KVRVEAVGCT
1690	1700	1710	1720	1730	1740	1750	1760
RRLVVQQAGQ	AEAGEYSCEA	GGQQLSFRLQ	VAELEPQISE	RPCRREPLVV	KEHEDIILTA	TLATPSAATV	TWLKDGVEIR
1770	1780	1790	1800	1810	1820	1830	1840
RSKRHETASQ	GDTHTLTVHG	AQVLDSAIYS	CRVGAEGQDF	PVQVEEVAAK	FCRLLEPVCG	ELGGTVTLAC	ELSPACAEVV
1850	1860	1870	1880	1890	1900	1910	1920
WRCGNTQLRV	GKRFQMVAEG	PVRSLTVLGL	RAEDAGEYVC	ESRDDHTSAQ	LTVSVPRVVK	FMSGLSTVVA	EEGGEATFQC
1930	1940	1950	1960	1970	1980	1990	2000
VVSPSDVAVV	WFRDGALLQP	SEKFAISQSG	ASHSLTISDL	VLEDAGQITV	EAEGASSSAA	LRVREAPVLF	KKKLEPQTVE
2010	2020	2030	2040	2050	2060	2070	2080
ERSSVTLEVE	LTRPWPELRW	TRNATALAPG	KNVEIHAEGA	RHRLVLHNVG	FADRGFFGCE	TPDDKTQAKL	TVEMRQVRLV
2090	2100	2110	2120	2130	2140	2150	2160
RGLQAVEARE	QGTATMEVQL	SHADVDGSWT	RDGLRFQQGP	TCHLAVRGPM	HTLTLSGLRP	EDSGLMVFKA	EGVHTSARLV
2170	2180	2190	2200	2210	2220	2230	2240
VTELPVSFSR	PLQDVVTTEK	EKVTLECELS	RPNVDVRWLK	DGVELRAGKT	MAIAAQGACR	SLTIYRCEFA	DQGVYVCDAH
2250	2260	2270	2280	2290	2300	2310	2320
DAQSSASVKV	QGRTYTLIYR	RVLAEDAGEI	QFVAENAESR	AQLRVKELPV	TLVRPLRDKI	AMEKHRGVLE	CQVSRASAQV
2330	2340	2350	2360	2370	2380	2390	2400

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2872	1	686.8855	-49.05	2	64.6	10.5	2	881-892	R.LRVSEPKVVFAK.E	
1563	1	927.4401	-8.97	3	48.2	13.0	1	5326-5351	R.EDSGQYAAYISNAMGAAYSSARLLVR.G	Oxidation: 14

Detailed Protein Report

Protein 349: neuropeptides B/W receptor type 1 [Homo sapiens]

Accession:	gi|53828924	**Score:**	23.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	36.1
Database Date:	2015-11-30	**pI:**	10.1
		Sequence Coverage [%]:	3.4
		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	2	604.3472	17.95	2	34.1	23.5	2	146-156	R.RVAGRTYSAAR.A	

Detailed Protein Report

Protein 350: plasminogen isoform 1 precursor [Homo sapiens]

Accession:	gi|4505881	**Score:**	23.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	90.5
Database Date:	2015-11-30	**pI:**	7.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.1
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 1.93 **CV:** 0.00 % **No. of 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	Ratios
1599	1	1073.5631	49.12	2	48.7	12.7	1	236-252	R.NPDRELRPWCFTTDPNK.R	Carbamidomethyl: 10	WD:WU 1.93

Detailed Protein Report

Protein 351: vacuolar protein sorting-associated protein 13D isoform 1 [Homo sapiens]

Accession:	gi|54607139	**Score:**	23.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	491.6
Database Date:	2015-11-30	**pI:**	6.1
Modification(s):	Oxidation	**Sequence Coverage [%]:**	0.8
		No. of unique Peptides:	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MLEGLVAWVL	NTYLGKYVNN	LNTDQLSVAL	LKGAVELENL	PLKKDALKEL	ELPFEVKAGF	IGKVTLQIPF	YRPHVDPWVI
90	100	110	120	130	140	150	160
SISSLHLIGA	PEKIQDFNDE	KEKLLERERK	KALLQALEEK	WKNDRQQKGE	SYWYSVTASV	VTRIVENIEL	KIQDVHLRFE
170	180	190	200	210	220	230	240
DGVTNPSHPF	AFGICIKNVS	MQNAVNEPVQ	KLMRKKQLDV	AEFSIYWDVD	CTLLGDLPQM	ELQEAMARSM	ESRSHHYVLE
250	260	270	280	290	300	310	320
PVFASALLKR	NCSKKPLRSR	HSPRIDCDIQ	LETIPLKLSQ	LQYRQIMEFL	KELERKERQV	KFRRWKPKVA	ISKNCREWWY
330	340	350	360	370	380	390	400
FALNANLYEI	REQRKRCTWD	FMLHRARDAV	SYTDKYFNKL	KGGLLSTDDK	EEMCRIEEEQ	SFEELKILRE	LVHDRFHKQE
410	420	430	440	450	460	470	480
ELAESLREPQ	FDSPGACPGA	PEPGGGSGML	QYLQSWFPGW	GGWYGQQTPE	GNVVEGLSAE	QQEQWIPEEI	LGTEEFFDPT
490	500	510	520	530	540	550	560
ADASCMNTYT	KRDHVFAKLN	LQLQRGTVTL	LHKEQGTPQM	NESAFMQLEF	SDVKLLAESL	PRRNSSLLSV	RLGGLFLRDL
570	580	590	600	610	620	630	640
ATEGTMFPLL	VFPNPQKEVG	RVSQSFGLQT	TSADRSDHYP	AADPDGPVFE	MLYERNPAHS	HFERRLNVST	RPLNIIYNPQ
650	660	670	680	690	700	710	720
AIKKVADFFY	KGKVHTSGFG	YQSELELRVA	EAARRQYNKL	KMQTKAEIRQ	TLDRLLVGDF	IEESKRWTVR	LDISAPQVIF
730	740	750	760	770	780	790	800
PDDFKFKNPV	LVVVDLGRML	LTNTQDNSRR	KSRDGSASEE	TQFSDDEYKT	PLATPPNTPP	PESSSSNGEK	TPPFSGVEFS
810	820	830	840	850	860	870	880
EEQLQAHLMS	TKMYERYSLS	FMDLQIMVGR	VKDNWKHVQD	IDVGPTHVVE	KFNVHLQLER	RLIYTSDPKY	PGAVLSGNLP
890	900	910	920	930	940	950	960
DLKIHINEDK	ISALKNCFAL	LTTPEMKTSD	TQIKEKIFPQ	EEQRGSLQDS	VMNLTQSIVL	LEQHTREVLV	ESQLLLAEFK
970	980	990	1000	1010	1020	1030	1040
VNCMQLGVES	NGRYISVLKV	FGTNAHFVKR	PYDAEVSLTV	HGLLLVDTMQ	TYGADFDLLM	ASHKNLSFDI	PTGSLRDSRA
1050	1060	1070	1080	1090	1100	1110	1120
QSPVSGPNVA	HLTDGATLND	RSATSVSLDK	ILTKEQESLI	KLEYQFVSSE	CPSMNLDSTL	QVISLQVNNL	DIILNPETIV
1130	1140	1150	1160	1170	1180	1190	1200
ELIGFLQKSF	PKEKDDLSPQ	PLMTDFERSF	REQGTYQSTY	EQNTEVAVEI	HRLNLLLLRT	VGMANREKYG	RKIATASIGG
1210	1220	1230	1240	1250	1260	1270	1280
TKVNVSMGST	FDMNGSLGCL	QLMDLTQDNV	KNQYVVSIGN	SVGYENIISD	IGYFESVFVR	MEDAALTEAL	SFTFVERSKQ
1290	1300	1310	1320	1330	1340	1350	1360
ECFLNLKMAS	LHYNHSAKFL	KELTLSMDEL	EENFRGMLKS	AATKVTTVLA	TKTAEYSEMV	SLFETPRKTR	EPFILEENEI
1370	1380	1390	1400	1410	1420	1430	1440
YGFDLASSHL	DTVKLILNIN	IESPVVSIPR	KPGSPELLVG	HLGQIFIQNF	VAGDDESRSD	RLQVEIKDIK	LYSLNCTQLA
1450	1460	1470	1480	1490	1500	1510	1520
GREAVGSEGS	RMFCPPSGSG	SANSQEEAHF	TRHDFFESLH	RGQAFHILNN	TTIQFKLEKI	PIERESELTF	SLSPDDLGTS
1530	1540	1550	1560	1570	1580	1590	1600
SIMKIEGKFV	NPVQVVLAKH	VYEQVLQTLD	NLVYSEDLNK	YPASATSSPC	PDSPLPPLST	CGESSVERKE	NGLFSHSSLS
1610	1620	1630	1640	1650	1660	1670	1680
NTSQKSLSVK	EVKSFTQIQA	TFCISELQVQ	LSGDLTLGAQ	GLVSLKFQDF	EVEFSKDHPQ	TLSIQIALHS	LLMEDLLEKN
1690	1700	1710	1720	1730	1740	1750	1760
PDSKYKNLMV	SRGAPKPSSL	AQKEYLSQSC	PSVSNVEYPD	MPRSLPSHME	EAPNVFQLYQ	RPTSASRKKQ	KEVQDKDYPL
1770	1780	1790	1800	1810	1820	1830	1840
TPPPSPTVDE	PKILVGKSKF	DDSLVHINIF	LVDKKHPEFS	SSYNRVNRSI	DVDFNCLDVL	ITLQTWVVIL	DFFGIGSTAD
1850	1860	1870	1880	1890	1900	1910	1920
NHAMRLPPEG	ILHNVKLEPH	ASMESGLQDP	VNTKLDLKVH	SLSLVLNKTT	SELAKANVSK	LVAHLEMIEG	DLALQGSIGS
1930	1940	1950	1960	1970	1980	1990	2000
LSLSDLTCHG	EFYRERFTTS	GEEALIFQTF	KYGRPDPLLR	REHDIRVSLR	MASVQYVHTQ	RFQAEVVAFI	QHFTQLQDVL
2010	2020	2030	2040	2050	2060	2070	2080
GRQRAAIEGQ	TVRDQAQRCS	RVLLDIEAGA	PVLLIPESSR	SNNLIVANLG	KLKVKNKFLF	AGFPGTFSLQ	DKESVPSASP
2090	2100	2110	2120	2130	2140	2150	2160
TGIPKHSLRK	TTSTEEPRGT	HSQGQFTMPL	AGMSLGSLKS	EFVPSTSTKQ	QGPQPTLSVG	QESSSPEDHV	CLLDCVVVDL
2170	2180	2190	2200	2210	2220	2230	2240
QDMDIFAAER	HPREYSKAPE	DSSGDLIFPS	YFVRQTGGSL	LTEPCRLKLQ	VERNLDKEIS	HTVPDISIHG	NLSSVHCSLD
2250	2260	2270	2280	2290	2300	2310	2320
LYKYKLIRGL	LENNLGEPIE	EFMRPYDLQD	PRIHTVLSGE	VYTCMCFLID	MVNVSLELKD	PKRKEGAGSL	ARFDFKKCKL
2330	2340	2350	2360	2370	2380	2390	2400

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2118	1	900.3217	-110.13	3	54.8	10.2	0	2835-2858	K.SEDWMGSSVDPPCFGQSLPLVYLR.T	Oxidation: 5

Detailed Protein Report

Protein 352: **regulator of G-protein signaling 11 isoform 3 [Homo sapiens]**

Accession: gi|557129067
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 23.4
MW [kDa]: 51.5
pI: 9.9
Sequence Coverage [%]: 7.7
No. of unique Peptides: 2

```
        10         20         30         40         50         60         70         80
MAAGPAPPPG RPRAQMPHLR KMERVVVSMQ DPDQGVKMRS QRLLVTVIPH AVTGSDVVQW LAQKFCVSEE EALHLGAVLV
        90        100        110        120        130        140        150        160
QHGYIYPLRD PRSLMLRPDE TPYRFQVRLG GAAIYLAKKN IRKRGTLVDY EKDCYDRLHK KINHAWDLVL MQAREQLRAA
       170        180        190        200        210        220        230        240
KQRSKGDRLV IACQEQTYWL VNRPPPGAPD VLEQGPGRGS CAASRVLMTK SADFHKREIE YFRKALGRTR VKSSVCLEAY
       250        260        270        280        290        300        310        320
LSFCGQRGPH DPLVSGCLPS NPWISDNDAY WVMNAPTVAA PTKLRVERWG FSFRELLEDP VGRAHFMDFL GKEFSGENLS
       330        340        350        360        370        380        390        400
FWEACEELRY GAQAQVPTLV DAVYEQFLAP GAAHWVNIDS RTMEQTLEGL RQPHRYVLDD AQLHIYMLMK KDSYPRFLKS
       410        420        430        440        450        460
DMYKALLAEA GIPLEMKRRV FPFTWRPRHS SPSPALLPTP VEPTAACGPG GGDGVA
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2916	1	973.5104	15.53	2	65.2	12.7	2	21-37	R.KMERVVVSMQDPDQGVK.M	
1806	1	697.3618	15.85	3	50.9	10.7	1	295-312	R.ELLEDPVGRAHFMDFLGK.E	Oxidation: 13

Detailed Protein Report

Protein 353: 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 354: acetylcholine receptor subunit delta isoform 2 precursor [Homo sapiens]

Accession:	gi|375331911	**Score:**	23.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	57.0
Database Date:	2015-11-30	**pI:**	6.6
		Sequence Coverage [%]:	5.4
		No. of unique Peptides:	2

Quantitation

WD:WU **Median:** 1.45 **CV:** 0.00 % **No. of 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	Ratios
1638	2	823.4155	-56.77	2	48.8	12.6	2	28-40	R.LIRHLFQEKGYNK.E		
1931	1	734.3090	-177.58	2	52.5	10.8	1	283-296	K.RLPATSMAIPLIGK.F		WD:WU 1.45

Detailed Protein Report

Protein 355: PREDICTED: polycystic kidney disease protein 1-like 1 isoform X1 [Homo sapiens]

Accession:	gi|578813318	**Score:**	23.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	223.0
Database Date:	2015-11-30	**pI:**	6.1
		Sequence Coverage [%]:	1.3
		No. of unique Peptides:	2

Quantitation

WD:WU	**Median:** 0.71	**CV:** 0.00 %	**No. of Peptides:** 1

Detailed Protein Report

10	20	30	40	50	60	70	80
MAEEAAQNIS	DDQERCLQAA	CCLSFGGELS	VSTDKSWGLH	LCSCSPPGGG	LWVEVYANHV	LLMSDGKCGC	PWCALNGKAE
90	100	110	120	130	140	150	160
DRESQSPSSS	ASRQKNIWKT	TSEAALSVVN	EKTQAVVNEK	TQAPLDCDNS	ADRIPHKPFI	IIARAWSSGG	PRFHHRRLCA
170	180	190	200	210	220	230	240
TGTADSTFSA	LLQLQGTTSA	AAPCSLKMEA	SCCVLRLLCC	AEDVATGLLP	GTVTMETPTK	VARPTQTSSQ	RVPLWPISHF
250	260	270	280	290	300	310	320
PTSPRSSHGL	PPGIPRTPSF	TASQSGSEIL	YPPTQHPPVA	ILARNSDNFM	NPVLNCSLEV	EARAPPNLGF	RVHMASGEAL
330	340	350	360	370	380	390	400
CLMMDFGDSS	GVEMRLHNMS	EAMAVTAYHQ	YSKEDWQRNS	QEGVYMLKAV	IYNEFHGTEV	ELGPYYVEIG	HEAVSAFMNS
410	420	430	440	450	460	470	480
SSVHEDEVLV	FADSQVNQKS	TVVIHHFPSI	PSYNVSFISQ	TQVGDSQAWH	SMTVWYKMQS	VSVYTNGTVF	ATDTDITFTA
490	500	510	520	530	540	550	560
VTKETIPLEF	EWYFGEDPPV	RTTSRSIKKR	LSIPQWYRVM	VKASNRMSSV	VSEPHVIRVQ	KKIVANRLTS	PSSALVNASV
570	580	590	600	610	620	630	640
AFECWINFGT	DVAYLWDFGD	GTVSLGSSSS	SHVYSREGEF	TVEVLAFNNV	SASTLRQQLF	IVCEPCQPPL	VKNMGPGKVQ
650	660	670	680	690	700	710	720
IWRSQPVRLG	VTFEAAVFCD	ISQGLSYTWN	LMDSEGLPVS	LPAAVDTHRQ	TLILPSHTLE	YGNYTALAKV	QIEGSVVYSN
730	740	750	760	770	780	790	800
YCVGLEVRAQ	APVSVISEGT	HLFFSRTTSS	PIVLRGTQSF	DPDDPGATLR	YHWECATAGS	PAHPCFDSST	AHQLDAAAPT
810	820	830	840	850	860	870	880
VSFEAQWLSD	SYDQFLVMLR	VSSGGRNSSE	TRVFLSPYPD	SAFRFVHISW	VSFKDTFVNW	NDELSLQAMC	EDCSEIPNLS
890	900	910	920	930	940	950	960
YSWDLFLVNA	TEKNRIEVPF	CRVVGLLGSL	GLGAISESSQ	LNLLPTEPGT	ADPDATTTPF	SREPSPVTLG	QPATSAPRGT
970	980	990	1000	1010	1020	1030	1040
PTEPMTGVYW	IPPAGDSAVL	GEAPEEGSLD	LEPGPQSKGS	LMTGRSERSQ	PTHSPDPHLS	DFEAYYSDIQ	EAIPSGGRQP
1050	1060	1070	1080	1090	1100	1110	1120
AKDTSFPGSG	PSLSAEESPG	DGDNLVDPSL	SAGRAEPVLM	IDWPKALLGR	AVFQGYSSSG	ITEQTVTIKP	YSLSSGETYV
1130	1140	1150	1160	1170	1180	1190	1200
LQVSVASKHG	LLGKAQLYLT	VNPAPRDMAC	QVQPHHGLEA	HTVFSVFCMS	GKPDFHYEFS	YQIGNTSKHT	LYHGRDTQYY
1210	1220	1230	1240	1250	1260	1270	1280
FVLPAGEHLD	NYKVMVSTEI	TDGKGSKVQP	CTVVVTVLPR	YHGNDCLGED	LYNSSLKNLS	TLQLMGSYTE	IRNYITVITR
1290	1300	1310	1320	1330	1340	1350	1360
ILSRLSKEDK	TASCNQWSRI	QDALISSVCR	LAFVDQEEMI	GSVLMLRDLV	SFSNKLGFMS	AVLILKYTRA	LLAQGQFSGP
1370	1380	1390	1400	1410	1420	1430	1440
FVIDKGVRLE	LIGLISRVWE	VSEQENSKEE	VYRHEEGITV	ISDLLLGCLS	LNHVSTGQME	FRTLLHYNLQ	SSVQSLGSVQ
1450	1460	1470	1480	1490	1500	1510	1520
VHLPGDLAGH	SPAGAETQSP	CYISQLILFK	KNPYPGSQAP	GQIGGVVGLN	LYTCSSRRPI	NRQWLRKPVM	VEFGEEDGLD
1530	1540	1550	1560	1570	1580	1590	1600
NRRNKTTFVL	LRDKVNLHQF	TELSENPQES	LQIEIEFSKP	VTRAFPVMLL	VRFSEKPTPS	DFLVKQIYFW	DESIVQIYIP
1610	1620	1630	1640	1650	1660	1670	1680
AASQKDASVG	YLSLLDADYD	RKPPNRYLAK	AVNYTVHFQW	IRCLFWDKRE	WKSERFSPQP	GTSPEKVNCS	YHRLAAFALL
1690	1700	1710	1720	1730	1740	1750	1760
RRKLKASFEV	SDISKLQSHP	ENLLPSIFIM	GSVILYGFLV	AKSRQVDHHE	KKKAGYIFLQ	EASLPGHQLY	AVVIDTGFRA
1770	1780	1790	1800	1810	1820	1830	1840
PARLTSKVYI	VLCGDNGLSE	TKELSCPEKP	LFERNSRHTF	ILSAPAQLGL	LRKIRLWHDS	RGPSPGWFIS	HVMVKELHTG
1850	1860	1870	1880	1890	1900	1910	1920
QGWFFPAQCW	LSAGRHDGRV	ERELTCLQGG	LGFRKLFYCK	FTEYLEDFHV	WLSVYSRPSS	SRYLHTPRLT	VSFSLLCVYA
1930	1940	1950	1960	1970	1980	1990	2000
CLTALVAAGG	QEQPHLDVSP	TLGSFRVGLL	CTLLASPGAQ	LLSLLFRLSK	EAPGSARVEP	HSPLRGGAQT	EAPHGPNSWG
2010	2020	2030					
RIPDAQEPRK	VNQSLCAAAN	LLA					

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

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
465	1	667.6915	-184.62	2	34.3	10.3	0	1378-1388	R.VWEVSEQENSK.E		WD:WU 0.71
714	1	541.1775	-140.74	3	37.4	13.0	0	1986-2001	R.GGAQTEAPHGPNSWGR.I		

Detailed Protein Report

Protein 356: coiled-coil domain-containing protein 168 [Homo sapiens]

Accession:	gi|226246554	**Score:**	23.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	801.4
Database Date:	2015-11-30	**pI:**	9.6
		Sequence Coverage [%]:	0.5
		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

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	
2180	4	974.2038	45.87	3	55.6	12.3	2	5658-5682	R.DEDIYFTGFGTIRSGKRPEWLFTGK.K	

Detailed Protein Report

Protein 357: G protein-regulated inducer of neurite outgrowth 1 [Homo sapiens]

Accession: gi|112821681
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 23.3
MW [kDa]: 102.3
pI: 9.3
Sequence Coverage [%]: 3.5
No. of unique Peptides: 1

Alias proteins:

Accession	Name	Description
gi|530380833	refseq_human (refseq_human_20140103.fasta)	PREDICTED: G protein-regulated inducer of neurite outgrowth 1 isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MDTAEDPAWL	QLLQKDSSPP	GPRPTAFFCP	QDGSLGAGSS	AMRDYCPSQQ	KASPAPPRHT	PDQSPGMESR	HRSPSGAGEG
90	100	110	120	130	140	150	160
ASCSDGPRGS	LACPSPTCFS	PQESPSKETL	EAHGASISGT	PEATTSGKPE	PVSSVKTEPK	SSDDRNPMFL	EKMDFKSSKQ
170	180	190	200	210	220	230	240
ADSTSIGKED	PGSSRKADPM	FTGKAEPEIL	GKGDPVAPGR	MDPMTVRKED	LGSLGKVDPL	CSSKTYTVSP	RKEDPGSLRK
250	260	270	280	290	300	310	320
VDPVSSDKVD	PVFPRKEEPR	YSGKEHPVSS	EKVAPTSAEK	VDLVLSGKRD	PGPSGKADPM	PLESMDSAST	GKTEPGLLGK
330	340	350	360	370	380	390	400
LIPGSSGKNG	PVSSGTGAPG	SLGRLDPTCL	GMADPASVGN	VETVPATKED	SRFLGKMDPA	SSGEGRPVSG	HTDTTASAKT
410	420	430	440	450	460	470	480
DLTSLKNVDP	MSSGKVDPVS	LGKMDPMCSG	KPELLSPGQA	ERVSVGKAGT	VSPGKEDPVS	SRREDPISAG	SRKTSSEKVN
490	500	510	520	530	540	550	560
PESSGKTNPV	SSGPGDPRSL	GTAGPPSAVK	AEPATGGKGD	PLSSEKAGLV	ASGKAAPTAS	GKAEPLAVGK	EDPVSKGKAD
570	580	590	600	610	620	630	640
AGPSGQGDSV	SIGKVVSTPG	KTVPVPSGKV	DPVSLGKAEA	IPEGKVGSLP	LEKGSPVTTT	KADPRASGKA	QPQSGGKAET
650	660	670	680	690	700	710	720
KLPGQEGAAA	PGEAGAVCLK	KETPQASEKV	DPGSCRKAEP	LASGKGEPVS	LGKADSAPSR	KTESPSLGKV	VPLSLEKTKP
730	740	750	760	770	780	790	800
SSSSRQLDRK	ALGSARSPEG	ARGSEGRVEP	KAEPVSSTEA	SSLGQKDLEA	AGAERSPCPE	AAAPPPGPRT	RDNFTKAPSW
810	820	830	840	850	860	870	880
EASAPPPPRE	DAGTQAGAQA	CVSVAVSPMS	PQDGAGGSAF	SFQAAPRAPS	PPSRRDAGLQ	VSLGAAETRS	VATGPMTPQA
890	900	910	920	930	940	950	960
AAPPAFPEVR	VRPGSALAAA	VAPPEPAEPV	RDVSWDEKGM	TWEVYGAAME	VEVLGMAIQK	HLERQIEEHG	RQGAPAPPPA
970	980	990	1000	1010			
ARAGPGRSGS	VRTAPPDGAA	KRPPGLFRAL	LQSVRRPRCC	SRAGPTAE			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2330	1	682.5941	-86.77	3	57.6	11.6	0	424-442	K.MDPMCSGKPELLSPGQAER.V	

Detailed Protein Report

Protein 358: PREDICTED: sperm flagellar protein 2 isoform X4 [Homo sapiens]

Accession:	gi|578809999	**Score:**	23.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	202.4
Database Date:	2015-11-30	**pI:**	5.2
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.0
		No. of unique Peptides:	2

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	MKSDTFQEQY	LNRRRQNEIM	AKIQAAIIQI
170	180	190	200	210	220	230	240
PKPASNRTLK	ALEAQKMMKK	KKEAEDVADE	IKKFEALIKK	DLQAKESASK	TSLDTAGQTT	TDLLNTYSDD	EYIKKIQKRL
250	260	270	280	290	300	310	320
EEDAFAREQR	EKRRRKLLMD	QLIAHEAQEE	AYREEQLINR	LMRQSQQERR	IAVQLMHVRH	EKEVLWQNRI	FREKQHEERR
330	340	350	360	370	380	390	400
LKDFQDALDR	EAALAKQAKI	DFEEQFLKEK	RFHDQIAVER	AQARYEKHYS	VCAEILDQIV	DLSTKVADYR	MLTNNLIPYK
410	420	430	440	450	460	470	480
LMHDWKELFF	NAKPIYEQAS	VKTLPANPSR	EQLTELEKRD	LLDTNDYEEY	KNMVGEWALP	EEMVDNLPPS	NNCILGHILH
490	500	510	520	530	540	550	560
RLAEKSLPPR	AESTTPELPS	FAVKGCLLGK	TLSGKTTILR	SLQKDFPIQI	LSIDTLVQEA	IQAFHDNEKV	SEVLPIQKND
570	580	590	600	610	620	630	640
EEDALPVLQE	EIKESQDPQH	VFSAGPVSDE	VLPETEGETM	LSANADKTPK	AEEVKSSDSF	LKLTTRAQLG	AKSEQLLKKG
650	660	670	680	690	700	710	720
KSIPDVLLVD	IIVNAINEIP	VNQDCILDGF	PMTLNQAQLL	EEALTGCNRN	LTEVERKKAQ	KSTLAIDPAT	SKEIPLPSPA
730	740	750	760	770	780	790	800
FDFVILLDVS	DTSSMSRMND	IIAEELSYKT	AHEDISQRVA	AENQDKDGDQ	NLRDQIQHRI	IGFLDNWPLL	EQWFSEPENI
810	820	830	840	850	860	870	880
LIKINAEIDK	ESLCEKVKEI	LTTEIAKKKN	KVEKKLEEKE	AEKKAAASLA	ELPLPTPPPA	PPPEPEKEKE	IHQSHVASKT
890	900	910	920	930	940	950	960
PTAKGKPQSE	APHGKQESLQ	EGKGKKGETA	LKRKGSPKGK	SSGGKVPVKK	SPADSTDTSP	VAIVPQPPKP	GSEEWVYVNE
970	980	990	1000	1010	1020	1030	1040
PVPEEMPLFL	VPYWELIENS	YINTIKTVLR	HLREDQHTVL	AYLYEIRTSF	QEFLKRPDHK	QDFVAQWQAD	FNSLPDDLWD
1050	1060	1070	1080	1090	1100	1110	1120
DEETKAELHQ	RVNDLRDRLW	DICDARKEEA	EQERLDIINE	SWLQDTLGMT	MNHFFSLMQA	ELNRFQDTKR	LLQDYYWGME
1130	1140	1150	1160	1170	1180	1190	1200
SKIPVEDNKR	FTRIPLVQLD	SKDNSESQLR	IPLVPRISIS	LETVTPKPKT	KSVLKGKMDN	SLENVESNFE	ADEKLVMDTW
1210	1220	1230	1240	1250	1260	1270	1280
QQASLAVSHM	VAAEIHQRLM	EEEKENQPAD	PKEKSPQMGA	NKKVKKEPPK	KKQEDKKPKG	KSPPMAEATP	VIVTTEEIAE
1290	1300	1310	1320	1330	1340	1350	1360
IKRKNELRVK	IKEEHLAALQ	FEEIATQFRL	ELIKTKALAL	LEDLVTKVVD	VYKLMEKWLG	ERYLNEMAST	EKLTDVARYH
1370	1380	1390	1400	1410	1420	1430	1440
IETSTKIQNE	LYLSQEDFFI	NGNIKVFPDP	PPSIRPPPVE	KEEDGTLTIE	QLDSLRDQFL	DMAPKGIIGN	KAFTDILIDL
1450	1460	1470	1480	1490	1500	1510	1520
VTLNLGTNNF	PSNWMHLTQP	ELQELTSLLT	VNSEFVDWRK	FLLVTSMPWP	IPLEEELLET	LQKFKAVDKE	QLGTITFEQY
1530	1540	1550	1560	1570	1580	1590	1600
MQAGLWFTGD	EDIKIPENPL	EPLPFNRQEH	LIEFFFRLFA	DYEKDPPQLD	YTQMLLYFAC	HPDTVEGVYR	ALSVAVGTHV
1610	1620	1630	1640	1650	1660	1670	1680
FQQVKASIPS	AEKTSSTDAG	PAEEFPEPEE	NAAREERKLK	DDTEKREQKD	EEIPENANNE	KMSMETLLKV	FKGGSEAQDS
1690	1700	1710	1720	1730	1740	1750	1760
NRFASHLKIE	NIYAEGFIKT	FQDLGAKNLE	PIEVAVLLKH	PFIQDLISNY	SDYKFPVHII	YVVEMIVCAK	GWAPLPSGKQ
1770							
CARWRN							

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

Detailed Protein Report

	Cmpds.		[ppm]		[min]					
1496	1	1006.5889	17.49	3	47.4	12.9	2	1143- 1169	K.DNSESQLRIPLVPRISISLETVTPKPK.T	
2688	1	484.7720	59.46	2	62.0	10.3	0	1662- 1669	K.MSMETLLK.V	Oxidation: 1

Detailed Protein Report

Protein 359: **TBC1 domain family member 8B isoform b [Homo sapiens]**

Accession:	gi|38570103	**Score:**	23.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	72.6
Database Date:	2015-11-30	**pI:**	5.9
		Sequence Coverage [%]:	4.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MWLKPEEVLL	KNALKLWLME	RSNDYFVLQR	RRGYGEEGGG	GLTGLLVGTL	DSVLDSTAKV	APFRILHQTP	DSQVYLSIAC
90	100	110	120	130	140	150	160
GANREEITKH	WDWLEQNIMK	TLSVFDSNED	ITNFVQGKIR	GLIAEEGKHC	FAKEDDPEKF	REALLKFEKC	FGLPEKEKLV
170	180	190	200	210	220	230	240
TYYSCSYWKG	RVPCQGWLYL	STNFLSFYSF	LLGSEIKLII	SWDEVSKLEK	TSNVILTESI	HVCSQGENHY	FSMFLHINQT
250	260	270	280	290	300	310	320
YLLMEQLANY	AIRRLFDKET	FDNDPVLYNP	LQITKRGLEN	RAHSEQFNAF	FRLPKGESLK	EVHECFLWVP	FSHFNTHGKM
330	340	350	360	370	380	390	400
CISENYICFA	SQDGNQCSVI	IPLREVLAID	KTNDSSKSVI	ISIKGKTAFR	FHEVKDFEQL	VAKLRLRCGA	ASTQYHDIST
410	420	430	440	450	460	470	480
ELAISSESTE	PSDNFEVQSL	TSQRECSKTV	NTEALMTVFH	PQNLETLNSK	MLKEKMKEQS	WKILFAECGR	GVSMFRTKKT
490	500	510	520	530	540	550	560
RDLVVRGIPE	TLRGELWMLF	SGAVNDMATN	PDYYTEVVEQ	SLGTCNLATE	EIERDLRRSL	PEHPAFQSDT	GISALRRVLT
570	580	590	600	610	620	630	640
AYAYRNPKIG	YCQAMNILTS	VLLLYAKEEE	AFWLLVAVCE	RMLPDYFNRR	IIGSDDFMPL	VRIQGQCVIG	EK

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2720	1	941.9748	14.19	2	62.5	10.1	2	157-171	K.EKLVTYYSCSYWKGR.V	

Detailed Protein Report

Protein 360: fibronectin type-III domain-containing protein 3A isoform 2 [Homo sapiens]

Accession:	gi|118918397	**Score:**	23.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	125.7
Database Date:	2015-11-30	**pI:**	6.8
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	2.9
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MSGPAQVPMM	SPNGSVPPIY	VPPGYAPQVI	EDNGVRRVVV	VPQAPEFHPG	SHTVLHRSPH	PPLPGFIPVP	TMMPPPPRHM
90	100	110	120	130	140	150	160
YSPVTGAGDM	TTQYMPQYQS	SQVYGDVDAH	STHGRSNFRD	ERSSKTYERL	QKKLKDRQGT	QKDKMSSPPS	SPQKCPSPIN
170	180	190	200	210	220	230	240
EHNGLIKGQI	AGGINTGSAK	IKSGKGKGGT	QVDTEIEEKD	EETKAFEALL	SNIVKPVASD	IQARTVVLTW	SPPSSLINGE
250	260	270	280	290	300	310	320
TDESSVPELY	GYEVLISSTG	KDGKYKSVYV	GEETNITLND	LKPAMDYHAK	VQAEYNSIKG	TPSEAEIFTT	LSCEPDIPNP
330	340	350	360	370	380	390	400
PRIANRTKNS	LTLQWKAPSD	NGSKIQNFVL	EWDEGKGNGE	FCQCYMGSQK	QFKITKLSPA	MGCKFRLSAR	NDYGTSGFSE
410	420	430	440	450	460	470	480
EVLYYTSGCA	PSMPASPVLT	KAGITWLSLQ	WSKPSGTPSD	EGISYILEME	EETSGYGFKP	KYDGEDLAYT	VKNLRRSTKY
490	500	510	520	530	540	550	560
KFKVIAYNSE	GKSNPSEVVE	FTTCPDKPGI	PVKPSVKGKI	HSHSFKITWD	PPKDNGGATI	NKYVVEMAEG	SNGNKWEMIY
570	580	590	600	610	620	630	640
SGATREHLCD	RLNPGCFYRL	RVYCISDGGQ	SAVSESLLVQ	TPAVPPGPCL	PPRLQGRPKA	KEIQLRWGPP	LVDGGSPISC
650	660	670	680	690	700	710	720
YSVEMSPIEK	DEPREVYQGS	EVECTVSSLL	PGKTYSFRLR	AANKMGFGPF	SEKCDITTAP	GPPDQCKPPQ	VTCRSATCAQ
730	740	750	760	770	780	790	800
VNWEVPLSNG	TDVTEYRLEW	GGVEGSMQIC	YCGPGLSYEI	KGLSPATTYY	CRVQALSVVG	AGPFSEVVAC	VTPPSVPGIV
810	820	830	840	850	860	870	880
TCLQEISDDE	IENPHYSPST	CLAISWEKPC	DHGSEILAYS	IDFGDKQSLT	VGKVTSYIIN	NLQPDTTYRI	RIQALNSLGA
890	900	910	920	930	940	950	960
GPFSHMIKLK	TKPLPPDPPR	LECVAFSHQN	LKLKWGEGTP	KTLSTDSIQY	HLQMEDKNGR	FVSLYRGPCH	TYKVQRLNES
970	980	990	1000	1010	1020	1030	1040
TSYKFCIQAC	NEAGEGPLSQ	EYIFTTPKSV	PAALKAPKIE	KVNDHICEIT	WECLQPMKGD	PVIYSLQVML	GKDSEFKQIY
1050	1060	1070	1080	1090	1100	1110	1120
KGPDSSFRYS	SLQLNCEYRF	RVCAIRQCQD	SLGHQDLVGP	YSTTVLFISQ	RTEPPASTNR	DTVESTRTRR	ALSDEQCAAV
1130	1140	1150					
ILVLFAFFSI	LIAFIIQYFV	IK					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2160	1	734.3496	-60.68	2	55.4	13.1	2	374-386	K.ITKLSPAMGCKFR.L	Oxidation: 8
1739	1	626.2821	-30.30	4	50.1	10.2	1	999-1018	K.IEKVNDHICEITWECLQPMK.G	Carbamidomethyl: 15; Oxidation: 19

Detailed Protein Report

Protein 361: 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:	2

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

	Cmpds.		[ppm]		[min]					
2532	1	729.9581	43.06	2	59.9	12.6	2	584-596	K.LIAKAASIRDICK.Q	Carbamidomethyl: 12
882	1	647.8007	-127.22	2	39.8	10.6	1	1629-1640	R.IVSHANTGVLKR.M	

Detailed Protein Report

Protein 362: PREDICTED: inositol 1,4,5-trisphosphate receptor type 2 isoform X1 [Homo sapiens]

Accession:	gi|578822836	**Score:**	23.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	212.9
Database Date:	2015-11-30	**pI:**	6.3
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.3
		No. of unique Peptides:	1

Quantitation

WD:WU	**Median:** 0.82	**CV:** 0.00 %	**No. of Peptides:** 1

```
        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	Ratios
1156	1	867.9132	-54.78	2	43.1	10.9	2	1647-1661	R.IRCGAFMSKLINHTK.K	Oxidation: 7	WD:WU 0.82

Detailed Protein Report

Protein 363: **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 364: glycogen phosphorylase, liver form isoform 2 [Homo sapiens]

Accession:	gi|255653002	**Score:**	23.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	93.1
Database Date:	2015-11-30	**pI:**	7.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAKPLTDQEK	RRQISIRGIV	GVENVAELKK	SFNRHLHFTL	VKDRNVATTR	DYYFALAHTV	RDHLVGRWIR	TQQHYYDKCP
90	100	110	120	130	140	150	160
KLGLDIEELE	EIEEDAGLGN	GGLGRLAACF	LDSMATLGLA	AYGYGIRYEY	GIFNQKIRDG	WQVEEADDWL	RYGNPWEKSR
170	180	190	200	210	220	230	240
PEFMLPVHFY	GKVEHTNTGT	KWIDTQVVLA	LPYDTPVPGY	MNNTVNTMRL	WSARAPNDFN	LRDFNVGDYI	QAVLDRNLAE
250	260	270	280	290	300	310	320
NISRVLYPND	NFFEGKELRL	KQEYFVVAAT	LQDIIRRFKA	SKFGSTRGAG	TVFDAFPDQV	AIQLNDTHPA	LAIPELMRIF
330	340	350	360	370	380	390	400
VDIEKLPWSK	AWELTQKTFA	YTNHTVLPEA	LERWPVDLVE	KLLPRHLEII	YEINQKHLDR	IVALFPKDVD	RLRRMSLIEE
410	420	430	440	450	460	470	480
EGSKRINMAH	LCIVGSHAVN	GVAKIHSDIV	KTKVFKDFSE	LEPDKFQNKT	NGITPRRWLL	LCNPGLAELI	AEKIGEDYVK
490	500	510	520	530	540	550	560
DLSQLTKLHS	FLGDDVFLRE	LAKVKQENKL	KFSQFLETEY	KVKINPSSMF	DVQVKRIHEY	KRQLLNCLHV	ITMYNRIKKD
570	580	590	600	610	620	630	640
PKKLFVPRTV	IIGGKAAPGY	HMAKMIIKLI	TSVADVVNND	PMVGSKLKVI	FLENYRVSLA	EKVIPATDLS	EQISTAGTEA
650	660	670	680	690	700	710	720
SGTGNMKFML	NGALTIGTMD	GANVEMAEEA	GEENLFIFGM	RIDDVAALDK	KGYEAKEYYE	ALPELKLVID	QIDNGFFSPK
730	740	750	760	770	780	790	800
QPDLFKDIIN	MLFYHDRFKV	FADYEAYVKC	QDKVSQLYMN	PKAWNTMVLK	NIAASGKFSS	DRTIKEYAQN	IWNVEPSDLK
810	820						
ISLSNESNKV	NGN						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
772	1	647.8341	23.34	2	38.5	10.2	1	394-404	R.RMSLIEEEGSK.R	Oxidation: 2

Detailed Protein Report

Protein 365: **1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase eta-1 isoform c [Homo sapiens]**

Accession:	gi|195972873	**Score:**	23.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	114.4
Database Date:	2015-11-30	**pI:**	8.3
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	4.0
		No. of unique Peptides:	2

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
2076	1	649.2852	-47.07	3	54.3	10.8	2	18-33	R.CMSVMQSGTQMIKLKR.G	Carbamidomethyl: 1; Oxidation: 2, 5, 11
845	1	1419.3283	69.70	2	39.4	12.2	1	379-402	K.HAFVKNEFPVILSIENHCSIQQQR.K	

Detailed Protein Report

Protein 366: dynein heavy chain 11, axonemal [Homo sapiens]

Accession:	gi|459642365	**Score:**	23.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	520.0
Database Date:	2015-11-30	**pI:**	6.0
		Sequence Coverage [%]:	0.5
		No. of unique Peptides:	1

Quantitation

WD:WU	**Median:** 0.42	**CV:** 0.00 %	**No. of Peptides:** 1

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

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
36	1	779.3158	-100.01	2	29.7	10.1	1	2083-2095	R.GDKNRPEDQVLMR.A		WD:WU 0.42

Detailed Protein Report

Protein 367: condensin complex subunit 1 [Homo sapiens]

Accession:	gi|178056552	**Score:**	22.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	157.1
Database Date:	2015-11-30	**pI:**	6.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.9
		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
1660	1	927.4336	-29.14	3	49.5	11.3	2	286-310	K.CPQELSRDPSGTKGFAAFLTELAER.V	Carbamidomethyl: 1
2825	1	913.4475	-27.71	2	63.9	11.6	0	1086-1100	R.FPNLVDPWTPHLYAR.L	

Detailed Protein Report

Protein 368: thymidine phosphorylase isoform 1 proprotein [Homo sapiens]

Accession:	gi|4503445	**Score:**	22.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	49.9
Database Date:	2015-11-30	**pI:**	5.2
Modification(s):	Oxidation	**Sequence Coverage [%]:**	6.4
		No. of unique Peptides:	2

Quantitation

WD:WU	**Median:**	1.63	**CV:**	0.00 %	**No. of Peptides:**	1

Alias proteins:

Accession	Name	Description
gi|384229049	refseq_huma (refseq_human_20140103.fasta)	thymidine phosphorylase isoform 1 proprotein [Homo sapiens]
gi|166158925	refseq_huma (refseq_human_20140103.fasta)	thymidine phosphorylase isoform 1 proprotein [Homo sapiens]
gi|166158922	refseq_huma (refseq_human_20140103.fasta)	thymidine phosphorylase isoform 1 proprotein [Homo sapiens]

10	20	30	40	50	60	70	80
MAALMTPGTG	APPAPGDFSG	EGSQGLPDPS	PEPKQLPELI	RMKRDGGRLS	EADIRGFVAA	VVNGSAQGAQ	IGAMLMAIRL
90	100	110	120	130	140	150	160
RGMDLEETSV	LTQALAQSGQ	QLEWPEAWRQ	QLVDKHSTGG	VGDKVSLVLA	PALAACGCKV	PMISGRGLGH	TGGTLDKLES
170	180	190	200	210	220	230	240
IPGFNVIQSP	EQMQVLLDQA	GCCIVGQSEQ	LVPADGILYA	ARDVTATVDS	LPLITASILS	KKLVEGLSAL	VVDVKFGGAA
250	260	270	280	290	300	310	320
VFPNQEQARE	LAKTLVGVGA	SLGLRVAAAL	TAMDKPLGRC	VGHALEVEEA	LLCMDGAGPP	DLRDLVTTLG	GALLWLSGHA
330	340	350	360	370	380	390	400
GTQAQGAARV	AAALDDGSAL	GRFERMLAAQ	GVDPGLARAL	CSGSPAERRQ	LLPRAREQEE	LLAPADGTVE	LVRALPLALV
410	420	430	440	450	460	470	480
LHELGAGRSR	AGEPLRLGVG	AELLVDVGQR	LRRGTPWLRV	HRDGPALSGP	QSRALQEALV	LSDRAPFAAP	SPFAELVLPP
490							
QQ							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
41	1	906.3675	-118.89	2	29.5	10.9	1	140-157	K.VPMISGRGLGHTGGTLDK.L	Oxidation: 3	WD:WU 1.63
1488	1	671.3911	-17.76	2	47.0	12.0	0	223-235	K.LVEGLSALVVDVK.F		

Detailed Protein Report

Protein 369: PREDICTED: stabilin-1 isoform X3 [Homo sapiens]

Accession:	gi|530372115	**Score:**	22.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	273.1
Database Date:	2015-11-30	**pI:**	6.1
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	0.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAGPRGLLPL	CLLAFCLAGF	SFVRGQVLFK	GCDVKTTFVT	HVPCTSCAAI	KKQTCPSGWL	RELPDQITQD	CRYEVQLGGS
90	100	110	120	130	140	150	160
MVSMSGCRRK	CRKQVVQKAC	CPGYWGSRCH	ECPGGAETPC	NGHGTCLDGM	DRNGTCVCQE	NFRGSACQEC	QDPNRFGPDC
170	180	190	200	210	220	230	240
QSVCSCVHGV	CNHGPRGDGS	CLCFAGYTGP	HCDQELPVCQ	ELRCPQNTQC	SAEAPSCRCL	PGYTQQGSEC	RAPNPCWPSP
250	260	270	280	290	300	310	320
CSLLAQCSVS	PKGQAQCHCP	ENYHGDGMVC	LPKDPCTDNL	GGCPSNSTLC	VYQKPGQAFC	TCRPGLVSIN	SNASAGCFAF
330	340	350	360	370	380	390	400
CSPFSCDRSA	TCQVTADGKT	SCVCRESEVG	DGRACYGHLL	HEVQKATQTG	RVFLQLRVAV	AMMDQGCREI	LTTAGPFTVL
410	420	430	440	450	460	470	480
VPSVSSFSSR	TMNASLAQQL	CRQHIIAGQH	ILEDTRTQQT	RRWWTLAGQE	ITVTFNQFTK	YSYKYKDQPQ	QTFNIYKANN
490	500	510	520	530	540	550	560
IAANGVFHVV	TGLRWQAPSG	TPGDPKRTIG	QILASTEAFS	RFETILENCG	LPSILDGPGP	FTVFAPSNEA	VDSLRDGRLI
570	580	590	600	610	620	630	640
YLFTAGLSKL	QELVRYHIYN	HGQLTVEKLI	SKGRILTMAN	QVLAVNISEE	GRILLGPEGV	PLQRVDVMAA	NGVIHMLDGI
650	660	670	680	690	700	710	720
LLPPTILPIL	PKHCSEEQHK	IVAGSCVDCQ	ALNTSTCPPN	SVKLDIFPKE	CVYIHDPTGL	NVLKKGCASY	CNQTIMEQGC
730	740	750	760	770	780	790	800
CKGFFGPDCT	QCPGGFSNPC	YGKGNCSDGI	QGNGACLCFP	DYKGIACHIC	SNPNKHGEQC	QEDCGCVHGL	CDNRPGSGGV
810	820	830	840	850	860	870	880
CQQGTCAPGF	SGRFCNESMG	DCGPTGLAQH	CHLHARCVSQ	EGVARCRCLD	GFEGDGFSCT	PSNPCSHPDR	GGCSENAECV
890	900	910	920	930	940	950	960
PGSLGTHHCT	CHKGWSGDGR	VCVAIDECEL	DMRGGCHTDA	LCSYVGPGQS	RCTCKLGFAG	DGYQCSPIDP	CRAGNGGCHG
970	980	990	1000	1010	1020	1030	1040
LATCRAVGGG	QRVCTCPPGF	GGDGFSCYGD	IFRELEANAH	FSIFYQWLKS	AGITLPADRR	VTALVPSEAA	VRQLSPEDRA
1050	1060	1070	1080	1090	1100	1110	1120
FWLQPRTLPN	LVRAHFLQGA	LFEEELARLG	GQEVATLNPT	TRWEIRNISG	RVWVQNASVD	VADLLATNGV	LHILSQVLLP
1130	1140	1150	1160	1170	1180	1190	1200
PRGDVPGGQG	LLQQLDLVPA	FSLFRELLQH	HGLVPQIEAA	TAYTIFVPTN	RSLEAQGNSS	HLDADTVRHH	VVLGEALSME
1210	1220	1230	1240	1250	1260	1270	1280
TLRKGGHRNS	LLGPAHWIVF	YNHSGQPEVN	HVPLEGPMLE	APGRSLIGLS	GVLTVGSSRC	LHSHAEALRE	KCVNCTRRFR
1290	1300	1310	1320	1330	1340	1350	1360
CTQGFQLQDT	PRKSCVYRSG	FSFSRGCSYT	CAKKIQVPDC	CPGFFGTLCE	PCPGGLGGVC	SGHGQCQDRF	LGSGECHCHE
1370	1380	1390	1400	1410	1420	1430	1440
GFHGTACEVC	ELGRYGPNCT	GVCDCAHGLC	QEGLQGDGSC	VCNVGWQGLR	CDQKITSPQC	PRKCDPNANC	VQDSAGASTC
1450	1460	1470	1480	1490	1500	1510	1520
ACAAGYSGNG	IFCSEVDPCA	HGHGGCSPHA	NCTKVAPGQR	TCTCQDGYMG	DGELCQEINS	CLIHHGGCHI	HAECIPTGPQ
1530	1540	1550	1560	1570	1580	1590	1600
QVSCSCREGY	SGDGIRTCEL	LDPCSKNNGG	CSPYATCKST	GDGQRTCTCD	TAHTVGDGLT	CRARVGLELL	RDKHASFFSL
1610	1620	1630	1640	1650	1660	1670	1680
RLLEYKELKG	DGPFTIFVPH	ADLMSNLSQD	ELARIRAHRQ	LVFRYHVVGC	RRLRSEDLLE	QGYATALSGH	PLRFSEREGS
1690	1700	1710	1720	1730	1740	1750	1760
IYLNDFARVV	SSDHEAVNGI	LHFIDRVLLP	PEALHWEPDD	APIPRRNVTA	AAQGFGYKIF	SGLLKVAGLL	PLLREASHRP
1770	1780	1790	1800	1810	1820	1830	1840
FTMLWPTDAA	FRALPPDRQA	WLYHEDHRDK	LAAILRGHMI	RNVEALASDL	PNLGPLRTMH	GTPISFSCSR	TRAGELMVGE
1850	1860	1870	1880	1890	1900	1910	1920
DDARIVQRHL	PFEGGLAYGI	DQLLEPPGLG	ARCDHFETRP	LRLNTCSICG	LEPPCPEGSQ	EQGSPEACWR	FYPKFWTSPP
1930	1940	1950	1960	1970	1980	1990	2000
LHSLGLRSVW	VHPSLWGRPQ	GLGRGCHRNC	VTTTWKPSCC	PGHYGSECQA	CRCTVHGRCD	EGLGGSGSCF	CDEGWTGPRC
2010	2020	2030	2040	2050	2060	2070	2080
EVQLELQPVC	TPPCAPEAVC	RAGNSCECSL	GYEGDGRVCT	VADLCQDGHG	GCSEHANCSQ	VGTMVTCTCL	PDYEGDGWSC
2090	2100	2110	2120	2130	2140	2150	2160
RARNPCTDGH	RGGCSEHANC	LSTGLNTRRC	ECHAGYVGDG	LQCLEESEPP	VDRCLGQPPP	CHSDAMCTDL	HFQEKRAGVF
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2603	1	637.1527	-199.59	2	60.8	12.7	0	953-965	R.AGNGGCHGLATCR.A	Carbamidomethyl: 12

Detailed Protein Report

Protein 370: **DNA repair protein XRCC1 [Homo sapiens]**

Accession:	gi|190684675	**Score:**	22.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	69.5
Database Date:	2015-11-30	**pI:**	5.9
		Sequence Coverage [%]:	5.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPEIRLRHVV	SCSSQDSTHC	AENLLKADTY	RKWRAAKAGE	KTISVVLQLE	KEEQIHSVDI	GNDGSAFVEV	LVGSSAGGAG
90	100	110	120	130	140	150	160
EQDYEVLLVT	SSFMSPSESR	SGSNPNRVRM	FGPDKLVRAA	AEKRWDRVKI	VCSQPYSKDS	PFGLSFVRFH	SPPDKDEAEA
170	180	190	200	210	220	230	240
PSQKVTVTKL	GQFRVKEEDE	SANSLRPGAL	FFSRINKTSP	VTASDPAGPS	YAAATLQASS	AASSASPVSR	AIGSTSKPQE
250	260	270	280	290	300	310	320
SPKGKRKLDL	NQEEKKTPSK	PPAQLSPSVP	KRPKLPAPTR	TPATAPVPAR	AQGAVTGKPR	GEGTEPRRPR	AGPEELGKIL
330	340	350	360	370	380	390	400
QGVVVVLSGF	QNPFRSELRD	KALELGAKYR	PDWTRDSTHL	ICAFANTPKY	SQVLGLGGRI	VRKEWVLDCH	RMRRRLPSQR
410	420	430	440	450	460	470	480
YLMAGPGSSS	EEDEASHSGG	SGDEAPKLPQ	KQPQTKTKPT	QAAGPSSPQK	PPTPEETKAA	SPVLQEDIDI	EGVQSEGQDN
490	500	510	520	530	540	550	560
GAEDSGDTED	ELRRVAEQKE	HRLPPGQEEN	GEDPYAGSTD	ENTDSEEHQE	PPDLPVPELP	DFFQGKHFFL	YGEFPGDERR
570	580	590	600	610	620	630	640
KLIRYVTAFN	GELEDYMSDR	VQFVITAQEW	DPSFEEALMD	NPSLAFVRPR	WIYSCNEKQK	LLPHQLYGVV	PQA

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2390	1	767.3810	-70.91	2	58.1	11.1	0	257-271	K.TPSKPPAQLSPSVPK.R	

Detailed Protein Report

Protein 371: 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: 22.9
MW [kDa]: 190.8
pI: 9.1
Sequence Coverage [%]: 2.1
No. of unique Peptides: 2

Quantitation

WD:WU **Median:** 0.65 **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
2747	5	913.4548	46.11	2	62.8	12.3	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		WD:WU 0.65

Detailed Protein Report

Protein 372: TBC1 domain family member 2A isoform 2 [Homo sapiens]

Accession:	gi|222352143	**Score:**	22.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	104.0
Database Date:	2015-11-30	**pI:**	6.0
		Sequence Coverage [%]:	2.9
		No. of unique Peptides:	2

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	
2673	1	676.8390	-7.24	2	61.8	10.3	1	344-356	K.RASSAYLAAAEDK.D	

Detailed Protein Report

Protein 373: 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:	2

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
977	1	512.1767	-143.10	2	41.0	10.1	0	35-42	R.DVMLENFR.N	
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 374: ephrin type-A receptor 5 isoform e [Homo sapiens]

Accession:	gi|528881091	**Score:**	22.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	110.9
Database Date:	2015-11-30	**pI:**	6.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.9
		No. of unique Peptides:	2

Quantitation

WD:WU **Median:** 1.09 **CV:** 33.58 % **No. of Peptides:** 2

10	20	30	40	50	60	70	80
MRGSGPRGAG	RRRPPSGGGD	TPITPASLAG	CYSAPRRAPL	WTCLLLCAAL	RTLLASPSNE	VNLLDSRTVM	GDLGWIAFPK
90	100	110	120	130	140	150	160
NGWEEIGEVD	ENYAPIHTYQ	VCKVMEQNQN	NWLLTSWISN	EGASRIFIEL	KFTLRDCNSL	PGGLGTCKET	FNMYYFESDD
170	180	190	200	210	220	230	240
QNGRNIKENQ	YIKIDTIAAD	ESFTELDLGD	RVMKLNTEVR	DVGPLSKKGF	YLAFQDVGAC	IALVSVRVYY	KKCPSVVRHL
250	260	270	280	290	300	310	320
AVFPDTITGA	DSSQLLEVSG	SCVNHSVTDE	PPKMHCSAEG	EWLVPIGKCM	CKAGYEEKNG	TCQVCRPGFF	KASPHIQSCG
330	340	350	360	370	380	390	400
KCPPHSYTHE	EASTSCVCEK	DYFRRESDPP	TMACTRPPSA	PRNAISNVNE	TSVFLEWIPP	ADTGGRKDVS	YYIACKKCNS
410	420	430	440	450	460	470	480
HAGVCEECGG	HVRYLPRQSG	LKNTSVMMVD	LLAHTNYTFE	IEAVNGVSDL	SPGARQYVSV	NVTTNQAAPS	PVTNVKKGKI
490	500	510	520	530	540	550	560
AKNSISLSWQ	EPDRPNGIIL	EYEIKYFEKD	QETSYTIIKS	KETTITAEGL	KPASVYVFQI	RARTAAGYGV	FSRRFEFETT
570	580	590	600	610	620	630	640
PVSVAASSDQ	SQIPVIAVSV	TVGVILLAVV	IGVLLSGSCC	ECGCGRASSL	CAVAHPSLIW	RCGYSKAKQD	PEEEKMHFHN
650	660	670	680	690	700	710	720
GHIKLPGVRT	YIDPHTYEDP	NQAVHEFAKE	IEASCITIER	VIGAGEFGEV	CSGRLKLPGK	RELPVAIKTL	KVGYTEKQRR
730	740	750	760	770	780	790	800
DFLGEASIMG	QFDHPNIIHL	EGVVTKSKPV	MIVTEYMENG	SLDTFLKKND	GQFTVIQLVG	MLRGISAGMK	YLSDMGYVHR
810	820	830	840	850	860	870	880
DLAARNILIN	SNLVCKVSDF	GLSRVLEDDP	EAAYTTRGGK	IPIRWTAPEA	IAFRKFTSAS	DVWSYGIVMW	EVVSYGERPY
890	900	910	920	930	940	950	960
WEMTNQDVIK	AVEEGYRLPS	PMDCPAALYQ	LMLDCWQKER	NSRPKFDEIV	NMLDKLIRNP	SSLKTLVNAS	CRVSNLLAEH
970	980	990	1000	1010			
SPLGSGAYRS	VGEWLEAIKM	GRYTEIFMEN	GYSSMDAVAQ	VTLE			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
2043	1	661.2613	-54.57	2	53.9	10.7	0	136-148	R.DCNSLPGGLGTCK.E	Carbamidomethyl: 2	WD:WU	1.51
51	1	857.9018	65.31	2	29.6	12.1	0	398-413	K.CNSHAGVCEECGGHVR.Y	Carbamidomethyl: 11	WD:WU	0.79

Detailed Protein Report

Protein 375: PREDICTED: rho GTPase-activating protein SYDE2 isoform X5 [Homo sapiens]

Accession:	gi|530363440	**Score:**	22.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	105.4
Database Date:	2015-11-30	**pI:**	6.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MKGRELEELK	DNIEFRGHKP	LNSITVSKKR	NWLYQSTLRP	LNLEEENKKC	QDRSHLSISP	VSLPKHQLSQ	SFLKSSKEYC
90	100	110	120	130	140	150	160
TYVVCNATNS	SLSKNCALDF	NEENDADDEG	EIWYNPIPED	DDLGISSALS	FGEADSAVLK	LPAVNLSMLS	GSDLMKAERH
170	180	190	200	210	220	230	240
TEDSLCSSEH	AGDIQTTRSN	GMNPIHPAHS	TEFVQQYKQK	LGHKTQEGIM	VEDSPMLKSP	FAGSGILAAT	NSTELGIMEP
250	260	270	280	290	300	310	320
SSPNPSPVKK	GSSINWSLPD	KIKSPRTVRK	LSMKMKKLPE	FSRKLSVKGT	LNYINSPDNT	PSLSKYNCRE	VHHTDILPSG
330	340	350	360	370	380	390	400
NTTTAAKRNV	ISRYHLDTSV	SSQQSYQKKN	SMSSKYSCKG	GYLSDGDSPE	LTTKASKHGS	ENKFGKGKEI	ISNSCSKNEI
410	420	430	440	450	460	470	480
DIDAFRHYSF	SDQPKCSQYI	SGLMSVHFYG	AEDLKPPRID	SKDVFCAIQV	DSVNKARTAL	LTCRTTFLDM	DHTFNIEIEN
490	500	510	520	530	540	550	560
AQHLKLVVFS	WEPTPRKNRV	CCHGTVVLPT	LFRVTKTHQL	AVKLEPRGLI	YVKVTLMEQW	ENSLHGLDIN	QEPIIFGVDI
570	580	590	600	610	620	630	640
QKVVEKENIG	LMVPLLIQKC	IMEIEKRGCQ	VVGLYRLCGS	AAVKKELREA	FERDSKAVGL	CENQYPDINV	ITGVLKDYLR
650	660	670	680	690	700	710	720
ELPSPLITKQ	LYEAVLDAMA	KSPLKMSSNG	CENDPGDSKY	TVDLLDCLPE	IEKATLKMLL	DHLKLVASYH	EVNKMTCQNL
730	740	750	760	770	780	790	800
AVCFGPVLLS	QRQEPSTHNN	RVFTDSEELA	SALDFKKHIE	VLHYLLQLWP	VQRLTVKKST	DNLFPEQKSS	LNYLRQKKER
810	820	830	840	850	860	870	880
PHMLNLSGTD	SSGVLRPRQN	RLDSPLSNRY	AGDWSSCGEN	YFLNTKENLN	DVDYDDVPSE	DRKIGENYSK	MDGPEVMIEQ
890	900	910	920	930	940		
PIPMSKECTF	QTYLTMQTVE	STVDRKNNLK	DLQESIDTLI	GNLERELNKN	KLNMSF		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2968	1	964.7824	-62.98	3	65.9	11.8	2	50-74	K.CQDRSHLSISPVSLPKHQLSQSFLK.S	Carbamidomethyl: 1

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Detailed Protein Report

Protein 376: keratin, type II cuticular Hb2 [Homo sapiens]

Accession:	gi|27477127	**Score:**	22.7
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 377: PREDICTED: rho GTPase-activating protein 32 isoform X2 [Homo sapiens]

Accession:	gi|578822484	**Score:**	22.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	156.7
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
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 378: PREDICTED: coiled-coil domain-containing protein 74B isoform X9 [Homo sapiens]

Accession:	gi|578805131	**Score:**	22.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	36.8
Database Date:	2015-11-30	**pI:**	12.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	10.2
		No. of unique Peptides:	2

```
        10         20         30         40         50         60         70         80
MSGAGVAAGT RPPSSPTPGS RRRRQRPSVG VQSLRPQSPQ LRQSDPQKRN LDLEKSLQFL QQQHSEMLAK LHEEIEHLKR
        90        100        110        120        130        140        150        160
ENKGEPARGP RPALPPQAHS TLPLPQHRNT AINSSTRLGS GGTQDDLRYK LIMNQTSQKK DGPSGNHLSR ASAPLGARWV
       170        180        190        200        210        220        230        240
CINGVWVEPG GPSPARLKEG SSRTHRPGGK HGRLAGGSAD TVRSPADSLS TSSFQSVKSI SNSANSQGKA RPQPGSFNKQ
       250        260        270        280        290        300        310        320
DSKADVPQKA DLEEEPLLHN SKLDKVPGVQ GQASPPHLGS AKCSSASCGI PTSCRPKSCS TSSPSWKGAR GPRQSRRKLA
       330        340        350
FPGTKKPRIS PRSPPRASPR NACF
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2681	1	945.9624	-37.93	2	61.9	11.2	2	140-158	K.KDGPSGNHLSRASAPLGAR.W	
1874	1	860.9002	-14.63	2	51.8	11.4	2	298-313	K.SCSTSSPSWKGARGPR.Q	Carbamidomethyl: 2

Detailed Protein Report

Protein 379: **sphingosine 1-phosphate receptor 4 precursor [Homo sapiens]**

Accession:	gi|4503459	**Score:**	22.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	41.6
Database Date:	2015-11-30	**pI:**	11.8
		Sequence Coverage [%]:	7.3
		No. of unique Peptides:	2

```
        10         20         30         40         50         60         70         80
MNATGTPVAP ESCQQLAAGG HSRLIVLHYN HSGRLAGRGG PEDGGLGALR GLSVAASCLV VLENLLVLAA ITSHMRSRRW
        90        100        110        120        130        140        150        160
VYYCLVNITL SDLLTGAAYL ANVLLSGART FRLAPAQWFL REGLLFTALA ASTFSLLFTA GERFATMVRP VAESGATKTS
       170        180        190        200        210        220        230        240
RVYGFIGLCW LLAALLGMLP LLGWNCLCAF DRCSSLLPLY SKRYILFCLV IFAGVLATIM GLYGAIFRLV QASGQKAPRP
       250        260        270        280        290        300        310        320
AARRKARRLL KTVLMILLAF LVCWGPLFGL LLADVFGSNL WAQEYLRGMD WILALAVLNS AVNPIIYSFR SREVCRAVLS
       330        340        350        360        370        380        390
FLCCGCLRLG MRGPGDCLAR AVEAHSGAST TDSSLRPRDS FRGSRSLSFR MREPLSSISS VRSI
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1600	1	853.3743	-147.58	2	48.3	12.4	2	229-244	R.LVQASGQKAPRPAARR.K	
94	1	707.7845	-110.73	2	30.1	10.1	2	359-370	R.DSFRGSRSLSFR.M	

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Detailed Protein Report

Protein 380: transmembrane protein 194A isoform a [Homo sapiens]

Accession:	gi|195972881	**Score:**	22.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	50.6
Database Date:	2015-11-30	**pI:**	6.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	6.8
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MAGGMKVAVS PAVGPGPWGS GVGGGGTVRL LLILSGCLVY GTAETDVNVV MLQESQVCEK RASQQFCYTN VLIPKWHDIW
        90        100        110        120        130        140        150        160
TRIQIRVNSS RLVRVTQVEN EEKLKELEQF SIWNFFSSFL KEKLNDTYVN VGLYSTKTCL KVEIIEKDTK YSVIVIRRFD
       170        180        190        200        210        220        230        240
PKLFLVFLLG LMLFFCGDLL SRSQIFYYST GMTVGIVASL LIIIFILSKF MPKKSPIYVI LVGGWSFSLY LIQLVFKNLQ
       250        260        270        280        290        300        310        320
EIWRCYWQYL LSYVLTVGFM SFAVCYKYGP LENERSINLL TWTLQLMGLC FMYSGIQIPH IALAIIIIAL CTKNLEHPIQ
       330        340        350        360        370        380        390        400
WLYITCRKVC KGAEKPVPPR LLTEEEYRIQ GEVETRKALE ELREFCNSPD CSAWKTVSRI QSPKRFADFV EGSSHLTPNE
       410        420        430        440        450
VSVHEQEYGL GSIIAQDEIY EEASSEEEDS YSRCPAITQN NFLT
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1826	1	1045.0325	-2.71	2	51.2	10.5	1	124-141	K.LNDTYVNVGLYSTKTCLK.V	Carbamidomethyl: 16

Detailed Protein Report

Protein 381: PREDICTED: WD repeat-containing protein 11 isoform X1 [Homo sapiens]

Accession:	gi|530393962	**Score:**	22.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	108.0
Database Date:	2015-11-30	**pI:**	5.9
		Sequence Coverage [%]:	3.4
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530393964	refseq_human (refseq_human_20140103.fasta)	PREDICTED: WD repeat-containing protein 11 isoform X2 [Homo sapiens]

10	20	30	40	50	60	70	80
MLLLYPREIL	ILDLEVNQTV	GVIAIERTGV	PFLQVIPCFQ	RDGLFCLHEN	GCITLRVRRS	YNNIFTTSNE	EPDPDPVQEL
90	100	110	120	130	140	150	160
TYDLRSQCDA	IRVTKTVRPF	SMVCCPVNEN	AAALVVSDGR	VMIWELKSAV	CNRNSRNSSS	GVSPLYSPVS	FCGIPVGVLQ
170	180	190	200	210	220	230	240
NKLPDLSLDN	MIGQSAIAGE	EHPRGSILRE	VHLKFLLTGL	LSGLPAPQFA	IRMCPPLTTK	NIKMYQPLLA	VGTSNGSVLV
250	260	270	280	290	300	310	320
YHLTSGLLHK	ELSIHSCEVK	GIEWTSLTSF	LSFATSTPNN	MGLVRNELQL	VDLPTGRSIA	FRGERGNDES	AIEMIKVSHL
330	340	350	360	370	380	390	400
KQYLAVVFRD	KPLELWDVRT	CTLLREMSKN	FPTITALEWS	PSHNLKSLRK	KQLATREAMA	RQTVVSDTEL	SIVESSVISL
410	420	430	440	450	460	470	480
LQEAESKSEL	SQNISAREHF	VFTDIDGQVY	HLTVEGNSVK	DSARIPPDGS	MGSITCIAWK	GDTLVLGDMD	GNLNFWDLKG
490	500	510	520	530	540	550	560
RVSRGIPTHR	SWVRKIRFAP	GKGNQKLIAM	YNDGAEVWDT	KEVQMVSSLR	SGRNVTFRIL	DVDWCTSDKV	ILASDDGCIR
570	580	590	600	610	620	630	640
VLEMSMKSAC	FRMDEQELTE	PVWCPYLLVP	RASLALKAFL	LHQPWNGQYS	LDISHVDYPE	NEEIKNLLQE	QLNSLSNDIK
650	660	670	680	690	700	710	720
KLLLDPEFTL	LQRCLLVSRL	YGDESELHFW	TVAAHYLHSL	SQEKSASTTA	PKEAAPRDKL	SNPLDICYDV	LCENAYFQKF
730	740	750	760	770	780	790	800
QLERVNLQEV	KRSTYDHTRK	CTDQLLLLGQ	TDRAVQLLLE	TSADNQHYYC	DSLKACLVTT	VTSSGPSQST	IKLVATNMIA
810	820	830	840	850	860	870	880
NGKLAEGVQL	LCLIDKAADA	CRYLQTYGEW	NRAAWLAKVR	LNPEECADVL	RRWVDHLCSP	QVNQKSKALL	VLLSLGCFFS
890	900	910	920	930	940	950	960
VAETLHSMRY	FDRAALFVEA	CLKYGAFEVT	EDTEKLITAI	YADYARSLKN	LGFKQGAVLF	ASKAGAAGKD	LLNELESPKE
970							
EPIEE							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2753	1	973.5005	10.37	2	62.9	11.5	1	42-58	R.DGLFCLHENGCITLRVR.R	

Detailed Protein Report

Protein 382: protein Hook homolog 1 [Homo sapiens]

Accession:	gi|7705415	**Score:**	22.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	84.6
Database Date:	2015-11-30	**pI:**	5.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.7
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530362743	refseq_human (refseq_human_20140103.fasta)	PREDICTED: protein Hook homolog 1 isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MEETQPPPQP	KLPLCDSLMI	WLQTFNTASP	CQDVKQLTSG	VAMAQVLHQI	DAAWFNESWL	SRIKEDVGDN	WRIKASNVKK
90	100	110	120	130	140	150	160
VLQGIMSYYH	EFLGQQISEA	LIPDLNQITE	CSDPVELGRL	LQLILGCAIN	CEKKQEHIQN	IMTLEESVQH	VVMTAIQELM
170	180	190	200	210	220	230	240
SKEILSSPPN	DAVGELEQQL	KRALEELQEA	LAEKEELRQR	CEELDMQVTT	LQDEKNSLVS	ENEMMNEKLD	QLDGSFDDPN
250	260	270	280	290	300	310	320
TVVAKKYFHA	QLQLEQLQEE	NFRLEAAKDD	YRVHCEELEK	QLIEFQHRND	ELTSLAEETR	ALKDEIDVLR	ATSDKANKLE
330	340	350	360	370	380	390	400
STVEIYRQKL	QDLNDLRKQV	KTLQETNMMY	MHNTVSLEEE	LKKANAARTQ	LETYKRQVQD	LHVKLSSESK	RADTLAFEMK
410	420	430	440	450	460	470	480
RLEEKHEALL	KEKERLIEQR	DTLKETNEEL	RCSQVQQDHL	NQTDASATKS	YENLAAEIMP	VEYREVFIRL	QHENKMLRLQ
490	500	510	520	530	540	550	560
QEGSENERIE	ELQEQLEQKH	RKMNELETEQ	RLSKERIREL	QQQIEDLQKS	LQEQGSKSEG	ESSSKLKQKL	EAHMEKLTEV
570	580	590	600	610	620	630	640
HEELQKKQEL	IEDLQPDINQ	NVQKINELEA	ALQKKDEDMK	AMEERYKMYL	EKARNVIKTL	DPKLNPASAE	IMLLRKQLAE
650	660	670	680	690	700	710	720
KERRIEILES	ECKVAKFRDY	EEKLIVSAWY	NKSLAFQKLG	MESRLVSGGG	ACSDTGACTP	ARSFLAQQRH	ITNTRRNLSV
730							
KVPATTSD							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1597	1	685.8641	-18.30	2	48.3	10.6	2	546-556	K.LKQKLEAHMEK.L	Oxidation: 9

Detailed Protein Report

Protein 383: V-type proton ATPase subunit E 2 [Homo sapiens]

Accession:	gi|18087815	**Score:**	22.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	26.1
Database Date:	2015-11-30	**pI:**	9.4
Modification(s):	Oxidation	**Sequence Coverage [%]:**	10.6
		No. of unique Peptides:	1

Quantitation

WD:WU	**Median:**	0.61	**CV:**	0.00 %	**No. of Peptides:**	1

Alias proteins:

Accession	Name	Description
gi|530368262	refseq_human (refseq_human_20140103.fasta)	PREDICTED: V-type proton ATPase subunit E 2 isoform X2 [Homo sapiens]
gi|530368260	refseq_human (refseq_human_20140103.fasta)	PREDICTED: V-type proton ATPase subunit E 2 isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MALSDVDVKK	QIKHMMAFIE	QEANEKAEEI	DAKAEEEFNI	EKGRLVQTQR	LKIMEYYEKK	EKQIEQQKKI	LMSTMRNQAR
90	100	110	120	130	140	150	160
LKVLRARNDL	ISDLLSEAKL	RLSRIVEDPE	VYQGLLDKLV	LQGLLRLLEP	VMIVRCRPQD	LLLVEAAVQK	AIPEYMTISQ
170	180	190	200	210	220	230	
KHVEVQIDKE	AYLAVNAAGG	VEVYSGNQRI	KVSNTLESRL	DLSAKQKMPE	IRMALFGANT	NRKFFI	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
792	1	555.7879	29.14	2	38.3	11.6	0	213-222	R.MALFGANTNR.K	Oxidation: 1	WD:WU 0.61

Detailed Protein Report

Protein 384: PREDICTED: replication factor C subunit 2 isoform X1 [Homo sapiens]

Accession: gi|578814487
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 22.4
MW [kDa]: 24.5
pI: 7.8
Sequence Coverage [%]: 16.1
No. of unique Peptides: 1

Quantitation

WD:WU **Median:** 0.62 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MCPTSSLRMT	DGAQQALRRT	MEIYSKTTRF	ALACNASDKI	IEPIQSRCAV	LRYTKLTDAQ	ILTRLMNVIE	KERVPYTDDG
90	100	110	120	130	140	150	160
LEAIIFTAQG	DMRQALNNLQ	STFSGFGFIN	SENVFKVCDE	PHPLLVKEMI	QHCVNANIDE	AYKILAHLWH	LGYSPEDIIG
170	180	190	200	210	220		
NIFRVCKTFQ	MAEYLKLEFI	KEIGYTHMKI	AEGVNSLLQM	AGLLARLCQK	TMAPVAS		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1044	1	983.4577	-11.26	2	41.8	10.1	1	1-18	-.MCPTSSLRMTDGAQQALR.R		WD:WU 0.62

Detailed Protein Report

Protein 385: PREDICTED: EH domain-binding protein 1 isoform X4 [Homo sapiens]

Accession:	gi|530367409	**Score:**	22.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	108.6
Database Date:	2015-11-30	**pI:**	5.2
		Sequence Coverage [%]:	2.5
		No. of unique Peptides:	2

Quantitation

WD:WU **Median:** 0.94 **CV:** 77.37 % **No. of Peptides:** 2

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
804	1	660.3468	-45.46	2	38.5	12.3	2	111-122	R.RKALATSSINMK.Q		WD:WU 1.86
157	2	688.1811	-190.45	2	31.2	10.1	0	558-569	K.HNTNTATPFCNR.Q		WD:WU 0.47

Detailed Protein Report

Protein 386: PHD and RING finger domain-containing protein 1 isoform 4 [Homo sapiens]

Accession:	gi|557440810	**Score:**	22.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	178.1
Database Date:	2015-11-30	**pI:**	10.1
		Sequence Coverage [%]:	1.8
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 1.82 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MDDDSLDELV	ARSPGPDGHP	QVGPADPAES	SVGSSGDSGD	DSDSEHGDT	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	Ratios
1190	1	500.7991	12.23	2	43.5	10.8	2	347-356	R.KKTPSGPSAK.S		WD:WU 1.82

Detailed Protein Report

Protein 387: **PREDICTED: protein transport protein Sec16A isoform X5 [Homo sapiens]**

Accession:	gi|530426857	**Score:**	22.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	240.9
Database Date:	2015-11-30	**pI:**	5.7
		Sequence Coverage [%]:	1.0
		No. of unique Peptides:	1

Quantitation

WD:WU	**Median:** 0.81	**CV:** 0.00 %	**No. of Peptides:** 1

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

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2722	2	607.3395	-24.29	2	62.5	12.3	2	2001-2011	K.RPGQAAKKETK.E		WD:WU 0.81

Detailed Protein Report

Protein 388: PREDICTED: microspherule protein 1 isoform X2 [Homo sapiens]

Accession:	gi|530399608	**Score:**	22.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	42.5
Database Date:	2015-11-30	**pI:**	9.7
		Sequence Coverage [%]:	9.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MVKDYIEVSK	APSTPVPPSP	APAPGLTKRV	KKSKQPLQVT	KDLGRWKPAD	DLLLINAVLQ	TNDLTSVHLG	VKFSCRFTLR
90	100	110	120	130	140	150	160
EVQERWYALL	YDPVISKLAC	QAMRQLHPEA	IAAIQSKALF	SKAEEQLLSK	VGSTSQPTLE	TFQDLLHRHP	DAFYLARTAK
170	180	190	200	210	220	230	240
ALQAHWQLMK	QYYLLEDQTV	QPLPKGDQVL	NFSDAEDLID	DSKLKDMRDE	VLEHELMVAD	RRQKREIRQL	EQELHKWQVL
250	260	270	280	290	300	310	320
VDSITGMSSP	DFDNQTLAVL	RGRMVRYLMR	SREITLGRAT	KDNQIDVDLS	LEGPAWKISR	KQGVIKLKNN	GDFFIANEGR
330	340	350	360	370	380		
RPIYIDGRPV	LCGSKWRLSN	NSVVEIASLR	FVFLINQDLI	ALIRAEAAKI	TPQ		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1814	1	689.9700	-142.87	3	51.0	11.1	2	11-31	K.APSTPVPPSPAPAPGLTKRVK.K	

Detailed Protein Report

Protein 389: **PREDICTED: olfactomedin-like protein 2A isoform X2 [Homo sapiens]**

Accession: gi|530390640
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 22.3
MW [kDa]: 64.4
pI: 9.5
Sequence Coverage [%]: 6.0
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MAAAALPPRP	LLLLPLVLLL	SGRPTRADSK	VFGDLDQVRM	TSEGSDCRCK	CIMRPLSKDA	CSRVRSGRAR	VEDFYTVETV
90	100	110	120	130	140	150	160
SSGTDCRCSC	TAPPSSLNPC	ENEWKMEKLK	KQAPELLKLQ	SMVDLLEGTL	YSMDLMKVHA	YVHKVASQMN	TLEESIKANL
170	180	190	200	210	220	230	240
SRENEVVKDS	VRHLSEQLRH	YENHSAIMLG	IKKELSRLGL	QLLQKDAAAA	PATPATGTGS	KAQDTARGKG	KDISKYGSVQ
250	260	270	280	290	300	310	320
KSFADRGLPK	PPKEKLLQVE	KLRKESGKGS	FLQPTAKPRA	LAQQQAVIRG	FTYYKAGKQE	VTEAVAGREA	SCEGTLRAVD
330	340	350	360	370	380	390	400
PPVRHHSYGR	HEGAWMKDPA	ARDDRIYVTN	YYYGNSLVEF	RNLENFKQGR	WSNMYKLPYN	WIGTGHVVYQ	GAFYYNRAFT
410	420	430	440	450	460	470	480
KNIIKYDLRQ	RFVASWALLP	DVVYEDTTPW	KWRGHSDIDF	AVDESGLWVI	YPAVDDRDEA	QPEVIVLSRL	DPGDLSVHRE
490	500	510	520	530	540	550	560
TTWKTRLRRN	SYGNCFLVCG	ILYAVDTYNQ	QEGQVAYAFD	THTGTDARPQ	LPFLNEHAYT	TQIDYNPKER	VLYAWDNGHQ
570							
LTYTLHFVV							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2186	1	1159.9541	-101.22	2	55.8	11.4	2	296-317	K.AGKQEVTEAVAGREASCEGTLR.A	Carbamidomethyl: 17

Detailed Protein Report

Protein 390: 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	1	665.3626	67.46	2	63.7	12.3	0	972-983	R.DIAPSEEAINDR.T	

Detailed Protein Report

Protein 391: **protocadherin beta-15 precursor [Homo sapiens]**

Accession: gi|9256610
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 22.3
MW [kDa]: 86.3
pI: 4.6
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 392: testis-specific protein 10-interacting protein [Homo sapiens]

Accession:	gi|154759273	**Score:**	22.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	62.3
Database Date:	2015-11-30	**pI:**	10.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.3
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MGQDTDMLNT	YQQLVRTPSV	RPGQDVRLQA	PGTRTGLLKL	LSTVSQDKQG	CLGSGDGVPN	QDLQQRSQSS	RQTAKKDRKP
90	100	110	120	130	140	150	160
RGQSKKGQGS	EESEDHFPLL	PRKPSFPFQW	AWESIATDVR	AVLQPSSPTP	GHQALPMPSS	FSQRQSRRKS	TANLPEAHGC
170	180	190	200	210	220	230	240
CWKTEAQNLK	ARQQLGAWGG	VSIPTGKGEL	GSEPPSGLQL	PGRRPGSGSA	SDKQVQLQSL	GAEEAERGLS	SGVLPQRPRR
250	260	270	280	290	300	310	320
GSISEEEQFS	EATEEAEEGE	HRTPCRRRAG	CQRKGQISGE	EASDEGEVQG	QSQGSSPSFN	NLRRRQWRKT	RAKELQGPWD
330	340	350	360	370	380	390	400
LEKLHRQLQR	DLDCGPQKLP	WKTLRAAFQA	SKRNGKAYAS	GYDETFVSAN	LPNRTFHKRQ	EATRSLLQAW	ERQRQEERQQ
410	420	430	440	450	460	470	480
AELRRARTQH	VQRQVAHCLA	AYAPRGSRGP	GAAQRKLEEL	RRQERQRFAE	YQAELQGIQH	RVQARPFLFQ	QAMQANARLT
490	500	510	520	530	540	550	560
VTRRFSQVLS	ALGLDEEQLL	SEAGKVDREG	TPRKPRSHRS	MGVRMEHSPQ	RPPRTEPTGS	QPDRHYNPSL	DPECSP

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2105	1	707.2250	-208.16	2	54.7	11.8	1	312-323	R.AKELQGPWDLEK.L	
467	1	708.1877	-156.38	2	34.3	10.4	0	545-556	R.HYNPSLDPECSP.-	Carbamidomethyl: 10

Detailed Protein Report

Protein 393: **transient receptor potential cation channel subfamily M member 3 isoform d [Homo sapiens]**

Accession:	gi|154091318	**Score:**	22.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	176.1
Database Date:	2015-11-30	**pI:**	6.4
		Sequence Coverage [%]:	1.4
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 0.46 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MYVRVSFDTK PDLLLHLMTK EWQLELPKLL ISVHGGLQNF ELQPKLKQVF GKGLIKAAMT TGAWIFTGGV NTGVIRHVGD
        90        100        110        120        130        140        150        160
ALKDHASKSR GKICTIGIAP WGIVENQEDL IGRDVVRPYQ TMSNPMSKLT VLNSMHSHFI LADNGTTGKY GAEVKLRRQL
       170        180        190        200        210        220        230        240
EKHISLQKIN TRIGQGVPVV ALIVEGGPNV ISIVLEYLRD TPPVPVVVCD GSGRASDILA FGHKYSEEGG LINESLRDQL
       250        260        270        280        290        300        310        320
LVTIQKTFTY TRTQAQHLFI ILMECMKKKE LITVFRMGSE GHQDIDLAIL TALLKGANAS APDQLSLALA WNRVDIARSQ
       330        340        350        360        370        380        390        400
IFIYGQQWPV GSLEQAMLDA LVLDRVDFVK LLIENGVSMH RFLTISRLEE LYNTRHGPSN TLYHLVRDVK KGNLPPDYRI
       410        420        430        440        450        460        470        480
SLIDIGLVIE YLMGGAYRCN YTRKRFRTLY HNLFGPKRDD IPLRRGRKTT KKREEEVDID LDDPEINHFP FPFHELMVWA
       490        500        510        520        530        540        550        560
VLMKRQKMAL FFWQHGEEAM AKALVACKLC KAMAHEASEN DMVDDISQEL NHNSRDFGQL AVELLDQSYK QDEQLAMKLL
       570        580        590        600        610        620        630        640
TYELKNWSNA TCLQLAVAAK HRDFIAHTCS QMLLTDMWMG RLRMRKNSGL KVILGILLPP SILSLEFKNK DDMPYMSQAQ
       650        660        670        680        690        700        710        720
EIHLQEKEAE EPEKPTKEKE EEDMELTAML GRNNGESSRK KDEEEVQSKH RLIPLGRKIY EFYNAPIVKF WFYTLAYIGY
       730        740        750        760        770        780        790        800
LMLFNYIVLV KMERWPSTQE WIVISYIFTL GIEKMREILM SEPGKLLQKV KVWLQEYWNV TDLIAILLFS VGMILRLQDQ
       810        820        830        840        850        860        870        880
PFRSDGRVIY CVNIIYWYIR LLDIFGVNKY LGPYVMMIGK MMIDMMYFVI IMLVVLMSFG VARQAILFPN EEPSWKLAKN
       890        900        910        920        930        940        950        960
IFYMPYWMIY GEVFADQIDP PCGQNETRED GKIIQLPPCK TGAWIVPAIM ACYLLVANIL LVNLLIAVFN NTFFEVKSIS
       970        980        990       1000       1010       1020       1030       1040
NQVWKFQRYQ LIMTFHERPV LPPPLIIFSH MTMIFQHLCC RWRKHESDPD ERDYGLKLFI TDDELKKVHD FEEQCIEEYF
      1050       1060       1070       1080       1090       1100       1110       1120
REKDDRFNSS NDERIRVTSE RVENMSMRLE EVNEREHSMK ASLQTVDIRL AQLEDLIGRM ATALERLTGL ERAESNKIRS
      1130       1140       1150       1160       1170       1180       1190       1200
RTSSDCTDAA YIVRQSSFNS QEGNTFKLQE SIDPAGEETM SPTSPTLMPR MRSHSFYSVN MKDKGGIEKL ESIFKERSLS
      1210       1220       1230       1240       1250       1260       1270       1280
LHRATSSHSV AKEPKAPAAP ANTLAIVPDS RRPSSCIDIY VSAMDELHCD IDPLDNSVNI LGLGEPSFST PVPSTAPSSS
      1290       1300       1310       1320       1330       1340       1350       1360
AYATLAPTDR PPSRSIDFED ITSMDTRSFS SDYTHLPECQ NPWDSEPPMY HTIERSKSSR YLATTPFLLE EAPIVKSHSF
      1370       1380       1390       1400       1410       1420       1430       1440
MFSPSRSYYA NFGVPVKTAE YTSITDCIDT RCVNAPQAIA DRAAFPGGLG DKVEDLTCCH PEREAELSHP SSDSEENEAK
      1450       1460       1470       1480       1490       1500       1510       1520
GRRATIAISS QEGDNSERTL SNNITVPKIE RANSYSAEEP SAPYAHTRKS FSISDKLDRQ RNTASLRNPF QRSKSSKPEG
      1530       1540       1550
RGDSLSMRRL SRTSAFQSFE SKHN
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
317	1	442.6411	-248.40	2	33.0	10.9	1	438-444	K.RDDIPLR.R		WD:WU	0.46

Detailed Protein Report

Protein 394: dynein heavy chain 10, axonemal [Homo sapiens]

Accession:	gi|198442844	**Score:**	22.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	514.5
Database Date:	2015-11-30	**pI:**	5.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	0.7
		No. of unique Peptides:	1

Detailed Protein Report

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

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2662	1	835.4217	30.04	2	61.6	11.7	1	2516-2528	K.RLLVFMDDMNMPR.V	Oxidation: 6, 9

Detailed Protein Report

Protein 395: PREDICTED: protein LAP2 isoform X4 [Homo sapiens]

Accession:	gi|578810464	**Score:**	22.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	139.9
Database Date:	2015-11-30	**pI:**	5.1
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	2.5
		No. of unique Peptides:	2

Quantitation

WD:WU **Median:** 0.92 **CV:** 0.00 % **No. of 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	Ratios
486	1	668.2076	-211.28	2	34.5	10.8	0	1177-1189	R.VGSEHSLLDPPGK.S		WD:WU 0.92
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 396: PREDICTED: ATP-binding cassette sub-family A member 1 isoform X4 [Homo sapiens]

Accession:	gi|530390674	**Score:**	22.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	247.0
Database Date:	2015-11-30	**pI:**	6.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.0
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MPSAGTLPWV	QGIICNANNP	CFRYPTPGEA	PGVVGNFNKS	IVARLFSDAR	RLLLYSQKDT	SMKDMRKVLR	TLQQIKKSSS
90	100	110	120	130	140	150	160
NLKLQDFLVD	NETFSGFLYH	NLSLPKSTVD	KMLRADVILH	KVFLQGYQLH	LTSLCNGSKS	EEMIQLGDQE	VSELCGLPRE
170	180	190	200	210	220	230	240
KLAAAERVLR	SNMDILKPIL	RTLNSTSPFP	SKELAEATKT	LLHSLGTLAQ	ELFSMRSWSD	MRQEVMFLTN	VNSSSSSTQI
250	260	270	280	290	300	310	320
YQAVSRIVCG	HPEGGGLKIK	SLNWYEDNNY	KALFGGNGTE	EDAETFYDNS	TTPYCNDLMK	NLESSPLSRI	IWKALKPLLV
330	340	350	360	370	380	390	400
GKILYTPDTP	ATRQVMAEVN	KTFQELAVFH	DLEGMWEELS	PKIWTFMENS	QEMDLVRMLL	DSRDNDHFWE	QQLDGLDWTA
410	420	430	440	450	460	470	480
QDIVAFLAKH	PEDVQSSNGS	VYTWREAFNE	TNQAIRTISR	FMECVNLNKL	EPIATEVWLI	NKSMELLDER	KFWAGIVFTG
490	500	510	520	530	540	550	560
ITPGSIELPH	HVKYKIRMDI	DNVERTNKIK	DGYWDPGPRA	DPFEDMRYVW	GGFAYLQDVV	EQAIIRVLTG	TEKKTGVYMQ
570	580	590	600	610	620	630	640
QMPYPCYVDD	IFLRVMSRSM	PLFMTLAWIY	SVAVIIKGIV	YEKEARLKET	MRIMGLDNSI	LWFSWFISSL	IPLLVSAGLL
650	660	670	680	690	700	710	720
VVILKLGNLL	PYSDPSVVFV	FLSVFAVVTI	LQCFLISTLF	SRANLAAACG	GIIYFTLYLP	YVLCVAWQDY	VGFTLKIFAS
730	740	750	760	770	780	790	800
LLSPVAFGFG	CEYFALFEEQ	GIGVQWDNLF	ESPVEEDGFN	LTTSVSMMLF	DTFLYGVMTW	YIEAVFPGQY	GIPRPWYFPC
810	820	830	840	850	860	870	880
TKSYWFGEES	DEKSHPGSNQ	KRISEICMEE	EPTHLKLGVS	IQNLVKVYRD	GMKVAVDGLA	LNFYEGQITS	FLGHNGAGKT
890	900	910	920	930	940	950	960
TTMSILTGLF	PPTSGTAYIL	GKDIRSEMST	IRQNLGVCPQ	HNVLFDMLTV	EEHIWFYARL	KGLSEKHVKA	EMEQMALDVG
970	980	990	1000	1010	1020	1030	1040
LPSSKLKSKT	SQLSGGMQRK	LSVALAFVGG	SKVVILDEPT	AGVDPYSRRG	IWELLLKYRQ	GRTIILSTHH	MDEADVLGDR
1050	1060	1070	1080	1090	1100	1110	1120
IAIISHGKLC	CVGSSLFLKN	QLGTGYYLTL	VKKDVESSLS	SCRNSSSTVS	YLKKVVPELP	PAGQSGGRGG	EVQRLVALTQ
1130	1140	1150	1160	1170	1180	1190	1200
DVSAISNLIR	KHVSEARLVE	DIGHELTYVL	PYEAAKEGAF	VELFHEIDDR	LSDLGISSYG	ISETTLEEIF	LKVAEESGVD
1210	1220	1230	1240	1250	1260	1270	1280
AETSDGTLPA	RRNRRAFGDK	QSCLRPFTED	DAADPNDSDI	DPESRETDLL	SGMDGKGSYQ	VKGWKLTQQQ	FVALLWKRLL
1290	1300	1310	1320	1330	1340	1350	1360
IARRSRKGFF	AQIVLPAVFV	CIALVFSLIV	PPFGKYPSLE	LQPWMYNEQY	TFVSNDAPED	TGTLELLNAL	TKDPGFGTRC
1370	1380	1390	1400	1410	1420	1430	1440
MEGNPIPDTP	CQAGEEEWTT	APVPQTIMDL	FQNGNWTMQN	PSPACQCSSD	KIKKMLPVCP	PGAGGLPPPQ	RKQNTADILQ
1450	1460	1470	1480	1490	1500	1510	1520
DLTGRNISDY	LVKTYVQIIA	KSLKNKIWVN	EFRYGGFSLG	VSNTQALPPS	QEVNDAIKQM	KKHLKLAKDS	SADRFLNSLG
1530	1540	1550	1560	1570	1580	1590	1600
RFMTGLDTKN	NVKVWFNNKG	WHAISSFLNV	INNAILRANL	QKGENPSHYG	ITAFNHPLNL	TKQQLSEVAL	MTTSVDVLVS
1610	1620	1630	1640	1650	1660	1670	1680
ICVIFAMSFV	PASFVVFLIQ	ERVSKAKHLQ	FISGVKPVIY	WLSNFVWDMC	NYVVPATLVI	IIFICFQQKS	YVSSTNLPVL
1690	1700	1710	1720	1730	1740	1750	1760
ALLLLLYGWS	ITPLMYPASF	VFKIPSTAYV	VLTSVNLFIG	INGSVATFVL	ELFTDNKLNN	INDILKSVFL	IFPHFCLGRG
1770	1780	1790	1800	1810	1820	1830	1840
LIDMVKNQAM	ADALERFGEN	RFVSPLSWDL	VGRNLFAMAV	EGVVFFLITV	LIQYRFFIRP	RPVNAKLSPL	NDEDEDVRRE
1850	1860	1870	1880	1890	1900	1910	1920
RQRILDGGGQ	NDILEIKELT	KIYRRKRKPA	VDRICVGIPP	GECFGLLGVN	GAGKSSTFKM	LTGDTTVTRG	DAFLNKNSIL
1930	1940	1950	1960	1970	1980	1990	2000
SNIHEVHQNM	GYCPQFDAIT	ELLTGREHVE	FFALLRGVPE	KEVGKVGEWA	IRKLGLVKYG	EKYAGNYSGG	NKRKLSTAMA
2010	2020	2030	2040	2050	2060	2070	2080
LIGGPPVVFL	DEPTTGMDPK	ARRFLWNCAL	SVVKEGRSVV	LTSHSMEECE	ALCTRMAIMV	NGRFRCLGSV	QHLKNRFGDG
2090	2100	2110	2120	2130	2140	2150	2160
YTIVVRIAGS	NPDLKPVQDF	FGLAFPGSVL	KEKHRNMLQY	QLPSSLSSLA	RIFSILSQSK	KRLHIEDYSV	SQTTLDQVFV
2170	2180	2190	2200	2210			

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1993	1	1051.4220	-89.87	2	53.6	11.9	1	947-965	K.HVKAEMEQMALDVGLPSSK.L	Oxidation: 6, 9
2097	1	900.3873	-102.80	3	54.6	10.3	1	2174-2197	K.DLSLHKNQTVVDVAVLTSFLQDEK.V	

Detailed Protein Report

Protein 397: 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 398: PREDICTED: collagen alpha-1(XIV) chain isoform X1 [Homo sapiens]

Accession:	gi|530389313	**Score:**	22.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	191.8
Database Date:	2015-11-30	**pI:**	5.1
		Sequence Coverage [%]:	1.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
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	m/z meas.	Δ m/z	z	Rt	Score	P	Range	Sequence	Modification

	Cmpds.		[ppm]		[min]					
64	1	809.3817	-76.89	2	30.0	10.1	1	740-754	R.NLVVGDETTSSLRVK.W	

Detailed Protein Report

Protein 399: 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 400: **PREDICTED: maestro heat-like repeat-containing protein family member 2A isoform X1 [Homo sapiens]**

Accession:	gi|578804228	**Score:**	22.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	189.4
Database Date:	2015-11-30	**pI:**	6.2
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.7
		No. of unique Peptides:	2

```
        10         20         30         40         50         60         70         80
MTEAITEAAV ASSEEVSEER DDLGPLELHD SGTFQQVVNL LDIIDSESAK TDTTGAGLDM RKTLASVIIM EKATTEPSVV
        90        100        110        120        130        140        150        160
INTLIRCLQV PEISTQRKVN IYNILQDIIQ QEGELEEQCV QRLVAIASKE MREIPEMEGY MKAEVASDTL VALSRNHFSL
       170        180        190        200        210        220        230        240
VMYELQHHLK PLNLTDEFVI ITLAKLANGN VFEFMPYMGI TLATIFTMLR LANEAKIRQA ICSAMETFCE TVQFYLKHLE
       250        260        270        280        290        300        310        320
ESVYPVMTEE EFALKVFPMY RYFVTVWLRH YNPEVKLGVI KSLKPMLGLL LPNDDLREQV YDYIPLLLAE YQGSLEVLFV
       330        340        350        360        370        380        390        400
TQVLRQILEL SVTTNTPVPQ MQLHTIFTEL HVQVCNKAPA QHQYSSQNLM EMVHCFVALA RSYPKELMKF FFSQMETNKE
       410        420        430        440        450        460        470        480
AVRVGTLNLI RAIVSADEPR MSIRAIYLAI RVVKNTISDT RSKVRMAILH IIGQLALCGY QERIKGWGLK YLSVQLTLST
       490        500        510        520        530        540        550        560
YKLTNRREKF YQRDLEERMV HKVTMDTVKI ITSSVSGMTT EFWVRLLCYI METDYVEALT PICISLTNLA EHQLHGQDVD
       570        580        590        600        610        620        630        640
VSVAGKSRQV DLPAPQKLLA RLLVLMSSPY KGEGRGIAML NLLRTLSQSI APSMADMWEL EIALLVRYLE EHTEFTWDQK
       650        660        670        680        690        700        710        720
AWEDKLIQFL RNSLKKTRGS SWSLRLSKEL NNQIASFDSP SLEKGFLYRA LGFTLATGLE ASKVEVLLLE LLYKTDYSND
       730        740        750        760        770        780        790        800
FDSEGVIMCF GLCARGQVKT VLNVLHDFEE RIQESEQSWQ ISAWRKDHPW RRETVKSALM VMYSCVASYC HPQLLLNLVD
       810        820        830        840        850        860        870        880
SPITAKIIHH YVSSCQDICL KMAFMKSVVQ VTKAINNIKD LEDFHFAQKT TLTSIIVAVI KAEPTDNLVS PVRALAMEAL
       890        900        910        920        930        940        950        960
SHLSKLKPFY STEENSELMD ISIHSVISLQ LPGEDNESIK TLYANALSSL EQLMESLLQR QLDPKGLQEM VQLLEKWILS
       970        980        990       1000       1010       1020       1030       1040
EKEWEREKAV SLHLYLMWIY VHSTAVCIHL KLGQFGTMVG LIAPCTCDAH QRTRMASMNV LSSLLDLHAS QTCSLWGPSK
      1050       1060       1070       1080       1090       1100       1110       1120
QKELEKCKGD LQSTDVEKIF CASSRIAKVV CMEFSCDEVV SLIQKLCENT GAMNLQHDKA SVTWIAFFLQ MRAKELEDKV
      1130       1140       1150       1160       1170       1180       1190       1200
AEILSAILVH LPVVDHPEVR RLLIDGILLL AHHHQETILT SLLRQPLPME SHLAEVWLAV SENVPFARTM LHSLMGRLQS
      1210       1220       1230       1240       1250       1260       1270       1280
RLSPRISATS KADIWRLAAV DPLMTLCTIH LLIQKLDEND KLPDFLPDLI YTLLLQLGSS HRPEAAPPVL KMWKLVHTTP
      1290       1300       1310       1320       1330       1340       1350       1360
LPEEMNLQRV TIKSMQLLFK RVKSQHLAHT LDEQAVWDLL QDGGTFLEGV SLLARLCMQH VEGHRQRLAE LVLRGMDSEV
      1370       1380       1390       1400       1410       1420       1430       1440
LSCRISSTAV CFMSGPVLYQ EKLLKPAALL LEKGADQEED EALRVLSLRA LGNMALGAPK KVKQYRKVLL EKCLGPLREP
      1450       1460       1470       1480       1490       1500       1510       1520
VSNSVTAEGM EALTKILAEL REGDVGSSFD AMSEQCRIFF DNESELLRLK AFILFGKLAR VVGMSKKHFF KGEVKKAWIP
      1530       1540       1550       1560       1570       1580       1590       1600
LMLHSQDPCS NAAQACMATM FQCVHFWGWK SLEHPSGPSD TATDDKMTVF QTTMCSILTR KKPAVLYRFL LETMAYVKNN
      1610       1620       1630       1640       1650       1660       1670       1680
LSRIRIAACN LAGIIMKQMS THYLKKLDFP ALRNSLQELQ LDPDPGVRRA ALETLTVLDS CSQHGFLASP QGMS
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2646	1	616.8461	-35.09	2	61.4	11.5	1	62-72	R.KTLASVIIMEK.A	
288	1	636.2301	-155.37	3	32.3	10.6	1	1348-1364	R.LAELVLRGMDSEVLSCR.I	Oxidation: 9

Detailed Protein Report

Protein 401: activator of apoptosis harakiri [Homo sapiens]

Accession:	gi|4504493	**Score:**	22.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	9.9
Database Date:	2015-11-30	**pI:**	12.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	34.1
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MCPCPLHRGR GPPAVCACSA GRLGLRSSAA QLTAARLKAL GDELHQRTMW RRRARSRRAP APGALPTYWP WLCAAAQVAA
        90        100
LAAWLLGRRN L
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1505	1	599.9721	-16.93	3	47.2	10.9	2	9-26	R.GRGPPAVCACSAGRLGLR.S	Carbamidomethyl: 8

Detailed Protein Report

Protein 402: olfactory receptor 2T27 [Homo sapiens]

Accession:	gi|49227791	**Score:**	22.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	35.5
Database Date:	2015-11-30	**pI:**	9.4
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	10.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEQSNYSVYA	DFILLGLFSN	ARFPWLLFAL	ILLVFLTSIA	SNVVKIILIH	IDSRLHTPMY	FLLSQLSLRD	ILYISTIVPK
90	100	110	120	130	140	150	160
MLVDQVMSQR	AISFAGCTAQ	HFLYLTLAGA	EFFLLGLMSY	DRYVAICNPL	HYPVLMSRKI	CWLIVAAAWL	GGSIDGFLLT
170	180	190	200	210	220	230	240
PVTMQFPFCA	SREINHFFCE	VPALLKLSCT	DTSAYETAMY	VCCIMMLLIP	FSVISGSYTR	ILITVYRMSE	AEGRGKAVAT
250	260	270	280	290	300	310	320
CSSHMVVVSL	FYGAAMYTYV	LPHSYHTPEQ	DKAVSAFYTI	LTPMLNPLIY	SLRNKDVTGA	LQKVVGRCVS	SGKVTTF

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
128	1	1319.6098	4.84	3	30.5	22.1	0	187-220	K.LSCTDTSAYETAMYVCCIMMLLIPFSVISGSYTR.I	Carbamidomethyl: 3, 16, 17; Oxidation: 13

Detailed Protein Report

Protein 403: desmin [Homo sapiens]

Accession:	gi|55749932	**Score:**	22.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	53.5
Database Date:	2015-11-30	**pI:**	5.1
		Sequence Coverage [%]:	6.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSQAYSSSQR	VSSYRRTFGG	APGFPLGSPL	SSPVFPRAGF	GSKGSSSSVT	SRVYQVSRTS	GGAGGLGSLR	ASRLGTTRTP
90	100	110	120	130	140	150	160
SSYGAGELLD	FSLADAVNQE	FLTTRTNEKV	ELQELNDRFA	NYIEKVRFLE	QQNAALAAEV	NRLKGREPTR	VAELYEEELR
170	180	190	200	210	220	230	240
ELRRQVEVLT	NQRARVDVER	DNLLDDLQRL	KAKLQEEIQL	KEEAENNLAA	FRADVDAATL	ARIDLERRIE	SLNEEIAFLK
250	260	270	280	290	300	310	320
KVHEEEIREL	QAQLQEQQVQ	VEMDMSKPDL	TAALRDIRAQ	YETIAAKNIS	EAEEWYKSKV	SDLTQAANKN	NDALRQAKQE
330	340	350	360	370	380	390	400
MMEYRHQIQS	YTCEIDALKG	TNDSLMRQMR	ELEDRFASEA	SGYQDNIARL	EEEIRHLKDE	MARHLREYQD	LLNVKMALDV
410	420	430	440	450	460	470	480
EIATYRKLLE	GEESRINLPI	QTYSALNFRE	TSPEQRGSEV	HTKKTVMIKT	IETRDGEVVS	EATQQQHEVL	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
80	1	707.7702	-112.32	2	29.9	10.9	1	38-52	R.AGFGSKGSSSSVTSR.V	

Detailed Protein Report

Protein 404: **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	

Protein 405: thrombospondin type-1 domain-containing protein 7B [Homo sapiens]

Accession: gi|122937257
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 22.0
MW [kDa]: 175.5
pI: 9.1
Sequence Coverage [%]: 1.6
No. of unique Peptides: 1

Quantitation

WD:WU **Median:** 1.31 **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
417	1	475.6019	-263.42	2	33.8	10.3	1	1052-1060	R.CGGGTQSRK.I	Carbamidomethyl: 1	WD:WU 1.31

Detailed Protein Report

Protein 406: PREDICTED: dystonin isoform X15 [Homo sapiens]

Accession:	gi|530382446	**Score:**	22.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	825.5
Database Date:	2015-11-30	**pI:**	5.0
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	0.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MHSSSYSYRS	SDSVFSNTTS	TRTSLDSNEN	LLLVHCGPTL	INSCISFGSE	SFDGHRLEML	QQIANRVQRD	SVICEDKLIL
90	100	110	120	130	140	150	160
AGNALQSDSK	RLESGVQFQN	EAEIAGYILE	CENLLRQHVI	DVQILIDGKY	YQADQLVQRV	AKLRDEIMAL	RNECSSVYSK
170	180	190	200	210	220	230	240
GRILTTEQTK	LMISGITQSL	NSGFAQTLHP	SLTSGLTQSL	TPSLTSSSMT	SGLSSGMTSR	LTPSVTPAYT	PGFPSGLVPN
250	260	270	280	290	300	310	320
FSSGVEPNSL	QTLKLMQIRK	PLLKSSLLDQ	NLTEEEINMK	FVQDLLNWVD	EMQVQLDRTE	WGSDLPSVES	HLENHKNVHR
330	340	350	360	370	380	390	400
AIEEFESSLK	EAKISEIQMT	APLKLTYAEK	LHRLESQYAK	LLNTSRNQER	HLDTLHNFVS	RATNELIWLN	EKEEEEVAYD
410	420	430	440	450	460	470	480
WSERNTNIAR	KKDYHAELMR	ELDQKEENIK	SVQEIAEQLL	LENHPARLTI	EAYRAAMQTQ	WSWILQLCQC	VEQHIKENTA
490	500	510	520	530	540	550	560
YFEFFNDAKE	ATDYLRNLKD	AIQRKYSCDR	SSSIHKLEDL	VQESMEEKEE	LLQYKSTIAN	LMGKAKTIIQ	LKPRNSDCPL
570	580	590	600	610	620	630	640
KTSIPIKAIC	DYRQIEITIY	KDDECVLANN	SHRAKWKVIS	PTGNEAMVPS	VCFTVPPPNK	EAVDLANRIE	QQYQNVLTLW
650	660	670	680	690	700	710	720
HESHINMKSV	VSWHYLINEI	DRIRASNVAS	IKTMLPGEHQ	QVLSNLQSRF	EDFLEDSQES	QVFSGSDITQ	LEKEVNVCKQ
730	740	750	760	770	780	790	800
YYQELLKSAE	REEQEESVYN	LYISEVRNIR	LRLENCEDRL	IRQIRTPLER	DDLHESVFRI	TEQEKLKKEL	ERLKDDLGTI
810	820	830	840	850	860	870	880
TNKCEEFFSQ	AAASSSVPTL	RSELNVVLQN	MNQVYSMSST	YIDKLKTVNL	VLKNTQAAEA	LVKLYETKLC	EEEAVIADKN
890	900	910	920	930	940	950	960
NIENLISTLK	QWRSEVDEKR	QVFHALEDEL	QKAKAISDEM	FKTYKERDLD	FDWHKEKADQ	LVERWQNVHV	QIDNRLRDLE
970	980	990	1000	1010	1020	1030	1040
GIGKSLKYYR	DTYHPLDDWI	QQVETTQRKI	QENQPENSKT	LATQLNQQKM	LVSEIEMKQS	KMDECQKYAE	QYSATVKDYE
1050	1060	1070	1080	1090	1100	1110	1120
LQTMTYRAMV	DSQQKSPVKR	RRMQSSADLI	IQEFMDLRTR	YTALVTLMTQ	YIKFAGDSLK	RLEEEEKSLE	EEKKEHVEKA
1130	1140	1150	1160	1170	1180	1190	1200
KELQKWVSNI	SKTLKDAEKA	GKPPFSKQKI	SSEEISTKKE	QLSEALQTIQ	LFLAKHGDKM	TDEERNELEK	QVKTLQESYN
1210	1220	1230	1240	1250	1260	1270	1280
LLFSESLKQL	QESQTSGDVK	VEEKLDKVIA	GTIDQTTGEV	LSVFQAVLRG	LIDYDTGIRL	LETQLMISGL	ISPELRKCFD
1290	1300	1310	1320	1330	1340	1350	1360
LKDAKSHGLI	DEQILCQLKE	LSKAKEIISA	ASPTTIPVLD	ALAQSMITES	MAIKVLEILL	STGSLVIPAT	GEQLTLQKAF
1370	1380	1390	1400	1410	1420	1430	1440
QQNLVSSALF	SKVLERQNMC	KDLIDPCTSE	KVSLIDMVQR	STLQENTGMW	LLPVRPQEGG	RITLKCGRNI	SILRAAHEGL
1450	1460	1470	1480	1490	1500	1510	1520
IDRETMFRLL	SAQLLSGGLI	NSNSGQRMTV	EEAVREGVID	RDTASSILTY	QVQTGGIIQS	NPAKRLTVDE	AVQCDLITSS
1530	1540	1550	1560	1570	1580	1590	1600
SALLVLEAQR	GYVGLIWPHS	GEIFPTSSSL	QQELITNELA	YKILNGRQKI	AALYIPESSQ	VIGLDAAKQL	GIIDNNTASI
1610	1620	1630	1640	1650	1660	1670	1680
LKNITLPDKM	PDLGDLEACK	NARRWLSFCK	FQPSTVHDYR	QEEDVFDGEE	PVTTQTSEET	KKLFLSYLMI	NSYMDANTGQ
1690	1700	1710	1720	1730	1740	1750	1760
RLLLYDGDLD	EAVGMLLEGC	HAEFDGNTAI	KECLDVLSSS	GVFLNNASGR	EKDECTATPS	SFNKCHCGEP	EHEETPENRK
1770	1780	1790	1800	1810	1820	1830	1840
CAIDEEFNEM	RNTVINSEFS	QSGKLASTIS	IDPKVNSSPS	VCVPSLISYL	TQTELADISM	LRSDSENILT	NYENQSRVET
1850	1860	1870	1880	1890	1900	1910	1920
NERANECSHS	KNIQNFPSDL	IENPIMKSKM	SKFCGVNETE	NEDNTNRDSP	IFDYSPRLSA	LLSHDKLMHS	QGSFNDTHTP
1930	1940	1950	1960	1970	1980	1990	2000
ESNGNKCEAP	ALSFSDKTML	SGQRIGEKFQ	DQFLGIAAIN	ISLPGEQYGQ	KSLNMISSNP	QVQYHNDKYI	SNTSGEDEKT
2010	2020	2030	2040	2050	2060	2070	2080
HPGFQQMPED	KEDESEIEEY	SCAVTPGGDT	DNAIVSLTCA	TPLLDETISA	SDYETSLLND	QQNNTGTDTD	SDDDFYDTPL
2090	2100	2110	2120	2130	2140	2150	2160
FEDDDHDSLL	LDGDDRDCLH	PEDYDTLQEE	NDETASPADV	FYDVSKENEN	SMVPQGAPVG	SLSVKNKAHC	LQDFLMDVEK
2170	2180	2190	2200	2210	2220	2230	2240
DELDSGEKIH	LNPVGSDKVN	GQSLETGSER	ECTNILEGDE	SDSLTDYDIV	GGKESFTASL	KFDDSGSWRG	RKEEYVTGQE
2250	2260	2270	2280	2290	2300	2310	2320
FHSDTDHLDS	MQSEESYGDY	IYDSNDQDDD	DDDGIDEEGG	GIRDENGKPR	CQNVAEDMDI	QLCASILNEN	SDENENINTM
2330	2340	2350	2360	2370	2380	2390	2400

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1982	1	927.8655	-42.70	2	53.4	10.5	1	1377-1391	R.QNMCKDLIDPCTSEK.V	Carbamidomethyl: 4, 11; Oxidation: 3

Detailed Protein Report

Protein 407: sedoheptulokinase [Homo sapiens]

Accession: gi|74315356
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 22.0
MW [kDa]: 51.5
pI: 6.4
Sequence Coverage [%]: 7.3
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MAARPITLGI	DLGTTSVKAA	LLRAAPDDPS	GFAVLASCAR	AARAEAAVES	AVAGPQGREQ	DVSRILQALH	ECLAALPRPQ
90	100	110	120	130	140	150	160
LRSVVGIGVS	GQMHGVVFWK	TGQGCEWTEG	GITPVFEPRA	VSHLVTWQDG	RCSSEFLASL	PQPKSHLSVA	TGFGCATIFW
170	180	190	200	210	220	230	240
LLKYRPEFLK	SYDAAGTIHD	YVVAMLCGLP	RPLMSDQNAA	SWGYFNTQSQ	SWNVETLRSS	GFPVHLLPDI	AEPGSVAGRT
250	260	270	280	290	300	310	320
SHMWFEIPKG	TQVGVALGDL	QASVYSCMAQ	RTDAVLNIST	SVQLAASMPS	GFQPAQTPDP	TAPVAYFPYF	NRTYLGVAAS
330	340	350	360	370	380	390	400
LNGGNVLATF	VHMLVQWMAD	LGLEVEESTV	YSRMIQAAVQ	QRDTHLTITP	TVLGERHLPD	QLASVTRISS	SDLSLGHVTR
410	420	430	440	450	460	470	480
ALCRGIVQNL	HSMLPIQQLQ	EWGVERVMGS	GSALSRNDVL	KQEVQRAFPL	PMSFGQDVDA	AVGAALVMLR	RHLNQKES

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
425	1	767.5397	173.85	2	33.9	10.6	1	427-441	R.VMGSGSALSRNDVLK.Q	

Detailed Protein Report

Protein 408: PREDICTED: stabilin-2 isoform X1 [Homo sapiens]

Accession:	gi|578823928	**Score:**	22.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	243.6
Database Date:	2015-11-30	**pI:**	6.1
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.1
		No. of unique Peptides:	2

Detailed Protein Report

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        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
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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
2882	2	648.3630	73.51	2	64.8	11.7	1	220-229	K.LECKCLPNYR.G	Carbamidomethyl: 3
424	1	761.9985	164.95	2	34.3	10.3	0	568-581	K.DGTLDYLLSPEGSR.K	

Detailed Protein Report

Protein 409: CCR4-NOT transcription complex subunit 1 isoform c [Homo sapiens]

Accession:	gi|388454220	**Score:**	22.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	266.2
Database Date:	2015-11-30	**pI:**	6.6
		Sequence Coverage [%]:	0.9
		No. of unique Peptides:	1

Quantitation

WD:WU	**Median:** 0.63	**CV:** 0.00 %	**No. of Peptides:** 1

10	20	30	40	50	60	70	80
MNLDSLSLAL	SQISYLVDNL	TKKNYRASQQ	EIQHIVNRHG	PEADRHLLRC	LFSHVDFSGD	GKSSGKDFHQ	TQFLIQECAL
90	100	110	120	130	140	150	160
LITKPNFIST	LSYAIDNPLH	YQKSLKPAPH	LFAQLSKVLK	LSKVQEVIFG	LALLNSSSSD	LRGFAAQFIK	QKLPDLLRSY
170	180	190	200	210	220	230	240
IDADVSGNQE	GGFQDIAIEV	LHLLLSHLLF	GQKGAFGVGQ	EQIDAFLKTL	RRDFPQERCP	VVLAPLLYPE	KRDILMDRIL
250	260	270	280	290	300	310	320
PDSGGVAKTM	MESSLADFMQ	EVGYGFCASI	EECRNIIVQF	GVREVTAAQV	ARVLGMMART	HSGLTDGIPL	QSISAPGSGI
330	340	350	360	370	380	390	400
WSDGKDKSDG	AQAHTWNVEV	LIDVLKELNP	SLNFKEVTYE	LDHPGFQIRD	SKGLHNVVYG	IQRGLGMEVF	PVDLIYRPWK
410	420	430	440	450	460	470	480
HAEGQLSFIQ	HSLINPEIFC	FADYPCHTVA	TDILKAPPED	DNREIATWKS	LDLIESLLRL	AEVGQYEQVK	QLFSFPIKHC
490	500	510	520	530	540	550	560
PDMLVLALLQ	INTSWHTLRH	ELISTLMPIF	LGNHPNSAII	LHYAWHGQGQ	SPSIRQLIMH	AMAEWYMRGE	QYDQAKLSRI
570	580	590	600	610	620	630	640
LDVAQDLKAL	SMLLNGTPFA	FVIDLAALAS	RREYLKLDKW	LTDKIREHGE	PFIQACMTFL	KRRCPSILGG	LAPEKDQPKS
650	660	670	680	690	700	710	720
AQLPPETLAT	MLACLQACAG	SVSQELSETI	LTMVANCSNV	MNKARQPPPG	VMPKGRPPSA	SSLDAISPVQ	IDPLAGMTSL
730	740	750	760	770	780	790	800
SIGGSAAPHT	QSMQGFPPNL	GSAFSTPQSP	AKAFPPLSTP	NQTTAFSGIG	GLSSQLPVGG	LGTGSLTGIG	TGALGLPAVN
810	820	830	840	850	860	870	880
NDPFVQRKLG	TSGLNQPTFQ	QTDLSQVWPE	ANQHFSKEID	DEANSYFQRI	YNHPPHPTMS	VDEVLEMLQR	FKDSTIKRER
890	900	910	920	930	940	950	960
EVFNCMLRNL	FEEYRFFPQY	PDKELHITAC	LFGGIIEKGL	VTYMALGLAL	RYVLEALRKP	FGSKMYYFGI	AALDRFKNRL
970	980	990	1000	1010	1020	1030	1040
KDYPQYCQHL	ASISHFMQFP	HHLQEYIEYG	QQSRDPPVKM	QGSITTPGSI	ALAQAQAQAQ	VPAKAPLAGQ	VSTMVTTSTT
1050	1060	1070	1080	1090	1100	1110	1120
TTVAKTVTVT	RPTGVSFKKD	VPPSINTTNI	DTLLVATDQT	ERIVEPPENI	QEKIAFIFNN	LSQSNMTQKV	EELKETVKEE
1130	1140	1150	1160	1170	1180	1190	1200
FMPWVSQYLV	MKRVSIEPNF	HSLYSNFLDT	LKNPEFNKMV	LNETYRNIKV	LLTSDKAAAN	FSDRSLLKNL	GHWLGMITLA
1210	1220	1230	1240	1250	1260	1270	1280
KNKPILHTDL	DVKSLLLEAY	VKGQQELLYV	VPFVAKVLES	SIRSVVFRPP	NPWTMAIMNV	LAELHQEHDL	KLNLKFEIEV
1290	1300	1310	1320	1330	1340	1350	1360
LCKNLALDIN	ELKPGNLLKD	KDRLKNLDEQ	LSAPKKDVKQ	PEELPPITTT	TTSTTPATNT	TCTATVPPQP	QYSYHDINVY
1370	1380	1390	1400	1410	1420	1430	1440
SLAGLAPHIT	LNPTIPLFQA	HPQLKQCVRQ	AIERAVQELV	HPVVDRSIKI	AMTTCEQIVR	KDFALDSEES	RMRIAAHHMM
1450	1460	1470	1480	1490	1500	1510	1520
RNLTAGMAMI	TCREPLLMSI	STNLKNSFAS	ALRTASPQQR	EMMDQAAAQL	AQDNCELACC	FIQKTAVEKA	GPEMDKRLAT
1530	1540	1550	1560	1570	1580	1590	1600
EFELRKHARQ	EGRRYCDPVV	LTYQAERMPE	QIRLKVGGVD	PKQLAVYEEF	ARNVPGFLPT	NDLSQPTGFL	AQPMKQAWAT
1610	1620	1630	1640	1650	1660	1670	1680
DDVAQIYDKC	ITELEQHLHA	IPPTLAMNPQ	AQALRSLLEV	VVLSRNSRDA	IAALGLLQKA	VEGLLDATSG	ADADLLLRYR
1690	1700	1710	1720	1730	1740	1750	1760
ECHLLVLKAL	QDGRAYGSPW	CNKQITRCLI	ECRDEYKYNV	EAVELLIRNH	LVNMQQYDLH	LAQSMENGLN	YMAVAFAMQL
1770	1780	1790	1800	1810	1820	1830	1840
VKILLVDERS	VAHVTEADLF	HTIETLMRIN	AHSRGNAPEG	LPQLMEVVRS	NYEAMIDRAH	GGPNFMMHSG	ISQASEYDDP
1850	1860	1870	1880	1890	1900	1910	1920
PGLREKAEYL	LREWVNLYHS	AAAGRDSTKA	FSAFVGQMHQ	QGILKTDDLI	TRFFRLCTEM	CVEISYRAQA	EQQHNPAANP
1930	1940	1950	1960	1970	1980	1990	2000
TMIRAKCYHN	LDAFVRLIAL	LVKHSGEATN	TVTKINLLNK	VLGIVVGVLL	QDHDVRQSEF	QQLPYHRIFI	MLLLELNAPE
2010	2020	2030	2040	2050	2060	2070	2080
HVLETINFQT	LTAFCNTFHI	LRPTKAPGFV	YAWLELISHR	IFIARMLAHT	PQQKGWPMYA	QLLIDLFKYL	APFLRNVELT
2090	2100	2110	2120	2130	2140	2150	2160
KPMQILYKGT	LRVLLVLLHD	FPEFLCDYHY	GFCDVIPPNC	IQLRNLILSA	FPRNMRLPDP	FTPNLKVDML	SEINIAPRIL
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
585	1	603.8101	58.84	2	36.2	10.4	0	2360-2371	K.QAQQVMEGTGAS.-		WD:WU 0.63

Detailed Protein Report

Protein 410: PREDICTED: multiple PDZ domain protein isoform X3 [Homo sapiens]

Accession:	gi|530390235	**Score:**	21.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	213.7
Database Date:	2015-11-30	**pI:**	4.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	0.8
		No. of unique Peptides:	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MLEAIDKNRA	LHAAERLQTK	LRERGDVANE	DKLSLLKSVL	QSPLFSQILS	LQTSVQQLKD	QVNIATSATS	NIEYAHVPHL
90	100	110	120	130	140	150	160
SPAVIPTLQN	ESFLLSPNNG	NLEALTGPGI	PHINGKPACD	EFDQLIKNMA	QGRHVEVFEL	LKPPSGGLGF	SVVGLRSENR
170	180	190	200	210	220	230	240
GELGIFVQEI	QEGSVAHRDG	RLKETDQILA	INGQALDQTI	THQQAISILQ	KAKDTVQLVI	ARGSLPQLVS	PIVSRSPSAA
250	260	270	280	290	300	310	320
STISAHSNPV	HWQHMETIEL	VNDGSGLGFG	IIGGKATGVI	VKTILPGGVA	DQHGRLCSGD	HILKIGDTDL	AGMSSEQVAQ
330	340	350	360	370	380	390	400
VLRQCGNRVK	LMIARGAIEE	RTAPTALGIT	LSSSPTSTPE	LRVDASTQKG	EESETFDVEL	TKNVQGLGIT	IAGYIGDKKL
410	420	430	440	450	460	470	480
EPSGIFVKSI	TKSSAVEHDG	RIQIGDQIIA	VDGTNLQGFT	NQQAVEVLRH	TGQTVLLTLM	RRGMKQEAEL	MSREDVTKDA
490	500	510	520	530	540	550	560
DLSPVNASII	KENYEKDEDF	LSSTRNTNIL	PTEEEGYPLL	SAEIEEIEDA	QKQEAALLTK	WQRIMGINYE	IVVAHVSKFS
570	580	590	600	610	620	630	640
ENSGLGISLE	ATVGHHFIRS	VLPEGPVGHS	GKLFSGDELL	EVNGITLLGE	NHQDVVNILK	ELPIEVTMVC	CRRTVPPTTQ
650	660	670	680	690	700	710	720
SELDSLDLCD	IELTEKPHVD	LGEFIGSSET	EDPVLAMTDA	GQSTEEVQAP	LAMWEAGIQH	IELEKGSKGL	GFSILDYQDP
730	740	750	760	770	780	790	800
IDPASTVIII	RSLVPGGIAE	KDGRLLPGDR	LMFVNDVNLE	NSSLEEAVEA	LKGAPSGTVR	IGVAKPLPLS	PEEGYVSAKE
810	820	830	840	850	860	870	880
DSFLYPPHSC	EEAGLADKPL	FRADLALVGT	NDADLVDEST	FESPYSPEND	SIYSTQASIL	SLHGSSCGDG	LNYGSSLPSS
890	900	910	920	930	940	950	960
PPKDVIENSC	DPVLDLHMSL	EELYTQNLLQ	RQDENTPSVD	ISMGPASGFT	INDYTPANAI	EQQYECENTI	VWTESHLPSE
970	980	990	1000	1010	1020	1030	1040
VISSAELPSV	LPDSAGKGSE	YLLEQSSLAC	NAECVMLQNV	SKESFERTIN	IAKGNSSLGM	TVSANKDGLG	MIVRSIIHGG
1050	1060	1070	1080	1090	1100	1110	1120
AISRDGRIAI	GDCILSINEE	STISVTNAQA	RAMLRRHSLI	GPDIKITYVP	AEHLEEFKIS	LGQQSGRVMA	LDIFSSYTGR
1130	1140	1150	1160	1170	1180	1190	1200
DIPELPEREE	GEGEESELQN	TAYSNWNQPR	RVELWREPSK	SLGISIVGGR	GMGSRLSNGE	VMRGIFIKHV	LEDSPAGKNG
1210	1220	1230	1240	1250	1260	1270	1280
TLKPGDRIVE	APSQSESEPE	KAPLCSVPPP	PPSAFAEMGS	DHTQSSASKI	SQDVDKEDEF	GYSWKNIRER	YGTLTGELHM
1290	1300	1310	1320	1330	1340	1350	1360
IELEKGHSGL	GLSLAGNKDR	SRMSVFIVGI	DPNGAAGKDG	RLQIADELLE	INGQILYGRS	HQNASSIIKC	APSKVKIIFI
1370	1380	1390	1400	1410	1420	1430	1440
RNKDAVNQMA	VCPGNAVEPL	PSNSENLQNK	ETEPTVTTSD	AAVDLSSFKN	VQHLELPKDQ	GGLGIAISEE	DTLSGVIIKS
1450	1460	1470	1480	1490	1500	1510	1520
LTEHGVAATD	GRLKVGDQIL	AVDDEIVVGY	PIEKFISLLK	TAKMTVKLTI	HAENPDSQAV	PSAAGAASGE	KKNSSQSLMV
1530	1540	1550	1560	1570	1580	1590	1600
PQSGSPEPES	IRNTSRSSTP	AIFASDPATC	PIIPGCETTI	EISKGRTGLG	LSIVGGSDTL	LGAIIIHEVY	EEGAACKDGR
1610	1620	1630	1640	1650	1660	1670	1680
LWAGDQILEV	NGIDLRKATH	DEAINVLRQT	PQRVRLTLYR	DEAPYKEEEV	CDTLTIELQK	KPGKGLGLSI	VGKRNDTGVF
1690	1700	1710	1720	1730	1740	1750	1760
VSDIVKGGIA	DADGRLMQGD	QILMVNGEDV	RNATQEAVAA	LLKCSLGTVT	LEVGRIKAGP	FHSERRPSQS	SQVSEGSLSS
1770	1780	1790	1800	1810	1820	1830	1840
FTFPLSGSST	SESLESSSKK	NALASEIQGL	RTVEMKKGPT	DSLGISIAGG	VGSPLGDVPI	FIAMMHPTGV	AAQTQKLRVG
1850	1860	1870	1880	1890	1900	1910	1920
DRIVTICGTS	TEGMTHTQAV	NLLKNASGSI	EMQVVAGGDV	SVVTGHQQEP	ASSSLSFTGL	TSSSIFQDDL	GPPQCKSITL
1930	1940	1950	1960	1970	1980	1990	2000
ERGPDGLGFS	IVGGYGSPHG	DLPIYVKTVF	AKGAASEDGR	LKRGDQIIAV	NGQSLEGVTH	EEAVAILKRT	KGTVTLMVLS
2010							

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

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1954	1	618.9203	-128.74	3	53.1	10.4	2	1340-1356	R.SHQNASSIIKCAPSKVK.I	Carbamidomethyl: 11

Protein 411: PREDICTED: transcriptional regulator ATRX isoform X8 [Homo sapiens]

Accession: gi|578838421
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 21.9
MW [kDa]: 211.9
pI: 6.7
Sequence Coverage [%]: 0.8
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MTAEPMSESK	LNTLVQKLHD	FLAHSSEESE	ETSSPPRLAM	NQNTDKISGS	GSNSDMMENS	KEEGTSSSEK	SKSSGSSRSK
90	100	110	120	130	140	150	160
RKPSIVTKYV	ESDDEKPLDD	ETVNEDASNE	NSENDITMQS	LPKGTVIVQP	EPVLNEDKDD	FKGPEFRSRS	KMKTENLKKR
170	180	190	200	210	220	230	240
GEDGLHGIVS	CTACGQQVNH	FQKDSIYRHP	SLQVLICKNC	FKYYMSDDIS	RDSDGMDEQC	RWCAEGGNLI	CCDFCHNAFC
250	260	270	280	290	300	310	320
KKCILRNLGR	KELSTIMDEN	NQWYCYICHP	EPLLDLVTAC	NSVFENLEQL	LQQNKKKIKV	DSEKSNKVYE	HTSRFSPKKT
330	340	350	360	370	380	390	400
SSNCNGEEKK	LDDSCSGSVT	YSYSALIVPK	EMIKKAKKLI	ETTANMNSSY	VKFLKQATDN	SEISSATKLR	QLKAFKSVLA
410	420	430	440	450	460	470	480
DIKKAHLALE	EDLNSEFRAM	DAVNKEKNTK	EHKVIDAKFE	TKARKGEKPC	ALEKKDISKS	EAKLSRKQVD	SEHMHQNVPT
490	500	510	520	530	540	550	560
EEQRTNKSTG	GEHKKSDRKE	EPQYEPANTS	EDLDMDIVSV	PSSVPEDIFE	NLETAMEVQS	SVDHQGDGSS	GTEQEVESSS
570	580	590	600	610	620	630	640
VKLNISSKDN	RGGIKSKTTA	KVTKELYVKL	TPVSLSNSPI	KGADCQEVPQ	DKDGYKSCGL	NPKLEKCGLG	QENSDNEHLV
650	660	670	680	690	700	710	720
ENEVSLLLEE	SDLRRSPRVK	TTPLRRPTET	NPVTSNSDEE	CNETVKEKQK	LSVPVRKKDK	RNSSDSAIDN	PKPNKLPKSK
730	740	750	760	770	780	790	800
QSETVDQNSD	SDEMLAILKE	VSRMSHSSSS	DTDINEIHTN	HKTLYDLKTQ	AGKDDKGKRK	RKSSTSGSDF	DTKKGKSAKS
810	820	830	840	850	860	870	880
SIISKKKRQT	QSESSNYDSE	LEKEIKSMSK	IGAARTTKKR	IPNTKDFDSS	EDEKHSKKGM	DNQGHKNLKT	SQEGSSDDAE
890	900	910	920	930	940	950	960
RKQERETFSS	AEGTVDKDTT	IMELRDRLPK	KQQASASTDG	VDKLSGKEES	FTSLEVRKVA	ETKEKSKHLK	TKTCKKVQDG
970	980	990	1000	1010	1020	1030	1040
LSDIAEKFLK	KDQSDETSED	DKKQSKKGTE	EKKKPSDFKK	KVIKMEQQYE	SSSDGTEKLP	EREEICHFPK	GIKQIKNGTT
1050	1060	1070	1080	1090	1100	1110	1120
DGEKKSKKIR	DKTSKKKDEL	SDYAEKSTGK	GDSCDSSEDK	KSKNGAYGRE	KKRCKLLGKS	SRKRQDCSSS	DTEKYSMKED
1130	1140	1150	1160	1170	1180	1190	1200
GCNSSDKRLK	RIELRERRNL	SSKRNTKEIQ	SGSSSSDAEE	SSEDNKKKKQ	RTSSKKKAVI	VKEKKRNSLR	TSTKRKQADI
1210	1220	1230	1240	1250	1260	1270	1280
TSSSSSDIED	DDQNSIGEGS	SDEQKIKPVT	ENLVLSSHTG	FCQSSGDEAL	SKSVPVTVDD	DDDDNDPENR	IAKKMLLEEI
1290	1300	1310	1320	1330	1340	1350	1360
KANLSSDEDG	SSDDEPEEGK	KRTGKQNEEN	PGDEEAKNQV	NSESDSDSEE	SKKPRYRHRL	LRHKLTVSDG	ESGEEKKTKP
1370	1380	1390	1400	1410	1420	1430	1440
KEHKEVKGRN	RRKVSSEDSE	DSDFQESGVS	EEVSESEDEQ	RPRTRSAKKA	ELEENQRSYK	QKKKRRRIKV	QEDSSSENKS
1450	1460	1470	1480	1490	1500	1510	1520
NSEEEEEEKE	EEEEEEEEEE	EEEEDENDDS	KSPGKGRKKI	RKILKDDKLR	TETQNALKEE	EERRKRIAER	EREREKLREV
1530	1540	1550	1560	1570	1580	1590	1600
IEIEDASPTK	CPITTKLVLD	EDEETKEPLV	QVHRNMVIKL	KPHQVDGVQF	MWDCCCESVK	KTKKSPGSGC	ILAHCMGLGK
1610	1620	1630	1640	1650	1660	1670	1680
TLQVVSFLHT	VLLCDKLDFS	TALVVCPLNT	ALNWMNEFEK	WQEGLKDDEK	LEVSELATVK	RPQERSYMLQ	RWQEDGGVMI
1690	1700	1710	1720	1730	1740	1750	1760
IGYEMYRNLA	QGRNVKSRKL	KEIFNKALVD	PGPDFVVCDE	GHILKNEASA	VSKAMNSIRS	RRRIILTGTP	LQNNLIEYHC
1770	1780	1790	1800	1810	1820	1830	1840
MVNFIKENLL	GSIKEFRNRF	INPIQNGQCA	DSTMVDVRVM	KKRAHILYEM	LAGCVQRKDY	TALTKFLPPK	HEYVLAVRMT
1850	1860	1870	1880				
SIQCKLYQYY	LDHLTVLHLN	KMGMLKSIKY	F				

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2633	1	589.1691	-335.46	1	61.2	10.3	1	572-577	R.GGIKSK.T	

Detailed Protein Report

Protein 412: **PREDICTED: brain-specific angiogenesis inhibitor 3 isoform X3 [Homo sapiens]**

Accession:	gi|578812890	**Score:**	21.9
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:	2

```
        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
1966	1	590.7814	2.32	2	53.0	10.8	1	1120-1128	R.EVQDAFRCR.L	Carbamidomethyl: 8

Detailed Protein Report

Protein 413: nuclear receptor coactivator 3 isoform d [Homo sapiens]

Accession:	gi|291490685	**Score:**	21.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	154.3
Database Date:	2015-11-30	**pI:**	7.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.9
		No. of unique 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
286	1	881.1736	82.04	3	32.7	11.0	2	199-220	R.MLMKTPHDILEDINASPEMRQR.Y	Oxidation: 19

Detailed Protein Report

Protein 414: vesicular integral-membrane protein VIP36 precursor [Homo sapiens]

Accession:	gi|5803023	**Score:**	21.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	40.2
Database Date:	2015-11-30	**pI:**	6.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	6.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAAEGWIWRW	GWGRRCLGRP	GLLGPGPGPT	TPLFLLLLLG	SVTADITDGN	SEHLKREHSL	IKPYQGVGSS	SMPLWDFQGS
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
TMLTSQYVRL	TPDERSKEGS	IWNHQPCFLK	DWEMHVHFKV	HGTGKKNLHG	DGIALWYTRD	RLVPGPVFGS	KDNFHGLAIF
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
LDTYPNDETT	ERVFPYISVM	VNNGSLSYDH	SKDGRWTELA	GCTADFRNRD	HDTFLAVRYS	RGRLTVMTDL	EDKNEWKNCI
250	**260**	**270**	**280**	**290**	**300**	**310**	**320**
DITGVRLPTG	YYFGASAGTG	DLSDNHDIIS	MKLFQLMVEH	TPDEESIDWT	KIEPSVNFLK	SPKDNVDDPT	GNFRSGPLTG
330	**340**	**350**	**360**				
WRVFLLLLCA	LLGIVVCAVV	GAVVFQKRQE	RNKRFY				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
470	1	524.1609	-200.81	2	34.4	11.0	0	238-246	K.NCIDITGVR.L	Carbamidomethyl: 2

Detailed Protein Report

Protein 415: protocadherin Fat 4 precursor [Homo sapiens]

Accession:	gi|165932370	**Score:**	21.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	542.4
Database Date:	2015-11-30	**pI:**	4.6
		Sequence Coverage [%]:	0.6
		No. of unique Peptides:	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MDLAPDRATG	RPWLPLHTLS	VSQLLRVFWL	LSLLPGQAWV	HGAEPRQVFQ	VLEEQPPGTL	VGTIQTRPGF	TYRLSESHAL
90	100	110	120	130	140	150	160
FAINSSTGAL	YTTSTIDRES	LPSDVINLVV	LSSAPTYPTE	VRVLVRDLND	NAPVFPDPSI	VVTFKEDSSS	GRQVILDTAT
170	180	190	200	210	220	230	240
DSDIGSNGVD	HRSYRIIRGN	EAGRFRLDIT	LNPSGEGAFL	HLVSKGGLDR	EVTPQYQLLV	EVEDKGEPKR	RGYLQVNVTV
250	260	270	280	290	300	310	320
QDINDNPPVF	GSSHYQAGVP	EDAVVGSSVL	QVAAADADEG	TNADIRYRLQ	DEGTPFQMDP	ETGLITVREP	LDFEARRQYS
330	340	350	360	370	380	390	400
LTVQAMDRGV	PSLTGRAEAL	IQLLDVNDND	PVVKFRYFPA	TSRYASVDEN	AQVGTVVALL	TVTDADSPAA	NGNISVQILG
410	420	430	440	450	460	470	480
GNEQRHFEVQ	SSKVPNLSLI	KVASALDRER	IPSYNLTVSV	SDNYGAPPGA	AVQARSSVAS	LVIFVNDIND	HPPVFSQQVY
490	500	510	520	530	540	550	560
RVNLSEEAPP	GSYVSGISAT	DGDSGLNANL	RYSIVSGNGL	GWFHISEHSG	LVTTGSSGGL	DRELASQIVL	NISARDQGVH
570	580	590	600	610	620	630	640
PKVSYAQLVV	TLLDVNDEKP	VFSQPEGYDV	SVVENAPTGT	ELLMLRATDG	DLGDNGTVRF	SLQEAETDRR	SFRLDPVSGR
650	660	670	680	690	700	710	720
LSTISSLDRE	EQAFYSLLVL	ATDLGSPPQS	SMARINVSLL	DINDNSPVFY	PVQYFAHIKE	NEPGGSYITT	VSATDPDLGT
730	740	750	760	770	780	790	800
NGTVKYSISA	GDRSRFQVNA	QSGVISTRMA	LDREEKTAYQ	LQIVATDGGN	LQSPNQAIVT	ITVLDTQDNP	PVFSQVAYSF
810	820	830	840	850	860	870	880
VVFENVALGY	HVGSVSASTM	DLNSNISYLI	TTGDQKGMFA	INQVTGQLTT	ANVIDREEQS	FYQLKVVASG	GTVTGDTMVN
890	900	910	920	930	940	950	960
ITVKDLNDNS	PHFLQAIESV	NVVENWQAGH	SIFQAKAVDP	DEGVNGMVLY	SLKQNPKNLF	AINEKNGTIS	LLGPLDVHAG
970	980	990	1000	1010	1020	1030	1040
SYQIEILASD	MGVPQLSSSV	ILTVYVHDVN	DNSPVFDQLS	YEVTLSESEP	VNSRFFKVQA	SDKDSGANGE	IAYTIAEGNT
1050	1060	1070	1080	1090	1100	1110	1120
GDAFGIFPDG	QLYIKSELDR	ELQDRYVLMV	VASDRAVEPL	SATVNVTVIL	EDVNDNRPLF	NSTNYTFYFE	EEQRAGSFVG
1130	1140	1150	1160	1170	1180	1190	1200
KVSAVDKDFG	PNGEVRYSFE	MVQPDFELHA	ISGEITNTHQ	FDRESLMRRR	GTAVFSFTVI	ATDQGIPQPL	KDQATVHVYM
1210	1220	1230	1240	1250	1260	1270	1280
KDINDNAPKF	LKDFYQATIS	ESAANLTQVL	RVSASDVDEG	NNGLIHYSII	KGNEERQFAI	DSTSGQVTLI	GKLDYEATPA
1290	1300	1310	1320	1330	1340	1350	1360
YSLVIQAVDS	GTIPLNSTCT	LNIDILDEND	NTPSFPKSTL	FVDVLENMRI	GELVSSVTAT	DSDSGDNADL	YYSITGTNNH
1370	1380	1390	1400	1410	1420	1430	1440
GTFSISPNTG	SIFLAKKLDF	ETQSLYKLNI	TAKDQGRPPR	SSTMSVVIHV	RDFNDNPPSF	PPGDIFKSIV	ENIPIGTSVI
1450	1460	1470	1480	1490	1500	1510	1520
SVTAHDPDAD	INGQLSYTII	QQMPRGNHFT	IDEVKGTIYT	NAEIDREFAN	LFELTVKAND	QAVPIETRRY	ALKNVTILVT
1530	1540	1550	1560	1570	1580	1590	1600
DLNDNVPMFI	SQNALAADPS	AVIGSVLTTI	MAADPDEGAN	GEIEYEIING	DTDTFIVDRY	SGDLRVASAL	VPSQLIYNLI
1610	1620	1630	1640	1650	1660	1670	1680
VSATDLGPER	RKSTTELTII	LQGLDGPVFT	QPKYITILKE	GEPIGTNVIS	IEAASPRGSE	APVEYYIVSV	RCEEKTVGRL
1690	1700	1710	1720	1730	1740	1750	1760
FTIGRHTGII	QTAAILDREQ	GACLYLVDVY	AIEKSTAFPR	TQRAEVEITL	QDINDNPPVF	PTDMLDLTVE	ENIGDGSKIM
1770	1780	1790	1800	1810	1820	1830	1840
QLTAMDADEG	ANALVTYTII	SGADDSFRID	PESGDLIATR	RLDRERRSKY	SLLVRADDGL	QSSDMRINIT	VSDVNDHTPK
1850	1860	1870	1880	1890	1900	1910	1920
FSRPVYSFDI	PEDTIPGSLV	AAILATDDDS	GVNGEITYIV	NEDDEDGIFF	LNPITGVFNL	TRLLDYEVQQ	YYILTVRAED
1930	1940	1950	1960	1970	1980	1990	2000
GGGQFTTIRV	YFNILDVNDN	PPIFSLNSYS	TSLMENLPVG	STVLVFNVTD	ADDGINSQLT	YSIASGDSLG	QFTVDKNGVL
2010	2020	2030	2040	2050	2060	2070	2080
KVLKALDRES	QSFYNLVVQV	HDLPQIPASR	FTSTAQVSII	LLDVNDNPPT	FLSPKLTYIP	ENTPIDTVVF	KAQATDPDSG
2090	2100	2110	2120	2130	2140	2150	2160
PNSYIEYTLL	NPLGNKFSIG	TIDGEVRLTG	ELDREEVSNY	TLTVVATDKG	QPSLSSSTEV	VVMVLDINDN	NPIFAQALYK
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
654	1	602.1692	-235.73	2	37.0	11.0	1	3115-3125	R.DRDAAMNGLIK.Y	

Detailed Protein Report

Protein 416: PREDICTED: tetratricopeptide repeat protein 18 isoform X8 [Homo sapiens]

Accession:	gi|530392981	**Score:**	21.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	105.0
Database Date:	2015-11-30	**pI:**	5.6
		Sequence Coverage [%]:	2.3
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578818878	refseq_human(refseq_human_20140103.fasta)	PREDICTED: tetratricopeptide repeat protein 18 isoform X16 [Homo sapiens]
gi|578818876	refseq_human(refseq_human_20140103.fasta)	PREDICTED: tetratricopeptide repeat protein 18 isoform X15 [Homo sapiens]
gi|578818874	refseq_human(refseq_human_20140103.fasta)	PREDICTED: tetratricopeptide repeat protein 18 isoform X14 [Homo sapiens]

10	20	30	40	50	60	70	80
MVGLQVPSLG	EKDYPILFKN	GTLKLGGERE	PVPRPKKWPI	ANILAPGANN	IPDAFIVGGP	YEEEEGELNH	PEDSEFRNQA
90	100	110	120	130	140	150	160
ECIKKRIIWD	LESRCYLDPS	AVVSFQKRIA	DCRLWPVEIT	RVPLVTIPKG	KAGKTEKTDE	EAQLSFHGVA	YVNMVPLLYP
170	180	190	200	210	220	230	240
GVKRIRGAFH	VYPYLDSVVH	EKTKCLLSLF	RDIGHHLIHN	NKIGGINSLL	SKQAVSKNLK	EDKPVKEKDI	DGRPRPGDVQ
250	260	270	280	290	300	310	320
APSIKSQSSD	TPLEGEPPLS	HNPEGQQYVE	AGTYIVLEIQ	LDKALVPKRM	PEELARRVKE	MIPPRPPLTR	RTGGAQKAVS
330	340	350	360	370	380	390	400
DYHIQIKNIS	RAILDEYYRM	FGKQVAKLES	DMDSETLEEQ	KCQLSYELNC	SGKYFAFKEQ	LKHAVVKIVR	DKYLKTTSFE
410	420	430	440	450	460	470	480
SQEELQTFIS	ELYVFLVDQM	HVALNQTMPD	DVQGTVATIY	TSSEQLQLFA	FEAEVNENFE	MAAAYYKERL	VREPQNLDHW
490	500	510	520	530	540	550	560
LDYGAFCLLT	EDNIKAQECF	QKALSLNQSH	IHSLLLCGVL	AVLLENYEQA	EIFFEDATCL	EPTNVVAWTL	LGLYYEIQNN
570	580	590	600	610	620	630	640
DIRMEMAFHE	ASKQLQARML	QAQVTKQKST	GVEDTEERGK	RESSLGPWGI	TNGSATAIKV	EAPAGPGAAL	SILDKFLEES
650	660	670	680	690	700	710	720
SKLQSDSQEP	ILTTQTWDPS	ISQKPSNTFI	KEIPTKKEAS	KCQDSSALLH	PGLHYGVSQT	TTIFMETIHF	LMKVKAVQYV
730	740	750	760	770	780	790	800
HRVLAHELLC	PQGGPSCEYY	LVLAQTHILK	KNFAKAEEYL	QQAAQMDYLN	PNVWGLKGHL	YFLSGNHSEA	KACYERTISF
810	820	830	840	850	860	870	880
VVDASEMHFI	FLRLGLIYLE	EKEYEKAKKT	YMQACKRSPS	CLTWLGLGIA	CYRLEELTEA	EDALSEANAL	NNYNAEVWAY
890	900	910	920	930			
LALVCLKVGR	QLEAEQAYKY	MIKLKLKDEA	LLAEIHTLQE	TVGFGNPSF			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2801	1	813.9256	-11.47	2	63.6	11.1	1	814-826	R.LGLIYLEEKEYEK.A	

Detailed Protein Report

Protein 417: 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 418: PREDICTED: E3 ubiquitin-protein ligase UBR5 isoform X7 [Homo sapiens]

Accession:	gi|530389115	**Score:**	21.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	200.9
Database Date:	2015-11-30	**pI:**	5.2
		Sequence Coverage [%]:	1.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MMRRSLRAAG	LGRHEAGASS	SDHQDPVSPP	IAPPSWVPDP	PAMDPDGDID	FILAPAVGSL	TTAATGTGQG	PSTSTIPGPS
90	100	110	120	130	140	150	160
TEPSVVESKD	RKANAHFILK	LLCDSVVLQP	YLRELLSAKD	ARGMTPFMSA	VSGRAYPAAI	TILETAQKIA	KAEISSSEKE
170	180	190	200	210	220	230	240
EDVFMGMVCP	SGTNPDDSPL	YVLCCNDTCS	FTWTGAEHIN	QDIFECRTCG	LLESLCCCTE	CARVCHKGHD	CKLKRTSPTA
250	260	270	280	290	300	310	320
YCDCWEKCKC	KTLIAGQKSA	RLDLLYRLLT	ATNLVTLPNS	RGEHLLLFLV	QTVARQTVEH	CQYRPPRIRE	DRNRKTASPE
330	340	350	360	370	380	390	400
DSDMPDHDLE	PPRFAQLALE	RVLQDWNALK	SMIMFGSQEN	KDPLSASSRI	GHLLPEEQVY	LNQQSGTIRL	DCFTHCLIVK
410	420	430	440	450	460	470	480
CTADILLLDT	LLGTLVKELQ	NKYTPGRREE	AIAVTMRFLR	SVARVFVILS	VEMASSKKKN	NFIPQPIGKC	KRVFQALLPY
490	500	510	520	530	540	550	560
AVEELCNVAE	SLIVPVRMGI	ARPTAPFTLA	STSIDAMQGS	EELFSVEPLP	PRPSSDQSSS	SSQSQSSYII	RNPQQRRISQ
570	580	590	600	610	620	630	640
SQPVRGRDEE	QDDIVSADVE	EVEVVEGVAG	EEDHHDEQEE	HGEENAEAEG	QHDEHDEDGS	DMELDLLAAA	ETESDSESNH
650	660	670	680	690	700	710	720
SNQDNASGRR	SVVTAATAGS	EAGASSVPAF	FSEDDSQSND	SSDSDSSSSQ	SDDIEQETFM	LDEPLERTTN	SSHANGAAQA
730	740	750	760	770	780	790	800
PRSMQWAVRN	TQHQRAASTA	PSSTSTPAAS	SAGLIYIDPS	NLRRSGTIST	SAAAAAAALE	ASNASSYLTS	ASSLARAYSI
810	820	830	840	850	860	870	880
VIRQISDLMG	LIPKYNHLVY	SQIPAAVKLT	YQDAVNLQNY	VEEKLIPTWN	WMVSIMDSTE	AQLRYGSALA	SAGDPGHPNH
890	900	910	920	930	940	950	960
PLHASQNSAR	RERMTAREEA	SLRTLEGRRR	ATLLSARQGM	MSARGDFLNY	ALSLMRSHND	EHSDVLPVLD	VCSLKHVAYV
970	980	990	1000	1010	1020	1030	1040
FQALIYWIKA	MNQQTTLDTP	QLERKRTREL	LELGIDNEDS	EHENDDDTNQ	SATLNDKDDD	SLPAETGQNH	PFFRRSDSMT
1050	1060	1070	1080	1090	1100	1110	1120
FLGCIPPNPF	EVPLAEAIPL	ADQPHLLQPN	ARKEDLFGRP	SQGLYSSSAS	SGKCLMEVTV	DRNCLEVLPT	KMSYAANLKN
1130	1140	1150	1160	1170	1180	1190	1200
VMNMQNRQKK	EGEEQPVLPE	ETESSKPGPS	AHDLAAQLKS	SLLAEIGLTE	SEGPPLTSFR	PQCSFMGMVI	SHDMLLGRWR
1210	1220	1230	1240	1250	1260	1270	1280
LSLELFGRVF	MEDVGAEPGS	ILTELGGFEV	KESKFRREME	KLRNQQSRDL	SLEVKVDRDR	DLLIQQTMRQ	LNNHFGRRCA
1290	1300	1310	1320	1330	1340	1350	1360
TTPMAVHRVK	VTFKDEPGEG	SGVARSFYTA	IAQAFLSNEK	LPNLECIQNA	NKGTHTSLMQ	RLRNRGERDR	EREREREMRR
1370	1380	1390	1400	1410	1420	1430	1440
SSGLRAGSRR	DRDRDFRRQL	SIDTRPFRPA	SEGNPSDDPE	PLPAHRQALG	ERLYPRVQAM	QPAFASKITG	MLLELSPAQL
1450	1460	1470	1480	1490	1500	1510	1520
LLLLASEDSL	RARVDEAMEL	IIAHGRENGA	DSILDLGLVD	SSEKVQQENR	KRHGSSRSVV	DMDLDDTDDG	DDNAPLFYQP
1530	1540	1550	1560	1570	1580	1590	1600
GKRGFYTPRP	GKNTEARLNC	FRNIGRILGL	CLLQNELCPI	TLNRHVIKVL	LGRKVNWHDF	AFFDPVMYES	LRQLILASQS
1610	1620	1630	1640	1650	1660	1670	1680
SDADAVFSAM	DLAFAIDLCK	EEGGGQVELI	PNGVNIPVTP	QNVYEYVRKY	AEHRMLVVAE	QPLHAMRKGL	LDVLPKNSLE
1690	1700	1710	1720	1730	1740	1750	1760
DLTAEDFRLL	VNGCGEVNVQ	MLISFTSFND	ESGENAEKLL	QFKRWFWSIV	EKMSMTERQD	LVYFWTSSPS	LPASEEGFQP
1770	1780	1790	1800	1810	1820		
MPSITIRPPD	DQHLPTANTC	ISRLYVPLYS	SKQILKQKLL	LAIKTKNFGF	V		

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

	Cmpds.		[ppm]		[min]					
31	1	712.9884	0.22	3	29.6	11.4	1	315-333	R.KTASPEDSDMPDHDLEPPR.F	

Detailed Protein Report

Protein 419: PREDICTED: coiled-coil domain-containing protein 13 isoform X2 [Homo sapiens]

Accession:	gi|530371957	**Score:**	21.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	52.8
Database Date:	2015-11-30	**pI:**	9.0
		Sequence Coverage [%]:	7.1
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 0.44 **CV:** 0.00 % **No. of 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	Ratios
1302	1	857.8300	-157.01	2	45.0	11.4	0	393-407	K.QLQEILGSLSLQEEK.T		WD:WU 0.44

Detailed Protein Report

Protein 420: PREDICTED: PR domain zinc finger protein 16 isoform X3 [Homo sapiens]

Accession:	gi|530360370	**Score:**	21.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	129.7
Database Date:	2015-11-30	**pI:**	5.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.6
		No. of unique Peptides:	1

Quantitation

WD:WU	**Median:**	1.19	**CV:**	0.00 %	**No. of Peptides:**	1

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1511	1	1005.9710	-61.06	2	47.6	21.5	2	104-122	K.MEAGERLGPCVVVPRAAAK.E	Carbamidomethyl: 10	WD:WU 1.19

Detailed Protein Report

Protein 421: NACHT, LRR and PYD domains-containing protein 12 isoform 2 [Homo sapiens]

Accession:	gi|21955154	**Score:**	21.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	120.1
Database Date:	2015-11-30	**pI:**	6.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLRTAGRDGL	CRLSTYLEEL	EAVELKKFKL	YLGTATELGE	GKIPWGSMEK	AGPLEMAQLL	ITHFGPEEAW	RLALSTFERI
90	100	110	120	130	140	150	160
NRKDLWERGQ	REDLVRDTPP	GGPSSLGNQS	TCLLEVSLVT	PRKDPQETYR	DYVRRKFRLM	EDRNARLGEC	VNLSHRYTRL
170	180	190	200	210	220	230	240
LLVKEHSNPM	QVQQQLLDTG	RGHARTVGHQ	ASPIKIETLF	EPDEERPEPP	RTVVMQGAAG	IGKSMLAHKV	MLDWADGKLF
250	260	270	280	290	300	310	320
QGRFDYLFYI	NCREMNQSAT	ECSMQDLIFS	CWPEPSAPLQ	ELIRVPERLL	FIIDGFDELK	PSFHDPQGPW	CLCWEEKRPT
330	340	350	360	370	380	390	400
ELLLNSLIRK	KLLPELSLLI	TTRPTALEKL	HRLLEHPRHV	EILGFSEAER	KEYFYKYFHN	AEQAGQVFNY	VRDNEPLFTM
410	420	430	440	450	460	470	480
CFVPLVCWVV	CTCLQQQLEG	GGLLRQTSRT	TTAVYMLYLL	SLMQPKPGAP	RLQPPPNQRG	LCSLAADGLW	NQKILFEEQD
490	500	510	520	530	540	550	560
LRKHGLDGED	VSAFLNMNIF	QKDINCERYY	SFIHLSFQEF	FAAMYYILDE	GEGGAGPDQD	VTRLLTEYAF	SERSFLALTS
570	580	590	600	610	620	630	640
RFLFGLLNEE	TRSHLEKSLC	WKVSPHIKMD	LLQWIQSKAQ	SDGSTLQQGS	LEFFSCLYEI	QEEEFIQQAL	SHFQVIVVSN
650	660	670	680	690	700	710	720
IASKMEHMVS	SFCLKRCRSA	QVLHLYGATY	SADGEDRARC	SAGAHTLLVQ	LPERTVLLDA	YSEHLAAALC	TNPNLIELSL
730	740	750	760	770	780	790	800
YRNALGSRGV	KLLCQGLRHP	NCKLQNLRLK	RCRISSSACE	DLSAALIANK	NLTRMDLSGN	GVGFPGMMLL	CEGLRHPQCR
810	820	830	840	850	860	870	880
LQMIQLRKCQ	LESGACQEMA	SVLGTNPHLV	ELDLTGNALE	DLGLRLLCQG	LRHPVCRLRT	LWLKICRLTA	AACDELASTL
890	900	910	920	930	940	950	960
SVNQSLRELD	LSLNELGDLG	VLLLCEGLRH	PTCKLQTLRL	GICRLGSAAC	EGLSVVLQAN	HNLRELDLSF	NDLGDWGLWL
970	980	990	1000	1010	1020	1030	1040
LAEGLQHPAC	RLQKLWLDSC	GLTAKACENL	YFTLGINQTL	TDLYLTNNAL	GDTGVRLLCK	RLSHPGCKLR	VLWLFGMDLN
1050	1060	1070					
KMTHSRLAAL	RVTKPYLDIG	C					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2687	1	973.4884	-3.97	2	62.0	11.3	2	144-159	R.NARLGECVNLSHRYTR.L	Carbamidomethyl: 7

Detailed Protein Report

Protein 422: 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 423: regulator of G-protein signaling 9-binding protein [Homo sapiens]

Accession:	gi|115496700	**Score:**	21.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	25.1
Database Date:	2015-11-30	**pI:**	7.8
		Sequence Coverage [%]:	15.3
		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 424: heat shock protein 75 kDa, mitochondrial isoform 2 [Homo sapiens]

Accession:	gi|440309857	**Score:**	21.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	74.2
Database Date:	2015-11-30	**pI:**	8.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	4.9
		No. of unique Peptides:	2

```
        10         20         30         40         50         60         70         80
MARELRALLL WGRRLRPLLR APALAAVPGG STSKHEFQAE TKKLLDIVAR SLYSEKEVFI RELISNASDA LEKLRHKLVS
        90        100        110        120        130        140        150        160
DGQALPEMEI HLQTNAEKGT ITIQDTGIGM TQEELVSNLG TIARSGSKAF LDALQNQAEA SSKIIGQFGV GFYSAFMVAD
       170        180        190        200        210        220        230        240
RVEVYSRSAA PGSLGYQWLS DGSGVFEIAE ASGVRTGTKI IIHLKSDCKE FSSEARVRDV VTKYSNFVSF PLYLNGRRMN
       250        260        270        280        290        300        310        320
TLQAIWMMDP KDVREWQHEE FYRYVAQAHD KPRYTLHYKT DAPLNIRSIF YVPDMKPSMF DVSRELGSSV ALYSRKVLIQ
       330        340        350        360        370        380        390        400
TKATDILPKW LRFIRGVVDS EDIPLNLSRE LLQESALIRK LRDVLQQRLI KFFIDQSKKD AEKYAKFFED YGLFMREGIV
       410        420        430        440        450        460        470        480
TATEQEVKED IAKLLRYESS ALPSGQLTSL SEYASRMRAG TRNIYYLCAP NRHLAEHSPY YEAMKKKDTE VLFCFEQFDE
       490        500        510        520        530        540        550        560
LTLLHLREFD KKKLISVETD IVVDHYKEEK FEDRSPAAEC LSEKETEELM AWMRNVLGSR VTNVKVTLRL DTHPAMVTVL
       570        580        590        600        610        620        630        640
EMGAARHFLR MQQLAKTQEE RAQLLQPTLE INPRHALIKK LNQLRASEPG LAQLLVDQIY ENAMIAAGLV DDPRAMVGRL
       650        660
NELLVKALER H
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
35	1	796.7750	-156.03	2	29.7	10.7	0	129-143	K.AFLDALQNQAEASSK.I	
2046	1	1073.4473	-50.14	2	53.9	10.7	2	380-396	K.DAEKYAKFFEDYGLFMR.E	Oxidation: 16

Detailed Protein Report

Protein 425: myotubularin-related protein 8 [Homo sapiens]

Accession:	gi|21361759	**Score:**	21.4
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
1132	1	956.7332	257.45	1	42.4	10.9	0	1-8	-.MDHITVPK.V	Oxidation: 1

Detailed Protein Report

Protein 426: **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

Quantitation

WD:WU **Median:** 0.53 **CV:** 4.81 % **No. of 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	Ratios
1134	1	984.4501	-53.47	2	42.9	11.3	1	544-559	K.HCFKGHCIWLTPDILK.R	Carbamidomethyl: 2	WD:WU 0.56
2148	1	766.2823	-164.03	2	55.4	10.0	2	1183-1194	R.RPSPYEKTRNQR.I		WD:WU 0.51

Detailed Protein Report

Protein 427: integrin beta-1-binding protein 2 [Homo sapiens]

Accession:	gi|6912438	**Score:**	21.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	38.4
Database Date:	2015-11-30	**pI:**	4.9
		Sequence Coverage [%]:	6.6
		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 428: **protein-arginine deiminase type-2 [Homo sapiens]**

Accession:	gi|122939159	**Score:**	21.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	75.5
Database Date:	2015-11-30	**pI:**	5.3
		Sequence Coverage [%]:	5.6
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MLRERTVRLQ YGSRVEAVYV LGTYLWTDVY SAAPAGAQTF SLKHSEHVWV EVVRDGEAEE VATNGKQRWL LSPSTTLRVT
        90        100        110        120        130        140        150        160
MSQASTEASS DKVTVNYYDE EGSIPIDQAG LFLTAIEISL DVDADRDGVV EKNNPKKASW TWGPEGQGAI LLVNCDRETP
       170        180        190        200        210        220        230        240
WLPKEDCRDE KVYSKEDLKD MSQMILRTKG PDRLPAGYEI VLYISMSDSD KVGVFYVENP FFGQRYIHIL GRRKLYHVVK
       250        260        270        280        290        300        310        320
YTGGSAELLF FVEGLCFPDE GFSGLVSIHV SLLEYMAQDI PLTPIFTDTV IFRIAPWIMT PNILPPVSVF VCCMKDNYLF
       330        340        350        360        370        380        390        400
LKEVKNLVEK TNCELKVCFQ YLNRGDRWIQ DEIEFGYIEA PHKGFPVVLD SPRDGNLKDF PVKELLGPDF GYVTREPLFE
       410        420        430        440        450        460        470        480
SVTSLDSFGN LEVSPPVTVN GKTYPLGRIL IGSSFPLSGG RRMTKVVRDF LKAQQVQAPV ELYSDWLTVG HVDEFMSFVP
       490        500        510        520        530        540        550        560
IPGTKKFLLL MASTSACYKL FREKQKDGHG EAIMFKGLGG MSSKRITINK ILSNESLVQE NLYFQRCLDW NRDILKKELG
       570        580        590        600        610        620        630        640
LTEQDIIDLP ALFKMDEDHR ARAFFPNMVN MIVLDKDLGI PKPFGPQVEE ECCLEMHVRG LLEPLGLECT FIDDISAYHK
       650        660        670
FLGEVHCGTN VRRKPFTFKW WHMVP
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
183	1	823.9125	-36.73	2	31.1	10.2	2	323-336	K.EVKNLVEKTNCELK.V	

Protein 429: **NACHT, LRR and PYD domains-containing protein 2 isoform 3 [Homo sapiens]**

Accession:	gi|291463280	**Score:**	21.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	117.8
Database Date:	2015-11-30	**pI:**	5.8
		Sequence Coverage [%]:	1.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
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
1270	1	419.0769	-336.69	2	44.6	11.0	0	864-870	K.FLCEGLR.Y	

Detailed Protein Report

Protein 430: sulfiredoxin-1 [Homo sapiens]

Accession:	gi|22129778	**Score:**	21.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	14.3
Database Date:	2015-11-30	**pI:**	9.1
		Sequence Coverage [%]:	12.4
		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 431: PREDICTED: zinc finger protein 556 isoform X1 [Homo sapiens]

Accession:	gi|530425435	**Score:**	21.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	51.5
Database Date:	2015-11-30	**pI:**	11.1
		Sequence Coverage [%]:	7.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDTVVFEDVV	VDFTLEEWAL	LNPAQRKLYR	DVMLETFKHL	ASVDNEAQLK	ASGSISQQDT	SGEKLSLKQK	IEKFTRKNIW
90	100	110	120	130	140	150	160
ASLLGKNWEE	HSVKDKHNTK	ERHLRNPRVE	RPCKSSKGNK	RGRTFRKTRN	CNRHLRKNCC	TSVRRYECSQ	CGKLFTHSSS
170	180	190	200	210	220	230	240
LIRHKRAHSG	QKLYKCKECG	KAFSRPSYLQ	THEKTHSGEK	PYACQSCGKT	FLRSHSLTEH	VRTHTGEKPY	ECGQCGKGFS
250	260	270	280	290	300	310	320
CPKSFRAHVM	MHAGGRPYEC	KHCGKAFRCQ	KSFRVHMIMH	AGGRPYECKQ	CGKAYCWATS	FQRHVRIHNG	EKPYKCGKCG
330	340	350	360	370	380	390	400
KAFGWPSSLH	KHARTHAKKK	PVSGGSVGKS	SARPRPSTDV	KSQTREKVYK	CETCGKTYGW	SSSLHKHERK	HTGEKPVNAA
410	420	430	440	450	460		
SVGKPSGGLC	SSKNVRTQIG	QKPSKCEKCG	KAFSCPKAFQ	GHVRSHTGKK	SCTSK		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1615	1	853.4020	-19.62	2	48.9	10.3	2	316-331	K.CGKCGKAFGWPSSLHK.H	

Detailed Protein Report

Protein 432: OTU domain-containing protein 7A [Homo sapiens]

Accession:	gi|18702331	**Score:**	21.3
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 433: **PREDICTED: probable global transcription activator SNF2L1 isoform X5 [Homo sapiens]**

Accession:	gi|578838748	**Score:**	21.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	121.1
Database Date:	2015-11-30	**pI:**	9.0
		Sequence Coverage [%]:	1.2
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 2.90 **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
966	1	711.3525	2.57	2	40.4	21.3	1	434-446	K.DIDVLNSSGKMDK.M		WD:WU 2.90

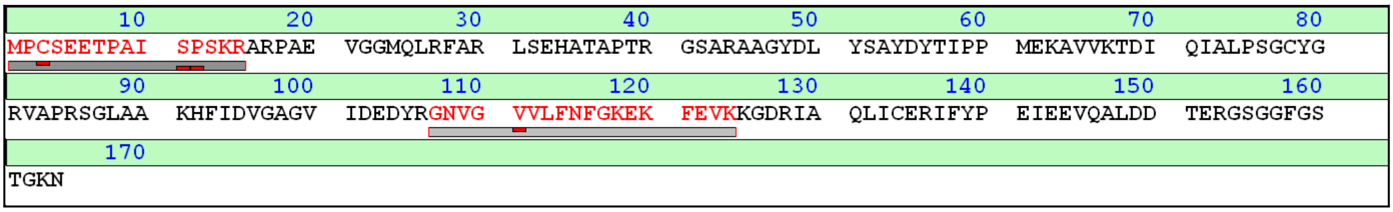
Detailed Protein Report

Protein 434: **deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial isoform 2 [Homo sapiens]**

Accession:	gi|4503423	**Score:**	21.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	17.7
Database Date:	2015-11-30	**pI:**	6.2
		Sequence Coverage [%]:	20.1
		No. of unique Peptides:	2

Quantitation

WD:WU **Median:** 0.88 **CV:** 31.40 % **No. of Peptides:** 2



```
        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		WD:WU	0.65
1576	1	671.0938	82.25	3	48.0	10.4	2	107-124	R.GNVGVVLFNFGKEKFEVK.K		WD:WU	1.19

Detailed Protein Report

Protein 435: DIS3-like exonuclease 1 isoform 2 [Homo sapiens]

Accession:	gi|19115966	**Score:**	21.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	111.0
Database Date:	2015-11-30	**pI:**	5.9
		Sequence Coverage [%]:	2.3
		No. of unique Peptides:	2

Quantitation

WD:WU	**Median:** 2.22	**CV:**	0.00 %	**No. of Peptides:**	1

Alias proteins:

Accession	Name	Description
gi|530405359	refseq_human (refseq_human_20140103.fasta)	PREDICTED: DIS3-like exonuclease 1 isoform X4 [Homo sapiens]
gi|530405355	refseq_human (refseq_human_20140103.fasta)	PREDICTED: DIS3-like exonuclease 1 isoform X2 [Homo sapiens]

10	20	30	40	50	60	70	80
MQTACQAVQH	QRGRRQYNKL	RNLLKDARHD	CILFANEFQQ	CCYLPRERGE	SMEKWQTRSI	YNAAVWYYHH	CQDRMPIVMV
90	100	110	120	130	140	150	160
TEDEEAIQQY	GSETEGVFVI	TFKNYLDNFW	PDLKAAHELC	DSILQSRRER	ENESQESHGK	EYPEHLPLEV	LEAGIKSGRY
170	180	190	200	210	220	230	240
IQGILNVNKH	RAQIEAFVRL	QGASSKDSDL	VSDILIHGMK	ARNRSIHGDV	VVVELLPKNE	WKGRTVALCE	NDCDDKASGE
250	260	270	280	290	300	310	320
SPSEPMPTGR	VVGILQKNWR	DYVVTFPSKE	EVQSQGKNAQ	KILVTPWDYR	IPKIRISTQQ	AETLQDFRVV	VRIDSWESTS
330	340	350	360	370	380	390	400
VYPNGHFVRV	LGRIGDLEGE	IATILVENSI	SVIPFSEAQM	CEMPVNTPES	PWKVSPEEEQ	KRKDLRKSHL	VFSIDPKGCE
410	420	430	440	450	460	470	480
DVDDTLSVRT	LNNGNLELGV	HIADVTHFVA	PNSYIDIEAR	TRATTYYLAD	RRYDMLPSVL	SADLCSLLGG	VDRYAVSIMW
490	500	510	520	530	540	550	560
ELDKASYEIK	KVWYGRTIIR	SAYKLFYEAA	QELLDGNLSV	VDDIPEFKDL	DEKSRQAKLE	ELVWAIGKLT	DIARHVRAKR
570	580	590	600	610	620	630	640
DGCGALELEG	VEVCVQLDDK	KNIHDLIPKQ	PLEVHETVAE	CMILANHWVA	KKIWESFPHQ	ALLRQHPPPH	QEFFSELREC
650	660	670	680	690	700	710	720
AKAKGFFIDT	RSNKTLADSL	DNANDPHDPI	VNRLLRSMAT	QAMSNALYFS	TGSCAEEEFH	HYGLALDKYT	HFTSPIRRYS
730	740	750	760	770	780	790	800
DIVVHRLLMA	AISKDKKMEI	KGNLFSNKDL	EELCRHINNR	NQAAQHSQKQ	STELFQCMYF	KDKDPATEER	CISDGVIYSI
810	820	830	840	850	860	870	880
RTNGVLLFIP	RFGIKGAAYL	KNKDGLVISC	GPDSCSEWKP	GSLQRFQNKI	TSTTTDGESV	TFHLFDHVTV	RISIQASRCH
890	900	910	920	930	940	950	960
SDTIRLEIIS	NKPYKIPNTE	LIHQSSPLLK	SELVKEVTKS	VEEAQLAQEV	KVNIIQEEYQ	EYRQTKGRSL	YTLLEEIRDL
970	980						
ALLDVSNNYG	I						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2734	1	639.3382	-4.54	2	62.6	10.8	1	709-718	K.YTHFTSPIRR.Y		
1921	1	655.2832	-155.36	2	52.4	10.4	2	812-823	R.FGIKGAAYLKNK.D		WD:WU 2.22

Detailed Protein Report

Protein 436: PREDICTED: protein Shroom2 isoform X1 [Homo sapiens]

Accession:	gi|578837883	**Score:**	21.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	176.2
Database Date:	2015-11-30	**pI:**	6.7
		Sequence Coverage [%]:	2.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEGAEPRARP	ERLAEAETRA	ADGGRLVEVQ	LSGGAPWGFT	LKGGREHGEP	LVITKIEEGS	KAAAVDKLLA	GDEIVGINDI
90	100	110	120	130	140	150	160
GLSGFRQEAI	CLVKGSHKTL	KLVVKRRSEL	GWRPHSWHAT	KFSDSHPELA	ASPFTSTSGC	PSWSGRHHAS	SSSHDLSSSW
170	180	190	200	210	220	230	240
EQTNLQRTLD	HFSSLGSVDS	LDHPSSRLSV	AKSNSSIDHL	GSHSKRDSAY	GSFSTSSSTP	DHTLSKADTS	SAENILYTVG
250	260	270	280	290	300	310	320
LWEAPRQGGR	QAQAAGDPQG	SEEKLSCFPP	RVPGDSGKGP	RPEYNAEPKL	AAPGRSNFGP	VWYVPDKKKA	PSSPPPPPPP
330	340	350	360	370	380	390	400
LRSDSFAATK	SHEKAQGPVF	SEAAAAQHFT	ALAQAQPRGD	RRPELTDRPW	RSAHPGSLGK	GSGGPGCPQE	AHADGSWPPS
410	420	430	440	450	460	470	480
KDGASSRLQA	SLSSSDVRFP	QSPHSGRHPP	LYSDHSPLCA	DSLGQEPGAA	SFQNDSPPQV	RGLSSCDQKL	GSGWQGPRPC
490	500	510	520	530	540	550	560
VQGDLQAAQL	WAGCWPSDTA	LGALESLPPP	TVGQSPRHHL	PQPEGPPDAR	ETGRCYPLDK	GAEGCSAGAQ	EPPRASRAEK
570	580	590	600	610	620	630	640
ASQRLAASIT	WADGESSRIC	PQETPLLHSL	TQEGKRRPES	SPEDSATRPP	PFDAHVGKPT	RRSDRFATTL	RNEIQMHRAK
650	660	670	680	690	700	710	720
LQKSRSTVAL	TAAGEAEDGT	GRWRAGLGGG	TQEGPLAGTY	KDHLKEAQAR	VLRATSFKRR	DLDPNPGDLY	PESLEHRMGD
730	740	750	760	770	780	790	800
PDTVPHFWEA	GLAQPPSSTS	GGPHPPRIGG	RRRFTAEQKL	KSYSEPEKMN	EVGLTRGYSP	HQHPRTSEDT	VGTFADRWKF
810	820	830	840	850	860	870	880
FEETSKPVPQ	RPAQKQALHG	IPRDKPERPR	TAGRTCEGTE	PWSRTTSLGD	SLNAHSAAEK	AGTSDLPRRL	GTFAEYQASW
890	900	910	920	930	940	950	960
KEQRKPLEAR	SSGRCHSADD	ILDVSLDPQE	RPQHVHGRSR	SSPSTDHYKQ	EASVELRRQA	GDPGEPREEL	PSAVRAEEGQ
970	980	990	1000	1010	1020	1030	1040
STPRQADAQC	REGSPGSQQH	PPSQKAPNPP	TFSELSHCRG	APELPREGRG	RAGTLPRDYR	YSEESTPADL	GPRAQSPGSP
1050	1060	1070	1080	1090	1100	1110	1120
LHARGQDSWP	VSSALLSKRP	APQRPPPPKR	EPRRYRATDG	APADAPVGVL	GRPFPTPSPA	SLDVYVARLS	LSHSPSVFSS
1130	1140	1150	1160	1170	1180	1190	1200
AQPQDTPKAT	VCERGSQHVS	GDASRPLPEA	LLPPKQQHLR	LQTATMETSR	SPSPQFAPQK	LTDKPPLLIQ	DEDSTRIERV
1210	1220	1230	1240	1250	1260	1270	1280
MDNNTTVKMV	PIKIVHSESQ	PEKESRQSLA	CPAEPPALPH	GLEKDQIKTL	STSEQFYSRF	CLYTRQGAEP	EAPHRAQPAE
1290	1300	1310	1320	1330	1340	1350	1360
PQPLGTQVPP	EKDRCTSPPG	LSYMKAKEKT	VEDLKSEELA	REIVGKDKSL	ADILDPSVKI	KTTMDLMEGI	FPKDEHLLEE
1370	1380	1390	1400	1410	1420	1430	1440
AQQRRKLLPK	IPSPRSTEER	KEEPSVPAAV	SLATNSTYYS	TSAPKAELLI	KMKDLQEQQE	HEEDSGSDLD	HDLSVKKELI
1450	1460	1470	1480	1490	1500	1510	1520
ESISRKLQVL	REARESLLED	VQANTVLGAE	VEAIVKGVCK	PSEFDKFRMF	IGDLDKVVNL	LLSLSGRLAR	VENALNNLDD
1530	1540	1550	1560	1570	1580	1590	1600
GASPGDRQSL	LEKQRVLIQQ	HEDAKELKEN	LDRRERIVFD	ILANYLSEES	LADYEHFVKM	KSALIIEQRE	LEDKIHLGEE
1610	1620						
QLKCLLDSLQ	PERGK						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2357	1	994.6851	148.86	2	57.7	11.2	2	1197-1213	R.IERVMDNNTTVKMVPIK.I	

Detailed Protein Report

Protein 437: supervillin isoform 1 [Homo sapiens]

Accession: gi|150417971
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 21.2
MW [kDa]: 200.7
pI: 6.5
Sequence Coverage [%]: 1.8
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MKRKERIARR	LEGIENDTQP	ILLQSCTGLV	THRLLEEDTP	RYMRASDPAS	PHIGRSNEEE	ETSDSSLEKQ	TRSKYCTETS
90	100	110	120	130	140	150	160
GVHGDSPYGS	GTMDTHSLES	KAERIARYKA	ERRRQLAEKY	GLTLDPEADS	EYLSRYTKSR	KEPDAVEKRG	GKSDKQEESS
170	180	190	200	210	220	230	240
RDASSLYPGT	ETMGLRTCAG	ESKDYALHVG	DGSSDPEVLL	NIENQRRGQE	LSATRQAHDL	SPAAESSSTF	SFSGRDSSFT
250	260	270	280	290	300	310	320
EVPRSPKHAH	SSSLQQAASR	SPSFGDPQLS	PEARPRCTSH	SETPTVDDEE	KVDERAKLSV	AAKRLLFREM	EKSFDEQNVP
330	340	350	360	370	380	390	400
KRRSRNTAVE	QRLRRLQDRS	LTQPITTEEV	VIAATLQASA	HQKALAKDQT	NEGKELAEQG	EPDSSTLSLA	EKLALFNKLS
410	420	430	440	450	460	470	480
QPVSKAISTR	NRIDTRQRRM	NARYQTQPVT	LGEVEQVQSG	KLIPFSPAVN	TSVSTVASTV	APMYAGDLRT	KPPLDHNASA
490	500	510	520	530	540	550	560
TDYKFSSSIE	NSDSPVRSIL	KSQAWQPLVE	GSENKGMLRE	YGETESKRAL	TGRDSGMEKY	GSFEEAEASY	PILNRAREGD
570	580	590	600	610	620	630	640
SHKESKYAVP	RRGSLERANP	PITHLGDEPK	EFSMAKMNAQ	GNLDLRDRLP	FEEKVEVENV	MKRKFSLRAA	EFGEPTSEQT
650	660	670	680	690	700	710	720
GTAAGKTIAQ	TTAPVSWKPQ	DSSEQPQEKL	CKNPCAMFAA	GEIKTPTGEG	LLDSPSKTMS	IKERLALLKK	SGEEDWRNRL
730	740	750	760	770	780	790	800
SRRQEGGKAP	ASSLHTQEAG	RSLIKKRVTE	SRESQMTIEE	RKQLITVREE	AWKTRGRGAA	NDSTQFTVAG	RMVKKGLASP
810	820	830	840	850	860	870	880
TAITPVASPI	CGKTRGTTPV	SKPLEDIEAR	PDMQLESDLK	LDRLETFLRR	LNNKVGGMHE	TVLTVTGKSV	KEVMKPDDDE
890	900	910	920	930	940	950	960
TFAKFYRSVD	YNMPRSPVEM	DEDFDVIFDP	YAPKLTSSVA	EHKRAVRPKR	RVQASKNPLK	MLAAREDLLQ	EYTEQRLNVA
970	980	990	1000	1010	1020	1030	1040
FMESKRMKVE	KMSSNSNFSE	VTLAGLASKE	NFSNVSLRSV	NLTEQNSNNS	AVPYKRLMLL	QIKGRRHVQT	RLVEPRASAL
1050	1060	1070	1080	1090	1100	1110	1120
NSGDCFLLLS	PHCCFLWVGE	FANVIEKAKA	SELATLIQTK	RELGCRATYI	QTIEEGINTH	THAAKDFWKL	LGGQTSYQSA
1130	1140	1150	1160	1170	1180	1190	1200
GDPKEDELYE	AAIIETNCIY	RLMDDKLVPD	DDYWGKIPKC	SLLQPKEVLV	FDFGSEVYVW	HGKEVTLAQR	KIAFQLAKHL
1210	1220	1230	1240	1250	1260	1270	1280
WNGTFDYENC	DINPLDPGEC	NPLIPRKGQG	RPDWAIFGRL	TEHNETILFK	EKFLDWTELK	RSNEKNPGEL	AQHKEDPRTD
1290	1300	1310	1320	1330	1340	1350	1360
VKAYDVTRMV	SMPQTTAGTI	LDGVNVGRGY	GLVEGHDRRQ	FEITSVSVDV	WHILEFDYSR	LPKQSIGQFH	EGDAYVVKWK
1370	1380	1390	1400	1410	1420	1430	1440
FMVSTAVGSR	QKGEHSVRAA	GKEKCVYFFW	QGRHSTVSEK	GTSALMTVEL	DEERGAQVQV	LQGKEPPCFL	QCFQGGMVVH
1450	1460	1470	1480	1490	1500	1510	1520
SGRREEEEEN	VQSEWRLYCV	RGEVPVEGNL	LEVACHCSSL	RSRTSMVVLN	VNKALIYLWH	GCKAQAHTKE	VGRTAANKIK
1530	1540	1550	1560	1570	1580	1590	1600
EQCPLEAGLH	SSSKVTIHEC	DEGSEPLGFW	DALGRRDRKA	YDCMLQDPGS	FNFAPRLFIL	SSSSGDFAAT	EFVYPARAPS
1610	1620	1630	1640	1650	1660	1670	1680
VVSSMPFLQE	DLYSAPQPAL	FLVDNHHEVY	LWQGWWPIEN	KITGSARIRW	ASDRKSAMET	VLQYCKGKNL	KKPAPKSYLI
1690	1700	1710	1720	1730	1740	1750	1760
HAGLEPLTFT	NMFPSWEHRE	DIAEITEMDT	EVSNQITLVE	DVLAKLCKTI	YPLADLLARP	LPEGVDPLKL	EIYLTDEDFE
1770	1780	1790					
FALDMTRDEY	NALPAWKQVN	LKKAKGLF					

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

	Cmpds.		[ppm]		[min]					
2904	1	974.3155	-109.14	2	65.1	10.9	0	1560-1576	K.AYDCMLQDPGSFNFAPR.L	Oxidation: 5

Detailed Protein Report

Protein 438: **zinc finger protein 425 [Homo sapiens]**

Accession:	gi|48717241	**Score:**	21.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	87.7
Database Date:	2015-11-30	**pI:**	10.6
		Sequence Coverage [%]:	3.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAEPASVTVT	FDDVALYFSE	QEWEILEKWQ	KQMYKQEMKT	NYETLDSLGY	AFSKPDLITW	MEQGRMLLIS	EQGCLDKTRR
90	100	110	120	130	140	150	160
TTSPPTDEQL	NMKNTGKLLC	FDDEGTPRTK	EEDCRLNGPQ	KQDLCAALRG	KERKILLAQT	ATFQSPSLRE	TEILNKKVSI
170	180	190	200	210	220	230	240
TAYDPDKKDL	RHKPRETPGR	LEIPTGPRCY	SCYVCRKVFQ	VRRDLLKHKR	SHSKSQLCRY	PKYKNSSRGK	SELRRTQRLL
250	260	270	280	290	300	310	320
CQKKRFQCSE	CEKSYFLKGS	LVTHQVVHTG	QRPYPCPECD	KTFRYRANLK	KHLCLHRGER	PFCCGECGRA	FVQQCELTEH
330	340	350	360	370	380	390	400
LRLHSGEKPF	QCPQCDRCFR	LKRGMKVHLT	QHSGKRPFHC	PECGRSFSRK	AALKTHQRTH	SEEKPFSCGE	CGRKFIYKIK
410	420	430	440	450	460	470	480
LDEHIRVHTG	EKPFSCPECN	KSFRLKRSLK	AHGLQHIGKR	PFQCPECSRG	FFWRNAMRAH	QRLHSEQKPF	PCAECGKRFT
490	500	510	520	530	540	550	560
RPSKLACHTR	VHDRQKEFPC	GECKKTFSQQ	SRLTQHLKVH	TTEKPFSCAE	CGRSFRRRAH	LTEHTRLHSG	EEPFQCPECD
570	580	590	600	610	620	630	640
KSFSWKASMK	FHQRMHRDEK	PFACGECDKT	YTHQSQLTEH	LRLHSGEKPY	QCPECEKTFR	LKGNLKSHLL	QHSGQKPFSC
650	660	670	680	690	700	710	720
VMCGKSFTQQ	YRLTEHIRVH	SGEKPFQCPE	CDKSYCIRGS	LKVHLYKHSG	ERPFQCPECG	KGFLQKRSLK	AHLCLHSGER
730	740	750	760				
PFSCDECGRS	FTYVGALKTH	IAVHAKEKPS	SL				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1689	1	1043.8593	-137.44	2	49.4	10.7	0	627-645	K.SHLLQHSGQKPFSCVMCGK.S	

Detailed Protein Report

Protein 439: von Willebrand factor A domain-containing protein 8 isoform a precursor [Homo sapiens]

Accession:	gi|57863271	**Score:**	21.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	214.7
Database Date:	2015-11-30	**pI:**	7.1
		Sequence Coverage [%]:	1.9
		No. of unique Peptides:	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MQSRLLLLGA	PGGHGGPASR	RMRLLLRQVV	QRRPGGDRQR	PEVRLLHAGS	GADTGDTVNI	GDVSYKLKIP	KNPELVPQNY
90	100	110	120	130	140	150	160
ISDSLAQSVV	QHLRWIMQKD	LLGQDVFLIG	PPGPLRRSIA	MQYLELTKRE	VEYIALSRDT	TETDLKQRRE	IRAGTAFYID
170	180	190	200	210	220	230	240
QCAVRAATEG	RTLILEGLEK	AERNVLPVLN	NLLENREMQL	EDGRFLMSAE	RYDKLLRDHT	KKELDSWKIV	RVSENFRVIA
250	260	270	280	290	300	310	320
LGLPVPRYSG	NPLDPPLRSR	FQARDIYYLP	FKDQLKLLYS	IGANVSAEKV	SQLLSFATTL	CSQESSTLGL	PDFPLDSLAA
330	340	350	360	370	380	390	400
AVQILDSFPM	MPIKHAIQWL	YPYSILLGHE	GKMAVEGVLK	RFELQDSGSS	LLPKEIVKVE	KMMENHVSQA	SVTIRIADKE
410	420	430	440	450	460	470	480
VTIKVPAGTR	LLSQPCASDR	FIQTLSHKQL	QAEMMQSHMV	KDICLIGGKG	CGKTVIAKNF	ADTLGYNIEP	IMLYQDMTAR
490	500	510	520	530	540	550	560
DLLQQRYTLP	NGDTAWRSSP	LVNAALEGKL	VLLDGIHRVN	AGTLAVLQRL	IHDRELSLYD	GSRLLREDRY	MRLKEELQLS
570	580	590	600	610	620	630	640
DEQLQKRSIF	PIHPSFRIIA	LAEPPVIGST	AHQWLGPEFL	TMFFFHYMKP	LVKSEEIQVI	KEKVPNVPQE	ALDKLLSFTH
650	660	670	680	690	700	710	720
KLRETQDPTA	QSLAASLSTR	QLLRISRRLS	QYPNENLHSA	VTKACLSRFL	PSLARSALEK	NLADATIEIN	TDDNLEPELK
730	740	750	760	770	780	790	800
DYKCEVTSGT	LRIGAVSAPI	YNAHEKMKVP	DVLFYDNIQH	VIVMEDMLKD	FLLGEHLLLV	GNQGVGKNKI	VDRFLHLLNR
810	820	830	840	850	860	870	880
PREYIQLHRD	TTVQTLTLQP	SVKDGLIVYE	DSPLVKAVKL	GHILVVDEAD	KAPTNVTCIL	KTLVENGEMI	LADGRRIVAN
890	900	910	920	930	940	950	960
SANVNGRENV	VVIHPDFRMI	VLANRPGFPF	LGNDFFGTLG	DIFSCHAVDN	PKPHSELEML	RQYGPNVPEP	ILQKLVAAFG
970	980	990	1000	1010	1020	1030	1040
ELRSLADQGI	INYPYSTREV	VNIVKHLQKF	PTEGLSSVVR	NVFDFDSYNN	DMREILINTL	HKYGIPIGAK	PTSVQLAKEL
1050	1060	1070	1080	1090	1100	1110	1120
TLPEQTFMGY	WTIGQARSGM	QKLLCPVETH	HIDIKGPALI	NIQEYPIERH	EERSLNFTEE	CASWRIPLDE	INIICDIATS
1130	1140	1150	1160	1170	1180	1190	1200
HENEQNTLYV	VTCNPASLYF	MNMTGKSGFF	VDFFDIFPRT	ANGVWHPFVT	VAPLGSPLKG	QVVLHEQQSN	VILLLDTTGR
1210	1220	1230	1240	1250	1260	1270	1280
ALHRLILPSE	KFTSKKPFWW	NKEEAETYKM	CKEFSHKNWL	VFYKEKGNSL	TVLDVLEGRT	HTISLPINLK	TVFLVAEDKW
1290	1300	1310	1320	1330	1340	1350	1360
LLVESKTNQK	YLLTKPAHIE	SEGSGVCQLY	VLKEEPPSTG	FGVTQETEFS	IPHKISSDQL	SSEHLSSAVE	QKIASPNRIL
1370	1380	1390	1400	1410	1420	1430	1440
SDEKNYATIV	VGFPDLMSPS	EVYSWKRPSS	LHKRSGTDTS	FYRGKKKRGT	PKQSNCVTLL	DTNQVVRILP	PGEVPLKDIY
1450	1460	1470	1480	1490	1500	1510	1520
PKDVTPPQTS	GYIEVTDLQS	KKLRYIPIPR	SESLSPYTTW	LSTISDTDAL	LAEWDKSGVV	TVDMGGHIRL	WETGLERLQR
1530	1540	1550	1560	1570	1580	1590	1600
SLMEWRNMIG	QDDRNMQITI	NRDSGEDVSS	PKHGKEDPDN	MPHVGGNTWA	GGTGGRDTAG	LGGKGGPYRL	DAGHTVYQVS
1610	1620	1630	1640	1650	1660	1670	1680
QAEKDAVPEE	VKRAAREMGQ	RAFQQRLKEI	QMSEYDAATY	ERFSGAVRRQ	VHSLRIILDN	LQAKGKERQW	LRHQATGELD
1690	1700	1710	1720	1730	1740	1750	1760
DAKIIDGLTG	EKAIYKRRGE	LEPQLGSPQQ	KPKRLRLVVD	VSGSMYRFNR	MDGRLERTME	AVCMVMEAFE	NYEEKFQYDI
1770	1780	1790	1800	1810	1820	1830	1840
VGHSGDGYNI	GLVPMNKIPK	DNKQRLEILK	TMHAHSQFCM	SGDHTLEGTE	HAIKEIVKEE	ADEYFVIVLS	DANLSRYGIH
1850	1860	1870	1880	1890	1900	1910	
PAKFAQILTR	DPQVNAFAIF	IGSLGDQATR	LQRTLPAGRS	FVAMDTKDIP	QILQQIFTST	MLSSV	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2188	1	958.6176	79.28	2	55.7	10.0	2	5-23	R.LLLLGAPGGHGGPASRRMR.L	

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Detailed Protein Report

Protein 440: **PREDICTED: multiple epidermal growth factor-like domains protein 6 isoform X4 [Homo sapiens]**

Accession:	gi|578798522	**Score:**	21.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	135.9
Database Date:	2015-11-30	**pI:**	5.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.0
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MGASRDRGLA ALWCLGLLGG LARVAGTHYR YLWRGCYPCH LGQAGYPVSA GDQRPDVDEC RTHNGGCQHR CVNTPGSYLC
        90        100        110        120        130        140        150        160
ECKPGFRLHT DSRTCLAINS CALGNGGCQH HCVQLTITRH RCQCRPGFQL QEDGRHCVRR SPCANRNGSC MHRCQVVRGL
       170        180        190        200        210        220        230        240
ARCECHVGYQ LAADGKACED VDECAAGLAQ CAHGCLNTQG SFKCVCHAGY ELGADGRQCY RIEMEIVNSC EANNGGCSHG
       250        260        270        280        290        300        310        320
CSHTSAGPLC TCPRGYELDT DQRTCIDVDD CADSPCCQQV CTNNPGGYEC GCYAGYRLSA DGCGCEDVDE CASSRGGCEH
       330        340        350        360        370        380        390        400
HCTNLAGSFQ CSCEAGYRLH EDRRGCSPLE EPMVDLDGEL PFVRPLPHIA VLQDELPQLF QDDDVGADEE EAELRGEHTL
       410        420        430        440        450        460        470        480
TEKFVCLDDS FGHDCSLTCD DCRNGGTCLL GLDGCDCPEG WTGLICNETC PPDTFGKNCS FSCSCQNGGT CDSVTGACRC
       490        500        510        520        530        540        550        560
PPGVSGTNCE DGCPKGYYGK HCRKKCNCAN RGRCHRLYGA CLCDPGLYGR FCHLTCPPWA FGPGCSEECQ CVQPHTQSCD
       570        580        590        600        610        620        630        640
KRDGSCSCKA GFRGERCQAE CELGYFGPGC WQACTCPVGV ACDSVSGECG KRCPAGFQGE DCGQECPVGT FGVNCSSSCS
       650        660        670        680        690        700        710        720
CGGAPCHGVT GQCRCPPGRT GEDCEAECPQ GHFGPGCEQR CQCQHGAACD HVSGACTCPA GWRGTFCEHA CPAGFFGLDC
       730        740        750        760        770        780        790        800
RSACNCTAGA ACDAVNGSCL CPAGRRGPRC AETCPAHTYG HNCSQACACF NGASCDPVHG QCHCAPGWMG PSCLQACPAG
       810        820        830        840        850        860        870        880
LYGDNCRHSC LCQNGGTCDP VSGHCACPEG WAGLACEKEC LPRDVRAGCR HSGGCLNGGL CDPHTGRCLC PAGWTGDKCQ
       890        900        910        920        930        940        950        960
SPCLRGWFGE ACAQRCSCPP GAACHHVTGA CRCPPGFTGS GCEQACPPGS FGEDCAQMCQ CPGENPACHP ATGTCSCAAG
       970        980        990       1000       1010       1020       1030       1040
YHGPSCQQRC PPGRYGPGCE QLCGCLNGGS CDAATGACRC PTGFLGTDCN LTCPQGRFGP NCTHVCGCGQ GAACDPVTGT
      1050       1060       1070       1080       1090       1100       1110       1120
CLCPPGRAGV RCERGCPQNR FGVGCEHTCS CRNGGLCHAS NGSCSCGLGW TGRHCELACP PGRYGAACHL ECSCHNNSTC
      1130       1140       1150       1160       1170       1180       1190       1200
EPATGTCRCG PGFYGQACEH PCPPGFHGAG CQGLCWCQHG APCDPISGRC LCPAGFHGHF CERGCEPGSF GEGCHQRCDC
      1210       1220       1230       1240       1250       1260       1270       1280
DGGAPCDPVT GLCLCPPGRS GATCNLDCRR GQFGPSCTLH CDCGGGADCD PVSGQCHCVD GYMGPTCREG GPLRLPENPS
      1290       1300       1310
LAQGSAGTLP ASSRPTSRSG GPARH
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
12	1	1103.5102	57.86	2	29.4	10.6	0	1198-1219	R.CDCDGGAPCDPVTGLCLCPPGR.S	Carbamidomethyl: 16

Detailed Protein Report

Protein 441: voltage-dependent R-type calcium channel subunit alpha-1E isoform 2 [Homo sapiens]

Accession:	gi|329663531	**Score:**	21.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	254.4
Database Date:	2015-11-30	**pI:**	9.3
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MARFGEAVVA	RPGSGDGDSD	QSRNRQGTPV	PASGQAAAYK	QTKAQRARTM	ALYNPIPVRQ	NCFTVNRSLF	IFGEDNIVRK
90	100	110	120	130	140	150	160
YAKKLIDWPP	FEYMILATII	ANCIVLALEQ	HLPEDDKTPM	SRRLEKTEPY	FIGIFCFEAG	IKIVALGFIF	HKGSYLRNGW
170	180	190	200	210	220	230	240
NVMDFIVVLS	GILATAGTHF	NTHVDLRTLR	AVRVLRPLKL	VSGIPSLQIV	LKSIMKAMVP	LLQIGLLLFF	AILMFAIIGL
250	260	270	280	290	300	310	320
EFYSGKLHRA	CFMNNSGILE	GFDPPHPCGV	QGCPAGYECK	DWIGPNDGIT	QFDNILFAVL	TVFQCITMEG	WTTVLYNTND
330	340	350	360	370	380	390	400
ALGATWNWLY	FIPLIIIGSF	FVLNLVLGVL	SGEFAKERER	VENRRAFMKL	RRQQQIEREL	NGYRAWIDKA	EEVMLAEENK
410	420	430	440	450	460	470	480
NAGTSALEVL	RRATIKRSRT	EAMTRDSSDE	HCVDISSVGT	PLARASIKSA	KVDGVSYFRH	KERLLRISIR	HMVKSQVFYW
490	500	510	520	530	540	550	560
IVLSLVALNT	ACVAIVHHNQ	PQWLTHLLYY	AEFLFLGLFL	LEMSLKMYGM	GPRLYFHSSF	NCFDFGVTVG	SIFEVVWAIF
570	580	590	600	610	620	630	640
RPGTSFGISV	LRALRLLRIF	KITKYWASLR	NLVVSLMSSM	KSIISLLFLL	FLFIVVFALL	GMQLFGGRFN	FNDGTPSANF
650	660	670	680	690	700	710	720
DTFPAAIMTV	FQILTGEDWN	EVMYNGIRSQ	GGVSSGMWSA	IYFIVLTLFG	NYTLLNVFLA	IAVDNLANAQ	ELTKDEQEEE
730	740	750	760	770	780	790	800
EAFNQKHALQ	KAKEVSPMSA	PNMPSIERER	RRRHHMSVWE	QRTSQLRKHM	QMSSQEALNR	EEAPTMNPLN	PLNPLSSLNP
810	820	830	840	850	860	870	880
LNAHPSLYRR	PRAIEGLALG	LALEKFEEER	ISRGGSLKGD	GGDRSSALDN	QRTPLSLGQR	EPPWLARPCH	GNCDPTQQEA
890	900	910	920	930	940	950	960
GGGEAVVTFE	DRARHRQSQR	RSRHRRVRTE	GKESSSASRS	RSASQERSLD	EAMPTEGEKD	HELRGNHGAK	EPTIQEERAQ
970	980	990	1000	1010	1020	1030	1040
DLRRTNSLMV	SRGSGLAGGL	DEADTPLVLP	HPELEVGKHV	VLTEQEPEGS	SEQALLGNVQ	LDMGRVISQS	EPDLSCITAN
1050	1060	1070	1080	1090	1100	1110	1120
TDKATTESTS	VTVAIPDVDP	LVDSTVVHIS	NKTDGEASPL	KEAEIREDEE	EVEKKKQKKE	KRETGKAMVP	HSSMFIFSTT
1130	1140	1150	1160	1170	1180	1190	1200
NPIRRACHYI	VNLRYFEMCI	LLVIAASSIA	LAAEDPVLTN	SERNKVLRYF	DYVFTGVFTF	EMVIKMIDQG	LILQDGSYFR
1210	1220	1230	1240	1250	1260	1270	1280
DLWNILDFVV	VVGALVAFAL	ANALGTNKGR	DIKTIKSLRV	LRVLRPLKTI	KRLPKLKAVF	DCVVTSLKNV	FNILIVYKLF
1290	1300	1310	1320	1330	1340	1350	1360
MFIFAVIAVQ	LFKGKFFYCT	DSSKDTEKEC	IGNYVDHEKN	KMEVKGREWK	RHEFHYDNII	WALLTLFTVS	TGEGWPQVLQ
1370	1380	1390	1400	1410	1420	1430	1440
HSVDVTEEDR	GPSRSNRMEM	SIFYVVYFVV	FPFFFVNIFV	ALIIITFQEQ	GDKMMEECSL	EKNERACIDF	AISAKPLTRY
1450	1460	1470	1480	1490	1500	1510	1520
MPQNRHTFQY	RVWHFVVSPS	FEYTIMAMIA	LNTVVLMMKY	YSAPCTYELA	LKYLNIAFTM	VFSLECVLKV	IAFGFLNYFR
1530	1540	1550	1560	1570	1580	1590	1600
DTWNIFDFIT	VIGSITEIIL	TDSKLVNTSG	FNMSFLKLFR	AARLIKLLRQ	GYTIRILLWT	FVQSFKALPY	VCLLIAMLFF
1610	1620	1630	1640	1650	1660	1670	1680
IYAIIGMQVF	GNIKLDEESH	INRHNNFRSF	FGSLMLLFRS	ATGEAWQEIM	LSCLGEKGCE	PDTTAPSGQN	ENERCGTDLA
1690	1700	1710	1720	1730	1740	1750	1760
YVYFVSFIFF	CSFLMLNLFV	AVIMDNFEYL	TRDSSILGPH	HLDEFVRVWA	EYDRAACGRI	HYTEMYEMLT	LMSPPLGLGK
1770	1780	1790	1800	1810	1820	1830	1840
RCPSKVAYKR	LVLMNMPVAE	DMTVHFTSTL	MALIRTALDI	KIAKGGADRQ	QLDSELQKET	LAIWPHLSQK	MLDLLVPMPK
1850	1860	1870	1880	1890	1900	1910	1920
ASDLTVGKIY	AAMMIMDYYK	QSKVKKQRQQ	LEEQKNAPMF	QRMEPSSLPQ	EIIANAKALP	YLQQDPVSGL	SGRSGYPSMS
1930	1940	1950	1960	1970	1980	1990	2000
PLSPQDIFQL	ACMDPADDGQ	FQERQSLVVT	DPSSMRRSFS	TIRDKRSNSS	WLEEFSMERS	SENTYKSRRR	SYHSSLRLSA
2010	2020	2030	2040	2050	2060	2070	2080
HRLNSDSGHK	SDTHRSGGRE	RGRSKERKHL	LSPDVSRCNS	EERGTQADWE	SPERRQSRSP	SEGRSQTPNR	QGTGSLSESS
2090	2100	2110	2120	2130	2140	2150	2160
IPSVSDTSTP	RRSRRQLPPV	PPKPRPLLSY	SSLIRHAGSI	SPPADGSEEG	SPLTSQALES	NNACLTESSN	SPHPQQSQHA
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2785	1	973.5222	64.95	2	63.4	10.8	1	734-750	K.EVSPMSAPNMPSIERER.R	Oxidation: 10

Detailed Protein Report

Protein 442: glycosyltransferase-like domain-containing protein 1 isoform d [Homo sapiens]

Accession:	gi|545746399	**Score:**	21.0
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 [%]:**	10.6
		No. of unique Peptides:	2

Quantitation

WD:WU **Median:** 0.72 **CV:** 0.00 % **No. of Peptides:** 1

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	Ratios	
48	1	518.2542	17.55	3	29.5	10.4	1	1-13	-.MESFLTSMGKFMK.L	Oxidation: 1	WD:WU	0.72
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 443: 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

Quantitation

WD:WU **Median:** 0.64 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MEKTKTKQGE	NEHMPVNNPS	TQIYQLQALA	SELKTGFTEA	MQELSRIQHG	EYALEEKVKS	CRCSMEEKVT	EMKNSLNYFK
90	100	110	120	130	140	150	160
EELSNAMSMI	QAITSKQEEM	QQKIEQLQQE	KRRESRKVKA	KKTQKEEHSS	QAGPAQAQGS	PFRSINIPEP	VLPSEDFTNL
170	180	190	200	210	220	230	240
LPSQAYEKAQ	ESRSVHVGDS	NVKGMMGPGV	NPTTPEAEEN	LKSCLSADIQ	SKGHLPSGMW	RQPKDGKEWG	EEYVTKDHPD
250	260	270	280	290	300	310	320
KLKEAGQGRH	SSLENVLCET	SLAAKRQTVA	LELLESERKY	VINISLILKI	KATFQGSDGK	RNSKERSLFP	GSLRYLVQQH
330	340	350	360	370	380	390	400
LDLLHALQER	VLKWPRQGVL	GDLFLKLTND	ENNFLDYYVA	YLRDLPECIS	LVHVVVLKEG	DEEIKSDIYT	LFFHIVQRIP
410	420	430	440	450	460	470	480
EYLIHLQNVL	KFTEQEHPDY	YLLLVCVQRL	RVFISHYTLL	FQCNEDLLIQ	KRKKLKKSSM	AKLYKGLASQ	CANAGQDASP
490	500	510	520	530	540	550	560
TAGPEAVRDT	GIHSEELLQP	YPSAPSSGPA	ITHLMPPVKK	SQQQQSLMES	MQPGKPSDWE	LEGRKHERPE	SLLAPTQFCA
570	580	590	600	610	620	630	640
AEQDVKALAG	PLQAIPEMDF	ESSPAEPLGN	VERSLRAPAE	LLPDARGFVP	AAYEEFEYGG	EIFALPAPYD	EEPFQAPALF
650	660	670	680	690	700	710	720
ENCSPASSES	SLDICFLRPV	SFAMEAERPE	HPLQPLPKSA	TSPAGSSSAY	KLEAAAQAHG	KAKPLSRSLK	EFPRAPPADG
730	740	750	760	770	780	790	800
VAPRLYSTRS	SSGGRAPIKA	ERAAQAHGPA	AAAVAARGAS	RTFFPQQRSQ	SEKQTYLEVR	REMHLEDTTR	FCPKEERESE
810	820	830	840	850	860	870	880
QTSFSDQNPR	QDQKGGFRSS	FRKLFKKKSS	GSEYREKTNE	NPSMDPSPTK	QDFFRNRLAL	ANDLDQGTAV	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
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		WD:WU 0.64

Detailed Protein Report

Protein 444: spermatogenesis-associated protein 31E1 [Homo sapiens]

Accession:	gi|155029550	**Score:**	20.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	157.0
Database Date:	2015-11-30	**pI:**	10.3
		Sequence Coverage [%]:	1.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGNLVIPLGK	GRAGRVESGQ	RIPPPAPRPS	VECTGDDIAL	QMEKMLFPLK	SPSATWLSPS	STPWMMDFIL	TSVCGLVLLF
90	100	110	120	130	140	150	160
LLLLYVHSDP	PSPPPGRKRS	SREPQRERSG	RSRSRKISAL	KACRILLREL	EETRDLNYLL	ESHLRKLAGE	GSSHLPLGGD
170	180	190	200	210	220	230	240
PLGDVCKPVP	AKAHQPHGKC	MQDPSPASLS	PPAPPAPLAS	TLSPGPMTFS	EPFGPHSTLS	ASGPPEPLLP	LKCPATQPHV
250	260	270	280	290	300	310	320
VFPPSPQPHG	PLASSPPPPD	SSLAGLQCGS	TTCPVPQSSP	LHNQVLPPPT	RVISGLGCSS	DPIWDLYCWR	EAATTWGLST
330	340	350	360	370	380	390	400
YSHGKSQPRH	LPDHTSEASF	WGDPTPKHME	VGGCTFIHPD	VQKLLETLIA	KRALMKMWQE	KERKRADHPH	MTSLGKEWDI
410	420	430	440	450	460	470	480
TTLNPFWNVS	TQPQQLPRPQ	QVSDATTVGN	HLQQKRSQLF	WDLPSLNSES	LATTVWVSRN	PSSQNAHSVP	LDKASTSLPG
490	500	510	520	530	540	550	560
EPEVEASSQL	SQAPPQPHHM	AQPQHFTPAW	PQSQPPPLAE	IQTQAHLSPP	VPSLGCSSPP	QIRGCGASYP	TSQERTQSVI
570	580	590	600	610	620	630	640
PTGKEYLEWP	LKKRPKWKRV	LPSLLKKSQA	VLSQPTAHLP	QERPASWSPK	SAPILPGVVT	SPELPEHWWQ	GRNAIHQEQS
650	660	670	680	690	700	710	720
CGPPSRLQAS	GDLLQPDGEF	PGRPQSQAED	TQQALLPSQP	SDFAGKGRKD	VQKTGFRSSG	RFSDKGCLGS	KLGPDPSRDQ
730	740	750	760	770	780	790	800
GSGRTSVKAL	DEDKEAEGDL	RRSWKYQSVS	STPRDPDKEH	LENKLQIHLA	RKVGEIKEGW	IPMPVRRSWL	MAKCAVPKSD
810	820	830	840	850	860	870	880
THRKPGKLAS	WRGGKAHVNT	SQELSFLHPC	TQQILEVHLV	RFCVRHSWGT	DLQSLEPINV	WSGEAQAPPF	PQSTFTPWAS
890	900	910	920	930	940	950	960
WVSRVESVPK	VPIFLGKRPQ	NGPGDNRTTS	KSVPTVSGPL	AAPPPEQEGV	QRPPRGSQSA	DTHGRSEAFP	TGHKGRGCSQ
970	980	990	1000	1010	1020	1030	1040
PPTCSLVGRT	WQSRTVLESG	KPKPRLEGSM	GSEMAGNEAW	LESESMSPGD	PCSSRALQVL	SIGSQWARAE	DALQALKVGE
1050	1060	1070	1080	1090	1100	1110	1120
KPPTWEVTLG	ASVRASSGSV	QEDLRSTGAL	GTTGNPSASS	VCVAQDPEQL	HLKAQVVSEI	ALIVQVDSEE	QLPGRAPGIL
1130	1140	1150	1160	1170	1180	1190	1200
LQDGATGLCL	PGRHMDMLTA	ADRLPTQAPL	STSQSVSGKN	MTASQGPCAL	LWKGGDSPGQ	QEPGSPKAKA	PQKSQKTLGC
1210	1220	1230	1240	1250	1260	1270	1280
ADKGEAHRRP	RTGEQGHRSK	GPRTSEASGR	SHPAQAREIG	DKQERKYNQL	QLEKGQTPPE	SHFQRKISHH	PQGLHPRKGG
1290	1300	1310	1320	1330	1340	1350	1360
TRWEDVLQKG	KPGADAFQSW	GSGPPRQFMD	CMADKAWTIS	RVVGQILVDK	LGLQWGRGPS	EVNRHKGDFR	AQENVPSCCH
1370	1380	1390	1400	1410	1420	1430	1440
RGHCHQERSR	EMRALACSPK	ATPKGHHCPV	KNRGIRDRDS	SWAPPPREPV	SPAGPHHHRP	RMASTSGGPH	PQLQELMSAQ
1450							
RCLAS							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2055	1	643.7814	-75.01	2	54.1	10.5	1	706-718	K.GCLGSKLGPDPSR.D	

Detailed Protein Report

Protein 445: PREDICTED: A-kinase anchor protein 12 isoform X3 [Homo sapiens]

Accession:	gi|530384249	**Score:**	20.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	180.9
Database Date:	2015-11-30	**pI:**	4.3
		Sequence Coverage [%]:	0.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MVGQRDSEDV	SKRDSDKEMA	TKSAVVHDIT	DDGQEETPEI	IEQIPSSESN	LEELTQPTES	QANDIGFKKV	FKFVGFKFTV
90	100	110	120	130	140	150	160
KKDKTEKPDT	VQLLTVKKDE	GEGAAGAGDH	KDPSLGAGEA	ASKESEPKQS	TEKPEETLKR	EQSHAEISPP	AESGQAVEEC
170	180	190	200	210	220	230	240
KEEGEEKQEK	EPSKSAESPT	SPVTSETGST	FKKFFTQGWA	GWRKKTSFRK	PKEDEVEASE	KKKEQEPEKV	DTEEDGKAEV
250	260	270	280	290	300	310	320
ASEKLTASEQ	AHPQEPAESA	HEPRLSAEYE	KVELPSEEQV	SGSQGPSEEK	PAPLATEVFD	EKIEVHQEEV	VAEVHVSTVE
330	340	350	360	370	380	390	400
ERTEEQKTEV	EETAGSVPAE	ELVEMDAEPQ	EAEPAKELVK	LKETCVSGED	PTQGADLSPD	EKVLSKPPEG	VVSEVEMLSS
410	420	430	440	450	460	470	480
QERMKVQGSP	LKKLFTSTGL	KKLSGKKQKG	KRGGGDEESG	EHTQVPADSP	DSQEEQKGES	SASSPEEPEE	ITCLEKGLAE
490	500	510	520	530	540	550	560
VQQDGEAEEG	ATSDGEKKRE	GVTPWASFKK	MVTPKKRVRR	PSESDKEDEL	DKVKSATLSS	TESTASEMQE	EMKGSVEEPK
570	580	590	600	610	620	630	640
PEEPKRKVDT	SVSWEALICV	GSSKKRARRG	SSSDEEGGPK	AMGGDHQKAD	EAGKDKETGT	DGILAGSQEH	DPGQGSSSPE
650	660	670	680	690	700	710	720
QAGSPTEGEG	VSTWESFKRL	VTPRKKSKSK	LEEKSEDSIA	GSGVEHSTPD	TEPGKEESWV	SIKKFIPGRR	KKRPDGKQEQ
730	740	750	760	770	780	790	800
APVEDAGPTG	ANEDDSDVPA	VVPLSEYDAV	EREKMEAQQA	QKSAEQPEQK	AATEVSKELS	ESQVHMMAAA	VADGTRAATI
810	820	830	840	850	860	870	880
IEERSPSWIS	ASVTEPLEQV	EAEAALLTEE	VLEREVIAEE	EPPTVTEPLP	ENREARGDTV	VSEAELTPEA	VTAAETAGPL
890	900	910	920	930	940	950	960
GAEEGTEASA	AEETTEMVSA	VSQLTDSPDT	TEEATPVQEV	EGGVPDIEEQ	ERRTQEVLQA	VAEKVKEESQ	LPGTGGPEDV
970	980	990	1000	1010	1020	1030	1040
LQPVQRAEAE	RPEEQAEASG	LKKETDVVLK	VDAQEAKTEP	FTQGKVVGQT	TPESFEKAPQ	VTESIESSEL	VTTCQAETLA
1050	1060	1070	1080	1090	1100	1110	1120
GVKSQEMVME	QAIPPDSVET	PTDSETDGST	PVADFDAPGT	TQKDEIVEIH	EENEVASGTQ	SGGTEAEAVP	AQKERPPAPS
1130	1140	1150	1160	1170	1180	1190	1200
SFVFQEETKE	QSKMEDTLEH	TDKEVSVETV	SILSKTEGTQ	EADQYADEKT	KDVPFFEGLE	GSIDTGITVS	REKVTEVALK
1210	1220	1230	1240	1250	1260	1270	1280
GEGTEEAECK	KDDALELQSH	AKSPPSPVER	EMVVQVEREK	TEAEPTHVNE	EKLEHETAVT	VSEEVSKQLL	QTVNVPIIDG
1290	1300	1310	1320	1330	1340	1350	1360
AKEVSSLEGS	PPPCLGQEEA	VCTKIQVQSS	EASFTLTAAA	EEEKVLGETA	NILETGETLE	PAGAHLVLEE	KSSEKNEDFA
1370	1380	1390	1400	1410	1420	1430	1440
AHPGEDAVPT	GPDCQAKSTP	VIVSATTKKG	LSSDLEGEKT	TSLKWKSDEV	DEQVACQEVK	VSVAIEDLEP	ENGILELETK
1450	1460	1470	1480	1490	1500	1510	1520
SSKLVQNIIQ	TAVDQFVRTE	ETATEMLTSE	LQTQAHVIKA	DSQDAGQETE	KEGEEPQASA	QDETPITSAK	EESESTAVGQ
1530	1540	1550	1560	1570	1580	1590	1600
AHSDISKDMS	EASEKTMTVE	VEGSTVNDQQ	LEEVVLPSEE	EGGGAGTKSV	PEDDGHALLA	ERIEKSLVEP	KEDEKGDDVD
1610	1620	1630	1640	1650	1660	1670	1680
DPENQNSALA	DTDASGGLTK	ESPDTNGPKQ	KEKEDAQEVE	LQEGKVHSES	DKAITPQAQE	ELQKQERESA	KSELTES

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2985	2	703.3668	-23.06	2	66.1	20.9	2	498-509	K.KREGVTPWASFK.K	

Detailed Protein Report

Protein 446: polycystic kidney disease protein 1-like 2 isoform d [Homo sapiens]

Accession:	gi|509155833	**Score:**	20.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	197.3
Database Date:	2015-11-30	**pI:**	6.0
		Sequence Coverage [%]:	1.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGEDSPVAMF	SWYLDNTPTE	QAEPLLDACR	LRGFWPRSLT	LLQSNTSTLL	LNSSFLQSRG	EVIRIRATAL	TRHAYGEDTY
90	100	110	120	130	140	150	160
VISTVPPREV	PACTIAPEEG	TVLTSFAIFC	NASTALGPLE	FCFCLESGSC	LHCGPEPALP	SVYLPLGEEN	NDFVLTVVIS
170	180	190	200	210	220	230	240
ATNRAGDTQQ	TQAMAKVALG	DTCVEDVAFQ	AAVSEKIPTA	LQGEGGPEQL	LQLAKAVSSM	LNQEHESQGS	GQSLSIDVRQ
250	260	270	280	290	300	310	320
KVREHVLGSL	SAVTTGLEDV	QRVQELAEVL	REVTCRSKEL	TPSAQWEASL	ALQHASEALL	TVSAKARPED	QRRQAATRDL
330	340	350	360	370	380	390	400
FQAVGSVLEA	SLSNRPEEPA	EASSSQIATV	LRLLRVMEHV	QTTLLLGKLP	GGLPAMLATP	SISVYTNRIQ	PWSWQGSSLR
410	420	430	440	450	460	470	480
PDAADSATFM	LPAASSLSSL	EGGQEPVDIK	IMSFPKSPFP	ARSHFDVSGT	VGGLRVTSPS	GQLIPVKNLS	ENIEILLPRH
490	500	510	520	530	540	550	560
SQRHSQPTVL	NLTSPEALWV	NVTSGEATLG	IQLHWRPDIA	LTLSLGYGYH	PNKSSYDAQT	HLVPMVAPDE	LPTWILSPQD
570	580	590	600	610	620	630	640
LRFGEGVYYL	TVVPESDLEP	APGRDLTVGI	TTFLSHCVFW	DEVQETWDDS	GCQVGPRTSP	YQTHCLCNHL	TFFGSTFLVM
650	660	670	680	690	700	710	720
SNAINIHQTA	ELFATFEDNP	VVVTTVGCLC	VVYVLVVIWA	RRKDAQDQAK	VKVTVLEDND	PFAQYHYLVT	VYTGHRRGAA
730	740	750	760	770	780	790	800
TSSKVTVTLY	GLDGEREPHH	LADPDTPVFE	RGAVDAFLLS	TLFPLGELRS	LRLWHDNSGD	RPSWYVSRVL	VYDLVMDRKW
810	820	830	840	850	860	870	880
YFLCNSWLSI	NVGDCVLDKV	FPVATEQDRK	QFSHLFFMKT	SAGFQDGHIW	YSIFSRCARS	SFTRVQRVSC	CFSLLLCTML
890	900	910	920	930	940	950	960
TSIMFWGVPK	DPAEQKMDLG	KIEFTWQEVM	IGLESSILMF	PINLLIVQIF	QNTRPRVAKE	QNTGKWDRGS	PNLTPSPQPM
970	980	990	1000	1010	1020	1030	1040
EDGLLTPEAV	TKDVSRIVSS	LFKALKVPSP	ALGWDSVNLM	DINSLLALVE	DVIYPQNTSG	QVFWEEAKKR	EDPVTLTLGS
1050	1060	1070	1080	1090	1100	1110	1120
SEMKEKSQCP	KPKAARSGPW	KDSAYRQCLY	LQLEHVEQEL	RLVGPRGFSQ	PHSHAQALRQ	LQTLKGGLGV	QPGTWAPAHA
1130	1140	1150	1160	1170	1180	1190	1200
SALQVSKPPQ	GLPWWCILVG	WLLVAATSGV	AAFFTMLYGL	HYGRASSLRW	LISMAVSFVE	SMFVTQPLKV	LGFAAFFALV
1210	1220	1230	1240	1250	1260	1270	1280
LKRVDDEEDT	VAPLPGHLLG	PDPYALFRAR	RNSSRDVYQP	PLTAAIEKMK	TTHLKEQKAF	ALIREILAYL	GFLWMLLLVA
1290	1300	1310	1320	1330	1340	1350	1360
YGQRDPSAYH	LNRHLQHSFT	RGFSGVLGFR	EFFKWANTTL	VSNLYGHPPG	FITDGNSKLV	GSAQIRQVRV	QESSCPLAQQ
1370	1380	1390	1400	1410	1420	1430	1440
PQAYLNGCRA	PYSLDAEDMA	DYGEGWNATT	LSEWQYQSQD	QRQGYPIWGK	LTVYRGGGYV	VPLGTDRQST	SRILRYLFDN
1450	1460	1470	1480	1490	1500	1510	1520
TWLDALTRAV	FVESTVYNAN	VNLFCIVTLT	LETSALGTFF	THAALQSLRL	YPFTDGWHPF	VVAAELIYFL	FLLYYMVVQG
1530	1540	1550	1560	1570	1580	1590	1600
KRMSKETWGY	FCSKWNLLEL	AIILASWSAL	AVFVKRAVLA	ERDLQRCRNH	REEGISFSET	AAADAALGYI	IAFLVLLSTV
1610	1620	1630	1640	1650	1660	1670	1680
KLWHLLRLNP	KMNMITAALR	RAWGDISGFM	IVILTMLLAY	SIASNLIFGW	KLRSYKTLFD	AAETMVSLQL	GIFNYEEVLD
1690	1700	1710	1720	1730	1740	1750	1760
YSPVLGSFLI	GSCIVFMTFV	VLNLFISVIL	VAFSEEQKYY	QLSEEGEIVD	LLLMKILSFL	GIKSKREEPG	SSREQPGSLS
1770	1780						
QTRHSRPAQA	LPKD						

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

	Cmpds.		[ppm]		[min]					
2783	1	616.3560	86.02	2	63.3	10.8	1	891-901	K.DPAEQKMDLGK.I	

Detailed Protein Report

Protein 447: **PREDICTED: zinc finger homeobox protein 3 isoform X1 [Homo sapiens]**

Accession:	gi|530423920	**Score:**	20.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	404.0
Database Date:	2015-11-30	**pI:**	5.8
		Sequence Coverage [%]:	0.8
		No. of unique Peptides:	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MEGCDSPVVS	GKDNGCGIPQ	HQQWTELNST	HLPDKPSSME	QSTGESHGPL	DSLRAPFNER	LAESTASAGP	PSEPASKEVT
90	100	110	120	130	140	150	160
CNECSASFAS	LQTYMEHHCP	SARPPPPLRE	ESASDTGEEG	DEESDVENLA	GEIVYQPDGS	AYIVESLSQL	TQGGGACGSG
170	180	190	200	210	220	230	240
SGSGPLPSLF	LNSLPGAGGK	QGDPSCAAPV	YPQIINTFHI	ASSFGKWFEG	PDQAFPNTSA	LAGLSPVLHS	FRVFDVRHKS
250	260	270	280	290	300	310	320
NKDYLNSDGS	AKSSCVSKDV	PNNVDLSKFD	GFVLYGKRKP	ILMCFLCKLS	FGYVRSFVTH	AVHDHRMTLS	EDERKILSNK
330	340	350	360	370	380	390	400
NISAIIQGIG	KDKEPLVSFL	EPKNKNFQHP	LVSTANLIGP	GHSFYGKFSG	IRMEGEEALP	AGSAAGPEQP	QAGLLTPSTL
410	420	430	440	450	460	470	480
LNLGGLTSSV	LKTPITSVPL	GPLASSPTKS	SEGKDSGAAE	GEKQEVGDGD	CFSEKVEPAE	EEAEEEEEEE	EAEEEEEEEE
490	500	510	520	530	540	550	560
EEEEEEEDEG	CKGLFPSELD	EELEDRPHEE	PGAAAGSSSK	KDLALSNQSI	SNSPLMPNVL	QTLSRGTAST	SSNSASSFVV
570	580	590	600	610	620	630	640
FDGANRRNRL	SFNSEGVRAN	VAEGGRRLDF	ADESANKDNA	TAPEPNESTE	GDDGGFVPHH	QHAGSLCELG	VGECPSGSGV
650	660	670	680	690	700	710	720
ECPKCDTVLG	SSRSLGGHMT	MMHSRNSCKT	LKCPKCNWHY	KYQQTLEAHM	KEKHPEPGGS	CVYCKSGQPH	PRLARGESYT
730	740	750	760	770	780	790	800
CGYKPFRCEV	CNYSTTTKGN	LSIHMQSDKH	LNNMQNLQNG	GGEQVFSHTA	GAAAAAVAAA	AAAANISSSC	GAPSPTKPKT
810	820	830	840	850	860	870	880
KPTWRCEVCD	YETNVARNLR	IHMTSEKHMH	NMMLLQQNMT	QIQHNRHLGL	GSLPSPAEAE	LYQYYLAQNM	NLPNLKMDSA
890	900	910	920	930	940	950	960
ASDAQFMMSG	FQLDPAGPMA	AMTPALVGGE	IPLDMRLGGG	QLVSEELMNL	GESFIQTNDP	SLKLFQCAVC	NKFTTDNLDM
970	980	990	1000	1010	1020	1030	1040
LGLHMNVERS	LSEDEWKAVM	GDSYQCKLCR	YNTQLKANFQ	LHCKTDKHVQ	KYQLVAHIKE	GGKANEWRLK	CVAIGNPVHL
1050	1060	1070	1080	1090	1100	1110	1120
KCNACDYYTN	SLEKLRLHTV	NSRHEASLKL	YKHLQQHESG	VEGESCYYHC	VLCNYSTKAK	LNLIQHVRSM	KHQRSESLRK
1130	1140	1150	1160	1170	1180	1190	1200
LQRLQKGLPE	EDEDLGQIFT	IRRCPSTDPE	AIEDVEGPSE	TAADPEELAK	DQEGGASSSQ	AEKELTDSPA	TSKRISFPGS
1210	1220	1230	1240	1250	1260	1270	1280
SESPLSSKRP	KTAEEIKPEQ	MYQCPYCKYS	NADVNRLRVH	AMTQHSVQPM	LRCPLCQDML	NNKIHLQLHL	THLHSVAPDC
1290	1300	1310	1320	1330	1340	1350	1360
VEKLIMTVTT	PEMVMPSSMF	LPAAVPDRDG	NSNLEEAGKQ	PETSEDLGKN	ILPSASTEQS	GDLKPSPADP	GSVREDSGFI
1370	1380	1390	1400	1410	1420	1430	1440
CWKKGCNQVF	KTSAALQTHF	NEVHAKRPQL	PVSDRHVYKY	RCNQCSLAFK	TIEKLQLHSQ	YHVIRAATMC	CLCQRSFRTF
1450	1460	1470	1480	1490	1500	1510	1520
QALKKHLETS	HLELSEADIQ	QLYGGLLANG	DLLAMGDPTL	AEDHTIIVEE	DKEEESDLED	KQSPTGSDSG	SVQEDSGSEP
1530	1540	1550	1560	1570	1580	1590	1600
KRALPFRKGP	NFTMEKFLDP	SRPYKCTVCK	ESFTQKNILL	VHYNSVSHLH	KLKRALQESA	TGQPEPTSSP	DNKPFKCNTC
1610	1620	1630	1640	1650	1660	1670	1680
NVAYSQSSTL	EIHMRSVLHQ	TKARAAKLEA	ASGSSNGTGN	SSSISLSSST	PSPVSTSGSN	TFTTSNPSSA	GIAPSSNLLS
1690	1700	1710	1720	1730	1740	1750	1760
QVPTESVGMP	PLGNPIGANI	ASPSEPKEAN	RKKLADMIAS	RQQQQQQQQQ	QQQQQQQQQQ	AQTLAQAQAQ	VQAHLQQELQ
1770	1780	1790	1800	1810	1820	1830	1840
QQAALIQSQL	FNPTLLPHFP	MTTETLLQLQ	QQQHLLFPFY	IPSAEFQLNP	EVSLPVTSGA	LTLTGTGPGL	LEDLKAQVQV
1850	1860	1870	1880	1890	1900	1910	1920
PQQSHQQILP	QQQQNQLSIA	QSHSALLQPS	QHPEKKNKLV	IKEKEKESQR	ERDSAEGGEG	NTGPKETLPD	ALKAKEKKEL
1930	1940	1950	1960	1970	1980	1990	2000
APGGGSEPSM	LPPRIASDAR	GNATKALLEN	FGFELVIQYN	ENKQKVQKKN	GKTDQGENLE	KLECDSCGKL	FSNILILKSH
2010	2020	2030	2040	2050	2060	2070	2080
QEHVHQNYFP	FKQLERFAKQ	YRDHYDKLYP	LRPQTPEPPP	PPPPPPPPPL	PAAPPQPAST	PAIPASAPPI	TSPTIAPAQP
2090	2100	2110	2120	2130	2140	2150	2160
SVPLTQLSMP	MELPIFSPLM	MQTMPLQTLP	AQLPPQLGPV	EPLPADLAQL	YQHQLNPTLL	QQQNKRPRTR	ITDDQLRVLR
2170	2180	2190	2200	2210	2220	2230	2240
QYFDINNSPS	EEQIKEMADK	SGLPQKVIKH	WFRNTLFKER	QRNKDSPYNF	SNPPITSLEE	LKIDSRPPSP	EPPKQEYWGS
2250	2260	2270	2280	2290	2300	2310	2320
KRSSRTRFTD	YQLRVLQDFF	DANAYPKDDE	FEQLSNLLNL	PTRVIVVWFQ	NARQKARKNY	ENQGEGKDGE	RRELTNDRYI
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
2701	1	973.4995	-53.38	2	62.2	10.8	1	2643-2658	R.LRTTITPEQLEILYQK.Y	

Detailed Protein Report

Protein 448: 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 449: serine/threonine-protein kinase WNK3 isoform 2 [Homo sapiens]

Accession:	gi|50845416	**Score:**	20.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	191.7
Database Date:	2015-11-30	**pI:**	5.4
		Sequence Coverage [%]:	1.2
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|578838231	refseq_human (refseq_human_20140103.fasta)	PREDICTED: serine/threonine-protein kinase WNK3 isoform X2 [Homo sapiens]
gi|578838229	refseq_human (refseq_human_20140103.fasta)	PREDICTED: serine/threonine-protein kinase WNK3 isoform X1 [Homo sapiens]

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	

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Detailed Protein Report

Protein 450: **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

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
2754	1	639.3520	54.35	2	62.8	10.3	0	265-276	H.IPGAWGSPSYSR.C	
2636	1	625.6343	-143.74	2	61.2	10.5	0	589-599	R.EQHTGAECMND.-	Oxidation: 9

Detailed Protein Report

Protein 451: latent-transforming growth factor beta-binding protein 4 isoform b [Homo sapiens]

Accession: gi|110347412
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 20.8
MW [kDa]: 169.3
pI: 5.0
Sequence Coverage [%]: 1.7
No. of unique Peptides: 2

Quantitation

WD:WU **Median:** 0.86 **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		
407	1	846.5265	154.58	2	33.7	10.2	1	541-555	R.LSPQGTRCIDVDECR.R		WD:WU 0.86

Detailed Protein Report

Protein 452: **zinc finger protein 467 [Homo sapiens]**

Accession:	gi|46409310	**Score:**	20.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	65.1
Database Date:	2015-11-30	**pI:**	11.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.0
		No. of unique Peptides:	2

Alias proteins:

Accession	Name	Description
gi|578813959	refseq_human (refseq_human_20140103.fasta)	PREDICTED: zinc finger protein 467 isoform X6 [Homo sapiens]
gi|530386928	refseq_human (refseq_human_20140103.fasta)	PREDICTED: zinc finger protein 467 isoform X3 [Homo sapiens]
gi|530386926	refseq_human (refseq_human_20140103.fasta)	PREDICTED: zinc finger protein 467 isoform X2 [Homo sapiens]
gi|530386924	refseq_human (refseq_human_20140103.fasta)	PREDICTED: zinc finger protein 467 isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MRETLEALSS	LGFSVGQPEM	APQSEPREGS	HNAQEQMSSS	REERALGVCS	GHEAPTPEEG	AHTEQAEAPC	RGQACSAQKA
90	100	110	120	130	140	150	160
QPVGTCPGEE	WMIRKVKVED	EDQEAEEEVE	WPQHLSLLPS	PFPAPDLGHL	AAAYKLEPGA	PGALSGLALS	GWGPMPEKPY
170	180	190	200	210	220	230	240
GCGECERRFR	DQLTLRLHQR	LHRGEGPCAC	PDCGRSFTQR	AHMLLHQRSH	RGERPFPCSE	CDKRFSKKAH	LTRHLRTHTG
250	260	270	280	290	300	310	320
ERPYPCAECG	KRFSQKIHLG	SHQKTHTGER	PFPCTECEKR	FRKKTHLIRH	QRIHTGERPY	QCAQCARSFT	HKQHLVRHQR
330	340	350	360	370	380	390	400
VHQTAGPARP	SPDSSASPHS	TAPSPTPSFP	GPKPFACSDC	GLSFGWKKNL	ATHQCLHRSE	GRPFGCDECA	LGATVDAPAA
410	420	430	440	450	460	470	480
KPLASAPGGP	GCGPGSDPVV	PQRAPSGERS	FFCPDCGRGF	SHGQHLARHP	RVHTGERPFA	CTQCDRRFGS	RPNLVAHSRA
490	500	510	520	530	540	550	560
HSGARPFACA	QCGRRFSRKS	HLGRHQAVHT	GSRPHACAVC	ARSFSSKTNL	VRHQAIHTGS	RPFSCPQCGK	SFSRKTHLVR
570	580	590	600				
HQLIHGEAAH	AAPDAALAAP	AWSAPPEVAP	PPLFF				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1902	1	785.7933	-55.89	2	52.1	10.0	1	181-195	R.LHRGEGPCACPDCGR.S	
340	3	544.7855	123.91	2	32.9	10.7	0	430-438	R.SFFCPDCGR.G	Carbamidomethyl: 7

Detailed Protein Report

Protein 453: trinucleotide repeat-containing gene 6B protein isoform 3 [Homo sapiens]

Accession:	gi|67782330	**Score:**	20.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	109.3
Database Date:	2015-11-30	**pI:**	7.0
		Sequence Coverage [%]:	2.3
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 1.32 **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
LLQQQQQQQL	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
325	1	564.6741	-207.76	2	32.8	10.1	0	503-511	R.QQQEQQLAR.M		WD:WU 1.32

Detailed Protein Report

Protein 454: PREDICTED: diphthine--ammonia ligase isoform X1 [Homo sapiens]

Accession:	gi|530406619	**Score:**	20.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	40.1
Database Date:	2015-11-30	**pI:**	7.8
		Sequence Coverage [%]:	4.4
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 2.21 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MSLPQGQGAK	VPHPPRSGVP	QAAAGLAAPI	RGQAAERTPG	RGPAVRHASC	GATSWLPPAL	AARTRTAPSM	RVAALISGGK
90	100	110	120	130	140	150	160
DSCYNMMQCI	AAGHQIVALA	NLRPAENQVG	SDELDSYMYQ	TVGHHAIDLY	AEAMALPLYR	RTIRGRSLDT	RQVYTKCEGD
170	180	190	200	210	220	230	240
EVEDLYELLK	LVKEKEEVEG	ISVGAILSDY	QRIRVENVCK	RLNLQPLAYL	WQRNQEDLLR	EMISSNIQAM	IIKVAALGLD
250	260	270	280	290	300	310	320
PDKHLGKTLD	QMEPYLIELS	KKYGVHVCGE	GGEYETFTLD	CPLFKKKIIV	DSSEVVIHSA	DAFAPVAYLR	FLELHLEDKA
330	340	350	360	370			
KEQKSDLSRW	SKVFTSLKPN	AVKLNETTWG	LNGCWAVGTA	GSLLL			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1742	1	480.7260	-88.12	2	50.1	10.3	1	193-200	R.IRVENVCK.R		WD:WU 2.21

Detailed Protein Report

Protein 455: RNA-binding protein 12B [Homo sapiens]

Accession: gi|118722349
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 20.6
MW [kDa]: 118.0
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 456: **latent-transforming growth factor beta-binding protein 4 isoform c precursor [Homo sapiens]**

Accession:	gi|110347437	**Score:**	20.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	165.6
Database Date:	2015-11-30	**pI:**	4.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.1
		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

Detailed Protein Report

Protein 457: receptor-type tyrosine-protein phosphatase-like N isoform 3 [Homo sapiens]

Accession:	gi|315113881	**Score:**	20.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	96.2
Database Date:	2015-11-30	**pI:**	6.1
		Sequence Coverage [%]:	3.3
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MSQGLSWHDD	LTQYVISQEM	ERIPRLRPPE	PRPRDRSGLA	PKRPGPAGEL	LLQDIPTGSA	PAAQHRLPQP	PVGKGGAGAS
90	100	110	120	130	140	150	160
SSLSPLQAEL	LPPLLEHLLL	PPQPPHPSLS	YEPALLQPYL	FHQFGSRDGS	RVSEGSPGMV	SVGPLPKAEA	PALFSRTASK
170	180	190	200	210	220	230	240
GIFGDHPGHS	YGDLPGPSPA	QLFQDSGLLY	LAQELPAPSR	ARVPRLPEQG	SSSRAEDSPE	GYEKEGLGDR	GEKPASPAVQ
250	260	270	280	290	300	310	320
PDAALQRLAA	VLAGYGVELR	QLTPEQLSTL	LTLLQLLPKG	AGRNPGGVVN	VGADIKKTME	GPVEGRDTAE	LPARTSPMPG
330	340	350	360	370	380	390	400
HPTASPTSSE	VQQVPSPVSS	EPPKAARPPV	TPVLLEKKSP	LGQSQPTVAG	QPSARPAAEE	YGYIVTDQKP	LSLAAGVKLL
410	420	430	440	450	460	470	480
EILAEHVHMS	SGSFINISVV	GPALTFRIRH	NEQNLSLADV	TQQAGLVKSE	LEAQTGLQIL	QTGVGQREEA	AAVLPQTAHS
490	500	510	520	530	540	550	560
TSPMRSVLLT	LVALAGVAGL	LVALAVALCV	RQHARQQDKE	RLAALGPEGA	HGDTTFEYQD	LCRQHMATKS	LFNRAEGPPE
570	580	590	600	610	620	630	640
PSRVSSVSSQ	FSDAAQASPS	SHSSTPSWCE	EPAQANMDIS	TGHMILAYME	DHLRNRDRLA	KEWQALCAYQ	AEPNTCATAQ
650	660	670	680	690	700	710	720
GEGNIKKNRH	PDFLPYDHAR	IKLKVESSPS	RSDYINASPI	IEHDPRMPAY	IATQGPLSHT	IADFWQMVWE	SGCTVIVMLT
730	740	750	760	770	780	790	800
PLVEDGVKQC	DRYWPDEGAS	LYHVYEVNLV	SEHIWCEDFL	VRSFYLKNVQ	TQETRTLTQF	HFLSWPAEGT	PASTRPLLDF
810	820	830	840	850	860	870	880
RRKVNKCYRG	RSCPIIVHCS	DGAGRTGTYI	LIDMVLNRMA	KGVKEIDIAA	TLEHVRDQRP	GLVRSKDQFE	FALTAVAEEV
890							
NAILKALPQ							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2983	1	863.9596	41.86	2	66.1	10.0	0	672-686	R.SDYINASPIIEHDPR.M	
531	1	472.2515	58.93	3	35.1	10.5	0	812-825	R.SCPIIVHCSDGAGR.T	

Detailed Protein Report

Protein 458: **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 459: **succinate dehydrogenase assembly factor 1, mitochondrial [Homo sapiens]**

Accession:	gi|111038124	**Score:**	20.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	12.8
Database Date:	2015-11-30	**pI:**	12.0
		Sequence Coverage [%]:	29.6
		No. of unique Peptides:	1

```
         10         20         30         40         50         60         70         80
MSRHSRLQRQ VLSLYRDLLR AGRGKPGAEA RVRAEFRQHA GLPRSDVLRI EYLYRRGRRQ LQLLRSGHAT AMGAFVRPRA
         90        100        110        120
PTGEPGGVGS QPDDGDSPRN PHDSTGAPET RPDGR
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2984	1	729.3744	-1.00	2	66.1	10.3	0	66-79	R.SGHATAMGAFVRPR.A	

Detailed Protein Report

Protein 460: PREDICTED: kelch-like protein 8 isoform X3 [Homo sapiens]

Accession:	gi|530378014	**Score:**	20.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	47.9
Database Date:	2015-11-30	**pI:**	7.2
		Sequence Coverage [%]:	2.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MASDSMSSKQ	ARNHITKGKR	QQQHQQIKNR	SSISDGDGED	SFIFEANEAW	KDFHGSLLRF	YENGELCDVT	LKVRLPLLPV
90	100	110	120	130	140	150	160
DFLMGVVAKE	QIVKQNLKCR	DLLDEARNYH	LHLSSRAVPD	FEYSIRTTPR	KHTAGVLFCV	GGRGGSGDPF	RSIECYSINK
170	180	190	200	210	220	230	240
NSWFFGPEMN	SRRRHVGVIS	VEGKVYAVGG	HDGNEHLGSM	EMFDPLTNKW	MMKASMNTKR	RGIALASLGG	PIYAIGGLDD
250	260	270	280	290	300	310	320
NTCFNDVERY	DIESDQWSTV	APMNTPRGGV	GSVALVNHVY	AVGGNDGMAS	LSSVERYDPH	LDKWIEVKEM	GQRRAGNGVS
330	340	350	360	370	380	390	400
KLHGCLYVVG	GFDDNSPLSS	VERYDPRSNK	WDYVAALTTP	RGGVGIATVM	GKIFAVGGHN	GNAYLNTVEA	FDPVLNRWEL
410	420	430	440				
VGSVSHCRAG	AGVAVCSCLT	SQIRDVGHGS	NNVVDCM				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
490	1	472.1760	-43.61	2	34.6	20.2	0	1-9	-.MASDSMSSK.Q	

Detailed Protein Report

Protein 461: PREDICTED: ubiquinone biosynthesis protein COQ7 homolog isoform X1 [Homo sapiens]

Accession:	gi|530407440	**Score:**	20.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	22.8
Database Date:	2015-11-30	**pI:**	6.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	9.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGSQCHLPQM	AYGRRTSVRF	RSSGMTLDNI	SRAAVDRIIR	VDHAGEYGAN	RIYAGQMAVL	GRTSVGPVIQ	KMWDQEKDHL
90	100	110	120	130	140	150	160
KKFNELMVTF	RVRPTVLMPL	WNVLGFALGA	GTALLGKEGA	MACTVAVEES	IAHHYNNQIR	TLMEEDPEKY	EELLQLIKKF
170	180	190	200	210			
RDEELEHHDI	GLDHDAELAP	AYAVLKSIIQ	AGCRVAIYLS	ERL			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1373	1	1045.9338	-113.36	2	45.5	20.1	2	22-40	R.SSGMTLDNISRAAVDRIIR.V	Oxidation: 4

Detailed Protein Report

Protein 462: PREDICTED: ankyrin-3 isoform X15 [Homo sapiens]

Accession:	gi|578819314	**Score:**	20.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	386.8
Database Date:	2015-11-30	**pI:**	5.6
		Sequence Coverage [%]:	0.4
		No. of unique Peptides:	1

Quantitation

WD:WU	**Median:** 0.79	**CV:** 0.00 %	**No. of Peptides:** 1

Detailed Protein Report

10	20	30	40	50	60	70	80
MALPQSEDAM	TGDTDKYLGP	QDLKELGDDS	LPAEGYMGFS	LGARSASSDR	SYTLNRSSYA	RDSMMIEELL	VPSKEQHLTF
90	100	110	120	130	140	150	160
TREFDSDSLR	HYSWAADTLD	NVNLVSSPIH	SGFLVSFMVD	ARGGSMRGSR	HHGMRIIIPP	RKCTAPTRIT	CRLVKRHKLA
170	180	190	200	210	220	230	240
NPPPMVEGEG	LASRLVEMGP	AGAQFLGPVI	VEIPHFGSMR	GKERELIVLR	SENGETWKEH	QFDSKNEDLT	ELLNGMDEEL
250	260	270	280	290	300	310	320
DSPEELGKKR	ICRIITKDFP	QYFAVVSRIK	QESNQIGPEG	GILSSTTVPL	VQASFPEGAL	TKRIRVGLQA	QPVPDEIVKK
330	340	350	360	370	380	390	400
ILGNKATFSP	IVTVEPRRRK	FHKPITMTIP	VPPPSGEGVS	NGYKGDTTPN	LRLLCSITGG	TSPAQWEDIT	GTTPLTFIKD
410	420	430	440	450	460	470	480
CVSFTTNVSA	RFWLADCHQV	LETVGLATQL	YRELICVPYM	AKFVVFAKMN	DPVESSLRCF	CMTDDKVDKT	LEQQENFEEV
490	500	510	520	530	540	550	560
ARSKDIEVLE	GKPIYVDCYG	NLAPLTKGGQ	QLVFNFYSFK	ENRLPFSIKI	RDTSQEPCGR	LSFLKEPKTT	KGLPQTAVCN
570	580	590	600	610	620	630	640
LNITLPAHKK	ETESDQDDEI	EKTDRRQSFA	SLALRKRYSY	LTEPGMKTVE	RSTGATRSLP	TTYSYKPFFS	TRPYQSWTTA
650	660	670	680	690	700	710	720
PITVPGPAKS	GFTSLSSSSS	NTPSASPLKS	IWSVSTPSPI	KSTLGASTTS	SVKSISDVAS	PIRSFRTMSS	PIKTVVSQSP
730	740	750	760	770	780	790	800
YNIQVSSGTL	ARAPAVTEAT	PLKGLASNST	FSSRTSPVTT	AGSLLERSSI	TMTPPASPKS	NINMYSSSLP	FKSIITSAAP
810	820	830	840	850	860	870	880
LISSPLKSVV	SPVKSAVDVI	SSAKITMASS	LSSPVKQMPG	HAEVALVNGS	ISPLKYPSSS	TLINGCKATA	TLQEKISSAT
890	900	910	920	930	940	950	960
NSVSSVVSAA	TDTVEKVFST	TTAMPFSPLR	SYVSAAPSAF	QSLRTPSASA	LYTSLGSSIS	ATTSSVTSSI	ITVPVYSVVN
970	980	990	1000	1010	1020	1030	1040
VLPEPALKKL	PDSNSFTKSA	AALLSPIKTL	TTETHPQPHF	SRTSSPVKSS	LFLAPSALKL	STPSSLSSSQ	EILKDVAEMK
1050	1060	1070	1080	1090	1100	1110	1120
EDLMRMTAIL	QTDVPEEKPF	QPELPKEGRI	DDEEPFKIVE	KVKEDLVKVS	EILKKDVCVD	NKGSPKSPKS	DKGHSPEDDW
1130	1140	1150	1160	1170	1180	1190	1200
IEFSSEEIRE	ARQQAAASQS	PSLPERVQVK	AKAASEKDYN	LTKVIDYLTN	DIGSSSLTNL	KYKFEDAKKD	GEERQKRVLK
1210	1220	1230	1240	1250	1260	1270	1280
PAIALQEHKL	KMPPASMRTS	TSEKELCKMA	DSFFGTDTIL	ESPDDFSQHD	QDKSPLSDSG	FETRSEKTPS	APQSAESTGP
1290	1300	1310	1320	1330	1340	1350	1360
KPLFHEVPIP	PVITETRTEV	VHVIRSYDPS	AGDVPQTQPE	EPVSPKPSPT	FMELEPKPTT	SSIKEKVKAF	QMKASSEEDD
1370	1380	1390	1400	1410	1420	1430	1440
HNRVLSKGMR	VKEETHITTT	TRMVYHSPPG	GEGASERIEE	TMSVHDIMKA	FQSGRDPSKE	LAGLFEHKSA	VSPDVHKSAA
1450	1460	1470	1480	1490	1500	1510	1520
ETSAQHAEKD	NQMKPKLERI	IEVHIEKGNQ	AEPTEVIIRE	TKKHPEKEMY	VYQKDLSRGD	INLKDFLPEK	HDAFPCSEEQ
1530	1540	1550	1560	1570	1580	1590	1600
GQQEEEELTA	EESLPSYLES	SRVNTPVSQE	EDSRPSSAQL	ISDDSYKTLK	LLSQHSIEYH	DDELSELRGE	SYRFAEKMLL
1610	1620	1630	1640	1650	1660	1670	1680
SEKLDVSHSD	TEESVTDHAG	PPSSELQGSD	KRSREKIATA	PKKEILSKIY	KDVSENGVGK	VSKDEHFDKV	TVLHYSGNVS
1690	1700	1710	1720	1730	1740	1750	1760
SPKHAMWMRF	TEDRLDRGRE	KLIYEDRVDR	TVKEAEEKLT	EVSQFFRDKT	EKLNDELQSP	EKKARPKNGK	EYSSQSPTSS
1770	1780	1790	1800	1810	1820	1830	1840
SPEKVLLTEL	LASNDEWVKA	RQHGPDGQGF	PKAEEKAPSL	PSSPEKMVLS	QQTEDSKSTV	EAKGSISQSK	APDGPQSGFQ
1850	1860	1870	1880	1890	1900	1910	1920
LKQSKLSSIR	LKFEQGTHAK	SKDMSQEDRK	SDGQSRIPVK	KIQESKLPVY	QVFAREKQQK	AIDLPDESVS	VQKDFMVLKT
1930	1940	1950	1960	1970	1980	1990	2000
KDEHAQSNEI	VVNDSGSDNV	KKQRTEMSSK	AMPDSFSEQQ	AKDLACHITS	DLATRGPWDK	KVFRTWESSG	ATNNKSQKEK
2010	2020	2030	2040	2050	2060	2070	2080
LSHVLVHDVR	ENHIGHPESK	SVDQKNEFMS	VTERERKLLT	NGSLSEIKEM	TVKSPSKKVL	YREYVVKEGD	HPGGLLDQPS
2090	2100	2110	2120	2130	2140	2150	2160
RRSESSAVSH	IPVRVADERR	MLSSNIPDGF	CEQSAFPKHE	LSQKLSQSSM	SKETVETQHF	NSIEDEKVTY	SEISKVSKHQ
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
534	1	676.8481	-14.81	2	35.1	20.1	1	3029-3041	K.TKALTTSSCVDVK.S		WD:WU 0.79

Detailed Protein Report

Protein 463: uncharacterized protein KIAA0226-like isoform f [Homo sapiens]

Accession:	gi|557947998	**Score:**	20.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	50.5
Database Date:	2015-11-30	**pI:**	8.6
		Sequence Coverage [%]:	2.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MIISAMEKMK	CNILSQQQTE	SWSKEVSGLL	GSDQPDSEMT	FDTNIKQESG	SSTSSYSGYE	GCAVLQVSPV	TETRTYHDVK
90	100	110	120	130	140	150	160
EICKCDVDEF	VILELGDFND	ITETCSCSCS	SSKSVTYEPD	FNSAELLAKE	LYRVFQKCWI	LSVVNSQLAG	SLSAAGSIVV
170	180	190	200	210	220	230	240
NEECVRKDFE	SSMNVVQEIK	FKSRIRGTED	WAPPRFQIIF	NIHPPLKRDL	VVAAQNFFCA	GCGTPVEPKF	VKRLRYCEYL
250	260	270	280	290	300	310	320
GKYFCDCCHS	YAESCIPARI	LMMWDFKKYY	VSNFSKQLLD	SIWHQPIFNL	LSIGQSLYAK	AKELDRVKEI	QEQLFHIKKL
330	340	350	360	370	380	390	400
LKTCRFANSA	LKEFEQVPGH	LTDELHLFSL	EDLVRIKKGL	LAPLLKDILK	ASLAHVAGCE	LCQGKGFICE	FCQNTTVIFP
410	420	430	440	450			
FQTATCRRCS	ACRACFHKQC	FQSSECPRCA	RITARRKLLE	SVASAAT			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2445	1	597.3363	-141.46	2	58.8	20.0	2	356-366	R.IKKGLLAPLLK.D	

Detailed Protein Report

Protein 464: **ovochymase-2 precursor [Homo sapiens]**

Accession:	gi|373838920	**Score:**	19.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	62.6
Database Date:	2015-11-30	**pI:**	6.2
		Sequence Coverage [%]:	2.5
		No. of unique Peptides:	1

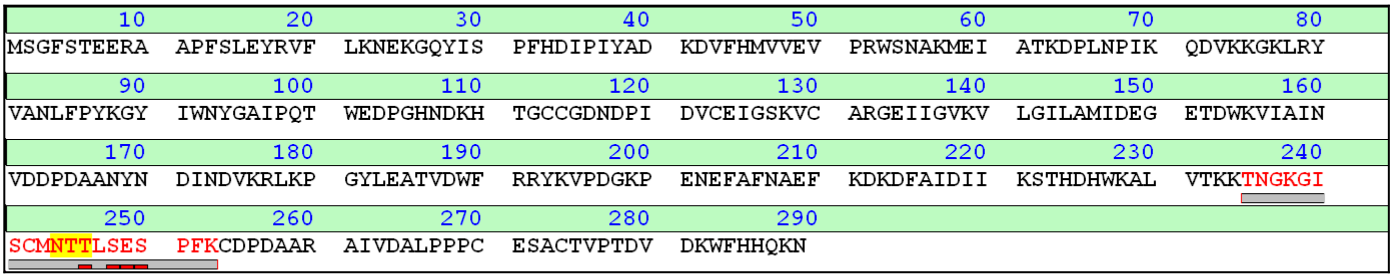
```
        10         20         30         40         50         60         70         80
MLISRNKLIL LLGIVFFERG KSATLSLPKA PSCGQSLVKV QPWNYFNIFS RILGGSQVEK GSYPWQVSLK QRQKHICGGS
        90        100        110        120        130        140        150        160
IVSPQWVITA AHCIANRNIV STLNVTAGEY DLSQTDPGEQ TLTIETVIIH PHFSTKKPMD YDIALLKMAG AFQFGHFVGP
       170        180        190        200        210        220        230        240
ICLPELREQF EAGFICTTAG WGRLTEGGVL SQVLQEVNLP ILTWEECVAA LLTLKRPISG KTFLCTGFPD GGRDACQGDS
       250        260        270        280        290        300        310        320
GGSLMCRNKK GAWTLAGVTS WGLGCGRGWR NNVRKSDQGS PGIFTDISKV LPWIHEHIQT GNRRKSSRAW CSEQDVIVSG
       330        340        350        360        370        380        390        400
AEGKLHFPES LHLYYESKQR CVWTLLVPEE MHVLLSFSHL DVESCHHSYL SMYSLEDRPI GKFCGESLPS SILIGSNSLR
       410        420        430        440        450        460        470        480
LKFVSDATDN AAGFNLTYKA LKPNYIPDSG CSYLTVLFEE GLIQSLNYPE NYSDKANCDW IFQASKHHLI KLSFQSLEIE
       490        500        510        520        530        540        550        560
ESGDCTSDYV TVHSDVERKK EIARLCGYDV PTPVLSPSSI MLISFQSDEN GTCRGFQATV SFIPKAVYPD LNISISEDES
       570
MFLET
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1535	1	850.5690	134.04	2	47.5	19.9	0	290-303	K.VLPWIHEHIQTGNR.R	

Detailed Protein Report

Protein 465: inorganic pyrophosphatase [Homo sapiens]

Accession:	gi|11056044	**Score:**	19.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	32.6
Database Date:	2015-11-30	**pI:**	5.5
Modification(s):	Carbamidomethyl, Oxidation	**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 466: retinol dehydrogenase 10 [Homo sapiens]

Accession:	gi|25282469	**Score:**	19.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	38.1
Database Date:	2015-11-30	**pI:**	7.9
		Sequence Coverage [%]:	2.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MNIVVEFFVV	TFKVLWAFVL	AAARWLVRPK	EKSVAGQVCL	ITGAGSGLGR	LFALEFARRR	ALLVLWDINT	QSNEETAGMV
90	100	110	120	130	140	150	160
RHIYRDLEAA	DAAALQAGNG	EEEILPHCNL	QVFTYTCDVG	KRENVYLTAE	RVRKEVGEVS	VLVNNAGVVS	GHHLLECPDE
170	180	190	200	210	220	230	240
LIERTMMVNC	HAHFWTTKAF	LPTMLEINHG	HIVTVASSLG	LFSTAGVEDY	CASKFGVVGF	HESLSHELKA	AEKDGIKTTL
250	260	270	280	290	300	310	320
VCPYLVDTGM	FRGCRIRKEI	EPFLPPLKPD	YCVKQAMKAI	LTDQPMICTP	RLMYIVTFMK	SILPFEAVVC	MYRFLGADKC
330	340	350					
MYPFIAQRKQ	ATNNNEAKNG	I					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
365	1	639.8907	24.31	2	33.2	19.8	2	51-60	R.LFALEFARRR.A	

Detailed Protein Report

Protein 467: **tuberin isoform 4 [Homo sapiens]**

Accession:	gi|116256350	**Score:**	19.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	193.1
Database Date:	2015-11-30	**pI:**	6.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	0.8
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 0.90 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MAKPTSKDSG	LKEKFKILLG	LGTPRPNPRS	AEGKQTEFII	TAEILRELSM	ECGLNNRIRM	IGQICEVAKT	KKFEEHAVEA
90	100	110	120	130	140	150	160
LWKAVADLLQ	PERPLEARHA	VLALLKAIVQ	GQGERLGVLR	ALFFKVIKDY	PSNEDLHERL	EVFKALTDNG	RHITYLEEEL
170	180	190	200	210	220	230	240
ADFVLQWMDV	GLSSEFLLVL	VNLVKFNSCY	LDEYIARMVQ	MICLLCVRTA	SSVDIEVSLQ	VLDAVVCYNC	LPAESLPLFI
250	260	270	280	290	300	310	320
VTLCRTINVK	ELCEPCWKLM	RNLLGTHLGH	SAIYNMCHLM	EDRAYMEDAP	LLRGAVFFVG	MALWGAHRLY	SLRNSPTSVL
330	340	350	360	370	380	390	400
PSFYQAMACP	NEVVSYEIVL	SITRLIKKYR	KELQVVAWDI	LLNIIERLLQ	QLQTLDSPEL	RTIVHDLLTT	VEELCDQNEF
410	420	430	440	450	460	470	480
HGSQERYFEL	VERCADQRPE	SSLLNLISYR	AQSIHPAKDG	WIQNLQALME	RFFRSESRGA	VRIKVLDVLS	FVLLINRQFY
490	500	510	520	530	540	550	560
EEELINSVVI	SQLSHIPEDK	DHQVRKLATQ	LLVDLAEGCH	THHFNSLLDI	IEKVMARSLS	PPPELEERDV	AAYSASLEDV
570	580	590	600	610	620	630	640
KTAVLGLLVI	LQTKLYTLPA	SHATRVYEML	VSHIQLHYKH	SYTLPIASSI	RLQAFDFLLL	LRADSLHRLG	LPNKDGVVRF
650	660	670	680	690	700	710	720
SPYCVCDYME	PERGSEKKTS	GPLSPPTGPP	GPAPAGPAVR	LGSVPYSLLF	RVLLQCLKQE	SDWKVLKLVL	GRLPESLRYK
730	740	750	760	770	780	790	800
VLIFTSPCSV	DQLCSALCSM	LSGPKTLERL	RGAPEGFSRT	DLHLAVVPVL	TALISYHNYL	DKTKQREMVY	CLEQGLIHRC
810	820	830	840	850	860	870	880
ASQCVVALSI	CSVEMPDIII	KALPVLVVKL	THISATASMA	VPLLEFLSTL	ARLPHLYRNF	AAEQYASVFA	ISLPYTNPSK
890	900	910	920	930	940	950	960
FNQYIVCLAH	HVIAMWFIRC	RLPFRKDFVP	FITKGLRSNV	LLSFDDTPEK	DSFRARSTSL	NERPKRIQTS	LTSASLGSAD
970	980	990	1000	1010	1020	1030	1040
ENSVAQADDS	LKNLHLELTE	TCLDMMARYV	FSNFTAVPKR	SPVGEFLLAG	GRTKTWLVGN	KLVTVTTSVG	TGTRSLLGLD
1050	1060	1070	1080	1090	1100	1110	1120
SGELQSGPES	SSSPGVHVRQ	TKEAPAKLES	QAGQQVSRGA	RDRVRSMSGG	HGLRVGALDV	PASQFLGSAT	SPGPRTAPAA
1130	1140	1150	1160	1170	1180	1190	1200
KPEKASAGTR	VPVQEKTNLA	AYVPLLTQGW	AEILVRRPTG	NTSWLMSLEN	PLSPFSSDIN	NMPLQELSNA	LMAAERFKEH
1210	1220	1230	1240	1250	1260	1270	1280
RDTALYKSLS	VPAASTAKPP	PLPRSNTDSA	VVMEEGSPGE	VPVLVEPPGL	EDVEAALGMD	RRTDAYSRSS	SVSSQEEKSL
1290	1300	1310	1320	1330	1340	1350	1360
HAEELVGRGI	PIERVVSSEG	GRPSVDLSFQ	PSQPLSKSSS	SPELQTLQDI	LGDPGDKADV	GRLSPEVKAR	SQSGTLDGES
1370	1380	1390	1400	1410	1420	1430	1440
AAWSASGEDS	RGQPEGPLPS	SSPRSPSGLR	PRGYTISDSA	PSRRGKRVER	DALKSRATAS	NAEKVPGINP	SFVFLQLYHS
1450	1460	1470	1480	1490	1500	1510	1520
PFFGDESNKP	ILLPNESQSF	ERSVQLLDQI	PSYDTHKIAV	LYVGEGQSNS	ELAILSNEHG	SYRYTEFLTG	LGRLIELKDC
1530	1540	1550	1560	1570	1580	1590	1600
QPDKVYLGGL	DVCGEDGQFT	YCWHDDIMQA	VFHIATLMPT	KDVDKHRCDK	KRHLGNDFVS	IVYNDSGEDF	KLGTIKGQFN
1610	1620	1630	1640	1650	1660	1670	1680
FVHVIVTPLD	YECNLVSLQC	RKDMEGLVDT	SVAKIVSDRN	LPFVARQMAL	HANMASQVHH	SRSNPTDIYP	SKWIARLRHI
1690	1700	1710	1720	1730	1740	1750	
KRLRQRICEE	AAYSNPSLPL	VHPPSHSKAP	AQTPAEPTPG	YEVGQRKRLI	SSVEDFTEFV		

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
52	4	768.2749	-173.91	2	29.9	19.8	2	1-14	-.MAKPTSKDSGLKEK.F	Oxidation: 1	WD:WU 0.90

Detailed Protein Report

Protein 468: **PREDICTED: DNA topoisomerase 2-binding protein 1 isoform X1 [Homo sapiens]**

Accession:	gi|530373836	**Score:**	19.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	170.0
Database Date:	2015-11-30	**pI:**	6.5
		Sequence Coverage [%]:	0.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSRNDKEPFF	VKFLKSSDNS	KCFFKALESI	KEFQSEEYLQ	IITEEEALKI	KENDRSLYIC	DPFSGVVFDH	LKKLGCRIVG
90	100	110	120	130	140	150	160
PQVVIFCMHH	QRCVPRAEHP	VYNMVMSDVT	ISCTSLEKEK	REEVHKYVQM	MGGRVYRDLN	VSVTHLIAGE	VGSKKYLVAA
170	180	190	200	210	220	230	240
NLKKPILLPS	WIKTLWEKSQ	EKKITRYTDI	NMEDFKCPIF	LGCIICVTGL	CGLDRKEVQQ	LTVKHGGQYM	GQLKMNECTH
250	260	270	280	290	300	310	320
LIVQEPKGQK	YECAKRWNVH	CVTTQWFFDS	IEKGFCQDES	IYKTEPRPEA	KTMPNSSTPT	SQINTIDNVS	NISNINASCV
330	340	350	360	370	380	390	400
SESICNSLNS	KLEPTLENLE	NLDVSAFQAP	EDLLDGCRIY	LCGFSGRKLD	KLRRLINSGG	GVRFNQLNED	VTHVIVGDYD
410	420	430	440	450	460	470	480
DELKQFWNKS	AHRPHVVGAK	WLLECFSKGY	MLSEEPYIHA	NYQPVEIPVS	HKPESKAALL	KKKNSSFSKK	DFAPSEKHEQ
490	500	510	520	530	540	550	560
ADEDLLSQYE	NGSSTVVEAK	TSEARPFNDS	THAEPLNDST	HISLQEENQS	SVSHCVPDVS	TITEEGLFSQ	KSFLVLGFSN
570	580	590	600	610	620	630	640
ENESNIANII	KENAGKIMSL	LSRTVADYAV	VPLLGCEVEA	TVGEVVTNTW	LVTCIDYQTL	FDPKSNPLFT	PVPVMTGMTP
650	660	670	680	690	700	710	720
LEDCVISFSQ	CAGAEKESLT	FLANLLGASV	QEYFVRKSNA	KKGMFASTHL	ILKERGGSKY	EAAKKWNLPA	VTIAWLLETA
730	740	750	760	770	780	790	800
RTGKRADESH	FLIENSTKEE	RSLETEITNG	INLNSDTAEH	PGTRLQTHRK	TVVTPLDMNR	FQSKAFRAVV	SQHARQVAAS
810	820	830	840	850	860	870	880
PAVGQPLQKE	PSLHLDTPSK	FLSKDKLFKP	SFDVKDALAA	LETPGRPSQQ	KRKPSTPLSE	VIVKNLQLAL	ANSSRNAVAL
890	900	910	920	930	940	950	960
SASPQLKEAQ	SEKEEAPKPL	HKVVVCVSKK	LSKKQSELNG	IAASLGADYR	WSFDETVTHF	IYQGRPNDTN	REYKSVKERG
970	980	990	1000	1010	1020	1030	1040
VHIVSEHWLL	DCAQECKHLP	ESLYPHTYNP	KMSLDISAVQ	DGRLCNSRLL	SAVSSTKDDE	PDPLILEEND	VDNMATNNKE
1050	1060	1070	1080	1090	1100	1110	1120
SAPSNGSGKN	DSKGVLTQTL	EMRENFQKQL	QEIMSATSIV	KPQGQRTSLS	RSGCNSASST	PDSTRSARSG	RSRVLEALRQ
1130	1140	1150	1160	1170	1180	1190	1200
SRQTVPDVNT	EPSQNEQIIW	DDPTAREERA	RLASNLQWPS	CPTQYSELQV	DIQNLEDSPF	QKPLHDSEIA	KQAVCDPGNI
1210	1220	1230	1240	1250	1260	1270	1280
RVTEAPKHPI	SEELETPIKD	SHLIPTPQAP	SIAFPLANPP	VAPHPREKII	TIEETHEELK	KQYIFQLSSL	NPQERIDYCH
1290	1300	1310	1320	1330	1340	1350	1360
LIEKLGGLVI	EKQCFDPTCT	HIVVGHPLRN	EKYLASVAAG	KWVLHRSYLE	ACRTAGHFVQ	EEDYEWGSSS	ILDVLTGINV
1370	1380	1390	1400	1410	1420	1430	1440
QQRRLALAAM	RWRKKIQQRQ	ESGIVEGAFS	GWKVILHVDQ	SREAGFKRLL	QSGGAKVLPG	HSVPLFKEAT	HLFSDLNKLK
1450	1460	1470	1480	1490	1500	1510	1520
PDDSGVNIAE	AAAQNVYCLR	TEYIADYLMQ	ESPPHVENYC	LPEAISFIQN	NKELGTGLSQ	KRKAPTEKNK	IKRPRVH

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1880	1	697.5427	213.85	2	51.8	19.8	0	796-809	R.QVAASPAVGQPLQK.E	

Detailed Protein Report

Protein 469: alpha-2-HS-glycoprotein preproprotein [Homo sapiens]

Accession:	gi|156523970	**Score:**	19.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	39.3
Database Date:	2015-11-30	**pI:**	5.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	6.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MKSLVLLLCL	AQLWGCHSAP	HGPGLIYRQP	NCDDPETEEA	ALVAIDYINQ	NLPWGYKHTL	NQIDEVKVWP	QQPSGELFEI
90	100	110	120	130	140	150	160
EIDTLETTCH	VLDPTPVARC	SVRQLKEHAV	EGDCDFQLLK	LDGKFSVVYA	KCDSSPDSAE	DVRKVCQDCP	LLAPLNDTRV
170	180	190	200	210	220	230	240
VHAAKAALAA	FNAQNNGSNF	QLEEISRAQL	VPLPPSTYVE	FTVSGTDCVA	KEATEAAKCN	LLAEKQYGFC	KATLSEKLGG
250	260	270	280	290	300	310	320
AEVAVTCMVF	QTQPVSSQPQ	PEGANEAVPT	PVVDPDAPPS	PPLGAPGLPP	AGSPPDSHVL	LAAPPGHQLH	RAHYDLRHTF
330	340	350	360	370			
MGVVSLGSPS	GEVSHPRKTR	TVVQPSVGAA	AGPVVPPCPG	RIRHFKV			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2906	1	860.4973	66.36	3	65.1	19.8	0	188-211	R.AQLVPLPPSTYVEFTVSGTDCVAK.E	Carbamidomethyl: 21

Detailed Protein Report

Protein 470: **PREDICTED: zinc finger CCCH domain-containing protein 7A isoform X4 [Homo sapiens]**

Accession:	gi|530407964	**Score:**	19.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	67.6
Database Date:	2015-11-30	**pI:**	9.6
		Sequence Coverage [%]:	1.6
		No. of unique Peptides:	1

```
        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
202	1	999.6888	178.38	1	31.7	19.7	0	327-335	R.NGQVIEPDK.N	

Detailed Protein Report

Protein 471: interferon regulatory factor 2-binding protein-like [Homo sapiens]

Accession:	gi|33457336	**Score:**	19.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	82.6
Database Date:	2015-11-30	**pI:**	9.6
		Sequence Coverage [%]:	1.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSAAQVSSSR	RQSCYLCDLP	RMPWAMIWDF	SEPVCRGCVN	YEGADRIEFV	IETARQLKRA	HGCFQDGRSP	GPPPPVGVKT
90	100	110	120	130	140	150	160
VALSAKEAAA	AAAAAAAAAA	AAQQQQQQQQ	QQQQQQQQQQ	QQQQQQQLNH	VDGSSKPAVL	AAPSGLERYG	LSAAAAAAAA
170	180	190	200	210	220	230	240
AAAAVEQRSR	FEYPPPPVSL	GSSSHTARLP	NGLGGPNGFP	KPTPEEGPPE	LNRQSPNSSS	AAASVASRRG	THGGLVTGLP
250	260	270	280	290	300	310	320
NPGGGGGPQL	TVPPNLLPQT	LLNGPASAAV	LPPPPPHALG	SRGPPTPAPP	GAPGGPACLG	GTPGVSATSS	SASSSTSSSV
330	340	350	360	370	380	390	400
AEVGVGAGGK	RPGSVSSTDQ	ERELKEKQRN	AEALAELSES	LRNRAEEWAS	KPKMVRDTLL	TLAGCTPYEV	RFKKDHSLLG
410	420	430	440	450	460	470	480
RVFAFDAVSK	PGMDYELKLF	IEYPTGSGNV	YSSASGVAKQ	MYQDCMKDFG	RGLSSGFKYL	EYEKKHGSGD	WRLLGDLLPE
490	500	510	520	530	540	550	560
AVRFFKEGVP	GADMLPQPYL	DASCPMLPTA	LVSLSRAPSA	PPGTGALPPA	APSGRGAAAS	LRKRKASPEP	PDSAEGALKL
570	580	590	600	610	620	630	640
GEEQQRQQWM	ANQSEALKLT	MSAGGFAAPG	HAAGGPPPPP	PPLGPHSNRT	TPPESAPQNG	PSPMAALMSV	ADTLGTAHSP
650	660	670	680	690	700	710	720
KDGSSVHSTT	ASARRNSSSP	VSPASVPGQR	RLASRNGDLN	LQVAPPPPSA	HPGMDQVHPQ	NIPDSPMANS	GPLCCTICHE
730	740	750	760	770	780	790	800
RLEDTHFVQC	PSVPSHKFCF	PCSRESIKAQ	GATGEVYCPS	GEKCPLVGSN	VPWAFMQGEI	ATILAGDVKV	KKERDP

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2766	1	659.8617	61.81	2	63.1	19.6	0	331-342	K.RPGSVSSTDQER.E	

Detailed Protein Report

Protein 472: serine protease 58 precursor [Homo sapiens]

Accession:	gi|48255915	**Score:**	19.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	27.1
Database Date:	2015-11-30	**pI:**	6.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	11.6
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MKFILLWALL NLTVALAFNP DYTVSSTPPY LVYLKSDYLP CAGVLIHPLW VITAAHCNLP KLRVILGVTI PADSNEKHLQ
        90        100        110        120        130        140        150        160
VIGYEKMIHH PHFSVTSIDH DIMLIKLKTE AELNDYVKLA NLPYQTISEN TMCSVSTWSY NVCDIYKEPD SLQTVNISVI
       170        180        190        200        210        220        230        240
SKPQCRDAYK TYNITENMLC VGIVPGRRQP CKEVSAAPAI CNGMLQGILS FADGCVLRAD VGIYAKIFYY IPWIENVIQN
       250
N
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1245	1	1072.1826	-52.32	3	43.9	19.6	1	36-63	K.SDYLPCAGVLIHPLWVITAAHCNLPKLR.V	Carbamidomethyl: 6, 22

Detailed Protein Report

Protein 473: 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 474: 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 475: 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

Quantitation

WD:WU **Median:** 1.09 **CV:** 0.00 % **No. of 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	Ratios
1043	1	630.9810	-97.07	3	41.8	19.5	2	8-24	R.ILGQPLSIPTSQPKQKR.T		WD:WU 1.09

Detailed Protein Report

Protein 476: rho GTPase-activating protein 19 isoform 3 [Homo sapiens]

Accession:	gi|374093192	**Score:**	19.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	54.9
Database Date:	2015-11-30	**pI:**	10.1
		Sequence Coverage [%]:	2.1
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MPHQKLSALI DAICSFVICN DSSLRGQPII FNPDFFVEKL RHEKPEIFTE LVVSNITRLI DLPGTELAQL MGEVDLKLPG

        90        100        110        120        130        140        150        160
GAGPASGFFR SLMSLKRKEK GVIFGSPLTE EGIAQIYQLI EYLHKNLRVE GLFRVPGNSV RQQILRDALN NGTDIDLESG

       170        180        190        200        210        220        230        240
EFHSNDVATL LKMFLGELPE PLLTHKHFNA HLKIADLMQF DDKGNKTNIP DKDRQIEALQ LLFLILPPPN RNLLKLLLDL

       250        260        270        280        290        300        310        320
LYQTAKKQDK NKMSAYNLAL MFAPHVLWPK NVTANDLQEN ITKLNSGMAF MIKHSQKLFK APAYIRECAR LHYLGSRTQA

       330        340        350        360        370        380        390        400
SKDDLDLIAS CHTKSFQLAK SQKRNRVDSC PHQEETQHHT EEALRELFQH VHDMPESAKK KQLIRQFNKQ SLTQTPGREP

       410        420        430        440        450        460        470        480
STSQVQKRAR SRSFSGLIKR KVLGNQMMSE KKKKNPTPES VAIGELKGTS KENRNLLFSG SPAVTMTPTR LKWSEGKKEG

       490
KKGFL
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
693	1	556.2788	-12.08	2	37.1	19.5	0	284-293	K.LNSGMAFMIK.H	

Detailed Protein Report

Protein 477: 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 478: mucin-17 precursor [Homo sapiens]

Accession:	gi|91982772	**Score:**	19.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	451.5
Database Date:	2015-11-30	**pI:**	3.9
		Sequence Coverage [%]:	0.2
		No. of unique Peptides:	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MPRPGTMALC	LLTLVLSLLP	PQAAAEQDLS	VNRAVWDGGG	CISQGDVLNR	QCQQLSQHVR	TGSAANTATG	TTSTNVVEPR
90	100	110	120	130	140	150	160
MYLSCSTNPE	MTSIESSVTS	DTPGVSSTRM	TPTESRTTSE	STSDSTTLFP	SSTEDTSSPT	TPEGTDVPMS	TPSEESISST
170	180	190	200	210	220	230	240
MAFVSTAPLP	SFEAYTSLTY	KVDMSTPLTT	STQASSSPTT	PESTTIPKST	NSEGSTPLTS	MPASTMKVAS	SEAITLLTTP
250	260	270	280	290	300	310	320
VEISTPVTIS	AQASSSPTTA	EGPSLSNSAP	SGGSTPLTRM	PLSVMLVVSS	EASTLSTTPA	ATNIPVITST	EASSSPTTAE
330	340	350	360	370	380	390	400
GTSIPTSTYT	EGSTPLTSTP	ASTMPVATSE	MSTLSITPVD	TSTLVTTSTE	PSSLPTTAEA	TSMLTSTLSE	GSTPLTNMPV
410	420	430	440	450	460	470	480
STILVASSEA	STTSTIPVDS	KTFVTTASEA	SSSPTTAEDT	SIATSTPSEG	STPLTSMPVS	TTPVASSEAS	NLSTTPVDSK
490	500	510	520	530	540	550	560
TQVTTSTEAS	SSPPTAEVNS	MPTSTPSEGS	TPLTSMSVST	MPVASSEAST	LSTTPVDTST	PVTTSSEASS	SSTTPEGTSI
570	580	590	600	610	620	630	640
PTSTPSEGST	PLTNMPVSTR	LVVSSEASTT	STTPADSNTF	VTTSSEASSS	STTAEGTSMP	TSTYSERGTT	ITSMSVSTTL
650	660	670	680	690	700	710	720
VASSEASTLS	TTPVDSNTPV	TTSTEATSSS	TTAEGTSMPT	STYTEGSTPL	TSMPVNTTLV	ASSEASTLST	TPVDTSTPVT
730	740	750	760	770	780	790	800
TSTEASSSPT	TADGASMPTS	TPSEGSTPLT	SMPVSKTLLT	SSEASTLSTT	PLDTSTHITT	STEASCSPTT	TEGTSMPIST
810	820	830	840	850	860	870	880
PSEGSPLLTS	IPVSITPVTS	PEASTLSTTP	VDSNSPVTTS	TEVSSSPTPA	EGTSMPTSTY	SEGRTPLTSM	PVSTTLVATS
890	900	910	920	930	940	950	960
AISTLSTTPV	DTSTPVTNST	EARSSPTTSE	GTSMPTSTPG	EGSTPLTSMP	DSTTPVVSSE	ARTLSATPVD	TSTPVTTSTE
970	980	990	1000	1010	1020	1030	1040
ATSSPTTAEG	TSIPTSTPSE	GTTPLTSTPV	SHTLVANSEA	STLSTTPVDS	NTPLTTSTEA	SSPPPTAEGT	SMPTSTPSEG
1050	1060	1070	1080	1090	1100	1110	1120
STPLTRMPVS	TTMVASSETS	TLSTTPADTS	TPVTTYSQAS	SSSTTADGTS	MPTSTYSEGS	TPLTSVPVST	RLVVSSEAST
1130	1140	1150	1160	1170	1180	1190	1200
LSTTPVDTSI	PVTTSTEASS	SPTTAEGTSI	PTSPPSEGTT	PLASMPVSTT	LVVSSEANTL	STTPVDSKTQ	VATSTEASSP
1210	1220	1230	1240	1250	1260	1270	1280
PPTAEVTSMP	TSTPGERSTP	LTSMPVRHTP	VASSEASTLS	TSPVDTSTPV	TTSAETSSSP	TTAEGTSLPT	STTSEGSTLL
1290	1300	1310	1320	1330	1340	1350	1360
TSIPVSTTLV	TSPEASTLLT	TPVDTKGPVV	TSNEVSSSPT	PAEGTSMPTS	TYSEGRTPLT	SIPVNTTLVA	SSAISILSTT
1370	1380	1390	1400	1410	1420	1430	1440
PVDNSTPVTT	STEACSSPTT	SEGTSMPNSN	PSEGTTPLTS	IPVSTTPVVS	SEASTLSATP	VDTSTPGTTS	AEATSSPTTA
1450	1460	1470	1480	1490	1500	1510	1520
EGISIPTSTP	SEGKTPLKSI	PVSNTPVANS	EASTLSTTPV	DSNSPVVTST	AVSSSPTPAE	GTSIAISTPS	EGSTALTSIP
1530	1540	1550	1560	1570	1580	1590	1600
VSTTTVASSE	INSLSTTPAV	TSTPVTTYSQ	ASSSPTTADG	TSMQTSTYSE	GSTPLTSLPV	STMLVVSSEA	NTLSTTPIDS
1610	1620	1630	1640	1650	1660	1670	1680
KTQVTASTEA	SSSTTAEGSS	MTISTPSEGS	PLLTSIPVST	TPVASPEAST	LSTTPVDSNS	PVITSTEVSS	SPTPAEGTSM
1690	1700	1710	1720	1730	1740	1750	1760
PTSTYTEGRT	PLTSITVRTT	PVASSAISTL	STTPVDNSTP	VTTSTEARSS	PTTSEGTSMP	NSTPSEGTTP	LTSIPVSTTP
1770	1780	1790	1800	1810	1820	1830	1840
VLSSEASTLS	ATPIDTSTPV	TTSTEATSSP	TTAEGTSIPT	STLSEGMTPL	TSTPVSHTLV	ANSEASTLST	TPVDSNSPVV
1850	1860	1870	1880	1890	1900	1910	1920
TSTAVSSSPT	PAEGTSIATS	TPSEGSTALT	SIPVSTTTVA	SSETNTLSTT	PAVTSTPVTT	YAQVSSSPTT	ADGSSMPTST
1930	1940	1950	1960	1970	1980	1990	2000
PREGRPPLTS	IPVSTTTVAS	SEINTLSTTL	ADTRTPVTTY	SQASSSPTTA	DGTSMPTPAY	SEGSTPLTSM	PLSTTLVVSS
2010	2020	2030	2040	2050	2060	2070	2080
EASTLSTTPV	DTSTPATTST	EGSSSPTTAG	GTSIQTSTPS	ERTTPLAGMP	VSTTLVVSSE	GNTLSTTPVD	SKTQVTNSTE
2090	2100	2110	2120	2130	2140	2150	2160
ASSSATAEGS	SMTISAPSEG	SPLLTSIPLS	TTPVASPEAS	TLSTTPVDSN	SPVITSTEVS	SSPIPTEGTS	MQTSTYSDRR
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
138	2	613.7562	-82.11	2	31.0	19.4	0	51-60	R.QCQQLSQHVR.T	

Detailed Protein Report

Protein 479: **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 480: PREDICTED: NT-3 growth factor receptor isoform X9 [Homo sapiens]

Accession:	gi|578827025	**Score:**	19.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	55.2
Database Date:	2015-11-30	**pI:**	6.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDVSLCPAKC	SFWRIFLLGS	VWLDYVGSVL	ACPANCVCSK	TEINCRRPDD	GNLFPLLEGQ	DSGNSNGNAS	INITDISRNI
90	100	110	120	130	140	150	160
TSIHIENWRS	LHTLNAVDME	LYTGLQKLTI	KNSGLRSIQP	RAFAKNPHLR	YINLSSNRLT	TLSWQLFQTL	SLRELQLEQN
170	180	190	200	210	220	230	240
FFNCSCDIRW	MQLWQEQGEA	KLNSQNLYCI	NADGSQLPLF	RMNISQCDLP	EISVSHVNLT	VREGDNAVIT	CNGSGSPLPD
250	260	270	280	290	300	310	320
VDWIVTGLQS	INTHQTNLNW	TNVHAINLTL	VNVTSEDNGF	TLTCIAENVV	GMSNASVALT	VYYPPRVVSL	EEPELRLEHC
330	340	350	360	370	380	390	400
IEFVVRGNPP	PTLHWLHNGQ	PLRESKIIHV	EYYQEGEISE	GCLLFNKPTH	YNNGNYTLIA	KNPLGTANQT	INGHFLKEPF
410	420	430	440	450	460	470	480
PVDEVSPTPP	ITVTHKPEED	TFGVSIAVGL	AAFACVLLVV	LFVMINKYGR	RSKFGMKDGL	ELLAVLLKCD	SKQLKNKEGN
490	500						
KMKNNNGKKK	RATSA						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
342	2	699.2835	-131.98	3	32.9	19.3	2	454-472	K.FGMKDGLELLAVLLKCDSK.Q	Oxidation: 3

Detailed Protein Report

Protein 481: 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

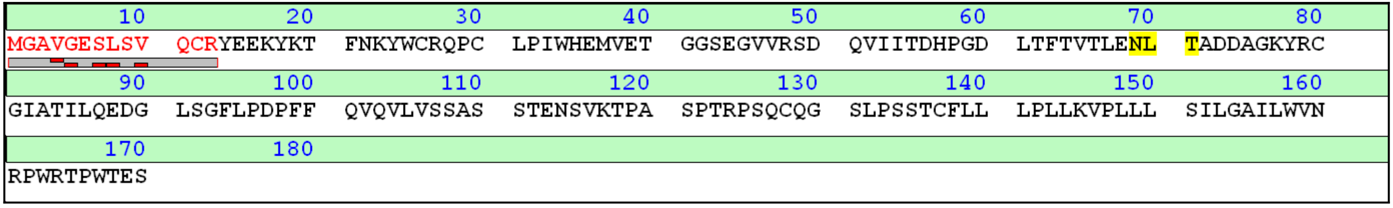
Detailed Protein Report

Protein 482: PREDICTED: CD300c molecule-like isoform X1 [Homo sapiens]

Accession:	gi|530356604	**Score:**	19.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	18.8
Database Date:	2015-11-30	**pI:**	5.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	7.6
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578846497	refseq_human (refseq_human_20140103.fasta)	PREDICTED: CD300c molecule-like isoform X4 [Homo sapiens]
gi|578831945	refseq_human (refseq_human_20140103.fasta)	PREDICTED: CD300c molecule-like isoform X3 [Homo sapiens]



```
        10         20         30         40         50         60         70         80
MGAVGESLSV QCRYEEKYKT FNKYWCRQPC LPIWHEMVET GGSEGVVRSD QVIITDHPGD LTFTVTLENL TADDAGKYRC
        90        100        110        120        130        140        150        160
GIATILQEDG LSGFLPDPFF QVQVLVSSAS STENSVKTPA SPTRPSQCQG SLPSSTCFLL LPLLKVPLLL SILGAILWVN
       170        180
RPWRTPWTES
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2788	2	676.8636	66.68	2	63.4	19.2	0	1-13	-.MGAVGESLSVQCR.Y	Oxidation: 1

Detailed Protein Report

Protein 483: 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 484: **PREDICTED: rho guanine nucleotide exchange factor 15 isoform X3 [Homo sapiens]**

Accession:	gi|578829770	**Score:**	18.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	85.0
Database Date:	2015-11-30	**pI:**	10.3
		Sequence Coverage [%]:	2.3
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MSAQSLPAAT PPTQKPPRII RPRPPSRSRA AQSPGPPHNG SSPQELPRNS NDAPTPMCTP IFWEPPAASL KPPALLPPSA
        90        100        110        120        130        140        150        160
SRASLDSQTS PDSPSSTPTP SPVSRRSASP EPAPRSPVPP PKPSGSPCTP LLPMAGVLAQ NGSASAPGTV RRLAGRFEGG
       170        180        190        200        210        220        230        240
AEGRAQDADA PEPGLQARAD VNGEREAPLT GSGSQENGAP DAGLACPPCC PCVCHTTRPG LELRWVPVGG YEEVPRVPRR
       250        260        270        280        290        300        310        320
ASPLRTSRSR PHPPSIGHPA VVLTSYRSTA ERKLLPLLKP PKPTRVRQDA TIFGDPPQPD LDLLSEDGIQ TGDSPDEAPQ
       330        340        350        360        370        380        390        400
NTPPATVEGR EEEGLEVLKE QNWELPLQDE PLYQTYRAAV LSEELWGVGE DGSPSPANAG DAPTFPRPPG PRNTLWQELP
       410        420        430        440        450        460        470        480
AVQASGLLDT LSPQERRMQE SLFEVVTSEA SYLRSLRLLT DTFVLSQALR DTLTPRDHHT LFSNVQRVQG VSERFLATLL
       490        500        510        520        530        540        550        560
SRVRSSPHIS DLCDVVHAHA VGPFSVYVDY VRNQQYQEET YSRLMDTNVR FSAELRRLQS LPKCERLPLP SFLLLPFQRI
       570        580        590        600        610        620        630        640
TRLRMLLQNI LRQTEEGSSR QENAQKALGA VSKIIERCSA EVGRMKQTEE LIRLTQRLRF HKVKALPLVS WSRRLEFQGE
       650        660        670        680        690        700        710        720
LTELGCRRGG VLFASRPRFT PLCLLLFSDL LLITQPKRPS RFRIHLDPLP SASPFSATTR AAPPTDYSKL LPYQTCSAGW
       730        740        750        760        770        780
EPSQPQAPFP APQTPSMRTV TVPRNCVQSR LHLPRLKDGV WSPGLPPNTC TRPLKVG
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1331	1	1023.0328	-98.25	2	45.4	18.8	2	268-285	R.STAERKLLPLLKPPKPTR.V	

Detailed Protein Report

Protein 485: 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 486: 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 487: 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 488: **PREDICTED: SH3-containing GRB2-like protein 3-interacting protein 1 isoform X9 [Homo sapiens]**

Accession:	gi|530363468	**Score:**	18.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	68.2
Database Date:	2015-11-30	**pI:**	9.4
		Sequence Coverage [%]:	1.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MMEGLKKRTR	KAFGIRKKEK	DTDSTGSPDR	DGIKKSNGAP	NGFYAEIDWE	RYNSPELDEE	GYSIRPEEPG	STKGKHFYSS
90	100	110	120	130	140	150	160
SESEEEEESH	KKFNIKIKPL	QSKDILKNAA	TVDELKASIG	NIALSPSPVG	AIKRNLSSEE	VARPRRSTPT	PELISKKPPD
170	180	190	200	210	220	230	240
DTTALAPLFG	PPLESAFDEQ	KTEVLLDQPE	IWGSGQPINP	SMESPKLTRP	FPTGTPPPLP	PKNVPATPPR	TGSPLTIGPG
250	260	270	280	290	300	310	320
ASSPARPATP	LVPCRSTTPP	PPPPRPPSRP	KLPPGKPGVG	DVSRPFSPPI	HSSSPPPIAP	LARAESTSSI	SSTNSLSAAT
330	340	350	360	370	380	390	400
TPTVENEQPS	LVWFDRGKFY	LTFEGSSRGP	SPLTMGAQDT	LPVAAAFTET	VNAYFKGADP	SKCIVKITGE	MVLSFPAGIT
410	420	430	440	450	460	470	480
RHFANNPSPA	ALTFRVINFS	RLEHVLPNPQ	LLCCDNTQND	ANTKEFWVNM	PNLMTHLKKV	SEQKPQATYY	NVDMLKYQVS
490	500	510	520	530	540	550	560
AQGIQSTPLN	LAVNWRCEPS	STDLRIDYKY	NTDAMTTAVA	LNNVQFLVPI	DGGVTKLQAV	LPPAVWNAEQ	QRILWKIPDI
570	580	590	600	610	620	630	
SQKSENGGVG	SLLARFQLSE	GPSKPSPLVV	QFTSEGSTLS	GCDIELVGAG	YRFSLIKKRF	AAGKYLADN	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
363	3	629.3611	47.90	2	33.2	18.5	0	135-145	R.NLSSEEVARPR.R	

Detailed Protein Report

Protein 489: PREDICTED: probable G-protein coupled receptor 142 isoform X1 [Homo sapiens]

Accession:	gi|530412100	**Score:**	18.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	41.1
Database Date:	2015-11-30	**pI:**	10.3
Modification(s):	Oxidation	**Sequence Coverage [%]:**	4.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLTGSCGDPQ	KKPQVTQDSG	PQSMGLEGRE	TAGQPRVTLL	PTPHVSGLSQ	EFESHWPEIA	ERSPCVAGVI	PVIYYSVLLG
90	100	110	120	130	140	150	160
LGLPVSLLTA	VALARLATRT	RRPSYYYLLA	LTASDIIIQV	VIVFAGFLLQ	GAVLARQVPQ	AVVRTANILE	FAANHASVWI
170	180	190	200	210	220	230	240
AILLTVDRYT	ALCHPLHHRA	ASSPGRTRRA	IAAVLSAALL	TGIPFYWWLD	MWRDTDSPRT	LDEVLKWAHC	LTVYFIPCGV
250	260	270	280	290	300	310	320
FLVTNSAIIH	RLRRRGRSGL	QPRVGKSTAI	LLGITTLFTL	LWAPRVFVML	YHMYVAPVHR	DWRVHLALDV	ANMVAMLHTA
330	340	350	360	370	380		
ANFGLYCFVS	KTFRATVRQV	IHDAYLPCTL	ASQPEGMAAK	PVMEPPGLPT	GAEV		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2323	1	965.9652	-2.87	2	57.3	18.4	0	12-29	K.KPQVTQDSGPQSMGLEGR.E	Oxidation: 13

Detailed Protein Report

Protein 490: PREDICTED: anamorsin isoform X3 [Homo sapiens]

Accession:	gi|530424142	**Score:**	18.3
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
1841	2	785.8992	-40.49	2	51.4	18.3	1	27-41	K.GLVDKLQALTGNEGR.V	

Detailed Protein Report

Protein 491: **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 492: protein FAM107A isoform a [Homo sapiens]

Accession:	gi|6005924	**Score:**	18.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	17.4
Database Date:	2015-11-30	**pI:**	10.3
		Sequence Coverage [%]:	12.5
		No. of unique Peptides:	1

Quantitation

WD:WU	**Median:** 5.87	**CV:** 0.00 %	**No. of Peptides:** 1

Alias proteins:

Accession	Name	Description
gi|530371819	refseq_human (refseq_human_20140103.fasta)	PREDICTED: protein FAM107A isoform X3 [Homo sapiens]
gi|115583665	refseq_human (refseq_human_20140103.fasta)	protein FAM107A isoform a [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MYSEIQRERA DIGGLMARPE YREWNPELIK PKKLLNPVKA SRSHQELHRE LLMNHRRGLG VDSKPELQRV LEHRRRNQLI
        90        100        110        120        130        140        150
KKKKEELEAK RLQCPFEQEL LRRQQRLNQL EKPPEKEEDH APEFIKVREN LRRIATLTSE EREL
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2090	1	696.9638	-136.58	3	54.5	18.1	2	57-74	R.RGLGVDSKPELQRVLEHR.R		WD:WU 5.87

Detailed Protein Report

Protein 493: eosinophil peroxidase preproprotein [Homo sapiens]

Accession:	gi|4503595	**Score:**	18.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	81.0
Database Date:	2015-11-30	**pI:**	11.5
		Sequence Coverage [%]:	2.2
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578831504	refseq_human (refseq_human_20140103.fasta)	PREDICTED: eosinophil peroxidase isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MHLLPALAGV	LATLVLAQPC	EGTDPASPGA	VETSVLRDCI	AEAKLLVDAA	YNWTQKSIKQ	RLRSGSASPM	DLLSYFKQPV
90	100	110	120	130	140	150	160
AATRTVVRAA	DYMHVALGLL	EEKLQPQRSG	PFNVTDVLTE	PQLRLLSQAS	GCALRDQAER	CSDKYRTITG	RCNNKRRPLL
170	180	190	200	210	220	230	240
GASNQALARW	LPAEYEDGLS	LPFGWTPSRR	RNGFLLPLVR	AVSNQIVRFP	NERLTSDRGR	ALMFMQWGQF	IDHDLDFSPE
250	260	270	280	290	300	310	320
SPARVAFTAG	VDCERTCAQL	PPCFPIKIPP	NDPRIKNQRD	CIPFFRSAPS	CPQNKNRVRN	QINALTSFVD	ASMVYGSEVS
330	340	350	360	370	380	390	400
LSLRLRNRTN	YLGLLAINQR	FQDNGRALLP	FDNLHDDPCL	LTNRSARIPC	FLAGDTRSTE	TPKLAAMHTL	FMREHNRLAT
410	420	430	440	450	460	470	480
ELRRLNPRWN	GDKLYNEARK	IMGAMVQIIT	YRDFLPLVLG	KARARRTLGH	YRGYCSNVDP	RVANVFTLAF	RFGHTMLQPF
490	500	510	520	530	540	550	560
MFRLDSQYRA	SAPNSHVPLS	SAFFASWRIV	YEGGIDPILR	GLMATPAKLN	RQDAMLVDEL	RDRLFRQVRR	IGLDLAALNM
570	580	590	600	610	620	630	640
QRSRDHGLPG	YNAWRRFCGL	SQPRNLAQLS	RVLKNQDLAR	KFLNLYGTPD	NIDIWIGAIA	EPLLPGARVG	PLLACLFENQ
650	660	670	680	690	700	710	720
FRRARDGDRF	WWQKRGVFTK	RQRKALSRIS	LSRIICDNTG	ITTVSRDIFR	ANIYPRGFVN	CSRIPRLNLS	AWRGT

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2217	1	927.3936	-145.10	2	56.1	18.0	2	547-562	R.QVRRIGLDLAALNMQR.S	

Detailed Protein Report

Protein 494: 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 495: transmembrane protein 151A [Homo sapiens]

Accession:	gi|23397566	**Score:**	17.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	51.2
Database Date:	2015-11-30	**pI:**	9.3
		Sequence Coverage [%]:	3.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPEDGAGDGG	EVPALIPDGE	PLREEQRPLK	QSLGSSLCRE	SHWKCLLLTL	LIHACGAVVA	WCRLATVPRL	VLGPEAALAR
90	100	110	120	130	140	150	160
GAGGPPPTYP	ASPCSDGYLY	IPLAFVSLLY	LLYLAECWHC	HVRSCQAPRT	DAHTVLALIR	RLQQAPPCVW	WKATSYHYVR
170	180	190	200	210	220	230	240
RTRQITRYRN	GDAYTTTQVY	HERADSRTAR	GEFDYSAHGV	RDVSKELVGL	AEHAATRLRF	TKCFSFGSAE	AEASYLTQRA
250	260	270	280	290	300	310	320
RFFSANEGLD	DYLEAREGMH	LKDVDFRESL	MVFADPRSPP	WYARAWVFWL	VSAATLSWPL	RVVAAYGTAH	VHYQVEKLFG
330	340	350	360	370	380	390	400
ASSPPPGAVP	SGPPLSRVAT	VDFTELEWHI	CSNRQLVPSY	SEAVVMGAGS	GAYLRGCQRC	RRSVSSNSLP	PARPSGPRLP
410	420	430	440	450	460	470	
FSRSRLSLGA	GGRATPGVFR	SLSGGPLGRR	GEDTEPLESP	PCYEDALYFP	VLIVHGDSGC	QGDGQGAL	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1863	1	864.4736	-15.26	2	52.0	17.8	2	414-430	R.ATPGVFRSLSGGPLGRR.G	

Detailed Protein Report

Protein 496: **NUT family member 1 isoform 3 [Homo sapiens]**

Accession:	gi|50233787	**Score:**	17.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	120.3
Database Date:	2015-11-30	**pI:**	5.2
		Sequence Coverage [%]:	1.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MASDGASALP	GPDMSMKPSA	ALSPSPALPF	LPPTSDPPDH	PPREPPPQPI	MPSVFSPDNP	LMLSAFPSSL	LVTGDGGPCL
90	100	110	120	130	140	150	160
SGAGAGKVIV	KVKTEGGSAE	PSQTQNFILT	QTALNSTAPG	TPCGGLEGPA	PPFVTASNVK	TILPSKAVGV	SQEGPPGLPP
170	180	190	200	210	220	230	240
QPPPPVAQLV	PIVPLEKAWP	GPHGTTGEGG	PVATLSKPSL	GDRSKISKDV	YENFRQWQRY	KALARRHLSQ	SPDTEALSCF
250	260	270	280	290	300	310	320
LIPVLRSLAR	LKPTMTLEEG	LPLAVQEWEH	TSNFDRMIFY	EMAERFMEFE	AEEMQIQNTQ	LMNGSQGLSP	ATPLKLDPLG
330	340	350	360	370	380	390	400
PLASEVCQQP	VYIPKKAASK	TRAPRRRQRK	AQRPPAPEAP	KEIPPEAVKE	YVDIMEWLVG	THLATGESDG	KQEEEGQQQE
410	420	430	440	450	460	470	480
EEGMYPDPGL	LSYINELCSQ	KVFVSKVEAV	IHPQFLADLL	SPEKQRDPLA	LIEELEQEEG	LTLAQLVQKR	LMALEEEEDA
490	500	510	520	530	540	550	560
EAPPSFSGAQ	LDSSPSGSVE	DEDGDGRLRP	SPGLQGAGGA	ACLGKVSSSG	KRAREVHGGQ	EQALDSPRGM	HRDGNTLPSP
570	580	590	600	610	620	630	640
SSWDLQPELA	APQGTPGPLG	VERRGSGKVI	NQVSLHQDGH	LGGAGPPGHC	LVADRTSEAL	PLCWQGGFQP	ESTPSLDAGL
650	660	670	680	690	700	710	720
AELAPLQGQG	LEKQVLGLQK	GQQTGGRGVL	PQGKEPLAVP	WEGSSGAMWG	DDRGTPMAQS	YDQNPSPRAA	GERDDVCLSP
730	740	750	760	770	780	790	800
GVWLSSEMDA	VGLELPVQIE	EVIESFQVEK	CVTEYQEGCQ	GLGSRGNISL	GPGETLVPGD	TESSVIPCGG	TVAAAALEKR
810	820	830	840	850	860	870	880
NYCSLPGPLR	ANSPPLRSKE	NQEQSCETVG	HPSDLWAEGC	FPLLESGDST	LGSSKETLPP	TCQGNLLIMG	TEDASSLPEA
890	900	910	920	930	940	950	960
SQEAGSRGNS	FSPLLETIEP	VNILDVKDDC	GLQLRVSEDT	CPLNVHSYDP	QGEGRVDPDL	SKPKNLAPLQ	ESQESYTTGT
970	980	990	1000	1010	1020	1030	1040
PKATSSHQGL	GSTLPRRGTR	NAIVPRETSV	SKTHRSADRA	KGKEKKKKEA	EEEDEELSNF	AYLLASKLSL	SPREHPLSPH
1050	1060	1070	1080	1090	1100	1110	1120
HASGGQGSQR	ASHLLPAGAK	GPSKLPYPVA	KSGKRALAGG	PAPTEKTPHS	GAQLGVPREK	PLALGVVRPS	QPRKRRCDSF
1130	1140						
VTGRRKKRRR	SQ						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1503	1	671.1069	119.58	3	47.1	17.8	2	800-817	K.RNYCSLPGPLRANSPPLR.S	

Detailed Protein Report

Protein 497: **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

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
940	2	567.1435	-248.79	2	40.6	17.8	0	77-86	K.GEMPVQLTSR.R	Oxidation: 3

Detailed Protein Report

Protein 498: 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 499: PREDICTED: Golgin-45 isoform X1 [Homo sapiens]

Accession:	gi|530365531	**Score:**	17.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	30.1
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
MTTKNLETKV	TVTSSPIRGA	GDGMETEEPP	KSVEVTSGVQ	SRKHHSLQSP	WKKAVPSESP	GVLQLGKMLT	EKAMEVKAVR
90	100	110	120	130	140	150	160
ILVPKAAITH	DIPNKNTKVK	SLGHHKGEFL	GQSEGVIEPN	KELSEVKNVL	EKLKNSERRL	LQDKEGLSNQ	LRVQTEVNRE
170	180	190	200	210	220	230	240
LKKLLVASVG	DDLQYHFERL	AREKNQLILE	NEALGRNTAQ	LSEQLERMSI	QCDVWRSKFL	ASRVMADELT	NSRAALQRQN
250	260	270					
RDAHGAIQDL	LSEREQFRQE	MIATQKF					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
131	2	608.2888	-81.31	2	30.9	17.7	1	153-162	R.VQTEVNRELK.K	

Detailed Protein Report

Protein 500: PREDICTED: complement factor H-related protein 2 isoform X1 [Homo sapiens]

Accession:	gi|530364612	**Score:**	17.7
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
11	1	1069.4808	-32.42	3	29.1	17.7	2	129-155	R.NGQWSEPPKCLDPCVISQEIMEKYNIK.L	Carbamidomethyl: 10

Detailed Protein Report

Protein 501: 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 502: E-selectin precursor [Homo sapiens]

Accession:	gi|187960042	**Score:**	17.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	66.6
Database Date:	2015-11-30	**pI:**	5.1
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	2.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MIASQFLSAL	TLVLLIKESG	AWSYNTSTEA	MTYDEASAYC	QQRYTHLVAI	QNKEEIEYLN	SILSYSPSYY	WIGIRKVNNV
90	100	110	120	130	140	150	160
WVWVGTQKPL	TEEAKNWAPG	EPNNRQKDED	CVEIYIKREK	DVGMWNDERC	SKKKLALCYT	AACTNTSCSG	HGECVETINN
170	180	190	200	210	220	230	240
YTCKCDPGFS	GLKCEQIVNC	TALESPEHGS	LVCSHPLGNF	SYNSSCSISC	DRGYLPSSME	TMQCMSSGEW	SAPIPACNVV
250	260	270	280	290	300	310	320
ECDAVTNPAN	GFVECFQNPG	SFPWNTTCTF	DCEEGFELMG	AQSLQCTSSG	NWDNEKPTCK	AVTCRAVRQP	QNGSVRCSHS
330	340	350	360	370	380	390	400
PAGEFTFKSS	CNFTCEEGFM	LQGPAQVECT	TQGQWTQQIP	VCEAFQCTAL	SNPERGYMNC	LPSASGSFRY	GSSCEFSCEQ
410	420	430	440	450	460	470	480
GFVLKGSKRL	QCGPTGEWDN	EKPTCEAVRC	DAVHQPPKGL	VRCAHSPIGE	FTYKSSCAFS	CEEGFELHGS	TQLECTSQGQ
490	500	510	520	530	540	550	560
WTEEVPSCQV	VKCSSLAVPG	KINMSCSGEP	VFGTVCKFAC	PEGWTLNGSA	ARTCGATGHW	SGLLPTCEAP	TESNIPLVAG
570	580	590	600	610	620		
LSAAGLSLLT	LAPFLLWLRK	CLRKAKKFVP	ASSCQSLESD	GSYQKPSYIL			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2878	1	872.9387	57.19	2	64.7	17.6	0	502-517	K.INMSCSGEPVFGTVCK.F	Carbamidomethyl: 15; Oxidation: 3

Detailed Protein Report

Protein 503: **amiloride-sensitive sodium channel subunit alpha isoform 1 [Homo sapiens]**

Accession:	gi|4506815	**Score:**	17.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	75.7
Database Date:	2015-11-30	**pI:**	8.5
		Sequence Coverage [%]:	2.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEGNKLEEQD	SSPPQSTPGL	MKGNKREEQG	LGPEPAAPQQ	PTAEEEALIE	FHRSYRELFE	FFCNNTTIHG	AIRLVCSQHN
90	100	110	120	130	140	150	160
RMKTAFWAVL	WLCTFGMMYW	QFGLLFGEYF	SYPVSLNINL	NSDKLVFPAV	TICTLNPYRY	PEIKEELEEL	DRITEQTLFD
170	180	190	200	210	220	230	240
LYKYSSFTTL	VAGSRSRRDL	RGTLPHPLQR	LRVPPPPHGA	RRARSVASSL	RDNNPQVDWK	DWKIGFQLCN	QNKSDCFYQT
250	260	270	280	290	300	310	320
YSSGVDAVRE	WYRFHYINIL	SRLPETLPSL	EEDTLGNFIF	ACRFNQVSCN	QANYSHFHHP	MYGNCYTFND	KNNSNLWMSS
330	340	350	360	370	380	390	400
MPGINNGLSL	MLRAEQNDFI	PLLSTVTGAR	VMVHGQDEPA	FMDDGGFNLR	PGVETSISMR	KETLDRLGGD	YGDCTKNGSD
410	420	430	440	450	460	470	480
VPVENLYPSK	YTQQVCIHSC	FQESMIKECG	CAYIFYPRPQ	NVEYCDYRKH	SSWGYCYYKL	QVDFSSDHLG	CFTKCRKPCS
490	500	510	520	530	540	550	560
VTSYQLSAGY	SRWPSVTSQE	WVFQMLSRQN	NYTVNNKRNG	VAKVNIFFKE	LNYKTNSESP	SVTMVTLLSN	LGSQWSLWFG
570	580	590	600	610	620	630	640
SSVLSVVEMA	ELVFDLLVIM	FLMLLRRFRS	RYWSPGRGGR	GAQEVASTLA	SSPPSHFCPH	PMSLSLSQPG	PAPSPALTAP
650	660	670					
PPAYATLGPR	PSPGGSAGAS	SSTCPLGGP					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2868	1	873.7778	-171.39	2	64.6	17.6	0	477-492	R.KPCSVTSYQLSAGYSR.W	

Detailed Protein Report

Protein 504: **PREDICTED: leucine-rich repeat and IQ domain-containing protein 1 isoform X6 [Homo sapiens]**

Accession:	gi|578824314	**Score:**	17.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	191.8
Database Date:	2015-11-30	**pI:**	5.8
		Sequence Coverage [%]:	1.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDDDDAKLKA	EIEAELDKLS	ISSLEKEDIE	SDAKSETQSD	DSDTDSVELP	ESVLHCINII	KNRSKAVEEL	ILQDLEDTDI
90	100	110	120	130	140	150	160
LSCSYGAVSN	NHMHLRTGLS	TEYEESSEQL	IKILSEIEKE	EFMRSKTDCA	TPDFVPEPSP	HDLPMDEHVL	PDDADINFGY
170	180	190	200	210	220	230	240
CEVEEKCRQS	FEAWQEKQKE	LEDKEKQTLK	AQRDREEKQF	QEEEEKRHCW	MKQFKVEKKK	LENIQKQEQD	KMNDELYKEE
250	260	270	280	290	300	310	320
KIWKEKFKQH	EEYIRNLHLQ	MEEERTRFKD	QQEKEKNSLL	KQQNNAAVKI	QAKYKAFVAY	QKYGPIIKEQ	IESKKRKAQE
330	340	350	360	370	380	390	400
WKEKEAKIRQ	KEEENRKRLE	EEQRIKEERK	KQKEEERKRR	EKEYEEKKNI	VKQEREQLIS	KEKIILREDA	SQQLIISSAL
410	420	430	440	450	460	470	480
KKSGYNNKHL	SLEDISNDKG	DIAKNLVDEN	SKKQEDVLLW	LVEESNMKEN	VDRQTILKES	IQVKLKESIS	SQTILADFKM
490	500	510	520	530	540	550	560
EEKNENLAKK	RCSEELVKQE	RKYENTDNKT	ELGNSDLKGN	LKEQFPLQEL	KSDAQKEEKI	MKHVINENTG	QKTQIILGHN
570	580	590	600	610	620	630	640
QEISEVKTNE	EQKIIKDNQQ	KKIQKVEKEE	IQEQNGLLYK	DKDTLVISVK	QRSLSLTSEN	SKDVRENVIL	QEKEIYSKSK
650	660	670	680	690	700	710	720
EIEENPKDNA	WNSGIVIFNT	TDTMINIEGK	RNDQDYVLGR	HAPCEGLSNY	NAESSMVSKE	VNSLKSEIRN	ISEKCHENAP
730	740	750	760	770	780	790	800
EPDSMTCCVS	ESTLLYSIEE	RRLAWIKSFK	PWLEIFKQNQ	QKKIVRRKRP	VKCPANMTPA	LDKLEILRCG	PWDTLQQVTT
810	820	830	840	850	860	870	880
VTFQDLPGCV	LSTLAECTNL	QFLSLRRCGL	TSLHSLSNCK	KLKYIDAQEN	HIEAIECENL	ENLCVVLLNK	NQLTSLHGLD
890	900	910	920	930	940	950	960
GCTNIQCLEL	SYNKITRIGG	LESLKNLQQL	ILDHNQLINT	KGLCDTPTIV	YLDCSHNHLT	DVEGVENCGL	LQILKLQGNY
970	980	990	1000	1010	1020	1030	1040
LSELPSLENL	VLLRELHLDD	NSISTVEAFS	SYWLPLLQNI	TISQNSLTKI	VPLFHFVSLE	KLDVSHNCLS	DLKSAIKWFD
1050	1060	1070	1080	1090	1100	1110	1120
ACYSLHELSL	TGNPLLQETN	WRDSLLKVLP	ALRILNGNIL	NSNSESRTEE	HNQLGSAGFL	ALCQSQIREF	NLLIENYITG
1130	1140	1150	1160	1170	1180	1190	1200
KGDVFTLDTA	ENLCHYFKKL	MILSTEYRHA	HERGDVTITK	KDESEAQKNH	LAPTNSDSTL	QNGVFYSCAR	EGEPDSPDIP
1210	1220	1230	1240	1250	1260	1270	1280
EKWMDSVSSH	SPLSKSATCE	NMEGRHQEIL	VCQKREDSKA	SSIPTIRIPF	KEVVMTNSLL	RNHQNIEPSE	KIMAAVVIQS
1290	1300	1310	1320	1330	1340	1350	1360
YWRGYLMRRQ	THFSTRLHTA	ATEGLPNSSI	KNQTILKKGK	RENIVNIRKQ	REKAAILIQA	VWKGFILRKK	LTTALEAIKN
1370	1380	1390	1400	1410	1420	1430	1440
EESDEEYREI	DLEDFIFDEA	ALEEEWLALD	STRFPSQTLL	LSNQLHWPKI	PGNLKWDDTS	FNLPSNPAQA	WLCNDKENLS
1450	1460	1470	1480	1490	1500	1510	1520
SSEHTQFNSR	SENKTSSWTP	ESKTSRKSLL	KSEKEKKISE	EWGFKDISTA	QQMLKRAQKM	KSKKLKKKID	STVRLALFKN
1530	1540	1550	1560	1570	1580	1590	1600
NENKVSLPKS	PKMVQPRRDG	YFEGIEEDPI	HKDTTANEKL	ERNREYTYQW	LHTQVGVHET	TSSRNMKCNH	FLPELDPDVL
1610	1620	1630	1640	1650	1660		
NGGRVQLVAR	LVSREDTDLD	LFSMTNGSAL	SVNREKKNQA	HRHSAGSSSK	LWFPSKLI		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
862	1	1198.5391	-67.11	2	39.2	17.6	1	1290-1311	R.QTHFSTRLHTAATEGLPNSSIK.N	

Detailed Protein Report

Protein 505: 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 506: 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	1	676.1711	-187.18	2	37.3	17.5	1	137-147	R.CHREDQVYACK.L	

Detailed Protein Report

Protein 507: uncharacterized protein KIAA0947 [Homo sapiens]

Accession:	gi|149363685	**Score:**	17.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	247.7
Database Date:	2015-11-30	**pI:**	5.2
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MMPGETHSAA	PGTAADLSRC	QGCASLQQNL	NEYVEALITL	KQKIINTDNL	LTEYQKKCDE	LQFARRENSN	LHHQVEEMLQ
90	100	110	120	130	140	150	160
KISPLQKCQE	ELGSLKAELE	EKKSSLKLYQ	DTHQEYARVK	EECLKSDAQK	KKLEAKVKKL	QEAAVKQTQD	FKQLRNEKKI
170	180	190	200	210	220	230	240
LEKEFKKTQE	RLDEFSKQKN	EKELRHIGTQ	ISSDSYGSID	KRKVKLLLKE	LWLCVNTTHR	LPGEGSRCVP	EKPAKAITSS
250	260	270	280	290	300	310	320
RVPGEDGTLP	PTQGSPLRTS	NVQTCLTKLS	MEIKEDFLCQ	NVEKQSSSGT	NCSSDHVFNE	NGNLEVLVQS	HRDGGSTEFV
330	340	350	360	370	380	390	400
DHDHFFDEDL	QAAIDFFKLP	PPLLSPVPSP	PPMSSPHPGS	LPSSFAPETY	FGEYTDSSDN	DSVQLRNSAE	CVSEDDTTES
410	420	430	440	450	460	470	480
QNYFGSLRKN	KGSGTWEEKP	KSHEAIQALN	TWEVNKVTTS	GLETFTATLR	ESSATHSLVG	EKHWTTASRS	MSDRKRDILH
490	500	510	520	530	540	550	560
ETKTQMEVRE	MDKSVQTEKT	IHKLTRGLCI	ERLSASPAQE	KEAAPGKSEL	CSSPLGKRPL	NELMESEGKT	VLSKMMGSPK
570	580	590	600	610	620	630	640
SEFTKWTRIN	EITSEPDRIT	VSGHFHRLSR	ELEKEKEDTQ	GFTLGESPES	EDDDSGDGMD	VAGLDIETSF	SSSSTLVALS
650	660	670	680	690	700	710	720
VGSNPQSSSG	LDCGNDTDIT	TKVFSTEPHH	SEHKLQTKTL	NTLHLQSEPP	ECSIGGNNLE	NSLCALSPEL	GASNFNDQKS
730	740	750	760	770	780	790	800
SGIEYTKVVK	GLTKIHSLPR	SVFMKATKDG	QCESQDPRIE	LTLNKPDFTS	LIGSQAALIK	SGLGFVKSTS	WHHSDLLRKG
810	820	830	840	850	860	870	880
GEESLRAKSE	HEQKTSHQLQ	KAMPFLQNRG	PTPKPDLLRE	NNNPVEFKTT	ASVLPNQVSV	ITKQTRPEKV	QSAKLEHLRP
890	900	910	920	930	940	950	960
HRVEPTLVTE	NSGNKTGMST	VAKCDGERDD	TTQNITEVAA	VKSISPEVSA	SRRKLDFNSP	GGSSPVENSD	CSTNSRLSFS
970	980	990	1000	1010	1020	1030	1040
PENILIQNQD	IVREAAVQGD	GQKQRQPQAT	DLDSSGTHGS	EMLPATEVTV	SGGFSVEETS	CGDTGRSGGE	ALAVANDSTS
1050	1060	1070	1080	1090	1100	1110	1120
TPQNANGLWK	LKSTTPGGAL	PECFGTTDTT	FSSAFCRKHG	ETQDTSQSSL	PGTLHCYTGI	REGGDDTEVE	SEAFSCSEGS
1130	1140	1150	1160	1170	1180	1190	1200
EQQDAPDDSQ	KNLGDTDAAV	AEVRPSLEVG	YLTSALQDFN	ISTFSELDRL	STSEVVMFLE	SCQLGDYSSG	DSVSECSSKG
1210	1220	1230	1240	1250	1260	1270	1280
TLSKEMNKEL	KASEIGEKYR	KQPCEEETLG	TCEEWIESEE	DDYSLKNTSQ	LTQCSLETLS	EVLTKIRQEL	QTNSEDCNGK
1290	1300	1310	1320	1330	1340	1350	1360
DTGSLLLLNV	NNNMTTENLK	EKSPFRETTG	SSSHASEPTP	QAAALDTEGS	SPISGMPQNE	NPQSRPEARS	DAGRQTDGGE
1370	1380	1390	1400	1410	1420	1430	1440
EDLPEPVEPS	ALCSDSVMEP	SIEQSSNCEA	ETTFQCQIAT	VTSEVINVLI	NKDQNLVIEK	GDNWTIISGV	AVLPHVDQVT
1450	1460	1470	1480	1490	1500	1510	1520
LCDIPGDIPI	SQDQGELEAG	CIPVTSAEKS	PEASHTGPAF	QEAPCGNNLS	CPQEDVSSSG	QSTNFDKSRL	RNRPVKPSIW
1530	1540	1550	1560	1570	1580	1590	1600
ISSQIYDQNF	ETQIVASDHT	YYNSKLEPSG	KNKNRSKISN	KDQSNKPVKT	SASSRVETHQ	SEVAQSFSGE	KANTKTQRSQ
1610	1620	1630	1640	1650	1660	1670	1680
TQTILANADT	STPTDCSPDT	LSKIRQEVGP	PLPPLLAPLI	ATPPRTSQPL	SPLISSSSPS	SPASPVGQVS	PFRETPVPPA
1690	1700	1710	1720	1730	1740	1750	1760
MSPWPEDPRR	ASPPDPSPSP	SAASASERVV	PSPLQFCAAT	PKHALPVPGR	LPPCASGHAA	VGGPQENSVK	ILDTMYPELS
1770	1780	1790	1800	1810	1820	1830	1840
ARARTLNILK	GNIQLTRGPP	ADCKNLPGPA	SAMIGFKTIT	SAATAFVKTG	SSSGGDCNQD	KSRDLGTQQD	SSGKRTLSTS
1850	1860	1870	1880	1890	1900	1910	1920
TLRSAKRLRL	DTGSPEPETR	GVTAEGIHKN	LPGNLPPAEV	ATTNEERSCS	SPAVSAVSQL	PLSPKETVES	HDKAIANALK
1930	1940	1950	1960	1970	1980	1990	2000
KIAEFSFDLL	PVIRSHVYVG	NISKKPVMRD	QEKEVVYEFS	TTKKHLAECL	LHSILSELKI	QKISMDHNYI	HALCRVYVGI
2010	2020	2030	2040	2050	2060	2070	2080
CRQLGDLERA	RLFCYSLLKE	DFPESEKLTL	FIANMWHDIF	LSQSVINKAM	QLVARQRAKG	EVLNCLRAFL	NWEKNAPVDV
2090	2100	2110	2120	2130	2140	2150	2160
GFMVSKLLLT	IQLCPKTEFQ	PSEKFGEDLS	DNTWEYIFAI	DLLCCHQKWI	WTHDNIISKE	LWPVMDKWIK	YRKGHANIAY
2170	2180	2190	2200	2210	2220	2230	2240
TPDIIIASIL	RLIGRLGQLG	LKEGFPSAVK	NISSVIGMFI	QHAHDEDIPW	GIQLAAVYAL	CDLSPSNPAE	ISKILEAWRR
2250	2260	2270					
EASKSVPSAI	VSCLEEVSAL	STEELG					

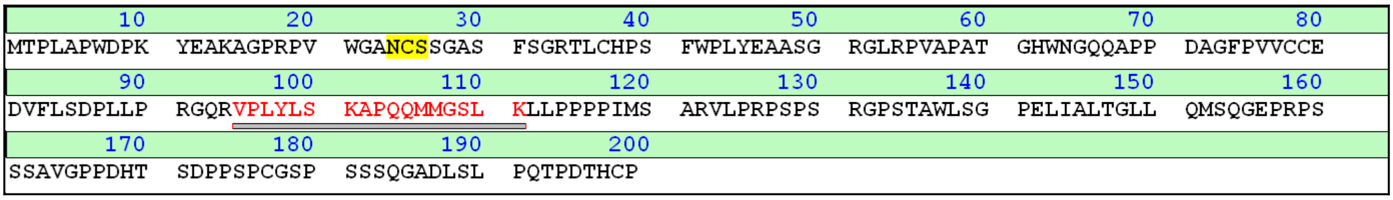
Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
9	1	803.7023	-79.81	3	29.3	17.5	1	1785-1808	K.NLPGPASAMIGFKTITSAATAFVK.T	Oxidation: 9

Detailed Protein Report

Protein 508: histone deacetylase complex subunit SAP25 [Homo sapiens]

Accession:	gi|284004891	**Score:**	17.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	20.9
Database Date:	2015-11-30	**pI:**	9.2
		Sequence Coverage [%]:	8.5
		No. of unique Peptides:	1



10	20	30	40	50	60	70	80
MTPLAPWDPK	YEAKAGPRPV	WGANCSSGAS	FSGRTLCHPS	FWPLYEAASG	RGLRPVAPAT	GHWNGQQAPP	DAGFPVVCCE
90	100	110	120	130	140	150	160
DVFLSDPLLP	RGQRVPLYLS	KAPQQMMGSL	KLLPPPPIMS	ARVLPRPSPS	RGPSTAWLSG	PELIALTGLL	QMSQGEPRPS
170	180	190	200				
SSAVGPPDHT	SDPPSPCGSP	SSSQGADLSL	PQTPDTHCP				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2810	2	945.9828	-31.58	2	63.7	17.5	1	95-111	R.VPLYLSKAPQQMMGSLK.L	

Detailed Protein Report

Protein 509: **sushi, von Willebrand factor type A, EGF and pentraxin domain-containing protein 1 precursor [Homo sapiens]**

Accession:	gi|148886654	**Score:**	17.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	389.9
Database Date:	2015-11-30	**pI:**	5.2
		Sequence Coverage [%]:	0.3
		No. of unique Peptides:	1

Quantitation

WD:WU	**Median:** 2.71	**CV:** 0.00 %	**No. of Peptides:** 1

Detailed Protein Report

10	20	30	40	50	60	70	80
MWPRLAFCCW	GLALVSGWAT	FQQMSPSRNF	SFRLFPETAP	GAPGSIPAPP	APGDEAAGSR	VERLGQAFRR	RVRLLRELSE
90	100	110	120	130	140	150	160
RLELVFLVDD	SSSVGEVNFR	SELMFVRKLL	SDFPVVPTAT	RVAIVTFSSK	NYVVPRVDYI	STRRARQHKC	ALLLQEIPAI
170	180	190	200	210	220	230	240
SYRGGGTYTK	GAFQQAAQIL	LHARENSTKV	VFLITDGYSN	GGDPRPIAAS	LRDSGVEIFT	FGIWQGNIRE	LNDMASTPKE
250	260	270	280	290	300	310	320
EHCYLLHSFE	EFEALARRAL	HEDLPSGSFI	QDDMVHCSYL	CDEGKDCCDR	MGSCKCGTHT	GHFECICEKG	YYGKGLQYEC
330	340	350	360	370	380	390	400
TACPSGTYKP	EGSPGGISSC	IPCPDENHTS	PPGSTSPEDC	VCREGYRASG	QTCELVHCPA	LKPPENGYFI	QNTCNNHFNA
410	420	430	440	450	460	470	480
ACGVRCHPGF	DLVGSSIILC	LPNGLWSGSE	SYCRVRTCPH	LRQPKHGHIS	CSTREMLYKT	TCLVACDEGY	RLEGSDKLTC
490	500	510	520	530	540	550	560
QGNSQWDGPE	PRCVERHCST	FQMPKDVIIS	PHNCGKQPAK	FGTICYVSCR	QGFILSGVKE	MLRCTTSGKW	NVGVQAAVCK
570	580	590	600	610	620	630	640
DVEAPQINCP	KDIEAKTLEQ	QDSANVTWQI	PTAKDNSGEK	VSVHVHPAFT	PPYLFPIGDV	AIVYTATDLS	GNQASCIFHI
650	660	670	680	690	700	710	720
KVIDAEPPVI	DWCRSPPPVQ	VSEKVHAASW	DEPQFSDNSG	AELVITRSHT	QGDLFPQGET	IVQYTATDPS	GNNRTCDIHI
730	740	750	760	770	780	790	800
VIKGSPCEIP	FTPVNGDFIC	TPDNTGVNCT	LTCLEGYDFT	EGSTDKYYCA	YEDGVWKPTY	TTEWPDCAKK	RFANHGFKSF
810	820	830	840	850	860	870	880
EMFYKAARCD	DTDLMKKFSE	AFETTLGKMV	PSFCSDAEDI	DCRLEENLTK	KYCLEYNYDY	ENGFAIGPGG	WGAANRLDYS
890	900	910	920	930	940	950	960
YDDFLDTVQE	TATSIGNAKS	SRIKRSAPLS	DYKIKLIFNI	TASVPLPDER	NDTLEWENQQ	RLLQTLETIT	NKLKRTLNKD
970	980	990	1000	1010	1020	1030	1040
PMYSFQLASE	ILIADSNSLE	TKKASPFCRP	GSVLRGRMCV	NCPLGTYYNL	EHFTCESCRI	GSYQDEEGQL	ECKLCPSGMY
1050	1060	1070	1080	1090	1100	1110	1120
TEYIHSRNIS	DCKAQCKQGT	YSYSGLETCE	SCPLGTYQPK	FGSRSCLSCP	ENTSTVKRGA	VNISACGVPC	PEGKFSRSGL
1130	1140	1150	1160	1170	1180	1190	1200
MPCHPCPRDY	YQPNAGKAFC	LACPFYGTTP	FAGSRSITEC	SSFSSTFSAA	EESVVPPASL	GHIKKRHEIS	SQVFHECFFN
1210	1220	1230	1240	1250	1260	1270	1280
PCHNSGTCQQ	LGRGYVCLCP	LGYTGLKCET	DIDECSPLPC	LNNGVCKDLV	GEFICECPSG	YTGQRCEENI	NECSSSPCLN
1290	1300	1310	1320	1330	1340	1350	1360
KGICVDGVAG	YRCTCVKGFV	GLHCETEVNE	CQSNPCLNNA	VCEDQVGGFL	CKCPPGFLGT	RCGKNVDECL	SQPCKNGATC
1370	1380	1390	1400	1410	1420	1430	1440
KDGANSFRCL	CAAGFTGSHC	ELNINECQSN	PCRNQATCVD	ELNSYSCKCQ	PGFSGKRCET	EQSTGFNLDF	EVSGIYGYVM
1450	1460	1470	1480	1490	1500	1510	1520
LDGMLPSLHA	LTCTFWMKSS	DDMNYGTPIS	YAVDNGSDNT	LLLTDYNGWV	LYVNGREKIT	NCPSVNDGRW	HHIAITWTSA
1530	1540	1550	1560	1570	1580	1590	1600
NGIWKVYIDG	KLSDGGAGLS	VGLPIPGGGA	LVLGQEQDKK	GEGFSPAESF	VGSISQLNLW	DYVLSPQQVK	SLATSCPEEL
1610	1620	1630	1640	1650	1660	1670	1680
SKGNVLAWPD	FLSGIVGKVK	IDSKSIFCSD	CPRLGGSVPH	LRTASEDLKP	GSKVNLFCDP	GFQLVGNPVQ	YCLNQGQWTQ
1690	1700	1710	1720	1730	1740	1750	1760
PLPHCERISC	GVPPPLENGF	HSADDFYAGS	TVTYQCNNGY	YLLGDSRMFC	TDNGSWNGVS	PSCLDVDECA	VGSDCSEHAS
1770	1780	1790	1800	1810	1820	1830	1840
CLNVDGSYIC	SCVPPYTGDG	KNCAEPIKCK	APGNPENGHS	SGEIYTVGAE	VTFSCQEGYQ	LMGVTKITCL	ESGEWNHLIP
1850	1860	1870	1880	1890	1900	1910	1920
YCKAVSCGKP	AIPENGCIEE	LAFTFGSKVT	YRCNKGYTLA	GDKESSCLAN	SSWSHSPPVC	EPVKCSSPEN	INNGKYILSG
1930	1940	1950	1960	1970	1980	1990	2000
LTYLSTASYS	CDTGYSLQGP	SIIECTASGI	WDRAPPACHL	VFCGEPPAIK	DAVITGNNFT	FRNTVTYTCK	EGYTLAGLDT
2010	2020	2030	2040	2050	2060	2070	2080
IECLADGKWS	RSDQQCLAVS	CDEPPIVDHA	SPETAHRLFG	DIAFYYCSDG	YSLADNSQLL	CNAQGKWVPP	EGQDMPRCIA
2090	2100	2110	2120	2130	2140	2150	2160
HFCEKPPSVS	YSILESVSKA	KFAAGSVVSF	KCMEGFVLNT	SAKIECMRGG	QWNPSPMSIQ	CIPVRCGEPP	SIMNGYASGS
2170	2180	2190	2200	2210	2220	2230	2240
NYSFGAMVAY	SCNKGFYIKG	EKKSTCEATG	QWSSPIPTCH	PVSCGEPPKV	ENGFLEHTTG	RIFESEVRYQ	CNPGYKSVGS
2250	2260	2270	2280	2290	2300	2310	2320
PVFVCQANRH	WHSESPLMCV	PLDCGKPPPI	QNGFMKGENF	EVGSKVQFFC	NEGYELVGDS	SWTCQKSGKW	NKKSNPKCMP
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
2764	2	639.3642	-0.12	2	63.1	17.4	2	903-913	R.IKRSAPLSDYK.I		WD:WU 2.71

Detailed Protein Report

Protein 510: PREDICTED: chromodomain-helicase-DNA-binding protein 7 isoform X4 [Homo sapiens]

Accession:	gi|578815680	**Score:**	17.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	214.1
Database Date:	2015-11-30	**pI:**	5.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	0.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
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
2811	1	995.0043	51.30	2	63.6	17.4	0	995-1010	K.LCQPSLDLPEWWECGR.H	Carbamidomethyl: 14

Detailed Protein Report

Protein 511: t-SNARE domain-containing protein 1 [Homo sapiens]

Accession:	gi|223972648	**Score:**	17.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	55.9
Database Date:	2015-11-30	**pI:**	10.2
		Sequence Coverage [%]:	1.6
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 1.10 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MSYGSIARGG	GLGSRGPFGG	PSRQGCQPLE	CARCWTEYGI	RHFPCPSPES	KLQNRCVGKD	GEGDLGPAGT	PIVPRARKRG
90	100	110	120	130	140	150	160
PGVAPEGSRM	PEPTSSPTIG	PRKDSAAGPH	GRMAGPSTTR	AKKRKPNFCP	QETEVLVSKV	SKHHQLLFGT	GLLKAEPTRR
170	180	190	200	210	220	230	240
YRVWSRILQA	VNALGYCRRD	VVDLKHKWRD	LRAVVRRKLG	DLRKAAHGPS	PGSGKPQALA	LTPVEQVVAK	TFSCQALPSE
250	260	270	280	290	300	310	320
GFSLEPPRAT	QVDPCNLQEL	FQEMSANVFR	INSSVTSLER	SLQSLGTPSD	TQELRDSLHT	AQQETNKTIA	ASASSVKQMA
330	340	350	360	370	380	390	400
ELLRSSCPQE	RLQQERPQLD	RLKTQLSDAI	QCYGVVQKKI	AEKSRALLPM	AQRGSKQSPQ	APFAELADDE	KVFNGSDNMW
410	420	430	440	450	460	470	480
QGQEQALLPD	ITEEDLEAIR	LREEAILQME	SNLLDVNQII	KDLASMVSEQ	GEAVDSIEAS	LEAASSHAEA	ARQLLAGASR
490	500	510	520				
HQLQRHKIKC	CFLSAGVTAL	LVIIIIIATS	VRK				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
258	1	442.7344	36.28	2	32.0	17.4	0	1-8	-.MSYGSIAR.G		WD:WU 1.10

Detailed Protein Report

Protein 512: **peptidyl-prolyl cis-trans isomerase A-like 4G [Homo sapiens]**

Accession:	gi|178057341	**Score:**	17.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	18.2
Database Date:	2015-11-30	**pI:**	10.0
Modification(s):	Oxidation	**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 513: PREDICTED: YLP motif-containing protein 1 isoform X1 [Homo sapiens]

Accession:	gi|530404193	**Score:**	17.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	231.6
Database Date:	2015-11-30	**pI:**	6.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	0.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MYPNWGRYGG	SSHYPPPPVP	PPPPVALPEA	SPGPGYSSST	TPAAPSSSGF	MSFREQHLAQ	LQQLQQMHQK	QMQCVLQPHH
90	100	110	120	130	140	150	160
LPPPPLPPPP	VMPGGGYGDW	QPPPPPMPPP	PGPALSYQKQ	QQYKHQMLHH	QRDGPPGLVP	MELESPPESP	PVPPGSYMPP
170	180	190	200	210	220	230	240
SQSYMPPPQP	PPSYYPPTSS	QPYLPPAQPS	PSQSPPSQSY	LAPTPSYSSS	SSSSQSYLSH	SQSYLPSSQA	SPSRPSQGHS
250	260	270	280	290	300	310	320
KSQLLAPPPP	SAPPGNKTTV	QQEPLESGAK	NKSTEQQQAA	PEPDPSTMTP	QEQQQYWYRQ	HLLSLQQRTK	VHLPGHKKGP
330	340	350	360	370	380	390	400
VVAKDTPEPV	KEEVTVPATS	QVPESPSSEE	PPLPPPNEEV	PPPLPPEEPQ	SEDPEEDARL	KQLQAAAAHW	QQHQQHRVGF
410	420	430	440	450	460	470	480
QYQGIMQKHT	QLQQILQQYQ	QIIQPPPHIQ	TMSVDMQLRH	YEMQQQQFQH	LYQEWEREFQ	LWEEQLHSYP	HKDQLQEYEK
490	500	510	520	530	540	550	560
QWKTWQGHMK	ATQSYLQEKV	NSFQNMKNQY	MGNMSMPPPF	VPYSQMPPPL	PTMPPPVLPP	SLPPPVMPPA	LPATVPPPGM
570	580	590	600	610	620	630	640
PPPVMPPSLP	TSVPPPGMPP	SLSSAGPPPV	LPPPSLSSAG	PPPVLPPPSL	SSTAPPPVMP	LPPLSSATPP	PGIPPPGVPQ
650	660	670	680	690	700	710	720
GIPPQLTAAP	VPPASSSQSS	QVPEKPRPAL	LPTPVSFGSA	PPTTYHPPLQ	SAGPSEQVNS	KAPLSKSALP	YSSFSSDQGL
730	740	750	760	770	780	790	800
GESSAAPSQP	ITAVKDMPVR	SGGLLPDPPR	SSYLESPRGP	RFDGPRRFED	LGSRCEGPRP	KGPRFEGNRP	DGPRPRYEGH
810	820	830	840	850	860	870	880
PAEGTKSKWG	MIPRGPASQF	YITPSTSLSP	RQSGPQWKGP	KPAFGQQHQQ	QPKSQAEPLS	GNKEPLADTS	SNQQKNFKMQ
890	900	910	920	930	940	950	960
SAAFSIAADV	KDVKAAQSNE	NLSDSQQEPP	KSEVSEGPVE	PSNWDQNVQS	METQIDKAQA	VTQPVPLANK	PVPAQSTFPS
970	980	990	1000	1010	1020	1030	1040
KTGGMEGGTA	VATSSLTADN	DFKPVGIGLP	HSENNQDKGL	PRPDNRDNRL	EGNRGNSSSY	RGPGQSRMED	TRDKGLVNRG
1050	1060	1070	1080	1090	1100	1110	1120
RGQAISRGPG	LVKQEDFRDK	MMGRREDSRE	KMNRGEGSRD	RGLVRPGSSR	EKVPGGLQGS	QDRGAAGSRE	RGPPRRAGSQ
1130	1140	1150	1160	1170	1180	1190	1200
ERGPLRRAGS	RERIPPRRAG	SRERGPPRGP	GSRERGLGRS	DFGRDRGPFR	PEPGDGGEKM	YPYHRDEPPR	APWNHGEERG
1210	1220	1230	1240	1250	1260	1270	1280
HEEFPLDGRN	APMERERLDD	WDRERYWREC	ERDYQDDTLE	LYNREDRFSA	PPSRSHDGDR	RGPWWDDWER	DQDMDEDYNR
1290	1300	1310	1320	1330	1340	1350	1360
EMERDMDRDV	DRISRPMDMY	DRSLDNEWDR	DYGRPLDEQE	SQFRERDIPS	LPPLPPLPPL	PPLDRYRDDR	WREERNREHG
1370	1380	1390	1400	1410	1420	1430	1440
YDRDFRDRGE	LRIREYPERG	DTWREKRDYV	PDRMDWERER	LSDRWYPSDV	DRHSPMAEHM	PSSHHSSEMM	GSDASLDSDQ
1450	1460	1470	1480	1490	1500	1510	1520
GLGGVMVLSQ	RQHEIILKAA	QELKMLREQK	EQLQKMKDFG	SEPQMADHLP	PQESRLQNTS	SRPGMYPPPG	SYRPPPPMGK
1530	1540	1550	1560	1570	1580	1590	1600
PPGSIVRPSA	PPARSSVPVT	RPPVPIPPPP	PPPPLPPPPP	VIKPQTSAVE	QERWDEDSFY	GLWDTNDEQG	LNSEFKSETA
1610	1620	1630	1640	1650	1660	1670	1680
AIPSAPVLPP	PPVHSSIPPP	GPVPMGMPPM	SKPPPVQQTV	DYGHGRDIST	NKVEQIPYGE	RITLRPDPLP	ERSTFETEHA
1690	1700	1710	1720	1730	1740	1750	1760
GQRDRYDRER	DREPYFDRQS	NVIADHRDFK	RDRETHRDRD	RDRGVIDYDR	DRFDRERRPR	DDRAQSYRDK	KDHSSSRRGG
1770	1780	1790	1800	1810	1820	1830	1840
FDRPSYDRKS	DRPVYEGPSM	FGGERRTYPE	ERMPLPAPSL	SHQPPPAPRV	EKKPESKNVD	DILKPPGRES	RPERIVVIMR
1850	1860	1870	1880	1890	1900	1910	1920
GLPGSGKTHV	AKLIRDKEVE	FGGPAPRVLS	LDDYFITEVE	KEEKDPDSGK	KVKKKVMEYE	YEAEMEETYR	TSMFKTFKKT
1930	1940	1950	1960	1970	1980	1990	2000
LDDGFFPFII	LDAINDRVRH	FDQFWSAAKT	KGFEVYLAEM	SADNQTCGKR	NIHGRKLKEI	NKMADHWETA	PRHMMRLDIR
2010	2020	2030	2040	2050	2060	2070	
SLLQDAAIEE	VEMEDFDANI	EEQKEEKKDA	EEEESELGYI	PKSKWEMDTS	EAKLVCHVEE	V	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2835	3	746.4789	26.21	1	64.1	17.2	0	1835-1840	R.IVVIMR.G	Oxidation: 5

Detailed Protein Report

Protein 514: trichohyalin [Homo sapiens]

Accession:	gi|148746195	**Score:**	17.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	253.8
Database Date:	2015-11-30	**pI:**	5.6
		Sequence Coverage [%]:	0.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSPLLRSICD	ITEIFNQYVS	HDCDGAALTK	KDLKNLLERE	FGAVLRRPHD	PKTVDLILEL	LDLDSNGRVD	FNEFLLFIFK
90	100	110	120	130	140	150	160
VAQACYYALG	QATGLDEEKR	ARCDGKESLL	QDRRQEEDQR	RFEPRDRQLE	EEPGQRRRQK	RQEQERELAE	GEEQSEKQER
170	180	190	200	210	220	230	240
LEQRDRQRRD	EELWRQRQEW	QEREERRAEE	EQLQSCKGHE	TEEFPDEEQL	RRRELLELRR	KGREEKQQQR	RERQDRVFQE
250	260	270	280	290	300	310	320
EEEKEWRKRE	TVLRKEEEKL	QEEEPQRQRE	LQEEEEQLRK	LERQELRRER	QEEEQQQQRL	RREQQLRRKQ	EEERREQQEE
330	340	350	360	370	380	390	400
RREQQERREQ	QEERREQQLR	REQEERREQQ	LRREQEEERR	EQQLRREQEE	ERREQQLRRE	QQLRREQQLR	REQQLRREQQ
410	420	430	440	450	460	470	480
LRREQQLRRE	QQLRREQQLR	REQQLRREQE	EERHEQKHEQ	ERREQRLKRE	QEERRDWLKR	EEETERHEQE	RRKQQLKRDQ
490	500	510	520	530	540	550	560
EEERRERWLK	LEEEERREQQ	ERREQQLRRE	QEERREQRLK	RQEEEERLQQ	RLRSEQQLRR	EQEERREQLL	KREEEKRLEQ
570	580	590	600	610	620	630	640
ERREQRLKRE	QEERRDQLLK	REEERRQQRL	KREQEERLEQ	RLKREEVERL	EQEERREQRL	KREEPEEERR	QQLLKSEEQE
650	660	670	680	690	700	710	720
ERRQQQLRRE	QQERREQRLK	REEEEERLEQ	RLKREHEEER	REQELAEEEQ	EQARERIKSR	IPKWQWQLES	EADARQSKVY
730	740	750	760	770	780	790	800
SRPRKQEGQR	RRQEQEEKRR	RRESELQWQE	EERAHRQQQE	EEQRRDFTWQ	WQAEEKSERG	RQRLSARPPL	REQRERQLRA
810	820	830	840	850	860	870	880
EERQQREQRF	LPEEEEKEQR	RRQRREREKE	LQFLEEEEQL	QRRERAQQLQ	EEEDGLQEDQ	ERRRSQEQRR	DQKWRWQLEE
890	900	910	920	930	940	950	960
ERKRRRHTLY	AKPALQEQLR	KEQQLLQEEE	EELQREEREK	RRRQEQERQY	REEEQLQQEE	EQLLREEREK	RRRQERERQY
970	980	990	1000	1010	1020	1030	1040
RKDKKLQQKE	EQLLGEEPEK	RRRQEREKKY	REEEELQQEE	EQLLREEREK	RRRQEWERQY	RKKDELQQEE	EQLLREEREK
1050	1060	1070	1080	1090	1100	1110	1120
RRLQERERQY	REEEELQQEE	EQLLGEERET	RRRQELERQY	RKEEELQQEE	EQLLREEPEK	RRRQERERQC	REEEELQQEE
1130	1140	1150	1160	1170	1180	1190	1200
EQLLREEREK	RRRQELERQY	REEEEVQQEE	EQLLREEPEK	RRRQELERQY	REEEELQQEE	EQLLREEQEK	RRQERERQYR
1210	1220	1230	1240	1250	1260	1270	1280
EEEELQRQKR	KQRYRDEDQR	SDLKWQWEPE	KENAVRDNKV	YCKGRENEQF	RQLEDSQLRD	RQSQQDLQHL	LGEQQERDRE
1290	1300	1310	1320	1330	1340	1350	1360
QERRRWQQRD	RHFPEEEQLE	REEQKEAKRR	DRKSQEEKQL	LREEREEKRR	RQETDRKFRE	EEQLLQEREE	QPLRRQERDR
1370	1380	1390	1400	1410	1420	1430	1440
KFREEELRHQ	EQGRKFLEEE	QRLRRQERER	KFLKEEQQLR	CQEREQQLRQ	DRDRKFREEE	QQLSRQERDR	KFREEEQQVR
1450	1460	1470	1480	1490	1500	1510	1520
RQERERKFLE	EEQQLRQERH	RKFREEEQLL	QEREEQQLHR	QERDRKFLEE	EQQLRRQERD	RKFREQELRS	QEPERKFLEE
1530	1540	1550	1560	1570	1580	1590	1600
EQQLHRQQRQ	RKFLQEEQQL	RRQERGQQRR	QDRDRKFREE	EQLRQEREEQ	QLSRQERDRK	FRLEEQKVRR	QEQERKFMED
1610	1620	1630	1640	1650	1660	1670	1680
EQQLRRQEGQ	QQLRQERDRK	FREDEQLLQE	REEQQLHRQE	RDRKFLEEEP	QLRRQEREQQ	LRHDRDRKFR	EEEQLLQEGE
1690	1700	1710	1720	1730	1740	1750	1760
EQQLRRQERD	RKFREEEQQL	RRQERERKFL	QEEQQLRRQE	LERKFREEEQ	LRQETEQEQL	RRQERYRKIL	EEEQLRPERE
1770	1780	1790	1800	1810	1820	1830	1840
EQQLRRQERD	RKFREEEQLR	QEREEQQLRS	QESDRKFREE	EQLRQEREEQ	QLRPQQRDGK	YRWEEEQLQL	EEQEQRLRQE
1850	1860	1870	1880	1890	1900	1910	1920
RDRQYRAEEQ	FATQEKSRRE	EQELWQEEEQ	KRRQERERKL	REEHIRRQQK	EEQRHRQVGE	IKSQEGKGHG	RLLEPGTHQF
1930	1940	1950					
ASVPVRSSPL	YEYIQEQRSQ	YRP					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2093	2	974.3559	-134.06	2	54.5	17.2	1	828-842	R.EKELQFLEEEEQLQR.R	

Detailed Protein Report

Protein 515: PREDICTED: uncharacterized protein KIAA1211 isoform X7 [Homo sapiens]

Accession:	gi|578808650	**Score:**	17.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	124.6
Database Date:	2015-11-30	**pI:**	5.5
		Sequence Coverage [%]:	1.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEEKVAPVKP	SRPKRHFSSA	GTIESVNLDA	IPLAIARLDN	SAAKHKLAVK	PKKQRVSKKH	RRLAQDPQHE	QGGLESRPCL
90	100	110	120	130	140	150	160
DQNGHPGEDK	PTWHEEEPNP	LDSEEERRRQ	EDYWRELEAK	CKRQKAEAAE	KRRLEEQRLQ	ALERRLWEEN	RRQELLEEEG
170	180	190	200	210	220	230	240
EGQEPPLEAE	RAPREEQQRS	LEAPGWEDAE	RREREERERL	EAEEERRRLQ	AQAQAEERRR	LEEDARLEER	RRQEEEEGRC
250	260	270	280	290	300	310	320
AEELKRQEEE	EAEGWEELEQ	QEAEVQGPPE	ALEETGEGRR	GAEEEDLGEE	EEEGQAHLED	WRGQLSELLN	DFEERLEDQE
330	340	350	360	370	380	390	400
RLKPEGQREH	SEEPGICEEQ	NPEAERRREQ	QGRSGDFQGA	DRPGPEEKRE	EGDTEPLLKQ	EGPVEAAQPP	VERKEAAALE
410	420	430	440	450	460	470	480
QGRKVEELRW	QEVDERQTMP	RPYTFQVSSG	GKQILFPKVN	LSPVTPAKDT	GLTAAPQEPK	APKASPVQHA	LPSSLSVPHT
490	500	510	520	530	540	550	560
AILVTGAQLC	GPAVNLSQIK	DTACKSLLGL	EEKKHAEAPA	GENPPRGPGD	ARAGSGKAKP	RQESPSSASA	LAEWASIRSR
570	580	590	600	610	620	630	640
ILKNAESDPR	SSERDQLRPG	DESTPRGRCD	SRGNQRKTPP	VNAKFSIMPA	WQKFSDGGTE	TSKQSTEAES	IRKRPMLGPS
650	660	670	680	690	700	710	720
EETAPQPPPA	GVRELGKGPE	KSEMHREPAD	TTEGCKFAKD	LPSFLVPSLP	YPPQKVVAHT	EFTTSSDSET	ANGIAKPDPV
730	740	750	760	770	780	790	800
MPGGEEKASP	FGIKLRRTNY	SLRFNCDQQA	EQKKKKRHSS	TGDSADAGPP	AAGSARGEKE	MEGVALKHGP	SLPQERKQAP
810	820	830	840	850	860	870	880
STRRDSAEPS	SSRSVPVAHP	GPPPASSQTP	APEHDKAANK	MPLAQKPALA	PKPTSQTPPA	SPLSKLSRPY	LVELLSRRAG
890	900	910	920	930	940	950	960
RPDPEPSEPS	KEDQESSDRR	PPSPPGPEER	KGQKRDEEEE	ATERKPASPP	LPATQQEKPS	QTPEAGRKEK	PMLQSRHSLD
970	980	990	1000	1010	1020	1030	1040
GSKLTEKVET	AQPLWITLAL	QKQKGFREQQ	ATREERKQAR	EAKQAEKLSK	ENVSVSVQPG	SSSVSRAGSL	HKSTALPEEK
1050	1060	1070	1080	1090	1100	1110	1120
RPETAVSRLE	RREQLKKANT	LPTSVTVEIS	DSAPPAPLVK	EVTKRFSTPD	AAPVSTEPAW	LALAKRKAKA	WSDCPQIIK

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1846	3	734.2644	-176.08	2	51.4	17.1	1	1027-1040	R.AGSLHKSTALPEEK.R	

Detailed Protein Report

Protein 516: protein cramped-like [Homo sapiens]

Accession:	gi|223972612	**Score:**	17.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	134.6
Database Date:	2015-11-30	**pI:**	9.1
		Sequence Coverage [%]:	1.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MTVKLGDGGS	GEDGLKKLGK	RAADEESLEG	EGAGGADAAE	ESSGTKRDEK	TPRAGADGPP	APPGAPQAPS	PPQGSPQDQH
90	100	110	120	130	140	150	160
HFLRSSVRPQ	SKRPRKDPPS	AVGSGNAGGS	GPRGKGAEGG	GSSSGNVSGV	APAAPAGGSR	SSSRNLGSSG	GEKEEGKKVR
170	180	190	200	210	220	230	240
RQWESWSTED	KNTFFEGLYE	HGKDFEAIQN	NIALKYKKKG	KPASMVKNKE	QVRHFYYRTW	HKITKYIDFD	HVFSRGLKKS
250	260	270	280	290	300	310	320
SQELYGLICY	GELRKKIGGC	MDDKNATKLN	ELIQVGATTV	RYKGRNLRIK	APMCRALKKL	CDPDGLSDEE	DQKPVRLPLK
330	340	350	360	370	380	390	400
VPIELQPRNN	HAWARVQSLA	QNPRLRMIVE	LHRKVSSLIE	FLKQKWALHE	VRVRKTLEER	QLQDSCSAPM	QEKVTLHLFP
410	420	430	440	450	460	470	480
GENCTLTPLP	GVARVVHSKA	FCTVHWQEGG	RCKQSAKDAH	VLPPAQILGI	QSGQGTARGQ	VKCPRSGAEG	KGVGRPPPAA
490	500	510	520	530	540	550	560
DALQSSGESS	PESAPGEGAA	LSLSSPDAPD	RPPPRHQDTG	PCLEKTPAEG	RDSPTREPGA	LPCACGQLPD	LEDELSLLDP
570	580	590	600	610	620	630	640
LPRYLKSCQD	LIVPEQCRCA	DTRPGSEQPP	LGGAASPEVL	APVSKEAADL	APTGPSPRPG	PGLLLDVCTK	DLADAPAEEL
650	660	670	680	690	700	710	720
QEKGSPAGPP	PSQGQPAARP	PKEVPASRLA	QQLREEGWNL	QTSESLTLAE	VYLMMGKPSK	LQLEYDWLGP	GRQDPRPGSL
730	740	750	760	770	780	790	800
PTALHKQRLL	SCLLKLISTE	VNPKLALEAN	TISTASVRPA	QEEQSMTPPG	KVVTVSSRSP	RCPRNQASLR	SSKTFPPSSA
810	820	830	840	850	860	870	880
PCSSGLRNPP	RPLLVPGPSS	TGSNDSDGGL	FAVPTTLPPN	SRHGKLFSPS	KEAELTFRQH	LNSISMQSDF	FLPKPRKLRN
890	900	910	920	930	940	950	960
RHLRKPLVVQ	RTLLPRPSEN	QSHNVCSFSI	LSNSSVTGRG	SFRPIQSSLT	KAALSRPIVP	KVLPPQATSH	LASAIDLAAT
970	980	990	1000	1010	1020	1030	1040
SAGILSGNPL	PALDTEGLSG	ISPLSSDEVT	GAISGQDSTG	THQDGDTLPT	VGGSDPFVSI	PSRPEQEPVA	DSFQGSSVLS
1050	1060	1070	1080	1090	1100	1110	1120
LSELPKAPLQ	NGLSIPLSSS	ESSSTRLSPP	DVSALLDISL	PGPPEDALSQ	GEPATHISDS	IIEIAISSGQ	YGEGVPLSPA
1130	1140	1150	1160	1170	1180	1190	1200
KLNGSDSSKS	LPSPSSSPQP	HWIASPTHDP	QWYPSDSTDS	SLSSLFASFI	SPEKSRKMLP	TPIGTNSGTS	LLGPSLLDGN
1210	1220	1230	1240	1250	1260	1270	
SRDSFVSRSL	ADVAEVVDSQ	LVCMMNENSI	DYISRFNDLA	QELSIAEPGR	REALFDGGGG	GPAVSDLSQ	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2985	1	846.4337	-1.84	2	66.1	17.1	2	1-17	-.MTVKLGDGGSGEDGLKK.L	

Detailed Protein Report

Protein 517: PREDICTED: mucin-3A [Homo sapiens]

Accession:	gi|578844260	**Score:**	17.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	21.4
Database Date:	2015-11-30	**pI:**	4.4
		Sequence Coverage [%]:	9.9
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MLCADVVETE VGMEVSVDQQ FSPDLNDNTS QAYRDFNKTF WNQMQKIFAD MQGFTFKGVE ILSLRNGSIV VDYLVLLEMP
        90        100        110        120        130        140        150        160
FSPQLESEYE QVKTTLKEGL QNASQDANSC QDSQTLCFKP DSIKVNNNSK TELTPEAICR RAAPTGYEEF YFPLVEATRL
       170        180        190        200
RCVTKCTSGV DNAIDCHQGQ CVLETSGPAC R
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1444	1	1086.6084	26.40	2	46.4	17.1	1	47-65	K.IFADMQGFTFKGVEILSLR.N	

Detailed Protein Report

Protein 518: **alpha-1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase [Homo sapiens]**

Accession:	gi|167857778	**Score:**	17.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	50.8
Database Date:	2015-11-30	**pI:**	9.8
		Sequence Coverage [%]:	3.6
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578811120	refseq_human (refseq_human_20140103.fasta)	PREDICTED: alpha-1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase isoform X4 [Homo sapiens]
gi|578811118	refseq_human (refseq_human_20140103.fasta)	PREDICTED: alpha-1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase isoform X3 [Homo sapiens]
gi|530381058	refseq_human (refseq_human_20140103.fasta)	PREDICTED: alpha-1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase isoform X2 [Homo sapiens]
gi|530381056	refseq_human (refseq_human_20140103.fasta)	PREDICTED: alpha-1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase isoform X1 [Homo sapiens]
gi|167857786	refseq_human (refseq_human_20140103.fasta)	alpha-1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase [Homo sapiens]
gi|167857784	refseq_human (refseq_human_20140103.fasta)	alpha-1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase [Homo sapiens]
gi|167857782	refseq_human (refseq_human_20140103.fasta)	alpha-1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase [Homo sapiens]
gi|167857780	refseq_human (refseq_human_20140103.fasta)	alpha-1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase [Homo sapiens]

10	20	30	40	50	60	70	80
MLKKQSAGLV	LWGAILFVAW	NALLLLFFWT	RPAPGRPPSV	SALDGDPASL	TREVIRLAQD	AEVELERQRG	LLQQIGDALS
90	100	110	120	130	140	150	160
SQRGRVPTAA	PPAQPRVPVT	PAPAVIPILV	IACDRSTVRR	CLDKLLHYRP	SAELFPIIVS	QDCGHEETAQ	AIASYGSAVT
170	180	190	200	210	220	230	240
HIRQPDLSSI	AVPPDHRKFQ	GYYKIARHYR	WALGQVFRQF	RFPAAVVVED	DLEVAPDFFE	YFRATYPLLK	ADPSLWCVSA
250	260	270	280	290	300	310	320
WNDNGKEQMV	DASRPELLYR	TDFFPGLGWL	LLAELWAELE	PKWPKAFWDD	WMRRPEQRQG	RACIRPEISR	TMTFGRKGVS
330	340	350	360	370	380	390	400
HGQFFDQHLK	FIKLNQQFVH	FTQLDLSYLQ	REAYDRDFLA	RVYGAPQLQV	EKVRTNDRKE	LGEVRVQYTG	RDSFKAFAKA
410	420	430	440	450			
LGVMDDLKSG	VPRAGYRGIV	TFQFRGRRVH	LAPPLTWEGY	DPSWN			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1777	1	881.9118	17.60	2	50.6	17.1	0	231-246	K.ADPSLWCVSAWNDNGK.E	

Detailed Protein Report

Protein 519: deoxyribonuclease-1-like 2 precursor [Homo sapiens]

Accession:	gi|4503347	**Score:**	17.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	32.8
Database Date:	2015-11-30	**pI:**	4.6
		Sequence Coverage [%]:	5.4
		No. of unique Peptides:	1

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
1326	1	939.1023	103.59	2	45.3	17.0	2	214-229	R.AQDWAAIRLRSSEVFK.W	

Detailed Protein Report

Protein 520: protocadherin alpha-1 isoform 2 precursor [Homo sapiens]

Accession:	gi|14165400	**Score:**	17.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	87.6
Database Date:	2015-11-30	**pI:**	4.6
		Sequence Coverage [%]:	1.1
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 0.39 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MVFSRRGGLG	ARDLLLWLLL	LAAWEVGSGQ	LHYSIPEEAK	HGTFVGRVAQ	DLGLELAELV	PRLFRVASKT	HRDLLEVNLQ
90	100	110	120	130	140	150	160
NGILFVNSRI	DREELCQWSA	ECSIHLELIA	DRPLQVFHVE	VKVKDINDNP	PVFRGREQII	FIPESRLLNS	RFPIEGAADA
170	180	190	200	210	220	230	240
DIGANALLTY	TLSPSDYFSL	DVEASDELSK	SLWLELRKYL	DREETPELHL	LLTATDGGKP	ELQGTVELLI	TVLDVNDNAP
250	260	270	280	290	300	310	320
LFDQAVYRVH	LLETTANGTL	VTTLNASDAD	EGVNGEVVFS	FDSGISRDIQ	EKFKVDSSSG	EIRLIDKLDY	EETKSYEIQV
330	340	350	360	370	380	390	400
KAVDKGSPPM	SNHCKVLVKV	LDVNDNAPEL	AVTSLYLPIR	EDAPLSTVIA	LITVSDRDSG	ANGQVTCSLM	PHVPFKLVST
410	420	430	440	450	460	470	480
FKNYYSLVLD	SALDRESLSV	YELVVTARDG	GSPSLWATAR	VSVEVADVND	NAPAFAQPEY	TVFVKENNPP	GCHIFTVSAR
490	500	510	520	530	540	550	560
DADAQENALV	SYSLVERRVG	ERALSNYVSV	HAESGKVYAL	QPLDHEELEL	LQFQVSARDA	GVPPLGSNVT	LQVFVLDEND
570	580	590	600	610	620	630	640
NAPALLAPRV	GGTIGAVSEL	VPRLVGAGHV	VAKVRAVDAD	SGYNAWLSYE	LQPAAGGARI	PFRVGLYTGE	ISTTRVLDEA
650	660	670	680	690	700	710	720
DLSRYRLLVL	VKDHGEPALT	ATATVLVSLV	ESGQAPKASS	RASVGVAGPE	AALVDVNVYL	IIAICAVSSL	LVLTLLLYTA
730	740	750	760	770	780	790	800
LRCSVPPTEG	AYVPGKPTLV	CSSALGSWSN	SQQRRQRVCS	SEGPPKTDLM	AFSPGLSPSL	NTSERNEQPE	ANLDLSGNVS
810							
PTFEFWL							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
642	1	509.1279	-267.69	2	36.9	17.0	0	636-644	R.VLDEADLSR.Y		WD:WU 0.39

Detailed Protein Report

Protein 521: fibrinogen-like protein 1 precursor [Homo sapiens]

Accession: gi|42544189
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 16.9
MW [kDa]: 36.4
pI: 5.5
Sequence Coverage [%]: 3.5
No. of unique Peptides: 1

Alias proteins:

Accession	Name	Description
gi|42544202	refseq_huma (refseq_human_20140103.fasta)	fibrinogen-like protein 1 precursor [Homo sapiens]
gi|42544200	refseq_huma (refseq_human_20140103.fasta)	fibrinogen-like protein 1 precursor [Homo sapiens]
gi|42544198	refseq_huma (refseq_human_20140103.fasta)	fibrinogen-like protein 1 precursor [Homo sapiens]

10	20	30	40	50	60	70	80
MAKVFSFILV	TTALTMGREI	SALEDCAQEQ	MRLRAQVRLL	ETRVKQQQVK	IKQLLQENEV	QFLDKGDENT	VIDLGSKRQY
90	100	110	120	130	140	150	160
ADCSEIFNDG	YKLSGFYKIK	PLQSPAEFSV	YCDMSDGGGW	TVIQRRSDGS	ENFNRGWKDY	ENGFGNFVQK	HGEYWLGNKN
170	180	190	200	210	220	230	240
LHFLTTQEDY	TLKIDLADFE	KNSRYAQYKN	FKVGDEKNFY	ELNIGEYSGT	AGDSLAGNFH	PEVQWWASHQ	RMKFSTWDRD
250	260	270	280	290	300	310	320
HDNYEGNCAE	EDQSGWWFNR	CHSANLNGVY	YSGPYTAKTD	NGIVWYTWHG	WWYSLKSVVM	KIRPNDFIPN	VI

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1103	1	1355.1276	221.32	1	42.5	16.9	2	33-43	R.LRAQVRLLETR.V	

Detailed Protein Report

Protein 522: formin-1 isoform c [Homo sapiens]

Accession:	gi|472235321	**Score:**	16.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	71.8
Database Date:	2015-11-30	**pI:**	10.1
		Sequence Coverage [%]:	1.4
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 0.98 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MEGTHCTLQL	HKPITELCYI	SFCLPKGEVR	GFSYKGTVTL	DRSNKGFHNC	YQVREESDII	SLSQEPDEHP	GDIFFKQTPT
90	100	110	120	130	140	150	160
KDILTELYKL	TTERERLLTN	LLSSDHILGI	TMGNQEGKLQ	ELSVSLAPED	DCFQSAGDWQ	GELPVGPLNK	RSTHGNKKPR
170	180	190	200	210	220	230	240
RSSGRRESFG	ALPQKRTKRK	GRGGRESAPL	MGKDKICSSH	SLPLSRTRPN	LWVLEEKGNL	LPNGALACSL	QRRESCPPDI
250	260	270	280	290	300	310	320
PKTPDTDLGF	GSFETAFKDT	GLGREVLPPD	CSSTEAGGDG	IRRPPSGLEH	QQTGLSESHQ	DPEKHPEAEK	DEMEKPAKRT
330	340	350	360	370	380	390	400
CKQKPVSKVV	AKVQDLSSQV	QRVVKTHSKG	KETIAIRPAA	HAEFVPKADL	LTLPGAEAGA	HGSRRQGKER	QGDRSSQSPA
410	420	430	440	450	460	470	480
GETASISSVS	ASAEGAVNKV	PLKVIESEKL	DEAPEGKRLG	FPVHTSVPHT	RPETRNKRRA	GLPLGGHKSL	FLDLPHKVGP
490	500	510	520	530	540	550	560
DSSQPRGDKK	KPSPPAPAAL	GKVFNNSASQ	SSTHKQTSPV	PSPLSPRLPS	PQQHHRILRL	PALPGEREAA	LNDSPCRKSR
570	580	590	600	610	620	630	640
VFSGCVSADT	LEPPSSAKVT	ETKGASPAFL	RAGQPRLVPG	ETLEKSLGPG	KTTAEPQHQS	PPAFHWDLQQ	HFQEPVIRTV
650	660	670					
SISCASNLIK	EEAGKGKESR	SG					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
787	1	509.7081	-159.31	2	38.3	16.9	1	320-328	R.TCKQKPVSK.V		WD:WU 0.98

Detailed Protein Report

Protein 523: E3 ubiquitin-protein ligase ZNF645 [Homo sapiens]

Accession:	gi|22749189	**Score:**	16.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	48.8
Database Date:	2015-11-30	**pI:**	10.3
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MNKMPAGEQE	CEYNKEGKYY	SKGVKLVRKK	KKIPGYRWGD	IKINIIGEKD	DLPIHFCDKC	DLPIKIYGRI	IPCKHAFCYH
90	100	110	120	130	140	150	160
CANLYDKVGY	KVCPRCRYPV	LRIEAHKRGS	VFMCSIVQQC	KRTYLSQKSL	QAHIKRRHKR	ARKQVTSASL	EKVRPHIAPP
170	180	190	200	210	220	230	240
QTEISDIPKR	LQDRDHLSYI	PPEQHTMVSL	PSVQHMLQEQ	HNQPHKDIQA	PPPELSLSLP	FPIQWETVSI	FTRKHGNLTV
250	260	270	280	290	300	310	320
DHIQNNSDSG	AKKPTPPDYY	PECQSQPAVS	SPHHIIPQKQ	HYAPPPSPSS	PVNHQMPYPP	QDVVTPNSVR	SQVPALTTTY
330	340	350	360	370	380	390	400
DPSSGYIIVK	VPPDMNSPPL	RAPQSQNGNP	SASEFASHHY	NLNILPQFTE	NQETLSPQFT	QTDAMDHRRW	PAWKRLSPCP
410	420	430					
PTRSPPPSTL	HGRSHHSHQR	RHRRY					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2100	1	707.7227	-87.06	2	54.8	16.9	0	4-15	K.MPAGEQECEYNK.E	Oxidation: 1

Detailed Protein Report

Protein 524: **PREDICTED: thrombospondin type-1 domain-containing protein 7A isoform X4 [Homo sapiens]**

Accession:	gi|578813343	**Score:**	16.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	169.7
Database Date:	2015-11-30	**pI:**	9.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGLQARRWAS	GSRGAAGPRR	GVLQLLPLPL	PLPLLLLLLL	RPGAGRAAAQ	GEAEAPTLYL	WKTGPWGRCM	GDECGPGGIQ
90	100	110	120	130	140	150	160
TRAVWCAHVE	GWTTLHTNCK	QAERPNNQQN	CFKVCDWHKE	LYDWRLGPWN	QCQPVISKSL	EKPLECIKGE	EGIQVREIAC
170	180	190	200	210	220	230	240
IQKDKDIPAE	DIICEYFEPK	PLLEQACLIP	CQQDCIVSEF	SAWSECSKTC	GSGLQHRTRH	VVAPPQFGGS	GCPNLTEFQV
250	260	270	280	290	300	310	320
CQSSPCEAEE	LRYSLHVGPW	STCSMPHSRQ	VRQARRRGKN	KEREKDRSKG	VKDPEARELI	KKKRNRNRQN	RQENKYWDIQ
330	340	350	360	370	380	390	400
IGYQTREVMC	INKTGKAADL	SFCQQEKLPM	TFQSCVITKE	CQVSEWSEWS	PCSKTCHDMV	SPAGTRVRTR	TIRQFPIGSE
410	420	430	440	450	460	470	480
KECPEFEEKE	PCLSQGDGVV	PCATYGWRTT	EWTECRVDPL	LSQQDKRRGN	QTALCGGGIQ	TREVYCVQAN	ENLLSQLSTH
490	500	510	520	530	540	550	560
KNKEASKPMD	LKLCTGPIPN	TTQLCHIPCP	TECEVSPWSA	WGPCTYENCN	DQQGKKGFKL	RKRRITNEPT	GGSGVTGNCP
570	580	590	600	610	620	630	640
HLLEAIPCEE	PACYDWKAVR	LGNCEPDNGK	ECGPGTQVQE	VVCINSDGEE	VDRQLCRDAI	FPIPVACDAP	CPKDCVLSTW
650	660	670	680	690	700	710	720
STWSSCSHTC	SGKTTEGKQI	RARSILAYAG	EEGGIRCPNS	SALQEVRSCN	EHPCTVYHWQ	TGPWGQCIED	TSVSSFNTTT
730	740	750	760	770	780	790	800
TWNGEASCSV	GMQTRKVICV	RVNVGQVGPK	KCPESLRPET	VRPCLLPCKK	DCIVTPYSDW	TSCPSSCKEG	DSSIRKQSRH
810	820	830	840	850	860	870	880
RVIIQLPANG	GRDCTDPLYE	EKACEAPQAC	QSYRWKTHKW	RRCQLVPWSV	QQDSPGAQEG	CGPGRQARAI	TCRKQDGGQA
890	900	910	920	930	940	950	960
GIHECLQYAG	PVPALTQACQ	IPCQDDCQLT	SWSKFSSCNG	DCGAVRTRKR	TLVGKSKKKE	KCKNSHLYPL	IETQYCPCDK
970	980	990	1000	1010	1020	1030	1040
YNAQPVGNWS	DCILPEGKVE	VLLGMKVQGD	IKECGQGYRY	QAMACYDQNG	RLVETSRCNS	HGYIEEACII	PCPSDCKLSE
1050	1060	1070	1080	1090	1100	1110	1120
WSNWSRCSKS	CGSGVKVRSK	WLREKPYNGG	RPCPKLDHVN	QAQVYEVVPC	HSDCNQYLWV	TEPWSICKVT	FVNMRENCGE
1130	1140	1150	1160	1170	1180	1190	1200
GVQTRKVRCM	QNTADGPSEH	VEDYLCDPEE	MPLGSRVCKL	PCPEDCVISE	WGPWTQCVLP	CNQSSFRQRS	ADPIRQPADE
1210	1220	1230	1240	1250	1260	1270	1280
GRSCPNAVEK	EPCNLNKNCY	HYDYNVTDWS	TCQLSEKAVC	GNGIKTRMLD	CVRSDGKSVD	LKYCEALGLE	KNWQMNTSCM
1290	1300	1310	1320	1330	1340	1350	1360
VECPVNCQLS	DWSPWSECSQ	TCGLTGKMIR	RRTVTQPFQG	DGRPCPSLMD	QSKPCPVKPC	YRWQYGQWSP	CQVQEAQCGE
1370	1380	1390	1400	1410	1420	1430	1440
GTRTRNISCV	VSDGSADDFS	KVVDEEFCAD	IELIIDGNKN	MVLEESCSQP	CPGDCYLKDW	SSWSLCQLTC	VNGEDLGFGG
1450	1460	1470	1480	1490	1500	1510	1520
IQVRSRPVII	QELENQHLCP	EQMLETKSCY	DGQCYEYKWM	ASAWKGSSRT	VWCQRSDGIN	VTAKSQRNPK	EGKTTD

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2861	1	795.7251	11.18	3	64.4	16.9	1	253-272	R.YSLHVGPWSTCSMPHSRQVR.Q	Carbamidomethyl: 11

Detailed Protein Report

Protein 525: PREDICTED: uncharacterized protein KIAA1551 isoform X1 [Homo sapiens]

Accession:	gi|530399223	**Score:**	16.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	194.7
Database Date:	2015-11-30	**pI:**	9.7
		Sequence Coverage [%]:	0.6
		No. of unique Peptides:	1

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
120	1	585.2911	-66.24	2	30.4	16.8	0	1662-1672	K.EQAPLQVSGIK.S	

Detailed Protein Report

Protein 526: 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

WD:WU **Median:** 0.56 **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		WD:WU 0.56

Detailed Protein Report

Protein 527: **PREDICTED: HMG box transcription factor BBX isoform X10 [Homo sapiens]**

Accession:	gi|578807613	**Score:**	16.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	98.5
Database Date:	2015-11-30	**pI:**	9.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.9
		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 528: HEAT repeat-containing protein 4 [Homo sapiens]

Accession:	gi|333805657	**Score:**	16.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	117.1
Database Date:	2015-11-30	**pI:**	9.9
		Sequence Coverage [%]:	1.4
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|578825794	refseq_human(refseq_human_20140103.fasta)	PREDICTED: HEAT repeat-containing protein 4 isoform X1 [Homo sapiens]
gi|333805659	refseq_human(refseq_human_20140103.fasta)	HEAT repeat-containing protein 4 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MTRTQKGKTF LPHCFYQSLP PRLGWGMILN YSKLKGKEEC ASVSSVPMVF FSSQYRLHRK SQYLKMAAAN LTFSQEVVWQ
        90        100        110        120        130        140        150        160
RGLPSIPYSQ YSFDHLYNTN DIIHTPQIRK ARPQKPVSFK FLGSSSPLTG DTSLAVKTES SANPEKKLKK SKPASTVREA
       170        180        190        200        210        220        230        240
PRPLIHHPCM HPDMLGRPPS LDVNLEEREA WLLPPEKEAR AWEATVLEKL NERTARWIQS KRPRRPGASP NKWQSFLRQQ
       250        260        270        280        290        300        310        320
YDWSHIRDEL TSASDLELLK QLEAEETAEF EDQSVILPPQ EKKKPELLLP VYYRLPSYFQ QAETVEIMPG NKSTEDIHEK
       330        340        350        360        370        380        390        400
TSLSQPQTQS YFRQVTPRAG KFAYSTDNTF EQEIYFDEVQ IIHQIGAKRD QIVLENLNRY NKQLSKVFPE TPEKWSAQAI
       410        420        430        440        450        460        470        480
PEASYRPVQG ALRWTALPTP AKDMLLQVGE KDVPIKTRRL KKQAKSLQED VTWELVVLRR MLKEWKTAWA LIIEWHHETV
       490        500        510        520        530        540        550        560
ENLLQSLGDL HDDVRIKAIT TCATAALERP RIATSQRDSD KTIQDLPEVL LPALEAALCD KNAHVRMAAA ICQYAIQSHN
       570        580        590        600        610        620        630        640
PLARNIMQTA LLKGNSVDSW AAAQCLALEG TATYPVIKRI LHQLFTKKNE DTEEQSYILL SYLSEKTTLI HTMLAVELNS
       650        660        670        680        690        700        710        720
CQWKNRIVAC QAFSRISGNV CLDMKHKLIQ LMWNDWNKEV RRAAAQALGQ MSLGKEVHDI IRVKLGQGNS QERVEALYLI
       730        740        750        760        770        780        790        800
GELKLMTAKL LPSFLHCFSD DFTAVRRAAC LAAGALQIRD KMVLECLLNL MQRDPYWKIK AFAIRALGQI GQVSPELTDL
       810        820        830        840        850        860        870        880
LLWAIHYEES PGVRLEACRS ILALKLQGDR VRDTFLDVLL LENHDAVLKE MYQTMKILNL GNEGNQEMLQ EIKNRIKTLS
       890        900        910        920        930        940        950        960
QKDLLTHKIL KLEMVMGKVR EEAKRVYLKP KGEQGPLTLQ TLLQETFQDE MVLPRRPSEV CDTEAVIKPV KPRAPNPWLQ
       970        980        990       1000       1010       1020       1030
SSVPGLTTRS KVRSSLVKDL RTSPEKRIAV GPFRSDYPAL YLGKFSERTF FSPIMSSPSG KKGAHL
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2100	1	757.3120	-102.39	2	54.6	16.7	1	1009-1022	R.TFFSPIMSSPSGKK.G	

Detailed Protein Report

Protein 529: **protein FAM122A [Homo sapiens]**

Accession:	gi|49472830	**Score:**	16.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	30.5
Database Date:	2015-11-30	**pI:**	6.4
		Sequence Coverage [%]:	3.5
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MAQEKMELDL ELPPGTGGSP AEGGGSGGGG GLRRSNSAPL IHGLSDTSPV FQAEAPSARR NSTTFPSRHG LLLPASPVRM
        90        100        110        120        130        140        150        160
HSSRLHQIKQ EEGMDLINRE TVHEREVQTA MQISHSWEES FSLSDNDVEK SASPKRIDFI PVSPAPSPTR GIGKQCFSPS
       170        180        190        200        210        220        230        240
LQSFVSSNGL PPSPIPSPTT RFTTRRSQSP INCIRPSVLG PLKRKCEMET EYQPKRFFQG ITNMLSSDVA QLSDPGVCVS
       250        260        270        280        290
SDTLDGNSSS AGSSCNSPAK VSTTTDSPVS PAQAASPFIP LDELSSK
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
588	1	602.8102	41.84	2	35.8	16.6	0	90-99	K.QEEGMDLINR.E	

Detailed Protein Report

Protein 530: PREDICTED: zinc finger protein 646 isoform X3 [Homo sapiens]

Accession:	gi|530409439	**Score:**	16.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	198.5
Database Date:	2015-11-30	**pI:**	6.8
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	0.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEDTPPSLSC	SDCQRHFPSL	PELSRHRELL	HPSPNQDSEE	ADSIPRPYRC	QQCGRGYRHP	GSLVNHRRTH	ETGLFPCTTC
90	100	110	120	130	140	150	160
GKDFSNPMAL	KSHMRTHAPE	GRRRHRPPRP	KEATPHLQGE	TVSTDSWGQR	LGSSEGWENQ	TKHTEETPDC	ESVPDPRAAS
170	180	190	200	210	220	230	240
GTWEDLPTRQ	REGLASHPGP	EDGADGWGPS	TNSARAPPLP	IPASSLLSNL	EQYLAESVVN	FTGGQEPTQS	PPAEEERRYK
250	260	270	280	290	300	310	320
CSQCGKTYKH	AGSLTNHRQS	HTLGIYPCAI	CFKEFSNLMA	LKNHSRLHAQ	YRPYHCPHCP	RVFRLPRELL	EHQQSHEGER
330	340	350	360	370	380	390	400
QEPRWEEKGM	PTTNGHTDES	SQDQLPSAQM	LNGSAELSTS	GELEDSGLEE	YRPFRCGDCG	RTYRHAGSLI	NHRKSHQTGV
410	420	430	440	450	460	470	480
YPCSLCSKQL	FNAAALKNHV	RAHHRPRQGV	GENGQPSVPP	APLLLAETTH	KEEEDPTTTL	DHRPYKCSEC	GRAYRHRGSL
490	500	510	520	530	540	550	560
VNHRHSHRTG	EYQCSLCPRK	YPNLMALRNH	VRVHCKAARR	SADIGAEGAP	SHLKVELPPD	PVEAEAAPHT	DQDHVCKHEE
570	580	590	600	610	620	630	640
EATDITPAAD	KTAAHICSIC	GLLFEDAESL	ERHGLTHGAG	EKENSRTETT	MSPPRAFACR	DCGKSYRHSG	SLINHRQTHQ
650	660	670	680	690	700	710	720
TGDFSCGACA	KHFHTMAAMK	NHLRRHSRRR	SRRHRKRAGG	ASGGREAKLL	AAESWTRELE	DNEGLESPQD	PSGESPHGAE
730	740	750	760	770	780	790	800
GNLESDGDCL	QAESEGDKCG	LERDETHFQG	DKESGGTGEG	LERKDASLLD	NLDIPGEEGG	GTHFCDSLTG	VDEDQKPATG
810	820	830	840	850	860	870	880
QPNSSSHSAN	AVTGWQAGAA	HTCSDCGHSF	PHATGLLSHR	PCHPPGIYQC	SLCPKEFDSL	PALRSHFQNH	RPGEATSAQP
890	900	910	920	930	940	950	960
FLCCLCGMIF	PGRAGYRLHR	RQAHSSSGMT	EGSEEEGEEE	GVAEAAPARS	PPLQLSEAEL	LNQLQREVEA	LDSAGYGHIC
970	980	990	1000	1010	1020	1030	1040
GCCGQTYDDL	GSLERHHQSQ	SSGTTADKAP	SPLGVAGDAM	EMVVDSVLED	IVNSVSGEGG	DAKSQEGAGT	PLGDSLCIQG
1050	1060	1070	1080	1090	1100	1110	1120
GESLLEAQPR	PFRCNQCGKT	YRHGGSLVNH	RKIHQTGDFL	CPVCSRCYPN	LAAYRNHLRN	HPRCKGSEPQ	VGPIPEAAGS
1130	1140	1150	1160	1170	1180	1190	1200
SELQVGPIPE	GGSNKPQHMA	EEGPGQAEVE	KLQEELKVEP	LEEVARVKEE	VWEETTVKGE	EIEPRLETAE	KGCQTEASSE
1210	1220	1230	1240	1250	1260	1270	1280
RPFSCEVCGR	SYKHAGSLIN	HRQSHQTGHF	GCQACSKGFS	NLMSLKNHRR	IHADPRRFRC	SECGKAFRLR	KQLASHQRVH
1290	1300	1310	1320	1330	1340	1350	1360
MERRGGGGTR	KATREDRPFR	CGQCGRTYRH	AGSLLNHRRS	HETGQYSCPT	CPKTYSNRMA	LKDHQRLHSE	NRRRRAGRSR
1370	1380	1390	1400	1410	1420	1430	1440
RTAVRCALCG	RSFPGRGSLE	RHLREHEETE	REPANGQGGL	DGTAASEANL	TGSQGLETQL	GGAEPVPHLE	DGVPRPGERS
1450	1460	1470	1480	1490	1500	1510	1520
QSPIRAASSE	APEPLSWGAG	KAGGWPVGGG	LGNHSGGWVP	QFLTRSEEPE	DSVHRSPCHA	GDCQLNGPTL	SHMDSWDNRD
1530	1540	1550	1560	1570	1580	1590	1600
NSSQLQPGSH	SSCSQCGKTY	CQSGSLLNHN	TNKTDRHYCL	LCSKEFLNPV	ATKSHSHNHI	DAQTFACPDC	GKAFESHQEL
1610	1620	1630	1640	1650	1660	1670	1680
ASHLQAHARG	HSQVPAQMEE	ARDPKAGTGE	DQVVLPGQGK	AQEAPSETPR	GPGESVERAR	GGQAVTSMAA	EDKERPFRCT
1690	1700	1710	1720	1730	1740	1750	1760
QCGRSYRHAG	SLLNHQKAHT	TGLYPCSLCP	KLLPNLLSLK	NHSRTHTDPK	RHCCSICGKA	FRTAARLEGH	GRVHAPREGP
1770	1780	1790	1800	1810			
FTCPHCPRHF	RRRISFVQHQ	QQHQEEWTVA	GSGRGHEGSQ	EEEPQWHQ			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2876	1	899.9560	111.44	2	64.7	16.6	0	1-15	-.MEDTPPSLSCSDCQR.H	Carbamidomethyl: 10, 13; Oxidation: 1

Detailed Protein Report

Protein 531: SKI/DACH domain-containing protein 1 [Homo sapiens]

Accession:	gi|148762982	**Score:**	16.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	98.1
Database Date:	2015-11-30	**pI:**	9.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.9
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578818410	refseq_human (refseq_human_20140103.fasta)	PREDICTED: SKI/DACH domain-containing protein 1 isoform X3 [Homo sapiens]
gi|530392158	refseq_human (refseq_human_20140103.fasta)	PREDICTED: SKI/DACH domain-containing protein 1 isoform X2 [Homo sapiens]
gi|530392156	refseq_human (refseq_human_20140103.fasta)	PREDICTED: SKI/DACH domain-containing protein 1 isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MGDLKSGFEE	VDGVRLGYLI	IKGKQMFALS	QVFTDLLKNI	PRTTVHKRMD	HLKVKKHHCD	LEELRKLKAI	NSIAFHAAKC
90	100	110	120	130	140	150	160
TLISREDVEA	LYTSCKTERV	LKTKRRRVGR	ALATKAPPPE	RAAAASPRPG	FWKDKHQLWR	GLSGAARPLP	ISAQSQRPGA
170	180	190	200	210	220	230	240
AAARPAAHLP	QIFSKYPGSH	YPEIVRSPCK	PPLNYETAPL	QGNYVAFPSD	PAYFRSLLCS	KHPAAAAAAA	AAAAAAAAAA
250	260	270	280	290	300	310	320
AAAAYYQVSA	AGPQPKAAAG	AGGPGSLSYR	CKRKRGGAKD	CLLAPHAGAR	RLLLLPRSYK	AKAAAAAAAA	AAAAAAAAGA
330	340	350	360	370	380	390	400
TCLERFHLVN	GFCPPPHHHH	HHHHHHHHHH	HRAQPPQQSH	HPPHHHRPQP	HLGSFPESCS	SDSESSSYSD	HAANDSDFGS
410	420	430	440	450	460	470	480
SLSSSSNSVS	SEEEEEEGEE	EEEEEEEEGG	SGASDSSEVS	SEEEDSSTES	DSSSGSSQVS	VQSIRFRRTS	FCKPPSVQAQ
490	500	510	520	530	540	550	560
ANFLYHLASA	AAATKPAAFE	DAGRLPDLKS	SVKAESPAEW	NLQSWAPKAS	PVYCPASLGS	CFAEIRNDRV	SEITFPHSEI
570	580	590	600	610	620	630	640
SNAVKRTDLT	INCLAEGASS	PSPKTNNAFP	QQRILREARK	CLQTTPTTHC	ADNNTIAARF	LNNDSSGAEA	NSEKYSKILH
650	660	670	680	690	700	710	720
CPEFATDLPS	SQTDPEVNAA	GAAATKAENP	CTDTGDKTLP	FLHNIKIKVE	DSSANEEYEP	HLFTNKLKCE	CNDTKGEFYS
730	740	750	760	770	780	790	800
VTESKEEDAL	LTTAKEGFAC	PEKETPSLNP	LAQSQGLSCT	LGSPKPEDGE	YKFGARVRKN	YRTLVLGKRP	VLQTPPVKPN
810	820	830	840	850	860	870	880
LKSARSPRPT	GKTETNEGTL	DDFTVINRRK	KVASNVASAV	KRPFHFMANF	PCPPSLIIGR	DGDLWPAYSL	NTTKDSQTPH
890	900	910					
KAHPIWKWQL	GGSAIPLPPS	HKFRKFNS					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2905	1	1023.0342	45.64	2	65.1	16.6	1	80-96	K.CTLISREDVEALYTSCK.T	Carbamidomethyl: 1, 16

Detailed Protein Report

Protein 532: **calcium/calmodulin-dependent protein kinase kinase 2 isoform 6 [Homo sapiens]**

Accession:	gi|27437023	**Score:**	16.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	54.1
Database Date:	2015-11-30	**pI:**	7.0
		Sequence Coverage [%]:	3.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
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
1288	1	917.4243	-149.73	2	44.9	16.6	2	430-445	K.NPESRIVVPEIKILVK.T	

Detailed Protein Report

Protein 533: POC1 centriolar protein homolog A isoform 2 [Homo sapiens]

Accession:	gi|239787760	**Score:**	16.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	39.8
Database Date:	2015-11-30	**pI:**	9.5
		Sequence Coverage [%]:	3.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAAPCAEDPS	LERHFKGHRD	AVTCVDFSIN	TKQLASGSMD	SCLMVWHMKP	QSRAYRFTGH	KDAVTCVNFS	PSGHLLASGS
90	100	110	120	130	140	150	160
RDKTVRIWVP	NVKGESTVFR	AHTATVRSVH	FCSDGQSFVT	ASDDKTVKVW	ATHRQKFLFS	LSQHINWVRC	AKFSPDGRLI
170	180	190	200	210	220	230	240
VSASDDKTVK	LWDKSSRECV	HSYCEHGGFV	TYVDFHPSGT	CIAAAGMDNT	VKVWDVRTHR	LLQHYQLHSA	AVNGLSFHPS
250	260	270	280	290	300	310	320
GNYLITASSD	STLKILDLME	GRLLYTLHGH	QGPATTVAFS	RTGEYFASGG	SDEQVMVWKS	NFDIVDHGEV	TKVPRPPATL
330	340	350	360				
ASSMGNLTVS	ILEQRLTLTE	DKLKQCLENQ	QLIMQRATP				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2441	1	638.3753	21.87	2	58.8	16.6	1	159-170	R.LIVSASDDKTVK.L	

Detailed Protein Report

Protein 534: 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 535: forkhead box protein J3 isoform 2 [Homo sapiens]

Accession:	gi|311893307	**Score:**	16.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	65.5
Database Date:	2015-11-30	**pI:**	6.8
		Sequence Coverage [%]:	3.2
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 0.96 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MGLYGQACPS VTSLRMTSEL ESSLTSMDWL PQLTMRAAIQ KSDATQNAHG TGISKKNALL DPNTTLDQEE VQQHKDGKPP
        90        100        110        120        130        140        150        160
YSYASLITFA INSSPKKKMT LSEIYQWICD NFPYYREAGS GWKNSIRHNL SLNKCFLKVP RSKDDPGKGS YWAIDTNPKE
       170        180        190        200        210        220        230        240
DVLPTRPKKR ARSVERVTLY NTDQDGSDSP RSSLNNSLSD QSLASVNLNS VGSVHSYTPV TSHPESVSQS LTPQQQPQYN
       250        260        270        280        290        300        310        320
LPERDKQLLF SEYNFEDLSA SFRSLYKSVF EQSLSQQGLM NIPSESSQQS HTSCTYQHSP SSTVSTHPHS NQSSLSNSHG
       330        340        350        360        370        380        390        400
SGLNTTGSNS VAQVSLSHPQ MHTQPSPHPP HRPHGLPQHP QRSPHPAPHP QQHSQLQSPH PQHPSPHQHI QHHPNHQHQT
       410        420        430        440        450        460        470        480
LTHQAPPPPQ QVSCNSGVSN DWYATLDMLK ESCRIASSVN WSDVDLSQFQ GLMESMRQAD LKNWSLDQVQ FADLCSSLNQ
       490        500        510        520        530        540        550        560
FFTQTGLIHS QSNVQQNVCH GAMHPTKPSQ HIGTGNLYID SRQNLPPSVM PPPGYPHIPQ ALSTPGTTMA GHHRAMNQQH
       570        580        590
MMPSQAFQMR RSLPPDDIQD DFDWDSIV
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
36	1	1096.9864	-51.33	2	29.4	16.4	0	57-75	K.NALLDPNTTLDQEEVQQHK.D		WD:WU 0.96

Detailed Protein Report

Protein 536: **PREDICTED: TBC domain-containing protein kinase-like protein isoform X1 [Homo sapiens]**

Accession:	gi|578809649	**Score:**	16.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	84.9
Database Date:	2015-11-30	**pI:**	5.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.9
		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 537: PREDICTED: transmembrane protein 2 isoform X2 [Homo sapiens]

Accession:	gi|578817261	**Score:**	16.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	136.2
Database Date:	2015-11-30	**pI:**	9.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	0.5
		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
EGVSLSGFRV  EVVDGVKLNL  LDDVSSWKPG  DQIVVASTDY  SMYQAEEFTL  LPCSECSHFQ  VKVKETPQFL  HMGEIIDGVD
       490         500         510         520         530         540         550         560
MRAEVGILTR  NIVIQGEVED  SCYAENQCQF  FDYDTFGGHI  MIMKNFTSVH  LSYVELKHMG  QQQMGRYPVH  FHLCGDVDYK
       570         580         590         600         610         620         630         640
GGYRHATFVD  GLSIHHSFSR  CITVHGTNGL  LIKDTIGFDT  LGHCFFLEDG  IEQRNTLFHN  LGLLTKPGTL  LPTDRNNSMC
       650         660         670         680         690         700         710         720
TTMRDKVFGN  YIPVPATDCM  AVSTFWIAHP  NNNLINNAAA  GSQDAGIWYL  FHKEPTGESS  GLQLLAKPEL  TPLGIFYNNR
       730         740         750         760         770         780         790         800
VHSNFKAGLF  IDKGVKTTNS  SAADPREYLC  LDNSARFRPH  QDANPEKPRV  AALIDRLIAF  KNNDNGAWVR  GGDIIVQNSA
       810         820         830         840         850         860         870         880
FADNGIGLTF  ASDGSFPSDE  GSSQEVSESL  FVGESRNYGF  QGGQNKYVGT  GGIDQKPRTL  PRNRTFPIRG  FQIYDGPIHL
       890         900         910         920         930         940         950         960
TRSTFKKYVP  TPDRYSSAIG  FLMKNSWQIT  PRNNISLVKF  GPHVSLNVFF  GKPGPWFEDC  EMDGDKNSIF  HDIDGSVTGY
       970         980         990        1000        1010        1020        1030        1040
KDAYVGRMDN  YLIRHPSCVN  VSKWNAVICS  GTYAQVYVQT  WSTQNLSMTI  TRDEYPSNPM  VLRGINQKAA  FPQYQPVVML
      1050        1060        1070        1080        1090        1100        1110        1120
EKGYTIHWNG  PAPRTTFLYL  VNFNKNDWIR  VGLCYPSNTS  FQVTFGYLQR  QNGSLSKIEE  YEPVHSLEEL  QRKQSERKFY
      1130        1140        1150        1160        1170        1180        1190        1200
FDSSTGLLFL  YLKAKSHRHG  HSYCSSQGCE  RVKIQAATDS  KDISNCMAKA  YPQYYRKPSV  VKRMPAMLTG  LCQGCGTRQM
      1210        1220
AAYWISRKHC  NESEPKI
```

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 538: 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 539: **PREDICTED: NACHT, LRR and PYD domains-containing protein 8 isoform X1 [Homo sapiens]**

Accession:	gi|530415693	**Score:**	16.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	117.3
Database Date:	2015-11-30	**pI:**	9.5
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	1.7
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 0.63 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MSDVNPPSDT PIPFSSSSTH SSHIPPWTFS CYPGSPCENG VMLYMRNVSH EELQRFKQLL LTELSTGTMP ITWDQVETAS
        90        100        110        120        130        140        150        160
WAEVVHLLIE RFPGRRAWDV TSNIFAIMNC DKMCVVVRRE INAILPTLEP EDLNVGETQV NLEEGESGKI RRYKSNVMEK
       170        180        190        200        210        220        230        240
FFPIWDITTW PGNQRDFFYQ GVHRHEEYLP CLLLPKRPQG RQPKTVAIQG APGIGKTILA KKVMFEWARN KFYAHKRWCA
       250        260        270        280        290        300        310        320
FYFHCQEVNQ TTDQSFSELI EQKWPGSQDL VSKIMSKPDQ LLLLLDGFEE LTSTLIDRLE DLSEDWRQKL PGSVLLSSLL
       330        340        350        360        370        380        390        400
SKTMLPEATL LIMIRFTSWQ TCKPLLKCPS LVTLPGFNTM EKIKYFQMYF GHTEEGDQVL SFAMENTILF SMCRVPVVCW
       410        420        430        440        450        460        470        480
MVCSGLKQQM ERGNNLTQSC PNATSVFVRY ISSLFPTRAE NFSRKIHQAQ LEGLCHLAAD SMWHRKWVLG KEDLEEAKLD
       490        500        510        520        530        540        550        560
QTGVTAFLGM SILRRIAGEE DHYVFTLVTF QEFFAALFYV LCFPQRLKNF HVLSHVNIQR LIASPRGSKS YLSHMGLFLF
       570        580        590        600        610        620        630        640
GFLNEACASA VEQSFQCKVS FGNKRKLLKV IPLLHKCDPP SPGSGVPQLF YCLHEIREEA FVSQALNDYH KVVLRIGNNK
       650        660        670        680        690        700        710        720
EVQVSAFCLK RCQYLHEVEL TVTLNFMNVW KLSSSSHPGS EAPESNGLHR WWQDLCSVFA TNDKLEVLTM TNSVLGPPFL
       730        740        750        760        770        780        790        800
KALAAALRHP QCKLQKLLLR RVNSTMLNQD LIGVLTGNQH LRYLEIQHVE VESKAVKLLC RVLRSPRCRL QCLRLEDCLA
       810        820        830        840        850        860        870        880
TPRIWTDLGN NLQGNGHLKT LILRKNSLEN CGAYYLSVAQ LERLSQSKML THLSLAENAL KDEGAKHIWN ALPHLRCPLQ
       890        900        910        920        930        940        950        960
RLVLRKCDLT FNCCQDMISA LCKNKTLKSL DLSFNSLKDD GVILLCEALK NPDCTLQILE LENCLFTSIC CQAMASMLRK
       970        980        990       1000       1010       1020       1030
NQHLRHLDLS KNAIGVYGIL TLCEAFSSQK KREEVIFCIP AWTRITSFSP TPHPPDFTGK SDCLSQINP
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1190	1	660.9872	74.48	3	43.1	16.4	0	887-903	K.CDLTFNCCQDMISALCK.N	Carbamidomethyl: 16; Oxidation: 11	WD:WU 0.63

Detailed Protein Report

Protein 540: **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

Protein 541: 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 542: **cathepsin Z preproprotein [Homo sapiens]**

Accession:	gi|22538442	**Score:**	16.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	33.8
Database Date:	2015-11-30	**pI:**	6.9
Modification(s):	Carbamidomethyl, Oxidation	**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 543: WAP four-disulfide core domain protein 3 precursor [Homo sapiens]

Accession:	gi|32307109	**Score:**	16.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	24.7
Database Date:	2015-11-30	**pI:**	9.4
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	10.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MMLSCLFLLK	ALLALGSLES	WITAGEHAKE	GECPPHKNPC	KELCQGDELC	PAEQKCCTTG	CGRICRDIPK	GRKRDCPRVI
90	100	110	120	130	140	150	160
RKQSCLKRCI	TDETCPGVKK	CCTLGCNKSC	VVPISKQKLA	EFGGECPADP	LPCEELCDGD	ASCPQGHKCC	STGCGRTCLG
170	180	190	200	210	220	230	240
DIEGGRGGDC	PKVLVGLCIV	GCVMDENCQA	GEKCCKSGCG	RFCVPPVLPP	KLTMNPNWTV	RSDSELEIPV	P

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1720	1	863.0927	43.31	3	50.2	16.2	1	173-196	K.VLVGLCIVGCVMDENCQAGEKCCK.S	Carbamidomethyl: 10; Oxidation: 12

Detailed Protein Report

Protein 544: 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

Detailed Protein Report

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 545: 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 546: protein phosphatase 1D [Homo sapiens]

Accession: gi|4505997
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 16.1
MW [kDa]: 66.6
pI: 10.0
Sequence Coverage [%]: 2.1
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MAGLYSLGVS	VFSDQGGRKY	MEDVTQIVVE	PEPTAEEKPS	PRRSLSQPLP	PRPSPAALPG	GEVSGKGPAV	AAREARDPLP
90	100	110	120	130	140	150	160
DAGASPAPSR	CCRRRSSVAF	FAVCDGHGGR	EAAQFAREHL	WGFIKKQKGF	TSSEPAKVCA	AIRKGFLACH	LAMWKKLAEW
170	180	190	200	210	220	230	240
PKTMTGLPST	SGTTASVVII	RGMKMYVAHV	GDSGVVLGIQ	DDPKDDFVRA	VEVTQDHKPE	LPKERERIEG	LGGSVMNKSG
250	260	270	280	290	300	310	320
VNRVVWKRPR	LTHNGPVRRS	TVIDQIPFLA	VARALGDLWS	YDFFSGEFVV	SPEPDTSVHT	LDPQKHKYII	LGSDGLWNMI
330	340	350	360	370	380	390	400
PPQDAISMCQ	DQEEKKYLMG	EHGQSCAKML	VNRALGRWRQ	RMLRADNTSA	IVICISPEVD	NQGNFTNEDE	LYLNLTDSPS
410	420	430	440	450	460	470	480
YNSQETCVMT	PSPCSTPPVK	SLEEDPWPRV	NSKDHIPALV	RSNAFSENFL	EVSAEIAREN	VQGVVIPSKD	PEPLEENCAK
490	500	510	520	530	540	550	560
ALTLRIHDSL	NNSLPIGLVP	TNSTNTVMDQ	KNLKMSTPGQ	MKAQEIERTP	PTNFKRTLEE	SNSGPLMKKH	RRNGLSRSSG
570	580	590	600	610			
AQPASLPTTS	QRKNSVKLTM	RRRLRGQKKI	GNPLLHQHRK	TVCVC			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2103	1	734.3073	-43.91	2	54.7	16.1	1	336-348	K.KYLMGEHGQSCAK.M	Oxidation: 4

Detailed Protein Report

Protein 547: **PREDICTED: putative E3 ubiquitin-protein ligase SH3RF2 isoform X3 [Homo sapiens]**

Accession:	gi|578810803	**Score:**	16.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	64.0
Database Date:	2015-11-30	**pI:**	10.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDDLTLLDLL	ECPVCFEKLD	VTAKVLPCQH	TFCKPCLQRV	FKAHKELRCP	ECRTPVFSNI	EALPANLLLV	RLLDGVRSGQ
90	100	110	120	130	140	150	160
SSGRGGSFRR	PGTMTLQDGR	KSRTNPRRLQ	ASPFRLVPNV	RIHMDGVPRA	KALCNYRGQN	PGDLRFNKGD	IILLRRQLDE
170	180	190	200	210	220	230	240
NWYQGEINGI	SGNFPASSVE	VIKQLPQPPP	LCRALYNFDL	RGKDKSENQD	CLTFLKDDII	TVISRVDENW	AEGKLGDKVG
250	260	270	280	290	300	310	320
IFPILFVEPN	LTARHLLEKN	KGRQSSRTKN	LSLVSSSSRG	NTSTLRRGPG	SRRKVPGQFS	ITTALNTLNR	MVHSPSGRHM
330	340	350	360	370	380	390	400
VEISTPVLIS	SSNPSVITQP	MEKADVPSSC	VGQVSTYHPA	PVSPGHSTAV	VSLPGSQQHL	SANMFVALHS	YSAHGPDELD
410	420	430	440	450	460	470	480
LQKGEGVRVL	GKCQDGWLRG	VSLVTGRVGI	FPNNYVIPIF	RKTSSFPDSR	SPGLYTTWTL	STSSVSSQGS	ISEGDPRQSR
490	500	510	520	530	540	550	560
PFKSVFVPTA	IVNPVRSTAG	PGTLGQGSLR	KGRSSMRKSK	WWQRECNELL	IPQVTYRIYV	QWMGISCLPE	NLRGRNDLFL
570	580						
RQDHLNLKKK	KKGKEKQ						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1746	1	916.9097	-57.96	2	50.5	16.1	2	130-145	R.AKALCNYRGQNPGDLR.F	Carbamidomethyl: 5

Detailed Protein Report

Protein 548: **PREDICTED: alpha-(1,3)-fucosyltransferase 11 isoform X4 [Homo sapiens]**

Accession:	gi|578819000	**Score:**	16.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	51.4
Database Date:	2015-11-30	**pI:**	5.7
		Sequence Coverage [%]:	1.5
		No. of unique Peptides:	1

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
310	1	464.6377	-111.51	2	32.6	16.1	0	343-349	K.NDEEYMK.Y	

Detailed Protein Report

Protein 549: **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	1	840.6326	169.50	2	60.5	16.0	0	1025-1039	R.KPPVIPVLQEIFDGK.Q	

Detailed Protein Report

Protein 550: **olfactory receptor 2AK2 [Homo sapiens]**

Accession:	gi|52317190	**Score:**	15.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	37.7
Database Date:	2015-11-30	**pI:**	10.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.0
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 0.57 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MNISDVISFD ILVSAMKTGN QSFGTDFLLV GLFQYGWINS LLFVVIATLF TVALTGNIML IHLIRLNTRL HTPMYFLLSQ
        90        100        110        120        130        140        150        160
LSIVDLMYIS TTVPKMAVSF LSQSKTIRFL GCEIQTYVFL ALGGTEALLL GFMSYDRYVA ICHPLHYPML MSKKICCLMV
       170        180        190        200        210        220        230        240
ACAWASGSIN AFIHTLYVFQ LPFCRSRLIN HFFCEVPALL SLVCQDTSQY EYTVLLSGLI ILLLPFLAIL ASYARVLIVV
       250        260        270        280        290        300        310        320
FQMSSGKGQA KAVSTCSSHL IVASLFYATT LFTYTRPHSL RSPSRDKAVA VFYTIVTPLL NPFIYSLRNK EVTGAVRRLL
       330        340
GYWICCRKYD FRSLY
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
108	1	557.2530	-55.78	2	30.6	15.9	0	96-105	K.MAVSFLSQSK.T	Oxidation: 1	WD:WU	0.57

Detailed Protein Report

Protein 551: PREDICTED: ras-related GTP-binding protein D isoform X1 [Homo sapiens]

Accession:	gi|530383216	**Score:**	15.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	34.2
Database Date:	2015-11-30	**pI:**	4.1
		Sequence Coverage [%]:	3.3
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 1.81 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MSQVLGKPQP	QDEDDAEEEE	EEDELVGLAD	YGDGPDSSDA	DPDSGTEEGV	LDFSDPFSTE	VKPRILLMGL	RRSGKSSIQK
90	100	110	120	130	140	150	160
VVFHKMSPNE	TLFLESTNKI	CREDVSNSSF	VNFQIWDFPG	QIDFFDPTFD	YEMIFRGTGA	LIFVIDSQDD	YMEALARLHL
170	180	190	200	210	220	230	240
TVTRAYKVNT	DINFEVFIHK	VDGLSDDHKI	ETQRDIHQRA	NDDLADAGLE	KIHLSFYLTS	IYDHSIFEAF	SKVVQKLIPQ
250	260	270	280	290	300	310	
LPTLENLLNI	FISNSGIEKA	FLFDVVSKIY	IATDSTPVDM	QTYELCCDMI	DVVIDISCIY	GAN	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2830	1	648.3562	18.22	2	63.9	15.9	1	190-199	K.IETQRDIHQR.A		WD:WU 1.81

Detailed Protein Report

Protein 552: uncharacterized protein KIAA0355 [Homo sapiens]

Accession:	gi|46276868	**Score:**	15.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	115.9
Database Date:	2015-11-30	**pI:**	6.8
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	1.3
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530417641	refseq_human (refseq_human_20140103.fasta)	PREDICTED: uncharacterized protein KIAA0355 isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MYCCSAQDSK	MDYKRRFLLG	GSKQKVQQHQ	QYPMPELGRA	LSAPLASTAT	TAPLGSLTAA	GSCHHAMPHT	TPIADIQQGI
90	100	110	120	130	140	150	160
SKYLDALNVF	CRASTFLTDL	FSTVFRNSHY	SKAATQLKDV	QEHVMEAASR	LTSAIKPEIA	KMLMELSAGA	ANFTDQKEFS
170	180	190	200	210	220	230	240
LQDIEVLGRC	FLTVVQVHFQ	FLTHALQKVQ	PVAHSCFAEV	IVPEKKNSGS	GGGLSGMGHT	PEVEEAVRSW	RGAAEATSRL
250	260	270	280	290	300	310	320
RERGCDGCLA	GIEVQQLFCS	QSAAIPEHQL	KELNIKIDSA	LQAYKIALES	LGHCEYAMKA	GFHLNPKAIE	ASLQGCCSEA
330	340	350	360	370	380	390	400
EAQQTGRRQT	PPQPMQCELP	TVPVQIGSHF	LKGVSFNESA	ADNLKLKTHT	MLQLMKEAGC	YNGITSRDDF	PVTEVLNQVC
410	420	430	440	450	460	470	480
PSTWRGACKT	AVQLLFGQAG	LVVVDTAQIE	NKEAYAPQIS	LEGSRIVVQV	PSTWCLKEDP	ATMSLLQRSL	DPEKTLGLVD
490	500	510	520	530	540	550	560
VLYTAVLDLN	RWRAGREQAL	PCIQIQLQRE	ICDFGNQADL	PSGNGNKSSG	GLQKTFSKLT	SRFTKKASCT	SSSSSTNYSI
570	580	590	600	610	620	630	640
QNTPSKNIFI	AGCSEEKAKM	PGNIDTRLQS	ILNIGNFPRT	TDPSQSAQNS	SNTVANGFLM	ERRENFLHGD	DGKDEKGMNL
650	660	670	680	690	700	710	720
PTDQEMQEVI	DFLSGFNMGQ	SHQGSPLVTR	HNSAATAMVT	EQKAGAMQPQ	QPSLPVPPPP	RAPQAGAHTP	LTPQPGLAPQ
730	740	750	760	770	780	790	800
QQSPKQQQPQ	VQYYQHLLQP	IGPQQPPPQP	RAPGKWVHGS	SQQPAQAVGA	GLSPLGQWPG	ISDLSSDLYS	LGLVSSYMDN
810	820	830	840	850	860	870	880
VMSEVLGQKP	QGPRNNTWPN	RDQSDGVFGM	LGEILPFDPA	VGSDPEFARY	VAGVSQAMQQ	KRQAQHGRRP	GNPRGNWPPM
890	900	910	920	930	940	950	960
DDAHRTWPFP	EFFTEGDGLH	GGWSGAQGDS	ASSSDETSSA	NGDSLFSMFS	GPDLVAAVKQ	RRKHSSGEQD	TSTLPSPPLL
970	980	990	1000	1010	1020	1030	1040
TTVEDVNQDN	KTKTWPPKAP	WQHPSPLPST	LPSPSAPLYA	VTSPGSQWND	TMQMLQSPVW	AATNDCSAAA	FSYVQTPPQP
1050	1060	1070	1080				
PPPPAHKAAP	KGFKAFPGKG	ERRPAYLPQY					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1382	1	873.4411	120.85	2	45.6	15.8	1	1-14	-.MYCCSAQDSKMDYK.R	Carbamidomethyl: 3; Oxidation: 11

Detailed Protein Report

Protein 553: **PREDICTED: disintegrin and metalloproteinase domain-containing protein 10 isoform X1 [Homo sapiens]**

Accession:	gi|530405298	**Score:**	15.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	80.5
Database Date:	2015-11-30	**pI:**	8.7
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	3.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MVLLRVLILL	LSWAAGMGGQ	YGNPLNKYIR	HYEGLSYNVD	SLHQKHQRAK	RAVSHEDQFL	RLDFHAHGRH	FNLRMKRDTS
90	100	110	120	130	140	150	160
LFSDEFKVET	SNKVLDYDTS	HIYTGHIYGE	EGSFSHGSVI	DGRFEGFIQT	RGGTFYVEPA	ERYIKDRTLP	FHSVIYHEDD
170	180	190	200	210	220	230	240
INYPHKYGPQ	GGCADHSVFE	RMRKYQMTGV	EEVTQIPQEE	HAANGPELLR	KKRTTSAEKN	TCQLYIQTDH	LFFKYYGTRE
250	260	270	280	290	300	310	320
AVIAQINTTA	DEKDPTNPFR	FPNIGVEKFL	ELNSEQNHDD	YCLAYVFTDR	DFDDGVLGLA	WVGAPSGSSG	GICEKSKLYS
330	340	350	360	370	380	390	400
DGKKKSLNTG	IITVQNYGSH	VPPKVSHITF	AHEVGHNFGS	PHDSGTECTP	GESKNLGQKE	NGNYIMYARA	TSGDKLNNNK
410	420	430	440	450	460	470	480
FSLCSIRNIS	QVLEKKRNNC	FVESGQPICG	NGMVEQGEEC	DCGYSDQCKD	ECCFDANQPE	GRKCKLKPGK	QCSPSQGPCC
490	500	510	520	530	540	550	560
TAQCAFKSKS	EKCRDDSDCA	REGICNGFTA	LCPASDPKPN	FTDCNRHTQV	CINGQCAGSI	CEKYGLEECT	CASSDGKDDK
570	580	590	600	610	620	630	640
ELCHVCCMKK	MDPSTCASTG	SVQWSRHFSG	RTITLQPGSP	CNDFRGYCDV	FMRCRLVDAD	GPLARLKKAI	FSPELYENIA
650	660	670	680	690	700	710	720
EWIVAHWWAV	LLMGIALIML	MAGFIKICSV	HTPSSNPKLP	PPKPLPGTLK	RRRPPQPIQQ	PQRQRPRESY	QMGHMRR

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1896	1	1056.6778	-73.07	3	52.0	15.8	2	544-569	K.YGLEECTCASSDGKDDKELCHVCCMK.K	Carbamidomethyl: 6, 8, 20, 23, 24; Oxidation: 25

Detailed Protein Report

Protein 554: PREDICTED: pre-B-cell leukemia transcription factor 3 isoform X3 [Homo sapiens]

Accession: gi|578817531
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 15.7
MW [kDa]: 38.7
pI: 9.3
Sequence Coverage [%]: 4.6
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MDDQSRMLQT	LAGVNLAGHS	VQGGMALPPP	PHGHEGADGD	GRKQDIGDIL	HQIMTITDQS	LDEAQAKKHA	LNCHRMKPAL
90	100	110	120	130	140	150	160
FSVLCEIKEK	TGLSIRGAQE	EDPPDPQLMR	LDNMLLAEGV	SGPEKGGGSA	AAAAAAAASG	GSSDNSIEHS	DYRAKLTQIR
170	180	190	200	210	220	230	240
QIYHTELEKY	EQACNEFTTH	VMNLLREQSR	TRPISPKEIE	RMVGIIHRKF	SSIQMQLKQS	TCEAVMILRS	RFLDARRKRR
250	260	270	280	290	300	310	320
NFSKQATEIL	NEYFYSHLSN	PYPSEEAKEE	LAKKCSITVS	QVSNWFGNKR	IRYKKNIGKF	QEEANLYAAK	TAVTAAHAVA
330	340	350	360				
AAVQNNQTNS	PTTPNSGGYP	PSCYQSDGRL	Q				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1938	1	618.9208	-90.90	3	52.6	15.7	1	274-289	K.KCSITVSQVSNWFGNK.R	Carbamidomethyl: 2

Detailed Protein Report

Protein 555: **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 556: 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 557: PREDICTED: cytoplasmic tyrosine-protein kinase BMX isoform X1 [Homo sapiens]

Accession:	gi|578837945	**Score:**	15.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	77.9
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
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
2432	1	701.1001	113.81	3	58.7	15.7	0	592-609	K.SDVWAFGILMWEVFSLGK.Q	Oxidation: 10

Detailed Protein Report

Protein 558: BTB/POZ domain-containing protein KCTD18 [Homo sapiens]

Accession:	gi|45387953	**Score:**	15.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	46.7
Database Date:	2015-11-30	**pI:**	9.9
		Sequence Coverage [%]:	2.1
		No. of unique Peptides:	1

Quantitation

WD:WU	**Median:** 1.58	**CV:** 0.00 %	**No. of Peptides:** 1

Alias proteins:

Accession	Name	Description
gi|530369815	refseq_human (refseq_human_20140103.fasta)	PREDICTED: BTB/POZ domain-containing protein KCTD18 isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MEGHKAEEEV	LDVLRLNVGG	CIYTARRESL	CRFKDSMLAS	MFSGRFPLKT	DESGACVIDR	DGRLFKYLLD	YLHGEVQIPT
90	100	110	120	130	140	150	160
DEQTRIALQE	EADYFGIPYP	YSLSDHLANE	METYSLRSNI	ELKKALTDFC	DSYGLVCNKP	TVWVLHYLNT	SGASCESRII
170	180	190	200	210	220	230	240
GVYATKTDGT	DAIEKQLGGR	IHSKGIFKRE	AGNNVQYIWS	YYSVAELKKM	MDAFDAWEGK	GVSYWRVPHE	LIECWTLEER
250	260	270	280	290	300	310	320
PLLGSLRHMA	PIRKRRLITF	NEADESVNYK	TGPKPVRFLG	PSTSTQIKVK	NSASVTVSPA	SAIQTSAGAT	ANRFQSGSRR
330	340	350	360	370	380	390	400
KAAQRSAPSR	ATALVGTGAP	GHPQASPGAA	SAENGGTHLP	PAKVLLSDKK	PTPQRVIKLK	RTPLCATAPC	LPSPTATRQA
410	420	430					
NSLKPLPGEA	ARALGVRTEN	GKNKGN					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
587	1	472.2712	30.05	2	36.2	15.6	1	322-330	K.AAQRSAPSR.A		WD:WU 1.58

Detailed Protein Report

Protein 559: 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

Quantitation

WD:WU **Median:** 5.86 **CV:** 0.00 % **No. of 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	Ratios
2291	2	666.2683	-223.38	2	57.1	15.5	2	193-204	R.IIGVKVHPGQRK.E		WD:WU 5.86

Detailed Protein Report

Protein 560: gastric inhibitory polypeptide receptor precursor [Homo sapiens]

Accession:	gi|4503999	**Score:**	15.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	53.1
Database Date:	2015-11-30	**pI:**	10.1
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	1.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MTTSPILQLL	LRLSLCGLLL	QRAETGSKGQ	TAGELYQRWE	RYRRECQETL	AAAEPPSGLA	CNGSFDMYVC	WDYAAPNATA
90	100	110	120	130	140	150	160
RASCPWYLPW	HHHVAAGFVL	RQCGSDGQWG	LWRDHTQCEN	PEKNEAFLDQ	RLILERLQVM	YTVGYSLSLA	TLLLALLILS
170	180	190	200	210	220	230	240
LFRRLHCTRN	YIHINLFTSF	MLRAAAILSR	DRLLPRPGPY	LGDQALALWN	QALAACRTAQ	IVTQYCVGAN	YTWLLVEGVY
250	260	270	280	290	300	310	320
LHSLLVLVGG	SEEGHFRYYL	LLGWGAPALF	VIPWVIVRYL	YENTQCWERN	EVKAIWWIIR	TPILMTILIN	FLIFIRILGI
330	340	350	360	370	380	390	400
LLSKLRTRQM	RCRDYRLRLA	RSTLTLVPLL	GVHEVVFAPV	TEEQARGALR	FAKLGFEIFL	SSFQGFLVSV	LYCFINKEVQ
410	420	430	440	450	460	470	
SEIRRGWHHC	RLRRSLGEEQ	RQLPERAFRA	LPSGSGPGEV	PTSRGLSSGT	LPGPGNEASR	ELESYC	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1605	3	1023.6518	154.68	1	48.8	15.5	2	327-333	R.TRQMRCR.D	Carbamidomethyl: 6; Oxidation: 4

Detailed Protein Report

Protein 561: **uncharacterized protein KIAA0408 [Homo sapiens]**

Accession:	gi|59806363	**Score:**	15.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	79.1
Database Date:	2015-11-30	**pI:**	9.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.9
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 2.23 **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	5	841.8664	-25.81	2	61.9	15.5	1	17-29	K.EKMELLDQFDNER.K	Oxidation: 3	WD:WU 2.23

Detailed Protein Report

Protein 562: 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

Quantitation

WD:WU	**Median:** 0.75	**CV:** 0.00 %	**No. of 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	Ratios
14	1	788.3704	-3.92	3	29.4	15.5	1	172-191	K.MASCSYVAHERLSYAFSVWR.M		WD:WU 0.75

Detailed Protein Report

Protein 563: 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

Quantitation

WD:WU **Median:** 1.22 **CV:** 0.00 % **No. of 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	Ratios
2031	1	652.2575	-58.70	2	54.0	15.4	1	76-86	K.KESMGMCFIGK.R	Carbamidomethyl: 7; Oxidation: 6	WD:WU 1.22

Detailed Protein Report

Protein 564: histone deacetylase 1 [Homo sapiens]

Accession:	gi|13128860	**Score:**	15.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	55.1
Database Date:	2015-11-30	**pI:**	5.2
		Sequence Coverage [%]:	2.7
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 1.72 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MAQTQGTRRK	VCYYYDGDVG	NYYYGQGHPM	KPHRIRMTHN	LLLNYGLYRK	MEIYRPHKAN	AEEMTKYHSD	DYIKFLRSIR
90	100	110	120	130	140	150	160
PDNMSEYSKQ	MQRFNVGEDC	PVFDGLFEFC	QLSTGGSVAS	AVKLNKQQTD	IAVNWAGGLH	HAKKSEASGF	CYVNDIVLAI
170	180	190	200	210	220	230	240
LELLKYHQRV	LYIDIDIHHG	DGVEEAFYTT	DRVMTVSFHK	YGEYFPGTGD	LRDIGAGKGK	YYAVNYPLRD	GIDDESYEAI
250	260	270	280	290	300	310	320
FKPVMSKVME	MFQPSAVVLQ	CGSDSLSGDR	LGCFNLTIKG	HAKCVEFVKS	FNLPMLMLGG	GGYTIRNVAR	CWTYETAVAL
330	340	350	360	370	380	390	400
DTEIPNELPY	NDYFEYFGPD	FKLHISPSNM	TNQNTNEYLE	KIKQRLFENL	RMLPHAPGVQ	MQAIPEDAIP	EESGDEDEDD
410	420	430	440	450	460	470	480
PDKRISICSS	DKRIACEEEF	SDSEEEGEGG	RKNSSNFKKA	KRVKTEDEKE	KDPEEKKEVT	EEEKTKEEKP	EAKGVKEEVK
490							
LA							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
184	1	530.6117	41.73	3	31.2	15.4	2	452-464	K.DPEEKKEVTEEEK.T		WD:WU 1.72

Detailed Protein Report

Protein 565: **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

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
2175	2	666.2454	-213.60	2	55.7	15.4	1	143-154	K.EPVKIAAPELHK.G	

Detailed Protein Report

Protein 566: WD repeat-containing protein 74 [Homo sapiens]

Accession:	gi|221219004	**Score:**	15.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	42.4
Database Date:	2015-11-30	**pI:**	9.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	6.5
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530396902	refseq_human (refseq_human_20140103.fasta)	PREDICTED: WD repeat-containing protein 74 isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MAAAAARWNH	VWVGTETGIL	KGVNLQRKQA	ANFTAGGQPR	REEAVSALCW	GTGGETQMLV	GCADRTVKHF	STEDGIFQGQ
90	100	110	120	130	140	150	160
RHCPGGEGMF	RGLAQADGTL	ITCVDSGILR	VWHDKDKDTS	SDPLLELRVG	PGVCRMRQDP	AHPHVVATGG	KENALKIWDL
170	180	190	200	210	220	230	240
QGSEEPVFRA	KNVRNDWLDL	RVPIWDQDIQ	FLPGSQKLVT	CTGYHQVRVY	DPASPQRRPV	LETTYGEYPL	TAMTLTPGGN
250	260	270	280	290	300	310	320
SVIVGNTHGQ	LAEIDLRQGR	LLGCLKGLAG	SVRGLQCHPS	KPLLASCGLD	RVLRIHRIQN	PRGLEHKVYL	KSQLNCLLLS
330	340	350	360	370	380	390	
GRDNWEDEPQ	EPQEPNKVPL	EDTETDELWA	SLEAAAKRKL	SGLEQPQGAL	QTRRRKKKRP	GSTSP	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1187	1	918.4360	17.92	3	43.1	15.4	1	41-65	R.REEAVSALCWGTGGETQMLVGCADR.T	Carbamidomethyl: 9, 22

Detailed Protein Report

Protein 567: 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

Quantitation

WD:WU **Median:** 1.11 **CV:** 0.00 % **No. of 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	Ratios
588	1	469.2361	-75.04	2	36.2	15.4	1	724-731	K.KGVTYEIK.V		WD:WU 1.11

Detailed Protein Report

Protein 568: insulin receptor-related protein precursor [Homo sapiens]

Accession:	gi|31657140	**Score:**	15.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	143.6
Database Date:	2015-11-30	**pI:**	6.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAVPSLWPWG	ACLPVIFLSL	GFGLDTVEVC	PSLDIRSEVA	ELRQLENCSV	VEGHLQILLM	FTATGEDFRG	LSFPRLTQVT
90	100	110	120	130	140	150	160
DYLLLFRVYG	LESLRDLFPN	LAVIRGTRLF	LGYALVIFEM	PHLRDVALPA	LGAVLRGAVR	VEKNQELCHL	STIDWGLLQP
170	180	190	200	210	220	230	240
APGANHIVGN	KLGEECADVC	PGVLGAAGEP	CAKTTFSGHT	DYRCWTSSHC	QRVCPCPHGM	ACTARGECCH	TECLGGCSQP
250	260	270	280	290	300	310	320
EDPRACVACR	HLYFQGACLW	ACPPGTYQYE	SWRCVTAERC	ASLHSVPGRA	STFGIHQGSC	LAQCPSGFTR	NSSSIFCHKC
330	340	350	360	370	380	390	400
EGLCPKECKV	GTKTIDSIQA	AQDLVGCTHV	EGSLILNLRQ	GYNLEPQLQH	SLGLVETITG	FLKIKHSFAL	VSLGFFKNLK
410	420	430	440	450	460	470	480
LIRGDAMVDG	NYTLYVLDNQ	NLQQLGSWVA	AGLTIPVGKI	YFAFNPRLCL	EHIYRLEEVT	GTRGRQNKAE	INPRTNGDRA
490	500	510	520	530	540	550	560
ACQTRTLRFV	SNVTEADRIL	LRWERYEPLE	ARDLLSFIVY	YKESPFQNAT	EHVGPDACGT	QSWNLLDVEL	PLSRTQEPGV
570	580	590	600	610	620	630	640
TLASLKPWTQ	YAVFVRAITL	TTEEDSPHQG	AQSPIVYLRT	LPAAPTVPQD	VISTSNSSSH	LLVRWKPPTQ	RNGNLTYYLV
650	660	670	680	690	700	710	720
LWQRLAEDGD	LYLNDYCHRG	LRLPTSNNDP	RFDGEDGDPE	AEMESDCCPC	QHPPPGQVLP	PLEAQEASFQ	KKFENFLHNA
730	740	750	760	770	780	790	800
ITIPISPWKV	TSINKSPQRD	SGRHRRAAGP	LRLGGNSSDF	EIQEDKVPRE	RAVLSGLRHF	TEYRIDIHAC	NHAAHTVGCS
810	820	830	840	850	860	870	880
AATFVFARTM	PHREADGIPG	KVAWEASSKN	SVLLRWLEPP	DPNGLILKYE	IKYRRLGEEA	TVLCVSRLRY	AKFGGVHLAL
890	900	910	920	930	940	950	960
LPPGNYSARV	RATSLAGNGS	WTDSVAFYIL	GPEEEDAGGL	HVLLTATPVG	LTLLIVLAAL	GFFYGKKRNR	TLYASVNPEY
970	980	990	1000	1010	1020	1030	1040
FSASDMYVPD	EWEVPREQIS	IIRELGQGSF	GMVYEGLARG	LEAGEESTPV	ALKTVNELAS	PRECIEFLKE	ASVMKAFKCH
1050	1060	1070	1080	1090	1100	1110	1120
HVVRLLGVVS	QGQPTLVIME	LMTRGDLKSH	LRSLRPEAEN	NPGLPQPALG	EMIQMAGEIA	DGMAYLAANK	FVHRDLAARN
1130	1140	1150	1160	1170	1180	1190	1200
CMVSQDFTVK	IGDFGMTRDV	YETDYYRKGG	KGLLPVRWMA	PESLKDGIFT	THSDVWSFGV	VLWEIVTLAE	QPYQGLSNEQ
1210	1220	1230	1240	1250	1260	1270	1280
VLKFVMDGGV	LEELEGCPLQ	LQELMSRCWQ	PNPRLRPSFT	HILDSIQEEL	RPSFRLLSFY	YSPECRGARG	SLPTTDAEPD
1290	1300						
SSPTPRDCSP	QNGGPGH						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
571	1	730.2246	-112.42	2	36.0	15.3	0	213-225	R.VCPCPHGMACTAR.G	Carbamidomethyl: 2, 4

Detailed Protein Report

Protein 569: PREDICTED: kazrin isoform X2 [Homo sapiens]

Accession:	gi|530360946	**Score:**	15.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	51.7
Database Date:	2015-11-30	**pI:**	6.6
		Sequence Coverage [%]:	1.9
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 1.67 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MTNTKDPKRA	MESTLATSNS	ATGPVTFSHV	FGQQCQLMQA	AVQSLHTLND	QISHFIVTKS	KALEEDKDPF	LPTEKETLKS
90	100	110	120	130	140	150	160
SMILMRHLLM	DAQAKILSMM	EDNKQLALRI	DGAVQSASQE	VTNLRAELTA	TNRRLAELSG	GGGPGPGPGA	AASASAAGDS
170	180	190	200	210	220	230	240
AATNMENPQL	GAQVLLREEV	SRLQEEVHLL	RQMKEMLAKD	LEESQGGKSS	EVLSATELRV	QLAQKEQELA	RAKEALQAMK
250	260	270	280	290	300	310	320
ADRKRLKGEK	TDLVSQMQQL	YATLESREEQ	LRDFIRNYEQ	HRKESEDAVK	ALAKEKDLLE	REKWELRRQA	KEATDHATAL
330	340	350	360	370	380	390	400
RSQLDLKDNR	MKELEAELAM	AKQSLATLTK	DVPKRHSLAM	PGETVLNGNQ	EWVVQADLPL	TAAIRQSQQT	LYHSHPPHPA
410	420	430	440	450	460	470	
DRQAVRVSPC	HSRQPSVISD	ASAAEGDRSS	TPSDINSPRH	RTHSLWRQSR	PSSEEPAQPY	CTVTRGS	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
989	2	540.6455	-205.92	2	40.7	15.3	0	96-104	K.ILSMMEDNK.Q		WD:WU 1.67

Detailed Protein Report

Protein 570: **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	

Detailed Protein Report

Protein 571: 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

Quantitation

WD:WU	**Median:**	0.80	**CV:**	0.00 %	**No. of Peptides:**	1	

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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	Ratios
714	1	512.2777	86.29	2	37.7	15.3	0	1100-1109	R.CVAECGASVK.G	Carbamidomethyl: 1	WD:WU 0.80

Detailed Protein Report

Protein 572: tumor necrosis factor alpha-induced protein 8-like protein 1 [Homo sapiens]

Accession:	gi|269846912	**Score:**	15.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	20.8
Database Date:	2015-11-30	**pI:**	10.4
		Sequence Coverage [%]:	5.4
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530425099	refseq_human (refseq_human_20140103.fasta)	PREDICTED: tumor necrosis factor alpha-induced protein 8-like protein 1 isoform X1 [Homo sapiens]
gi|269846918	refseq_human (refseq_human_20140103.fasta)	tumor necrosis factor alpha-induced protein 8-like protein 1 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MDTFSTKSLA LQAQKKLLSK MASKAVVAVL VDDTSSEVLD ELYRATREFT RSRKEAQKML KNLVKVALKL GLLLRGDQLG
        90        100        110        120        130        140        150        160
GEELALLRRF RHRARCLAMT AVSFHQVDFT FDRRVLAAGL LECRDLLHQA VGPHLTAKSH GRINHVFGHL ADCDFLAALY
       170        180        190
GPAEPYRSHL RRICEGLGRM LDEGSL
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1438	1	1095.6551	-96.87	1	46.4	15.3	1	66-75	K.VALKLGLLLR.G	

Detailed Protein Report

Protein 573: patatin-like phospholipase domain-containing protein 5 isoform 1 [Homo sapiens]

Accession:	gi|20304127	**Score:**	15.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	47.9
Database Date:	2015-11-30	**pI:**	6.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGFLEEEGRW	NLSFSGAGYL	GAHHVGATEC	LRQRAPRLLQ	GARRIYGSSS	GALNAVSIVC	GKSVDFCCSH	LLGMVGQLER
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
LSLSILHPAY	APIEHVKQQL	QDALPPDAHV	LASQRLGISL	TRWPDGRNFL	VTDFATCDEL	IQALVCTLYF	PFYCGLIPPE
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
FRGERYIDGA	LSNNLPFADC	PSTITVSPFH	GTVDICPQST	SPNLHELNVF	NFSFQISTEN	FFLGLICLIP	PSLEVVADNC
250	**260**	**270**	**280**	**290**	**300**	**310**	**320**
RQGYLDALRF	LERRGLTKEP	VLWTLVSKEP	PAPADGNWDA	GCDQRWKGGL	SLNWKVPHVQ	VKDVPNFEQL	SPELEAALKK
330	**340**	**350**	**360**	**370**	**380**	**390**	**400**
ACTRDPSRWA	RFWHSGPGQV	LTYLLLPCTL	PFEYIYFRSR	RLVVWLPDVP	ADLWWMQGLL	RNMALEVFSR	TKAQLLGPIS
410	**420**	**430**					
PPATRVLETS	PLQPQIAPHR	EELGPTHQA					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
958	1	684.2638	-84.66	3	40.3	15.3	0	63-80	K.SVDFCCSHLLGMVGQLER.L	Carbamidomethyl: 5

Detailed Protein Report

Protein 574: **mannan-binding lectin serine protease 2 isoform 1 preproprotein [Homo sapiens]**

Accession:	gi|21264363	**Score:**	15.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	75.7
Database Date:	2015-11-30	**pI:**	5.3
		Sequence Coverage [%]:	2.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MRLLTLLGLL	CGSVATPLGP	KWPEPVFGRL	ASPGFPGEYA	NDQERRWTLT	APPGYRLRLY	FTHFDLELSH	LCEYDFVKLS
90	100	110	120	130	140	150	160
SGAKVLATLC	GQESTDTERA	PGKDTFYSLG	SSLDITFRSD	YSNEKPFTGF	EAFYAAEDID	ECQVAPGEAP	TCDHHCHNHL
170	180	190	200	210	220	230	240
GGFYCSCRAG	YVLHRNKRTC	SALCSGQVFT	QRSGELSSPE	YPRPYPKLSS	CTYSISLEEG	FSVILDFVES	FDVETHPETL
250	260	270	280	290	300	310	320
CPYDFLKIQT	DREEHGPFCG	KTLPHRIETK	SNTVTITFVT	DESGDHTGWK	IHYTSTAQPC	PYPMAPPNGH	VSPVQAKYIL
330	340	350	360	370	380	390	400
KDSFSIFCET	GYELLQGHLP	LKSFTAVCQK	DGSWDRPMPA	CSIVDCGPPD	DLPSGRVEYI	TGPGVTTYKA	VIQYSCEETF
410	420	430	440	450	460	470	480
YTMKVNDGKY	VCEADGFWTS	SKGEKSLPVC	EPVCGLSART	TGGRIYGGQK	AKPGDFPWQV	LILGGTTAAG	ALLYDNWVLT
490	500	510	520	530	540	550	560
AAHAVYEQKH	DASALDIRMG	TLKRLSPHYT	QAWSEAVFIH	EGYTHDAGFD	NDIALIKLNN	KVVINSNITP	ICLPRKEAES
570	580	590	600	610	620	630	640
FMRTDDIGTA	SGWGLTQRGF	LARNLMYVDI	PIVDHQKCTA	AYEKPPYPRG	SVTANMLCAG	LESGGKDSCR	GDSGGALVFL
650	660	670	680	690			
DSETERWFVG	GIVSWGSMNC	GEAGQYGVYT	KVINYIPWIE	NIISDF			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
16	1	1068.4952	-116.47	2	29.4	15.2	2	538-556	K.LNNKVVINSNITPICLPRK.E	

Detailed Protein Report

Protein 575: **serine/threonine-protein kinase MRCK gamma [Homo sapiens]**

Accession:	gi|156766068	**Score:**	15.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	172.4
Database Date:	2015-11-30	**pI:**	5.9
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MERRLRALEQ	LARGEAGGCP	GLDGLLDLLL	ALHHELSSGP	LRRERSVAQF	LSWASPFVSK	VKELRLQRDD	FEILKVIGRG
90	100	110	120	130	140	150	160
AFGEVTVVRQ	RDTGQIFAMK	MLHKWEMLKR	AETACFREER	DVLVKGDSRW	VTTLHYAFQD	EEYLYLVMDY	YAGGDLLTLL
170	180	190	200	210	220	230	240
SRFEDRLPPE	LAQFYLAEMV	LAIHSLHQLG	YVHRDVKPDN	VLLDVNGHIR	LADFGSCLRL	NTNGMVDSSV	AVGTPDYISP
250	260	270	280	290	300	310	320
EILQAMEEGK	GHYGPQCDWW	SLGVCAYELL	FGETPFYAES	LVETYGKIMN	HEDHLQFPPD	VPDVPASAQD	LIRQLLCRQE
330	340	350	360	370	380	390	400
ERLGRGGLDD	FRNHPFFEGV	DWERLASSTA	PYIPELRGPM	DTSNFDVDDD	TLNHPGTLPP	PSHGAFSGHH	LPFVGFTYTS
410	420	430	440	450	460	470	480
GSHSPESSSE	AWAALERKLQ	CLEQEKVELS	RKHQEALHAP	TDHRELEQLR	KEVQTLRDRL	PEMLRDKASL	SQTDGPPAGS
490	500	510	520	530	540	550	560
PGQDSDLRQE	LDRLHRELAE	GRAGLQAQEQ	ELCRAQGQQE	ELLQRLQEAQ	EREAATASQT	RALSSQLEEA	RAAQRELEAQ
570	580	590	600	610	620	630	640
VSSLSRQVTQ	LQGQWEQRLE	ESSQAKTIHT	ASETNGMGPP	EGGPQEAQLR	KEVAALREQL	EQAHSHRPSG	KEEALCQLQE
650	660	670	680	690	700	710	720
ENRRLSREQE	RLEAELAQEQ	ESKQRLEGER	RETESNWEAQ	LADILSWVND	EKVSRGYLQA	LATKMAEELE	SLRNVGTQTL
730	740	750	760	770	780	790	800
PARPLDHQWK	ARRLQKMEAS	ARLELQSALE	AEIRAKQGLQ	ERLTQVQEAQ	LQAERRLQEA	EKQSQALQQE	LAMLREELRA
810	820	830	840	850	860	870	880
RGPVDTKPSN	SLIPFLSFRS	SEKDSAKDPG	ISGEATRHGG	EPDLRPEGRR	SLRMGAVFPR	APTANTASTE	GLPAKPGSHT
890	900	910	920	930	940	950	960
LRPRSFPSPT	KCLRCTSLML	GLGRQGLGCD	ACGYFCHTTC	APQAPPCPVP	PDLLRTALGV	HPETGTGTAY	EGFLSVPRPS
970	980	990	1000	1010	1020	1030	1040
GVRRGWQRVF	AALSDSRLLL	FDAPDLRLSP	PSGALLQVLD	LRDPQFSATP	VLASDVIHAQ	SRDLPRIFRV	TTSQLAVPPT
1050	1060	1070	1080	1090	1100	1110	1120
TCTVLLLAES	EGERERWLQV	LGELQRLLLD	ARPRPRPVYT	LKEAYDNGLP	LLPHTLCAAI	LDQDRLALGT	EEGLFVIHLR
1130	1140	1150	1160	1170	1180	1190	1200
SNDIFQVGEC	RRVQQLTLSP	SAGLLVVLCG	RGPSVRLFAL	AELENIEVAG	AKIPESRGCQ	VLAAGSILQA	RTPVLCVAVK
1210	1220	1230	1240	1250	1260	1270	1280
RQVLCYQLGP	GPGPWQRRIR	ELQAPATVQS	LGLLGDRLCV	GAAGGFALYP	LLNEAAPLAL	GAGLVPEELP	PSRGGLGEAL
1290	1300	1310	1320	1330	1340	1350	1360
GAVELSLSEF	LLLFTTAGIY	VDGAGRKSRG	HELLWPAAPM	GWGYAAPYLT	VFSENSIDVF	DVRRAEWVQT	VPLKKVRPLN
1370	1380	1390	1400	1410	1420	1430	1440
PEGSLFLYGT	EKVRLTYLRN	QLAEKDEFDI	PDLTDNSRRQ	LFRTKSKRRF	FFRVSEEQQK	QQRREMLKDP	FVRSKLISPP
1450	1460	1470	1480	1490	1500	1510	1520
TNFNHLVHVG	PANGRPGARD	KSPAPEEKGR	VARGSGPQRP	HSFSEALRRP	ASMGSEGLGG	DADPMKRKPW	TSLSSESVSC
1530	1540	1550	1560				
PQGSLSPATS	LMQVSERPRS	LPLSPELESS	P				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2153	1	974.3330	-124.42	2	55.3	15.2	1	1489-1507	R.RPASMGSEGLGGDADPMKR.K	Oxidation: 5

Detailed Protein Report

Protein 576: PREDICTED: ATP-dependent RNA helicase DDX19B isoform X1 [Homo sapiens]

Accession:	gi|578828798	**Score:**	15.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	52.0
Database Date:	2015-11-30	**pI:**	7.7
		Sequence Coverage [%]:	4.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLSNLHLKEE	KIKPDTNGAV	VKTNANAEKT	DEEEKEDRAA	QSLLNKLIRS	NLVDNTNQVE	VLQRDPNSPL	YSVKSFEELR
90	100	110	120	130	140	150	160
LKPQLLQGVY	AMGFNRPSKI	QENALPLMLA	EPPQNLIAQS	QSGTGKTAAF	VLAMLSQVEP	ANKYPQCLCL	SPTYELALQT
170	180	190	200	210	220	230	240
GKVIEQMGKF	YPELKLAYAV	RGNKLERGQK	ISEQIVIGTP	GTVLDWCSKL	KFIDPKKIKV	FVLDEADVMI	ATQGHQDQSI
250	260	270	280	290	300	310	320
RIQRMLPRNC	QMLLFSATFE	DSVWKFAQKV	VPDPNVIKLK	REEETLDTIK	QYYVLCSSRD	EKFQALCNLY	GAITIAQAMI
330	340	350	360	370	380	390	400
FCHTRKTASW	LAAELSKEGH	QVALLSGEMM	VEQRAAVIER	FREGKEKVLV	TTNVCARGID	VEQVSVVINF	DLPVDKDGNP
410	420	430	440	450	460	470	
DNETYLHRIG	RTGRFGKRGL	AVNMVDSKHS	MNILNRIQEH	FNKKIERLDT	DDLDEIEKIA	N	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1837	2	716.3485	-69.03	3	51.6	15.2	0	81-99	R.LKPQLLQGVYAMGFNRPSK.I	

Detailed Protein Report

Protein 577: polyadenylate-binding protein 4 isoform 3 [Homo sapiens]

Accession:	gi|208431836	**Score:**	15.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	69.5
Database Date:	2015-11-30	**pI:**	10.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MNAAASSYPM	ASLYVGDLHS	DVTEAMLYEK	FSPAGPVLSI	RVCRDMITRR	SLGYAYVNFQ	QPADAERALD	TMNFDVIKGK
90	100	110	120	130	140	150	160
PIRIMWSQRD	PSLRKSGVGN	VFIKNLDKSI	DNKALYDTFS	AFGNILSCKV	VCDENGSKGY	AFVHFETQEA	ADKAIEKMNG
170	180	190	200	210	220	230	240
MLLNDRKVFV	GRFKSRKERE	AELGAKAKEF	TNVYIKNFGE	EVDDESLKEL	FSQFGKTLSV	KVMRDPNGKS	KGFGFVSYEK
250	260	270	280	290	300	310	320
HEDANKAVEE	MNGKEISGKI	IFVGRAQKKV	ERQAELKRKF	EQLKQERISR	YQGVNLYIKN	LDDTIDDEKL	RKEFSPFGSI
330	340	350	360	370	380	390	400
TSAKVMLEDG	RSKGFGFVCF	SSPEEATKAV	TEMNGRIVGS	KPLYVALAQR	KEERKAHLTN	QYMQRVAGMR	ALPANAILNQ
410	420	430	440	450	460	470	480
FQPAAGGYFV	PAVPQAQGRP	PYYTPNQLAQ	MRPNPRWQQG	GRPQGFQGMP	SAIRQSGPRP	TLRHLAPTGN	APASRGLPTT
490	500	510	520	530	540	550	560
TQRVGVPTAV	QNLAPRAAVA	AAAPRAVAPY	KYASSVRSPH	PAIQPLQAPQ	PAVHVQGQEP	LTASMLAAAP	PQEQKQMLGE
570	580	590	600	610	620	630	640
RLFPLIQTMH	SNLAGKITGM	LLEIDNSELL	HMLESPESLR	SKVDEAVAVL	QAHHAKKEAA	QKVGAVAAAT	S

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2973	1	1051.5430	46.04	2	65.9	15.2	2	241-259	K.HEDANKAVEEMNGKEISGK.I	Oxidation: 11

Detailed Protein Report

Protein 578: **GLIPR1-like protein 2 isoform 1 [Homo sapiens]**

Accession:	gi|394025727	**Score:**	15.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	40.2
Database Date:	2015-11-30	**pI:**	4.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	4.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
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 579: **PREDICTED: mitogen-activated protein kinase-binding protein 1 isoform X2 [Homo sapiens]**

Accession:	gi|578826739	**Score:**	15.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	99.8
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
MISCGADKSI	YFRTAQKSGD	GVQFTRTHHV	VRKTTLYDMD	VEPSWKYTAI	GCQDRNIRIF	NISSGKQKKL	FKGSQGEDGT
90	100	110	120	130	140	150	160
LIKVQTDPSG	IYIATSCSDK	NLSIFDFSSG	ECVATMFGHS	EIVTGMKFSN	DCKHLISVSG	DSCIFVWRLS	SEMTISMRQR
170	180	190	200	210	220	230	240
LAELRQRQRG	GKQQGPSSPQ	RASGPNRHQA	PSMLSPGPAL	SSDSDKEGED	EGTEEELPAL	PVLAKSTKKA	LASVPSPALP
250	260	270	280	290	300	310	320
RSLSHWEMSR	AQESVGFLDP	APAANPGPRR	RGRWVQPGVE	LSVRSMLDLR	QLETLAPSLQ	DPSQDSLAII	PSGPRKHGQE
330	340	350	360	370	380	390	400
ALETSLTSQN	EKPPRPQASQ	PCSYPHIIRL	LSQEEGVFAQ	DLEPAPIEDG	IVYPEPSDNP	TMDTSEFQVQ	APARGTLGRV
410	420	430	440	450	460	470	480
YPGSRSSEKH	SPDSACSVDY	SSSCLSSPEH	PTEDSESTEP	LSVDGISSDL	EEPAEGDEEE	EEEEGGMGPY	GLQEGSPQTP
490	500	510	520	530	540	550	560
DQEQFLKQHF	ETLASGAAPG	APVQVPERSE	SRSISSRFLL	QVQTRPLREP	SPSSSSLALM	SRPAQVPQAS	GEQPRGNGAN
570	580	590	600	610	620	630	640
PPGAPPEVEP	SSGNPSPQQA	ASVLLPRCRL	NPDSSWAPKR	VATASPFSGL	QKAQSVHSLV	PQERHEASLQ	APSPGALLSR
650	660	670	680	690	700	710	720
EIEAQDGLGS	LPPADGRPSR	PHSYQNPTTS	SMAKISRSIS	VGENLGLVAE	PQAHAPIRVS	PLSKLALPSR	AHLVLDIPKP
730	740	750	760	770	780	790	800
LPDRPTLAAF	SPVTKGRAPG	EAEKPGFPVG	LGKAHSTTER	WACLGEGTTP	KPRTECQAHP	GPSSPCAQQL	PVSSLFQGPE
810	820	830	840	850	860	870	880
NLQPPPPEKT	PNPMECTKPG	AALSQDSEPA	VSLEQCEQLV	AELRGSVRQA	VRLYHSVAGC	KMPSAEQSRI	AQLLRDTFSS
890	900	910	920	930	940		
VRQELEAVAG	AVLSSPGSSP	GAVGAEQTQA	LLEQYSELLL	RAVERRMERK	L		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
809	2	697.8381	-23.89	2	38.9	15.1	1	14-26	R.TAQKSGDGVQFTR.T	

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Detailed Protein Report

Protein 580: **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

WD:WU **Median:** 0.84 **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	WD:WU	0.84

Detailed Protein Report

Protein 581: armadillo repeat-containing X-linked protein 2 [Homo sapiens]

Accession:	gi|7662162	**Score:**	15.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	65.6
Database Date:	2015-11-30	**pI:**	9.3
		Sequence Coverage [%]:	2.5
		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 582: **breast cancer anti-estrogen resistance protein 3 isoform 2 [Homo sapiens]**

Accession:	gi|387157911	**Score:**	15.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	82.3
Database Date:	2015-11-30	**pI:**	9.4
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	1.9
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MPKECSAFHA LSAALCCFYH RKSFIGVKFS KERHIMDRTP EKLKKELEEE LLLSSEDLRS HAWYHGRIPR QVSENLVQRD

        90        100        110        120        130        140        150        160
GDFLVRDSLS SPGNFVLTCQ WKNLAQHFKI NRTVLRLSEA YSRVQYQFEM ESFDSIPGLV RCYVGNRRPI SQQSGAIIFQ

       170        180        190        200        210        220        230        240
PINRTVPLRC LEEHYGTSPG QAREGSLTKG RPDVAKRLSL TMGGVQAREQ NLPRGNLLRN KEKSGSQPAC LDHMQDRRAL

       250        260        270        280        290        300        310        320
SLKAHQSESY LPIGCKLPPQ SSGVDTSPCP NSPVFRTGSE PALSPAVVRR VSSDARAGEA LRGSDSQLCP KPPPKPCKVP

       330        340        350        360        370        380        390        400
FLKVPSSPSA WLNSEANYCE LNPAFATGCG RGAKLPSCAQ GSHTELLTAK QNEAPGPRNS GVNYLILDDD DRERPWEPAA

       410        420        430        440        450        460        470        480
AQMEKGQWDK GEFVTPLLET VSSFRPNEFE SKFLPPENKP LETAMLKRAK ELFTNNDPKV IAQHVLSMDC RVARILGVSE

       490        500        510        520        530        540        550        560
EMRRNMGVSS GLELITLPHG HQLRLDIIER HNTMAIGIAV DILGCTGTLE DRAATLSKII QVAVELKDSM GDLYSFSALM

       570        580        590        600        610        620        630        640
KALEMPQITR LEKTWTALRH QYTQTAILYE KQLKPFSKLL HEGRESTCVP PNNVSVPLLM PLVTLMERQA VTFEGTDMWE

       650        660        670        680        690        700        710        720
KNDQSCEIML NHLATARFMA EAADSYRMNA ERILAGFQPD EEMNEICKTE FQMRLLWGSK GAQVNQTERY EKFNQILTAL

       730        740
SRKLEPPPVK QAEL
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
46	1	809.3894	59.94	2	29.5	15.0	0	224-237	K.SGSQPACLDHMQDR.R	Carbamidomethyl: 7; Oxidation: 11

Detailed Protein Report

Protein 583: 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 584: cyclin-dependent kinase 5 activator 1 [Homo sapiens]

Accession:	gi|4502737	**Score:**	15.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	34.0
Database Date:	2015-11-30	**pI:**	10.2
		Sequence Coverage [%]:	5.2
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 0.88 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MGTVLSLSPS	YRKATLFEDG	AATVGHYTAV	QNSKNAKDKN	LKRHSIISVL	PWKRIVAVSA	KKKNSKKVQP	NSSYQNNITH
90	100	110	120	130	140	150	160
LNNENLKKSL	SCANLSTFAQ	PPPAQPPAPP	ASQLSGSQTG	GSSSVKKAPH	PAVTSAGTPK	RVIVQASTSE	LLRCLGEFLC
170	180	190	200	210	220	230	240
RRCYRLKHLS	PTDPVLWLRS	VDRSLLLQGW	QDQGFITPAN	VVFLYMLCRD	VISSEVGSDH	ELQAVLLTCL	YLSYSYMGNE
250	260	270	280	290	300	310	
ISYPLKPFLV	ESCKEAFWDR	CLSVINLMSS	KMLQINADPH	YFTQVFSDLK	NESGQEDKKR	LLLGLDR	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
2666	1	945.9810	-33.71	2	61.6	15.0	1	168-183	K.HLSPTDPVLWLRSVDR.S		WD:WU	0.88

Detailed Protein Report

Protein 585: PDZ domain-containing protein MAGIX isoform d [Homo sapiens]

Accession:	gi|532164745	**Score:**	15.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	26.7
Database Date:	2015-11-30	**pI:**	11.6
		Sequence Coverage [%]:	5.1
		No. of unique Peptides:	1

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1817	2	1273.5520	-62.61	1	51.4	15.0	0	238-250	R.GAAQLAQEMAAGR.R	

Detailed Protein Report

Protein 586: **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 587: toll-like receptor 9 precursor [Homo sapiens]

Accession:	gi|8394456	**Score:**	14.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	115.8
Database Date:	2015-11-30	**pI:**	9.7
		Sequence Coverage [%]:	1.3
		No. of unique Peptides:	1

Quantitation

WD:WU	**Median:** 0.91	**CV:** 0.00 %	**No. of Peptides:** 1

10	20	30	40	50	60	70	80
MGFCRSALHP	LSLLVQAIML	AMTLALGTLP	AFLPCELQPH	GLVNCNWLFL	KSVPHFSMAA	PRGNVTSLSL	SSNRIHHLHD
90	100	110	120	130	140	150	160
SDFAHLPSLR	HLNLKWNCPP	VGLSPMHFPC	HMTIEPSTFL	AVPTLEELNL	SYNNIMTVPA	LPKSLISLSL	SHTNILMLDS
170	180	190	200	210	220	230	240
ASLAGLHALR	FLFMDGNCYY	KNPCRQALEV	APGALLGLGN	LTHLSLKYNN	LTVVPRNLPS	SLEYLLLSYN	RIVKLAPEDL
250	260	270	280	290	300	310	320
ANLTALRVLD	VGGNCRRCDH	APNPCMECPR	HFPQLHPDTF	SHLSRLEGLV	LKDSSLSWLN	ASWFRGLGNL	RVLDLSENFL
330	340	350	360	370	380	390	400
YKCITKTKAF	QGLTQLRKLN	LSFNYQKRVS	FAHLSLAPSF	GSLVALKELD	MHGIFFRSLD	ETTLRPLARL	PMLQTLRLQM
410	420	430	440	450	460	470	480
NFINQAQLGI	FRAFPGLRYV	DLSDNRISGA	SELTATMGEA	DGGEKVWLQP	GDLAPAPVDT	PSSEDFRPNC	STLNFTLDLS
490	500	510	520	530	540	550	560
RNNLVTVQPE	MFAQLSHLQC	LRLSHNCISQ	AVNGSQFLPL	TGLQVLDLSH	NKLDLYHEHS	FTELPRLEAL	DLSYNSQPFG
570	580	590	600	610	620	630	640
MQGVGHNFSF	VAHLRTLRHL	SLAHNNIHSQ	VSQQLCSTSL	RALDFSGNAL	GHMWAEGDLY	LHFFQGLSGL	IWLDLSQNRL
650	660	670	680	690	700	710	720
HTLLPQTLRN	LPKSLQVLRL	RDNYLAFFKW	WSLHFLPKLE	VLDLAGNQLK	ALTNGSLPAG	TRLRRLDVSC	NSISFVAPGF
730	740	750	760	770	780	790	800
FSKAKELREL	NLSANALKTV	DHSWFGPLAS	ALQILDVSAN	PLHCACGAAF	MDFLLEVQAA	VPGLPSRVKC	GSPGQLQGLS
810	820	830	840	850	860	870	880
IFAQDLRLCL	DEALSWDCFA	LSLLAVALGL	GVPMLHHLCG	WDLWYCFHLC	LAWLPWRGRQ	SGRDEDALPY	DAFVVFDKTQ
890	900	910	920	930	940	950	960
SAVADWVYNE	LRGQLEECRG	RWALRLCLEE	RDWLPGKTLF	ENLWASVYGS	RKTLFVLAHT	DRVSGLLRAS	FLLAQQRLLE
970	980	990	1000	1010	1020	1030	1040
DRKDVVVLVI	LSPDGRRSRY	VRLRQRLCRQ	SVLLWPHQPS	GQRSFWAQLG	MALTRDNHHF	YNRNFCQGPT	AE

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
1392	1	698.8594	-48.59	2	45.8	14.9	0	235-247	K.LAPEDLANLTALR.V		WD:WU	0.91

Detailed Protein Report

Protein 588: 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 589: PREDICTED: pyruvate carboxylase, mitochondrial isoform X6 [Homo sapiens]

Accession:	gi|578821481	**Score:**	14.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	73.3
Database Date:	2015-11-30	**pI:**	5.6
		Sequence Coverage [%]:	2.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MVNGPTTPIP	VKASPSPTDP	VVPAVPIGPP	PAGFRDILLR	EGPEGFARAV	RNHPGLLLMD	TTFRDAHQSL	LATRVRTHDL
90	100	110	120	130	140	150	160
KKIAPYVAHN	FSKLFSMENW	GGATFDVAMR	FLYECPWRRL	QELRELIPNI	PFQMLLRGAN	AVGYTNYPDN	VVFKFCEVAK
170	180	190	200	210	220	230	240
ENGMDVFRVF	DSLNYLPNML	LGMEAAGSAG	GVVEAAISYT	GDVADPSRTK	YSLQYYMGLA	EELVRAGTHI	LCIKDMAGLL
250	260	270	280	290	300	310	320
KPTACTMLVS	SLRDRFPDLP	LHIHTHDTSG	AGVAAMLACA	QAGADVVDVA	ADSMSGMTSQ	PSMGALVACT	RGTPLDTEVP
330	340	350	360	370	380	390	400
MERVFDYSEY	WEGARGLYAA	FDCTATMKSG	NSDVYENEIP	GGQYTNLHFQ	AHSMGLGSKF	KEVKKAYVEA	NQMLGDLIKV
410	420	430	440	450	460	470	480
TPSSKIVGDL	AQFMVQNGLS	RAEAEAQAEE	LSFPRSVVEF	LQGYIGVPHG	GFPEPFRSKV	LKDLPRVEGR	PGASLPPLDL
490	500	510	520	530	540	550	560
QALEKELVDR	HGEEVTPEDV	LSAAMYPDVF	AHFKDFTATF	GPLDSLNTRL	FLQGPKIAEE	FEVELERGKT	LHIKALAVSD
570	580	590	600	610	620	630	640
LNRAGQRQVF	FELNGQLRSI	LVKDTQAMKE	MHFHPKALKD	VKGQIGAPMP	GKVIDIKVVA	GAKVAKGQPL	CVLSAMKMET
650	660	670	680				
VVTSPMEGTV	RKVHVTKDMT	LEGDDLILEI	E				

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	613-626	K.VIDIKVVAGAKVAK.G	

Protein 590: 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

WD:WU **Median:** 0.93 **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		WD:WU 0.93

Detailed Protein Report

Protein 591: myosin-IIIb isoform 1 [Homo sapiens]

Accession:	gi|284172510	**Score:**	14.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	148.5
Database Date:	2015-11-30	**pI:**	8.7
		Sequence Coverage [%]:	1.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
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	

BRUKER

Detailed Protein Report

Protein 592: PREDICTED: RANBP2-like and GRIP domain-containing protein 5/6 isoform X5 [Homo sapiens]

Accession:	gi|530369376	**Score:**	14.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	165.9
Database Date:	2015-11-30	**pI:**	6.1
		Sequence Coverage [%]:	1.1
		No. of unique Peptides:	1

Alias proteins:

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

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2775	1	557.2986	22.82	3	63.1	14.9	1	623-638	K.STKEGFSIPVSADGFK.F	

Detailed Protein Report

Protein 593: ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial precursor [Homo sapiens]

Accession: gi|7242140

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Modification(s): Carbamidomethyl

Score: 14.8

MW [kDa]: 69.2

pI: 8.5

Sequence Coverage [%]: 3.9

No. of unique Peptides: 1

Quantitation

WD:WU **Median:** 1.13 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MPSCGACTCG	AAAVRLITSS	LASAQRGISG	GRIHMSVLGR	LGTFETQILQ	RAPLRSFTET	PAYFASKDGI	SKDGSGDGNK
90	100	110	120	130	140	150	160
KSASEGSSKK	SGSGNSGKGG	NQLRCPKCGD	LCTHVETFVS	STRFVKCEKC	HHFFVVLSEA	DSKKSIIKEP	ESAAEAVKLA
170	180	190	200	210	220	230	240
FQQKPPPPPK	KIYNYLDKYV	VGQSFAKKVL	SVAVYNHYKR	IYNNIPANLR	QQAEVEKQTS	LTPRELEIRR	REDEYRFTKL
250	260	270	280	290	300	310	320
LQIAGISPHG	NALGASMQQQ	VNQQIPQEKR	GGEVLDSSHD	DIKLEKSNIL	LLGPTGSGKT	LLAQTLAKCL	DVPFAICDCT
330	340	350	360	370	380	390	400
TLTQAGYVGE	DIESVIAKLL	QDANYNVEKA	QQGIVFLDEV	DKIGSVPGIH	QLRDVGGEGV	QQGLLKLLEG	TIVNVPEKNS
410	420	430	440	450	460	470	480
RKLRGETVQV	DTTNILFVAS	GAFNGLDRII	SRRKNEKYLG	FGTPSNLGKG	RRAAAAADLA	NRSGESNTHQ	DIEEKDRLLR
490	500	510	520	530	540	550	560
HVEARDLIEF	GMIPEFVGRL	PVVVPLHSLD	EKTLVQILTE	PRNAVIPQYQ	ALFSMDKCEL	NVTEDALKAI	ARLALERKTG
570	580	590	600	610	620	630	640
ARGLRSIMEK	LLLEPMFEVP	NSDIVCVEVD	KEVVEGKKEP	GYIRAPTKES	SEEEYDSGVE	EEGWPRQADA	ANS

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
524	1	817.7754	49.53	3	35.0	14.8	1	2-26	M. PSCGACTCGAAAVRLITSSLASAQ G	Carbamidomethyl: 3	WD:WU 1.13

Detailed Protein Report

Protein 594: **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

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
48	1	505.2491	-51.14	2	29.8	14.8	0	151-159	R.VHGLEIEGR.D	

Detailed Protein Report

Protein 595: PREDICTED: keratin, type I cuticular Ha1 isoform X1 [Homo sapiens]

Accession:	gi|530412192	**Score:**	14.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	42.2
Database Date:	2015-11-30	**pI:**	4.6
		Sequence Coverage [%]:	2.5
		No. of unique Peptides:	1

Quantitation

WD:WU	**Median:**	1.94	**CV:**	0.00 %	**No. of Peptides:**	1	

Alias proteins:

Accession	Name	Description
gi|530431086	refseq_human (refseq_human_20140103.fasta)	PREDICTED: keratin, type I cuticular Ha1 isoform X1 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MPYNFCLPSL SCRTSCSSRP CVPPSCHSCT LPGACNIPAN VSNCNWFCEG SFNGSEKETM QFLNDRLASY LEKVRQLERD
        90        100        110        120        130        140        150        160
NAELENLIRE RSQQQEPLLC PSYQSYFKTI EELQQKILCT KSENARLVVQ IDNAKLAADD FRTKYQTELS LRQLVESDIN
       170        180        190        200        210        220        230        240
GLRRILDELT LCKSDLEAQV ESLKEELLCL KSNHEQEVNT LRCQLGDRLN VEVDAAPTVD LNRVLNETRS QYEALVETNR
       250        260        270        280        290        300        310        320
REVEQWFTTQ TEELNKQVVS SSEQLQSYQA EIIELRRTVN ALEIELQAQH NLRDSLENTL TESEARYSSQ LSQVQSLITN
       330        340        350        360        370
VESQLAEIRS DLERQNQEYQ VLLDVRARLE CEINTYRSLL ESEDCK
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
881	1	512.1602	-149.56	2	39.4	14.7	0	358-366	R.SLLESEDCK.-		WD:WU 1.94

Detailed Protein Report

Protein 596: 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

Quantitation

WD:WU **Median:** 0.90 **CV:** 0.00 % **No. of 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	Ratios
930	1	974.4715	15.67	2	40.4	14.7	0	51-68	R.TQGVCSFPAMPQAPIDGR.I	Carbamidomethyl: 5; Oxidation: 10	WD:WU 0.90

Detailed Protein Report

Protein 597: 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

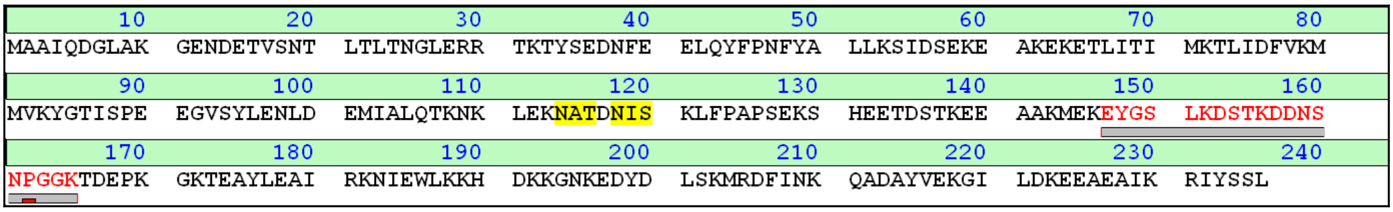
10	20	30	40	50	60	70	80
MEHRIVGPGP	YRATRLWNET	VELFRAKMPL	RKHRCRFKSY	EHCFTAAEAV	DWLHELLRCS	QNFGPEVTRK	QTVQLLKKFL
90	100	110	120	130	140	150	160
KNHVIEDIKG	KWGEEDFEDN	RHLYRFPPSS	PLKPYPKKPP	NQKDVIKFPE	WNDLPPGTSQ	ENIPVRPVVM	NSEMWYKRHS
170	180	190	200	210	220	230	240
IAIGEVPACR	LVHRRQLTEA	NVEEIWKSMT	LSYLQKILGL	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 598: 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 599: PREDICTED: uncharacterized protein CXorf65 isoform X1 [Homo sapiens]

Accession:	gi|530421697	**Score:**	14.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	18.6
Database Date:	2015-11-30	**pI:**	11.1
		Sequence Coverage [%]:	8.8
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MFIFIKHGDN QQFLVNTNCA VVVLLYYIRS KVKLPKTNTI DLCEQTGKMK MLFLMKPNHA EYASKYLTAR STYYVCKVER
        90        100        110        120        130        140        150        160
GPPVALRIQC DALERRRIQM LKMKEAKKVV IIEPPASVPS KQSGRSDKKK STRKSPTFRN RPDFRKNKGR QLNKTTKQKK
       170
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2029	1	732.3134	-180.02	2	53.8	14.7	1	108-121	K.KVVIIEPPASVPSK.Q	

Detailed Protein Report

Protein 600: PDZ domain-containing protein 4 [Homo sapiens]

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

Score: 14.6
MW [kDa]: 86.1
pI: 5.7
Sequence Coverage [%]: 4.0
No. of unique Peptides: 1

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
450	1	1100.7316	-85.85	3	34.6	14.6	0	326-356	R.DFHFSMDSLLAEGAGLGGGDVPGLTDEEYER.Y	Oxidation: 6

Detailed Protein Report

Protein 601: ATP-binding cassette sub-family A member 5 [Homo sapiens]

Accession:	gi|27262624	**Score:**	14.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	186.4
Database Date:	2015-11-30	**pI:**	6.5
		Sequence Coverage [%]:	0.9
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|27262626	refseq_human(refseq_human_20140103.fasta)	ATP-binding cassette sub-family A member 5 [Homo sapiens]

10	20	30	40	50	60	70	80
MSTAIREVGV	WRQTRTLLLK	NYLIKCRTKK	SSVQEILFPL	FFLFWLILIS	MMHPNKKYEE	VPNIELNPMD	KFTLSNLILG
90	100	110	120	130	140	150	160
YTPVTNITSS	IMQKVSTDHL	PDVIITEEYT	NEKEMLTSSL	SKPSNFVGVV	FKDSMSYELR	FFPDMIPVSS	IYMDSRAGCS
170	180	190	200	210	220	230	240
KSCEAAQYWS	SGFTVLQASI	DAAIIQLKTN	VSLWKELEST	KAVIMGETAV	VEIDTFPRGV	ILIYLVIAFS	PFGYFLAIHI
250	260	270	280	290	300	310	320
VAEKEKKIKE	FLKIMGLHDT	AFWLSWVLLY	TSLIFLMSLL	MAVIATASLL	FPQSSSIVIF	LLFFLYGLSS	VFFALMLTPL
330	340	350	360	370	380	390	400
FKKSKHVGIV	EFFVTVAFGF	IGLMIILIES	FPKSLVWLFS	PFCHCTFVIG	IAQVMHLEDF	NEGASFSNLT	AGPYPLIITI
410	420	430	440	450	460	470	480
IMLTLNSIFY	VLLAVYLDQV	IPGEFGLRRS	SLYFLKPSYW	SKSKRNYEEL	SEGNVNGNIS	FSEIIEPVSS	EFVGKEAIRI
490	500	510	520	530	540	550	560
SGIQKTYRKK	GENVEALRNL	SFDIYEGQIT	ALLGHSGTGK	STLMNILCGL	CPPSDGFASI	YGHRVSEIDE	MFEARKMIGI
570	580	590	600	610	620	630	640
CPQLDIHFDV	LTVEENLSIL	ASIKGIPANN	IIQEVQKVLL	DLDMQTIKDN	QAKKLSGGQK	RKLSLGIAVL	GNPKILLLDE
650	660	670	680	690	700	710	720
PTAGMDPCSR	HIVWNLLKYR	KANRVTVFST	HFMDEADILA	DRKAVISQGM	LKCVGSSMFL	KSKWGIGYRL	SMYIDKYCAT
730	740	750	760	770	780	790	800
ESLSSLVKQH	IPGATLLQQN	DQQLVYSLPF	KDMDKFSGLF	SALDSHSNLG	VISYGVSMTT	LEDVFLKLEV	EAEIDQADYS
810	820	830	840	850	860	870	880
VFTQQPLEEE	MDSKSFDEME	QSLLILSETK	AALVSTMSLW	KQQMYTIAKF	HFFTLKRESK	SVRSVLLLLL	IFFTVQIFMF
890	900	910	920	930	940	950	960
LVHHSFKNAV	VPIKLVPDLY	FLKPGDKPHK	YKTSLLLQNS	ADSDISDLIS	FFTSQNIMVT	MINDSDYVSV	APHSAALNVM
970	980	990	1000	1010	1020	1030	1040
HSEKDYVFAA	VFNSTMVYSL	PILVNIISNY	YLYHLNVTET	IQIWSTPFFQ	EITDIVFKIE	LYFQAALLGI	IVTAMPPYFA
1050	1060	1070	1080	1090	1100	1110	1120
MENAENHKIK	AYTQLKLSGL	LPSAYWIGQA	VVDIPLFFII	LILMLGSLLA	FHYGLYFYTV	KFLAVVFCLI	GYVPSVILFT
1130	1140	1150	1160	1170	1180	1190	1200
YIASFTFKKI	LNTKEFWSFI	YSVAALACIA	ITEITFFMGY	TIATILHYAF	CIIIPIYPLL	GCLISFIKIS	WKNVRKNVDT
1210	1220	1230	1240	1250	1260	1270	1280
YNPWDRLSVA	VISPYLQCVL	WIFLLQYYEK	KYGGRSIRKD	PFFRNLSTKS	KNRKLPEPPD	NEDEDEDVKA	ERLKVKELMG
1290	1300	1310	1320	1330	1340	1350	1360
CQCCEEKPSI	MVSNLHKEYD	DKKDFLLSRK	VKKVATKYIS	FCVKKGEILG	LLGPNGAGKS	TIINILVGDI	EPTSGQVFLG
1370	1380	1390	1400	1410	1420	1430	1440
DYSSETSEDD	DSLKCMGYCP	QINPLWPDTT	LQEHFEIYGA	VKGMSASDMK	EVISRITHAL	DLKEHLQKTV	KKLPAGIKRK
1450	1460	1470	1480	1490	1500	1510	1520
LCFALSMLGN	PQITLLDEPS	TGMDPKAKQH	MWRAIRTAFK	NRKRAAILTT	HYMEEAEAVC	DRVAIMVSGQ	LRCIGTVQHL
1530	1540	1550	1560	1570	1580	1590	1600
KSKFGKGYFL	EIKLKDWIEN	LEVDRLQREI	QYIFPNASRQ	ESFSSILAYK	IPKEDVQSLS	QSFFKLEEAK	HAFAIEEYSF
1610	1620	1630	1640	1650			
SQATLEQVFV	ELTKEQEEED	NSCGTLNSTL	WWERTQEDRV	VF			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2136	1	805.8396	-128.42	2	55.1	14.6	1	1560-1573	R.QESFSSILAYKIPK.E	

Detailed Protein Report

Protein 602: **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 603: **PREDICTED: cGMP-inhibited 3',5'-cyclic phosphodiesterase A isoform X1 [Homo sapiens]**

Accession:	gi|578822894	**Score:**	14.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	118.5
Database Date:	2015-11-30	**pI:**	5.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.0
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 0.68 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MAVPGDAARV	RDKPVHSGVS	QAPTAGRDCH	HRADPASPRD	SGCRGCWGDL	VLQPLRSSRK	LSSALCAGSL	SFLLALLVRL
90	100	110	120	130	140	150	160
VRGEVGCDLE	QCKEAAAAEE	EEAAPGAEGG	VFPGPRGGAP	GGGARLSPWL	QPSALLFSLL	CAFFWMGLYL	LRAGVRLPLA
170	180	190	200	210	220	230	240
VALLAACCGG	EALVQIGLGV	GEDHLLSLPA	AGVVLSCLAA	ATWLVLRLRL	GVLMIALTSA	VRTVSLISLE	RFKVAWRPYL
250	260	270	280	290	300	310	320
AYLAGVLGIL	LARYVEQILP	QSAEAAPREH	LGSQLIAGTK	EDIPVFKRRR	RSSSVVSAEM	SGCSSKSHRR	TSLPCIPREQ
330	340	350	360	370	380	390	400
LMGHSEWDHK	RGPRGSQSSG	TSITVDIAVM	GEAHGLITDL	LADPSLPPNV	CTSLRAVSNL	LSTQLTFQAI	HKPRVNPVTS
410	420	430	440	450	460	470	480
LSENYTCSDS	EESSEKDKLA	IPKRLRRSLP	PGLLRRVSST	WTTTTSATGL	PTLEPAPVRR	DRSTSIKLQE	APSSSPDSWN
490	500	510	520	530	540	550	560
NPVMMTLTKS	RSFTSSYAIS	AANHVKAKKQ	SRPGALAKIS	PLSSPCSSPL	QGTPASSLVS	KISAVQFPES	ADTTAKQSLG
570	580	590	600	610	620	630	640
SHRALTYTQS	APDLSPQILT	PPVICSSCGR	PYSQGNPADE	PLERSGVATR	TPSRTDDTAQ	VTSDYETNNN	SDSSDIVQNE
650	660	670	680	690	700	710	720
DETECLREPL	RKASACSTYA	PETMMFLDKP	ILAPEPLVMD	NLDSIMEQLN	TWNFPIFDLV	ENIGRKCGRI	LSQVSYRLFE
730	740	750	760	770	780	790	800
DMGLFEAFKI	PIREFMNYFH	ALEIGYRDIP	YHNRIHATDV	LHAVWYLTTQ	PIPGLSTVIN	DHGSTSDSDS	DSGFTHGHMG
810	820	830	840	850	860	870	880
YVFSKTYNVT	DDKYGCLSGN	IPALELMALY	VAAAMHDYDH	PGRTNAFLVA	TSAPQAVLYN	DRSVLENHHA	AAAWNLFMSR
890	900	910	920	930	940	950	960
PEYNFLINLD	HVEFKHFRFL	VIEAILATDL	KKHFDFVAKF	NGKVNDDVGI	DWTNENDRLL	VCQMCIKLAD	INGPAKCKEL
970	980	990	1000	1010	1020	1030	1040
HLQWTDGIVN	EFYEQGDEEA	SLGLPISPFM	DRSAPQLANL	QESFISHIVG	PLCNSYDSAG	LMPGKWVEDS	DESGDTDDPE
1050	1060	1070	1080	1090			
EEEEEAPAPN	EEETCENNES	PSKYQMPLAY	RLEDTLQDKF	LKGGMLR			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
645	1	647.6267	-227.08	2	36.5	14.5	0	83-93	R.GEVGCDLEQCK.E	Carbamidomethyl: 5, 10	WD:WU 0.68

Detailed Protein Report

Protein 604: inhibitor of nuclear factor kappa-B kinase subunit alpha [Homo sapiens]

Accession: gi|62241001
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 14.5
MW [kDa]: 84.6
pI: 6.3
Sequence Coverage [%]: 1.1
No. of unique Peptides: 1

Quantitation

WD:WU **Median:** 0.52 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MERPPGLRPG	AGGPWEMRER	LGTGGFGNVC	LYQHRELDLK	IAIKSCRLEL	STKNRERWCH	EIQIMKKLNH	ANVVKACDVP
90	100	110	120	130	140	150	160
EELNILIHDV	PLLAMEYCSG	GDLRKLLNKP	ENCCGLKESQ	ILSLLSDIGS	GIRYLHENKI	IHRDLKPENI	VLQDVGGKII
170	180	190	200	210	220	230	240
HKIIDLGYAK	DVDQGSLCTS	FVGTLQYLAP	ELFENKPYTA	TVDYWSFGTM	VFECIAGYRP	FLHHLQPFTW	HEKIKKKDPK
250	260	270	280	290	300	310	320
CIFACEEMSG	EVRFSSHLPQ	PNSLCSLVVE	PMENWLQLML	NWDPQQRGGP	VDLTLKQPRC	FVLMDHILNL	KIVHILNMTS
330	340	350	360	370	380	390	400
AKIISFLLPP	DESLHSLQSR	IERETGINTG	SQELLSETGI	SLDPRKPASQ	CVLDGVRGCD	SYMVYLFDKS	KTVYEGPFAS
410	420	430	440	450	460	470	480
RSLSDCVNYI	VQDSKIQLPI	IQLRKVWAEA	VHYVSGLKED	YSRLFQGQRA	AMLSLLRYNA	NLTKMKNTLI	SASQQLKAKL
490	500	510	520	530	540	550	560
EFFHKSIQLD	LERYSEQMTY	GISSEKMLKA	WKEMEEKAIH	YAEVGVIGYL	EDQIMSLHAE	IMELQKSPYG	RRQGDLMESL
570	580	590	600	610	620	630	640
EQRAIDLYKQ	LKHRPSDHSY	SDSTEMVKII	VHTVQSQDRV	LKELFGHLSK	LLGCKQKIID	LLPKVEVALS	NIKEADNTVM
650	660	670	680	690	700	710	720
FMQGKRQKEI	WHLLKIACTQ	SSARSLVGSS	LEGAVTPQTS	AWLPPTSAEH	DHSLSCVVTP	QDGETSAQMI	EENLNCLGHL
730	740	750					
STIIHEANEE	QGNSMMNLDW	SWLTE					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1405	1	533.6158	-246.47	2	45.9	14.5	1	510-517	K.AWKEMEEK.A	Oxidation: 5	WD:WU 0.52

Detailed Protein Report

Protein 605: zinc finger and BTB domain-containing protein 5 [Homo sapiens]

Accession:	gi|7662074	**Score:**	14.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	74.2
Database Date:	2015-11-30	**pI:**	5.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.5
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|530390257	refseq_human (refseq_human_20140103.fasta)	PREDICTED: zinc finger and BTB domain-containing protein 5 isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MDFPGHFEQI	FQQLNYQRLH	GQLCDCVIVV	GNRHFKAHRS	VLAACSTHFR	ALFSVAEGDQ	TMNMIQLDSE	VVTAEAFAAL
90	100	110	120	130	140	150	160
IDMMYTSTLM	LGESNVMDVL	LAASHLHLNS	VVKACKHYLT	TRTLPMSPPS	ERVQEQSARM	QRSFMLQQLG	LSIVSSALNS
170	180	190	200	210	220	230	240
SQNGEEQPAP	MSSSMRSNLD	QRTPFPMRRL	HKRKQSAEER	ARQRLRPSID	ESAISDVTPE	NGPSGVHSRE	EFFSPDSLKI
250	260	270	280	290	300	310	320
VDNPKADGMT	DNQEDSAIMF	DQSFGTQEDA	QVPSQSDNSA	GNMAQLSMAS	RATQVETSFD	QEAAPEKSSF	QCENPEVGLG
330	340	350	360	370	380	390	400
EKEHMRVVVK	SEPLSSPEPQ	DEVSDVTSQA	EGSESVEVEG	VVVSAEKIDL	SPESSDRSFS	DPQSSTDRVG	DIHILEVTNN
410	420	430	440	450	460	470	480
LEHKSTFSIS	NFLNKSRGNN	FTANQNNDDN	IPNTTSDCRL	ESEAPYLLSP	EAGPAGGPSS	APGSHVENPF	SEPADSHFVR
490	500	510	520	530	540	550	560
PMQEVMGLPC	VQTSGYQGGE	QFGMDFSRSG	LGLHSSFSRV	MIGSPRGGAS	NFPYYRRIAP	KMPVVTSVRS	SQIPENSTSS
570	580	590	600	610	620	630	640
QLMMNGATSS	FENGHPSQPG	PPQLTRASAD	VLSKCKKALS	EHNVLVVEGA	RKYACKICCK	TFLTLTDCKK	HIRVHTGEKP
650	660	670	680				
YACLKCGKRF	SQSSHLYKHS	KTTCLRWQSS	NLPSTLL				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1742	1	689.9841	-17.31	3	50.5	14.5	2	613-629	K.YACKICCKTFLTLTDCK.K	Carbamidomethyl: 6, 7

Detailed Protein Report

Protein 606: **beta-1-syntrophin [Homo sapiens]**

Accession:	gi|11321640	**Score:**	14.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	58.0
Database Date:	2015-11-30	**pI:**	9.5
		Sequence Coverage [%]:	2.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAVAAAAAAA	GPAGAGGGRA	QRSGLLEVLV	RDRWHKVLVN	LSEDALVLSS	EEGAAAYNGI	GTATNGSFCR	GAGAGHPGAG
90	100	110	120	130	140	150	160
GAQPPDSPAG	VRTAFTDLPE	QVPESISNQK	RGVKVLKQEL	GGLGISIKGG	KENKMPILIS	KIFKGLAADQ	TQALYVGDAI
170	180	190	200	210	220	230	240
LSVNGADLRD	ATHDEAVQAL	KRAGKEVLLE	VKYMREATPY	VKKGSPVSEI	GWETPPPESP	RLGGSTSDPP	SSQSFSFHRD
250	260	270	280	290	300	310	320
RKSIPLKMCY	VTRSMALADP	ENRQLEIHSP	DAKHTVILRS	KDSATAQAWF	SAIHSNVNDL	LTRVIAEVRE	QLGKTGIAGS
330	340	350	360	370	380	390	400
REIRHLGWLA	EKVPGESKKQ	WKPALVVLTE	KDLLIYDSMP	RRKEAWFSPV	HTYPLLATRL	VHSGPGKGSP	QAGVDLSFAT
410	420	430	440	450	460	470	480
RTGTRQGIET	HLFRAETSRD	LSHWTRSIVQ	GCHNSAELIA	EISTACTYKN	QECRLTIHYE	NGFSITTEPQ	EGAFPKTIIQ
490	500	510	520	530	540		
SPYEKLKMSS	DDGIRMLYLD	FGGKDGEIQL	DLHSCPKPIV	FIIHSFLSAK	ITRLGLVA		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2302	1	703.3364	-29.47	2	57.1	14.4	0	388-401	K.GSPQAGVDLSFATR.T	

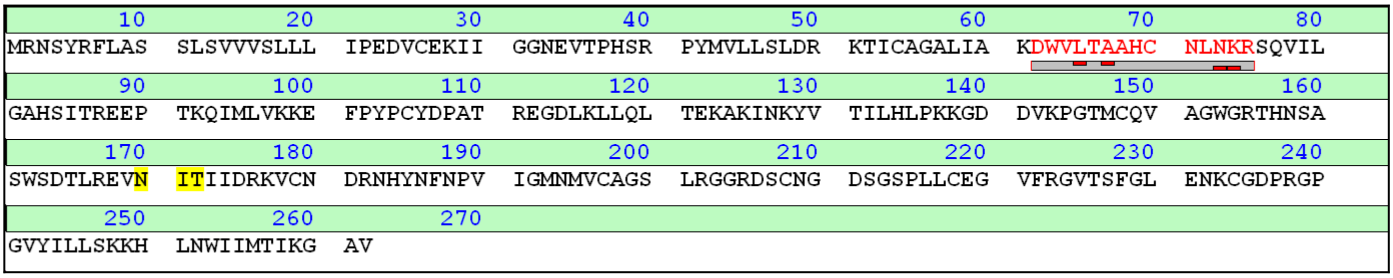
Detailed Protein Report

Protein 607: granzyme A precursor [Homo sapiens]

Accession:	gi|5453676	**Score:**	14.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	28.9
Database Date:	2015-11-30	**pI:**	10.1
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	5.3
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 0.78 **CV:** 0.00 % **No. of Peptides:** 1



```
        10         20         30         40         50         60         70         80
MRNSYRFLAS SLSVVVSLLL IPEDVCEKII GGNEVTPHSR PYMVLLSLDR KTICAGALIA KDWVLTAAHC NLNKRSQVIL
        90        100        110        120        130        140        150        160
GAHSITREEP TKQIMLVKKE FPYPCYDPAT REGDLKLLQL TEKAKINKYV TILHLPKKGD DVKPGTMCQV AGWGRTHNSA
       170        180        190        200        210        220        230        240
SWSDTLREVN ITIIDRKVCN DRNHYNFNPV IGMNMVCAGS LRGGRDSCNG DSGSPLLCEG VFRGVTSFGL ENKCGDPRGP
       250        260        270
GVYILLSKKH LNWIIMTIKG AV
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
92	1	566.5853	-66.20	3	30.1	14.4	1	62-75	K.DWVLTAAHCNLNKR.S	Carbamidomethyl: 9	WD:WU 0.78

Detailed Protein Report

Protein 608: putative dehydrogenase/reductase SDR family member 4-like 2 [Homo sapiens]

Accession:	gi|482628371	**Score:**	14.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	16.3
Database Date:	2015-11-30	**pI:**	9.1
Modification(s):	Oxidation	**Sequence Coverage [%]:**	8.7
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 1.24 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MTGTVCHVGK MKDWERLVAT VSCREMGTEP GGGKGSQPEP PSLLSWTALG FSPYNVSKTA LLGLNKTLAI ELAPRNIRVN
        90        100        110        120        130        140        150        160
CLAPGLIKTS FSRMLWMDKE KEESMKETLR IRRLGEPEDS LGIVSFLCSE DASYLTGETV MVGGGTPSRL
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
717	1	866.9167	38.74	2	37.8	14.4	2	94-106	R.MLWMDKEKEESMK.E	Oxidation: 1, 4, 12	WD:WU	1.24

Detailed Protein Report

Protein 609: PREDICTED: catenin alpha-1 isoform X2 [Homo sapiens]

Accession:	gi|530379718	**Score:**	14.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	59.5
Database Date:	2015-11-30	**pI:**	5.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.2
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530379720	refseq_human (refseq_human_20140103.fasta)	PREDICTED: catenin alpha-1 isoform X3 [Homo sapiens]

10	20	30	40	50	60	70	80
MTKKTRDLRR	QLRKAVMDHV	SDSFLETNVP	LLVLIEAAKN	GNEKEVKEYA	QVFREHANKL	IEVANLACSI	SNNEEGVKLV
90	100	110	120	130	140	150	160
RMSASQLEAL	CPQVINAALA	LAAKPQSKLA	QENMDLFKEQ	WEKQVRVLTD	AVDDITSIDD	FLAVSENHIL	EDVNKCVIAL
170	180	190	200	210	220	230	240
QEKDVDGLDR	TAGAIRGRAA	RVIHVVTSEM	DNYEPGVYTE	KVLEATKLLS	NTVMPRFTEQ	VEAAVEALSS	DPAQPMDENE
250	260	270	280	290	300	310	320
FIDASRLVYD	GIRDIRKAVL	MIRTPEELDD	SDFETEDFDV	RSRTSVQTED	DQLIAGQSAR	AIMAQLPQEQ	KAKIAEQVAS
330	340	350	360	370	380	390	400
FQEEKSKLDA	EVSKWDDSGN	DIIVLAKQMC	MIMMEMTDFT	RGKGPLKNTS	DVISAAKKIA	EAGSRMDKLG	RTIADHCPDS
410	420	430	440	450	460	470	480
ACKQDLLAYL	QRIALYCHQL	NICSKVKAEV	QNLGGELVVS	GVDSAMSLIQ	AAKNLMNAVV	QTVKASYVAS	TKYQKSQGMA
490	500	510	520	530	540		
SLNLPAVSWK	MKAPEKKPLV	KREKQDETQT	KIKRASQKKH	VNPVQALSEF	KAMDSI		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2652	3	659.3500	103.51	2	61.5	14.3	0	392-403	R.TIADHCPDSACK.Q	Carbamidomethyl: 11

Detailed Protein Report

Protein 610: probable ATP-dependent RNA helicase DHX58 [Homo sapiens]

Accession:	gi|149408122	**Score:**	14.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	76.6
Database Date:	2015-11-30	**pI:**	7.1
		Sequence Coverage [%]:	2.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MELRSYQWEV	IMPALEGKNI	IIWLPTGAGK	TRAAAYVAKR	HLETVDGAKV	VVLVNRVHLV	TQHGEEFRRM	LDGRWTVTTL
90	100	110	120	130	140	150	160
SGDMGPRAGF	GHLARCHDLL	ICTAELLQMA	LTSPEEEEHV	ELTVFSLIVV	DECHHTHKDT	VYNVIMSQYL	ELKLQRAQPL
170	180	190	200	210	220	230	240
PQVLGLTASP	GTGGASKLDG	AINHVLQLCA	NLDTWCIMSP	QNCCPQLQEH	SQQPCKQYNL	CHRRSQDPFG	DLLKKLMDQI
250	260	270	280	290	300	310	320
HDHLEMPELS	RKFGTQMYEQ	QVVKLSEAAA	LAGLQEQRVY	ALHLRRYNDA	LLIHDTVRAV	DALAALQDFY	HREHVTKTQI
330	340	350	360	370	380	390	400
LCAERRLLAL	FDDRKNELAH	LATHGPENPK	LEMLEKILQR	QFSSSNSPRG	IIFTRTRQSA	HSLLLWLQQQ	QGLQTVDIRA
410	420	430	440	450	460	470	480
QLLIGAGNSS	QSTHMTQRDQ	QEVIQKFQDG	TLNLLVATSV	AEEGLDIPHC	NVVVRYGLLT	NEISMVQARG	RARADQSVYA
490	500	510	520	530	540	550	560
FVATEGSREL	KRELINEALE	TLMEQAVAAV	QKMDQAEYQA	KIRDLQQAAL	TKRAAQAAQR	ENQRQQFPVE	HVQLLCINCM
570	580	590	600	610	620	630	640
VAVGHGSDLR	KVEGTHHVNV	NPNFSNYYNV	SRDPVVINKV	FKDWKPGGVI	SCRNCGEVWG	LQMIYKSVKL	PVLKVRSMLL
650	660	670	680				
ETPQGRIQAK	KWSRVPFSVP	DFDFLQHCAE	NLSDLSLD				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1926	1	618.9091	-113.75	3	52.4	14.3	1	614-629	R.NCGEVWGLQMIYKSVK.L	

Detailed Protein Report

Protein 611: probable ATP-dependent RNA helicase DHX36 isoform 2 [Homo sapiens]

Accession:	gi|167830436	**Score:**	14.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	113.1
Database Date:	2015-11-30	**pI:**	8.3
		Sequence Coverage [%]:	1.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSYDYHQNWG	RDGGPRSSGG	GYGGGPAGGH	GGNRGSGGGG	GGGGGGRGGR	GRHPGHLKGR	EIGMWYAKKQ	GQKNKEAERQ
90	100	110	120	130	140	150	160
ERAVVHMDER	REEQIVQLLN	SVQAKNDKES	EAQISWFAPE	DHGYGTEVST	KNTPCSENKL	DIQEKKLINQ	EKKMFRIRNR
170	180	190	200	210	220	230	240
SYIDRDSEYL	LQENEPDGTL	DQKLLEDLQK	KKNDLRYIEM	QHFREKLPSY	GMQKELVNLI	DNHQVTVISG	ETGCGKTTQV
250	260	270	280	290	300	310	320
TQFILDNYIE	RGKGSACRIV	CTQPRRISAI	SVAERVAAER	AESCGSGNST	GYQIRLQSRL	PRKQGSILYC	TTGIILQWLQ
330	340	350	360	370	380	390	400
SDPYLSSVSH	IVLDEIHERN	LQSDVLMTVV	KDLLNFRSDL	KVILMSATLN	AEKFSEYFGN	CPMIHIPGFT	FPVVEYLLED
410	420	430	440	450	460	470	480
VIEKIRYVPE	QKEHRSQFKR	GFMQGHVNRQ	EKEEKEAIYK	ERWPDYVREL	RRRYSASTVD	VIEMMEDDKV	DLNLIVALIR
490	500	510	520	530	540	550	560
YIVLEEEDGA	ILVFLPGWDN	ISTLHDLLMS	QVMFKSVNQT	QVFKRTPPGV	RKIVIATNIA	ETSITIDDVV	YVIDGGKIKE
570	580	590	600	610	620	630	640
THFDTQNNIS	TMSAEWVSKA	NAKQRKGRAG	RVQPGHCYHL	YNGLRASLLD	DYQLPEILRT	PLEELCLQIK	ILRLGGIAYF
650	660	670	680	690	700	710	720
LSRLMDPPSN	EAVLLSIRHL	MELNALDKQE	ELTPLGVHLA	RLPVEPHIGK	MILFGALFCC	LDPVLTIAAS	LSFKDPFVIP
730	740	750	760	770	780	790	800
LGKEKIADAR	RKELAKDTRS	DHLTVVNAFE	GWEEARRRGF	RYEKDYCWEY	FLSSNTLQML	HNMKGQFAEH	LLGAGFVSSR
810	820	830	840	850	860	870	880
NPKDPESNIN	SDNEKIIKAV	ICAGLYPKVA	KIRLNLGKKR	KMVKVYTKTD	GLVAVHPKSV	NVEQTDFHYN	WLIYHLKMRT
890	900	910	920	930	940	950	960
SSIYLYDCTE	VSPYCLLFFG	GDISIQKDND	QETIAVDEWI	VFQSPARIAH	LVKELRKELD	ILLQEKIESP	HPVDWNDTKS
970	980	990	1000				
RDCAVLSAII	DLIKTQEKAT	PRNFPPRFQD	GYYS				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
338	2	686.9336	150.15	2	32.9	14.3	2	35-52	R.GSGGGGGGGGGGRGGRGR.H	

Detailed Protein Report

Protein 612: glypican-5 precursor [Homo sapiens]

Accession:	gi|4758464	**Score:**	14.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	63.7
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
MDAQTWPVGF RCLLLLALVG SARSEGVQTC EEVRKLFQWR LLGAVRGLPD SPRAGPDLQV CISKKPTCCT RKMEERYQIA
        90        100        110        120        130        140        150        160
ARQDMQQFLQ TSSSTLKFLI SRNAAAFQET LETLIKQAEN YTSILFCSTY RNMALEAAAS VQEFFTDVGL YLFGADVNPE
       170        180        190        200        210        220        230        240
EFVNRFFDSL FPLVYNHLIN PGVTDSSLEY SECIRMARRD VSPFGNIPQR VMGQMGRSLL PSRTFLQALN LGIEVINTTD
       250        260        270        280        290        300        310        320
YLHFSKECSR ALLKMQYCPH CQGLALTKPC MGYCLNVMRG CLAHMAELNP HWHAYIRSLE ELSDAMHGTY DIGHVLLNFH
       330        340        350        360        370        380        390        400
LLVNDAVLQA HLNGQKLLEQ VNRICGRPVR TPTQSPRCSF DQSKEKHGMK TTTRNSEETL ANRRKEFINS LRLYRSFYGG
       410        420        430        440        450        460        470        480
LADQLCANEL AAADGLPCWN GEDIVKSYTQ RVVGNGIKAQ SGNPEVKVKG IDPVINQIID KLKHVVQLLQ GRSPKPDKWE
       490        500        510        520        530        540        550        560
LLQLGSGGGM VEQVSGDCDD EDGCGGSGSG EVKRTLKITD WMPDDMNFSD VKQIHQTDTG STLDTTGAGC AVATESMTFT
       570        580
LISVVMLLPG IW
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1972	1	973.3912	-90.24	2	53.0	14.3	2	367-383	K.HGMKTTTRNSEETLANR.R	

Detailed Protein Report

Protein 613: 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	

Detailed Protein Report

Protein 614: **SH3 domain-binding glutamic acid-rich-like protein [Homo sapiens]**

Accession:	gi|4506925	**Score:**	14.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	12.8
Database Date:	2015-11-30	**pI:**	5.1
		Sequence Coverage [%]:	14.0
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MVIRVYIASS SGSTAIKKKQ QDVLGFLEAN KIGFEEKDIA ANEENRKWMR ENVPENSRPA TGYPLPPQIF NESQYRGDYD
        90        100        110        120
AFFEARENNA VYAFLGLTAP PGSKEAEVQA KQQA
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2960	1	826.4281	-53.76	2	65.8	14.3	1	2-17	M.VIRVYIASSSGSTAIK.K	

Detailed Protein Report

Protein 615: selenium-binding protein 1 isoform 2 [Homo sapiens]

Accession:	gi|385137128	**Score:**	14.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	45.4
Database Date:	2015-11-30	**pI:**	5.2
Modification(s):	Oxidation	**Sequence Coverage [%]:**	4.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MATKCGNCGP	GYSTPLEAMK	GPREEIVYLP	CIYRNTGTEA	PDYLATVDVD	PKSPQYCQVI	EPKDIHAKCE	LAFLHTSHCL
90	100	110	120	130	140	150	160
ASGEVMISSL	GDVKGNGKGG	FVLLDGETFE	VKGTWERPGG	AAPLGYDFWY	QPRHNVMIST	EWAAPNVLRD	GFNPADVEAG
170	180	190	200	210	220	230	240
LYGSHLYVWD	WQRHEIVQTL	SLKDGLIPLE	IRFLHNPDAA	QGFVGCALSS	TIQRFYKNEG	GTWSVEKVIQ	VPPKKVKGWL
250	260	270	280	290	300	310	320
LPEMPGLITD	ILLSLDDRFL	YFSNWLHGDL	RQYDISDPQR	PRLTGQLFLG	GSIVKGGPVQ	VLEDEELKSQ	PEPLVVKGKR
330	340	350	360	370	380	390	400
VAGGPQMIQL	SLDGKRLYIT	TSLYSAWDKQ	FYPDLIREGS	VMLQVDVDTV	KGGLKLNPNF	LVDFGKEPLG	PALAHELRYP
410	420						
GGDCSSDIWI							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1766	1	1045.8477	-101.94	2	50.4	14.3	1	1-20	-.MATKCGNCGPGYSTPLEAMK.G	Oxidation: 1, 19

Detailed Protein Report

Protein 616: **chymotrypsinogen B precursor [Homo sapiens]**

Accession:	gi|118498341	**Score:**	14.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	27.7
Database Date:	2015-11-30	**pI:**	7.7
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	10.6
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 1.11 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MASLWLLSCF SLVGAAFGCG VPAIHPVLSG LSRIVNGEDA VPGSWPWQVS LQDKTGFHFC GGSLISEDWV VTAAHCGVRT
        90        100        110        120        130        140        150        160
SDVVVAGEFD QGSDEENIQV LKIAKVFKNP KFSILTVNND ITLLKLATPA RFSQTVSAVC LPSADDDFPA GTLCATTGWG
       170        180        190        200        210        220        230        240
KTKYNANKTP DKLQQAALPL LSNAECKKSW GRRITDVMIC AGASGVSSCM GDSGGPLVCQ KDGAWTLVGI VSWGSDTCST
       250        260        270
SSPGVYARVT KLIPWVQKIL AAN
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
323	1	939.4727	58.29	3	32.7	14.2	0	194-221	R. ITDVMICAGASGVSSCMGDSGGP D	Carbamidomethyl: 16, 26; Oxidation: 17	WD:WU 1.11

Detailed Protein Report

Protein 617: PREDICTED: putative uncharacterized protein FLJ46235-like [Homo sapiens]

Accession:	gi|530359082	**Score:**	14.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	24.4
Database Date:	2015-11-30	**pI:**	13.0
		Sequence Coverage [%]:	6.0
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530435845	refseq_human (refseq_human_20140103.fasta)	PREDICTED: putative uncharacterized protein FLJ46235-like [Homo sapiens]
gi|530386771	refseq_human (refseq_human_20140103.fasta)	PREDICTED: putative uncharacterized protein FLJ46235-like [Homo sapiens]

10	20	30	40	50	60	70	80
MPSPSLQTAA	SDSARAQIPA	AFVRPKPPPA	QLSRPTCGLA	VASPGPDLAS	RWPSPAVFLP	ASQRPRQAHR	MPLTGLWRSS
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
SSLTVASPGP	APARPDGVSR	PRVSQVGPSR	AQLLPPGRWP	VRAQSVLKSA	SPGPAPACRR	PLDLRHGLCL	LTVDPHQAQL
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
LPQHGRLRPG	SCSACGQPPR	ARLSPLAILS	RPRSVSSQPL	QAQLSLPAAP	AGPAPASQQP	RSAQLLPSSW	QPL

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2544	1	694.4688	179.47	2	60.1	14.2	0	2-15	M.PSPSLQTAASDSAR.A	

Detailed Protein Report

Protein 618: **PREDICTED: probable E3 ubiquitin-protein ligase HECTD2 isoform X2 [Homo sapiens]**

Accession:	gi|530393122	**Score:**	14.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	76.8
Database Date:	2015-11-30	**pI:**	8.4
		Sequence Coverage [%]:	2.7
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 0.88 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MDASSSEMKA	PVLPEPILPI	QPKTVKDFQE	DVEKVKSSGD	WKAVHDFYLT	TFDSFPELNA	AFKKDATASF	NTIEDSGINA
90	100	110	120	130	140	150	160
KFVNAVYDTL	LNTPQDVQKT	VLKGIINSLL	REWKGPRTKD	DLRAYFILLQ	NPQFNNTSTY	VIYAHLLRQI	ATLVEADHHF
170	180	190	200	210	220	230	240
LVHWFKKLSQ	KRFKQLVERL	LQFISLRLFP	AKPEEFPPIT	KCSWWIPSAA	KVLALLNTAN	NLVHPPLIPY	TDFYNSTLDH
250	260	270	280	290	300	310	320
IDLMEEYHTW	QNFGNSHRFS	FCQYPFVISV	AAKKIIIQRD	SEQQMINIAR	QSLVDKVSRR	QRPDMNILFL	NMKVRRTHLV
330	340	350	360	370	380	390	400
SDSLDELTRK	RADLKKKLKV	TFVGEAGLDM	GGLTKEWFLL	LIRQIFHPDY	GMFTYHKDSH	CHWFSSFKCD	NYSEFRLVGI
410	420	430	440	450	460	470	480
LMGLAVYNSI	TLDIRFPPCC	YKKLLSPPII	PSDQNIPVGI	CNVTVDDLCQ	IMPELAHGLS	ELLSHEGNVE	EDFYSTFQVF
490	500	510	520	530	540	550	560
QEEFGIIKSY	NLKPGGDKIS	VTNQNRKEYV	QLYTDFLLNK	SIYKQFAAFY	YGFHSVCASN	ALMLLRPEEV	EILVCGSPDL
570	580	590	600	610	620	630	640
DMHALQRSTQ	YDGYAKTDLT	IKYFWDVVLG	FPLDLQKKLL	HFTTGSDRVP	VGGMADLNFK	ISKNETSTNC	LPVAHTCFNQ
650	660	670					
LCLPPYKSKK	DLKQKLIIGI	SNSEGFGLE					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1946	1	918.3545	-158.85	2	52.7	14.2	1	338-355	K.LKVTFVGEAGLDMGGLTK.E		WD:WU 0.88

Detailed Protein Report

Protein 619: cardiomyopathy-associated protein 5 [Homo sapiens]

Accession:	gi|62241003	**Score:**	14.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	448.9
Database Date:	2015-11-30	**pI:**	4.6
		Sequence Coverage [%]:	0.3
		No. of unique Peptides:	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MASRDSNHAG	ESFLGSDGDE	EATRELETEE	ESEGEEDETA	AESEEEPDSR	LSDQDEEGKI	KQEYIISDPS	FSMVTVQRED
90	100	110	120	130	140	150	160
SGITWETNSS	RSSTPWASEE	SQTSGVCSRE	GSTVNSPPGN	VSFIVDEVKK	VRKRTHKSKH	GSPSLRRKGN	RKRNSFESQD
170	180	190	200	210	220	230	240
VPTNKKGSPL	TSASQVLTTE	KEKSYTGIYD	KARKKKTTSN	TPPITGAIYK	EHKPLVLRPV	YIGTVQYKIK	MFNSVKEELI
250	260	270	280	290	300	310	320
PLQFYGTLPK	GYVIKEIHYR	KGKDASISLE	PDLDNSGSNT	VSKTRKLVAQ	SIEDKVKEVF	PPWRGALSKG	SESLTLMFSH
330	340	350	360	370	380	390	400
EDQKKIYADS	PLNATSALEH	TVPSYSSSGR	AEQGIQLRHS	QSVPQQPEDE	AKPHEVEPPS	VTPDTPATMF	LRTTKEECEL
410	420	430	440	450	460	470	480
ASPGTAASEN	DSSVSPSFAN	EVKKEDVYSA	HHSISLEAAS	PGLAASTQDG	LDPDQEQPDL	TSIERAEPVS	AKLTPTHPSV
490	500	510	520	530	540	550	560
KGEKEENMLE	PSISLSEPLM	LEEPEKEEIE	TSLPIAITPE	PEDSNLVEEE	IVELDYPESP	LVSEKPFPPH	MSPEVEHKEE
570	580	590	600	610	620	630	640
ELILPLLAAS	SPEHVALSEE	EREEIASVST	GSAFVSEYSV	PQDLNHELQE	QEGEPVPPSN	VEAIAEHAVL	SEEENEEFEA
650	660	670	680	690	700	710	720
YSPAAAPTSE	SSLSPSTTEK	TSENQSPLFS	TVTPEYMVLS	GDEASESGCY	TPDSTSASEY	SVPSLATKES	LKKTIDRKSP
730	740	750	760	770	780	790	800
LILKGVSEYM	IPSEEKEDTG	SFTPAVAPAS	EPSLSPSTTE	KTSECQSPLP	STATSEHVVP	SEGEDLGSER	FTPDSKLISK
810	820	830	840	850	860	870	880
YAAPLNATQE	SQKKIINEAS	QFKPKGISEH	TVLSVDGKEV	IGPSSPDLVV	ASEHSFPPHT	TEMTSECQAP	PLSATPSEYV
890	900	910	920	930	940	950	960
VLSDEEAVEL	ERYTPSSTSA	SEFSVPPYAT	PEAQEEEIVH	RSLNLKGASS	PMNLSEEDQE	DIGPFSPDSA	FVSEFSFPPY
970	980	990	1000	1010	1020	1030	1040
ATQEAEKREF	ECDSPICLTS	PSEHTILSDE	DTEEAELFSP	DSASQVSIPP	FRISETEKNE	LEPDSLLTAV	SASGYSCFSE
1050	1060	1070	1080	1090	1100	1110	1120
ADEEDIGSTA	ATPVSEQFSS	SQKQKAETFP	LMSPLEDLSL	PPSTDKSEKA	EIKPEIPTTS	TSVSEYLILA	QKQKTQAYLE
1130	1140	1150	1160	1170	1180	1190	1200
PESEDLIPSH	LTSEVEKGER	EASSSVAAIP	AALPAQSSIV	KEETKPASPH	SVLPDSVPAI	KKEQEPTAAL	TLKAADEQMA
1210	1220	1230	1240	1250	1260	1270	1280
LSKVRKEEIV	PDSQEATAHV	SQDQKMEPQP	PNVPESEMKY	SVLPDMVDEP	KKGVKPKLVL	NVTSELEQRK	LSKNEPEVIK
1290	1300	1310	1320	1330	1340	1350	1360
PYSPLKETSL	SGPEALSAVK	MEMKHDSKIT	TTPIVLHSAS	SGVEKQVEHG	PPALAFSALS	EEIKKEIEPS	SSTTTASVTK
1370	1380	1390	1400	1410	1420	1430	1440
LDSNLTRAVK	EEIPTDSSLI	TPVDRPVLTK	VGKGELGSGL	PPLVTSADEH	SVLAEEDKVA	IKGASPIETS	SKHLAWSEAE
1450	1460	1470	1480	1490	1500	1510	1520
KEIKFDSLPS	VSSIAEHSVL	SEVEAKEVKA	GLPVIKTSSS	QHSDKSEEAR	VEDKQDLLFS	TVCDSERLVS	SQKKSLMSTS
1530	1540	1550	1560	1570	1580	1590	1600
EVLEPEHELP	LSLWGEIKKK	ETELPSSQNV	SPASKHIIPK	GKDEETASSS	PELENLASGL	APTLLLLSDD	KNKPAVEVSS
1610	1620	1630	1640	1650	1660	1670	1680
TAQGDFPSEK	QDVALAELSL	EPEKKDKPHQ	PLELPNAGSE	FSSDLGRQSG	SIGTKQAKSP	ITETEDSVLE	KGPAELRSRE
1690	1700	1710	1720	1730	1740	1750	1760
GKEENRELCA	SSTMPAISEL	SSLLREESQN	EEIKPFSPKI	ISLESKEPPA	SVAEGGNPEE	FQPFTFSLKG	LSEEVSHPAD
1770	1780	1790	1800	1810	1820	1830	1840
FKKGGNQEIG	PLPPTGNLKA	QVMGDILDKL	SEETGHPNSS	QVLQSITEPS	KIAPSDLLVE	QKKTEKALHS	DQTVKLPDVS
1850	1860	1870	1880	1890	1900	1910	1920
TSSEDKQDLG	IKQFSLMREN	LPLEQSKSFM	TTKPADVKET	KMEEFFISPK	DENWMLGKPE	NVASQHEQRI	AGSVQLDSSS
1930	1940	1950	1960	1970	1980	1990	2000
SNELRPGQLK	AAVSSKDHTC	EVRKQVLPHS	AEESHLSSQE	AVSALDTSSG	NTETLSSKSY	SSEEVKLAEE	PKSLVLAGNV
2010	2020	2030	2040	2050	2060	2070	2080
ERNIAEGKEI	HSLMESESLL	LEKANTELSW	PSKEDSQEKI	KLPPERFFQK	PVSGLSVEQV	KSETISSSVK	TAHFPAEGVE
2090	2100	2110	2120	2130	2140	2150	2160
PALGNEKEAH	RSTPPFPEEK	PLEESKMVQS	KVIDDADEGK	KPSPEVKIPT	QRKPISSIHA	REPQSPESPE	VTQNPPTQPK
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1989	3	703.2718	-183.94	2	53.2	14.2	2	251-261	K.GYVIKEIHYRK.G	

Detailed Protein Report

Protein 620: 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 621: **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 622: mitogen-activated protein kinase kinase kinase 11 [Homo sapiens]

Accession:	gi|4505195	**Score:**	14.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	92.6
Database Date:	2015-11-30	**pI:**	9.4
		Sequence Coverage [%]:	2.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
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 623: **dynein heavy chain 17, axonemal [Homo sapiens]**

Accession:	gi|256542310	**Score:**	14.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	509.0
Database Date:	2015-11-30	**pI:**	5.4
		Sequence Coverage [%]:	0.3
		No. of unique Peptides:	1

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

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2850	1	869.4224	-91.80	2	64.2	14.1	0	3728-3742	K.LIFLAQVTFQVLSMK.K	

Detailed Protein Report

Protein 624: zinc finger imprinted 2 [Homo sapiens]

Accession:	gi|33354273	**Score:**	14.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	61.1
Database Date:	2015-11-30	**pI:**	6.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.8
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|226423929	refseq_human(refseq_human_20140103.fasta)	zinc finger imprinted 2 [Homo sapiens]
gi|226423927	refseq_human(refseq_human_20140103.fasta)	zinc finger imprinted 2 [Homo sapiens]

10	20	30	40	50	60	70	80
MYQPEDDNNS	DVTSDDDMTR	NRRESSPPHS	VHSFSGDRDW	DRRGRSRDME	PRDRWSHTRN	PRSRMPPRDL	SLPVVAKTSF
90	100	110	120	130	140	150	160
EMDREDDRDS	RAYESRSQDA	ESYQNVVDLA	EDRKPHNTIQ	DNMENYRKLL	SLGFLAQDSV	PAEKRNTEML	DNLPSAGSQF
170	180	190	200	210	220	230	240
PDFKHLGTFL	VFEELVTFED	VLVDFSPEEL	SSLSAAQRNL	YREVMLENYR	NLVSLGHQFS	KPDIISRLEE	EESYAMETDS
250	260	270	280	290	300	310	320
RHTVICQGES	HDDPLEPHQG	NQEKLLTPIT	MNDPKTLTPE	RSYGSDEFER	SSNLSKQSKD	PLGKDPQEGT	APGICTSPQS
330	340	350	360	370	380	390	400
ASQENKHNRC	EFCKRTFSTQ	VALRRHERIH	TGKKPYECKQ	CAEAFYLMPH	LNRHQKTHSG	RKTSGCNEGR	KPSVQCANLC
410	420	430	440	450	460	470	480
ERVRIHSQED	YFECFQCGKA	FLQNVHLLQH	LKAHEAARVL	PPGLSHSKTY	LIRYQRKHDY	VGERACQCCD	CGRVFSRNSY
490	500	510	520	530			
LIQHYRTHTQ	ERPYQCQLCG	KCFGRPSYLT	QHYQLHSQEK	TVECDHC			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2843	1	616.8649	-144.67	3	64.2	14.1	0	487-501	R.THTQERPYQCQLCGK.C	Carbamidomethyl: 13

Detailed Protein Report

Protein 625: **zinc finger protein 688 isoform b [Homo sapiens]**

Accession:	gi|67010013	**Score:**	14.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	28.9
Database Date:	2015-11-30	**pI:**	11.6
		Sequence Coverage [%]:	6.5
		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 626: PREDICTED: zinc finger protein 197 isoform X2 [Homo sapiens]

Accession:	gi|578805510	**Score:**	14.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	96.1
Database Date:	2015-11-30	**pI:**	10.1
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	1.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MALMLLTAQP	QELVMFEEVS	VCFTSEEWAC	LGPIQRALYW	DVMLENYGNV	TSLEWETMTE	NEEVTSKPSS	SQRADSHKGT
90	100	110	120	130	140	150	160
SKRLQGSVPQ	VLDFEEECEW	QVLASQWGNE	TDERADTVKK	VSLCERDKKK	RTPPEKQGQK	WKELGDSLTF	GSAISESLIG
170	180	190	200	210	220	230	240
TEGKKFYKCD	MCCKHFNKIS	HLINHRRIHT	GEKPHKCKEC	GKGFIQRSSL	LMHLRNHSGE	KPYKCNECGK	AFSQSAYLLN
250	260	270	280	290	300	310	320
HQRIHTGEKP	YKCKECGKGF	YRHSGLIIHL	RRHSGERPYK	CNECGKVFSQ	NAYLIDHQRL	HKGEEPYKCN	KCQKAFILKK
330	340	350	360	370	380	390	400
SLILHQRIHS	GEKPYKCDEC	GKTFAQTTYL	IDHQRLHSAE	NPYKCKECGK	VFIRSKSLLL	HQRVHTEKKT	FGCKKCGKIF
410	420	430	440	450	460	470	480
SSKSNFIDHK	RMHSREKPYK	CTECGKAFTQ	SAYLFDHQRL	HNGEKPYECN	ECGKVFILKK	SLILHQRFHT	GENLYECKDC
490	500	510	520	530	540	550	560
GKVFGSNRNL	IDHERLHNGE	KPYECRECGK	TFIMSKSFMV	HQKLHTQEKA	YKCEDCGKAF	SYNSSLLVHR	RIHTGEKPFE
570	580	590	600	610	620	630	640
CSECGRAFSS	NRNLIEHKRI	HSGEKPYECD	ECGKCFILKK	SLIGHQRIHT	REKSYKCNDC	GKVFSYRSNL	IAHQRIHTGE
650	660	670	680	690	700	710	720
KPYACSECGK	GFTYNRNLIE	HQRIHSGEKT	YECHVCRKVL	TSSRNLMVHQ	RIHTGEKPYK	CNECGKDFSQ	NKNLVVHQRM
730	740	750	760	770	780	790	800
HTGEKPYECD	KCRKSFTSKR	NLVGHQRIHT	GEKPYGCNDC	SKVFRQRKNL	TVHQKIHTDE	KPCECDVSEK	EFSQTSNLHL
810	820	830					
QQKIHTIEEF	SWLQNTNESK	IEIQKI					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1461	1	671.4129	203.04	2	46.6	14.0	2	165-174	K.KFYKCDMCCK.H	Carbamidomethyl: 8; Oxidation: 7

Detailed Protein Report

Protein 627: **ribosomal protein S6 kinase alpha-1 isoform b [Homo sapiens]**

Accession:	gi|55743134	**Score:**	14.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	83.9
Database Date:	2015-11-30	**pI:**	9.5
		Sequence Coverage [%]:	2.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEQDPKPPRL	RLWALIPWLP	RKQRPRISQT	SLPVPGPGSG	PQRDSDEGVL	KEISITHHVK	AGSEKADPSH	FELLKVLGQG
90	100	110	120	130	140	150	160
SFGKVFLVRK	VTRPDSGHLY	AMKVLKKATL	KVRDRVRTKM	ERDILADVNH	PFVVKLHYAF	QTEGKLYLIL	DFLRGGDLFT
170	180	190	200	210	220	230	240
RLSKEVMFTE	EDVKFYLAEL	ALGLDHLHSL	GIIYRDLKPE	NILLDEEGHI	KLTDFGLSKE	AIDHEKKAYS	FCGTVEYMAP
250	260	270	280	290	300	310	320
EVVNRQGHSH	SADWWSYGVL	MFEMLTGSLP	FQGKDRKETM	TLILKAKLGM	PQFLSTEAQS	LLRALFKRNP	ANRLGSGPDG
330	340	350	360	370	380	390	400
AEEIKRHVFY	STIDWNKLYR	REIKPPFKPA	VAQPDDTFYF	DTEFTSRTPK	DSPGIPPSAG	AHQLFRGFSF	VATGLMEDDG
410	420	430	440	450	460	470	480
KPRAPQAPLH	SVVQQLHGKN	LVFSDGYVVK	ETIGVGSYSE	CKRCVHKATN	MEYAVKVIDK	SKRDPSEEIE	ILLRYGQHPN
490	500	510	520	530	540	550	560
IITLKDVYDD	GKHVYLVTEL	MRGGELLDKI	LRQKFFSERE	ASFVLHTIGK	TVEYLHSQGV	VHRDLKPSNI	LYVDESGNPE
570	580	590	600	610	620	630	640
CLRICDFGFA	KQLRAENGLL	MTPCYTANFV	APEVLKRQGY	DEGCDIWSLG	ILLYTMLAGY	TPFANGPSDT	PEEILTRIGS
650	660	670	680	690	700	710	720
GKFTLSGGNW	NTVSETAKDL	VSKMLHVDPH	QRLTAKQVLQ	HPWVTQKDKL	PQSQLSHQDL	QLVKGAMAAT	YSALNSSKPT
730	740	750					
PQLKPIESSI	LAQRRVRKLP	STTL					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1051	1	839.4103	-46.72	2	41.9	14.0	0	27-43	R.ISQTSLPVPGPGSGPQR.D	

Detailed Protein Report

Protein 628: cytokine receptor common subunit beta precursor [Homo sapiens]

Accession:	gi|4559408	**Score:**	14.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	97.3
Database Date:	2015-11-30	**pI:**	5.2
		Sequence Coverage [%]:	2.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MVLAQGLLSM	ALLALCWERS	LAGAEETIPL	QTLRCYNDYT	SHITCRWADT	QDAQRLVNVT	LIRRVNEDLL	EPVSCDLSDD
90	100	110	120	130	140	150	160
MPWSACPHPR	CVPRRCVIPC	QSFVVTDVDY	FSFQPDRPLG	TRLTVTLTQH	VQPPEPRDLQ	ISTDQDHFLL	TWSVALGSPQ
170	180	190	200	210	220	230	240
SHWLSPGDLE	FEVVYKRLQD	SWEDAAILLS	NTSQATLGPE	HLMPSSTYVA	RVRTRLAPGS	RLSGRPSKWS	PEVCWDSQPG
250	260	270	280	290	300	310	320
DEAQPQNLEC	FFDGAAVLSC	SWEVRKEVAS	SVSFGLFYKP	SPDAGEEECS	PVLREGLGSL	HTRHHCQIPV	PDPATHGQYI
330	340	350	360	370	380	390	400
VSVQPRRAEK	HIKSSVNIQM	APPSLNVTKD	GDSYSLRWET	MKMRYEHIDH	TFEIQYRKDT	ATWKDSKTET	LQNAHSMALP
410	420	430	440	450	460	470	480
ALEPSTRYWA	RVRVRTSRTG	YNGIWSEWSE	ARSWDTESVL	PMWVLALIVI	FLTIAVLLAL	RFCGIYGYRL	RRKWEEKIPN
490	500	510	520	530	540	550	560
PSKSHLFQNG	SAELWPPGSM	SAFTSGSPPH	QGPWGSRFPE	LEGVFPVGFG	DSEVSPLTIE	DPKHVCDPPS	GPDTTPAASD
570	580	590	600	610	620	630	640
LPTEQPPSPQ	PGPPAASHTP	EKQASSFDFN	GPYLGPPHSR	SLPDILGQPE	PPQEGGSQKS	PPPGSLEYLC	LPAGGQVQLV
650	660	670	680	690	700	710	720
PLAQAMGPGQ	AVEVERRPSQ	GAAGSPSLES	GGGPAPPALG	PRVGGQDQKD	SPVAIPMSSG	DTEDPGVASG	YVSSADLVFT
730	740	750	760	770	780	790	800
PNSGASSVSL	VPSLGLPSDQ	TPSLCPGLAS	GPPGAPGPVK	SGFEGYVELP	PIEGRSPRSP	RNNPVPPEAK	SPVLNPGERP
810	820	830	840	850	860	870	880
ADVSPTSPQP	EGLLVLQQVG	DYCFLPGLGP	GPLSLRSKPS	SPGPGPEIKN	LDQAFQVKKP	PGQAVPQVPV	IQLFKALKQQ
890	900						
DYLSLPPWEV	NKPGEVC						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2606	1	495.0590	111.94	4	60.9	14.0	0	601-619	R.SLPDILGQPEPPQEGGSQK.S	

Detailed Protein Report

Protein 629: **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 630: 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 631: **PREDICTED: golgin subfamily A member 6-like protein 2-like [Homo sapiens]**

Accession:	gi|578845630	**Score:**	14.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	23.1
Database Date:	2015-11-30	**pI:**	5.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	4.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MRGAGGEDAG	DRRRRCGGQE	EKMREQEEKM	REQEEKMQGQ	EEKMREQEEK	MRGQEEKMRE	QEEKMRGQEE	KMWGQEEKMW
90	100	110	120	130	140	150	160
GQEEKMWGQE	EMMREKEERI	RDQKEKMQER	LPEHEERCSE	PCLPPSKVLC	NMSHTGSVEP	AGGEAGEGSP	QDNPTAQEIM
170	180	190	200				
QLFCGMKNAQ	QCPGLGSTSC	IPFFYRGDKR	KMKIINI				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1953	1	590.7822	0.87	2	52.8	14.0	2	51-59	K.MRGQEEKMR.E	Oxidation: 8

Detailed Protein Report

Protein 632: 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 633: TGF-beta receptor type-1 isoform 1 precursor [Homo sapiens]

Accession:	gi|4759226	**Score:**	14.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	55.9
Database Date:	2015-11-30	**pI:**	8.7
		Sequence Coverage [%]:	1.6
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 0.70 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MEAAVAAPRP	RLLLLVLAAA	AAAAAALLPG	ATALQCFCHL	CTKDNFTCVT	DGLCFVSVTE	TTDKVIHNSM	CIAEIDLIPR
90	100	110	120	130	140	150	160
DRPFVCAPSS	KTGSVTTTYC	CNQDHCNKIE	LPTTVKSSPG	LGPVELAAVI	AGPVCFVCIS	LMLMVYICHN	RTVIHHRVPN
170	180	190	200	210	220	230	240
EEDPSLDRPF	ISEGTTLKDL	IYDMTTSGSG	SGLPLLVQRT	IARTIVLQES	IGKGRFGEVW	RGKWRGEEVA	VKIFSSREER
250	260	270	280	290	300	310	320
SWFREAEIYQ	TVMLRHENIL	GFIAADNKDN	GTWTQLWLVS	DYHEHGSLFD	YLNRYTVTVE	GMIKLALSTA	SGLAHLHMEI
330	340	350	360	370	380	390	400
VGTQGKPAIA	HRDLKSKNIL	VKKNGTCCIA	DLGLAVRHDS	ATDTIDIAPN	HRVGTKRYMA	PEVLDDSINM	KHFESFKRAD
410	420	430	440	450	460	470	480
IYAMGLVFWE	IARRCSIGGI	HEDYQLPYYD	LVPSDPSVEE	MRKVVCEQKL	RPNIPNRWQS	CEALRVMAKI	MRECWYANGA
490	500	510					
ARLTALRIKK	TLSQLSQQEG	IKM					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
684	1	450.6291	-320.69	2	37.0	14.0	0	109-116	K.IELPTTVK.S		WD:WU 0.70

Detailed Protein Report

Protein 634: PREDICTED: zinc finger protein 91 isoform X4 [Homo sapiens]

Accession:	gi|578833582	**Score:**	13.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	101.7
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
MPGTPGSLEM	GLLTFRDVAI	EFSPEEWQCL	DTAQQNLYRN	VMLENYRNLA	FLGIALSKPD	LITYLEQGKE	PWNMKQHEMV
90	100	110	120	130	140	150	160
DEPTGICPHF	PQDFWPEQSM	EDSFQKVLLR	KYEKCGHENL	QLRKGCKSVD	ECKVHKEGYN	KLNQCLTTAQ	SKVFQCGKYL
170	180	190	200	210	220	230	240
KVFYKFLNSN	RHTIRHTGKK	CFKCKKCVKS	FCIRLHKTQH	KCVYITEKSC	KCKECEKTFH	WSSTLTNHKE	IHTEDKPYKC
250	260	270	280	290	300	310	320
EECGKAFKQL	STLTTHKIIC	AKEKIYKCEE	CGKAFLWSST	LTRHKRIHTG	EKPYKCEECG	KAFSHSSTLA	KHKRIHTGEK
330	340	350	360	370	380	390	400
PYKCEECGKA	FSRSSTLAKH	KRIHTGEKPY	KCKECGKAFS	NSSTLANHKI	THTEEKPYKC	KECDKAFKRL	STLTKHKIIH
410	420	430	440	450	460	470	480
AGEKLYKCEE	CGKAFNRSSN	LTIHKFIHTG	EKPYKCEECG	KAFNWSSSLT	KHKRFHTREK	PFKCKECGKA	FIWSSTLTRH
490	500	510	520	530	540	550	560
KRIHTGEKPY	KCEECGKAFR	QSSTLTKHKI	IHTGEKPYKF	EECGKAFRQS	LTLNKHKIIH	SREKPYKCKE	CGKAFKQFST
570	580	590	600	610	620	630	640
LTTHKIIHAG	KKLYKCEECG	KAFNHSSSLS	THKIIHTGEK	SYKCEECGKA	FLWSSTLRRH	KRIHTGEKPY	KCEECGKAFS
650	660	670	680	690	700	710	720
QSSTLTTHKI	IHTGEKPYKC	EECGKAFRKS	STLTEHKIIH	TGEKPYKCEE	CGKAFSQSST	LTRHTRMHTG	EKPYKCEECG
730	740	750	760	770	780	790	800
KAFNRSSKLT	THKIIHTGEK	PYKCEECGKA	FISSSTLNGH	KRIHTREKPY	KCEECGKAFS	QSSTLTRHKR	LHTGEKPYKC
810	820	830	840	850	860	870	880
GECGKAFKES	SALTKHKIIH	TGEKPYKCEK	CGKAFNQSSI	LTNHKKIHTI	TPVIPLLWEA	EAGGSRGQEM	ETILANTVKP
890							
LLY							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2677	1	665.3406	42.21	2	61.8	13.9	2	263-273	K.EKIYKCEECGK.A	

Detailed Protein Report

Protein 635: 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 636: 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 637: **PREDICTED: zinc finger CCHC domain-containing protein 10 isoform X4 [Homo sapiens]**

Accession: gi|530380033
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 13.9
MW [kDa]: 13.8
pI: 11.3
Sequence Coverage [%]: 6.1
No. of unique Peptides: 1

```
        10         20         30         40         50         60         70         80
MATPMHRLIA RRQAFDTELQ PVKTFWILIQ PSIVISEANK QHVRCQKCLE FGHWTYECTG KRKYLHRPSR TAELKKALKE
        90        100        110        120
KENRLLLQQR SFFPPRVYQH WRNQCRKKGQ EKKV
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
422	1	464.6450	-245.69	2	34.3	13.9	0	64-70	K.YLHRPSR.T	

Detailed Protein Report

Protein 638: protein FAM222B isoform 1 [Homo sapiens]

Accession:	gi|568786296	**Score:**	13.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	59.8
Database Date:	2015-11-30	**pI:**	10.3
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.5
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578831131	refseq_human (refseq_human_20140103.fasta)	PREDICTED: protein FAM222B isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MRSSFPLASA	KKNLRVGTNL	EQRDSSTHQG	DTTQKMRTAH	YPTPAELDAY	AKKVANNPLT	IKIFPNSVKV	PQRKHVRRTV
90	100	110	120	130	140	150	160
NGLDTSAQRY	SPYPTQAATK	AGLLAIVKVP	AKSILKDFDG	TRARLLPEAI	MNPPVAPYAT	VAPSTLAHPQ	AQALARQQAL
170	180	190	200	210	220	230	240
QHAQTLAHAP	PQTLQHPQGI	PPPQALSHPQ	SLQQPQGLGH	PQPMAQTQGL	VHPQALAHQG	LQHPHNPLLH	GGRKMPDSDA
250	260	270	280	290	300	310	320
PPNVTVSTST	IPLSMAATLQ	HSQPPDLSSI	VHQINQFCQT	RAGISTTSVC	EGQIANPSPI	SRSLLINAST	RVSTHSVPTP
330	340	350	360	370	380	390	400
MPSCVVNPME	HTHAATAALP	AAGPVNLPTG	ISRVPTGYPS	DLKPVTWNQH	QLAHLQQMCS	EASGTPAPGL	TGKHAAGREL
410	420	430	440	450	460	470	480
AGPGFVGKAP	AYPQELCLAQ	SFHLKPPLEK	PTPSPPVNGM	AAPLAYPNGH	YFQPLWNNIL	PTPNSDSSGS	QDLAMPFHGG
490	500	510	520	530	540	550	560
QPTGAPLDCA	AAPGAHYRAG	TGGGPVASQN	SLMQTVDYLS	GDFQQACFRE	QSLAMLSKAH	RAPGNRAPDP	TESRSLHIQH
570							
PGYR							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
7	1	804.3526	-6.18	2	29.0	13.9	1	24-37	R.DSSTHQGDTTQKMR.T	Oxidation: 13

Protein 639: **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 640: protein phosphatase 1 regulatory subunit 26 [Homo sapiens]

Accession:	gi|45387958	**Score:**	13.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	127.3
Database Date:	2015-11-30	**pI:**	9.8
		Sequence Coverage [%]:	1.5
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578818032	refseq_human (refseq_human_20140103.fasta)	PREDICTED: protein phosphatase 1 regulatory subunit 26 isoform X5 [Homo sapiens]
gi|578818030	refseq_human (refseq_human_20140103.fasta)	PREDICTED: protein phosphatase 1 regulatory subunit 26 isoform X4 [Homo sapiens]
gi|578818028	refseq_human (refseq_human_20140103.fasta)	PREDICTED: protein phosphatase 1 regulatory subunit 26 isoform X3 [Homo sapiens]
gi|530426639	refseq_human (refseq_human_20140103.fasta)	PREDICTED: protein phosphatase 1 regulatory subunit 26 isoform X2 [Homo sapiens]
gi|530426637	refseq_human (refseq_human_20140103.fasta)	PREDICTED: protein phosphatase 1 regulatory subunit 26 isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MFLMNASPVV	ALQSKWEAFG	PPGSCRFPRC	FSEADEGVES	ASVSARVQML	ISTLQRDGAA	RGTSDERAAQ	RGHRAEGCHD
90	100	110	120	130	140	150	160
ARPAAKPTVH	KEPPALAVCG	LVADFDPMGE	EETTDFGPLV	LDSDSDDSVD	RDIEEAIQEY	LKAKSGAAQP	GAGGAQPGAA
170	180	190	200	210	220	230	240
QPSRAAGGGS	RCKPEPAHGS	APTALCPPKL	VPGSGGGPGS	QVGSSKDQGS	ASPVSVSSDD	SFEQSIRAEI	EQFLNEKRQH
250	260	270	280	290	300	310	320
ETQKCDGSVE	KKPDTNENSA	KSLLKSHQEP	PTKVVHRQGL	LGVQKEFAFR	KPPRLAKMNV	QPRSLRSKVT	TTQENEGSTK
330	340	350	360	370	380	390	400
PATPCRPSEA	AQNKGGIKRS	ASAARRGKRV	MSAAQASEAS	DSSSDDGIEE	AIQLYQLQKT	RKEADGDLPQ	RVQLREERAP
410	420	430	440	450	460	470	480
DPPAHSTSSA	TKSALPETHR	KTPSKKKLVA	TKTMDPGPGG	LDTDHAPKLL	KETKAPPPAS	PASRSEFVER	SSCRADTSAE
490	500	510	520	530	540	550	560
LMCAEAILDI	SKTILPAPVE	GSDGSLSASP	LFYSPNVPSR	SDGDSSSVDS	DDSIEQEIRT	FLALKAQSGS	LLARGESCPQ
570	580	590	600	610	620	630	640
AAQGPLLPPG	LNSQTGGHKT	PLSKTPDPLL	GCKRKRRGGG	HVRPSTPKKM	QEVVKDGSQD	ADHSQGRAEP	GHERRDLPIQ
650	660	670	680	690	700	710	720
GKASEALGGE	GTARGPGDTR	MSQGQGKTDE	ARRLDEKESS	EDKSSSLDSD	EDLDTAIKDL	LRSKRKLKKR	CREPRAACRK
730	740	750	760	770	780	790	800
KVRFSTAQTH	FLEQLGGLRR	DWKDRGPPVL	KSCLSKSKRD	SGEGPGKKPP	SVFGSTAERM	RQEGAASQDA	ALAFRVRRPA
810	820	830	840	850	860	870	880
SASASEGNPF	PRESQGPAPS	PGSLSDDSSS	VDSNDSIELE	IRKFLAEKAK	ESVSSSEVQA	EGPTALGTGG	PARPEVLCRK
890	900	910	920	930	940	950	960
EPAPPPGVCT	RSQRARGVPH	LAEGLRGTES	AGAQGTAGLF	SQGGKGLPAA	PARGDPVPPR	STSGGVSAKG	LSVSRRNVYV
970	980	990	1000	1010	1020	1030	1040
HKDQSPRGAE	PAAKSAFGQL	PSCATAGTEA	GGARGTFHMG	CGSPSFLTPS	PGAERDAGAQ	ADRTPPWSDF	AHQSRLPSPW
1050	1060	1070	1080	1090	1100	1110	1120
VLRSEGRDAV	WRGGVGSERD	KGSEGPARGL	PSLPLAGFSP	LLSTQLFHFG	KGVSWGGRQA	GLFSPHLGLP	LQGPSFSAFR
1130	1140	1150	1160	1170	1180	1190	1200
EAQAGPSPVF	GSPHLLAKKD	GGPWPTRKAQ	AGLSLHDRRS	SGSEESILDL	RYRRRVNRDD	QEQDALGSDA	SDFSDTSTED
1210							
SGGSSVVKV							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1424	1	627.5982	-62.69	3	46.2	13.9	0	475-492	R.ADTSAELMCAEAILDISK.T	

Detailed Protein Report

Protein 641: serine/threonine-protein kinase Nek4 isoform 2 [Homo sapiens]

Accession:	gi|302058308	**Score:**	13.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	84.3
Database Date:	2015-11-30	**pI:**	8.8
		Sequence Coverage [%]:	2.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPLAAYCYLR	VVGKGSYGEV	TLVKHRRDGK	QYLHEKHILH	RDLKTQNVFL	TRTNIIKVGD	LGIARVLENH	CDMASTLIGT
90	100	110	120	130	140	150	160
PYYMSPELFS	NKPYNYKSDV	WALGCCVYEM	ATLKHAFNAK	DMNSLVYRII	EGKLPPMPRD	YSPELAELIR	TMLSKRPEER
170	180	190	200	210	220	230	240
PSVRSILRQP	YIKRQISFFL	EATKIKTSKN	NIKNGDSQSK	PFATVVSGEA	ESNHEVIHPQ	PLSSEGSQTY	IMGEGKCLSQ
250	260	270	280	290	300	310	320
EKPRASGLLK	SPASLKAHTC	KQDLSNTTEL	ATISSVNIDI	LPAKGRDSVS	DGFVQENQPR	YLDASNELGG	ICSISQVEEE
330	340	350	360	370	380	390	400
MLQDNTKSSA	QPENLIPMWS	SDIVTGEKNE	PVKPLQPLIK	EQKPKDQSLA	LSPKLECSGT	ILAHSNLRLL	GSSDSPASAS
410	420	430	440	450	460	470	480
RVAGITGVCH	HAQDQVAGEC	IIEKQGRIHP	DLQPHNSGSE	PSLSRQRRQK	RREQTEHRGE	KRQVRRDLFA	FQESPPRFLP
490	500	510	520	530	540	550	560
SHPIVGKVDV	TSTQKEAENQ	RRVVTGSVSS	SRSSEMSSSK	DRPLSARERR	RLKQSQEEMS	SSGPSVRKAS	LSVAGPGKPQ
570	580	590	600	610	620	630	640
EEDQPLPARR	LSSDCSVTQE	RKQIHCLSED	ELSSSTSSTD	KSDGDYGEGK	GQTNEINALV	QLMTQTLKLD	SKESCEDVPV
650	660	670	680	690	700	710	720
ANPVSEFKLH	RKYRDTLILH	GKVAEEAEEI	HFKELPSAIM	PGSEKIRRLV	EVLRTDVIRG	LGVQLLEQVY	DLLEEEDEFD
730	740	750	760				
REVRLREHMG	EKYTTYSVKA	RQLKFFEENM	NF				

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	549-569	K.ASLSVAGPGKPQEEDQPLPAR.R	

Detailed Protein Report

Protein 642: PREDICTED: apoptosis-resistant E3 ubiquitin protein ligase 1 isoform X2 [Homo sapiens]

Accession:	gi|530404992	**Score:**	13.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	75.6
Database Date:	2015-11-30	**pI:**	6.3
		Sequence Coverage [%]:	1.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MVVPSKTKIV	CHFSTLVLTC	GQPHTLQIVP	RDEYDNPTNN	SMSLRDEHNY	TLSIHELGPQ	EEESTGVSFE	KSVTSNRQTF
90	100	110	120	130	140	150	160
QVFLRLTLHS	RGCFHACISY	QNQPINNGEF	DIIVLSEDEK	NIVERNVSTS	GVSIYFEAYL	YNATNCSSTP	WHLPPMHMTS
170	180	190	200	210	220	230	240
SQRRPSTAVD	EEDEDSPSEC	HTPEKVKKPK	KVYCYVSPKQ	FSVKEFYLKI	IPWRLYTFRV	CPGTKFSYLG	PDPVHKLLTL
250	260	270	280	290	300	310	320
VVDDGIQPPV	ELSCKERNIL	AATFIRSLHK	NIGGSETFQD	KVNFFQRELR	QVHMKRPHSK	VTLKVSRHAL	LESSLKATRN
330	340	350	360	370	380	390	400
FSISDWSKNF	EVVFQDEEAL	DWGGPRREWF	ELICKALFDT	TNQLFTRFSD	NNQALVHPNP	NRPAHLRLKM	YEFAGRLVGK
410	420	430	440	450	460	470	480
CLYESSLGGA	YKQLVRARFT	RSFLAQIIGL	RMHYKYFETD	DPEFYKSKVC	FILNNDMSEM	ELVFAEEKYN	KSGQLDKVVE
490	500	510	520	530	540	550	560
LMTGGAQTPV	TNANKIFYLN	LLAQYRLASQ	VKEEVEHFLK	GLNELVPENL	LAIFDENELE	LLMCGTGDIS	VSDFKAHAVV
570	580	590	600	610	620	630	640
VGGSWHFREK	VMRWFWTVVS	SLTQEELARL	LQFTTGSSQL	PPGGFAALCP	SFQIIAAPTH	STLPTAHTCF	NQLCLPTYDS
650	660	670					
YEEVHRMLQL	AISEGCEGFG	ML					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2591	1	557.8482	105.51	2	60.7	13.8	1	388-396	R.LKMYEFAGR.L	

Detailed Protein Report

Protein 643: 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	1	701.2818	-9.24	3	54.8	13.8	0	339-356	R.EPEEINADDEIEDTCDHK.E	

Detailed Protein Report

Protein 644: 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 645: phosphatidylinositol 3-kinase regulatory subunit beta [Homo sapiens]

Accession:	gi|4826908	**Score:**	13.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	81.6
Database Date:	2015-11-30	**pI:**	6.1
Modification(s):	Oxidation	**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 646: metabotropic glutamate receptor 5 isoform b precursor [Homo sapiens]

Accession:	gi|4504143	**Score:**	13.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	128.8
Database Date:	2015-11-30	**pI:**	8.6
		Sequence Coverage [%]:	1.5
		No. of unique Peptides:	1

Quantitation

WD:WU	**Median:**	0.89	**CV:**	0.00 %	**No. of Peptides:**	1

Alias proteins:

Accession	Name	Description
gi|578822167	refseq_human (refseq_human_20140103.fasta)	PREDICTED: metabotropic glutamate receptor 5 isoform X3 [Homo sapiens]

10	20	30	40	50	60	70	80
MVLLLILSVL	LLKEDVRGSA	QSSERRVVAH	MPGDIIIGAL	FSVHHQPTVD	KVHERKCGAV	REQYGIQRVE	AMLHTLERIN
90	100	110	120	130	140	150	160
SDPTLLPNIT	LGCEIRDSCW	HSAVALEQSI	EFIRDSLISS	EEEEGLVRCV	DGSSSSFRSK	KPIVGVIGPG	SSSVAIQVQN
170	180	190	200	210	220	230	240
LLQLFNIPQI	AYSATSMDLS	DKTLFKYFMR	VVPSDAQQAR	AMVDIVKRYN	WTYVSAVHTE	GNYGESGMEA	FKDMSAKEGI
250	260	270	280	290	300	310	320
CIAHSYKIYS	NAGEQSFDKL	LKKLTSHLPK	ARVVACFCEG	MTVRGLLMAM	RRLGLAGEFL	LLGSDGWADR	YDVTDGYQRE
330	340	350	360	370	380	390	400
AVGGITIKLQ	SPDVKWFDDY	YLKLRPETNH	RNPWFQEFWQ	HRFQCRLEGF	PQENSKYNKT	CNSSLTLKTH	HVQDSKMGFV
410	420	430	440	450	460	470	480
INAIYSMAYG	LHNMQMSLCP	GYAGLCDAMK	PIDGRKLLES	LMKTNFTGVS	GDTILFDENG	DSPGRYEIMN	FKEMGKDYFD
490	500	510	520	530	540	550	560
YINVGSWDNG	ELKMDDDEVW	SKKSNIIRSV	CSEPCEKGQI	KVIRKGEVSC	CWTCTPCKEN	EYVFDEYTCK	ACQLGSWPTD
570	580	590	600	610	620	630	640
DLTGCDLIPV	QYLRWGDPEP	IAAVVFACLG	LLATLFVTVV	FIIYRDTPVV	KSSSRELCYI	ILAGICLGYL	CTFCLIAKPK
650	660	670	680	690	700	710	720
QIYCYLQRIG	IGLSPAMSYS	ALVTKTNRIA	RILAGSKKKI	CTKKPRFMSA	CAQLVIAFIL	ICIQLGIIVA	LFIMEPPDIM
730	740	750	760	770	780	790	800
HDYPSIREVY	LICNTTNLGV	VTPLGYNGLL	ILSCTFYAFK	TRNVPANFNE	AKYIAFTMYT	TCIIWLAFVP	IYFGSNYKII
810	820	830	840	850	860	870	880
TMCFSVSLSA	TVALGCMFVP	KVYIILAKPE	RNVRSAFTTS	TVVRMHVGDG	KSSSAASRSS	SLVNLWKRRG	SSGETLSSNG
890	900	910	920	930	940	950	960
KSVTWAQNEK	SSRGQHLWQR	LSIHINKKEN	PNQTAVIKPF	PKSTESRGLG	AGAGAGGSAG	GVGATGGAGC	AGAGPGGPES
970	980	990	1000	1010	1020	1030	1040
PDAGPKALYD	VAEAEEHFPA	PARPRSPSPI	STLSHRAGSA	SRTDDDVPSL	HSEPVARSSS	SQGSLMEQIS	SVVTRFTANI
1050	1060	1070	1080	1090	1100	1110	1120
SELNSMMLST	AAPSPGVGAP	LCSSYLIPKE	IQLPTTMTTF	AEIQPLPAIE	VTGGAQPAAG	AQAAGDAARE	SPAAGPEAAA
1130	1140	1150	1160	1170	1180	1190	
AKPDLEELVA	LTPPSPFRDS	VDSGSTTPNS	PVSESALCIP	SSPKYDTLII	RDYTQSSSSL		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2722	1	941.9859	24.92	2	62.4	13.8	0	1018-1035	R.SSSSQGSLMEQISSVVTR.F		WD:WU 0.89

Detailed Protein Report

Protein 647: 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

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Detailed Protein Report

Protein 648: coiled-coil domain-containing protein 71L [Homo sapiens]

Accession:	gi|57242766	**Score:**	13.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	26.2
Database Date:	2015-11-30	**pI:**	12.4
Modification(s):	Oxidation	**Sequence Coverage [%]:**	6.0
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 1.10 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MRRSMKRRRR	RRPVAPATAA	RGGDFRAEDG	AGLEAREEKV	VYSRSQLSLA	DSTKALGDAF	KLFMPRSTEF	MSSDAELWSF
90	100	110	120	130	140	150	160
LCSLKHQFSP	HILRSKDVYG	YSSCRALVPD	PPGPPTARGQ	ARRPVPRAAA	RRRRRGARAA	AARRRKPRPP	PPPPPPPEES
170	180	190	200	210	220	230	240
CPAKPVAPGP	CFGGRTLEEI	WRAATPTLTT	FPTIRVGSDV	WGERSLAAAR	RRARQVLRVN	LEPMVRLRRF	PVPRA

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
811	1	848.9801	-6.53	2	39.0	13.8	2	213-226	R.ARQVLRVNLEPMVR.L	Oxidation: 12	WD:WU 1.10

Detailed Protein Report

Protein 649: SH3 domain-containing protein 21 isoform 1 [Homo sapiens]

Accession:	gi|242117953	**Score:**	13.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	83.9
Database Date:	2015-11-30	**pI:**	5.9
		Sequence Coverage [%]:	1.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEVLVLAGYR	AQKEDELSLA	PGDVVRQVRW	VPARGWLRGE	FGGRYGLFPE	RLVQEIPETL	RGSGEARRPR	CARRRGHPAK
90	100	110	120	130	140	150	160
HPRPQRWCKV	NFSYSPEQAD	ELKLQAGEIV	EMIKEIEDGW	WLGKKNGQLG	AFPSNFVELL	DSGPPSLGNP	DMPSVSPGPQ
170	180	190	200	210	220	230	240
RPPKLSSLAY	DSPPDYLQTV	SHPEVYRVLF	DYQPEAPDEL	ALRRGDVVKV	LSKTTEDKGW	WEGECQGRRG	VFPDNFVLPP
250	260	270	280	290	300	310	320
PPIKKLVPRK	VVSRESAPIK	EPKKLMPKTS	LPTVKKLATA	TTGPSKAKTS	RTPSRDSQKL	TSRDSGPNGG	FQSGGSYHPG
330	340	350	360	370	380	390	400
RKRSKTQTPQ	QRSVSSQEEE	HSSPVKAPSV	KRTPMPDKTA	TPERPPAPEN	APSSKKIPAP	DKVPSPEKTL	TLGDKASIPG
410	420	430	440	450	460	470	480
NSTSGKIPAP	DKVPTPEKMV	TPEDKASIPE	NSIIPEETLT	VDKPSTPERV	FSVEESPALE	APPMDKVPNP	KMAPLGDEAP
490	500	510	520	530	540	550	560
TLEKVLTPEL	SEEEVSTRDD	IQFHHFSSEE	ALQKVKYFVA	KEDPSSQEEA	HTPEAPPPQP	PSSERCLGEM	KCTLVRGDSS
570	580	590	600	610	620	630	640
PRQAELKSGP	ASRPALEKPH	PHEEATTLPE	EAPSNDERTP	EEEAPPNEQR	PLREEVLPKE	GVASKEEVTL	KEELPPKEEV
650	660	670	680	690	700	710	720
APKEEVPPIE	RAFAQKTRPI	KPPPDSQETL	ALPSLVPQNY	TENKNEGVDV	TSLRGEVESL	RRALELMEVQ	LERKLTDIWE
730	740	750	760				
ELKSEKEQRR	RLEVQVMQGT	QKSQTPRVIH	TQTQTY				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
328	1	658.3980	85.56	2	32.8	13.8	2	62-73	R.GSGEARRPRCAR.R	

Detailed Protein Report

Protein 650: rho GTPase-activating protein 12 isoform 5 [Homo sapiens]

Accession:	gi|398303814	**Score:**	13.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	87.7
Database Date:	2015-11-30	**pI:**	9.3
		Sequence Coverage [%]:	2.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MKMADRSGKI	IPGQVYIEVE	YDYEYEAKDR	KIVIKQGERY	ILVKKTNDDW	WQVKPDENSK	AFYVPAQYVK	EVTRKALMPP
90	100	110	120	130	140	150	160
VKQVAGLPNN	STKIMQSLHL	QRSTENVNKL	PELSSFGKPS	SSVQGTGLIR	DANQNFGPSY	NQGQTVNLSL	DLTHNNGKFN
170	180	190	200	210	220	230	240
NDSHSPKVSS	QNRTRSFGHF	PGPEFLDVEK	TSFSQEQSCD	SAGEGSERIH	QDSESGDELS	SSSTEQIRAT	TPPNQGRPDS
250	260	270	280	290	300	310	320
PVYANLQELK	ISQSALPPLP	GSPAIQINGE	WETHKDSSGR	CYYYNRGTQE	RTWKPPRWTR	DASISKGDFQ	NPGDQEWLKH
330	340	350	360	370	380	390	400
VDDQGRQYYY	SADGSRSEWE	LPKYNASSQQ	QREIIKSRSL	DRRLQEPIVL	TKWRHSTIVL	DTNDKDQEKY	GLLNVTKIAE
410	420	430	440	450	460	470	480
NGKKVRKNWL	SSWAVLQGSS	LLFTKTQGSS	TSWFGSNQSK	PEFTVDLKGA	TIEMASKDKS	SKKNVFELKT	RQGTELLIQS
490	500	510	520	530	540	550	560
DNDTVINDWF	KVLSSTINNQ	AVETDEGIEE	EIPDSPGIEK	HDKEKEQKDP	KKLRSFKVSS	IDSSEQKKTK	KNLKKFLTRR
570	580	590	600	610	620	630	640
PTLQAVREKG	YIKDQVFGSN	LANLCQRENG	TVPKFVKLCI	EHVEEHGLDI	DGIYRVSGNL	AVIQKLRFAV	NHDEKLDLND
650	660	670	680	690	700	710	720
SKWEDIHVIT	GALKMFFREL	PEPLFTFNHF	NDFVNAIKQE	PRQRVAAVKD	LIRQLPKPNQ	DTMQILFRHL	RRVIENGEKN
730	740	750	760	770			
RMTYQSIAIV	FGPTLLKPEK	ETGNIAVHTV	YQNQIVELIL	LELSSIFGR			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1695	1	865.1582	65.82	3	49.5	13.8	1	470-491	K.TRQGTELLIQSDNDTVINDWFK.V	

Detailed Protein Report

Protein 651: **PREDICTED: ubiquitin carboxyl-terminal hydrolase isozyme L5 isoform X14 [Homo sapiens]**

Accession:	gi|578801073	**Score:**	13.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	23.7
Database Date:	2015-11-30	**pI:**	6.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	8.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MKGLALSNSD	VIRQVHNSFA	RQQMFEFDTK	TSAKEEDAFH	FVSYVPVNGR	LYELDGLREG	PIDLGACNQD	DWISAVRPVI
90	100	110	120	130	140	150	160
EKRIQKYSEG	EIRFNLMAIV	SDRKMIYEQK	IAELQRQLAE	EPMDTDQGNS	MLSAIQSEVA	KNQMLIEEEV	QKLKRYKIEN
170	180	190	200	210			
IRRKHNYLPF	IMELLKTLAE	HQQLIPLVEK	AKEKQNAKKA	QETK			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2419	1	1051.5349	-7.05	2	58.6	13.7	2	94-110	R.FNLMAIVSDRKMIYEQK.I	Oxidation: 4

Detailed Protein Report

Protein 652: **amyloid beta A4 precursor protein-binding family B member 1 isoform b [Homo sapiens]**

Accession:	gi|22035554	**Score:**	13.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	76.9
Database Date:	2015-11-30	**pI:**	4.8
		Sequence Coverage [%]:	3.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSVPSSLSQS	AINANSHGGP	ALSLPLPLHA	AHNQLLNAKL	QATAVGPKDL	RSAMGEGGGP	EPGPANAKWL	KEGQNQLRRA
90	100	110	120	130	140	150	160
ATAHRDQNRN	VTLTLAEEAS	QEPEMAPLGP	KGLIHLYSEL	ELSAHNAANR	GLRGPGLIIS	TQEQGPDEGE	EKAAGEAEEE
170	180	190	200	210	220	230	240
EEDDDDEEEE	EDLSSPPGLP	EPLESVEAPP	RPQALTDGPR	EHSKSASLLF	GMRNSAASDE	DSSWATLSQG	SPSYGSPEDT
250	260	270	280	290	300	310	320
DSFWNPNAFE	TDSDLPAGWM	RVQDTSGTYY	WHIPTGTTQW	EPPGRASPSQ	GSSPQEESQL	TWTGFAHGEG	FEDGEFWKDE
330	340	350	360	370	380	390	400
PSDEAPMELG	LKEPEEGTLT	FPAQSLSPEP	LPQEEEKLPP	RNTNPGIKCF	AVRSLGWVEM	TEEELAPGRS	SVAVNNCIRQ
410	420	430	440	450	460	470	480
LSYHKNNLHD	PMSGGWGEGK	DLLLQLEDET	LKLVEPQSQA	LLHAQPIISI	RVWGVGRDSG	RDFAYVARDK	LTQMLKCHVF
490	500	510	520	530	540	550	560
RCEAPAKNIA	TSLHEICSKI	MAERRNARCL	VNGLSLDHSK	LVDVPFQVEF	PAPKNELVQK	FQVYYLGNVP	VAKPVGVDVI
570	580	590	600	610	620	630	640
NGALESVLSS	SSREQWTPSH	VSVAPATLTI	LHQQTEAVLG	ECRVRFLSFL	AVGRDVHTFA	FIMAAGPASF	CCHMFWCEPN
650	660	670	680	690	700	710	
AASLSEAVQA	ACMLRYQKCL	DARSQASTSC	LPAPPAESVA	RRVGWTVRRG	VQSLWGSLKP	KRLGAHTP	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2594	1	946.7123	-95.55	3	60.7	13.7	1	86-111	R.DQNRNVTLTLAEEASQEPEMAPLGPK.G	

Detailed Protein Report

Protein 653: **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	1	695.9396	-46.71	2	46.3	13.7	2	540-551	R.LARILVRLPALR.L	

Detailed Protein Report

Protein 654: 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 655: PREDICTED: STE20-related kinase adapter protein alpha isoform X6 [Homo sapiens]

Accession:	gi|530413123	**Score:**	13.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	33.1
Database Date:	2015-11-30	**pI:**	6.4
		Sequence Coverage [%]:	5.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSFLVSKPER	IRRWVSEKFI	VEGLRDLELF	GEQPPGDTRR	KTNDASSESI	ASFSKQEVMS	SFLPEGGCYE	LLTVIGKGFE
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
DLMTVNLARY	KPTGEYVTVR	RINLEACSNE	MVTFLQGELH	VSKLFNHPNI	VPYRATFIAD	NELWVVTSFM	AYGSAKDLIC
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
THFMDGMNEL	AIAYILQGVL	KALDYIHHMG	YVHRSVKASH	ILISVDGKVY	LSGLRSNLSM	ISHGQRQRVV	HDFPKYSVKV
250	**260**	**270**	**280**	**290**	**300**		
LPWLSPEVLQ	QNLQGYDAKS	DIYSVGITAC	ELANGHVPFK	DMPATQGEDS	TVKGI		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
58	1	516.8847	-52.61	3	29.7	13.7	1	281-295	K.DMPATQGEDSTVKGI.-	

Detailed Protein Report

Protein 656: 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 657: FERM domain-containing protein 6 isoform 1 [Homo sapiens]

Accession:	gi|22748721	**Score:**	13.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	70.9
Database Date:	2015-11-30	**pI:**	7.4
		Sequence Coverage [%]:	2.3
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 3.24 **CV:** 0.00 % **No. of 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	Ratios	
255	1	795.3881	-62.20	2	32.4	13.7	1	233-246	K.REIEASLTLGLTMR.G		WD:WU	3.24

Detailed Protein Report

Protein 658: schwannomin-interacting protein 1 isoform 4 [Homo sapiens]

Accession:	gi|308193348	**Score:**	13.7
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

WD:WU **Median:** 1.13 **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
2028	2	909.8408	-159.06	2	53.7	13.7	1	121-137	K.LQAEAKMALAMAKPMAK.M	Oxidation: 15	WD:WU 1.13

Detailed Protein Report

Protein 659: **electroneutral sodium bicarbonate exchanger 1 isoform c [Homo sapiens]**

Accession:	gi|385719213	**Score:**	13.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	117.1
Database Date:	2015-11-30	**pI:**	6.5
Modification(s):	Oxidation	**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 660: PREDICTED: putative uncharacterized protein LOC400499 [Homo sapiens]

Accession:	gi|578846033	**Score:**	13.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	74.9
Database Date:	2015-11-30	**pI:**	10.1
		Sequence Coverage [%]:	2.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGWSDLQPAM	GGEAERFQAQ	LEVKLVTGGS	PVVFTGNLTR	QVGSKLAFSA	SLSHLLSDQA	NVTALLERKE	ENGRRVAALG
90	100	110	120	130	140	150	160
AELFVPGLVG	LRALGLLQQR	GQLWTNSLRI	QYSLLGQAKQ	AAHECSTSQK	LRADSGSDGA	YRLELRHELH	CTQILAFSHK
170	180	190	200	210	220	230	240
VQLWHEEDSR	HLHSQLEVSY	GKHWDKNSNK	RHLRVSQTFK	NDSGPALSNH	FMEFVLQVPE	RQVDCRVQLY	HLSLRLPYVE
250	260	270	280	290	300	310	320
SSSHLKVQYN	GRPLFVAGGQ	WKDTSRATLW	KWEGALNLDS	PWLMVSAAHR	LYWPHRAVFQ	AVLELTLGKA	WTLKDLVVSV
330	340	350	360	370	380	390	400
GCRSQGPNRE	GKIQVYTAAT	TYLRVSTVTV	LAQSLFHSWS	ELESAWNTAV	QGEIHAENSR	DRKILNCWLK	GPQQELNLTA
410	420	430	440	450	460	470	480
AYRHLEWPRK	TQVSLTAVWI	GAQGQPRGLQ	LEGELEELRQ	DRTLYRKRGA	LLLRHPLHLP	IPQSLLLQET	FTADRRHQRY
490	500	510	520	530	540	550	560
SLETRVVLNG	REETLQTMVL	GCQAGHPYVC	AGLMHPYDGK	VIPRNTEGCL	VTWNQHTAKN	REVEATLKVH	RKVVLHLKGL
570	580	590	600	610	620	630	640
HHDRSQHGEI	RHSLALDLAH	SYQLSFPQAL	SLDGGIIFRQ	SPQGTFNFGM	DARAAVNHNV	TSQASVQLNG	SDSDFAFFFQ
650	660	670					
LRHPHGPTFP	PNFQVWTLLP	WR					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
170	1	793.8952	-14.93	2	31.4	13.6	1	315-329	K.DLVVSVGCRSQGPNR.E	

Detailed Protein Report

Protein 661: **integral membrane protein 2B [Homo sapiens]**

Accession:	gi|11527402	**Score:**	13.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	30.3
Database Date:	2015-11-30	**pI:**	4.9
		Sequence Coverage [%]:	4.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MVKVTFNSAL	AQKEAKKDEP	KSGEEALIIP	PDAVAVDCKD	PDDVVPVGQR	RAWCWCMCFG	LAFMLAGVIL	GGAYLYKYFA
90	100	110	120	130	140	150	160
LQPDDVYYCG	IKYIKDDVIL	NEPSADAPAA	LYQTIEENIK	IFEEEEVEFI	SVPVPEFADS	DPANIVHDFN	KKLTAYLDLN
170	180	190	200	210	220	230	240
LDKCYVIPLN	TSIVMPPRNL	LELLINIKAG	TYLPQSYLIH	EHMVITDRIE	NIDHLGFFIY	RLCHDKETYK	LQRRETIKGI
250	260	270					
QKREASNCFA	IRHFENKFAV	ETLICS					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
591	1	676.8296	-29.37	2	36.2	13.6	1	40-51	K.DPDDVVPVGQRR.A	

Detailed Protein Report

Protein 662: PREDICTED: helicase POLQ-like isoform X8 [Homo sapiens]

Accession:	gi|578808747	**Score:**	13.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	82.5
Database Date:	2015-11-30	**pI:**	9.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLQELLCCRK	DVLMILPYVA	IVQEKISGLS	SFGIELGFFV	EEYAGSKGRF	PPTKRREKKS	LYIATIEKGH	SLVNSLIETG
90	100	110	120	130	140	150	160
RIDSLGLVVV	DELHMIGEGS	RGATLEMTLA	KILYTSKTTQ	IIGMSATLNN	VEDLQKFLQA	EYYTSQFRPV	ELKEYLKIND
170	180	190	200	210	220	230	240
TIYEVDSKAE	NGMTFSRLLN	YKYSDTLKKM	DPDHLVALVT	EVIPNYSCLV	FCPSKKNCEN	VAEMICKFLS	KEYLKHKEKE
250	260	270	280	290	300	310	320
KCEVIKNLKN	IGNGNLCPVL	KRTIPFGVAY	HHSGLTSDER	KLLEEAYSTG	VLCLFTCTST	LAAGVNLPAR	RVILRAPYVA
330	340	350	360	370	380	390	400
KEFLKRNQYK	QMIGRAGRAG	IDTIGESILI	LQEKDKQQVL	ELITKPLENC	YSHLVQEFTK	GIQTLFLSLI	GLKIATNLDD
410	420	430	440	450	460	470	480
IYHFMNGTFF	GVQQKVLLKE	KSLWEITVES	LRYLTEKGLL	QKDTIYKSEE	EVQYNFHITK	LGRASFKGTI	DLAYCDILYR
490	500	510	520	530	540	550	560
DLKKGLEGLV	LESLLHLIYL	TTPYDLVSQC	NPDWMIYFRQ	FSQLSPAEQN	VAAILGVSES	FIGKKASGQA	IGKKVDKNVV
570	580	590	600	610	620	630	640
NRLYLSFVLY	TLLKETNIWT	VSEKFNMPRG	YIQNLLTGTA	SFSSCVLHFC	EELEEFWVYR	ALLVELTKKL	TYCVKAELIP
650	660	670	680	690	700	710	720
LMEVTGVLEG	RAKQLYSAGY	KSLMHLANAN	PEVLVRTIDH	LSRRQAKQIV	SSAKMLLHEK	AEALQEEVEE	LLRLPSDFPG
730							
AVASSTDKA							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1448	1	626.6972	-186.66	2	46.5	13.6	1	1-10	-.MLQELLCCRK.D	Oxidation: 1

Detailed Protein Report

Protein 663: poly [ADP-ribose] polymerase 10 [Homo sapiens]

Accession:	gi|157738665	**Score:**	13.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	109.9
Database Date:	2015-11-30	**pI:**	4.8
		Sequence Coverage [%]:	1.9
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 0.92 **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		WD:WU 0.92

Detailed Protein Report

Protein 664: structural maintenance of chromosomes protein 1B [Homo sapiens]

Accession:	gi|71565160	**Score:**	13.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	143.7
Database Date:	2015-11-30	**pI:**	7.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.1
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 0.95 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MAHLELLLVE	NFKSWRGRQV	IGPFRRFTCI	IGPNGSGKSN	VMDALSFVMG	EKIANLRVKN	IQELIHGAHI	GKPISSSASV
90	100	110	120	130	140	150	160
KIIYVEESGE	EKTFARIIRG	GCSEFRFNDN	LVSRSVYIAE	LEKIGIIVKA	QNCLVFQGTV	ESISVKKPKE	RTQFFEEIST
170	180	190	200	210	220	230	240
SGELIGEYEE	KKRKLQKAEE	DAQFNFNKKK	NIAAERRQAK	LEKEEAERYQ	SLLEELKMNK	IQLQLFQLYH	NEKKIHLLNT
250	260	270	280	290	300	310	320
KLEHVNRDLS	VKRESLSHHE	NIVKARKKEH	GMLTRQLQQT	EKELKSVETL	LNQKRPQYIK	AKENTSHHLK	KLDVAKKSIK
330	340	350	360	370	380	390	400
DSEKQCSKQE	DDIKALETEL	ADLDAAWRSF	EKQIEEEILH	KKRDIELEAS	QLDRYKELKE	QVRKKVATMT	QQLEKLQWEQ
410	420	430	440	450	460	470	480
KTDEERLAFE	KRRHGEVQGN	LKQIKEQIED	HKKRIEKLEE	YTKTCMDCLK	EKKQQEETLV	DEIEKTKSRM	SEFNEELNLI
490	500	510	520	530	540	550	560
RSELQNAGID	THEGKRQQKR	AEVLEHLKRL	YPDSVFGRLF	DLCHPIHKKY	QLAVTKVFGR	FITAIVVASE	KVAKDCIRFL
570	580	590	600	610	620	630	640
KEERAEPETF	LALDYLDIKP	INERLRELKG	CKMVIDVIKT	QFPQLKKVIQ	FVCGNGLVCE	TMEEARHIAL	SGPERQKTVA
650	660	670	680	690	700	710	720
LDGTLFLKSG	VISGGSSDLK	YKARCWDEKE	LKNLRDRRSQ	KIQELKGLMK	TLRKETDLKQ	IQTLIQGTQT	RLKYSQNELE
730	740	750	760	770	780	790	800
MIKKKHLVAF	YQEQSQLQSE	LLNIESQCIM	LSEGIKERQR	RIKEFQEKID	KVEDDIFQHF	CEEIGVENIR	EFENKHVKRQ
810	820	830	840	850	860	870	880
QEIDQKRLEF	EKQKTRLNVQ	LEYSRSHLKK	KLNKINTLKE	TIQKGSEDID	HLKKAEENCL	QTVNELMAKQ	QQLKDIRVTQ
890	900	910	920	930	940	950	960
NSSAEKVQTQ	IEEERKKFLA	VDREVGKLQK	EVVSIQTSLE	QKRLEKHNLL	LDCKVQDIEI	ILLSGSLDDI	IEVEMGTEAE
970	980	990	1000	1010	1020	1030	1040
STQATIDIYE	KEEAFEIDYS	SLKEDLKALQ	SDQEIEAHLR	LLLQQVASQE	DILLKTAAPN	LRALENLKTV	RDKFQESTDA
1050	1060	1070	1080	1090	1100	1110	1120
FEASRKEARL	CRQEFEQVKK	RRYDLFTQCF	EHVSISIDQI	YKKLCRNNSA	QAFLSPENPE	EPYLEGISYN	CVAPGKRFMP
1130	1140	1150	1160	1170	1180	1190	1200
MDNLSGGEKC	VAALALLFAV	HSFRPAPFFV	LDEVDAALDN	TNIGKVSSYI	KEQTQDQFQM	IVISLKEEFY	SRADALIGIY
1210	1220	1230	1240				
PEYDDCMFSR	VLTLDLSQYP	DTEGQESSKR	HGESR				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2132	1	757.3003	-55.47	2	55.0	13.6	1	1117-1129	K.RFMPMDNLSGGEK.C	Oxidation: 3, 5	WD:WU 0.95

Detailed Protein Report

Protein 665: sodium/hydrogen exchanger 5 precursor [Homo sapiens]

Accession:	gi|4759144	**Score:**	13.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	98.9
Database Date:	2015-11-30	**pI:**	7.9
		Sequence Coverage [%]:	1.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLRAALSLLA	LPLAGAAEEP	TQKPESPGEP	PPGLELFRWQ	WHEVEAPYLV	ALWILVASLA	KIVFHLSRKV	TSLVPESCLL
90	100	110	120	130	140	150	160
ILLGLVLGGI	VLAVAKKAEY	QLEPGTFFLF	LLPPIVLDSG	YFMPSRLFFD	NLGAILTYAV	VGTLWNAFTT	GAALWGLQQA
170	180	190	200	210	220	230	240
GLVAPRVQAG	LLDFLLFGSL	ISAVDPVAVL	AVFEEVHVNE	TLFIIVFGES	LLNDAVTVVL	YKVCNSFVEM	GSANVQATDY
250	260	270	280	290	300	310	320
LKGVASLFVV	SLGGAAVGLV	FAFLLALTTR	FTKRVRIIEP	LLVFLLAYAA	YLTAEMASLS	AILAVTMCGL	GCKKYVEANI
330	340	350	360	370	380	390	400
SHKSRTTVKY	TMKTLASCAE	TVIFMLLGIS	AVDSSKWAWD	SGLVLGTLIF	ILFFRALGVV	LQTWVLNQFR	LVPLDKIDQV
410	420	430	440	450	460	470	480
VMSYGGLRGA	VAFALVILLD	RTKVPAKDYF	VATTIVVVFF	TVIVQGLTIK	PLVKWLKVKR	SEHHKPTLNQ	ELHEHTFDHI
490	500	510	520	530	540	550	560
LAAVEDVVGH	HGYHYWRDRW	EQFDKKYLSQ	LLMRRSAYRI	RDQIWDVYYR	LNIRDAISFV	DQGGHVLSST	GLTLPSMPSR
570	580	590	600	610	620	630	640
NSVAETSVTN	LLRESGSGAC	LDLQVIDTVR	SGRDREDAVM	HHLLCGGLYK	PRRRYKASCS	RHFISEDAQE	RQDKEVFQQN
650	660	670	680	690	700	710	720
MKRRLESFKS	TKHNICFTKS	KPRPRKTGRR	KKDGVANAEA	TNGKHRGLGF	QDTAAVILTV	ESEEEEEESD	SSETEKEDDE
730	740	750	760	770	780	790	800
GIIFVARATS	EVLQEGKVSG	SLEVCPSPRI	IPPSPTCAEK	ELPWKSGQGD	LAVYVSSETT	KIVPVDMQTG	WNQSISSLES
810	820	830	840	850	860	870	880
LASPPCNQAP	ILTCLPPHPR	GTEEPQVPLH	LPSDPRSSFA	FPPSLAKAGR	SRSESSADLP	QQQELQPLMG	HKDHTHLSPG
890	900						
TATSHWCIQF	NRGSRL						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1364	1	669.3350	-19.03	2	45.8	13.6	0	397-408	K.IDQVVMSYGGLR.G	

Detailed Protein Report

Protein 666: 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

Detailed Protein Report

Protein 667: 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 668: PREDICTED: cyclin-L2 isoform X7 [Homo sapiens]

Accession:	gi|578799847	**Score:**	13.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	33.8
Database Date:	2015-11-30	**pI:**	11.5
		Sequence Coverage [%]:	2.3
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 1.11 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MNDSLRTDVF	VRFQPESIAC	ACIYLAARTL	EIPLPNRPHW	FLLFGATEEE	IQEICLKILQ	LYARKKVDLT	HLEGEVEKRK
90	100	110	120	130	140	150	160
HAIEEAKAQA	RGLLPGGTQV	LDGTSGFSPA	PKLVESPKEG	KGSKPSPLSV	KNTKRRLEGA	KKAKADSPVN	GLPKGRESRS
170	180	190	200	210	220	230	240
RSRSREQSYS	RSPSRSASPK	RRKSDSGSTS	GGSKSQSRSR	SRSDSPPRQA	PRSAPYKGSE	IRGSRKSKDC	KYPQKPHKSR
250	260	270	280	290	300		
SRSSSRSRSR	SRERADNPGK	YKKKSHYYRD	QRRERSRSYE	RTGRRYERDH	PGHSRHRR		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
510	1	469.1462	-224.93	2	34.8	13.5	2	282-288	R.TGRRYER.D		WD:WU 1.11

Detailed Protein Report

Protein 669: PREDICTED: cytochrome P450 2U1 isoform X4 [Homo sapiens]

Accession:	gi|530377130	**Score:**	13.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	37.1
Database Date:	2015-11-30	**pI:**	10.4
		Sequence Coverage [%]:	6.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSSPGPSQPP	AEDPPWPARL	LRAPLGLLRL	DPSGGALLLC	GLVALLGWSW	LRRRRARGIP	PGPTPWPLVG	NFGHVLLPPF
90	100	110	120	130	140	150	160
LRRRSWLSSR	TRAAGIDPSV	IGPQVLLAHL	ARVYGSIFSF	FIGHYLVVVL	SDFHSVREAL	VQQAEVFSDR	PRVPLISIVT
170	180	190	200	210	220	230	240
KEKEKVHEEI	ERVIGANRAP	SLTDKAQMPY	TEATIMEVQR	LTVVVPLAIP	HMTSENTVLQ	GYTIPKGTLI	LPNLWSVHRD
250	260	270	280	290	300	310	320
PAIWEKPEDF	YPNRFLDDQG	QLIKKETFIP	FGIGKRVCMG	EQLAKMELFL	MFVSLMQSFA	FALPEDSKKP	LLTGRFGLTL
330	340						
APHPFNITIS	RR						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
332	1	752.4965	78.30	3	32.8	13.5	1	91-112	R.TRAAGIDPSVIGPQVLLAHLAR.V	

Detailed Protein Report

Protein 670: lysozyme C precursor [Homo sapiens]

Accession:	gi|4557894	**Score:**	13.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	16.5
Database Date:	2015-11-30	**pI:**	10.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	18.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MKALIVLGLV	LLSVTVQGKV	FERCELARTL	KRLGMDGYRG	ISLANWMCLA	KWESGYNTRA	TNYNAGDRST	DYGIFQINSR
90	100	110	120	130	140	150	
YWCNDGKTPG	AVNACHLSCS	ALLQDNIADA	VACAKRVVRD	PQGIRAWVAW	RNRCQNRDVR	QYVQGCGV	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2481	1	938.4534	2.74	3	59.3	13.5	0	88-115	K.TPGAVNACHLSCSALLQDNIADAVACAK.R	Carbamidomethyl: 26

Detailed Protein Report

Protein 671: neuronal pentraxin receptor [Homo sapiens]

Accession:	gi|17402888	**Score:**	13.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	52.8
Database Date:	2015-11-30	**pI:**	5.8
		Sequence Coverage [%]:	3.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MKFLAVLLAA	GMLAFLGAVI	CIIASVPLAA	SPARALPGGA	DNASVASGAA	ASPGPQRSLS	ALHGAGGSAG	PPALPGAPAA
90	100	110	120	130	140	150	160
SAHPLPPGPL	FSRFLCTPLA	AACPSGAQQG	DAAGAAPGER	EELLLLQSTA	EQLRQTALQQ	EARIRADQDT	IRELTGKLGR
170	180	190	200	210	220	230	240
CESGLPRGLQ	GAGPRRDTMA	DGPWDSPALI	LELEDAVRAL	RDRIDRLEQE	LPARVNLSAA	PAPVSAVPTG	LHSKMDQLEG
250	260	270	280	290	300	310	320
QLLAQVLALE	KERVALSHSS	RRQRQEVEKE	LDVLQGRVAE	LEHGSSAYSP	PDAFKISIPI	RNNYMYARVR	KALPELYAFT
330	340	350	360	370	380	390	400
ACMWLRSRSS	GTGQGTPFSY	SVPGQANEIV	LLEAGHEPME	LLINDKVAQL	PLSLKDNGWH	HICIAWTTRD	GLWSAYQDGE
410	420	430	440	450	460	470	480
LQGSGENLAA	WHPIKPHGIL	ILGQEQDTLG	GRFDATQAFV	GDIAQFNLWD	HALTPAQVLG	IANCTAPLLG	NVLPWEDKLV
490	500	510					
EAFGGATKAA	FDVCKGRAKA						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2151	1	863.8612	-97.34	2	55.4	13.5	1	479-495	K.LVEAFGGATKAAFDVCK.G	

Detailed Protein Report

Protein 672: PREDICTED: gastrin/cholecystokinin type B receptor isoform X1 [Homo sapiens]

Accession:	gi|530395959	**Score:**	13.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	55.8
Database Date:	2015-11-30	**pI:**	11.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MELLKLNRSV	QGTGPGPGAS	LCRPGAPLLN	SSSVGNLSCE	PPRIRGAGTR	ELELAIRITL	YAVIFLMSVG	GNMLIIVVLG
90	100	110	120	130	140	150	160
LSRRLRTVTN	AFLLSLAVSD	LLLAVACMPF	TLLPNLMGTF	IFGTVICKAV	SYLMGVSVSV	STLSLVAIAL	ERYSAICRPL
170	180	190	200	210	220	230	240
QARVWQTRSH	AARVIVATWL	LSGLLMVPYP	VYTVVQPVGP	RVLQCVHRWP	SARVRQTWSV	LLLLLLFFIP	GVVMAVAYGL
250	260	270	280	290	300	310	320
ISRELYLGLR	FDGDSDSDSQ	SRVRNQGGLP	GGAGPREQNL	GEAELWRATG	PAGVGGTEMK	VRVRRKLEME	LSWERRSGGD
330	340	350	360	370	380	390	400
WAGDWGDSPF	SLTAHPLCSG	AVHQNGRCRP	ETGAVGEDSD	GCYVQLPRSR	PALELTALTA	PGPGSGSRPT	QAKLLAKKRV
410	420	430	440	450	460	470	480
VRMLLVIVVL	FFLCWLPVYS	ANTWRAFDGP	GAHRALSGAP	ISFIHLLSYA	SACVNPLVYC	FMHRRFRQAC	LETCARCCPR
490	500	510	520				
PPRARPRALP	DEDPPTPSIA	SLSRLSYTTI	STLGPG				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1548	1	851.5588	119.65	2	47.7	13.5	2	288-304	R.ATGPAGVGGTEMKVRVR.R	Oxidation: 12

Detailed Protein Report

Protein 673: **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

```
        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
711	1	665.1654	-215.52	2	37.7	13.5	1	252-263	R.KSCSGFVQSDSK.R	Carbamidomethyl: 3

Detailed Protein Report

Protein 674: **integral membrane protein GPR180 precursor [Homo sapiens]**

Accession:	gi|30725877	**Score:**	13.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	49.4
Database Date:	2015-11-30	**pI:**	7.2
		Sequence Coverage [%]:	3.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGGLRLLAVA	LTCCWWPQGS	QGKTLRGSFS	STAAQDAQGQ	RIGHFEFHGD	HALLCVRINN	IAVAVGKEAK	LYLFQAQEWL
90	100	110	120	130	140	150	160
KLQQSSHGYS	CSEKLSKAQL	TMTMNQTEHN	LTVSQIPSPQ	TWHVFYADKY	TCQDDKENSQ	VEDIPFEMVL	LNPDAEGNPF
170	180	190	200	210	220	230	240
DHFSAGESGL	HEFFFLLVLV	YFVIACIYAQ	SLWQAIKKGG	PMHMILKVLT	TALLLQAGSA	LANYIHFSSY	SKDGIGVPFM
250	260	270	280	290	300	310	320
GSLAEFFDIA	SQIQMLYLLL	SLCMGWTIVR	MKKSQSRPLQ	WDSTPASTGI	AVFIVMTQSV	LLLWEQFEDI	SHHSYHSHHN
330	340	350	360	370	380	390	400
LAGILLIVLR	ICLALSLGCG	LYQIITVERS	TLKREFYITF	AKGCILWFLC	HPVLACISVI	FSDYQRDKVI	TIGVILCQSV
410	420	430	440	450			
SMVILYRLFL	SHSLYWEVSS	LSSVTLPLTI	SSGHKSRPHF				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1390	1	727.2022	-165.33	2	45.7	13.5	0	82-94	K.LQQSSHGYSCSEK.L	

Detailed Protein Report

Protein 675: **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 676: PREDICTED: hephaestin isoform X3 [Homo sapiens]

Accession:	gi|578838557	**Score:**	13.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	97.3
Database Date:	2015-11-30	**pI:**	5.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.4
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 0.29 **CV:** 0.00 % **No. of Peptides:** 1

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	Ratios
2643	1	784.0056	-47.59	3	61.3	13.5	0	271-291	R. MHAINGFVFGNLPELNMCAQK.R	Oxidation: 17	WD:WU 0.29

Detailed Protein Report

Protein 677: alpha-protein kinase 3 [Homo sapiens]

Accession: gi|115511036
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 13.4
MW [kDa]: 201.1
pI: 8.8
Sequence Coverage [%]: 0.7
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MEVAWLVYVL	GQQPLARQGE	GQSRLVPGRG	LVLWLPGLPR	SSPSWPAVDL	APLAPARPRG	PLICHTGHEQ	AGREPGPGSS
90	100	110	120	130	140	150	160
TKGPVLHDQD	TRCAFLPRPP	GPLQTRRYCR	HQGRQGSGLG	AGPGAGTWAP	APPGVSKPRC	PGRARPGEGQ	QQVTTARPPA
170	180	190	200	210	220	230	240
INRGARQPRA	GAAAAGRGPG	AGAWRTGEAA	ASAGPAVGEG	GAMGSRRAPS	RGWGAGGRSG	AGGDGEDDGP	VWIPSPASRS
250	260	270	280	290	300	310	320
YLLSVRPETS	LSSNRLSHPS	SGRSTFCSII	AQLTEETQPL	FETTLKSRSV	SEDSDVRFTC	IVTGYPEPEV	TWYKDDTELD
330	340	350	360	370	380	390	400
RYCGLPKYEI	THQGNRHTLQ	LYRCREEDAA	IYQASAQNSK	GIVSCSGVLE	VGTMTEYKIH	QRWFAKLKRK	AAAKLREIEQ
410	420	430	440	450	460	470	480
SWKHEKAVPG	EVDTLRKLSP	DRFQRKRRLS	GAQAPGPSVP	TREPEGGTLA	AWQEGETETA	QHSGLGLINS	FASGEVTTNG
490	500	510	520	530	540	550	560
EAAPENGEDG	EHGLLTYICD	AMELGPQRAL	KEESGAKKKK	KDEESKQGLR	KPELEKAAQS	RRSSENCIPS	SDEPDSCGTQ
570	580	590	600	610	620	630	640
GPVGVEQVQT	QPRGRAARGP	GSSGTDSTRK	PASAVGTPDK	AQKAPGPGPG	QEVYFSLKDM	YLENTQAVRP	LGEEGPQTLS
650	660	670	680	690	700	710	720
VRAPGESPKG	KAPLRARSEG	VPGAPGQPTH	SLTPQPTRPF	NRKRFAPPKP	KGEATTDSKP	ISSLSQAPEC	GAQSLGKAPP
730	740	750	760	770	780	790	800
QASVQVPTPP	ARRRHGTRDS	TLQGQAGHRT	PGEVLECQTT	TAPTMSASSS	SDVASIGVST	SGSQGIIEPM	DMETQEDGRT
810	820	830	840	850	860	870	880
SANQRTGSKK	NVQADGKIQV	DGRTRGDGTQ	TAQRTRADRK	TQVDAGTQES	KRPQSDRSAQ	KGMMTQGRAE	TQLETTQAGE
890	900	910	920	930	940	950	960
KIQEDRKAQA	DKGTQEDRRM	QGEKGMQGEK	GTQSEGSAPT	AMEGQSEQEV	ATSLGPPSRT	PKLPPTAGPR	APLNIECFVQ
970	980	990	1000	1010	1020	1030	1040
TPEGSCFPKK	PGCLPRSEEA	VVTASRNHEQ	TVLGPLSGNL	MLPAQPPHEG	SVEQVGGERC	RGPQSSGPVE	AKQEDSPFQC
1050	1060	1070	1080	1090	1100	1110	1120
PKEERPGGVP	CMDQGGCPLA	GLSQEVPTMP	SLPGTGLTAS	PKAGPCSTPT	SQHGSTATFL	PSEDQVLMSS	APTLHLGLGT
1130	1140	1150	1160	1170	1180	1190	1200
PTQSHPPETM	ATSSEGACAQ	VPDVEGRTPG	PRSCDPGLID	SLKNYLLLLL	KLSSTETSGA	GGESQVGAAT	GGLVPSATLT
1210	1220	1230	1240	1250	1260	1270	1280
PTVEVAGLSP	RTSRRILERV	ENNHLVQSAQ	TLLLSPCTSR	RLTGLLDREV	QAGRQALAAA	RGSWGPGPSS	LTVPAIVVDE
1290	1300	1310	1320	1330	1340	1350	1360
EDPGLASEGA	SEGEGEVSPE	GPGLLGASQE	SSMAGRLGEA	GGQAAPGQGP	SAESIAQEPS	QEEKFPGEAL	TGLPAATPEE
1370	1380	1390	1400	1410	1420	1430	1440
LALGARRKRF	LPKVRAAGDG	EATTPEERES	PTVSPRGPRK	SLVPGSPGTP	GRERRSPTQG	RKASMLEVPR	AEEELAAGDL
1450	1460	1470	1480	1490	1500	1510	1520
GPSPKAGGLD	TEVALDEGKQ	ETLAKPRKAK	DLLKAPQVIR	KIRVEQFPDA	SGSLKLWCQF	FNILSDSVLT	WAKDQRPVGE
1530	1540	1550	1560	1570	1580	1590	1600
VGRSAGDEGP	AALAIVQASP	VDCGVYRCTI	HNEHGSASTD	FCLSPEVLSG	FISREEGEVG	EEIEMTPMVF	AKGLADSGCW
1610	1620	1630	1640	1650	1660	1670	1680
GDKLFGRLVS	EELRGGGYGC	GLRKASQAKV	IYGLEPIFES	GRTCIIKVSS	LLVFGPSSET	SLVGRNYDVT	IQGCKIQNMS
1690	1700	1710	1720	1730	1740	1750	1760
REYCKIFAAE	ARAAPGFGEV	PEIIPLYLIY	RPANNIPYAT	LEEDLGKPLE	SYCSREWGCA	EAPTASGSSE	AMQKCQTFQH
1770	1780	1790	1800	1810	1820	1830	1840
WLYQWTNGSF	LVTDLAGVDW	KMTDVQIATK	LRGYQGLKES	CFPALLDRFA	SSHQCNAYCE	LLGLTPLKGP	EAAHPQAKAK
1850	1860	1870	1880	1890	1900	1910	
GSKSPSAGRK	GSQLSPQPQK	KGLPSPQGTR	KSAPSSKATP	QASEPVTTQL	LGQPPTQEEG	SKAQGMR	

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1359	1	669.3184	-65.41	2	45.3	13.4	0	429-442	R.LSGAQAPGPSVPTR.E	

Detailed Protein Report

Protein 678: photoreceptor-specific nuclear receptor isoform a [Homo sapiens]

Accession:	gi|7706515	**Score:**	13.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	39.6
Database Date:	2015-11-30	**pI:**	8.0
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	6.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
METRPTALMS	STVAAAAPAA	GAASRKESPG	RWGLGEDPTG	VSPSLQCRVC	GDSSSGKHYG	IYACNGCSGF	FKRSVRRRLI
90	100	110	120	130	140	150	160
YRCQVGAGMC	PVDKAHRNQC	QACRLKKCLQ	AGMNQDAVQN	ERQPRSTAQV	HLDSMESNTE	SRPESLVAPP	APAGRSPRGP
170	180	190	200	210	220	230	240
TPMSAARALG	HHFMASLITA	ETCAKLEPED	ADENIDVTSN	DPEFPSSPYS	SSSPCGLDSI	HETSARLLFM	AVKWAKNLPV
250	260	270	280	290	300	310	320
FSSLPFRDQV	ILLEEAWSEL	FLLGAIQWSL	PLDSCPLLAP	PEASAAGGAQ	GRLTLASMET	RVLQETISRF	RALAVDPTEF
330	340	350	360	370			
ACMKALVLFK	PETRGLKDPE	HVEALQDQSQ	VMLSQHSKAH	HPSQPVR			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2476	1	900.2164	98.29	3	59.2	13.4	2	302-324	R.VLQETISRFRALAVDPTEFACMK.A	Carbamidomethyl: 21; Oxidation: 22

Detailed Protein Report

Protein 679: 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 680: cerebral cavernous malformations 2 protein-like [Homo sapiens]

Accession:	gi|31542255	**Score:**	13.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	46.7
Database Date:	2015-11-30	**pI:**	10.4
		Sequence Coverage [%]:	4.4
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578835776	refseq_human (refseq_human_20140103.fasta)	PREDICTED: cerebral cavernous malformations 2 protein-like isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MEYEVKKGKK	GFVSPIRRLV	FPKAGRRAAC	RSSVSRRPLH	SMPLYPPDYL	IDPQILLCDY	LEKEVKFLGH	LTWVTSSLNP
90	100	110	120	130	140	150	160
SSRDELLQLL	DTARQLKELP	LKTTAEQDSI	LSLSARCLLL	TWRDNEELIL	RIPTHEIAAA	SYLQDDALHL	LVLKTGLGVD
170	180	190	200	210	220	230	240
PVPAGVDASP	GGAGRDPGPP	GGAPEKRRVG	TAERRHTICS	LDWRMGWGGG	AAEARAGGGG	GGSLERQRAG	ARASGSWERR
250	260	270	280	290	300	310	320
QTFSGSWERR	HGGGGGGGGA	GKPGGSWERR	QAGSGGGGSW	ERRHPGPNPL	DPQDPSPDAY	CNLVILAVAN	RDAAEESCAL
330	340	350	360	370	380	390	400
ICQVFQIIYG	DQSIECVDRA	GYHYTSTPER	PWLCSRIMAP	RTPLKHVTAA	RPHLLSMAPT	AAAATTAVWA	WSSYRITWSR
410	420	430	440				
CGVSWGPSRS	SSLRCCCGST	GWGCPSRTIA	QAC				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2317	1	819.4008	25.39	2	57.3	13.4	0	251-269	R.HGGGGGGGGAGKPGGSWER.R	

Detailed Protein Report

Protein 681: prickle-like protein 4 [Homo sapiens]

Accession:	gi|118722347	**Score:**	13.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	41.7
Database Date:	2015-11-30	**pI:**	5.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSVQNSGWPH	QEDSPKPQDP	GPPANSDSDS	GHLPGEDPED	THAQGPAVLS	LGSLCLDTNQ	APNWTGLQTL	LQQLPPQDID
90	100	110	120	130	140	150	160
ERYCLALGEE	ERAELQLFCA	RRKQEALGQG	VARLVLPKLE	GHTCEKCREL	LKPGEYGVFA	ARAGEQRCWH	QPCFACQACG
170	180	190	200	210	220	230	240
QALINLIYFY	HDGQLYCGRH	HAELLRPRCP	ACDQLIFSWR	CTEAEGQRWH	ENHFCCQDCA	GPLGGGRYAL	PGGSPCCPSC
250	260	270	280	290	300	310	320
FENRYSDAGS	SWAGALEGQA	FLGETGLDRT	EGRDQTSVNS	ATLSRTLLAA	AGGSSLQTQR	GLPGSSPQQE	NRPGDKAEAP
330	340	350	360	370	380	390	
KGQEQCRLET	IRDPKDTPFS	TCSSSSDSEP	EGFFLGERLP	QSWKTPGSLQ	AEDSNASKTH	CTMC	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1234	1	1136.1482	87.82	2	43.7	13.4	1	83-101	R.YCLALGEEERAELQLFCAR.R	Carbamidomethyl: 2

Detailed Protein Report

Protein 682: **PREDICTED: uveal autoantigen with coiled-coil domains and ankyrin repeats isoform X3 [Homo sapiens]**

Accession:	gi|530406156	**Score:**	13.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	160.2
Database Date:	2015-11-30	**pI:**	6.8
		Sequence Coverage [%]:	1.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MMNCWFSCTP	KNRHAADWNK	YDDRLMKAAE	RGDVEKVTSI	LAKKGVNPGK	LDVEGRSVFH	VVTSKGNLEC	LNAILIHGVD
90	100	110	120	130	140	150	160
ITTSDTAGRN	ALHLAAKYGH	ALCLQKLLQY	NCPTEHADLQ	GRTALHDAAM	ADCPSSIQLL	CDHGASVNAK	DVDGRTPLVL
170	180	190	200	210	220	230	240
ATQMSRPTIC	QLLIDRGADV	NSRDKQNRTA	LMLGCEYGCR	DAVEVLIKNG	ADISLLDALG	HDSSYYARIG	DNLDILTLLK
250	260	270	280	290	300	310	320
TASENTNKGR	ELWKKGPSLQ	QRNLTHMQDE	VNVKSHQREH	QNIQDLEIEN	EDLKERLRKI	QQEQRILLDK	VNGLQLQLNE
330	340	350	360	370	380	390	400
REKLKSLLAA	KEKQHEESLR	TIEALKNRFK	YFESDHLGSG	SHFSNRKEDM	LLKQGQMYMA	DSQCTSPGIP	AHMQSRSMLR
410	420	430	440	450	460	470	480
PLELSLPSQT	SYSENEILKK	ELEAMRTFCE	SAKQDRLKLQ	NELAHKVAEC	KALALECERV	KEDSDEQIKQ	LEDALKDVQK
490	500	510	520	530	540	550	560
RMYESEGKVK	QMQTHFLALK	EHLTSEAASG	NHRLTEELKD	QLKDLKVKYE	GASAEVGKLR	NQIKQNEMIV	EEFKRDEGKL
570	580	590	600	610	620	630	640
IEENKRLQKE	LSMCEMEREK	KGRKVTEMEG	QAKELSAKLA	LSIPAEKFEN	MKSSLSNEVN	EKAKKLVEME	REHEKSLSEI
650	660	670	680	690	700	710	720
RQLKRELENV	KAKLAQHVKP	EEHEQVKSRL	EQKSGELGKK	ITELTLKNQT	LQKEIEKVYL	DNKLLKEQAH	NLTIEMKNHY
730	740	750	760	770	780	790	800
VPLKVSEDMK	KSHDAIIDDL	NRKLLDVTQK	YTEKKLEMEK	LLLENDSLSK	DVSRLETVFV	PPEKHEKEII	ALKSNIVELK
810	820	830	840	850	860	870	880
KQLSELKKKC	GEDQEKIHAL	TSENTNLKKM	MSNQYVPVKT	HEEVKMTLND	TLAKTNRELL	DVKKKFEDIN	QEFVKIKDKN
890	900	910	920	930	940	950	960
EILKRNLENT	QNQIKAEYIS	LAEHEAKMSS	LSQSMRKVQD	SNAEILANYR	KGQEEIVTLH	AEIKAQKKEL	DTIQECIKVK
970	980	990	1000	1010	1020	1030	1040
YAPIVSFEEC	ERKFKATEKE	LKDQLSEQTQ	KYSVSEEEVK	KNKQENDKLK	KEIFTLQKDL	RDKTVLIEKS	HEMERALSRK
1050	1060	1070	1080	1090	1100	1110	1120
TDELNKQLKD	LSQKYTEVKN	VKEKLVEENA	KQTSEILAVQ	NLLQKQHVPL	EQVEALKKSL	NGTIENLKEE	LKSMQRCYEK
1130	1140	1150	1160	1170	1180	1190	1200
EQQTVTKLHQ	LLENQKNSSV	PLAEHLQIKE	AFEKEVGIIK	ASLREKEEES	QNKMEEVSKL	QSEVQNTKQA	LKKLETREVV
1210	1220	1230	1240	1250	1260	1270	1280
DLSKYKATKS	DLETQISSLN	EKLANLNRKY	EEVCEEVLHA	KKKEISAKDE	KELLHFSIEQ	EIKDQKERCD	KSLTTITELQ
1290	1300	1310	1320	1330	1340	1350	1360
RRIQESAKQI	EAKDNKITEL	LNDVERLKQA	LNGLSQLTYT	SGNPTKRQSQ	LIDTLQHQVK	SLEQQLADAD	RQHQEVIAIY
1370	1380	1390	1400				
RTHLLSAAQG	HMDEDVQEAL	LQIIQMRQGL	VC				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1985	1	599.9122	-110.16	3	53.2	13.4	2	959-973	K.VKYAPIVSFEECERK.F	

Detailed Protein Report

Protein 683: **dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A isoform b [Homo sapiens]**

Accession:	gi|511630717	**Score:**	13.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	69.5
Database Date:	2015-11-30	**pI:**	8.7
		Sequence Coverage [%]:	1.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MITSAAIYHV	LHFFHITIDI	RNVCVFLAPL	FSSFTTIVTY	HLTKELKDAG	AGLLAAAMIA	VVPGYISRSV	AGSYDNEGIA
90	100	110	120	130	140	150	160
IFCMLLTYYM	WIKAVKTGSI	CWAAKCALAY	FYMVSSWGGY	VFLINLIPLH	VLVLMLTGRF	SHRIYVAYCT	VYCLGTILSM
170	180	190	200	210	220	230	240
QISFVGFQPV	LSSEHMAAFG	VFGLCQIHAF	VDYLRSKLNP	QQFEVLFRSV	ISLVGFVLLT	VGALLMLTGK	ISPWTGRFYS
250	260	270	280	290	300	310	320
LLDPSYAKNN	IPIIASVSEH	QPTTWSSYYF	DLQLLVFMFP	VGLYYCFSNL	SDARIFIIMY	GVTSMYFSAV	MVRLMLVLAP
330	340	350	360	370	380	390	400
VMCILSGIGV	SQVLSTYMKN	LDISRPDKKS	KKQQDSTYPI	KNEVASGMIL	VMAFFLITYT	FHSTWVTSEA	YSSPSIVLSA
410	420	430	440	450	460	470	480
RGGDGSRIIF	DDFREAYYWL	RHNTPEDAKV	MSWWDYGYQI	TAMANRTILV	DNNTWNNTHI	SRVGQAMAST	EEKAYEIMRE
490	500	510	520	530	540	550	560
LDVSYVLVIF	GGLTGYSSDD	INKFLWMVRI	GGSTDTGKHI	KENDYYTPTG	EFRVDREGSP	VLLNCLMYKM	CYYRFGQVYT
570	580	590	600	610	620		
EAKRPPGFDR	VRNAEIGNKD	FELDVLEEAY	TTEHWLVRIY	KVKDLDNRGL	SRT		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1173	1	500.6606	-239.16	2	43.3	13.4	1	571-579	R.VRNAEIGNK.D	

Detailed Protein Report

Protein 684: malcavernin isoform 4 [Homo sapiens]

Accession: gi|269308190
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 13.4
MW [kDa]: 39.4
pI: 5.6
Sequence Coverage [%]: 4.0
No. of unique Peptides: 1

Quantitation

WD:WU **Median:** 0.16 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MEEEGKKGKK	PGIVSPFKRV	FLKGEKSRDK	KAHEKVTERR	PLHTVVLSLP	ERVEPDRLLS	DYIEKEVKYL	GQLTSIPGYL
90	100	110	120	130	140	150	160
NPSSRTEILH	FIDNAKRAHQ	LPGHLTQEHD	AVLSLSAYNV	KLAWRDGEDI	ILRVPIHDIA	AVSYVRDDAA	HLVVLKTDDS
170	180	190	200	210	220	230	240
STKVDIKETY	EVEASTFCFP	ESVDVGGASP	HSKTISESEL	SASATELLQD	YMLTLRTKLS	SQEIQQFAAL	LHEYRNGASI
250	260	270	280	290	300	310	320
HEFCINLRQL	YGDSRKFLLL	GLRPFIPEKD	SQHFENFLET	IGVKDGRGII	TDSFGRHRRA	LSTTSSSTTN	GNRATGSSDD
330	340	350	360				
RSAPSEGDEW	DRMISDISSD	IEALGCSMDQ	DSA				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1332	1	698.9025	94.05	2	45.0	13.4	0	300-313	R.ALSTTSSSTTNGNR.A		WD:WU 0.16

Detailed Protein Report

Protein 685: 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

Alias proteins:

Accession	Name	Description
gi|313151197	refseq_human (refseq_human_20140103.fasta)	pyridoxal phosphate phosphatase PHOSPHO2 [Homo sapiens]
gi|313151195	refseq_human (refseq_human_20140103.fasta)	pyridoxal phosphate phosphatase PHOSPHO2 [Homo sapiens]
gi|313151193	refseq_human (refseq_human_20140103.fasta)	pyridoxal phosphate phosphatase PHOSPHO2 [Homo sapiens]
gi|313151191	refseq_human (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
1387	1	695.3741	-31.67	2	46.1	13.4	2	30-40	K.KLPIELRDSYR.K	

Detailed Protein Report

Protein 686: **sodium/hydrogen exchanger 11 [Homo sapiens]**

Accession:	gi|224465231	**Score:**	13.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	129.0
Database Date:	2015-11-30	**pI:**	6.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.2
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 1.14 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MSSYFWAQNE	SNRPDLLCGQ	PADYLVEEKH	FTTLVCFIVV	LGGLLKMCLK	NCEVIVLTIL	SLSGFVIGHM	AYNSVEVHQI
90	100	110	120	130	140	150	160
VYPLLRTSSF	SLYSYFSPLI	IFMVALDVEF	YTLKKMFWQV	LLTGLISFST	ASIIIGYVVI	KFNKDSWDLQ	SCLLFSITLG
170	180	190	200	210	220	230	240
IIDPLRSVNS	LKTIGISKIY	IDLIRGESLI	ICSIASIFFG	NFRGNRIHFS	IFRDLHVGIE	LSYDILGSII	FGYWCAKIIQ
250	260	270	280	290	300	310	320
CILADVFSNM	LTNIILCFSM	VYMTFYIVEF	LGMSGTLALA	AVGLNLDSLT	FKPKIELVIT	KFLRIFSSVY	EHLIYAFFGI
330	340	350	360	370	380	390	400
VIGCGELSHY	EFHTIPFIFI	LFTTVNLVRL	LTILLVSPIL	MHSNYEYNWR	WGVVITWSGI	KGVFNLLWAP	DVYNLAERKV
410	420	430	440	450	460	470	480
EVPQMFILYV	QVISLLTMGI	NSYVMTQSAR	KLDLCVLSLP	RQMILQNATQ	HIQEIVQNTI	TLFKTEKILT	NVNWTLVEDK
490	500	510	520	530	540	550	560
TRIEYIPFSH	VSHNDMKTES	TTDEALMEEA	RLHVAAIQMS	SFEKQRNNGI	LEIEAARILI	GAAKCYYSIQ	GKFMSIYDVS
570	580	590	600	610	620	630	640
TYMRTRSWLI	KFKNVLTFLE	YCIEKIHFIP	PESNTFLTFI	FHIVFSEEFE	YTGQIINLIY	IYPMIIHLWP	MARGLNVSAL
650	660	670	680	690	700	710	720
ISINYYFMFL	YVLESTLKII	ILKRKYFQQC	WNTLEFFILV	IGIIDIFCVY	FVKLRPDNLA	LIQLTVIMGY	LRIIRFLPLF
730	740	750	760	770	780	790	800
KIIVPILIRI	ADVQIKKRLS	LMYSITKGYI	KSQEDAKLLI	KQIAVCESIY	QKLCEILETN	KQDAVKELVL	MEHEGRDVVI
810	820	830	840	850	860	870	880
ALKTKQAIRN	VIAKALKNLT	FLCSRGIIDK	HEVIEINKVL	LKKLKALNNF	PKAIPPPTPD	IYLHNIIWLE	GKDVLIDFFK
890	900	910	920	930	940	950	960
ERAKLACFDS	GDTICKGGEM	PQGIYLIISG	MAILHSLSPT	FGIESNQRCD	RGSRDMFTEF	CTTGDIIGEL	SCLLKREIEY
970	980	990	1000	1010	1020	1030	1040
TVICETSLQA	CFISLEDLYE	GFDAFWPSLE	YKIWLKLALS	TAYQYFESSL	IDEDLRFQNC	VMFNQAYVET	LSSYSDMIID
1050	1060	1070	1080	1090	1100	1110	1120
NMTMKFVIIV	YGSVIDTKTE	EPYFAPCIIP	TTCEQVQGTS	DLSKLLIIQA	SELTQRNSNT	NVMASVNTVF	EQPGKNINGR
1130							
QKMS							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2425	1	893.4053	-14.86	2	58.6	13.4	1	553-566	K.FMSIYDVSTYMRTR.S	Oxidation: 2	WD:WU 1.14

Protein 687: uncharacterized protein ARIH2OS [Homo sapiens]

Accession: gi|176866318
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 13.4
MW [kDa]: 30.4
pI: 12.4
Sequence Coverage [%]: 8.3
No. of unique Peptides: 1

```
        10         20         30         40         50         60         70         80
MLGQRAGDGE RPGLPGDGEG GVPARPGRRA ERPPQRPAKV NKAVTCAAHL PGAAASRPLS PNKPDRVRPG QRDRIGAKRQ
        90        100        110        120        130        140        150        160
RRRRADAGQA RAASSRRVVP TAPEVLGAVA SLPDRGRPTV ARVATGSRLE GLFSAASLKL SALTQSLTRV RQAPTASGAT
       170        180        190        200        210        220        230        240
IRLPASPVEM FLTSAFLTGF SFHCLYSGIG HGEDILASVE QITIVSRPLS GQRGAGPGNS AYTPRRSQGG PRAATTPGFR
       250        260        270        280        290        300
FPCRGLVRRA VLRLTVTVQD CILTALLAVS FHSIGVVIMT SSYLLGPVVK
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
573	1	819.8424	95.39	3	35.6	13.4	0	43-66	K.AVTCAAHLPGAAASRPLSPNKPDR.V	Carbamidomethyl: 4

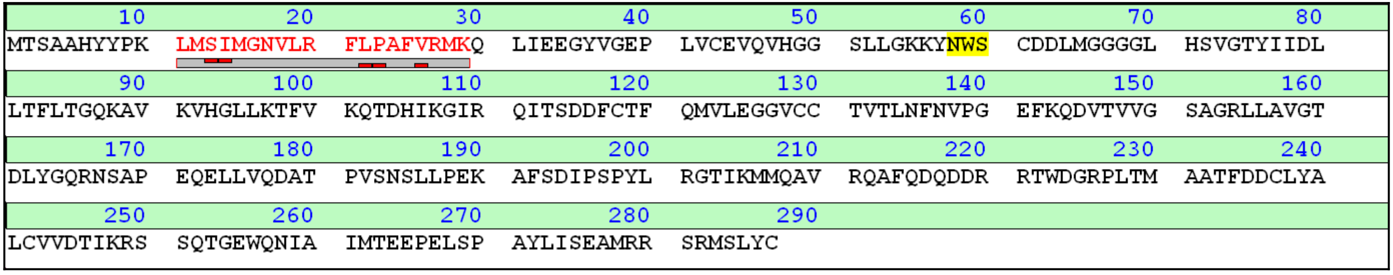
Detailed Protein Report

Protein 688: **glucose-fructose oxidoreductase domain-containing protein 1 isoform 2 [Homo sapiens]**

Accession:	gi|336285206	**Score:**	13.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	31.8
Database Date:	2015-11-30	**pI:**	5.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	6.6
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|336285213	refseq_human (refseq_human_20140103.fasta)	glucose-fructose oxidoreductase domain-containing protein 1 isoform 2 [Homo sapiens]



10	20	30	40	50	60	70	80
MTSAAHYYPK	LMSIMGNVLR	FLPAFVRMKQ	LIEEGYVGEP	LVCEVQVHGG	SLLGKKYNWS	CDDLMGGGGL	HSVGTYIIDL
90	100	110	120	130	140	150	160
LTFLTGQKAV	KVHGLLKTFV	KQTDHIKGIR	QITSDDFCTF	QMVLEGGVCC	TVTLNFNVPG	EFKQDVTVVG	SAGRLLAVGT
170	180	190	200	210	220	230	240
DLYGQRNSAP	EQELLVQDAT	PVSNSLLPEK	AFSDIPSPYL	RGTIKMMQAV	RQAFQDQDDR	RTWDGRPLTM	AATFDDCLYA
250	260	270	280	290			
LCVVDTIKRS	SQTGEWQNIA	IMTEEPELSP	AYLISEAMRR	SRMSLYC			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
348	1	752.5027	120.14	3	33.0	13.3	2	11-29	K.LMSIMGNVLRFLPAFVRMK.Q	Oxidation: 5, 18

Detailed Protein Report

Protein 689: PREDICTED: PEX5-related protein isoform X2 [Homo sapiens]

Accession:	gi|530374762	**Score:**	13.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	72.3
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
MSDSEMDGRT	HIPSLLNALL	SRNRVMQMSY	LKSKEQGYGK	LSSDEDLEII	VDQKQGKGSR	AADKAVAMVM	KEIPREESAE
90	100	110	120	130	140	150	160
EKPLLTMTSQ	LVNEQQESRP	LLSPSIDDFL	CETKSEAIAR	PVTSNTAVLT	TGLDLLDLSE	PVSQTQTKAK	KSEPSSKTSS
170	180	190	200	210	220	230	240
LKKKADGSDL	ISTDAEQRGQ	PLRVPETSSL	DLDIQTQLEK	WDDVKFHGDR	NTKGHPMAER	KSSSSRTGSK	ELLWSSEHRS
250	260	270	280	290	300	310	320
QPELSGGKSA	LNSESASELE	LVAPTQARLT	KEHRWGSALL	SRNHSLEEEF	ERAKAAVESD	TEFWDKMQAE	WEEMARRNWI
330	340	350	360	370	380	390	400
SENQEAQNQV	TISASEKGYY	FHTENPFKDW	PGAFEEGLKR	LKEGDLPVTI	LFMEAAILQD	PGDAEAWQFL	GITQAENENE
410	420	430	440	450	460	470	480
QAAIVALQRC	LELQPNNLKA	LMALAVSYTN	TGHQQDACDA	LKNWIKQNPK	YKYLVKSKKG	SPGLTRRMSK	SPVDSSVLEG
490	500	510	520	530	540	550	560
VKELYLEAAH	QNGDMIDPDL	QTGLGVLFHL	SGEFNRAIDA	FNAALTVRPE	DYSLWNRLGA	TLANGDRSEE	AVEAYTRALE
570	580	590	600	610	620	630	640
IQPGFIRSRY	NLGISCINLG	AYREAVSNFL	TALSLQRKSR	NQQQVPHPAI	SGNIWAALRI	ALSLMDQPEL	FQAANLGDLD
650	660						
VLLRAFNLDP							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1782	2	938.9355	-35.07	2	50.6	13.3	2	25-40	R.VMQMSYLKSKEQGYGK.L	

Detailed Protein Report

Protein 690: alcohol dehydrogenase 4 [Homo sapiens]

Accession:	gi|71565152	**Score:**	13.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	40.2
Database Date:	2015-11-30	**pI:**	9.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGTKGKVIKC	KAAIAWEAGK	PLCIEEVEVA	PPKAHEVRIQ	IIATSLCHTD	ATVIDSKFEG	LAFPVIVGHE	AAGIVESIGP
90	100	110	120	130	140	150	160
GVTNVKPGDK	VIPLYAPLCR	KCKFCLSPLT	NLCGKISNLK	SPASDQQLME	DKTSRFTCKG	KPVYHFFGTS	TFSQYTVVSD
170	180	190	200	210	220	230	240
INLAKIDDDA	NLERVCLLGC	GFSTGYGAAI	NNAKVTPGST	CAVFGLGGVG	LSAVMGCKAA	GASRIIGIDI	NSEKFVKAKA
250	260	270	280	290	300	310	320
LGATDCLNPR	DLHKPIQEVI	IELTKGGVDF	ALDCAGGSET	MKAALDCTTA	GWGSCTFIGV	AAGSKGLTIF	PEELIIGRTI
330	340	350	360	370	380	390	
NGTFFGGWKS	VDSIPKLVTD	YKNKKFNLDA	LVTHTLPFDK	ISEAFDLMNQ	GKSVRTILIF		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1369	1	676.8982	87.95	2	45.4	13.3	0	104-115	K.FCLSPLTNLCGK.I	Carbamidomethyl: 10

Detailed Protein Report

Protein 691: **PREDICTED: probable ATP-dependent RNA helicase DDX60-like isoform X7 [Homo sapiens]**

Accession: gi|578809624
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 13.3
MW [kDa]: 152.1
pI: 7.0
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 692: kanadaptin [Homo sapiens]

Accession:	gi|155722990	**Score:**	13.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	88.8
Database Date:	2015-11-30	**pI:**	5.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.0
		No. of unique Peptides:	1

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
2677	1	973.4892	-48.43	2	61.8	13.3	2	249-264	R.IPPRTYCRVHVGHVVR.F	Carbamidomethyl: 7

Detailed Protein Report

Protein 693: 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

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
836	1	585.7806	55.65	2	39.3	13.3	0	1-11	-.MCSGAGVMMAR.W	Carbamidomethyl: 2

Detailed Protein Report

Protein 694: protein ECT2 isoform b [Homo sapiens]

Accession:	gi|21735572	**Score:**	13.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	100.0
Database Date:	2015-11-30	**pI:**	7.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.9
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|385198081	refseq_human (refseq_human_20140103.fasta)	protein ECT2 isoform b [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MAENSVLTST TGRTSLADSS IFDSKVTEIS KENLLIGSTS YVEEEMPQIE TRVILVQEAG KQEELIKALK DIKVGFVKME
        90        100        110        120        130        140        150        160
SVEEFEGLDS PEFENVFVVT DFQDSVFNDL YKADCRVIGP PVVLNCSQKG EPLPFSCRPL YCTSMMNLVL CFTGFRKKEE
       170        180        190        200        210        220        230        240
LVRLVTLVHH MGGVIRKDFN SKVTHLVANC TQGEKFRVAV SLGTPIMKPE WIYKAWERRN EQDFYAAVDD FRNEFKVPPF
       250        260        270        280        290        300        310        320
QDCILSFLGF SDEEKTNMEE MTEMQGGKYL PLGDERCTHL VVEENIVKDL PFEPSKKLYV VKQEWFWGSI QMDARAGETM
       330        340        350        360        370        380        390        400
YLYEKANTPE LKKSVSMLSL NTPNSNRKRR RLKETLAQLS RETDVSPFPP RKRPSAEHSL SIGSLLDISN TPESSINYGD
       410        420        430        440        450        460        470        480
TPKSCTKSSK SSTPVPSKQS ARWQVAKELY QTESNYVNIL ATIIQLFQVP LEEEGQRGGP ILAPEEIKTI FGSIPDIFDV
       490        500        510        520        530        540        550        560
HTKIKDDLED LIVNWDESKS IGDIFLKYSK DLVKTYPPFV NFFEMSKETI IKCEKQKPRF HAFLKINQAK PECGRQSLVE
       570        580        590        600        610        620        630        640
LLIRPVQRLP SVALLLNDLK KHTADENPDK STLEKAIGSL KEVMTHINED KRKTEAQKQI FDVVYEVDGC PANLLSSHRS
       650        660        670        680        690        700        710        720
LVQRVETISL GEHPCDRGEQ VTLFLFNDCL EIARKRHKVI GTFRSPHGQT RPPASLKHIH LMPLSQIKKV LDIRETEDCH
       730        740        750        760        770        780        790        800
NAFALLVRPP TEQANVLLSF QMTSDELPKE NWLKMLCRHV ANTICKADAE NLIYTADPES FEVNTKDMDS TLSRASRAIK
       810        820        830        840        850        860        870        880
KTSKKVTRAF SFSKTPKRAL RRALMTSHGS VEGRSPSSND KHVMSRLSST SSLAGIPSPS LVSLPSFFER RSHTLSRSTT
       890
HLI
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2201	1	928.4175	-66.81	2	55.9	13.3	1	113-129	K.ADCRVIGPPVVLNCSQK.G	Carbamidomethyl: 14

Detailed Protein Report

Protein 695: **syntaxin-7 [Homo sapiens]**

Accession:	gi|170932494	**Score:**	13.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	29.8
Database Date:	2015-11-30	**pI:**	5.3
		Sequence Coverage [%]:	5.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSYTPGVGGD	PAQLAQRISS	NIQKITQCSV	EIQRTLNQLG	TPQDSPELRQ	QLQQKQQYTN	QLAKETDKYI	KEFGSLPTTP
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
SEQRQRKIQK	DRLVAEFTTS	LTNFQKVQRQ	AAEREKEFVA	RVRASSRVSG	SFPEDSSKER	NLVSWESQTQ	PQVQVQDEEI
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
TEDDLRLIHE	RESSIRQLEA	DIMDINEIFK	DLGMMIHEQG	DVIDSIEANV	ENAEVHVQQA	NQQLSRAADY	QRKSRKTLCI
250	**260**	**270**					
IILILVIGVA	IISLIIWGLN	H					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2771	1	616.3212	-15.13	3	63.2	13.2	1	50-64	R.QQLQQKQQYTNQLAK.E	

Detailed Protein Report

Protein 696: PREDICTED: collagen alpha-1(XXII) chain isoform X2 [Homo sapiens]

Accession:	gi|578815852	**Score:**	13.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	129.6
Database Date:	2015-11-30	**pI:**	7.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.4
		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 697: **ras-GEF domain-containing family member 1C [Homo sapiens]**

Accession: gi|40255197
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 13.2
MW [kDa]: 52.8
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 698: P2Y purinoceptor 8 [Homo sapiens]

Accession:	gi|30023826	**Score:**	13.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	40.6
Database Date:	2015-11-30	**pI:**	10.7
		Sequence Coverage [%]:	5.6
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578838987	refseq_human (refseq_human_20140103.fasta)	PREDICTED: P2Y purinoceptor 8 isoform X6 [Homo sapiens]
gi|578837768	refseq_human (refseq_human_20140103.fasta)	PREDICTED: P2Y purinoceptor 8 isoform X5 [Homo sapiens]
gi|530423005	refseq_human (refseq_human_20140103.fasta)	PREDICTED: P2Y purinoceptor 8 isoform X4 [Homo sapiens]
gi|530423003	refseq_human (refseq_human_20140103.fasta)	PREDICTED: P2Y purinoceptor 8 isoform X3 [Homo sapiens]
gi|530420927	refseq_human (refseq_human_20140103.fasta)	PREDICTED: P2Y purinoceptor 8 isoform X2 [Homo sapiens]
gi|530420925	refseq_human (refseq_human_20140103.fasta)	PREDICTED: P2Y purinoceptor 8 isoform X1 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MQVPNSTGPD NATLQMLRNP AIAVALPVVY SLVAAVSIPG NLFSLWVLCR RMGPRSPSVI FMINLSVTDL MLASVLPFQI

        90        100        110        120        130        140        150        160
YYHCNRHHWV FGVLLCNVVT VAFYANMYSS ILTMTCISVE RFLGVLYPLS SKRWRRRRYA VAACAGTWLL LLTALSPLAR

       170        180        190        200        210        220        230        240
TDLTYPVHAL GIITCFDVLK WTMLPSVAMW AVFLFTIFIL LFLIPFVITV ACYTATILKL LRTEEAHGRE QRRRAVGLAA

       250        260        270        280        290        300        310        320
VVLLAFVTCF APNNFVLLAH IVSRLFYGKS YYHVYKLTLC LSCLNNCLDP FVYYFASREF QLRLREYLGC RRVPRDTLDT

       330        340        350        360
RRESLFSART TSVRSEAGAH PEGMEGATRP GLQRQESVF
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
961	1	1025.8925	-94.87	2	40.3	13.2	0	335-354	R.SEAGAHPEGMEGATRPGLQR.Q	

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Detailed Protein Report

Protein 699: G-protein coupled receptor 35 isoform a [Homo sapiens]

Accession:	gi|33695097	**Score:**	13.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	34.0
Database Date:	2015-11-30	**pI:**	10.3
		Sequence Coverage [%]:	5.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MNGTYNTCGS	SDLTWPPAIK	LGFYAYLGVL	LVLGLLLNSL	ALWVFCCRMQ	QWTETRIYMT	NLAVADLCLL	CTLPFVLHSL
90	100	110	120	130	140	150	160
RDTSDTPLCQ	LSQGIYLTNR	YMSISLVTAI	AVDRYVAVRH	PLRARGLRSP	RQAAAVCAVL	WVLVIGSLVA	RWLLGIQEGG
170	180	190	200	210	220	230	240
FCFRSTRHNF	NSMAFPLLGF	YLPLAVVVFC	SLKVVTALAQ	RPPTDVGQAE	ATRKAARMVW	ANLLVFVVCF	LPLHVGLTVR
250	260	270	280	290	300	310	
LAVGWNACAL	LETIRRALYI	TSKLSDANCC	LDAICYYYMA	KEFQEASALA	VAPSAKAHKS	QDSLCVTLA	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2988	1	619.0064	18.19	3	66.1	13.2	1	282-299	K.EFQEASALAVAPSAKAHK.S	

Detailed Protein Report

Protein 700: **alpha-2-macroglobulin-like protein 1 isoform 2 [Homo sapiens]**

Accession: gi|539846446
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 13.2
MW [kDa]: 105.9
pI: 5.7
Sequence Coverage [%]: 1.8
No. of unique Peptides: 1

```
        10         20         30         40         50         60         70         80
MLIGKGSLVM EGQKHLNSKK KGLKASFSLS LTFTSRLAPD PSLVIYAIFP SGGVVADKIQ FSVEMCFDNQ VSLGFSPSQQ
        90        100        110        120        130        140        150        160
LPGAEVELQL QAAPGSLCAL RAVDESVLLL RPDRELSNRS VYGMFPFWYG HYPYQVAEYD QCPVSGPWDF PQPLIDPMPQ
       170        180        190        200        210        220        230        240
GHSSQRSIIW RPSFSEGTDL FSFFRDVGLK ILSNAKIKKP VDCSHRSPEY STAMGAGGGH PEAFESSTPL HQAEDSQVRQ
       250        260        270        280        290        300        310        320
YFPETWLWDL FPIGNSGKEA VHVTVPDAIT EWKAMSFCTS QSRGFGLSPT VGLTAFKPFF VDLTLPYSVV RGESFRLTAT
       330        340        350        360        370        380        390        400
IFNYLKDCIR VQTDLAKSHE YQLESWADSQ TSSCLCADEA KTHHWNITAV KLGHINFTIS TKILDSNEPC GGQKGFVPQK
       410        420        430        440        450        460        470        480
GRSDTLIKPV LVKPEGVLVE KTHSSLLCPK GKVASESVSL ELPVDIVPDS TKAYVTVLGD IMGTALQNLD GLVQMPSGCG
       490        500        510        520        530        540        550        560
EQNMVLFAPI IYVLQYLEKA GLLTEEIRSR AVGFLEIGYQ KELMYKHSNG SYSAFGERDG NGNTWLTAFV TKCFGQAQKF
       570        580        590        600        610        620        630        640
IFIDPKNIQD ALKWMAGNQL PSGCYANVGN LLHTAMKGGV DDEVSLTAYV TAALLEMGKD VDDPMVSQGL RCLKNSATST
       650        660        670        680        690        700        710        720
TNLYTQALLA YIFSLAGEMD IRNILLKQLD QQAIISGESI YWSQKPTPSS NASPWSEPAA VDVELTAYAL LAQLTKPSLT
       730        740        750        760        770        780        790        800
QKEIAKATSI VAWLAKQRNA YGGFSSTQDT VVALQALAKY ATTAYMPSEE INLVVKSTEN FQRTFNIQSV NRLVFQQDTL
       810        820        830        840        850        860        870        880
PNVPGMYTLE ASGQGCVYVQ TVLRYNILPP TNMKTFSLSV EIGKARCEQP TSPRSLTLTI HTSYVGSRSS SNMAIVEVKM
       890        900        910        920        930        940        950        960
LSGFSPMEGT NQLLLQQPLV KKVEFGTDTL NIYLDELIKN TQTYTFTISQ SVLVTNLKPA TIKVYDYYLP DEQATIQYSD
       970
PCE
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2228	1	972.9750	-10.10	2	56.2	13.2	0	760-776	K.YATTAYMPSEEINLVVK.S	Oxidation: 7

Detailed Protein Report

Protein 701: pentraxin-4 [Homo sapiens]

Accession: gi|61966763
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 13.2
MW [kDa]: 51.3
pI: 10.8
Sequence Coverage [%]: 3.2
No. of unique Peptides: 1

Quantitation

WD:WU **Median:** 2.88 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MGSGNWEVTG	PPCGSRCERP	PGLPRGVHGQ	FRSAVGLSGL	RWFRRFQEVT	WTHLQNIASN	YNVSYNVDVR	FRSLAEESQA
90	100	110	120	130	140	150	160
VAQAVNRSQA	SVQGELAQLK	AWVRKLQRRG	RKVDTRLRAL	DLTLGERSQQ	RARERKAHKA	QRDALQDSLA	RLEGLVHSQG
170	180	190	200	210	220	230	240
ARLAALEGRL	PVAHPGTAAL	GPALVPTPTQ	PEELGPTSLK	LQRDRQELRA	ASEHRGPPQD	SSAPLQGRRE	PPASGSHRVL
250	260	270	280	290	300	310	320
SGTAPKDPRQ	QAWSPQVPGE	ICGVGPTLVF	PNASTRNVVF	LSPGFVTALR	ALSFCSWVRT	ASGRLGTLLS	YATEDNDNKL
330	340	350	360	370	380	390	400
VLHGRDSLLP	GSIHFVIGDP	AFRELPLQLL	LDGQWHHICV	IWTSTQGRYW	LHVDRRLVAT	GSRFREGYEI	PPGGSLVLGQ
410	420	430	440	450	460	470	480
EQDSVGGGFD	SSEAFVGSMS	GLAIWDRALV	PGEVANLAIG	KEFPTGAILT	LANAALAGGF	VQGANCTCLE	RCP

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
424	1	787.0347	168.04	2	33.8	13.2	0	73-87	R.SLAEESQAVAQAVNR.S		WD:WU 2.88

Detailed Protein Report

Protein 702: helicase SRCAP [Homo sapiens]

Accession:	gi|146219843	**Score:**	13.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	343.3
Database Date:	2015-11-30	**pI:**	5.6
		Sequence Coverage [%]:	0.6
		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 703: **potassium voltage-gated channel subfamily KQT member 2 isoform e [Homo sapiens]**

Accession: gi|26051268
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 13.2
MW [kDa]: 44.2
pI: 10.6
Sequence Coverage [%]: 3.3
No. of unique Peptides: 1

Quantitation

WD:WU **Median:** 2.72 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MVQKSRNGGV	YPGPSGEKKL	KVGFVGLDPG	APDSTRDGAL	LIAGSEAPKR	GSILSKPRAG	GAGAGKPPKR	NAFYRKLQNF
90	100	110	120	130	140	150	160
LYNVLERPRG	WAFIYHAYVF	LLVFSCLVLS	VFSTIKEYEK	SSEGALYILE	IVTIVVFGVE	YFVRIWAAGC	CCRYRGWRGR
170	180	190	200	210	220	230	240
LKFARKPFCV	IDIMVLIASI	AVLAAGSQGN	VFATSALRSL	RFLQILRMIR	MDRRGGTWKL	LGSVVYAHSK	ELVTAWYIGF
250	260	270	280	290	300	310	320
LCLILASFLV	YLAEKGENDH	FDTYADALWW	GLITLTTIGY	GDKYPQTWNG	RLLAATFTLI	GVSFFALPAG	ILGSGFALKV
330	340	350	360	370	380	390	400
QEQHRQKHFE	KRRNPAAGLI	QSAWRFYATN	LSRTDLHSTW	QYYERTVTVP	MYRYRRRAPA	TKQLFHFLFS	ICS

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1607	1	720.3800	-23.52	2	48.4	13.2	1	333-345	R.RNPAAGLIQSAWR.F		WD:WU 2.72

Detailed Protein Report

Protein 704: **metallothionein-1G [Homo sapiens]**

Accession: gi|10835230

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Modification(s): Carbamidomethyl

Score: 13.2

MW [kDa]: 6.1

pI: 10.5

Sequence Coverage [%]: 41.0

No. of unique Peptides: 1

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1987	2	862.6346	-31.70	3	53.2	13.2	2	1-25	-.MDPNCSCAAGVSCTCASSCKCKECK.C	Carbamidomethyl: 7

Detailed Protein Report

Protein 705: stathmin isoform a [Homo sapiens]

Accession:	gi|5031851	**Score:**	13.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	17.3
Database Date:	2015-11-30	**pI:**	5.7
		Sequence Coverage [%]:	12.1
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|44890052	refseq_human (refseq_human_20140103.fasta)	stathmin isoform a [Homo sapiens]
gi|44890050	refseq_human (refseq_human_20140103.fasta)	stathmin isoform a [Homo sapiens]

```
         10         20         30         40         50         60         70         80
MASSDIQVKE LEKRASGQAF ELILSPRSKE SVPEFPLSPP KKKDLSLEEI QKKLEAAEER RKSHEAEVLK QLAEKREHEK
         90        100        110        120        130        140        150
EVLQKAIEEN NNFSKMAEEK LTHKMEANKE NREAQMAAKL ERLREKDKHI EEVRKNKESK DPADETEAD
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2763	1	1022.5215	-40.47	2	63.0	13.2	2	10-27	K.ELEKRASGQAFELILSPR.S	

Detailed Protein Report

Protein 706: PREDICTED: protein PRR14L isoform X4 [Homo sapiens]

Accession:	gi|578837142	**Score:**	13.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	219.9
Database Date:	2015-11-30	**pI:**	6.2
		Sequence Coverage [%]:	0.8
		No. of unique Peptides:	1

Quantitation

WD:WU	**Median:**	0.75	**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
140	1	793.8794	36.37	2	31.0	13.1	0	632-646	K.NVSQENMCSASAAFK.S		WD:WU 0.75

Detailed Protein Report

Protein 707: ryanodine receptor 3 isoform 2 [Homo sapiens]

Accession:	gi|345842488	**Score:**	13.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	551.1
Database Date:	2015-11-30	**pI:**	5.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	0.4
		No. of unique Peptides:	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MAEGGEGGED	EIQFLRTEDE	VVLQCIATIH	KEQRKFCLAA	EGLGNRLCFL	EPTSEAKYIP	PDLCVCNFVL	EQSLSVRALQ
90	100	110	120	130	140	150	160
EMLANTGENG	GEGAAQGGGH	RTLLYGHAVL	LRHSFSGMYL	TCLTTSRSQT	DKLAFDVGLR	EHATGEACWW	TIHPASKQRS
170	180	190	200	210	220	230	240
EGEKVRIGDD	LILVSVSSER	YLHLSVSNGN	IQVDASFMQT	LWNVHPTCSG	SSIEEGYLLG	GHVVRLFHGH	DECLTIPSTD
250	260	270	280	290	300	310	320
QNDSQHRRIF	YEAGGAGTRA	RSLWRVEPLR	ISWSGSNIRW	GQAFRLRHLT	TGHYLALTED	QGLILQDRAK	SDTKSTAFSF
330	340	350	360	370	380	390	400
RASKELKEKL	DSSHKRDIEG	MGVPEIKYGD	SVCFVQHIAS	GLWVTYKAQD	AKTSRLGPLK	RKVILHQEGH	MDDGLTLQRC
410	420	430	440	450	460	470	480
QREESQAARI	IRNTTALFSQ	FVSGNNRTAA	PITLPIEEVL	QTLQDLIAYF	QPPEEEMRHE	DKQNKLRSLK	NRQNLFKEEG
490	500	510	520	530	540	550	560
MLALVLNCID	RLNVYNSVAH	FAGIAREESG	MAWKEILNLL	YKLLAALIRG	NRNNCAQFSN	NLDWLISKLD	RLESSSGILE
570	580	590	600	610	620	630	640
VLHCILTESP	EALNLIAEGH	IKSIISLLDK	HGRNHKVLDI	LCSLCLCNGV	AVRANQNLIC	DNLLPRRNLL	LQTRLINDVT
650	660	670	680	690	700	710	720
SIRPNIFLGV	AEGSAQYKKW	YFELIIDQVD	PFLTAEPTHL	RVGWASSSGY	APYPGGGEGW	GGNGVGDDLY	SYGFDGLHLW
730	740	750	760	770	780	790	800
SGRIPRAVAS	INQHLLRSDD	VVSCCLDLGV	PSISFRINGQ	PVQGMFENFN	TDGLFFPVMS	FSAGVKVRFL	MGGRHGEFKF
810	820	830	840	850	860	870	880
LPPSGYAPCY	EALLPKEKMR	LEPVKEYKRD	ADGIRDLLGT	TQFLSQASFI	PCPVDTSQVI	LPPHLEKIRD	RLAENIHELW
890	900	910	920	930	940	950	960
GMNKIELGWT	FGKIRDDNKR	QHPCLVEFSK	LPETEKNYNL	QMSTETLKTL	LALGCHIAHV	NPAAEEDLKK	VKLPKNYMMS
970	980	990	1000	1010	1020	1030	1040
NGYKPAPLDL	SDVKLLPPQE	ILVDKLAENA	HNVWAKDRIK	QGWTYGIQQD	LKNKRNPRLV	PYALLDERTK	KSNRDSLREA
1050	1060	1070	1080	1090	1100	1110	1120
VRTFVGYGYN	IEPSDQELAD	SAVEKVSIDK	IRFFRVERSY	AVRSGKWYFE	FEVVTGGDMR	VGWARPGCRP	DVELGADDQA
1130	1140	1150	1160	1170	1180	1190	1200
FVFEGNRGQR	WHQGSGYFGR	TWQPGDVVGC	MINLDDASMI	FTLNGELLIT	NKGSELAFAD	YEIENGFVPI	CCLGLSQIGR
1210	1220	1230	1240	1250	1260	1270	1280
MNLGTDASTF	KFYTMCGLQE	GFEPFAVNMN	RDVAMWFSKR	LPTFVNVPKD	HPHIEVMRID	GTMDSPPCLK	VTHKTFGTQN
1290	1300	1310	1320	1330	1340	1350	1360
SNADMIYCRL	SMPVECHSSF	SHSPCLDSEA	FQKRKQMQEI	LSHTTTQCYY	AIRIFAGQDP	SCVWVGWVTP	DYHLYSEKFD
1370	1380	1390	1400	1410	1420	1430	1440
LNKNCTVTVT	LGDERGRVHE	SVKRSNCYMV	WGGDIVASSQ	RSNRSNVDLE	IGCLVDLAMG	MLSFSANGKE	LGTCYQVEPN
1450	1460	1470	1480	1490	1500	1510	1520
TKVFPAVFLQ	PTSTSLFQFE	LGKLKNAMPL	SAAIFRSEEK	NPVPQCPPRL	DVQTIQPVLW	SRMPNSFLKV	ETERVSERHG
1530	1540	1550	1560	1570	1580	1590	1600
WVVQCLEPLQ	MMALHIPEEN	RCVDILELCE	QEDLMRFHYH	TLRLYSAVCA	LGNSRVAYAL	CSHVDLSQLF	YAIDNKYLPG
1610	1620	1630	1640	1650	1660	1670	1680
LLRSGFYDLL	ISIHLASAKE	RKLMMKNEYI	IPITSTTRNI	RLFPDESKRH	GLPGVGLRTC	LKPGFRFSTP	CFVVTGEDHQ
1690	1700	1710	1720	1730	1740	1750	1760
KQSPEIPLES	LRTKALSMLT	EAVQCSGAHI	RDPVGGSVEF	QFVPVLKLIG	TLLVMGVFDD	DDVRQILLLI	DPSVFGEHSA
1770	1780	1790	1800	1810	1820	1830	1840
GTEEGAEKEE	VTQVEEKAVE	AGEKAGKEAP	VKGLLQTRLP	ESVKLQMCEL	LSYLCDCELQ	HRVEAIVAFG	DIYVSKLQAN
1850	1860	1870	1880	1890	1900	1910	1920
QKFRYNELMQ	ALNMSAALTA	RKTKEFRSPP	QEQINMLLNF	QLGENCPCPE	EIREELYDFH	EDLLLHCGVP	LEEEEEEEED
1930	1940	1950	1960	1970	1980	1990	2000
TSWTGKLCAL	VYKIKGPPKP	EKEQPTEEEE	RCPTTLKELI	SQTMICWAQE	DQIQDSELVR	MMFNLLRRQY	DSIGELLQAL
2010	2020	2030	2040	2050	2060	2070	2080
RKTYTISHTS	VSDTINLLAA	LGQIRSLLSV	RMGKEEELLM	INGLGDIMNN	KVFYQHPNLM	RVLGMHETVM	EVMVNVLGTE
2090	2100	2110	2120	2130	2140	2150	2160
KSQIAFPKMV	ASCCRFLCYF	CRISRQNQKA	MFEHLSYLLE	NSSVGLASPS	MRGSTPLDVA	ASSVMDNNEL	ALSLEEPDLE
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
58	1	845.3504	-92.64	3	29.9	13.1	2	382-402	R.KVILHQEGHMDDGLTLQRCQR.E	Carbamidomethyl: 19

Detailed Protein Report

Protein 708: protein ARV1 [Homo sapiens]

Accession:	gi|12232479	**Score:**	13.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	31.0
Database Date:	2015-11-30	**pI:**	9.5
		Sequence Coverage [%]:	3.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGNGGRSGLQ	QGKGNVDGVA	ATPTAASASC	QYRCIECNQE	AKELYRDYNH	GVLKITICKS	CQKPVDKYIE	YDPVIILINA
90	100	110	120	130	140	150	160
ILCKAQAYRH	ILFNTQINIH	GKLCIFCLLC	EAYLRWWQLQ	DSNQNTAPDD	LIRYAKEWDF	YRMFAIAALE	QTAYFIGIFT
170	180	190	200	210	220	230	240
FLWVERPMTA	KKKPNFILLL	KALLLSSYGK	LLLIPAVIWE	HDYTSVCLKL	IKVFVLTSNF	QAIRVTLNIN	RKLSFLAVLS
250	260	270	280				
GLLLESIMVY	FFQSMEWDVG	SDYAIFKSQD	F				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2796	1	639.3467	71.37	2	63.5	13.1	1	134-142	R.YAKEWDFYR.M	

Detailed Protein Report

Protein 709: uncharacterized protein LOC100132994 [Homo sapiens]

Accession:	gi|223468690	**Score:**	13.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	54.4
Database Date:	2015-11-30	**pI:**	10.1
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.1
		No. of unique Peptides:	1

Quantitation

WD:WU	**Median:**	0.78	**CV:**	0.00 %	**No. of Peptides:**	1

Alias proteins:

Accession	Name	Description
gi|223468693	refseq_huma (refseq_human_20140103.fasta)	putative uncharacterized protein CXorf49 [Homo sapiens]

10	20	30	40	50	60	70	80
MSSPDKVSVC	GAGFDLEGGK	KAGSRTASPG	APGAHSHGLD	LGVPGSGDGK	SESGFTDPEG	FSFESESELI	EQGRVVLWGR
90	100	110	120	130	140	150	160
EGRPGTPVDD	QGDVVDYSFY	LADEPAAIVP	PPSVQGHPFP	EGAAAEGSAE	NWADAEVGPS	GRDVLGHSPG	KWQQASAGRL
170	180	190	200	210	220	230	240
HLCGPGPVRA	WKNPERGSKS	RWSLRVDPQQ	PSAKGPTRLP	THDSDSADES	SDLPLMKVGI	CRNEGSQAKP	GSPKKRADTS
250	260	270	280	290	300	310	320
RQASFHCKES	YLPVPGRFLT	SAPRGLTPVA	ERPAVGELED	SPQKKMQSRA	WGKVEVRPSC	SGAAAAGALP	QGLSRRKMAG
330	340	350	360	370	380	390	400
GKKSLGGASQ	LALGRGFPAC	GERLSAAPPE	PATFPPFSGV	RPQGMSKKPQ	KPKHSSPGKK	PAGRKTRESQ	AAAREDNDPN
410	420	430	440	450	460	470	480
RDEVPRAQLP	THRPGLPRLS	VRRGEFSSSD	PNIRAPQLPG	TSEPSAYSPG	GLVPRRHAPS	GNQQPPVHPP	RPERQQQPPG
490	500	510	520				
AQGCPRCIWL	QREIEDLTQQ	LAAMQFLTDK	FQDL				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
198	1	938.4465	-16.72	2	31.3	13.1	1	242-257	R.QASFHCKESYLPVPGR.F	Carbamidomethyl: 6	WD:WU	0.78

Detailed Protein Report

Protein 710: 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	1	635.5460	-95.49	3	33.3	13.1	2	407-422	R.CPCYSNRKACLDCICR.G	Carbamidomethyl: 1

Detailed Protein Report

Protein 711: U11/U12 small nuclear ribonucleoprotein 25 kDa protein [Homo sapiens]

Accession: gi|13443018
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 13.1
MW [kDa]: 15.3
pI: 9.0
Sequence Coverage [%]: 5.3
No. of unique Peptides: 1

```
         10         20         30         40         50         60         70         80
MDVFQEGLAM VVQDPLLCDL PIQVTLEEVN SQIALEYGQA MTVRVCKMDG EVMPVVVVQS ATVLDLKKAI QRYVQLKQER
         90        100        110        120        130        140
EGGIQHISWS YVWRTYHLTS AGEKLTEDRK KLRDYGIRNR DEVSFIKKLR QK
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1247	1	419.0865	-321.45	2	43.9	13.1	0	121-127	R.DEVSFIK.K	

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Detailed Protein Report

Protein 712: ran GTPase-activating protein 1 [Homo sapiens]

Accession:	gi|4506411	**Score:**	13.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	63.5
Database Date:	2015-11-30	**pI:**	4.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.0
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578837322	refseq_human (refseq_human_20140103.fasta)	PREDICTED: ran GTPase-activating protein 1 isoform X3 [Homo sapiens]
gi|520975387	refseq_human (refseq_human_20140103.fasta)	ran GTPase-activating protein 1 [Homo sapiens]

10	20	30	40	50	60	70	80
MASEDIAKLA	ETLAKTQVAG	GQLSFKGKSL	KLNTAEDAKD	VIKEIEDFDS	LEALRLEGNT	VGVEAARVIA	KALEKKSELK
90	100	110	120	130	140	150	160
RCHWSDMFTG	RLRTEIPPAL	ISLGEGLITA	GAQLVELDLS	DNAFGPDGVQ	GFEALLKSSA	CFTLQELKLN	NCGMGIGGGK
170	180	190	200	210	220	230	240
ILAAALTECH	RKSSAQGKPL	ALKVFVAGRN	RLENDGATAL	AEAFRVIGTL	EEVHMPQNGI	NHPGITALAQ	AFAVNPLLRV
250	260	270	280	290	300	310	320
INLNDNTFTE	KGAVAMAETL	KTLRQVEVIN	FGDCLVRSKG	AVAIADAIRG	GLPKLKELNL	SFCEIKRDAA	LAVAEAMADK
330	340	350	360	370	380	390	400
AELEKLDLNG	NTLGEEGCEQ	LQEVLEGFNM	AKVLASLSDD	EDEEEEEEGE	EEEEEAEEEE	EEDEEEEEEE	EEEEEEEPQQ
410	420	430	440	450	460	470	480
RGQGEKSATP	SRKILDPNTG	EPAPVLSSPP	PADVSTFLAF	PSPEKLLRLG	PKSSVLIAQQ	TDTSDPEKVV	SAFLKVSSVF
490	500	510	520	530	540	550	560
KDEATVRMAV	QDAVDALMQK	AFNSSSFNSN	TFLTRLLVHM	GLLKSEDKVK	AIANLYGPLM	ALNHMVQQDY	FPKALAPLLL
570	580	590					
AFVTKPNSAL	ESCSFARHSL	LQTLYKV					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2615	1	589.1847	-155.39	2	61.0	13.1	0	149-160	K.LNNCGMGIGGGK.I	Carbamidomethyl: 4

Protein 713: 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 714: UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 7 [Homo sapiens]

Accession: gi|21687139
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 13.1
MW [kDa]: 46.0
pI: 10.0
Sequence Coverage [%]: 4.0
No. of unique Peptides: 1

```
        10         20         30         40         50         60         70         80
MSLWKKTVYR SLCLALALLV AVTVFQRSLT PGQFLQEPPP PTLEPQKAQK PNGQLVNPNN FWKNPKDVAA PTPMASQGPQ
        90        100        110        120        130        140        150        160
AWDVTTTNCS ANINLTHQPW FQVLEPQFRQ FLFYRHCRYF PMLLNHPEKC RGDVYLLVVV KSVITQHDRR EAIRQTWGRE
       170        180        190        200        210        220        230        240
RQSAGGGRGA VRTLFLLGTA SKQEERTHYQ QLLAYEDRLY GDILQWGFLD TFFNLTLKEI HFLKWLDIYC PHVPFIFKGD
       250        260        270        280        290        300        310        320
DDVFVNPTNL LEFLADRQPQ ENLFVGDVLQ HARPIRRKDN KYYIPGALYG KASYPPYAGG GGFLMAGSLA RRLHHACDTL
       330        340        350        360        370        380        390        400
ELYPIDDVFL GMCLEVLGVQ PTAHEGFKTF GISRNRNSRM NKEPCFFRAM LVVHKLLPPE LLAMWGLVHS NLTCSRKLQV
       410
L
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2975	1	619.0047	20.87	3	66.0	13.1	0	48-63	K.AQKPNGQLVNPNNFWK.N	

Detailed Protein Report

Protein 715: **small conductance calcium-activated potassium channel protein 1 [Homo sapiens]**

Accession:	gi|25777643	**Score:**	13.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	59.9
Database Date:	2015-11-30	**pI:**	9.8
		Sequence Coverage [%]:	2.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MNSHSYNGSV	GRPLGSGPGA	LGRDPPDPEA	GHPPQPPHSP	GLQVVVAKSE	PARPSPGSPR	GQPQDQDDDE	DDEEDEAGRQ
90	100	110	120	130	140	150	160
RASGKPSNVG	HRLGHRRALF	EKRKRLSDYA	LIFGMFGIVV	MVTETELSWG	VYTKESLYSF	ALKCLISLST	AILLGLVVLY
170	180	190	200	210	220	230	240
HAREIQLFMV	DNGADDWRIA	MTCERVFLIS	LELAVCAIHP	VPGHYRFTWT	ARLAFTYAPS	VAEADVDVLL	SIPMFLRLYL
250	260	270	280	290	300	310	320
LGRVMLLHSK	IFTDASSRSI	GALNKITFNT	RFVMKTLMTI	CPGTVLLVFS	ISSWIIAAWT	VRVCERYHDK	QEVTSNFLGA
330	340	350	360	370	380	390	400
MWLISITFLS	IGYGDMVPHT	YCGKGVCLLT	GIMGAGCTAL	VVAVVARKLE	LTKAEKHVHN	FMMDTQLTKR	VKNAAANVLR
410	420	430	440	450	460	470	480
ETWLIYKHTR	LVKKPDQARV	RKHQRKFLQA	IHQAQKLRSV	KIEQGKLNDQ	ANTLTDLAKT	QTVMYDLVSE	LHAQHEELEA
490	500	510	520	530	540	550	
RLATLESRLD	ALGASLQALP	GLIAQAIRPP	PPPLPPRPGP	GPQDQAARSS	PCRWTPVAPS	DCG	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2958	1	724.8727	-73.27	2	65.7	13.1	2	408-419	K.HTRLVKKPDQAR.V	

Detailed Protein Report

Protein 716: ICOS ligand isoform a precursor [Homo sapiens]

Accession:	gi|27477039	**Score:**	13.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	33.3
Database Date:	2015-11-30	**pI:**	5.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	5.3
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578836292	refseq_human (refseq_human_20140103.fasta)	PREDICTED: ICOS ligand-like isoform X2 [Homo sapiens]
gi|578797797	refseq_human (refseq_human_20140103.fasta)	PREDICTED: ICOS ligand-like isoform X2 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MRLGSPGLLF LLFSSLRADT QEKEVRAMVG SDVELSCACP EGSRFDLNDV YVYWQTSESK TVVTYHIPQN SSLENVDSRY
        90        100        110        120        130        140        150        160
RNRALMSPAG MLRGDFSLRL FNVTPQDEQK FHCLVLSQSL GFQEVLSVEV TLHVAANFSV PVVSAPHSPS QDELTFTCTS
       170        180        190        200        210        220        230        240
INGYPRPNVY WINKTDNSLL DQALQNDTVF LNMRGLYDVV SVLRIARTPS VNIGCCIENV LLQQNLTVGS QTGNDIGERD
       250        260        270        280        290        300        310
KITENPVSTG EKNAATWSIL AVLCLLVVVA VAIGWVCRDR CLQHSYAGAW AVSPETELTG HV
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2987	2	869.4191	-26.75	2	66.1	13.0	1	84-99	R.ALMSPAGMLRGDFSLR.L	Oxidation: 3

Detailed Protein Report

Protein 717: PREDICTED: UPF0692 protein C19orf54 isoform X1 [Homo sapiens]

Accession:	gi|530416253	**Score:**	13.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	33.2
Database Date:	2015-11-30	**pI:**	11.1
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.2
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578834306	refseq_human(refseq_human_20140103.fasta)	PREDICTED: UPF0692 protein C19orf54 isoform X6 [Homo sapiens]
gi|578834304	refseq_human(refseq_human_20140103.fasta)	PREDICTED: UPF0692 protein C19orf54 isoform X5 [Homo sapiens]

10	20	30	40	50	60	70	80
MTSPCSPPLK	PPISPPKTPV	PQASSIPSPP	LPPSPLDFSA	LPSPPWSQQT	PVPPPLPLPP	PPAATGPAPR	HVFGLEKSQL
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
LKEAFDKAGP	VPKGREDVKR	LLKLHKDRFR	GDLRWILFCA	DLPSLIQEGP	QCGLVALWMA	GTLLSPPSGV	PLERLIRVAT
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
ERGYTAQGEM	FSVADMGRLA	QEVLGCQAKL	LSGGLGGPNR	DLVLQHLVTG	HPLLIPYDED	FNHEPCQRKG	HKAHWAGSCW
250	**260**	**270**	**280**	**290**	**300**	**310**	
VFGLCPVSAT	LRTLSCRACS	TQCWARPANH	HPCQRRAPRE	LSTCCPSRAR	VGTISCGTTT	RSGRATCS	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2691	1	690.3641	10.83	2	62.0	13.0	1	289-301	R.ARVGTISCGTTTR.S	Carbamidomethyl: 8

Detailed Protein Report

Protein 718: **PREDICTED: double zinc ribbon and ankyrin repeat-containing protein 1 isoform X7 [Homo sapiens]**

Accession:	gi|578835454	**Score:**	13.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	76.5
Database Date:	2015-11-30	**pI:**	9.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.0
		No. of unique 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
1524	2	829.3909	-6.37	2	47.8	13.0	0	22-35	K.ANHEIDNNTLLEMK.S	Oxidation: 13

Detailed Protein Report

Protein 719: 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 720: transcription factor p65 isoform 4 [Homo sapiens]

Accession: gi|345842445
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 13.0
MW [kDa]: 49.5
pI: 7.8
Sequence Coverage [%]: 6.0
No. of unique Peptides: 1

```
        10         20         30         40         50         60         70         80
MDELFPLIFP AEPAQASGPY VEIIEQPKQR GMRFRYKCEG RSAGSIPGER STDTTKTHPT IKINGYTGPG TVRISLVTKD
        90        100        110        120        130        140        150        160
PPHRPHPHEL VGKDCRDGFY EAELCPDRCI HSFQNLGIQC VKKRDLEQAI SQRIQTNNNP FQVPIEEQRG DYDLNAVRLC
       170        180        190        200        210        220        230        240
FQVTVRDPSG RPLRLPPVLS HPIFDNRAPN TAELKICRVN RNSGSCLGGD EIFLLCDKVQ KEDIEVYFTG PGWEARGSFS
       250        260        270        280        290        300        310        320
QADVHRQVAI VFRTPPYADP SLQAPVRVSM QLRRPSDREL SEPMEFQYLP DTDDRHRIEE KRKRTYETFK SIMKKSPFSG
       330        340        350        360        370        380        390        400
PTDPRPPPRR IAVPSRSSAS VPKPAPQPYP FTSSLSTINY DEFPTMVFPS GQISQASALA PAPPQVLPQA PAPAPAPAMV
       410        420        430        440        450
SALAQRPPDP APAPLGAPGL PNGLLSGDED FSSIADMDFS ALLSQISS
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1871	1	1057.5041	3.81	3	51.7	13.0	2	97-123	R.DGFYEAELCPDRCIHSFQNLGIQCVKK.R	Carbamidomethyl: 24

Detailed Protein Report

Protein 721: 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

Detailed Protein Report

Protein 722: gamma-glutamylcyclotransferase isoform 3 [Homo sapiens]

Accession:	gi|315360620	**Score:**	13.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	12.9
Database Date:	2015-11-30	**pI:**	9.6
		Sequence Coverage [%]:	14.0
		No. of unique Peptides:	1

```
         10         20         30         40         50         60         70         80
MANSGCKDVT GPDEESFLYF AYGSNLLTER IHLRNPSAAF FCVARLQDFK LDFGNSQGKT SQTWHGGIAT IFQSPGDEVW
         90        100        110        120
GVVWKMNKSN LNSLDELFAW VQKKMVCRWS IKRS
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2373	1	907.3649	-100.81	2	57.9	13.0	1	35-50	R.NPSAAFFCVARLQDFK.L	

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Detailed Protein Report

Protein 723: peptidyl-prolyl cis-trans isomerase FKBP5 isoform 1 [Homo sapiens]

Accession:	gi|4758384	**Score:**	13.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	51.2
Database Date:	2015-11-30	**pI:**	5.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.7
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|224809329	refseq_human (refseq_human_20140103.fasta)	peptidyl-prolyl cis-trans isomerase FKBP5 isoform 1 [Homo sapiens]
gi|224809327	refseq_human (refseq_human_20140103.fasta)	peptidyl-prolyl cis-trans isomerase FKBP5 isoform 1 [Homo sapiens]

10	20	30	40	50	60	70	80
MTTDEGAKNN	EESPTATVAE	QGEDITSKKD	RGVLKIVKRV	GNGEETPMIG	DKVYVHYKGK	LSNGKKFDSS	HDRNEPFVFS
90	100	110	120	130	140	150	160
LGKGQVIKAW	DIGVATMKKG	EICHLLCKPE	YAYGSAGSLP	KIPSNATLFF	EIELLDFKGE	DLFEDGGIIR	RTKRKGEGYS
170	180	190	200	210	220	230	240
NPNEGATVEI	HLEGRCGGRM	FDCRDVAFTV	GEGEDHDIPI	GIDKALEKMQ	REEQCILYLG	PRYGFGEAGK	PKFGIEPNAE
250	260	270	280	290	300	310	320
LIYEVTLKSF	EKAKESWEMD	TKEKLEQAAI	VKEKGTVYFK	GGKYMQAVIQ	YGKIVSWLEM	EYGLSEKESK	ASESFLLAAF
330	340	350	360	370	380	390	400
LNLAMCYLKL	REYTKAVECC	DKALGLDSAN	EKGLYRRGEA	QLLMNEFESA	KGDFEKVLEV	NPQNKAARLQ	ISMCQKKAKE
410	420	430	440	450	460		
HNERDRRIYA	NMFKKFAEQD	AKEEANKAMG	KKTSEGVTNE	KGTDSQAMEE	EKPEGHV		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2372	1	911.8056	-124.45	2	57.9	13.0	1	336-352	K.AVECCDKALGLDSANEK.G	Carbamidomethyl: 4

Detailed Protein Report

Protein 724: myelin transcription factor 1 [Homo sapiens]

Accession:	gi|17975763	**Score:**	13.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	122.3
Database Date:	2015-11-30	**pI:**	4.7
		Sequence Coverage [%]:	0.9
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 1.14 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MSLENEDKRA	RTRSKALRGP	PETTAADLSC	PTPGCTGSGH	VRGKYSRHRS	LQSCPLAKKR	KLEGAEAEHL	VSKRKSHPLK
90	100	110	120	130	140	150	160
LALDEGYGVD	SDGSEDTEVK	DASVSDESEG	TLEGAEAETS	GQDEIHRPET	AEGRSPVKSH	FGSNPIGSAT	ASSKGSYSSY
170	180	190	200	210	220	230	240
QGIIATSLLN	LGQIAEETLV	EEDLGQAAKP	GPGIVHLLQE	AAEGAASEEG	EKGLFIQPED	AEEVVEVTTE	RSQDLCPQSL
250	260	270	280	290	300	310	320
EDAASEESSK	QKGILSHEEE	DEEEEEEEEE	EEEDEEEEEE	EEEEEEEEEE	EEEEEEEEEE	EEEEEEAAPD	VIFQEDTSHT
330	340	350	360	370	380	390	400
SAQKAPELRG	PESPSPKPEY	SVIVEVRSDD	DKDEDTHSRK	STVTDESEMQ	DMMTRGNLGL	LEQAIALKAE	QVRTVCEPGC
410	420	430	440	450	460	470	480
PPAEQSQLGL	GEPGKAAKPL	DTVRKSYYSK	DPSRAEKREI	KCPTPGCDGT	GHVTGLYPHH	RSLSGCPHKD	RIPPEILAMH
490	500	510	520	530	540	550	560
ENVLKCPTPG	CTGQGHVNSN	RNTHRSLSGC	PIAAAEKLAK	SHEKQQPQTG	DPSKSSSNSD	RILRPMCFVK	QLEVPPYGSY
570	580	590	600	610	620	630	640
RPNVAPATPR	ANLAKELEKF	SKVTFDYASF	DAQVFGKRML	APKIQTSETS	PKAFQCFDYS	QDAEAAHMAA	TAILNLSTRC
650	660	670	680	690	700	710	720
WEMPENLSTK	PQDLPSKSVD	IEVDENGTLD	LSMHKHRKRE	NAFPSSSSCS	SSPGVKSPDA	SQRHSSTSAP	SSSMTSPQSS
730	740	750	760	770	780	790	800
QASRQDEWDR	PLDYTKPSRL	REEEPEESEP	AAHSFASSEA	DDQEVSEENF	EERKYPGEVT	LTNFKLKFLS	KDIKKELLTC
810	820	830	840	850	860	870	880
PTPGCDGSGH	ITGNYASHRS	LSGCPLADKS	LRNLMAAHSA	DLKCPTPGCD	GSGHITGNYA	SHRSLSGCPR	AKKSGVKVAP
890	900	910	920	930	940	950	960
TKDDKEDPEL	MKCPVPGCVG	LGHISGKYAS	HRSASGCPLA	ARRQKEGSLN	GSSFSWKSLK	NEGPTCPTPG	CDGSGHANGS
970	980	990	1000	1010	1020	1030	1040
FLTHRSLSGC	PRATFAGKKG	KLSGDEVLSP	KFKTSDVLEN	DEEIKQLNQE	IRDLNESNSE	MEAAMVQLQS	QISSMEKNLK
1050	1060	1070	1080	1090	1100	1110	1120
NIEEENKLIE	EQNEALFLEL	SGLSQALIQS	LANIRLPHME	PICEQNFDAY	VSTLTDMYSN	QDPENKDLLE	SIKQAVRGIQ
1130							
V							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
234	1	1074.6988	94.18	1	31.7	13.0	1	50-59	R.SLQSCPLAKK.R		WD:WU	1.14

Detailed Protein Report

Protein 725: **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 726: 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 727: **NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial isoform 2 [Homo sapiens]**

Accession:	gi|548923801	**Score:**	13.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	20.0
Database Date:	2015-11-30	**pI:**	7.8
		Sequence Coverage [%]:	9.3
		No. of unique Peptides:	1

```
         10         20         30         40         50         60         70         80
MAVARAGVLG VQWLQRASRN VMPLGARTAS HMTKDMFPGP YPRTPEERAA AAKKYNMRVE DYEPYPDDGM GYGDYPKLPD
         90        100        110        120        130        140        150        160
RSQHERDPWY SWDQPGLRLN WGEPMHWHLD MYNRNRVDTS PTPVSWHVMC MQLFGFLAFM IFMCWVGDVY PVYQPVCRHH
        170        180
FSYNLGFLSA LG
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1939	1	918.3463	-93.31	2	52.9	13.0	1	28-43	R.TASHMTKDMFPGPYPR.T	

Detailed Protein Report

Protein 728: centromere protein J [Homo sapiens]

Accession:	gi|130980075	**Score:**	13.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	152.9
Database Date:	2015-11-30	**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 729: splicing factor, arginine/serine-rich 19 [Homo sapiens]

Accession:	gi|226509740	**Score:**	13.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	139.2
Database Date:	2015-11-30	**pI:**	9.9
		Sequence Coverage [%]:	1.4
		No. of unique Peptides:	1

Quantitation

WD:WU	**Median:** 0.73	**CV:** 0.00 %	**No. of Peptides:** 1

Alias proteins:

Accession	Name	Description
gi|530416968	refseq_human (refseq_human_20140103.fasta)	PREDICTED: splicing factor, arginine/serine-rich 19 isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MEEEDESRGK	TEESGEDRGD	GPPDRDPTLS	PSAFILRAIQ	QAVGSSLQGD	LPNDKDGSRC	HGLRWRRCRS	PRSEPRSQES
90	100	110	120	130	140	150	160
GGTDTATVLD	MATDSFLAGL	VSVLDPPDTW	VPSRLDLRPG	ESEDMLELVA	EVRIGDRDPI	PLPVPSLLPR	LRAWRTGKTV
170	180	190	200	210	220	230	240
SPQSNSSRPT	CARHLTLGTG	DGGPAPPPAP	SSASSSPSPS	PSSSSPSPPP	PPPPPAPPAP	PAPRFDIYDP	FHPTDEAYSP
250	260	270	280	290	300	310	320
PPAPEQKYDP	FEPTGSNPSS	SAGTPSPEEE	EEEEEEEEEE	EEDEEEEEGL	SQSISRISET	LAGIYDDNSL	SQDFPGDESP
330	340	350	360	370	380	390	400
RPDAQPTQPT	PAPGTPPQVD	STRADGAMRR	RVFVVGTEAE	ACREGKVSVE	VVTAGGAALP	PPLLPPGDSE	IEEGEIVQPE
410	420	430	440	450	460	470	480
EEPRLALSLF	RPGGRAARPT	PAASATPTAQ	PLPQPPAPRA	PEGDDFLSLH	AESDGEGALQ	VDLGEPAPAP	PAADSRWGGL
490	500	510	520	530	540	550	560
DLRRKILTQR	RERYRQRSPS	PAPAPAPAAA	AGPPTRKKSR	RERKRSGEAK	EAASSSSGTQ	PAPPAPASPW	DSKKHRSRDR
570	580	590	600	610	620	630	640
KPGSHASSSA	RRRSRSRSRS	RSTRRRSRST	DRRRGGSRRS	RSREKRRRRR	RSASPPPATS	SSSSSRRERH	RGKHRDGGGS
650	660	670	680	690	700	710	720
KKKKKRSRSR	GEKRSGDGSE	KAPAPAPPPS	GSTSCGDRDS	RRRGAVPPSI	QDLTDHDLFA	IKRTITVGRL	DKSDPRGPSP
730	740	750	760	770	780	790	800
APASSPKREV	LYDSEGLSGE	ERGGKSSQKD	RRRSGAASSS	SSSREKGSRR	KALDGGDRDR	DRDRDRDRDR	SSKKARPPKE
810	820	830	840	850	860	870	880
SAPSSGPPPK	PPVSSGSGSS	SSSSSCSSRK	VKLQSKVAVL	IREGVSSTTP	AKDAASAGLG	SIGVKFSRDR	ESRSPFLKPD
890	900	910	920	930	940	950	960
ERAPTEMAKA	APGSTKPKKT	KVKAKAGAKK	TKGTKGKTKP	SKTRKKVRSG	GGSGGSGGQV	SLKKSKADSC	SQAAGTKGAE
970	980	990	1000	1010	1020	1030	1040
ETSWSGEERA	AKVPSTPPPK	AAPPPPALTP	DSQTVDSSCK	TPEVSFLPEE	ATEEAGVRGG	AEEEEEEEEE	EEEEEEEEEQ
1050	1060	1070	1080	1090	1100	1110	1120
QPATTTATST	AAAAPSTAPS	AGSTAGDSGA	EDGPASRVSQ	LPTLPPPMPW	NLPAGVDCTT	SGVLALTALL	FKMEEANLAS
1130	1140	1150	1160	1170	1180	1190	1200
RAKAQELIQA	TNQILSHRKP	PSSLGMTPAP	VPTSLGLPPG	PSSYLLPGSL	PLGGCGSTPP	TPTGLAATSD	KREGSSSSEG
1210	1220	1230	1240	1250	1260	1270	1280
RGDTDKYLKK	LHTQERAVEE	VKLAIKPYYQ	KKDITKEEYK	DILRKAVHKI	CHSKSGEINP	VKVSNLVRAY	VQRYRYFRKH
1290	1300	1310	1320				
GRKPGDPPGP	PRPPKEPGPP	DKGGPGLPLP	PL				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
54	1	809.3848	-64.53	2	29.9	13.0	2	927-944	K.VRSGGGSGGSGGQVSLKK.S		WD:WU 0.73

Detailed Protein Report

Protein 730: methylcytosine dioxygenase TET1 [Homo sapiens]

Accession:	gi|156139122	**Score:**	13.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	235.2
Database Date:	2015-11-30	**pI:**	9.4
Modification(s):	Oxidation	**Sequence Coverage [%]:**	0.8
		No. of unique Peptides:	1

Quantitation

WD:WU	**Median:**	0.65	**CV:**	0.00 %	**No. of Peptides:**	1	

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		

Detailed Protein Report

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	WD:WU 0.65

Detailed Protein Report

Protein 731: 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 732: gamma-aminobutyric acid receptor subunit delta precursor [Homo sapiens]

Accession:	gi|34734071	**Score:**	13.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	50.7
Database Date:	2015-11-30	**pI:**	9.3
		Sequence Coverage [%]:	2.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDAPARLLAP	LLLLCAQQLR	GTRAMNDIGD	YVGSNLEISW	LPNLDGLIAG	YARNFRPGIG	GPPVNVALAL	EVASIDHISE
90	100	110	120	130	140	150	160
ANMEYTMTVF	LHQSWRDSRL	SYNHTNETLG	LDSRFVDKLW	LPDTFIVNAK	SAWFHDVTVE	NKLIRLQPDG	VILYSIRITS
170	180	190	200	210	220	230	240
TVACDMDLAK	YPMDEQECML	DLESYGYSSE	DIVYYWSESQ	EHIHGLDKLQ	LAQFTITSYR	FTTELMNFKS	AGQFPRLSLH
250	260	270	280	290	300	310	320
FHLRRNRGVY	IIQSYMPSVL	LVAMSWVSFW	ISQAAVPARV	SLGITTVLTM	TTLMVSARSS	LPRASAIKAL	DVYFWICYVF
330	340	350	360	370	380	390	400
VFAALVEYAF	AHFNADYRKK	QKAKVKVSRP	RAEMDVRNAI	VLFSLSAAGV	TQELAISRRQ	RRVPGNLMGS	YRSVGVETGE
410	420	430	440	450	460		
TKKEGAARSG	GQGGIRARLR	PIDADTIDIY	ARAVFPAAFA	AVNVIYWAAY	AM		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1088	2	565.6602	-213.89	2	41.9	13.0	0	221-229	R.FTTELMNFK.S	

Detailed Protein Report

Protein 733: protein dispatched homolog 2 [Homo sapiens]

Accession: gi|25121980
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 12.9
MW [kDa]: 151.9
pI: 9.3
Sequence Coverage [%]: 0.6
No. of unique Peptides: 1

Quantitation

WD:WU **Median:** 0.64 **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	1	1011.8041	245.60	1	51.7	12.9	0	811-818	R.WLLALCHR.A		WD:WU 0.64

Detailed Protein Report

Protein 734: 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 735: 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 736: 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 737: apolipoprotein L3 isoform 3 [Homo sapiens]

Accession:	gi|22035648	**Score:**	12.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	21.6
Database Date:	2015-11-30	**pI:**	9.5
		Sequence Coverage [%]:	8.9
		No. of unique Peptides:	1

Quantitation

WD:WU	**Median:** 0.69	**CV:**	0.00 %	**No. of Peptides:**	1

Alias proteins:

Accession	Name	Description
gi|22035650	refseq_human (refseq_human_20140103.fasta)	apolipoprotein L3 isoform 3 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MSLAGLVLAP FTAGTSLALT AAGVGLGAAS AVTGITTSIV EHSYTSSAEA EASRLTATSI DRLKVFKEVM RDITPNLLSL
        90        100        110        120        130        140        150        160
LNNYYEATQT IGSEIRAIRQ ARARARLPVT TWRISAGSGG QAERTIAGTT RAVSRGARIL SATTSGIFLA LDVVNLVYES
       170        180        190        200        210
KHLHEGAKSA SAEELRRQAQ ELEENLMELT QIYQRLNPCH TH
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
729	1	866.9494	-1.19	2	37.9	12.9	1	114-131	R.ISAGSGGQAERTIAGTTR.A		WD:WU 0.69

Detailed Protein Report

Protein 738: relaxin receptor 2 isoform 1 [Homo sapiens]

Accession:	gi|18677729	**Score:**	12.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	86.4
Database Date:	2015-11-30	**pI:**	10.0
		Sequence Coverage [%]:	2.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MIVFLVFKHL	FSLRLITMFF	LLHFIVLINV	KDFALTQGSM	ITPSCQKGYF	PCGNLTKCLP	RAFHCDGKDD	CGNGADEENC
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
GDTSGWATIF	GTVHGNANSV	ALTQECFLKQ	YPQCCDCKET	ELECVNGDLK	SVPMISNNVT	LLSLKKNKIH	SLPDKVFIKY
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
TKLKKIFLQH	NCIRHISRKA	FFGLCNLQIL	YLNHNCITTL	RPGIFKDLHQ	LTWLILDDNP	ITRISQRLFT	GLNSLFFLSM
250	**260**	**270**	**280**	**290**	**300**	**310**	**320**
VNNYLEALPK	QMCAQMPQLN	WVDLEGNRIK	YLTNSTFLSC	DSLTVLFLPR	NQIGFVPEKT	FSSLKNLGEL	DLSSNTITEL
330	**340**	**350**	**360**	**370**	**380**	**390**	**400**
SPHLFKDLKL	LQKLNLSSNP	LMYLHKNQFE	SLKQLQSLDL	ERIEIPNINT	RMFQPMKNLS	HIYFKNFRYC	SYAPHVRICM
410	**420**	**430**	**440**	**450**	**460**	**470**	**480**
PLTDGISSFE	DLLANNILRI	FVWVIAFITC	FGNLFVIGMR	SFIKAENTTH	AMSIKILCCA	DCLMGVYLFF	VGIFDIKYRG
490	**500**	**510**	**520**	**530**	**540**	**550**	**560**
QYQKYALLWM	ESVQCRLMGF	LAMLSTEVSV	LLLTYLTLEK	FLVIVFPFSN	IRPGKRQTSV	ILICIWMAGF	LIAVIPFWNK
570	**580**	**590**	**600**	**610**	**620**	**630**	**640**
DYFGNFYGKN	GVCFPLYYDQ	TEDIGSKGYS	LGIFLGVNLL	AFLIIVFSYI	TMFCSIQKTA	LQTTEVRNCF	GREVAVANRF
650	**660**	**670**	**680**	**690**	**700**	**710**	**720**
FFIVFSDAIC	WIPVFVVKIL	SLFRVEIPDT	MTSWIVIFFL	PVNSALNPIL	YTLTTNFFKD	KLKQLLHKHQ	RKSIFKIKKK
730	**740**	**750**	**760**				
SLSTSIVWIE	DSSSLKLGVL	NKITLGDSIM	KPVS				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
869	1	764.0295	-45.76	3	39.3	12.9	0	271-290	K.YLTNSTFLSCDSLTVLFLPR.N	

Detailed Protein Report

Protein 739: metallothionein-1B [Homo sapiens]

Accession:	gi|27414495	**Score:**	12.9
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	

Protein 740: 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 741: 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 742: **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 743: **F-box/LRR-repeat protein 19 isoform 3 [Homo sapiens]**

Accession:	gi|537544651	**Score:**	12.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	42.2
Database Date:	2015-11-30	**pI:**	11.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MCQLLERVPD	TSSSSSDSDS	DSDSSGTSLS	EDEAPGEARN	GRRPARGSSG	EKENRGGRRA	VRPGSGGPLL	SWPLGPAPPP
90	100	110	120	130	140	150	160
RPPQLERHVV	RPPPRSPEPD	TLPLAAGSDH	PLPRAAWLRV	FQHLGPRELC	ICMRVCRTWS	RWCYDKRLWP	RMDLSRRKSL
170	180	190	200	210	220	230	240
TPPMLSGVVR	RQPRALDLSW	TGVSKKQLMW	LLNRLQGLQE	LVLSGCSWLS	VSALGSAPLP	ALRLLDLRWI	EDVKDSQLRE
250	260	270	280	290	300	310	320
LLLPPPDTKP	GQTESRGRLQ	GVAELRLAGL	ELTDASLRLL	LRHAPQLSAL	DLSHCAHVGD	PSVHLLTAPT	SPLRETLVHL
330	340	350	360	370	380	390	
NLAGCHRLTD	HCLPLFRRCP	RLRRLDLRSC	RQLSPEACAR	LAAAGPPGPF	RCPEEKLLLK	DS	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
601	1	460.1164	-274.12	2	35.9	12.8	1	345-351	R.LDLRSCR.Q	Carbamidomethyl: 6

Detailed Protein Report

Protein 744: **zinc finger SWIM domain-containing protein 3 [Homo sapiens]**

Accession:	gi|57863255	**Score:**	12.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	79.4
Database Date:	2015-11-30	**pI:**	7.9
Modification(s):	Carbamidomethyl	**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

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Detailed Protein Report

Protein 745: PREDICTED: pre-mRNA-splicing factor CWC22-like [Homo sapiens]

Accession:	gi|578818185	**Score:**	12.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	41.1
Database Date:	2015-11-30	**pI:**	13.2
		Sequence Coverage [%]:	5.0
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 0.92 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MGPPPPPLPP	RNNQNHIQGR	CVPSVPGKVI	LSPMGDLCLV	PELPAYSRRF	AGIVNFQGFH	RLAKTVCSEQ	RRRGIGSPGR
90	100	110	120	130	140	150	160
PRVSSLRTTT	RDLGRANARR	QLRQGHARAG	LRSSKWKRIL	HRTRSSQLHP	RGRLPGQWLG	SARRHSNPSR	PRLLDLLTGH
170	180	190	200	210	220	230	240
RGRGLGPATS	PRSPPPPPPP	GFSLTHGSRP	LPLFSLTARA	PGGECVSRPG	RGAVCISYAG	SLAPGSRAAS	PAVAGAAKSA
250	260	270	280	290	300	310	320
ISGPLRPQAS	RRAVRSPSSS	AQPAACGGVR	RRQASASSSV	SRCGRRSSLH	LLLGPPSLPS	SHFPSSGVSR	PRSTLLQEQR
330	340	350	360	370	380	390	
KTPRRRRRHL	RLLLRPAPGP	RRRHQGARLS	LPGGLGPASS	CRLRARTRLS	HLGPCRALKR	SL	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1664	1	932.4654	-19.93	2	49.1	12.8	1	344-362	R.HQGARLSLPGGLGPASSCR.L		WD:WU 0.92

Detailed Protein Report

Protein 746: insulin gene enhancer protein ISL-1 [Homo sapiens]

Accession:	gi|115387114	**Score:**	12.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	39.0
Database Date:	2015-11-30	**pI:**	9.8
		Sequence Coverage [%]:	6.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGDMGDPPKK	KRLISLCVGC	GNQIHDQYIL	RVSPDLEWHA	ACLKCAECNQ	YLDESCTCFV	RDGKTYCKRD	YIRLYGIKCA
90	100	110	120	130	140	150	160
KCSIGFSKND	FVMRARSKVY	HIECFRCVAC	SRQLIPGDEF	ALREDGLFCR	ADHDVVERAS	LGAGDPLSPL	HPARPLQMAA
170	180	190	200	210	220	230	240
EPISARQPAL	RPHVHKQPEK	TTRVRTVLNE	KQLHTLRTCY	AANPRPDALM	KEQLVEMTGL	SPRVIRVWFQ	NKRCKDKKRS
250	260	270	280	290	300	310	320
IMMKQLQQQQ	PNDKTNIQGM	TGTPMVAASP	ERHDGGLQAN	PVEVQSYQPP	WKVLSDFALQ	SDIDQPAFQQ	LVNFSEGGPG
330	340	350					
SNSTGSEVAS	MSSQLPDTPN	SMVASPIEA					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2453	1	900.1989	108.21	3	58.9	12.8	2	107-130	R.CVACSRQLIPGDEFALREDGLFCR.A	

Detailed Protein Report

Protein 747: 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	

Protein 748: PREDICTED: cip1-interacting zinc finger protein isoform X8 [Homo sapiens]

Accession:	gi|578817288	**Score:**	12.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	94.4
Database Date:	2015-11-30	**pI:**	5.8
		Sequence Coverage [%]:	1.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPRGMADPSG	RQTDLGLRAS	PSRCGGRGTE	ATMFSQQQQQ	QLQQQQQQLQ	QLQQQQLQQQ	QLQQQQLLQL	QQLLQQSPPQ
90	100	110	120	130	140	150	160
APLPMAVSRG	LPPQQPQQPL	LNLQGTNSAS	LLNGSMLQRA	LLLQQLQGNL	RGYGMASPGL	AAPSLTPPQL	ATPNLQQFFP
170	180	190	200	210	220	230	240
QATRQSLLGP	PPVGVPMNPS	QFNLSGRNPQ	KQARTSSSTT	PNRKDSSSQT	MPVEDKSDPP	EGSEEAAEPR	MDTPEDQDLP
250	260	270	280	290	300	310	320
PCPEDIAKEK	RTPAPEPEPC	EASELPAKRL	RSSEEPTEKE	PPGQLQVKAQ	PQARMTVPKQ	TQTPDLLPEA	LEAQVLPRFQ
330	340	350	360	370	380	390	400
PRVLQVQAQV	QSQTQPRIPS	TDTQVQPKLQ	KQAQTQTSPE	HLVLQQKQVQ	PQLQQEAEPQ	KQVQPQVHTQ	AQPSVQPQEH
410	420	430	440	450	460	470	480
PPAQVSVQPP	EQTHEQPHTQ	PQVSLLAPEQ	TPVVVHVCGL	EMPPDAVEAG	GGMEKTLPEP	VGTQVSMEEI	QNESACGLDV
490	500	510	520	530	540	550	560
GECENRAREM	PGVWGAGGSL	KVTILQSSDS	RAFSTVPLTP	VPRPSDSVSS	TPAATSTPSK	QALQFFCYIC	KASCSSQQEF
570	580	590	600	610	620	630	640
QDHMSEPQHQ	QRLGEIQHMS	QACLLSLLPV	PRDVLETEDE	EPPPRRWCNT	CQLYYMGDLI	QHRRTQDHKI	AKQSLRPFCT
650	660	670	680	690	700	710	720
VCNRYFKTPR	KFVEHVKSQG	HKDKAKELKS	LEKEIAGQDE	DHFITVDAVG	CFEGDEEEEE	DDEDEEEIEV	EEELCKQVRS
730	740	750	760	770	780	790	800
RDISREEWKG	SETYSPNTAY	GVDFLVPVMG	YICRICHKFY	HSNSGAQLSH	CKSLGHFENL	QKYKAAKNPS	PTTRPVSRRC
810	820	830	840	850	860		
AINARNALTA	LFTSSGRPPS	QPNTQDKTPS	KVTARPSQPP	LPRRSTRLKT			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
38	1	837.3492	-94.93	2	29.4	12.8	2	12-27	R.QTDLGLRASPSRCGGR.G	

Detailed Protein Report

Protein 749: UDP-glucuronosyltransferase 2A3 precursor [Homo sapiens]

Accession:	gi|193211427	**Score:**	12.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	60.2
Database Date:	2015-11-30	**pI:**	9.1
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	2.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MRSDKSALVF	LLLQLFCVGC	GFCGKVLVWP	CDMSHWLNVK	VILEELIVRG	HEVTVLTHSK	PSLIDYRKPS	ALKFEVVHMP
90	100	110	120	130	140	150	160
QDRTEENEIF	VDLALNVLPG	LSTWQSVIKL	NDFFVEIRGT	LKMMCESFIY	NQTLMKKLQE	TNYDVMLIDP	VIPCGDLMAE
170	180	190	200	210	220	230	240
LLAVPFVLTL	RISVGGNMER	SCGKLPAPLS	YVPVPMTGLT	DRMTFLERVK	NSMLSVLFHF	WIQDYDYHFW	EEFYSKALGR
250	260	270	280	290	300	310	320
PTTLCETVGK	AEIWLIRTYW	DFEFPQPYQP	NFEFVGGLHC	KPAKALPKEM	ENFVQSSGED	GIVVFSLGSL	FQNVTEEKAN
330	340	350	360	370	380	390	400
IIASALAQIP	QKVLWRYKGK	KPSTLGANTR	LYDWIPQNDL	LGHPKTKAFI	THGGMNGIYE	AIYHGVPMVG	VPIFGDQLDN
410	420	430	440	450	460	470	480
IAHMKAKGAA	VEINFKTMTS	EDLLRALRTV	ITDSSYKENA	MRLSRIHHDQ	PVKPLDRAVF	WIEFVMRHKG	AKHLRSAAHD
490	500	510	520	530			
LTWFQHYSID	VIGFLLACVA	TAIFLFTKCF	LFSCQKFNKT	RKIEKRE			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1155	1	652.5392	-138.06	3	42.7	12.8	1	123-137	K.MMCESFIYNQTLMKK.L	Carbamidomethyl: 3; Oxidation: 1, 13

Detailed Protein Report

Protein 750: **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 751: hypoxia-inducible factor 1-alpha isoform 2 [Homo sapiens]

Accession: gi|31077211
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 12.8
MW [kDa]: 82.7
pI: 5.1
Sequence Coverage [%]: 1.5
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MEGAGGANDK	KKISSERRKE	KSRDAARSRR	SKESEVFYEL	AHQLPLPHNV	SSHLDKASVM	RLTISYLRVR	KLLDAGDLDI
90	100	110	120	130	140	150	160
EDDMKAQMNC	FYLKALDGFV	MVLTDDGDMI	YISDNVNKYM	GLTQFELTGH	SVFDFTHPCD	HEEMREMLTH	RNGLVKKGKE
170	180	190	200	210	220	230	240
QNTQRSFFLR	MKCTLTSRGR	TMNIKSATWK	VLHCTGHIHV	YDTNSNQPQC	GYKKPPMTCL	VLICEPIPHP	SNIEIPLDSK
250	260	270	280	290	300	310	320
TFLSRHSLDM	KFSYCDERIT	ELMGYEPEEL	LGRSIYEYYH	ALDSDHLTKT	HHDMFTKGQV	TTGQYRMLAK	RGGYVWVETQ
330	340	350	360	370	380	390	400
ATVIYNTKNS	QPQCIVCVNY	VVSGIIQHDL	IFSLQQTECV	LKPVESSDMK	MTQLFTKVES	EDTSSLFDKL	KKEPDALTLL
410	420	430	440	450	460	470	480
APAAGDTIIS	LDFGSNDTET	DDQQLEEVPL	YNDVMLPSPN	EKLQNINLAM	SPLPTAETPK	PLRSSADPAL	NQEVALKLEP
490	500	510	520	530	540	550	560
NPESLELSFT	MPQIQDQTPS	PSDGSTRQSS	PEPNSPSEYC	FYVDSDMVNE	FKLELVEKLF	AEDTEAKNPF	STQDTDLDLE
570	580	590	600	610	620	630	640
MLAPYIPMDD	DFQLRSFDQL	SPLESSSASP	ESASPQSTVT	VFQQTQIQEP	TANATTTTAT	TDELKTVTKD	RMEDIKILIA
650	660	670	680	690	700	710	720
SPSPTHIHKE	TTSATSSPYR	DTQSRTASPN	RAGKGVIEQT	EKSHPRSPNV	LSVALSQRTT	VPEEELNPKI	LALQNAQRKR
730	740						
KMEHDGSLFQ	AVGII						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2689	2	616.8502	77.22	2	62.0	12.8	1	661-671	R.DTQSRTASPNR.A	

Detailed Protein Report

Protein 752: **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

Quantitation

WD:WU **Median:** 0.87 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MELFQAKDHY	ILQQGERALW	CSRRDGGLQL	RPATDLLLAW	NPICLGLVEG	VIGKIQLHSD	LPWWLILIRQ	KALVGKLPGD
90	100	110	120	130	140	150	160
HEVCKVTKIA	VLSLSEMEPQ	DLELELCKKH	HFGINKPEKI	IPSPDDSKFL	LKTFTHIKSN	VSAPNKKKVK	ESKEKEKLER
170	180	190	200	210	220	230	240
RLLEELLKMF	MDSESFYYSL	TYDLTNSVQR	QSTGERDGRP	LWQKVDDRFF	WNKYMIQDLT	EIGTPDVDFW	IIPMIQGFVQ
250	260	270	280	290	300	310	320
IEELVVNYTE	SSDDEKSSPE	TPPQESTCVD	DIHPRFLVAL	ISRRSRHRAG	MRYKRRGVDK	NGNVANYVET	EQLIHVHNHT
330	340	350	360	370	380	390	400
LSFVQTRGSV	PVFWSQVGYR	YNPRPRLDRS	EKETVAYFCA	HFEEQLNIYK	KQVIINLVDQ	AGREKIIGDA	YLKQVLLFNN
410	420	430	440	450	460	470	480
SHLTYVSFDF	HEHCRGMKFE	NVQTLTDAIY	DIILDMKWCW	VDEAGVICKQ	EGIFRVNCMD	CLDRTNVVQA	AIARVVMEQQ
490	500	510	520	530	540	550	560
LKKLGVMPPE	QPLPVKCNRI	YQIMWANNGD	SISRQYAGTA	ALKGDFTRTG	ERKLAGVMKD	GVNSANRYYL	NRFKDAYRQA
570	580	590	600	610	620	630	640
VIDLMQGIPV	TEDLYSIFTK	EKEHEALHKE	NQRSHQELIS	QLLQSYMKLL	LPDDEKFHGG	WALIDCDPRK	PPTLSTAGKR
650							
L							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1334	1	727.3902	-51.85	2	45.4	12.8	1	371-383	K.KQVIINLVDQAGR.E		WD:WU 0.87

Protein 753: uncharacterized protein C21orf62 precursor [Homo sapiens]

Accession:	gi|254911037	**Score:**	12.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	24.8
Database Date:	2015-11-30	**pI:**	9.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.1
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|254911043	refseq_huma (refseq_human_20140103.fasta)	uncharacterized protein C21orf62 precursor [Homo sapiens]
gi|254911041	refseq_huma (refseq_human_20140103.fasta)	uncharacterized protein C21orf62 precursor [Homo sapiens]

10	20	30	40	50	60	70	80
MAPPSRHCLL	LISTLGVFAL	NCFTKGQKNS	TLIFTRENTI	RNCSCSADIR	DCDYSLANLM	CNCKTVLPLA	VERTSYNGHL
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
TIWFTDTSAL	GHLLNFTLVQ	DLKLSLCSTN	TLPTEYLAIC	GLKRLRINME	AKHPFPEQSL	LIHSGGDSDS	REKPMWLHKG
170	**180**	**190**	**200**	**210**	**220**		
WQPCMYISFL	DMALFNRDSA	LKSYSIENVT	SIANNFPDFS	YFRTFPMPSN	KSYVVTFIY		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1513	1	513.1408	-136.07	2	47.3	12.8	0	42-50	R.NCSCSADIR.D	Carbamidomethyl: 4

Detailed Protein Report

Protein 754: rho-associated protein kinase 1 [Homo sapiens]

Accession: gi|4885583
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 12.8
MW [kDa]: 158.1
pI: 5.6
Sequence Coverage [%]: 1.3
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MSTGDSFETR	FEKMDNLLRD	PKSEVNSDCL	LDGLDALVYD	LDFPALRKNK	NIDNFLSRYK	DTINKIRDLR	MKAEDYEVVK
90	100	110	120	130	140	150	160
VIGRGAFGEV	QLVRHKSTRK	VYAMKLLSKF	EMIKRSDSAF	FWEERDIMAF	ANSPWVVQLF	YAFQDDRYLY	MVMEYMPGGD
170	180	190	200	210	220	230	240
LVNLMSNYDV	PEKWARFYTA	EVVLALDAIH	SMGFIHRDVK	PDNMLLDKSG	HLKLADFGTC	MKMNKEGMVR	CDTAVGTPDY
250	260	270	280	290	300	310	320
ISPEVLKSQG	GDGYYGRECD	WWSVGVFLYE	MLVGDTPFYA	DSLVGTYSKI	MNHKNSLTFP	DDNDISKEAK	NLICAFLTDR
330	340	350	360	370	380	390	400
EVRLGRNGVE	EIKRHLFFKN	DQWAWETLRD	TVAPVVPDLS	SDIDTSNFDD	LEEDKGEEET	FPIPKAFVGN	QLPFVGFTYY
410	420	430	440	450	460	470	480
SNRRYLSSAN	PNDNRTSSNA	DKSLQESLQK	TIYKLEEQLH	NEMQLKDEME	QKCRTSNIKL	DKIMKELDEE	GNQRRNLEST
490	500	510	520	530	540	550	560
VSQIEKEKML	LQHRINEYQR	KAEQENEKRR	NVENEVSTLK	DQLEDLKKVS	QNSQLANEKL	SQLQKQLEEA	NDLLRTESDT
570	580	590	600	610	620	630	640
AVRLRKSHTE	MSKSISQLES	LNRELQERNR	ILENSKSQTD	KDYYQLQAIL	EAERRDRGHD	SEMIGDLQAR	ITSLQEEVKH
650	660	670	680	690	700	710	720
LKHNLEKVEG	ERKEAQDMLN	HSEKEKNNLE	IDLNYKLKSL	QQRLEQEVNE	HKVTKARLTD	KHQSIEEAKS	VAMCEMEKKL
730	740	750	760	770	780	790	800
KEEREAREKA	ENRVVQIEKQ	CSMLDVDLKQ	SQQKLEHLTG	NKERMEDEVK	NLTLQLEQES	NKRLLLQNEL	KTQAFEADNL
810	820	830	840	850	860	870	880
KGLEKQMKQE	INTLLEAKRL	LEFELAQLTK	QYRGNEGQMR	ELQDQLEAEQ	YFSTLYKTQV	KELKEEIEEK	NRENLKKIQE
890	900	910	920	930	940	950	960
LQNEKETLAT	QLDLAETKAE	SEQLARGLLE	EQYFELTQES	KKAASRNRQE	ITDKDHTVSR	LEEANSMLTK	DIEILRRENE
970	980	990	1000	1010	1020	1030	1040
ELTEKMKKAE	EEYKLEKEEE	ISNLKAAFEK	NINTERTLKT	QAVNKLAEIM	NRKDFKIDRK	KANTQDLRKK	EKENRKLQLE
1050	1060	1070	1080	1090	1100	1110	1120
LNQEREKFNQ	MVVKHQKELN	DMQAQLVEEC	AHRNELQMQL	ASKESDIEQL	RAKLLDLSDS	TSVASFPSAD	ETDGNLPESR
1130	1140	1150	1160	1170	1180	1190	1200
IEGWLSVPNR	GNIKRYGWKK	QYVVVSSKKI	LFYNDEQDKE	QSNPSMVLDI	DKLFHVRPVT	QGDVYRAETE	EIPKIFQILY
1210	1220	1230	1240	1250	1260	1270	1280
ANEGECRKDV	EMEPVQQAEK	TNFQNHKGHE	FIPTLYHFPA	NCDACAKPLW	HVFKPPPALE	CRRCHVKCHR	DHLDKKEDLI
1290	1300	1310	1320	1330	1340	1350	1360
CPCKVSYDVT	SARDMLLLAC	SQDEQKKWVT	HLVKKIPKNP	PSGFVRASPR	TLSTRSTANQ	SFRKVVKNTS	GKTS

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1917	1	696.9347	-101.57	3	52.3	12.8	1	290-307	K.IMNHKNSLTFPDDNDISK.E	

Detailed Protein Report

Protein 755: PREDICTED: protein crumbs homolog 2 isoform X1 [Homo sapiens]

Accession:	gi|530391003	**Score:**	12.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	99.8
Database Date:	2015-11-30	**pI:**	5.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.5
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 0.82 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MAMEPGALWT	FLGHLWLLAG	PTCEEDVDEC	LSDPCLHGGT	CSDTVAGYIC	RCPETWGGRD	CSVQLTGCQG	HTCPLAATCI
90	100	110	120	130	140	150	160
PIFESGVHSY	VCHCPPGTHG	PFCGQNTTFS	VMAGSPIQAS	VPAGGPLGLA	LRFRTTLPAG	TLATRNDTKE	SLELALVAAT
170	180	190	200	210	220	230	240
LQATLWSYST	TVLVLRLPDL	ALNDGHWHQV	EVVLHLATLE	LRLWHEGCPA	RLCVASGPVA	LASTASATPL	PAGISSAQLG
250	260	270	280	290	300	310	320
DATFAGCLQD	VRVDGHLLLP	EDLGENVLLG	CERREQCRPL	PCVHGGSCVD	LWTHFRCDCA	RPHRGPTCAD	EIPAATFGLG
330	340	350	360	370	380	390	400
GAPSSASFLL	QELPGPNLTV	SFLLRTRESA	GLLLQFANDS	AAGLTVFLSE	GRIRAEVPGS	PAVVLPGRWD	DGLRHLVMLS
410	420	430	440	450	460	470	480
FGPDQLQDLG	QHVHVGGRLL	AADSQPWGGP	FRGCLQDLRL	DGCHLPFFPL	PLDNSSQPSE	LGGRQSWNLT	AGCVSEDMCS
490	500	510	520	530	540	550	560
PDPCFNGGTC	LVTWNDFHCT	CPANFTGPTC	AQQLWCPGQP	CLPPATCEEV	PDGFVCVAEA	TFREGPPAAF	SGHNASSGRL
570	580	590	600	610	620	630	640
LGGLSLAFRT	RDSEAWLLRA	AAGALEGVWL	AVRNGSLAGG	VRGGHGLPGA	VLPIPGPRVA	DGAWHRVRLA	MERPAATTSR
650	660	670	680	690	700	710	720
WLLWLDGAAT	PVALRGLASD	LGFLQGPGAV	RILLAENFTG	CLGRVALGGL	PLPLARPRPG	AAPGAREHFA	SWPGTPAPIL
730	740	750	760	770	780	790	800
GCRGAPVCAP	SPCLHDGACR	DLFDAFACAC	GPGWEGPRCE	AHVDPCHSAP	CARGRCHTHP	DGRFECRCPP	GFGGPRCRLP
810	820	830	840	850	860	870	880
VPSKECSLNV	TCLDGSPCEG	GSPAANCSCL	EGLAGQRCQV	PTLPCEANPC	LNGGTCRAAG	GVSECICNAR	FSGQFCEVAK
890	900	910	920	930	940	950	960
GLPLPLPFPL	LEVAVPAACA	CLLLLLLGLL	SGILAARKRR	QSEGTYSPSQ	QEVAGARLEM	DSVLKVPPEE	RLI

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
47	1	829.3877	-47.23	2	29.5	12.8	1	938-951	R.LEMDSVLKVPPEER.L	Oxidation: 3	WD:WU	0.82

Detailed Protein Report

Protein 756: PREDICTED: inhibitor of Bruton tyrosine kinase isoform X3 [Homo sapiens]

Accession:	gi|578812678	**Score:**	12.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	148.9
Database Date:	2015-11-30	**pI:**	8.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSSPMPDCTS	KCRSLKHALD	VLSVVTKGSE	NQIKAFLSSH	CYNAATIKDV	FGRNALHLVS	SCGKKGVLDW	LIQKGVDLLV
90	100	110	120	130	140	150	160
KDKESGWTAL	HRSIFYGHID	CVWSLLKHGV	SLYIQDKEGL	SALDLVMKDR	PTHVVFKNTD	PTDVYTWGDN	TNFTLGHGSQ
170	180	190	200	210	220	230	240
NSKHHPELVD	LFSRSGIYIK	QVVLCKFHSV	FLSQKGQVYT	CGHGPGGRLG	HGDEQTCLVP	RLVEGLNGHN	CSQVAAAKDH
250	260	270	280	290	300	310	320
TVVLTEDGCV	YTFGLNIFHQ	LGIIPPPSSC	NVPRQIQAKY	LKGRTIIGVA	AGRFHTVLWT	REAVYTMGLN	GGQLGCLLDP
330	340	350	360	370	380	390	400
NGEKCVTAPR	QVSALHHKDI	ALSLVAASDG	ATVCVTTRGD	IYLLADYQCK	KMASKQLNLK	KVLVSGGHME	YKVDPEHLKE
410	420	430	440	450	460	470	480
NGGQKICILA	MDGAGRVFCW	RSVNSSLKQC	RWAYPRQVFI	SDIALNRNEI	LFVTQDGEGF	RGRWFEEKRK	SSEKKEILSN
490	500	510	520	530	540	550	560
LHNSSSDVSY	VSDINSVYER	IRLEKLTFAH	RAVSVSTDPS	GCNFAILQSD	PKTSLYEIPA	VSSSSFFEEF	GKLLREADEM
570	580	590	600	610	620	630	640
DSIHDVTFQV	GNRLFPAHKY	ILAVHSDFFQ	KLFLSDGNTS	EFTDIYQKDE	DSAGCHLFVV	EKVHPDMFEY	LLQFIYTDTC
650	660	670	680	690	700	710	720
DFLTHGFKPR	IHLNKNPEEY	QGTLNSHLNK	VNFHEDDNQK	SAFEVYKSNQ	AQTVSERQKS	KPKSCKKGKN	IREDDPVRML
730	740	750	760	770	780	790	800
QTVAKKFDFS	NLSSRLDGVR	FENEKINVIA	KNTGNKLKLS	QKKCSFLCDV	TMKSVDGKEF	PCHKCVLCAR	LEYFHSMLSS
810	820	830	840	850	860	870	880
SWIEASSCAA	LEMPIHSDIL	KVILDYLYTD	EAVVIKESQN	VDFICSVLVV	ADQLLITRLK	EICEVALTEK	LTLKNAAMLL
890	900	910	920	930	940	950	960
EFAAMYSAKQ	LKLSCLQFIG	LNMAALLEAR	SLDVLSDGVL	KDLSEFYRKM	IPAMDRRVIT	PYQDGPDISY	LEVEDGDIFL
970	980	990	1000	1010	1020	1030	1040
KEEINMEQNH	SETMFKKAKT	KAKKKPRKRS	DSSGGYNLSD	IIQSPSSTEL	LTSDSEGSYA	GVGSPRDLQS	PDFTTGFHSD
1050	1060	1070	1080	1090	1100	1110	1120
KIEAKVKPYV	NGTSPVYSRE	DLKPWEKSPI	LKISAPQPIP	SNRIDTTSSA	SWVAGSFSPV	SPPVVDLRTI	MEIEESRQKC
1130	1140	1150	1160	1170	1180	1190	1200
GATPKSHLGK	TVSHGVKLSQ	KQRKMIALTT	KENNSGMNSM	ETVLFTPSKA	PKPVNAWASS	LHSVSSKSFR	DFLLEEKKSV
1210	1220	1230	1240	1250	1260	1270	1280
TSHSSGDHVK	KVSFKGIENS	QAPKIVRCST	HGTPGPEGNH	ISDLPLLDSP	NPWLSSSVTA	PSMVAPVTFA	SIVEEELQQE
1290	1300	1310	1320	1330	1340		
AALIRSREKP	LALIQIEEHA	IQDLLVFYEA	FGNPEEFVIV	ERTPQGPLAV	PMWNKHGC		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2082	1	701.2889	-119.01	3	54.6	12.7	1	871-889	K.LTLKNAAMLLEFAAMYSAK.Q	Oxidation: 15

Detailed Protein Report

Protein 757: 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		

Detailed Protein Report

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 758: 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 759: **PREDICTED: heterogeneous nuclear ribonucleoprotein M isoform X6 [Homo sapiens]**

Accession:	gi|530427511	**Score:**	12.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	60.5
Database Date:	2015-11-30	**pI:**	9.8
		Sequence Coverage [%]:	4.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEESMKKAAE	VLNKHSLSGR	PLKVKEDPDG	EHARRAMQKA	GRLGSTVFVA	NLDYKVGWKK	LKEVFSMAGV	VVRADILEDK
90	100	110	120	130	140	150	160
DGKSRGIGTV	TFEQSIEAVQ	AISMFNGQLL	FDRPMHVKMD	ERALPKGDFF	PPERPQQLPH	GLGGIGMGLG	PGGQPIDANH
170	180	190	200	210	220	230	240
LNKGIGMGNI	GPAGMGMEGI	GFGINKMGGM	EGPFGGGMEN	MGRFGSGMNM	GRINEILSNA	LKRGEIIAKQ	GGGGGGGSVP
250	260	270	280	290	300	310	320
GIERMGPGID	RLGGAGMERM	GAGLGHGMDR	VGSEIERMGL	VMDRMGSVER	MGSGIERMGP	LGLDHMASSI	ERMGQTMERI
330	340	350	360	370	380	390	400
GSGVERMGAG	MGFGLERMAA	PIDRVGQTIE	RMGSGVERMG	PAIERMGLSM	ERMVPAGMGA	GLERMGPVMD	RMATGLERMG
410	420	430	440	450	460	470	480
ANNLERMGLE	RMGANSLERM	GLERMGANSL	ERMGPAMGPA	LGAGIERMGL	AMGGGGGASF	DRAIEMERGN	FGGSFAGSFG
490	500	510	520	530	540	550	560
GAGGHAPGVA	RKACQIFVRN	LPFDFTWKML	KDKFNECGHV	LYADIKMENG	KSKGCGVVKF	ESPEVAERAC	RMMNGMKLSG
570	580						
REIDVRIDRN	A						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1622	1	927.1215	17.83	3	49.0	12.7	2	366-391	R.MGLSMERMVPAGMGAGLERMGPVMDR.M	

Detailed Protein Report

Protein 760: **serine/threonine-protein kinase ATR [Homo sapiens]**

Accession:	gi|157266317	**Score:**	12.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	301.2
Database Date:	2015-11-30	**pI:**	7.3
		Sequence Coverage [%]:	0.6
		No. of unique Peptides:	1

Detailed Protein Report

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 761: rap guanine nucleotide exchange factor 1 isoform a [Homo sapiens]

Accession:	gi|38373675	**Score:**	12.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	120.5
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
MDTDSQRSHL	SSFTMKLMDK	FHSPKIKRTP	SKKGKPAEVS	VKIPEKPVNK	EATDRFLPEG	YPLPLDLEQQ	AVEFMSTSAV
90	100	110	120	130	140	150	160
ASRSQRQKNL	SWLEEKEKEV	VSALRYFKTI	VDKMAIDKKV	LEMLPGSASK	VLEAILPLVQ	NDPRIQHSSA	LSSCYSRVYQ
170	180	190	200	210	220	230	240
SLANLIRWSD	QVMLEGVNSE	DKEMVTTVKG	VIKAVLDGVK	ELVRLTIEKQ	GRPSPTSPVK	PSSPASKPDG	PAELPLTDRE
250	260	270	280	290	300	310	320
VEILNKTTGM	SQSTELLPDA	TDEEVAPPKP	PLPGIRVVDN	SPPPALPPKK	RQSAPSPTRV	AVVAPMSRAT	SGSSLPVGIN
330	340	350	360	370	380	390	400
RQDFDVDCYA	QRRLSGGSHS	YGGESPRLSP	CSSIGKLSKS	DEQLSSLDRD	SGQCSRNTSC	ETLDHYDPDY	EFLQQDLSNA
410	420	430	440	450	460	470	480
DQIPQQTAWN	LSPLPESLGE	SGSPFLGPPF	QLPLGGHPQP	DGPLAPGQQT	DTPPALPEKK	RRSAASQTAD	GSGCRVSYER
490	500	510	520	530	540	550	560
HPSQYDNISG	EDLQSTAPIP	SVPYAPFAAI	LPFQHGGSSA	PVEFVGDFTA	PESTGDPEKP	PPLPEKKNKH	MLAYMQLLED
570	580	590	600	610	620	630	640
YSEPQPSMFY	QTPQNEHIYQ	QKNKLLMEVY	GFSDSFSGVD	SVQELAPPPA	LPPKQRQLEP	PAGKDGHPRD	PSAVSGVPGK
650	660	670	680	690	700	710	720
DSRDGSERAP	KSPDALESAQ	SEEEVDELSL	IDHNEIMSRL	TLKQEGDDGP	DVRGGSGDIL	LVHATETDRK	DLVLYCEAFL
730	740	750	760	770	780	790	800
TTYRTFISPE	ELIKKLQYRY	EKFSPFADTF	KKRVSKNTFF	VLVRVVDELC	LVELTEEILK	LLMELVFRLV	CNGELSLARV
810	820	830	840	850	860	870	880
LRKNILDKVD	QKKLLRCATS	SQPLAARGVA	ARPGTLHDFH	SHEIAEQLTL	LDAELFYKIE	IPEVLLWAKE	QNEEKSPNLT
890	900	910	920	930	940	950	960
QFTEHFNNMS	YWVRSIIMLQ	EKAQDRERLL	LKFIKIMKHL	RKLNNFNSYL	AILSALDSAP	IRRLEWQKQT	SEGLAEYCTL
970	980	990	1000	1010	1020	1030	1040
IDSSSSFRAY	RAALSEVEPP	CIPYLGLILQ	DLTFVHLGNP	DYIDGKVNFS	KRWQQFNILD	SMRCFQQAHY	DMRRNDDIIN
1050	1060	1070	1080				
FFNDFSDHLA	EEALWELSLK	IKPRNITRRK	TDREEKT				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1627	1	686.4490	148.95	2	48.7	12.7	1	630-643	R.DPSAVSGVPGKDSR.D	

Detailed Protein Report

Protein 762: **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 763: testis-specific gene 10 protein [Homo sapiens]

Accession:	gi|13376858	**Score:**	12.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	81.4
Database Date:	2015-11-30	**pI:**	5.7
		Sequence Coverage [%]:	2.0
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 1.02 **CV:** 0.00 % **No. of Peptides:** 1

Alias proteins:

Accession	**Name**	**Description**
gi|578804977	refseq_human (refseq_human_20140103.fasta)	PREDICTED: testis-specific gene 10 protein isoform X11 [Homo sapiens]
gi|578804975	refseq_human (refseq_human_20140103.fasta)	PREDICTED: testis-specific gene 10 protein isoform X10 [Homo sapiens]
gi|530368823	refseq_human (refseq_human_20140103.fasta)	PREDICTED: testis-specific gene 10 protein isoform X8 [Homo sapiens]
gi|530368819	refseq_human (refseq_human_20140103.fasta)	PREDICTED: testis-specific gene 10 protein isoform X6 [Homo sapiens]
gi|530368817	refseq_human (refseq_human_20140103.fasta)	PREDICTED: testis-specific gene 10 protein isoform X5 [Homo sapiens]
gi|530368815	refseq_human (refseq_human_20140103.fasta)	PREDICTED: testis-specific gene 10 protein isoform X4 [Homo sapiens]
gi|530368813	refseq_human (refseq_human_20140103.fasta)	PREDICTED: testis-specific gene 10 protein isoform X3 [Homo sapiens]
gi|530368811	refseq_human (refseq_human_20140103.fasta)	PREDICTED: testis-specific gene 10 protein isoform X2 [Homo sapiens]
gi|188528616	refseq_human (refseq_human_20140103.fasta)	testis-specific gene 10 protein [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MMRSRSKSPR RPSPTARGAN CDVELLKTTT RDREELKCML EKYERHLAEI QGNVKVLKSE RDKIFLLYEQ AQEEITRLRR
        90        100        110        120        130        140        150        160
EMMKSCKSPK STTAHAILRR VETERDVAFT DLRRMTTERD SLRERLKIAQ ETAFNEKAHL EQRIEELECT VHNLDDERME
       170        180        190        200        210        220        230        240
QMSNMTLMKE TISTVEKEMK SLARKAMDTE SELGRQKAEN NSLRLLYENT EKDLSDTQRH LAKKKYELQL TQEKIMCLDE
       250        260        270        280        290        300        310        320
KIDNFTRQNI AQREEISILG GTLNDLAKEK ECLQACLDKK SENIASLGES LAMKEKTISG MKNIIAEMEQ ASRQCTEALI
       330        340        350        360        370        380        390        400
VCEQDVSRMR RQLDETNDEL AQIARERDIL AHDNDNLQEQ FAKAKQENQA LSKKLNDTHN ELNDIKQKVQ DTNLEVNKLK
       410        420        430        440        450        460        470        480
NILKSEESEN RQMMEQLRKA NEDAENWENK ARQSEADNNT LKLELITAEA EGNRLKEKVD SLNREVEQHL NAERSYKSQI
       490        500        510        520        530        540        550        560
STLHKSVVKM EEELQKVQFE KVSALADLSS TRELCIKLDS SKELLNRQLV AKDQEIEMRE NELDSAHSEI ELLRSQMANE
       570        580        590        600        610        620        630        640
RISMQNLEAL LVANRDKEYQ SQIALQEKES EIQLLKEHLC LAENKMAIQS RDVAQFRNVV TQLEADLDIT KRQLGTERFE
       650        660        670        680        690        700
RERAVQELRR QNYSSNAYHM SSTMKPNTKC HSPERAHHRS PDRGLDRSLE ENLCYRDF
```

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	18-31	R.GANCDVELLKTTTR.D		WD:WU 1.02

Detailed Protein Report

Protein 764: protein RRNAD1 isoform 2 [Homo sapiens]

Accession:	gi|216548564	**Score:**	12.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	29.7
Database Date:	2015-11-30	**pI:**	9.8
		Sequence Coverage [%]:	5.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPGISARGLS	HEGRKQLAVN	LTRVLALYRS	ILDAYIIEFF	TDNLWDTLPC	SWQEALDGLK	PPQLATMLLG	MPGEGEVVRY
90	100	110	120	130	140	150	160
RSVWPLTLLA	LKSTACALAF	TRMPGFQTPS	EFLENPSQSS	RLTAPFRKHV	RPKKQHEIRR	LGELVKKLSD	FTGCTQVVDV
170	180	190	200	210	220	230	240
GSGQGHLSRF	MALGLGLMVK	SIEGDQRLVE	RAQRLDQELL	QALEKEEKRN	PQICAAGATA	SGARSPAATE	SGCPSGPRGP
250	260	270	280				
GEPCGGLLQP	GSTACPTGGD	AYSTGPAAVP	SGTGFPC				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2066	1	734.3148	-85.92	2	54.2	12.7	1	1-14	-.MPGISARGLSHEGR.K	

Detailed Protein Report

Protein 765: 6-phosphofructokinase, muscle type isoform 2 [Homo sapiens]

Accession:	gi|4505749	**Score:**	12.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	85.1
Database Date:	2015-11-30	**pI:**	9.2
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.9
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578823895	refseq_human (refseq_human_20140103.fasta)	PREDICTED: 6-phosphofructokinase, muscle type isoform X9 [Homo sapiens]
gi|578823893	refseq_human (refseq_human_20140103.fasta)	PREDICTED: 6-phosphofructokinase, muscle type isoform X8 [Homo sapiens]
gi|266453768	refseq_human (refseq_human_20140103.fasta)	6-phosphofructokinase, muscle type isoform 2 [Homo sapiens]
gi|266453748	refseq_human (refseq_human_20140103.fasta)	6-phosphofructokinase, muscle type isoform 2 [Homo sapiens]

10	20	30	40	50	60	70	80
MTHEEHHAAK	TLGIGKAIAV	LTSGGDAQGM	NAAVRAVVRV	GIFTGARVFF	VHEGYQGLVD	GGDHIKEATW	ESVSMMLQLG
90	100	110	120	130	140	150	160
GTVIGSARCK	DFREREGRLR	AAYNLVKRGI	TNLCVIGGDG	SLTGADTFRS	EWSDLLSDLQ	KAGKITDEEA	TKSSYLNIVG
170	180	190	200	210	220	230	240
LVGSIDNDFC	GTDMTIGTDS	ALHRIMEIVD	AITTTAQSHQ	RTFVLEVMGR	HCGYLALVTS	LSCGADWVFI	PECPPDDDWE
250	260	270	280	290	300	310	320
EHLCRRLSET	RTRGSRLNII	IVAEGAIDKN	GKPITSEDIK	NLVVKRLGYD	TRVTVLGHVQ	RGGTPSAFDR	ILGSRMGVEA
330	340	350	360	370	380	390	400
VMALLEGTPD	TPACVVSLSG	NQAVRLPLME	CVQVTKDVTK	AMDEKKFDEA	LKLRGRSFMN	NWEVYKLLAH	VRPPVSKSGS
410	420	430	440	450	460	470	480
HTVAVMNVGA	PAAGMNAAVR	STVRIGLIQG	NRVLVVHDGF	EGLAKGQIEE	AGWSYVGGWT	GQGGSKLGTK	RTLPKKSFEQ
490	500	510	520	530	540	550	560
ISANITKFNI	QGLVIIGGFE	AYTGGLELME	GRKQFDELCI	PFVVIPATVS	NNVPGSDFSV	GADTALNTIC	TTCDRIKQSA
570	580	590	600	610	620	630	640
AGTKRRVFII	ETMGGYCGYL	ATMAGLAAGA	DAAYIFEEPF	TIRDLQANVE	HLVQKMKTTV	KRGLVLRNEK	CNENYTTDFI
650	660	670	680	690	700	710	720
FNLYSEEGKG	IFDSRKNVLG	HMQQGGSPTP	FDRNFATKMG	AKAMNWMSGK	IKESYRNGRI	FANTPDSGCV	LGMRKRALVF
730	740	750	760	770	780	790	
QPVAELKDQT	DFEHRIPKEQ	WWLKLRPILK	ILAKYEIDLD	TSDHAHLEHI	TRKRSGEAAV		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1805	1	1273.5509	-63.73	2	51.2	12.7	2	656-678	R.KNVLGHMQQGGSPTPFDRNFATK.M	Oxidation: 7

Detailed Protein Report

Protein 766: PREDICTED: zinc finger protein 407 isoform X3 [Homo sapiens]

Accession:	gi|578832590	**Score:**	12.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	180.5
Database Date:	2015-11-30	**pI:**	6.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MMDSENKPEN	DEDEKINKEA	QDLTKLSSHN	EDGGPVSDVI	ASFPENSMGK	RGFSESSNSD	SVVIGEDRNK	HASKRRKLDE
90	100	110	120	130	140	150	160
AEPLKSGKQG	ICRLETSESS	VTEGGIALDE	TGKETFLSDC	TVGGTCLPNA	LSPSCNFSTI	DVVSLKTDTE	KTSAQEMVSL
170	180	190	200	210	220	230	240
DLERESPFPP	KEISVSCTIG	NVDTVLKCSI	CGHLFSSCSD	LEKHAESHMQ	QPKEHTCCHC	SHKAESSSAL	HMHIKQAHGP
250	260	270	280	290	300	310	320
QKVFSCDLCG	FQCSEENLLN	AHYLGKTHLR	RQNLAARGGF	VQILTKQPFP	KKSRTMATKN	VHSKPRTSKS	IAKNSDSKGL
330	340	350	360	370	380	390	400
RNVGSTFKDF	RGSISKQSGS	SSELLVEMMP	SRNTLSQEVE	IVEEHVTSLG	LAQNPENQSR	KLDTLVTSEG	LLEKLESTKN
410	420	430	440	450	460	470	480
TLQAAHGNSV	TSRPRPERNI	LVLGNSFRRR	SSTFTLKGQA	KKRFNLLGIK	RGTSETQRMY	MKHLRTQMKT	HDAESVLKHL
490	500	510	520	530	540	550	560
EACSSVQRVC	VTTSETQEAE	QGQGSARPPD	SGLHSLTVKP	ASGSQTLCAC	TDCGQVATNR	TDLEIHVKRC	HAREMKFYCR
570	580	590	600	610	620	630	640
TCDFSSMSRR	DLDEHLHSNQ	HQQTASVLSC	QCCSFISLDE	INLRDHMKEK	HNMHFLCTPC	NLFFLSEKDV	EEHKATEKHI
650	660	670	680	690	700	710	720
NSLVQPKTLQ	SSNSDLVLQT	LPLSTLESEN	AKESMDDSGK	ASQEEPLKSR	VSHGNEVRHS	SKPQFQCKKC	FYKTRSSTVL
730	740	750	760	770	780	790	800
TRHIKLRHGQ	DYHFLCKACN	LYSLSKEGME	KHIKRSKHLE	NAKKNNIGLS	FEECIERVCI	GANDKKEEFD	VSGNGRIEGH
810	820	830	840	850	860	870	880
IGVQLQEHSY	LEKGMLASEE	LSQSGGSTKD	DELASTTTPK	RGRPKGNISR	TCSHCGLLAS	SITNLTVHIR	RKHSHQYSYL
890	900	910	920	930	940	950	960
CKVCKYYTVT	KGDMERHCAT	KKHKGRVEIE	ASGKHSSDII	VGPEGGSLEA	GKKNAGSAVT	MSDEHANKPA	ESPTSVLEKP
970	980	990	1000	1010	1020	1030	1040
DRGNSIEAEV	ENVFHSLDGE	VNSHLLDKKE	QISSEPEDFA	QPGDVYSQRD	VTGTGENKCL	HCEFSAHSSA	SLELHVKRKH
1050	1060	1070	1080	1090	1100	1110	1120
TKEFEFYCMA	CDYYAVTRRE	MTRHAATEKH	KMKRQSYLNS	ANVEAGSADM	SKNIIMPEEE	HQQNSEEFQI	ISGQPSDTLK
1130	1140	1150	1160	1170	1180	1190	1200
SRNAADCSIL	NENTNLDMSK	VLCAADSVEV	ETEEESNFNE	DHSFCETFQQ	APVKDKVRKP	EEMMSLTMSS	NYGSPSRFQN
1210	1220	1230	1240	1250	1260	1270	1280
ENSGSSALNC	ETAKKNHEIS	NDAGELRVHC	EGEGGNAGDG	GGVVPHRHLC	PVTLDGERSA	ESPVLVVTRI	TREQGNLESG
1290	1300	1310	1320	1330	1340	1350	1360
GQNRVARGHG	LEDLKGVQED	PVLGNKEILM	NSQHETEFIL	EEDGPASDST	VESSDVYETI	ISIDDKGQAM	YSFGRFDSSI
1370	1380	1390	1400	1410	1420	1430	1440
IRIKNPEDGE	LIDQSEEGLI	ATGVRISELP	LKDCAQGVKK	KKSEGSSIGE	STRIRCDDCG	FLADGLSGLN	VHIAMKHPTK
1450	1460	1470	1480	1490	1500	1510	1520
EKHFHCLLCG	KSFYTESNLH	QHLASAGHMR	NEQASVEELP	EGGATFKCVK	CTEPFDSEQN	LFLHIKGQHE	ELLREVNKYI
1530	1540	1550	1560	1570	1580	1590	1600
VEDTEQINRE	REENQGNVCK	YCGKMCRSSN	SMAFLAHIRT	HTGSKPFKCK	ICHFATAQLG	DARNHVKRHL	GMREYKCHVC
1610	1620	1630					
GVAFVMKKHL	NTHLLGKHGV	GTPKERQI					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2427	1	1103.9913	-10.11	2	58.6	12.6	2	1541-1559	K.YCGKMCRSSNSMAFLAHIR.T	Oxidation: 5, 12

Detailed Protein Report

Protein 767: zinc finger protein Aiolos isoform 14 [Homo sapiens]

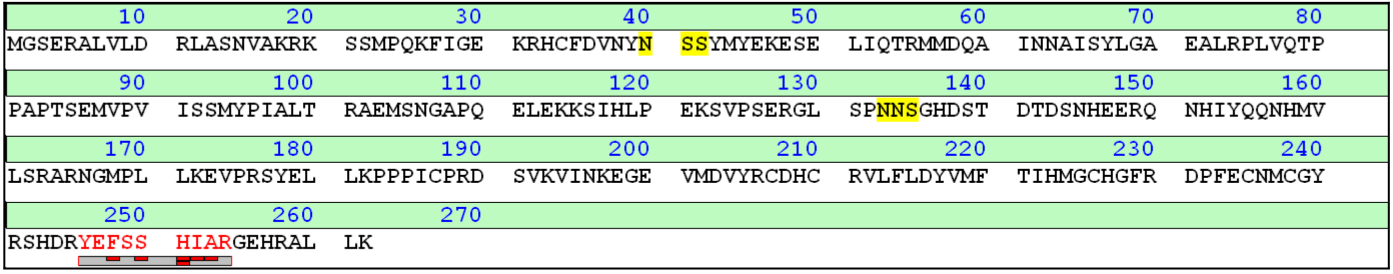
Accession:	gi|548962170	**Score:**	12.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	30.0
Database Date:	2015-11-30	**pI:**	7.9
		Sequence Coverage [%]:	3.4
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 1.31 **CV:** 0.00 % **No. of Peptides:** 1

Alias proteins:

Accession	**Name**	**Description**
gi|548962174	refseq_human (refseq_human_20140103.fasta)	zinc finger protein Aiolos isoform 14 [Homo sapiens]
gi|548962172	refseq_human (refseq_human_20140103.fasta)	zinc finger protein Aiolos isoform 14 [Homo sapiens]



```
        10         20         30         40         50         60         70         80
MGSERALVLD RLASNVAKRK SSMPQKFIGE KRHCFDVNYN SSYMYEKESE LIQTRMMDQA INNAISYLGA EALRPLVQTP
        90        100        110        120        130        140        150        160
PAPTSEMVPV ISSMYPIALT RAEMSNGAPQ ELEKKSIHLP EKSVPSERGL SPNNSGHDST DTDSNHEERQ NHIYQQNHMV
       170        180        190        200        210        220        230        240
LSRARNGMPL LKEVPRSYEL LKPPPICPRD SVKVINKEGE VMDVYRCDHC RVLFLDYVMF TIHMGCHGFR DPFECNMCGY
       250        260        270
RSHDRYEFSS HIARGEHRAL LK
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
775	1	555.1616	-199.44	2	38.1	12.6	0	246-254	R.YEFSSHIAR.G		WD:WU 1.31

Detailed Protein Report

Protein 768: PREDICTED: protein SON isoform X3 [Homo sapiens]

Accession:	gi|578836658	**Score:**	12.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	228.0
Database Date:	2015-11-30	**pI:**	5.2
		Sequence Coverage [%]:	0.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MATNIEQIFR	SFVVSKFREI	QQELSSGRNE	GQLNGETNTP	IEGNQAGDAA	ASARSLPNEE	IVQKIEEVLS	GVLDTELRYK
90	100	110	120	130	140	150	160
PDLKEGSRKS	RCVSVQTDPT	DEIPTKKSKK	HKKHKNKKKK	KKKEKEKKYK	RQPEESESKT	KSHDDGNIDL	ESDSFLKFDS
170	180	190	200	210	220	230	240
EPSAVALELP	TRAFGPSETN	ESPAVVLEPP	VVSMEVSEPH	ILETLKPATK	TAELSVVSTS	VISEQSEQSV	AVMPEPSMTK
250	260	270	280	290	300	310	320
ILDSFAAAPV	PTTTLVLKSS	EPVVTMSVEY	QMKSVLKSVE	STSPEPSKIM	LVEPPVAKVL	EPSETLVVSS	ETPTEVYPEP
330	340	350	360	370	380	390	400
STSTTMDFPE	SSAIEALRLP	EQPVDVPSEI	ADSSMTRPQE	LPELPKTTAL	ELQESSVASA	MELPGPPATS	MPELQGPPVT
410	420	430	440	450	460	470	480
PVLELPGPSA	TPVPELPGPL	STPVPELPGP	PATAVPELPG	PSVTPVPQLS	QELPGLPAPS	MGLEPPQEVP	EPPVMAQELP
490	500	510	520	530	540	550	560
GLPLVTAAVE	LPEQPAVTVA	MELTEQPVTT	TELEQPVGMT	TVEHPGHPEV	TTATGLLGQP	EATMVLELPG	QPVATTALEL
570	580	590	600	610	620	630	640
PGQPSVTGVP	ELPGLPSATR	ALELSGQPVA	TGALELPGPL	MAAGALEFSG	QSGAAGALEL	LGQPLATGVL	ELPGQPGAPE
650	660	670	680	690	700	710	720
LPGQPVATVA	LEISVQSVVT	TSELSTMTVS	QSLEVPSTTA	LESYNTVAQE	LPTTLVGETS	VTVGVDPLMA	PESHILASNT
730	740	750	760	770	780	790	800
METHILASNT	MDSQMLASNT	MDSQMLASNT	MDSQMLASST	MDSQMLATSS	MDSQMLATSS	MDSQMLATST	MDSQMLATSS
810	820	830	840	850	860	870	880
MDSQMLATSS	MDSQMLATSS	MDSQMLATSS	MDSQMLATST	MDSQMLATST	MDSQMLATSS	MDSQMLASGT	MDSQMLASGT
890	900	910	920	930	940	950	960
MDAQMLASGT	MDAQMLASST	QDSAMLGSKS	PDPYRLAQDP	YRLAQDPYRL	GHDPYRLGHD	AYRLGQDPYR	LGHDPYRLTP
970	980	990	1000	1010	1020	1030	1040
DPYRMSPRPY	RIAPRSYRIA	PRPYRLAPRP	LMLASRRSMM	MSYAAERSMM	SSYERSMMSY	ERSMMSPMAE	RSMMSAYERS
1050	1060	1070	1080	1090	1100	1110	1120
MMSAYERSMM	SPMAERSMMS	AYERSMMSAY	ERSMMSPMAD	RSMMSMGADR	SMMSSYSAAD	RSMMSSYSAA	DRSMMSSYTA
1130	1140	1150	1160	1170	1180	1190	1200
DRSMMSMAAD	SYTDSYTDTY	TEAYMVPPLP	PEEPPTMPPL	PPEEPPMTPP	LPPEEPPEGP	ALPTEQSALT	AENTWPTEVP
1210	1220	1230	1240	1250	1260	1270	1280
SSPSEESVSQ	PEPPVSQSEI	SEPSAVPTDY	SVSASDPSVL	VSEAAVTVPE	PPPEPESSIT	LTPVESAVVA	EEHEVVPERP
1290	1300	1310	1320	1330	1340	1350	1360
VTCMVSETPA	MSAEPTVLAS	EPPVMSETAE	TFDSMRASGH	VASEVSTSLL	VPAVTTPVLA	ESILEPPAMA	APESSAMAVL
1370	1380	1390	1400	1410	1420	1430	1440
ESSAVTVLES	STVTVLESST	VTVLEPSVVT	VPEPPVVAEP	DYVTIPVPVV	SALEPSVPVL	EPAVSVLQPS	MIVSEPSVSV
1450	1460	1470	1480	1490	1500	1510	1520
QESTVTVSEP	AVTVSEQTQV	IPTEVAIEST	PMILESSIMS	SHVMKGINLS	SGDQNLAPEI	GMQEIALHSG	EEPHAEEHLK
1530	1540	1550	1560	1570	1580	1590	1600
GDFYESEHGI	NIDLNINNHL	IAKEMEHNTV	CAAGTSPVGE	IGEEKILPTS	ETKQRTVLDT	YPGVSEADAG	ETLSSTGPFA
1610	1620	1630	1640	1650	1660	1670	1680
LEPDATGTSK	GIEFTTASTL	SLVNKYDVDL	SLTTQDTEHD	MVISTSPSGG	SEADIEGPLP	AKDIHLDLPS	NNNLVSKDTE
1690	1700	1710	1720	1730	1740	1750	1760
EPLPVKESDQ	TLAALLSPKE	SSGGEKEVPP	PPKETLPDSG	FSANIEDINE	ADLVRPLLPK	DMERLTSLRA	GIEGPLLASD
1770	1780	1790	1800	1810	1820	1830	1840
VGRDRSAASP	VVSSMPERAS	ESSSEEKDDY	EIFVKVKDTH	EKSKKNKNRD	KGEKEKKRDS	SLRSRSKRSK	SSEHKSRKRT
1850	1860	1870	1880	1890	1900	1910	1920
SESRSRARKR	SSKSKSHRSQ	TRSRSRSRRR	RRSSRSRSKS	RGRRSVSKEK	RKRSPKHRSK	SRERKRKRSS	SRDNRKTVRA
1930	1940	1950	1960	1970	1980	1990	2000
RSRTPSRRSR	SHTPSRRRRS	RSVGRRRSFS	ISPSRRSRTP	SRRSRTPSRR	SRTPSRRSRT	PSRRSRTPSR	RSRTPSRRRR
2010	2020	2030	2040	2050	2060	2070	2080
SRSVVRRRSF	SISPVRLRRS	RTPLRRRFSR	SPIRRKRSRS	SERGRSPKRL	TDLDKAQLLE	IAKANAAAMC	AKAGVPLPPN
2090	2100	2110					
LKPAPPPTIE	EKVAKKSGGA	TIEELTEF					

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1554	1	513.1087	-205.66	2	47.7	12.6	0	1073-1081	R.SMMSPMADR.S	

Detailed Protein Report

Protein 769: uncharacterized protein LOC388780 [Homo sapiens]

Accession:	gi|567315929	**Score:**	12.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	14.2
Database Date:	2015-11-30	**pI:**	10.7
		Sequence Coverage [%]:	7.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MATAGSQHRR	RENEDRSRVT	ALAFEQPRES	LCVLQPPLPF	MSEVLSPQRS	PQRAFPDAYE	TGSAWAQVEE	GPAWPPPRSP
90	**100**	**110**	**120**	**130**			
WGPCPFRRFS	RVLHHGNSGV	GSVGCEPSGW	GSRRALSASP	REVTQEHH			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2121	1	557.8753	170.20	2	54.9	12.6	1	1-10	-.MATAGSQHRR.R	

Detailed Protein Report

Protein 770: prokineticin-1 precursor [Homo sapiens]

Accession:	gi|14165282	**Score:**	12.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	11.7
Database Date:	2015-11-30	**pI:**	11.6
Modification(s):	Carbamidomethyl, Oxidation	**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

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Detailed Protein Report

Protein 771: PREDICTED: calcyphosin-like protein isoform X2 [Homo sapiens]

Accession:	gi|578809847	**Score:**	12.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	23.1
Database Date:	2015-11-30	**pI:**	8.9
Modification(s):	Oxidation	**Sequence Coverage [%]:**	7.5
		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
2813	1	895.4559	30.47	2	63.8	12.6	1	80-94	K.EFMKGLNDYAVVMEK.E	Oxidation: 3

Detailed Protein Report

Protein 772: **melanoma-associated antigen B17 [Homo sapiens]**

Accession: gi|472235301

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Score: 12.6

MW [kDa]: 37.6

pI: 9.8

Sequence Coverage [%]: 2.7

No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MPRGQASKRR	AREKRRQARG	EDQCLGGAQA	TAAEKEKLPS	SSSPACQSPP	QSFPNAGIPQ	ESQRASYPSS	PASAVSLTSS
90	100	110	120	130	140	150	160
DEGAKGQKGE	SPNSFHGPSS	SESTGRDLLN	TKTGELVQFL	LNKYIRKEPI	TREAMLKVIN	RKYKQHFPEI	LRRSTENVEV
170	180	190	200	210	220	230	240
VFGLYLKEMD	PSRQSYVLVG	KLDFPNQGSL	SDGGGFPLSG	LLMVLLSTIF	MHGNRATEEE	MWECLNALGM	YKGRKHFIYG
250	260	270	280	290	300	310	320
EPQELVTKDL	VREGYLEYQQ	VPSSDPPRYE	FLWGPRARAE	TSKMKVLEFV	AKLNDTVAST	YKSRYEEALR	EEEEQARARA
330	340						
VARDSARARA	SRSFQP						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1134	1	510.1594	-222.02	2	42.4	12.6	2	328-336	R.ARASRSFQP.-	

Detailed Protein Report

Protein 773: **PREDICTED: 3 beta-hydroxysteroid dehydrogenase type 7 isoform X1 [Homo sapiens]**

Accession:	gi|530409203	**Score:**	12.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	51.3
Database Date:	2015-11-30	**pI:**	10.0
		Sequence Coverage [%]:	5.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MRSPLAPPTA	PDPFSPLCKF	ELHPHQVLRW	TQMPVEHRAA	ARGRLGARVV	GVVAGRVSVP	GMGQEGEGGA	SGRTVCGPAS
90	100	110	120	130	140	150	160
PGRKKRAPPG	QSGHPGIAAA	GMADSAQAQK	LVYLVTGGCG	FLGEHVVRML	LQREPRLGEL	RVFDQHLGPW	LEELKTGPVR
170	180	190	200	210	220	230	240
VTAIQGDVTQ	AHEVAAAVAG	AHVVIHTAGL	VDVFGRASPK	TIHEVNVQGT	RNVIEACVQT	GTRFLVYTSS	MEVVGPNTKG
250	260	270	280	290	300	310	320
HPFYRGNEDT	PYEAVHRHPY	PCSKALAEWL	VLEANGRKVR	GGLPLVTCAL	RPTGIYGEGH	QIMRDFYRQG	LRLGGWLFRA
330	340	350	360	370	380	390	400
IPASVEHGRV	YVGNVAWMHV	LAARELEQRA	TLMGGQVYFC	YDGSPYRSYE	DFNMEFLGPC	GLRLVGARPL	LPYWLLVFLA
410	420	430	440	450	460	470	480
ALNALLQWLL	RPLVLYAPLL	NPYTLAVANT	TFTVSTDKAQ	RHFGYEPLFS	WEDSRTRTIL	WVQAATGSAQ	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1753	1	626.2639	-91.47	4	50.3	12.6	2	85-110	K.KRAPPGQSGHPGIAAAGMADSAQAQK.L	

Detailed Protein Report

Protein 774: **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 775: 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

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
344	1	952.8297	-93.31	2	33.4	12.5	1	1-17	-.MGNLCYCIQGDSKNSSK.K	Carbamidomethyl: 5

Detailed Protein Report

Protein 776: epithelial cell adhesion molecule precursor [Homo sapiens]

Accession:	gi|218505670	**Score:**	12.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	34.9
Database Date:	2015-11-30	**pI:**	8.7
		Sequence Coverage [%]:	4.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAPPQVLAFG	LLLAAATATF	AAAQEECVCE	NYKLAVNCFV	NNNRQCQCTS	VGAQNTVICS	KLAAKCLVMK	AEMNGSKLGR
90	100	110	120	130	140	150	160
RAKPEGALQN	NDGLYDPDCD	ESGLFKAKQC	NGTSMCWCVN	TAGVRRTDKD	TEITCSERVR	TYWIIIELKH	KAREKPYDSK
170	180	190	200	210	220	230	240
SLRTALQKEI	TTRYQLDPKF	ITSILYENNV	ITIDLVQNSS	QKTQNDVDIA	DVAYYFEKDV	KGESLFHSKK	MDLTVNGEQL
250	260	270	280	290	300	310	320
DLDPGQTLIY	YVDEKAPEFS	MQGLKAGVIA	VIVVVVIAVV	AGIVVLVISR	KKRMAKYEKA	EIKEMGEMHR	ELNA

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
98	1	850.1495	168.44	2	30.2	12.5	2	139-151	R.VRTYWIIIELKHK.A	

Detailed Protein Report

Protein 777: olfactory receptor 13J1 [Homo sapiens]

Accession:	gi|52218862	**Score:**	12.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	34.7
Database Date:	2015-11-30	**pI:**	10.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEPLNRTEVS	EFFLKGFSGY	PALEHLLFPL	CSAMYLVTLL	GNTAIMAVSV	LDIHLHTPVY	FFLGNLSTLD	ICYTPTFVPL
90	100	110	120	130	140	150	160
MLVHLLSSRK	TISFAVCAIQ	MCLSLSTGST	ECLLLAITAY	DRYLAICQPL	RYHVLMSHRL	CVLLMGAAWV	LCLLKSVTEM
170	180	190	200	210	220	230	240
VISMRLPFCG	HHVVSHFTCK	ILAVLKLACG	NTSVSEDFLL	AGSILLLPVP	LAFICLSYLL	ILATILRVPS	AARCCKAFST
250	260	270	280	290	300	310	320
CLAHLAVVLL	FYGTIIFMYL	KPKSKEAHIS	DEVFTVLYAM	VTTMLNPTIY	SLRNKEVKEA	ARKVWGRSRA	SR

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2253	1	524.7006	-103.56	2	56.5	12.5	1	228-236	R.VPSAARCCK.A	Carbamidomethyl: 7, 8

Detailed Protein Report

Protein 778: PREDICTED: orexin receptor type 1 isoform X2 [Homo sapiens]

Accession:	gi|530362467	**Score:**	12.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	32.0
Database Date:	2015-11-30	**pI:**	10.8
Modification(s):	Oxidation	**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 779: **complement C4-A isoform 2 preproprotein [Homo sapiens]**

Accession:	gi|356582273	**Score:**	12.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	187.6
Database Date:	2015-11-30	**pI:**	6.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	0.8
		No. of unique Peptides:	1

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
946	2	872.2583	-156.84	2	40.6	12.5	0	730-743	R.EPFLSCCQFAESLR.K	Carbamidomethyl: 6, 7

Detailed Protein Report

Protein 780: zinc finger protein 609 [Homo sapiens]

Accession:	gi|71725360	**Score:**	12.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	151.1
Database Date:	2015-11-30	**pI:**	9.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	0.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSLSSGASGG	KGVDANPVET	YDSGDEWDIG	VGNLIIDLDA	DLEKDQQKLE	MSGSKEVGIP	APNAVATLPD	NIKFVTPVPG
90	100	110	120	130	140	150	160
PQGKEGKSKS	KRSKSGKDTS	KPTPGTSLFT	PSEGAASKKE	VQGRSGDGAN	AGGLVAAIAP	KGSEKAAKAS	RSVAGSKKEK
170	180	190	200	210	220	230	240
ENSSSKSKKE	RSEGVGTCSE	KDPGVLQPVP	LGGRGGQYDG	SAGVDTGAVE	PLGSIAIEPG	AALNPLGTKP	EPEEGENECR
250	260	270	280	290	300	310	320
LLKKVKSEKM	ESPVSTPAVL	PIHLLVPVVN	NDISSPCEQI	MVRTRSVGVN	TCDVALATEP	ECLGPCEPGT	SVNLEGIVWQ
330	340	350	360	370	380	390	400
ETEDGMLVVN	VTWRNKTYVG	TLLDCTRHDW	APPRFCDSPT	SDLEMRNGRG	RGKRMRPNSN	TPVNETATAS	DSKGTSNSSK
410	420	430	440	450	460	470	480
TRAGANSKGR	RGSQNSSEHR	PPASSTSEDV	KASPSSANKR	KNKPLSDMEL	NSSSEDSKGS	KRVRTNSMGS	ATGPLPGTKV
490	500	510	520	530	540	550	560
EPTVLDRNCP	SPVLIDCPHP	NCNKKYKHIN	GLKYHQAHAH	TDDDSKPEAD	GDSEYGEEPI	LHADLGSCNG	ASVSQKGSLS
570	580	590	600	610	620	630	640
PARSATPKVR	LVEPHSPSPS	SKFSTKGLCK	KKLSGEGDTD	LGALSNDGSD	DGPSVMDETS	NDAFDSLERK	CMEKEKCKKP
650	660	670	680	690	700	710	720
SSLKPEKIPS	KSLKSARPIA	PAIPPQQIYT	FQTATFTAAS	PGSSSGLTAT	VAQAMPNSPQ	LKPIQPKPTV	MGEPFTVNPA
730	740	750	760	770	780	790	800
LTPAKDKKKK	DKKKKESSKE	LESPLTPGKV	CRAEEGKSPF	RESSGDGMKM	EGLLNGSSDP	HQSRLASIKA	EADKIYSFTD
810	820	830	840	850	860	870	880
NAPSPSIGGS	SRLENTTPTQ	PLTPLHVVTQ	NGAEASSVKT	NSPAYSDISD	AGEDGEGKVD	SVKSKDAEQL	VKEGAKKTLF
890	900	910	920	930	940	950	960
PPQPQSKDSP	YYQGFESYYS	PSYAQSSPGA	LNPSSQAGVE	SQALKTKRDE	EPESIEGKVK	NDICEEKKPE	LSSSSQQPSV
970	980	990	1000	1010	1020	1030	1040
IQQRPNMYMQ	SLYYNQYAYV	PPYGYSDQSY	HTHLLSTNTA	YRQQYEEQQK	RQSLEQQQRG	VDKKAEMGLK	EREAALKEEW
1050	1060	1070	1080	1090	1100	1110	1120
KQKPSIPPTL	TKAPSLTDLV	KSGPGKAKEP	GADPAKSVII	PKLDDSSKLP	GQAPEGLKVK	LSDASHLSKE	ASEAKTGAEC
1130	1140	1150	1160	1170	1180	1190	1200
GRQAEMDPIL	WYRQEAEPRM	WTYVYPAKYS	DIKSEDERWK	EERDRKLKEE	RSRSKDSVPK	EDGKESTSSD	CKLPTSEESR
1210	1220	1230	1240	1250	1260	1270	1280
LGSKEPRPSV	HVPVSSPLTQ	HQSYIPYMHG	YSYSQSYDPN	HPSYRSMPAV	MMQNYPGSYL	PSSYSFSPYG	SKVSGGEDAD
1290	1300	1310	1320	1330	1340	1350	1360
KARASPSVTC	KSSSESKALD	ILQQHASHYK	SKSPTISDKT	SQERDRGGCG	VVGGGGSCSS	VGGASGGERS	VDRPRTSPSQ
1370	1380	1390	1400	1410	1420		
RLMSTHHHHH	HLGYSLLPAQ	YNLPYAAGLS	STAIVASQQG	STPSLYPPPR	R		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2845	1	657.3625	105.46	2	64.2	12.5	1	758-769	K.SPFRESSGDGMK.M	Oxidation: 11

Detailed Protein Report

Protein 781: PREDICTED: integrator complex subunit 8 isoform X1 [Homo sapiens]

Accession: gi|578816078
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 12.5
MW [kDa]: 107.3
pI: 6.8
Sequence Coverage [%]: 2.0
No. of unique Peptides: 1

Quantitation

WD:WU **Median:** 0.55 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MSAEAADREA ATSSRPCTPP QTCWFEFLLE ESLLEKHLRK PCPDPAPVQL IVQFLEQASK PSVNEQNQVQ PPPDNKRNRI

        90        100        110        120        130        140        150        160
LKLLALKVAA HLKWDLDILE KSLSVPVLNM LLNELLCISK VPPGTKHVDM DLATLPPTTA MAVLLYNRWA IRTIVQSSFP

       170        180        190        200        210        220        230        240
VKQAKPGPPQ LSVMNQMQQE KELTENILKV LKEQAADSIL VLEAALKLNK DLYVHTMRTL DLLAMEPGMV NGETESSTAG

       250        260        270        280        290        300        310        320
LKVKTEEMQC QVCYDLGAAY FQQGSTNSAV YENAREKFFR TKELIAEEVI QIFIEDNLTL SLPVQFRQSV LRELFKKAQQ

       330        340        350        360        370        380        390        400
GNEALDEICF KVCACNTVRD ILEGRTISVQ FNQLFLRPNK EKIDFLLEVC SRSVNLEKAS ESLKGNMAAF LKNVCLGLED

       410        420        430        440        450        460        470        480
LQYVFMISSH ELFITLLKDE ERKLLVDQMR KRSPRVNLCI KPVTSFYDIP ASASVNIGQL EHQLILSVDP WRIRQILIEL

       490        500        510        520        530        540        550        560
HGMTSERQFW TVSNKWEVPS VYSGVILGIK DNLTRDLVYI LMAKGLHCST VKDFSHAKQL FAACLELVTE FSPKLRQVML

       570        580        590        600        610        620        630        640
NEMLLLDIHT HEAGTGQAGE RPPSDLISRV RGYLEMRLPD IPLRQVIAEE CVAFMLNWRE NEYLTLQVPA FLLQSNPYVK

       650        660        670        680        690        700        710        720
LGQLLAATCK ELPGPKESRR TAKDLWEVVV QICSVSSQHK RGNDGRVSLI KQRESTLGIM YRSELLSFIK KLREPLVLTI

       730        740        750        760        770        780        790        800
ILSLFVKLHN VREDIVNDIT AEHISIWPSS IPNLQSVDFE AVAITVKELV RYTLSINPNN HSWLIIQADI YFATNQYSAA

       810        820        830        840        850        860        870        880
LHYYLQAGAV CSDFFNKAVP PDVYTDQVIK RMIKCCSLLN CHTQVAILCQ FLREIDYKTA FKSLQEQNSH DAMDSYYDYI

       890        900        910        920        930        940        950
WDVTILEYLT YLHHKRGETD KRQIAIKAIG QTELNASNPE EVLQLAAQRR KKKFLQAMAK LYF
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2583	1	701.3615	-42.72	3	60.6	12.5	0	102-120	K.SLSVPVLNMLLNELLCISK.V	Oxidation: 9	WD:WU 0.55

Detailed Protein Report

Protein 782: 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 783: cadherin-6 preproprotein [Homo sapiens]

Accession:	gi|4826673	**Score:**	12.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	88.3
Database Date:	2015-11-30	**pI:**	4.6
		Sequence Coverage [%]:	1.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MRTYRYFLLL	FWVGQPYPTL	STPLSKRTSG	FPAKKRALEL	SGNSKNELNR	SKRSWMWNQF	FLLEEYTGSD	YQYVGKLHSD
90	100	110	120	130	140	150	160
QDRGDGSLKY	ILSGDGAGDL	FIINENTGDI	QATKRLDREE	KPVYILRAQA	INRRTGRPVE	PESEFIIKIH	DINDNEPIFT
170	180	190	200	210	220	230	240
KEVYTATVPE	MSDVGTFVVQ	VTATDADDPT	YGNSAKVVYS	ILQGQPYFSV	ESETGIIKTA	LLNMDRENRE	QYQVVIQAKD
250	260	270	280	290	300	310	320
MGGQMGGLSG	TTTVNITLTD	VNDNPPRFPQ	STYQFKTPES	SPPGTPIGRI	KASDADVGEN	AEIEYSITDG	EGLDMFDVIT
330	340	350	360	370	380	390	400
DQETQEGIIT	VKKLLDFEKK	KVYTLKVEAS	NPYVEPRFLY	LGPFKDSATV	RIVVEDVDEP	PVFSKLAYIL	QIREDAQINT
410	420	430	440	450	460	470	480
TIGSVTAQDP	DAARNPVKYS	VDRHTDMDRI	FNIDSGNGSI	FTSKLLDRET	LLWHNITVIA	TEINNPKQSS	RVPLYIKVLD
490	500	510	520	530	540	550	560
VNDNAPEFAE	FYETFVCEKA	KADQLIQTLH	AVDKDDPYSG	HQFSFSLAPE	AASGSNFTIQ	DNKDNTAGIL	TRKNGYNRHE
570	580	590	600	610	620	630	640
MSTYLLPVVI	SDNDYPVQSS	TGTVTVRVCA	CDHHGNMQSC	HAEALIHPTG	LSTGALVAIL	LCIVILLVTV	VLFAALRRQR
650	660	670	680	690	700	710	720
KKEPLIISKE	DIRDNIVSYN	DEGGGEEDTQ	AFDIGTLRNP	EAIEDNKLRR	DIVPEALFLP	RRTPTARDNT	DVRDFINQRL
730	740	750	760	770	780	790	800
KENDTDPTAP	PYDSLATYAY	EGTGSVADSL	SSLESVTTDA	DQDYDYLSDW	GPRFKKLADM	YGGVDSDKDS	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2689	1	701.4103	66.95	2	62.0	12.4	2	702-713	R.RTPTARDNTDVR.D	

Detailed Protein Report

Protein 784: lck-interacting transmembrane adapter 1 precursor [Homo sapiens]

Accession:	gi|157388906	**Score:**	12.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	31.3
Database Date:	2015-11-30	**pI:**	11.1
		Sequence Coverage [%]:	4.1
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 1.99 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MGLPVSWAPP	ALWVLGCCAL	LLSLWALCTA	CRRPEDAVAP	RKRARRQRAR	LQGSATAAEA	SLLRRTHLCS	LSKSDTRLHE
90	100	110	120	130	140	150	160
LHRGPRSSRA	LRPASMDLLR	PHWLEVSRDI	TGPQAAPSAF	PHQELPRALP	AAAATAGCAG	LEATYSNVGL	AALPGVSLAA
170	180	190	200	210	220	230	240
SPVVAEYARV	QKRKGTHRSP	QEPQQGKTEV	TPAAQVDVLY	SRVCKPKRRD	PGPTTDPLDP	KGQGAILALA	GDLAYQTLPL
250	260	270	280	290	300		
RALDVDSGPL	ENVYESIREL	GDPAGRSSTC	GAGTPPASSC	PSLGRGWRPL	PASLP		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2206	1	626.6775	-205.72	2	55.9	12.4	0	210-221	R.DPGPTTDPLDPK.G		WD:WU 1.99

Detailed Protein Report

Protein 785: PREDICTED: N-glycosylase/DNA lyase isoform X1 [Homo sapiens]

Accession:	gi|530372567	**Score:**	12.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	35.9
Database Date:	2015-11-30	**pI:**	9.2
Modification(s):	Oxidation	**Sequence Coverage [%]:**	8.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPARALLPRR	MGHRTLASTP	ALWASIPCPR	SELRLDLVLP	SGQSFRWREQ	SPAHWSGVLA	DQVWTLTQTE	EQLHCTVYRG
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
DKSQASRPTP	DELEAVRKYF	QLDVTLAQLY	HHWGSVDSHF	QEVAQKFQGV	RLLRQDPIEC	LFSFICSSNN	NIARITGMVE
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
RLCQAFGPRL	IQLDDVTYHG	FPSLQALAGP	EVEAHLRKLG	LGYRARYVSA	SARAILEEQG	GLAWLQQLRE	SSYEEAHKAL
250	**260**	**270**	**280**	**290**	**300**	**310**	**320**
CILPGVGTKV	ADCICLMALD	KPQAVPVDVH	MWHIAQRDYS	WHPTTSQAKG	PSPQTNKELG	NFFRSLWGPY	AGWAQAINF

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1563	1	1059.1172	-72.43	3	47.9	12.4	0	250-277	K.VADCICLMALDKPQAVPVDVHMWHIAQR.D	Oxidation: 8

Detailed Protein Report

Protein 786: **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 787: 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 788: furin preproprotein [Homo sapiens]

Accession:	gi|4505579	**Score:**	12.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	86.6
Database Date:	2015-11-30	**pI:**	6.0
Modification(s):	Oxidation	**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 789: 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 790: **PREDICTED: DNA repair and recombination protein RAD54-like isoform X1 [Homo sapiens]**

Accession:	gi|578799949	**Score:**	12.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	64.0
Database Date:	2015-11-30	**pI:**	9.1
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.0
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MADEMGLGKT LQCITLMWTL LRQSPECKPE IDKAVVVSPS SLVKNWYNEV GKWLGGRIQP LAIDGGSKDE IDQKLEGFMN
        90        100        110        120        130        140        150        160
QRGARVSSPI LIISYETFRL HVGVLQKGSV GLVICDEGHR LKNSENQTYQ ALDSLNTSRR VLISGTPIQN DLLEYFSLVH
       170        180        190        200        210        220        230        240
FVNSGILGTA HEFKKHFELP ILKGRDAAAS EADRQLGEER LRELTSIVNR CLIRRTSDIL SKYLPVKIEQ VVCCRLTPLQ
       250        260        270        280        290        300        310        320
TELYKRFLRQ AKPAEELLEG KMSVSSLSSI TSLKKLCNHP ALIYDKCVEE EDGFVGALDL FPPGYSSKAL EPQLSGKMLV
       330        340        350        360        370        380        390        400
LDYILAVTRS RSSDKVVLVS NYTQTLDLFE KLCRARRYLY VRLDGTMSIK KRAKVVERFN SPSSPDFVFM LSSKAGGCGL
       410        420        430        440        450        460        470        480
NLIGANRLVM FDPDWNPAND EQAMARVWRD GQKKTCYIYR LLSAGTIEEK IFQRQSHKKA LSSCVVDEEQ DVERHFSLGE
       490        500        510        520        530        540        550        560
LKELFILDEA SLSDTHDRLH CRRCVNSRQI RPPPDGSDCT SDLAGWNHCT DKWGLRDEVL QAAWDAASTA ITFVFHQRSH
       570
EEQRGLR
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1960	1	1022.8951	-142.08	2	53.2	12.4	2	434-450	K.KTCYIYRLLSAGTIEEK.I	Carbamidomethyl: 3

Detailed Protein Report

Protein 791: DDB1- and CUL4-associated factor 13 [Homo sapiens]

Accession:	gi|229892270	**Score:**	12.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	67.5
Database Date:	2015-11-30	**pI:**	10.2
		Sequence Coverage [%]:	2.8
		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 792: **PREDICTED: asparagine synthetase domain-containing protein 1 isoform X1 [Homo sapiens]**

Accession:	gi|530370551	**Score:**	12.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	72.0
Database Date:	2015-11-30	**pI:**	6.4
		Sequence Coverage [%]:	2.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
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 793: **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

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	m/z meas.		z	Rt	Score	P	Range	Sequence	Modification

Detailed Protein Report

	Cmpds.		Δ m/z [ppm]		[min]					
1647	1	938.9364	-41.92	2	49.3	12.4	2	813-829	K.VMGLLNCKMPPAEKASR.I	Oxidation: 2, 9

Detailed Protein Report

Protein 794: **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

Quantitation

WD:WU **Median:** 0.72 **CV:** 0.00 % **No. of 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	Ratios
70	1	518.2613	-57.00	3	30.1	12.4	0	547-560	K.SLNLVDSPQPLLEK.V		WD:WU 0.72

Detailed Protein Report

Protein 795: **mitochondrial uncoupling protein 3 isoform UCP3S [Homo sapiens]**

Accession:	gi|13259546	**Score:**	12.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	29.8
Database Date:	2015-11-30	**pI:**	9.9
		Sequence Coverage [%]:	5.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MVGLKPSDVP	PTMAVKFLGA	GTAACFADLV	TFPLDTAKVR	LQIQGENQAV	QTARLVQYRG	VLGTILTMVR	TEGPCSPYNG
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
LVAGLQRQMS	FASIRIGLYD	SVKQVYTPKG	ADNSSLTTRI	LAGCTTGAMA	VTCAQPTDVV	KVRFQASIHL	GPSRSDRKYS
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
GTMDAYRTIA	REEGVRGLWK	GTLPNIMRNA	IVNCAEVVTY	DILKEKLLDY	HLLTDNFPCH	FVSAFGAGFC	ATVVASPVDV
250	**260**	**270**	**280**				
VKTRYMNSPP	GQYFSPLDCM	IKMVAQEGPT	AFYKG				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2964	2	869.4193	-26.04	2	65.8	12.4	1	104-119	K.QVYTPKGADNSSLTTR.I	

Detailed Protein Report

Protein 796: potassium voltage-gated channel subfamily C member 1 isoform A [Homo sapiens]

Accession:	gi|163792201	**Score:**	12.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	65.8
Database Date:	2015-11-30	**pI:**	5.8
Modification(s):	Carbamidomethyl	**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 797: PREDICTED: transcription initiation factor TFIID subunit 6 isoform X2 [Homo sapiens]

Accession:	gi|578814558	**Score:**	12.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	71.4
Database Date:	2015-11-30	**pI:**	9.6
		Sequence Coverage [%]:	4.5
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578814560	refseq_human (refseq_human_20140103.fasta)	PREDICTED: transcription initiation factor TFIID subunit 6 isoform X3 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MAEEKKLKLS NTVLPSESMK VVAESMGIAQ IQEETCQLLT DEDALKFMHM GKRQKLTTSD IDYALKLKNV EPLYGFHAQE

        90        100        110        120        130        140        150        160
FIPFRFASGG GRELYFYEEK EVDLSDIINT PLPRVPLDVC LKAHWLSIEG CQPAIPENPP PAPKEQQKAE ATEPLKSAKP

       170        180        190        200        210        220        230        240
GQEEDGPLKG KGQGATTADG KGKEKKAPPL LEGAPLRLKP RSIHELSVEQ QLYYKEITEA CVGSCEAKRA EALQSIATDP

       250        260        270        280        290        300        310        320
GLYQMLPRFS TFISEGVRVN VVQNNLALLI YLMRMVKALM DNPTLYLEKY VHELIPAVMT CIVSRQLCLR PDVDNHWALR

       330        340        350        360        370        380        390        400
DFAARLVAQI CKHFSTTTNN IQSRITKTFT KSWVDEKTPW TTRYGSIAGL AELGHDVIKT LILPRLQQEG ERIRSVLDGP

       410        420        430        440        450        460        470        480
VLSNIDRIGA DHVQSLLLKH CAPVLAKLRP PPDNQDAYRA EFGSLGPLLC SQVVKARAQA ALQAQQVNRT TLTITQPRPT

       490        500        510        520        530        540        550        560
LTLSQAPQPG PRTPGLLKVP GSIALPVQTL VSARAAAPPQ PSPPPTKFIV MSSSSSAPST QQVLSLSTSA PGSGSTTTSP

       570        580        590        600        610        620        630        640
VTTTVPSVQP IVKLVSTATT APPSTAPSGP GSVQKYIVVS LPPTGEGKGG PTSHPSPVPP PASSPSPLSG SALCGGKQEA

       650        660        670
GDSPPPAPGT PKANGSQPNS GSPQPAP
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
868	1	946.6986	-87.24	3	39.3	12.4	1	638-667	K.QEAGDSPPPAPGTPKANGSQPNSGSPQPAP.-	

Detailed Protein Report

Protein 798: 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 799: insulin receptor substrate 1 [Homo sapiens]

Accession:	gi|5031805	**Score:**	12.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	131.5
Database Date:	2015-11-30	**pI:**	9.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.0
		No. of unique 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
1995	1	719.2866	-53.40	2	53.6	12.3	0	952-964	R.AAWQESTGVEMGR.L	Oxidation: 11

Detailed Protein Report

Protein 800: PREDICTED: caspase-10 isoform X6 [Homo sapiens]

Accession:	gi|578805020	**Score:**	12.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	30.8
Database Date:	2015-11-30	**pI:**	9.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	6.3
		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 801: 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 802: **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 803: 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

Quantitation

WD:WU **Median:** 0.88 **CV:** 0.00 % **No. of 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	Ratios
1887	1	918.4473	8.72	2	52.3	12.3	2	324-338	R.MHLGEKPYKCRECGK.A	Carbamidomethyl: 10	WD:WU 0.88

Detailed Protein Report

Protein 804: PREDICTED: WD repeat-containing protein 19 isoform X3 [Homo sapiens]

Accession:	gi|578808579	**Score:**	12.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	144.7
Database Date:	2015-11-30	**pI:**	6.1
		Sequence Coverage [%]:	1.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MKRIFSLLEK	TWLGAPIQFA	WQKTSGNYLA	VTGADYIVKI	FDRHGQKRSE	INLPGNCVAM	DWDKDGDVLA	VIAEKSSCIY
90	100	110	120	130	140	150	160
LWDANTNKTS	QLDNGMRDQM	SFLLWSKVGS	FLAVGTVKGN	LLIYNHQTSR	KIPVLGKHTK	RITCGCWNAE	NLLALGGEDK
170	180	190	200	210	220	230	240
MITVSNQEGD	TIRQTQVRSE	PSNMQFFLMK	MDDRTSAAES	MISVVLGKKT	LFFLNLNEPD	NPADLEFQQD	FGNIVCYNWY
250	260	270	280	290	300	310	320
GDGRIMIGFS	CGHFVVISTH	TGELGQEIFQ	ARNHKDNLTS	IAVSQTLNKV	ATCGDNCIKI	QDLVDLKDMY	VILNLDEENK
330	340	350	360	370	380	390	400
GLGTLSWTDD	GQLLALSTQR	GSLHVFLTKL	PILGDACSTR	IAYLTSLLEV	TVANPVEGEL	PITVSVDVEP	NFVAVGLYHL
410	420	430	440	450	460	470	480
AVGMNNRAWF	YVLGENAVKK	LKDMEYLGTV	ASICLHSDYA	AALFEGKVQL	HLIESEILDA	QEERETRLFP	AVDDKCRILC
490	500	510	520	530	540	550	560
HALTSDFLIY	GTDTGVVQYF	YIEDWQFVND	YRHPVSVKKI	FPDPNGTRLV	FIDEKSDGFV	YCPVNDATYE	IPDFSPTIKG
570	580	590	600	610	620	630	640
VLWENWPMDK	GVFIAYDDDK	VYTYVFHKDT	IQGAKVILAG	STKVPFAHKP	LLLYNGELTC	QTQSGKVNNI	YLSTHGFLSN
650	660	670	680	690	700	710	720
LKDTGPDELR	PMLAQNLMLK	RFSDAWEMCR	ILNDEAAWNE	LARACLHHME	VEFAIRVYRR	IGNVGIVMSL	EQIKGIEDYN
730	740	750	760	770	780	790	800
LLAGHLAMFT	NDYNLAQDLY	LASSCPIAAL	EMRRDLQHWD	SALQLAKHLA	PDQIPFISKE	YAIQLEFAGD	YVNALAHYEK
810	820	830	840	850	860	870	880
GITGDNKEHD	EACLAGVAQM	SIRMGDIRRG	VNQALKHPSR	VLKRDCGAIL	ENMKQFSEAA	QLYEKGLYYD	KAASVYIRSK
890	900	910	920	930	940	950	960
NWAKVGDLLP	HVSSPKIHLQ	YAKAKEADGR	YKEAVVAYEN	AKQWQSVIRI	YLDHLNNPEK	AVNIVRETQS	LDGAKMVARF
970	980	990	1000	1010	1020	1030	1040
FLQLGDYGSA	IQFLVMSKCN	NEAFTLAQQH	NKMEIYADII	GSEDTTNEDY	QSIALYFEGE	KRYLQAGKFF	LLCGQYSRAL
1050	1060	1070	1080	1090	1100	1110	1120
KHFLKCPSSE	DNVAIEMAIE	TVGQAKDELL	TNQLIDHLLG	ENDGMPKDAK	YLFRLYMALK	QYREAAQTAI	IIAREEQSAG
1130	1140	1150	1160	1170	1180	1190	1200
NYRNAHDVLF	SMYAELKSQK	IKIPSEMATN	LMILHSYILV	KIHVKNGDHM	KGARMLIRVA	NNISKFPSHI	VPILTSTVIE
1210	1220	1230	1240	1250	1260	1270	1280
CHRAGLKNSA	FSFAAMLMRP	EYRSKIDAKY	KKKIEGMVRE	RQRENTKLTT	PVAQEERRPQ	DLPMLSAVEC	AMNSSSQRWP
1290							
M							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
389	1	733.4679	112.36	3	33.5	12.3	1	643-661	K.DTGPDELRPMLAQNLMLKR.F	

Detailed Protein Report

Protein 805: PREDICTED: LOW QUALITY PROTEIN: BCL-6 corepressor-like [Homo sapiens]

Accession:	gi|578797994	**Score:**	12.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	70.6
Database Date:	2015-11-30	**pI:**	9.6
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	1.9
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 0.90 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MMGSEFPTAR	LSNSKYPETL	EVGESAQPVP	MYTWKTVAQD	RKDGVSPPLL	EKQSITKSIS	NKPVELSSKV	VEVDASKADH
90	100	110	120	130	140	150	160
MKKMASMGLV	HSMAGSGLVL	SRSEILKEIS	SLRNGCAIYR	SEFISTDPSS	WVVPRPRTNE	ENNGESMLKN	KVMDWMIIQQ
170	180	190	200	210	220	230	240
QSSFYLCMNG	KGTMIPNVLG	SVSCAGHPTS	ILTLYYQSPT	PHRADGTRTN	RSSVDTTSSI	IQQVGQPPTV	PVKQSSSTSS
250	260	270	280	290	300	310	320
KVAKASSPEL	SFKANXDGLQ	PSPLFLPPNE	AFRPPSISHP	RSYFPYPVPK	ATAIRPFSLH	DKGPVYPHPV	LLPNNSLFLG
330	340	350	360	370	380	390	400
CLASKPRLPY	VVPMGHPEFL	IYQDALGFGM	VQPMLITHRP	IEITKKEKPE	RRSHSQERAC	RKDPTLQNQF	SEMLEASSTA
410	420	430	440	450	460	470	480
FHPEVPNDSL	KLNPSWNQGK	IIIRSDKVVY	VDHLQEKTDA	KTDANVSKPS	FIMKSVGQNA	DPASPPIVKP	YLQQHGDFIT
490	500	510	520	530	540	550	560
LREKLGHIDD	FHEPYTIKQT	PTNKEKKEVE	AGTNKENIGM	PVSTSFLEPT	LVSDGHAVTF	GKIQEYPKPY	CLGSAPLSMD
570	580	590	600	610	620	630	640
IISTYTKDGA	NEAKSSDGKL	LKPKPSNLVK	RVTTSAGCMA	DRLKCVTTEL	YADSSQLSWE	QRALQVTPST	HLLATLPVVT
650							
V							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1042	1	670.8061	0.27	2	41.8	12.3	1	591-602	K.RVTTSAGCMADR.L	Carbamidomethyl: 8; Oxidation: 9	WD:WU 0.90

Detailed Protein Report

Protein 806: PREDICTED: schlafen-like protein 1 isoform X6 [Homo sapiens]

Accession:	gi|530362078	**Score:**	12.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	39.4
Database Date:	2015-11-30	**pI:**	6.0
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	8.0
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|530362080	refseq_human (refseq_human_20140103.fasta)	PREDICTED: schlafen-like protein 1 isoform X7 [Homo sapiens]

10	20	30	40	50	60	70	80
MTPMKRSVQT	QVSEPFMESW	GEESLPELPA	EQSLTEYSDL	EEAPSAHTLY	VGHLNPQFSV	PVLACLLRDT	LERLEMPVAR
90	100	110	120	130	140	150	160
EHIEVVRRPR	KAYALVQVTV	HRDTLASLPW	RLQTALEEHL	ILKELAARGK	DLLLSEAQGP	FSHREQIVGK	DQLFQGAFLG
170	180	190	200	210	220	230	240
SETRNMEFKR	GSGEYLSLAF	KHHVRRYVCA	FLNSEGGSLL	VGVEDSGLVQ	GIRCSHRDED	RARLLVDSIL	QGFKPQIFPD
250	260	270	280	290	300	310	320
AYTLTFIPVI	STSETSVPLK	VIRLTVHTPK	AQSQPQLYQT	DQGEVFLRRD	GSIQGPLSAS	AIQEWCRQRW	LVELGKLEEK
330	340	350					
MKALMMEKEQ	LQQQLQQHGP	VSCTCCVL					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2423	1	1131.2820	75.37	3	58.6	12.3	2	321-348	K.MKALMMEKEQLQQQLQQHGPVSCTCCVL.-	Carbamidomethyl: 23, 25, 26; Oxidation: 1

Detailed Protein Report

Protein 807: **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 808: PREDICTED: sterol regulatory element-binding protein 1 isoform X2 [Homo sapiens]

Accession: gi|578830023
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 12.3
MW [kDa]: 119.1
pI: 9.9
Sequence Coverage [%]: 1.1
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MDCTFEDMLQ	LINNQDSDFP	GLFDPPYAGS	GAGGTDPASP	DTSSPGSLSP	PPATLSSSLE	AFLSGPQAAP	SPLSPPQPAP
90	100	110	120	130	140	150	160
TPLKMYPSMP	AFSPGPGIKE	ESVPLSILQT	PTPQPLPGAL	LPQSFPAPAP	PQFSSTPVLG	YPSPPGGFST	GSPPGNTQQP
170	180	190	200	210	220	230	240
LPGLPLASPP	GVPPVSLHTQ	VQSVVPQQLL	TVTAAPTAAP	VTTTVTSQIQ	QVPVLLQPHF	IKADSLLLTA	MKTDGATVKA
250	260	270	280	290	300	310	320
AGLSPLVSGT	TVQTGPLPTL	VSGGTILATV	PLVVDAEKLP	INRLAAGSKA	PASAQSRGEK	RTAHNAIEKR	YRSSINDKII
330	340	350	360	370	380	390	400
ELKDLVVGTE	AKLNKSAVLR	KAIDYIRFLQ	HSNQKLKQEN	LSLRTAVHKS	KSLKDLVSAC	GSGGNTDVLM	EGVKTEVEDT
410	420	430	440	450	460	470	480
LTPPPSDAGS	PFQSSPLSLG	SRGSGSGGSG	SDSEPDSPVF	EDSKAKPEQR	PSLHSRGMLD	RSRLALCTLV	FLCLSCNPLA
490	500	510	520	530	540	550	560
SLLGARGLPS	PSDTTSVYHS	PGRNVLGTES	RDGPGWAQWL	LPPVVWLLNG	LLVLVSLVLL	FVYGEPVTRP	HSGPAVYFWR
570	580	590	600	610	620	630	640
HRKQADLDLA	RGDFAQAAQQ	LWLALRALGR	PLPTSHLDLA	CSLLWNLIRH	LLQRLWVGRW	LAGRAGGLQQ	DCALRVDASA
650	660	670	680	690	700	710	720
SARDAALVYH	KLHQLHTMGK	HTGGHLTATN	LALSALNLAE	CAGDAVSVAT	LAEIYVAAAL	RVKTSLPRAL	HFLTRFFLSS
730	740	750	760	770	780	790	800
ARQACLAQSG	SVPPAMQWLC	HPVGHRFFVD	GDWSVLSTPW	ESLYSLAGNP	VDPLAQVTQL	FREHLLERAL	NCVTQPNPSP
810	820	830	840	850	860	870	880
GSADGDKEFS	DALGYLQLLN	SCSDAAGAPA	YSFSISSSMA	TTTGVDPVAK	WWASLTAVVI	HWLRRDEEAA	ERLCPLVEHL
890	900	910	920	930	940	950	960
PRVLQESERP	LPRAALHSFK	AARALLGCAK	AESGPASLTI	CEKASGYLQD	SLATTPASSS	IDKAVQLFLC	DLLLVVRTSL
970	980	990	1000	1010	1020	1030	1040
WRQQQPPAPA	PAAQGTSSRP	QASALELRGF	QRDLSSLRRL	AQSFRPAMRR	VFLHEATARL	MAGASPTRTH	QLLDRSLRRR
1050	1060	1070	1080	1090	1100	1110	1120
AGPGGKGGAV	AELEPRPTRR	EHAEALLLAS	CYLPPGFLSA	PGQRVGMLAE	AARTLEKLGD	RRLLHDCQQM	LMRLGGGTTV
1130							
TSS							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2258	1	698.2825	-152.25	2	56.6	12.3	1	358-369	K.QENLSLRTAVHK.S	

Detailed Protein Report

Protein 809: PREDICTED: neurogenic locus notch homolog protein 2-like isoform X1 [Homo sapiens]

Accession:	gi|578801920	**Score:**	12.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	48.7
Database Date:	2015-11-30	**pI:**	10.1
		Sequence Coverage [%]:	5.6
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578842780	refseq_human (refseq_human_20140103.fasta)	PREDICTED: neurogenic locus notch homolog protein 2-like isoform X1 [Homo sapiens]

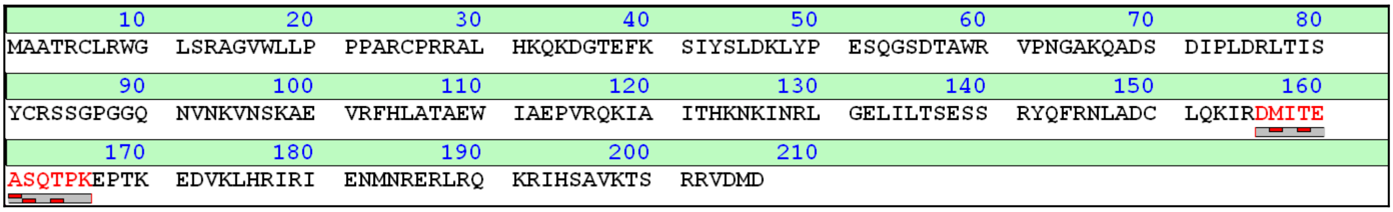
10	20	30	40	50	60	70	80
MRTGPVTRSR	SLRAELGPAL	LPAGNPWVPK	AAGPRPRRQW	GGACGGRRRL	RRKDTRGCFA	AHPRKFQPNF	GRLRRRPRSG
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
GLRARGVEAF	APGLRSVAPG	PEPLKQEEGR	REWGSSIGTP	SPCGSAQAAA	AEEATEKMPA	LRPALLWALL	ALWLCCATPA
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
HVILLPTSPI	MVEKNSVSWL	HQNLLGWILD	SAPRDSDKCR	DGYEPCVNEG	MCVTYHNGTG	YCKCPEGFLG	EYCQHRDPCE
250	**260**	**270**	**280**	**290**	**300**	**310**	**320**
KNRCQNGGTC	VAQAMLGKAT	CRCASGFTGE	DCQYSTSHPC	FVSRPCLNGG	TCHMLSRDTY	ECTCQVGFTG	KECQWTDACL
330	**340**	**350**	**360**	**370**	**380**	**390**	**400**
SHPCANGSTC	TTVANQFSCK	CLTGFTGQKC	ETDVNECDIP	GHCQHGGICL	NLPGSYQCQC	LQGFTGQYCD	SLYVPCAPSP
410	**420**	**430**	**440**	**450**			
CVNGGTCRQT	GDFTFECNCL	PETVRRGTEL	WERDREVWNG	KEHDEN			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2463	1	864.4574	-42.61	3	59.1	12.3	2	14-38	R.AELGPALLPAGNPWVPKAAGPRPRR.Q	

Detailed Protein Report

Protein 810: 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 811: **PREDICTED: tetratricopeptide repeat protein 7A isoform X2 [Homo sapiens]**

Accession:	gi|530367852	**Score:**	12.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	82.4
Database Date:	2015-11-30	**pI:**	6.4
		Sequence Coverage [%]:	2.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPSACTHGPG	LMTCPWRTSP	CIRCGCCRRL	LSSKHASGFL	GEHSPGGQRS	CRGGLSLERL	PNSIASRFRL	TEREEEVITC
90	100	110	120	130	140	150	160
FERASWIAQV	FLQELEKTTN	NSTSRHLKGC	HPLDYELTYF	LEAALQSAYV	KNLKKGNIVK	GMRELREVLR	TVETKATQNF
170	180	190	200	210	220	230	240
KVMAAKHLAG	VLLHSLSEEC	YWSPLSHPLP	EFMGKEESSF	ATQALRKPHL	YEGDNLYCPK	DNIEEALLLL	LISESMATRD
250	260	270	280	290	300	310	320
VVLSRVPEQE	EDRTVSLQNA	AAIYDLLSIT	LGRRGQYVML	SECLERAMKF	AFGEFHLWYQ	VALSMVACGK	SAYAVSLLRE
330	340	350	360	370	380	390	400
CVKLRPSDPT	VPLMAAKVCI	GSLRWLEEAE	HFAMMVISLG	EEAGEFLPKG	YLALGLTYSL	QATDATLKSK	QDELHRKALQ
410	420	430	440	450	460	470	480
TLERAQQLAP	SDPQVILYVS	LQLALVRQIS	SAMEQLQEAL	KVRKDDAHAL	HLLALLFSAQ	KHHQHALDVV	NMAITEHPEN
490	500	510	520	530	540	550	560
FNLMFTKVKL	EQVLKGPEEA	LVTCRQVLRL	WQTLYSFSQL	GGLEKDGSFG	EGLTMKKQSG	MHLTLPDAHD	ADSGSRRASS
570	580	590	600	610	620	630	640
IAASRLEEAM	SELTMPSSVL	KQGPMQLWTT	LEQIWLQAAE	LFMEQQHLKE	AGFCIQEAAG	LFPTSHSVLY	MRGRLAEVKG
650	660	670	680	690	700	710	720
NLEEAKQLYK	EALTVNPDGV	RIMHSLGLML	SRLGHKSLAQ	KVLRDAVERQ	STCHEAWQGL	GEVLQAQGQN	EAAVDCFLTA
730	740						
LELEASSPVL	PFSIIPREL						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2755	1	941.9676	29.42	2	62.9	12.2	1	35-52	K.HASGFLGEHSPGGQRSCR.G	

Detailed Protein Report

Protein 812: deleted in autism protein 1 isoform a precursor [Homo sapiens]

Accession:	gi|27734895	**Score:**	12.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	49.5
Database Date:	2015-11-30	**pI:**	9.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MWRLVPPKLG	RLSRSLKLAA	LGSLLVLMVL	HSPSLLASWQ	RNELTDRRFL	QLNKCPACFG	TSWCRRFLNG	QVVFEAWGRL
90	100	110	120	130	140	150	160
RLLDFLNVKN	VYFAQYGEPR	EGGRRRVVLK	RLGSQRELAQ	LDQSICKRAT	GRPRCDLLQA	MPRTEFARLN	GDVRLLTPEA
170	180	190	200	210	220	230	240
VEGWSDLVHC	PSQRLLDRLV	RRYAETKDSG	SFLLRNLKDS	ERMQLLLTLA	FNPEPLVLQS	FPSDEGWPFA	KYLGACGRMV
250	260	270	280	290	300	310	320
AVNYVGEELW	SYFNAPWEKR	VDLAWQLMEI	AEQLTNNDFE	FALYLLDVSF	DNFAVGPRDG	KVIIVDAENV	LVADKRLIRQ
330	340	350	360	370	380	390	400
NKPENWDVWY	ESKFDDCDKE	ACLSFSKEIL	CARATVDHNY	YAVCQNLLSR	HATWRGTSGG	LLHDPPSEIA	KDGRLEALLD
410	420	430	440				
ECANPKKRYG	RFQAAKELRE	YLAQLSNNVR					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2880	1	644.3218	100.55	2	64.7	12.2	0	55-65	K.CPACFGTSWCR.R	Carbamidomethyl: 10

Detailed Protein Report

Protein 813: PREDICTED: TNF receptor-associated factor 5 isoform X3 [Homo sapiens]

Accession: gi|578801456
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 12.2
MW [kDa]: 67.2
pI: 9.7
Sequence Coverage [%]: 4.1
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MTVSASSRPL	PARPLFPCAR	PRPSARAPAP	PQASPPLRRR	RRPQPGAAAA	PADRPRGARA	PSPTMAYSEE	HKGMPCGFIR
90	100	110	120	130	140	150	160
QNSGNSISLD	FEPSIEYQFV	ERLEERYKCA	FCHSVLHNPH	QTGCGHRFCQ	HCILSLRELN	TVPICPVDKE	VIKSQEVFKD
170	180	190	200	210	220	230	240
NCCKREVLNL	YVYCSNAPGC	NAKVILGRYQ	DHLQQCLFQP	VQCSNEKCRE	PVLRKDLKEH	LSASCQFRKE	KCLYCKKDVV
250	260	270	280	290	300	310	320
VINLQNHEEN	LCPEYPVFCP	NNCAKIILKT	EVDEHLAVCP	EAEQDCPFKH	YGCAVTISDL	HKSLEQKESK	IQQLAETIKK
330	340	350	360	370	380	390	400
LEKEFKQFAQ	LFGKNGSFLP	NIQVFASHID	KSAWLEAQVH	QLLQMVNQQQ	NKFDLRPLME	AVDTVKQKIT	LLENNDQRLA
410	420	430	440	450	460	470	480
VLEEETNKHD	THINIHKAQL	SKNEERFKLL	EGTCYNGKLI	WKVTDYKMKK	REAVDGHTVS	IFSQSFYTSR	CGYRLCARAY
490	500	510	520	530	540	550	560
LNGDGSGRGS	HLSLYFVVMR	GEFDSLLQWP	FRQRVTLMLL	DQSGKKNIME	TFKPDPNSSS	FKRPDGEMNI	ASGCPRFVAH
570	580	590	600				
SVLENAKNAY	IKDDTLFLKV	AVDLTDLEDL					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1679	1	865.0347	-46.70	3	49.3	12.2	2	57-80	R.GARAPSPTMAYSEEHKGMPCGFIR.Q	

Detailed Protein Report

Protein 814: **PREDICTED: histone-lysine N-methyltransferase 2B isoform X2 [Homo sapiens]**

Accession:	gi|578835223	**Score:**	12.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	212.5
Database Date:	2015-11-30	**pI:**	6.8
		Sequence Coverage [%]:	0.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPPLEKARIA	GVGSLPLSGV	EEKMFSLLKR	AKVQLFKIDQ	QQQQKVAASM	PLSPGGQMEE	VAGAVKQISD	RGPVRSEDES
90	100	110	120	130	140	150	160
VEAKRERPSG	PESPVQGPRI	KHVCRHAAVA	LGQARAMVPE	DVPRLSALPL	RDRQDLATED	TSSASETESV	PSRSRRGKVE
170	180	190	200	210	220	230	240
AAGPGGESEP	TGSGGTLAHT	PRRSLPSHHG	KKMRMARCGH	CRGCLRVQDC	GSCVNCLDKP	KFGGPNTKKQ	CCVYRKCDKI
250	260	270	280	290	300	310	320
EARKMERLAK	KGRTIVKTLL	PWDSDESPEA	SPGPPGPRRG	AGAGGPREEV	VAHPGPEEQD	SLLQRKSARR	CVKQRPSYDI
330	340	350	360	370	380	390	400
FEDSDDSEPG	GPPAPRRRTP	RENELPLPEP	EEQSRPRKPT	LQPVLQLKAR	RRLDKDALAP	GPFASFPNGW	TGKQKSPDGV
410	420	430	440	450	460	470	480
HRVRVDFKED	CDLENVWLMG	GLSVLTSVPG	GPPMVCLLCA	SKGLHELVFC	QVCCDPFHPF	CLEEAERPLP	QHHDTWCCRR
490	500	510	520	530	540	550	560
CKFCHVCGRK	GRGSKHLLEC	ERCRHAYHPA	CLGPSYPTRA	TRKRRHWVRD	EICSACVRCK	SCGATPGKNW	DVEWSGDYSL
570	580	590	600	610	620	630	640
CPRCTQLYEK	GNYCPICTRC	YEDNDYESKM	MQCAQCDHWV	HAKCEGLSDE	DYEILSGLPD	SVLYTCGPCA	GAAQPRWREA
650	660	670	680	690	700	710	720
LSGALQGGLR	QVLQGLLSSK	VVGPLLLCTQ	CGPDGKQLHP	GPCGLQAVSQ	RFEDGHYKSV	HSFMEDMVGI	LMRHSEEGET
730	740	750	760	770	780	790	800
PDRRAGGQMK	GLLLKLLESA	FGWFDAHDPK	YWRRSTRLPN	GVLPNAVLPP	SLDHVYAQWR	QQEPETPESG	QPPGDPSAAF
810	820	830	840	850	860	870	880
QGKDPAAFSH	LEDPRQCALC	LKYGDADSKE	AGRLLYIGQN	EWTHVNCAIW	SAEVFEENDG	SLKNVHAAVA	RGRQMRCELC
890	900	910	920	930	940	950	960
LKPGATVGCC	LSSCLSNFHF	MCARASYCIF	QDDKKVFCQK	HTDLLDGKEI	VNPDGFDVLR	RVYVDFEGIN	FKRKFLTGLE
970	980	990	1000	1010	1020	1030	1040
PDAINVLIGS	IRIDSLGTLS	DLSDCEGRLF	PIGYQCSRLY	WSTVDARRRC	WYRCRILEYR	PWGPREEPAH	LEAAEENQTI
1050	1060	1070	1080	1090	1100	1110	1120
VHSPAPSSEP	PGGEDPPLDT	DVLVPGAPER	HSPIQNLDPP	LRPDSGSAPP	PAPRSFSGAR	IKVPNYSPSR	RPLGGVSFGP
1130	1140	1150	1160	1170	1180	1190	1200
LPSPGSPSSL	THHIPTVGDP	DFPAPPRRSR	RPSPLAPRPP	PSRWASPPLK	TSPQLRVPPP	TSVVTALTPT	SGELAPPGPA
1210	1220	1230	1240	1250	1260	1270	1280
PSPPPPEDLG	PDFEDMEVVS	GLSAADLDFA	ASLLGTEPFQ	EEIVAAGAMG	SSHGGPGDSS	EEESSPTSRY	IHFPVTVVSA
1290	1300	1310	1320	1330	1340	1350	1360
PGLAPSATPG	APRIEQLDGV	DDGTDSEAEA	VQQPRGQGTP	PSGPGVVRAG	VLGAAGDRAR	PPEDLPSEIV	DFVLKNLGGP
1370	1380	1390	1400	1410	1420	1430	1440
GDGGAGPREE	SLPPAPPLAN	GSQPSQGLTA	SPADPTRTFA	WLPGAPGVRV	LSLGPAPEPP	KPATSKIILV	NKLGQVFVKM
1450	1460	1470	1480	1490	1500	1510	1520
AGEGEPVPPP	VKQPPLPPTI	SPTAPTSWTL	PPGPLLGVLP	VVGVVRPAPP	PPPPPLTLVL	SSGPASPPRQ	AIRVKRVSTF
1530	1540	1550	1560	1570	1580	1590	1600
SGRSPPAPPP	YKAPRLDEDG	EASEDTPQVP	GLGSGGFSRV	RMKTPTVRGV	LDLDRPGEPA	GEESPGPLQE	RSPLLPLPED
1610	1620	1630	1640	1650	1660	1670	1680
GPPQVPDGPP	DLLLESQWHH	YSGEASSSEE	EPPSPDDKEN	QAPKRTGPHL	RFEISSEDGF	SVEAESLEGA	WRTLIEKVQE
1690	1700	1710	1720	1730	1740	1750	1760
ARGHARLRHL	SFSGMSGARL	LGIHHDAVIF	LAEQLPGAQR	CQHYKFRYHQ	QGEGQEEPPL	NPHGAARAEV	YLRKCTFDMF
1770	1780	1790	1800	1810	1820	1830	1840
NFLASQHRVL	PEGATCDEEE	DEVQLRSTRR	ATSLELPMAM	RFRHLKKTSK	EAVGVYRSAI	HGRGLFCKRN	IDAGEMVIEY
1850	1860	1870	1880	1890	1900	1910	1920
SGIVIRSVLT	DKREKFYDGK	GIGCYMFRMD	DFDVVDATMH	GNAARFINHS	CEPNCFSRVI	HVEGQKHIVI	FALRRILRGE
1930	1940	1950	1960				
ELTYDYKFPI	EDASNKLPCN	CGAKRCRRFL	N				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2760	1	841.9053	-83.22	2	63.0	12.2	1	7-23	K.ARIAGVGSLPLSGVEEK.M	

Detailed Protein Report

Protein 815: PREDICTED: LOW QUALITY PROTEIN: spermatogenesis-associated protein 31D1, partial [Homo sapiens]

Accession:	gi|530436439	**Score:**	12.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	176.0
Database Date:	2015-11-30	**pI:**	10.1
		Sequence Coverage [%]:	0.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
NFICLSGLGL	FILYLFYMVL	TLYSSPTEKN	NDTQKHQGRA	RRKRKSVTFK	GFPDRKSLQK	EAEEERKLHS	FLKSFGPPVS
90	100	110	120	130	140	150	160
CSPLGQHHDT	TLFRRLLCPD	PVCRVCNRAT	ADIQRLLSWE	SLKDAAPSVS	PLASSASGAE	IVHSGFSSFT	LASTPSATTP
170	180	190	200	210	220	230	240
EDLILSSRPK	PSPPPPLILS	PDLITTLXLI	FTLTIADLFS	PSPLRDPLPP	QPTPLDSKFP	IDHSPPQQLP	FPLLPPHHIE
250	260	270	280	290	300	310	320
RVEPSLQPEA	SLSLNTIFSF	GSTLCQDISQ	AVNRTDSCAR	HHGPPTPSAL	PPEDCTVTQS	KSNLTVLKTF	PEMLSLGGSG
330	340	350	360	370	380	390	400
GSSTSAPTTK	GIDHSCPASS	EFSWWQPHAK	DSFSSNFVPS	DFMEELLTLH	SSEASLGGHS	VANIIQPVNI	SFLSHDIPAL
410	420	430	440	450	460	470	480
LERQVKRRGD	FLMWKENGKK	PGSFPTQLRP	NYQLNSSRNM	LTSTAVKHDL	AESFPFWASK	GKLEWQHIHQ	QPPYSKCFED
490	500	510	520	530	540	550	560
HLEQKYVQLF	WGLPSLHSES	LHPTVFVQHG	RSSMFVFFNG	ITNTSMSHES	PVLPPPQPLF	LPSTQPLPLP	QTLPRGQSLH
570	580	590	600	610	620	630	640
LTQVKSLAQP	QSPFPALPPS	PLFLIRVCGV	CFHRPQNEAR	SLMPSEINHL	EWNVLQKVQE	SVWGLPSVVQ	KSQEDFCPPA
650	660	670	680	690	700	710	720
PNPVLVRKSF	KVHVPISIIP	GDFPLSSEVR	KKLEQHIRKR	LIQRRWGLPR	RIHESLSLLR	PQNKISELSV	SESIHGPLNI
730	740	750	760	770	780	790	800
SLVEGQRCNV	LKKSASSFPR	SFHERSSNML	SMENVGNYQG	CSQETAPKNH	LLHDPETSSE	EDLRSNSERD	LGTHMMHLSG
810	820	830	840	850	860	870	880
NDSGVRLGQK	QLENALTVHL	SKKFEEINEG	RMPGTVHSSW	HSVKQTICLP	EKSHSQIKHR	NLAALVSEDH	RVDTSQEMSF
890	900	910	920	930	940	950	960
LSSNKQKMLS	PYXIFPYEAH	IKSFHMRMLW	GLPRKIREPT	EIFKSEEDIS	NSFSHFYLPS	SASFISQGDS	KDGVSKSCRR
970	980	990	1000	1010	1020	1030	1040
STFQGEKLGT	TSSVPVLNHP	QPVSSPIGKE	GQGTLRRQFS	DTDHDLIETD	AKDGASTPLR	RGTTYFQGEK	LETTSSFSIL
1050	1060	1070	1080	1090	1100	1110	1120
GHPHLVTSPV	DQEKQGTLRR	EFADTDEDLT	ESVWTTEDGR	QTFLPPTHSI	IDEVSQKQTV	LASRCSAELP	ILQAGVGRDS
1130	1140	1150	1160	1170	1180	1190	1200
RDKRESASNN	VNRLQGSRKT	FPVTNGSKEM	FKEEEICTLQ	SQTRNNLTTS	KSGSCLVTNV	KRSTSHETEI	FPPRISVPQT
1210	1220	1230	1240	1250	1260	1270	1280
PKSSYLKNQM	LSQLKLVQRK	HSQPQSHFTG	MSLALDNLSS	KDLLTHAQGI	SNQDLGTSQV	LHVHLEVRGI	RVAQQQEPRV
1290	1300	1310	1320	1330	1340	1350	1360
PTHVLQKCQV	KNFSPATKRV	SPLRPNGGEL	GGGDAGLGTS	QLRRKSHAIH	NKTSRESLGS	KSSPTLKTQP	PPENLFGTLM
1370	1380	1390	1400	1410	1420	1430	1440
KTFLQQSNKP	IITYGKQESS	XEKGSSLSSS	VQNRGRVKSR	AVFTGTIEAQ	KIRKDTGEFI	EEKLGHRHXI	DITCPQEPLS
1450	1460	1470	1480	1490	1500	1510	1520
SPVQLGKSQN	VPELQVRAEP	VQGYPCNYMA	PSCKVTCTKS	CSQQAIFVGQ	NYPAMIRQII	DKDRXPQEVX	TFKGKILCQR
1530	1540	1550	1560	1570	1580	1590	
HPQSMPHRKP	VPQPNPTCSX	EVNLVPPVIL	TSAKNTVFSD	VPLLTGQKIL	PKHLQGGKFP	PKK	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
149	1	636.2737	-54.29	3	30.8	12.2	1	0-0	.QESSPEKGSSLSSSVQNR.	

Detailed Protein Report

Protein 816: **PREDICTED: 1-acyl-sn-glycerol-3-phosphate acyltransferase delta isoform X4 [Homo sapiens]**

Accession:	gi|530383876	**Score:**	12.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	27.3
Database Date:	2015-11-30	**pI:**	10.2
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	5.6
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|578812839	refseq_human (refseq_human_20140103.fasta)	PREDICTED: 1-acyl-sn-glycerol-3-phosphate acyltransferase delta isoform X8 [Homo sapiens]

10	20	30	40	50	60	70	80
MDLAGLLKSQ	FLCHLVFCYV	FIASGLIINT	IQLFTLLLWP	INKQLFRKIN	CRLSYCISSQ	LVMLLEWWSG	TECTIFTDPR
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
AYLKYGKENA	IVVLNHKFEI	DFLCGWSLSE	RFGLLGGSKV	LAKKELAYVP	IIGWMWYFTE	MVFCSRKWEQ	DRKTVATSLQ
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
HLRDYPEKYF	FLIHCEGTRF	TEKKHEISMQ	VARAKGLPRL	KHHLLPRTKG	FAITVRSLRN	VEIMKIQHCW	ES

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
40	1	845.3297	-71.12	2	29.5	12.2	1	220-232	R.NVEIMKIQHCWES.-	Carbamidomethyl: 10; Oxidation: 5

Detailed Protein Report

Protein 817: 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

```
        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
2304	1	937.3088	-123.46	2	57.2	12.1	0	1-17	-.MSGACTSYVSAEQEVVR.G	Carbamidomethyl: 5

Detailed Protein Report

Protein 818: histone-lysine N-methyltransferase PRDM9 [Homo sapiens]

Accession: gi|147905620
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 12.1
MW [kDa]: 103.3
pI: 10.3
Sequence Coverage [%]: 1.7
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MSPEKSQEES	PEEDTERTER	KPMVKDAFKD	ISIYFTKEEW	AEMGDWEKTR	YRNVKRNYNA	LITIGLRATR	PAFMCHRRQA
90	100	110	120	130	140	150	160
IKLQVDDTED	SDEEWTPRQQ	VKPPWMALRV	EQRKHQKGMP	KASFSNESSL	KELSRTANLL	NASGSEQAQK	PVSPSGEAST
170	180	190	200	210	220	230	240
SGQHSRLKLE	LRKKETERKM	YSLRERKGHA	YKEVSEPQDD	DYLYCEMCQN	FFIDSCAAHG	PPTFVKDSAV	DKGHPNRSAL
250	260	270	280	290	300	310	320
SLPPGLRIGP	SGIPQAGLGV	WNEASDLPLG	LHFGPYEGRI	TEDEEAANNG	YSWLITKGRN	CYEYVDGKDK	SWANWMRYVN
330	340	350	360	370	380	390	400
CARDDEEQNL	VAFQYHRQIF	YRTCRVIRPG	CELLVWYGDE	YGQELGIKWG	SKWKKELMAG	REPKPEIHPC	PSCCLAFSSQ
410	420	430	440	450	460	470	480
KFLSQHVERN	HSSQNFPGPS	ARKLLQPENP	CPGDQNQEQQ	YPDPHSRNDK	TKGQEIKERS	KLLNKRTWQR	EISRAFSSPP
490	500	510	520	530	540	550	560
KGQMGSCRVG	KRIMEEESRT	GQKVNPGNTG	KLFVGVGISR	IAKVKYGECG	QGFSVKSDVI	THQRTHTGEK	LYVCRECGRG
570	580	590	600	610	620	630	640
FSWKSHLLIH	QRIHTGEKPY	VCRECGRGFS	WQSVLLTHQR	THTGEKPYVC	RECGRGFSRQ	SVLLTHQRRH	TGEKPYVCRE
650	660	670	680	690	700	710	720
CGRGFSRQSV	LLTHQRRHTG	EKPYVCRECG	RGFSWQSVLL	THQRTHTGEK	PYVCRECGRG	FSWQSVLLTH	QRTHTGEKPY
730	740	750	760	770	780	790	800
VCRECGRGFS	NKSHLLRHQR	THTGEKPYVC	RECGRGFRDK	SHLLRHQRTH	TGEKPYVCRE	CGRGFRDKSN	LLSHQRTHTG
810	820	830	840	850	860	870	880
EKPYVCRECG	RGFSNKSHLL	RHQRTHTGEK	PYVCRECGRG	FRNKSHLLRH	QRTHTGEKPY	VCRECGRGFS	DRSSLCYHQR
890	900						
THTGEKPYVC	REDE						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2778	1	941.4753	-36.22	2	63.3	12.1	1	99-113	R.QQVKPPWMALRVEQR.K	Oxidation: 8

Detailed Protein Report

Protein 819: PREDICTED: SH2B adapter protein 2 isoform X1 [Homo sapiens]

Accession: gi|530431159
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 12.1
MW [kDa]: 72.2
pI: 5.6
Sequence Coverage [%]: 4.9
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MDPSYCPAHG	FPSQDPLWPL	SSQQWSSAHY	SEPAAGGCDG	TEAMNGAGPG	PAAAAPVPVP	VPVPDWRQFC	ELHAQAAAVD
90	100	110	120	130	140	150	160
FAHKFCRFLR	DNPAYDTPDA	GASFSRHFAA	NFLDVFGEEV	RRVLVAGPTT	RGAAVSAEAM	EPELADTSAL	KAAPYGHSRS
170	180	190	200	210	220	230	240
SEDVSTHAAT	KARVRKGFSL	RNMSLCVVDG	VRDMWHRRAS	PEPDAAAAPR	TAEPRDKWTR	RLRLSRTLAA	KVELVDIQRE
250	260	270	280	290	300	310	320
GALRFMVADD	AAAGSGGSAQ	WQKCRLLLRR	AVAEERFRLE	FFVPPKASRP	KVSIPLSAII	EVRTTMPLEM	PEKDNTFVLK
330	340	350	360	370	380	390	400
VENGAEYILE	TIDSLQKHSW	VADIQGCVDP	GDSEEDTELS	CTRGGCLASR	VASCSCELLT	DVDLPRPPET	TAVGAVVTAP
410	420	430	440	450	460	470	480
HSRGRDAVRE	SLIHVPLETF	LQTLESPGGS	GSDSNNTGEQ	GAETDPEAEP	ELELSDYPWF	HGTLSRVKAA	QLVLAGGPRN
490	500	510	520	530	540	550	560
HGLFVIRQSE	TRPGEYVLTF	NFQGKAKHLR	LSLNGHGQCH	VQHLWFQSVL	DMLRHFHTHP	IPLESGGSAD	ITLRSYVRAQ
570	580	590	600	610	620	630	640
DPPPEPGPTP	PAAPASPACW	SDSPGQHYFS	SLAAAACPPA	SPSDAAGASS	SSASSSSAAS	GPAPPRPVEG	QLSARSRSNS
650	660	670	680				
AERLLEAVAA	TAAEEPPEAA	PGRARAVENQ	YSFY				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2484	1	1131.1716	-58.41	3	59.3	12.1	0	371-403	R.VASCSCELLTDVDLPRPPETTAVGAVVTAPHSR.G	

Detailed Protein Report

Protein 820: 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

WD:WU **Median:** 1.31 **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		WD:WU 1.31

Detailed Protein Report

Protein 821: PREDICTED: LETM1 and EF-hand domain-containing protein 1, mitochondrial isoform X3 [Homo sapiens]

Accession:	gi|578808155	**Score:**	12.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	83.2
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
MASILLRSCR	GRAPARLPPP	PRYTVPRGSP	GDPAHLSCAS	TLGLRNCLNV	PFGCCTPIHP	VYTSSRGDHL	GCWALRPECL
90	100	110	120	130	140	150	160
RIVSRAPWTS	TSVGFVAVGP	QCLPVRGWHS	SRPVRDDSVV	EKSLKSLKDK	NKKLEEGGPV	YSPPAEVVVK	KSLGQRVLDE
170	180	190	200	210	220	230	240
LKHYYHGFRL	LWIDTKIAAR	MLWRILNGHS	LTRRERRQFL	RICADLFRLV	PFLVFVVVPF	MEFLLPVAVK	LFPNMLPSTF
250	260	270	280	290	300	310	320
ETQSLKEERL	KKELRVKLEL	AKFLQDTIEE	MALKNKAAKG	SATKDFSVFF	QKIRETGERP	SNEEIMRFSK	LFEDELTLDN
330	340	350	360	370	380	390	400
LTRPQLVALC	KLLELQSIGT	NNFLRFQLTM	RLRSIKADDK	LIAEEGVDSL	NVKELQAACR	ARGMRALGVT	EDRLRGQLKQ
410	420	430	440	450	460	470	480
WLDLHLHQEI	PTSLLILSRA	MYLPDTLSPA	DQLKSTLQTL	PEIVAKEAQV	KVAEVEGEQV	DNKAKLEATL	QEEAAIQQEH
490	500	510	520	530	540	550	560
REKELQKRSE	VADFEPERVV	AAPQRPGTEP	QPEMPDTVLQ	SETLKDTAPV	LEGLKEEEIT	KEEIDILSDA	CSKLQEQKKS
570	580	590	600	610	620	630	640
LTKEKEELEL	LKEDVQDYSE	DLQEIKKELS	KTGEEKYVEE	SKASKRLTKR	VQQMIGQIDG	LISQLEMDQQ	AGKLAPANGM
650	660	670	680	690	700	710	720
PTGENVISVA	ELINAMKQVK	HIPESKLTSL	AAALDENKDG	KVNIDDLVKV	IELVDKEDVH	ISTSQVAEIV	ATLEKEEKVE
730	740						
EKEKAKEKAE	KEVAEVKS						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1166	1	509.6492	-285.95	2	43.2	12.1	1	2-10	M.ASILLRSCR.G	

Detailed Protein Report

Protein 822: endophilin-A3 [Homo sapiens]

Accession:	gi|223468657	**Score:**	12.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	39.3
Database Date:	2015-11-30	**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 823: angiogenin precursor [Homo sapiens]

Accession:	gi|4557313	**Score:**	12.1
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

WD:WU	**Median:**	0.81	**CV:**	0.00 %	**No. of Peptides:**	1	

Alias proteins:

Accession	Name	Description
gi|148277046	refseq_huma (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
2679	4	607.3390	64.12	2	61.9	12.1	2	49-57	R.YCESIMRRR.G		WD:WU 0.81

Detailed Protein Report

Protein 824: steroid hormone receptor ERR2 [Homo sapiens]

Accession:	gi|238550159	**Score:**	12.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	56.2
Database Date:	2015-11-30	**pI:**	9.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.8
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 0.62 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MSSDDRHLGS	SCGSFIKTEP	SSPSSGIDAL	SHHSPSGSSD	ASGGFGLALG	THANGLDSPP	MFAGAGLGGT	PCRKSYEDCA
90	100	110	120	130	140	150	160
SGIMEDSAIK	CEYMLNAIPK	RLCLVCGDIA	SGYHYGVASC	EACKAFFKRT	IQGNIEYSCP	ATNECEITKR	RRKSCQACRF
170	180	190	200	210	220	230	240
MKCLKVGMLK	EGVRLDRVRG	GRQKYKRRLD	SESSPYLSLQ	ISPPAKKPLT	KIVSYLLVAE	PDKLYAMPPP	GMPEGDIKAL
250	260	270	280	290	300	310	320
TTLCDLADRE	LVVIIGWAKH	IPGFSSLSLG	DQMSLLQSAW	MEILILGIVY	RSLPYDDKLV	YAEDYIMDEE	HSRLAGLLEL
330	340	350	360	370	380	390	400
YRAILQLVRR	YKKLKVEKEE	FVTLKALALA	NSDSMYIEDL	EAVQKLQDLL	HEALQDYELS	QRHEEPWRTG	KLLLTLPLLR
410	420	430	440	450	460	470	480
QTAAKAVQHF	YSVKLQGKVP	MHKLFLEMLE	AKVGQEQLRG	SPKDERMSSH	DGKCPFQSAA	FTSRDQSNSP	GIPNPRPSSP
490	500	510					
TPLNERGRQI	SPSTRTPGGQ	GKHLWLTM					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
56	1	773.7195	-167.88	2	29.6	12.1	2	440-453	R.GSPKDERMSSHDGK.C	Oxidation: 8	WD:WU 0.62

Detailed Protein Report

Protein 825: PREDICTED: serologically defined colon cancer antigen 3 isoform X2 [Homo sapiens]

Accession:	gi|530426675	**Score:**	12.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	42.4
Database Date:	2015-11-30	**pI:**	4.8
		Sequence Coverage [%]:	3.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSGYQRRPGA	TPLSRARSLA	IPDDFGYGKG	KCSKQSPSGA	HGTHFGDDRF	EDLEEANPFS	FREFLKTKNL	GLSKEDPASR
90	100	110	120	130	140	150	160
IYAKEASRHS	LGLDHNSPPS	QTGGYGLEYQ	QPFFEDPTGA	GDLLDEEEDE	DTGWSGAYLP	SAIEQTHPER	VPAGTSPCST
170	180	190	200	210	220	230	240
YLSFFSTPSE	LAGPESLPSW	ALSDTDSRVS	PASPAGSPSA	DFAVHGESLG	DRHLRTLQIS	YDALKDENSK	LRRKLNEVQS
250	260	270	280	290	300	310	320
FSEAQTEMVR	TLERKLEAKM	IKEESDYHDL	ESVVQQVEQN	LELMTKRAVK	AENHVVKLKQ	EISLLQAQVS	NFQRENEALR
330	340	350	360	370	380	390	
CGQGASLTVV	KQNADVALQN	LRVVMNSAQA	SIKQLVSGAE	TLNLVAEILK	SIDRISEVKD	EEEDS	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2089	1	734.3401	-51.03	2	54.5	12.1	1	18-31	R.SLAIPDDFGYGKGK.C	

Detailed Protein Report

Protein 826: zinc finger protein 20 isoform 2 [Homo sapiens]

Accession:	gi|322303718	**Score:**	12.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	61.1
Database Date:	2015-11-30	**pI:**	10.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDSVAFEDVA	VSFTQEEWAL	LDPSQKNLYR	DVMQETFKNL	TSVGKTWKVQ	NIEDEYKNPR	RNLSLMREKL	CESKESHHCG
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
ESFNQIADDM	LNRKTLPGIT	PCESSVCGEV	GTGHSSLNTH	IRADTGHKSS	EYQEYGENPY	RNKECKKAFS	YLDSFQSHDK
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
ACTKEKPYDG	KECTETFISH	SCIQRHRVMH	SGDGPYKCKF	CGKAFYFLNL	CLIHERIHTG	VKPYKCKQCG	KAFTRSTTLP
250	**260**	**270**	**280**	**290**	**300**	**310**	**320**
VHERTHTGVN	ADECKECGNA	FSFPSEIRRH	KRSHTGEKPY	ECKQCGKVFI	SFSSIQYHKM	THTGEKPYEC	KQCGKAFRCG
330	**340**	**350**	**360**	**370**	**380**	**390**	**400**
SHLQKHGRTH	TGEKPYECRQ	CGKAFRCTSD	LQRHEKTHTE	DKPYGCKQCG	KGFRCASQLQ	IHERTHSGEK	PHECKECGKV
410	**420**	**430**	**440**	**450**	**460**	**470**	**480**
FKYFSSLRIH	ERTHTGEKPH	ECKQCGKAFR	YFSSLHIHER	THTGDKPYEC	KVCGKAFTCS	SSIRYHERTH	TGEKPYECKH
490	**500**	**510**	**520**	**530**			
CGKAFISNYI	RYHERTHTGE	KPYQCKQCGK	AFIRASSCRE	HERTHTINR			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2376	1	1130.4062	-64.30	2	58.0	12.0	0	75-93	K.ESHHCGESFNQIADDMLNR.K	Carbamidomethyl: 5

Detailed Protein Report

Protein 827: **MAM and LDL-receptor class A domain-containing protein C10orf112 precursor [Homo sapiens]**

Accession:	gi|565671710	**Score:**	12.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	240.9
Database Date:	2015-11-30	**pI:**	4.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	0.7
		No. of unique 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
777	1	541.1764	-129.12	3	38.5	12.0	1	2032-2046	R.NGGTCVVEKNGPMCR.C	Carbamidomethyl: 5

Detailed Protein Report

Protein 828: **PREDICTED: targeting protein for Xklp2 isoform X2 [Homo sapiens]**

Accession: gi|530417959
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 12.0
MW [kDa]: 85.0
pI: 10.0
Sequence Coverage [%]: 2.3
No. of unique Peptides: 1

```
        10         20         30         40         50         60         70         80
MSQVKSSYSY DAPSDFINFS SLDDEGDTQN IDSWFEEKAN LENKLLGKNG TGGLFQGKTP LRKANLQQAI VTPLKPVDNT

        90        100        110        120        130        140        150        160
YYKEAEKENL VEQSIPSNAC SSLEVEAAIS RKTPAQPQRR SLRLSAQKDL EQKEKHHVKM KAKRCATPVI IDEILPSKKM

       170        180        190        200        210        220        230        240
KVSNNKKKPE EEGSAHQDTA EKNASSPEKA KGRHTVPCMP PAKQKFLKST EEQELEKSMK MQQEVVEMRK KNEEFKKLAL

       250        260        270        280        290        300        310        320
AGIGQPVKKS VSQVTKSVDF HFRTDERIKQ HPKNQEEYKE VNFTSELRKH PSSPARVTKG CTIVKPFNLS QGKKRTFDET

       330        340        350        360        370        380        390        400
VSTYVPLAQQ VEDFHKRTPN RYHLRSKKDD INLLPSKSSV TKICRDPQTP VLQTKHRARA VTCKSTAELE AEELEKLQQY

       410        420        430        440        450        460        470        480
KFKARELDPR ILEGGPILPK KPPVKPPTEP IGFDLEIEKR IQERESKKKT EDEHFEFHSR PCPTKILEDV VGVPEKKVLP

       490        500        510        520        530        540        550        560
ITVPKSPAFA LKNRIRMPTK EDEEEDEPVV IKAQPVPHYG VPFKPQIPEA RTVEICPFSF DSRDKERQLQ KEKKIKELQK

       570        580        590        600        610        620        630        640
GEVPKFKALP LPHFDTINLP EKKVKNVTQI EPFCLETDRR GALKAQTWKH QLEEELRQQK EAACFKARPN TVISQEPFVP

       650        660        670        680        690        700        710        720
KKEKKSVAVQ EPFQLATEKR AKERQELEKR MAEVEAQKAQ QLEEARLQEE EQKKEELARL RRELVHKANP IRKYQGLEIK

       730        740        750
SSDQPLTVPV SPKFSTRFHC
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1899	1	973.3824	-143.79	2	52.1	12.0	2	349-365	K.DDINLLPSKSSVTKICR.D	Carbamidomethyl: 16

Detailed Protein Report

Protein 829: PREDICTED: NEDD4-binding protein 1 isoform X1 [Homo sapiens]

Accession:	gi|530424557	**Score:**	12.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	75.8
Database Date:	2015-11-30	**pI:**	5.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.2
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 0.44 **CV:** 0.00 % **No. of Peptides:** 1

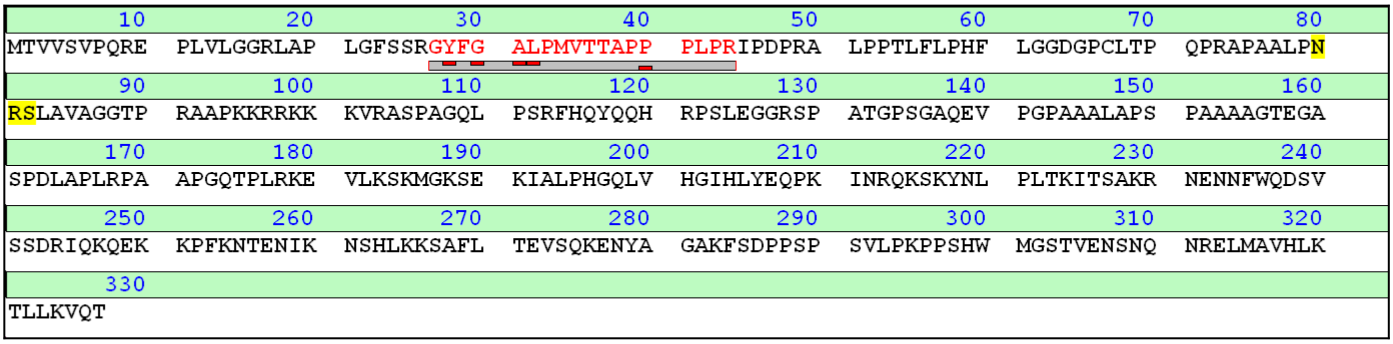
10	20	30	40	50	60	70	80
MAARAVLDEF	TAPAEKAELL	EQSRGRIEGL	FGVSLAVLGA	LGAEEPLPAR	IWLQLCGAQE	AVHSAKEYIK	GICEPELEER
90	100	110	120	130	140	150	160
ECYPKDMHCI	FVGAESLFLK	SLIQDTCADL	CILDIGLLGI	RGSAEAVVMA	RSHIQQFVKL	FENKENLPSS	QKESEVKREF
170	180	190	200	210	220	230	240
KQFVEAHADN	YTMDLLILPT	SLKKELLTLT	QGEENLFETG	DDEVIEMRDS	QQTEFTQNAA	TGLNISRDET	VLQEEARNKA
250	260	270	280	290	300	310	320
GTPVSELTKQ	MDTVLSSSPD	VLFDPINGLT	PDEEALSNER	ICQKRRFSDS	EERHTKKQFS	LENVQEGEIL	HDAKTLAGNV
330	340	350	360	370	380	390	400
IADLSDSSAD	SENLSPDIKE	TTEEMEYNIL	VNFFKTMGYS	QEIVEKVIKV	YGPSTEPLLL	LEEIEKENKR	FQEDREFSAG
410	420	430	440	450	460	470	480
TVYPETNKTK	NKGVYSSTNE	LTTDSTPKKT	QAHTQQNMVE	KFSQLPFKVE	AKPCTSNCRI	NTFRTVPIEQ	KHEVWGSNQN
490	500	510	520	530	540	550	560
YICNTDPETD	GLSPSVASPS	PKEVNFVSRG	ASSHQPRVPL	FPENGLHQQP	EPLLPNNMKS	ACEKRLGCCS	SPHSKPNCST
570	580	590	600	610	620	630	640
LSPPMPLPQL	LPSVTDARSA	GPSDHIDSSV	TGVQRFRDTL	KIPYKLELKN	EPGRTDLKHI	VIDGSNVAIT	HGLKKFFSCR
650	660	670	680				
GIAIAVEYFW	KLGNRNITVF	VPQWRTRRDP	NVTGFYYT				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
1036	1	954.9665	41.36	2	41.7	12.0	1	71-85	K.GICEPELEERECYPK.D	Carbamidomethyl: 3, 12	WD:WU	0.44

Detailed Protein Report

Protein 830: proline-rich nuclear receptor coactivator 1 [Homo sapiens]

Accession:	gi|5802982	**Score:**	12.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	35.2
Database Date:	2015-11-30	**pI:**	11.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	5.5
		No. of unique Peptides:	1



```
        10         20         30         40         50         60         70         80
MTVVSVPQRE PLVLGGRLAP LGFSSRGYFG ALPMVTTAPP PLPRIPDPRA LPPTLFLPHF LGGDGPCLTP QPRAPAALPN
        90        100        110        120        130        140        150        160
RSLAVAGGTP RAAPKKRRKK KVRASPAGQL PSRFHQYQQH RPSLEGGRSP ATGPSGAQEV PGPAAALAPS PAAAAGTEGA
       170        180        190        200        210        220        230        240
SPDLAPLRPA APGQTPLRKE VLKSKMGKSE KIALPHGQLV HGIHLYEQPK INRQKSKYNL PLTKITSAKR NENNFWQDSV
       250        260        270        280        290        300        310        320
SSDRIQKQEK KPFKNTENIK NSHLKKSAFL TEVSQKENYA GAKFSDPPSP SVLPKPPSHW MGSTVENSNQ NRELMAVHLK
       330
TLLKVQT
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2381	1	951.1462	150.40	2	58.0	12.0	0	27-44	R.GYFGALPMVTTAPPPLPR.I	Oxidation: 8

Detailed Protein Report

Protein 831: **tryptophan 5-hydroxylase 2 [Homo sapiens]**

Accession:	gi|31795563	**Score:**	12.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	56.0
Database Date:	2015-11-30	**pI:**	6.0
		Sequence Coverage [%]:	2.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MQPAMMMFSS	KYWARRGFSL	DSAVPEEHQL	LGSSTLNKPN	SGKNDDKGNK	GSSKREAATE	SGKTAVVFSL	KNEVGGLVKA
90	100	110	120	130	140	150	160
LRLFQEKRVN	MVHIESRKSR	RRSSEVEIFV	DCECGKTEFN	ELIQLLKFQT	TIVTLNPPEN	IWTEEEELED	VPWFPRKISE
170	180	190	200	210	220	230	240
LDKCSHRVLM	YGSELDADHP	GFKDNVYRQR	RKYFVDVAMG	YKYGQPIPRV	EYTEEETKTW	GVVFRELSKL	YPTHACREYL
250	260	270	280	290	300	310	320
KNFPLLTKYC	GYREDNVPQL	EDVSMFLKER	SGFTVRPVAG	YLSPRDFLAG	LAYRVFHCTQ	YIRHGSDPLY	TPEPDTCHEL
330	340	350	360	370	380	390	400
LGHVPLLADP	KFAQFSQEIG	LASLGASDED	VQKLATCYFF	TIEFGLCKQE	GQLRAYGAGL	LSSIGELKHA	LSDKACVKAF
410	420	430	440	450	460	470	480
DPKTTCLQEC	LITTFQEAYF	VSESFEEAKE	KMRDFAKSIT	RPFSVYFNPY	TQSIEILKDT	RSIENVVQDL	RSDLNTVCDA
490	500						
LNKMNQYLGI							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
852	1	683.3354	-83.47	2	39.4	12.0	1	238-248	R.EYLKNFPLLTK.Y	

Detailed Protein Report

Protein 832: 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	2	593.1800	-194.20	2	34.7	12.0	1	180-194	R.RGAGGGGGGAGAQGR.A	

Detailed Protein Report

Protein 833: RNA-binding protein 14 isoform 1 [Homo sapiens]

Accession:	gi|5454064	**Score:**	12.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	69.4
Database Date:	2015-11-30	**pI:**	10.0
		Sequence Coverage [%]:	1.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MKIFVGNVDG	ADTTPEELAA	LFAPYGTVMS	CAVMKQFAFV	HMRENAGALR	AIEALHGHEL	RPGRALVVEM	SRPRPLNTWK
90	100	110	120	130	140	150	160
IFVGNVSAAC	TSQELRSLFE	RRGRVIECDV	VKDYAFVHME	KEADAKAAIA	QLNGKEVKGK	RINVELSTKG	QKKGPGLAVQ
170	180	190	200	210	220	230	240
SGDKTKKPGA	GDTAFPGTGG	FSATFDYQQA	FGNSTGGFDG	QARQPTPPFF	GRDRSPLRRS	PPRASYVAPL	TAQPATYRAQ
250	260	270	280	290	300	310	320
PSVSLGAAYR	AQPSASLGVG	YRTQPMTAQA	ASYRAQPSVS	LGAPYRGQLA	SPSSQSAAAS	SLGPYGGAQP	SASALSSYGG
330	340	350	360	370	380	390	400
QAAAASSLNS	YGAQGSSLAS	YGNQPSSYGA	QAASSYGVRA	AASSYNTQGA	ASSLGSYGAQ	AASYGAQSAA	SSLAYGAQAA
410	420	430	440	450	460	470	480
SYNAQPSASY	NAQSAPYAAQ	QAASYSSQPA	AYVAQPATAA	AYASQPAAYA	AQATTPMAGS	YGAQPVVQTQ	LNSYGAQASM
490	500	510	520	530	540	550	560
GLSGSYGAQS	AAAATGSYGA	AAAYGAQPSA	TLAAPYRTQS	SASLAASYAA	QQHPQAAASY	RGQPGNAYDG	AGQPSAAYLS
570	580	590	600	610	620	630	640
MSQGAVANAN	STPPPYERTR	LSPPRASYDD	PYKKAVAMSK	RYGSDRRLAE	LSDYRRLSES	QLSFRRSPTK	SSLDYRRLPD
650	660	670					
AHSDYARYSG	SYNDYLRAAQ	MHSGYQRRM					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
349	1	639.8896	62.99	2	33.0	12.0	2	607-616	R.RLAELSDYRR.L	

Detailed Protein Report

Protein 834: **carbohydrate sulfotransferase 11 isoform 2 [Homo sapiens]**

Accession:	gi|291219907	**Score:**	12.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	41.0
Database Date:	2015-11-30	**pI:**	9.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	5.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MKPALLEVMR	MNRICRMVLA	TCLGSFILVI	FYFQIMRRNP	FGVDICCRKG	SRSPLQELYN	PIQLELSNTA	VLHQMRRDQV
90	100	110	120	130	140	150	160
TDTCRANSAT	SRKRRVLTPN	DLKHLVVDED	HELIYCYVPK	VACTNWKRLM	MVLTGRGKYS	DPMEIPANEA	HVSANLKTLN
170	180	190	200	210	220	230	240
QYSIPEINHR	LKSYMKFLFV	REPFERLVSA	YRNKFTQKYN	ISFHKRYGTK	IIKRQRKNAT	QEALRKGDDV	KFEEFVAYLI
250	260	270	280	290	300	310	320
DPHTQREEPF	NEHWQTVYSL	CHPCHIHYDL	VGKYETLEED	SNYVLQLAGV	GSYLKFPTYA	KSTRTTDEMT	TEFFQNISSE
330	340	350					
HQTQLYEVYK	LDFLMFNYSV	PSYLKLE					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2642	1	784.3526	-74.09	3	61.3	12.0	2	158-176	K.TLNQYSIPEINHRLKSYMK.F	Oxidation: 18

Detailed Protein Report

Protein 835: **tigger transposable element-derived protein 3 [Homo sapiens]**

Accession:	gi|23312394	**Score:**	12.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	52.0
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
MELSSKKKLH	ALSLAEKIQV	LELLDESKMS	QSEVARRFQV	SQPQISRICK	NKEKLLADWC	SGTANRERKR	KRESKYSGID
90	100	110	120	130	140	150	160
EALLCWYHIA	RAKAWDVTGP	MLLHKAKELA	DIMGQDFVPS	IGWLVRWKRR	NNVGFGARHV	LAPSFPPEPP	PPGLTSQAQL
170	180	190	200	210	220	230	240
PLSLKDFSPE	DVFGCAELPL	LYRAVPGSFG	ACDQVQVLLC	ANSRGTEKRR	VLLGGLQAAP	RCFFGIRSEA	LPASYHPDLG
250	260	270	280	290	300	310	320
IPWLEWLAQF	DRDMGQQGRQ	VALLLAARVV	EELAGLPGLY	HVKLLPLAAS	STTPPLPSSV	VRAFKAHYRH	RLLGKLAAIQ
330	340	350	360	370	380	390	400
SERDGTSLAE	AGAGITVLDA	LHVASAAWAK	VPPQLIFSSF	IQEGLAPGKT	PPSSHKTSEM	PPVPGGLSLE	EFSRFVDLEG
410	420	430	440	450	460	470	480
EEPRSGVCKE	EIGTEDEKGD	REGAFEPLPT	KADALRALGT	LRRWFECNST	SPELFEKFYD	CEEEVERLCC	L

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
974	1	547.7654	-131.86	2	40.5	12.0	0	211-221	R.VLLGGLQAAPR.C	

Detailed Protein Report

Protein 836: 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 837: unconventional myosin-VIIa isoform 3 [Homo sapiens]

Accession:	gi|256355179	**Score:**	12.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	135.7
Database Date:	2015-11-30	**pI:**	9.5
		Sequence Coverage [%]:	1.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
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		
KLTEEVTKRL	HDGESTVQGN	SMLEDRPTSN	LEKLHFIIGN	GILRPALRSV	PGGGDTRA		

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	

Detailed Protein Report

Protein 838: PREDICTED: SAC3 domain-containing protein 1 isoform X3 [Homo sapiens]

Accession:	gi|530396707	**Score:**	12.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	23.7
Database Date:	2015-11-30	**pI:**	7.9
		Sequence Coverage [%]:	8.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPGCELPVGT	CPDMCPAAER	AQREREHRLH	RLEVVPGCRQ	DPPRADPQRA	VKEYSRPAAG	KPRPPPSQLR	PPSVLLATVR
90	100	110	120	130	140	150	160
YLAGEVAESA	DIARAEVASF	VADRLRAVLL	DLALQGAGDA	EAAVVLEAAL	ATLLTVVARL	GPDAARGPAD	PVLLQAQVQE
170	180	190	200	210	220	230	
GFGSLRRCYA	RGAGPHPRQP	AFQGLFLLYN	LEMGSRMLPL	EFLGSSDPPA	PPSQVAGCGH	HAQ	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2655	1	973.4798	64.10	2	61.5	12.0	0	2-20	M.PGCELPVGTCPDMCPAAER.A	

Detailed Protein Report

Protein 839: **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 840: 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 841: PREDICTED: cyclic nucleotide-gated cation channel beta-3 isoform X1 [Homo sapiens]

Accession:	gi|578816058	**Score:**	11.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	76.5
Database Date:	2015-11-30	**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 842: melanoma-associated antigen D1 isoform b [Homo sapiens]

Accession:	gi|52632377	**Score:**	11.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	86.1
Database Date:	2015-11-30	**pI:**	5.5
		Sequence Coverage [%]:	1.5
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|52632379	refseq_human (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 843: beta-catenin-interacting protein 1 [Homo sapiens]

Accession:	gi|9910390	**Score:**	11.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	9.2
Database Date:	2015-11-30	**pI:**	5.2
		Sequence Coverage [%]:	22.2
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578799481	refseq_human (refseq_human_20140103.fasta)	PREDICTED: beta-catenin-interacting protein 1 isoform X1 [Homo sapiens]
gi|59889555	refseq_human (refseq_human_20140103.fasta)	beta-catenin-interacting protein 1 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MNREGAPGKS PEEMYIQQKV RVLLMLRKMG SNLTASEEEF LRTYAGVVNS QLSQLPPHSI DQGAEDVVMA FSRSETEDRR
        90
Q
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2513	1	1023.9000	-114.74	2	59.7	11.9	2	4-21	R.EGAPGKSPEEMYIQQKVR.V	

Detailed Protein Report

Protein 844: ret finger protein-like 4A [Homo sapiens]

Accession:	gi|222446629	**Score:**	11.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	32.2
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
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
1612	1	746.4374	48.07	3	48.9	11.9	0	196-215	K.VFAASTVPMTPLWVSPQLHR.V	

Detailed Protein Report

Protein 845: 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

Quantitation

WD:WU **Median:** 1.07 **CV:** 0.00 % **No. of 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	Ratios
2116	2	766.2591	-184.33	2	55.0	11.9	2	62-74	K.RSDESVRLSVNNR.E		WD:WU 1.07

Detailed Protein Report

Protein 846: 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

WD:WU **Median:** 6.88 **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		WD:WU	6.88

Detailed Protein Report

Protein 847: PREDICTED: sodium/hydrogen exchanger 7 isoform X6 [Homo sapiens]

Accession: gi|578838129
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 11.9
MW [kDa]: 77.7
pI: 6.3
Sequence Coverage [%]: 2.3
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MEPGDAARPG	SGRATGAPPP	RLLLLPLLLG	WGLRVAAAAS	ASSSGAAAED	SSAMEELATE	KEAEESHRQD	SVSLLTFILL
90	100	110	120	130	140	150	160
LTLTILTIWL	FKHRRVRFLH	ETGLAMIYGL	IVGVILRYGT	PATSGRDKSL	SCTQEDRAFS	TLLVNVSGKF	FEYTLKGEIS
170	180	190	200	210	220	230	240
PGKINSVEQN	DMLRKVTFDP	EVFFNILLPP	IIFHAGYSLK	KRHFFRNLGS	ILAYAFLGTA	VSCFIIGNLM	YGVVKLMKIM
250	260	270	280	290	300	310	320
GQLSDKFYYT	DCLFFGAIIS	ATDPVTVLAI	FNELHADVDL	YALLFGESVL	NDAVAIVLSS	SIVAYQPAGL	NTHAFDAAAF
330	340	350	360	370	380	390	400
FKSVGIFLGI	FSGSFTMGAV	TGVVTALVTK	FTKLHCFPLL	ETALFFLMSW	STFLLAEACG	FTGVVAVLFC	GITQAHYTYN
410	420	430	440	450	460	470	480
NLSVESRSRT	KQLFEVLHFL	AENFIFSYMG	LALFTFQKHV	FSPIFIIGAF	VAIFLGRAAH	IYPLSFFLNL	GRRHKIGWNF
490	500	510	520	530	540	550	560
QHMMMFSGLR	GAMAFALAIR	DTASYARQMM	FTTTLLIVFF	TVWIIGGGTT	PMLSWLNIRV	GVDPDQDPPP	NNDSFQVLQG
570	580	590	600	610	620	630	640
DGPDSARGNR	TKQESAWIFR	LWYSFDHNYL	KPILTHSGPP	LTTTLPAWCG	LLARCLTSPQ	VYDNQEPLRE	EDSDFILTEG
650	660	670	680	690	700	710	
DLTLTYGDST	VTANGSSSSH	TASTSLEGSR	RTKSSSEEVL	ERDLGMGDQK	VSSRGTRLVF	PLEDNA	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
843	2	937.9669	-59.83	2	38.9	11.9	1	458-473	R.AAHIYPLSFFLNLGRR.H	

Detailed Protein Report

Protein 848: PREDICTED: DNA-(apurinic or apyrimidinic site) lyase isoform X2 [Homo sapiens]

Accession:	gi|530403617	**Score:**	11.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	33.8
Database Date:	2015-11-30	**pI:**	9.0
		Sequence Coverage [%]:	6.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MYEPEAKKSK	TAAKKNDKEA	AGEGPALYED	PPDQKTSPSG	KPATLKICSW	NVDGLRAWIK	KKGLDWVKEE	APDILCLQET
90	100	110	120	130	140	150	160
KCSENKLPAE	LQELPGLSHQ	YWSAPSDKEG	YSGVGLLSRQ	CPLKVSYGIG	DEEHDQEGRV	IVAEFDSFVL	VTAYVPNAGR
170	180	190	200	210	220	230	240
GLVRLEYRQR	WDEAFRKFLK	GLASRKPLVL	CGDLNVAHEE	IDLRNPKGNK	KNAGFTPQER	QGFGELLQAV	PLADSFRHLY
250	260	270	280	290	300	310	
PNTPYAYTFW	TYMMNARSKN	VGWRLDYFLL	SHSLLPALCD	SKIRSKALGS	DHCPITLYLA	L	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1621	1	1130.4868	-28.13	2	48.6	11.9	1	120-139	R.QCPLKVSYGIGDEEHDQEGR.V	

Detailed Protein Report

Protein 849: 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 850: 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 851: 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 852: 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

Quantitation

WD:WU	**Median:** 0.91	**CV:** 0.00 %	**No. of 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	Ratios
803	1	541.1573	-169.31	3	38.9	11.9	2	87-100	K.CGHNKGYKGLDNCR.F	Carbamidomethyl: 1	WD:WU 0.91

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Detailed Protein Report

Protein 853: 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 854: diacylglycerol kinase eta isoform 4 [Homo sapiens]

Accession:	gi|325197221	**Score:**	11.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	120.5
Database Date:	2015-11-30	**pI:**	5.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLCAENRKEM	EDWISSLKSV	QTREPYEVAQ	FNVEHFSGMH	NWYACSHARP	TFCNVCRESL	SGVTSHGLSC	EVCKFKAHKR
90	100	110	120	130	140	150	160
CAVRATNNCK	WTTLASIGKD	IIEDEDGVAM	PHQWLEGNLP	VSAKCAVCDK	TCGSVLRLQD	WKCLWCKTMV	HTACKDLYHP
170	180	190	200	210	220	230	240
ICPLGQCKVS	IIPPIALNST	DSDGFCRATF	SFCVSPLLVF	VNSKSGDNQG	VKFLRRFKQL	LNPAQVFDLM	NGGPHLGLRL
250	260	270	280	290	300	310	320
FQKFDNFRIL	VCGGDGSVGW	VLSEIDKLNL	NKQCQLGVLP	LGTGNDLARV	LGWGGSYDDD	TQLPQILEKL	ERASTKMLDR
330	340	350	360	370	380	390	400
WSIMTYELKL	PPKASLLPGP	PEASEEFYMT	IYEDSVATHL	TKILNSDEHA	VVISSAKTLC	ETVKDFVAKV	EKTYDKTLEN
410	420	430	440	450	460	470	480
AVVADAVASK	CSVLNEKLEQ	LLQALHTDSQ	AAPVLPGLSP	LIVEEDAVES	SSEESLGESK	EQLGDDVTKP	SSQKAVKPRE
490	500	510	520	530	540	550	560
IMLRANSLKK	AVRQVIEEAG	KVMDDPTVHP	CEPANQSSDY	DSTETDESKE	EAKDDGAKES	ITVKTAPRSP	DARASYGHSQ
570	580	590	600	610	620	630	640
TDSVPGPAVA	ASKENLPVLN	TRIICPGLRA	GLAASIAGSS	IINKMLLANI	DPFGATPFID	PDLDSVDGYS	EKCVMNNYFG
650	660	670	680	690	700	710	720
IGLDAKISLE	FNNKREEHPE	KCRSRTKNLM	WYGVLGTREL	LQRSYKNLEQ	RVQLECDGQY	IPLPSLQGIA	VLNIPSYAGG
730	740	750	760	770	780	790	800
TNFWGGTKED	DIFAAPSFDD	KILEVVAIFD	SMQMAVSRVI	KLQHHRIAQC	RTVKITIFGD	EGVPVQVDGE	AWVQPPGIIK
810	820	830	840	850	860	870	880
IVHKNRAQML	TRDRAFESTL	KSWEDKQKCD	SGKPVLRTHL	YIHHAIDLAT	EEVSQMQLCS	QAAEELITRI	CDAATIHCLL
890	900	910	920	930	940	950	960
EQELAHAVNA	CSHALNKANP	RCPESLTRDT	ATEIAINVKA	LYNETESLLV	GRVPLQLESP	HEERVSNALH	SVEVELQKLT
970	980	990	1000	1010	1020	1030	1040
EIPWLYYILH	PNEDEEPPMD	CTKRNNRSTV	FRIVPKFKKE	KVQKQKTSSQ	PVQKWGTEEV	AAWLDLLNLG	EYKDIFIRHD
1050	1060	1070	1080	1090			
IRGAELLHLE	RRDLKDLGIP	KVGHVKRILQ	GIKELGRSTP	QSEV			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1474	1	689.9970	-3.59	3	46.8	11.9	1	58-76	R.ESLSGVTSHGLSCEVCKFK.A	Carbamidomethyl: 13

Detailed Protein Report

Protein 855: PREDICTED: DNA mismatch repair protein Mlh3 isoform X4 [Homo sapiens]

Accession:	gi|530403519	**Score:**	11.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	143.6
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
MIKCLSVEVQ	AKLRSGLAIS	SLGQCVEELA	LNSIDAEAKC	VAVRVNMETF	QVQVIDNGFG	MGSDDVEKVG	NRYFTSKCHS
90	100	110	120	130	140	150	160
VQDLENPRFY	GFRGEALANI	ADMASAVEIS	SKKNRTMKTF	VKLFQSGKAL	KACEADVTRA	SAGTTVTVYN	LFYQLPVRRK
170	180	190	200	210	220	230	240
CMDPRLEFEK	VRQRIEALSL	MHPSISFSLR	NDVSGSMVLQ	LPKTKDVCSR	FCQIYGLGKS	QKLREISFKY	KEFELSGYIS
250	260	270	280	290	300	310	320
SEAHYNKNMQ	FLFVNKRLVL	RTKLHKLIDF	LLRKESIICK	PKNGPTSRQM	NSSLRHRSTP	ELYGIYVINV	QCQFCEYDVC
330	340	350	360	370	380	390	400
MEPAKTLIEF	QNWDTLLFCI	QEGVKMFLKQ	EKLFVELSGE	DIKEFSEDNG	FSLFDATLQK	RVTSDERSNF	QEACNNILDS
410	420	430	440	450	460	470	480
YEMFNLQSKA	VKRKTTAENV	NTQSSRDSEA	TRKNTNDAFL	YIYESGGPGH	SKMTEPSLQN	KDSSCSESKM	LEQETIVASE
490	500	510	520	530	540	550	560
AGENEKHKKS	FLEHSSLENP	CGTSLEMFLS	PFQTPCHFEE	SGQDLEIWKE	STTVNGMAAN	ILKNNRIQNQ	PKRFKDATEV
570	580	590	600	610	620	630	640
GCQPLPFATT	LWGVHSAQTE	KEKKKESSNC	GRRNVFSYGR	VKLCSTGFIT	HVVQNEKTKS	TETEHSFKNY	VRPGPTRAQE
650	660	670	680	690	700	710	720
TFGNRTRHSV	ETPDIKDLAS	TLSKESGQLP	NKKNCRTNIS	YGLENEPTAT	YTMFSAFQEG	SKKSQTDCIL	SDTSPSFPWY
730	740	750	760	770	780	790	800
RHVSNDSRKT	DKLIGFSKPI	VRKKLSLSSQ	LGSLEKFKRQ	YGKVENPLDT	EVEESNGVTT	NLSLQVEPDI	LLKDKNRLEN
810	820	830	840	850	860	870	880
SDVCKITTME	HSDSDSSCQP	ASHILNSEKF	PFSKDEDCLE	QQMPSLRESP	MTLKELSLFN	RKPLDLEKSS	ESLASKLSRL
890	900	910	920	930	940	950	960
KGSERETQTM	GMMSRFNELP	NSDSSRKDSK	LCSVLTQDFC	MLFNNKHEKT	ENGVIPTSDS	ATQDNSFNKN	SKTHSNSNTT
970	980	990	1000	1010	1020	1030	1040
ENCVISETPL	VLPYNNSKVT	GKDSDVLIRA	SEQQIGSLDS	PSGMLMNPVE	DATGDQNGIC	FQSEESKARA	CSETEESNTC
1050	1060	1070	1080	1090	1100	1110	1120
CSDWQRHFDV	ALGRMVYVNK	MTGLSTFIAP	TEDIQAACTK	DLTTVAVDVV	LENGSQYRCQ	PFRSDLVLPF	LPRARAERTV
1130	1140	1150	1160	1170	1180	1190	1200
MRQDNRDTVD	DTVSSESLQS	LFSEWDNPVF	ARYPEVAVDV	SSGQAESLAV	KIHNILYPYR	FTKGMIHSMQ	VLQQVDNKFI
1210	1220	1230	1240	1250	1260	1270	1280
ACLMSTKTEE	NGEAGGNLLV	LVDQHAAHER	IRLEQLIIDS	YEKQQAQGSG	RKKLLSSTLI	PPLEITVTEE	QRRLL

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
964	1	523.2194	-171.68	2	40.4	11.9	2	877-885	K.LSRLKGSER.E	

Detailed Protein Report

Protein 856: 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 857: PREDICTED: transketolase isoform X1 [Homo sapiens]

Accession: gi|578806532
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 11.8
MW [kDa]: 68.8
pI: 9.0
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 858: **dickkopf-related protein 1 precursor [Homo sapiens]**

Accession:	gi|7110719	**Score:**	11.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	28.7
Database Date:	2015-11-30	**pI:**	10.2
		Sequence Coverage [%]:	3.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MMALGAAGAT	RVFVAMVAAA	LGGHPLLGVS	ATLNSVLNSN	AIKNLPPPLG	GAAGHPGSAV	SAAPGILYPG	GNKYQTIDNY
90	100	110	120	130	140	150	160
QPYPCAEDEE	CGTDEYCASP	TRGGDAGVQI	CLACRKRRKR	CMRHAMCCPG	NYCKNGICVS	SDQNHFRGEI	EETITESFGN
170	180	190	200	210	220	230	240
DHSTLDGYSR	RTTLSSKMYH	TKGQEGSVCL	RSSDCASGLC	CARHFWSKIC	KPVLKEGQVC	TKHRRKGSHG	LEIFQRCYCG
250	260	270					
EGLSCRIQKD	HHQASNSSRL	HTCQRH					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1338	1	569.8185	115.24	2	45.1	11.8	0	250-259	K.DHHQASNSSR.L	

Detailed Protein Report

Protein 859: 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 860: amyloid-like protein 1 isoform 2 precursor [Homo sapiens]

Accession:	gi|4885065	**Score:**	11.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	72.1
Database Date:	2015-11-30	**pI:**	5.5
		Sequence Coverage [%]:	1.4
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 1.07 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MGPASPAARG	LSRRPGQPPL	PLLLPLLLLL	LRAQPAIGSL	AGGSPGAAEA	PGSAQVAGLC	GRLTLHRDLR	TGRWEPDPQR
90	100	110	120	130	140	150	160
SRRCLRDPQR	VLEYCRQMYP	ELQIARVEQA	TQAIPMERWC	GGSRSGSCAH	PHHQVVPFRC	LPGEFVSEAL	LVPEGCRFLH
170	180	190	200	210	220	230	240
QERMDQCESS	TRRHQEAQEA	CSSQGLILHG	SGMLLPCGSD	RFRGVEYVCC	PPPGTPDPSG	TAVGDPSTRS	WPPGSRVEGA
250	260	270	280	290	300	310	320
EDEEEEESFP	QPVDDYFVEP	PQAEEEEETV	PPPSSHTLAV	VGKVTPTPRP	TDGVDIYFGM	PGEISEHEGF	LRAKMDLEER
330	340	350	360	370	380	390	400
RMRQINEVMR	EWAMADNQSK	NLPKADRQAL	NEHFQSILQT	LEEQVSGERQ	RLVETHATRV	IALINDQRRA	ALEGFLAALQ
410	420	430	440	450	460	470	480
ADPPQAERVL	LALRRYLRAE	QKEQRHTLRH	YQHVAAVDPE	KAQQMRFQVH	THLQVIEERV	NQSLGLLDQN	PHLAQELRPQ
490	500	510	520	530	540	550	560
IQELLHSEHL	GPSELEAPAP	GGSSEDKGGL	QPPDSKDDTP	MTLPKGSTEQ	DAASPEKEKM	NPLEQYERKV	NASVPRGFPF
570	580	590	600	610	620	630	640
HSSEIQRDEL	APAGTGVSRE	AVSGLLIMGA	GGGSLIVLSM	LLLRRKKPYG	AISHGVVEVD	PMLTLEEQQL	RELQRHGYEN
650	660						
PTYRFLEERP							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2604	1	449.6284	-237.08	2	60.8	11.8	0	508-516	K.GGLQPPDSK.D		WD:WU 1.07

Detailed Protein Report

Protein 861: protein SCO2 homolog, mitochondrial precursor [Homo sapiens]

Accession:	gi|153791313	**Score:**	11.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	29.8
Database Date:	2015-11-30	**pI:**	9.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.0
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|281182727	refseq_human (refseq_human_20140103.fasta)	protein SCO2 homolog, mitochondrial precursor [Homo sapiens]
gi|281182722	refseq_human (refseq_human_20140103.fasta)	protein SCO2 homolog, mitochondrial precursor [Homo sapiens]
gi|281182716	refseq_human (refseq_human_20140103.fasta)	protein SCO2 homolog, mitochondrial precursor [Homo sapiens]

10	20	30	40	50	60	70	80
MLLLTRSPTA	WHRLSQLKPR	VLPGTLGGQA	LHLRSWLLSR	QGPAETGGQG	QPQGPGLRTR	LLITGLFGAG	LGGAWLALRA
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
EKERLQQQKR	TEALRQAAVG	QGDFHLLDHR	GRARCKADFR	GQWVLMYFGF	THCPDICPDE	LEKLVQVVRQ	LEAEPGLPPV
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
QPVFITVDPE	RDDVEAMARY	VQDFHPRLLG	LTGSTKQVAQ	ASHSYRVYYN	AGPKDEDQDY	IVDHSIAIYL	LNPDGLFTDY
250	**260**	**270**					
YGRSRSAEQI	SDSVRRHMAA	FRSVLS					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
896	1	512.1549	-207.64	2	39.6	11.8	2	113-120	R.ARCKADFR.G	Carbamidomethyl: 3

Detailed Protein Report

Protein 862: PREDICTED: receptor-type tyrosine-protein phosphatase T isoform X5 [Homo sapiens]

Accession:	gi|578835723	**Score:**	11.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	155.9
Database Date:	2015-11-30	**pI:**	6.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.4
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 1.93 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MLDQAVPTGS	FMMVNSSGRA	SGQKAHLLLP	TLKENDTHCI	DFHYYFSSRD	RSSPGALNVY	VKVNGGPQGN	PVWNVSGVVT
90	100	110	120	130	140	150	160
EGWVKAELAI	STFWPHFYQV	IFESVSLKGH	PGYIAVDEVR	VLAHPCRKAP	HFLRLQNVEV	NVGQNATFQC	IAGGKWSQHD
170	180	190	200	210	220	230	240
KLWLQQWNGR	DTALMVTRVV	NHRRFSATVS	VADTAQRSVS	KYRCVIRSDG	GSGVSNYAEL	IVKEPPTPIA	PPELLAVGAT
250	260	270	280	290	300	310	320
YLWIKPNANS	IIGDGPIILK	EVEYRTTTGT	WAETHIVDSP	NYKLWHLDPD	VEYEIRVLLT	RPGEGGTGPP	GPPLTTRTKC
330	340	350	360	370	380	390	400
ADPVHGPQNV	EIVDIRARQL	TLQWEPFGYA	VTRCHSYNLT	VQYQYVFNQQ	QYEAEEVIQT	SSHYTLRGLR	PFMTIRLRLL
410	420	430	440	450	460	470	480
LSNPEGRMES	EELVVQTEED	VPGAVPLESI	QGGPFEEKIY	IQWKPPNETN	GVITLYEINY	KAVGSLDPSA	DLSSQRGKVF
490	500	510	520	530	540	550	560
KLRNETHHLF	VGLYPGTTYS	FTIKASTAKG	FGPPVTTRIA	TKISAPSMPE	YDTDTPLNET	DTTITVMLKP	AQSRGAPVSV
570	580	590	600	610	620	630	640
YQLVVKEERL	QKSRRAADII	ECFSVPVSYR	NASSLDSLHY	FAAELKPANL	PVTQPFTVGD	NKTYNGYWNP	PLSPLKSYSI
650	660	670	680	690	700	710	720
YFQALSKANG	ETKINCVRLA	TKAPMGSAQV	TPGTPLCLLT	TGASTQNSNT	VEPEKQVDNT	VKMAGVIAGL	LMFIIILLGV
730	740	750	760	770	780	790	800
MLTIKRRKLA	KKQKETQSGA	QREMGPVASA	DKPTTKLSAS	RNDEGFSSSS	QDVNGFTDGS	RGELSQPTLT	IQTHPYRTCD
810	820	830	840	850	860	870	880
PVEMSYPRDQ	FQPAIRVADL	LQHITQMKRG	QGYGFKEEYE	ALPEGQTASW	DTAKEDENRN	KNRYGNIISY	DHSRVRLLVL
890	900	910	920	930	940	950	960
DGDPHSDYIN	ANYIDGYHRP	RHYIATQGPM	QETVKDFWRM	IWQENSASIV	MVTNLVEVGR	VKCVRYWPDD	TEVYGDIKVT
970	980	990	1000	1010	1020	1030	1040
LIETEPLAEY	VIRTFTVQKK	GYHEIRELRL	FHFTSWPDHG	VPCYATGLLG	FVRQVKFLNP	PEAGPIVVHC	SAGAGRTGCF
1050	1060	1070	1080	1090	1100	1110	1120
IAIDTMLDMA	ENEGVVDIFN	CVRELRAQRV	NLVQTEEQYV	FVHDAILEAC	LCGNTAIPVC	EFRSLYYNIS	RLDPQTNSSQ
1130	1140	1150	1160	1170	1180	1190	1200
IKDEFQTLNI	VTPRVRPEDC	SIGLLPRNHD	KNRSMDVLPL	DRCLPFLISV	DGESSNYINA	ALMDSHKQPA	AFVVTQHPLP
1210	1220	1230	1240	1250	1260	1270	1280
NTVADFWRLV	FDYNCSSVVM	LNEMDTAQFC	MQYWPEKTSG	CYGPIQVEFV	SADIDEDIIH	RIFRICNMAR	PQDGYRIVQH
1290	1300	1310	1320	1330	1340	1350	1360
LQYIGWPAYR	DTPPSKRSLL	KVVRRLEKWQ	EQYDGREGRT	VVHCLNGGGR	SGTFCAICSV	CEMIQQQNII	DVFHIVKTLR
1370	1380	1390					
NNKSNMVETL	EQYKFVYEVA	LEYLSSF					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2030	1	715.9422	-125.78	3	53.8	11.8	1	320-338	K.CADPVHGPQNVEIVDIRAR.Q	Carbamidomethyl: 1	WD:WU 1.93

Detailed Protein Report

Protein 863: Krueppel-like factor 10 isoform b [Homo sapiens]

Accession:	gi|73760403	**Score:**	11.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	51.4
Database Date:	2015-11-30	**pI:**	10.3
		Sequence Coverage [%]:	3.0
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MEERMEMISE RPKESMYSWN KTAEKSDFEA VEALMSMSCS WKSDFKKYVE NRPVTPVSDL SEEENLLPGT PDFHTIPAFC

        90        100        110        120        130        140        150        160
LTPPYSPSDF EPSQVSNLMA PAPSTVHFKS LSDTAKPHIA APFKEEEKSP VSAPKLPKAQ ATSVIRHTAD AQLCNHQTCP

       170        180        190        200        210        220        230        240
MKAASILNYQ NNSFRRRTHL NVEAARKNIP CAAVSPNRSK CERNTVADVD EKASAALYDF SVPSSETVIC RSQPAPVSPQ

       250        260        270        280        290        300        310        320
QKSVLVSPPA VSAGGVPPMP VICQMVPLPA NNPVVTTVVP STPPSQPPAV CPPVVFMGTQ VPKGAVMFVV PQPVVQSSKP

       330        340        350        360        370        380        390        400
PVVSPNGTRL SPIAPAPGFS PSAAKVTPQI DSSRIRSHIC SHPGCGKTYF KSSHLKAHTR THTGEKPFSC SWKGCERRFA

       410        420        430        440        450        460        470
RSDELSRHRR THTGEKKFAC PMCDRRFMRS DHLTKHARRH LSAKKLPNWQ MEVSKLNDIA LPPTPAPTQ
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
19	1	797.4613	101.35	2	29.2	11.8	2	199-212	R.SKCERNTVADVDEK.A	

Detailed Protein Report

Protein 864: 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 865: zinc finger protein 573 isoform 4 [Homo sapiens]

Accession:	gi|289577063	**Score:**	11.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	77.9
Database Date:	2015-11-30	**pI:**	10.2
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MFPVLEPHQV	GLIRSYNSKT	MTCELVTFRD	VAIDFSRQEW	EYLDPNQRDL	YRDVMLENYR	NLVSLGGHSI	SKPVVVDLLE
90	100	110	120	130	140	150	160
RGKEPWMILR	EETQFTDLDL	QCEIISYIEV	PTYETDISST	QLQSIYKREK	LYECKKCQKK	FSSGYQLILH	HRFHVIERPY
170	180	190	200	210	220	230	240
ECKECGKNFR	SGYQLTLHQR	FHTGEKPYEC	TECGKNFRSG	YQLTVHQRFH	TGEKTYECRQ	CGKAFIYASH	IVQHERIHTG
250	260	270	280	290	300	310	320
GKPYECQECG	RAFSQGGHLR	IHQRVHTGEK	PYKCKECGKT	FSRRSNLVEH	GQFHTDEKPY	ICEKCGKAFR	RGHQLTVHQR
330	340	350	360	370	380	390	400
VHTGKKPYEC	KECGKGYTTA	SYFLLHQRIH	KGGKPYECKE	CKKTFTLYRN	LTRHQNIHTG	EKLFECKQCG	KTYTTGSKLF
410	420	430	440	450	460	470	480
QHQKTHTGEK	PYECKECGKA	FSLYGYLKQH	QKIHTGMKHF	ECKECKKTFT	LYRNLTRHQN	IHTGKKLFEC	QECGKAYSTG
490	500	510	520	530	540	550	560
SNLIQHRKTH	TGEKPYKCKE	CGKTFSLHGY	LNQHQKIHTG	MKPYECKVCR	KTFTFYRNLT	LHQSIHTDEK	PFECKECGKT
570	580	590	600	610	620	630	640
FRRSSHLTAH	QSIHADKKPY	ECKECGKAFK	MYGYLTQHQK	IHTGGKPYEC	KECGKAFSRA	SNLVQHERIH	TGEKPYVCKQ
650	660	670					
CGKTFRYGSA	LKAHQRIHRS	IKV					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2167	1	900.3438	-97.52	3	55.5	11.8	2	15-37	R.SYNSKTMTCELVTFRDVAIDFSR.Q	Oxidation: 7

Detailed Protein Report

Protein 866: SWI/SNF complex subunit SMARCC2 isoform b [Homo sapiens]

Accession:	gi|21237808	**Score:**	11.8
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 [%]:**	1.1
		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
2077	1	696.2716	-109.38	2	54.6	11.8	1	488-499	R.RNLAGDVCAIMR.V	Carbamidomethyl: 8; Oxidation: 11

Detailed Protein Report

Protein 867: kinetochore-associated protein NSL1 homolog isoform 1 [Homo sapiens]

Accession:	gi|110349759	**Score:**	11.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	32.1
Database Date:	2015-11-30	**pI:**	6.4
		Sequence Coverage [%]:	4.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAGSPELVVL	DPPWDKELAA	GTESQALVSA	TPREDFRVRC	TSKRAVTEML	QLCGRFVQKL	GDALPEEIRE	PALRDAQWTF
90	100	110	120	130	140	150	160
ESAVQENISI	NGQAWQEASD	NCFMDSDIKV	LEDQFDEIIV	DIATKRKQYP	RKILECVIKT	IKAKQEILKQ	YHPVVHPLDL
170	180	190	200	210	220	230	240
KYDPDPAPHM	ENLKCRGETV	AKEISEAMKS	LPALIEQGEG	FSQVLRMQPV	IHLQRIHQEV	FSSCHRKPDA	KPENFITQIE
250	260	270	280	290			
TTPTETASRK	TSDMVLKRKQ	TKDCPQRKWY	PLRPKKINLD	T			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2922	1	822.4610	-7.35	2	65.3	11.8	2	269-281	K.WYPLRPKKINLDT.-	

Detailed Protein Report

Protein 868: 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 869: diacylglycerol O-acyltransferase 2 isoform 2 [Homo sapiens]

Accession:	gi|359806523	**Score:**	11.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	39.0
Database Date:	2015-11-30	**pI:**	10.0
		Sequence Coverage [%]:	3.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MKTLIAAYSG	VLRGERQAEA	DRSQRSHGGP	ALSREGSGRW	GVACSAILMY	IFCTDCWLIA	VLYFTWLVFD	WNTPKKGGRR
90	100	110	120	130	140	150	160
SQWVRNWAVW	RYFRDYFPIQ	LVKTHNLLTT	RNYIFGYHPH	GIMGLGAFCN	FSTEATEVSK	KFPGIRPYLA	TLAGNFRMPV
170	180	190	200	210	220	230	240
LREYLMSGGI	CPVSRDTIDY	LLSKNGSGNA	IIIVVGGAAE	SLSSMPGKNA	VTLRNRKGFV	KLALRHGADL	VPIYSFGENE
250	260	270	280	290	300	310	320
VYKQVIFEEG	SWGRWVQKKF	QKYIGFAPCI	FHGRGLFSSD	TWGLVPYSKP	ITTVVGEPIT	IPKLEHPTQQ	DIDLYHTMYM
330	340	350					
EALVKLFDKH	KTKFGLPETE	VLEVN					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2815	1	626.8578	46.04	2	63.8	11.7	1	23-34	R.SQRSHGGPALSR.E	

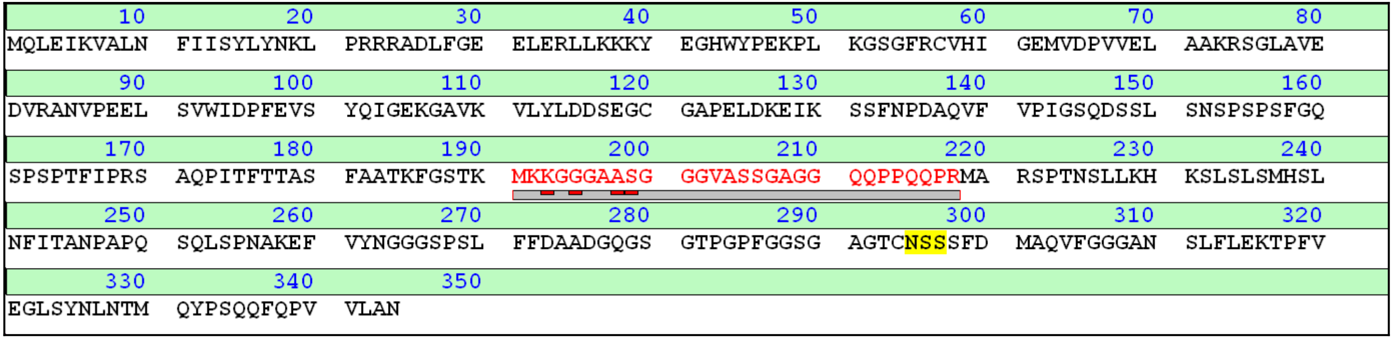
Detailed Protein Report

Protein 870: 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	

Detailed Protein Report

Protein 871: 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

Quantitation

WD:WU **Median:** 1.40 **CV:** 0.00 % **No. of 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	Ratios
927	1	625.5184	-139.00	3	40.4	11.7	1	254-270	R.CMCKAGFEAVENGTVCR.G	Carbamidomethyl: 16	WD:WU 1.40

Detailed Protein Report

Protein 872: PREDICTED: uncharacterized protein KIAA1841 isoform X3 [Homo sapiens]

Accession:	gi|530368202	**Score:**	11.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	66.0
Database Date:	2015-11-30	**pI:**	9.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.1
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MVIHVCDEAK NLKEDFTCPR DLLISEMKYF AEYLSMDAQR WEEVDISVHC DVHIFNWLIK YIKRNTKENK DCEMPTLEPG
        90        100        110        120        130        140        150        160
NVISILISSE FLKMDSLVEQ CIQYCHKNMN AIVATPCNMN CINANLLTRI ADLFSHNEVD DLKDKKDKFK SKLFCKKIER
       170        180        190        200        210        220        230        240
LFDPEYLNPD SRSNAATLYR CCLCKKLLTK ETERRIPCIP GKINVDRRGN IVYIHIRDKT WDVHEYLNSL FEELKSWRDV
       250        260        270        280        290        300        310        320
YWRLWGTINW LTCSRCYQAF LCIEFSHCQY HSETVVYPTA ASSLNTVGTG IYPCCNQKVL RFDPTQLTKG CKVRDHMVTL
       330        340        350        360        370        380        390        400
RDQGEGGDLP SCPTARMLDD LHKYRDVIVV PFSKDTVSDV GVGLCDEKGI ECDVLLEPNT PWGPKTGELN AFLSLKNWTL
       410        420        430        440        450        460        470        480
QLKQQSLFSE EEEYTTGSEV TEDEVGDEEE VSKKQRKKEK PKKFTRQPKK QVSSPCAQRK EKALEKSASR DVSPFVMSMQ
       490        500        510        520        530        540        550        560
KNKWDATRSL RFNQDAQRED DQRRMTEITG HLIKMRLGDL DRVKSKEAKE FAGGIYSRLE AQIKASVPVS ARQSSSEKNT
       570        580
RSKSRFGQGR PA
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2891	1	713.3518	-39.00	2	64.9	11.7	1	2-13	M.VIHVCDEAKNLK.E	Carbamidomethyl: 5

Detailed Protein Report

Protein 873: 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 874: **elongation factor G, mitochondrial [Homo sapiens]**

Accession:	gi|18390331	**Score:**	11.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	83.4
Database Date:	2015-11-30	**pI:**	6.6
		Sequence Coverage [%]:	1.7
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 1.00 **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		WD:WU 1.00

Detailed Protein Report

Protein 875: **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

WD:WU **Median:** 0.58 **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		WD:WU 0.58

Detailed Protein Report

Protein 876: **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 877: PREDICTED: formin-binding protein 1 isoform X20 [Homo sapiens]

Accession:	gi|530390795	**Score:**	11.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	64.0
Database Date:	2015-11-30	**pI:**	5.0
		Sequence Coverage [%]:	1.8
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 0.34 **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		WD:WU 0.34

Detailed Protein Report

Protein 878: **PREDICTED: phosphatidylinositol 3,4,5-trisphosphate-dependent Rac exchanger 1 protein isoform X1 [Homo sapiens]**

Accession:	gi|530418228	**Score:**	11.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	106.0
Database Date:	2015-11-30	**pI:**	5.2
		Sequence Coverage [%]:	1.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGLEQIIKIP	DQPDTLCFQI	RGAAPPYVYA	VGRGSEAMAA	GLCAGQCILK	VNGSNVMNDG	APEVLEHFQA	FRSRREEALG
90	100	110	120	130	140	150	160
LYQWIYHTHE	DAQEARASQE	ASTEDPSGEQ	AQEEDQADSA	FPLLSLGPRL	SLCEDSPMVT	LTVDNVHLEH	GVVYEYVSTA
170	180	190	200	210	220	230	240
GVRCHVLEKI	VEPRGCFGLT	AKILEAFAAN	DSVFVENCRR	LMALSSAIVT	MPHFEFRNIC	DTKLESIGQR	IACYQEFAAQ
250	260	270	280	290	300	310	320
LKSRVSPPFK	QAPLEPHPLC	GLDFCPTNCH	INLMEVSYPK	TTPSVGRSFS	IRFGRKPSLI	GLDPEQGHLN	PMSYTQHCIT
330	340	350	360	370	380	390	400
TMAAPSWKCL	PAAEGDPQGQ	GLHDGSFGPA	SGTLGQEDRG	LSFLLKQEDR	EIQDAYLQLF	TKLDVALKEM	KQYVTQINRL
410	420	430	440	450	460	470	480
LSTITEPTSG	GSCDASLAEE	ASSLPLVSEE	SEMDRSDHGG	IKKVCFKVAE	EDQEDSGHDT	MSYRDSYSEC	NSNRDSVLSY
490	500	510	520	530	540	550	560
TSVRSNSSYL	GSDEMGSGDE	LPCDMRIPSD	KQDKLHGCLE	HLFNQVDSIN	ALLKGPVMSR	AFEETKHFPM	NHSLQEFKQK
570	580	590	600	610	620	630	640
EECTIRGRSL	IQISIQEDPW	NLPNSIKTLV	DNIQRYVEDG	KNQLLLALLK	CTDTELQLRR	DAIFCQALVA	AVCTFSKQLL
650	660	670	680	690	700	710	720
AALGYRYNNN	GEYEESSRDA	SRKWLEQVAA	TGVLLHCQSL	LSPATVKEER	TMLEDIWVTL	SELDNVTFSF	KQLDENYVAN
730	740	750	760	770	780	790	800
TNVFYHIEGS	RQALKVIFYL	DSYHFSKLPS	RLEGGASLRL	HTALFTKVLE	NVEGLPSPGS	QAAEDLQQDI	NAQSLEKVQQ
810	820	830	840	850	860	870	880
YYRKLRAFYL	ERSNLPTDAS	TTAVKIDQLI	RPINALDELC	RLMKSFVHPK	PGAAGSVGAG	LIPISSELCY	RLGACQMVMC
890	900	910	920	930	940	950	960
GTGMQRSTLS	VSLEQAAILA	RSHGLLPKCI	MQATDIMRKQ	GPRVEILAKN	LRVKDQMPQG	APRLYRLCQP	PVDGDL

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2874	1	734.8534	-46.80	2	64.7	11.7	0	371-382	R.EIQDAYLQLFTK.L	

Detailed Protein Report

Protein 879: olfactory receptor 14A16 [Homo sapiens]

Accession:	gi|50233854	**Score:**	11.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	34.3
Database Date:	2015-11-30	**pI:**	9.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	5.2
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578802205	refseq_human(refseq_human_20140103.fasta)	PREDICTED: olfactory receptor 14A16 isoform X2 [Homo sapiens]

10	20	30	40	50	60	70	80
MANLTIVTEF	ILMGFSTNKN	MCILHSILFL	LIYLCALMGN	VLIIMITTLD	HHLHTPVYFF	LKNLSFLDLC	LISVTAPKSI
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
ANSLIHNNSI	SFLGCVSQVF	LLLSSASAEL	LLLTVMSFDR	YTAICHPLHY	DVIMDRSTCV	QRATVSWLYG	GLIAVMHTAG
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
TFSLSYCGSN	MVHQFFCDIP	QLLAISCSEN	LIREIALILI	NVVLDFCCFI	VIIITYVHVF	STVKKIPSTE	GQSKAYSICL
250	**260**	**270**	**280**	**290**	**300**	**310**	
PHLLVVLFLS	TGFIAYLKPA	SESPSILDAV	ISVFYTMLPP	TFNPIIYSLR	NKAIKVALGM	LIKGKLTKK	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2229	1	597.6218	-67.53	3	56.3	11.7	0	63-78	K.NLSFLDLCLISVTAPK.S	Carbamidomethyl: 8

Detailed Protein Report

Protein 880: **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 881: ubiquitin carboxyl-terminal hydrolase 6 [Homo sapiens]

Accession:	gi|109638751	**Score:**	11.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	158.6
Database Date:	2015-11-30	**pI:**	8.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.4
		No. of unique Peptides:	1

Alias proteins:

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

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2697	1	1175.5508	58.82	2	62.1	11.6	1	1039-1058	R.AFTSEEELGESEMYYCSKCK.T	Oxidation: 13

Detailed Protein Report

Protein 882: PREDICTED: PDZ domain-containing protein 2 isoform X9 [Homo sapiens]

Accession:	gi|578809883	**Score:**	11.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	269.5
Database Date:	2015-11-30	**pI:**	9.0
		Sequence Coverage [%]:	0.7
		No. of unique Peptides:	1

Detailed Protein Report

```
        10         20         30         40         50         60         70         80
MTNAASQKVG RRTSNRVTAW HGRKLAEYGR WSCSKNRMGW EFRDGRLSLG DELLVINGHL LVGLSHEEAV AILRSATGMV

        90        100        110        120        130        140        150        160
QLVVASKENS AEDLLRLTSK SLPDLTSSVE DVSSWTDNED QEADGEEDEG TSSSVQRAMP GTDEPQDVCG AEESKGNLES

       170        180        190        200        210        220        230        240
PKQGSNKIKL KSRLSGGVHR LESVEEYNEL MVRNGDPRIR MLEVSRDGRK HSLPQLLDSS SASQEYHIVK KSTRSLSTTQ

       250        260        270        280        290        300        310        320
VESPWRLIRP SVISIIGLYK EKGKGLGFSI AGGRDCIRGQ MGIFVKTIFP NGSAAEDGRL KEGDEILDVN GIPIKGLTFQ

       330        340        350        360        370        380        390        400
EAIHTFKQIR SGLFVLTVRT KLVSPSLTPC STPTHMSRSA SPNFNTSGGA SAGGSDEGSS SSLGRKTPGP KDRIVMEVTL

       410        420        430        440        450        460        470        480
NKEPRVGLGI GACCLALENS PPGIYIHSLA PGSVAKMESN LSRGDQILEV NSVNVRHAAL SKVHAILSKC PPGPVRLVIG

       490        500        510        520        530        540        550        560
RHPNPKVSEQ EMDEVIARST YQESKEANSS PGLGTPLKSP SLAKKDSLIS ESELSQYFAH DVPGPLSDFM VAGSEDEDHP

       570        580        590        600        610        620        630        640
GSGCSTSEEG SLPPSTSTHK EPGKPRANSL VTLGSHRASG LFHKQVTVAR QASLPGSPQA LRNPLLRQRK VGCYDANDAS

       650        660        670        680        690        700        710        720
DEEEFDREGD CISLPGALPG PIRPLSEDDP RRVSISSSKG MDVHNQEERP RKTLVSKAIS APLLGSSVDL EESIPEGMVD

       730        740        750        760        770        780        790        800
AASYAANLTD SAEAPKGSPG SWWKKELSGS SSAPKLEYTV RTDTQSPTNT GSPSSPQQKS EGLGSRHRPV ARVSPHCKRS

       810        820        830        840        850        860        870        880
EAEAKPSGSQ TVNLTGRAND PCDLDSRVQA TSVKVTVAGF QPGGAVEKES LGKLTTGDAC VSTSCELASA LSHLDASHLT

       890        900        910        920        930        940        950        960
ENLPKAASEL GQQPMTELDS SSDLISSPGK KGAAHPDPSK TSVDTGQVSR PENPSQPASP RVTKCKARSP VRLPHEGSPS

       970        980        990       1000       1010       1020       1030       1040
PGEKAAAPPD YSKTRSASET STPHNTRRVA ALRGAGPGAE GMTPAGAVLP GDPLTSQEQR QGAPGNHSKA LEMTGIHAPE

      1050       1060       1070       1080       1090       1100       1110       1120
SSQEPSLLEG ADSVSSRAPQ ASLSMLPSTD NTKEACGHVS GHCCPGGSRE SPVTDIDSFI KELDASAARS PSSQTGDSGS

      1130       1140       1150       1160       1170       1180       1190       1200
QEGSAQGHPP AGAGGGSSCR AEPVPGGQTS SPRRAWAAGA PAYPQWASQP SVLDSINPDK HFTVNKNFLS NYSRNFSSFH

      1210       1220       1230       1240       1250       1260       1270       1280
EDSTSLSGLG DSTEPSLSSM YGDAEDSSSD PESLTEAPRA SARDGWSPPR SRVSLHKEDP SESEEEQIEI CSTRGCPNPP

      1290       1300       1310       1320       1330       1340       1350       1360
SSPAHLPTQA AICPASAKVL SLKYSTPRES VASPREKAAC LPGSYTSGPD SSQPSSLLEM SSQEHETHAD ISTSQNHRPS

      1370       1380       1390       1400       1410       1420       1430       1440
CAEETTEVTS ASSAMENSPL SKVARHFHSP PIILSSPNMV NGLEHDLLDD ETLNQYETSI NAAASLSSFS VDVPKNGESV

      1450       1460       1470       1480       1490       1500       1510       1520
LENLHISESQ DLDDLLQKPK MIARRPIMAW FKEINKHNQG THLRSKTEKE QPLMPARSPD SKIQMVSSSQ KKGVTVPHSP

      1530       1540       1550       1560       1570       1580       1590       1600
PQPKTNLENK DLSKKSPAEM LLTNGQKAKC GPKLKRLSLK GKAKVNSEAP AANAVKAGGT DHRKPLISPQ TSHKTLSKAV

      1610       1620       1630       1640       1650       1660       1670       1680
SQRLHVADHE DPDRNTTAAP RSPQCVLESK PPLATSGPLK PSVSDTSIRT FVSPLTSPKP VPEQGMWSRF HMAVLSEPDR

      1690       1700       1710       1720       1730       1740       1750       1760
GCPTTPKSPK CRAEGRAPRA DSGPVSPAAS RNGMSVAGNR QSEPRLASHV AADTAQPRPT GEKGGNIMAS DRLERTNQLK

      1770       1780       1790       1800       1810       1820       1830       1840
IVEISAEAVS ETVCGNKPAE SDRRGGCLAQ GNCQEKSEIR LYRQVAESST SHPSSLPSHA SQAEQEMSRS FSMAKLASSS

      1850       1860       1870       1880       1890       1900       1910       1920
SSLQTAIRKA EYSQGKSSLM SDSRGVPRNS IPGGPSGEDH LYFTPRPATR TYSMPAQFSS HFGREGHPPH SLGRSRDSQV

      1930       1940       1950       1960       1970       1980       1990       2000
PVTSSVVPEA KASRGGLPSL ANGQGIYSVK PLLDTSRNLP ATDEGDIISV QETSCLVTDK IKVTRRHYCY EQNWPHESTS

      2010       2020       2030       2040       2050       2060       2070       2080
FFSVKQRIKS FENLANADRP VAKSGASPFL SVSSKPPIGR RSSGSIVSGS LGHPGDAAAR LLRRSLSSCS ENQSEAGTLL

      2090       2100       2110       2120       2130       2140       2150       2160
PQMAKSPSIM TLTISRQNPP ETSSKGSDSE LKKSLGPLGI PTPTMTLASP VKRNKSSVRH TQPSPVSRSK LQELRALSMP

      2170       2180       2190       2200       2210       2220       2230       2240
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2006	1	917.8396	-134.11	2	53.5	11.6	1	2297-2315	R.KEGSGLGFSVAGGTDVEPK.S	

Detailed Protein Report

Protein 883: **carcinoembryonic antigen-related cell adhesion molecule 20 isoform 4S precursor [Homo sapiens]**

Accession:	gi|156564388	**Score:**	11.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	54.1
Database Date:	2015-11-30	**pI:**	5.9
		Sequence Coverage [%]:	5.3
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 1.34 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MGPADSWGHH WMGILLSASL CTVWSPPAAA QLTLNANPLD ATQSEDVVLP VFGTPRTPQI HGRSRELAKP SIAVSPGTAI
        90        100        110        120        130        140        150        160
EQKDMVTFYC TTKDVNITIH WVSNNLSVVF HERMQLSKDG KILTILIVQR EDSGTYQCEA RDALLSQRSD PIFLDVKYGP
       170        180        190        200        210        220        230        240
DPVEIKLESG VASGEVVEVM EGSSMTFLAE TKSHPPCAYT WFLLDSILSH TTRTFTIHAV SREHEGLYRC LVSNSATHLS
       250        260        270        280        290        300        310        320
SLGTLKVRVL ETLTMPQVVP SSLNLVENAR SVDLTCQTVN QSVNVQWFLS GQPLLPSEHL QLSADNRTLI IHGLQRNDTG
       330        340        350        360        370        380        390        400
PYACEVWNWG SRARSEPLEL TINCPQSSSL SSGAIAGIVI GILAVIAVAS ELGYFLYIRN ARRPSRKTTE DPSHETSQPI
       410        420        430        440        450        460        470        480
PKEEHPTEPS SESLSPEYCN ISQLQGRIRV ELTKLPSASR RGNSFSPWKP PPKPLMPPLR LVSTVPKNME SIYEELVNPE
       490        500
PNTYIQINPS V
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
95	1	896.4310	-0.22	3	30.1	11.6	0	167-192	K.LESGVASGEVVEVMEGSSMTFLAS		WD:WU 1.34

Detailed Protein Report

Protein 884: fibulin-5 precursor [Homo sapiens]

Accession:	gi|19743803	**Score:**	11.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	50.1
Database Date:	2015-11-30	**pI:**	4.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPGIKRILTV	TILALCLPSP	GNAQAQCTNG	FDLDRQSGQC	LDIDECRTIP	EACRGDMMCV	NQNGGYLCIP	RTNPVYRGPY
90	100	110	120	130	140	150	160
SNPYSTPYSG	PYPAAAPPLS	APNYPTISRP	LICRFGYQMD	ESNQCVDVDE	CATDSHQCNP	TQICINTEGG	YTCSCTDGYW
170	180	190	200	210	220	230	240
LLEGQCLDID	ECRYGYCQQL	CANVPGSYSC	TCNPGFTLNE	DGRSCQDVNE	CATENPCVQT	CVNTYGSFIC	RCDPGYELEE
250	260	270	280	290	300	310	320
DGVHCSDMDE	CSFSEFLCQH	ECVNQPGTYF	CSCPPGYILL	DDNRSCQDIN	ECEHRNHTCN	LQQTCYNLQG	GFKCIDPIRC
330	340	350	360	370	380	390	400
EEPYLRISDN	RCMCPAENPG	CRDQPFTILY	RDMDVVSGRS	VPADIFQMQA	TTRYPGAYYI	FQIKSGNEGR	EFYMRQTGPI
410	420	430	440	450			
SATLVMTRPI	KGPREIQLDL	EMITVNTVIN	FRGSSVIRLR	IYVSQYPF			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2359	1	911.7720	-114.30	2	57.8	11.6	1	327-342	R.ISDNRCMCPAENPGCR.D	Carbamidomethyl: 6

Detailed Protein Report

Protein 885: PREDICTED: 6-phosphofructokinase, liver type isoform X4 [Homo sapiens]

Accession:	gi|530419271	**Score:**	11.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	82.2
Database Date:	2015-11-30	**pI:**	7.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MNAAVRAVTR	MGIYVGAKVF	LIYEGYEGLV	EGGENIKQAN	WLSVSNIIQL	GGTIIGSARC	KAFTTREGRR	AAAYNLVQHG
90	100	110	120	130	140	150	160
ITNLCVIGGD	GSLTGANIFR	SEWGSLLEEL	VAEGKISETT	ARTYSHLNIA	GLVGSIDNDF	CGTDMTIGTD	SALHRIMEVI
170	180	190	200	210	220	230	240
DAITTTAQSH	QRTFVLEVMG	RHCGYLALVS	ALASGADWLF	IPEAPPEDGW	ENFMCERLGE	TRSRGSRLNI	IIIAEGAIDR
250	260	270	280	290	300	310	320
NGKPISSSYV	KDLVVQRLGF	DTRVTVLGHV	QRGGTPSAFD	RILSSKMGME	AVMALLEATP	DTPACVVTLS	GNQSVRLPLM
330	340	350	360	370	380	390	400
ECVQMTKEVQ	KAMDDKRFDE	ATQLRGGSFE	NNWNIYKLLA	HQKPPKEKSN	FSLAILNVGA	PAAGMNAAVR	SAVRTGISHG
410	420	430	440	450	460	470	480
HTVYVVHDGF	EGLAKGQVQE	VGWHDVAGWL	GRGGSMLGTK	RTLPKGQLES	IVENIRIYGI	HALLVVGGFE	AYEGVLQLVE
490	500	510	520	530	540	550	560
ARGRYEELCI	VMCVIPATIS	NNVPGTDFSL	GSDTAVNAAM	ESCDRIKQSA	SGTKRRVFIV	ETMGGYCGYL	ATVTGIAVGA
570	580	590	600	610	620	630	640
DAAYVFEDPF	NIHDLKVNVE	HMTEKMKTDI	QRGLVLRNEK	CHDYYTTEFL	YNLYSSEGKG	VFDCRTNVLG	HLQQGGAPTP
650	660	670	680	690	700	710	720
FDRNYGTKLG	VKAMLWLSEK	LREVYRKGRV	FANAPDSACV	IGLKKKAVAF	SPVTELKKDT	DFEHRMPREQ	WWLSLRLMLK
730	740	750	760				
MLAQYRISMA	AYVSGELEHV	TRRTLSMDKG	F				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1744	1	647.3021	-75.58	4	50.5	11.6	1	38-61	K.QANWLSVSNIIQLGGTIIGSARCK.A	Carbamidomethyl: 23

Detailed Protein Report

Protein 886: neuronal pentraxin-2 precursor [Homo sapiens]

Accession: gi|28195384
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 11.6
MW [kDa]: 47.0
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 887: PREDICTED: zinc finger protein 334 isoform X4 [Homo sapiens]

Accession:	gi|578836054	**Score:**	11.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	78.3
Database Date:	2015-11-30	**pI:**	10.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.2
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578836058	refseq_human (refseq_human_20140103.fasta)	PREDICTED: zinc finger protein 334 isoform X6 [Homo sapiens]
gi|578836056	refseq_human (refseq_human_20140103.fasta)	PREDICTED: zinc finger protein 334 isoform X5 [Homo sapiens]

10	20	30	40	50	60	70	80
MAATGPCSEA	PVQGCDAGEL	QQLGLCGVSD	VQRSWSKFCN	FPLTGYHVSK	PDVIFKLEQG	EEPWIVEEFS	NQNYPDIDDA
90	100	110	120	130	140	150	160
LEKNKEIQDK	HLTQTVFFSN	KTLITERENV	FGKTLNLGMN	SVPSRKMPYK	CNPGGNSLKT	NSEVIVAKKS	KENRKIPDGY
170	180	190	200	210	220	230	240
SGFGKHEKSH	LGMKKYRYNP	MRKASNQNEN	LILHQNIQIL	KQPFDYNKCG	KTFFKRAILI	TQKGRQTERK	PNECNECRKT
250	260	270	280	290	300	310	320
FSKRSTLIVH	QRIHTGEKPY	VCSDCRKTFR	VKTSLTRHRR	IHTGERPYEC	SECRKTFIDK	SALIVHQKIH	GGEKSYECNE
330	340	350	360	370	380	390	400
CGKTFFRKSA	LAEHFRSHTG	EKPYECKECG	NAFSKKSYLV	VHQRTHRGEK	PNECKECGKT	FFCQSALTAH	QRIHTGEKPY
410	420	430	440	450	460	470	480
ECSECEKTFF	CQSALNVHRR	SHTGEKPYEC	SQCGKFLCTK	SALIAHQITH	RGKKSYECNE	CGKFFCHKST	LTIHQRTHTG
490	500	510	520	530	540	550	560
EKHGVFNKCG	RISIVKSNCS	QCKRMNTKEN	LYECSEHGHA	VSKNSHLIVH	QRTIWERPYE	CNECGRTYCR	KSALTHHQRT
570	580	590	600	610	620	630	640
HTGQRPYECN	ECGKTFCQKF	SFVEHQRTHT	GEKPYECNEC	GKSFCHKSAF	RVHRRIHTGE	KPYECNQCGK	TYRRLWTLTE
650	660	670	680				
HQKIHTGEKP	YECNKCEKTF	RHKSNFLLHQ	KSHKE				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1665	1	967.4326	-7.08	2	49.1	11.6	2	224-238	K.GRQTERKPNECNECR.K	Carbamidomethyl: 11, 14

Detailed Protein Report

Protein 888: microtubule-associated tumor suppressor candidate 2 isoform a [Homo sapiens]

Accession:	gi|140161498	**Score:**	11.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	151.1
Database Date:	2015-11-30	**pI:**	6.3
		Sequence Coverage [%]:	1.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
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 889: transport and Golgi organization protein 6 homolog [Homo sapiens]

Accession:	gi|153791502	**Score:**	11.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	120.7
Database Date:	2015-11-30	**pI:**	5.7
		Sequence Coverage [%]:	1.2
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MAARQAVGSG AQETCGLDRI LEALKLLLSP GGSGSSSLQV TKHDVLLATL KSNLSALEDK FLKDPQWKNL KLLRDEIADK

        90        100        110        120        130        140        150        160
AEWPQNSVDV TWSFTSQTLL LLLCLKETMI RLAANFNPGK PNPRTPEVAP ALSPDALSIS QQKTVQFVLQ FVVTLGICPY

       170        180        190        200        210        220        230        240
LMPGVGVPLR YRTEFGAVVQ DVVCFDAAPD ATRRLYTSCK ALLNVAQHTS LGSLIFCHHF GDIAAGLCQL GFCPTKRKLL

       250        260        270        280        290        300        310        320
TPAEEVLTEE ERTLSRGALR DMLDQVYQPL AVRELLILQG GPPQSCTDVK TQMRCRAPAW LRRLCGQLLS ERLMRPNGVQ

       330        340        350        360        370        380        390        400
AVVRGILEGA GAGAAGGSDA EVTAADWKKC DLIAKILASC PQQSLSPENY YRDICPQVLD LFHFQDKLTA RQFQRVATTT

       410        420        430        440        450        460        470        480
FITLSRERPH LAAKYLLQPV LAPLHRCLNT AELSESDMVP GTILVTEEEL SRCIEDVFKV YVVGNEPLTV LMDSLLPVLG

       490        500        510        520        530        540        550        560
VLFLLYCFTK QSVSHIRSLC QEILLWILGK LERKKAIASL KGFAGLDKAV PSLHSLCQFR VATQGGIMIT IKEAISDEDE

       570        580        590        600        610        620        630        640
DEALYQKVSS EQGRVEHLGD LLSHCQECGL AGDFFIFCLK ELTHVASENE TELKTEPFSS KSLLELEQHQ TLLVEGQERK

       650        660        670        680        690        700        710        720
LLVLQLMAVL CERMSEQIFT NVTQVVDFVA ATLQRACASL AHQAESTVES QTLSMSMGLV AVMLGGAVQL KSSDFAVLKQ

       730        740        750        760        770        780        790        800
LLPLLEKVSN TYPDPVIQEL AVDLRITIST HGAFATEAVS MAAQSTLNRK DLEGKIEEQQ QTSHERPTDV AHSHLEQQQS

       810        820        830        840        850        860        870        880
HETAPQTGLQ SNAPIIPQGV NEPSTTTSQK SGSVTTEQLQ EVLLSAYDPQ IPTRAAALRT LSHWIEQREA KALEMQEKLL

       890        900        910        920        930        940        950        960
KIFLENLEHE DTFVYLSAIQ GVALLSDVYP EKILPDLLAQ YDSSKDKHTP ETRMKVGEVL MRIVRALGDM VSKYREPLIH

       970        980        990       1000       1010       1020       1030       1040
TFLRGVRDPD GAHRASSLAN LGELCQRLDF LLGSVVHEVT ACLIAVAKTD GEVQVRRAAI HVVVLLLRGL SQKATEVLSA

      1050       1060       1070       1080       1090       1100
VLKDLYHLLK HVVCLEPDDV AKLHAQLALE ELDDIMKNFL FPPQKLEKKI MVLP
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2164	1	698.2954	-118.56	2	55.4	11.6	0	112-124	R.LAANFNPGKPNPR.T	

Detailed Protein Report

Protein 890: **teashirt homolog 2 isoform 2 [Homo sapiens]**

Accession: gi|301171536
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 11.6
MW [kDa]: 114.5
pI: 7.5
Sequence Coverage [%]: 1.2
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MMAAALLHYT	GYAQEEQLKE	EEEIKEEEEE	EDSGSVAQLQ	GGNDTGTDEE	LETGPEQKGC	FSYQNSPGSH	LSNQDAENES
90	100	110	120	130	140	150	160
LLSDASDQVS	DIKSVCGRDA	SDKKAHTHVR	LPNEAHNCMD	KMTAVYANIL	SDSYWSGLGL	GFKLSNSERR	NCDTRNGSNK
170	180	190	200	210	220	230	240
SDFDWHQDAL	SKSLQQNLPS	RSVSKPSLFS	SVQLYRQSSK	MCGTVFTGAS	RFRCRQCSAA	YDTLVELTVH	MNETGHYQDD
250	260	270	280	290	300	310	320
NRKKDKLRPT	SYSKPRKRAF	QDMDKEDAQK	VLKCMFCGDS	FDSLQDLSVH	MIKTKHYQKV	PLKEPVPTIS	SKMVTPAKKR
330	340	350	360	370	380	390	400
VFDVNRPCSP	DSTTGSFADS	FSSQKNANLQ	LSSNNRYGYQ	NGASYTWQFE	ACKSQILKCM	ECGSSHDTLQ	QLTTHMMVTG
410	420	430	440	450	460	470	480
HFLKVTSSAS	KKGKQLVLDP	LAVEKMQSLS	EAPNSDSLAP	KPSSNSASDC	TASTTELKKE	SKKERPEETS	KDEKVVKSED
490	500	510	520	530	540	550	560
YEDPLQKPLD	PTIKYQYLRE	EDLEDGSKGG	GDILKSLENT	VTTAINKAQN	GAPSWSAYPS	IHAAYQLSEG	TKPPLPMGSQ
570	580	590	600	610	620	630	640
VLQIRPNLTN	KLRPIAPKWK	VMPLVSMPTH	LAPYTQVKKE	SEDKDEAVKE	CGKESPHEEA	SSFSHSEGDS	FRKSETPPEA
650	660	670	680	690	700	710	720
KKTELGPLKE	EEKLMKEGSE	KEKPQPLEPT	SALSNGCALA	NHAPALPCIN	PLSALQSVLN	NHLGKATEPL	RSPSCSSPSS
730	740	750	760	770	780	790	800
STISMFHKSN	LNVMDKPVLS	PASTRSASVS	RRYLFENSDQ	PIDLTKSKSK	KAESSQAQSC	MSPPQKHALS	DIADMVKVLP
810	820	830	840	850	860	870	880
KATTPKPASS	SRVPPMKLEM	DVRRFEDVSS	EVSTLHKRKG	RQSNWNPQHL	LILQAQFASS	LFQTSEGKYL	LSDLGPQERM
890	900	910	920	930	940	950	960
QISKFTGLSM	TTISHWLANV	KYQLRKTGGT	KFLKNMDKGH	PIFYCSDCAS	QFRTPSTYIS	HLESHLGFQM	KDMTRLSVDQ
970	980	990	1000	1010	1020	1030	1040
QSKVEQEISR	VSSAQRSPET	IAAEEDTDSK	FKCKLCCRTF	VSKHAVKLHL	SKTHSKSPEH	HSQFVTDVDE	E

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
50	1	645.8133	-54.63	2	29.6	11.6	0	516-527	K.SLENTVTTAINK.A	

Detailed Protein Report

Protein 891: 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 892: jerky protein homolog isoform b [Homo sapiens]

Accession:	gi|525342477	**Score:**	11.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	61.8
Database Date:	2015-11-30	**pI:**	9.2
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	2.5
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 4.52 **CV:** 0.00 % **No. of Peptides:** 1

Alias proteins:

Accession	Name	Description
gi|578816229	refseq_human (refseq_human_20140103.fasta)	PREDICTED: jerky protein homolog isoform X3 [Homo sapiens]
gi|525342488	refseq_human (refseq_human_20140103.fasta)	jerky protein homolog isoform b [Homo sapiens]

10	20	30	40	50	60	70	80
MASKPAAGKS	RGEKRKRVVL	TLKEKIDICT	RLEKGESRKA	LMQEYNVGMS	TLYDIRAHKA	QLLRFFASSD	SNKALEQRRT
90	100	110	120	130	140	150	160
LHTPKLEHLD	RVLYEWFLGK	RSEGVPVSGP	MLIEKAKDFY	EQMQLTEPCV	FSGGWLWRFK	ARHGIKKLDA	SSEKQSADHQ
170	180	190	200	210	220	230	240
AAEQFCAFFR	SLAAEHGLSA	EQVYNADETG	LFWRCLPNPT	PEGGAVPGPK	QGKDRLTVLM	CANATGSHRL	KPLAIGKCSG
250	260	270	280	290	300	310	320
PRAFKGIQHL	PVAYKAQGNA	WVDKEIFSDW	FHHIFVPSVR	EHFRTIGLPE	DSKAVLLLDS	SRAHPQEAEL	VSSNVFTIFL
330	340	350	360	370	380	390	400
PASVASLVQP	MEQGIRRDFM	RNFINPPVPL	QGPHARYNMN	DAIFSVACAW	NAVPSHVFRR	AWRKLWPSVA	FAEGSSSEEE
410	420	430	440	450	460	470	480
LEAECFPVKP	HNKSFAHILE	LVKEGSSCPG	QLRQRQAASW	GVAGREAEGG	RPPAATSPAE	VVWSSEKTPK	ADQDGRGDPG
490	500	510	520	530	540	550	560
EGEEVAWEQA	AVAFDAVLRF	AERQPCFSAQ	EVGQLRALRA	VFRSQQQETV	GLEDVVVTSP	EELAIPKCCL	EASTET

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
69	1	773.7368	-181.03	2	29.8	11.6	0	216-229	R.LTVLMCANATGSHR.L	Carbamidomethyl: 6; Oxidation: 5	WD:WU	4.52

Detailed Protein Report

Protein 893: 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 894: endophilin-A2 isoform 3 [Homo sapiens]

Accession:	gi|317108193	**Score:**	11.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	34.5
Database Date:	2015-11-30	**pI:**	5.5
		Sequence Coverage [%]:	3.3
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 2.27 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MSVAGLKKQF	YKASQLVSEK	VGGAEGTKLD	DDFKEMEKKV	DVTSKAVTEV	LARTIEYLQP	NPASRAKLTM	LNTVSKIRGQ
90	100	110	120	130	140	150	160
NLCEKDLKEI	QHHLKKLEGR	RLDFDYKKKR	QGKIPDEELR	QALEKFEESK	EVAETSMHNL	LETDIEQVSQ	LSALVDAQLD
170	180	190	200	210	220	230	240
YHRQAVQILD	ELAEKLKRRM	REASSRPKRE	YKPKPREPFD	LGEPEQSNGG	FPCTTAPKIA	ASSSFRSSDK	PIRTPSRSMP
250	260	270	280	290	300	310	
PLDQPSCKAL	YDFEPENDGE	LGFHEGDVIT	LTNQIDENWY	EGMLDGQSGF	FPLSYVEVLV	PLPQ	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
818	1	635.1543	-208.98	2	38.6	11.6	1	29-38	K.LDDDFKEMEK.K		WD:WU 2.27

Detailed Protein Report

Protein 895: ferrochelatase, mitochondrial isoform b precursor [Homo sapiens]

Accession: gi|60499021

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Modification(s): Oxidation

Score: 11.6

MW [kDa]: 47.8

pI: 9.8

Sequence Coverage [%]: 4.7

No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MRSLGANMAA	ALRAAGVLLR	DPLASSSWRV	CQPWRWKSGA	AAAAVTTETA	QHAQGAKPQV	QPQKRKPKTG	ILMLNMGGPE
90	100	110	120	130	140	150	160
TLGDVHDFLL	RLFLDRDLMT	LPIQNKLAPF	IAKRRTPKIQ	EQYRRIGGGS	PIKIWTSKQG	EGMVKLLDEL	SPNTAPHKYY
170	180	190	200	210	220	230	240
IGFRYVHPLT	EEAIEEMERD	GLERAIAFTQ	YPQYSCSTTG	SSLNAIYRYY	NQVGRKPTMK	WSTIDRWPTH	HLLIQCFADH
250	260	270	280	290	300	310	320
ILKELDHFPL	EKRSEVVILF	SAHSLPMSVV	NRGDPYPQEV	SATVQKVMER	LEYCNPYRLV	WQSKVGPMPW	LGPQTDESIK
330	340	350	360	370	380	390	400
GLCERGRKNI	LLVPIAFTSD	HIETLYELDI	EYSQVLAKEC	GVENIRRAES	LNGNPLFSKA	LADLVHSHIQ	SNELCSKQLT
410	420	430					
LSCPLCVNPV	CRETKSFFTS	QQL					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2339	1	1029.7232	144.15	2	57.5	11.6	2	1-20	-.MRSLGANMAAALRAAGVLLR.D	Oxidation: 8

Detailed Protein Report

Protein 896: NEDD4 family-interacting protein 1 [Homo sapiens]

Accession:	gi|13386480	**Score:**	11.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	24.9
Database Date:	2015-11-30	**pI:**	4.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	7.7
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 0.75 **CV:** 0.00 % **No. of Peptides:** 1

```
         10         20         30         40         50         60         70         80
MALALAALAA VEPACGSRYQ QLQNEEESGE PEQAAGDAPP PYSSISAESA AYFDYKDESG FPKPPSYNVA TTLPSYDEAE
         90        100        110        120        130        140        150        160
RTKAEATIPL VPGRDEDFVG RDDFDDADQL RIGNDGIFML TFFMAFLFNW IGFFLSFCLT TSAAGRYGAI SGFGLSLIKW
        170        180        190        200        210        220        230
ILIVRFSTYF PGYFDGQYWL WWVFLVLGFL LFLRGFINYA KVRKMPETFS NLPRTRVLFI Y
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1839	1	547.6443	24.04	3	51.3	11.6	0	2-18	M.ALALAALAAVEPACGSR.Y	Carbamidomethyl: 14	WD:WU 0.75

Detailed Protein Report

Protein 897: **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 898: tricarboxylate transport protein, mitochondrial isoform c [Homo sapiens]

Accession:	gi|568786339	**Score:**	11.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	23.2
Database Date:	2015-11-30	**pI:**	10.3
Modification(s):	Oxidation	**Sequence Coverage [%]:**	4.8
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MFEFLSNHMR DAQGRLDSTR GLLCGLGAGV AEAVVVVCPM ETIKVKFIHD QTSPNPKYRG FFHGVREIVR EQGLKGTYQG
        90        100        110        120        130        140        150        160
LTATVLKQGS NQAIRFFVMT SLRNWYRGDN PNKPMNPLIT GVFGAIAGAA SVFGNTPLDV IKTRMQGLEA HKYRNTWDCG
       170        180        190        200        210
LQILKKEGLK AFYKGTVPRL GRVCLDVAIV FVIYDEVVKL LNKVWKTD
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
610	1	593.6757	-215.17	2	36.0	11.6	1	143-152	K.TRMQGLEAHK.Y	Oxidation: 3

Detailed Protein Report

Protein 899: leukotriene-B(4) omega-hydroxylase 1 precursor [Homo sapiens]

Accession: gi|13435391
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 11.6
MW [kDa]: 59.8
pI: 6.7
Sequence Coverage [%]: 4.2
No. of unique Peptides: 1

Quantitation

WD:WU **Median:** 0.73 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MSQLSLSWLG	LWPVAASPWL	LLLLVGASWL	LAHVLAWTYA	FYDNCRRLRC	FPQPPRRNWF	WGHQGMVNPT	EEGMRVLTQL
90	100	110	120	130	140	150	160
VATYPQGFKV	WMGPISPLLS	LCHPDIIRSV	INASAAIAPK	DKFFYSFLEP	WLGDGLLLSA	GDKWSRHRRM	LTPAFHFNIL
170	180	190	200	210	220	230	240
KPYMKIFNES	VNIMHAKWQL	LASEGSACLD	MFEHISLMTL	DSLQKCVFSF	DSHCQEKPSE	YIAAILELSA	LVSKRHHEIL
250	260	270	280	290	300	310	320
LHIDFLYYLT	PDGQRFRRAC	RLVHDFTDAV	IQERRRTLPS	QGVDDFLQAK	AKSKTLDFID	VLLLSKDEDG	KKLSDEDIRA
330	340	350	360	370	380	390	400
EADTFMFEGH	DTTASGLSWV	LYHLAKHPEY	QERCRQEVQE	LLKDREPKEI	EWDDLAHLPF	LTMCMKESLR	LHPPVPVISR
410	420	430	440	450	460	470	480
HVTQDIVLPD	GRVIPKGIIC	LISVFGTHHN	PAVWPDPEVY	DPFRFDPENI	KERSPLAFIP	FSAGPRNCIG	QTFAMAEMKV
490	500	510	520	530			
VLALTLLRFR	VLPDHTEPRR	KPELVLRAEG	GLWLRVEPLS				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
169	1	898.4349	4.83	3	31.3	11.6	1	369-390	K. EIEWDDLAHLPFLTMCMKESLR. L	Oxidation: 15	WD:WU 0.73

Detailed Protein Report

Protein 900: **homeobox protein BarH-like 1 [Homo sapiens]**

Accession:	gi|153218470	**Score:**	11.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	27.3
Database Date:	2015-11-30	**pI:**	10.3
		Sequence Coverage [%]:	7.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MQRPGEPGAA	RFGPPEGCAD	HRPHRYRSFM	IEEILTEPPG	PKGAAPAAAA	AAAGELLKFG	VQALLAARPF	HSHLAVLKAE
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
QAAVFKFPLA	PLGCSGLSSA	LLAAGPGLPG	AAGAPHLPLE	LQLRGKLEAA	GPGEPGTKAK	KGRRSRTVFT	ELQLMGLEKR
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
FEKQKYLSTP	DRIDLAESLG	LSQLQVKTWY	QNRRMKWKKI	VLQGGGLESP	TKPKGRPKKN	SIPTSEQLTE	QERAKDAEKP
250	**260**						
AEVPGEPSDR	SRED						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1733	1	697.3497	-100.24	3	50.0	11.6	2	200-219	K.IVLQGGGLESPTKPKGRPKK.N	

Detailed Protein Report

Protein 901: signal recognition particle 9 kDa protein isoform 2 [Homo sapiens]

Accession:	gi|4507217	**Score:**	11.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	10.1
Database Date:	2015-11-30	**pI:**	9.1
Modification(s):	Oxidation	**Sequence Coverage [%]:**	17.4
		No. of unique Peptides:	1

```
         10         20         30         40         50         60         70         80
MPQYQTWEEF SRAAEKLYLA DPMKARVVLK YRHSDGNLCV KVTDDLVCLV YKTDQAQDVK KIEKFHSQLM RLMVAKEARN
         90
VTMETE
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2901	1	869.4256	-4.05	2	65.0	11.5	2	72-86	R.LMVAKEARNVTMETE.-	Oxidation: 12

Detailed Protein Report

Protein 902: 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 903: **tropomyosin alpha-3 chain isoform 6 [Homo sapiens]**

Accession:	gi|499137516	**Score:**	11.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	21.3
Database Date:	2015-11-30	**pI:**	4.7
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	4.9
		No. of unique Peptides:	1

```
         10         20         30         40         50         60         70         80
MMQRSELSAS SEKLREKGGP GNRGMKVIEN RALKDEEKME LQEIQLKEAK HIAEEADRKY EEVARKLVII EGDLERTEER
         90        100        110        120        130        140        150        160
AELAESRCRE MDEQIRLMDQ NLKCLSAAEE KYSQKEDKYE EEIKILTDKL KEAETRAEFA ERSVAKLEKT IDDLEDKLKC
        170        180        190
TKEEHLCTQR MLDQTLLDLN EM
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2779	2	626.8528	125.66	2	63.3	11.5	1	88-96	R.CREMDEQIR.L	Carbamidomethyl: 1; Oxidation: 4

Detailed Protein Report

Protein 904: zinc finger protein 865 [Homo sapiens]

Accession:	gi|307219238	**Score:**	11.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	111.0
Database Date:	2015-11-30	**pI:**	10.6
		Sequence Coverage [%]:	1.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEANPAGSGA	GGGGSSGIGG	EDGVHFQSYP	FDFLEFLNHQ	RFEPMELYGE	HAKAVAALPC	APGPPPQPPP	QPPPPQYDYP
90	100	110	120	130	140	150	160
PQSTFKPKAE	VPSSSSSSSS	SSSSSSSSSS	SSSSSSSQAK	KPDPPLPPAF	GAPPPPLFDA	AFPTPQWGIV	DLSGHQHLFG
170	180	190	200	210	220	230	240
NLKRGGPASG	PGVTPGLGAP	AGAPGPLPAP	SQTPPGPPAA	AACDPTKDDK	GYFRRLKYLM	ERRFPCGVCQ	KSFKQSSHLV
250	260	270	280	290	300	310	320
QHMLVHSGER	PYECGVCGRT	YNHVSSLIRH	RRCHKDVPPA	AGGPPQPGPH	LPPLGLPAPA	ASAATAAAPS	TVSSGPPATP
330	340	350	360	370	380	390	400
VAPAPSADGS	AAPAGVGVPP	PATGGGDGPF	ACPLCWKVFK	KPSHLHQHQI	IHTGEKPFSC	SVCSKSFNRR	ESLKRHVKTH
410	420	430	440	450	460	470	480
SADLLRLPCG	ICGKAFRDAS	YLLKHQAAHA	GAGAGGPRPV	YPCDLCGKSY	SAPQSLLRHK	AAHAPPAAAA	EAPKDGAASA
490	500	510	520	530	540	550	560
PQPPPTFPPG	PYLLPPDPPT	TDSEKAAAAA	AAVVYGAVPV	PLLGAHPLLL	GGAGTSGAGG	SGASVPGKTF	CCGICGRGFG
570	580	590	600	610	620	630	640
RRETLKRHER	IHTGEKPHQC	PVCGKRFRES	FHLSKHHVVH	TRERPYKCEL	CGKVFGYPQS	LTRHRQVHRL	QLPCALAGAA
650	660	670	680	690	700	710	720
GLPSTQGTPG	ACGPGASGTS	AGPTDGLSYA	CSDCGEHFPD	LFHVMSHKEV	HMAEKPYGCD	ACGKTFGFIE	NLMWHKLVHQ
730	740	750	760	770	780	790	800
AAPERLLPPA	PGGLQPPDGS	SGTDAASVLD	NGLAGEVGAA	VAALAGVSGG	EDAGGAAVAG	AGGGASSGPE	RFSCATCGQS
810	820	830	840	850	860	870	880
FKHFLGLVTH	KYVHLVRRTL	GCGLCGQSFA	GAYDLLLHRR	SHRQKRGFRC	PVCGKRFWEA	ALLMRHQRCH	TEQRPYRCGV
890	900	910	920	930	940	950	960
CGRGFLRSWY	LRQHRVVHTG	ERAFKCGVCA	KRFAQSSSLA	EHRRLHAVAR	PQRCSACGKT	FRYRSNLLEH	QRLHLGERAY
970	980	990	1000	1010	1020	1030	1040
RCEHCGKGFF	YLSSVLRHQR	AHEPPRPELR	CPACLKAFKD	PGYFRKHLAA	HQGGRPFRCS	SCGEGFANTY	GLKKHRLAHK
1050	1060						
AENLGGPGAG	AGTLAGKDA						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2853	1	650.6072	-69.86	3	64.3	11.5	2	906-923	K.CGVCAKRFAQSSSLAEHR.R	

Detailed Protein Report

Protein 905: **protein sidekick-1 isoform 2 [Homo sapiens]**

Accession:	gi|119220550	**Score:**	11.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	74.3
Database Date:	2015-11-30	**pI:**	5.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MQVRELPRGE	WQTYSSSISH	EATACVVDRL	RPFTSYKLRL	KATNDIGDSD	FSSETEAVTT	LQDVPGEPPG	SVSATPHTTS
90	100	110	120	130	140	150	160
SVLIQWQPPR	DESLNGLLQG	YRIYYRELEY	EAGSGTEAKT	LKNPIALHAE	LTAQSSFKTV	NSSSTSTMCE	LTHLKKYRRY
170	180	190	200	210	220	230	240
EVIMTAYNII	GESPASAPVE	VFVGEAAPAM	APQNVQVTPL	TASQLEVTWD	PPPPESQNGN	IQGYKIYYWE	ADSQNETEKM
250	260	270	280	290	300	310	320
KVLFLPEPVV	RLKNLTSHTK	YLVSISAFNA	AGDGPKSDPQ	QGRTHQAAPG	APSFLAFSEI	TSTTLNVSWG	EPAAANGILQ
330	340	350	360	370	380	390	400
GYRVVYEPLA	PVQGVSKVVT	VEVRGNWQRW	LKVRDLTKGV	TYFFRVQART	ITYGPELQAN	ITAGPAEGSP	GSPRDVLVTK
410	420	430	440	450	460	470	480
SASELTLQWT	EGHSGDTPTT	GYVIEARPSD	EGLWDMFVKD	IPRSATSYTL	SLDKLRQGVT	YEFRVVAVNE	AGYGEPSNPS
490	500	510	520	530	540	550	560
TAVSAQVEAP	FYEEWWFLLV	MALSSLIVIL	LVVFALVLHG	QNKKYKNCST	GKGISTMEES	VTLDNGGFAA	LELSSRHLNV
570	580	590	600	610	620	630	640
KSTFSKKNGT	RSPPRPSPGG	LHYSDEDICN	KYNGAVLTES	VSLKEKSADA	SESEATDSDY	EDALPKHSFV	NHYMSDPTYY
650	660	670	680				
NSWKRRAQGR	APAPHSVAIL	LTSNPSAYLS	VAPRGSASW				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2162	1	618.9457	-18.66	3	55.4	11.5	0	139-155	K.TVNSSSTSTMCELTHLK.K	Oxidation: 10

Detailed Protein Report

Protein 906: 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 907: PREDICTED: zinc finger protein 708 isoform X1 [Homo sapiens]

Accession:	gi|578833563	**Score:**	11.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	57.3
Database Date:	2015-11-30	**pI:**	10.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.0
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 0.64 **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	
245	1	605.6544	-222.19	2	32.2	11.5	2	102-111	K.NPFKCKECGK.S	Carbamidomethyl: 8	WD:WU	0.64

Detailed Protein Report

Protein 908: 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 909: **PREDICTED: V-type proton ATPase 116 kDa subunit a isoform 3 isoform X2 [Homo sapiens]**

Accession:	gi|530396189	**Score:**	11.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	53.0
Database Date:	2015-11-30	**pI:**	10.8
		Sequence Coverage [%]:	2.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGSMFRSEEV	ALVQLFLPTA	AAYTCVSRLG	ELGLVEFRDL	NASVSAFQRR	FVVDVRRCEE	LEKTFTFLQE	EVRRAGLVLP
90	100	110	120	130	140	150	160
PPKGRLPAPP	PRDLLRIQEE	TERLAQELRD	VRGNQQALRA	QLHQLQLHAA	VLRQGHEPQL	AAAHTDGASE	RTPLLQAPGG
170	180	190	200	210	220	230	240
PHQDLRVNFV	AGAVEPHKAP	ALERLLWRAC	RGFLIASFRE	LEQPLEHPVT	GEPATWMTFL	ISYWGEQIGQ	KIRKITDCAS
250	260	270	280	290	300	310	320
SLQLPLPRLP	VSAAGGGPPR	GPAAAATAEP	GAAGGPRGDR	AVPEPGARPG	AAAAAARAGA	GPQDEGRVPG	PEPVQREHHA
330	340	350	360	370	380	390	400
QVPHCRGLVL	CARPARPAGG	PAGQLDGGGS	ECRGSPHPLP	GHAPHTHPHQ	PLHGQLPGHR	GCLRRGPLPG	GQPRSLHHHH
410	420	430	440	450	460	470	480
LPLPVCCDVR	GCGPRAAHVP	VRPGHGPCGE	PTGCEGRAER	DLADFLQGPL	PAPAYGPVLH	LHRLHLQRVL	QSRHQHLPLG
490	500						
LECGRHGQPV	WLE						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2945	1	713.3534	-34.35	2	65.6	11.5	1	64-74	K.TFTFLQEEVRR.A	

Detailed Protein Report

Protein 910: protocadherin-16 precursor [Homo sapiens]

Accession:	gi|16933557	**Score:**	11.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	346.0
Database Date:	2015-11-30	**pI:**	4.6
		Sequence Coverage [%]:	0.4
		No. of unique Peptides:	1

Quantitation

WD:WU	**Median:**	3.50	**CV:**	0.00 %	**No. of Peptides:**	1

10	20	30	40	50	60	70	80
MQKELGIVPS	CPGMKSPRPH	LLLPLLLLLL	LLLGAGVPGA	WGQAGSLDLQ	IDEEQPAGTL	IGDISAGLPA	GTAAPLMYFI
90	100	110	120	130	140	150	160
SAQEGSGVGT	DLAIDEHSGV	VRTARVLDRE	QRDRYRFTAV	TPDGATVEVT	VRVADINDHA	PAFPQARAAL	QVPEHTAFGT
170	180	190	200	210	220	230	240
RYPLEPARDA	DAGRLGTQGY	ALSGDGAGET	FRLETRPGPD	GTPVPELVVT	GELDRENRSH	YMLQLEAYDG	GSPPRRAQAL
250	260	270	280	290	300	310	320
LDVTLLDIND	HAPAFNQSRY	HAVVSESLAP	GSPVLQVFAS	DADAGVNGAV	TYEINRRQSE	GDGPFSIDAH	TGLLQLERPL
330	340	350	360	370	380	390	400
DFEQRRVHEL	VVQARDGGAH	PELGSAFVTV	HVRDANDNQP	SMTVIFLSAD	GSPQVSEAAP	PGQLVARISV	SDPDDGDFAH
410	420	430	440	450	460	470	480
VNVSLEGGEG	HFALSTQDSV	IYLVCVARRL	DREERDAYNL	RVTATDSGSP	PLRAEAAFVL	HVTDVNDNAP	AFDRQLYRPE
490	500	510	520	530	540	550	560
PLPEVALPGS	FVVRVTARDP	DQGTNGQVTY	SLAPGAHTHW	FSIDPTSGII	TTAASLDYEL	EPQPQLIVVA	TDGGLPPLAS
570	580	590	600	610	620	630	640
SATVSVALQD	VNDNEPQFQR	TFYNASLPEG	TQPGTCFLQV	TATDADSGPF	GLLSYSLGAG	LGSSGSPPFR	IDAHSGDVCT
650	660	670	680	690	700	710	720
TRTLDRDQGP	SSFDFTVTAV	DGGGLKSMVY	VKVFLSDEND	NPPQFYPREY	AASISAQSPP	GTAVLRLRAH	DPDQGSHGRL
730	740	750	760	770	780	790	800
SYHILAGNSP	PLFTLDEQSG	LLTVAWPLAR	RANSVVQLEI	GAEDGGGLQA	EPSARVDISI	VPGTPTPPIF	EQLQYVFSVP
810	820	830	840	850	860	870	880
EDVAPGTSVG	IVQAHNPPGR	LAPVTLSLSG	GDPRGLFSLD	AVSGLLQTLR	PLDRELLGPV	LELEVRAGSG	VPPAFAVARV
890	900	910	920	930	940	950	960
RVLLDDVNDN	SPAFPAPEDT	VLLPPNTAPG	TPIYTLRALD	PDSGVNSRVT	FTLLAGGGGA	FTVDPTTGHV	RLMRPLGPSG
970	980	990	1000	1010	1020	1030	1040
GPAHELELEA	RDGGSPPRTS	HFRLRVVVQD	VGTRGLAPRF	NSPTYRVDLP	SGTTAGTQVL	QVQAQAPDGG	PITYHLAAEG
1050	1060	1070	1080	1090	1100	1110	1120
ASSPFGLEPQ	SGWLWVRAAL	DREAQELYIL	KVMAVSGSKA	ELGQQTGTAT	VRVSILNQNE	HSPRLSEDPT	FLAVAENQPP
1130	1140	1150	1160	1170	1180	1190	1200
GTSVGRVFAT	DRDSGPNGRL	TYSLQQLSED	SKAFRIHPQT	GEVTTLQTLD	REQQSSYQLL	VQVQDGGSPP	RSTTGTVHVA
1210	1220	1230	1240	1250	1260	1270	1280
VLDLNDNSPT	FLQASGAAGG	GLPIQVPDRV	PPGTLVTTLQ	AKDPDEGENG	TILYTLTGPG	SELFSLHPHS	GELLTAAPLI
1290	1300	1310	1320	1330	1340	1350	1360
RAERPHYVLT	LSAHDQGSPP	RSASLQLLVQ	VLPSARLAEP	PPDLAERDPA	APVPVVLTVT	AAEGLRPGSL	LGSVAAPEPA
1370	1380	1390	1400	1410	1420	1430	1440
GVGALTYTLV	GGADPEGTFA	LDAASGRLYL	ARPLDFEAGP	PWRALTVRAE	GPGGAGARLL	RVQVQVQDEN	EHAPAFARDP
1450	1460	1470	1480	1490	1500	1510	1520
LALALPENPE	PGAALYTFRA	SDADGPGPNS	DVRYRLLRQE	PPVPALRLDA	RTGALSAPRG	LDRETTPALL	LLVEATDRPA
1530	1540	1550	1560	1570	1580	1590	1600
NASRRRAARV	SARVFVTDEN	DNAPVFASPS	RVRLPEDQPP	GPAALHVVAR	DPDLGEAARV	SYRLASGGDG	HFRLHSSTGA
1610	1620	1630	1640	1650	1660	1670	1680
LSVVRPLDRE	QRAEHVLTVV	ASDHGSPPRS	ATQVLTVSVA	DVNDEAPTFQ	QQEYSVLLRE	NNPPGTSLLT	LRATDPDVGA
1690	1700	1710	1720	1730	1740	1750	1760
NGQVTYGGVS	SESFSLDPDT	GVLTTLRALD	REEQEEINLT	VYAQDRGSPP	QLTHVTVRVA	VEDENDHAPT	FGSAHLSLEV
1770	1780	1790	1800	1810	1820	1830	1840
PEGQDPQTLT	MLRASDPDVG	ANGQLQYRIL	DGDPSGAFVL	DLASGEFGTM	RPLDREVEPA	FQLRIEARDG	GQPALSATLL
1850	1860	1870	1880	1890	1900	1910	1920
LTVTVLDAND	HAPAFPVPAY	SVEVPEDVPA	GTLLLQLQAH	DPDAGANGHV	TYYLGAGTAG	AFLLEPSSGE	LRTAAALDRE
1930	1940	1950	1960	1970	1980	1990	2000
QCPSYTFSVS	AVDGAAAGPL	STTVSVTITV	RDVNDHAPTF	PTSPLRLRLP	RPGPSFSTPT	LALATLRAED	RDAGANASIL
2010	2020	2030	2040	2050	2060	2070	2080
YRLAGTPPPG	TTVDSYTGEI	RVARSPVALG	PRDRVLFIVA	TDLGRPARSA	TGVIIVGLQG	EAERGPRFPR	ASSEATIREN
2090	2100	2110	2120	2130	2140	2150	2160
APPGTPIVSP	RAVHAGGTNG	PITYSILSGN	EKGTFSIQPS	TGAITVRSAE	GLDFEVSPRL	RLVLQAESGG	AFAFTVLTLT
2170	2180	2190	2200	2210	2220	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
701	1	606.1713	-219.57	2	37.2	11.5	0	2537-2549	R.LAEAGESAGPGPR.A		WD:WU 3.50

Detailed Protein Report

Protein 911: 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

WD:WU **Median:** 0.91 **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	WD:WU 0.91

Detailed Protein Report

Protein 912: 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

Quantitation

WD:WU **Median:** 1.19 **CV:** 0.00 % **No. of 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	Ratios
173	1	424.2196	-47.66	3	31.4	11.4	2	147-158	R.TGCIGAKHRISK.E		WD:WU 1.19

Detailed Protein Report

Protein 913: **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

WD:WU **Median:** 0.82 **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		WD:WU 0.82

Detailed Protein Report

Protein 914: guanylate cyclase soluble subunit alpha-3 isoform D [Homo sapiens]

Accession:	gi|194595482	**Score:**	11.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	70.1
Database Date:	2015-11-30	**pI:**	7.8
		Sequence Coverage [%]:	1.4
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 1.56	**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		WD:WU 1.56

Detailed Protein Report

Protein 915: dedicator of cytokinesis protein 8 isoform 2 [Homo sapiens]

Accession:	gi|299473744	**Score:**	11.4
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
44	1	1097.5125	-75.08	1	29.8	11.4	0	800-810	K.SGAPTALLDPR.S	

Detailed Protein Report

Protein 916: inositol 1,4,5-trisphosphate receptor type 1 isoform 2 [Homo sapiens]

Accession:	gi|269954692	**Score:**	11.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	306.6
Database Date:	2015-11-30	**pI:**	5.9
		Sequence Coverage [%]:	0.3
		No. of unique Peptides:	1

Quantitation

WD:WU	**Median:** 3.89	**CV:** 0.00 %	**No. of Peptides:** 1

Detailed Protein Report

```
        10         20         30         40         50         60         70         80
MSDKMSSFLH IGDICSLYAE GSTNGFISTL GLVDDRCVVQ PETGDLNNPP KKFRDCLFKL CPMNRYSAQK QFWKAAKPGA
        90        100        110        120        130        140        150        160
NSTTDAVLLN KLHHAADLEK KQNETENRKL LGTVIQYGNV IQLLHLKSNK YLTVNKRLPA LLEKNAMRVT LDEAGNEGSW
       170        180        190        200        210        220        230        240
FYIQPFYKLR SIGDSVVIGD KVVLNPVNAG QPLHASSHQL VDNPGCNEVN SVNCNTSWKI VLFMKWSDNK DDILKGGDVV
       250        260        270        280        290        300        310        320
RLFHAEQEKF LTCDEHRKKQ HVFLRTTGRQ SATSATSSKA LWEVEVVQHD PCRGGAGYWN SLFRFKHLAT GHYLAAEVDP
       330        340        350        360        370        380        390        400
DQDASRSRLR NAQEKMVYSL VSVPEGNDIS SIFELDPTTL RGGDSLVPRN SYVRLRHLCT NTWVHSTNIP IDKEEEKPVM
       410        420        430        440        450        460        470        480
LKIGTSPVKE DKEAFAIVPV SPAEVRDLDF ANDASKVLGS IAGKLEKGTI TQNERRSVTK LLEDLVYFVT GGTNSGQDVL
       490        500        510        520        530        540        550        560
EVVFSKPNRE RQKLMREQNI LKQIFKLLQA PFTDCGDGPM LRLEELGDQR HAPFRHICRL CYRVLRHSQQ DYRKNQEYIA
       570        580        590        600        610        620        630        640
KQFGFMQKQI GYDVLAEDTI TALLHNNRKL LEKHITAAEI DTFVSLVRKN REPRFLDYLS DLCVSMNKSI PVTQELICKA
       650        660        670        680        690        700        710        720
VLNPTNADIL IETKLVLSRF EFEGVSSTGE NALEAGEDEE EVWLFWRDSN KEIRSKSVRE LAQDAKEGQK EDRDVLSYYR
       730        740        750        760        770        780        790        800
YQLNLFARMC LDRQYLAINE ISGQLDVDLI LRCMSDENLP YDLRASFCRL MLHMHVDRDP QEQVTPVKYA RLWSEIPSEI
       810        820        830        840        850        860        870        880
AIDDYDSSGA SKDEIKERFA QTMEFVEEYL RDVVCQRFPF SDKEKNKLTF EVVNLARNLI YFGFYNFSDL LRLTKILLAI
       890        900        910        920        930        940        950        960
LDCVHVTTIF PISKMAKGEE NKGSNVMRSI HGVGELMTQV VLRGGGFLPM TPMAAAPEGN VKQAEPEKED IMVMDTKLKI
       970        980        990       1000       1010       1020       1030       1040
IEILQFILNV RLDYRISCLL CIFKREFDES NSQTSETSSG NSSQEGPSNV PGALDFEHIE EQAEGIFGGS EENTPLDLDD
      1050       1060       1070       1080       1090       1100       1110       1120
HGGRTFLRVL LHLTMHDYPP LVSGALQLLF RHFSQRQEVL QAFKQVQLLV TSQDVDNYKQ IKQDLDQLRS IVEKSELWVY
      1130       1140       1150       1160       1170       1180       1190       1200
KGQGPDETMD GASGENEHKK TEEGNNKPQK HESTSSYNYR VVKEILIRLS KLCVQESASV RKSRKQQQRL LRNMGAHAVV
      1210       1220       1230       1240       1250       1260       1270       1280
LELLQIPYEK AEDTKMQEIM RLAHEFLQNF CAGNQQNQAL LHKHINLFLN PGILEAVTMQ HIFMNNFQLC SEINERVVQH
      1290       1300       1310       1320       1330       1340       1350       1360
FVHCIETHGR NVQYIKFLQT IVKAEGKFIK KCQDMVMAEL VNSGEDVLVF YNDRASFQTL IQMMRSERDR MDENSPLMYH
      1370       1380       1390       1400       1410       1420       1430       1440
IHLVELLAVC TEGKNVYTEI KCNSLLPLDD IVRVVTHEDC IPEVKIAYIN FLNHCYVDTE VEMKEIYTSN HMWKLFENFL
      1450       1460       1470       1480       1490       1500       1510       1520
VDICRACNNT SDRKHADSIL EKYVTEIVMS IVTTFFSSPF SDQSTTLQTR QPVFVQLLQG VFRVYHCNWL MPSQKASVES
      1530       1540       1550       1560       1570       1580       1590       1600
CIRVLSDVAK SRAIAIPVDL DSQVNNLFLK SHSIVQKTAM NWRLSARNAA RRDSVLAASR DYRNIIERLQ DIVSALEDRL
      1610       1620       1630       1640       1650       1660       1670       1680
RPLVQAELSV LVDVLHRPEL LFPENTDARR KCESGGFICK LIKHTKQLLE ENEEKLCIKV LQTLREMMTK DRGYGEKGEA
      1690       1700       1710       1720       1730       1740       1750       1760
LRQVLVNRYY GNVRPSGRRE SLTSFGNGPL SAGGPGKPGG GGGGSGSSSM SRGEMSLAEV QCHLDKEGAS NLVIDLIMNA
      1770       1780       1790       1800       1810       1820       1830       1840
SSDRVFHESI LLAIALLEGG NTTIQHSFFC RLTEDKKSEK FFKVFYDRMK VAQQEIKATV TVNTSDLGNK KKDDEVDRDA
      1850       1860       1870       1880       1890       1900       1910       1920
PSRKKAKEPT TQITEEVRDQ LLEASAATRK AFTTFRREAD PDDHYQPGEG TQATADKAKD DLEMSAVITI MQPILRFLQL
      1930       1940       1950       1960       1970       1980       1990       2000
LCENHNRDLQ NFLRCQNNKT NYNLVCETLQ FLDCICGSTT GGLGLLGLYI NEKNVALINQ TLESLTEYCQ GPCHENQNCI
      2010       2020       2030       2040       2050       2060       2070       2080
ATHESNGIDI ITALILNDIN PLGKKRMDLV LELKNNASKL LLAIMESRHD SENAERILYN MRPKELVEVI KKAYMQGEVE
      2090       2100       2110       2120       2130       2140       2150       2160
FEDGENGEDG AASPRNVGHN IYILAHQLAR HNKELQSMLK PGGQVDGDEA LEFYAKHTAQ IEIVRLDRTM EQIVFPVPSI
      2170       2180       2190       2200       2210       2220       2230       2240
CEFLTKESKL RIYYTTERDE QGSKINDFFL RSEDLFNEMN WQKKLRAQPV LYWCARNMSF WSSISFNLAV LMNLLVAFFY
      2250       2260       2270       2280       2290       2300       2310       2320
PFKGVRGGTL EPHWSGLLWT AMLISLAIVI ALPKPHGIRA LIASTILRLI FSVGLQPTLF LLGAFNVCNK IIFLMSFVGN
      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
1212	1	533.7834	-38.28	2	43.8	11.4	0	2137-2145	K.HTAQIEIVR.L		WD:WU 3.89

Detailed Protein Report

Protein 917: PREDICTED: clusterin-associated protein 1 isoform X1 [Homo sapiens]

Accession:	gi|578828036	**Score:**	11.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	39.5
Database Date:	2015-11-30	**pI:**	4.5
		Sequence Coverage [%]:	3.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MATKAHIKLN	TKKLYQADGY	AVKELLKITS	VLYNAMKTKG	MEGSEIVEED	VNKFKFDLGS	KIADLKAARQ	LASEITSKGA
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
SLYDLLGMEV	ELREMRTEAI	ARPLEINETE	KVMRIAIKEI	LTQVQKTKDL	LNNVASDEAN	LEAKIEKRKL	ELERNRKRLE
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
TLQSVRPCFM	DEYEKTEEEL	QKQYDTYLEK	FQNLTYLEQQ	LEDHHRMEQE	RFEEAKNTLC	LIQNKLKEEE	KRLLKSGSND
250	**260**	**270**	**280**	**290**	**300**	**310**	**320**
DSDIDIQEDD	ESDSELEERR	LPKPQTAMEM	LMQGRPGKRI	VGTMQGGDSD	DNEDSEESEI	DMEDDDDEDD	DLEDESISLS
330	**340**	**350**					
PTKPNRRVRK	SEPLDESDND	F					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2301	1	741.3566	-87.91	2	57.1	11.4	2	54-66	K.FKFDLGSKIADLK.A	

Detailed Protein Report

Protein 918: **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 919: proteasome activator complex subunit 3 isoform 1 [Homo sapiens]

Accession:	gi|30410794	**Score:**	11.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	29.5
Database Date:	2015-11-30	**pI:**	5.6
		Sequence Coverage [%]:	6.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MASLLKVDQE	VKLKVDSFRE	RITSEAEDLV	ANFFPKKLLE	LDSFLKEPIL	NIHDLTQIHS	DMNLPVPDPI	LLTNSHDGLD
90	100	110	120	130	140	150	160
GPTYKKRRLD	ECEEAFQGTK	VFVMPNGMLK	SNQQLVDIIE	KVKPEIRLLI	EKCNTVKMWV	QLLIPRIEDG	NNFGVSIQEE
170	180	190	200	210	220	230	240
TVAELRTVES	EAASYLDQIS	RYYITRAKLV	SKIAKYPHVE	DYRRTVTEID	EKEYISLRLI	ISELRNQYVT	LHDMILKNIE
250	260						
KIKRPRSSNA	ETLY						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2745	1	941.9477	-120.25	2	62.8	11.4	2	122-137	K.VKPEIRLLIEKCNTVK.M	

Detailed Protein Report

Protein 920: PREDICTED: RNA-binding protein 44 isoform X1 [Homo sapiens]

Accession: gi|530371379
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 11.4
MW [kDa]: 117.5
pI: 5.4
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 921: 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 922: **PREDICTED: extended synaptotagmin-3 isoform X2 [Homo sapiens]**

Accession:	gi|578807790	**Score:**	11.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	91.8
Database Date:	2015-11-30	**pI:**	9.2
		Sequence Coverage [%]:	0.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MRAEEPCAPG	APSALGAQRT	PGPELRLSSQ	LLPELCTFVV	RVLFYLGPVY	LAGYLGLSIT	WLLLGALLWM	WWRRNRRGKL
90	100	110	120	130	140	150	160
GRLAAAFEFL	DNEREFISRE	LRGQHLPAWI	HFPDVERVEW	ANKIISQTWP	YLSMIMESKF	REKLEPKIRE	KSIHLRTFTF
170	180	190	200	210	220	230	240
TKLYFGQKCP	RVNGVKAHTN	TCNRRRVTVD	LQICYIGDCE	ISVELQKIQA	GVNGIQLQGT	LRVILEPLLV	DKPFVGAVTV
250	260	270	280	290	300	310	320
FFLQKPHLQI	NWTGLTNLLD	APGINDVSDS	LLEDLIATHL	VLPNRVTVPV	KKGLDLTNLR	FPLPCGVIRV	HLLEAEQLAQ
330	340	350	360	370	380	390	400
KDNFLGLRGK	SDPYAKVSIG	LQHFRSRTIY	RNLNPTWNEV	FEFMVYEVPG	QDLEVDLYDE	DTDRDDFLGS	LQICLGDVMT
410	420	430	440	450	460	470	480
NRVVDEWFVL	NDTTSGRLHL	RLEWLSLLTD	QEVLTEDHGG	LSTAILVVFL	ESACNLPRNP	FDYLNGEYRA	KKLSRFARNK
490	500	510	520	530	540	550	560
VSKDPSSYVK	LSVGKKTHTS	KTCPHNKDPV	WSQVFSFFVH	NVATERLHLK	VLDDDQECAL	GMLEVPLCQI	LPYADLTLEQ
570	580	590	600	610	620	630	640
RFQLDHSGLD	SLISMRLVLR	FLQVEERELG	SPYTGPEALK	KGPLLIKKVA	TNQGPKAQPQ	EEGPTDLPCP	PDPASDTKDV
650	660	670	680	690	700	710	720
SRSTTTTTSA	TTVATEPTSQ	ETGPEPKGKD	SAKRFCEPIG	EKKSPATIFL	TVPGPHSPGP	IKSPRPMKCP	ASPFAWPPKR
730	740	750	760	770	780	790	800
LAPSMSSLNS	LASSCFDLAD	ISLNIEYAPL	CLIFSKIACM	KNTSLDGKVD	MNLHFCASCF	FTKYLPKRQH	GVVERTQDKG
810	820						
ERAKQAVYGS	SCVLTIK						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
374	1	734.1603	-282.65	1	33.3	11.4	0	762-768	K.NTSLDGK.V	

Detailed Protein Report

Protein 923: 7SK snRNA methylphosphate capping enzyme isoform A [Homo sapiens]

Accession:	gi|47271406	**Score:**	11.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	74.3
Database Date:	2015-11-30	**pI:**	10.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.3
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 0.48 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MIEMAAEKEP FLVPAPPPPL KDESGGGGGP TVPPHQEAAS GELRGGTERG PGRCAPSAGS PAAAVGRESP GAAATSSSGP
        90        100        110        120        130        140        150        160
QAQQHRGGGP QAQSHGEARL SDPPGRAAPP DVGEERRGGG GTELGPPAPP RPRNGYQPHR PPGGGGGKRR NSCNVGGGGG
       170        180        190        200        210        220        230        240
GFKHPAFKRR RRVNSDCDSV LPSNFLLGGN IFDPLNLNSL LDEEVSRTLN AETPKSSPLP AKGRDPVEIL IPKDITDPLS
       250        260        270        280        290        300        310        320
LNTCTDEGHV VLASPLKTGR KRHRHRGQHH QQQQAAGGSE SHPVPPTAPL TPLLHGEGAS QQPRHRGQNR DAPQPYELNT
       330        340        350        360        370        380        390        400
AINCRDEVVS PLPSALQGPS GSLSAPPAAS VISAPPSSSS RHRKRRRTSS KSEAGARGGG QGSKEKGRGS WGGRHHHHHP
       410        420        430        440        450        460        470        480
LPAAGFKKQQ RKFQYGNYCK YYGYRNPSCE DGRLRVLKPE WFRGRDVLDL GCNVGHLTLS IACKWGPSRM VGLDIDSRLI
       490        500        510        520        530        540        550        560
HSARQNIRHY LSEELRLPPQ TLEGDPGAEG EEGTTTVRKR SCFPASLTAS RGPIAAPQVP LDGADTSVFP NNVVFVTGNY
       570        580        590        600        610        620        630        640
VLDRDDLVEA QTPEYDVVLC LSLTKWVHLN WGDEGLKRMF RRIYRHLRPG GILVLEPQPW SSYGKRKTLT ETIYKNYYRI
       650        660        670        680        690
QLKPEQFSSY LTSPDVGFSS YELVATPHNT SKGFQRPVYL FHKARSPSH
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1179	1	1070.0301	2.64	2	43.0	11.4	2	45-67	R. GGTERGPGRCAPSAGSPAAAVGI E	Carbamidomethyl: 10	WD:WU 0.48

Detailed Protein Report

Protein 924: 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	3	715.6762	49.39	3	48.8	11.4	0	1-20	-.MGCSLSEDGGMLAQCQGLSK.E	Carbamidomethyl: 3, 15; Oxidation: 11

Detailed Protein Report

Protein 925: PREDICTED: autism susceptibility gene 2 protein isoform X1 [Homo sapiens]

Accession:	gi|530385715	**Score:**	11.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	90.0
Database Date:	2015-11-30	**pI:**	9.7
		Sequence Coverage [%]:	2.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MFAPPTALPP	PPPLTSGSLQ	VAGHPAGSTY	SEQDILRQEL	NTRFLASQSA	DRGASLGPPP	YLRTEFHQHQ	HQHQHTHQHT
90	100	110	120	130	140	150	160
HQHTFTPFPH	AIPPTAIMPT	PAPPMVRTPG	RNFDKYPTKV	DPFYRHSLFH	SYPPAVSGIP	PMIPPTGPFG	SLQGAFQPKT
170	180	190	200	210	220	230	240
SNPIDVAARP	GTVPHTLLQK	DPRLTDPFRP	MLRKPGKWCA	MHVHIAWQIY	HHQQKVKKQM	QSDPHKLDFG	LKPEFLSRPP
250	260	270	280	290	300	310	320
GPSLFGAIHH	PHDLARPSTL	FSAAGAAHPT	GTPFGPPPHH	SNFLNPAAHL	EPFNRPSTFT	GLAAVGGNAF	GGLGNPSVTP
330	340	350	360	370	380	390	400
NSMFGHKDGP	SVQNFSNPHE	PWNRLHRTPP	SFPTPPPWLK	PGELERSASA	AAHDRDRDVD	KRDSSVSKDD	KERESVEKRH
410	420	430	440	450	460	470	480
SSHPSPAPVL	PVNALGHTRS	STEQIRAHLN	TEAREKDKPK	ERERDHSESR	KDLAADEHKA	KEGHLPEKDG	HGHEGRAAGE
490	500	510	520	530	540	550	560
EAKQLARVPS	PYVRTPVVES	ARPNSTSSRE	AEPRKGEPAY	ENPKKSSEVK	VKEERKEDHD	LPPEAPQTHR	ASEPPPPNSS
570	580	590	600	610	620	630	640
SSVHPGPLAS	MPMTVGVTGI	HPMNSISSLD	RTRMMTPFMG	ISPLPGGERF	PYPSFHWDPI	RDPLRDPYRE	LDIHRRDPLG
650	660	670	680	690	700	710	720
RDFLLRNDPL	HRLSTPRLYE	ADRSFRDREP	HDYSHHHHHH	HHPLSVDPRR	EHERGGHLDE	RERLHMLRED	YEHTRLHSVH
730	740	750	760	770	780	790	800
PASLDGHLPH	PSLITPGLPS	MHYPRISPTA	GNQNGLLNKT	PPTAALSAPP	PLISTLGGRP	VSPRRTTPLS	AEIRERPPSH
810							
TLKDIEAR							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1863	1	860.9061	-9.89	2	51.6	11.4	0	594-609	R.MMTPFMGISPLPGGER.F	

Detailed Protein Report

Protein 926: oxysterol-binding protein-related protein 1 isoform 1 [Homo sapiens]

Accession: gi|19718746
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 11.4
MW [kDa]: 50.2
pI: 6.2
Sequence Coverage [%]: 3.0
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MSEEKDCGGG	DALSNGIKKH	RTSLPSPMFS	RNDFSIWSIL	RKCIGMELSK	ITMPVIFNEP	LSFLQRLTEY	MEHTYLIHKA
90	100	110	120	130	140	150	160
SSLSDPVERM	QCVAAFAVSA	VASQWERTGK	PFNPLLGETY	ELVRDDLGFR	LISEQVSHHP	PISAFHAEGL	NNDFIFHGSI
170	180	190	200	210	220	230	240
YPKLKFWGKS	VEAEPKGTIT	LELLEHNEAY	TWTNPTCCVH	NIIVGKLWIE	QYGNVEIINH	KTGDKCVLNF	KPCGLFGKEL
250	260	270	280	290	300	310	320
HKVEGYIQDK	SKKKLCALYG	KWTECLYSVD	PATFDAYKKN	DKKNTEEKKN	SKQMSTSEEL	DEMPVPDSES	VFIIPGSVLL
330	340	350	360	370	380	390	400
WRIAPRPPNS	AQMYNFTSFA	MVLNEVDKDM	ESVIPKTDCR	LRPDIRAMEN	GEIDQASEEK	KRLEEKQRAA	RKNRSKSEED
410	420	430	440				
WKTRWFHQGP	NPYNGAQDWI	YSGSYWDRNY	FNLPDIY				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2915	1	713.3417	-43.47	2	65.2	11.4	0	226-238	K.CVLNFKPCGLFGK.E	

Detailed Protein Report

Protein 927: **PREDICTED: NAD-dependent protein deacylase sirtuin-5, mitochondrial isoform X3 [Homo sapiens]**

Accession:	gi|530381706	**Score:**	11.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	31.7
Database Date:	2015-11-30	**pI:**	11.1
Modification(s):	Oxidation	**Sequence Coverage [%]:**	4.2
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MRPLQIVPSR LISQLYCGLK PPASTRNQIC LKMARPSSSM ADFRKFFAKA KHIVIISGAG VSAESGVPTF RGAGGYWRKW
        90        100        110        120        130        140        150        160
QAQDLATPLA FAHNPSRVWE FYHYRREVMG SKEPNAGHRA IAECETRLGK QGRRVVVITQ NIDELHRKAG TKNLLEIHGS
       170        180        190        200        210        220        230        240
LFKTRCTSCG VVAENYKSPI CPALSGKGAP EPGTQDASIP VEKLPRWALP LWCTQQPCLP PRWLPGACQW LNLTRRPPQL
       250        260        270        280        290
RTDSGFISRD PVERLFLKPL PVMKMKLFLK CPGEERNYSI SKN
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
324	1	686.3446	49.16	2	32.7	11.4	0	33-44	K.MARPSSSMADFR.K	Oxidation: 8

Detailed Protein Report

Protein 928: **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 929: separin [Homo sapiens]

Accession:	gi|134276943	**Score:**	11.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	233.0
Database Date:	2015-11-30	**pI:**	8.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.0
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|578824487	refseq_human (refseq_human_20140103.fasta)	PREDICTED: separin isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MRSFKRVNFG	TLLSSQKEAE	ELLPALKEFL	SNPPAGFPSS	RSDAERRQAC	DAILRACNQQ	LTAKLACPRH	LGSLLELAEL
90	100	110	120	130	140	150	160
ACDGYLVSTP	QRPPLYLERI	LFVLLRNAAA	QGSPEATLRL	AQPLHACLVQ	CSREAAPQDY	EAVARGSFSL	LWKGAEALLE
170	180	190	200	210	220	230	240
RRAAFAARLK	ALSFLVLLED	ESTPCEVPHF	ASPTACRAVA	AHQLFDASGH	GLNEADADFL	DDLLSRHVIR	ALVGERGSSS
250	260	270	280	290	300	310	320
GLLSPQRALC	LLELTLEHCR	RFCWSRHHDK	AISAVEKAHS	YLRNTNLAPS	LQLCQLGVKL	LQVGEEGPQA	VAKLLIKASA
330	340	350	360	370	380	390	400
VLSKSMEAPS	PPLRALYESC	QFFLSGLERG	TKRRYRLDAI	LSLFAFLGGY	CSLLQQLRDD	GVYGGSSKQQ	QSFLQMYFQG
410	420	430	440	450	460	470	480
LHLYTVVVYD	FAQGCQIVDL	ADLTQLVDSC	KSTVVWMLEA	LEGLSGQELT	DHMGMTASYT	SNLAYSFYSH	KLYAEACAIS
490	500	510	520	530	540	550	560
EPLCQHLGLV	KPGTYPEVPP	EKLHRCFRLQ	VESLKKLGKQ	AQGCKMVILW	LAALQPCSPE	HMAEPVTFWV	RVKMDAARAG
570	580	590	600	610	620	630	640
DKELQLKTLR	DSLSGWDPET	LALLLREELQ	AYKAVRADTG	QERFNIICDL	LELSPEETPA	GAWARATHLV	ELAQVLCYHD
650	660	670	680	690	700	710	720
FTQQTNCSAL	DAIREALQLL	DSVRPEAQAR	DQLLDDKAQA	LLWLYICTLE	AKMQEGIERD	RRAQAPGNLE	EFEVNDLNYE
730	740	750	760	770	780	790	800
DKLQEDRFLY	SNIAFNLAAD	AAQSKCLDQA	LALWKELLTK	GQAPAVRCLQ	QTAASLQILA	ALYQLVAKPM	QALEVLLLLR
810	820	830	840	850	860	870	880
IVSERLKDHS	KAAGSSCHIT	QLLLTLGCPS	YAQLHLEEAA	SSLKHLDQTT	DTYLLLSLTC	DLLRSQLYWT	HQKVTKGVSL
890	900	910	920	930	940	950	960
LLSVLRDPAL	QKSSKAWYLL	RVQVLQLVAA	YLSLPSNNLS	HSLWEQLCAQ	GWQTPEIALI	DSHKLLRSII	LLLMGSDILS
970	980	990	1000	1010	1020	1030	1040
TQKAAVETSF	LDYGENLVQK	WQVLSEVLSC	SEKLVCHLGR	LGSVSEAKAF	CLEALKLTTK	LQIPRQCALF	LVLKGELELA
1050	1060	1070	1080	1090	1100	1110	1120
RNDIDLCQSD	LQQVLFLLES	CTEFGGVTQH	LDSVKKVHLQ	KGKQQAQVPC	PPQLPEEELF	LRGPALELVA	TVAKEPGPIA
1130	1140	1150	1160	1170	1180	1190	1200
PSTNSSPVLK	TKPQPIPNFL	SHSPTCDCSL	CASPVLTAVC	LRWVLVTAGV	RLAMGHQAQG	LDLLQVVLKG	CPEAAERLTQ
1210	1220	1230	1240	1250	1260	1270	1280
ALQASLNHKT	PPSLVPSLLD	EILAQAYTLL	ALEGLNQPSN	ESLQKVLQSG	LKFVAARIPH	LEPWRASLLL	IWALTKLGGL
1290	1300	1310	1320	1330	1340	1350	1360
SCCTTQLFAS	SWGWQPPLIK	SVPGSEPSKT	QGQKRSGRGR	QKLASAPLRL	NNTSQKGLEG	RGLPCTPKPP	DRIRQAGPHV
1370	1380	1390	1400	1410	1420	1430	1440
PFTVFEEVCP	TESKPEVPQA	PRVQQRVQTR	LKVNFSDDSD	LEDPVSAEAW	LAEEPKRRGT	ASRGRGRARK	GLSLKTDAVV
1450	1460	1470	1480	1490	1500	1510	1520
APGSAPGNPG	LNGRSRRAKK	VASRHCEERR	PQRASDQARP	GPEIMRTIPE	EELTDNWRKM	SFEILRGSDG	EDSASGGKTP
1530	1540	1550	1560	1570	1580	1590	1600
APGPEAASGE	WELLRLDSSK	KKLPSPCPDK	ESDKDLGPRL	RLPSAPVATG	LSTLDSICDS	LSVAFRGISH	CPPSGLYAHL
1610	1620	1630	1640	1650	1660	1670	1680
CRFLALCLGH	RDPYATAFLV	TESVSITCRH	QLLTHLHRQL	SKAQKHRGSL	EIADQLQGLS	LQEMPGDVPL	ARIQRLFSFR
1690	1700	1710	1720	1730	1740	1750	1760
ALESGHFPQP	EKESFQERLA	LIPSGVTVCV	LALATLQPGT	VGNTLLLTRL	EKDSPPVSVQ	IPTGQNKLHL	RSVLNEFDAI
1770	1780	1790	1800	1810	1820	1830	1840
QKAQKENSSC	TDKREWWTGR	LALDHRMEVL	IASLEKSVLG	CWKGLLLPSS	EEPGPAQEAS	RLQELLQDCG	WKYPDRTLLK
1850	1860	1870	1880	1890	1900	1910	1920
IMLSGAGALT	PQDIQALAYG	LCPTQPERAQ	ELLNEAVGRL	QGLTVPSNSH	LVLVLDKDLQ	KLPWESMPSL	QALPVTRLPS
1930	1940	1950	1960	1970	1980	1990	2000
FRFLLSYSII	KEYGASPVLS	QGVDPRSTFY	VLNPHNNLSS	TEEQFRANFS	SEAGWRGVVG	EVPRPEQVQE	ALTKHDLYIY
2010	2020	2030	2040	2050	2060	2070	2080
AGHGAGARFL	DGQAVLRLSC	RAVALLFGCS	SAALAVRGNL	EGAGIVLKYI	MAGCPLFLGN	LWDVTDRDID	RYTEALLQGW
2090	2100	2110	2120	2130			
LGAGPGAPLL	YYVNQARQAP	RLKYLIGAAP	IAYGLPVSLR				

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
138	1	879.3993	-65.99	3	30.6	11.3	1	678-699	K.AQALLWLYICTLEAKMQEGIER.D	Carbamidomethyl: 10

Detailed Protein Report

Protein 930: **PREDICTED: EF-hand calcium-binding domain-containing protein 4B isoform X6 [Homo sapiens]**

Accession:	gi|578822705	**Score:**	11.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	77.3
Database Date:	2015-11-30	**pI:**	4.9
		Sequence Coverage [%]:	1.5
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 2.19 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MAAPDGRVVS	RPQRLGQGSG	QGPKGSGACL	HPLDSLEQKE	TQEQTSGQLV	MLRKAQEFFQ	TCDAEGKGFI	ARKDMQRLHK
90	100	110	120	130	140	150	160
ELPLSLEELE	DVFDALDADG	NGYLTPQEFT	TGFSHFFFSQ	NNPSQEDAGE	QVAQRHEEKV	YLSRGDEDLG	DMGEDEEAQF
170	180	190	200	210	220	230	240
RMLMDRLGAQ	KVLEDESDVK	QLWLQLKKEE	PHLLSNFEDF	LTRIISQLQE	AHEEKNELEC	ALKRKIAAYD	EEIQHLYEEM
250	260	270	280	290	300	310	320
EQQIKSEKEQ	FLLKDTERFQ	ARSQELEQKL	LCKEQELEQL	TQKQKRLEGQ	CTALHHDKHE	TKAENTKLKL	TNQELARELE
330	340	350	360	370	380	390	400
RTSWELQDAQ	QQLESLQQEA	CKLHQEKEME	VYRVTESLQR	EKAGLLKQLD	FLSSQSEEEE	EVFGIPRRSS	LGLSGYPLTE
410	420	430	440	450	460	470	480
EEPGTGEPGP	GGPYPRPLRR	IISVEEDPLP	QLLDGGFEQP	LSKCSEEEEV	SDQGVQGQIP	EAPPLKLTPT	SPRGQPVGKE
490	500	510	520	530	540	550	560
ALCKEESSPS	APDRLFKIVF	VGNSAVGKTS	FLRRFCEDRF	SPGMAATVGI	DYRVKTLNVD	NSQVALQLWD	TAGQERYRCI
570	580	590	600	610	620	630	640
TQQFFRKADG	VIVMYDLTDK	QSFLSVRRWL	SSVEEAVGDR	VPVLLLGNKL	DNEKEREVPR	GLGEQLATVK	SKHFHLSGQS
650	660	670	680	690			
VTPREVGQVP	KSLGGDFLWK	CHGKEATGKH	GCLGILGMAQ	LLCM			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1025	3	508.1580	-265.04	2	41.1	11.3	0	621-630	R.GLGEQLATVK.S		WD:WU 2.19

Detailed Protein Report

Protein 931: 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 932: PREDICTED: adenylate cyclase type 8 isoform X1 [Homo sapiens]

Accession:	gi|530388711	**Score:**	11.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	136.6
Database Date:	2015-11-30	**pI:**	6.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	0.8
		No. of unique Peptides:	1

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
158	1	659.9157	162.56	2	31.2	11.3	1	704-713	K.YSQMRDEVFK.S	Oxidation: 4

Detailed Protein Report

Protein 933: **APC membrane recruitment protein 1 [Homo sapiens]**

Accession:	gi|124244056	**Score:**	11.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	124.0
Database Date:	2015-11-30	**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	

Detailed Protein Report

Protein 934: 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 935: leukocyte immunoglobulin-like receptor subfamily B member 1 isoform 6 precursor [Homo sapiens]

Accession:	gi|508772614	**Score:**	11.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	49.3
Database Date:	2015-11-30	**pI:**	5.6
		Sequence Coverage [%]:	3.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MTPILTVLIC	LGLSLGPRTH	VQAGHLPKPT	LWAEPGSVIT	QGSPVTLRCQ	GGQETQEYRL	YREKKTALWI	TRIPQELVKK
90	100	110	120	130	140	150	160
GQFPIPSITW	EHAGRYRCYY	GSDTAGRSES	SDPLELVVTG	AYIKPTLSAQ	PSPVVNSGGN	VILQCDSQVA	FDGFSLCKEG
170	180	190	200	210	220	230	240
EDEHPQCLNS	QPHARGSSRA	IFSVGPVSPS	RRWWYRCYAY	DSNSPYEWSL	PSDLLELLVL	GVSKKPSLSV	QPGPIVAPEE
250	260	270	280	290	300	310	320
TLTLQCGSDA	GYNRFVLYKD	GERDFLQLAG	AQPQAGLSQA	NFTLGPVSRS	YGGQYRCYGA	HNLSSEWSAP	SDPLDILIAG
330	340	350	360	370	380	390	400
QFYDRVSLSV	QPGPTVASGE	NVTLLCQSQG	WMQTFLLTKE	GAADDPWRLR	STYQSQKYQA	EFPMGPVTSA	HAGTYRCYGS
410	420	430	440	450	460		
QSSKPYLLTH	PSDPLELVVS	GPSGGPSSPT	TGPTSTSAGP	EDQPLTPTGS	DPQSGE		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1584	1	949.1716	123.54	2	48.1	11.3	0	1-18	-.MTPILTVLICLGLSLGPR.T	

Detailed Protein Report

Protein 936: 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 937: PREDICTED: zinc finger protein 35 isoform X4 [Homo sapiens]

Accession:	gi|530373105	**Score:**	11.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	41.7
Database Date:	2015-11-30	**pI:**	10.4
		Sequence Coverage [%]:	3.8
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530373109	refseq_human (refseq_human_20140103.fasta)	PREDICTED: zinc finger protein 35 isoform X6 [Homo sapiens]
gi|530373107	refseq_human (refseq_human_20140103.fasta)	PREDICTED: zinc finger protein 35 isoform X5 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MLKRQRIKRE KKDFRQVIVN DCHLPESFKE EENQKCKKSG GKYSLNSGAV KNPKTQLGQK PFTCSVCGKG FSQSANLVVH
        90        100        110        120        130        140        150        160
QRIHTGEKPF ECHECGKAFI QSANLVVHQR IHTGQKPYVC SKCGKAFTQS SNLTVHQKIH SLEKTFKCNE CEKAFSYSSQ
       170        180        190        200        210        220        230        240
LARHQKVHIT EKCYECNECG KTFTRSSNLI VHQRIHTGEK PFACNDCGKA FTQSANLIVH QRSHTGEKPY ECKECGKAFS
       250        260        270        280        290        300        310        320
CFSHLIVHQR IHTAEKPYDC SECGKAFSQL SCLIVHQRIH SGDLPYVCNE CGKAFTCSSY LLIHQRIHNG EKPYTCNECG
       330        340        350        360        370
KAFRQRSSLT VHQRTHTGEK PYECEKCGAA FISNSHLMRH HRTHLVE
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2227	2	698.3590	-34.60	2	56.2	11.3	2	38-51	K.KSGGKYSLNSGAVK.N	

Detailed Protein Report

Protein 938: **nuclear RNA export factor 3 [Homo sapiens]**

Accession:	gi|11545757	**Score:**	11.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	60.1
Database Date:	2015-11-30	**pI:**	6.3
		Sequence Coverage [%]:	2.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSLPSGHTTG	HTDQVVQRRA	RCWDIYQRRF	SSRSEPVNPG	MHSSSHQQQD	GDAAMHGAHM	DSPVRYTPYT	ISPYNRKGSF
90	100	110	120	130	140	150	160
RKQDQTHVNM	EREQKPPERR	MEGNMPDGTL	GSWFKITVPF	GIKYNEKWLL	NLIQNECSVP	FVPVEFHYEN	MHASFFVENA
170	180	190	200	210	220	230	240
SIAYALKNVS	GKIWDEDNEK	ISIFVNPAGI	PHFVHRELKS	EKVEQIKLAM	NQQCDVSQEA	LDIQRLPFYP	DMVNRDTKMA
250	260	270	280	290	300	310	320
SNPRKCMAAS	LDVHEENIPT	VMSAGEMDKW	KGIEPGEKCA	DRSPVCTTFS	DTSSNINSIL	ELFPKLLCLD	GQQSPRATLC
330	340	350	360	370	380	390	400
GTEAHKRLPT	CKGSFFGSEM	LKNLVLQFLQ	QYYLIYDSGD	RQGLLSAYHD	EACFSLSIPF	NPEDSAPSSF	CKFFKDSRNI
410	420	430	440	450	460	470	480
KILKDPYLRG	ELLKHTKLDI	VDSLSALPKT	QHDLSSFLVD	MWYQTEWMLC	FSVNGVFKEV	EGQSQGSVLA	FTRTFIATPG
490	500	510	520	530	540		
SSSSLCIVND	KLFVRDTSHQ	GTQSALFTLV	PTAFSSSVPA	FSQEQQKMLP	S		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2683	1	835.4519	96.70	2	61.9	11.3	0	101-115	R.MEGNMPDGTLGSWFK.I	

Detailed Protein Report

Protein 939: **PREDICTED: amyotrophic lateral sclerosis 2 chromosomal region candidate gene 12 protein isoform X2 [Homo sapiens]**

Accession:	gi|578803684	**Score:**	11.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	31.0
Database Date:	2015-11-30	**pI:**	9.6
		Sequence Coverage [%]:	6.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MYPNPLIYCT	CWDPWNLGPR	KLIKTPQLPR	KNSTGSSKLT	PLVPAPKNHN	YLQPTKPVVS	PKMKIHSARQ	EETNKSFYEV
90	100	110	120	130	140	150	160
INVSPGYQLV	RNREQISVTL	GDEMFDRKKR	WESEIPDKGR	FSRTNIISDL	EEQISELTAI	IEQMNRDHQS	AQKLLSSEMD
170	180	190	200	210	220	230	240
LRCAEMKQNF	ENKNRELKEA	HEAELSELEN	NYKAALKAEK	LAAQEKLEEM	GKEYKYLKNM	FRTYQDSIYD	EMEEKWSKQK
250	260	270					
AKWKKDEKFE	RENILLQQKK	KR					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2079	1	715.9597	-76.99	3	54.4	11.3	1	176-193	R.ELKEAHEAELSELENNYK.A	

Detailed Protein Report

Protein 940: 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 941: azurocidin preproprotein [Homo sapiens]

Accession:	gi|11342670	**Score:**	11.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	26.9
Database Date:	2015-11-30	**pI:**	11.9
		Sequence Coverage [%]:	5.2
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MTRLTVLALL AGLLASSRAG SSPLLDIVGG RKARPRQFPF LASIQNQGRH FCGGALIHAR FVMTAASCFQ SQNPGVSTVV
        90        100        110        120        130        140        150        160
LGAYDLRRRE RQSRQTFSIS SMSENGYDPQ QNLNDLMLLQ LDREANLTSS VTILPLPLQN ATVEAGTRCQ VAGWGSQRSG
       170        180        190        200        210        220        230        240
GRLSRFPRFV NVTVTPEDQC RPNNVCTGVL TRRGGICNGD GGTPLVCEGL AHGVASFSLG PCGRGPDFFT RVALFRDWID
       250        260
GVLNNPGPGP A
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2248	1	753.2914	-139.59	2	56.4	11.3	0	37-49	R.QFPFLASIQNQGR.H	

Detailed Protein Report

Protein 942: smad nuclear-interacting protein 1 [Homo sapiens]

Accession:	gi|21314720	**Score:**	11.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	45.8
Database Date:	2015-11-30	**pI:**	10.4
		Sequence Coverage [%]:	3.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MKAVKSERER	GSRRRHRDGD	VVLPAGVVVK	QERLSPEVAP	PAHRRPDHSG	GSPSPPTSEP	ARSGHRGNRA	RGVSRSPPKK
90	100	110	120	130	140	150	160
KNKASGRRSK	SPRSKRNRSP	HHSTVKVKQE	REDHPRRGRE	DRQHREPSEQ	EHRRARNSDR	DRHRGHSHQR	RTSNERPGSG
170	180	190	200	210	220	230	240
QGQGRDRDTQ	NLQAQEEERE	FYNARRREHR	QRNDVGGGGS	ESQELVPRPG	GNNKEKEVPA	KEKPSFELSG	ALLEDTNTFR
250	260	270	280	290	300	310	320
GVVIKYSEPP	EARIPKKRWR	LYPFKNDEVL	PVMYIHRQSA	YLLGRHRRIA	DIPIDHPSCS	KQHAVFQYRL	VEYTRADGTV
330	340	350	360	370	380	390	400
GRRVKPYIID	LGSGNGTFLN	NKRIEPQRYY	ELKEKDVLKF	GFSSREYVLL	HESSDTSEID	RKDDEDEEEE	EEVSDS

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2242	1	698.3431	-10.52	2	56.4	11.3	0	289-301	R.IADIPIDHPSCSK.Q	

Detailed Protein Report

Protein 943: transcriptional repressor CTCF isoform 2 [Homo sapiens]

Accession:	gi|300388142	**Score:**	11.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	46.0
Database Date:	2015-11-30	**pI:**	9.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	4.0
		No. of unique 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
1114	1	612.2788	-15.06	3	42.6	11.3	2	25-40	K.CSMCDYASVEVSKLKR.H	Oxidation: 3

Detailed Protein Report

Protein 944: zinc finger protein 41 homolog [Homo sapiens]

Accession:	gi|27883846	**Score:**	11.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	22.8
Database Date:	2015-11-30	**pI:**	10.5
		Sequence Coverage [%]:	5.1
		No. of unique Peptides:	1

Quantitation

WD:WU	**Median:** 2.98	**CV:** 0.00 %	**No. of Peptides:** 1

Alias proteins:

Accession	Name	Description
gi|403048741	refseq_human (refseq_human_20140103.fasta)	zinc finger protein 41 homolog [Homo sapiens]

```
         10         20         30         40         50         60         70         80
MEKPAGRKKK TPTPREEADV QKSALREEKV SGDRKPPERP TVPRKPRTEP CLSPEDEEHV FDAFDASFKD DFEGVPVFIP
         90        100        110        120        130        140        150        160
FQRKKPYECS ECGRIFKHKT DHIRHQRVHT GEKPFKCAQC GKAFRHSSDV TKHQRTHTGE KPFKCGECGK AFNCGSNLLK
        170        180        190        200
HQKTHTGEKP YECTHCGKAF AYSSCLIRHQ KRHPRKKP
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1184	1	586.1188	-218.96	2	43.0	11.3	0	85-94	K.KPYECSECGR.I		WD:WU 2.98

Detailed Protein Report

Protein 945: PREDICTED: enhancer of polycomb homolog 2 isoform X1 [Homo sapiens]

Accession:	gi|578804049	**Score:**	11.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	77.3
Database Date:	2015-11-30	**pI:**	9.9
		Sequence Coverage [%]:	2.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDSEDETLLN	RLNRKMEIKP	LQFEIMIDRL	EKASSNQLVT	LQEAKLLLNE	DDYLIKAVYD	YWVRKRKNCR	GPSLIPQIKQ
90	100	110	120	130	140	150	160
EKRDGSTNND	PYVAFRRRTE	KMQTRKNRKN	DEASYEKMLK	LRREFSRAIT	ILEMIKRREK	TKRELLHLTL	EVVEKRYHLG
170	180	190	200	210	220	230	240
DYGGEILNEV	KISRSEKELY	ATPATLHNGN	HHKVQECKTK	HPHHLSLKEE	ASDVVRQKKK	YPKKPKAEAL	ITSQQPTPET
250	260	270	280	290	300	310	320
LPVINKSDIK	QYDFHSSDED	EFPQVLSPVS	EPEEENDPDG	PCAFRRRAGC	QYYAPRLDQA	NHSCENSELA	DLDKLRYRHC
330	340	350	360	370	380	390	400
LTTLTVPRRC	IGFARRRIGR	GGRVIMDRIS	TEHDPVLKQI	DPEMLNSFSS	SSQTIDFSSN	FSRTNASSKH	CENRLSLSEI
410	420	430	440	450	460	470	480
LSNIRSCRLQ	CFQPRLLNLQ	DSDSEECTSR	KPGQTVNNKR	VSAASVALLN	TSKNGISGGI	TEEQFQTHQQ	QLVQMQRQQL
490	500	510	520	530	540	550	560
AQLQQKQQSQ	HSSQQTHPKA	QGSSTSDCMS	KTLDSASAHF	AASAVVSAPV	PSRSEVAKEQ	NTGHNNINGV	VQPSGTSKTL
570	580	590	600	610	620	630	640
YSTNMALSSS	PGISAVQLVR	TVGHTTTNHL	IPALCTSSPQ	TLPMNNSCLT	NAVHLNNVSV	VSPVNVHINT	RTSAPSPTAL
650	660	670	680	690			
KLATVAASMD	RVPKVTPSSA	ISSIARENHE	PERLGLNGIA	ETTVAMEVT			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
956	1	757.0581	154.93	2	40.3	11.3	1	652-666	R.VPKVTPSSAISSIAR.E	

Detailed Protein Report

Protein 946: uncharacterized protein LOC402160 [Homo sapiens]

Accession: gi|300797344
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 11.3
MW [kDa]: 74.8
pI: 10.3
Sequence Coverage [%]: 2.5
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MAYYGKCIET	VIEQLDKFTP	KRDNPEQFLE	AAATSLQALS	PQKQSFVLEV	LSGCLEYRKL	LTVVVDAFYV	EDGRLCLRVD
90	100	110	120	130	140	150	160
HSRFEVICYL	ATFLLEELGF	QLFCNIIKSQ	PVDKMCKFLR	FFFNPLHLCS	WIKDEWSLIY	EPAHVKENWI	DPLMRWQPEV
170	180	190	200	210	220	230	240
QELINHLEGV	SASQSSPLKT	KAKVTEPKEF	NLTAPRPRTI	PAPEPVPVVA	KPRPVPQSTY	QPPKEQQQLE	TVKRYNRRKA
250	260	270	280	290	300	310	320
EELLLRANIE	ELCCAMPRSC	RERVQGSKQQ	LRLQFPPRIR	KTPKLTFYRP	DNILVKLNTT	AILREGALYQ	RQVEQELQRV
330	340	350	360	370	380	390	400
DKLVDGAGDF	SEFFEWQKKM	QAKDREEQLA	ASECRRLQGK	LSHEEAVLAR	QSLMQENKQR	VEQQKEQMAK	LMLQRAERRL
410	420	430	440	450	460	470	480
REDRSRKELV	EQVIEGQKNA	KAAQTKLAKG	RQQTVQEAIE	ESRGLLQRRA	QAAQEEQRRR	CELISQLRAL	ETQPTRKGKL
490	500	510	520	530	540	550	560
VDLTQIPGYG	LEGEMSIVEL	RERLALLKEN	QRRKEEEKRD	QIIQGKHTKS	QELQNMVEQI	SLCRAAMGRS	AALRWEEKKA
570	580	590	600	610	620	630	640
LAAAPAAPSQ	DERVQQLRRR	ISERAAERSR	QAALLHVSAP	RTARPKPRAQ	LEAQHWLELE	RSRERRLQAL	QQGGSGPGPA
650							
RRLEAA							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
814	1	965.4561	-29.93	2	39.0	11.3	1	2-17	M.AYYGKCIETVIEQLDK.F	Carbamidomethyl: 6

Detailed Protein Report

Protein 947: **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 948: CD109 antigen isoform 2 precursor [Homo sapiens]

Accession:	gi|227430301	**Score:**	11.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	159.6
Database Date:	2015-11-30	**pI:**	5.5
		Sequence Coverage [%]:	1.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MQGPPLLTAA	HLLCVCTAAL	AVAPGPRFLV	TAPGIIRPGG	NVTIGVELLE	HCPSQVTVKA	ELLKTASNLT	VSVLEAEGVF
90	100	110	120	130	140	150	160
EKGSFKTLTL	PSLPLNSADE	IYELRVTGRT	QDEILFSNST	RLSFETKRIS	VFIQTDKALY	KPKQEVKFRI	VTLFSDFKPY
170	180	190	200	210	220	230	240
KTSLNILIKD	PKSNLIQQWL	SQQSDLGVIS	KTFQLSSHPI	LGDWSIQVQV	NDQTYYQSFQ	VSEYVLPKFE	VTLQTPLYCS
250	260	270	280	290	300	310	320
MNSKHLNGTI	TAKYTYGKPV	KGDVTLTFLP	LSFWGKKKNI	TKTFKINGSA	NFSFNDEEMK	NVMDSSNGLS	EYLDLSSPGP
330	340	350	360	370	380	390	400
VEILTTVTES	VTGISRNVST	NVFFKQHDYI	IEFFDYTTVL	KPSLNFTATV	KVTRADGNQL	TLEERRNNVV	ITVTQRNYTE
410	420	430	440	450	460	470	480
YWSGSNSGNQ	KMEAVQKINY	TVPQSGTFKI	EFPILEDSSE	LQLKAYFLGS	KSSMAVHSLF	KSPSKTYIQL	KTRDENIKVG
490	500	510	520	530	540	550	560
SPFELVVSGN	KRLKELSYMV	VSRGQLVAVG	KQNSTMFSLT	PENSWTPKAC	VIVYYIEDDG	EIISDVLKIP	VQLVFKNKIK
570	580	590	600	610	620	630	640
LYWSKVKAEP	SEKVSLRISV	TQPDSIVGIV	AVDKSVNLMN	ASNDITMENV	VHELELYNTG	YYLGMFMNSF	AVFQECGLWV
650	660	670	680	690	700	710	720
LTDANLTKDY	IDGVYDNAEY	AERFMEENEG	HIVDIHDFSL	GSSPHVRKHF	PETWIWLDTN	MGYRIYQEFE	VTVPDSITSW
730	740	750	760	770	780	790	800
VATGFVISED	LGLGLTTTPV	ELQAFQPFFI	FLNLPYSVIR	GEEFALEITI	FNYLKDATEV	KVIIEKSDKF	DILMTSNEIN
810	820	830	840	850	860	870	880
ATGHQQTLLV	PSEDGATVLF	PIRPTHLGEI	PITVTALSPT	ASDAVTQMIL	VKAEGIEKSY	SQSILLDLTD	NRLQSTLKTL
890	900	910	920	930	940	950	960
SFSFPPNTVT	GSERVQITAI	GDVLGPSING	LASLIRMPYG	CGEQNMINFA	PNIYILDYLT	KKKQLTDNLK	EKALSFMRQG
970	980	990	1000	1010	1020	1030	1040
YQRELLYQRE	DGSFSAFGNY	DPSGSTWLSA	FVLRCFLEAD	PYIDIDQNVL	HRTYTWLKGH	QKSNGEFWDP	GRVIHSELQG
1050	1060	1070	1080	1090	1100	1110	1120
GNKSPVTLTA	YIVTSLLGYR	KYQPNIDVQE	SIHFLESEFS	RGISDNYTLA	LITYALSSVG	SPKAKEALNM	LTWRAEQEGG
1130	1140	1150	1160	1170	1180	1190	1200
MQFWVSSESK	LSDSWQPRSL	DIEVAAYALL	SHFLQFQTSE	GIPIMRWLSR	QRNSLGGFAS	TQDTTVALKA	LSEFAALMNT
1210	1220	1230	1240	1250	1260	1270	1280
ERTNIQVTVT	GPSSPSPLAV	VQPTAVNISA	NGFGFAICQL	NVVYNVKASG	SSRRRRSIQN	QEAFDLDVAV	KENKDDLNHV
1290	1300	1310	1320	1330	1340	1350	1360
DLNVCTSFSG	PGRSGMALME	VNLLSGFMVP	SEAISLSETV	KKVEYDHGKL	NLYLDSVNET	QFCVNIPAVR	NFKVSNTQDA
1370	1380	1390	1400	1410	1420	1430	
SVSIVDYYEP	RRQAVRSYNS	EVKLSSCDLC	SDVQGCRPCE	DGASGSHHHS	SVIFIFCFKL	LYFMELWL	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1508	3	705.9840	-55.85	3	47.2	11.3	1	110-127	R.TQDEILFSNSTRLSFETK.R	

Detailed Protein Report

Protein 949: 39S ribosomal protein L18, mitochondrial [Homo sapiens]

Accession:	gi|21265080	**Score:**	11.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	20.6
Database Date:	2015-11-30	**pI:**	10.6
		Sequence Coverage [%]:	5.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MALRSRFWGL	FSVCRNPGCR	FAALSTSSEP	AAKPEVDPVE	NEAVAPEFTN	RNPRNLELLS	VARKERGWRT	VFPSREFWHR
90	100	110	120	130	140	150	160
LRVIRTQHHV	EALVEHQNGK	VVVSASTREW	AIKKHLYSTR	NVVACESIGR	VLAQRCLEAG	INFMVYQPTP	WEAASDSMKR
170	180	190					
LQSAMTEGGV	VLREPQRIYE						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
373	1	524.1226	-273.97	2	33.3	11.3	0	121-130	R.NVVACESIGR.V	

Detailed Protein Report

Protein 950: 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 951: **PREDICTED: mitochondrial sodium/hydrogen exchanger 9B2 isoform X6 [Homo sapiens]**

Accession:	gi|578808778	**Score:**	11.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	45.1
Database Date:	2015-11-30	**pI:**	8.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.1
		No. of unique Peptides:	1

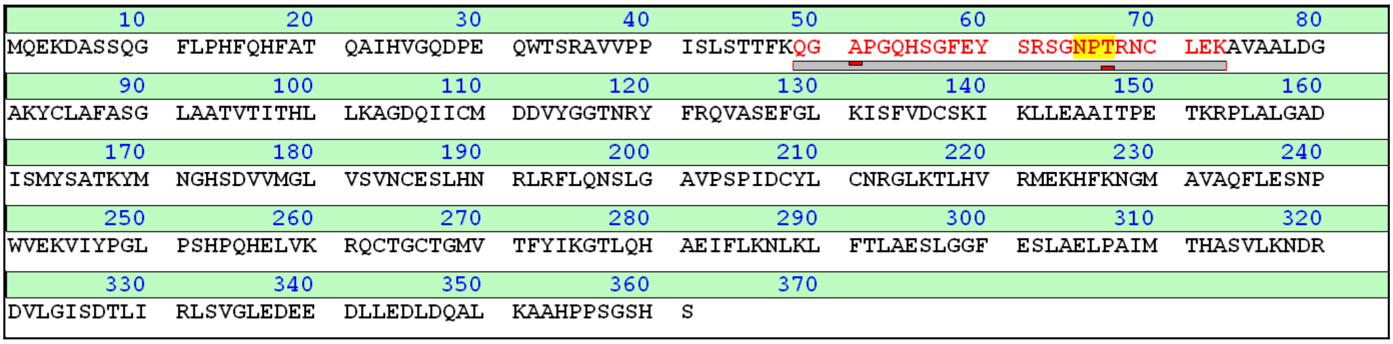
10	20	30	40	50	60	70	80
MGDEDKRITY	EDSEPSTGMN	YTPSMHQEAQ	EETVMKLKGI	DANEPTEGSI	LLKSSEKKLQ	ETPTEANHVQ	RLRQMLACPP
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
HGLLDRVITN	GMLLAGFLIR	NIPVINDNVQ	IKHKWSSSLR	SIALSIILVR	AGLGLDSKAL	KKLKGVCVRL	SMGPCIVEAC
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
TSALLAHYLL	GLPWQWGFIL	GFVLGAVSPA	VVVPSMLLLQ	GGGYGVEKGV	PTLLMAAGSF	DDILAITGFN	TCLGIAFSTG
250	**260**	**270**	**280**	**290**	**300**	**310**	**320**
STVFNVLRGV	LEVVIGVATG	SVLGFFIQYF	PSRDQDKLVC	KRTFLVLGLS	VLAVFSSVHF	GFPGSGGLCT	LVMAFLAGMG
330	**340**	**350**	**360**	**370**	**380**	**390**	**400**
WTSEKAEVEK	IIAVAWDIFQ	PLLFGLIGAE	VSIASLRPET	VGCNRICGFG	HSKVTWRETI	RRLWNGCVDS	GIFVHPHHSP
410	**420**						
NWKSAYWFTG	PQASAES						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2407	1	754.4199	54.17	2	58.4	11.3	0	74-86	R.QMLACPPHGLLDR.V	Carbamidomethyl: 5

Detailed Protein Report

Protein 952: 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 953: PREDICTED: zinc finger protein 513 isoform X2 [Homo sapiens]

Accession: gi|530367236

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Modification(s): Carbamidomethyl

Score: 11.2

MW [kDa]: 40.2

pI: 10.9

Sequence Coverage [%]: 5.1

No. of unique Peptides: 1

```
        10         20         30         40         50         60         70         80
MQTHSGEKPF RCGRCPYASA QLVNLTRHTR THTGEKPYRC PHCPFACSSL GNLRRHQRTH AGPPTPPCPT CGFRCCTPRP

        90        100        110        120        130        140        150        160
ARPPSPTEQE GAVPRRPEDA LLLPDLSLHV PPGGASFLPD CGQLRGEGEG LCGTGSEPLP ELLFPWTCRG CGQELEEGEG

       170        180        190        200        210        220        230        240
SRLGAAMCGR CMRGEAGGGA SGGPQGPSDK GFACSLCPFA THYPNHLARH MKTHSGEKPF RCARCPYASA HLDNLKRHQR

       250        260        270        280        290        300        310        320
VHTGEKPYKC PLCPYACGNL ANLKRHGRIH SGDKPFRCSL CNYSCNQSMN LKRHMLRHTG EKPFRCATCA YTTGHWDNYK

       330        340        350        360        370        380
RHQKVHGHGG AGGPGLSASE GWAPPHSPPS VLSSRGPPAL GTAGSRAVHT DSS
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1243	1	715.1105	125.80	3	43.8	11.2	2	250-268	K.CPLCPYACGNLANLKRHGR.I	Carbamidomethyl: 8

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Detailed Protein Report

Protein 954: 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

WD:WU **Median:** 3.36 **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		WD:WU 3.36

Detailed Protein Report

Protein 955: PREDICTED: peroxisomal biogenesis factor 5 isoform X9 [Homo sapiens]

Accession:	gi|578822993	**Score:**	11.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	63.0
Database Date:	2015-11-30	**pI:**	4.2
		Sequence Coverage [%]:	2.3
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 1.14 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MDDLLAEMQQ IEQSNFRQAP QRAPGVADLA LSENWAQEFL AAGDAVDVTQ DYNETDWSQE FISEVTDPLS VSPARWAEEY
        90        100        110        120        130        140        150        160
LEQSEEKLWL GEPEGTATDR WYDEYHPEED LQHTASDFVA KVDDPKLANS EWPVCVSVPQ FLKFVRQIGE GQVSLESGAG
       170        180        190        200        210        220        230        240
SGRAQAEQWA AEFIQQQGTS DAWVDQFTRP VNTSALDMEF ERAKSAIESD VDFWDKLQAE LEEMAKRDAE AHPWLSDYDD
       250        260        270        280        290        300        310        320
LTSATYDKGY QFEEENPLRD HPQPFEEGLR RLQEGDLPNA VLLFEAAVQQ DPKHMEAWQY LGTTQAENEQ ELLAISALRR
       330        340        350        360        370        380        390        400
CLELKPDNQT ALMALAVSFT NESLQRQACE TLRDWLRYTP AYAHLVTPAE EGAGGAGLGP SKRILGSLLS DSLFLEVKEL
       410        420        430        440        450        460        470        480
FLAAVRLDPT SIDPDVQCGL GVLFNLSGEY DKAVDCFTAA LSVRPNDYLL WNKLGATLAN GNQSEEAVAA YRRALELQPG
       490        500        510        520        530        540        550        560
YIRSRYNLGI SCINLGAHRE AVEHFLEALN MQRKSRGPRG EGGAMSENIW STLRLALSML GQSDAYGAAD ARDLSTLLTM
       570
FGLPQ
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
438	1	718.3578	-29.07	2	34.0	11.2	0	553-565	R.DLSTLLTMFGLPQ.-		WD:WU 1.14

Detailed Protein Report

Protein 956: 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 957: 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 958: **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 959: 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

Quantitation

WD:WU **Median:** 0.74 **CV:** 0.00 % **No. of 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	Ratios
1468	1	620.0709	76.55	3	47.1	11.2	2	94-108	K.WKEQNRAKPVHLVPR.R		WD:WU 0.74

Detailed Protein Report

Protein 960: PREDICTED: centriolar coiled-coil protein of 110 kDa isoform X4 [Homo sapiens]

Accession: gi|578828704
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 11.2
MW [kDa]: 109.0
pI: 9.3
Sequence Coverage [%]: 1.2
No. of unique Peptides: 1

Quantitation

WD:WU **Median:** 0.18 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MEEYEKFCEK	SLARIQEASL	STESFLPAQS	ESISLIRFHG	VAILSPLLNI	EKRKEMQQEK	QKALDVEARK	QVNRKKALLT
90	100	110	120	130	140	150	160
RVQEILDNVQ	VRKAPNASDF	DQWEMETVYS	NSEVRNLNVP	ATFPNSFPSH	TEHSTAAKLD	KIAGILPLDN	EDQCKTDGID
170	180	190	200	210	220	230	240
LARDSEGFNS	PKQCDSSNIS	HVENEAFPKT	SSATPQETLI	SDGPFSVNEQ	QDLPLLAEVI	PDPYVMSLQN	LMKKSKEYIE
250	260	270	280	290	300	310	320
REQSRRSLRG	SINRIVNESH	LDKEHDAVEV	ADCVKEKGQL	TGKHCVSVIP	DKPSLNKSNV	LLQGASTQAS	SMSMPVLASF
330	340	350	360	370	380	390	400
SKVDIPIRTG	HPTVLESNSD	FKVIPTFVTE	NNVIKSLTGS	YAKLPSPEPS	MSPKMHRRRS	RTSSACHILI	NNPINACELS
410	420	430	440	450	460	470	480
PKGKEQAMDL	IIQDTDENTN	VPEIMPKLPT	DLAGVCSSKV	YVGKNTSEVK	EDVVLGKSNQ	VCQSSGNHLE	NKVTHGLVTV
490	500	510	520	530	540	550	560
EGQLTSDERG	AHIMNSTCAA	MPKLHEPYAS	SQCIASPNFG	TVSGLKPASM	LEKNCSLQTE	LNKSYDVKNP	SPLLMQNQNT
570	580	590	600	610	620	630	640
RQQMDTPMVS	CGNEQFLDNS	FEKVKRRLDL	DIDGLQKENC	PYVITSGITE	QERQHLPEKR	YPKGSGFVNK	NKMLGTSSKE
650	660	670	680	690	700	710	720
SEELLKSKML	AFEEMRKRLE	EQHAQQLSLL	IAEQEREQER	LQKEIEEQEK	MLKEKKAMTA	EASELDINNA	VELEWRKISD
730	740	750	760	770	780	790	800
SSLLETMLSQ	ADSLHTSNSN	SSGFTNSAMQ	YSFVSANEAP	FYLWGSSTSG	LTKLSVTRPF	GRAKTRWSQV	FSLEIQAKFN
810	820	830	840	850	860	870	880
KITAVAKGFL	TRRLMQTDKL	KQLRQTVKDT	MEFIRSFQSE	APLKRGIVSA	QDASLQERVL	AQLRAALYGI	HDIFFVMDAA
890	900	910	920	930	940	950	960
ERMSILHHDR	EVRKEKMLRQ	MDKMKSPRVA	LSAATQKSLD	RKKYMKAAEM	GMPNKKFLVK	QNPSETRSIC	RKNPKKAAKC
970	980						
CDNLRRQHSL	G						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2559	1	693.6709	-206.81	2	60.3	11.2	1	924-935	K.YMKAAEMGMPNK.K	Oxidation: 7	WD:WU 0.18

Detailed Protein Report

Protein 961: **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 962: liprin-beta-1 isoform 3 [Homo sapiens]

Accession:	gi|312032471	**Score:**	11.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	96.9
Database Date:	2015-11-30	**pI:**	6.1
		Sequence Coverage [%]:	1.0
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 1.45 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MLQQELLSRT	SLETQKLDLM	AEISNLKLKL	TAVEKDRLDY	EDKFRDTEGL	IQEINDLRLK	VSEMDSERLQ	YEKKLKSTKS
90	100	110	120	130	140	150	160
LMAKLSSMKI	KVGQMQYEKQ	RMEQKWESLK	DELASLKEQL	EEKESEVKRL	QEKLVCKMKG	EGVEIVDRDI	EVQKMKKAVE
170	180	190	200	210	220	230	240
SLMAANEEKD	RKIEDLRQCL	NRYKKMQDTV	VLAQGKDGEY	EELLNSSSIS	SLLDAQGFSD	LEKSPSPTPV	MGSPSCDPFN
250	260	270	280	290	300	310	320
TSVPEEFHTT	ILQVSIPSLL	PATVSMETSE	KSKLTPKPET	SFEENDGNII	LGATVDTQLC	DKLLTSSLQK	SSSLGNLKKE
330	340	350	360	370	380	390	400
TSDGEKETIQ	KTSEDRAPAE	SRPFGTLPPR	PPGQDTSMDD	NPFGTRKVRS	SFGRGFFKIK	SNKRTASAPN	LAETEKETAE
410	420	430	440	450	460	470	480
HLDLAGASSR	PKDSQRNSPF	QIPPPSPDSK	KKSRGIMKLF	GKLRRSQSTT	FNPDDMSEPE	FKRGGTRATA	GPRLGWSRDL
490	500	510	520	530	540	550	560
GQSNSDLDMP	FAKWTKEQVC	NWLMEQGLGS	YLNSGKHWIA	SGQTLLQASQ	QDLEKELGIK	HSLHRKKLQL	ALQALGSEEE
570	580	590	600	610	620	630	640
TNHGKLDFNW	VTRWLDDIGL	PQYKTQFDEG	RVDGRMLHYM	TVDDLLSLKV	VSVLHHLSIK	RAIQVLRINN	FEPNCLRRRP
650	660	670	680	690	700	710	720
SDENTIAPSE	VQKWTNHRVM	EWLRSVDLAE	YAPNLRGSGV	HGGLMVLEPR	FNVETMAQLL	NIPPNKTLLR	RHLATHFNLL
730	740	750	760	770	780	790	800
IGAEAQHQKR	DAMELPDYVL	LTATAKVKPK	KLAFSNFGNL	RKKKQEDGEE	YVCPMELGQA	SGSASKKGFK	PGLDMRLYEE
810	820	830	840	850	860		
DDLDRLEQME	DSEGTVRQIG	AFSEGINNLT	HMLKEDDMFK	DFAARSPSAS	ITDEDSNV		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
901	1	559.2818	-42.07	2	39.7	11.2	0	1-9	-.MLQQELLSR.T		WD:WU	1.45

Detailed Protein Report

Protein 963: **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 964: keratin-associated protein 5-1 [Homo sapiens]

Accession:	gi|54400749	**Score:**	11.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	24.2
Database Date:	2015-11-30	**pI:**	12.2
Modification(s):	Carbamidomethyl	**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 965: PREDICTED: T-lymphoma invasion and metastasis-inducing protein 1 isoform X4 [Homo sapiens]

Accession:	gi|530419050	**Score:**	11.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	161.7
Database Date:	2015-11-30	**pI:**	6.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.1
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 0.63 **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	WD:WU 0.63

Detailed Protein Report

Protein 966: PREDICTED: zinc finger protein 844 isoform X3 [Homo sapiens]

Accession:	gi|578833194	**Score:**	11.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	58.8
Database Date:	2015-11-30	**pI:**	10.4
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	3.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MQEKAHTGEK	LYDCKECGKT	FISHSSIQRH	MIMHNGDGTY	KCKFCGKACP	CLSIYLIHER	VHTGEKPYKC	KQCGKAFSYS
90	100	110	120	130	140	150	160
TSLQIHERTH	TGEKPYECKE	CGKAFGSPNS	LYEHRRTHTG	EKPYECKQCG	KAFRWFHSFQ	IHERTHSEEK	AYECTKCGKA
170	180	190	200	210	220	230	240
FKCPSYLCRH	EVTHSGKKPC	ECKQCGKALS	YLNFQRHMKM	HTRMRPYKCK	TVEKPLILPV	RFEDMKELTL	ERNLMNASTV
250	260	270	280	290	300	310	320
VKPSIVPVPF	TIMKGLTLER	NPMNVSSVVK	PSFLPLPFDI	MKGLTLERNR	MSVSNVGKPS	DLPHTFKCME	GLTLKRNPMN
330	340	350	360	370	380	390	400
VSSVVKPSFF	PLPFDIMKGL	TLERNPMSVS	NVGKPSHLPH	TFKCMKGLTL	ESNCMNLNNV	KKPLDLSETF	KFMKRHTLER
410	420	430	440	450	460	470	480
NPIRNMEKHS	TISLPFKYMQ	QCTEDRMPMN	VKSVTKHSYL	PRSFEYMQEH	TLERNPMNVR	NAEKRSIIFL	LCVYTKGCTL
490	500	510					
ERNHINVRIV	GKHSVCLVPF	VDIKGLTLE					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
85	1	695.6045	-76.90	3	30.0	11.1	1	364-381	K.CMKGLTLESNCMNLNNVK.K	Carbamidomethyl: 11; Oxidation: 12

Detailed Protein Report

Protein 967: **thrombospondin-type laminin G domain and EAR repeat-containing protein isoform 1 precursor [Homo sapiens]**

Accession:	gi|22001420	**Score:**	11.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	74.9
Database Date:	2015-11-30	**pI:**	6.0
		Sequence Coverage [%]:	1.5
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 1.37 **CV:** 0.00 % **No. of 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	Ratios	
1797	1	1011.7680	171.47	1	51.1	11.1	0	58-67	R.GLQLSVAAPR.T		WD:WU	1.37

Detailed Protein Report

Protein 968: **PREDICTED: centrosomal protein of 120 kDa isoform X2 [Homo sapiens]**

Accession:	gi|530379724	**Score:**	11.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	107.6
Database Date:	2015-11-30	**pI:**	5.7
		Sequence Coverage [%]:	2.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MVSKSDQLLI	VVSILEGRHF	PKRPKHMLVV	EAKFDGEQLA	TDPVDHTDQP	EFATELAWEI	DRKALHQHRL	QRTPIKLQCF
90	100	110	120	130	140	150	160
ALDPVTSAKE	TIGYIVLDLR	TAQETKQAPK	WYQLLSNKYT	KFKSEIQISI	ALETDTKPPV	DSFKAKGAPP	RDGKVPAILA
170	180	190	200	210	220	230	240
GLDPRDIVAV	LNEEGGYHQI	GPAEYCTDSF	IMSVTIAFAT	QLEQLIPCTM	KLPERQPEFF	FYYSLLGNDV	TNEPFNDLIN
250	260	270	280	290	300	310	320
PNFEPERASV	RIRSSVEILR	VYLALQSKLQ	IHLCCGDQSL	GSTEIPLTGL	LKKGSTEINQ	HPVTVEGAFT	LDPPNRAKQK
330	340	350	360	370	380	390	400
LAPIPVELAP	TVGVSVALQR	EGIDSQSPPT	KDDATESEVE	SLQYDKDTKP	NPKASSSVPA	SLAQLVTTSN	ASEVASGQKI
410	420	430	440	450	460	470	480
AVPATSHHFC	FSIDLRSIHA	LEIGFPINCI	LRYSYPFFGS	AAPIMTNPPV	EVRKNMEVFL	PQSYCAFDFA	TMPHQLQDTF
490	500	510	520	530	540	550	560
LRIPLLVELW	HKDKMSKDLL	LGIARIQLSN	ILSSEKTRFL	GSNGEQCWRQ	TYSESVPVIA	AQGSNNRIAD	LSYTVTLEDY
570	580	590	600	610	620	630	640
GLVKMREIFI	SDSSQGVSAV	QQKPSSLPPA	PCPSEIQTEP	RETLEYKAAL	ELEMWKEMQE	DIFENQLKQK	ELAHMQALAE
650	660	670	680	690	700	710	720
EWKKRDRERE	SLVKKKVAEY	TILEGKLQKT	LIDLEKREQQ	LASVESELQR	EKKELQSERQ	RNLQELQDSI	RRAKEDCIHQ
730	740	750	760	770	780	790	800
VELERLKIKQ	LEEDKHRLQQ	QLNDAENKYK	ILEKEFQQFK	DQQNNKPEIR	LQSEINLLTL	EKVELERKLE	SATKSKLHYK
810	820	830	840	850	860	870	880
QQWGRALKEL	ARLKQREQES	QMARLKKQQE	ELEQMRLRYL	AAEEKDTVKT	ERQELLDIRN	ELNRLRQQEQ	KQYQDSTEIA
890	900	910	920	930	940	950	
SGKKDGPHGS	VLEEGLDDYL	TRLIEERDTL	MRTGVYNHED	RIISELDRQI	REILAKSNAS	N	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
605	1	1106.2245	18.50	3	36.0	11.1	2	617-643	K.EMQEDIFENQLKQKELAHMQALAEEWK.K	

Detailed Protein Report

Protein 969: **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

WD:WU **Median:** 0.78 **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		WD:WU 0.78

Detailed Protein Report

Protein 970: **nicotinate-nucleotide pyrophosphorylase [carboxylating] precursor [Homo sapiens]**

Accession:	gi|45269149	**Score:**	11.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	30.8
Database Date:	2015-11-30	**pI:**	5.8
		Sequence Coverage [%]:	5.4
		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 971: 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 972: neurogenic differentiation factor 2 [Homo sapiens]

Accession:	gi|98986461	**Score:**	11.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	41.3
Database Date:	2015-11-30	**pI:**	6.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	5.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLTRLFSEPG	LLSDVPKFAS	WGDGEDDEPR	SDKGDAPPPP	PPAPGPGAPG	PARAAKPVPL	RGEEGTEATL	AEVKEEGELG
90	100	110	120	130	140	150	160
GEEEEEEEEE	EGLDEAEGER	PKKRGPKKRK	MTKARLERSK	LRRQKANARE	RNRMHDLNAA	LDNLRKVVPC	YSKTQKLSKI
170	180	190	200	210	220	230	240
ETLRLAKNYI	WALSEILRSG	KRPDLVSYVQ	TLCKGLSQPT	TNLVAGCLQL	NSRNFLTEQG	ADGAGRFHGS	GGPFAMHPYP
250	260	270	280	290	300	310	320
YPCSRLAGAQ	CQAAGGLGGG	AAHALRTHGY	CAAYETLYAA	AGGGGASPDY	NSSEYEGPLS	PPLCLNGNFS	LKQDSSPDHE
330	340	350	360	370	380	390	
KSYHYSMHYS	ALPGSRPTGH	GLVFGSSAVR	GGVHSENLLS	YDMHLHHDRG	PMYEELNAFF	HN	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
276	1	636.2276	-156.14	3	32.2	11.1	0	246-266	R.LAGAQCQAAGGLGGGAAHALR.T	Carbamidomethyl: 6

Detailed Protein Report

Protein 973: protein shisa-7 precursor [Homo sapiens]

Accession:	gi|223633890	**Score:**	11.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	56.2
Database Date:	2015-11-30	**pI:**	11.1
		Sequence Coverage [%]:	3.5
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 0.89 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MPALLLLVLL	ASSAGQARAR	PSNATSAEPA	GPLPALLAHL	RRLTGALTGG	GGAASPGANG	TRTGPAGGAG	AAARAPPPAE
90	100	110	120	130	140	150	160
LCHGYYDVMG	QYDATFNCST	GSYRFCCGTC	HYRFCCEHRH	MRLAQASCSN	YDTPRWATTP	PPLAGGAGGA	GGAGGGPGPG
170	180	190	200	210	220	230	240
QAGWLEGGRT	GGAGGRGGEG	PGGSTAYVVC	GVISFALAVG	VGAKVAFSKA	SRAPRAHRDI	NVPRALVDIL	RHQAGPGTRP
250	260	270	280	290	300	310	320
DRARSSSLTP	GIGGPDSMPP	RTPKNLYNTV	KTPNLDWRAL	PPPSPSLHYS	TLSCSRSFHN	LSHLPPSYEA	AVKSELNRYS
330	340	350	360	370	380	390	400
SLKRLAEKDL	DEAYLKRRPL	ELPRGTLPLH	ALRRPGTGGG	YRMEAWGGPE	ELGLAPAPNP	RRVMSQEHLL	GDGGRSRYEF
410	420	430	440	450	460	470	480
TLPRARLVSQ	EHLLLSSPEA	LRQSREHLLS	PPRSPALPPD	PTARASLAAS	HSNLLLGPGG	PPTPLRGLPP	PSSLHAHHHH
490	500	510	520	530	540		
ALHGSPQPAW	MSDAGGGGGT	LARRPPFQRQ	GTLEQLQFIP	GHHLPQHLRT	ASKNEVTV		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2765	1	941.9760	0.36	2	63.1	11.1	1	243-261	R.ARSSSLTPGIGGPDSMPPR.T		WD:WU 0.89

Detailed Protein Report

Protein 974: **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

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        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	

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Detailed Protein Report

Protein 975: 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	

BRUKER

Detailed Protein Report

Protein 976: PREDICTED: V(D)J recombination-activating protein 1 isoform X1 [Homo sapiens]

Accession:	gi|530395605	**Score:**	11.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	119.0
Database Date:	2015-11-30	**pI:**	9.8
		Sequence Coverage [%]:	1.1
		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 977: receptor-type tyrosine-protein kinase FLT3 [Homo sapiens]

Accession:	gi|121114304	**Score:**	11.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	112.8
Database Date:	2015-11-30	**pI:**	5.4
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPALARDGGQ	LPLLVVFSAM	IFGTITNQDL	PVIKCVLINH	KNNDSSVGKS	SSYPMVSESP	EDLGCALRPQ	SSGTVYEAAA
90	100	110	120	130	140	150	160
VEVDVSASIT	LQVLVDAPGN	ISCLWVFKHS	SLNCQPHFDL	QNRGVVSMVI	LKMTETQAGE	YLLFIQSEAT	NYTILFTVSI
170	180	190	200	210	220	230	240
RNTLLYTLRR	PYFRKMENQD	ALVCISESVP	EPIVEWVLCD	SQGESCKEES	PAVVKKEEKV	LHELFGTDIR	CCARNELGRE
250	260	270	280	290	300	310	320
CTRLFTIDLN	QTPQTTLPQL	FLKVGEPLWI	RCKAVHVNHG	FGLTWELENK	ALEEGNYFEM	STYSTNRTMI	RILFAFVSSV
330	340	350	360	370	380	390	400
ARNDTGYYTC	SSSKHPSQSA	LVTIVEKGFI	NATNSSEDYE	IDQYEEFCFS	VRFKAYPQIR	CTWTFSRKSF	PCEQKGLDNG
410	420	430	440	450	460	470	480
YSISKFCNHK	HQPGEYIFHA	ENDDAQFTKM	FTLNIRRKPQ	VLAEASASQA	SCFSDGYPLP	SWTWKKCSDK	SPNCTEEITE
490	500	510	520	530	540	550	560
GVWNRKANRK	VFGQWVSSST	LNMSEAIKGF	LVKCCAYNSL	GTSCETILLN	SPGPFPFIQD	NISFYATIGV	CLLFIVVLTL
570	580	590	600	610	620	630	640
LICHKYKKQF	RYESQLQMVQ	VTGSSDNEYF	YVDFREYEYD	LKWEFPRENL	EFGKVLGSGA	FGKVMNATAY	GISKTGVSIQ
650	660	670	680	690	700	710	720
VAVKMLKEKA	DSSEREALMS	ELKMMTQLGS	HENIVNLLGA	CTLSGPIYLI	FEYCCYGDLL	NYLRSKREKF	HRTWTEIFKE
730	740	750	760	770	780	790	800
HNFSFYPTFQ	SHPNSSMPGS	REVQIHPDSD	QISGLHGNSF	HSEDEIEYEN	QKRLEEEEDL	NVLTFEDLLC	FAYQVAKGME
810	820	830	840	850	860	870	880
FLEFKSCVHR	DLAARNVLVT	HGKVVKICDF	GLARDIMSDS	NYVVRGNARL	PVKWMAPESL	FEGIYTIKSD	VWSYGILLWE
890	900	910	920	930	940	950	960
IFSLGVNPYP	GIPVDANFYK	LIQNGFKMDQ	PFYATEEIYI	IMQSCWAFDS	RKRPSFPNLT	SFLGCQLADA	EEAMYQNVDG
970	980	990	1000				
RVSECPHTYQ	NRRPFSREMD	LGLLSPQAQV	EDS				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1473	1	655.3406	24.71	2	46.8	11.1	2	645-655	K.MLKEKADSSER.E	Oxidation: 1

Detailed Protein Report

Protein 978: 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 979: **epidermal growth factor receptor substrate 15-like 1 isoform 4 [Homo sapiens]**

Accession:	gi|385648259	**Score:**	11.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	66.4
Database Date:	2015-11-30	**pI:**	5.0
		Sequence Coverage [%]:	1.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
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 980: **alpha-2,8-sialyltransferase 8F precursor [Homo sapiens]**

Accession:	gi|54234057	**Score:**	11.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	44.8
Database Date:	2015-11-30	**pI:**	9.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	7.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MRPGGALLAL	LASLLLLLLL	RLLWCPADAP	GRARILVEES	REATHGTPAA	LRTLRSPATA	VPRATNSTYL	NEKSLQLTEK
90	100	110	120	130	140	150	160
CKNLQYGIES	FSNKTKGYSE	NDYLQIITDI	QSCPWKRQAE	EYANFRAKLA	SCCDAVQNFV	VSQNNTPVGT	NMSYEVESKK
170	180	190	200	210	220	230	240
EIPIKKNIFH	MFPVSQPFVD	YPYNQCAVVG	NGGILNKSLC	GTEIDKSDFV	FRCNLPPTTG	DVSKDVGSKT	NLVTINPSII
250	260	270	280	290	300	310	320
TLKYGNLKEK	KALFLEDIAT	YGDAFFLLPA	FSFRANTGTS	FKVYYTLEES	KARQKVLFFH	PKYLKDLALF	WRTKGVTAYR
330	340	350	360	370	380	390	400
LSTGLMITSV	AVELCKNVKL	YGFWPFSKTV	EDIPVSHHYY	DNKLPKHGFH	QMPKEYSQIL	QLHMKGILKL	QFSKCEVA

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1694	1	1131.2170	33.19	3	49.5	11.1	0	129-159	K.LASCCDAVQNFVVSQNNTPVGTNMSYEVESK.K	Carbamidomethyl: 4

Detailed Protein Report

Protein 981: **phosphatidylinositol 3,4,5-trisphosphate 3-phosphatase TPTE2 isoform delta [Homo sapiens]**

Accession: gi|213972593

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Score: 11.0

MW [kDa]: 48.4

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 982: 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 983: **PREDICTED: phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic subunit beta isoform isoform X3 [Homo sapiens]**

Accession:	gi|530374778	**Score:**	11.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	121.0
Database Date:	2015-11-30	**pI:**	7.1
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.4
		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
2131	1	899.4303	1.31	2	55.0	11.0	0	292-306	K.MYEQEMIAIEAAINR.N	Oxidation: 6

Detailed Protein Report

Protein 984: PREDICTED: hemicentin-2 isoform X1 [Homo sapiens]

Accession:	gi|578796176	**Score:**	11.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	139.5
Database Date:	2015-11-30	**pI:**	7.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.8
		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 985: 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

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
309	1	646.7814	-69.45	2	33.0	11.0	1	244-254	K.RSHLESSSRPH.-	

Detailed Protein Report

Protein 986: **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 987: **recombining binding protein suppressor of hairless-like protein isoform 2 [Homo sapiens]**

Accession:	gi|527122116	**Score:**	11.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	51.2
Database Date:	2015-11-30	**pI:**	10.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDPAGAADPS	VPPNPLTHLS	LQDRSEMQLQ	SEADRRSLPG	TWTRSSPEHT	TILRGGVRRC	LQQQCEQTVR	ILHAKVAQKS
90	100	110	120	130	140	150	160
YGNEKRFFCP	PPCVYLSGPG	WRVKPGQDQA	HQAGETGPTV	CGYMGLDSAS	GSATETQKLN	FEQQPDSREF	GCAKTLYISD
170	180	190	200	210	220	230	240
ADKRKHFRLV	LRLVLRGGRE	LGTFHSRLIK	VISKPSQKKQ	SLKNTDLCIS	SGSKVSLFNR	LRSQTVSTRY	LSVEDGAFVA
250	260	270	280	290	300	310	320
SARQWAAFTL	HLADGHSAQG	DFPPREGYVR	YGSLVQLVCT	VTGITLPPMI	IRKVAKQCAL	LDVDEPISQL	HKCAFQFPGS
330	340	350	360	370	380	390	400
PPGGGGTYLC	LATEKVVQFQ	ASPCPKEANR	ALLNDSSCWT	IIGTESVEFS	FSTSLACTLE	PVTPVPLIST	LELSGGGDVA
410	420	430	440	450	460	470	480
TLELHGENFH	AGLKVWFGDV	EAETMYRYGV	EPAVPGVRGA	GRGGLLQRLA	LAARSHHNPH	EPGARRRALL	P

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1915	1	655.2467	-63.21	2	52.6	11.0	0	25-35	R.SEMQLQSEADR.R	Oxidation: 3

Detailed Protein Report

Protein 988: 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 989: PREDICTED: solute carrier organic anion transporter family member 2B1 isoform X1 [Homo sapiens]

Accession: gi|578821116
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 11.0
MW [kDa]: 68.1
pI: 9.6
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 990: **PREDICTED: serine/threonine-protein kinase ULK4 isoform X4 [Homo sapiens]**

Accession:	gi|530372727	**Score:**	11.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	100.6
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
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 991: 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 992: protein Jade-1 isoform 2 [Homo sapiens]

Accession:	gi|19923609	**Score:**	11.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	58.3
Database Date:	2015-11-30	**pI:**	5.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.2
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|566006111	refseq_human (refseq_human_20140103.fasta)	protein Jade-1 isoform 2 [Homo sapiens]

10	20	30	40	50	60	70	80
MKRGRLPSSS	EDSDDNGSLS	TTWSQNSRSQ	HRRSSCSRHE	DRKPSEVFRT	DLITAMKLHD	SYQLNPDEYY	VLADPWRQEW
90	100	110	120	130	140	150	160
EKGVQVPVSP	GTIPQPVARV	VSEEKSLMFI	RPKKYIVSSG	SEPPELGYVD	IRTLADSVCR	YDLNDMDAAW	LELTNEEFKE
170	180	190	200	210	220	230	240
MGMPELDEYT	MERVLEEFEQ	RCYDNMNHAI	ETEEGLGIEY	DEDVVCDVCQ	SPDGEDGNEM	VFCDKCNICV	HQACYGILKV
250	260	270	280	290	300	310	320
PEGSWLCRTC	ALGVQPKCLL	CPKKGGAMKP	TRSGTKWVHV	SCALWIPEVS	IGSPEKMEPI	TKVSHIPSSR	WALVCSLCNE
330	340	350	360	370	380	390	400
KFGASIQCSV	KNCRTAFHVT	CAFDRGLEMK	TILAENDEVK	FKSYCPKHSS	HRKPEESLGK	GAAQENGAPE	CSPRNPLEPF
410	420	430	440	450	460	470	480
ASLEQNREEA	HRVSVRKQKL	QQLEDEFYTF	VNLLDVARAL	RLPEEVVDFL	YQYWKLKRKV	NFNKPLITPK	KDEEDNLAKR
490	500	510					
EQDVLFRRLQ	LFTHLRQDLE	RVMIDTDTL					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
565	1	661.8568	62.79	2	35.5	11.0	0	311-321	R.WALVCSLCNEK.F	Carbamidomethyl: 8

Detailed Protein Report

Protein 993: **leucine-rich repeat and IQ domain-containing protein 4 [Homo sapiens]**

Accession:	gi|122937315	**Score:**	11.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	63.9
Database Date:	2015-11-30	**pI:**	9.3
		Sequence Coverage [%]:	2.0
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578807342	refseq_human (refseq_human_20140103.fasta)	PREDICTED: leucine-rich repeat and IQ domain-containing protein 4 isoform X2 [Homo sapiens]
gi|530374547	refseq_human (refseq_human_20140103.fasta)	PREDICTED: leucine-rich repeat and IQ domain-containing protein 4 isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MSKDIKSVEH	SPKIHQRNDP	QHVNDRTFFI	DASNQSLTAI	PLEIFTFTEL	EEVHLENNQI	EEIPQEIQRL	KNIRVLYLDK
90	100	110	120	130	140	150	160
NNLRSLCPAL	GLLSSLESLD	LSYNPIFSSS	LVVVSFLHAL	RELRLYQTDL	KEIPVVIFKN	LHHLELLGLT	GNHLKCLPKE
170	180	190	200	210	220	230	240
IVNQTKLREI	YLKRNQFEVF	PQELCVLYTL	EIIDLDENKI	GAIPEEIGHL	TGLQKFYMAS	NNLPVLPASL	CQCSQLSVLD
250	260	270	280	290	300	310	320
LSHNLLHSIP	KSFAELRKMT	EIGLSGNRLE	KVPRLICRWT	SLHLLYLGNT	GLHRLRGSFR	CLVNLRFLDL	SQNHLHHCPL
330	340	350	360	370	380	390	400
QICALKNLEV	LGLDDNKIGQ	LPSELGSLSK	LKILGLTGNE	FLSFPEEVLS	LASLEKLYIG	QDQGFKLTYV	PEHIRKLQSL
410	420	430	440	450	460	470	480
KELYIENNHL	EYLPVSLGSM	PNLEVLDCRH	NLLKQLPDAI	CQAQALKELR	LEDNLLTHLP	ENLDSLVNLK	VLTLMDNPME
490	500	510	520	530	540	550	560
EPPKEVCAEG	NEAIWKYLKE	NRNRNIMATK	IQAWWRGTMV	QRGFGKFGEL	LKPQKKGKTS	PKDKKGKKDV	KGKPGKGKKK
570							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2663	1	659.3506	-6.24	2	61.6	11.0	1	7-17	K.SVEHSPKIHQR.N	

Detailed Protein Report

Protein 994: 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 995: 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 996: **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

WD:WU **Median:** 0.73 **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		WD:WU 0.73

Detailed Protein Report

Protein 997: 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 998: 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 999: PREDICTED: phosphatidate phosphatase PPAPDC1A isoform X5 [Homo sapiens]

Accession: gi|578819062
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 10.9
MW [kDa]: 21.5
pI: 9.8
Sequence Coverage [%]: 3.6
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MRELAIEIGV	RALLFGVFVF	TEFLDPFQRV	IQPEEIWLYK	NPLVQSDNIP	TRLMFAISFL	TPLAVICVVK	IIRRTDKTEI
90	100	110	120	130	140	150	160
KEAFLAVSLA	LALNGVCTNT	IKLIVGSCLF	GPWLHDVLLG	GQAALLHREW	AGKELAALCC	HPALVLRHDD	CPVPHVRLQA
170	180	190	200				
SLARFLCGWS	HRPHFCIHLL	QTALSSSGQH	SLP				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1787	1	901.3035	-281.98	1	50.7	10.9	2	71-77	K.IIRRTDK.T	

Detailed Protein Report

Protein 1000: **neurensin-1 [Homo sapiens]**

Accession: gi|189217874
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 10.9
MW [kDa]: 21.5
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 1001: 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 1002: syntaphilin [Homo sapiens]

Accession:	gi|38202246	**Score:**	10.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	53.5
Database Date:	2015-11-30	**pI:**	5.3
		Sequence Coverage [%]:	3.6
		No. of unique Peptides:	1

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	

BRUKER

Detailed Protein Report

Protein 1003: ubiquitin-like protein 7 isoform a [Homo sapiens]

Accession:	gi|14249682	**Score:**	10.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	40.5
Database Date:	2015-11-30	**pI:**	4.7
		Sequence Coverage [%]:	5.3
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|557948089	refseq_human (refseq_human_20140103.fasta)	ubiquitin-like protein 7 isoform a [Homo sapiens]
gi|557947994	refseq_human (refseq_human_20140103.fasta)	ubiquitin-like protein 7 isoform a [Homo sapiens]
gi|41152107	refseq_human (refseq_human_20140103.fasta)	ubiquitin-like protein 7 isoform a [Homo sapiens]

10	20	30	40	50	60	70	80
MSLSDWHLAV	KLADQPLTPK	SILRLPETEL	GEYSLGGYSI	SFLKQLIAGK	LQESVPDPEL	IDLIYCGRKL	KDDQTLDFYG
90	100	110	120	130	140	150	160
IQPGSTVHVL	RKSWPEPDQK	PEPVDKVAAM	REFRVLHTAL	HSSSSYREAV	FKMLSNKESL	DQIIVATPGL	SSDPIALGVL
170	180	190	200	210	220	230	240
QDKDLFSVFA	DPNMLDTLVP	AHPALVNAIV	LVLHSVAGSA	PMPGTDSSSR	SMPSSSYRDM	PGGFLFEGLS	DDEDDFHPNT
250	260	270	280	290	300	310	320
RSTPSSSTPS	SRPASLGYSG	AAGPRPITQS	ELATALALAS	TPESSSHTPT	PGTQGHSSGT	SPMSSGVQSG	TPITNDLFSQ
330	340	350	360	370	380	390	
ALQHALQASG	QPSLQSQWQP	QLQQLRDMGI	QDDELSLRAL	QATGGDIQAA	LELIFAGGAP		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2456	1	754.4649	115.07	3	59.0	10.9	0	72-91	K.DDQTLDFYGIQPGSTVHVLR.K	

Detailed Protein Report

Protein 1004: disintegrin and metalloproteinase domain-containing protein 18 isoform 1 preproprotein [Homo sapiens]

Accession:	gi|7656861	**Score:**	10.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	82.8
Database Date:	2015-11-30	**pI:**	7.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MFLLLALLTE	LGRLQAHEGS	EGIFLHVTVP	RKIKSNDSEV	SERKMIYIIT	IDGQPYTLHL	GKQSFLPQNF	LVYTYNETGS
90	100	110	120	130	140	150	160
LHSVSPYFMM	HCHYQGYAAE	FPNSFVTLSI	CSGLRGFLQF	ENISYGIEPV	ESSARFEHII	YQMKNNDPNV	SILAVNYSHI
170	180	190	200	210	220	230	240
WQKDQPYKVP	LNSQIKNLSK	LLPQYLEIYI	IVEKALYDYM	GSEMMAVTQK	IVQVIGLVNT	MFTQFKLTVI	LSSLELWSNE
250	260	270	280	290	300	310	320
NQISTSGDAD	DILQRFLAWK	RDYLILRPHD	IAYLLVYRKH	PKYVGATFPG	TVCNKSYDAG	IAMYPDAIGL	EGFSVIIAQL
330	340	350	360	370	380	390	400
LGLNVGLTYD	DITQCFCLRA	TCIMNHEAVS	ASGRKIFSNC	SMHDYRYFVS	KFETKCLQKL	SNLQPLHQNQ	PVCGNGILES
410	420	430	440	450	460	470	480
NEECDCGNKN	ECQFKKCCDY	NTCKLKGSVK	CGSGPCCTSK	CELSIAGTPC	RKSIDPECDF	TEYCNGTSSN	CVPDTYALNG
490	500	510	520	530	540	550	560
RLCKLGTAYC	YNGQCQTTDN	QCAKIFGKGA	QGAPFACFKE	VNSLHERSEN	CGFKNSQPLP	CERKDVLCGK	LACVQPHKNA
570	580	590	600	610	620	630	640
NKSDAQSTVY	SYIQDHVCVS	IATGSSMRSD	GTDNAYVADG	TMCGPEMYCV	NKTCRKVHLM	GYNCNATTKC	KGKGICNNFG
650	660	670	680	690	700	710	720
NCQCFPGHRP	PDCKFQFGSP	GGSIDDGNFQ	KSGDFYTEKG	YNTHWNNWFI	LSFCIFLPFF	IVFTTVIFKR	NEISKSCNRE
730	740						
NAEYNRNSSV	VSESDDVGH						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2129	1	734.3188	-28.32	2	55.0	10.9	0	617-629	K.VHLMGYNCNATTK.C	Oxidation: 4

Detailed Protein Report

Protein 1005: **PREDICTED: voltage-dependent L-type calcium channel subunit beta-1 isoform X3 [Homo sapiens]**

Accession:	gi|530412809	**Score:**	10.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	40.5
Database Date:	2015-11-30	**pI:**	5.4
		Sequence Coverage [%]:	3.8
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MRPIILVGPS LKGYEVTDMM QKALFDFLKH RFDGRISITR VTADISLAKR SVLNNPSKHI IIERSNTRSS LAEVQSEIER
        90        100        110        120        130        140        150        160
IFELARTLQL VALDADTINH PAQLSKTSLA PIIVYIKITS PKVLQRLIKS RGKSQSKHLN VQIAASEKLA QCPPEMFDII
       170        180        190        200        210        220        230        240
LDENQLEDAC EHLAEYLEAY WKATHPPSST PPNPLLNRTM ATAALAASPA PVSNLQGPYL ASGDQPLERA TGEHASMHEY
       250        260        270        280        290        300        310        320
PGELGQPPGL YPSSHPPGRA GTLRALSRQD TFDADTPGSR NSAYTELGDS CVDMETDPSE GPGLGDPAGG GTPPARQGSW
       330        340        350        360        370        380
EDEEEDYEEE LTDNRNRGRN KARYCAEGGG PVLGRNKNEL EGWGRGVYIR
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1903	1	703.2558	-139.52	2	52.2	10.9	1	342-355	K.ARYCAEGGGPVLGR.N	

Detailed Protein Report

Protein 1006: BEN domain-containing protein 4 isoform a [Homo sapiens]

Accession:	gi|148762950	**Score:**	10.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	58.3
Database Date:	2015-11-30	**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 1007: tyrosine-protein kinase SYK isoform 2 [Homo sapiens]

Accession:	gi|205277435	**Score:**	10.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	69.5
Database Date:	2015-11-30	**pI:**	7.8
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	2.0
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|293332611	refseq_human (refseq_human_20140103.fasta)	tyrosine-protein kinase SYK isoform 2 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MASSGMADSA NHLPFFFGNI TREEAEDYLV QGGMSDGLYL LRQSRNYLGG FALSVAHGRK AHHYTIEREL NGTYAIAGGR

        90        100        110        120        130        140        150        160
THASPADLCH YHSQESDGLV CLLKKPFNRP QGVQPKTGPF EDLKENLIRE YVKQTWNLQG QALEQAIISQ KPQLEKLIAT

       170        180        190        200        210        220        230        240
TAHEKMPWFH GKISREESEQ IVLIGSKTNG KFLIRARDNN GSYALCLLHE GKVLHYRIDK DKTGKLSIPE GKKFDTLWQL

       250        260        270        280        290        300        310        320
VEHYSYKADG LLRVLTVPCQ KIGTQGNVNF GGRPQLPGSH PASSPAQGNR QESTVSFNPY EPELAPWAAD KGPQREALPM

       330        340        350        360        370        380        390        400
DTEVYESPYA DPEEIRPKEV YLDRKLLTLE DKELGSGNFG TVKKGYYQMK KVVKTVAVKI LKNEANDPAL KDELLAEANV

       410        420        430        440        450        460        470        480
MQQLDNPYIV RMIGICEAES WMLVMEMAEL GPLNKYLQQN RHVKDKNIIE LVHQVSMGMK YLEESNFVHR DLAARNVLLV

       490        500        510        520        530        540        550        560
TQHYAKISDF GLSKALRADE NYYKAQTHGK WPVKWYAPEC INYYKFSSKS DVWSFGVLMW EAFSYGQKPY RGMKGSEVTA

       570        580        590        600        610        620
MLEKGERMGC PAGCPREMYD LMNLCWTYDV ENRPGFAAVE LRLRNYYYDV VN
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1105	1	653.6417	-205.60	2	42.1	10.9	1	565-576	K.GERMGCPAGCPR.E	Carbamidomethyl: 10; Oxidation: 4

Detailed Protein Report

Protein 1008: zinc finger protein 211 isoform 6 [Homo sapiens]

Accession:	gi|388240796	**Score:**	10.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	57.5
Database Date:	2015-11-30	**pI:**	10.3
		Sequence Coverage [%]:	2.0
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 0.61 **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		WD:WU 0.61

Detailed Protein Report

Protein 1009: 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 1010: ATP-dependent zinc metalloprotease YME1L1 isoform 4 [Homo sapiens]

Accession:	gi|359718987	**Score:**	10.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	75.9
Database Date:	2015-11-30	**pI:**	9.2
		Sequence Coverage [%]:	2.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MFSLSSTVQP	QVTVPLSHLI	NAFHTPKNTS	VSLSGVSVSQ	NQHRDVVPEH	EAPSSEPSLN	LRDLGLSELK	IGQIDQLVEN
90	100	110	120	130	140	150	160
LLPGFCKGKN	ISSHWHTSHV	SAQSFFENKY	VFIQSRGFKT	LKSRTRRLQS	TSERLAETQN	IAPSFVKGFL	LRDRGSDVES
170	180	190	200	210	220	230	240
LDKLMKTKNI	PEAHQDAFKT	GFAEGFLKAQ	ALTQKTNDSL	RRTRLILFVL	LLFGIYGLLK	NPFLSVRFRT	TTGLDSAVDP
250	260	270	280	290	300	310	320
VQMKNVTFEH	VKGVEEAKQE	LQEVVEFLKN	PQKFTILGGK	LPKGILLVGP	PGTGKTLLAR	AVAGEADVPF	YYASGSEFDE
330	340	350	360	370	380	390	400
MFVGVGASRI	RNLFREAKAN	APCVIFIDEL	DSVGGKRIES	PMHPYSRQTI	NQLLAEMDGF	KPNEGVIIIG	ATNFPEALDN
410	420	430	440	450	460	470	480
ALIRPGRFDM	QVTVPRPDVK	GRTEILKWYL	NKIKFDQSVD	PEIIARGTVG	FSGAELENLV	NQAALKAAVD	GKEMVTMKEL
490	500	510	520	530	540	550	560
EFSKDKILMG	PERRSVEIDN	KNKTITAYHE	SGHAIIAYYT	KDAMPINKAT	IMPRGPTLGH	VSLLPENDRW	NETRAQLLAQ
570	580	590	600	610	620	630	640
MDVSMGGRVA	EELIFGTDHI	TTGASSDFDN	ATKIAKRMVT	KFGMSEKLGV	MTYSDTGKLS	PETQSAIEQE	IRILLRDSYE
650	660	670	680	690			
RAKHILKTHA	KEHKNLAEAL	LTYETLDAKE	IQIVLEGKKL	EVR			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1920	1	600.5632	-124.56	3	52.7	10.9	0	28-44	K.NTSVSLSGVSVSQNQHR.D	

Detailed Protein Report

Protein 1011: PREDICTED: multifunctional protein ADE2 isoform X1 [Homo sapiens]

Accession: gi|578808622
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 10.9
MW [kDa]: 93.9
pI: 9.2
Sequence Coverage [%]: 1.6
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MESGAGKHWT	EEEVKALLSV	WAEKNIRKQL	YGTLRNKGIF	IYIAKRLQSL	GVYRDWKQCW	AKYKNLKYEY	RTVKYAHNSG
90	100	110	120	130	140	150	160
DSSKTMKFFH	DLDVILQYEP	ATQFTEEDAN	GRYLETLSPS	TAPETTEGKM	SIASVDKEDV	SGNPLLLVSH	VRPMELGIST
170	180	190	200	210	220	230	240
SVLEPSNNTT	FIPTVANEGG	KHWTVPEVRA	LIDIWSDKSI	QRQLEGTVRN	KRIFQQIAAK	LQKFGIDRDW	KQCRTKYKNL
250	260	270	280	290	300	310	320
KHEYKIVRTA	QDLGMTKSMK	FFTELDAILG	PNKTEKSRDQ	ESQDGEHVTE	CANVKMGEDQ	TVHPDREELI	TKTSENRRLT
330	340	350	360	370	380	390	400
NVKKESSDIE	LFEGHNKSQG	TLSFKRKAHE	DEPVSKSLKK	SAPEIITNQF	PQSVITEPKD	STECFCRQKT	QLHQSSASLP
410	420	430	440	450	460	470	480
GAVAALSPLR	IMATAEVLNI	GKKLYEGKTK	EVYELLDSPG	KVLLQSKDQI	TAGNAARKNH	LEGKAAISNK	ITSCIFQLLQ
490	500	510	520	530	540	550	560
EAGIKTAFTR	KCGETAFIAP	QCEMIPIEWV	CRRIATGSFL	KRNPGVKEGY	KFYPPKVELF	FKDDANNDPQ	WSEEQLIAAK
570	580	590	600	610	620	630	640
FCFAGLLIGQ	TEVDIMSHAT	QAIFEILEKS	WLPQNCTLVD	MKIEFGVDVT	TKEIVLADVI	DNDSWRLWPS	GDRSQQKDKQ
650	660	670	680	690	700	710	720
SYRDLKEVTP	EGLQMVKKNF	EWVAERVELL	LKSESQCRVV	VLMGSTSDLG	HCEKIKKACG	NFGIPCELRV	TSAHKGPDET
730	740	750	760	770	780	790	800
LRIKAEYEGD	GIPTVFVAVA	GRSNGLGPVM	SGNTAYPVIS	CPPLTPDWGV	QDVWSSLRLP	SGLGCSTVLS	PEGSAQFAAQ
810	820	830	840				
IFGLSNHLVW	SKLRASILNT	WISLKQADKK	IRECNL				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2231	1	734.3310	-85.49	2	56.2	10.9	2	348-360	K.AHEDEPVSKSLKK.S	

Detailed Protein Report

Protein 1012: 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

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
120	1	679.7199	-180.53	2	30.8	10.9	2	400-411	R.KPKCGKGTHCSR.N	Carbamidomethyl: 4

Detailed Protein Report

Protein 1013: sorting nexin-18 isoform b [Homo sapiens]

Accession: gi|157057543

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Modification(s): Oxidation

Score: 10.9

MW [kDa]: 68.9

pI: 5.3

Sequence Coverage [%]: 1.4

No. of unique Peptides: 1

```
        10         20         30         40         50         60         70         80
MALRARALYD FRSENPGEIS LREHEVLSLC SEQDIEGWLE GVNSRGDRGL FPASYVQVIR APEPGPAGDG GPGAPARYAN
        90        100        110        120        130        140        150        160
VPPGGFEPLP VAPPASFKPP PDAFQALLQP QQAPPPSTFQ PPGAGFPYGG GALQPSPQQL YGGYQASQGS DDDWDDEWDD
       170        180        190        200        210        220        230        240
SSTVADEPGA LGSGAYPDLD GSSSAGVGAA GRYRLSTRSD LSLGSRGGSV PPQHHPSGPK SSATVSRNLN RFSTFVKSGG
       250        260        270        280        290        300        310        320
EAFVLGEASG FVKDGDKLCV VLGPYGPEWQ ENPYPFQCTI DDPTKQTKFK GMKSYISYKL VPTHTQVPVH RRYKHFDWLY
       330        340        350        360        370        380        390        400
ARLAEKFPVI SVPHLPEKQA TGRFEEDFIS KRRKGLIWWM NHMASHPVLA QCDVFQHFLT CPSSTDEKAW KQGKRKAEKD
       410        420        430        440        450        460        470        480
EMVGANFFLT LSTPPAAALD LQEVESKIDG FKCFTKKMDD SALQLNHTAN EFARKQVTGF KKEYQKVGQS FRGLSQAFEL
       490        500        510        520        530        540        550        560
DQQAFSVGLN QAIAFTGDAY DAIGELFAEQ PRQDLDPVMD LLALYQGHLA NFPDIIHVQK GKAWPLEQVI WSVLCRLKGA
       570        580        590        600        610        620        630
TLTAVPLWVS ESYSTGEEAS RDVDAWVFSL ECKLDCSTGS FLLEYLALGN EYSFSKVQRV PLMTVLSF
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1470	1	1022.6762	114.58	1	46.8	10.9	0	620-628	R.VPLMTVLSF.-	Oxidation: 4

Protein 1014: PREDICTED: bromodomain adjacent to zinc finger domain protein 2B isoform X27 [Homo sapiens]

Accession:	gi|578804191	**Score:**	10.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	215.9
Database Date:	2015-11-30	**pI:**	5.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.1
		No. of unique Peptides:	1

Detailed Protein Report

```
        10         20         30         40         50         60         70         80
MESGERLPSS AASSTTPTSS STPSVASVVS KGGLSTGVAS LSSTINPCGH LFRTAGDQPF NLSTVSSAFP MVSHPVFGLH

        90        100        110        120        130        140        150        160
SASSGHSEFG GLGTLGTPTA LAAHPQLASF PGAEWWRTTD AHTRTGATFF PPLLGIPPLF APPAQNHDSS SFHSRTSGKS

       170        180        190        200        210        220        230        240
NRNGPEKGVN GSINGSNTSS VIGINTSVLS TTASSSMGQT KSTSSGGGNR KCNQEQSKNQ PLDARVDKIK DKKPRKKAME

       250        260        270        280        290        300        310        320
SSSNSDSDSG TSSDTSSEGI SSSDSDDLEE DEEEEDQSIE ESEDDDSDSE SEAQHKSNNQ VLLHGISDPK ADGQKATEKA

       330        340        350        360        370        380        390        400
QEKRIHQPLP LASESQTHSF QSQQKQPQVL SQQLPFIFQS SQAKEESVNK HTSVIQSTGL VSNVKPLSLV NQAKKETYMK

       410        420        430        440        450        460        470        480
LIVPSPDVLK AGNKNTSEES SLLTSELRSK REQYKQAFPS QLKKQESSKS LKKVIAALSN PKATSSSPAH PKQTLENNHP

       490        500        510        520        530        540        550        560
NPFLTNALLG NHQPNGVIQS VIQEAPLALT TKTKMQSKIN ENIAAASSTP FSSPVNLSTS GRRTPGNQTP VMPSASPILH

       570        580        590        600        610        620        630        640
SQGKEKAVSN NVNPVKTQHH SHPAKSLVEQ FRGTDSDIPS SKDSEDSNED EEEDDEEEDE EDDEDDESDD SQSESDSNSE

       650        660        670        680        690        700        710        720
SDTEGSEEED DDDKDQDESD SDTEGEKTSM KLNKTTSSVK SPSMSLTGHS TPRNLHIAKA PGSAPAALCS ESQSPAFLGT

       730        740        750        760        770        780        790        800
SSSTLTSSPH SGTSKRRRVT DERELRIPLE YGWQRETRIR NFGGRLQGEV AYYAPCGKKL RQYPEVIKYL SRNGIMDISR

       810        820        830        840        850        860        870        880
DNFSFSAKIR VGDFYEARDG PQGMQWCLLK EEDVIPRIRA MEGRRGRPPN PDRQRAREES RMRRRKGRPP NVGNAEFLDN

       890        900        910        920        930        940        950        960
ADAKLLRKLQ AQEIARQAAQ IKLLRKLQKQ EQARVAKEAK KQQAIMAAEE KRKQKEQIKI MKQQEKIKRI QQIRMEKELR

       970        980        990       1000       1010       1020       1030       1040
AQQILEAKKK KKEEAANAKL LEAEKRIKEK EMRRQQAVLL KHQELERHRL DMVWERERRR QHMMLMKAME ARKKAEEKER

      1050       1060       1070       1080       1090       1100       1110       1120
LKQEKRDEKR LNKERKLEQR RLELEMAKEL KKPNEDMCLA DQKPLPELPR IPGLVLSGST FSDCLMVVQF LRNFGKVLGF

      1130       1140       1150       1160       1170       1180       1190       1200
DVNIDVPNLS VLQEGLLNIG DSMGEVQDLL VRLLSAAVCD PGLITGYKAK TALGEHLLNV GVNRDNVSEI LQIFMEAHCG

      1210       1220       1230       1240       1250       1260       1270       1280
QTELTESLKT KAFQAHTPAQ KASVLAFLIN ELACSKSVVS EIDKNIDYMS NLRRDKWVVE GKLRKLRIIH AKKTGKRDTS

      1290       1300       1310       1320       1330       1340       1350       1360
GGIDLGEEQH PLGTPTPGRK RRRKGGDSDY DDDDDDDSDD QGDEDDEDEE DKEDKKGKKT DICEDEDEGD QAASVEELEK

      1370       1380       1390       1400       1410       1420       1430       1440
QIEKLSKQQS QYRRKLFDAS HSLRSVMFGQ DRYRRRYWIL PQCGGIFVEG MESGEGLEEI AKEREKLKKA ESVQIKEEMF

      1450       1460       1470       1480       1490       1500       1510       1520
ETSGDSLNCS NTDHCEQKED LKEKDNTNLF LQKPGSFSKL SKLLEVAKMP PESEVMTPKP NAGANGCTLS YQNSGKHSLG

      1530       1540       1550       1560       1570       1580       1590       1600
SVQSTATQSN VEKADSNNLF NTGSSGPGKF YSPLPNDQLL KTLTEKNRQW FSLLPRTPCD DTSLTHADMS TASLVTPQSQ

      1610       1620       1630       1640       1650       1660       1670       1680
PPSKSPSPTP APLGSSAQNP VGLNPFALSP LQVKGGVSMM GLQFCGWPTG VVTSNIPFTS SVPSLGSGLG LSEGNGNSFL

      1690       1700       1710       1720       1730       1740       1750       1760
TSNVASSKSE SPVPQNEKAT SAQPAAVEVA KPVDFPSPKP IPEEMQFGWW RIIDPEDLKA LLKVLHLRGI REKALQKQIQ

      1770       1780       1790       1800       1810       1820       1830       1840
KHLDYITQAC LKNKDVAIIE LNENEENQVT RDIVENWSVE EQAMEMDLSV LQQVEDLERR VASASLQVKG WMCPEPASER

      1850       1860       1870       1880       1890       1900       1910       1920
EDLVYFEHKS FTKLCKEHDG EFTGEDESSA HALERKSDNP LDIAVTRLAD LERNIERSTA KSVEREIMKN CFFFVMAVTK

      1930       1940       1950       1960
AVIPTAIDPR LQQSQMETGF VQLALLRQVV KL
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1818	1	1273.0889	-96.81	2	51.1	10.9	2	1931-1952	R.LQQSQMETGFVQLALLRQVVKL.-	Oxidation: 6

Detailed Protein Report

Protein 1015: coiled-coil domain-containing protein 178 isoform 2 [Homo sapiens]

Accession:	gi|157671917	**Score:**	10.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	97.5
Database Date:	2015-11-30	**pI:**	5.9
		Sequence Coverage [%]:	1.1
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 2.25 **CV:** 0.00 % **No. of Peptides:** 1

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
253	1	559.2713	-28.25	2	31.9	10.9	2	152-160	K.RDEKCPELK.Q		WD:WU 2.25

Detailed Protein Report

Protein 1016: PREDICTED: SH3 domain-containing RING finger protein 3 isoform X2 [Homo sapiens]

Accession: gi|578804249
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 10.9
MW [kDa]: 63.9
pI: 9.8
Sequence Coverage [%]: 1.8
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MLLGASWLCA	SKAAAAAAQS	EGDEDRPGER	RRRRAAATAA	GAGEDMDESS	LLDLLECSVC	LERLDTTAKV	LPCQHTFCRR
90	100	110	120	130	140	150	160
CLESIVCSRH	ELRCPECRIL	VGCGVDELPA	NILLVRLLDG	IRQRPRAGTS	PGGSPPARPI	PGQSAAPTLA	GGGGGAAGST
170	180	190	200	210	220	230	240
PGSPVFLSAA	AGSTAGSLRE	LATSRTAPAA	KNPCLLPYGK	ALYSYEGKEP	GDLKFNKGDI	IVLRRKVDEQ	WYHGELHGTQ
250	260	270	280	290	300	310	320
GFLPASYIQC	IQPLPHAPPQ	GKALYDFEMK	DKDQDKDCLT	FTKDEILTVL	RRVDENWAEG	MLGDKIGIFP	LLYVELNDSA
330	340	350	360	370	380	390	400
KQLIEMDKPC	PAAASSCNAS	LPSDSGAVAS	VAPSPTLSSS	GAVSAFQRRV	DGKKNTKKRH	SFTALSVTHR	SSQAASHRHS
410	420	430	440	450	460	470	480
MEISAPVLIS	SSDPRAAARI	GDLAHLSCAA	PTQDVSSSAG	STPTAVPRAA	SVSGEQGTPP	KVQLPLNVYL	ALYAYKPQKS
490	500	510	520	530	540	550	560
DELELHKGEM	YRVLEKCQDG	WFKGASLRTG	VSGVFPGNYV	TPVSRVPAGG	AGPPRNNVVG	GSPLAKGITT	TMHPGSGSLS
570	580	590	600	610	620		
SLATATRPAL	PITTPQAHAQ	HPTASPPTGS	CLRHSAQPTA	SQARSTISTG			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
447	1	705.2428	-148.77	2	34.1	10.9	1	493-503	R.VLEKCQDGWFK.G	Carbamidomethyl: 5

Detailed Protein Report

Protein 1017: PREDICTED: tumor necrosis factor receptor superfamily member 3 isoform X3 [Homo sapiens]

Accession:	gi|578822606	**Score:**	10.9
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 1018: **TFIIH basal transcription factor complex helicase XPD subunit isoform 2 [Homo sapiens]**

Accession:	gi|195947407	**Score:**	10.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	46.2
Database Date:	2015-11-30	**pI:**	9.7
		Sequence Coverage [%]:	4.7
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 2.21 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MRELKRTLDA	KGHGVLEMPS	GTGKTVSLLA	LIMAYQRAYP	LEVTKLIYCS	RTVPEIEKVI	EELRKLLNFY	EKQEGEKLPF
90	100	110	120	130	140	150	160
LGLALSSRKN	LCIHPEVTPL	RFGKDVDGKC	HSLTASYVRA	QYQHDTSLPH	CRFYEEFDAH	GREVPLPAGI	YNLDDLKALG
170	180	190	200	210	220	230	240
RRQGWCPYFL	ARYSILHANV	VVYSYHYLLD	PKIADLVSKE	LARKAVVVFD	EAHNIDNVCI	DSMSVNLTRR	TLDRCQGNLE
250	260	270	280	290	300	310	320
TLQKTVLRIK	ETDEQRLRDE	YRRLVEGLRE	ASAARETDAH	LANPVLPDEV	LQEAVPGSIR	TAEHFLGFLR	RLLEYVKWRL
330	340	350	360	370	380	390	400
RVQHVVQESP	PAFLSGLAQR	VCIQRKPLRF	CAERLRSLLH	TLEITDLADF	SPLTLLANFA	TLVSTYAKGQ	AQHCGSSRNQ
410							
KRSHP							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1633	1	977.4534	-60.37	2	48.7	10.9	2	6-24	K.RTLDAKGHGVLEMPSGTGK.T		WD:WU 2.21

Detailed Protein Report

Protein 1019: PREDICTED: ubiquitin carboxyl-terminal hydrolase 37 isoform X8 [Homo sapiens]

Accession:	gi|530370695	**Score:**	10.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	83.2
Database Date:	2015-11-30	**pI:**	5.9
		Sequence Coverage [%]:	2.2
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MKITLRKMIH HRLLPLQSSS FYGSRAGSKE HSSGGTNLDR TNVSSQTPSA KRSLGFLPQP VPLSVKKLRC NQDYTGWNKP
        90        100        110        120        130        140        150        160
RVPLSSHQQQ QLQGFSNLGN TCYMNAILQS LFSLQSFAND LLKQGIPWKK IPLNALIRRF AHLLVKKDIC NSETKKDLLK
       170        180        190        200        210        220        230        240
KVKNAISATA ERFSGYMQND AHEFLSQCLD QLKEDMEKLN KTWKTEPVSG EENSPDISAT RAYTCPVITN LEFEVQHSII
       250        260        270        280        290        300        310        320
CKACGEIIPK REQFNDLSID LPRRKKPLPP RSIQDSLDLF FRAEELEYSC EKCGGKCALV RHKFNRLPRV LILHLKRYSF
       330        340        350        360        370        380        390        400
NVALSLNNKI GQQVIIPRYL TLSSHCTENT KPPFTLGWSA HMAISRPLKA SQMVNSCITS PSTPSKKFTF KSKSSLALCL
       410        420        430        440        450        460        470        480
DSDSEDELKR SVALSQRLCE MLGNEQQQED LEKDSKLCPI EPDKSELENS GFDRMSEEEL LAAVLEISKR DASPSLSHED
       490        500        510        520        530        540        550        560
DDKPTSSPDT GFAEDDIQEM PENPDTMETE KPKTITELDP ASFTEITKDC DENKENKTPE GSQGEVDWLQ QYDMEREREE
       570        580        590        600        610        620        630        640
QELQQALAQS LQEQEAWEQK EDDDLKRATE LSLQEFNNSF VDALGSDEDS GNEDVFDMEY TEAEAEELKR NAEVITLVMY
       650        660        670        680        690        700        710        720
MTLRSKRGLL TMTWRYQKSK RLPCRVIEIG VATSSFICTR RSLMSCWKQK RTLSHLARKW GRLPVRPCEE QTPGLAACTA
       730        740
YLLLLPTSPF LC
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
241	1	862.8312	-77.86	2	31.8	10.8	0	394-409	K.SSLALCLDSDSEDELK.R	

Detailed Protein Report

Protein 1020: 60S ribosomal protein L23a [Homo sapiens]

Accession:	gi|17105394	**Score:**	10.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	17.7
Database Date:	2015-11-30	**pI:**	10.9
		Sequence Coverage [%]:	5.1
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MAPKAKKEAP APPKAEAKAK ALKAKKAVLK GVHSHKKKKI RTSPTFRRPK TLRLRRQPKY PRKSAPRRNK LDHYAIIKFP
        90        100        110        120        130        140        150        160
LTTESAMKKI EDNNTLVFIV DVKANKHQIK QAVKKLYDID VAKVNTLIRP DGEKKAYVRL APDYDALDVA NKIGII
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2608	1	974.3100	-249.41	1	60.9	10.8	2	60-67	K.YPRKSAPR.R	

Detailed Protein Report

Protein 1021: olfactory receptor 6T1 [Homo sapiens]

Accession:	gi|52353278	**Score:**	10.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	36.3
Database Date:	2015-11-30	**pI:**	10.4
		Sequence Coverage [%]:	5.3
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MNPENWTQVT SFVLLGFPSS HLIQFLVFLG LMVTYIVTAT GKLLIIVLSW IDQRLHIQMY FFLRNFSFLE LLLVTVVVPK
        90        100        110        120        130        140        150        160
MLVVILTGDH TISFVSCIIQ SYLYFFLGTT DFFLLAVMSL DRYLAICRPL RYETLMNGHV CSQLVLASWL AGFLWVLCPT
       170        180        190        200        210        220        230        240
VLMASLPFCG PNGIDHFFRD SWPLLRLSCG DTHLLKLVAF MLSTLVLLGS LALTSVSYAC ILATVLRAPT AAERRKAFST
       250        260        270        280        290        300        310        320
CASHLTVVVI IYGSSIFLYI RMSEAQSKLL NKGASVLSCI ITPLLNPFIF TLRNDKVQQA LREALGWPRL TAVMKLRVTS
       330
QRK
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1150	1	977.4905	-24.45	2	43.1	10.8	1	180-196	R.DSWPLLRLSCGDTHLLK.L	

Detailed Protein Report

Protein 1022: platelet-derived growth factor D isoform 2 precursor [Homo sapiens]

Accession:	gi|15451921	**Score:**	10.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	42.1
Database Date:	2015-11-30	**pI:**	9.4
		Sequence Coverage [%]:	3.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MHRLIFVYTL	ICANFCSCRD	TSATPQSASI	KALRNANLRR	DDLYRRDETI	QVKGNGYVQS	PRFPNSYPRN	LLLTWRLHSQ
90	100	110	120	130	140	150	160
ENTRIQLVFD	NQFGLEEAEN	DICRYDFVEV	EDISETSTII	RGRWCGHKEV	PPRIKSRTNQ	IKITFKSDDY	FVAKPGFKIY
170	180	190	200	210	220	230	240
YSLLEDFQPA	AASETNWESV	TSSISGVSYN	SPSVTDPTLI	ADALDKKIAE	FDTVEDLLKY	FNPESWQEDL	ENMYLDTPRY
250	260	270	280	290	300	310	320
RGRSYHDRKS	KVDLDRLNDD	AKRYSCTPRN	YSVNIREELK	LANVVFFPRC	LLVQRCGGNC	GCGTVNWRSC	TCNSGKTVKK
330	340	350	360	370			
YHEVLQFEPG	HIKRRGRAKT	MALVDIQLDH	HERCDCICSS	RPPR			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2901	1	682.8331	-42.36	2	65.0	10.8	1	270-280	R.NYSVNIREELK.L	

Detailed Protein Report

Protein 1023: uncharacterized protein C17orf80 isoform d [Homo sapiens]

Accession:	gi|571026655	**Score:**	10.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	60.8
Database Date:	2015-11-30	**pI:**	10.1
		Sequence Coverage [%]:	2.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSDNPPRMEV	CPYCKKPFKR	LKSHLPYCKM	IGPTIPTDQK	VYQSKPATLP	RAKKMKGPIK	DLIKAKGKEL	ETENEERNSK
90	100	110	120	130	140	150	160
LVVDKPEQTV	KTFPLPAVGL	ERAATTKADK	DIKNPIQPSF	KMLKNTKPMT	TFQEETKAQF	YASEKTSPKR	ELAKDLPKSG
170	180	190	200	210	220	230	240
ESRCNPSEAG	ASLLVGSIEP	SLSNQDRKYS	STLPNDVQTT	SGDLKLDKID	PQRQELLVKL	LDVPTGDCHI	SPKNVSDGVK
250	260	270	280	290	300	310	320
RVRTLLSNER	DSKGRDHLSG	VPTDVTVTET	PEKNTESLIL	SLKMSSLGKI	QVMEKQEKGL	TLGVETCGSK	GNAEKSMSAT
330	340	350	360	370	380	390	400
EKQERTVMSH	GCENFNTRDS	VTGKESQGER	PHLSLFIPRE	TTYQFHSVSQ	SSSQSLASLA	TTFLQEKKAE	AQNHNCVPDV
410	420	430	440	450	460	470	480
KALMESPEGQ	LSLEPKSDSQ	FQASHTGCQS	PLCSAQRHTP	QSPFTNHAAA	AGRKTLRSCM	GLEWFPELYP	GYLGLGVLPG
490	500	510	520	530	540	550	
KPQCWNAMTQ	KPQLISPQGE	RLSQGWIRCN	TTIRKSGFGG	ITMLFTGYFV	LCCSWSFRRL	KLQRWRK	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
555	1	712.9189	120.57	2	35.4	10.8	0	389-401	K.AEAQNHNCVPDVK.A	

Detailed Protein Report

Protein 1024: 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

WD:WU **Median:** 1.56 **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	WD:WU 1.56

Detailed Protein Report

Protein 1025: E3 ubiquitin-protein ligase RNF103 isoform 2 [Homo sapiens]

Accession:	gi|312147324	**Score:**	10.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	78.6
Database Date:	2015-11-30	**pI:**	5.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.3
		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 1026: G patch domain-containing protein 3 [Homo sapiens]

Accession:	gi|205277458	**Score:**	10.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	59.3
Database Date:	2015-11-30	**pI:**	4.8
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	3.8
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 0.65 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MAVPGEAEEE	ATVYLVVSGI	PSVLRSAHLR	SYFSQFREER	GGGFLCFHYR	HRPERAPPQA	APNSALIPTD	PAAEGQLLSQ
90	100	110	120	130	140	150	160
TSATDVRPLS	TRDSTPIQTR	TCCCVISVRG	LAQAQRLIRM	YSGRRWLDSH	GTWLPGRCLI	RRLRLPTEAS	GLGSFPFKTR
170	180	190	200	210	220	230	240
KELQSWKAEN	EAFTLADLKQ	LPELNPPVLM	PRGNVGTPLR	VFLELIRACR	LPPRIITQLQ	LQFPKTGSSR	RYGNVPFEYE
250	260	270	280	290	300	310	320
DSETVEQEEL	VYTAEGEEIP	QGTYLADIPA	SPCGEPEEEV	GKEEEEESHS	DEDDDRGEEW	ERHEALHEDV	TGQERTTEQL
330	340	350	360	370	380	390	400
FEEEIELKWE	KGGSGLVFYT	DAQFWQEEEG	DFDEQTADDW	DVDMSVYYDR	DGGDKDARDS	VQMRLEQRLR	DGQEDGSVIE
410	420	430	440	450	460	470	480
RQVGTFERHT	KGIGRKVMER	QGWAEGQGLG	CRCSGVPEAL	DSDGQHPRCK	RGLGYHGEKL	QPFGQLKRPR	RNGLGLISTI
490	500	510	520	530			
YDEPLPQDQT	ESLLRRQPPT	SMKFRTDMAF	VRGSSCASDS	PSLPD			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1493	1	705.9667	-4.88	3	47.0	10.8	1	506-525	R.TDMAFVRGSSCASDSPSLPD.-	Carbamidomethyl: 11; Oxidation: 3	WD:WU 0.65

Detailed Protein Report

Protein 1027: **PREDICTED: probable E3 ubiquitin-protein ligase TRIML1 isoform X2 [Homo sapiens]**

Accession:	gi|578809099	**Score:**	10.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	32.2
Database Date:	2015-11-30	**pI:**	5.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	7.0
		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 1028: PREDICTED: serine/threonine-protein kinase TAO3 isoform X4 [Homo sapiens]

Accession:	gi|578823854	**Score:**	10.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	101.7
Database Date:	2015-11-30	**pI:**	7.3
		Sequence Coverage [%]:	1.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MRKGVLKDPE	IADLFYKDDP	EELFIGLHEI	GHGSFGAVYF	ATNAHTSEVV	AIKKMSYSGK	QTHEKWQDIL	KEVKFLRQLK
90	100	110	120	130	140	150	160
HPNTIEYKGC	YLKEHTAWLV	MEYCLGSASD	LLEVHKKPLQ	EVEIAAITHG	ALHGLAYLHS	HALIHRDIKA	GNILLTEPGQ
170	180	190	200	210	220	230	240
VKLADFGSAS	MASPANSFVG	TPYWMAPEVI	LAMDEGQYDG	KVDIWSLGIT	CIELAERKPP	LFNMNAMSAL	YHIAQNDSPT
250	260	270	280	290	300	310	320
LQSNEWTDSF	RRFVDYCLQK	IPQERPTSAE	LLRHDFVRRD	RPLRVLIDLI	QRTKDAVREL	DNLQYRKMKK	ILFQETRNGP
330	340	350	360	370	380	390	400
LNESQEDEED	SEHGTSLNRE	MDSLGSNHSI	PSMSVSTGSQ	SSSVNSMQEV	MDESSSELVM	MHDDESTINS	SSSVVHKKVG
410	420	430	440	450	460	470	480
FLVPSTEDHV	FIRDEAGHGD	PRPEPRPTQS	VQSQALHYRN	RERFATIKSA	SLVTRQIHEH	EQENELREQM	SGYKRMRRQH
490	500	510	520	530	540	550	560
QKQLIALENK	LKAEMDEHRL	KLQKEVETHA	NNSSIELEKL	AKKQVAIIEK	EAKVAAADEK	KFQQQILAQQ	KKDLTTFLES
570	580	590	600	610	620	630	640
QKKQYKICKE	KIKEEMNEDH	STPKKEKQER	ISKHKENLQH	TQAEEEAHLL	TQQRLYYDKN	CRFFKRKIMI	KRHEVEQQNI
650	660	670	680	690	700	710	720
REELNKKRTQ	KEMEHAMLIR	HDESTRELEY	RQLHTLQKLR	MDLIRLQHQT	ELENQLEYNK	RRERELHRKH	VMELRQQPKN
730	740	750	760	770	780	790	800
LKAMEMQIKK	QFQDTCKVQT	KQYKALKNHQ	LEVTPKNEHK	TILKTLKDEQ	TRKLAILAEQ	YEQSINEMMA	SQALRLDEAQ
810	820	830	840	850	860	870	880
EAECQALRLQ	LQQEMELLNA	YQSKIKMQTE	AQHERELQKL	EQRVSLRRAH	LEQKETLNVP	SQRNDVGCWG	G

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2240	1	927.9733	43.59	2	56.5	10.8	1	652-666	K.EMEHAMLIRHDESTR.E	

Detailed Protein Report

Protein 1029: septin-9 isoform f [Homo sapiens]

Accession:	gi|164698504	**Score:**	10.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	38.5
Database Date:	2015-11-30	**pI:**	7.8
		Sequence Coverage [%]:	3.6
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578830273	refseq_human (refseq_human_20140103.fasta)	PREDICTED: septin-9 isoform X7 [Homo sapiens]
gi|530411385	refseq_human (refseq_human_20140103.fasta)	PREDICTED: septin-9 isoform X5 [Homo sapiens]
gi|530411383	refseq_human (refseq_human_20140103.fasta)	PREDICTED: septin-9 isoform X4 [Homo sapiens]
gi|530411381	refseq_human (refseq_human_20140103.fasta)	PREDICTED: septin-9 isoform X3 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MADTPRDAGL KQAPASRNEK APVDFGYVGI DSILEQMRRK AMKQGFEFNI MVVGQSGLGK STLINTLFKS KISRKSVQPT

        90        100        110        120        130        140        150        160
SEERIPKTIE IKSITHDIEE KGVRMKLTVI DTPGFGDHIN NENCWQPIMK FINDQYEKYL QEEVNINRKK RIPDTRVHCC

       170        180        190        200        210        220        230        240
LYFIPATGHS LRPLDIEFMK RLSKVVNIVP VIAKADTLTL EERVHFKQRI TADLLSNGID VYPQKEFDED SEDRLVNEKF

       250        260        270        280        290        300        310        320
REMIPFAVVG SDHEYQVNGK RILGRKTKWG TIEVENTTHC EFAYLRDLLI RTHMQNIKDI TSSIHFEAYR VKRLNEGSSA

       330        340
MANGMEEKEP EAPEM
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2038	1	719.7894	-86.50	2	53.9	10.8	0	299-310	K.DITSSIHFEAYR.V	

Detailed Protein Report

Protein 1030: decorin isoform c precursor [Homo sapiens]

Accession:	gi|19743850	**Score:**	10.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	23.3
Database Date:	2015-11-30	**pI:**	6.8
		Sequence Coverage [%]:	5.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MKATIILLLL	AQVSWAGPFQ	QRGLFDFMLE	DEASGIGPEV	PDDRDFEPSL	GPVCPFRCQC	HLRVVQCSDL	GLPPSLTELH
90	100	110	120	130	140	150	160
LDGNKISRVD	AASLKGLNNL	AKLGLSFNSI	SAVDNGSLAN	TPHLRELHLD	NNKLTRVPGG	LAEHKYIQVV	YLHNNNISVV
170	180	190	200	210	220		
GSSDFCPPGH	NTKKASYSGV	SLFSNPVQYW	EIQPSTFRCV	YVRSAIQLGN	YK		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2807	1	639.3549	-23.37	2	63.7	10.8	1	134-145	K.LTRVPGGLAEHK.Y	

Detailed Protein Report

Protein 1031: 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 1032: PREDICTED: uncharacterized protein LOC101928352 [Homo sapiens]

Accession:	gi|578796908	**Score:**	10.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	24.9
Database Date:	2015-11-30	**pI:**	11.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	13.0
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578845616	refseq_human (refseq_human_20140103.fasta)	PREDICTED: uncharacterized protein LOC101928352 [Homo sapiens]
gi|578826487	refseq_human (refseq_human_20140103.fasta)	PREDICTED: uncharacterized protein LOC101928352 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MARGGWRVVR AGTAKSFVGA LKRPTGGPAL GGTRAARPEP RVRAPTPAGL ARLLHLRASS LCLQPSEGDP DGFIFGNLPR
        90        100        110        120        130        140        150        160
LFRLFYPHQA PSSEGQLSPL ITGEGARNSS NTHFGTGKPA GGERAARGIN PCGAGGGAGL TQALVGQMAP ATTGTLGRLS
       170        180        190        200        210        220        230        240
PALGKFELQT CPESFSRPSP QGPSLDRGTQ AAALQPKGLD QQGCPWHICT AYFPERQSEG AGMWAPVHNL PHHTKDKPR
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2465	1	938.4759	3.50	3	59.1	10.8	0	128-158	R.GINPCGAGGGAGLTQALVGQMAPATTGTLGR.L	Oxidation: 21

Detailed Protein Report

Protein 1033: PREDICTED: brain mitochondrial carrier protein 1 isoform X8 [Homo sapiens]

Accession:	gi|578838760	**Score:**	10.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	24.3
Database Date:	2015-11-30	**pI:**	10.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	8.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSFGRGGVEM	AAPRLPKQRF	GYFRWFQCFR	VGAAVAFPTV	GASASQSSDE	PEQHQKSTTV	SHEMSGLNWK	PFVYGGLASI
90	100	110	120	130	140	150	160
VAEFGTFPVD	LTKTRLQVQG	QSIDARFKEI	KYRGMFHALF	RICKEEGVLA	LYSGIAPALL	RQASYGTIKI	GIYQSLKRLF
170	180	190	200	210	220		
VERLEDSNAG	SRKLVPREHD	WKLYRYIPTR	RHQGSVEGCG	SNCSACCHRC	RSRATSL		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
867	1	631.1419	-155.18	3	39.3	10.8	0	192-209	R.HQGSVEGCGSNCSACCHR.C	Carbamidomethyl: 16

Detailed Protein Report

Protein 1034: 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 1035: mitochondrial dynamic protein MID49 isoform 3 [Homo sapiens]

Accession:	gi|222080060	**Score:**	10.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	20.5
Database Date:	2015-11-30	**pI:**	10.7
		Sequence Coverage [%]:	3.9
		No. of unique 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
773	1	450.7679	13.60	2	38.5	10.8	1	153-160	R.AWGAALRR.A	

Detailed Protein Report

Protein 1036: bcl-2-like protein 12 isoform 2 [Homo sapiens]

Accession:	gi|542133130	**Score:**	10.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	19.1
Database Date:	2015-11-30	**pI:**	12.2
		Sequence Coverage [%]:	10.8
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MGRPAGLFPP LCPFLGFRPE ACWERHMQIE RAPSVPPFLR WAGYRPGPVR RRGKVELIKF VRVQWRRPQV EWRRRRWGPG
        90        100        110        120        130        140        150        160
PGASMAGSEE LGLREDTLRV LAAFLRRGEA AGSPVPTPPR PSYSRLLCFG GPAAGTAGPR AAEISAQPRI TGSPIDREGS
       170        180
HTAEAGGPAG GGGRSH
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
256	1	846.3810	3.99	2	32.0	10.8	1	158-176	R.EGSHTAEAGGPAGGGGRSH.-	

Detailed Protein Report

Protein 1037: PREDICTED: PR domain zinc finger protein 1 isoform X1 [Homo sapiens]

Accession:	gi|530383954	**Score:**	10.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	73.8
Database Date:	2015-11-30	**pI:**	9.9
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.5
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 1.25 **CV:** 0.00 % **No. of 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	Ratios
1153	2	598.6557	-197.29	2	42.7	10.7	0	129-138	R.GSPEMPFYPR.V	Oxidation: 5	WD:WU 1.25

Detailed Protein Report

Protein 1038: 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

Quantitation

WD:WU	**Median:** 0.69	**CV:** 0.00 %	**No. of 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	Ratios
905	1	654.8549	64.59	2	40.1	10.7	0	416-428	R.EVGIGGDQGPHDK.G		WD:WU 0.69

Protein 1039: 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	

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Detailed Protein Report

Protein 1040: **PREDICTED: X-linked retinitis pigmentosa GTPase regulator isoform X1 [Homo sapiens]**

Accession:	gi|530421509	**Score:**	10.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	77.8
Database Date:	2015-11-30	**pI:**	5.1
		Sequence Coverage [%]:	1.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MREPEELMPD	SGAVFTFGKS	KFAENNPGKF	WFKNDVPVHL	SCGDEHSAVV	TGNNKLYMFG	SNNWGQLGLG	SKSAISKPTC
90	100	110	120	130	140	150	160
VKALKPEKVK	LAACGRNHTL	VSTEGGNVYA	TGGNNEGQLG	LGDTEERNTF	HVISFFTSEH	KIKQLSAGSN	TSAALTEDGR
170	180	190	200	210	220	230	240
LFMWGDNSEG	QIGLKNVSNV	CVPQQVTIGK	PVSWISCGYY	HSAFVTTDGE	LYVFGEPENG	KLGLPNQLLG	NHRTPQLVSE
250	260	270	280	290	300	310	320
IPEKVIQVAC	GGEHTVVLTE	NAVYTFGLGQ	FGQLGLGTFL	FETSEPKVIE	NIRDQTISYI	SCGENHTALI	TDIGLMYTFG
330	340	350	360	370	380	390	400
DGRHGKLGLG	LENFTNHFIP	TLCSNFLRFI	VKLVACGGCH	MVVFAAPHRG	VAKEIEFDEI	NDTCLSVATF	LPYSSLTSGN
410	420	430	440	450	460	470	480
VLQRTLSARM	RRRERERSPD	SFSMRRTLPP	IEGTLGLSAC	FLPNSVFPRC	SERNLQESVL	SEQDLMQPEE	PDYLLDEMTK
490	500	510	520	530	540	550	560
EAEIDNSSTV	ESLGETTDIL	NMTHIMSLNS	NEKSLKLSPV	QKQKDHEFSK	TEELKLEDVD	EEINAENVES	KKKTVGDDES
570	580	590	600	610	620	630	640
VPTGYHSKTE	GAERTNDDSS	AETIEKKEKA	NLEERAICEY	NENPKGYMLD	DADSSSLEIL	ENSETTPSKD	MKKTKKIFLF
650	660	670	680	690	700	710	
KRVPSINQKI	VKNNNEPLPE	IKSIGDQIIL	KSDNKDADQN	HMSQNHQNIP	PTNTERRSKS	CTIL	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2271	1	666.3126	-102.24	2	56.7	10.7	0	222-233	K.LGLPNQLLGNHR.T	

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Detailed Protein Report

Protein 1041: zinc finger protein 93 [Homo sapiens]

Accession:	gi|38708324	**Score:**	10.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	70.9
Database Date:	2015-11-30	**pI:**	10.3
		Sequence Coverage [%]:	1.6
		No. of unique 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
645	1	512.6921	-185.63	2	36.9	10.7	0	237-246	K.AFIASSTLSK.H	

Detailed Protein Report

Protein 1042: 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 1043: **PREDICTED: microtubule-associated serine/threonine-protein kinase 4 isoform X12 [Homo sapiens]**

Accession:	gi|578810348	**Score:**	10.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	247.6
Database Date:	2015-11-30	**pI:**	9.5
		Sequence Coverage [%]:	0.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MRPRSRSLSP	GRSPACCDHE	IIMMNHVYKE	RFPKATAQME	ERLKEIITSY	SPDNVLPLAD	GVLSFTHHQI	IELARDCLDK
90	100	110	120	130	140	150	160
SHQGLITSRY	FLELQHKLDK	LLQEAHDRSE	SGELAFIKQL	VRKILIVIAR	PARLLECLEF	DPEEFYYLLE	AAEGHAKEGQ
170	180	190	200	210	220	230	240
GIKTDIPRYI	ISQLGLNKDP	LEEMAHLGNY	DSGTAETPET	DESVSSSNAS	LKLRRKPRES	DFETIKLISN	GAYGAVYFVR
250	260	270	280	290	300	310	320
HKESRQRFAM	KKINKQNLIL	RNQIQQAFVE	RDILTFAENP	FVVSMYCSFE	TRRHLCMVME	YVEGGDCATL	MKNMGPLPVD
330	340	350	360	370	380	390	400
MARMYFAETV	LALEYLHNYG	IVHRDLKPDN	LLVTSMGHIK	LTDFGLSKVG	LMSMTTNLYE	GHIEKDAREF	LDKQVCGTPE
410	420	430	440	450	460	470	480
YIAPEVILRQ	GYGKPVDWWA	MGIILYEFLV	GCVPFFGDTP	EELFGQVISD	EINWPEKDEA	PPPDAQDLIT	LLLRQNPLER
490	500	510	520	530	540	550	560
LGTGGAYEVK	QHRFFRSLDW	NSLLRQKAEF	IPQLESEDDT	SYFDTRSEKY	HHMETEEEDD	TNDEDFNVEI	RQFSSCSHRF
570	580	590	600	610	620	630	640
SKVFSSIDRI	TQNSAEEKED	SVDKTKSTTL	PSTETLSWSS	EYSEMQQLST	SNSSDTESNR	HKLSSGLLPK	LAISTEGEQD
650	660	670	680	690	700	710	720
EAASCPGDPH	EEPGKPALPP	EECAQEEPEV	TTPASTISSS	TLSVGSFSEH	LDQINGRSEC	VDSTDNSSKP	SSEPASHMAR
730	740	750	760	770	780	790	800
QRLESTEKKK	ISGKVTKSLS	ASALSLMIPG	DMFAVSPLGS	PMSPHSLSSD	PSSSRDSSPS	RDSSAASASP	HQPIVIHSSG
810	820	830	840	850	860	870	880
KNYGFTIRAI	RVYVGDSDIY	TVHHIVWNVE	EGSPACQAGL	KAGDLITHIN	GEPVHGLVHT	EVIELLLKSG	NKVSITTTPF
890	900	910	920	930	940	950	960
ENTSIKTGPA	RRNSYKSRMV	RRSKKSKKKE	SLERRRSLFK	KLAKQPSPLL	HTSRSFSCLN	RSLSSGESLP	GSPTHSLSPR
970	980	990	1000	1010	1020	1030	1040
SPTPSYRSTP	DFPSGTNSSQ	SSSPSSSAPN	SPAGSGHIRP	STLHGLAPKL	GGQRYRSGRR	KSAGNIPLSP	LARTPSPTPQ
1050	1060	1070	1080	1090	1100	1110	1120
PTSPQRSPSP	LLGHSLGNSK	IAQAFPSKMH	SPPTIVRHIV	RPKSAEPPRS	PLLKRVQSEE	KLSPSYGSDK	KHLCSRKHSL
1130	1140	1150	1160	1170	1180	1190	1200
EVTQEEVQRE	QSQREAPLQS	LDENVCDVPP	LSRARPVEQG	CLKRPVSRKV	GRQESVDDLD	RDKLKAKVVV	KKADGFPEKQ
1210	1220	1230	1240	1250	1260	1270	1280
ESHQKSHGPG	SDLENFALFK	LEEREKKVYP	KAVERSSTFE	NKASMQEAPP	LGSLLKDALH	KQASVRASEG	AMSDGRVPAE
1290	1300	1310	1320	1330	1340	1350	1360
HRQGGGDFRR	APAPGTLQDG	LCHSLDRGIS	GKGEGTEKSS	QAKELLRCEK	LDSKLANIDY	LRKKMSLEDK	EDNLCPVLKP
1370	1380	1390	1400	1410	1420	1430	1440
KMTAGSHECL	PGNPVRPTGG	QQEPPPASES	RAFVSSTHAA	QMSAVSFVPL	KALTGRVDSG	TEKPGLVAPE	SPVRKSPSEY
1450	1460	1470	1480	1490	1500	1510	1520
KLEGRSVSCL	KPIEGTLDIA	LLSGPQASKT	ELPSPESAQS	PSPSGDVRAS	VPPVLPSSSG	KKNDTTSARE	LSPSSLKMNK
1530	1540	1550	1560	1570	1580	1590	1600
SYLLEPWFLP	PSRGLQNSPA	VSLPDPEFKR	DRKGPHPTAR	SPGTVMESNP	QQREGSSPKH	QDHTTDPKLL	TCLGQNLHSP
1610	1620	1630	1640	1650	1660	1670	1680
DLARPRCPLP	PEASPSREKP	GLRESSERGP	PTARSERSAA	RADTCREPSM	ELCFPETAKT	SDNSKNLLSV	GRTHPDFYTQ
1690	1700	1710	1720	1730	1740	1750	1760
TQAMEKAWAP	GGKTNHKDGP	GEARPPPRDN	SSLHSAGIPC	EKELGKVRRG	VEPKPEALLA	RRSLQPPGIE	SEKSEKLSSF
1770	1780	1790	1800	1810	1820	1830	1840
PSLQKDGAKE	PERKEQPLQR	HPSSIPPPPL	TAKDLSSPAA	RQHCSSPSHA	SGREPGAKPS	TAEPSSSPQD	PPKPVAAHSE
1850	1860	1870	1880	1890	1900	1910	1920
SSSHKPRPGP	DPGPPKTKHP	DRSLSSQKPS	VGATKGKEPA	TQSLGGSSRE	GKGHSKSGPD	VFPATPGSQN	KASDGIGQGE
1930	1940	1950	1960	1970	1980	1990	2000
GGPSVPLHTD	RAPLDAKPQP	TSGGRPLEVL	EKPVHLPRPG	HPGPSEPADQ	KLSAVGEKQT	LSPKHPKPST	VKDCPTLCKQ
2010	2020	2030	2040	2050	2060	2070	2080
TDNRQTDKSP	SQPAANTDRR	AEGKKCTEAL	YAPAEGDKLE	AGLSFVHSEN	RLKGAERPAA	GVGKGFPEAR	GKGPGPQKPP
2090	2100	2110	2120	2130	2140	2150	2160
TEADKPNGMK	RSPSATGQSS	FRSTALPEKS	LSCSSSFPET	RAGVREASAA	SSDTSSAKAA	GGMLELPAPS	NRDHRKAQPA
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2513	1	694.6522	-36.12	3	59.7	10.7	0	1135-1153	R.EAPLQSLDENVCDVPPLSR.A	

Detailed Protein Report

Protein 1044: uncharacterized protein C15orf65 [Homo sapiens]

Accession:	gi|311771669	**Score:**	10.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	13.8
Database Date:	2015-11-30	**pI:**	9.5
		Sequence Coverage [%]:	10.7
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 1.37 **CV:** 0.00 % **No. of Peptides:** 1

```
         10         20         30         40         50         60         70         80
MTDRNRDKKS TSPSNSDTEM KSEQLPPCVN PGNPVFSCML DPKTLQTATS LSKPQMIMYK TNSSHYGEFL PIPQFFPCNY
         90        100        110        120        130
TPKEQVFSSH IRATGFYQNN TLNTAPDRTR TLDFPNIQHT L
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
835	1	706.2186	-146.50	2	38.8	10.7	1	9-21	K.KSTSPSNSDTEMK.S		WD:WU 1.37

Protein 1045: PREDICTED: otoferlin isoform X1 [Homo sapiens]

Accession:	gi|530368284	**Score:**	10.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	225.9
Database Date:	2015-11-30	**pI:**	5.3
		Sequence Coverage [%]:	0.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MALLIHLKTV	SELRGRGDRI	AKVTFRGQSF	YSRVLENCED	VADFDETFRW	PVASSIDRNE	MLEIQVFNYS	KVFSNKLIGT
90	100	110	120	130	140	150	160
FRMVLQKVVE	ESHVEVTDTL	IDDNNAIIKT	SLCVEVRYQA	TDGTVGSWDD	GDFLGDESLQ	EEEKDSQETD	GLLPGSRPSS
170	180	190	200	210	220	230	240
RPPGEKSFRS	KGREKTKGGR	DDEHKAGRSV	FSAMKLGKNR	SHKEEPQRPD	EPAVLEMEDL	DHLAIRLGDG	LDPDSVSLAS
250	260	270	280	290	300	310	320
VTALTTNVSN	KRSKPDIKME	PSAGRPMDYQ	VSITVIEARQ	LVGLNMDPVV	CVEVGDDKKY	TSMKESTNCP	YYNEYFVFDF
330	340	350	360	370	380	390	400
HVSPDVMFDK	IIKISVIHSK	NLLRSGTLVG	SFKMDVGTVY	SQPEHQFHHK	WAILSDPDDI	SSGLKGYVKC	DVAVVGKGDN
410	420	430	440	450	460	470	480
IKTPHKANET	DEDDIEGNLL	LPEGVPPERQ	WARFYVKIYR	AEGLPRMNTS	LMANVKKAFI	GENKDLVDPY	VQVFFAGQKG
490	500	510	520	530	540	550	560
KTSVQKSSYE	PLWNEQVVFT	DLFPPLCKRM	KVQIRDSDKV	NDVAIGTHFI	DLRKISNDGD	KGFLPTLGPA	WVNMYGSTRN
570	580	590	600	610	620	630	640
YTLLDEHQDL	NEGLGEGVSF	RARLLLGLAV	EIVDTSNPEL	TSSTEVQVEQ	ATPISESCAG	KMEEFFLFGA	FLEASMIDRR
650	660	670	680	690	700	710	720
NGDKPITFEV	TIGNYGNEVD	GLSRPQRPRP	RKEPGDEEEV	DLIQNASDDE	AGDAGDLASV	SSTPPMRPQV	TDRNYFHLPY
730	740	750	760	770	780	790	800
LERKPCIYIK	SWWPDQRRRL	YNANIMDHIA	DKLEEGLNDI	QEMIKTEKSY	PERRLRGVLE	ELSCGCCRFL	SLADKDQGHS
810	820	830	840	850	860	870	880
SRTRLDRERL	KSCMRELENM	GQQARMLRAQ	VKRHTVRDKL	RLCQNFLQKL	RFLADEPQHS	IPDIFIWMMS	NNKRVAYARV
890	900	910	920	930	940	950	960
PSKDLLFSIV	EEETGKDCAK	VKTLFLKLPG	KRGFGSAGWT	VQAKVELYLW	LGLSKQRKEF	LCGLPCGFQE	VKAAQGLGLH
970	980	990	1000	1010	1020	1030	1040
AFPPVSLVYT	KKQAFQLRAH	MYQARSLFAA	DSSGLSDPFA	RVFFINQSQC	TEVLNETLCP	TWDQMLVFDN	LELYGEAHEL
1050	1060	1070	1080	1090	1100	1110	1120
RDDPPIIVIE	IYDQDSMGKA	DFMGRTFAKP	LVKMADEAYC	PPRFPPQLEY	YQIYRGNATA	GDLLAAFELL	QIGPAGKADL
1130	1140	1150	1160	1170	1180	1190	1200
PPINGPVDVD	RGPIMPVPMG	IRPVLSKYRV	EVLFWGLRDL	KRVNLAQVDR	PRVDIECAGK	GVQSSLIHNY	KKNPNFNTLV
1210	1220	1230	1240	1250	1260	1270	1280
KWFEVDLPEN	ELLHPPLNIR	VVDCRAFGRY	TLVGSHAVSS	LRRFIYRPPD	RSAPSWNTTG	EVVVTMEPEV	PIKKLETMVK
1290	1300	1310	1320	1330	1340	1350	1360
LDATSEAVVK	VDVAEEEKEK	KKKKKGTAEE	PEEEEPDESM	LDWWSKYFAS	IDTMKEQLRQ	QEPSGIDLEE	KEEVDNTEGL
1370	1380	1390	1400	1410	1420	1430	1440
KGSMKGKEKA	RAAKEEKKKK	TQSSGSGQGS	EAPEKKKPKI	DELKVYPKEL	ESEFDNFEDW	LHTFNLLRGK	TGDDEDGSTE
1450	1460	1470	1480	1490	1500	1510	1520
EERIVGRFKG	SLCVYKVPLP	EDVSREAGYD	STYGMFQGIP	SNDPINVLVR	VYVVRATDLH	PADINGKADP	YIAIRLGKTD
1530	1540	1550	1560	1570	1580	1590	1600
IRDKENYISK	QLNPVFGKSF	DIEASFPMES	MLTVAVYDWD	LVGTDDLIGE	TKIDLENRFY	SKHRATCGIA	QTYSTHGYNI
1610	1620	1630	1640	1650	1660	1670	1680
WRDPMKPSQI	LTRLCKDGKV	DGPHFGPPGR	VKVANRVFTG	PSEIEDENGQ	RKPTDEHVAL	LALRHWEDIP	RAGCRLVPEH
1690	1700	1710	1720	1730	1740	1750	1760
VETRPLLNPD	KPGIEQGRLE	LWVDMFPMDM	PAPGTPLDIS	PRKPKKYELR	VIIWNTDEVV	LEDDDFFTGE	KSSDIFVRGW
1770	1780	1790	1800	1810	1820	1830	1840
LKGQQEDKQD	TDVHYHSLTG	EGNFNWRYLF	PFDYLAAEEK	IVISKKESMF	SWDETEYKIP	ARLTLQIWDA	DHFSADDFLG
1850	1860	1870	1880	1890	1900	1910	1920
AIELDLNRFP	RGAKTAKQCT	MEMATGEVDV	PLVSIFKQKR	VKGWWPLLAR	NENDEFELTG	KVEAELHLLT	AEEAEKNPVG
1930	1940	1950	1960	1970	1980	1990	2000
LARNEPDPLE	KPNRPDTAFV	WFLNPLKSIK	YLICTRYKWL	IIKIVLALLG	LLMLGLFLYS	LPGYMVKKLL	GA

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1207	1	984.1444	151.03	2	43.4	10.7	0	542-559	K.GFLPTLGPAWVNMYGSTR.N	

Detailed Protein Report

Protein 1046: PREDICTED: protein unc-80 homolog isoform X8 [Homo sapiens]

Accession:	gi|578804137	**Score:**	10.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	278.5
Database Date:	2015-11-30	**pI:**	6.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	0.8
		No. of unique Peptides:	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MVKRKSSEGQ	EQDGGRGIPL	PIQTFLWRQT	SAFLRPKLGK	QYEASCVSFE	RVLVENKLHG	LSPALSEAIQ	SISRWELVQA
90	100	110	120	130	140	150	160
ALPHVLHCTA	TLLSNRNKLG	HQDKLGVAET	KLLHTLHWML	LEAPQDCNNE	RFGGTDRGSS	WGGSSSAFIH	QVENQGSPGQ
170	180	190	200	210	220	230	240
PCQSSSNDEE	ENNRRKIFQN	SMATVELFVF	LFAPLVHRIK	ESDLTFRLAS	GLVIWQPMWE	HRQPGVSGFT	ALVKPIRNII
250	260	270	280	290	300	310	320
TAKRSSPINS	QSRTCESPNQ	DARHLEGLQV	VCETFQSDSI	SPKATISGCH	RGNSFDGSLS	SQTSQERGPS	HSRASLVIPP
330	340	350	360	370	380	390	400
CQRSRYATYF	DVAVLRCLLQ	PHWSEEGTQW	SLMYYLQRLR	HMLEEKPEKP	PEPDIPLLPR	PRSSSMVAAA	PSLVNTHKTQ
410	420	430	440	450	460	470	480
DLTMKCNEEE	KSLSSEAFSK	VSLTNLRRSA	VPDLSSDLGM	NIFKKFKSRK	EDRERKGSIP	FHHTGKRRPR	RMGVPFLLHE
490	500	510	520	530	540	550	560
DHLDVSPTRS	TFSFGSFSGL	GEDRRGIEKG	GWQTTILGKL	TRRGSSDAAT	EMESLSARHS	HSHHTLVSDL	PDPSNSHGEN
570	580	590	600	610	620	630	640
TVKEVRSQIS	TITVATFNTT	LASFNVGYAD	FFNEHMRKLC	NQVPIPEMPH	EPLACANLPR	SLTDSCINYS	YLEDTEHIDG
650	660	670	680	690	700	710	720
TNNFVHKNGM	LDLSVVLKAV	YLVLNHDISS	RICDVALNIV	ECLLQLGVVP	CVEKNRKKSE	NKENETLEKR	PSEGAFQFKG
730	740	750	760	770	780	790	800
VSGSSTCGFG	GPAVSGAGDG	GGEEGGGGDG	GGGGGDGGGG	GGGGGGPYEK	NDKNQEKDES	TPVSNHRLAL	TMLIKIVKSL
810	820	830	840	850	860	870	880
GCAYGCGEGH	RGLSGDRLRH	QVFRENAQNC	LTKLYKLDKM	QFRQTMRDYV	NKDSLNNVVD	FLHALLGFCM	EPVTDNKAGF
890	900	910	920	930	940	950	960
GNNFTTVDNK	STAQNVEGII	VSAMFKSLIT	RCASTTHELH	SPENLGLYCD	IRQLVQFIKE	AHGNVFRRVA	LSALLDSAEK
970	980	990	1000	1010	1020	1030	1040
LAPGKKVEEN	EQESKPAGSK	RSEAGSIVDK	GQVSSAPEEC	RSFMSGRPSQ	TPEHDEQMQG	ANLGRKDFWR	KMFKSQSAAS
1050	1060	1070	1080	1090	1100	1110	1120
DTSSQSEQDT	SECTTAHSGT	TSDRRARSRS	RRISLRKKLK	LPIGNWLKRS	SLSGLADGVE	DLLDISSVDR	LSFIRQSSKV
1130	1140	1150	1160	1170	1180	1190	1200
KFTSAVKLSE	GGPGSGMENG	RDEEENFFKR	LGCHSFDDHL	SPNQDGGKSK	NVVNLGAIRQ	GMKRFQFLLN	CCEPGTIPDA
1210	1220	1230	1240	1250	1260	1270	1280
SILAAALDLE	APVVARAALF	LECARFVHRC	NRGNWPEWMK	GHHVNITKKG	LSRGRSPIVG	NKRNQKLQWN	AAKLFYQWGD
1290	1300	1310	1320	1330	1340	1350	1360
AIGVRLNELC	HGESESPANL	LGLIYDEETK	RRLRKEDEEE	DFLDDSTVNP	SKCGCPFALK	MAACQLLLEI	TTFLRETFSC
1370	1380	1390	1400	1410	1420	1430	1440
LPRPRTEPLV	DLESCRLRLD	PELDRHRYER	KISFAGVLDE	NEDSKDSLHS	SSHTLKSDAG	VEEKKVPSRK	IRIGGSRLLQ
1450	1460	1470	1480	1490	1500	1510	1520
IKGTRSFQVK	KGGSLSSIRR	VGSLKSSKLS	RQDSESEAEE	LQLSQSRDTV	TDLEGSPWSA	SEPSIEPEGM	SNAGAEENYH
1530	1540	1550	1560	1570	1580	1590	1600
RNMSWLHVMI	LLCNQQSFIC	THVDYCHPHC	YLHHSRSCAR	LVRAIKLLYG	DSVDSLRESS	NISSVALRGK	KQKECSDKSC
1610	1620	1630	1640	1650	1660	1670	1680
LRTPSLKKRV	SDANLEGKKD	SGMLKYIRLQ	VMSLSPAPLS	LLIKAAPILT	EEMYGDIQPA	AWELLLSMDE	HMAGAAAAMF
1690	1700	1710	1720	1730	1740	1750	1760
LLCAVKVPEA	VSDMLMSEFH	HPETVQRLNA	VLKFHTLWRF	RYQVWPRMEE	GAQQIFKIPP	PSINFTLPSP	VLGMPSVPMF
1770	1780	1790	1800	1810	1820	1830	1840
DPPWVPQCSG	SVQDPINEDQ	SKSFSARAVS	RSHQRAEHIL	KNLQQEEEKK	RLGREASLIT	AIPITQEACY	EPTCTPNSEP
1850	1860	1870	1880	1890	1900	1910	1920
EEEVEEVTNL	ASRRLSVSPS	CTSSTSHRNY	SFRRGSVWSV	RSAVSAEDEE	HTTEHTPNHH	VPQPPQAVFP	ACICAAVLPI
1930	1940	1950	1960	1970	1980	1990	2000
VHLMEDGEVR	EDGVAVSAVA	QQVLWNCLIE	DPSTVLRHFL	EKLTISNRQD	ELMYMLRKLL	LNIGDFPAQT	SHILFNYLVG
2010	2020	2030	2040	2050	2060	2070	2080
LIMYFVRTPC	EWGMDAISAT	LTFLWEVVGY	VEGLFFKDLK	QTMKKEQCEV	KLLVTASMPG	TKTLVVHGQN	ECDIPTQLPV
2090	2100	2110	2120	2130	2140	2150	2160
HEDTQFEALL	KECLEFFNIP	ESQSTHYFLM	DKRWNLIHYN	KTYVRDIYPF	RRSVSPQLNL	VHMHPEKGQE	LIQKQVFTRK
2170	2180	2190	2200	2210	2220	2230	2240

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2444	1	754.6487	-64.65	3	58.8	10.7	2	981-1001	K.RSEAGSIVDKGQVSSAPEECR.S	Carbamidomethyl: 20

Detailed Protein Report

Protein 1047: mediator of RNA polymerase II transcription subunit 23 isoform c [Homo sapiens]

Accession:	gi|395455064	**Score:**	10.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	155.5
Database Date:	2015-11-30	**pI:**	7.2
		Sequence Coverage [%]:	0.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
METQLQSIFE	EVVKTEVIEE	AFPGMFMDTP	EDEKTKLISC	LGAFRQFWGG	LSQESHEQCI	QWIVKFIHGQ	HSPKRISFLY
90	100	110	120	130	140	150	160
DCLAMAVETG	LLPPRLVCES	LINSDTLEWE	RTQLWALTFK	LVRKIIGGVD	YKGVRDLLKV	ILEKILTIPN	TVSSAVVQQL
170	180	190	200	210	220	230	240
LAAREVIAYI	LERNACLLPA	YFAVTEIRKL	YPEGKLPHWL	LGNLVSDFVD	TFRPTARINS	ICGRCSLLPV	VNNSGAICNS
250	260	270	280	290	300	310	320
WKLDPATLRF	PLKGLLPYDK	DLFEPQTALL	RYVLEQPYSR	DMVCNMLGLN	KQHKQRCPVL	EDQLVDLVVY	AMERSETEEK
330	340	350	360	370	380	390	400
FDDGGTSQLL	WQHLSSQLIF	FVLFQFASFP	HMVLSLHQKL	AGRGLIKGRD	HLMWVLLQFI	SGSIQKNALA	DFLPVMKLFD
410	420	430	440	450	460	470	480
LLYPEKEYIP	VPDINKPQST	HAFAMTCIWI	HLNRKAQNDN	SKLQIPIPHS	LRLHHEFLQQ	SLRNKSLQMN	DYKIALLCNA
490	500	510	520	530	540	550	560
YSTNSECFTL	PMGALVETIY	GNGIMRIPLP	GTNCMASGSI	TPLPMNLLDS	LTVHAKMSLI	HSIATRVIKL	AHAKSSVALA
570	580	590	600	610	620	630	640
PALVETYSRL	LVYMEIESLG	IKGFISQLLP	TVFKSHAWGI	LHTLLEMFSY	RMHHIQPHYR	VQLLSHLHTL	AAVAQTNQNQ
650	660	670	680	690	700	710	720
LHLCVESTAL	RLITALGSSE	VQPQFTRFLS	DPKTVLSAES	EELNRALILT	LARATHVTDF	FTGSDSIQGT	WCKDILQTIM
730	740	750	760	770	780	790	800
SFTPHNWASH	TLSCFPGPLQ	AFFKQNNVPQ	ESRFNLKKNV	EEEYRKWKSM	SNENDIITHF	SMQGSPPLFL	CLLWKMLLET
810	820	830	840	850	860	870	880
DHINQIGYRV	LERIGARALV	AHVRTFADFL	VYEFSTSAGG	QQLNKCIEIL	NDMVWKYNIV	TLDRLILCLA	MRSHEGNEAQ
890	900	910	920	930	940	950	960
VCYFIIQLLL	LKPNDFRNRV	SDFVKENSPE	HWLQNDWHTK	HMNYHKKYPE	KLYFEGLAEQ	VDPPVQIQSP	YLPIYFGNVC
970	980	990	1000	1010	1020	1030	1040
LRFLPVFDIV	IHRFLELLPV	SKSLETLLDH	LGGLYKFHDR	PVTYLYNTLH	YYEMHLRDRA	FLKRKLVHAI	IGSLKDNRPQ
1050	1060	1070	1080	1090	1100	1110	1120
GWCLSDTYLK	CAMNAREENP	WVPDDTYYCR	LIGRLVDTMA	GKSPGPFPNC	DWRFNEFPNP	AAHALHVTCV	ELMALAVSGK
1130	1140	1150	1160	1170	1180	1190	1200
EVGNALLNVV	LKSQPLVPRE	NITAWMNAIG	LIITALPEPY	WIVLHDRIVS	VISSPSLTSE	TEWVGYPFRL	FDFTACHQSY
1210	1220	1230	1240	1250	1260	1270	1280
SEMSCSYTLA	LAHAVWHHSS	IGQLSLIPKF	LTEVLLPIVK	TEFQLLYVYH	LVGPFLQRFQ	QERTRCMIEI	GVAFYDMLLN
1290	1300	1310	1320	1330	1340	1350	1360
VDQCSTHLNY	MDPICDFLYH	MKYMFTGDSV	KEQVEKIICN	LKPALKLRLR	FITHISKMEP	AAVPPQAMNS	GSPAPQSNQ

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2623	1	964.2392	-292.20	1	61.1	10.7	1	898-905	R.NRVSDFVK.E	

Detailed Protein Report

Protein 1048: 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

WD:WU	**Median:** 0.61	**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		WD:WU 0.61

Detailed Protein Report

Protein 1049: translational activator of cytochrome c oxidase 1 [Homo sapiens]

Accession: gi|27545315
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 10.7
MW [kDa]: 32.5
pI: 9.5
Sequence Coverage [%]: 4.7
No. of unique Peptides: 1

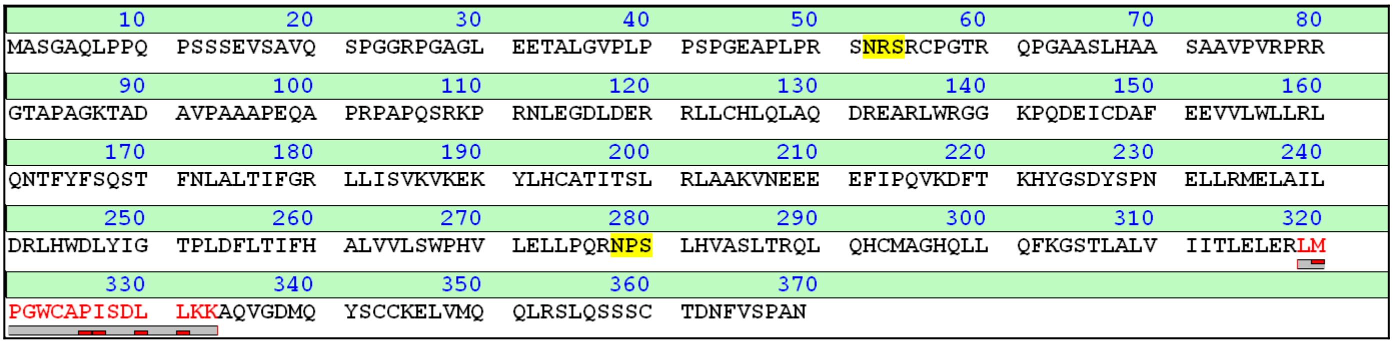
10	20	30	40	50	60	70	80
MSAWAAASLS	RAAARCLLAR	GPGVRAAPPR	DPRPSHPEPR	GCGAAPGRTL	HFTAAVPAGH	NKWSKVRHIK	GPKDVERSRI
90	100	110	120	130	140	150	160
FSKLCLNIRL	AVKEGGPNPE	HNSNLANILE	VCRSKHMPKS	TIETALKMEK	SKDTYLLYEG	RGPGGSSLLI	EALSNSSHKC
170	180	190	200	210	220	230	240
QADIRHILNK	NGGVMAVGAR	HSFDKKGVIV	VEVEDREKKA	VNLERALEMA	IEAGAEDVKE	TEDEEERNVF	KFICDASSLH
250	260	270	280	290	300		
QVRKKLDSLG	LCSVSCALEF	IPNSKVQLAE	PDLEQAAHLI	QALSNHEDVI	HVYDNIE		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
430	1	706.0114	144.80	2	33.9	10.7	2	12-25	R.AAARCLLARGPGVR.A	

Detailed Protein Report

Protein 1050: 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 1051: fibroblast growth factor 13 isoform 1 [Homo sapiens]

Accession:	gi|4758366	**Score:**	10.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	27.5
Database Date:	2015-11-30	**pI:**	10.5
		Sequence Coverage [%]:	5.7
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MAAAIASSLI RQKRQARERE KSNACKCVSS PSKGKTSCDK NKLNVFSRVK LFGSKKRRRR RPEPQLKGIV TKLYSRQGYH
        90        100        110        120        130        140        150        160
LQLQADGTID GTKDEDSTYT LFNLIPVGLR VVAIQGVQTK LYLAMNSEGY LYTSELFTPE CKFKESVFEN YYVTYSSMIY
       170        180        190        200        210        220        230        240
RQQQSGRGWY LGLNKEGEIM KGNHVKKNKP AAHFLPKPLK VAMYKEPSLH DLTEFSRSGS GTPTKSRSVS GVLNGGKSMS
       250
HNEST
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2152	1	698.2417	-140.23	2	55.3	10.7	2	22-35	K.SNACKCVSSPSKGK.T	

Detailed Protein Report

Protein 1052: putative uncharacterized protein C15orf56 [Homo sapiens]

Accession:	gi|90017700	**Score:**	10.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	17.0
Database Date:	2015-11-30	**pI:**	12.8
		Sequence Coverage [%]:	9.3
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MPRAGRAPAE GGPAPGTRSS RCLRPRPLAW RRLVPNFGAW APRKGAARVG RPVLSPRTSG AAGEPTCGAG SPGTLEEGVA
        90        100        110        120        130        140        150        160
SGRTRRRTQS AGEVAKCRWG LGQEPLCPRG AVLLNSFSPP AWPQFPPALR LRALAWPQPR GPACGSTAQW PPRGDPTWRI
       170
S
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2360	1	682.7875	-99.01	2	57.9	10.6	1	4-18	R.AGRAPAEGGPAPGTR.S	

Detailed Protein Report

Protein 1053: protein phosphatase 1 regulatory subunit 12B isoform f [Homo sapiens]

Accession:	gi|268607514	**Score:**	10.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	43.2
Database Date:	2015-11-30	**pI:**	4.7
		Sequence Coverage [%]:	3.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAELEHLGGK	RAESARMRRA	EQLRRWRGSL	TEQEPAERRG	AGRQPLTRRG	SPRVRFEDGA	VFLAACSSGD	TDEVRKLLAR
90	100	110	120	130	140	150	160
GADINTVNVD	GLTALHQACI	DENLDMVKFL	VENRANVNQQ	DNEGWTPLHA	AASCGYLNIA	EYFINHGASV	GIVNSEGEVP
170	180	190	200	210	220	230	240
SDLAEEPAMK	DLLLEQVKKQ	GVDLEQSRKE	EEQQMLQDAR	QWLNSGKIED	VRQARSGATA	LHVAAAKGYS	EVLRLLIQAG
250	260	270	280	290	300	310	320
YELNVQDYDG	WTPLHAAAHW	GVKEACSILA	EALCDMDIRN	KLGQTPFDVA	DEGLVEHLEL	LQKKQNVLRS	EKETRNKLIE
330	340	350	360	370	380	390	
SDLNSKIQSG	FFKNKEKMLY	EEETPKSQEM	EEENKESSSS	SSEEEEGEDE	ASESETEKEA	VLFWPF	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1674	1	900.4535	-28.47	2	49.3	10.6	2	201-215	R.QWLNSGKIEDVRQAR.S	

Detailed Protein Report

Protein 1054: PREDICTED: uncharacterized protein LOC102724147 [Homo sapiens]

Accession:	gi|578824644	**Score:**	10.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	38.4
Database Date:	2015-11-30	**pI:**	11.8
		Sequence Coverage [%]:	3.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGVGDDLQEP	SAIIGASPVQ	SGFLGGRKEQ	DLGKRCHKGK	AAGPGSRGSK	ALMCSTGVSK	APLTYLMSYG	FELGWRKGNR
90	100	110	120	130	140	150	160
AVACREDRGG	ESVGMGQESI	LSQCESSEYK	TTVETIPAFK	AFTMDRRAYV	VCGVRSVAGR	KSFMCDGGAG	RLSDWLRRRP
170	180	190	200	210	220	230	240
LRIARPPPRA	QPAPSRRLRA	AARRRQDAQG	WDRRPSPSPG	PGRAGTPGPA	ASRVRRGGAA	RCRPAACAPS	RGPGSGSGAP
250	260	270	280	290	300	310	320
RARAHGGQSA	EAVPSACNER	NPGEPPGASE	ELGCCVQGCC	CRRGCLKLLK	VESRLEGAAR	REPEGKEVGR	CKSDRHGQTD
330	340	350	360	370			
AQTFGRHCVG	SLPGAHEAPQ	HRLTQERGKN	TFNSEEATQS	SLL			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2833	1	616.3620	86.61	2	64.0	10.6	2	302-312	R.EPEGKEVGRCK.S	

Detailed Protein Report

Protein 1055: neuralized-like protein 4 isoform 2 [Homo sapiens]

Accession:	gi|53829368	**Score:**	10.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	166.6
Database Date:	2015-11-30	**pI:**	5.5
		Sequence Coverage [%]:	0.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
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
2675	1	715.3668	-42.44	2	61.8	10.6	1	1139-1151	K.NILLSNGNRTATR.V	

Detailed Protein Report

Protein 1056: cadherin-15 preproprotein [Homo sapiens]

Accession:	gi|4826669	**Score:**	10.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	88.9
Database Date:	2015-11-30	**pI:**	4.7
		Sequence Coverage [%]:	1.8
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 0.69 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MDAAFLLVLG	LLAQSLCLSL	GVPGWRRPTT	LYPWRRAPAL	SRVRRAWVIP	PISVSENHKR	LPYPLVQIKS	DKQQLGSVIY
90	100	110	120	130	140	150	160
SIQGPGVDEE	PRGVFSIDKF	TGKVFLNAML	DREKTDRFRL	RAFALDLGGS	TLEDPTDLEI	VVVDQNDNRP	AFLQEAFTGR
170	180	190	200	210	220	230	240
VLEGAVPGTY	VTRAEATDAD	DPETDNAALR	FSILQQGSPE	LFSIDELTGE	IRTVQVGLDR	EVVAVYNLTL	QVADMSGDGL
250	260	270	280	290	300	310	320
TATASAIITL	DDINDNAPEF	TRDEFFMEAI	EAVSGVDVGR	LEVEDRDLPG	SPNWVARFTI	LEGDPDGQFT	IRTDPKTNEG
330	340	350	360	370	380	390	400
VLSIVKALDY	ESCEHYELKV	SVQNEAPLQA	AALRAERGQA	KVRVHVQDTN	EPPVFQENPL	RTSLAEGAPP	GTLVATFSAR
410	420	430	440	450	460	470	480
DPDTEQLQRL	SYSKDYDPED	WLQVDAATGR	IQTQHVLSPA	SPFLKGGWYR	AIVLAQDDAS	QPRTATGTLS	IEILEVNDHA
490	500	510	520	530	540	550	560
PVLAPPPPGS	LCSEPHQGPG	LLLGATDEDL	PPHGAPFHFQ	LSPRLPELGR	NWSLSQVNVS	HARLRPRHQV	PEGLHRLSLL
570	580	590	600	610	620	630	640
LRDSGQPPQQ	REQPLNVTVC	RCGKDGVCLP	GAAALLAGGT	GLSLGALVIV	LASALLLLVL	VLLVALRARF	WKQSRGKGLL
650	660	670	680	690	700	710	720
HGPQDDLRDN	VLNYDEQGGG	EEDQDAYDIS	QLRHPTALSL	PLGPPPLRRD	APQGRLHPQP	PRVLPTSPLD	IADFINDGLE
730	740	750	760	770	780	790	800
AADSDPSVPP	YDTALIYDYE	GDGSVAGTLS	SILSSQGDED	QDYDYLRDWG	PRFARLADMY	GHPCGLEYGA	RWDHQAREGL
810	820						
SPGALLPRHR	GRTA						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
851	1	578.2825	-67.04	3	39.0	10.6	1	45-59	R.RAWVIPPISVSENHK.R		WD:WU 0.69

Detailed Protein Report

Protein 1057: ankyrin-2 isoform 1 [Homo sapiens]

Accession:	gi|52426735	**Score:**	10.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	433.4
Database Date:	2015-11-30	**pI:**	4.9
		Sequence Coverage [%]:	0.5
		No. of unique Peptides:	1

Quantitation

WD:WU	**Median:** 1.07	**CV:** 0.00 %	**No. of Peptides:** 1

10	20	30	40	50	60	70	80
MMNEDAAQKS	DSGEKFNGSS	QRRKRPKKSD	SNASFLRAAR	AGNLDKVVEY	LKGGIDINTC	NQNGLNALHL	AAKEGHVGLV
90	100	110	120	130	140	150	160
QELLGRGSSV	DSATKKGNTA	LHIASLAGQA	EVVKVLVKEG	ANINAQSQNG	FTPLYMAAQE	NHIDVVKYLL	ENGANQSTAT
170	180	190	200	210	220	230	240
EDGFTPLAVA	LQQGHNQAVA	ILLENDTKGK	VRLPALHIAA	RKDDTKSAAL	LLQNDHNADV	QSKMMVNRTT	ESGFTPLHIA
250	260	270	280	290	300	310	320
AHYGNVNVAT	LLLNRGAAVD	FTARNGITPL	HVASKRGNTN	MVKLLLDRGG	QIDAKTRDGL	TPLHCAARSG	HDQVVELLLE
330	340	350	360	370	380	390	400
RGAPLLARTK	NGLSPLHMAA	QGDHVECVKH	LLQHKAPVDD	VTLDYLTALH	VAAHCGHYRV	TKLLLDKRAN	PNARALNGFT
410	420	430	440	450	460	470	480
PLHIACKKNR	IKVMELLVKY	GASIQAITES	GLTPIHVAAF	MGHLNIVLLL	LQNGASPDVT	NIRGETALHM	AARAGQVEVV
490	500	510	520	530	540	550	560
RCLLRNGALV	DARAREEQTP	LHIASRLGKT	EIVQLLLQHM	AHPDAATTNG	YTPLHISARE	GQVDVASVLL	EAGAAHSLAT
570	580	590	600	610	620	630	640
KKGFTPLHVA	AKYGSLDVAK	LLLQRRAAAD	SAGKNGLTPL	HVAAHYDNQK	VALLLLEKGA	SPHATAKNGY	TPLHIAAKKN
650	660	670	680	690	700	710	720
QMQIASTLLN	YGAETNIVTK	QGVTPLHLAS	QEGHTDMVTL	LLDKGANIHM	STKSGLTSLH	LAAQEDKVNV	ADILTKHGAD
730	740	750	760	770	780	790	800
QDAHTKLGYT	PLIVACHYGN	VKMVNFLLKQ	GANVNAKTKN	GYTPLHQAAQ	QGHTHIINVL	LQHGAKPNAT	TANGNTALAI
810	820	830	840	850	860	870	880
AKRLGYISVV	DTLKVVTEEV	TTTTTTITEK	HKLNVPETMT	EVLDVSDEEG	DDTMTGDGGE	YLRPEDLKEL	GDDSLPSSQF
890	900	910	920	930	940	950	960
LDGMNYLRYS	LEGGRSDSLR	SFSSDRSHTL	SHASYLRDSA	VMDDSVVIPS	HQVSTLAKEA	ERNSYRLSWG	TENLDNVALS
970	980	990	1000	1010	1020	1030	1040
SSPIHSGFLV	SFMVDARGGA	MRGCRHNGLR	IIIPPRKCTA	PTRVTCRLVK	RHRLATMPPM	VEGEGLASRL	IEVGPSGAQF
1050	1060	1070	1080	1090	1100	1110	1120
LGKLHLPTAP	PPLNEGESLV	SRILQLGPPG	TKFLGPVIVE	IPHFAALRGK	ERELVVLRSE	NGDSWKEHFC	DYTEDELNEI
1130	1140	1150	1160	1170	1180	1190	1200
LNGMDEVLDS	PEDLEKKRIC	RIITRDFPQY	FAVVSRIKQD	SNLIGPEGGV	LSSTVVPQVQ	AVFPEGALTK	RIRVGLQAQP
1210	1220	1230	1240	1250	1260	1270	1280
MHSELVKKIL	GNKATFSPIV	TLEPRRRKFH	KPITMTIPVP	KASSDVMLNG	FGGDAPTLRL	LCSITGGTTP	AQWEDITGTT
1290	1300	1310	1320	1330	1340	1350	1360
PLTFVNECVS	FTTNVSARFW	LIDCRQIQES	VTFASQVYRE	IICVPYMAKF	VVFAKSHDPI	EARLRCFCMT	DDKVDKTLEQ
1370	1380	1390	1400	1410	1420	1430	1440
QENFAEVARS	RDVEVLEGKP	IYVDCFGNLV	PLTKSGQHHI	FSFFAFKENR	LPLFVKVRDT	TQEPCGRLSF	MKEPKSTRGL
1450	1460	1470	1480	1490	1500	1510	1520
VHQAICNLNI	TLPIYTKESE	SDQEQEEEID	MTSEKNDETE	STETSVLKSH	LVNEVPVLAS	PDLLSEVSEM	KQDLIKMTAI
1530	1540	1550	1560	1570	1580	1590	1600
LTTDVSDKAG	SIKVKELVKA	AEEEPGEPFE	IVERVKEDLE	KVNEILRSGT	CTRDESSVQS	SRSERGLVEE	EWVIVSDEEI
1610	1620	1630	1640	1650	1660	1670	1680
EEARQKAPLE	ITEYPCVEVR	IDKEIKGKVE	KDSTGLVNYL	TDDLNTCVPL	PKEQLQTVQD	KAGKKCEALA	VGRSSEKEGK
1690	1700	1710	1720	1730	1740	1750	1760
DIPPDETQST	QKQHKPSLGI	KKPVRRKLKE	KQKQKEEGLQ	ASAEKAELKK	GSSEESLGED	PGLAPEPLPT	VKATSPLIEE
1770	1780	1790	1800	1810	1820	1830	1840
TPIGSIKDKV	KALQKRVEDE	QKGRSKLPIR	VKGKEDVPKK	TTHRPHPAAS	PSLKSERHAP	GSPSPKTERH	STLSSSAKTE
1850	1860	1870	1880	1890	1900	1910	1920
RHPPVSPSSK	TEKHSPVSPS	AKTERHSPAS	SSSKTEKHSP	VSPSTKTERH	SPVSSTKTER	HPPVSPSGKT	DKRPPVSPSG
1930	1940	1950	1960	1970	1980	1990	2000
RTEKHPPVSP	GRTEKRLPVS	PSGRTDKHQP	VSTAGKTEKH	LPVSPSGKTE	KQPPVSPTSK	TERIEETMSV	RELMKAFQSG
2010	2020	2030	2040	2050	2060	2070	2080
QDPSKHKTGL	FEHKSAKQKQ	PQEKGKVRVE	KEKGPILTQR	EAQKTENQTI	KRGQRLPVTG	TAESKRGVRV	SSIGVKKEDA
2090	2100	2110	2120	2130	2140	2150	2160
AGGKEKVLSH	KIPEPVQSVP	EEESHRESEV	PKEKMADEQG	DMDLQISPDR	KTSTDFSEVI	KQELEDNDKY	QQFRLSEETE
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	
1579	1	993.5096	20.62	2	48.1	10.6	1	3371-3389	K.TVAPQGQDMASIAPDNRSK.S		WD:WU	1.07

Detailed Protein Report

Protein 1058: ATPase ASNA1 [Homo sapiens]

Accession:	gi|50428938	**Score:**	10.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	38.8
Database Date:	2015-11-30	**pI:**	4.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.7
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MAAGVAGWGV EAEEFEDAPD VEPLEPTLSN IIEQRSLKWI FVGGKGGVGK TTCSCSLAVQ LSKGRESVLI ISTDPAHNIS
        90        100        110        120        130        140        150        160
DAFDQKFSKV PTKVKGYDNL FAMEIDPSLG VAELPDEFFE EDNMLSMGKK MMQEAMSAFP GIDEAMSYAE VMRLVKGMNF
       170        180        190        200        210        220        230        240
SVVVFDTAPT GHTLRLLNFP TIVERGLGRL MQIKNQISPF ISQMCNMLGL GDMNADQLAS KLEETLPVIR SVSEQFKDPE
       250        260        270        280        290        300        310        320
QTTFICVCIA EFLSLYETER LIQELAKCKI DTHNIIVNQL VFPDPEKPCK MCEARHKIQA KYLDQMEDLY EDFHIVKLPL
       330        340        350
LPHEVRGADK VNTFSALLLE PYKPPSAQ
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1356	1	699.4617	171.51	2	45.3	10.6	0	51-63	K.TTCSCSLAVQLSK.G	Carbamidomethyl: 5

Detailed Protein Report

Protein 1059: 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 1060: **PREDICTED: inositol hexakisphosphate and diphosphoinositol-pentakisphosphate kinase 1-like [Homo sapiens]**

Accession:	gi|578798047	**Score:**	10.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	90.7
Database Date:	2015-11-30	**pI:**	7.0
		Sequence Coverage [%]:	1.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MRIHGFFVSL	SRNTIMRELA	PQFQIPWSIP	TEAEDIPIVP	TTSGTMMELR	CVIAIIRHGD	RTPKQKMKME	VKHPRFFALF
90	100	110	120	130	140	150	160
EKHGGYKTGK	LKLKRPEQLQ	EVLDITRLLL	AELEKEPGGE	IEEKTGKLEQ	LKSVLEMYGH	FSGINRKVQL	TYYPHGVKAS
170	180	190	200	210	220	230	240
NEGQDPQRET	LAPSLLLVLK	WGGELTPAGR	VQAEELGRAF	RCMYPGGQGD	YAGFPGCGLL	RLHSTFRHDL	KIYASDEGRV
250	260	270	280	290	300	310	320
QMTAAAFAKG	LLALEGELTP	ILVQMVKSAN	MNGLLDSDGD	SLSSCQHRVK	ARLHHILQQD	APFGPEDYDQ	LAPTRSTSLL
330	340	350	360	370	380	390	400
NSMTIIQNPV	KVCDQVFALI	ENLTHQIRER	MQDPRSVDLQ	LYHSETLELM	LQRWSKLERD	FRQKSGRYDI	SKIPDIYDCV
410	420	430	440	450	460	470	480
KYDVQHNGSL	GLQGTAELLR	LSKALADVVI	PQEYGISREE	KLEIAVGFCL	PLLRKILLDL	QRTHEDESVN	KLHPLYSRGV
490	500	510	520	530	540	550	560
LSPGRHVRTR	LYFTSESHVH	SLLSVFRYGG	LLDETQDAQW	QRALDYLSAI	SELNYMTQIV	IMLYEDNTQD	PLSEERFHVE
570	580	590	600	610	620	630	640
LHFSPGVKGV	EEEGSARLAV	DSNEEMKTNQ	GSMENLCPGK	ASDEPDRALQ	TSPQPPEGPG	LPRRSPLIRN	RKAGSMEVLS
650	660	670	680	690	700	710	720
ETSSSRPGGY	RLFSSSRPPT	EMKQSGLGSQ	CTGLFSTTVL	GGSSSAPNLQ	DYARSHGKKL	PPASLKHRDE	LLFVPAVKRF
730	740	750	760	770	780	790	800
SVSFAKHPTN	ELLDDQHPVV	RLLRSFSSDC	TGGRPVSLDA	TLAHHLHQCS	YHLRLFRNWL	RSGQDDPECL	YGTPCHQTGC
810							
CHYPGWV							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2855	1	626.8538	4.88	2	64.4	10.6	1	51-61	R.CVIAIIRHGDR.T	

Detailed Protein Report

Protein 1061: lengsin isoform a [Homo sapiens]

Accession:	gi|221307485	**Score:**	10.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	57.2
Database Date:	2015-11-30	**pI:**	5.9
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.5
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 0.66 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MNNEEDLLQE	DSTRDEGNET	EANSMNTLRR	TRKKVTKPYV	CSTEVGETDM	SNSNDCMRDS	SQILTPPQLS	SRMKHIRQAM
90	100	110	120	130	140	150	160
AKNRLQFVRF	EATDLHGVSR	SKTIPAHFFQ	EKVSHGVCMP	RGYLEVIPNP	KDNEMNNIRA	TCFNSDIVLM	PELSTFRVLP
170	180	190	200	210	220	230	240
WADRTARVIC	DTFTVTGEPL	LTSPRYIAKR	QLSHLQASGF	SLLSAFIYDF	CIFGVPEILN	SKIISFPALT	FLNNHDQPFM
250	260	270	280	290	300	310	320
QELVDGLYHT	GANVESFSSS	TRPGQMEISF	LPEFGISSAD	NAFTLRTGVK	EVARKYNYIA	SFFIETGFCD	SGILSHSLWD
330	340	350	360	370	380	390	400
VDRKKNMFCS	TSGTEQLTIT	GKKWLAGLLK	HSAALSCLMA	PSVSCRKRYS	KDRKDLKKSV	PTTWGYNDNS	CIFNIKCHGE
410	420	430	440	450	460	470	480
KGTRIENKLG	SATANPYLVL	AATVAAGLDG	LHSSNEVLAG	PDESTDFYQV	EPSEIPLKLE	DALVALEEDQ	CLRQALGETF
490	500	510					
IRYFVAMKKY	ELENEEIAAE	RNKFLEYFI					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
109	1	981.4823	13.57	2	30.3	10.6	1	326-343	K.NMFCSTSGTEQLTITGKK.W	Oxidation: 2	WD:WU	0.66

Detailed Protein Report

Protein 1062: DEP domain-containing protein 5 isoform 2 [Homo sapiens]

Accession:	gi|55749924	**Score:**	10.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	63.7
Database Date:	2015-11-30	**pI:**	7.2
		Sequence Coverage [%]:	2.3
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 1.24 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MRTTKVYKLV	IHKKGFGGSD	DELVVNPKVF	PHIKLGDIVE	IAHPNDEYSP	LLLQVKSLKE	DLQKETISVD	QTVTQVFRLR
90	100	110	120	130	140	150	160
PYQDVYVNVV	DPKDVTLDLV	ELTFKDQYIG	RGDMWRLKKS	LVSTCAYITQ	KVEFAGIRAQ	AGELWVKNEK	VMCGYISEDT
170	180	190	200	210	220	230	240
RVVFRSTSAM	VYIFIQMSCE	MWDFDIYGDL	YFEKAVNGFL	ADLFTKWKEK	NCSHEVTVVL	FSRTFYDAKS	VDEFPEINRA
250	260	270	280	290	300	310	320
SIRQDHKGRF	YEDFYKVVVQ	NERREEWTSL	LVTIKKLFIQ	YPVLVRLEQA	EGFPQGDNST	SAQGNYLEAI	NLSFNVFDKH
330	340	350	360	370	380	390	400
YINRNFDRTG	QMSVVITPGV	GVFEVDRLLM	ILTKQRMIDN	GIGVDLVCMG	EQPLHAVPLF	KLHNRSAPRD	SRLGDDYNIP
410	420	430	440	450	460	470	480
HWINHSFYTS	KSQLFCNSFT	PRIKLAGKKP	ASEKAKNGRD	TSLGSPKESE	NALPIQVDYD	AYDAQVFRLP	GPSRAQCLTT
490	500	510	520	530	540	550	560
CRSVRERESH	SRKSASSCDV	SSSPSLPSRT	LPTEEVRSQA	SDDSSLGKSA	NILMIPHPHL	HQYEVSSSLG	YTSTREHLG

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
853	1	866.9126	5.90	2	39.1	10.6	2	244-256	R.QDHKGRFYEDFYK.V		WD:WU 1.24

Detailed Protein Report

Protein 1063: PREDICTED: spectrin beta chain, non-erythrocytic 4 isoform X1 [Homo sapiens]

Accession:	gi|578834710	**Score:**	10.6
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

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
1037	2	530.6333	-249.62	2	41.3	10.6	2	2383-2392	R.EGGDRRASGR.R	

Detailed Protein Report

Protein 1064: **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 1065: SKI family transcriptional corepressor 1 [Homo sapiens]

Accession:	gi|384407369	**Score:**	10.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	93.7
Database Date:	2015-11-30	**pI:**	8.5
		Sequence Coverage [%]:	2.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MIPKSLVQAA	ETQRGLCEPG	GKGREGRSGG	KGETRPRGVG	TQEGKGTIPG	SPREKRGERG	EGDPALLPAE	DLWRLPGSKD
90	100	110	120	130	140	150	160
RLRSSLLPPP	GPPSSDSGPG	PPSSHSGKTA	QGPRTLNWAR	KQSARTSSNL	CAWSLAMATK	MAEIPSSPYE	PGQRGMKDTQ
170	180	190	200	210	220	230	240
RGDAPQRGSP	EPRILQLARV	GNVYLKEESS	RSGRLEAKKW	IPTKFLENLS	VPHVDLGGNQ	LWSGGMEALT	TQLGPGREGS
250	260	270	280	290	300	310	320
SSPNSKQELQ	PYSGSSALKP	NQVGETSLYG	VPIVSLVIDG	QERLCLAQIS	NTLLKNYSYN	EIHNRRVALG	ITCVQCTPVQ
330	340	350	360	370	380	390	400
LEILRRAGAM	PISSRRCGMI	TKREAERLCK	SFLGEHKPPK	LPENFAFDVV	HECAWGSRGS	FIPARYNSSR	AKCIKCGYCS
410	420	430	440	450	460	470	480
MYFSPNKFIF	HSHRTPDAKY	TQPDAANFNS	WRRHLKLSDK	SATDELSHAW	EDRGLGLATG	ASGPAGPGGP	GGGAGVRSYP
490	500	510	520	530	540	550	560
VIPVPSKGFG	LLQKLPPPLF	PHPYGFPTAF	GLCPKKDDPV	LGAGEPKGGS	YVSAFRPVVK	DTESIAKLYG	SAREAYGAGP
570	580	590	600	610	620	630	640
ARGPGPGAGS	GGYVSPDFLS	EGSSSYNSAS	PDVDTADEPE	VDVESNRFPD	DEDAQEETEP	SAPSAGGGPD	AGRPAFGDLA
650	660	670	680	690	700	710	720
AEDLVRRPER	SPPSGGGGYE	LREPCGPLGG	PAPAKVFAPE	RDEHVKSAAV	ALGPAASYVC	TPEAHEPDKE	DNHSPADDLE
730	740	750	760	770	780	790	800
TRKSYPDQRS	ISQPSPANTD	RGEDGLTLDV	TGTHLVEKDI	ENLAREELQK	LLLEQMELRK	KLEREFQSLK	DNFQDQMKRE
810	820	830	840	850	860	870	
LAYREEMVQQ	LQIVRDTLCN	ELDQERKARY	AIQQKLKEAH	DALHHFSCKM	LTPRHCTGNC	SFKPPLLP	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1961	1	599.9124	-123.71	3	52.9	10.6	2	38-55	R.GVGTQEGKGTIPGSPREK.R	

Detailed Protein Report

Protein 1066: lysosomal-associated transmembrane protein 4A [Homo sapiens]

Accession:	gi|7661916	**Score:**	10.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	26.8
Database Date:	2015-11-30	**pI:**	6.1
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.4
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 0.77 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MVSMSFKRNR	SDRFYSTRCC	GCCHVRTGTI	ILGTWYMVVN	LLMAILLTVE	VTHPNSMPAV	NIQYEVIGNY	YSSERMADNA
90	100	110	120	130	140	150	160
CVLFAVSVLM	FIISSMLVYG	AISYQVGWLI	PFFCYRLFDF	VLSCLVAISS	LTYLPRIKEY	LDQLPDFPYK	DDLLALDSSC
170	180	190	200	210	220	230	240
LLFIVLVFFA	LFIIFKAYLI	NCVWNCYKYI	NNRNVPEIAV	YPAFEAPPQY	VLPTYEMAVK	MPEKEPPPPY	LPA

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
574	1	469.1409	-54.78	2	36.0	10.6	0	19-26	R.CCGCCHVR.T	Carbamidomethyl: 1	WD:WU	0.77

Detailed Protein Report

Protein 1067: 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

WD:WU	**Median:** 1.17	**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	WD:WU 1.17

Detailed Protein Report

Protein 1068: 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

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
912	1	679.3350	-108.10	2	40.2	10.6	2	1114-1125	R.LGNAMLRIVRSK.A	

Detailed Protein Report

Protein 1069: 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 1070: collagen alpha-1(XIX) chain precursor [Homo sapiens]

Accession: gi|47778921
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 10.6
MW [kDa]: 115.1
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 1071: tumor suppressor candidate gene 1 protein [Homo sapiens]

Accession:	gi|51944974	**Score:**	10.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	23.4
Database Date:	2015-11-30	**pI:**	11.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	8.5
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MGPMWRMRGG ATRRGSCCGG DGAADGRGPG RSGRARGGGS PSGGGGGVGW RGRADGARQQ LEERFADLAA SHLEAIRARD
        90        100        110        120        130        140        150        160
EWDRQNARLR QENARLRLEN RRLKRENRSL FRQALRLPGE GGNGTPAEAR RVPEEASTNR RARDSGREDE PGSPRALRAR
       170        180        190        200        210        220
LEKLEAMYRR ALLQLHLEQR GPRPSGDKEE QPLQEPDSGL RSRDSEPSGP WL
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1610	1	853.3997	39.87	2	48.5	10.6	2	14-31	R.RGSCCGGDGAADGRGPGR.S	Carbamidomethyl: 4

Detailed Protein Report

Protein 1072: PREDICTED: glycine--tRNA ligase isoform X1 [Homo sapiens]

Accession:	gi|578813403	**Score:**	10.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	69.9
Database Date:	2015-11-30	**pI:**	5.7
		Sequence Coverage [%]:	2.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEDTLKRRFF	YDQAFAIYGG	VSGLYDFGPV	GCALKNNIIQ	TWRQHFIQEE	QILEIDCTML	TPEPVLKTSG	HVDKFADFMV
90	100	110	120	130	140	150	160
KDVKNGECFR	ADHLLKAHLQ	KLMSDKKCSV	EKKSEMESVL	AQLDNYGQQE	LADLFVNYNV	KSPITGNDLS	PPVSFNLMFK
170	180	190	200	210	220	230	240
TFIGPGGNMP	GYLRPETAQG	IFLNFKRLLE	FNQGKLPFAA	AQIGNSFRNE	ISPRSGLIRV	REFTMAEIEH	FVDPSEKDHP
250	260	270	280	290	300	310	320
KFQNVADLHL	YLYSAKAQVS	GQSARKMRLG	DAVEQGVINN	TVLGYFIGRI	YLYLTKVGIS	PDKLRFRQHM	ENEMAHYACD
330	340	350	360	370	380	390	400
CWDAESKTSY	GWIEIVGCAD	RSCYDLSCHA	RATKVPLVAE	KPLKEPKTVN	VVQFEPSKGA	IGKAYKKDAK	LVMEYLAICD
410	420	430	440	450	460	470	480
ECYITEMEML	LNEKGEFTIE	TEGKTFQLTK	DMINVKRFQK	TLYVEEVVPN	VIEPSFGLGR	IMYTVFEHTF	HVREGDEQRT
490	500	510	520	530	540	550	560
FFSFPAVVAP	FKCSVLPLSQ	NQEFMPFVKE	LSEALTRHGV	SHKVDDSSGS	IGRRYARTDE	IGVAFGVTID	FDTVNKTPHT
570	580	590	600	610	620		
ATLRDRDSMR	QIRAEISELP	SIVQDLANGN	ITWADVEARY	PLFEGQETGK	KETIEE		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1178	1	660.7641	128.35	3	43.0	10.6	2	85-101	K.NGECFRADHLLKAHLQK.L	

Detailed Protein Report

Protein 1073: glutamyl aminopeptidase [Homo sapiens]

Accession:	gi|132814467	**Score:**	10.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	109.2
Database Date:	2015-11-30	**pI:**	5.2
		Sequence Coverage [%]:	1.4
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 0.14 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MNFAEREGSK	RYCIQTKHVA	ILCAVVVGVG	LIVGLAVGLT	RSCDSSGDGG	PGTAPAPSHL	PSSTASPSGP	PAQDQDICPA
90	100	110	120	130	140	150	160
SEDESGQWKN	FRLPDFVNPV	HYDLHVKPLL	EEDTYTGTVS	ISINLSAPTR	YLWLHLRETR	ITRLPELKRP	SGDQVQVRRC
170	180	190	200	210	220	230	240
FEYKKQEYVV	VEAEEELTPS	SGDGLYLLTM	EFAGWLNGSL	VGFYRTTYTE	NGQVKSIVAT	DHEPTDARKS	FPCFDEPNKK
250	260	270	280	290	300	310	320
ATYTISITHP	KEYGALSNMP	VAKEESVDDK	WTRTTFEKSV	PMSTYLVCFA	VHQFDSVKRI	SNSGKPLTIY	VQPEQKHTAE
330	340	350	360	370	380	390	400
YAANITKSVF	DYFEEYFAMN	YSLPKLDKIA	IPDFGTGAME	NWGLITYRET	NLLYDPKESA	SSNQQRVATV	VAHELVHQWF
410	420	430	440	450	460	470	480
GNIVTMDWWE	DLWLNEGFAS	FFEFLGVNHA	ETDWQMRDQM	LLEDVLPVQE	DDSLMSSHPI	IVTVTTPDEI	TSVFDGISYS
490	500	510	520	530	540	550	560
KGSSILRMLE	DWIKPENFQK	GCQMYLEKYQ	FKNAKTSDFW	AALEEASRLP	VKEVMDTWTR	QMGYPVLNVN	GVKNITQKRF
570	580	590	600	610	620	630	640
LLDPRANPSQ	PPSDLGYTWN	IPVKWTEDNI	TSSVLFNRSE	KEGITLNSSN	PSGNAFLKIN	PDHIGFYRVN	YEVATWDSIA
650	660	670	680	690	700	710	720
TALSLNHKTF	SSADRASLID	DAFALARAQL	LDYKVALNLT	KYLKREENFL	PWQRVISAVT	YIISMFEDDK	ELYPMIEEYF
730	740	750	760	770	780	790	800
QGQVKPIADS	LGWNDAGDHV	TKLLRSSVLG	FACKMGDREA	LNNASSLFEQ	WLNGTVSLPV	NLRLLVYRYG	MQNSGNEISW
810	820	830	840	850	860	870	880
NYTLEQYQKT	SLAQEKEKLL	YGLASVKNVT	LLSRYLDLLK	DTNLIKTQDV	FTVIRYISYN	SYGKNMAWNW	IQLNWDYLVN
890	900	910	920	930	940	950	960
RYTLNNRNLG	RIVTIAEPFN	TELQLWQMES	FFAKYPQAGA	GEKPREQVLE	TVKNNIEWLK	QHRNTIREWF	FNLLESG

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
793	1	709.9203	61.50	2	38.3	10.6	0	541-553	R.QMGYPVLNVNGVK.N		WD:WU 0.14

Detailed Protein Report

Protein 1074: 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 1075: transmembrane channel-like protein 1 [Homo sapiens]

Accession:	gi|21071070	**Score:**	10.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	87.7
Database Date:	2015-11-30	**pI:**	6.2
		Sequence Coverage [%]:	1.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSPKKVQIKV	EEKEDETEES	SSEEEEEVED	KLPRRESLRP	KRKRTRDVIN	EDDPEPEPED	EETRKAREKE	RRRRLKRGAE
90	100	110	120	130	140	150	160
EEEIDEEELE	RLKAELDEKR	QIIATVKCKP	WKMEKKIEVL	KEAKKFVSEN	EGALGKGKGK	RWFAFKMMMA	KKWAKFLRDF
170	180	190	200	210	220	230	240
ENFKAACVPW	ENKIKAIESQ	FGSSVASYFL	FLRWMYGVNM	VLFILTFSLI	MLPEYLWGLP	YGSLPRKTVP	RAEEASAANF
250	260	270	280	290	300	310	320
GVLYDFNGLA	QYSVLFYGYY	DNKRTIGWMN	FRLPLSYFLV	GIMCIGYSFL	VVLKAMTKNI	GDDGGGDDNT	FNFSWKVFTS
330	340	350	360	370	380	390	400
WDYLIGNPET	ADNKFNSITM	NFKEAITEEK	AAQVEENVHL	IRFLRFLANF	FVFLTLGGSG	YLIFWAVKRS	QEFAQQDPDT
410	420	430	440	450	460	470	480
LGWWEKNEMN	MVMSLLGMFC	PTLFDLFAEL	EDYHPLIALK	WLLGRIFALL	LGNLYVFILA	LMDEINNKIE	EEKLVKANIT
490	500	510	520	530	540	550	560
LWEANMIKAY	NASFSENSTG	PPFFVHPADV	PRGPCWETMV	GQEFVRLTVS	DVLTTYVTIL	IGDFLRACFV	RFCNYCWCWD
570	580	590	600	610	620	630	640
LEYGYPSYTE	FDISGNVLAL	IFNQGMIWMG	SFFAPSLPGI	NILRLHTSMY	FQCWAVMCCN	VPEARVFKAS	RSNNFYLGML
650	660	670	680	690	700	710	720
LLILFLSTMP	VLYMIVSLPP	SFDCGPFSGK	NRMFEVIGET	LEHDFPSWMA	KILRQLSNPG	LVIAVILVMV	LAIYYLNATA
730	740	750	760	770			
KGQKAANLDL	KKKMKMQALE	NKMRNKKMAA	ARAAAAAGRQ				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
962	1	529.1944	-206.45	2	40.8	10.6	1	722-731	K.GQKAANLDLK.K	

Detailed Protein Report

Protein 1076: PREDICTED: ATP-binding cassette sub-family A member 9 isoform X4 [Homo sapiens]

Accession:	gi|530411334	**Score:**	10.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	163.3
Database Date:	2015-11-30	**pI:**	8.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	0.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGNGKQVKMS	KRRMSVGQQT	WALLCKNCLK	KWRMKRQTLL	EWLFSFLLVL	FLYLFFSNLH	QVHDTPQMSS	MDLGRVDSFN
90	100	110	120	130	140	150	160
DTNYVIAFAP	ESKTTQEIMN	KVASAPFLKG	RTIMGWPDEK	SMDELDLNYS	IDAVRVIFTD	TFSYHLKFSW	GHRIPMMKEH
170	180	190	200	210	220	230	240
RDHSAHCQAV	NEKMKCEGSE	FWEKGFVAFQ	AAINAAIIEI	ATNHSVMEQL	MSVTGVHMKI	LPFVAQGGVA	TDFFIFFCII
250	260	270	280	290	300	310	320
SFSTFIYYVS	VNVTQERQYI	TSLMTMMGLR	ESAFWLSWGL	MYAGFILIMA	TLMALIVKSA	QIVVLTGFVM	VFTLFLLYGL
330	340	350	360	370	380	390	400
SLITLAFLMS	VLIKKPFLTG	LVVFLLIVFW	GILGFPALYT	RLPAFLEWTL	CLLSPFAFTV	GMAQLIHLDY	DVNSNAHLDS
410	420	430	440	450	460	470	480
SQNPYLIIAT	LFMLVFDTLL	YLVLTLYFDK	ILPAEYGHRC	SPLFFLKSCF	WFQHGRANHV	VLENETDSDP	TPNDCFEPVS
490	500	510	520	530	540	550	560
PEFCGKEAIR	IKNLKKEYAG	KCERVEALKG	VVFDIYEGQI	TALLGHSGAG	KTTLLNILSG	LSVPTSGSVT	VYNHTLSRMA
570	580	590	600	610	620	630	640
DIENISKFTG	FCPQSNVQFG	FLTVKENLRL	FAKIKGILPH	EVEKEVQRVV	QELEMENIQD	ILAQNLSGGQ	NRKLTFGIAI
650	660	670	680	690	700	710	720
LGDPQVLLLD	EPTAGLDPLS	RHRIWNLLKE	GKSDRVILFS	TQFIDEADIL	ADRKVFISNG	KLKCAGSSLF	LKKKWGIGYH
730	740	750	760	770	780	790	800
LSLHLNERCD	PESITSLVKQ	HISDAKLTAQ	SEEKLVYILP	LERTNKFPEL	YRDLDRCSNQ	GIEDYGVSIT	TLNEVFLKLE
810	820	830	840	850	860	870	880
GKSTIDESDI	GIWGQLQTDG	AKDIGSLVEL	EQVLSSFHET	RKTISGVALW	RQQVCAIAKV	RFLKLKKERK	SLWTILLLFG
890	900	910	920	930	940	950	960
ISFIPQLLEH	LFYESYQKSY	PWELSPNTYF	LSPGQQPQDP	LTHLLVINKT	GSTIDNFLHS	LRRQNIAIEV	DAFGTRNGTD
970	980	990	1000	1010	1020	1030	1040
DPSYNGAIIV	SGDEKDHRFS	IACNTKRLNC	FPVLLDVISN	GLLGIFNSSE	HIQTDRSTFF	EEHMDYEYGY	RSNTFFWIPM
1050	1060	1070	1080	1090	1100	1110	1120
AASFTPYIAM	SSIGDYKKKA	HSQLRISGLY	PSAYWFGQAL	VDVSLYFLIL	LLMQIMDYIF	SPEEIIFIIQ	NLLIQILCSI
1130	1140	1150	1160	1170	1180	1190	1200
GYVSSLVFLT	YVISFIFRNG	RKNSGIWSFF	FLIVVIFSIV	ATDLNEYGFL	GLFFGTMLIP	PFTLIGSLFI	FSEISPDSMD
1210	1220	1230	1240	1250	1260	1270	1280
YLGASESEIV	YLALLIPYLH	FLIFLFILRC	LEMNCRKKLM	RKDPVFRISP	RSNAIFPNPE	EPEGEEEDIQ	MERMRTVNAM
1290	1300	1310	1320	1330	1340	1350	1360
AVRDFDETPV	IIASCLRKEY	AGKKKNCFSK	RKKKIATRNV	SFCVKKGEVI	GLLGHNGAGK	STTIKMITGD	TKPTAGQVIL
1370	1380	1390	1400	1410	1420	1430	1440
KGSGGGEPLG	FLGYCPQENA	LWPNLTVRQH	LEVYAAVKGL	RKGDAMIAIT	RLVDALKLQD	QLKAPVKTLS	EGIKRKAGDS
1450							
GHL							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
882	1	470.6496	-174.02	2	39.4	10.6	0	979-986	R.FSIACNTK.R	Carbamidomethyl: 5

Detailed Protein Report

Protein 1077: probable ATP-dependent RNA helicase DHX35 isoform 2 [Homo sapiens]

Accession: gi|299829255
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 10.6
MW [kDa]: 75.4
pI: 9.5
Sequence Coverage [%]: 2.2
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MAAPVGPVKF	WRPGTEGPGV	SISEERQSLA	ENSGTTVVYN	PYAALSIEQQ	RQKLPVFKYL	AEAGWTAEGR	VVGVTQPRRV
90	100	110	120	130	140	150	160
AAVTVAGRVA	EERGAVLGHE	VGYCIRFDDC	TDQLATRIKF	LTDGMLVREM	MVDPLLTKYS	VIMLDEAHER	TLYTDIAIGL
170	180	190	200	210	220	230	240
LKKIQKKRGD	LRLIVASATL	DADKFRDFFN	QNETSDPARD	TCVILTVEGR	TFPVDIFYLQ	SPVPDYIKST	VETVVKIHQT
250	260	270	280	290	300	310	320
EGDGDVLAFL	TGQEEVETVV	SMLIEQARAL	ARTGMKRHLR	VLPMYAGLPS	FEQMKVFERV	SRSVRKVIVA	TNVAETSITI
330	340	350	360	370	380	390	400
SGIVYVIDCG	FVKLRAYNPR	TAIECLVVVP	VSQASANQRA	GRGGRSRSGK	CYRLYTEEAF	DKLPQSTVPE	MQRSNLAPVI
410	420	430	440	450	460	470	480
LQLKALGIDN	VLRFHFMSPP	PAQSMVQALE	LLYALGGLDK	DCRLTEPLGM	RIAEFPLNPM	FAKMLLESGN	FGCSQEILSI
490	500	510	520	530	540	550	560
AAMMQIQNIF	VVPPNQKSHA	IRVHRKFAVE	EGDHLTMLNI	YEAFIKHNKD	SKWCQEHFLN	YKGLVRAATV	REQLKKLLVK
570	580	590	600	610	620	630	640
FQVPRKSSEG	DPDLVLRCIV	SGFFANAARF	HSTGAYRTIR	DDHELHIHPA	SVLYAEKPPR	WVIYNEVIQT	SKYYMRDVTA
650	660	670	680				
IESAWLLELA	PHFYQQGTHL	SLKAKRAKVQ	DP				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2138	1	863.8534	-89.53	2	55.3	10.6	0	281-295	R.VLPMYAGLPSFEQMK.V	Oxidation: 4

Detailed Protein Report

Protein 1078: matrix-remodeling-associated protein 5 precursor [Homo sapiens]

Accession:	gi|139948432	**Score:**	10.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	312.0
Database Date:	2015-11-30	**pI:**	9.3
		Sequence Coverage [%]:	0.8
		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

Detailed Protein Report

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 1079: 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 1080: calcium-activated potassium channel subunit alpha-1 isoform c [Homo sapiens]

Accession:	gi|238624130	**Score:**	10.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	137.5
Database Date:	2015-11-30	**pI:**	6.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	0.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MANGGGGGGG	SSGGGGGGGG	SSLRMSSNIH	ANHLSLDASS	SSSSSSSSSS	SSSSSSSSSS	VHEPKMDALI	IPVTMEVPCD
90	100	110	120	130	140	150	160
SRGQRMWWAF	LASSMVTFFG	GLFIILLWRT	LKYLWTVCCH	CGGKTKEAQK	INNGSSQADG	TLKPVDEKEE	AVAAEVGWMT
170	180	190	200	210	220	230	240
SVKDWAGVMI	SAQTLTGRVL	VVLVFALSIG	ALVIYFIDSS	NPIESCQNFY	KDFTLQIDMA	FNVFFLLYFG	LRFIAANDKL
250	260	270	280	290	300	310	320
WFWLEVNSVV	DFFTVPPVFV	SVYLNRSWLG	LRFLRALRLI	QFSEILQFLN	ILKTSNSIKL	VNLLSIFIST	WLTAAGFIHL
330	340	350	360	370	380	390	400
VENSGDPWEN	FQNNQALTYW	ECVYLLMVTM	STVGYGDVYA	KTTLGRLFMV	FFILGGLAMF	ASYVPEIIEL	IGNRKKYGGS
410	420	430	440	450	460	470	480
YSAVSGRKHI	VVCGHITLES	VSNFLKDFLH	KDRDDVNVEI	VFLHNISPNL	ELEALFKRHF	TQVEFYQGSV	LNPHDLARVK
490	500	510	520	530	540	550	560
IESADACLIL	ANKYCADPDA	EDASNIMRVI	SIKNYHPKIR	IITQMLQYHN	KAHLLNIPSW	NWKEGDDAIC	LAELKLGFIA
570	580	590	600	610	620	630	640
QSCLAQGLST	MLANLFSMRS	FIKIEEDTWQ	KYYLEGVSNE	MYTEYLSSAF	VGLSFPTVCE	LCFVKLKLLM	IAIEYKSANR
650	660	670	680	690	700	710	720
ESRILINPGN	HLKIQEGTLG	FFIASDAKEV	KRAFFYCKAC	HDDITDPKRI	KKCGCKRPKM	SIYKRMRRAC	CFDCGRSERD
730	740	750	760	770	780	790	800
CSCMSGRVRG	NVDTLERAFP	LSSVSVNDCS	TSFRAFEDEQ	PSTLSPKKKQ	RNGGMRNSPN	TSPKLMRHDP	LLIPGNDQID
810	820	830	840	850	860	870	880
NMDSNVKKYD	STGMFHWCAP	KEIEKVILTR	SEAAMTVLSG	HVVVCIFGDV	SSALIGLRNL	VMPLRASNFH	YHELKHIVFV
890	900	910	920	930	940	950	960
GSIEYLKREW	ETLHNFPKVS	ILPGTPLSRA	DLRAVNINLC	DMCVILSANQ	NNIDDTSLQD	KECILASLNI	KSMQFDDSIG
970	980	990	1000	1010	1020	1030	1040
VLQANSQGFT	PPGMDRSSPD	NSPVHGMLRQ	PSITTGVNIP	IITELVNDTN	VQFLDQDDDD	DPDTELYLTQ	PFACGTAFAV
1050	1060	1070	1080	1090	1100	1110	1120
SVLDSLMSAT	YFNDNILTLI	RTLVTGGATP	ELEALIAEEN	ALRGGYSTPQ	TLANRDRCRV	AQLALLDGPF	ADLGDGGCYG
1130	1140	1150	1160	1170	1180	1190	1200
DLFCKALKTY	NMLCFGIYRL	RDAHLSTPSQ	CTKRYVITNP	PYEFELVPTD	LIFCLMQFDH	NAGQSRASLS	HSSHSSQSSS
1210	1220	1230	1240				
KKSSSVHSIP	STANRQNRPK	SRESRDKQKY	VQEERL				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2635	1	644.1226	-193.67	2	61.2	10.5	1	717-727	R.SERDCSCMSGR.V	Carbamidomethyl: 5

Protein 1081: sterile alpha motif domain-containing protein 9-like [Homo sapiens]

Accession: gi|51339291
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 10.5
MW [kDa]: 184.4
pI: 9.0
Sequence Coverage [%]: 1.1
No. of unique Peptides: 1

Alias proteins:

Accession	Name	Description
gi|578814011	refseq_human(refseq_human_20140103.fasta)	PREDICTED: sterile alpha motif domain-containing protein 9-like isoform X6 [Homo sapiens]
gi|578814009	refseq_human(refseq_human_20140103.fasta)	PREDICTED: sterile alpha motif domain-containing protein 9-like isoform X5 [Homo sapiens]
gi|578814007	refseq_human(refseq_human_20140103.fasta)	PREDICTED: sterile alpha motif domain-containing protein 9-like isoform X4 [Homo sapiens]
gi|530385585	refseq_human(refseq_human_20140103.fasta)	PREDICTED: sterile alpha motif domain-containing protein 9-like isoform X3 [Homo sapiens]
gi|530385581	refseq_human(refseq_human_20140103.fasta)	PREDICTED: sterile alpha motif domain-containing protein 9-like isoform X1 [Homo sapiens]

Detailed Protein Report

10	20	30	40	50	60	70	80
MSKQVSLPEM	IKDWTKEHVK	KWVNEDLKIN	EQYGQILLSE	EVTGLVLQEL	TEKDLVEMGL	PWGPALLIKR	SYNKLNSKSP
90	100	110	120	130	140	150	160
ESDNHDPGQL	DNSKPSKTEH	QKNPKHTKKE	EENSMSSNID	YDPREIRDIK	QEESILMKEN	VLDEVANAKH	KKKGKLKPEQ
170	180	190	200	210	220	230	240
LTCMPYPFDQ	FHDSHRYIEH	YTLQPETGAL	NLIDPIHEFK	ALTNTETATE	VDIKMKFSNE	VFRFASACMN	SRTNGTIHFG
250	260	270	280	290	300	310	320
VKDKPHGEIV	GVKITSKAAF	IDHFNVMIKK	YFEESEINEA	KKCIREPRFV	EVLLQNNTPS	DRFVIEVDTI	PKHSICNDKY
330	340	350	360	370	380	390	400
FYIQMQICKD	KIWKQNQNLS	LFVREGASSR	DILANSKQRD	VDFKAFLQNL	KSLVASRKEA	EEEYGMKAMK	KESEGLKLVK
410	420	430	440	450	460	470	480
LLIGNRDSLD	NSYYDWYILV	TNKCHPNQIK	HLDFLKEIKW	FAVLEFDPES	MINGVVKAYK	ESRVANLHFP	NQYEDKTTNM
490	500	510	520	530	540	550	560
WEKISTLNLY	QQPSWIFCNG	RSDLKSETYK	PLEPHLWQRE	RASEVRKLIL	FLTDENIMTR	GKFLVVFLLL	SSVESPGDPL
570	580	590	600	610	620	630	640
IETFWAFYQA	LKGMENMLCI	SVNSHIYQRW	KDLLQTRMKM	EDELTNHSIS	TLNIELVNST	ILKLKSVTRS	SRRFLPARGS
650	660	670	680	690	700	710	720
SSVILEKKKE	DVLTALEILC	ENECTETDIE	KDKSKFLEFK	KSKEEHFYRG	GKVSWWNFYF	SSENYSSDFV	KRDSYEKLKD
730	740	750	760	770	780	790	800
LIHCWAESPK	PIFAKIINLY	HHPGCGGTTL	AMHVLWDLKK	NFRCAVLKNK	TTDFAEIAEQ	VINLVTYRAK	SHQDYIPVLL
810	820	830	840	850	860	870	880
LVDDFEEQEN	VYFLQNAIHS	VLAEKDLRYE	KTLVIILNCM	RSRNPDESAK	LADSIALNYQ	LSSKEQRAFG	AKLKEIEKQH
890	900	910	920	930	940	950	960
KNCENFYSFM	IMKSNFDETY	IENVVRNILK	GQDVDSKEAQ	LISFLALLSS	YVTDSTISVS	QCEIFLGIIY	TSTPWEPESL
970	980	990	1000	1010	1020	1030	1040
EDKMGTYSTL	LIKTEVAEYG	RYTGVRIIHP	LIALYCLKEL	ERSYHLDKCQ	IALNILEENL	FYDSGIGRDK	FQHDVQTLLL
1050	1060	1070	1080	1090	1100	1110	1120
TRQRKVYGDE	TDTLFSPLME	ALQNKDIEKV	LSAGSRRFPQ	NAFICQALAR	HFYIKEKDFN	TALDWARQAK	MKAPKNSYIS
1130	1140	1150	1160	1170	1180	1190	1200
DTLGQVYKSE	IKWWLDGNKN	CRSITVNDLT	HLLEAAEKAS	RAFKESQRQT	DSKNYETENW	SPQKSQRRYD	MYNTACFLGE
1210	1220	1230	1240	1250	1260	1270	1280
IEVGLYTIQI	LQLTPFFHKE	NELSKKHMVQ	FLSGKWTIPP	DPRNECYLAL	SKFTSHLKNL	QSDLKRCFDF	FIDYMVLLKM
1290	1300	1310	1320	1330	1340	1350	1360
RYTQKEIAEI	MLSKKVSRCF	RKYTELFCHL	DPCLLQSKES	QLLQEENCRK	KLEALRADRF	AGLLEYLNPN	YKDATTMESI
1370	1380	1390	1400	1410	1420	1430	1440
VNEYAFLLQQ	NSKKPMTNEK	QNSILANIIL	SCLKPNSKLI	QPLTTLKKQL	REVLQFVGLS	HQYPGPYFLA	CLLFWPENQE
1450	1460	1470	1480	1490	1500	1510	1520
LDQDSKLIEK	YVSSLNRSFR	GQYKRMCRSK	QASTLFYLGK	RKGLNSIVHK	AKIEQYFDKA	QNTNSLWHSG	DVWKKNEVKD
1530	1540	1550	1560	1570	1580	1590	
LLRRLTGQAE	GKLISVEYGT	EEKIKIPVIS	VYSGPLRSGR	NIERVSFYLG	FSIEGPLAYD	IEVI	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
372	1	699.2836	-142.88	3	33.3	10.5	1	718-735	K.LKDLIHCWAESPKPIFAK.I	

Detailed Protein Report

Protein 1082: cyclic nucleotide-gated olfactory channel [Homo sapiens]

Accession:	gi|42718011	**Score:**	10.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	76.0
Database Date:	2015-11-30	**pI:**	5.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.1
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 0.79 **CV:** 0.00 % **No. of 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	Ratios
1498	1	798.9215	3.49	2	47.5	10.5	2	485-498	K.GDIGKEMYIIKEGK.L	Oxidation: 7	WD:WU 0.79

Detailed Protein Report

Protein 1083: tripartite motif-containing protein 46 isoform 4 [Homo sapiens]

Accession:	gi|375298680	**Score:**	10.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	81.8
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
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

Detailed Protein Report

Protein 1084: endogenous Bornavirus-like nucleoprotein 2 [Homo sapiens]

Accession:	gi|40538806	**Score:**	10.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	30.4
Database Date:	2015-11-30	**pI:**	10.0
		Sequence Coverage [%]:	7.0
		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	

Protein 1085: 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

Quantitation

WD:WU **Median:** 0.85 **CV:** 0.00 % **No. of 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	Ratios
643	1	820.5020	122.11	2	36.9	10.5	1	114-127	K.MVVECKMNNIVSTR.I	Oxidation: 1	WD:WU 0.85

Detailed Protein Report

Protein 1086: amyloid protein-binding protein 2 isoform 2 [Homo sapiens]

Accession:	gi|541862246	**Score:**	10.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	58.5
Database Date:	2015-11-30	**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 1087: 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 1088: transcription factor Sp8 isoform 2 [Homo sapiens]

Accession:	gi|39812501	**Score:**	10.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	48.6
Database Date:	2015-11-30	**pI:**	10.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLAATCNKIG	SPSPSPSSLS	DSSSSFGKGF	HPWKRSSSSS	SASCNVVGSS	LSSFGVSGAS	RNGGSSSAAA	AAAAAAAAAA
90	100	110	120	130	140	150	160
ALVSDSFSCG	GSPGSSAFSL	TSSSAAAAAA	AAAAAASSSP	FANDYSVFQA	PGVSGGSGGG	GGGGGGGSSA	HSQDGSHQPV
170	180	190	200	210	220	230	240
FISKVHTSVD	GLQGIYPRVG	MAHPYESWFK	PSHPGLGAAG	EVGSAGASSW	WDVGAGWIDV	QNPNSAAALP	GSLHPAAGGL
250	260	270	280	290	300	310	320
QTSLHSPLGG	YNSDYSGLSH	SAFSSGASSH	LLSPAGQHLM	DGFKPVLPGS	YPDSAPSPLA	GAGGSMLSAG	PSAPLGGSPR
330	340	350	360	370	380	390	400
SSARRYSGRA	TCDCPNCQEA	ERLGPAGASL	RRKGLHSCHI	PGCGKVYGKT	SHLKAHLRWH	TGERPFVCNW	LFCGKRFTRS
410	420	430	440	450	460	470	480
DELQRHLRTH	TGEKRFACPV	CNKRFMRSDH	LSKHVKTHSG	GGGGGGSAGS	GSGGKKGSDT	DSEHSAAGSP	PCHSPELLQP
490	500						
PEPGHRNGLE							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2670	1	980.4483	58.67	2	61.7	10.5	1	326-342	R.YSGRATCDCPNCQEAER.L	Carbamidomethyl: 12

Detailed Protein Report

Protein 1089: PREDICTED: GDP-mannose 4,6 dehydratase isoform X1 [Homo sapiens]

Accession:	gi|578811609	**Score:**	10.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	32.3
Database Date:	2015-11-30	**pI:**	9.5
		Sequence Coverage [%]:	2.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAHAPARCPS	ARGSGDGEMG	KPRNVALITG	ITGQDGSYLA	EFLLEKGYEV	HGIVRRSSSF	NTGRIEHLYK	NPQAHIEGNM
90	100	110	120	130	140	150	160
KLHYGDLTDS	TCLVKIINEV	KPTEIYNLGA	QSHVKISFDL	AEYTADVDGV	GTLRLLDAVK	TCGLINSVKF	YQASTSELYG
170	180	190	200	210	220	230	240
KVQEIPQKET	TPFYPRSPYG	AAKLYAYWIV	VNFREAYNLF	AVNGILFNHE	SPRRGANFVT	RKISRSVAKI	YLGQLECFSL
250	260	270	280	290	300		
GNLDAKRDWG	HAKDYVEHTS	SQMSHSSGLW	ILIGSLLSYT	RNPIFKNHCS			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1480	1	428.0689	-309.31	2	46.9	10.5	0	57-64	R.SSSFNTGR.I	

Detailed Protein Report

Protein 1090: dual specificity tyrosine-phosphorylation-regulated kinase 2 isoform 1 [Homo sapiens]

Accession:	gi|4503427	**Score:**	10.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	59.7
Database Date:	2015-11-30	**pI:**	10.2
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MNDHLHVGSH	AHGQIQVQQL	FEDNSNKRTV	LTTQPNGLTT	VGKTGLPVVP	ERQLDSIHRR	QGSSTSLKSM	EGMGKVKATP
90	100	110	120	130	140	150	160
MTPEQAMKQY	MQKLTAFEHH	EIFSYPEIYF	LGLNAKKRQG	MTGGPNNGGY	DDDQGSYVQV	PHDHVAYRYE	VLKVIGKGSF
170	180	190	200	210	220	230	240
GQVVKAYDHK	VHQHVALKMV	RNEKRFHRQA	AEEIRILEHL	RKQDKDNTMN	VIHMLENFTF	RNHICMTFEL	LSMNLYELIK
250	260	270	280	290	300	310	320
KNKFQGFSLP	LVRKFAHSIL	QCLDALHKNR	IIHCDLKPEN	ILLKQQGRSG	IKVIDFGSSC	YEHQRVYTYI	QSRFYRAPEV
330	340	350	360	370	380	390	400
ILGARYGMPI	DMWSLGCILA	ELLTGYPLLP	GEDEGDQLAC	MIELLGMPSQ	KLLDASKRAK	NFVSSKGYPR	YCTVTTLSDG
410	420	430	440	450	460	470	480
SVVLNGGRSR	RGKLRGPPES	REWGNALKGC	DDPLFLDFLK	QCLEWDPAVR	MTPGQALRHP	WLRRRLPKPP	TGEKTSVKRI
490	500	510	520	530			
TESTGAITSI	SKLPPPSSSA	SKLRTNLAQM	TDANGNIQQR	TVLPKLVS			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
959	1	546.7312	-52.04	4	40.3	10.5	2	69-88	K.SMEGMGKVKATPMTPEQAMK.Q	Oxidation: 2, 5

Detailed Protein Report

Protein 1091: 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 1092: PREDICTED: src substrate cortactin isoform X2 [Homo sapiens]

Accession:	gi|578821165	**Score:**	10.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	41.2
Database Date:	2015-11-30	**pI:**	6.6
		Sequence Coverage [%]:	3.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MWKASAGHAV	SIAQDDAGAD	DWETDPDFVN	DVSEKEQRWG	AKTVQGSGHQ	EHINIHKLRE	NVFQEHQTLK	EKELETGPKA
90	100	110	120	130	140	150	160
SHGYGGKFGV	EQDRMDKSAV	GHEYQSKLSK	HCSQVDSVRG	FGGKFGVQMD	RVDQSAVGFE	YQGKTEKHAS	QKDYSSGFGG
170	180	190	200	210	220	230	240
KYGVQADRVD	KSAVGFDYQG	KTEKHESQRD	YSKGFGGKYG	IDKDKVDKSA	VGFEYQGKTE	KHESQKDYVK	GFGGKFGVQT
250	260	270	280	290	300	310	320
DRQDKCALGW	DHQEKLQLHE	SQKDYKTGFG	GKFGVQSERQ	DSAAVGFDYK	EKLAKHESQQ	DYSKGFGGKY	GVQKDRMDKN
330	340	350	360	370			
ASTFEDVTQV	SSAYQKTVPV	EAVTSFWEQL	GPAQLPEPLG	RSCDRRKTS			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2947	1	694.8617	-0.54	2	65.6	10.5	1	256-266	K.LQLHESQKDYK.T	

Detailed Protein Report

Protein 1093: kinetochore-associated protein 1 [Homo sapiens]

Accession:	gi|7661960	**Score:**	10.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	250.6
Database Date:	2015-11-30	**pI:**	5.6
		Sequence Coverage [%]:	0.7
		No. of unique Peptides:	1

Quantitation

WD:WU	**Median:**	0.88	**CV:**	0.00 %	**No. of Peptides:**	1

Alias proteins:

Accession	Name	Description
gi|578824490	refseq_human (refseq_human_20140103.fasta)	PREDICTED: kinetochore-associated protein 1 isoform X1 [Homo sapiens]

Detailed Protein Report

10	20	30	40	50	60	70	80
MWNDIELLTN	DDTGSGYLSV	GSRKEHGTAL	YQVDLLVKIS	SEKASLNPKI	QACSLSDGFI	IVADQSVILL	DSICRSLQLH
90	100	110	120	130	140	150	160
LVFDTEVDVV	GLCQEGKFLL	VGERSGNLHL	IHVTSKQTLL	TNAFVQKAND	ENRRTYQNLV	IEKDGSNEGT	YYMLLLTYSG
170	180	190	200	210	220	230	240
FFCITNLQLL	KIQQAIENVD	FSTAKKLQGQ	IKSSFISTEN	YHTLGCLSLV	AGDLASEVPV	IIGGTGNCAF	SKWEPDSSKK
250	260	270	280	290	300	310	320
GMTVKNLIDA	EIIKGAKKFQ	LIDNLLFVLD	TDNVLSLWDI	YTLTPVWNWP	SLHVEEFLLT	TEADSPSSVT	WQGITNLKLI
330	340	350	360	370	380	390	400
ALTASANKKM	KNLMVYSLPT	MEILYSLEVS	SVSSLVQTGI	STDTIYLLEG	VCKNDPKLSE	DSVSVLVLRC	LTEALPENRL
410	420	430	440	450	460	470	480
SRLLHKHRFA	EAESFAIQFG	LDVELVYKVK	SNHILEKLAL	SSVDASEQTE	WQQLVDDAKE	NLHKIQDDEF	VVNYCLKAQW
490	500	510	520	530	540	550	560
ITYETTQEML	NYAKTRLLKK	EDKTALIYSD	GLKEVLRAHA	KLTTFYGAFG	PEKFSGSSWI	EFLNNEDDLK	DIFLQLKEGN
570	580	590	600	610	620	630	640
LVCAQYLWLR	HRANFESRFD	VKMLESLLNS	MSASVSLQKL	CPWFKNDVIP	FVRRTVPEGQ	IILAKWLEQA	ARNLELTDKA
650	660	670	680	690	700	710	720
NWPENGLQLA	EIFFTAEKTD	ELGLASSWHW	ISLKDYQNTE	EVCQLRTLVN	NLRELITLHR	KYNCKLALSD	FEKENTTTIV
730	740	750	760	770	780	790	800
FRMFDKVLAP	ELIPSILEKF	IRVYMREHDL	QEEELLLLYI	EDLLNRCSSK	STSLFETAWE	AKAMAVIACL	SDTDLIFDAV
810	820	830	840	850	860	870	880
LKIMYAAVVP	WSAAVEQLVK	QHLEMDHPKV	KLLQESYKLM	EMKKLLRGYG	IREVNLLNKE	IMRVVRYILK	QDVPSSLEDA
890	900	910	920	930	940	950	960
LKVAQAFMLS	DDEIYSLRII	DLIDREQGED	CLLLLKSLPP	AEAEKTAERV	IIWARLALQE	EPDHSKEGKA	WRMSVAKTSV
970	980	990	1000	1010	1020	1030	1040
DILKILCDIQ	KDNLQKKDEC	EEMLKLFKEV	ASLQENFEVF	LSFEDYSNSS	LVADLREQHI	KAHEVAQAKH	KPGSTPEPIA
1050	1060	1070	1080	1090	1100	1110	1120
AEVRSPSMES	KLHRQALALQ	MSKQELEAEL	TLRALKDGNI	KTALKKCSDL	FKYHCNADTG	KLLFLTCQKL	CQMLADNVPV
1130	1140	1150	1160	1170	1180	1190	1200
TVPVGLNLPS	MIHDLASQAA	TICSPDFLLD	ALELCKHTLM	AVELSRQCQM	DDCGILMKAS	FGTHKDPYEE	WSYSDFFSED
1210	1220	1230	1240	1250	1260	1270	1280
GIVLESQMVL	PVIYELISSL	VPLAESKRYP	LESTSLPYCS	LNEGDGLVLP	VINSISALLQ	NLQESSQWEL	ALRFVVGSFG
1290	1300	1310	1320	1330	1340	1350	1360
TCLQHSVSNF	MNATLSEKLF	GETTLVKSRH	VVMELKEKAV	IFIRENATTL	LHKVFNCRLV	DLDLALGYCT	LLPQKDVFEN
1370	1380	1390	1400	1410	1420	1430	1440
LWKLIDKAWQ	NYDKILAISL	VGSELASLYQ	EIEMGLKFRE	LSTDAQWGIR	LGKLGISFQP	VFRQHFLTKK	DLIKALVENI
1450	1460	1470	1480	1490	1500	1510	1520
DMDTSLILEY	CSTFQLDCDA	VLQLFIETLL	HNTNAGQGQG	DASMDSAKRR	HPKLLAKALE	MVPLLTSTKD	LVISLSGILH
1530	1540	1550	1560	1570	1580	1590	1600
KLDPYDYEMI	EVVLKVIERA	DEKITNININ	QALSILKHLK	SYRRISPPVD	LEYQYMLEHV	ITLPSAAQTR	LPFHLIFFGT
1610	1620	1630	1640	1650	1660	1670	1680
AQNFWKILST	ELSEESFPTL	LLISKLMKFS	LDTLYVSTAK	HVFEKKLKPK	LLKLTQAKSS	TLINKEITKI	TQTIESCLLS
1690	1700	1710	1720	1730	1740	1750	1760
IVNPEWAVAI	AISLAQDIPE	GSFKISALKF	CLYLAERWLQ	NIPSQDEKRE	KAEALLKKLH	IQYRRSGTEA	VLIAHKLNTE
1770	1780	1790	1800	1810	1820	1830	1840
EYLRVIGKPA	HLIVSLYEHP	SINQRIQNSS	GTDYPDIHAA	AKEIAEVNEI	NLEKVWDMLL	EKWLCPSTKP	GEKPSELFEL
1850	1860	1870	1880	1890	1900	1910	1920
QEDEALRRVQ	YLLLSRPIDY	SSRMLFVFAT	STTTTLGMHQ	LTFAHRTRAL	QCLFYLADKE	TIESLFKKPI	EEVKSYLRCI
1930	1940	1950	1960	1970	1980	1990	2000
TFLASFETLN	IPITYELFCS	SPKEGMIKGL	WKNHSHESMA	VRLVTELCLE	YKIYDLQLWN	GLLQKLLGFN	MIPYLRKVLK
2010	2020	2030	2040	2050	2060	2070	2080
AISSIHSLWQ	VPYFSKAWQR	VIQIPLLSAS	CPLSPDQLSD	CSESLIAVLE	CPVSGDLDLI	GVARQYIQLE	LPAFALACLM
2090	2100	2110	2120	2130	2140	2150	2160
LMPHSEKRHQ	QIKNFLGSCD	PQVILKQLEE	HMNTGQLAGF	SHQIRSLILN	NIINKKEFGI	LAKTKYFQML	KMHAMNTNNI
2170	2180	2190	2200	2210			
TELVNYLAND	LSLDEASVLI	TEYSKHCGKP	VPPDTAPCEI	LKMFLSGLS			

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

Detailed Protein Report

	Cmpds.		[ppm]		[min]						
1494	1	981.9243	-80.41	2	47.0	10.5	2	128-143	K.ANDENRRTYQNLVIEK.D		WD:WU 0.88

Detailed Protein Report

Protein 1094: 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 1095: 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 1096: PREDICTED: filamin-B isoform X7 [Homo sapiens]

Accession:	gi|578805877	**Score:**	10.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	225.9
Database Date:	2015-11-30	**pI:**	5.6
		Sequence Coverage [%]:	0.6
		No. of unique Peptides:	1

Quantitation

WD:WU	**Median:** 0.88	**CV:** 0.00 %	**No. of Peptides:** 1

Detailed Protein Report

```
        10         20         30         40         50         60         70         80
MPVTEKDLAE DAPWKKIQQN TFTRWCNEHL KCVNKRIGNL QTDLSDGLRL IALLEVLSQK RMYRKYHQRP TFRQMQLENV
        90        100        110        120        130        140        150        160
SVALEFLDRE SIKLVSIDSK AIVDGNLKLI LGLVWTLILH YSISMPVWED EGDDDAKKQT PKQRLLGWIQ NKIPYLPITN
       170        180        190        200        210        220        230        240
FNQNWQDGKA LGALVDSCAP GLCPDWESWD PQKPVDNARE AMQQADDWLG VPQVITPEEI IHPDVDEHSV MTYLSQFPKA
       250        260        270        280        290        300        310        320
KLKPGAPLKP KLNPKKARAY GRGIEPTGNM VKQPAKFTVD TISAGQGDVM VFVEDPEGNK EEAQVTPDSD KNKTYSVEYL
       330        340        350        360        370        380        390        400
PKVTGLHKVT VLFAGQHISK SPFEVSVDKA QGDASKVTAK GPGLEAVGNI ANKPTYFDIY TAGAGVGDIG VEVEDPQGKN
       410        420        430        440        450        460        470        480
TVELLVEDKG NQVYRCVYKP MQPGPHVVKI FFAGDTIPKS PFVVQVGEAC NPNACRASGR GLQPKGVRIR ETTDFKVDTK
       490        500        510        520        530        540        550        560
AAGSGELGVT MKGPKGLEEL VKQKDFLDGV YAFEYYPSTP GRYSIAITWG GHHIPKSPFE VQVGPEAGMQ KVRAWGPGLH
       570        580        590        600        610        620        630        640
GGIVGRSADF VVESIGSEVG SLGFAIEGPS QAKIEYNDQN DGSCDVKYWP KEPGEYAVHI MCDDEDIKDS PYMAFIHPAT
       650        660        670        680        690        700        710        720
GGYNPDLVRA YGPGLEKSGC IVNNLAEFTV DPKDAGKAPL KIFAQDGEGQ RIDIQMKNRM DGTYACSYTP VKAIKHTIAV
       730        740        750        760        770        780        790        800
VWGGVNIPHS PYRVNIGQGS HPQKVKVFGP GVERSGLKAN EPTHFTVDCT EAGEGDVSVG IKCDARVLSE DEEDVDFDII
       810        820        830        840        850        860        870        880
HNANDTFTVK YVPPAAGRYT IKVLFASQEI PASPFRVKVD PSHDASKVKA EGPGLSKAGV ENGKPTHFTV YTKGAGKAPL
       890        900        910        920        930        940        950        960
NVQFNSPLPG DAVKDLDIID NYDYSHTVKY TPTQQGNMQV LVTYGGDPIP KSPFTVGVAA PLDLSKIKLN GLENRVEVGK
       970        980        990       1000       1010       1020       1030       1040
DQEFTVDTRG AGGQGKLDVT ILSPSRKVVP CLVTPVTGRE NSTAKFIPRE EGLYAVDVTY DGHPVPGSPY TVEASLPPDP
      1050       1060       1070       1080       1090       1100       1110       1120
SKVKAHGPGL EGGLVGKPAE FTIDTKGAGT GGLGLTVEGP CEAKIECSDN GDGTCSVSYL PTKPGEYFVN ILFEEVHIPG
      1130       1140       1150       1160       1170       1180       1190       1200
SPFKADIEMP FDPSKVVASG PGLEHGKVGE AGLLSVDCSE AGPGALGLEA VSDSGTKAEV SIQNNKDGTY AVTYVPLTAG
      1210       1220       1230       1240       1250       1260       1270       1280
MYTLTMKYGG ELVPHFPARV KVEPAVDTSR IKVFGPGIEG KDVFREATTD FTVDSRPLTQ VGGDHIKAHI ANPSGASTEC
      1290       1300       1310       1320       1330       1340       1350       1360
FVTDNADGTY QVEYTPFEKG LHVVEVTYDD VPIPNSPFKV AVTEGCQPSR VQAQGPGLKE AFTNKPNVFT VVTRGAGIGG
      1370       1380       1390       1400       1410       1420       1430       1440
LGITVEGPSE SKINCRDNKD GSCSAEYIPF APGDYDVNIT YGGAHIPGSP FTAKITDDSR RCSQVKLGSA ADFLLDISET
      1450       1460       1470       1480       1490       1500       1510       1520
DLSSLTASIK APSGRDEPCL LKRLPNNHIG ISFIPREVGE HLVSIKKNGN HVANSPVSIM VVQSEIGDAR RAKVYGRGLS
      1530       1540       1550       1560       1570       1580       1590       1600
EGRTFEMSDF IVDTRDAGYG GISLAVEGPS KVDIQTEDLE DGTCKVSYFP TVPGVYIVST KFADEHVPGS PFTVKISGEG
      1610       1620       1630       1640       1650       1660       1670       1680
RVKESITRTS RAPSVATVGS ICDLNLKIPE INSSDMSAHV TSPSGRVTEA EIVPMGKNSH CVRFVPQEMG VHTVSVKYRG
      1690       1700       1710       1720       1730       1740       1750       1760
QHVTGSPFQF TVGPLGEGGA HKVRAGGPGL ERGEAGVPAE FSIWTREAGA GGLSIAVEGP SKAEITFDDH KNGSCGVSYI
      1770       1780       1790       1800       1810       1820       1830       1840
AQEPGNYEVS IKFNDEHIPE SPYLVPVIAP SDDARRLTVM SLQESGLKVN QPASFAIRLN GAKGKIDAKV HSPSGAVEEC
      1850       1860       1870       1880       1890       1900       1910       1920
HVSELEPDKY AVRFIPHENG VHTIDVKFNG SHVVGSPFKV RVGEPGQAGN PALVSAYGTG LEGGTTGIQS EFFINTTRAG
      1930       1940       1950       1960       1970       1980       1990       2000
PGTLSVTIEG PSKVKMDCQE TPEGYKVMYT PMAPGNYLIS VKYGGPNHIV GSPFKAKVTG QRLVSPGSAN ETSSILVESV
      2010       2020       2030       2040       2050       2060       2070       2080
TRSSTETCYS AIPKASSDAS KVTSKGAGLS KAFVGQKSSF LVDCSKAGSN MLLIGVHGPT TPCEEVSMKH VGNQQYNVTY
      2090       2100       2110
VVKERGDYVL AVKWGEEHIP GSPFHVTVP
```

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
224	1	575.6716	-248.03	2	31.6	10.4	0	1136-1147	K.VVASGPGLEHGK.V		WD:WU 0.88

Detailed Protein Report

Protein 1097: 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 1098: mastermind-like protein 2 [Homo sapiens]

Accession: gi|33286444
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 10.4
MW [kDa]: 125.1
pI: 10.0
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 1099: 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 1100: PREDICTED: serine/threonine-protein kinase tousled-like 1 isoform X3 [Homo sapiens]

Accession: gi|578805282
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 10.4
MW [kDa]: 45.8
pI: 10.3
Sequence Coverage [%]: 2.2
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MSVQSSSGSL	EGPPSWSQLS	TSPTPGSAAA	ARSLLNHTPP	SGRPREGAMD	ELHSLDPRRQ	ELLEARFTGV	ASGSTGSTGS
90	100	110	120	130	140	150	160
CSVGAKASTN	NESSNHSFGS	LGSLSDKESE	TPEKKQSESS	RGRKRKAENQ	NESSQGKSIG	GRGHKISDYF	EYQGGNGSSP
170	180	190	200	210	220	230	240
VRGIPPAIRS	PQNSHSHSTP	SSSVRPNSPS	PTALAFGDHP	IVQPKQLSFK	IIQTDLTMLK	LAALESNKIQ	DLEKKEGRID
250	260	270	280	290	300	310	320
DLLRANCDLR	RQIDEQQKLL	EKYKERLNKC	ISMSKKLLIE	KSTQEKLSSR	EKSMQDRLRL	GHFTTVRHGA	SFTEQWTDGF
330	340	350	360	370	380	390	400
AFQNLVKQQE	WVNQQREDIE	RQRKLLAKRK	PPTANNSQAP	STNSEPKQRK	NKAVNGAEND	PFVRPNLPQL	LTLAEYHEQE
410	420						
EIFKLRLGHL	KKR						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1076	1	540.6516	-238.63	2	41.7	10.4	1	267-275	R.LNKCISMSK.K	Carbamidomethyl: 4

Detailed Protein Report

Protein 1101: PREDICTED: interleukin-4 receptor subunit alpha isoform X6 [Homo sapiens]

Accession:	gi|578828546	**Score:**	10.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	53.7
Database Date:	2015-11-30	**pI:**	4.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	5.1
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MKRDEDPHKA AKEMPFQGSG KSAWCPVEIS KTVLWPESIS VVRCVELFEA PVECEEEEEV EEEKGSFCAS PESSRDDFQE
        90        100        110        120        130        140        150        160
GREGIVARLT ESLFLDLLGE ENGGFCQQDM GESCLLPPSG STSAHMPWDE FPSAGPKEAP PWGKEQPLHL EPSPPASPTQ
       170        180        190        200        210        220        230        240
SPDNLTCTET PLVIAGNPAY RSFSNSLSQS PCPRELGPDP LLARHLEEVE PEMPCVPQLS EPTTVPQPEP ETWEQILRRN
       250        260        270        280        290        300        310        320
VLQHGAAAAP VSAPTSGYQE FVHAVEQGGT QASAVVGLGP PGEAGYKAFS SLLASSAVSP EKCGFGASSG EEGYKPFQDL
       330        340        350        360        370        380        390        400
IPGCPGDPAP VPVPLFTFGL DREPPRSPQS SHLPSSSPEH LGLEPGEKVE DMPKPPLPQE QATDPLVDSL GSGIVYSALT
       410        420        430        440        450        460        470        480
CHLCGHLKQC HGQEDGGQTP VMASPCCGCC CGDRSSPPTT PLRAPDPSPG GVPLEASLCP ASLAPSGISE KSKSSSSFHP
       490        500        510
APGNAQSSSQ TPKIVNFVSV GPTYMRVS
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1710	1	900.2977	-32.09	3	49.7	10.4	0	409-434	K.QCHGQEDGGQTPVMASPCCGCCCGDR.S	Carbamidomethyl: 19

Detailed Protein Report

Protein 1102: 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 1103: dickkopf-related protein 2 precursor [Homo sapiens]

Accession: gi|7657023
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl, Oxidation

Score: 10.4
MW [kDa]: 28.4
pI: 10.9
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 1104: secretin preproprotein [Homo sapiens]

Accession:	gi|11345450	**Score:**	10.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	13.0
Database Date:	2015-11-30	**pI:**	12.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	10.7
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 0.93 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MAPRPLLLLL LLLGGSAARP APPRARRHSD GTFTSELSRL REGARLQRLL QGLVGKRSEQ DAENSMAWTR LSAGLLCPSG
        90        100        110        120        130
SNMPILQAWM PLDGTWSPWL PPGPMVSEPA GAAAEGTLRP R
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
918	1	770.6818	-179.60	2	39.9	10.4	0	58-70	R.SEQDAENSMAWTR.L	Oxidation: 9	WD:WU	0.93

Detailed Protein Report

Protein 1105: SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1-related [Homo sapiens]

Accession:	gi|83715964	**Score:**	10.4
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 [%]:**	2.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSHGPKQPGA	AAAPAGGKAP	GQHGGFVVTV	KQERGEGPRA	GEKGSHEEEP	VKKRGWPKGK	KRKKILPNGP	KAPVTGYVRF
90	100	110	120	130	140	150	160
LNERREQIRT	RHPDLPFPEI	TKMLGAEWSK	LQPTEKQRYL	DEAEREKQQY	MKELRAYQQS	EAYKMCTEKI	QEKKIKKEDS
170	180	190	200	210	220	230	240
SSGLMNTLLN	GHKGGDCDGF	STFDVPIFTE	EFLDQNKARE	AELRRLRKMN	VAFEEQNAVL	QRHTQSMSSA	RERLEQELAL
250	260	270	280	290	300	310	320
EERRTLALQQ	QLQAVRQALT	ASFASLPVPG	TGETPTLGTL	DFYMARLHGA	IERDPAQHEK	LIVRIKEILA	QVASEHL

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
318	1	591.7318	-78.66	2	33.1	10.4	1	145-153	K.MCTEKIQEK.K	Carbamidomethyl: 2; Oxidation: 1

Detailed Protein Report

Protein 1106: 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

Quantitation

WD:WU **Median:** 0.91 **CV:** 0.00 % **No. of 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	Ratios
492	1	689.6601	-214.61	2	35.1	10.4	1	84-95	K.CGSTDHEITKCK.A	Carbamidomethyl: 1	WD:WU 0.91

Detailed Protein Report

Protein 1107: CD27 antigen precursor [Homo sapiens]

Accession:	gi|4507587	**Score:**	10.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	29.1
Database Date:	2015-11-30	**pI:**	9.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	10.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MARPHPWWLC	VLGTLVGLSA	TPAPKSCPER	HYWAQGKLCC	QMCEPGTFLV	KDCDQHRKAA	QCDPCIPGVS	FSPDHHTRPH
90	100	110	120	130	140	150	160
CESCRHCNSG	LLVRNCTITA	NAECACRNGW	QCRDKECTEC	DPLPNPSLTA	RSSQALSPHP	QPTHLPYVSE	MLEARTAGHM
170	180	190	200	210	220	230	240
QTLADFRQLP	ARTLSTHWPP	QRSLCSSDFI	RILVIFSGMF	LVFTLAGALF	LHQRRKYRSN	KGESPVEPAE	PCRYSCPREE
250	260	270					
EGSTIPIQED	YRKPEPACSP						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1812	1	1045.8095	11.98	3	51.0	10.4	1	58-85	R.KAAQCDPCIPGVSFSPDHHTRPHCESCR.H	Carbamidomethyl: 8

Detailed Protein Report

Protein 1108: 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

WD:WU	**Median:** 0.79	**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	WD:WU	0.79

Detailed Protein Report

Protein 1109: 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

WD:WU **Median:** 0.93 **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		WD:WU 0.93

Detailed Protein Report

Protein 1110: 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

Quantitation

WD:WU **Median:** 0.68 **CV:** 0.00 % **No. of 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	Ratios
829	1	647.8199	-30.73	2	39.2	10.4	2	142-151	R.RAQHNEVERR.R		WD:WU 0.68

Detailed Protein Report

Protein 1111: 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

WD:WU **Median:** 0.91 **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		WD:WU 0.91

Protein 1112: 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 1113: PREDICTED: vacuolar protein sorting-associated protein 53 homolog isoform X2 [Homo sapiens]

Accession:	gi|530410472	**Score:**	10.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	72.4
Database Date:	2015-11-30	**pI:**	9.0
		Sequence Coverage [%]:	4.2
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|578829979	refseq_human (refseq_human_20140103.fasta)	PREDICTED: vacuolar protein sorting-associated protein 53 homolog isoform X3 [Homo sapiens]

10	20	30	40	50	60	70	80
MGIPQIRQLS	ERVKAAQTEL	GQQILADFEE	AFPSQGTKRP	GGPSNVLRDA	CLVANILDPR	IKQEIIKKFI	KQHLSEYLVL
90	100	110	120	130	140	150	160
FQENQDVAWL	DKIDRRYAWI	KRQLVDYEEK	YGRMFPREWC	MAERIAVEFC	HVTRAELAKI	MRTRAKEIEV	KLLLFAIQRT
170	180	190	200	210	220	230	240
TNFEGFLAKR	FSGCTLTDGT	LKKLESPPPS	TNPFLEDEPT	PEMEELATEK	GDLDQPKKPK	APDNPFHGIV	SKCFEPHLYV
250	260	270	280	290	300	310	320
YIESQDKNLG	ELIDRFVADF	KAQGPPKPNT	DEGGAVLPSC	ADLFVYYKKC	MVQCSQLSTG	EPMIALTTIF	QKYLREYAWK
330	340	350	360	370	380	390	400
ILSGNLPKTT	TSSGGLTISS	LLKEKEGSEV	AKFTLEELCL	ICNILSTAEY	CLATTQQLEE	KLKEKVDVSL	IERINLTGEM
410	420	430	440	450	460	470	480
DTFSTVISSS	IQLLVQDLDA	ACDPALTAMS	KMQWQNVEHV	GDQSPYVTSV	ILHIKQNVPI	IRDNLASTRK	YFTQFCVKFA
490	500	510	520	530	540	550	560
NSFIPKFITH	LFKCKPISMV	GAEQLLLDTH	SLKMVLLDLP	SISSQVVRKA	PASYTKIVVK	GMTRAEMILK	VVMAPHEPLV
570	580	590	600	610	620	630	640
VFVDNYIKLL	TDCNTETFQK	ILDMKGLKRS	EQSSMLELLR	QRLPAPPSGA	ESSGSLSLTA	PTPEQESSRI	RKLEKLIKKR
650							
L							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2698	1	946.5530	92.66	3	62.2	10.4	0	262-288	K.AQGPPKPNTDEGGAVLPSCADLFVYYK.K	

Detailed Protein Report

Protein 1114: 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

Score: 10.4
MW [kDa]: 160.7
pI: 9.2
Sequence Coverage [%]: 1.1
No. of unique Peptides: 1

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
1604	1	882.0680	124.94	2	48.8	10.4	0	476-490	K.CLYYLYATLDLNAVK.A	

Detailed Protein Report

Protein 1115: PREDICTED: nuclear envelope pore membrane protein POM 121 isoform X2 [Homo sapiens]

Accession:	gi|530386697	**Score:**	10.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	121.6
Database Date:	2015-11-30	**pI:**	11.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSPAAAAAGA	GERRRPIASV	RDGRGRGCGG	PARAVLLGLS	LVGLLLYLVP	AAAALAWLTV	GATAAWWGLS	REPRGSRPLS
90	100	110	120	130	140	150	160
SFVRKARHRR	PLSSFVRKAR	HRRTLFASPL	AKSTANGNLL	EPRTLLEGPD	PAELLLMGSY	LGKPGPPQPA	AAPEGQDLRD
170	180	190	200	210	220	230	240
RPGRRPPARP	APRSPPPRSP	PPRSPPPSPP	THRAHHVYPS	LPTPLLRPSR	RPSPRDCGTL	PNRFVITPRR	RYPIHQAQYS
250	260	270	280	290	300	310	320
CLGVLPTVCW	NGYHKKAVLS	PRNSRMVCSP	VTVRIAPPDR	RFSRSAIPEQ	IISSTLSSPS	SNAPDPCAKE	TVLSALKEKE
330	340	350	360	370	380	390	400
KKRTVEEEDQ	IFLDGQENKR	RRHDSSGSGH	SAFEPLVANG	VPASFVPKPG	SLKRGLNSQS	SDDHLNKRSR	SSSMSSLTGA
410	420	430	440	450	460	470	480
YASGIPSSSR	NAITSSYSST	RGISQLWKRN	GPSSSPFSSP	ASSRSQTPER	PAKKIREEEL	CHHSSSSTPL	AADRESQGEK
490	500	510	520	530	540	550	560
AADTTPRKKQ	NSNSQSTPGS	SGQRKRKVQL	LPSRRGEQLT	LPPPPQLGYS	ITAEDLDLEK	KASLQWFNQA	LEDKSESAGA
570	580	590	600	610	620	630	640
ATTEALSPPK	TPSLLPPLGL	SQSGPPGLLP	SPSFDSKPPT	TLLGLIPAPS	MVPATDTKAP	PTLQAETATK	PQATSAPSPA
650	660	670	680	690	700	710	720
PKQSFLFGTQ	NTSPSSPAAP	AASSAPPMFK	PIFTAPPKSE	KEGPTPPGPS	VTATAPSSSS	LPTTTSTTAP	TFQPVFSSMG
730	740	750	760	770	780	790	800
PPASVPLPAP	FFKQTTTPAT	APTTTAPLFT	GLASATSAVA	PITSASPSTD	SASKPAFGFG	INSVSSSSVS	TTTSTATAAS
810	820	830	840	850	860	870	880
QPFLFGAPQA	SAASFTPAMG	SIFQFGKPPA	LPTTTTVTTF	SQSLHTAVPT	ATSSSAADFS	GFGSTLATSA	PATSSQPTLT
890	900	910	920	930	940	950	960
FSNTSTPTFN	IPFGSSAKSP	LPSYPGANPQ	PAFGAAEGQP	PGAAKPALAP	SFGSSFTFGN	SAAPAAAPTP	APPSMIKVVP
970	980	990	1000	1010	1020	1030	1040
AYVPTPIHPI	FGGATHSAFG	LKATASAFGA	PASSQPAFGG	STAVFFGAAT	SSGFGATTQT	ASSGSSSSVF	GSTTPSPFTF
1050	1060	1070	1080	1090	1100	1110	1120
GGSAAPAGSG	SFGINVATPG	SSTTTGAFSF	GAGQSGSTAT	STPFAGGLGQ	NALGTTGQST	PFAFNVSSTT	ESKPVFGGTA
1130	1140	1150	1160	1170	1180	1190	1200
TPTFGLNTPA	PGVGTSGSSL	SFGASSAPAQ	GFVGVAPFGS	AALSFSIGAG	SKTPGARQRL	QARRQHTRKK	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2272	1	703.3240	-44.91	2	56.7	10.4	1	263-274	R.NSRMVCSPVTVR.I	Carbamidomethyl: 6

Protein 1116: PREDICTED: melanoma inhibitory activity protein 3 isoform X3 [Homo sapiens]

Accession: gi|578800895
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 10.4
MW [kDa]: 209.3
pI: 4.6
Sequence Coverage [%]: 0.6
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MAAAPGLLVW	LLVLRLPWRV	PGQLDPSTGR	RFSEHKLCAD	DECSMLMYRG	EALEDFTGPD	CRFVNFKKGD	PVYVYYKLAR
90	100	110	120	130	140	150	160
GWPEVWAGSV	GRTFGYFPKD	LIQVVHEYTK	EELQVPTDET	DFVCFDGGRD	DFHNYNVEEL	LGFLELYNSA	ATDSEKAVEK
170	180	190	200	210	220	230	240
TLQDMEKNPE	LSKEREPEPE	PVEANSEESD	SVFSENTEDL	QEQFTTQKHH	SHANSQANHA	QGEQASFESF	EEMLQDKLKV
250	260	270	280	290	300	310	320
PESENNKTSN	SSQVSNEQDK	IDAYKLLKKE	MTLDLKTKFG	STADALVSDD	ETTRLVTSLE	DDFDEELDTE	YYAVGKEDEE
330	340	350	360	370	380	390	400
NQEDFDELPL	LTFTDGEDMK	TPAKSGVEKY	PTDKEQNSNE	EDKVQLTVPP	GIKNDDKNIL	TTWGDTIFSI	VTGGEETRDT
410	420	430	440	450	460	470	480
MDLESSSSEE	EKEDDDDALV	PDSKQGKPQS	ATDYSDPDNV	DDGLFIVDIP	KTNNDKEVNA	EHHIKGKGRG	VQESKRGLVQ
490	500	510	520	530	540	550	560
DKTELEDENQ	EGMTVHSSVH	SNNLNSMPAA	EKGKDTLKSA	YDDTENDLKG	AAIHISKGML	HEEKPGEQIL	EGGSESESAQ
570	580	590	600	610	620	630	640
KAAGNQMNDR	KIQQESLGSA	PLMGDDHPNA	SRDSVEGDAL	VNGAKLHTLS	VEHQREELKE	ELVLKTQNQP	RFSSPDEIDL
650	660	670	680	690	700	710	720
PRELEDEVPI	LGRNLPWQQE	RDVAATASKQ	MSEKIRLSEG	EAKEDSLDEE	FFHHKAMQGT	EVGQTDQTDS	TGGPAFLSKV
730	740	750	760	770	780	790	800
EEDDYPSEEL	LEDENAINAK	RSKEKNPGNQ	GRQFDVNLQV	PDRAVLGTIH	PDPEIEESKQ	ETSMILDSEK	TSETAAKGVN
810	820	830	840	850	860	870	880
TGGREPNTMV	EKERPLADKK	AQRPFERSDF	SDSIKIQTPE	LGEVFQNKDS	DYLKNDNPEE	HLKTSGLAGE	PEGELSKEDH
890	900	910	920	930	940	950	960
ENTEKYMGTE	SQGSAAAEPE	DDSFHWTPHT	SVEPGHSDKR	EDLLIISSFF	KEQQSLQRFQ	KYFNVHELEA	LLQEMSSKLK
970	980	990	1000	1010	1020	1030	1040
SAQQESLPYN	MEKVLDKVFR	ASESQILSIA	EKMLDTRVAE	NRDLGMNENN	IFEEAAVLDD	IQDLIYFVRY	KHSTAEETAT
1050	1060	1070	1080	1090	1100	1110	1120
LVMAPPLEEG	LGGAMEEMQP	LHEDNFSREK	TAELNVQVPE	EPTHLDQRVI	GDTHASEVSQ	KPNTEKDLDP	GPVTTEDTPM
1130	1140	1150	1160	1170	1180	1190	1200
DAIDANKQPE	TAAEEPASVT	PLENAILLIY	SFMFYLTKSL	VATLPDDVQP	GPDFYGLPWK	PVFITAFLGI	ASFAIFLWRT
1210	1220	1230	1240	1250	1260	1270	1280
VLVVKDRVYQ	VTEQQISEKL	KTIMKENTEL	VQKLSNYEQK	IKESKKHVQE	TRKQNMILSD	EAIKYKDKIK	TLEKNQEILD
1290	1300	1310	1320	1330	1340	1350	1360
DTAKNLRVML	ESEREQNVKN	QDLLQQEIED	WSKLHAELSE	QIKSFEKSQK	DLEVALTHKD	DNINALTNCI	TQLNLLECES
1370	1380	1390	1400	1410	1420	1430	1440
ESEGQNKGGN	DSDELANGEV	GGDRNEKMKN	QIKQMMDVSR	TQTAISVVEE	DLKLLQLKLR	ASVSTKCNLE	DQVKKLEDDR
1450	1460	1470	1480	1490	1500	1510	1520
NSLQAAKAGL	EDECKTLRQK	VEILNELYQQ	KEMALQKKLS	QEEYERQERE	HRLSAADEKA	VSAAEEVKTY	KRRIEEMEDE
1530	1540	1550	1560	1570	1580	1590	1600
LQKTERSFKN	QIATHEKKAH	ENWLKARAAE	RAIAEEKREA	ANLRHKLLEL	TQKMAMLQEE	PVIVKPMPGK	PNTQNPPRRG
1610	1620	1630	1640	1650	1660	1670	1680
PLSQNGSFGP	SPVSGGECSP	PLTVEPPVRP	LSATLNRRDM	PRSEFGSVDG	PLPHPRWSAE	ASGKPSPSDP	GSGTATMMNS
1690	1700	1710	1720	1730	1740	1750	1760
SSRGSSPTRV	LDEGKQTVLQ	EPEVPSVPSI	TSLAERPVAV	NMAPKGPPPF	PGVPLMSTPM	GGPVPPPIRY	GPPPQLCGPF
1770	1780	1790	1800	1810	1820	1830	1840
GPRPLPPPFG	PGMRPPLGLR	EFAPGVPPGR	RDLPLHPRGF	LPGHAPFRPL	GSLGPREYFI	PGTRLPPPTH	GPQEYPPPPA
1850	1860	1870	1880				
VRDLLPSGSR	DEPPPASQST	SQDCSQALKQ	SP				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2077	1	734.3308	-113.16	2	54.4	10.4	1	920-931	K.REDLLIISSFFK.E	

Detailed Protein Report

Protein 1117: PREDICTED: ubiquitin carboxyl-terminal hydrolase 15 isoform X3 [Homo sapiens]

Accession:	gi|530401067	**Score:**	10.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	74.4
Database Date:	2015-11-30	**pI:**	4.9
		Sequence Coverage [%]:	2.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MRGEIAKSYA	ELIKQMWSGK	FSYVTPRAFK	TQVGRFAPQF	SGYQQQDCQE	LLAFLLDGLH	EDLNRIRKKP	YIQLKDADGR
90	100	110	120	130	140	150	160
PDKVVAEEAW	ENHLKRNDSI	IVDIFHGLFK	STLVCPECAK	ISVTFDPFCY	LTLPLPMKKE	RTLEVYLVRM	DPLTKPMQYK
170	180	190	200	210	220	230	240
VVVPKIGNIL	DLCTALSALS	GIPADKMIVT	DIYNHRFHRI	FAMDENLSSI	MERDDIYVFE	ININRTEDTE	HVIIPVCLRE
250	260	270	280	290	300	310	320
KFRHSSYTHH	TGSSLFGQPF	LMAVPRNNTE	DKLYNLLLLR	MCRYVKISTE	TEETEGSLHC	CKDQNINGNG	PNGIHEEGSP
330	340	350	360	370	380	390	400
SEMETDEPDD	ESSQDQELPS	ENENSQSEDS	VGGDNDSENG	LCTEDTCKGQ	LTGHKKRLFT	FQFNNLGNTD	INYIKDDTRH
410	420	430	440	450	460	470	480
IRFDDRQLRL	DERSFLALDW	DPDLKKRYFD	ENAAEDFEKH	ESVEYKPPKK	PFVKLKDCIE	LFTTKEKLGA	EDPWYCPNCK
490	500	510	520	530	540	550	560
EHQQATKKLD	LWSLPPVLVV	HLKRFSYSRY	MRDKLDTLVD	FPINDLDMSE	FLINPNAGPC	RYNLIAVSNH	YGGMGGGHYT
570	580	590	600	610	620	630	640
AFAKNKDDGK	WYYFDDSSVS	TASEDQIVSK	AAYVLFYQRQ	DTFSGTGFFP	LDRETKGASA	ATGIPLESDE	DSNDNDNDIE
650							
NENCMHTN							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1496	1	619.7680	82.44	3	47.1	10.3	1	488-503	K.KLDLWSLPPVLVVHLK.R	

Detailed Protein Report

Protein 1118: 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 1119: PREDICTED: small G protein signaling modulator 3 isoform X6 [Homo sapiens]

Accession:	gi|530420028	**Score:**	10.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	71.6
Database Date:	2015-11-30	**pI:**	5.8
		Sequence Coverage [%]:	2.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSGSHTPACG	PFSALTPSIW	PQEILAKYTQ	KEESAEQPEF	YYDEFGFRVY	KEEGDEPGSS	LLANSPLMED	APQRLRWQAH
90	100	110	120	130	140	150	160
LEFTHNHDVG	DLTWDKIAVS	LPRSEKLRSL	VLAGIPHGMR	PQLWMRLSGA	LQKKRNSELS	YREIVKNSSN	DETIAAKQIE
170	180	190	200	210	220	230	240
KDLLRTMPSN	ACFASMGSIG	VPRLRRVLRA	LAWLYPEIGY	CQGTGMVAAC	LLLFLEEEDA	FWMMSAIIED	LLPASYFSTT
250	260	270	280	290	300	310	320
LLGVQTDQRV	LRHLIVQYLP	RLDKLLQEHD	IELSLITLHW	FLTAFASVVD	IKLLLRIWDL	FFYEGSRVLF	QLTLGMLHLK
330	340	350	360	370	380	390	400
EEELIQSENS	ASIFNTLSDI	PSQMEDAELL	LGVAMRLAGS	LTDVAVETQR	RKHLAYLIAD	QGQLLGAGTL	TNLSQVVRRR
410	420	430	440	450	460	470	480
TQRRKSTITA	LLFGEDDLEA	LKAKNIKQTE	LVADLREAIL	RVARHFQCTD	PKNCSVELTP	DYSMESHQRD	HENYVACSRS
490	500	510	520	530	540	550	560
HRRRAKALLD	FERHDDDELG	FRKNDIITIV	SQKDEHCWVG	ELNGLRGWFP	AKFVEVLDER	SKEYSIAGDD	SVTEGVTDLV
570	580	590	600	610	620	630	640
RGTLCPALKA	LFEHGLKKPS	LLGGACHPWL	FIEEAAGREV	ERDFASVYSR	LVLCKTFRSF	GVPSGWMKMA	KS

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
563	1	756.9503	105.42	2	35.5	10.3	2	619-632	R.SFGVPSGWMKMAKS.-	

Detailed Protein Report

Protein 1120: **ATP synthase F(0) complex subunit C3, mitochondrial isoform B precursor [Homo sapiens]**

Accession: gi|298358756
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl, Oxidation

Score: 10.3
MW [kDa]: 10.6
pI: 11.3
Sequence Coverage [%]: 14.3
No. of unique Peptides: 1

```
        10         20         30         40         50         60         70         80
MFACAKLACT PSLIRAGSRV AYRPISASVL SRPEASRTGE GSTVFNGAQN GVSQLIQREF QTSAISRDID TAAKFIGAGA
        90        100        110
ATVGVAGSGA GIGTVFGSLI IGYAR
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
115	1	849.4132	-20.25	2	30.4	10.3	1	1-15	-.MFACAKLACTPSLIR.A	Carbamidomethyl: 9; Oxidation: 1

Detailed Protein Report

Protein 1121: 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 1122: heterogeneous nuclear ribonucleoprotein D0 isoform c [Homo sapiens]

Accession: gi|14110414
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 10.3
MW [kDa]: 32.8
pI: 9.0
Sequence Coverage [%]: 4.2
No. of unique Peptides: 1

Quantitation

WD:WU **Median:** 0.52 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MSEEQFGGDG	AAAAATAAVG	GSAGEQEGAM	VAATQGAAAA	AGSGAGTGGG	TASGGTEGGS	AESEGAKIDA	SKNEEDEGHS
90	100	110	120	130	140	150	160
NSSPRHSEAA	TAQREEWKMF	IGGLSWDTTK	KDLKDYFSKF	GEVVDCTLKL	DPITGRSRGF	GFVLFKESES	VDKVMDQKEH
170	180	190	200	210	220	230	240
KLNGKVIDPK	RAKAMKTKEP	VKKIFVGGLS	PDTPEEKIRE	YFGGFGEVES	IELPMDNKTN	KRRGFCFITF	KEEEPVKKIM
250	260	270	280	290	300	310	
EKKYHNVGLS	KCEIKVAMSK	EQYQQQQQWG	SRGGFAGRAR	GRGGDQQSGY	GKVSRRGGHQ	NSYKPY	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2535	1	729.3445	63.67	2	60.0	10.3	0	73-85	K.NEEDEGHSNSSPR.H		WD:WU 0.52

Detailed Protein Report

Protein 1123: transmembrane protein 126B isoform d [Homo sapiens]

Accession:	gi|375065842	**Score:**	10.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	21.1
Database Date:	2015-11-30	**pI:**	10.3
		Sequence Coverage [%]:	10.9
		No. of unique Peptides:	1

```
        10          20          30          40          50          60          70          80
MRLGLSQGIQ  VWCRWELRKR  PRTQNIYQMA  TFGTTAGFSG  IFSNFLFRRC  FKVKHDALKT  YASLATLPFL  STVVTDKLFV
        90         100         110         120         130         140         150         160
IDALYSDNIS  KENCVFRSSL  IGIVCGVFYP  SSLAFTKNGR  LATKYHTVPL  PPKGRVLIHW  MTLCQTQMKL  MAIPLVFQIM
       170         180         190
FGILNGLYHY  AVFEETLEKT  IHEE
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1806	1	697.0294	-14.46	3	51.2	10.3	0	98-117	R.SSLIGIVCGVFYPSSLAFTK.N	

Detailed Protein Report

Protein 1124: PREDICTED: leucine-rich repeat-containing protein 49 isoform X3 [Homo sapiens]

Accession:	gi|530406077	**Score:**	10.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	45.4
Database Date:	2015-11-30	**pI:**	9.0
		Sequence Coverage [%]:	2.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
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 1125: mediator of RNA polymerase II transcription subunit 13 [Homo sapiens]

Accession:	gi|102468717	**Score:**	10.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	239.1
Database Date:	2015-11-30	**pI:**	5.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	0.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSASFVPNGA	SLEDCHCNLF	CLADLTGIKW	KKYVWQGPTS	APILFPVTEE	DPILSSFSRC	LKADVLGVWR	RDQRPGRREL
90	100	110	120	130	140	150	160
WIFWWGEDPS	FADLIHHDLS	EEEDGVWENG	LSYECRTLLF	KAVHNLLERC	LMNRNFVRIG	KWFVKPYEKD	EKPINKSEHL
170	180	190	200	210	220	230	240
SCSFTFFLHG	DSNVCTSVEI	NQHQPVYLLS	EEHITLAQQS	NSPFQVILCP	FGLNGTLTGQ	AFKMSDSATK	KLIGEWKQFY
250	260	270	280	290	300	310	320
PISCCLKEMS	EEKQEDMDWE	DDSLAAVEVL	VAGVRMIYPA	CFVLVPQSDI	PTPSPVGSTH	CSSSCLGVHQ	VPASTRDPAM
330	340	350	360	370	380	390	400
SSVTLTPPTS	PEEVQTVDPQ	SVQKWVKFSS	VSDGFNSDST	SHHGGKIPRK	LANHVVDRVW	QECNMNRAQN	KRKYSASSGG
410	420	430	440	450	460	470	480
LCEEATAAKV	ASWDFVEATQ	RTNCSCLRHK	NLKSRNAGQQ	GQAPSLGQQQ	QILPKHKTNE	KQEKSEKPQK	RPLTPFHHRV
490	500	510	520	530	540	550	560
SVSDDVGMDA	DSASQRLVIS	APDSQVRFSN	IRTNDVAKTP	QMHGTEMANS	PQPPPLSPHP	CDVVDEGVTK	TPSTPQSQHF
570	580	590	600	610	620	630	640
YQMPTPDPLV	PSKPMEDRID	SLSQSFPPQY	QEAVEPTVYV	GTAVNLEEDE	ANIAWKYYKF	PKKKDVEFLP	PQLPSDKFKD
650	660	670	680	690	700	710	720
DPVGPFGQES	VTSVTELMVQ	CKKPLKVSDE	LVQQYQIKNQ	CLSAIASDAE	QEPKIDPYAF	VEGDEEFLFP	DKKDRQNSER
730	740	750	760	770	780	790	800
EAGKKHKVED	GTSSVTVLSH	EEDAMSLFSP	SIKQDAPRPT	SHARPPSTSL	IYDSDLAVSY	TDLDNLFNSD	EDELTPGSKK
810	820	830	840	850	860	870	880
SANGSDDKAS	CKESKTGNLD	PLSCISTADL	HKMYPTPPSL	EQHIMGFSPM	NMNNKEYGSM	DTTPGGTVLE	GNSSSIGAQF
890	900	910	920	930	940	950	960
KIEVDEGFCS	PKPSEIKDFS	YVYKPENCQI	LVGCSMFAPL	KTLPSQYLPP	IKLPEECIYR	QSWTVGKLEL	LSSGPSMPFI
970	980	990	1000	1010	1020	1030	1040
KEGDGSNMDQ	EYGTAYTPQT	HTSFGMPPSS	APPSNSGAGI	LPSPSTPRFP	TPRTPRTPRT	PRGAGGPASA	QGSVKYENSD
1050	1060	1070	1080	1090	1100	1110	1120
LYSPASTPST	CRPLNSVEPA	TVPSIPEAHS	LYVNLILSES	VMNLFKDCNF	DSCCICVCNM	NIKGADVGVY	IPDPTQEAQY
1130	1140	1150	1160	1170	1180	1190	1200
RCTCGFSAVM	NRKFGNNSGL	FLEDELDIIG	RNTDCGKEAE	KRFEALRATS	AEHVNGGLKE	SEKLSDDLIL	LLQDQCTNLF
1210	1220	1230	1240	1250	1260	1270	1280
SPFGAADQDP	FPKSGVISNW	VRVEERDCCN	DCYLALEHGR	QFMDNMSGGK	VDEALVKSSC	LHPWSKRNDV	SMQCSQDILR
1290	1300	1310	1320	1330	1340	1350	1360
MLLSLQPVLQ	DAIQKKRTVR	PWGVQGPLTW	QQFHKMAGRG	SYGTDESPEP	LPIPTFLLGY	DYDYLVLSPF	ALPYWERLML
1370	1380	1390	1400	1410	1420	1430	1440
EPYGSQRDIA	YVVLCPENEA	LLNGAKSFFR	DLTAIYESCR	LGQHRPVSRL	LTDGIMRVGS	TASKKLSEKL	VAEWFSQAAD
1450	1460	1470	1480	1490	1500	1510	1520
GNNEAFSKLK	LYAQVCRYDL	GPYLASLPLD	SSLLSQPNLV	APTSQSLITP	PQMTNTGNAN	TPSATLASAA	SSTMTVTSGV
1530	1540	1550	1560	1570	1580	1590	1600
AISTSVATAN	STLTTASTSS	SSSSNLNSGV	SSNKLPSFPP	FGSMNSNAAG	SMSTQANTVQ	SGQLGGQQTS	ALQTAGISGE
1610	1620	1630	1640	1650	1660	1670	1680
SSSLPTQPHP	DVSESTMDRD	KVGIPTDGDS	HAVTYPPAIV	VYIIDPFTYE	NTDESTNSSS	VWTLGLLRCF	LEMVQTLPPH
1690	1700	1710	1720	1730	1740	1750	1760
IKSTVSVQII	PCQYLLQPVK	HEDREIYPQH	LKSLAFSAFT	QCRRPLPTST	NVKTLTGFGP	GLAMETALRS	PDRPECIRLY
1770	1780	1790	1800	1810	1820	1830	1840
APPFILAPVK	DKQTELGETF	GEAGQKYNVL	FVGYCLSHDQ	RWILASCTDL	YGELLETCII	NIDVPNRARR	KKSSARKFGL
1850	1860	1870	1880	1890	1900	1910	1920
QKLWEWCLGL	VQMSSLPWRV	VIGRLGRIGH	GELKDWSCLL	SRRNLQSLSK	RLKDMCRMCG	ISAADSPSIL	SACLVAMEPQ
1930	1940	1950	1960	1970	1980	1990	2000
GSFVIMPDSV	STGSVFGRST	TLNMQTSQLN	TPQDTSCTHI	LVFPTSASVQ	VASATYTTEN	LDLAFNPNND	GADGMGIFDL
2010	2020	2030	2040	2050	2060	2070	2080
LDTGDDLDPD	IINILPASPT	GSPVHSPGSH	YPHGGDAGKG	QSTDRLLSTE	PHEEVPNILQ	QPLALGYFVS	TAKAGPLPDW
2090	2100	2110	2120	2130	2140	2150	2160
FWSACPQAQY	QCPLFLKASL	HLHVPSVQSD	ELLHSKHSHP	LDSNQTSDVL	RFVLEQYNAL	SWLTCDPATQ	DRRSCLPIHF
2170	2180						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1464	1	1006.5988	75.55	2	46.7	10.3	2	1251-1267	K.VDEALVKSSCLHPWSKR.N	Carbamidomethyl: 10

Detailed Protein Report

Protein 1126: 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

Quantitation

WD:WU **Median:** 0.38 **CV:** 0.00 % **No. of 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	Ratios
1673	1	1045.0313	-28.88	2	49.6	10.3	2	178-195	K.FLLMVRDGRASVHSMITR.K		WD:WU 0.38

Detailed Protein Report

Protein 1127: 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 1128: AP-2 complex subunit alpha-1 isoform 2 [Homo sapiens]

Accession:	gi|19913416	**Score:**	10.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	105.3
Database Date:	2015-11-30	**pI:**	8.7
		Sequence Coverage [%]:	1.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPAVSKGDGM	RGLAVFISDI	RNCKSKEAEI	KRINKELANI	RSKFKGDKAL	DGYSKKKYVC	KLLFIFLLGH	DIDFGHMEAV
90	100	110	120	130	140	150	160
NLLSSNKYTE	KQIGYLFISV	LVNSNSELIR	LINNAIKNDL	ASRNPTFMCL	ALHCIANVGS	REMGEAFAAD	IPRILVAGDS
170	180	190	200	210	220	230	240
MDSVKQSAAL	CLLRLYKASP	DLVPMGEWTA	RVVHLLNDQH	MGVVTAAVSL	ITCLCKKNPD	DFKTCVSLAV	SRLSRIVSSA
250	260	270	280	290	300	310	320
STDLQDYTYY	FVPAPWLSVK	LLRLLQCYPP	PEDAAVKGRL	VECLETVLNK	AQEPPKSKKV	QHSNAKNAIL	FETISLIIHY
330	340	350	360	370	380	390	400
DSEPNLLVRA	CNQLGQFLQH	RETNLRYLAL	ESMCTLASSE	FSHEAVKTHI	DTVINALKTE	RDVSVRQRAA	DLLYAMCDRS
410	420	430	440	450	460	470	480
NAKQIVSEML	RYLETADYAI	REEIVLKVAI	LAEKYAVDYS	WYVDTILNLI	RIAGDYVSEE	VWYRVLQIVT	NRDDVQGYAA
490	500	510	520	530	540	550	560
KTVFEALQAP	ACHENMVKVG	GYILGEFGNL	IAGDPRSSPP	VQFSLLHSKF	HLCSVATRAL	LLSTYIKFIN	LFPETKATIQ
570	580	590	600	610	620	630	640
GVLRAGSQLR	NADVELQQRA	VEYLTLSSVA	STDVLATVLE	EMPPFPERES	SILAKLKRKK	GPGAGSALDD	GRRDPSSNDI
650	660	670	680	690	700	710	720
NGGMEPTPST	VSTPSPSADL	LGLRAAPPPA	APPASAGAGN	LLVDVFDGPA	AQPSLGPTPE	EAFLSPGPED	IGPPIPEADE
730	740	750	760	770	780	790	800
LLNKFVCKNN	GVLFENQLLQ	IGVKSEFRQN	LGRMYLFYGN	KTSVQFQNFS	PTVVHPGDLQ	TQLAVQTKRV	AAQVDGGAQV
810	820	830	840	850	860	870	880
QQVLNIECLR	DFLTPPLLSV	RFRYGGAPQA	LTLKLPVTIN	KFFQPTEMAA	QDFFQRWKQL	SLPQQEAQKI	FKANHPMDAE
890	900	910	920	930	940	950	960
VTKAKLLGFG	SALLDNVDPN	PENFVGAGII	QTKALQVGCL	LRLEPNAQAQ	MYRLTLRTSK	EPVSRHLCEL	LAQQF

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2708	1	974.0860	30.01	2	62.3	10.3	1	548-564	K.FINLFPETKATIQGVLR.A	

Detailed Protein Report

Protein 1129: phosphorylated adapter RNA export protein [Homo sapiens]

Accession:	gi|66392146	**Score:**	10.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	44.4
Database Date:	2015-11-30	**pI:**	5.1
Modification(s):	Oxidation	**Sequence Coverage [%]:**	6.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MALEVGDMED	GQLSDSDSDM	TVAPSDRPLQ	LPKVLGGDSA	MRAFQNTATA	CAPVSHYRAV	ESVDSSEESF	SDSDDDSCLW
90	100	110	120	130	140	150	160
KRKRQKCFNP	PPKPEPFQFG	QSSQKPPVAG	GKKINNIWGA	VLQEQNQDAV	ATELGILGME	GTIDRSRQSE	TYNYLLAKKL
170	180	190	200	210	220	230	240
RKESQEHTKD	LDKELDEYMH	GGKKMGSKEE	ENGQGHLKRK	RPVKDRLGNR	PEMNYKGRYE	ITAEDSQEKV	ADEISFRLQE
250	260	270	280	290	300	310	320
PKKDLIARVV	RIIGNKKAIE	LLMETAEVEQ	NGGLFIMNGS	RRRTPGGVFL	NLLKNTPSIS	EEQIKDIFYI	ENQKEYENKK
330	340	350	360	370	380	390	400
AARKRRTQVL	GKKMKQAIKS	LNFQEDDDTS	RETFASDTNE	ALASLDESQE	GHAEAKLEAE	EAIEVDHSHD	LDIF

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1012	1	984.1752	8.05	3	41.0	10.3	2	258-283	K.AIELLMETAEVEQNGGLFIMNGSRRR.T	Oxidation: 6

Detailed Protein Report

Protein 1130: 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 1131: pancreatic lipase-related protein 3 precursor [Homo sapiens]

Accession: gi|190341077
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 10.3
MW [kDa]: 52.2
pI: 9.4
Sequence Coverage [%]: 1.9
No. of unique Peptides: 1

Quantitation

WD:WU **Median:** 0.90 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MLGIWIVAFL	FFGTSRGKEV	CYERLGCFKD	GLPWTRTFST	ELVGLPWSPE	KINTRFLLYT	IHNPNAYQEI	SAVNSSTIQA
90	100	110	120	130	140	150	160
SYFGTDKITR	INIAGWKTDG	KWQRDMCNVL	LQLEDINCIN	LDWINGSREY	IHAVNNLRVV	GAEVAYFIDV	LMKKFEYSPS
170	180	190	200	210	220	230	240
KVHLIGHSLG	AHLAGEAGSR	IPGLGRITGL	DPAGPFFHNT	PKEVRLDPSD	ANFVDVIHTN	AARILFELGV	GTIDACGHLD
250	260	270	280	290	300	310	320
FYPNGGKHMP	GCEDLITPLL	KFNFNAYKKE	MASFFDCNHA	RSYQFYAESI	LNPDAFIAYP	CRSYTSFKAG	NCFFCSKEGC
330	340	350	360	370	380	390	400
PTMGHFADRF	HFKNMKTNGS	HYFLNTGSLS	PFARWRHKLS	VKLSGSEVTQ	GTVFLRVGGA	VRKTGEFAIV	SGKLEPGMTY
410	420	430	440	450	460	470	
TKLIDADVNV	GNITSVQFIW	KKHLFEDSQN	KLGAEMVINT	SGKYGYKSTF	CSQDIMGPNI	LQNLKPC	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
261	1	528.1590	-186.43	2	32.0	10.3	0	394-402	K.LEPGMTYTK.L	Oxidation: 5	WD:WU 0.90

Detailed Protein Report

Protein 1132: 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

Quantitation

WD:WU	**Median:**	1.24	**CV:**	0.00 %	**No. of Peptides:**	1

Alias proteins:

Accession	Name	Description
gi|573014793	refseq_huma (refseq_human_20140103.fasta)	protein lin-54 homolog isoform b [Homo sapiens]
gi|169234723	refseq_huma (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	Ratios
107	1	504.5800	42.14	3	30.6	10.2	1	405-417	K.CIGCKNFEESPER.K		WD:WU 1.24

Detailed Protein Report

Protein 1133: probable inactive ribonuclease-like protein 12 precursor [Homo sapiens]

Accession: gi|67459908
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 10.2
MW [kDa]: 17.2
pI: 6.8
Sequence Coverage [%]: 11.6
No. of unique Peptides: 1

```
         10         20         30         40         50         60         70         80
MIIMVIIFLV LLFWENEVND EAVMSTLEHL HVDYPQNDVP VPARYCNHMI IQRVIREPDH TCKKEHVFIH ERPRKINGIC
         90        100        110        120        130        140        150
ISPKKVACQN LSAIFCFQSE TKFKMTVCQL IEGTRYPACR YHYSPTEGFV LVTCDDLRPD SFLGYVK
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1960	1	973.3783	-84.95	2	52.9	10.2	0	86-102	K.VACQNLSAIFCFQSETK.F	Carbamidomethyl: 3

Detailed Protein Report

Protein 1134: tetratricopeptide repeat protein 40 [Homo sapiens]

Accession:	gi|359385708	**Score:**	10.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	303.3
Database Date:	2015-11-30	**pI:**	7.2
Modification(s):	Oxidation	**Sequence Coverage [%]:**	0.8
		No. of unique Peptides:	1

Detailed Protein Report

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        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
LNEMPPTFWI  LFLHLSGDRS  RLYGAAYEKP  KFITAAKGKV  QAVGGSCKVM  RLAISPTAFS  HLLACAQQFR  KQTQAQVYSE
      2250        2260        2270        2280        2290        2300        2310        2320
DMALNIGSEP  EGLQVEEKER  PVQRLSSVLG  PLEELLQPLF  PLLSLSKARV  QTPAVVADSG  KSKGKDKERK  TSTGQHSTVQ
      2330        2340        2350        2360        2370        2380        2390        2400
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Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2308	1	841.6632	-116.58	3	57.3	10.2	2	972-994	K.KFGPEESRLVAEMLCTATAIQGR.S	Oxidation: 13

Detailed Protein Report

Protein 1135: 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: 10.2
MW [kDa]: 145.8
pI: 9.9
Sequence Coverage [%]: 1.3
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
2371	1	937.3024	-144.74	2	57.9	10.2	1	975-991	R.HEQSGGPEHGPERGPFR.G	

Detailed Protein Report

Protein 1136: PREDICTED: 6-phosphofructokinase type C isoform X3 [Homo sapiens]

Accession:	gi|530392193	**Score:**	10.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	81.7
Database Date:	2015-11-30	**pI:**	8.5
		Sequence Coverage [%]:	1.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MNAAVRAVVR	MGIYVGAKVY	FIYEGYQGMV	DGGSNIAEAD	WESVSSILQV	GGTIIGSARC	QAFRTREGRL	KAACNLLQRG
90	100	110	120	130	140	150	160
ITNLCVIGGD	GSLTGANLFR	KEWSGLLEEL	ARNGQIDKEA	VQKYAYLNVV	GMVGSIDNDF	CGTDMTIGTD	SALHRIIEVV
170	180	190	200	210	220	230	240
DAIMTTAQSH	QRTFVLEVMG	RHCGYLALVS	ALACGADWVF	LPESPPEEGW	EEQMCVKLSE	NRARKKRLNI	IIVAEGAIDT
250	260	270	280	290	300	310	320
QNKPITSEKI	KELVVTQLGY	DTRVTILGHV	QRGGTPSAFD	RILASRMGVE	AVIALLEATP	DTPACVVSLN	GNHAVRLPLM
330	340	350	360	370	380	390	400
ECVQMTQDVQ	KAMDERRFQD	AVRLRGRSFA	GNLNTYKRLA	IKLPDDQIPK	TNCNVAVINV	GAPAAGMNAA	VRSAVRVGIA
410	420	430	440	450	460	470	480
DGHRMLAIYD	GFDGFAKGQI	KEIGWTDVGG	WTGQGGSILG	TKRVLPGKYL	EEIATQMRTH	SINALLIIGG	FEAYLGLLEL
490	500	510	520	530	540	550	560
SAAREKHEEF	CVPMVMVPAT	VSNNVPGSDF	SIGADTALNT	ITDTCDRIKQ	SASGTKRRVF	IIETMGGYCG	YLANMGGLAA
570	580	590	600	610	620	630	640
GADAAYIFEE	PFDIRDLQSN	VEHLTEKMKT	TIQRGLVLRN	ESCSENYTTD	FIYQLYSEEG	KGVFDCRKNV	LGHMQQGGAP
650	660	670	680	690	700	710	720
SPFDRNFGTK	ISARAMEWIT	AKLKEARGRG	KKFTTDDSIC	VLGISKRNVI	FQPVAELKKQ	TDFEHRIPKE	QWWLKLRPLM
730	740	750					
KILAKYKASY	DVSDSGQLEH	VQPWSV					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2259	1	619.2475	-151.99	2	56.6	10.2	1	393-404	R.SAVRVGIADGHR.M	

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Detailed Protein Report

Protein 1137: PREDICTED: uncharacterized protein LOC728637 isoform X2 [Homo sapiens]

Accession:	gi|578810543	**Score:**	10.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	24.1
Database Date:	2015-11-30	**pI:**	8.9
		Sequence Coverage [%]:	6.8
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MWPLRVYTRK KREGQRLNLT PTPDLGSPAK AEAPPGSKRK GKVHGLSKIA EKAERSRQGG SGSGPFSPRL GVTGEKSLQE
        90        100        110        120        130        140        150        160
NRSSEDTQDE KIASLRESVT DDLQVDSSSS NSELVSDWEC PNLEEHMQWK NSTLLDTSKA VAIEKAPQFS NVSAIFSTSS
       170        180        190        200        210        220        230
EDYQKCHRKT VMTVADQNVS PKAKCASNSE SDNAACEILL AEKTCPSTPE KTKKKASIEA E
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
246	1	530.5813	-91.19	3	32.2	10.2	1	131-145	K.NSTLLDTSKAVAIEK.A	

Detailed Protein Report

Protein 1138: PREDICTED: nck-associated protein 5 isoform X5 [Homo sapiens]

Accession:	gi|578804245	**Score:**	10.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	193.9
Database Date:	2015-11-30	**pI:**	9.3
		Sequence Coverage [%]:	0.5
		No. of unique Peptides:	1

Quantitation

WD:WU	**Median:** 3.89	**CV:** 0.00 %	**No. of Peptides:** 1

Detailed Protein Report

10	20	30	40	50	60	70	80
MLHIYKTELI	IVSAKNDDFE	NCYKSKAENS	ALALENENQR	EQYERCLDEV	ANQVVQALLT	QKDLREECVK	LKTRVFDLEQ
90	100	110	120	130	140	150	160
QNRTLSILFQ	QRVRPTSDLL	LQKLHSRLLD	LSSGDLLSEV	ERNRSLTQSR	TDAEVHEHQL	NTKSALKCPG	LGAVIPGHLC
170	180	190	200	210	220	230	240
PRNSYSSSSE	LSLSSTCSEY	SSGSSYTWHD	GKNLRKRQSS	QNWDKRLSID	SSLPSGFASP	TNELPPTRIK	ESHILEGLRK
250	260	270	280	290	300	310	320
LQKRKVLLEP	PSVITKWGYK	DCMNSNEGIY	SPGIKSSSLK	EYPPCKTADL	GSPCKEPHKT	FVYDLDSHVD	ADDDPSTLAL
330	340	350	360	370	380	390	400
LQAVPNQSCR	PHGSKLTHSV	SDSLFGWETN	RKHFLEGTSS	VYPKERPEKL	TSCASSCPLE	MKLCPSVQTP	QVQRERGPQG
410	420	430	440	450	460	470	480
QGHGRMALNL	QLSDTDDNET	FDELHIESSD	EKSPSDVSLA	ADTDKSVENL	DVLVGFGKSL	CGSPEEEEKQ	VPIPSETRPK
490	500	510	520	530	540	550	560
TFSFIKQQRV	VKRTSSEECV	TVIFDAEDGE	PIEFSSHQTG	VVTVTRNEIS	INSTPAGPKA	EHTELLPQGI	ACLQPRAAAR
570	580	590	600	610	620	630	640
DYTFFKRSEE	DTEKNIPKDN	VDNVPRVSTE	SFSSRTVTQN	PQQQKLVKPT	HNISCQSNSR	SSAPMGIYQK	QNLTKIPPRG
650	660	670	680	690	700	710	720
KSSPQKSKLM	EPEATTLLPS	SGLVTLEKSP	ALAPGKLSRF	MKTESSGPLF	ELRSDPHIPK	HSAQLPHSSR	MPSRRDWVQC
730	740	750	760	770	780	790	800
PKSQTPGSRS	RPAIESSDSG	EPPTRDEHCG	SGPEAGVKSP	SPPPPPGRSV	SLLARPSYDY	SPAPSSTKSE	TRVPSETART
810	820	830	840	850	860	870	880
PFKSPLLKGI	SAPVISSNPA	TTEVQRKKPS	VAFKKPIFTH	PMPSPEAVIQ	TRCPAHAPSS	SFTVMALGPP	KVSPKRGVPK
890	900	910	920	930	940	950	960
TSPRQTLGTP	QRDIGLQTPR	ISPSTHEPLE	MTSSKSVSPG	RKGQLNDSAS	TPPKPSFLGV	NESPSSQVSS	SSSSSSPAKS
970	980	990	1000	1010	1020	1030	1040
HNSPHGCQSA	HEKGLKTRLP	VGLKVLMKSP	QLLRKSSTVP	GKHEKDSLNE	ASKSSVAVNK	SKPEDSKNPA	SMEITAGERN
1050	1060	1070	1080	1090	1100	1110	1120
VTLPDSQAQG	SLADGLPLET	ALQEPLESSI	PGSDGRDGVD	NRSMRRSLSS	SKPHLKPALG	MNGAKARSHS	FSTHSGDKPS
1130	1140	1150	1160	1170	1180	1190	1200
TPPIEGSGKV	RTQIITNTAE	RGNSLTRQNS	STESSPNKAP	SAPMLESLPS	VGRPSGHPSS	GKGSLGSSGS	FSSQHGSPSK
1210	1220	1230	1240	1250	1260	1270	1280
LPLRIPPKSE	GLLIPPGKED	QQAFTQGECP	SANVAVLGEP	GSDRRSCPPT	PTDCPEALQS	PGRTQHPSTF	ETSSTSKLET
1290	1300	1310	1320	1330	1340	1350	1360
SGRHPDASAT	ATDAVSSEAP	LSPTIEEKVM	LCIQENVEKG	QVQTKPTSVE	AKQKPGPSFA	SWFGFRKSRL	PALSSRKMDI
1370	1380	1390	1400	1410	1420	1430	1440
SKTKVEKKDA	KVLGFGNRQL	KSERKKEKKK	PELQCETENE	LIKDTKSADN	PDGGLQSKNN	RRTPQDIYNQ	LKIEPRNRHS
1450	1460	1470	1480	1490	1500	1510	1520
PVACSTKDTF	MTELLNRVDK	KAAPQTESGS	SNASCRNVLK	GSSQGSCLIG	SSISTQGNHK	KNMKIKADME	VPKDSLVKEA
1530	1540	1550	1560	1570	1580	1590	1600
NENLQEDEDD	AVADSVFQSH	IIESNCQMRT	LDSGIGTFPL	PDSGNRSTGR	YLCQPDSPED	AEPLLPLQSA	LSAVSSMRAQ
1610	1620	1630	1640	1650	1660	1670	1680
TLEREVPSST	DGQRPADSAI	VHSTSDPIMT	ARGMRPLQSR	LPKPASSGKV	SSQKQNEAEP	RPQTCSSFGY	AEDPMASQPL
1690	1700	1710	1720	1730	1740	1750	1760
PDWGSEVAAT	GTQKLRQLEE	TKDDPENRLS	KISLESFNKF	NSNTVILLEK	EKNSLNKVEG	QKEEKEKNEE	TSLSSSDRPG
1770	1780	1790					
VDNLESLSDS	LYDSFSSCAS	QGSNDV					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1394	1	533.7488	-137.10	2	45.8	10.2	1	631-639	K.QNLTKIPPR.G		WD:WU 3.89

Detailed Protein Report

Protein 1139: 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 1140: cleavage and polyadenylation specificity factor subunit 2 [Homo sapiens]

Accession: gi|34101288
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 10.2
MW [kDa]: 88.4
pI: 4.8
Sequence Coverage [%]: 1.7
No. of unique Peptides: 1

Alias proteins:

Accession	Name	Description
gi|530403998	refseq_human(refseq_human_20140103.fasta)	PREDICTED: cleavage and polyadenylation specificity factor subunit 2 isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MTSIIKLTTL	SGVQEESALC	YLLQVDEFRF	LLDCGWDEHF	SMDIIDSLRK	HVHQIDAVLL	SHPDPLHLGA	LPYAVGKLGL
90	100	110	120	130	140	150	160
NCAIYATIPV	YKMGQMFMYD	LYQSRHNTED	FTLFTLDDVD	AAFDKIQQLK	FSQIVNLKGK	GHGLSITPLP	AGHMIGGTIW
170	180	190	200	210	220	230	240
KIVKDGEEEI	VYAVDFNHKR	EIHLNGCSLE	MLSRPSLLIT	DSFNATYVQP	RRKQRDEQLL	TNVLETLRGD	GNVLIAVDTA
250	260	270	280	290	300	310	320
GRVLELAQLL	DQIWRTKDAG	LGVYSLALLN	NVSYNVVEFS	KSQVEWMSDK	LMRCFEDKRN	NPFQFRHLSL	CHGLSDLARV
330	340	350	360	370	380	390	400
PSPKVVLASQ	PDLECGFSRD	LFIQWCQDPK	NSIILTYRTT	PGTLARFLID	NPSEKITEIE	LRKRVKLEGK	ELEEYLEKEK
410	420	430	440	450	460	470	480
LKKEAAKKLE	QSKEADIDSS	DESDIEEDID	QPSAHKTKHD	LMMKGEGSRK	GSFFKQAKKS	YPMFPAPEER	IKWDEYGEII
490	500	510	520	530	540	550	560
KPEDFLVPEL	QATEEEKSKL	ESGLTNGDEP	MDQDLSDVPT	KCISTTESIE	IKARVTYIDY	EGRSDGDSIK	KIINQMKPRQ
570	580	590	600	610	620	630	640
LIIVHGPPEA	SQDLAECCRA	FGGKDIKVYM	PKLHETVDAT	SETHIYQVRL	KDSLVSSLQF	CKAKDAELAW	IDGVLDMRVS
650	660	670	680	690	700	710	720
KVDTGVILEE	GELKDDGEDS	EMQVEAPSDS	SVIAQQKAMK	SLFGDDEKET	GEESEIIPTL	EPLPPHEVPG	HQSVFMNEPR
730	740	750	760	770	780	790	
LSDFKQVLLR	EGIQAEFVGG	VLVCNNQVAV	RRTETGRIGL	EGCLCQDFYR	IRDLLYEQYA	IV	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1834	1	734.4148	23.62	2	51.3	10.2	1	610-622	R.LKDSLVSSLQFCK.A	

Detailed Protein Report

Protein 1141: collagen triple helix repeat-containing protein 1 isoform 2 [Homo sapiens]

Accession:	gi|368711292	**Score:**	10.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	24.8
Database Date:	2015-11-30	**pI:**	9.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	7.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MWPPGRSITV	KLREKTVSRK	LEMNGPSAFQ	GLICGKYNGM	CLQGPAGVPG	RDGSPGANGI	PGTPGIPGRD	GFKGEKGECL
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
RESFEESWTP	NYKQCSWSSL	NYGIDLGKIA	ECTFTKMRSN	SALRVLFSGS	LRLKCRNACC	QRWYFTFNGA	ECSGPLPIEA
170	**180**	**190**	**200**	**210**	**220**	**230**	
IIYLDQGSPE	MNSTINIHRT	SSVEGLCEGI	GAGLVDVAIW	VGTCSDYPKG	DASTGWNSVS	RIIIEELPK	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1998	1	840.7992	-129.23	2	53.6	10.2	0	21-36	K.LEMNGPSAFQGLICGK.Y	Oxidation: 3

Detailed Protein Report

Protein 1142: 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	

Detailed Protein Report

Protein 1143: retinal guanylyl cyclase 1 [Homo sapiens]

Accession:	gi|4504217	**Score:**	10.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	120.0
Database Date:	2015-11-30	**pI:**	7.4
Modification(s):	Oxidation	**Sequence Coverage [%]:**	0.9
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 1.64 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MTACARRAGG	LPDPGLCGPA	WWAPSLPRLP	RALPRLPLLL	LLLLLQPPAL	SAVFTVGVLG	PWACDPIFSR	ARPDLAARLA
90	100	110	120	130	140	150	160
AARLNRDPGL	AGGPRFEVAL	LPEPCRTPGS	LGAVSSALAR	VSGLVGPVNP	AACRPAELLA	EEAGIALVPW	GCPWTQAEGT
170	180	190	200	210	220	230	240
TAPAVTPAAD	ALYALLRAFG	WARVALVTAP	QDLWVEAGRS	LSTALRARGL	PVASVTSMEP	LDLSGAREAL	RKVRDGPRVT
250	260	270	280	290	300	310	320
AVIMVMHSVL	LGGEEQRYLL	EAAEELGLTD	GSLVFLPFDT	IHYALSPGPE	ALAALANSSQ	LRRAHDAVLT	LTRHCPSEGS
330	340	350	360	370	380	390	400
VLDSLRRAQE	RRELPSDLNL	QQVSPLFGTI	YDAVFLLARG	VAEARAAAGG	RWVSGAAVAR	HIRDAQVPGF	CGDLGGDEEP
410	420	430	440	450	460	470	480
PFVLLDTDAA	GDRLFATYML	DPARGSFLSA	GTRMHFPRGG	SAPGPDPSCW	FDPNNICGGG	LEPGLVFLGF	LLVVGMGLAG
490	500	510	520	530	540	550	560
AFLAHYVRHR	LLHMQMVSGP	NKIILTVDDI	TFLHPHGGTS	RKVAQGSRSS	LGARSMSDIR	SGPSQHLDSP	NIGVYEGDRV
570	580	590	600	610	620	630	640
WLKKFPGDQH	IAIRPATKTA	FSKLQELRHE	NVALYLGLFL	ARGAEGPAAL	WEGNLAVVSE	HCTRGSLQDL	LAQREIKLDW
650	660	670	680	690	700	710	720
MFKSSLLLDL	IKGIRYLHHR	GVAHGRLKSR	NCIVDGRFVL	KITDHGHGRL	LEAQKVLPEP	PRAEDQLWTA	PELLRDPALE
730	740	750	760	770	780	790	800
RRGTLAGDVF	SLAIIMQEVV	CRSAPYAMLE	LTPEEVVQRV	RSPPPLCRPL	VSMDQAPVEC	ILLMKQCWAE	QPELRPSMDH
810	820	830	840	850	860	870	880
TFDLFKNINK	GRKTNIIDSM	LRMLEQYSSN	LEDLIRERTE	ELELEKQKTD	RLLTQMLPPS	VAEALKTGTP	VEPEYFEQVT
890	900	910	920	930	940	950	960
LYFSDIVGFT	TISAMSEPIE	VVDLLNDLYT	LFDAIIGSHD	VYKVETIGDA	YMVASGLPQR	NGQRHAAEIA	NMSLDILSAV
970	980	990	1000	1010	1020	1030	1040
GTFRMRHMPE	VPVRIRIGLH	SGPCVAGVVG	LTMPRYCLFG	DTVNTASRME	STGLPYRIHV	NLSTVGILRA	LDSGYQVELR
1050	1060	1070	1080	1090	1100	1110	
GRTELKGKGA	EDTFWLVGRR	GFNKPIPKPP	DLQPGSSNHG	ISLQEIPPER	RRKLEKARPG	QFS	

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	965-974	R.MRHMPEVPVR.I	Oxidation: 1, 4	WD:WU 1.64

Detailed Protein Report

Protein 1144: zinc finger protein 592 [Homo sapiens]

Accession:	gi|108860697	**Score:**	10.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	137.4
Database Date:	2015-11-30	**pI:**	9.3
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	1.2
		No. of unique Peptides:	1

Quantitation

WD:WU	**Median:** 0.90	**CV:** 0.00 %	**No. of Peptides:**	1

Alias proteins:

Accession	Name	Description
gi|530407316	refseq_human (refseq_human_20140103.fasta)	PREDICTED: zinc finger protein 592 isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MGDMKTPDFD	DLLAAFDIPD	PTSLDAKEAI	QTPSEENESP	LKPPGICMDE	SVSLSHSGSA	PDVPAVSVIV	KNTSRQESFE
90	100	110	120	130	140	150	160
AEKDHITPSL	LHNGFRGSDL	PPDPHNCGKF	DSTFMNGDSA	RSFPGKLEPP	KSEPLPTFNQ	FSPISSPEPE	DPIKDNGFGI
170	180	190	200	210	220	230	240
KPKHSDSYFP	PPLGCGAVGG	PVLEALAKFP	VPELHMFDHF	CKKEPKPEPL	PLGSQQEHEQ	SGQNTVEPHK	DPDATRFFGE
250	260	270	280	290	300	310	320
ALEFNSHPSN	SIGESKGLAR	ELGTCSSVPP	RQRLKPAHSK	LSSCVAALVA	LQAKRVASVT	KEDQPGHTKD	LSGPTKESSK
330	340	350	360	370	380	390	400
GSPKMPKSPK	SPRSPLEATR	KSIKPSDSPR	SICSDSSSKG	SPSVAASSPP	AIPKVRIKTI	KTSSGEIKRT	VTRILPDPDD
410	420	430	440	450	460	470	480
PSKSPVGSPL	GSAIAEAPSE	MPGDEVPVEE	HFPEAGTNSG	SPQGARKGDE	SMTKASDSSS	PSCSSGPRVP	KGAAPGSQTG
490	500	510	520	530	540	550	560
KKQQSTALQA	STLAPANLLP	KAVHLANLNL	VPHSVAASVT	AKSSVQRRSQ	PQLTQMSVPL	VHQVKKAAPL	IVEVFNKVLH
570	580	590	600	610	620	630	640
SSNPVPLYAP	NLSPPADSRI	HVPASGYCCL	ECGDAFALEK	SLSQHYGRRS	VHIEVLCTLC	SKTLLFFNKC	SLLRHARDHK
650	660	670	680	690	700	710	720
SKGLVMQCSQ	LLVKPISADQ	MFVSAPVNST	APAAPAPSSS	PKHGLTSGSA	SPPPPALPLY	PDPVRLIRYS	IKCLECHKQM
730	740	750	760	770	780	790	800
RDYMVLAAHF	QRTTEETEGL	TCQVCQMLLP	NQCSFCAHQR	IHAHKSPYCC	PECGVLCRSA	YFQTHVKENC	LHYARKVGYR
810	820	830	840	850	860	870	880
CIHCGVVHLT	LALLKSHIQE	RHCQVFHKCA	FCPMAFKTAS	STADHSATQH	PTQPHRPSQL	IYKCSCEMVF	NKKRHIQQHF
890	900	910	920	930	940	950	960
YQNVSKTQVG	VFKCPECPLL	FVQKPELMQH	VKSTHGVPRN	VDELSSLQSS	ADTSSSRPGS	RVPTEPPATS	VAARSSSLPS
970	980	990	1000	1010	1020	1030	1040
GRWGRPEAHR	RVEARPRLRN	TGWTCQECQE	WVPDRESYVS	HMKKSHGRTL	KRYPCRQCEQ	SFHTPNSLRK	HIRNNHDTVK
1050	1060	1070	1080	1090	1100	1110	1120
KFYTCGYCTE	DSPSFPRPSL	LESHISLMHG	IRNPDLSQTS	KVKPPGGHSP	QVNHLKRPVS	GVGDAPGTSN	GATVSSTKRH
1130	1140	1150	1160	1170	1180	1190	1200
KSLFQCAKCS	FATDSGLEFQ	SHIPQHQVDS	STAQCLLCGL	CYTSASSLSR	HLFIVHKVRD	QEEEEEEEAA	AAEMAVEVAE
1210	1220	1230	1240	1250	1260	1270	
PEEGSGEEVP	METRENGLEE	CAGEPLSADP	EARRLLGPAP	EDDGGHNDHS	QPQASQDQDS	HTLSPQV	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
852	1	974.4621	-3.82	2	39.1	10.2	1	189-203	K.FPVPELHMFDHFCKK.E	Carbamidomethyl: 13; Oxidation: 8	WD:WU 0.90

Detailed Protein Report

Protein 1145: 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	

Detailed Protein Report

Protein 1146: neuromedin-U receptor 1 [Homo sapiens]

Accession:	gi|188497623	**Score:**	10.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	47.3
Database Date:	2015-11-30	**pI:**	10.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MTPLCLNCSV	LPGDLYPGGA	RNPMACNGSA	ARGHFDPEDL	NLTDEALRLK	YLGPQQTELF	MPICATYLLI	FVVGAVGNGL
90	100	110	120	130	140	150	160
TCLVILRHKA	MRTPTNYYLF	SLAVSDLLVL	LVGLPLELYE	MWHNYPFLLG	VGGCYFRTLL	FEMVCLASVL	NVTALSVERY
170	180	190	200	210	220	230	240
VAVVHPLQAR	SMVTRAHVRR	VLGAVWGLAM	LCSLPNTSLH	GIRQLHVPCR	GPVPDSAVCM	LVRPRALYNM	VVQTTALLFF
250	260	270	280	290	300	310	320
CLPMAIMSVL	YLLIGLRLRR	ERLLLMQEAK	GRGSAAARSR	YTCRLQQHDR	GRRQVTKMLF	VLVVVFGICW	APFHADRVMW
330	340	350	360	370	380	390	400
SVVSQWTDGL	HLAFQHVHVI	SGIFFYLGSA	ANPVLYSLMS	SRFRETFQEA	LCLGACCHRL	RPRHSSHSLS	RMTTGSTLCD
410	420	430					
VGSLGSWVHP	LAGNDGPEAQ	QETDPS					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2913	1	869.4027	27.32	2	65.2	10.2	0	365-379	R.ETFQEALCLGACCHR.L	Carbamidomethyl: 12

Detailed Protein Report

Protein 1147: 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

Quantitation

WD:WU **Median:** 1.13 **CV:** 0.00 % **No. of 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	Ratios
2209	1	1131.3087	-184.38	1	56.1	10.2	0	741-750	R.SEVPCAPMPK.K	Carbamidomethyl: 5; Oxidation: 8	WD:WU 1.13

Detailed Protein Report

Protein 1148: 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	

Detailed Protein Report

Protein 1149: 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 1150: probable gluconokinase isoform 3 [Homo sapiens]

Accession:	gi|379642551	**Score:**	10.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	15.7
Database Date:	2015-11-30	**pI:**	5.9
		Sequence Coverage [%]:	5.0
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 3.01 **CV:** 0.00 % **No. of 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	Ratios
702	1	387.7050	-42.29	2	37.6	10.1	0	46-52	R.DILTQGK.D		WD:WU 3.01

Detailed Protein Report

Protein 1151: PREDICTED: outer dense fiber protein 3B isoform X8 [Homo sapiens]

Accession:	gi|578837697	**Score:**	10.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	21.9
Database Date:	2015-11-30	**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 1152: **PREDICTED: kynurenine/alpha-aminoadipate aminotransferase, mitochondrial isoform X1 [Homo sapiens]**

Accession:	gi|578809158	**Score:**	10.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	51.7
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
MLKFVLVAGM	LPRRVPRVSL	TKDGPQPLKK	KLDAWLSEDM	NYARFITAAS	AARNPSPIRT	MTDILSRGPK	SMISLAGGLP
90	100	110	120	130	140	150	160
NPNMFPFKTA	VITVENGKTI	QFGEEMMKRA	LQYSPSAGIP	ELLSWLKQLQ	IKLHNPPTIH	YPPSQGQMDL	CVTSGSQQGL
170	180	190	200	210	220	230	240
CKVFEMIINP	GDNVLLDEPA	YSGTLQSLHP	LGCNIINVAS	DESGIVPDSL	RDILSRWKPE	DAKNPQKNTP	KFLYTVPNGN
250	260	270	280	290	300	310	320
NPTGNSLTSE	RKKEIYELAR	KYDFLIIEDD	PYYFLQFNKF	RVPTFLSMDV	DGRVIRADSF	SKIISSGLRI	GFLTGPKPLI
330	340	350	360	370	380	390	400
ERVILHIQVS	TLHPSTFNQL	MISQLLHEWG	EEGFMAHVDR	VIDFYSNQKD	AILAAADKWL	TGLAEWHVPA	AGMFLWIKVK
410	420	430	440	450	460	470	
GINDVKELIE	EKAVKMGVLM	LPGNAFYVDS	SAPSPYLRAS	FSSASPEQMD	VAFQVLAQLI	KESL	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2581	1	637.8494	-38.12	2	60.5	10.1	1	4-14	K.FVLVAGMLPRR.V	Oxidation: 7

Detailed Protein Report

Protein 1153: transmembrane protein 68 isoform 3 [Homo sapiens]

Accession:	gi|557786131	**Score:**	10.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	15.8
Database Date:	2015-11-30	**pI:**	6.2
		Sequence Coverage [%]:	12.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MIDKNQTCGV	GQDSVPYMIC	LIHILEEWFG	VEQLEDYLNF	ANYLLWVFTP	LILLILPYFT	IFLLYLTIIF	LHIYKRKNVL
90	**100**	**110**	**120**	**130**	**140**		
KEAYSHNLWD	GARKTVATLW	DGHAAVWHGK	QGYFHLCVAI	HVCCIGTVLP	FHFID		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1673	1	938.9125	-87.28	2	49.2	10.1	1	94-110	R.KTVATLWDGHAAVWHGK.Q	

Detailed Protein Report

Protein 1154: angiotensin-converting enzyme 2 precursor [Homo sapiens]

Accession:	gi|11225609	**Score:**	10.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	92.4
Database Date:	2015-11-30	**pI:**	5.3
		Sequence Coverage [%]:	0.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSSSSWLLLS	LVAVTAAQST	IEEQAKTFLD	KFNHEAEDLF	YQSSLASWNY	NTNITEENVQ	NMNNAGDKWS	AFLKEQSTLA
90	100	110	120	130	140	150	160
QMYPLQEIQN	LTVKLQLQAL	QQNGSSVLSE	DKSKRLNTIL	NTMSTIYSTG	KVCNPDNPQE	CLLLEPGLNE	IMANSLDYNE
170	180	190	200	210	220	230	240
RLWAWESWRS	EVGKQLRPLY	EEYVVLKNEM	ARANHYEDYG	DYWRGDYEVN	GVDGYDYSRG	QLIEDVEHTF	EEIKPLYEHL
250	260	270	280	290	300	310	320
HAYVRAKLMN	AYPSYISPIG	CLPAHLLGDM	WGRFWTNLYS	LTVPFGQKPN	IDVTDAMVDQ	AWDAQRIFKE	AEKFFVSVGL
330	340	350	360	370	380	390	400
PNMTQGFWEN	SMLTDPGNVQ	KAVCHPTAWD	LGKGDFRILM	CTKVTMDDFL	TAHHEMGHIQ	YDMAYAAQPF	LLRNGANEGF
410	420	430	440	450	460	470	480
HEAVGEIMSL	SAATPKHLKS	IGLLSPDFQE	DNETEINFLL	KQALTIVGTL	PFTYMLEKWR	WMVFKGEIPK	DQWMKKWWEM
490	500	510	520	530	540	550	560
KREIVGVVEP	VPHDETYCDP	ASLFHVSNDY	SFIRYYTRTL	YQFQFQEALC	QAAKHEGPLH	KCDISNSTEA	GQKLFNMLRL
570	580	590	600	610	620	630	640
GKSEPWTLAL	ENVVGAKNMN	VRPLLNYFEP	LFTWLKDQNK	NSFVGWSTDW	SPYADQSIKV	RISLKSALGD	KAYEWNDNEM
650	660	670	680	690	700	710	720
YLFRSSVAYA	MRQYFLKVKN	QMILFGEEDV	RVANLKPRIS	FNFFVTAPKN	VSDIIPRTEV	EKAIRMSRSR	INDAFRLNDN
730	740	750	760	770	780	790	800
SLEFLGIQPT	LGPPNQPPVS	IWLIVFGVVM	GVIVVGIVIL	IFTGIRDRKK	KNKARSGENP	YASIDISKGE	NNPGFQNTDD
810							
VQTSF							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2742	1	817.4866	67.39	1	62.7	10.1	0	535-541	K.HEGPLHK.C	

Detailed Protein Report

Protein 1155: 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 1156: apolipoprotein D precursor [Homo sapiens]

Accession:	gi|4502163	**Score:**	10.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	21.3
Database Date:	2015-11-30	**pI:**	4.9
Modification(s):	Oxidation	**Sequence Coverage [%]:**	6.3
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 0.90 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MVMLLLLLSA	LAGLFGAAEG	QAFHLGKCPN	PPVQENFDVN	KYLGRWYEIE	KIPTTFENGR	CIQANYSLME	NGKIKVLNQE
90	100	110	120	130	140	150	160
LRADGTVNQI	EGEATPVNLT	EPAKLEVKFS	WFMPSAPYWI	LATDYENYAL	VYSCTCIIQL	FHVDFAWILA	RNPNLPPETV
170	180	190					
DSLKNILTSN	NIDVKKMTVT	DQVNCPKLS					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
368	1	690.4400	149.87	2	33.2	10.1	1	176-187	K.KMTVTDQVNCPK.L	Oxidation: 2	WD:WU 0.90

Detailed Protein Report

Protein 1157: PREDICTED: coiled-coil domain-containing protein 158 isoform X8 [Homo sapiens]

Accession:	gi|578809093	**Score:**	10.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	122.8
Database Date:	2015-11-30	**pI:**	6.4
		Sequence Coverage [%]:	2.3
		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 1158: fetal and adult testis-expressed transcript protein [Homo sapiens]

Accession:	gi|14861838	**Score:**	10.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	20.7
Database Date:	2015-11-30	**pI:**	9.9
		Sequence Coverage [%]:	6.6
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 1.48 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MAGGPPNTKA EMEMSLAEEL NHGRQGENQE HLVIAEMMEL GSRSRGASQK KQKLEQKAAG SASAKRVWNM TATRPKKMGS
        90        100        110        120        130        140        150        160
QLPKPRMLRE SGHGDAHLQE YAGNFQGIRF HYDRNPGTDA VAQTSLEEFN VLEMEVMRRQ LYAVNRRLRA LEEQGATWRH
       170        180        190
RETLIIAVLV SASIANLWLW MNQ
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2684	1	715.3525	-39.72	2	61.9	10.1	1	148-159	R.LRALEEQGATWR.H		WD:WU 1.48

Detailed Protein Report

Protein 1159: ATP-dependent RNA helicase DDX18 [Homo sapiens]

Accession:	gi|38327634	**Score:**	10.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	75.4
Database Date:	2015-11-30	**pI:**	10.1
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSHLPMKLLR	KKIEKRNLKL	RQRNLKFQGA	SNLTLSETQN	GDVSEETMGS	RKVKKSKQKP	MNVGLSETQN	GGMSQEAVGN
90	100	110	120	130	140	150	160
IKVTKSPQKS	TVLTNGEAAM	QSSNSESKKK	KKKKRKMVND	AEPDTKKAKT	ENKGKSEEES	AETTKETENN	VEKPDNDEDE
170	180	190	200	210	220	230	240
SEVPSLPLGL	TGAFEDTSFA	SLCNLVNENT	LKAIKEMGFT	NMTEIQHKSI	RPLLEGRDLL	AAAKTGSGKT	LAFLIPAVEL
250	260	270	280	290	300	310	320
IVKLRFMPRN	GTGVLILSPT	RELAMQTFGV	LKELMTHHVH	TYGLIMGGSN	RSAEAQKLGN	GINIIVATPG	RLLDHMQNTP
330	340	350	360	370	380	390	400
GFMYKNLQCL	VIDEADRILD	VGFEEELKQI	IKLLPTRRQT	MLFSATQTRK	VEDLARISLK	KEPLYVGVDD	DKANATVDGL
410	420	430	440	450	460	470	480
EQGYVVCPSE	KRFLLLFTFL	KKNRKKKLMV	FFSSCMSVKY	HYELLNYIDL	PVLAIHGKQK	QNKRTTTFFQ	FCNADSGTLL
490	500	510	520	530	540	550	560
CTDVAARGLD	IPEVDWIVQY	DPPDDPKEYI	HRVGRTARGL	NGRGHALLIL	RPEELGFLRY	LKQSKVPLSE	FDFSWSKISD
570	580	590	600	610	620	630	640
IQSQLEKLIE	KNYFLHKSAQ	EAYKSYIRAY	DSHSLKQIFN	VNNLNLPQVA	LSFGFKVPPF	VDLNVNSNEG	KQKKRGGGGG
650	660	670	680				
FGYQKTKKVE	KSKIFKHISK	KSSDSRQFSH					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1269	1	697.8175	-17.16	2	44.2	10.1	0	428-439	K.LMVFFSSCMSVK.Y	Oxidation: 9

Detailed Protein Report

Protein 1160: 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 1161: PREDICTED: prothymosin alpha-like [Homo sapiens]

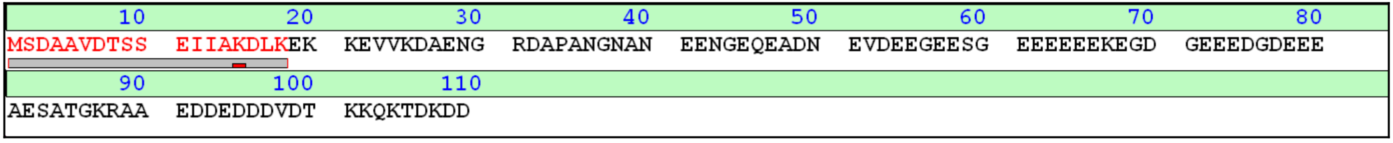
Accession:	gi|113420837	**Score:**	10.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	11.9
Database Date:	2015-11-30	**pI:**	3.7
		Sequence Coverage [%]:	16.5
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 1.08 **CV:** 0.00 % **No. of 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	Ratios
2007	1	947.3382	-146.89	2	53.7	10.1	1	1-18	-.MSDAAVDTSSEIIAKDLK.E		WD:WU 1.08

Detailed Protein Report

Protein 1162: synaptotagmin-13 isoform 2 [Homo sapiens]

Accession:	gi|351542146	**Score:**	10.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	31.3
Database Date:	2015-11-30	**pI:**	8.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.9
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578820656	refseq_human (refseq_human_20140103.fasta)	PREDICTED: synaptotagmin-13 isoform X1 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
METWNPEKAA SWNQAPKLHY CLDYDCQKAE LFVTRLEAVT SNHDGGCDCY VQGSVANRTG SVEAQTALKK RQLHTTWEEG
        90        100        110        120        130        140        150        160
LVLPLAEEEL PTATLTLTLR TCDRFSRHSV AGELRLGLDG TSVPLGAAQW GELKTSAKEP SAGAGEVLLS ISYLPAANRL
       170        180        190        200        210        220        230        240
LVVLIKAKNL HSNQSKELLG KDVSVKVTLK HQARKLKKKQ TKRAKHKINP VWNEMIMFEL PDDLLQASSV ELEVLGQDDS
       250        260        270        280        290
GQSCALGHCS LGLHTSGSER SHWEEMLKNP RRQIAMWHQL HL
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2945	1	729.3727	81.79	2	65.6	10.1	0	18-28	K.LHYCLDYDCQK.A	Carbamidomethyl: 9

Detailed Protein Report

Protein 1163: **type 1 phosphatidylinositol 4,5-bisphosphate 4-phosphatase isoform 2 [Homo sapiens]**

Accession:	gi|154816184	**Score:**	10.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	29.4
Database Date:	2015-11-30	**pI:**	10.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAADGERSPL	LSEPIDGGAG	GNGLVGPGGS	GAGPGGGLTP	SAPPYGAAFP	PFPEGHPAVL	PGEDPPPYSP	LTSPDSGSAP
90	100	110	120	130	140	150	160
MITCRVCQSL	INVEGKMHQH	VVKCGVCNEA	TPIKNAPPGK	KYVRCPCNCL	LICKVTSQRI	ACPRPYCKRI	INLGPVHPGP
170	180	190	200	210	220	230	240
LSPEPQPMGV	RVICGHCKNT	FLWTEFTDRT	LARCPHCRKV	SSIGRRYPRK	RCICCFLLGL	LLAVTATGLA	FGTWKHARRY
250	260	270	280				
GGIYAAWAFV	ILLAVLCLGR	ALYWACMKVS	HPVQNFS				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2003	1	621.2942	-43.69	2	53.4	10.1	2	190-199	R.TLARCPHCRK.V	Carbamidomethyl: 8

Detailed Protein Report

Protein 1164: zinc finger protein 219 [Homo sapiens]

Accession:	gi|156415996	**Score:**	10.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	76.8
Database Date:	2015-11-30	**pI:**	10.9
Modification(s):	Carbamidomethyl	**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]

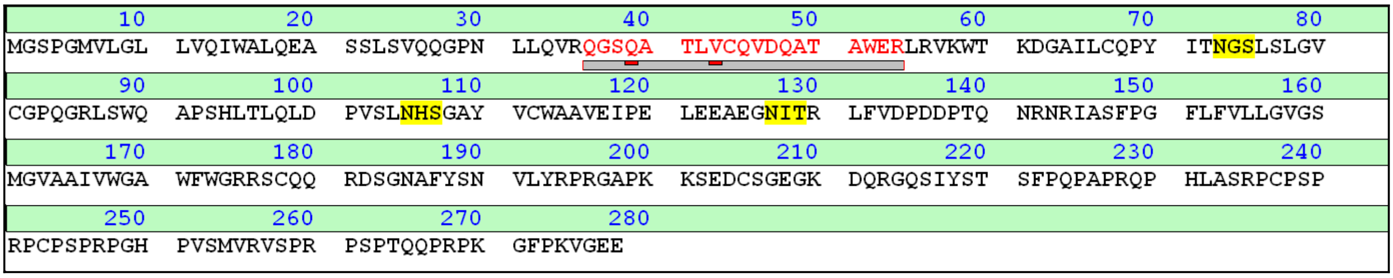
10	20	30	40	50	60	70	80
MEGSRPRAPS	GHLAPSPPAF	DGELDLQRYS	NGPAVSAGSL	GMGAVSWSES	RAGERRFPCP	VCGKRFRFNS	ILALHLRAHP
90	100	110	120	130	140	150	160
GAQAFQCPHC	GHRAAQRALL	RSHLRTHQPE	RPRSPAARLL	LELEERALLR	EARLGRARSS	GGMQATPATE	GLARPQAPSS
170	180	190	200	210	220	230	240
SAFRCPYCKG	KFRTSAERER	HLHILHRPWK	CGLCSFGSSQ	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 1165: **transmembrane and immunoglobulin domain-containing protein 2 isoform 2 precursor [Homo sapiens]**

Accession:	gi|281306840	**Score:**	10.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	30.3
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
MGSPGMVLGL	LVQIWALQEA	SSLSVQQGPN	LLQVRQGSQA	TLVCQVDQAT	AWERLRVKWT	KDGAILCQPY	ITNGSLSLGV
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
CGPQGRLSWQ	APSHLTLQLD	PVSLNHSGAY	VCWAAVEIPE	LEEAEGNITR	LFVDPDDPTQ	NRNRIASFPG	FLFVLLGVGS
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
MGVAAIVWGA	WFWGRRSCQQ	RDSGNAFYSN	VLYRPRGAPK	KSEDCSGEGK	DQRGQSIYST	SFPQPAPRQP	HLASRPCPSP
250	**260**	**270**	**280**				
RPCPSPRPGH	PVSMVRVSPR	PSPTQQPRPK	GFPKVGEE				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1886	1	1045.8876	-107.32	2	51.9	10.1	0	36-54	R.QGSQATLVCQVDQATAWER.L	

Detailed Protein Report

Protein 1166: PREDICTED: adenylate kinase 8 isoform X2 [Homo sapiens]

Accession:	gi|578817081	**Score:**	10.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	49.8
Database Date:	2015-11-30	**pI:**	5.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	5.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDATIAPHRI	PPEMPQYGEE	NHIFELMQAM	WLCKHLNSSL	LTLENLILNE	FSYTATEARR	LYLQRKTVPS	ALLVQLIQER
90	100	110	120	130	140	150	160
LAEEDCIKQG	WILDGIPETR	EQALRIQTLG	ITPRHVIVLS	APDTVLIERN	LGKRIDPQTG	EIYHTTFDWP	PESEIQNRLM
170	180	190	200	210	220	230	240
VPEDISELET	AQKLLEYHRN	IVRVIPSYPK	ILKVISADQP	CVDVFYQALT	YVQSNHRTNA	PFTPRVLLLG	PVGSGKSLQA
250	260	270	280	290	300	310	320
ALLAQKYRLV	NVCCGQLLKE	AVADRTTFGE	LIQPFFEKEM	AVPDSLLMKV	LSQRLDQQDC	IQKGWVLHGV	PRDLDQAHLL
330	340	350	360	370	380	390	400
NRLGYNPNRV	FFLNVPFDSI	MERLTLRRID	PVTGERYHLM	YKPPPTMEIQ	ARLLQNPKDA	EEQVKLKMDL	FYRNSADLEQ
410	420	430	440				
LYGSAITLNG	DQDPYTVFEY	IESGIINPLP	KKIP				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1430	1	1022.7032	-95.12	3	46.3	10.1	0	10-34	R.IPPEMPQYGEENHIFELMQAMWLCK.H	Oxidation: 18, 21

Protein 1167: PREDICTED: angiomotin-like protein 1 isoform X6 [Homo sapiens]

Accession:	gi|578822001	**Score:**	10.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	76.0
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
MDLSEKWTLE	EGAWLSHAGI	HHFASTRADS	EFVEASPASY	SPDELGSPSA	CYSPSSPVQV	LEDSTYFSPD	FQLYSGRHET
90	100	110	120	130	140	150	160
SALTVEATSS	IREKVVEDPL	CNFHSPNFLR	ISEVEMRGSE	DAAAGTVLQR	LIQEQLRYGT	PTENMNLLAI	QHQATGSAGP
170	180	190	200	210	220	230	240
AHPTNNFSST	ENLTQEDPQM	VYQSARQEPQ	GQEHQVDNTV	MEKQVRSTQP	QQNNEELPTY	EEAKAQSQFF	RGQQQQQQQQ
250	260	270	280	290	300	310	320
GAVGHGYYMA	GGTSQKSRTE	GRPTVNRANS	GQAHKDEALK	ELKQGHVRSL	SERIMQLSLE	RNGAKQHLPG	SGNGKGFKVG
330	340	350	360	370	380	390	400
GGPSPAQPAG	KVLDPRGPPP	EYPFKTKQMM	SPVSKTQEHG	LFYGDQHPGM	LHEMVKPYPA	PQPVRTDVAV	LRYQPPPEYG
410	420	430	440	450	460	470	480
VTSRPCQLPF	PSTMQQHSPM	SSQTSSASGP	LHSVSLPLPL	PMALGAPQPP	PAASPSQQLG	PDAFAIVERA	QQMVEILTEE
490	500	510	520	530	540	550	560
NRVLHQELQG	YYDNADKLHK	FEKELQRISE	AYESLVKSTT	KRESLDKAMR	NKLEGEIRRL	HDFNRDLRDR	LETANRQLSS
570	580	590	600	610	620	630	640
REYEGHEDKA	AEGHYASQNK	EFLKEKEKLE	MELAAVRTAS	EDHRRHIEIL	DQALSNAQAR	VIKLEEELRE	KQAYVEKVEK
650	660	670	680				
LQQALTQLQS	ACEKREQMER	RLRTWLEREL	DALRTQQ				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
825	1	848.9721	28.99	2	39.1	10.0	2	302-318	R.NGAKQHLPGSGNGKGFK.V	

Detailed Protein Report

Protein 1168: carbamoyl-phosphate synthase [ammonia], mitochondrial isoform c [Homo sapiens]

Accession:	gi|170295797	**Score:**	10.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	116.0
Database Date:	2015-11-30	**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 1169: PDZ and LIM domain protein 4 isoform 1 [Homo sapiens]

Accession:	gi|19923181	**Score:**	10.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	35.4
Database Date:	2015-11-30	**pI:**	9.2
		Sequence Coverage [%]:	6.4
		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 1170: carnosine synthase 1 isoform 2 [Homo sapiens]

Accession: gi|148839342
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 10.0
MW [kDa]: 88.4
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 1171: calsyntenin-3 precursor [Homo sapiens]

Accession:	gi|42475534	**Score:**	10.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	106.0
Database Date:	2015-11-30	**pI:**	5.1
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MTLLLLPLLL	ASLLASCSCN	KANKHKPWIE	AEYQGIVMEN	DNTVLLNPPL	FALDKDAPLR	YAGEICGFRL	HGSGVPFEAV
90	100	110	120	130	140	150	160
ILDKATGEGL	IRAKEPVDCE	AQKEHTFTIQ	AYDCGEGPDG	ANTKKSHKAT	VHVRVNDVNE	FAPVFVERLY	RAAVTEGKLY
170	180	190	200	210	220	230	240
DRILRVEAID	GDCSPQYSQI	CYYEILTPNT	PFLIDNDGNI	ENTEKLQYSG	ERLYKFTVTA	YDCGKKRAAD	DAEVEIQVKP
250	260	270	280	290	300	310	320
TCKPSWQGWN	KRIEYAPGAG	SLALFPGIRL	ETCDEPLWNI	QATIELQTSH	VAKGCDRDNY	SERALRKLCG	AATGEVDLLP
330	340	350	360	370	380	390	400
MPGPNANWTA	GLSVHYSQDS	SLIYWFNGTQ	AVQVPLGGPS	GLGSGPQDSL	SDHFTLSFWM	KHGVTPNKGK	KEEETIVCNT
410	420	430	440	450	460	470	480
VQNEDGFSHY	SLTVHGCRIA	FLYWPLLESA	RPVKFLWKLE	QVCDDEWHHY	ALNLEFPTVT	LYTDGISFDP	ALIHDNGLIH
490	500	510	520	530	540	550	560
PPRREPALMI	GACWTEEKNK	EKEKGDNSTD	TTQGDPLSIH	HYFHGYLAGF	SVRSGRLESR	EVIECLYACR	EGLDYRDFES
570	580	590	600	610	620	630	640
LGKGMKVHVN	PSQSLLTLEG	DDVETFNHAL	QHVAYMNTLR	FATPGVRPLR	LTTAVKCFSE	ESCVSIPEVE	GYVVVLQPDA
650	660	670	680	690	700	710	720
PQILLSGTAH	FARPAVDFEG	TNGVPLFPDL	QITCSISHQV	EAKKDESWQG	TVTDTRMSDE	IVHNLDGCEI	SLVGDDLDPE
730	740	750	760	770	780	790	800
RESLLLDTTS	LQQRGLELTN	TSAYLTIAGV	ESITVYEEIL	RQARYRLRHG	AALYTRKFRL	SCSEMNGRYS	SNEFIVEVNV
810	820	830	840	850	860	870	880
LHSMNRVAHP	SHVLSSQQFL	HRGHQPPPEM	AGHSLASSHR	NSMIPSAATL	IIVVCVGFLV	LMVVLGLVRI	HSLHRRVSGA
890	900	910	920	930	940	950	960
GGPPGASSDP	KDPDLFWDDS	ALTIIVNPME	SYQNRQSCVT	GAVGGQQEDE	DSSDSEVADS	PSSDERRIIE	TPPHRY

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2025	1	899.3750	-66.39	2	53.7	10.0	1	537-550	R.LESREVIECLYACR.E	Carbamidomethyl: 9, 13

Detailed Protein Report

Protein 1172: prohibitin-2 isoform 3 [Homo sapiens]

Accession:	gi|390608669	**Score:**	10.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	29.0
Database Date:	2015-11-30	**pI:**	10.4
		Sequence Coverage [%]:	6.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAQNLKDLAG	RLPAGPRGMG	TALKLLLGAG	AVAYGVRESV	FTVEGGHRAI	FFNRIGGVQQ	DTILAEGLHF	RIPWFQYPII
90	100	110	120	130	140	150	160
YDIRARPRKI	SSPTGSKDLQ	MVNISLRVLS	RPNAQELPSM	YQRLGLDYEE	RVLPSIVNEV	LKSVVAKFNA	SQLITQRAQV
170	180	190	200	210	220	230	240
SLLIRRELTE	RAKDFSLILD	DVAITELSFS	REYTAAVEAK	QVALSKNPGY	IKLRKIRAAQ	NISKTIATSQ	NRIYLTADNL
250	260	270					
VLNLQDESFT	RGSDSLIKGK	K					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2763	1	973.5204	-2.06	2	63.1	10.0	1	90-107	K.ISSPTGSKDLQMVNISLR.V	

Detailed Protein Report

Protein 1173: properdin precursor [Homo sapiens]

Accession:	gi|4505737	**Score:**	10.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	51.2
Database Date:	2015-11-30	**pI:**	10.1
		Sequence Coverage [%]:	3.0
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 1.03 **CV:** 0.00 % **No. of Peptides:** 1

Alias proteins:

Accession	Name	Description
gi|223671861	refseq_human (refseq_human_20140103.fasta)	properdin precursor [Homo sapiens]

10	20	30	40	50	60	70	80
MITEGAQAPR	LLLPPLLLLL	TLPATGSDPV	LCFTQYEESS	GKCKGLLGGG	VSVEDCCLNT	AFAYQKRSGG	LCQPCRSPRW
90	100	110	120	130	140	150	160
SLWSTWAPCS	VTCSEGSQLR	YRRCVGWNGQ	CSGKVAPGTL	EWQLQACEDQ	QCCPEMGGWS	GWGPWEPCSV	TCSKGTRTRR
170	180	190	200	210	220	230	240
RACNHPAPKC	GGHCPGQAQE	SEACDTQQVC	PTHGAWATWG	PWTPCSASCH	GGPHEPKETR	SRKCSAPEPS	QKPPGKPCPG
250	260	270	280	290	300	310	320
LAYEQRRCTG	LPPCPVAGGW	GPWGPVSPCP	VTCGLGQTME	QRTCNHPVPQ	HGGPFCAGDA	TRTHICNTAV	PCPVDGEWDS
330	340	350	360	370	380	390	400
WGEWSPCIRR	NMKSISCQEI	PGQQSRGRTC	RGRKFDGHRC	AGQQQDIRHC	YSIQHCPLKG	SWSEWSTWGL	CMPPCGPNPT
410	420	430	440	450	460	470	
RARQRLCTPL	LPKYPPTVSM	VEGQGEKNVT	FWGRPLPRCE	ELQGQKLVVE	EKRPCLHVPA	CKDPEEEEL	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1362	1	816.4149	-5.18	2	45.4	10.0	1	439-452	R.CEELQGQKLVVEEK.R		WD:WU 1.03

Detailed Protein Report

Protein 1174: 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

WD:WU	**Median:** 3.22	**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]

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	WD:WU	3.22

Detailed Protein Report

Protein 1175: putative polypeptide N-acetylgalactosaminyltransferase-like protein 5 [Homo sapiens]

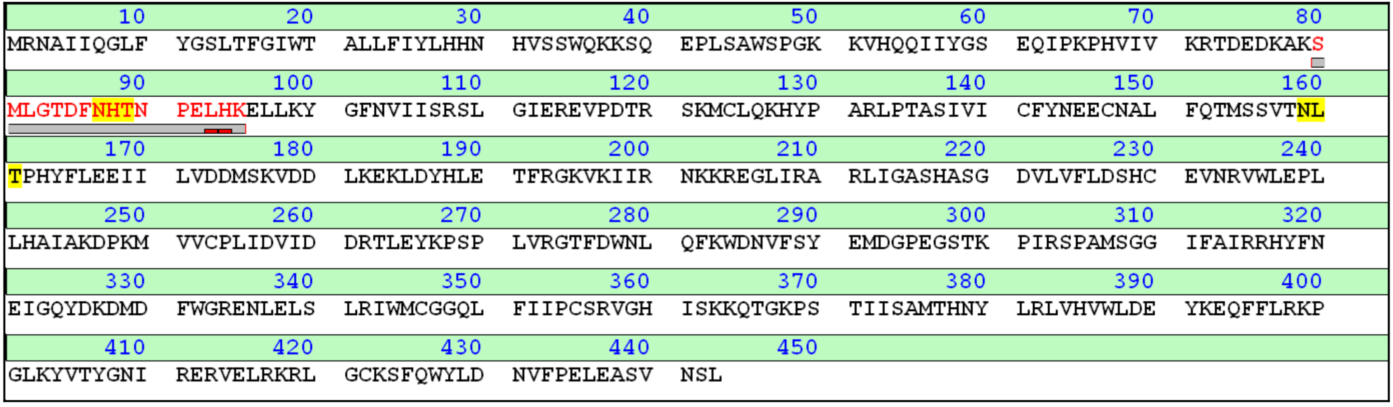
Accession:	gi|281485547	**Score:**	10.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	51.4
Database Date:	2015-11-30	**pI:**	9.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.6
		No. of unique Peptides:	1

Quantitation

WD:WU	**Median:**	0.42	**CV:**	0.00 %		**No. of Peptides:**	1

Alias proteins:

Accession	Name	Description
gi|578813950	refseq_human (refseq_human_20140103.fasta)	PREDICTED: putative polypeptide N-acetylgalactosaminyltransferase-like protein 5 isoform X2 [Homo sapiens]
gi|578813948	refseq_human (refseq_human_20140103.fasta)	PREDICTED: putative polypeptide N-acetylgalactosaminyltransferase-like protein 5 isoform X1 [Homo sapiens]



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        10         20         30         40         50         60         70         80
MRNAIIQGLF YGSLTFGIWT ALLFIYLHHN HVSSWQKKSQ EPLSAWSPGK KVHQQIIYGS EQIPKPHVIV KRTDEDKAKS
        90        100        110        120        130        140        150        160
MLGTDFNHTN PELHKELLKY GFNVIISRSL GIEREVPDTR SKMCLQKHYP ARLPTASIVI CFYNEECNAL FQTMSSVTNL
       170        180        190        200        210        220        230        240
TPHYFLEEII LVDDMSKVDD LKEKLDYHLE TFRGKVKIIR NKKREGLIRA RLIGASHASG DVLVFLDSHC EVNRVWLEPL
       250        260        270        280        290        300        310        320
LHAIAKDPKM VVCPLIDVID DRTLEYKPSP LVRGTFDWNL QFKWDNVFSY EMDGPEGSTK PIRSPAMSGG IFAIRRHYFN
       330        340        350        360        370        380        390        400
EIGQYDKDMD FWGRENLELS LRIWMCGGQL FIIPCSRVGH ISKKQTGKPS TIISAMTHNY LRLVHVWLDE YKEQFFLRKP
       410        420        430        440        450
GLKYVTYGNI RERVELRKRL GCKSFQWYLD NVFPELEASV NSL
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2735	1	928.9724	42.01	2	62.7	10.0	0	80-95	K.SMLGTDFNHTNPELHK.E	Oxidation: 2	WD:WU 0.42

Detailed Protein Report

Protein 1176: protein salvador homolog 1 [Homo sapiens]

Accession:	gi|11141889	**Score:**	10.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	44.6
Database Date:	2015-11-30	**pI:**	9.5
		Sequence Coverage [%]:	2.1
		No. of unique Peptides:	1

Quantitation

WD:WU **Median:** 1.58 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MLSRKKTKNE	VSKPAEVQGK	YVKKETSPLL	RNLMPSFIRH	GPTIPRRTDI	CLPDSSPNAF	STSGDVVSRN	QSFLRTPIQR
90	100	110	120	130	140	150	160
TPHEIMRRES	NRLSAPSYLA	RSLADVPREY	GSSQSFVTEV	SFAVENGDSG	SRYYYSDNFF	DGQRKRPLGD	RAHEDYRYYE
170	180	190	200	210	220	230	240
YNHDLFQRMP	QNQGRHASGI	GRVAATSLGN	LTNHGSEDLP	LPPGWSVDWT	MRGRKYYIDH	NTNTTHWSHP	LEREGLPPGW
250	260	270	280	290	300	310	320
ERVESSEFGT	YYVDHTNKKA	QYRHPCAPSV	PRYDQPPPVT	YQPQQTERNQ	SLLVPANPYH	TAEIPDWLQV	YARAPVKYDH
330	340	350	360	370	380	390	
ILKWELFQLA	DLDTYQGMLK	LLFMKELEQI	VKMYEAYRQA	LLTELENRKQ	RQQWYAQQHG	KNF	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
504	1	472.1588	-261.22	2	34.7	10.0	1	24-31	K.KETSPLLR.N		WD:WU 1.58

Detailed Protein Report

Protein 1177: 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	