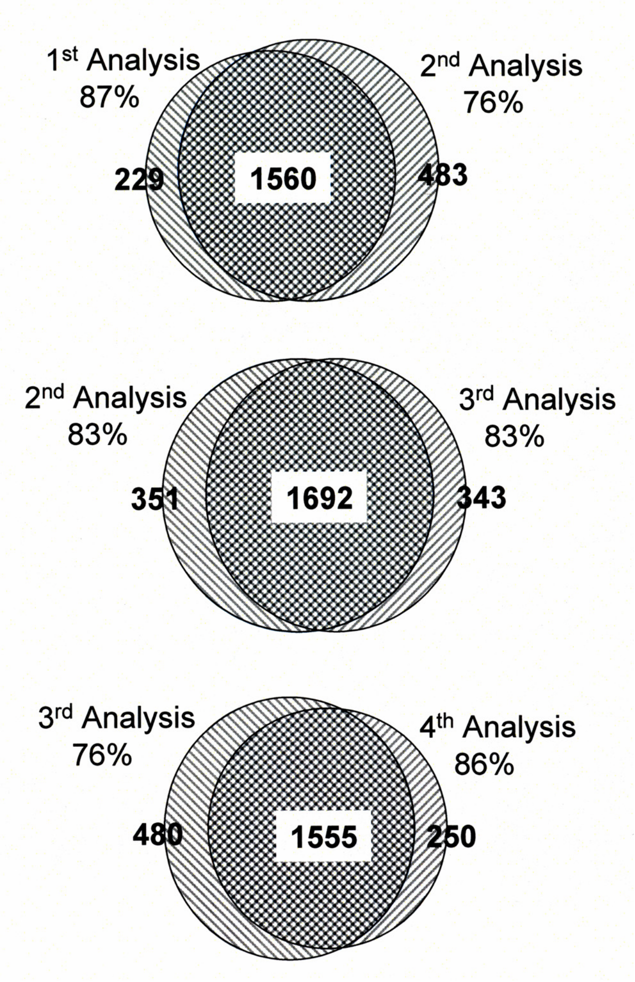
Supplemental Figures and Tables



Supplemental Figure 1. Reproducibility along repetitive analyses of the 2-D samples. In each Venn diagram, common protein counts and unique protein counts were labeled. Percentages illustrate the proportion of proteins identified in each analysis that were common with the other analysis being compared. Only proteins identified by two or more peptides were counted.

Supplemental Table 1. Identification of different closely related isoforms in a protein family by the 2-D/repetitive and 3-D methods.

2-D Protein			3-D Protein			
Protein Entry ID[a]	**# Unique Peptides**[b]	**Unique to Dataset**[c]	**Protein Entry ID**	**# Unique Peptides**[b]	**# Common Peptides**	**Sequence Identity (%)**
Q5U0I1	1	0	Q15907	1	10	99.54
			Q6FHR0			99.08
Q5VU66[d]	1	0	Q6QA25	3	12	93.95
UPI0000D61FF9[d]			UPI000020489E			93.55
Q4LE56	8	7	UPI0000F0A52B	6	19	94.44
Q6IAH3	1	0	Q9UBQ0	1	4	97.31
UPI000045667B						97.84
Q02952	3	1	Q4LE68	15	43	99.49
Q02952-2						98.99
Q59H74	2	1	UPI000052D444	5	4	98.48
			P13612			98.48
			UPI0000456EB4			98.48
Q8HXW2	2	1	Q53GR7	6	5	98.07
			Q9UJS0			98.37
			Q546F9			98.37
Q5U0I7	2	1	P67775	5	8	97.09
P62714						97.41
Q8WZ56						97.73
UPI00004576CB	2	1	UPI0000E9B14C	5	4	81.98
Q99475	3	3	Q6FI31	6	15	99.8
UPI0000D6223A						99.8
P11413-2	2	1	Q2Q9H2	4	22	99.79

a These 11 proteins were identified by ≥ 3 peptides in the 2-D/repetitive runs dataset but were not identified in the 3-D dataset. However, in all cases, highly homologous proteins with many common peptides were identified in the 3-D dataset due to database redundancy and variations in building consensus protein lists in different datasets.

b Number of peptides not shared with the corresponding most homologous protein in the other dataset.

c Most peptides that were apparently "unique" to the 2-D/repetitive-run dataset actually could be found assigned to other homologous proteins in the 3-D dataset, indicating further variations in assignments of peptides among multiple proteins in a protein family.

d These two proteins have a sequence identity of 98.7%.

Supplemental Table 2. Protein List of 2-D Dataset

uniref100 database (May, 2007); DTA
At least two unique peptide sequence

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
1	Q15149	236	3840	55.9	4684	531738	5.9	Plectin-1
1	Q6S380	236	3840	55.9	4684	531796	6	Plectin 6
2	UPI00004EC29C	183	4206	37	5890	629114	6.1	AHNAK nucleoprotein isoform 1
3	Q5HY53	103	1383	54	2639	280016	6	Filamin A, alpha
3	P21333	103	1383	53.9	2647	280737	6.1	Filamin-A
4	P78527	102	1059	28.1	4128	469093	7.1	DNA-dependent protein kinase catalytic subunit
4	UPI000045790C	102	1059	28.1	4127	468980	7.1	DNA-dependent protein kinase catalytic subunit (EC 2.7.11.1) (DNA-PK catalytic subunit) (DNA-PKcs) (DNPK1) (p460).
5	P35579	101	1639	55.5	1960	226530	5.6	Myosin-9
6	Q14204	98	561	26.3	4646	532412	6.4	Dynein heavy chain, cytosolic
6	UPI000021D4C1	98	561	26.3	4647	532371	6.4	Dynein heavy chain, cytosolic (DYHC) (Cytoplasmic dynein heavy chain 1) (DHC1) (Dynein heavy chain 1, cytoplasmic 1).
7	Q13813	94	728	43.6	2472	284538	5.3	Spectrin alpha chain, brain
7	UPI00004577B5	94	728	43.5	2480	285480	5.4	Spectrin alpha chain, brain (Spectrin, non-erythroid alpha chain) (Alpha-II spectrin) (Fodrin alpha chain).
7	Q13813-2	94	728	43.5	2477	285093	5.4	Isoform 2 of Q13813
7	UPI0000D61917	94	728	43.4	2485	286012	5.4	Spectrin alpha chain, brain (Spectrin, non-erythroid alpha chain) (Alpha-II spectrin) (Fodrin alpha chain).
8	Q53R99	84	716	45.1	2314	268714	5.6	Hypothetical protein SPTBN1
8	Q01082	84	716	44.2	2364	274608	5.6	Spectrin beta chain, brain 1
9	Q9Y490	79	887	44.8	2541	269765	6.1	Talin-1
9	UPI0000167B7F	79	887	44.8	2541	269665	6	talin 1
10	Q00610-2	75	1005	59.6	1639	187889	5.7	Isoform 2 of Q00610
10	Q00610	75	1005	58.3	1675	191613	5.7	Clathrin heavy chain 1
11	Q5SYZ6	73	1536	53.7	1621	177438	4.4	Nestin
12	O75369-2	67	436	35.3	2578	275697	5.8	Isoform 2 of O75369
12	Q60FE7	67	436	35.1	2591	276936	5.7	Filamin B
12	O75369	67	436	35	2602	278193	5.7	Filamin-B
12	UPI00001AEC01	67	436	35	2602	278162	5.7	filamin B, beta (actin binding protein 278)
13	P35580	61	297	46.6	1976	228937	5.5	Myosin-10
13	Q149N3	61	297	46.6	1976	228997	5.5	Myosin, heavy chain 10, non-muscle
13	P35580-3	61	297	46.1	1997	231307	5.5	Isoform 3 of P35580
13	Q4LE45	61	297	45.6	2018	233847	5.6	MYH10 variant protein
14	Q9NZM1-6	59	361	36.4	2048	233474	6.2	Isoform 6 of Q9NZM1
14	Q9NZM1	59	361	36.2	2061	234706	6.2	Myoferlin
15	O43707	55	1008	67.8	911	104854	5.4	Alpha-actinin-4
16	Q4LE83	54	412	28.3	2548	277368	6.6	FASN variant protein
16	UPI0000D623B2	54	412	28.3	2548	277428	6.6	Fatty acid synthase (EC 2.3.1.85) [Includes: [Acyl-carrier-protein] S-acetyltransferase (EC 2.3.1.38); [Acyl-carrier-protein] S-malonyltransferase (EC 2.3.1.39); 3-oxoacyl-[acyl-carrier-protein] synthase (EC 2.3.1.41); 3-oxoacyl-[acyl-carrier-protein] r

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
17	P46940	50	360	39.6	1657	189251	6.5	Ras GTPase-activating-like protein IQGAP1
18	Q6ZUD8	49	342	44	1394	157961	6.1	CDNA FLJ43793 fis, clone TESTI4000014, highly similar to 130 kDa leucine-rich protein
19	Q9P2E9	49	587	40.6	1410	152472	8.6	Ribosome-binding protein 1
20	P18206-2	48	231	52.5	1066	116722	6.1	Isoform 1 of P18206
20	P18206	48	231	49.4	1134	123799	5.7	Vinculin
21	O75643	48	209	27.1	2136	244505	6.1	U5 small nuclear ribonucleoprotein 200 kDa helicase
22	Q02952-2	46	250	37.7	1683	181646	4.4	Isoform 2 of Q02952
22	Q02952	46	250	35.7	1781	191438	4.4	A-kinase anchor protein 12
23	Q5T201	44	188	43.7	1224	138345	7.7	Coatomer protein complex, subunit alpha
24	UPI000014054E	42	191	29.5	1600	175618	5.3	Eukaryotic translation initiation factor 4 gamma 1 (eIF-4-gamma 1) (eIF-4G1) (eIF-4G 1) (p220).
25	P46821	42	215	22.6	2468	270618	4.8	Microtubule-associated protein 1B (MAP 1B) [Contains: MAP1 light chain LC1]
25	UPI000013E382	42	215	22.6	2468	270632	4.8	Microtubule-associated protein 1B (MAP 1B) [Contains: MAP1 light chain LC1].
26	Q5CAQ5	41	777	55.6	802	92340	4.9	Tumor rejection antigen (Gp96) 1
26	P14625	41	777	55.5	803	92469	4.8	Endoplasmin precursor
27	P13639	40	827	58.3	858	95338	6.8	Elongation factor 2
28	Q08211	40	410	36.9	1270	140958	6.8	ATP-dependent RNA helicase A
28	UPI0000D62059	40	410	35.7	1315	146474	6.9	ATP-dependent RNA helicase A (EC 3.6.1.-) (Nuclear DNA helicase II) (NDH II) (DEAH box protein 9).
29	P02545	39	793	58.3	664	74140	7	Lamin-A/C
29	Q5I6Y6	39	793	58.3	664	74082	7.2	Lamin A/C transcript variant 1
30	P11216	39	444	58.2	843	96696	6.9	Glycogen phosphorylase, brain form
31	P33176	39	125	51.2	963	109685	6.5	Kinesin heavy chain
32	Q00341	39	188	40.9	1268	141439	6.9	Vigilin
33	Q9NYU2	39	155	31.6	1531	174976	5.6	UDP-glucose:glycoprotein glucosyltransferase 1 precursor
33	UPI0000D61230	39	155	31.1	1557	177373	5.6	UDP-glucose:glycoprotein glucosyltransferase 1 precursor (EC 2.4.1.-) (UDP-glucose ceramide glucosyltransferase-like 1) (UDP-- Glc:glycoprotein glucosyltransferase) (HUGT1).
33	UPI00000707D8	39	155	31.1	1555	177189	5.6	UDP-glucose ceramide glucosyltransferase-like 1 isoform 1
34	P08670	38	4318	74	466	53652	5.1	Vimentin
35	Q7KZF4	37	354	49.3	910	101997	7.2	Staphylococcal nuclease domain-containing protein 1
35	Q59FF0	37	354	46.6	964	107433	7.5	EBNA-2 co-activator variant
36	Q14152	36	142	28	1382	166569	6.8	Eukaryotic translation initiation factor 3 subunit 10
36	Q24JU4	36	142	28	1382	166470	6.7	Eukaryotic translation initiation factor 3, subunit 10 theta, 150/170kDa

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
37	P14618	35	1202	68.4	531	57937	7.8	Pyruvate kinase isozymes M1/M2
37	Q53GK4	35	1202	68.4	531	57984	8.1	Pyruvate kinase 3 isoform 1 variant
38	Q5CAQ7	34	610	43	854	98113	5.2	Heat shock protein HSP 90-alpha 2
39	P05023	34	411	37.6	1023	112896	5.5	Sodium/potassium-transporting ATPase alpha-1 chain precursor (EC 3.6.3.9) (Sodium pump 1) (Na(+)/K(+) ATPase 1)
40	Q86UP2-2	34	143	28.5	1300	149610	5.7	Isoform 2 of Q86UP2
40	Q86UP2	34	143	27.3	1357	156275	5.6	Kinectin
41	P11717	32	111	13.3	2491	274274	5.9	Cation-independent mannose-6-phosphate receptor precursor
41	UPI0000072478	32	111	13.3	2491	274373	5.9	Cation-independent mannose-6-phosphate receptor precursor (CI Man-6-P receptor) (CI-MPR) (M6PR) (Insulin-like growth factor 2 receptor) (Insulin-like growth factor II receptor) (IGF-II receptor) (M6P/IGF2 receptor) (M6P/IGF2R) (300 kDa mannose 6-phosphate
42	P10809	31	1321	68.9	573	61055	5.9	60 kDa heat shock protein, mitochondrial precursor
42	UPI000013D97A	31	1321	68.7	575	61213	5.9	60 kDa heat shock protein, mitochondrial precursor (Hsp60) (60 kDa chaperonin) (CPN60) (Heat shock protein 60) (HSP-60) (Mitochondrial matrix protein P1) (P60 lymphocyte protein) (HuCHA60).
43	P50990	31	166	63.7	548	59621	5.6	T-complex protein 1 subunit theta
44	UPI000004D059	31	135	37.6	1048	116052	5.7	integrin alpha-V precursor
45	UPI0000225CC0	31	131	35.6	1091	119772	7.3	ATP citrate lyase isoform 2
45	P53396	31	131	35.2	1101	120839	7.3	ATP-citrate synthase (EC 2.3.3.8) (ATP-citrate (pro-S-)-lyase)
46	Q86VP6	31	118	32.4	1230	136375	5.8	Cullin-associated NEDD8-dissociated protein 1
47	P12814	30	300	63	892	103058	5.4	Alpha-actinin-1
48	P11142	30	613	53.9	646	70898	5.5	Heat shock cognate 71 kDa protein
49	P13667	30	410	51.3	645	72933	5.1	Protein disulfide-isomerase A4 precursor
50	P55072	30	444	50.6	806	89322	5.3	Transitional endoplasmic reticulum ATPase (TER ATPase) (15S Mg(2+)- ATPase p97 subunit)
50	Q0V924	30	444	50.6	806	89344	5.3	Valosin-containing protein
51	Q9Y4L1	30	255	40.4	999	111335	5.2	150 kDa oxygen-regulated protein precursor
52	P16615-2	30	383	38.8	997	109691	5.4	Isoform SERCA2A of P16615

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
52	P16615	30	383	37.1	1042	114757	5.3	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 (EC 3.6.3.8) (Calcium pump 2) (SERCA2) (SR Ca(2+)-ATPase 2) (Calcium-transporting ATPase sarcoplasmic reticulum type, slow twitch skeletal muscle isoform) (Endoplasmic reticulum class 1/2 Ca(2+) ATPase)
53	P27816	30	149	33.5	1152	121019	5.4	Microtubule-associated protein 4
53	UPI000020A6A4	30	149	33.5	1152	121005	5.4	microtubule-associated protein 4 isoform 1
53	Q59FT2	30	149	33.2	1163	122941	6.7	Microtubule-associated protein 4 isoform 1 variant
54	Q6UVK1	30	197	17.1	2322	250494	5.5	Chondroitin sulfate proteoglycan 4 precursor
54	UPI00001AEEB6	30	197	17.1	2322	250534	5.5	chondroitin sulfate proteoglycan 4
55	P12270	30	109	14.7	2349	265598	5.1	Nucleoprotein TPR
55	Q5SWY0	30	109	14.6	2363	267290	5	Translocated promoter region
56	Q2TAL4	29	157	46.5	840	94331	5.2	Heat shock 70kDa protein 4
57	P22314	29	132	41.9	1058	117849	5.8	Ubiquitin-activating enzyme E1
58	A0AVA9	29	123	25	1512	170590	7.3	EPRS protein
58	Q5H9S5	29	123	25	1512	170643	7.2	Hypothetical protein DKFZp313B047
59	P27824	28	603	47.3	592	67568	4.6	Calnexin precursor
60	P26038	28	315	46.4	577	67820	6.4	Moesin
61	Q4LE33	28	153	17	2233	244402	4.9	TNC variant protein
62	P07237	27	259	60.4	508	57116	4.9	Protein disulfide-isomerase precursor
63	Q16658	27	267	58.4	493	54530	7.2	Fascin
63	UPI0000D61BF6	27	267	58.4	493	54640	7.8	Fascin (Singed-like protein) (55 kDa actin-bundling protein) (p55).
63	Q96IH1	27	267	57.6	500	55136	7.2	FSCN1 protein
64	P11021	27	368	47.4	654	72333	5.2	78 kDa glucose-regulated protein precursor (GRP 78) (Heat shock 70 kDa protein 5) (Immunoglobulin heavy chain-binding protein) (BiP) (Endoplasmic reticulum lumenal Ca(2+)-binding protein grp78)
65	Q92598-2	27	116	42.9	814	92116	5.6	Isoform Beta of Q92598
65	Q92598	27	116	40.7	858	96865	5.4	Heat-shock protein 105 kDa
66	Q00839-2	27	216	35.6	806	88980	5.8	Isoform Short of Q00839
66	Q00839	27	216	34.8	824	90514	6	Heterogeneous nuclear ribonucleoprotein U
67	O14980	27	129	34.5	1071	123386	6.1	Exportin-1
67	UPI0000456DC8	27	129	34.5	1070	123299	6.1	Exportin-1 (Exp1) (Chromosome region maintenance 1 protein homolog).
68	Q4LE56	27	80	29.4	1097	125055	9.5	MYO1C variant protein
69	UPI00003677FD	27	122	14.6	2330	256509	5.8	fibronectin 1 isoform 4 preproprotein
69	UPI0000167B25	27	122	14.5	2355	259223	5.7	fibronectin 1 isoform 3 preproprotein
69	P02751-3	27	122	14.5	2355	259195	5.7	Isoform 3 of P02751
69	P02751	27	122	14.3	2386	262604	5.7	Fibronectin precursor

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
69	Q6N025	27	122	14	2444	268675	6.1	Hypothetical protein DKFZp686M2451
70	P07355	26	785	73.5	339	38604	7.8	Annexin A2
70	Q8TBV2	26	785	73.5	339	38576	7.8	Annexin A2
70	UPI0000366A50	26	785	69.7	357	40411	8.4	annexin A2 isoform 1
71	Q07065	26	361	51.7	602	66023	5.9	Cytoskeleton-associated protein 4
72	Q9BSJ8	26	162	35.1	1104	122856	5.8	Protein FAM62A
72	Q9BSJ8-2	26	162	34.8	1114	124003	5.8	Isoform 2 of Q9BSJ8
73	Q15393	26	80	27.9	1217	135577	5.3	Splicing factor 3B subunit 3
74	Q16531	26	57	25.1	1140	126968	5.3	DNA damage-binding protein 1
74	UPI0000D62613	26	57	25.1	1140	126966	5.3	DNA damage-binding protein 1 (Damage-specific DNA-binding protein 1) (UV-damaged DNA-binding factor) (DDB p127 subunit) (DDBa) (UV-damaged DNA-binding protein 1) (UV-DDB 1) (Xeroderma pigmentosum group E-complementing protein) (XPCe) (XPE-binding factor)
75	Q53SY7	26	72	15.4	2151	235175	6.6	Hypothetical protein CAD
75	P27708	26	72	14.9	2225	242981	6.5	CAD protein [Includes: Glutamine-dependent carbamoyl-phosphate synthase (EC 6.3.5.5); Aspartate carbamoyltransferase (EC 2.1.3.2); Dihydroorotase (EC 3.5.2.3)]
76	P50395	25	147	69.2	445	50663	6.5	Rab GDP dissociation inhibitor beta
77	P04843	25	529	53.9	607	68569	6.4	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 67 kDa subunit precursor
77	Q6IBR0	25	529	53.9	607	68607	6.4	RPN1 protein
78	P40939	25	176	48.8	763	83000	9	Trifunctional enzyme subunit alpha, mitochondrial precursor (TP-alpha) (78 kDa gastrin-binding protein) [Includes: Long-chain enoyl-CoA hydratase (EC 4.2.1.17); Long chain 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.211)]
79	P11940	25	148	45.1	636	70671	9.5	Polyadenylate-binding protein 1 (Poly(A)-binding protein 1)
80	P43243	25	140	35.1	847	94623	6.3	Matrin-3
81	P19338	25	265	34.8	710	76615	4.7	Nucleolin
82	Q14764	25	129	34.6	893	99327	5.5	Major vault protein
83	P09874	25	81	29.1	1014	113084	8.9	Poly [ADP-ribose] polymerase 1 (EC 2.4.2.30) (PARP-1) (ADPRT) (NAD(+) ADP-ribosyltransferase 1)
84	O75533	25	118	24.5	1304	145815	7	Splicing factor 3B subunit 1
84	UPI000013D493	25	118	24.5	1304	145830	7.1	splicing factor 3b, subunit 1 isoform 1
85	Q9NTJ3	25	78	22.7	1288	147182	6.8	Structural maintenance of chromosomes protein 4
86	Q9BQG0	25	88	22.1	1328	148854	9.3	Myb-binding protein 1A
86	Q9BQG0-2	25	88	22.1	1332	149366	9.3	Isoform 2 of Q9BQG0
87	Q92616	25	166	13.3	2671	292742	7.4	GCN1-like protein 1

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
87	UPI0000451CA7	25	166	13.3	2671	292708	7.4	GCN1 general control of amino-acid synthesis 1-like 1
88	Q6P2Q9	25	102	12.6	2335	273599	8.8	Pre-mRNA-processing-splicing factor 8
89	P00558	24	129	67.6	417	44615	8.1	Phosphoglycerate kinase 1
90	P78371	24	105	60.9	535	57488	6.4	T-complex protein 1 subunit beta
91	P30101	24	259	60.6	505	56782	6.4	Protein disulfide-isomerase A3 precursor
92	P11413-2	24	68	53.3	561	63827	6.9	Isoform Long of P11413
93	P29401	24	277	49.4	623	67878	7.7	Transketolase
94	Q05682-5	24	253	41.4	532	61213	6.7	Isoform 5 of Q05682
94	Q05682-4	24	253	40.9	538	62663	6.4	Isoform 4 of Q05682
95	P52272-2	24	228	42.5	691	73621	8.8	Isoform 2 of P52272
95	P52272	24	228	40.3	730	77516	8.7	Heterogeneous nuclear ribonucleoprotein M
96	P17844	24	160	39.6	614	69148	8.9	Probable ATP-dependent RNA helicase DDX5
97	Q9Y678	24	188	38.9	874	97718	5.5	Coatomer subunit gamma
98	Q14697	24	216	30.7	944	106874	6.1	Neutral alpha-glucosidase AB precursor
98	UPI00003667D2	24	216	30.7	944	106847	6.2	Neutral alpha-glucosidase AB precursor (EC 3.2.1.84) (Glucosidase II subunit alpha).
99	P31939	23	80	57.4	592	64616	6.7	Bifunctional purine biosynthesis protein PURH [Includes: Phosphoribosylaminoimidazolecarboxamide formyltransferase (EC 2.1.2.3) (5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase) (AICAR transformylase); IMP cyclohydrolase (EC 3.5.4.10) (Inosinicase) (IMP synthetase) (ATIC)]
100	P38646	23	186	39.9	679	73681	6.2	Stress-70 protein, mitochondrial precursor
101	Q13200	23	102	36.2	908	100200	5.2	26S proteasome non-ATPase regulatory subunit 2
101	Q53XQ4	23	102	36.2	908	100249	5.2	Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 2
101	Q59EG8	23	102	36	913	100588	5.2	Proteasome 26S non-ATPase subunit 2 variant
102	P41252	23	62	23.4	1266	144958	6.2	Isoleucyl-tRNA synthetase, cytoplasmic
102	Q59G75	23	62	23.1	1279	146344	6.4	Isoleucyl-tRNA synthetase, cytoplasmic variant
103	UPI000013C8EF	23	78	15.6	1912	218003	5.9	chromodomain helicase DNA binding protein 4
103	UPI00001AE66A	23	78	15.4	1940	220846	6	Chromodomain helicase-DNA-binding protein 4 (EC 3.6.1.-) (ATP-dependent helicase CHD4) (CHD-4) (Mi-2 autoantigen 218 kDa protein) (Mi2-beta).
104	P07437	22	700	72.3	444	49671	4.9	Tubulin beta chain
105	P06576	22	340	63.7	529	56560	5.4	ATP synthase subunit beta, mitochondrial precursor
106	P68104	22	1104	49.1	462	50141	9	Elongation factor 1-alpha 1
106	Q6IPT9	22	1104	49.1	462	50185	9.1	Eukaryotic translation elongation factor 1 alpha 1

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
106	Q6IPN6	22	1104	49.1	462	50123	9	Eukaryotic translation elongation factor 1 alpha 1
106	Q5VTE0	22	1104	49.1	462	50185	9.1	Eukaryotic translation elongation factor 1 alpha-like 3
106	Q53HR5	22	1104	49.1	462	50125	9	Eukaryotic translation elongation factor 1 alpha 1 variant
106	Q53HQ7	22	1104	49.1	462	50199	8.9	Eukaryotic translation elongation factor 1 alpha 1 variant
106	Q53HM9	22	1104	49.1	462	50142	8.9	Eukaryotic translation elongation factor 1 alpha 1 variant
107	P48643	22	115	48.1	541	59671	5.6	T-complex protein 1 subunit epsilon
108	UPI0000D61699	22	121	43	670	75529	5.6	Annexin A6 (Annexin VI) (Lipocortin VI) (P68) (P70) (Protein III) (Chromobindin-20) (67 kDa calelectrin) (Calphobindin-II) (CPB-II).
108	P08133	22	121	42.8	673	75873	5.6	Annexin A6
109	Q5M7Z9	22	91	42.4	682	78606	6.9	TARS protein
109	P26639	22	91	40	723	83435	6.7	Threonyl-tRNA synthetase, cytoplasmic
109	Q53GX7	22	91	40	723	83445	6.7	Threonyl-tRNA synthetase variant
110	P55060-3	22	165	30.6	945	107777	5.8	Isoform 3 of P55060
110	P55060	22	165	29.8	971	110417	5.8	Exportin-2
111	O00410	22	124	28.3	1097	123630	4.9	Importin beta-3
111	UPI0000163C1C	22	124	27.8	1115	125545	4.9	RAN binding protein 5
112	P78347-2	22	48	25.4	957	107970	7.9	Isoform 2 of P78347
112	Q499G6	22	48	24.9	976	110080	7.6	General transcription factor II, i
112	P78347-4	22	48	24.9	977	110106	7.4	Isoform 4 of P78347
112	P78347-3	22	48	24.8	978	110280	6.7	Isoform 3 of P78347
112	P78347	22	48	24.3	998	112416	6.4	General transcription factor II-I
113	P04075	21	250	70.9	364	39420	8.1	Fructose-bisphosphate aldolase A
114	P06733	21	553	68.4	434	47169	7.4	Alpha-enolase
114	Q53FT9	21	553	68.4	434	47197	7.4	Enolase 1 variant
115	P60842	21	129	64	406	46154	5.5	Eukaryotic initiation factor 4A-I
116	P50454	21	244	55.3	418	46441	8.7	Serpin H1 precursor
117	P08238	21	345	49.3	724	83264	5	Heat shock protein HSP 90-beta
117	UPI00001AE8D8	21	345	48.5	736	84758	5.4	Heat shock protein HSP 90-beta (HSP 84) (HSP 90).
118	P25705	21	177	48.6	553	59751	9.1	ATP synthase subunit alpha, mitochondrial precursor
119	P17987	21	104	45.9	556	60344	6.1	T-complex protein 1 subunit alpha
120	P17655	21	94	45.4	700	80009	5	Calpain-2 catalytic subunit precursor
120	UPI000003475E	21	94	45.4	700	80007	5	calpain 2, large subunit
120	Q59EF6	21	94	43.6	729	83109	5.1	Calpain 2, large [catalytic] subunit variant
121	P31948	21	68	41.6	543	62639	6.8	Stress-induced-phosphoprotein 1
122	P20700	21	90	40.4	586	66408	5.2	Lamin-B1
123	Q53T76	21	99	40.8	693	77252	6.9	Hypothetical protein GPD2
123	P43304	21	99	38.9	727	80834	7.5	Glycerol-3-phosphate dehydrogenase, mitochondrial precursor
124	Q14974	21	166	36.3	876	97170	4.8	Importin beta-1 subunit
125	Q01813	21	59	36.1	784	85596	7.6	6-phosphofructokinase type C

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
126	P23246	21	153	35.1	707	76150	9.4	Splicing factor, proline- and glutamine-rich
127	P53618	21	94	29.6	953	107142	6	Coatomer subunit beta
128	P49588	21	89	27.6	968	106810	5.5	Alanyl-tRNA synthetase, cytoplasmic
128	UPI0000D61A0F	21	89	27.6	968	106710	5.5	Alanyl-tRNA synthetase, cytoplasmic (EC 6.1.1.7) (Alanine--tRNA ligase) (AlaRS) (Renal carcinoma antigen NY-REN-42).
129	Q9H0A0	21	65	25.3	1025	115704	8.3	N-acetyltransferase 10
129	UPI000015F46F	21	65	25.3	1025	115748	8.3	N-acetyltransferase-like protein
129	UPI000013CF8E	21	65	25.3	1025	115730	8.3	N-acetyltransferase 10 (EC 2.3.1.-).
130	O15061	21	71	17.1	1565	172767	5.2	Desmuslin
130	UPI0000DC3AA9	21	71	17.1	1565	172867	5.2	desmuslin isoform A
131	P68363	20	581	58.3	451	50152	5.1	Tubulin alpha-ubiquitous chain
132	Q53HV2	20	128	54	543	59341	7.6	Chaperonin containing TCP1, subunit 7 (Eta) variant
132	Q99832	20	128	54	543	59367	7.6	T-complex protein 1 subunit eta
133	P08107	20	129	48.7	641	70038	5.6	Heat shock 70 kDa protein 1
133	UPI000013C67D	20	129	48.7	641	70025	5.6	heat shock 70kDa protein 1B
133	Q5JQI4	20	129	48.7	641	70052	5.6	Heat shock 70kDa protein 1A
133	Q59EJ3	20	129	44	709	77496	6.3	Heat shock 70kDa protein 1A variant
134	Q5SZY0	20	136	49.4	522	57972	6.9	Chaperonin containing TCP1, subunit 3
134	UPI00004CA9C4	20	136	47.4	544	60463	6.5	chaperonin containing TCP1, subunit 3 isoform b
134	P49368	20	136	47.3	545	60534	6.5	T-complex protein 1 subunit gamma
135	P46063	20	93	42.1	649	73456	8.1	ATP-dependent DNA helicase Q1
135	UPI0000167E2F	20	93	42.1	649	73457	7.9	RecQ protein-like isoform 1
136	P13010	20	125	39.9	732	82705	5.8	ATP-dependent DNA helicase 2 subunit 2
137	UPI0000136C97	20	164	33.9	760	84901	6.6	transferrin receptor
138	Q15459	20	58	30.3	793	88886	5.2	Splicing factor 3 subunit 1
139	Q8IXJ3	20	63	34.5	850	95372	6	Small nuclear ribonucleoprotein component
139	Q15029	20	63	30.1	972	109436	5	116 kDa U5 small nuclear ribonucleoprotein component
139	UPI0000169E0D	20	63	30.1	972	109478	5	U5 snRNP-specific protein, 116 kD
139	Q6IBM8	20	63	30.1	972	109460	5	U5-116KD protein
140	O95373	20	120	25.1	1038	119516	4.8	Importin-7
140	UPI0000D625B4	20	120	25.1	1040	119702	4.8	Importin-7 (Imp7) (Ran-binding protein 7) (RanBP7).
141	Q15155	20	45	22.2	1222	134352	5.8	Nodal modulator 1 precursor
141	UPI00001AF3F1	20	45	22.2	1222	134133	5.7	nodal modulator 3
141	UPI000013D37E	20	45	22.2	1222	134324	5.8	nodal modulator 1
141	UPI00001AE864	20	45	21.4	1267	139381	5.7	Nodal modulator 3 precursor (pM5 protein 3).
141	Q5JPE7	20	45	21.4	1267	139439	5.8	Nodal modulator 2 precursor
142	P26640	20	88	18.2	1264	140476	7.6	Valyl-tRNA synthetase
142	UPI0000457409	20	88	18.2	1264	140376	7.8	Valyl-tRNA synthetase (EC 6.1.1.9) (Valine--tRNA ligase) (ValRS) (Protein G7a).
143	Q6YHK3	20	121	17.8	1445	161688	5.8	CD109 antigen precursor
144	Q71UH4	20	50	14.3	1598	180613	7.9	DNA topoisomerase II beta
144	Q02880-2	20	50	14.1	1621	182661	8.1	Isoform Beta
144	Q02880	20	50	14	1626	183266	8	DNA topoisomerase 2-beta
145	P60174	19	298	85.1	249	26669	6.9	Triosephosphate isomerase

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146	P63104	19	866	72.2	245	27745	4.8	14-3-3 protein zeta/delta
147	P08758	19	217	71.6	320	35937	5	Annexin A5
148	P40926	19	257	67.8	338	35531	8.7	Malate dehydrogenase, mitochondrial precursor
148	UPI000013DA68	19	257	67.8	338	35503	8.7	mitochondrial malate dehydrogenase precursor
148	Q6FHZ0	19	257	67.8	338	35559	8.7	MDH2 protein
149	P04083	19	171	62.7	346	38714	7	Annexin A1
150	Q02790	19	64	55.1	459	51805	5.4	FK506-binding protein 4
151	Q05CK9	19	131	55.6	453	50651	6.7	Hypothetical protein
151	Q5TCG3	19	131	44.8	562	62656	7.6	OTTHUMP00000016816
151	O60506	19	131	40.4	623	69603	8.6	Heterogeneous nuclear ribonucleoprotein Q
152	P49748	19	102	39.4	655	70390	8.8	Very-long-chain specific acyl-CoA dehydrogenase, mitochondrial precursor
153	O00429-4	19	100	39.6	699	78100	6.8	Isoform 4 of O00429
153	UPI0000D621CC	19	100	39	710	79224	7.1	Dynamin-1-like protein (EC 3.6.5.5) (Dynamin-like protein) (Dnm1p/Vps1p-like protein) (DVLP) (Dynamin family member proline-rich carboxyl-terminal domain less) (Dymple) (Dynamin-related protein 1) (Dynamin-like protein 4) (Dynamin-like protein IV) (HdynIV
153	O00429-5	19	100	39	710	79109	6.9	Isoform 5 of O00429
153	O00429-3	19	100	39	710	79442	6.9	Isoform 3 of O00429
153	O00429-2	19	100	38.2	725	80536	6.7	Isoform 2 of O00429
153	O00429	19	100	37.6	736	81877	6.8	Dynamin-1-like protein
153	Q59GN9	19	100	36.9	751	83579	7.7	Dynamin-like protein DYNIV-11 variant
154	A4D210	19	88	29.8	775	88681	5.1	Eukaryotic translation initiation factor 3, subunit 9 eta, 116kDa
154	A4D208	19	88	28.4	814	92482	5	Eukaryotic translation initiation factor 3, subunit 9 eta, 116kDa
154	P55884	19	88	28.4	814	92492	5	Eukaryotic translation initiation factor 3 subunit 9
154	P55884-2	19	88	26.5	873	99039	5.1	Isoform 2 of P55884
155	Q5T567	19	65	27.4	793	87089	7.1	Aldehyde dehydrogenase 18 family, member A1
155	P54886	19	65	27.3	795	87302	7.1	Delta 1-pyrroline-5-carboxylate synthetase (P5CS) (Aldehyde dehydrogenase 18 family member A1) [Includes: Glutamate 5-kinase (EC 2.7.2.11) (Gamma-glutamyl kinase) (GK); Gamma-glutamyl phosphate reductase (GPR) (EC 1.2.1.41) (Glutamate-5-semialdehyde dehydrogenase) (Glutamyl-gamma-semialdehyde dehydrogenase)]
156	O43143	19	91	26.8	795	90933	7.5	Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15
157	Q12906-5	19	125	32.8	690	74607	8.2	Isoform 5 of Q12906
157	Q12906-4	19	125	32.4	698	75509	8.4	Isoform 4 of Q12906
157	Q12906-2	19	125	32.2	702	76033	7.8	Isoform 2 of Q12906
157	Q12906-6	19	125	32	706	76502	7.9	Isoform 6 of Q12906
157	Q12906-3	19	125	29.6	764	82802	8.2	Isoform 3 of Q12906

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157	UPI0000366D19	19	125	29.5	765	82924	8.2	Interleukin enhancer-binding factor 3 (Nuclear factor of activated T-cells 90 kDa) (NF-AT-90) (Double-stranded RNA-binding protein 76) (DRBP76) (Translational control protein 80) (TCP80) (Nuclear factor associated with dsRNA) (NFAR) (M-phase phosphoprote
157	Q12906	19	125	25.3	894	95339	8.8	Interleukin enhancer-binding factor 3
158	UPI000013E942	19	94	23.9	905	101085	6.9	Hexokinase-1 (EC 2.7.1.1) (Hexokinase type I) (HK I) (Brain form hexokinase).
158	P19367-4	19	94	23.9	905	101104	7	Isoform 4 of P19367
158	P19367	19	94	23.6	917	102486	6.8	Hexokinase-1
159	P11586	19	51	22.2	935	101559	7.3	C-1-tetrahydrofolate synthase, cytoplasmic (C1-THF synthase) [Includes: Methylenetetrahydrofolate dehydrogenase (EC 1.5.1.5); Methenyltetrahydrofolate cyclohydrolase (EC 3.5.4.9); Formyltetrahydrofolate synthetase (EC 6.3.4.3)]
159	UPI0000161BEA	19	51	22.2	935	101531	7.2	methylenetetrahydrofolate dehydrogenase 1
160	Q14203	19	54	19.6	1278	141694	5.8	Dynactin-1
160	Q6MZZ3	19	54	19.6	1278	141550	5.9	Hypothetical protein DKFZp686I0746
161	O60841	19	50	18.4	1220	138799	5.5	Eukaryotic translation initiation factor 5B
161	UPI0000D61206	19	50	18.4	1220	138681	5.6	Eukaryotic translation initiation factor 5B (eIF-5B) (Translation initiation factor IF-2).
161	UPI0000207EC7	19	50	18.4	1220	138827	5.5	eukaryotic translation initiation factor 5B
161	Q8N5A0	19	50	18.4	1220	138800	5.5	Eukaryotic translation initiation factor 5B
162	O60264	19	38	18.1	1052	121905	8.1	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5
162	UPI0000161FA8	19	38	18.1	1052	121933	8.1	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin a5
163	Q14980-2	19	59	11.4	2101	236513	5.8	Isoform 2 of Q14980
164	Q5T3Q7	19	81	11	2063	233274	6.6	Protein BAP28
164	Q9H583	19	81	10.6	2144	242368	6.5	HEAT repeat-containing protein 1
165	Q96HG5	18	1607	67.1	368	41005	5.8	Actin, beta
165	P60709	18	1607	65.9	375	41737	5.5	Actin, cytoplasmic 1
165	Q53GK6	18	1607	65.9	375	41723	5.5	Beta actin variant
165	Q53G99	18	1607	65.9	375	41765	5.6	Beta actin variant
165	Q53G76	18	1607	65.9	375	41721	5.5	Beta actin variant
165	P63261	18	1607	65.9	375	41793	5.5	Actin, cytoplasmic 2
166	O43852	18	204	65.1	315	37107	4.6	Calumenin precursor
167	P00338	18	750	63	332	36689	8.3	L-lactate dehydrogenase A chain
168	Q99475	18	102	53.9	549	60212	6.7	KM-102-derived reductase-like factor

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168	UPI0000D6223A	18	102	45.5	651	71153	7.5	CDNA FLJ46672 fis, clone TRACH3009008, highly similar to Thioredoxin reductase (EC 1.6.4.5).
169	P52209	18	89	51.3	483	53140	7.2	6-phosphogluconate dehydrogenase, decarboxylating
169	UPI0000D61E45	18	89	51.1	485	53339	7.4	6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44).
170	P09493-3	18	142	47.2	284	32876	4.8	Isoform 3 of P09493
171	Q16851	18	83	47	508	56940	8.1	UTP--glucose-1-phosphate uridylyltransferase 2
172	P05455	18	67	46.1	408	46837	7.1	Lupus La protein
173	P47895	18	89	44.9	512	56109	7.3	Aldehyde dehydrogenase 1A3
173	UPI0000129264	18	89	44.9	512	56009	7	aldehyde dehydrogenase 1A3
174	Q15233	18	86	44.6	471	54232	8.9	Non-POU domain-containing octamer-binding protein (NonO protein) (54 kDa nuclear RNA- and DNA-binding protein) (p54(nrb))
175	P50991	18	84	44.3	539	57924	7.8	T-complex protein 1 subunit delta
176	Q5T6W5	18	193	47.9	428	47557	5.6	Heterogeneous nuclear ribonucleoprotein K
176	P61978-3	18	193	46.6	440	48562	5.5	Isoform 3 of P61978
176	P61978	18	193	44.3	463	50976	5.5	Heterogeneous nuclear ribonucleoprotein K
176	Q6IBN1	18	193	44.2	464	51028	5.3	HNRPK protein
177	Q03252	18	57	37	600	67689	5.3	Lamin-B2
178	O00571	18	106	34.6	662	73244	7.2	ATP-dependent RNA helicase DDX3X
179	P12956	18	125	34	609	69843	6.6	ATP-dependent DNA helicase 2 subunit 1
179	UPI000045708A	18	125	34	609	69870	6.6	ATP-dependent DNA helicase 2 subunit 1 (ATP-dependent DNA helicase II 70 kDa subunit) (Lupus Ku autoantigen protein p70) (Ku70) (70 kDa subunit of Ku antigen) (Thyroid-lupus autoantigen) (TLAA) (CTC box- binding factor 75 kDa subunit) (CTCBF) (CTC75) (DNA
179	Q6FG89	18	125	34	609	69873	6.6	G22P1 protein
180	O60568	18	92	31.2	738	84785	6.1	Procollagen-lysine,2-oxoglutarate 5 dioxygenase 3 precursor
181	O95573	18	180	30.6	720	80420	8.4	Long-chain-fatty-acid--CoA ligase 3
182	P54136	18	59	30.6	660	75379	6.7	Arginyl-tRNA synthetase, cytoplasmic
183	Q7Z451	18	86	28.8	880	98118	5.2	Beta adaptin subunit
183	P63010	18	86	27	937	104553	5.4	AP-2 complex subunit beta-1
183	UPI0000456A82	18	86	26.9	939	104711	5.4	AP-2 complex subunit beta-1 (Adapter-related protein complex 2 beta-1 subunit) (Beta-adaptin) (Plasma membrane adaptor HA2/AP2 adaptin beta subunit) (Clathrin assembly protein complex 2 beta large chain) (AP105B).
183	Q3ZB97	18	86	26.6	951	105692	5.3	Ap2b1 protein

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183	UPI0000456A83	18	86	26.5	953	105850	5.3	AP-2 complex subunit beta-1 (Adapter-related protein complex 2 beta-1 subunit) (Beta-adaptin) (Plasma membrane adaptor HA2/AP2 adaptin beta subunit) (Clathrin assembly protein complex 2 beta large chain) (AP105B).
184	A1KYQ7	18	74	22.2	913	105404	5.7	Cell migration-inducing protein 17
184	Q99613	18	74	22.2	913	105344	5.7	Eukaryotic translation initiation factor 3 subunit 8
185	Q8WUM6	18	107	22.3	798	88415	5.4	Integrin, beta 1
185	Q7Z3V1	18	107	21.6	823	91131	5.5	Integrin beta
186	Q86VX4	18	43	18.5	1217	141507	7.2	Structural maintenance of chromosomes 3
186	UPI0000D60FCC	18	43	18.5	1217	141557	7.4	Structural maintenance of chromosomes protein 3 (Chondroitin sulfate proteoglycan 6) (Chromosome-associated polypeptide) (hCAP) (Bamacan) (Basement membrane-associated chondroitin proteoglycan).
186	Q9UQE7	18	43	18.5	1217	141541	7.2	Structural maintenance of chromosomes protein 3
187	Q15075	18	31	16.2	1411	162465	5.7	Early endosome antigen 1
187	UPI000013C754	18	31	16.2	1411	162465	5.7	Early endosome antigen 1 (Endosome-associated protein p162) (Zinc finger FYVE domain-containing protein 2).
188	Q5XG74	18	83	17.6	1106	121651	6.9	SEC31 homolog A
188	Q17RR5	18	83	16.2	1205	131534	6.9	SEC31 homolog A
188	Q9UM05	18	83	16	1220	133031	6.9	ABP130
188	Q7LCX9	18	83	16	1220	133015	6.9	Sec31 protein
188	O94979	18	83	15.9	1229	134238	7	SEC31 homolog A
189	P49792	18	53	6.4	3224	358201	6.2	E3 SUMO-protein ligase RanBP2
189	UPI0000167B4B	18	53	6.4	3224	358173	6.2	RAN binding protein 2
190	P23396	17	176	74.5	243	26688	9.7	40S ribosomal protein S3
191	P23528	17	317	70.5	166	18502	8.1	Cofilin-1
192	P07195	17	715	59.9	334	36639	6.1	L-lactate dehydrogenase B chain
193	P61158	17	89	57.9	418	47371	5.9	Actin-like protein 3
194	Q6PIN5	17	75	55.2	373	41681	7.5	PA2G4 protein
194	Q9UQ80	17	75	52.3	394	43787	6.6	Proliferation-associated protein 2G4
194	Q05D08	17	75	50.7	406	45151	8.9	Hypothetical protein
195	UPI0000126EBE	17	131	46.7	475	51673	8	adenylyl cyclase-associated protein
196	P60228	17	77	45.8	445	52221	6	Eukaryotic translation initiation factor 3 subunit 6
196	Q6IAX5	17	77	45.8	445	52206	6	EIF3S6 protein
197	UPI0000D61084	17	221	46.2	599	65668	5.5	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit precursor (EC 2.4.1.119) (Ribophorin II) (RPN-II) (RIBIIR).
197	Q5JYR6	17	221	45	615	67723	6.1	Ribophorin II
197	P04844	17	221	43.9	631	69284	5.7	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit precursor

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198	Q8TC62	17	75	42.9	417	48659	8.6	Septin 7
198	Q3LIE9	17	75	42.8	418	48774	8.6	Predicted protein product of Nbla02942
198	A4GYY8	17	75	41.3	433	50263	8.6	Hypothetical protein DKFZp686F17268
198	Q16181-2	17	75	41.1	436	50581	8.6	Isoform 2 of Q16181
198	Q16181	17	75	41	437	50680	8.6	Septin-7
198	UPI0000D61C26	17	75	40.9	438	50809	8.5	Septin-7 (CDC10 protein homolog).
199	P61221	17	56	37.7	599	67314	8.3	ATP-binding cassette sub-family E member 1
200	Q86UE4	17	193	36.4	582	63837	9.3	Protein LYRIC
201	P21980	17	51	34.9	687	77329	5.2	Protein-glutamine gamma-glutamyltransferase 2 (EC 2.3.2.13) (Tissue transglutaminase) (TGase C) (TGC) (TG(C))
202	O94973	17	53	27.5	939	103960	7	AP-2 complex subunit alpha-2
202	Q53ET1	17	53	27.4	940	104089	6.9	Adaptor-related protein complex 2, alpha 2 subunit variant
203	Q5U4P6	17	74	26.3	710	72897	7.9	KHSRP protein
203	UPI0000D61707	17	74	26.1	717	73805	8.1	Far upstream element-binding protein 2 (FUSE-binding protein 2) (KH type-splicing regulatory protein) (KSRP) (p75).
204	P22102	17	43	24.4	1010	107767	6.7	Trifunctional purine biosynthetic protein adenosine-3 [Includes: Phosphoribosylamine--glycine ligase (EC 6.3.4.13) (GARS) (Glycinamide ribonucleotide synthetase) (Phosphoribosylglycinamide synthetase); Phosphoribosylformylglycinamidine cyclo-ligase (EC 6.3.3.1) (AIRS) (Phosphoribosyl-aminoimidazole synthetase) (AIR synthase); Phosphoribosylglycinamide formyltransferase (EC 2.1.2.2) (GART) (GAR transformylase) (5'-phosphoribosylglycinamide transformylase)]
204	Q3B7A7	17	43	24.4	1010	107723	6.8	Phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase
204	Q59HH3	17	43	23.5	1046	112138	7.4	Phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase isoform 1 variant
205	Q9UDX0	17	50	22.8	1023	115935	6.9	Oxoglutarate (Alpha-ketoglutarate) dehydrogenase
206	Q9NSE4	17	58	20.9	1012	113791	7.2	Isoleucyl-tRNA synthetase, mitochondrial precursor
207	Q13423	17	76	18.3	1086	113895	8.1	NAD(P) transhydrogenase, mitochondrial precursor

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
207	Q2TB59	17	76	18.3	1086	113883	8.1	Nicotinamide nucleotide transhydrogenase
208	Q13045	17	56	17	1269	144751	6.1	Protein flightless-1 homolog
209	Q14683	17	53	14.6	1233	143233	7.6	Structural maintenance of chromosomes protein 1A
210	P11047	17	37	11.7	1609	177606	5.1	Laminin subunit gamma-1 precursor
210	UPI0000034928	17	37	11.7	1609	177572	5.1	laminin, gamma 1 precursor
210	Q5VYE7	17	37	11.7	1609	177602	5.1	Laminin, gamma 1
211	Q14690	17	45	10.5	1871	208699	8.9	RRP5 protein homolog
212	P63244	16	146	72.6	317	35077	7.7	Guanine nucleotide-binding protein subunit beta 2-like 1
212	Q5VLR4	16	146	66.3	347	37889	8.2	Lung cancer oncogene 7
213	Q99623	16	112	57.5	299	33296	9.8	Prohibitin-2
214	P62701	16	167	55.9	263	29598	10.2	40S ribosomal protein S4, X isoform
215	P62191	16	41	44.5	440	49185	6.2	26S protease regulatory subunit 4
215	Q53HB3	16	41	44.5	440	49213	6.2	Proteasome 26S ATPase subunit 1 variant
216	P37837	16	148	44.2	337	37540	6.8	Transaldolase
217	Q53G71	16	122	45.3	406	46919	4.4	Calreticulin variant
217	P27797	16	122	44.1	417	48142	4.4	Calreticulin precursor
218	P14866	16	68	40.5	558	60187	7.1	Heterogeneous nuclear ribonucleoprotein L
218	Q6NTA2	16	68	40.5	558	60233	7.1	HNRPL protein
218	UPI0000D6179A	16	68	38.4	589	64195	8.3	Heterogeneous nuclear ribonucleoprotein L (hnRNP L).
218	UPI00004432FA	16	68	38.4	589	64133	8.2	heterogeneous nuclear ribonucleoprotein L isoform a
219	P23526	16	61	39.1	432	47716	6.3	Adenosylhomocysteinase
220	UPI0000D6261A	16	88	36.3	435	49917	6.7	Elongation factor 1-gamma (EF-1-gamma) (eEF-1B gamma).
220	P26641	16	88	36.2	437	50119	6.7	Elongation factor 1-gamma
220	UPI0000D6261B	16	88	36.2	436	50016	6.7	Elongation factor 1-gamma (EF-1-gamma) (eEF-1B gamma).
221	P08195	16	213	36.1	529	57945	5.3	4F2 cell-surface antigen heavy chain
221	UPI0000405902	16	213	31.9	599	64873	5.1	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2 isoform d
221	UPI00004EC298	16	213	30.3	631	68101	5	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2 isoform b
221	UPI000013E757	16	213	30.3	630	67994	5	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2 isoform c
221	UPI00004EC297	16	213	28.9	661	71123	5	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2 isoform a
222	P00367	16	46	36	558	61398	7.8	Glutamate dehydrogenase 1, mitochondrial precursor
223	P13797	16	54	32.5	627	70436	5.8	Plastin-3
223	UPI000000D962	16	54	32.4	630	70811	5.6	plastin 3
224	Q8NBJ5	16	101	28.6	622	71636	7.3	Glycosyltransferase 25 domain-containing protein 1
225	UPI0000161BCB	16	43	28.6	681	76747	6.9	glucosamine-fructose-6-phosphate aminotransferase

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225	Q06210-2	16	43	28.6	681	76759	6.9	Isoform 2 of Q06210
225	Q06210	16	43	27.9	699	78806	7.1	Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] 1
226	UPI0000161B4F	16	95	29.6	685	77531	6.2	Glycyl-tRNA synthetase (EC 6.1.1.14) (Glycine--tRNA ligase) (GlyRS).
226	P41250	16	95	27.5	739	83140	7	Glycyl-tRNA synthetase
226	UPI00005A885C	16	95	27.5	739	83166	7	glycyl-tRNA synthetase
227	P35606	16	76	25.2	906	102487	5.3	Coatomer subunit beta'
228	Q12797	16	141	25.1	758	85863	5	Aspartyl/asparaginyl beta-hydroxylase
228	UPI0000D624CD	16	141	25	759	86006	5.1	Aspartyl/asparaginyl beta-hydroxylase (EC 1.14.11.16) (Aspartate beta- hydroxylase) (ASP beta-hydroxylase) (Peptide-aspartate beta- dioxygenase).
229	O43491	16	43	22.1	1005	112588	5.4	Band 4.1-like protein 2
230	Q5T665	16	70	21.2	956	106077	8.3	Inter-alpha inhibitor H5
230	UPI00003B5D4F	16	70	21.2	956	106017	8.3	inter-alpha trypsin inhibitor heavy chain precursor 5 isoform 1
231	Q9P2J5	16	45	17.4	1176	134466	7.3	Leucyl-tRNA synthetase, cytoplasmic
232	O60610	16	52	15.4	1248	138978	5.4	Protein diaphanous homolog 1
232	UPI0000EA87E7	16	52	15.2	1263	140289	5.4	diaphanous 1 isoform 2
232	UPI0000DBEE89	16	52	15.2	1263	140255	5.4	Protein diaphanous homolog 1 (Diaphanous-related formin-1) (DRF1).
232	UPI0000DBEE88	16	52	15.2	1264	140416	5.4	Protein diaphanous homolog 1 (Diaphanous-related formin-1) (DRF1).
232	Q17RN4	16	52	15.2	1262	140192	5.4	Diaphanous homolog 1
232	Q6URC4	16	52	15.1	1272	141303	5.5	Diaphanous 1
232	Q59FH8	16	52	14.8	1299	143786	5.4	Diaphanous 1 variant
233	Q15021	16	57	15.4	1401	157168	6.6	Condensin complex subunit 1
233	UPI000013C8CA	16	57	15.4	1401	157182	6.6	Condensin complex subunit 1 (Non-SMC condensin I complex subunit D2) (Chromosome condensation-related SMC-associated protein 1) (Chromosome-associated protein D2) (hCAP-D2) (XCAP-D2 homolog).
234	Q06830	15	171	72.9	199	22110	8.1	Peroxiredoxin-1
235	P35232	15	154	70.2	272	29804	5.8	Prohibitin
235	Q6FHP5	15	154	70.2	272	29832	5.8	PHB protein
236	UPI00001AF1AB	15	53	68.6	389	42931	5.3	Interleukin enhancer-binding factor 2 (Nuclear factor of activated T-cells 45 kDa).
236	Q12905	15	53	68.5	390	43062	5.3	Interleukin enhancer-binding factor 2
237	P21796	15	227	67.8	283	30773	8.5	Voltage-dependent anion-selective channel protein 1
238	P04406	15	1418	64.5	335	36053	8.5	Glyceraldehyde-3-phosphate dehydrogenase
239	O15144	15	110	58.3	300	34333	7.3	Actin-related protein 2/3 complex subunit 2
240	P61247	15	291	54.2	264	29945	9.7	40S ribosomal protein S3a
240	Q6NXR8	15	291	54.2	264	29975	9.7	Ribosomal protein S3A
241	P62136	15	88	53.9	330	37512	6.3	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit

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242	UPI00006D1D75	15	191	56.6	320	34223	9.2	Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabilizing protein) (Single-strand RNA-binding protein) (hnRNP core protein A1).
242	P49312	15	191	56.6	320	34196	9.2	Heterogeneous nuclear ribonucleoprotein A1
242	P09651	15	191	48.7	372	38846	9.2	Heterogeneous nuclear ribonucleoprotein A1
242	UPI0000161BF2	15	191	48.7	372	38747	9.1	heterogeneous nuclear ribonucleoprotein A1 isoform b
243	P26599	15	104	43.5	531	57221	9.2	Polypyrimidine tract-binding protein 1
243	P26599-2	15	104	42	550	59037	9.2	Isoform 2 of P26599
243	UPI0000D616E2	15	104	41.5	557	59693	9.2	Polypyrimidine tract-binding protein 1 (PTB) (Heterogeneous nuclear ribonucleoprotein I) (hnRNP I) (57 kDa RNA-binding protein PPTB-1).
243	Q9BUQ0	15	104	41.5	557	59633	9.2	Polypyrimidine tract binding protein 1
244	Q59ET3	15	126	42.5	529	57762	6.7	Chaperonin containing TCP1, subunit 6A isoform a variant
244	P40227	15	126	42.4	531	58024	6.7	T-complex protein 1 subunit zeta
245	Q16555	15	97	42	572	62294	6.4	Dihydropyrimidinase-related protein 2
245	Q59GB4	15	97	38.2	628	68184	6.2	Dihydropyrimidinase-like 2 variant
246	P12081	15	36	39.3	509	57411	5.9	Histidyl-tRNA synthetase, cytoplasmic
247	UPI000013EC8B	15	129	39	426	47566	11.1	60S ribosomal protein L4 (L1).
247	P36578	15	129	38.9	427	47697	11.1	60S ribosomal protein L4
247	Q59GY2	15	129	37.6	441	48996	11	Ribosomal protein L4 variant
248	Q6DD88	15	69	38.4	541	60542	5.7	DKFZP564J0863 protein
249	Q9Y230	15	54	36.9	463	51157	5.6	RuvB-like 2
250	O94925	15	55	33.5	669	73461	7.8	Glutaminase kidney isoform, mitochondrial precursor
250	UPI0000163E16	15	55	33.5	669	73427	7.8	glutaminase C
251	P38606	15	50	32.7	617	68304	5.5	Vacuolar ATP synthase catalytic subunit A
252	Q53HQ1	15	111	31.7	564	66696	6.2	Eukaryotic translation initiation factor 3 subunit 6 interacting protein variant
252	Q9Y262	15	111	31.7	564	66727	6.3	Eukaryotic translation initiation factor 3 subunit 6-interacting protein
252	Q5QTR1	15	111	31.7	564	66739	6.3	MSTP005
252	Q53HT4	15	111	31.7	564	66753	6.3	Eukaryotic translation initiation factor 3 subunit 6 interacting protein variant
252	Q6ICD2	15	111	29.5	607	70902	6.7	DJ1014D13.1 protein
253	Q16891-2	15	66	26.8	747	82625	6.6	Isoform 2 of Q16891
253	Q16891	15	66	26.4	758	83678	6.5	Mitochondrial inner membrane protein
253	UPI0000456DEF	15	66	26.4	758	83847	6.5	Mitochondrial inner membrane protein (Mitofilin) (p87/89) (Proliferation-inducing gene 4 protein).
253	UPI000006DE12	15	66	26.4	758	83668	6.5	inner membrane protein, mitochondrial
254	P35221	15	72	26	906	100071	6.3	Catenin alpha-1
255	Q32MZ4-3	15	72	25.8	752	82689	4.6	Isoform 3 of Q32MZ4

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
255	UPI000006DC73	15	72	24.7	784	86438	4.7	leucine rich repeat (in FLII) interacting protein 1
255	Q32MZ4-2	15	72	24.7	784	86404	4.7	Isoform 2 of Q32MZ4
255	Q32MZ4	15	72	24	808	89253	4.7	Leucine-rich repeat flightless-interacting protein 1
256	Q13263	15	72	22.2	835	88550	5.8	Transcription intermediary factor 1-beta
257	Q8TDQ5	15	68	22	788	89187	5.8	Arsenite-resistant protein ASR2
257	A4D2E6	15	68	21.7	796	90251	5.7	Arsenate resistance protein ARS2
257	Q6NT74	15	68	21.3	812	92194	5.8	ARS2 protein
257	Q32MI4	15	68	19.9	871	100147	6	ARS2 protein
257	A4D2E5	15	68	19.8	875	100537	6	Arsenate resistance protein ARS2
257	Q9BXP5-2	15	68	19.8	872	100276	6	Isoform B of Q9BXP5
257	Q9BXP5	15	68	19.7	876	100667	6	Arsenite-resistance protein 2
257	UPI000013C800	15	68	19.6	884	101567	6.1	Arsenite-resistance protein 2.
258	P17301	15	40	15.7	1181	129295	5.3	Integrin alpha-2 precursor
258	UPI0000169C36	15	40	15.7	1181	129296	5.3	integrin alpha 2 precursor
259	P29144	15	33	15.2	1249	138349	6.3	Tripeptidyl-peptidase 2
259	UPI0000137276	15	33	15.2	1249	138449	6.4	tripeptidyl peptidase II
260	Q7L576	15	98	14	1253	145182	6.9	Cytoplasmic FMR1-interacting protein 1
261	Q13428	15	38	10.8	1488	152103	9	Treacle protein
261	Q13428-3	15	38	10.7	1489	152203	9	Isoform 3 of Q13428
261	Q13428-4	15	38	10.5	1524	155926	8.9	Isoform 4 of Q13428
262	P46013-2	15	82	6.2	2896	319444	9.5	Isoform Short of P46013
262	P46013	15	82	5.6	3256	358695	9.4	Antigen KI-67
263	Q5T4S7	15	46	3.9	5183	573849	6	Zinc finger UBR1-type protein 1
263	Q8TDN5	15	46	3.9	5183	573909	6	P600
264	Q99714	14	80	75.9	261	26923	7.8	3-hydroxyacyl-CoA dehydrogenase type-2
265	P62258	14	240	69.4	255	29174	4.7	14-3-3 protein epsilon
266	P30041	14	113	66.5	224	25035	6.4	Peroxiredoxin-6
267	P23919	14	53	57.5	212	23819	8.3	Thymidylate kinase
268	P05141	14	196	53.7	298	32895	9.7	ADP/ATP translocase 2
269	UPI0000247080	14	361	48	352	37298	9.1	Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2 / hnRNP B1).
269	P22626	14	361	47.9	353	37430	8.9	Heterogeneous nuclear ribonucleoproteins A2/B1
270	Q02878	14	93	45.1	288	32728	10.6	60S ribosomal protein L6
270	Q8TBK5	14	93	45.1	288	32742	10.6	Ribosomal protein L6
270	Q8N5Z7	14	93	45.1	288	32726	10.6	Ribosomal protein L6
270	Q9HBB3	14	93	45	289	32891	10.6	DNA-binding protein TAXREB107
271	Q9NTK5	14	47	43.2	396	44744	7.8	Putative GTP-binding protein 9
272	Q15084	14	134	43	440	48121	5.1	Protein disulfide-isomerase A6 precursor
272	Q15084-2	14	134	38.4	492	53901	5.3	Isoform 2 of Q15084
273	P09543	14	45	42.5	421	47579	9.1	2',3'-cyclic-nucleotide 3'-phosphodiesterase
274	UPI0000134091	14	100	38.6	402	45978	10.2	60S ribosomal protein L3 (HIV-1 TAR RNA-binding protein B) (TARBP-B).
274	P39023	14	100	38.5	403	46109	10.2	60S ribosomal protein L3
275	O00148	14	76	36.8	427	49130	5.7	ATP-dependent RNA helicase DDX39
276	UPI0000E9BBC7	14	117	32.5	582	64677	5.2	Protein phosphatase 2
276	P30153	14	117	32.1	589	65309	5.1	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform

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277	Q92841	14	51	35.8	650	72372	8.6	Probable ATP-dependent RNA helicase DDX17
277	Q92841-3	14	51	35.7	652	72557	8.7	Isoform 3 of Q92841
277	UPI00003670EA	14	51	32	729	80255	8.3	Probable ATP-dependent RNA helicase DDX17 (EC 3.6.1.-) (DEAD box protein 17) (RNA-dependent helicase p72) (DEAD box protein p72).
277	UPI000021BFBA	14	51	32	729	80273	8.3	DEAD box polypeptide 17 isoform p82
277	Q59F66	14	51	31.6	737	81068	7.9	DEAD box polypeptide 17 isoform p82 variant
278	P55084	14	42	31.4	474	51294	9.4	Trifunctional enzyme subunit beta, mitochondrial precursor (TP-beta) [Includes: 3-ketoacyl-CoA thiolase (EC 2.3.1.16) (Acetyl-CoA acyltransferase) (Beta-ketothiolase)]
278	Q5R1W7	14	42	31.4	475	51396	9.4	Trifunctional enzyme subunit beta, mitochondrial precursor (TP-beta) [Includes: 3-ketoacyl-CoA thiolase (EC 2.3.1.16) (Acetyl-CoA acyltransferase) (Beta-ketothiolase)]
279	Q96AY3	14	64	30.2	582	64245	5.6	FK506-binding protein 10 precursor
279	UPI000015C65C	14	64	30.2	582	64305	5.6	FK506 binding protein 10, 65 kDa
280	Q10471	14	63	27.3	571	64733	8.4	Polypeptide N-acetylgalactosaminyltransferase 2 (EC 2.4.1.41) (Protein-UDP acetylgalactosaminyltransferase 2) (UDP- GalNAc:polypeptide N-acetylgalactosaminyltransferase 2) (Polypeptide GalNAc transferase 2) (GalNAc-T2) (pp-GaNTase 2) [Contains: Polypeptide N-acetylgalactosaminyltransferase 2 soluble form]
281	Q92499	14	54	25.1	740	82432	7.2	ATP-dependent RNA helicase DDX1
282	Q15046	14	42	25	597	68048	6.4	Lysyl-tRNA synthetase
282	UPI00001405CB	14	42	23.8	625	71497	6.8	Lysyl-tRNA synthetase (EC 6.1.1.6) (Lysine--tRNA ligase) (LysRS).
282	Q9HB23	14	42	23.8	625	71384	6.7	Lysyl-tRNA synthetase
283	P49915	14	50	24.5	693	76715	6.9	GMP synthase [glutamine-hydrolyzing]
284	Q9NR30	14	57	22.7	783	87344	9.3	Nucleolar RNA helicase 2
285	P46087	14	35	21.2	812	89302	9.2	Putative RNA methyltransferase NOL1
285	Q3KQS4	14	35	20.4	845	92860	9.2	NOL1 protein
285	UPI0000D62194	14	35	20.3	846	92974	9.2	Proliferating-cell nucleolar antigen p120 (Proliferation-associated nucleolar protein p120).
285	UPI00004565C2	14	35	20.1	855	94098	9.2	Proliferating-cell nucleolar antigen p120 (Proliferation-associated nucleolar protein p120).
286	Q99460-2	14	42	21.6	922	102258	5.3	Isoform 2 of Q99460

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286	Q99460	14	42	20.9	953	105836	5.4	26S proteasome non-ATPase regulatory subunit 1
287	Q13435	14	43	20	872	97657	5.7	Splicing factor 3B subunit 2
287	Q7Z627	14	43	19.8	877	98116	5.5	SF3B2 protein
287	Q9BWD2	14	43	19.5	894	100097	5.7	SF3B2 protein
288	Q9Y5B9	14	64	17.3	1047	119914	5.7	FACT complex subunit SPT16
289	O14617-5	14	51	16.5	1215	136651	7.6	Isoform 5 of O14617
290	O75694	14	45	13.8	1391	155199	6.2	Nuclear pore complex protein Nup155
291	Q9HD20-2	14	40	15.1	1086	121110	7.8	Isoform B of Q9HD20
291	Q9HD20	14	40	13.6	1204	132955	8.1	Probable cation-transporting ATPase 13A1
292	P11388	14	44	13.1	1531	174384	8.7	DNA topoisomerase 2-alpha
292	P11388-2	14	44	12.9	1557	177500	8.8	Isoform 2 of P11388
292	UPI0000D6231D	14	44	12.8	1568	178882	8.7	TOP2A_HUMAN Isoform 2 of P11388 - Homo sapiens (Human)
292	P11388-3	14	44	12.8	1567	178711	8.8	Isoform 3 of P11388
292	P11388-4	14	44	12.5	1612	182680	8.6	Isoform 4 of P11388
293	P55265-3	14	28	13.5	1181	131099	8.6	Isoform 3 of P55265
293	P55265-2	14	28	13.2	1200	133203	8.5	Isoform 2 of P55265
293	P55265	14	28	13	1226	135995	8.6	Double-stranded RNA-specific adenosine deaminase
293	Q59EC0	14	28	12.8	1244	137833	8.5	Adenosine deaminase, RNA-specific isoform ADAR-a variant
294	Q14160	14	24	11.5	1630	174930	5.1	Protein LAP4
294	UPI00001408BD	14	24	11.5	1630	174884	5.1	Protein LAP4 (Protein scribble homolog) (hScrib).
294	UPI0000D62517	14	24	11.4	1654	177194	5.1	Protein LAP4 (Protein scribble homolog) (hScrib).
294	UPI00004576FD	14	24	11.4	1655	177693	5.1	Protein LAP4 (Protein scribble homolog) (hScrib).
294	Q14160-4	14	24	11.4	1654	177240	5.1	Isoform 4 of Q14160
294	Q14160-3	14	24	11.4	1655	177739	5.1	Isoform 3 of Q14160
295	P26358	14	34	11	1616	183164	7.8	DNA (cytosine-5)-methyltransferase 1
295	A0AV63	14	34	10.8	1632	184818	7.9	DNMT1 protein
296	UPI0000DD79CB	14	37	8.8	1808	203142	4.8	PREDICTED: similar to melanoma inhibitory activity 3 isoform 14
296	UPI0000DD7931	14	37	8.8	1808	203141	4.8	PREDICTED: similar to melanoma inhibitory activity 3 isoform 3
296	Q5JRA6	14	37	8.4	1907	213700	4.8	Melanoma inhibitory activity family member 3
296	UPI00006C03EC	14	37	8.4	1907	213701	4.8	PREDICTED: similar to melanoma inhibitory activity 3 isoform 1
297	UPI000013F255	14	46	8.6	1972	218524	8.1	colonic and hepatic tumor over-expressed protein isoform b
297	Q0VAX8	14	46	8.3	2032	225493	7.8	Cytoskeleton associated protein 5
297	Q14008	14	46	8.3	2032	225507	7.9	Cytoskeleton-associated protein 5
298	Q7Z6Z7	14	54	4.1	4374	481896	5.2	E3 ubiquitin-protein ligase HUWE1
298	UPI0000D626C3	14	54	4.1	4374	481985	5.2	HECT, UBA and WWE domain-containing protein 1 (EC 6.3.2.-) (E3 ubiquitin protein ligase URE-B1) (Mcl-1 ubiquitin ligase E3) (Mule) (ARF-binding protein 1) (ARF-BP1).
298	Q7Z6Z7-3	14	54	4.1	4365	481023	5.2	Isoform 3 of Q7Z6Z7

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
298	Q7Z6Z7-2	14	54	4.1	4358	480203	5.2	Isoform 2 of Q7Z6Z7
299	P61106	13	94	73.5	215	23897	6.2	Ras-related protein Rab-14
300	P51149	13	172	72.9	207	23490	6.7	Ras-related protein Rab-7a
301	Q5R370	13	87	72.4	185	21228	7.9	Calcyclin binding protein
301	Q9HB71	13	87	58.8	228	26210	8.2	Calcyclin-binding protein
302	P37802	13	305	70.4	199	22391	8.2	Transgelin-2
302	UPI000013D3E3	13	305	63.6	220	24454	8.2	Transgelin-2 (SM22-alpha homolog).
303	Q9UJZ1	13	57	62.1	356	38534	7.4	Stomatin-like protein 2
304	Q5RLJ0	13	57	61.9	244	27969	6.4	CLE
304	Q9Y224	13	57	61.9	244	28068	6.7	Protein C14orf166
305	Q15365	13	112	60.4	356	37498	7.1	Poly(rC)-binding protein 1
305	UPI00001313C8	13	112	60.4	356	37526	7.1	poly(rC) binding protein 1
306	P05388	13	114	59	317	34274	6	60S acidic ribosomal protein P0
306	Q53HW2	13	114	59	317	34302	6	Ribosomal protein P0 variant
307	P04899	13	56	51.3	355	40451	5.5	Guanine nucleotide-binding protein G(i), alpha-2 subunit
308	P15880	13	70	50.2	293	31324	10.2	40S ribosomal protein S2
308	UPI000013EEA4	13	70	50.2	293	31438	10.2	similar to ribosomal protein S2 (LOC646294), mRNA
309	Q5VU66	13	112	50	248	28870	4.8	Tropomyosin 3
309	UPI0000D61FF9	13	112	50	248	28916	4.8	Tropomyosin alpha-3 chain (Tropomyosin-3) (Tropomyosin gamma) (hTM5).
310	P00387	13	54	48.8	301	34235	7.6	NADH-cytochrome b5 reductase (EC 1.6.2.2) (B5R) (Diaphorase-1) (Cytochrome b5 reductase 3) [Contains: NADH-cytochrome b5 reductase membrane-bound form; NADH-cytochrome b5 reductase soluble form]
311	Q5T7C4	13	106	65.2	158	18311	9.7	High-mobility group box 1
311	Q5T7C6	13	106	63.6	162	18808	9.7	High-mobility group box 1
311	Q59GW1	13	106	58.5	176	20164	9.7	High-mobility group box 1 variant
311	P09429	13	106	47.9	215	24894	5.7	High mobility group protein B1
311	Q14321	13	106	47.9	215	24993	5.9	HMG-1
312	P05198	13	37	46	315	36112	5.1	Eukaryotic translation initiation factor 2 subunit 1
313	P62495	13	34	42.3	437	49031	5.7	Eukaryotic peptide chain release factor subunit 1
314	UPI0000D62378	13	60	42.3	402	45292	8.2	26S protease regulatory subunit 8 (Proteasome 26S subunit ATPase 5) (Proteasome subunit p45) (p45/SUG) (Thyroid hormone receptor- interacting protein 1) (TRIP1).
314	P62195	13	60	41.9	406	45626	7.5	26S protease regulatory subunit 8
315	O60701	13	39	40.9	494	55024	7.1	UDP-glucose 6-dehydrogenase
316	P07910-2	13	98	39.6	293	32338	5.1	Isoform C1 of P07910
317	P35241	13	87	39.6	583	68564	6.4	Radixin
318	P23381	13	38	39.3	471	53165	6.2	Tryptophanyl-tRNA synthetase, cytoplasmic
319	P21281	13	38	38	511	56501	5.8	Vacuolar ATP synthase subunit B, brain isoform
320	P06744	13	76	36.6	558	63147	8.3	Glucose-6-phosphate isomerase

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
321	P22234	13	56	35.8	425	47079	7.2	Multifunctional protein ADE2 [Includes: Phosphoribosylaminoimidazole-succinocarboxamide synthase (EC 6.3.2.6) (SAICAR synthetase); Phosphoribosylaminoimidazole carboxylase (EC 4.1.1.21) (AIR carboxylase) (AIRC)]
321	UPI000013D4E4	13	56	33.7	451	49679	7.5	Multifunctional protein ADE2 [Includes: Phosphoribosylaminoimidazole-succinocarboxamide synthase (EC 6.3.2.6) (SAICAR synthetase); Phosphoribosylaminoimidazole carboxylase (EC 4.1.1.21) (AIR carboxylase) (AIRC)].
322	P38159	13	82	35.5	391	42332	10.1	Heterogeneous nuclear ribonucleoprotein G
323	P21589	13	93	34.7	574	63368	7	5'-nucleotidase precursor
323	Q6NZX3	13	93	34.7	574	63308	7	5'-nucleotidase, ecto
323	Q53Z63	13	93	34.7	574	63338	7	5'-nucleotidase
324	Q96I99	13	36	34.3	432	46511	6.4	Succinyl-CoA ligase [GDP-forming] beta-chain, mitochondrial precursor
325	P54577	13	43	31.8	528	59144	7	Tyrosyl-tRNA synthetase, cytoplasmic
326	P35052	13	60	31.4	558	61650	7.3	Glypican-1 precursor
326	Q53QM4	13	60	31.4	558	61680	7.3	Hypothetical protein GPC1
327	Q9UHB9	13	27	26.3	627	70730	8.6	Signal recognition particle 68 kDa protein
328	UPI0000D6239D	13	93	26.5	562	62865	8.4	Septin-9 (MLL septin-like fusion protein) (MLL septin-like fusion protein MSF-A) (Ovarian/Breast septin) (Ov/Br septin) (Septin D1).
328	Q9UHD8-2	13	93	26.2	568	63666	8.4	Isoform 2 of Q9UHD8
328	Q9UHD8-5	13	93	25.7	579	64682	7.6	Isoform 5 of Q9UHD8
328	Q9UHD8	13	93	25.4	586	65402	9	Septin-9
329	Q53FJ5	13	209	24	524	58141	5.2	Prosaposin (Variant Gaucher disease and variant metachromatic leukodystrophy) variant
330	P47897	13	24	20.9	775	87799	7.2	Glutaminyl-tRNA synthetase
330	Q53HS0	13	24	20.9	775	87711	7.2	Glutaminyl-tRNA synthetase variant
331	P11387	13	35	20	765	90726	9.3	DNA topoisomerase 1
332	Q86W92-4	13	29	19	980	110297	5.4	Isoform 4 of Q86W92
332	Q86W92-2	13	29	18.5	1005	113181	5.7	Isoform 2 of Q86W92
332	Q86W92	13	29	18.4	1011	114024	5.6	Liprin-beta-1
333	Q96FS1	13	33	21.3	830	92388	7.2	CTNND1 protein
333	O60716-21	13	33	21.3	832	92675	7.2	Isoform 3A of O60716
333	O60716-19	13	33	21.1	838	93496	7	Isoform 3AC of O60716
333	O60716-18	13	33	20.6	861	95868	6.3	Isoform 3AB of O60716
333	O60716-13	13	33	20.1	879	98049	7.5	Isoform 2A of O60716
333	O60716-11	13	33	20	885	98870	7.3	Isoform 2AC of O60716
333	O60716-10	13	33	19.5	908	101242	6.6	Isoform 2AB of O60716
333	Q6DHZ7	13	33	19	933	104098	7	CTNND1 protein
333	O60716-5	13	33	19	933	104156	7	Isoform 1A of O60716
333	UPI0000D62606	13	33	18.8	939	105005	7	Catenin delta-1 (p120 catenin) (p120(ctn)) (Cadherin-associated Src substrate) (CAS) (p120(cas)).

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
333	O60716-3	13	33	18.8	939	104977	6.9	Isoform 1AC of O60716
333	O60716-2	13	33	18.4	962	107349	6.3	Isoform 1AB of O60716
333	O60716	13	33	18.3	968	108170	6.2	Catenin delta-1 (p120 catenin) (p120(ctn)) (Cadherin-associated Src substrate) (CAS) (p120(cas))
334	P05106	13	38	18	788	87058	5.2	Integrin beta-3 precursor
335	UPI0000F58EF5	13	63	22	705	78878	5.8	Programmed cell death 6-interacting protein
335	Q4W4Y1	13	63	17.9	868	96079	6.5	Dopamine receptor interacting protein 4
335	Q8WUM4	13	63	17.9	868	96023	6.5	Programmed cell death 6-interacting protein
335	Q6NUS1	13	63	17.8	873	96818	6.5	PDCD6IP protein
336	Q92974	13	42	19.4	893	101174	8.4	Rho/Rac guanine nucleotide exchange factor 2
336	Q9H023	13	42	18.1	958	108242	6.9	Hypothetical protein DKFZp547L106 (Rho/rac guanine nucleotide exchange factor (GEF) 2)
336	Q8TDA3	13	42	17.6	985	111471	7.3	Guanine nucleotide exchange factor GEF-H1 (Rho/rac guanine nucleotide exchange factor (GEF) 2)
336	Q5VY92	13	42	17.5	986	111543	7.3	Rho/rac guanine nucleotide exchange factor (GEF) 2
336	Q5VY93	13	42	17.5	987	111493	7	Rho/rac guanine nucleotide exchange factor (GEF) 2
337	Q9Y2L1	13	31	17.1	958	109003	7.1	Exosome complex exonuclease RRP44
337	UPI0000D61A7F	13	31	17.1	960	109187	7.1	Exosome complex exonuclease RRP44 (EC 3.1.13.-) (Ribosomal RNA- processing protein 44) (DIS3 protein homolog).
337	UPI00001610C4	13	31	17.1	958	108976	7.1	KIAA1008
338	UPI0000136781	13	72	15.4	955	108694	10.2	thyroid hormone receptor associated protein 3
339	Q9Y2A7	13	27	12.8	1128	128790	6.6	Nck-associated protein 1
339	UPI00001693F2	13	27	12.7	1134	129517	6.7	NCK-associated protein 1 isoform 2
340	Q68CZ2	13	47	12.5	1445	155237	6.8	Tensin-3
340	UPI0000457557	13	47	12.5	1445	155293	6.8	tensin-like SH2 domain containing 1
340	UPI00001AE9DA	13	47	12.5	1445	155265	6.8	tensin 3
340	Q8IZW7	13	47	12.5	1445	155277	6.8	Tensin 3
341	Q5VYK3	13	42	8.7	1845	204289	7.1	Proteasome-associated protein ECM29 homolog
341	UPI0000D618EB	13	42	8.7	1833	203186	7.2	Proteasome-associated protein ECM29 homolog (Ecm29).
341	UPI00001D76EA	13	42	8.7	1839	203992	7.2	Proteasome-associated protein ECM29 homolog (Ecm29).
341	UPI0000DD7F7A	13	42	7.9	2017	223692	8.7	PREDICTED: similar to Proteasome-associated protein ECM29 homolog (Ecm29)
342	Q9Y520	13	54	5.3	2701	295829	9	Hypothetical protein
342	UPI0000203BC5	13	54	5.3	2703	295999	9	HBxAg transactivated protein 2
342	UPI0000E265EC	13	54	5	2817	308606	9.1	HBxAg transactivated protein 2
343	P61604	12	305	76.5	102	10932	8.9	10 kDa heat shock protein, mitochondrial

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
344	Q9Y696	12	41	61.7	253	28772	5.6	Chloride intracellular channel protein 4
345	P61019	12	126	60.8	212	23546	6.5	Ras-related protein Rab-2A
346	Q13162	12	52	60.1	271	30540	6.3	Peroxiredoxin-4
347	P18669	12	86	59.4	254	28804	7.2	Phosphoglycerate mutase 1
347	UPI00001AF8FE	12	86	59.4	254	28850	7.2	PREDICTED: similar to Phosphoglycerate mutase 1 (Phosphoglycerate mutase isozyme B) (PGAM-B) (BPG-dependent PGAM 1) isoform 1
347	Q6P6D7	12	86	59.4	254	28820	7.2	Phosphoglycerate mutase 1
347	Q53G35	12	86	59.4	254	28832	7.2	Phosphoglycerate mutase 1 (Brain) variant
348	P16152	12	50	55.6	277	30375	8.3	Carbonyl reductase [NADPH] 1 (EC 1.1.1.184) (NADPH-dependent carbonyl reductase 1) (Prostaglandin-E(2) 9-reductase)
349	P12004	12	61	52.9	261	28769	4.7	Proliferating cell nuclear antigen
349	Q6FHF5	12	61	52.9	261	28706	4.7	Proliferating cell nuclear antigen
350	P38117	12	77	51.8	255	27844	8.1	Electron transfer flavoprotein subunit beta
351	P55145	12	67	51.4	179	20257	8.4	ARMET protein precursor
351	UPI00004542F2	12	67	49.7	185	21144	8.9	arginine-rich, mutated in early stage tumors
352	Q07955	12	84	48	248	27745	10.4	Splicing factor, arginine/serine-rich 1
353	P13804	12	58	46.2	333	35080	8.4	Electron transfer flavoprotein subunit alpha, mitochondrial precursor
354	Q92820	12	56	44.3	318	35964	7.1	Gamma-glutamyl hydrolase precursor
355	Q13347	12	32	42.8	325	36502	5.6	Eukaryotic translation initiation factor 3 subunit 2
355	Q53HU7	12	32	42.8	325	36500	5.6	Eukaryotic translation initiation factor 3, subunit 2 beta, 36kDa variant
356	P46781	12	102	41.2	194	22591	10.7	40S ribosomal protein S9
357	P22695	12	35	40.8	453	48443	8.6	Ubiquinol-cytochrome-c reductase complex core protein 2, mitochondrial precursor
358	Q5VU20	12	112	39.7	393	43135	8.4	PAI-1 mRNA-binding protein
358	Q8NC51	12	112	38.2	408	44965	8.6	Plasminogen activator inhibitor 1 RNA-binding protein
359	Q9Y266	12	42	39.6	331	38243	5.4	Nuclear migration protein nudC
360	Q9HDC9	12	46	37.7	416	46480	6.2	Adipocyte plasma membrane-associated protein
360	UPI0000456F75	12	46	37.7	416	46528	6.2	Adipocyte plasma membrane-associated protein (BSCv protein).
361	P13489	12	43	35.6	461	49974	4.8	Ribonuclease inhibitor
361	Q9BQ80	12	43	35.6	461	49954	4.8	Ribonuclease/angiogenin inhibitor 1
362	P31943	12	162	34.3	449	49229	6.3	Heterogeneous nuclear ribonucleoprotein H
362	Q6IBM4	12	162	34.3	449	49130	6.2	HNRPH1 protein
362	UPI00001AF4DD	12	162	32.6	472	51230	6.8	Heterogeneous nuclear ribonucleoprotein H (hnRNP H).
363	P35998	12	60	33.5	433	48634	5.9	26S protease regulatory subunit 7

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
363	Q3LIA5	12	60	33.5	433	48618	6.1	Hypothetical protein Nbla10058
364	P31930	12	33	32.7	480	52646	6.4	Ubiquinol-cytochrome-c reductase complex core protein 1, mitochondrial precursor
365	P49411	12	34	32.1	452	49542	7.6	Elongation factor Tu, mitochondrial precursor
366	A4D2I9	12	30	32	431	48294	5	Src homology 3 domain-containing protein HIP-55
367	P09622	12	74	32	509	54150	7.7	Dihydrolipoyl dehydrogenase, mitochondrial precursor
367	Q8WTS4	12	74	32	509	54177	7.9	Dihydrolipoamide dehydrogenase
367	Q59EV8	12	74	31.3	520	55594	8.5	Dihydrolipoamide dehydrogenase, variant
368	P00505	12	41	30.5	430	47476	9	Aspartate aminotransferase, mitochondrial precursor
368	UPI000013CB99	12	41	30.5	430	47518	9	aspartate aminotransferase 2 precursor
368	Q53FL3	12	41	30.5	430	47548	9	Aspartate aminotransferase 2 variant
369	Q9H4M9	12	24	30.3	534	60627	6.8	EH domain-containing protein 1
370	P48735	12	36	29.2	452	50909	8.7	Isocitrate dehydrogenase [NADP], mitochondrial precursor (EC 1.1.1.42) (Oxalosuccinate decarboxylase) (IDH) (NADP(+)-specific ICDH)
370	Q53GL5	12	36	29.2	452	50910	8.5	Isocitrate dehydrogenase 2 (NADP+), mitochondrial variant
371	Q9Y2X3	12	50	28.9	529	59578	8.9	Nucleolar protein NOP5
372	Q53H17	12	43	28.1	606	66228	6.7	WD repeat-containing protein 1 isoform 1 variant
372	Q59ER5	12	43	27.2	624	68171	7.2	WD repeat-containing protein 1 isoform 1 variant
373	P55809	12	35	27.9	520	56158	7.5	Succinyl-CoA:3-ketoacid-coenzyme A transferase 1, mitochondrial precursor
374	P07384	12	26	22.1	714	81890	5.7	Calpain-1 catalytic subunit
374	Q6DHV4	12	26	22.1	714	81831	5.6	CAPN1 protein
375	Q02809	12	49	21.7	727	83550	6.9	Procollagen-lysine,2-oxoglutarate 5 dioxygenase 1 precursor
376	Q15436	12	51	20.1	765	86161	7.1	Protein transport protein Sec23A
377	UPI0000161B5A	12	43	20.5	835	93394	5.1	Ubiquitin isopeptidase T
377	P45974-2	12	43	20.5	835	93308	5.1	Isoform Short of P45974
377	P45974	12	43	19.9	858	95786	5	Ubiquitin carboxyl-terminal hydrolase 5
378	Q9UGP8	12	42	18.2	760	87997	5.3	Translocation protein SEC63 homolog
379	P42285	12	35	15.2	1042	117805	6.5	Superkiller viralicidic activity 2-like 2
379	Q6MZZ8	12	35	15.2	1042	117761	6.7	Hypothetical protein DKFZp686K2075
380	Q9H0D6-2	12	29	15.6	874	99962	8	Isoform 2 of Q9H0D6
380	Q9H0D6	12	29	14.3	950	108583	7.5	5'-3' exoribonuclease 2
381	Q6PKG0-3	12	44	15.3	1019	116465	9.1	Isoform 3 of Q6PKG0
381	Q6PKG0	12	44	14.2	1096	123510	8.8	La-related protein 1
381	UPI0000457378	12	44	14.2	1095	122812	9.1	La-related protein 1 (La ribonucleoprotein domain family member 1).
381	Q6PKG0-2	12	44	14.2	1096	122940	9.1	Isoform 2 of Q6PKG0

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
382	P20020-6	12	42	14.9	1184	130617	6	Isoform K of P20020
382	P20020-3	12	42	14.5	1220	134685	5.9	Isoform B of P20020
382	P20020-4	12	42	14.2	1249	137804	6	Isoform C of P20020
382	P20020	12	42	14.1	1258	138755	6	Plasma membrane calcium-transporting ATPase 1
383	Q9BPX3	12	30	13.8	1015	114334	5.6	Condensin complex subunit 3
384	O43795-2	12	27	14.2	1078	124951	9.2	Isoform 2 of O43795
384	O43795	12	27	13.5	1136	131985	9.4	Myosin-Ib
385	A3KQ42	12	17	12.6	1126	118693	5.6	HLA-B associated transcript 3
385	Q5HYL9	12	17	12.6	1126	118725	5.6	Hypothetical protein DKFZp686L0653
385	UPI0000161DCF	12	17	12.5	1132	119419	5.6	HLA-B associated transcript-3 isoform a
385	UPI000013C678	12	17	12.5	1140	120258	5.6	HLA-B associated transcript 3
385	P46379	12	17	12.5	1132	119409	5.6	Large proline-rich protein BAT3
385	Q5SQ39	12	17	12.2	1162	122342	5.7	HLA-B associated transcript 3
386	Q9NQW6-2	12	31	11.7	1087	120016	8.2	Isoform 2 of Q9NQW6
386	Q9NQW6	12	31	11.3	1124	124199	8.1	Actin-binding protein anillin
387	Q14573	12	32	5.5	2671	304037	6.5	Inositol 1,4,5-trisphosphate receptor type 3
387	UPI0000161B31	12	32	5.5	2671	304115	6.5	inositol 1,4,5-triphosphate receptor, type 3
387	Q5TAQ2	12	32	5.5	2671	304105	6.5	Inositol 1,4,5-triphosphate receptor, type 3
388	Q99497	11	66	76.2	189	19891	6.8	Protein DJ-1
389	P62937	11	325	70.3	165	18012	7.8	Peptidyl-prolyl cis-trans isomerase A
390	P32969	11	123	66.1	192	21863	10	60S ribosomal protein L9
391	P04792	11	174	64.4	205	22783	6.4	Heat-shock protein beta-1
392	Q13509	11	86	64.2	450	50433	4.9	Tubulin beta-3 chain
393	UPI00004A67B3	11	99	68.2	148	16621	8.3	destrin isoform b
393	P60981	11	99	61.2	165	18506	7.9	Destrin
394	O00299	11	82	61	241	26923	5.2	Chloride intracellular channel protein 1
394	Q53FB0	11	82	61	241	27015	5.2	Chloride intracellular channel 1 variant
395	P28066	11	81	60.6	241	26411	4.8	Proteasome subunit alpha type 5
396	P27348	11	164	60	245	27764	4.8	14-3-3 protein theta
397	P61026	11	94	57.5	200	22541	8.4	Ras-related protein Rab-10
397	UPI0000072ACD	11	94	57.5	200	22469	8.6	ras-related GTP-binding protein RAB10
398	P08865	11	87	56.9	295	32854	4.9	40S ribosomal protein SA
399	P21266	11	51	56.9	225	26560	5.5	Glutathione S-transferase Mu 3
400	Q5U0I1	11	76	56.4	218	24489	5.7	RAB11B, member RAS oncogene family
401	Q13126	11	52	55.8	283	31236	7.2	S-methyl-5-thioadenosine phosphorylase
401	Q6FHT1	11	52	55.8	283	31254	7.2	MTAP protein
401	Q6FHP1	11	52	55.8	283	31210	7.2	MTAP protein
402	Q2TNB3	11	77	54.8	239	27349	5.6	Cell migration-inducing protein 22
402	Q9UL46	11	77	54.8	239	27362	5.6	Proteasome activator complex subunit 2
402	Q86SZ7	11	77	54.8	239	27402	5.7	Full-length cDNA clone CS0DJ015YJ12 of T cells (Jurkat cell line) of Homo sapiens
403	Q7Z4Y4	11	37	54.2	227	25620	9.3	GTP:AMP phosphotransferase
403	Q9UIJ7	11	37	54.2	227	25565	9.2	GTP:AMP phosphotransferase mitochondrial
404	P30085	11	53	52.6	196	22222	5.6	UMP-CMP kinase
405	P67809	11	55	50.9	324	35924	9.9	Nuclease sensitive element-binding protein 1

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
406	Q9Y5M8	11	55	50.6	271	29702	9	Signal recognition particle receptor subunit beta
407	Q53GQ0	11	63	50	312	34350	9.3	Estradiol 17-beta-dehydrogenase 12
407	UPI000004C79B	11	63	50	312	34324	9.3	steroid dehydrogenase homolog
408	P67936	11	96	49.2	248	28522	4.7	Tropomyosin alpha-4 chain
409	P24539	11	66	48.8	256	28909	9.4	ATP synthase B chain, mitochondrial precursor
410	P25786	11	36	48.7	263	29556	6.6	Proteasome subunit alpha type 1
410	P25786-2	11	36	47.6	269	30239	7	Isoform Long of P25786
411	P29692	11	119	48.4	281	31122	5	Elongation factor 1-delta
411	Q96I38	11	119	21	647	71422	6.4	EEF1D protein
412	O60664	11	49	47.7	434	47047	5.4	Mannose-6-phosphate receptor-binding protein 1
413	A2VBX9	11	52	47.6	273	31655	6	MHC class I antigen
414	P46782	11	108	47.5	204	22876	9.7	40S ribosomal protein S5
415	P27695	11	29	46.5	318	35554	8.1	DNA-(apurinic or apyrimidinic site) lyase
416	Q15019	11	63	44.6	361	41487	6.6	Septin-2
417	P40925	11	87	40.7	334	36426	7.3	Malate dehydrogenase, cytoplasmic
418	P09525	11	71	40.4	319	35883	6.1	Annexin A4
419	Q53GN6	11	49	37.2	376	42917	5.7	Proteasome 26S non-ATPase subunit 13 isoform 1 variant
419	UPI0000158430	11	49	37.2	376	42946	5.8	26S proteasome non-ATPase regulatory subunit 13 (26S proteasome regulatory subunit S11) (26S proteasome regulatory subunit p40.5).
419	Q9UNM6	11	49	37.2	376	42918	5.8	26S proteasome non-ATPase regulatory subunit 13
419	Q9Y6E3	11	49	37.1	377	42671	6.1	HSPC027
420	P07339	11	139	37.1	412	44552	6.5	Cathepsin D precursor (EC 3.4.23.5) [Contains: Cathepsin D light chain; Cathepsin D heavy chain]
421	Q02978	11	47	36.9	314	34062	9.9	Mitochondrial 2-oxoglutarate/malate carrier protein
422	P61160	11	82	35.3	394	44761	6.7	Actin-like protein 2
423	Q5D0C4	11	109	35.3	397	44000	9.4	SERPINE2 protein
424	P07954-2	11	32	38.1	467	50213	7.4	Isoform Cytoplasmic of P07954
424	P07954	11	32	34.9	510	54637	8.8	Fumarate hydratase, mitochondrial precursor
425	Q6IBS1	11	32	34.4	404	45250	5.5	PSMC3 protein
426	Q96ND2	11	56	34	377	43084	4.9	CDNA FLJ31051 fis, clone HSYRA2000605, weakly similar to MYOSIN HEAVY CHAIN, CLONE 203
427	P51572	11	300	33.7	246	27992	8.4	B-cell receptor-associated protein 31
427	Q53HT6	11	300	33.7	246	27962	8.4	B-cell receptor-associated protein 31 variant
427	Q53G72	11	300	33.7	246	27931	8.4	B-cell receptor-associated protein 31 variant
428	Q9BS26	11	29	33.7	406	46971	5.3	Thioredoxin domain-containing protein 4 precursor
429	P15311	11	63	33.3	586	69413	6.3	Ezrin
429	Q6NUR7	11	63	33.3	586	69242	6.3	Villin 2
429	UPI0000D61508	11	63	33.1	589	69688	6.3	Ezrin (p81) (Cytovillin) (Villin-2).

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
430	Q7L1Q6	11	33	33.7	419	48043	5.9	Basic leucine zipper and W2 domain-containing protein 1
430	Q53FN7	11	33	33.3	424	48618	6.1	BZW1 protein variant
431	P62333	11	26	32.6	389	44173	7.5	26S protease regulatory subunit S10B
432	P39656	11	103	32.3	439	48810	5.7	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit precursor
432	UPI0000163BD0	11	103	31.1	456	50702	6.4	dolichyl-diphosphooligosaccharide-protein glycosyltransferase precursor
432	Q5VWA5	11	103	31.1	456	50801	6.5	Dolichyl-diphosphooligosaccharide-protein glycosyltransferase
433	P43686	11	46	32.3	418	47366	5.2	26S protease regulatory subunit 6B
434	O00231	11	27	32	422	47464	6.5	26S proteasome non-ATPase regulatory subunit 11
435	Q9Y265	11	39	31.1	456	50228	6.4	RuvB-like 1
436	P28838	11	25	31	519	56166	7.9	Cytosol aminopeptidase
437	Q9NVA2	11	44	30.3	429	49398	6.8	Septin-11
438	P41091	11	27	29.9	472	51110	8.4	Eukaryotic translation initiation factor 2 subunit 3
438	Q53HK3	11	27	29.9	472	51083	8.4	Eukaryotic translation initiation factor 2, subunit 3 gamma, 52kDa variant
439	Q96D94	11	29	29.7	499	54025	5.3	SIAHBP1 protein
439	Q969E7	11	29	28.7	516	55729	5.3	SIAHBP1 protein
439	UPI00004576FF	11	29	27.4	541	58115	5.3	fuse-binding protein-interacting repressor isoform b
439	Q99628	11	29	27.4	541	57996	5.3	Siah binding protein 1
439	Q9NZA0	11	29	27.3	542	58172	5.3	FBP-interacting repressor
439	Q9UJY7	11	29	26.6	556	59572	5.3	Poly-U binding splicing factor PUF60
439	UPI00004576FE	11	29	26.5	558	59819	5.3	fuse-binding protein-interacting repressor isoform b
439	Q9UHX1	11	29	26.5	559	59876	5.3	Ro ribonucleoprotein-binding protein 1
440	Q15008	11	31	28.3	389	45531	5.6	26S proteasome non-ATPase regulatory subunit 6
441	P43490	11	31	27.7	491	55521	7.2	Nicotinamide phosphoribosyltransferase
442	P05362	11	62	25.8	532	57825	8	Intercellular adhesion molecule 1 precursor
443	Q5JTV8	11	37	25.2	583	66248	8.2	Torsin-1A-interacting protein 1
444	O43776	11	29	25	548	62943	6.3	Asparaginyl-tRNA synthetase, cytoplasmic
445	Q5T0M6	11	24	25.5	466	50316	6.6	Annexin A7
445	Q53HM8	11	24	25.5	466	50228	7.2	Annexin VII isoform 1 variant
445	P20073	11	24	24.4	488	52739	5.7	Annexin A7
445	Q5T0M7	11	24	24.4	488	52739	5.7	Annexin A7
446	P48444	11	65	24.1	511	57210	6.2	Coatomer subunit delta
446	UPI000049DD56	11	65	22.3	552	61626	5.8	Coatomer subunit delta (Delta-coat protein) (Delta-COP) (Archain).
446	Q6MZV5	11	65	22.3	552	61598	5.8	Hypothetical protein DKFZp686M09245
447	Q02818	11	41	24.1	461	53879	5.2	Nucleobindin-1 precursor
447	Q53GX6	11	41	24.1	461	53907	5.2	Nucleobindin 1 variant
448	P50995	11	34	23.8	505	54390	7.7	Annexin A11
449	Q68CR9	11	32	29.2	401	45771	5.7	Hypothetical protein DKFZp781B11202

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
449	P14868	11	32	23.4	501	57136	6.5	Aspartyl-tRNA synthetase, cytoplasmic
450	Q53G58	11	32	22.8	474	53281	7.1	Coronin, actin binding protein, 1C variant
450	Q9ULV4	11	32	22.8	474	53249	7.1	Coronin-1C
451	Q96AE4	11	80	22.7	644	67560	7.6	Far upstream element-binding protein 1
451	UPI00004561FD	11	80	22.4	651	68491	7.3	Far upstream element-binding protein 1 (FUSE-binding protein 1) (FBP) (DNA helicase V) (HDH V).
451	Q96AE4-2	11	80	22.4	653	68605	7.3	Isoform 2 of Q96AE4
451	UPI000059CFF9	11	80	22.3	655	68904	7.9	Far upstream element-binding protein 1 (FUSE-binding protein 1) (FBP) (DNA helicase V) (HDH V).
452	A2A418	11	87	21.5	731	80641	5.8	Gelsolin
452	P06396	11	87	20.1	782	85697	6.3	Gelsolin precursor
453	P46060	11	24	21.3	587	63542	4.7	Ran GTPase-activating protein 1
454	P07686	11	80	20.7	556	63111	6.8	Beta-hexosaminidase beta chain precursor (EC 3.2.1.52) (N-acetyl-beta- glucosaminidase) (Beta-N-acetylhexosaminidase) (Hexosaminidase B) (Cervical cancer proto-oncogene 7) (HCC-7) [Contains: Beta- hexosaminidase beta-B chain; Beta-hexosaminidase beta-A chain]
455	O75746	11	38	20.6	678	74756	8.4	Calcium-binding mitochondrial carrier protein Aralar1
455	Q96AM8	11	38	20.6	678	74762	8.4	Solute carrier family 25 (Mitochondrial carrier, Aralar), member 12
456	Q99798	11	44	21.2	780	85425	7.6	Aconitate hydratase, mitochondrial precursor
456	Q8TAQ6	11	44	21.2	780	85565	7.7	Aconitase 2, mitochondrial
456	Q6FHX0	11	44	21.2	780	85467	7.5	ACO2 protein
456	A2A274	11	44	20.5	805	87820	7.4	Aconitase 2, mitochondrial
457	Q8IXB1	11	36	18.4	793	91080	7.2	DnaJ homolog subfamily C member 10 precursor
458	A4D229	11	44	16.9	893	98902	8.7	KIAA1228 protein
459	Q6P179	11	18	15.5	915	105526	6.8	LRAP protein
459	Q9HBX2	11	18	14.8	960	110462	6.7	Aminopeptidase
459	Q7Z5K1	11	18	14.8	960	110447	6.7	Leukocyte-derived arginine aminopeptidase long form variant
460	Q15042	11	30	15.2	981	110524	5.6	Rab3 GTPase-activating protein catalytic subunit
461	Q8N163	11	26	15	923	102902	5.2	Protein KIAA1967
461	Q8N163-2	11	26	15	923	103143	5.4	Isoform 2 of Q8N163
461	UPI00001AEEB7	11	26	14.9	925	103030	5.2	p30 DBC protein
462	P49736	11	22	14.7	904	101896	5.5	DNA replication licensing factor MCM2
463	Q5JRX3	11	19	12.4	1037	117455	7	Presequence protease, mitochondrial precursor
463	UPI000045634B	11	19	12.4	1037	117448	6.9	Presequence protease, mitochondrial precursor (EC 3.4.24.-) (hPreP) (Pitrilysin metalloproteinase 1) (Metalloprotease 1) (hMP1).
463	UPI00001F8A38	11	19	12.4	1037	117413	6.9	metalloprotease 1

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
463	UPI000013C859	11	19	12.4	1037	117410	7	Presequence protease, mitochondrial precursor (EC 3.4.24.-) (hPreP) (Pitrilysin metalloproteinase 1) (Metalloprotease 1) (hMP1).
463	Q5JRX3-2	11	19	12.4	1038	117554	7	Isoform 2 of Q5JRX3
464	UPI0000441EF9	11	26	11.6	1092	124106	7.7	formin-like 2
464	Q96PY5	11	26	11.4	1112	126314	8.2	Formin-like protein 2
465	O95819	11	25	11.1	1239	142101	7.5	Mitogen-activated protein kinase kinase kinase kinase 4
466	P26006-2	11	37	11.2	1051	116612	6.8	Isoform Alpha
466	P26006	11	37	11.1	1066	118698	7	Integrin alpha-3 precursor (Galactoprotein B3) (GAPB3) (VLA-3 alpha chain) (FRP-2) (CD49c antigen) [Contains: Integrin alpha-3 heavy chain; Integrin alpha-3 light chain]
466	UPI0000140781	11	37	11.1	1066	118756	7	integrin alpha 3 isoform b, precursor
467	Q8TAQ2-2	11	35	11.2	1130	124841	5.6	Isoform 2 of Q8TAQ2
467	Q59G16	11	35	11	1156	127377	5.5	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin c2 isoform b variant
467	Q59GV3	11	35	10.9	1164	128088	5.6	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin c2 isoform b variant
467	Q8TAQ2	11	35	10.5	1214	132879	5.7	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily C member 2
468	UPI00001610D5	11	30	11.3	1155	129438	8.5	DEAH (Asp-Glu-Ala-His) box polypeptide 30 isoform 2
468	Q7L2E3	11	30	11	1194	133938	8.8	Putative ATP-dependent RNA helicase DHX30
469	P55011-3	11	27	10.9	1196	129679	6.5	Isoform 2 of P55011
469	P55011	11	27	10.7	1212	131447	6.4	Solute carrier family 12 member 2 (Bumetanide-sensitive sodium-(potassium)-chloride cotransporter 1)
469	UPI0000D61674	11	27	10.7	1211	131391	6.5	Solute carrier family 12 member 2 (Bumetanide-sensitive sodium-(potassium)-chloride cotransporter 1) (Basolateral Na-K-Cl symporter).
470	UPI000046FFDC	11	25	10.8	1588	179483	7.7	Ras GTPase-activating-like protein IQGAP3.
470	A2RRC9	11	25	10.5	1631	184517	7.5	IQ motif containing GTPase activating protein 3
470	UPI0000231C93	11	25	10.5	1631	184598	7.6	IQ motif containing GTPase activating protein 3
470	UPI000021D298	11	25	10.5	1633	184856	7.6	Ras GTPase-activating-like protein IQGAP3.
470	Q86VI3	11	25	10.5	1631	184545	7.5	Ras GTPase-activating-like protein IQGAP3
470	Q5T3H8	11	25	10.5	1631	184698	7.6	IQ motif containing GTPase activating protein 3

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471	UPI0000D62364	11	24	10.4	1309	144909	5.2	C-jun-amino-terminal kinase-interacting protein 4 (JNK-interacting protein 4) (JIP-4) (JNK-associated leucine-zipper protein) (JLP) (Sperm-associated antigen 9) (Mitogen-activated protein kinase 8- interacting protein 4) (Human lung cancer protein 6) (HLC
471	UPI0000D62363	11	24	10.4	1313	145362	5.2	C-jun-amino-terminal kinase-interacting protein 4 (JNK-interacting protein 4) (JIP-4) (JNK-associated leucine-zipper protein) (JLP) (Sperm-associated antigen 9) (Mitogen-activated protein kinase 8- interacting protein 4) (Human lung cancer protein 6) (HLC
471	O60271-4	11	24	10.4	1307	144681	5.2	Isoform 4 of O60271
471	O60271-2	11	24	10.4	1311	145135	5.2	Isoform 2 of O60271
471	O60271	11	24	10.3	1321	146205	5.1	C-jun-amino-terminal kinase-interacting protein 4
472	P52701	11	33	9.6	1360	152785	6.9	DNA mismatch repair protein MSH6
473	O95347	11	28	9.5	1197	135780	8.6	Structural maintenance of chromosomes protein 2
473	UPI0000457786	11	28	9.5	1195	135549	8.6	Structural maintenance of chromosomes protein 2 (Chromosome-associated protein E) (hCAP-E) (XCAP-E homolog).
473	Q6IEE0	11	28	9.5	1197	135656	8.4	SMC2 protein
474	Q9Y451	11	23	9.9	1391	158035	8.6	Androgen-induced prostate proliferative shutoff associated protein
474	Q9NTI5	11	23	9.5	1447	164666	8.5	Hypothetical protein
474	UPI0000D61A5E	11	23	9.5	1449	164824	8.5	androgen-induced prostate proliferative shutoff associated protein
474	Q9Y2I5	11	23	9.3	1483	168415	8.6	Androgen-induced proliferation inhibitor
475	Q7Z460-2	11	34	8.8	1471	162110	8.8	Isoform 2 of Q7Z460
475	A2RU21	11	34	8.7	1479	162914	8.8	CLASP1 protein
475	Q7Z460-3	11	34	8.6	1494	164565	8.5	Isoform 3 of Q7Z460
475	Q7Z460	11	34	8.4	1538	169450	9	CLIP-associating protein 1
476	Q5QNZ9	11	18	7.3	1724	192593	5.7	Poly (ADP-ribose) polymerase family, member 4
476	Q9UKK3	11	18	7.3	1724	192587	5.7	Poly [ADP-ribose] polymerase 4 (EC 2.4.2.30) (PARP-4) (Vault poly(ADP- ribose) polymerase)
477	Q9Y4I1-2	11	22	7.3	1828	212287	8.6	Isoform 2 of Q9Y4I1
477	Q9Y4I1	11	22	7.2	1855	215419	8.5	Myosin-Va
477	UPI0000E445E1	11	22	7.2	1855	215403	8.5	myosin VA (heavy polypeptide 12, myoxin)
478	O75165	11	51	5.8	2243	254417	6.7	DnaJ homolog subfamily C member 13
478	Q3L0T1	11	51	5.8	2243	254412	6.7	DnaJ domain-containing protein RME-8
479	Q9UQ35	11	37	5.5	2752	299616	12.1	Serine/arginine repetitive matrix protein 2
480	Q14019	10	100	75.4	142	15945	5.7	Coactosin-like protein
481	P22392	10	206	71.7	152	17298	8.4	Nucleoside diphosphate kinase B

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482	UPI00005E7FE3	10	92	68.9	167	19488	8.4	Tubulin--tyrosine ligase-like protein 3 (HOTTL).
482	P59998	10	92	68.5	168	19667	8.4	Actin-related protein 2/3 complex subunit 4
483	P09211	10	236	63.8	210	23356	5.6	Glutathione S-transferase P
484	Q5TIF8	10	37	60.3	232	25615	7.9	Adenylate kinase 2
484	P54819	10	37	58.6	239	26478	7.8	Adenylate kinase isoenzyme 2, mitochondrial
485	P62249	10	133	58.2	146	16445	10.2	40S ribosomal protein S16
486	P32119	10	79	56.6	198	21892	6	Peroxiredoxin-2
487	P20618	10	61	56.4	241	26489	8.1	Proteasome subunit beta type 1 precursor
487	Q53FT8	10	61	56.4	241	26491	8.1	Proteasome beta 1 subunit variant
488	P00568	10	43	56.2	194	21635	8.6	Adenylate kinase isoenzyme 1
488	Q53EY8	10	43	56.2	194	21619	8.9	Adenylate kinase 1 variant
488	Q5T9B7	10	43	51.9	210	23411	8.6	Adenylate kinase 1
489	P07203	10	47	56.2	201	21899	6.5	Glutathione peroxidase 1
489	UPI00001B07C3	10	47	55.7	203	21938	6.5	glutathione peroxidase 1 isoform 1
490	P62269	10	213	52.6	152	17719	11	40S ribosomal protein S18
491	Q92520	10	162	50.2	227	24680	8.3	Protein FAM3C precursor
492	P62241	10	161	50	208	24205	10.3	40S ribosomal protein S8
493	P23284	10	260	49.5	208	22742	9.3	Peptidyl-prolyl cis-trans isomerase B precursor
493	UPI0000072333	10	260	47.7	216	23743	9.4	peptidylprolyl isomerase B precursor
493	Q6IBH5	10	260	47.7	216	23728	9.4	Peptidyl-prolyl cis-trans isomerase
494	Q15691	10	29	48.9	268	29999	5.1	Microtubule-associated protein RP/EB family member 1
495	Q15417	10	51	47.7	329	36414	6.1	Calponin-3
496	P62714	10	41	47.2	309	35575	5.4	Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform
496	Q8WZ56	10	41	47.2	309	35631	5.4	Protein phosphatase type 2A catalytic subunit
496	Q5U0I7	10	41	47.2	309	35605	5.4	Protein phosphatase 2 (Formerly 2A), catalytic subunit, beta isoform
497	UPI0000129B77	10	57	46.6	290	31371	8.1	mitochondrial short-chain enoyl-coenzyme A hydratase 1 precursor
498	Q6IPN0	10	225	44.9	343	36918	4.8	RTN4 protein
498	Q7L7Q6	10	225	41.3	373	40318	4.8	RTN4
499	Q16698	10	58	44.5	335	36068	9.3	2,4-dienoyl-CoA reductase, mitochondrial precursor
500	P60900	10	99	43.9	246	27399	6.7	Proteasome subunit alpha type 6
501	P06493	10	43	42.8	297	34095	8.4	Cell division control protein 2 homolog
501	UPI000013EBE9	10	43	42.8	297	34081	8.4	Cell division control protein 2 homolog (EC 2.7.11.22) (EC 2.7.11.23) (p34 protein kinase) (Cyclin-dependent kinase 1) (CDK1).
502	P28482	10	27	42.5	360	41390	7	Mitogen-activated protein kinase 1
502	UPI0000F0A51A	10	27	40.3	380	43553	7.3	Mitogen-activated protein kinase 1
503	UPI000013EEE0	10	70	47.8	293	31479	7.6	PREDICTED: similar to voltage-dependent anion channel 2
503	P45880-5	10	70	47.6	294	31566	7.6	Isoform 5 of P45880

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503	UPI0000D611B0	10	70	47.3	296	31721	7.6	UPI0000D611B0 UniRef100 entry
503	UPI00003666E7	10	70	42.3	331	36232	6.7	Voltage-dependent anion-selective channel protein 2 (VDAC-2) (hVDAC2) (Outer mitochondrial membrane protein porin 2).
503	P45880-3	10	70	42.2	332	36288	6.7	Isoform 3 of P45880
504	P07858	10	66	41	339	37822	6.3	Cathepsin B precursor (EC 3.4.22.1) (Cathepsin B1) (APP secretase) (APPS) [Contains: Cathepsin B light chain; Cathepsin B heavy chain]
505	P62826	10	76	39.8	216	24423	7.5	GTP-binding nuclear protein Ran
506	P46777	10	82	38.4	297	34363	9.7	60S ribosomal protein L5
507	P18124	10	110	37.9	248	29226	10.7	60S ribosomal protein L7
507	Q3KQU0	10	110	29.6	318	37022	10.7	RPL7 protein
508	Q53HL6	10	30	37.2	374	42471	5.6	Dendritic cell protein variant
508	Q7L2H7	10	30	37.2	374	42503	5.6	PCI domain containing 1
509	P62424	10	65	35	266	29996	10.6	60S ribosomal protein L7a
509	UPI0000D62425	10	65	34.4	270	30548	10.7	similar to 60S ribosomal protein L7a (Surfeit locus protein 3) (LOC645846), mRNA
510	Q96DB5	10	30	34.7	314	35808	8.5	Protein FAM82B
510	UPI0000DD7F20	10	30	20.1	541	59651	9.4	PREDICTED: similar to Protein FAM82B
511	O00303	10	63	34.2	357	37564	5.4	Eukaryotic translation initiation factor 3 subunit 5
512	Q96BS4	10	59	41.5	260	28449	9.4	FBL protein
512	P22087	10	59	33.6	321	33784	10.2	rRNA 2'-O-methyltransferase fibrillarin
513	Q13148	10	33	33.1	414	44740	6.2	TAR DNA-binding protein 43
514	P51991-2	10	93	34.6	356	37029	8.3	Isoform 2 of P51991
514	P51991	10	93	32.5	378	39595	9	Heterogeneous nuclear ribonucleoprotein A3
515	O00154-6	10	52	37.4	329	36568	7.8	Isoform 6 of O00154
515	O00154-4	10	52	36.4	338	37420	7.3	Isoform 4 of O00154
515	O00154	10	52	32.4	380	41796	8.5	Cytosolic acyl coenzyme A thioester hydrolase
516	Q99733	10	75	31.7	375	42823	4.7	Nucleosome assembly protein 1-like 4
516	UPI0000D6258B	10	75	31.6	377	43011	4.7	Nucleosome assembly protein 1-like 4 (Nucleosome assembly protein 2) (NAP2).
517	O43390	10	48	29.1	633	70943	8.1	Heterogeneous nuclear ribonucleoprotein R
518	Q9Y6E2	10	28	28.9	419	48162	6.7	Basic leucine zipper and W2 domain-containing protein 2
519	Q13283	10	71	28.8	466	52164	5.5	Ras GTPase-activating protein-binding protein 1
519	Q6FI03	10	71	28.8	466	52164	5.6	G3BP protein
520	O15371	10	38	28.6	548	63973	6	Eukaryotic translation initiation factor 3 subunit 7
521	UPI0000163C03	10	32	29.2	472	53216	8.7	DEAD (Asp-Glu-Ala-Asp) box polypeptide 6
521	P26196	10	32	28.6	483	54417	8.7	Probable ATP-dependent RNA helicase DDX6
522	P04062	10	19	28	536	59716	7.6	Glucosylceramidase precursor
523	O94808	10	22	26.8	682	76931	7.4	Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] 2

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523	UPI000049E025	10	22	26.8	684	77190	7.5	Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] 2 (EC 2.6.1.16) (Hexosephosphate aminotransferase 2) (D-fructose-6-phosphate amidotransferase 2) (GFAT 2) (GFAT2).
524	P04040	10	17	25.4	527	59756	7.4	Catalase
525	O00232	10	27	25	456	52904	7.6	26S proteasome non-ATPase regulatory subunit 12
526	Q5HYG8	10	48	25.3	483	53465	8.2	Hypothetical protein DKFZp686P09201
526	P34897	10	48	24.2	504	55993	8.5	Serine hydroxymethyltransferase, mitochondrial precursor
526	Q53ET4	10	48	24.2	504	55974	8.4	Serine hydroxymethyltransferase 2 (Mitochondrial) variant
527	Q13418	10	20	22.8	452	51419	8.1	Integrin-linked protein kinase
528	Q7Z5D5	10	30	32	384	43736	5.5	Medulloblastoma antigen MU-MB-2.50
528	Q7RTQ9	10	30	22.9	538	61202	5.8	Kinesin light chain 1A
528	Q7RTQ7	10	30	22.5	547	62192	5.7	Kinesin light chain 1F
528	Q07866-8	10	30	22.5	547	62302	6	Isoform S of Q07866
528	Q07866-2	10	30	22.1	556	63293	5.9	Isoform C of Q07866
528	UPI00004567D3	10	30	22	559	63686	5.9	Kinesin light chain 1 (KLC 1).
528	Q07866-3	10	30	22	560	63796	6.4	Isoform G of Q07866
528	UPI00004567D1	10	30	21.7	568	64656	6.4	Kinesin light chain 1 (KLC 1).
528	Q07866	10	30	21.6	569	64786	6.3	Kinesin light chain 1
528	UPI0000D62453	10	30	21.2	579	65565	6	Kinesin light chain 1 (KLC 1).
528	Q07866-7	10	30	21.2	580	65768	6	Isoform P of Q07866
528	Q7RTQ8	10	30	20.3	607	68964	7.3	Kinesin light chain 1O
528	Q7RTQ2	10	30	20.2	609	68762	6	Kinesin light chain 1E
528	UPI0000D62452	10	30	20	616	69894	7.3	Kinesin light chain 1 (KLC 1).
528	Q7RTQ3	10	30	20	614	69242	6	Kinesin light chain 1D
528	Q7RTQ1	10	30	20	616	69954	7.1	Kinesin light chain 1K
528	Q7RTQ0	10	30	19.7	624	70496	6.8	Kinesin light chain 1N
528	Q07866-6	10	30	19.7	624	70482	6.8	Isoform N of Q07866
528	UPI00004567D4	10	30	19.5	632	71342	6.8	Kinesin light chain 1 (KLC 1).
528	UPI00004567D2	10	30	19.4	634	71744	7.8	Kinesin light chain 1 (KLC 1).
528	Q7RTP8	10	30	19.4	633	71487	6.7	Kinesin light chain 1J
528	Q07866-9	10	30	19.4	635	71874	7.7	Isoform I of Q07866
528	Q07866-4	10	30	19.4	633	71473	6.7	Isoform J of Q07866
529	P42166	10	42	21.5	694	75492	7.7	Lamina-associated polypeptide 2 isoform alpha (Thymopoietin isoform alpha) (TP alpha) (Thymopoietin-related peptide isoform alpha) (TPRP isoform alpha) [Contains: Thymopoietin (TP) (Splenin); Thymopentin (TP5)]
530	Q96GF2	10	27	21.5	633	68448	5.3	GSPT1 protein
531	P12268	10	34	21.4	514	55805	6.9	Inosine-5'-monophosphate dehydrogenase 2
532	Q96N86	10	60	21.3	517	59574	8.6	CDNA FLJ31237 fis, clone KIDNE2004846, highly similar to 26S PROTEASOME REGULATORY SUBUNIT S3
532	O43242	10	60	20.6	534	60978	8.4	26S proteasome non-ATPase regulatory subunit 3
532	Q6IBN0	10	60	20.6	534	60946	8.4	PSMD3 protein
533	Q8N4P8	10	22	19.6	632	73709	9.6	GTPBP4 protein

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533	UPI00001AE86D	10	22	19.6	634	73852	9.5	Nucleolar GTP-binding protein 1 (Chronic renal failure gene protein) (GTP-binding protein NGB).
533	Q9BZE4	10	22	19.6	634	73965	9.5	Nucleolar GTP-binding protein 1
534	Q27J83	10	32	19.7	707	77762	5.9	Chromosome 14 open reading frame 173 isoform 1
534	Q27J81	10	32	19.4	716	78769	5.6	Uncharacterized protein C14orf173
535	P51659	10	33	18.5	736	79686	8.8	Peroxisomal multifunctional enzyme type 2
536	P42224	10	22	18	750	87335	6.1	Signal transducer and activator of transcription 1-alpha/beta
536	Q68D00	10	22	18	750	87363	6.1	Hypothetical protein DKFZp686B04100
537	Q08J23	10	31	18	767	86499	6.9	Putative 5-methycytoisine methyltransferase
537	UPI000020BF2B	10	31	18	767	86471	6.8	NOL1/NOP2/Sun domain family 2 protein
538	Q9H845	10	23	17.6	621	68760	8	Acyl-CoA dehydrogenase family member 9, mitochondrial precursor
539	P33993	10	20	16.4	719	81308	6.5	DNA replication licensing factor MCM7
540	Q9H307	10	24	15.8	717	81614	7.2	Pinin
540	UPI000013C70D	10	24	15.8	717	81628	7.2	Pinin (140 kDa nuclear and cell adhesion-related phosphoprotein) (Domain-rich serine protein) (DRS-protein) (DRSP) (Melanoma metastasis clone A protein) (Desmosome-associated protein) (SR-like protein) (Nuclear protein SDK3).
541	Q86XP3	10	25	15.4	938	102975	7	ATP-dependent RNA helicase DDX42
541	UPI0000456AEB	10	25	15.4	938	103005	6.9	DEAD box polypeptide 42 protein
542	Q96P70	10	48	14.5	1041	115963	4.8	Importin-9
543	A0AV56	10	28	13.4	917	102855	5.5	Scaffold attachment factor B
543	Q15424	10	28	13.4	915	102642	5.5	Scaffold attachment factor B
544	P53992	10	28	13.2	1094	118315	7.1	Protein transport protein Sec24C
544	UPI000013F621	10	28	13.2	1094	118325	7.1	SEC24-related protein C
545	A0AVT1	10	20	12.6	1052	117970	6.1	Ubiquitin-activating enzyme E1-like protein 2
545	UPI00001910DA	10	20	12.6	1052	117955	6.2	ubiquitin-activating enzyme E1-like 2
546	O94804	10	18	12.1	968	112135	6.9	Serine/threonine-protein kinase 10
546	UPI0000457386	10	18	12	974	112748	6.8	Serine/threonine-protein kinase 10 (EC 2.7.11.1) (Lymphocyte-oriented kinase).
547	Q8TCJ2	10	71	11.7	826	93674	8.9	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B
548	Q59EA1	10	14	11.7	1081	122130	8.6	Transcription elongation regulator 1 variant
548	O14776	10	14	11.6	1098	123960	8.7	Transcription elongation regulator 1
548	UPI000013E374	10	14	11.6	1098	123901	8.6	transcription elongation regulator 1 isoform 1

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549	P35442	10	26	11.3	1172	129955	4.8	Thrombospondin-2 precursor
549	Q5RI52	10	26	11.3	1172	129991	4.8	Thrombospondin 2
550	Q9HAV4	10	32	11.1	1204	136311	5.8	Exportin-5
550	UPI00004A3AA6	10	32	11.1	1204	136260	5.8	Exportin-5 (Exp5) (Ran-binding protein 21).
551	P29317	10	36	11	976	108254	6.2	Ephrin type-A receptor 2 precursor
551	Q8N3Z2	10	36	11	976	108266	6.2	Ephrin receptor
552	P07996	10	28	10.3	1170	129383	4.9	Thrombospondin-1 precursor
552	Q59E99	10	28	9.9	1225	134849	5	Thrombospondin 1 variant
553	UPI00004565B7	10	22	11.1	993	114069	6.3	ELKS/RAB6-interacting/CAST family member 1 (RAB6-interacting protein 2) (ERC protein 1).
553	Q8IUD2-2	10	22	11.1	992	113920	6.3	Isoform 2 of Q8IUD2
553	Q8IUD2-3	10	22	10.1	1088	124904	6.1	Isoform 3 of Q8IUD2
553	Q8IUD2	10	22	9.9	1116	128086	6	ELKS/RAB6-interacting/CAST family member 1
554	Q13523	10	31	9.6	1007	116973	10.3	Serine/threonine-protein kinase PRP4 homolog
554	Q8IVC3	10	31	9.6	1007	116991	10.3	PRP4 pre-mRNA processing factor 4 homolog B
554	Q5TAY8	10	31	9.6	1007	116987	10.3	PRP4 pre-mRNA processing factor 4 homolog B
555	Q92900-2	10	27	9.4	1118	123036	6.7	Isoform 2 of Q92900
555	Q92900	10	27	9.3	1129	124345	6.6	Regulator of nonsense transcripts 1
556	Q5SW80	10	14	8.3	1557	171972	7.4	Centrosomal protein 170kDa
556	Q5SW79	10	14	8.1	1584	175292	7.1	Centrosomal protein of 170 kDa
556	UPI000045632C	10	14	8.1	1585	175435	7.2	centrosomal protein 170kDa isoform gamma
557	Q9H2M9	10	16	8	1393	155984	5.6	Rab3 GTPase-activating protein non-catalytic subunit
557	UPI00004562FB	10	16	8	1393	155941	5.6	Rab3 GTPase-activating protein non-catalytic subunit (Rab3 GTPase- activating protein 150 kDa subunit) (Rab3-GAP p150) (Rab3-GAP regulatory subunit) (RAB3-GAP150) (RGAP-iso).
558	P51532	10	19	7.4	1647	184644	7.9	Probable global transcription activator SNF2L4
558	Q9HBD4	10	19	7.3	1679	188147	8.2	SMARCA4 isoform 2
559	P07942	10	34	7.1	1786	198065	5	Laminin subunit beta-1 precursor
560	Q9Y6D6	10	23	6.8	1849	208766	5.9	Brefeldin A-inhibited guanine nucleotide-exchange protein 1
561	Q92621	10	22	5.3	2012	227918	6.2	Nuclear pore complex protein Nup205
561	UPI00001D74D8	10	22	5.3	2012	227919	6.2	Nuclear pore complex protein Nup205 (Nucleoporin Nup205) (205 kDa nucleoporin).
562	O75691	10	32	4	2785	318426	7.4	Small subunit processome component 20 homolog
562	UPI00001FB38B	10	32	4	2785	318385	7.4	down-regulated in metastasis
562	UPI0000031EE4	10	32	4	2785	318400	7.4	PREDICTED: similar to Small subunit processome component 20 homolog (Down-regulated in metastasis protein) (Protein Key-1A6) (Novel nucleolar protein 73) (NNP73)

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563	UPI0000D626C7	10	28	2.2	5300	606141	5.4	Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5 (Actin cross-linking family protein 7) (Macrophin-1) (Trabeculin-alpha) (620 kDa actin-binding protein) (ABP620).
563	Q9UPN3	10	28	2.1	5430	620426	5.4	Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5
563	UPI0000D626C8	10	28	2.1	5374	614212	5.4	Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5 (Actin cross-linking family protein 7) (Macrophin-1) (Trabeculin-alpha) (620 kDa actin-binding protein) (ABP620).
563	UPI00004578EC	10	28	2.1	5430	620397	5.4	Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5 (Actin cross-linking family protein 7) (Macrophin-1) (Trabeculin-alpha) (620 kDa actin-binding protein) (ABP620).
563	Q9UPN3-1	10	28	2.1	5374	614160	5.4	Isoform 1 of Q9UPN3
564	P07737	9	248	70	140	15054	8.3	Profilin-1
565	P30086	9	59	69	187	21057	7.5	Phosphatidylethanolamine-binding protein 1 (PEBP-1) (Prostatic-binding protein) (HCNPpp) (Neuropolypeptide h3) (Raf kinase inhibitor protein) (RKIP) [Contains: Hippocampal cholinergic neurostimulating peptide (HCNP)]
566	O75947	9	58	65.8	161	18491	5.3	ATP synthase D chain, mitochondrial
567	P62820	9	204	64.4	205	22678	6.2	Ras-related protein Rab-1A
568	P84085	9	231	63.3	180	20530	6.8	ADP-ribosylation factor 5
569	P60660	9	149	60.3	151	16930	4.7	Myosin light polypeptide 6
569	Q561V9	9	149	60.3	151	16961	4.6	Myosin, light chain 6, alkali, smooth muscle and non-muscle
569	UPI0000D62206	9	149	58.3	156	17353	4.7	Myosin light polypeptide 6 (Smooth muscle and nonmuscle myosin light chain alkali 6) (Myosin light chain alkali 3) (Myosin light chain 3) (MLC-3) (LC17).
570	P25787	9	69	59.4	234	25899	7.4	Proteasome subunit alpha type 2
570	Q53GF5	9	69	59.4	234	25841	8	Proteasome alpha 2 subunit variant
571	P08708	9	107	57	135	15550	9.8	40S ribosomal protein S17
572	A2VCL0	9	1006	56.9	102	11377	11.4	HIST2H4B protein
572	P62805	9	1006	56.3	103	11367	11.4	Histone H4
573	Q04917	9	45	56.9	246	28219	4.8	14-3-3 protein eta
574	P62081	9	107	56.2	194	22127	10.1	40S ribosomal protein S7
575	Q9Y2B0	9	45	56	182	20652	4.9	MIR-interacting saposin-like protein precursor
576	P48047	9	88	54.5	213	23277	10	ATP synthase O subunit, mitochondrial precursor
577	O75396	9	107	53.5	215	24741	8.5	Vesicle-trafficking protein SEC22b
578	Q05DH1	9	42	55.5	238	26714	8.9	Hypothetical protein

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578	O14818	9	42	53.2	248	27887	8.5	Proteasome subunit alpha type 7
579	Q9NP72	9	39	52.9	206	22977	5.2	Ras-related protein Rab-18
580	Q13938	9	45	52.4	189	20967	4.9	Calcyphosin
581	O75347	9	75	51.9	108	12855	5.3	Tubulin-specific chaperone A
582	P39019	9	213	50.3	145	16060	10.3	40S ribosomal protein S19
582	Q8WVX7	9	213	46.5	157	17282	10.5	Ribosomal protein S19
583	Q5VYC2	9	43	50.2	227	24636	7.2	Protein-L-isoaspartate (D-aspartate) O-methyltransferase
583	Q5VYC1	9	43	50	228	24679	6.5	Protein-L-isoaspartate (D-aspartate) O-methyltransferase
584	Q02543	9	125	48.3	176	20762	10.7	60S ribosomal protein L18a
585	P28074	9	52	46.6	208	22897	8.5	Proteasome subunit beta type 5 precursor
585	Q7Z3B5	9	52	36.5	266	28810	6.5	Hypothetical protein DKFZp686I0180
586	P61254	9	103	45.5	145	17258	10.6	60S ribosomal protein L26
586	Q6IBH6	9	103	45.5	145	17244	10.6	RPL26 protein
587	O43399	9	39	45.1	206	22238	5.4	Tumor protein D54
587	UPI0000D610E3	9	39	42.5	219	23739	6.2	Tumor protein D54 (hD54) (Tumor protein D52-like 2).
587	Q5U0E0	9	39	42.3	220	23787	5.7	Tumor protein D52-like 2
587	Q5JWU6	9	39	40.6	229	24854	6.4	Tumor protein D52-like 2
588	P00491	9	31	45	289	32118	6.9	Purine nucleoside phosphorylase
589	Q15631	9	97	44.7	228	26183	6.4	Translin
590	Q9Y6C9	9	48	44.2	303	33331	8	Mitochondrial carrier homolog 2
591	P54920	9	29	42.7	295	33233	5.4	Alpha-soluble NSF attachment protein
592	Q96AG4	9	81	40.7	307	34930	9.6	Leucine-rich repeat-containing protein 59
593	UPI0000185FC9	9	128	40.6	155	17662	10.4	PREDICTED: similar to 60S ribosomal protein L23a
593	P62750	9	128	40.4	156	17695	10.4	60S ribosomal protein L23a
594	Q06323	9	26	40.2	249	28723	6	Proteasome activator complex subunit 1
594	UPI000045675C	9	26	39.7	252	28837	5.4	Proteasome activator complex subunit 1 (Proteasome activator 28-alpha subunit) (PA28alpha) (PA28a) (Activator of multicatalytic protease subunit 1) (11S regulator complex subunit alpha) (REG-alpha) (Interferon gamma up-regulated I-5111 protein) (IGUP I-51
595	P62280	9	49	39.9	158	18431	10.3	40S ribosomal protein S11
596	Q6FHN1	9	59	59.8	164	17748	6.6	DUT protein
596	UPI000045684C	9	59	39.2	250	26552	9.6	Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial precursor (EC 3.6.1.23) (dUTPase) (dUTP pyrophosphatase).
596	P33316	9	59	38.9	252	26706	9.6	Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial precursor
596	Q6NSA3	9	59	38.9	252	26563	9.4	DUTP pyrophosphatase
597	Q0MQG7	9	34	38.8	263	30168	7.5	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial precursor

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597	O75489	9	34	38.6	264	30242	7.5	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial precursor
597	Q53FM7	9	34	38.6	264	30160	6.7	NADH dehydrogenase (Ubiquinone) Fe-S protein 3, 30kDa (NADH-coenzyme Q reductase) variant
598	P61313	9	90	38.2	204	24146	11.6	60S ribosomal protein L15
598	Q5T6E0	9	90	38.2	204	24174	11.6	Ribosomal protein L15 pseudogene 3
599	O15372	9	24	37.5	352	39930	6.5	Eukaryotic translation initiation factor 3 subunit 3
599	Q53HR0	9	24	37.5	352	39914	6.5	Eukaryotic translation initiation factor 3, subunit 3 gamma, 40kDa variant
600	P52788	9	17	37.4	366	41268	5	Spermine synthase
600	UPI0000D61D37	9	17	37.4	366	41272	5	Spermine synthase (EC 2.5.1.22) (Spermidine aminopropyltransferase) (SPMSY).
601	P09661	9	36	36.5	255	28416	8.6	U2 small nuclear ribonucleoprotein A'
601	Q53G61	9	36	36.5	255	28402	8.6	Small nuclear ribonucleoprotein polypeptide A' variant
601	Q53G21	9	36	36.5	255	28474	8.6	Small nuclear ribonucleoprotein polypeptide A' variant
602	Q12907	9	37	36.5	356	40229	7	Vesicular integral-membrane protein VIP36 precursor
603	P78417	9	48	36.1	241	27566	6.6	Glutathione transferase omega-1
604	P15559	9	74	35.4	274	30868	8.9	NAD(P)H dehydrogenase [quinone] 1 (EC 1.6.5.2) (Quinone reductase 1) (NAD(P)H:quinone oxidoreductase 1)
605	Q14165	9	20	34.6	292	32234	5.4	Uncharacterized protein KIAA0152 precursor
606	Q15785	9	26	33	309	34559	9	Mitochondrial import receptor subunit TOM34
607	Q5TZT4	9	29	32.3	350	38380	5.2	Unr-interacting protein
607	Q9Y3F4	9	29	32.3	350	38438	5.1	Serine-threonine kinase receptor-associated protein
607	Q9NTK0	9	29	32.3	350	38452	5.1	Hypothetical protein DKFZp564N1778
608	Q9UHQ9	9	22	29.8	305	34095	9.4	NADH-cytochrome b5 reductase isoform
609	P20042	9	30	29.1	333	38388	5.8	Eukaryotic translation initiation factor 2 subunit 2
610	Q7Z7N7	9	101	28.8	361	39959	9.4	Solute carrier family 25 (Mitochondrial carrier; phosphate carrier), member 3
610	Q8NCF7	9	101	28.8	361	39933	9.4	CDNA FLJ90278 fis, clone NT2RP1000325, highly similar to Phosphate carrier protein, mitochondrialprecursor
611	O00505	9	18	28.6	521	57811	4.9	Importin alpha-3 subunit
612	P10644	9	12	28.1	381	42982	5.3	cAMP-dependent protein kinase type I-alpha regulatory subunit
612	Q68DQ4	9	12	28.1	381	42948	5.3	Hypothetical protein DKFZp779L0468
613	Q15942	9	77	28.1	572	61277	6.7	Zyxin

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
614	Q32Q68	9	45	26.1	272	30629	6	Capping protein (Actin filament) muscle Z-line, beta
614	Q5VVZ5	9	45	23.6	301	33781	6.4	Capping protein (Actin filament) muscle Z-line, beta
615	Q8NB01	9	24	26.8	388	44997	5.5	CDNA FLJ34453 fis, clone HLUNG2002429, highly similar to Homo sapiens cartilage-associated protein
615	O75718	9	24	25.9	401	46562	5.7	Cartilage-associated protein precursor
615	UPI0000D61AEC	9	24	25.7	404	46847	5.7	Cartilage-associated protein precursor.
616	Q9NR12	9	14	25.6	457	49845	8.4	PDZ and LIM domain protein 7
617	Q0IJ47	9	64	25.5	467	48086	4.9	KRT9 protein
618	Q5QPL9	9	64	32.5	237	24665	10.5	RNA binding protein, autoantigenic (HnRNP-associated with lethal yellow homolog (Mouse))
618	Q9UKM9-2	9	64	26.6	290	30364	9.6	Isoform 1 of Q9UKM9
618	Q9UKM9	9	64	25.2	306	32463	9.2	RNA-binding protein Raly
618	Q53GL6	9	64	25.1	307	32550	9.2	RNA binding protein (Autoantigenic, hnRNP-associated with lethal yellow) long isoform variant (RNA binding protein, autoantigenic) (HnRNP-associated with lethal yellow homolog (Mouse))
619	UPI000045648D	9	24	25.1	371	42252	6.3	Alpha-parvin (Calponin-like integrin-linked kinase-binding protein) (CH-ILKBP) (Matrix-remodelling-associated protein 2).
619	Q9NVD7	9	24	25	372	42244	5.9	Alpha-parvin
620	A0PJ92	9	50	24.8	447	49757	9.1	Hypothetical protein
620	O00567	9	50	18.7	594	66050	9.2	Nucleolar protein Nop56
621	P52292	9	30	23.8	529	57862	5.4	Importin alpha-2 subunit
621	Q6NVW7	9	30	23.8	529	57965	5.4	Karyopherin alpha 2
621	Q53YE3	9	30	23.8	529	57876	5.3	Karyopherin alpha 2
622	Q59GY3	9	92	29.4	279	31865	11	Arginine/serine-rich splicing factor 6 variant
622	Q13247-3	9	92	24.5	335	38419	11	Isoform SRP55
622	Q13247	9	92	23.8	344	39587	11.4	Splicing factor, arginine/serine-rich 6
623	P30520	9	20	23.5	456	50097	6.6	Adenylosuccinate synthetase isozyme 2
624	P51114-3	9	30	26.7	536	59919	6.9	Isoform 3 of P51114
624	P51114	9	30	23	621	69692	6.3	Fragile X mental retardation syndrome-related protein 1
624	UPI000013EA6E	9	30	23	621	69721	6.2	fragile X mental retardation-related protein 1 isoform a
625	Q13409-4	9	28	23.6	605	67552	5.1	Isoform 2D of Q13409
625	UPI0000D61269	9	28	23.5	608	67805	5.2	Cytoplasmic dynein 1 intermediate chain 2 (Dynein intermediate chain 2, cytosolic) (DH IC-2) (Cytoplasmic dynein intermediate chain 2).
625	Q7Z4X1	9	28	23.4	612	68354	5.3	Cytoplasmic dynein intermediate chain 2C
625	Q5BJF8	9	28	23.4	612	68426	5.3	DYNC1I2 protein
625	Q13409-6	9	28	23.4	611	68298	5.3	Isoform 2F of Q13409
625	Q13409-2	9	28	22.6	632	70645	5.2	Isoform 2B of Q13409
625	Q13409	9	28	22.4	638	71457	5.2	Cytoplasmic dynein 1 intermediate chain 2
625	Q13409-5	9	28	22.4	637	71328	5.2	Isoform 2E of Q13409

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
625	UPI0000456EA1	9	28	22.3	641	71709	5.2	Cytoplasmic dynein 1 intermediate chain 2 (Dynein intermediate chain 2, cytosolic) (DH IC-2) (Cytoplasmic dynein intermediate chain 2).
626	UPI0000378489	9	66	22.5	525	59178	4.4	protein kinase C substrate 80K-H isoform 2
626	P14314	9	66	22.3	528	59425	4.4	Glucosidase 2 subunit beta precursor
627	Q9Y3I0	9	21	22	505	55210	7.2	UPF0027 protein C22orf28
628	P07099	9	27	21.1	455	52949	7.3	Epoxide hydrolase 1
629	O75131	9	23	20.9	537	60131	5.8	Copine-3
630	Q99829	9	26	20.9	537	59059	5.8	Copine-1
631	Q15758	9	96	20.5	541	56598	5.5	Neutral amino acid transporter B(0) (ATB(0))
631	Q71UA6	9	96	20.5	541	56583	5.5	Neutral amino acid transporter
632	Q86UX7-2	9	30	20.7	663	75430	6.8	Isoform 2 of Q86UX7
632	Q86UX7	9	30	20.5	667	75953	7	Unc-112-related protein 2
633	P13674	9	22	20.2	534	61049	6	Prolyl 4-hydroxylase subunit alpha-1 precursor
633	Q5VSQ6	9	22	20.2	534	60967	6	Procollagen-proline, 2-oxoglutarate 4-dioxygenase (Proline 4-hydroxylase), alpha polypeptide I (Procollagen-proline, 2-oxoglutarate 4-dioxygenase (Proline 4-hydroxylase), alpha polypeptide I variant)
634	O75390	9	28	19.7	466	51712	8.3	Citrate synthase, mitochondrial precursor
635	Q2T9F7	9	34	18.2	713	79612	6.8	UNC84B protein
635	Q9UH99	9	34	18.1	717	80311	6.7	Sad1/unc-84-like protein 2
635	Q504T5	9	34	17.6	738	82575	6.6	UNC84B protein
636	P49321	9	26	17.8	788	85238	4.3	Nuclear autoantigenic sperm protein
637	Q14247	9	41	17.1	550	61636	5.4	Src substrate cortactin
637	UPI0000D62647	9	41	17.1	551	61762	5.4	Src substrate cortactin (Amplaxin) (Oncogene EMS1).
637	UPI000013D657	9	41	17.1	550	61586	5.4	cortactin isoform a
637	Q53HG7	9	41	17.1	550	61558	5.4	Cortactin isoform a variant
638	O95831-3	9	25	16.6	609	66295	8.9	Isoform 3 of O95831
638	O95831	9	25	16.5	613	66901	9	Apoptosis-inducing factor 1, mitochondrial precursor
639	Q96TA1	9	18	16.8	733	82683	6.2	Niban-like protein
639	Q5VVW7	9	18	16.5	746	84138	6.2	Chromosome 9 open reading frame 88
640	P18084	9	38	16.4	799	88054	6.1	Integrin beta-5 precursor
640	UPI0000DD7BBB	9	38	13.7	958	104706	7.3	PREDICTED: similar to Integrin beta-5 precursor
641	Q6GMQ6	9	31	17.4	610	66393	8.8	Phosphatidylinositol binding clathrin assembly protein
641	Q13492-2	9	31	16.8	632	68764	7.9	Isoform 2 of Q13492
641	Q13492	9	31	16.3	652	70755	7.9	Phosphatidylinositol-binding clathrin assembly protein
641	Q4LE54	9	31	14.7	721	77397	8.4	PICALM variant protein
642	Q9BR63	9	46	16.1	585	65701	6.8	FARSB protein
642	UPI00002096AC	9	46	16	589	66116	6.8	phenylalanyl-tRNA synthetase, beta subunit
642	Q9NSD9	9	46	16	589	66130	6.8	Phenylalanyl-tRNA synthetase beta chain
643	Q6IMN7	9	58	16	694	76862	5.1	Cytoplasmic activation/proliferation-associated protein 1

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643	Q9BV09	9	58	15.7	709	78366	5.2	GPI-anchored membrane protein 1
643	UPI0000366799	9	58	15.6	712	78612	5.2	GPI-anchored membrane protein 1 (GPI-anchored protein p137) (p137GPI) (Membrane component chromosome 11 surface marker 1).
644	Q75MP2	9	28	19.1	591	66914	6.4	Hypothetical protein PDE1C
644	Q8TAE4	9	28	17.8	634	72226	6.6	PDE1C protein
644	Q14123-2	9	28	17.8	634	72208	6.6	Isoform PDE1C1 of Q14123
644	Q14123	9	28	15.9	709	80760	8.8	Calcium/calmodulin-dependent 3',5'-cyclic nucleotide phosphodiesterase 1C
644	UPI000045753D	9	28	14.7	769	86915	8.6	Calcium/calmodulin-dependent 3',5'-cyclic nucleotide phosphodiesterase 1C (EC 3.1.4.17) (Cam-PDE 1C) (hCam-3).
644	Q8NB10	9	28	14.7	769	86910	8.5	CDNA FLJ34415 fis, clone HEART2004764, highly similar to CALCIUM/CALMODULIN-DEPENDENT 3',5'-CYCLIC NUCLEOTIDE PHOSPHODIESTERASE 1C
645	Q96PK6	9	29	15.7	669	69492	9.7	RNA-binding protein 14
646	P08582	9	26	14.9	738	80242	6	Melanotransferrin precursor
646	UPI000013E329	9	26	14.9	738	80215	5.9	melanoma-associated antigen p97 isoform 1, precursor
647	Q16643	9	27	14.9	649	71425	4.5	Drebrin
647	UPI0000457394	9	27	14.9	649	71429	4.5	Drebrin (Developmentally-regulated brain protein).
647	UPI000013E0B5	9	27	14.9	649	71439	4.5	drebrin 1 isoform a
648	Q92973	9	42	14.7	890	101310	5	Transportin-1
648	UPI000020CAB6	9	42	14.6	898	102355	5	transportin 1 isoform 1
649	P23921	9	18	14.4	792	90070	7.1	Ribonucleoside-diphosphate reductase large subunit
649	Q53GZ5	9	18	14.4	792	89972	7.3	Ribonucleoside-diphosphate reductase M1 chain variant
650	O00541-2	9	35	14.2	583	67456	7.5	Isoform 2 of O00541
650	O00541	9	35	14.1	588	68003	7.3	Pescadillo homolog 1
651	Q32P28	9	44	12.6	736	83394	5.1	Prolyl 3-hydroxylase 1 precursor
652	Q8NE71	9	30	12.4	845	95926	6.8	ATP-binding cassette sub-family F member 1
653	Q9NZB2-3	9	15	11.3	1118	121888	8.9	Isoform C of Q9NZB2
654	Q9P2B2	9	21	10.9	879	98556	6.6	Prostaglandin F2 receptor negative regulator precursor
655	P52732	9	21	10.4	1056	119159	5.6	Kinesin-like protein KIF11
656	UPI0000456910	9	19	10.3	1102	128316	5.6	Ubiquitin carboxyl-terminal hydrolase 7 (EC 3.1.2.15) (Ubiquitin thioesterase 7) (Ubiquitin specific-processing protease 7) (Deubiquitinating enzyme 7) (Herpesvirus-associated ubiquitin-specific protease).

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
656	UPI000013F0BE	9	19	10.3	1102	128302	5.6	Ubiquitin carboxyl-terminal hydrolase 7 (EC 3.1.2.15) (Ubiquitin thioesterase 7) (Ubiquitin-specific-processing protease 7) (Deubiquitinating enzyme 7) (Herpesvirus-associated ubiquitin-specific protease).
656	Q93009	9	19	10.3	1102	128272	5.6	Ubiquitin carboxyl-terminal hydrolase 7
656	Q6U8A4	9	19	10.2	1112	129004	5.8	Ubiquitin-specific protease 7 isoform
656	UPI0000D6198F	9	19	10.2	1110	128925	5.8	Ubiquitin carboxyl-terminal hydrolase 7 (EC 3.1.2.15) (Ubiquitin thioesterase 7) (Ubiquitin-specific-processing protease 7) (Deubiquitinating enzyme 7) (Herpesvirus-associated ubiquitin-specific protease).
657	Q9H2G2-2	9	22	10.3	1204	138995	5.1	Isoform 2 of Q9H2G2
657	Q9H2G2	9	22	10	1235	142695	5.1	STE20-like serine/threonine-protein kinase
658	O00203	9	21	9.9	1094	121350	6	AP-3 complex subunit beta-1
658	UPI00001AE77D	9	21	9.9	1094	121320	6	adaptor-related protein complex 3, beta 1 subunit
659	Q92878	9	18	9.2	1312	153892	6.9	DNA repair protein RAD50
659	UPI000045733E	9	18	9.2	1311	153750	6.9	DNA repair protein RAD50 (EC 3.6.-.-) (hRAD50).
659	Q92878-2	9	18	9.2	1318	154587	6.9	Isoform 2 of Q92878
660	Q5TBK6	9	22	8.5	1349	153670	7.8	LIM domain 7
660	Q8WWI1-3	9	22	8.5	1349	153684	7.8	Isoform 3 of Q8WWI1
660	UPI0000456709	9	22	7.1	1614	185153	8	LIM domain only protein 7 (LOMP) (F-box only protein 20).
660	Q8WWI1-4	9	22	7.1	1614	185229	8	Isoform 4 of Q8WWI1
660	UPI0000456708	9	22	6.9	1670	190813	7	LIM domain only protein 7 (LOMP) (F-box only protein 20).
660	Q8WWI1-2	9	22	6.9	1670	190889	7	Isoform 2 of Q8WWI1
660	UPI0000456707	9	22	6.8	1683	192754	8.1	LIM domain only protein 7 (LOMP) (F-box only protein 20).
660	Q8WWI1	9	22	6.8	1683	192708	8.1	LIM domain only protein 7
661	Q9UBG0	9	24	7.8	1479	166655	5.8	Macrophage mannose receptor 2 precursor
661	UPI000013E895	9	24	7.8	1479	166674	5.8	mannose receptor, C type 2
662	Q9C0C2	9	22	6.5	1729	181780	4.9	182 kDa tankyrase 1-binding protein
662	UPI000013DB72	9	22	6.5	1729	181795	4.9	tankyrase 1-binding protein 1
663	Q9Y5S2	9	10	6.1	1711	194314	6.4	Serine/threonine-protein kinase MRCK beta
664	Q14669	9	31	6	1992	220432	8.5	Probable E3 ubiquitin-protein ligase TRIP12
664	UPI0000456F1C	9	31	6	1991	220245	8.5	Thyroid receptor-interacting protein 12 (TRIP12).
664	Q14CA3	9	31	5.8	2040	225518	8.7	TRIP12 protein
665	Q149P0	9	22	5.1	1855	206015	5.8	GBF1 protein
665	Q92538	9	22	5.1	1859	206444	5.7	Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1

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666	UPI0000D62536	9	23	5.6	2142	232541	6	SON protein (SON3) (Negative regulatory element-binding protein) (NRE- binding protein) (DBP-5) (Bax antagonist selected in saccharomyces 1) (BASS1).
666	P18583-2	9	23	5.6	2140	232322	6	Isoform A of P18583
666	P18583-10	9	23	5.3	2282	247836	5.4	Isoform J of P18583
666	UPI0000140BF6	9	23	5.2	2325	252251	5.4	SON protein (SON3) (Negative regulatory element-binding protein) (NRE- binding protein) (DBP-5) (Bax antagonist selected in saccharomyces 1) (BASS1).
666	UPI000013E646	9	23	5.2	2303	250386	5.6	SON DNA-binding protein isoform B
666	P18583-4	9	23	5.2	2325	252267	5.4	Isoform C of P18583
666	P18583-3	9	23	5.2	2303	250402	5.6	Isoform B of P18583
666	UPI0000D62537	9	23	5	2388	259821	5.7	SON protein (SON3) (Negative regulatory element-binding protein) (NRE- binding protein) (DBP-5) (Bax antagonist selected in saccharomyces 1) (BASS1).
666	P18583-7	9	23	5	2386	259608	5.7	Isoform G of P18583
666	P18583	9	23	4.9	2426	263843	5.6	SON protein
666	UPI0000140BFD	9	23	4.9	2426	263827	5.6	SON DNA-binding protein isoform F
666	P18583-9	9	23	4.9	2466	268106	5.6	Isoform I of P18583
666	P18583-5	9	23	4.9	2459	267048	5.7	Isoform D of P18583
667	Q07954	9	17	2.3	4544	504579	5.4	Low-density lipoprotein receptor-related protein 1 precursor
667	UPI00001B044F	9	17	2.3	4544	504610	5.4	low density lipoprotein-related protein 1
668	Q9GZT3	8	70	64.2	109	12349	10.2	SRA stem-loop-interacting RNA-binding protein, mitochondrial precursor
669	P09382	8	570	61.5	135	14716	5.5	Galectin-1
670	Q96TD5	8	31	57.2	243	26349	4.7	P27BBP protein
670	P56537	8	31	56.7	245	26599	4.7	Eukaryotic translation initiation factor 6 (eIF-6) (B4 integrin interactor) (CAB) (p27(BBP)) (B(2)GCN homolog)
671	P51148	8	103	54.2	216	23483	8.4	Ras-related protein Rab-5C
672	P61981	8	128	53	247	28303	4.9	14-3-3 protein gamma
673	P19105	8	92	50.9	171	19794	4.8	Myosin regulatory light chain 2, nonsarcomeric
673	Q3THE2	8	92	50.6	172	19779	4.8	Myosin regulatory light chain 2-B, smooth muscle isoform
674	P62807	8	507	50.4	125	13819	10.3	Histone H2B type 1-C/E/F/G/I
674	A0AVI3	8	507	50	126	13916	10.3	H2B histone family, member S
674	Q99880	8	507	50	126	13952	10.3	Histone H2B type 1-L
674	Q99879	8	507	50	126	13989	10.3	Histone H2B type 1-M
674	Q99877	8	507	50	126	13922	10.3	Histone H2B type 1-N
674	Q93079	8	507	50	126	13892	10.3	Histone H2B type 1-H
674	Q5QNW6	8	507	50	126	13920	10.3	Histone H2B type 2-F
674	P58876	8	507	50	126	13936	10.3	Histone H2B type 1-D
674	P57053	8	507	50	126	13944	10.4	Histone H2B type F-S
674	O60814	8	507	50	126	13890	10.3	Histone H2B type 1-K
675	P51153	8	39	48.3	203	22774	9.2	Ras-related protein Rab-13
676	P63241	8	65	48.1	154	16832	5.2	Eukaryotic translation initiation factor 5A-1
676	P63241-2	8	65	40.2	184	20170	7	Isoform 2 of P63241

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677	Q9Y3B7	8	19	47.9	192	20683	9.9	39S ribosomal protein L11, mitochondrial precursor
678	P20340-2	8	58	47.1	208	23549	5.5	Isoform 2 of P20340
678	Q6FGX3	8	58	47.1	208	23550	5.4	RAB6A protein
679	P46783	8	124	46.7	165	18898	10.2	40S ribosomal protein S10
680	P61758	8	47	45.7	197	22658	7.1	Prefoldin subunit 3
681	P61224	8	86	45.1	184	20825	5.8	Ras-related protein Rap-1b precursor
682	UPI00004075C6	8	33	50.2	253	28226	6.8	S-formylglutathione hydrolase (EC 3.1.2.12) (FGH) (Esterase D).
682	P10768	8	33	45	282	31463	7	S-formylglutathione hydrolase
683	P35270	8	34	44.1	261	28048	8	Sepiapterin reductase
684	P29966	8	38	43.7	332	31555	4.4	Myristoylated alanine-rich C-kinase substrate
685	P47755	8	33	43.7	286	32949	5.8	F-actin capping protein subunit alpha-2
685	Q53GC7	8	33	43.7	286	32967	5.8	Capping protein (Actin filament) muscle Z-line, alpha 2 variant
686	P00492	8	43	43.6	218	24579	6.7	Hypoxanthine-guanine phosphoribosyltransferase
686	Q6LET3	8	43	43.6	218	24588	6.8	HPRT1 protein
687	P61586	8	72	43.5	193	21768	6.1	Transforming protein RhoA precursor
688	Q15286	8	43	43.3	201	23025	8.3	Ras-related protein Rab-35
688	UPI0000456691	8	43	43.3	201	23053	8	Ras-related protein Rab-35 (Rab-1C) (GTP-binding protein RAY).
689	P21964-2	8	51	52	221	24449	5.3	Isoform Soluble of P21964
689	P21964	8	51	42.4	271	30037	5.5	Catechol O-methyltransferase
689	Q6ICE6	8	51	42.4	271	30069	5.5	COMT protein
690	P04179	8	43	42.3	222	24722	8.3	Superoxide dismutase [Mn], mitochondrial precursor
690	UPI000006D275	8	43	42.3	222	24750	8.3	manganese superoxide dismutase isoform A precursor
691	Q99653	8	34	42.1	195	22456	5.1	Calcium-binding protein p22
692	P62917	8	132	42	257	28025	11	60S ribosomal protein L8
693	O95816	8	37	41.7	211	23772	6.7	BAG family molecular chaperone regulator 2
694	UPI00002263A8	8	57	44.8	183	20345	5.3	sorcin isoform b
694	P30626	8	57	41.4	198	21676	5.6	Sorcin
695	Q86V81	8	36	40.5	257	26888	11.2	THO complex subunit 4
696	Q9BVK6	8	73	40.2	214	25105	7.2	Transmembrane emp24 domain-containing protein 9 precursor
696	UPI00001D6EC0	8	73	36.6	235	27277	8	transmembrane emp24 protein transport domain containing 9
697	P37235	8	57	39.9	193	22313	5.4	Hippocalcin-like protein 1
698	Q9Y2Q3	8	41	39.8	226	25497	8.4	Glutathione S-transferase kappa 1
699	O43809	8	43	39.6	227	26227	8.8	Cleavage and polyadenylation specificity factor 5
700	P47985	8	68	39.4	274	29668	8.3	Ubiquinol-cytochrome c reductase iron-sulfur subunit, mitochondrial precursor
701	Q13185	8	54	39.3	183	20811	5.3	Chromobox protein homolog 3
702	UPI0000456411	8	69	40.8	238	25889	7.8	Thioredoxin-dependent peroxide reductase, mitochondrial precursor (EC 1.11.1.15) (Peroxiredoxin-3) (PRX III) (Antioxidant protein 1) (AOP-1) (Protein MER5 homolog) (HBC189).

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702	UPI00001B216B	8	69	40.8	238	25839	7.5	peroxiredoxin 3 isoform b
702	P30048	8	69	37.9	256	27693	7.8	Thioredoxin-dependent peroxide reductase, mitochondrial precursor
703	Q9NX63	8	78	37.9	227	26152	8.3	Coiled-coil-helix-coiled-coil-helix domain-containing protein 3
704	Q9UBQ7	8	30	39.3	328	35668	7.4	Glyoxylate reductase/hydroxypyruvate reductase
704	Q5M7Z5	8	30	37.8	341	36824	6.4	GRHPR protein
705	P53004	8	23	37.5	296	33428	6.4	Biliverdin reductase A precursor
706	P26373	8	86	37.4	211	24261	11.7	60S ribosomal protein L13
706	Q6NZ55	8	86	37.4	211	24265	11.7	Ribosomal protein L13
707	P40261	8	42	36	264	29574	5.7	Nicotinamide N-methyltransferase
708	Q99685	8	25	36	303	33261	7	Monoglyceride lipase
708	UPI0000D61B71	8	25	34.8	313	34305	6.7	Monoglyceride lipase (EC 3.1.1.23) (MGL) (HU-K5) (Lysophospholipase homolog) (Lysophospholipase-like).
709	P52565	8	43	35.3	204	23207	5.1	Rho GDP-dissociation inhibitor 1
710	P48556	8	23	34.2	257	30005	7.3	26S proteasome non-ATPase regulatory subunit 8
710	Q5U0B3	8	23	34.2	257	29922	7.3	Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 8
711	Q5TAM6	8	28	34.2	333	37805	5.2	SGT1, suppressor of G2 allele of SKP1
711	Q9Y2Z0	8	28	31.2	365	41024	5.2	Suppressor of G2 allele of SKP1 homolog
712	UPI000049DDE7	8	30	39.9	208	23873	3.9	Acidic leucine-rich nuclear phosphoprotein 32 family member A (Potent heat-stable protein phosphatase 2A inhibitor I1PP2A) (Acidic nuclear phosphoprotein pp32) (Leucine-rich acidic nuclear protein) (Lanp) (Putative HLA-DR-associated protein I) (PHAPI) (Ma
712	UPI000049DDE6	8	30	33.6	247	28325	4.1	Acidic leucine-rich nuclear phosphoprotein 32 family member A (Potent heat-stable protein phosphatase 2A inhibitor I1PP2A) (Acidic nuclear phosphoprotein pp32) (Leucine-rich acidic nuclear protein) (Lanp) (Putative HLA-DR-associated protein I) (PHAPI) (Ma
712	P39687	8	30	33.3	249	28585	4.1	Acidic leucine-rich nuclear phosphoprotein 32 family member A
712	Q53FK4	8	30	33.3	249	28557	4.1	Acidic (Leucine-rich) nuclear phosphoprotein 32 family, member A variant
713	P51665	8	39	33.3	324	37025	6.8	26S proteasome non-ATPase regulatory subunit 7
714	O00233	8	22	32.3	223	24654	7	26S proteasome non-ATPase regulatory subunit 9

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
714	UPI000013D207	8	22	32.3	223	24682	7	proteasome 26S non-ATPase subunit 9
715	Q13501	8	26	29.1	440	47687	5.2	Sequestosome-1
715	UPI0000D616D2	8	26	29	441	47822	5.4	Sequestosome-1 (Phosphotyrosine independent ligand for the Lck SH2 domain of 62 kDa) (Ubiquitin-binding protein p62) (EBI3-associated protein of 60 kDa) (p60) (EBIAP).
715	UPI0000D616D1	8	26	28.9	443	47871	5.4	Sequestosome-1 (Phosphotyrosine independent ligand for the Lck SH2 domain of 62 kDa) (Ubiquitin-binding protein p62) (EBI3-associated protein of 60 kDa) (p60) (EBIAP).
716	P36542	8	34	28.9	298	32996	9.2	ATP synthase gamma chain, mitochondrial precursor
717	Q9Y295	8	18	28.6	367	40542	8.9	Developmentally-regulated GTP-binding protein 1
718	P38919	8	28	28.5	411	46871	6.7	Eukaryotic initiation factor 4A-III
719	Q86UY0	8	25	28.3	360	40369	5.8	TXNDC5 protein
719	Q8NBS9	8	25	23.6	432	47629	6	Thioredoxin domain-containing protein 5 precursor
720	P23193	8	21	27.6	301	33970	8.4	Transcription elongation factor A protein 1
721	Q13561	8	13	26.4	401	44231	5.2	Dynactin subunit 2
721	UPI000045662F	8	13	26.1	406	44722	5.2	Dynactin subunit 2 (Dynactin complex 50 kDa subunit) (50 kDa dynein- associated polypeptide) (p50 dynamitin) (DCTN-50).
721	UPI000004EFD1	8	13	26.1	406	44820	5.2	dynactin 2
721	Q53H88	8	13	26.1	406	44821	5.1	Dynactin 2 variant
722	P43034	8	15	25.6	410	46638	7.4	Platelet-activating factor acetylhydrolase IB subunit alpha
723	O75874	8	24	25.1	414	46659	7	Isocitrate dehydrogenase [NADP] cytoplasmic (EC 1.1.1.42) (Cytosolic NADP-isocitrate dehydrogenase) (Oxalosuccinate decarboxylase) (IDH) (NADP(+)-specific ICDH)
723	Q7Z3V0	8	24	25.1	414	46527	7.2	Hypothetical protein DKFZp686M0959
723	Q6FIA4	8	24	25.1	414	46568	6.8	IDH1 protein
724	P04181	8	40	24.1	439	48535	7	Ornithine aminotransferase, mitochondrial precursor (EC 2.6.1.13) (Ornithine--oxo-acid aminotransferase) [Contains: Ornithine aminotransferase, hepatic form; Ornithine aminotransferase, renal form]
725	Q96S43	8	56	41.4	244	27191	8.6	JKTBP1delta6
725	Q7KZ75	8	56	33.6	301	33589	7.3	HnRNP JKTBP protein
725	O14979	8	56	24	420	46437	9.6	Heterogeneous nuclear ribonucleoprotein D-like
726	Q07960	8	22	23	439	50436	6.3	Rho GTPase-activating protein 1
727	Q9Y383	8	27	23	392	46514	10	Putative RNA-binding protein Luc7-like 2

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727	UPI000013D41E	8	27	22.4	401	47506	10	Putative RNA-binding protein Luc7-like 2.
728	Q13217	8	16	22.8	504	57580	6.2	DnaJ homolog subfamily C member 3
729	O15355	8	45	21.6	546	59272	4.4	Protein phosphatase 2C isoform gamma
730	P08559	8	15	20.8	390	43296	8.1	Pyruvate dehydrogenase E1 component alpha subunit, somatic form, mitochondrial precursor
731	O95747	8	15	20.3	527	58022	6.4	Serine/threonine-protein kinase OSR1
732	Q96HE7	8	20	20.3	468	54393	5.7	ERO1-like protein alpha precursor
733	Q9HCJ6	8	16	20	419	45899	5.1	Probable oxidoreductase KIAA1576
734	O43175	8	13	19.9	533	56651	6.7	D-3-phosphoglycerate dehydrogenase
735	O95340	8	12	19.5	614	69501	8	Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthetase 2 (PAPS synthetase 2) (PAPSS 2) (Sulfurylase kinase 2) (SK2) (SK 2) [Includes: Sulfate adenylyltransferase (EC 2.7.7.4) (Sulfate adenylate transferase) (SAT) (ATP-sulfurylase); Adenylyl-sulfate kinase (EC 2.7.1.25) (Adenylylsulfate 3'-phosphotransferase) (APS kinase) (Adenosine-5'-phosphosulfate 3'-phosphotransferase) (3'-phosphoadenosine-5'-phosphosulfate synthetase)]
735	UPI000049DD01	8	12	19.4	619	70062	8.2	Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthetase 2 (PAPS synthetase 2) (PAPSS 2) (Sulfurylase kinase 2) (SK2) (SK 2) [Includes: Sulfate adenylyltransferase (EC 2.7.7.4) (Sulfate adenylate transferase) (SAT) (ATP-sulfurylase); Adenylyl-sulfate
735	O95340-2	8	12	19.4	619	69970	8	Isoform B of O95340
736	Q9UHG3	8	18	19.4	505	56640	6.2	Prenylcysteine oxidase precursor
736	UPI000013D518	8	18	19.4	505	56700	6.2	prenylcysteine oxidase 1
737	P61619-2	8	89	21	423	46045	7.3	Isoform 2 of P61619
737	P61619	8	89	18.7	476	52265	8.1	Protein transport protein Sec61 subunit alpha isoform 1
738	O95302	8	21	18.2	570	63084	5.1	FK506-binding protein 9 precursor
739	Q16222-2	8	19	18.2	505	57028	6.4	Isoform AGX1 of Q16222
739	Q16222-3	8	19	17.7	521	58682	6.3	Isoform 3 of Q16222

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739	Q16222	8	19	17.6	522	58769	6.3	UDP-N-acetylhexosamine pyrophosphorylase (Antigen X) (AGX) (Sperm- associated antigen 2) [Includes: UDP-N-acetylgalactosamine pyrophosphorylase (EC 2.7.7.-) (AGX-1); UDP-N-acetylglucosamine pyrophosphorylase (EC 2.7.7.23) (AGX-2)]
740	P17812	8	32	17.3	591	66690	6.5	CTP synthase 1
741	Q5SSJ5	8	33	16.3	553	61207	9.7	Heterochromatin protein 1, binding protein 3
741	UPI0000D61E73	8	33	16.2	555	61434	9.7	HP1-BP74
742	Q69YH4	8	36	16.2	622	70064	8.7	Hypothetical protein DKFZp666E065
742	UPI00003FF926	8	36	14.7	689	77151	9.1	hypothetical protein LOC54867 isoform 1
743	Q96JZ5	8	47	16.1	545	62941	7.5	CDNA FLJ14882 fis, clone PLACE1003537, weakly similar to ENDOSOMAL P24A PROTEIN
743	UPI0000169B24	8	47	14.9	589	67870	7.2	transmembrane 9 superfamily member 3
743	Q9HD45	8	47	14.9	589	67888	7.2	Transmembrane 9 superfamily protein member 3 precursor
744	UPI0000456CFE	8	17	15.7	955	105371	7.9	AP-2 complex subunit alpha-1 (Adapter-related protein complex 2 alpha- 1 subunit) (Alpha-adaptin A) (Adaptor protein complex AP-2 alpha-1 subunit) (Clathrin assembly protein complex 2 alpha-A large chain) (100 kDa coated vesicle protein A) (Plasma membran
744	UPI0000037C08	8	17	15.7	955	105361	7.7	adaptor-related protein complex 2, alpha 1 subunit isoform 2
744	O95782-2	8	17	15.7	955	105370	7.7	Isoform B of O95782
744	O95782	8	17	15.4	977	107555	7.1	AP-2 complex subunit alpha-1
744	UPI0000456CFD	8	17	15.4	977	107555	7.3	AP-2 complex subunit alpha-1 (Adapter-related protein complex 2 alpha- 1 subunit) (Alpha-adaptin A) (Adaptor protein complex AP-2 alpha-1 subunit) (Clathrin assembly protein complex 2 alpha-A large chain) (100 kDa coated vesicle protein A) (Plasma membran
744	UPI0000167B50	8	17	15.4	977	107546	7	adaptor-related protein complex 2, alpha 1 subunit isoform 1
745	P50443	8	42	15.2	739	81649	8.4	Sulfate transporter
745	UPI000013DE3D	8	42	15.2	739	81662	8.4	solute carrier family 26 member 2
746	Q12874	8	9	15.2	501	58849	5.4	Splicing factor 3A subunit 3
746	Q53HM6	8	9	15.2	501	58877	5.4	Splicing factor 3a, subunit 3 variant
747	P11166	8	50	14	492	54084	8.7	Solute carrier family 2, facilitated glucose transporter member 1

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747	UPI000004F0B2	8	50	14	492	54118	8.7	solute carrier family 2 (facilitated glucose transporter), member 1
747	Q0P512	8	50	14	492	54054	8.9	Solute carrier family 2 (Facilitated glucose transporter), member 1
748	Q9NVP1	8	22	13.6	670	75407	9.5	ATP-dependent RNA helicase DDX18
749	Q53FR4	8	30	13.3	796	91681	5.5	Vacuolar protein sorting 35 variant
749	Q96QK1	8	30	13.3	796	91707	5.5	Vacuolar protein sorting-associated protein 35
750	Q9NTJ5	8	39	13.5	587	66979	7.3	Hypothetical protein DKFZp434O1328
750	Q96AX7	8	39	13.5	587	66951	7.1	SAC1 suppressor of actin mutations 1-like
750	O94935	8	39	13	607	69474	8	SAC1 suppressor of actin mutations 1-like protein
751	UPI00004703AF	8	60	50	140	15079	8.9	sterol carrier protein 2 isoform 2 precursor
751	P22307-2	8	60	49	143	15401	8.9	Isoform SCP2 of P22307
751	P22307	8	60	12.8	547	58994	6.9	Nonspecific lipid-transfer protein
752	Q1KMD3	8	22	12.7	747	85105	4.9	Heterogeneous nuclear ribonucleoprotein U-like protein 2
753	UPI0000D62355	8	20	12.7	739	82092	6.8	Vesicle-fusing ATPase (EC 3.6.4.6) (Vesicular-fusion protein NSF) (N- ethylmaleimide sensitive fusion protein) (NEM-sensitive fusion protein).
753	P46459	8	20	12.6	744	82560	7	Vesicle-fusing ATPase
754	P46977	8	82	12.6	705	80472	8.2	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A
754	Q8WUB4	8	82	12.6	705	80530	8.1	STT3, subunit of the oligosaccharyltransferase complex, homolog A
755	O60763	8	27	12.4	962	107895	4.9	General vesicular transport factor p115
755	UPI00001382BE	8	27	12.4	962	107907	4.9	vesicle docking protein p115
755	Q86TB8	8	27	12.2	973	109187	4.9	Hypothetical protein DKFZp451D234
756	Q9H5A4	8	271	26	338	36733	5.4	CD44 molecule
756	P16070-14	8	271	22.2	396	43157	5.3	Isoform 14 of P16070
756	P16070-13	8	271	20.7	425	46249	5.2	Isoform 13 of P16070
756	P16070-11	8	271	20.5	429	46565	5.7	Isoform 11 of P16070
756	Q9H5A6	8	271	18.7	470	50728	5.4	CD44 molecule
756	UPI000037848D	8	271	17.8	493	53411	5.4	CD44 antigen isoform 3 precursor
756	P16070-10	8	271	17.8	493	53399	5.4	Isoform 10 of P16070
756	P16070-16	8	271	13.2	668	73138	5.4	Isoform 16 of P16070
756	P16070-8	8	271	13.1	674	74404	5.2	Isoform 8 of P16070
756	Q9H5A7	8	271	13	676	73929	5.3	CD44 molecule
756	P16070-17	8	271	12.7	691	75945	5.3	Isoform 17 of P16070
756	UPI000037848C	8	271	12.6	699	76612	5.3	CD44 antigen isoform 2 precursor
756	P16070-6	8	271	12.6	699	76692	5.3	Isoform 6 of P16070
756	P16070-4	8	271	12.6	699	76628	5.3	Isoform 4 of P16070
756	P16070-3	8	271	12.4	711	77999	5.4	Isoform 3 of P16070
756	P16070-7	8	271	12.3	713	78461	5.4	Isoform 7 of P16070
756	Q9H5A5	8	271	12.2	719	78854	5.3	CD44 molecule

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756	P16070-5	8	271	12	734	80806	5.3	Isoform 5 of P16070
756	P16070	8	271	11.9	742	81554	5.3	CD44 antigen precursor
756	UPI000013D3FE	8	271	11.9	742	81538	5.3	CD44 antigen isoform 1 precursor
757	Q9GZV0	8	32	11.9	767	85730	6.3	CDNA FLJ12466 fis, clone NT2RM1000826, highly similar to UNR PROTEIN
757	O75534-2	8	32	11.9	767	85747	6.2	Isoform Short of O75534
757	O75534	8	32	11.4	798	88885	6.2	Cold shock domain-containing protein E1
757	UPI0000456228	8	32	11.4	798	88986	6.5	GTPase NRas precursor (Transforming protein N-Ras).
757	UPI0000D61F93	8	32	11.2	813	90706	6.7	GTPase NRas precursor (Transforming protein N-Ras).
757	Q68DF1	8	32	11.2	813	90555	6.5	Hypothetical protein DKFZp779B0247
758	Q8TEX9-2	8	29	12.3	1083	118901	4.9	Isoform 2 of Q8TEX9
758	Q8TEX9	8	29	12.3	1081	118715	5	Importin-4
758	Q59FI4	8	29	10.5	1264	138200	5.3	Importin 4 variant
759	Q5TG62	8	21	9.8	971	109421	7.9	KIAA0090
759	Q8N766-2	8	21	9.6	992	111631	7.7	Isoform 2 of Q8N766
759	Q8N766	8	21	9.6	993	111759	7.7	Uncharacterized protein KIAA0090 precursor
760	UPI00001AFA18	8	20	9.7	979	111479	7.6	Probable ATP-dependent RNA helicase DHX36 (EC 3.6.1.-) (DEAH box protein 36) (MLE-like protein 1) (RNA helicase associated with AU-rich element ARE).
760	Q9H2U1-3	8	20	9.7	979	111495	7.6	Isoform 3 of Q9H2U1
760	Q9H2U1-2	8	20	9.6	994	113169	7.7	Isoform 2 of Q9H2U1
760	Q9H2U1	8	20	9.4	1008	114776	7.7	Probable ATP-dependent RNA helicase DHX36
760	UPI000013ED25	8	20	9.4	1008	114760	7.7	Probable ATP-dependent RNA helicase DHX36 (EC 3.6.1.-) (DEAH box protein 36) (MLE-like protein 1) (RNA helicase associated with AU-rich element ARE).
761	O95486	8	29	9.2	1078	118792	8.1	Protein transport protein Sec24A
761	UPI0000457346	8	29	9.2	1077	118677	8.2	Protein transport protein Sec24A (SEC24-related protein A)
761	UPI0000185FF9	8	29	9.1	1093	119749	7.7	SEC24 related gene family, member A
762	Q9UP95	8	27	8.8	1085	120650	6.4	Solute carrier family 12 member 4
763	Q9NPK3	8	28	8.8	1245	137624	6.1	DJ34F7.7 (Superkiller viralicidic activity 2 (S. cerevisiae homolog)-like (SKI2W))
763	O76046	8	28	8.7	1246	137794	6.1	Putative RNA helicase Ski2w
763	Q5ST66	8	28	8.7	1246	137755	6.1	Superkiller viralicidic activity 2-like
763	Q5JP73	8	28	8.7	1246	137737	6.1	Superkiller viralicidic activity 2-like
763	Q15477	8	28	8.7	1246	137799	6.1	Helicase SKI2W
764	UPI00003E59F4	8	21	10.9	836	95843	6	SLIT-ROBO Rho GTPase activating protein 2 isoform b
764	A2RUF3	8	21	8.5	1071	120870	6.7	SLIT-ROBO Rho GTPase activating protein 2
764	O75044	8	21	8.5	1071	120880	6.7	SLIT-ROBO Rho GTPase-activating protein 2

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765	Q96F88	8	29	8.4	1024	114681	9.2	Processing of 1, ribonuclease P/MRP subunit
765	Q99575	8	29	8.4	1024	114709	9.2	Ribonucleases P/MRP protein subunit POP1
766	Q53RX7	8	29	8.4	1073	119476	6.8	Hypothetical protein ITGA6
766	P23229-4	8	29	8.4	1068	119074	7.3	Isoform Alpha
766	P23229-2	8	29	8.4	1073	119462	6.8	Isoform Alpha
766	UPI0000366FA3	8	29	8.3	1086	121665	7.4	Integrin alpha-6 precursor (VLA-6) (CD49f antigen) [Contains: Integrin alpha-6 heavy chain; Integrin alpha-6 light chain].
766	P23229-5	8	29	8.3	1086	121678	7.6	Isoform Alpha
766	UPI0000EA87E5	8	29	8.2	1091	122053	6.8	integrin alpha chain, alpha 6 isoform a precursor
766	P23229-3	8	29	8.2	1091	122066	7	Isoform Alpha
766	UPI0000D6126A	8	29	8.1	1112	124028	6.6	Integrin alpha-6 precursor (VLA-6) (CD49f antigen) [Contains: Integrin alpha-6 heavy chain; Integrin alpha-6 light chain].
766	P23229-6	8	29	8.1	1112	124014	6.6	Isoform Alpha
766	P23229	8	29	8	1130	126618	6.8	Integrin alpha-6 precursor (VLA-6) (CD49f antigen) [Contains: Integrin alpha-6 heavy chain; Integrin alpha-6 light chain]
766	UPI000013D4BA	8	29	8	1130	126605	6.6	Integrin alpha-6 precursor (VLA-6) (CD49f antigen) [Contains: Integrin alpha-6 heavy chain; Integrin alpha-6 light chain].
767	O75153	8	15	7.9	1309	146669	6.1	Putative eukaryotic translation initiation factor 3 subunit
767	UPI0000D622A0	8	15	7.9	1310	146826	6.2	Putative eukaryotic translation initiation factor 3 subunit (eIF-3).
768	O15067	8	14	7.8	1338	144664	5.8	Phosphoribosylformylglycinamidine synthase
768	UPI00001A95E5	8	14	7.8	1338	144734	5.8	phosphoribosylformylglycinamidine synthase
769	UPI0000D625ED	8	34	8.3	1316	149100	5.6	Nuclear pore complex protein Nup160 (Nucleoporin Nup160) (160 kDa nucleoporin).
769	Q12769	8	34	8.3	1316	149001	5.6	Nuclear pore complex protein Nup160
769	Q08AD3	8	34	7.6	1436	162091	5.5	Nucleoporin 160kDa
769	UPI0000185FEB	8	34	7.6	1436	162121	5.5	nucleoporin 160kDa
770	Q9Y6M7-4	8	37	8.9	1000	112448	7.1	Isoform 4 of Q9Y6M7
770	UPI0000D61AE5	8	37	8.8	1017	114060	6.8	Sodium bicarbonate cotransporter 3 (Sodium bicarbonate cotransporter 2) (Sodium bicarbonate cotransporter 2b) (Bicarbonate transporter) (Solute carrier family 4 member 7).
770	Q9Y6M7-3	8	37	8.7	1018	114205	7.3	Isoform 3 of Q9Y6M7
770	UPI0000D61AE4	8	37	8.2	1092	123253	6.9	Sodium bicarbonate cotransporter 3 (Sodium bicarbonate cotransporter 2) (Sodium bicarbonate cotransporter 2b) (Bicarbonate transporter) (Solute carrier family 4 member 7).
770	Q9Y6M7-2	8	37	8.2	1090	123081	6.9	Isoform 2 of Q9Y6M7
770	Q9Y6M7	8	37	7.3	1214	136043	6.8	Sodium bicarbonate cotransporter 3

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770	UPI0000DBEEB7	8	37	7.3	1214	136044	6.7	solute carrier family 4, sodium bicarbonate cotransporter, member 7
770	UPI0000D61AE3	8	37	7.3	1224	137157	6.8	Sodium bicarbonate cotransporter 3 (Sodium bicarbonate cotransporter 2) (Sodium bicarbonate cotransporter 2b) (Bicarbonate transporter) (Solute carrier family 4 member 7).
771	Q9UKV3	8	25	7.1	1341	151887	6.4	Apoptotic chromatin condensation inducer in the nucleus
771	UPI000013D308	8	25	7.1	1341	151861	6.4	Apoptotic chromatin condensation inducer in the nucleus (Acinus).
772	O15085	8	18	6.4	1522	167704	5.5	Rho guanine nucleotide exchange factor 11
772	UPI0000456283	8	18	6.2	1560	172038	5.6	Rho guanine nucleotide exchange factor 11 (PDZ-RhoGEF).
772	Q6PFW2	8	18	6.2	1562	172243	5.5	Rho guanine nucleotide exchange factor (GEF) 11
773	Q53SJ7	8	16	6.2	1337	155520	6	Hypothetical protein ROCK2
773	O75116	8	16	6	1388	160912	6	Rho-associated protein kinase 2
773	UPI000049DEE3	8	16	6	1388	160981	6.2	Rho-associated protein kinase 2 (EC 2.7.11.1) (Rho-associated, coiled- coil-containing protein kinase 2) (p164 ROCK-2) (Rho kinase 2).
773	UPI000034ECB0	8	16	6	1388	160899	6	Rho-associated, coiled-coil containing protein kinase 2
774	Q5UIP0	8	13	4.8	2472	274464	5.5	Telomere-associated protein RIF1
774	UPI0000D6124A	8	13	4.8	2448	271915	5.4	Telomere-associated protein RIF1 (Rap1-interacting factor 1 homolog).
774	UPI0000D61249	8	13	4.8	2474	274691	5.5	Telomere-associated protein RIF1 (Rap1-interacting factor 1 homolog).
774	Q5UIP0-2	8	13	4.8	2446	271688	5.4	Isoform 2 of Q5UIP0
775	UPI00006C1433	8	11	4.2	2146	241643	6.6	PREDICTED: similar to YLP motif-containing protein 1 (Nuclear protein ZAP3) (ZAP113) isoform 2
776	Q63HN8	8	10	3.1	3280	373981	6.9	RING finger protein 213
776	UPI0000D623A6	8	10	3.1	3279	373852	6.9	CDNA FLJ13809 fis, clone THYRO1000270 (C17orf27 protein).
777	Q14789	8	14	2.9	3259	376019	5	Golgin subfamily B member 1
777	UPI000012B42C	8	14	2.9	3259	376078	5	golgi autoantigen, golgin subfamily b, macrogolgin (with transmembrane signal), 1
778	O75368	7	42	71.1	114	12774	5.2	SH3 domain-binding glutamic acid-rich-like protein
779	P62888	7	110	59.1	115	12784	9.6	60S ribosomal protein L30
780	P61326	7	34	58.9	146	17164	6.1	Protein mago nashi homolog
780	Q96A72	7	34	58.1	148	17276	6.4	Protein mago nashi homolog 2
781	P62244	7	120	58.5	130	14839	10.1	40S ribosomal protein S15a
782	Q2YDC2	7	33	57.1	189	21664	5.4	Programmed cell death 6
782	O75340	7	33	56.5	191	21868	5.4	Programmed cell death protein 6

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
783	Q8NBT2	7	26	55.8	197	22443	4.7	Kinetochore protein Spc24
784	Q9UHV9	7	33	54.5	154	16648	6.6	Prefoldin subunit 2
785	P46405	7	49	53.8	132	14515	7.2	40S ribosomal protein S12
786	Q9ULC4	7	39	52.5	181	20555	8.8	Malignant T cell amplified sequence 1
787	Q9NVJ2	7	28	51.6	186	21539	8.4	ADP-ribosylation factor-like protein 8B
788	P10599	7	146	51.4	105	11737	4.9	Thioredoxin
789	Q01469	7	43	49.6	135	15164	7	Fatty acid-binding protein, epidermal
790	Q9UBQ5	7	67	49.1	218	25060	4.9	Eukaryotic translation initiation factor 3 subunit 12
791	P61006	7	24	48.8	207	23668	9.1	Ras-related protein Rab-8A
792	P16949	7	90	48.3	149	17302	6	Stathmin
793	Q9BSD7	7	19	47.9	190	20713	9.5	Probable UPF0334 kinase-like protein C1orf57
794	Q9NYG7	7	96	50.3	179	19718	5.4	Bax-sigma
794	Q07812	7	96	46.9	192	21184	5.2	Apoptosis regulator BAX, membrane isoform alpha
794	Q07814	7	96	41.3	218	24220	7.9	Apoptosis regulator BAX, cytoplasmic isoform beta
795	P30044	7	78	44.4	214	22026	8.6	Peroxiredoxin-5, mitochondrial precursor
795	UPI000013D62C	7	78	44.4	214	22086	8.7	Peroxiredoxin-5, mitochondrial precursor (EC 1.11.1.15) (Prx-V) (Peroxisomal antioxidant enzyme) (PLP) (Thioredoxin reductase) (Thioredoxin peroxidase PMP20) (Antioxidant enzyme B166) (AOEB166) (TPx type VI) (Liver tissue 2D-page spot 71B) (Alu corepresso
796	P62158	7	89	44.3	149	16838	4.2	Calmodulin
797	Q9BUF5	7	25	43.7	446	49857	4.9	Tubulin beta-6 chain
798	P31150	7	25	43	447	50583	5.1	Rab GDP dissociation inhibitor alpha
799	Q53F37	7	21	42.4	198	22410	6.1	SAR1a gene homolog 2 variant
799	Q9Y6B6	7	21	42.4	198	22410	6.1	GTP-binding protein SAR1b
800	P04632	7	73	41.4	268	28316	5.2	Calpain small subunit 1
801	P62277	7	92	41.1	151	17222	10.5	40S ribosomal protein S13
802	P25789	7	26	40.6	261	29484	7.7	Proteasome subunit alpha type 4
803	P46779	7	95	40.1	137	15747	12	60S ribosomal protein L28
804	P02792	7	79	40	175	20020	5.8	Ferritin light chain
804	Q96CU0	7	79	40	175	20039	5.8	Ferritin, light polypeptide
804	Q8WU07	7	79	40	175	20062	5.8	Ferritin, light polypeptide
804	Q6IBT7	7	79	40	175	19992	5.8	Ferritin
805	Q6IPF4	7	59	39.9	366	38651	6.8	Poly(RC) binding protein 2
805	UPI0000456618	7	59	39.9	366	38634	6.8	Poly(rC)-binding protein 2 (Alpha-CP2) (hnRNP-E2).
806	P63000	7	46	43.2	192	21450	8.5	Ras-related C3 botulinum toxin substrate 1 precursor
806	A4D2P0	7	46	39.3	211	23467	8.6	Ras-related C3 botulinum toxin substrate 1
807	Q9NWU5	7	15	39.3	206	23641	9.9	39S ribosomal protein L22, mitochondrial precursor
807	UPI000013D5D9	7	15	35.7	227	26063	9.6	39S ribosomal protein L22, mitochondrial precursor (L22mt) (MRP-L22).
808	O95336	7	18	39.1	258	27547	6.1	6-phosphogluconolactonase
809	Q0QEW2	7	90	44.5	164	18732	11.8	Ribosomal protein L18
809	Q07020	7	90	38.8	188	21634	11.7	60S ribosomal protein L18

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810	P51858	7	34	37.5	240	26788	4.7	Hepatoma-derived growth factor
811	P08579	7	48	37.3	225	25486	9.7	U2 small nuclear ribonucleoprotein B''
812	Q9UL25	7	41	37.3	225	24348	7.9	Ras-related protein Rab-21
813	Q969H8	7	77	37	173	18795	6.7	Uncharacterized protein C19orf10 precursor
814	O14579	7	24	36	308	34482	5.1	Coatomer subunit epsilon
814	Q9UGP6	7	24	36	308	34494	5.1	Epsilon COP
814	Q53HJ6	7	24	36	308	34528	5.1	Epsilon subunit of coatomer protein complex isoform a variant
815	Q6IPH7	7	68	35.5	220	23787	10.9	RPL14 protein
816	Q9NRX2	7	16	35.4	175	20050	10.1	39S ribosomal protein L17, mitochondrial precursor
817	P49755	7	132	35.2	219	24976	7.5	Transmembrane emp24 domain-containing protein 10 precursor
817	Q53GF9	7	132	34.2	225	25637	6.7	Full-length cDNA 5-PRIME end of clone CS0DF013YM24 of Fetal brain of Homo sapiens (Human) variant
818	Q15404	7	21	34.7	277	31540	8.6	Ras suppressor protein 1
819	UPI000013D771	7	12	34.7	357	38325	8	Sorbitol dehydrogenase (EC 1.1.1.14) (L-iditol 2-dehydrogenase).
820	Q9BRG1	7	26	33.5	176	20748	6.3	Vacuolar protein sorting-associated protein 25
821	Q9BUP3	7	24	33.5	242	27118	8.6	Oxidoreductase HTATIP2
822	Q9Y3A5	7	37	32.4	250	28764	8.7	Shwachman-Bodian-Diamond syndrome protein
823	P52597	7	29	32.3	415	45672	5.6	Heterogeneous nuclear ribonucleoprotein F
824	Q9UKD2	7	13	32.2	239	27560	8.3	mRNA turnover protein 4 homolog
825	Q13242	7	22	32.1	221	25542	8.6	Splicing factor, arginine/serine-rich 9
826	Q14257	7	32	31.9	317	36876	4.4	Reticulocalbin-2 precursor
827	Q14696	7	25	31.2	234	26077	7.8	Mesoderm development candidate 2
828	Q6IBS0	7	26	31.2	349	39548	6.9	Twinfilin-2
829	P39748	7	15	31.1	380	42593	8.6	Flap endonuclease 1
830	P06748-2	7	178	34.3	265	29465	4.6	Isoform 2 of P06748
830	P06748	7	178	31	294	32575	4.8	Nucleophosmin
831	Q9NX40	7	26	31	245	27626	7.5	OCIA domain-containing protein 1
832	P50479	7	14	30.6	330	35398	7.9	PDZ and LIM domain protein 4
833	P31937	7	20	29.8	336	35329	8.1	3-hydroxyisobutyrate dehydrogenase, mitochondrial precursor
834	Q13011	7	26	28.7	328	35816	8	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial precursor
835	P62753	7	75	28.5	249	28681	10.8	40S ribosomal protein S6
835	Q96DV6	7	75	28.5	249	28709	10.9	Ribosomal protein S6
836	UPI00006C0D04	7	26	28.4	370	40821	8.9	PREDICTED: similar to Actin-related protein 2/3 complex subunit 1B (ARP2/3 complex 41 kDa subunit) (p41-ARC)
836	O15143	7	26	28.2	372	40950	8.4	Actin-related protein 2/3 complex subunit 1B
837	Q12771	7	78	28	286	31481	7.4	P37 AUF1
837	Q14103-4	7	78	27.9	287	30672	8.4	Isoform 4 of Q14103
837	Q14103-3	7	78	26.1	306	32835	8.2	Isoform 3 of Q14103

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837	UPI0000D6158B	7	78	24.2	330	36464	8.5	Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1).
837	Q14103-2	7	78	23.8	336	36272	8.1	Isoform 2 of Q14103
837	Q14103	7	78	22.5	355	38434	7.8	Heterogeneous nuclear ribonucleoprotein D0
838	Q15717	7	68	27.3	326	36092	9.2	ELAV-like protein 1
839	P62873	7	34	27.1	340	37377	6	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1
840	O43684	7	26	26.8	328	37155	6.8	Mitotic checkpoint protein BUB3
841	P30443	7	30	26.8	365	40846	6.5	HLA class I histocompatibility antigen, A-1 alpha chain precursor
841	P30455	7	30	26.8	365	40934	6.4	HLA class I histocompatibility antigen, A-36 alpha chain precursor
842	P61289	7	44	26.8	254	29506	6	Proteasome activator complex subunit 3
842	P61289-2	7	44	25.5	267	30887	6.1	Isoform 2 of P61289
843	Q8TBC0	7	19	30.4	342	39732	5.6	Similar to GNAS complex locus
843	Q14433	7	19	27.4	379	44179	6.3	Guanine nucleotide-binding protein G-s-alpha-3
843	P63092-2	7	19	27.4	380	44266	6.3	Isoform Gnas
843	P63092	7	19	26.4	394	45665	5.8	Guanine nucleotide-binding protein G(s) subunit alpha isoforms short
843	UPI000004D202	7	19	26.3	395	45752	5.8	GNAS complex locus isoform f
843	UPI0000D610C3	7	19	21.5	484	54674	8.9	Neuroendocrine secretory protein 55 (NESP55) [Contains: LHAL tetrapeptide; GPIPIRRH peptide].
843	UPI0000D610C1	7	19	14.4	721	78734	5.8	Neuroendocrine secretory protein 55 (NESP55) [Contains: LHAL tetrapeptide; GPIPIRRH peptide].
843	UPI00004A39FA	7	19	14.4	722	78821	5.8	Neuroendocrine secretory protein 55 (NESP55) [Contains: LHAL tetrapeptide; GPIPIRRH peptide].
843	UPI0000456FBC	7	19	11.5	908	97549	5.3	Neuroendocrine secretory protein 55 (NESP55) [Contains: LHAL tetrapeptide; GPIPIRRH peptide].
843	Q5JWF2-2	7	19	10.2	1023	109626	5.1	Isoform XLas
843	Q5JWF2	7	19	10	1037	111024	5	Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas
844	Q7Z518	7	13	26.3	354	40677	8.5	NADH dehydrogenase
844	O95299	7	13	26.2	355	40751	8.5	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial precursor
844	Q5R9E8	7	13	26.2	355	40719	8.5	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial precursor
845	P25788-2	7	33	26.6	248	27647	5.3	Isoform 2 of P25788
845	P25788	7	33	25.9	255	28433	5.3	Proteasome subunit alpha type 3
845	Q6IB71	7	33	25.9	255	28415	5.3	Proteasome subunit alpha type

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846	P68400	7	14	25.3	391	45144	7.7	Casein kinase II subunit alpha
846	UPI0000D61015	7	14	25.1	395	45682	7.9	Casein kinase II subunit alpha (EC 2.7.11.1) (CK II).
846	Q5U5J2	7	14	24.9	397	45909	7.9	CSNK2A1 protein
847	Q8TDN6	7	19	24.9	353	41401	9.9	Brix domain-containing protein 2
848	P31350	7	16	24.7	389	44878	5.4	Ribonucleoside-diphosphate reductase M2 subunit
849	Q16543	7	26	24.6	378	44468	5.2	Hsp90 co-chaperone Cdc37
850	Q8WXE8	7	23	24.4	393	45571	6.6	Paraspeckle protein 1 beta isoform
850	Q8WXF1	7	23	18.4	523	58744	6.7	Paraspeckle component 1
851	P35237	7	12	24.2	376	42590	5.3	Serpin B6
851	Q5TD06	7	12	24.2	376	42622	5.3	Serpin peptidase inhibitor, clade B (Ovalbumin), member 6
851	Q59F97	7	12	23.2	393	44446	5.2	Hypothetical protein
851	UPI0000D613D8	7	12	22.2	409	46331	5.9	Serpin B6 (Placental thrombin inhibitor) (Cytoplasmic antiproteinase) (CAP) (Protease inhibitor 6) (PI-6).
852	P24752	7	24	23	427	45200	8.8	Acetyl-CoA acetyltransferase, mitochondrial precursor
853	P49585	7	25	22.6	367	41732	6.9	Choline-phosphate cytidylyltransferase A
853	Q86Y88	7	25	22.6	367	41731	7.3	Phosphate cytidylyltransferase 1, choline, alpha
854	A0PJ61	7	33	22.5	440	49490	10.1	Hypothetical protein
854	Q32Q62	7	33	21.3	464	52165	10.2	RSL1D1 protein
854	O76021	7	33	20.2	490	54973	10.1	Ribosomal L1 domain-containing protein 1
855	P53007	7	16	22.5	311	34013	9.9	Tricarboxylate transport protein, mitochondrial precursor
855	Q6LAP8	7	16	22	318	34788	9.9	Mitochondrial citrate transport protein
856	O43237	7	16	22.4	492	54099	6.4	Cytoplasmic dynein 1 light intermediate chain 2
857	Q7Z503	7	15	24.1	403	43611	5.6	Beta-succinyl CoA synthetase
857	Q5T9Q6	7	15	22	441	48040	7.1	Succinate-CoA ligase, ADP-forming, beta subunit
857	Q9P2R7	7	15	21	463	50317	7.4	Succinyl-CoA ligase [ADP-forming] beta-chain, mitochondrial precursor
858	O60884	7	14	21.8	412	45746	6.5	DnaJ homolog subfamily A member 2
859	O75367-2	7	20	22	369	39183	9.8	Isoform 1 of O75367
859	O75367	7	20	21.8	372	39617	9.8	Core histone macro-H2A.1
860	Q9UM22	7	26	33	224	25437	6.7	Mammalian ependymin-related protein 1 precursor
860	A4D1W8	7	26	21.5	344	38151	9.6	Upregulated in colorectal cancer gene 1
860	Q96J80	7	26	21.5	344	38141	9.6	Mammalian ependymin related protein 1
861	Q5U8W9	7	22	21.4	327	37557	5.7	Protein arginine methyltransferase 1 isoform 4
861	Q2VP93	7	22	20.4	343	39602	5.6	Protein arginine methyltransferase 1
861	Q99873-3	7	22	20.4	343	39572	5.7	Isoform 3 of Q99873
861	Q99873-2	7	22	20.2	347	39899	5.7	Isoform 2 of Q99873
861	Q6LEU5	7	22	20.2	347	39929	5.6	HRMT1L2 protein
861	Q8WUW5	7	22	19.9	352	40417	5.5	PRMT1 protein

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861	UPI000013CBFF	7	22	19.5	359	41255	5.5	Protein arginine N-methyltransferase 1 (EC 2.1.1.-) (Interferon receptor 1-bound protein 4).
861	Q99873	7	22	19.4	361	41486	5.5	Protein arginine N-methyltransferase 1
862	P49257	7	87	20.2	510	57549	6.8	ERGIC-53 protein precursor
862	Q53FS4	7	87	20.2	510	57558	6.8	Lectin, mannose-binding, 1 variant
863	Q6NZI2	7	43	20	390	43476	5.6	Polymerase I and transcript release factor
864	Q05DA4	7	11	21	504	57378	5.6	P4HA2 protein
864	Q5HYD8	7	11	19.9	533	60617	5.7	Hypothetical protein DKFZp686M0919
864	O15460-2	7	11	19.9	533	60633	5.7	Isoform IIa of O15460
864	O15460	7	11	19.8	535	60902	5.7	Prolyl 4-hydroxylase subunit alpha-2 precursor
865	Q16630-3	7	30	22.2	478	52326	6.4	Isoform 3 of Q16630
865	Q16630	7	30	19.2	551	59210	7.2	Cleavage and polyadenylation specificity factor 6
865	UPI000006D566	7	30	19.2	551	59209	7.4	cleavage and polyadenylation specific factor 6, 68 kD subunit
865	Q16630-2	7	30	18	588	63471	7.7	Isoform 2 of Q16630
866	Q8HXW2	7	17	18.8	674	74003	8.4	Calcium-binding mitochondrial carrier protein Aralar2
867	P22570	7	14	18.5	491	53837	8.4	NADPH:adrenodoxin oxidoreductase, mitochondrial precursor (EC 1.18.1.2) (Adrenodoxin reductase) (AR) (Ferredoxin reductase) (Ferredoxin--NADP(+) reductase)
867	P22570-2	7	14	18.3	497	54479	8.4	Isoform Long of P22570
868	P18031	7	8	18.4	435	49967	6.3	Tyrosine-protein phosphatase non-receptor type 1
869	Q8TCT9-5	7	90	20.6	335	36814	6.7	Isoform 5 of Q8TCT9
869	Q8TCT9	7	90	18.3	377	41488	6.4	Minor histocompatibility antigen H13
870	Q9BZZ5-3	7	26	24.1	373	42020	4.8	Isoform 3 of Q9BZZ5
870	Q9BZZ5-4	7	26	18	500	56099	5.9	Isoform 4 of Q9BZZ5
870	Q5R644	7	26	17.9	504	56770	5.9	Apoptosis inhibitor 5
870	Q9BZZ5	7	26	17.6	510	57561	6.1	Apoptosis inhibitor 5
870	UPI0000D625E5	7	26	17.3	521	58472	7.3	Apoptosis inhibitor 5 (API-5) (Fibroblast growth factor 2-interacting factor) (FIF) (Protein XAGL) (Antiapoptosis clone 11 protein) (AAC- 11).
871	Q9UMS4	7	14	17.9	504	55181	6.6	Pre-mRNA-processing factor 19
872	Q8N2L6	7	20	17.7	447	49824	9.4	CDNA FLJ90138 fis, clone HEMBB1000905, weakly similar to TRANSCRIPTIONAL REPRESSOR RCO-1
872	Q9Y4P3	7	20	17.7	447	49798	9.4	Transducin beta-like 2 protein
873	Q16843	7	45	19.1	460	52444	6.5	Thromboxane synthase
873	P24557	7	45	16.5	533	60544	7.6	Thromboxane-A synthase
873	UPI000006DC94	7	45	16.5	534	60676	7.6	thromboxane A synthase 1 (platelet, cytochrome P450, family 5, subfamily A) isoform TXS-I
873	Q53F23	7	45	16.5	534	60650	7.6	Thromboxane A synthase 1 (Platelet, cytochrome P450, family 5, subfamily A) isoform TXS-I variant

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874	Q9BRD2	7	89	21.8	308	33376	8.4	LAMP1 protein
874	P11279	7	89	16.1	416	44773	9.1	Lysosome-associated membrane glycoprotein 1 precursor
874	UPI000049DDA7	7	89	16.1	415	44591	8.9	Lysosome-associated membrane glycoprotein 1 precursor (LAMP-1) (CD107a antigen).
874	Q8WU33	7	89	16.1	417	44882	8.7	Lysosomal-associated membrane protein 1
875	Q7Z4V5	7	15	15.5	671	74317	7.5	Hepatoma-derived growth factor 2
875	Q9BW08	7	15	15.5	670	74230	7.5	Hepatoma-derived growth factor-related protein 2
876	Q8TAT6	7	25	15.5	608	68120	6.4	Nuclear protein localization protein 4 homolog
876	UPI0000D623AF	7	25	15.5	607	67987	6.4	Nuclear protein localization protein 4 homolog (Protein NPL4).
876	UPI000006F9F7	7	25	15.5	608	68183	6.3	nuclear protein localization 4
876	UPI0000D623B0	7	25	15.3	616	69360	6.7	Nuclear protein localization protein 4 homolog (Protein NPL4).
876	Q8TAT6-2	7	25	15.2	617	69461	6.7	Isoform 2 of Q8TAT6
877	Q2PZI1	7	39	14.7	675	77319	9	Dpy-19-like protein 1
877	UPI0000DD7E92	7	39	14.7	675	77361	9	PREDICTED: similar to dpy-19-like 1, like
878	Q5JW30	7	16	17	494	54709	9.5	Staufen, RNA binding protein, homolog 1
878	O95793-2	7	16	16.9	496	54934	9.5	Isoform Short of O95793
878	Q5JW29	7	16	16.7	502	55635	9.5	Staufen, RNA binding protein, homolog 1
878	O95793	7	16	14.6	577	63182	9.4	Double-stranded RNA-binding protein Staufen homolog 1
879	UPI00005A4215	7	12	16	694	75927	6.6	PREDICTED: similar to catenin (cadherin-associated protein), beta 1, 88kDa
879	UPI00006C0700	7	12	15.8	702	77207	6.6	PREDICTED: similar to Beta-catenin
879	UPI0000DD7B92	7	12	14.3	774	84766	5.9	PREDICTED: similar to catenin (cadherin-associated protein), beta 1, 88kDa
879	P35222	7	12	14.2	781	85497	5.9	Catenin beta-1
880	P55290	7	15	14.2	713	78287	5	Cadherin-13 precursor
881	Q9Y6M1	7	22	15.1	556	61843	8.3	Insulin-like growth factor 2 mRNA-binding protein 2
881	A0A4Z0	7	22	14	598	65990	8.5	Insulin-like growth factor 2 mRNA binding protein 2
882	Q08945	7	22	14	709	81075	6.9	FACT complex subunit SSRP1
883	P31040	7	27	13.7	664	72692	7.4	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial precursor
884	P17858	7	8	13.6	780	85018	7.5	6-phosphofructokinase, liver type
885	Q5JPR5	7	18	19.4	427	46610	8.8	SH3-domain kinase binding protein 1
885	Q5JPT5	7	18	13.2	628	68550	7.5	SH3-domain kinase binding protein 1
885	Q5JPR3	7	18	12.9	645	70443	8.6	SH3-domain kinase binding protein 1
885	Q96B97	7	18	12.5	665	73126	6.6	SH3 domain-containing kinase-binding protein 1
886	Q9NVI7-2	7	16	12.6	586	66218	9.2	Isoform 2 of Q9NVI7

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
887	O43747	7	22	12	822	91391	6.8	AP-1 complex subunit gamma-1
887	UPI000016A4AD	7	22	12	825	91723	6.8	adaptor-related protein complex 1, gamma 1 subunit isoform a
887	UPI000013E60C	7	22	12	822	91351	6.8	adaptor-related protein complex 1, gamma 1 subunit isoform b
887	Q8IY97	7	22	12	825	91757	6.8	Adaptor-related protein complex 1, gamma 1 subunit
888	Q5T207	7	40	12	689	76744	5.7	Nicastrin
888	Q92542	7	40	11.7	709	78411	6	Nicastrin precursor
889	Q9GZR7	7	10	10.1	859	96332	9.1	ATP-dependent RNA helicase DDX24
890	P13591	7	15	9.6	848	93361	4.9	Neural cell adhesion molecule 1, 140 kDa isoform precursor
890	UPI0000E445E3	7	15	9.4	858	94574	4.9	neural cell adhesion molecule 1 isoform 2
890	Q86X47	7	15	9.4	858	94601	4.9	Neural cell adhesion molecule 1
891	Q13620	7	17	9.6	895	102299	7.9	Cullin-4B
891	UPI000059DB7F	7	17	9.6	900	102756	8	Cullin-4B (CUL-4B).
891	UPI0000457880	7	17	9.4	917	104645	8	Cullin-4B (CUL-4B).
891	Q5JRZ4	7	17	9.4	913	103982	7.4	Cullin 4B
892	Q53X12	7	14	9.6	831	95751	6.7	Vacuolar-type H(+)-ATPase
892	UPI0000D62334	7	14	9.6	837	96477	6.7	Vacuolar proton translocating ATPase 116 kDa subunit a isoform 1 (V- ATPase 116 kDa isoform a1) (Clathrin-coated vesicle/synaptic vesicle proton pump 116 kDa subunit) (Vacuolar proton pump subunit 1) (Vacuolar adenosine triphosphatase subunit Ac116).
892	Q93050-1	7	14	9.6	831	95756	6.7	Isoform 2 of Q93050
892	Q93050	7	14	9.6	837	96413	6.4	Vacuolar proton translocating ATPase 116 kDa subunit a isoform 1
892	Q5CZH6	7	14	9.5	838	96603	6.6	Hypothetical protein DKFZp686N0561
893	UPI0000456E7C	7	13	10.2	827	95332	7.5	Pre-mRNA-processing factor 40 homolog A (Formin-binding protein 3) (Formin-binding protein 11) (Huntingtin-interacting protein HYPA) (Huntingtin yeast partner A) (Fas ligand-associated factor 1) (NY-REN- 6 antigen).
893	O75400-2	7	13	9.2	915	104363	7.6	Isoform 2 of O75400
893	O75400-3	7	13	8.9	939	106907	7.4	Isoform 3 of O75400
893	O75400	7	13	8.8	957	108805	7.6	Pre-mRNA-processing factor 40 homolog A
893	UPI0000DD7A6A	7	13	8.6	974	110497	8.2	PREDICTED: similar to Pre-mRNA-processing factor 40 homolog A (Formin-binding protein 3) (Huntingtin yeast partner A) (Huntingtin-interacting protein HYPA/FBP11) (Fas ligand-associated factor 1) (NY-REN-6 antigen) isoform 1
894	UPI000013FCDE	7	13	9	808	89467	10.1	arginine/proline rich coiled-coil 1

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894	Q3KQU3	7	13	8.7	841	92820	10.1	Arginine/proline-rich coiled-coil protein 1
895	Q5JTH9	7	27	8.5	1297	143702	8.8	RRP12-like protein
895	UPI00000712A5	7	27	8.5	1297	143732	8.8	ribosomal RNA processing 12 homolog
896	Q9P0K7	7	12	8.5	980	110041	6.2	Ankycorbin
896	UPI0000074005	7	12	8.5	980	110042	6.2	retinoic acid induced 14
896	Q9P0K7-3	7	12	8.5	972	109080	6	Isoform 3 of Q9P0K7
896	Q9P0K7-2	7	12	8.4	983	110423	6.1	Isoform 2 of Q9P0K7
897	Q14157-1	7	17	9.2	983	103930	7	Isoform 2 of Q14157
897	Q14157-3	7	17	8.4	1068	112580	6.6	Isoform 3 of Q14157
897	Q14157	7	17	8.3	1087	114534	7.1	Ubiquitin-associated protein 2-like
897	UPI00000735C4	7	17	8.3	1087	114543	7.1	ubiquitin associated protein 2-like
898	UPI0000457885	7	12	8.2	1231	141328	5.4	Cohesin subunit SA-2 (Stromal antigen 2) (SCC3 homolog 2).
898	Q8N3U4	7	12	8.2	1231	141326	5.4	Cohesin subunit SA-2
898	Q6MZM4	7	12	8.2	1231	141306	5.4	Hypothetical protein DKFZp686P16143
898	Q6MZM3	7	12	8.2	1231	141301	5.4	Hypothetical protein DKFZp686C21148
898	Q5JTI5	7	12	8	1268	145751	5.5	Stromal antigen 2
898	UPI0000D61DCF	7	12	8	1268	145753	5.5	Cohesin subunit SA-2 (Stromal antigen 2) (SCC3 homolog 2).
898	Q6MZP3	7	12	8	1268	145675	5.5	Hypothetical protein DKFZp686I05169
898	Q68DE9	7	12	8	1268	145781	5.5	Hypothetical protein DKFZp781H1753
899	Q6P2E9	7	13	8	1401	151661	5.9	Enhancer of mRNA-decapping protein 4
900	Q01970	7	16	7.9	1234	138799	5.9	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta 3
901	Q7Z406	7	35	7.5	1995	228000	5.9	Myosin-14
901	UPI0000E59250	7	35	7.5	2003	228663	5.6	myosin, heavy chain 14 isoform 1
901	UPI0000E5924F	7	35	7.5	1995	227868	5.6	myosin, heavy chain 14 isoform 2
901	Q7Z406-2	7	35	7.4	2028	231214	5.6	Isoform 2 of Q7Z406
902	Q4KMR3	7	15	7.1	1108	127062	8.9	Myosin IE
903	Q7L014	7	8	7.1	1031	117362	9.3	Probable ATP-dependent RNA helicase DDX46
903	UPI0000457348	7	8	7.1	1032	117462	9.3	Probable ATP-dependent RNA helicase DDX46 (EC 3.6.1.-) (DEAD box protein 46) (PRP5 homolog).
903	UPI0000457347	7	8	7.1	1033	117575	9.3	Probable ATP-dependent RNA helicase DDX46 (EC 3.6.1.-) (DEAD box protein 46) (PRP5 homolog).
904	UPI0000D6250D	7	9	8.2	878	99204	6.4	Focal adhesion kinase 1 (EC 2.7.10.2) (FADK 1) (pp125FAK) (Protein- tyrosine kinase 2).
904	Q05397-2	7	9	8.2	879	99358	6.4	Isoform 2 of Q05397
904	Q59GN8	7	9	7.4	975	110234	6.2	PTK2 protein tyrosine kinase 2 isoform b variant
904	Q8IYN9	7	9	7.2	1006	114253	6.8	PTK2 protein
904	Q59GM6	7	9	7.1	1007	114157	6.6	PTK2 protein tyrosine kinase 2 isoform b variant
904	Q05397	7	9	6.8	1052	119233	6.6	Focal adhesion kinase 1
905	Q14692	7	16	6.1	1282	145807	6.4	Ribosome biogenesis protein BMS1 homolog

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905	UPI000000DA33	7	16	6.1	1282	145821	6.4	BMS1-like, ribosome assembly protein
906	Q59GJ0	7	23	6.1	1780	195956	5.6	Eukaryotic translation initiation factor 4 gamma, 3 variant
907	Q08378-3	7	14	6.1	1458	162985	5.4	Isoform 3 of Q08378
907	Q08378	7	14	5.9	1498	167354	5.4	Golgin subfamily A member 3
908	Q9UIG0	7	7	5.9	1483	170902	8.5	Bromodomain adjacent to zinc finger domain protein 1B
908	Q9UIG0-2	7	7	5.9	1479	170446	8.5	Isoform 2 of Q9UIG0
909	Q9P2D5	7	22	5.8	1386	154717	8.1	Transmembrane protein 2
910	UPI0000D612FA	7	13	5.7	1676	187847	6.7	Tight junction protein ZO-1 (Zonula occludens 1 protein) (Zona occludens 1 protein) (Tight junction protein 1).
910	Q07157-2	7	13	5.7	1668	186965	6.8	Isoform Short of Q07157
910	Q6MZU1	7	13	5.6	1692	189616	6.8	Hypothetical protein DKFZp686A1195
910	UPI0000D612F9	7	13	5.5	1736	194834	6.8	Tight junction protein ZO-1 (Zonula occludens 1 protein) (Zona occludens 1 protein) (Tight junction protein 1).
910	Q07157	7	13	5.4	1748	195457	6.7	Tight junction protein ZO-1
911	P52948	7	8	4.5	1729	187789	6.3	Nuclear pore complex protein Nup98-Nup96 precursor [Contains: Nuclear pore complex protein Nup98 (Nucleoporin Nup98) (98 kDa nucleoporin); Nuclear pore complex protein Nup96 (Nucleoporin Nup96) (96 kDa nucleoporin)]
911	UPI0000D62592	7	8	4.5	1729	187780	6.4	Nuclear pore complex protein Nup98-Nup96 precursor [Contains: Nuclear pore complex protein Nup98 (Nucleoporin Nup98) (98 kDa nucleoporin); Nuclear pore complex protein Nup96 (Nucleoporin Nup96) (96 kDa nucleoporin)].
911	P52948-5	7	8	4.3	1800	195816	6.4	Isoform 5 of P52948
912	P24928	7	9	4.2	1970	217204	7.4	DNA-directed RNA polymerase II largest subunit
912	UPI0000D622B7	7	9	4.2	1972	217430	7.4	DNA-directed RNA polymerase II largest subunit (EC 2.7.7.6) (RPB1).
912	UPI0000140EB9	7	9	4.2	1970	217174	7.4	DNA-directed RNA polymerase II largest subunit (EC 2.7.7.6) (RPB1).
913	Q6IEH8	7	21	2.9	2804	316066	7.9	Transcriptional regulator
913	Q6KC79	7	21	2.9	2804	316051	7.9	Nipped-B-like protein
914	Q8WUH6	6	26	79.3	116	11748	9.3	Uncharacterized protein C12orf23
915	P58546	6	92	66.9	118	12895	5.5	Myotrophin
916	P41567	6	41	61.1	113	12732	7.5	Eukaryotic translation initiation factor 1
917	P31946-2	6	79	59.4	244	27850	4.8	Isoform Short of P31946
917	P31946	6	79	58.9	246	28082	4.8	14-3-3 protein beta/alpha
918	P09669	6	34	58.7	75	8781	10.4	Cytochrome c oxidase polypeptide VIc precursor
919	O75531	6	69	56.2	89	10059	6.1	Barrier-to-autointegration factor
920	P49773	6	45	55.6	126	13802	7	Histidine triad nucleotide-binding protein 1
921	P99999	6	110	55.2	105	11749	9.6	Cytochrome c

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922	Q99471	6	31	55.2	154	17328	6.3	Prefoldin subunit 5
923	Q53HV6	6	56	50.3	151	16584	7.7	Niemann-Pick disease, type C2 variant
924	P63173	6	88	50	70	8218	10.1	60S ribosomal protein L38
925	Q04837	6	88	49.3	148	17260	9.6	Single-stranded DNA-binding protein, mitochondrial precursor
925	Q567R6	6	88	49.3	148	17359	9.7	Single-stranded DNA binding protein 1
926	Q9P0J0	6	29	49.3	144	16698	8.4	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13
926	UPI0000163BED	6	29	31.3	227	25865	9.8	cell death-regulatory protein GRIM19
927	P62316	6	93	49.2	118	13527	9.9	Small nuclear ribonucleoprotein Sm D2
928	P61088	6	52	48.7	152	17138	6.6	Ubiquitin-conjugating enzyme E2 N
929	P68133	6	154	48.3	377	42051	5.4	Actin, alpha skeletal muscle
930	P30050	6	155	47.9	165	17819	9.4	60S ribosomal protein L12
930	UPI0000D6190D	6	155	34.5	229	24724	9.9	60S ribosomal protein L12.
931	O75964	6	83	47.6	103	11428	9.6	ATP synthase subunit g, mitochondrial
932	P40616	6	35	47	181	20418	5.7	ADP-ribosylation factor-like protein 1
933	P84095	6	8	46.1	191	21308	8.1	Rho-related GTP-binding protein RhoG precursor
934	Q9Y221	6	16	45.6	180	20463	8.5	60S ribosome subunit biogenesis protein NIP7 homolog
935	P57105	6	24	45.5	145	15928	6.3	Synaptojanin-2-binding protein
936	Q9Y5S9	6	40	45.4	174	19889	5.7	RNA-binding protein 8A
937	O15511	6	62	45	151	16320	5.7	Actin-related protein 2/3 complex subunit 5
938	Q15370	6	47	44.9	118	13133	4.9	Transcription elongation factor B polypeptide 2
938	UPI0000353500	6	47	32.9	161	17911	6.1	elongin B isoform b
939	Q9BTQ7	6	222	46.3	134	14150	10.3	Similar to ribosomal protein L23
939	P62829	6	222	44.3	140	14865	10.5	60S ribosomal protein L23
939	UPI0000D62314	6	222	44.3	140	14811	10.4	60S ribosomal protein L23 (Ribosomal protein L17).
940	P13693	6	75	44.2	172	19595	4.9	Translationally-controlled tumor protein
941	Q4VBQ4	6	33	42.9	140	15088	6.1	Profilin 2
942	Q8CFN2	6	48	42.4	191	21259	6.5	Cell division control protein 42 homolog precursor
942	UPI0000EFE353	6	48	42.2	192	21346	6.5	Human Cell Division Cycle 42 (CDC42)
943	P60983	6	24	42.3	142	16713	5.3	Glia maturation factor beta
943	Q9BS35	6	24	39	154	18110	5.3	GMFB protein
944	O43324	6	14	42	174	19811	8.6	Eukaryotic translation elongation factor 1 epsilon-1
945	Q8TED1	6	30	41.1	209	23909	9.4	CDNA FLJ23636 fis, clone CAS07176
946	Q03135	6	233	41	178	20472	6	Caveolin-1
947	Q9BYC9	6	16	40.9	149	17443	10.9	39S ribosomal protein L20, mitochondrial precursor
948	O00264	6	17	40.5	195	21671	4.7	Membrane-associated progesterone receptor component 1
949	A3KQT0	6	95	39.8	201	23072	10	Ribosomal protein L10
949	Q6ZWV3	6	95	37.4	214	24604	10.1	60S ribosomal protein L10
949	Q53FH7	6	95	37.4	214	24543	10.1	Ribosomal protein L10 variant

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949	P27635	6	95	37.4	214	24577	10.1	60S ribosomal protein L10
949	Q5HY50	6	95	34.8	230	26593	10.2	Ribosomal protein L10
950	P21291	6	21	39.4	193	20567	8.6	Cysteine and glycine-rich protein 1
951	P13073	6	61	38.5	169	19577	9.5	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial precursor
951	Q6P666	6	61	38.5	169	19607	9.5	Cytochrome c oxidase subunit IV isoform 1
952	P49720	6	63	38.5	205	22949	6.5	Proteasome subunit beta type 3
953	P61086	6	19	38.5	200	22407	5.4	Ubiquitin-conjugating enzyme E2-25 kDa (EC 6.3.2.19) (Ubiquitin-protein ligase) (Ubiquitin carrier protein) (E2(25K))
954	UPI0000251F42	6	59	38.7	124	13614	10.1	PREDICTED: similar to 40S ribosomal protein S25
954	UPI000013DA0C	6	59	38.7	124	13615	10	PREDICTED: similar to 40S ribosomal protein S25
954	P62851	6	59	38.4	125	13742	10.1	40S ribosomal protein S25
955	P02794	6	40	37.7	183	21226	5.6	Ferritin heavy chain
955	UPI0000EB65CC	6	40	37.7	183	21198	5.4	FERRITIN HEAVY CHAIN
955	UPI0000EB65CB	6	40	37.7	183	21212	5.4	FERRITIN HEAVY CHAIN
955	UPI0000EB65CA	6	40	37.7	183	21212	5.4	FERRITIN HEAVY CHAIN
955	Q6NZ44	6	40	37.7	183	21242	5.3	FTH1 protein
955	UPI0000D62618	6	40	28.3	244	27725	7	Ferritin heavy chain (EC 1.16.3.1) (Ferritin H subunit) (Proliferation-inducing gene 15 protein).
956	P52943	6	11	37.5	208	22493	8.7	Cysteine-rich protein 2
956	Q53FN1	6	11	37.5	208	22494	8.5	Cysteine-rich protein 2 variant
957	Q15185	6	54	37.5	160	18697	4.5	Prostaglandin E synthase 3
958	Q9BYD1	6	11	37.1	178	20692	9.1	39S ribosomal protein L13, mitochondrial
959	UPI0000EFE339	6	27	37.2	180	20639	7.8	NEDD8-conjugating enzyme Ubc12
959	P61081	6	27	36.6	183	20900	7.7	NEDD8-conjugating enzyme Ubc12
960	P28070	6	26	36.4	264	29204	6	Proteasome subunit beta type 4 precursor
960	Q6IBI4	6	26	36.4	264	29190	6	Proteasome subunit beta type
961	P83731	6	63	35.7	157	17779	11.3	60S ribosomal protein L24
962	P63208	6	33	35.6	163	18658	4.5	S-phase kinase-associated protein 1A
963	P46778	6	48	35	160	18565	10.5	60S ribosomal protein L21
963	Q59GK9	6	48	34.4	163	18891	10.5	Ribosomal protein L21 variant
964	P37108	6	35	34.6	136	14570	10	Signal recognition particle 14 kDa protein
964	Q96Q14	6	35	34.6	136	14514	10	Signal recognition particle 14kD
965	P05090	6	20	34.4	189	21276	5.1	Apolipoprotein D precursor
966	Q15126	6	22	34.4	192	21995	5.7	Phosphomevalonate kinase
967	Q9H061	6	10	34.4	195	21527	9.3	Transmembrane protein 126A
968	UPI000046D37E	6	14	34.9	292	31762	7.5	syntenin isoform 2
968	O00560	6	14	34.2	298	32444	7.5	Syntenin-1
969	Q13257	6	14	33.7	205	23510	5.1	Mitotic spindle assembly checkpoint protein MAD2A
969	Q6IRW7	6	14	33.7	205	23496	5.1	MAD2 mitotic arrest deficient-like 1
969	Q53F56	6	14	33.7	205	23526	5.1	MAD2-like 1 variant
970	Q9HAV7	6	16	33.6	217	24279	8.1	GrpE protein homolog 1, mitochondrial precursor

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971	O75223	6	26	33.5	188	21008	5.1	Uncharacterized protein C7orf24
972	Q08ES8	6	57	33.3	177	20094	9.6	Cell growth-inhibiting protein 34
972	P62913-2	6	57	33.3	177	20124	9.6	Isoform 2 of P62913
972	P62913	6	57	33.1	178	20252	9.6	60S ribosomal protein L11
973	UPI000015B7BA	6	23	32.9	210	24611	6	DNA directed RNA polymerase II polypeptide E
974	P18621	6	95	32.6	184	21397	10.2	60S ribosomal protein L17
974	Q6NZ54	6	95	32.6	184	21416	10.2	Ribosomal protein L17
974	UPI0000456877	6	95	32.4	185	21441	10.1	60S ribosomal protein L17 (L23).
975	Q9GZZ1	6	47	32.5	169	19398	8.8	N-acetyltransferase 13
976	Q85KS8	6	44	32.2	227	25566	4.8	Cytochrome oxidase subunit II
977	Q00688	6	34	31.2	224	25177	9.3	FK506-binding protein 3
977	Q53GD8	6	34	31.2	224	25204	9.4	FK506-binding protein 3 variant
978	P41227	6	9	30.2	235	26458	5.6	N-terminal acetyltransferase complex ARD1 subunit homolog A
979	P62266	6	78	30.1	143	15808	10.5	40S ribosomal protein S23
979	UPI00005E9ED6	6	78	30.1	143	15790	10.5	40S ribosomal protein S23.
980	P35625	6	19	29.9	211	24145	8.7	Metalloproteinase inhibitor 3 precursor
980	Q9TUL9	6	19	29.9	211	24147	8.7	Metalloproteinase inhibitor 3 precursor
981	Q59G46	6	13	30.7	280	31355	4.8	Thioredoxin-like 1 variant
981	O43396	6	13	29.8	289	32251	5	Thioredoxin-like protein 1
982	Q01105-2	6	43	29.2	277	32103	4.2	Isoform 2 of Q01105
982	UPI0000161B37	6	43	29.2	277	32134	4.2	SET translocation (myeloid leukemia-associated)
983	Q9H3H0	6	9	29.1	247	28275	9.4	Vacuolar ATP synthase subunit D homolog
983	Q9Y5K8	6	9	29.1	247	28263	9.4	Vacuolar ATP synthase subunit D
984	P16989-3	6	14	31.6	342	37021	9.9	Isoform 3 of P16989
984	P16989	6	14	29	372	40090	9.8	DNA-binding protein A
984	UPI0000128F30	6	14	29	372	40060	9.8	cold shock domain protein A
985	Q6IAX4	6	37	28.8	208	23562	8.9	RTN1 protein
985	Q9BQ59	6	37	28.8	208	23576	8.9	Reticulon 1
986	UPI000002552E	6	47	28.7	216	24700	9.9	60S ribosomal protein L10a (CSA-19).
986	P62906	6	47	28.6	217	24831	9.9	60S ribosomal protein L10a
987	Q04760	6	48	28.3	184	20778	5.3	Lactoylglutathione lyase
988	P29218	6	17	28.2	277	30189	5.3	Inositol monophosphatase (EC 3.1.3.25) (IMPase) (IMP) (Inositol-1(or 4)-monophosphatase)
989	Q13637	6	25	28	225	24997	6.5	Ras-related protein Rab-32
990	Q9BSQ6	6	33	27.9	201	23375	10.9	RPL13A protein
990	P40429	6	33	27.6	203	23577	10.9	60S ribosomal protein L13a
990	UPI000013DB4D	6	33	27.6	203	23619	10.9	PREDICTED: similar to ribosomal protein L13a isoform 1
990	Q5QTS3	6	33	27.6	203	23662	11	FWP004
990	Q53H34	6	33	27.6	203	23558	10.9	Ribosomal protein L13a variant
991	Q96C19	6	29	27.5	240	26697	5.2	EF-hand domain-containing protein 2
992	Q5T429	6	27	27.3	242	26279	8.9	Guanylate kinase 1
993	P27105	6	22	27.1	288	31731	7.9	Erythrocyte band 7 integral membrane protein
994	Q8N5D1	6	26	27	230	27086	10.3	MRPL47 protein
994	UPI000013D022	6	26	24.8	250	29450	10.4	mitochondrial ribosomal protein L47 isoform a

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
994	UPI0000D61BB3	6	26	24.6	252	29787	10.4	39S ribosomal protein L47, mitochondrial precursor (L47mt) (MRP-L47).
994	Q9HD33	6	26	24.6	252	29577	10.3	39S ribosomal protein L47, mitochondrial precursor
995	Q92979	6	12	27	244	26720	9.2	Probable ribosome biogenesis protein NEP1
996	P48739	6	19	26.9	271	31540	6.9	Phosphatidylinositol transfer protein beta isoform
996	P48739-2	6	19	26.8	272	31638	6.2	Isoform 2 of P48739
997	Q99598	6	29	26.9	290	33112	6.6	Translin-associated protein X
998	P30040	6	30	26.8	261	28993	7.3	Endoplasmic reticulum protein ERp29 precursor
999	P46108	6	22	26	304	33872	5.7	Proto-oncogene C-crk
999	Q96HJ0	6	22	26	304	33831	5.6	V-crk sarcoma virus CT10 oncogene homolog
1000	P31942-2	6	51	26.9	331	35239	6.9	Isoform 2 of P31942
1000	P31942	6	51	25.7	346	36926	6.9	Heterogeneous nuclear ribonucleoprotein H3
1000	Q53F48	6	51	25.7	346	36926	7.4	Heterogeneous nuclear ribonucleoprotein H3 isoform a variant
1001	Q99729-3	6	38	29.5	285	30588	7.9	Isoform 3 of Q99729
1001	UPI000013EBF8	6	38	25.5	329	36187	8.6	Heterogeneous nuclear ribonucleoprotein A/B (hnRNP A/B) (APOBEC-1- binding protein 1) (ABBP-1).
1001	Q53F64	6	38	25.3	332	35996	7.4	Heterogeneous nuclear ribonucleoprotein AB isoform a variant
1001	Q99729-2	6	38	25.3	332	35968	6.9	Isoform 2 of Q99729
1002	Q9H4A6	6	24	25.2	298	33811	6.4	Golgi phosphoprotein 3
1003	O95571	6	16	24.8	254	27873	6.8	ETHE1 protein, mitochondrial precursor
1004	UPI000069648D	6	35	27.5	204	23587	9	vacuolar H+ ATPase E1 isoform b
1004	P36543	6	35	24.8	226	26145	8	Vacuolar ATP synthase subunit E 1
1005	P50402	6	32	24.8	254	28994	5.5	Emerin
1006	Q8NBQ5	6	18	24.7	300	32964	9.2	Dehydrogenase/reductase SDR family member 8 precursor
1006	UPI00006C088F	6	18	24.7	300	33014	9.3	PREDICTED: similar to Dehydrogenase/reductase SDR family member 8 precursor (17-beta-hydroxysteroid dehydrogenase 11) (17-beta-HSD 11) (17-beta-HSD XI) (17betaHSDXI) (17bHSD11) (17betaHSD11) (Retinal short-chain dehydrogenase/reductase 2) (retSDR2) (Cutaneous...
1006	UPI000013FB48	6	18	24.7	300	32936	9.1	Dehydrogenase/reductase SDR family member 8 precursor (EC 1.1.1.-) (17-beta-hydroxysteroid dehydrogenase 11) (17-beta-HSD 11) (17-beta- HSD XI) (17betaHSDXI) (17bHSD11) (17betaHSD11) (Retinal short-chain dehydrogenase/reductase 2) (retSDR2) (Cutaneous T-c
1007	Q16831	6	20	24.5	310	33934	7.9	Uridine phosphorylase 1

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1008	Q8NBX0	6	22	24.5	429	47151	9.1	Probable saccharopine dehydrogenase
1009	P54709	6	32	24	279	31513	8.3	Sodium/potassium-transporting ATPase subunit beta-3
1010	Q9H2U2-3	6	32	26.2	305	34658	8.5	Isoform 3 of Q9H2U2
1010	Q9H2U2	6	32	24	334	37920	7.4	Inorganic pyrophosphatase 2, mitochondrial precursor
1010	Q9H2U2-2	6	32	22.9	349	39638	6.9	Isoform 2 of Q9H2U2
1011	Q15006	6	16	23.6	297	34833	6.6	Tetratricopeptide repeat protein 35
1011	Q53HG5	6	16	23.6	297	34761	6.8	KIAA0103 variant
1012	O60762	6	18	23.5	260	29634	9.6	Dolichol-phosphate mannosyltransferase
1012	Q5QPK2	6	18	21.3	287	32426	9.1	Dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit
1012	Q5QPK0	6	18	20.7	294	33218	9.1	Dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit
1013	P57088	6	34	23.5	247	27978	9.7	Transmembrane protein 33
1013	UPI000015F326	6	34	23.5	247	27951	9.7	transmembrane protein 33
1014	Q14847	6	42	23.4	261	29717	7	LIM and SH3 domain protein 1
1014	UPI0000D62315	6	42	18.9	322	35773	8.5	LIM and SH3 domain protein 1 (LASP-1) (MLN 50).
1014	Q14847-2	6	42	18.9	323	36014	8.6	Isoform 2 of Q14847
1015	P17931	6	11	23.2	250	26188	8.5	Galectin-3
1015	Q6IBA7	6	11	23.2	250	26152	8.5	LGALS3 protein
1015	Q6FGL0	6	11	23.2	250	26161	8.5	LGALS3 protein
1015	Q59FR8	6	11	22.5	258	27118	8.4	LGALS3 protein variant
1016	Q9BTT5	6	30	25.7	338	38442	9.7	Similar to NADH dehydrogenase (Ubiquinone) 1 alpha subcomplex, 9
1016	Q16795	6	30	23.1	377	42510	9.8	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial precursor
1017	Q9Y5K5-2	6	9	25.6	316	36079	5.2	Isoform 2 of Q9Y5K5
1017	Q9Y5K5-3	6	9	24.7	328	37478	5.4	Isoform 3 of Q9Y5K5
1017	Q9Y5K5	6	9	24.6	329	37607	5.3	Ubiquitin carboxyl-terminal hydrolase isozyme L5
1017	Q5LJA5	6	9	22.8	355	40423	5.3	Ubiquitin carboxyl-terminal hydrolase L5
1017	Q5LJA9	6	9	22	368	41695	5.5	Ubiquitin carboxyl-terminal hydrolase L5
1018	P50213	6	21	22.1	366	39592	6.9	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial precursor (EC 1.1.1.41) (Isocitric dehydrogenase) (NAD(+)-specific ICDH)
1018	Q53GF8	6	21	22.1	366	39620	6.9	Isocitrate dehydrogenase 3 (NAD+) alpha variant
1019	O75821	6	25	21.9	320	35611	6.1	Eukaryotic translation initiation factor 3 subunit 4
1020	Q3ZCQ8	6	17	21.8	353	39646	8.4	Import inner membrane translocase subunit TIM50, mitochondrial precursor
1020	Q3ZCQ8-2	6	17	16.9	456	50465	9.4	Isoform 2 of Q3ZCQ8
1021	O76003	6	22	21.2	335	37432	5.4	Thioredoxin-like protein 2
1022	P25685	6	16	21.2	340	38044	8.6	DnaJ homolog subfamily B member 1
1022	Q6FI51	6	16	21.2	340	38010	8.6	DNAJB1 protein

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1023	P11766	6	16	21.1	374	39724	7.5	Alcohol dehydrogenase class 3 (EC 1.1.1.1) (Alcohol dehydrogenase class III) (Alcohol dehydrogenase class chi chain) (S-(hydroxymethyl)glutathione dehydrogenase)
1023	Q6FI45	6	16	21.1	374	39690	7.5	ADH5 protein
1024	Q53H12	6	18	21.1	422	47137	8.1	Acylglycerol kinase, mitochondrial precursor
1025	Q96HI4	6	14	21.1	494	56604	7.8	NMT1 protein
1025	P30419	6	14	21	496	56806	7.8	Glycylpeptide N-tetradecanoyltransferase 1
1025	UPI0000D6234C	6	14	20.9	498	56978	7.8	Glycylpeptide N-tetradecanoyltransferase 1 (EC 2.3.1.97) (Peptide N-myristoyltransferase 1) (Myristoyl-CoA:protein N-myristoyltransferase 1) (NMT 1) (Type I N-myristoyltransferase).
1026	P11177-2	6	21	22	341	37200	5.9	Isoform 2 of P11177
1026	P11177	6	21	20.9	359	39233	6.6	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial precursor
1026	UPI0000161B07	6	21	20.9	359	39249	6.6	pyruvate dehydrogenase (lipoamide) beta
1027	P31689	6	17	20.7	397	44868	7.1	DnaJ homolog subfamily A member 1
1028	P54727	6	9	20.3	409	43171	4.8	UV excision repair protein RAD23 homolog B
1028	Q53F10	6	9	20.3	409	43113	4.9	UV excision repair protein RAD23 homolog B variant
1029	UPI00004BEBE5	6	11	20.2	392	43449	8	TIA-1 related protein isoform 2
1030	Q6FHU0	6	24	20.2	272	29696	5.8	PSMB8 protein
1030	Q5JNW6	6	24	20.2	272	29770	5.8	Proteasome subunit beta type
1030	P28062	6	24	19.9	276	30354	7.8	Proteasome subunit beta type 8 precursor
1030	Q5QNR8	6	24	19.9	276	30354	7.4	Proteasome subunit beta type
1031	Q1XBU6	6	29	28.6	255	28366	8.8	Aging-associated protein 14b
1031	P50502	6	29	19.8	369	41332	5.3	Hsc70-interacting protein
1032	UPI0000D617D3	6	32	35.7	207	22366	9.1	Vasodilator-stimulated phosphoprotein (VASP).
1032	P50552	6	32	19.5	380	39830	8.9	Vasodilator-stimulated phosphoprotein
1033	P16402	6	83	19	221	22350	11	Histone H1.3
1034	Q542Y9	6	13	18.7	358	40500	6.2	CDNA FLJ90819 fis, clone Y79AA1001264, highly similar to DnaJ homolog subfamily B member 11
1034	Q9UBS4	6	13	18.7	358	40514	6.2	DnaJ homolog subfamily B member 11 precursor
1034	Q6IAQ8	6	13	18.7	358	40542	6.2	DNAJB11 protein
1035	Q13077	6	15	18.5	416	46164	6.1	TNF receptor-associated factor 1
1036	Q15293	6	66	18.4	331	38890	5	Reticulocalbin-1 precursor
1037	Q96HC5	6	18	18.3	471	53121	9.1	U2 small nuclear RNA auxiliary factor 2
1037	P26368	6	18	18.1	475	53501	9.1	Splicing factor U2AF 65 kDa subunit (U2 auxiliary factor 65 kDa subunit) (U2 snRNP auxiliary factor large subunit) (hU2AF(65))

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
1037	UPI0000D6181E	6	18	18	477	53728	9.2	Splicing factor U2AF 65 kDa subunit (U2 auxiliary factor 65 kDa subunit) (U2 snRNP auxiliary factor large subunit) (hU2AF(65)).
1038	Q53GI0	6	17	18.1	420	46337	7.2	GDP-mannose pyrophosphorylase A
1038	Q9NWC3	6	17	18.1	420	46351	7.2	CDNA FLJ10137 fis, clone HEMBA1003136, weakly similar to MANNOSE-1- PHOSPHATE GUANYLTRANSFERASE
1038	Q96IJ6	6	17	18.1	420	46291	7.2	GDP-mannose pyrophosphorylase A
1038	UPI000066D9A1	6	17	16.1	473	52018	7.2	GDP-mannose pyrophosphorylase A
1039	O75955	6	8	18	427	47355	7.5	Flotillin-1
1039	Q53HQ0	6	8	18	427	47354	8.1	Flotillin 1 variant
1040	Q9UBT2	6	24	17.5	640	71224	5.3	SUMO-activating enzyme subunit 2
1041	P36507	6	17	16.8	400	44424	6.5	Dual specificity mitogen-activated protein kinase kinase 2
1042	UPI0000233611	6	27	16.5	370	42210	6.6	ubiquitin-conjugating enzyme E2 Kua-UEV isoform 1
1043	Q0VGU9	6	33	22.6	367	39818	6.6	Rbm39 protein
1043	A2RRD3	6	33	16.3	508	57090	10	RBM39 protein
1043	Q68DD9	6	33	16.2	513	57444	10.3	Hypothetical protein DKFZp781C0423
1043	Q5RC80	6	33	15.8	524	58657	10.1	RNA-binding protein 39
1043	Q14498	6	33	15.7	530	59380	10.1	RNA-binding protein 39
1044	O96019	6	17	16.1	429	47461	5.6	Actin-like protein 6A
1044	Q6FI97	6	17	16.1	429	47381	5.7	BAF53A protein
1044	Q53FS0	6	17	16.1	429	47481	5.7	Actin-like 6A isoform 1 variant
1045	Q53GF0	6	26	16.1	434	48329	7.9	Cytidine 5'-monophosphate N-acetylneuraminic acid synthetase variant
1045	Q8NFW8	6	26	16.1	434	48379	7.9	N-acylneuraminate cytidylyltransferase
1046	P36871	6	14	16	562	61449	6.8	Phosphoglucomutase-1
1046	UPI0000D61F2F	6	14	16	564	61633	6.8	Phosphoglucomutase-1 (EC 5.4.2.2) (Glucose phosphomutase 1) (PGM 1).
1046	Q86U74	6	14	16	562	61370	6.6	Phosphoglucomutase 1
1046	Q6NW22	6	14	16	562	61439	6.8	Phosphoglucomutase 1
1047	Q59H65	6	16	16.7	461	51892	6.8	Aldehyde dehydrogenase 3A2 variant
1047	P51648	6	16	15.9	485	54848	7.9	Fatty aldehyde dehydrogenase
1047	P51648-2	6	16	15.2	508	57669	8.9	Isoform 2 of P51648
1048	Q0VGA5	6	9	15.9	511	58407	6.4	SARS protein
1048	P49591	6	9	15.8	514	58777	6.4	Seryl-tRNA synthetase, cytoplasmic
1048	Q53HA4	6	9	15.8	514	58690	6.4	Seryl-tRNA synthetase variant
1048	UPI0000D61F7C	6	9	15.1	536	61285	7.1	Seryl-tRNA synthetase, cytoplasmic (EC 6.1.1.11) (Serine--tRNA ligase) (SerRS).
1048	Q5T5C7	6	9	15.1	536	61313	7.1	Seryl-tRNA synthetase
1049	Q99961	6	11	15.5	368	41490	5.4	SH3-containing GRB2-like protein 1
1050	P55010	6	20	15.3	431	49223	5.6	Eukaryotic translation initiation factor 5
1050	Q6IBU0	6	20	15.3	431	49152	5.5	EIF5 protein
1051	Q96JJ7	6	14	15.2	454	51872	4.9	Protein disulfide-isomerase TXNDC10 precursor

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1052	P08621-2	6	12	15.4	428	50618	9.9	Isoform 2 of P08621
1052	P08621	6	12	15.1	437	51557	9.9	U1 small nuclear ribonucleoprotein 70 kDa
1053	P00390	6	14	14.9	522	56257	8.5	Glutathione reductase, mitochondrial precursor
1054	A0PJJ5	6	10	14.8	559	62644	8.3	Hypothetical protein
1054	Q0D2M6	6	10	14.8	560	62730	8.2	Hypothetical protein
1054	Q71V07	6	10	12.4	671	74607	9.2	Putative signal recognition particle
1054	O76094	6	10	12.4	671	74606	9.3	Signal recognition particle 72 kDa protein
1055	O60832	6	9	14.8	514	57674	9.4	H/ACA ribonucleoprotein complex subunit 4
1056	P49189	6	11	14.8	494	53802	5.9	4-trimethylaminobutyraldehyde dehydrogenase
1057	Q7Z4H8	6	32	14.8	507	58573	8.2	KDEL motif-containing protein 2 precursor
1057	UPI00001B5C05	6	32	14.8	507	58489	8.1	KDEL (Lys-Asp-Glu-Leu) containing 2
1058	P23634-5	6	30	16.3	1122	124007	7.3	Isoform ZK of P23634
1058	P23634-4	6	30	16.1	1134	125344	7.7	Isoform XK of P23634
1058	P23634-3	6	30	15.8	1158	128066	7.1	Isoform ZA of P23634
1058	Q5T0B3	6	30	15.6	1170	129403	7.5	Cation-transporting ATPase
1058	P23634-7	6	30	15.3	1193	132594	6.2	Isoform ZB of P23634
1058	Q7Z3S1	6	30	15.2	1205	133874	6.5	Cation-transporting ATPase
1058	Q5T0B2	6	30	15.2	1205	133930	6.4	Cation-transporting ATPase
1058	P23634-8	6	30	14.9	1229	136583	6.4	Isoform ZD of P23634
1058	P23634	6	30	14.7	1241	137920	6.6	Plasma membrane calcium-transporting ATPase 4
1059	Q13098	6	9	14.6	471	53372	6.7	COP9 signalosome complex subunit 1
1059	Q13098-2	6	9	14.5	475	53816	6.9	Isoform 2 of Q13098
1059	UPI0000231C2E	6	9	13.1	527	59050	6.3	G protein pathway suppressor 1 isoform 1
1060	Q8NF37	6	26	14.6	534	59151	6	1-acylglycerophosphocholine O-acyltransferase 1
1061	Q96I24	6	10	14.5	572	61640	8.4	Far upstream element-binding protein 3
1062	Q59H57	6	32	25	300	31994	9.5	Fusion (Involved in t(12;16) in malignant liposarcoma) isoform a variant
1062	P35637	6	32	14.3	526	53426	9.4	RNA-binding protein FUS
1062	Q8TBR3	6	32	14.3	526	53400	9.4	Fusion (Involved in t(12;16) in malignant liposarcoma)
1062	P35637-2	6	32	14.3	525	53355	9.4	Isoform Short of P35637
1062	Q13344	6	32	14.2	528	53377	9.4	Fus-like protein
1063	Q9P129	6	16	16.5	411	45819	5.5	Calcium-binding transporter
1063	Q6NUK1	6	16	14.3	477	53338	6.3	Solute carrier family 25 member 24
1063	UPI00001BDC72	6	16	14.3	476	53251	6.3	solute carrier family 25 member 24 isoform 1
1063	Q6PJJ9	6	16	14.3	477	53354	6.3	Solute carrier family 25 (Mitochondrial carrier; phosphate carrier), member 24
1064	UPI00005A6C9C	6	11	15.3	459	52386	5.8	ubiquitin specific protease 14 isoform b
1064	P54578	6	11	14.2	494	56069	5.3	Ubiquitin carboxyl-terminal hydrolase 14
1065	Q86WL4	6	9	14.7	518	58511	8.4	Gastric cancer multi-drug resistance protein variant
1065	Q5LJ98	6	9	14.7	518	58483	8.4	TROVE domain family, member 2
1065	Q5LJA0	6	9	14.5	525	59270	8.5	TROVE domain family, member 2

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1065	Q86WL3	6	9	14.2	534	60197	8.1	Gastric cancer multi-drug resistance protein variant
1065	Q5LJ99	6	9	14.2	534	60169	8.1	TROVE domain family, member 2
1065	P10155	6	9	14.1	538	60671	8	60 kDa SS-A/Ro ribonucleoprotein
1066	Q09028	6	22	14.1	425	47656	4.9	Histone-binding protein RBBP4
1067	Q13177	6	14	13.7	524	58043	6	Serine/threonine-protein kinase PAK 2
1068	Q53HE9	6	42	13.6	487	53598	8.2	Ankylosis, progressive homolog
1068	Q9HCJ1	6	42	13.4	492	54241	7.9	Progressive ankylosis protein homolog
1069	Q4ZG30	6	39	13.1	579	66087	6.1	Hypothetical protein ARL6IP2
1069	Q9H5M7	6	39	13.1	579	66159	6	CDNA: FLJ23293 fis, clone HEP10514
1069	Q8NHH8	6	39	13.1	579	66057	6.2	ARL6IP2
1069	UPI00001B00A2	6	39	13	583	66229	5.5	ADP-ribosylation factor-like 6 interacting protein 2
1069	Q8NHH9	6	39	13	583	66199	5.5	ADP-ribosylation factor-like protein 6-interacting protein 2
1070	Q9NZ37	6	9	13.4	397	45398	7.1	Uncharacterized hypothalamus protein HT010
1070	UPI0000D6127F	6	9	12.9	412	47015	6.4	erythropoietin 4 immediate early response
1070	Q5QTQ4	6	9	12.8	413	47143	6.6	MSTP012
1070	Q9NUZ3	6	9	12.4	426	48631	5.4	CDNA FLJ11039 fis, clone PLACE1004376
1070	Q8WU90	6	9	12.4	426	48603	5.3	Zinc finger CCCH-type containing 15
1070	Q9P079	6	9	11.6	458	51851	5.2	HSPC303
1071	Q969V3	6	10	12.6	563	62974	6.9	Nicalin precursor
1071	Q969V3-2	6	10	12.6	562	62846	6.9	Isoform 2 of Q969V3
1072	Q12996	6	15	12.4	717	82922	8.1	Cleavage stimulation factor 77 kDa subunit
1073	Q8NFM1	6	10	12	585	65060	8.9	Eukaryotic translation initiation factor 2A
1073	UPI00000473DB	6	10	12	585	64990	8.9	eukaryotic translation initiation factor 2A
1073	Q96K81	6	10	12	585	64986	8.9	CDNA FLJ14450 fis, clone HEMBB1001736, weakly similar to EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 9
1073	Q96EW9	6	10	12	585	64989	9	Eukaryotic translation initiation factor 2A, 65kDa
1073	UPI000045718C	6	10	11.5	608	67707	8.9	eukaryotic translation initiation factor 2A
1073	Q9BY44	6	10	11.5	609	67851	9	Eukaryotic translation initiation factor 2A 65 kDa

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1074	P53634	6	18	11.7	463	51842	7	Dipeptidyl-peptidase 1 precursor (EC 3.4.14.1) (Dipeptidyl-peptidase I) (DPP-I) (DPPI) (Cathepsin C) (Cathepsin J) (Dipeptidyl transferase) [Contains: Dipeptidyl-peptidase 1 exclusion domain chain (Dipeptidyl- peptidase I exclusion domain chain); Dipeptidyl peptidase 1 heavy chain (Dipeptidyl-peptidase I heavy chain); Dipeptidyl-peptidase 1 light chain (Dipeptidyl-peptidase I light chain)]
1074	UPI000006D22D	6	18	11.7	463	51854	7	Dipeptidyl-peptidase 1 precursor (EC 3.4.14.1) (Dipeptidyl-peptidase I) (DPP-I) (DPPI) (Cathepsin C) (Cathepsin J) (Dipeptidyl transferase) [Contains: Dipeptidyl-peptidase 1 exclusion domain chain (Dipeptidyl- peptidase I exclusion domain chain); Dipeptid
1074	Q8WY99	6	18	11.7	463	51902	7	Cathepsin C
1074	Q71E76	6	18	11.7	463	51816	7	Cathepsin C
1075	Q8NA80	6	27	12.4	534	58309	9.2	CDNA FLJ35762 fis, clone TESTI2004793, moderately similar to Homo sapiens NY-REN-2 antigen mRNA
1075	UPI0000D624D2	6	27	11.4	579	63076	9	YTH domain family protein 3.
1075	Q7Z739	6	27	11.3	585	63861	9	YTH domain family protein 3
1076	P28288	6	27	11.1	659	75476	9.4	ATP-binding cassette sub-family D member 3
1077	P35610	6	8	11.1	550	64735	8.9	Sterol O-acyltransferase 1
1078	Q8IYB3-2	6	16	11.1	902	102126	11.8	Isoform 2 of Q8IYB3
1078	Q8IYB3	6	16	11.1	904	102335	11.8	Serine/arginine repetitive matrix protein 1
1078	Q5VVN3	6	16	11	913	103390	11.8	Serine/arginine repetitive matrix 1
1079	Q96AC1-2	6	14	11.5	633	72397	7.5	Isoform 2 of Q96AC1
1079	Q96AC1	6	14	10.7	680	77861	6.7	Pleckstrin homology domain-containing family C member 1
1080	P28331	6	15	10.6	727	79468	6.2	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial precursor
1081	O00461	6	10	10.1	696	81880	4.8	Golgi phosphoprotein 4
1082	Q14978	6	27	10	699	73603	9.5	Nucleolar phosphoprotein p130
1082	UPI00001303C3	6	27	10	699	73720	9.5	nucleolar and coiled-body phosphoprotein 1
1082	Q9BUV3	6	27	10	700	73745	9.5	Nucleolar and coiled-body phosphoprotein 1
1082	Q14978-2	6	27	9.9	709	74747	9.5	Isoform Beta of Q14978
1083	P30825	6	35	9.9	629	67638	5.4	High-affinity cationic amino acid transporter 1
1084	P53794	6	28	9.2	718	79694	7.3	Sodium/myo-inositol cotransporter (Na(+)/myo-inositol cotransporter)
1085	Q8N556	6	31	9	730	80741	8.6	Actin filament associated protein 1

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1085	UPI0000233618	6	31	9	730	80725	8.7	actin filament associated protein 1
1085	Q9HBY1	6	31	9	730	80727	8.7	Actin filament associated protein
1086	Q5T3X0	6	31	16.9	414	46139	9.6	Interferon, gamma-inducible protein 16
1086	Q16666-2	6	31	9.6	729	82096	9.3	Isoform 2 of Q16666
1086	Q16666	6	31	8.9	785	88256	9.3	Gamma-interferon-inducible protein Ifi-16
1087	Q2TTR2	6	14	8.6	928	103136	4.8	Cell growth inhibiting protein 39
1087	Q9BZQ8	6	14	8.6	928	103135	4.8	Niban protein
1088	Q7Z5K2	6	10	8.2	1190	132945	5.4	Wings apart-like protein homolog
1088	UPI0000D60F87	6	10	8	1228	137363	5.9	Wings apart-like protein homolog (Friend of EBNA2 protein).
1088	Q7Z5K2-2	6	10	8	1227	137314	5.9	Isoform 2 of Q7Z5K2
1089	UPI00004576CB	6	8	8.2	777	89028	9.6	RNA-binding protein 12B (RNA-binding motif protein 12B).
1090	Q13616	6	18	8.1	776	89678	8	Cullin-1
1091	O94855	6	19	8	1032	113000	7.2	Protein transport protein Sec24D
1091	UPI00001AEA4F	6	19	8	1032	113010	7.2	Protein transport protein Sec24D (SEC24-related protein D).
1091	Q8IYI7	6	19	8	1033	113081	7.2	SEC24 related gene family, member D
1092	Q53HG6	6	19	8.3	726	82804	7	Cysteine-tRNA ligase isoform a variant
1092	P49589-2	6	19	8.3	726	82846	7	Isoform 2 of P49589
1092	UPI00004F8E1C	6	19	8.1	738	84472	6.4	cysteinyl-tRNA synthetase isoform d
1092	P49589	6	19	8	748	85473	6.7	Cysteinyl-tRNA synthetase, cytoplasmic
1092	Q5HYE4	6	19	7.2	831	94638	6.8	Hypothetical protein DKFZp686F1612
1093	Q3ZAQ6	6	25	8	839	94447	6.7	Autophagy 9-like 1 protein
1093	UPI0000456EF3	6	25	8	839	94471	6.7	Autophagy-related protein 9A (APG9-like 1).
1093	Q7Z3C6	6	25	8	839	94466	6.7	Autophagy-related protein 9A
1094	Q59H74	6	10	8	854	95158	5.9	Integrin alpha 4 variant
1095	Q14739	6	26	7.8	615	70703	9.4	Lamin-B receptor
1096	UPI0000D620CF	6	9	8.1	1084	120372	5.2	Nuclear pore complex protein Nup133 (Nucleoporin Nup133) (133 kDa nucleoporin).
1096	Q8WUM0	6	9	7.6	1156	128979	5.1	Nuclear pore complex protein Nup133
1097	Q6Y7W6-2	6	14	8.7	1100	127290	5.4	Isoform 2 of Q6Y7W6
1097	Q6Y7W6	6	14	7.4	1299	150070	5.5	PERQ amino acid-rich with GYF domain-containing protein 2
1097	UPI0000D612CD	6	14	7.4	1301	150271	5.5	PERQ amino acid-rich with GYF domain-containing protein 2 (Grb10- interacting GYF protein 2) (Trinucleotide repeat-containing protein 15).
1098	Q9H7I6	6	33	10	672	71623	7.9	FLJ00100 protein
1098	Q9H7Q7	6	33	8.7	772	81919	8.3	FLJ00010 protein
1098	Q9BXP2	6	33	7.3	914	96110	8.1	Solute carrier family 12 member 9
1098	Q9NQR5	6	33	7.3	914	96171	8.1	Cation-chloride cotransporter-interacting protein
1098	Q9BYI0	6	33	7.3	914	96079	8.3	Cation chloride cotransporter 6
1099	Q4LE61	6	13	7.2	1073	118793	7	SYMPK variant protein

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1099	UPI00000622E6	6	13	6.7	1142	126500	6.4	Symplekin.
1099	Q92797	6	13	6	1274	141148	6.1	Symplekin
1100	Q9NT51	6	8	9.1	859	96782	7.7	Hypothetical protein DKFZp434P1818
1100	Q2T9J4	6	8	6.9	1132	128394	7	Inositol polyphosphate-5-phosphatase F
1100	Q9Y2H2	6	8	6.8	1150	130166	7.1	Inositol polyphosphate-5-phosphatase F
1101	Q8IY37	6	10	6.7	1157	129545	8.1	Probable ATP-dependent RNA helicase DHX37
1102	Q15020	6	10	6.5	963	109935	5.6	Squamous cell carcinoma antigen recognized by T-cells 3
1103	Q96KR1	6	7	6.2	1057	115287	9.3	Zinc finger RNA-binding protein
1103	UPI00001BBB38	6	7	6.1	1074	117012	9	zinc finger RNA binding protein
1104	Q92626	6	16	5.7	1496	167210	7.3	Peroxidasin homolog
1105	P32004	6	10	5.5	1257	140003	6.2	Neural cell adhesion molecule L1 precursor
1105	UPI00001AEDC0	6	10	5.5	1248	138907	6.2	Neural cell adhesion molecule L1 precursor (N-CAM L1) (CD171 antigen).
1105	P32004-2	6	10	5.5	1253	139517	6.2	Isoform 2 of P32004
1106	Q10570	6	12	5.5	1443	160883	6.4	Cleavage and polyadenylation specificity factor subunit 1
1107	Q13464	6	9	5.4	1354	158174	5.9	Rho-associated protein kinase 1
1107	UPI000022A6D8	6	9	5.4	1354	158243	5.9	Rho-associated protein kinase 1 (EC 2.7.11.1) (Rho-associated, coiled- coil-containing protein kinase 1) (p160 ROCK-1) (p160ROCK) (Renal carcinoma antigen NY-REN-35).
1107	Q2KHM4	6	9	5.4	1354	158127	5.9	Rho-associated, coiled-coil containing protein kinase 1
1108	Q92620	6	15	5.4	1227	140502	6.5	Pre-mRNA-splicing factor ATP-dependent RNA helicase PRP16
1109	O95239-2	6	12	5.7	1127	128459	6.2	Isoform 2 of O95239
1109	O95239	6	12	5.2	1232	139881	6.3	Chromosome-associated kinesin KIF4A
1110	P42695	6	27	5.1	1498	168890	7.5	Condensin-II complex subunit D3
1110	UPI0000D626A5	6	27	5.1	1501	169232	7.6	Condensin-II complex subunit D3 (Non-SMC condensin II complex subunit D3) (hCAP-D3).
1111	Q5VT25-3	6	17	5.4	1638	186112	6.3	Isoform 3 of Q5VT25
1111	Q5VT25-5	6	17	5.2	1719	195921	6.5	Isoform 5 of Q5VT25
1111	Q5VT25	6	17	5.1	1732	197306	6.6	Serine/threonine-protein kinase MRCK alpha
1111	Q5VT25-2	6	17	5.1	1754	199809	6.4	Isoform 2 of Q5VT25
1112	Q86UU1-2	6	6	4.9	1319	144739	8.6	Isoform 2 of Q86UU1
1113	Q16363	6	45	4.8	1823	202527	6.3	Laminin subunit alpha-4 precursor
1113	Q5D044	6	45	4.8	1816	201882	6.3	LAMA4 protein
1113	Q16363-2	6	45	4.8	1816	201779	6.3	Isoform 2 of Q16363
1114	Q8IZN6	6	20	4.7	1278	144200	8.2	ATP-binding cassette protein C4 splice variant A
1114	O15439	6	20	4.5	1325	149540	8.3	Multidrug resistance-associated protein 4
1114	Q9BX28	6	20	4.5	1325	149526	8.2	ATP-binding cassette, sub-family C (CFTR/MRP), member 4

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1114	Q8NEW8	6	20	4.5	1325	149355	8.3	Multidrug resistance-associated protein
1115	Q69YN4	6	9	4.2	1810	201700	5	Protein KIAA1429
1115	UPI00001BBB23	6	9	4.2	1812	202023	5	hypothetical protein LOC25962 isoform 1
1115	Q9P2B8	6	9	4.2	1795	200853	4.8	KIAA1429 protein
1116	Q7KZ85	6	9	3.8	1726	199071	4.9	Transcription elongation factor SPT6
1116	UPI0000D622EF	6	9	3.8	1728	199271	4.9	Transcription elongation factor SPT6 (hSPT6) (Tat-cotransactivator 2 protein) (Tat-CT2 protein).
1117	UPI0000D6119F	6	15	4	1734	198891	6.9	proteasome (prosome, macropain) activator subunit 4
1117	Q14997	6	15	3.7	1843	211332	6.9	Proteasome activator complex subunit 4
1118	UPI000066D92A	6	12	3.5	1922	208475	4.7	Tumor suppressor p53-binding protein 1 (p53-binding protein 1) (p53BP1) (53BP1).
1118	Q12888	6	12	3.4	1972	213573	4.7	Tumor suppressor p53-binding protein 1
1119	Q6MZL5	6	6	3.9	1694	195643	5.2	Hypothetical protein DKFZp686C06243
1119	Q15643	6	6	3.3	1979	227637	5.3	Thyroid receptor-interacting protein 11
1119	UPI000013D767	6	6	3.3	1979	227584	5.3	Thyroid receptor-interacting protein 11 (TRIP-11) (Golgi-associated microtubule-binding protein 210) (GMAP-210) (Trip230) (Clonal evolution-related gene on chromosome 14).
1120	Q9BTC0	6	22	3.3	2240	243870	7.9	Death-inducer obliterator 1
1120	UPI000056322E	6	22	3.3	2240	243840	7.9	death inducer-obliterator 1 isoform c
1121	Q0KKZ9	6	19	3.2	2090	239618	7	Mib
1121	Q92508	6	19	3.2	2035	233040	6.9	Protein FAM38A
1122	Q93008	6	9	2.6	2547	289539	5.7	Probable ubiquitin carboxyl-terminal hydrolase FAF-X
1122	UPI0000D61D4F	6	9	2.6	2563	291447	5.7	Probable ubiquitin carboxyl-terminal hydrolase FAF-X (EC 3.1.2.15) (Ubiquitin thioesterase FAF-X) (Ubiquitin-specific-processing protease FAF-X) (Deubiquitinating enzyme FAF-X) (Fat facets protein-related, X-linked) (Ubiquitin-specific protease 9, X chro
1122	UPI0000D61D4E	6	9	2.6	2564	291492	5.8	Probable ubiquitin carboxyl-terminal hydrolase FAF-X (EC 3.1.2.15) (Ubiquitin thioesterase FAF-X) (Ubiquitin-specific-processing protease FAF-X) (Deubiquitinating enzyme FAF-X) (Fat facets protein-related, X-linked) (Ubiquitin-specific protease 9, X chro
1122	UPI00006AB82F	6	9	2.6	2554	290495	5.8	ubiquitin specific protease 9, X-linked isoform 4
1122	UPI00006AB82E	6	9	2.6	2570	292312	5.8	ubiquitin specific protease 9, X-linked isoform 3
1122	Q93008-2	6	9	2.6	2563	291356	5.7	Isoform Long of Q93008

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1123	UPI000034ECE6	6	8	2.3	3097	346901	6.4	triple functional domain (PTPRF interacting)
1124	P46939	6	19	2	3433	394495	5.3	Utrophin
1124	UPI000049E05A	6	19	2	3433	394520	5.3	Utrophin (Dystrophin-related protein 1) (DRP1) (DRP).
1124	Q5SZ57	6	19	2	3433	394467	5.3	Utrophin
1125	Q8WZ42	6	12	0.2	34350	3816081	6.3	Titin
1125	Q8WZ42-8	6	12	0.2	34474	3829767	6.4	Isoform 8 of Q8WZ42
1125	Q8WZ42-2	6	12	0.2	34258	3805759	6.3	Isoform 2 of Q8WZ42
1126	P05387	5	50	73.9	115	11665	4.5	60S acidic ribosomal protein P2
1127	P18859	5	12	65.7	108	12587	9.5	ATP synthase coupling factor 6, mitochondrial precursor
1128	Q6IB68	5	11	65	103	11953	5.9	MYCBP protein
1128	Q99417	5	11	65	103	11967	5.9	C-Myc-binding protein
1129	Q9NS69	5	67	62	142	15522	4.3	Mitochondrial import receptor subunit TOM22 homolog
1130	P18085	5	60	59.4	180	20511	7.2	ADP-ribosylation factor 4
1131	P62314	5	45	54.6	119	13282	11.6	Small nuclear ribonucleoprotein Sm D1
1132	P09132	5	15	54.2	144	16156	9.8	Signal recognition particle 19 kDa protein
1133	P12236	5	116	53	298	32866	9.7	ADP/ATP translocase 3
1134	Q13526	5	18	51.5	163	18243	8.8	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1
1135	Q64152	5	50	50	204	22031	9.5	Transcription factor BTF3
1135	P20290	5	50	49.5	206	22168	9.4	Transcription factor BTF3
1136	P50583	5	17	48.3	147	16829	5.3	Bis(5'-nucleosyl)-tetraphosphatase [asymmetrical]
1137	Q9Y3B4	5	28	48	125	14585	9.4	Pre-mRNA branch site protein p14
1138	O14737	5	49	47.2	125	14285	6	Programmed cell death protein 5
1139	P31949	5	83	46.7	105	11740	7.2	Protein S100-A11
1140	Q15121	5	60	44.6	130	15040	5	Astrocytic phosphoprotein PEA-15
1140	Q6FHL9	5	60	44.6	130	15068	5	PEA15 protein
1141	Q99584	5	60	41.8	98	11471	6.2	Protein S100-A13
1142	Q9BYN0	5	11	41.6	137	14259	8.2	Sulfiredoxin-1
1143	P0C0S5	5	202	40.6	128	13553	10.6	Histone H2A.Z
1143	Q71UI9	5	202	40.6	128	13509	10.6	Histone H2AV
1144	P62330	5	22	40.6	175	20082	9	ADP-ribosylation factor 6
1144	Q5U025	5	22	40.6	175	20211	9	ADP-ribosylation factor 6
1145	P14927	5	37	39.6	111	13530	8.8	Ubiquinol-cytochrome c reductase complex 14 kDa protein
1146	P24666	5	17	39.2	158	18042	6.8	Low molecular weight phosphotyrosine protein phosphatase
1146	Q59EH3	5	17	37.6	165	18698	7.9	Acid phosphatase 1 isoform c variant
1147	P82932	5	24	39.2	125	14227	9.3	Mitochondrial 28S ribosomal protein S6
1148	P30405	5	20	39.1	207	22040	9.4	Peptidyl-prolyl cis-trans isomerase, mitochondrial precursor
1149	Q4VC31	5	16	38.9	144	16620	7.8	Coiled-coil domain-containing protein 58
1150	Q8IXM3	5	27	38.7	137	15383	9.6	39S ribosomal protein L41, mitochondrial precursor
1151	O95881	5	15	38.4	172	19206	5.4	Thioredoxin domain-containing protein 12 precursor

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1152	P07741	5	27	38.3	180	19608	6	Adenine phosphoribosyltransferase
1153	Q53GL9	5	24	39	428	49019	5.8	HLA-B associated transcript 1 variant
1153	Q13838	5	24	39	428	48991	5.7	Spliceosome RNA helicase BAT1
1153	Q0EFA1	5	24	37.7	443	50679	5.9	BAT1 protein
1154	P51970	5	13	37.2	172	20105	7.6	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8
1155	P53680	5	14	36.6	142	17018	6.2	AP-2 complex subunit sigma-1
1156	P01111	5	12	36.5	189	21229	5.2	GTPase NRas precursor
1157	P24534	5	55	36.4	225	24764	4.7	Elongation factor 1-beta
1157	UPI000013DA8E	5	55	36.4	225	24932	4.7	PREDICTED: similar to eukaryotic translation elongation factor 1 beta 2
1158	P51571	5	80	36.4	173	18999	6.2	Translocon-associated protein subunit delta precursor
1159	P62263	5	120	36.4	151	16273	10.1	40S ribosomal protein S14
1160	P07951-2	5	25	36.3	284	32990	4.7	Isoform 2 of P07951
1161	P61353	5	44	36	136	15798	10.6	60S ribosomal protein L27
1162	Q96DE0	5	7	35.4	195	21273	6.9	Nucleoside diphosphate-linked moiety X motif 16
1163	Q9UBI1	5	15	35.4	195	22151	6	COMM domain-containing protein 3
1164	P60033	5	26	35.2	236	25809	5.3	CD81 antigen
1164	UPI000066D8DE	5	26	30.3	274	29806	6.9	CD81 antigen (26 kDa cell surface protein TAPA-1) (Target of the antiproliferative antibody 1) (Tetraspanin-28) (Tspan-28).
1165	O60493-4	5	28	40	140	16316	6.8	Isoform 4 of O60493
1165	O60493	5	28	34.6	162	18762	8.7	Sorting nexin-3
1166	P10301	5	12	34.4	218	23480	6.9	Ras-related protein R-Ras precursor
1167	Q3MIH3	5	263	34.4	128	14728	9.8	Ubiquitin A-52 residue ribosomal protein fusion product 1
1168	P36404	5	18	34.2	184	20878	6.4	ADP-ribosylation factor-like protein 2
1169	Q92572	5	27	34.2	193	21732	5.4	AP-3 complex subunit sigma-1
1170	P55327	5	14	33.7	184	19863	5	Tumor protein D52
1170	Q6FGS3	5	14	33.7	184	19847	5	TPD52 protein
1170	UPI00005520F0	5	14	30	207	22477	5.4	tumor protein D52 isoform 2
1170	UPI0000D624DE	5	14	29.7	209	22635	5.4	Tumor protein D52 (N8 protein).
1170	Q53EK8	5	14	27.9	222	23782	5.9	N8 protein long isoform variant
1170	Q86YZ2	5	14	27.7	224	24327	4.8	Prostate and colon associated protein
1170	UPI0000D624DF	5	14	27.4	226	24485	4.8	Tumor protein D52 (N8 protein).
1170	Q9UCX8	5	14	25	248	26382	6.4	N8 protein long isoform
1170	UPI0000D624DD	5	14	24.8	250	26480	5.9	Tumor protein D52 (N8 protein).
1171	Q9NRV9	5	29	33.3	189	21097	5.8	Heme-binding protein 1
1172	Q13765	5	42	32.6	215	23384	4.6	Nascent polypeptide-associated complex subunit alpha
1173	O75663	5	9	32	272	31444	5.9	TIP41-like protein
1174	Q9UMX5	5	5	32	172	18856	5.7	Neudesin precursor
1175	P15374	5	18	31.3	230	26183	4.9	Ubiquitin carboxyl-terminal hydrolase isozyme L3

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1176	UPI000045667B	5	18	31.4	185	20796	7	Vacuolar protein sorting-associated protein 29 (Vesicle protein sorting 29) (hVPS29) (PEP11).
1176	Q6IAH3	5	18	31.2	186	20927	7	VPS29 protein
1177	P49207	5	70	30.8	117	13293	11.5	60S ribosomal protein L34
1178	Q15363	5	81	30.8	201	22761	5.2	Transmembrane emp24 domain-containing protein 2 precursor
1179	Q9Y3D9	5	10	30.5	190	21771	8.9	Mitochondrial ribosomal protein S23
1180	Q9Y3U8	5	40	30.5	105	12254	11.6	60S ribosomal protein L36
1181	Q9Y6A4	5	12	30.1	193	22774	9.8	Uncharacterized protein C16orf80
1182	Q3T0Q6	5	28	31.2	170	18742	7.7	Cellular nucleic acid-binding protein
1182	Q4JGY1	5	28	31	171	18871	7.6	Cellular nucleic acid binding protein beta variant 1
1182	Q4JGY0	5	28	30.8	172	18970	7.6	Cellular nucleic acid binding protein beta variant 2
1182	P62633	5	28	29.9	177	19463	7.7	Cellular nucleic acid-binding protein
1182	P53996	5	28	29.8	178	19592	7.6	Cellular nucleic acid-binding protein
1183	UPI0000456547	5	15	29.5	224	24849	8.5	Signal peptidase complex subunit 2 (EC 3.4.-.-) (Microsomal signal peptidase 25 kDa subunit) (SPase 25 kDa subunit).
1183	Q15005	5	15	29.2	226	25003	8.5	Signal peptidase complex subunit 2
1183	UPI000047EFF7	5	15	29.2	226	24976	8	hypothetical protein LOC653566
1184	Q53F20	5	17	28.9	266	30434	3.9	Acidic (Leucine-rich) nuclear phosphoprotein 32 family, member E variant
1184	Q9BTT0	5	17	28.7	268	30692	3.8	Acidic leucine-rich nuclear phosphoprotein 32 family member E
1185	Q15382	5	25	28.8	184	20497	5.9	GTP-binding protein Rheb precursor
1185	Q6NZ61	5	25	28.8	184	20558	5.9	Ras homolog enriched in brain
1186	P68431	5	49	28.7	136	15404	11.1	Histone H3.1
1186	Q71DI3	5	49	28.7	136	15388	11.3	Histone H3.2
1186	Q16695	5	49	28.7	136	15508	11.1	Histone H3.1t
1186	P84243	5	49	28.7	136	15328	11.3	Histone H3.3
1186	UPI00006C1BEF	5	49	27.5	142	16181	10.6	PREDICTED: similar to H3 histone, family 3B
1186	UPI00006C029D	5	49	21.7	180	20527	10.2	PREDICTED: similar to H3 histone, family 2 isoform 2
1187	O00217	5	16	28.6	210	23705	6.3	NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial precursor
1188	Q53S50	5	16	30.1	249	28345	6.5	Hypothetical protein MTX2
1188	Q8IZ68	5	16	29.6	253	28823	6.5	Metaxin 2
1188	O75431	5	16	28.5	263	29763	6.3	Metaxin-2
1189	A0JLN5	5	31	28.4	169	19872	9.9	Hypothetical protein
1189	Q99442	5	31	12	399	45862	7.1	Translocation protein SEC62
1190	Q53F35	5	21	28.4	250	28673	4.1	Acidic (Leucine-rich) nuclear phosphoprotein 32 family, member B variant
1190	Q92688	5	21	28.3	251	28788	4.1	Acidic leucine-rich nuclear phosphoprotein 32 family member B

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
1191	Q8N183	5	12	28.4	169	19856	9	Mimitin, mitochondrial precursor
1192	Q9UES0	5	39	29.3	191	21607	6.5	SNARE protein Ykt6
1192	O15498	5	39	28.3	198	22418	6.9	Synaptobrevin homolog YKT6
1193	P24390	5	36	28.3	212	24542	8.6	ER lumen protein retaining receptor 1
1194	O43617	5	17	27.8	180	20274	5	Trafficking protein particle complex subunit 3
1195	O43447	5	18	27.7	177	19208	8.1	Peptidyl-prolyl cis-trans isomerase H
1196	Q9UK41	5	20	27.6	221	25425	5.5	Vacuolar protein sorting-associated protein 28 homolog
1197	O15145	5	44	27.5	178	20547	8.6	Actin-related protein 2/3 complex subunit 3
1197	Q2LE71	5	44	27.5	178	20565	8.6	Actin related protein 2/3 complex
1198	O14735	5	16	27.2	213	23539	8	CDP-diacylglycerol--inositol 3-phosphatidyltransferase
1198	Q53HA5	5	16	27.2	213	23558	8.3	CDP-diacylglycerol--inositol 3-phosphatidyltransferase isoform 1 variant
1199	Q15181	5	23	27	289	32660	5.9	Inorganic pyrophosphatase
1200	Q13442	5	19	26.5	181	20630	8.9	28 kDa heat- and acid-stable phosphoprotein
1201	P83881	5	47	26.4	106	12441	10.6	60S ribosomal protein L36a
1201	UPI00006C193F	5	47	26.4	106	12366	10.4	PREDICTED: similar to large subunit ribosomal protein L36a
1201	UPI00001AFE47	5	47	26.4	106	12475	10.4	PREDICTED: similar to large subunit ribosomal protein L36a
1201	UPI000016174B	5	47	26.4	106	12338	10.3	PREDICTED: similar to large subunit ribosomal protein L36a
1202	Q15056-2	5	31	28.1	228	25200	8.1	Isoform Short of Q15056
1202	Q15056	5	31	25.8	248	27385	7.2	Eukaryotic translation initiation factor 4H
1203	A3KFL4	5	9	25.5	263	29408	7.2	Exosome component 2
1203	Q13868	5	9	22.9	293	32789	7.5	Exosome complex exonuclease RRP4
1204	O00629	5	27	25.5	521	57887	5	Importin alpha-4 subunit
1205	P68402	5	30	25.3	229	25569	5.9	Platelet-activating factor acetylhydrolase IB subunit beta
1206	Q9H9B4	5	23	24.8	322	35619	9.1	Sideroflexin-1
1207	Q5U071	5	24	24.5	208	23905	8.1	High-mobility group box 2
1207	P26583	5	24	24.4	209	24034	7.8	High mobility group protein B2
1208	Q13151	5	48	23.6	305	30841	9.3	Heterogeneous nuclear ribonucleoprotein A0
1209	Q13155	5	21	23.4	320	35349	8.2	Multisynthetase complex auxiliary component p38
1210	Q969G5	5	11	23.4	261	27642	6.2	Protein kinase C delta-binding protein
1210	UPI000013E910	5	11	23.4	261	27701	6.4	protein kinase C, delta binding protein
1211	UPI00006C03E4	5	26	57.5	106	12581	9.4	PREDICTED: similar to FUS interacting protein (serine-arginine rich) 1
1211	Q5JRI1	5	26	35.5	172	20913	10.5	FUS interacting protein (Serine/arginine-rich) 1
1211	Q5JRI2	5	26	35.3	173	21000	10.5	FUS interacting protein (Serine/arginine-rich) 1
1211	Q5JRI3	5	26	33.5	182	22135	10.3	FUS interacting protein (Serine/arginine-rich) 1
1211	Q5JRI4	5	26	33.3	183	22222	10.3	FUS interacting protein (Serine/arginine-rich) 1

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
1211	UPI0000DD7961	5	26	25	244	29195	11.1	PREDICTED: similar to FUS-interacting serine-arginine-rich protein 1 (TLS-associated protein with Ser-Arg repeats) (TLS-associated protein with SR repeats) (TASR) (TLS-associated serine-arginine protein) (TLS-associated SR protein) (Neural-specific SR protein... isoform 3
1211	Q5JRI0	5	26	23.4	261	31213	11.3	FUS interacting protein (Serine/arginine-rich) 1
1211	O75494	5	26	23.3	262	31301	11.3	FUS-interacting serine-arginine-rich protein 1
1211	Q53GD7	5	26	23.3	262	31282	11.3	FUS interacting protein (Serine-arginine rich) 1 isoform 2 variant
1212	Q3B7K3	5	14	23.2	267	30368	9	IKIP protein
1213	Q502X2	5	14	23.1	186	21233	4.8	Diablo homolog
1213	Q9NR28	5	14	18	239	27131	5.9	Diablo homolog, mitochondrial precursor
1214	P01584	5	10	22.7	269	30748	4.8	Interleukin-1 beta precursor
1214	Q53X59	5	10	22.7	269	30747	4.9	IL1B protein
1215	P52815	5	34	22.7	198	21348	8.9	39S ribosomal protein L12, mitochondrial precursor
1216	O95292	5	51	22.6	243	27228	7.3	Vesicle-associated membrane protein-associated protein B/C
1217	Q8IWR8	5	61	25.4	173	20820	11.4	Ribosomal protein L19
1217	UPI0000192A4A	5	61	22.6	195	23335	11.5	60S ribosomal protein L19.
1217	P84098	5	61	22.4	196	23466	11.5	60S ribosomal protein L19
1217	Q53G49	5	61	22.4	196	23467	11.4	Ribosomal protein L19 variant
1218	Q9BUN8	5	12	22.3	251	28801	9.5	Derlin-1
1219	Q9Y3A6	5	22	22.3	229	26005	4.8	Transmembrane emp24 domain-containing protein 5 precursor
1220	P31431	5	26	22.2	198	21642	4.5	Syndecan-4 precursor
1220	Q53FN9	5	26	22.2	198	21608	4.5	Syndecan 4 variant
1221	Q07021	5	30	22	282	31362	4.8	Complement component 1 Q subcomponent-binding protein, mitochondrial precursor
1222	P61421	5	12	21.9	351	40329	5	Vacuolar ATP synthase subunit d
1223	Q9BWM7	5	17	21.8	321	35503	9.1	Sideroflexin-3
1223	UPI00004563F7	5	17	21.5	325	35979	9	Sideroflexin-3.
1223	UPI000006EE3D	5	17	21.5	325	35979	9.1	sideroflexin 3
1224	A4D0R4	5	8	21.7	240	28191	9.6	B-cell receptor-associated protein 29
1224	Q9UHQ4	5	8	21.6	241	28320	9.5	B-cell receptor-associated protein 29
1224	UPI000049A623	5	8	21.3	244	28731	9.5	B-cell receptor-associated protein BAP29 isoform d
1224	UPI000049A622	5	8	15.4	337	39102	9.3	B-cell receptor-associated protein BAP29 isoform c
1224	UPI000049A621	5	8	14.9	348	40797	9.7	B-cell receptor-associated protein BAP29 isoform a
1225	Q9UJ70	5	20	21.5	344	37376	6.2	N-acetylglucosamine kinase
1226	Q6IBT1	5	54	21.3	277	29937	7.7	Proteasome subunit beta type
1226	Q99436	5	54	21.3	277	29965	7.7	Proteasome subunit beta type 7 precursor
1226	Q86U62	5	54	21.3	277	30018	8	Proteasome (Prosome, macropain) subunit, beta type, 7
1227	Q9H690	5	26	24.7	291	32973	7.5	CDNA: FLJ22484 fis, clone HRC10868

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
1227	Q9GZY8	5	26	21.1	342	38465	9	Uncharacterized protein C2orf33
1228	Q68D08	5	9	21	324	36750	6.1	Hypothetical protein DKFZp686B04128
1228	Q9NUQ9	5	9	21	324	36748	6.1	Protein FAM49B
1229	Q99426	5	28	20.9	244	27326	5.1	Tubulin folding cofactor B
1230	O15260-2	5	117	35.2	159	17970	6.1	Isoform 2 of O15260
1230	UPI0000D6193B	5	117	30.1	186	21115	7.2	Surfeit locus protein 4.
1230	Q5T8U5	5	117	30.1	186	21128	6.5	Surfeit 4
1230	Q5T8U7	5	117	29.8	188	21130	8.6	Surfeit 4
1230	UPI0000D6193C	5	117	29.5	190	21331	8.6	Surfeit locus protein 4.
1230	O15260	5	117	20.8	269	30394	7.8	Surfeit locus protein 4
1231	Q16836	5	28	20.4	314	34278	8.9	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial precursor
1231	UPI000013EECF	5	28	20.4	314	34294	8.9	L-3-hydroxyacyl-Coenzyme A dehydrogenase precursor
1231	UPI000013D5C7	5	28	16.4	390	42123	9.3	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial precursor (EC 1.1.1.35) (Short chain 3-hydroxyacyl-CoA dehydrogenase) (HCDH) (Medium and short chain L-3-hydroxyacyl-coenzyme A dehydrogenase).
1231	Q16836-2	5	28	16.4	390	42123	9.3	Isoform 2 of Q16836
1232	P61163	5	24	20.2	376	42614	6.6	Alpha-centractin
1233	O75323	5	18	19.6	286	33743	9.4	Protein NipSnap2
1234	Q5U000	5	26	19.5	303	33868	7.1	Cathepsin Z
1235	P11908	5	22	19.2	318	34769	6.6	Ribose-phosphate pyrophosphokinase II
1235	Q0VDI0	5	22	19	321	35054	6.4	Phosphoribosyl pyrophosphate synthetase 2
1236	P08574	5	14	19.1	325	35390	9	Cytochrome c1 heme protein, mitochondrial precursor
1236	UPI000014046B	5	14	19.1	325	35422	9	Cytochrome c1 heme protein, mitochondrial precursor (Cytochrome c-1).
1237	P46926	5	8	19	289	32668	6.9	Glucosamine-6-phosphate isomerase
1238	P18754	5	13	18.8	421	44969	7.5	Regulator of chromosome condensation
1238	UPI0000E26242	5	13	18	438	46753	8.1	regulator of chromosome condensation 1 isoform b
1238	Q6NT97	5	13	17.5	452	48146	8.2	Regulator of chromosome condensation 1
1239	Q5QPQ6	5	11	20.3	300	31735	7.6	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase
1239	P35914	5	11	18.8	325	34360	8.5	Hydroxymethylglutaryl-CoA lyase, mitochondrial precursor
1240	Q5T5B4	5	12	18.8	368	40781	6.3	Serine/threonine kinase 24
1240	Q6P0Y1	5	12	16	431	47941	5.4	Serine/threonine kinase 24
1240	Q5U0E6	5	12	16	431	47913	5.4	Serine/threonine kinase 24
1240	Q9Y6E0	5	12	15.6	443	49308	5.7	Serine/threonine-protein kinase 24
1241	P09486	5	13	18.5	303	34632	4.8	SPARC precursor
1242	Q9HC38-2	5	10	18.5	298	33233	5.6	Isoform 2 of Q9HC38
1242	UPI000006E21F	5	10	18.5	298	33249	5.6	glyoxalase domain containing 4
1242	Q9Y3E8	5	10	10.9	504	55012	8.7	Uncharacterized protein C17orf25
1243	Q5JTA8	5	21	18.4	250	28743	10	Novel protein
1243	Q9H0U3	5	21	13.7	335	38037	9.6	Implantation-associated protein precursor

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1244	P53597	5	34	18.3	333	35047	8.9	Succinyl-CoA ligase [GDP-forming] subunit alpha, mitochondrial precursor
1244	UPI000014BF59	5	34	17.6	346	36250	8.8	succinate-CoA ligase, GDP-forming, alpha subunit
1245	Q59EL5	5	29	21.9	260	29156	7	Aldo-keto reductase family 1, member B1 variant
1245	P15121	5	29	18	316	35853	7	Aldose reductase
1246	Q8WWC4	5	11	17.9	291	32545	9.2	Uncharacterized protein C2orf47
1246	Q9H671	5	11	17.9	291	32487	9.3	CDNA: FLJ22555 fis, clone HSI01193
1247	O95433	5	19	17.8	338	38274	5.5	Activator of 90 kDa heat shock protein ATPase homolog 1
1248	UPI0000202E29	5	21	33.2	205	22764	5.5	basigin isoform 4
1248	P35613	5	21	17.7	385	42200	5.7	Basigin precursor
1249	P06737	5	19	16.9	847	97149	7.2	Glycogen phosphorylase, liver form
1249	UPI0000D62406	5	19	16.8	849	97334	7.2	Glycogen phosphorylase, liver form (EC 2.4.1.1).
1250	Q96C36	5	9	16.9	320	33637	7.8	Pyrroline-5-carboxylate reductase 2
1251	Q9NZ01	5	45	16.9	308	36034	9.4	Synaptic glycoprotein SC2
1252	Q9Y394-2	5	7	19.7	289	32268	8.9	Isoform 2 of Q9Y394
1252	Q9Y394	5	7	16.8	339	38299	8.3	Dehydrogenase/reductase SDR family member 7 precursor
1253	Q5SQ52	5	19	19.4	186	21609	4.9	Casein kinase 2, beta polypeptide
1253	P67870	5	19	16.7	215	24942	5.6	Casein kinase II subunit beta
1253	Q5SRQ6	5	19	15.4	234	26926	6	Casein kinase 2, beta polypeptide
1254	UPI00006C1BBA	5	21	16.7	305	35024	8.6	PREDICTED: similar to Ran-specific GTPase-activating protein (Ran-binding protein 1) (RanBP1)
1255	Q6YN16	5	10	16.5	418	45395	8	Hydroxysteroid dehydrogenase-like protein 2
1255	UPI0000D618EF	5	10	16.5	417	45361	8.4	hydroxysteroid dehydrogenase like 2
1256	Q9Y3B3	5	15	29.5	224	25172	6.9	Transmembrane emp24 domain-containing protein 7 precursor
1256	Q6JUT2	5	15	16.3	404	46173	5.1	Toll-like receptor adapter molecule 2
1257	Q9Y570	5	13	16.1	386	42315	6	Protein phosphatase methylesterase 1
1257	UPI0000D62652	5	13	15.9	389	42669	5.8	Protein phosphatase methylesterase 1 (EC 3.1.1.-) (PME-1).
1258	P21283	5	27	16	382	43942	7.5	Vacuolar ATP synthase subunit C
1259	Q8NCJ3	5	8	15.7	413	46904	7.1	CDNA FLJ90220 fis, clone MAMMA1003126, moderately similar to Human Hpast (HPAST) mRNA
1259	Q9NZN4	5	8	12	543	61161	6.5	EH domain-containing protein 2
1260	Q6E0B2	5	16	15.5	476	52627	6.7	Small intestine SPAK-like kinase

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1260	UPI000049DF21	5	16	13.6	545	59524	6.4	STE20/SPS1-related proline-alanine-rich protein kinase (EC 2.7.11.1) (Ste-20-related kinase) (Serine/threonine-protein kinase 39) (DCHT).
1260	UPI000013D46D	5	16	13.6	545	59474	6.3	serine threonine kinase 39 (STE20/SPS1 homolog, yeast)
1260	Q9UEW8	5	16	13.5	547	59642	6.3	STE20/SPS1-related proline-alanine-rich protein kinase
1261	Q9Y305	5	9	15.5	406	46355	8	Acyl-coenzyme A thioesterase 9
1261	UPI0000D61D39	5	9	14.5	434	49270	8.3	Acyl-coenzyme A thioesterase 9 (EC 3.1.2.-) (Acyl-CoA thioesterase 9) (Acyl-CoA thioester hydrolase 9).
1261	UPI000013F264	5	9	14.4	439	49902	8.6	acyl-Coenzyme A thioesterase 2, mitochondrial isoform b
1261	UPI0000D61D38	5	9	14.2	445	50474	8.4	Acyl-coenzyme A thioesterase 9 (EC 3.1.2.-) (Acyl-CoA thioesterase 9) (Acyl-CoA thioester hydrolase 9).
1261	UPI00003D7D31	5	9	14.1	448	50851	8.5	acyl-Coenzyme A thioesterase 2, mitochondrial isoform a
1262	Q4VX89	5	9	15.2	453	50354	7.5	HBS1-like
1262	Q9Y450	5	9	10.1	684	75473	6.6	HBS1-like protein
1263	Q9H488	5	9	15.2	388	43956	8.5	GDP-fucose protein O-fucosyltransferase 1 precursor
1264	O95232	5	13	15	432	51466	9.8	Cisplatin resistance-associated overexpressed protein
1265	P12955	5	11	15	493	54548	6	Xaa-Pro dipeptidase
1266	P55036	5	18	14.9	377	40737	4.8	26S proteasome non-ATPase regulatory subunit 4
1266	Q5VWC4	5	18	14.7	380	41079	4.8	Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 4
1267	P17174	5	11	14.8	413	46248	7	Aspartate aminotransferase, cytoplasmic
1267	Q2TU84	5	11	14.8	413	46320	6.8	Growth-inhibiting protein 18
1268	Q1WAI7	5	7	14.1	306	34583	6.5	Methionine adenosyltransferase II beta variant 2
1268	Q9UJ54	5	7	13.3	323	36401	6.7	DTDP-4-keto-6-deoxy-D-glucose 4-reductase
1268	Q9BS89	5	7	13.3	323	36431	6.7	Methionine adenosyltransferase II, beta
1268	Q9NZL9	5	7	12.9	334	37552	7.4	Methionine adenosyltransferase regulatory beta subunit
1268	Q567T7	5	7	12.9	334	37480	7.6	Methionine adenosyltransferase 2 beta
1269	Q7Z4X0	5	15	14.1	341	39774	7.5	MO25-like protein
1269	Q9Y376	5	15	14.1	341	39869	6.9	Calcium-binding protein 39
1270	UPI0000208801	5	15	15.3	437	45880	5.6	trans-golgi network protein 2
1270	Q96QL2	5	15	15.3	437	45866	5.6	Trans-golgi network protein 2
1270	O43493-2	5	15	15.3	437	45774	5.6	Isoform TGN46 of O43493
1270	Q8N6T8	5	15	15	447	47058	5.6	TGOLN2 protein
1270	UPI000020880A	5	15	14.8	453	47774	6	Trans-Golgi network integral membrane protein 2 precursor (Trans-Golgi network protein TGN51) (TGN46) (TGN48) (TGN38 homolog).
1270	O43493-3	5	15	14.8	453	47592	6	Isoform TGN48 of O43493

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
1270	O43493	5	15	14	480	51007	5.7	Trans-Golgi network integral membrane protein 2 precursor
1271	Q8N8S7-2	5	7	14.6	570	63925	6.4	Isoform 2 of Q8N8S7
1271	Q8N8S7	5	7	14	591	66510	6.9	Protein enabled homolog
1272	Q9UNF1	5	5	14	606	64954	9.3	Melanoma-associated antigen D2
1273	Q15645	5	13	13.9	432	48551	6.1	Thyroid receptor-interacting protein 13
1274	Q9BXS5	5	9	15.4	423	48587	7.3	AP-1 complex subunit mu-1
1274	Q59EK3	5	9	13.9	466	53263	8.9	Adaptor-related protein complex 1, mu 1 subunit variant
1275	O43837	5	5	13.8	385	42212	8.5	Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial precursor (EC 1.1.1.41) (Isocitric dehydrogenase) (NAD(+)-specific ICDH)
1275	UPI00004709E4	5	5	13.7	387	42411	8.5	Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial precursor (EC 1.1.1.41) (Isocitric dehydrogenase) (NAD(+)-specific ICDH).
1276	UPI00002371B1	5	13	15.3	406	45169	9.2	DEAD (Asp-Glu-Ala-Asp) box polypeptide 47 isoform 2
1276	Q53GJ1	5	13	13.8	448	49882	9.2	DEAD (Asp-Glu-Ala-Asp) box polypeptide 47 isoform 1 variant
1276	Q9H0S4	5	13	13.6	455	50647	9.1	Probable ATP-dependent RNA helicase DDX47
1277	UPI0000D61BB9	5	13	13.9	433	49390	9.5	AP-2 complex subunit mu-1 (Adaptin mu-1) (AP-2 mu-2 chain) (Clathrin coat assembly protein AP50) (Clathrin coat-associated protein AP50) (Plasma membrane adaptor AP-2 50 kDa protein) (HA2 50 kDa subunit) (Clathrin assembly protein complex 2 medium chain).
1277	Q96CW1	5	13	13.8	435	49655	9.5	AP-2 complex subunit mu-1
1277	UPI00004571AB	5	13	13.8	435	49656	9.5	AP-2 complex subunit mu-1 (Adaptin mu-1) (AP-2 mu-2 chain) (Clathrin coat assembly protein AP50) (Clathrin coat-associated protein AP50) (Plasma membrane adaptor AP-2 50 kDa protein) (HA2 50 kDa subunit) (Clathrin assembly protein complex 2 medium chain).
1278	Q9NPQ8-2	5	8	13.9	524	58846	6.6	Isoform 2 of Q9NPQ8
1278	Q9NPQ8	5	8	13.8	530	59612	5.3	Synembryn-A
1278	UPI0000037C19	5	8	13.6	537	60372	5.3	resistance to inhibitors of cholinesterase 8 homolog A
1278	Q9NPQ8-3	5	8	13.6	536	60275	5.3	Isoform 3 of Q9NPQ8
1279	O15554	5	18	13.6	427	47696	9.8	Intermediate conductance calcium-activated potassium channel protein 4
1280	UPI0000F0A4F3	5	11	17.6	336	37229	6.5	C-terminal-binding protein 2
1280	P56545	5	11	13.3	445	48945	6.9	C-terminal-binding protein 2
1280	Q86SV0	5	11	13.3	445	48933	6.9	CTBP2 protein
1280	Q5SQP8	5	11	11.5	513	56102	7	C-terminal binding protein 2

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
1280	Q5SQP7	5	11	6	985	106187	8	C-terminal binding protein 2
1281	Q12765	5	32	13.3	414	46382	4.8	Secernin-1
1281	UPI000007450E	5	32	13.3	414	46422	4.8	secernin 1
1282	Q16719	5	15	13.3	465	52352	7	Kynureninase
1282	Q53F63	5	15	13.3	465	52325	6.8	Kynureninase (L-kynurenine hydrolase) variant
1283	O00116	5	20	13.2	658	72912	7.3	Alkyldihydroxyacetonephosphate synthase, peroxisomal precursor
1284	Q9H857-4	5	8	17.4	390	45998	8.1	Isoform 4 of Q9H857
1284	Q9H857-3	5	8	14.8	461	54177	7	Isoform 3 of Q9H857
1284	Q9H857-2	5	8	14	486	57204	7.1	Isoform 2 of Q9H857
1284	Q9H857	5	8	13.1	520	60719	6.8	5'-nucleotidase domain-containing protein 2
1285	Q9H223	5	5	12.9	541	61175	6.8	EH domain-containing protein 4
1286	P30837	5	13	12.8	517	57238	6.8	Aldehyde dehydrogenase X, mitochondrial precursor
1287	Q02318	5	9	12.6	531	60235	8.9	Cytochrome P450 27, mitochondrial precursor (EC 1.14.13.15) (Cytochrome P-450C27/25) (Sterol 26-hydroxylase) (Sterol 27-hydroxylase) (Vitamin D(3) 25-hydroxylase)
1288	Q15637-6	5	24	12.6	571	61889	9.3	Isoform 6 of Q15637
1289	O15427	5	30	12.5	465	49469	8	Monocarboxylate transporter 4
1289	Q53G91	5	30	12.5	465	49483	8	Solute carrier family 16, member 3 variant
1290	Q9Y285	5	18	12.4	508	57564	7.8	Phenylalanyl-tRNA synthetase alpha chain
1291	UPI000013E7A3	5	7	14	477	52812	9.7	DNA polymerase-transactivated protein 6 (DNAPTP6), mRNA
1291	Q8WV53	5	7	13.7	488	54050	9.6	DNAPTP6 protein
1291	Q53T22	5	7	12.3	545	60234	9.7	Hypothetical protein DKFZP564A2416
1291	UPI000013F0CD	5	7	12.3	546	60362	9.7	DNA polymerase-transactivated protein 6 (DNAPTP6), mRNA
1291	Q9NUQ6	5	7	12	558	61759	9.6	CDNA FLJ11202 fis, clone PLACE1007746
1291	Q9NTW4	5	7	12	558	61728	9.7	Hypothetical protein DKFZp564A2416
1292	UPI000049E047	5	35	13.5	394	43130	9.4	Adenosine 3'-phospho 5'-phosphosulfate transporter 1 (PAPS transporter 1) (Solute carrier family 35 member B2) (Putative MAPK-activating protein PM15) (Putative NF-kappa-B-activating protein 48).
1292	Q8TB61-2	5	35	13.5	392	42967	9.4	Isoform 2 of Q8TB61
1292	Q8TB61	5	35	12.3	432	47515	9.2	Adenosine 3'-phospho 5'-phosphosulfate transporter 1
1293	Q9H4A4	5	9	12.2	650	72596	5.8	Aminopeptidase B
1294	Q8NC56	5	6	12.1	503	56975	9	LEM domain-containing protein 2
1295	O75844	5	37	12	475	54813	7.5	CAAX prenyl protease 1 homolog

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
1296	P10619	5	24	11.7	480	54466	6.6	Lysosomal protective protein precursor (EC 3.4.16.5) (Cathepsin A) (Carboxypeptidase C) (Protective protein for beta-galactosidase) [Contains: Lysosomal protective protein 32 kDa chain; Lysosomal protective protein 20 kDa chain]
1296	Q59EV6	5	24	11.3	497	56120	6.6	Carrier family 6 , member 8 variant
1297	P23368	5	8	11.6	584	65444	7.6	NAD-dependent malic enzyme, mitochondrial precursor
1298	Q6PI48	5	9	11.6	645	73563	8	Aspartyl-tRNA synthetase, mitochondrial precursor
1299	Q14166	5	14	11.5	644	74404	5.5	Tubulin--tyrosine ligase-like protein 12
1300	Q9P258	5	9	11.3	522	56085	8.8	Protein RCC2
1301	Q01650	5	63	11.2	507	55010	7.7	Large neutral amino acids transporter small subunit 1
1302	Q96A33	5	9	11.2	483	55874	4.9	Coiled-coil domain-containing protein 47 precursor
1302	UPI0000073E7C	5	9	11.2	483	55816	4.9	coiled-coil domain containing 47
1302	Q96A33-2	5	9	11.2	480	55318	4.7	Isoform 2 of Q96A33
1303	O94826	5	12	10.9	608	67455	7.1	Mitochondrial precursor proteins import receptor
1303	Q6P0M2	5	12	10.9	607	67398	7.1	Translocase of outer mitochondrial membrane 70 homolog A
1304	P61011	5	8	10.9	504	55705	8.8	Signal recognition particle 54 kDa protein
1305	Q14108	5	60	10.9	478	54290	5.1	Lysosome membrane protein 2
1306	Q6UW63	5	11	10.8	502	58043	7.7	KDEL motif-containing protein 1 precursor
1306	UPI000006ED28	5	11	10.8	502	58029	7.7	KDEL (Lys-Asp-Glu-Leu) containing 1
1307	Q8IY81	5	17	10.3	847	96576	8.2	Putative rRNA methyltransferase 3 (EC 2.1.1.-) (rRNA (uridine-2'-O-)-methyltransferase 3)
1307	UPI000013C87B	5	17	10.3	847	96558	8.4	Putative rRNA methyltransferase 3 (EC 2.1.1.-) (rRNA (uridine-2'-O-)-methyltransferase 3).
1308	Q09161	5	8	10	790	91839	6.4	Nuclear cap-binding protein subunit 1
1309	P19022	5	7	9.9	906	99809	4.8	Cadherin-2 precursor
1310	P52294	5	12	9.9	538	60249	5	Importin alpha-1 subunit
1310	UPI000013D524	5	12	9.9	538	60222	5	Importin alpha-1 subunit (Karyopherin alpha-1 subunit) (SRP1-beta) (RAG cohort protein 2) (Nucleoprotein interactor 1) (NPI-1).
1310	Q5BKZ2	5	12	9.9	538	60309	5	Karyopherin alpha 1
1311	Q8TCS8	5	12	9.7	783	85951	7.8	Polyribonucleotide nucleotidyltransferase 1, mitochondrial precursor

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1311	UPI0000D611A9	5	12	9.7	785	86123	7.8	Polyribonucleotide nucleotidyltransferase 1, mitochondrial precursor (EC 2.7.7.8) (PNPase 1) (Polynucleotide phosphorylase-like protein) (PNPase old-35) (3'-5' RNA exonuclease OLD35).
1311	UPI000007136D	5	12	9.7	783	85937	7.8	polyribonucleotide nucleotidyltransferase 1
1312	UPI000015D937	5	5	9.7	620	71320	6.5	protein arginine methyltransferase 5 isoform b
1312	O14744	5	5	9.4	637	72684	6.3	Protein arginine N-methyltransferase 5
1313	Q9Y5L0-4	5	15	9.4	909	102541	5.6	Isoform 4 of Q9Y5L0
1313	A4D1K9	5	15	9.2	923	104203	5.6	Transportin 3
1314	Q9BRC2	5	7	9.1	750	83856	6.8	TBCD protein
1314	Q9BTW9-5	5	7	9	757	84263	6.4	Isoform 5 of Q9BTW9
1314	UPI000020053F	5	7	5.7	1192	132600	6.2	beta-tubulin cofactor D
1314	Q9BTW9	5	7	5.7	1192	132528	6.2	Tubulin-specific chaperone D
1314	Q9BTW9-4	5	7	5.4	1248	138597	6.4	Isoform 4 of Q9BTW9
1315	Q17RS0	5	6	9	1105	122867	5.8	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1
1315	UPI0000167B18	5	6	9	1105	122721	5.8	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin c1
1315	Q92922	5	6	9	1105	122753	5.8	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily C member 1
1315	Q58EY4	5	6	9	1105	122911	5.7	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1
1316	Q7L5N7	5	15	9	544	60208	6.6	Acyltransferase-like 1
1317	Q9BUJ2-4	5	8	9.9	756	84794	8.8	Isoform 4 of Q9BUJ2
1317	Q9BUJ2-2	5	8	9.3	804	90292	6.9	Isoform 2 of Q9BUJ2
1317	Q9BUJ2	5	8	8.8	856	95739	6.9	Heterogeneous nuclear ribonucleoprotein U-like protein 1
1318	O94901	5	11	10	812	90064	7.1	Sad1/unc-84 protein-like 1
1318	UPI000013E40F	5	11	9.9	822	91113	7.2	Sad1/unc-84 protein-like 1 (Unc-84 homolog A).
1318	A4D2Q0	5	11	8.3	974	108455	8	Unc-84 homolog A
1319	Q00653	5	13	8.3	900	96749	6.2	Nuclear factor NF-kappa-B p100 subunit (DNA-binding factor KBF2) (H2TF1) (Lymphocyte translocation chromosome 10) (Oncogene Lyt-10) (Lyt10) [Contains: Nuclear factor NF-kappa-B p52 subunit]
1319	UPI000012DC55	5	13	8.3	899	96678	6.2	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 isoform b

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
1319	UPI00004563FB	5	13	8.1	930	100358	6.6	Nuclear factor NF-kappa-B p100 subunit (DNA-binding factor KBF2) (H2TF1) (Lymphocyte translocation chromosome 10) (Oncogene Lyt-10) (Lyt10) [Contains: Nuclear factor NF-kappa-B p52 subunit].
1320	Q15061	5	16	8.3	720	79119	5.9	WD repeat protein 43
1321	UPI000012B30D	5	24	8.3	836	91840	9.1	mannosyl-oligosaccharide glucosidase
1321	Q13724	5	24	8.2	837	91918	8.9	Mannosyl-oligosaccharide glucosidase
1321	Q58F09	5	24	8.2	837	91907	9	Glucosidase I
1322	Q14566	5	13	8.2	821	92889	5.4	DNA replication licensing factor MCM6
1323	O00469	5	14	8.1	737	84686	6.7	Procollagen-lysine,2-oxoglutarate 5 dioxygenase 2 precursor
1323	O00469-2	5	14	7.9	758	87098	6.7	Isoform 2 of O00469
1324	UPI000048AB3C	5	10	10	652	72532	8.6	Zinc finger CCCH domain-containing protein 11A.
1324	O75152	5	10	8	810	89131	8.4	Zinc finger CCCH domain-containing protein 11A
1324	UPI0000D62084	5	10	8	812	89346	8.4	Zinc finger CCCH domain-containing protein 11A.
1325	P33992	5	11	8	734	82286	8.4	DNA replication licensing factor MCM5
1325	Q53FG5	5	11	8	734	82237	8.3	Minichromosome maintenance deficient protein 5 variant
1326	O96005	5	19	7.8	669	76097	6.3	Cleft lip and palate transmembrane protein 1
1326	O96005-2	5	19	7.6	686	77959	6.3	Isoform 2 of O96005
1327	Q13618-2	5	8	7.8	744	86234	8	Isoform 2 of Q13618
1327	Q13618	5	8	7.6	768	88930	8.5	Cullin-3
1328	Q9UHB6-2	5	8	9.7	599	67120	5.9	Isoform Alpha of Q9UHB6
1328	Q53GG0	5	8	7.6	759	85254	6.8	Epithelial protein lost in neoplasm beta variant
1328	Q9UHB6	5	8	7.6	759	85226	6.8	LIM domain and actin-binding protein 1
1328	Q59FE8	5	8	7.5	769	86107	6.8	Epithelial protein lost in neoplasm beta variant
1329	Q2Y124	5	5	7.6	824	92904	7.6	Transient receptor potencial vanilloid 4 channel variant C
1329	Q2Y123	5	5	7.5	837	94998	8.2	Transient receptor potencial vanilloid 4 channel variant D
1329	Q9HBA0-3	5	5	7.4	853	96449	8.4	Isoform 3 of Q9HBA0
1329	Q9HBA0	5	5	7.2	871	98281	7.8	Transient receptor potential cation channel subfamily V member 4
1330	UPI000013CEE9	5	15	7.5	1037	119938	5.2	importin 8
1331	UPI0000456C02	5	12	7.2	866	97663	7.3	Dynamin-2 (EC 3.6.5.5).
1331	P50570-2	5	12	7.2	866	97652	7.6	Isoform 2 of P50570
1331	P50570	5	12	7.1	870	98064	7.5	Dynamin-2
1331	UPI0000456C01	5	12	7.1	870	98021	7.3	Dynamin-2 (EC 3.6.5.5).
1332	Q52MB3	5	12	7.1	672	78029	10.3	SAFB-like transcription modulator
1332	UPI0000039EA4	5	12	4.6	1034	117149	7.9	modulator of estrogen induced transcription isoform a
1333	Q9NXF1	5	9	7.1	929	105674	9.4	Testis-expressed sequence 10 protein
1333	UPI0000071D99	5	9	7.1	929	105693	9.4	testis expressed sequence 10

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1334	UPI0000456EF2	5	21	7.7	764	85458	8.5	Mitochondrial ATP-binding cassette sub-family B member 6 (Mitochondrial ABC transporter 3) (Mt-ABC transporter 3) (Ubiquitously expressed mammalian ABC half transporter) (P-glycoprotein-related protein).
1334	Q9NP58-4	5	21	7.7	766	85685	8.5	Isoform 4 of Q9NP58
1334	Q9NP58	5	21	7	842	93886	8.5	Mitochondrial ATP-binding cassette sub-family B member 6
1335	P25205	5	9	6.9	808	90981	5.8	DNA replication licensing factor MCM3
1335	Q53HJ4	5	9	6.9	808	90981	5.7	Minichromosome maintenance protein 3 variant
1336	Q6ZXV5	5	26	6.9	915	104009	8.9	Transmembrane and TPR repeat-containing protein 3
1336	UPI00001A9DBE	5	26	6.9	914	103835	8.9	transmembrane and tetratricopeptide repeat containing 3
1336	Q6ZXV5-2	5	26	6.9	914	103880	8.8	Isoform 2 of Q6ZXV5
1337	Q5SYX5	5	7	7	952	107946	5	Golgi autoantigen, golgin subfamily a, 2
1337	Q08379	5	7	6.8	990	111659	5	Golgin subfamily A member 2
1337	UPI00004577B2	5	7	6.8	991	111652	5	Golgin subfamily A member 2 (Cis-Golgi matrix protein GM130) (Gm130 autoantigen) (Golgin-95).
1338	Q99805	5	22	6.8	663	75776	7.4	Transmembrane 9 superfamily protein member 2 precursor
1339	Q5H9R7-3	5	14	7.1	791	88909	4.6	Isoform 3 of Q5H9R7
1339	Q5H9R7-6	5	14	6.6	844	94445	4.6	Isoform 6 of Q5H9R7
1339	Q5H9R7-2	5	14	6.5	867	96957	4.6	Isoform 2 of Q5H9R7
1339	Q5H9R7	5	14	6.4	873	97669	4.6	SAPS domain family member 3
1339	Q5H9R7-5	5	14	6.4	879	98485	4.6	Isoform 5 of Q5H9R7
1340	P56192	5	9	6.3	900	101116	6.2	Methionyl-tRNA synthetase, cytoplasmic
1341	Q03701	5	38	6.3	1054	120988	5.9	CCAAT/enhancer-binding protein zeta
1341	UPI0000072AAB	5	38	6.3	1054	120974	5.9	CCAAT/enhancer binding protein zeta
1342	Q2M2I8	5	11	6.3	863	93578	8.5	AP2-associated protein kinase 1
1343	Q53SY9	5	16	6.3	1016	106667	5.1	Hypothetical protein EMILIN1
1343	Q9Y6C2	5	16	6.3	1016	106695	5.2	EMILIN-1 precursor
1344	Q6P275	5	7	6.2	1221	140090	5.5	STAG1 protein
1344	Q4LE48	5	7	6	1275	146338	5.7	STAG1 variant protein
1344	UPI000020A2DE	5	7	6	1258	144427	5.6	stromal antigen 1
1344	Q8WVM7	5	7	6	1258	144445	5.6	Cohesin subunit SA-1
1345	Q9Y4F1	5	8	6	1045	118633	8.2	FERM, RhoGEF and pleckstrin domain-containing protein 1
1345	UPI000041C6E3	5	8	5.9	1076	122095	8.5	FERM, RhoGEF and pleckstrin domain-containing protein 1 (Chondrocyte- derived ezrin-like protein).
1345	Q9Y4F1-2	5	8	5.9	1076	122113	8.5	Isoform 2 of Q9Y4F1
1346	Q29RF7	5	8	5.8	1337	150830	7.9	SCC-112 protein
1347	O76024	5	14	5.6	890	100305	8	Wolframin
1347	UPI00000715C3	5	14	5.6	890	100291	8	Wolframin.
1348	P12109	5	19	5.6	1028	108529	5.4	Collagen alpha-1(VI) chain precursor

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1349	Q53EP0	5	15	5.6	1204	132878	5.9	Fibronectin type III domain-containing protein 3B
1349	UPI00001AE8B2	5	15	5.6	1204	132888	5.9	fibronectin type III domain containing 3B
1349	Q8IXB2	5	15	5.6	1204	132900	5.9	FAD104
1349	Q5U5T8	5	15	5.6	1204	132957	5.9	Fibronectin type III domain containing 3B
1350	Q15386	5	11	5.5	1083	123923	6.7	Ubiquitin-protein ligase E3C
1350	UPI000013D26C	5	11	5.5	1085	124150	6.7	Ubiquitin-protein ligase E3C (EC 6.3.2.-).
1350	UPI0000071402	5	11	5.5	1083	123937	6.7	ubiquitin protein ligase E3C
1351	O00291	5	6	5.2	1030	115442	5.3	Huntingtin-interacting protein 1
1351	UPI0000D61C73	5	6	5.2	1039	116414	5.3	Huntingtin-interacting protein 1 (HIP-I).
1351	Q2TB58	5	6	5.2	1037	116221	5.3	Huntingtin interacting protein 1
1352	UPI000020D228	5	8	5.3	1253	145015	8.6	Myosin-6 (Myosin VI) (Unconventional myosin VI).
1352	Q9UM54-5	5	8	5.3	1253	145041	8.6	Isoform 5 of Q9UM54
1352	Q9UM54-2	5	8	5.3	1262	146047	8.5	Isoform 2 of Q9UM54
1352	Q9UM54	5	8	5.2	1294	149691	8.5	Myosin-VI
1352	Q9UM54-4	5	8	5.2	1285	148684	8.6	Isoform 4 of Q9UM54
1352	Q9UM54-1	5	8	5.2	1285	148713	8.5	Isoform 1 of Q9UM54
1353	UPI0000D61296	5	15	5.4	1252	135490	8.8	Ras-associated and pleckstrin homology domains-containing protein 1 (RAPH1) (Lamellipodin) (Proline-rich EVH1 ligand 2) (PREL-2) (Protein RMO1) (Amyotrophic lateral sclerosis 2 chromosomal region candidate 9 gene protein).
1353	UPI000020940F	5	15	5.4	1250	135256	8.9	Ras association and pleckstrin homology domains 1 isoform 1
1353	Q70E73-10	5	15	5.4	1250	135242	8.9	Isoform RMO1
1353	Q70E73	5	15	5.1	1302	141165	8.9	Ras-associated and pleckstrin homology domains-containing protein 1
1353	UPI0000D61297	5	15	5.1	1304	141414	8.9	Ras-associated and pleckstrin homology domains-containing protein 1 (RAPH1) (Lamellipodin) (Proline-rich EVH1 ligand 2) (PREL-2) (Protein RMO1) (Amyotrophic lateral sclerosis 2 chromosomal region candidate 9 gene protein).
1354	Q9NVI1	5	11	5.1	1268	142581	6.8	Uncharacterized membrane protein KIAA1794
1354	UPI0000603C25	5	11	5.1	1268	142569	6.8	hypothetical protein LOC55215
1354	Q9NVI1-2	5	11	5.1	1267	142452	6.8	Isoform 2 of Q9NVI1
1354	Q9NVI1-3	5	11	4.9	1328	149335	6.7	Isoform 3 of Q9NVI1
1355	O75976	5	10	4.2	1380	152931	6	Carboxypeptidase D precursor
1356	O15118	5	32	4.1	1278	142166	5.4	Niemann-Pick C1 protein precursor
1356	UPI00001303D7	5	32	4.1	1278	142148	5.4	Niemann-Pick disease, type C1 precursor
1356	Q59GR1	5	32	4.1	1289	143231	5.4	Niemann-Pick disease, type C1 variant
1357	Q92896	5	7	4.1	1179	134593	6.9	Golgi apparatus protein 1 precursor
1357	Q6P9D1	5	7	4	1203	137222	6.9	Golgi apparatus protein 1
1358	Q6PGP7	5	6	3.5	1564	175485	7.5	Tetratricopeptide repeat protein 37

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
1359	Q9H3S7	5	7	3.5	1636	178972	6.9	Tyrosine-protein phosphatase non-receptor type 23
1360	UPI000049DE09	5	9	3.5	1615	182150	9.7	Retinoblastoma-binding protein 6 (p53-associated cellular protein of testis) (Proliferation potential-related protein) (Protein P2P-R) (Retinoblastoma-binding Q protein 1) (Protein RBQ-1).
1360	Q7Z6E9-2	5	9	3.2	1758	197286	9.6	Isoform 2 of Q7Z6E9
1360	Q7Z6E9	5	9	3.1	1792	201563	9.6	Retinoblastoma-binding protein 6
1361	Q12789	5	8	2.6	2109	238270	7.3	General transcription factor 3C polypeptide 1
1361	UPI0000D619C5	5	8	2.6	2110	238556	7.4	General transcription factor 3C polypeptide 1 (Transcription factor IIIC-subunit alpha) (TF3C-alpha) (TFIIIC 220 kDa subunit) (TFIIIC220) (TFIIIC box B-binding subunit).
1361	UPI0000D619C4	5	8	2.6	2112	239270	7.4	General transcription factor 3C polypeptide 1 (Transcription factor IIIC-subunit alpha) (TF3C-alpha) (TFIIIC 220 kDa subunit) (TFIIIC220) (TFIIIC box B-binding subunit).
1361	UPI00001FF123	5	8	2.6	2109	238873	7.3	general transcription factor IIIC, polypeptide 1, alpha 220kDa
1361	Q6AWA4	5	8	2.6	2112	238179	7.5	Hypothetical protein DKFZp686O0870
1361	Q6AHZ7	5	8	2.6	2109	238799	7.4	Hypothetical protein DKFZp686A111
1361	Q12789-2	5	8	2.6	2109	238885	7.3	Isoform 2 of Q12789
1362	UPI0000D60F33	5	6	2.9	1788	200772	7.1	Supervillin (Archvillin) (p205/p250).
1362	UPI0000366679	5	6	2.9	1788	200846	6.9	Supervillin (Archvillin) (p205/p250).
1362	UPI000006D31C	5	6	2.9	1788	200820	6.9	supervillin isoform 1
1362	O95425-2	5	6	2.9	1788	200792	6.9	Isoform 2 of O95425
1362	O95425	5	6	2.3	2214	247704	7	Supervillin
1362	UPI0000D60F34	5	6	2.3	2214	247670	7.1	Supervillin (Archvillin) (p205/p250).
1362	UPI0000366678	5	6	2.3	2214	247744	7	Supervillin (Archvillin) (p205/p250).
1363	Q59FH1	5	15	1.7	3587	405818	8.2	Transformation/transcription domain-associated protein variant
1363	A4D265	5	15	1.6	3830	434416	8.2	Transformation/transcription domain-associated protein
1363	Q9Y4A5	5	15	1.6	3859	437603	8.2	Transformation/transcription domain-associated protein
1364	P98160	5	7	1.4	4391	468830	6.5	Basement membrane-specific heparan sulfate proteoglycan core protein precursor
1364	UPI0000D626C6	5	7	1.4	4346	464081	6.5	Basement membrane-specific heparan sulfate proteoglycan core protein precursor (HSPG) (Perlecan) (PLC).
1364	Q5VU27	5	7	1.4	4391	468835	6.5	Heparan sulfate proteoglycan 2
1365	P68371	4	50	68.3	445	49831	4.9	Tubulin beta-2C chain
1365	Q8IZ29	4	50	68.3	445	49840	4.9	Tubulin, beta 2C
1365	Q8IWP6	4	50	68.3	445	49753	4.9	Class IVb beta tubulin
1366	P15531	4	94	65.1	152	17149	6.2	Nucleoside diphosphate kinase A

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
1367	Q9H0U4	4	51	62.7	201	22171	5.7	Ras-related protein Rab-1B
1368	P56385	4	28	62.3	69	7933	9.4	ATP synthase e chain, mitochondrial
1369	Q9Y333	4	36	60	95	10835	6.5	U6 snRNA-associated Sm-like protein LSm2
1370	Q96FJ2	4	19	57.3	89	10350	7.4	Dynein light chain 2, cytoplasmic
1371	Q9UBI6	4	98	56.9	72	8006	9	Guanine nucleotide-binding protein G(I)/G(S)/G(O) gamma-12 subunit precursor
1372	P04080	4	37	55.1	98	11140	7.6	Cystatin-B
1373	Q8WUW1	4	18	54.7	75	8745	5.5	Probable protein BRICK1
1373	Q8WUW1-2	4	18	38.7	106	12046	6.8	Isoform 2 of Q8WUW1
1373	UPI00004570B9	4	18	38	108	12158	6.8	UPI00004570B9 UniRef100 entry
1374	P82909	4	8	53.4	103	11466	10	Mitochondrial 28S ribosomal protein S36
1375	Q9Y5L4	4	19	52.6	95	10500	8.2	Mitochondrial import inner membrane translocase subunit Tim13
1376	Q15369	4	26	50.9	112	12473	4.8	Transcription elongation factor B polypeptide 1
1377	Q9Y3D0	4	9	50.3	163	17663	5.2	Protein FAM96B
1378	Q92930	4	9	48.3	207	23584	9.1	Ras-related protein Rab-8B
1379	O00483	4	48	46.9	81	9370	9.4	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4
1380	Q86Y39	4	20	46.8	141	14852	8.7	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11
1381	Q15843	4	16	45.7	81	9072	8.4	NEDD8 precursor
1381	UPI0000EFE33A	4	16	45.7	81	8905	7.2	NEDD8
1382	P14854	4	48	45.3	86	10192	7	Cytochrome c oxidase subunit VIb isoform 1
1383	Q96FQ6	4	65	44.7	103	11801	6.8	Protein S100-A16
1384	Q9Y2Q5	4	12	44	125	13507	5.4	Mitogen-activated protein-binding protein-interacting protein
1385	P62312	4	46	43.8	80	9128	9.6	U6 snRNA-associated Sm-like protein LSm6
1386	UPI0000158C34	4	12	67	100	10905	4.5	PREDICTED: similar to basic transcription factor 3-like 4
1386	UPI0000D61F1B	4	12	44.1	152	16409	5.6	Transcription factor BTF3 homolog 4 (Basic transcription factor 3-like 4).
1386	Q6PJ77	4	12	43.8	153	16470	5.6	BTF3L4 protein
1386	Q96K17	4	12	42.4	158	17271	6.4	Transcription factor BTF3 homolog 4
1387	Q96EL3	4	14	42.9	112	12107	8.8	39S ribosomal protein L53, mitochondrial precursor
1388	Q9UI30	4	26	42.4	125	14199	5.3	TRM112-like protein
1389	O43678	4	24	41.4	99	10922	9.6	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2
1390	Q4W5L2	4	16	56.9	102	10190	9.5	Hypothetical protein SNCA
1390	P37840-2	4	16	51.8	112	11372	8.3	Isoform 2
1390	P37840	4	16	41.4	140	14460	4.7	Alpha-synuclein
1391	Q16864	4	12	41.2	119	13370	5.5	Vacuolar ATP synthase subunit F
1392	Q9BPX5	4	12	41.2	153	16941	6.6	Actin-related protein 2/3 complex subunit 5-like protein
1393	Q8WVC2	4	61	42	81	8850	8.5	RPS21 protein
1393	P63220	4	61	41	83	9111	8.5	40S ribosomal protein S21
1394	P52758	4	12	40.9	137	14494	8.7	Ribonuclease UK114

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
1395	Q9NR31	4	33	40.9	198	22367	6.7	GTP-binding protein SAR1a
1396	P49458	4	35	40.7	86	10112	8	Signal recognition particle 9 kDa protein
1397	P42677	4	52	39.3	84	9461	9.5	40S ribosomal protein S27
1398	P68036	4	32	39	154	17862	8.5	Ubiquitin-conjugating enzyme E2 L3
1399	Q9BRA2	4	20	38.2	123	13941	5.5	Thioredoxin-like protein 5
1400	P61513	4	79	38	92	10275	10.4	60S ribosomal protein L37a
1401	Q6GMV3	4	11	37.9	140	15805	9.1	Similar to CG14903-PA
1402	O95182	4	14	37.2	113	12551	10.2	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 7
1402	Q6IB89	4	14	35.6	118	13279	10.5	NDUFA7 protein
1402	Q6FG42	4	14	35.6	118	13180	10.5	NDUFA7 protein
1403	P00441	4	38	37	154	15936	6.1	Superoxide dismutase [Cu-Zn]
1403	UPI00001AE968	4	38	36.5	156	16122	6.3	Superoxide dismutase [Cu-Zn] (EC 1.15.1.1).
1404	P20339	4	6	36.7	215	23659	8.1	Ras-related protein Rab-5A
1405	P62854	4	45	36.5	115	13015	11	40S ribosomal protein S26
1405	Q5JVH5	4	45	36.5	115	13001	11	OTTHUMP00000018641
1406	Q8NB37	4	5	35.9	220	23298	6.6	CDNA FLJ34283 fis, clone FEBRA2003926, weakly similar to NonF
1407	P30046	4	41	35.6	118	12712	7.3	D-dopachrome decarboxylase
1408	P52907	4	20	35.3	286	32923	5.7	F-actin capping protein subunit alpha-1
1409	P55769	4	41	35.2	128	14174	8.5	NHP2-like protein 1
1409	UPI0000F53459	4	41	34.6	130	14318	8.5	U4/U6.U5 tri-snRNP 15.5 kDa protein
1410	Q9P0M9	4	15	35.1	148	16073	10.4	Mitochondrial 39S ribosomal protein L27
1411	gi|21689593|gb|AA	4	9	34.8	138	14722	5.2	rubber elongation factor [Hevea brasiliensis]
1412	O75828	4	7	33.9	277	30850	6.2	Carbonyl reductase [NADPH] 3
1413	Q9GZM3	4	6	33.9	115	13074	6.3	RPB11b1alpha protein
1413	P52435	4	6	33.3	117	13293	5.9	DNA-directed RNA polymerase II subunit J
1413	Q9H1A6	4	6	30.7	127	14131	5.9	RPB11a protein
1413	Q0VGM6	4	6	28.3	138	15027	6.9	MGC13098 protein
1413	Q8IZ67	4	6	24.4	160	17172	6.9	MGC13098 protein
1413	UPI0000D61CA1	4	6	21.9	178	18673	6.2	DNA-directed RNA polymerase II subunit J (EC 2.7.7.6) (DNA-directed RNA polymerase II 13.3 kDa polypeptide) (RPB11).
1413	Q6PJD2	4	6	21.8	179	18885	6.4	MGC13098 protein
1413	Q59FR2	4	6	21.7	180	19038	6.7	MGC13098 protein variant
1414	Q14011	4	18	33.1	172	18648	9.5	Cold-inducible RNA-binding protein
1415	P62899	4	31	32.8	125	14463	10.5	60S ribosomal protein L31
1416	Q8N5K1	4	13	36.3	135	15278	9.6	Zinc finger, CDGSH-type domain 2
1416	Q7Z3D5	4	13	32.7	150	16793	9.4	Zinc finger CDGSH domain-containing protein 2
1417	Q9Y3E5	4	14	31.8	179	19194	8.7	Peptidyl-tRNA hydrolase 2, mitochondrial precursor
1418	P61923	4	32	31.6	177	20198	4.8	Coatomer subunit zeta-1
1418	Q53FU3	4	32	31.6	177	20267	4.9	Coatomer protein complex, subunit zeta 1 variant
1419	O14602	4	25	31.2	144	16442	5.2	Eukaryotic translation initiation factor 1A, Y-chromosomal
1420	Q96DA6	4	11	31	116	12499	10.1	Mitochondrial import inner membrane translocase subunit TIM14

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
1421	P51452	4	12	30.8	185	20478	7.8	Dual specificity protein phosphatase 3
1422	Q13232	4	7	30.8	169	19015	7.8	Nucleoside diphosphate kinase 3
1423	P36405	4	20	30.2	182	20456	7.2	ADP-ribosylation factor-like protein 3
1423	Q53X83	4	20	30.2	182	20474	7.2	ARL3 protein
1424	P67812	4	59	30.2	179	20625	9.5	Signal peptidase complex catalytic subunit SEC11A
1424	Q6IAM7	4	59	30.2	179	20611	9.5	SPC18 protein
1425	Q16718	4	42	30.2	116	13459	6	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5
1425	Q5H9R2	4	42	30.2	116	13563	5.6	Hypothetical protein DKFZp781K1356
1426	Q8IV95	4	14	34	156	17984	5.1	Nudix (Nucleoside diphosphate linked moiety X)-type motif 1
1426	Q7Z7N6	4	14	34	156	17951	5.1	Nudix (Nucleoside diphosphate linked moiety X)-type motif 1
1426	A4D205	4	14	29.6	179	20296	5	Nudix (Nucleoside diphosphate linked moiety X)-type motif 1
1426	P36639	4	14	26.9	197	22552	5.3	7,8-dihydro-8-oxoguanine triphosphatase
1427	Q5W0X3	4	16	31.1	103	11424	9.1	Peptidyl-prolyl cis-trans isomerase
1427	P62942	4	16	29.6	108	11951	8.2	FK506-binding protein 1A
1428	Q5T0P8	4	69	30	130	15069	10.9	Ribosomal protein S24
1428	Q7Z3D1	4	69	29.5	132	15326	10.8	Hypothetical protein DKFZp686N1586
1428	P62847	4	69	29.3	133	15423	10.8	40S ribosomal protein S24
1429	P46776	4	31	29.1	148	16561	11	60S ribosomal protein L27a
1429	UPI0000160A16	4	31	29.1	148	16622	11.1	PREDICTED: similar to 60S ribosomal protein L27a
1429	Q6NZ52	4	31	29.1	148	16478	11	Ribosomal protein L27a
1430	Q9UDC2	4	68	31.1	135	15812	10.4	RIG homolog
1430	P62841	4	68	29	145	17040	10.4	40S ribosomal protein S15
1431	P26447	4	41	28.7	101	11728	6.1	Protein S100-A4
1432	P32321	4	18	28.7	178	20016	7.6	Deoxycytidylate deaminase
1432	Q5M7Z8	4	18	27	189	21014	7.5	DCMP deaminase
1433	Q8TB65	4	30	28.7	150	16762	6.8	Cytochrome c oxidase subunit Va
1434	P09104	4	8	28.1	434	47269	5	Gamma-enolase
1435	P56556	4	13	28.1	128	15137	10	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6
1435	Q6IBT8	4	13	28.1	128	15185	10	NDUFA6 protein
1436	Q9P299	4	13	28.1	210	23548	5.2	Coatomer subunit zeta-2
1437	Q5J8M3-2	4	12	34.2	149	16745	10.1	Isoform 2 of Q5J8M3
1437	Q5J8M3	4	12	27.9	183	20087	8.6	Transmembrane protein 85
1438	P20338	4	11	27.7	213	23871	6.1	Ras-related protein Rab-4A
1438	Q5T7P7	4	11	27.1	218	24390	6.1	RAB4A, member RAS oncogene family
1438	Q53GC2	4	11	27.1	218	24332	6.6	RAB4A, member RAS oncogene family variant
1438	UPI0000D620CE	4	11	26.9	219	24446	7.2	Protein SPHAR (S-phase response protein).
1438	UPI0000D620CD	4	11	26.9	219	24432	6.6	Protein SPHAR (S-phase response protein).
1439	O43583	4	11	27.3	198	22092	5.3	Density-regulated protein
1439	UPI00004566A8	4	11	27.1	199	22285	5.6	Density-regulated protein (DRP) (Protein DRP1) (Smooth muscle cell- associated protein 3) (SMAP-3).

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
1440	P30043	4	22	27.2	206	22119	7.6	Flavin reductase
1440	UPI000013D3F5	4	22	26.5	211	22594	7.6	Flavin reductase (EC 1.5.1.30) (FR) (NADPH-dependent diaphorase) (NADPH-flavin reductase) (FLR) (Biliverdin reductase B) (EC 1.3.1.24) (BVR-B) (Biliverdin-IX beta-reductase) (Green heme-binding protein) (GHBP).
1441	O95298	4	7	26.9	119	14187	9	NADH dehydrogenase [ubiquinone] 1 subunit C2
1441	Q6FIH8	4	7	26.9	119	14173	9	NDUFC2 protein
1442	Q9NRW3	4	5	26.8	190	22826	7.6	Probable DNA dC- dU-editing enzyme APOBEC-3C
1443	Q2PFU1	4	7	26.4	129	14665	4.9	Huntingtin-interacting protein HYPK
1443	Q9NX55	4	7	19.4	175	19332	5.4	Huntingtin-interacting protein HYPK
1444	UPI0000E9BBA8	4	70	28.7	150	16821	6.4	Fusion protein consists of immunoglobin G-Bin
1444	UPI0000E9BBA7	4	70	28.7	150	16835	6.4	Fusion protein consists of immunoglobin G-Bin
1444	P84103	4	70	26.2	164	19330	11.6	Splicing factor, arginine/serine-rich 3
1445	Q96IU4	4	9	26.2	210	22346	6.4	Abhydrolase domain-containing protein 14B
1446	Q9BQ61	4	7	26.1	176	18419	9.4	Uncharacterized protein C19orf43
1447	Q86U28	4	5	26	154	16476	5.2	Iron-sulfur cluster assembly 2 homolog, mitochondrial precursor
1448	P41223	4	19	25.7	144	17000	8.8	Protein BUD31 homolog
1449	P62256	4	10	25.7	183	20655	4.7	Ubiquitin-conjugating enzyme E2 H
1450	O96000	4	19	25.6	172	20777	8.5	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10
1451	Q9NV31	4	13	25.5	184	21850	9.5	U3 small nucleolar ribonucleoprotein protein IMP3
1452	Q8IZQ5	4	21	25.4	122	13407	9.6	Selenoprotein H
1452	UPI0000163E14	4	21	25.4	122	13303	9.7	selenoprotein H
1453	Q5SPS5	4	7	26.3	615	67971	9.5	Poly(A) binding protein, cytoplasmic 4
1453	Q13310	4	7	25.2	644	70783	9.3	Polyadenylate-binding protein 4 (Poly(A)-binding protein 4) (PABP 4) (Inducible poly(A)-binding protein)
1453	Q6IQ30	4	7	24.5	660	72361	9.3	PABPC4 protein
1453	Q5SPS6	4	7	24.5	660	72391	9.3	Poly(A) binding protein, cytoplasmic 4
1454	gi|12345|prg	4	1466	26	223	23476	7.9	Promega sequencing grade modified trypsin
1454	IPITrypsinPIG	4	1466	25.1	231	24409	7.2	TRYP_PIG
1455	P13987	4	106	25	128	14177	6.5	CD59 glycoprotein precursor
1456	Q16527	4	14	24.9	193	20954	8.6	Cysteine and glycine-rich protein 2
1457	Q9UL26	4	13	24.7	194	21855	8.2	Ras-related protein Rab-22A
1458	Q9H444	4	7	24.6	224	24950	4.8	Charged multivesicular body protein 4b
1459	Q96EK6	4	9	24.5	184	20749	8	Glucosamine 6-phosphate N-acetyltransferase
1460	Q9UM00-2	4	27	27.2	169	18766	9.6	Isoform 2 of Q9UM00

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1460	Q9UM00	4	27	24.5	188	21175	9.7	Transmembrane and coiled-coil domain-containing protein 1
1461	P49721	4	53	24.4	201	22836	7	Proteasome subunit beta type 2
1462	Q9Y3D6	4	39	24.3	152	16938	8.8	Mitochondrial fission 1 protein
1462	UPI0000073ACD	4	39	24.3	152	16980	8.8	tetratricopeptide repeat domain 11
1463	Q9UF68	4	4	24.1	270	30658	7	Hypothetical protein DKFZp434A149
1463	Q6BCY4	4	4	23.6	276	31458	8.5	Cytochrome b5 reductase 2
1464	UPI00001405F0	4	16	25.9	270	29500	7	calponin 2 isoform b
1464	Q53GK7	4	16	22.7	309	33621	7.6	Calponin 2 isoform a variant
1464	Q99439	4	16	22.7	309	33697	7.3	Calponin-2
1464	Q6FHE4	4	16	22.7	309	33709	7.3	CNN2 protein
1465	Q9NQ88	4	17	22.6	270	30063	7.7	Uncharacterized protein C12orf5
1466	Q15202	4	81	22.9	109	11959	3.7	Prothymosin alpha
1466	Q8TBK9	4	81	22.7	110	12016	3.8	Prothymosin, alpha
1466	Q86YS2	4	81	22.7	110	12044	3.8	Prothymosin alpha protein
1466	Q5VYG3	4	81	22.7	110	12055	3.8	OTTHUMP00000018545
1466	Q15204	4	81	22.7	110	12047	3.7	Prothymosin alpha
1466	Q15200	4	81	22.7	110	12085	3.8	Prothymosin alpha
1466	P06454-2	4	81	22.7	110	12074	3.8	Isoform 2 of P06454
1466	P06454	4	81	22.5	111	12203	3.8	Prothymosin alpha [Contains: Thymosin alpha-1]
1467	Q92522	4	42	22.5	213	22487	10.8	Histone H1x
1468	Q9BYN8	4	4	22.4	205	24212	10.4	28S ribosomal protein S26, mitochondrial precursor
1469	P30042	4	22	22	268	28170	8.3	ES1 protein homolog, mitochondrial precursor
1470	P15927	4	10	21.9	270	29247	6.1	Replication protein A 32 kDa subunit
1470	P15927-2	4	10	21.2	278	30156	7	Isoform 2 of P15927
1470	P15927-3	4	10	16.5	358	38810	8.9	Isoform 3 of P15927
1471	Q9NRX1	4	10	21.8	252	27924	9.7	RNA-binding protein PNO1
1472	P13984	4	9	21.7	249	28380	9.2	Transcription initiation factor IIF subunit beta
1472	UPI00004566E9	4	9	21.6	250	28473	9.3	Transcription initiation factor IIF subunit beta (EC 3.6.1.-) (TFIIF-beta) (ATP-dependent helicase GTF2F2) (General transcription factor IIF subunit 2) (Transcription initiation factor RAP30).
1473	P61009	4	11	21.7	180	20313	8.6	Signal peptidase complex subunit 3
1473	UPI00004572A7	4	11	21.3	183	20779	9.3	Signal peptidase complex subunit 3 (EC 3.4.-.-) (Microsomal signal peptidase 23 kDa subunit) (SPase 22 kDa subunit) (SPC22/23).
1474	Q96GC5	4	9	21.7	212	23935	9	39S ribosomal protein L48, mitochondrial precursor
1475	Q9Y296	4	5	21.5	219	24340	6.2	Trafficking protein particle complex subunit 4
1476	Q96HX4	4	8	21.5	274	28649	7.5	Pyrroline-5-carboxylate reductase-like
1476	Q53H96	4	8	21.4	276	28886	7.5	Pyrroline-5-carboxylate reductase-like protein
1477	Q96C86	4	7	21.4	337	38609	6.4	Scavenger mRNA-decapping enzyme DcpS
1478	O14828	4	19	21.3	347	38319	7.6	Secretory carrier-associated membrane protein 3

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
1478	UPI0000456274	4	19	21.3	347	38315	7.2	Secretory carrier-associated membrane protein 3 (Secretory carrier membrane protein 3).
1478	Q6FHJ5	4	19	21.3	347	38243	7.6	SCAMP3 protein
1478	Q4VX17	4	19	21.3	347	38287	7.6	Secretory carrier membrane protein 3
1479	Q53FX5	4	15	21.3	197	21820	8	Lin-7 homolog C variant
1479	Q9NUP9	4	15	21.3	197	21834	8.4	Lin-7 homolog C
1480	Q6V3B2	4	10	21.3	221	25726	6.1	FK506-binding protein 7
1480	Q9Y680-2	4	10	21.2	222	25794	6.3	Isoform 2 of Q9Y680
1480	UPI0000456EAC	4	10	18.4	256	29688	6.5	FK506-binding protein 7 precursor (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPIase) (Rotamase) (FKBP-23).
1480	Q9Y680	4	10	18.1	259	30009	6.5	FK506-binding protein 7 precursor
1481	P09496-2	4	24	21.1	218	23662	4.5	Isoform Non
1482	Q6DKI1	4	10	21.1	246	28661	10.5	Ribosomal protein L7-like 1
1483	P36969-2	4	14	24.1	170	19478	7.9	Isoform Cytoplasmic of P36969
1483	P36969	4	14	20.8	197	22128	8.3	Phospholipid hydroperoxide glutathione peroxidase, mitochondrial precursor
1483	UPI00001AAC3F	4	14	20.8	197	22025	8.4	glutathione peroxidase 4 isoform A precursor
1483	Q6PI42	4	14	20.8	197	22166	8.4	Glutathione peroxidase 4
1483	UPI000096F213	4	14	17.5	234	26948	10.1	glutathione peroxidase 4 isoform C precursor
1484	Q9BUL8	4	12	20.8	212	24702	8.2	Programmed cell death protein 10
1485	P35219	4	8	20.7	290	32973	4.9	Carbonic anhydrase-related protein
1486	O43402	4	10	20.5	210	23773	6.4	Neighbor of COX4
1487	P62341	4	7	20.5	195	22277	8.5	Selenoprotein T precursor
1487	UPI000034ECC3	4	7	20.5	195	22174	8.6	selenoprotein T
1488	P11233	4	25	20.4	206	23567	7.1	Ras-related protein Ral-A precursor
1489	O00422	4	8	20.3	153	17561	9.4	Histone deacetylase complex subunit SAP18
1490	P09012	4	31	20.2	282	31280	9.8	U1 small nuclear ribonucleoprotein A
1491	UPI0000457067	4	26	20.9	919	101348	5.1	AP-1 complex subunit beta-1 (Adapter-related protein complex 1 beta-1 subunit) (Beta-adaptin 1) (Adaptor protein complex AP-1 beta-1 subunit) (Golgi adaptor HA1/AP1 adaptin beta subunit) (Clathrin assembly protein complex 1 beta large chain).
1491	Q86X54	4	26	20.9	919	101318	5.1	AP1B1 protein
1491	UPI0000140030	4	26	20.4	942	103921	5.1	adaptor-related protein complex 1 beta 1 subunit isoform b
1491	Q20WL3	4	26	20.4	939	103534	5.2	AP1B1 protein
1491	Q10567-2	4	26	20.4	942	103891	5.1	Isoform B of Q10567
1491	Q10567	4	26	20.2	949	104607	5.1	AP-1 complex subunit beta-1
1491	UPI000013CED0	4	26	20.2	949	104637	5.1	adaptor-related protein complex 1 beta 1 subunit isoform a

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
1492	Q16740	4	10	20.2	277	30180	8.1	Putative ATP-dependent Clp protease proteolytic subunit, mitochondrial precursor
1493	Q96QR8	4	15	20.2	312	33241	5.4	Transcriptional activator protein Pur-beta
1494	Q96CN7	4	9	20.1	298	32237	7.4	Isochorismatase domain-containing protein 1
1495	Q9H8S9	4	12	19.9	216	25080	7	Mps one binder kinase activator-like 1B
1495	UPI0000047AC8	4	12	19.9	216	25008	7.2	Mob4B protein
1496	Q5T3I2	4	19	19.8	288	31675	7.7	Apolipoprotein A-I-binding protein
1496	Q8NCW5	4	19	19.8	288	31689	7.7	ApoA-I binding protein precursor
1497	Q3SY19	4	24	19.4	247	26556	4.8	PRSS1 protein
1498	P42765	4	7	19.1	397	41924	8.1	3-ketoacyl-CoA thiolase, mitochondrial
1498	UPI0000136E5A	4	7	19.1	397	42039	8.3	acetyl-coenzyme A acyltransferase 2
1499	P55209	4	17	18.9	391	45374	4.5	Nucleosome assembly protein 1-like 1
1500	O95330	4	19	18.7	198	22396	6.4	Hypothetical protein
1500	UPI0000D61079	4	19	14.9	248	28113	5.5	Endoplasmic reticulum-Golgi intermediate compartment protein 3 (Serologically defined breast cancer antigen NY-BR-84).
1500	Q9Y282	4	19	9.7	383	43222	6.1	Endoplasmic reticulum-Golgi intermediate compartment protein 3
1500	UPI0000456F87	4	19	9.5	390	44008	5.9	Endoplasmic reticulum-Golgi intermediate compartment protein 3 (Serologically defined breast cancer antigen NY-BR-84).
1500	Q5JWS3	4	19	9.5	388	43772	6	ERGIC and golgi 3
1500	Q5JWS0	4	19	9.3	396	44568	6.5	ERGIC and golgi 3
1501	P51809	4	18	18.6	220	24935	8.6	Synaptobrevin-like protein 1
1502	Q66K91	4	20	19	231	23656	10.9	Small nuclear ribonucleoprotein polypeptides B and B1
1502	Q5XPV6	4	20	19	231	23657	10.7	Small nuclear ribonucleoprotein polypeptide B
1502	Q6PKB4	4	20	18.8	234	24088	10.8	SNRPB protein
1502	UPI0000D612F2	4	20	18.6	236	26362	9.3	Small nuclear ribonucleoprotein-associated protein N (snRNP-N) (Sm protein N) (Sm-N) (SmN) (Sm-D) (Tissue-specific-splicing protein).
1502	P14678	4	20	18.3	240	24610	11.2	Small nuclear ribonucleoprotein-associated proteins B and B'
1502	P63162	4	20	18.3	240	24614	11.2	Small nuclear ribonucleoprotein-associated protein N
1502	UPI0000D6101C	4	20	18.2	242	27236	9.4	Small nuclear ribonucleoprotein-associated proteins B and B' (snRNP-B) (Sm protein B/B') (Sm-B/Sm-B') (SmB/SmB').
1502	Q9UIS4	4	20	18.1	243	27267	9.4	Small nuclear ribonucleoprotein B'
1502	Q15182	4	20	15.4	285	29671	10.1	SNRPB protein

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
1502	UPI0000D6101B	4	20	15.3	287	29862	10.2	Small nuclear ribonucleoprotein-associated proteins B and B' (snRNP-B) (Sm protein B/B') (Sm-B/Sm-B') (SmB/SmB').
1502	P14678-3	4	20	15.2	289	30032	10.2	Isoform SM
1503	O75937	4	6	18.2	253	29842	9.1	DnaJ homolog subfamily C member 8
1503	UPI0000456194	4	6	17.5	263	30829	8.9	DnaJ homolog subfamily C member 8 (Splicing protein spf31).
1504	Q8TB70	4	8	21.8	188	22199	5.8	TXNDC9 protein
1504	O14530	4	8	18.1	226	26534	5.9	Thioredoxin domain-containing protein 9
1504	Q53HG4	4	8	18.1	226	26535	5.7	ATP binding protein associated with cell differentiation variant
1505	Q13951	4	9	18.1	182	21508	6.6	Core-binding factor subunit beta
1506	P43307	4	14	17.8	286	32235	4.5	Translocon-associated protein subunit alpha precursor
1506	UPI000016789F	4	14	17.8	286	32183	4.5	signal sequence receptor, alpha
1507	Q96GG9	4	5	17.8	259	30124	5.3	DCN1-like protein 1
1507	UPI000013E0D4	4	5	17.8	258	29993	5.3	DCN1-like protein 1 (Defective in cullin neddylation protein 1-like protein 1) (DCUN1 domain-containing protein 1) (Squamous cell carcinoma-related oncogene).
1508	Q9BYD2	4	6	17.6	267	30185	10.1	39S ribosomal protein L9, mitochondrial precursor
1508	UPI000013D8FA	4	6	17.6	267	30243	10.1	mitochondrial ribosomal protein L9
1509	Q9UBV8	4	11	17.6	284	30381	6.5	Peflin
1510	Q6IN49	4	6	17.5	332	37490	7.9	Cysteine and histidine-rich domain-containing protein 1
1510	Q9UHD1	4	6	17.5	332	37437	7.7	CHORD containing protein-1
1511	O75822	4	11	17.4	258	29062	4.8	Eukaryotic translation initiation factor 3 subunit 1
1512	O94905	4	11	17.4	339	37840	5.6	SPFH domain-containing protein 2 precursor
1513	Q96A35	4	7	17.1	216	24915	9.3	39S ribosomal protein L24, mitochondrial precursor
1514	Q53H82	4	13	17	288	32790	6.8	Lactamase beta-2
1514	Q9Y392	4	13	17	288	32806	6.8	CGI-83 protein
1515	Q9UKK9	4	9	16.9	219	24328	4.9	ADP-sugar pyrophosphatase
1515	UPI000059D108	4	9	15.9	232	25895	5.2	ADP-sugar pyrophosphatase (EC 3.6.1.13) (EC 3.6.1.-) (Nucleoside diphosphate-linked moiety X motif 5) (Nudix motif 5) (YSA1H).
1516	Q6P1N9	4	6	16.8	297	33572	7	TatD DNAse domain-containing protein 1
1516	Q9BY40	4	6	16.8	297	33602	7	CDA11
1517	Q7L5N1	4	7	16.8	327	36163	5.7	COP9 signalosome complex subunit 6
1518	Q53Y37	4	9	16.6	211	23181	4.7	Clathrin, light polypeptide
1519	Q9H8Y8	4	7	16.4	452	47145	4.8	Golgi reassembly-stacking protein 2
1520	O43765	4	14	16.3	313	34063	4.9	Small glutamine-rich tetratricopeptide repeat-containing protein A
1521	O60711	4	5	16.3	386	43332	6	Leupaxin
1521	Q53FW6	4	5	16.3	386	43346	6	Leupaxin variant

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1522	Q96DH6-2	4	10	21.1	251	28421	8.5	Isoform 2 of Q96DH6
1522	Q96DH6	4	10	16.2	328	35197	8.5	RNA-binding protein Musashi homolog 2
1523	Q9H7Z7	4	8	16.2	377	41943	9.2	Prostaglandin E synthase 2 (EC 5.3.99.3) (Microsomal prostaglandin E synthase 2) (mPGES-2) [Contains: Prostaglandin E synthase 2 truncated form]
1524	Q9UBE0	4	19	16.2	346	38450	5.3	SUMO-activating enzyme subunit 1
1525	Q15435-2	4	11	18.3	317	36837	5.2	Isoform 2 of Q15435
1525	Q15435	4	11	16.1	360	41564	4.9	Protein phosphatase 1 regulatory subunit 7
1526	Q8NBU5	4	10	16.1	361	40744	6.9	ATPase family AAA domain-containing protein 1
1527	P62995-3	4	34	24.5	188	21935	10.2	Isoform 3 of P62995
1527	Q68DZ9	4	34	16.7	276	32321	11.4	Hypothetical protein DKFZp686F18120
1527	Q59GA1	4	34	16.5	278	32274	11.1	Splicing factor, arginine/serine-rich 10 (Transformer 2 homolog, Drosophila) variant
1527	P62995	4	34	16	288	33666	11.2	Arginine/serine-rich-splicing factor 10
1527	UPI0000D61BC0	4	34	15.9	289	33699	10.8	Arginine/serine-rich-splicing factor 10 (Transformer-2-beta) (HTRA2-beta) (Transformer 2 protein homolog).
1528	Q12904	4	10	16	312	34353	8.4	Multisynthetase complex auxiliary component p43 [Contains: Endothelial monocyte-activating polypeptide 2 (EMAP-II) (Small inducible cytokine subfamily E member 1)]
1529	Q9BYG3	4	10	16	293	34222	9.9	MKI67 FHA domain-interacting nucleolar phosphoprotein
1529	UPI000006F493	4	10	16	293	34253	9.9	MKI67 (FHA domain) interacting nucleolar phosphoprotein
1530	P53582	4	7	15.8	386	43215	7.2	Methionine aminopeptidase 1
1531	Q59FA6	4	13	16.8	303	33553	6.2	SEC13-like 1 isoform b variant
1531	P55735	4	13	15.8	322	35541	5.5	Protein SEC13 homolog
1532	O95861	4	6	15.6	308	33392	5.7	3'(2'),5'-bisphosphate nucleotidase 1
1533	Q9GZL7	4	6	15.6	423	47708	5.9	WD repeat protein 12
1533	UPI000015F4D0	4	6	15.6	423	47544	6	WD repeat domain 12 protein
1534	Q9NQG5	4	5	15.6	326	36900	6	Uncharacterized protein C20orf77
1535	O75251	4	15	15.5	213	23564	10	NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial precursor
1535	UPI0000130964	4	15	15.5	213	23580	10	NADH-ubiquinone oxidoreductase Fe-S protein 7
1535	Q8NAS7	4	15	15.5	213	22962	9.4	CDNA FLJ34850 fis, clone NT2NE2011758, highly similar to NADH- UBIQUINONE OXIDOREDUCTASE 20 kDa SUBUNIT
1536	Q6PD63	4	23	15.5	362	43160	8.9	Protein tyrosine phosphatase-like A domain containing 1

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1536	Q96T12	4	23	15.5	362	43159	9.1	CDNA FLJ14515 fis, clone NT2RM1000800, weakly similar to Mus musculus partial B-IND1 protein
1536	Q8NC86	4	23	15.5	362	43126	8.9	CDNA FLJ90417 fis, clone NT2RP3000171, weakly similar to Mus musculus partial B-IND1 protein
1536	Q8IUI5	4	23	15.5	361	42908	9	PTPLAD1 protein
1536	Q9NQA7	4	23	15.1	370	43543	8	B-ind1 protein
1536	UPI0000D61358	4	23	15	373	44323	9.2	butyrate-induced transcript 1
1536	Q9P035	4	23	15	373	44423	9.1	Protein-tyrosine phosphatase-like A domain-containing protein 1
1537	Q96FW1	4	10	15.5	271	31284	4.9	Ubiquitin thioesterase OTUB1
1538	UPI0000203595	4	10	21.6	236	26072	5.6	regulator of G-protein signalling 19 interacting protein 1 isoform 2
1538	O14908	4	10	15.3	333	36049	6.3	PDZ domain-containing protein GIPC1
1539	Q86XR1	4	17	16	238	26108	9.1	Prion protein
1539	Q540C4	4	17	15.4	246	26884	9.3	Prion protein
1539	A2A2V1	4	17	15.3	249	27279	9	Prion protein
1539	A1YVW6	4	17	15	253	27703	9.1	Prion protein
1539	Q6FGR8	4	17	15	253	27599	9.1	PRNP protein
1539	Q6FGN5	4	17	15	253	27629	9	Major prion protein
1539	Q27H91	4	17	15	253	27635	9	Prion protein PrP
1539	P04156	4	17	15	253	27661	9	Major prion protein precursor
1539	Q6SES1	4	17	13.7	277	29992	9	Prion protein
1539	O75942	4	17	13.3	285	30768	9	Prion protein
1540	Q08170	4	13	15	494	56678	11.5	Splicing factor, arginine/serine-rich 4
1541	Q8NBJ7	4	18	15	301	33857	8	Sulfatase-modifying factor 2 precursor
1541	UPI000013E405	4	18	15	301	33843	8	Sulfatase-modifying factor 2 precursor (C-alpha-formyglycine-generating enzyme 2).
1541	UPI0000DAC779	4	18	14.8	304	34290	8.4	sulfatase modifying factor 2 isoform a precursor
1542	Q9NUJ1	4	18	15	306	33933	8.6	Abhydrolase domain-containing protein 10, mitochondrial precursor
1543	P31153	4	23	14.7	395	43661	6.5	S-adenosylmethionine synthetase isoform type-2
1543	UPI0000DB12F5	4	23	14.6	396	43748	6.5	S-adenosylmethionine synthetase isoform type-
1544	P19623	4	10	14.6	302	33825	5.5	Spermidine synthase
1545	P61201	4	6	14.4	443	51597	5.5	COP9 signalosome complex subunit 2
1545	Q53HJ0	4	6	14.4	443	51570	5.5	COP9 constitutive photomorphogenic homolog subunit 2 variant
1546	Q05BK6	4	9	14.2	366	40691	6.4	TFG protein
1546	Q7Z426	4	9	13.1	396	43006	5.2	Putative MAPK activating protein
1546	Q969I2	4	9	13	400	43448	5.1	TRK-fused gene
1546	Q92734	4	9	13	400	43434	5.1	Protein TFG
1546	Q8TDJ5	4	9	6.5	803	88671	6.3	TRK-fused gene/anaplastic large cell lymphoma kinase extra long form
1547	Q15654	4	8	14.1	476	50288	7.4	Thyroid receptor-interacting protein 6

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1548	UPI000006FDB9	4	8	14.4	397	41296	6.7	acetyl-Coenzyme A acetyltransferase 2
1548	Q9BWD1	4	8	14.4	397	41351	6.9	Acetyl-CoA acetyltransferase, cytosolic
1548	Q59GW6	4	8	14.1	404	42136	7.4	Acetyl-CoA acetyltransferase, cytosolic variant
1549	Q96G23	4	6	13.9	380	44876	9	LAG1 longevity assurance homolog 2
1550	Q9H3N1	4	26	13.9	280	31791	5	Thioredoxin domain-containing protein 1 precursor
1550	UPI000006E5F1	4	26	13.9	280	31806	5	thioredoxin domain containing
1551	Q9UI12-2	4	12	14.4	465	54151	6.5	Isoform 2 of Q9UI12
1551	Q9UI12	4	12	13.9	483	55883	6.5	Vacuolar ATP synthase subunit H
1552	P48509	4	35	13.8	253	28295	7.5	CD151 antigen
1553	Q6FI81-3	4	4	14.4	299	32213	5.6	Isoform 3 of Q6FI81
1553	Q6FI81	4	4	13.8	312	33582	5.6	Anamorsin
1553	UPI00000739FB	4	4	11.7	367	40003	5.8	CPIN1_HUMAN Isoform 2 of Q6FI81 - Homo sapiens (Human)
1554	UPI0000456DE4	4	8	14.3	280	32431	9.6	39S ribosomal protein L19, mitochondrial precursor (L19mt) (MRP-L19) (MRP-L15).
1554	P49406	4	8	13.7	292	33535	9.5	39S ribosomal protein L19, mitochondrial precursor
1555	Q2L696	4	9	14.4	390	46630	5.2	Nucb2 splice variant
1555	P80303	4	9	13.3	420	50223	5.1	Nucleobindin-2 precursor
1555	UPI00001AF3CE	4	9	13.3	420	50201	5.1	Nucleobindin-2 precursor (DNA-binding protein NEFA) (Gastric cancer antigen Zg4).
1556	Q07666-3	4	24	14.6	404	44027	7.3	Isoform 3 of Q07666
1556	Q07666	4	24	13.3	443	48227	8.7	KH domain-containing, RNA-binding, signal transduction-associated protein 1
1557	Q13510	4	50	13.2	395	44650	7.6	Acid ceramidase precursor (EC 3.5.1.23) (Acylsphingosine deacylase) (N-acylsphingosine amidohydrolase) (AC) (Putative 32 kDa heart protein) (PHP32) [Contains: Acid ceramidase subunit alpha; Acid ceramidase subunit beta]
1557	Q53H01	4	50	13.2	395	44692	7.6	N-acylsphingosine amidohydrolase (Acid ceramidase) 1 preproprotein isoform a variant
1557	UPI0000190976	4	50	12.7	411	46494	7.9	N-acylsphingosine amidohydrolase (acid ceramidase) 1 isoform b
1558	P11172	4	4	13.1	480	52222	7.2	Uridine 5'-monophosphate synthase (UMP synthase) [Includes: Orotate phosphoribosyltransferase (EC 2.4.2.10) (OPRTase); Orotidine 5'-phosphate decarboxylase (EC 4.1.1.23) (OMPdecase)]
1559	Q9BVC6	4	27	12.8	243	26210	10.5	Transmembrane protein 109 precursor
1560	Q9Y639	4	13	12.8	282	31291	6.9	Neuroplastin precursor
1560	Q9Y639-2	4	13	9	398	44387	8	Isoform 2 of Q9Y639
1561	UPI0000457335	4	8	19.4	304	32825	5.6	proline-rich coiled-coil 1
1561	Q8NEZ7	4	8	19.3	305	32896	5.6	FLJ00410 protein

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1561	Q96M27	4	8	13.3	445	46701	5.8	CDNA FLJ32875 fis, clone TESTI2004031
1561	Q8IVL4	4	8	12.8	462	48907	5.3	Hypothetical protein
1561	Q86Y42	4	8	12.7	464	48525	5.4	Proline-rich coiled-coil protein 1
1561	UPI0000D61673	4	8	12.7	466	48637	5.5	proline-rich coiled-coil 1
1562	Q9H0C8	4	6	12.5	392	42907	7.1	Integrin-linked kinase-associated serine/threonine phosphatase 2C
1563	Q9HAB8	4	6	12.5	311	34005	6.7	Phosphopantothenate--cysteine ligase
1564	Q9BUB1	4	6	12.8	382	43067	5.1	PRKAR2A protein
1564	P13861	4	6	12.1	404	45518	5.1	cAMP-dependent protein kinase type II-alpha regulatory subunit
1565	Q0VDF9	4	6	12	509	54795	5.6	Heat shock 70 kDa protein 14
1565	Q9UI07	4	6	12	509	54778	5.6	Heat shock protein hsp70-related protein
1565	Q9P0X2	4	6	12	509	54824	5.5	Heat shock protein HSP60
1566	Q8N684-2	4	10	12.1	462	51096	7.8	Isoform 2 of Q8N684
1566	Q8N684	4	10	11.9	471	52050	8	Cleavage and polyadenylation specificity factor 7
1567	UPI0000D61B8E	4	25	15.9	258	28857	4.9	Glycogenin-1 (EC 2.4.1.186).
1567	P46976-3	4	25	15.8	260	29057	4.9	Isoform GN
1567	Q8N5Y3	4	25	12.4	331	37246	5.4	GYG1 protein
1567	Q6FHZ1	4	25	12.3	333	37479	5.4	GYG protein
1567	P46976	4	25	11.7	350	39384	5.5	Glycogenin-1
1568	P82650	4	5	11.7	360	41280	7.9	Mitochondrial 28S ribosomal protein S22
1569	UPI0000D62170	4	10	13.9	395	44603	5.6	Ataxin-10 (Spinocerebellar ataxia type 10 protein) (Brain protein E46 homolog).
1569	Q9UBB4	4	10	11.6	475	53489	5.2	Ataxin-10
1570	UPI000014188D	4	7	12.3	439	46796	8.6	UPI000014188D UniRef100 entry
1570	Q9UKX7	4	7	11.5	468	50144	7.1	Nucleoporin 50 kDa
1571	O75306	4	5	11.2	463	52546	7.6	NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial precursor
1571	Q53HG2	4	5	11.2	463	52561	7.6	NADH dehydrogenase (Ubiquinone) Fe-S protein 2, 49kDa (NADH-coenzyme Q reductase) variant
1572	P06865	4	6	11.2	529	60689	5.2	Beta-hexosaminidase alpha chain precursor
1572	Q6AI32	4	6	11.2	529	60719	5.1	Hypothetical protein DKFZp781C13106
1572	Q53HS8	4	6	11.2	529	60699	5.2	Hexosaminidase A preproprotein variant
1573	Q9BR76	4	7	11.2	489	54235	5.9	Coronin-1B
1574	UPI0000071403	4	9	11.4	537	60540	8.8	guanine nucleotide binding protein-like 3 isoform 2
1574	Q5PU80	4	9	11.1	549	61957	9.1	Nucleostemin
1574	UPI000003C48A	4	9	11.1	549	61993	9.2	guanine nucleotide binding protein-like 3 isoform 1
1574	Q9BVP2	4	9	11.1	549	61997	9.1	Guanine nucleotide-binding protein-like 3

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
1575	UPI0000D625AE	4	17	11.2	555	60357	6.4	Tripeptidyl-peptidase 1 precursor (EC 3.4.14.9) (Tripeptidyl-peptidase I) (TPP-1) (TPP-I) (Tripeptidyl aminopeptidase) (Lysosomal pepstatin insensitive protease) (LPIC) (Cell growth-inhibiting gene 1 protein).
1575	O14773-3	4	17	11.2	556	60458	6.4	Isoform 3 of O14773
1575	O14773	4	17	11	563	61248	6.5	Tripeptidyl-peptidase 1 precursor
1575	Q53HP2	4	17	11	563	61213	6.5	Tripeptidyl-peptidase I variant
1576	P36957	4	18	11	453	48640	8.8	Dihydrolipoyllysine-residue succinyltransferase component of 2- oxoglutarate dehydrogenase complex, mitochondrial precursor
1576	Q7LDY7	4	18	11	453	48755	9	Alpha-KG-E2
1577	Q99541	4	7	11	437	48075	6.8	Adipophilin
1578	Q9H9J5	4	8	10.9	521	59844	6	CDNA FLJ12694 fis, clone NT2RP1000358, highly similar to Homo sapiens mRNA; cDNA DKFZp564C186
1578	UPI000041820C	4	8	7.6	749	84919	5.6	Nucleolar complex protein 2 homolog (Protein NOC2 homolog) (NOC2- like).
1578	UPI0000161C39	4	8	7.6	749	84878	5.5	nucleolar complex associated 2 homolog
1578	Q9Y3T9	4	8	7.6	749	84905	5.6	Nucleolar complex protein 2 homolog
1579	Q6ZP32	4	12	10.7	448	52953	7.9	CDNA FLJ26613 fis, clone MPB05565, highly similar to Serine/threonine protein phosphatase 2A, 55 kDa regulatory subunit B, alpha isoform
1579	UPI0000D624A2	4	12	10.7	448	52925	7.9	Dedicator of cytokinesis protein 5.
1580	Q59FQ9	4	7	16.3	313	35616	7.9	DDX19-like protein variant
1580	Q68DY7	4	7	15.5	328	37429	7.6	Hypothetical protein DKFZp686C21137
1580	Q69YM2	4	7	14.2	360	40711	7.3	Hypothetical protein DKFZp762C1313
1580	Q96KE7	4	7	13.8	370	41779	7.9	Testicular DEAD-box helicase protein (DEAD (Asp-Glu-Ala-As) box polypeptide 19B)
1580	Q9UMR2-2	4	7	11.4	448	50490	6.1	Isoform 2 of Q9UMR2
1580	Q9NUU7	4	7	10.7	478	53975	6.6	ATP-dependent RNA helicase DDX19A
1580	Q53G16	4	7	10.6	479	53914	6.5	DEAD (Asp-Glu-Ala-As) box polypeptide 19 variant
1580	Q9UMR2	4	7	10.6	479	53927	6.3	ATP-dependent RNA helicase DDX19B
1581	Q8WUX9	4	9	10.6	453	50911	5.3	Protein CHMP7
1582	P43897	4	7	10.5	325	35391	8.4	Elongation factor Ts, mitochondrial precursor
1583	Q13867	4	4	10.5	455	52562	6.3	Bleomycin hydrolase

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1584	O43252	4	8	10.4	624	70833	6.9	Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthetase 1 (PAPS synthetase 1) (PAPSS 1) (Sulfurylase kinase 1) (SK1) (SK 1) [Includes: Sulfate adenylyltransferase (EC 2.7.7.4) (Sulfate adenylate transferase) (SAT) (ATP-sulfurylase); Adenylyl-sulfate kinase (EC 2.7.1.25) (Adenylylsulfate 3'-phosphotransferase) (APS kinase) (Adenosine-5'-phosphosulfate 3'-phosphotransferase) (3'-phosphoadenosine-5'-phosphosulfate synthetase)]
1585	Q9UN86-2	4	22	11.1	449	50817	5.4	Isoform B of Q9UN86
1585	Q9UN86	4	22	10.4	482	54121	5.6	Ras GTPase-activating protein-binding protein 2
1586	Q13619	4	7	10.3	759	87680	8.1	Cullin-4A
1586	UPI0000D61AB1	4	7	10.2	763	88235	8.1	Cullin-4A (CUL-4A).
1587	Q15629	4	20	10.2	374	43072	9.6	Translocation-associated membrane protein 1
1588	Q15437	4	6	10	767	86479	6.9	Protein transport protein Sec23B
1588	Q503A9	4	6	10	767	86495	6.9	Sec23 homolog B
1589	P48637	4	4	9.7	474	52385	5.9	Glutathione synthetase
1590	UPI000014FCE3	4	8	12.4	508	57508	8.8	KIAA0020 (KIAA0020), mRNA
1590	Q15397	4	8	9.7	648	73584	9.6	Protein KIAA0020
1591	Q8TB21	4	9	9.7	667	73533	9	Stimulated by retinoic acid gene 6 homolog
1591	Q9BX79	4	9	9.7	667	73503	9	STRA6 isoform 1
1592	Q5T2T8	4	5	18.6	204	22890	7.3	Prion protein interacting protein
1592	Q5TG35	4	5	17.1	222	25009	6.5	Prion protein interacting protein
1592	UPI0000D4E859	4	5	10.4	365	40077	8	prion protein interacting protein
1592	O43414	4	5	9.6	397	43076	8.7	Prion protein-interacting protein
1593	Q9UNH7	4	6	9.6	406	46649	6.2	Sorting nexin-6
1594	O14929	4	6	9.5	419	49513	5.7	Histone acetyltransferase type B catalytic subunit
1595	Q05BU5	4	8	9.5	461	52106	9.7	Hypothetical protein
1595	UPI0000D61501	4	8	3.5	1273	140703	8.3	Putative RNA-binding protein 16 (RNA-binding motif protein 16).
1595	Q9UPN6	4	8	3.5	1271	140519	8.3	Putative RNA-binding protein 16
1595	Q6NSK3	4	8	3.5	1271	140518	8.3	RBM16 protein
1596	Q9HB40	4	12	9.5	452	50831	5.8	Retinoid-inducible serine carboxypeptidase precursor
1597	A4D1I8	4	18	9.4	561	64400	6.8	Asparagine synthetase
1597	P08243	4	18	9.4	561	64370	6.9	Asparagine synthetase [glutamine-hydrolyzing]
1598	P48147	4	5	9.4	710	80764	5.8	Prolyl endopeptidase
1598	Q9UM02	4	5	9.4	710	80734	5.9	Prolyl endopeptidase
1598	Q8N6D4	4	5	9.4	710	80700	5.9	Prolyl endopeptidase
1599	P13473	4	104	9.3	410	44961	5.6	Lysosome-associated membrane glycoprotein 2 precursor
1599	Q9UD93	4	104	9.3	410	45043	5.9	Lysosomal membrane glycoprotein LAMP-2 homolog
1599	P13473-2	4	104	9.3	410	44956	5.7	Isoform LAMP
1599	Q6Q3G8	4	104	9.2	411	45170	5.9	Lysosomal-associated membrane protein 2C

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1600	Q2Z2K8	4	7	9.3	754	85562	5.8	Endothelin-converting enzyme-1c
1600	P42892-2	4	7	9.2	758	85808	6.5	Isoform A of P42892
1600	P42892	4	7	9.1	770	87164	5.9	Endothelin-converting enzyme 1
1600	P42892-4	4	7	9.1	767	87023	5.8	Isoform D of P42892
1601	Q8N2N3	4	12	16.9	243	27824	7.8	CDNA FLJ90102 fis, clone HEMBA1006299, highly similar to Putative NFkB activating protein 373
1601	Q5JRS7	4	12	9.1	450	51571	7.3	G protein-coupled receptor 177
1601	Q5T9L3-2	4	12	7.6	543	62552	7.6	Isoform 2 of Q5T9L3
1601	Q5T9L3	4	12	7.6	541	62253	7.4	Integral membrane protein GPR177 precursor
1601	Q8N108-9	4	12	5.8	710	81719	4.7	Isoform 9 of Q8N108
1602	O00400	4	16	8.9	549	60909	7.3	Acetyl-coenzyme A transporter 1
1603	Q5BKZ1	4	5	8.9	582	65654	5.2	Zinc finger protein 326
1604	Q9NQW7-2	4	15	9.2	599	67227	5.8	Isoform 2 of Q9NQW7
1604	Q9NQW7	4	15	8.8	623	69918	5.7	Xaa-Pro aminopeptidase 1
1605	P49821-2	4	8	8.8	455	49868	8.2	Isoform 2 of P49821
1605	P49821	4	8	8.6	464	50817	8.2	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial precursor
1605	Q53G70	4	8	8.6	464	50801	8.2	NADH dehydrogenase (Ubiquinone) flavoprotein 1, 51kDa variant
1606	Q9HAB1	4	12	9.4	438	47170	6.8	CDNA FLJ11863 fis, clone HEMBA1006926
1606	UPI000045716A	4	12	9.3	439	47299	6.8	solute carrier family 41, member 3 isoform 4
1606	Q8NB27	4	12	8.6	478	51507	7.2	CDNA FLJ34352 fis, clone FEBRA2011593
1606	UPI00003D2133	4	12	8.4	487	52449	6.9	solute carrier family 41, member 3 isoform 2
1606	UPI00001AF113	4	12	8.3	496	53923	7.2	solute carrier family 41, member 3 isoform 4
1606	UPI000013D523	4	12	8.1	507	54767	7.8	solute carrier family 41, member 3 isoform 4
1606	Q96GZ6	4	12	8.1	507	54737	7.8	Solute carrier family 41 member 3
1607	Q6FIA3	4	12	8.5	445	51353	5.4	PACSIN2 protein
1607	UPI000003EE3B	4	12	7.8	486	55905	5.2	protein kinase C and casein kinase substrate in neurons 2
1607	Q9UNF0	4	12	7.8	486	55739	5.2	Protein kinase C and casein kinase substrate in neurons protein 2
1608	Q8TED0	4	5	8.5	518	58355	9.1	U3 small nucleolar RNA-associated protein 15 homolog
1608	UPI000020CADC	4	5	8.5	518	58415	9.1	UTP15, U3 small nucleolar ribonucleoprotein, homolog
1609	Q969Y5	4	14	8.5	635	68642	8.3	Solute carrier family 5 (Sodium-dependent vitamin transporter), member 6
1609	Q9Y289	4	14	8.5	635	68702	8.3	Sodium-dependent multivitamin transporter (Na(+)-dependent multivitamin transporter)
1610	Q96CP5	4	9	8.5	480	53509	6.7	PMPCB protein
1610	O75439	4	9	8.4	489	54366	6.8	Mitochondrial-processing peptidase subunit beta, mitochondrial precursor

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1610	UPI0000D61CA8	4	9	8.4	491	54524	6.8	Mitochondrial-processing peptidase subunit beta, mitochondrial precursor (EC 3.4.24.64) (Beta-MPP) (P-52).
1611	Q14161-11	4	8	10	631	70183	6.6	Isoform 11 of Q14161
1611	UPI0000D6224B	4	8	9.8	646	71956	6.6	ARF GTPase-activating protein GIT2 (G protein-coupled receptor kinase- interactor 2) (GRK-interacting protein 2) (Cool-interacting tyrosine-phosphorylated protein 2) (CAT2) (CAT-2).
1611	Q14161-7	4	8	9.8	646	71967	6.7	Isoform 7 of Q14161
1611	UPI0000D6224A	4	8	9.5	661	73392	6.7	ARF GTPase-activating protein GIT2 (G protein-coupled receptor kinase- interactor 2) (GRK-interacting protein 2) (Cool-interacting tyrosine-phosphorylated protein 2) (CAT2) (CAT-2).
1611	Q14161-6	4	8	9.5	661	73403	6.7	Isoform 6 of Q14161
1611	UPI0000D62249	4	8	9.3	681	76061	7.3	ARF GTPase-activating protein GIT2 (G protein-coupled receptor kinase- interactor 2) (GRK-interacting protein 2) (Cool-interacting tyrosine-phosphorylated protein 2) (CAT2) (CAT-2).
1611	UPI0000167B56	4	8	9.3	679	75734	7.2	G protein-coupled receptor kinase-interactor 2 isoform 3
1611	Q14161-10	4	8	9.3	681	76072	7.5	Isoform 10 of Q14161
1611	Q14161-8	4	8	9.1	694	77518	7.3	Isoform 8 of Q14161
1611	UPI0000D62248	4	8	8.9	709	78943	7.3	ARF GTPase-activating protein GIT2 (G protein-coupled receptor kinase- interactor 2) (GRK-interacting protein 2) (Cool-interacting tyrosine-phosphorylated protein 2) (CAT2) (CAT-2).
1611	Q14161-4	4	8	8.9	709	78954	7.5	Isoform 4 of Q14161
1611	UPI0000D62247	4	8	8.6	729	81311	6.9	ARF GTPase-activating protein GIT2 (G protein-coupled receptor kinase- interactor 2) (GRK-interacting protein 2) (Cool-interacting tyrosine-phosphorylated protein 2) (CAT2) (CAT-2).
1611	Q14161-5	4	8	8.6	729	81322	7	Isoform 5 of Q14161
1611	Q14161-3	4	8	8.5	744	82759	7.1	Isoform 3 of Q14161
1611	Q14161	4	8	8.3	759	84543	7.2	ARF GTPase-activating protein GIT2
1611	UPI0000D62246	4	8	8.3	759	84532	7.1	ARF GTPase-activating protein GIT2 (G protein-coupled receptor kinase- interactor 2) (GRK-interacting protein 2) (Cool-interacting tyrosine-phosphorylated protein 2) (CAT2) (CAT-2).
1612	Q2TAY7	4	8	8.2	513	57544	7.2	Smu-1 suppressor of mec-8 and unc-52 protein homolog
1613	Q92544	4	11	8.2	625	72541	6.7	Transmembrane 9 superfamily protein member 4
1614	Q9H8H0	4	4	8.1	719	81124	6.1	Nucleolar protein 11

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1615	UPI0000366EEE	4	19	8.6	510	57391	8	Interferon-induced, double-stranded RNA-activated protein kinase (EC 2.7.11.1) (Interferon-inducible RNA-dependent protein kinase) (Protein kinase RNA-activated) (PKR) (p68 kinase) (P1/eIF-2A protein kinase).
1615	Q8IW76	4	19	8.6	513	57620	8.3	EIF2AK2 protein
1615	Q7Z6F6	4	19	8.6	510	57478	8.2	Interferon-inducible double-stranded RNA-dependent protein kinase
1615	P19525	4	19	8	551	62094	8.4	Interferon-induced, double-stranded RNA-activated protein kinase
1616	O75475	4	6	7.9	530	60103	9.1	PC4 and SFRS1-interacting protein
1617	Q9UG63	4	13	7.9	623	71290	7.4	ATP-binding cassette sub-family F member 2
1618	Q14554	4	6	7.7	519	59594	7.9	Protein disulfide-isomerase A5 precursor
1619	Q9H074-2	4	5	9.2	400	45631	4.5	Isoform 2 of Q9H074
1619	Q9H074	4	5	7.7	479	53525	4.8	Polyadenylate-binding protein-interacting protein 1 (Poly(A)-binding protein-interacting protein 1)
1620	O95817	4	5	7.5	575	61595	7	BAG family molecular chaperone regulator 3
1620	Q53GY1	4	5	7.5	575	61604	7.4	BCL2-associated athanogene 3 variant
1621	Q53GW1	4	5	7.5	642	72308	6.4	Vesicle transport-related protein isoform a variant
1621	Q8WVM8	4	5	7.5	642	72380	6.3	Sec1 family domain-containing protein 1
1622	O43395	4	10	7.3	683	77529	9.5	U4/U6 small nuclear ribonucleoprotein Prp3
1622	Q53GV6	4	10	7.3	683	77441	9.5	PRP3 pre-mRNA processing factor 3 homolog
1622	O43395-2	4	10	7.3	682	77472	9.5	Isoform 2 of O43395
1623	O94776	4	5	7.3	668	75023	9.7	Metastasis-associated protein MTA2
1624	P51812	4	6	7.3	740	83736	6.9	Ribosomal protein S6 kinase alpha-3
1625	O94874	4	10	7.2	794	89595	6.8	Uncharacterized protein KIAA0776
1626	P16435	4	8	7.2	677	76690	5.6	NADPH--cytochrome P450 reductase
1626	Q63HL4	4	8	7.2	680	77018	5.6	Hypothetical protein DKFZp686G04235
1627	P50281	4	5	7.2	582	65884	7.8	Matrix metalloproteinase-14 precursor
1627	UPI0000048136	4	5	7.2	582	65894	7.8	matrix metalloproteinase 14 preproprotein
1628	Q6P1M0	4	11	7.2	643	72064	8.5	Long-chain fatty acid transport protein 4
1629	Q9NZW5	4	5	7.2	540	61117	6.2	MAGUK p55 subfamily member 6
1630	Q9NVH1-3	4	5	7.7	507	57197	7.5	Isoform 3 of Q9NVH1
1630	UPI0000D61E3A	4	5	7.5	523	59173	7.6	DnaJ homolog subfamily C member 11.
1630	Q9NVH1-2	4	5	7.5	521	58947	7.6	Isoform 2 of Q9NVH1
1630	Q9NVH1	4	5	7	559	63278	8.4	DnaJ homolog subfamily C member 11

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1630	UPI000006D6B2	4	5	7	559	63336	8.4	DnaJ (Hsp40) homolog, subfamily C, member 11
1631	UPI000020A59A	4	15	7	660	76329	7.4	hypothetical protein LOC55129
1632	A4D1C5	4	16	6.9	780	88106	5.6	Protein tyrosine phosphatase, non-receptor type 12
1632	Q05209	4	16	6.9	780	88120	5.6	Tyrosine-protein phosphatase non-receptor type 12
1633	Q6DCA8	4	11	6.9	680	77948	10.2	BCLAF1 protein
1633	Q9NYF8-4	4	11	6.3	747	85937	10.4	Isoform 4 of Q9NYF8
1633	UPI00004574B1	4	11	5.4	869	100202	10	Bcl-2-associated transcription factor 1 (Btf).
1633	Q9NYF8-3	4	11	5.4	869	100232	10	Isoform 3 of Q9NYF8
1633	Q9NYF8-2	4	11	5.1	918	105948	10	Isoform 2 of Q9NYF8
1633	Q9NYF8	4	11	5.1	920	106122	10	Bcl-2-associated transcription factor 1
1634	P13798	4	8	6.8	732	81225	5.5	Acylamino-acid-releasing enzyme
1635	Q15003	4	11	6.7	741	82563	5.1	Condensin complex subunit 2
1636	Q86SZ6	4	17	8.2	489	55251	7.1	Full-length cDNA clone CS0DJ012YD11 of T cells (Jurkat cell line) of Homo sapiens
1636	O15321	4	17	6.6	606	68861	7.2	Transmembrane 9 superfamily protein member 1 precursor
1637	P40222	4	4	6.6	546	61891	6.5	Alpha-taxilin
1638	UPI0000DA4C59	4	7	6.9	750	80265	5.1	calpastatin isoform f
1638	UPI0000DA4C58	4	7	6.9	756	81169	5.2	calpastatin isoform e
1638	UPI0000DA4C5B	4	7	6.8	769	82437	5.2	calpastatin isoform h
1638	UPI0000DA4C5A	4	7	6.7	772	82771	5.3	calpastatin isoform g
1638	Q59HE3	4	7	6.6	784	84228	5.3	Calpastatin isoform a variant
1639	P98194-2	4	9	6.8	888	96960	6.3	Isoform 2 of P98194
1639	P98194-4	4	9	6.6	903	98733	6.6	Isoform 4 of P98194
1639	P98194	4	9	6.5	919	100577	6.7	Calcium-transporting ATPase type 2C member 1 (EC 3.6.3.8) (ATPase 2C1) (ATP-dependent Ca(2+) pump PMR1)
1639	P98194-3	4	9	6.5	923	101163	6.4	Isoform 3 of P98194
1639	P98194-5	4	9	6.4	939	103007	6.5	Isoform 5 of P98194
1639	UPI00001969A3	4	9	6.3	949	104032	6.4	calcium-transporting ATPase 2C1 isoform 1d
1639	P98194-6	4	9	6.3	959	105057	6.3	Isoform 6 of P98194
1639	UPI0000D61B7A	4	9	6.2	960	105298	6.1	Calcium-transporting ATPase type 2C member 1 (EC 3.6.3.8) (ATPase 2C1) (ATP-dependent Ca(2+) pump PMR1).
1640	Q9Y5S1	4	13	6.5	764	85981	5.8	Transient receptor potential cation channel subfamily V member 2
1640	UPI0000D622C9	4	13	6.5	766	86151	5.9	Transient receptor potential cation channel subfamily V member 2 (TrpV2) (osm-9-like TRP channel 2) (OTRPC2) (Vanilloid receptor-like protein 1) (VRL-1).
1641	Q2TU89	4	19	8	701	79614	6.7	Aging-associated protein 1
1641	Q2NKW9	4	19	6.4	869	98150	7	Eukaryotic translation initiation factor 4 gamma, 2
1641	P78344	4	19	6.2	907	102362	7.1	Eukaryotic translation initiation factor 4 gamma 2

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1641	UPI000013C8BE	4	19	6.2	907	102330	7.1	Eukaryotic translation initiation factor 4 gamma 2 (eIF-4-gamma 2) (eIF-4G 2) (eIF4G 2) (p97) (Death-associated protein 5) (DAP-5).
1641	Q49A79	4	19	6.2	907	102389	7.1	Eukaryotic translation initiation factor 4 gamma, 2
1641	Q0VH01	4	19	6.2	907	102335	7.1	Eukaryotic translation initiation factor 4 gamma, 2
1641	Q59G42	4	19	6	940	105828	7.4	Eukaryotic translation initiation factor 4 gamma, 2 variant
1642	Q68E01	4	12	6.2	1043	118070	5.8	Integrator complex subunit 3
1642	Q68E01-2	4	12	6.2	1042	118013	5.8	Isoform 2 of Q68E01
1643	Q96C62	4	15	6.2	682	76915	10	Transmembrane protein 112B
1643	Q9BU23	4	15	5.9	707	79698	10.1	Transmembrane protein 153
1644	O60502-2	4	7	6.5	849	95331	5	Isoform 2 of O60502
1644	O60502	4	7	6	916	102915	4.9	Bifunctional protein NCOAT (Nuclear cytoplasmic O-GlcNAcase and acetyltransferase) (Meningioma-expressed antigen 5) [Includes: Beta- hexosaminidase (EC 3.2.1.52) (N-acetyl-beta-glucosaminidase) (Beta-N-acetylhexosaminidase) (Hexosaminidase C) (N-acetyl-beta-D- glucosaminidase) (O-GlcNAcase); Histone acetyltransferase (EC 2.3.1.48) (HAT)]
1645	UPI000015C445	4	10	6.3	875	98503	5.4	aminopeptidase puromycin sensitive
1645	P55786	4	10	6	919	103276	5.7	Puromycin-sensitive aminopeptidase
1646	P28340	4	8	5.9	1107	123631	7	DNA polymerase delta catalytic subunit
1646	UPI00001297C1	4	8	5.9	1107	123635	7	polymerase (DNA directed), delta 1, catalytic subunit 125kDa
1646	Q308M6	4	8	5.7	1133	126338	7.4	DNA-directed polymerase delta 1
1647	P33991	4	13	5.9	863	96558	6.7	DNA replication licensing factor MCM4
1648	O60341	4	6	5.8	852	92903	6.5	Lysine-specific histone demethylase 1
1648	UPI0000D61E80	4	6	5.6	876	95223	6.2	Lysine-specific histone demethylase 1 (EC 1.-.-.-) (Flavin-containing amine oxidase domain-containing protein 2) (BRAF35-HDAC complex protein BHC110).
1648	O60341-2	4	6	5.6	876	95155	6.2	Isoform 2 of O60341
1649	P58215	4	8	5.8	753	83166	6.9	Lysyl oxidase homolog 3 precursor
1650	Q63ZY3	4	8	5.8	851	91174	5.6	Ankyrin repeat domain-containing protein 25
1650	Q63ZY3-3	4	8	5.8	841	90044	6	Isoform 3 of Q63ZY3
1651	Q9BVJ6	4	7	5.8	771	87978	7.9	U3 small nucleolar RNA-associated protein 14 homolog A
1652	Q96RP9	4	11	5.7	751	83472	7	Elongation factor G 1, mitochondrial precursor

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1652	UPI0000D61B9E	4	11	5.7	753	83632	7	Elongation factor G 1, mitochondrial precursor (mEF-G 1) (Elongation factor G1).
1653	P50416-2	4	15	5.7	756	86239	8.4	Isoform 2 of P50416
1653	P50416	4	15	5.6	773	88368	8.7	Carnitine O-palmitoyltransferase I, liver isoform
1654	Q92888-2	4	13	6	879	98768	5.6	Isoform 2 of Q92888
1654	Q92888	4	13	5.8	912	102435	5.7	Rho guanine nucleotide exchange factor 1
1654	Q6NX52	4	13	5.6	948	105854	6.5	ARHGEF1 protein
1654	UPI0000D617B4	4	13	5.6	947	105660	6.6	Rho guanine nucleotide exchange factor 1 (p115-RhoGEF) (p115RhoGEF) (115 kDa guanine nucleotide exchange factor) (Sub1.5).
1655	Q8N1F7	4	14	5.6	819	93488	5.7	Nuclear pore complex protein Nup93
1655	UPI0000070C22	4	14	5.6	819	93557	5.8	nucleoporin 93kDa
1656	A4D169	4	5	5.3	856	97687	6.5	Oxysterol binding protein-like 3
1656	Q9H4L5	4	5	5.1	887	101224	6.9	Oxysterol-binding protein-related protein 3
1657	Q14CX7	4	6	5.1	972	112292	6.6	Uncharacterized protein C12orf30
1657	Q7Z4N6	4	6	5.1	972	112277	6.6	P120
1658	O94906	4	7	5	941	106925	8.3	Pre-mRNA-processing factor 6
1659	P00533-4	4	5	9.7	628	69228	7.1	Isoform 4 of P00533
1659	Q68GS6	4	5	9.5	645	70823	7.1	Epidermal growth factor receptor
1659	P00533	4	5	5	1210	134277	6.7	Epidermal growth factor receptor precursor
1659	Q2TTR7	4	5	5	1210	134323	6.7	Cell growth inhibiting protein 40
1660	Q59E90	4	13	5	1007	113305	7.2	Mannosidase, alpha, class 2B, member 1 variant
1661	Q7RTP6-2	4	4	5.2	948	106837	8.2	Isoform 2 of Q7RTP6
1661	UPI0000DD85C8	4	4	5.1	963	108956	8.4	PREDICTED: similar to Protein MICAL-3
1661	Q7RTP6	4	4	5	976	109911	8.4	Protein MICAL-3
1662	O15451	4	14	4.9	1021	109140	4.3	Proline and glutamic acid rich nuclear protein isoform
1662	UPI0000D622A9	4	14	4.8	1042	110225	4.3	PELP1_HUMAN Isoform 2 of Q8IZL8 - Homo sapiens (Human)
1662	UPI00000740E9	4	14	4.4	1130	119624	4.3	proline-, glutamic acid-, leucine-rich protein 1
1662	Q8IZL8	4	14	4.4	1130	119700	4.3	Proline-, glutamic acid- and leucine-rich protein 1
1662	UPI000013E710	4	14	3.9	1272	135374	4.4	PELP1_HUMAN Isoform 2 of Q8IZL8 - Homo sapiens (Human)
1662	Q8IZL8-2	4	14	3.9	1275	135495	4.4	Isoform 2 of Q8IZL8
1663	Q8WTT2	4	9	4.9	800	92548	9.2	Nucleolar complex protein 3 homolog
1663	UPI0000D60F9F	4	9	4.9	800	92624	9.2	Nucleolar complex protein 3 homolog (NOC3 protein homolog) (NOC3-like protein) (Nucleolar complex-associated protein 3-like protein) (Factor for adipocyte differentiation 24).
1664	Q96JM3	4	5	4.9	812	89099	8.4	Zinc finger protein KIAA1802
1665	Q96T88	4	5	4.9	793	89814	7.6	E3 ubiquitin-protein ligase UHRF1

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1665	UPI0000456BDE	4	5	4.9	792	89743	7.6	E3 ubiquitin-protein ligase UHRF1 (EC 6.3.2.-) (Ubiquitin-like PHD and RING finger domain-containing protein 1) (Ubiquitin-like-containing PHD and RING finger domains protein 1) (Inverted CCAAT box-binding protein of 90 kDa) (Transcription factor ICBP90)
1665	UPI0000D48B65	4	5	4.8	806	91100	7.4	ubiquitin-like, containing PHD and RING finger domains, 1 isoform 2
1666	Q9Y6Y8-2	4	11	5.3	924	102187	5.8	Isoform 2 of Q9Y6Y8
1666	Q9Y6Y8	4	11	4.9	1000	111076	5.5	SEC23-interacting protein
1667	A4D228	4	4	4.7	1156	132195	6.8	More than blood homolog
1667	Q86XI2	4	4	4.7	1143	130960	6.9	Condensin-II complex subunit G2
1668	Q8NFA7	4	4	5.1	940	103581	7.1	Transmembrane receptor PTK7-3
1668	UPI0000457445	4	4	4.7	1015	112354	6.9	Tyrosine-protein kinase-like 7 precursor (Colon carcinoma kinase 4) (CCK-4).
1668	Q8NFA8	4	4	4.7	1030	113805	7	Transmembrane receptor PTK7-2
1668	Q8NFA6	4	4	4.7	1014	112261	7	Transmembrane receptor PTK7-4
1668	Q13308	4	4	4.5	1070	118392	7.1	Tyrosine-protein kinase-like 7 precursor
1668	Q6IQ54	4	4	4.5	1070	118376	7.1	PTK7 protein tyrosine kinase 7
1669	Q9HAU5	4	6	4.5	1272	147810	5.7	Regulator of nonsense transcripts 2
1670	Q6PD62	4	6	4.4	1173	133502	6.8	RNA polymerase-associated protein CTR9 homolog
1671	Q6NX72	4	15	4.3	1160	132322	5.8	EHBP1 protein
1671	Q6QNV2	4	15	4.2	1196	136237	5.4	EH domain binding protein 1
1671	UPI000013D49A	4	15	4.1	1231	140017	5.3	EH domain binding protein 1
1671	Q8NDI1	4	15	4.1	1231	139858	5.4	EH domain-binding protein 1
1672	Q7Z7M9	4	23	4.3	940	106266	9.5	Polypeptide N-acetylgalactosaminyltransferase 5
1673	Q9UIA9	4	18	4.3	1087	123907	6.3	Exportin-7
1673	UPI000049E0B7	4	18	4.3	1087	123975	6.3	Exportin-7 (Exp7) (Ran-binding protein 16).
1673	UPI0000073676	4	18	4.3	1087	123953	6.3	exportin 7
1674	Q59HA5	4	12	4.6	1196	130790	5.8	Cyclin G-associated kinase variant
1674	Q5U4P5	4	12	4.5	1232	134410	5.8	GAK protein
1674	O14976	4	12	4.2	1311	143190	5.7	Cyclin G-associated kinase
1674	UPI0000161B7C	4	12	4.2	1311	143164	5.7	cyclin G associated kinase
1675	P30876	4	5	4.1	1174	133896	6.9	DNA-directed RNA polymerase II 140 kDa polypeptide
1676	P56199	4	8	4.1	1179	130848	6.3	Integrin alpha-1 precursor
1676	UPI0000D61624	4	8	4.1	1180	130988	6.3	Integrin alpha-1 precursor (Laminin and collagen receptor) (VLA-1) (CD49a antigen).
1677	Q14527	4	13	4.1	1009	113928	8.6	Helicase-like transcription factor
1677	Q59GQ7	4	13	4.1	992	111966	8.7	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin a3 variant
1678	Q16706	4	20	4	1144	131084	7.6	Alpha-mannosidase 2

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1678	UPI000013D193	4	20	4	1144	131140	7.6	mannosidase, alpha, class 2A, member 1
1679	Q6PL18	4	8	4	1390	158554	6.3	ATPase family AAA domain-containing protein 2
1680	O95197-3	4	55	16.5	236	25609	8.5	Isoform 3 of O95197
1680	O95197-4	4	55	15.3	255	27568	8.2	Isoform 4 of O95197
1680	UPI0000D62622	4	55	15.2	257	27753	8.2	Reticulon-3 (Neuroendocrine-specific protein-like 2) (NSP-like protein II) (NSPLII).
1680	O95197	4	55	3.8	1032	112611	5	Reticulon-3
1680	UPI0000D62623	4	55	3.8	1034	112754	5	Reticulon-3 (Neuroendocrine-specific protein-like 2) (NSP-like protein II) (NSPLII).
1680	O95197-2	4	55	3.8	1013	110652	5	Isoform 2 of O95197
1681	Q9NVU3	4	5	5.3	864	96378	6.7	CDNA FLJ10506 fis, clone NT2RP2000510
1681	Q9BZH6	4	5	3.8	1224	136685	6.9	Bromodomain and WD repeat domain-containing protein 2
1682	A0JP11	4	5	3.7	1358	153158	7.2	Phosphoinositide-3-kinase, regulatory subunit 4, p150
1682	Q99570	4	5	3.7	1358	153103	7.2	Phosphoinositide 3-kinase regulatory subunit 4
1683	P35251	4	7	3.6	1148	128254	9.4	Replication factor C subunit 1
1683	P35251-2	4	7	3.6	1147	128183	9.4	Isoform 2 of P35251
1684	Q08AD0	4	10	3.6	1516	174700	6.9	UDP-glucose ceramide glucosyltransferase-like 2
1684	UPI00001FC9AA	4	10	3.6	1516	174734	6.9	UDP-glucose:glycoprotein glucosyltransferase 2 precursor (EC 2.4.1.-) (UDP-glucose ceramide glucosyltransferase-like 1) (UDP-- Glc:glycoprotein glucosyltransferase 2) (HUGT2).
1684	UPI0000137AEE	4	10	3.6	1516	174760	6.9	UDP-glucose:glycoprotein glucosyltransferase 2
1684	Q9NYU1	4	10	3.6	1516	174718	6.9	UDP-glucose:glycoprotein glucosyltransferase 2 precursor
1685	Q8WWM7-6	4	11	3.9	968	102895	8.6	Isoform 6 of Q8WWM7
1685	Q63ZY4	4	11	3.6	1062	112091	8.7	ATXN2L protein
1685	UPI0000161370	4	11	3.6	1044	110143	8.8	ataxin 2 related protein isoform E
1685	UPI000015FF26	4	11	3.6	1062	111920	8.7	ataxin 2 related protein isoform B
1685	Q8WWM7-5	4	11	3.6	1044	110177	8.8	Isoform 5 of Q8WWM7
1685	Q8WWM7-4	4	11	3.6	1044	110326	8.9	Isoform 4 of Q8WWM7
1685	Q8WWM7-2	4	11	3.6	1062	111954	8.7	Isoform 2 of Q8WWM7
1685	Q8WWM7-3	4	11	3.5	1097	115582	8.7	Isoform 3 of Q8WWM7
1685	Q8WWM7	4	11	3.5	1075	113374	8.6	Ataxin-2-like protein
1686	Q96K76-2	4	5	3.7	1287	147179	5.1	Isoform 2 of Q96K76
1686	Q96K76	4	5	3.5	1375	157268	5.1	Ubiquitin carboxyl-terminal hydrolase 47
1686	UPI0000D625BB	4	5	3.5	1362	155859	5.1	Ubiquitin carboxyl-terminal hydrolase 47 (EC 3.1.2.15) (Ubiquitin thioesterase 47) (Ubiquitin-specific-processing protease 47) (Deubiquitinating enzyme 47).
1687	UPI00001D7C42	4	8	3.5	1593	182774	8.4	THO complex 2 isoform 1
1688	Q9H7M7	4	14	3.6	1415	148907	4.7	FLJ00043 protein
1688	Q8N3D4	4	14	3.4	1510	160311	4.8	EH domain-binding protein 1-like protein 1

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1688	UPI000013EE70	4	14	3.4	1510	160283	4.8	Signal-induced proliferation-associated protein 1 (Sipa-1) (GTPase- activating protein Spa-1) (p130 SPA-1).
1689	P08572	4	9	3.2	1712	167553	8.7	Collagen alpha-2(IV) chain precursor [Contains: Canstatin]
1689	UPI0000D61AA5	4	9	3.2	1706	167211	8.6	Collagen alpha-2(IV) chain precursor.
1689	UPI0000D61AA4	4	9	3.2	1712	167607	8.6	Collagen alpha-2(IV) chain precursor.
1689	UPI00004588A6	4	9	3.2	1706	167157	8.6	Collagen alpha-2(IV) chain precursor.
1690	UPI00004FCB0F	4	8	3.3	1400	159300	5	Remodeling and spacing factor 1 (Rsf-1) (Hepatitis B virus X-associated protein) (HBV pX-associated protein 8) (p325 subunit of RSF chromatin remodelling complex).
1690	Q96T23-2	4	8	3.3	1400	159314	5	Isoform 2 of Q96T23
1690	Q96T23	4	8	3.2	1431	163005	5	Remodeling and spacing factor 1
1690	UPI00001FB001	4	8	3.2	1441	163820	5	remodeling and spacing factor 1
1691	Q9BZF9	4	7	3	1416	162504	7	Uveal autoantigen with coiled-coil domains and ankyrin repeats
1692	Q29RG0	4	6	2.9	1392	156767	5.4	CAP-GLY domain containing linker protein 1
1692	P30622-2	4	6	2.9	1392	156781	5.4	Isoform Short of P30622
1692	A0AVD3	4	6	2.8	1438	162246	5.4	CLIP1 protein
1692	Q17RS4	4	6	2.8	1438	162270	5.4	CLIP1 protein
1692	P30622	4	6	2.8	1427	160989	5.4	CAP-Gly domain-containing linker protein 1
1693	P48634	4	8	2.5	2157	228858	9.5	Large proline-rich protein BAT2
1693	UPI000020E69E	4	8	2.5	2157	228829	9.5	Large proline-rich protein BAT2 (HLA-B-associated transcript 2).
1693	UPI000020E56F	4	8	2.5	2157	228861	9.5	HLA-B associated transcript 2 (BAT2), transcript variant 1, mRNA
1693	UPI00000703A1	4	8	2.5	2157	228869	9.5	HLA-B associated transcript-2 isoform a
1693	Q05BK4	4	8	2.5	2157	228706	9.4	BAT2 protein
1694	Q96N67	4	7	2.3	2140	242558	6.8	Dedicator of cytokinesis protein 7
1694	UPI0000D61F29	4	7	2.3	2107	239160	6.8	Dedicator of cytokinesis protein 7.
1694	Q96N67-6	4	7	2.3	2131	241670	6.8	Isoform 6 of Q96N67
1694	Q96N67-5	4	7	2.3	2109	239420	6.8	Isoform 5 of Q96N67
1694	Q96N67-4	4	7	2.3	2098	238272	6.8	Isoform 4 of Q96N67
1694	Q96N67-3	4	7	2.3	2100	238532	6.8	Isoform 3 of Q96N67
1694	Q96N67-2	4	7	2.3	2129	241410	6.8	Isoform 2 of Q96N67
1695	Q5VTN2	4	5	2.2	2193	250502	7.2	OTTHUMP00000016904
1695	UPI000014145A	4	5	2.2	2202	251458	7.1	activating signal cointegrator 1 complex subunit 3 isoform a
1695	Q8N3C0	4	5	2.2	2202	251488	7.1	Activating signal cointegrator 1 complex subunit 3
1696	Q8WYP5	4	7	1.9	2275	253458	6.6	AT-hook-containing transcription factor 1
1696	UPI0000DD79DA	4	7	1.9	2223	247774	6.7	PREDICTED: similar to transcription factor ELYS

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1696	UPI000059D0E4	4	7	1.9	2301	255998	6.6	AT-hook-containing transcription factor 1 (Embryonic large molecule derived from yolk sac).
1696	UPI0000456336	4	7	1.9	2302	256411	7	AT-hook-containing transcription factor 1 (Embryonic large molecule derived from yolk sac).
1696	Q8WYP5-2	4	7	1.9	2304	256273	6.6	Isoform 2 of Q8WYP5
1697	UPI0000366852	4	21	2.2	2136	225686	6.4	Serine/threonine-protein kinase WNK1 (EC 2.7.11.1) (Protein kinase with no lysine 1) (Protein kinase, lysine-deficient 1) (Kinase deficient protein) (Erythrocyte 65 kDa protein) (p65).
1697	Q9H4A3-2	4	21	2.2	2136	225648	6.4	Isoform 2 of Q9H4A3
1697	Q9H4A3	4	21	1.9	2382	250753	6.3	Serine/threonine-protein kinase WNK1
1697	UPI000013CD65	4	21	1.9	2382	250791	6.3	Serine/threonine-protein kinase WNK1 (EC 2.7.11.1) (Protein kinase with no lysine 1) (Protein kinase, lysine-deficient 1) (Kinase deficient protein) (Erythrocyte 65 kDa protein) (p65).
1698	P42858	4	6	1.8	3144	347859	6.2	Huntingtin
1698	UPI0000D61535	4	6	1.8	3142	347775	6.2	Huntingtin (Huntington disease protein) (HD protein).
1698	UPI000013D567	4	6	1.8	3142	347603	6.2	Huntingtin (Huntington disease protein) (HD protein).
1699	Q5TBT1	4	4	1.3	5457	625004	5.7	Dystonin
1699	UPI0000457907	4	4	1.3	5497	629750	5.7	Bullous pemphigoid antigen 1, isoforms 1/2/3/4/5/8 (230 kDa bullous pemphigoid antigen) (BPA) (Hemidesmosomal plaque protein) (Dystonia musculorum protein) (Dystonin)
1699	UPI00001C1576	4	4	1.3	5497	629794	5.7	dystonin isoform 1
1699	UPI0000D626B7	4	4	1	7545	857472	5.2	Bullous pemphigoid antigen 1, isoforms 1/2/3/4/5/8 (230 kDa bullous pemphigoid antigen) (BPA) (Hemidesmosomal plaque protein) (Dystonia musculorum protein) (Dystonin)
1699	Q5TBT2	4	4	1	7543	857331	5.2	Dystonin
1700	Q709C8	4	11	1.1	3753	422393	6.8	Vacuolar protein sorting-associated protein 13C
1700	UPI000023BD43	4	11	1.1	3585	403087	6.4	vacuolar protein sorting 13C protein isoform 1B
1700	Q709C8-4	4	11	1.1	3584	402957	6.4	Isoform 4 of Q709C8
1700	Q709C8-3	4	11	1.1	3710	417279	6.6	Isoform 3 of Q709C8
1700	Q709C8-2	4	11	1.1	3627	408072	6.6	Isoform 2 of Q709C8
1701	P14618-2	3	15	64.8	531	58062	7.7	Isoform M1 of P14618
1702	O75506	3	11	64.5	76	8544	4.4	Heat shock factor-binding protein 1
1702	UPI000013E5CF	3	11	59	83	9349	4.4	Heat shock factor-binding protein 1 (Nasopharyngeal carcinoma-associated antigen 13) (NPC-A-13).
1703	P61960	3	22	60	85	9118	9.3	Ubiquitin-fold modifier 1 precursor

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1704	UPI0000D621E1	3	49	58.7	448	49764	5.1	Tubulin alpha-6 chain (Alpha-tubulin 6).
1704	Q53GA7	3	49	58.6	449	49823	5.1	Tubulin alpha 6 variant
1704	Q9BQE3	3	49	58.6	449	49895	5.1	Tubulin alpha-6 chain
1705	Q13885	3	8	57.8	445	49907	4.9	Tubulin beta-2A chain
1706	P61204	3	60	53.6	181	20601	7.4	ADP-ribosylation factor 3
1706	P84077	3	60	53.6	181	20697	6.8	ADP-ribosylation factor 1
1707	O95167	3	14	50	84	9279	8.5	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 3
1708	P62857	3	104	46.4	69	7841	10.7	40S ribosomal protein S28
1708	UPI000013E08B	3	104	46.4	69	7823	10.7	ribosomal protein S28 (RPS28), mRNA
1709	Q9C005	3	20	45.5	99	11250	4.9	Dpy-30-like protein
1710	Q9Y281	3	10	45.2	166	18737	7.9	Cofilin-2
1711	P62834	3	7	45.1	184	20987	6.6	Ras-related protein Rap-1A precursor
1712	P62140	3	13	43.4	327	37187	6.2	Serine/threonine-protein phosphatase PP1-beta catalytic subunit
1713	P04271	3	64	40.2	92	10713	4.6	Protein S100-B
1714	Q9BZL1	3	26	39.7	73	8547	8.4	Ubiquitin-like protein 5
1715	Q9Y3D7	3	10	39.2	125	13825	9.7	Mitochondrial import inner membrane translocase subunit TIM16
1716	Q9BWJ5	3	22	38.4	86	10135	6.4	Splicing factor 3B subunit 5
1717	A4FU11	3	8	38.2	262	29294	10.2	RPS4Y1 protein
1717	Q496E4	3	8	38	263	29426	10.2	Ribosomal protein S4, Y-linked 1
1717	P22090	3	8	38	263	29456	10.2	40S ribosomal protein S4, Y isoform 1
1718	O00244	3	21	38.2	68	7402	7.2	Copper transport protein ATOX1
1718	UPI0000D6169C	3	21	38.2	68	7449	7.2	Copper transport protein ATOX1 (Metal transport protein ATX1).
1718	Q6IBA3	3	21	38.2	68	7388	7.2	ATOX1 protein
1719	Q9Y5J7	3	9	38.2	89	10378	7.2	Mitochondrial import inner membrane translocase subunit Tim9
1720	P62304	3	35	38	92	10804	9.4	Small nuclear ribonucleoprotein E
1721	P35244	3	13	37.2	121	13569	5.1	Replication protein A 14 kDa subunit
1722	P05114	3	10	37	100	10659	9.6	Nonhistone chromosomal protein HMG-14
1723	Q5RI17	3	6	36.7	723	79844	7.9	Heterogeneous nuclear ribonucleoprotein U
1724	P14174	3	28	36.5	115	12476	7.9	Macrophage migration inhibitory factor
1725	Q99622	3	10	36.5	126	13178	5.1	Putative C10 protein
1726	UPI000016062E	3	4	36.4	118	12951	9.6	PREDICTED: similar to BC003940 protein
1727	Q99878	3	232	36.7	128	13936	10.9	Histone H2A type 1-J
1727	Q96KK5	3	232	36.7	128	13906	10.9	Histone H2A type 1-H
1727	Q9BTM1	3	232	36.4	129	14019	10.9	H2A histone family, member J
1727	Q16777	3	232	36.4	129	13988	10.9	Histone H2A type 2-C
1727	P0C0S8	3	232	36.2	130	14091	10.9	Histone H2A type 1
1727	Q6FI13	3	232	36.2	130	14095	10.9	Histone H2A type 2-A
1727	P20671	3	232	36.2	130	14107	10.9	Histone H2A type 1-D
1727	UPI000013C8E5	3	232	30.3	155	16610	10.2	H2A histone family, member J isoform 2

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
1728	P61769	3	35	35.3	119	13715	6.5	Beta-2-microglobulin precursor [Contains: Beta-2-microglobulin variant pI 5.3]
1728	Q6IAT8	3	35	35.3	119	13697	6.5	B2M protein
1729	Q3ZAQ7	3	12	34.7	101	11354	7.2	Hypothetical protein LOC203547
1730	P63027	3	40	34.5	116	12649	8.1	Vesicle-associated membrane protein 2
1730	Q9N0Y0	3	40	34.5	116	12663	8.1	Vesicle-associated membrane protein 2
1731	A2VBZ8	3	9	37.4	273	31456	5.8	MHC class I antigen
1731	A0JKD2	3	9	34.2	298	34040	5.8	MHC class I
1732	P62306	3	52	33.7	86	9725	4.7	Small nuclear ribonucleoprotein F
1732	Q6IBQ1	3	52	33.7	86	9711	4.7	SNRPF protein
1733	P84090	3	47	33.7	104	12259	5.9	Enhancer of rudimentary homolog
1734	Q7Z7F7	3	8	33.6	128	15128	11.2	39S ribosomal protein L55, mitochondrial precursor
1735	Q8NDD5	3	7	43	128	14098	5.9	Hypothetical protein DKFZp586L2318
1735	UPI00001B5789	3	7	40.1	137	15614	4.6	ubiquitin-conjugating enzyme E2G 2 isoform 2
1735	P60604	3	7	33.3	165	18566	4.7	Ubiquitin-conjugating enzyme E2 G2
1736	Q5T179	3	5	38.8	67	8027	6.4	CDC28 protein kinase regulatory subunit 1B
1736	P61024	3	5	32.9	79	9660	8.9	Cyclin-dependent kinases regulatory subunit 1
1736	UPI0000161698	3	5	32.9	79	9660	8.7	PREDICTED: similar to Cyclin-dependent kinases regulatory subunit 1 (CKS-1) (Sid 1334)
1737	Q49AP7	3	15	32.6	92	10739	8.5	C1orf212 protein
1738	P07108	3	23	32.2	87	10044	6.5	Acyl-CoA-binding protein
1738	Q4VWZ6	3	23	31.8	88	10145	6.5	Diazepam binding inhibitor, splice form 1c
1738	Q3I231	3	23	26.9	104	11793	5.5	Diazepam-binding protein
1739	A2IDD8	3	8	32.1	140	16241	6.6	Vesicle-associated membrane protein 4
1739	O75379	3	8	31.9	141	16397	7.4	Vesicle-associated membrane protein 4
1740	Q8N4H5	3	4	52.9	51	6035	9.7	Uncharacterized protein C9orf105
1740	Q5JRT7	3	4	31.8	85	9655	7.2	Chromosome 9 open reading frame 105
1741	P62318	3	26	31.7	126	13916	10.3	Small nuclear ribonucleoprotein Sm D3
1742	Q8WYJ5	3	12	39.8	128	13918	7	Protein kinase C inhibitor-2
1742	Q53HJ8	3	12	31.3	163	17174	9.5	PKCI-1-related HIT protein variant
1742	Q9BX68	3	12	31.3	163	17162	9.1	Histidine triad nucleotide-binding protein 2
1743	P62072	3	9	31.1	90	10333	6.3	Mitochondrial import inner membrane translocase subunit Tim10
1744	O96033	3	8	30.7	88	9755	4.7	Molybdenum cofactor synthesis protein 2 small subunit
1745	Q53FH6	3	11	30.6	124	13563	7.4	Mitogen-activated protein kinase kinase 1 interacting protein 1 variant
1745	Q9UHA4	3	11	30.6	124	13623	7.4	Mitogen-activated protein kinase kinase 1-interacting protein 1

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1746	Q8N4V1	3	7	30.5	131	14686	9.1	Transmembrane protein 32
1747	P83916	3	10	30.3	185	21418	4.9	Chromobox protein homolog 1
1748	Q6P1L8	3	10	29.7	145	15948	10.2	39S ribosomal protein L14, mitochondrial precursor
1749	O43920	3	20	29.2	106	12517	9.1	NADH dehydrogenase [ubiquinone] iron-sulfur protein 5
1750	O60783	3	14	28.9	128	15139	11.4	Mitochondrial 28S ribosomal protein S14
1751	P26885	3	14	28.9	142	15649	9.1	FK506-binding protein 2 precursor
1752	O43676	3	20	28.6	98	11402	9.2	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3
1753	Q8N9N8	3	3	28.5	165	19053	5.2	CDNA FLJ36810 fis, clone ASTRO2001249
1754	Q9NQP4	3	15	28.4	134	15314	4.5	Prefoldin subunit 4
1755	Q86U75	3	8	28.3	619	67017	6	Dihydropyrimidinase-like 2
1756	Q86SX6	3	16	28	157	16628	6.8	Glutaredoxin-related protein 5
1757	O15212	3	5	27.9	129	14583	8.9	Prefoldin subunit 6
1758	P61020	3	11	27.9	215	23707	8.1	Ras-related protein Rab-5B
1759	O95563	3	8	27.6	127	14279	10.4	Brain protein 44
1760	Q8N111	3	6	27.5	149	14954	9.2	Cell cycle exit and neuronal differentiation protein 1
1761	P62910	3	25	27.4	135	15860	11.3	60S ribosomal protein L32
1761	UPI0000073979	3	25	27.4	135	15751	10.9	PREDICTED: similar to 60S ribosomal protein L32
1762	P42167	3	10	26.9	454	50670	9.4	Lamina-associated polypeptide 2, isoforms beta/gamma (Thymopoietin, isoforms beta/gamma) (TP beta/gamma) (Thymopoietin-related peptide isoforms beta/gamma) (TPRP isoforms beta/gamma) [Contains: Thymopoietin (TP) (Splenin); Thymopentin (TP5)]
1763	Q9Y5R8	3	3	26.9	145	16832	9.2	Trafficking protein particle complex subunit 1
1764	O75607	3	5	26.4	178	19344	4.6	Nucleoplasmin-3
1765	Q7Z4G1	3	3	38.8	85	9638	6	COMM domain-containing protein 6
1765	UPI000034ECDC	3	3	33.7	98	10908	6	COMM domain containing 6 isoform a
1765	Q5TBK3	3	3	26.4	125	14211	9.8	COMM domain containing 6
1765	UPI0000D61A83	3	3	26.4	125	14257	9.8	COMM domain-containing protein 6.
1766	Q9Y2R0	3	22	26.4	106	11731	9.6	Coiled-coil domain-containing protein 56
1767	P60866	3	54	26.1	119	13373	9.9	40S ribosomal protein S20
1768	P53999	3	26	26	127	14395	9.6	Activated RNA polymerase II transcriptional coactivator p15
1768	UPI000006EEC7	3	26	26	127	14365	9.6	activated RNA polymerase II transcription cofactor 4
1768	Q59G24	3	26	24.6	134	15135	9.4	Activated RNA polymerase II transcription cofactor 4 variant
1769	Q9NP97	3	12	39.6	96	10922	7.2	Dynein light chain roadblock-type 1
1769	Q5TC71	3	12	25.7	148	16253	7	Dynein, light chain, roadblock-type 1
1770	Q5JW33	3	3	25.4	134	15055	4.6	ASF1 anti-silencing function 1 homolog A
1770	UPI00004153B3	3	3	20.2	168	18809	4.5	ASF1 anti-silencing function 1 homolog A

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1770	UPI0000F24423	3	3	19.4	175	19812	4.5	ASF1A protein
1770	Q9Y294	3	3	16.7	204	22969	4.4	Histone chaperone ASF1A
1771	O60613	3	24	25.3	162	17743	5	15 kDa selenoprotein precursor
1771	UPI000034ECC1	3	24	24.8	165	17942	5	15 kDa selenoprotein isoform 1 precursor
1772	Q7Z7H5	3	9	25.1	227	25943	8.3	Transmembrane emp24 domain-containing protein 4 precursor
1772	UPI0000D61C37	3	9	24.9	229	26170	8.6	Transmembrane emp24 domain-containing protein 4 precursor.
1773	O75348	3	22	24.6	118	13758	8.8	Vacuolar ATP synthase subunit G 1
1774	Q9H7C9	3	4	24.6	122	13332	8.4	UPF0366 protein C11orf67
1775	P06703	3	134	24.4	90	10180	5.5	Protein S100-A6
1776	P98179	3	66	24.2	157	17170	8.9	Putative RNA-binding protein 3
1777	Q16540	3	14	24.2	153	17781	9.7	Mitochondrial 39S ribosomal protein L23
1777	UPI0000D62587	3	14	24.2	153	17834	10	Mitochondrial 39S ribosomal protein L23 (L23mt) (MRP-L23) (L23 mitochondrial-related protein) (Ribosomal protein L23-like).
1777	UPI00001678B9	3	14	24.2	153	17811	9.7	mitochondrial ribosomal protein L23
1777	UPI00001F9AD4	3	14	22.7	163	18530	10.9	Mitochondrial 39S ribosomal protein L23 (L23mt) (MRP-L23) (L23 mitochondrial-related protein) (Ribosomal protein L23-like).
1778	Q9NWU2	3	4	23.7	228	26749	5	Protein C20orf11
1779	Q13405	3	14	23.5	166	19198	9.5	Mitochondrial 39S ribosomal protein L49
1780	Q86WX3	3	5	23.5	136	15434	10.7	40S ribosomal protein S19-binding protein 1
1781	Q9BRJ6	3	9	23.2	194	22083	9.6	MGC11257 protein
1782	O60925	3	16	23	122	14210	6.8	Prefoldin subunit 1
1783	Q53G62	3	8	23	187	20771	9.3	Mitochondrial ribosomal protein S28 variant
1783	Q9Y2Q9	3	8	23	187	20843	9.1	Mitochondrial 28S ribosomal protein S28
1784	UPI0000470085	3	5	32.7	104	11447	10.1	DnaJ homolog subfamily C member 15 (Methylation-controlled J protein) (MCJ).
1784	Q9Y5T4	3	5	22.7	150	16383	10.1	DnaJ homolog subfamily C member 15
1785	P30049	3	24	22.6	168	17490	5.5	ATP synthase delta chain, mitochondrial precursor
1786	Q9UI09	3	18	22.8	145	17114	9.6	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12
1786	Q53XX0	3	18	22.8	145	17084	9.6	13kDa differentiation-associated protein
1786	Q53HG1	3	18	22.6	146	17215	9.6	13kDa differentiation-associated protein variant
1787	O95372	3	7	22.5	231	24737	7.2	Acyl-protein thioesterase 2
1788	P20962	3	50	22.5	102	11530	4.2	Parathymosin
1789	P82930	3	7	22.5	218	25650	10	Mitochondrial 28S ribosomal protein S34
1790	Q6IAA8	3	12	22.4	161	17745	5.1	UPF0404 protein C11orf59
1791	P09417	3	5	22.1	244	25789	7.4	Dihydropteridine reductase
1791	UPI000004C79F	3	5	22.1	244	25804	7.4	quinoid dihydropteridine reductase

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1792	Q6GMR2	3	5	22.1	208	22808	11	MGC70857 protein
1792	Q6P2Q7	3	5	21.3	216	23889	9.1	Similar to RIKEN cDNA C030006K11 gene
1792	Q6P1X6	3	5	21.3	216	23875	9.1	Similar to RIKEN cDNA C030006K11 gene
1793	Q9BWN5	3	8	23.7	224	23195	8.3	IlvB (Bacterial acetolactate synthase)-like
1793	UPI0000456C2D	3	8	23.6	225	23392	8.5	ilvB (bacterial acetolactate synthase)-like isoform 1
1793	A1L0T0	3	8	22	241	25613	9.6	FLJ39061 protein
1793	Q59GP4	3	8	12.4	427	45645	8.9	IlvB (Bacterial acetolactate synthase)-like isoform 1 variant
1793	Q99651	3	8	8.4	632	67924	8.1	Acetolactate synthase homolog
1793	Q96F08	3	8	8.4	632	67869	8	IlvB (Bacterial acetolactate synthase)-like
1793	O43341	3	8	8.4	632	67868	8.1	IlvB-like protein
1794	A2IDC8	3	7	22	168	18601	10.9	Non-metastatic cells 4, protein expressed in
1794	O00746	3	7	19.8	187	20659	10.3	Nucleoside diphosphate kinase, mitochondrial precursor
1794	Q4TT34	3	7	19	195	21522	10.6	Non-metastatic cells 4, protein expressed in
1795	P52434	3	19	22	150	17143	4.7	DNA-directed RNA polymerases I, II, and III 17.1 kDa polypeptide
1796	Q9Y5J5	3	8	22	127	13891	9.7	Pleckstrin homology-like domain family A member 3
1797	Q8WW12	3	8	21.9	178	18925	7.5	PEST proteolytic signal-containing nuclear protein
1798	Q5TGM0	3	3	21.7	249	27331	5.2	Chromosome 6 open reading frame 55
1798	Q9NP79	3	3	17.6	307	33879	6.3	Uncharacterized protein C6orf55
1798	Q6IAE8	3	3	17.6	307	33865	6.3	C6orf55 protein
1799	P63272	3	11	21.4	117	13193	8.1	Transcription elongation factor SPT4
1800	Q9HBM1	3	4	21.4	224	26153	8	Kinetochore protein Spc25
1801	Q53EQ5	3	5	21.2	208	23144	9	Hypothetical protein
1801	Q8N511	3	5	21.2	208	23130	9	Uncharacterized protein C17orf32
1802	Q9Y3C6	3	8	21.1	166	18237	8	Peptidyl-prolyl cis-trans isomerase-like 1
1803	P55957	3	15	21	195	21995	5.4	BH3-interacting domain death agonist (BID) (p22 BID) [Contains: BH3- interacting domain death agonist p15 (p15 BID); BH3-interacting domain death agonist p13 (p13 BID); BH3-interacting domain death agonist p11 (p11 BID)]
1804	Q9Y4Z0	3	21	20.9	139	15350	10	U6 snRNA-associated Sm-like protein LSm4
1805	A1XKG3	3	5	20.8	260	29544	6.4	Protein kinase CDK5 splicing variant
1805	Q6IAW3	3	5	18.5	292	33288	7.7	CDK5 protein
1805	Q00535	3	5	18.5	292	33304	7.7	Cell division protein kinase 5
1806	Q9BVJ7	3	7	20.7	150	16588	8.2	Dual specificity protein phosphatase 23
1807	P52298	3	7	20.5	156	18001	8.2	Nuclear cap-binding protein subunit 2
1808	Q9H2H8	3	7	20.5	161	18155	6.8	Peptidyl-prolyl cis-trans isomerase-like 3

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1809	Q9NR77	3	4	20.5	195	22253	10.6	Peroxisomal membrane protein 2
1810	O00161-2	3	12	27.2	158	17789	4.7	Isoform SNAP
1810	O00161	3	12	20.4	211	23354	5	Synaptosomal-associated protein 23
1811	UPI000059DB3B	3	7	20.9	158	18342	7.3	Sorting nexin-12.
1811	Q3SYF1	3	7	20.4	162	18885	8.4	Sorting nexin 12
1811	UPI0000D61D89	3	7	19.2	172	19819	7.8	Sorting nexin-12.
1811	Q9UMY4	3	7	19.2	172	19730	7.9	Sorting nexin-12
1812	Q9BZX2	3	3	20.3	261	29299	6.7	Uridine-cytidine kinase 2
1813	Q99627	3	11	20.1	209	23226	5.4	COP9 signalosome complex subunit 8
1814	Q9GZS3	3	21	20	305	33581	5.5	WD repeat protein 61
1815	Q96GN0	3	10	19.9	181	21210	7.5	Regulator of G-protein signalling 10
1816	Q8WW59	3	7	19.8	207	23098	6.9	SPRY domain-containing protein 4
1816	UPI00001418EE	3	7	19.8	207	23129	6.9	SPRY domain-containing protein 4.
1817	P60510	3	9	19.5	307	35080	5.1	Serine/threonine-protein phosphatase 4 catalytic subunit
1818	Q58P21	3	8	21.3	188	20917	7.8	Tissue inhibitor of metalloproteinase 1
1818	P01033	3	8	19.3	207	23171	8.1	Metalloproteinase inhibitor 1 precursor
1819	Q7Z7H8	3	7	19.2	261	29297	9.6	39S ribosomal protein L10, mitochondrial precursor
1819	UPI000004FA30	3	7	19.2	261	29283	9.6	mitochondrial ribosomal protein L10 isoform a
1819	UPI000013DFCA	3	7	18.5	271	30307	9.2	mitochondrial ribosomal protein L10 isoform b
1820	Q8WVJ2	3	5	19.1	157	17676	5.1	NudC domain-containing protein 2
1821	Q9NX08	3	7	19.1	183	21090	5.4	COMM domain-containing protein 8
1822	P10606	3	33	18.6	129	13696	8.8	Cytochrome c oxidase subunit 5B, mitochondrial precursor
1822	Q6FHM4	3	33	18.6	129	13705	8.8	COX5B protein
1823	P30154	3	4	18.5	601	66214	4.9	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform
1823	Q8NHV8	3	4	16.6	667	73585	5.1	Protein phosphatase 2 (Formerly 2A), regulatory subunit A, beta isoform
1824	Q9BRJ7	3	6	18.5	211	23338	8.9	Protein syndesmos
1825	Q9NQ50	3	9	18.4	206	24490	9.6	39S ribosomal protein L40, mitochondrial precursor
1826	Q16629-3	3	31	32.6	132	15257	9.6	Isoform 3 of Q16629
1826	Q16629-2	3	31	31.9	135	15573	9.8	Isoform 2 of Q16629
1826	UPI000013D48B	3	31	31.4	137	15763	9.8	Splicing factor, arginine/serine-rich 7 (Splicing factor 9G8).
1826	Q16629	3	31	18.1	238	27367	11.8	Splicing factor, arginine/serine-rich 7
1827	Q8IW87	3	5	18.1	227	24434	6.9	Candidate tumor suppressor in ovarian cancer 2
1827	Q8WZ82	3	5	18.1	227	24418	6.9	Candidate tumor suppressor OVCA2
1828	Q14197	3	6	18	206	23630	10.1	Immature colon carcinoma transcript 1 protein precursor
1829	Q6UW68	3	3	18	189	21198	8.6	MBC3205
1830	Q9BY32	3	6	18	194	21446	5.6	Inosine triphosphate pyrophosphatase

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1831	Q9NYL4	3	17	17.9	201	22180	9.4	FK506-binding protein 11 precursor
1832	Q9UBX3	3	3	17.8	287	31282	9.5	Mitochondrial dicarboxylate carrier
1832	Q9UBX3-2	3	3	17.2	296	32145	9.3	Isoform 2 of Q9UBX3
1833	UPI0000D61D3B	3	7	19.6	179	20084	9.4	Protein FAM121B precursor.
1833	Q9BUR5-2	3	7	19.4	180	20199	9.3	Isoform 2 of Q9BUR5
1833	Q9BUR5	3	7	17.7	198	22285	9.1	Apolipoprotein O precursor
1834	Q9H0A8-2	3	5	25	140	15458	8.3	Isoform 2 of Q9H0A8
1834	Q9H0A8	3	5	17.6	199	21764	7.3	COMM domain-containing protein 4
1835	P04183	3	6	17.5	234	25469	8.5	Thymidine kinase, cytosolic
1835	UPI0000F58EFA	3	6	17.5	234	25354	8.5	Thymidine kinase
1835	UPI0000161B4B	3	6	17.5	234	25501	8.5	thymidine kinase 1, soluble
1836	P60903	3	62	17.5	97	11203	7.4	Protein S100-A10
1836	Q6FGE5	3	62	17.5	97	11187	7.4	S100A10 protein
1837	Q9CSU2	3	17	20.8	259	28772	7.1	10 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2610303K13 product:26S proteasome-associated pad1 homolog, full insert sequence
1837	O00487	3	17	17.4	310	34577	6.5	26S proteasome non-ATPase regulatory subunit 14
1838	Q9BU61	3	15	17.4	184	20350	8.2	Uncharacterized protein C3orf60
1839	UPI000045652F	3	7	19.1	188	20857	10.1	39S ribosomal protein L21, mitochondrial precursor (L21mt) (MRP-L21).
1839	Q7Z2W9	3	7	17.2	209	23159	9.9	39S ribosomal protein L21, mitochondrial precursor
1840	Q9UHY7	3	8	17.2	261	28933	4.8	Enolase-phosphatase E1
1841	Q16595	3	7	17.1	210	23135	8.7	Frataxin, mitochondrial precursor (Friedreich ataxia protein) (Fxn) [Contains: Frataxin intermediate form]
1842	Q5TIF0	3	10	17.1	234	26761	5	Syntaxin 12
1842	Q6LEU0	3	10	14.9	269	30878	5.8	STX12 protein
1842	Q86Y82	3	10	14.5	276	31642	5.6	Syntaxin-12
1843	Q8N0U8	3	38	17	176	19836	9.1	Vitamin K epoxide reductase complex subunit 1-like protein 1
1844	Q9NR45	3	4	17	359	40308	6.7	Sialic acid synthase
1845	Q6P587	3	8	18.8	224	24843	7.4	Fumarylacetoacetate hydrolase domain-containing protein 1
1845	A2A2C3	3	8	18.6	226	24910	7.7	Fumarylacetoacetate hydrolase domain containing 1
1845	A2A2C2	3	8	16.9	248	27128	7.7	Fumarylacetoacetate hydrolase domain containing 1
1846	Q9Y3L5	3	8	16.9	183	20745	4.9	Ras-related protein Rap-2c precursor
1847	Q9Y6M9	3	8	16.8	179	21831	8.4	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9
1848	A4FVB3	3	9	16.7	299	32568	7.9	SPRY4 protein
1848	Q9C004	3	9	16.7	299	32541	7.9	Sprouty homolog 4
1849	Q14919	3	11	16.6	205	22350	5.2	Dr1-associated corepressor
1849	Q14919-2	3	11	16.1	211	23148	5.3	Isoform 2 of Q14919
1849	UPI0000D62635	3	11	16	212	23205	5.3	Dr1-associated corepressor (Dr1-associated protein 1) (Negative co-factor 2 alpha) (NC2 alpha).

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
1850	Q96CT7	3	9	16.6	223	25835	9.5	Coiled-coil domain-containing protein 124
1851	O75608-2	3	15	17.8	214	22875	6.5	Isoform 2 of O75608
1851	O75608	3	15	16.5	230	24670	6.8	Acyl-protein thioesterase 1
1852	P07305	3	22	16.5	194	20863	10.8	Histone H1.0 (Histone H1(0))
1853	P34741	3	18	16.4	201	22174	4.9	Syndecan-2 precursor
1853	Q6PIS6	3	18	16.4	201	22160	4.9	Syndecan 2
1854	Q52LJ0	3	12	16.4	330	37191	6.3	Protein FAM98B
1854	UPI0000DA182F	3	12	12.5	433	45547	8.7	family with sequence similarity 98, member B isoform 1
1855	Q53GA4	3	6	16.4	152	17092	9.2	Pleckstrin homology-like domain family A member 2
1856	Q5W111-2	3	6	20.4	157	17487	5.9	Isoform 2 of Q5W111
1856	Q5W111	3	6	16.3	196	21666	6.7	Chronic lymphocytic leukemia deletion region gene 6 protein
1857	Q01081	3	17	16.2	240	27872	8.8	Splicing factor U2AF 35 kDa subunit
1858	Q9NQR4	3	4	15.6	276	30608	7.2	Nit protein 2
1859	UPI00006C03F3	3	6	19.5	241	27027	4.9	PREDICTED: hypothetical protein
1859	Q658P1	3	6	15.5	304	34805	6.6	Hypothetical protein DKFZp666C185
1859	UPI000013EF67	3	6	15.4	306	34925	6.7	PREDICTED: hypothetical protein LOC64853
1859	Q9H9E8	3	6	15.4	306	34951	6.7	CDNA FLJ12806 fis, clone NT2RP2002235
1859	Q96BJ3	3	6	15.4	306	35023	6.6	Uncharacterized protein C1orf80
1860	O14561	3	22	15.4	156	17417	4.9	Acyl carrier protein, mitochondrial precursor
1861	UPI0000456EE0	3	6	15.9	220	23901	5.4	Ribulose-phosphate 3-epimerase (EC 5.1.3.1) (Ribulose-5-phosphate-3- epimerase).
1861	Q96AT9-2	3	6	15.9	220	23924	5.6	Isoform 2 of Q96AT9
1861	Q96AT9	3	6	15.4	228	24928	5.6	Ribulose-phosphate 3-epimerase
1862	Q53HV0	3	5	15.3	346	38954	7.9	SPFH domain family, member 1 variant
1863	A0PJ79	3	6	15.2	302	34446	9.4	Hypothetical protein
1863	UPI0000D61582	3	6	15.2	303	34492	8.1	39S ribosomal protein L1, mitochondrial precursor (L1mt) (MRP-L1).
1863	Q9BYD6	3	6	15.2	303	34453	8.1	39S ribosomal protein L1, mitochondrial precursor
1864	UPI00001B2F34	3	16	18	150	16676	8	ubiquitin-conjugating enzyme E2C isoform 3
1864	O00762	3	16	15.1	179	19652	7.4	Ubiquitin-conjugating enzyme E2 C
1865	O75934	3	5	15.1	225	26131	5.6	Breast carcinoma amplified sequence 2
1866	Q8N9N7	3	4	15.1	239	26754	8.4	Leucine-rich repeat-containing protein 57
1866	UPI000006FF78	3	4	15.1	239	26740	8.2	leucine rich repeat containing 57
1867	O15305	3	10	15	246	28082	6.8	Phosphomannomutase 2
1868	Q12974	3	5	15	167	19127	8.4	Protein tyrosine phosphatase type IVA protein 2 (EC 3.1.3.48) (Protein-tyrosine phosphatase 4a2) (Protein-tyrosine phosphatase of regenerating liver 2) (PRL-2) (PTP(CAAXII))
1869	Q08257	3	16	14.9	329	35207	8.4	Quinone oxidoreductase

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
1870	Q5SY58	3	3	14.8	243	26326	6.3	Nitrilase 1
1870	Q86X76-4	3	3	11.5	312	34323	7.4	Isoform 5 of Q86X76
1870	Q86X76	3	3	11	327	35896	7.7	Nitrilase homolog 1
1870	Q86X76-3	3	3	9.8	367	40200	6.9	Isoform 4 of Q86X76
1871	Q9ULC3	3	4	14.8	237	26659	6.6	Ras-related protein Rab-23
1872	P62993	3	6	14.7	217	25206	6.3	Growth factor receptor-bound protein 2
1873	P60673	3	12	14.6	137	14596	9.3	Profilin-3
1874	Q9GZZ9	3	10	14.6	404	44863	4.8	Ubiquitin-activating enzyme E1 domain-containing protein 1
1875	Q59FM5	3	5	14.6	357	41891	5.7	Guanine nucleotide-binding protein G, alpha subunit variant
1875	P29992	3	5	14.5	359	42123	5.7	Guanine nucleotide-binding protein subunit alpha-11 (G alpha-11) (Guanine nucleotide-binding protein G(y) subunit alpha)
1876	UPI0000456B12	3	18	16.2	197	22761	11.9	Splicing factor, arginine/serine-rich 2 (Splicing factor SC35) (SC-35) (Splicing component, 35 kDa) (Protein PR264).
1876	Q01130	3	18	14.5	221	25476	11.9	Splicing factor, arginine/serine-rich 2
1876	Q53FN0	3	18	14.5	221	25502	11.9	Splicing factor, arginine/serine-rich 2 variant
1877	Q15257-3	3	4	17.7	294	33467	6.3	Isoform 3 of Q15257
1877	Q15257-2	3	4	16.1	323	36775	6.3	Isoform 1 of Q15257
1877	Q15257	3	4	14.5	358	40668	5.9	Serine/threonine-protein phosphatase 2A regulatory subunit B'
1878	UPI0000161188	3	9	14.6	316	33341	6.8	pyrroline-5-carboxylate reductase 1 isoform 2
1878	P32322	3	9	14.4	319	33361	7.6	Pyrroline-5-carboxylate reductase 1
1879	P40937	3	6	14.4	340	38497	7.2	Replication factor C subunit 5
1879	Q6LES9	3	6	14.4	340	38397	6.9	RFC5 protein
1879	Q59GW7	3	6	14	351	39643	7.8	Replication factor C 5 isoform 1 variant
1880	P82664	3	4	14.4	201	22999	8	Mitochondrial 28S ribosomal protein S10
1881	Q13243	3	17	14.3	272	31264	11.6	Splicing factor, arginine/serine-rich 5
1882	Q561W0	3	5	14.3	258	29642	8.7	TXNDC14 protein
1882	Q9Y320	3	5	12.5	296	34038	8.7	CGI-31 protein
1882	Q5J7Q7	3	5	12.5	296	34012	8.7	Proliferation-inducing gene 26 protein
1882	UPI000024706C	3	5	10	371	42472	8.6	Catenin delta-1 (p120 catenin) (p120(ctn)) (Cadherin-associated Src substrate) (CAS) (p120(cas)).
1882	Q9H3L1	3	5	9.9	372	42478	8.7	My009 protein
1882	Q8NBP9	3	5	9.9	372	42543	8.6	Thioredoxin domain-containing protein 14
1883	UPI00003667A5	3	49	15.7	242	26818	5.1	CD82 antigen isoform 2
1883	P27701	3	49	14.2	267	29626	5.2	CD82 antigen
1883	Q7Z2D4	3	49	14.2	267	29611	5.2	CD82 molecule
1883	Q6LET0	3	49	14.2	267	29644	5.2	KAI1 protein
1884	P84157-2	3	5	17.1	170	17493	4.1	Isoform 2 of P84157
1884	P84157-3	3	5	16.4	177	18207	4.1	Isoform 3 of P84157
1884	P84157	3	5	14.2	204	21466	4.3	Matrix-remodelling-associated protein 7
1885	Q53GB6	3	6	14.2	365	40954	8	Actin related protein 2/3 complex subunit 1A variant

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1885	Q92747	3	6	14.1	370	41569	8.2	Actin-related protein 2/3 complex subunit 1A
1886	Q5T1C6	3	7	14.2	240	27130	8.3	Thioesterase superfamily member 4
1886	Q96KR2	3	7	14.2	240	27173	8.4	C-terminal modulator protein
1887	Q9Y316	3	7	14.1	297	33733	7.2	Protein memo
1887	Q5R2V8	3	7	14	300	34294	7.3	Chromosome 2 open reading frame 4 short form
1888	Q9Y2R9	3	9	14	242	28162	10	28S ribosomal protein S7, mitochondrial precursor
1888	UPI000013CBA7	3	9	14	242	28134	10	28S ribosomal protein S7, mitochondrial precursor (S7mt) (MRP-S7) (bMRP27a) (bMRP-27a).
1889	UPI00005199BA	3	6	14.3	342	37980	5.7	paraoxonase 2 isoform 2
1889	Q5FBX7	3	6	14.3	342	38022	5.7	Paraoxonase nirs variant 1
1889	UPI00004575B2	3	6	13.9	352	38946	5.5	Serum paraoxonase/arylesterase 2 (EC 3.1.1.2) (EC 3.1.8.1) (PON 2) (Serum aryldialkylphosphatase 2) (A-esterase 2) (Aromatic esterase 2).
1889	A4D1H7	3	6	13.8	354	39381	5.6	Paraoxonase 2
1889	Q15165-2	3	6	13.8	354	39397	5.6	Isoform 2 of Q15165
1889	Q15165	3	6	13.8	354	39398	5.5	Serum paraoxonase/arylesterase 2
1890	Q9UEH5	3	18	14.7	231	25430	7.4	24-kDa subunit of complex I
1890	P19404	3	18	13.7	249	27392	8.1	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial precursor
1890	Q6IPW4	3	18	13.7	249	27364	8.1	NADH dehydrogenase (Ubiquinone) flavoprotein 2, 24kDa
1890	Q6IB76	3	18	13.7	249	27349	8.1	NDUFV2 protein
1891	P23258	3	6	13.7	451	51170	6.1	Tubulin gamma-1 chain
1891	UPI0000456AAD	3	6	13.7	451	51006	5.7	Tubulin gamma-2 chain (Gamma-2 tubulin).
1891	Q9NRH3	3	6	13.7	451	51092	5.8	Tubulin gamma-2 chain
1892	P49841	3	4	13.6	420	46744	8.8	Glycogen synthase kinase-3 beta
1892	P49841-2	3	4	13.2	433	48034	8.8	Isoform 2 of P49841
1893	P48163	3	9	13.5	572	64150	6.1	NADP-dependent malic enzyme
1894	Q6FGR9	3	3	14.4	229	25695	7.6	ARHE protein
1894	Q6FGN7	3	3	14.4	229	25637	7.8	ARHE protein
1894	P61587	3	3	13.5	244	27368	8.5	Rho-related GTP-binding protein RhoE precursor
1894	UPI0000D61248	3	3	13.4	247	27782	8.6	Rho-related GTP-binding protein RhoE (Rho family GTPase 3) (Rnd3) (Rho8) (MemB protein).
1895	Q9NPD3	3	10	13.5	245	26383	6.5	Exosome complex exonuclease RRP41
1895	UPI0000D6251B	3	10	13.4	247	26610	6.7	Exosome complex exonuclease RRP41 (EC 3.1.13.-) (Ribosomal RNA- processing protein 41) (Exosome component 4) (p12A).
1896	Q9UPY8-2	3	5	14.3	266	30380	5.3	Isoform 2 of Q9UPY8
1896	Q9UPY8	3	5	13.5	281	31982	5.5	Microtubule-associated protein RP/EB family member 3
1897	Q567R9	3	5	18.7	150	16830	9.7	CIP29 protein

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1897	P82979	3	5	13.3	210	23671	6.4	Nuclear protein Hcc-1
1898	Q96HS1	3	6	13.3	255	28006	7.3	Phosphoglycerate mutase family member 5
1898	UPI00001400B6	3	6	13.3	255	28020	7.3	Bcl-XL-binding protein v68
1899	Q5RKV6	3	6	13.2	272	28235	6.3	Exosome component 6
1900	O00764	3	10	13.1	312	35102	6.1	Pyridoxal kinase
1901	Q13630	3	11	13.1	321	35893	6.6	GDP-L-fucose synthetase (EC 1.1.1.271) (Protein FX) (Red cell NADP(H)- binding protein)
1902	P28072	3	29	13	239	25358	4.9	Proteasome subunit beta type 6 precursor
1903	P32970	3	14	13	193	21118	8.5	Tumor necrosis factor ligand superfamily member 7
1904	Q5JW12	3	12	21.4	159	17853	9.9	Mitochondrial ribosomal protein L43
1904	Q5JW13	3	12	20.7	164	18311	9.7	Mitochondrial ribosomal protein L43
1904	Q5JW14	3	12	20.2	168	18657	8.5	Mitochondrial ribosomal protein L43
1904	Q5JW08	3	12	18.5	184	20539	10.3	Mitochondrial ribosomal protein L43
1904	UPI000013E565	3	12	17.3	196	21780	9.5	39S ribosomal protein L43, mitochondrial precursor (L43mt) (MRP-L43) (Mitochondrial ribosomal protein bMRP36a).
1904	Q8N983-5	3	12	17.3	197	21881	9.5	Isoform 5 of Q8N983
1904	Q5JW09	3	12	16.8	202	22580	9.3	Mitochondrial ribosomal protein L43
1904	Q8N983	3	12	15.8	215	23431	8.6	39S ribosomal protein L43, mitochondrial precursor
1904	UPI0000167F88	3	12	14.5	235	25862	9	mitochondrial ribosomal protein L43 isoform d
1904	Q5JW07	3	12	13	261	28676	8.3	Mitochondrial ribosomal protein L43
1905	Q6DRA6	3	32	15.2	164	18018	10.6	Histone H2B type 2-D
1905	Q6DN03	3	32	13	193	21472	10.7	Histone H2B type 2-C
1906	Q9HC03	3	7	13	324	36964	9.3	Dolichyl-phosphate beta-glucosyltransferase
1906	Q9Y673	3	7	13	324	36946	9.3	Dolichyl-phosphate beta-glucosyltransferase
1907	O95478	3	4	12.7	260	30065	10.3	TGF-beta-inducible nuclear protein 1
1908	Q05DR2	3	4	12.7	308	34755	9.1	RNASEH2B protein
1908	UPI000006CECF	3	4	12.5	312	35105	9.1	deleted in lymphocytic leukemia 8
1908	Q5TBB1	3	4	12.5	312	35139	9.1	Ribonuclease H2 subunit B
1908	UPI0000246C16	3	4	11.8	331	37360	9	Ribonuclease H2 subunit B (RNase H2 subunit B) (Ribonuclease HI subunit B) (Aicardi-Goutieres syndrome 2 protein) (AGS2) (Deleted in lymphocytic leukemia 8).
1908	Q8N451	3	4	11.8	331	37359	9.1	RNASEH2B protein
1909	Q8N959	3	11	15.5	323	35226	6.3	CDNA FLJ38330 fis, clone FCBBF3025280, highly similar to NDRG1 PROTEIN
1909	Q53EU7	3	11	12.7	394	42863	5.8	N-myc downstream regulated gene 1 variant

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1909	UPI0000D62506	3	11	12.7	394	42834	5.8	Protein NDRG1 (N-myc downstream-regulated gene 1 protein) (Differentiation-related gene 1 protein) (DRG-1) (Reducing agents and tunicamycin-responsive protein) (RTP) (Nickel-specific induction protein Cap43) (Rit42).
1909	Q92597	3	11	12.7	394	42835	5.8	Protein NDRG1
1909	Q597H1	3	11	12.7	394	42819	5.8	Transformation-related protein 14
1910	O43681	3	4	12.6	348	38793	4.9	Arsenical pump-driving ATPase
1910	UPI0000D61731	3	4	12.1	363	40226	5.1	Arsenical pump-driving ATPase (EC 3.6.3.16) (Arsenite-translocating ATPase) (Arsenical resistance ATPase) (Arsenite-transporting ATPase) (ARSA) (ASNA-I).
1911	O95721	3	11	12.4	258	28970	5.8	Synaptosomal-associated protein 29
1912	Q8NFV4-4	3	11	12.7	308	33863	9.2	Isoform 4 of Q8NFV4
1912	Q8NFV4	3	11	12.4	315	34690	9.5	Abhydrolase domain-containing protein 11
1913	Q96E11-3	3	8	14.7	218	24115	9.6	Isoform 3 of Q96E11
1913	Q96E11	3	8	12.2	262	29277	9.8	Ribosome recycling factor, mitochondrial precursor
1914	P11310	3	10	12.1	421	46588	8.4	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial precursor
1914	Q5T4U5	3	10	11.2	454	50271	7.8	Acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain
1914	Q5HYG7	3	10	11.2	454	50309	7.8	Hypothetical protein DKFZp686M24262
1915	P49593	3	8	12.1	454	49831	5.1	Ca(2+)/calmodulin-dependent protein kinase phosphatase
1915	Q6IPC0	3	8	12.1	453	49702	5.1	Protein phosphatase 1F
1916	Q8NBZ7	3	10	12.1	420	47577	8.9	UDP-glucuronic acid decarboxylase 1
1916	UPI0000D6120F	3	10	12	425	48179	8.9	UDP-glucuronic acid decarboxylase 1 (EC 4.1.1.35) (UDP-glucuronate decarboxylase 1) (UGD) (UXS-1).
1916	Q8NBZ7-2	3	10	12	425	48152	8.9	Isoform 2 of Q8NBZ7
1917	UPI0000456F5C	3	13	12.1	314	35595	5.2	Uncharacterized protein C20orf116 precursor.
1918	Q9Y277	3	32	12	283	30659	8.6	Voltage-dependent anion-selective channel protein 3
1918	Q9Y277-2	3	32	12	284	30790	8.6	Isoform 2 of Q9Y277
1919	Q9Y3Q3	3	5	12	217	24777	5.6	Transmembrane emp24 domain-containing protein 3 precursor
1920	A1JUI9	3	3	11.9	505	54843	7.9	WASL protein
1920	O00401	3	3	11.9	505	54827	7.9	Neural Wiskott-Aldrich syndrome protein
1921	P05026-2	3	13	12	301	34893	8.6	Isoform 2 of P05026
1921	P05026	3	13	11.9	303	35061	8.5	Sodium/potassium-transporting ATPase subunit beta-1
1921	Q6LEU2	3	13	11.9	303	35049	8.5	ATP1B1 protein

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1921	UPI0000D6203C	3	13	11.8	305	35246	8.5	Sodium/potassium-transporting ATPase subunit beta-1 (Sodium/potassium- dependent ATPase beta-1 subunit).
1922	Q96D15	3	9	11.9	328	37493	4.9	Reticulocalbin-3 precursor
1923	Q9NPL8	3	6	11.6	285	32178	8.5	Uncharacterized protein C3orf1
1924	Q9UNE7	3	4	11.6	303	34856	5.9	STIP1 homology and U box-containing protein 1
1925	Q8WXX5	3	5	11.5	260	29910	5.7	DnaJ homolog subfamily C member 9
1926	UPI000049E0CA	3	13	12.2	229	24770	7.9	Collagen triple helix repeat-containing protein 1 precursor (NMTC1 protein).
1926	Q96CG8	3	13	11.5	243	26224	8	Collagen triple helix repeat-containing protein 1 precursor
1927	Q96GK7	3	4	11.5	314	34596	8.2	Fumarylacetoacetate hydrolase domain-containing protein 2A
1927	Q9Y3B0	3	4	11.5	314	34582	8.2	CGI-105 protein
1928	O14656	3	8	11.4	332	37809	7	Torsin A precursor
1928	UPI00004577BB	3	8	11.4	332	37812	7.2	Torsin A precursor (Torsin family 1 member A) (Dystonia 1 protein).
1929	Q00059	3	5	11.4	246	29097	9.7	Transcription factor A, mitochondrial precursor
1929	Q6LES8	3	5	11.4	246	29083	9.7	TFAM protein
1930	Q53FU2	3	4	11.4	342	36751	5.2	Methylosome protein 50 variant
1930	Q9BQA1	3	4	11.4	342	36724	5.2	Methylosome protein 50
1931	Q5HYI8	3	10	11.4	236	26423	7.1	Rab-like protein 3
1931	Q8WUD3	3	10	11.4	236	26308	6.8	RAB, member of RAS oncogene family-like 3
1932	Q14151	3	6	11.3	953	107474	6.2	Scaffold attachment factor B2
1933	Q8NFQ8	3	13	11.3	470	51263	5	Torsin-1A-interacting protein 2
1934	O96011	3	8	11.2	259	28431	9.8	Peroxisomal membrane protein 11B
1935	Q8N5M1	3	3	11.1	289	32772	7.1	ATP synthase mitochondrial F1 complex assembly factor 2, mitochondrial precursor
1935	UPI0000456A37	3	3	11	290	32882	7.5	ATP synthase mitochondrial F1 complex assembly factor 2, mitochondrial precursor (ATP12 homolog).
1936	Q99848	3	6	11.1	306	34852	10.1	Probable rRNA-processing protein EBP2
1936	UPI0000129B3E	3	6	11.1	306	34820	10.1	EBNA1 binding protein 2
1937	Q9NX58	3	9	11.1	379	43615	9.5	Cell growth-regulating nucleolar protein
1937	UPI0000037C40	3	9	11.1	379	43634	9.6	hypothetical protein FLJ20425
1938	UPI0000F2442B	3	8	13.8	195	22469	9.4	EUKARYOTIC TRANSLATION INITIATION FACTOR 4E T
1938	Q59FE1	3	8	11.1	243	27829	7.5	Eukaryotic translation initiation factor 4E member 2 variant
1938	O60573	3	8	11	245	28362	8.9	Eukaryotic translation initiation factor 4E type 2

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
1938	UPI0000D612CB	3	8	10.6	255	29289	8	Eukaryotic translation initiation factor 4E type 2 (eIF4E type 2) (eIF-4E type 2) (mRNA cap-binding protein type 3) (Eukaryotic translation initiation factor 4E-like 3) (Eukaryotic translation initiation factor 4E homologous protein) (mRNA cap-binding pro
1939	P13995	3	12	10.9	350	37895	8.7	Bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase, mitochondrial precursor [Includes: NAD-dependent methylenetetrahydrofolate dehydrogenase (EC 1.5.1.15); Methenyltetrahydrofolate cyclohydrolase (EC 3.5.4.9)]
1940	Q13572	3	4	10.9	414	45621	6.2	Inositol-tetrakisphosphate 1-kinase (EC 2.7.1.134) (Inositol-triphosphate 5/6-kinase) (EC 2.7.1.159) (Inositol 1,3,4-trisphosphate 5/6-kinase) (Ins(1,3,4)P(3) 5/6-kinase)
1941	Q99536	3	4	10.9	393	41920	6.3	Synaptic vesicle membrane protein VAT-1 homolog
1942	Q9H1E5	3	10	10.9	349	38952	4.4	Thioredoxin domain-containing protein 13 precursor
1943	Q14192	3	11	10.8	279	32193	7.5	Four and a half LIM domains protein 2
1943	Q2TSB7	3	11	10.8	279	32246	7.7	Aging-associated gene 11
1943	UPI000023C3A9	3	11	8.1	372	42073	8	Four and a half LIM domains protein 2 (FHL-2) (Skeletal muscle LIM- protein 3) (SLIM 3) (LIM domain protein DRAL).
1943	Q2XQU9	3	11	7.7	389	44177	8.1	FHL2 isoform 5
1944	Q96EP5	3	6	10.8	407	43383	8.6	DAZ-associated protein 1
1945	UPI0000D61DD0	3	5	11.1	1005	117261	8	Probable global transcription activator SNF2L1 (EC 3.6.1.-) (Nucleosome remodeling factor subunit SNF2L) (ATP-dependent helicase SMARCA1) (SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 1).
1945	Q5JZ57	3	5	11.1	1005	117265	7.8	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1
1945	P28370-2	3	5	10.7	1042	121142	8.2	Isoform 2 of P28370
1945	P28370	3	5	10.6	1054	122605	8.1	Probable global transcription activator SNF2L1
1946	P82914	3	4	10.5	257	29842	10.5	28S ribosomal protein S15, mitochondrial precursor
1947	Q8TC12	3	7	10.4	318	35386	8.8	Retinol dehydrogenase 11

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1947	UPI0000D6241F	3	7	10.4	318	35415	8.9	Retinol dehydrogenase 11 (EC 1.1.1.-) (Retinal reductase 1) (RalR1) (Prostate short-chain dehydrogenase/reductase 1) (Androgen-regulated short-chain dehydrogenase/reductase 1) (HCV core-binding protein HCBP12).
1947	UPI0000070F53	3	7	10.4	318	35414	8.8	androgen-regulated short-chain dehydrogenase/reductase 1
1948	O43488	3	12	10.3	359	39589	7.2	Aflatoxin B1 aldehyde reductase member 2
1949	O95400	3	3	10.3	341	37646	4.6	CD2 antigen cytoplasmic tail-binding protein 2
1950	P35250-2	3	9	11.2	320	35244	5.5	Isoform 2 of P35250
1950	P35250	3	9	10.2	354	39157	6.4	Replication factor C subunit 2
1951	Q8IZ81	3	10	10.2	293	34961	8.1	ELMO domain-containing protein 2
1952	P20645	3	12	10.1	277	30993	5.8	Cation-dependent mannose-6-phosphate receptor precursor
1952	Q6I9U3	3	12	10.1	277	30975	5.8	M6PR protein
1952	Q53GY9	3	12	10.1	277	31019	5.8	Cation-dependent mannose-6-phosphate receptor variant
1953	Q10588	3	3	10.1	318	35724	7.8	ADP-ribosyl cyclase 2 precursor
1953	UPI0000126AFB	3	3	10.1	318	35738	7.8	bone marrow stromal cell antigen 1 precursor
1953	UPI000066D9E4	3	3	9.6	333	37482	8	ADP-ribosyl cyclase 2 precursor (EC 3.2.2.5) (Cyclic ADP-ribose hydrolase 2) (cADPr hydrolase 2) (Bone marrow stromal antigen 1) (BST- 1) (CD157 antigen).
1954	UPI000045619C	3	5	11.9	370	38212	4.6	Syndecan-3 (SYND3).
1954	O75056-2	3	5	11.9	370	38246	4.6	Isoform 3 of O75056
1954	O75056-1	3	5	11.5	384	39636	4.6	Isoform 2 of O75056
1954	O75056	3	5	10	442	45497	4.7	Syndecan-3
1954	UPI000006FA8A	3	5	10	442	45496	4.7	syndecan 3
1954	UPI0000DD798E	3	5	9.4	467	49600	4.9	PREDICTED: similar to syndecan 3 isoform 2
1955	Q969X5-2	3	11	14.6	198	22160	9.1	Isoform 2 of Q969X5
1955	Q969X5	3	11	10	290	32592	7.1	Endoplasmic reticulum-Golgi intermediate compartment protein 1
1956	Q92905	3	7	9.9	334	37579	6.5	COP9 signalosome complex subunit 5
1957	Q14232	3	5	9.8	305	33712	7.3	Translation initiation factor eIF-2B subunit alpha
1957	UPI00004566B0	3	5	9.8	305	33648	6.9	Translation initiation factor eIF-2B subunit alpha (eIF-2B GDP-GTP exchange factor subunit alpha).
1958	Q5VT94	3	18	9.8	325	35282	10.1	Growth hormone inducible transmembrane protein
1958	UPI0000D60F83	3	18	9.8	325	35169	10.1	Growth hormone-inducible transmembrane protein (Dermal papilla-derived protein 2) (Transmembrane BAX inhibitor motif-containing protein 5).
1958	Q9H3K2	3	18	9.3	345	37205	9.9	Growth hormone-inducible transmembrane protein

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1958	Q6FIA7	3	18	9.3	345	37279	10	GHITM protein
1959	Q6PIU2	3	19	9.8	408	45808	7.2	Arylacetamide deacetylase-like 1
1959	UPI0000050344	3	19	9.1	440	49063	7.9	arylacetamide deacetylase-like 1
1960	Q59EQ4	3	3	17.6	262	29663	6.8	Serine palmitoyltransferase subunit 1 isoform a variant
1960	O15269	3	3	9.7	473	52744	6	Serine palmitoyltransferase 1
1960	Q6NUL7	3	3	9	513	57396	7.5	SPTLC1 protein
1961	Q14914	3	6	9.7	329	35870	8.3	NADP-dependent leukotriene B4 12-hydroxydehydrogenase
1961	UPI0000074210	3	6	9.7	329	35886	8.3	NADP-dependent leukotriene B4 12-hydroxydehydrogenase
1962	Q8WVY7	3	3	9.7	318	36805	6.5	Ubiquitin-like domain-containing CTD phosphatase 1
1962	UPI000007368C	3	3	9.7	318	36733	6.7	ubiquitin-like domain containing CTD phosphatase 1
1963	Q96KP4	3	4	9.7	475	52878	6	Cytosolic nonspecific dipeptidase
1963	UPI0000D60EF3	3	4	9.7	475	52897	6	Cytosolic nonspecific dipeptidase (Glutamate carboxypeptidase-like protein 1) (CNDP dipeptidase 2).
1963	UPI0000049A46	3	4	9.7	475	52779	5.9	CNDP dipeptidase 2 (metallopeptidase M20 family)
1964	Q5T7G5	3	4	9.6	324	35189	6.7	Phosphoserine aminotransferase 1
1964	Q9Y617	3	4	8.4	370	40423	7.7	Phosphoserine aminotransferase
1965	P30566	3	6	9.5	484	54889	7.1	Adenylosuccinate lyase
1965	Q71UA4	3	6	9.5	484	54871	7.1	Adenylosuccinate lyase
1966	Q99816	3	6	9.5	390	43944	6.4	Tumor susceptibility gene 101 protein
1967	O00151	3	11	9.4	329	36072	7	PDZ and LIM domain protein 1
1968	O75787	3	6	9.4	350	39008	6.1	Renin receptor precursor (Renin/prorenin receptor) (ATPase H(+)- transporting lysosomal accessory protein 2) (ATPase H(+)-transporting lysosomal-interacting protein 2)
1969	O96008-2	3	10	10.3	329	34441	7.2	Isoform 2 of O96008
1969	O96008	3	10	9.4	361	37893	7.3	Probable mitochondrial import receptor subunit TOM40 homolog
1970	P31321	3	7	9.4	381	43158	5.8	cAMP-dependent protein kinase type I-beta regulatory subunit
1970	UPI0000DD7E3F	3	7	9.4	381	43011	5.7	PREDICTED: similar to protein kinase, cAMP-dependent, regulatory, type I, beta
1970	Q8N422	3	7	9.4	381	43073	5.7	Protein kinase, cAMP-dependent, regulatory, type I, beta
1971	Q8N367	3	7	17.4	213	23600	4.8	HS1BP3 protein
1971	UPI000013CA23	3	7	12.3	302	32835	5.4	HCLS1 binding protein 3
1971	Q9H7U7	3	7	12.3	302	32888	6.1	CDNA FLJ14249 fis, clone OVARC1001200, weakly similar to Mus musculus HS1 binding protein 3
1971	Q53T59	3	7	9.4	392	42780	5	HCLS1-binding protein 3
1971	Q86VC2	3	7	9.4	392	42842	5	HCLS1 binding protein 3
1972	Q9NP81	3	3	9.3	518	58283	8.1	Seryl-tRNA synthetase, mitochondrial precursor

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1972	UPI0000456CB2	3	3	9.3	518	58182	8.3	Seryl-tRNA synthetase, mitochondrial precursor (EC 6.1.1.11) (Serine-- tRNA ligase) (SerRSmt).
1973	P53985	3	4	9	500	53958	8.7	Monocarboxylate transporter 1
1974	Q6NVY7	3	12	8.9	359	38724	6.4	Inositol monophosphatase domain-containing protein 1
1974	Q9NX62	3	12	8.9	359	38681	6.9	CDNA FLJ20421 fis, clone KAT02467
1975	UPI0000D6159B	3	9	9.5	515	56404	5.4	Rap1 GTPase-GDP dissociation stimulator 1 (SMG P21 stimulatory GDP/GTP exchange protein) (SMG GDS protein) (Exchange factor smgGDS).
1975	Q6U7G8	3	9	9.5	516	56488	5.4	GTP-GDP dissociation stimulator 1 isoform A
1975	Q499L7	3	9	8.8	559	61108	5.4	RAP1GDS1 protein
1975	Q4KMV2	3	9	8.8	558	61037	5.4	RAP1GDS1 protein
1975	UPI000004A01F	3	9	8.1	608	66388	5.3	Rap1 GTPase-GDP dissociation stimulator 1 (SMG P21 stimulatory GDP/GTP exchange protein) (SMG GDS protein) (Exchange factor smgGDS).
1975	Q9BUX6	3	9	8.1	607	66331	5.3	RAP1, GTP-GDP dissociation stimulator 1
1975	Q4QQI8	3	9	8.1	608	66316	5.4	RAP1, GTP-GDP dissociation stimulator 1
1976	O94766	3	6	8.7	335	37122	8.3	Galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase 3
1976	Q5U676	3	6	8.5	341	37828	8.6	B3GAT3 protein
1977	P30533	3	13	8.7	357	41466	8.8	Alpha-2-macroglobulin receptor-associated protein precursor
1978	UPI0000470A40	3	4	11.7	274	30220	5.1	NSFL1 cofactor p47 (p97 cofactor p47).
1978	Q5JXA4	3	4	9.4	339	37325	5.1	NSFL1 (P97) cofactor
1978	Q53FE8	3	4	8.6	370	40572	5.1	P47 protein isoform a variant
1978	Q9UNZ2	3	4	8.6	370	40573	5.1	NSFL1 cofactor p47
1978	Q5JXA5	3	4	8.6	372	40816	5.1	NSFL1 (P97) cofactor
1978	Q53FF5	3	4	8.6	370	40500	5.2	P47 protein isoform a variant
1979	Q8WWH5	3	3	8.6	349	37253	8.3	Probable tRNA pseudouridine synthase 1
1980	Q9Y5A9-2	3	4	9.5	529	56877	8.9	Isoform 2 of Q9Y5A9
1980	UPI0000456197	3	4	8.8	569	61192	9.1	YTH domain family protein 2 (High-glucose-regulated protein 8) (CLL-associated antigen KW-14) (Renal carcinoma antigen NY-REN-2).
1980	Q9Y5A9	3	4	8.6	579	62334	8.8	YTH domain family protein 2
1981	P14324	3	7	8.5	353	40532	5.2	Farnesyl pyrophosphate synthetase (FPP synthetase) (FPS) (Farnesyl diphosphate synthetase) [Includes: Dimethylallyltranstransferase (EC 2.5.1.1); Geranyltranstransferase (EC 2.5.1.10)]
1982	Q7Z3B4-2	3	4	14.8	291	33180	6.4	Isoform 2 of Q7Z3B4
1982	Q53H29	3	4	8.5	508	55564	7	Nucleoporin 54kDa variant
1982	Q7Z3B4	3	4	8.5	507	55436	7	Nucleoporin p54
1983	Q7L5N2	3	15	8.5	471	52634	9	LENG4 protein

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1983	Q9BPV2	3	15	8.5	472	52765	9	Leukocyte receptor cluster (LRC) member 4
1983	Q96N66	3	15	8.5	472	52775	9	Leukocyte receptor cluster member 4
1984	Q96CS3	3	4	8.3	445	52624	5.6	UBX domain-containing protein 8
1985	Q9NR56-3	3	8	9.3	302	33050	8.8	Isoform EXP35 of Q9NR56
1985	Q96RE3	3	8	8.9	314	34211	8.8	36 kDa muscleblind protein EXP36
1985	Q86UV8	3	8	8.2	342	37074	8.6	Muscleblind-like protein EXP41s
1985	UPI0000246E53	3	8	8.2	340	36992	8.6	muscleblind-like 1 isoform f
1985	Q86UV9	3	8	8.2	341	37063	8.6	Muscleblind-like protein EXP40s
1985	Q9NR56-2	3	8	7.6	370	39831	8.8	Isoform EXP40 of Q9NR56
1985	Q96P92	3	8	7.3	382	40992	8.7	Muscleblind 41kD isoform
1985	Q9NR56	3	8	7.2	388	41817	8.9	Muscleblind-like protein 1
1986	Q9BTV4	3	18	8.2	400	44876	8.1	Transmembrane protein 43
1987	O00425	3	9	8.1	579	63720	8.9	Insulin-like growth factor 2 mRNA-binding protein 3
1987	UPI0000D61C0E	3	9	8.1	583	64160	9	insulin-like growth factor 2 mRNA binding protein 3
1987	UPI0000117172	3	9	8.1	579	63705	8.9	insulin-like growth factor 2 mRNA binding protein 3
1988	Q53XA7	3	3	9.7	349	38614	7.2	Hypothetical protein DKFZp686F13224
1988	P16930	3	3	8.1	419	46374	6.9	Fumarylacetoacetase
1989	Q05BU6	3	8	15.9	246	24847	6.3	Hypothetical protein
1989	Q6PJY9	3	8	15.8	247	24976	6.8	SFRS11 protein
1989	Q6PKC9	3	8	12.1	321	34277	11.5	SFRS11 protein
1989	Q5T760	3	8	10	389	42316	11.7	Splicing factor, arginine/serine-rich 11
1989	Q6PJB9	3	8	9.9	394	42957	11.7	SFRS11 protein
1989	Q05519	3	8	8.1	484	53542	10.5	Splicing factor arginine/serine-rich 11
1989	Q8IWE6	3	8	8.1	483	53414	10.5	Splicing factor, arginine/serine-rich 11
1990	Q68E00	3	11	10.5	315	32580	6.8	Hypothetical protein DKFZp686G2045
1990	UPI0000D610D0	3	11	8.5	387	40237	5.1	Adhesion-regulating molecule 1 precursor (110 kDa cell membrane glycoprotein) (Gp110).
1990	Q16186	3	11	8.1	407	42153	5.1	Adhesion-regulating molecule 1 precursor
1991	Q9BQ04	3	7	8.1	359	40150	6.7	RNA-binding protein 4B
1991	Q9BWF3	3	7	8	364	40314	7.1	RNA-binding protein 4
1991	UPI00001413BF	3	7	7.9	365	40841	8.2	RNA binding motif protein 4 (RBM4), mRNA
1992	P48651	3	19	8	473	55528	8.4	Phosphatidylserine synthase 1
1993	Q13454-2	3	7	8.1	347	39558	10.1	Isoform 2 of Q13454
1993	Q13454	3	7	8	348	39676	9.9	Tumor suppressor candidate 3
1994	Q6UWP7	3	10	8	414	48920	8.6	Lysocardiolipin acyltransferase
1995	Q9UHD9	3	7	7.9	624	65696	5.2	Ubiquilin-2
1996	Q9Y302-2	3	6	10.7	335	38484	9.4	Isoform 2 of Q9Y302
1996	UPI0000D4C36B	3	6	9.5	379	43772	9.4	PREDICTED: similar to G protein-coupled receptor 89
1996	Q9Y302	3	6	7.9	455	52917	9.3	Protein GPR89A
1996	UPI0000D61FC4	3	6	7.9	458	53279	9.3	Protein GPR89A (Putative MAPK-activating protein PM01) (Putative NF- kappa-B-activating protein 90).

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1997	UPI000012759A	3	6	7.9	469	51962	6.9	sorting and assembly machinery component 50 homolog
1998	A0S2X6	3	8	7.8	603	67055	9	NADH dehydrogenase subunit 5
1998	Q4F2Y8	3	8	7.8	603	66963	9	NADH dehydrogenase subunit 5
1998	Q4F2K8	3	8	7.8	603	67012	9	NADH dehydrogenase subunit 5
1998	Q4F2F6	3	8	7.8	603	67027	9	NADH dehydrogenase subunit 5
1998	Q4F200	3	8	7.8	603	67043	9	NADH dehydrogenase subunit 5
1998	Q4F1S2	3	8	7.8	603	67069	9	NADH dehydrogenase subunit 5
1998	Q4F0F4	3	8	7.8	603	67011	9	NADH dehydrogenase subunit 5
1998	Q4F050	3	8	7.8	603	67039	9	NADH dehydrogenase subunit 5
1998	Q4EZT3	3	8	7.8	603	67013	9	NADH dehydrogenase subunit 5
1998	Q4EZS0	3	8	7.8	603	67027	9	NADH dehydrogenase subunit 5
1998	Q4EZP4	3	8	7.8	603	67041	9	NADH dehydrogenase subunit 5
1998	Q4EZ36	3	8	7.8	603	67023	9	NADH dehydrogenase subunit 5
1998	Q4EYP3	3	8	7.8	603	67000	9	NADH dehydrogenase subunit 5
1998	Q4EY48	3	8	7.8	603	66981	9	NADH dehydrogenase subunit 5
1998	Q4EXY9	3	8	7.8	603	66971	9	NADH dehydrogenase subunit 5
1998	Q4EXW4	3	8	7.8	603	67018	9	NADH dehydrogenase subunit 5
1998	Q4EXU5	3	8	7.8	603	67004	9	NADH dehydrogenase subunit 5
1998	Q4EXP2	3	8	7.8	603	67040	9	NADH dehydrogenase subunit 5
1998	Q4EXM9	3	8	7.8	603	67043	9.1	NADH dehydrogenase subunit 5
1998	Q4EWD7	3	8	7.8	603	67023	9	NADH dehydrogenase subunit 5
1998	Q3S9H4	3	8	7.8	603	67057	9	NADH dehydrogenase subunit 5
1998	Q306C1	3	8	7.8	603	67013	9	NADH dehydrogenase subunit 5
1998	Q305W9	3	8	7.8	603	67000	9	NADH dehydrogenase subunit 5
1998	Q2LHU9	3	8	7.8	603	66997	9	NADH dehydrogenase subunit 5
1998	Q2LHB7	3	8	7.8	603	67017	9	NADH dehydrogenase subunit 5
1998	Q2LH26	3	8	7.8	603	67057	9	NADH dehydrogenase subunit 5
1998	Q2L743	3	8	7.8	603	67057	9	NADH dehydrogenase subunit 5
1998	Q2HKQ7	3	8	7.8	603	67025	9	NADH dehydrogenase subunit 5
1998	Q2HKK5	3	8	7.8	603	67012	9	NADH dehydrogenase subunit 5
1998	Q2HJQ6	3	8	7.8	603	66967	9	NADH dehydrogenase subunit 5

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1998	Q27H51	3	8	7.8	603	67057	9	NADH dehydrogenase subunit 5
1998	Q27H25	3	8	7.8	603	67043	9	NADH dehydrogenase subunit 5
1998	Q1ZY31	3	8	7.8	603	67072	9	NADH dehydrogenase subunit 5
1998	Q1W0U7	3	8	7.8	603	67042	9	NADH dehydrogenase subunit 5
1998	Q1ADM1	3	8	7.8	603	66998	9	NADH dehydrogenase subunit 5
1998	Q1ADK8	3	8	7.8	603	67040	9	NADH dehydrogenase subunit 5
1998	Q15II4	3	8	7.8	603	67013	9	NADH dehydrogenase subunit 5
1998	Q15ID2	3	8	7.8	603	67051	9	NADH dehydrogenase subunit 5
1998	Q15HM4	3	8	7.8	603	66986	9	NADH dehydrogenase subunit 5
1998	Q15HL1	3	8	7.8	603	67000	9	NADH dehydrogenase subunit 5
1998	Q15HH2	3	8	7.8	603	67042	9	NADH dehydrogenase subunit 5
1998	Q15HE6	3	8	7.8	603	67027	9	NADH dehydrogenase subunit 5
1998	Q15H42	3	8	7.8	603	66983	9	NADH dehydrogenase subunit 5
1998	Q15GZ0	3	8	7.8	603	67013	9	NADH dehydrogenase subunit 5
1998	Q15GW4	3	8	7.8	603	67013	9	NADH dehydrogenase subunit 5
1998	Q0ZK24	3	8	7.8	603	66997	9	NADH dehydrogenase subunit 5
1998	Q0ZFK3	3	8	7.8	603	67039	9	NADH dehydrogenase subunit 5
1998	Q0ZFC5	3	8	7.8	603	66999	9	NADH dehydrogenase subunit 5
1998	Q0Z7P8	3	8	7.8	603	66967	9	NADH dehydrogenase subunit 5
1998	Q0Z7K9	3	8	7.8	603	66971	9	NADH dehydrogenase subunit 5
1998	Q06V50	3	8	7.8	603	67000	9	NADH dehydrogenase subunit 5
1998	Q06UH9	3	8	7.8	603	67031	9	NADH dehydrogenase subunit 5
1998	Q06UC7	3	8	7.8	603	67000	9	NADH dehydrogenase subunit 5
1998	P03915	3	8	7.8	603	67027	9	NADH-ubiquinone oxidoreductase chain 5
1998	A3R0P4	3	8	7.8	603	67027	9	NADH dehydrogenase subunit 5
1998	A3R0N1	3	8	7.8	603	67069	9	NADH dehydrogenase subunit 5
1998	A3R0L8	3	8	7.8	603	67026	9.1	NADH dehydrogenase subunit 5
1998	A1Z550	3	8	7.8	603	67007	9	NADH dehydrogenase subunit 5
1998	A1Z4K5	3	8	7.8	603	67027	9	NADH dehydrogenase subunit 5
1998	A1Z4H9	3	8	7.8	603	67083	9	NADH dehydrogenase subunit 5
1998	A1Z4G6	3	8	7.8	603	66997	9	NADH dehydrogenase subunit 5
1998	A1E1L3	3	8	7.8	603	67005	9	NADH dehydrogenase subunit 5

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1998	A1DVU9	3	8	7.8	603	67051	9	NADH dehydrogenase subunit 5
1998	A1DVT6	3	8	7.8	603	67054	9	NADH dehydrogenase subunit 5
1998	A1DVN4	3	8	7.8	603	67054	9	NADH dehydrogenase subunit 5
1998	A1DV00	3	8	7.8	603	67011	9	NADH dehydrogenase subunit 5
1998	A1DTY1	3	8	7.8	603	67044	9	NADH dehydrogenase subunit 5
1998	A1DTP0	3	8	7.8	603	67028	9	NADH dehydrogenase subunit 5
1998	A1DTE9	3	8	7.8	603	67000	9	NADH dehydrogenase subunit 5
1998	A1DTD6	3	8	7.8	603	67000	9	NADH dehydrogenase subunit 5
1998	A1DT71	3	8	7.8	603	67014	9	NADH dehydrogenase subunit 5
1998	A1DSY0	3	8	7.8	603	67070	9	NADH dehydrogenase subunit 5
1998	A1DSV4	3	8	7.8	603	67070	9	NADH dehydrogenase subunit 5
1998	A1DSU1	3	8	7.8	603	67026	9	NADH dehydrogenase subunit 5
1998	A1DSK0	3	8	7.8	603	67010	9	NADH dehydrogenase subunit 5
1998	A1DSD5	3	8	7.8	603	67010	9	NADH dehydrogenase subunit 5
1998	A0SBQ0	3	8	7.8	603	66953	8.9	NADH dehydrogenase subunit 5
1998	A0SBN6	3	8	7.8	603	66983	9	NADH dehydrogenase subunit 5
1998	A0SBJ7	3	8	7.8	603	67043	9	NADH dehydrogenase subunit 5
1998	A0SBH1	3	8	7.8	603	67017	9	NADH dehydrogenase subunit 5
1998	A0SB29	3	8	7.8	603	67087	9	NADH dehydrogenase subunit 5
1998	A0S952	3	8	7.8	603	67033	9	NADH dehydrogenase subunit 5
1998	A0S939	3	8	7.8	603	67033	9	NADH dehydrogenase subunit 5
1998	A0S8Q9	3	8	7.8	603	67081	9	NADH dehydrogenase subunit 5
1998	A0S8I1	3	8	7.8	603	67033	9	NADH dehydrogenase subunit 5
1998	A0S4F9	3	8	7.8	603	67015	9	NADH dehydrogenase subunit 5
1998	A0S481	3	8	7.8	603	66979	9	NADH dehydrogenase subunit 5
1998	A0S302	3	8	7.8	603	67041	9	NADH dehydrogenase subunit 5
1999	O43818	3	10	7.8	475	51841	7.9	U3 small nucleolar RNA-interacting protein 2
2000	P33240-2	3	7	8	560	59251	6.8	Isoform 2 of P33240
2000	P33240	3	7	7.8	577	60959	6.8	Cleavage stimulation factor 64 kDa subunit
2000	UPI0000D61DA0	3	7	7.4	611	64388	7.5	Cleavage stimulation factor 64 kDa subunit (CSTF 64 kDa subunit) (CF-1 64 kDa subunit) (CstF-64).
2001	Q53GS9	3	5	7.8	565	65381	8.9	U4/U6.U5 tri-snRNP-associated protein 2
2002	P35659	3	5	7.7	375	42674	8.6	Protein DEK

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
2003	Q6P1S1	3	3	7.7	414	47611	6.2	Mitochondrial ribosomal protein S27
2004	Q13895	3	4	7.6	437	49601	8.1	Bystin
2005	UPI0000D612BA	3	7	8.4	367	41317	6.9	WD repeat and FYVE domain-containing protein 1 (WD40- and FYVE domain- containing protein 1) (Phosphoinositide-binding protein 1) (FENS-1) (Zinc finger FYVE domain-containing protein 17).
2005	Q8IWB7	3	7	7.6	410	46324	7.3	WD repeat and FYVE domain-containing protein 1
2006	Q9Y5J1	3	5	7.6	556	62004	8.8	U3 small nucleolar RNA-associated protein 18 homolog
2007	Q59F45	3	10	8.3	386	43659	6.8	MAD, mothers against decapentaplegic homolog 3 variant
2007	P84022	3	10	7.5	425	48081	7.2	Mothers against decapentaplegic homolog 3
2008	Q9Y5X2	3	4	7.5	465	52569	7.4	Sorting nexin-8
2009	Q2TU87	3	4	10.8	287	32821	6	Growth-inhibiting protein 25
2009	P01011	3	4	7.3	423	47651	5.5	Alpha-1-antichymotrypsin precursor (ACT) [Contains: Alpha-1- antichymotrypsin His-Pro-less]
2010	Q32MB2	3	12	7.3	381	42010	8.2	KRT73 protein
2011	Q6IP98	3	14	7.2	349	40317	4.9	KRT17 protein
2012	Q14738-3	3	7	8.7	496	58453	6.8	Isoform Delta
2012	Q59EF0	3	7	8.5	503	59336	7.4	Delta isoform of regulatory subunit B56, protein phosphatase 2A isoform 1 variant
2012	Q14738-2	3	7	7.5	570	66181	7.6	Isoform Delta
2012	Q14738	3	7	7.1	602	69992	8.1	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform
2013	O43172	3	5	6.9	522	58449	7.4	U4/U6 small nuclear ribonucleoprotein Prp4
2013	Q6IAP9	3	5	6.9	521	58307	7.4	PRPF4 protein
2013	Q5T1M7	3	5	6.9	521	58321	7.4	PRP4 pre-mRNA processing factor 4 homolog
2013	Q59EL4	3	5	6.7	537	60022	7.6	PRPF4 protein variant
2014	Q9UPE4	3	3	7.5	415	47366	7.4	Putative mitochondrial inner membrane protein import receptor
2014	O43615	3	3	6.9	452	51356	8.3	Import inner membrane translocase subunit TIM44, mitochondrial precursor
2014	Q53G69	3	3	6.9	452	51324	8.3	Translocase of inner mitochondrial membrane 44 homolog
2015	Q86VP5	3	6	6.9	507	58579	7.5	SEPT10 protein
2015	Q9P0V9	3	6	6.8	517	59982	7.1	Septin-10
2015	UPI0000456E33	3	6	6.7	519	60191	6.9	Septin-10.
2015	UPI0000D61215	3	6	6.4	547	63282	6.8	Septin-10.
2016	Q9BV38	3	6	6.9	432	47405	6.7	WD repeat protein 18
2017	Q59EH7	3	9	6.8	483	55418	7.5	DnaJ (Hsp40) homolog, subfamily C, member 7 variant
2017	Q99615	3	9	6.7	494	56441	7	DnaJ homolog subfamily C member 7
2018	UPI000045753E	3	11	8.5	520	57444	5.7	KIAA0241 (KIAA0241), mRNA
2018	Q8NBF6-2	3	11	7.4	591	65313	6	Isoform 2 of Q8NBF6
2018	Q8NBF6	3	11	6.8	648	71947	6.2	Protein KIAA0241

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
2019	Q13131	3	3	6.7	550	62808	7.6	5'-AMP-activated protein kinase catalytic subunit alpha-1
2019	UPI000020C9F6	3	3	6.6	559	64009	8.1	protein kinase, AMP-activated, alpha 1 catalytic subunit isoform 1
2019	UPI00002263A3	3	3	6.5	565	64322	7.7	5'-AMP-activated protein kinase catalytic subunit alpha-1 (EC 2.7.11.1) (AMPK alpha-1 chain).
2019	UPI00003529FB	3	3	6.4	574	65523	8.2	protein kinase, AMP-activated, alpha 1 catalytic subunit isoform 2
2019	Q86VS1	3	3	6.4	574	65505	8.2	Protein kinase, AMP-activated, alpha 1 catalytic subunit
2020	Q59GU6	3	7	8.1	432	50099	7	Sorting nexin 1 isoform a variant
2020	Q13596-2	3	7	7.7	457	51813	5.6	Isoform 1A of Q13596
2020	UPI0000D61352	3	7	7.6	460	52225	5.9	Sorting nexin-1.
2020	UPI000045686A	3	7	7.4	473	53189	5.1	Sorting nexin-1.
2020	UPI000013FEB0	3	7	7.4	474	53304	5	sorting nexin 1 isoform c
2020	Q13596	3	7	6.7	522	59070	5.1	Sorting nexin-1
2020	UPI0000456869	3	7	6.7	521	58955	5.2	Sorting nexin-1.
2020	Q53HL9	3	7	6.7	522	59022	5.2	Sorting nexin 1 isoform a variant
2020	Q53GY8	3	7	6.7	522	59012	5.2	Sorting nexin 1 isoform a variant
2021	Q14258	3	15	6.7	630	70990	8.1	Tripartite motif-containing protein 25
2021	UPI00001AE6B8	3	15	6.7	630	70974	8.1	tripartite motif-containing 25
2021	Q59GW5	3	15	6.5	644	72250	8.1	Tripartite motif-containing 25 variant
2022	Q7Z434	3	9	6.7	540	56528	5.5	Mitochondrial antiviral-signaling protein
2023	P07196	3	3	6.6	543	61517	4.6	Neurofilament light polypeptide
2023	UPI0000246DBD	3	3	6.6	542	61430	4.6	Neurofilament triplet L protein (68 kDa neurofilament protein) (Neurofilament light polypeptide) (NF-L).
2024	Q16566	3	3	6.6	473	51926	5.8	Calcium/calmodulin-dependent protein kinase type IV
2025	Q6P1A2	3	5	6.6	487	56035	8.7	Membrane-bound O-acyltransferase domain-containing protein 5
2026	Q8NHP8	3	9	6.6	589	65472	7	Hypothetical protein LOC196463
2026	UPI000013DC40	3	9	6.6	589	65472	6.8	UPI000013DC40 UniRef100 entry
2027	Q8NG18	3	3	6.5	554	63522	5.1	Chronic myelogenous leukemia tumor antigen 66 short form
2027	UPI000021048A	3	3	6.2	583	66756	5.1	NudC domain containing 1
2027	Q9BVR5	3	3	6.2	583	66790	5.1	NudC domain containing 1
2027	Q96SI4	3	3	6.2	583	66729	5.1	CDNA FLJ14991 fis, clone Y79AA1001781
2027	Q96RS6	3	3	6.2	583	66776	5.1	NudC domain-containing protein 1
2028	Q08AM6	3	6	6.3	782	87973	6.1	Vac14 homolog
2028	UPI0000DD83A9	3	6	4	1240	135879	8.6	PREDICTED: similar to Vac14 homolog
2029	P10515	3	6	6.2	614	65781	6.1	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial precursor

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2029	Q86YI5	3	6	5.9	647	68997	7.8	Dihydrolipoamide S-acetyltransferase
2029	Q53EP3	3	6	5.9	647	68996	8	Dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex) variant
2030	P43007	3	11	6.2	532	55723	6.3	Neutral amino acid transporter A
2030	Q53F03	3	11	6.2	532	55723	6.3	Solute carrier family 1, member 4 variant
2031	Q05BM8	3	9	6.2	499	57337	7.8	GALNT1 protein
2031	Q10472	3	9	5.5	559	64219	7.7	Polypeptide N-acetylgalactosaminyltransferase 1 (EC 2.4.1.41) (Protein-UDP acetylgalactosaminyltransferase 1) (UDP- GalNAc:polypeptide N-acetylgalactosaminyltransferase 1) (Polypeptide GalNAc transferase 1) (GalNAc-T1) (pp-GaNTase 1) [Contains: Polypeptide N-acetylgalactosaminyltransferase 1 soluble form]
2032	Q5T2B5	3	5	6.5	706	82359	6.7	Cullin 2
2032	Q13617	3	5	6.2	745	86983	6.9	Cullin-2
2033	Q53HB9	3	6	6.2	547	61566	9.3	DEAD (Asp-Glu-Ala-Asp) box polypeptide 56 variant
2033	Q9NY93	3	6	6.2	547	61590	9.3	Probable ATP-dependent RNA helicase DDX56
2033	Q6IAE2	3	6	6.2	547	61640	9.3	DDX56 protein
2034	Q5R363	3	6	6.2	547	62033	5.7	SFRS protein kinase 1
2034	UPI000020DBDD	3	6	5.2	655	74325	6.2	SFRS protein kinase 1
2034	UPI000015FF90	3	6	5.2	654	74226	6.2	Serine/threonine-protein kinase SRPK1 (EC 2.7.11.1) (Serine/arginine- rich protein-specific kinase 1) (SR-protein-specific kinase 1) (SFRS protein kinase 1).
2034	Q96SB4-2	3	6	5.2	655	74320	6.2	Isoform 2 of Q96SB4
2034	UPI0000D61435	3	6	4.1	825	92447	7.9	Serine/threonine-protein kinase SRPK1 (EC 2.7.11.1) (Serine/arginine- rich protein-specific kinase 1) (SR-protein-specific kinase 1) (SFRS protein kinase 1).
2034	Q96SB4	3	6	4.1	826	92407	7.7	Serine/threonine-protein kinase SRPK1
2035	Q96K12	3	6	6.2	515	59439	9.4	Fatty acyl-CoA reductase 2
2036	Q8WXA9-2	3	3	6.1	624	71650	10.2	Isoform 2 of Q8WXA9
2037	UPI00004572F1	3	10	6	974	112369	5.2	Importin-11 (Imp11) (Ran-binding protein 11) (RanBP11).
2037	Q9UI26	3	10	5.9	975	112535	5.3	Importin-11
2038	Q53H59	3	3	5.8	756	84451	6.2	Estrogen receptor binding protein variant
2038	Q76MJ8	3	3	5.8	756	84469	6.2	TdT interacting factor 2
2038	Q6TLI0	3	3	5.8	756	84444	6	Estrogen receptor binding protein
2038	Q5QJE6	3	3	5.8	756	84455	6.2	LPTS-RP2
2038	Q5TFJ4	3	3	5.4	810	90670	6	Deoxynucleotidyltransferase terminal-interacting protein 2
2039	P20839-2	3	11	7	489	52598	6.6	Isoform 2 of P20839

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
2039	P20839	3	11	6.6	514	55406	6.9	Inosine-5'-monophosphate dehydrogenase 1
2039	UPI0000D61CCC	3	11	6.4	528	56788	7.1	Inosine-5'-monophosphate dehydrogenase 1 (EC 1.1.1.205) (IMP dehydrogenase 1) (IMPDH-I) (IMPD 1).
2039	Q6ZNB1	3	11	6.4	530	57050	7.3	CDNA FLJ16255 fis, clone HLUNG2015548, highly similar to INOSINE-5'- MONOPHOSPHATE DEHYDROGENASE 1
2039	UPI0000D61CCB	3	11	6.1	561	60210	6.6	Inosine-5'-monophosphate dehydrogenase 1 (EC 1.1.1.205) (IMP dehydrogenase 1) (IMPDH-I) (IMPD 1).
2039	UPI0000D61CCD	3	11	5.8	587	63025	6.7	Inosine-5'-monophosphate dehydrogenase 1 (EC 1.1.1.205) (IMP dehydrogenase 1) (IMPDH-I) (IMPD 1).
2039	A4D0Z6	3	11	5.7	599	64320	7	IMP (Inosine monophosphate) dehydrogenase 1
2039	UPI0000D61CCA	3	11	5.7	597	64093	6.9	Inosine-5'-monophosphate dehydrogenase 1 (EC 1.1.1.205) (IMP dehydrogenase 1) (IMPDH-I) (IMPD 1).
2039	Q5H9Q6	3	11	5.7	599	64537	8	Hypothetical protein DKFZp781N0678
2040	Q14680	3	5	5.7	651	74642	8.7	Maternal embryonic leucine zipper kinase
2040	Q53GX0	3	5	5.7	651	74642	8.7	Maternal embryonic leucine zipper kinase variant
2041	P27694	3	8	5.5	616	68138	7.2	Replication protein A 70 kDa DNA-binding subunit
2042	O95352	3	9	5.4	703	77960	6.2	Autophagy-related protein 7
2043	Q8N9Z3	3	52	6.6	579	66047	7.3	CDNA FLJ36025 fis, clone TESTI2016701, highly similar to TUMOR NECROSIS FACTOR TYPE 1 RECEPTOR ASSOCIATED PROTEIN
2043	Q12931	3	52	5.4	704	80110	8.2	Heat shock protein 75 kDa, mitochondrial precursor
2043	UPI0000001C1A	3	52	5.4	704	80011	8	TNF receptor-associated protein 1
2043	Q9BV61	3	52	5.4	699	79357	7.8	TRAP1 protein
2043	Q53G55	3	52	5.4	704	80039	8	TNF receptor-associated protein 1 variant
2043	Q53FS6	3	52	5.4	704	80091	8	TNF receptor-associated protein 1 variant
2044	Q9Y5X1	3	3	5.4	595	66592	5.6	Sorting nexin-9
2045	UPI0000160BED	3	9	6	583	61287	9.1	Ewing sarcoma breakpoint region 1 isoform EWS-b
2045	Q01844-2	3	9	6	583	61217	9.1	Isoform EWS
2045	UPI0000457066	3	9	5.8	600	62508	9.4	RNA-binding protein EWS (EWS oncogene) (Ewing sarcoma breakpoint region 1 protein).
2045	Q96MN4	3	9	5.8	600	62478	9.4	CDNA FLJ32119 fis, clone PEBLM1000034, highly similar to RNA-BINDING PROTEIN EWS
2045	Q01844	3	9	5.3	656	68478	9.3	RNA-binding protein EWS

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2045	Q96MX4	3	9	5.3	661	68966	9.3	CDNA FLJ31747 fis, clone NT2RI2007377, highly similar to RNA-BINDING PROTEIN EWS
2045	Q96FE8	3	9	5.3	655	68391	9.3	Ewing sarcoma breakpoint region 1
2046	Q3YEC7	3	5	5.3	729	79549	5.2	Putative GTP-binding protein Parf
2046	Q3YEC7-2	3	5	5.3	730	79636	5.2	Isoform 2 of Q3YEC7
2047	Q5R914	3	8	5.3	511	57659	6.3	Serine/threonine protein phosphatase
2048	Q96ST2-2	3	5	8.7	494	56109	5.4	Isoform 2 of Q96ST2
2048	Q96ST2-3	3	5	7	612	69108	4.9	Isoform 3 of Q96ST2
2048	Q96ST2	3	5	5.3	819	91955	4.7	IWS1 homolog
2049	P05067-3	3	18	5.9	677	76760	4.8	Isoform L
2049	P05067-4	3	18	5.8	695	78663	4.8	Isoform APP695 of P05067
2049	P05067-5	3	18	5.7	696	78866	4.8	Isoform L
2049	P05067-6	3	18	5.6	714	80769	4.8	Isoform APP714 of P05067
2049	P05067-7	3	18	5.5	733	82916	4.8	Isoform L
2049	Q6GSC0	3	18	5.3	751	84819	4.8	Amyloid beta (A4) protein
2049	P05067-9	3	18	5.3	752	85040	4.8	Isoform L
2049	P05067	3	18	5.2	770	86943	4.8	Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer disease amyloid protein) (Cerebral vascular amyloid peptide) (CVAP) (Protease nexin-II) (PN-II) (APPI) (PreA4) [Contains: Soluble APP-alpha (S-APP- alpha); Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59) (Amyloid intracellular domain 59) (AID(59)) (AICD-59); Gamma-CTF(57) (Gamma-secretase C-terminal fragment 57) (Amyloid intracellular domain 57) (AID(57)) (AICD-57); Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50) (Amyloid intracellular domain 50) (AID(50)) (AICD-50); C31]
2050	Q13416	3	3	5.2	577	65972	6.5	Origin recognition complex subunit 2
2051	Q9UBY2	3	3	5.2	712	77243	5.5	Neurochondrin-2
2051	Q9UBB6	3	3	5.1	729	78864	5.5	Neurochondrin-1
2051	Q9Y4D9	3	3	5.1	731	79158	5.6	Neurochondrin
2051	Q9Y4A6	3	3	5.1	730	78963	5.5	Hypothetical protein WUGSC:H_DJ0728D04.2
2052	Q9Y2W2	3	10	5.1	641	69998	8.4	WW domain-binding protein 11
2053	P43121	3	6	5	646	71608	5.8	Cell surface glycoprotein MUC18 precursor
2054	Q9H3U1-2	3	14	5.1	929	101675	6.1	Isoform 2 of Q9H3U1
2054	Q9H3U1	3	14	5	944	103077	6.1	UNC45 homolog A
2055	O95202	3	12	4.9	739	83354	6.7	Leucine zipper-EF-hand-containing transmembrane protein 1, mitochondrial precursor

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2056	O95834	3	4	4.9	649	70679	6.3	Echinoderm microtubule-associated protein-like 2
2057	P21399	3	4	4.9	889	98399	6.7	Iron-responsive element-binding protein 1
2058	O60518	3	13	4.8	1105	124713	5	Ran-binding protein 6
2059	A4D1R2	3	3	4.6	699	77903	8.4	Zinc finger CCCH type, antiviral 1
2059	UPI0000457619	3	3	3.5	902	101444	8.3	Zinc finger CCCH type antiviral protein 1 (Zinc finger CCCH domain- containing protein 2).
2059	Q7Z2W4	3	3	3.5	902	101444	8.3	Zinc finger CCCH type antiviral protein 1
2059	A4D1S4	3	3	3.5	902	101431	8.4	Zinc finger CCCH type, antiviral 1
2060	P33121-2	3	4	4.7	688	76871	7	Isoform 2 of P33121
2060	P33121	3	4	4.6	698	77943	7.1	Long-chain-fatty-acid--CoA ligase 1
2061	Q6NX51	3	5	4.5	974	110498	6.5	Exocyst complex component 4
2061	Q96A65	3	5	4.5	974	110498	6.5	Exocyst complex component 4
2062	UPI0000141B4C	3	25	4.9	932	102639	6.4	MMS19-like protein (hMMS19) (MET18 homolog).
2062	Q96T76-5	3	25	4.9	932	102625	6.4	Isoform 5 of Q96T76
2062	Q96T76	3	25	4.5	1030	113275	6.4	MMS19-like protein
2062	UPI000013DDF7	3	25	4.5	1030	113289	6.4	MMS19-like protein (hMMS19) (MET18 homolog).
2062	UPI000007172D	3	25	4.5	1030	113318	6.3	MMS19-like (MET18 homolog, S. cerevisiae)
2063	Q8WUM9	3	8	4.4	679	73700	7.1	Sodium-dependent phosphate transporter 1
2064	Q9Y2J2-2	3	5	5.5	865	96514	5.4	Isoform B of Q9Y2J2
2064	Q9Y2J2	3	5	4.4	1087	120677	5.2	Band 4.1-like protein 3
2065	P43246	3	6	4.3	934	104743	5.8	DNA mismatch repair protein Msh2
2066	Q14562	3	9	4.3	1220	139314	8.3	ATP-dependent RNA helicase DHX8
2066	Q86YB2	3	9	4.3	1220	139314	8.4	DEAH (Asp-Glu-Ala-His) box polypeptide 8
2066	Q86X36	3	9	4.3	1220	139287	8.1	DEAH (Asp-Glu-Ala-His) box polypeptide 8
2067	Q9UPT8	3	9	4.3	1303	140256	6.3	Zinc finger CCCH domain-containing protein C19orf7
2067	UPI0000D617DC	3	9	4.3	1317	141672	6.2	Zinc finger CCCH domain-containing protein C19orf7.
2068	O15042-3	3	25	6.9	620	72524	7.6	Isoform 3 of O15042
2068	O15042	3	25	4.2	1029	118292	8.5	U2-associated protein SR140
2068	UPI0000457184	3	25	4.2	1029	118305	8.5	U2-associated SR140 protein
2068	O15042-2	3	25	4.2	1028	118235	8.5	Isoform 2 of O15042
2069	O43290	3	7	4.2	800	90255	6.1	U4/U6.U5 tri-snRNP-associated protein 1
2069	UPI0000D62637	3	7	4.2	800	90310	6.2	U4/U6.U5 tri-snRNP-associated protein 1 (U4/U6.U5 tri-snRNP-associated 110 kDa protein) (Squamous cell carcinoma antigen recognized by T cells 1) (SART-1) (hSART-1) (hSnu66).
2070	P08648	3	3	4.2	1049	114536	5.8	Integrin alpha-5 precursor (Fibronectin receptor subunit alpha) (Integrin alpha-F) (VLA-5) (CD49e antigen) [Contains: Integrin alpha-5 heavy chain; Integrin alpha-5 light chain]
2071	UPI00004569D8	3	5	5.3	756	83908	5.6	conserved nuclear protein NHN1

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
2071	Q96MP7	3	5	5.3	757	84074	5.7	CDNA FLJ32070 fis, clone OCBBF1000119
2071	Q86VM9	3	5	4.2	953	106359	8.2	Conserved nuclear protein NHN1
2071	UPI00001FF676	3	5	4.2	953	106379	8.3	conserved nuclear protein NHN1
2072	Q96QU8	3	4	4.2	1125	128883	6.4	Exportin-6
2073	P49756	3	6	4.3	784	94122	6.2	Probable RNA-binding protein 25
2073	A0PJL9	3	6	4.1	839	99723	6.3	RBM25 protein
2073	UPI0000373D58	3	6	4	843	100186	6.3	RNA binding motif protein 25
2074	P23588	3	12	4.1	611	69224	5.7	Eukaryotic translation initiation factor 4B
2074	UPI0000D621F8	3	12	4.1	610	69167	5.8	Eukaryotic translation initiation factor 4B (eIF-4B).
2074	Q8WYK5	3	12	4.1	611	69151	5.7	Eukaryotic initiation factor 4B
2074	Q6IB46	3	12	4.1	611	69137	5.7	EIF4B protein
2074	Q6GPH5	3	12	4.1	611	69166	5.7	Eukaryotic translation initiation factor 4B
2074	Q53HQ2	3	12	4.1	611	69151	5.7	Eukaryotic translation initiation factor 4B variant
2074	Q4G0E3	3	12	4.1	611	69098	5.7	Eukaryotic translation initiation factor 4B
2075	Q8N3F8	3	3	4.1	863	93441	7.2	MICAL-like protein 1
2076	Q93063-2	3	6	4	728	83598	6.4	Isoform 2 of Q93063
2077	Q0VG75	3	5	3.9	1124	127436	5.1	Exportin 4
2077	Q9C0E2	3	5	3.8	1151	130139	5	Exportin-4
2078	Q13488	3	13	3.9	830	92998	7	Vacuolar proton translocating ATPase 116 kDa subunit a isoform 3
2078	Q8WVC5	3	13	3.9	830	92968	7.1	T-cell, immune regulator 1, ATPase, H+ transporting, lysosomal V0 subunit A3
2079	Q5H8A4-4	3	5	8.2	463	51267	7.6	Isoform 4 of Q5H8A4
2079	Q5H8A4	3	5	3.9	983	108173	7.1	GPI ethanolamine phosphate transferase 2
2079	UPI000006FDE7	3	5	3.9	975	107284	7.3	GPI7 protein
2079	Q5H8A4-2	3	5	3.9	975	107376	7.2	Isoform 2 of Q5H8A4
2080	UPI00004C2784	3	4	3.9	1506	164886	8.2	CLIP-associating protein 2
2081	O75150	3	4	3.8	1001	113678	6.3	E3 ubiquitin-protein ligase BRE1B
2081	UPI000013D2CF	3	4	3.8	1001	113650	6.2	Ubiquitin-protein ligase BRE1B (EC 6.3.2.-) (BRE1-B) (RING finger protein 40) (95 kDa retinoblastoma-associated protein) (RBP95).
2082	Q5T8P6-5	3	3	6.9	534	60007	8.9	Isoform 5 of Q5T8P6
2082	Q5T8P6-4	3	3	6.6	558	62580	9.1	Isoform 4 of Q5T8P6
2082	Q5T8P6-3	3	3	3.8	980	110666	9.1	Isoform 3 of Q5T8P6
2083	Q8N3L8	3	12	3.8	1061	112497	7.4	Hypothetical protein DKFZp761H0722
2084	Q8N596	3	4	3.8	811	90794	6.8	Oxysterol binding protein-like 5
2084	UPI0000366761	3	4	3.8	821	91898	6.9	Oxysterol-binding protein-related protein 5 (OSBP-related protein 5) (ORP-5).
2084	UPI00001AF3AD	3	4	3.5	889	99721	7.6	Oxysterol-binding protein-related protein 5 (OSBP-related protein 5) (ORP-5).
2084	Q9H0X9	3	4	3.5	879	98617	7.5	Oxysterol-binding protein-related protein 5
2085	Q6DHZ8	3	9	3.7	1102	123447	7.4	Activity-dependent neuroprotector
2085	Q9H2P0	3	9	3.7	1102	123563	7.3	Activity-dependent neuroprotector

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2086	Q96L67	3	4	4.3	948	108513	5	Nardilysin
2086	O43847	3	4	3.6	1150	131571	5	Nardilysin precursor
2086	UPI0000458A54	3	4	3.6	1151	131700	5	Nardilysin precursor (EC 3.4.24.61) (N-arginine dibasic convertase) (NRD convertase) (NRD-C).
2086	UPI00004561DA	3	4	3.6	1150	131572	5	Nardilysin precursor (EC 3.4.24.61) (N-arginine dibasic convertase) (NRD convertase) (NRD-C).
2086	UPI000004EC94	3	4	3.4	1219	139328	5	nardilysin (N-arginine dibasic convertase)
2086	Q5VUL1	3	4	3.4	1219	139413	5	Nardilysin
2086	O43847-2	3	4	3.4	1218	139284	5	Isoform 2 of O43847
2087	Q5VTR2	3	5	3.6	975	113662	5.9	E3 ubiquitin-protein ligase BRE1A
2087	UPI000013DE3A	3	5	3.6	977	113977	6	Ubiquitin-protein ligase BRE1A (EC 6.3.2.-) (BRE1-A) (hBRE1) (RING finger protein 20).
2088	Q9Y2U8	3	5	3.6	911	99997	7.5	Inner nuclear membrane protein Man1
2089	Q13563	3	10	3.5	968	109691	5.7	Polycystin-2
2090	O00267	3	7	3.4	1087	121000	5.1	Transcription elongation factor SPT5
2090	UPI0000D6179E	3	7	3.4	1083	120527	5.1	Transcription elongation factor SPT5 (hSPT5) (DRB sensitivity-inducing factor large subunit) (DSIF large subunit) (DSIF p160) (Tat- cotransactivator 1 protein) (Tat-CT1 protein).
2090	UPI0000456CB7	3	7	3.4	1087	121028	5	Transcription elongation factor SPT5 (hSPT5) (DRB sensitivity-inducing factor large subunit) (DSIF large subunit) (DSIF p160) (Tat- cotransactivator 1 protein) (Tat-CT1 protein).
2090	O00267-2	3	7	3.4	1083	120499	5.1	Isoform 2 of O00267
2091	UPI000004729B	3	8	3.6	924	107568	8	optic atrophy 1 isoform 2
2091	O60313-8	3	8	3.5	952	110721	7.6	Isoform 8 of O60313
2091	O60313	3	8	3.4	960	111657	7.9	Dynamin-like 120 kDa protein, mitochondrial precursor (Optic atrophy protein 1) [Contains: Dynamin-like 120 kDa protein, form S1]
2091	UPI000049DFC2	3	8	3.4	978	113490	7.8	Dynamin-like 120 kDa protein, mitochondrial precursor (Optic atrophy protein 1) [Contains: Dynamin-like 120 kDa protein, form S1].
2091	UPI00000472A0	3	8	3.4	979	113681	7.9	optic atrophy 1 isoform 6
2091	UPI000004729F	3	8	3.4	961	111821	8	optic atrophy 1 isoform 4
2091	UPI000004729C	3	8	3.4	978	113517	7.8	optic atrophy 1 isoform 5
2091	O60313-7	3	8	3.4	969	112524	7.5	Isoform 7 of O60313
2091	O60313-4	3	8	3.4	977	113460	7.8	Isoform 4 of O60313
2091	UPI0000422965	3	8	3.3	1015	117743	7.8	Dynamin-like 120 kDa protein, mitochondrial precursor (Optic atrophy protein 1) [Contains: Dynamin-like 120 kDa protein, form S1].

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2091	UPI0000422960	3	8	3.3	997	115884	7.9	Dynamin-like 120 kDa protein, mitochondrial precursor (Optic atrophy protein 1) [Contains: Dynamin-like 120 kDa protein, form S1].
2091	UPI00000472A1	3	8	3.3	1015	117770	7.8	optic atrophy 1 isoform 8
2091	O60313-6	3	8	3.3	1014	117713	7.8	Isoform 6 of O60313
2091	O60313-5	3	8	3.3	989	114975	7.6	Isoform 5 of O60313
2091	O60313-3	3	8	3.3	1006	116777	7.5	Isoform 3 of O60313
2091	O60313-2	3	8	3.3	997	115911	7.9	Isoform 2 of O60313
2092	Q0VG08	3	15	3.5	1233	133629	7.4	SEC24 related gene family, member B
2092	O95487	3	15	3.4	1268	137789	6.7	Protein transport protein Sec24B
2092	UPI00004F6ED7	3	15	3.4	1268	137417	6.7	SEC24 (S. cerevisiae) homolog B isoform a
2092	UPI00001AE8CE	3	15	3.4	1266	137573	6.7	Protein transport protein Sec24B (SEC24-related protein B).
2093	Q3MJA4	3	3	3.4	831	94132	6.8	Solute carrier family 39 (Zinc transporter), member 10
2093	Q9ULF5	3	3	3.4	835	94559	6.8	Solute carrier family 39 member 10
2093	Q68CR5	3	3	3.4	831	94120	6.8	Hypothetical protein DKFZp781L10106
2094	Q9UFY1	3	5	6.7	629	71370	6	Hypothetical protein DKFZp434N101
2094	A2A284	3	5	3.3	1291	148660	6	Phospholipase C, gamma 1
2094	P19174	3	5	3.3	1290	148532	6	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase gamma 1
2094	UPI0000D61091	3	5	3	1412	161314	7.2	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase gamma 1 (EC 3.1.4.11) (Phosphoinositide phospholipase C) (PLC-gamma-1) (Phospholipase C-gamma-1) (PLC-II) (PLC-148).
2094	Q4LE43	3	5	3	1412	161302	7.2	PLCG1 variant protein
2095	Q59ER0	3	3	4.3	1138	130427	6.4	Rho GTPase activating protein 5 variant
2095	Q05BU8	3	3	4.1	1189	136660	6.7	Hypothetical protein
2095	Q05BE8	3	3	3.3	1502	172429	6.7	ARHGAP5 protein
2095	UPI000057B85C	3	3	3.3	1502	172459	6.6	Rho GTPase activating protein 5 isoform a
2095	UPI000057B85B	3	3	3.3	1501	172331	6.6	Rho GTPase activating protein 5 isoform b
2096	O14974-4	3	5	3.3	971	109104	5.4	Isoform 4 of O14974
2096	O14974-3	3	5	3.3	974	109728	5.3	Isoform 3 of O14974
2096	O14974-2	3	5	3.2	995	111185	5.4	Isoform 2 of O14974
2096	O14974	3	5	3.1	1030	115281	5.4	Protein phosphatase 1 regulatory subunit 12A
2096	Q2NKL4	3	5	3.1	1030	115281	5.4	PPP1R12A protein
2097	Q9BUM6	3	5	7.5	425	47451	5.5	COL6A2 protein
2097	P12110	3	5	3.1	1019	108579	6.2	Collagen alpha-2(VI) chain precursor
2098	Q14146	3	6	3.1	1524	170569	7.3	Uncharacterized protein KIAA0133
2098	Q5VYC9	3	6	3.1	1524	170543	7.3	KIAA0133
2099	Q9HC35	3	4	3.1	981	108903	6.3	Echinoderm microtubule-associated protein-like 4

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2099	UPI0000140350	3	4	3.1	981	108916	6.4	Echinoderm microtubule-associated protein-like 4 (EMAP-4) (Restrictedly overexpressed proliferation-associated protein) (Ropp 120).
2100	O60524	3	3	3	1076	122970	6.3	Serologically defined colon cancer antigen 1
2100	UPI0000246D16	3	3	3	1076	122954	6.3	Serologically defined colon cancer antigen 1 (Antigen NY-CO-1).
2101	Q9UDQ3	3	3	4.4	745	84397	5.3	WUGSC:H_DJ0560O14.1 protein
2101	UPI0000D61C7B	3	3	3.1	1071	121188	5.4	Dihydropyridine-sensitive L-type calcium channel subunits alpha-2/delta precursor [Contains: L-type calcium channel subunit alpha-2; L-type calcium channel subunit delta].
2101	P54289	3	3	3	1091	123183	5.2	Dihydropyridine-sensitive L-type calcium channel subunits alpha-2/delta precursor [Contains: L-type calcium channel subunit alpha-2; L-type calcium channel subunit delta]
2101	Q9UIU0	3	3	3	1110	125308	5.4	Dihydropyridine receptor alpha 2 subunit
2101	Q17R45	3	3	3	1091	123183	5.2	Calcium channel, voltage-dependent, alpha 2/delta subunit 1
2102	Q12913	3	7	3	1337	145927	5.6	Receptor-type tyrosine-protein phosphatase eta precursor
2102	UPI00004564C8	3	7	3	1337	145941	5.6	Receptor-type tyrosine-protein phosphatase eta precursor (EC 3.1.3.48) (Protein-tyrosine phosphatase eta) (R-PTP-eta) (HPTP eta) (Protein- tyrosine phosphatase receptor type J) (Density-enhanced phosphatase 1) (DEP-1) (CD148 antigen).
2103	Q6WCQ1	3	3	3	1024	116446	6.2	Myosin phosphatase Rho-interacting protein
2103	UPI0000366BAD	3	3	3	1025	116533	6.2	myosin phosphatase-Rho interacting protein isoform 2
2103	UPI0000200A77	3	3	3	1038	118103	6.4	myosin phosphatase-Rho interacting protein isoform 1
2103	Q6WCQ1-2	3	3	3	1037	118016	6.4	Isoform 2 of Q6WCQ1
2104	Q8IX12	3	16	3	1150	132821	5.8	Cell division cycle and apoptosis regulator protein 1
2105	Q9H7L6	3	7	3.6	1310	141544	6.1	FLJ00056 protein
2105	UPI00001FCFB7	3	7	3.1	1519	164657	6.1	hypothetical protein LOC55701
2105	Q8TER5	3	7	3	1546	167672	6.4	FLJ00128 protein
2106	Q5VT52	3	4	2.9	1461	156019	7.4	Uncharacterized protein KIAA0460
2106	Q5VT52-3	3	4	2.9	1435	152875	7	Isoform 3 of Q5VT52
2107	Q8TEQ8	3	4	2.9	1089	118699	8.1	GPI ethanolamine phosphate transferase 3
2108	P28290	3	13	2.8	1259	138386	5.2	Sperm-specific antigen 2
2109	Q548W1	3	3	3	920	103012	6.9	HRNT1
2109	O15294	3	3	2.7	1046	116924	6.7	UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit

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2109	O15294-3	3	3	2.7	1036	115706	6.7	Isoform 1 of O15294
2110	O14981	3	9	2.5	1849	206886	6.5	TATA-binding protein-associated factor 172 (EC 3.6.1.-) (ATP-dependent helicase BTAF1) (TBP-associated factor 172) (TAF-172) (TAF(II)170)
2111	Q7Z478	3	13	2.5	1369	155235	8.1	Putative ATP-dependent RNA helicase DHX29
2112	P78357	3	3	2.4	1384	156266	7.1	Contactin-associated protein 1 precursor
2112	UPI0000D62337	3	3	2.4	1384	156280	7.1	Contactin-associated protein 1 precursor (Caspr) (Caspr1) (Neurexin 4) (Neurexin IV) (p190).
2113	Q59GM0	3	6	2.4	1469	162246	6.7	Nuclear receptor co-repressor 2 variant
2113	UPI0000E59244	3	6	1.4	2524	274674	7.6	nuclear receptor co-repressor 2 isoform 1
2113	UPI0000E59243	3	6	1.4	2462	268358	7.8	nuclear receptor co-repressor 2 isoform 2
2113	UPI0000D62278	3	6	1.4	2521	274528	7.5	Nuclear receptor corepressor 2 (N-CoR2) (Silencing mediator of retinoic acid and thyroid hormone receptor) (SMRT) (SMRTe) (Thyroid-, retinoic-acid-receptor-associated corepressor) (T3 receptor- associating factor) (TRAC) (CTG repeat protein 26) (SMAP270).
2113	Q9Y618	3	6	1.4	2517	274032	8.1	Nuclear receptor corepressor 2
2114	Q96ST3	3	7	2.4	1273	145175	7.3	Paired amphipathic helix protein Sin3a
2115	P39880	3	5	2.3	1505	164272	6	Homeobox protein cut-like 1
2115	UPI00004575CB	3	5	2.3	1494	163149	5.8	Protein CASP.
2115	UPI0000246CDF	3	5	2.3	1505	164187	5.9	Protein CASP.
2115	UPI00001A95D7	3	5	2.3	1505	164312	6	CCAAT displacement protein isoform a
2115	P39880-5	3	5	2.3	1449	157980	5.8	Isoform 6 of P39880
2115	P39880-2	3	5	2.3	1483	161734	5.9	Isoform 2 of P39880
2115	P39880-3	3	5	2.2	1516	165687	5.9	Isoform 3 of P39880
2116	Q7LBC6	3	7	2.3	1761	191610	7.2	JmjC domain-containing histone demethylation protein 2B
2116	UPI000020C6A8	3	7	2.3	1761	191580	7.2	JmjC domain-containing histone demethylation protein 2B (EC 1.14.11.-) (Jumonji domain-containing protein 1B) (Nuclear protein 5qNCA).
2117	Q8TCU6-3	3	3	2.4	1561	175847	6.8	Isoform 3 of Q8TCU6
2117	Q8TCU6	3	3	2.2	1659	186203	6.4	Phosphatidylinositol 3,4,5-trisphosphate-dependent Rac exchanger 1 protein
2117	UPI000013D375	3	3	2.2	1659	186202	6.4	Phosphatidylinositol 3,4,5-trisphosphate-dependent Rac exchanger 1 protein (P-Rex1 protein).
2118	P42356	3	6	2.1	2044	231290	6.9	Phosphatidylinositol 4-kinase alpha

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2118	UPI00001AE78E	3	6	2.1	2044	231317	6.9	Phosphatidylinositol 4-kinase alpha (EC 2.7.1.67) (PI4-kinase alpha) (PtdIns-4-kinase alpha) (PI4K-alpha).
2118	Q4LE69	3	6	2	2121	238695	7.1	PIK4CA variant protein
2119	Q5QD01	3	4	2	1581	180550	5.9	SP-A receptor subunit SP-R210 alphaS
2120	A1L4N4	3	19	1.9	1672	185545	6.8	KIDINS220 protein
2120	Q9ULH0	3	19	1.8	1777	197210	6.7	KIAA1250 protein
2121	Q68DX7	3	13	1.9	2127	239113	7	Hypothetical protein DKFZp686E0722
2121	Q7Z3K2	3	13	1.9	2150	241011	7.1	CCR4-NOT transcription complex subunit 1
2121	UPI00001FF2F6	3	13	1.7	2376	266937	7.1	CCR4-NOT transcription complex, subunit 1 isoform a
2122	Q68CP7	3	8	2.2	1215	134927	6.6	Hypothetical protein DKFZp781G125
2122	P33527-8	3	8	2	1351	151631	7.6	Isoform 8 of P33527
2122	UPI000059D323	3	8	1.9	1416	158948	7.4	ATP-binding cassette, sub-family C, member 1 isoform 4
2122	UPI000013D386	3	8	1.9	1400	157240	7.5	Multidrug resistance-associated protein 1 (ATP-binding cassette sub- family C member 1) (Leukotriene C(4) transporter) (LTC4 transporter).
2122	UPI000013D384	3	8	1.9	1456	163262	7.7	Multidrug resistance-associated protein 1 (ATP-binding cassette sub- family C member 1) (Leukotriene C(4) transporter) (LTC4 transporter).
2122	UPI000013D383	3	8	1.9	1459	163861	7	Multidrug resistance-associated protein 1 (ATP-binding cassette sub- family C member 1) (Leukotriene C(4) transporter) (LTC4 transporter).
2122	UPI000013D381	3	8	1.9	1450	162595	7.4	Multidrug resistance-associated protein 1 (ATP-binding cassette sub- family C member 1) (Leukotriene C(4) transporter) (LTC4 transporter).
2122	Q9UQ98	3	8	1.9	1400	157210	7.5	Multidrug resistance protein
2122	P33527-7	3	8	1.9	1410	158251	7.1	Isoform 7 of P33527
2122	P33527-6	3	8	1.9	1407	157652	7.8	Isoform 6 of P33527
2122	A3RJX2	3	8	1.8	1531	171590	7.1	ATP-binding cassette, sub-family C (CFTR/MRP), member 1
2122	UPI000059D326	3	8	1.8	1472	164970	7.6	ATP-binding cassette, sub-family C, member 1 isoform 2
2122	UPI000059D325	3	8	1.8	1466	164303	7.3	ATP-binding cassette, sub-family C, member 1 isoform 5
2122	UPI00004091AF	3	8	1.8	1475	165569	6.9	ATP-binding cassette, sub-family C, member 1 isoform 3
2122	UPI00001604C7	3	8	1.8	1482	166166	7.3	ATP-binding cassette, sub-family C, member 1 isoform 7
2122	UPI00001604C6	3	8	1.8	1489	166653	7.4	ATP-binding cassette, sub-family C, member 1 isoform 6

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2122	UPI000013D385	3	8	1.8	1473	164975	7.6	Multidrug resistance-associated protein 1 (ATP-binding cassette sub- family C member 1) (Leukotriene C(4) transporter) (LTC4 transporter).
2122	UPI000013D382	3	8	1.8	1466	164488	7.4	Multidrug resistance-associated protein 1 (ATP-binding cassette sub- family C member 1) (Leukotriene C(4) transporter) (LTC4 transporter).
2122	UPI000013D380	3	8	1.8	1515	169882	7.2	Multidrug resistance-associated protein 1 (ATP-binding cassette sub- family C member 1) (Leukotriene C(4) transporter) (LTC4 transporter).
2122	P33527-9	3	8	1.8	1541	172609	6.8	Isoform 9 of P33527
2122	P33527-4	3	8	1.8	1466	164273	7.3	Isoform 4 of P33527
2122	P33527-3	3	8	1.8	1475	165538	6.9	Isoform 3 of P33527
2122	P33527-2	3	8	1.8	1472	164940	7.6	Isoform 2 of P33527
2122	P33527	3	8	1.8	1531	171560	7.1	Multidrug resistance-associated protein 1 (ATP-binding cassette sub- family C member 1) (Leukotriene C(4) transporter)
2123	P12883	3	3	1.8	1935	223095	5.8	Myosin-7
2123	UPI0000D623D8	3	3	1.8	1940	223470	5.8	Myosin heavy chain, cardiac muscle beta isoform (MyHC-beta).
2124	O14578	3	3	1.7	2027	231429	6.6	Citron Rho-interacting kinase
2124	Q2M5E1	3	3	1.7	2069	236605	6.7	Citron
2125	O14646	3	5	1.7	1709	196517	7.2	Chromodomain-helicase-DNA-binding protein 1
2125	UPI000013DD75	3	5	1.7	1710	196687	7.1	chromodomain helicase DNA binding protein 1
2125	Q17RZ3	3	5	1.7	1709	196589	7.1	Chromodomain helicase DNA binding protein 1
2126	Q8IVF4	3	4	1.7	3051	349503	5.9	Ciliary dynein heavy chain 10
2127	O95071	3	3	1.6	2799	309352	5.8	E3 ubiquitin-protein ligase EDD1
2127	UPI000052A0EC	3	3	1.6	2796	309192	6.1	PREDICTED: similar to E3 ubiquitin protein ligase, HECT domain containing, 1
2127	UPI00004576D7	3	3	1.6	2798	309307	5.9	Ubiquitin-protein ligase EDD1 (EC 6.3.2.-) (Hyperplastic discs protein homolog) (hHYD) (Progestin-induced protein).
2128	P51610	3	5	1.5	2035	208840	7.5	Host cell factor (HCF) (HCF-1) (C1 factor) (VP16 accessory protein) (VCAF) (CFF) [Contains: HCF N-terminal chain 1; HCF N-terminal chain 2; HCF N-terminal chain 3; HCF N-terminal chain 4; HCF N-terminal chain 5; HCF N-terminal chain 6; HCF C-terminal chain 1; HCF C- terminal chain 2; HCF C-terminal chain 3; HCF C-terminal chain 4; HCF C-terminal chain 5; HCF C-terminal chain 6]

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
2128	UPI000059DBED	3	5	1.5	1980	202848	7.1	Host cell factor (HCF) (HCF-1) (C1 factor) (VP16 accessory protein) (VCAF) (CFF) [Contains: HCF N-terminal chain 1; HCF N-terminal chain 2; HCF N-terminal chain 3; HCF N-terminal chain 4; HCF N-terminal chain 5; HCF N-terminal chain 6; HCF C-terminal chai
2128	UPI000059DBEB	3	5	1.5	1936	198175	7.2	Host cell factor (HCF) (HCF-1) (C1 factor) (VP16 accessory protein) (VCAF) (CFF) [Contains: HCF N-terminal chain 1; HCF N-terminal chain 2; HCF N-terminal chain 3; HCF N-terminal chain 4; HCF N-terminal chain 5; HCF N-terminal chain 6; HCF C-terminal chai
2128	UPI000036779B	3	5	1.5	1966	201848	7.5	Host cell factor (HCF) (HCF-1) (C1 factor) (VP16 accessory protein) (VCAF) (CFF) [Contains: HCF N-terminal chain 1; HCF N-terminal chain 2; HCF N-terminal chain 3; HCF N-terminal chain 4; HCF N-terminal chain 5; HCF N-terminal chain 6; HCF C-terminal chai
2128	UPI0000142F1F	3	5	1.5	2035	208730	7.5	host cell factor 1
2128	P51610-2	3	5	1.5	1966	201957	7.5	Isoform 2 of P51610
2129	Q59EW8	3	3	2.6	1310	152553	5.6	Golgi autoantigen, golgin subfamily a, 4 variant
2129	UPI0000367131	3	3	1.6	2184	255638	5.4	Golgin subfamily A member 4 (Trans-Golgi p230) (256 kDa golgin) (Golgin-245) (Protein 72.1).
2129	Q13439-2	3	3	1.6	2185	255737	5.4	Isoform 2 of Q13439
2129	Q13439	3	3	1.5	2230	261137	5.4	Golgin subfamily A member 4
2129	Q13439-4	3	3	1.5	2228	260948	5.4	Isoform 4 of Q13439
2129	Q13439-3	3	3	1.5	2223	260322	5.4	Isoform 3 of Q13439
2130	UPI0000E8AC98	3	15	1.5	2610	289383	5.4	HECT domain containing 1
2131	P23471-2	3	6	2.2	1454	163443	5.2	Isoform Short of P23471
2131	P23471	3	6	1.4	2314	254528	4.9	Receptor-type tyrosine-protein phosphatase zeta precursor
2132	UPI000016001C	3	4	1.6	2288	259840	6.8	transcriptional regulator ATRX isoform 3
2132	UPI0000D61D94	3	4	1.5	2424	274983	6.4	Transcriptional regulator ATRX (EC 3.6.1.-) (ATP-dependent helicase ATRX) (X-linked helicase II) (X-linked nuclear protein) (XNP) (Znf- HX).
2132	UPI000016001B	3	4	1.5	2454	278226	6.5	transcriptional regulator ATRX isoform 2
2132	P46100-4	3	4	1.5	2454	278206	6.6	Isoform 3 of P46100
2132	P46100-3	3	4	1.5	2375	269789	7	Isoform 2 of P46100
2132	P46100	3	4	1.4	2492	282564	6.6	Transcriptional regulator ATRX
2132	UPI0000DD8684	3	4	1.4	2493	282810	6.6	PREDICTED: similar to transcriptional regulator ATRX isoform 1
2132	UPI0000161F78	3	4	1.4	2492	282584	6.6	transcriptional regulator ATRX isoform 1
2133	O94915	3	6	1.3	3013	339598	5.6	Protein furry homolog-like

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
2134	Q02224	3	3	1.3	2663	312089	5.6	Centromeric protein E
2134	UPI0000D615A1	3	3	1.3	2585	302383	5.6	centromere protein E
2134	UPI000020B28A	3	3	1.3	2701	316414	5.6	centromere protein E
2134	Q4LE75	3	3	1.3	2585	302323	5.6	CENPE variant protein
2135	Q6AI22	3	6	1.1	2810	318870	5	Hypothetical protein DKFZp686H16106
2135	Q9NU22	3	6	0.6	5596	632827	5.7	Midasin
2136	Q8WXH0	3	3	0.5	6885	796457	5.4	Nesprin-2
2136	Q8WXH0-2	3	3	0.5	6907	798877	5.4	Isoform 2 of Q8WXH0
2137	Q15149-4	2	17	57	4547	516174	5.8	Isoform 4 of Q15149
2137	UPI0000233FD1	2	17	57	4547	516204	5.8	plectin 1 isoform 11
2138	Q96G68	2	19	48.7	39	4414	9.7	C1orf151 protein
2139	P12235	2	11	47.7	298	33064	9.8	ADP/ATP translocase 1
2140	Q3LIF5	2	25	46.7	1018	110665	4.1	Nestin
2141	A2Q118	2	13	44	273	31636	5.8	MHC class I antigen
2141	A2VBZ9	2	13	44	273	31799	6.1	MHC class I antigen
2142	Q9HB66	2	12	41.3	63	7264	9.6	PNAS-117
2143	Q71UM5	2	20	39.3	84	9477	9.5	40S ribosomal protein S27-like protein
2143	UPI000049DDE1	2	20	33	100	11346	9.3	40S ribosomal protein S27-like protein.
2144	O94925-3	2	6	38.8	598	65460	7.9	Isoform GAC of O94925
2145	Q9UDW1	2	12	38.1	63	7308	9.5	Ubiquinol-cytochrome c reductase complex 7.2 kDa protein
2146	Q9Y5U9	2	16	34.1	82	8969	8.3	Immediate early response 3-interacting protein 1
2147	Q14240	2	2	33.9	407	46402	5.5	Eukaryotic initiation factor 4A-II
2147	Q14240-2	2	2	33.8	408	46489	5.5	Isoform 2 of Q14240
2148	UPI00004576A1	2	15	33.3	144	16384	8	Ubiquitin-conjugating enzyme E2 variant 2 (MMS2) (Enterocyte differentiation-associated factor EDAF-1) (Enterocyte differentiation-promoting factor) (EDPF-1) (Vitamin D3-inducible protein) (DDVit 1).
2148	Q15819	2	15	33.1	145	16363	8	Ubiquitin-conjugating enzyme E2 variant 2
2149	O43504	2	5	33	91	9614	4.9	Hepatitis B virus X-interacting protein
2149	UPI0000205288	2	5	17.3	173	18158	5.5	hepatitis B virus x-interacting protein
2150	P16104	2	19	32.9	143	15145	10.7	Histone H2A.x
2151	Q8WVE3	2	5	32.9	85	9509	5.9	MGC13017 protein
2151	Q96HQ2	2	5	24.1	116	13196	5	Similar to RIKEN cDNA A430101B06 gene
2152	Q9NPE3	2	17	32.8	64	7706	10	H/ACA ribonucleoprotein complex subunit 3
2153	UPI000013ED5D	2	7	32.6	129	14687	10	PREDICTED: similar to ribosomal protein S15a
2154	P59768	2	11	32.4	71	7850	8	Guanine nucleotide-binding protein G(I)/G(S)/G(O) gamma-2 subunit precursor
2155	P61970	2	11	32.3	127	14478	5.4	Nuclear transport factor 2
2156	Q85KX8	2	19	32.2	227	25575	4.8	Cytochrome oxidase subunit II
2157	UPI0000140BDB	2	2	31.2	462	50154	9	UPI0000140BDB UniRef100 entry
2158	Q9BT73	2	4	30.3	122	13104	7.9	Uncharacterized protein C7orf48
2159	Q9HB72	2	3	30.3	76	8468	10.2	PNAS-106
2159	Q9Y5V0	2	3	30.3	76	8498	10	Zinc finger protein 706

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2160	UPI000006FE7A	2	3	30.1	156	17967	9.5	PREDICTED: similar to ubiquitin and ribosomal protein S27a precursor
2161	P62875	2	14	29.9	67	7645	7.8	DNA-directed RNA polymerase II 7.6 kDa polypeptide
2162	UPI0000161022	2	2	29.9	157	17722	10.5	PREDICTED: similar to 60S ribosomal protein L23a
2163	Q6FG99	2	33	29.8	114	11568	4.4	RPLP1 protein
2164	UPI00001975C1	2	12	29.5	176	20867	10.8	PREDICTED: similar to ribosomal protein L18a
2165	Q9H3K6	2	8	29.1	86	10117	6.5	BolA-like protein 2
2166	Q13015	2	10	28.9	90	10061	4.5	Protein AF1q
2167	Q5T123	2	61	28.4	88	9380	9.4	SH3 domain binding glutamic acid-rich protein like 3
2167	Q9H299	2	61	26.9	93	10438	4.9	SH3 domain-binding glutamic acid-rich-like protein 3
2167	UPI0000D61E9C	2	61	11.1	225	23699	9.1	SH3 domain-binding glutamic acid-rich-like protein 3 (SH3 domain-binding protein 1) (SH3BP-1).
2167	Q86Z22	2	61	11.1	226	23838	9.1	Hypothetical protein
2168	O14907	2	6	28.2	124	13735	8.5	Tax1-binding protein 3
2169	Q8NI22	2	4	28.1	146	16390	4.6	Multiple coagulation factor deficiency protein 2 precursor
2170	O15523	2	2	28	660	73154	7.6	ATP-dependent RNA helicase DDX3Y
2171	P14406	2	23	27.7	83	9396	9.7	Cytochrome c oxidase polypeptide VIIa-liver/heart, mitochondrial precursor
2171	Q496I0	2	23	27.7	83	9426	9.6	Cytochrome c oxidase subunit VIIa polypeptide 2
2171	UPI000015A446	2	23	20	115	12844	9.1	Cytochrome c oxidase polypeptide VIIa-liver/heart, mitochondrial precursor (EC 1.9.3.1) (Cytochrome c oxidase subunit VIIa-L) (VIIaL).
2172	Q567R0	2	11	29.4	85	9953	5.5	UQCRH protein
2172	P07919	2	11	27.5	91	10739	4.4	Ubiquinol-cytochrome c reductase complex 11 kDa protein, mitochondrial precursor
2173	Q86XF3	2	18	38.8	67	7371	4.9	LSM8 protein
2173	O95777	2	18	27.1	96	10403	4.5	U6 snRNA-associated Sm-like protein LSm8
2174	P62879	2	14	27.1	340	37331	6	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 2
2175	P62273	2	9	26.8	56	6677	10.1	40S ribosomal protein S29
2176	O75380	2	6	26.6	124	13712	8.3	NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial precursor
2177	Q969Q0	2	8	26.4	106	12469	10.7	60S ribosomal protein L36a-like
2178	Q9Y547	2	5	25.7	144	16297	5	Placental protein 25
2179	Q6FIE5	2	5	25.6	125	13792	6.1	PHP14 protein
2179	Q9NRX4	2	5	25.6	125	13833	6.1	14 kDa phosphohistidine phosphatase
2179	UPI0000DD5CDC	2	5	22.2	144	16144	6.4	14 kDa phosphohistidine phosphatase
2180	UPI000041A257	2	90	43.6	55	6295	8.9	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F2 isoform 2c
2180	P56134-2	2	90	27.3	88	10363	9.9	Isoform 2 of P56134

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2180	P56134	2	90	25.5	94	10918	9.7	ATP synthase f chain, mitochondrial
2181	Q49AN9	2	42	29.7	64	7101	7.2	SNRPG protein
2181	P62308	2	42	25	76	8496	8.9	Small nuclear ribonucleoprotein G
2182	Q8TBQ9	2	26	25	72	8060	9	Transmembrane protein 167 precursor
2183	P63172	2	13	24.8	113	12452	5.1	Dynein light chain Tctex-type 1
2184	O15155	2	8	24.6	118	13289	9.1	BET1 homolog
2185	P09972	2	14	24.5	364	39456	6.9	Fructose-bisphosphate aldolase C
2186	O95139	2	5	24.2	128	15489	9.6	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 6
2187	Q9NPA8	2	5	23.8	101	11529	9.3	Enhancer of yellow 2 homolog
2187	UPI0000503EA4	2	5	23.8	101	11526	9.3	enhancer of yellow 2 homolog
2188	P51808	2	14	23.3	116	13062	5.7	Dynein light chain Tctex-type 3
2188	UPI0000211E80	2	14	17.8	152	16979	5.9	Dynein light chain Tctex-type 3 (T-complex-associated testis-expressed 1-like) (Protein 91/23).
2189	UPI00001FD8B2	2	6	31.5	73	8322	9.5	Acylphosphatase-1 (EC 3.6.1.7) (Acylphosphate phosphohydrolase 1) (Acylphosphatase, organ-common type isozyme) (Acylphosphatase, erythrocyte isozyme).
2189	P07311	2	6	23.2	99	11261	9.3	Acylphosphatase-1
2190	UPI000013CABC	2	39	23.2	164	18111	6.9	PREDICTED: similar to peptidylprolyl isomerase A isoform 1
2191	P82921	2	13	23	87	10742	10.2	Mitochondrial 28S ribosomal protein S21
2192	O60220	2	8	22.7	97	10998	5.2	Mitochondrial import inner membrane translocase subunit Tim8 A
2193	Q9NU23	2	4	22.7	88	10449	10.5	LYR motif-containing protein 2
2194	UPI000013EB83	2	10	22.6	376	42003	5.6	hypothetical protein LOC345651
2195	Q9Y6H1	2	5	22.5	151	15513	9.2	Coiled-coil-helix-coiled-coil-helix domain-containing protein 2
2196	P00167-2	2	5	30.6	98	11268	5.1	Isoform 2 of P00167
2196	Q59F44	2	5	22.7	132	14572	5.7	Cytochrome b-5 isoform 1 variant
2196	P00167	2	5	22.4	134	15330	5	Cytochrome b5
2197	Q9H0N5	2	2	22.3	103	11761	7.6	Pterin-4-alpha-carbinolamine dehydratase 2
2197	UPI000013F545	2	2	17.7	130	14365	9.1	pterin-4 alpha-carbinolamine dehydratase 2
2198	P61457	2	5	22.1	104	12000	6.8	Pterin-4-alpha-carbinolamine dehydratase
2198	Q6FGB3	2	5	22.1	104	12010	6.8	PCBD protein
2199	Q5RI15	2	11	22	118	13291	8.8	Protein FAM36A
2199	Q5RI15-2	2	11	20	130	14669	8.8	Isoform 2 of Q5RI15
2200	P60468	2	67	21.9	96	9974	11.6	Protein transport protein Sec61 subunit beta
2201	Q96B45	2	5	21.9	105	11564	6.8	Uncharacterized protein C10orf32
2201	UPI00004563FD	2	5	21.9	105	11608	8	Uncharacterized protein C10orf32.
2202	O15514	2	11	21.8	142	16311	4.8	DNA-directed RNA polymerase II 16 kDa polypeptide

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2203	Q9Y6G3	2	6	21.8	142	16661	8.4	Mitochondrial 28S ribosomal protein S32, mitochondrial precursor
2203	UPI000016020B	2	6	21.8	142	16602	7	mitochondrial ribosomal protein L42 isoform b
2204	Q8N4D3	2	7	23.5	119	13921	9.8	Hypothetical protein
2204	UPI000045715C	2	7	23.3	120	14026	9.8	PREDICTED: similar to NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4, 15kDa isoform 1
2204	O95168	2	7	21.7	129	15209	9.8	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4
2205	P33947	2	71	21.7	212	24422	8.7	ER lumen protein retaining receptor 2
2206	Q9Y5J9	2	5	21.7	83	9344	5.1	Mitochondrial import inner membrane translocase subunit Tim8 B
2207	O95183	2	2	21.6	116	12805	7.8	Vesicle-associated membrane protein 5
2208	Q9NX14	2	3	22.2	153	17317	5.2	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11, mitochondrial precursor
2208	Q7Z4X2	2	3	21.5	158	17942	5.4	Neuronal protein
2208	Q9NX14-2	2	3	20.9	163	18364	5.2	Isoform 2 of Q9NX14
2209	UPI00006C034D	2	4	21.5	293	32072	5.4	PREDICTED: similar to Heterogeneous nuclear ribonucleoprotein C-like 1 (hnRNP core protein C-like 1)
2210	Q7Z3H5	2	4	24.8	323	37501	7.1	Hypothetical protein DKFZp686O0215
2210	UPI0000140DA1	2	4	23.9	335	38275	6.2	Mitogen-activated protein kinase 3 (EC 2.7.11.24) (Extracellular signal-regulated kinase 1) (ERK-1) (Insulin-stimulated MAP2 kinase) (MAP kinase 1) (MAPK 1) (p44-ERK1) (ERT2) (p44-MAPK) (Microtubule- associated protein 2 kinase).
2210	UPI0000D579B4	2	4	22.4	357	40088	7.5	mitogen-activated protein kinase 3 isoform 2
2210	P27361	2	4	21.1	379	43136	6.8	Mitogen-activated protein kinase 3
2211	Q9BUE6	2	5	20.9	129	14179	9.1	Iron-sulfur cluster assembly 1 homolog, mitochondrial precursor
2211	UPI0000141215	2	5	20.9	129	14177	9.1	OTTHUMP00000021591.
2211	UPI00006C0905	2	5	20.5	132	14630	9.9	similar to HESB like domain containing 2
2211	UPI0000DD7CF0	2	5	12.4	218	24137	10.2	PREDICTED: similar to HESB like domain containing 2 isoform 2
2212	Q3MHD2	2	4	20.6	131	14328	5.9	LSM12 protein
2212	Q96NL5	2	4	13.8	195	21701	7.8	CDNA FLJ30656 fis, clone DFNES2000292
2213	P55854	2	39	20.4	103	11637	5.5	Small ubiquitin-related modifier 3 precursor
2214	Q9NRF9	2	4	20.4	147	16860	4.7	DNA polymerase epsilon subunit 3
2214	UPI0000070E87	2	4	20.4	147	16872	4.7	DNA polymerase epsilon subunit 3

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2215	Q9NZ45	2	6	20.4	108	12199	9.1	Zinc finger CDGSH domain-containing protein 1
2216	UPI0000F0A512	2	5	20.6	350	40110	5.7	Guanine nucleotide-binding protein G(k) subun
2216	P08754	2	5	20.3	354	40532	5.7	Guanine nucleotide-binding protein G(k) subunit alpha (G(i) alpha-3)
2217	Q96C01	2	8	20.3	138	15641	7.6	Hypothetical protein FLJ14668
2218	O14519	2	13	20	115	12365	9.4	Cyclin-dependent kinase 2-associated protein 1
2219	P81605	2	3	20	110	11284	6.5	Dermcidin precursor (Preproteolysin) [Contains: Survival-promoting peptide; DCD-1]
2220	Q53HB4	2	4	20	160	18995	5.3	M-phase phosphoprotein 6 variant
2220	UPI00001AE7AB	2	4	20	160	19024	5.2	M-phase phosphoprotein 6
2220	Q99547	2	4	20	160	18996	5.2	M-phase phosphoprotein 6
2221	Q9BV81	2	3	20	110	12017	10.1	Transmembrane protein 93
2222	P11234	2	2	19.9	206	23409	6.6	Ras-related protein Ral-B precursor
2222	Q6ZS74	2	2	18.1	227	25710	8.7	CDNA FLJ45773 fis, clone NETRP2003448, highly similar to Ras-related protein RAL-B
2223	P68014	2	6	19.9	146	15808	8.4	Hemoglobin subunit delta
2224	Q96RP6	2	11	24.6	118	13635	8.3	Ubiquitin-conjugating enzyme
2224	P61077	2	11	19.7	147	16687	7.8	Ubiquitin-conjugating enzyme E2 D3 (EC 6.3.2.19) (Ubiquitin-protein ligase D3) (Ubiquitin carrier protein D3) (Ubiquitin-conjugating enzyme E2-17 kDa 3) (E2(17)KB 3)
2224	P62837	2	11	19.7	147	16735	7.8	Ubiquitin-conjugating enzyme E2 D2 (EC 6.3.2.19) (Ubiquitin-protein ligase D2) (Ubiquitin carrier protein D2) (Ubiquitin-conjugating enzyme E2-17 kDa 2) (E2(17)KB 2)
2224	Q8N924	2	11	19.6	148	16785	7.3	CDNA FLJ38503 fis, clone HCHON2000056, highly similar to UBIQUITIN- CONJUGATING ENZYME E2-17 kDa 3
2224	UPI00001B31EA	2	11	19.5	149	16893	7.8	ubiquitin-conjugating enzyme E2D 3 isoform 3
2224	UPI0000D6159F	2	11	19.3	150	16910	6.8	Ubiquitin-conjugating enzyme E2 D3 (EC 6.3.2.19) (Ubiquitin-protein ligase D3) (Ubiquitin carrier protein D3) (Ubiquitin-conjugating enzyme E2-17 kDa 3) (E2(17)KB 3).
2224	UPI0000D6159E	2	11	19.3	150	16943	7.3	Ubiquitin-conjugating enzyme E2 D3 (EC 6.3.2.19) (Ubiquitin-protein ligase D3) (Ubiquitin carrier protein D3) (Ubiquitin-conjugating enzyme E2-17 kDa 3) (E2(17)KB 3).
2225	Q6P5R6	2	10	19.7	122	14606	9.4	Ribosomal protein L22-like 1
2226	P61803	2	37	19.5	113	12497	7.1	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1
2227	Q9P2X0	2	19	23.9	92	10094	5.9	Dolichol-phosphate mannosyltransferase subunit 3
2227	Q6P184	2	19	20.8	106	11564	6	DPM3 protein

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
2227	Q3SX58	2	19	19.5	113	12339	6	DPM3 protein
2228	Q15714	2	2	19.4	144	15680	5.2	TSC22 domain family protein 1
2229	O14548	2	6	19.3	114	12615	9.4	Cytochrome c oxidase subunit VIIa-related protein, mitochondrial precursor
2230	O14966	2	2	19.2	203	23155	7.2	Ras-related protein Rab-7L1
2230	Q53EX5	2	2	19.2	203	23139	7.2	RAB7, member RAS oncogene family-like 1 variant
2231	O95295	2	5	19.1	136	14874	9.3	SNARE-associated protein Snapin
2232	P18077	2	23	19.1	110	12538	11.1	60S ribosomal protein L35a
2233	Q9NX24	2	8	19	153	17201	8.2	H/ACA ribonucleoprotein complex subunit 2
2234	UPI0000D610B1	2	2	19	189	20461	5.8	Breast carcinoma amplified sequence 4.
2235	UPI00001AE467	2	13	20.6	102	11138	7.3	blocked early in transport 1 homolog (S. cerevisiae) like
2235	Q9NYM9	2	13	18.9	111	12388	8.2	BET1-like protein
2236	Q9P0S2	2	3	18.9	106	12293	9.5	COX16-like protein C14orf112, mitochondrial precursor
2237	O15173	2	8	18.8	223	23818	4.9	Membrane-associated progesterone receptor component 2
2238	UPI0000DD7B6E	2	40	33.3	72	8132	11.1	PREDICTED: similar to 60S ribosomal protein L22 (Heparin-binding protein HBp15)
2238	P35268	2	40	18.8	128	14787	9.2	60S ribosomal protein L22
2238	Q7Z4W8	2	40	18.8	128	14818	9.3	Heparin-binding protein HBp15
2239	P62861	2	13	18.6	59	6648	12.1	40S ribosomal protein S30
2240	Q93096	2	4	18.5	173	19815	9	Protein tyrosine phosphatase type IVA protein 1 (EC 3.1.3.48) (Protein-tyrosine phosphatase 4a1) (Protein-tyrosine phosphatase of regenerating liver 1) (PRL-1) (PTP(CAAXI))
2241	Q9NQ29-2	2	2	20.9	325	38405	10	Isoform 2 of Q9NQ29
2241	Q9NQ29-3	2	2	19.2	354	41929	9.9	Isoform 3 of Q9NQ29
2241	Q9NQ29	2	2	18.3	371	43728	9.9	Putative RNA-binding protein Luc7-like 1
2242	Q96A26	2	14	18.2	154	17342	9.8	E2-induced gene 5 protein
2243	Q9Y3E0	2	60	18.1	138	15426	10.3	Vesicle transport protein GOT1B
2244	O14880	2	32	17.8	152	16516	9.4	Microsomal glutathione S-transferase 3
2244	Q53GB9	2	32	17.8	152	16530	9.4	Microsomal glutathione S-transferase 3 variant
2245	P45973	2	7	17.8	191	22225	5.9	Chromobox protein homolog 5
2246	Q75M90	2	2	17.7	113	12749	10.1	Hypothetical protein HSPC268
2246	Q96HJ9	2	2	17.7	113	12733	10.1	Hypothetical protein HSPC268
2247	P05161	2	2	17.6	165	17887	7.5	Interferon-induced 17 kDa protein precursor [Contains: Ubiquitin cross-reactive protein (hUCRP) (Interferon-induced 15 kDa protein)]
2248	P39210	2	4	17.6	176	19733	9.5	Protein Mpv17
2249	P78537	2	2	17.6	125	14311	8.2	Biogenesis of lysosome-related organelles complex-1 subunit 1
2250	Q5TDQ4	2	5	17.6	170	19550	5.6	HD domain containing 2
2250	Q9Y3D1	2	5	17.6	170	19491	5.4	CGI-130 protein
2250	Q6NZ49	2	5	14.7	204	23419	5.7	HD domain containing 2
2250	Q9BTT2	2	5	13.8	218	24850	6.2	HD domain-containing protein 2

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
2251	Q4R6Q8	2	6	17.5	171	18756	9	Testis cDNA, clone: QtsA-17369, similar to human 1-acylglycerol-3-phosphate O-acyltransferase 1(lysophosphatidic acid acyltransferase, alpha) (AGPAT1),transcript variant 2,
2251	Q71VH6	2	6	12.3	244	27083	9.4	Hypothetical protein
2251	Q99943	2	6	10.6	283	31717	9.4	1-acyl-sn-glycerol-3-phosphate acyltransferase alpha
2252	Q9BX83	2	3	24	100	10710	7.7	Hemoglobin alpha 1 globin chain
2252	Q4ZGM8	2	3	24	100	10796	9	Hemoglobin alpha-2 globin mutant
2252	P69905	2	3	16.9	142	15258	8.7	Hemoglobin subunit alpha
2252	Q53F97	2	3	16.9	142	15281	8.7	Alpha 2 globin variant
2252	Q1HDT5	2	3	16.9	142	15272	9	Hemoglobin alpha 1-2 hybrid
2253	P83876	2	3	16.9	142	16786	5.8	Thioredoxin-like protein 4A
2254	P84101	2	5	16.9	59	6900	10.4	Small EDRK-rich factor 2
2255	Q8NCS4	2	2	16.9	154	16885	9.2	ZMYM6 protein
2256	Q53EN2	2	4	16.8	190	21307	6.2	MURR1 variant
2256	Q8N668	2	4	16.8	190	21178	6.2	COMM domain-containing protein 1
2257	UPI000016176F	2	3	18.6	264	30084	9.1	cyclin-dependent kinase 2 isoform 2
2257	P24941	2	3	16.4	298	33930	8.7	Cell division protein kinase 2
2258	O60282	2	4	16.1	957	109495	6.2	Kinesin heavy chain isoform 5C
2259	O75915	2	50	16	188	21615	9.8	PRA1 family protein 3
2260	Q9NPJ3	2	13	15.7	140	14960	9.1	Thioesterase superfamily member 2
2261	Q9BY50	2	12	15.6	192	21542	9.2	Signal peptidase complex catalytic subunit SEC11C
2262	Q9Y237	2	3	16.8	131	13810	9.8	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4
2262	Q3MHV0	2	3	15.6	141	14892	9.9	PIN4 protein
2262	Q0D2H3	2	3	15.5	142	15069	9.8	PIN4 protein
2262	UPI00002263A9	2	3	14.1	156	16608	10	protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting, 4 (parvulin)
2263	Q9BRT6	2	8	15.5	129	15225	10.4	Uncharacterized protein C12orf31
2264	UPI0000D616EE	2	6	15.7	102	11528	5.3	U6 snRNA-associated Sm-like protein LSm7.
2264	Q9UK45	2	6	15.5	103	11602	5.3	U6 snRNA-associated Sm-like protein LSm7
2265	P42766	2	20	15.4	123	14551	11	60S ribosomal protein L35
2266	P63098	2	13	15.3	170	19300	4.8	Calcineurin subunit B isoform 1
2266	P63100-2	2	13	12	216	24979	5.2	Isoform 2 of P63100
2266	Q86YQ0	2	13	3.4	765	84721	8.1	HZGJ
2267	Q9NZZ4	2	5	19.4	139	16059	6.8	HSPC176
2267	Q9UL33	2	5	19.3	140	16146	6.8	Trafficking protein particle complex 2-like protein
2267	Q6ZTA7	2	5	15.3	177	20021	8.2	CDNA FLJ44827 fis, clone BRACE3046837
2268	Q9NQT4	2	4	15.3	235	25249	7.6	Exosome complex exonuclease RRP46
2269	Q05BV9	2	5	15.2	138	15774	5.2	Hypothetical protein
2269	Q05DM1	2	5	15.1	139	15901	5.5	Hypothetical protein
2269	UPI0000456571	2	5	9.2	228	26510	5.7	Adrenal gland protein AD-002 (Hypothetical protein HSPC148) (Hypothetical protein ORF5).

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
2269	Q9UI29	2	5	9.2	229	26624	5.7	Adrenal gland protein AD-002
2269	Q9P013	2	5	9.2	229	26610	5.7	HSPC148
2270	Q8N5N7	2	2	15.2	158	18325	7.9	Mitochondrial 39S ribosomal protein L50
2271	Q8TDP1-2	2	7	15.3	163	17712	4.9	Isoform 2 of Q8TDP1
2271	Q8TDP1	2	7	15.2	164	17840	5	Ribonuclease H2 subunit C
2272	Q96AB3	2	3	15.1	205	22337	7.8	Isochorismatase domain-containing protein 2, mitochondrial precursor
2272	Q96AB3-2	2	3	14	221	24097	7.8	Isoform 2 of Q96AB3
2273	P51151	2	2	14.9	201	22838	5.5	Ras-related protein Rab-9
2274	Q6PII1	2	2	14.9	174	19423	5.9	GPR180 protein
2274	Q86V85	2	2	5.9	440	49395	7.4	Integral membrane protein GPR180 precursor
2275	Q5T091	2	25	15.5	187	21024	8.7	RER1 retention in endoplasmic reticulum 1 homolog
2275	O15258	2	25	14.8	196	22958	9.5	Protein RER1
2275	UPI000049DC68	2	25	14.1	205	23050	6.9	Protein RER1.
2275	UPI0000D61E27	2	25	13.6	213	24689	9.6	Protein RER1.
2275	Q9P0H9	2	25	13.6	214	24817	9.6	RER1 protein
2276	P52657	2	14	14.7	109	12457	6.8	Transcription initiation factor IIA gamma chain
2277	P17568	2	9	14.6	137	16402	8.9	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7
2278	UPI000015FD55	2	23	14.8	155	17219	11.1	PREDICTED: similar to 60S ribosomal protein L29 (Cell surface heparin-binding protein HIP)
2278	P47914	2	23	14.5	159	17752	11.7	60S ribosomal protein L29
2278	Q6IPI1	2	23	14.3	161	17951	11.7	Ribosomal protein L29
2279	P82663	2	7	14.5	173	20116	8.8	Mitochondrial 28S ribosomal protein S25
2280	Q16495	2	2	14.5	145	15156	11.3	Thyroid peroxidase
2281	Q5TBA5	2	9	14.5	275	30009	5.3	OTTHUMP00000018264
2281	Q96B26	2	9	14.5	276	30040	5.3	Exosome complex exonuclease RRP43
2282	Q9BV57	2	4	14.5	179	21498	5.7	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase
2282	UPI0000070FDE	2	4	14.5	179	21483	5.7	membrane-type 1 matrix metalloproteinase cytoplasmic tail binding protein-1
2283	Q9BW83	2	8	14.5	186	20480	5.4	Putative GTP-binding protein RAY-like
2283	UPI000013C6D3	2	8	14.4	187	20424	5.6	Putative GTP-binding protein RAY-like (Rab-like protein 4).
2284	Q5HYD9	2	13	19.6	107	11873	4.8	Hypothetical protein DKFZp686M0619
2284	O43169	2	13	14.4	146	16332	5	Cytochrome b5 type B precursor
2285	P49006	2	7	14.4	195	19529	4.7	MARCKS-related protein
2286	Q8WY22	2	2	14.3	251	27836	9.4	BRI3-binding protein
2287	Q9HBL7	2	7	14.3	147	17201	9.6	Uncharacterized protein C9orf46
2287	UPI0000073DFC	2	7	14.3	147	17229	9.7	hypothetical protein LOC55848
2288	Q9Y3C4	2	11	14.3	175	19661	6.8	TP53RK-binding protein
2288	Q9Y3C4-3	2	11	11.7	214	23854	7.4	Isoform 3 of Q9Y3C4
2289	A2BEH4	2	16	15.8	196	20942	4.9	Proteasome (Prosome, macropain) subunit beta type 9
2289	P28065-2	2	16	14.8	209	22328	5	Isoform LMP2.S of P28065
2289	A2BEH1	2	16	14.2	219	23245	5	Proteasome (Prosome, macropain) subunit beta type 9

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
2289	P28065	2	16	14.2	219	23264	5	Proteasome subunit beta type 9 precursor
2290	O43752	2	5	14.1	255	29176	4.9	Syntaxin-6
2291	O43716	2	2	14	136	15086	5	Putative protein 15E1.2
2292	P00374	2	10	13.9	187	21453	7.4	Dihydrofolate reductase
2293	P63279	2	23	13.9	158	18007	8.7	SUMO-conjugating enzyme UBC9
2293	UPI00001AF46D	2	23	12	184	20458	8.5	SUMO-conjugating enzyme UBC9 (EC 6.3.2.-) (SUMO-protein ligase) (Ubiquitin-conjugating enzyme E2 I) (Ubiquitin-protein ligase I) (Ubiquitin carrier protein I) (Ubiquitin carrier protein 9) (p18).
2293	Q7KZS0	2	23	12	184	20444	8.5	Ubiquitin-conjugating enzyme E2I
2294	Q496C9	2	4	13.9	209	23484	8.3	D-tyrosyl-tRNA deacylase 1 homolog
2294	Q8TEA8	2	4	13.9	209	23424	8.2	Probable D-tyrosyl-tRNA(Tyr) deacylase 1
2295	UPI0000D624C1	2	4	14.2	134	15535	8.1	Golgin subfamily A member 7 (Golgi complex-associated protein of 16 kDa).
2295	Q7Z5G4-2	2	4	14.2	134	15578	8.4	Isoform 2 of Q7Z5G4
2295	Q7Z5G4	2	4	13.9	137	15824	7	Golgin subfamily A member 7
2296	Q9H0U6	2	8	13.9	180	20577	9.5	39S ribosomal protein L18, mitochondrial precursor
2297	Q9Y2R5	2	2	13.8	130	14502	9.8	28S ribosomal protein S17, mitochondrial precursor
2298	Q5JYY5	2	2	16.8	185	20217	5.6	Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 10
2298	Q5JYY4	2	2	16.1	193	20808	6.6	Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 10
2298	O75832	2	2	13.7	226	24428	6.1	26S proteasome non-ATPase regulatory subunit 10
2299	Q13084	2	5	13.7	256	30157	8.3	39S ribosomal protein L28, mitochondrial precursor
2299	Q4TT38	2	5	13.7	256	30046	8	Mitochondrial ribosomal protein L28
2300	Q7LG56	2	7	13.7	351	40737	5	Ribonucleoside-diphosphate reductase M2 subunit B
2301	Q0VAE4	2	3	13.6	235	26879	9.2	MORF4L1 protein
2301	Q9Y690	2	3	13.6	235	26733	8.4	Transcription factor-like protein MORF4
2301	Q569V4	2	3	9.9	323	37231	9.2	Mortality factor 4 like 1
2301	Q9UBU8	2	3	8.8	362	41474	9.3	Mortality factor 4-like protein 1
2302	Q16576	2	6	13.6	425	47820	5	Histone-binding protein RBBP7
2303	Q5QP91	2	2	13.6	221	24843	8.1	Eukaryotic translation initiation factor 2B, subunit 3 gamma, 58kDa
2304	Q7RTV0	2	11	13.6	110	12405	8.4	PHD finger-like domain-containing protein 5A
2305	Q6IQ22	2	3	13.5	244	27248	8.4	Ras-related protein Rab-12
2306	Q9NRP0	2	34	13.4	149	16829	9.1	DC2
2306	Q9P1R4	2	34	12.5	160	17895	9.5	HDCMD45P
2306	Q9P075	2	34	12	167	18667	9.5	HSPC307
2307	Q9H2D1	2	5	13.3	315	35407	9.5	Mitochondrial folate transporter/carrier
2308	Q9NWM8	2	2	13.3	211	24172	6.1	FK506-binding protein 14 precursor

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2309	P09234	2	23	13.2	159	17394	9.7	U1 small nuclear ribonucleoprotein C
2309	Q53G33	2	23	13.2	159	17452	9.6	Small nuclear ribonucleoprotein polypeptide C variant
2309	Q5TAL3	2	23	11.7	180	19687	9.6	Small nuclear ribonucleoprotein polypeptide C
2310	UPI000013EC4C	2	17	13.3	181	20792	9.6	jagunal homolog 1
2310	Q8N5M9	2	17	13.1	183	21125	9.7	Protein jagunal homolog 1
2310	Q96SW1	2	17	13.1	183	21072	9.6	CDNA FLJ14602 fis, clone NT2RP1000191
2311	O15347	2	9	13	200	22980	8.4	High mobility group protein B3
2311	UPI0000DD7F4E	2	9	12.5	208	23744	8.8	PREDICTED: similar to high-mobility group box 3
2312	Q00169	2	3	13	270	31806	6.5	Phosphatidylinositol transfer protein alpha isoform
2312	UPI00004569F0	2	3	12.9	271	31934	6.7	Phosphatidylinositol transfer protein alpha isoform (PtdIns transfer protein alpha) (PtdInsTP) (PI-TP-alpha).
2312	Q6NUL6	2	3	11.1	316	35900	8	PITPNA protein
2313	Q5T6Z8	2	5	13	192	21860	5.3	Transmembrane protein 59
2313	Q6P5R1	2	5	10.5	239	27100	5	TMEM59 protein
2313	Q9BXS4	2	5	7.7	323	36223	5.1	Transmembrane protein 59 precursor
2314	Q9Y2V2	2	6	12.9	147	15892	8.2	Calcium-regulated heat stable protein 1
2315	Q04323	2	2	12.8	297	33325	5.3	SAPK substrate protein 1
2316	Q6MZY9	2	5	12.8	172	19092	6.5	Hypothetical protein DKFZp686M14237
2316	UPI0000229DA7	2	5	12.8	172	19036	6.5	CDNA FLJ11151 fis, clone PLACE1006883.
2316	UPI000013D1D1	2	5	7	314	35548	6.2	CDNA FLJ11151 fis, clone PLACE1006883.
2316	Q9H9M9	2	5	7	314	35624	6.3	CDNA FLJ12648 fis, clone NT2RM4002018
2316	Q9BRF8	2	5	7	314	35620	6.1	Hypothetical protein FLJ11151
2317	A2TDT2	2	3	12.7	157	18221	6.5	Mutant B-cell CLL/lymphoma 10
2317	O95999	2	3	8.6	233	26252	5.8	B-cell lymphoma/leukemia 10
2318	Q561V6	2	14	17.5	137	15667	7.6	NDUFB5 protein
2318	O43674	2	14	12.7	189	21750	9.6	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 5, mitochondrial precursor
2319	Q96IP9	2	2	12.7	213	22079	5.8	CDV3 protein
2319	Q9UKY7	2	2	10.5	258	27335	6.4	Protein CDV3 homolog
2320	Q00534	2	2	12.6	326	36938	6.5	Cell division protein kinase 6
2321	Q9NRG7-2	2	5	12.6	293	31077	9	Isoform 2 of Q9NRG7
2321	UPI000059D223	2	5	12.6	293	31077	9	hypothetical protein LOC56948
2322	Q96HR9	2	20	12.5	184	20733	8.6	Receptor expression-enhancing protein 6
2323	Q9P0S3	2	5	12.4	153	17371	9.6	ORM1-like protein 1
2324	UPI000006FB06	2	6	13.4	292	33242	4.6	BRCA2 and CDKN1A-interacting protein isoform C
2324	Q9P287-3	2	6	13.4	292	33442	4.6	Isoform 3 of Q9P287
2324	Q9P287	2	6	12.4	314	35979	4.6	BRCA2 and CDKN1A-interacting protein
2324	Q9P287-2	2	6	12.1	322	36215	4.7	Isoform 2 of Q9P287
2325	O14949	2	24	12.2	82	9906	10.1	Ubiquinol-cytochrome c reductase complex ubiquinone-binding protein QP-C

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
2326	P62487	2	2	12.2	172	19294	5.5	DNA-directed RNA polymerase II 19 kDa polypeptide
2327	Q16539	2	4	12.2	360	41293	5.8	Mitogen-activated protein kinase 14
2327	Q95NE7	2	4	12.2	360	41493	5.9	Mitogen-activated protein kinase 14
2327	UPI0000E8DA32	2	4	12	367	42109	6.4	Mitogen-activated protein kinase 14
2327	UPI0000E8DA31	2	4	12	367	42143	6.4	Mitogen-activated protein kinase 14
2327	UPI0000E8DA30	2	4	12	367	42083	6.4	Mitogen-activated protein kinase 14
2328	Q9H2W6	2	4	12.2	279	31705	7	39S ribosomal protein L46, mitochondrial precursor
2329	P11441	2	5	12.1	157	17776	8.7	Ubiquitin-like protein 4A
2329	Q5HY81	2	5	10.6	180	20570	9.7	Ubiquitin-like 4
2330	Q5T0S6	2	10	13.3	279	30743	7.9	Palmitoyl-protein thioesterase 1
2330	P50897	2	10	12.1	306	34193	6.5	Palmitoyl-protein thioesterase 1 precursor
2331	Q567U8	2	12	12.1	248	27317	5.5	COPS7A protein
2331	Q9UBW8	2	12	10.9	275	30277	8.2	COP9 signalosome complex subunit 7a
2332	Q5T653	2	6	12.1	305	33301	11.3	39S ribosomal protein L2, mitochondrial precursor
2333	Q96LJ7	2	6	12.1	313	33909	7.8	Dehydrogenase/reductase SDR family member 1
2334	Q9P000	2	3	12.1	198	21819	5.9	COMM domain-containing protein 9
2334	UPI00000731DD	2	3	12.1	198	21918	6.2	COMM domain containing 9
2335	P02511	2	2	12	175	20159	7.3	Alpha crystallin B chain (Alpha(B)-crystallin)
2336	P40855	2	5	12	299	32807	4.3	Peroxisomal biogenesis factor 19
2337	Q5VXM9	2	4	12	208	24158	9.5	Brix domain containing 1
2337	Q9H7B2	2	4	8.2	306	35583	10	Brix domain-containing protein 1
2338	UPI00001400A6	2	4	12.2	164	18593	8.9	28S ribosomal protein S24, mitochondrial precursor (S24mt) (MRP-S24) (bMRP47) (bMRP-47).
2338	Q96EL2	2	4	12	167	19015	9.4	28S ribosomal protein S24, mitochondrial precursor
2339	Q6ZRV1	2	14	11.9	243	26419	8	CDNA FLJ46073 fis, clone TESTI2001364, highly similar to Homo sapiens lactate dehydrogenase A -like
2340	Q9Y3B8	2	11	11.8	237	26833	6.9	Oligoribonuclease, mitochondrial precursor
2340	UPI0000130E83	2	11	11.8	237	26861	6.9	small fragment nuclease
2341	Q96EY5-2	2	2	13.7	233	24532	8.3	Isoform 2 of Q96EY5
2341	Q96EY5-3	2	2	12.5	257	27050	9.4	Isoform 3 of Q96EY5
2341	Q96EY5	2	2	11.7	273	28783	8.9	Protein FAM125A
2342	Q587I9	2	3	11.6	215	21790	9.9	Vesicle transport protein SFT2C
2343	Q969T4	2	7	11.6	207	22913	7.2	Ubiquitin-conjugating enzyme E2 E3
2344	Q9Y324	2	2	11.6	198	23370	9.7	rRNA-processing protein FCF1 homolog
2345	Q2MD55	2	2	11.5	174	20081	5.1	B-cell linker protein
2346	Q9BTE1	2	10	11.5	182	20127	8	Dynactin subunit 5
2347	Q12981	2	2	11.4	228	26132	8.9	Vesicle transport protein SEC20

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
2347	UPI000002AF30	2	2	11.4	228	26217	9.1	BCL2/adenovirus E1B 19kD interacting protein 1 isoform BNIP1
2347	UPI000013019D	2	2	9.6	271	31198	9.1	BCL2/adenovirus E1B 19kD interacting protein 1 isoform BNIP1-b
2347	Q12981-1	2	2	9.6	271	31113	8.9	Isoform 3 of Q12981
2348	P35754	2	5	11.3	106	11776	8.1	Glutaredoxin-1
2349	Q16763	2	4	11.3	222	23845	8.4	Ubiquitin-conjugating enzyme E2 S
2350	P61599	2	8	11.2	178	20368	5	N-acetyltransferase 5
2351	Q6NVV8	2	9	11.7	231	25635	6.6	IAH1 protein
2351	Q6PCA9	2	9	11.5	234	25845	6	IAH1 protein
2351	Q05D21	2	9	11.2	240	26443	6.5	IAH1 protein
2351	Q2TAA2	2	9	10.9	248	27599	5.3	Isoamyl acetate-hydrolyzing esterase 1 homolog
2352	Q53FT3	2	5	11.2	197	21628	5.5	Uncharacterized protein C11orf73
2353	Q6FIG5	2	2	11.2	197	21963	7.4	FN3KRP protein
2353	Q9HA64	2	2	7.1	309	34412	7.3	Ketosamine-3-kinase
2354	Q9Y5Z4-2	2	3	12.5	184	20859	4.8	Isoform 2 of Q9Y5Z4
2354	Q9Y5Z4	2	3	11.2	205	22875	4.6	Heme-binding protein 2
2355	Q8WZA0	2	6	11.1	190	21495	4.9	Protein LZIC
2356	Q9HC07	2	7	11.1	324	34906	7	Transmembrane protein 165
2357	Q08AR5	2	3	11	246	27857	8.5	ZRF1 protein
2357	UPI00001AE640	2	3	4.8	568	65914	9.1	Zuotin-related factor 1 (M-phase phosphoprotein 11).
2357	Q99543-2	2	3	4.8	568	65814	9	Isoform 2 of Q99543
2357	UPI000020F858	2	3	4.3	621	71996	8.7	zuotin related factor 1
2357	Q99543	2	3	4.3	621	71897	8.6	DnaJ homolog subfamily C member 2
2358	Q9UMS0	2	7	14.3	196	21802	4.3	NFU1 iron-sulfur cluster scaffold homolog
2358	Q7Z5B1	2	7	12.2	230	25924	4.7	Cytosolic iron-sulfur cluster scaffold protein Nfu
2358	Q7Z2Y4	2	7	11.6	242	27114	6	Hypothetical protein DKFZp686H1983
2358	Q6VNZ8	2	7	11	254	28460	5.2	NifU-like protein HIRIP5
2358	Q7Z5B2	2	7	11	254	28463	5.1	Iron-sulfur cluster scaffold protein Nfu
2359	Q5W145	2	3	12.9	155	18479	5.5	NADH dehydrogenase (Ubiquinone) 1 beta subcomplex, 8, 19kDa
2359	O95169	2	3	10.8	186	21766	6.8	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial precursor
2360	P08397	2	8	10.8	361	39330	7.2	Porphobilinogen deaminase
2361	Q9Y3C8	2	4	10.8	167	19458	7.4	Ufm1-conjugating enzyme 1
2361	UPI0000167880	2	4	10.8	167	19467	7.5	Ufm1-conjugating enzyme 1
2362	Q53EX1	2	5	10.7	419	47535	7.9	BCS1-like variant
2362	Q9Y276	2	5	10.7	419	47534	8.5	Mitochondrial chaperone BCS1
2363	Q9GZQ3	2	2	10.7	224	24670	7	COMM domain-containing protein 5
2364	O14494	2	4	10.6	284	32156	8	Lipid phosphate phosphohydrolase 1
2365	P31483	2	8	10.6	386	42961	8.2	Nucleolysin TIA-1 isoform p40 (RNA-binding protein TIA-1) (p40-TIA-1) [Contains: Nucleolysin TIA-1 isoform p15 (p15-TIA-1)]
2365	UPI0000161C6C	2	8	10.6	386	42962	8	TIA1 protein isoform 2
2365	Q53SS9	2	8	10.6	386	42963	7.8	Hypothetical protein TIA1
2365	Q59G98	2	8	8.8	464	51330	7.8	TIA1 protein variant

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2366	Q00765	2	38	10.6	189	21493	8.1	Receptor expression-enhancing protein 5
2367	Q86WV7	2	5	10.6	227	25564	4.9	Hypothetical protein
2367	UPI0000456ABD	2	5	10.6	227	25757	5	Coiled-coil domain-containing protein 43.
2368	P35249	2	3	10.5	363	39682	8	Replication factor C subunit 4
2369	P08590	2	22	10.3	195	21932	5.1	Myosin light polypeptide 3
2370	P63302	2	2	10.3	87	9401	9.1	Selenoprotein W
2370	UPI0000161B36	2	2	10.3	87	9298	9.2	selenoprotein W, 1
2370	UPI0000456CEF	2	2	10.1	89	9561	8.9	Selenoprotein W.
2371	Q9BUH6	2	4	10.3	204	21640	5.5	Uncharacterized protein C9orf142
2372	O75935-3	2	9	12	158	18001	6	Isoform 3 of O75935
2372	O75935	2	9	10.2	186	21119	5.5	Dynactin subunit 3
2373	Q8N6S5	2	3	10.2	226	24676	6.3	ADP-ribosylation-like factor 6 interacting protein 6
2374	O00194	2	3	10.1	218	24608	5.5	Ras-related protein Rab-27B
2375	Q5VXF4	2	4	10.1	326	35290	6.6	Fibronectin type III domain containing 3A
2375	UPI00001C1F5D	2	4	2.9	1142	125822	7.1	fibronectin type III domain containing 3A isoform 2
2375	Q9Y2H6	2	4	2.9	1134	125054	7.1	Fibronectin type-III domain-containing protein 3a
2375	Q6EVH4	2	4	2.8	1198	131852	6.7	Gene expressed in odontoblast protein
2376	Q712K3	2	4	10.1	238	27166	4.4	Ubiquitin-conjugating enzyme E2 R2
2377	Q96H20	2	4	10.1	258	28864	6.7	Vacuolar sorting protein SNF8
2377	Q96H20-2	2	4	10.1	257	28736	6.4	Isoform 2 of Q96H20
2378	Q9BT09	2	8	10.1	278	30748	5.5	Trinucleotide repeat-containing protein 5
2379	P24311	2	15	10	80	9160	10.3	Cytochrome c oxidase polypeptide VIIb, mitochondrial precursor
2380	P51159-2	2	4	10.3	213	24041	5.7	Isoform Short of P51159
2380	P51159	2	4	10	221	24868	5.2	Ras-related protein Rab-27A
2380	Q6IAS8	2	4	10	221	24898	5.2	RAB27A protein
2381	Q16563	2	14	10	259	28565	8.4	Synaptophysin-like protein 1
2382	UPI0000411C6A	2	3	11.6	258	29140	8	RCD1 required for cell differentiation1 homolog
2382	UPI0000ED4E8A	2	3	11.2	268	30485	8	RCD1 required for cell differentiation1 homol
2382	Q92600	2	3	10	299	33631	8	Protein RCD1 homolog
2383	P45877	2	6	9.9	212	22763	8.4	Peptidyl-prolyl cis-trans isomerase C
2384	Q9BZK7	2	4	9.9	514	55595	5.6	F-box-like/WD repeat protein TBL1XR1
2384	UPI00004571A4	2	4	9.9	514	55573	5.5	F-box-like/WD repeat protein TBL1XR1 (Transducin beta-like 1X-related protein 1) (Nuclear receptor corepressor/HDAC3 complex subunit TBLR1) (TBL1-related protein 1).
2385	Q9H1E3	2	3	9.9	243	27296	5.1	Nuclear ubiquitous casein and cyclin-dependent kinases substrate
2386	P10109	2	37	9.8	184	19393	5.8	Adrenodoxin, mitochondrial precursor
2387	P50461	2	2	9.8	194	20969	8.5	Cysteine and glycine-rich protein 3
2388	Q7Z2Q5	2	3	10	429	46405	6.6	C-terminal binding protein 1
2388	Q13363	2	3	9.8	440	47535	6.8	C-terminal-binding protein 1
2388	Q4KMQ8	2	3	9.8	440	47501	6.8	C-terminal binding protein 1

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2389	Q9BSK0	2	2	9.8	173	18914	9.6	MARVEL domain-containing protein 1
2390	UPI0000F58EC8	2	10	9.8	1075	121363	6.2	protein expressed in prostate, ovary, testis, and placenta 2
2391	Q96N63	2	19	19.8	121	13202	7.2	CDNA FLJ31361 fis, clone MESAN2008460, highly similar to Homo sapiens SL15 protein mRNA
2391	Q96K24	2	19	19	126	13431	9	CDNA FLJ14836 fis, clone OVARC1001702
2391	UPI000013E72D	2	19	18.9	127	13615	9	Mannose-P-dolichol utilization defect 1 protein (Suppressor of Lec15 and Lec35 glycosylation mutation homolog) (SL15).
2391	Q9H3L2	2	19	11.4	211	22609	8.3	My008 protein
2391	O75352	2	19	9.7	247	26707	9.1	Mannose-P-dolichol utilization defect 1 protein
2391	UPI000013CCA4	2	19	9.7	247	26638	8.9	mannose-P-dolichol utilization defect 1
2391	Q9BUU8	2	19	9.7	247	26668	8.9	Mannose-P-dolichol utilization defect 1
2391	Q1HDL3	2	19	8	299	32006	7.6	HBeAg-binding protein 2 binding protein A
2392	Q96PJ7	2	3	11.8	211	23758	8.7	Ras-related GTP-binding protein RAB39
2392	UPI0000D622F3	2	3	11.7	213	23958	8.5	Ras-related protein Rab-34 (Rab-39) (Ras-related protein Rah).
2392	Q6NXT3	2	3	9.7	259	29071	7.9	RAB34 protein
2392	UPI000015D94E	2	3	9.7	259	29058	7.9	RAB39
2392	Q9BZG1	2	3	9.7	259	29044	7.9	Ras-related protein Rab-34
2393	P46109	2	3	9.6	303	33777	6.7	Crk-like protein
2394	Q7Z677	2	2	11.4	132	15554	4.9	Hypothetical protein DKFZp779P0659
2394	Q53YA7	2	2	11.3	133	16011	8.1	Adaptor-related protein complex 1, sigma 1 subunit
2394	UPI000013E6B0	2	2	10.3	146	17448	7.1	UPI000013E6B0 UniRef100 entry
2394	P56377	2	2	9.6	157	18615	5.5	AP-1 complex subunit sigma-2
2394	P61966	2	2	9.5	158	18733	5.7	AP-1 complex subunit sigma-1A
2394	UPI00006C18A3	2	2	7.2	207	24133	9.3	PREDICTED: similar to adaptor-related protein complex 1 sigma 2 subunit
2394	UPI00006C17F0	2	2	7.2	207	24192	9.4	PREDICTED: similar to adaptor-related protein complex 1 sigma 2 subunit
2395	Q6PI78	2	5	9.6	240	25543	8.8	Transmembrane protein 65
2395	UPI00003675D1	2	5	9.6	240	25498	8.6	Transmembrane protein 65.
2396	Q9H3H3	2	5	9.6	251	27383	5.6	Uncharacterized protein C11orf68
2396	UPI0000228EAB	2	5	9.6	251	27355	5.5	Uncharacterized protein C11orf68 (Basophilic leukemia expressed protein Bles03) (Protein p5326).
2397	A2A2Q2	2	5	9.5	221	25490	9.1	Chromosome 20 open reading frame 44
2397	Q5T347	2	5	8.6	243	27909	9.1	Chromosome 20 open reading frame 44
2397	Q5T352	2	5	8.4	249	28939	8.8	Chromosome 20 open reading frame 44
2397	UPI0000456F84	2	5	7.7	273	31546	9	Basic FGF-repressed Zic-binding protein (bFZb).
2397	Q9NVA1-2	2	5	7.7	273	31517	8.8	Isoform 2 of Q9NVA1

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2397	Q9NVA1	2	5	7	299	34572	8.8	Basic FGF-repressed Zic-binding protein
2397	Q3KRB6	2	5	7	299	34600	8.9	Chromosome 20 open reading frame 44
2397	UPI0000D61074	2	5	6.7	313	36249	8.6	Basic FGF-repressed Zic-binding protein (bFZb).
2398	UPI0000DD79EA	2	27	9.5	273	30193	8.6	PREDICTED: similar to peptidylprolyl isomerase A isoform 1
2399	Q15427	2	15	9.4	424	44386	8.6	Splicing factor 3B subunit 4
2399	Q53FG6	2	15	9.4	424	44387	8.2	Splicing factor 3b, subunit 4 variant
2400	Q0QEY7	2	2	10.2	255	28906	8.5	Succinate dehydrogenase complex subunit B
2400	P21912	2	2	9.3	280	31630	8.8	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial precursor
2401	Q9HD15	2	8	9.3	236	25673	7	Steroid receptor RNA activator 1
2402	O75940	2	7	9.2	238	26711	7.3	Survival of motor neuron-related-splicing factor 30
2403	Q9C064	2	7	13.4	276	28417	7.6	LYST-interacting protein LIP4
2403	UPI0000457118	2	7	13.2	280	28857	7.6	Poly(rC)-binding protein 4 (Alpha-CP4).
2403	P57723-2	2	7	10.3	360	37078	8.7	Isoform 2 of P57723
2403	Q9HCU2	2	7	10	369	37858	8.4	RNA binding protein MCG10
2403	UPI0000457119	2	7	9.8	377	38834	7.2	Poly(rC)-binding protein 4 (Alpha-CP4).
2403	Q7Z4Y9	2	7	9.3	397	41345	7.9	CBP
2403	P57723	2	7	9.2	403	41482	8.2	Poly(rC)-binding protein 4
2403	Q9GZT1	2	7	8.7	424	43869	8.4	RNA binding protein MCG10
2404	Q6UX59	2	4	9.7	310	33524	9.3	DFIT212
2404	Q6IAN0	2	4	9.2	325	35089	9.6	Dehydrogenase/reductase SDR family member 7B
2404	Q9UFM6	2	4	9.2	325	35069	9.5	Hypothetical protein DKFZp566O084
2404	Q9BTF9	2	4	9.2	325	35119	9.6	Dehydrogenase/reductase (SDR family) member 7B
2405	UPI0000F0A4D4	2	5	11.7	196	21694	6.8	Cob(I)yrinic acid a,c-diamide adenosyltransfe
2405	Q96EY8	2	5	9.2	250	27388	8.6	Cob(I)yrinic acid a,c-diamide adenosyltransferase, mitochondrial precursor (EC 2.5.1.17) (Cob(I)alamin adenosyltransferase)
2406	Q9GZP9	2	8	9.2	239	27567	7.3	Derlin-2
2407	Q9NYK5	2	3	9.2	338	38722	7.6	Mitochondrial 39S ribosomal protein L39
2407	UPI00001AEE66	2	3	9.2	338	38712	7.6	Mitochondrial 39S ribosomal protein L39 (L39mt) (MRP-L39) (MRP-L5).
2407	UPI00001AEAC0	2	3	8.8	353	40458	7.9	Mitochondrial 39S ribosomal protein L39 (L39mt) (MRP-L39) (MRP-L5).
2407	Q9NYK5-2	2	3	8.8	353	40468	7.9	Isoform 2 of Q9NYK5
2408	P48507	2	3	9.1	274	30727	6	Glutamate--cysteine ligase regulatory subunit
2409	Q5TZX9	2	4	9.1	232	26616	9.2	Vesicle transport through interaction with t-SNAREs homolog 1B
2409	Q9UEU0	2	4	9.1	232	26688	9	Vesicle transport through interaction with t-SNAREs homolog 1B

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2410	Q96IZ0	2	2	9.1	340	36568	5.4	PRKC apoptosis WT1 regulator protein
2411	Q9H5L2	2	6	9.1	418	46982	6.7	CDNA: FLJ23330 fis, clone HEP12654
2411	Q9Y2T2	2	6	9.1	418	46939	6.9	AP-3 complex subunit mu-1
2412	Q96DI7	2	2	9	357	39311	8.1	WD repeat protein 57
2413	UPI0000D616A3	2	4	9.2	1256	145905	7	cytoplasmic FMR1 interacting protein 2
2413	Q96F07-2	2	4	9.2	1253	145673	7.1	Isoform 2 of Q96F07
2413	UPI0000D616A2	2	4	9.1	1258	146231	7.1	cytoplasmic FMR1 interacting protein 2
2413	Q96F07	2	4	9	1278	148398	7.3	Cytoplasmic FMR1-interacting protein 2
2414	Q99757	2	10	9	166	18383	8.3	Thioredoxin, mitochondrial precursor
2415	Q9BUT1	2	3	9	245	26724	7.6	3-hydroxybutyrate dehydrogenase type 2
2416	O43731	2	8	8.9	214	25027	8.9	ER lumen protein retaining receptor 3
2416	Q4V750	2	8	8.6	220	25648	8.1	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3
2416	O43731-2	2	8	8.6	220	25690	8.1	Isoform 2 of O43731
2417	P14550	2	12	8.9	325	36573	6.8	Alcohol dehydrogenase [NADP+]
2418	P48729	2	3	8.9	337	38915	9.6	Casein kinase I isoform alpha
2418	Q5U046	2	3	8.9	337	38905	9.6	Casein kinase 1, alpha 1
2418	P67962	2	3	8.9	337	38901	9.6	Casein kinase I isoform alpha
2418	UPI000053FD0F	2	3	8.2	365	41937	9.6	casein kinase 1, alpha 1 isoform 1
2418	Q4JJA0	2	3	8.2	365	41938	9.5	Casein kinase 1 alpha 1
2419	Q14331	2	2	8.9	258	29172	9	Protein FRG1
2420	Q15041	2	50	8.9	203	23363	9.3	ARL-6-interacting protein 1
2421	Q9H0P0	2	2	8.9	336	37948	7.1	Cytosolic 5'-nucleotidase III
2422	P17900	2	9	8.8	193	20822	5.3	Ganglioside GM2 activator precursor (GM2-AP) (Cerebroside sulfate activator protein) (Shingolipid activator protein 3) (SAP-3) [Contains: Ganglioside GM2 activator isoform short]
2422	UPI00001AEC37	2	9	8.8	193	20838	5.3	GM2 ganglioside activator precursor
2423	Q0P5W4	2	2	8.8	329	35350	9.2	RCE1 protein
2424	UPI00005D556B	2	2	9.1	296	33321	7	ubiquitin fusion degradation 1-like isoform B
2424	Q541A5	2	2	8.8	307	34500	6.7	Ubiquitin fusion degradation 1-like
2424	Q92890	2	2	7.9	343	38725	6.3	Ubiquitin fusion degradation protein 1 homolog
2425	Q9BUB7	2	11	8.8	260	28969	8.9	Transmembrane protein 70
2426	P19387	2	5	8.7	275	31441	4.9	DNA-directed RNA polymerase II 33 kDa polypeptide
2427	P80217	2	4	8.7	286	31514	6.1	Interferon-induced 35 kDa protein
2427	UPI0000200E4E	2	4	8.7	288	31777	6.1	Interferon-induced 35 kDa protein (IFP 35).
2427	P80217-2	2	4	8.7	288	31745	6.1	Isoform 2 of P80217
2428	Q4W5A9	2	4	8.7	309	34359	4.7	Hypothetical protein SET7
2428	Q8WTS6	2	4	7.4	366	40721	4.6	Histone-lysine N-methyltransferase, H3 lysine-4 specific SET7
2429	UPI000066DA0A	2	3	9.8	430	49916	6.2	Septin-8.
2429	Q92599-2	2	3	9.8	429	49814	6.1	Isoform 2 of Q92599

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2429	UPI000066DA0B	2	3	9.5	440	50928	6.2	Septin-8.
2429	UPI000020C588	2	3	9.5	442	51178	6.2	Septin-8.
2429	UPI000066DA0C	2	3	9.1	460	53163	6.5	Septin-8.
2429	Q92599	2	3	8.7	483	55756	6.3	Septin-8
2429	UPI0000457340	2	3	8.6	487	55908	6.4	Septin-8.
2430	Q96SD6	2	4	8.7	393	44071	4.8	Putative TCPTP-interacting protein
2430	Q9NVQ6	2	4	7.2	470	52118	5.1	CDNA FLJ10579 fis, clone NT2RP2003446
2430	Q96TC7	2	4	7.2	470	52070	5.1	Protein FAM82C
2431	Q0QVZ1	2	4	9.6	376	43217	8.7	Caspase-5/b
2431	P51878	2	4	8.6	418	47814	9	Caspase-5 precursor (EC 3.4.22.58) (CASP-5) (ICH-3 protease) (TY protease) (ICE(rel)-III) [Contains: Caspase-5 subunit p20; Caspase-5 subunit p10]
2431	UPI000013D0C0	2	4	8.6	418	47859	9	Caspase-5 precursor (EC 3.4.22.-) (CASP-5) (ICH-3 protease) (TY protease) (ICE(rel)-III) [Contains: Caspase-5 subunit p20; Caspase-5 subunit p10].
2431	Q6DJV7	2	4	8.6	418	47829	9	Caspase 5, apoptosis-related cysteine peptidase
2431	Q1HBJ3	2	4	8.6	418	47845	9	Caspase 5, apoptosis-related cysteine peptidase
2431	Q14DD6	2	4	8.6	418	47775	8.9	Caspase 5, apoptosis-related cysteine peptidase
2431	Q0QVZ2	2	4	8.3	434	49692	9.2	Caspase-5/a
2432	Q92665	2	3	8.6	395	45319	9.3	28S ribosomal protein S31, mitochondrial precursor
2432	UPI0000167B37	2	3	8.6	395	45318	9.4	mitochondrial ribosomal protein S31
2433	O43813	2	8	8.5	399	45283	7.8	LanC-like protein 1
2433	Q6FHH6	2	8	8.5	399	45267	7.8	LANCL1 protein
2434	Q15773	2	4	8.5	248	28147	6.9	Myeloid leukemia factor 2
2435	Q8IUR0	2	2	8.5	188	20783	9.7	Trafficking protein particle complex subunit 5
2436	Q9BTY7	2	3	8.5	390	42129	4.8	Brain protein 16
2436	UPI000013EBB5	2	3	8.5	390	42128	4.8	PREDICTED: similar to brain protein 16
2437	Q5VWZ2	2	4	8.4	237	26316	7.8	Lysophospholipase-like protein 1
2437	UPI00000709FC	2	4	8.4	237	26334	7.8	lysophospholipase-like 1
2438	O75911	2	4	8.3	302	33548	8.8	Short-chain dehydrogenase/reductase 3
2439	O95456-2	2	2	9	267	30288	7.8	Isoform 2 of O95456
2439	O95456	2	2	8.3	288	32854	7.2	Down syndrome critical region protein 2
2439	Q6FHA3	2	2	8.3	288	32840	7.2	DSCR2 protein
2440	O95758	2	3	8.3	521	56502	9.2	Regulator of differentiation 1
2440	Q5T8V9	2	3	8.2	524	56821	9.2	ROD1 regulator of differentiation 1
2440	Q5T4E6	2	3	7.8	552	59690	9	ROD1 regulator of differentiation 1
2440	O95758-2	2	3	7	614	66234	9.5	Isoform 2 of O95758
2441	P06730	2	6	8.3	217	25097	6.1	Eukaryotic translation initiation factor 4E
2441	Q32Q75	2	6	8.3	217	25067	6.1	Eukaryotic translation initiation factor 4E
2442	UPI0000DD7AE9	2	10	10.1	268	31695	8.8	PREDICTED: similar to LIM and senescent cell antigen-like domains 1

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
2442	P48059	2	10	8.3	325	37251	8	LIM and senescent cell antigen-like-containing domain protein 1
2442	UPI0000207FB5	2	10	7	387	44390	8	LIM and senescent cell antigen-like-containing domain protein 1 (Particularly interesting new Cys-His protein 1) (PINCH-1) (Renal carcinoma antigen NY-REN-48).
2442	UPI0000DBEE50	2	10	6.8	396	45508	7.9	LIM and senescent cell antigen-like-containing domain protein 3 (Particularly interesting new Cys-His protein 3) (PINCH-3).
2443	Q7Z5U4	2	7	8.3	277	32166	9.4	SDAD1 protein
2443	Q32Q11	2	7	8.2	279	32423	9.5	Hypothetical protein
2444	Q86TR7	2	13	8.2	279	30962	4.8	Uncharacterized protein C14orf151
2445	Q8N4L2	2	2	8.2	257	28081	8.7	Transmembrane protein 55A
2446	UPI0000D6168C	2	4	14.8	142	16349	4.2	Protein YIPF5 (YIP1 family member 5) (YPT-interacting protein 1 A) (Five-pass transmembrane protein localizing in the Golgi apparatus and the endoplasmic reticulum 5) (Smooth muscle cell-associated protein 5) (SMAP-5).
2446	Q969M3	2	4	8.2	257	27989	4.4	Protein YIPF5
2446	Q969M3-3	2	4	7.9	265	29107	4.5	Isoform 3 of Q969M3
2446	UPI0000D6168B	2	4	7.8	270	29739	4.5	Protein YIPF5 (YIP1 family member 5) (YPT-interacting protein 1 A) (Five-pass transmembrane protein localizing in the Golgi apparatus and the endoplasmic reticulum 5) (Smooth muscle cell-associated protein 5) (SMAP-5).
2447	Q9HD42	2	3	8.2	196	21703	8.1	Charged multivesicular body protein 1a
2448	P57764	2	9	8.1	484	52801	5.1	Gasdermin domain-containing protein 1
2449	Q15300	2	2	8.1	593	67050	6.2	RET tyrosine kinase/cAMP protein kinase A subunit RI
2450	Q9NZJ9	2	5	10.6	180	20306	6.4	Diphosphoinositol polyphosphate phosphohydrolase 2
2450	Q4AEJ6	2	5	8.1	234	25951	6.8	KIAA0487 protein
2451	Q9NXR1-2	2	4	8.4	335	37721	5.2	Isoform 2 of Q9NXR1
2451	Q9NXR1	2	4	8.1	346	38808	5.3	Nuclear distribution protein nudE homolog 1
2452	O94903	2	3	8	275	30344	7.5	Proline synthetase co-transcribed bacterial homolog protein
2453	Q53GS5	2	4	8	352	39934	4.5	SYAP1 protein variant
2453	Q96A49	2	4	8	352	39933	4.5	Synapse-associated protein 1
2454	Q5XKR6	2	14	8	373	41385	7.9	AUP1 protein
2454	UPI0000D611C1	2	14	8	375	41670	8.3	Ancient ubiquitous protein 1 precursor.
2454	Q68CX8	2	14	8	375	41587	8.3	Hypothetical protein DKFZp686P12272
2454	Q9Y679-2	2	14	7.3	410	45787	8.6	Isoform Short of Q9Y679

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
2454	UPI000013CFAF	2	14	6.3	474	52751	7.9	Ancient ubiquitous protein 1 precursor.
2454	Q9Y679	2	14	6.3	476	53028	8.1	Ancient ubiquitous protein 1 precursor
2455	Q6ZWP6	2	3	8	288	31024	9.1	CDNA FLJ90159 fis, clone HEMBB1002465, weakly similar to ACYL-COA DEHYDROGENASE
2455	Q9UKU7	2	3	5.5	415	45070	7.9	Acyl-CoA dehydrogenase family member 8, mitochondrial precursor
2456	Q9BTE7	2	2	8	237	27508	5.6	DCN1-like protein 5
2457	P51553	2	3	7.9	393	42794	8.5	Isocitrate dehydrogenase [NAD] subunit gamma, mitochondrial precursor (EC 1.1.1.41) (Isocitric dehydrogenase) (NAD(+)-specific ICDH)
2458	Q05048	2	2	7.9	431	48358	6.6	Cleavage stimulation factor 50 kDa subunit
2459	Q2LE81	2	3	9	244	25882	9.2	NADP(H)-dependent retinol dehydrogenase/reductase B1 isoform
2459	Q9BTZ2	2	3	8.5	260	27572	7.8	Dehydrogenase/reductase SDR family member 4
2459	Q20CR0	2	3	7.9	278	29537	8.5	NADP(H)-dependent retinol dehydrogenase/reductase short isoform
2459	Q71UQ6	2	3	7.9	278	29531	8.5	Hep27-like protein
2460	O60684	2	2	7.8	536	60030	5	Importin alpha-7 subunit
2460	UPI0000D61EBB	2	2	7.8	539	60342	5	Importin alpha-7 subunit (Karyopherin alpha-6).
2461	Q15102	2	5	7.8	231	25734	6.8	Platelet-activating factor acetylhydrolase IB subunit gamma
2462	Q96KB5	2	5	7.8	322	36085	5.1	T-lymphokine-activated killer cell-originated protein kinase
2463	Q9NVT9	2	8	7.8	282	31281	5.8	Armadillo repeat-containing protein 1
2464	O95218-2	2	5	8.4	311	35304	8.8	Isoform ZIS
2464	Q59F92	2	5	8.2	316	36032	9.8	Zinc finger protein 265 isoform 1 variant
2464	Q5VV33	2	5	8.1	320	36318	9.8	Zinc finger, RAN-binding domain containing 2
2464	Q5VV34	2	5	7.9	330	37404	10	Zinc finger, RAN-binding domain containing 2
2464	Q53GS3	2	5	7.9	330	37332	10.1	Zinc finger protein 265 isoform 1 variant
2464	O95218	2	5	7.7	337	38223	8.7	Zinc finger Ran-binding domain-containing protein 2
2464	UPI000013F68D	2	5	7.7	336	38136	8.7	Zinc finger Ran-binding domain-containing protein 2 (Zinc finger protein 265) (Zinc finger, splicing).
2465	P27707	2	3	7.7	260	30519	5.2	Deoxycytidine kinase
2465	Q5TZY7	2	3	7.7	260	30509	5.2	Deoxycytidine kinase
2465	UPI0000F0E9A9	2	3	7.1	280	32618	6.1	deoxycytidine kinase
2466	Q6P147	2	14	7.7	286	31668	8.8	Cytochrome b reductase 1
2466	Q9H0Q8	2	14	7.7	286	31638	9	Hypothetical protein DKFZp564E227
2467	Q8NFH5	2	2	7.7	326	34774	9.1	Nucleoporin NUP53
2468	UPI000041C7E5	2	6	8.9	305	34756	8.4	replication factor C 3 isoform 2
2468	P40938	2	6	7.6	356	40556	8.3	Replication factor C subunit 3

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2468	Q5U0C2	2	6	7.6	356	40570	8.3	Replication factor C (Activator 1) 3, 38kDa
2469	P42126-2	2	6	8.1	285	30896	8.9	Isoform 2 of P42126
2469	P42126	2	6	7.6	302	32816	8.6	3,2-trans-enoyl-CoA isomerase, mitochondrial precursor (EC 5.3.3.8) (Dodecenoyl-CoA isomerase) (Delta(3),Delta(2)-enoyl-CoA isomerase)
2470	Q13557-8	2	6	7.9	478	54128	7.3	Isoform Delta 6 of Q13557
2470	UPI0000D615AE	2	6	7.8	489	55378	7.7	Calcium/calmodulin-dependent protein kinase type II delta chain (EC 2.7.11.17) (CaM-kinase II delta chain) (CaM kinase II subunit delta) (CaMK-II subunit delta).
2470	Q13557-9	2	6	7.8	488	55250	7.6	Isoform Delta 7 of Q13557
2470	Q13557	2	6	7.6	499	56369	7.2	Calcium/calmodulin-dependent protein kinase type II delta chain
2470	Q13557-5	2	6	7.6	497	56102	7.3	Isoform Delta 8 of Q13557
2470	Q13557-11	2	6	7.6	498	56298	7.2	Isoform Delta 11 of Q13557
2470	Q13557-3	2	6	7.5	509	57492	7.5	Isoform Delta 3 of Q13557
2470	Q13557-6	2	6	7.4	512	57773	7	Isoform Delta 9 of Q13557
2470	Q13557-4	2	6	7.3	518	58344	7.2	Isoform Delta 4 of Q13557
2471	Q53HT2	2	21	7.5	279	32633	9.6	Elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1 variant
2471	Q9BW60	2	21	7.5	279	32663	9.6	Elongation of very long chain fatty acids protein 1
2471	Q8WXU3	2	21	7.5	279	32637	9.6	SSC1/ELOVL1
2472	Q7Z528	2	4	7.5	266	30425	5.2	E3-16
2472	Q9Y287	2	4	7.5	266	30338	5.1	Integral membrane protein 2B (Transmembrane protein BRI) [Contains: ABri/ADan amyloid peptide]
2472	Q9NX12	2	4	7.5	266	30312	5.2	CDNA FLJ20496 fis, clone KAT08729
2472	Q96B24	2	4	7.5	266	30368	5.1	Integral membrane protein 2B
2473	Q8IVD9	2	6	7.5	361	40822	5.3	NudC domain-containing protein 3
2474	Q8IVM0	2	3	7.5	306	35822	6.7	Coiled-coil domain-containing protein 50
2474	Q8IVM0-2	2	3	4.8	482	56340	8.2	Isoform 2 of Q8IVM0
2475	Q9H446	2	4	7.4	243	27939	4.2	RWD domain-containing protein 1
2476	A0SZW4	2	3	7.5	322	36792	6.4	Aryl hydrocarbon receptor interacting protein
2476	A0SZW3	2	3	7.3	330	37666	6.2	Aryl hydrocarbon receptor interacting protein
2476	UPI000013DBC1	2	3	7.3	330	37636	6.3	AH receptor-interacting protein (AIP) (Aryl-hydrocarbon receptor-interacting protein) (Immunophilin homolog ARA9) (HBV-X-associated protein 2).
2476	O00170	2	3	7.3	330	37664	6.5	AH receptor-interacting protein
2476	A0SZW6	2	3	7.3	330	37617	6.2	Aryl hydrocarbon receptor interacting protein
2476	A0SZW5	2	3	7.3	330	37637	6	Aryl hydrocarbon receptor interacting protein
2477	Q5T6G5	2	2	9	268	29411	4.6	DNAation factor, 45kDa, alpha polypeptide

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2477	O00273	2	2	7.3	331	36522	4.8	DNA fragmentation factor subunit alpha
2477	Q53HN4	2	2	7.3	331	36594	4.8	DNAation factor, 45kDa, alpha polypeptide isoform 1 variant
2478	P49023-2	2	4	7.7	557	60937	6.4	Isoform Alpha of P49023
2478	P49023	2	4	7.3	591	64533	6.1	Paxillin
2478	UPI00001AE664	2	4	7.3	587	64031	6.4	Paxillin.
2478	UPI0000D62268	2	4	7.2	601	65738	6.5	Paxillin.
2478	P49023-3	2	4	7.1	605	66183	6.4	Isoform Gamma of P49023
2479	O00115	2	5	7.2	360	39581	8	Deoxyribonuclease-2-alpha precursor
2480	O00625	2	12	7.2	290	32113	6.9	Pirin
2480	Q6FHD2	2	12	7.2	290	32157	6.8	PIR protein
2481	UPI0000D61CD4	2	3	7.9	430	47710	5.1	Nuclear-interacting partner of ALK (Nuclear-interacting partner of anaplastic lymphoma kinase) (hNIPA) (Zinc finger C3HC-type protein 1).
2481	Q86WB0-3	2	3	7.9	431	47771	5.2	Isoform 3 of Q86WB0
2481	A4D1L4	2	3	7.1	481	53603	6.2	Nuclear interacting partner of anaplastic lymphoma kinase
2481	UPI0000457601	2	3	7.1	480	53498	6.2	Nuclear-interacting partner of ALK (Nuclear-interacting partner of anaplastic lymphoma kinase) (hNIPA) (Zinc finger C3HC-type protein 1).
2481	Q86WB0-2	2	3	7.1	481	53559	6.4	Isoform 2 of Q86WB0
2481	UPI0000457602	2	3	6.8	501	55200	5.5	Nuclear-interacting partner of ALK (Nuclear-interacting partner of anaplastic lymphoma kinase) (hNIPA) (Zinc finger C3HC-type protein 1).
2481	Q86WB0	2	3	6.8	502	55262	5.6	Nuclear-interacting partner of ALK
2482	Q6FIC8	2	10	9.5	241	26900	7.6	DNAJB6 protein (DnaJ (Hsp40) homolog, subfamily B, member 6)
2482	O75190	2	10	7.1	326	36087	9.1	DnaJ homolog subfamily B member 6
2482	Q53EN8	2	10	7.1	326	36117	9.1	DnaJ (Hsp40) homolog, subfamily B, member 6 isoform a variant
2482	Q59EF2	2	10	6.9	335	36772	7.2	DnaJ (Hsp40) homolog, subfamily B, member 6 isoform a variant
2483	Q5TAW7	2	4	7.1	280	32424	7.5	Calcium binding protein 39-like
2483	Q9H9S4	2	4	5.9	337	39088	8.4	Calcium-binding protein 39-like
2484	Q96EM0	2	3	7.1	354	38168	6.6	Uncharacterized protein C14orf149
2484	Q96LJ5	2	3	7.1	354	38138	6.7	CDNA FLJ25436 fis, clone TST08261
2485	O60362	2	3	7	242	27310	8.9	Hypothetical protein 44M2.1
2485	Q9NXG2	2	3	4.8	353	39315	7.9	THUMP domain-containing protein 1
2485	UPI000059D337	2	3	3.9	439	48549	8.8	THUMP domain-containing protein 1.
2485	Q6MZT3	2	3	3.9	439	48491	8.9	Hypothetical protein DKFZp686C1054
2486	Q15813	2	2	7	527	59346	6.8	Tubulin-specific chaperone E
2487	Q16254	2	2	7	413	43960	4.7	Transcription factor E2F4

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2487	UPI0000D61A05	2	2	7	417	44403	4.8	Transcription factor E2F4 (E2F-4).
2488	Q7L5D6	2	3	7	327	36504	5.4	UPF0363 protein C7orf20
2489	A2AB02	2	5	6.9	261	29460	8.6	Nurim
2489	Q8IXM6	2	5	6.9	262	29379	8.6	Nurim
2490	P42574	2	11	6.9	277	31608	6.5	Caspase-3 precursor (EC 3.4.22.56) (CASP-3) (Apopain) (Cysteine protease CPP32) (Yama protein) (CPP-32) (SREBP cleavage activity 1) (SCA-1) [Contains: Caspase-3 p17 subunit; Caspase-3 p12 subunit]
2491	Q9NZX8	2	2	9.1	352	40091	5	HSPC058
2491	Q6AI06	2	2	8.1	394	45424	8.8	Hypothetical protein DKFZp781F2227
2491	Q3ZTU1	2	2	6.9	466	52985	6.4	CTD small phosphatase-like protein 2
2491	Q9P030	2	2	6.9	466	53129	6.6	HSPC129
2491	Q8IYI9	2	2	6.9	466	52999	6.4	CTDSPL2 protein
2492	Q5T7L6	2	2	10.3	242	28001	5.1	Stromal cell derived factor 4
2492	UPI000045610D	2	2	9.8	254	27868	5.8	45 kDa calcium-binding protein precursor (Cab45) (Stromal cell-derived factor 4) (SDF-4).
2492	Q9UN53	2	2	9.8	254	27826	5.8	Calcium binding protein
2492	Q5T7L8	2	2	7.2	348	39608	5.1	Stromal cell derived factor 4
2492	Q53G52	2	2	6.9	362	41819	4.9	Calcium binding protein Cab45 variant
2492	Q9BRK5	2	2	6.9	362	41807	4.9	45 kDa calcium-binding protein precursor
2492	Q53HQ9	2	2	6.9	362	41777	4.9	Calcium binding protein Cab45 variant
2493	Q5JB52	2	3	7.3	508	56467	7.6	Stromal RNA regulating factor
2493	Q5JB51	2	3	6.9	537	59648	7.7	Stromal RNA regulating factor
2493	Q8WVV9	2	3	6.8	542	60083	7.7	Heterogeneous nuclear ribonucleoprotein L-like
2494	Q86U42-2	2	7	7.1	296	31497	5	Isoform 2 of Q86U42
2494	Q86U42	2	7	6.9	306	32749	5.1	Polyadenylate-binding protein 2 (Poly(A)-binding protein 2) (Poly(A)-binding protein II) (PABII) (Polyadenylate-binding nuclear protein 1) (Nuclear poly(A)-binding protein 1)
2495	Q9H0V9	2	4	6.9	348	39711	8.4	VIP36-like protein precursor
2495	Q9H0V9-2	2	4	6.7	359	40982	8.9	Isoform 2 of Q9H0V9
2496	Q9H9J2	2	4	6.9	332	37535	8.4	39S ribosomal protein L44, mitochondrial precursor
2497	Q9NQZ2	2	6	6.9	479	54558	5.6	Something about silencing protein 10
2498	A0AUJ8	2	3	6.8	365	41750	9	MGC21874 protein
2499	O43819	2	8	6.8	266	29810	8.9	SCO2 protein homolog, mitochondrial precursor
2499	UPI0000167B35	2	8	6.8	266	29751	8.6	cytochrome oxidase deficient homolog 2
2500	Q8TAF6	2	5	7.2	670	74422	8	Acyl-CoA synthetase 4
2500	O60488	2	5	6.8	711	79188	8.4	Long-chain-fatty-acid--CoA ligase 4
2501	P51398	2	2	6.8	398	45566	8.9	Mitochondrial 28S ribosomal protein S29
2502	Q13287	2	2	6.8	307	35057	5.3	N-myc-interactor
2502	UPI000002FDB7	2	2	6.8	307	35117	5.3	N-myc and STAT interactor
2502	Q8WTW2	2	2	6.8	307	35085	5.3	N-myc (And STAT) interactor
2503	Q96SI1	2	3	6.7	283	31942	7.4	BTB/POZ domain-containing protein KCTD15

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
2504	Q9UNQ2	2	2	6.7	313	35236	10	Probable dimethyladenosine transferase (EC 2.1.1.-) (S-adenosylmethionine-6-N',N'-adenosyl(rRNA) dimethyltransferase)
2505	O00743	2	2	6.6	305	35144	5.7	Serine/threonine-protein phosphatase 6
2505	Q9UIC9	2	2	6.6	303	34814	5.9	Serine/threonine protein phosphatase catalytic subunit
2506	P20933	2	2	6.6	346	37194	6.3	N(4)-(beta-N-acetylglucosaminyl)-L asparaginase precursor (EC 3.5.1.26) (Glycosylasparaginase) (Aspartylglucosaminidase) (N4-(N-acetyl-beta-glucosaminyl)-L-asparagine amidase) (AGA) [Contains: Glycosylasparaginase alpha chain; Glycosylasparaginase beta chain]
2506	UPI000013D53C	2	2	6.6	346	37208	6.3	N(4)-(beta-N-acetylglucosaminyl)-L asparaginase precursor (EC 3.5.1.26) (Glycosylasparaginase) (Aspartylglucosaminidase) (N4-(N-acetyl-beta-glucosaminyl)-L-asparagine amidase) (AGA) [Contains: Glycosylasparaginase alpha chain; Glycosylasparaginase beta c
2507	P29279	2	2	6.6	349	38091	8	Connective tissue growth factor precursor
2507	Q6FHL8	2	2	6.6	349	38129	7.9	CTGF protein
2507	Q5M8T4	2	2	6.6	349	38069	7.9	Connective tissue growth factor
2508	P30740	2	2	6.6	379	42742	6.3	Leukocyte elastase inhibitor
2509	Q15007	2	3	6.6	396	44244	5.2	Wilms' tumor 1-associating protein (WT1-associated protein) (Putative pre-mRNA-splicing regulator female-lethal(2D) homolog)
2510	UPI0000DD7C47	2	5	9.5	211	24434	11.8	PREDICTED: similar to ribonucleic acid binding protein S1 isoform 1
2510	UPI00006C085C	2	5	7.1	282	31610	11.9	PREDICTED: similar to ribonucleic acid binding protein S1 isoform 7
2510	UPI0000237318	2	5	7.1	282	31591	11.8	PREDICTED: similar to ribonucleic acid binding protein S1
2510	Q15287-2	2	5	7.1	282	31709	11.9	Isoform 2 of Q15287
2510	Q15287	2	5	6.6	305	34208	11.8	RNA-binding protein with serine-rich domain 1
2510	UPI00006C085B	2	5	6.6	305	34109	11.8	PREDICTED: similar to ribonucleic acid binding protein S1 isoform 3
2510	UPI00001618F9	2	5	6.6	305	34090	11.8	PREDICTED: similar to ribonucleic acid binding protein S1
2511	Q86XZ2	2	4	7.1	435	50738	6.7	PPP2R5E protein
2511	Q58EX4	2	4	7	441	51523	7.4	PPP2R5E protein

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2511	Q16537	2	4	6.6	467	54699	6.9	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit epsilon isoform
2511	Q562F2	2	4	6.6	467	54681	6.9	Protein phosphatase 2, regulatory subunit B', epsilon isoform
2511	Q3ZCW9	2	4	6.6	467	54704	7.2	PPP2R5E protein
2511	Q59EK0	2	4	6.2	501	57956	8.2	Epsilon isoform of regulatory subunit B56, protein phosphatase 2A variant
2512	Q9UBP9	2	2	6.6	304	34490	7.9	GULP engulfment adaptor PTB domain-containing protein 1
2513	Q9UMY1	2	2	6.6	257	29426	9.7	Nucleolar protein 7
2514	Q9H0E2	2	9	8.4	274	30282	6	Toll-interacting protein
2514	Q59FB9	2	9	6.5	352	38895	8.5	Toll interacting protein variant
2514	UPI0000D6257D	2	9	6.5	355	39151	8.8	Toll-interacting protein.
2515	Q5HYL6	2	5	6.5	352	39555	5.2	Hypothetical protein DKFZp686E1899
2515	Q9NYL9	2	5	6.5	352	39595	5.2	Tropomodulin-3
2516	Q6UXH1-3	2	2	8.1	284	30712	5.1	Isoform 3 of Q6UXH1
2516	Q6UXH1-2	2	2	7.2	321	34958	4.6	Isoform 2 of Q6UXH1
2516	Q6UXH1-4	2	2	7.1	325	35288	4.7	Isoform 4 of Q6UXH1
2516	Q6UXH1	2	2	6.5	353	38192	4.6	Cysteine-rich with EGF-like domain protein 2 precursor
2516	UPI000018CEC3	2	2	6.5	353	38104	4.6	cysteine-rich with EGF-like domains 2
2516	Q6UXH1-6	2	2	6.2	373	40491	4.8	Isoform 6 of Q6UXH1
2516	Q6UXH1-5	2	2	5.7	402	43579	4.8	Isoform 5 of Q6UXH1
2517	Q96MH6-2	2	3	8.2	257	29542	7.4	Isoform 2 of Q96MH6
2517	Q96MH6	2	3	6.5	324	37425	7.9	Transmembrane protein 68
2518	Q9C0B1	2	8	6.5	507	58456	5.2	KIAA1752 protein
2518	UPI000013D7B3	2	8	6.5	505	58282	5.2	fatso
2519	Q6ZTV1	2	2	10.8	362	39472	5.9	CDNA FLJ44194 fis, clone THYMU2040975, weakly similar to PTB- ASSOCIATED SPLICING FACTOR
2519	A2AIB8	2	2	6.4	613	68042	5.5	KIAA1949
2519	UPI00006C0AE4	2	2	6.4	613	67844	5.4	PREDICTED: similar to Protein KIAA1949 isoform 7
2519	Q6NYC8	2	2	6.4	613	67943	5.4	Uncharacterized protein KIAA1949
2520	O75683	2	4	6.4	361	41450	10.6	Surfeit locus protein 6
2521	Q53GI6	2	8	6.4	437	50409	4.8	Synaptonemal complex protein SC65 variant
2521	Q92791	2	8	6.4	437	50381	4.8	Nucleolar autoantigen No55
2522	O14817	2	5	6.3	238	26118	6.5	Tetraspanin-4
2523	P15586	2	3	6.3	552	62082	8.3	N-acetylglucosamine-6-sulfatase precursor
2524	P25774	2	6	6.3	331	37496	8.3	Cathepsin S precursor
2524	Q6FHS5	2	6	6.3	331	37526	8.2	CTSS protein
2525	Q86WV4	2	4	8.3	302	35148	9.1	MRPS9 protein
2525	P82933	2	4	6.3	396	45823	9.6	28S ribosomal protein S9, mitochondrial precursor
2525	Q6PG40	2	4	6.3	396	45835	9.5	Mitochondrial ribosomal protein S9
2526	Q9NWL0	2	2	8.2	280	31863	5.3	CDNA FLJ20758 fis, clone HEP01508
2526	Q597H0	2	2	6.3	367	41893	6.3	Transformation-related protein 15
2526	Q658Y9	2	2	6.3	367	41919	6.3	Hypothetical protein DKFZp666K071
2526	Q9BUZ8	2	2	5.7	402	46050	6.2	PTCD3 protein

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
2526	UPI0000456DED	2	2	3.3	690	78624	6.4	Pentatricopeptide repeat domain 3
2526	Q96EY7	2	2	3.3	689	78550	6.4	Pentatricopeptide repeat domain-containing protein 3
2527	Q05D88	2	4	6.2	453	53181	9.4	Hypothetical protein
2527	Q9Y5B6-2	2	4	3.4	815	93170	5.7	Isoform B of Q9Y5B6
2527	Q9Y5B6	2	4	3.1	917	104804	5.7	GC-rich sequence DNA-binding factor homolog
2528	Q13190-3	2	2	8.2	267	29887	9.2	Isoform 3 of Q13190
2528	UPI0000DD80F5	2	2	7.5	295	33137	8	PREDICTED: similar to Syntaxin-5
2528	Q13190	2	2	6.2	355	39673	9.2	Syntaxin-5
2529	Q92604	2	2	6.2	370	43089	8.9	Acyl-CoA:lysophosphatidylglycerol acyltransferase 1
2530	Q96G21	2	3	6.2	291	33757	9.5	U3 small nucleolar ribonucleoprotein protein IMP4
2531	Q96JY6	2	7	6.2	352	37459	8.7	PDZ and LIM domain protein 2
2531	Q96JY6-3	2	7	6	366	39181	8.9	Isoform 3 of Q96JY6
2532	Q9BRJ2	2	4	6.2	306	35351	9	39S ribosomal protein L45, mitochondrial precursor
2532	UPI00001AEFFB	2	4	6.2	306	35243	9	mitochondrial ribosomal protein L45
2533	Q9NX31	2	5	6.2	292	31779	8.5	Uncharacterized protein C20orf111
2534	Q8WYK3	2	2	6.8	279	31759	7	Thymidylate synthase
2534	P04818	2	2	6.1	313	35716	7	Thymidylate synthase
2534	Q53FB7	2	2	6.1	313	35717	6.8	Thymidylate synthetase variant
2535	P09110	2	13	6.1	424	44292	8.4	3-ketoacyl-CoA thiolase, peroxisomal precursor
2536	Q53GY5	2	3	6.1	570	64487	6.7	DiGeorge syndrome critical region gene 8 variant
2537	Q6N049	2	8	6.1	477	54252	6.9	Hypothetical protein DKFZp686A05136
2537	Q8N404	2	8	6.1	477	54224	6.8	ZWILCH protein
2537	UPI000013EC73	2	8	4.9	591	67214	6.3	Zwilch
2537	Q9H900	2	8	4.9	591	67283	6.3	Protein zwilch homolog
2538	O00330	2	8	6	501	54122	8.7	Pyruvate dehydrogenase protein X component, mitochondrial precursor
2538	UPI0000168268	2	8	6	501	54208	8.8	pyruvate dehydrogenase complex, component X
2539	P42785	2	8	6	496	55800	7.2	Lysosomal Pro-X carboxypeptidase precursor
2539	UPI00001FB052	2	8	5.8	517	58100	7.4	prolylcarboxypeptidase isoform 2 preproprotein
2540	Q13547	2	8	6	482	55103	5.5	Histone deacetylase 1
2541	Q59FY9	2	10	6	600	66739	5.7	LEPREL2 protein variant
2541	UPI00001AF55A	2	10	4.9	735	81723	6.3	Probable G-protein coupled receptor 162 (Gene-rich cluster gene A protein).
2541	Q8IVL6	2	10	4.9	736	81837	6.3	Prolyl 3-hydroxylase 3 precursor
2542	Q5TDH0	2	2	6	399	44523	5	DNA-damage inducible protein 2
2542	Q7RTZ0	2	2	5.7	419	46571	5.1	Protein DDI1 homolog 2
2543	Q9Y2S7	2	2	6	368	42033	8.6	Polymerase delta-interacting protein 2
2543	UPI000013C4D8	2	2	6	367	41934	8.6	Polymerase delta-interacting protein 2 (38 kDa DNA polymerase delta interaction protein) (p38).
2544	Q8N6T3-3	2	6	6.1	396	43776	8.5	Isoform 3 of Q8N6T3

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
2544	Q53F62	2	6	5.9	406	44669	5.4	ADP-ribosylation factor GTPase activating protein 1 isoform a variant
2544	Q8N6T3	2	6	5.9	406	44668	5.7	ADP-ribosylation factor GTPase-activating protein 1
2544	Q8N6T3-2	2	6	5.8	414	45676	5.8	Isoform 2 of Q8N6T3
2545	Q53FV3	2	4	5.9	406	46268	6.1	COP9 signalosome subunit 4 variant
2545	Q9BT78	2	4	5.9	406	46269	5.8	COP9 signalosome complex subunit 4
2546	A4D0U6	2	5	5.8	412	46910	7.6	Testis derived transcript
2546	Q9UGI8	2	5	5.7	421	47996	7.7	Testin
2547	Q9NYD2	2	3	10.8	195	21589	8.8	Hepatocellular carcinoma-associated antigen 64
2547	Q59E94	2	3	9.1	232	25830	7.2	Peroxisomal D3,D2-enoyl-CoA isomerase isoform 1 variant
2547	O75521	2	3	5.8	359	39609	8.6	Peroxisomal 3,2-trans-enoyl-CoA isomerase (EC 5.3.3.8) (Dodecenoyl-CoA isomerase) (Delta(3),delta(2)-enoyl-CoA isomerase)
2547	Q6IBN4	2	3	5.8	364	40193	8.8	PECI protein
2547	Q53HG3	2	3	5.8	364	40111	8.9	Peroxisomal D3,D2-enoyl-CoA isomerase isoform 1 variant
2547	Q53GC8	2	3	5.8	364	40211	8.8	Peroxisomal D3,D2-enoyl-CoA isomerase isoform 1 variant
2548	Q13325	2	2	5.8	482	55847	7.4	Interferon-induced protein with tetratricopeptide repeats 5
2548	Q6IAX3	2	2	5.8	482	55874	7.4	IFIT5 protein
2549	Q6P1J9	2	2	5.8	531	60577	9.6	Parafibromin
2549	UPI0000D62067	2	2	5.8	531	60577	9.7	Parafibromin (Cell division cycle protein 73 homolog) (Hyperparathyroidism 2 protein).
2550	Q9UFF2	2	2	8.4	237	25759	8.3	Hypothetical protein DKFZp434L2027
2550	Q9H686	2	2	5.8	347	37754	9	CDNA: FLJ22500 fis, clone HRC11301
2550	Q9NWS9	2	2	4.4	450	48957	6.1	Zinc finger protein 446
2551	Q9Y6X3-3	2	2	15.9	189	21268	6.7	Isoform 3 of Q9Y6X3
2551	Q9Y6X3-2	2	2	13.8	218	24654	6.7	Isoform 2 of Q9Y6X3
2551	Q9Y4B3	2	2	5.8	514	58310	6.8	R29828_1
2551	UPI0000456C51	2	2	5.8	513	58097	6.8	K0892_HUMAN Isoform 2 of Q9Y6X3 - Homo sapiens (Human)
2551	Q9Y6X3	2	2	4.9	613	69082	7.3	Uncharacterized protein KIAA0892 precursor
2552	UPI00005A6223	2	9	5.8	394	43882	5.3	AP-3 complex subunit sigma-2 (Adapter-related protein complex 3 sigma- 2 subunit) (Sigma-adaptin 3b) (AP-3 complex sigma-3B subunit) (Sigma- 3B-adaptin).
2553	Q5TDC2	2	2	5.9	357	39099	7.3	Mitochondrial carrier homolog 1
2553	UPI0000140C95	2	2	5.8	362	39884	8.9	Mitochondrial carrier homolog 1 (Presenilin-associated protein).
2553	Q9Y374	2	2	5.8	363	40039	8.9	CGI-64 protein
2553	A4FVA6	2	2	5.7	370	39759	9.5	MTCH1 protein
2553	Q9NZJ7-2	2	2	5.6	372	39920	9.5	Isoform 2 of Q9NZJ7
2553	Q9NZJ7	2	2	5.4	389	41544	9.3	Mitochondrial carrier homolog 1

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2553	UPI0000D6143C	2	2	5.1	409	44618	9	Mitochondrial carrier homolog 1 (Presenilin-associated protein).
2553	Q8IW90	2	2	5.1	409	44619	9.1	MTCH1 protein
2554	Q8NFG7	2	5	6	318	36157	9.2	Alpha 2,3 sialyltransferase IV type A2-12
2554	Q11206-3	2	5	5.9	322	36745	9.2	Isoform 3 of Q11206
2554	Q8N6A6	2	5	5.8	328	37228	9.2	Alpha 2,3-sialyltransferase IV type A1-12
2554	Q6IBE6	2	5	5.8	329	37458	9.4	SIAT4C protein
2554	Q11206	2	5	5.7	333	38045	9.4	CMP-N-acetylneuraminate-beta-galactosamide-alpha-2,3-sialyltransferase
2554	Q11206-2	2	5	5.7	332	37816	9.2	Isoform 2 of Q11206
2554	UPI00004565A6	2	5	5.6	339	38649	9.3	CMP-N-acetylneuraminate-beta-galactosamide-alpha-2,3-sialyltransferase (EC 2.4.99.-) (Beta-galactoside alpha-2,3-sialyltransferase) (Alpha 2,3-sialyltransferase IV) (Alpha 2,3-ST) (Gal-NAc6S) (STZ) (SIAT4-C) (ST3Gal III) (SAT-3) (ST-4).
2554	Q8NFD3	2	5	5.6	338	38431	9.2	Alpha-2,3-sialyltransferase IV type A1+18
2554	Q11206-4	2	5	5.6	339	38660	9.4	Isoform 4 of Q11206
2554	UPI000013CA87	2	5	5.3	356	40914	9.4	CMP-N-acetylneuraminate-beta-galactosamide-alpha-2,3-sialyltransferase (EC 2.4.99.-) (Beta-galactoside alpha-2,3-sialyltransferase) (Alpha 2,3-sialyltransferase IV) (Alpha 2,3-ST) (Gal-NAc6S) (STZ) (SIAT4-C) (ST3Gal III) (SAT-3) (ST-4).
2554	Q9HAA9	2	5	5.3	356	40930	9.4	CDNA FLJ11867 fis, clone HEMBA1006976, weakly similar to H.sapiens Gal-beta(1-3/1-4)GlcNAc alpha-2.3-sialyltransferase
2555	Q14376	2	5	5.7	348	38282	6.7	UDP-glucose 4-epimerase
2556	Q15035	2	4	5.7	370	43328	9.2	Translocation-associated membrane protein 2
2557	Q9NUM4	2	9	6.6	274	31127	7	Transmembrane protein 106B
2557	Q8N353	2	9	5.7	314	35137	8.2	TMEM106B protein
2558	Q9H3P7	2	2	5.7	528	60593	5.1	Golgi resident protein GCP60
2559	O95905	2	4	5.6	644	72758	4.9	SGT1 protein
2559	Q6I9U8	2	4	5.6	644	72710	4.9	HSGT1 protein
2560	Q658J0	2	3	6.3	332	37029	6.5	Hypothetical protein DKFZp762L015
2560	Q9GZT8	2	3	6	350	38984	6.4	NIF3-like protein 1
2560	Q53TX4	2	3	5.6	377	41968	6.7	Hypothetical protein NIF3L1
2561	Q9BT22	2	4	5.6	464	52518	7.2	Chitobiosyldiphosphodolichol beta-mannosyltransferase
2562	Q9Y4G6	2	4	5.6	2542	271553	5.6	Talin-2
2562	UPI0000D6134E	2	4	5.6	2544	271795	5.6	Talin-2.
2562	UPI00001FE5FC	2	4	5.6	2542	271611	5.6	Talin-2.
2563	UPI0000DD81F6	2	3	5.6	378	38876	10.5	PREDICTED: similar to coiled-coil domain containing 86
2564	O60678	2	5	5.5	531	59903	5.3	Protein arginine N-methyltransferase 3

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2564	UPI0000198DED	2	5	5.5	531	59876	5.3	Protein arginine N-methyltransferase 3 (EC 2.1.1.-) (Heterogeneous nuclear ribonucleoprotein methyltransferase-like protein 3).
2564	UPI00001AFD06	2	5	5.3	548	61841	7.3	Protein arginine N-methyltransferase 3 (EC 2.1.1.-) (Heterogeneous nuclear ribonucleoprotein methyltransferase-like protein 3).
2564	Q8WUV3	2	5	5.3	548	61967	7.4	PRMT3 protein
2565	Q13685	2	2	5.5	434	46751	4.4	Angio-associated migratory cell protein
2566	UPI0000074015	2	2	5.6	359	39303	5.2	hsp70-interacting protein
2566	Q9NZL4	2	2	5.5	362	39474	5.2	Hsp70-binding protein 1
2567	P41236	2	3	5.4	205	23015	4.7	Protein phosphatase inhibitor 2
2567	UPI000013EC9E	2	3	5.4	205	23106	4.9	protein phosphatase 1, regulatory (inhibitor) subunit 2 pseudogene 3 (PPP1R2P3) on chromosome 5
2567	Q6NXS1	2	3	5.4	205	23048	4.9	PPP1R2P3 protein
2568	Q14318	2	3	5.4	355	38408	7.7	FK506-binding protein 8
2568	Q53GU3	2	3	5.1	372	40464	5.7	FK506-binding protein 8 variant
2568	UPI000020376E	2	3	4.6	413	44649	4.8	FK506-binding protein 8
2568	Q86YK6	2	3	4.6	412	44562	4.8	FK506-binding protein 38
2568	Q7Z349	2	3	4.2	451	48636	5	Hypothetical protein DKFZp686M22160
2569	Q53FA7	2	2	5.4	332	35536	7.2	Putative quinone oxidoreductase
2570	UPI0000D61A38	2	2	5.4	316	33124	7.2	procollagen (type III) N-endopeptidase (PCOLN3), mRNA
2571	Q59EJ1	2	6	10.3	185	21279	9.3	Etoposide-induced protein 2.4 variant
2571	UPI0000D6269D	2	6	7.3	261	29994	9.7	Etoposide-induced protein 2.4 (p53-induced protein 8).
2571	UPI00004703AE	2	6	7.3	262	30107	9.7	etoposide induced 2.4 isoform 2
2571	Q9BUQ1	2	6	5.6	340	38965	9.7	Etoposide induced 2.4 mRNA
2571	O14681	2	6	5.3	359	40979	9.5	Etoposide-induced protein 2.4
2571	UPI0000140B73	2	6	5.3	356	40694	9.4	Etoposide-induced protein 2.4 (p53-induced protein 8).
2572	O95219	2	4	5.3	450	51909	6	Sorting nexin-4
2573	P36551	2	3	5.3	454	50152	8.3	Coproporphyrinogen III oxidase, mitochondrial precursor
2573	Q53F08	2	3	5.3	454	50166	8.3	Coproporphyrinogen oxidase variant
2574	Q10713	2	8	5.3	525	58253	6.9	Mitochondrial-processing peptidase alpha subunit, mitochondrial precursor
2575	Q86VS8	2	6	5.3	718	83126	5.2	Hook homolog 3
2576	Q96NA3	2	5	5.3	434	48705	8.9	CDNA FLJ31187 fis, clone KIDNE2000349, moderately similar to Mus musculus putative lysophosphatidic acid acyltransferase mRNA
2577	Q9NXG7	2	21	5.3	525	55145	4.9	CDNA FLJ20261 fis, clone COLF7630
2578	O43670-2	2	9	5.4	463	49692	9.1	Isoform 2 of O43670
2578	O43670	2	9	5.2	478	50751	9.1	Zinc finger protein 207
2578	Q59G94	2	9	5	496	52856	9	Zinc finger protein 207 variant

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2579	Q16850	2	11	5.2	503	56806	8.5	Cytochrome P450 51A1
2580	Q8IWE2	2	4	5.2	563	60825	4.7	Protein NOXP20
2580	UPI00001DFE17	2	4	5.2	563	60742	4.7	family with sequence similarity 114, member A1 (FAM114A1), mRNA
2581	Q9HCC0-2	2	2	5.5	525	57519	7.7	Isoform 2 of Q9HCC0
2581	Q9HCC0	2	2	5.2	563	61333	7.7	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial precursor
2582	Q96HS5	2	4	11.2	179	21021	7.9	PSCD3 protein
2582	Q75MW6	2	4	5.2	387	45231	5.9	Hypothetical protein PSCD3
2582	A4D2N8	2	4	5	399	46292	5.5	Pleckstrin homology, Sec7 and coiled-coil domains 3
2582	O43739	2	4	5	400	46349	5.5	Cytohesin-3
2583	Q8N1G4	2	8	5	583	63473	8.3	Leucine-rich repeat-containing protein 47
2584	Q8NBN3-3	2	3	5.7	494	56774	5.7	Isoform 3 of Q8NBN3
2584	Q8NBN3	2	3	5	555	63430	6.7	Transmembrane protein 87A precursor
2584	UPI000045682C	2	3	5	562	64144	7	Transmembrane protein 87A precursor.
2585	UPI0000D625C4	2	5	7.6	342	38322	8.3	Fatty acyl-CoA reductase 1 (EC 1.2.1.-) (Male sterility domain-containing protein 2).
2585	Q9H600	2	5	7.6	342	38379	8.8	CDNA: FLJ22728 fis, clone HSI15617
2585	Q8WVX9	2	5	5	515	59357	9.2	Fatty acyl-CoA reductase 1
2585	UPI0000D625C5	2	5	5	518	59629	9.2	Fatty acyl-CoA reductase 1 (EC 1.2.1.-) (Male sterility domain-containing protein 2).
2586	Q92685	2	7	5	438	50126	9.4	Dolichyl-P-Man:Man(5)GlcNAc(2)-PP-dolichyl mannosyltransferase (EC 2.4.1.-) (Dol-P-Man-dependent alpha(1-3)-mannosyltransferase)
2587	Q9H936	2	3	5	323	34470	9.3	Mitochondrial glutamate carrier 1 (GC-1) (Glutamate/H(+) symporter 1)
2588	Q9UHY1	2	2	5	535	59845	5.1	Nuclear receptor-binding protein
2589	P53990-2	2	7	5.4	335	36622	5.4	Isoform 2 of P53990
2589	P53990-3	2	7	5	360	39928	7.8	Isoform 3 of P53990
2589	P53990	2	7	4.9	364	39751	5.3	Uncharacterized protein KIAA0174
2589	Q3SYM4	2	7	4.9	366	39979	5.3	KIAA0174 protein
2590	Q5J8M4	2	7	5.1	352	39479	7.8	Migration-inducing gene 14
2590	P78406	2	7	4.9	368	40968	7.8	mRNA-associated protein mrnp 41
2591	Q969G3-2	2	5	5.5	363	41780	6	Isoform 2 of Q969G3
2591	Q969G3	2	5	4.9	411	46649	4.9	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1
2592	Q9BQ39	2	3	4.9	737	82565	9.2	ATP-dependent RNA helicase DDX50
2593	Q9NRX5	2	6	4.9	453	50495	5.8	Serine incorporator 1
2594	O94919	2	5	4.8	500	55017	5.7	Endonuclease domain-containing 1 protein precursor
2595	Q4G0D9	2	2	6.3	567	64081	9.3	BOP1 protein
2595	Q14137	2	2	4.8	746	83630	6.2	Ribosome biogenesis protein BOP1
2596	Q86YF0	2	3	4.8	481	50803	8.3	ALDH16A1 protein

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2596	UPI000013E0FF	2	3	2.9	802	85127	6.8	aldehyde dehydrogenase 16 family, member A1
2596	Q8IZ83	2	3	2.9	802	85113	6.8	Aldehyde dehydrogenase family 16 member A1
2597	Q8NCH0	2	4	4.8	376	42997	9.5	Carbohydrate sulfotransferase D4ST1
2598	Q8WX92	2	2	4.8	580	65697	6.1	Negative elongation factor B
2599	Q9H173	2	5	4.8	461	52085	5.4	Nucleotide exchange factor SIL1 precursor
2600	Q9H490-2	2	3	5.1	415	47611	8.2	Isoform 2 of Q9H490
2600	Q9H490	2	3	4.8	435	50052	7.7	GPI transamidase component PIG-U
2601	Q9HA77	2	8	4.8	564	62224	8.3	Probable cysteinyl-tRNA synthetase, mitochondrial precursor
2602	Q9NYB0	2	4	4.8	399	44260	4.7	Telomeric repeat-binding factor 2-interacting protein 1
2603	Q9UJW0	2	3	4.8	460	52337	7.3	Dynactin subunit 4
2604	A2VDI4	2	12	4.7	674	76138	6.5	KIAA0143 protein
2604	UPI000041A085	2	12	4.1	785	88802	6.5	hypothetical protein LOC23167
2604	Q14156-3	2	12	4.1	777	87580	6.6	Isoform 3 of Q14156
2604	Q14156	2	12	3.9	821	92924	6.7	Protein EFR3-like
2605	Q05D48	2	6	5.4	771	87140	5.1	Hypothetical protein
2605	O14787	2	6	4.7	897	101387	5	Transportin-2
2605	UPI000013F0EA	2	6	4.7	897	101388	5	Transportin-2 (Karyopherin beta-2b).
2605	Q6IN77	2	6	4.7	887	100408	5	Transportin 2
2605	O14787-2	2	6	4.7	887	100403	5	Isoform 2 of O14787
2605	Q4LE60	2	6	4	1051	117677	5.6	TNPO2 variant protein
2606	UPI000013CA9C	2	5	5.2	481	52839	5.8	solute carrier family 39 (zinc transporter), member 14
2606	Q96BB3	2	5	5.2	481	52823	5.8	SLC39A14 protein
2606	UPI0000457680	2	5	5.1	492	54057	5.1	solute carrier family 39 (zinc transporter), member 14
2606	Q15043	2	5	4.7	531	58417	5.4	Solute carrier family 39 member 14
2607	Q8IXH7-4	2	2	4.8	581	65479	5.1	Isoform NELF
2607	Q8IXH7	2	2	4.7	590	66247	5.1	Negative elongation factor C/D
2608	O00186	2	7	4.6	592	67574	8	Syntaxin-binding protein 3
2608	Q5VTL6	2	7	4.6	592	67764	7.8	Syntaxin binding protein 3
2608	Q53FW1	2	7	4.6	592	67730	7.8	Syntaxin binding protein 3 variant
2609	O75525-2	2	2	5.9	271	30250	9.5	Isoform 2 of O75525
2609	O75525	2	2	4.6	346	38800	7.6	KH domain-containing, RNA-binding, signal transduction-associated protein 3
2610	O95470	2	2	4.6	568	63524	9.2	Sphingosine-1-phosphate lyase 1
2611	P37198	2	11	4.6	522	53255	5.3	Nuclear pore glycoprotein p62
2612	P56182	2	4	4.6	461	52839	9.3	RRP1-like protein
2612	UPI000013E05F	2	4	4.6	461	52942	9.4	NNP-1 protein (Novel nuclear protein 1) (Nucleolar protein Nop52) (D21S2056E).
2612	Q53FR7	2	4	4.6	461	52853	9.4	Nucleolar protein NOP52 variant
2612	Q6PJJ2	2	4	4.5	466	53413	9.5	D21S2056E protein
2613	Q05CS9	2	3	4.6	632	69119	9.2	Hypothetical protein
2614	UPI000000CBC7	2	4	4.8	419	46663	9.2	Inner membrane protein OXA1L, mitochondrial precursor (Oxidase assembly 1-like protein) (OXA1-like protein) (OXA1Hs) (Hsa).
2614	Q15070-2	2	4	4.8	419	46692	9.2	Isoform 2 of Q15070

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
2614	Q15070	2	4	4.6	435	48548	9.4	Inner membrane protein OXA1L, mitochondrial precursor
2614	UPI000013DE11	2	4	4	495	55270	9.7	Inner membrane protein OXA1L, mitochondrial precursor (Oxidase assembly 1-like protein) (OXA1-like protein) (OXA1Hs) (Hsa).
2614	UPI0000130F58	2	4	4	495	55298	9.7	oxidase (cytochrome c) assembly 1-like
2614	Q2M1J6	2	4	4	496	55385	9.7	Oxidase (Cytochrome c) assembly 1-like
2615	Q5T8B5	2	4	4.6	571	59481	8.6	Interferon regulatory factor 2 binding protein 2
2615	Q5T8B6	2	4	4.4	587	61025	8.7	Interferon regulatory factor 2-binding protein 2
2616	Q6PJG6	2	2	4.6	821	88119	5.3	HEAT repeat domain-containing protein C7orf27 precursor
2616	UPI0000001C11	2	2	4.6	821	88020	5.2	hypothetical protein LOC221927
2617	Q9UH65	2	3	4.6	585	68998	5.9	Switch-associated protein 70
2618	Q86TN5	2	8	4.7	676	78276	7.8	Similar to Origin recognition complex subunit 3
2618	A2A2T5	2	8	4.5	712	82325	7.6	Origin recognition complex, subunit 3-like
2618	Q9UBD5	2	8	4.5	711	82254	7.6	Origin recognition complex subunit 3
2618	Q53GY6	2	8	4.5	711	82332	7.6	Origin recognition complex, subunit 3 isoform 2 variant
2619	Q8IWA4-2	2	3	5.4	370	41883	6.4	Isoform 2 of Q8IWA4
2619	Q05CV7	2	3	4.5	447	50948	6.6	Hypothetical protein
2619	Q8IWA4-3	2	3	3.2	630	71401	6.3	Isoform 3 of Q8IWA4
2619	UPI000013D495	2	3	2.7	741	84100	6.3	Mitofusin-1 (EC 3.6.5.-) (Transmembrane GTPase MFN1) (Fzo homolog).
2619	Q8IWA4	2	3	2.7	741	84159	6.3	Mitofusin-1
2619	Q4AEJ4	2	3	2.6	769	86994	6.4	Mitochondrial transmembrane GTPase FZO-2
2620	Q9ULA6	2	3	8.4	287	33463	9.3	Homo sapiens chromosome 14 BAC containing genes for ABH and nuclear receptor coactivator NCoA-62, complete sequence
2620	Q13573	2	3	4.5	536	61495	9.5	SNW domain-containing protein 1
2620	Q6I9S2	2	3	4.5	536	61449	9.5	SNW1 protein
2621	Q308M8	2	3	4.5	494	52937	4.9	RAN binding protein 3 transcript variant a
2621	UPI00001619DB	2	3	4.4	499	53481	4.8	RAN binding protein 3 isoform RANBP3-b
2621	Q9H6Z4-3	2	3	4.4	499	53411	4.8	Isoform 3 of Q9H6Z4
2621	UPI00001AE593	2	3	3.9	560	59465	4.8	Ran-binding protein 3 (RanBP3).
2621	UPI000006EF22	2	3	3.9	562	59622	4.8	RAN binding protein 3 isoform RANBP3-a
2621	Q9H6Z4-2	2	3	3.9	562	59694	4.8	Isoform 2 of Q9H6Z4
2621	Q9H6Z4	2	3	3.9	567	60210	4.8	Ran-binding protein 3
2622	UPI00000622B6	2	6	5.6	665	75579	5.5	armadillo repeat containing 9
2622	Q7Z3E5	2	6	4.5	817	91762	6.2	LisH domain-containing protein ARMC9
2623	Q9UNS2	2	9	4.5	423	47873	6.7	COP9 signalosome complex subunit 3
2624	O75168	2	6	4.4	844	92602	6	TEL2 homolog

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
2624	Q9Y4R8	2	6	4.4	837	91775	5.8	Hypothetical protein DKFZp434A073
2624	Q7LDV4	2	6	4.4	837	91747	5.8	KIAA0683
2625	P35813-2	2	2	6.5	324	35958	5.8	Isoform Alpha
2625	Q4J6C2	2	2	6.4	327	36313	5.5	PPM1B beta isoform variant 4
2625	Q4J6C1	2	2	5.5	380	42086	5.4	PPM1B beta isoform variant 5
2625	P35813	2	2	5.5	382	42448	5.4	Protein phosphatase 2C isoform alpha
2625	Q461Q2	2	2	5.4	387	42771	5.2	PPM1B beta isoform variant 2
2625	UPI0000D61192	2	2	4.9	431	47769	6	Protein phosphatase 2C isoform beta (EC 3.1.3.16) (PP2C-beta).
2625	Q4J6C0	2	2	4.9	431	47810	6.1	PPM1B beta isoform variant 6
2625	O75688	2	2	4.4	479	52643	5	Protein phosphatase 2C isoform beta
2626	UPI0000246FF6	2	3	6.5	417	47287	6.3	Serum albumin precursor.
2626	P02768-2	2	3	6.5	417	47361	6.3	Isoform 2 of P02768
2626	P02768	2	3	4.4	609	69367	6.3	Serum albumin precursor
2626	Q56G89	2	3	4.4	609	69084	6.2	Serum albumin
2626	UPI0000D61578	2	3	4.3	626	71576	6.7	Serum albumin precursor.
2627	P31749	2	2	4.4	480	55686	6.1	RAC-alpha serine/threonine-protein kinase
2628	Q86X55	2	5	4.4	585	63460	6.6	Histone-arginine methyltransferase CARM1
2628	UPI000004B825	2	5	4.3	608	65854	6.7	coactivator-associated arginine methyltransferase 1
2629	Q9H174	2	2	4.5	493	55040	8.1	Alanine:glyoxylate aminotransferase 2 homolog 1, splice form 1
2629	Q8TBG4	2	2	4.4	499	55671	8.1	Alanine-glyoxylate aminotransferase 2-like protein 1
2630	UPI00000372F2	2	2	5.6	514	58604	6.2	WD repeat domain 26
2630	Q9H7D7-2	2	2	4.5	645	70460	6.2	Isoform 2 of Q9H7D7
2630	Q9H7D7	2	2	4.4	661	72124	6.2	WD repeat protein 26
2631	A1A693	2	3	4.3	913	99578	9.9	RNA binding motif protein 15 isoform L2
2631	Q96T37-2	2	3	4.1	957	104755	10.1	Isoform 2 of Q96T37
2631	Q86VW9	2	3	4.1	959	105284	10.1	RBM15 protein
2631	Q96T37	2	3	4	977	107188	10.1	Putative RNA-binding protein 15
2631	Q4V760	2	3	4	969	106366	10.1	RBM15 protein
2631	Q3ZB86	2	3	4	969	106365	10.1	RBM15 protein
2632	Q5TBH8	2	5	4.9	587	67046	6.3	Glyceronephosphate O-acyltransferase
2632	O15228	2	5	4.3	680	77188	6.6	Dihydroxyacetone phosphate acyltransferase
2632	Q53H08	2	5	4.3	680	77162	6.6	Glyceronephosphate O-acyltransferase variant
2632	Q53FI2	2	5	4.3	680	77089	6.4	Glyceronephosphate O-acyltransferase variant
2633	Q59H76	2	10	4.3	627	72827	6.2	Leucyl/cystinyl aminopeptidase variant
2633	Q9UIQ6	2	10	2.6	1025	117349	5.7	Leucyl-cystinyl aminopeptidase
2634	Q9NRV2	2	2	6.2	273	31841	8.9	X 010 protein
2634	Q8NBL1	2	2	4.3	392	46189	8.7	KTEL motif-containing protein 1 precursor
2634	UPI0000073BBD	2	2	4.3	392	46221	8.7	chromosome 3 open reading frame 9

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
2635	UPI000046FEE5	2	5	4.4	571	65202	5.2	Optineurin (Optic neuropathy-inducing protein) (E3-14.7K-interacting protein) (FIP-2) (Huntingtin-interacting protein HYPL) (NEMO-related protein) (Transcription factor IIIA-interacting protein) (TFIIIA- IntP).
2635	Q96CV9-2	2	5	4.4	571	65203	5.1	Isoform 2 of Q96CV9
2635	Q96CV9	2	5	4.3	577	65922	5.2	Optineurin
2635	UPI000013D38D	2	5	4.3	577	65921	5.2	Optineurin (Optic neuropathy-inducing protein) (E3-14.7K-interacting protein) (FIP-2) (Huntingtin-interacting protein HYPL) (NEMO-related protein) (Transcription factor IIIA-interacting protein) (TFIIIA- IntP).
2636	A2CEE0	2	5	4.2	698	77529	7.7	Quiescin Q6-like 1
2636	UPI0000D6194B	2	5	4.2	698	77420	7.4	Sulfhydryl oxidase 2 precursor (EC 1.8.3.2) (Quiescin Q6-like protein 1) (Neuroblastoma-derived sulfhydryl oxidase).
2636	Q6ZRP7	2	5	4.2	698	77543	7.7	Sulfhydryl oxidase 2 precursor
2636	UPI0000D6194A	2	5	4.1	700	77756	7.7	Sulfhydryl oxidase 2 precursor (EC 1.8.3.2) (Quiescin Q6-like protein 1) (Neuroblastoma-derived sulfhydryl oxidase).
2637	A4D2L3	2	3	4.2	521	58443	7	Transforming growth factor beta regulator 4
2637	Q969Z0	2	3	3.5	631	70738	7.4	Protein TBRG4
2638	O00592	2	2	4.2	528	55596	5.6	Podocalyxin-like protein 1 precursor
2638	UPI0000D61CD8	2	2	4.2	526	55347	5.7	Podocalyxin-like protein 1 precursor.
2638	Q96N83	2	2	4.2	518	54577	5.6	CDNA FLJ31254 fis, clone KIDNE2005526, highly similar to Homo sapiens podocalyxin-like protein mRNA
2638	Q53ER6	2	2	4.2	526	55400	5.6	Podocalyxin-like variant
2638	Q52LZ7	2	2	4.2	526	55386	5.6	Podocalyxin-like
2638	UPI000042467C	2	2	3.9	558	58635	5.5	podocalyxin-like precursor isoform 1
2639	O94964	2	2	4.2	518	55761	9.1	Uncharacterized protein C20orf117
2639	Q5T2J2	2	2	1.3	1661	183857	6.5	Novel protein
2640	Q9BPW0	2	5	4.3	484	55096	6.2	PPP5C protein
2640	P53041	2	5	4.2	499	56879	6.3	Serine/threonine-protein phosphatase 5
2640	Q53FR0	2	5	4.2	499	56907	6.3	Protein phosphatase 5, catalytic subunit variant
2641	Q6P1Q2	2	3	4.8	484	52550	8.8	N-PAC protein
2641	Q9BTI1	2	3	4.4	523	57215	9.2	Similar to RIKEN cDNA 3930401K13 gene
2641	UPI000059D307	2	3	4.3	536	58637	9.2	cytokine-like nuclear factor n-pac
2641	Q49A26	2	3	4.2	553	60606	9.2	Cytokine-like nuclear factor n-pac
2641	UPI00001FF8EE	2	3	4.2	553	60556	9.2	cytokine-like nuclear factor n-pac
2641	Q6V3W7	2	3	4.2	553	60547	9.2	Cytokine-like nuclear factor n-pac-like protein
2641	Q5U632	2	3	4.2	553	60548	9.1	Cytokine-like nuclear factor n-pac

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2642	Q96DP0	2	2	4.4	456	49245	9	CDNA FLJ31479 fis, clone NT2NE2001634, moderately similar to NADH- UBIQUINONE OXIDOREDUCTASE 9 KD SUBUNIT
2642	Q8WU60	2	2	4.2	473	50983	9.2	NADH dehydrogenase (Ubiquinone) flavoprotein 3, 10kDa
2642	UPI000037848B	2	2	4.2	473	50984	9.2	NADH-ubiquinone oxidoreductase flavoprotein 3 isoform a precursor
2643	Q96D46	2	4	4.2	503	57603	7.1	Protein NMD3 homolog
2643	Q9Y2Z6	2	4	4.2	503	57585	7.1	CGI-07 protein
2644	P17405	2	2	4.1	629	69851	7.4	Sphingomyelin phosphodiesterase precursor
2644	UPI000013E592	2	2	4.1	631	69936	7.3	sphingomyelin phosphodiesterase 1, acid lysosomal isoform 1 precursor
2644	UPI0000D625A9	2	2	3.9	664	73082	7.5	Sphingomyelin phosphodiesterase precursor (EC 3.1.4.12) (Acid sphingomyelinase) (aSMase).
2644	Q59EN6	2	2	3.9	664	73054	7.5	Sphingomyelin phosphodiesterase 1, acid lysosomal isoform 1 variant
2645	Q85KV2	2	8	4.1	459	51623	9.4	NADH dehydrogenase subunit 4
2646	UPI000014077B	2	2	4.3	414	47829	8.5	tRNA-nucleotidyltransferase 1, mitochondrial precursor (EC 2.7.7.25) (Mitochondrial tRNA nucleotidyl transferase, CCA-adding) (mt tRNA adenylyltransferase) (mt tRNA CCA-pyrophosphorylase) (mt tRNA CCA- diphosphorylase) (mt CCA-adding enzyme).
2646	Q96Q11-2	2	2	4.3	414	47845	8.5	Isoform 2 of Q96Q11
2646	Q96Q11	2	2	4.1	434	50144	8.1	tRNA-nucleotidyltransferase 1, mitochondrial precursor
2646	UPI000013CD08	2	2	4.1	434	50128	8.1	tRNA-nucleotidyltransferase 1, mitochondrial precursor (EC 2.7.7.25) (Mitochondrial tRNA nucleotidyl transferase, CCA-adding) (mt tRNA adenylyltransferase) (mt tRNA CCA-pyrophosphorylase) (mt tRNA CCA- diphosphorylase) (mt CCA-adding enzyme).
2647	Q9NY61	2	3	4.1	560	63133	4.9	Protein AATF
2647	UPI000013C869	2	3	4.1	562	63291	4.9	Protein AATF (Apoptosis-antagonizing transcription factor) (Rb-binding protein Che-1).
2648	P40763	2	9	4	770	88068	6.3	Signal transducer and activator of transcription 3
2648	P40763-2	2	9	4	769	87981	6.3	Isoform Del
2649	UPI000045647B	2	2	4.6	439	49848	7.2	Tripartite motif-containing protein 22 (RING finger protein 94) (50 kDa-stimulated trans-acting factor) (Staf-50).
2649	Q05CQ0	2	2	4	498	56946	7.8	Tripartite motif-containing 22

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2649	UPI000045647A	2	2	4	496	56398	7.5	Tripartite motif-containing protein 22 (RING finger protein 94) (50 kDa-stimulated trans-acting factor) (Staf-50).
2649	Q8IYM9-2	2	2	4	494	56429	7.7	Isoform 2 of Q8IYM9
2649	Q8IYM9	2	2	4	498	56947	7.7	Tripartite motif-containing protein 22
2650	Q5T4Q0	2	2	7.3	316	36595	5.3	Vacuolar protein sorting 45A
2650	Q53FR8	2	2	4	570	65070	8.2	Vacuolar protein sorting 45A variant
2650	Q9NRW7	2	2	4	570	65077	8.2	Vacuolar protein sorting-associated protein 45
2651	Q9BYH2	2	16	4	494	54424	9.2	Cystine/glutamate exchanger
2651	Q9UPY5	2	16	4	501	55423	9.2	Cystine/glutamate transporter
2652	Q13112	2	3	3.9	559	61493	7.5	Chromatin assembly factor 1 subunit B
2653	Q6DEN2	2	4	3.9	684	73910	6.6	DPYSL3 protein
2653	UPI000020CF0E	2	4	3.9	684	73911	6.4	Dihydropyrimidinase-related protein 3 (DRP-3) (Unc-33-like phosphoprotein) (ULIP protein) (Collapsin response mediator protein 4) (CRMP-4).
2654	Q8ND56	2	2	3.9	463	50530	9.5	LSM14 protein homolog A
2654	UPI000006F08C	2	2	3.9	463	50526	9.4	LSM14 homolog A
2654	Q8ND56-2	2	2	3.9	463	50554	9.5	Isoform 2 of Q8ND56
2655	UPI0000456DE5	2	2	3.9	768	88810	9.3	GC-rich sequence DNA-binding factor (GCF) (Transcription factor 9) (TCF-9).
2656	Q12873	2	2	3.8	2000	226590	7.3	Chromodomain helicase-DNA-binding protein 3
2656	UPI00004432F5	2	2	3.7	2045	231360	6.4	chromodomain helicase DNA binding protein 3 isoform 3
2657	Q14694	2	2	3.8	798	87134	5.3	Ubiquitin carboxyl-terminal hydrolase 10
2658	Q86VT2	2	2	3.9	511	55943	9	FAAH2 protein
2658	Q6GMR7	2	2	3.8	532	58304	9.1	Fatty acid amide hydrolase 2
2658	Q96N98	2	2	3.8	532	58332	9.1	CDNA FLJ31204 fis, clone KIDNE2003305, weakly similar to PUTATIVE AMIDASE AF1954
2659	Q96KG9-5	2	2	5	626	69238	8.7	Isoform 5 of Q96KG9
2659	Q96KG9-3	2	2	4.4	707	78696	8.4	Isoform 3 of Q96KG9
2659	UPI0000D62632	2	2	4	783	85686	8	N-terminal kinase-like protein (SCY1-like protein 1) (Teratoma-associated tyrosine kinase) (Telomerase transcriptional element- interacting factor) (Telomerase regulation-associated protein).
2659	Q96KG9-4	2	2	4	781	86312	6.6	Isoform 4 of Q96KG9
2659	Q96KG9-6	2	2	3.9	787	86371	8.7	Isoform 6 of Q96KG9
2659	Q96KG9-2	2	2	3.9	791	88089	6.3	Isoform 2 of Q96KG9
2659	Q96KG9	2	2	3.8	808	89631	6.3	N-terminal kinase-like protein
2660	UPI0000DD8621	2	2	3.8	560	57049	9.3	PREDICTED: hypothetical protein
2661	Q12884	2	3	3.7	760	87794	6.8	Seprase
2661	Q53TP5	2	3	3.7	760	87713	6.6	Hypothetical protein FAP
2662	Q13427-2	2	3	7.8	357	40299	9.7	Isoform 2 of Q13427
2662	Q6GMS9	2	3	7	402	46174	10.1	PPIG protein
2662	Q32LZ0	2	3	6.2	448	51715	10.2	Hypothetical protein
2662	Q2NKQ6	2	3	3.8	739	87103	10.3	PPIG protein
2662	Q13427	2	3	3.7	754	88618	10.3	Peptidyl-prolyl cis-trans isomerase G

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2662	UPI000013D124	2	3	3.7	754	88617	10.3	peptidyl-prolyl isomerase G (cyclophilin G)
2663	UPI0000EF7C5E	2	2	3.7	674	77378	6.2	Thimet oligopeptidase
2663	P52888	2	2	3.6	689	78840	6	Thimet oligopeptidase
2663	Q96CV8	2	2	3.6	689	78824	6	Thimet oligopeptidase 1
2664	Q9NVT0	2	4	4.4	656	75118	5.6	CDNA FLJ10534 fis, clone NT2RP2001065
2664	Q8WUY5	2	4	3.8	759	86857	6.3	TSR1 protein
2664	Q2NL82	2	4	3.6	804	91810	7.4	TSR1, 20S rRNA accumulation, homolog
2664	Q9P2E6	2	4	3.4	853	97049	8	Pre-rRNA-processing protein TSR1 homolog
2665	Q9UBU9	2	8	3.6	619	70182	8.5	Nuclear RNA export factor 1
2666	Q5UW38	2	4	3.5	596	64028	8.2	L9
2666	UPI00004C9B11	2	4	3.5	596	64002	8.2	PDZ and LIM domain 5 isoform a
2666	UPI00001401C7	2	4	3.5	596	63945	8.2	PDZ and LIM domain protein 5 (Enigma homolog) (Enigma-like PDZ and LIM domains protein).
2666	Q96HC4	2	4	3.5	596	63972	8.2	PDZ and LIM domain protein 5
2667	Q8IUH4	2	4	3.5	622	70889	8.1	Probable palmitoyltransferase ZDHHC13
2667	UPI0000D625CD	2	4	3.5	622	70818	8	Probable palmitoyltransferase ZDHHC13 (EC 2.3.1.-) (Zinc finger DHHC domain-containing protein 13) (DHHC-13) (Huntingtin-interacting protein 14-related protein) (HIP14-related protein) (Huntingtin- interacting protein HIP3RP) (Putative NF-kappa-B-activati
2667	UPI000015F967	2	4	3.5	622	70861	8.1	zinc finger, DHHC domain containing 13 isoform 1
2668	Q99459	2	5	3.5	802	92251	8.2	Cell division cycle 5-like protein
2669	O60645-2	2	9	4.1	641	73797	7.1	Isoform 2 of O60645
2669	O60645	2	9	3.4	756	86845	6.1	Exocyst complex component 3
2670	P35240-4	2	3	3.9	507	59096	7.2	Isoform 4 of P35240
2670	P35240-8	2	3	3.6	561	65350	6.6	Isoform 8 of P35240
2670	P35240-6	2	3	3.6	548	63997	6.2	Isoform 6 of P35240
2670	P35240-5	2	3	3.6	549	64189	8.2	Isoform 5 of P35240
2670	P35240	2	3	3.4	595	69690	6.5	Merlin
2670	P35240-3	2	3	3.4	590	69090	6.7	Isoform 3 of P35240
2670	UPI0000457069	2	3	3.2	617	72107	7.3	Merlin (Moesin-ezrin-radixin-like protein) (Neurofibromin-2) (Schwannomin) (Schwannomerlin).
2670	P35240-2	2	3	3.2	620	72514	7.1	Isoform 2 of P35240
2671	Q56A80	2	2	4.2	523	58330	8.8	IDUA protein
2671	P35475	2	2	3.4	653	72670	9.1	Alpha-L-iduronidase precursor
2672	Q12929	2	7	3.4	822	91882	7.5	Epidermal growth factor receptor kinase substrate 8
2672	UPI000013DC63	2	7	3.4	824	92040	7.5	Epidermal growth factor receptor kinase substrate 8.
2673	Q4G0J3	2	3	3.4	582	66899	9.6	La-related protein 7
2674	Q5RKV4	2	3	6.4	487	54778	6.2	Ankyrin repeat and FYVE domain containing 1
2674	Q5H9P4	2	3	3.4	924	99824	6.3	Hypothetical protein DKFZp686M19106
2674	UPI00004569F8	2	3	2.7	1168	128295	6.1	Ankyrin repeat and FYVE domain-containing protein 1 (Ankyrin repeats hooked to a zinc finger motif).

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
2674	Q9P2R3	2	3	2.7	1169	128399	6.1	Ankyrin repeat and FYVE domain-containing protein 1
2674	UPI0000D4BE3E	2	3	2.6	1170	128486	6.1	ankyrin repeat and FYVE domain containing 1 isoform 1
2675	Q9BTX1-4	2	2	4.2	542	61009	8.9	Isoform 4 of Q9BTX1
2675	Q9BTX1	2	2	3.4	674	76305	9.1	Nucleoporin NDC1
2675	UPI000006DFC8	2	2	3.4	674	76363	9	transmembrane protein 48
2675	Q9BTX1-2	2	2	3.4	673	76234	9.1	Isoform 2 of Q9BTX1
2676	UPI0000131B9E	2	4	3.7	738	80827	6.1	phospholipase A2-activating protein isoform 2
2676	Q9Y263	2	4	3.4	795	87157	6.4	Phospholipase A-2-activating protein
2677	Q9Y4W2-3	2	2	3.7	675	76845	4.7	Isoform 3 of Q9Y4W2
2677	Q9Y4W2-2	2	2	3.5	717	81243	4.7	Isoform 2 of Q9Y4W2
2677	Q9Y4W2	2	2	3.4	734	83065	4.7	LAS1-like protein
2678	P23786	2	2	3.3	658	73777	8.2	Carnitine O-palmitoyltransferase 2, mitochondrial precursor
2679	Q6NUM9-2	2	10	4.2	481	52439	8	Isoform 2 of Q6NUM9
2679	Q6NUM9	2	10	3.3	610	66820	8.3	All-trans-retinol 13,14-reductase precursor
2679	UPI0000072C67	2	10	3.3	610	66793	8.3	all-trans-13,14-dihydroretinol saturase
2680	Q9P263	2	2	3.3	785	83604	5.7	Immunoglobulin superfamily containing leucine-rich repeat 2
2681	O60231	2	2	3.2	1041	119263	6.8	Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16
2681	UPI0000161FB0	2	2	3.2	1041	119172	6.7	DEAH (Asp-Glu-Ala-His) box polypeptide 16
2682	O76031	2	6	3.2	633	69224	7.6	ATP-dependent Clp protease ATP-binding subunit ClpX-like, mitochondrial precursor
2683	Q9BSN5	2	5	6	517	57070	6.3	Hypothetical protein
2683	Q2VPA0	2	5	3.7	848	95097	6.7	PRSS15 protein
2683	Q8N8K8	2	5	3.5	895	100397	6.7	CDNA FLJ39307 fis, clone OCBBF2013208, highly similar to MITOCHONDRIAL LON PROTEASE
2683	P36776	2	5	3.2	959	106489	6.4	Lon protease homolog, mitochondrial precursor
2684	Q58F15	2	4	3.4	949	105744	6.2	EPHA4 protein
2684	P54764	2	4	3.2	986	109860	6.6	Ephrin type-A receptor 4 precursor
2685	Q6PJE1	2	5	4.4	686	79971	5.3	NUP107 protein
2685	P57740	2	5	3.2	925	106374	5.4	Nuclear pore complex protein Nup107
2686	Q9NPH3-3	2	4	5.2	346	39743	6.3	Isoform 3 of Q9NPH3
2686	Q9NPH3-2	2	4	5.1	356	41019	7.3	Isoform 2 of Q9NPH3
2686	Q9NPH3	2	4	3.2	570	65419	8.1	Interleukin-1 receptor accessory protein precursor
2687	UPI0000457706	2	2	3.4	563	61132	7.9	Glycosylphosphatidylinositol anchor attachment 1 protein (GPI anchor attachment protein 1) (GAA1 protein homolog) (hGAA1).
2687	O43292	2	2	3.1	621	67623	8.1	Glycosylphosphatidylinositol anchor attachment 1 protein
2687	UPI0000457705	2	2	3	623	67657	8.2	Glycosylphosphatidylinositol anchor attachment 1 protein (GPI anchor attachment protein 1) (GAA1 protein homolog) (hGAA1).

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
2688	Q04446	2	6	3.1	702	80460	6.3	1,4-alpha-glucan branching enzyme
2688	UPI0000457142	2	6	3.1	702	80540	6.3	1,4-alpha-glucan branching enzyme (EC 2.4.1.18) (Glycogen branching enzyme) (Brancher enzyme).
2688	UPI0000209A24	2	6	3.1	702	80474	6.3	glucan (1,4-alpha-), branching enzyme 1
2689	Q86SW2	2	2	8.1	273	31287	5.2	Full-length cDNA 5-PRIME end of clone CS0DK005YC03 of HeLa cells of Homo sapiens
2689	Q13330-2	2	2	5.1	430	49017	5.5	Isoform Short of Q13330
2689	Q13330	2	2	3.1	715	80788	9.3	Metastasis-associated protein MTA1
2689	UPI00003669FD	2	2	3.1	715	80786	9.3	metastasis associated protein
2690	Q2UZW3	2	3	3.1	818	91329	5.3	XB130
2690	Q8N4X5-2	2	3	3.1	814	90860	5.3	Isoform 2 of Q8N4X5
2690	Q8N4X5	2	3	3.1	818	91300	5.3	Actin filament-associated protein 1-like 2
2691	Q9H078-2	2	2	3.2	677	75449	9	Isoform 2 of Q9H078
2691	Q9H078	2	2	3.1	707	78729	9	Caseinolytic peptidase B protein homolog
2692	Q8TEG6	2	35	8.2	354	38908	5.2	FLJ00231 protein
2692	Q6ZVG3	2	35	8.2	352	38486	6.3	CDNA FLJ42617 fis, clone BRACE3014807
2692	UPI0000199C26	2	35	5.9	491	54139	5.3	tweety 3
2692	Q9C0H2	2	35	5.2	558	61119	6.1	Tweety homolog 3
2692	A4D201	2	35	3	951	102588	7.2	Tweety homolog 3
2693	O43772	2	3	3	301	32944	9.4	Mitochondrial carnitine/acylcarnitine carrier protein
2693	UPI00006C071D	2	3	3	303	33298	9.3	PREDICTED: similar to Mitochondrial carnitine/acylcarnitine carrier protein (Carnitine/acylcarnitine translocase) (CAC) (Solute carrier family 25 member 20)
2694	P23677	2	2	3	461	51009	7.7	Inositol-trisphosphate 3-kinase A
2695	P48960-2	2	11	3.4	742	81743	7.1	Isoform 2 of P48960
2695	P48960-3	2	11	3.2	786	86628	6.9	Isoform 3 of P48960
2695	P48960	2	11	3	835	91869	6.9	CD97 antigen precursor
2696	Q8N2B3	2	4	6.5	491	54656	6	CDNA FLJ33559 fis, clone BRAMY2009528
2696	Q96JJ0	2	4	5	639	70428	5.7	KIAA1837 protein
2696	Q9H7V0	2	4	4.6	691	76234	5.7	CDNA FLJ14225 fis, clone NT2RP3004051
2696	Q7L1C9	2	4	4.6	699	77176	5.7	KIAA0319L protein
2696	Q8NDA0	2	4	4.3	746	82461	5.5	Hypothetical protein DKFZp434C0829
2696	Q8WYZ5	2	4	3.4	946	103879	5.9	Hypothetical protein
2696	UPI00001B5642	2	4	3.2	996	109752	6.1	polycystic kidney disease 1-like isoform b
2696	UPI000003F081	2	4	3.1	1049	115658	6	polycystic kidney disease 1-like isoform a
2696	Q8WY39	2	4	3.1	1049	115732	6	PP791 protein
2696	Q8IZA0	2	4	3.1	1049	115718	6.1	Polycystic kidney disease 1-related protein
2696	Q6PJJ7	2	4	3.1	1049	115584	6	KIAA0319-like
2696	Q5T225	2	4	3	1058	116614	6	Protein KIAA0319-like
2697	Q8N0X7	2	2	3	666	72833	5.9	Spartin
2698	Q9H330-4	2	13	5.4	503	55419	9.3	Isoform 4 of Q9H330
2698	UPI0000D618E3	2	13	3.1	871	96251	8.8	Uncharacterized protein C9orf5 (Protein CG-2).

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
2698	Q9H330-2	2	13	3.1	879	97357	8.9	Isoform 2 of Q9H330
2698	Q9H330	2	13	3	911	100945	8.9	Uncharacterized protein C9orf5
2698	UPI000045778C	2	13	3	908	100541	8.9	Uncharacterized protein C9orf5 (Protein CG-2).
2699	Q9BXJ9-4	2	4	3.4	526	61602	8.2	Isoform 2 of Q9BXJ9
2699	Q58F05	2	4	2.9	614	72387	8.4	NARG1 protein
2699	Q9BXJ9	2	4	2.1	866	101272	7.4	NMDA receptor-regulated protein 1
2700	Q96A78	2	2	3	808	89035	6.9	TBL3 protein (Transducin (Beta)-like 3)
2700	Q8IVB7	2	2	3	808	88936	6.9	Transducin (Beta)-like 3
2700	Q59GD6	2	2	2.9	832	91238	7	Transducin beta-like 3 variant
2701	UPI0000141B46	2	3	6	418	47480	5	Leucine-rich repeat and IQ domain-containing protein 2.
2701	Q8NA71	2	3	6	418	47514	5	CDNA FLJ35781 fis, clone TESTI2005395
2701	Q8IW35	2	3	2.9	865	96981	5	Leucine-rich repeat and IQ domain-containing protein 2
2702	Q8NFP3	2	2	2.9	622	71762	8.8	Gag protein
2703	UPI000059DB76	2	2	3.2	597	68393	8.1	Angiomotin.
2703	A2BDD9	2	2	2.8	676	72637	6.7	AMOT protein
2703	Q4VCS5	2	2	1.8	1084	118085	7.6	Angiomotin
2704	Q06124-3	2	2	3.7	460	52828	7.4	Isoform 3 of Q06124
2704	Q06124-2	2	2	2.9	593	68011	7.3	Isoform 2 of Q06124
2704	Q06124	2	2	2.8	597	68436	7.3	Tyrosine-protein phosphatase non-receptor type 11
2705	Q13586	2	2	2.8	685	77493	6.7	Stromal interaction molecule 1 precursor
2705	Q8N382	2	2	2.8	685	77423	6.7	Stromal interaction molecule 1
2706	Q86UE8-3	2	2	3.1	718	82348	8.3	Isoform 3 of Q86UE8
2706	Q86UE8-2	2	2	2.9	750	85444	8.4	Isoform 2 of Q86UE8
2706	Q86UE8	2	2	2.8	772	87661	8.4	Serine/threonine-protein kinase tousled-like 2
2707	Q9P0V3	2	2	2.8	963	107496	7.7	SH3 domain-binding protein 4
2708	Q9P253	2	2	2.8	973	110186	6.1	Vacuolar protein sorting-associated protein 18 homolog
2709	Q9P2I0	2	10	2.8	782	88487	5.1	Cleavage and polyadenylation specificity factor subunit 2
2710	P11498	2	2	2.7	1178	129634	6.8	Pyruvate carboxylase, mitochondrial precursor
2711	Q08174	2	2	2.7	1026	111270	5	Protocadherin-1 precursor
2711	UPI000045735F	2	2	2.7	1031	111812	5	Protocadherin-1 precursor (Protocadherin-42) (PC42) (Cadherin-like protein 1).
2711	Q08174-2	2	2	2.7	1030	111704	5	Isoform 2 of Q08174
2711	Q8IUP2	2	2	2.6	1060	114743	5	Protocadherin 1
2711	UPI000016158F	2	2	2.3	1237	133722	5.1	protocadherin 1 isoform 2 precursor
2712	Q6VY07	2	3	2.7	963	104898	7.7	Phosphofurin acidic cluster sorting protein 1
2712	Q6VY07-2	2	3	2.6	1008	109342	7.4	Isoform 2 of Q6VY07
2713	Q9BZQ6	2	3	2.7	889	100305	4.9	ER degradation-enhancing alpha-mannosidase-like 3
2714	Q9Y3E9	2	2	5.2	404	45005	8.5	CGI-151 protein
2714	Q9Y2J6	2	2	2.7	772	83643	7.7	KIAA0992 protein
2715	Q9Y4E8	2	2	2.7	981	112419	5.2	Ubiquitin carboxyl-terminal hydrolase 15
2715	Q9Y4E8-3	2	2	2.7	956	109796	5.2	Isoform 3 of Q9Y4E8
2715	Q9Y4E8-2	2	2	2.7	952	109297	5.2	Isoform 2 of Q9Y4E8
2716	UPI0000074697	2	2	2.7	669	76394	7.5	EF hand domain family, member B
2716	UPI0000DBEEB5	2	2	2.7	669	76368	7.5	EF-hand domain-containing family member B.

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2716	UPI0000D61ADD	2	2	2.7	670	76467	7.5	EF-hand domain-containing family member B.
2716	UPI0000D61ADC	2	2	2.6	704	79671	7	EF-hand domain-containing family member B.
2717	P14735	2	5	2.6	1019	118022	6.8	Insulin-degrading enzyme
2717	Q5T5N2	2	5	2.6	1019	117968	6.6	Insulin-degrading enzyme
2718	Q6ZR79	2	2	14.9	154	17257	10.5	CDNA FLJ46573 fis, clone THYMU3041603, moderately similar to Homo sapiens tubulin, gamma complex associated protein 2
2718	UPI000045899B	2	2	3.2	721	82604	6.8	Gamma-tubulin complex component 2 (GCP-2) (Spindle pole body protein Spc97 homolog) (hSpc97) (hGCP2) (h103p).
2718	Q53EQ3	2	2	2.6	901	102449	6.8	Tubulin, gamma complex associated protein 2 variant
2718	Q9BSJ2	2	2	2.5	902	102534	6.8	Gamma-tubulin complex component 2
2719	Q53H65	2	4	2.6	759	85666	9.2	RNA binding motif protein 28 variant
2719	UPI000006F4A6	2	4	2.6	759	85766	9.2	RNA binding motif protein 28
2719	Q9NW13	2	4	2.6	759	85738	9.2	RNA-binding protein 28
2720	Q4G0Y5	2	3	11.4	193	21981	5.7	CHERP protein
2720	O00302	2	3	2.5	884	100015	9.2	ERPROT 213-21
2720	Q8WU30	2	3	2.5	884	99992	9.2	Calcium homeostasis endoplasmic reticulum protein
2720	UPI00001AE5BE	2	3	2.4	916	103702	9	calcium homeostasis endoplasmic reticulum protein
2720	Q8IWX8	2	3	2.4	916	103596	8.9	Calcium homeostasis endoplasmic reticulum protein
2721	P06400	2	2	2.5	928	106159	7.9	Retinoblastoma-associated protein
2721	Q59HH0	2	2	2.4	960	109774	8.2	Retinoblastoma-associated protein variant
2722	UPI000006F9CB	2	2	2.6	1452	158481	9.7	cell division cycle 2-like 5 isoform 2
2722	Q14004-2	2	2	2.6	1452	158434	9.7	Isoform 2 of Q14004
2722	Q14004	2	2	2.5	1512	164922	9.7	Cell division cycle 2-like protein kinase 5
2722	UPI000006DA35	2	2	2.5	1512	164969	9.7	cell division cycle 2-like 5 isoform 1
2723	Q6P5Y2	2	2	2.5	609	68927	6.6	MLL5 protein
2723	Q9NWE7	2	2	2.5	594	67514	6.9	CDNA FLJ10078 fis, clone HEMBA1001869
2723	Q8NFF8	2	2	0.8	1858	204786	7.6	MLL5
2723	Q8IZD2	2	2	0.8	1858	204963	7.6	Myeloid/lymphoid or mixed-lineage leukemia protein 5
2724	Q7Z2Z2	2	2	2.5	1069	119889	5.8	Elongation factor Tu GTP-binding domain-containing protein 1
2724	UPI00001FEA3A	2	2	2.5	1069	119887	5.8	elongation factor Tu GTP binding domain containing 1 isoform 2
2724	UPI00001FEA35	2	2	2.4	1120	125430	5.9	elongation factor Tu GTP binding domain containing 1 isoform 1
2725	Q8TA92	2	4	2.5	812	90194	9.1	Similar to AFG3 ATPase family gene 3-like 2
2725	Q9Y4W6	2	4	2.5	797	88584	8.7	AFG3-like protein 2
2726	Q8TD19	2	2	2.5	979	107168	5.7	Serine/threonine-protein kinase Nek9
2726	UPI0000070F8F	2	2	2.5	979	107034	5.7	NIMA related kinase 9

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
2727	Q59F19	2	2	2.8	949	102591	9	Proto-oncogene tyrosine-protein kinase ABL1 variant
2727	P00519	2	2	2.4	1130	122872	8.7	Proto-oncogene tyrosine-protein kinase ABL1
2727	Q59FK4	2	2	2.3	1167	127257	8.9	V-abl Abelson murine leukemia viral oncogene homolog 1 isoform b variant
2728	P20936-2	2	4	2.9	870	100398	7.6	Isoform 2 of P20936
2728	P20936	2	4	2.4	1047	116403	6.5	Ras GTPase-activating protein 1
2728	UPI000013DA03	2	4	2.4	1047	116391	6.5	Ras GTPase-activating protein 1 (GTPase-activating protein) (GAP) (Ras p21 protein activator) (p120GAP) (RasGAP).
2729	Q9BTX0	2	3	2.6	852	94370	6.7	RNA binding motif protein 10
2729	Q5JRR2	2	3	2.6	853	94469	6.7	RNA binding motif protein 10
2729	P98175	2	3	2.4	929	103459	6	RNA-binding protein 10
2729	Q9BTE4	2	3	2.4	930	103533	6	RNA binding motif protein 10
2729	Q7Z3D7	2	3	2.2	995	110338	6.2	Hypothetical protein DKFZp686E2459
2730	Q6ZMZ3	2	4	2.4	975	112216	6.2	Nesprin-3
2730	UPI0000225CD0	2	4	2.4	975	112244	6.2	nesprin-3
2730	Q6ZMZ3-2	2	4	2.4	970	111677	6.2	Isoform 2 of Q6ZMZ3
2731	Q8TD16	2	2	2.4	824	93533	5.4	Protein bicaudal D homolog 2
2731	Q8TD16-2	2	2	2.3	855	96806	5.4	Isoform 2 of Q8TD16
2732	Q9H2K8	2	2	2.4	898	105406	7.3	Serine/threonine-protein kinase TAO3
2732	UPI0000070EFD	2	2	2.4	898	105433	7.3	TAO kinase 3
2733	UPI000013E31F	2	3	2.5	1035	117309	5.3	retinoblastoma-associated protein 140
2733	Q9H2F7	2	3	2.5	1035	117350	5.3	CTCL tumor antigen se89-1
2733	A1L3A4	2	3	2.3	1116	126444	6.1	C3orf63 protein
2733	UPI000013E320	2	3	2.1	1233	139998	5.6	retinoblastoma-associated protein 140
2733	Q9UK61	2	3	2.1	1233	139954	5.7	Protein C3orf63
2734	UPI000059D1C3	2	9	2.8	680	76423	6.6	Fibroblast growth factor receptor 2 precursor (EC 2.7.10.1) (FGFR-2) (keratiocyte growth factor receptor 2) (CD332 antigen).
2734	P21802-4	2	9	2.8	682	76705	6.9	Isoform 4 of P21802
2734	UPI0000D60FEA	2	9	2.7	709	79843	5.8	Fibroblast growth factor receptor 2 precursor (EC 2.7.10.1) (FGFR-2) (keratiocyte growth factor receptor 2) (CD332 antigen).
2734	UPI0000D60FE8	2	9	2.7	707	79500	6.8	Fibroblast growth factor receptor 2 precursor (EC 2.7.10.1) (FGFR-2) (keratiocyte growth factor receptor 2) (CD332 antigen).
2734	UPI000059D1C5	2	9	2.7	707	79490	6.8	Fibroblast growth factor receptor 2 precursor (EC 2.7.10.1) (FGFR-2) (keratiocyte growth factor receptor 2) (CD332 antigen).
2734	UPI000013D40D	2	9	2.7	705	79290	6.8	Fibroblast growth factor receptor 2 precursor (EC 2.7.10.1) (FGFR-2) (keratiocyte growth factor receptor 2) (CD332 antigen).
2734	Q8IXC7	2	9	2.7	709	79833	5.8	Isoform of FGFR2
2734	P21802-20	2	9	2.7	704	79197	6.6	Isoform 20 of P21802

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
2734	P21802-15	2	9	2.7	705	79212	5.6	Isoform 15 of P21802
2734	UPI0000167E2D	2	9	2.6	731	82118	6.1	Fibroblast growth factor receptor 2 precursor (EC 2.7.10.1) (FGFR-2) (keratiocyte growth factor receptor 2) (CD332 antigen).
2734	P21802-8	2	9	2.5	766	85929	6.3	Isoform 8 of P21802
2734	P21802-2	2	9	2.5	768	86130	6.3	Isoform 2 of P21802
2734	P21802-17	2	9	2.5	769	86223	6.5	Isoform 17 of P21802
2734	P21802-12	2	9	2.5	771	86407	6.5	Isoform 12 of P21802
2734	UPI0000456416	2	9	2.4	788	88505	6.1	Fibroblast growth factor receptor 2 precursor (EC 2.7.10.1) (FGFR-2) (keratiocyte growth factor receptor 2) (CD332 antigen).
2734	Q1KHY5	2	9	2.4	785	88181	6	Fibroblast growth factor receptor 2
2734	P21802	2	9	2.3	821	92025	5.9	Fibroblast growth factor receptor 2 precursor
2734	UPI0000D60FE9	2	9	2.3	821	92035	5.9	Fibroblast growth factor receptor 2 precursor (EC 2.7.10.1) (FGFR-2) (keratiocyte growth factor receptor 2) (CD332 antigen).
2734	UPI0000D60FE7	2	9	2.3	822	92128	6	Fibroblast growth factor receptor 2 precursor (EC 2.7.10.1) (FGFR-2) (keratiocyte growth factor receptor 2) (CD332 antigen).
2734	UPI0000D60FE6	2	9	2.3	819	91536	6.3	Fibroblast growth factor receptor 2 precursor (EC 2.7.10.1) (FGFR-2) (keratiocyte growth factor receptor 2) (CD332 antigen).
2734	P21802-9	2	9	2.3	819	91566	6.3	Isoform 9 of P21802
2734	P21802-7	2	9	2.3	817	91620	7.1	Isoform 7 of P21802
2734	P21802-5	2	9	2.3	819	91825	5.9	Isoform 5 of P21802
2734	P21802-3	2	9	2.3	822	92118	6	Isoform 3 of P21802
2734	P21802-18	2	9	2.3	820	91918	6	Isoform 18 of P21802
2734	P21802-16	2	9	2.3	822	92165	6	Isoform 16 of P21802
2734	P21802-11	2	9	2.3	830	92733	6.9	Isoform 11 of P21802
2734	P21802-10	2	9	2.3	819	91641	6.5	Isoform 10 of P21802
2735	Q69YM3	2	2	2.5	651	68890	9.1	Hypothetical protein DKFZp762H2012
2735	Q13207	2	2	2.3	702	74068	9.1	T-box transcription factor TBX2
2736	UPI00004572D4	2	3	5.1	408	46390	8.6	PR domain zinc finger protein 9 (PR domain-containing protein 9).
2736	UPI00004572D5	2	3	3	695	80062	9.3	PR domain zinc finger protein 9 (PR domain-containing protein 9).
2736	Q9NQV7	2	3	3	689	79475	9.3	PR domain zinc finger protein 9
2736	Q27Q50	2	3	2.3	894	103377	9.2	PR domain-containing 9
2737	Q2TAM4	2	2	2.3	952	107812	7.7	POLR1B protein
2737	Q9H9Y6-2	2	2	2	1079	121988	7.6	Isoform 2 of Q9H9Y6
2737	Q9H9Y6	2	2	1.9	1135	128229	7.8	DNA-directed RNA polymerase I 135 kDa polypeptide
2738	Q5JSZ5	2	2	2.3	1535	165526	8.8	Uncharacterized protein KIAA0515
2739	Q96AP3	2	2	3.8	532	59372	9.1	CC2D1B protein
2739	Q5T0G1	2	2	3.2	627	69549	8.6	Coiled-coil and C2 domain containing 1B

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
2739	Q5T0G0	2	2	2.6	771	85030	5.6	Coiled-coil and C2 domain containing 1B
2739	Q5T0F8	2	2	2.3	852	93595	5.2	Coiled-coil and C2 domain containing 1B
2739	Q5T0F9	2	2	2.3	858	94224	5.3	Coiled-coil and C2 domain-containing protein 1B
2740	Q9H6M7	2	2	3.5	774	84408	7.6	CDNA: FLJ22087 fis, clone HEP15918
2740	Q9H6B3	2	2	3.5	774	84378	7.6	CDNA: FLJ22417 fis, clone HRC08579
2740	Q8TDM9	2	2	2.7	1013	110352	7.3	Amplified in breast cancer 1
2740	Q6AI08	2	2	2.3	1181	128781	7	Hypothetical protein DKFZp686D22141
2740	Q6MZX1	2	2	2.3	1181	128707	7.1	Hypothetical protein DKFZp686B03209
2741	Q6NUQ2	2	7	2.3	1002	111640	4.9	Calmin
2741	Q96JQ2	2	7	2.3	1002	111651	4.9	Calmin
2742	Q86VQ0	2	2	2.3	697	80554	7.7	Uncharacterized protein C6orf152
2742	UPI00001907F9	2	2	2.3	697	80530	7.7	hypothetical protein LOC167691
2743	Q8NEE8	2	2	2.3	873	98309	9	Tetratricopeptide repeat protein 16
2744	A1L3A9	2	6	2.2	1232	138540	5.3	TBC1 domain family, member 9B
2744	UPI000034ECFF	2	6	2.2	1250	140525	5.3	TBC1 domain family, member 9B (with GRAM domain) isoform a
2744	UPI000020CCFB	2	6	2.2	1233	138670	5.3	TBC1 domain family, member 9B (with GRAM domain) isoform b
2744	UPI000013D22E	2	6	2.1	1261	141519	5.3	TBC1 domain family, member 9B (with GRAM domain) isoform b
2744	O75163	2	6	2.1	1262	141589	5.3	TBC1 domain family member 9B
2745	Q9Y6D9	2	2	2.5	718	83067	5.9	Mitotic spindle assembly checkpoint protein MAD1
2745	A4D218	2	2	2.2	803	91721	8.1	MAD1 mitotic arrest deficient-like 1
2745	UPI0000140415	2	2	2.2	803	91771	8.1	Mitotic spindle assembly checkpoint protein MAD1 (Mitotic arrest deficient-like protein 1) (MAD1-like 1) (Mitotic checkpoint MAD1 protein-homolog) (HsMAD1) (hMAD1) (Tax-binding protein 181).
2745	Q9Y6D9-2	2	2	2.2	804	91859	8.1	Isoform 2 of Q9Y6D9
2746	P19838	2	2	2.2	968	105356	5.4	Nuclear factor NF-kappa-B p105 subunit (DNA-binding factor KBF1) (EBP- 1) [Contains: Nuclear factor NF-kappa-B p50 subunit]
2746	P19838-2	2	2	2.2	969	105427	5.4	Isoform 2 of P19838
2747	P49916-2	2	2	2.3	862	95802	9	Isoform Beta of P49916
2747	P49916	2	2	2.2	922	102691	8.8	DNA ligase 3
2748	Q86V48-3	2	2	2.3	1053	117555	8.9	Isoform 3 of Q86V48
2748	Q86V48-2	2	2	2.3	1026	114588	8.9	Isoform 2 of Q86V48
2748	Q86V48	2	2	2.2	1076	120275	8.5	Leucine zipper protein 1
2748	UPI0000445E0E	2	2	2.2	1076	120304	8.6	leucine zipper protein 1
2749	UPI0000457488	2	5	2.4	981	108579	6.5	NEDD9-interacting protein with calponin homology and LIM domains (Molecule interacting with CasL protein 1).

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
2749	Q8TDZ2-2	2	5	2.4	981	108552	6.5	Isoform 2 of Q8TDZ2
2749	Q8TDZ2	2	5	2.2	1067	117875	6.4	NEDD9-interacting protein with calponin homology and LIM domains
2749	UPI0000457487	2	5	2.2	1067	117902	6.4	NEDD9-interacting protein with calponin homology and LIM domains (Molecule interacting with CasL protein 1).
2749	UPI000012F0E5	2	5	2.2	1067	117932	6.5	microtubule associated monoxygenase, calponin and LIM domain containing 1
2750	Q8WXD9	2	12	2.2	1431	149813	9.1	Caskin-1
2750	UPI00004568FC	2	12	2.2	1432	149857	9.2	Caskin-1 (CASK-interacting protein 1).
2751	Q9H165	2	2	2.2	835	91197	6.6	B-cell lymphoma/leukemia 11A
2751	Q9H165-6	2	2	2.2	801	87554	6.5	Isoform 6 of Q9H165
2752	O75762	2	2	2.1	1119	127379	7	Transient receptor potential cation channel subfamily A member 1
2752	UPI00004576B7	2	2	2.1	1117	127274	7.1	Transient receptor potential cation channel subfamily A member 1 (Ankyrin-like with transmembrane domains protein 1) (Transformation sensitive-protein p120).
2752	UPI000021081A	2	2	2.1	1119	127501	7.1	ankyrin-like protein 1
2753	Q17RV9	2	2	2.1	1291	149769	6.1	KIF15 protein
2753	Q9NS87	2	2	1.9	1388	160159	6	Kinesin-like protein KIF15
2754	Q641R2	2	5	2.6	728	82554	7.1	OSBPL8 protein
2754	UPI0000130E99	2	5	2.2	847	96956	7.5	oxysterol-binding protein-like protein 8 isoform b
2754	Q9BZF1-2	2	5	2.2	874	99714	7.1	Isoform 2 of Q9BZF1
2754	Q68D75	2	5	2.2	847	96924	7.5	Oxysterol-binding protein
2754	Q5HYM3	2	5	2.1	890	101298	7.1	Oxysterol-binding protein
2754	Q9BZF1	2	5	2.1	889	101196	7	Oxysterol-binding protein-related protein 8
2755	Q7L590	2	4	2.1	875	98183	8.8	Protein MCM10 homolog
2756	Q9H7N4	2	2	2.1	1343	142483	9.4	FLJ00034 protein
2756	Q9NR59	2	2	2.1	1312	139269	9.2	Ser/arg-rich pre-mRNA splicing factor SR-A1
2757	Q9Y6X7	2	2	2.1	1402	158411	5.1	KIAA0864 protein
2757	UPI000013F560	2	2	2.1	1402	158412	5.1	Myosin phosphatase Rho-interacting protein (Rho-interacting protein 3) (M-RIP) (RIP3) (p116Rip).
2758	Q5TAX2	2	23	3.6	907	102314	6.3	Zinc finger, CCHC domain containing 11
2758	A2RRP0	2	23	2	1645	185251	8	Zinc finger, CCHC domain containing 11
2758	UPI000016057B	2	23	2	1640	184704	8	zinc finger, CCHC domain containing 11 isoform c
2758	Q5TAX3	2	23	2	1644	185164	8	Zinc finger CCHC domain-containing protein 11
2759	Q53TS3	2	2	2.4	808	91286	5.4	Hypothetical protein NRP2
2759	UPI0000456EDD	2	2	2.1	901	101497	5.6	Neuropilin-2 precursor (Vascular endothelial cell growth factor 165 receptor 2).
2759	UPI0000456EDC	2	2	2.1	909	102231	5.3	Neuropilin-2 precursor (Vascular endothelial cell growth factor 165 receptor 2).
2759	UPI0000456EDB	2	2	2.1	926	104304	5.2	Neuropilin-2 precursor (Vascular endothelial cell growth factor 165 receptor 2).

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
2759	UPI0000140230	2	2	2.1	906	101985	5.6	Neuropilin-2 precursor (Vascular endothelial cell growth factor 165 receptor 2).
2759	Q9H2E4	2	2	2.1	901	101380	5.8	Neuropilin-2b
2759	Q9H2E3	2	2	2.1	906	101956	5.8	Neuropilin-2b
2759	Q9H2D5	2	2	2.1	901	101381	5.6	Neuropilin-2b
2759	Q9H2D4	2	2	2.1	906	101957	5.6	Neuropilin-2b
2759	Q7LBX6	2	2	2.1	926	104255	5.2	Neuropilin-2a
2759	O60462-2	2	2	2.1	909	102215	5.3	Isoform A0 of O60462
2759	O60462	2	2	2	931	104831	5.2	Neuropilin-2 precursor
2759	UPI000014020F	2	2	2	931	104859	5.2	Neuropilin-2 precursor (Vascular endothelial cell growth factor 165 receptor 2).
2760	Q5TER5	2	3	2.1	860	98089	8.4	Exosome component 10
2760	Q01780	2	3	2	885	100831	8.5	Exosome component 10
2761	Q05481	2	3	2	1191	137226	9.3	Zinc finger protein 91
2761	UPI00002038F9	2	3	2	1191	137217	9.3	zinc finger protein 91
2762	Q96QC0	2	5	2	940	99058	9.2	Serine/threonine-protein phosphatase 1 regulatory subunit 10
2763	O75151	2	2	1.9	1101	121232	9.2	PHD finger protein 2
2763	UPI0000D618C2	2	2	1.9	1095	120501	9.4	PHD finger protein 2 (GRC5).
2763	Q4VXB9	2	2	1.9	1096	120775	9.2	PHD finger protein 2
2764	Q3LIC4	2	2	1.9	1072	118427	8.7	Hypothetical protein Nbla00003
2764	Q7Z3K3-3	2	2	1.5	1366	151213	7.3	Isoform 3 of Q7Z3K3
2764	Q7Z3K3-2	2	2	1.5	1357	150129	7.3	Isoform 2 of Q7Z3K3
2764	Q5SZS1	2	2	1.5	1315	145295	7.2	Pogo transposable element with ZNF domain
2764	Q7Z3K3	2	2	1.4	1410	155343	7.4	Pogo transposable element with ZNF domain
2765	Q59G54	2	2	1.9	1188	136621	6	Bromodomain adjacent to zinc finger domain, 1A isoform b variant
2765	UPI0000D623EF	2	2	1.4	1525	175440	6.9	Bromodomain adjacent to zinc finger domain protein 1A (ATP-utilizing chromatin assembly and remodeling factor 1) (hACF1) (ATP-dependent chromatin remodelling protein) (Williams syndrome transcription factor-related chromatin-remodeling factor 180) (WCRF18
2765	UPI0000D623EE	2	2	1.4	1557	178758	6.6	Bromodomain adjacent to zinc finger domain protein 1A (ATP-utilizing chromatin assembly and remodeling factor 1) (hACF1) (ATP-dependent chromatin remodelling protein) (Williams syndrome transcription factor-related chromatin-remodeling factor 180) (WCRF18
2765	Q9NRL2-2	2	2	1.4	1524	175384	6.8	Isoform 2 of Q9NRL2
2765	Q9NRL2	2	2	1.4	1556	178702	6.6	Bromodomain adjacent to zinc finger domain protein 1A
2766	Q6PJM4	2	2	2.6	915	105772	8.1	ZNFX1 protein
2766	Q5JXR6	2	2	1.9	1270	146226	8.4	Zinc finger, NFX1-type containing 1
2766	Q9P2E3	2	2	1.3	1918	220225	7.3	NFX1-type zinc finger-containing protein 1
2767	Q6DD85	2	2	3.6	662	74085	4.8	FKBP15 protein
2767	Q5T1M5	2	2	1.9	1244	136273	5.2	FK506-binding protein 15
2767	Q9Y4D0	2	2	1.9	1234	135179	5.2	KIAA0674 protein

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2767	UPI0000DD7F7E	2	2	1.8	1342	146538	5.6	PREDICTED: similar to Golgin subfamily A member 6 (Golgin linked to PML) (Golgin-like protein)
2768	Q8IWR0	2	2	1.9	971	110538	7.3	Zinc finger CCCH domain-containing protein 7A
2769	Q2NLD0	2	5	2.1	891	100275	6.6	ATP9A protein
2769	O75110	2	5	1.8	1047	118582	7.8	Probable phospholipid-transporting ATPase IIA
2770	O94909-2	2	2	2.1	989	109861	5.5	Isoform 2 of O94909
2770	O94909	2	2	1.8	1142	126526	5	Uncharacterized protein KIAA0819
2771	Q5TCZ1	2	2	1.8	1133	125289	8.9	SH3 and PX domain-containing protein 2A
2772	Q86Y65	2	7	3.3	900	104487	5.2	KIAA1529 protein
2772	Q5VV25	2	7	1.8	1646	191099	6	KIAA1529
2772	UPI0000D618D4	2	7	1.8	1708	198116	6	KIAA1529 (KIAA1529), mRNA
2772	Q9P1Z9	2	7	1.8	1680	194698	6.1	KIAA1529 protein
2772	Q68DP5	2	7	1.8	1708	198122	6	Protein KIAA1529
2773	Q96FS4	2	4	1.8	1042	112149	6.6	Signal-induced proliferation-associated protein 1
2773	UPI0000163B1E	2	4	1.8	1042	112116	6.6	signal-induced proliferation-associated protein 1
2774	Q68DI5	2	3	2.3	983	111509	6.3	Hypothetical protein DKFZp781H1425
2774	O95163	2	3	1.7	1332	150191	6	Elongator complex protein 1
2774	Q8N516	2	3	1.7	1332	150223	6	Inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase complex-associated protein
2774	Q4LE38	2	3	1.7	1342	151455	6	IKBKAP variant protein
2775	UPI0000D61533	2	2	1.8	1224	135907	6.5	Uncharacterized protein C4orf8 (Protein IT14).
2775	P78312-2	2	2	1.8	1224	135964	6.5	Isoform 2 of P78312
2775	P78312	2	2	1.7	1265	139988	6.5	Uncharacterized protein C4orf8
2775	UPI0000D61532	2	2	1.7	1265	139972	6.5	Uncharacterized protein C4orf8 (Protein IT14).
2776	Q14126	2	4	1.7	1117	122385	5.3	Desmoglein-2 precursor
2776	Q4KKU6	2	4	1.7	1118	122294	5.2	Desmoglein 2
2777	UPI0000074057	2	10	2	1518	170600	8.3	poly (ADP-ribose) polymerase family, member 14
2777	Q460N5-4	2	10	2	1517	170718	7.5	Isoform 4 of Q460N5
2777	Q460N5-2	2	10	1.8	1638	184342	7.9	Isoform 2 of Q460N5
2777	Q460N5	2	10	1.7	1720	193752	8	Poly [ADP-ribose] polymerase 14
2778	Q6ZV73	2	10	1.7	1430	160816	7	FYVE, RhoGEF and PH domain-containing protein 6
2778	UPI00001C0A5D	2	10	1.7	1430	160825	7	FYVE, RhoGEF and PH domain containing 6
2779	Q8TEQ6	2	7	1.7	1508	168560	6.6	Gem-associated protein 5
2779	UPI000020D072	2	7	1.7	1508	168589	6.6	Gem-associated protein 5 (Gemin5).
2780	UPI0000D6160C	2	2	2	1192	138141	8	Ribonuclease III (EC 3.1.26.3) (RNase III) (Drosha) (p241).
2780	Q9NRR4-3	2	2	2	1192	138157	8	Isoform 3 of Q9NRR4
2780	Q9NRR4-2	2	2	1.8	1306	151296	7.6	Isoform 2 of Q9NRR4
2780	Q9NRR4	2	2	1.7	1374	159315	7.9	Ribonuclease 3
2780	UPI000049E005	2	2	1.7	1373	159184	7.9	Ribonuclease III (EC 3.1.26.3) (RNase III) (Drosha) (p241).
2780	UPI0000163BD8	2	2	1.7	1374	159244	7.8	ribonuclease III, nuclear
2781	Q9UPX6	2	3	1.7	916	102993	7.3	UPF0258 protein KIAA1024
2782	A2RUB6	2	2	1.6	949	109526	8.3	CCDC66 protein
2783	O14672	2	2	1.6	748	84142	7.8	ADAM 10 precursor

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2784	O60266	2	3	1.6	1144	128960	6.6	Adenylate cyclase type 3
2784	UPI0000052BD3	2	3	1.6	1144	128970	6.6	adenylate cyclase 3
2785	O94913	2	2	1.6	1654	183980	8.9	Pre-mRNA cleavage complex 2 protein Pcf11
2786	Q6ZUT7	2	2	1.6	1281	145809	6.9	CDNA FLJ43337 fis, clone NT2RI3007158
2786	UPI0000D62441	2	2	0.8	2458	275431	6.3	KIAA1409 (KIAA1409), mRNA
2786	UPI000059F076	2	2	0.8	2458	275473	6.3	hypothetical protein LOC57578
2786	UPI0000231CA2	2	2	0.8	2508	281190	6.3	KIAA1409 (KIAA1409), mRNA
2786	Q9P2D8	2	2	0.8	2461	275484	6.3	Protein KIAA1409
2787	Q8IZH2	2	4	1.6	1706	194106	7.2	5'-3' exoribonuclease 1
2787	UPI0000480180	2	4	1.6	1693	192713	7.3	5""-3"" exoribonuclease 1 isoform b
2787	Q8IZH2-2	2	4	1.6	1694	192842	7.3	Isoform 2 of Q8IZH2
2788	Q8WXR4-3	2	2	1.8	1251	141339	7.6	Isoform 3 of Q8WXR4
2788	UPI0000D61265	2	2	1.7	1314	148838	7.9	Myosin IIIB (EC 2.7.11.1).
2788	UPI0000D61263	2	2	1.7	1278	144818	8.1	Myosin IIIB (EC 2.7.11.1).
2788	UPI0000D61262	2	2	1.7	1275	144552	8.2	Myosin IIIB (EC 2.7.11.1).
2788	UPI0000074403	2	2	1.7	1314	148590	7.7	myosin IIIB isoform 1
2788	Q8WXR4-5	2	2	1.7	1275	144287	8.1	Isoform 5 of Q8WXR4
2788	Q8WXR4-4	2	2	1.7	1314	148573	7.7	Isoform 4 of Q8WXR4
2788	Q8WXR4-2	2	2	1.7	1278	144552	8	Isoform 2 of Q8WXR4
2788	Q8WXR4	2	2	1.6	1341	151786	8.1	Myosin-IIIB
2788	UPI0000D61264	2	2	1.6	1341	152051	8.2	Myosin IIIB (EC 2.7.11.1).
2788	UPI0000074402	2	2	1.6	1341	151803	8.1	myosin IIIB isoform 2
2788	Q8WXR4-7	2	2	1.6	1350	152756	8.2	Isoform 7 of Q8WXR4
2789	Q9Y2H0	2	2	1.6	989	107567	7.3	Disks large-associated protein 4
2789	Q9Y2H0-2	2	2	1.6	992	108012	7.1	Isoform 2 of Q9Y2H0
2790	UPI0000DD7D5C	2	3	1.6	1977	209273	8.5	PREDICTED: similar to NHS-like 1 isoform 1
2791	Q96RT1-7	2	2	1.6	1302	146086	5.3	Isoform 7 of Q96RT1
2791	Q96RT1-6	2	2	1.6	1340	150601	5.5	Isoform 6 of Q96RT1
2791	Q96RT1-4	2	2	1.6	1346	151251	5.4	Isoform 4 of Q96RT1
2791	A0AVR1	2	2	1.5	1371	153952	5.5	Erbb2 interacting protein
2791	UPI0000D61630	2	2	1.5	1361	152723	5.4	Protein LAP2 (Erbb2-interacting protein) (Erbin) (Densin-180-like protein).
2791	Q96RT1-5	2	2	1.5	1356	152290	5.4	Isoform 5 of Q96RT1
2791	Q96RT1-3	2	2	1.5	1360	152652	5.4	Isoform 3 of Q96RT1
2791	Q96RT1-2	2	2	1.5	1371	153926	5.5	Isoform 2 of Q96RT1
2791	Q96RT1	2	2	1.5	1412	158297	5.5	Protein LAP2
2791	Q1RMD0	2	2	1.5	1371	153788	5.5	Erbb2 interacting protein
2791	Q1RMC9	2	2	1.5	1367	153515	5.5	ERBB2IP protein
2792	A1L0S8	2	8	1.5	1132	129465	5.3	CROCC protein
2792	A1L0S9	2	8	1.5	1132	129524	5.3	CROCC protein
2792	Q5TZA0	2	8	0.9	1898	214564	5.5	Ciliary rootlet coiled-coil, rootletin
2792	UPI0000DBEEE1	2	8	0.8	2009	227616	5.6	Rootletin (Ciliary rootlet coiled-coil protein).
2792	UPI000042B0BB	2	8	0.8	2017	228422	5.5	ciliary rootlet coiled-coil, rootletin
2792	Q5TZA2	2	8	0.8	2017	228521	5.5	Rootletin
2793	UPI000045728B	2	3	1.6	1386	154670	6.8	KIAA0922 (KIAA0922), mRNA
2793	Q86Y92	2	3	1.6	1387	154717	6.8	Protein KIAA0922
2793	A2VDJ0	2	3	1.5	1461	163446	7.1	KIAA0922
2793	UPI00001D1AD9	2	3	1.5	1462	163517	7.1	hypothetical protein LOC23240
2794	O60885-2	2	3	2.8	722	80463	8.6	Isoform 2 of O60885
2794	Q4G0X8	2	3	2.5	794	88289	8.4	BRD4 protein
2794	O60885	2	3	1.5	1362	152218	9.2	Bromodomain-containing protein 4
2794	Q86YS8	2	3	1.1	1846	200087	6.4	BRD4-NUT fusion oncoprotein

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
2795	UPI00004570A3	2	6	2.8	1007	111775	5.7	SET-binding factor 1 (Sbf1) (Myotubularin-related protein 5).
2795	O95248-2	2	6	2.8	1007	111702	5.7	Isoform 2 of O95248
2795	O95248	2	6	1.5	1866	208255	7.2	SET-binding factor 1
2795	UPI0000D6217C	2	6	1.5	1893	211075	7.1	SET-binding factor 1 (Sbf1) (Myotubularin-related protein 5).
2795	UPI00004570A2	2	6	1.5	1864	208137	7.2	SET-binding factor 1 (Sbf1) (Myotubularin-related protein 5).
2795	O95248-4	2	6	1.5	1893	211047	7.1	Isoform 4 of O95248
2795	O95248-3	2	6	1.5	1867	208313	6.9	Isoform 3 of O95248
2796	UPI00004577B6	2	6	1.6	1638	182237	6.9	nucleoporin 188kDa
2796	Q7Z3K8	2	6	1.6	1639	182478	6.9	Hypothetical protein DKFZp686L1653
2796	Q14675	2	6	1.5	1745	195697	6.7	KIAA0169 protein
2796	Q5SRE5	2	6	1.5	1749	196041	6.7	188 kDa nucleoporin
2797	Q504Q3	2	3	1.5	1202	135367	6	PAB-dependent poly(A)-specific ribonuclease subunit 2
2797	UPI0000577D0A	2	3	1.5	1202	135367	6	ubiquitin specific protease 52
2797	UPI00001AE7A6	2	3	1.5	1198	135008	5.9	ubiquitin specific protease 52
2797	UPI000007464B	2	3	1.5	1198	135035	5.9	ubiquitin specific protease 52
2797	Q504Q3-3	2	3	1.5	1201	135280	6	Isoform 3 of Q504Q3
2797	Q504Q3-2	2	3	1.5	1198	135008	5.9	Isoform 2 of Q504Q3
2798	Q92954-4	2	2	1.7	1270	136547	9.5	Isoform D of Q92954
2798	Q92954-3	2	2	1.6	1311	141106	9.4	Isoform C of Q92954
2798	Q92954	2	2	1.5	1404	151076	9.5	Proteoglycan-4 precursor (Lubricin) (Megakaryocyte-stimulating factor) (Superficial zone proteoglycan) [Contains: Proteoglycan-4 C-terminal part]
2798	Q92954-6	2	2	1.5	1361	146467	9.5	Isoform F of Q92954
2798	Q92954-2	2	2	1.5	1363	146517	9.6	Isoform B of Q92954
2799	O15056-3	2	2	1.6	1288	143445	7.6	Isoform 2A of O15056
2799	O15056	2	2	1.4	1496	165537	7.3	Synaptojanin-2
2799	UPI0000D61505	2	2	1.4	1451	160403	7.3	Synaptojanin-2 (EC 3.1.3.36) (Synaptic inositol-1,4,5-trisphosphate 5- phosphatase 2).
2799	O15056-2	2	2	1.4	1451	160433	7.3	Isoform 2B1 of O15056
2800	O95811	2	7	1.4	1580	179670	6.8	Retinoblastoma binding protein 2 homolog 1
2800	UPI00001AE68F	2	7	1.4	1580	179408	6.8	Jumonji, AT rich interactive domain 1B (RBP2-like)
2800	Q9Y3Q5	2	7	1.4	1544	175657	6.7	PLU-1 protein
2800	UPI00001AE781	2	7	1.3	1680	190102	7.4	Jumonji, AT rich interactive domain 1B (RBP2-like)
2800	Q9UGL1	2	7	1.3	1681	190118	7.4	Jumonji/ARID domain-containing protein 1B
2801	Q5VVH4	2	4	1.4	1821	206688	8.8	Pleckstrin homology domain-interacting protein
2801	Q8WWQ0	2	4	1.4	1821	206646	8.8	WD repeat domain 11 protein
2802	UPI0000140BED	2	4	1.8	997	104697	9.7	Nuclear factor related to kappa-B-binding protein (DNA-binding protein R kappa-B).
2802	Q6P4R8	2	4	1.4	1299	139001	9.2	Nuclear factor related to kappa-B-binding protein
2802	Q6P4R8-2	2	4	1.4	1324	141860	9	Isoform 2 of Q6P4R8
2803	Q9P2M7	2	2	1.4	1197	136386	5.5	Cingulin
2804	Q5VW08	2	2	2.3	1039	116940	8.2	OTTHUMP00000018324
2804	A3KMH1	2	2	1.3	1872	210922	7	KIAA0564 protein

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2804	UPI00001606AC	2	2	1.3	1905	214823	7.4	hypothetical protein LOC23078 isoform a
2805	O60287	2	3	1.3	2248	252316	6.4	Nucleolar preribosomal-associated protein 1
2806	Q5JPV5	2	3	1.6	1501	169350	6.3	Myeloid/lymphoid or mixed-lineage leukemia (Trithorax homolog, Drosophila); translocated to, 4
2806	UPI0000711FD9	2	3	1.5	1651	187671	6.5	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 4 isoform 2
2806	Q5TIG7	2	3	1.5	1612	181998	6.5	Myeloid/lymphoid or mixed-lineage leukemia (Trithorax homolog, Drosophila); translocated to, 4
2806	Q59FP0	2	3	1.5	1639	186298	6.5	Afadin variant
2806	P55196-2	2	3	1.5	1611	181899	6.5	Isoform 1 of P55196
2806	UPI0000D61519	2	3	1.4	1665	189138	6.5	Afadin (Protein AF-6).
2806	Q5TIG5	2	3	1.4	1665	189153	6.5	Myeloid/lymphoid or mixed-lineage leukemia (Trithorax homolog, Drosophila); translocated to, 4
2806	P55196-3	2	3	1.4	1743	197652	6.5	Isoform 3 of P55196
2806	P55196	2	3	1.3	1816	205604	6.8	Afadin
2806	UPI0000D61518	2	3	1.3	1824	206788	6.5	Afadin (Protein AF-6).
2806	UPI00004574E7	2	3	1.3	1816	205589	6.8	Afadin (Protein AF-6).
2806	P55196-4	2	3	1.3	1824	206803	6.5	Isoform 4 of P55196
2807	Q4G0A5	2	3	2.1	992	112857	7	KIF14 protein
2807	Q14CI8	2	3	1.3	1648	186464	7.9	Kinesin family member 14
2807	UPI00004562CC	2	3	1.3	1648	186615	7.9	Kinesin-like protein KIF14.
2807	Q15058	2	3	1.3	1648	186490	7.9	Kinesin-like protein KIF14
2808	Q9C0D5	2	2	1.3	1644	179425	8.4	Tetratricopeptide repeat, ankyrin repeat and coiled-coil-containing protein 1
2808	UPI0000D61252	2	2	1.2	1861	202244	8.3	TPR domain, ankyrin-repeat and coiled-coil-containing
2808	UPI00004B247A	2	2	1.2	1861	202191	8.3	TPR domain, ankyrin-repeat and coiled-coil-containing
2809	Q9UHB7-2	2	16	1.7	900	98205	9.3	Isoform 2 of Q9UHB7
2809	Q9UHB7	2	16	1.3	1163	127459	9.3	AF4/FMR2 family member 4
2810	Q5T5E1	2	2	1.5	1206	134308	7.9	Zinc finger, MYM-type 4
2810	A0JP20	2	2	1.5	1224	136344	8.1	ZMYM4 protein
2810	O43308	2	2	1.4	1270	141148	8.1	KIAA0425 protein
2810	Q7L3Q4	2	2	1.3	1434	160264	8	ZMYM4 protein
2810	A0JP19	2	2	1.2	1516	169250	6.9	ZMYM4 protein
2810	Q5VZL5	2	2	1.2	1548	172787	6.8	Zinc finger MYM-type protein 4
2811	Q2TAZ4	2	7	3.3	788	85874	5	MDC1 protein
2811	UPI0000D6113B	2	7	1.4	1825	197569	5.7	UPI0000D6113B UniRef100 entry
2811	A2BF04	2	7	1.2	2089	226606	5.5	Mediator of DNA damage checkpoint 1
2811	UPI00004A3B34	2	7	1.2	2089	226636	5.5	UPI00004A3B34 UniRef100 entry
2811	Q14676	2	7	1.2	2089	226664	5.5	Mediator of DNA damage checkpoint protein 1
2811	Q0EFC2	2	7	1.2	2089	226680	5.5	KIAA0170 protein
2812	Q6DT37	2	2	1.2	1551	172517	6.3	Serine/threonine-protein kinase MRCK gamma

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2812	UPI000047C9E2	2	2	1.2	1551	172458	6.3	Serine/threonine-protein kinase MRCK gamma (EC 2.7.11.1) (CDC42- binding protein kinase gamma) (Myotonic dystrophy kinase-related CDC42-binding kinase gamma) (Myotonic dystrophy protein kinase-like alpha) (MRCK gamma) (DMPK-like gamma).
2813	Q96Q89-4	2	4	1.3	1722	199862	5.2	Isoform 4 of Q96Q89
2813	Q96Q89	2	4	1.2	1820	210681	5.7	M-phase phosphoprotein 1
2813	UPI00001F9377	2	4	1.2	1780	206134	5.8	M-phase phosphoprotein 1
2813	UPI000013D104	2	4	1.2	1820	210628	5.7	M-phase phosphoprotein 1 (MPP1) (Kinesin-related motor interacting with PIN1).
2813	Q96Q89-3	2	4	1.2	1780	206187	5.8	Isoform 3 of Q96Q89
2813	Q96Q89-2	2	4	1.2	1853	214327	5.9	Isoform 2 of Q96Q89
2814	Q9P2K8	2	2	1.2	1649	186837	6.3	Eukaryotic translation initiation factor 2-alpha kinase 4
2814	UPI0000160791	2	2	1.2	1649	186909	6.3	eukaryotic translation initiation factor 2 alpha kinase 4
2814	Q9P2K8-2	2	2	1.2	1621	183644	6.5	Isoform 2 of Q9P2K8
2815	A1YCA4	2	2	1.1	2154	231133	5.7	SEC16L
2815	O15027-3	2	2	1.1	2159	231249	5.6	Isoform 3 of O15027
2815	O15027-2	2	2	1.1	2134	228868	5.6	Isoform 2 of O15027
2815	O15027	2	2	1.1	2179	233515	5.6	Uncharacterized protein KIAA0310
2816	Q2VPJ7	2	2	4	657	73637	6.4	NAG protein
2816	A2RRP1	2	2	1.1	2371	268583	6	Neuroblastoma-amplified protein
2816	UPI00001AEA68	2	2	1.1	2371	268569	6	neuroblastoma-amplified protein
2816	Q8NFY8	2	2	1.1	2371	268466	5.9	Neuroblastoma-amplified protein
2817	Q3LIB1	2	3	2.2	905	103147	6.1	Hypothetical protein Nbla00445
2817	O15031	2	3	1.1	1838	205126	6.2	Plexin-B2 precursor
2817	UPI00006C1B9B	2	3	1.1	1884	209692	6.5	PREDICTED: similar to Plexin-B2 precursor (MM1)
2818	UPI0000D6255B	2	2	1.5	1339	135917	6.5	Collagen alpha-1(XVIII) chain precursor [Contains: Endostatin].
2818	UPI00004F6EDB	2	2	1.5	1336	135510	6.5	alpha 1 type XVIII collagen isoform 2 precursor
2818	P39060-2	2	2	1.5	1339	135761	6.5	Isoform 3 of P39060
2818	UPI0000D6255C	2	2	1.4	1476	150048	5.7	Collagen alpha-1(XVIII) chain precursor [Contains: Endostatin].
2818	UPI0000DB273B	2	2	1.3	1516	153767	5.7	alpha 1 type XVIII collagen isoform 1 precursor
2818	P39060-1	2	2	1.3	1519	154018	5.7	Isoform 2 of P39060
2818	P39060	2	2	1.1	1754	178159	6	Collagen alpha-1(XVIII) chain precursor [Contains: Endostatin]
2818	UPI0000D6255D	2	2	1.1	1755	178377	6.1	Collagen alpha-1(XVIII) chain precursor [Contains: Endostatin].
2819	P42345	2	3	1.1	2549	288890	7.2	FKBP12-rapamycin complex-associated protein

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2819	UPI000049DC6B	2	3	1.1	2551	289062	7.2	FKBP12-rapamycin complex-associated protein (FK506-binding protein 12- rapamycin complex-associated protein 1) (Rapamycin target protein) (RAPT1) (Mammalian target of rapamycin) (mTOR).
2819	Q4LE76	2	3	1	2583	292863	7.6	FRAP1 variant protein
2820	Q14571	2	3	1.1	2701	308076	6.5	Inositol 1,4,5-trisphosphate receptor type 2
2820	UPI0000D621C2	2	3	1.1	2703	308290	6.4	Inositol 1,4,5-trisphosphate receptor type 2 (Type 2 inositol 1,4,5- trisphosphate receptor) (Type 2 InsP3 receptor) (IP3 receptor isoform 2) (InsP3R2).
2820	UPI00001FB7D2	2	3	1.1	2701	308062	6.4	inositol 1,4,5-triphosphate receptor, type 2
2821	UPI0000E4C8FD	2	2	1.2	1794	197398	6.5	myosin light chain kinase isoform 3B
2821	Q15746-4	2	2	1.2	1794	197631	6.8	Isoform 3B of Q15746
2821	Q15746	2	2	1.1	1914	210772	6.2	Myosin light chain kinase, smooth muscle
2821	UPI0000E4C8FC	2	2	1.1	1845	203054	6.2	myosin light chain kinase isoform 2
2821	UPI0000D61B67	2	2	1.1	1842	202643	6.1	Myosin light chain kinase, smooth muscle (EC 2.7.11.18) (MLCK) (Telokin) (Kinase-related protein) (KRP).
2821	UPI0000D61B66	2	2	1.1	1864	205349	6.8	Myosin light chain kinase, smooth muscle (EC 2.7.11.18) (MLCK) (Telokin) (Kinase-related protein) (KRP).
2821	UPI0000457165	2	2	1.1	1845	203085	6.1	Myosin light chain kinase, smooth muscle (EC 2.7.11.18) (MLCK) (Telokin) (Kinase-related protein) (KRP).
2821	UPI0000457163	2	2	1.1	1914	210744	6.1	Myosin light chain kinase, smooth muscle (EC 2.7.11.18) (MLCK) (Telokin) (Kinase-related protein) (KRP).
2821	UPI000020A0AE	2	2	1.1	1914	210713	6.2	myosin light chain kinase isoform 1
2821	UPI000013E30E	2	2	1.1	1863	205057	6.5	myosin light chain kinase isoform 3A
2821	Q15746-6	2	2	1.1	1913	210643	6.2	Isoform Del
2821	Q15746-5	2	2	1.1	1841	202568	6.2	Isoform 4 of Q15746
2821	Q15746-3	2	2	1.1	1863	205277	6.8	Isoform 3A of Q15746
2821	Q15746-2	2	2	1.1	1845	203127	6.2	Isoform 2 of Q15746
2822	Q96JI4	2	20	1.1	1778	200950	6.8	KIAA1843 protein
2823	Q9HCK1	2	4	1.1	1779	200909	6.3	KIAA1571 protein
2824	UPI00001FC8BF	2	2	1.1	1672	190329	5.5	RING finger protein 17.
2825	A0JP21	2	2	1	1770	198626	5.5	KIF13A protein
2825	UPI0000D613F5	2	2	1	1759	197274	5.6	Kinesin-like protein KIF13A (Kinesin-like protein RBKIN).
2825	UPI0000D613F4	2	2	1	1768	198431	5.5	Kinesin-like protein KIF13A (Kinesin-like protein RBKIN).
2825	UPI0000D613F3	2	2	1	1772	198816	5.5	Kinesin-like protein KIF13A (Kinesin-like protein RBKIN).
2825	UPI00004708ED	2	2	1	1768	198440	5.5	Kinesin-like protein KIF13A (Kinesin-like protein RBKIN).
2825	Q9H1H9-3	2	2	1	1749	196069	5.7	Isoform 3 of Q9H1H9
2825	A0JP22	2	2	1	1757	197084	5.6	KIF13A protein
2825	UPI00004708EC	2	2	0.9	1803	202121	5.6	Kinesin-like protein KIF13A (Kinesin-like protein RBKIN).

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2825	UPI00004573C6	2	2	0.9	1807	202497	5.6	Kinesin-like protein KIF13A (Kinesin-like protein RBKIN).
2825	UPI000012DAD8	2	2	0.9	1805	202258	5.6	kinesin family member 13A
2825	Q9H1H9	2	2	0.9	1805	202307	5.6	Kinesin-like protein KIF13A
2826	Q4LE74	2	5	1.1	2028	229712	8.6	MYO9B variant protein
2826	Q13459-2	2	5	1.1	2023	229298	8.5	Isoform Short of Q13459
2826	Q13459	2	5	1	2158	243555	8.7	Myosin-IXb
2826	UPI0000D61740	2	5	1	2157	243354	8.8	Myosin-9B (Myosin IXb) (Unconventional myosin-9b).
2826	UPI00001B55A5	2	5	1	2157	243398	8.8	myosin IXB
2827	UPI000037848A	2	2	1.2	1851	203621	6.8	sidekick 2
2827	Q58EX2-2	2	2	1.1	1919	210903	7.1	Isoform 2 of Q58EX2
2827	Q58EX2	2	2	1	2170	239118	7	Protein sidekick-2 precursor
2827	Q58EX2-4	2	2	1	2214	244092	7.1	Isoform 4 of Q58EX2
2827	Q58EX2-3	2	2	1	2151	236894	7	Isoform 3 of Q58EX2
2828	Q7Z3P7	2	2	2	1004	111594	8.7	Hypothetical protein DKFZp686D219
2828	Q8N3A2	2	2	1.5	1321	146863	6.9	Hypothetical protein DKFZp761J031
2828	Q5T5U3	2	2	1	1957	217329	7.8	Rho GTPase-activating protein 21
2828	Q9P2C3	2	2	1	1944	215997	7.8	KIAA1424 protein
2828	Q8NI19	2	2	1	1957	217325	7.8	Rho-GTPase activating protein 10
2829	Q8IYT8	2	2	1	1036	112726	8.5	Serine/threonine-protein kinase ULK2
2829	UPI0000167B55	2	2	1	1036	112756	8.5	unc-51-like kinase 2
2829	UPI000013D19B	2	2	1	1036	112694	8.5	Serine/threonine-protein kinase ULK2 (EC 2.7.11.1) (Unc-51-like kinase 2).
2830	Q8WXQ5	2	3	1	993	108961	8.6	Serine/threonine protein kinase kkialre-like 1
2831	Q9ULI4	2	2	1	1840	190320	8.8	Kinesin-like protein KIF26A
2832	UPI0000DBEEC3	2	2	1	2122	236458	6.3	CDNA FLJ46511 fis, clone THYMU3031868.
2832	Q8N201	2	2	1	2190	244295	6.1	Integrator complex subunit 1
2832	A4D212	2	2	0.9	2394	265754	6.7	DKFZP586J0619 protein
2832	UPI0000DD7DB8	2	2	0.9	2381	264069	6.6	integrator complex subunit 1
2832	A4D213	2	2	0.9	2408	266641	6.7	DKFZP586J0619 protein
2833	Q5S007	2	3	0.9	2527	286055	6.8	Leucine-rich repeat serine/threonine-protein kinase 2
2834	Q6Q759	2	3	0.9	2223	251739	6.2	Sperm-associated antigen 17
2835	Q9H2D6-5	2	3	3.5	593	68041	6.1	Isoform 1 of Q9H2D6
2835	Q9H2D6	2	3	0.9	2365	261373	8.5	TRIO and F-actin-binding protein
2835	Q9H2D6-2	2	3	0.9	2267	250721	8.2	Isoform 3 of Q9H2D6
2836	UPI000045890A	2	2	0.9	2884	315868	5.3	Collagen alpha-1(XII) chain precursor.
2836	Q5VYK1	2	2	0.8	3063	333147	5.5	Collagen type XII alpha 1
2836	UPI0000457469	2	2	0.8	3063	333256	5.6	Collagen alpha-1(XII) chain precursor.
2836	Q99715	2	2	0.8	3063	333194	5.5	Collagen alpha-1(XII) chain precursor
2837	Q6V0I7	2	4	0.8	3222	351192	5.1	FAT tumor suppressor homolog 4
2837	UPI0000DB85F8	2	4	0.5	4924	536560	4.9	FAT tumor suppressor homolog 4
2838	Q96Q15-2	2	2	0.9	3521	395454	6.3	Isoform 2 of Q96Q15
2838	Q96Q15	2	2	0.8	3657	410262	6.5	Serine/threonine-protein kinase SMG1

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
2838	UPI0000DBEEA7	2	2	0.8	3665	410958	6.5	Serine/threonine-protein kinase SMG1 (EC 2.7.11.1) (SMG-1) (hSMG-1) (Lambda/iota protein kinase C-interacting protein) (Lambda-interacting protein) (61E3.4).
2838	UPI00004F8E22	2	2	0.8	3661	410501	6.5	PI-3-kinase-related kinase SMG-1
2839	UPI00006C201C	2	2	0.8	4307	492627	6.5	PREDICTED: similar to dynein, cytoplasmic, heavy chain 2 isoform 3
2840	P21359-4	2	2	1.3	1598	180212	7	Isoform 4 of P21359
2840	P21359	2	2	0.7	2839	319372	7.4	Neurofibromin (Neurofibromatosis-related protein NF-1) [Contains: Neurofibromin truncated]
2840	P21359-2	2	2	0.7	2818	317032	7.3	Isoform 1 of P21359
2841	Q5VUA4	2	3	0.7	2099	231993	6.4	Zinc finger protein 318
2842	P98161	2	2	0.6	4303	462573	6.7	Polycystin-1 precursor
2842	UPI00001B0454	2	2	0.6	4303	462534	6.7	polycystin 1 isoform 1 precursor
2842	UPI0000156133	2	2	0.6	4302	462422	6.7	polycystin 1 isoform 2 precursor
2842	P98161-3	2	2	0.6	4302	462445	6.7	Isoform 3 of P98161
2842	P98161-2	2	2	0.6	4292	461409	6.8	Isoform 2 of P98161
2843	UPI00006C1DAD	2	2	0.8	2011	229391	7.3	PREDICTED: similar to ataxia telangiectasia and Rad3 related protein
2843	Q13535	2	2	0.6	2644	301365	7.4	Serine/threonine-protein kinase ATR
2843	UPI0000DD7BC9	2	2	0.6	2612	298136	7.6	PREDICTED: similar to Serine/threonine-protein kinase ATR (Ataxia telangiectasia and Rad3-related protein) (FRAP-related protein 1)
2843	UPI0000D61B87	2	2	0.6	2582	294417	7.5	Serine/threonine-protein kinase ATR (EC 2.7.11.1) (Ataxia telangiectasia and Rad3-related protein) (FRAP-related protein 1).
2843	UPI0000D61B86	2	2	0.6	2646	301564	7.5	Serine/threonine-protein kinase ATR (EC 2.7.11.1) (Ataxia telangiectasia and Rad3-related protein) (FRAP-related protein 1).
2843	UPI000002E542	2	2	0.6	2644	301450	7.5	ataxia telangiectasia and Rad3 related protein
2843	Q13535-2	2	2	0.6	2580	294217	7.4	Isoform 2 of Q13535
2844	P49454	2	4	0.5	3210	367595	5.1	Centromere protein F
2844	Q5VVM7	2	4	0.5	3114	357527	5.1	Centromere protein F, 350/400ka
2845	Q5VT06	2	2	0.5	3117	350931	6.3	Centrosome-associated protein 350
2845	UPI00004562B9	2	2	0.5	3117	351007	6.3	Centrosome-associated protein 350 (Centrosome-associated protein of 350 kDa).
2845	UPI0000203C9B	2	2	0.5	3116	350860	6.3	centrosome-associated protein 350
2846	Q9NR09	2	3	0.5	4829	527615	6	Baculoviral IAP repeat-containing protein 6
2846	UPI0000DBEF4D	2	3	0.5	4829	527615	6	Baculoviral IAP repeat-containing protein 6 (Ubiquitin-conjugating BIR domain enzyme apollon).

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
2846	UPI00004EC29E	2	3	0.5	4829	527629	6	baculoviral IAP repeat-containing 6
2846	UPI00004578FF	2	3	0.5	4829	527683	6.1	Baculoviral IAP repeat-containing protein 6 (Ubiquitin-conjugating BIR domain enzyme apollon).
2847	P20929	2	2	0.4	6669	773230	9.1	Nebulin
2847	UPI0000E445E4	2	2	0.4	6669	772918	9.1	nebulin
2847	UPI0000D626AB	2	2	0.4	6669	772957	9.1	Nebulin.
2848	Q96JB1	2	5	0.4	4490	514668	6.3	Ciliary dynein heavy chain 8
2848	UPI0000D626B6	2	5	0.4	4699	537743	6.2	Ciliary dynein heavy chain 8 (Axonemal beta dynein heavy chain 8).
2848	Q96JB1-2	2	5	0.4	4454	510452	6.3	Isoform 2 of Q96JB1
2849	UPI0000141B94	2	2	0.4	4563	515611	7	Apolipoprotein B-100 precursor (Apo B-100) [Contains: Apolipoprotein B-48 (Apo B-48)].
2849	UPI0000D820D0	2	2	0.4	4563	515537	7	apolipoprotein B precursor
2850	UPI0000DD87BC	2	6	0.4	5048	534427	5.3	PREDICTED: similar to AHNAK nucleoprotein isoform 1 isoform 1

Supplemental Table 3. Protein list of 3-D dataset

uniref100 database (May, 2007); DTASelect v1.9
At least two unique peptide sequences

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
1	Q15149	229	4235	52.6	4684	531738	5.9	Plectin-1
1	UPI0000457911	229	4235	52.6	4684	531668	5.9	Plectin-1 (PLTN) (PCN) (Hemidesmosomal protein 1) (HD1).
1	Q6S380	229	4235	52.6	4684	531796	6	Plectin 6
2	UPI00004EC29C	187	4256	36.8	5890	629114	6.1	AHNAK nucleoprotein isoform 1
3	P78527	105	1094	28.5	4128	469093	7.1	DNA-dependent protein kinase catalytic subunit
3	UPI000045790C	105	1094	28.5	4127	468980	7.1	DNA-dependent protein kinase catalytic subunit (EC 2.7.11.1) (DNA-PK catalytic subunit) (DNA-PKcs) (DNPK1) (p460).
4	Q13813	103	712	47.4	2472	284538	5.3	Spectrin alpha chain, brain
4	Q13813-2	103	712	47.3	2477	285093	5.4	Isoform 2 of Q13813
4	UPI00004577B5	103	712	47.2	2480	285480	5.4	Spectrin alpha chain, brain (Spectrin, non-erythroid alpha chain) (Alpha-II spectrin) (Fodrin alpha chain).
4	UPI0000D61917	103	712	47.1	2485	286012	5.4	Spectrin alpha chain, brain (Spectrin, non-erythroid alpha chain) (Alpha-II spectrin) (Fodrin alpha chain).
5	P35579	102	1675	54.1	1960	226530	5.6	Myosin-9
6	Q14204	97	574	24.2	4646	532412	6.4	Dynein heavy chain, cytosolic
6	UPI000021D4C1	97	574	24.2	4647	532371	6.4	Dynein heavy chain, cytosolic (DYHC) (Cytoplasmic dynein heavy chain 1) (DHC1) (Dynein heavy chain 1, cytoplasmic 1).
7	UPI0000D61DF7	94	1337	47.3	2639	280044	6	Filamin-A (Alpha-filamin) (Filamin-1) (Endothelial actin-binding protein) (Actin-binding protein 280) (ABP-280) (Nonmuscle filamin).
7	Q5HY53	94	1337	47.3	2639	280016	6	Filamin A, alpha
7	P21333	94	1337	47.1	2647	280737	6.1	Filamin-A
7	UPI00004578B4	94	1337	47.1	2647	280765	6	Filamin-A (Alpha-filamin) (Filamin-1) (Endothelial actin-binding protein) (Actin-binding protein 280) (ABP-280) (Nonmuscle filamin).
8	Q53R99	88	692	46.8	2314	268714	5.6	Hypothetical protein SPTBN1
8	Q01082	88	692	45.9	2364	274608	5.6	Spectrin beta chain, brain 1
8	Q59ER3	88	692	45.6	2377	276168	5.5	Spectrin, beta, non-erythrocytic 1 isoform 1 variant
9	Q9Y490	83	747	45.9	2541	269765	6.1	Talin-1
9	UPI0000167B7F	83	747	45.9	2541	269665	6	talin 1
10	Q00610-2	73	891	53.9	1639	187889	5.7	Isoform 2 of Q00610
10	Q00610	73	891	52.7	1675	191613	5.7	Clathrin heavy chain 1
11	Q5SYZ6	72	1573	51.7	1621	177438	4.4	Nestin
12	Q9NZM1-6	70	435	40.9	2048	233474	6.2	Isoform 6 of Q9NZM1
12	Q9NZM1	70	435	40.6	2061	234706	6.2	Myoferlin
13	UPI0000457129	64	439	32.2	2578	275692	5.8	Filamin-B (FLN-B) (Beta-filamin) (Actin-binding-like protein) (Thyroid autoantigen) (Truncated actin-binding protein) (Truncated ABP) (ABP- 280 homolog) (ABP-278) (Filamin 3) (Filamin homolog 1) (Fh1).
13	O75369-2	64	439	32.2	2578	275697	5.8	Isoform 2 of O75369
13	Q60FE7	64	439	32	2591	276936	5.7	Filamin B
13	O75369	64	439	31.9	2602	278193	5.7	Filamin-B
13	UPI0000457128	64	439	31.9	2602	278188	5.7	Filamin-B (FLN-B) (Beta-filamin) (Actin-binding-like protein) (Thyroid autoantigen) (Truncated actin-binding protein) (Truncated ABP) (ABP- 280 homolog) (ABP-278) (Filamin 3) (Filamin homolog 1) (Fh1).
13	UPI00001AEC01	64	439	31.9	2602	278162	5.7	filamin B, beta (actin binding protein 278)
14	Q4LE68	58	311	45.5	1791	192381	4.4	AKAP12 variant protein
15	O43707	57	994	70.1	911	104854	5.4	Alpha-actinin-4
16	P35580	56	316	42.2	1976	228937	5.5	Myosin-10
16	Q149N4	56	316	42.2	1976	228981	5.5	Myosin, heavy chain 10, non-muscle
16	Q149N3	56	316	42.2	1976	228997	5.5	Myosin, heavy chain 10, non-muscle
16	P35580-3	56	316	41.7	1997	231307	5.5	Isoform 3 of P35580
17	P46940	56	355	41.5	1657	189251	6.5	Ras GTPase-activating-like protein IQGAP1
18	Q6ZUD8	53	244	45.4	1394	157961	6.1	CDNA FLJ43793 fis, clone TESTI4000014, highly similar to 130 kDa leucine-rich protein
19	Q4LE83	50	334	26.3	2548	277368	6.6	FASN variant protein
19	UPI0000D623B2	50	334	26.3	2548	277428	6.6	Fatty acid synthase (EC 2.3.1.85) [Includes: [Acyl-carrier-protein] S- acetyltransferase (EC 2.3.1.38); [Acyl-carrier-protein] S- malonyltransferase (EC 2.3.1.39); 3-oxoacyl-[acyl-carrier-protein] synthase (EC 2.3.1.41); 3-oxoacyl-[acyl-carrier-protein] r
20	P46821	49	222	27.6	2468	270618	4.8	Microtubule-associated protein 1B (MAP 1B) [Contains: MAP1 light chain LC1]
20	UPI000013E382	49	222	27.6	2468	270632	4.8	Microtubule-associated protein 1B (MAP 1B) [Contains: MAP1 light chain LC1].
21	Q5CAQ5	47	664	58	802	92340	4.9	Tumor rejection antigen (Gp96) 1
21	P14625	47	664	57.9	803	92469	4.8	Endoplasmin precursor

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
22	O75643	46	196	24	2136	244505	6.1	U5 small nuclear ribonucleoprotein 200 kDa helicase
23	Q9P2E9	45	623	38.4	1410	152472	8.6	Ribosome-binding protein 1
24	Q5T201	44	178	45	1224	138345	7.7	Coatomer protein complex, subunit alpha
25	P11216	43	457	58.8	843	96696	6.9	Glycogen phosphorylase, brain form
26	P18206-2	43	175	48.5	1066	116722	6.1	Isoform 1 of P18206
26	P18206	43	175	45.6	1134	123799	5.7	Vinculin
27	Q9NYU2	43	195	34.2	1531	174976	5.6	UDP-glucose:glycoprotein glucosyltransferase 1 precursor
27	UPI0000D61230	43	195	33.7	1557	177373	5.6	UDP-glucose:glycoprotein glucosyltransferase 1 precursor (EC 2.4.1.-) (UDP-glucose ceramide glucosyltransferase-like 1) (UDP-- Glc:glycoprotein glucosyltransferase) (HUGT1).
27	UPI00000707D8	43	195	33.7	1555	177189	5.6	UDP-glucose ceramide glucosyltransferase-like 1 isoform 1
28	Q00341	42	211	40.5	1268	141439	6.9	Vigilin
29	Q08211	42	388	39.1	1270	140958	6.8	ATP-dependent RNA helicase A
29	UPI0000D62059	42	388	37.7	1315	146474	6.9	ATP-dependent RNA helicase A (EC 3.6.1.-) (Nuclear DNA helicase II) (NDH II) (DEAH box protein 9).
30	P08670	41	2866	78.8	466	53652	5.1	Vimentin
31	P02545	41	712	60.2	664	74140	7	Lamin-A/C
31	Q5I6Y6	41	712	60.2	664	74082	7.2	Lamin A/C transcript variant 1
32	UPI000004D059	41	170	47.4	1048	116052	5.7	integrin alpha-V precursor
33	P13639	39	551	50.7	858	95338	6.8	Elongation factor 2
34	Q14152	39	212	29.5	1382	166569	6.8	Eukaryotic translation initiation factor 3 subunit 10
34	Q24JU4	39	212	29.5	1382	166470	6.7	Eukaryotic translation initiation factor 3, subunit 10 theta, 150/170kDa
35	P55072	38	349	59.4	806	89322	5.3	Transitional endoplasmic reticulum ATPase (TER ATPase) (15S Mg(2+)- ATPase p97 subunit)
35	Q0V924	38	349	59.4	806	89344	5.3	Valosin-containing protein
36	Q9Y4L1	37	257	46.1	999	111335	5.2	150 kDa oxygen-regulated protein precursor
37	UPI000014054E	37	214	25.8	1600	175618	5.3	Eukaryotic translation initiation factor 4 gamma 1 (eIF-4-gamma 1) (eIF-4G1) (eIF-4G 1) (p220).
38	P10809	35	856	71.4	573	61055	5.9	60 kDa heat shock protein, mitochondrial precursor
38	UPI000013D97A	35	856	71.1	575	61213	5.9	60 kDa heat shock protein, mitochondrial precursor (Hsp60) (60 kDa chaperonin) (CPN60) (Heat shock protein 60) (HSP-60) (Mitochondrial matrix protein P1) (P60 lymphocyte protein) (HuCHA60).
39	P14618	35	817	66.9	531	57937	7.8	Pyruvate kinase isozymes M1/M2
39	Q53GK4	35	817	66.9	531	57984	8.1	Pyruvate kinase 3 isoform 1 variant
40	P13667	35	328	56.7	645	72933	5.1	Protein disulfide-isomerase A4 precursor
41	P08238	35	704	51.5	724	83264	5	Heat shock protein HSP 90-beta
41	UPI00001AE8D8	35	704	50.7	736	84758	5.4	Heat shock protein HSP 90-beta (HSP 84) (HSP 90).
42	UPI0000225CC0	35	144	38.7	1091	119772	7.3	ATP citrate lyase isoform 2
42	P53396	35	144	38.3	1101	120839	7.3	ATP-citrate synthase (EC 2.3.3.8) (ATP-citrate (pro-S-)-lyase)
43	P05023	35	467	37.1	1023	112896	5.5	Sodium/potassium-transporting ATPase alpha-1 chain precursor (EC 3.6.3.9) (Sodium pump 1) (Na(+)/K(+) ATPase 1)
44	P12814	34	303	66.3	892	103058	5.4	Alpha-actinin-1
45	Q92598	34	149	49.2	858	96865	5.4	Heat-shock protein 105 kDa
46	P33176	34	124	43.7	963	109685	6.5	Kinesin heavy chain
47	Q7KZF4	34	279	45.4	910	101997	7.2	Staphylococcal nuclease domain-containing protein 1
47	Q59FF0	34	279	42.8	964	107433	7.5	EBNA-2 co-activator variant
48	P27816	34	178	38.2	1152	121019	5.4	Microtubule-associated protein 4
48	UPI000020A6A4	34	178	38.2	1152	121005	5.4	microtubule-associated protein 4 isoform 1
48	Q59FT2	34	178	37.8	1163	122941	6.7	Microtubule-associated protein 4 isoform 1 variant
49	A0AVA9	34	160	27.8	1512	170590	7.3	EPRS protein
50	Q6UVK1	34	219	20	2322	250494	5.5	Chondroitin sulfate proteoglycan 4 precursor
50	UPI00001AEEB6	34	219	20	2322	250534	5.5	chondroitin sulfate proteoglycan 4
51	UPI00003677FD	34	130	19.5	2330	256509	5.8	fibronectin 1 isoform 4 preproprotein
51	UPI0000167B25	34	130	19.3	2355	259223	5.7	fibronectin 1 isoform 3 preproprotein
51	P02751-3	34	130	19.3	2355	259195	5.7	Isoform 3 of P02751
51	P02751	34	130	19.1	2386	262604	5.7	Fibronectin precursor
52	Q4LE33	34	178	18.5	2233	244402	4.9	TNC variant protein
53	P11717	33	126	13.6	2491	274274	5.9	Cation-independent mannose-6-phosphate receptor precursor
53	UPI0000072478	33	126	13.6	2491	274373	5.9	Cation-independent mannose-6-phosphate receptor precursor (CI Man-6-P receptor) (CI-MPR) (M6PR) (Insulin-like growth factor 2 receptor) (Insulin-like growth factor II receptor) (IGF-II receptor) (M6P/IGF2 receptor) (M6P/IGF2R) (300 kDa mannose 6-phosphate
54	P11142	32	585	55	646	70898	5.5	Heat shock cognate 71 kDa protein
55	P31948	32	79	52.1	543	62639	6.8	Stress-induced-phosphoprotein 1
56	Q9Y678	32	187	52.1	874	97718	5.5	Coatomer subunit gamma

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
57	Q2TAL4	32	144	50.7	840	94331	5.2	Heat shock 70kDa protein 4
58	Q86UP2-2	32	117	25.8	1300	149610	5.7	Isoform 2 of Q86UP2
58	Q86UP2	32	117	24.7	1357	156275	5.6	Kinectin
59	P09874	31	96	36.1	1014	113084	8.9	Poly [ADP-ribose] polymerase 1 (EC 2.4.2.30) (PARP-1) (ADPRT) (NAD(+) ADP-ribosyltransferase 1)
60	Q14683	31	84	23.9	1233	143233	7.6	Structural maintenance of chromosomes protein 1A
61	P50395	30	154	76.9	445	50663	6.5	Rab GDP dissociation inhibitor beta
62	P50990	30	154	64.8	548	59621	5.6	T-complex protein 1 subunit theta
63	P27824	30	576	48.8	592	67568	4.6	Calnexin precursor
64	Q15075	30	38	25.9	1411	162465	5.7	Early endosome antigen 1
64	UPI000013C754	30	38	25.9	1411	162465	5.7	Early endosome antigen 1 (Endosome-associated protein p162) (Zinc finger FYVE domain-containing protein 2).
65	Q14697	29	136	35.1	944	106874	6.1	Neutral alpha-glucosidase AB precursor
65	UPI00003667D2	29	136	35.1	944	106847	6.2	Neutral alpha-glucosidase AB precursor (EC 3.2.1.84) (Glucosidase II subunit alpha).
66	UPI00001B03B3	29	72	23.5	1564	172738	5.2	Desmuslin.
66	UPI0000DC3AA9	29	72	23.5	1565	172867	5.2	desmuslin isoform A
67	P07237	28	371	61.8	508	57116	4.9	Protein disulfide-isomerase precursor
68	Q16658	28	256	59.8	493	54530	7.2	Fascin
68	UPI0000D61BF6	28	256	59.8	493	54640	7.8	Fascin (Singed-like protein) (55 kDa actin-bundling protein) (p55).
68	Q96IH1	28	256	59	500	55136	7.2	FSCN1 protein
69	P40939	28	106	52.6	763	83000	9	Trifunctional enzyme subunit alpha, mitochondrial precursor (TP-alpha) (78 kDa gastrin-binding protein) [Includes: Long-chain enoyl-CoA hydratase (EC 4.2.1.17); Long chain 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.211)]
70	O00571	28	127	50.5	662	73244	7.2	ATP-dependent RNA helicase DDX3X
71	P11021	28	377	48.9	654	72333	5.2	78 kDa glucose-regulated protein precursor (GRP 78) (Heat shock 70 kDa protein 5) (Immunoglobulin heavy chain-binding protein) (BiP) (Endoplasmic reticulum lumenal Ca(2+)-binding protein grp78)
72	P26038	28	242	48.2	577	67820	6.4	Moesin
73	Q05682-5	28	203	47.7	532	61213	6.7	Isoform 5 of Q05682
73	Q05682-4	28	203	47.2	538	62663	6.4	Isoform 4 of Q05682
74	P38646	28	147	47	679	73681	6.2	Stress-70 protein, mitochondrial precursor
75	Q9NR30	28	85	42.7	783	87344	9.3	Nucleolar RNA helicase 2
76	P53618	28	136	39	953	107142	6	Coatomer subunit beta
77	Q14764	28	94	39	893	99327	5.5	Major vault protein
78	Q16531	28	40	26.8	1140	126968	5.3	DNA damage-binding protein 1
78	UPI0000D62613	28	40	26.8	1140	126966	5.3	DNA damage-binding protein 1 (Damage-specific DNA-binding protein 1) (UV-damaged DNA-binding factor) (DDB p127 subunit) (DDBa) (UV-damaged DNA-binding protein 1) (UV-DDB 1) (Xeroderma pigmentosum group E- complementing protein) (XPCe) (XPE-binding factor)
79	P26640	28	82	24.8	1264	140476	7.6	Valyl-tRNA synthetase
79	UPI0000457409	28	82	24.8	1264	140376	7.8	Valyl-tRNA synthetase (EC 6.1.1.9) (Valine--tRNA ligase) (ValRS) (Protein G7a).
80	Q6P2Q9	28	106	13.3	2335	273599	8.8	Pre-mRNA-processing-splicing factor 8
81	Q07065	27	348	51.7	602	66023	5.9	Cytoskeleton-associated protein 4
82	P26639	27	108	48.7	723	83435	6.7	Threonyl-tRNA synthetase, cytoplasmic
82	Q53GX7	27	108	48.7	723	83445	6.7	Threonyl-tRNA synthetase variant
83	P52272-2	27	206	45.6	691	73621	8.8	Isoform 2 of P52272
83	P52272	27	206	43.2	730	77516	8.7	Heterogeneous nuclear ribonucleoprotein M
84	Q16891-2	27	72	42.8	747	82625	6.6	Isoform 2 of Q16891
85	P22314	27	139	39.1	1058	117849	5.8	Ubiquitin-activating enzyme E1
86	Q86VX4	27	60	26	1217	141507	7.2	Structural maintenance of chromosomes 3
86	UPI0000D60FCC	27	60	26	1217	141557	7.4	Structural maintenance of chromosomes protein 3 (Chondroitin sulfate proteoglycan 6) (Chromosome-associated polypeptide) (hCAP) (Bamacan) (Basement membrane-associated chondroitin proteoglycan).
86	Q9UQE7	27	60	26	1217	141541	7.2	Structural maintenance of chromosomes protein 3
87	Q6YHK3	27	129	23.5	1445	161688	5.8	CD109 antigen precursor
88	Q9NTJ3	27	73	21.8	1288	147182	6.8	Structural maintenance of chromosomes protein 4
89	P07355	26	647	73.5	339	38604	7.8	Annexin A2
89	Q8TBV2	26	647	73.5	339	38576	7.8	Annexin A2
89	UPI0000366A50	26	647	69.7	357	40411	8.4	annexin A2 isoform 1
90	Q2Q9H2	26	81	66.5	475	54825	7.1	Glucose-6-phosphate 1-dehydrogenase
91	UPI0000D61699	26	85	48.5	670	75529	5.6	Annexin A6 (Annexin VI) (Lipocortin VI) (P68) (P70) (Protein III) (Chromobindin-20) (67 kDa calelectrin) (Calphobindin-II) (CPB-II).
91	P08133	26	85	48.3	673	75873	5.6	Annexin A6
92	A4D210	26	101	39.2	775	88681	5.1	Eukaryotic translation initiation factor 3, subunit 9 eta, 116kDa

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
92	A4D208	26	101	37.3	814	92482	5	Eukaryotic translation initiation factor 3, subunit 9 eta, 116kDa
92	P55884	26	101	37.3	814	92492	5	Eukaryotic translation initiation factor 3 subunit 9
92	P55884-2	26	101	34.8	873	99039	5.1	Isoform 2 of P55884
93	O43143	26	96	37	795	90933	7.5	Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15
94	P16615-2	26	404	34.1	997	109691	5.4	Isoform SERCA2A of P16615
94	P16615	26	404	32.6	1042	114757	5.3	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 (EC 3.6.3.8) (Calcium pump 2) (SERCA2) (SR Ca(2+)-ATPase 2) (Calcium-transporting ATPase sarcoplasmic reticulum type, slow twitch skeletal muscle isoform) (Endoplasmic reticulum class 1/2 Ca(2+) ATPase)
95	P55060-3	26	127	31.6	945	107777	5.8	Isoform 3 of P55060
95	P55060	26	127	30.8	971	110417	5.8	Exportin-2
96	Q86VP6	26	125	25.7	1230	136375	5.8	Cullin-associated NEDD8-dissociated protein 1
97	Q14839	26	68	15.4	1912	217989	5.9	Chromodomain helicase-DNA-binding protein 4
97	UPI000013C8EF	26	68	15.4	1912	218003	5.9	chromodomain helicase DNA binding protein 4
97	UPI00001AE66A	26	68	15.2	1940	220846	6	Chromodomain helicase-DNA-binding protein 4 (EC 3.6.1.-) (ATP- dependent helicase CHD4) (CHD-4) (Mi-2 autoantigen 218 kDa protein) (Mi2-beta).
97	Q14839-2	26	68	15.2	1940	220832	6	Isoform 2 of Q14839
98	P12270	26	74	13.1	2349	265598	5.1	Nucleoprotein TPR
98	Q5SWY0	26	74	13	2363	267290	5	Translocated promoter region
99	P00558	25	133	68.1	417	44615	8.1	Phosphoglycerate kinase 1
100	P30101	25	249	56.8	505	56782	6.4	Protein disulfide-isomerase A3 precursor
101	Q5SZY0	25	118	53.6	522	57972	6.9	Chaperonin containing TCP1, subunit 3
101	UPI00004CA9C4	25	118	51.5	544	60463	6.5	chaperonin containing TCP1, subunit 3 isoform b
101	P49368	25	118	51.4	545	60534	6.5	T-complex protein 1 subunit gamma
102	P29401	25	160	48.2	623	67878	7.7	Transketolase
102	Q53EM5	25	160	48.2	623	67906	7.8	Transketolase variant
103	Q53T76	25	80	46.3	693	77252	6.9	Hypothetical protein GPD2
103	P43304	25	80	44.2	727	80834	7.5	Glycerol-3-phosphate dehydrogenase, mitochondrial precursor
104	Q00839-2	25	230	32.1	806	88980	5.8	Isoform Short of Q00839
104	Q00839	25	230	31.4	824	90514	6	Heterogeneous nuclear ribonucleoprotein U
105	UPI0000F0A52B	25	90	27.2	1044	119628	9.5	myosin IC isoform b
106	P11388	25	85	18.8	1531	174384	8.7	DNA topoisomerase 2-alpha
106	P11388-2	25	85	18.5	1557	177500	8.8	Isoform 2 of P11388
106	UPI0000D6231D	25	85	18.4	1568	178882	8.7	TOP2A_HUMAN Isoform 2 of P11388 - Homo sapiens (Human)
106	P11388-3	25	85	18.4	1567	178711	8.8	Isoform 3 of P11388
106	P11388-4	25	85	17.9	1612	182680	8.6	Isoform 4 of P11388
107	P07437	24	612	72.5	444	49671	4.9	Tubulin beta chain
108	P35998	24	68	62.6	433	48634	5.9	26S protease regulatory subunit 7
108	Q3LIA5	24	68	62.6	433	48618	6.1	Hypothetical protein Nbla10058
109	P09493-3	24	194	55.6	284	32876	4.8	Isoform 3 of P09493
110	P25705	24	148	52.4	553	59751	9.1	ATP synthase subunit alpha, mitochondrial precursor
111	P04843	24	591	48.6	607	68569	6.4	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 67 kDa subunit precursor
111	Q6IBR0	24	591	48.6	607	68607	6.4	RPN1 protein
111	Q53EP4	24	591	48.6	607	68580	6.4	Ribophorin I variant
112	P49748	24	75	48.4	655	70390	8.8	Very-long-chain specific acyl-CoA dehydrogenase, mitochondrial precursor
113	Q5U4P6	24	97	41.7	710	72897	7.9	KHSRP protein
113	UPI0000D61707	24	97	41.3	717	73805	8.1	Far upstream element-binding protein 2 (FUSE-binding protein 2) (KH type-splicing regulatory protein) (KSRP) (p75).
114	P11940	24	100	41.4	636	70671	9.5	Polyadenylate-binding protein 1 (Poly(A)-binding protein 1)
115	Q14974	24	183	37	876	97170	4.8	Importin beta-1 subunit
116	Q13200	24	84	34	908	100200	5.2	26S proteasome non-ATPase regulatory subunit 2
116	Q53XQ4	24	84	34	908	100249	5.2	Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 2
116	Q59EG8	24	84	33.8	913	100588	5.2	Proteasome 26S non-ATPase subunit 2 variant
117	UPI0000161B5A	24	62	34.3	835	93394	5.1	Ubiquitin isopeptidase T
117	P45974-2	24	62	34.3	835	93308	5.1	Isoform Short of P45974
117	P45974	24	62	33.3	858	95786	5	Ubiquitin carboxyl-terminal hydrolase 5
118	Q12906	24	113	32.6	894	95339	8.8	Interleukin enhancer-binding factor 3
119	Q4W4Y1	24	62	31	868	96079	6.5	Dopamine receptor interacting protein 4
119	Q8WUM4	24	62	31	868	96023	6.5	Programmed cell death 6-interacting protein
119	Q6NUS1	24	62	30.8	873	96818	6.5	PDCD6IP protein
120	UPI0000456CFE	24	62	29	955	105371	7.9	AP-2 complex subunit alpha-1 (Adapter-related protein complex 2 alpha- 1 subunit) (Alpha-adaptin A) (Adaptor protein complex AP-2 alpha-1 subunit) (Clathrin assembly protein complex 2 alpha-A large chain) (100 kDa coated vesicle protein A) (Plasma membran

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120	UPI0000037C08	24	62	29	955	105361	7.7	adaptor-related protein complex 2, alpha 1 subunit isoform 2
120	O95782-2	24	62	29	955	105370	7.7	Isoform B of O95782
120	O95782	24	62	28.4	977	107555	7.1	AP-2 complex subunit alpha-1
120	UPI0000456CFD	24	62	28.4	977	107555	7.3	AP-2 complex subunit alpha-1 (Adapter-related protein complex 2 alpha- 1 subunit) (Alpha-adaptin A) (Adaptor protein complex AP-2 alpha-1 subunit) (Clathrin assembly protein complex 2 alpha-A large chain) (100 kDa coated vesicle protein A) (Plasma membran
120	UPI0000167B50	24	62	28.4	977	107546	7	adaptor-related protein complex 2, alpha 1 subunit isoform 1
121	Q86W92-2	24	57	28.4	1005	113181	5.7	Isoform 2 of Q86W92
122	O75533	24	110	24.2	1304	145815	7	Splicing factor 3B subunit 1
122	UPI000013D493	24	110	24.2	1304	145830	7.1	splicing factor 3b, subunit 1 isoform 1
123	P41252	24	64	21.2	1266	144958	6.2	Isoleucyl-tRNA synthetase, cytoplasmic
123	Q59G75	24	64	21	1279	146344	6.4	Isoleucyl-tRNA synthetase, cytoplasmic variant
124	Q53SY7	24	71	14.2	2151	235175	6.6	Hypothetical protein CAD
124	P27708	24	71	13.7	2225	242981	6.5	CAD protein [Includes: Glutamine-dependent carbamoyl-phosphate synthase (EC 6.3.5.5); Aspartate carbamoyltransferase (EC 2.1.3.2); Dihydroorotase (EC 3.5.2.3)]
125	P31939	23	61	54.1	592	64616	6.7	Bifunctional purine biosynthesis protein PURH [Includes: Phosphoribosylaminoimidazolecarboxamide formyltransferase (EC 2.1.2.3) (5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase) (AICAR transformylase); IMP cyclohydrolase (EC 3.5.4.10) (Inosinicase) (IMP synthetase) (ATIC)]
126	P47895	23	87	53.9	512	56109	7.3	Aldehyde dehydrogenase 1A3
126	UPI0000129264	23	87	53.9	512	56009	7	aldehyde dehydrogenase 1A3
127	Q53G71	23	164	53.2	406	46919	4.4	Calreticulin variant
127	P27797	23	164	51.8	417	48142	4.4	Calreticulin precursor
128	O60506-2	23	130	48.5	588	65682	8.6	Isoform 2 of O60506
128	O60506	23	130	45.7	623	69603	8.6	Heterogeneous nuclear ribonucleoprotein Q
129	P12956	23	145	43.3	609	69843	6.6	ATP-dependent DNA helicase 2 subunit 1
129	UPI000045708A	23	145	43.3	609	69870	6.6	ATP-dependent DNA helicase 2 subunit 1 (ATP-dependent DNA helicase II 70 kDa subunit) (Lupus Ku autoantigen protein p70) (Ku70) (70 kDa subunit of Ku antigen) (Thyroid-lupus autoantigen) (TLAA) (CTC box- binding factor 75 kDa subunit) (CTCBF) (CTC75) (DNA
129	Q6FG89	23	145	43.3	609	69873	6.6	G22P1 protein
130	O00429-4	23	101	43.3	699	78100	6.8	Isoform 4 of O00429
130	UPI0000D621CC	23	101	42.7	710	79224	7.1	Dynamin-1-like protein (EC 3.6.5.5) (Dynamin-like protein) (Dnm1p/Vps1p-like protein) (DVLP) (Dynamin family member proline-rich carboxyl-terminal domain less) (Dymple) (Dynamin-related protein 1) (Dynamin-like protein 4) (Dynamin-like protein IV) (HdynIV
130	O00429-5	23	101	42.7	710	79109	6.9	Isoform 5 of O00429
130	O00429-3	23	101	42.7	710	79442	6.9	Isoform 3 of O00429
130	O00429-2	23	101	41.8	725	80536	6.7	Isoform 2 of O00429
130	O00429	23	101	41.2	736	81877	6.8	Dynamin-1-like protein
130	Q59GN9	23	101	40.3	751	83579	7.7	Dynamin-like protein DYNIV-11 variant
131	Q5CAQ7	23	309	40.2	854	98113	5.2	Heat shock protein HSP 90-alpha 2
132	Q01813	23	74	38	784	85596	7.6	6-phosphofructokinase type C
133	P43243	23	166	34.6	847	94623	6.3	Matrin-3
134	P19338-2	23	229	33.5	687	74397	4.6	Isoform 2 of P19338
134	P19338	23	229	32.4	710	76615	4.7	Nucleolin
135	P63010	23	83	30.6	937	104553	5.4	AP-2 complex subunit beta-1
135	UPI0000456A82	23	83	30.6	939	104711	5.4	AP-2 complex subunit beta-1 (Adapter-related protein complex 2 beta-1 subunit) (Beta-adaptin) (Plasma membrane adaptor HA2/AP2 adaptin beta subunit) (Clathrin assembly protein complex 2 beta large chain) (AP105B).
135	Q3ZB97	23	83	30.2	951	105692	5.3	Ap2b1 protein
135	UPI0000456A83	23	83	30.1	953	105850	5.3	AP-2 complex subunit beta-1 (Adapter-related protein complex 2 beta-1 subunit) (Beta-adaptin) (Plasma membrane adaptor HA2/AP2 adaptin beta subunit) (Clathrin assembly protein complex 2 beta large chain) (AP105B).
136	Q9BSJ8	23	148	29.9	1104	122856	5.8	Protein FAM62A
136	Q9BSJ8-2	23	148	29.6	1114	124003	5.8	Isoform 2 of Q9BSJ8
137	UPI000013E942	23	117	29	905	101085	6.9	Hexokinase-1 (EC 2.7.1.1) (Hexokinase type I) (HK I) (Brain form hexokinase).
137	P19367-4	23	117	29	905	101104	7	Isoform 4 of P19367
137	P19367	23	117	28.6	917	102486	6.8	Hexokinase-1

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
138	UPI0000456DC8	23	97	27.8	1070	123299	6.1	Exportin-1 (Exp1) (Chromosome region maintenance 1 protein homolog).
138	O14980	23	97	27.7	1071	123386	6.1	Exportin-1
139	O00410	23	121	26	1097	123630	4.9	Importin beta-3
139	UPI0000163C1C	23	121	25.6	1115	125545	4.9	RAN binding protein 5
140	P78347-2	23	56	26.6	957	107970	7.9	Isoform 2 of P78347
140	P78347-4	23	56	26.1	977	110106	7.4	Isoform 4 of P78347
140	P78347-3	23	56	26.1	978	110280	6.7	Isoform 3 of P78347
140	P78347	23	56	25.6	998	112416	6.4	General transcription factor II-I
141	P11586	23	61	25.3	935	101559	7.3	C-1-tetrahydrofolate synthase, cytoplasmic (C1-THF synthase) [Includes: Methylenetetrahydrofolate dehydrogenase (EC 1.5.1.5); Methenyltetrahydrofolate cyclohydrolase (EC 3.5.4.9); Formyltetrahydrofolate synthetase (EC 6.3.4.3)]
141	UPI0000161BEA	23	61	25.3	935	101531	7.2	methylenetetrahydrofolate dehydrogenase 1
142	Q8IUD2	23	38	21	1116	128086	6	ELKS/RAB6-interacting/CAST family member 1
143	O95347	23	38	20.4	1197	135780	8.6	Structural maintenance of chromosomes protein 2
143	UPI0000457786	23	38	20.4	1195	135549	8.6	Structural maintenance of chromosomes protein 2 (Chromosome-associated protein E) (hCAP-E) (XCAP-E homolog).
143	Q6IEE0	23	38	20.4	1197	135656	8.4	SMC2 protein
144	P11047	23	51	16.7	1609	177606	5.1	Laminin subunit gamma-1 precursor
144	UPI0000034928	23	51	16.7	1609	177572	5.1	laminin, gamma 1 precursor
144	Q5VYE7	23	51	16.7	1609	177602	5.1	Laminin, gamma 1
145	Q14690	23	54	13.7	1871	208699	8.9	RRP5 protein homolog
146	Q14980-2	23	49	13.2	2101	236513	5.8	Isoform 2 of Q14980
147	P06733	22	486	69.1	434	47169	7.4	Alpha-enolase
147	Q53FT9	22	486	69.1	434	47197	7.4	Enolase 1 variant
148	P06576	22	275	63.7	529	56560	5.4	ATP synthase subunit beta, mitochondrial precursor
149	Q02790	22	49	53.8	459	51805	5.4	FK506-binding protein 4
150	Q16851	22	105	50.6	508	56940	8.1	UTP--glucose-1-phosphate uridylyltransferase 2
151	P78371	22	113	50.1	535	57488	6.4	T-complex protein 1 subunit beta
152	UPI0000E9BBC7	22	93	48.8	582	64677	5.2	Protein phosphatase 2
152	P30153	22	93	48.2	589	65309	5.1	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform
153	P17655	22	72	45.4	700	80009	5	Calpain-2 catalytic subunit precursor
153	UPI000003475E	22	72	45.4	700	80007	5	calpain 2, large subunit
153	Q59EF6	22	72	43.6	729	83109	5.1	Calpain 2, large [catalytic] subunit variant
154	P46063	22	69	45	649	73456	8.1	ATP-dependent DNA helicase Q1
154	UPI0000167E2F	22	69	45	649	73457	7.9	RecQ protein-like isoform 1
155	P49915	22	48	40	693	76715	6.9	GMP synthase [glutamine-hydrolyzing]
156	Q15393	22	78	23.8	1217	135577	5.3	Splicing factor 3B subunit 3
157	Q7L576	22	102	19.4	1253	145182	6.9	Cytoplasmic FMR1-interacting protein 1
158	UPI000013F255	22	64	13.2	1972	218524	8.1	colonic and hepatic tumor over-expressed protein isoform b
158	Q0VAX8	22	64	12.8	2032	225493	7.8	Cytoskeleton associated protein 5
158	Q14008	22	64	12.8	2032	225507	7.9	Cytoskeleton-associated protein 5
159	P46013	22	111	7.3	3256	358695	9.4	Antigen KI-67
160	P08758	21	228	75	320	35937	5	Annexin A5
161	P04075	21	223	69	364	39420	8.1	Fructose-bisphosphate aldolase A
162	Q6FI31	21	92	58.6	497	54575	6.5	TXNRD1 protein
163	P68363	21	517	58.5	451	50152	5.1	Tubulin alpha-ubiquitous chain
164	P50454	21	210	54.8	418	46441	8.7	Serpin H1 precursor
165	P17987	21	67	47.1	556	60344	6.1	T-complex protein 1 subunit alpha
166	P48643	21	99	45.3	541	59671	5.6	T-complex protein 1 subunit epsilon
167	P49321	21	46	41.5	788	85238	4.3	Nuclear autoantigenic sperm protein
168	P20700	21	68	39.9	586	66408	5.2	Lamin-B1
169	P13010	21	120	39.8	732	82705	5.8	ATP-dependent DNA helicase 2 subunit 2
170	Q92499	21	73	37.4	740	82432	7.2	ATP-dependent RNA helicase DDX1
171	P17844	21	114	37	614	69148	8.9	Probable ATP-dependent RNA helicase DDX5
172	UPI0000136C97	21	180	34.3	760	84901	6.6	transferrin receptor
173	Q1KMD3	21	66	32.8	747	85105	4.9	Heterogeneous nuclear ribonucleoprotein U-like protein 2
174	P49588	21	60	25.8	968	106810	5.5	Alanyl-tRNA synthetase, cytoplasmic
174	UPI0000D61A0F	21	60	25.8	968	106710	5.5	Alanyl-tRNA synthetase, cytoplasmic (EC 6.1.1.7) (Alanine--tRNA ligase) (AlaRS) (Renal carcinoma antigen NY-REN-42).
175	Q8WUM6	21	146	26.4	798	88415	5.4	Integrin, beta 1
175	Q7Z3V1	21	146	25.6	823	91131	5.5	Integrin beta
176	Q9P2J5	21	47	22.3	1176	134466	7.3	Leucyl-tRNA synthetase, cytoplasmic
177	Q14203	21	43	20.5	1278	141694	5.8	Dynactin-1
178	P07942	21	46	14	1786	198065	5	Laminin subunit beta-1 precursor
179	Q5T3Q7	21	82	11.6	2063	233274	6.6	Protein BAP28
179	Q9H583	21	82	11.2	2144	242368	6.5	HEAT repeat-containing protein 1
180	P04083	20	206	62.4	346	38714	7	Annexin A1
181	P00338	20	304	62	332	36689	8.3	L-lactate dehydrogenase A chain
182	P60842	20	131	57.6	406	46154	5.5	Eukaryotic initiation factor 4A-I

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183	Q59ET3	20	103	51.6	529	57762	6.7	Chaperonin containing TCP1, subunit 6A isoform a variant
183	P40227	20	103	51.4	531	58024	6.7	T-complex protein 1 subunit zeta
184	P08107	20	110	51.3	641	70038	5.6	Heat shock 70 kDa protein 1
184	UPI000013C67D	20	110	51.3	641	70025	5.6	heat shock 70kDa protein 1B
184	Q5JQI4	20	110	51.3	641	70052	5.6	Heat shock 70kDa protein 1A
184	Q59EJ3	20	110	46.4	709	77496	6.3	Heat shock 70kDa protein 1A variant
185	P50991	20	76	49	539	57924	7.8	T-complex protein 1 subunit delta
186	P14866	20	75	48.6	558	60187	7.1	Heterogeneous nuclear ribonucleoprotein L
186	Q6NTA2	20	75	48.6	558	60233	7.1	HNRPL protein
186	UPI00004432FA	20	75	46	589	64133	8.2	heterogeneous nuclear ribonucleoprotein L isoform a
187	O60701	20	33	47.4	494	55024	7.1	UDP-glucose 6-dehydrogenase
188	P68104	20	615	46.1	462	50141	9	Elongation factor 1-alpha 1
188	Q6IPT9	20	615	46.1	462	50185	9.1	Eukaryotic translation elongation factor 1 alpha 1
188	Q6IPN6	20	615	46.1	462	50123	9	Eukaryotic translation elongation factor 1 alpha 1
188	Q5VTE0	20	615	46.1	462	50185	9.1	Eukaryotic translation elongation factor 1 alpha-like 3
188	Q53HR5	20	615	46.1	462	50125	9	Eukaryotic translation elongation factor 1 alpha 1 variant
188	Q53HQ7	20	615	46.1	462	50199	8.9	Eukaryotic translation elongation factor 1 alpha 1 variant
188	Q53HM9	20	615	46.1	462	50142	8.9	Eukaryotic translation elongation factor 1 alpha 1 variant
188	Q53G85	20	615	46.1	462	50113	9	Eukaryotic translation elongation factor 1 alpha 1 variant
189	UPI0000D6239D	20	89	45.9	562	62865	8.4	Septin-9 (MLL septin-like fusion protein) (MLL septin-like fusion protein MSF-A) (Ovarian/Breast septin) (Ov/Br septin) (Septin D1).
189	Q9UHD8-2	20	89	45.4	568	63666	8.4	Isoform 2 of Q9UHD8
189	Q9UHD8-5	20	89	44.6	579	64682	7.6	Isoform 5 of Q9UHD8
189	Q9UHD8	20	89	44	586	65402	9	Septin-9
190	UPI0000D6261A	20	109	40.2	435	49917	6.7	Elongation factor 1-gamma (EF-1-gamma) (eEF-1B gamma).
190	UPI0000D6261B	20	109	40.1	436	50016	6.7	Elongation factor 1-gamma (EF-1-gamma) (eEF-1B gamma).
190	P26641	20	109	40	437	50119	6.7	Elongation factor 1-gamma
191	Q53FJ5	20	103	38.2	524	58141	5.2	Prosaposin (Variant Gaucher disease and variant metachromatic leukodystrophy) variant
192	P23246	20	102	37.5	707	76150	9.4	Splicing factor, proline- and glutamine-rich
193	P54136	20	46	37.1	660	75379	6.7	Arginyl-tRNA synthetase, cytoplasmic
194	O95573	20	168	35.8	720	80420	8.4	Long-chain-fatty-acid--CoA ligase 3
195	Q99798	20	48	36.4	780	85425	7.6	Aconitate hydratase, mitochondrial precursor
195	Q8TAQ6	20	48	36.4	780	85565	7.7	Aconitase 2, mitochondrial
195	Q6FHX0	20	48	36.4	780	85467	7.5	ACO2 protein
195	A2A274	20	48	35.3	805	87820	7.4	Aconitase 2, mitochondrial
196	UPI0000161BCB	20	68	34.7	681	76747	6.9	glucosamine-fructose-6-phosphate aminotransferase
196	Q06210-2	20	68	34.7	681	76759	6.9	Isoform 2 of Q06210
196	Q06210	20	68	33.8	699	78806	7.1	Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] 1
197	P47897	20	38	31.6	775	87799	7.2	Glutaminyl-tRNA synthetase
197	Q53HS0	20	38	31.6	775	87711	7.2	Glutaminyl-tRNA synthetase variant
198	P54886	20	65	31.1	795	87302	7.1	Delta 1-pyrroline-5-carboxylate synthetase (P5CS) (Aldehyde dehydrogenase 18 family member A1) [Includes: Glutamate 5-kinase (EC 2.7.2.11) (Gamma-glutamyl kinase) (GK); Gamma-glutamyl phosphate reductase (GPR) (EC 1.2.1.41) (Glutamate-5-semialdehyde dehydrogenase) (Glutamyl-gamma-semialdehyde dehydrogenase)]
198	Q5T567	20	65	31.1	793	87089	7.1	Aldehyde dehydrogenase 18 family, member A1
199	Q9GZV0	20	33	32.2	767	85730	6.3	CDNA FLJ12466 fis, clone NT2RM1000826, highly similar to UNR PROTEIN
199	O75534-2	20	33	32.2	767	85747	6.2	Isoform Short of O75534
199	O75534	20	33	31	798	88885	6.2	Cold shock domain-containing protein E1
199	Q68DF1	20	33	30.4	813	90555	6.5	Hypothetical protein DKFZp779B0247
200	Q15459	20	41	29.3	793	88886	5.2	Splicing factor 3 subunit 1
201	Q13263	20	96	29	835	88550	5.8	Transcription intermediary factor 1-beta
202	Q99460-2	20	45	27.8	922	102258	5.3	Isoform 2 of Q99460
202	Q99460	20	45	26.9	953	105836	5.4	26S proteasome non-ATPase regulatory subunit 1
203	Q9UDX0	20	59	24.7	1023	115935	6.9	Oxoglutarate (Alpha-ketoglutarate) dehydrogenase
204	O60264	20	57	19.4	1052	121905	8.1	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5
204	UPI0000161FA8	20	57	19.4	1052	121933	8.1	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin a5
205	P29144	20	41	18.9	1249	138349	6.3	Tripeptidyl-peptidase 2
205	UPI0000137276	20	41	18.9	1249	138449	6.4	tripeptidyl peptidase II
205	Q5VZU9	20	41	18.7	1262	139765	6.5	Tripeptidyl peptidase II
206	P62258	19	349	69.4	255	29174	4.7	14-3-3 protein epsilon

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
207	UPI0000247080	19	288	64.2	352	37298	9.1	Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2 / hnRNP B1).
207	P22626	19	288	64	353	37430	8.9	Heterogeneous nuclear ribonucleoproteins A2/B1
208	Q6PIN5	19	78	61.1	373	41681	7.5	PA2G4 protein
208	Q9UQ80	19	78	57.9	394	43787	6.6	Proliferation-associated protein 2G4
209	P61158	19	88	60.8	418	47371	5.9	Actin-like protein 3
210	P62136	19	93	60.3	330	37512	6.3	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit
211	Q9HDC9	19	50	57	416	46480	6.2	Adipocyte plasma membrane-associated protein
212	Q53HV2	19	76	51.9	543	59341	7.6	Chaperonin containing TCP1, subunit 7 (Eta) variant
212	Q99832	19	76	51.9	543	59367	7.6	T-complex protein 1 subunit eta
213	Q96I24	19	42	50.9	572	61640	8.4	Far upstream element-binding protein 3
214	P37837	19	146	47.5	337	37540	6.8	Transaldolase
215	P48444	19	66	42.7	511	57210	6.2	Coatomer subunit delta
215	UPI000049DD56	19	66	39.5	552	61626	5.8	Coatomer subunit delta (Delta-coat protein) (Delta-COP) (Archain).
215	Q6MZV5	19	66	39.5	552	61598	5.8	Hypothetical protein DKFZp686M09245
216	O60568	19	81	33.6	738	84785	6.1	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3 precursor
217	P33993	19	32	31.4	719	81308	6.5	DNA replication licensing factor MCM7
218	P35221	19	58	29.1	906	100071	6.3	Catenin alpha-1
219	Q9Y5B9	19	76	22	1047	119914	5.7	FACT complex subunit SPT16
220	Q13045	19	71	17.6	1269	144751	6.1	Protein flightless-1 homolog
221	Q5XG74	19	84	17.7	1106	121651	6.9	SEC31 homolog A
221	Q17RR5	19	84	16.3	1205	131534	6.9	SEC31 homolog A
221	Q9UM05	19	84	16.1	1220	133031	6.9	ABP130
221	Q7LCX9	19	84	16.1	1220	133015	6.9	Sec31 protein
221	O94979	19	84	15.9	1229	134238	7	SEC31 homolog A
222	Q9BQG0	19	79	15.5	1328	148854	9.3	Myb-binding protein 1A
222	Q9BQG0-2	19	79	15.5	1332	149366	9.3	Isoform 2 of Q9BQG0
223	Q92616	19	74	9.7	2671	292742	7.4	GCN1-like protein 1
223	UPI0000451CA7	19	74	9.7	2671	292708	7.4	GCN1 general control of amino-acid synthesis 1-like 1
224	P63244	18	105	75.4	317	35077	7.7	Guanine nucleotide-binding protein subunit beta 2-like 1
224	Q5VLR4	18	105	68.9	347	37889	8.2	Lung cancer oncogene 7
225	Q96HG5	18	1024	67.1	368	41005	5.8	Actin, beta
225	P60709	18	1024	65.9	375	41737	5.5	Actin, cytoplasmic 1
225	Q53GK6	18	1024	65.9	375	41723	5.5	Beta actin variant
225	Q53G99	18	1024	65.9	375	41765	5.6	Beta actin variant
225	Q53G76	18	1024	65.9	375	41721	5.5	Beta actin variant
225	P63261	18	1024	65.9	375	41793	5.5	Actin, cytoplasmic 2
226	P40926	18	119	65.4	338	35531	8.7	Malate dehydrogenase, mitochondrial precursor
226	UPI000013DA68	18	119	65.4	338	35503	8.7	mitochondrial malate dehydrogenase precursor
226	Q6FHZ0	18	119	65.4	338	35559	8.7	MDH2 protein
227	P13489	18	35	61.4	461	49974	4.8	Ribonuclease inhibitor
228	O43852	18	191	59.4	315	37107	4.6	Calumenin precursor
229	O00231	18	44	50.9	422	47464	6.5	26S proteasome non-ATPase regulatory subunit 11
230	Q16555	18	51	49	572	62294	6.4	Dihydropyrimidinase-related protein 2
230	Q59GB4	18	51	44.6	628	68184	6.2	Dihydropyrimidinase-like 2 variant
231	UPI0000126EBE	18	119	48.4	475	51673	8	adenylyl cyclase-associated protein
232	P28838	18	39	46.1	519	56166	7.9	Cytosol aminopeptidase
233	Q5T6W5	18	260	47.9	428	47557	5.6	Heterogeneous nuclear ribonucleoprotein K
233	P61978-3	18	260	46.6	440	48562	5.5	Isoform 3 of P61978
233	P61978	18	260	44.3	463	50976	5.5	Heterogeneous nuclear ribonucleoprotein K
233	Q6IBN1	18	260	44.2	464	51028	5.3	HNRPK protein
234	Q9Y230	18	65	41.9	463	51157	5.6	RuvB-like 2
235	P23526	18	63	41.4	432	47716	6.3	Adenosylhomocysteinase
236	Q15233	18	104	41.4	471	54232	8.9	Non-POU domain-containing octamer-binding protein (NonO protein) (54 kDa nuclear RNA- and DNA-binding protein) (p54(nrb))
237	P14868	18	32	40.3	501	57136	6.5	Aspartyl-tRNA synthetase, cytoplasmic
238	O94925	18	88	39.3	669	73461	7.8	Glutaminase kidney isoform, mitochondrial precursor
238	UPI0000163E16	18	88	39.3	669	73427	7.8	glutaminase C
239	Q96AY3	18	56	39.2	582	64245	5.6	FK506-binding protein 10 precursor
239	UPI000015C65C	18	56	39.2	582	64305	5.6	FK506 binding protein 10, 65 kDa
240	P42166	18	55	37.9	694	75492	7.7	Lamina-associated polypeptide 2 isoform alpha (Thymopoietin isoform alpha) (TP alpha) (Thymopoietin-related peptide isoform alpha) (TPRP isoform alpha) [Contains: Thymopoietin (TP) (Splenin); Thymopentin (TP5)]
241	Q7RTQ9	18	29	37.4	538	61202	5.8	Kinesin light chain 1A
241	Q7RTQ7	18	29	36.7	547	62192	5.7	Kinesin light chain 1F
241	Q07866-8	18	29	36.7	547	62302	6	Isoform S of Q07866
241	Q07866-2	18	29	36.2	556	63293	5.9	Isoform C of Q07866
241	UPI00004567D3	18	29	36	559	63686	5.9	Kinesin light chain 1 (KLC 1).
241	Q07866-3	18	29	35.9	560	63796	6.4	Isoform G of Q07866
241	UPI00004567D1	18	29	35.4	568	64656	6.4	Kinesin light chain 1 (KLC 1).

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241	Q07866	18	29	35.3	569	64786	6.3	Kinesin light chain 1
241	UPI0000D62453	18	29	34.7	579	65565	6	Kinesin light chain 1 (KLC 1).
241	Q07866-7	18	29	34.7	580	65768	6	Isoform P of Q07866
241	Q7RTQ8	18	29	33.1	607	68964	7.3	Kinesin light chain 1O
241	Q7RTQ2	18	29	33	609	68762	6	Kinesin light chain 1E
241	Q7RTQ3	18	29	32.7	614	69242	6	Kinesin light chain 1D
241	UPI0000D62452	18	29	32.6	616	69894	7.3	Kinesin light chain 1 (KLC 1).
241	Q7RTQ1	18	29	32.6	616	69954	7.1	Kinesin light chain 1K
241	Q7RTQ0	18	29	32.2	624	70496	6.8	Kinesin light chain 1N
241	Q07866-6	18	29	32.2	624	70482	6.8	Isoform N of Q07866
241	UPI00004567D4	18	29	31.8	632	71342	6.8	Kinesin light chain 1 (KLC 1).
241	Q7RTP8	18	29	31.8	633	71487	6.7	Kinesin light chain 1J
241	Q07866-4	18	29	31.8	633	71473	6.7	Isoform J of Q07866
241	UPI00004567D2	18	29	31.7	634	71744	7.8	Kinesin light chain 1 (KLC 1).
241	Q07866-9	18	29	31.7	635	71874	7.7	Isoform I of Q07866
242	A2A418	18	82	34.9	731	80641	5.8	Gelsolin
242	P06396	18	82	32.6	782	85697	6.3	Gelsolin precursor
243	Q02809	18	71	31.4	727	83550	6.9	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1 precursor
244	Q32MZ4-3	18	67	33.2	752	82689	4.6	Isoform 3 of Q32MZ4
244	UPI000006DC73	18	67	31.9	784	86438	4.7	leucine rich repeat (in FLII) interacting protein 1
244	Q32MZ4-2	18	67	31.9	784	86404	4.7	Isoform 2 of Q32MZ4
244	Q32MZ4	18	67	30.9	808	89253	4.7	Leucine-rich repeat flightless-interacting protein 1
245	Q8NBJ5	18	86	29.9	622	71636	7.3	Glycosyltransferase 25 domain-containing protein 1
246	Q96AM8	18	30	29.2	678	74762	8.4	Solute carrier family 25 (Mitochondrial carrier, Aralar), member 12
247	Q15029	18	55	26.1	972	109436	5	116 kDa U5 small nuclear ribonucleoprotein component
247	UPI0000169E0D	18	55	26.1	972	109478	5	U5 snRNP-specific protein, 116 kD
247	Q6IBM8	18	55	26.1	972	109460	5	U5-116KD protein
248	P25205	18	36	25.1	808	90981	5.8	DNA replication licensing factor MCM3
248	Q53HJ4	18	36	25.1	808	90981	5.7	Minichromosome maintenance protein 3 variant
249	P05106	18	51	25	788	87058	5.2	Integrin beta-3 precursor
250	P35606	18	70	24.1	906	102487	5.3	Coatomer subunit beta'
251	O43491	18	44	23.5	1005	112588	5.4	Band 4.1-like protein 2
252	O60313-8	18	33	21.1	952	110721	7.6	Isoform 8 of O60313
252	O60313	18	33	20.9	960	111657	7.9	Dynamin-like 120 kDa protein, mitochondrial precursor (Optic atrophy protein 1) [Contains: Dynamin-like 120 kDa protein, form S1]
252	O60313-7	18	33	20.7	969	112524	7.5	Isoform 7 of O60313
252	O60313-4	18	33	20.6	977	113460	7.8	Isoform 4 of O60313
252	O60313-5	18	33	20.3	989	114975	7.6	Isoform 5 of O60313
252	UPI0000422960	18	33	20.2	997	115884	7.9	Dynamin-like 120 kDa protein, mitochondrial precursor (Optic atrophy protein 1) [Contains: Dynamin-like 120 kDa protein, form S1].
252	O60313-2	18	33	20.2	997	115911	7.9	Isoform 2 of O60313
252	O60313-3	18	33	20	1006	116777	7.5	Isoform 3 of O60313
252	O60313-6	18	33	19.8	1014	117713	7.8	Isoform 6 of O60313
253	Q9H0A0	18	53	20	1025	115704	8.3	N-acetyltransferase 10
253	UPI000015F46F	18	53	20	1025	115748	8.3	N-acetyltransferase-like protein
253	UPI000013CF8E	18	53	20	1025	115730	8.3	N-acetyltransferase 10 (EC 2.3.1.-).
254	P07996	18	35	17.5	1170	129383	4.9	Thrombospondin-1 precursor
254	Q59E99	18	35	16.7	1225	134849	5	Thrombospondin 1 variant
255	P17301	18	55	17.5	1181	129295	5.3	Integrin alpha-2 precursor
255	UPI0000169C36	18	55	17.5	1181	129296	5.3	integrin alpha 2 precursor
256	Q68CZ2	18	56	17.4	1445	155237	6.8	Tensin-3
256	UPI0000457557	18	56	17.4	1445	155293	6.8	tensin-like SH2 domain containing 1
256	UPI00001AE9DA	18	56	17.4	1445	155265	6.8	tensin 3
256	Q8IZW7	18	56	17.4	1445	155277	6.8	Tensin 3
257	Q92900-2	18	54	17.4	1118	123036	6.7	Isoform 2 of Q92900
257	Q92900	18	54	17.3	1129	124345	6.6	Regulator of nonsense transcripts 1
258	O60610	18	68	16.3	1248	138978	5.4	Protein diaphanous homolog 1
258	UPI0000EA87E7	18	68	16.1	1263	140289	5.4	diaphanous 1 isoform 2
258	UPI0000DBEE89	18	68	16.1	1263	140255	5.4	Protein diaphanous homolog 1 (Diaphanous-related formin-1) (DRF1).
258	UPI0000DBEE88	18	68	16.1	1264	140416	5.4	Protein diaphanous homolog 1 (Diaphanous-related formin-1) (DRF1).
258	Q17RN4	18	68	16.1	1262	140192	5.4	Diaphanous homolog 1
258	Q6URC4	18	68	16	1272	141303	5.5	Diaphanous 1
258	Q59FH8	18	68	15.6	1299	143786	5.4	Diaphanous 1 variant
259	P60174	17	211	84.7	249	26669	6.9	Triosephosphate isomerase
260	P23396	17	179	74.5	243	26688	9.7	40S ribosomal protein S3
261	P23528	17	171	70.5	166	18502	8.1	Cofilin-1
262	P38117	17	52	58.8	255	27844	8.1	Electron transfer flavoprotein subunit beta
263	P05198	17	70	57.5	315	36112	5.1	Eukaryotic translation initiation factor 2 subunit 1
264	Q5TZT4	17	49	57.4	350	38380	5.2	Unr-interacting protein
264	Q9Y3F4	17	49	57.4	350	38438	5.1	Serine-threonine kinase receptor-associated protein
264	Q9NTK0	17	49	57.4	350	38452	5.1	Hypothetical protein DKFZp564N1778
265	P05455	17	82	44.4	408	46837	7.1	Lupus La protein

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266	Q9Y2X3	17	49	42.5	529	59578	8.9	Nucleolar protein NOP5
267	P00367	17	50	38.7	558	61398	7.8	Glutamate dehydrogenase 1, mitochondrial precursor
268	Q86UE4	17	191	36.4	582	63837	9.3	Protein LYRIC
269	Q53H17	17	55	35.6	606	66228	6.7	WD repeat-containing protein 1 isoform 1 variant
269	Q59ER5	17	55	34.6	624	68171	7.2	WD repeat-containing protein 1 isoform 1 variant
270	P13797	17	32	35.1	627	70436	5.8	Plastin-3
270	UPI000000D962	17	32	34.9	630	70811	5.6	plastin 3
271	Q86UX7-2	17	38	34.2	663	75430	6.8	Isoform 2 of Q86UX7
271	Q86UX7	17	38	34	667	75953	7	Unc-112-related protein 2
272	UPI0000378489	17	93	33.3	525	59178	4.4	protein kinase C substrate 80K-H isoform 2
273	Q53HQ1	17	83	31.6	564	66696	6.2	Eukaryotic translation initiation factor 3 subunit 6 interacting protein variant
273	Q9Y262	17	83	31.6	564	66727	6.3	Eukaryotic translation initiation factor 3 subunit 6-interacting protein
273	Q5QTR1	17	83	31.6	564	66739	6.3	MSTP005
273	Q53HT4	17	83	31.6	564	66753	6.3	Eukaryotic translation initiation factor 3 subunit 6 interacting protein variant
273	Q6ICD2	17	83	29.3	607	70902	6.7	DJ1014D13.1 protein
274	Q15436	17	73	30.6	765	86161	7.1	Protein transport protein Sec23A
275	UPI0000161B4F	17	77	32	685	77531	6.2	Glycyl-tRNA synthetase (EC 6.1.1.14) (Glycine--tRNA ligase) (GlyRS).
275	P41250	17	77	29.6	739	83140	7	Glycyl-tRNA synthetase
275	UPI00005A885C	17	77	29.6	739	83166	7	glycyl-tRNA synthetase
275	UPI0000D61C1A	17	77	29.2	749	84392	7.5	Glycyl-tRNA synthetase (EC 6.1.1.14) (Glycine--tRNA ligase) (GlyRS).
276	Q16643	17	43	28.7	649	71425	4.5	Drebrin
276	UPI0000457394	17	43	28.7	649	71429	4.5	Drebrin (Developmentally-regulated brain protein).
276	UPI000013E0B5	17	43	28.7	649	71439	4.5	drebrin 1 isoform a
277	Q16666-2	17	59	27.6	729	82096	9.3	Isoform 2 of Q16666
277	Q16666	17	59	25.6	785	88256	9.3	Gamma-interferon-inducible protein Ifi-16
278	P11387	17	58	24.2	765	90726	9.3	DNA topoisomerase 1
279	Q9NSE4	17	55	21.5	1012	113791	7.2	Isoleucyl-tRNA synthetase, mitochondrial precursor
280	A1KYQ7	17	75	21.2	913	105404	5.7	Cell migration-inducing protein 17
280	Q99613	17	75	21.2	913	105344	5.7	Eukaryotic translation initiation factor 3 subunit 8
281	UPI0000136781	17	106	20.2	955	108694	10.2	thyroid hormone receptor associated protein 3
282	O95373	17	126	19.7	1038	119516	4.8	Importin-7
282	UPI0000D625B4	17	126	19.6	1040	119702	4.8	Importin-7 (Imp7) (Ran-binding protein 7) (RanBP7).
283	O60841	17	51	14.8	1220	138799	5.5	Eukaryotic translation initiation factor 5B
283	UPI0000D61206	17	51	14.8	1220	138681	5.6	Eukaryotic translation initiation factor 5B (eIF-5B) (Translation initiation factor IF-2).
283	UPI0000207EC7	17	51	14.8	1220	138827	5.5	eukaryotic translation initiation factor 5B
283	Q8N5A0	17	51	14.8	1220	138800	5.5	Eukaryotic translation initiation factor 5B
284	Q92878	17	22	13.7	1312	153892	6.9	DNA repair protein RAD50
284	UPI000045733E	17	22	13.7	1311	153750	6.9	DNA repair protein RAD50 (EC 3.6.-.-) (hRAD50).
284	Q92878-2	17	22	13.7	1318	154587	6.9	Isoform 2 of Q92878
285	P26358	17	42	13	1616	183164	7.8	DNA (cytosine-5)-methyltransferase 1
285	A0AV63	17	42	12.9	1632	184818	7.9	DNMT1 protein
286	UPI0000D626C7	17	37	3.9	5300	606141	5.4	Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5 (Actin cross-linking family protein 7) (Macrophin-1) (Trabeculin-alpha) (620 kDa actin-binding protein) (ABP620).
286	Q9UPN3	17	37	3.8	5430	620426	5.4	Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5
286	UPI0000D626C8	17	37	3.8	5374	614212	5.4	Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5 (Actin cross-linking family protein 7) (Macrophin-1) (Trabeculin-alpha) (620 kDa actin-binding protein) (ABP620).
286	UPI00004578EC	17	37	3.8	5430	620397	5.4	Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5 (Actin cross-linking family protein 7) (Macrophin-1) (Trabeculin-alpha) (620 kDa actin-binding protein) (ABP620).
286	Q9UPN3-1	17	37	3.8	5374	614160	5.4	Isoform 1 of Q9UPN3
287	P21796	16	168	70.7	283	30773	8.5	Voltage-dependent anion-selective channel protein 1
288	P35232	16	94	68.8	272	29804	5.8	Prohibitin
288	Q6FHP5	16	94	68.8	272	29832	5.8	PHB protein
289	Q9HB71	16	46	63.2	228	26210	8.2	Calcyclin-binding protein
290	P09525	16	68	53.9	319	35883	6.1	Annexin A4
291	UPI0000D62378	16	53	50.5	402	45292	8.2	26S protease regulatory subunit 8 (Proteasome 26S subunit ATPase 5) (Proteasome subunit p45) (p45/SUG) (Thyroid hormone receptor- interacting protein 1) (TRIP1).
291	P62195	16	53	50	406	45626	7.5	26S protease regulatory subunit 8
292	UPI00006D1D75	16	138	57.5	320	34223	9.2	Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabilizing protein) (Single-strand RNA-binding protein) (hnRNP core protein A1).
292	P49312	16	138	57.5	320	34196	9.2	Heterogeneous nuclear ribonucleoprotein A1
292	P09651	16	138	49.5	372	38846	9.2	Heterogeneous nuclear ribonucleoprotein A1

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
292	UPI0000161BF2	16	138	49.5	372	38747	9.1	heterogeneous nuclear ribonucleoprotein A1 isoform b
293	P62333	16	42	45.8	389	44173	7.5	26S protease regulatory subunit S10B
294	P62495	16	34	43	437	49031	5.7	Eukaryotic peptide chain release factor subunit 1
295	P35241	16	81	37.4	583	68564	6.4	Radixin
296	O15355	16	54	36.4	546	59272	4.4	Protein phosphatase 2C isoform gamma
297	P06744	16	87	33.3	558	63147	8.3	Glucose-6-phosphate isomerase
298	P21980	16	40	32.5	687	77329	5.2	Protein-glutamine gamma-glutamyltransferase 2 (EC 2.3.2.13) (Tissue transglutaminase) (TGase C) (TGC) (TG(C))
299	O00567	16	47	32	594	66050	9.2	Nucleolar protein Nop56
300	Q03252	16	54	31.2	600	67689	5.3	Lamin-B2
301	Q14247	16	57	30.5	550	61636	5.4	Src substrate cortactin
301	UPI0000D62647	16	57	30.5	551	61762	5.4	Src substrate cortactin (Amplaxin) (Oncogene EMS1).
301	UPI000013D657	16	57	30.5	550	61586	5.4	cortactin isoform a
301	Q53HG7	16	57	30.5	550	61558	5.4	Cortactin isoform a variant
302	P07384	16	29	25.9	714	81890	5.7	Calpain-1 catalytic subunit
302	Q6DHV4	16	29	25.9	714	81831	5.6	CAPN1 protein
303	Q92973	16	37	24.8	890	101310	5	Transportin-1
303	UPI000020CAB6	16	37	24.6	898	102355	5	transportin 1 isoform 1
304	P50570-2	16	32	23.8	866	97652	7.6	Isoform 2 of P50570
304	P50570	16	32	23.7	870	98064	7.5	Dynamin-2
305	P55265-3	16	37	15.9	1181	131099	8.6	Isoform 3 of P55265
305	P55265-2	16	37	15.7	1200	133203	8.5	Isoform 2 of P55265
305	P55265	16	37	15.3	1226	135995	8.6	Double-stranded RNA-specific adenosine deaminase
305	Q59EC0	16	37	15.1	1244	137833	8.5	Adenosine deaminase, RNA-specific isoform ADAR-a variant
306	P52701	16	50	14.5	1360	152785	6.9	DNA mismatch repair protein MSH6
307	Q9UKK3	16	31	10.3	1724	192587	5.7	Poly [ADP-ribose] polymerase 4 (EC 2.4.2.30) (PARP-4) (Vault poly(ADP- ribose) polymerase)
308	Q07954	16	41	3.8	4544	504579	5.4	Low-density lipoprotein receptor-related protein 1 precursor
308	UPI00001B044F	16	41	3.8	4544	504610	5.4	low density lipoprotein-related protein 1
309	P61106	15	106	84.7	215	23897	6.2	Ras-related protein Rab-14
310	P51149	15	148	77.8	207	23490	6.7	Ras-related protein Rab-7a
311	P51858	15	53	70	240	26788	4.7	Hepatoma-derived growth factor
312	P12004	15	101	66.7	261	28769	4.7	Proliferating cell nuclear antigen
313	P16152	15	48	65.3	277	30375	8.3	Carbonyl reductase [NADPH] 1 (EC 1.1.1.184) (NADPH-dependent carbonyl reductase 1) (Prostaglandin-E(2) 9-reductase)
314	P63104	15	421	65.3	245	27745	4.8	14-3-3 protein zeta/delta
315	UPI00001AF1AB	15	39	58.4	389	42931	5.3	Interleukin enhancer-binding factor 2 (Nuclear factor of activated T- cells 45 kDa).
315	Q12905	15	39	58.2	390	43062	5.3	Interleukin enhancer-binding factor 2
316	P62701	15	135	55.1	263	29598	10.2	40S ribosomal protein S4, X isoform
317	Q99623	15	73	54.8	299	33296	9.8	Prohibitin-2
318	Q6QA25	15	99	50.8	248	29033	4.8	Tropomyosin 3
318	UPI000020489E	15	99	50.8	248	29079	4.8	Tropomyosin alpha-3 chain (Tropomyosin-3) (Tropomyosin gamma) (hTM5).
319	P07195	15	292	46.1	334	36639	6.1	L-lactate dehydrogenase B chain
320	P43034	15	34	45.9	410	46638	7.4	Platelet-activating factor acetylhydrolase IB subunit alpha
321	P52209	15	46	44.9	483	53140	7.2	6-phosphogluconate dehydrogenase, decarboxylating
322	Q15942	15	57	44.2	572	61277	6.7	Zyxin
323	O00232	15	28	41	456	52904	7.6	26S proteasome non-ATPase regulatory subunit 12
324	Q53GL9	15	74	41.1	428	49019	5.8	HLA-B associated transcript 1 variant
324	Q13838	15	74	41.1	428	48991	5.7	Spliceosome RNA helicase BAT1
324	Q0EFA1	15	74	39.7	443	50679	5.9	BAT1 protein
325	Q15008	15	52	39.1	389	45531	5.6	26S proteasome non-ATPase regulatory subunit 6
326	Q6DD88	15	49	38.4	541	60542	5.7	DKFZP564J0863 protein
327	Q96AE4	15	46	35.1	644	67560	7.6	Far upstream element-binding protein 1
327	UPI00004561FD	15	46	34.7	651	68491	7.3	Far upstream element-binding protein 1 (FUSE-binding protein 1) (FBP) (DNA helicase V) (HDH V).
327	Q96AE4-2	15	46	34.6	653	68605	7.3	Isoform 2 of Q96AE4
327	UPI000059CFF9	15	46	34.5	655	68904	7.9	Far upstream element-binding protein 1 (FUSE-binding protein 1) (FBP) (DNA helicase V) (HDH V).
328	UPI00003670EA	15	39	34	729	80255	8.3	Probable ATP-dependent RNA helicase DDX17 (EC 3.6.1.-) (DEAD box protein 17) (RNA-dependent helicase p72) (DEAD box protein p72).
328	UPI000021BFBA	15	39	34	729	80273	8.3	DEAD box polypeptide 17 isoform p82
328	Q59F66	15	39	33.6	737	81068	7.9	DEAD box polypeptide 17 isoform p82 variant
329	Q53G58	15	44	31.6	474	53281	7.1	Coronin, actin binding protein, 1C variant
329	Q9ULV4	15	44	31.6	474	53249	7.1	Coronin-1C
330	Q15046	15	46	27.1	597	68048	6.4	Lysyl-tRNA synthetase
330	UPI00001405CB	15	46	25.9	625	71497	6.8	Lysyl-tRNA synthetase (EC 6.1.1.6) (Lysine--tRNA ligase) (LysRS).

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330	Q9HB23	15	46	25.9	625	71384	6.7	Lysyl-tRNA synthetase
331	Q08J23	15	41	27	767	86499	6.9	Putative 5-methycytoisine methyltransferase
331	UPI000020BF2B	15	41	27	767	86471	6.8	NOL1/NOP2/Sun domain family 2 protein
332	P06737	15	39	26.1	847	97149	7.2	Glycogen phosphorylase, liver form
332	UPI0000D62406	15	39	26	849	97334	7.2	Glycogen phosphorylase, liver form (EC 2.4.1.1).
333	Q96PK6	15	24	25	669	69492	9.7	RNA-binding protein 14
334	UPI0000D62355	15	26	24	739	82092	6.8	Vesicle-fusing ATPase (EC 3.6.4.6) (Vesicular-fusion protein NSF) (N- ethylmaleimide sensitive fusion protein) (NEM-sensitive fusion protein).
334	P46459	15	26	23.8	744	82560	7	Vesicle-fusing ATPase
335	P08582	15	41	23.2	738	80242	6	Melanotransferrin precursor
335	UPI000013E329	15	41	23.2	738	80215	5.9	melanoma-associated antigen p97 isoform 1, precursor
336	P23921	15	29	21.8	792	90070	7.1	Ribonucleoside-diphosphate reductase large subunit
336	Q53GZ5	15	29	21.8	792	89972	7.3	Ribonucleoside-diphosphate reductase M1 chain variant
337	Q9Y6C2	15	36	20.8	1016	106695	5.2	EMILIN-1 precursor
338	Q13435	15	45	20.2	872	97657	5.7	Splicing factor 3B subunit 2
338	Q7Z627	15	45	20.1	877	98116	5.5	SF3B2 protein
338	Q9BWD2	15	45	19.7	894	100097	5.7	SF3B2 protein
339	Q6NT74	15	59	19.8	812	92194	5.8	ARS2 protein
339	Q9BXP5-2	15	59	18.5	872	100276	6	Isoform B of Q9BXP5
339	Q32MI4	15	59	18.5	871	100147	6	ARS2 protein
339	A4D2E5	15	59	18.4	875	100537	6	Arsenate resistance protein ARS2
339	Q9BXP5	15	59	18.4	876	100667	6	Arsenite-resistance protein 2
339	UPI000013C800	15	59	18.2	884	101567	6.1	Arsenite-resistance protein 2.
340	Q9Y2L1	15	32	18.3	958	109003	7.1	Exosome complex exonuclease RRP44
340	UPI00001610C4	15	32	18.3	958	108976	7.1	KIAA1008
340	UPI0000D61A7F	15	32	18.2	960	109187	7.1	Exosome complex exonuclease RRP44 (EC 3.1.13.-) (Ribosomal RNA- processing protein 44) (DIS3 protein homolog).
341	P22102	15	47	17.9	1010	107767	6.7	Trifunctional purine biosynthetic protein adenosine-3 [Includes: Phosphoribosylamine--glycine ligase (EC 6.3.4.13) (GARS) (Glycinamide ribonucleotide synthetase) (Phosphoribosylglycinamide synthetase); Phosphoribosylformylglycinamidine cyclo-ligase (EC 6.3.3.1) (AIRS) (Phosphoribosyl-aminoimidazole synthetase) (AIR synthase); Phosphoribosylglycinamide formyltransferase (EC 2.1.2.2) (GART) (GAR transformylase) (5'-phosphoribosylglycinamide transformylase)]
341	Q3B7A7	15	47	17.9	1010	107723	6.8	Phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase
341	Q59HH3	15	47	17.3	1046	112138	7.4	Phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase isoform 1 variant
342	Q5T665	15	81	17.9	956	106077	8.3	Inter-alpha inhibitor H5
342	UPI00003B5D4F	15	81	17.9	956	106017	8.3	inter-alpha trypsin inhibitor heavy chain precursor 5 isoform 1
343	P26006-2	15	47	17.9	1051	116612	6.8	Isoform Alpha
343	P26006	15	47	17.6	1066	118698	7	Integrin alpha-3 precursor (Galactoprotein B3) (GAPB3) (VLA-3 alpha chain) (FRP-2) (CD49c antigen) [Contains: Integrin alpha-3 heavy chain; Integrin alpha-3 light chain]
343	UPI0000140781	15	47	17.6	1066	118756	7	integrin alpha 3 isoform b, precursor
344	Q2NKW9	15	39	18.4	869	98150	7	Eukaryotic translation initiation factor 4 gamma, 2
344	P78344	15	39	17.6	907	102362	7.1	Eukaryotic translation initiation factor 4 gamma 2
344	UPI000013C8BE	15	39	17.6	907	102330	7.1	Eukaryotic translation initiation factor 4 gamma 2 (eIF-4-gamma 2) (eIF-4G 2) (eIF4G 2) (p97) (Death-associated protein 5) (DAP-5).
344	Q49A79	15	39	17.6	907	102389	7.1	Eukaryotic translation initiation factor 4 gamma, 2
344	Q0VH01	15	39	17.6	907	102335	7.1	Eukaryotic translation initiation factor 4 gamma, 2
344	Q59G42	15	39	17	940	105828	7.4	Eukaryotic translation initiation factor 4 gamma, 2 variant
345	P23229-4	15	32	18.1	1068	119074	7.3	Isoform Alpha
345	Q53RX7	15	32	18	1073	119476	6.8	Hypothetical protein ITGA6
345	P23229-2	15	32	18	1073	119462	6.8	Isoform Alpha
345	UPI0000366FA3	15	32	17.8	1086	121665	7.4	Integrin alpha-6 precursor (VLA-6) (CD49f antigen) [Contains: Integrin alpha-6 heavy chain; Integrin alpha-6 light chain].
345	P23229-5	15	32	17.8	1086	121678	7.6	Isoform Alpha
345	UPI0000EA87E5	15	32	17.7	1091	122053	6.8	integrin alpha chain, alpha 6 isoform a precursor
345	P23229-3	15	32	17.7	1091	122066	7	Isoform Alpha
345	UPI0000D6126A	15	32	17.4	1112	124028	6.6	Integrin alpha-6 precursor (VLA-6) (CD49f antigen) [Contains: Integrin alpha-6 heavy chain; Integrin alpha-6 light chain].

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345	P23229-6	15	32	17.4	1112	124014	6.6	Isoform Alpha
345	P23229	15	32	17.1	1130	126618	6.8	Integrin alpha-6 precursor (VLA-6) (CD49f antigen) [Contains: Integrin alpha-6 heavy chain; Integrin alpha-6 light chain]
345	UPI000013D4BA	15	32	17.1	1130	126605	6.6	Integrin alpha-6 precursor (VLA-6) (CD49f antigen) [Contains: Integrin alpha-6 heavy chain; Integrin alpha-6 light chain].
346	Q15021	15	49	13.3	1401	157168	6.6	Condensin complex subunit 1
346	UPI000013C8CA	15	49	13.3	1401	157182	6.6	Condensin complex subunit 1 (Non-SMC condensin I complex subunit D2) (Chromosome condensation-related SMC-associated protein 1) (Chromosome-associated protein D2) (hCAP-D2) (XCAP-D2 homolog).
347	Q71UH4	15	33	12.5	1598	180613	7.9	DNA topoisomerase II beta
347	Q02880	15	33	12.3	1626	183266	8	DNA topoisomerase 2-beta
347	Q02880-2	15	33	12.3	1621	182661	8.1	Isoform Beta
348	Q9C0C2	15	33	10.5	1729	181780	4.9	182 kDa tankyrase 1-binding protein
348	UPI000013DB72	15	33	10.5	1729	181795	4.9	tankyrase 1-binding protein 1
349	Q92621	15	33	8.1	2012	227918	6.2	Nuclear pore complex protein Nup205
349	UPI00001D74D8	15	33	8.1	2012	227919	6.2	Nuclear pore complex protein Nup205 (Nucleoporin Nup205) (205 kDa nucleoporin).
350	Q9UQ35	15	57	7.3	2752	299616	12.1	Serine/arginine repetitive matrix protein 2
351	P49792	15	47	5.2	3224	358201	6.2	E3 SUMO-protein ligase RanBP2
351	UPI0000167B4B	15	47	5.2	3224	358173	6.2	RAN binding protein 2
352	P30041	14	88	66.5	224	25035	6.4	Peroxiredoxin-6
353	Q15365	14	94	59.3	356	37498	7.1	Poly(rC)-binding protein 1
353	UPI00001313C8	14	94	59.3	356	37526	7.1	poly(rC) binding protein 1
354	Q13162	14	61	59	271	30540	6.3	Peroxiredoxin-4
355	Q13347	14	51	57.8	325	36502	5.6	Eukaryotic translation initiation factor 3 subunit 2
356	Q5TAM6	14	49	57.1	333	37805	5.2	SGT1, suppressor of G2 allele of SKP1
357	UPI00006C059A	14	84	62.5	293	31445	7.6	PREDICTED: similar to voltage-dependent anion channel 2
357	UPI000013EEE0	14	84	62.5	293	31479	7.6	PREDICTED: similar to voltage-dependent anion channel 2
357	P45880-5	14	84	62.2	294	31566	7.6	Isoform 5 of P45880
357	UPI0000D611B0	14	84	61.8	296	31721	7.6	UPI0000D611B0 UniRef100 entry
357	UPI00003666E7	14	84	55.3	331	36232	6.7	Voltage-dependent anion-selective channel protein 2 (VDAC-2) (hVDAC2) (Outer mitochondrial membrane protein porin 2).
357	P45880-3	14	84	55.1	332	36288	6.7	Isoform 3 of P45880
358	P27695	14	32	55	318	35554	8.1	DNA-(apurinic or apyrimidinic site) lyase
359	P04406	14	967	54.3	335	36053	8.5	Glyceraldehyde-3-phosphate dehydrogenase
360	UPI00004115F3	14	30	60.6	188	21064	8.7	PREDICTED: similar to deoxythymidylate kinase (thymidylate kinase) isoform 1
360	P23919	14	30	53.8	212	23819	8.3	Thymidylate kinase
361	P61247	14	169	53.4	264	29945	9.7	40S ribosomal protein S3a
361	Q6NXR8	14	169	53.4	264	29975	9.7	Ribosomal protein S3A
362	P29692	14	144	51.6	281	31122	5	Elongation factor 1-delta
362	Q96I38	14	144	22.4	647	71422	6.4	EEF1D protein
363	P04899	14	60	50.7	355	40451	5.5	Guanine nucleotide-binding protein G(i), alpha-2 subunit
364	Q53GN6	14	37	47.9	376	42917	5.7	Proteasome 26S non-ATPase subunit 13 isoform 1 variant
364	UPI0000158430	14	37	47.9	376	42946	5.8	26S proteasome non-ATPase regulatory subunit 13 (26S proteasome regulatory subunit S11) (26S proteasome regulatory subunit p40.5).
364	Q9UNM6	14	37	47.9	376	42918	5.8	26S proteasome non-ATPase regulatory subunit 13
365	O00154	14	76	47.6	380	41796	8.5	Cytosolic acyl coenzyme A thioester hydrolase
366	P17174	14	23	45.3	413	46248	7	Aspartate aminotransferase, cytoplasmic
367	Q02878	14	244	45.1	288	32728	10.6	60S ribosomal protein L6
367	Q8TBK5	14	244	45.1	288	32742	10.6	Ribosomal protein L6
367	Q8N5Z7	14	244	45.1	288	32726	10.6	Ribosomal protein L6
367	Q9HBB3	14	244	45	289	32891	10.6	DNA-binding protein TAXREB107
368	O15144	14	98	45	300	34333	7.3	Actin-related protein 2/3 complex subunit 2
369	Q32Q68	14	57	44.9	272	30629	6	Capping protein (Actin filament) muscle Z-line, beta
369	Q5VVZ5	14	57	40.5	301	33781	6.4	Capping protein (Actin filament) muscle Z-line, beta
370	P23381	14	44	43.9	471	53165	6.2	Tryptophanyl-tRNA synthetase, cytoplasmic
371	Q15084	14	133	43	440	48121	5.1	Protein disulfide-isomerase A6 precursor
371	Q15084-2	14	133	38.4	492	53901	5.3	Isoform 2 of Q15084
372	P31930	14	34	41.9	480	52646	6.4	Ubiquinol-cytochrome-c reductase complex core protein 1, mitochondrial precursor
373	O75874	14	28	41.1	414	46659	7	Isocitrate dehydrogenase [NADP] cytoplasmic (EC 1.1.1.42) (Cytosolic NADP-isocitrate dehydrogenase) (Oxalosuccinate decarboxylase) (IDH) (NADP(+)-specific ICDH)
373	Q6FIA4	14	28	41.1	414	46568	6.8	IDH1 protein
374	P26599	14	85	39.4	531	57221	9.2	Polypyrimidine tract-binding protein 1
374	P26599-2	14	85	38	550	59037	9.2	Isoform 2 of P26599

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374	UPI0000D616E2	14	85	37.5	557	59693	9.2	Polypyrimidine tract-binding protein 1 (PTB) (Heterogeneous nuclear ribonucleoprotein I) (hnRNP I) (57 kDa RNA-binding protein PPTB-1).
374	Q9BUQ0	14	85	37.5	557	59633	9.2	Polypyrimidine tract binding protein 1
375	UPI000013EC8B	14	151	39	426	47566	11.1	60S ribosomal protein L4 (L1).
375	P36578	14	151	38.9	427	47697	11.1	60S ribosomal protein L4
375	Q59GY2	14	151	37.6	441	48996	11	Ribosomal protein L4 variant
376	Q8TC62	14	52	39.6	417	48659	8.6	Septin 7
376	Q3LIE9	14	52	39.5	418	48774	8.6	Predicted protein product of Nbla02942
376	A4GYY8	14	52	38.1	433	50263	8.6	Hypothetical protein DKFZp686F17268
376	Q16181-2	14	52	37.8	436	50581	8.6	Isoform 2 of Q16181
376	Q16181	14	52	37.8	437	50680	8.6	Septin-7
376	UPI0000D61C26	14	52	37.7	438	50809	8.5	Septin-7 (CDC10 protein homolog).
377	P49411	14	46	38.1	452	49542	7.6	Elongation factor Tu, mitochondrial precursor
378	Q9NTK5	14	37	37.9	396	44744	7.8	Putative GTP-binding protein 9
379	P21589	14	66	37.6	574	63368	7	5'-nucleotidase precursor
379	Q6NZX3	14	66	37.6	574	63308	7	5'-nucleotidase, ecto
379	Q53Z63	14	66	37.6	574	63338	7	5'-nucleotidase
380	Q9Y265	14	41	37.5	456	50228	6.4	RuvB-like 1
381	Q6NUK1	14	22	36.1	477	53338	6.3	Solute carrier family 25 member 24
381	UPI00001BDC72	14	22	36.1	476	53251	6.3	solute carrier family 25 member 24 isoform 1
381	Q6PJJ9	14	22	36.1	477	53354	6.3	Solute carrier family 25 (Mitochondrial carrier; phosphate carrier), member 24
382	P00505	14	40	36	430	47476	9	Aspartate aminotransferase, mitochondrial precursor
382	UPI000013CB99	14	40	36	430	47518	9	aspartate aminotransferase 2 precursor
382	Q53FL3	14	40	36	430	47548	9	Aspartate aminotransferase 2 variant
383	P60228	14	90	36	445	52221	6	Eukaryotic translation initiation factor 3 subunit 6
383	Q6IAX5	14	90	36	445	52206	6	EIF3S6 protein
384	Q7Z4H8	14	35	35.9	507	58573	8.2	KDEL motif-containing protein 2 precursor
385	Q9NVA2	14	47	35.9	429	49398	6.8	Septin-11
386	UPI0000D61084	14	179	37.6	599	65668	5.5	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit precursor (EC 2.4.1.119) (Ribophorin II) (RPN-II) (RIBIIR).
386	Q5JYR6	14	179	36.6	615	67723	6.1	Ribophorin II
386	P04844	14	179	35.7	631	69284	5.7	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit precursor
387	P41091	14	23	35	472	51110	8.4	Eukaryotic translation initiation factor 2 subunit 3
388	P55809	14	30	33.8	520	56158	7.5	Succinyl-CoA:3-ketoacid-coenzyme A transferase 1, mitochondrial precursor
389	P38606	14	22	33.1	617	68304	5.5	Vacuolar ATP synthase catalytic subunit A
390	P08195	14	266	32.3	529	57945	5.3	4F2 cell-surface antigen heavy chain
390	UPI0000405902	14	266	28.5	599	64873	5.1	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2 isoform d
390	UPI00004EC298	14	266	27.1	631	68101	5	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2 isoform b
390	UPI000013E757	14	266	27.1	630	67994	5	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2 isoform c
390	UPI00004EC297	14	266	25.9	661	71123	5	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2 isoform a
391	P27694	14	27	29.5	616	68138	7.2	Replication protein A 70 kDa DNA-binding subunit
392	P54577	14	33	28	528	59144	7	Tyrosyl-tRNA synthetase, cytoplasmic
393	Q2T9F7	14	39	27.8	713	79612	6.8	UNC84B protein
393	Q9UH99	14	39	27.6	717	80311	6.7	Sad1/unc-84-like protein 2
393	Q504T5	14	39	26.8	738	82575	6.6	UNC84B protein
394	Q8N4P8	14	25	27.5	632	73709	9.6	GTPBP4 protein
394	UPI00001AE86D	14	25	27.4	634	73852	9.5	Nucleolar GTP-binding protein 1 (Chronic renal failure gene protein) (GTP-binding protein NGB).
394	Q9BZE4	14	25	27.4	634	73965	9.5	Nucleolar GTP-binding protein 1
395	Q12797	14	118	22.6	758	85863	5	Aspartyl/asparaginyl beta-hydroxylase
395	UPI0000D624CD	14	118	22.5	759	86006	5.1	Aspartyl/asparaginyl beta-hydroxylase (EC 1.14.11.16) (Aspartate beta- hydroxylase) (ASP beta-hydroxylase) (Peptide-aspartate beta- dioxygenase).
396	Q96TA1	14	40	21.3	733	82683	6.2	Niban-like protein
396	Q5VVW7	14	40	20.9	746	84138	6.2	Chromosome 9 open reading frame 88
397	Q96FS1	14	34	22.7	830	92388	7.2	CTNND1 protein
397	O60716-21	14	34	22.6	832	92675	7.2	Isoform 3A of O60716
397	O60716-19	14	34	22.4	838	93496	7	Isoform 3AC of O60716
397	O60716-18	14	34	21.8	861	95868	6.3	Isoform 3AB of O60716
397	O60716-13	14	34	21.4	879	98049	7.5	Isoform 2A of O60716
397	O60716-11	14	34	21.2	885	98870	7.3	Isoform 2AC of O60716
397	O60716-10	14	34	20.7	908	101242	6.6	Isoform 2AB of O60716
397	Q6DHZ7	14	34	20.2	933	104098	7	CTNND1 protein
397	O60716-5	14	34	20.2	933	104156	7	Isoform 1A of O60716
397	UPI0000D62606	14	34	20	939	105005	7	Catenin delta-1 (p120 catenin) (p120(ctn)) (Cadherin-associated Src substrate) (CAS) (p120(cas)).
397	O60716-3	14	34	20	939	104977	6.9	Isoform 1AC of O60716
397	O60716-2	14	34	19.5	962	107349	6.3	Isoform 1AB of O60716

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
397	O60716	14	34	19.4	968	108170	6.2	Catenin delta-1 (p120 catenin) (p120(ctn)) (Cadherin-associated Src substrate) (CAS) (p120(cas))
398	Q9P2B2	14	29	18	879	98556	6.6	Prostaglandin F2 receptor negative regulator precursor
399	Q5SYX5	14	20	18.3	952	107946	5	Golgi autoantigen, golgin subfamily a, 2
399	Q08379	14	20	17.6	990	111659	5	Golgin subfamily A member 2
400	O14617-4	14	48	16.8	1021	114707	8	Isoform 4 of O14617
400	O14617	14	48	14.9	1153	130158	8.5	AP-3 complex subunit delta-1
400	O14617-5	14	48	14.2	1215	136651	7.6	Isoform 5 of O14617
401	O43795-2	14	29	15.6	1078	124951	9.2	Isoform 2 of O43795
401	O43795	14	29	14.8	1136	131985	9.4	Myosin-Ib
402	Q15155	14	38	14.6	1222	134352	5.8	Nodal modulator 1 precursor
402	UPI00001AF3F1	14	38	14.6	1222	134133	5.7	nodal modulator 3
402	UPI000013D37E	14	38	14.6	1222	134324	5.8	nodal modulator 1
402	UPI00001AE864	14	38	14	1267	139381	5.7	Nodal modulator 3 precursor (pM5 protein 3).
402	Q5JPE7	14	38	14	1267	139439	5.8	Nodal modulator 2 precursor
403	UPI00001610D5	14	29	14.3	1155	129438	8.5	DEAH (Asp-Glu-Ala-His) box polypeptide 30 isoform 2
403	Q7L2E3	14	29	13.8	1194	133938	8.8	Putative ATP-dependent RNA helicase DHX30
404	O60271-4	14	30	13.5	1307	144681	5.2	Isoform 4 of O60271
404	O60271-2	14	30	13.4	1311	145135	5.2	Isoform 2 of O60271
404	UPI0000D62364	14	30	13.4	1309	144909	5.2	C-jun-amino-terminal kinase-interacting protein 4 (JNK-interacting protein 4) (JIP-4) (JNK-associated leucine-zipper protein) (JLP) (Sperm-associated antigen 9) (Mitogen-activated protein kinase 8-interacting protein 4) (Human lung cancer protein 6) (HLC
404	UPI0000D62363	14	30	13.4	1313	145362	5.2	C-jun-amino-terminal kinase-interacting protein 4 (JNK-interacting protein 4) (JIP-4) (JNK-associated leucine-zipper protein) (JLP) (Sperm-associated antigen 9) (Mitogen-activated protein kinase 8-interacting protein 4) (Human lung cancer protein 6) (HLC
405	O95819	14	35	13.1	1239	142101	7.5	Mitogen-activated protein kinase kinase kinase kinase 4
406	P28290	14	24	13.1	1259	138386	5.2	Sperm-specific antigen 2
407	Q14160	14	27	9.8	1630	174930	5.1	Protein LAP4
407	UPI00001408BD	14	27	9.8	1630	174884	5.1	Protein LAP4 (Protein scribble homolog) (hScrib).
407	UPI0000D62517	14	27	9.7	1654	177194	5.1	Protein LAP4 (Protein scribble homolog) (hScrib).
407	UPI00004576FD	14	27	9.7	1655	177693	5.1	Protein LAP4 (Protein scribble homolog) (hScrib).
407	Q14160-4	14	27	9.7	1654	177240	5.1	Isoform 4 of Q14160
407	Q14160-3	14	27	9.7	1655	177739	5.1	Isoform 3 of Q14160
408	Q59ES2	14	31	6.5	2341	267021	6.3	Inositol 1,4,5-trisphosphate receptor type 3 variant
408	UPI0000161B31	14	31	5.7	2671	304115	6.5	inositol 1,4,5-triphosphate receptor, type 3
408	Q5TAQ2	14	31	5.7	2671	304105	6.5	Inositol 1,4,5-triphosphate receptor, type 3
409	Q14789	14	24	5.2	3259	376019	5	Golgin subfamily B member 1
409	UPI000012B42C	14	24	5.2	3259	376078	5	golgi autoantigen, golgin subfamily b, macrogolgin (with transmembrane signal), 1
410	Q5T4S7	14	37	2.9	5183	573849	6	Zinc finger UBR1-type protein 1
410	Q8TDN5	14	37	2.9	5183	573909	6	P600
411	Q14019	13	80	81.7	142	15945	5.7	Coactosin-like protein
412	P07737	13	170	73.6	140	15054	8.3	Profilin-1
413	Q99714	13	46	70.5	261	26923	7.8	3-hydroxyacyl-CoA dehydrogenase type-2
414	P37802	13	153	70.4	199	22391	8.2	Transgelin-2
414	UPI000013D3E3	13	153	63.6	220	24454	8.2	Transgelin-2 (SM22-alpha homolog).
415	O00299	13	88	68.5	241	26923	5.2	Chloride intracellular channel protein 1
415	Q53FB0	13	88	68.5	241	27015	5.2	Chloride intracellular channel 1 variant
416	P61019	13	106	67.9	212	23546	6.5	Ras-related protein Rab-2A
417	Q99497	13	41	67.2	189	19891	6.8	Protein DJ-1
418	Q9Y696	13	41	64.8	253	28772	5.6	Chloride intracellular channel protein 4
419	Q13509	13	76	64.4	450	50433	4.9	Tubulin beta-3 chain
420	Q5RLJ0	13	36	61.1	244	27969	6.4	CLE
420	Q9Y224	13	36	61.1	244	28068	6.7	Protein C14orf166
421	P67775	13	26	60.8	309	35594	5.5	Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform
422	P54920	13	30	60	295	33233	5.4	Alpha-soluble NSF attachment protein
423	P31150	13	29	59.3	447	50583	5.1	Rab GDP dissociation inhibitor alpha
424	Q9UJZ1	13	46	56.7	356	38534	7.4	Stomatin-like protein 2
425	Q15019	13	93	54.3	361	41487	6.6	Septin-2
426	P13804	13	40	53.5	333	35080	8.4	Electron transfer flavoprotein subunit alpha, mitochondrial precursor
427	Q9BUP3	13	30	53.3	242	27118	8.6	Oxidoreductase HTATIP2
428	P55145	13	31	51.4	179	20257	8.4	ARMET protein precursor
428	UPI00004542F2	13	31	49.7	185	21144	8.9	arginine-rich, mutated in early stage tumors
429	Q15631	13	57	51.3	228	26183	6.4	Translin
430	Q06323	13	38	47.8	249	28723	6	Proteasome activator complex subunit 1

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430	UPI000045675C	13	38	47.2	252	28837	5.4	Proteasome activator complex subunit 1 (Proteasome activator 28-alpha subunit) (PA28alpha) (PA28a) (Activator of multicatalytic protease subunit 1) (11S regulator complex subunit alpha) (REG-alpha) (Interferon gamma up-regulated I-5111 protein) (IGUP I-51
431	Q5T7C4	13	80	64.6	158	18311	9.7	High-mobility group box 1
431	Q5T7C6	13	80	63	162	18808	9.7	High-mobility group box 1
431	Q59GW1	13	80	58	176	20164	9.7	High-mobility group box 1 variant
431	P09429	13	80	47.4	215	24894	5.7	High mobility group protein B1
431	Q14321	13	80	47.4	215	24993	5.9	HMG-1
432	P46781	13	126	46.4	194	22591	10.7	40S ribosomal protein S9
433	P07339	13	114	45.1	412	44552	6.5	Cathepsin D precursor (EC 3.4.23.5) [Contains: Cathepsin D light chain; Cathepsin D heavy chain]
434	P24752	13	32	44.7	427	45200	8.8	Acetyl-CoA acetyltransferase, mitochondrial precursor
435	P52788	13	35	44.3	366	41268	5	Spermine synthase
436	Q6IBS1	13	35	42.3	404	45250	5.5	PSMC3 protein
437	P28482	13	43	42.2	360	41390	7	Mitogen-activated protein kinase 1
437	UPI0000F0A51A	13	43	40	380	43553	7.3	Mitogen-activated protein kinase 1
438	P31943	13	168	41.9	449	49229	6.3	Heterogeneous nuclear ribonucleoprotein H
438	Q6IBM4	13	168	41.9	449	49130	6.2	HNRPH1 protein
438	UPI00001AF4DD	13	168	39.8	472	51230	6.8	Heterogeneous nuclear ribonucleoprotein H (hnRNP H).
439	O75955	13	19	41	427	47355	7.5	Flotillin-1
439	Q53HQ0	13	19	41	427	47354	8.1	Flotillin 1 variant
440	P50213	13	40	40.7	366	39592	6.9	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial precursor (EC 1.1.1.41) (Isocitric dehydrogenase) (NAD(+)-specific ICDH)
440	Q53GF8	13	40	40.7	366	39620	6.9	Isocitrate dehydrogenase 3 (NAD+) alpha variant
441	P07910-2	13	123	40.3	293	32338	5.1	Isoform C1 of P07910
442	Q5VU20	13	58	40.2	393	43135	8.4	PAI-1 mRNA-binding protein
442	Q8NC51	13	58	38.7	408	44965	8.6	Plasminogen activator inhibitor 1 RNA-binding protein
443	Q96ND2	13	64	39.8	377	43084	4.9	CDNA FLJ31051 fis, clone HSYRA2000605, weakly similar to MYOSIN HEAVY CHAIN, CLONE 203
444	P36507	13	17	39.5	400	44424	6.5	Dual specificity mitogen-activated protein kinase kinase 2
445	P21281	13	28	38.7	511	56501	5.8	Vacuolar ATP synthase subunit B, brain isoform
446	P43686	13	31	38.5	418	47366	5.2	26S protease regulatory subunit 6B
447	Q12765	13	34	38.4	414	46382	4.8	Secernin-1
448	P22695	13	34	37.5	453	48443	8.6	Ubiquinol-cytochrome-c reductase complex core protein 2, mitochondrial precursor
449	P38159	13	71	35.5	391	42332	10.1	Heterogeneous nuclear ribonucleoprotein G
450	P04040	13	28	34	527	59756	7.4	Catalase
451	Q16222-3	13	31	31.7	521	58682	6.3	Isoform 3 of Q16222
451	Q16222	13	31	31.6	522	58769	6.3	UDP-N-acetylhexosamine pyrophosphorylase (Antigen X) (AGX) (Sperm- associated antigen 2) [Includes: UDP-N-acetylgalactosamine pyrophosphorylase (EC 2.7.7.-) (AGX-1); UDP-N-acetylglucosamine pyrophosphorylase (EC 2.7.7.23) (AGX-2)]
452	O94973	13	38	30	939	103960	7	AP-2 complex subunit alpha-2
452	Q53ET1	13	38	30	940	104089	6.9	Adaptor-related protein complex 2, alpha 2 subunit variant
453	Q6IAP9	13	14	29	521	58307	7.4	PRPF4 protein
453	Q5T1M7	13	14	29	521	58321	7.4	PRP4 pre-mRNA processing factor 4 homolog
453	O43172	13	14	28.9	522	58449	7.4	U4/U6 small nuclear ribonucleoprotein Prp4
453	Q59EL4	13	14	28.1	537	60022	7.6	PRPF4 protein variant
454	P12268	13	28	28.8	514	55805	6.9	Inosine-5'-monophosphate dehydrogenase 2
455	P61221	13	31	27.9	599	67314	8.3	ATP-binding cassette sub-family E member 1
456	Q8WXF1	13	22	27.9	523	58744	6.7	Paraspeckle component 1
457	Q96N86	13	47	27.9	517	59574	8.6	CDNA FLJ31237 fis, clone KIDNE2004846, highly similar to 26S PROTEASOME REGULATORY SUBUNIT S3
457	O43242	13	47	27	534	60978	8.4	26S proteasome non-ATPase regulatory subunit 3
457	Q6IBN0	13	47	27	534	60946	8.4	PSMD3 protein
458	P28331	13	25	26.4	727	79468	6.2	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial precursor
459	P46060	13	31	25.7	587	63542	4.7	Ran GTPase-activating protein 1
460	O76094	13	29	25.5	671	74606	9.3	Signal recognition particle 72 kDa protein
461	O60216	13	15	25	631	71690	4.7	Double-strand-break repair protein rad21 homolog
462	Q9UHB9	13	26	24.9	627	70730	8.6	Signal recognition particle 68 kDa protein
463	P07686	13	67	23.7	556	63111	6.8	Beta-hexosaminidase beta chain precursor (EC 3.2.1.52) (N-acetyl-beta- glucosaminidase) (Beta-N-acetylhexosaminidase) (Hexosaminidase B) (Cervical cancer proto-oncogene 7) (HCC-7) [Contains: Beta- hexosaminidase beta-B chain; Beta-hexosaminidase beta-A chain]

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464	Q8TAE4	13	31	24.8	634	72226	6.6	PDE1C protein
464	Q14123-2	13	31	24.8	634	72208	6.6	Isoform PDE1C1 of Q14123
464	Q14123	13	31	22.1	709	80760	8.8	Calcium/calmodulin-dependent 3',5'-cyclic nucleotide phosphodiesterase 1C
465	Q9H845	13	32	21.7	621	68760	8	Acyl-CoA dehydrogenase family member 9, mitochondrial precursor
466	O00469	13	35	21.6	737	84686	6.7	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 2 precursor
466	O00469-2	13	35	21	758	87098	6.7	Isoform 2 of O00469
467	Q8TCS8	13	20	20.9	783	85951	7.8	Polyribonucleotide nucleotidyltransferase 1, mitochondrial precursor
467	UPI0000D611A9	13	20	20.9	785	86123	7.8	Polyribonucleotide nucleotidyltransferase 1, mitochondrial precursor (EC 2.7.7.8) (PNPase 1) (Polynucleotide phosphorylase-like protein) (PNPase old-35) (3'-5' RNA exonuclease OLD35).
467	UPI000007136D	13	20	20.9	783	85937	7.8	polyribonucleotide nucleotidyltransferase 1
468	Q13616	13	24	20.7	776	89678	8	Cullin-1
469	Q99459	13	25	20.4	802	92251	8.2	Cell division cycle 5-like protein
470	Q53FR4	13	39	18.7	796	91681	5.5	Vacuolar protein sorting 35 variant
470	Q96QK1	13	39	18.7	796	91707	5.5	Vacuolar protein sorting-associated protein 35
471	Q86XP3	13	21	18.6	938	102975	7	ATP-dependent RNA helicase DDX42
471	UPI0000456AEB	13	21	18.6	938	103005	6.9	DEAD box polypeptide 42 protein
472	P49736	13	28	18.1	904	101896	5.5	DNA replication licensing factor MCM2
473	Q14566	13	25	18	821	92889	5.4	DNA replication licensing factor MCM6
474	Q15424	13	35	16	915	102642	5.5	Scaffold attachment factor B
474	A0AV56	13	35	15.9	917	102855	5.5	Scaffold attachment factor B
475	Q8TEX9	13	31	15.9	1081	118715	5	Importin-4
475	Q8TEX9-2	13	31	15.9	1083	118901	4.9	Isoform 2 of Q8TEX9
476	Q13423	13	50	15	1086	113895	8.1	NAD(P) transhydrogenase, mitochondrial precursor
476	Q2TB59	13	50	15	1086	113883	8.1	Nicotinamide nucleotide transhydrogenase
477	Q96F88	13	40	14.2	1024	114681	9.2	Processing of 1, ribonuclease P/MRP subunit
477	Q99575	13	40	14.2	1024	114709	9.2	Ribonucleases P/MRP protein subunit POP1
478	Q6PKG0	13	32	12.8	1096	123510	8.8	La-related protein 1
479	Q9Y2A7	13	24	12.3	1128	128790	6.6	Nck-associated protein 1
479	UPI00001693F2	13	24	12.3	1134	129517	6.7	NCK-associated protein 1 isoform 2
480	Q9UBG0	13	37	11.3	1479	166655	5.8	Macrophage mannose receptor 2 precursor
480	UPI000013E895	13	37	11.3	1479	166674	5.8	mannose receptor, C type 2
481	Q08378-2	13	22	11.2	1390	155682	5.4	Isoform 2 of Q08378
481	Q08378-3	13	22	10.6	1458	162985	5.4	Isoform 3 of Q08378
481	Q08378	13	22	10.3	1498	167354	5.4	Golgin subfamily A member 3
482	Q9UIG0-2	13	30	9.7	1479	170446	8.5	Isoform 2 of Q9UIG0
482	Q9UIG0	13	30	9.6	1483	170902	8.5	Bromodomain adjacent to zinc finger domain protein 1B
483	UPI000066D92A	13	25	8.6	1922	208475	4.7	Tumor suppressor p53-binding protein 1 (p53-binding protein 1) (p53BP1) (53BP1).
483	Q12888	13	25	8.4	1972	213573	4.7	Tumor suppressor p53-binding protein 1
484	P62937	12	192	77.6	165	18012	7.8	Peptidyl-prolyl cis-trans isomerase A
485	P60981	12	50	65.5	165	18506	7.9	Destrin
486	Q9Y2Q3	12	27	60.6	226	25497	8.4	Glutathione S-transferase kappa 1
487	Q7Z4Y4	12	32	56.8	227	25620	9.3	GTP:AMP phosphotransferase
487	Q9UIJ7	12	32	56.8	227	25565	9.2	GTP:AMP phosphotransferase mitochondrial
488	P05388	12	107	55.8	317	34274	6	60S acidic ribosomal protein P0
488	Q53HW2	12	107	55.8	317	34302	6	Ribosomal protein P0 variant
489	P23284	12	164	55.3	208	22742	9.3	Peptidyl-prolyl cis-trans isomerase B precursor
489	UPI0000072333	12	164	53.2	216	23743	9.4	peptidylprolyl isomerase B precursor
489	Q6IBH5	12	164	53.2	216	23728	9.4	Peptidyl-prolyl cis-trans isomerase
490	Q9Y5M8	12	50	53.9	271	29702	9	Signal recognition particle receptor subunit beta
491	O14579	12	29	52.3	308	34482	5.1	Coatomer subunit epsilon
491	Q53HJ6	12	29	52.3	308	34528	5.1	Epsilon subunit of coatomer protein complex isoform a variant
492	P06493	12	47	52.2	297	34095	8.4	Cell division control protein 2 homolog
492	UPI000013EBE9	12	47	52.2	297	34081	8.4	Cell division control protein 2 homolog (EC 2.7.11.22) (EC 2.7.11.23) (p34 protein kinase) (Cyclin-dependent kinase 1) (CDK1).
493	UPI000013D771	12	25	51.8	357	38325	8	Sorbitol dehydrogenase (EC 1.1.1.14) (L-iditol 2-dehydrogenase).
494	A2VBX9	12	59	50.5	273	31655	6	MHC class I antigen
495	P67936	12	80	49.6	248	28522	4.7	Tropomyosin alpha-4 chain
496	P00387	12	65	49.5	301	34235	7.6	NADH-cytochrome b5 reductase (EC 1.6.2.2) (B5R) (Diaphorase-1) (Cytochrome b5 reductase 3) [Contains: NADH-cytochrome b5 reductase membrane-bound form; NADH-cytochrome b5 reductase soluble form]
497	P08865	12	123	49.2	295	32854	4.9	40S ribosomal protein SA
498	Q07955	12	71	49.2	248	27745	10.4	Splicing factor, arginine/serine-rich 1
499	P15880	12	79	47.8	293	31324	10.2	40S ribosomal protein S2
499	UPI000013EEA4	12	79	47.8	293	31438	10.2	similar to ribosomal protein S2 (LOC646294), mRNA
500	O43809	12	30	46.7	227	26227	8.8	Cleavage and polyadenylation specificity factor 5

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
501	Q6IBS0	12	43	45.8	349	39548	6.9	Twinfilin-2
502	Q12907	12	38	44.9	356	40229	7	Vesicular integral-membrane protein VIP36 precursor
503	Q99733	12	55	43.7	375	42823	4.7	Nucleosome assembly protein 1-like 4
504	P05141	12	189	42.3	298	32895	9.7	ADP/ATP translocase 2
504	Q6NVC0	12	189	39	323	35294	9.8	SLC25A5 protein
505	Q13501	12	32	42.3	440	47687	5.2	Sequestosome-1
506	P40925	12	63	40.7	334	36426	7.3	Malate dehydrogenase, cytoplasmic
507	P07954-2	12	37	43.7	467	50213	7.4	Isoform Cytoplasmic of P07954
507	P07954	12	37	40	510	54637	8.8	Fumarate hydratase, mitochondrial precursor
508	P61160	12	85	39.6	394	44761	6.7	Actin-like protein 2
509	P04181	12	25	37.8	439	48535	7	Ornithine aminotransferase, mitochondrial precursor (EC 2.6.1.13) (Ornithine--oxo-acid aminotransferase) [Contains: Ornithine aminotransferase, hepatic form; Ornithine aminotransferase, renal form]
510	P51991	12	91	36.8	378	39595	9	Heterogeneous nuclear ribonucleoprotein A3
511	Q0IJ47	12	130	36.4	467	48086	4.9	KRT9 protein
512	P39656	12	123	35.8	439	48810	5.7	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit precursor
512	UPI0000163BD0	12	123	34.4	456	50702	6.4	dolichyl-diphosphooligosaccharide-protein glycosyltransferase precursor
512	Q5VWA5	12	123	34.4	456	50801	6.5	Dolichyl-diphosphooligosaccharide-protein glycosyltransferase
513	P50552	12	24	35.5	380	39830	8.9	Vasodilator-stimulated phosphoprotein
514	P38919	12	19	34.8	411	46871	6.7	Eukaryotic initiation factor 4A-III
515	UPI0000134091	12	60	34.6	402	45978	10.2	60S ribosomal protein L3 (HIV-1 TAR RNA-binding protein B) (TARBP-B).
515	P39023	12	60	34.5	403	46109	10.2	60S ribosomal protein L3
516	P22234	12	47	34.4	425	47079	7.2	Multifunctional protein ADE2 [Includes: Phosphoribosylaminoimidazole- succinocarboxamide synthase (EC 6.3.2.6) (SAICAR synthetase); Phosphoribosylaminoimidazole carboxylase (EC 4.1.1.21) (AIR carboxylase) (AIRC)]
516	UPI000013D4E4	12	47	32.4	451	49679	7.5	Multifunctional protein ADE2 [Includes: Phosphoribosylaminoimidazole- succinocarboxamide synthase (EC 6.3.2.6) (SAICAR synthetase); Phosphoribosylaminoimidazole carboxylase (EC 4.1.1.21) (AIR carboxylase) (AIRC)].
517	Q96D94	12	30	32.5	499	54025	5.3	SIAHBP1 protein
517	UPI00004576FF	12	30	29.9	541	58115	5.3	fuse-binding protein-interacting repressor isoform b
517	Q9NZA0	12	30	29.9	542	58172	5.3	FBP-interacting repressor
517	Q99628	12	30	29.9	541	57996	5.3	Siah binding protein 1
518	O43390	12	51	32.4	633	70943	8.1	Heterogeneous nuclear ribonucleoprotein R
519	P20042	12	21	32.4	333	38388	5.8	Eukaryotic translation initiation factor 2 subunit 2
520	A4D2I9	12	41	32.3	431	48294	5	Src homology 3 domain-containing protein HIP-55
520	UPI0000D61C36	12	41	31.7	438	48886	5.2	Drebrin-like protein (SH3 domain-containing protein 7) (Drebrin-F) (Cervical SH3P7) (HPK1-interacting protein of 55 kDa) (HIP-55) (Cervical mucin-associated protein).
520	Q9UJU6-3	12	41	31.7	439	49042	5	Isoform 3 of Q9UJU6
521	P09622	12	49	31.8	509	54150	7.7	Dihydrolipoyl dehydrogenase, mitochondrial precursor
521	Q8WTS4	12	49	31.8	509	54177	7.9	Dihydrolipoamide dehydrogenase
521	Q59EV8	12	49	31.2	520	55594	8.5	Dihydrolipoamide dehydrogenase, variant
522	P43490	12	29	31.6	491	55521	7.2	Nicotinamide phosphoribosyltransferase
523	P48735	12	23	31.4	452	50909	8.7	Isocitrate dehydrogenase [NADP], mitochondrial precursor (EC 1.1.1.42) (Oxalosuccinate decarboxylase) (IDH) (NADP(+)-specific ICDH)
523	Q53GL5	12	23	31.4	452	50910	8.5	Isocitrate dehydrogenase 2 (NADP+), mitochondrial variant
524	P22570	12	17	30.3	491	53837	8.4	NADPH:adrenodoxin oxidoreductase, mitochondrial precursor (EC 1.18.1.2) (Adrenodoxin reductase) (AR) (Ferredoxin reductase) (Ferredoxin--NADP(+) reductase)
524	P22570-2	12	17	30	497	54479	8.4	Isoform Long of P22570
525	O15371	12	41	29.4	548	63973	6	Eukaryotic translation initiation factor 3 subunit 7
526	Q9H4M9	12	28	29.4	534	60627	6.8	EH domain-containing protein 1
527	Q5JTV8	12	33	29.2	583	66248	8.2	Torsin-1A-interacting protein 1
528	P12081	12	24	27.7	509	57411	5.9	Histidyl-tRNA synthetase, cytoplasmic
529	P55084	12	29	27.6	474	51294	9.4	Trifunctional enzyme subunit beta, mitochondrial precursor (TP-beta) [Includes: 3-ketoacyl-CoA thiolase (EC 2.3.1.16) (Acetyl-CoA acyltransferase) (Beta-ketothiolase)]

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
529	Q5R1W7	12	29	27.6	475	51396	9.4	Trifunctional enzyme subunit beta, mitochondrial precursor (TP-beta) [Includes: 3-ketoacyl-CoA thiolase (EC 2.3.1.16) (Acetyl-CoA acyltransferase) (Beta-ketothiolase)]
530	Q02818	12	32	27.3	461	53879	5.2	Nucleobindin-1 precursor
530	Q53GX6	12	32	27.3	461	53907	5.2	Nucleobindin 1 variant
531	Q5T0M6	12	35	26.4	466	50316	6.6	Annexin A7
531	Q53HM8	12	35	26.4	466	50228	7.2	Annexin VII isoform 1 variant
531	P20073	12	35	25.2	488	52739	5.7	Annexin A7
531	Q5T0M7	12	35	25.2	488	52739	5.7	Annexin A7
532	Q96GF2	12	31	25.1	633	68448	5.3	GSPT1 protein
533	Q96S43	12	69	42.2	244	27191	8.6	JKTBP1delta6
533	Q7KZ75	12	69	34.2	301	33589	7.3	HnRNP JKTBP protein
533	O14979	12	69	24.5	420	46437	9.6	Heterogeneous nuclear ribonucleoprotein D-like
534	Q9Y6M1	12	33	26.1	556	61843	8.3	Insulin-like growth factor 2 mRNA-binding protein 2
534	A0A4Z0	12	33	24.2	598	65990	8.5	Insulin-like growth factor 2 mRNA binding protein 2
535	P17812	12	26	24	591	66690	6.5	CTP synthase 1
536	P51659	12	28	23.4	736	79686	8.8	Peroxisomal multifunctional enzyme type 2
537	Q15042	12	27	17.8	981	110524	5.6	Rab3 GTPase-activating protein catalytic subunit
538	Q32P28	12	51	17.7	736	83394	5.1	Prolyl 3-hydroxylase 1 precursor
539	O60763	12	32	16.9	962	107895	4.9	General vesicular transport factor p115
539	UPI00001382BE	12	32	16.9	962	107907	4.9	vesicle docking protein p115
539	Q86TB8	12	32	16.8	973	109187	4.9	Hypothetical protein DKFZp451D234
540	Q9BPX3	12	24	13.9	1015	114334	5.6	Condensin complex subunit 3
541	UPI000013F0BE	12	25	13.3	1102	128302	5.6	Ubiquitin carboxyl-terminal hydrolase 7 (EC 3.1.2.15) (Ubiquitin thioesterase 7) (Ubiquitin-specific-processing protease 7) (Deubiquitinating enzyme 7) (Herpesvirus-associated ubiquitin-specific protease).
541	Q93009	12	25	13.3	1102	128272	5.6	Ubiquitin carboxyl-terminal hydrolase 7
541	Q6U8A4	12	25	13.2	1112	129004	5.8	Ubiquitin-specific protease 7 isoform
542	Q7Z460-2	12	23	10	1471	162110	8.8	Isoform 2 of Q7Z460
542	A2RU21	12	23	9.9	1479	162914	8.8	CLASP1 protein
542	Q7Z460-3	12	23	9.8	1494	164565	8.5	Isoform 3 of Q7Z460
542	Q7Z460	12	23	9.6	1538	169450	9	CLIP-associating protein 1
543	Q53SJ7	12	24	9.9	1337	155520	6	Hypothetical protein ROCK2
543	O75116	12	24	9.6	1388	160912	6	Rho-associated protein kinase 2
543	UPI000049DEE3	12	24	9.6	1388	160981	6.2	Rho-associated protein kinase 2 (EC 2.7.11.1) (Rho-associated, coiled- coil-containing protein kinase 2) (p164 ROCK-2) (Rho kinase 2).
543	UPI000034ECB0	12	24	9.6	1388	160899	6	Rho-associated, coiled-coil containing protein kinase 2
544	P51532	12	25	8.3	1647	184644	7.9	Probable global transcription activator SNF2L4
544	Q9HBD4	12	25	8.2	1679	188147	8.2	SMARCA4 isoform 2
545	UPI0000E265EC	12	48	4.9	2817	308606	9.1	HBxAg transactivated protein 2
546	Q7Z6Z7	12	33	3.6	4374	481896	5.2	E3 ubiquitin-protein ligase HUWE1
546	UPI0000D626C3	12	33	3.6	4374	481985	5.2	HECT, UBA and WWE domain-containing protein 1 (EC 6.3.2.-) (E3 ubiquitin protein ligase URE-B1) (Mcl-1 ubiquitin ligase E3) (Mule) (ARF-binding protein 1) (ARF-BP1).
546	Q7Z6Z7-3	12	33	3.6	4365	481023	5.2	Isoform 3 of Q7Z6Z7
546	Q7Z6Z7-2	12	33	3.6	4358	480203	5.2	Isoform 2 of Q7Z6Z7
547	O75947	11	29	73.9	161	18491	5.3	ATP synthase D chain, mitochondrial
548	P15531	11	120	69.7	152	17149	6.2	Nucleoside diphosphate kinase A
549	P04792	11	119	67.8	205	22783	6.4	Heat-shock protein beta-1
550	P09211	11	157	66.2	210	23356	5.6	Glutathione S-transferase P
551	P37235	11	44	61.1	193	22313	5.4	Hippocalcin-like protein 1
552	P27348	11	131	60	245	27764	4.8	14-3-3 protein theta
553	Q13938	11	40	58.2	189	20967	4.9	Calcyphosin
554	Q2TNB3	11	54	56.5	239	27349	5.6	Cell migration-inducing protein 22
554	Q9UL46	11	54	56.5	239	27362	5.6	Proteasome activator complex subunit 2
554	Q86SZ7	11	54	56.5	239	27402	5.7	Full-length cDNA clone CS0DJ015YJ12 of T cells (Jurkat cell line) of Homo sapiens
555	Q15907	11	71	56.4	218	24488	5.9	Ras-related protein Rab-11B
555	Q6FHR0	11	71	56.4	218	24435	5.7	RAB11B protein
556	P29966	11	43	53.3	332	31555	4.4	Myristoylated alanine-rich C-kinase substrate
557	P30085	11	31	52.6	196	22222	5.6	UMP-CMP kinase
558	Q13126	11	32	52.3	283	31236	7.2	S-methyl-5-thioadenosine phosphorylase
559	Q15691	11	35	51.9	268	29999	5.1	Microtubule-associated protein RP/EB family member 1
560	P21266	11	32	51.1	225	26560	5.5	Glutathione S-transferase Mu 3
561	Q9UKK9	11	23	50.2	219	24328	4.9	ADP-sugar pyrophosphatase
561	UPI000059D108	11	23	47.4	232	25895	5.2	ADP-sugar pyrophosphatase (EC 3.6.1.13) (EC 3.6.1.-) (Nucleoside diphosphate-linked moiety X motif 5) (Nudix motif 5) (YSA1H).
562	Q99685	11	22	49.5	303	33261	7	Monoglyceride lipase
562	UPI0000D61B71	11	22	47.9	313	34305	6.7	Monoglyceride lipase (EC 3.1.1.23) (MGL) (HU-K5) (Lysophospholipase homolog) (Lysophospholipase-like).

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563	UPI0000456C19	11	84	64.2	148	16102	6.6	Peroxiredoxin-2 (EC 1.11.1.15) (Thioredoxin peroxidase 1) (Thioredoxin-dependent peroxide reductase 1) (Thiol-specific antioxidant protein) (TSA) (PRP) (Natural killer cell-enhancing factor B) (NKEF-B).
563	P32119	11	84	48	198	21892	6	Peroxiredoxin-2
564	O14818	11	32	47.6	248	27887	8.5	Proteasome subunit alpha type 7
565	Q96HJ0	11	21	45.4	304	33831	5.6	V-crk sarcoma virus CT10 oncogene homolog
566	Q9BWM7	11	13	45.2	321	35503	9.1	Sideroflexin-3
566	UPI00004563F7	11	13	44.6	325	35979	9	Sideroflexin-3.
566	UPI000006EE3D	11	13	44.6	325	35979	9.1	sideroflexin 3
567	P50479	11	14	44.8	330	35398	7.9	PDZ and LIM domain protein 4
568	P60900	11	54	44.7	246	27399	6.7	Proteasome subunit alpha type 6
569	Q15717	11	35	44.5	326	36092	9.2	ELAV-like protein 1
570	Q12904	11	15	44.2	312	34353	8.4	Multisynthetase complex auxiliary component p43 [Contains: Endothelial monocyte-activating polypeptide 2 (EMAP-II) (Small inducible cytokine subfamily E member 1)]
571	P48739	11	26	43.9	271	31540	6.9	Phosphatidylinositol transfer protein beta isoform
571	P48739-2	11	26	43.8	272	31638	6.2	Isoform 2 of P48739
572	Q16831	11	23	43.2	310	33934	7.9	Uridine phosphorylase 1
573	P25786	11	46	42.6	263	29556	6.6	Proteasome subunit alpha type 1
573	Q53YE8	11	46	42.6	263	29598	6.6	Proteasome (Prosome, macropain) subunit, alpha type, 1
573	P25786-2	11	46	41.6	269	30239	7	Isoform Long of P25786
574	P07858	11	63	41.6	339	37822	6.3	Cathepsin B precursor (EC 3.4.22.1) (Cathepsin B1) (APP secretase) (APPS) [Contains: Cathepsin B light chain; Cathepsin B heavy chain]
575	Q9Y5K5-2	11	16	44.9	316	36079	5.2	Isoform 2 of Q9Y5K5
575	Q9Y5K5-3	11	16	43.3	328	37478	5.4	Isoform 3 of Q9Y5K5
575	Q9Y5K5	11	16	43.2	329	37607	5.3	Ubiquitin carboxyl-terminal hydrolase isozyme L5
575	Q5LJA5	11	16	40	355	40423	5.3	Ubiquitin carboxyl-terminal hydrolase L5
575	Q5LJA9	11	16	38.6	368	41695	5.5	Ubiquitin carboxyl-terminal hydrolase L5
576	Q02978	11	43	39.2	314	34062	9.9	Mitochondrial 2-oxoglutarate/malate carrier protein
577	P42765	11	16	39	397	41924	8.1	3-ketoacyl-CoA thiolase, mitochondrial
577	UPI0000136E5A	11	16	39	397	42039	8.3	acetyl-coenzyme A acyltransferase 2
578	Q9BWF3	11	25	39	364	40314	7.1	RNA-binding protein 4
579	P46777	11	95	38.4	297	34363	9.7	60S ribosomal protein L5
580	P16989	11	51	37.9	372	40090	9.8	DNA-binding protein A
580	UPI0000128F30	11	51	37.9	372	40060	9.8	cold shock domain protein A
581	Q9Y295	11	26	37.6	367	40542	8.9	Developmentally-regulated GTP-binding protein 1
582	Q15293	11	58	37.5	331	38890	5	Reticulocalbin-1 precursor
583	P78417	11	28	37.3	241	27566	6.6	Glutathione transferase omega-1
584	Q96DB5	11	36	35.7	314	35808	8.5	Protein FAM82B
584	UPI0000DD7F20	11	36	20.7	541	59651	9.4	PREDICTED: similar to Protein FAM82B
585	Q9NYB0	11	13	35.1	399	44260	4.7	Telomeric repeat-binding factor 2-interacting protein 1
586	Q5D0C4	11	56	35	397	44000	9.4	SERPINE2 protein
587	P30520	11	20	34.2	456	50097	6.6	Adenylosuccinate synthetase isozyme 2
588	UPI0000D6135C	11	56	40.6	207	23652	4.4	Acidic leucine-rich nuclear phosphoprotein 32 family member A (Potent heat-stable protein phosphatase 2A inhibitor I1PP2A) (Acidic nuclear phosphoprotein pp32) (Leucine-rich acidic nuclear protein) (Lanp) (Putative HLA-DR-associated protein I) (PHAPI) (Ma
588	Q6PKH8	11	56	40.2	209	24068	4.8	ANP32A protein
588	Q08AJ6	11	56	35.3	238	27298	4.1	ANP32A protein
588	UPI000049DDE6	11	56	34	247	28325	4.1	Acidic leucine-rich nuclear phosphoprotein 32 family member A (Potent heat-stable protein phosphatase 2A inhibitor I1PP2A) (Acidic nuclear phosphoprotein pp32) (Leucine-rich acidic nuclear protein) (Lanp) (Putative HLA-DR-associated protein I) (PHAPI) (Ma
588	P39687	11	56	33.7	249	28585	4.1	Acidic leucine-rich nuclear phosphoprotein 32 family member A
588	Q53FK4	11	56	33.7	249	28557	4.1	Acidic (Leucine-rich) nuclear phosphoprotein 32 family, member A variant
589	P11766	11	21	33.2	374	39724	7.5	Alcohol dehydrogenase class 3 (EC 1.1.1.1) (Alcohol dehydrogenase class III) (Alcohol dehydrogenase class chi chain) (S- (hydroxymethyl)glutathione dehydrogenase)
589	UPI0000D6159C	11	21	33.2	373	39617	7.7	Alcohol dehydrogenase class 3 chi chain (EC 1.1.1.1) (Alcohol dehydrogenase class III chi chain) (S-(hydroxymethyl)glutathione dehydrogenase) (EC 1.1.1.284) (Glutathione-dependent formaldehyde dehydrogenase) (FDH).
589	Q6FI45	11	21	33.2	374	39690	7.5	ADH5 protein
590	P23193	11	20	33.2	301	33970	8.4	Transcription elongation factor A protein 1

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591	P13995	11	15	33.1	350	37895	8.7	Bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase, mitochondrial precursor [Includes: NAD-dependent methylenetetrahydrofolate dehydrogenase (EC 1.5.1.15); Methenyltetrahydrofolate cyclohydrolase (EC 3.5.4.9)]
592	P08559	11	27	32.8	390	43296	8.1	Pyruvate dehydrogenase E1 component alpha subunit, somatic form, mitochondrial precursor
593	O75367	11	28	32.5	372	39617	9.8	Core histone macro-H2A.1
594	O00505	11	21	31.9	521	57811	4.9	Importin alpha-3 subunit
594	Q8IYQ9	11	21	31.9	521	57901	4.9	Karyopherin alpha 3
595	A0PJ61	11	36	30.5	440	49490	10.1	Hypothetical protein
595	Q32Q62	11	36	28.9	464	52165	10.2	RSL1D1 protein
595	O76021	11	36	27.3	490	54973	10.1	Ribosomal L1 domain-containing protein 1
596	Q5T9Q6	11	19	30.4	441	48040	7.1	Succinate-CoA ligase, ADP-forming, beta subunit
596	Q9P2R7	11	19	28.9	463	50317	7.4	Succinyl-CoA ligase [ADP-forming] beta-chain, mitochondrial precursor
597	UPI0000163C03	11	33	30.7	472	53216	8.7	DEAD (Asp-Glu-Ala-Asp) box polypeptide 6
597	P26196	11	33	30	483	54417	8.7	Probable ATP-dependent RNA helicase DDX6
598	Q53GR7	11	19	29.6	675	74116	8.4	Solute carrier family 25, member 13 (Citrin) variant
598	Q9UJS0	11	19	29.6	675	74176	8.6	Calcium-binding mitochondrial carrier protein Aralar2
598	Q546F9	11	19	29.6	676	74304	8.6	Mitochondrial aspartate-glutamate carrier protein
599	Q5HYG8	11	31	30.4	483	53465	8.2	Hypothetical protein DKFZp686P09201
599	P34897	11	31	29.2	504	55993	8.5	Serine hydroxymethyltransferase, mitochondrial precursor
599	Q53ET4	11	31	29.2	504	55974	8.4	Serine hydroxymethyltransferase 2 (Mitochondrial) variant
600	O43175	11	18	27.8	533	56651	6.7	D-3-phosphoglycerate dehydrogenase
601	P52292	11	30	27.4	529	57862	5.4	Importin alpha-2 subunit
601	Q7Z726	11	30	27.4	529	57876	5.4	Karyopherin alpha 2
601	Q6NVW7	11	30	27.4	529	57965	5.4	Karyopherin alpha 2
601	Q53YE3	11	30	27.4	529	57876	5.3	Karyopherin alpha 2
602	Q9Y6E2	11	29	27	419	48162	6.7	Basic leucine zipper and W2 domain-containing protein 2
603	Q8IWE2	11	17	26.1	563	60825	4.7	Protein NOXP20
603	UPI00001DFE17	11	17	26.1	563	60742	4.7	family with sequence similarity 114, member A1 (FAM114A1), mRNA
604	P05362	11	88	25.9	532	57825	8	Intercellular adhesion molecule 1 precursor
605	O43776	11	31	25.4	548	62943	6.3	Asparaginyl-tRNA synthetase, cytoplasmic
606	O95747	11	24	25	527	58022	6.4	Serine/threonine-protein kinase OSR1
607	P35052	11	53	24.9	558	61650	7.3	Glypican-1 precursor
607	Q53QM4	11	53	24.9	558	61680	7.3	Hypothetical protein GPC1
608	Q9H9A6	11	13	24.8	602	68250	6.4	Leucine-rich repeat-containing protein 40
609	Q08170	11	51	24.1	494	56678	11.5	Splicing factor, arginine/serine-rich 4
610	Q7Z4X1	11	28	25.2	612	68354	5.3	Cytoplasmic dynein intermediate chain 2C
610	Q5BJF8	11	28	25.2	612	68426	5.3	DYNC1I2 protein
610	Q32LY9	11	28	25.2	612	68412	5.3	DYNC1I2 protein
610	Q13409-6	11	28	25.2	611	68298	5.3	Isoform 2F of Q13409
610	Q13409-2	11	28	24.4	632	70645	5.2	Isoform 2B of Q13409
610	Q13409-5	11	28	24.2	637	71328	5.2	Isoform 2E of Q13409
610	Q13409	11	28	24.1	638	71457	5.2	Cytoplasmic dynein 1 intermediate chain 2
610	UPI0000456EA1	11	28	24	641	71709	5.2	Cytoplasmic dynein 1 intermediate chain 2 (Dynein intermediate chain 2, cytosolic) (DH IC-2) (Cytoplasmic dynein intermediate chain 2).
611	O75390	11	23	23.8	466	51712	8.3	Citrate synthase, mitochondrial precursor
612	Q5SSJ5	11	26	23.5	553	61207	9.7	Heterochromatin protein 1, binding protein 3
612	UPI0000D61E73	11	26	23.4	555	61434	9.7	HP1-BP74
613	O75131	11	20	22.9	537	60131	5.8	Copine-3
614	Q13217	11	21	22.6	504	57580	6.2	DnaJ homolog subfamily C member 3
615	P17858	11	19	22.2	780	85018	7.5	6-phosphofructokinase, liver type
616	Q9BR63	11	52	19.5	585	65701	6.8	FARSB protein
616	UPI00002096AC	11	52	19.4	589	66116	6.8	phenylalanyl-tRNA synthetase, beta subunit
616	Q9NSD9	11	52	19.4	589	66130	6.8	Phenylalanyl-tRNA synthetase beta chain
617	UPI00005A4215	11	17	21.5	694	75927	6.6	PREDICTED: similar to catenin (cadherin-associated protein), beta 1, 88kDa
617	UPI00006C0700	11	17	21.2	702	77207	6.6	PREDICTED: similar to Beta-catenin
617	UPI0000DD7B92	11	17	19.3	774	84766	5.9	PREDICTED: similar to catenin (cadherin-associated protein), beta 1, 88kDa
617	P35222	11	17	19.1	781	85497	5.9	Catenin beta-1
618	P16435	11	16	18.2	677	76690	5.6	NADPH--cytochrome P450 reductase
619	P22307	11	35	17.9	547	58994	6.9	Nonspecific lipid-transfer protein
620	UPI0000131B9E	11	12	18.4	738	80827	6.1	phospholipase A2-activating protein isoform 2
620	Q9Y263	11	12	17.1	795	87157	6.4	Phospholipase A-2-activating protein
621	O94874	11	15	16.6	794	89595	6.8	Uncharacterized protein KIAA0776
621	UPI0000D6149C	11	15	16.6	797	89951	6.9	KIAA0776 (KIAA0776), mRNA
622	Q6IMN7	11	63	16	694	76862	5.1	Cytoplasmic activation/proliferation-associated protein 1
622	Q9BV09	11	63	15.7	709	78366	5.2	GPI-anchored membrane protein 1

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
622	UPI0000366799	11	63	15.6	712	78612	5.2	GPI-anchored membrane protein 1 (GPI-anchored protein p137) (p137GPI) (Membrane component chromosome 11 surface marker 1).
623	P21399	11	16	15.7	889	98399	6.7	Iron-responsive element-binding protein 1
624	Q13619	11	23	15.4	759	87680	8.1	Cullin-4A
625	A4D229	11	36	15.1	893	98902	8.7	KIAA1228 protein
626	A4D1S4	11	18	14	902	101431	8.4	Zinc finger CCCH type, antiviral 1
626	UPI0000457619	11	18	14	902	101444	8.3	Zinc finger CCCH type antiviral protein 1 (Zinc finger CCCH domain- containing protein 2).
626	Q7Z2W4	11	18	14	902	101444	8.3	Zinc finger CCCH type antiviral protein 1
627	P35442	11	23	13	1172	129955	4.8	Thrombospondin-2 precursor
627	Q5RI52	11	23	13	1172	129991	4.8	Thrombospondin 2
628	A0AVT1	11	22	12.7	1052	117970	6.1	Ubiquitin-activating enzyme E1-like protein 2
628	UPI00001910DA	11	22	12.7	1052	117955	6.2	ubiquitin-activating enzyme E1-like 2
629	O94855	11	20	12.5	1032	113000	7.2	Protein transport protein Sec24D
629	UPI00001AEA4F	11	20	12.5	1032	113010	7.2	Protein transport protein Sec24D (SEC24-related protein D).
629	Q8IYI7	11	20	12.5	1033	113081	7.2	SEC24 related gene family, member D
630	Q5SQ43	11	18	12.3	1078	113910	5.9	HLA-B associated transcript 3
630	A3KQ42	11	18	11.8	1126	118693	5.6	HLA-B associated transcript 3
630	Q5HYL9	11	18	11.8	1126	118725	5.6	Hypothetical protein DKFZp686L0653
630	UPI0000161DCF	11	18	11.7	1132	119419	5.6	HLA-B associated transcript-3 isoform a
630	UPI000013C678	11	18	11.7	1140	120258	5.6	HLA-B associated transcript 3
630	P46379	11	18	11.7	1132	119409	5.6	Large proline-rich protein BAT3
630	Q5SQ39	11	18	11.4	1162	122342	5.7	HLA-B associated transcript 3
631	UPI0000D61C7B	11	16	11.6	1071	121188	5.4	Dihydropyridine-sensitive L-type calcium channel subunits alpha- 2/delta precursor [Contains: L-type calcium channel subunit alpha-2; L-type calcium channel subunit delta].
631	P54289	11	16	11.4	1091	123183	5.2	Dihydropyridine-sensitive L-type calcium channel subunits alpha- 2/delta precursor [Contains: L-type calcium channel subunit alpha-2; L-type calcium channel subunit delta]
631	Q17R45	11	16	11.4	1091	123183	5.2	Calcium channel, voltage-dependent, alpha 2/delta subunit 1
631	Q9UIU0	11	16	11.2	1110	125308	5.4	Dihydropyridine receptor alpha 2 subunit
632	Q9BXJ9	11	21	11.4	866	101272	7.4	NMDA receptor-regulated protein 1
633	A2RRC9	11	17	10.7	1631	184517	7.5	IQ motif containing GTPase activating protein 3
633	UPI0000231C93	11	17	10.7	1631	184598	7.6	IQ motif containing GTPase activating protein 3
633	UPI000021D298	11	17	10.7	1633	184856	7.6	Ras GTPase-activating-like protein IQGAP3.
633	Q86VI3	11	17	10.7	1631	184545	7.5	Ras GTPase-activating-like protein IQGAP3
633	Q5T3H8	11	17	10.7	1631	184698	7.6	IQ motif containing GTPase activating protein 3
634	O95239	11	16	10.2	1232	139881	6.3	Chromosome-associated kinesin KIF4A
635	Q29RF7	11	25	9.7	1337	150830	7.9	SCC-112 protein
636	P78357	11	17	9.3	1384	156266	7.1	Contactin-associated protein 1 precursor
636	UPI0000D62337	11	17	9.3	1384	156280	7.1	Contactin-associated protein 1 precursor (Caspr) (Caspr1) (Neurexin 4) (Neurexin IV) (p190).
637	Q13523	11	18	9	1007	116973	10.3	Serine/threonine-protein kinase PRP4 homolog
637	Q8IVC3	11	18	9	1007	116991	10.3	PRP4 pre-mRNA processing factor 4 homolog B
637	Q5TAY8	11	18	9	1007	116987	10.3	PRP4 pre-mRNA processing factor 4 homolog B
638	P30086	10	25	74.9	187	21057	7.5	Phosphatidylethanolamine-binding protein 1 (PEBP-1) (Prostatic-binding protein) (HCNPpp) (Neuropolypeptide h3) (Raf kinase inhibitor protein) (RKIP) [Contains: Hippocampal cholinergic neurostimulating peptide (HCNP)]
639	UPI00005E7FE3	10	69	68.9	167	19488	8.4	Tubulin--tyrosine ligase-like protein 3 (HOTTL).
639	P59998	10	69	68.5	168	19667	8.4	Actin-related protein 2/3 complex subunit 4
640	P28066	10	53	66	241	26411	4.8	Proteasome subunit alpha type 5
641	P60660	10	83	62.9	151	16930	4.7	Myosin light polypeptide 6
641	Q561V9	10	83	62.9	151	16961	4.6	Myosin, light chain 6, alkali, smooth muscle and non-muscle
641	UPI0000D62206	10	83	60.9	156	17353	4.7	Myosin light polypeptide 6 (Smooth muscle and nonmuscle myosin light chain alkali 6) (Myosin light chain alkali 3) (Myosin light chain 3) (MLC-3) (LC17).
642	P32969	10	90	62	192	21863	10	60S ribosomal protein L9
643	Q04917	10	53	60.2	246	28219	4.8	14-3-3 protein eta
644	A2VCL0	10	646	57.8	102	11377	11.4	HIST2H4B protein
644	P62805	10	646	57.3	103	11367	11.4	Histone H4
645	P07203	10	45	56.2	201	21899	6.5	Glutathione peroxidase 1
645	UPI00001B07C3	10	45	55.7	203	21938	6.5	glutathione peroxidase 1 isoform 1
646	P62249	10	110	55.5	146	16445	10.2	40S ribosomal protein S16
647	P61026	10	72	54	200	22541	8.4	Ras-related protein Rab-10
647	UPI0000072ACD	10	72	54	200	22469	8.6	ras-related GTP-binding protein RAB10
648	P28074	10	28	53.8	208	22897	8.5	Proteasome subunit beta type 5 precursor
648	Q7Z3B5	10	28	42.1	266	28810	6.5	Hypothetical protein DKFZp686I0180
649	P62269	10	140	52.6	152	17719	11	40S ribosomal protein S18
650	Q15126	10	24	52.6	192	21995	5.7	Phosphomevalonate kinase
651	O75347	10	42	51.9	108	12855	5.3	Tubulin-specific chaperone A
652	Q9H9B4	10	14	51.6	322	35619	9.1	Sideroflexin-1

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
653	O43399	10	38	51.5	206	22238	5.4	Tumor protein D54
653	UPI0000D610E3	10	38	48.4	219	23739	6.2	Tumor protein D54 (hD54) (Tumor protein D52-like 2).
653	Q5U0E0	10	38	48.2	220	23787	5.7	Tumor protein D52-like 2
653	Q5JWU6	10	38	46.3	229	24854	6.4	Tumor protein D52-like 2
654	P47755	10	58	49.3	286	32949	5.8	F-actin capping protein subunit alpha-2
654	Q53GC7	10	58	49.3	286	32967	5.8	Capping protein (Actin filament) muscle Z-line, alpha 2 variant
655	P19623	10	16	49	302	33825	5.5	Spermidine synthase
656	P00491	10	30	47.4	289	32118	6.9	Purine nucleoside phosphorylase
657	O95571	10	18	47.2	254	27873	6.8	ETHE1 protein, mitochondrial precursor
658	Q99598	10	14	47.2	290	33112	6.6	Translin-associated protein X
659	Q96AG4	10	92	45.9	307	34930	9.6	Leucine-rich repeat-containing protein 59
660	UPI0000129B77	10	47	45.9	290	31371	8.1	mitochondrial short-chain enoyl-coenzyme A hydratase 1 precursor
661	Q04760	10	40	44	184	20778	5.3	Lactoylglutathione lyase
662	O60664	10	34	43.8	434	47047	5.4	Mannose-6-phosphate receptor-binding protein 1
663	Q14257	10	22	43.8	317	36876	4.4	Reticulocalbin-2 precursor
664	P62873	10	61	43.2	340	37377	6	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1
665	Q15417	10	52	42.6	329	36414	6.1	Calponin-3
666	Q92820	10	45	41.8	318	35964	7.1	Gamma-glutamyl hydrolase precursor
667	P53004	10	34	41.6	296	33428	6.4	Biliverdin reductase A precursor
668	P11177-2	10	24	43.4	341	37200	5.9	Isoform 2 of P11177
668	P11177	10	24	41.2	359	39233	6.6	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial precursor
668	UPI0000161B07	10	24	41.2	359	39249	6.6	pyruvate dehydrogenase (lipoamide) beta
669	P36543	10	32	41.2	226	26145	8	Vacuolar ATP synthase subunit E 1
670	Q16698	10	32	41.2	335	36068	9.3	2,4-dienoyl-CoA reductase, mitochondrial precursor
671	P15121	10	29	39.9	316	35853	7	Aldose reductase
672	P62826	10	78	39.8	216	24423	7.5	GTP-binding nuclear protein Ran
673	P55036	10	20	39.3	377	40737	4.8	26S proteasome non-ATPase regulatory subunit 4
674	P35249	10	11	38.8	363	39682	8	Replication factor C subunit 4
675	Q53HL6	10	31	37.2	374	42471	5.6	Dendritic cell protein variant
675	Q7L2H7	10	31	37.2	374	42503	5.6	PCI domain containing 1
676	Q15785	10	34	36.9	309	34559	9	Mitochondrial import receptor subunit TOM34
677	Q5BKY2	10	37	36.1	349	39610	6.4	Hypothetical protein
677	O15372	10	37	35.8	352	39930	6.5	Eukaryotic translation initiation factor 3 subunit 3
677	Q53HR0	10	37	35.8	352	39914	6.5	Eukaryotic translation initiation factor 3, subunit 3 gamma, 40kDa variant
677	Q53HG0	10	37	35.8	352	39870	6.5	Eukaryotic translation initiation factor 3, subunit 3 gamma, 40kDa variant
678	P61163	10	27	35.6	376	42614	6.6	Alpha-centractin
679	P09110	10	19	35.4	424	44292	8.4	3-ketoacyl-CoA thiolase, peroxisomal precursor
680	P25685	10	20	35.3	340	38044	8.6	DnaJ homolog subfamily B member 1
680	Q6FI51	10	20	35.3	340	38010	8.6	DNAJB1 protein
681	Q9UKM9	10	56	34.6	306	32463	9.2	RNA-binding protein Raly
681	Q53GL6	10	56	34.5	307	32550	9.2	RNA binding protein (Autoantigenic, hnRNP-associated with lethal yellow) long isoform variant (RNA binding protein, autoantigenic) (HnRNP-associated with lethal yellow homolog (Mouse))
682	Q96I99	10	19	34.3	432	46511	6.4	Succinyl-CoA ligase [GDP-forming] beta-chain, mitochondrial precursor
683	O00303	10	45	34.2	357	37564	5.4	Eukaryotic translation initiation factor 3 subunit 5
684	P62191	10	53	31.4	440	49185	6.2	26S protease regulatory subunit 4
684	Q53HB3	10	53	31.4	440	49213	6.2	Proteasome 26S ATPase subunit 1 variant
685	Q9BS26	10	23	31.3	406	46971	5.3	Thioredoxin domain-containing protein 4 precursor
686	Q8NFW8	10	20	31.1	434	48379	7.9	N-acylneuraminate cytidylyltransferase
687	P51572	10	289	30.9	246	27992	8.4	B-cell receptor-associated protein 31
687	Q53HT6	10	289	30.9	246	27962	8.4	B-cell receptor-associated protein 31 variant
687	Q53G72	10	289	30.9	246	27931	8.4	B-cell receptor-associated protein 31 variant
688	Q9BRK5	10	21	30.7	362	41807	4.9	45 kDa calcium-binding protein precursor
689	Q13148	10	34	29.5	414	44740	6.2	TAR DNA-binding protein 43
690	P49257	10	77	28.6	510	57549	6.8	ERGIC-53 protein precursor
690	Q53FS4	10	77	28.6	510	57558	6.8	Lectin, mannose-binding, 1 variant
691	P15311	10	47	28.3	586	69413	6.3	Ezrin
691	Q6NUR7	10	47	28.3	586	69242	6.3	Villin 2
691	UPI0000D61508	10	47	28.2	589	69688	6.3	Ezrin (p81) (Cytovillin) (Villin-2).
692	P21283	10	22	27.2	382	43942	7.5	Vacuolar ATP synthase subunit C
693	P30533	10	15	26.3	357	41466	8.8	Alpha-2-macroglobulin receptor-associated protein precursor
694	P54727	10	34	25.9	409	43171	4.8	UV excision repair protein RAD23 homolog B
695	UPI000013EA6E	10	25	25.9	621	69721	6.2	fragile X mental retardation-related protein 1 isoform a
696	Q6FIA3	10	19	25.8	445	51353	5.4	PACSIN2 protein
696	Q9UNF0	10	19	23.7	486	55739	5.2	Protein kinase C and casein kinase substrate in neurons protein 2
697	Q9NPQ8-2	10	17	25.6	524	58846	6.6	Isoform 2 of Q9NPQ8
697	Q9NPQ8	10	17	25.3	530	59612	5.3	Synembryn-A

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697	UPI0000037C19	10	17	25	537	60372	5.3	resistance to inhibitors of cholinesterase 8 homolog A
697	Q9NPQ8-3	10	17	25	536	60275	5.3	Isoform 3 of Q9NPQ8
698	P50995	10	23	25.1	505	54390	7.7	Annexin A11
699	O00425	10	25	25	579	63720	8.9	Insulin-like growth factor 2 mRNA-binding protein 3
699	UPI0000117172	10	25	25	579	63705	8.9	insulin-like growth factor 2 mRNA binding protein 3
700	Q96EW9	10	14	24.1	585	64989	9	Eukaryotic translation initiation factor 2A, 65kDa
700	UPI00000473DB	10	14	24.1	585	64990	8.9	eukaryotic translation initiation factor 2A
700	Q96K81	10	14	24.1	585	64986	8.9	CDNA FLJ14450 fis, clone HEMBB1001736, weakly similar to EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 9
700	UPI000045718C	10	14	23.2	608	67707	8.9	eukaryotic translation initiation factor 2A
700	Q9BY44	10	14	23.2	609	67851	9	Eukaryotic translation initiation factor 2A 65 kDa
701	O94808	10	28	23.8	682	76931	7.4	Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] 2
701	UPI000049E025	10	28	23.7	684	77190	7.5	Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] 2 (EC 2.6.1.16) (Hexosephosphate aminotransferase 2) (D-fructose-6- phosphate amidotransferase 2) (GFAT 2) (GFAT2).
702	O95817	10	14	23.8	575	61595	7	BAG family molecular chaperone regulator 3
703	O95302	10	27	23.5	570	63084	5.1	FK506-binding protein 9 precursor
704	P13674	10	19	23.4	534	61049	6	Prolyl 4-hydroxylase subunit alpha-1 precursor
704	Q5VSQ6	10	19	23.4	534	60967	6	Procollagen-proline, 2-oxoglutarate 4-dioxygenase (Proline 4- hydroxylase), alpha polypeptide I (Procollagen-proline, 2-oxoglutarate 4-dioxygenase (Proline 4-hydroxylase), alpha polypeptide I variant)
705	Q8WZA9	10	17	21.3	623	62717	4.9	Immunity-related GTPase family Q protein
706	P06865	10	22	21.2	529	60689	5.2	Beta-hexosaminidase alpha chain precursor
706	Q6AI32	10	22	21.2	529	60719	5.1	Hypothetical protein DKFZp781C13106
707	Q9Y3I0	10	32	21.2	505	55210	7.2	UPF0027 protein C22orf28
708	Q6NZY4	10	12	20.5	707	78577	4.9	Zinc finger CCHC domain-containing protein 8
709	P31040	10	26	20.2	664	72692	7.4	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial precursor
710	Q96HC4	10	15	20	596	63972	8.2	PDZ and LIM domain protein 5
710	UPI00004C9B11	10	15	20	596	64002	8.2	PDZ and LIM domain 5 isoform a
711	Q12996	10	21	19.2	717	82922	8.1	Cleavage stimulation factor 77 kDa subunit
712	Q14694	10	20	18.8	798	87134	5.3	Ubiquitin carboxyl-terminal hydrolase 10
713	UPI00001619DB	10	18	20.8	499	53481	4.8	RAN binding protein 3 isoform RANBP3-b
713	Q9H6Z4-3	10	18	20.8	499	53411	4.8	Isoform 3 of Q9H6Z4
713	UPI00001AE593	10	18	18.6	560	59465	4.8	Ran-binding protein 3 (RanBP3).
713	Q9H6Z4-2	10	18	18.5	562	59694	4.8	Isoform 2 of Q9H6Z4
713	Q9H6Z4	10	18	18.3	567	60210	4.8	Ran-binding protein 3
714	Q9NVP1	10	21	18.2	670	75407	9.5	ATP-dependent RNA helicase DDX18
715	Q9Y2J2-2	10	17	18.2	865	96514	5.4	Isoform B of Q9Y2J2
716	Q10471	10	77	18	571	64733	8.4	Polypeptide N-acetylgalactosaminyltransferase 2 (EC 2.4.1.41) (Protein-UDP acetylgalactosaminyltransferase 2) (UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase 2) (Polypeptide GalNAc transferase 2) (GalNAc-T2) (pp-GaNTase 2) [Contains: Polypeptide N-acetylgalactosaminyltransferase 2 soluble form]
717	Q08945	10	25	17.9	709	81075	6.9	FACT complex subunit SSRP1
718	P42224	10	28	17.3	750	87335	6.1	Signal transducer and activator of transcription 1-alpha/beta
718	Q68D00	10	28	17.3	750	87363	6.1	Hypothetical protein DKFZp686B04100
719	P18084	10	30	16.8	799	88054	6.1	Integrin beta-5 precursor
719	UPI0000DD7BBB	10	30	14	958	104706	7.3	PREDICTED: similar to Integrin beta-5 precursor
720	Q9Y5L0-4	10	27	16.5	909	102541	5.6	Isoform 4 of Q9Y5L0
720	A4D1K9	10	27	16.3	923	104203	5.6	Transportin 3
721	Q8N1F7	10	26	16.2	819	93488	5.7	Nuclear pore complex protein Nup93
721	UPI0000070C22	10	26	16.2	819	93557	5.8	nucleoporin 93kDa
722	Q96RP9	10	15	16	751	83472	7	Elongation factor G 1, mitochondrial precursor
722	UPI0000D61B9E	10	15	15.9	753	83632	7	Elongation factor G 1, mitochondrial precursor (mEF-G 1) (Elongation factor G1).
723	P51812	10	10	15.7	740	83736	6.9	Ribosomal protein S6 kinase alpha-3
724	P46087	10	31	15.6	812	89302	9.2	Putative RNA methyltransferase NOL1
724	UPI0000D62194	10	31	15	846	92974	9.2	Proliferating-cell nucleolar antigen p120 (Proliferation-associated nucleolar protein p120).
724	Q3KQS4	10	31	15	845	92860	9.2	NOL1 protein
725	Q14137	10	18	15	746	83630	6.2	Ribosome biogenesis protein BOP1
726	Q86YQ0	10	17	15	765	84721	8.1	HZGJ
727	UPI000015C445	10	16	15.7	875	98503	5.4	aminopeptidase puromycin sensitive
727	P55786	10	16	14.9	919	103276	5.7	Puromycin-sensitive aminopeptidase
728	P33991	10	23	14.6	863	96558	6.7	DNA replication licensing factor MCM4
729	Q9BUJ2-4	10	20	16.3	756	84794	8.8	Isoform 4 of Q9BUJ2
729	Q9BUJ2-2	10	20	15.3	804	90292	6.9	Isoform 2 of Q9BUJ2

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
729	Q9BUJ2	10	20	14.4	856	95739	6.9	Heterogeneous nuclear ribonucleoprotein U-like protein 1
730	P46977	10	117	14.2	705	80472	8.2	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A
730	Q8WUB4	10	117	14.2	705	80530	8.1	STT3, subunit of the oligosaccharyltransferase complex, homolog A
731	Q8NE71	10	30	13.6	845	95926	6.8	ATP-binding cassette sub-family F member 1
732	P42566	10	12	13.1	896	98656	4.6	Epidermal growth factor receptor substrate 15
733	Q2TBF3	10	11	13.1	900	97675	6.9	MTHFD1L protein
733	Q9UFU8	10	11	12.9	917	99439	6.9	Hypothetical protein DKFZp586G1517
733	Q6UB35	10	11	12.1	978	105790	8.1	C1-tetrahydrofolate synthase (EC 6.3.4.3) (EC 3.5.4.9) (EC 1.5.1.5) (Methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like)
734	Q59E90	10	27	12.7	1007	113305	7.2	Mannosidase, alpha, class 2B, member 1 variant
735	Q8N163	10	18	11.7	923	102902	5.2	Protein KIAA1967
735	UPI00001AEEB7	10	18	11.7	925	103030	5.2	p30 DBC protein
735	Q8N163-2	10	18	11.7	923	103143	5.4	Isoform 2 of Q8N163
736	Q5JRX3	10	14	10.6	1037	117455	7	Presequence protease, mitochondrial precursor
736	UPI00001F8A38	10	14	10.6	1037	117413	6.9	metalloprotease 1
736	UPI000013C859	10	14	10.6	1037	117410	7	Presequence protease, mitochondrial precursor (EC 3.4.24.-) (hPreP) (Pitrilysin metalloproteinase 1) (Metalloprotease 1) (hMP1).
736	Q5JRX3-2	10	14	10.6	1038	117554	7	Isoform 2 of Q5JRX3
737	Q9H2G2-2	10	21	10.3	1204	138995	5.1	Isoform 2 of Q9H2G2
737	Q9H2G2	10	21	10	1235	142695	5.1	STE20-like serine/threonine-protein kinase
738	Q8TAQ2-2	10	32	10.2	1130	124841	5.6	Isoform 2 of Q8TAQ2
738	Q59G16	10	32	9.9	1156	127377	5.5	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin c2 isoform b variant
738	Q59GV3	10	32	9.9	1164	128088	5.6	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin c2 isoform b variant
738	Q8TAQ2	10	32	9.5	1214	132879	5.7	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily C member 2
739	Q9H2M9	10	19	9.4	1393	155984	5.6	Rab3 GTPase-activating protein non-catalytic subunit
739	UPI00004562FB	10	19	9.4	1393	155941	5.6	Rab3 GTPase-activating protein non-catalytic subunit (Rab3 GTPase- activating protein 150 kDa subunit) (Rab3-GAP p150) (Rab3-GAP regulatory subunit) (RAB3-GAP150) (RGAP-iso).
740	Q7Z406	10	31	8.9	1995	228000	5.9	Myosin-14
740	UPI0000E59250	10	31	8.9	2003	228663	5.6	myosin, heavy chain 14 isoform 1
740	UPI0000E5924F	10	31	8.9	1995	227868	5.6	myosin, heavy chain 14 isoform 2
740	Q7Z406-2	10	31	8.8	2028	231214	5.6	Isoform 2 of Q7Z406
741	Q9UKV3	10	20	8.8	1341	151887	6.4	Apoptotic chromatin condensation inducer in the nucleus
741	UPI000013D308	10	20	8.8	1341	151861	6.4	Apoptotic chromatin condensation inducer in the nucleus (Acinus).
742	O75694	10	28	8.7	1391	155199	6.2	Nuclear pore complex protein Nup155
743	Q9NQW6	10	22	8.6	1124	124199	8.1	Actin-binding protein anillin
744	Q5SW79	10	17	8.3	1584	175292	7.1	Centrosomal protein of 170 kDa
744	UPI000045632C	10	17	8.3	1585	175435	7.2	centrosomal protein 170kDa isoform gamma
745	A0JLU0	10	19	7.5	1414	144138	8.5	Hypothetical protein
745	UPI0000D61693	10	19	7.5	1412	144411	9	Treacher Collins-Franceschetti syndrome 1 isoform b
745	UPI000045736E	10	19	7.5	1411	144314	9	Treacher Collins-Franceschetti syndrome 1 isoform b
745	Q13428-2	10	19	7.5	1412	144411	9	Isoform 2 of Q13428
745	UPI0000D61694	10	19	7.3	1451	148350	8.9	Treacher Collins-Franceschetti syndrome 1 isoform b
745	UPI00004B247E	10	19	7.3	1450	148253	8.9	Treacher Collins-Franceschetti syndrome 1 isoform a
745	Q13428-3	10	19	7.1	1489	152203	9	Isoform 3 of Q13428
745	Q13428	10	19	7.1	1488	152103	9	Treacle protein
745	Q13428-4	10	19	7	1524	155926	8.9	Isoform 4 of Q13428
746	Q8WZ42	10	13	0.3	34350	3816081	6.3	Titin
746	UPI0000DACAD1	10	13	0.3	33423	3713573	6.5	titin isoform N2-A
746	Q8WZ42-8	10	13	0.3	34474	3829767	6.4	Isoform 8 of Q8WZ42
746	Q8WZ42-7	10	13	0.3	33615	3734713	6.5	Isoform 7 of Q8WZ42
746	Q8WZ42-5	10	13	0.3	32900	3653161	6.4	Isoform 5 of Q8WZ42
746	Q8WZ42-4	10	13	0.3	33445	3716096	6.5	Isoform 4 of Q8WZ42
746	Q8WZ42-2	10	13	0.3	34258	3805759	6.3	Isoform 2 of Q8WZ42
747	Q8NBT2	9	28	66.5	197	22443	4.7	Kinetochore protein Spc24
748	Q01469	9	33	65.2	135	15164	7	Fatty acid-binding protein, epidermal
749	P84085	9	71	63.3	180	20530	6.8	ADP-ribosylation factor 5
750	Q9BSD7	9	14	61.1	190	20713	9.5	Probable UPF0334 kinase-like protein C1orf57
751	Q9UNM1	9	133	61.9	97	10295	9	Chaperonin 10-related protein
751	P61604	9	133	58.8	102	10932	8.9	10 kDa heat shock protein, mitochondrial
752	P63208	9	18	58.3	163	18658	4.5	S-phase kinase-associated protein 1A
753	Q06830	9	67	56.8	199	22110	8.1	Peroxiredoxin-1
754	P25787	9	44	56.4	234	25899	7.4	Proteasome subunit alpha type 2

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
754	Q53GF5	9	44	56.4	234	25841	8	Proteasome alpha 2 subunit variant
755	P62081	9	83	56.2	194	22127	10.1	40S ribosomal protein S7
756	Q9Y2B0	9	33	56	182	20652	4.9	MIR-interacting saposin-like protein precursor
757	Q9GZZ1	9	14	55.6	169	19398	8.8	N-acetyltransferase 13
758	O95816	9	31	55.5	211	23772	6.7	BAG family molecular chaperone regulator 2
759	Q9P0J0	9	26	54.2	144	16698	8.4	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13
759	UPI0000163BED	9	26	34.4	227	25865	9.8	cell death-regulatory protein GRIM19
760	Q9BUF5	9	23	52.7	446	49857	4.9	Tubulin beta-6 chain
761	Q99653	9	32	52.3	195	22456	5.1	Calcium-binding protein p22
762	P39019	9	151	50.3	145	16060	10.3	40S ribosomal protein S19
762	Q8WVX7	9	151	46.5	157	17282	10.5	Ribosomal protein S19
763	P00492	9	34	49.5	218	24579	6.7	Hypoxanthine-guanine phosphoribosyltransferase
763	Q6LET3	9	34	49.5	218	24588	6.8	HPRT1 protein
764	Q9NP72	9	32	49.5	206	22977	5.2	Ras-related protein Rab-18
765	Q9H2J4	9	13	47.7	239	27614	4.8	Phosducin-like protein 3
766	Q96DI7	9	14	47.1	357	39311	8.1	WD repeat protein 57
767	P62241	9	87	46.6	208	24205	10.3	40S ribosomal protein S8
768	P61254	9	79	45.5	145	17258	10.6	60S ribosomal protein L26
768	Q6IBH6	9	79	45.5	145	17244	10.6	RPL26 protein
769	Q9H444	9	18	45.5	224	24950	4.8	Charged multivesicular body protein 4b
770	Q6ICE6	9	48	45	271	30069	5.5	COMT protein
771	Q9NX63	9	62	44.9	227	26152	8.3	Coiled-coil-helix-coiled-coil-helix domain-containing protein 3
772	Q5TIF8	9	29	46.1	232	25615	7.9	Adenylate kinase 2
772	P54819	9	29	44.8	239	26478	7.8	Adenylate kinase isoenzyme 2, mitochondrial
773	UPI00002263A8	9	31	47.5	183	20345	5.3	sorcin isoform b
773	P30626	9	31	43.9	198	21676	5.6	Sorcin
774	Q96HX4	9	14	43.8	274	28649	7.5	Pyrroline-5-carboxylate reductase-like
775	Q0MQG7	9	36	43.7	263	30168	7.5	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial precursor
775	O75489	9	36	43.6	264	30242	7.5	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial precursor
776	P62158	9	39	43	149	16838	4.2	Calmodulin
777	P18669	9	52	42.9	254	28804	7.2	Phosphoglycerate mutase 1
777	UPI00001AF8FE	9	52	42.9	254	28850	7.2	PREDICTED: similar to Phosphoglycerate mutase 1 (Phosphoglycerate mutase isozyme B) (PGAM-B) (BPG-dependent PGAM 1) isoform 1
777	Q6P6D7	9	52	42.9	254	28820	7.2	Phosphoglycerate mutase 1
777	Q53G35	9	52	42.9	254	28832	7.2	Phosphoglycerate mutase 1 (Brain) variant
778	P24539	9	57	42.6	256	28909	9.4	ATP synthase B chain, mitochondrial precursor
779	UPI000045684C	9	43	42.4	250	26552	9.6	Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial precursor (EC 3.6.1.23) (dUTPase) (dUTP pyrophosphatase).
779	P33316	9	43	42.1	252	26706	9.6	Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial precursor
779	Q6NSA3	9	43	42.1	252	26563	9.4	DUTP pyrophosphatase
780	Q92520	9	87	41.9	227	24680	8.3	Protein FAM3C precursor
781	Q9Y6C9	9	23	41.6	303	33331	8	Mitochondrial carrier homolog 2
782	P29218	9	28	40.1	277	30189	5.3	Inositol monophosphatase (EC 3.1.3.25) (IMPase) (IMP) (Inositol-1(or 4)-monophosphatase)
783	P46109	9	14	39.9	303	33777	6.7	Crk-like protein
784	Q9Y3A5	9	31	39.6	250	28764	8.7	Shwachman-Bodian-Diamond syndrome protein
785	O75521	9	14	38.7	359	39609	8.6	Peroxisomal 3,2-trans-enoyl-CoA isomerase (EC 5.3.3.8) (Dodecenoyl-CoA isomerase) (Delta(3),delta(2)-enoyl-CoA isomerase)
785	Q53HG3	9	14	38.2	364	40111	8.9	Peroxisomal D3,D2-enoyl-CoA isomerase isoform 1 variant
785	Q53GC8	9	14	38.2	364	40211	8.8	Peroxisomal D3,D2-enoyl-CoA isomerase isoform 1 variant
786	P52565	9	37	38.7	204	23207	5.1	Rho GDP-dissociation inhibitor 1
787	P61313	9	92	38.2	204	24146	11.6	60S ribosomal protein L15
787	Q5T6E0	9	92	38.2	204	24174	11.6	Ribosomal protein L15 pseudogene 3
788	Q3B7K3	9	15	38.2	267	30368	9	IKIP protein
789	Q9UBQ7	9	27	37.5	328	35668	7.4	Glyoxylate reductase/hydroxypyruvate reductase
790	Q53H82	9	11	36.8	288	32790	6.8	Lactamase beta-2
790	Q9Y392	9	11	36.8	288	32806	6.8	CGI-83 protein
791	O75821	9	29	36.6	320	35611	6.1	Eukaryotic translation initiation factor 3 subunit 4
792	P09661	9	35	36.5	255	28416	8.6	U2 small nuclear ribonucleoprotein A'
792	Q53G61	9	35	36.5	255	28402	8.6	Small nuclear ribonucleoprotein polypeptide A' variant
792	Q53G21	9	35	36.5	255	28474	8.6	Small nuclear ribonucleoprotein polypeptide A' variant
793	P51665	9	47	36.4	324	37025	6.8	26S proteasome non-ATPase regulatory subunit 7
794	Q12771	9	78	36.4	286	31481	7.4	P37 AUF1
794	Q14103-4	9	78	36.2	287	30672	8.4	Isoform 4 of Q14103
794	Q14103-3	9	78	34	306	32835	8.2	Isoform 3 of Q14103

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
794	UPI0000D6158B	9	78	31.5	330	36464	8.5	Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1).
794	Q14103-2	9	78	31	336	36272	8.1	Isoform 2 of Q14103
794	Q14103	9	78	29.3	355	38434	7.8	Heterogeneous nuclear ribonucleoprotein D0
795	P61421	9	23	36.2	351	40329	5	Vacuolar ATP synthase subunit d
796	Q0QEY7	9	18	39.6	255	28906	8.5	Succinate dehydrogenase complex subunit B
796	P21912	9	18	36.1	280	31630	8.8	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial precursor
797	Q14165	9	26	35.6	292	32234	5.4	Uncharacterized protein KIAA0152 precursor
798	P06748-2	9	177	39.2	265	29465	4.6	Isoform 2 of P06748
798	P06748	9	177	35.4	294	32575	4.8	Nucleophosmin
799	P15559	9	75	35.4	274	30868	8.9	NAD(P)H dehydrogenase [quinone] 1 (EC 1.6.5.2) (Quinone reductase 1) (NAD(P)H:quinone oxidoreductase 1)
800	P09486	9	15	35.3	303	34632	4.8	SPARC precursor
801	P30154	9	18	34.1	601	66214	4.9	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform
801	Q8NHV8	9	18	30.7	667	73585	5.1	Protein phosphatase 2 (Formerly 2A), regulatory subunit A, beta isoform
802	Q53GS5	9	11	33.8	352	39934	4.5	SYAP1 protein variant
802	Q96A49	9	11	33.8	352	39933	4.5	Synapse-associated protein 1
803	P61289	9	33	33.5	254	29506	6	Proteasome activator complex subunit 3
803	P61289-2	9	33	31.8	267	30887	6.1	Isoform 2 of P61289
804	P63092	9	15	32.5	394	45665	5.8	Guanine nucleotide-binding protein G(s) subunit alpha isoforms short
804	UPI000004D202	9	15	32.4	395	45752	5.8	GNAS complex locus isoform f
804	UPI0000456FBC	9	15	14.1	908	97549	5.3	Neuroendocrine secretory protein 55 (NESP55) [Contains: LHAL tetrapeptide; GPIPIRRH peptide].
804	Q5JWF2	9	15	12.3	1037	111024	5	Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas
805	O00233	9	17	32.3	223	24654	7	26S proteasome non-ATPase regulatory subunit 9
805	UPI000013D207	9	17	32.3	223	24682	7	proteasome 26S non-ATPase subunit 9
806	O43684	9	29	32.3	328	37155	6.8	Mitotic checkpoint protein BUB3
807	P35250	9	17	31.9	354	39157	6.4	Replication factor C subunit 2
808	P62424	9	53	31.6	266	29996	10.6	60S ribosomal protein L7a
808	UPI0000D62425	9	53	31.1	270	30548	10.7	similar to 60S ribosomal protein L7a (Surfeit locus protein 3) (LOC645846), mRNA
809	Q96BS4	9	26	38.8	260	28449	9.4	FBL protein
809	P22087	9	26	31.5	321	33784	10.2	rRNA 2'-O-methyltransferase fibrillarin
810	P31689	9	21	31.5	397	44868	7.1	DnaJ homolog subfamily A member 1
811	P36542	9	36	31.5	298	32996	9.2	ATP synthase gamma chain, mitochondrial precursor
812	Q5JNZ9	9	23	31.9	420	47273	5	Retinoblastoma binding protein 7
812	Q16576	9	23	31.5	425	47820	5	Histone-binding protein RBBP7
812	Q5JP00	9	23	28.6	469	52314	5.3	Retinoblastoma binding protein 7
813	P31153	9	31	31.4	395	43661	6.5	S-adenosylmethionine synthetase isoform type-2
813	UPI0000DB12F5	9	31	31.3	396	43748	6.5	S-adenosylmethionine synthetase isoform type-
814	Q9H2U2-3	9	22	34.1	305	34658	8.5	Isoform 3 of Q9H2U2
814	Q9H2U2	9	22	31.1	334	37920	7.4	Inorganic pyrophosphatase 2, mitochondrial precursor
814	Q9H2U2-2	9	22	29.8	349	39638	6.9	Isoform 2 of Q9H2U2
815	O43837	9	23	30.9	385	42212	8.5	Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial precursor (EC 1.1.1.41) (Isocitric dehydrogenase) (NAD(+)-specific ICDH)
815	UPI00004709E4	9	23	30.7	387	42411	8.5	Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial precursor (EC 1.1.1.41) (Isocitric dehydrogenase) (NAD(+)-specific ICDH).
816	P31350	9	13	30.8	389	44878	5.4	Ribonucleoside-diphosphate reductase M2 subunit
817	O14908	9	21	30.6	333	36049	6.3	PDZ domain-containing protein GIPC1
818	Q8TDN6	9	18	30.6	353	41401	9.9	Brix domain-containing protein 2
819	P49585	9	16	30	367	41732	6.9	Choline-phosphate cytidylyltransferase A
819	Q86Y88	9	16	30	367	41731	7.3	Phosphate cytidylyltransferase 1, choline, alpha
820	UPI00004BEBE5	9	26	29.6	392	43449	8	TIA-1 related protein isoform 2
821	Q13077	9	17	29.3	416	46164	6.1	TNF receptor-associated factor 1
822	Q3ZCQ8	9	23	28.6	353	39646	8.4	Import inner membrane translocase subunit TIM50, mitochondrial precursor
822	Q3ZCQ8-2	9	23	22.1	456	50465	9.4	Isoform 2 of Q3ZCQ8
823	Q9GZL7	9	11	28.6	423	47708	5.9	WD repeat protein 12
824	Q9NVD7	9	19	28.2	372	42244	5.9	Alpha-parvin
825	Q9Y617	9	12	28.1	370	40423	7.7	Phosphoserine aminotransferase
826	Q9Y266	9	33	27.8	331	38243	5.4	Nuclear migration protein nudC
827	Q6NZI2	9	49	27.4	390	43476	5.6	Polymerase I and transcript release factor
828	P09543	9	30	26.8	421	47579	9.1	2',3'-cyclic-nucleotide 3'-phosphodiesterase
829	Q2VP93	9	27	25.9	343	39602	5.6	Protein arginine methyltransferase 1
829	Q6LEU5	9	27	25.6	347	39929	5.6	HRMT1L2 protein
829	Q8WUW5	9	27	25.3	352	40417	5.5	PRMT1 protein
829	UPI000013CBFF	9	27	24.8	359	41255	5.5	Protein arginine N-methyltransferase 1 (EC 2.1.1.-) (Interferon receptor 1-bound protein 4).

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830	Q92783-2	9	14	34.5	403	44972	4.9	Isoform 2 of Q92783
830	Q92783	9	14	25.7	540	59180	4.8	Signal transducing adapter molecule 1
831	Q9UGI8	9	12	25.7	421	47996	7.7	Testin
832	Q13283	9	47	25.5	466	52164	5.5	Ras GTPase-activating protein-binding protein 1
832	Q6FI03	9	47	25.5	466	52164	5.6	G3BP protein
833	Q542Y9	9	22	24.9	358	40500	6.2	CDNA FLJ90819 fis, clone Y79AA1001264, highly similar to DnaJ homolog subfamily B member 11
833	Q9UBS4	9	22	24.9	358	40514	6.2	DnaJ homolog subfamily B member 11 precursor
833	Q6IAQ8	9	22	24.9	358	40542	6.2	DNAJB11 protein
834	Q96CP5	9	11	25	480	53509	6.7	PMPCB protein
834	O75439	9	11	24.5	489	54366	6.8	Mitochondrial-processing peptidase subunit beta, mitochondrial precursor
834	UPI0000D61CA8	9	11	24.4	491	54524	6.8	Mitochondrial-processing peptidase subunit beta, mitochondrial precursor (EC 3.4.24.64) (Beta-MPP) (P-52).
835	P11310	9	11	24.2	421	46588	8.4	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial precursor
835	Q5T4U5	9	11	22.5	454	50271	7.8	Acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain
835	Q5HYG7	9	11	22.5	454	50309	7.8	Hypothetical protein DKFZp686M24262
836	Q99816	9	11	24.1	390	43944	6.4	Tumor susceptibility gene 101 protein
837	Q9NZ37	9	11	24.9	397	45398	7.1	Uncharacterized hypothalamus protein HT010
837	Q5QTQ4	9	11	24	413	47143	6.6	MSTP012
837	UPI0000D6127F	9	11	24	412	47015	6.4	erythropoietin 4 immediate early response
837	Q9NUZ3	9	11	23.2	426	48631	5.4	CDNA FLJ11039 fis, clone PLACE1004376
837	Q8WU90	9	11	23.2	426	48603	5.3	Zinc finger CCCH-type containing 15
838	Q7L1Q6	9	29	23.9	419	48043	5.9	Basic leucine zipper and W2 domain-containing protein 1
838	Q53FN7	9	29	23.6	424	48618	6.1	BZW1 protein variant
839	Q10713	9	17	23.4	525	58253	6.9	Mitochondrial-processing peptidase alpha subunit, mitochondrial precursor
840	Q0VGU9	9	51	32.2	367	39818	6.6	Rbm39 protein
840	A2RRD3	9	51	23.2	508	57090	10	RBM39 protein
840	Q68DD9	9	51	23	513	57444	10.3	Hypothetical protein DKFZp781C0423
840	Q5RC80	9	51	22.5	524	58657	10.1	RNA-binding protein 39
840	Q14498	9	51	22.3	530	59380	10.1	RNA-binding protein 39
841	UPI0000D61BB9	9	25	23.3	433	49390	9.5	AP-2 complex subunit mu-1 (Adaptin mu-1) (AP-2 mu-2 chain) (Clathrin coat assembly protein AP50) (Clathrin coat-associated protein AP50) (Plasma membrane adaptor AP-2 50 kDa protein) (HA2 50 kDa subunit) (Clathrin assembly protein complex 2 medium chain).
841	Q96CW1	9	25	23.2	435	49655	9.5	AP-2 complex subunit mu-1
841	UPI00004571AB	9	25	23.2	435	49656	9.5	AP-2 complex subunit mu-1 (Adaptin mu-1) (AP-2 mu-2 chain) (Clathrin coat assembly protein AP50) (Clathrin coat-associated protein AP50) (Plasma membrane adaptor AP-2 50 kDa protein) (HA2 50 kDa subunit) (Clathrin assembly protein complex 2 medium chain).
842	P04062	9	19	22.9	536	59716	7.6	Glucosylceramidase precursor
843	Q9H223	9	16	22.7	541	61175	6.8	EH domain-containing protein 4
844	Q9UNH7	9	11	22.7	406	46649	6.2	Sorting nexin-6
845	Q12874	9	14	22.4	501	58849	5.4	Splicing factor 3A subunit 3
845	Q53HM6	9	14	22.4	501	58877	5.4	Splicing factor 3a, subunit 3 variant
846	Q15813	9	10	22.4	527	59346	6.8	Tubulin-specific chaperone E
847	Q9Y285	9	24	22.4	508	57564	7.8	Phenylalanyl-tRNA synthetase alpha chain
848	Q9HBZ9	9	12	21.5	478	54020	6.3	RNA helicase
848	Q9NUU7	9	12	21.5	478	53975	6.6	ATP-dependent RNA helicase DDX19A
849	Q6UW63	9	13	21.1	502	58043	7.7	KDEL motif-containing protein 1 precursor
849	UPI000006ED28	9	13	21.1	502	58029	7.7	KDEL (Lys-Asp-Glu-Leu) containing 1
850	Q9UMS4	9	16	20.8	504	55181	6.6	Pre-mRNA-processing factor 19
851	Q9NZW5	9	14	20.7	540	61117	6.2	MAGUK p55 subfamily member 6
852	P10155	9	21	20.4	538	60671	8	60 kDa SS-A/Ro ribonucleoprotein
853	Q9UBT2	9	17	19.7	640	71224	5.3	SUMO-activating enzyme subunit 2
854	O60684	9	16	19.6	536	60030	5	Importin alpha-7 subunit
854	UPI0000D61EBB	9	16	19.5	539	60342	5	Importin alpha-7 subunit (Karyopherin alpha-6).
855	Q5JW30	9	15	22.9	494	54709	9.5	Staufen, RNA binding protein, homolog 1
855	O95793-2	9	15	22.8	496	54934	9.5	Isoform Short of O95793
855	Q5JW29	9	15	22.5	502	55635	9.5	Staufen, RNA binding protein, homolog 1
855	O95793	9	15	19.6	577	63182	9.4	Double-stranded RNA-binding protein Staufen homolog 1
856	P53634	9	22	19.2	463	51842	7	Dipeptidyl-peptidase 1 precursor (EC 3.4.14.1) (Dipeptidyl-peptidase I) (DPP-I) (DPPI) (Cathepsin C) (Cathepsin J) (Dipeptidyl transferase) [Contains: Dipeptidyl-peptidase 1 exclusion domain chain (Dipeptidyl- peptidase I exclusion domain chain); Dipeptidyl-peptidase 1 heavy chain (Dipeptidyl-peptidase I heavy chain); Dipeptidyl-peptidase 1 light chain (Dipeptidyl-peptidase I light chain)]

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
856	UPI000006D22D	9	22	19.2	463	51854	7	Dipeptidyl-peptidase 1 precursor (EC 3.4.14.1) (Dipeptidyl-peptidase I) (DPP-I) (DPPI) (Cathepsin C) (Cathepsin J) (Dipeptidyl transferase) [Contains: Dipeptidyl-peptidase 1 exclusion domain chain (Dipeptidyl- peptidase I exclusion domain chain); Dipeptid
856	Q8WY99	9	22	19.2	463	51902	7	Cathepsin C
856	Q71E76	9	22	19.2	463	51816	7	Cathepsin C
857	O00116	9	21	18.7	658	72912	7.3	Alkyldihydroxyacetonephosphate synthase, peroxisomal precursor
858	Q15637-4	9	13	21.7	548	59712	9.5	Isoform 4 of Q15637
858	Q15637-6	9	13	20.8	571	61889	9.3	Isoform 6 of Q15637
858	UPI0000456506	9	13	19.1	624	67309	9	Splicing factor 1 (Zinc finger protein 162) (Transcription factor ZFM1) (Zinc finger gene in MEN1 locus) (Mammalian branch point-binding protein mBBP) (BBP).
858	Q15637-3	9	13	19.1	623	67277	9.2	Isoform 3 of Q15637
858	Q15637-2	9	13	18.7	638	68633	9.2	Isoform 2 of Q15637
858	Q15637	9	13	18.6	639	68330	9	Splicing factor 1
858	UPI0000D6262C	9	13	15.6	764	80370	9.2	Splicing factor 1 (Zinc finger protein 162) (Transcription factor ZFM1) (Zinc finger gene in MEN1 locus) (Mammalian branch point-binding protein mBBP) (BBP).
858	Q15637-5	9	13	15.6	764	80621	9.5	Isoform 5 of Q15637
859	O95831-3	9	16	18.4	609	66295	8.9	Isoform 3 of O95831
859	O95831	9	16	18.3	613	66901	9	Apoptosis-inducing factor 1, mitochondrial precursor
860	O00541-2	9	20	17.2	583	67456	7.5	Isoform 2 of O00541
860	O00541	9	20	17	588	68003	7.3	Pescadillo homolog 1
861	P48147	9	19	17	710	80764	5.8	Prolyl endopeptidase
861	Q9UM02	9	19	17	710	80734	5.9	Prolyl endopeptidase
861	Q8N6D4	9	19	17	710	80700	5.9	Prolyl endopeptidase
862	Q2PZI1	9	45	16.3	675	77319	9	Dpy-19-like protein 1
862	UPI0000DD7E92	9	45	16.3	675	77361	9	PREDICTED: similar to dpy-19-like 1, like
863	P07196	9	21	16.2	543	61517	4.6	Neurofilament light polypeptide
863	UPI0000246DBD	9	21	16.2	542	61430	4.6	Neurofilament triplet L protein (68 kDa neurofilament protein) (Neurofilament light polypeptide) (NF-L).
864	Q86VS8	9	10	15.6	718	83126	5.2	Hook homolog 3
865	Q6PI48	9	12	15.5	645	73563	8	Aspartyl-tRNA synthetase, mitochondrial precursor
866	Q6AWC9	9	9	13.8	879	99245	6.5	Hypothetical protein DKFZp686J1643
867	Q09161	9	20	13.7	790	91839	6.4	Nuclear cap-binding protein subunit 1
868	Q9UGP8	9	30	13.3	760	87997	5.3	Translocation protein SEC63 homolog
869	Q8IXB1	9	21	12.5	793	91080	7.2	DnaJ homolog subfamily C member 10 precursor
870	Q2TTR2	9	20	12.4	928	103136	4.8	Cell growth inhibiting protein 39
870	Q9BZQ8	9	20	12.4	928	103135	4.8	Niban protein
871	UPI000059D172	9	16	12.7	1042	111985	6.4	Protein transport protein Sec24C (SEC24-related protein C).
871	P53992	9	16	12.1	1094	118315	7.1	Protein transport protein Sec24C
871	UPI000013F621	9	16	12.1	1094	118325	7.1	SEC24-related protein C
872	Q5TG62	9	26	12	971	109421	7.9	KIAA0090
872	Q8N766-2	9	26	11.8	992	111631	7.7	Isoform 2 of Q8N766
872	Q8N766	9	26	11.8	993	111759	7.7	Uncharacterized protein KIAA0090 precursor
873	Q96P70	9	39	11.8	1041	115963	4.8	Importin-9
874	P12110	9	9	11.4	1019	108579	6.2	Collagen alpha-2(VI) chain precursor
875	Q2VPA0	9	20	12.9	848	95097	6.7	PRSS15 protein
875	Q8N8K8	9	20	12.2	895	100397	6.7	CDNA FLJ39307 fis, clone OCBBF2013208, highly similar to MITOCHONDRIAL LON PROTEASE
875	P36776	9	20	11.4	959	106489	6.4	Lon protease homolog, mitochondrial precursor
876	Q9NZB2	9	12	11.3	1069	116701	9	UPF0318 protein FAM120A
876	UPI000013D2D9	9	12	11.3	1068	116588	9	UPF0318 protein FAM120A.
876	Q9NZB2-3	9	12	10.8	1118	121888	8.9	Isoform C of Q9NZB2
877	P42285	9	27	11.1	1042	117805	6.5	Superkiller viralicidic activity 2-like 2
878	O95486	9	21	10.5	1078	118792	8.1	Protein transport protein Sec24A
878	UPI0000457346	9	21	10.5	1077	118677	8.2	Protein transport protein Sec24A (SEC24-related protein A)
878	UPI0000185FF9	9	21	10.3	1093	119749	7.7	SEC24 related gene family, member A
879	UPI0000E9B14C	9	13	10.5	1001	118103	6.8	RNA binding motif protein 12B
880	Q8WWM7	9	16	9.8	1075	113374	8.6	Ataxin-2-like protein
881	Q9P0K7-3	9	13	9.8	972	109080	6	Isoform 3 of Q9P0K7
881	Q9P0K7	9	13	9.7	980	110041	6.2	Ankycorbin
881	UPI0000074005	9	13	9.7	980	110042	6.2	retinoic acid induced 14
881	Q9P0K7-2	9	13	9.7	983	110423	6.1	Isoform 2 of Q9P0K7
882	P23634-5	9	54	10.6	1122	124007	7.3	Isoform ZK of P23634
882	P23634-4	9	54	10.5	1134	125344	7.7	Isoform XK of P23634
882	P23634-3	9	54	10.3	1158	128066	7.1	Isoform ZA of P23634
882	Q5T0B3	9	54	10.2	1170	129403	7.5	Cation-transporting ATPase
882	P23634-7	9	54	10	1193	132594	6.2	Isoform ZB of P23634
882	Q7Z3S1	9	54	9.9	1205	133874	6.5	Cation-transporting ATPase
882	Q5T0B2	9	54	9.9	1205	133930	6.4	Cation-transporting ATPase
882	P23634-8	9	54	9.7	1229	136583	6.4	Isoform ZD of P23634

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
882	P23634	9	54	9.6	1241	137920	6.6	Plasma membrane calcium-transporting ATPase 4
883	UPI000052D444	9	20	9.6	1032	114899	6.5	integrin alpha 4 precursor
883	P13612	9	20	9.5	1038	115333	6.4	Integrin alpha-4 precursor
883	UPI0000456EB4	9	20	9.5	1037	115304	6.3	Integrin alpha-4 precursor (Integrin alpha-IV) (VLA-4) (CD49d antigen).
884	UPI0000D61AE5	9	35	9.5	1017	114060	6.8	Sodium bicarbonate cotransporter 3 (Sodium bicarbonate cotransporter 2) (Sodium bicarbonate cotransporter 2b) (Bicarbonate transporter) (Solute carrier family 4 member 7).
885	Q7L014	9	19	9.3	1031	117362	9.3	Probable ATP-dependent RNA helicase DDX46
885	UPI0000457348	9	19	9.3	1032	117462	9.3	Probable ATP-dependent RNA helicase DDX46 (EC 3.6.1.-) (DEAD box protein 46) (PRP5 homolog).
885	UPI0000457347	9	19	9.3	1033	117575	9.3	Probable ATP-dependent RNA helicase DDX46 (EC 3.6.1.-) (DEAD box protein 46) (PRP5 homolog).
886	Q12965	9	21	9.1	1109	127041	8.9	Myosin-Ie
886	Q4KMR3	9	21	9.1	1108	127062	8.9	Myosin IE
887	O00203	9	14	9	1094	121350	6	AP-3 complex subunit beta-1
887	UPI00001AE77D	9	14	9	1094	121320	6	adaptor-related protein complex 3, beta 1 subunit
888	Q9HD20-2	9	22	9.9	1086	121110	7.8	Isoform B of Q9HD20
888	Q9HD20	9	22	8.9	1204	132955	8.1	Probable cation-transporting ATPase 13A1
889	Q9NTI5	9	16	8.8	1447	164666	8.5	Hypothetical protein
889	UPI0000D61A5E	9	16	8.8	1449	164824	8.5	androgen-induced prostate proliferative shutoff associated protein
889	Q9Y2I5	9	16	8.6	1483	168415	8.6	Androgen-induced proliferation inhibitor
890	Q59EA1	9	15	8.9	1081	122130	8.6	Transcription elongation regulator 1 variant
890	O14776	9	15	8.7	1098	123960	8.7	Transcription elongation regulator 1
890	UPI000013E374	9	15	8.7	1098	123901	8.6	transcription elongation regulator 1 isoform 1
891	Q5TBK6	9	21	8.4	1349	153670	7.8	LIM domain 7
891	Q8WWI1-3	9	21	8.4	1349	153684	7.8	Isoform 3 of Q8WWI1
891	UPI0000456709	9	21	7	1614	185153	8	LIM domain only protein 7 (LOMP) (F-box only protein 20).
891	Q8WWI1-4	9	21	7	1614	185229	8	Isoform 4 of Q8WWI1
891	UPI0000456708	9	21	6.8	1670	190813	7	LIM domain only protein 7 (LOMP) (F-box only protein 20).
891	Q8WWI1-2	9	21	6.8	1670	190889	7	Isoform 2 of Q8WWI1
891	UPI0000456707	9	21	6.7	1683	192754	8.1	LIM domain only protein 7 (LOMP) (F-box only protein 20).
891	Q8WWI1	9	21	6.7	1683	192708	8.1	LIM domain only protein 7
892	O75153	9	19	8	1309	146669	6.1	Putative eukaryotic translation initiation factor 3 subunit
892	UPI0000D622A0	9	19	8	1310	146826	6.2	Putative eukaryotic translation initiation factor 3 subunit (eIF-3).
893	Q9BZF9	9	16	7.1	1416	162504	7	Uveal autoantigen with coiled-coil domains and ankyrin repeats
894	Q5D044	9	50	6.4	1816	201882	6.3	LAMA4 protein
895	Q149P0	9	15	5.8	1855	206015	5.8	GBF1 protein
895	Q92538	9	15	5.8	1859	206444	5.7	Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1
896	Q9Y5S2	9	11	5.8	1711	194314	6.4	Serine/threonine-protein kinase MRCK beta
897	UPI0000D61343	9	23	5.5	1828	212180	8.6	Myosin-5A (Myosin Va) (Dilute myosin heavy chain, non-muscle) (Myosin heavy chain 12) (Myoxin).
897	Q9Y4I1-2	9	23	5.5	1828	212287	8.6	Isoform 2 of Q9Y4I1
897	Q9Y4I1	9	23	5.4	1855	215419	8.5	Myosin-Va
897	UPI0000E445E1	9	23	5.4	1855	215403	8.5	myosin VA (heavy polypeptide 12, myoxin)
897	UPI0000D61342	9	23	5.4	1855	215312	8.5	Myosin-5A (Myosin Va) (Dilute myosin heavy chain, non-muscle) (Myosin heavy chain 12) (Myoxin).
897	UPI0000D61341	9	23	5.3	1880	218515	8.5	Myosin-5A (Myosin Va) (Dilute myosin heavy chain, non-muscle) (Myosin heavy chain 12) (Myoxin).
898	UPI0000DD79CB	9	18	5.3	1808	203142	4.8	PREDICTED: similar to melanoma inhibitory activity 3 isoform 14
898	UPI0000DD7931	9	18	5.3	1808	203141	4.8	PREDICTED: similar to melanoma inhibitory activity 3 isoform 3
898	UPI00006C03F1	9	18	5.2	1848	206889	4.8	PREDICTED: similar to melanoma inhibitory activity 3 isoform 23
898	Q5JRA6	9	18	5	1907	213700	4.8	Melanoma inhibitory activity family member 3
898	UPI0000D620B3	9	18	5	1907	213686	4.8	melanoma inhibitory activity family, member 3
898	UPI00006C03EC	9	18	5	1907	213701	4.8	PREDICTED: similar to melanoma inhibitory activity 3 isoform 1
899	UPI0000D62536	9	19	5.4	2142	232541	6	SON protein (SON3) (Negative regulatory element-binding protein) (NRE- binding protein) (DBP-5) (Bax antagonist selected in saccharomyces 1) (BASS1).
899	P18583-2	9	19	5.4	2140	232322	6	Isoform A of P18583
899	UPI0000D62537	9	19	4.8	2388	259821	5.7	SON protein (SON3) (Negative regulatory element-binding protein) (NRE- binding protein) (DBP-5) (Bax antagonist selected in saccharomyces 1) (BASS1).
899	P18583-7	9	19	4.8	2386	259608	5.7	Isoform G of P18583
899	P18583	9	19	4.7	2426	263843	5.6	SON protein
899	UPI0000140BFD	9	19	4.7	2426	263827	5.6	SON DNA-binding protein isoform F
899	P18583-9	9	19	4.7	2466	268106	5.6	Isoform I of P18583

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899	P18583-5	9	19	4.7	2459	267048	5.7	Isoform D of P18583
900	O75165	9	44	4.5	2243	254417	6.7	DnaJ homolog subfamily C member 13
900	Q3L0T1	9	44	4.5	2243	254412	6.7	DnaJ domain-containing protein RME-8
901	P05387	8	50	77.4	115	11665	4.5	60S acidic ribosomal protein P2
902	P49773	8	24	75.4	126	13802	7	Histidine triad nucleotide-binding protein 1
903	O75368	8	26	71.9	114	12774	5.2	SH3 domain-binding glutamic acid-rich-like protein
904	O75531	8	51	65.2	89	10059	6.1	Barrier-to-autointegration factor
905	Q9BVJ7	8	9	61.3	150	16588	8.2	Dual specificity protein phosphatase 23
906	P09382	8	202	58.5	135	14716	5.5	Galectin-1
907	P08708	8	84	57	135	15550	9.8	40S ribosomal protein S17
908	Q96TD5	8	29	57.2	243	26349	4.7	P27BBP protein
908	P56537	8	29	56.7	245	26599	4.7	Eukaryotic translation initiation factor 6 (eIF-6) (B4 integrin interactor) (CAB) (p27(BBP)) (B(2)GCN homolog)
909	P61981	8	107	56.3	247	28303	4.9	14-3-3 protein gamma
910	P15374	8	34	54.8	230	26183	4.9	Ubiquitin carboxyl-terminal hydrolase isozyme L3
911	Q9NYG7	8	87	58.7	179	19718	5.4	Bax-sigma
911	Q07812	8	87	54.7	192	21184	5.2	Apoptosis regulator BAX, membrane isoform alpha
911	Q07814	8	87	48.2	218	24220	7.9	Apoptosis regulator BAX, cytoplasmic isoform beta
912	P62820	8	85	54.6	205	22678	6.2	Ras-related protein Rab-1A
913	P63241	8	63	53.2	154	16832	5.2	Eukaryotic translation initiation factor 5A-1
913	P63241-2	8	63	44.6	184	20170	7	Isoform 2 of P63241
914	Q16774	8	22	52.8	197	21726	6.5	Guanylate kinase
914	Q5T435	8	22	47.9	217	23711	7.5	Guanylate kinase 1
914	Q5T433	8	22	41.1	253	27578	5.6	Guanylate kinase 1
915	P19105	8	62	50.9	171	19794	4.8	Myosin regulatory light chain 2, nonsarcomeric
915	Q3THE2	8	62	50.6	172	19779	4.8	Myosin regulatory light chain 2-B, smooth muscle isoform
916	P48047	8	50	49.3	213	23277	10	ATP synthase O subunit, mitochondrial precursor
917	Q13405	8	13	48.2	166	19198	9.5	Mitochondrial 39S ribosomal protein L49
918	O75340	8	28	47.1	191	21868	5.4	Programmed cell death protein 6
919	P25789	8	28	46.7	261	29484	7.7	Proteasome subunit alpha type 4
920	Q86SZ2	8	11	46.2	158	17983	8.7	Trafficking protein particle complex subunit 6B
921	P20618	8	40	46.1	241	26489	8.1	Proteasome subunit beta type 1 precursor
921	Q53FT8	8	40	46.1	241	26491	8.1	Proteasome beta 1 subunit variant
922	P52943	8	14	45.2	208	22493	8.7	Cysteine-rich protein 2
922	Q53FN1	8	14	45.2	208	22494	8.5	Cysteine-rich protein 2 variant
923	Q16836	8	10	44.9	314	34278	8.9	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial precursor
923	UPI000013EECF	8	10	44.9	314	34294	8.9	L-3-hydroxyacyl-Coenzyme A dehydrogenase precursor
923	UPI000013D5C7	8	10	36.2	390	42123	9.3	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial precursor (EC 1.1.1.35) (Short chain 3-hydroxyacyl-CoA dehydrogenase) (HCDH) (Medium and short chain L-3-hydroxyacyl-coenzyme A dehydrogenase).
923	Q16836-2	8	10	36.2	390	42123	9.3	Isoform 2 of Q16836
924	P07951-2	8	37	44.7	284	32990	4.7	Isoform 2 of P07951
925	P00568	8	32	44.3	194	21635	8.6	Adenylate kinase isoenzyme 1
925	Q53EY8	8	32	44.3	194	21619	8.9	Adenylate kinase 1 variant
925	Q5T9B7	8	32	41	210	23411	8.6	Adenylate kinase 1
926	P04632	8	49	44	268	28316	5.2	Calpain small subunit 1
927	Q02543	8	73	43.8	176	20762	10.7	60S ribosomal protein L18a
928	P61586	8	41	43.5	193	21768	6.1	Transforming protein RhoA precursor
929	Q5VYC2	8	33	43.6	227	24636	7.2	Protein-L-isoaspartate (D-aspartate) O-methyltransferase
929	Q5VYC1	8	33	43.4	228	24679	6.5	Protein-L-isoaspartate (D-aspartate) O-methyltransferase
930	Q92979	8	14	43.4	244	26720	9.2	Probable ribosome biogenesis protein NEP1
931	P36969-2	8	16	50	170	19478	7.9	Isoform Cytoplasmic of P36969
931	P36969	8	16	43.1	197	22128	8.3	Phospholipid hydroperoxide glutathione peroxidase, mitochondrial precursor
931	UPI00001AAC3F	8	16	43.1	197	22025	8.4	glutathione peroxidase 4 isoform A precursor
931	UPI000096F213	8	16	36.3	234	26948	10.1	glutathione peroxidase 4 isoform C precursor
932	P35270	8	17	42.9	261	28048	8	Sepiapterin reductase
933	Q15366	8	48	42.5	365	38580	6.8	Poly(rC)-binding protein 2
933	Q6IPF4	8	48	42.3	366	38651	6.8	Poly(RC) binding protein 2
934	Q9NWU5	8	23	42.2	206	23641	9.9	39S ribosomal protein L22, mitochondrial precursor
934	UPI000013D5D9	8	23	38.3	227	26063	9.6	39S ribosomal protein L22, mitochondrial precursor (L22mt) (MRP-L22).
935	Q9BRG1	8	31	42	176	20748	6.3	Vacuolar protein sorting-associated protein 25
936	O96000	8	13	41.9	172	20777	8.5	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10
937	Q9HBM1	8	12	41.5	224	26153	8	Kinetochore protein Spc25
938	P10768	8	17	41.1	282	31463	7	S-formylglutathione hydrolase
939	P20340	8	62	40.9	208	23593	5.5	Ras-related protein Rab-6A
939	Q6FGX3	8	62	40.9	208	23550	5.4	RAB6A protein
939	P20340-2	8	62	40.9	208	23549	5.5	Isoform 2 of P20340
940	P02792	8	55	40.6	175	20020	5.8	Ferritin light chain

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
940	Q96CU0	8	55	40.6	175	20039	5.8	Ferritin, light polypeptide
940	Q8WU07	8	55	40.6	175	20062	5.8	Ferritin, light polypeptide
940	Q6IBT7	8	55	40.6	175	19992	5.8	Ferritin
941	Q9BVK6	8	51	40.2	214	25105	7.2	Transmembrane emp24 domain-containing protein 9 precursor
941	UPI00001D6EC0	8	51	36.6	235	27277	8	transmembrane emp24 protein transport domain containing 9
942	Q13185	8	32	39.9	183	20811	5.3	Chromobox protein homolog 3
943	Q15181	8	24	39.8	289	32660	5.9	Inorganic pyrophosphatase
944	P61758	8	33	39.6	197	22658	7.1	Prefoldin subunit 3
945	P47985	8	28	39.4	274	29668	8.3	Ubiquinol-cytochrome c reductase iron-sulfur subunit, mitochondrial precursor
946	UPI000002552E	8	55	38.9	216	24700	9.9	60S ribosomal protein L10a (CSA-19).
946	P62906	8	55	38.7	217	24831	9.9	60S ribosomal protein L10a
947	Q13151	8	35	38	305	30841	9.3	Heterogeneous nuclear ribonucleoprotein A0
948	P18124	8	95	37.1	248	29226	10.7	60S ribosomal protein L7
948	Q3KQU0	8	95	28.9	318	37022	10.7	RPL7 protein
949	Q6FHE4	8	29	36.9	309	33709	7.3	CNN2 protein
949	Q99439	8	29	36.9	309	33697	7.3	Calponin-2
950	P62280	8	40	36.7	158	18431	10.3	40S ribosomal protein S11
951	Q9Y277	8	23	36.7	283	30659	8.6	Voltage-dependent anion-selective channel protein 3
951	Q9Y277-2	8	23	36.6	284	30790	8.6	Isoform 2 of Q9Y277
952	Q6IPN0	8	195	36.4	343	36918	4.8	RTN4 protein
952	Q7L7Q6	8	195	33.5	373	40318	4.8	RTN4
953	Q59G46	8	26	37.1	280	31355	4.8	Thioredoxin-like 1 variant
953	O43396	8	26	36	289	32251	5	Thioredoxin-like protein 1
954	O00629	8	23	35.5	521	57887	5	Importin alpha-4 subunit
955	UPI0000185FC9	8	73	35.5	155	17662	10.4	PREDICTED: similar to 60S ribosomal protein L23a
955	P62750	8	73	35.3	156	17695	10.4	60S ribosomal protein L23a
956	Q9BVG4	8	12	35.2	233	26057	4.8	UPF0368 protein Cxorf26
957	Q8WUF0	8	13	35.1	276	30580	7.2	Nitrilase family member 2
957	Q9NQR4	8	13	35.1	276	30608	7.2	Nit protein 2
958	Q96C19	8	35	35	240	26697	5.2	EF-hand domain-containing protein 2
959	Q6UXN9	8	11	34.8	313	35079	7.7	WD repeat protein 82
960	Q9NX40	8	16	34.3	245	27626	7.5	OCIA domain-containing protein 1
961	O00764	8	14	33.3	312	35102	6.1	Pyridoxal kinase
962	P04179	8	36	33.3	222	24722	8.3	Superoxide dismutase [Mn], mitochondrial precursor
962	UPI000006D275	8	36	33.3	222	24750	8.3	manganese superoxide dismutase isoform A precursor
963	P62753	8	89	33.3	249	28681	10.8	40S ribosomal protein S6
963	Q96DV6	8	89	33.3	249	28709	10.9	Ribosomal protein S6
964	Q15382	8	16	33.2	184	20497	5.9	GTP-binding protein Rheb precursor
964	Q6NZ61	8	16	33.2	184	20558	5.9	Ras homolog enriched in brain
965	Q96QR8	8	13	33	312	33241	5.4	Transcriptional activator protein Pur-beta
966	Q9BY32	8	11	33	194	21446	5.6	Inosine triphosphate pyrophosphatase
967	P55735	8	15	32.9	322	35541	5.5	Protein SEC13 homolog
968	Q9HC38-2	8	11	32.9	298	33233	5.6	Isoform 2 of Q9HC38
968	Q9Y3E8	8	11	19.4	504	55012	8.7	Uncharacterized protein C17orf25
969	P46782	8	82	32.4	204	22876	9.7	40S ribosomal protein S5
970	Q53F35	8	36	32.4	250	28673	4.1	Acidic (Leucine-rich) nuclear phosphoprotein 32 family, member B variant
970	Q92688	8	36	32.3	251	28788	4.1	Acidic leucine-rich nuclear phosphoprotein 32 family member B
971	UPI00006C0D04	8	31	32.2	370	40821	8.9	PREDICTED: similar to Actin-related protein 2/3 complex subunit 1B (ARP2/3 complex 41 kDa subunit) (p41-ARC)
971	O15143	8	31	32	372	40950	8.4	Actin-related protein 2/3 complex subunit 1B
972	Q53F20	8	21	32	266	30434	3.9	Acidic (Leucine-rich) nuclear phosphoprotein 32 family, member E variant
972	Q9BTT0	8	21	31.7	268	30692	3.8	Acidic leucine-rich nuclear phosphoprotein 32 family member E
973	O43765	8	25	31.6	313	34063	4.9	Small glutamine-rich tetratricopeptide repeat-containing protein A
974	Q96FW1	8	20	31.4	271	31284	4.9	Ubiquitin thioesterase OTUB1
975	Q9P287	8	12	31.2	314	35979	4.6	BRCA2 and CDKN1A-interacting protein
976	Q9BY40	8	9	31	297	33602	7	CDA11
977	P40261	8	31	30.7	264	29574	5.7	Nicotinamide N-methyltransferase
978	P55209	8	39	30.4	391	45374	4.5	Nucleosome assembly protein 1-like 1
979	P57088	8	33	30.4	247	27978	9.7	Transmembrane protein 33
979	UPI000015F326	8	33	30.4	247	27951	9.7	transmembrane protein 33
980	Q14847	8	39	30.3	261	29717	7	LIM and SH3 domain protein 1
980	UPI0000D62315	8	39	24.5	322	35773	8.5	LIM and SH3 domain protein 1 (LASP-1) (MLN 50).
980	Q14847-2	8	39	24.5	323	36014	8.6	Isoform 2 of Q14847
981	Q5HYL6	8	12	30.1	352	39555	5.2	Hypothetical protein DKFZp686E1899
981	Q9NYL9	8	12	30.1	352	39595	5.2	Tropomodulin-3
982	Q9UJ70	8	22	29.9	344	37376	6.2	N-acetylglucosamine kinase
983	P51398	8	9	29.6	398	45566	8.9	Mitochondrial 28S ribosomal protein S29
984	P50402	8	43	29.5	254	28994	5.5	Emerin
985	Q53GQ0	8	50	29.5	312	34350	9.3	Estradiol 17-beta-dehydrogenase 12

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
985	UPI000004C79B	8	50	29.5	312	34324	9.3	steroid dehydrogenase homolog
986	Q96C36	8	16	29.4	320	33637	7.8	Pyrroline-5-carboxylate reductase 2
987	UPI0000D618EF	8	11	29.3	417	45361	8.4	hydroxysteroid dehydrogenase like 2
987	Q6YN16	8	11	29.2	418	45395	8	Hydroxysteroid dehydrogenase-like protein 2
988	UPI0000457067	8	15	30	919	101348	5.1	AP-1 complex subunit beta-1 (Adapter-related protein complex 1 beta-1 subunit) (Beta-adaptin 1) (Adaptor protein complex AP-1 beta-1 subunit) (Golgi adaptor HA1/AP1 adaptin beta subunit) (Clathrin assembly protein complex 1 beta large chain).
988	Q86X54	8	15	30	919	101318	5.1	AP1B1 protein
988	Q20WL3	8	15	29.4	939	103534	5.2	AP1B1 protein
988	UPI0000140030	8	15	29.3	942	103921	5.1	adaptor-related protein complex 1 beta 1 subunit isoform b
988	Q10567-2	8	15	29.3	942	103891	5.1	Isoform B of Q10567
988	Q10567	8	15	29.1	949	104607	5.1	AP-1 complex subunit beta-1
988	UPI000013CED0	8	15	29.1	949	104637	5.1	adaptor-related protein complex 1 beta 1 subunit isoform a
989	Q9NQG5	8	24	29.1	326	36900	6	Uncharacterized protein C20orf77
990	O76003	8	15	29	335	37432	5.4	Thioredoxin-like protein 2
991	P30443	8	29	29	365	40846	6.5	HLA class I histocompatibility antigen, A-1 alpha chain precursor
991	P30455	8	29	29	365	40934	6.4	HLA class I histocompatibility antigen, A-36 alpha chain precursor
992	P31937	8	23	28.9	336	35329	8.1	3-hydroxyisobutyrate dehydrogenase, mitochondrial precursor
993	P17931	8	11	28.8	250	26188	8.5	Galectin-3
993	Q6IBA7	8	11	28.8	250	26152	8.5	LGALS3 protein
993	Q6FGL0	8	11	28.8	250	26161	8.5	LGALS3 protein
993	Q59FR8	8	11	27.9	258	27118	8.4	LGALS3 protein variant
994	P78406	8	11	28.8	368	40968	7.8	mRNA-associated protein mrnp 41
995	Q13011	8	18	28.7	328	35816	8	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial precursor
996	Q9H488	8	14	28.6	388	43956	8.5	GDP-fucose protein O-fucosyltransferase 1 precursor
997	Q86UY0	8	16	28.3	360	40369	5.8	TXNDC5 protein
997	Q8NBS9	8	16	23.6	432	47629	6	Thioredoxin domain-containing protein 5 precursor
998	Q96PU8-5	8	9	30.3	317	35233	6.2	Isoform 5 of Q96PU8
998	Q96PU8-8	8	9	30.1	319	35248	7.4	Isoform 8 of Q96PU8
998	Q96PU8-3	8	9	28.8	333	36926	8.5	Isoform 3 of Q96PU8
998	Q96PU8	8	9	28.2	341	37671	8.5	Quaking protein
998	Q96PU8-2	8	9	28.2	341	37466	8.4	Isoform 2 of Q96PU8
998	Q96PU8-7	8	9	27.7	347	38313	7	Isoform 7 of Q96PU8
999	Q9BTT5	8	19	31.4	338	38442	9.7	Similar to NADH dehydrogenase (Ubiquinone) 1 alpha subcomplex, 9
999	Q16795	8	19	28.1	377	42510	9.8	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial precursor
1000	Q567T7	8	14	27.8	334	37480	7.6	Methionine adenosyltransferase 2 beta
1000	Q9NZL9	8	14	27.8	334	37552	7.4	Methionine adenosyltransferase regulatory beta subunit
1001	O75323	8	18	26.9	286	33743	9.4	Protein NipSnap2
1002	Q9BTV4	8	32	25.8	400	44876	8.1	Transmembrane protein 43
1003	Q96HI4	8	22	25.7	494	56604	7.8	NMT1 protein
1003	P30419	8	22	25.6	496	56806	7.8	Glycylpeptide N-tetradecanoyltransferase 1
1003	UPI0000D6234C	8	22	25.5	498	56978	7.8	Glycylpeptide N-tetradecanoyltransferase 1 (EC 2.3.1.97) (Peptide N- myristoyltransferase 1) (Myristoyl-CoA:protein N-myristoyltransferase 1) (NMT 1) (Type I N-myristoyltransferase).
1004	UPI00002371B1	8	17	27.6	406	45169	9.2	DEAD (Asp-Glu-Ala-Asp) box polypeptide 47 isoform 2
1004	Q53GJ1	8	17	25	448	49882	9.2	DEAD (Asp-Glu-Ala-Asp) box polypeptide 47 isoform 1 variant
1004	Q9H0S4	8	17	24.6	455	50647	9.1	Probable ATP-dependent RNA helicase DDX47
1005	P18031	8	14	24.6	435	49967	6.3	Tyrosine-protein phosphatase non-receptor type 1
1006	O60884	8	17	24.3	412	45746	6.5	DnaJ homolog subfamily A member 2
1007	Q7Z518	8	15	24.3	354	40677	8.5	NADH dehydrogenase
1007	O95299	8	15	24.2	355	40751	8.5	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial precursor
1008	UPI0000D612BA	8	13	26.7	367	41317	6.9	WD repeat and FYVE domain-containing protein 1 (WD40- and FYVE domain- containing protein 1) (Phosphoinositide-binding protein 1) (FENS-1) (Zinc finger FYVE domain-containing protein 17).
1008	Q8IWB7	8	13	23.9	410	46324	7.3	WD repeat and FYVE domain-containing protein 1
1009	Q9UQD4	8	9	24.9	353	39840	5.2	SH3-containing Grb-2-like 1 protein
1009	Q99961	8	9	23.9	368	41490	5.4	SH3-containing GRB2-like protein 1
1010	Q8NCF7	8	94	23.3	361	39933	9.4	CDNA FLJ90278 fis, clone NT2RP1000325, highly similar to Phosphate carrier protein, mitochondrialprecursor

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1010	Q7Z7N7	8	94	23.3	361	39959	9.4	Solute carrier family 25 (Mitochondrial carrier; phosphate carrier), member 3
1010	Q53HC3	8	94	23.3	361	39929	9.4	Solute carrier family 25 member 3 isoform b variant
1010	Q00325	8	94	23.2	362	40095	9.4	Phosphate carrier protein, mitochondrial precursor
1011	Q9Y376	8	21	23.2	341	39869	6.9	Calcium-binding protein 39
1012	P35237	8	12	22.9	376	42590	5.3	Serpin B6
1012	Q5TD06	8	12	22.9	376	42622	5.3	Serpin peptidase inhibitor, clade B (Ovalbumin), member 6
1012	Q59F97	8	12	21.9	393	44446	5.2	Hypothetical protein
1012	UPI0000D613D8	8	12	21	409	46331	5.9	Serpin B6 (Placental thrombin inhibitor) (Cytoplasmic antiproteinase) (CAP) (Protease inhibitor 6) (PI-6).
1013	Q9Y383	8	32	22.7	392	46514	10	Putative RNA-binding protein Luc7-like 2
1013	UPI000013D41E	8	32	22.2	401	47506	10	Putative RNA-binding protein Luc7-like 2.
1014	Q5H907	8	15	22.5	521	55796	7.8	Melanoma antigen family D, 2
1014	UPI0000D61D7D	8	15	22.5	521	55830	7.8	Melanoma-associated antigen D2 (MAGE-D2 antigen) (MAGE-D) (Breast cancer-associated gene 1 protein) (BCG-1) (11B6) (Hepatocellular carcinoma-associated protein JCL-1).
1014	UPI0000D61D7E	8	15	21.3	549	59453	9.7	Melanoma-associated antigen D2 (MAGE-D2 antigen) (MAGE-D) (Breast cancer-associated gene 1 protein) (BCG-1) (11B6) (Hepatocellular carcinoma-associated protein JCL-1).
1014	Q5H909	8	15	21.3	550	59525	9.7	Melanoma antigen family D, 2
1014	UPI0000457842	8	15	19.9	588	63151	9.3	Melanoma-associated antigen D2 (MAGE-D2 antigen) (MAGE-D) (Breast cancer-associated gene 1 protein) (BCG-1) (11B6) (Hepatocellular carcinoma-associated protein JCL-1).
1014	Q9UNF1-2	8	15	19.9	588	63167	9.3	Isoform 2 of Q9UNF1
1014	Q9UNF1	8	15	19.3	606	64954	9.3	Melanoma-associated antigen D2
1015	Q0VGA5	8	12	21.9	511	58407	6.4	SARS protein
1015	P49591	8	12	21.8	514	58777	6.4	Seryl-tRNA synthetase, cytoplasmic
1015	Q53HA4	8	12	21.8	514	58690	6.4	Seryl-tRNA synthetase variant
1015	UPI0000D61F7C	8	12	20.9	536	61285	7.1	Seryl-tRNA synthetase, cytoplasmic (EC 6.1.1.11) (Serine--tRNA ligase) (SerRS).
1015	Q5T5C7	8	12	20.9	536	61313	7.1	Seryl-tRNA synthetase
1016	Q9H3N1	8	33	21.8	280	31791	5	Thioredoxin domain-containing protein 1 precursor
1016	UPI000006E5F1	8	33	21.8	280	31806	5	thioredoxin domain containing
1017	Q9NY27	8	11	21.8	495	54704	4.7	Protein phosphatase 4 regulatory subunit 2
1018	O60784	8	11	21.7	492	53818	4.7	Target of Myb protein 1
1018	Q86X74	8	11	21.7	493	53875	4.7	Target of myb1
1019	Q8TCT9-5	8	108	23.9	335	36814	6.7	Isoform 5 of Q8TCT9
1019	Q8TCT9	8	108	21.2	377	41488	6.4	Minor histocompatibility antigen H13
1020	Q07960	8	20	21	439	50436	6.3	Rho GTPase-activating protein 1
1021	Q53GI6	8	14	20.8	437	50409	4.8	Synaptonemal complex protein SC65 variant
1021	Q92791	8	14	20.8	437	50381	4.8	Nucleolar autoantigen No55
1022	Q8N1G4	8	18	20.8	583	63473	8.3	Leucine-rich repeat-containing protein 47
1023	Q96A33-2	8	13	20.6	480	55318	4.7	Isoform 2 of Q96A33
1023	Q96A33	8	13	20.5	483	55874	4.9	Coiled-coil domain-containing protein 47 precursor
1023	UPI0000073E7C	8	13	20.5	483	55816	4.9	coiled-coil domain containing 47
1024	Q13418	8	12	20.4	452	51419	8.1	Integrin-linked protein kinase
1025	Q59EH7	8	10	20.3	483	55418	7.5	DnaJ (Hsp40) homolog, subfamily C, member 7 variant
1025	Q99615	8	10	19.8	494	56441	7	DnaJ homolog subfamily C member 7
1026	P07099	8	18	20	455	52949	7.3	Epoxide hydrolase 1
1027	O75306	8	15	19.9	463	52546	7.6	NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial precursor
1028	Q8N2L6	8	19	19.5	447	49824	9.4	CDNA FLJ90138 fis, clone HEMBB1000905, weakly similar to TRANSCRIPTIONAL REPRESSOR RCO-1
1028	Q9Y4P3	8	19	19.5	447	49798	9.4	Transducin beta-like 2 protein
1029	Q14166	8	17	19.1	644	74404	5.5	Tubulin--tyrosine ligase-like protein 12
1030	Q14554	8	15	18.3	519	59594	7.9	Protein disulfide-isomerase A5 precursor
1031	O75475	8	18	17.4	530	60103	9.1	PC4 and SFRS1-interacting protein
1032	Q53GW1	8	9	17.3	642	72308	6.4	Vesicle transport-related protein isoform a variant
1032	Q8WVM8	8	9	17.3	642	72380	6.3	Sec1 family domain-containing protein 1
1033	Q59GU6	8	13	20.8	432	50099	7	Sorting nexin 1 isoform a variant
1033	Q13596-2	8	13	19.7	457	51813	5.6	Isoform 1A of Q13596
1033	UPI0000D61352	8	13	19.6	460	52225	5.9	Sorting nexin-1.
1033	UPI0000456869	8	13	17.3	521	58955	5.2	Sorting nexin-1.
1033	Q13596	8	13	17.2	522	59070	5.1	Sorting nexin-1
1033	Q53GY8	8	13	17.2	522	59012	5.2	Sorting nexin 1 isoform a variant
1033	Q6ZRJ8	8	13	16.2	557	63022	5.5	CDNA FLJ46302 fis, clone TESTI4036048, highly similar to Sorting nexin 1

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1034	O43252	8	16	17	624	70833	6.9	Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthetase 1 (PAPS synthetase 1) (PAPSS 1) (Sulfurylase kinase 1) (SK1) (SK 1) [Includes: Sulfate adenylyltransferase (EC 2.7.7.4) (Sulfate adenylate transferase) (SAT) (ATP-sulfurylase); Adenylyl-sulfate kinase (EC 2.7.1.25) (Adenylylsulfate 3'-phosphotransferase) (APS kinase) (Adenosine-5'-phosphosulfate 3'-phosphotransferase) (3'-phosphoadenosine-5'-phosphosulfate synthetase)]
1035	Q8IW76	8	26	17.7	513	57620	8.3	EIF2AK2 protein
1035	P19525	8	26	16.5	551	62094	8.4	Interferon-induced, double-stranded RNA-activated protein kinase
1036	Q15758	8	86	16.3	541	56598	5.5	Neutral amino acid transporter B(0) (ATB(0))
1036	Q71UA6	8	86	16.3	541	56583	5.5	Neutral amino acid transporter
1037	Q5JPT5	8	17	16.6	628	68550	7.5	SH3-domain kinase binding protein 1
1037	Q5JPR3	8	17	16.1	645	70443	8.6	SH3-domain kinase binding protein 1
1037	Q96B97	8	17	15.6	665	73126	6.6	SH3 domain-containing kinase-binding protein 1
1038	Q6GMQ6	8	30	16.9	610	66393	8.8	Phosphatidylinositol binding clathrin assembly protein
1038	Q13492-2	8	30	16.3	632	68764	7.9	Isoform 2 of Q13492
1038	Q13492	8	30	15.8	652	70755	7.9	Phosphatidylinositol-binding clathrin assembly protein
1038	Q4LE54	8	30	14.3	721	77397	8.4	PICALM variant protein
1039	Q69YH4	8	32	15.4	622	70064	8.7	Hypothetical protein DKFZp666E065
1039	UPI00003FF926	8	32	13.9	689	77151	9.1	hypothetical protein LOC54867 isoform 1
1040	Q05BV5	8	10	15.2	660	71801	7	OGFR protein
1041	Q2Z2K8	8	13	14.7	754	85562	5.8	Endothelin-converting enzyme-1c
1041	P42892-2	8	13	14.6	758	85808	6.5	Isoform A of P42892
1041	P42892-4	8	13	14.5	767	87023	5.8	Isoform D of P42892
1041	P42892	8	13	14.4	770	87164	5.9	Endothelin-converting enzyme 1
1042	Q9BV61	8	47	13.9	699	79357	7.8	TRAP1 protein
1042	Q12931	8	47	13.8	704	80110	8.2	Heat shock protein 75 kDa, mitochondrial precursor
1042	UPI0000001C1A	8	47	13.8	704	80011	8	TNF receptor-associated protein 1
1042	Q53G55	8	47	13.8	704	80039	8	TNF receptor-associated protein 1 variant
1042	Q53FS6	8	47	13.8	704	80091	8	TNF receptor-associated protein 1 variant
1043	Q96AC1-2	8	18	14.8	633	72397	7.5	Isoform 2 of Q96AC1
1043	Q96AC1	8	18	13.8	680	77861	6.7	Pleckstrin homology domain-containing family C member 1
1044	Q9NVI7-2	8	15	14.7	586	66218	9.2	Isoform 2 of Q9NVI7
1044	Q9NVI7	8	15	13.6	634	71369	9	ATPase family AAA domain-containing protein 3A
1044	UPI0000073837	8	15	13.6	634	71357	9	ATPase family, AAA domain containing 3A
1045	P19022	8	10	13.2	906	99809	4.8	Cadherin-2 precursor
1046	P33992	8	12	13.2	734	82286	8.4	DNA replication licensing factor MCM5
1046	Q53FG5	8	12	13.2	734	82237	8.3	Minichromosome maintenance deficient protein 5 variant
1047	Q96A78	8	14	13.4	808	89035	6.9	TBL3 protein (Transducin (Beta)-like 3)
1047	Q8IVB7	8	14	13.4	808	88936	6.9	Transducin (Beta)-like 3
1047	Q59GD6	8	14	13	832	91238	7	Transducin beta-like 3 variant
1048	Q96JZ5	8	40	13	545	62941	7.5	CDNA FLJ14882 fis, clone PLACE1003537, weakly similar to ENDOSOMAL P24A PROTEIN
1048	UPI0000169B24	8	40	12.1	589	67870	7.2	transmembrane 9 superfamily member 3
1048	Q9HD45	8	40	12.1	589	67888	7.2	Transmembrane 9 superfamily protein member 3 precursor
1049	Q15003	8	19	12.8	741	82563	5.1	Condensin complex subunit 2
1050	P49589-2	8	24	12.9	726	82846	7	Isoform 2 of P49589
1050	UPI00004F8E1C	8	24	12.7	738	84472	6.4	cysteinyl-tRNA synthetase isoform d
1050	P49589	8	24	12.6	748	85473	6.7	Cysteinyl-tRNA synthetase, cytoplasmic
1050	Q5HYE4	8	24	11.3	831	94638	6.8	Hypothetical protein DKFZp686F1612
1051	Q13617	8	13	12.5	745	86983	6.9	Cullin-2
1052	Q9H5A4	8	262	26	338	36733	5.4	CD44 molecule
1052	P16070-14	8	262	22.2	396	43157	5.3	Isoform 14 of P16070
1052	P16070-13	8	262	20.7	425	46249	5.2	Isoform 13 of P16070
1052	P16070-11	8	262	20.5	429	46565	5.7	Isoform 11 of P16070
1052	Q9H5A6	8	262	18.7	470	50728	5.4	CD44 molecule
1052	UPI000037848D	8	262	17.8	493	53411	5.4	CD44 antigen isoform 3 precursor
1052	P16070-10	8	262	17.8	493	53399	5.4	Isoform 10 of P16070
1052	P16070-16	8	262	13.2	668	73138	5.4	Isoform 16 of P16070
1052	P16070-8	8	262	13.1	674	74404	5.2	Isoform 8 of P16070
1052	Q9H5A7	8	262	13	676	73929	5.3	CD44 molecule
1052	P16070-17	8	262	12.7	691	75945	5.3	Isoform 17 of P16070
1052	UPI000037848C	8	262	12.6	699	76612	5.3	CD44 antigen isoform 2 precursor
1052	P16070-6	8	262	12.6	699	76692	5.3	Isoform 6 of P16070
1052	P16070-4	8	262	12.6	699	76628	5.3	Isoform 4 of P16070
1052	P16070-3	8	262	12.4	711	77999	5.4	Isoform 3 of P16070
1052	P16070-7	8	262	12.3	713	78461	5.4	Isoform 7 of P16070
1052	Q9H5A5	8	262	12.2	719	78854	5.3	CD44 molecule
1052	P16070-5	8	262	12	734	80806	5.3	Isoform 5 of P16070
1052	P16070	8	262	11.9	742	81554	5.3	CD44 antigen precursor

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
1052	UPI000013D3FE	8	262	11.9	742	81538	5.3	CD44 antigen isoform 1 precursor
1053	A4D1C5	8	16	11.5	780	88106	5.6	Protein tyrosine phosphatase, non-receptor type 12
1053	Q05209	8	16	11.5	780	88120	5.6	Tyrosine-protein phosphatase non-receptor type 12
1054	Q9H3U1-2	8	9	11.7	929	101675	6.1	Isoform 2 of Q9H3U1
1054	Q9H3U1	8	9	11.5	944	103077	6.1	UNC45 homolog A
1055	P56192	8	15	10.4	900	101116	6.2	Methionyl-tRNA synthetase, cytoplasmic
1056	Q53GS1	8	15	10.7	878	98262	5.6	MutS homolog 2 variant
1056	Q53FK0	8	15	10.7	878	98222	5.7	MutS homolog 2 variant
1056	P43246	8	15	10.1	934	104743	5.8	DNA mismatch repair protein Msh2
1057	O14964	8	12	10	777	86192	6.2	Hepatocyte growth factor-regulated tyrosine kinase substrate
1058	Q8TCJ2	8	58	10	826	93674	8.9	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B
1059	Q9H0D6-2	8	21	10.5	874	99962	8	Isoform 2 of Q9H0D6
1059	Q9H0D6	8	21	9.7	950	108583	7.5	5'-3' exoribonuclease 2
1060	Q8IYB3-2	8	21	9.5	902	102126	11.8	Isoform 2 of Q8IYB3
1060	Q8IYB3	8	21	9.5	904	102335	11.8	Serine/arginine repetitive matrix protein 1
1060	Q5VVN3	8	21	9.4	913	103390	11.8	Serine/arginine repetitive matrix 1
1061	Q01970	8	15	8.3	1234	138799	5.9	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta 3
1062	Q15020	8	20	8.3	963	109935	5.6	Squamous cell carcinoma antigen recognized by T-cells 3
1063	O00267	8	13	7.8	1087	121000	5.1	Transcription elongation factor SPT5
1063	UPI0000D6179E	8	13	7.8	1083	120527	5.1	Transcription elongation factor SPT5 (hSPT5) (DRB sensitivity-inducing factor large subunit) (DSIF large subunit) (DSIF p160) (Tat- cotransactivator 1 protein) (Tat-CT1 protein).
1063	UPI0000456CB7	8	13	7.8	1087	121028	5	Transcription elongation factor SPT5 (hSPT5) (DRB sensitivity-inducing factor large subunit) (DSIF large subunit) (DSIF p160) (Tat- cotransactivator 1 protein) (Tat-CT1 protein).
1063	O00267-2	8	13	7.8	1083	120499	5.1	Isoform 2 of O00267
1064	UPI0000D625BB	8	10	6.9	1362	155859	5.1	Ubiquitin carboxyl-terminal hydrolase 47 (EC 3.1.2.15) (Ubiquitin thioesterase 47) (Ubiquitin-specific-processing protease 47) (Deubiquitinating enzyme 47).
1064	Q96K76	8	10	6.8	1375	157268	5.1	Ubiquitin carboxyl-terminal hydrolase 47
1065	Q96ST3	8	13	6.8	1273	145175	7.3	Paired amphipathic helix protein Sin3a
1066	P08572	8	26	6.6	1712	167553	8.7	Collagen alpha-2(IV) chain precursor [Contains: Canstatin]
1066	UPI0000D61AA5	8	26	6.6	1706	167211	8.6	Collagen alpha-2(IV) chain precursor.
1066	UPI0000D61AA4	8	26	6.6	1712	167607	8.6	Collagen alpha-2(IV) chain precursor.
1066	UPI00004588A6	8	26	6.6	1706	167157	8.6	Collagen alpha-2(IV) chain precursor.
1067	Q10570	8	15	6.4	1443	160883	6.4	Cleavage and polyadenylation specificity factor subunit 1
1068	Q6PFW2	8	21	5.8	1562	172243	5.5	Rho guanine nucleotide exchange factor (GEF) 11
1069	P52948	8	11	5.6	1729	187789	6.3	Nuclear pore complex protein Nup98-Nup96 precursor [Contains: Nuclear pore complex protein Nup98 (Nucleoporin Nup98) (98 kDa nucleoporin); Nuclear pore complex protein Nup96 (Nucleoporin Nup96) (96 kDa nucleoporin)]
1069	UPI0000D62592	8	11	5.6	1729	187780	6.4	Nuclear pore complex protein Nup98-Nup96 precursor [Contains: Nuclear pore complex protein Nup98 (Nucleoporin Nup98) (98 kDa nucleoporin); Nuclear pore complex protein Nup96 (Nucleoporin Nup96) (96 kDa nucleoporin)].
1069	P52948-5	8	11	5.4	1800	195816	6.4	Isoform 5 of P52948
1070	UPI000059DBEB	8	14	5.5	1936	198175	7.2	Host cell factor (HCF) (HCF-1) (C1 factor) (VP16 accessory protein) (VCAF) (CFF) [Contains: HCF N-terminal chain 1; HCF N-terminal chain 2; HCF N-terminal chain 3; HCF N-terminal chain 4; HCF N-terminal chain 5; HCF N-terminal chain 6; HCF C-terminal chai
1070	UPI000059DBED	8	14	5.4	1980	202848	7.1	Host cell factor (HCF) (HCF-1) (C1 factor) (VP16 accessory protein) (VCAF) (CFF) [Contains: HCF N-terminal chain 1; HCF N-terminal chain 2; HCF N-terminal chain 3; HCF N-terminal chain 4; HCF N-terminal chain 5; HCF N-terminal chain 6; HCF C-terminal chai
1070	UPI000036779B	8	14	5.4	1966	201848	7.5	Host cell factor (HCF) (HCF-1) (C1 factor) (VP16 accessory protein) (VCAF) (CFF) [Contains: HCF N-terminal chain 1; HCF N-terminal chain 2; HCF N-terminal chain 3; HCF N-terminal chain 4; HCF N-terminal chain 5; HCF N-terminal chain 6; HCF C-terminal chai
1070	UPI0000142F1F	8	14	5.2	2035	208730	7.5	host cell factor 1
1071	Q9Y6D6	8	22	5.1	1849	208766	5.9	Brefeldin A-inhibited guanine nucleotide-exchange protein 1
1072	Q5UIP0	8	15	4.7	2472	274464	5.5	Telomere-associated protein RIF1

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
1072	UPI0000D6124A	8	15	4.7	2448	271915	5.4	Telomere-associated protein RIF1 (Rap1-interacting factor 1 homolog).
1072	Q5UIP0-2	8	15	4.7	2446	271688	5.4	Isoform 2 of Q5UIP0
1072	UPI0000D61249	8	15	4.6	2474	274691	5.5	Telomere-associated protein RIF1 (Rap1-interacting factor 1 homolog).
1073	UPI00004569DB	8	11	4.5	2036	233241	6.9	Protein FAM38A.
1073	Q92508	8	11	4.5	2035	233040	6.9	Protein FAM38A
1073	Q0KKZ9	8	11	4.4	2090	239618	7	Mib
1074	Q9GZT3	7	33	63.3	109	12349	10.2	SRA stem-loop-interacting RNA-binding protein, mitochondrial precursor
1075	Q99471	7	23	59.7	154	17328	6.3	Prefoldin subunit 5
1076	P62888	7	100	59.1	115	12784	9.6	60S ribosomal protein L30
1077	Q9Y3E5	7	14	57	179	19194	8.7	Peptidyl-tRNA hydrolase 2, mitochondrial precursor
1078	Q9BYN0	7	19	56.9	137	14259	8.2	Sulfiredoxin-1
1079	Q9Y221	7	11	56.1	180	20463	8.5	60S ribosome subunit biogenesis protein NIP7 homolog
1080	Q9UHV9	7	34	54.5	154	16648	6.6	Prefoldin subunit 2
1081	P61088	7	36	53.3	152	17138	6.6	Ubiquitin-conjugating enzyme E2 N
1082	Q53HV6	7	54	51.7	151	16584	7.7	Niemann-Pick disease, type C2 variant
1083	P10599	7	110	51.4	105	11737	4.9	Thioredoxin
1084	P67809	7	46	50.9	324	35924	9.9	Nuclease sensitive element-binding protein 1
1085	Q04837	7	44	50	148	17260	9.6	Single-stranded DNA-binding protein, mitochondrial precursor
1085	Q567R6	7	44	50	148	17359	9.7	Single-stranded DNA binding protein 1
1086	P16949	7	74	48.3	149	17302	6	Stathmin
1087	P61006	7	17	48.3	207	23668	9.1	Ras-related protein Rab-8A
1088	Q03135	7	159	47.2	178	20472	6	Caveolin-1
1089	P11441	7	12	47.1	157	17776	8.7	Ubiquitin-like protein 4A
1090	Q15185	7	47	46.9	160	18697	4.5	Prostaglandin E synthase 3
1091	O75828	7	12	46.6	277	30850	6.2	Carbonyl reductase [NADPH] 3
1092	P61326	7	27	46.6	146	17164	6.1	Protein mago nashi homolog
1092	Q96A72	7	27	45.9	148	17276	6.4	Protein mago nashi homolog 2
1093	Q96DE0	7	11	45.6	195	21273	6.9	Nucleoside diphosphate-linked moiety X motif 16
1094	Q9NRV9	7	24	45.5	189	21097	5.8	Heme-binding protein 1
1095	P61224	7	35	45.1	184	20825	5.8	Ras-related protein Rap-1b precursor
1096	P30044	7	38	44.4	214	22026	8.6	Peroxiredoxin-5, mitochondrial precursor
1096	UPI000013D62C	7	38	44.4	214	22086	8.7	Peroxiredoxin-5, mitochondrial precursor (EC 1.11.1.15) (Prx-V) (Peroxisomal antioxidant enzyme) (PLP) (Thioredoxin reductase) (Thioredoxin peroxidase PMP20) (Antioxidant enzyme B166) (AOEB166) (TPx type VI) (Liver tissue 2D-page spot 71B) (Alu corepresso
1097	Q4VBQ4	7	29	43.6	140	15088	6.1	Profilin 2
1098	P25398	7	42	43.2	132	14526	6.7	40S ribosomal protein S12
1099	O75223	7	21	42.6	188	21008	5.1	Uncharacterized protein C7orf24
1100	Q07020	7	93	42	188	21634	11.7	60S ribosomal protein L18
1101	P37108	7	35	41.9	136	14570	10	Signal recognition particle 14 kDa protein
1101	Q96Q14	7	35	41.9	136	14514	10	Signal recognition particle 14kD
1102	P13073	7	64	41.4	169	19577	9.5	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial precursor
1102	Q6P666	7	64	41.4	169	19607	9.5	Cytochrome c oxidase subunit IV isoform 1
1103	Q9NR31	7	14	41.4	198	22367	6.7	GTP-binding protein SAR1a
1104	Q9BPX5	7	18	41.2	153	16941	6.6	Actin-related protein 2/3 complex subunit 5-like protein
1105	Q9UL26	7	17	40.7	194	21855	8.2	Ras-related protein Rab-22A
1106	O75396	7	98	40.5	215	24741	8.5	Vesicle-trafficking protein SEC22b
1107	Q9GZS3	7	13	40	305	33581	5.5	WD repeat protein 61
1108	P19387	7	12	39.6	275	31441	4.9	DNA-directed RNA polymerase II 33 kDa polypeptide
1109	P01111	7	16	39.2	189	21229	5.2	GTPase NRas precursor
1110	UPI0000456547	7	30	39.3	224	24849	8.5	Signal peptidase complex subunit 2 (EC 3.4.-.-) (Microsomal signal peptidase 25 kDa subunit) (SPase 25 kDa subunit).
1110	Q15005	7	30	38.9	226	25003	8.5	Signal peptidase complex subunit 2
1110	UPI000047EFF7	7	30	38.9	226	24976	8	hypothetical protein LOC653566
1111	Q9HAV7	7	13	38.2	217	24279	8.1	GrpE protein homolog 1, mitochondrial precursor
1112	Q567R9	7	14	53.3	150	16830	9.7	CIP29 protein
1112	P82979	7	14	38.1	210	23671	6.4	Nuclear protein Hcc-1
1113	UPI000015B7BA	7	15	38.1	210	24611	6	DNA directed RNA polymerase II polypeptide E
1114	P13693	7	52	37.2	172	19595	4.9	Translationally-controlled tumor protein
1115	Q9UHY7	7	18	37.2	261	28933	4.8	Enolase-phosphatase E1
1116	Q9Y296	7	13	37	219	24340	6.2	Trafficking protein particle complex subunit 4
1117	Q9NRX1	7	16	36.9	252	27924	9.7	RNA-binding protein PNO1
1118	P41227	7	18	36.2	235	26458	5.6	N-terminal acetyltransferase complex ARD1 subunit homolog A
1119	UPI0000EFE339	7	26	36.7	180	20639	7.8	NEDD8-conjugating enzyme Ubc12
1119	P61081	7	26	36.1	183	20900	7.7	NEDD8-conjugating enzyme Ubc12
1120	P63000	7	35	39.1	192	21450	8.5	Ras-related C3 botulinum toxin substrate 1 precursor
1120	A4D2P0	7	35	35.5	211	23467	8.6	Ras-related C3 botulinum toxin substrate 1

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
1121	Q8NFH5	7	9	35.3	326	34774	9.1	Nucleoporin NUP53
1122	Q8WW59	7	10	35.3	207	23098	6.9	SPRY domain-containing protein 4
1122	UPI00001418EE	7	10	35.3	207	23129	6.9	SPRY domain-containing protein 4.
1123	P49755	7	107	35.2	219	24976	7.5	Transmembrane emp24 domain-containing protein 10 precursor
1123	Q53GF9	7	107	34.2	225	25637	6.7	Full-length cDNA 5-PRIME end of clone CS0DF013YM24 of Fetal brain of Homo sapiens (Human) variant
1124	O43447	7	10	35	177	19208	8.1	Peptidyl-prolyl cis-trans isomerase H
1125	Q15404	7	11	35	277	31540	8.6	Ras suppressor protein 1
1125	Q32Q10	7	11	34.6	280	31359	9.1	RSU1 protein
1126	P06730	7	12	33.6	217	25097	6.1	Eukaryotic translation initiation factor 4E
1126	Q32Q75	7	12	33.6	217	25067	6.1	Eukaryotic translation initiation factor 4E
1127	Q08257	7	8	33.4	329	35207	8.4	Quinone oxidoreductase
1128	P26373	7	65	33.2	211	24261	11.7	60S ribosomal protein L13
1128	Q6NZ55	7	65	33.2	211	24265	11.7	Ribosomal protein L13
1129	Q541A5	7	12	33.2	307	34500	6.7	Ubiquitin fusion degradation 1-like
1129	Q92890	7	12	29.7	343	38725	6.3	Ubiquitin fusion degradation protein 1 homolog
1130	O00151	7	9	33.1	329	36072	7	PDZ and LIM domain protein 1
1131	Q03405	7	14	32.8	335	36978	6.6	Urokinase plasminogen activator surface receptor precursor
1132	Q53G42	7	14	32.3	337	38610	6.4	MRNA decapping enzyme variant
1132	Q96C86	7	14	32.3	337	38609	6.4	Scavenger mRNA-decapping enzyme DcpS
1133	Q13242	7	16	32.1	221	25542	8.6	Splicing factor, arginine/serine-rich 9
1134	Q9UKD2	7	20	31.8	239	27560	8.3	mRNA turnover protein 4 homolog
1135	Q5T3I2	7	12	31.2	288	31675	7.7	Apolipoprotein A-I-binding protein
1135	Q8NCW5	7	12	31.2	288	31689	7.7	ApoA-I binding protein precursor
1136	O60762	7	22	30.8	260	29634	9.6	Dolichol-phosphate mannosyltransferase
1136	Q5QPK2	7	22	27.9	287	32426	9.1	Dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit
1136	Q5QPK0	7	22	27.2	294	33218	9.1	Dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit
1137	P30040	7	19	30.7	261	28993	7.3	Endoplasmic reticulum protein ERp29 precursor
1138	Q5VYD7	7	9	33.7	252	28491	4.9	HCLS1 associated protein X-1
1138	O00165	7	9	30.5	279	31621	4.9	HS1-associating protein X-1
1139	P62917	7	62	30.4	257	28025	11	60S ribosomal protein L8
1140	Q9GZZ9	7	10	30	404	44863	4.8	Ubiquitin-activating enzyme E1 domain-containing protein 1
1141	Q01105-2	7	35	29.6	277	32103	4.2	Isoform 2 of Q01105
1141	UPI0000161B37	7	35	29.6	277	32134	4.2	SET translocation (myeloid leukemia-associated)
1142	Q9UBP9	7	12	29.6	304	34490	7.9	GULP engulfment adaptor PTB domain-containing protein 1
1143	P13984	7	7	28.5	249	28380	9.2	Transcription initiation factor IIF subunit beta
1143	UPI00004566E9	7	7	28.4	250	28473	9.3	Transcription initiation factor IIF subunit beta (EC 3.6.1.-) (TFIIF- beta) (ATP-dependent helicase GTF2F2) (General transcription factor IIF subunit 2) (Transcription initiation factor RAP30).
1144	UPI0000456411	7	53	30.7	238	25889	7.8	Thioredoxin-dependent peroxide reductase, mitochondrial precursor (EC 1.11.1.15) (Peroxiredoxin-3) (PRX III) (Antioxidant protein 1) (AOP-1) (Protein MER5 homolog) (HBC189).
1144	UPI00001B216B	7	53	30.7	238	25839	7.5	peroxiredoxin 3 isoform b
1144	P30048	7	53	28.5	256	27693	7.8	Thioredoxin-dependent peroxide reductase, mitochondrial precursor
1145	Q9BY43	7	8	28.4	222	25098	4.7	Charged multivesicular body protein 4a
1146	O76071	7	8	28	339	37840	5	Protein CIAO1
1147	O94905	7	18	28	339	37840	5.6	SPFH domain-containing protein 2 precursor
1148	Q8NBJ7	7	19	27.9	301	33857	8	Sulfatase-modifying factor 2 precursor
1148	UPI000013E405	7	19	27.9	301	33843	8	Sulfatase-modifying factor 2 precursor (C-alpha-formyglycine- generating enzyme 2).
1148	UPI0000DAC779	7	19	27.6	304	34290	8.4	sulfatase modifying factor 2 isoform a precursor
1149	Q8NFV4-4	7	17	28.6	308	33863	9.2	Isoform 4 of Q8NFV4
1149	Q8NFV4	7	17	27.9	315	34690	9.5	Abhydrolase domain-containing protein 11
1150	O75937	7	9	27.7	253	29842	9.1	DnaJ homolog subfamily C member 8
1150	UPI0000456194	7	9	26.6	263	30829	8.9	DnaJ homolog subfamily C member 8 (Splicing protein spf31).
1151	O00273	7	10	27.5	331	36522	4.8	DNA fragmentation factor subunit alpha
1151	Q53HN4	7	10	27.5	331	36594	4.8	DNAation factor, 45kDa, alpha polypeptide isoform 1 variant
1152	Q9UBE0	7	21	27.5	346	38450	5.3	SUMO-activating enzyme subunit 1
1153	O96008	7	10	27.4	361	37893	7.3	Probable mitochondrial import receptor subunit TOM40 homolog
1154	P46926	7	18	27.3	289	32668	6.9	Glucosamine-6-phosphate isomerase
1155	O00170	7	10	27	330	37664	6.5	AH receptor-interacting protein
1156	Q9H8Y8	7	13	27	452	47145	4.8	Golgi reassembly-stacking protein 2
1157	Q92905	7	12	26.6	334	37579	6.5	COP9 signalosome complex subunit 5
1158	P82650	7	13	26.4	360	41280	7.9	Mitochondrial 28S ribosomal protein S22
1159	P53367	7	9	26.3	373	41738	6.7	Arfaptin-1
1160	Q53Y37	7	17	26.1	211	23181	4.7	Clathrin, light polypeptide

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
1161	P31942-3	7	33	30	297	31525	7.3	Isoform 3 of P31942
1161	P31942-2	7	33	26.9	331	35239	6.9	Isoform 2 of P31942
1161	P31942	7	33	25.7	346	36926	6.9	Heterogeneous nuclear ribonucleoprotein H3
1161	Q53F48	7	33	25.7	346	36926	7.4	Heterogeneous nuclear ribonucleoprotein H3 isoform a variant
1162	O95861	7	10	25.6	308	33392	5.7	3'(2'),5'-bisphosphate nucleotidase 1
1163	Q6FHU0	7	11	25.4	272	29696	5.8	PSMB8 protein
1163	Q5JNW6	7	11	25.4	272	29770	5.8	Proteasome subunit beta type
1163	P28062	7	11	25	276	30354	7.8	Proteasome subunit beta type 8 precursor
1163	Q5QNR8	7	11	25	276	30354	7.4	Proteasome subunit beta type
1164	Q96D15	7	19	25	328	37493	4.9	Reticulocalbin-3 precursor
1165	P14550	7	13	24.6	325	36573	6.8	Alcohol dehydrogenase [NADP+]
1166	Q05048	7	12	24.6	431	48358	6.6	Cleavage stimulation factor 50 kDa subunit
1167	Q16543	7	25	24.6	378	44468	5.2	Hsp90 co-chaperone Cdc37
1168	P18754	7	16	24.2	421	44969	7.5	Regulator of chromosome condensation
1168	UPI0000E26242	7	16	23.3	438	46753	8.1	regulator of chromosome condensation 1 isoform b
1168	Q6NT97	7	16	22.6	452	48146	8.2	Regulator of chromosome condensation 1
1169	Q9Y305	7	13	23.6	406	46355	8	Acyl-coenzyme A thioesterase 9
1169	UPI0000D61D39	7	13	22.1	434	49270	8.3	Acyl-coenzyme A thioesterase 9 (EC 3.1.2.-) (Acyl-CoA thioesterase 9) (Acyl-CoA thioester hydrolase 9).
1169	UPI000013F264	7	13	21.9	439	49902	8.6	acyl-Coenzyme A thioesterase 2, mitochondrial isoform b
1169	UPI0000D61D38	7	13	21.6	445	50474	8.4	Acyl-coenzyme A thioesterase 9 (EC 3.1.2.-) (Acyl-CoA thioesterase 9) (Acyl-CoA thioester hydrolase 9).
1169	UPI00003D7D31	7	13	21.4	448	50851	8.5	acyl-Coenzyme A thioesterase 2, mitochondrial isoform a
1170	Q53FE8	7	8	23.5	370	40572	5.1	P47 protein isoform a variant
1170	Q9UNZ2	7	8	23.5	370	40573	5.1	NSFL1 cofactor p47
1170	Q5JXA5	7	8	23.4	372	40816	5.1	NSFL1 (P97) cofactor
1171	UPI000006FDB9	7	11	23.7	397	41296	6.7	acetyl-Coenzyme A acetyltransferase 2
1171	Q9BWD1	7	11	23.7	397	41351	6.9	Acetyl-CoA acetyltransferase, cytosolic
1171	Q59GW6	7	11	23.3	404	42136	7.4	Acetyl-CoA acetyltransferase, cytosolic variant
1172	P50502	7	25	23	369	41332	5.3	Hsc70-interacting protein
1173	P68400	7	13	22.8	391	45144	7.7	Casein kinase II subunit alpha
1173	UPI0000D61015	7	13	22.5	395	45682	7.9	Casein kinase II subunit alpha (EC 2.7.11.1) (CK II).
1173	Q5U5J2	7	13	22.4	397	45909	7.9	CSNK2A1 protein
1174	P23258	7	8	22.6	451	51170	6.1	Tubulin gamma-1 chain
1175	Q9Y570	7	8	22	386	42315	6	Protein phosphatase methylesterase 1
1175	UPI0000D62652	7	8	21.9	389	42669	5.8	Protein phosphatase methylesterase 1 (EC 3.1.1.-) (PME-1).
1176	Q96EP5	7	16	21.9	407	43383	8.6	DAZ-associated protein 1
1177	Q99747	7	7	21.8	312	34746	5.4	Gamma-soluble NSF attachment protein
1177	UPI0000456B5E	7	7	21.8	312	34920	5.2	Gamma-soluble NSF attachment protein (SNAP-gamma) (N-ethylmaleimide- sensitive factor attachment protein, gamma).
1178	Q96HC5	7	16	21.9	471	53121	9.1	U2 small nuclear RNA auxiliary factor 2
1178	P26368	7	16	21.7	475	53501	9.1	Splicing factor U2AF 65 kDa subunit (U2 auxiliary factor 65 kDa subunit) (U2 snRNP auxiliary factor large subunit) (hU2AF(65))
1178	UPI0000D6181E	7	16	21.6	477	53728	9.2	Splicing factor U2AF 65 kDa subunit (U2 auxiliary factor 65 kDa subunit) (U2 snRNP auxiliary factor large subunit) (hU2AF(65)).
1179	Q9UM22	7	36	33	224	25437	6.7	Mammalian ependymin-related protein 1 precursor
1179	A4D1W8	7	36	21.5	344	38151	9.6	Upregulated in colorectal cancer gene 1
1179	Q96J80	7	36	21.5	344	38141	9.6	Mammalian ependymin related protein 1
1180	O43237	7	12	21.3	492	54099	6.4	Cytoplasmic dynein 1 light intermediate chain 2
1181	Q15645	7	8	20.6	432	48551	6.1	Thyroid receptor-interacting protein 13
1182	P51570	7	11	20.4	392	42272	6.5	Galactokinase
1183	Q53GI0	7	15	20.2	420	46337	7.2	GDP-mannose pyrophosphorylase A
1183	Q9NWC3	7	15	20.2	420	46351	7.2	CDNA FLJ10137 fis, clone HEMBA1003136, weakly similar to MANNOSE-1- PHOSPHATE GUANYLTRANSFERASE
1183	Q96IJ6	7	15	20.2	420	46291	7.2	GDP-mannose pyrophosphorylase A
1184	Q9P0V9-2	7	13	22.2	454	52593	6.8	Isoform 2 of Q9P0V9
1184	Q86VP5	7	13	19.9	507	58579	7.5	SEPT10 protein
1184	UPI0000456E33	7	13	19.5	519	60191	6.9	Septin-10.
1184	Q9P0V9	7	13	19.5	517	59982	7.1	Septin-10
1184	UPI0000D61215	7	13	18.5	547	63282	6.8	Septin-10.
1185	Q9HAB8	7	7	19.9	311	34005	6.7	Phosphopantothenate--cysteine ligase
1186	UPI0000F0A4F3	7	12	25.9	336	37229	6.5	C-terminal-binding protein 2
1186	P56545	7	12	19.6	445	48945	6.9	C-terminal-binding protein 2
1186	Q86SV0	7	12	19.6	445	48933	6.9	CTBP2 protein
1186	Q5SQP8	7	12	17	513	56102	7	C-terminal binding protein 2
1186	Q5SQP7	7	12	8.8	985	106187	8	C-terminal binding protein 2
1187	P49821-2	7	9	19.6	455	49868	8.2	Isoform 2 of P49821
1187	P49821	7	9	19.2	464	50817	8.2	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial precursor

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
1188	Q5T6J5	7	14	19.1	561	59220	5.1	Ubiquilin 1
1188	Q9UMX0	7	14	18.2	589	62519	5.1	Ubiquilin-1
1189	Q9NZN4	7	21	19	543	61161	6.5	EH domain-containing protein 2
1190	P52594-2	7	10	20.3	522	54182	8.9	Isoform 2 of P52594
1190	P52594	7	10	18.9	562	58260	8.6	Nucleoporin-like protein RIP
1190	P52594-3	7	10	18.9	560	58132	8.6	Isoform 3 of P52594
1191	Q9HCJ6	7	13	18.9	419	45899	5.1	Probable oxidoreductase KIAA1576
1192	P61201	7	7	18.7	443	51597	5.5	COP9 signalosome complex subunit 2
1192	Q53HJ0	7	7	18.7	443	51570	5.5	COP9 constitutive photomorphogenic homolog subunit 2 variant
1192	Q59EL2	7	7	18.4	451	52533	5.5	COP9 constitutive photomorphogenic homolog subunit 2 variant
1192	Q3V3N6	7	7	18.4	450	52405	5.5	16 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A130047E19 product:COP9 (constitutive photomorphogenic) homolog, subunit 2 (Arabidopsis thaliana), full insert sequence (COP9 (Constitutive photomorphogenic) homolog, subunit 2)
1192	UPI00006D3674	7	7	18.3	453	52737	5.5	COP9 signalosome complex subunit 2 (Signalosome subunit 2) (SGN2) (JAB1-containing signalosome subunit 2) (Thyroid receptor-interacting protein 15) (Alien homolog).
1193	Q96CS3	7	11	18.4	445	52624	5.6	UBX domain-containing protein 8
1194	Q16630-3	7	23	21.1	478	52326	6.4	Isoform 3 of Q16630
1194	Q16630	7	23	18.3	551	59210	7.2	Cleavage and polyadenylation specificity factor 6
1194	UPI000006D566	7	23	18.3	551	59209	7.4	cleavage and polyadenylation specific factor 6, 68 kD subunit
1194	Q16630-2	7	23	17.2	588	63471	7.7	Isoform 2 of Q16630
1195	Q9BZZ5-3	7	20	24.7	373	42020	4.8	Isoform 3 of Q9BZZ5
1195	Q9BZZ5-4	7	20	18.4	500	56099	5.9	Isoform 4 of Q9BZZ5
1195	Q5R644	7	20	18.3	504	56770	5.9	Apoptosis inhibitor 5
1195	Q9BZZ5	7	20	18	510	57561	6.1	Apoptosis inhibitor 5
1195	UPI0000D625E5	7	20	17.7	521	58472	7.3	Apoptosis inhibitor 5 (API-5) (Fibroblast growth factor 2-interacting factor) (FIF) (Protein XAGL) (Antiapoptosis clone 11 protein) (AAC- 11).
1196	Q9Y6I3-3	7	12	18.4	550	57504	4.9	Isoform 3 of Q9Y6I3
1196	Q9Y6I3	7	12	18.3	551	57575	4.9	Epsin-1
1196	Q9Y6I3-2	7	12	17.5	576	60293	4.8	Isoform 2 of Q9Y6I3
1197	O75312	7	12	17.9	459	50925	4.7	Zinc-finger protein ZPR1
1198	Q92769	7	16	17.6	488	55364	5.9	Histone deacetylase 2
1199	P16930	7	11	17.4	419	46374	6.9	Fumarylacetoacetase
1200	P36871	7	15	17.4	562	61449	6.8	Phosphoglucomutase-1
1200	UPI0000D61F2F	7	15	17.4	564	61633	6.8	Phosphoglucomutase-1 (EC 5.4.2.2) (Glucose phosphomutase 1) (PGM 1).
1200	Q86U74	7	15	17.4	562	61370	6.6	Phosphoglucomutase 1
1201	P55010	7	18	17.4	431	49223	5.6	Eukaryotic translation initiation factor 5
1201	Q6IBU0	7	18	17.4	431	49152	5.5	EIF5 protein
1202	Q9UPE4	7	17	18.8	415	47366	7.4	Putative mitochondrial inner membrane protein import receptor
1202	O43615	7	17	17.3	452	51356	8.3	Import inner membrane translocase subunit TIM44, mitochondrial precursor
1202	Q53G69	7	17	17.3	452	51324	8.3	Translocase of inner mitochondrial membrane 44 homolog
1203	P23368	7	15	17	584	65444	7.6	NAD-dependent malic enzyme, mitochondrial precursor
1204	P61619-2	7	109	19.1	423	46045	7.3	Isoform 2 of P61619
1204	P61619	7	109	17	476	52265	8.1	Protein transport protein Sec61 subunit alpha isoform 1
1205	P61011	7	10	16.7	504	55705	8.8	Signal recognition particle 54 kDa protein
1206	Q9H0C8	7	17	16.6	392	42907	7.1	Integrin-linked kinase-associated serine/threonine phosphatase 2C
1207	Q7Z3B4	7	11	16.6	507	55436	7	Nucleoporin p54
1207	Q53H29	7	11	16.5	508	55564	7	Nucleoporin 54kDa variant
1208	Q96HE7	7	11	16.5	468	54393	5.7	ERO1-like protein alpha precursor
1209	Q4QQI8	7	8	16.4	608	66316	5.4	RAP1, GTP-GDP dissociation stimulator 1
1209	UPI000004A01F	7	8	16.4	608	66388	5.3	Rap1 GTPase-GDP dissociation stimulator 1 (SMG P21 stimulatory GDP/GTP exchange protein) (SMG GDS protein) (Exchange factor smgGDS).
1210	Q99829	7	17	16.4	537	59059	5.8	Copine-1
1211	Q9H074	7	13	16.1	479	53525	4.8	Polyadenylate-binding protein-interacting protein 1 (Poly(A)-binding protein-interacting protein 1)
1212	O95202	7	13	16	739	83354	6.7	Leucine zipper-EF-hand-containing transmembrane protein 1, mitochondrial precursor
1213	Q8TAF6	7	9	16.7	670	74422	8	Acyl-CoA synthetase 4
1213	O60488	7	9	15.8	711	79188	8.4	Long-chain-fatty-acid--CoA ligase 4
1214	Q13177	7	17	15.8	524	58043	6	Serine/threonine-protein kinase PAK 2
1215	UPI000013E7A3	7	20	18	477	52812	9.7	DNA polymerase-transactivated protein 6 (DNAPTP6), mRNA
1215	Q8WV53	7	20	17.6	488	54050	9.6	DNAPTP6 protein

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
1215	Q53T22	7	20	15.8	545	60234	9.7	Hypothetical protein DKFZP564A2416
1215	UPI000013F0CD	7	20	15.8	546	60362	9.7	DNA polymerase-transactivated protein 6 (DNAPTP6), mRNA
1215	Q9NUQ6	7	20	15.4	558	61759	9.6	CDNA FLJ11202 fis, clone PLACE1007746
1215	Q9NTW4	7	20	15.4	558	61728	9.7	Hypothetical protein DKFZp564A2416
1216	Q5PU80	7	9	15.8	549	61957	9.1	Nucleostemin
1216	Q9BVP2	7	9	15.8	549	61997	9.1	Guanine nucleotide-binding protein-like 3
1217	Q8NA80	7	17	16.9	534	58309	9.2	CDNA FLJ35762 fis, clone TESTI2004793, moderately similar to Homo sapiens NY-REN-2 antigen mRNA
1217	UPI0000D624D2	7	17	15.5	579	63076	9	YTH domain family protein 3.
1217	Q7Z739	7	17	15.4	585	63861	9	YTH domain family protein 3
1218	P33240-2	7	12	15.7	560	59251	6.8	Isoform 2 of P33240
1218	P33240	7	12	15.3	577	60959	6.8	Cleavage stimulation factor 64 kDa subunit
1218	UPI0000D61DA0	7	12	14.4	611	64388	7.5	Cleavage stimulation factor 64 kDa subunit (CSTF 64 kDa subunit) (CF-1 64 kDa subunit) (CstF-64).
1219	Q8TAT6	7	20	14.8	608	68120	6.4	Nuclear protein localization protein 4 homolog
1219	UPI0000D623AF	7	20	14.8	607	67987	6.4	Nuclear protein localization protein 4 homolog (Protein NPL4).
1219	UPI000006F9F7	7	20	14.8	608	68183	6.3	nuclear protein localization 4
1219	UPI0000D623B0	7	20	14.6	616	69360	6.7	Nuclear protein localization protein 4 homolog (Protein NPL4).
1219	Q8TAT6-2	7	20	14.6	617	69461	6.7	Isoform 2 of Q8TAT6
1220	Q6PJG6	7	9	14.7	821	88119	5.3	HEAT repeat domain-containing protein C7orf27 precursor
1220	UPI0000001C11	7	9	14.7	821	88020	5.2	hypothetical protein LOC221927
1221	O94826	7	13	14.3	608	67455	7.1	Mitochondrial precursor proteins import receptor
1221	Q6P0M2	7	13	14.3	607	67398	7.1	Translocase of outer mitochondrial membrane 70 homolog A
1222	Q99442	7	34	14	399	45862	7.1	Translocation protein SEC62
1223	Q27J83	7	21	14	707	77762	5.9	Chromosome 14 open reading frame 173 isoform 1
1223	Q27J81	7	21	13.8	716	78769	5.6	Uncharacterized protein C14orf173
1224	Q9UG63	7	11	13.8	623	71290	7.4	ATP-binding cassette sub-family F member 2
1225	Q8N8S7-2	7	20	13.7	570	63925	6.4	Isoform 2 of Q8N8S7
1225	Q8N8S7	7	20	13.2	591	66510	6.9	Protein enabled homolog
1225	UPI0000458AAB	7	20	9.5	817	88946	7.9	Protein enabled homolog.
1226	Q5BKZ1	7	14	12.9	582	65654	5.2	Zinc finger protein 326
1227	Q5R914	7	15	12.9	511	57659	6.3	Serine/threonine protein phosphatase
1228	Q68E10	7	7	13.2	889	98916	6	Hypothetical protein DKFZp686M1669
1228	UPI0000E8DA43	7	7	13	902	100479	6	Hexokinase-2
1228	P52789	7	7	12.8	917	102380	6.1	Hexokinase-2
1229	P08237	7	11	12.6	780	85182	8	6-phosphofructokinase, muscle type
1229	Q6ZTT1	7	11	11.5	851	93220	8	CDNA FLJ44241 fis, clone THYMU3008436, highly similar to 6- phosphofructokinase, muscle type
1230	Q9P2I0	7	9	12.3	782	88487	5.1	Cleavage and polyadenylation specificity factor subunit 2
1231	Q5T207	7	43	12	689	76744	5.7	Nicastrin
1231	Q92542	7	43	11.7	709	78411	6	Nicastrin precursor
1232	O43747	7	19	11.6	822	91391	6.8	AP-1 complex subunit gamma-1
1232	UPI000013E60C	7	19	11.6	822	91351	6.8	adaptor-related protein complex 1, gamma 1 subunit isoform b
1232	UPI000016A4AD	7	19	11.5	825	91723	6.8	adaptor-related protein complex 1, gamma 1 subunit isoform a
1232	Q8IY97	7	19	11.5	825	91757	6.8	Adaptor-related protein complex 1, gamma 1 subunit
1233	P55290	7	21	10.9	713	78287	5	Cadherin-13 precursor
1234	Q96T76	7	22	10.8	1030	113275	6.4	MMS19-like protein
1234	UPI000013DDF7	7	22	10.8	1030	113289	6.4	MMS19-like protein (hMMS19) (MET18 homolog).
1235	O94804	7	18	9.9	968	112135	6.9	Serine/threonine-protein kinase 10
1235	UPI0000457386	7	18	9.9	974	112748	6.8	Serine/threonine-protein kinase 10 (EC 2.7.11.1) (Lymphocyte-oriented kinase).
1235	Q6NSK0	7	18	9.9	968	112121	6.9	Serine/threonine kinase 10
1236	Q6WCQ1	7	12	9.6	1024	116446	6.2	Myosin phosphatase Rho-interacting protein
1236	UPI0000366BAD	7	12	9.6	1025	116533	6.2	myosin phosphatase-Rho interacting protein isoform 2
1236	Q6WCQ1-2	7	12	9.5	1037	118016	6.4	Isoform 2 of Q6WCQ1
1236	UPI0000200A77	7	12	9.4	1038	118103	6.4	myosin phosphatase-Rho interacting protein isoform 1
1237	Q59FL7	7	18	9.9	807	89176	5.4	Neural cell adhesion molecule 1, 120 kDa isoform variant
1237	P13591	7	18	9.4	848	93361	4.9	Neural cell adhesion molecule 1, 140 kDa isoform precursor
1237	UPI0000E445E3	7	18	9.3	858	94574	4.9	neural cell adhesion molecule 1 isoform 2
1237	Q86X47	7	18	9.3	858	94601	4.9	Neural cell adhesion molecule 1
1238	Q96T88	7	12	9.3	793	89814	7.6	E3 ubiquitin-protein ligase UHRF1

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1238	UPI0000456BDE	7	12	9.3	792	89743	7.6	E3 ubiquitin-protein ligase UHRF1 (EC 6.3.2.-) (Ubiquitin-like PHD and RING finger domain-containing protein 1) (Ubiquitin-like-containing PHD and RING finger domains protein 1) (Inverted CCAAT box-binding protein of 90 kDa) (Transcription factor ICBP90)
1238	UPI0000D48B65	7	12	9.2	806	91100	7.4	ubiquitin-like, containing PHD and RING finger domains, 1 isoform 2
1239	A4D169	7	19	9.1	856	97687	6.5	Oxysterol binding protein-like 3
1239	Q9H4L5	7	19	8.8	887	101224	6.9	Oxysterol-binding protein-related protein 3
1240	Q6PJE1	7	9	12.2	686	79971	5.3	NUP107 protein
1240	P57740	7	9	9.1	925	106374	5.4	Nuclear pore complex protein Nup107
1241	UPI0000D620CF	7	12	9.4	1084	120372	5.2	Nuclear pore complex protein Nup133 (Nucleoporin Nup133) (133 kDa nucleoporin).
1241	Q8WUM0	7	12	8.8	1156	128979	5.1	Nuclear pore complex protein Nup133
1242	UPI00001AFA18	7	11	8.9	979	111479	7.6	Probable ATP-dependent RNA helicase DHX36 (EC 3.6.1.-) (DEAH box protein 36) (MLE-like protein 1) (RNA helicase associated with AU-rich element ARE).
1242	Q9H2U1-3	7	11	8.9	979	111495	7.6	Isoform 3 of Q9H2U1
1242	Q9H2U1	7	11	8.6	1008	114776	7.7	Probable ATP-dependent RNA helicase DHX36
1242	UPI000013ED25	7	11	8.6	1008	114760	7.7	Probable ATP-dependent RNA helicase DHX36 (EC 3.6.1.-) (DEAH box protein 36) (MLE-like protein 1) (RNA helicase associated with AU-rich element ARE).
1243	Q9Y6Y8	7	13	8.6	1000	111076	5.5	SEC23-interacting protein
1244	Q92974	7	32	9.4	893	101174	8.4	Rho/Rac guanine nucleotide exchange factor 2
1244	Q9H023	7	32	8.8	958	108242	6.9	Hypothetical protein DKFZp547L106 (Rho/rac guanine nucleotide exchange factor (GEF) 2)
1244	Q5VY92	7	32	8.5	986	111543	7.3	Rho/rac guanine nucleotide exchange factor (GEF) 2
1244	Q8TDA3	7	32	8.5	985	111471	7.3	Guanine nucleotide exchange factor GEF-H1 (Rho/rac guanine nucleotide exchange factor (GEF) 2)
1244	Q5VY93	7	32	8.5	987	111493	7	Rho/rac guanine nucleotide exchange factor (GEF) 2
1245	Q14157	7	14	8.4	1087	114534	7.1	Ubiquitin-associated protein 2-like
1245	UPI00000735C4	7	14	8.4	1087	114543	7.1	ubiquitin associated protein 2-like
1246	O76046	7	18	8.3	1246	137794	6.1	Putative RNA helicase Ski2w
1246	Q9NPK3	7	18	8.3	1245	137624	6.1	DJ34F7.7 (Superkiller viralicidic activity 2 (S. cerevisiae homolog)- like (SKI2W))
1246	Q5ST66	7	18	8.3	1246	137755	6.1	Superkiller viralicidic activity 2-like
1246	Q5JP73	7	18	8.3	1246	137737	6.1	Superkiller viralicidic activity 2-like
1247	P08648	7	13	8	1049	114536	5.8	Integrin alpha-5 precursor (Fibronectin receptor subunit alpha) (Integrin alpha-F) (VLA-5) (CD49e antigen) [Contains: Integrin alpha-5 heavy chain; Integrin alpha-5 light chain]
1248	Q5VTR2	7	10	7.9	975	113662	5.9	E3 ubiquitin-protein ligase BRE1A
1248	UPI000013DE3A	7	10	7.9	977	113977	6	Ubiquitin-protein ligase BRE1A (EC 6.3.2.-) (BRE1-A) (hBRE1) (RING finger protein 20).
1249	O15042-3	7	18	12.9	620	72524	7.6	Isoform 3 of O15042
1249	O15042	7	18	7.8	1029	118292	8.5	U2-associated protein SR140
1249	O15042-2	7	18	7.8	1028	118235	8.5	Isoform 2 of O15042
1250	Q9NTZ6	7	10	7.8	932	97396	8.6	RNA-binding protein 12
1251	Q14126	7	10	7.7	1117	122385	5.3	Desmoglein-2 precursor
1251	Q4KKU6	7	10	7.7	1118	122294	5.2	Desmoglein 2
1252	Q9HAV4	7	22	7.7	1204	136311	5.8	Exportin-5
1252	UPI00004A3AA6	7	22	7.7	1204	136260	5.8	Exportin-5 (Exp5) (Ran-binding protein 21).
1253	Q03701	7	18	7.1	1054	120988	5.9	CCAAT/enhancer-binding protein zeta
1253	UPI0000072AAB	7	18	7.1	1054	120974	5.9	CCAAT/enhancer binding protein zeta
1254	O15067	7	11	7	1338	144664	5.8	Phosphoribosylformylglycinamidine synthase
1254	UPI00001A95E5	7	11	7	1338	144734	5.8	phosphoribosylformylglycinamidine synthase
1255	Q0VG08	7	9	7.1	1233	133629	7.4	SEC24 related gene family, member B
1255	O95487	7	9	6.9	1268	137789	6.7	Protein transport protein Sec24B
1255	UPI00004F6ED7	7	9	6.9	1268	137417	6.7	SEC24 (S. cerevisiae) homolog B isoform a
1255	UPI00001AE8CE	7	9	6.9	1266	137573	6.7	Protein transport protein Sec24B (SEC24-related protein B).
1256	P82094	7	8	6.9	1093	123171	5	TATA element modulatory factor
1256	UPI0000457136	7	8	6.9	1091	122812	5	TATA element modulatory factor (TMF).
1256	Q59GK0	7	8	6.8	1096	123027	4.9	TATA element modulatory factor 1 variant
1257	UPI0000D625ED	7	22	7.5	1316	149100	5.6	Nuclear pore complex protein Nup160 (Nucleoporin Nup160) (160 kDa nucleoporin).
1257	Q12769	7	22	7.5	1316	149001	5.6	Nuclear pore complex protein Nup160
1257	Q08AD3	7	22	6.9	1436	162091	5.5	Nucleoporin 160kDa
1257	UPI0000185FEB	7	22	6.9	1436	162121	5.5	nucleoporin 160kDa
1258	Q96L67	7	11	8.2	948	108513	5	Nardilysin
1258	O43847	7	11	6.8	1150	131571	5	Nardilysin precursor
1258	UPI0000458A54	7	11	6.8	1151	131700	5	Nardilysin precursor (EC 3.4.24.61) (N-arginine dibasic convertase) (NRD convertase) (NRD-C).

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
1258	UPI00004561DA	7	11	6.8	1150	131572	5	Nardilysin precursor (EC 3.4.24.61) (N-arginine dibasic convertase) (NRD convertase) (NRD-C).
1258	UPI000004EC94	7	11	6.4	1219	139328	5	nardilysin (N-arginine dibasic convertase)
1258	Q5VUL1	7	11	6.4	1219	139413	5	Nardilysin
1258	O43847-2	7	11	6.4	1218	139284	5	Isoform 2 of O43847
1259	P55011-3	7	14	6.9	1196	129679	6.5	Isoform 2 of P55011
1259	P55011	7	14	6.8	1212	131447	6.4	Solute carrier family 12 member 2 (Bumetanide-sensitive sodium- (potassium)-chloride cotransporter 1)
1259	UPI0000D61674	7	14	6.8	1211	131391	6.5	Solute carrier family 12 member 2 (Bumetanide-sensitive sodium- (potassium)-chloride cotransporter 1) (Basolateral Na-K-Cl symporter).
1260	Q9UP95-2	7	17	6.8	1068	118619	6.7	Isoform 2 of Q9UP95
1260	Q9UP95	7	17	6.7	1085	120650	6.4	Solute carrier family 12 member 4
1261	P30876	7	9	6.6	1174	133896	6.9	DNA-directed RNA polymerase II 140 kDa polypeptide
1262	UPI00001AEDC0	7	11	6.5	1248	138907	6.2	Neural cell adhesion molecule L1 precursor (N-CAM L1) (CD171 antigen).
1262	P32004-2	7	11	6.5	1253	139517	6.2	Isoform 2 of P32004
1262	P32004	7	11	6.4	1257	140003	6.2	Neural cell adhesion molecule L1 precursor
1263	UPI0000457885	7	14	6.4	1231	141328	5.4	Cohesin subunit SA-2 (Stromal antigen 2) (SCC3 homolog 2).
1263	Q8N3U4	7	14	6.4	1231	141326	5.4	Cohesin subunit SA-2
1263	Q6MZM4	7	14	6.4	1231	141306	5.4	Hypothetical protein DKFZp686P16143
1263	Q6MZM3	7	14	6.4	1231	141301	5.4	Hypothetical protein DKFZp686C21148
1263	Q5JTI5	7	14	6.2	1268	145751	5.5	Stromal antigen 2
1263	UPI0000D61DCF	7	14	6.2	1268	145753	5.5	Cohesin subunit SA-2 (Stromal antigen 2) (SCC3 homolog 2).
1263	Q6MZP3	7	14	6.2	1268	145675	5.5	Hypothetical protein DKFZp686I05169
1263	Q68DE9	7	14	6.2	1268	145781	5.5	Hypothetical protein DKFZp781H1753
1264	UPI0000D61296	7	14	6.3	1252	135490	8.8	Ras-associated and pleckstrin homology domains-containing protein 1 (RAPH1) (Lamellipodin) (Proline-rich EVH1 ligand 2) (PREL-2) (Protein RMO1) (Amyotrophic lateral sclerosis 2 chromosomal region candidate 9 gene protein).
1264	UPI000020940F	7	14	6.3	1250	135256	8.9	Ras association and pleckstrin homology domains 1 isoform 1
1264	Q70E73-10	7	14	6.3	1250	135242	8.9	Isoform RMO1
1264	Q70E73	7	14	6.1	1302	141165	8.9	Ras-associated and pleckstrin homology domains-containing protein 1
1264	UPI0000D61297	7	14	6.1	1304	141414	8.9	Ras-associated and pleckstrin homology domains-containing protein 1 (RAPH1) (Lamellipodin) (Proline-rich EVH1 ligand 2) (PREL-2) (Protein RMO1) (Amyotrophic lateral sclerosis 2 chromosomal region candidate 9 gene protein).
1265	Q92896	7	20	6.1	1179	134593	6.9	Golgi apparatus protein 1 precursor
1265	Q6P9D1	7	20	6	1203	137222	6.9	Golgi apparatus protein 1
1266	Q92626	7	17	5.9	1496	167210	7.3	Peroxidasin homolog
1267	P30622-2	7	7	5.5	1392	156781	5.4	Isoform Short of P30622
1267	A0AVD3	7	7	5.4	1438	162246	5.4	CLIP1 protein
1267	Q17RS4	7	7	5.4	1438	162270	5.4	CLIP1 protein
1267	P30622	7	7	5.4	1427	160989	5.4	CAP-Gly domain-containing linker protein 1
1268	UPI0000D612FA	7	14	4.6	1676	187847	6.7	Tight junction protein ZO-1 (Zonula occludens 1 protein) (Zona occludens 1 protein) (Tight junction protein 1).
1268	Q6MZU1	7	14	4.6	1692	189616	6.8	Hypothetical protein DKFZp686A1195
1268	Q07157-2	7	14	4.6	1668	186965	6.8	Isoform Short of Q07157
1268	Q07157	7	14	4.4	1748	195457	6.7	Tight junction protein ZO-1
1268	UPI0000D612F9	7	14	4.4	1736	194834	6.8	Tight junction protein ZO-1 (Zonula occludens 1 protein) (Zona occludens 1 protein) (Tight junction protein 1).
1269	Q14CF1	7	37	5.1	1722	192074	6.5	TRIP12 protein
1269	Q14669	7	37	4.4	1992	220432	8.5	Probable E3 ubiquitin-protein ligase TRIP12
1269	UPI0000456F1C	7	37	4.4	1991	220245	8.5	Thyroid receptor-interacting protein 12 (TRIP12).
1269	Q14CA3	7	37	4.3	2040	225518	8.7	TRIP12 protein
1270	Q14997	7	12	4.1	1843	211332	6.9	Proteasome activator complex subunit 4
1271	UPI0000367131	7	9	3.6	2184	255638	5.4	Golgin subfamily A member 4 (Trans-Golgi p230) (256 kDa golgin) (Golgin-245) (Protein 72.1).
1271	Q13439-2	7	9	3.6	2185	255737	5.4	Isoform 2 of Q13439
1271	Q13439	7	9	3.5	2230	261137	5.4	Golgin subfamily A member 4
1271	Q13439-4	7	9	3.5	2228	260948	5.4	Isoform 4 of Q13439
1271	Q13439-3	7	9	3.5	2223	260322	5.4	Isoform 3 of Q13439
1272	Q8WUH6	6	21	79.3	116	11748	9.3	Uncharacterized protein C12orf23
1273	Q9Y5L4	6	15	62.1	95	10500	8.2	Mitochondrial import inner membrane translocase subunit Tim13
1274	O60361	6	49	61.3	137	15529	8.6	Putative nucleoside diphosphate kinase
1275	P41567	6	23	61.1	113	12732	7.5	Eukaryotic translation initiation factor 1
1276	P99999	6	77	55.2	105	11749	9.6	Cytochrome c
1277	Q9Y3B4	6	13	53.6	125	14585	9.4	Pre-mRNA branch site protein p14

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
1278	P62244	6	76	53.1	130	14839	10.1	40S ribosomal protein S15a
1279	O14737	6	34	52.8	125	14285	6	Programmed cell death protein 5
1280	Q2PFU1	6	11	51.2	129	14665	4.9	Huntingtin-interacting protein HYPK
1280	Q9NX55	6	11	37.7	175	19332	5.4	Huntingtin-interacting protein HYPK
1281	Q9BTQ7	6	107	52.2	134	14150	10.3	Similar to ribosomal protein L23
1281	P62829	6	107	50	140	14865	10.5	60S ribosomal protein L23
1281	UPI0000D62314	6	107	50	140	14811	10.4	60S ribosomal protein L23 (Ribosomal protein L17).
1282	Q4W5L2	6	10	67.6	102	10190	9.5	Hypothetical protein SNCA
1282	P37840-2	6	10	61.6	112	11372	8.3	Isoform 2
1282	P37840	6	10	49.3	140	14460	4.7	Alpha-synuclein
1283	P62316	6	95	49.2	118	13527	9.9	Small nuclear ribonucleoprotein Sm D2
1284	O15212	6	9	48.8	129	14583	8.9	Prefoldin subunit 6
1285	P30050	6	59	47.9	165	17819	9.4	60S ribosomal protein L12
1285	UPI0000D6190D	6	59	34.5	229	24724	9.9	60S ribosomal protein L12.
1286	O75964	6	52	47.6	103	11428	9.6	ATP synthase subunit g, mitochondrial
1287	Q13232	6	7	47.3	169	19015	7.8	Nucleoside diphosphate kinase 3
1288	Q8N5N7	6	11	46.8	158	18325	7.9	Mitochondrial 39S ribosomal protein L50
1289	P30043	6	22	46.6	206	22119	7.6	Flavin reductase
1289	UPI000013D3F5	6	22	45.5	211	22594	7.6	Flavin reductase (EC 1.5.1.30) (FR) (NADPH-dependent diaphorase) (NADPH-flavin reductase) (FLR) (Biliverdin reductase B) (EC 1.3.1.24) (BVR-B) (Biliverdin-IX beta-reductase) (Green heme-binding protein) (GHBP).
1290	Q9ULC4	6	18	46.4	181	20555	8.8	Malignant T cell amplified sequence 1
1291	Q15370	6	20	45.8	118	13133	4.9	Transcription elongation factor B polypeptide 2
1291	UPI0000353500	6	20	33.5	161	17911	6.1	elongin B isoform b
1292	P24666	6	18	45.6	158	18042	6.8	Low molecular weight phosphotyrosine protein phosphatase
1292	Q59EH3	6	18	43.6	165	18698	7.9	Acid phosphatase 1 isoform c variant
1293	Q9Y5S9	6	29	45.4	174	19889	5.7	RNA-binding protein 8A
1294	Q8N5K1	6	9	50.4	135	15278	9.6	Zinc finger, CDGSH-type domain 2
1294	Q7Z3D5	6	9	45.3	150	16793	9.4	Zinc finger CDGSH domain-containing protein 2
1295	P30405	6	19	44.4	207	22040	9.4	Peptidyl-prolyl cis-trans isomerase, mitochondrial precursor
1296	P16104	6	108	44.1	143	15145	10.7	Histone H2A.x
1297	O43324	6	12	43.7	174	19811	8.6	Eukaryotic translation elongation factor 1 epsilon-1
1298	Q9NVJ2	6	21	43.5	186	21539	8.4	ADP-ribosylation factor-like protein 8B
1299	P14927	6	23	43.2	111	13530	8.8	Ubiquinol-cytochrome c reductase complex 14 kDa protein
1300	Q53G62	6	7	42.8	187	20771	9.3	Mitochondrial ribosomal protein S28 variant
1300	Q9Y2Q9	6	7	42.8	187	20843	9.1	Mitochondrial 28S ribosomal protein S28
1301	Q15819	6	42	41.4	145	16363	8	Ubiquitin-conjugating enzyme E2 variant 2
1302	Q6IAA8	6	15	41	161	17745	5.1	UPF0404 protein C11orf59
1303	P24534	6	83	40.9	225	24764	4.7	Elongation factor 1-beta
1303	UPI000013DA8E	6	83	40.9	225	24932	4.7	PREDICTED: similar to eukaryotic translation elongation factor 1 beta 2
1304	Q9NWU2	6	8	40.8	228	26749	5	Protein C20orf11
1305	P51970	6	10	40.7	172	20105	7.6	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8
1306	Q9UBI1	6	10	40	195	22151	6	COMM domain-containing protein 3
1307	P36404	6	9	39.7	184	20878	6.4	ADP-ribosylation factor-like protein 2
1308	P36405	6	14	39.6	182	20456	7.2	ADP-ribosylation factor-like protein 3
1308	Q53X83	6	14	39.6	182	20474	7.2	ARL3 protein
1309	P20338	6	12	39	213	23871	6.1	Ras-related protein Rab-4A
1309	Q5T7P7	6	12	38.1	218	24390	6.1	RAB4A, member RAS oncogene family
1309	Q53GC2	6	12	38.1	218	24332	6.6	RAB4A, member RAS oncogene family variant
1309	UPI0000D620CE	6	12	37.9	219	24446	7.2	Protein SPHAR (S-phase response protein).
1309	UPI0000D620CD	6	12	37.9	219	24432	6.6	Protein SPHAR (S-phase response protein).
1310	P62807	6	285	39.2	125	13819	10.3	Histone H2B type 1-C/E/F/G/I
1310	A0AVI3	6	285	38.9	126	13916	10.3	H2B histone family, member S
1310	Q99880	6	285	38.9	126	13952	10.3	Histone H2B type 1-L
1310	Q99879	6	285	38.9	126	13989	10.3	Histone H2B type 1-M
1310	Q99877	6	285	38.9	126	13922	10.3	Histone H2B type 1-N
1310	Q93079	6	285	38.9	126	13892	10.3	Histone H2B type 1-H
1310	Q5QNW6	6	285	38.9	126	13920	10.3	Histone H2B type 2-F
1310	P58876	6	285	38.9	126	13936	10.3	Histone H2B type 1-D
1310	P57053	6	285	38.9	126	13944	10.4	Histone H2B type F-S
1310	O60814	6	285	38.9	126	13890	10.3	Histone H2B type 1-K
1311	O00161	6	17	38.9	211	23354	5	Synaptosomal-associated protein 23
1312	P49720	6	37	38.5	205	22949	6.5	Proteasome subunit beta type 3
1313	UPI0000251F42	6	45	38.7	124	13614	10.1	PREDICTED: similar to 40S ribosomal protein S25
1313	UPI000013DA0C	6	45	38.7	124	13615	10	PREDICTED: similar to 40S ribosomal protein S25
1313	P62851	6	45	38.4	125	13742	10.1	40S ribosomal protein S25
1314	P46783	6	66	38.2	165	18898	10.2	40S ribosomal protein S10
1315	Q502X2	6	17	38.2	186	21233	4.8	Diablo homolog
1315	Q9NR28	6	17	29.7	239	27131	5.9	Diablo homolog, mitochondrial precursor
1316	Q9UBQ5	6	29	37.2	218	25060	4.9	Eukaryotic translation initiation factor 3 subunit 12
1317	Q969H8	6	47	37	173	18795	6.7	Uncharacterized protein C19orf10 precursor
1318	P49207	6	39	36.8	117	13293	11.5	60S ribosomal protein L34

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1319	Q9BYD1	6	11	36.5	178	20692	9.1	39S ribosomal protein L13, mitochondrial
1320	P62277	6	58	36.4	151	17222	10.5	40S ribosomal protein S13
1321	P28070	6	29	35.6	264	29204	6	Proteasome subunit beta type 4 precursor
1321	Q6IBI4	6	29	35.6	264	29190	6	Proteasome subunit beta type
1322	P62256	6	15	35.5	183	20655	4.7	Ubiquitin-conjugating enzyme E2 H
1323	P21291	6	23	35.2	193	20567	8.6	Cysteine and glycine-rich protein 1
1324	Q00169	6	6	35.2	270	31806	6.5	Phosphatidylinositol transfer protein alpha isoform
1325	P61086	6	11	34.5	200	22407	5.4	Ubiquitin-conjugating enzyme E2-25 kDa (EC 6.3.2.19) (Ubiquitin- protein ligase) (Ubiquitin carrier protein) (E2(25K))
1326	P05090	6	37	34.4	189	21276	5.1	Apolipoprotein D precursor
1327	P51148	6	59	34.3	216	23483	8.4	Ras-related protein Rab-5C
1328	Q86V81	6	41	33.9	257	26888	11.2	THO complex subunit 4
1329	P46779	6	60	33.6	137	15747	12	60S ribosomal protein L28
1330	Q08ES8	6	48	33.3	177	20094	9.6	Cell growth-inhibiting protein 34
1330	P62913-2	6	48	33.3	177	20124	9.6	Isoform 2 of P62913
1330	P62913	6	48	33.1	178	20252	9.6	60S ribosomal protein L11
1331	Q9UL25	6	29	32.9	225	24348	7.9	Ras-related protein Rab-21
1332	Q9UES0	6	19	34	191	21607	6.5	SNARE protein Ykt6
1332	O15498	6	19	32.8	198	22418	6.9	Synaptobrevin homolog YKT6
1333	Q9Y5Z4	6	11	32.7	205	22875	4.6	Heme-binding protein 2
1334	P18621	6	112	32.6	184	21397	10.2	60S ribosomal protein L17
1334	Q6NZ54	6	112	32.6	184	21416	10.2	Ribosomal protein L17
1334	UPI0000456877	6	112	32.4	185	21441	10.1	60S ribosomal protein L17 (L23).
1335	Q13155	6	11	32.5	320	35349	8.2	Multisynthetase complex auxiliary component p38
1336	Q85KS8	6	41	32.2	227	25566	4.8	Cytochrome oxidase subunit II
1337	P40855	6	8	32.1	299	32807	4.3	Peroxisomal biogenesis factor 19
1338	Q9UK41	6	16	32.1	221	25425	5.5	Vacuolar protein sorting-associated protein 28 homolog
1339	P35625	6	18	31.3	211	24145	8.7	Metalloproteinase inhibitor 3 precursor
1340	Q53S50	6	8	32.9	249	28345	6.5	Hypothetical protein MTX2
1340	Q8IZ68	6	8	32.4	253	28823	6.5	Metaxin 2
1340	O75431	6	8	31.2	263	29763	6.3	Metaxin-2
1341	Q53G20	6	44	31.2	218	23645	10.9	Ribosomal protein L14 variant
1342	Q9NQ88	6	16	31.1	270	30063	7.7	Uncharacterized protein C12orf5
1343	Q15286	6	28	30.8	201	23025	8.3	Ras-related protein Rab-35
1343	UPI0000456691	6	28	30.8	201	23053	8	Ras-related protein Rab-35 (Rab-1C) (GTP-binding protein RAY).
1344	O95292	6	46	30.5	243	27228	7.3	Vesicle-associated membrane protein-associated protein B/C
1345	Q9HCT2	6	9	30.5	187	21991	5.6	Core binding factor beta isoform PEBP2B
1346	Q9GZQ3	6	6	30.4	224	24670	7	COMM domain-containing protein 5
1347	Q9UPY8	6	8	30.2	281	31982	5.5	Microtubule-associated protein RP/EB family member 3
1348	P62266	6	62	30.1	143	15808	10.5	40S ribosomal protein S23
1348	UPI00005E9ED6	6	62	30.1	143	15790	10.5	40S ribosomal protein S23.
1349	Q96HY6	6	9	29.6	314	35611	5.1	Uncharacterized protein C20orf116 precursor
1349	UPI0000456F5C	6	9	29.6	314	35595	5.2	Uncharacterized protein C20orf116 precursor.
1350	Q15056	6	19	29	248	27385	7.2	Eukaryotic translation initiation factor 4H
1351	P08579	6	27	28.9	225	25486	9.7	U2 small nuclear ribonucleoprotein B''
1352	Q6IAX4	6	36	28.8	208	23562	8.9	RTN1 protein
1352	Q9BQ59	6	36	28.8	208	23576	8.9	Reticulon 1
1353	P09496-2	6	22	28.4	218	23662	4.5	Isoform Non
1354	P52597	6	15	28.4	415	45672	5.6	Heterogeneous nuclear ribonucleoprotein F
1355	P68402	6	26	28.4	229	25569	5.9	Platelet-activating factor acetylhydrolase IB subunit beta
1356	P39748	6	10	28.2	380	42593	8.6	Flap endonuclease 1
1357	A3KFL4	6	8	27.8	263	29408	7.2	Exosome component 2
1357	Q13868	6	8	24.9	293	32789	7.5	Exosome complex exonuclease RRP4
1358	Q9BSQ6	6	49	27.9	201	23375	10.9	RPL13A protein
1358	P40429	6	49	27.6	203	23577	10.9	60S ribosomal protein L13a
1358	UPI000013DB4D	6	49	27.6	203	23619	10.9	PREDICTED: similar to ribosomal protein L13a isoform 1
1358	Q5QTS3	6	49	27.6	203	23662	11	FWP004
1358	Q53H34	6	49	27.6	203	23558	10.9	Ribosomal protein L13a variant
1359	Q13630	6	13	27.4	321	35893	6.6	GDP-L-fucose synthetase (EC 1.1.1.271) (Protein FX) (Red cell NADP(H)- binding protein)
1360	Q14696	6	20	27.4	234	26077	7.8	Mesoderm development candidate 2
1361	Q8WXX5	6	9	26.9	260	29910	5.7	DnaJ homolog subfamily C member 9
1362	Q6IN49	6	10	26.8	332	37490	7.9	Cysteine and histidine-rich domain-containing protein 1
1363	Q5VWZ2	6	11	26.6	237	26316	7.8	Lysophospholipase-like protein 1
1363	UPI00000709FC	6	11	26.6	237	26334	7.8	lysophospholipase-like 1
1364	P04183	6	8	26.5	234	25469	8.5	Thymidine kinase, cytosolic
1364	UPI0000F58EFA	6	8	26.5	234	25354	8.5	Thymidine kinase
1364	UPI0000161B4B	6	8	26.5	234	25501	8.5	thymidine kinase 1, soluble
1365	Q13505	6	9	26.5	317	35777	6.3	Metaxin-1
1366	Q96LJ7	6	7	26.5	313	33909	7.8	Dehydrogenase/reductase SDR family member 1
1367	O95336	6	24	26.4	258	27547	6.1	6-phosphogluconolactonase

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
1368	O00625	6	12	26.2	290	32113	6.9	Pirin
1368	Q6FHD2	6	12	26.2	290	32157	6.8	PIR protein
1369	Q9H4A6	6	15	26.2	298	33811	6.4	Golgi phosphoprotein 3
1370	Q15006	6	17	25.9	297	34833	6.6	Tetratricopeptide repeat protein 35
1370	Q53HG5	6	17	25.9	297	34761	6.8	KIAA0103 variant
1371	Q59FE1	6	7	25.9	243	27829	7.5	Eukaryotic translation initiation factor 4E member 2 variant
1371	O60573	6	7	25.7	245	28362	8.9	Eukaryotic translation initiation factor 4E type 2
1371	UPI0000D612CB	6	7	24.7	255	29289	8	Eukaryotic translation initiation factor 4E type 2 (eIF4E type 2) (eIF-4E type 2) (mRNA cap-binding protein type 3) (Eukaryotic translation initiation factor 4E-like 3) (Eukaryotic translation initiation factor 4E homologous protein) (mRNA cap-binding pro
1372	P32322	6	8	25.7	319	33361	7.6	Pyrroline-5-carboxylate reductase 1
1373	P48556	6	16	25.7	257	30005	7.3	26S proteasome non-ATPase regulatory subunit 8
1373	Q5U0B3	6	16	25.7	257	29922	7.3	Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 8
1374	O15305	6	11	25.6	246	28082	6.8	Phosphomannomutase 2
1375	Q16629-3	6	70	46.2	132	15257	9.6	Isoform 3 of Q16629
1375	Q16629-2	6	70	45.2	135	15573	9.8	Isoform 2 of Q16629
1375	UPI000013D48B	6	70	44.5	137	15763	9.8	Splicing factor, arginine/serine-rich 7 (Splicing factor 9G8).
1375	Q16629	6	70	25.6	238	27367	11.8	Splicing factor, arginine/serine-rich 7
1376	Q9BUN8	6	20	25.5	251	28801	9.5	Derlin-1
1377	P62993	6	11	25.3	217	25206	6.3	Growth factor receptor-bound protein 2
1377	Q6ICN0	6	11	25.3	217	25148	6.5	GRB2 protein
1378	Q99729-3	6	48	29.5	285	30588	7.9	Isoform 3 of Q99729
1378	UPI000013EBF8	6	48	25.5	329	36187	8.6	Heterogeneous nuclear ribonucleoprotein A/B (hnRNP A/B) (APOBEC-1- binding protein 1) (ABBP-1).
1378	Q53F64	6	48	25.3	332	35996	7.4	Heterogeneous nuclear ribonucleoprotein AB isoform a variant
1378	Q99729-2	6	48	25.3	332	35968	6.9	Isoform 2 of Q99729
1379	Q9Y3A6	6	27	25.3	229	26005	4.8	Transmembrane emp24 domain-containing protein 5 precursor
1380	P08574	6	16	25.2	325	35390	9	Cytochrome c1 heme protein, mitochondrial precursor
1380	UPI000014046B	6	16	25.2	325	35422	9	Cytochrome c1 heme protein, mitochondrial precursor (Cytochrome c-1).
1381	P25788-2	6	44	25.8	248	27647	5.3	Isoform 2 of P25788
1381	P25788	6	44	25.1	255	28433	5.3	Proteasome subunit alpha type 3
1381	Q6IB71	6	44	25.1	255	28415	5.3	Proteasome subunit alpha type
1382	Q9HCU2	6	10	27.4	369	37858	8.4	RNA binding protein MCG10
1382	UPI0000457119	6	10	26.8	377	38834	7.2	Poly(rC)-binding protein 4 (Alpha-CP4).
1382	P57723	6	10	25.1	403	41482	8.2	Poly(rC)-binding protein 4
1382	Q9GZT1	6	10	23.8	424	43869	8.4	RNA binding protein MCG10
1383	O00442	6	9	24.9	366	39337	7.9	RNA 3'-terminal phosphate cyclase
1383	Q5VSV0	6	9	24	379	40709	8.3	RNA terminal phosphate cyclase domain 1
1384	Q13561	6	7	24.9	401	44231	5.2	Dynactin subunit 2
1384	UPI000045662F	6	7	24.6	406	44722	5.2	Dynactin subunit 2 (Dynactin complex 50 kDa subunit) (50 kDa dynein- associated polypeptide) (p50 dynamitin) (DCTN-50).
1384	UPI000004EFD1	6	7	24.6	406	44820	5.2	dynactin 2
1385	Q59GY3	6	34	30.5	279	31865	11	Arginine/serine-rich splicing factor 6 variant
1385	Q13247-3	6	34	25.4	335	38419	11	Isoform SRP55
1385	Q13247	6	34	24.7	344	39587	11.4	Splicing factor, arginine/serine-rich 6
1386	P50897	6	9	24.5	306	34193	6.5	Palmitoyl-protein thioesterase 1 precursor
1387	Q86XR1	6	25	25.6	238	26108	9.1	Prion protein
1387	A2A2V1	6	25	24.5	249	27279	9	Prion protein
1387	A1YVW6	6	25	24.1	253	27703	9.1	Prion protein
1387	Q6FGR8	6	25	24.1	253	27599	9.1	PRNP protein
1387	Q6FGN5	6	25	24.1	253	27629	9	Major prion protein
1387	Q27H91	6	25	24.1	253	27635	9	Prion protein PrP
1387	P04156	6	25	24.1	253	27661	9	Major prion protein precursor
1387	Q6SES1	6	25	22	277	29992	9	Prion protein
1387	O75942	6	25	21.4	285	30768	9	Prion protein
1388	Q14192	6	14	24	279	32193	7.5	Four and a half LIM domains protein 2
1388	Q2TSB7	6	14	24	279	32246	7.7	Aging-associated gene 11
1388	UPI000023C3A9	6	14	18	372	42073	8	Four and a half LIM domains protein 2 (FHL-2) (Skeletal muscle LIM- protein 3) (SLIM 3) (LIM domain protein DRAL).
1388	Q2XQU9	6	14	17.2	389	44177	8.1	FHL2 isoform 5
1389	Q6FI81-3	6	10	25.1	299	32213	5.6	Isoform 3 of Q6FI81
1389	Q6FI81	6	10	24	312	33582	5.6	Anamorsin
1389	UPI00000739FB	6	10	20.4	367	40003	5.8	CPIN1_HUMAN Isoform 2 of Q6FI81 - Homo sapiens (Human)
1390	Q9NUJ1	6	11	23.9	306	33933	8.6	Abhydrolase domain-containing protein 10, mitochondrial precursor
1391	P40937	6	12	23.5	340	38497	7.2	Replication factor C subunit 5

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
1391	Q6LES9	6	12	23.5	340	38397	6.9	RFC5 protein
1391	Q59GW7	6	12	22.8	351	39643	7.8	Replication factor C 5 isoform 1 variant
1392	P53701	6	9	23.5	268	30602	6.7	Cytochrome c-type heme lyase
1392	Q68D50	6	9	23.5	268	30529	7	Hypothetical protein DKFZp779I1858
1393	Q15202	6	30	23.9	109	11959	3.7	Prothymosin alpha
1393	Q8TBK9	6	30	23.6	110	12016	3.8	Prothymosin, alpha
1393	Q86YS2	6	30	23.6	110	12044	3.8	Prothymosin alpha protein
1393	Q5VYG3	6	30	23.6	110	12055	3.8	OTTHUMP00000018545
1393	Q15204	6	30	23.6	110	12047	3.7	Prothymosin alpha
1393	Q15200	6	30	23.6	110	12085	3.8	Prothymosin alpha
1393	P06454-2	6	30	23.6	110	12074	3.8	Isoform 2 of P06454
1393	P06454	6	30	23.4	111	12203	3.8	Prothymosin alpha [Contains: Thymosin alpha-1]
1394	Q99426	6	25	23.4	244	27326	5.1	Tubulin folding cofactor B
1395	O75822	6	11	23.3	258	29062	4.8	Eukaryotic translation initiation factor 3 subunit 1
1396	Q9BQP7	6	7	22.7	344	39421	7.7	Uncharacterized protein C20orf72
1397	P13716	6	9	22.4	330	36295	6.8	Delta-aminolevulinic acid dehydratase
1397	UPI000042B0B5	6	9	20.6	359	39034	7.6	delta-aminolevulinic acid dehydratase isoform a
1397	Q6ZMU0	6	9	20.6	359	39050	7.6	CDNA FLJ16678 fis, clone TLIVE2002046, highly similar to DELTA- AMINOLEVULINIC ACID DEHYDRATASE
1398	Q9NR56	6	7	22.4	388	41817	8.9	Muscleblind-like protein 1
1399	Q9BTY7	6	10	22.1	390	42129	4.8	Brain protein 16
1399	UPI000013EBB5	6	10	22.1	390	42128	4.8	PREDICTED: similar to brain protein 16
1400	O43488	6	22	22	359	39589	7.2	Aflatoxin B1 aldehyde reductase member 2
1401	Q9NX62	6	14	22	359	38681	6.9	CDNA FLJ20421 fis, clone KAT02467
1402	O14656	6	6	21.7	332	37809	7	Torsin A precursor
1402	UPI00004577BB	6	6	21.7	332	37812	7.2	Torsin A precursor (Torsin family 1 member A) (Dystonia 1 protein).
1403	O95433	6	18	21.3	338	38274	5.5	Activator of 90 kDa heat shock protein ATPase homolog 1
1404	Q9BUB1	6	12	22.5	382	43067	5.1	PRKAR2A protein
1404	P13861	6	12	21.3	404	45518	5.1	cAMP-dependent protein kinase type II-alpha regulatory subunit
1405	Q9BXY0	6	6	21.3	300	35369	5.4	MAK16-like protein RBM13
1406	A0PJ79	6	7	20.9	302	34446	9.4	Hypothetical protein
1406	UPI0000D61582	6	7	20.8	303	34492	8.1	39S ribosomal protein L1, mitochondrial precursor (L1mt) (MRP-L1).
1406	Q9BYD6	6	7	20.8	303	34453	8.1	39S ribosomal protein L1, mitochondrial precursor
1407	Q6IAE8	6	7	20.2	307	33865	6.3	C6orf55 protein
1407	Q9NP79	6	7	20.2	307	33879	6.3	Uncharacterized protein C6orf55
1408	Q7LDY7	6	21	20.1	453	48755	9	Alpha-KG-E2
1409	Q6IPC0	6	11	20.1	453	49702	5.1	Protein phosphatase 1F
1409	P49593	6	11	20	454	49831	5.1	Ca(2+)/calmodulin-dependent protein kinase phosphatase
1410	P80303	6	16	19.8	420	50223	5.1	Nucleobindin-2 precursor
1411	P17050	6	11	19.7	411	46565	5.2	Alpha-N-acetylgalactosaminidase precursor
1412	Q53FV3	6	8	19.7	406	46268	6.1	COP9 signalosome subunit 4 variant
1412	Q9BT78	6	8	19.7	406	46269	5.8	COP9 signalosome complex subunit 4
1413	Q53T59	6	9	19.6	392	42780	5	HCLS1-binding protein 3
1413	Q86VC2	6	9	19.6	392	42842	5	HCLS1 binding protein 3
1414	O96019	6	10	19.3	429	47461	5.6	Actin-like protein 6A
1414	Q6FI97	6	10	19.3	429	47381	5.7	BAF53A protein
1414	Q53FS0	6	10	19.3	429	47481	5.7	Actin-like 6A isoform 1 variant
1415	P10644	6	9	18.9	381	42982	5.3	cAMP-dependent protein kinase type I-alpha regulatory subunit
1415	Q68DQ4	6	9	18.9	381	42948	5.3	Hypothetical protein DKFZp779L0468
1416	Q53H12	6	12	18.7	422	47137	8.1	Acylglycerol kinase, mitochondrial precursor
1417	Q5JB52	6	8	19.7	508	56467	7.6	Stromal RNA regulating factor
1417	Q5JB51	6	8	18.6	537	59648	7.7	Stromal RNA regulating factor
1417	Q8WVV9	6	8	18.5	542	60083	7.7	Heterogeneous nuclear ribonucleoprotein L-like
1418	P30740	6	10	18.5	379	42742	6.3	Leukocyte elastase inhibitor
1419	P36551	6	9	18.5	454	50152	8.3	Coproporphyrinogen III oxidase, mitochondrial precursor
1419	Q53F08	6	9	18.5	454	50166	8.3	Coproporphyrinogen oxidase variant
1420	Q7Z426	6	23	18.2	396	43006	5.2	Putative MAPK activating protein
1420	Q969I2	6	23	18	400	43448	5.1	TRK-fused gene
1420	Q92734	6	23	18	400	43434	5.1	Protein TFG
1421	UPI0000202E29	6	29	33.7	205	22764	5.5	basigin isoform 4
1421	P35613	6	29	17.9	385	42200	5.7	Basigin precursor
1422	Q5U0E6	6	12	17.9	431	47913	5.4	Serine/threonine kinase 24
1422	Q6P0Y1	6	12	17.9	431	47941	5.4	Serine/threonine kinase 24
1422	Q6FG81	6	12	17.9	431	47879	5.4	STK24 protein
1422	Q9Y6E0	6	12	17.4	443	49308	5.7	Serine/threonine-protein kinase 24
1423	Q9NZ01	6	49	17.5	308	36034	9.4	Synaptic glycoprotein SC2
1424	Q13685	6	10	17.1	434	46751	4.4	Angio-associated migratory cell protein
1425	Q0VDF9	6	8	16.9	509	54795	5.6	Heat shock 70 kDa protein 14
1425	Q9UI07	6	8	16.9	509	54778	5.6	Heat shock protein hsp70-related protein
1425	Q9P0X2	6	8	16.9	509	54824	5.5	Heat shock protein HSP60

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1426	Q8NB01	6	22	17.3	388	44997	5.5	CDNA FLJ34453 fis, clone HLUNG2002429, highly similar to Homo sapiens cartilage-associated protein
1426	O75718	6	22	16.7	401	46562	5.7	Cartilage-associated protein precursor
1426	UPI0000D61AEC	6	22	16.6	404	46847	5.7	Cartilage-associated protein precursor.
1427	Q9UKX7	6	10	16.7	468	50144	7.1	Nucleoporin 50 kDa
1428	Q9H3P7	6	7	16.5	528	60593	5.1	Golgi resident protein GCP60
1429	UPI00005A6C9C	6	7	17.6	459	52386	5.8	ubiquitin specific protease 14 isoform b
1429	P54578	6	7	16.4	494	56069	5.3	Ubiquitin carboxyl-terminal hydrolase 14
1430	Q96KP4	6	10	16.4	475	52878	6	Cytosolic nonspecific dipeptidase
1430	UPI0000D60EF3	6	10	16.4	475	52897	6	Cytosolic nonspecific dipeptidase (Glutamate carboxypeptidase-like protein 1) (CNDP dipeptidase 2).
1430	UPI0000049A46	6	10	16.4	475	52779	5.9	CNDP dipeptidase 2 (metallopeptidase M20 family)
1431	UPI0000D625AE	6	19	16.2	555	60357	6.4	Tripeptidyl-peptidase 1 precursor (EC 3.4.14.9) (Tripeptidyl-peptidase I) (TPP-1) (TPP-I) (Tripeptidyl aminopeptidase) (Lysosomal pepstatin insensitive protease) (LPIC) (Cell growth-inhibiting gene 1 protein).
1431	O14773-3	6	19	16.2	556	60458	6.4	Isoform 3 of O14773
1431	O14773	6	19	16	563	61248	6.5	Tripeptidyl-peptidase 1 precursor
1431	Q53HP2	6	19	16	563	61213	6.5	Tripeptidyl-peptidase I variant
1432	Q9HB40	6	18	15.9	452	50831	5.8	Retinoid-inducible serine carboxypeptidase precursor
1433	O75844	6	19	15.8	475	54813	7.5	CAAX prenyl protease 1 homolog
1434	Q16719	6	11	15.7	465	52352	7	Kynureninase
1434	Q53F63	6	11	15.7	465	52325	6.8	Kynureninase (L-kynurenine hydrolase) variant
1435	P26440	6	8	15.6	423	46319	8.2	Isovaleryl-CoA dehydrogenase, mitochondrial precursor
1435	Q53XZ9	6	8	15.6	423	46236	8.2	Isovaleryl Coenzyme A dehydrogenase
1436	O60832	6	11	15.4	514	57674	9.4	H/ACA ribonucleoprotein complex subunit 4
1437	Q53G15	6	16	15.4	408	47169	10.3	DEAD (Asp-Glu-Ala-Asp) box polypeptide 27 variant
1437	UPI0000161F44	6	16	7.9	796	89865	9.3	DEAD (Asp-Glu-Ala-Asp) box polypeptide 27
1437	Q96GQ7	6	16	7.9	796	89835	9.3	Probable ATP-dependent RNA helicase DDX27
1438	Q7L0Y3	6	7	15.4	397	46685	9.3	RG9MTD1 protein
1438	Q9NRG5	6	7	15.1	403	47347	9.4	RNA (guanine-9-) methyltransferase domain-containing protein 1
1439	P49023-2	6	7	16.2	557	60937	6.4	Isoform Alpha of P49023
1439	UPI00001AE664	6	7	15.3	587	64031	6.4	Paxillin.
1439	P49023	6	7	15.2	591	64533	6.1	Paxillin
1439	UPI0000D62268	6	7	15	601	65738	6.5	Paxillin.
1439	P49023-3	6	7	14.9	605	66183	6.4	Isoform Gamma of P49023
1440	Q96JJ7	6	13	15.2	454	51872	4.9	Protein disulfide-isomerase TXNDC10 precursor
1441	Q9H857-2	6	10	16.3	486	57204	7.1	Isoform 2 of Q9H857
1441	Q9H857	6	10	15.2	520	60719	6.8	5'-nucleotidase domain-containing protein 2
1442	Q05DA4	6	10	16.1	504	57378	5.6	P4HA2 protein
1442	Q5HYD8	6	10	15.2	533	60617	5.7	Hypothetical protein DKFZp686M0919
1442	O15460-2	6	10	15.2	533	60633	5.7	Isoform IIa of O15460
1442	O15460	6	10	15.1	535	60902	5.7	Prolyl 4-hydroxylase subunit alpha-2 precursor
1443	P15586	6	13	14.9	552	62082	8.3	N-acetylglucosamine-6-sulfatase precursor
1444	P49189	6	12	14.8	494	53802	5.9	4-trimethylaminobutyraldehyde dehydrogenase
1445	Q9NR12	6	13	14.7	457	49845	8.4	PDZ and LIM domain protein 7
1446	P11172	6	15	14.4	480	52222	7.2	Uridine 5'-monophosphate synthase (UMP synthase) [Includes: Orotate phosphoribosyltransferase (EC 2.4.2.10) (OPRTase); Orotidine 5'- phosphate decarboxylase (EC 4.1.1.23) (OMPdecase)]
1447	Q9BRD2	6	89	19.2	308	33376	8.4	LAMP1 protein
1447	Q9NP13	6	89	16.6	355	38358	8.2	Lysosomal-associated membrane glycoprotein-1
1447	P11279	6	89	14.2	416	44773	9.1	Lysosome-associated membrane glycoprotein 1 precursor
1447	UPI000049DDA7	6	89	14.2	415	44591	8.9	Lysosome-associated membrane glycoprotein 1 precursor (LAMP-1) (CD107a antigen).
1447	Q8WU33	6	89	14.1	417	44882	8.7	Lysosomal-associated membrane protein 1
1448	P12955	6	10	13.6	493	54548	6	Xaa-Pro dipeptidase
1449	Q14108	6	49	13.6	478	54290	5.1	Lysosome membrane protein 2
1450	Q8NHP8	6	23	13.4	589	65472	7	Hypothetical protein LOC196463
1450	UPI000013DC40	6	23	13.4	589	65472	6.8	UPI000013DC40 UniRef100 entry
1451	Q9BXS5	6	11	14.7	423	48587	7.3	AP-1 complex subunit mu-1
1451	Q59EK3	6	11	13.3	466	53263	8.9	Adaptor-related protein complex 1, mu 1 subunit variant

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1452	O95340	6	12	13.2	614	69501	8	Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthetase 2 (PAPS synthetase 2) (PAPSS 2) (Sulfurylase kinase 2) (SK2) (SK 2) [Includes: Sulfate adenylyltransferase (EC 2.7.7.4) (Sulfate adenylate transferase) (SAT) (ATP-sulfurylase); Adenylyl-sulfate kinase (EC 2.7.1.25) (Adenylylsulfate 3'-phosphotransferase) (APS kinase) (Adenosine-5'-phosphosulfate 3'-phosphotransferase) (3'-phosphoadenosine-5'-phosphosulfate synthetase)]
1452	UPI000049DD01	6	12	13.1	619	70062	8.2	Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthetase 2 (PAPS synthetase 2) (PAPSS 2) (Sulfurylase kinase 2) (SK2) (SK 2) [Includes: Sulfate adenylyltransferase (EC 2.7.7.4) (Sulfate adenylate transferase) (SAT) (ATP-sulfurylase); Adenylyl-sulfate
1452	O95340-2	6	12	13.1	619	69970	8	Isoform B of O95340
1453	Q86VD2	6	7	13.3	851	96061	6.6	Dynamin 1
1453	Q6P3T6	6	7	13.3	851	96041	7	Dynamin 1
1453	Q05193	6	7	13.1	864	97407	7.3	Dynamin-1
1453	Q5SYX2	6	7	13.1	864	97408	7.2	Dynamin 1
1454	P08240	6	9	12.5	638	69811	9	Signal recognition particle receptor subunit alpha
1454	Q6IAX9	6	9	12.5	638	69894	9	SRPR protein
1455	Q9H8H0	6	8	12.5	719	81124	6.1	Nucleolar protein 11
1456	Q86YM9	6	11	20.2	435	47714	4.7	Calpastatin
1456	P20810-3	6	11	14.9	590	63666	4.8	Isoform 3 of P20810
1456	Q7Z4K0	6	11	13.2	667	71895	4.9	Calpastatin
1456	UPI0000DA4C5C	6	11	13.1	673	72799	5	calpastatin isoform k
1456	P20810-2	6	11	12.7	695	75305	5.1	Isoform 2 of P20810
1456	P20810	6	11	12.4	708	76573	5.1	Calpastatin
1456	UPI0000DA4C59	6	11	11.7	750	80265	5.1	calpastatin isoform f
1456	UPI0000DA4C58	6	11	11.6	756	81169	5.2	calpastatin isoform e
1456	UPI0000DA4C5B	6	11	11.4	769	82437	5.2	calpastatin isoform h
1456	UPI0000DA4C5A	6	11	11.4	772	82771	5.3	calpastatin isoform g
1457	UPI0000D610D0	6	9	12.7	387	40237	5.1	Adhesion-regulating molecule 1 precursor (110 kDa cell membrane glycoprotein) (Gp110).
1457	Q16186	6	9	12	407	42153	5.1	Adhesion-regulating molecule 1 precursor
1458	Q6P996	6	7	12.2	788	86708	5.3	KIAA0251 protein
1458	O00236	6	7	11.7	820	90027	5.5	KIAA0251 protein
1459	Q9P258	6	12	11.5	522	56085	8.8	Protein RCC2
1460	Q6DCA8	6	25	11.3	680	77948	10.2	BCLAF1 protein
1460	Q9NYF8-4	6	25	10.3	747	85937	10.4	Isoform 4 of Q9NYF8
1460	UPI00004574B1	6	25	8.9	869	100202	10	Bcl-2-associated transcription factor 1 (Btf).
1460	Q9NYF8-3	6	25	8.9	869	100232	10	Isoform 3 of Q9NYF8
1460	Q9NYF8-2	6	25	8.4	918	105948	10	Isoform 2 of Q9NYF8
1460	Q9NYF8	6	25	8.4	920	106122	10	Bcl-2-associated transcription factor 1
1461	A2A2P8	6	9	11.2	662	73333	6.5	Adducin 1
1461	P35611	6	9	10	737	80955	5.8	Alpha-adducin
1461	P35611-3	6	9	9.6	768	84303	6	Isoform 3 of P35611
1462	P50443	6	26	11	739	81649	8.4	Sulfate transporter
1462	UPI000013DE3D	6	26	11	739	81662	8.4	solute carrier family 26 member 2
1463	O95394	6	6	10.7	542	59852	6.3	Phosphoacetylglucosamine mutase
1464	O76031	6	9	10.6	633	69224	7.6	ATP-dependent Clp protease ATP-binding subunit ClpX-like, mitochondrial precursor
1465	P52888	6	9	10.4	689	78840	6	Thimet oligopeptidase
1465	Q96CV8	6	9	10.4	689	78824	6	Thimet oligopeptidase 1
1466	Q06124-2	6	8	10.5	593	68011	7.3	Isoform 2 of Q06124
1466	Q06124	6	8	10.4	597	68436	7.3	Tyrosine-protein phosphatase non-receptor type 11
1467	Q13724	6	45	10.2	837	91918	8.9	Mannosyl-oligosaccharide glucosidase
1468	Q5RF14	6	8	10.2	713	80478	7.2	Hypothetical protein DKFZp469L1232
1468	Q99797	6	8	10.2	713	80612	7.2	Mitochondrial intermediate peptidase, mitochondrial precursor
1468	Q96G65	6	8	10.2	713	80611	7	Mitochondrial intermediate peptidase
1468	Q5T9Q9	6	8	10.2	713	80641	7	Mitochondrial intermediate peptidase
1469	P40222	6	15	9.9	546	61891	6.5	Alpha-taxilin
1470	Q9NTJ5	6	18	10.1	587	66979	7.3	Hypothetical protein DKFZp434O1328
1470	Q96AX7	6	18	10.1	587	66951	7.1	SAC1 suppressor of actin mutations 1-like
1470	O94935	6	18	9.7	607	69474	8	SAC1 suppressor of actin mutations 1-like protein
1471	P53794	6	15	9.7	718	79694	7.3	Sodium/myo-inositol cotransporter (Na(+)/myo-inositol cotransporter)
1472	Q12884	6	13	9.6	760	87794	6.8	Seprase
1472	Q53TP5	6	13	9.6	760	87713	6.6	Hypothetical protein FAP
1473	A2RRF3	6	7	9.2	754	83248	5.1	EPS15L1 protein
1473	Q9UBC2	6	7	8	864	94255	5.1	Epidermal growth factor receptor substrate 15-like 1
1474	Q53H65	6	9	9.2	759	85666	9.2	RNA binding motif protein 28 variant
1474	UPI000006F4A6	6	9	9.2	759	85766	9.2	RNA binding motif protein 28
1474	Q9NW13	6	9	9.2	759	85738	9.2	RNA-binding protein 28
1475	Q6GSC0	6	19	9.3	751	84819	4.8	Amyloid beta (A4) protein

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
1475	P05067	6	19	9.1	770	86943	4.8	Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer disease amyloid protein) (Cerebral vascular amyloid peptide) (CVAP) (Protease nexin-II) (PN-II) (APPI) (PreA4) [Contains: Soluble APP-alpha (S-APP- alpha); Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59) (Amyloid intracellular domain 59) (AID(59)) (AICD-59); Gamma-CTF(57) (Gamma-secretase C-terminal fragment 57) (Amyloid intracellular domain 57) (AID(57)) (AICD-57); Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50) (Amyloid intracellular domain 50) (AID(50)) (AICD-50); C31]
1476	P11166	6	65	9.1	492	54084	8.7	Solute carrier family 2, facilitated glucose transporter member 1
1476	UPI000004F0B2	6	65	9.1	492	54118	8.7	solute carrier family 2 (facilitated glucose transporter), member 1
1476	Q0P512	6	65	9.1	492	54054	8.9	Solute carrier family 2 (Facilitated glucose transporter), member 1
1477	P58215	6	14	9	753	83166	6.9	Lysyl oxidase homolog 3 precursor
1478	Q9UHB6-2	6	10	11.4	599	67120	5.9	Isoform Alpha of Q9UHB6
1478	Q53GG0	6	10	9	759	85254	6.8	Epithelial protein lost in neoplasm beta variant
1478	Q9UHB6	6	10	9	759	85226	6.8	LIM domain and actin-binding protein 1
1478	Q59FE8	6	10	8.8	769	86107	6.8	Epithelial protein lost in neoplasm beta variant
1479	Q8N556	6	18	9	730	80741	8.6	Actin filament associated protein 1
1479	UPI0000233618	6	18	9	730	80725	8.7	actin filament associated protein 1
1479	Q9HBY1	6	18	9	730	80727	8.7	Actin filament associated protein
1480	P13798	6	10	8.9	732	81225	5.5	Acylamino-acid-releasing enzyme
1481	Q92615	6	8	8.9	738	80552	6.9	La-related protein 5
1481	UPI000046FFBF	6	8	8.9	743	81090	7.1	La ribonucleoprotein domain family, member 5
1481	UPI0000456346	6	8	8.8	753	82204	6.8	La ribonucleoprotein domain family, member 5
1482	Q9BWU0	6	7	8.7	796	88814	5.2	Kanadaptin
1482	UPI0000D6117A	6	7	8.6	798	89014	5.2	Kanadaptin (Kidney anion exchanger adapter protein) (Solute carrier family 4 anion exchanger member 1 adapter protein) (Lung cancer oncogene 3 protein).
1483	Q13618-2	6	16	8.9	744	86234	8	Isoform 2 of Q13618
1483	Q13618	6	16	8.6	768	88930	8.5	Cullin-3
1484	Q92888	6	13	8.6	912	102435	5.7	Rho guanine nucleotide exchange factor 1
1485	Q6P179	6	8	8.1	915	105526	6.8	LRAP protein
1485	Q9HBX2	6	8	7.7	960	110462	6.7	Aminopeptidase
1485	Q7Z5K1	6	8	7.7	960	110447	6.7	Leukocyte-derived arginine aminopeptidase long form variant
1486	P12109	6	8	8	1028	108529	5.4	Collagen alpha-1(VI) chain precursor
1487	Q8WTT2	6	10	7.9	800	92548	9.2	Nucleolar complex protein 3 homolog
1487	UPI0000D60F9F	6	10	7.9	800	92624	9.2	Nucleolar complex protein 3 homolog (NOC3 protein homolog) (NOC3-like protein) (Nucleolar complex-associated protein 3-like protein) (Factor for adipocyte differentiation 24).
1488	O43592	6	12	7.8	962	109964	5.4	Exportin-T (tRNA exportin) (Exportin(tRNA))
1489	UPI0000456E7C	6	12	8.9	827	95332	7.5	Pre-mRNA-processing factor 40 homolog A (Formin-binding protein 3) (Formin-binding protein 11) (Huntingtin-interacting protein HYPA) (Huntingtin yeast partner A) (Fas ligand-associated factor 1) (NY-REN- 6 antigen).
1489	O75400-2	6	12	8.1	915	104363	7.6	Isoform 2 of O75400
1489	O75400-3	6	12	7.9	939	106907	7.4	Isoform 3 of O75400
1489	O75400	6	12	7.7	957	108805	7.6	Pre-mRNA-processing factor 40 homolog A
1489	UPI0000DD7A6A	6	12	7.6	974	110497	8.2	PREDICTED: similar to Pre-mRNA-processing factor 40 homolog A (Formin-binding protein 3) (Huntingtin yeast partner A) (Huntingtin-interacting protein HYPA/FBP11) (Fas ligand-associated factor 1) (NY-REN-6 antigen) isoform 1
1490	Q5H9R7-3	6	15	8.5	791	88909	4.6	Isoform 3 of Q5H9R7
1490	Q5H9R7-6	6	15	7.9	844	94445	4.6	Isoform 6 of Q5H9R7
1490	Q5H9R7	6	15	7.7	873	97669	4.6	SAPS domain family member 3
1490	Q5H9R7-2	6	15	7.7	867	96957	4.6	Isoform 2 of Q5H9R7
1490	Q5H9R7-5	6	15	7.6	879	98485	4.6	Isoform 5 of Q5H9R7
1491	Q96KR1	6	7	7.5	1057	115287	9.3	Zinc finger RNA-binding protein
1491	UPI0000D6160F	6	7	7.5	1055	115092	9.2	zinc finger RNA binding protein
1491	UPI0000D6160E	6	7	7.4	1074	117078	9	zinc finger RNA binding protein
1491	UPI00001BBB38	6	7	7.4	1074	117012	9	zinc finger RNA binding protein
1492	Q8N3Z2	6	20	7.4	976	108266	6.2	Ephrin receptor
1493	UPI0000D6167D	6	7	8.3	835	91015	4.7	Bromodomain-containing protein 8 (p120) (Skeletal muscle abundant protein) (Thyroid hormone receptor coactivating protein 120kDa) (TrCP120).
1493	Q9H0E9-4	6	7	8	866	94297	4.7	Isoform 4 of Q9H0E9

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
1493	Q9H0E9-2	6	7	7.3	951	102839	4.7	Isoform 2 of Q9H0E9
1494	Q92797	6	9	6.9	1274	141148	6.1	Symplekin
1495	P14735	6	8	6.8	1019	118022	6.8	Insulin-degrading enzyme
1495	Q5T5N2	6	8	6.8	1019	117968	6.6	Insulin-degrading enzyme
1496	Q59GN8	6	12	7.2	975	110234	6.2	PTK2 protein tyrosine kinase 2 isoform b variant
1496	Q8IYN9	6	12	7	1006	114253	6.8	PTK2 protein
1496	Q59GM6	6	12	7	1007	114157	6.6	PTK2 protein tyrosine kinase 2 isoform b variant
1496	Q05397	6	12	6.7	1052	119233	6.6	Focal adhesion kinase 1
1497	Q6NX72	6	18	6.6	1160	132322	5.8	EHBP1 protein
1497	Q6QNV2	6	18	6.4	1196	136237	5.4	EH domain binding protein 1
1497	UPI000013D49A	6	18	6.2	1231	140017	5.3	EH domain binding protein 1
1497	Q8NDI1	6	18	6.2	1231	139858	5.4	EH domain-binding protein 1
1498	Q8N3E0	6	12	6.6	1009	114456	7.8	Hypothetical protein DKFZp761P0824
1498	UPI0000441EF9	6	12	6.1	1092	124106	7.7	formin-like 2
1498	Q96PY5	6	12	6	1112	126314	8.2	Formin-like protein 2
1499	Q6Y7W6-2	6	12	7.5	1100	127290	5.4	Isoform 2 of Q6Y7W6
1499	Q6Y7W6	6	12	6.4	1299	150070	5.5	PERQ amino acid-rich with GYF domain-containing protein 2
1499	UPI0000D612CD	6	12	6.4	1301	150271	5.5	PERQ amino acid-rich with GYF domain-containing protein 2 (Grb10- interacting GYF protein 2) (Trinucleotide repeat-containing protein 15).
1500	O43290	6	12	6.1	800	90255	6.1	U4/U6.U5 tri-snRNP-associated protein 1
1500	UPI0000D62637	6	12	6.1	800	90310	6.2	U4/U6.U5 tri-snRNP-associated protein 1 (U4/U6.U5 tri-snRNP-associated 110 kDa protein) (Squamous cell carcinoma antigen recognized by T cells 1) (SART-1) (hSART-1) (hSnu66).
1501	Q13464	6	13	6.1	1354	158174	5.9	Rho-associated protein kinase 1
1501	UPI000022A6D8	6	13	6.1	1354	158243	5.9	Rho-associated protein kinase 1 (EC 2.7.11.1) (Rho-associated, coiled- coil-containing protein kinase 1) (p160 ROCK-1) (p160ROCK) (Renal carcinoma antigen NY-REN-35).
1501	Q2KHM4	6	13	6.1	1354	158127	5.9	Rho-associated, coiled-coil containing protein kinase 1
1502	Q5JTH9	6	17	5.2	1297	143702	8.8	RRP12-like protein
1502	UPI00000712A5	6	17	5.2	1297	143732	8.8	ribosomal RNA processing 12 homolog
1503	Q2T9J4	6	13	5.1	1132	128394	7	Inositol polyphosphate-5-phosphatase F
1503	Q9Y2H2	6	13	5	1150	130166	7.1	Inositol polyphosphate-5-phosphatase F
1504	O60524	6	10	5	1076	122970	6.3	Serologically defined colon cancer antigen 1
1504	UPI0000246D16	6	10	5	1076	122954	6.3	Serologically defined colon cancer antigen 1 (Antigen NY-CO-1).
1505	Q7KZ85	6	8	4.1	1726	199071	4.9	Transcription elongation factor SPT6
1505	UPI0000D622EF	6	8	4.1	1728	199271	4.9	Transcription elongation factor SPT6 (hSPT6) (Tat-cotransactivator 2 protein) (Tat-CT2 protein).
1506	Q5VYK3	6	25	4	1845	204289	7.1	Proteasome-associated protein ECM29 homolog
1506	UPI0000D618EB	6	25	4	1833	203186	7.2	Proteasome-associated protein ECM29 homolog (Ecm29).
1506	UPI00001D76EA	6	25	4	1839	203992	7.2	Proteasome-associated protein ECM29 homolog (Ecm29).
1506	UPI0000DD7F7A	6	25	3.7	2017	223692	8.7	PREDICTED: similar to Proteasome-associated protein ECM29 homolog (Ecm29)
1507	Q6MZL5	6	7	3.8	1694	195643	5.2	Hypothetical protein DKFZp686C06243
1507	Q15643	6	7	3.2	1979	227637	5.3	Thyroid receptor-interacting protein 11
1507	UPI000013D767	6	7	3.2	1979	227584	5.3	Thyroid receptor-interacting protein 11 (TRIP-11) (Golgi-associated microtubule-binding protein 210) (GMAP-210) (Trip230) (Clonal evolution-related gene on chromosome 14).
1508	O75691	6	26	2.4	2785	318426	7.4	Small subunit processome component 20 homolog
1508	UPI00001FB38B	6	26	2.4	2785	318385	7.4	down-regulated in metastasis
1508	UPI0000031EE4	6	26	2.4	2785	318400	7.4	PREDICTED: similar to Small subunit processome component 20 homolog (Down-regulated in metastasis protein) (Protein Key-1A6) (Novel nucleolar protein 73) (NNP73)
1509	P46939	6	12	2.2	3433	394495	5.3	Utrophin
1509	UPI000049E05A	6	12	2.2	3433	394520	5.3	Utrophin (Dystrophin-related protein 1) (DRP1) (DRP).
1509	Q5SZ57	6	12	2.2	3433	394467	5.3	Utrophin
1510	Q5VVM7	6	8	2.3	3114	357527	5.1	Centromere protein F, 350/400ka
1510	P49454	6	8	2.2	3210	367595	5.1	Centromere protein F
1511	UPI000023BD43	6	11	1.8	3585	403087	6.4	vacuolar protein sorting 13C protein isoform 1B
1511	Q709C8-4	6	11	1.8	3584	402957	6.4	Isoform 4 of Q709C8
1511	Q709C8-3	6	11	1.8	3710	417279	6.6	Isoform 3 of Q709C8
1511	Q709C8-2	6	11	1.8	3627	408072	6.6	Isoform 2 of Q709C8
1511	Q709C8	6	11	1.7	3753	422393	6.8	Vacuolar protein sorting-associated protein 13C
1512	Q8IWP6	5	53	72.4	445	49753	4.9	Class IVb beta tubulin
1513	Q9Y333	5	20	67.4	95	10835	6.5	U6 snRNA-associated Sm-like protein LSm2
1514	Q6IB68	5	14	65	103	11953	5.9	MYCBP protein
1514	Q99417	5	14	65	103	11967	5.9	C-Myc-binding protein
1515	P18085	5	50	59.4	180	20511	7.2	ADP-ribosylation factor 4
1516	Q96EL3	5	11	58.9	112	12107	8.8	39S ribosomal protein L53, mitochondrial precursor

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1517	Q15369	5	23	58	112	12473	4.8	Transcription elongation factor B polypeptide 1
1518	Q8WUW1	5	22	54.7	75	8745	5.5	Probable protein BRICK1
1518	Q8WUW1-2	5	22	38.7	106	12046	6.8	Isoform 2 of Q8WUW1
1518	UPI00004570B9	5	22	38	108	12158	6.8	UPI00004570B9 UniRef100 entry
1519	P31946-2	5	51	54.5	244	27850	4.8	Isoform Short of P31946
1519	P31946	5	51	54.1	246	28082	4.8	14-3-3 protein beta/alpha
1520	O43678	5	9	49.5	99	10922	9.6	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2
1521	Q64152	5	18	50	204	22031	9.5	Transcription factor BTF3
1521	P20290	5	18	49.5	206	22168	9.4	Transcription factor BTF3
1522	O60925	5	14	49.2	122	14210	6.8	Prefoldin subunit 1
1523	P58546	5	83	49.2	118	12895	5.5	Myotrophin
1524	Q13526	5	11	47.2	163	18243	8.8	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1
1525	Q8WVC2	5	45	46.9	81	8850	8.5	RPS21 protein
1525	P63220	5	45	45.8	83	9111	8.5	40S ribosomal protein S21
1526	P68133	5	92	45.6	377	42051	5.4	Actin, alpha skeletal muscle
1527	Q8TDP1-2	5	11	45.4	163	17712	4.9	Isoform 2 of Q8TDP1
1527	Q8TDP1	5	11	45.1	164	17840	5	Ribonuclease H2 subunit C
1528	Q16718	5	25	44	116	13459	6	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5
1529	Q9H910	5	6	43.7	190	20063	9.3	Hematological and neurological expressed 1-like protein
1530	P68036	5	15	43.5	154	17862	8.5	Ubiquitin-conjugating enzyme E2 L3
1531	Q9UHA4	5	10	43.5	124	13623	7.4	Mitogen-activated protein kinase kinase 1-interacting protein 1
1532	P62879	5	14	43.2	340	37331	6	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 2
1533	P49458	5	17	43	86	10112	8	Signal recognition particle 9 kDa protein
1534	Q7RTV0	5	9	41.8	110	12405	8.4	PHD finger-like domain-containing protein 5A
1535	Q99584	5	32	41.8	98	11471	6.2	Protein S100-A13
1536	Q9BRJ6	5	12	41.8	194	22083	9.6	MGC11257 protein
1537	P12236	5	97	41.6	298	32866	9.7	ADP/ATP translocase 3
1537	UPI000015FDB7	5	97	41.6	298	32926	9.7	solute carrier family 25, member A6
1538	Q9BZL1	5	17	41.1	73	8547	8.4	Ubiquitin-like protein 5
1539	Q8NB37	5	7	40.5	220	23298	6.6	CDNA FLJ34283 fis, clone FEBRA2003926, weakly similar to NonF
1540	P84090	5	54	40.4	104	12259	5.9	Enhancer of rudimentary homolog
1541	Q4VC31	5	12	40.3	144	16620	7.8	Coiled-coil domain-containing protein 58
1542	O75380	5	7	38.7	124	13712	8.3	NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial precursor
1543	Q8IXM3	5	22	38.7	137	15383	9.6	39S ribosomal protein L41, mitochondrial precursor
1544	P52907	5	18	38.5	286	32923	5.7	F-actin capping protein subunit alpha-1
1545	Q15121	5	37	38.5	130	15040	5	Astrocytic phosphoprotein PEA-15
1545	Q6FHL9	5	37	38.5	130	15068	5	PEA15 protein
1546	O95881	5	14	38.4	172	19206	5.4	Thioredoxin domain-containing protein 12 precursor
1547	P07741	5	16	38.3	180	19608	6	Adenine phosphoribosyltransferase
1548	Q8CFN2	5	42	38.2	191	21259	6.5	Cell division control protein 42 homolog precursor
1548	UPI0000EFE353	5	42	38	192	21346	6.5	Human Cell Division Cycle 42 (CDC42)
1549	Q9Y2Q5	5	12	45.6	125	13507	5.4	Mitogen-activated protein-binding protein-interacting protein
1549	Q5VY97	5	12	38	150	15609	7.8	Mitogen-activated protein-binding protein-interacting protein
1550	P51153	5	25	37.4	203	22774	9.2	Ras-related protein Rab-13
1551	P60983	5	12	37.3	142	16713	5.3	Glia maturation factor beta
1551	UPI0000D6240C	5	12	34.4	154	18218	5.5	Glia maturation factor beta (GMF-beta).
1551	Q9BS35	5	12	34.4	154	18110	5.3	GMFB protein
1552	O00148	5	18	36.8	427	49130	5.7	ATP-dependent RNA helicase DDX39
1553	P30046	5	25	36.4	118	12712	7.3	D-dopachrome decarboxylase
1554	P51571	5	55	36.4	173	18999	6.2	Translocon-associated protein subunit delta precursor
1555	P62263	5	86	36.4	151	16273	10.1	40S ribosomal protein S14
1556	O14602	5	31	36.1	144	16442	5.2	Eukaryotic translation initiation factor 1A, Y-chromosomal
1557	P84095	5	6	36.1	191	21308	8.1	Rho-related GTP-binding protein RhoG precursor
1558	P61353	5	37	36	136	15798	10.6	60S ribosomal protein L27
1559	P55769	5	22	35.9	128	14174	8.5	NHP2-like protein 1
1559	UPI0000F53459	5	22	35.4	130	14318	8.5	U4/U6.U5 tri-snRNP 15.5 kDa protein
1560	P57105	5	19	35.9	145	15928	6.3	Synaptojanin-2-binding protein
1561	Q8IV95	5	15	41	156	17984	5.1	Nudix (Nucleoside diphosphate linked moiety X)-type motif 1
1561	Q7Z7N6	5	15	41	156	17951	5.1	Nudix (Nucleoside diphosphate linked moiety X)-type motif 1
1561	A4D205	5	15	35.8	179	20296	5	Nudix (Nucleoside diphosphate linked moiety X)-type motif 1
1561	P36639	5	15	32.5	197	22552	5.3	7,8-dihydro-8-oxoguanine triphosphatase
1562	Q16527	5	14	35.8	193	20954	8.6	Cysteine and glycine-rich protein 2
1563	P63173	5	53	35.7	70	8218	10.1	60S ribosomal protein L38
1564	Q9NV31	5	13	35.3	184	21850	9.5	U3 small nucleolar ribonucleoprotein protein IMP3

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
1565	Q6P1X6	5	12	34.7	216	23875	9.1	Similar to RIKEN cDNA C030006K11 gene
1565	Q6P2Q7	5	12	34.7	216	23889	9.1	Similar to RIKEN cDNA C030006K11 gene
1566	Q9BRJ7	5	9	34.6	211	23338	8.9	Protein syndesmos
1567	A2A2V9	5	8	34.5	113	13188	5.1	Novel protein
1567	UPI00000373C5	5	8	34.5	113	13171	5.1	family with sequence similarity 127, member A
1567	Q9BWD3	5	8	34.5	113	13204	5.1	Family with sequence similarity 127, member B
1568	P40616	5	18	34.3	181	20418	5.7	ADP-ribosylation factor-like protein 1
1569	Q96EK6	5	5	34.2	184	20749	8	Glucosamine 6-phosphate N-acetyltransferase
1570	P55957	5	12	33.3	195	21995	5.4	BH3-interacting domain death agonist (BID) (p22 BID) [Contains: BH3- interacting domain death agonist p15 (p15 BID); BH3-interacting domain death agonist p13 (p13 BID); BH3-interacting domain death agonist p11 (p11 BID)]
1571	Q9UMS0	5	13	33.2	196	21802	4.3	NFU1 iron-sulfur cluster scaffold homolog
1572	UPI000013EB83	5	11	33.2	376	42003	5.6	hypothetical protein LOC345651
1573	P60866	5	39	32.8	119	13373	9.9	40S ribosomal protein S20
1574	Q5W111	5	7	32.7	196	21666	6.7	Chronic lymphocytic leukemia deletion region gene 6 protein
1575	P10606	5	22	32.6	129	13696	8.8	Cytochrome c oxidase subunit 5B, mitochondrial precursor
1575	Q6FHM4	5	22	32.6	129	13705	8.8	COX5B protein
1576	Q13765	5	37	32.6	215	23384	4.6	Nascent polypeptide-associated complex subunit alpha
1577	P26885	5	9	32.4	142	15649	9.1	FK506-binding protein 2 precursor
1578	Q9UBQ0	5	11	32.4	182	20506	6.8	Vacuolar protein sorting-associated protein 29
1579	P63279	5	11	32.3	158	18007	8.7	SUMO-conjugating enzyme UBC9
1579	UPI00001AF46D	5	11	27.7	184	20458	8.5	SUMO-conjugating enzyme UBC9 (EC 6.3.2.-) (SUMO-protein ligase) (Ubiquitin-conjugating enzyme E2 I) (Ubiquitin-protein ligase I) (Ubiquitin carrier protein I) (Ubiquitin carrier protein 9) (p18).
1579	Q7KZS0	5	11	27.7	184	20444	8.5	Ubiquitin-conjugating enzyme E2I
1580	P02794	5	31	32.2	183	21226	5.6	Ferritin heavy chain
1580	UPI0000EB65CC	5	31	32.2	183	21198	5.4	FERRITIN HEAVY CHAIN
1580	UPI0000EB65CB	5	31	32.2	183	21212	5.4	FERRITIN HEAVY CHAIN
1580	UPI0000EB65CA	5	31	32.2	183	21212	5.4	FERRITIN HEAVY CHAIN
1580	Q6NZ44	5	31	32.2	183	21242	5.3	FTH1 protein
1580	UPI0000D62618	5	31	24.2	244	27725	7	Ferritin heavy chain (EC 1.16.3.1) (Ferritin H subunit) (Proliferation-inducing gene 15 protein).
1581	O00746	5	10	32.1	187	20659	10.3	Nucleoside diphosphate kinase, mitochondrial precursor
1581	Q4TT34	5	10	30.8	195	21522	10.6	Non-metastatic cells 4, protein expressed in
1582	P30042	5	10	32.1	268	28170	8.3	ES1 protein homolog, mitochondrial precursor
1583	Q8TED1	5	15	31.6	209	23909	9.4	CDNA FLJ23636 fis, clone CAS07176
1583	UPI000013E37B	5	15	31.6	209	23881	9.4	similar to RIKEN cDNA 2310016C16 (LOC493869), mRNA
1584	Q9UF68	5	5	31.9	270	30658	7	Hypothetical protein DKFZp434A149
1584	Q6BCY4	5	5	31.2	276	31458	8.5	Cytochrome b5 reductase 2
1585	Q5JQ44	5	9	31.5	181	20294	4.8	Hypothetical protein DKFZp547A0616
1585	P61225	5	9	31.1	183	20504	4.8	Ras-related protein Rap-2b precursor
1586	UPI000046D37E	5	13	31.5	292	31762	7.5	syntenin isoform 2
1586	O00560	5	13	30.9	298	32444	7.5	Syntenin-1
1587	Q53S90	5	16	30.9	363	39555	8.6	Hypothetical protein STK39
1587	UPI000013D46D	5	16	20.6	545	59474	6.3	serine threonine kinase 39 (STE20/SPS1 homolog, yeast)
1587	Q9UEW8	5	16	20.5	547	59642	6.3	STE20/SPS1-related proline-alanine-rich protein kinase
1588	Q15363	5	66	30.8	201	22761	5.2	Transmembrane emp24 domain-containing protein 2 precursor
1589	P46778	5	46	30.6	160	18565	10.5	60S ribosomal protein L21
1589	UPI000006FC44	5	46	30.6	160	18595	10.5	PREDICTED: similar to 60S ribosomal protein L21
1589	Q59GK9	5	46	30.1	163	18891	10.5	Ribosomal protein L21 variant
1590	O00264	5	14	30.3	195	21671	4.7	Membrane-associated progesterone receptor component 1
1591	Q3T0Q6	5	17	31.8	170	18742	7.7	Cellular nucleic acid-binding protein
1591	Q4JGY1	5	17	31.6	171	18871	7.6	Cellular nucleic acid binding protein beta variant 1
1591	Q4JGY0	5	17	31.4	172	18970	7.6	Cellular nucleic acid binding protein beta variant 2
1591	P62633	5	17	30.5	177	19463	7.7	Cellular nucleic acid-binding protein
1591	P53996	5	17	30.3	178	19592	7.6	Cellular nucleic acid-binding protein
1592	Q6P587	5	12	33.5	224	24843	7.4	Fumarylacetoacetate hydrolase domain-containing protein 1
1592	A2A2C3	5	12	33.2	226	24910	7.7	Fumarylacetoacetate hydrolase domain containing 1
1592	A2A2C2	5	12	30.2	248	27128	7.7	Fumarylacetoacetate hydrolase domain containing 1
1593	O15145	5	31	29.8	178	20547	8.6	Actin-related protein 2/3 complex subunit 3
1593	Q2LE71	5	31	29.8	178	20565	8.6	Actin related protein 2/3 complex
1594	Q02750	5	6	29.5	393	43439	6.6	Dual specificity mitogen-activated protein kinase kinase 1
1595	P62070	5	16	28.9	204	23400	6	Ras-related protein R-Ras2 precursor
1596	Q9UKY7	5	6	28.7	258	27335	6.4	Protein CDV3 homolog
1597	Q9Y3C1	5	9	28.7	178	21188	9.9	UPF0384 protein CGI-117

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
1597	UPI000004EC74	5	9	28.7	178	21148	9.9	hypothetical protein LOC51491
1598	Q92572	5	21	28.5	193	21732	5.4	AP-3 complex subunit sigma-1
1599	O75663	5	8	28.3	272	31444	5.9	TIP41-like protein
1600	P24390	5	33	28.3	212	24542	8.6	ER lumen protein retaining receptor 1
1601	P49721	5	34	27.9	201	22836	7	Proteasome subunit beta type 2
1602	O43617	5	18	27.8	180	20274	5	Trafficking protein particle complex subunit 3
1603	Q00688	5	28	27.7	224	25177	9.3	FK506-binding protein 3
1603	Q53GD8	5	28	27.7	224	25204	9.4	FK506-binding protein 3 variant
1604	Q53SS9	5	9	27.7	386	42963	7.8	Hypothetical protein TIA1
1604	Q59G98	5	9	23.1	464	51330	7.8	TIA1 protein variant
1605	P53680	5	13	27.5	142	17018	6.2	AP-2 complex subunit sigma-1
1606	P11233	5	23	27.2	206	23567	7.1	Ras-related protein Ral-A precursor
1607	Q9BSH4	5	8	26.9	297	32477	8.1	Coiled-coil domain-containing protein 44
1608	A3KQT0	5	56	26.4	201	23072	10	Ribosomal protein L10
1608	Q6ZWV3	5	56	24.8	214	24604	10.1	60S ribosomal protein L10
1608	Q53FH7	5	56	24.8	214	24543	10.1	Ribosomal protein L10 variant
1608	P27635	5	56	24.8	214	24577	10.1	60S ribosomal protein L10
1608	Q5HY50	5	56	23	230	26593	10.2	Ribosomal protein L10
1609	P41223	5	10	26.4	144	17000	8.8	Protein BUD31 homolog
1610	P83881	5	39	26.4	106	12441	10.6	60S ribosomal protein L36a
1610	UPI00006C193F	5	39	26.4	106	12366	10.4	PREDICTED: similar to large subunit ribosomal protein L36a
1610	UPI00001AFE47	5	39	26.4	106	12475	10.4	PREDICTED: similar to large subunit ribosomal protein L36a
1610	UPI000016174B	5	39	26.4	106	12338	10.3	PREDICTED: similar to large subunit ribosomal protein L36a
1611	P01583	5	9	26.2	271	30607	5.2	Interleukin-1 alpha precursor
1612	O60493-4	5	15	30	140	16316	6.8	Isoform 4 of O60493
1612	O60493	5	15	25.9	162	18762	8.7	Sorting nexin-3
1613	O00487	5	8	25.2	310	34577	6.5	26S proteasome non-ATPase regulatory subunit 14
1614	Q00535	5	5	25	292	33304	7.7	Cell division protein kinase 5
1615	Q16270	5	6	24.8	282	29130	7.9	Insulin-like growth factor-binding protein 7 precursor
1616	Q9H9H4	5	10	24.6	285	31307	7.3	Vacuolar protein sorting-associated protein 37 homolog B
1617	O75940	5	8	24.4	238	26711	7.3	Survival of motor neuron-related-splicing factor 30
1618	Q5U071	5	19	24.5	208	23905	8.1	High-mobility group box 2
1618	P26583	5	19	24.4	209	24034	7.8	High mobility group protein B2
1619	Q9Y2R9	5	8	24.4	242	28162	10	28S ribosomal protein S7, mitochondrial precursor
1619	UPI000013CBA7	5	8	24.4	242	28134	10	28S ribosomal protein S7, mitochondrial precursor (S7mt) (MRP-S7) (bMRP27a) (bMRP-27a).
1620	Q9BUL8	5	14	24.1	212	24702	8.2	Programmed cell death protein 10
1621	Q9H690	5	16	27.8	291	32973	7.5	CDNA: FLJ22484 fis, clone HRC10868
1621	Q9GZY8	5	16	23.7	342	38465	9	Uncharacterized protein C2orf33
1622	UPI00006C03E4	5	21	57.5	106	12581	9.4	PREDICTED: similar to FUS interacting protein (serine-arginine rich) 1
1622	Q5JRI1	5	21	35.5	172	20913	10.5	FUS interacting protein (Serine/arginine-rich) 1
1622	Q5JRI2	5	21	35.3	173	21000	10.5	FUS interacting protein (Serine/arginine-rich) 1
1622	Q5JRI3	5	21	33.5	182	22135	10.3	FUS interacting protein (Serine/arginine-rich) 1
1622	Q5JRI4	5	21	33.3	183	22222	10.3	FUS interacting protein (Serine/arginine-rich) 1
1622	UPI0000DD7961	5	21	25	244	29195	11.1	PREDICTED: similar to FUS-interacting serine-arginine-rich protein 1 (TLS-associated protein with Ser-Arg repeats) (TLS-associated protein with SR repeats) (TASR) (TLS-associated serine-arginine protein) (TLS-associated SR protein) (Neural-specific SR protein... isoform 3
1622	Q5JRI0	5	21	23.4	261	31213	11.3	FUS interacting protein (Serine/arginine-rich) 1
1622	O75494	5	21	23.3	262	31301	11.3	FUS-interacting serine-arginine-rich protein 1
1622	Q53GD7	5	21	23.3	262	31282	11.3	FUS interacting protein (Serine-arginine rich) 1 isoform 2 variant
1623	Q5SQ52	5	19	26.9	186	21609	4.9	Casein kinase 2, beta polypeptide
1623	P67870	5	19	23.3	215	24942	5.6	Casein kinase II subunit beta
1623	Q5SRQ6	5	19	21.4	234	26926	6	Casein kinase 2, beta polypeptide
1624	Q4W5A9	5	9	23.3	309	34359	4.7	Hypothetical protein SET7
1624	Q8WTS6	5	9	19.7	366	40721	4.6	Histone-lysine N-methyltransferase, H3 lysine-4 specific SET7
1625	Q96A35	5	14	23.1	216	24915	9.3	39S ribosomal protein L24, mitochondrial precursor
1626	Q969G5	5	23	23	261	27642	6.2	Protein kinase C delta-binding protein
1626	UPI000013E910	5	23	23	261	27701	6.4	protein kinase C, delta binding protein
1627	P53597	5	16	22.8	333	35047	8.9	Succinyl-CoA ligase [GDP-forming] subunit alpha, mitochondrial precursor
1627	UPI000014BF59	5	16	22	346	36250	8.8	succinate-CoA ligase, GDP-forming, alpha subunit
1628	P31431	5	14	22.7	198	21642	4.5	Syndecan-4 precursor
1628	Q53FN9	5	14	22.7	198	21608	4.5	Syndecan 4 variant
1629	P52815	5	24	22.7	198	21348	8.9	39S ribosomal protein L12, mitochondrial precursor
1630	UPI0000D611BE	5	17	22.9	214	24962	7	Mps one binder kinase activator-like 1B (Mob1 homolog 1B) (Mob1 alpha) (Mob1A) (Protein Mob4B).
1630	Q9H8S9	5	17	22.7	216	25080	7	Mps one binder kinase activator-like 1B

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1630	UPI0000D611BD	5	17	22.7	216	25122	7	Mps one binder kinase activator-like 1B (Mob1 homolog 1B) (Mob1 alpha) (Mob1A) (Protein Mob4B).
1630	UPI0000047AC8	5	17	22.7	216	25008	7.2	Mob4B protein
1631	Q04323	5	8	22.6	297	33325	5.3	SAPK substrate protein 1
1631	Q04323-2	5	8	21.5	312	35107	5.3	Isoform 2 of Q04323
1632	Q96DH6-2	5	7	29.5	251	28421	8.5	Isoform 2 of Q96DH6
1632	Q96DH6	5	7	22.6	328	35197	8.5	RNA-binding protein Musashi homolog 2
1633	P41236	5	9	22.4	205	23015	4.7	Protein phosphatase inhibitor 2
1634	Q8IWR8	5	48	25.4	173	20820	11.4	Ribosomal protein L19
1634	UPI0000192A4A	5	48	22.6	195	23335	11.5	60S ribosomal protein L19.
1634	P84098	5	48	22.4	196	23466	11.5	60S ribosomal protein L19
1634	Q53G49	5	48	22.4	196	23467	11.4	Ribosomal protein L19 variant
1635	Q14919	5	18	22.4	205	22350	5.2	Dr1-associated corepressor
1635	Q14919-2	5	18	21.8	211	23148	5.3	Isoform 2 of Q14919
1635	UPI0000D62635	5	18	21.7	212	23205	5.3	Dr1-associated corepressor (Dr1-associated protein 1) (Negative co- factor 2 alpha) (NC2 alpha).
1636	Q8N5D1	5	14	22.2	230	27086	10.3	MRPL47 protein
1636	UPI000013D022	5	14	20.4	250	29450	10.4	mitochondrial ribosomal protein L47 isoform a
1636	UPI0000D61BB3	5	14	20.2	252	29787	10.4	39S ribosomal protein L47, mitochondrial precursor (L47mt) (MRP-L47).
1636	Q9HD33	5	14	20.2	252	29577	10.3	39S ribosomal protein L47, mitochondrial precursor
1637	Q07021	5	41	22	282	31362	4.8	Complement component 1 Q subcomponent-binding protein, mitochondrial precursor
1638	O43402	5	7	21.9	210	23773	6.4	Neighbor of COX4
1639	UPI00006D2BD0	5	10	24	208	22627	8.5	Acyl-protein thioesterase 2 (EC 3.1.2.-) (Lysophospholipase II) (LPL- I).
1639	O95372	5	10	21.6	231	24737	7.2	Acyl-protein thioesterase 2
1640	Q6DKI1	5	13	21.5	246	28661	10.5	Ribosomal protein L7-like 1
1641	P11908	5	10	21.4	318	34769	6.6	Ribose-phosphate pyrophosphokinase II
1641	Q0VDI0	5	10	21.2	321	35054	6.4	Phosphoribosyl pyrophosphate synthetase 2
1642	Q1XII0	5	6	26.2	260	29326	6.8	Bone marrow stromal cell antigen 1 nirs variant 1
1642	Q10588	5	6	21.4	318	35724	7.8	ADP-ribosyl cyclase 2 precursor
1642	UPI0000126AFB	5	6	21.4	318	35738	7.8	bone marrow stromal cell antigen 1 precursor
1642	UPI000066D9E4	5	6	20.4	333	37482	8	ADP-ribosyl cyclase 2 precursor (EC 3.2.2.5) (Cyclic ADP-ribose hydrolase 2) (cADPr hydrolase 2) (Bone marrow stromal antigen 1) (BST- 1) (CD157 antigen).
1643	Q969X5-2	5	11	31.3	198	22160	9.1	Isoform 2 of Q969X5
1643	Q969X5	5	11	21.4	290	32592	7.1	Endoplasmic reticulum-Golgi intermediate compartment protein 1
1644	Q00765	5	27	21.2	189	21493	8.1	Receptor expression-enhancing protein 5
1645	Q8NBX0	5	21	21.2	429	47151	9.1	Probable saccharopine dehydrogenase
1646	Q9BYG3	5	10	21.2	293	34222	9.9	MKI67 FHA domain-interacting nucleolar phosphoprotein
1646	UPI000006F493	5	10	21.2	293	34253	9.9	MKI67 (FHA domain) interacting nucleolar phosphoprotein
1647	Q9H7Z7	5	9	21.2	377	41943	9.2	Prostaglandin E synthase 2 (EC 5.3.99.3) (Microsomal prostaglandin E synthase 2) (mPGES-2) [Contains: Prostaglandin E synthase 2 truncated form]
1648	P54709	5	35	21.1	279	31513	8.3	Sodium/potassium-transporting ATPase subunit beta-3
1649	Q8TC12	5	12	21.1	318	35386	8.8	Retinol dehydrogenase 11
1649	UPI0000D6241F	5	12	21.1	318	35415	8.9	Retinol dehydrogenase 11 (EC 1.1.1.-) (Retinal reductase 1) (RalR1) (Prostate short-chain dehydrogenase/reductase 1) (Androgen-regulated short-chain dehydrogenase/reductase 1) (HCV core-binding protein HCBP12).
1649	UPI0000070F53	5	12	21.1	318	35414	8.8	androgen-regulated short-chain dehydrogenase/reductase 1
1650	Q5RKV6	5	9	21	272	28235	6.3	Exosome component 6
1651	UPI000049E0CA	5	19	22.3	229	24770	7.9	Collagen triple helix repeat-containing protein 1 precursor (NMTC1 protein).
1651	Q96CG8	5	19	21	243	26224	8	Collagen triple helix repeat-containing protein 1 precursor
1652	O76054	5	6	20.8	403	46145	7.8	SEC14-like protein 2
1652	Q53EQ2	5	6	20.8	403	46117	7.8	SEC14-like 2 variant
1653	P25774	5	8	20.8	331	37496	8.3	Cathepsin S precursor
1653	Q6FHS5	5	8	20.8	331	37526	8.2	CTSS protein
1654	Q01081	5	19	20.8	240	27872	8.8	Splicing factor U2AF 35 kDa subunit
1655	UPI0000456FB4	5	7	21.6	287	31935	8.1	Uncharacterized protein C20orf43.
1655	Q9BY42-2	5	7	21.6	287	31903	8.1	Isoform 2 of Q9BY42
1655	Q9BY42	5	7	20.3	306	33855	8.6	Uncharacterized protein C20orf43
1655	UPI000013C542	5	7	20.3	306	33887	8.6	Uncharacterized protein C20orf43.
1656	P27105	5	15	20.1	288	31731	7.9	Erythrocyte band 7 integral membrane protein
1657	Q5QPQ6	5	6	21.7	300	31735	7.6	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase

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1657	P35914	5	6	20	325	34360	8.5	Hydroxymethylglutaryl-CoA lyase, mitochondrial precursor
1658	Q99541	5	5	19.9	437	48075	6.8	Adipophilin
1659	P01584	5	15	19.7	269	30748	4.8	Interleukin-1 beta precursor
1659	Q53X59	5	15	19.7	269	30747	4.9	IL1B protein
1660	O75934	5	7	19.6	225	26131	5.6	Breast carcinoma amplified sequence 2
1661	Q7Z2Q5	5	8	20	429	46405	6.6	C-terminal binding protein 1
1661	Q13363	5	8	19.5	440	47535	6.8	C-terminal-binding protein 1
1662	Q5U000	5	31	19.5	303	33868	7.1	Cathepsin Z
1663	UPI0000074210	5	13	19.5	329	35886	8.3	NADP-dependent leukotriene B4 12-hydroxydehydrogenase
1664	Q15435-2	5	14	21.5	317	36837	5.2	Isoform 2 of Q15435
1664	Q15435	5	14	18.9	360	41564	4.9	Protein phosphatase 1 regulatory subunit 7
1665	UPI000041C7E5	5	8	21.6	305	34756	8.4	replication factor C 3 isoform 2
1665	P40938	5	8	18.5	356	40556	8.3	Replication factor C subunit 3
1666	Q658J0	5	9	20.5	332	37029	6.5	Hypothetical protein DKFZp762L015
1666	Q9GZT8	5	9	19.4	350	38984	6.4	NIF3-like protein 1
1666	Q53TX4	5	9	18	377	41968	6.7	Hypothetical protein NIF3L1
1667	Q99848	5	6	18	306	34852	10.1	Probable rRNA-processing protein EBP2
1667	UPI0000129B3E	5	6	18	306	34820	10.1	EBNA1 binding protein 2
1668	Q12792-2	5	5	18.9	350	40283	7	Isoform 1 of Q12792
1668	Q12792	5	5	17.9	368	42209	7	Twinfilin-1
1668	UPI0000D621D3	5	5	17.9	368	42362	7.6	Twinfilin-1 (Protein A6) (Protein tyrosine kinase 9).
1668	Q6NUK9	5	5	17.7	372	42389	7.3	TWF1 protein
1669	Q96GG9	5	7	17.8	259	30124	5.3	DCN1-like protein 1
1669	UPI000013E0D4	5	7	17.8	258	29993	5.3	DCN1-like protein 1 (Defective in cullin neddylation protein 1-like protein 1) (DCUN1 domain-containing protein 1) (Squamous cell carcinoma-related oncogene).
1670	Q68D08	5	15	17.6	324	36750	6.1	Hypothetical protein DKFZp686B04128
1670	Q9NUQ9	5	15	17.6	324	36748	6.1	Protein FAM49B
1671	P30519	5	8	17.4	316	36033	5.4	Heme oxygenase 2
1671	Q6IBP2	5	8	17.4	316	36015	5.4	HMOX2 protein
1671	Q6FHB5	5	8	17.4	316	36049	5.4	HMOX2 protein
1671	Q53HF1	5	8	17.4	316	35934	5.4	Heme oxygenase (Decyclizing) 2 variant
1672	P53007	5	15	17.4	311	34013	9.9	Tricarboxylate transport protein, mitochondrial precursor
1672	Q6LAP8	5	15	17	318	34788	9.9	Mitochondrial citrate transport protein
1673	Q15654	5	5	17.4	476	50288	7.4	Thyroid receptor-interacting protein 6
1674	Q8NFQ8	5	14	17.4	470	51263	5	Torsin-1A-interacting protein 2
1675	Q9BZK7	5	7	17.1	514	55595	5.6	F-box-like/WD repeat protein TBL1XR1
1676	Q9H0V9	5	7	17	348	39711	8.4	VIP36-like protein precursor
1676	Q9H0V9-2	5	7	16.4	359	40982	8.9	Isoform 2 of Q9H0V9
1677	Q9ULA0	5	8	17.3	475	52428	7.4	Aspartyl aminopeptidase
1677	Q53SB6	5	8	16.9	485	53439	7.6	Hypothetical protein DNPEP
1678	Q8WVY7	5	9	16.7	318	36805	6.5	Ubiquitin-like domain-containing CTD phosphatase 1
1678	UPI000007368C	5	9	16.7	318	36733	6.7	ubiquitin-like domain containing CTD phosphatase 1
1679	Q96HS5	5	7	36.9	179	21021	7.9	PSCD3 protein
1679	Q75MW6	5	7	17.1	387	45231	5.9	Hypothetical protein PSCD3
1679	A4D2N8	5	7	16.5	399	46292	5.5	Pleckstrin homology, Sec7 and coiled-coil domains 3
1679	O43739	5	7	16.5	400	46349	5.5	Cytohesin-3
1680	Q9UIC9	5	8	16.5	303	34814	5.9	Serine/threonine protein phosphatase catalytic subunit
1680	O00743	5	8	16.4	305	35144	5.7	Serine/threonine-protein phosphatase 6
1681	P52294	5	7	16.4	538	60249	5	Importin alpha-1 subunit
1681	UPI000013D524	5	7	16.4	538	60222	5	Importin alpha-1 subunit (Karyopherin alpha-1 subunit) (SRP1-beta) (RAG cohort protein 2) (Nucleoprotein interactor 1) (NPI-1).
1681	Q5BKZ2	5	7	16.4	538	60309	5	Karyopherin alpha 1
1682	Q14151	5	12	16.4	953	107474	6.2	Scaffold attachment factor B2
1683	Q9NZU5	5	5	16.4	365	40833	7.9	LIM and cysteine-rich domains protein 1
1684	O75436	5	9	16.2	327	38170	6.5	Vacuolar protein sorting-associated protein 26A
1685	Q9Y2S7	5	5	15.8	368	42033	8.6	Polymerase delta-interacting protein 2
1685	UPI000013C4D8	5	5	15.8	367	41934	8.6	Polymerase delta-interacting protein 2 (38 kDa DNA polymerase delta interaction protein) (p38).
1686	Q53FH8	5	6	15.6	404	46816	7.1	Sorting nexin 5 variant
1686	Q9Y5X3	5	6	15.6	404	46817	6.8	Sorting nexin-5
1686	Q6P5V6	5	6	15.3	412	47438	7.5	SNX5 protein
1687	Q9UI12-2	5	14	16.1	465	54151	6.5	Isoform 2 of Q9UI12
1687	Q9UI12	5	14	15.5	483	55883	6.5	Vacuolar ATP synthase subunit H
1688	Q53F73	5	9	15.4	305	34114	9.5	Cytochrome b5 reductase 1
1688	Q9UHQ9	5	9	15.4	305	34095	9.4	NADH-cytochrome b5 reductase isoform
1688	Q8NCL5	5	9	15.4	305	34035	9.4	CDNA FLJ90173 fis, clone MAMMA1000457, highly similar to Cytochrome b5 reductase 1

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1689	Q13510	5	18	15.2	395	44650	7.6	Acid ceramidase precursor (EC 3.5.1.23) (Acylsphingosine deacylase) (N-acylsphingosine amidohydrolase) (AC) (Putative 32 kDa heart protein) (PHP32) [Contains: Acid ceramidase subunit alpha; Acid ceramidase subunit beta]
1689	Q53H01	5	18	15.2	395	44692	7.6	N-acylsphingosine amidohydrolase (Acid ceramidase) 1 preproprotein isoform a variant
1689	UPI0000190976	5	18	14.6	411	46494	7.9	N-acylsphingosine amidohydrolase (acid ceramidase) 1 isoform b
1690	P37198	5	9	15.1	522	53255	5.3	Nuclear pore glycoprotein p62
1691	UPI00004561A1	5	19	16	419	45958	7.6	KH domain-containing, RNA-binding, signal transduction-associated protein 1 (p21 Ras GTPase-activating protein-associated p62) (GAP- associated tyrosine phosphoprotein p62) (Src-associated in mitosis 68 kDa protein) (Sam68) (p68).
1691	Q07666-2	5	19	16	418	45861	7.6	Isoform 2 of Q07666
1691	Q07666	5	19	15.1	443	48227	8.7	KH domain-containing, RNA-binding, signal transduction-associated protein 1
1692	O75886	5	5	15	525	58164	5.1	Signal transducing adapter molecule 2
1692	UPI0000167B90	5	5	15	525	58193	5	signal transducing adaptor molecule 2
1693	Q8N5Y3	5	25	15.7	331	37246	5.4	GYG1 protein
1693	Q6FHZ1	5	25	15.6	333	37479	5.4	GYG protein
1693	P46976	5	25	14.9	350	39384	5.5	Glycogenin-1
1694	Q9UH62	5	7	14.8	379	42501	8.4	Armadillo repeat-containing X-linked protein 3
1695	UPI0000D62170	5	8	17.7	395	44603	5.6	Ataxin-10 (Spinocerebellar ataxia type 10 protein) (Brain protein E46 homolog).
1695	Q9UBB4	5	8	14.7	475	53489	5.2	Ataxin-10
1696	O14929	5	7	14.6	419	49513	5.7	Histone acetyltransferase type B catalytic subunit
1697	Q5M8T4	5	7	14.6	349	38069	7.9	Connective tissue growth factor
1697	Q6FHL8	5	7	14.6	349	38129	7.9	CTGF protein
1698	O15382-2	5	5	18.7	300	33777	7.7	Isoform B of O15382
1698	O15382	5	5	14.3	392	44288	8.6	Branched-chain-amino-acid aminotransferase, mitochondrial precursor (EC 2.6.1.42) (BCAT(m))
1698	Q53EW7	5	5	14.3	392	44274	8.5	Branched chain aminotransferase 2, mitochondrial variant
1699	Q13610	5	10	14.2	501	55828	4.8	Periodic tryptophan protein 1 homolog
1699	Q9BV37	5	10	14.2	501	55879	4.8	PWP1 homolog
1699	Q53FW9	5	10	14.2	501	55729	4.7	Nuclear phosphoprotein similar to S. cerevisiae PWP1 variant
1700	UPI0000DD87AF	5	7	14.3	615	68209	7	PREDICTED: similar to kinesin light chain 2
1700	Q9H0B6	5	7	14.1	622	68935	7.2	Kinesin light chain 2
1701	P30566	5	9	14	484	54889	7.1	Adenylosuccinate lyase
1701	Q71UA4	5	9	14	484	54871	7.1	Adenylosuccinate lyase
1702	Q6I9S2	5	6	13.8	536	61449	9.5	SNW1 protein
1703	Q6IP98	5	23	13.8	349	40317	4.9	KRT17 protein
1704	Q15437	5	12	13.6	767	86479	6.9	Protein transport protein Sec23B
1704	Q503A9	5	12	13.6	767	86495	6.9	Sec23 homolog B
1705	Q9NY61	5	8	13.4	560	63133	4.9	Protein AATF
1705	UPI000013C869	5	8	13.3	562	63291	4.9	Protein AATF (Apoptosis-antagonizing transcription factor) (Rb-binding protein Che-1).
1706	Q00613-2	5	8	14.3	489	52881	6.1	Isoform Short of Q00613
1706	UPI0000DD7F38	5	8	13.5	518	56201	5.7	PREDICTED: similar to Heat shock factor protein 1 (HSF 1) (Heat shock transcription factor 1) (HSTF 1)
1706	UPI0000DD7F05	5	8	13.5	518	56205	5.7	PREDICTED: similar to Heat shock factor protein 1 (HSF 1) (Heat shock transcription factor 1) (HSTF 1)
1706	Q00613	5	8	13.2	529	57261	5.2	Heat shock factor protein 1
1707	Q8N7H5	5	5	12.8	485	55501	5.4	CDNA FLJ25557 fis, clone JTH02756
1707	Q9NUU9	5	5	11.7	531	59798	4.6	CDNA FLJ11123 fis, clone PLACE1006167
1707	Q9H166	5	5	11.7	531	59976	4.6	RNA polymerase-associated protein 1 homolog
1708	Q8N422	5	7	12.6	381	43073	5.7	Protein kinase, cAMP-dependent, regulatory, type I, beta
1708	UPI0000DD7E3F	5	7	12.6	381	43011	5.7	PREDICTED: similar to protein kinase, cAMP-dependent, regulatory, type I, beta
1709	O15427	5	24	12.5	465	49469	8	Monocarboxylate transporter 4
1709	Q53G91	5	24	12.5	465	49483	8	Solute carrier family 16, member 3 variant
1710	Q59F45	5	11	13.7	386	43659	6.8	MAD, mothers against decapentaplegic homolog 3 variant
1710	P84022	5	11	12.5	425	48081	7.2	Mothers against decapentaplegic homolog 3
1711	Q53HC4	5	7	12.4	469	51904	7.1	CGI-51 protein variant
1711	Q9Y512	5	7	12.4	469	51976	6.9	Sorting and assembly machinery component 50 homolog
1712	Q53EL7	5	5	12.2	584	61692	8.1	Interferon regulatory factor 2-binding protein 1
1712	Q8IU81	5	5	12.2	584	61688	8.2	Interferon regulatory factor 2 binding protein 1
1712	Q6DC95	5	5	12.2	584	61617	8	Interferon regulatory factor 2 binding protein 1
1713	Q9H4A4	5	6	12.2	650	72596	5.8	Aminopeptidase B
1714	O60678	5	7	12.1	531	59903	5.3	Protein arginine N-methyltransferase 3
1714	UPI0000198DED	5	7	12.1	531	59876	5.3	Protein arginine N-methyltransferase 3 (EC 2.1.1.-) (Heterogeneous nuclear ribonucleoprotein methyltransferase-like protein 3).

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
1714	UPI00001AFD06	5	7	11.7	548	61841	7.3	Protein arginine N-methyltransferase 3 (EC 2.1.1.-) (Heterogeneous nuclear ribonucleoprotein methyltransferase-like protein 3).
1714	Q8WUV3	5	7	11.7	548	61967	7.4	PRMT3 protein
1715	Q15067	5	5	12.1	660	74424	8.2	Acyl-coenzyme A oxidase 1, peroxisomal
1715	Q15067-2	5	5	12.1	660	74668	7.6	Isoform 2 of Q15067
1715	Q7Z3W5	5	5	12	666	75286	7.6	Hypothetical protein DKFZp686L1882
1716	P20839-2	5	8	14.7	489	52598	6.6	Isoform 2 of P20839
1716	P20839	5	8	14	514	55406	6.9	Inosine-5'-monophosphate dehydrogenase 1
1716	UPI0000D61CCC	5	8	13.6	528	56788	7.1	Inosine-5'-monophosphate dehydrogenase 1 (EC 1.1.1.205) (IMP dehydrogenase 1) (IMPDH-I) (IMPD 1).
1716	Q6ZNB1	5	8	13.6	530	57050	7.3	CDNA FLJ16255 fis, clone HLUNG2015548, highly similar to INOSINE-5'- MONOPHOSPHATE DEHYDROGENASE 1
1716	UPI0000D61CCB	5	8	12.8	561	60210	6.6	Inosine-5'-monophosphate dehydrogenase 1 (EC 1.1.1.205) (IMP dehydrogenase 1) (IMPDH-I) (IMPD 1).
1716	UPI0000D61CCD	5	8	12.3	587	63025	6.7	Inosine-5'-monophosphate dehydrogenase 1 (EC 1.1.1.205) (IMP dehydrogenase 1) (IMPDH-I) (IMPD 1).
1716	UPI0000D61CCA	5	8	12.1	597	64093	6.9	Inosine-5'-monophosphate dehydrogenase 1 (EC 1.1.1.205) (IMP dehydrogenase 1) (IMPDH-I) (IMPD 1).
1716	A4D0Z6	5	8	12	599	64320	7	IMP (Inosine monophosphate) dehydrogenase 1
1716	Q5H9Q6	5	8	12	599	64537	8	Hypothetical protein DKFZp781N0678
1717	Q16843	5	21	13.9	460	52444	6.5	Thromboxane synthase
1717	P24557	5	21	12	533	60544	7.6	Thromboxane-A synthase
1717	UPI000006DC94	5	21	12	534	60676	7.6	thromboxane A synthase 1 (platelet, cytochrome P450, family 5, subfamily A) isoform TXS-I
1717	Q53F23	5	21	12	534	60650	7.6	Thromboxane A synthase 1 (Platelet, cytochrome P450, family 5, subfamily A) isoform TXS-I variant
1718	Q13098	5	8	11.9	471	53372	6.7	COP9 signalosome complex subunit 1
1718	Q13098-2	5	8	11.8	475	53816	6.9	Isoform 2 of Q13098
1718	UPI0000231C2E	5	8	10.6	527	59050	6.3	G protein pathway suppressor 1 isoform 1
1719	Q9UHG3	5	7	11.9	505	56640	6.2	Prenylcysteine oxidase precursor
1719	UPI000013D518	5	7	11.9	505	56700	6.2	prenylcysteine oxidase 1
1720	Q9UN86-2	5	19	12.7	449	50817	5.4	Isoform B of Q9UN86
1720	Q9UN86	5	19	11.8	482	54121	5.6	Ras GTPase-activating protein-binding protein 2
1721	P10619	5	23	11.7	480	54466	6.6	Lysosomal protective protein precursor (EC 3.4.16.5) (Cathepsin A) (Carboxypeptidase C) (Protective protein for beta-galactosidase) [Contains: Lysosomal protective protein 32 kDa chain; Lysosomal protective protein 20 kDa chain]
1721	Q59EV6	5	23	11.3	497	56120	6.6	Carrier family 6 , member 8 variant
1722	Q59H57	5	29	20.3	300	31994	9.5	Fusion (Involved in t(12;16) in malignant liposarcoma) isoform a variant
1722	P35637	5	29	11.6	526	53426	9.4	RNA-binding protein FUS
1722	Q8TBR3	5	29	11.6	526	53400	9.4	Fusion (Involved in t(12;16) in malignant liposarcoma)
1722	Q13344	5	29	11.6	528	53377	9.4	Fus-like protein
1722	P35637-2	5	29	11.6	525	53355	9.4	Isoform Short of P35637
1723	Q9Y3B3	5	18	21	224	25172	6.9	Transmembrane emp24 domain-containing protein 7 precursor
1723	Q6JUT2	5	18	11.6	404	46173	5.1	Toll-like receptor adapter molecule 2
1724	A4D1I8	5	14	11.4	561	64400	6.8	Asparagine synthetase
1724	P08243	5	14	11.4	561	64370	6.9	Asparagine synthetase [glutamine-hydrolyzing]
1725	UPI0000D61DD0	5	16	11.9	1005	117261	8	Probable global transcription activator SNF2L1 (EC 3.6.1.-) (Nucleosome remodeling factor subunit SNF2L) (ATP-dependent helicase SMARCA1) (SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 1).
1725	Q5JZ57	5	16	11.9	1005	117265	7.8	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1
1725	P28370	5	16	11.4	1054	122605	8.1	Probable global transcription activator SNF2L1
1726	P63151	5	11	11.4	447	51692	6.2	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform
1726	Q56VW8	5	11	11.4	447	51648	6.2	Lung cancer-related protein 9
1727	Q92879-2	5	11	12.9	482	51546	8.5	Isoform 2 of Q92879
1727	Q92879-3	5	11	12.8	483	51617	8.5	Isoform 3 of Q92879
1727	Q92879	5	11	12.8	486	52063	8.5	CUG triplet repeat RNA-binding protein 1
1727	Q4LE52	5	11	11.4	544	58344	7.8	CUGBP1 variant protein
1728	Q9BQ39	5	9	11.4	737	82565	9.2	ATP-dependent RNA helicase DDX50
1729	Q01650	5	65	11.2	507	55010	7.7	Large neutral amino acids transporter small subunit 1
1730	Q8NF37	5	25	11.2	534	59151	6	1-acylglycerophosphocholine O-acyltransferase 1
1731	Q9HCC0-2	5	9	12	525	57519	7.7	Isoform 2 of Q9HCC0

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1731	Q9HCC0	5	9	11.2	563	61333	7.7	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial precursor
1732	Q8TF42	5	6	11.1	649	72696	6.9	Suppressor of T-cell receptor signaling 1
1733	Q96G03	5	9	11.1	612	68283	6.7	Phosphoglucomutase-2
1734	P00390	5	19	10.5	522	56257	8.5	Glutathione reductase, mitochondrial precursor
1735	P48637	5	11	10.5	474	52385	5.9	Glutathione synthetase
1736	Q12929	5	11	10.5	822	91882	7.5	Epidermal growth factor receptor kinase substrate 8
1736	UPI000013DC63	5	11	10.4	824	92040	7.5	Epidermal growth factor receptor kinase substrate 8.
1737	O43823	5	6	10.3	692	76108	5.1	A-kinase anchor protein 8
1738	Q6DEN2	5	6	9.8	684	73910	6.6	DPYSL3 protein
1738	UPI000020CF0E	5	6	9.8	684	73911	6.4	Dihydropyrimidinase-related protein 3 (DRP-3) (Unc-33-like phosphoprotein) (ULIP protein) (Collapsin response mediator protein 4) (CRMP-4).
1739	Q14258	5	13	9.7	630	70990	8.1	Tripartite motif-containing protein 25
1739	UPI00001AE6B8	5	13	9.7	630	70974	8.1	tripartite motif-containing 25
1739	Q59GW5	5	13	9.5	644	72250	8.1	Tripartite motif-containing 25 variant
1740	Q9BR76	5	10	9.6	489	54235	5.9	Coronin-1B
1741	Q13586	5	6	9.2	685	77493	6.7	Stromal interaction molecule 1 precursor
1741	Q8N382	5	6	9.2	685	77423	6.7	Stromal interaction molecule 1
1742	Q8NG18	5	5	9.2	554	63522	5.1	Chronic myelogenous leukemia tumor antigen 66 short form
1742	UPI000021048A	5	5	8.7	583	66756	5.1	NudC domain containing 1
1742	Q9BVR5	5	5	8.7	583	66790	5.1	NudC domain containing 1
1742	Q96SI4	5	5	8.7	583	66729	5.1	CDNA FLJ14991 fis, clone Y79AA1001781
1742	Q96RS6	5	5	8.7	583	66776	5.1	NudC domain-containing protein 1
1743	Q8IVL6	5	11	9.1	736	81837	6.3	Prolyl 3-hydroxylase 3 precursor
1743	UPI00001AF55A	5	11	9.1	735	81723	6.3	Probable G-protein coupled receptor 162 (Gene-rich cluster gene A protein).
1744	P30825	5	34	8.6	629	67638	5.4	High-affinity cationic amino acid transporter 1
1745	Q15397	5	13	8.6	648	73584	9.6	Protein KIAA0020
1746	Q14978	5	18	8.4	699	73603	9.5	Nucleolar phosphoprotein p130
1746	UPI00001303C3	5	18	8.4	699	73720	9.5	nucleolar and coiled-body phosphoprotein 1
1746	Q9BUV3	5	18	8.4	700	73745	9.5	Nucleolar and coiled-body phosphoprotein 1
1746	Q14978-2	5	18	8.3	709	74747	9.5	Isoform Beta of Q14978
1747	Q15061	5	15	8.3	720	79119	5.9	WD repeat protein 43
1748	Q96EY7	5	6	8.3	689	78550	6.4	Pentatricopeptide repeat domain-containing protein 3
1748	UPI0000456DED	5	6	8.3	690	78624	6.4	Pentatricopeptide repeat domain 3
1749	Q9H078-2	5	6	8.7	677	75449	9	Isoform 2 of Q9H078
1749	Q9H078	5	6	8.3	707	78729	9	Caseinolytic peptidase B protein homolog
1750	Q9Y2W2	5	9	8.3	641	69998	8.4	WW domain-binding protein 11
1751	O95352	5	12	8.1	703	77960	6.2	Autophagy-related protein 7
1752	Q96ST2	5	9	7.9	819	91955	4.7	IWS1 homolog
1753	Q9Y5S1	5	17	7.9	764	85981	5.8	Transient receptor potential cation channel subfamily V member 2
1753	UPI0000D622C9	5	17	7.8	766	86151	5.9	Transient receptor potential cation channel subfamily V member 2 (TrpV2) (osm-9-like TRP channel 2) (OTRPC2) (Vanilloid receptor-like protein 1) (VRL-1).
1754	O94776	5	10	7.8	668	75023	9.7	Metastasis-associated protein MTA2
1755	O60341	5	5	7.7	852	92903	6.5	Lysine-specific histone demethylase 1
1755	UPI0000D61E80	5	5	7.5	876	95223	6.2	Lysine-specific histone demethylase 1 (EC 1.-.-.-) (Flavin-containing amine oxidase domain-containing protein 2) (BRAF35-HDAC complex protein BHC110).
1755	O60341-2	5	5	7.5	876	95155	6.2	Isoform 2 of O60341
1756	O75150	5	8	7.7	1001	113678	6.3	E3 ubiquitin-protein ligase BRE1B
1756	UPI000013D2CF	5	8	7.7	1001	113650	6.2	Ubiquitin-protein ligase BRE1B (EC 6.3.2.-) (BRE1-B) (RING finger protein 40) (95 kDa retinoblastoma-associated protein) (RBP95).
1757	Q9Y4K0	5	8	7.6	774	86725	6.4	Lysyl oxidase homolog 2 precursor
1757	UPI00001AE795	5	8	7.6	777	87020	6.4	Lysyl oxidase homolog 2 precursor (EC 1.4.3.-) (Lysyl oxidase-like protein 2) (Lysyl oxidase-related protein 2) (Lysyl oxidase-related protein WS9-14).
1758	Q5JTZ4	5	9	7.5	949	104235	5.1	A kinase (PRKA) anchor protein 2
1758	UPI000002A38A	5	9	6.5	1090	120630	5	PALM2-AKAP2 protein isoform 2
1759	Q9H307	5	17	7.4	717	81614	7.2	Pinin
1759	UPI000013C70D	5	17	7.4	717	81628	7.2	Pinin (140 kDa nuclear and cell adhesion-related phosphoprotein) (Domain-rich serine protein) (DRS-protein) (DRSP) (Melanoma metastasis clone A protein) (Desmosome-associated protein) (SR-like protein) (Nuclear protein SDK3).
1760	Q9NZ08	5	10	7.3	929	105847	6.4	Adipocyte-derived leucine aminopeptidase precursor
1760	Q9NZ08-2	5	10	7.3	936	106453	6.2	Isoform 2 of Q9NZ08
1760	UPI0000041388	5	10	7.2	941	107235	6.5	type 1 tumor necrosis factor receptor shedding aminopeptidase regulator isoform b
1761	Q2M2I8	5	7	7.2	863	93578	8.5	AP2-associated protein kinase 1

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1762	Q99805	5	19	6.8	663	75776	7.4	Transmembrane 9 superfamily protein member 2 precursor
1763	Q9UPN7	5	6	6.7	881	96724	4.6	SAPS domain family member 1
1763	UPI0000D61817	5	6	6.7	880	96637	4.6	SAPS domain family member 1.
1763	UPI000046D380	5	6	6.6	891	97792	4.6	SAPS domain family, member 1
1764	O95479	5	5	6.6	791	88893	7.3	GDH/6PGL endoplasmic bifunctional protein precursor [Includes: Glucose 1-dehydrogenase (EC 1.1.1.47) (Hexose-6-phosphate dehydrogenase); 6-phosphogluconolactonase (EC 3.1.1.31) (6PGL)]
1765	UPI00003672DD	5	8	9.2	552	58818	6	Disabled homolog 2 (Differentially expressed protein 2) (DOC-2).
1765	P98082-2	5	8	9.2	552	58861	5.7	Isoform 2 of P98082
1765	P98082	5	8	6.6	770	82448	5.5	Disabled homolog 2
1765	UPI0000161C97	5	8	6.6	770	82588	5.7	disabled homolog 2
1765	UPI000013DD18	5	8	6.6	770	82405	5.7	Disabled homolog 2 (Differentially expressed protein 2) (DOC-2).
1766	Q8IWA0	5	8	6.6	830	94499	6	WD repeat protein 75
1767	Q14739	5	20	6.5	615	70703	9.4	Lamin-B receptor
1768	O60502	5	6	6.4	916	102915	4.9	Bifunctional protein NCOAT (Nuclear cytoplasmic O-GlcNAcase and acetyltransferase) (Meningioma-expressed antigen 5) [Includes: Beta-hexosaminidase (EC 3.2.1.52) (N-acetyl-beta-glucosaminidase) (Beta-N- acetylhexosaminidase) (Hexosaminidase C) (N-acetyl-beta-D-glucosaminidase) (O-GlcNAcase); Histone acetyltransferase (EC 2.3.1.48) (HAT)]
1769	P23786	5	5	6.4	658	73777	8.2	Carnitine O-palmitoyltransferase 2, mitochondrial precursor
1770	Q53EP0	5	13	6	1204	132878	5.9	Fibronectin type III domain-containing protein 3B
1770	UPI00001AE8B2	5	13	6	1204	132888	5.9	fibronectin type III domain containing 3B
1770	Q8IXB2	5	13	6	1204	132900	5.9	FAD104
1770	Q5U5T8	5	13	6	1204	132957	5.9	Fibronectin type III domain containing 3B
1771	Q9HC35	5	7	5.8	981	108903	6.3	Echinoderm microtubule-associated protein-like 4
1771	UPI0000140350	5	7	5.8	981	108916	6.4	Echinoderm microtubule-associated protein-like 4 (EMAP-4) (Restrictedly overexpressed proliferation-associated protein) (Ropp 120).
1772	UPI000045664D	5	10	5.8	993	110953	5.4	Protein phosphatase 1 regulatory subunit 12A (Myosin phosphatase- targeting subunit 1) (Myosin phosphatase target subunit 1) (Protein phosphatase myosin-binding subunit).
1772	O14974-2	5	10	5.8	995	111185	5.4	Isoform 2 of O14974
1772	O14974	5	10	5.6	1030	115281	5.4	Protein phosphatase 1 regulatory subunit 12A
1772	UPI000045664E	5	10	5.6	1028	115048	5.4	Protein phosphatase 1 regulatory subunit 12A (Myosin phosphatase- targeting subunit 1) (Myosin phosphatase target subunit 1) (Protein phosphatase myosin-binding subunit).
1772	Q2NKL4	5	10	5.6	1030	115281	5.4	PPP1R12A protein
1773	P56199	5	12	5.3	1179	130848	6.3	Integrin alpha-1 precursor
1773	UPI0000D61624	5	12	5.3	1180	130988	6.3	Integrin alpha-1 precursor (Laminin and collagen receptor) (VLA-1) (CD49a antigen).
1774	Q15386	5	7	5.1	1083	123923	6.7	Ubiquitin-protein ligase E3C
1774	UPI000013D26C	5	7	5.1	1085	124150	6.7	Ubiquitin-protein ligase E3C (EC 6.3.2.-).
1774	UPI0000071402	5	7	5.1	1083	123937	6.7	ubiquitin protein ligase E3C
1775	Q59HA5	5	8	5.4	1196	130790	5.8	Cyclin G-associated kinase variant
1775	Q5U4P5	5	8	5.3	1232	134410	5.8	GAK protein
1775	O14976	5	8	5	1311	143190	5.7	Cyclin G-associated kinase
1775	UPI0000161B7C	5	8	5	1311	143164	5.7	cyclin G associated kinase
1776	Q8NFA7	5	6	5.5	940	103581	7.1	Transmembrane receptor PTK7-3
1776	UPI0000457445	5	6	5.1	1015	112354	6.9	Tyrosine-protein kinase-like 7 precursor (Colon carcinoma kinase 4) (CCK-4).
1776	Q8NFA6	5	6	5.1	1014	112261	7	Transmembrane receptor PTK7-4
1776	Q8NFA8	5	6	5	1030	113805	7	Transmembrane receptor PTK7-2
1776	Q13308	5	6	4.9	1070	118392	7.1	Tyrosine-protein kinase-like 7 precursor
1776	Q6IQ54	5	6	4.9	1070	118376	7.1	PTK7 protein tyrosine kinase 7
1777	Q16706	5	21	4.9	1144	131084	7.6	Alpha-mannosidase 2
1777	UPI000013D193	5	21	4.9	1144	131140	7.6	mannosidase, alpha, class 2A, member 1
1778	Q08AD0	5	7	4.8	1516	174700	6.9	UDP-glucose ceramide glucosyltransferase-like 2
1778	UPI00001FC9AA	5	7	4.8	1516	174734	6.9	UDP-glucose:glycoprotein glucosyltransferase 2 precursor (EC 2.4.1.-) (UDP-glucose ceramide glucosyltransferase-like 1) (UDP-- Glc:glycoprotein glucosyltransferase 2) (HUGT2).
1778	UPI0000137AEE	5	7	4.8	1516	174760	6.9	UDP-glucose:glycoprotein glucosyltransferase 2
1778	Q9NYU1	5	7	4.8	1516	174718	6.9	UDP-glucose:glycoprotein glucosyltransferase 2 precursor
1779	O14802	5	6	4.7	1391	155748	8.5	DNA-directed RNA polymerase III largest subunit
1779	Q8IW34	5	6	4.7	1390	155641	8.5	DNA-directed RNA polymerase
1780	P19174	5	9	4.7	1290	148532	6	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase gamma 1
1780	A2A284	5	9	4.6	1291	148660	6	Phospholipase C, gamma 1

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1780	UPI0000D61091	5	9	4.2	1412	161314	7.2	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase gamma 1 (EC 3.1.4.11) (Phosphoinositide phospholipase C) (PLC-gamma-1) (Phospholipase C-gamma-1) (PLC-II) (PLC-148).
1780	Q4LE43	5	9	4.2	1412	161302	7.2	PLCG1 variant protein
1781	Q14692	5	7	4.6	1282	145807	6.4	Ribosome biogenesis protein BMS1 homolog
1781	UPI000000DA33	5	7	4.6	1282	145821	6.4	BMS1-like, ribosome assembly protein
1782	Q5VT25-3	5	10	4.8	1638	186112	6.3	Isoform 3 of Q5VT25
1782	Q5VT25	5	10	4.6	1732	197306	6.6	Serine/threonine-protein kinase MRCK alpha
1782	Q5VT25-5	5	10	4.6	1719	195921	6.5	Isoform 5 of Q5VT25
1782	Q5VT25-2	5	10	4.5	1754	199809	6.4	Isoform 2 of Q5VT25
1783	Q8IZN6	5	10	3.9	1278	144200	8.2	ATP-binding cassette protein C4 splice variant A
1783	O15439	5	10	3.8	1325	149540	8.3	Multidrug resistance-associated protein 4
1783	Q9BX28	5	10	3.8	1325	149526	8.2	ATP-binding cassette, sub-family C (CFTR/MRP), member 4
1783	Q8NEW8	5	10	3.8	1325	149355	8.3	Multidrug resistance-associated protein
1784	Q9C0D5	5	6	3.8	1644	179425	8.4	Tetratricopeptide repeat, ankyrin repeat and coiled-coil-containing protein 1
1784	UPI0000D61252	5	6	3.3	1861	202244	8.3	TPR domain, ankyrin-repeat and coiled-coil-containing
1784	UPI00004B247A	5	6	3.3	1861	202191	8.3	TPR domain, ankyrin-repeat and coiled-coil-containing
1785	Q4ZG46	5	5	3.7	1583	184656	5.1	Ran-binding protein 2-like 4
1785	Q8IWJ2	5	5	3.7	1583	184657	5.1	GRIP and coiled-coil domain-containing protein 2
1785	UPI000049DF0C	5	5	3.4	1684	195908	5.1	Ran-binding protein 2-like 4 (RanBP2L4).
1786	UPI00001D7C42	5	12	3.6	1593	182774	8.4	THO complex 2 isoform 1
1787	Q8TCU6	5	11	3.2	1659	186203	6.4	Phosphatidylinositol 3,4,5-trisphosphate-dependent Rac exchanger 1 protein
1787	UPI000013D375	5	11	3.2	1659	186202	6.4	Phosphatidylinositol 3,4,5-trisphosphate-dependent Rac exchanger 1 protein (P-Rex1 protein).
1788	Q9P2B8	5	6	3.2	1795	200853	4.8	KIAA1429 protein
1788	Q69YN4	5	6	3.1	1810	201700	5	Protein KIAA1429
1788	UPI00001BBB23	5	6	3.1	1812	202023	5	hypothetical protein LOC25962 isoform 1
1789	UPI000049DE09	5	10	3.3	1615	182150	9.7	Retinoblastoma-binding protein 6 (p53-associated cellular protein of testis) (Proliferation potential-related protein) (Protein P2P-R) (Retinoblastoma-binding Q protein 1) (Protein RBQ-1).
1789	Q7Z6E9	5	10	3	1792	201563	9.6	Retinoblastoma-binding protein 6
1789	Q7Z6E9-2	5	10	3	1758	197286	9.6	Isoform 2 of Q7Z6E9
1790	Q12789-2	5	6	2.8	2109	238885	7.3	Isoform 2 of Q12789
1790	UPI0000D619C4	5	6	2.8	2112	239270	7.4	General transcription factor 3C polypeptide 1 (Transcription factor IIIC-subunit alpha) (TF3C-alpha) (TFIIIC 220 kDa subunit) (TFIIIC220) (TFIIIC box B-binding subunit).
1790	UPI00001FF123	5	6	2.8	2109	238873	7.3	general transcription factor IIIC, polypeptide 1, alpha 220kDa
1790	Q6AHZ7	5	6	2.8	2109	238799	7.4	Hypothetical protein DKFZp686A111
1791	Q9H2D6-5	5	5	10.6	593	68041	6.1	Isoform 1 of Q9H2D6
1791	Q9H2D6-2	5	5	2.8	2267	250721	8.2	Isoform 3 of Q9H2D6
1791	Q9H2D6	5	5	2.7	2365	261373	8.5	TRIO and F-actin-binding protein
1792	UPI00001FF2F6	5	15	2.4	2376	266937	7.1	CCR4-NOT transcription complex, subunit 1 isoform a
1793	UPI0000366852	5	21	2.5	2136	225686	6.4	Serine/threonine-protein kinase WNK1 (EC 2.7.11.1) (Protein kinase with no lysine 1) (Protein kinase, lysine-deficient 1) (Kinase deficient protein) (Erythrocyte 65 kDa protein) (p65).
1793	Q9H4A3-2	5	21	2.5	2136	225648	6.4	Isoform 2 of Q9H4A3
1793	Q9H4A3	5	21	2.2	2382	250753	6.3	Serine/threonine-protein kinase WNK1
1793	UPI000013CD65	5	21	2.2	2382	250791	6.3	Serine/threonine-protein kinase WNK1 (EC 2.7.11.1) (Protein kinase with no lysine 1) (Protein kinase, lysine-deficient 1) (Kinase deficient protein) (Erythrocyte 65 kDa protein) (p65).
1794	Q6IEH8	5	16	2	2804	316066	7.9	Transcriptional regulator
1794	Q6KC79	5	16	2	2804	316051	7.9	Nipped-B-like protein
1795	Q03001-6	5	5	1.8	2586	301815	6.7	Isoform 8 of Q03001
1795	UPI0000D6147A	5	5	1.6	3031	351796	6.3	Bullous pemphigoid antigen 1, isoforms 1/2/3/4/5/8 (230 kDa bullous pemphigoid antigen) (BPA) (Hemidesmosomal plaque protein) (Dystonia musculorum protein) (Dystonin)
1795	Q03001-5	5	5	1.6	2950	342758	6.8	Isoform 5 of Q03001
1795	Q03001-2	5	5	1.6	3030	351839	6.3	Isoform 2 of Q03001
1795	Q03001	5	5	1.5	3214	372210	6.8	Bullous pemphigoid antigen 1, isoforms 1/2/3/4/5/8
1795	UPI0000D61479	5	5	1.5	3212	371786	6.8	Bullous pemphigoid antigen 1, isoforms 1/2/3/4/5/8 (230 kDa bullous pemphigoid antigen) (BPA) (Hemidesmosomal plaque protein) (Dystonia musculorum protein) (Dystonin)
1796	P56385	4	11	62.3	69	7933	9.4	ATP synthase e chain, mitochondrial
1797	Q13885	4	12	61.3	445	49907	4.9	Tubulin beta-2A chain
1798	Q96FJ2	4	19	57.3	89	10350	7.4	Dynein light chain 2, cytoplasmic

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1799	P04080	4	21	55.1	98	11140	7.6	Cystatin-B
1800	P62140	4	18	54.1	327	37187	6.2	Serine/threonine-protein phosphatase PP1-beta catalytic subunit
1801	Q9NS69	4	33	50.7	142	15522	4.3	Mitochondrial import receptor subunit TOM22 homolog
1802	Q9Y3D0	4	8	50.3	163	17663	5.2	Protein FAM96B
1803	Q9BT73	4	6	50	122	13104	7.9	Uncharacterized protein C7orf48
1804	Q6FIG4	4	27	49.3	201	22198	5.7	RAB1B protein
1804	Q9H0U4	4	27	49.3	201	22171	5.7	Ras-related protein Rab-1B
1805	O00483	4	21	46.9	81	9370	9.4	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4
1806	O96033	4	9	46.6	88	9755	4.7	Molybdenum cofactor synthesis protein 2 small subunit
1807	P14209	4	23	45.4	185	18848	4.7	CD99 antigen precursor
1808	P52434	4	9	44.7	150	17143	4.7	DNA-directed RNA polymerases I, II, and III 17.1 kDa polypeptide
1809	Q96FQ6	4	43	44.7	103	11801	6.8	Protein S100-A16
1810	Q5JW33	4	10	44	134	15055	4.6	ASF1 anti-silencing function 1 homolog A
1810	UPI00004153B3	4	10	35.1	168	18809	4.5	ASF1 anti-silencing function 1 homolog A
1810	Q9Y294	4	10	28.9	204	22969	4.4	Histone chaperone ASF1A
1811	A4FU11	4	11	43.9	262	29294	10.2	RPS4Y1 protein
1811	Q496E4	4	11	43.7	263	29426	10.2	Ribosomal protein S4, Y-linked 1
1811	P22090	4	11	43.7	263	29456	10.2	40S ribosomal protein S4, Y isoform 1
1812	P62312	4	10	43.8	80	9128	9.6	U6 snRNA-associated Sm-like protein LSm6
1813	P31949	4	48	42.9	105	11740	7.2	Protein S100-A11
1814	Q16864	4	7	42.9	119	13370	5.5	Vacuolar ATP synthase subunit F
1815	P82909	4	5	42.7	103	11466	10	Mitochondrial 28S ribosomal protein S36
1816	A0JKD2	4	9	42.6	298	34040	5.8	MHC class I
1817	P62854	4	34	42.6	115	13015	11	40S ribosomal protein S26
1817	Q5JVH5	4	34	42.6	115	13001	11	OTTHUMP00000018641
1818	Q9UI30	4	12	42.4	125	14199	5.3	TRM112-like protein
1819	Q8WUH1	4	7	42	112	12887	4.8	Churchill protein
1820	P07108	4	16	41.4	87	10044	6.5	Acyl-CoA-binding protein
1820	Q4VWZ6	4	16	40.9	88	10145	6.5	Diazepam binding inhibitor, splice form 1c
1820	Q3I231	4	16	34.6	104	11793	5.5	Diazepam-binding protein
1821	P07311	4	5	41.4	99	11261	9.3	Acylphosphatase-1
1822	Q49AP7	4	8	41.3	92	10739	8.5	C1orf212 protein
1823	P52758	4	10	40.9	137	14494	8.7	Ribonuclease UK114
1824	Q96C01	4	8	40.6	138	15641	7.6	Hypothetical protein FLJ14668
1825	O14548	4	6	40.4	114	12615	9.4	Cytochrome c oxidase subunit VIIa-related protein, mitochondrial precursor
1826	P83916	4	9	40	185	21418	4.9	Chromobox protein homolog 1
1827	P62306	4	37	39.5	86	9725	4.7	Small nuclear ribonucleoprotein F
1827	Q6IBQ1	4	37	39.5	86	9711	4.7	SNRPF protein
1828	P42677	4	55	39.3	84	9461	9.5	40S ribosomal protein S27
1829	Q9BRA2	4	13	38.2	123	13941	5.5	Thioredoxin-like protein 5
1830	P62314	4	35	37.8	119	13282	11.6	Small nuclear ribonucleoprotein Sm D1
1831	O95182	4	10	37.2	113	12551	10.2	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 7
1831	Q6IB89	4	10	35.6	118	13279	10.5	NDUFA7 protein
1831	Q6FG42	4	10	35.6	118	13180	10.5	NDUFA7 protein
1832	P00441	4	21	37	154	15936	6.1	Superoxide dismutase [Cu-Zn]
1832	UPI00001AE968	4	21	36.5	156	16122	6.3	Superoxide dismutase [Cu-Zn] (EC 1.15.1.1).
1833	Q9NX24	4	12	36.6	153	17201	8.2	H/ACA ribonucleoprotein complex subunit 2
1834	Q8IZQ5	4	12	36.1	122	13407	9.6	Selenoprotein H
1834	UPI0000163E14	4	12	36.1	122	13303	9.7	selenoprotein H
1835	Q9Y2R0	4	13	35.8	106	11731	9.6	Coiled-coil domain-containing protein 56
1836	Q9P0M9	4	10	35.1	148	16073	10.4	Mitochondrial 39S ribosomal protein L27
1837	Q9BYC9	4	11	34.9	149	17443	10.9	39S ribosomal protein L20, mitochondrial precursor
1838	O43716	4	4	34.6	136	15086	5	Putative protein 15E1.2
1839	UPI0000F0A512	4	10	34.9	350	40110	5.7	Guanine nucleotide-binding protein G(k) subun
1839	P08754	4	10	34.5	354	40532	5.7	Guanine nucleotide-binding protein G(k) subunit alpha (G(i) alpha-3)
1840	P61020	4	13	34.4	215	23707	8.1	Ras-related protein Rab-5B
1841	Q3MIH3	4	287	34.4	128	14728	9.8	Ubiquitin A-52 residue ribosomal protein fusion product 1
1842	Q9UI09	4	7	34.5	145	17114	9.6	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12
1842	Q53XX0	4	7	34.5	145	17084	9.6	13kDa differentiation-associated protein
1842	Q53HG1	4	7	34.2	146	17215	9.6	13kDa differentiation-associated protein variant
1843	Q86U75	4	14	33.6	619	67017	6	Dihydropyrimidinase-like 2
1844	Q9BSY4	4	5	48.2	110	12395	6.7	Coiled-coil-helix-coiled-coil-helix domain-containing protein 5
1844	Q8N8C4	4	5	33.5	158	17713	7.9	CDNA FLJ39671 fis, clone SMINT2008917
1845	P62072	4	11	33.3	90	10333	6.3	Mitochondrial import inner membrane translocase subunit Tim10
1846	P62910	4	26	33.3	135	15860	11.3	60S ribosomal protein L32
1846	UPI0000073979	4	26	33.3	135	15751	10.9	PREDICTED: similar to 60S ribosomal protein L32
1847	O95298	4	6	32.8	119	14187	9	NADH dehydrogenase [ubiquinone] 1 subunit C2

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1847	Q6FIH8	4	6	32.8	119	14173	9	NDUFC2 protein
1848	P62899	4	44	32.8	125	14463	10.5	60S ribosomal protein L31
1849	P42167	4	10	32.4	454	50670	9.4	Lamina-associated polypeptide 2, isoforms beta/gamma (Thymopoietin, isoforms beta/gamma) (TP beta/gamma) (Thymopoietin-related peptide isoforms beta/gamma) (TPRP isoforms beta/gamma) [Contains: Thymopoietin (TP) (Splenin); Thymopentin (TP5)]
1850	P09669	4	22	32	75	8781	10.4	Cytochrome c oxidase polypeptide VIc precursor
1851	P50583	4	10	32	147	16829	5.3	Bis(5'-nucleosyl)-tetraphosphatase [asymmetrical]
1852	Q5TDQ4	4	4	31.2	170	19550	5.6	HD domain containing 2
1852	Q9Y3D1	4	4	31.2	170	19491	5.4	CGI-130 protein
1852	Q6NZ49	4	4	26	204	23419	5.7	HD domain containing 2
1852	Q9BTT2	4	4	24.3	218	24850	6.2	HD domain-containing protein 2
1853	P84103	4	33	31.1	164	19330	11.6	Splicing factor, arginine/serine-rich 3
1854	Q8N4D3	4	6	33.6	119	13921	9.8	Hypothetical protein
1854	UPI000045715C	4	6	33.3	120	14026	9.8	PREDICTED: similar to NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4, 15kDa isoform 1
1854	O95168	4	6	31	129	15209	9.8	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4
1855	P83876	4	9	31	142	16786	5.8	Thioredoxin-like protein 4A
1856	Q8WW12	4	9	30.9	178	18925	7.5	PEST proteolytic signal-containing nuclear protein
1857	P51452	4	9	30.8	185	20478	7.8	Dual specificity protein phosphatase 3
1858	Q9H2H8	4	6	30.4	161	18155	6.8	Peptidyl-prolyl cis-trans isomerase-like 3
1859	Q99627	4	8	30.1	209	23226	5.4	COP9 signalosome complex subunit 8
1860	Q9P000	4	5	29.8	198	21819	5.9	COMM domain-containing protein 9
1861	P09104	4	7	29.7	434	47269	5	Gamma-enolase
1862	Q5W0X3	4	9	31.1	103	11424	9.1	Peptidyl-prolyl cis-trans isomerase
1862	P62942	4	9	29.6	108	11951	8.2	FK506-binding protein 1A
1863	Q9H0A8	4	5	29.6	199	21764	7.3	COMM domain-containing protein 4
1864	Q59HE4	4	6	37.9	103	11698	7.8	Hypothetical protein
1864	O15540	4	6	29.5	132	14889	5.6	Fatty acid-binding protein, brain
1864	Q9H047	4	6	23.5	166	18829	5.9	Hypothetical protein DKFZp547J2313
1865	Q9Y3U8	4	45	29.5	105	12254	11.6	60S ribosomal protein L36
1866	Q5T0P8	4	49	30	130	15069	10.9	Ribosomal protein S24
1866	Q7Z3D1	4	49	29.5	132	15326	10.8	Hypothetical protein DKFZp686N1586
1866	P62847	4	49	29.3	133	15423	10.8	40S ribosomal protein S24
1867	O15511	4	35	29.1	151	16320	5.7	Actin-related protein 2/3 complex subunit 5
1868	Q9Y5R8	4	5	29	145	16832	9.2	Trafficking protein particle complex subunit 1
1869	P82932	4	11	28.8	125	14227	9.3	Mitochondrial 28S ribosomal protein S6
1870	Q16540	4	9	28.8	153	17781	9.7	Mitochondrial 39S ribosomal protein L23
1870	UPI0000D62587	4	9	28.8	153	17834	10	Mitochondrial 39S ribosomal protein L23 (L23mt) (MRP-L23) (L23 mitochondrial-related protein) (Ribosomal protein L23-like).
1870	UPI00001678B9	4	9	28.8	153	17811	9.7	mitochondrial ribosomal protein L23
1870	UPI00001F9AD4	4	9	27	163	18530	10.9	Mitochondrial 39S ribosomal protein L23 (L23mt) (MRP-L23) (L23 mitochondrial-related protein) (Ribosomal protein L23-like).
1871	Q9NZZ4	4	8	36.7	139	16059	6.8	HSPC176
1871	Q9UL33	4	8	36.4	140	16146	6.8	Trafficking protein particle complex 2-like protein
1871	Q6ZTA7	4	8	28.8	177	20021	8.2	CDNA FLJ44827 fis, clone BRACE3046837
1872	P26447	4	21	28.7	101	11728	6.1	Protein S100-A4
1873	Q8TB65	4	22	28.7	150	16762	6.8	Cytochrome c oxidase subunit Va
1874	Q9Y3B2	4	7	28.7	195	21452	8.2	3'-5' exoribonuclease CSL4 homolog
1875	P60033	4	17	28.4	236	25809	5.3	CD81 antigen
1875	UPI000066D8DE	4	17	24.5	274	29806	6.9	CD81 antigen (26 kDa cell surface protein TAPA-1) (Target of the antiproliferative antibody 1) (Tetraspanin-28) (Tspan-28).
1876	P56556	4	11	28.1	128	15137	10	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6
1876	Q6IBT8	4	11	28.1	128	15185	10	NDUFA6 protein
1877	Q8IW87	4	6	27.8	227	24434	6.9	Candidate tumor suppressor in ovarian cancer 2
1877	Q8WZ82	4	6	27.8	227	24418	6.9	Candidate tumor suppressor OVCA2
1878	O00762	4	7	27.4	179	19652	7.4	Ubiquitin-conjugating enzyme E2 C
1879	O43583	4	13	27.3	198	22092	5.3	Density-regulated protein
1879	UPI00004566A8	4	13	27.1	199	22285	5.6	Density-regulated protein (DRP) (Protein DRP1) (Smooth muscle cell- associated protein 3) (SMAP-3).
1880	Q9NRW3	4	6	26.8	190	22826	7.6	Probable DNA dC- dU-editing enzyme APOBEC-3C
1881	P00374	4	8	26.7	187	21453	7.4	Dihydrofolate reductase
1882	A2BEH4	4	13	29.6	196	20942	4.9	Proteasome (Prosome, macropain) subunit beta type 9
1882	P28065-2	4	13	27.8	209	22328	5	Isoform LMP2.S of P28065
1882	A2BEH1	4	13	26.5	219	23245	5	Proteasome (Prosome, macropain) subunit beta type 9
1882	P28065	4	13	26.5	219	23264	5	Proteasome subunit beta type 9 precursor
1883	P55795	4	12	26.5	449	49264	6.3	Heterogeneous nuclear ribonucleoprotein H'
1884	Q99470	4	7	26.5	211	23026	7.3	Stromal cell-derived factor 2 precursor
1885	Q9H0U6	4	8	26.1	180	20577	9.5	39S ribosomal protein L18, mitochondrial precursor

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
1886	P32970	4	15	25.9	193	21118	8.5	Tumor necrosis factor ligand superfamily member 7
1887	Q9H773	4	5	25.9	170	18681	5	CDNA: FLJ21190 fis, clone CAS12333
1888	P15927	4	4	25.6	270	29247	6.1	Replication protein A 32 kDa subunit
1888	P15927-2	4	4	24.8	278	30156	7	Isoform 2 of P15927
1888	P15927-3	4	4	19.3	358	38810	8.9	Isoform 3 of P15927
1889	P83731	4	49	25.5	157	17779	11.3	60S ribosomal protein L24
1890	Q8N6M0	4	5	25.3	293	33813	6	OTU domain-containing protein 6B
1891	gi|12345|prg	4	1405	26	223	23476	7.9	Promega sequencing grade modified trypsin
1891	IPITrypsinPIG	4	1405	25.1	231	24409	7.2	TRYP_PIG
1892	P13987	4	63	25	128	14177	6.5	CD59 glycoprotein precursor
1893	P52298	4	6	25	156	18001	8.2	Nuclear cap-binding protein subunit 2
1894	P05161	4	4	24.8	165	17887	7.5	Interferon-induced 17 kDa protein precursor [Contains: Ubiquitin cross-reactive protein (hUCRP) (Interferon-induced 15 kDa protein)]
1895	P62166	4	5	24.7	190	21879	4.8	Neuronal calcium sensor 1
1896	Q9H061	4	6	24.6	195	21527	9.3	Transmembrane protein 126A
1897	Q13257	4	10	24.4	205	23510	5.1	Mitotic spindle assembly checkpoint protein MAD2A
1897	Q6IRW7	4	10	24.4	205	23496	5.1	MAD2 mitotic arrest deficient-like 1
1897	Q53F56	4	10	24.4	205	23526	5.1	MAD2-like 1 variant
1898	Q9Y3D6	4	26	24.3	152	16938	8.8	Mitochondrial fission 1 protein
1898	UPI0000073ACD	4	26	24.3	152	16980	8.8	tetratricopeptide repeat domain 11
1899	P24941	4	5	24.2	298	33930	8.7	Cell division protein kinase 2
1900	Q9NPA0	4	10	24	242	26471	9.2	Uncharacterized protein C15orf24 precursor
1901	O00217	4	17	23.8	210	23705	6.3	NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial precursor
1902	P60510	4	11	23.8	307	35080	5.1	Serine/threonine-protein phosphatase 4 catalytic subunit
1903	P35219	4	9	23.4	290	32973	4.9	Carbonic anhydrase-related protein
1904	Q5SPS5	4	8	24.6	615	67971	9.5	Poly(A) binding protein, cytoplasmic 4
1904	Q13310	4	8	23.4	644	70783	9.3	Polyadenylate-binding protein 4 (Poly(A)-binding protein 4) (PABP 4) (Inducible poly(A)-binding protein)
1904	Q6IQ30	4	8	22.9	660	72361	9.3	PABPC4 protein
1904	Q5SPS6	4	8	22.9	660	72391	9.3	Poly(A) binding protein, cytoplasmic 4
1905	Q9NYL4	4	11	23.4	201	22180	9.4	FK506-binding protein 11 precursor
1906	Q5TBA5	4	5	23.3	275	30009	5.3	OTTHUMP00000018264
1906	Q96B26	4	5	23.2	276	30040	5.3	Exosome complex exonuclease RRP43
1907	Q09028	4	8	23.1	425	47656	4.9	Histone-binding protein RBBP4
1908	O15173	4	8	22.9	223	23818	4.9	Membrane-associated progesterone receptor component 2
1909	P02511	4	6	22.9	175	20159	7.3	Alpha crystallin B chain (Alpha(B)-crystallin)
1910	Q9H081	4	5	22.9	205	24140	5.7	Protein MIS12 homolog
1911	P01033	4	4	22.7	207	23171	8.1	Metalloproteinase inhibitor 1 precursor
1912	Q53FP0	4	4	22.6	261	29916	7.4	Pyridoxine 5'-phosphate oxidase variant
1912	Q9NVS9	4	4	22.6	261	29988	7.1	Pyridoxine-5'-phosphate oxidase
1913	Q92522	4	25	22.5	213	22487	10.8	Histone H1x
1914	Q96CT7	4	10	22.4	223	25835	9.5	Coiled-coil domain-containing protein 124
1915	UPI0000456BFD	4	7	22.3	309	34948	9.3	Mitochondrial 39S ribosomal protein L4 (L4mt) (MRP-L4).
1915	Q9BYD3	4	7	22.2	311	34919	9.7	Mitochondrial 39S ribosomal protein L4
1916	Q9UFW8	4	4	22.2	167	18820	9	CGG triplet repeat-binding protein 1
1917	O14735	4	23	22.1	213	23539	8	CDP-diacylglycerol--inositol 3-phosphatidyltransferase
1917	Q53HA5	4	23	22.1	213	23558	8.3	CDP-diacylglycerol--inositol 3-phosphatidyltransferase isoform 1 variant
1918	Q13442	4	14	22.1	181	20630	8.9	28 kDa heat- and acid-stable phosphoprotein
1919	Q9Y3D9	4	9	22.1	190	21771	8.9	Mitochondrial ribosomal protein S23
1920	Q13637	4	15	21.8	225	24997	6.5	Ras-related protein Rab-32
1921	Q9Y3A4	4	4	21.8	280	32334	9.6	Gastric cancer antigen Zg14
1922	UPI00003667A5	4	51	24	242	26818	5.1	CD82 antigen isoform 2
1922	P27701	4	51	21.7	267	29626	5.2	CD82 antigen
1922	Q7Z2D4	4	51	21.7	267	29611	5.2	CD82 molecule
1922	Q6LET0	4	51	21.7	267	29644	5.2	KAI1 protein
1923	Q96GC5	4	11	21.7	212	23935	9	39S ribosomal protein L48, mitochondrial precursor
1924	Q8N0U8	4	44	21.6	176	19836	9.1	Vitamin K epoxide reductase complex subunit 1-like protein 1
1925	Q5TIF0	4	9	21.4	234	26761	5	Syntaxin 12
1925	Q6LEU0	4	9	18.6	269	30878	5.8	STX12 protein
1925	Q86Y82	4	9	18.1	276	31642	5.6	Syntaxin-12
1926	Q9Y3A3-2	4	7	24.9	193	22318	6.1	Isoform 2 of Q9Y3A3
1926	Q9Y3A3	4	7	21.3	225	26032	5.8	Preimplantation protein 3
1927	UPI0000D61D3B	4	7	23.5	179	20084	9.4	Protein FAM121B precursor.
1927	Q9BUR5-2	4	7	23.3	180	20199	9.3	Isoform 2 of Q9BUR5
1927	Q9BUR5	4	7	21.2	198	22285	9.1	Apolipoprotein O precursor
1928	P09012	4	14	20.9	282	31280	9.8	U1 small nuclear ribonucleoprotein A
1929	Q7LG56	4	8	20.8	351	40737	5	Ribonucleoside-diphosphate reductase M2 subunit B
1930	P67812	4	66	20.7	179	20625	9.5	Signal peptidase complex catalytic subunit SEC11A
1930	Q6IAM7	4	66	20.7	179	20611	9.5	SPC18 protein

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1930	Q53FQ8	4	66	20.7	179	20613	9.5	Signal peptidase complex (18kD) variant
1931	A4D0R4	4	11	20.4	240	28191	9.6	B-cell receptor-associated protein 29
1931	Q9UHQ4	4	11	20.3	241	28320	9.5	B-cell receptor-associated protein 29
1931	UPI000049A623	4	11	20.1	244	28731	9.5	B-cell receptor-associated protein BAP29 isoform d
1931	UPI000049A622	4	11	14.5	337	39102	9.3	B-cell receptor-associated protein BAP29 isoform c
1931	UPI000049A621	4	11	14.1	348	40797	9.7	B-cell receptor-associated protein BAP29 isoform a
1932	Q9BUB7	4	11	20.4	260	28969	8.9	Transmembrane protein 70
1933	Q9BUT1	4	9	20.4	245	26724	7.6	3-hydroxybutyrate dehydrogenase type 2
1934	O43633	4	7	20.3	222	25104	6	Charged multivesicular body protein 2a
1935	Q16740	4	11	20.2	277	30180	8.1	Putative ATP-dependent Clp protease proteolytic subunit, mitochondrial precursor
1936	Q9BYD2	4	8	20.2	267	30185	10.1	39S ribosomal protein L9, mitochondrial precursor
1936	UPI000013D8FA	4	8	20.2	267	30243	10.1	mitochondrial ribosomal protein L9
1937	Q96CN7	4	5	20.1	298	32237	7.4	Isochorismatase domain-containing protein 1
1938	P34741	4	7	19.9	201	22174	4.9	Syndecan-2 precursor
1938	Q6PIS6	4	7	19.9	201	22160	4.9	Syndecan 2
1939	Q13243	4	16	19.9	272	31264	11.6	Splicing factor, arginine/serine-rich 5
1940	A4FVB3	4	10	19.4	299	32568	7.9	SPRY4 protein
1940	Q9C004	4	10	19.4	299	32541	7.9	Sprouty homolog 4
1941	P48507	4	5	19	274	30727	6	Glutamate--cysteine ligase regulatory subunit
1942	Q8N4B7	4	4	18.9	301	31905	4.4	Cell growth regulator with EF-hand domain 1
1942	UPI0000456D95	4	4	18.7	305	32178	4.4	Cell growth regulator with EF hand domain protein 1 (Cell growth regulatory gene 11 protein).
1943	P10109	4	10	18.5	184	19393	5.8	Adrenodoxin, mitochondrial precursor
1944	Q53FU2	4	5	18.4	342	36751	5.2	Methylosome protein 50 variant
1944	Q9BQA1	4	5	18.4	342	36724	5.2	Methylosome protein 50
1945	Q9HD15	4	7	18.2	236	25673	7	Steroid receptor RNA activator 1
1946	Q9UEH5	4	14	19.5	231	25430	7.4	24-kDa subunit of complex I
1946	P19404	4	14	18.1	249	27392	8.1	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial precursor
1946	Q6IPW4	4	14	18.1	249	27364	8.1	NADH dehydrogenase (Ubiquinone) flavoprotein 2, 24kDa
1946	Q6IB76	4	14	18.1	249	27349	8.1	NDUFV2 protein
1947	P62995-3	4	22	27.7	188	21935	10.2	Isoform 3 of P62995
1947	Q68DZ9	4	22	18.8	276	32321	11.4	Hypothetical protein DKFZp686F18120
1947	Q59GA1	4	22	18.7	278	32274	11.1	Splicing factor, arginine/serine-rich 10 (Transformer 2 homolog, Drosophila) variant
1947	P62995	4	22	18.1	288	33666	11.2	Arginine/serine-rich-splicing factor 10
1947	UPI0000D61BC0	4	22	18	289	33699	10.8	Arginine/serine-rich-splicing factor 10 (Transformer-2-beta) (HTRA2- beta) (Transformer 2 protein homolog).
1948	Q96HS1	4	7	18	255	28006	7.3	Phosphoglycerate mutase family member 5
1948	UPI00001400B6	4	7	18	255	28020	7.3	Bcl-XL-binding protein v68
1949	Q9P015	4	6	17.9	296	33420	10	39S ribosomal protein L15, mitochondrial precursor
1950	O15260-2	4	94	30.2	159	17970	6.1	Isoform 2 of O15260
1950	UPI0000D6193B	4	94	25.8	186	21115	7.2	Surfeit locus protein 4.
1950	Q5T8U5	4	94	25.8	186	21128	6.5	Surfeit 4
1950	Q5T8U7	4	94	25.5	188	21130	8.6	Surfeit 4
1950	UPI0000D6193C	4	94	25.3	190	21331	8.6	Surfeit locus protein 4.
1950	O15260	4	94	17.8	269	30394	7.8	Surfeit locus protein 4
1951	P43307	4	17	17.8	286	32235	4.5	Translocon-associated protein subunit alpha precursor
1951	UPI000016789F	4	17	17.8	286	32183	4.5	signal sequence receptor, alpha
1952	Q96GK7	4	8	17.8	314	34596	8.2	Fumarylacetoacetate hydrolase domain-containing protein 2A
1953	Q9NZ43	4	6	17.8	259	29345	9.1	Vesicle transport protein USE1
1953	UPI0000456C39	4	6	17.8	259	29369	9.1	Vesicle transport protein USE1 (USE1-like protein) (Putative MAPK- activating protein PM26) (Protein p31).
1954	UPI00001D7FA4	4	4	17.7	294	33620	5.3	hypothetical protein LOC285636
1955	Q96AH2	4	10	28.6	168	18793	5.2	Similar to mannose-6-phosphate receptor
1955	P20645	4	10	17.3	277	30993	5.8	Cation-dependent mannose-6-phosphate receptor precursor
1955	Q6I9U3	4	10	17.3	277	30975	5.8	M6PR protein
1955	Q53GY9	4	10	17.3	277	31019	5.8	Cation-dependent mannose-6-phosphate receptor variant
1956	Q96GA7	4	4	17.3	329	34674	6.9	Serine dehydratase-like
1957	O95721	4	12	17.1	258	28970	5.8	Synaptosomal-associated protein 29
1958	Q5J9I4	4	5	17.4	293	32186	9.4	Proliferation-inducing protein 16
1958	P29372-2	4	5	17.4	293	32181	9.4	Isoform 2 of P29372
1958	P29372	4	5	17.1	298	32864	9.6	DNA-3-methyladenine glycosylase
1958	Q1W6H1	4	5	17.1	298	32869	9.6	DNA-3-methyladenine glycosylase
1959	Q92600	4	7	17.1	299	33631	8	Protein RCD1 homolog
1960	P42574	4	6	17	277	31608	6.5	Caspase-3 precursor (EC 3.4.22.56) (CASP-3) (Apopain) (Cysteine protease CPP32) (Yama protein) (CPP-32) (SREBP cleavage activity 1) (SCA-1) [Contains: Caspase-3 p17 subunit; Caspase-3 p12 subunit]
1961	O60362	4	6	16.9	242	27310	8.9	Hypothetical protein 44M2.1

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1961	Q9NXG2	4	6	11.6	353	39315	7.9	THUMP domain-containing protein 1
1961	UPI000059D337	4	6	9.3	439	48549	8.8	THUMP domain-containing protein 1.
1961	Q6MZT3	4	6	9.3	439	48491	8.9	Hypothetical protein DKFZp686C1054
1962	Q9Y619	4	4	16.9	301	32736	9.1	Mitochondrial ornithine transporter 1
1963	Q9HD42	4	7	16.8	196	21703	8.1	Charged multivesicular body protein 1a
1964	Q9Y394-2	4	6	19.7	289	32268	8.9	Isoform 2 of Q9Y394
1964	Q9Y394	4	6	16.8	339	38299	8.3	Dehydrogenase/reductase SDR family member 7 precursor
1965	P28072	4	24	16.7	239	25358	4.9	Proteasome subunit beta type 6 precursor
1966	Q53GB6	4	6	16.7	365	40954	8	Actin related protein 2/3 complex subunit 1A variant
1966	Q92747	4	6	16.5	370	41569	8.2	Actin-related protein 2/3 complex subunit 1A
1967	Q6FIA0	4	7	16.7	329	36568	4.6	HSPC142 protein
1967	UPI000013C7E6	4	7	16.7	329	36427	4.7	CDNA FLJ20571 fis, clone REC01040 (HSPC142 protein) (Hypothetical protein DKFZp564N2378).
1967	Q9NWV8	4	7	16.7	329	36560	4.6	CDNA FLJ20571 fis, clone REC01040
1968	Q969Q5	4	6	16.7	203	23124	6.2	Ras-related protein Rab-24
1969	UPI00001FC123	4	12	22.3	247	28285	7	AMP-activated protein kinase, noncatalytic gamma-1 subunit isoform 2
1969	P54619	4	12	16.6	331	37579	6.9	5'-AMP-activated protein kinase subunit gamma-1
1969	Q8N7V9	4	12	16.2	340	38533	7.1	CDNA FLJ40287 fis, clone TESTI2027909, highly similar to 5'-AMP- ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT
1970	Q8N959	4	12	20.1	323	35226	6.3	CDNA FLJ38330 fis, clone FCBBF3025280, highly similar to NDRG1 PROTEIN
1970	Q597H1	4	12	16.5	394	42819	5.8	Transformation-related protein 14
1970	UPI0000D62506	4	12	16.5	394	42834	5.8	Protein NDRG1 (N-myc downstream-regulated gene 1 protein) (Differentiation-related gene 1 protein) (DRG-1) (Reducing agents and tunicamycin-responsive protein) (RTP) (Nickel-specific induction protein Cap43) (Rit42).
1970	Q92597	4	12	16.5	394	42835	5.8	Protein NDRG1
1971	Q9NRN7	4	7	16.5	309	35776	6.8	L-aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase
1972	Q712K3	4	9	16.4	238	27166	4.4	Ubiquitin-conjugating enzyme E2 R2
1973	Q96B36	4	6	16.4	256	27383	4.7	Proline-rich AKT1 substrate 1
1973	UPI0000071F14	4	6	16.4	256	27409	4.7	AKT1 substrate 1 (proline-rich)
1974	Q9NR45	4	5	16.4	359	40308	6.7	Sialic acid synthase
1975	Q8NBQ5	4	12	16.3	300	32964	9.2	Dehydrogenase/reductase SDR family member 8 precursor
1975	UPI00006C088F	4	12	16.3	300	33014	9.3	PREDICTED: similar to Dehydrogenase/reductase SDR family member 8 precursor (17-beta-hydroxysteroid dehydrogenase 11) (17-beta-HSD 11) (17-beta-HSD XI) (17betaHSDXI) (17bHSD11) (17betaHSD11) (Retinal short-chain dehydrogenase/reductase 2) (retSDR2) (Cutaneous...
1975	UPI000013FB48	4	12	16.3	300	32936	9.1	Dehydrogenase/reductase SDR family member 8 precursor (EC 1.1.1.-) (17-beta-hydroxysteroid dehydrogenase 11) (17-beta-HSD 11) (17-beta- HSD XI) (17betaHSDXI) (17bHSD11) (17betaHSD11) (Retinal short-chain dehydrogenase/reductase 2) (retSDR2) (Cutaneous T-c
1976	O96011	4	8	16.2	259	28431	9.8	Peroxisomal membrane protein 11B
1977	Q15257-3	4	5	19.7	294	33467	6.3	Isoform 3 of Q15257
1977	Q15257-2	4	5	18	323	36775	6.3	Isoform 1 of Q15257
1977	Q15257	4	5	16.2	358	40668	5.9	Serine/threonine-protein phosphatase 2A regulatory subunit B'
1978	O43681	4	8	16.1	348	38793	4.9	Arsenical pump-driving ATPase
1978	UPI0000D61731	4	8	15.4	363	40226	5.1	Arsenical pump-driving ATPase (EC 3.6.3.16) (Arsenite-translocating ATPase) (Arsenical resistance ATPase) (Arsenite-transporting ATPase) (ARSA) (ASNA-I).
1979	P42126-2	4	14	16.8	285	30896	8.9	Isoform 2 of P42126
1979	P42126	4	14	15.9	302	32816	8.6	3,2-trans-enoyl-CoA isomerase, mitochondrial precursor (EC 5.3.3.8) (Dodecenoyl-CoA isomerase) (Delta(3),Delta(2)-enoyl-CoA isomerase)
1980	Q9UBV8	4	9	15.8	284	30381	6.5	Peflin
1981	Q99447	4	5	15.7	389	43835	6.9	Ethanolamine-phosphate cytidylyltransferase
1982	P61964	4	5	15.6	334	36589	8.3	WD repeat protein 5
1983	Q8TED6	4	4	15.5	245	28043	7	Carboxymethylenebutenolidase homolog
1983	Q96DG6	4	4	15.5	245	28048	7.2	Carboxymethylenebutenolidase homolog
1984	Q9H1E5	4	8	15.5	349	38952	4.4	Thioredoxin domain-containing protein 13 precursor
1985	Q9Y2Z4	4	4	15.5	477	53199	9	Tyrosyl-tRNA synthetase, mitochondrial precursor
1986	Q9Y316	4	7	15.5	297	33733	7.2	Protein memo
1986	Q5R2V8	4	7	15.3	300	34294	7.3	Chromosome 2 open reading frame 4 short form
1987	Q99536	4	4	15.3	393	41920	6.3	Synaptic vesicle membrane protein VAT-1 homolog

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
1988	Q96KB5	4	6	15.2	322	36085	5.1	T-lymphokine-activated killer cell-originated protein kinase
1989	P16403	4	106	15.5	213	21365	10.9	Histone H1.2
1989	A3R0T7	4	106	15.1	219	21879	11	Liver histone H1e
1989	Q4VB24	4	106	15.1	219	21893	11	Histone cluster 1, H1e
1989	P10412	4	106	15.1	219	21865	11	Histone H1.4
1989	P16402	4	106	14.9	221	22350	11	Histone H1.3
1990	Q6UXH1-4	4	6	16.3	325	35288	4.7	Isoform 4 of Q6UXH1
1990	Q6UXH1	4	6	15	353	38192	4.6	Cysteine-rich with EGF-like domain protein 2 precursor
1990	Q6UXH1-6	4	6	14.2	373	40491	4.8	Isoform 6 of Q6UXH1
1990	Q6UXH1-5	4	6	13.2	402	43579	4.8	Isoform 5 of Q6UXH1
1991	Q9UNE7	4	5	14.9	303	34856	5.9	STIP1 homology and U box-containing protein 1
1992	Q5JTA8	4	27	14.8	250	28743	10	Novel protein
1992	Q9H0U3	4	27	11	335	38037	9.6	Implantation-associated protein precursor
1993	Q5T8A0	4	5	14.8	270	30479	9.6	Mitochondrial ribosomal protein S2
1993	Q9Y399	4	5	13.5	296	33249	9.3	Mitochondrial 28S ribosomal protein S2
1994	O75792	4	5	14.7	299	33395	5.3	Ribonuclease H2 subunit A (EC 3.1.26.4) (RNase H2 subunit A) (Ribonuclease HI subunit A) (Ribonuclease HI large subunit) (RNase HI large subunit) (RNase H(35))
1994	Q6UQL6	4	5	14.7	299	33425	5.2	Ribonuclease H2
1994	Q6IBG3	4	5	14.7	299	33353	5.3	JUNB protein
1995	Q00059	4	6	14.6	246	29097	9.7	Transcription factor A, mitochondrial precursor
1995	Q6LES8	4	6	14.6	246	29083	9.7	TFAM protein
1996	Q8IUI5	4	30	14.7	361	42908	9	PTPLAD1 protein
1996	Q6PD63	4	30	14.6	362	43160	8.9	Protein tyrosine phosphatase-like A domain containing 1
1996	Q96T12	4	30	14.6	362	43159	9.1	CDNA FLJ14515 fis, clone NT2RM1000800, weakly similar to Mus musculus partial B-IND1 protein
1996	Q8NC86	4	30	14.6	362	43126	8.9	CDNA FLJ90417 fis, clone NT2RP3000171, weakly similar to Mus musculus partial B-IND1 protein
1996	Q9NQA7	4	30	14.3	370	43543	8	B-ind1 protein
1996	UPI0000D61358	4	30	14.2	373	44323	9.2	butyrate-induced transcript 1
1996	Q9P035	4	30	14.2	373	44423	9.1	Protein-tyrosine phosphatase-like A domain-containing protein 1
1997	Q9BYN8	4	5	14.6	205	24212	10.4	28S ribosomal protein S26, mitochondrial precursor
1998	P08397	4	10	14.4	361	39330	7.2	Porphobilinogen deaminase
1999	Q14318	4	9	14.4	355	38408	7.7	FK506-binding protein 8
1999	Q86YK6	4	9	12.4	412	44562	4.8	FK506-binding protein 38
1999	UPI000020376E	4	9	12.3	413	44649	4.8	FK506-binding protein 8
1999	Q7Z349	4	9	11.3	451	48636	5	Hypothetical protein DKFZp686M22160
2000	Q2LE81	4	5	16.4	244	25882	9.2	NADP(H)-dependent retinol dehydrogenase/reductase B1 isoform
2000	Q9BTZ2	4	5	15.4	260	27572	7.8	Dehydrogenase/reductase SDR family member 4
2000	Q20CR0	4	5	14.4	278	29537	8.5	NADP(H)-dependent retinol dehydrogenase/reductase short isoform
2000	Q71UQ6	4	5	14.4	278	29531	8.5	Hep27-like protein
2001	Q6IBT1	4	43	14.4	277	29937	7.7	Proteasome subunit beta type
2001	Q99436	4	43	14.4	277	29965	7.7	Proteasome subunit beta type 7 precursor
2001	Q86U62	4	43	14.4	277	30018	8	Proteasome (Prosome, macropain) subunit, beta type, 7
2002	Q8N474	4	5	14.3	314	35386	8.9	Secreted frizzled-related protein 1 precursor
2003	Q9NYK5	4	4	13.9	338	38722	7.6	Mitochondrial 39S ribosomal protein L39
2003	UPI00001AEE66	4	4	13.9	338	38712	7.6	Mitochondrial 39S ribosomal protein L39 (L39mt) (MRP-L39) (MRP-L5).
2003	UPI00001AEAC0	4	4	13.3	353	40458	7.9	Mitochondrial 39S ribosomal protein L39 (L39mt) (MRP-L39) (MRP-L5).
2003	Q9NYK5-2	4	4	13.3	353	40468	7.9	Isoform 2 of Q9NYK5
2004	P48509	4	40	13.8	253	28295	7.5	CD151 antigen
2005	P53582	4	5	13.7	386	43215	7.2	Methionine aminopeptidase 1
2006	Q53GE7	4	4	13.7	292	33595	4.9	Tetratricopeptide repeat domain 1 variant
2006	Q99614	4	4	13.7	292	33526	4.8	Tetratricopeptide repeat protein 1
2006	Q53HD9	4	4	13.7	292	33454	4.9	Tetratricopeptide repeat domain 1 variant
2007	Q8IZ81	4	8	13.7	293	34961	8.1	ELMO domain-containing protein 2
2008	P49903	4	4	13.3	392	42911	6	Selenide, water dikinase 1
2009	P09001	4	6	13.2	348	38633	9.5	Mitochondrial 39S ribosomal protein L3
2010	Q86W42-2	4	6	14.2	317	34849	7.4	Isoform 2 of Q86W42
2010	Q86W42	4	6	13.2	341	37535	7.4	THO complex subunit 6 homolog
2011	Q9UNS2	4	6	13.2	423	47873	6.7	COP9 signalosome complex subunit 3
2012	Q7L5N1	4	14	13.1	327	36163	5.7	COP9 signalosome complex subunit 6
2013	Q9Y680-2	4	5	15.3	222	25794	6.3	Isoform 2 of Q9Y680
2013	UPI0000456EAC	4	5	13.3	256	29688	6.5	FK506-binding protein 7 precursor (EC 5.2.1.8) (Peptidyl-prolyl cis- trans isomerase) (PPIase) (Rotamase) (FKBP-23).
2013	Q9Y680	4	5	13.1	259	30009	6.5	FK506-binding protein 7 precursor
2014	P50148	4	5	13	353	41467	5.8	Guanine nucleotide-binding protein G(q) subunit alpha

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2014	Q6NT27	4	5	12.8	359	42142	5.7	Guanine nucleotide binding protein (G protein), q polypeptide
2015	O94766	4	6	12.8	335	37122	8.3	Galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase 3
2015	Q5U676	4	6	12.6	341	37828	8.6	B3GAT3 protein
2016	P06280	4	5	12.8	429	48767	5.6	Alpha-galactosidase A precursor
2016	Q53HF3	4	5	12.8	429	48753	5.6	Galactosidase, alpha variant
2017	Q9BVC6	4	42	12.8	243	26210	10.5	Transmembrane protein 109 precursor
2018	UPI0000457335	4	14	19.4	304	32825	5.6	proline-rich coiled-coil 1
2018	Q8NEZ7	4	14	19.3	305	32896	5.6	FLJ00410 protein
2018	Q96M27	4	14	13.3	445	46701	5.8	CDNA FLJ32875 fis, clone TESTI2004031
2018	Q8IVL4	4	14	12.8	462	48907	5.3	Hypothetical protein
2018	Q86Y42	4	14	12.7	464	48525	5.4	Proline-rich coiled-coil protein 1
2018	UPI0000D61673	4	14	12.7	466	48637	5.5	proline-rich coiled-coil 1
2019	Q9BRJ2	4	8	12.7	306	35351	9	39S ribosomal protein L45, mitochondrial precursor
2019	UPI00001AEFFB	4	8	12.7	306	35243	9	mitochondrial ribosomal protein L45
2020	Q9BV38	4	6	12.7	432	47405	6.7	WD repeat protein 18
2021	Q13620	4	8	12.6	895	102299	7.9	Cullin-4B
2021	UPI000059DB7F	4	8	12.6	900	102756	8	Cullin-4B (CUL-4B).
2021	Q5JRZ4	4	8	12.4	913	103982	7.4	Cullin 4B
2022	Q8N6T3-3	4	5	12.9	396	43776	8.5	Isoform 3 of Q8N6T3
2022	Q8N6T3	4	5	12.6	406	44668	5.7	ADP-ribosylation factor GTPase-activating protein 1
2022	Q8N6T3-2	4	5	12.3	414	45676	5.8	Isoform 2 of Q8N6T3
2023	Q6PKC2	4	13	22.5	236	27016	8.2	CROP protein
2023	Q86Y74	4	13	21.1	251	28926	7	CROP protein
2023	O95232	4	13	12.3	432	51466	9.8	Cisplatin resistance-associated overexpressed protein
2024	O00115	4	6	12.2	360	39581	8	Deoxyribonuclease-2-alpha precursor
2025	Q86U79	4	5	12.8	345	38737	6.7	Adenosine kinase
2025	Q5VXR3	4	5	12.8	345	38703	6.7	Adenosine kinase
2025	P55263	4	5	12.2	362	40545	6.7	Adenosine kinase
2026	Q14376	4	7	12.1	348	38282	6.7	UDP-glucose 4-epimerase
2027	Q9UNQ2	4	4	12.1	313	35236	10	Probable dimethyladenosine transferase (EC 2.1.1.-) (S- adenosylmethionine-6-N',N'-adenosyl(rRNA) dimethyltransferase)
2028	Q8N684-2	4	4	12.1	462	51096	7.8	Isoform 2 of Q8N684
2028	Q8N684	4	4	11.9	471	52050	8	Cleavage and polyadenylation specificity factor 7
2029	Q9Y6G9	4	10	11.9	523	56579	6.4	Cytoplasmic dynein 1 light intermediate chain 1
2029	UPI000006E91C	4	10	11.9	523	56627	6.6	dynein light chain-A
2030	P11182	4	4	11.8	482	53487	8.5	Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial precursor (EC 2.3.1.168) (Dihydrolipoyllysine-residue (2-methylpropanoyl)transferase)
2030	Q5VVL8	4	4	11.8	482	53517	8.5	Dihydrolipoamide branched chain transacylase E2
2031	O75351	4	7	11.7	444	49302	7.2	Vacuolar protein sorting-associating protein 4B (Suppressor of K(+) transport growth defect 1)
2032	Q86X76-4	4	6	12.2	312	34323	7.4	Isoform 5 of Q86X76
2032	Q86X76	4	6	11.6	327	35896	7.7	Nitrilase homolog 1
2032	Q86X76-3	4	6	10.4	367	40200	6.9	Isoform 4 of Q86X76
2033	Q15428	4	9	11.9	464	49256	9.6	Splicing factor 3A subunit 2
2033	Q05DF2	4	9	11.4	481	51476	10.1	SF3A2 protein
2034	O15554	4	8	11.2	427	47696	9.8	Intermediate conductance calcium-activated potassium channel protein 4
2035	Q13572-2	4	4	14.6	314	35632	5.7	Isoform 2 of Q13572
2035	UPI0000F0E9AF	4	4	14	328	37047	5.7	Inositol-tetrakisphosphate 1-kinase
2035	Q13572	4	4	11.1	414	45621	6.2	Inositol-tetrakisphosphate 1-kinase (EC 2.7.1.134) (Inositol- triphosphate 5/6-kinase) (EC 2.7.1.159) (Inositol 1,3,4-trisphosphate 5/6-kinase) (Ins(1,3,4)P(3) 5/6-kinase)
2036	Q12849-3	4	11	11.8	415	47041	5.6	Isoform 3 of Q12849
2036	UPI0000457223	4	11	11.6	422	47545	5.6	G-rich sequence factor 1 (GRSF-1).
2036	Q12849-2	4	11	11.6	424	47981	5.6	Isoform 2 of Q12849
2036	Q12849	4	11	11	447	50170	6	G-rich sequence factor 1
2036	UPI0000D61572	4	11	11	446	49970	6	G-rich sequence factor 1 (GRSF-1).
2037	Q8WXI9	4	5	11	593	65261	9.7	Transcriptional repressor p66 beta
2038	Q9BRP4-2	4	4	11.5	375	40439	6.7	Isoform 2 of Q9BRP4
2038	Q9BRP4	4	4	11	392	42190	6.3	WD repeat protein 71
2038	UPI0000D6264F	4	4	10.9	394	42374	6.3	WD repeat protein 71 (Protein G-16).
2039	UPI0000140FE5	4	7	11.5	453	49612	9.4	DnaJ homolog subfamily A member 3, mitochondrial precursor (Tumorous imaginal discs protein Tid56 homolog) (DnaJ protein Tid-1) (hTid-1).
2039	Q96EY1-2	4	7	11.5	453	49661	9.4	Isoform 2 of Q96EY1
2039	Q53G26	4	7	10.8	480	52489	9.3	DnaJ (Hsp40) homolog, subfamily A, member 3 variant
2039	Q96EY1	4	7	10.8	480	52538	9.3	DnaJ homolog subfamily A member 3, mitochondrial precursor
2040	UPI000013DC30	4	4	10.9	617	67723	8.6	decapping enzyme Dcp1b
2040	Q8IZD4	4	4	10.8	618	67851	8.6	mRNA-decapping enzyme 1B

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2041	P82675	4	5	10.7	430	48006	9.9	Mitochondrial 28S ribosomal protein S5
2042	Q5SXB7	4	4	10.7	328	36437	8	ATP synthase mitochondrial F1 complex assembly factor 1
2042	Q9H6E3	4	4	10.7	328	36407	8	CDNA: FLJ22351 fis, clone HRC06325
2043	Q9H9J5	4	6	10.6	521	59844	6	CDNA FLJ12694 fis, clone NT2RP1000358, highly similar to Homo sapiens mRNA; cDNA DKFZp564C186
2043	UPI000041820C	4	6	7.3	749	84919	5.6	Nucleolar complex protein 2 homolog (Protein NOC2 homolog) (NOC2- like).
2043	UPI0000161C39	4	6	7.3	749	84878	5.5	nucleolar complex associated 2 homolog
2043	Q9Y3T9	4	6	7.3	749	84905	5.6	Nucleolar complex protein 2 homolog
2044	O43639	4	5	10.5	380	42915	7	Cytoplasmic protein NCK2
2045	Q6ZVM7	4	7	10.5	507	55556	4.8	TOM1-like protein 2
2046	Q6IBT5	4	4	10.4	415	45493	5.9	NEU1 protein
2046	Q99519	4	4	10.4	415	45467	5.9	Sialidase-1 precursor
2047	Q8TB61-2	4	35	11.5	392	42967	9.4	Isoform 2 of Q8TB61
2047	UPI000049E047	4	35	11.4	394	43130	9.4	Adenosine 3'-phospho 5'-phosphosulfate transporter 1 (PAPS transporter 1) (Solute carrier family 35 member B2) (Putative MAPK-activating protein PM15) (Putative NF-kappa-B-activating protein 48).
2047	Q8TB61	4	35	10.4	432	47515	9.2	Adenosine 3'-phospho 5'-phosphosulfate transporter 1
2048	UPI0000F5345A	4	6	20	260	28847	5.7	U4/U6 small nuclear ribonucleoprotein Prp31
2048	Q8WWY3-3	4	6	18.7	278	30966	8.1	Isoform 3 of Q8WWY3
2048	UPI0000140A41	4	6	14.3	364	40749	5.1	U4/U6 small nuclear ribonucleoprotein Prp31 (Pre-mRNA-processing factor 31) (U4/U6 snRNP 61 kDa protein) (hPrp31) (Protein 61K) (Serologically defined breast cancer antigen NY-BR-99).
2048	Q8WWY3-2	4	6	14.3	364	40779	5.1	Isoform 2 of Q8WWY3
2048	Q8WWY3	4	6	10.4	499	55456	5.8	U4/U6 small nuclear ribonucleoprotein Prp31
2048	UPI0000072864	4	6	10.4	499	55442	5.8	pre-mRNA processing factor 31 homolog
2049	Q9BWS9-3	4	6	11.3	362	41678	8.6	Isoform 3 of Q9BWS9
2049	Q9BWS9	4	6	10.4	393	44941	8.6	Chitinase domain-containing protein 1 precursor
2049	UPI000006DA84	4	6	10.4	393	44883	8.8	chitinase domain containing 1
2050	UPI0000208801	4	13	11.2	437	45880	5.6	trans-golgi network protein 2
2050	Q96QL2	4	13	11.2	437	45866	5.6	Trans-golgi network protein 2
2050	Q53GV2	4	13	11.2	437	45850	5.6	Trans-golgi network protein 2 variant
2050	Q53G68	4	13	11.2	437	45936	5.5	Trans-golgi network protein 2 variant
2050	O43493-2	4	13	11.2	437	45774	5.6	Isoform TGN46 of O43493
2050	Q8N6T8	4	13	11	447	47058	5.6	TGOLN2 protein
2050	UPI000020880A	4	13	10.8	453	47774	6	Trans-Golgi network integral membrane protein 2 precursor (Trans-Golgi network protein TGN51) (TGN46) (TGN48) (TGN38 homolog).
2050	O43493-3	4	13	10.8	453	47592	6	Isoform TGN48 of O43493
2050	O43493	4	13	10.2	480	51007	5.7	Trans-Golgi network integral membrane protein 2 precursor
2051	Q9UJW0	4	6	10.2	460	52337	7.3	Dynactin subunit 4
2052	Q6UWP7	4	8	10.1	414	48920	8.6	Lysocardiolipin acyltransferase
2053	Q7L9G1	4	8	10	560	61988	9.4	CDNA FLJ12541 fis, clone NT2RM4000433, moderately similar to Mus musculus retinoic acid-responsive protein (Stra6) mRNA
2053	Q9BX78	4	8	8.5	658	72583	9.1	STRA6 isoform 2
2053	Q9BX79	4	8	8.4	667	73503	9	STRA6 isoform 1
2053	Q8TB21	4	8	8.4	667	73533	9	Stimulated by retinoic acid gene 6 homolog
2054	Q59H65	4	8	10.4	461	51892	6.8	Aldehyde dehydrogenase 3A2 variant
2054	P51648	4	8	9.9	485	54848	7.9	Fatty aldehyde dehydrogenase
2054	P51648-2	4	8	9.4	508	57669	8.9	Isoform 2 of P51648
2055	Q2L9C1	4	5	9.9	534	54823	7.7	Dha kinase/FMN cyclase splice variant
2055	UPI00000718B9	4	5	9.2	575	58947	7.5	dihydroxyacetone kinase 2
2055	Q3LXA3	4	5	9.2	575	58977	7.5	Dihydroxyacetone kinase
2056	Q16822	4	7	9.7	640	70637	7.6	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial precursor
2056	UPI000013C708	4	7	9.7	640	70730	7.6	mitochondrial phosphoenolpyruvate carboxykinase 2 isoform 1 precursor
2056	Q6IB91	4	7	9.7	640	70697	7.6	PCK2 protein
2057	Q5T160	4	4	9.7	578	65505	8.2	Probable arginyl-tRNA synthetase, mitochondrial precursor
2058	Q6P1A2	4	8	9.7	487	56035	8.7	Membrane-bound O-acyltransferase domain-containing protein 5
2059	O00330	4	7	9.6	501	54122	8.7	Pyruvate dehydrogenase protein X component, mitochondrial precursor
2059	UPI0000168268	4	7	9.6	501	54208	8.8	pyruvate dehydrogenase complex, component X
2060	P31749	4	6	9.6	480	55686	6.1	RAC-alpha serine/threonine-protein kinase
2061	Q5T8B5	4	7	9.6	571	59481	8.6	Interferon regulatory factor 2 binding protein 2
2061	Q5T8B6	4	7	9.4	587	61025	8.7	Interferon regulatory factor 2-binding protein 2
2062	Q5VTA2	4	9	9.6	490	55999	5.1	Fas (TNFRSF6) associated factor 1
2062	UPI0000D61F14	4	9	9.4	498	57040	5.1	FAS-associated factor 1 (Protein FAF1) (hFAF1).
2062	Q9UNN5-2	4	9	9.4	498	56934	5.1	Isoform Short of Q9UNN5
2062	Q9UNN5	4	9	7.2	650	73954	4.9	FAS-associated factor 1

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2063	UPI0000457066	4	19	10.3	600	62508	9.4	RNA-binding protein EWS (EWS oncogene) (Ewing sarcoma breakpoint region 1 protein).
2063	Q96MN4	4	19	10.3	600	62478	9.4	CDNA FLJ32119 fis, clone PEBLM1000034, highly similar to RNA-BINDING PROTEIN EWS
2063	Q01844	4	19	9.5	656	68478	9.3	RNA-binding protein EWS
2063	Q96FE8	4	19	9.5	655	68391	9.3	Ewing sarcoma breakpoint region 1
2063	Q96MX4	4	19	9.4	661	68966	9.3	CDNA FLJ31747 fis, clone NT2RI2007377, highly similar to RNA-BINDING PROTEIN EWS
2064	O95219	4	7	9.3	450	51909	6	Sorting nexin-4
2065	P13473	4	94	9.3	410	44961	5.6	Lysosome-associated membrane glycoprotein 2 precursor
2065	Q9UD93	4	94	9.3	410	45043	5.9	Lysosomal membrane glycoprotein LAMP-2 homolog
2065	P13473-2	4	94	9.3	410	44956	5.7	Isoform LAMP
2065	Q6Q3G8	4	94	9.2	411	45170	5.9	Lysosomal-associated membrane protein 2C
2066	P31146	4	4	9.3	461	51026	6.7	Coronin-1A
2067	Q5T6K6	4	7	16.5	254	28450	5.7	Nuclear transcription factor Y, gamma
2067	Q5T6K9	4	7	14	301	33702	5.1	Nuclear transcription factor Y, gamma
2067	UPI0000D61EEA	4	7	13.4	313	34243	6.4	Nuclear transcription factor Y subunit gamma (Nuclear transcription factor Y subunit C) (NF-YC) (CAAT-box DNA-binding protein subunit C) (Transactivator HSM-1/2).
2067	Q5T6K5	4	7	13.4	313	34213	6.4	Nuclear transcription factor Y, gamma
2067	Q13952-2	4	7	12.5	335	37194	5	Isoform 1 of Q13952
2067	Q59GY4	4	7	11.1	378	41595	6.1	Nuclear transcription factor Y, gamma variant
2067	Q13952-3	4	7	9.6	439	48150	5.4	Isoform 2 of Q13952
2067	Q13952	4	7	9.2	458	50302	6.1	Nuclear transcription factor Y subunit gamma
2068	Q4ZG30	4	31	9.2	579	66087	6.1	Hypothetical protein ARL6IP2
2068	Q9H5M7	4	31	9.2	579	66159	6	CDNA: FLJ23293 fis, clone HEP10514
2068	Q8NHH8	4	31	9.2	579	66057	6.2	ARL6IP2
2068	UPI00001B00A2	4	31	9.1	583	66229	5.5	ADP-ribosylation factor-like 6 interacting protein 2
2068	Q8NHH9	4	31	9.1	583	66199	5.5	ADP-ribosylation factor-like protein 6-interacting protein 2
2069	P14324	4	15	9.1	353	40532	5.2	Farnesyl pyrophosphate synthetase (FPP synthetase) (FPS) (Farnesyl diphosphate synthetase) [Includes: Dimethylallyltranstransferase (EC 2.5.1.1); Geranyltranstransferase (EC 2.5.1.10)]
2070	Q86YF0	4	10	9.1	481	50803	8.3	ALDH16A1 protein
2070	UPI000013E0FF	4	10	5.5	802	85127	6.8	aldehyde dehydrogenase 16 family, member A1
2070	Q8IZ83	4	10	5.5	802	85113	6.8	Aldehyde dehydrogenase family 16 member A1
2071	Q53HE9	4	26	9	487	53598	8.2	Ankylosis, progressive homolog
2071	Q9HCJ1	4	26	8.9	492	54241	7.9	Progressive ankylosis protein homolog
2072	O95208-3	4	5	10.5	545	57904	7.1	Isoform 3 of O95208
2072	UPI000013F8F2	4	5	9.8	584	62300	7.5	Epsin-2 (EPS-15-interacting protein 2).
2072	Q52LD0	4	5	9.8	584	62272	7.5	Epsin 2
2072	O95208-2	4	5	9.8	584	62285	7.5	Isoform 2 of O95208
2072	O95208	4	5	8.9	642	68554	7.5	Epsin-2
2072	UPI000013D197	4	5	8.9	641	68482	7.5	Epsin-2 (EPS-15-interacting protein 2).
2072	UPI000007255B	4	5	8.9	641	68454	7.5	epsin 2 isoform b
2072	O95208-4	4	5	8.9	641	68467	7.5	Isoform 4 of O95208
2073	P50542-2	4	4	9.5	602	66830	4.5	Isoform 2 of P50542
2073	P50542-3	4	4	9	631	69872	4.6	Isoform 3 of P50542
2073	P50542	4	4	8.9	639	70865	4.5	Peroxisomal targeting signal 1 receptor
2074	Q53HS1	4	6	8.8	546	59584	7.5	Achalasia, adrenocortical insufficiency, alacrimia (Allgrove, triple- A) variant
2074	Q9NRG9	4	6	8.8	546	59574	7.5	Aladin
2075	Q93052	4	6	8.8	612	65746	7.4	Lipoma-preferred partner
2076	Q9NQW7-2	4	10	9.2	599	67227	5.8	Isoform 2 of Q9NQW7
2076	Q9NQW7	4	10	8.8	623	69918	5.7	Xaa-Pro aminopeptidase 1
2077	Q6QNY5	4	5	8.7	722	79374	6.9	UDP-N-acetylglucosamine-2-epimerase / N-acetylmannosamine kinase
2077	Q9Y223	4	5	8.7	722	79275	6.8	Bifunctional UDP-N-acetylglucosamine 2-epimerase/N-acetylmannosamine kinase (UDP-GlcNAc-2-epimerase/ManAc kinase) [Includes: UDP-N- acetylglucosamine 2-epimerase (EC 5.1.3.14) (Uridine diphosphate-N- acetylglucosamine-2-epimerase) (UDP-GlcNAc-2-epimerase); N-acetylmannosamine kinase (EC 2.7.1.60) (ManAc kinase)]
2077	Q6QNY7	4	5	8.7	722	79305	6.7	UDP-N-acetylglucosamine-2-epimerase / N-acetylmannosamine kinase
2077	Q6QNY6	4	5	8.7	722	79232	6.7	UDP-N-acetylglucosamine-2-epimerase / N-acetylmannosamine kinase
2078	O00400	4	8	8.4	549	60909	7.3	Acetyl-coenzyme A transporter 1
2079	P20020-5	4	7	9.1	1171	129152	6.2	Isoform E of P20020
2079	P20020-6	4	7	9	1184	130617	6	Isoform K of P20020
2079	P20020-2	4	7	9	1176	129516	6.2	Isoform A of P20020
2079	P20020-3	4	7	8.7	1220	134685	5.9	Isoform B of P20020
2079	P20020-4	4	7	8.5	1249	137804	6	Isoform C of P20020

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
2079	P20020	4	7	8.4	1258	138755	6	Plasma membrane calcium-transporting ATPase 1
2080	O00186	4	5	8.3	592	67574	8	Syntaxin-binding protein 3
2080	Q5VTL6	4	5	8.3	592	67764	7.8	Syntaxin binding protein 3
2080	Q53FW1	4	5	8.3	592	67730	7.8	Syntaxin binding protein 3 variant
2081	Q6ZMM9	4	5	13.9	317	35359	6.7	CDNA FLJ16815 fis, clone THYMU3044175, highly similar to Adenosylhomocysteinase
2081	Q2NKW8	4	5	8.7	505	56469	7.8	AHCYL1 protein
2081	O43865	4	5	8.3	530	58951	6.9	Putative adenosylhomocysteinase 2
2082	Q13425	4	5	8.3	540	57950	8.8	Beta-2-syntrophin
2083	Q8N0X7	4	8	8.3	666	72833	5.9	Spartin
2084	Q96SB3	4	5	8.3	815	89192	5	Neurabin-2
2085	Q9Y608	4	7	8.3	721	82171	6.9	Leucine-rich repeat flightless-interacting protein 2
2086	Q9Y5X1	4	9	8.2	595	66592	5.6	Sorting nexin-9
2087	Q32MB2	4	13	8.1	381	42010	8.2	KRT73 protein
2088	Q53GT4	4	5	8.1	737	82565	5.1	Dipeptidylpeptidase III isoform 1 variant
2088	Q9NY33	4	5	8.1	737	82589	5.1	Dipeptidyl-peptidase 3
2088	Q5JPB8	4	5	8.1	737	82617	5.1	Hypothetical protein DKFZp686O1117
2088	Q53HL4	4	5	8.1	737	82549	5.1	Dipeptidylpeptidase III isoform 1 variant
2089	P16278	4	7	8	677	76091	6.6	Beta-galactosidase precursor
2089	UPI0000E9BBE7	4	7	8	677	76075	6.6	galactosidase, beta 1 isoform a
2089	UPI000049DF8F	4	7	8	677	76038	6.5	Beta-galactosidase-related protein precursor (Beta-galactosidase-like protein) (S-Gal) (Elastin-binding protein) (EBP).
2089	Q53H18	4	7	8	677	76110	6.4	Galactosidase, beta 1 variant
2089	Q53G40	4	7	8	677	76069	6.6	Galactosidase, beta 1 variant
2090	Q53FR8	4	7	7.9	570	65070	8.2	Vacuolar protein sorting 45A variant
2090	Q9NRW7	4	7	7.9	570	65077	8.2	Vacuolar protein sorting-associated protein 45
2091	Q8IW24	4	5	7.9	708	81952	6.8	Exocyst complex component 5
2092	Q9UBU9	4	12	7.9	619	70182	8.5	Nuclear RNA export factor 1
2093	Q14677	4	8	7.8	625	68259	6.4	Clathrin interactor 1
2093	Q14677-2	4	8	7.8	625	68166	6.4	Isoform 2 of Q14677
2094	Q59FS7	4	4	7.8	676	75048	8.5	DEAD (Asp-Glu-Ala-Asp) box polypeptide 24 variant
2094	Q9GZR7	4	4	6.2	859	96332	9.1	ATP-dependent RNA helicase DDX24
2095	Q8N2N3	4	12	17.3	243	27824	7.8	CDNA FLJ90102 fis, clone HEMBA1006299, highly similar to Putative NFkB activating protein 373
2095	Q5T9L3	4	12	7.8	541	62253	7.4	Integral membrane protein GPR177 precursor
2095	Q5T9L3-2	4	12	7.7	543	62552	7.6	Isoform 2 of Q5T9L3
2095	Q8N108-9	4	12	5.9	710	81719	4.7	Isoform 9 of Q8N108
2096	Q969V3	4	4	7.8	563	62974	6.9	Nicalin precursor
2096	Q969V3-2	4	4	7.8	562	62846	6.9	Isoform 2 of Q969V3
2097	Q8WXA9-2	4	5	7.7	624	71650	10.2	Isoform 2 of Q8WXA9
2098	O43815-2	4	4	8.1	731	80761	5.2	Isoform 2 of O43815
2098	UPI0000D61189	4	4	7.9	743	81688	5.1	Striatin.
2098	Q3B874	4	4	7.8	755	84267	5.4	STRN protein
2098	O43815	4	4	7.6	780	86132	5.3	Striatin
2099	Q13123	4	5	7.5	557	65630	6.6	Protein Red
2099	Q9UK43	4	5	7.5	557	65586	6.6	Chondrosarcoma-associated protein 2
2099	Q95HA6	4	5	7.5	557	65632	6.6	IK cytokine, down-regulator of HLA II
2099	Q6IPD8	4	5	7.5	557	65602	6.6	IK cytokine, down-regulator of HLA II
2100	O43719	4	4	7.4	755	85853	4.4	HIV Tat-specific factor 1
2101	Q5T176	4	5	7.4	702	77684	5.4	Pre-B-cell leukemia transcription factor interacting protein 1
2101	Q9HA02	4	5	7.4	702	77760	5.4	CDNA FLJ12435 fis, clone NT2RM1000059
2101	Q9HD85	4	5	7.1	731	80727	5.3	Hematopoietic PBX-interacting protein
2101	Q96AQ6	4	5	7.1	731	80643	5.3	Pre-B-cell leukemia transcription factor-interacting protein 1
2102	O43395	4	13	7.3	683	77529	9.5	U4/U6 small nuclear ribonucleoprotein Prp3
2102	Q53GV6	4	13	7.3	683	77441	9.5	PRP3 pre-mRNA processing factor 3 homolog
2102	O43395-2	4	13	7.3	682	77472	9.5	Isoform 2 of O43395
2103	O60504	4	6	7.3	671	75329	9.5	Vinexin
2104	P61764	4	5	7.2	594	67569	7	Syntaxin-binding protein 1
2104	Q5JU62	4	5	7.1	603	68736	6.8	Syntaxin binding protein 1
2105	Q96CW5-2	4	4	7.9	824	93885	7.8	Isoform 2 of Q96CW5
2105	Q96CW5	4	4	7.2	907	103571	8.1	Gamma-tubulin complex component 3
2106	Q8NEU8	4	5	7.1	664	74521	4.9	DCC-interacting protein 13 beta
2106	UPI000006D221	4	5	7.1	664	74493	4.9	DIP13 beta
2107	Q9ULX6	4	4	7.1	646	71640	5	A-kinase anchor protein 8-like
2108	Q52MB3	4	6	7	672	78029	10.3	SAFB-like transcription modulator
2108	UPI0000039EA4	4	6	4.5	1034	117149	7.9	modulator of estrogen induced transcription isoform a
2109	UPI000020A59A	4	14	7	660	76329	7.4	hypothetical protein LOC55129
2110	P10515	4	4	6.8	614	65781	6.1	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial precursor
2110	Q86YI5	4	4	6.5	647	68997	7.8	Dihydrolipoamide S-acetyltransferase
2110	Q53EP3	4	4	6.5	647	68996	8	Dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex) variant

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
2111	P19447	4	4	6.8	782	89278	7.2	TFIIH basal transcription factor complex helicase XPB subunit
2111	UPI0000D61228	4	4	6.8	784	89463	7.2	TFIIH basal transcription factor complex helicase XPB subunit (EC 3.6.1.-) (Basic transcription factor 2 89 kDa subunit) (BTF2-p89) (TFIIH 89 kDa subunit) (DNA-repair protein complementing XP-B cells) (Xeroderma pigmentosum group B-complementing protein)
2112	P49959-2	4	4	7.1	680	77642	5.8	Isoform 2 of P49959
2112	P49959	4	4	6.8	708	80593	5.9	Double-strand break repair protein MRE11A
2113	O95453	4	4	6.7	639	73451	6.2	Poly(A)-specific ribonuclease PARN
2113	UPI0000D6199C	4	4	6.7	641	73696	6.2	Poly(A)-specific ribonuclease PARN (EC 3.1.13.4) (Polyadenylate- specific ribonuclease) (Deadenylating nuclease) (Deadenylation nuclease).
2114	O00461	4	8	6.6	696	81880	4.8	Golgi phosphoprotein 4
2115	Q86SZ6	4	15	8.2	489	55251	7.1	Full-length cDNA clone CS0DJ012YD11 of T cells (Jurkat cell line) of Homo sapiens
2115	O15321	4	15	6.6	606	68861	7.2	Transmembrane 9 superfamily protein member 1 precursor
2116	A4FVC0	4	7	6.4	808	91496	9.4	EIF2C2 protein
2116	UPI0000168652	4	7	6.1	859	97208	9.2	eukaryotic translation initiation factor 2C, 2
2116	Q9UKV8	4	7	6.1	851	96799	9.2	Eukaryotic translation initiation factor 2C 2
2116	UPI0000D6250C	4	7	6	861	97407	9.2	Eukaryotic translation initiation factor 2C 2 (eIF2C 2) (eIF-2C 2) (Argonaute-2) (Slicer protein) (PAZ Piwi domain protein) (PPD).
2117	UPI000013FCDE	4	9	6.6	808	89467	10.1	arginine/proline rich coiled-coil 1
2117	Q9ULN3	4	9	6.5	813	89681	10	KIAA1187 protein
2117	Q3KQU3	4	9	6.3	841	92820	10.1	Arginine/proline-rich coiled-coil protein 1
2118	A2AIB8	4	6	6.2	613	68042	5.5	KIAA1949
2118	UPI00006C0AE4	4	6	6.2	613	67844	5.4	PREDICTED: similar to Protein KIAA1949 isoform 7
2118	Q6NYC8	4	6	6.2	613	67943	5.4	Uncharacterized protein KIAA1949
2119	Q0D2N8	4	4	6.2	710	77782	6.4	SARM1 protein
2119	Q6SZW1	4	4	6.1	724	79388	6.6	Sterile alpha and TIR motif-containing protein 1
2120	P33121-2	4	6	6	688	76871	7	Isoform 2 of P33121
2120	P33121	4	6	5.9	698	77943	7.1	Long-chain-fatty-acid--CoA ligase 1
2121	Q9BVJ6	4	10	5.8	771	87978	7.9	U3 small nucleolar RNA-associated protein 14 homolog A
2122	Q04446	4	4	5.7	702	80460	6.3	1,4-alpha-glucan branching enzyme
2123	Q68D75	4	8	5.7	847	96924	7.5	Oxysterol-binding protein
2123	UPI0000130E99	4	8	5.7	847	96956	7.5	oxysterol-binding protein-like protein 8 isoform b
2123	Q9BZF1-2	4	8	5.5	874	99714	7.1	Isoform 2 of Q9BZF1
2123	Q9BZF1	4	8	5.4	889	101196	7	Oxysterol-binding protein-related protein 8
2124	Q9Y4F1	4	10	5.6	1045	118633	8.2	FERM, RhoGEF and pleckstrin domain-containing protein 1
2124	UPI000041C6E3	4	10	5.5	1076	122095	8.5	FERM, RhoGEF and pleckstrin domain-containing protein 1 (Chondrocyte- derived ezrin-like protein).
2124	Q9Y4F1-2	4	10	5.5	1076	122113	8.5	Isoform 2 of Q9Y4F1
2125	Q3ZAQ6	4	19	5.5	839	94447	6.7	Autophagy 9-like 1 protein
2125	UPI0000456EF3	4	19	5.5	839	94471	6.7	Autophagy-related protein 9A (APG9-like 1).
2125	Q7Z3C6	4	19	5.5	839	94466	6.7	Autophagy-related protein 9A
2126	Q96JM3	4	5	5.5	812	89099	8.4	Zinc finger protein KIAA1802
2127	Q9BRC2	4	5	5.5	750	83856	6.8	TBCD protein
2127	Q9BTW9-5	4	5	5.4	757	84263	6.4	Isoform 5 of Q9BTW9
2127	UPI000020053F	4	5	3.4	1192	132600	6.2	beta-tubulin cofactor D
2127	Q9BTW9	4	5	3.4	1192	132528	6.2	Tubulin-specific chaperone D
2127	Q9BTW9-4	4	5	3.3	1248	138597	6.4	Isoform 4 of Q9BTW9
2128	P23588	4	10	5.4	611	69224	5.7	Eukaryotic translation initiation factor 4B
2128	UPI0000D621F8	4	10	5.4	610	69167	5.8	Eukaryotic translation initiation factor 4B (eIF-4B).
2128	Q8WYK5	4	10	5.4	611	69151	5.7	Eukaryotic initiation factor 4B
2128	Q6IB46	4	10	5.4	611	69137	5.7	EIF4B protein
2128	Q6GPH5	4	10	5.4	611	69166	5.7	Eukaryotic translation initiation factor 4B
2128	Q53HQ2	4	10	5.4	611	69151	5.7	Eukaryotic translation initiation factor 4B variant
2128	Q4G0E3	4	10	5.4	611	69098	5.7	Eukaryotic translation initiation factor 4B
2129	Q9BZQ6	4	7	5.4	889	100305	4.9	ER degradation-enhancing alpha-mannosidase-like 3
2130	Q15269	4	12	5.3	919	102452	6.1	Periodic tryptophan protein 2 homolog
2131	Q9H7I6	4	24	7.1	672	71623	7.9	FLJ00100 protein
2131	Q9H7Q7	4	24	6.2	772	81919	8.3	FLJ00010 protein
2131	Q9BXP2	4	24	5.3	914	96110	8.1	Solute carrier family 12 member 9
2131	Q9NQR5	4	24	5.3	914	96171	8.1	Cation-chloride cotransporter-interacting protein
2131	Q9BYI0	4	24	5.3	914	96079	8.3	Cation chloride cotransporter 6
2132	Q9H7C8	4	9	6.1	824	94301	7	CDNA: FLJ21040 fis, clone CAE10642
2132	Q7L371	4	9	5.8	869	99589	7.1	MGC16824 protein
2132	Q6PDA0	4	9	5.2	963	109530	7.2	Esophageal cancer associated protein
2132	Q86W66	4	9	5.2	963	109562	7.2	Esophageal cancer associated protein
2132	Q7Z3J2	4	9	5.1	972	110472	7.4	Hypothetical protein DKFZp313H1733
2133	Q08AF4	4	6	5.1	936	106183	6.4	PKN2 protein

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
2133	UPI0000D61F53	4	6	4.9	984	112117	6.4	Serine/threonine-protein kinase N2 (EC 2.7.11.13) (Protein kinase C- like 2) (Protein-kinase C-related kinase 2).
2133	Q16513	4	6	4.9	984	112035	6.3	Serine/threonine-protein kinase N2
2134	Q9BSJ2	4	10	5.1	902	102534	6.8	Gamma-tubulin complex component 2
2135	UPI00003E59F4	4	15	6.5	836	95843	6	SLIT-ROBO Rho GTPase activating protein 2 isoform b
2135	A2RUF3	4	15	5	1071	120870	6.7	SLIT-ROBO Rho GTPase activating protein 2
2135	O75044	4	15	5	1071	120880	6.7	SLIT-ROBO Rho GTPase-activating protein 2
2136	UPI000051912A	4	10	5.1	984	111145	9	RNA-binding protein 26 (RNA-binding motif protein 26) (CTCL tumor antigen se70-2).
2136	Q5T8P6-3	4	10	5.1	980	110666	9.1	Isoform 3 of Q5T8P6
2136	Q5T8P6-2	4	10	5.1	983	111024	9.1	Isoform 2 of Q5T8P6
2136	Q5T8P6	4	10	5	1007	113597	9.2	RNA-binding protein 26
2136	UPI0000519129	4	10	5	1008	113718	9.1	RNA-binding protein 26 (RNA-binding motif protein 26) (CTCL tumor antigen se70-2).
2137	Q9UNX4	4	6	5	943	106099	6.6	WD repeat protein 3
2138	Q53ET5	4	9	4.9	831	95804	6.7	ATPase, H+ transporting, lysosomal V0 subunit a isoform 1 variant
2138	UPI0000D62334	4	9	4.9	837	96477	6.7	Vacuolar proton translocating ATPase 116 kDa subunit a isoform 1 (V- ATPase 116 kDa isoform a1) (Clathrin-coated vesicle/synaptic vesicle proton pump 116 kDa subunit) (Vacuolar proton pump subunit 1) (Vacuolar adenosine triphosphatase subunit Ac116).
2138	Q93050-1	4	9	4.9	831	95756	6.7	Isoform 2 of Q93050
2138	Q93050	4	9	4.9	837	96413	6.4	Vacuolar proton translocating ATPase 116 kDa subunit a isoform 1
2138	Q5CZH6	4	9	4.9	838	96603	6.6	Hypothetical protein DKFZp686N0561
2138	Q53X12	4	9	4.9	831	95751	6.7	Vacuolar-type H(+)-ATPase
2139	Q6ZXV5	4	26	4.9	915	104009	8.9	Transmembrane and TPR repeat-containing protein 3
2139	UPI00001A9DBE	4	26	4.9	914	103835	8.9	transmembrane and tetratricopeptide repeat containing 3
2139	Q6ZXV5-2	4	26	4.9	914	103880	8.8	Isoform 2 of Q6ZXV5
2140	Q96PD2	4	5	4.9	775	85035	7.2	Discoidin, CUB and LCCL domain-containing protein 2 precursor
2140	Q96PD2-2	4	5	4.8	789	86657	7.2	Isoform 2 of Q96PD2
2141	O75157-2	4	9	4.9	756	76392	4.9	Isoform 2 of O75157
2141	O75157	4	9	4.7	780	79228	5	TSC22 domain family protein 2
2142	Q7Z5K2	4	4	4.7	1190	132945	5.4	Wings apart-like protein homolog
2142	UPI0000D60F87	4	4	4.6	1228	137363	5.9	Wings apart-like protein homolog (Friend of EBNA2 protein).
2142	Q7Z5K2-2	4	4	4.6	1227	137314	5.9	Isoform 2 of Q7Z5K2
2143	O94906	4	7	4.6	941	106925	8.3	Pre-mRNA-processing factor 6
2144	Q9BTX0	4	8	5	852	94370	6.7	RNA binding motif protein 10
2144	Q5JRR2	4	8	5	853	94469	6.7	RNA binding motif protein 10
2144	P98175	4	8	4.6	929	103459	6	RNA-binding protein 10
2144	Q9BTE4	4	8	4.6	930	103533	6	RNA binding motif protein 10
2144	Q7Z3D7	4	8	4.3	995	110338	6.2	Hypothetical protein DKFZp686E2459
2145	P52732	4	14	4.5	1056	119159	5.6	Kinesin-like protein KIF11
2146	Q9Y4E8-3	4	5	4.5	956	109796	5.2	Isoform 3 of Q9Y4E8
2146	Q9Y4E8-2	4	5	4.5	952	109297	5.2	Isoform 2 of Q9Y4E8
2146	Q9Y4E8	4	5	4.4	981	112419	5.2	Ubiquitin carboxyl-terminal hydrolase 15
2147	O00291	4	4	4.3	1030	115442	5.3	Huntingtin-interacting protein 1
2147	UPI0000D61C73	4	4	4.2	1039	116414	5.3	Huntingtin-interacting protein 1 (HIP-I).
2147	Q2TB58	4	4	4.2	1037	116221	5.3	Huntingtin interacting protein 1
2148	Q13488	4	6	4.3	830	92998	7	Vacuolar proton translocating ATPase 116 kDa subunit a isoform 3
2148	Q8WVC5	4	6	4.3	830	92968	7.1	T-cell, immune regulator 1, ATPase, H+ transporting, lysosomal V0 subunit A3
2149	Q14562	4	9	4.2	1220	139314	8.3	ATP-dependent RNA helicase DHX8
2149	Q86YB2	4	9	4.2	1220	139314	8.4	DEAH (Asp-Glu-Ala-His) box polypeptide 8
2149	Q86X36	4	9	4.2	1220	139287	8.1	DEAH (Asp-Glu-Ala-His) box polypeptide 8
2150	Q96H94	4	8	5.6	806	85041	8.8	MAP1S protein
2150	Q9BRC6	4	8	4.7	962	101969	7.6	MAP1S protein
2150	Q66K74	4	8	4.2	1059	112227	7.3	Microtubule-associated protein 1S
2150	Q8N3W5	4	8	4.2	1059	112239	7.3	VCY2 interacting protein-1
2150	Q8N3L8	4	8	4.2	1061	112497	7.4	Hypothetical protein DKFZp761H0722
2150	Q6NXF1	4	8	4.2	1061	112437	7.4	Microtubule-associated protein 1S
2151	Q8IZL8	4	12	4.2	1130	119700	4.3	Proline-, glutamic acid- and leucine-rich protein 1
2151	UPI00000740E9	4	12	4.2	1130	119624	4.3	proline-, glutamic acid-, leucine-rich protein 1
2152	Q9BZH6	4	8	4.2	1224	136685	6.9	Bromodomain and WD repeat domain-containing protein 2
2153	P28340	4	5	4.1	1107	123631	7	DNA polymerase delta catalytic subunit
2153	UPI00001297C1	4	5	4.1	1107	123635	7	polymerase (DNA directed), delta 1, catalytic subunit 125kDa
2153	Q308M6	4	5	4	1133	126338	7.4	DNA-directed polymerase delta 1
2154	Q5TER5	4	6	4.2	860	98089	8.4	Exosome component 10

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
2154	Q01780	4	6	4.1	885	100831	8.5	Exosome component 10
2155	Q9H8Z6	4	5	5.1	857	96078	6.4	CDNA FLJ13119 fis, clone NT2RP3002671, weakly similar to ELONGATION FACTOR 2
2155	Q7Z2Z2	4	5	4.1	1069	119889	5.8	Elongation factor Tu GTP-binding domain-containing protein 1
2155	UPI00001FEA3A	4	5	4.1	1069	119887	5.8	elongation factor Tu GTP binding domain containing 1 isoform 2
2155	UPI00001FEA35	4	5	3.9	1120	125430	5.9	elongation factor Tu GTP binding domain containing 1 isoform 1
2156	Q7Z7M9	4	12	4	940	106266	9.5	Polypeptide N-acetylgalactosaminyltransferase 5
2157	Q9UDY2	4	6	3.9	1190	133972	7.4	Tight junction protein ZO-2
2157	UPI0000141800	4	6	3.9	1190	133958	7.4	tight junction protein 2 (zona occludens 2) isoform 1
2157	Q9UDY2-3	4	6	3.9	1167	131382	7.1	Isoform C1 of Q9UDY2
2158	Q8IX12	4	7	3.7	1150	132821	5.8	Cell division cycle and apoptosis regulator protein 1
2159	Q8IZH2	4	7	3.6	1706	194106	7.2	5'-3' exoribonuclease 1
2159	UPI0000480180	4	7	3.6	1693	192713	7.3	5""-3"" exoribonuclease 1 isoform b
2159	Q8IZH2-2	4	7	3.6	1694	192842	7.3	Isoform 2 of Q8IZH2
2160	O15118	4	32	3.5	1278	142166	5.4	Niemann-Pick C1 protein precursor
2160	UPI00001303D7	4	32	3.5	1278	142148	5.4	Niemann-Pick disease, type C1 precursor
2160	Q59GR1	4	32	3.5	1289	143231	5.4	Niemann-Pick disease, type C1 variant
2161	Q6PGP7	4	5	3.5	1564	175485	7.5	Tetratricopeptide repeat protein 37
2162	Q6PL18	4	5	3.4	1390	158554	6.3	ATPase family AAA domain-containing protein 2
2163	Q9NRY4	4	9	3.3	1513	172228	6.8	Glucocorticoid receptor DNA-binding factor 1
2163	UPI0000D617DA	4	9	3.3	1514	172419	6.8	Glucocorticoid receptor DNA-binding factor 1 (Glucocorticoid receptor repression factor 1) (GRF-1) (Rho GAP p190A) (p190-A).
2163	Q9NRY4-2	4	9	3.3	1499	170513	6.6	Isoform 2 of Q9NRY4
2164	Q5K651	4	9	3.2	1589	184280	7.8	Sterile alpha motif domain-containing protein 9
2165	O75976	4	8	3.1	1380	152931	6	Carboxypeptidase D precursor
2166	UPI0000470061	4	4	3.8	1071	120732	5.3	AT rich interactive domain 4B isoform 2
2166	Q4LE39-3	4	4	3.6	1153	130418	5	Isoform 3 of Q4LE39
2166	Q4LE39-2	4	4	3.3	1226	137607	5.5	Isoform 2 of Q4LE39
2166	Q4LE39	4	4	3.1	1312	147809	5.1	AT-rich interactive domain-containing protein 4B
2167	Q9H7M7	4	5	3.3	1415	148907	4.7	FLJ00043 protein
2167	Q8N3D4	4	5	3.1	1510	160311	4.8	EH domain-binding protein 1-like protein 1
2167	UPI000013EE70	4	5	3.1	1510	160283	4.8	Signal-induced proliferation-associated protein 1 (Sipa-1) (GTPase- activating protein Spa-1) (p130 SPA-1).
2168	P48634	4	5	2.8	2157	228858	9.5	Large proline-rich protein BAT2
2168	UPI000020E69E	4	5	2.8	2157	228829	9.5	Large proline-rich protein BAT2 (HLA-B-associated transcript 2).
2168	UPI000020E56F	4	5	2.8	2157	228861	9.5	HLA-B associated transcript 2 (BAT2), transcript variant 1, mRNA
2168	UPI00000703A1	4	5	2.8	2157	228869	9.5	HLA-B associated transcript-2 isoform a
2168	Q05BK4	4	5	2.8	2157	228706	9.4	BAT2 protein
2169	Q8TER5	4	5	2.8	1546	167672	6.4	FLJ00128 protein
2169	UPI00001FCFB7	4	5	2.8	1519	164657	6.1	hypothetical protein LOC55701
2170	UPI00004577B6	4	8	2.9	1638	182237	6.9	nucleoporin 188kDa
2170	Q7Z3K8	4	8	2.9	1639	182478	6.9	Hypothetical protein DKFZp686L1653
2170	Q14675	4	8	2.7	1745	195697	6.7	KIAA0169 protein
2170	Q5SRE5	4	8	2.7	1749	196041	6.7	188 kDa nucleoporin
2171	Q5VVH4	4	4	2.7	1821	206688	8.8	Pleckstrin homology domain-interacting protein
2171	Q8WWQ0	4	4	2.7	1821	206646	8.8	WD repeat domain 11 protein
2172	Q75R47	4	4	2.7	2091	213689	7.5	KIAA0023 splice variant 1
2173	A1IGE7	4	5	2.3	1843	212619	6	PKB/Akt-binding protein
2174	Q9BTC0	4	8	2.3	2240	243870	7.9	Death-inducer obliterator 1
2174	UPI000056322E	4	8	2.3	2240	243840	7.9	death inducer-obliterator 1 isoform c
2175	UPI0000D61F29	4	9	2.3	2107	239160	6.8	Dedicator of cytokinesis protein 7.
2175	Q96N67-6	4	9	2.3	2131	241670	6.8	Isoform 6 of Q96N67
2175	Q96N67-5	4	9	2.3	2109	239420	6.8	Isoform 5 of Q96N67
2175	Q96N67-4	4	9	2.3	2098	238272	6.8	Isoform 4 of Q96N67
2175	Q96N67-3	4	9	2.3	2100	238532	6.8	Isoform 3 of Q96N67
2175	Q96N67-2	4	9	2.3	2129	241410	6.8	Isoform 2 of Q96N67
2175	Q96N67	4	9	2.2	2140	242558	6.8	Dedicator of cytokinesis protein 7
2176	UPI000034ECE6	4	10	1.5	3097	346901	6.4	triple functional domain (PTPRF interacting)
2177	P61960	3	7	60	85	9118	9.3	Ubiquitin-fold modifier 1 precursor
2178	UPI0000D621E1	3	34	58.9	448	49764	5.1	Tubulin alpha-6 chain (Alpha-tubulin 6).
2178	Q53GA7	3	34	58.8	449	49823	5.1	Tubulin alpha 6 variant
2178	Q9BQE3	3	34	58.8	449	49895	5.1	Tubulin alpha-6 chain
2179	P61204	3	43	53.6	181	20601	7.4	ADP-ribosylation factor 3
2179	P84077	3	43	53.6	181	20697	6.8	ADP-ribosylation factor 1
2180	Q9H3K6	3	11	51.2	86	10117	6.5	BolA-like protein 2
2181	O95167	3	10	50	84	9279	8.5	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 3
2182	Q9UBI6	3	40	47.2	72	8006	9	Guanine nucleotide-binding protein G(I)/G(S)/G(O) gamma-12 subunit precursor
2183	A0JCS1	3	12	46.9	273	31682	5.8	MHC class I antigen
2184	P62857	3	26	46.4	69	7841	10.7	40S ribosomal protein S28
2184	UPI000013E08B	3	26	46.4	69	7823	10.7	ribosomal protein S28 (RPS28), mRNA

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2185	Q9Y281	3	8	45.2	166	18737	7.9	Cofilin-2
2186	P61513	3	30	42.4	92	10275	10.4	60S ribosomal protein L37a
2187	Q9BTM1	3	138	41.9	129	14019	10.9	H2A histone family, member J
2188	Q92930	3	5	41.5	207	23584	9.1	Ras-related protein Rab-8B
2189	P0C0S5	3	31	40.6	128	13553	10.6	Histone H2A.Z
2189	Q71UI9	3	31	40.6	128	13509	10.6	Histone H2AV
2190	P04271	3	15	40.2	92	10713	4.6	Protein S100-B
2191	O15523	3	4	40	660	73154	7.6	ATP-dependent RNA helicase DDX3Y
2192	P18859	3	9	39.8	108	12587	9.5	ATP synthase coupling factor 6, mitochondrial precursor
2193	Q9Y3D7	3	4	39.2	125	13825	9.7	Mitochondrial import inner membrane translocase subunit TIM16
2194	Q9BWJ5	3	14	38.4	86	10135	6.4	Splicing factor 3B subunit 5
2195	O00244	3	6	38.2	68	7402	7.2	Copper transport protein ATOX1
2195	UPI0000D6169C	3	6	38.2	68	7449	7.2	Copper transport protein ATOX1 (Metal transport protein ATX1).
2195	Q6IBA3	3	6	38.2	68	7388	7.2	ATOX1 protein
2196	Q9Y5J7	3	7	38.2	89	10378	7.2	Mitochondrial import inner membrane translocase subunit Tim9
2197	Q96B45	3	5	38.1	105	11564	6.8	Uncharacterized protein C10orf32
2198	P35244	3	12	37.2	121	13569	5.1	Replication protein A 14 kDa subunit
2199	O15116	3	8	36.8	133	15179	5.2	U6 snRNA-associated Sm-like protein LSm1
2200	P14174	3	12	36.5	115	12476	7.9	Macrophage migration inhibitory factor
2201	Q99622	3	8	36.5	126	13178	5.1	Putative C10 protein
2202	Q86Y39	3	6	36.2	141	14852	8.7	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11
2203	Q6FIE5	3	5	35.2	125	13792	6.1	PHP14 protein
2203	Q9NRX4	3	5	35.2	125	13833	6.1	14 kDa phosphohistidine phosphatase
2203	UPI0000DD5CDC	3	5	30.6	144	16144	6.4	14 kDa phosphohistidine phosphatase
2204	Q8WYJ5	3	10	35.2	128	13918	7	Protein kinase C inhibitor-2
2204	Q9BX68	3	10	27.6	163	17162	9.1	Histidine triad nucleotide-binding protein 2
2205	Q3ZAQ7	3	9	34.7	101	11354	7.2	Hypothetical protein LOC203547
2206	Q15843	3	7	34.6	81	9072	8.4	NEDD8 precursor
2206	UPI0000EFE33A	3	7	34.6	81	8905	7.2	NEDD8
2207	P63027	3	30	34.5	116	12649	8.1	Vesicle-associated membrane protein 2
2207	Q9N0Y0	3	30	34.5	116	12663	8.1	Vesicle-associated membrane protein 2
2208	Q9Y547	3	6	33.3	144	16297	5	Placental protein 25
2209	Q05639	3	3	33	463	50470	9	Elongation factor 1-alpha 2
2210	Q5T179	3	6	38.8	67	8027	6.4	CDC28 protein kinase regulatory subunit 1B
2210	P61024	3	6	32.9	79	9660	8.9	Cyclin-dependent kinases regulatory subunit 1
2210	UPI0000161698	3	6	32.9	79	9660	8.7	PREDICTED: similar to Cyclin-dependent kinases regulatory subunit 1 (CKS-1) (Sid 1334)
2211	P81605	3	3	32.7	110	11284	6.5	Dermcidin precursor (Preproteolysin) [Contains: Survival-promoting peptide; DCD-1]
2212	Q56VW3	3	13	32.6	175	19800	6.6	Transformation-related gene 7
2212	Q7Z7H5	3	13	25.1	227	25943	8.3	Transmembrane emp24 domain-containing protein 4 precursor
2212	UPI0000D61C37	3	13	24.9	229	26170	8.6	Transmembrane emp24 domain-containing protein 4 precursor.
2213	Q5JTJ3-3	3	4	50.6	79	9428	7.7	Isoform 3 of Q5JTJ3
2213	Q5JTJ3	3	4	32	125	14116	8.3	Uncharacterized protein C1orf31
2213	UPI00001D7D6B	3	4	25.8	155	18007	10.1	Novel protein.
2213	Q5JTJ3-2	3	4	25.6	156	18094	10.1	Isoform 2 of Q5JTJ3
2214	P62318	3	25	31.7	126	13916	10.3	Small nuclear ribonucleoprotein Sm D3
2215	Q9Y6H1	3	3	31.1	151	15513	9.2	Coiled-coil-helix-coiled-coil-helix domain-containing protein 2
2216	Q9BUE6	3	4	31	129	14179	9.1	Iron-sulfur cluster assembly 1 homolog, mitochondrial precursor
2216	UPI0000141215	3	4	31	129	14177	9.1	OTTHUMP00000021591.
2217	Q8N4V1	3	9	30.5	131	14686	9.1	Transmembrane protein 32
2218	Q9Y3E2	3	4	29.9	137	14289	8	BolA-like protein 1
2219	UPI0000158C34	3	5	45	100	10905	4.5	PREDICTED: similar to basic transcription factor 3-like 4
2219	UPI0000D61F1B	3	5	29.6	152	16409	5.6	Transcription factor BTF3 homolog 4 (Basic transcription factor 3-like 4).
2219	Q6PJ77	3	5	29.4	153	16470	5.6	BTF3L4 protein
2219	Q96K17	3	5	28.5	158	17271	6.4	Transcription factor BTF3 homolog 4
2220	O43920	3	16	29.2	106	12517	9.1	NADH dehydrogenase [ubiquinone] iron-sulfur protein 5
2221	P60468	3	73	29.2	96	9974	11.6	Protein transport protein Sec61 subunit beta
2222	O60783	3	7	28.9	128	15139	11.4	Mitochondrial 28S ribosomal protein S14
2223	O43676	3	22	28.6	98	11402	9.2	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3
2224	P62273	3	9	28.6	56	6677	10.1	40S ribosomal protein S29
2225	P09132	3	9	28.5	144	16156	9.8	Signal recognition particle 19 kDa protein
2226	Q9NQP4	3	6	28.4	134	15314	4.5	Prefoldin subunit 4
2227	Q9BX83	3	3	40	100	10710	7.7	Hemoglobin alpha 1 globin chain
2227	P69905	3	3	28.2	142	15258	8.7	Hemoglobin subunit alpha
2227	Q53F97	3	3	28.2	142	15281	8.7	Alpha 2 globin variant

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2227	Q1HDT5	3	3	28.2	142	15272	9	Hemoglobin alpha 1-2 hybrid
2228	Q6VUD0	3	8	29.1	117	12976	8.3	Endosulfine-alpha variant 3
2228	Q6NUL2	3	8	29.1	117	12961	8.3	Endosulfine alpha
2228	Q6IAM4	3	8	29.1	117	12976	7.2	ENSA protein
2228	O43768	3	8	28.1	121	13389	7.2	Alpha-endosulfine
2228	Q6VUC9	3	8	24.8	137	15281	6	Endosulfine-alpha variant 2
2228	UPI0000D61FE3	3	8	24.3	140	15634	8.3	Alpha-endosulfine (ARPP-19e).
2228	Q68D48	3	8	24.3	140	15534	8.7	Hypothetical protein DKFZp779B2258
2228	Q5T5H1	3	8	18.2	187	20994	7.8	Endosulfine alpha
2229	Q8NI22	3	5	28.1	146	16390	4.6	Multiple coagulation factor deficiency protein 2 precursor
2230	Q86SX6	3	12	28	157	16628	6.8	Glutaredoxin-related protein 5
2231	O95295	3	3	27.9	136	14874	9.3	SNARE-associated protein Snapin
2232	Q7Z6L8	3	5	34.3	245	28385	4.8	Tropomyosin 1
2232	Q59GR8	3	5	27.7	303	34402	5.4	TPM1 protein variant
2233	Q8N111	3	14	27.5	149	14954	9.2	Cell cycle exit and neuronal differentiation protein 1
2234	Q5HYD9	3	7	37.4	107	11873	4.8	Hypothetical protein DKFZp686M0619
2234	O43169	3	7	27.4	146	16332	5	Cytochrome b5 type B precursor
2235	P42025	3	8	27.1	376	42293	6.4	Beta-centractin
2236	Q53HB4	3	7	26.9	160	18995	5.3	M-phase phosphoprotein 6 variant
2236	UPI00001AE7AB	3	7	26.9	160	19024	5.2	M-phase phosphoprotein 6
2236	Q99547	3	7	26.9	160	18996	5.2	M-phase phosphoprotein 6
2237	Q9NVP2	3	4	26.7	202	22434	4.6	Histone chaperone ASF1B
2238	P61803	3	30	26.5	113	12497	7.1	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1
2239	O75607	3	7	26.4	178	19344	4.6	Nucleoplasmin-3
2240	O75817	3	5	26.4	140	15651	8.9	Ribonuclease P protein subunit p20
2241	Q7Z4G1	3	6	38.8	85	9638	6	COMM domain-containing protein 6
2241	UPI000034ECDC	3	6	33.7	98	10908	6	COMM domain containing 6 isoform a
2241	Q5TBK3	3	6	26.4	125	14211	9.8	COMM domain containing 6
2241	UPI0000D61A83	3	6	26.4	125	14257	9.8	COMM domain-containing protein 6.
2242	Q9NUG6	3	3	26.3	133	15511	6	p53 and DNA damage-regulated protein 1
2243	Q9Y3C0	3	4	26.3	194	21173	4.5	Coiled-coil domain-containing protein 53
2244	Q53GP2	3	3	26.2	149	16989	6.3	Thioredoxin-like 4B variant
2244	Q9NX01	3	3	26.2	149	17015	6	Thioredoxin-like protein 4B
2245	P17677	3	3	26.1	238	24803	4.7	Neuromodulin
2246	P53999	3	22	26	127	14395	9.6	Activated RNA polymerase II transcriptional coactivator p15
2246	UPI000006EEC7	3	22	26	127	14365	9.6	activated RNA polymerase II transcription cofactor 4
2246	Q59G24	3	22	24.6	134	15135	9.4	Activated RNA polymerase II transcription cofactor 4 variant
2247	P68014	3	8	26	146	15808	8.4	Hemoglobin subunit delta
2248	UPI000059DB3B	3	6	26.6	158	18342	7.3	Sorting nexin-12.
2248	Q3SYF1	3	6	25.9	162	18885	8.4	Sorting nexin 12
2248	UPI0000D61D89	3	6	24.4	172	19819	7.8	Sorting nexin-12.
2248	Q9UMY4	3	6	24.4	172	19730	7.9	Sorting nexin-12
2249	Q9NX14	3	3	26.8	153	17317	5.2	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11, mitochondrial precursor
2249	Q7Z4X2	3	3	25.9	158	17942	5.4	Neuronal protein
2249	Q9NX14-2	3	3	25.2	163	18364	5.2	Isoform 2 of Q9NX14
2250	UPI0000E200C7	3	5	31.6	95	10300	10.5	PREDICTED: translocase of the inner mitochondrial membrane 14 isoform 1
2250	Q96DA6	3	5	25.9	116	12499	10.1	Mitochondrial import inner membrane translocase subunit TIM14
2251	Q3SZ52	3	7	38.8	147	16495	8	Ubiquitin-conjugating enzyme E2 variant 1
2251	Q13404-7	3	7	33.5	170	19307	8.5	Isoform 7 of Q13404
2251	Q13404-2	3	7	33.5	170	19228	8.2	Isoform 2 of Q13404
2251	Q13404	3	7	25.8	221	25797	8.3	Ubiquitin-conjugating enzyme E2 variant 1
2251	UPI0000233611	3	7	15.4	370	42210	6.6	ubiquitin-conjugating enzyme E2 Kua-UEV isoform 1
2252	Q9NP97	3	12	39.6	96	10922	7.2	Dynein light chain roadblock-type 1
2252	Q5TC71	3	12	25.7	148	16253	7	Dynein, light chain, roadblock-type 1
2253	P17568	3	6	25.5	137	16402	8.9	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7
2254	A2ABE5	3	7	25	368	41206	6.6	Major histocompatibility complex, class I, C
2254	A2ABE6	3	7	24.7	372	41363	6	Major histocompatibility complex, class I, C
2254	A2ABE7	3	7	23.2	397	44216	7	Major histocompatibility complex, class I, C
2255	Q6GMV3	3	8	25	140	15805	9.1	Similar to CG14903-PA
2256	UPI0000509F05	3	4	25.4	169	19805	4.7	TAF9 RNA polymerase II isoform c
2256	Q9Y3D8	3	4	25	172	20061	4.6	Adenylate kinase isoenzyme 6
2257	P32321	3	5	24.7	178	20016	7.6	Deoxycytidylate deaminase
2257	Q5M7Z8	3	5	23.3	189	21014	7.5	DCMP deaminase
2258	O75348	3	10	24.6	118	13758	8.8	Vacuolar ATP synthase subunit G 1
2259	P45973	3	6	24.6	191	22225	5.9	Chromobox protein homolog 5
2260	P98179	3	33	24.2	157	17170	8.9	Putative RNA-binding protein 3
2261	Q3KRA6	3	3	23.8	126	14609	6.9	LOC130355 protein
2261	Q4VC35	3	3	23.8	126	14623	6.9	Hypothetical protein LOC130355
2262	Q9Y2V2	3	4	23.8	147	15892	8.2	Calcium-regulated heat stable protein 1
2263	P54725	3	3	23.7	363	39609	4.6	UV excision repair protein RAD23 homolog A
2263	Q59EU8	3	3	22.7	379	41256	4.7	UV excision repair protein RAD23 homolog A variant

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
2264	O60613	3	13	23.5	162	17743	5	15 kDa selenoprotein precursor
2264	UPI000034ECC1	3	13	23	165	17942	5	15 kDa selenoprotein isoform 1 precursor
2265	Q9P299	3	12	23.3	210	23548	5.2	Coatomer subunit zeta-2
2266	Q96AB3	3	3	22.9	205	22337	7.8	Isochorismatase domain-containing protein 2, mitochondrial precursor
2266	Q96AB3-2	3	3	21.3	221	24097	7.8	Isoform 2 of Q96AB3
2267	P30049	3	13	22.6	168	17490	5.5	ATP synthase delta chain, mitochondrial precursor
2268	P61923	3	15	22.6	177	20198	4.8	Coatomer subunit zeta-1
2268	Q53FU3	3	15	22.6	177	20267	4.9	Coatomer protein complex, subunit zeta 1 variant
2269	P20962	3	62	22.5	102	11530	4.2	Parathymosin
2270	Q9Y530	3	4	22.4	152	17025	8.3	Uncharacterized protein C6orf130
2270	UPI00001415EB	3	4	21.7	157	17607	8.3	Uncharacterized protein C6orf130.
2271	Q9BQQ5	3	29	31.1	106	12015	11.5	Ribosomal protein L27a
2271	P46776	3	29	22.3	148	16561	11	60S ribosomal protein L27a
2271	UPI0000160A16	3	29	22.3	148	16622	11.1	PREDICTED: similar to 60S ribosomal protein L27a
2271	Q6NZ52	3	29	22.3	148	16478	11	Ribosomal protein L27a
2272	P54652	3	6	22.2	639	70021	5.7	Heat shock-related 70 kDa protein 2
2273	Q9BRX5	3	3	22.2	216	24535	5.3	GINS complex subunit 3
2273	UPI0000D619FA	3	3	22	218	24719	5.3	GINS complex subunit 3 (Psf3 homolog)
2274	P09417	3	9	22.1	244	25789	7.4	Dihydropteridine reductase
2274	UPI000004C79F	3	9	22.1	244	25804	7.4	quinoid dihydropteridine reductase
2275	Q9UDC2	3	33	23.7	135	15812	10.4	RIG homolog
2275	P62841	3	33	22.1	145	17040	10.4	40S ribosomal protein S15
2276	Q5TZN6	3	3	23.1	208	22629	4.2	Nucleolar protein 3
2276	O60936	3	3	21.9	219	24327	11.3	Nucleolar protein 3
2277	P63302	3	4	21.8	87	9401	9.1	Selenoprotein W
2277	UPI0000161B36	3	4	21.8	87	9298	9.2	selenoprotein W, 1
2277	UPI0000456CEF	3	4	21.3	89	9561	8.9	Selenoprotein W.
2278	Q9P0S2	3	3	21.7	106	12293	9.5	COX16-like protein C14orf112, mitochondrial precursor
2279	Q9UMX5	3	4	21.5	172	18856	5.7	Neudesin precursor
2280	P63272	3	4	21.4	117	13193	8.1	Transcription elongation factor SPT4
2281	Q93096	3	3	21.4	173	19815	9	Protein tyrosine phosphatase type IVA protein 1 (EC 3.1.3.48) (Protein-tyrosine phosphatase 4a1) (Protein-tyrosine phosphatase of regenerating liver 1) (PRL-1) (PTP(CAAXI))
2282	Q9UKK6	3	5	21.4	140	15847	5	NTF2-related export protein 1
2283	Q9H5X1	3	4	21.2	160	18355	4.9	Protein FAM96A
2284	Q9Y3C6	3	8	21.1	166	18237	8	Peptidyl-prolyl cis-trans isomerase-like 1
2285	UPI000013C8D5	3	3	21.1	166	17870	9.6	Iron-sulfur cluster assembly enzyme ISCU, mitochondrial precursor (NifU-like N-terminal domain-containing protein) (NifU-like protein).
2285	Q9H1K1	3	3	21	167	17937	9.5	Iron-sulfur cluster assembly enzyme ISCU, mitochondrial precursor
2285	UPI000021CA9A	3	3	21	167	17999	9.5	iron-sulfur cluster assembly enzyme isoform ISCU2 precursor
2286	Q86YS6	3	3	20.8	212	23339	5.7	Ras-related protein Rab-43
2287	O14582	3	4	20.7	140	16445	6.5	Trafficking protein particle complex subunit 2
2287	UPI0000457806	3	4	20.1	144	17020	6.5	Trafficking protein particle complex subunit 2 (Sedlin) (MBP-1- interacting protein 2A) (MIP-2A).
2287	O14582-2	3	4	19.7	147	17260	6.7	Isoform 2 of O14582
2288	Q96NT0	3	4	20.6	180	19761	7	Coiled-coil domain-containing protein 115
2289	P51151	3	5	20.4	201	22838	5.5	Ras-related protein Rab-9
2290	P82664	3	5	20.4	201	22999	8	Mitochondrial 28S ribosomal protein S10
2291	Q9HBL7	3	8	20.4	147	17201	9.6	Uncharacterized protein C9orf46
2291	UPI0000073DFC	3	8	20.4	147	17229	9.7	hypothetical protein LOC55848
2292	Q9HD47	3	3	20.4	186	20448	4.9	MOG1 isoform A
2293	Q9UM00-2	3	27	22.5	169	18766	9.6	Isoform 2 of Q9UM00
2293	Q9UM00	3	27	20.2	188	21175	9.7	Transmembrane and coiled-coil domain-containing protein 1
2294	A2TDT2	3	5	19.7	157	18221	6.5	Mutant B-cell CLL/lymphoma 10
2294	O95999	3	5	13.3	233	26252	5.8	B-cell lymphoma/leukemia 10
2295	O75915	3	38	19.7	188	21615	9.8	PRA1 family protein 3
2296	Q9BQE4	3	4	19.6	189	21116	9.6	Selenoprotein S
2296	UPI00001B2973	3	4	19.6	189	21013	9.7	selenoprotein S
2297	Q13795	3	3	19.4	201	22614	7.6	ADP-ribosylation factor-related protein 1
2298	Q32P46	3	5	19.3	166	18205	9.7	Mitochondrial ribosomal protein L11
2298	Q9Y3B7	3	5	16.7	192	20683	9.9	39S ribosomal protein L11, mitochondrial precursor
2298	Q53G19	3	5	16.7	192	20655	9.9	Mitochondrial ribosomal protein L11 isoform a variant
2299	Q8WVJ2	3	7	19.1	157	17676	5.1	NudC domain-containing protein 2
2300	Q9NX08	3	7	19.1	183	21090	5.4	COMM domain-containing protein 8
2301	P55327	3	9	19	184	19863	5	Tumor protein D52
2301	Q6FGS3	3	9	19	184	19847	5	TPD52 protein
2301	UPI00005520F0	3	9	16.9	207	22477	5.4	tumor protein D52 isoform 2
2301	UPI0000D624DE	3	9	16.7	209	22635	5.4	Tumor protein D52 (N8 protein).
2301	Q53EK8	3	9	15.8	222	23782	5.9	N8 protein long isoform variant
2301	Q86YZ2	3	9	15.6	224	24327	4.8	Prostate and colon associated protein
2301	UPI0000D624DF	3	9	15.5	226	24485	4.8	Tumor protein D52 (N8 protein).

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
2301	Q9UCX8	3	9	14.1	248	26382	6.4	N8 protein long isoform
2301	UPI0000D624DD	3	9	14	250	26480	5.9	Tumor protein D52 (N8 protein).
2302	Q561V4	3	5	18.9	169	19119	6.3	COMMD2 protein
2302	Q86X83	3	5	16.1	199	22745	6.7	COMM domain-containing protein 2
2303	Q9BU89	3	3	18.9	302	32904	4.8	Deoxyhypusine hydroxylase
2304	Q9NQ50	3	8	18.9	206	24490	9.6	39S ribosomal protein L40, mitochondrial precursor
2305	Q9BW83	3	4	18.8	186	20480	5.4	Putative GTP-binding protein RAY-like
2305	UPI000013C6D3	3	4	18.7	187	20424	5.6	Putative GTP-binding protein RAY-like (Rab-like protein 4).
2306	Q9Y3E0	3	65	18.8	138	15426	10.3	Vesicle transport protein GOT1B
2307	Q9Y6G5	3	4	18.8	202	22966	6.5	COMM domain-containing protein 10
2308	Q6MZY9	3	5	18.6	172	19092	6.5	Hypothetical protein DKFZp686M14237
2308	UPI0000229DA7	3	5	18.6	172	19036	6.5	CDNA FLJ11151 fis, clone PLACE1006883.
2308	UPI000013D1D1	3	5	10.2	314	35548	6.2	CDNA FLJ11151 fis, clone PLACE1006883.
2308	Q9H9M9	3	5	10.2	314	35624	6.3	CDNA FLJ12648 fis, clone NT2RM4002018
2308	Q9BRF8	3	5	10.2	314	35620	6.1	Hypothetical protein FLJ11151
2309	Q2QD04	3	5	18.5	222	23769	8.9	RcUBE2S
2309	Q6NXQ4	3	5	18.5	222	23771	8.7	UBE2S protein
2310	O43752	3	5	18.4	255	29176	4.9	Syntaxin-6
2311	Q53GA4	3	3	18.4	152	17092	9.2	Pleckstrin homology-like domain family A member 2
2312	Q9BV86	3	3	18.4	223	25387	5.5	UPF0351 protein C9orf32
2313	P62330	3	11	18.3	175	20082	9	ADP-ribosylation factor 6
2313	Q5U025	3	11	18.3	175	20211	9	ADP-ribosylation factor 6
2314	Q659F8	3	13	18.2	225	23874	9	Hypothetical protein DKFZp434F152
2314	Q9Y289	3	13	6.5	635	68702	8.3	Sodium-dependent multivitamin transporter (Na(+)-dependent multivitamin transporter)
2314	Q969Y5	3	13	6.5	635	68642	8.3	Solute carrier family 5 (Sodium-dependent vitamin transporter), member 6
2315	Q86U28	3	6	18.2	154	16476	5.2	Iron-sulfur cluster assembly 2 homolog, mitochondrial precursor
2316	Q7Z5G8	3	4	18.1	276	31625	7.1	P15RS protein
2316	Q96FY9	3	4	17.3	289	32917	6.7	P15RS protein
2316	Q96P16	3	4	16	312	35720	7.5	Cyclin-dependent kinase inhibitor-related protein
2317	Q969J3	3	5	17.9	196	22222	6.4	Loss of heterozygosity 12 chromosomal region 1 protein
2318	P61009	3	14	17.8	180	20313	8.6	Signal peptidase complex subunit 3
2318	UPI00004572A7	3	14	17.5	183	20779	9.3	Signal peptidase complex subunit 3 (EC 3.4.-.-) (Microsomal signal peptidase 23 kDa subunit) (SPase 22 kDa subunit) (SPC22/23).
2319	Q9H2D1	3	3	17.8	315	35407	9.5	Mitochondrial folate transporter/carrier
2320	Q496C9	3	5	17.7	209	23484	8.3	D-tyrosyl-tRNA deacylase 1 homolog
2320	Q8TEA8	3	5	17.7	209	23424	8.2	Probable D-tyrosyl-tRNA(Tyr) deacylase 1
2321	Q9BUH6	3	5	17.6	204	21640	5.5	Uncharacterized protein C9orf142
2322	P60903	3	29	17.5	97	11203	7.4	Protein S100-A10
2322	Q6FGE5	3	29	17.5	97	11187	7.4	S100A10 protein
2323	Q9NRI8	3	4	17.6	210	24121	5.8	HT014
2323	Q9GZP4	3	4	17.5	211	24178	5.8	Uncharacterized protein C1orf128
2324	UPI000036655D	3	3	21.5	233	26007	5.1	Probable diphthine synthase (EC 2.1.1.98) (Diphthamide biosynthesis methyltransferase).
2324	UPI000036655C	3	3	21.5	233	25938	5.1	Probable diphthine synthase (EC 2.1.1.98) (Diphthamide biosynthesis methyltransferase).
2324	Q9H2P9-2	3	3	21.4	234	26122	5	Isoform 2 of Q9H2P9
2324	UPI0000D61F6B	3	3	17.6	284	31518	5.3	Probable diphthine synthase (EC 2.1.1.98) (Diphthamide biosynthesis methyltransferase).
2324	UPI000059D01C	3	3	17.6	284	31580	5.3	diphthine synthase isoform b
2324	Q9H2P9	3	3	17.5	285	31651	5.3	Probable diphthine synthase
2324	Q9H2P9-4	3	3	17.5	285	31440	5.3	Isoform 4 of Q9H2P9
2324	Q9H2P9-5	3	3	16.8	297	33005	5.5	Isoform 5 of Q9H2P9
2325	P61599	3	6	17.4	178	20368	5	N-acetyltransferase 5
2326	Q9BU61	3	12	17.4	184	20350	8.2	Uncharacterized protein C3orf60
2327	Q8IWT0	3	6	17.3	179	20675	4.6	Zinc finger and BTB domain-containing opposite strand protein 8
2328	Q9Y3B8	3	6	17.3	237	26833	6.9	Oligoribonuclease, mitochondrial precursor
2328	UPI0000130E83	3	6	17.3	237	26861	6.9	small fragment nuclease
2329	Q9NRX2	3	8	17.1	175	20050	10.1	39S ribosomal protein L17, mitochondrial precursor
2330	Q9Y676	3	3	17.1	258	29396	9.4	28S ribosomal protein S18b, mitochondrial precursor
2331	Q8N2G6	3	3	17	241	26955	8.7	Zinc finger CCHC domain-containing protein C10orf56
2331	UPI000006DF92	3	3	17	241	26925	8.8	hypothetical protein LOC219654
2331	UPI0000D60F78	3	3	13.7	299	31988	9.3	C10orf56 protein
2332	Q9UHD9	3	5	17	624	65696	5.2	Ubiquilin-2
2333	Q561V6	3	9	23.4	137	15667	7.6	NDUFB5 protein
2333	O43674	3	9	16.9	189	21750	9.6	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 5, mitochondrial precursor
2334	UPI000020400A	3	35	18.7	123	14053	11.3	Histone H3.3.
2334	P68431	3	35	16.9	136	15404	11.1	Histone H3.1
2334	Q71DI3	3	35	16.9	136	15388	11.3	Histone H3.2
2334	Q16695	3	35	16.9	136	15508	11.1	Histone H3.1t

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
2334	P84243	3	35	16.9	136	15328	11.3	Histone H3.3
2334	UPI00006C1BEF	3	35	16.2	142	16181	10.6	PREDICTED: similar to H3 histone, family 3B
2334	UPI00006C029D	3	35	12.8	180	20527	10.2	PREDICTED: similar to H3 histone, family 2 isoform 2
2335	A1L179	3	6	16.8	863	99099	6.1	KIF5C protein
2335	UPI0000DD7A67	3	6	16.8	863	99040	6.1	PREDICTED: similar to Kinesin heavy chain isoform 5C (Kinesin heavy chain neuron-specific 2)
2335	O60282	3	6	15.2	957	109495	6.2	Kinesin heavy chain isoform 5C
2336	P40306	3	5	16.8	273	28936	7.8	Proteasome subunit beta type 10 precursor
2336	Q6IB22	3	5	16.8	273	28936	8.1	Proteasome subunit beta type
2337	Q96HR9	3	14	16.8	184	20733	8.6	Receptor expression-enhancing protein 6
2338	Q9Y3C8	3	7	16.8	167	19458	7.4	Ufm1-conjugating enzyme 1
2338	UPI0000167880	3	7	16.8	167	19467	7.5	Ufm1-conjugating enzyme 1
2339	P42773	3	4	16.7	168	18127	6.5	Cyclin-dependent kinase 6 inhibitor
2340	UPI000045652F	3	6	18.6	188	20857	10.1	39S ribosomal protein L21, mitochondrial precursor (L21mt) (MRP-L21).
2340	Q7Z2W9	3	6	16.7	209	23159	9.9	39S ribosomal protein L21, mitochondrial precursor
2341	UPI0000D624A0	3	4	16.7	252	29580	8	Bridging integrator 3.
2341	Q53HW0	3	4	16.6	253	29702	8.1	Bridging integrator 3 variant
2341	Q9NQY0	3	4	16.6	253	29665	7.5	Bridging integrator 3
2342	Q9Y6A4	3	5	16.6	193	22774	9.8	Uncharacterized protein C16orf80
2343	O75608-2	3	12	17.8	214	22875	6.5	Isoform 2 of O75608
2343	O75608	3	12	16.5	230	24670	6.8	Acyl-protein thioesterase 1
2344	Q13084	3	4	16.4	256	30157	8.3	39S ribosomal protein L28, mitochondrial precursor
2344	Q4TT38	3	4	16.4	256	30046	8	Mitochondrial ribosomal protein L28
2345	Q53FX5	3	16	16.2	197	21820	8	Lin-7 homolog C variant
2345	Q9NUP9	3	16	16.2	197	21834	8.4	Lin-7 homolog C
2346	Q9UM13	3	4	16.2	185	21252	9.1	Anaphase-promoting complex subunit 10
2346	UPI000007167D	3	4	16.2	185	21223	9.1	anaphase promoting complex subunit 10
2347	Q9BZS6	3	6	16	194	22615	5.3	SSU72 RNA polymerase II CTD phosphatase homolog
2347	Q9NP77	3	6	16	194	22574	5.3	CDNA FLJ10947 fis, clone PLACE1000066, weakly similar to SSU72 PROTEIN
2348	Q4VX17	3	6	15.9	347	38287	7.6	Secretory carrier membrane protein 3
2348	UPI0000456274	3	6	15.9	347	38315	7.2	Secretory carrier-associated membrane protein 3 (Secretory carrier membrane protein 3).
2348	Q6FHJ5	3	6	15.9	347	38243	7.6	SCAMP3 protein
2349	Q5VXM9	3	4	15.9	208	24158	9.5	Brix domain containing 1
2349	Q9H7B2	3	4	10.8	306	35583	10	Brix domain-containing protein 1
2350	P07738	3	3	15.8	259	30005	6.5	Bisphosphoglycerate mutase
2351	UPI0000456EE0	3	6	16.4	220	23901	5.4	Ribulose-phosphate 3-epimerase (EC 5.1.3.1) (Ribulose-5-phosphate-3- epimerase).
2351	Q96AT9-2	3	6	16.4	220	23924	5.6	Isoform 2 of Q96AT9
2351	Q96AT9	3	6	15.8	228	24928	5.6	Ribulose-phosphate 3-epimerase
2352	Q9H6K1	3	3	15.8	298	32872	4.6	Uncharacterized protein C6orf106
2353	Q96IU4	3	9	15.7	210	22346	6.4	Abhydrolase domain-containing protein 14B
2354	O75935-4	3	7	27.9	104	11882	9.8	Isoform 4 of O75935
2354	UPI0000D61856	3	7	27.4	106	12123	10	Dynactin subunit 3 (Dynactin complex subunit 22 kDa subunit) (p22).
2354	O75935-3	3	7	18.4	158	18001	6	Isoform 3 of O75935
2354	Q5T1I6	3	7	18	161	18240	8.3	Dynactin 3
2354	O75935-2	3	7	16.5	176	19468	7	Isoform 2 of O75935
2354	O75935	3	7	15.6	186	21119	5.5	Dynactin subunit 3
2355	P49247	3	3	15.6	237	26091	7.5	Ribose-5-phosphate isomerase
2356	Q00534	3	4	15.6	326	36938	6.5	Cell division protein kinase 6
2357	Q92599-2	3	5	17.5	429	49814	6.1	Isoform 2 of Q92599
2357	UPI000066DA0A	3	5	17.4	430	49916	6.2	Septin-8.
2357	UPI000066DA0B	3	5	17	440	50928	6.2	Septin-8.
2357	UPI000020C588	3	5	17	442	51178	6.2	Septin-8.
2357	UPI000066DA0C	3	5	16.3	460	53163	6.5	Septin-8.
2357	Q92599	3	5	15.5	483	55756	6.3	Septin-8
2357	UPI0000457340	3	5	15.4	487	55908	6.4	Septin-8.
2358	O14561	3	3	15.4	156	17417	4.9	Acyl carrier protein, mitochondrial precursor
2359	P07478	3	25	15.4	247	26488	4.9	Trypsin-2 precursor
2359	Q3SY20	3	25	15.4	247	26472	4.9	Protease, serine, 2
2359	Q3SY19	3	25	15.4	247	26556	4.8	PRSS1 protein
2359	UPI0000D61CF1	3	25	14.6	261	28220	5.4	Trypsin-2 precursor (EC 3.4.21.4) (Trypsin II) (Anionic trypsinogen) (Serine protease 2).
2359	Q7Z5F3	3	25	14.6	261	28137	5.4	Protease serine 2 isoform B
2360	Q6LBS1	3	10	17	218	21993	11.4	SmB /B' autoimmune antigene
2360	Q66K91	3	10	16	231	23656	10.9	Small nuclear ribonucleoprotein polypeptides B and B1
2360	Q5XPV6	3	10	16	231	23657	10.7	Small nuclear ribonucleoprotein polypeptide B
2360	Q6PKB4	3	10	15.8	234	24088	10.8	SNRPB protein
2360	UPI0000D612F2	3	10	15.7	236	26362	9.3	Small nuclear ribonucleoprotein-associated protein N (snRNP-N) (Sm protein N) (Sm-N) (SmN) (Sm-D) (Tissue-specific-splicing protein).
2360	P14678	3	10	15.4	240	24610	11.2	Small nuclear ribonucleoprotein-associated proteins B and B'

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
2360	P63162	3	10	15.4	240	24614	11.2	Small nuclear ribonucleoprotein-associated protein N
2360	UPI0000D6101C	3	10	15.3	242	27236	9.4	Small nuclear ribonucleoprotein-associated proteins B and B' (snRNP-B) (Sm protein B/B') (Sm-B/Sm-B') (SmB/SmB').
2360	Q9UIS4	3	10	15.2	243	27267	9.4	Small nuclear ribonucleoprotein B'
2360	Q15182	3	10	13	285	29671	10.1	SNRPB protein
2360	UPI0000D6101B	3	10	12.9	287	29862	10.2	Small nuclear ribonucleoprotein-associated proteins B and B' (snRNP-B) (Sm protein B/B') (Sm-B/Sm-B') (SmB/SmB').
2360	P14678-3	3	10	12.8	289	30032	10.2	Isoform SM
2361	P43487	3	16	15.4	201	23310	5.3	Ran-specific GTPase-activating protein
2361	UPI00006C1BBA	3	16	10.2	305	35024	8.6	PREDICTED: similar to Ran-specific GTPase-activating protein (Ran-binding protein 1) (RanBP1)
2362	Q5T653	3	7	15.4	305	33301	11.3	39S ribosomal protein L2, mitochondrial precursor
2363	Q6NW29	3	4	15.4	188	21251	5.3	RWD domain-containing protein 4A
2364	Q8TF59	3	5	15.3	445	49260	4.9	KIAA1942 protein
2364	Q8NCK5	3	5	15.2	446	49346	4.9	CDNA FLJ90195 fis, clone MAMMA1001310
2364	Q9BQ67	3	5	15.2	446	49419	4.9	Glutamate-rich WD repeat-containing protein 1
2365	Q86WV7	3	5	15	227	25564	4.9	Hypothetical protein
2365	UPI0000456ABD	3	5	15	227	25757	5	Coiled-coil domain-containing protein 43.
2366	P62341	3	4	14.9	195	22277	8.5	Selenoprotein T precursor
2366	UPI000034ECC3	3	4	14.9	195	22174	8.6	selenoprotein T
2367	Q9NR77	3	7	14.9	195	22253	10.6	Peroxisomal membrane protein 2
2368	Q9NVT9	3	7	14.9	282	31281	5.8	Armadillo repeat-containing protein 1
2369	O95983-2	3	6	16.6	259	29014	5.2	Isoform 2 of O95983
2369	O95983	3	6	14.8	291	32844	5.3	Methyl-CpG-binding domain protein 3
2370	Q52LJ0	3	4	14.8	330	37191	6.3	Protein FAM98B
2370	UPI0000DA182F	3	4	11.3	433	45547	8.7	family with sequence similarity 98, member B isoform 1
2371	Q9H1E3	3	7	14.8	243	27296	5.1	Nuclear ubiquitous casein and cyclin-dependent kinases substrate
2372	Q9NPD8	3	3	14.7	197	22521	8	Ubiquitin-conjugating enzyme E2 T
2373	Q5T1C6	3	4	14.6	240	27130	8.3	Thioesterase superfamily member 4
2373	Q96KR2	3	4	14.6	240	27173	8.4	C-terminal modulator protein
2374	Q9H944	3	5	14.6	212	23222	6.9	TRF-proximal protein homolog
2375	UPI0000074015	3	4	14.8	359	39303	5.2	hsp70-interacting protein
2375	Q9NZL4	3	4	14.6	362	39474	5.2	Hsp70-binding protein 1
2376	O75391	3	3	14.5	227	26034	7.9	Sperm-associated antigen 7
2376	UPI000013C65B	3	3	11.3	292	32693	8.7	Sperm-associated antigen 7.
2377	O94903	3	3	14.5	275	30344	7.5	Proline synthetase co-transcribed bacterial homolog protein
2378	P51159-2	3	6	15	213	24041	5.7	Isoform Short of P51159
2378	P51159	3	6	14.5	221	24868	5.2	Ras-related protein Rab-27A
2378	Q6IAS8	3	6	14.5	221	24898	5.2	RAB27A protein
2379	UPI0000456B12	3	26	16.2	197	22761	11.9	Splicing factor, arginine/serine-rich 2 (Splicing factor SC35) (SC-35) (Splicing component, 35 kDa) (Protein PR264).
2379	Q01130	3	26	14.5	221	25476	11.9	Splicing factor, arginine/serine-rich 2
2379	Q53FN0	3	26	14.5	221	25502	11.9	Splicing factor, arginine/serine-rich 2 variant
2380	Q08623	3	5	14.5	214	23730	5.3	Haloacid dehalogenase-like hydrolase domain-containing protein 1A
2381	Q15024	3	3	14.4	291	31835	5.2	Exosome complex exonuclease RRP42
2381	UPI000020A5E9	3	3	14.4	291	31821	5.2	Exosome complex exonuclease RRP42 (EC 3.1.13.-) (Ribosomal RNA- processing protein 42) (Exosome component 7) (p8).
2382	Q15427	3	5	14.4	424	44386	8.6	Splicing factor 3B subunit 4
2382	Q53FG6	3	5	14.4	424	44387	8.2	Splicing factor 3b, subunit 4 variant
2383	Q16539-3	3	3	17.5	297	34092	8.2	Isoform Mxi2 of Q16539
2383	Q16539-4	3	3	16.9	307	35453	8.7	Isoform Exip of Q16539
2383	Q16539	3	3	14.4	360	41293	5.8	Mitogen-activated protein kinase 14
2383	Q95NE7	3	3	14.4	360	41493	5.9	Mitogen-activated protein kinase 14
2384	Q9H446	3	3	14.4	243	27939	4.2	RWD domain-containing protein 1
2385	P51580	3	3	14.3	245	28180	6.2	Thiopurine S-methyltransferase
2385	Q9BS45	3	3	14.3	245	28233	6.4	Thiopurine S-methyltransferase
2386	Q9H3H0	3	7	14.2	247	28275	9.4	Vacuolar ATP synthase subunit D homolog
2386	Q9Y5K8	3	7	14.2	247	28263	9.4	Vacuolar ATP synthase subunit D
2387	O60888	3	6	15.6	179	19116	5.5	Protein CutA precursor
2387	A2AB26	3	6	14.1	198	20925	5.5	CutA divalent cation tolerance homolog
2388	O95330	3	7	14.1	198	22396	6.4	Hypothetical protein
2388	UPI0000D61079	3	7	11.3	248	28113	5.5	Endoplasmic reticulum-Golgi intermediate compartment protein 3 (Serologically defined breast cancer antigen NY-BR-84).
2388	Q9Y282	3	7	7.3	383	43222	6.1	Endoplasmic reticulum-Golgi intermediate compartment protein 3
2388	UPI0000456F87	3	7	7.2	390	44008	5.9	Endoplasmic reticulum-Golgi intermediate compartment protein 3 (Serologically defined breast cancer antigen NY-BR-84).
2388	Q5JWS3	3	7	7.2	388	43772	6	ERGIC and golgi 3

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2388	Q5JWS0	3	7	7.1	396	44568	6.5	ERGIC and golgi 3
2389	Q5T8T7	3	6	20.9	134	15855	4.9	Surfeit 5
2389	Q5T8T8	3	6	20.4	137	16032	4.8	Surfeit 5
2389	Q15528-2	3	6	20	140	16480	5	Isoform Surf5A of Q15528
2389	Q15528	3	6	14	200	22221	4.7	Surfeit locus protein 5
2390	Q7Z4W1	3	3	13.9	244	25913	8.1	L-xylulose reductase
2391	Q13595	3	5	13.8	282	32689	11.3	Transformer-2 protein homolog
2392	UPI00003675D1	3	4	13.8	240	25498	8.6	Transmembrane protein 65.
2393	Q0VAQ8	3	5	13.7	249	26525	12.2	Chromosome 1 open reading frame 77
2393	Q9Y3Y2	3	5	13.7	248	26397	12.2	Uncharacterized protein C1orf77
2394	P49841	3	3	13.6	420	46744	8.8	Glycogen synthase kinase-3 beta
2394	P49841-2	3	3	13.2	433	48034	8.8	Isoform 2 of P49841
2395	P25325	3	4	13.5	297	33178	6.6	3-mercaptopyruvate sulfurtransferase
2396	P27144	3	6	13.5	223	25268	8.4	Adenylate kinase isoenzyme 4, mitochondrial
2396	UPI00006C1315	3	6	13.5	223	25240	8.4	PREDICTED: similar to Adenylate kinase isoenzyme 4, mitochondrial (Adenylate kinase 3-like 1) (ATP-AMP transphosphorylase)
2396	UPI0000141B7B	3	6	13.5	223	25208	8.4	PREDICTED: similar to Adenylate kinase isoenzyme 4, mitochondrial (Adenylate kinase 3-like 1) (ATP-AMP transphosphorylase)
2396	Q8IUU9	3	6	13.5	223	25252	8.6	Adenylate kinase 3-like 1
2396	Q6NXQ5	3	6	13.5	223	25296	8.7	Adenylate kinase 3-like 1
2397	Q96PJ7	3	4	16.6	211	23758	8.7	Ras-related GTP-binding protein RAB39
2397	UPI0000D622F3	3	4	16.4	213	23958	8.5	Ras-related protein Rab-34 (Rab-39) (Ras-related protein Rah).
2397	Q6NXT3	3	4	13.5	259	29071	7.9	RAB34 protein
2397	UPI000015D94E	3	4	13.5	259	29058	7.9	RAB39
2397	Q9BZG1	3	4	13.5	259	29044	7.9	Ras-related protein Rab-34
2398	Q9BTE7	3	3	13.5	237	27508	5.6	DCN1-like protein 5
2399	Q9H3H3	3	6	13.5	251	27383	5.6	Uncharacterized protein C11orf68
2399	UPI0000228EAB	3	6	13.5	251	27355	5.5	Uncharacterized protein C11orf68 (Basophilic leukemia expressed protein Bles03) (Protein p5326).
2400	Q8N9N7	3	6	13.4	239	26754	8.4	Leucine-rich repeat-containing protein 57
2400	UPI000006FF78	3	6	13.4	239	26740	8.2	leucine rich repeat containing 57
2401	Q96MF7	3	6	13.4	247	27932	7.7	E3 SUMO-protein ligase NSE2
2402	Q8TB70	3	3	16	188	22199	5.8	TXNDC9 protein
2402	O14530	3	3	13.3	226	26534	5.9	Thioredoxin domain-containing protein 9
2402	Q53HG4	3	3	13.3	226	26535	5.7	ATP binding protein associated with cell differentiation variant
2403	Q567U8	3	6	13.3	248	27317	5.5	COPS7A protein
2403	Q9UBW8	3	6	12	275	30277	8.2	COP9 signalosome complex subunit 7a
2404	Q8WUN9	3	3	13.4	246	28051	4.7	MGC40499 protein
2404	Q8N129	3	3	13.3	248	28310	4.6	PRotein Associated with Tlr4
2404	UPI0000DD7E73	3	3	9.8	336	37824	6.3	PREDICTED: similar to PRotein Associated with Tlr4
2405	UPI0000F0A4D4	3	5	16.8	196	21694	6.8	Cob(I)yrinic acid a,c-diamide adenosyltransfe
2405	Q96EY8	3	5	13.2	250	27388	8.6	Cob(I)yrinic acid a,c-diamide adenosyltransferase, mitochondrial precursor (EC 2.5.1.17) (Cob(I)alamin adenosyltransferase)
2406	O95478	3	3	13.1	260	30065	10.3	TGF-beta-inducible nuclear protein 1
2407	P17900	3	7	13	193	20822	5.3	Ganglioside GM2 activator precursor (GM2-AP) (Cerebroside sulfate activator protein) (Shingolipid activator protein 3) (SAP-3) [Contains: Ganglioside GM2 activator isoform short]
2407	UPI00001AEC37	3	7	13	193	20838	5.3	GM2 ganglioside activator precursor
2408	Q15102	3	3	13	231	25734	6.8	Platelet-activating factor acetylhydrolase IB subunit gamma
2409	Q6DRA6	3	18	15.2	164	18018	10.6	Histone H2B type 2-D
2409	Q6DN03	3	18	13	193	21472	10.7	Histone H2B type 2-C
2410	Q9HC03	3	6	13	324	36964	9.3	Dolichyl-phosphate beta-glucosyltransferase
2410	Q9Y673	3	6	13	324	36946	9.3	Dolichyl-phosphate beta-glucosyltransferase
2411	Q9HA64	3	4	12.9	309	34412	7.3	Ketosamine-3-kinase
2412	Q9NZD2	3	5	12.9	209	23850	7.4	Glycolipid transfer protein
2413	UPI0000D61C3C	3	3	13.3	278	30640	8.5	Insulin-like growth factor-binding protein 3 precursor (IGFBP-3) (IBP- 3) (IGF-binding protein 3).
2413	P17936	3	3	12.7	291	31674	8.7	Insulin-like growth factor-binding protein 3 precursor
2413	UPI00004F8E1F	3	3	12.5	297	32223	8.6	insulin-like growth factor binding protein 3 isoform a precursor
2414	Q5HYI8	3	12	12.7	236	26423	7.1	Rab-like protein 3
2414	Q8WUD3	3	12	12.7	236	26308	6.8	RAB, member of RAS oncogene family-like 3
2415	Q8NDC9	3	3	12.7	322	34529	5.7	Hypothetical protein DKFZp547E2313
2415	Q9BV20	3	3	11.1	369	39150	6.3	Hypothetical protein MGC3207
2416	Q9NW68	3	4	12.6	430	47163	4.5	BSD domain-containing protein 1
2416	Q9NW68-2	3	4	12.6	428	46860	4.8	Isoform 2 of Q9NW68
2416	Q9NW68-3	3	4	11.4	474	51167	4.6	Isoform 3 of Q9NW68
2417	O95758	3	4	12.5	521	56502	9.2	Regulator of differentiation 1
2417	Q5T8V9	3	4	12.4	524	56821	9.2	ROD1 regulator of differentiation 1
2417	Q5T4E6	3	4	11.8	552	59690	9	ROD1 regulator of differentiation 1

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2417	O95758-2	3	4	10.6	614	66234	9.5	Isoform 2 of O95758
2418	P49366	3	4	12.5	369	40971	5.4	Deoxyhypusine synthase
2419	Q15555	3	3	12.5	327	37031	5.6	Microtubule-associated protein RP/EB family member 2
2420	Q15773	3	7	12.5	248	28147	6.9	Myeloid leukemia factor 2
2421	Q561W0	3	8	14.3	258	29642	8.7	TXNDC14 protein
2421	Q53G73	3	8	12.5	296	34025	8.7	Thioredoxin-related transmembrane protein 2 variant
2421	Q9Y320	3	8	12.5	296	34038	8.7	CGI-31 protein
2421	Q5J7Q7	3	8	12.5	296	34012	8.7	Proliferation-inducing gene 26 protein
2421	UPI000024706C	3	8	10	371	42472	8.6	Catenin delta-1 (p120 catenin) (p120(ctn)) (Cadherin-associated Src substrate) (CAS) (p120(cas)).
2421	Q9H3L1	3	8	9.9	372	42478	8.7	My009 protein
2421	Q8NBP9	3	8	9.9	372	42543	8.6	Thioredoxin domain-containing protein 14
2422	Q53HT2	3	15	12.5	279	32633	9.6	Elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1 variant
2422	Q9BW60	3	15	12.5	279	32663	9.6	Elongation of very long chain fatty acids protein 1
2422	Q8WXU3	3	15	12.5	279	32637	9.6	SSC1/ELOVL1
2423	Q96NM0	3	3	12.5	279	31716	6.7	Uncharacterized protein C5orf33
2424	Q9H0L4	3	4	12.5	616	64436	7.3	Cleavage stimulation factor 64 kDa subunit, tau variant
2425	Q9H3F6-2	3	3	13.4	290	32779	6.6	Isoform 2 of Q9H3F6
2425	Q9H3F6	3	3	12.5	313	35432	6.3	BTB/POZ domain-containing protein KCTD10
2426	O00422	3	7	12.4	153	17561	9.4	Histone deacetylase complex subunit SAP18
2427	P49770	3	4	12.3	351	38990	6.2	Translation initiation factor eIF-2B subunit beta
2427	Q9BPX4	3	4	12.3	351	39004	6.2	Eukaryotic translation initiation factor 2B, subunit 2 beta, 39kDa
2428	Q6J203	3	6	12.1	199	22558	10.1	HCV F-transactivated protein 1
2429	Q8NBZ7	3	8	12.1	420	47577	8.9	UDP-glucuronic acid decarboxylase 1
2429	UPI0000D6120F	3	8	12	425	48179	8.9	UDP-glucuronic acid decarboxylase 1 (EC 4.1.1.35) (UDP-glucuronate decarboxylase 1) (UGD) (UXS-1).
2429	Q8NBZ7-2	3	8	12	425	48152	8.9	Isoform 2 of Q8NBZ7
2430	Q9NXR1-2	3	5	12.5	335	37721	5.2	Isoform 2 of Q9NXR1
2430	Q9NXR1	3	5	12.1	346	38808	5.3	Nuclear distribution protein nudE homolog 1
2431	Q13547	3	5	12	482	55103	5.5	Histone deacetylase 1
2432	Q9NZJ9	3	4	15.6	180	20306	6.4	Diphosphoinositol polyphosphate phosphohydrolase 2
2432	Q4AEJ6	3	4	12	234	25951	6.8	KIAA0487 protein
2433	Q96CX2	3	3	12	325	35701	5.6	BTB/POZ domain-containing protein KCTD12
2434	P05026-2	3	15	12	301	34893	8.6	Isoform 2 of P05026
2434	P05026	3	15	11.9	303	35061	8.5	Sodium/potassium-transporting ATPase subunit beta-1
2434	Q6LEU2	3	15	11.9	303	35049	8.5	ATP1B1 protein
2434	UPI0000D6203C	3	15	11.8	305	35246	8.5	Sodium/potassium-transporting ATPase subunit beta-1 (Sodium/potassium- dependent ATPase beta-1 subunit).
2435	Q9H2W6	3	4	11.8	279	31705	7	39S ribosomal protein L46, mitochondrial precursor
2436	Q9ULW3	3	3	11.8	272	31079	9.9	Activator of basal transcription 1
2437	O75190	3	8	11.7	326	36087	9.1	DnaJ homolog subfamily B member 6
2437	Q53EN8	3	8	11.7	326	36117	9.1	DnaJ (Hsp40) homolog, subfamily B, member 6 isoform a variant
2438	UPI0000DD7AE9	3	8	14.2	268	31695	8.8	PREDICTED: similar to LIM and senescent cell antigen-like domains 1
2438	P48059	3	8	11.7	325	37251	8	LIM and senescent cell antigen-like-containing domain protein 1
2438	UPI0000207FB5	3	8	9.8	387	44390	8	LIM and senescent cell antigen-like-containing domain protein 1 (Particularly interesting new Cys-His protein 1) (PINCH-1) (Renal carcinoma antigen NY-REN-48).
2439	Q6PQ81	3	6	11.7	350	38340	4.7	Putative tumor suppressor Dkk-3/REIC
2439	UPI00001694CA	3	6	11.7	350	38390	4.7	dickkopf homolog 3 precursor
2439	Q9UBP4	3	6	11.7	350	38291	4.6	Dickkopf-related protein 3 precursor
2440	Q96B24	3	8	11.7	266	30368	5.1	Integral membrane protein 2B
2440	Q9Y287	3	8	11.7	266	30338	5.1	Integral membrane protein 2B (Transmembrane protein BRI) [Contains: ABri/ADan amyloid peptide]
2440	Q9NX12	3	8	11.7	266	30312	5.2	CDNA FLJ20496 fis, clone KAT08729
2441	Q9H5L2	3	5	11.7	418	46982	6.7	CDNA: FLJ23330 fis, clone HEP12654
2441	Q9Y2T2	3	5	11.7	418	46939	6.9	AP-3 complex subunit mu-1
2442	P49753-2	3	3	16.3	301	32997	8.1	Isoform 2 of P49753
2442	A1L172	3	3	11.6	421	46296	7.5	Acyl-CoA thioesterase 1
2442	Q86TX2	3	3	11.6	421	46277	7.3	Acyl-coenzyme A thioesterase 1
2442	UPI0000161F5B	3	3	10.1	483	53266	8.6	peroxisomal long-chain acyl-coA thioesterase
2442	UPI000013CA4E	3	3	10.1	483	53219	8.5	Acyl-coenzyme A thioesterase 2 (EC 3.1.2.2) (Acyl-CoA thioesterase 2) (Peroxisomal acyl-coenzyme A thioester hydrolase 2a) (Peroxisomal long-chain acyl-coA thioesterase 2) (ZAP128) (CTE-Ia).
2442	Q3I5F8	3	3	10.1	483	53227	8.8	Mitochondrial acyl-CoA thioesterase 2
2442	P49753	3	3	10.1	483	53257	8.7	Acyl-coenzyme A thioesterase 2
2443	O95218-2	3	7	12.5	311	35304	8.8	Isoform ZIS
2443	Q59F92	3	7	12.3	316	36032	9.8	Zinc finger protein 265 isoform 1 variant

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2443	Q5VV33	3	7	12.2	320	36318	9.8	Zinc finger, RAN-binding domain containing 2
2443	Q5VV34	3	7	11.8	330	37404	10	Zinc finger, RAN-binding domain containing 2
2443	Q53GS3	3	7	11.8	330	37332	10.1	Zinc finger protein 265 isoform 1 variant
2443	O95218	3	7	11.6	337	38223	8.7	Zinc finger Ran-binding domain-containing protein 2
2443	UPI000013F68D	3	7	11.6	336	38136	8.7	Zinc finger Ran-binding domain-containing protein 2 (Zinc finger protein 265) (Zinc finger, splicing).
2444	Q4G0F5	3	4	11.6	336	39155	7.3	Vacuolar protein sorting-associated protein 26B
2445	Q99496	3	4	11.6	336	37655	6.8	E3 ubiquitin-protein ligase RING2
2446	Q15287-2	3	7	12.4	282	31709	11.9	Isoform 2 of Q15287
2446	Q15287	3	7	11.5	305	34208	11.8	RNA-binding protein with serine-rich domain 1
2447	Q9NT62-2	3	5	11.6	311	35467	4.8	Isoform 2 of Q9NT62
2447	Q9NT62	3	5	11.5	314	35864	4.7	Autophagy-related protein 3
2448	Q6NXE6	3	3	11.4	501	54142	6.2	Armadillo repeat-containing protein 6
2449	Q6ZMK1	3	3	11.4	289	33274	7.7	Cysteine/histidine-rich protein 1
2450	O95297	3	3	11.2	269	29082	8.7	Myelin protein zero-like protein 1 precursor
2450	Q5U0H8	3	3	11.2	269	29096	8.7	Myelin protein zero-like 1
2450	O95297-2	3	3	11.2	268	28981	8.7	Isoform 2 of O95297
2451	Q5T446	3	6	21.2	193	21459	5.2	Uroporphyrinogen decarboxylase
2451	UPI0000D61F00	3	6	20	205	22886	5.4	Uroporphyrinogen decarboxylase (EC 4.1.1.37) (URO-D) (UPD).
2451	P06132	3	6	11.2	367	40787	6.1	Uroporphyrinogen decarboxylase
2451	Q53ZP6	3	6	11.2	367	40803	6.1	Uroporphyrinogen decarboxylase
2451	Q53YB8	3	6	11.2	367	40829	6.1	Uroporphyrinogen decarboxylase
2452	A0FIK6	3	3	11.1	324	36673	9.6	HRB2 variant B
2452	Q13601	3	3	9.4	381	43665	9.8	KRR1 small subunit processome component homolog
2453	UPI00002109D3	3	7	14.6	288	34729	5.8	farnesyltransferase, CAAX box, alpha isoform b
2453	UPI0000520A1B	3	7	13.5	312	36493	5.2	farnesyltransferase, CAAX box, alpha isoform c
2453	P49354	3	7	11.1	379	44409	5.1	Protein farnesyltransferase/geranylgeranyltransferase type I alpha subunit
2454	O43813	3	5	11	399	45283	7.8	LanC-like protein 1
2454	Q6FHH6	3	5	11	399	45267	7.8	LANCL1 protein
2455	P49406	3	9	11	292	33535	9.5	39S ribosomal protein L19, mitochondrial precursor
2456	P55039	3	3	11	364	40746	8.9	Developmentally-regulated GTP-binding protein 2
2456	Q53Y50	3	3	11	364	40777	8.9	Developmentally regulated GTP binding protein 2
2457	Q9NPD3	3	12	11	245	26383	6.5	Exosome complex exonuclease RRP41
2457	UPI0000D6251B	3	12	10.9	247	26610	6.7	Exosome complex exonuclease RRP41 (EC 3.1.13.-) (Ribosomal RNA- processing protein 41) (Exosome component 4) (p12A).
2458	Q9Y3B9	3	3	11	282	31484	5.5	RRP15-like protein
2459	Q8TDX7	3	5	10.9	302	34551	8.3	Serine/threonine-protein kinase Nek7
2460	P80217	3	3	10.8	286	31514	6.1	Interferon-induced 35 kDa protein
2460	UPI0000200E4E	3	3	10.8	288	31777	6.1	Interferon-induced 35 kDa protein (IFP 35).
2460	P80217-2	3	3	10.8	288	31745	6.1	Isoform 2 of P80217
2461	Q06547-4	3	4	11.2	348	36950	4.9	Isoform 4 of Q06547
2461	Q06547-3	3	4	10.8	360	38111	4.9	Isoform 3 of Q06547
2462	Q8IVM0	3	6	10.8	306	35822	6.7	Coiled-coil domain-containing protein 50
2462	Q8IVM0-2	3	6	6.8	482	56340	8.2	Isoform 2 of Q8IVM0
2463	Q96SD6	3	4	10.7	393	44071	4.8	Putative TCPTP-interacting protein
2463	Q9NVQ6	3	4	8.9	470	52118	5.1	CDNA FLJ10579 fis, clone NT2RP2003446
2463	Q96TC7	3	4	8.9	470	52070	5.1	Protein FAM82C
2464	UPI00004EC068	3	3	16.2	198	22945	5.9	cyclin C isoform b
2464	Q7Z4L3	3	3	11.3	283	33243	7.3	Cyclin C
2464	P24863	3	3	10.6	303	35559	8.2	Cyclin-C
2464	UPI000045747B	3	3	10.6	302	35416	8.1	Cyclin-C.
2465	Q6NUK4	3	3	10.6	255	29264	9.6	Receptor expression-enhancing protein 3
2466	Q8N954-2	3	5	17.9	156	18587	5	Isoform 2 of Q8N954
2466	Q8N954	3	5	10.6	263	30685	5.3	Coiled-coil domain-containing protein 75
2466	UPI0000160624	3	5	9.8	285	33277	5.9	coiled-coil domain containing 75
2467	Q9BR61	3	3	10.6	282	31151	5.1	Acyl-CoA-binding domain-containing protein 6
2468	UPI00005199BA	3	7	10.8	342	37980	5.7	paraoxonase 2 isoform 2
2468	Q5FBX7	3	7	10.8	342	38022	5.7	Paraoxonase nirs variant 1
2468	A4D1H7	3	7	10.5	354	39381	5.6	Paraoxonase 2
2468	UPI00004575B2	3	7	10.5	352	38946	5.5	Serum paraoxonase/arylesterase 2 (EC 3.1.1.2) (EC 3.1.8.1) (PON 2) (Serum aryldialkylphosphatase 2) (A-esterase 2) (Aromatic esterase 2).
2468	Q15165-2	3	7	10.5	354	39397	5.6	Isoform 2 of Q15165
2468	Q15165	3	7	10.5	354	39398	5.5	Serum paraoxonase/arylesterase 2
2469	UPI0000F24437	3	5	11.7	350	38802	6.1	2-OXOISOVALERATE DEHYDROGENASE BETA SUBUNIT
2469	P21953	3	5	10.5	392	43123	6.3	2-oxoisovalerate dehydrogenase subunit beta, mitochondrial precursor
2470	Q14232	3	3	10.5	305	33712	7.3	Translation initiation factor eIF-2B subunit alpha
2470	UPI00004566B0	3	3	10.5	305	33648	6.9	Translation initiation factor eIF-2B subunit alpha (eIF-2B GDP-GTP exchange factor subunit alpha).
2471	Q8NBL1	3	4	10.5	392	46189	8.7	KTEL motif-containing protein 1 precursor
2471	UPI0000073BBD	3	4	10.5	392	46221	8.7	chromosome 3 open reading frame 9

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
2472	Q96EQ0	3	4	10.5	304	33429	4.9	Small glutamine-rich tetratricopeptide repeat-containing protein B
2473	Q86WV4	3	4	13.6	302	35148	9.1	MRPS9 protein
2473	P82933	3	4	10.4	396	45823	9.6	28S ribosomal protein S9, mitochondrial precursor
2473	Q6PG40	3	4	10.4	396	45835	9.5	Mitochondrial ribosomal protein S9
2474	O43660-2	3	5	10.5	505	56290	9.2	Isoform 2 of O43660
2474	O43660	3	5	10.3	514	57194	9.2	Pleiotropic regulator 1
2475	O95400	3	3	10.3	341	37646	4.6	CD2 antigen cytoplasmic tail-binding protein 2
2476	Q8IZV5	3	4	10.3	341	38087	7.4	Retinol dehydrogenase 10
2477	O75569-2	3	6	10.6	302	33123	8.4	Isoform 2 of O75569
2477	O75569	3	6	10.2	313	34404	8.4	Interferon-inducible double stranded RNA-dependent protein kinase activator A
2478	P35813	3	3	10.2	382	42448	5.4	Protein phosphatase 2C isoform alpha
2479	P50452	3	3	10.2	374	42786	5.6	Serpin B8
2479	UPI000013C5F2	3	3	10.2	374	42767	5.6	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 8 isoform a
2479	Q7Z2V6	3	3	10.2	374	42737	5.6	Hypothetical protein DKFZp686O02190
2480	Q96JY6	3	6	10.2	352	37459	8.7	PDZ and LIM domain protein 2
2481	Q05DL3	3	3	14.7	232	26702	9.7	Hypothetical protein
2481	Q6PJ06	3	3	13	261	29825	9.8	CSNK1A1 protein
2481	P67827	3	3	10.5	325	37567	9.5	Casein kinase I isoform alpha
2481	P48729	3	3	10.1	337	38915	9.6	Casein kinase I isoform alpha
2481	Q5U046	3	3	10.1	337	38905	9.6	Casein kinase 1, alpha 1
2481	P67962	3	3	10.1	337	38901	9.6	Casein kinase I isoform alpha
2481	UPI000053FD0F	3	3	9.3	365	41937	9.6	casein kinase 1, alpha 1 isoform 1
2481	Q4JJA0	3	3	9.3	365	41938	9.5	Casein kinase 1 alpha 1
2482	Q14344	3	11	10.1	377	44050	8	Guanine nucleotide-binding protein alpha-13 subunit
2483	UPI00001C156B	3	6	12.6	254	28263	8.6	peroxisomal acyl-CoA thioesterase 1 isoform c
2483	O14734	3	6	10	319	35914	7.6	Acyl-coenzyme A thioesterase 8
2483	Q6FHI2	3	6	10	319	35957	7.8	PTE1 protein
2484	UPI000045619C	3	8	11.9	370	38212	4.6	Syndecan-3 (SYND3).
2484	O75056-2	3	8	11.9	370	38246	4.6	Isoform 3 of O75056
2484	O75056-1	3	8	11.5	384	39636	4.6	Isoform 2 of O75056
2484	O75056	3	8	10	442	45497	4.7	Syndecan-3
2484	UPI000006FA8A	3	8	10	442	45496	4.7	syndecan 3
2484	UPI0000DD798E	3	8	9.4	467	49600	4.9	PREDICTED: similar to syndecan 3 isoform 2
2485	Q14320	3	6	10	339	40242	6.8	Protein FAM50A
2486	Q6I9T0	3	4	10	280	31236	6	FHL3 protein
2486	Q9P100	3	4	10	280	31282	6.2	LIM-only protein FHL3
2486	Q9BVA2	3	4	10	280	31192	6.2	Four and a half LIM domains 3
2487	O60547	3	4	9.9	372	41950	7.3	GDP-mannose 4,6 dehydratase
2488	Q6I9R1	3	4	10.7	373	40539	8.5	MSSP-1
2488	P29558-3	3	4	10.7	373	40516	8.4	Isoform 3 of P29558
2488	UPI00001606B9	3	4	10.3	389	42348	8.8	RNA binding motif, single stranded interacting protein 1 isoform b
2488	Q14869	3	4	10.3	389	42335	8.7	MSSP-2 protein
2488	P29558	3	4	9.9	406	44505	8.8	RNA-binding motif, single-stranded-interacting protein 1
2488	P29558-2	3	4	9.9	403	44137	8.7	Isoform 2 of P29558
2489	UPI00001E058D	3	3	12.7	363	40729	5.6	ubiquitin-activating enzyme E1C isoform 3
2489	UPI000015F415	3	3	10.2	449	50072	5.3	ubiquitin-activating enzyme E1C isoform 2
2489	Q8TBC4	3	3	9.9	463	51852	5.5	NEDD8-activating enzyme E1 catalytic subunit
2489	UPI0000EFE338	3	3	5.7	805	89241	5.5	Maltose binding protein/NEDD8-activating enzy
2490	Q53RY7	3	4	9.8	522	57458	9.4	Hypothetical protein EIF2B4
2490	Q9UI10	3	4	9.8	523	57557	9.4	Translation initiation factor eIF-2B subunit delta
2490	UPI000016A377	3	4	9.4	543	59630	9.4	eukaryotic translation initiation factor 2B, subunit 4 delta isoform 1
2490	Q9UI10-2	3	4	9.4	544	59715	9.4	Isoform 2 of Q9UI10
2491	Q5VT94	3	17	9.8	325	35282	10.1	Growth hormone inducible transmembrane protein
2491	UPI0000D60F83	3	17	9.8	325	35169	10.1	Growth hormone-inducible transmembrane protein (Dermal papilla-derived protein 2) (Transmembrane BAX inhibitor motif-containing protein 5).
2491	Q9H3K2	3	17	9.3	345	37205	9.9	Growth hormone-inducible transmembrane protein
2491	Q6FIA7	3	17	9.3	345	37279	10	GHITM protein
2492	Q6PIU2	3	6	9.8	408	45808	7.2	Arylacetamide deacetylase-like 1
2492	UPI0000050344	3	6	9.1	440	49063	7.9	arylacetamide deacetylase-like 1
2493	Q9NPL8	3	4	9.8	285	32178	8.5	Uncharacterized protein C3orf1
2494	Q9Y5A9-2	3	6	10.8	529	56877	8.9	Isoform 2 of Q9Y5A9
2494	UPI0000456197	3	6	10	569	61192	9.1	YTH domain family protein 2 (High-glucose-regulated protein 8) (CLL- associated antigen KW-14) (Renal carcinoma antigen NY-REN-2).
2494	Q9Y5A9	3	6	9.8	579	62334	8.8	YTH domain family protein 2
2495	P46937	3	3	9.7	454	48755	5.1	65 kDa Yes-associated protein
2495	Q7Z574	3	3	9	488	52748	5.1	Yes-associated protein 2
2495	Q8IUY9	3	3	8.7	504	54462	5.2	YAP1 protein
2496	Q96DZ1	3	3	9.7	483	54858	6.3	XTP3-transactivated gene B protein precursor
2496	UPI0000D6119E	3	3	9.7	485	55058	6.4	XTP3-transactivated gene B protein precursor.
2497	Q96J01	3	3	9.7	351	38772	6.1	THO complex subunit 3
2497	UPI000013E86B	3	3	9.7	350	38659	6.1	UPI000013E86B UniRef100 entry

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
2498	A2AB02	3	4	9.6	261	29460	8.6	Nurim
2498	Q8IXM6	3	4	9.5	262	29379	8.6	Nurim
2499	Q86XZ2	3	3	10.3	435	50738	6.7	PPP2R5E protein
2499	Q58EX4	3	3	10.2	441	51523	7.4	PPP2R5E protein
2499	Q16537	3	3	9.6	467	54699	6.9	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit epsilon isoform
2499	Q562F2	3	3	9.6	467	54681	6.9	Protein phosphatase 2, regulatory subunit B', epsilon isoform
2499	Q3ZCW9	3	3	9.6	467	54704	7.2	PPP2R5E protein
2499	Q59EK0	3	3	9	501	57956	8.2	Epsilon isoform of regulatory subunit B56, protein phosphatase 2A variant
2500	Q8WWH5	3	3	9.5	349	37253	8.3	Probable tRNA pseudouridine synthase 1
2501	Q96ER3	3	4	9.5	475	53655	4.5	Protein SAAL1
2501	UPI00001F9E3B	3	4	9.5	474	53558	4.5	serum amyloid A-like 1
2502	Q9BRX2	3	4	9.4	385	43377	6.3	Protein pelota homolog
2502	UPI000013D9FE	3	4	9.4	385	43359	6.3	pelota homolog
2503	Q15050	3	5	9.3	365	41193	10.7	Ribosome biogenesis regulatory protein homolog
2504	Q9Y4A4	3	3	9.4	381	41787	5.8	F22162_1
2504	Q8NFZ8	3	3	9.3	388	42785	6.3	Immunoglobulin superfamily member 4C
2505	Q16254	3	5	9.2	413	43960	4.7	Transcription factor E2F4
2505	UPI0000D61A05	3	5	9.1	417	44403	4.8	Transcription factor E2F4 (E2F-4).
2506	Q8TD55	3	3	9.2	490	53350	5.4	Pleckstrin homology domain-containing family Q member 1
2507	Q96S82	3	4	9.2	380	40510	5.1	Ubiquitin-like protein 7
2508	Q9NZD8	3	3	9.1	308	34960	6.3	Maspardin
2509	UPI00001F9B06	3	3	11.3	265	27935	7.1	Protein TSSC4 (Tumor-suppressing subchromosomal transferable fragment candidate gene 4 protein) (Tumor-suppressing STF cDNA 4 protein).
2509	Q9Y5U2-2	3	3	11.3	265	27895	7.1	Isoform 2 of Q9Y5U2
2509	Q9Y5U2	3	3	9.1	329	34285	5.1	Protein TSSC4
2509	UPI0000161FA5	3	3	9.1	329	34326	5.2	tumor suppressing subtransferable candidate 4
2510	UPI000013ED31	3	6	9.7	360	39834	6.6	GDP-mannose pyrophosphorylase B isoform 2
2510	Q9Y5P6	3	6	9.7	360	39862	6.8	GDP-mannose pyrophosphorylase B
2510	Q9H7U3	3	6	9	387	42650	6.4	CDNA FLJ14257 fis, clone PLACE1000547, highly similar to Homo sapiens GDP-mannose pyrophosphorylase B (GMPPB) mRNA
2510	UPI000013ED26	3	6	9	387	42622	6.3	GDP-mannose pyrophosphorylase B isoform 2
2511	P42785	3	3	8.9	496	55800	7.2	Lysosomal Pro-X carboxypeptidase precursor
2511	UPI00001FB052	3	3	8.5	517	58100	7.4	prolylcarboxypeptidase isoform 2 preproprotein
2512	UPI0000D612A0	3	6	13	231	25489	6	cAMP response element-binding protein (CREB).
2512	Q6V963	3	6	13	230	25445	5.5	CREB
2512	Q53X93	3	6	9.2	327	35136	5.3	CREB1 protein
2512	P16220	3	6	8.8	341	36688	5.6	cAMP response element-binding protein
2513	P22694-4	3	3	9.2	338	39379	8.8	Isoform 4 of P22694
2513	P22694-3	3	3	9.1	339	39477	8.8	Isoform 3 of P22694
2513	P22694	3	3	8.8	351	40623	8.8	cAMP-dependent protein kinase, beta-catalytic subunit
2513	P22694-5	3	3	8.8	354	40947	8.7	Isoform 5 of P22694
2513	P22694-7	3	3	8.7	355	41046	8.7	Isoform 7 of P22694
2513	P22694-6	3	3	8.7	357	41296	8.6	Isoform 6 of P22694
2513	Q14VH1	3	3	7.8	398	46236	8.7	Protein kinase, cAMP-dependent, catalytic, beta
2514	P08621-2	3	10	8.9	428	50618	9.9	Isoform 2 of P08621
2514	P08621	3	10	8.7	437	51557	9.9	U1 small nuclear ribonucleoprotein 70 kDa
2515	Q53FA7	3	5	8.7	332	35536	7.2	Putative quinone oxidoreductase
2516	Q969G3-2	3	6	9.6	363	41780	6	Isoform 2 of Q969G3
2516	Q969G3	3	6	8.5	411	46649	4.9	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1
2517	Q9Y5B8	3	3	8.5	376	42492	6.5	Nucleoside diphosphate kinase 7
2518	Q2NLD4	3	5	9.5	285	32015	7	PURA protein
2518	Q2NLC9	3	5	9	300	34166	9.2	PURA protein
2518	Q00577	3	5	8.4	322	34911	6.4	Transcriptional activator protein Pur-alpha
2518	Q56A79	3	5	8.4	322	34939	6.7	Purine-rich element binding protein A
2519	Q08752	3	5	8.4	370	40764	7.2	40 kDa peptidyl-prolyl cis-trans isomerase
2519	Q6FGM6	3	5	8.4	370	40773	7.2	PPID protein
2520	Q9NR50	3	4	8.4	452	50240	6.5	Translation initiation factor eIF-2B subunit gamma
2521	Q96JB5	3	5	8.3	506	56921	4.8	CDK5 regulatory subunit-associated protein 3
2521	UPI000021D212	3	5	8.3	507	56947	4.8	CDK5 regulatory subunit-associated protein 3 (CDK5 activator-binding protein C53) (HSF-27 protein).
2522	Q9NXW2	3	4	8.3	375	41860	8.7	DnaJ homolog subfamily B member 12
2523	P49419	3	4	8.2	511	55366	6.9	Alpha-aminoadipic semialdehyde dehydrogenase
2523	UPI0000DD7CFB	3	4	7.7	549	59228	8	PREDICTED: similar to antiquitin
2524	Q53EY9	3	3	8.2	403	44478	7	F-box only protein 22 isoform a variant
2524	Q8NEZ5	3	3	8.2	403	44508	7	F-box only protein 22
2525	Q5JRG1	3	6	8.2	463	49095	7.8	Nucleoporin like 1
2525	Q5JRG2	3	6	7.8	485	50210	8.7	Nucleoporin like 1
2525	UPI00004A074B	3	6	7.4	516	53913	7.8	nucleoporin like 1 isoform c
2525	UPI00004A074A	3	6	6.5	587	59754	9.3	nucleoporin like 1 isoform b

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
2525	Q9BVL2	3	6	6.3	599	60897	9.3	Nucleoporin p58/p45
2526	Q96FZ2	3	3	8.2	354	40575	8.1	UPF0361 protein DC12
2526	UPI0000D61B75	3	3	7.8	371	42244	8.9	UPF0361 protein DC12.
2527	Q05BU6	3	5	15.9	246	24847	6.3	Hypothetical protein
2527	Q6PJY9	3	5	15.8	247	24976	6.8	SFRS11 protein
2527	Q6PKC9	3	5	12.1	321	34277	11.5	SFRS11 protein
2527	Q5T760	3	5	10	389	42316	11.7	Splicing factor, arginine/serine-rich 11
2527	Q6PJB9	3	5	9.9	394	42957	11.7	SFRS11 protein
2527	Q05519	3	5	8.1	484	53542	10.5	Splicing factor arginine/serine-rich 11
2527	Q8IWE6	3	5	8.1	483	53414	10.5	Splicing factor, arginine/serine-rich 11
2528	Q8IX04-4	3	3	11.1	341	37611	6.2	Isoform 4 of Q8IX04
2528	Q8IX04-3	3	3	10.6	357	39778	6.4	Isoform 3 of Q8IX04
2528	Q8IX04-2	3	3	10	379	42292	6.5	Isoform 2 of Q8IX04
2528	Q8IX04	3	3	8.1	471	52264	7.1	Ubiquitin-conjugating enzyme E2 variant 3
2529	Q96P63	3	3	8.4	405	46276	5.5	Serpin B12
2529	Q3SYB4	3	3	8	425	48446	5.4	SERPINB12 protein
2530	Q9Y606	3	4	8	427	47470	8.4	tRNA pseudouridine synthase A
2531	UPI0000519472	3	3	9.4	445	50625	5.3	amyloid beta precursor protein-binding protein 1 isoform c
2531	UPI0000519471	3	3	8	528	59420	5.2	amyloid beta precursor protein-binding protein 1 isoform b
2531	Q13564	3	3	7.9	534	60246	5.4	NEDD8-activating enzyme E1 regulatory subunit
2531	UPI0000EFE337	3	3	7.8	536	60391	5.4	NEDD8-activating enzyme E1 regulatory subunit
2532	Q6P1J9	3	4	7.9	531	60577	9.6	Parafibromin
2532	UPI0000D62067	3	4	7.9	531	60577	9.7	Parafibromin (Cell division cycle protein 73 homolog) (Hyperparathyroidism 2 protein).
2533	O60861-2	3	4	9.5	336	39206	6.7	Isoform 2 of O60861
2533	O60861	3	4	7.8	412	47266	7.6	Growth-arrest-specific protein 7
2533	Q59GS9	3	4	7.7	415	47577	7.8	Growth arrest-specific 7 isoform b variant
2534	Q96F86	3	3	7.7	508	56078	7.1	Enhancer of mRNA-decapping protein 3
2535	A2A302	3	3	7.6	646	73140	7.2	Rho guanine nucleotide exchange factor (GEF) 7
2535	Q5W9H0	3	3	7.2	680	77070	6.8	KIAA0142 splice variant 2
2535	Q5T2V0	3	3	7	705	79832	6.7	Rho guanine nucleotide exchange factor (GEF) 7
2536	O94919	3	6	7.6	500	55017	5.7	Endonuclease domain-containing 1 protein precursor
2537	P56182	3	3	7.6	461	52839	9.3	RRP1-like protein
2537	UPI000013E05F	3	3	7.6	461	52942	9.4	NNP-1 protein (Novel nuclear protein 1) (Nucleolar protein Nop52) (D21S2056E).
2537	Q53FR7	3	3	7.6	461	52853	9.4	Nucleolar protein NOP52 variant
2537	Q6PJJ2	3	3	7.5	466	53413	9.5	D21S2056E protein
2538	Q06265	3	4	7.6	423	46978	5.2	Exosome complex exonuclease RRP45
2538	Q86Y48	3	4	7.3	439	48949	5.3	Polymyositis/scleroderma autoantigen 1
2538	Q86Y41	3	4	7	456	50803	5.3	Polymyositis/scleroderma autoantigen 1
2539	Q53GS9	3	8	7.6	565	65381	8.9	U4/U6.U5 tri-snRNP-associated protein 2
2540	Q86T14	3	4	9.7	320	34597	7.7	Full-length cDNA clone CS0DH001YP08 of T cells (Jurkat cell line) of Homo sapiens
2540	UPI00003669A7	3	4	8.9	347	38088	8.6	guanosine monophosphate reductase 2 (GMPR2), transcript variant 2, mRNA
2540	Q9P2T1	3	4	8.9	348	37874	7.2	GMP reductase 2
2540	Q7Z527	3	4	8.9	350	38517	8.8	GMP dehydrogenase
2540	Q6PKC0	3	4	7.6	409	45008	8.3	GMPR2 protein
2541	Q9BUL2	3	3	8.1	482	53004	8.5	PNKP protein
2541	Q96T60	3	3	7.5	521	57076	8.5	Bifunctional polynucleotide phosphatase/kinase (Polynucleotide kinase- 3'-phosphatase) (DNA 5'-kinase/3'-phosphatase) [Includes: Polynucleotide 3'-phosphatase (EC 3.1.3.32) (2'(3')-polynucleotidase); Polynucleotide 5'-hydroxyl-kinase (EC 2.7.1.78)]
2542	Q9Y5X2	3	6	7.5	465	52569	7.4	Sorting nexin-8
2543	P80404	3	6	7.4	500	56439	8	4-aminobutyrate aminotransferase, mitochondrial precursor (EC 2.6.1.19) ((S)-3-amino-2-methylpropionate transaminase)
2544	Q16610	3	7	7.4	540	60674	6.7	Extracellular matrix protein 1 precursor
2544	UPI0000043C2E	3	7	7.4	540	60704	6.7	extracellular matrix protein 1 isoform 1 precursor
2544	Q8IZ60	3	7	7.4	540	60734	6.7	Extracellular matrix protein 1
2544	Q5T5G4	3	7	7.1	567	63563	6.9	Extracellular matrix protein 1
2545	UPI000045753E	3	5	9.2	520	57444	5.7	KIAA0241 (KIAA0241), mRNA
2545	Q8NBF6-2	3	5	8.1	591	65313	6	Isoform 2 of Q8NBF6
2545	Q8NBF6	3	5	7.4	648	71947	6.2	Protein KIAA0241
2546	UPI000014077B	3	4	7.7	414	47829	8.5	tRNA-nucleotidyltransferase 1, mitochondrial precursor (EC 2.7.7.25) (Mitochondrial tRNA nucleotidyl transferase, CCA-adding) (mt tRNA adenylyltransferase) (mt tRNA CCA-pyrophosphorylase) (mt tRNA CCA-diphosphorylase) (mt CCA-adding enzyme).
2546	Q96Q11-2	3	4	7.7	414	47845	8.5	Isoform 2 of Q96Q11
2546	Q96Q11	3	4	7.4	434	50144	8.1	tRNA-nucleotidyltransferase 1, mitochondrial precursor

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2546	UPI000013CD08	3	4	7.4	434	50128	8.1	tRNA-nucleotidyltransferase 1, mitochondrial precursor (EC 2.7.7.25) (Mitochondrial tRNA nucleotidyl transferase, CCA-adding) (mt tRNA adenylyltransferase) (mt tRNA CCA-pyrophosphorylase) (mt tRNA CCA-diphosphorylase) (mt CCA-adding enzyme).
2547	Q2TU87	3	6	10.8	287	32821	6	Growth-inhibiting protein 25
2547	P01011	3	6	7.3	423	47651	5.5	Alpha-1-antichymotrypsin precursor (ACT) [Contains: Alpha-1- antichymotrypsin His-Pro-less]
2548	Q1RMZ4	3	5	7.3	453	49673	6.3	LOC148756 protein
2548	Q6ZV30	3	5	5.4	606	66524	6.9	CDNA FLJ43068 fis, clone BRTHA3008778, moderately similar to Acetyl- coenzyme A synthetase
2548	Q9NUB1-2	3	5	4.8	687	74626	7.2	Isoform 2 of Q9NUB1
2548	Q9NUB1	3	5	4.8	689	74857	7.1	Acetyl-coenzyme A synthetase 2-like, mitochondrial precursor
2548	Q7Z5G3	3	5	4.8	687	74659	7.2	Acyl-CoA synthetase short-chain family member 1
2549	Q8NBF2	3	4	7.3	726	79444	5.6	NHL repeat-containing protein 2
2550	UPI0000D62147	3	4	8.9	337	37122	7	Apolipoprotein-L2 (Apolipoprotein L-II) (ApoL-II).
2550	Q9BQE5	3	4	8.9	337	37092	6.7	Apolipoprotein-L2
2550	Q59GW9	3	4	7.2	415	45687	8.6	Apolipoprotein L2 variant
2551	Q96D46	3	4	7.2	503	57603	7.1	Protein NMD3 homolog
2551	Q9Y2Z6	3	4	7.2	503	57585	7.1	CGI-07 protein
2552	Q13895	3	3	7.1	437	49601	8.1	Bystin
2553	UPI00000372F2	3	4	9.1	514	58604	6.2	WD repeat domain 26
2553	Q9H7D7-2	3	4	7.3	645	70460	6.2	Isoform 2 of Q9H7D7
2553	Q9H7D7	3	4	7.1	661	72124	6.2	WD repeat protein 26
2554	Q9UHY1	3	6	7.1	535	59845	5.1	Nuclear receptor-binding protein
2555	P35243	3	4	7	200	23130	5.2	Recoverin
2556	O00499-9	3	4	10	409	45563	5.5	Isoform BIN1
2556	O00499-10	3	4	9.7	424	47491	6.6	Isoform BIN1
2556	O00499-7	3	4	9.3	439	48258	5.2	Isoform II3 of O00499
2556	O00499-8	3	4	9	454	50185	5.9	Isoform BIN1 of O00499
2556	O00499-4	3	4	8.6	475	51737	5	Isoform IIC2 of O00499
2556	O00499-6	3	4	8.5	482	53020	5.3	Isoform II2 of O00499
2556	Q8WWH9	3	4	8.4	490	53167	5.1	Amphiphysin IIb-1
2556	O00499-11	3	4	8.2	497	54948	6	Isoform BIN1+12A of O00499
2556	O00499-3	3	4	8.1	506	55175	5.2	Isoform IIC1 of O00499
2556	O00499-2	3	4	7.9	518	56499	5.1	Isoform IIB of O00499
2556	O00499-5	3	4	7.5	550	59937	5	Isoform IID of O00499
2556	O00499	3	4	6.9	593	64699	5.1	Myc box-dependent-interacting protein 1
2557	P35610	3	4	6.9	550	64735	8.9	Sterol O-acyltransferase 1
2557	UPI0000D62050	3	4	6.9	552	64907	8.9	Sterol O-acyltransferase 1 (EC 2.3.1.26) (Cholesterol acyltransferase 1) (Acyl coenzyme A:cholesterol acyltransferase 1) (ACAT-1).
2558	Q969S3	3	3	6.9	477	54272	6.2	Zinc finger protein 622
2559	P48723	3	6	6.8	471	51928	5.8	Stress 70 protein chaperone microsome-associated 60 kDa protein precursor
2559	Q53FK2	3	6	6.8	471	51867	5.8	Stress 70 protein chaperone, microsome-associated, 60kDa variant
2560	Q5R363	3	3	6.8	547	62033	5.7	SFRS protein kinase 1
2560	UPI000015FF90	3	3	5.7	654	74226	6.2	Serine/threonine-protein kinase SRPK1 (EC 2.7.11.1) (Serine/arginine- rich protein-specific kinase 1) (SR-protein-specific kinase 1) (SFRS protein kinase 1).
2560	UPI000020DBDD	3	3	5.6	655	74325	6.2	SFRS protein kinase 1
2560	Q96SB4-2	3	3	5.6	655	74320	6.2	Isoform 2 of Q96SB4
2560	UPI0000D61435	3	3	4.5	825	92447	7.9	Serine/threonine-protein kinase SRPK1 (EC 2.7.11.1) (Serine/arginine- rich protein-specific kinase 1) (SR-protein-specific kinase 1) (SFRS protein kinase 1).
2560	Q96SB4	3	3	4.5	826	92407	7.7	Serine/threonine-protein kinase SRPK1
2561	Q5TFE4	3	4	6.8	455	51845	6.3	5'-nucleotidase domain-containing protein 1
2562	Q92685	3	7	6.8	438	50126	9.4	Dolichyl-P-Man:Man(5)GlcNAc(2)-PP-dolichyl mannosyltransferase (EC 2.4.1.-) (Dol-P-Man-dependent alpha(1-3)-mannosyltransferase)
2563	Q9Y6W5	3	7	6.8	498	54284	5.5	Wiskott-Aldrich syndrome protein family member 2
2564	UPI000053FD0C	3	3	7.1	438	48733	6.1	argininosuccinate lyase isoform 3
2564	UPI0000D61C56	3	3	7	442	49095	6.2	Argininosuccinate lyase (EC 4.3.2.1) (Arginosuccinase) (ASAL).
2564	P04424	3	3	6.7	464	51658	6.5	Argininosuccinate lyase
2565	Q13131	3	5	6.7	550	62808	7.6	5'-AMP-activated protein kinase catalytic subunit alpha-1
2565	UPI000020C9F6	3	5	6.6	559	64009	8.1	protein kinase, AMP-activated, alpha 1 catalytic subunit isoform 1
2565	UPI00002263A3	3	5	6.5	565	64322	7.7	5'-AMP-activated protein kinase catalytic subunit alpha-1 (EC 2.7.11.1) (AMPK alpha-1 chain).
2565	UPI00003529FB	3	5	6.4	574	65523	8.2	protein kinase, AMP-activated, alpha 1 catalytic subunit isoform 2

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2565	Q86VS1	3	5	6.4	574	65505	8.2	Protein kinase, AMP-activated, alpha 1 catalytic subunit
2566	Q13188	3	5	6.7	491	56301	5.2	Serine/threonine-protein kinase 3
2566	UPI00004576D2	3	5	6.7	491	56234	5.2	Serine/threonine-protein kinase 3 (EC 2.7.11.1) (STE20-like kinase MST2) (MST-2) (Mammalian STE20-like protein kinase 2) (Serine/threonine-protein kinase Krs-1).
2567	Q9H1B7	3	6	6.7	796	82659	8.2	RING finger protein C14orf4
2568	P20933	3	6	6.6	346	37194	6.3	N(4)-(beta-N-acetylglucosaminyl)-L-asparaginase precursor (EC 3.5.1.26) (Glycosylasparaginase) (Aspartylglucosaminidase) (N4-(N- acetyl-beta-glucosaminyl)-L-asparagine amidase) (AGA) [Contains: Glycosylasparaginase alpha chain; Glycosylasparaginase beta chain]
2568	UPI000013D53C	3	6	6.6	346	37208	6.3	N(4)-(beta-N-acetylglucosaminyl)-L-asparaginase precursor (EC 3.5.1.26) (Glycosylasparaginase) (Aspartylglucosaminidase) (N4-(N- acetyl-beta-glucosaminyl)-L-asparagine amidase) (AGA) [Contains: Glycosylasparaginase alpha chain; Glycosylasparaginase beta c
2569	Q6NUM9-2	3	9	8.3	481	52439	8	Isoform 2 of Q6NUM9
2569	Q6NUM9	3	9	6.6	610	66820	8.3	All-trans-retinol 13,14-reductase precursor
2569	UPI0000072C67	3	9	6.6	610	66793	8.3	all-trans-13,14-dihydroretinol saturase
2570	Q96GQ5	3	3	6.6	468	51018	6.9	UPF0420 protein C16orf58
2570	UPI0000072B44	3	3	6.6	468	50960	7.2	hypothetical protein LOC64755
2571	Q9H900	3	9	6.6	591	67283	6.3	Protein zwilch homolog
2571	UPI000013EC73	3	9	6.6	591	67214	6.3	Zwilch
2572	Q9HA77	3	4	6.6	564	62224	8.3	Probable cysteinyl-tRNA synthetase, mitochondrial precursor
2573	Q5T2T8	3	4	12.7	204	22890	7.3	Prion protein interacting protein
2573	Q5TG35	3	4	11.7	222	25009	6.5	Prion protein interacting protein
2573	UPI0000D4E859	3	4	7.1	365	40077	8	prion protein interacting protein
2573	O43414	3	4	6.5	397	43076	8.7	Prion protein-interacting protein
2574	UPI0000DD7F7B	3	4	6.5	602	66578	8.5	PREDICTED: similar to sorting nexin family member 30 isoform 1
2575	Q9BR60	3	3	11.5	373	42522	4.7	OS-9 protein
2575	Q13438	3	3	6.4	667	75562	4.9	Protein OS-9 precursor
2576	Q14746	3	4	6.4	738	83208	6.6	Conserved oligomeric Golgi complex component 2
2576	Q86U99	3	4	6.4	737	83136	6.6	Component of oligomeric golgi complex 2
2577	Q9BRR6-2	3	5	6.5	496	53961	6.2	Isoform 2 of Q9BRR6
2577	Q9BRR6	3	5	6.4	497	54089	6.2	ADP-dependent glucokinase
2578	Q13330-2	3	5	10.5	430	49017	5.5	Isoform Short of Q13330
2578	Q13330	3	5	6.3	715	80788	9.3	Metastasis-associated protein MTA1
2578	UPI00003669FD	3	5	6.3	715	80786	9.3	metastasis associated protein
2579	P98170	3	3	6.2	497	56685	6.6	Baculoviral IAP repeat-containing protein 4
2580	Q2TAY7	3	4	6.2	513	57544	7.2	Smu-1 suppressor of mec-8 and unc-52 protein homolog
2581	Q93034	3	6	6.2	780	90955	8	Cullin-5
2582	Q9UBV2	3	3	6.2	794	88755	5.4	Sel-1 homolog precursor
2583	Q59FI5	3	6	8.9	461	52976	7.1	Protein kinase C, alpha variant
2583	P17252	3	6	6.1	672	76764	7	Protein kinase C alpha type
2583	UPI000013DD98	3	6	6.1	672	76750	7	Protein kinase C alpha type (EC 2.7.11.13) (PKC-alpha) (PKC-A).
2583	Q2TSD3	3	6	6.1	672	76762	7.1	Aging-associated gene 6 protein
2584	Q14738-3	3	4	7.5	496	58453	6.8	Isoform Delta
2584	Q59EF0	3	4	7.4	503	59336	7.4	Delta isoform of regulatory subunit B56, protein phosphatase 2A isoform 1 variant
2584	Q14738-2	3	4	6.5	570	66181	7.6	Isoform Delta
2584	Q14738	3	4	6.1	602	69992	8.1	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform
2585	Q8IY67-2	3	5	6.1	739	77860	8.8	Isoform 2 of Q8IY67
2585	UPI0000E042A4	3	5	6	756	79579	8.9	RAVER1
2586	O43818	3	5	5.9	475	51841	7.9	U3 small nucleolar RNA-interacting protein 2
2587	UPI0000246FF6	3	3	8.6	417	47287	6.3	Serum albumin precursor.
2587	P02768-2	3	3	8.6	417	47361	6.3	Isoform 2 of P02768
2587	P02768	3	3	5.9	609	69367	6.3	Serum albumin precursor
2587	UPI0000D61578	3	3	5.8	626	71576	6.7	Serum albumin precursor.
2588	P17405	3	5	5.9	629	69851	7.4	Sphingomyelin phosphodiesterase precursor
2588	UPI000013E592	3	5	5.9	631	69936	7.3	sphingomyelin phosphodiesterase 1, acid lysosomal isoform 1 precursor
2588	UPI0000D625A9	3	5	5.6	664	73082	7.5	Sphingomyelin phosphodiesterase precursor (EC 3.1.4.12) (Acid sphingomyelinase) (aSMase).
2588	Q59EN6	3	5	5.6	664	73054	7.5	Sphingomyelin phosphodiesterase 1, acid lysosomal isoform 1 variant
2589	Q8IYU3	3	3	7.6	472	52175	7.8	2'-PDE protein
2589	Q8TE78	3	3	6.7	535	58920	6.8	CDNA FLJ23843 fis, clone KAT07393
2589	Q6L8Q7	3	3	5.9	609	67382	6.5	2'-phosphodiesterase
2589	UPI000053E488	3	3	5.9	609	67405	6.6	2""-phosphodiesterase
2589	UPI000049DFA7	3	3	5.9	609	67352	6.6	2'-phosphodiesterase

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2590	Q9P2B4	3	3	5.9	639	70158	8.1	CTTNBP2 N-terminal-like protein
2591	Q9UID3	3	4	5.9	782	86042	6.5	Uncharacterized protein C11orf2
2592	UPI00001AE640	3	4	6.3	568	65914	9.1	Zuotin-related factor 1 (M-phase phosphoprotein 11).
2592	Q99543-2	3	4	6.3	568	65814	9	Isoform 2 of Q99543
2592	Q99543	3	4	5.8	621	71897	8.6	DnaJ homolog subfamily C member 2
2592	UPI000020F858	3	4	5.8	621	71996	8.7	zuotin related factor 1
2593	P50281	3	3	5.7	582	65884	7.8	Matrix metalloproteinase-14 precursor
2593	UPI0000048136	3	3	5.7	582	65894	7.8	matrix metalloproteinase 14 preproprotein
2594	Q8IWH5	3	5	5.7	574	63830	8	Similar to chromosome 1 open reading frame 25
2594	UPI0000190FB4	3	5	4.5	733	81790	8	N2,N2-dimethylguanosine tRNA methyltransferase-like
2594	Q9BZQ1	3	5	4.5	733	81747	7.9	C1orf25
2595	O15397	3	19	5.6	1037	119974	5.2	Importin-8
2595	UPI000013CEE9	3	19	5.6	1037	119938	5.2	importin 8
2596	O94842	3	3	5.5	621	66195	5.1	Epidermal Langerhans cell protein LCP1
2597	P40763	3	3	5.5	770	88068	6.3	Signal transducer and activator of transcription 3
2597	P40763-2	3	3	5.5	769	87981	6.3	Isoform Del
2598	P48449	3	4	5.5	732	83309	6.6	Lanosterol synthase
2599	P85037	3	8	5.5	733	75457	9.3	Forkhead box protein K1
2600	Q0ZF97	3	5	5.5	380	42700	8	Cytochrome b
2601	Q9UI26	3	5	5.5	975	112535	5.3	Importin-11
2601	UPI00004572F1	3	5	5.5	974	112369	5.2	Importin-11 (Imp11) (Ran-binding protein 11) (RanBP11).
2602	UPI0000456943	3	3	5.8	537	59662	4.8	Rab GTPase-binding effector protein 2 (Rabaptin-5beta).
2602	Q9H5N1-2	3	3	5.8	533	59316	4.8	Isoform 2 of Q9H5N1
2602	Q9H5N1	3	3	5.4	569	63543	4.8	Rab GTPase-binding effector protein 2
2603	Q9NUQ8	3	5	5.4	709	79745	6.3	ATP-binding cassette sub-family F member 3
2603	UPI000004C4CA	3	5	5.4	709	79773	6.3	ATP-binding cassette, sub-family F (GCN20), member 3
2603	Q9NUQ8-2	3	5	5.4	703	78984	6.2	Isoform 2 of Q9NUQ8
2604	O15484	3	3	5.3	640	73169	7.6	Calpain-5
2604	UPI0000D62659	3	3	5	680	77293	7.4	Calpain-5 (EC 3.4.22.-) (nCL-3) (htra-3).
2604	Q6ZRM8	3	3	5	680	77309	7.5	CDNA FLJ46245 fis, clone TESTI4020596, highly similar to Homo sapiens calpain 5
2604	Q59GM2	3	3	5	678	76602	7.6	Hypothetical protein
2605	Q5T9B9	3	4	5.6	625	67542	6.6	Endoglin
2605	P17813	3	4	5.3	658	70578	6.6	Endoglin precursor
2606	Q59GV6	3	3	5.3	755	80589	5.4	Zinedin variant
2606	Q9NRL3	3	3	5.3	753	80582	5.4	Striatin-4
2606	Q8NE53	3	3	5.3	753	80596	5.4	Striatin, calmodulin binding protein 4
2607	UPI0000DD7E96	3	5	6	753	83389	6.4	PREDICTED: similar to Heat repeats-containing protein FLJ20397
2607	Q86Y56	3	5	5.3	855	93533	6.4	HEAT repeat-containing protein 2
2607	UPI0000D61BE2	3	5	5.3	855	93521	6.4	HEAT repeat-containing protein 2.
2607	UPI000000DBC0	3	5	5.3	855	93579	6.4	HEAT repeat containing 2
2608	Q8IWA4	3	5	5.3	741	84159	6.3	Mitofusin-1
2608	UPI000013D495	3	5	5.3	741	84100	6.3	Mitofusin-1 (EC 3.6.5.-) (Transmembrane GTPase MFN1) (Fzo homolog).
2609	Q96PZ0	3	3	5.3	661	75035	6.4	Pseudouridylate synthase 7 homolog
2610	Q9UH65	3	7	5.3	585	68998	5.9	Switch-associated protein 70
2611	Q6NUL5	3	3	5.5	823	90776	6.5	COG5 protein
2611	A4D0R6	3	3	5.2	860	94901	6.6	Component of oligomeric golgi complex 5
2612	Q8WUY5	3	4	5.5	759	86857	6.3	TSR1 protein
2612	Q2NL82	3	4	5.2	804	91810	7.4	TSR1, 20S rRNA accumulation, homolog
2612	Q9P2E6	3	4	4.9	853	97049	8	Pre-rRNA-processing protein TSR1 homolog
2613	Q5T2E6	3	3	5.2	689	78710	6.6	Uncharacterized protein C10orf76
2614	Q96KG9-5	3	3	6.7	626	69238	8.7	Isoform 5 of Q96KG9
2614	Q96KG9-3	3	3	5.9	707	78696	8.4	Isoform 3 of Q96KG9
2614	UPI0000D62632	3	3	5.4	783	85686	8	N-terminal kinase-like protein (SCY1-like protein 1) (Teratoma- associated tyrosine kinase) (Telomerase transcriptional element- interacting factor) (Telomerase regulation-associated protein).
2614	Q96KG9-4	3	3	5.4	781	86312	6.6	Isoform 4 of Q96KG9
2614	Q96KG9-6	3	3	5.3	787	86371	8.7	Isoform 6 of Q96KG9
2614	Q96KG9-2	3	3	5.3	791	88089	6.3	Isoform 2 of Q96KG9
2614	Q96KG9	3	3	5.2	808	89631	6.3	N-terminal kinase-like protein
2615	Q9NQZ2	3	5	5.2	479	54558	5.6	Something about silencing protein 10
2616	Q9Y5J1	3	5	5.2	556	62004	8.8	U3 small nucleolar RNA-associated protein 18 homolog
2617	O96005	3	12	5.1	669	76097	6.3	Cleft lip and palate transmembrane protein 1
2617	O96005-2	3	12	5	686	77959	6.3	Isoform 2 of O96005
2618	P57737	3	5	5.1	925	100575	5.8	Coronin-7
2618	UPI00006AB831	3	5	5.1	925	100635	5.8	coronin 7
2618	Q17RK4	3	5	5.1	925	100605	5.8	Coronin 7
2619	Q7L5N7	3	11	5.1	544	60208	6.6	Acyltransferase-like 1
2620	Q969X6-2	3	7	6.1	571	64119	8.7	Isoform 2 of Q969X6
2620	Q969X6	3	7	5.1	686	76890	8.8	Cirhin
2620	UPI000006E989	3	7	5.1	686	76922	8.8	cirhin

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
2621	P22059	3	3	5	807	89421	7.3	Oxysterol-binding protein 1
2622	Q00653	3	4	5	900	96749	6.2	Nuclear factor NF-kappa-B p100 subunit (DNA-binding factor KBF2) (H2TF1) (Lymphocyte translocation chromosome 10) (Oncogene Lyt-10) (Lyt10) [Contains: Nuclear factor NF-kappa-B p52 subunit]
2622	UPI000012DC55	3	4	5	899	96678	6.2	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 isoform b
2622	UPI00004563FB	3	4	4.8	930	100358	6.6	Nuclear factor NF-kappa-B p100 subunit (DNA-binding factor KBF2) (H2TF1) (Lymphocyte translocation chromosome 10) (Oncogene Lyt-10) (Lyt10) [Contains: Nuclear factor NF-kappa-B p52 subunit].
2623	Q5TEK9	3	4	5	862	98676	6.3	Itchy homolog E3 ubiquitin protein ligase
2623	UPI0000D6106F	3	4	5	862	98702	6.3	E3 ubiquitin-protein ligase Itchy homolog (EC 6.3.2.-) (Itch) (Atrophin-1-interacting protein 4) (AIP4) (NFE2-associated polypeptide 1) (NAPP1).
2623	UPI0000456F80	3	4	4.8	903	102829	6.3	E3 ubiquitin-protein ligase Itchy homolog (EC 6.3.2.-) (Itch) (Atrophin-1-interacting protein 4) (AIP4) (NFE2-associated polypeptide 1) (NAPP1).
2623	Q96J02	3	4	4.8	903	102803	6.3	E3 ubiquitin-protein ligase Itchy homolog
2624	Q9BUG9	3	6	8.7	439	48419	6.2	ITGB8 protein
2624	P26012	3	6	4.9	769	85632	7.2	Integrin beta-8 precursor
2625	UPI0000D6224C	3	3	7.9	471	52566	6.5	ARF GTPase-activating protein GIT2 (G protein-coupled receptor kinase- interactor 2) (GRK-interacting protein 2) (Cool-interacting tyrosine-phosphorylated protein 2) (CAT2) (CAT-2).
2625	UPI0000161FB2	3	3	7.9	471	52609	6.6	G protein-coupled receptor kinase-interactor 2 isoform 4
2625	Q6FI58	3	3	7.9	471	52577	6.6	GIT2 protein
2625	Q14161-11	3	3	5.9	631	70183	6.6	Isoform 11 of Q14161
2625	UPI0000D6224B	3	3	5.7	646	71956	6.6	ARF GTPase-activating protein GIT2 (G protein-coupled receptor kinase- interactor 2) (GRK-interacting protein 2) (Cool-interacting tyrosine-phosphorylated protein 2) (CAT2) (CAT-2).
2625	Q14161-7	3	3	5.7	646	71967	6.7	Isoform 7 of Q14161
2625	UPI0000D6224A	3	3	5.6	661	73392	6.7	ARF GTPase-activating protein GIT2 (G protein-coupled receptor kinase- interactor 2) (GRK-interacting protein 2) (Cool-interacting tyrosine-phosphorylated protein 2) (CAT2) (CAT-2).
2625	Q14161-6	3	3	5.6	661	73403	6.7	Isoform 6 of Q14161
2625	UPI0000D62249	3	3	5.4	681	76061	7.3	ARF GTPase-activating protein GIT2 (G protein-coupled receptor kinase- interactor 2) (GRK-interacting protein 2) (Cool-interacting tyrosine-phosphorylated protein 2) (CAT2) (CAT-2).
2625	UPI0000167B56	3	3	5.4	679	75734	7.2	G protein-coupled receptor kinase-interactor 2 isoform 3
2625	Q14161-10	3	3	5.4	681	76072	7.5	Isoform 10 of Q14161
2625	Q14161-8	3	3	5.3	694	77518	7.3	Isoform 8 of Q14161
2625	UPI0000D62248	3	3	5.2	709	78943	7.3	ARF GTPase-activating protein GIT2 (G protein-coupled receptor kinase- interactor 2) (GRK-interacting protein 2) (Cool-interacting tyrosine-phosphorylated protein 2) (CAT2) (CAT-2).
2625	Q14161-4	3	3	5.2	709	78954	7.5	Isoform 4 of Q14161
2625	UPI0000D62247	3	3	5.1	729	81311	6.9	ARF GTPase-activating protein GIT2 (G protein-coupled receptor kinase- interactor 2) (GRK-interacting protein 2) (Cool-interacting tyrosine-phosphorylated protein 2) (CAT2) (CAT-2).
2625	Q14161-5	3	3	5.1	729	81322	7	Isoform 5 of Q14161
2625	Q14161-3	3	3	5	744	82759	7.1	Isoform 3 of Q14161
2625	Q14161	3	3	4.9	759	84543	7.2	ARF GTPase-activating protein GIT2
2625	UPI0000D62246	3	3	4.9	759	84532	7.1	ARF GTPase-activating protein GIT2 (G protein-coupled receptor kinase- interactor 2) (GRK-interacting protein 2) (Cool-interacting tyrosine-phosphorylated protein 2) (CAT2) (CAT-2).
2626	P43121	3	4	4.8	646	71608	5.8	Cell surface glycoprotein MUC18 precursor
2627	P52735	3	4	4.8	878	101257	7.1	Protein vav-2
2627	Q5T1S1	3	4	4.8	878	101289	7.1	Vav 2 oncogene
2628	Q15057	3	3	4.8	778	88029	6.8	Centaurin-beta 2
2628	UPI00002132C7	3	3	4.8	778	88101	6.7	centaurin, beta 2
2629	Q92544	3	10	4.8	625	72541	6.7	Transmembrane 9 superfamily protein member 4
2630	Q6ULP2-3	3	3	5.2	820	89720	4.5	Isoform 3 of Q6ULP2
2630	Q53GW0	3	3	4.7	909	99488	4.6	Aftiphilin protein isoform b variant
2630	Q6ULP2-5	3	3	4.7	908	99371	4.6	Isoform 5 of Q6ULP2
2630	Q6ULP2-2	3	3	4.7	909	99458	4.6	Isoform 2 of Q6ULP2
2630	Q6ULP2-4	3	3	4.6	936	102113	4.5	Isoform 4 of Q6ULP2
2630	Q6ULP2	3	3	4.6	937	102200	4.5	Aftiphilin
2631	Q63ZY3-3	3	3	4.8	841	90044	6	Isoform 3 of Q63ZY3
2631	Q63ZY3	3	3	4.7	851	91174	5.6	Ankyrin repeat domain-containing protein 25

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
2632	Q9NXF1	3	8	4.7	929	105674	9.4	Testis-expressed sequence 10 protein
2632	UPI0000071D99	3	8	4.7	929	105693	9.4	testis expressed sequence 10
2633	UPI000015D937	3	5	4.7	620	71320	6.5	protein arginine methyltransferase 5 isoform b
2633	O14744	3	5	4.6	637	72684	6.3	Protein arginine N-methyltransferase 5
2634	P48960-2	3	7	5.1	742	81743	7.1	Isoform 2 of P48960
2634	P48960-3	3	7	4.8	786	86628	6.9	Isoform 3 of P48960
2634	P48960	3	7	4.6	835	91869	6.9	CD97 antigen precursor
2635	P19838	3	3	4.5	968	105356	5.4	Nuclear factor NF-kappa-B p105 subunit (DNA-binding factor KBF1) (EBP- 1) [Contains: Nuclear factor NF-kappa-B p50 subunit]
2635	P19838-2	3	3	4.5	969	105427	5.4	Isoform 2 of P19838
2636	P22033	3	5	4.5	750	83120	6.9	Methylmalonyl-CoA mutase, mitochondrial precursor
2636	UPI000013DA28	3	5	4.5	750	83135	6.9	Methylmalonyl-CoA mutase, mitochondrial precursor (EC 5.4.99.2) (MCM) (Methylmalonyl-CoA isomerase).
2636	UPI000004981E	3	5	4.5	750	83101	6.8	methylmalonyl Coenzyme A mutase precursor
2637	Q96EK5	3	3	4.5	621	71814	5.5	Uncharacterized protein KIAA1279
2638	Q9Y6D9	3	3	4.9	718	83067	5.9	Mitotic spindle assembly checkpoint protein MAD1
2638	A4D218	3	3	4.4	803	91721	8.1	MAD1 mitotic arrest deficient-like 1
2638	UPI0000140415	3	3	4.4	803	91771	8.1	Mitotic spindle assembly checkpoint protein MAD1 (Mitotic arrest deficient-like protein 1) (MAD1-like 1) (Mitotic checkpoint MAD1 protein-homolog) (HsMAD1) (hMAD1) (Tax-binding protein 181).
2638	Q9Y6D9-2	3	3	4.4	804	91859	8.1	Isoform 2 of Q9Y6D9
2639	Q5VXS9	3	3	5.2	907	102289	6.2	Hect domain and RLD 4
2639	Q5GLZ8-6	3	3	5	947	106715	6.5	Isoform 6 of Q5GLZ8
2639	Q5GLZ8-3	3	3	4.8	979	109585	6.5	Isoform 3 of Q5GLZ8
2639	Q5GLZ8-2	3	3	4.5	1049	117697	6.3	Isoform 2 of Q5GLZ8
2639	Q5GLZ8	3	3	4.4	1057	118563	6.2	Probable E3 ubiquitin-protein ligase HERC4
2640	P10253	3	7	4.3	952	105338	6	Lysosomal alpha-glucosidase precursor (EC 3.2.1.20) (Acid maltase) (Aglucosidase alfa) [Contains: 76 kDa lysosomal alpha-glucosidase; 70 kDa lysosomal alpha-glucosidase]
2641	Q9BTT9	3	4	4.8	673	76483	6.5	GYS1 protein
2641	P13807	3	4	4.3	737	83786	6.2	Glycogen [starch] synthase, muscle
2641	Q53ER0	3	4	4.3	737	83858	6.1	Glycogen synthase 1 (Muscle) variant
2642	O60231	3	6	4.2	1041	119263	6.8	Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16
2642	UPI0000161FB0	3	6	4.2	1041	119172	6.7	DEAH (Asp-Glu-Ala-His) box polypeptide 16
2643	Q9H911	3	4	4.8	852	98441	6.4	CDNA FLJ13089 fis, clone NT2RP3002108, weakly similar to DEC1 PROTEIN
2643	Q14CX7	3	4	4.2	972	112292	6.6	Uncharacterized protein C12orf30
2643	Q7Z4N6	3	4	4.2	972	112277	6.6	P120
2644	Q9UDY8-2	3	7	4.3	813	91081	5.9	Isoform 2 of Q9UDY8
2644	Q9UDY8	3	7	4.2	824	92272	5.7	Mucosa-associated lymphoid tissue lymphoma translocation protein 1
2645	O75152	3	4	4.1	810	89131	8.4	Zinc finger CCCH domain-containing protein 11A
2645	UPI0000D62084	3	4	4.1	812	89346	8.4	Zinc finger CCCH domain-containing protein 11A.
2646	Q8TD16	3	4	4.1	824	93533	5.4	Protein bicaudal D homolog 2
2646	Q8TD16-2	3	4	4	855	96806	5.4	Isoform 2 of Q8TD16
2647	Q7Z5I3	3	3	5.3	509	57954	6.6	Kinesin heavy chain member 2
2647	O00139	3	3	4	679	76955	6.4	Kinesin-like protein KIF2A
2647	UPI000012DE53	3	3	4	679	76927	6.4	kinesin heavy chain member 2
2647	UPI0000414107	3	3	3.9	686	77749	6.6	Kinesin-like protein KIF2A (Kinesin-2) (HK2).
2648	P30260	3	3	4	824	91867	7	Cell division cycle protein 27 homolog
2649	Q59G44	3	6	5.9	627	68685	8.1	Calcium-transporting ATPase 2C1 isoform 1d variant
2649	P98194-2	3	6	4.2	888	96960	6.3	Isoform 2 of P98194
2649	P98194-4	3	6	4.1	903	98733	6.6	Isoform 4 of P98194
2649	P98194	3	6	4	919	100577	6.7	Calcium-transporting ATPase type 2C member 1 (EC 3.6.3.8) (ATPase 2C1) (ATP-dependent Ca(2+) pump PMR1)
2649	P98194-3	3	6	4	923	101163	6.4	Isoform 3 of P98194
2649	UPI0000D61B7A	3	6	3.9	960	105298	6.1	Calcium-transporting ATPase type 2C member 1 (EC 3.6.3.8) (ATPase 2C1) (ATP-dependent Ca(2+) pump PMR1).
2649	UPI00001969A3	3	6	3.9	949	104032	6.4	calcium-transporting ATPase 2C1 isoform 1d
2649	P98194-6	3	6	3.9	959	105057	6.3	Isoform 6 of P98194
2649	P98194-5	3	6	3.9	939	103007	6.5	Isoform 5 of P98194
2650	Q61624	3	3	4	794	88751	6.5	Zinc finger protein 148
2650	UPI0000163B55	3	3	4	794	88992	6.5	zinc finger protein 148 (pHZ-52)
2650	Q9UQR1	3	3	4	794	88976	6.5	Zinc finger protein 148
2650	Q8TDH4	3	3	4	794	88988	6.5	CLL-associated antigen KW-10
2651	Q6NX51	3	7	4	974	110498	6.5	Exocyst complex component 4
2651	Q96A65	3	7	4	974	110498	6.5	Exocyst complex component 4
2652	Q96T37-2	3	4	4	957	104755	10.1	Isoform 2 of Q96T37
2652	Q86VW9	3	4	4	959	105284	10.1	RBM15 protein
2652	Q3ZB86	3	4	3.9	969	106365	10.1	RBM15 protein
2652	Q96T37	3	4	3.9	977	107188	10.1	Putative RNA-binding protein 15

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
2652	Q4V760	3	4	3.9	969	106366	10.1	RBM15 protein
2653	Q5T377	3	5	3.9	1039	115458	8.9	Novel protein
2654	Q68E01	3	6	3.9	1043	118070	5.8	Integrator complex subunit 3
2654	Q68E01-2	3	6	3.9	1042	118013	5.8	Isoform 2 of Q68E01
2655	UPI000049DE88	3	6	3.8	1104	124019	5.9	KIAA1468 (KIAA1468), mRNA
2656	Q6P275	3	8	3.8	1221	140090	5.5	STAG1 protein
2656	Q4LE48	3	8	3.7	1275	146338	5.7	STAG1 variant protein
2656	UPI000020A2DE	3	8	3.7	1258	144427	5.6	stromal antigen 1
2656	Q8WVM7	3	8	3.7	1258	144445	5.6	Cohesin subunit SA-1
2657	UPI00001C1F5D	3	5	3.9	1142	125822	7.1	fibronectin type III domain containing 3A isoform 2
2657	Q9Y2H6	3	5	3.9	1134	125054	7.1	Fibronectin type-III domain-containing protein 3a
2657	Q6EVH4	3	5	3.7	1198	131852	6.7	Gene expressed in odontoblast protein
2658	Q92620	3	6	3.7	1227	140502	6.5	Pre-mRNA-splicing factor ATP-dependent RNA helicase PRP16
2659	P49916-2	3	4	3.8	862	95802	9	Isoform Beta of P49916
2659	P49916	3	4	3.6	922	102691	8.8	DNA ligase 3
2660	UPI0000456EF2	3	7	3.9	764	85458	8.5	Mitochondrial ATP-binding cassette sub-family B member 6 (Mitochondrial ABC transporter 3) (Mt-ABC transporter 3) (Ubiquitously expressed mammalian ABC half transporter) (P-glycoprotein-related protein).
2660	Q9NP58-4	3	7	3.9	766	85685	8.5	Isoform 4 of Q9NP58
2660	Q9NP58	3	7	3.6	842	93886	8.5	Mitochondrial ATP-binding cassette sub-family B member 6
2661	Q9Y6D5	3	4	3.6	1785	202037	6.3	Brefeldin A-inhibited guanine nucleotide-exchange protein 2
2661	UPI000012693A	3	4	3.6	1785	202092	6.5	ADP-ribosylation factor guanine nucleotide-exchange factor 2
2662	Q5JSH3	3	3	3.5	913	101366	5.5	WD repeat protein 44
2662	Q5JSH3-2	3	3	3.5	905	100403	5.5	Isoform 2 of Q5JSH3
2663	Q6P2E9	3	4	3.5	1401	151661	5.9	Enhancer of mRNA-decapping protein 4
2664	Q9H4L7	3	4	3.5	1026	117374	5.6	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A containing DEAD/H box 1
2664	UPI000020B1CF	3	4	3.5	1028	117602	5.6	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A containing DEAD/H box 1 (EC 3.6.1.-) (ATP- dependent helicase 1) (hHEL1).
2664	UPI000013E22F	3	4	3.5	1026	117402	5.6	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A containing DEAD/H box 1 (EC 3.6.1.-) (ATP- dependent helicase 1) (hHEL1).
2664	Q9H4L7-2	3	4	3.5	1028	117574	5.6	Isoform 2 of Q9H4L7
2665	Q9UIA9	3	17	3.5	1087	123907	6.3	Exportin-7
2665	UPI000049E0B7	3	17	3.5	1087	123975	6.3	Exportin-7 (Exp7) (Ran-binding protein 16).
2665	UPI0000073676	3	17	3.5	1087	123953	6.3	exportin 7
2666	O76024	3	3	3.4	890	100305	8	Wolframin
2666	UPI00000715C3	3	3	3.4	890	100291	8	Wolframin.
2667	Q504U8	3	5	3.8	1091	120692	6.8	EGFR protein
2667	P00533	3	5	3.4	1210	134277	6.7	Epidermal growth factor receptor precursor
2667	Q2TTR7	3	5	3.4	1210	134323	6.7	Cell growth inhibiting protein 40
2668	Q13136-2	3	3	3.5	1185	133970	6.3	Isoform 2 of Q13136
2668	Q13136	3	3	3.4	1202	135778	6.3	Liprin-alpha-1
2668	UPI000013CE04	3	3	3.4	1206	136121	6.3	Liprin-alpha-1 (Protein tyrosine phosphatase receptor type f polypeptide-interacting protein alpha-1) (PTPRF-interacting protein alpha-1) (LAR-interacting protein 1) (LIP.1).
2669	Q9Y5Q9	3	6	3.4	886	101272	5.1	General transcription factor 3C polypeptide 3
2670	UPI0000161590	3	3	3.4	1011	111723	6.8	CAP-GLY domain containing linker protein 2 isoform 2
2671	Q8NC75	3	3	6	613	69848	8.8	CDNA FLJ90437 fis, clone NT2RP3000838, weakly similar to TRICHOHYALIN
2671	Q96D60	3	3	5.4	691	77897	7	PHLDB1 protein
2671	UPI0000D62692	3	3	5.1	730	82831	7	Pleckstrin homology-like domain family B member 1 (Protein LL5-alpha).
2671	Q6ZUD6	3	3	5.1	731	82988	6.9	CDNA FLJ43795 fis, clone TESTI4000079
2671	Q86UU1-3	3	3	3.7	995	107381	8.5	Isoform 3 of Q86UU1
2671	Q5W9G0	3	3	3.3	1125	124523	8.5	KIAA0638 splice variant 2
2671	Q86UU1-2	3	3	2.8	1319	144739	8.6	Isoform 2 of Q86UU1
2671	Q86UU1	3	3	2.7	1377	151161	8.6	Pleckstrin homology-like domain family B member 1
2672	Q12873-2	3	3	3.3	1966	222859	7.5	Isoform 2 of Q12873
2672	Q12873	3	3	3.2	2000	226590	7.3	Chromodomain helicase-DNA-binding protein 3
2672	UPI00004432F5	3	3	3.2	2045	231360	6.4	chromodomain helicase DNA binding protein 3 isoform 3
2673	Q15031	3	4	3.2	903	101976	8.2	Probable leucyl-tRNA synthetase, mitochondrial precursor
2674	UPI000059D6BC	3	3	3.4	1040	116286	8.6	Putative splicing factor, arginine/serine-rich 14 (Arginine/serine- rich-splicing factor 14).
2674	Q8IX01-4	3	3	3.4	1030	115216	8.6	Isoform 4 of Q8IX01

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2674	Q8IX01-3	3	3	3.4	1040	116316	8.6	Isoform 3 of Q8IX01
2674	Q8IX01	3	3	3.2	1082	120237	7.3	Putative splicing factor, arginine/serine-rich 14
2674	UPI000019825D	3	3	3.2	1082	120207	7.3	Putative splicing factor, arginine/serine-rich 14 (Arginine/serine- rich-splicing factor 14).
2675	Q8N3X1	3	4	3.2	1015	110064	4.7	Formin binding protein 4
2675	Q9NT81	3	4	3.2	1013	109875	4.7	Hypothetical protein DKFZp434M2023
2675	UPI0000DBEF37	3	4	3.1	1017	110266	4.7	formin binding protein 4
2675	UPI0000D625EC	3	4	3.1	1019	110451	4.8	formin binding protein 4
2675	Q9Y2L7	3	4	3	1050	113630	4.8	Formin-binding protein 4
2676	P20936-2	3	5	3.7	870	100398	7.6	Isoform 2 of P20936
2676	P20936	3	5	3.1	1047	116403	6.5	Ras GTPase-activating protein 1
2676	UPI000013DA03	3	5	3.1	1047	116391	6.5	Ras GTPase-activating protein 1 (GTPase-activating protein) (GAP) (Ras p21 protein activator) (p120GAP) (RasGAP).
2677	P31327	3	9	3.1	1500	164939	6.7	Carbamoyl-phosphate synthase [ammonia], mitochondrial precursor
2677	Q59HF8	3	9	3.1	1510	166117	6.8	Carbamoyl-phosphate synthetase 1 variant
2678	O95197-3	3	63	13.1	236	25609	8.5	Isoform 3 of O95197
2678	O95197-4	3	63	12.2	255	27568	8.2	Isoform 4 of O95197
2678	UPI0000D62622	3	63	12.1	257	27753	8.2	Reticulon-3 (Neuroendocrine-specific protein-like 2) (NSP-like protein II) (NSPLII).
2678	O95197-2	3	63	3.1	1013	110652	5	Isoform 2 of O95197
2678	O95197	3	63	3	1032	112611	5	Reticulon-3
2678	UPI0000D62623	3	63	3	1034	112754	5	Reticulon-3 (Neuroendocrine-specific protein-like 2) (NSP-like protein II) (NSPLII).
2679	Q01831	3	3	3	940	105981	8.9	DNA-repair protein complementing XP-C cells
2679	UPI000013DDC9	3	3	3	937	105723	8.9	DNA-repair protein complementing XP-C cells (Xeroderma pigmentosum group C-complementing protein) (p125).
2679	UPI0000073ED0	3	3	3	940	105953	8.9	xeroderma pigmentosum, complementation group C
2680	Q12913	3	6	3	1337	145927	5.6	Receptor-type tyrosine-protein phosphatase eta precursor
2680	UPI00004564C8	3	6	3	1337	145941	5.6	Receptor-type tyrosine-protein phosphatase eta precursor (EC 3.1.3.48) (Protein-tyrosine phosphatase eta) (R-PTP-eta) (HPTP eta) (Protein-tyrosine phosphatase receptor type J) (Density-enhanced phosphatase 1) (DEP-1) (CD148 antigen).
2681	Q5VT52-3	3	7	3	1435	152875	7	Isoform 3 of Q5VT52
2681	Q5VT52	3	7	2.9	1461	156019	7.4	Uncharacterized protein KIAA0460
2682	Q96PV8	3	3	5.1	664	71749	5.9	KIAA1930 protein
2682	Q9H8D9	3	3	4	858	91131	5.4	CDNA FLJ13725 fis, clone PLACE3000009, weakly similar to DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
2682	Q6ZS17	3	3	2.8	1223	132307	6.3	Protein FAM65A
2682	UPI0000231CA4	3	3	2.8	1219	131873	6.3	hypothetical protein LOC79567
2683	Q9H7N4	3	4	2.8	1343	142483	9.4	FLJ00034 protein
2683	Q9NR59	3	4	2.8	1312	139269	9.2	Ser/arg-rich pre-mRNA splicing factor SR-A1
2684	UPI000013F07D	3	10	4.6	802	90609	6.3	KIAA1794 (KIAA1794), mRNA
2684	Q9NVI1-3	3	10	2.8	1328	149335	6.7	Isoform 3 of Q9NVI1
2685	Q68DI5	3	5	3.7	983	111509	6.3	Hypothetical protein DKFZp781H1425
2685	O95163	3	5	2.7	1332	150191	6	Elongator complex protein 1
2685	Q8N516	3	5	2.7	1332	150223	6	Inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase complex-associated protein
2685	Q4LE38	3	5	2.7	1342	151455	6	IKBKAP variant protein
2686	Q9ULU4-6	3	3	2.8	1023	112892	6.7	Isoform 6 of Q9ULU4
2686	Q2HXV4	3	3	2.7	1088	120828	6.3	RACK7 isoform i
2686	Q2HXV1	3	3	2.6	1134	126415	6.7	RACK7 isoform l
2686	UPI000053F609	3	3	2.6	1107	123518	6.4	Protein kinase C-binding protein 1 (Rack7) (Cutaneous T-cell lymphoma- associated antigen se14-3) (CTCL tumor antigen se14-3) (Zinc finger MYND domain-containing protein 8).
2686	Q9ULU4-8	3	3	2.6	1106	123387	6.4	Isoform 8 of Q9ULU4
2686	Q2HXW0	3	3	2.6	1135	125470	6.5	RACK7 isoform c
2686	Q9ULU4-5	3	3	2.5	1180	130926	6.9	Isoform 5 of Q9ULU4
2686	Q2HXW1	3	3	2.5	1160	128371	6.4	RACK7 isoform b
2686	Q2HXV9	3	3	2.5	1163	128680	6.7	RACK7 isoform d
2686	Q2HXV7	3	3	2.5	1181	131057	6.9	RACK7 isoform f
2686	Q9ULU4-7	3	3	2.4	1233	137036	7.1	Isoform 7 of Q9ULU4
2686	Q9ULU4	3	3	2.4	1186	131692	7.2	Protein kinase C-binding protein 1
2686	Q2HXW2	3	3	2.4	1188	131580	6.6	RACK7 isoform a
2686	Q2HXV8	3	3	2.4	1234	137167	7.1	RACK7 isoform e
2687	Q8WXD9	3	3	2.6	1431	149813	9.1	Caskin-1
2687	UPI00004568FC	3	3	2.6	1432	149857	9.2	Caskin-1 (CASK-interacting protein 1).
2688	Q96RT1-7	3	8	2.6	1302	146086	5.3	Isoform 7 of Q96RT1
2688	A0AVR1	3	8	2.5	1371	153952	5.5	Erbb2 interacting protein
2688	UPI0000D61630	3	8	2.5	1361	152723	5.4	Protein LAP2 (Erbb2-interacting protein) (Erbin) (Densin-180-like protein).
2688	Q96RT1-6	3	8	2.5	1340	150601	5.5	Isoform 6 of Q96RT1

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
2688	Q96RT1-5	3	8	2.5	1356	152290	5.4	Isoform 5 of Q96RT1
2688	Q96RT1-4	3	8	2.5	1346	151251	5.4	Isoform 4 of Q96RT1
2688	Q96RT1-3	3	8	2.5	1360	152652	5.4	Isoform 3 of Q96RT1
2688	Q96RT1-2	3	8	2.5	1371	153926	5.5	Isoform 2 of Q96RT1
2688	Q1RMD0	3	8	2.5	1371	153788	5.5	Erbb2 interacting protein
2688	Q1RMC9	3	8	2.5	1367	153515	5.5	ERBB2IP protein
2688	Q96RT1	3	8	2.4	1412	158297	5.5	Protein LAP2
2689	Q9NP73	3	3	17	165	18225	6.5	Probable glycosyltransferase GLT28D1
2689	A2A2G2	3	3	2.5	1137	126056	6.7	Chromosome X open reading frame 45
2690	O14646	3	5	2.5	1709	196517	7.2	Chromodomain-helicase-DNA-binding protein 1
2690	UPI000013DD75	3	5	2.5	1710	196687	7.1	chromodomain helicase DNA binding protein 1
2690	Q17RZ3	3	5	2.5	1709	196589	7.1	Chromodomain helicase DNA binding protein 1
2691	O14981	3	7	2.5	1849	206886	6.5	TATA-binding protein-associated factor 172 (EC 3.6.1.-) (ATP-dependent helicase BTAF1) (TBP-associated factor 172) (TAF-172) (TAF(II)170)
2692	Q7Z478	3	9	2.5	1369	155235	8.1	Putative ATP-dependent RNA helicase DHX29
2693	Q9P2D5	3	10	2.5	1386	154717	8.1	Transmembrane protein 2
2694	O95104	3	19	2.4	1147	125869	9.6	Splicing factor, arginine/serine-rich 15
2694	Q0P607	3	19	2.4	1146	125740	9.6	Splicing factor, arginine/serine-rich 15
2694	O95104-2	3	19	2.4	1125	123643	9.6	Isoform 2 of O95104
2695	Q14671-2	3	3	2.5	1162	124420	6.8	Isoform 2 of Q14671
2695	Q14671	3	3	2.4	1186	126473	6.8	Pumilio homolog 1
2695	UPI0000203D8E	3	3	2.4	1188	126685	6.8	pumilio 1 isoform 1
2695	Q5VXY8	3	3	2.4	1189	126756	6.8	Pumilio homolog 1
2695	Q5VXY5	3	3	2.4	1224	130108	6.9	Pumilio homolog 1
2695	Q53HH5	3	3	2.4	1188	126708	6.8	Pumilio homolog 1 variant
2696	Q96T23	3	5	2.4	1431	163005	5	Remodeling and spacing factor 1
2696	UPI00004FCB0F	3	5	2.4	1400	159300	5	Remodeling and spacing factor 1 (Rsf-1) (Hepatitis B virus X- associated protein) (HBV pX-associated protein 8) (p325 subunit of RSF chromatin remodelling complex).
2696	UPI00001FB001	3	5	2.4	1441	163820	5	remodeling and spacing factor 1
2696	Q96T23-2	3	5	2.4	1400	159314	5	Isoform 2 of Q96T23
2697	P42695	3	6	2.3	1498	168890	7.5	Condensin-II complex subunit D3
2697	UPI0000D626A5	3	6	2.3	1501	169232	7.6	Condensin-II complex subunit D3 (Non-SMC condensin II complex subunit D3) (hCAP-D3).
2698	Q2Q1W1	3	3	2.4	1439	160772	5.2	Rab5-activating protein 6
2698	Q14C86	3	3	2.3	1460	162897	5.2	GTPase activating protein and VPS9 domain-containing protein 1
2698	UPI00001D76F1	3	3	2.3	1487	166168	5.2	GTPase activating protein and VPS9 domains 1
2698	Q9P207	3	3	2.3	1484	165637	5.2	KIAA1521 protein
2699	P42356	3	4	2.2	2044	231290	6.9	Phosphatidylinositol 4-kinase alpha
2699	UPI00001AE78E	3	4	2.2	2044	231317	6.9	Phosphatidylinositol 4-kinase alpha (EC 2.7.1.67) (PI4-kinase alpha) (PtdIns-4-kinase alpha) (PI4K-alpha).
2699	Q4LE69	3	4	2.1	2121	238695	7.1	PIK4CA variant protein
2700	O95602	3	3	2.1	1717	194190	7.2	DNA-directed RNA polymerase I largest subunit
2700	UPI0000456DEC	3	3	2.1	1716	194130	7.1	DNA-directed RNA polymerase I largest subunit (EC 2.7.7.6) (RNA polymerase I 194 kDa subunit) (RPA194).
2700	Q0VG05	3	3	2.1	1720	194810	7	Polymerase (RNA) I polypeptide A, 194kDa
2701	Q8TEQ6	3	4	2.1	1508	168560	6.6	Gem-associated protein 5
2701	UPI000020D072	3	4	2.1	1508	168589	6.6	Gem-associated protein 5 (Gemin5).
2702	Q13395	3	4	2	1621	181674	7.1	Probable methyltransferase TARBP1
2703	Q96JI4	3	17	2	1778	200950	6.8	KIAA1843 protein
2704	Q9Y4K1	3	3	2	1723	188675	5.9	Absent in melanoma 1 protein
2704	UPI000050B6CA	3	3	2	1723	188616	5.9	absent in melanoma 1
2705	UPI0000DD7D5C	3	3	2	1977	209273	8.5	PREDICTED: similar to NHS-like 1 isoform 1
2706	Q5T2J2	3	4	1.9	1661	183857	6.5	Novel protein
2707	Q9NZM3-2	3	3	2	1669	190364	8.2	Isoform 2 of Q9NZM3
2707	Q9NZM3	3	3	1.9	1696	193329	8.1	Intersectin-2
2708	Q460N5	3	5	1.8	1720	193752	8	Poly [ADP-ribose] polymerase 14
2709	Q9H3S7	3	3	1.8	1636	178972	6.9	Tyrosine-protein phosphatase non-receptor type 23
2710	A1YCA4	3	7	1.7	2154	231133	5.7	SEC16L
2710	O15027-3	3	7	1.7	2159	231249	5.6	Isoform 3 of O15027
2710	O15027-2	3	7	1.7	2134	228868	5.6	Isoform 2 of O15027
2710	O15027	3	7	1.7	2179	233515	5.6	Uncharacterized protein KIAA0310
2711	A2RUU9	3	5	1.6	1859	209905	5	PCM1 protein
2711	UPI0000F58ED3	3	5	1.5	2024	228531	5	pericentriolar material 1
2711	UPI000049E0B4	3	5	1.5	2022	228454	5	Pericentriolar material 1 protein (PCM-1) (hPCM-1).
2711	Q15154-2	3	5	1.5	1968	222209	5	Isoform 2 of Q15154
2711	Q15154	3	5	1.5	2023	228533	5	Pericentriolar material 1 protein
2712	Q5VTN2	3	4	1.5	2193	250502	7.2	OTTHUMP00000016904
2712	UPI0000D614A0	3	4	1.5	2192	250507	7.1	Activating signal cointegrator 1 complex subunit 3 (EC 3.6.1.-) (ASC-1 complex subunit p200) (Trip4 complex subunit p200) (Helicase, ATP binding 1).
2712	UPI000014145A	3	4	1.5	2202	251458	7.1	activating signal cointegrator 1 complex subunit 3 isoform a
2712	Q8N3C0-2	3	4	1.5	2193	250651	7.1	Isoform 2 of Q8N3C0

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
2712	Q8N3C0	3	4	1.5	2202	251488	7.1	Activating signal cointegrator 1 complex subunit 3
2713	UPI000016001C	3	3	1.5	2288	259840	6.8	transcriptional regulator ATRX isoform 3
2713	P46100	3	3	1.4	2492	282564	6.6	Transcriptional regulator ATRX
2713	UPI0000DD8684	3	3	1.4	2493	282810	6.6	PREDICTED: similar to transcriptional regulator ATRX isoform 1
2713	UPI0000D61D94	3	3	1.4	2424	274983	6.4	Transcriptional regulator ATRX (EC 3.6.1.-) (ATP-dependent helicase ATRX) (X-linked helicase II) (X-linked nuclear protein) (XNP) (Znf- HX).
2713	UPI0000161F78	3	3	1.4	2492	282584	6.6	transcriptional regulator ATRX isoform 1
2713	UPI000016001B	3	3	1.4	2454	278226	6.5	transcriptional regulator ATRX isoform 2
2713	P46100-4	3	3	1.4	2454	278206	6.6	Isoform 3 of P46100
2713	P46100-3	3	3	1.4	2375	269789	7	Isoform 2 of P46100
2714	UPI0000E8AC98	3	15	1.4	2610	289383	5.4	HECT domain containing 1
2715	Q4LE74	3	8	1.4	2028	229712	8.6	MYO9B variant protein
2715	Q13459-2	3	8	1.4	2023	229298	8.5	Isoform Short of Q13459
2715	Q13459	3	8	1.3	2158	243555	8.7	Myosin-IXb
2715	UPI0000D61740	3	8	1.3	2157	243354	8.8	Myosin-9B (Myosin IXb) (Unconventional myosin-9b).
2715	UPI00001B55A5	3	8	1.3	2157	243398	8.8	myosin IXB
2716	Q93008	3	7	1.3	2547	289539	5.7	Probable ubiquitin carboxyl-terminal hydrolase FAF-X
2716	UPI0000D61D4F	3	7	1.3	2563	291447	5.7	Probable ubiquitin carboxyl-terminal hydrolase FAF-X (EC 3.1.2.15) (Ubiquitin thioesterase FAF-X) (Ubiquitin-specific-processing protease FAF-X) (Deubiquitinating enzyme FAF-X) (Fat facets protein-related, X- linked) (Ubiquitin-specific protease 9, X chro
2716	UPI0000D61D4E	3	7	1.3	2564	291492	5.8	Probable ubiquitin carboxyl-terminal hydrolase FAF-X (EC 3.1.2.15) (Ubiquitin thioesterase FAF-X) (Ubiquitin-specific-processing protease FAF-X) (Deubiquitinating enzyme FAF-X) (Fat facets protein-related, X- linked) (Ubiquitin-specific protease 9, X chro
2716	UPI00006AB82F	3	7	1.3	2554	290495	5.8	ubiquitin specific protease 9, X-linked isoform 4
2716	UPI00006AB82E	3	7	1.3	2570	292312	5.8	ubiquitin specific protease 9, X-linked isoform 3
2716	Q93008-2	3	7	1.3	2563	291356	5.7	Isoform Long of Q93008
2717	O95071	3	3	1.2	2799	309352	5.8	E3 ubiquitin-protein ligase EDD1
2717	UPI000052A0EC	3	3	1.2	2796	309192	6.1	PREDICTED: similar to E3 ubiquitin protein ligase, HECT domain containing, 1
2717	UPI00004576D7	3	3	1.2	2798	309307	5.9	Ubiquitin-protein ligase EDD1 (EC 6.3.2.-) (Hyperplastic discs protein homolog) (hHYD) (Progestin-induced protein).
2718	A4D265	3	6	1	3830	434416	8.2	Transformation/transcription domain-associated protein
2718	Q9Y4A5	3	6	1	3859	437603	8.2	Transformation/transcription domain-associated protein
2719	UPI000051946B	3	4	0.9	4588	506278	5	FAT tumor suppressor 1 precursor
2719	Q14517	3	4	0.8	4590	506283	5	Cadherin-related tumor suppressor homolog precursor
2719	UPI0000457904	3	4	0.8	4594	506958	5	Cadherin-related tumor suppressor homolog precursor (Protein fat homolog).
2720	P14618-2	2	8	62	531	58062	7.7	Isoform M1 of P14618
2721	Q15149-4	2	25	53.3	4547	516174	5.8	Isoform 4 of Q15149
2721	UPI0000457914	2	25	53.3	4547	516075	5.8	Plectin-1 (PLTN) (PCN) (Hemidesmosomal protein 1) (HD1).
2721	UPI0000233FD1	2	25	53.3	4547	516204	5.8	plectin 1 isoform 11
2722	O43852-2	2	4	50.5	315	37135	4.6	Isoform 2 of O43852
2723	Q96G68	2	10	48.7	39	4414	9.7	C1orf151 protein
2724	Q9UNX3	2	3	45.5	145	17256	10.6	60S ribosomal protein L26-like 1
2725	P62834	2	2	45.1	184	20987	6.6	Ras-related protein Rap-1A precursor
2726	P06753	2	3	42.6	284	32819	4.7	Tropomyosin alpha-3 chain
2726	UPI0000456267	2	3	42.5	285	32996	4.7	Tropomyosin alpha-3 chain (Tropomyosin-3) (Tropomyosin gamma) (hTM5).
2726	UPI000013D90D	2	3	42.5	285	32950	4.7	tropomyosin 3 isoform 1
2727	O94925-3	2	5	42.1	598	65460	7.9	Isoform GAC of O94925
2728	Q16143	2	3	41.8	134	14288	4.4	Beta-synuclein
2729	Q9HB66	2	5	41.3	63	7264	9.6	PNAS-117
2730	O75506	2	8	39.5	76	8544	4.4	Heat shock factor-binding protein 1
2730	UPI000013E5CF	2	8	36.1	83	9349	4.4	Heat shock factor-binding protein 1 (Nasopharyngeal carcinoma- associated antigen 13) (NPC-A-13).
2731	Q71UM5	2	15	39.3	84	9477	9.5	40S ribosomal protein S27-like protein
2731	UPI000049DDE1	2	15	33	100	11346	9.3	40S ribosomal protein S27-like protein.
2732	Q96A08	2	11	38.6	127	14167	10.3	Histone H2B type 1-A
2733	Q9UDW1	2	4	38.1	63	7308	9.5	Ubiquinol-cytochrome c reductase complex 7.2 kDa protein
2734	Q9GZV4	2	2	37.9	153	16793	5.6	Eukaryotic translation initiation factor 5A-2
2735	P12235	2	7	36.2	298	33064	9.8	ADP/ATP translocase 1
2736	O75438	2	2	34.5	58	6961	8.9	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 1

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
2737	Q9Y5U9	2	6	34.1	82	8969	8.3	Immediate early response 3-interacting protein 1
2738	Q6NS89	2	3	33.3	117	13129	5.9	Mediator of RNA polymerase II transcription, subunit 11 homolog
2738	Q9P086	2	3	28.7	136	15301	8.8	Mediator of RNA polymerase II transcription subunit 11
2739	O43504	2	6	33	91	9614	4.9	Hepatitis B virus X-interacting protein
2739	UPI0000205288	2	6	17.3	173	18158	5.5	hepatitis B virus x-interacting protein
2740	Q8WVE3	2	3	32.9	85	9509	5.9	MGC13017 protein
2740	Q96HQ2	2	3	24.1	116	13196	5	Similar to RIKEN cDNA A430101B06 gene
2741	P01112	2	5	32.8	189	21298	5.3	GTPase HRas precursor
2742	Q5RI17	2	6	32.8	723	79844	7.9	Heterogeneous nuclear ribonucleoprotein U
2743	Q8NHG7	2	4	32.5	77	8443	8.9	Small VCP/p97-interacting protein
2743	UPI00006C1109	2	4	31.6	79	9023	9.8	PREDICTED: similar to Small VCP/p97-interacting protein isoform 6
2743	UPI00006C1108	2	4	31.6	79	8649	8	PREDICTED: similar to Small VCP/p97-interacting protein isoform 5
2744	A1L188	2	2	32.4	74	7756	9.3	Hypothetical LOC284184
2745	P59768	2	6	32.4	71	7850	8	Guanine nucleotide-binding protein G(I)/G(S)/G(O) gamma-2 subunit precursor
2746	P61970	2	6	32.3	127	14478	5.4	Nuclear transport factor 2
2747	Q85KX8	2	20	32.2	227	25575	4.8	Cytochrome oxidase subunit II
2748	Q15714	2	5	31.2	144	15680	5.2	TSC22 domain family protein 1
2749	Q9HB72	2	4	30.3	76	8468	10.2	PNAS-106
2749	Q9Y5V0	2	4	30.3	76	8498	10	Zinc finger protein 706
2750	UPI000006FE7A	2	2	30.1	156	17967	9.5	PREDICTED: similar to ubiquitin and ribosomal protein S27a precursor
2751	UPI0000DD7A6C	2	2	30.1	73	8254	8.4	PREDICTED: similar to ATP synthase alpha chain, mitochondrial precursor
2752	P62875	2	3	29.9	67	7645	7.8	DNA-directed RNA polymerase II 7.6 kDa polypeptide
2753	Q6FG99	2	15	29.8	114	11568	4.4	RPLP1 protein
2754	Q9NSA3	2	2	29.6	81	9170	5.4	Beta-catenin-interacting protein 1
2755	Q13015	2	5	28.9	90	10061	4.5	Protein AF1q
2756	Q5EBL8	2	4	28.6	140	16131	7.2	PDZ domain-containing protein 11
2756	Q5EBL8-2	2	4	23.4	171	19492	7.6	Isoform 2 of Q5EBL8
2757	Q5T123	2	33	28.4	88	9380	9.4	SH3 domain binding glutamic acid-rich protein like 3
2757	Q9H299	2	33	26.9	93	10438	4.9	SH3 domain-binding glutamic acid-rich-like protein 3
2757	UPI0000D61E9C	2	33	11.1	225	23699	9.1	SH3 domain-binding glutamic acid-rich-like protein 3 (SH3 domain- binding protein 1) (SH3BP-1).
2757	Q86Z22	2	33	11.1	226	23838	9.1	Hypothetical protein
2758	O14907	2	8	28.2	124	13735	8.5	Tax1-binding protein 3
2759	Q8NDD5	2	4	35.9	128	14098	5.9	Hypothetical protein DKFZp586L2318
2759	UPI00001B5789	2	4	33.6	137	15614	4.6	ubiquitin-conjugating enzyme E2G 2 isoform 2
2759	P60604	2	4	27.9	165	18566	4.7	Ubiquitin-conjugating enzyme E2 G2
2760	P14406	2	5	27.7	83	9396	9.7	Cytochrome c oxidase polypeptide VIIa-liver/heart, mitochondrial precursor
2760	Q496I0	2	5	27.7	83	9426	9.6	Cytochrome c oxidase subunit VIIa polypeptide 2
2760	UPI000015A446	2	5	20	115	12844	9.1	Cytochrome c oxidase polypeptide VIIa-liver/heart, mitochondrial precursor (EC 1.9.3.1) (Cytochrome c oxidase subunit VIIa-L) (VIIaL).
2761	Q567R0	2	6	29.4	85	9953	5.5	UQCRH protein
2761	P07919	2	6	27.5	91	10739	4.4	Ubiquinol-cytochrome c reductase complex 11 kDa protein, mitochondrial precursor
2762	UPI0000DD7D46	2	8	27.3	77	7941	8.4	PREDICTED: similar to ribosomal protein S14
2763	Q5SQX9	2	5	27.6	435	48726	5.1	Novel protein similar to beta-tubulin 4Q
2763	Q3ZCM7	2	5	27.2	441	49360	4.9	TUBB8 protein
2763	Q8WZ78	2	5	27	444	49776	4.9	Beta-tubulin 4Q
2764	Q86XF3	2	13	38.8	67	7371	4.9	LSM8 protein
2764	O95777	2	13	27.1	96	10403	4.5	U6 snRNA-associated Sm-like protein LSm8
2765	P10301	2	8	27.1	218	23480	6.9	Ras-related protein R-Ras precursor
2766	Q9Y605	2	2	26.8	127	14650	4.7	MORF4 family-associated protein 1
2767	Q9NRP2	2	2	26.6	79	9460	7.9	UPF0287 protein C16orf61
2768	Q9Y6A9	2	6	26.5	102	11805	9.3	Signal peptidase complex subunit 1
2769	Q969Q0	2	6	26.4	106	12469	10.7	60S ribosomal protein L36a-like
2770	Q9UHA2	2	2	26	77	8835	5.9	SS18-like protein 2
2771	O95716	2	3	25.6	219	24267	4.9	Ras-related protein Rab-3D
2772	Q49B96	2	3	25.6	90	10394	8.7	Cytochrome c oxidase assembly protein COX19
2773	UPI000041A257	2	108	43.6	55	6295	8.9	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F2 isoform 2c
2773	P56134-2	2	108	27.3	88	10363	9.9	Isoform 2 of P56134
2773	P56134	2	108	25.5	94	10918	9.7	ATP synthase f chain, mitochondrial
2774	Q0VGL1	2	6	25.3	99	10741	6.5	Similar to CG14977-PA
2775	Q13636	2	3	25.3	194	21569	7.1	Ras-related protein Rab-31
2775	UPI00000729DB	2	3	25.1	195	21700	7.1	RAB31, member RAS oncogene family
2775	Q53EY4	2	3	25.1	195	21686	7.1	RAB31, member RAS oncogene family variant
2776	Q9C005	2	7	25.3	99	11250	4.9	Dpy-30-like protein
2777	P62304	2	28	25	92	10804	9.4	Small nuclear ribonucleoprotein E
2778	Q49AN9	2	17	29.7	64	7101	7.2	SNRPG protein
2778	P62308	2	17	25	76	8496	8.9	Small nuclear ribonucleoprotein G

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
2779	Q8TBQ9	2	36	25	72	8060	9	Transmembrane protein 167 precursor
2780	P63172	2	10	24.8	113	12452	5.1	Dynein light chain Tctex-type 1
2781	O15155	2	8	24.6	118	13289	9.1	BET1 homolog
2782	Q96DE5	2	3	24.5	110	11667	5	Uncharacterized protein C10orf104
2783	UPI0000470B2C	2	5	24.8	125	14703	10.9	39S ribosomal protein L55, mitochondrial precursor (L55mt) (MRP-L55).
2783	Q7Z7F7	2	5	24.2	128	15128	11.2	39S ribosomal protein L55, mitochondrial precursor
2783	Q7Z7F7-2	2	5	18.9	164	18903	11	Isoform 2 of Q7Z7F7
2784	UPI000066D9CA	2	2	26.7	90	9536	9.1	Nonhistone chromosomal protein HMG-14 (High-mobility group nucleosome- binding domain-containing protein 1).
2784	UPI000013E8E4	2	2	26.7	90	9561	9.4	UPI000013E8E4 UniRef100 entry
2784	P05114	2	2	24	100	10659	9.6	Nonhistone chromosomal protein HMG-14
2784	UPI00001AEDD6	2	2	24	100	10659	9.5	PREDICTED: similar to Nonhistone chromosomal protein HMG-14 (High-mobility group nucleosome-binding domain-containing protein 1)
2784	Q6NSG7	2	2	24	100	10689	9.6	High-mobility group nucleosome binding domain 1
2784	Q3B790	2	2	24	100	10675	9.5	High-mobility group nucleosome binding domain 1
2784	UPI0000206EC6	2	2	20.7	116	12435	9.4	Nonhistone chromosomal protein HMG-14 (High-mobility group nucleosome- binding domain-containing protein 1).
2784	UPI0000DD82D7	2	2	14.2	169	17681	10	PREDICTED: similar to Nonhistone chromosomal protein HMG-14 (High-mobility group nucleosome-binding domain-containing protein 1)
2785	Q96F85	2	2	23.8	164	18648	8	Uncharacterized protein C2orf32
2786	Q9NPA8	2	4	23.8	101	11529	9.3	Enhancer of yellow 2 homolog
2786	UPI0000503EA4	2	4	23.8	101	11526	9.3	enhancer of yellow 2 homolog
2787	P23297	2	16	23.4	94	10546	4.5	Protein S100-A1
2787	Q5T7Y6	2	16	15	147	15895	4.5	S100 calcium binding protein A1
2788	P51808	2	6	23.3	116	13062	5.7	Dynein light chain Tctex-type 3
2788	UPI0000211E80	2	6	17.8	152	16979	5.9	Dynein light chain Tctex-type 3 (T-complex-associated testis-expressed 1-like) (Protein 91/23).
2789	UPI000013CABC	2	14	23.2	164	18111	6.9	PREDICTED: similar to peptidylprolyl isomerase A isoform 1
2790	P10114	2	8	23	183	20615	4.8	Ras-related protein Rap-2a precursor
2791	P82921	2	4	23	87	10742	10.2	Mitochondrial 28S ribosomal protein S21
2792	Q9Y3L5	2	5	23	183	20745	4.9	Ras-related protein Rap-2c precursor
2793	Q8WW01	2	3	22.8	171	18641	4.6	tRNA-splicing endonuclease subunit Sen15
2794	P17096	2	11	22.4	107	11676	10.3	High mobility group protein HMG-I/HMG-Y (HMG-
2794	UPI0000D6142E	2	11	13.4	179	19552	11.6	High mobility group protein HMG-I/HMG-Y (HMG-I(Y)) (High mobility group AT-hook protein 1) (High mobility group protein A1) (High mobility group protein-R).
2794	P17096-3	2	11	13.4	179	19694	11.7	Isoform HMG
2795	P20339	2	3	22.3	215	23659	8.1	Ras-related protein Rab-5A
2796	Q9H0N5	2	3	22.3	103	11761	7.6	Pterin-4-alpha-carbinolamine dehydratase 2
2796	UPI000013F545	2	3	17.7	130	14365	9.1	pterin-4 alpha-carbinolamine dehydratase 2
2797	Q5JVG7	2	4	22.2	72	8839	9.2	Hypothetical protein DKFZp566O173
2797	Q9Y6M9	2	4	8.9	179	21831	8.4	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9
2798	A2IDD8	2	8	22.1	140	16241	6.6	Vesicle-associated membrane protein 4
2798	O75379	2	8	22	141	16397	7.4	Vesicle-associated membrane protein 4
2799	P61457	2	2	22.1	104	12000	6.8	Pterin-4-alpha-carbinolamine dehydratase
2799	Q6FGB3	2	2	22.1	104	12010	6.8	PCBD protein
2800	Q9UK76	2	4	22.1	154	16015	5.6	Hematological and neurological expressed 1 protein
2800	UPI0000456B01	2	4	22.1	154	16080	8.5	Hematological and neurological expressed 1 protein (Androgen-regulated protein 2).
2800	Q9UK76-2	2	4	18.8	181	19916	8.3	Isoform 2 of Q9UK76
2801	Q5RI15	2	7	22	118	13291	8.8	Protein FAM36A
2801	Q5RI15-2	2	7	20	130	14669	8.8	Isoform 2 of Q5RI15
2802	O15514	2	3	21.8	142	16311	4.8	DNA-directed RNA polymerase II 16 kDa polypeptide
2803	Q9Y6G3	2	7	21.8	142	16661	8.4	Mitochondrial 28S ribosomal protein S32, mitochondrial precursor
2803	UPI000016020B	2	7	21.8	142	16602	7	mitochondrial ribosomal protein L42 isoform b
2804	P33947	2	15	21.7	212	24422	8.7	ER lumen protein retaining receptor 2
2805	Q5QPM4	2	7	21.7	106	11487	10.4	Proteasome (Prosome, macropain) inhibitor subunit 1
2805	UPI0000D61016	2	7	13.9	165	18335	6.3	Proteasome inhibitor PI31 subunit (hPI31).
2805	UPI000006D075	2	7	10.4	222	24393	10.2	Proteasome inhibitor PI31 subunit (hPI31).
2805	Q5QPM7	2	7	8.7	263	28957	6.4	Proteasome (Prosome, macropain) inhibitor subunit 1
2805	UPI000013279C	2	7	8.5	271	29773	5.7	proteasome inhibitor subunit 1 isoform 1
2805	Q92530	2	7	8.5	271	29817	5.7	Proteasome inhibitor PI31 subunit
2806	Q9Y5J9	2	5	21.7	83	9344	5.1	Mitochondrial import inner membrane translocase subunit Tim8 B
2807	P14649	2	2	21.6	208	22764	5.7	Myosin light polypeptide 6B
2808	P62699	2	4	21.5	121	13842	7.3	Protein yippee-like 5

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
2809	UPI00006C034D	2	2	21.5	293	32072	5.4	PREDICTED: similar to Heterogeneous nuclear ribonucleoprotein C-like 1 (hnRNP core protein C-like 1)
2810	Q53TK7	2	6	34.4	61	6700	8.2	Hypothetical protein ACYP2
2810	P00820	2	6	21.2	99	10992	9.6	Acylphosphatase-2
2810	P14621	2	6	21.2	99	11140	9.5	Acylphosphatase-2
2811	P60891	2	4	20.8	318	34834	7	Ribose-phosphate pyrophosphokinase I
2811	Q53FW2	2	4	20.8	318	34864	6.8	Phosphoribosyl pyrophosphate synthetase 1 variant
2812	P13929	2	32	20.7	434	46987	7.7	Beta-enolase
2812	UPI0000169F85	2	32	20.7	434	46932	7.7	Beta-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Muscle-specific enolase) (MSE) (Skeletal muscle enolase) (Enolase 3).
2812	UPI0000161C26	2	32	20.7	434	46959	7.7	enolase 3
2813	UPI0000457013	2	5	21.9	319	33784	8.7	Poly(rC)-binding protein 3 (Alpha-CP3).
2813	P57721-5	2	5	21.9	319	33814	8.5	Isoform 5 of P57721
2813	P57721-4	2	5	20.7	338	35810	8.1	Isoform 4 of P57721
2813	P57721	2	5	20.6	339	35938	8.1	Poly(rC)-binding protein 3
2813	Q5MJP6	2	5	19.4	361	38153	8.1	Poly(RC) binding protein 3
2814	Q3MHD2	2	5	20.6	131	14328	5.9	LSM12 protein
2814	Q96NL5	2	5	13.8	195	21701	7.8	CDNA FLJ30656 fis, clone DFNES2000292
2815	P55854	2	23	20.4	103	11637	5.5	Small ubiquitin-related modifier 3 precursor
2816	Q9NZ45	2	4	20.4	108	12199	9.1	Zinc finger CDGSH domain-containing protein 1
2817	O14519	2	7	20	115	12365	9.4	Cyclin-dependent kinase 2-associated protein 1
2818	Q9BTT4	2	3	20	135	15688	6.2	Mediator of RNA polymerase II transcription, subunit 10 homolog
2819	Q9BV81	2	3	20	110	12017	10.1	Transmembrane protein 93
2820	P11234	2	3	19.9	206	23409	6.6	Ras-related protein Ral-B precursor
2820	Q6ZS74	2	3	18.1	227	25710	8.7	CDNA FLJ45773 fis, clone NETRP2003448, highly similar to Ras-related protein RAL-B
2821	Q9UQL0	2	3	26.6	109	12463	7.9	Ubiquitin-conjugating enzyme 1 isoform
2821	UPI0000D60F6C	2	3	19.9	146	16490	8.1	Ubiquitin-conjugating enzyme E2 D1 (EC 6.3.2.19) (Ubiquitin-protein ligase D1) (Ubiquitin carrier protein D1) (UbcH5) (Ubiquitin- conjugating enzyme E2-17 kDa 1) (E2(17)KB 1).
2821	P51668	2	3	19.7	147	16602	7.4	Ubiquitin-conjugating enzyme E2 D1 (EC 6.3.2.19) (Ubiquitin-protein ligase D1) (Ubiquitin carrier protein D1) (UbcH5) (Ubiquitin- conjugating enzyme E2-17 kDa 1) (E2(17)KB 1)
2821	Q9Y2X8	2	3	19.7	147	16649	7.4	Ubiquitin-conjugating enzyme E2 D4
2822	Q6P5R6	2	7	19.7	122	14606	9.4	Ribosomal protein L22-like 1
2823	P35609	2	24	19.6	894	103854	5.5	Alpha-actinin-2
2824	O95139	2	5	19.5	128	15489	9.6	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 6
2825	Q9P2X0	2	10	23.9	92	10094	5.9	Dolichol-phosphate mannosyltransferase subunit 3
2825	Q6P184	2	10	20.8	106	11564	6	DPM3 protein
2825	Q3SX58	2	10	19.5	113	12339	6	DPM3 protein
2826	O14966	2	2	19.2	203	23155	7.2	Ras-related protein Rab-7L1
2826	Q53EX5	2	2	19.2	203	23139	7.2	RAB7, member RAS oncogene family-like 1 variant
2827	P18077	2	17	19.1	110	12538	11.1	60S ribosomal protein L35a
2828	Q96IX5	2	10	19	58	6458	9.8	Up-regulated during skeletal muscle growth protein 5
2828	UPI00001618AA	2	10	19	58	6617	9.9	UPI00001618AA UniRef100 entry
2829	UPI00001AE467	2	6	20.6	102	11138	7.3	blocked early in transport 1 homolog (S. cerevisiae) like
2829	Q9NYM9	2	6	18.9	111	12388	8.2	BET1-like protein
2830	UPI0000DD7B6E	2	32	33.3	72	8132	11.1	PREDICTED: similar to 60S ribosomal protein L22 (Heparin-binding protein HBp15)
2830	P35268	2	32	18.8	128	14787	9.2	60S ribosomal protein L22
2830	Q7Z4W8	2	32	18.8	128	14818	9.3	Heparin-binding protein HBp15
2831	Q9BQ61	2	5	18.8	176	18419	9.4	Uncharacterized protein C19orf43
2832	P14854	2	11	18.6	86	10192	7	Cytochrome c oxidase subunit VIb isoform 1
2833	P29777	2	2	18.6	354	40087	5.9	Guanine nucleotide-binding protein G(o) subunit alpha 2
2833	UPI000016A9CA	2	2	18.6	354	40073	5.9	guanine nucleotide binding protein, alpha activating polypeptide O
2834	P62861	2	15	18.6	59	6648	12.1	40S ribosomal protein S30
2835	Q02539	2	5	18.6	215	21842	11	Histone H1.1
2836	UPI000016062E	2	2	18.6	118	12951	9.6	PREDICTED: similar to BC003940 protein
2837	P01034	2	3	18.5	146	15799	8.8	Cystatin-C precursor
2838	Q9HAV0	2	3	18.5	340	37567	6	Guanine nucleotide-binding protein subunit beta 4
2839	Q96A48	2	2	18.3	142	15397	10.6	FKSG19
2840	Q9BRT3	2	2	18.3	115	12403	4.4	Uncharacterized protein C17orf37
2841	Q96A26	2	8	18.2	154	17342	9.8	E2-induced gene 5 protein
2842	O43573	2	2	17.9	134	14780	9.7	Methylmalonate semialdehyde dehydrogenase precursor
2842	Q53H94	2	2	4.5	535	57826	8.5	Aldehyde dehydrogenase 6A1 variant
2842	Q53FN8	2	2	4.5	535	57967	8.6	Aldehyde dehydrogenase 6A1 variant
2842	Q02252	2	2	4.5	535	57840	8.5	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial precursor

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
2843	Q9GZM3	2	4	18.3	115	13074	6.3	RPB11b1alpha protein
2843	P52435	2	4	17.9	117	13293	5.9	DNA-directed RNA polymerase II subunit J
2843	Q9H1A6	2	4	16.5	127	14131	5.9	RPB11a protein
2843	Q0VGM6	2	4	15.2	138	15027	6.9	MGC13098 protein
2843	Q8IZ67	2	4	13.1	160	17172	6.9	MGC13098 protein
2843	UPI0000D61CA1	2	4	11.8	178	18673	6.2	DNA-directed RNA polymerase II subunit J (EC 2.7.7.6) (DNA-directed RNA polymerase II 13.3 kDa polypeptide) (RPB11).
2843	Q6PJD2	2	4	11.7	179	18885	6.4	MGC13098 protein
2843	Q59FR2	2	4	11.7	180	19038	6.7	MGC13098 protein variant
2844	Q9NR33	2	4	17.9	117	12209	4.9	DNA polymerase epsilon subunit 4
2845	O14880	2	23	17.8	152	16516	9.4	Microsomal glutathione S-transferase 3
2845	Q53GB9	2	23	17.8	152	16530	9.4	Microsomal glutathione S-transferase 3 variant
2846	Q75M90	2	2	17.7	113	12749	10.1	Hypothetical protein HSPC268
2846	Q96HJ9	2	2	17.7	113	12733	10.1	Hypothetical protein HSPC268
2847	Q9Y244	2	3	17.7	141	15789	5.1	Proteasome maturation protein
2847	UPI0000D61A56	2	3	15.6	160	18042	4.9	Proteasome maturation protein (Proteassemblin) (Protein UMP1 homolog) (hUMP1) (Voltage-gated K channel beta subunit 4.1).
2848	P78537	2	4	17.6	125	14311	8.2	Biogenesis of lysosome-related organelles complex-1 subunit 1
2849	UPI00001D7C91	2	2	17.6	262	28060	8.9	UPI00001D7C91 UniRef100 entry
2850	Q7Z3H5	2	3	20.4	323	37501	7.1	Hypothetical protein DKFZp686O0215
2850	UPI0000140DA1	2	3	19.7	335	38275	6.2	Mitogen-activated protein kinase 3 (EC 2.7.11.24) (Extracellular signal-regulated kinase 1) (ERK-1) (Insulin-stimulated MAP2 kinase) (MAP kinase 1) (MAPK 1) (p44-ERK1) (ERT2) (p44-MAPK) (Microtubule- associated protein 2 kinase).
2850	UPI0000D579B4	2	3	18.5	357	40088	7.5	mitogen-activated protein kinase 3 isoform 2
2850	P27361	2	3	17.4	379	43136	6.8	Mitogen-activated protein kinase 3
2851	Q6QN92	2	3	24	125	13813	4.3	Mitochondrial glycine cleavage system H-protein
2851	P23434	2	3	17.3	173	18911	4.9	Glycine cleavage system H protein, mitochondrial precursor
2851	UPI000013FAFB	2	3	17.3	173	18885	4.9	glycine cleavage system protein H (aminomethyl carrier)
2851	Q6IAT2	2	3	17.3	173	19026	4.9	GCSH protein
2852	Q9H7C9	2	4	17.2	122	13332	8.4	UPF0366 protein C11orf67
2853	Q6ZSR9	2	4	17.1	216	23110	8.4	CDNA FLJ45252 fis, clone BRHIP2011199
2854	Q9Y3C4-2	2	4	21.1	142	16093	6.3	Isoform 2 of Q9Y3C4
2854	Q9Y3C4	2	4	17.1	175	19661	6.8	TP53RK-binding protein
2854	Q9Y3C4-3	2	4	14	214	23854	7.4	Isoform 3 of Q9Y3C4
2855	O96007	2	3	17	188	20944	5.4	Molybdenum cofactor synthesis protein 2 large subunit
2856	P84101	2	3	16.9	59	6900	10.4	Small EDRK-rich factor 2
2857	Q8TCD5	2	3	16.9	201	23383	6.6	5'(3')-deoxyribonucleotidase, cytosolic type
2858	P61769	2	26	16.8	119	13715	6.5	Beta-2-microglobulin precursor [Contains: Beta-2-microglobulin variant pI 5.3]
2858	Q6IAT8	2	26	16.8	119	13697	6.5	B2M protein
2859	P06703	2	66	16.7	90	10180	5.5	Protein S100-A6
2860	Q6P1L8	2	3	16.6	145	15948	10.2	39S ribosomal protein L14, mitochondrial precursor
2861	Q9BQ15	2	2	16.6	211	22338	9.1	Oligonucleotide/oligosaccharide-binding fold-containing protein 2B
2862	UPI0000456FC5	2	5	16.5	659	71779	4.9	Opioid growth factor receptor (OGFr) (Zeta-type opioid receptor) (7-60 protein).
2863	P00167-2	2	3	22.4	98	11268	5.1	Isoform 2 of P00167
2863	Q59F44	2	3	16.7	132	14572	5.7	Cytochrome b-5 isoform 1 variant
2863	P00167	2	3	16.4	134	15330	5	Cytochrome b5
2864	Q6IAZ6	2	6	16.8	167	19608	5.9	RGS10 protein
2864	O43665	2	6	16.2	173	20236	5.5	Regulator of G-protein signaling 10
2864	Q96GN0	2	6	15.5	181	21210	7.5	Regulator of G-protein signalling 10
2865	O43924	2	2	16	150	17420	5.7	Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit delta
2866	Q9Y5T4	2	3	16	150	16383	10.1	DnaJ homolog subfamily C member 15
2867	Q53HV0	2	8	15.9	346	38954	7.9	SPFH domain family, member 1 variant
2868	Q9NV35	2	2	15.9	164	18609	6.1	Probable 7,8-dihydro-8-oxoguanine triphosphatase NUDT15
2869	P61966	2	2	15.8	158	18733	5.7	AP-1 complex subunit sigma-1A
2870	Q9NPJ3	2	5	15.7	140	14960	9.1	Thioesterase superfamily member 2
2871	Q96E14	2	3	15.6	147	15865	7.9	Uncharacterized protein C16orf75
2872	Q9BY50	2	10	15.6	192	21542	9.2	Signal peptidase complex catalytic subunit SEC11C
2873	UPI0000D616EE	2	6	15.7	102	11528	5.3	U6 snRNA-associated Sm-like protein LSm7.
2873	Q9UK45	2	6	15.5	103	11602	5.3	U6 snRNA-associated Sm-like protein LSm7
2874	Q9HD34	2	5	15.4	91	10758	10.7	LYR motif-containing protein 4
2875	UPI00006C196D	2	26	15.4	136	15556	10.6	PREDICTED: similar to 60S ribosomal protein L35
2876	Q13541	2	2	15.3	118	12580	5.5	Eukaryotic translation initiation factor 4E-binding protein 1
2877	Q9UBK9	2	5	15.3	157	18246	7.6	Protein UXT
2878	Q86XN0	2	8	15.2	145	15961	8.7	MRPL43 protein
2879	Q9UBY6	2	3	16.2	154	16970	4.3	Kinase-related protein isoform 2

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
2879	Q05B97	2	3	15.1	166	18152	4.4	MYLK protein
2879	Q05B98	2	3	15	167	18253	4.4	MYLK protein
2879	Q68DK3	2	3	14.8	169	18482	4.4	Hypothetical protein DKFZp686I10125
2879	Q3B765	2	3	11	227	24647	4.5	MYLK protein
2879	Q05D81	2	3	10.6	236	25872	5	MYLK protein
2879	Q6ZNP1	2	3	4.4	572	62282	4.8	CDNA FLJ27411 fis, clone WMC04903, highly similar to Myosin light chain kinase, smooth muscle and non-muscle isozymes
2879	UPI0000E4C8FD	2	3	1.4	1794	197398	6.5	myosin light chain kinase isoform 3B
2879	UPI0000E4C8FC	2	3	1.4	1845	203054	6.2	myosin light chain kinase isoform 2
2879	UPI0000D61B67	2	3	1.4	1842	202643	6.1	Myosin light chain kinase, smooth muscle (EC 2.7.11.18) (MLCK) (Telokin) (Kinase-related protein) (KRP).
2879	UPI0000457165	2	3	1.4	1845	203085	6.1	Myosin light chain kinase, smooth muscle (EC 2.7.11.18) (MLCK) (Telokin) (Kinase-related protein) (KRP).
2879	Q15746-5	2	3	1.4	1841	202568	6.2	Isoform 4 of Q15746
2879	Q15746-4	2	3	1.4	1794	197631	6.8	Isoform 3B of Q15746
2879	Q15746-2	2	3	1.4	1845	203127	6.2	Isoform 2 of Q15746
2879	UPI0000D61B66	2	3	1.3	1864	205349	6.8	Myosin light chain kinase, smooth muscle (EC 2.7.11.18) (MLCK) (Telokin) (Kinase-related protein) (KRP).
2879	UPI0000457163	2	3	1.3	1914	210744	6.1	Myosin light chain kinase, smooth muscle (EC 2.7.11.18) (MLCK) (Telokin) (Kinase-related protein) (KRP).
2879	UPI000020A0AE	2	3	1.3	1914	210713	6.2	myosin light chain kinase isoform 1
2879	UPI000013E30E	2	3	1.3	1863	205057	6.5	myosin light chain kinase isoform 3A
2879	Q15746-6	2	3	1.3	1913	210643	6.2	Isoform Del
2879	Q15746-3	2	3	1.3	1863	205277	6.8	Isoform 3A of Q15746
2879	Q15746	2	3	1.3	1914	210772	6.2	Myosin light chain kinase, smooth muscle
2880	Q9Y5J5	2	5	15	127	13891	9.7	Pleckstrin homology-like domain family A member 3
2881	P52566	2	2	14.9	201	22988	5.2	Rho GDP-dissociation inhibitor 2
2882	Q13158	2	2	14.9	208	23279	5.7	Protein FADD
2883	Q5T091	2	26	15.5	187	21024	8.7	RER1 retention in endoplasmic reticulum 1 homolog
2883	O15258	2	26	14.8	196	22958	9.5	Protein RER1
2883	UPI000049DC68	2	26	14.1	205	23050	6.9	Protein RER1.
2883	UPI0000D61E27	2	26	13.6	213	24689	9.6	Protein RER1.
2883	Q9P0H9	2	26	13.6	214	24817	9.6	RER1 protein
2884	Q14353	2	3	14.8	236	26318	6.1	Guanidinoacetate N-methyltransferase
2885	P52657	2	10	14.7	109	12457	6.8	Transcription initiation factor IIA gamma chain
2886	Q86WX3	2	4	14.7	136	15434	10.7	40S ribosomal protein S19-binding protein 1
2887	O95989	2	2	14.5	172	19471	6.4	Diphosphoinositol polyphosphate phosphohydrolase 1
2888	UPI000015FD55	2	24	14.8	155	17219	11.1	PREDICTED: similar to 60S ribosomal protein L29 (Cell surface heparin-binding protein HIP)
2888	P47914	2	24	14.5	159	17752	11.7	60S ribosomal protein L29
2888	Q6IPI1	2	24	14.3	161	17951	11.7	Ribosomal protein L29
2889	P62487	2	3	14.5	172	19294	5.5	DNA-directed RNA polymerase II 19 kDa polypeptide
2890	P82663	2	5	14.5	173	20116	8.8	Mitochondrial 28S ribosomal protein S25
2891	Q6ZR81	2	10	18.5	135	15343	10.7	CDNA FLJ46566 fis, clone THYMU3040829, moderately similar to Cold- inducible RNA-binding protein
2891	Q14011	2	10	14.5	172	18648	9.5	Cold-inducible RNA-binding protein
2892	Q16674	2	3	14.5	131	14509	8.8	Melanoma-derived growth regulatory protein precursor
2893	Q5JS54	2	6	14.5	138	15196	6.9	Chromosome 6 open reading frame 86
2894	Q8WWX9	2	4	14.5	145	16185	5.5	Thioredoxin-like selenoprotein M precursor
2894	UPI0000D62134	2	4	14.5	145	16134	5.6	Thioredoxin-like selenoprotein M precursor (Protein SelM).
2894	UPI000016788A	2	4	14.5	145	16082	5.5	selenoprotein M precursor
2895	Q92882	2	4	14.5	214	23787	5.7	Osteoclast-stimulating factor 1
2895	UPI0000130EB3	2	4	14.5	214	23799	5.4	osteoclast stimulating factor 1
2896	P11217	2	2	14.4	842	97092	7	Glycogen phosphorylase, muscle form
2897	P49006	2	9	14.4	195	19529	4.7	MARCKS-related protein
2898	O43181	2	2	14.3	175	20108	10.3	NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial precursor
2899	UPI0000D624C1	2	6	14.2	134	15535	8.1	Golgin subfamily A member 7 (Golgi complex-associated protein of 16 kDa).
2899	Q7Z5G4-2	2	6	14.2	134	15578	8.4	Isoform 2 of Q7Z5G4
2899	Q7Z5G4	2	6	13.9	137	15824	7	Golgin subfamily A member 7
2900	O15235	2	3	13.8	138	15173	10.3	28S ribosomal protein S12, mitochondrial precursor
2901	O43598	2	5	13.8	174	19108	5	c-Myc-responsive protein Rcl
2902	Q3ZCS0	2	4	13.8	189	21054	9.6	TP53I11 protein
2902	UPI00004564BB	2	4	8.7	298	32348	10.5	p53-induced protein
2902	Q99785	2	4	8.7	299	32373	10.6	Hypothetical protein
2903	Q6P161	2	8	13.8	138	15819	9.6	39S ribosomal protein 54, mitochondrial precursor
2904	Q9Y2R5	2	4	13.8	130	14502	9.8	28S ribosomal protein S17, mitochondrial precursor
2905	Q96EH3	2	4	13.7	234	26170	5.5	Uncharacterized protein C7orf30
2906	Q53G08	2	3	13.5	185	21370	5.6	DNA replication complex GINS protein PSF2 variant

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
2906	Q9Y248	2	3	13.5	185	21428	5.4	DNA replication complex GINS protein PSF2
2907	Q5SXM8	2	3	13.5	178	19204	9.8	Chromosome 9 open reading frame 151
2908	Q6IQ22	2	3	13.5	244	27248	8.4	Ras-related protein Rab-12
2909	A4D0R9	2	4	13.4	418	46302	4.9	Protein kinase, cAMP-dependent, regulatory, type II, beta
2909	Q6DHZ2	2	4	13.4	418	46348	4.9	Protein kinase, cAMP-dependent, regulatory, type II, beta
2909	P31323	2	4	13.4	418	46346	4.9	cAMP-dependent protein kinase type II-beta regulatory subunit
2910	O43708	2	4	13.4	216	24182	8.5	Maleylacetoacetate isomerase
2910	UPI000013C6F0	2	4	13.4	216	24114	7.7	glutathione transferase zeta 1 isoform 1
2910	Q6IB17	2	4	13.4	216	24083	8.3	GSTZ1 protein
2911	Q9NRP0	2	33	13.4	149	16829	9.1	DC2
2911	Q9P1R4	2	33	12.5	160	17895	9.5	HDCMD45P
2911	Q9P075	2	33	12	167	18667	9.5	HSPC307
2912	Q9BWN5	2	2	14.3	224	23195	8.3	IlvB (Bacterial acetolactate synthase)-like
2912	A1L0T0	2	2	13.3	241	25613	9.6	FLJ39061 protein
2912	Q59GP4	2	2	7.5	427	45645	8.9	IlvB (Bacterial acetolactate synthase)-like isoform 1 variant
2912	Q99651	2	2	5.1	632	67924	8.1	Acetolactate synthase homolog
2912	Q96F08	2	2	5.1	632	67869	8	IlvB (Bacterial acetolactate synthase)-like
2912	O43341	2	2	5.1	632	67868	8.1	IlvB-like protein
2913	UPI0000D62162	2	3	22	123	13891	7	DNA-directed RNA polymerase III subunit 22.9 kDa polypeptide (EC 2.7.7.6) (RPC8).
2913	UPI0000511A82	2	3	22	123	13816	7	polymerase (RNA) III (DNA directed) polypeptide H (22.9kD) isoform c
2913	Q9Y535	2	3	13.2	204	22918	4.6	DNA-directed RNA polymerase III subunit 22.9 kDa polypeptide
2914	UPI000013EC4C	2	11	13.3	181	20792	9.6	jagunal homolog 1
2914	Q8N5M9	2	11	13.1	183	21125	9.7	Protein jagunal homolog 1
2914	Q96SW1	2	11	13.1	183	21072	9.6	CDNA FLJ14602 fis, clone NT2RP1000191
2915	UPI000049DF0A	2	5	17.5	120	13954	9.9	39S ribosomal protein L30, mitochondrial precursor (L30mt) (MRP-L30).
2915	Q8TCC3-3	2	5	16	131	15191	10.3	Isoform 3 of Q8TCC3
2915	Q0D2Q7	2	5	13	161	18576	10	Mitochondrial ribosomal protein L30
2915	Q8TCC3	2	5	13	161	18546	10	39S ribosomal protein L30, mitochondrial precursor
2915	UPI0000D61205	2	5	12.3	171	19668	10.1	39S ribosomal protein L30, mitochondrial precursor (L30mt) (MRP-L30).
2916	Q8N183	2	3	13	169	19856	9	Mimitin, mitochondrial precursor
2917	Q5SRD1	2	5	15.8	171	17870	7.9	Translocase of inner mitochondrial membrane 23 homolog B
2917	O14925	2	5	12.9	209	21943	8.6	Mitochondrial import inner membrane translocase subunit Tim23
2917	Q53FF8	2	5	12.9	209	21953	8.6	Translocase of inner mitochondrial membrane 23 (Yeast) homolog
2917	UPI0000DD7FFF	2	5	10.5	257	28048	9.4	PREDICTED: similar to Mitochondrial import inner membrane translocase subunit Tim23 isoform 1
2918	Q5TZX9	2	2	12.9	232	26616	9.2	Vesicle transport through interaction with t-SNAREs homolog 1B
2918	Q9UEU0	2	2	12.9	232	26688	9	Vesicle transport through interaction with t-SNAREs homolog 1B
2919	Q7Z4A2	2	3	12.9	233	24812	6.8	Ankyrin repeat and SOCS box-containing 9
2919	Q9BVF5	2	3	11.9	252	26849	6.6	ASB9 protein
2919	Q96DX5-2	2	3	11.5	262	27902	6.5	Isoform 2 of Q96DX5
2919	Q96DX5	2	3	10.2	294	31858	7	Ankyrin repeat and SOCS box protein 9
2920	Q9BVK8	2	3	12.9	224	25261	7.7	Transmembrane protein 147
2921	Q9H204	2	2	12.9	178	19520	5.6	Mediator of RNA polymerase II transcription subunit 28
2922	Q9P0L0	2	4	12.9	249	27893	8.6	Vesicle-associated membrane protein-associated protein A
2923	Q9Y2Y0	2	3	12.9	163	18822	4.3	ADP-ribosylation factor-like protein 2-binding protein
2924	Q5JYY6	2	5	26.4	110	11926	5.2	Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 10
2924	Q8IZK9	2	5	19.2	151	16137	6	Hepatocellular carcinoma-associated protein p28-II (Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 10)
2924	Q5JYY5	2	5	15.7	185	20217	5.6	Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 10
2924	Q5JYY4	2	5	15	193	20808	6.6	Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 10
2924	O75832	2	5	12.8	226	24428	6.1	26S proteasome non-ATPase regulatory subunit 10
2924	Q5U0B2	2	5	12.8	226	24458	6.1	Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 10
2925	P41208	2	3	12.8	172	19738	5	Centrin-2
2926	Q96GX9	2	2	12.8	242	27125	7.1	APAF1-interacting protein
2926	UPI000006DF8A	2	2	12.8	242	27012	7.1	APAF1 interacting protein
2927	UPI00002263A9	2	3	12.8	156	16608	10	protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting, 4 (parvulin)

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
2928	Q6QNY1	2	2	12.7	142	15961	4.9	Biogenesis of lysosome-related organelles complex-1 subunit 2
2929	Q14197	2	6	12.6	206	23630	10.1	Immature colon carcinoma transcript 1 protein precursor
2930	UPI0000212024	2	7	13.8	160	17188	8.8	PRA1 family protein 2.
2930	O60831	2	7	12.4	178	19258	9.2	PRA1 family protein 2
2931	Q9BSB4	2	2	12.4	218	25003	6.1	Uncharacterized protein C12orf44
2931	Q9HAE2	2	2	12.4	218	24991	6.1	CDNA FLJ11773 fis, clone HEMBA1005852
2932	Q53GG5-2	2	3	12.3	316	34280	7.7	Isoform 2 of Q53GG5
2933	Q658V9	2	4	12.3	171	19673	6.9	Hypothetical protein DKFZp666A212
2933	Q9H671	2	4	7.2	291	32487	9.3	CDNA: FLJ22555 fis, clone HSI01193
2933	Q8WWC4	2	4	7.2	291	32545	9.2	Uncharacterized protein C2orf47
2934	O14949	2	5	12.2	82	9906	10.1	Ubiquinol-cytochrome c reductase complex ubiquinone-binding protein QP-C
2935	Q9BS40	2	5	12.2	222	25769	5.8	Latexin
2935	UPI000006FB86	2	5	12.2	222	25750	5.8	Latexin (Endogenous carboxypeptidase inhibitor) (ECI) (Tissue carboxypeptidase inhibitor) (TCI) (MUM).
2936	Q5HYI7	2	3	12	158	17541	8.1	Hypothetical protein DKFZp313L052
2936	UPI0000E20823	2	3	12	158	17569	8.1	metaxin 3
2936	UPI0000D61653	2	3	12	158	17580	7.4	metaxin 3
2937	Q5T6Z8	2	3	12	192	21860	5.3	Transmembrane protein 59
2937	Q6P5R1	2	3	9.6	239	27100	5	TMEM59 protein
2937	Q9BXS4	2	3	7.1	323	36223	5.1	Transmembrane protein 59 precursor
2938	Q5TCK0	2	2	12	175	18977	5.1	Polyamine-modulated factor 1
2938	Q6ZVE6	2	2	11.7	180	20258	8.6	CDNA FLJ42655 fis, clone BRACE3045033, moderately similar to Homo sapiens polyamine-modulated factor 1
2938	Q5TCK1	2	2	11.7	180	20230	8.5	Polyamine-modulated factor 1
2938	Q6P1K2	2	2	10.2	205	23339	5.5	Polyamine-modulated factor 1
2938	Q5TCK2	2	2	10	211	23769	7.3	Polyamine-modulated factor 1
2938	Q6P1K2-5	2	2	9.5	220	24032	8.3	Isoform 5 of Q6P1K2
2939	Q9UIS3	2	4	32.8	58	6427	8.4	Transforming growth factor-alpha
2939	Q53SK7	2	4	14.8	128	13879	7.8	Hypothetical protein TGFA
2939	P01135	2	4	11.9	160	17006	7.5	Transforming growth factor alpha precursor
2939	Q9BS56	2	4	11.9	159	16935	7.5	Transforming growth factor, alpha
2940	Q6ZRV1	2	8	11.9	243	26419	8	CDNA FLJ46073 fis, clone TESTI2001364, highly similar to Homo sapiens lactate dehydrogenase A -like
2941	Q9P0I2-2	2	3	14.2	219	24915	9.7	Isoform 2 of Q9P0I2
2941	Q9P0I2	2	3	11.9	261	29952	6.8	Transmembrane protein 111
2942	Q9Y584	2	2	11.9	194	20031	7.6	Mitochondrial import inner membrane translocase subunit Tim22
2943	Q7Z6U1	2	4	17.2	128	14434	9.8	TBP-like 1
2943	Q7Z6U2	2	4	13.5	163	18282	9.6	TBP-like 1
2943	P62380	2	4	11.8	186	20887	9.5	TATA box-binding protein-like protein 1
2944	Q96HR3	2	4	11.8	178	20277	8.3	Thyroid hormone receptor-associated protein 6
2945	P25686-3	2	2	11.7	324	35580	6	Isoform 3 of P25686
2946	Q5TEG0	2	2	11.7	222	24341	5.7	OTTHUMP00000017168
2946	UPI0000D614CC	2	2	9.5	275	30446	8.9	Enoyl-CoA hydratase domain-containing protein 1.
2946	UPI0000D614CB	2	2	9.1	286	31306	8.3	Enoyl-CoA hydratase domain-containing protein 1.
2946	Q9NZ30	2	2	9.1	286	31303	8.9	Uncharacterized hypothalamus protein HCDASE
2946	UPI000013EEE5	2	2	8.6	303	33155	8.2	Enoyl-CoA hydratase domain-containing protein 1.
2946	Q9NTX5	2	2	8.5	307	33698	8.2	Enoyl-CoA hydratase domain-containing protein 1
2947	Q96EY5-2	2	2	13.7	233	24532	8.3	Isoform 2 of Q96EY5
2947	Q96EY5-3	2	2	12.5	257	27050	9.4	Isoform 3 of Q96EY5
2947	Q96EY5	2	2	11.7	273	28783	8.9	Protein FAM125A
2948	Q969T4	2	4	11.6	207	22913	7.2	Ubiquitin-conjugating enzyme E2 E3
2949	Q96GD0	2	2	11.5	296	31698	6.5	Pyridoxal phosphate phosphatase
2949	UPI0000F2440E	2	2	11.4	298	31826	6.5	PYRIDOXAL PHOSPHATE PHOSPHATASE
2949	UPI0000F51D2A	2	2	11.1	306	32907	6.8	Pyridoxal phosphate phosphatase
2950	P59780	2	4	11.4	193	22017	5.2	AP-3 complex subunit sigma-2
2950	Q53H83	2	4	11.4	193	22147	5.2	Adaptor-related protein complex 3, sigma 2 subunit variant
2951	UPI0000112548	2	3	19.8	121	13492	4.8	frataxin
2951	Q16595	2	3	11.4	210	23135	8.7	Frataxin, mitochondrial precursor (Friedreich ataxia protein) (Fxn) [Contains: Frataxin intermediate form]
2952	P35754	2	4	11.3	106	11776	8.1	Glutaredoxin-1
2953	Q9NYS3	2	2	39.2	79	8443	9.7	Apoptosis-related protein PNAS-3
2953	UPI00003FE520	2	2	18.9	164	17248	9.3	exosome component 3 isoform 2
2953	Q9NQT5	2	2	11.3	275	29572	8.1	Exosome complex exonuclease RRP40
2954	Q9NWV4	2	2	11.2	160	18048	5	Uncharacterized protein C1orf123
2955	Q9NX00	2	2	11.2	188	19657	8	Transmembrane protein 160
2956	Q6UW68	2	4	11.1	189	21198	8.6	MBC3205
2957	Q7Z7H8	2	3	11.1	261	29297	9.6	39S ribosomal protein L10, mitochondrial precursor
2957	UPI000004FA30	2	3	11.1	261	29283	9.6	mitochondrial ribosomal protein L10 isoform a
2957	UPI000013DFCA	2	3	10.7	271	30307	9.2	mitochondrial ribosomal protein L10 isoform b
2958	Q8WZA0	2	5	11.1	190	21495	4.9	Protein LZIC
2959	Q9HC07	2	6	11.1	324	34906	7	Transmembrane protein 165

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
2960	P13796	2	2	11	627	70289	5.3	Plastin-2
2960	Q5TBN4	2	2	11	627	70289	5.4	Lymphocyte cytosolic protein 1
2960	Q53FI1	2	2	11	627	70259	5.3	L-plastin variant
2961	Q969E8	2	4	11	191	20894	4.4	Pre-rRNA-processing protein TSR2 homolog
2962	P11802	2	3	10.9	303	33730	7	Cell division protein kinase 4
2963	Q9NUP3	2	2	16.4	483	54025	6.2	CDNA FLJ11224 fis, clone PLACE1008273, moderately similar to COATOMER GAMMA SUBUNIT
2963	Q2NLA0	2	2	10.9	726	81483	6.6	COPG2 protein
2963	Q9H9B7	2	2	9.9	799	89387	5.7	CDNA FLJ12872 fis, clone NT2RP2003760, highly similar to COATOMER GAMMA SUBUNIT
2963	Q9UBF2	2	2	9.1	871	97622	5.8	Coatomer subunit gamma-2
2964	UPI0000D616A3	2	7	11.1	1256	145905	7	cytoplasmic FMR1 interacting protein 2
2964	Q96F07-2	2	7	11.1	1253	145673	7.1	Isoform 2 of Q96F07
2964	UPI0000D616A2	2	7	11	1258	146231	7.1	cytoplasmic FMR1 interacting protein 2
2964	Q96F07	2	7	10.9	1278	148398	7.3	Cytoplasmic FMR1-interacting protein 2
2965	Q9P032	2	2	10.9	175	20266	8.8	UPF0240 protein C6orf66
2966	Q16775	2	3	10.8	260	28860	7.3	Hydroxyacylglutathione hydrolase
2967	Q9NX20	2	6	10.8	251	28449	10.1	39S ribosomal protein L16, mitochondrial precursor
2968	UPI00001FBCE1	2	2	10.8	251	28137	5.7	PREDICTED: similar to Unc119c isoform 3
2969	O14521	2	3	10.7	159	17043	8.6	Succinate dehydrogenase [ubiquinone] cytochrome b small subunit, mitochondrial precursor
2969	UPI0000D62687	2	3	10.7	159	17043	8.6	Succinate dehydrogenase [ubiquinone] cytochrome b small subunit, mitochondrial precursor (CybS) (Succinate-ubiquinone reductase membrane anchor subunit) (QPs3) (CII-4) (Succinate dehydrogenase complex subunit D) (Succinate-ubiquinone oxidoreductase cytoch
2969	UPI000016179F	2	3	10.7	159	17004	8.6	PREDICTED: similar to Succinate dehydrogenase [ubiquinone] cytochrome b small subunit, mitochondrial precursor (CybS) (Succinate-ubiquinone reductase membrane anchor subunit) (QPs3) (CII-4) (Succinate dehydrogenase complex subunit D) (Succinate-ubiquinone oxi...
2969	Q9CXV1	2	3	10.7	159	17014	9.1	Succinate dehydrogenase [ubiquinone] cytochrome b small subunit, mitochondrial precursor
2970	Q9Y315	2	3	11	318	35231	8.9	Putative deoxyribose-phosphate aldolase
2970	Q53HN9	2	3	10.7	326	35837	9.1	2-deoxyribose-5-phosphate aldolase homolog
2971	Q7Z5U5	2	2	10.7	177	20848	8.7	CCDC25 protein
2971	Q86WR0	2	2	9.1	208	24479	6.8	Coiled-coil domain-containing protein 25
2972	Q13907	2	2	10.6	227	26319	6.4	Isopentenyl-diphosphate Delta-isomerase 1
2972	UPI0000F5342F	2	2	10.3	233	26862	6.4	Isopentenyl-diphosphate delta isomerase
2972	Q53GQ6	2	2	9.8	245	28345	6.6	Isopentenyl-diphosphate delta isomerase variant
2972	Q32Q13	2	2	9.8	246	28515	6.8	IDI1 protein
2973	Q53EQ5	2	2	10.6	208	23144	9	Hypothetical protein
2973	Q8N511	2	2	10.6	208	23130	9	Uncharacterized protein C17orf32
2974	Q6Y1H2	2	4	10.6	254	28368	9.5	Protein-tyrosine phosphatase-like member B
2974	UPI0000D61B65	2	4	10.6	255	28638	9.5	protein tyrosine phosphatase-like (proline instead of catalytic arginine), member b
2975	O95456-2	2	3	11.2	267	30288	7.8	Isoform 2 of O95456
2975	O95456	2	3	10.4	288	32854	7.2	Down syndrome critical region protein 2
2975	Q6FHA3	2	3	10.4	288	32840	7.2	DSCR2 protein
2976	Q53GL1	2	2	10.4	279	31920	8.9	Nicotinamide nucleotide adenylyltransferase 1 variant
2976	Q9HAN9	2	2	10.4	279	31932	8.9	Nicotinamide mononucleotide adenylyltransferase 1
2977	UPI00006C136D	2	2	13.3	181	20878	10.5	PREDICTED: similar to Protein C21orf70 homolog
2977	Q9NSI2-2	2	2	11.2	215	23945	10.9	Isoform B of Q9NSI2
2977	Q9NSI2	2	2	10.4	230	25456	11.1	Uncharacterized protein C21orf70
2978	P60520	2	3	10.3	117	13667	8.1	Gamma-aminobutyric acid receptor-associated protein-like 2 (GABA(A) receptor-associated protein-like 2)
2979	UPI0000E87021	2	3	11.2	242	27488	6.2	Spindlin-1
2979	UPI000049E0E5	2	3	11	246	28053	6	Spindlin-1 (Ovarian cancer-related protein).
2979	Q9Y657	2	3	10.3	262	29601	7	Spindlin-1
2980	P55210	2	2	10.2	303	34277	6.1	Caspase-7 precursor (EC 3.4.22.60) (CASP-7) (ICE-like apoptotic protease 3) (ICE-LAP3) (Apoptotic protease Mch-3) (CMH-1) [Contains: Caspase-7 subunit p20; Caspase-7 subunit p11]
2980	Q53YD5	2	2	10.2	303	34291	6.1	Caspase 7, apoptosis-related cysteine protease
2981	P82930	2	4	10.1	218	25650	10	Mitochondrial 28S ribosomal protein S34
2982	Q5JXX1	2	2	18.4	158	17617	10.4	Mortality factor 4 like 2
2982	Q5JXX2	2	2	16.4	177	19831	10	Mortality factor 4 like 2
2982	Q5JXX3	2	2	16.3	178	19902	10	Mortality factor 4 like 2
2982	Q15014	2	2	10.1	288	32308	9.7	Mortality factor 4-like protein 2
2982	Q53EY5	2	2	10.1	288	32312	9.7	MORF-related gene X variant
2983	Q9BT09	2	4	10.1	278	30748	5.5	Trinucleotide repeat-containing protein 5
2984	Q9NY12-2	2	3	11.1	199	20834	10.4	Isoform 2 of Q9NY12
2984	Q9NY12	2	3	10.1	217	22348	10.9	H/ACA ribonucleoprotein complex subunit 1
2985	Q9Y324	2	3	10.1	198	23370	9.7	rRNA-processing protein FCF1 homolog

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
2986	O14593-2	2	2	11	237	25580	4.4	Isoform RFX
2986	Q24JQ1	2	2	10.9	238	25652	4.4	Regulatory factor X-associated ankyrin-containing protein
2986	O14593	2	2	10	260	28102	4.5	DNA-binding protein RFXANK
2986	Q6IB23	2	2	10	260	28088	4.5	RFXANK protein
2987	Q59FA5	2	2	17.9	112	12320	7.4	Transgelin variant
2987	Q53GC9	2	2	10.9	184	20889	8.7	Transgelin variant
2987	Q01995	2	2	10	201	22611	8.8	Transgelin
2987	Q6FI52	2	2	10	201	22551	8.8	TAGLN protein
2988	Q53FM2	2	2	10	281	32162	6.8	Chromosome 1 open reading frame 48 variant
2988	Q96IY1	2	2	10	281	32130	6.8	Kinetochore-associated protein NSL1 homolog
2989	Q8WVC6	2	4	10	231	26550	9.6	Dephospho-CoA kinase domain-containing protein
2989	Q9BR71	2	4	10	231	26549	9.6	Dephospho-CoA kinase domain containing
2990	Q8N5M4	2	3	9.9	171	20013	8.9	Tetratricopeptide repeat domain 9C
2991	P07305	2	11	9.8	194	20863	10.8	Histone H1.0 (Histone H1(0))
2992	Q6FGR9	2	7	10.5	229	25695	7.6	ARHE protein
2992	Q6FGN7	2	7	10.5	229	25637	7.8	ARHE protein
2992	P61587	2	7	9.8	244	27368	8.5	Rho-related GTP-binding protein RhoE precursor
2992	UPI0000D61248	2	7	9.7	247	27782	8.6	Rho-related GTP-binding protein RhoE (Rho family GTPase 3) (Rnd3) (Rho8) (MemB protein).
2993	Q9BSK0	2	5	9.8	173	18914	9.6	MARVEL domain-containing protein 1
2994	Q9NX58	2	3	9.8	379	43615	9.5	Cell growth-regulating nucleolar protein
2994	UPI0000037C40	2	3	9.8	379	43634	9.6	hypothetical protein FLJ20425
2995	Q96N63	2	16	19.8	121	13202	7.2	CDNA FLJ31361 fis, clone MESAN2008460, highly similar to Homo sapiens SL15 protein mRNA
2995	Q96K24	2	16	19	126	13431	9	CDNA FLJ14836 fis, clone OVARC1001702
2995	UPI000013E72D	2	16	18.9	127	13615	9	Mannose-P-dolichol utilization defect 1 protein (Suppressor of Lec15 and Lec35 glycosylation mutation homolog) (SL15).
2995	Q9H3L2	2	16	11.4	211	22609	8.3	My008 protein
2995	O75352	2	16	9.7	247	26707	9.1	Mannose-P-dolichol utilization defect 1 protein
2995	UPI000013CCA4	2	16	9.7	247	26638	8.9	mannose-P-dolichol utilization defect 1
2995	Q9BUU8	2	16	9.7	247	26668	8.9	Mannose-P-dolichol utilization defect 1
2995	Q1HDL3	2	16	8	299	32006	7.6	HBeAg-binding protein 2 binding protein A
2996	Q6NVW3	2	2	9.7	278	29197	8.6	YRDC protein
2996	Q86U90	2	2	9.7	279	29328	8.6	YrdC domain-containing protein
2996	Q7L4E4	2	2	9.2	292	30663	9.1	YRDC protein
2997	O15400-2	2	3	10.5	239	27400	5.1	Isoform 2 of O15400
2997	O15400	2	3	9.6	261	29816	5.6	Syntaxin-7
2997	UPI0000161DE1	2	3	9.6	261	29846	5.6	syntaxin 7
2998	Q15796-2	2	5	10.3	438	49043	7.1	Isoform Short of Q15796
2998	Q15796	2	5	9.6	467	52306	6.6	Mothers against decapentaplegic homolog 2
2999	Q5U602	2	26	9.6	229	25698	7	RAB33B, member RAS oncogene family
2999	Q9H082	2	26	9.6	229	25717	7.2	Ras-related protein Rab-33B
3000	A2A2Q2	2	9	9.5	221	25490	9.1	Chromosome 20 open reading frame 44
3000	Q5T347	2	9	8.6	243	27909	9.1	Chromosome 20 open reading frame 44
3000	Q5T352	2	9	8.4	249	28939	8.8	Chromosome 20 open reading frame 44
3000	UPI0000456F84	2	9	7.7	273	31546	9	Basic FGF-repressed Zic-binding protein (bFZb).
3000	Q9NVA1-2	2	9	7.7	273	31517	8.8	Isoform 2 of Q9NVA1
3000	Q9NVA1	2	9	7	299	34572	8.8	Basic FGF-repressed Zic-binding protein
3000	Q3KRB6	2	9	7	299	34600	8.9	Chromosome 20 open reading frame 44
3000	UPI0000D61074	2	9	6.7	313	36249	8.6	Basic FGF-repressed Zic-binding protein (bFZb).
3001	P51809	2	13	9.5	220	24935	8.6	Synaptobrevin-like protein 1
3002	Q00403	2	3	9.5	316	34833	8.4	Transcription initiation factor IIB
3003	Q9H0T5	2	2	9.5	179	20317	6	Hypothetical protein DKFZp564C1362
3004	O75208	2	2	9.4	318	35509	5.9	Ubiquinone biosynthesis protein COQ9, mitochondrial precursor
3004	UPI0000D619F5	2	2	9.3	324	35968	5.6	Ubiquinone biosynthesis protein COQ9, mitochondrial precursor.
3005	Q6ICJ4	2	6	10	230	25948	7.5	Em:AP000351.3 protein
3005	P30712	2	6	9.4	244	27507	6.4	Glutathione S-transferase theta-2
3005	UPI000006DC51	2	6	9.4	244	27506	7	glutathione S-transferase theta 2 (GSTT2), mRNA
3005	Q6IB75	2	6	9.4	244	27532	7	GSTT2 protein
3006	Q6IAH4	2	5	9.4	224	25320	8.2	HCCA3 protein
3006	Q9NRV1	2	5	9.4	224	25279	7.6	X 003 protein
3006	Q9P1R6	2	5	8.2	256	28616	7.6	HDCMC29P
3006	Q969U7	2	5	8	264	29396	7	Tumor necrosis factor superfamily, member 5-induced protein 1
3007	Q8TB37-2	2	3	17.3	173	18209	10.1	Isoform 2 of Q8TB37
3007	Q8TB37	2	3	9.4	319	34083	9	Nucleotide-binding protein-like
3008	Q9NQT4	2	2	9.4	235	25249	7.6	Exosome complex exonuclease RRP46
3009	O00193	2	6	9.3	183	20333	4.7	Small acidic protein
3010	P29084	2	2	9.3	291	33044	9.7	Transcription initiation factor IIE subunit beta
3011	P84157-2	2	4	11.2	170	17493	4.1	Isoform 2 of P84157
3011	P84157-3	2	4	10.7	177	18207	4.1	Isoform 3 of P84157
3011	P84157	2	4	9.3	204	21466	4.3	Matrix-remodelling-associated protein 7
3012	Q4VXZ8	2	2	9.3	280	29484	8.9	2,4-dienoyl CoA reductase 2, peroxisomal
3012	Q9NUI1	2	2	8.9	292	30778	9.2	Peroxisomal 2,4-dienoyl-CoA reductase
3013	Q9UMY1	2	2	9.3	257	29426	9.7	Nucleolar protein 7

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
3014	O95105	2	2	9.2	262	29411	5.4	Tetratricopeptide repeat protein 33
3014	Q6PID6	2	2	9.2	262	29439	5.4	Tetratricopeptide repeat domain 33
3015	Q5TGA2	2	2	9.8	296	33085	5.6	Peptidyl-prolyl cis-trans isomerase
3015	Q9UNP9	2	2	9.6	301	33431	5.6	Peptidyl-prolyl cis-trans isomerase E
3015	Q3S611	2	2	9.2	314	35020	6.2	Cyclophilin-33B
3015	Q5TGA3	2	2	9.2	314	34991	6.4	Peptidyl-prolyl cis-trans isomerase
3016	Q9GZP9	2	7	9.2	239	27567	7.3	Derlin-2
3017	Q9Y5N6	2	2	9.1	252	28107	8.7	Origin recognition complex subunit 6
3018	Q53SH3	2	3	9	321	34862	5.3	Hypothetical protein ABI-2
3018	Q9NYB9-3	2	3	7.2	401	44409	7.3	Isoform 3 of Q9NYB9
3018	Q9NYB9-2	2	3	6.1	475	52446	6	Isoform 2 of Q9NYB9
3018	UPI0000DD7B05	2	3	5.8	497	53977	6.8	PREDICTED: similar to Abl interactor 2 (Abelson interactor 2) (Abi-2) (Abl-binding protein 3) (AblBP3) (Arg-binding protein 1) (ArgBP1)
3018	Q9NYB9	2	3	5.7	513	55663	6.2	Abl interactor 2
3019	Q6PJL1	2	2	9	466	49577	5.5	Nicotinate phosphoribosyltransferase domain containing 1
3019	Q9BRG0	2	2	8.2	514	54993	6	NAPRT1 protein
3019	Q6XQN4	2	2	8	525	56085	5.7	Nicotinate phosphoribosyltransferase-like protein
3019	Q6XQN5	2	2	7.8	538	57564	5.7	Nicotinate phosphoribosyltransferase-like protein
3019	UPI0000D62514	2	2	7.4	566	60234	5.8	nicotinate phosphoribosyltransferase domain containing 1
3019	Q6XQN6	2	2	7.4	567	60277	5.8	Nicotinate phosphoribosyltransferase domain-containing protein 1
3020	Q99757	2	10	9	166	18383	8.3	Thioredoxin, mitochondrial precursor
3021	O43731	2	7	8.9	214	25027	8.9	ER lumen protein retaining receptor 3
3021	Q4V750	2	7	8.6	220	25648	8.1	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3
3021	O43731-2	2	7	8.6	220	25690	8.1	Isoform 2 of O43731
3022	Q14331	2	4	8.9	258	29172	9	Protein FRG1
3023	Q15041	2	46	8.9	203	23363	9.3	ARL-6-interacting protein 1
3024	Q59H03	2	2	8.9	224	25336	6.2	Hypothetical protein
3024	Q86VN1	2	2	5.2	386	43817	7.2	Vacuolar protein sorting-associated protein 36
3025	Q8TAA5	2	2	8.9	225	25431	7.7	GrpE protein homolog 2, mitochondrial precursor
3026	P24385	2	2	8.8	295	33729	5	G1/S-specific cyclin-D1
3027	Q498A9	2	3	9.1	309	33412	5.2	NUBP1 protein
3027	Q32M30	2	3	8.8	320	34535	5.3	Nucleotide binding protein 1
3027	Q53FS7	2	3	8.8	320	34508	5.3	Nucleotide binding protein 1 (MinD homolog, E. coli) variant
3028	Q6IN77	2	3	10.5	887	100408	5	Transportin 2
3028	Q4LE60	2	3	8.8	1051	117677	5.6	TNPO2 variant protein
3029	Q5VZM0	2	4	8.8	194	22919	5.9	Ras-related GTP binding B
3029	Q7L523	2	4	5.4	313	36566	7.7	Ras-related GTP-binding protein A
3029	Q5VZM2-2	2	4	4.9	346	40172	6.1	Isoform 2 of Q5VZM2
3029	Q5VZM2	2	4	4.5	374	43250	6.2	Ras-related GTP-binding protein B
3030	Q8TCZ3	2	2	8.8	239	26802	5.3	Proteinase-related protein
3030	UPI000013D49E	2	2	6.8	309	35028	4.6	solute carrier family 7, member 6 opposite strand
3030	Q9H8R8	2	2	6.8	309	35102	4.6	CDNA FLJ13291 fis, clone OVARC1001176
3030	Q96CW6	2	2	6.8	309	35086	4.6	Solute carrier family 7 member 6 opposite strand
3031	Q99766	2	2	8.8	215	24882	7.6	ATP synthase subunit s, mitochondrial precursor
3031	UPI000013F17D	2	2	8.8	215	24866	7.6	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit s isoform a precursor
3032	Q9Y3Q3	2	6	8.8	217	24777	5.6	Transmembrane emp24 domain-containing protein 3 precursor
3033	Q06136	2	2	8.7	332	36187	7.1	3-ketodihydrosphingosine reductase precursor
3034	Q969E4	2	7	9	200	22502	4.9	Transcription elongation factor A protein-like 3
3034	Q5H9L2	2	7	8.7	206	23307	4.8	Transcription elongation factor A protein-like 5
3035	Q9BUE0	2	2	8.7	208	23663	6.5	Mediator of RNA polymerase II transcription subunit 18
3035	Q9NXU9	2	2	8.7	208	23651	6.5	CDNA FLJ20045 fis, clone COL00548
3036	UPI0000117170	2	3	8.7	577	63481	9.2	insulin-like growth factor 2 mRNA binding protein 1
3037	Q5JB54	2	4	13.9	245	26749	9.1	Proliferation-inducing gene 5
3037	UPI000013E89A	2	4	10.4	328	36167	8.8	macrophage erythroblast attacher isoform 2
3037	Q9H9Z4	2	4	10.4	328	36095	8.9	CDNA FLJ12453 fis, clone NT2RM1000430, moderately similar to Homo sapiens erythroblast macrophage protein EMP mRNA
3037	Q9H9V6	2	4	9.6	355	40410	8.8	CDNA FLJ12524 fis, clone NT2RM2002145, moderately similar to Homo sapiens erythroblast macrophage protein EMP mRNA
3037	Q9BQ11	2	4	8.8	385	44171	8.8	MAEA protein
3037	O95285	2	4	8.6	395	43907	8.7	Erythroblast macrophage protein EMP
3037	Q9NW84	2	4	8.6	396	45315	8.7	CDNA FLJ10226 fis, clone HEMBB1000037, moderately similar to Homo sapiens erythroblast macrophage protein EMP mRNA
3037	Q7L5Y9	2	4	8.6	396	45287	8.7	Macrophage erythroblast attacher
3038	Q5VU10	2	2	10.8	212	23286	9	Ribonuclease P
3038	Q5VU11	2	2	9.1	254	28112	9.2	Ribonuclease P
3038	UPI00001F9391	2	2	8.9	258	28280	8.9	Ribonuclease P protein subunit p30 (EC 3.1.26.5) (RNaseP protein p30) (RNase P subunit 2).

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
3038	P78346	2	2	8.6	268	29321	8.9	Ribonuclease P protein subunit p30
3039	Q9H0P0	2	6	8.6	336	37948	7.1	Cytosolic 5'-nucleotidase III
3040	O75251	2	4	8.5	213	23564	10	NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial precursor
3040	UPI0000130964	2	4	8.5	213	23580	10	NADH-ubiquinone oxidoreductase Fe-S protein 7
3040	Q8NAS7	2	4	8.5	213	22962	9.4	CDNA FLJ34850 fis, clone NT2NE2011758, highly similar to NADH- UBIQUINONE OXIDOREDUCTASE 20 kDa SUBUNIT
3041	Q53G11	2	2	8.5	340	36594	6.8	Serine racemase variant
3041	Q9GZT4	2	2	8.5	340	36566	6.5	Serine racemase
3042	Q9BRQ6	2	2	8.5	235	26458	8.9	Coiled-coil-helix-coiled-coil-helix domain-containing protein 6
3043	Q9NRG7-2	2	3	8.5	293	31077	9	Isoform 2 of Q9NRG7
3043	UPI000059D223	2	3	8.5	293	31077	9	hypothetical protein LOC56948
3044	Q9NUQ2	2	6	8.5	364	42072	9.1	1-acyl-sn-glycerol-3-phosphate acyltransferase epsilon
3045	UPI000011DC0B	2	2	12.2	312	34866	6.5	Caspase-2 precursor (EC 3.4.22.-) (CASP-2) (ICH-1 protease) (ICH- 1L/1S) [Contains: Caspase-2 subunit p18; Caspase-2 subunit p13; Caspase-2 subunit p12].
3045	P42575-2	2	2	12.1	313	34923	6.5	Isoform ICH
3045	P42575	2	2	8.4	452	50685	6.8	Caspase-2 precursor (EC 3.4.22.55) (CASP-2) (ICH-1 protease) (ICH- 1L/1S) [Contains: Caspase-2 subunit p18; Caspase-2 subunit p13; Caspase-2 subunit p12]
3046	P46734-2	2	5	9.1	318	36173	6.3	Isoform 1 of P46734
3046	P46734	2	5	8.4	347	39318	7.4	Dual specificity mitogen-activated protein kinase kinase 3
3046	Q6FHG1	2	5	8.4	347	39265	7.1	MAP2K3 protein
3046	UPI000013D199	2	5	8.3	351	39853	7.5	Dual specificity mitogen-activated protein kinase kinase 3 (EC 2.7.12.2) (MAP kinase kinase 3) (MAPKK 3) (MAPK/ERK kinase 3).
3046	P46734-3	2	5	8.2	352	39940	7.5	Isoform 2 of P46734
3047	UPI00001F6D70	2	3	9.8	244	28228	4.9	CCR4-NOT transcription complex, subunit 7 isoform 2
3047	Q96IQ6	2	3	9.8	246	28364	4.8	CNOT7 protein
3047	Q7Z530	2	3	8.4	285	32815	4.8	CAF1
3047	Q9UIV1	2	3	8.4	285	32745	4.8	CCR4-NOT transcription complex subunit 7
3048	P50750	2	2	8.3	372	42778	8.8	Cell division protein kinase 9
3049	Q7L5D6	2	5	8.3	327	36504	5.4	UPF0363 protein C7orf20
3050	Q8NFH4	2	3	8.3	326	36708	5.9	Nucleoporin Nup37
3051	Q9Y375	2	2	8.3	327	37764	7.6	Complex I intermediate-associated protein 30, mitochondrial precursor
3052	P05121	2	5	8.2	402	45060	7.2	Plasminogen activator inhibitor 1 precursor
3053	Q5TZ92	2	2	8.9	291	33150	6	Novel protein
3053	UPI0000D61E00	2	2	8.8	297	33814	6.3	BRCA1/BRCA2-containing complex subunit 3.
3053	P46736	2	2	8.2	316	36072	5.9	BRCA1/BRCA2-containing complex subunit 3
3053	UPI0000D61DFF	2	2	8.1	322	36736	6.3	BRCA1/BRCA2-containing complex subunit 3.
3054	Q3B781	2	2	8.2	245	27979	5.3	CCDC90B protein
3054	Q9GZU6	2	2	7.9	254	29506	7.5	Hypothetical protein DKFZp434F1919
3054	Q9GZT6	2	2	7.9	254	29472	7.5	MDS011
3055	UPI00006C03F3	2	3	10.4	241	27027	4.9	PREDICTED: hypothetical protein
3055	Q658P1	2	3	8.2	304	34805	6.6	Hypothetical protein DKFZp666C185
3055	UPI000013EF67	2	3	8.2	306	34925	6.7	PREDICTED: hypothetical protein LOC64853
3055	Q9H9E8	2	3	8.2	306	34951	6.7	CDNA FLJ12806 fis, clone NT2RP2002235
3055	Q96BJ3	2	3	8.2	306	35023	6.6	Uncharacterized protein C1orf80
3056	Q86TR7	2	8	8.2	279	30962	4.8	Uncharacterized protein C14orf151
3057	Q96H20-2	2	7	8.2	257	28736	6.4	Isoform 2 of Q96H20
3057	Q96H20	2	7	8.1	258	28864	6.7	Vacuolar sorting protein SNF8
3058	UPI00004DFE95	2	3	10.2	197	22995	8.9	Protein NipSnap3A (NipSnap4) (Target for Salmonella secreted protein C) (TassC).
3058	Q9UFN0	2	3	8.1	247	28467	9.2	Protein NipSnap3A
3059	O60711	2	2	8	386	43332	6	Leupaxin
3059	Q6FI07	2	2	8	386	43336	6	LPXN protein
3060	P53990-2	2	3	8.7	335	36622	5.4	Isoform 2 of P53990
3060	P53990-3	2	3	8.1	360	39928	7.8	Isoform 3 of P53990
3060	P53990	2	3	8	364	39751	5.3	Uncharacterized protein KIAA0174
3060	Q3SYM4	2	3	7.9	366	39979	5.3	KIAA0174 protein
3061	Q96BI2	2	2	13	215	24190	10.9	ARL6IP4 protein
3061	Q9P2R9	2	2	12.8	218	24592	10.9	SRp25 nuclear protein
3061	UPI00003E1F8A	2	2	8.2	341	36612	11.2	SRp25 nuclear protein isoform 2
3061	Q504R8	2	2	8	352	37648	11.2	ADP-ribosylation-like factor 6 interacting protein 4
3061	UPI00003E1F8B	2	2	8	352	37638	11.2	SRp25 nuclear protein isoform 3
3061	Q66PJ3	2	2	7.8	360	38395	11.1	ADP-ribosylation factor-like protein 6-interacting protein 4
3061	Q8TEM4	2	2	6.5	432	46514	11.5	FLJ00169 protein
3062	Q6ZWP6	2	2	8	288	31024	9.1	CDNA FLJ90159 fis, clone HEMBB1002465, weakly similar to ACYL-COA DEHYDROGENASE

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
3062	Q9UKU7	2	2	5.5	415	45070	7.9	Acyl-CoA dehydrogenase family member 8, mitochondrial precursor
3063	Q8N1Q1	2	2	8	262	29443	7	Carbonic anhydrase 13
3064	Q96I25	2	4	8	401	44962	6	Splicing factor 45
3065	Q13867	2	3	7.9	455	52562	6.3	Bleomycin hydrolase
3066	Q92785	2	2	7.9	391	44156	6.3	Zinc-finger protein ubi-d4
3067	UPI0000DBEF1B	2	2	8	540	60102	8.4	Cyclin-K.
3067	UPI0000DBEF1A	2	2	7.9	547	60811	8.4	Cyclin-K.
3068	UPI0000D619C0	2	3	9.3	281	32456	6.8	Leucine carboxyl methyltransferase 1 (EC 2.1.1.-) (Protein-leucine O- methyltransferase).
3068	UPI00005B2DFC	2	3	9.3	279	32172	6.3	leucine carboxyl methyltransferase 1 isoform b
3068	Q9UIC8	2	3	7.8	334	38379	6	Leucine carboxyl methyltransferase 1
3068	UPI0000D619C1	2	3	7.7	338	38834	6.5	Leucine carboxyl methyltransferase 1 (EC 2.1.1.-) (Protein-leucine O- methyltransferase).
3068	UPI0000D619C2	2	3	7.3	357	41116	7.6	Leucine carboxyl methyltransferase 1 (EC 2.1.1.-) (Protein-leucine O- methyltransferase).
3068	Q9UIC8-2	2	3	7.3	357	41106	7	Isoform 2 of Q9UIC8
3069	UPI0000DD80FD	2	2	8.1	258	27451	6.2	PREDICTED: similar to Copper chaperone for superoxide dismutase (Superoxide dismutase copper chaperone)
3069	O14618	2	2	7.7	274	29041	5.6	Copper chaperone for superoxide dismutase
3069	Q8NEV0	2	2	7.7	274	29027	5.6	Superoxide dismutase copper chaperone
3070	Q53GI2	2	2	7.7	313	34188	5	Testis expressed sequence 264 variant
3070	Q9Y6I9	2	2	7.7	313	34189	4.9	Testis-expressed sequence 264 protein precursor
3071	Q6P147	2	8	7.7	286	31668	8.8	Cytochrome b reductase 1
3071	Q9H0Q8	2	8	7.7	286	31638	9	Hypothetical protein DKFZp564E227
3072	Q8WUY3	2	3	7.7	259	29491	4.9	Uncharacterized protein C9orf65
3073	UPI0000DD8590	2	3	7.7	337	36661	8.4	PREDICTED: hypothetical protein LOC140731
3074	A2NHL9	2	2	7.6	331	38056	6.6	Mih1/TX isoform beta
3074	P49662	2	2	6.6	377	43262	6	Caspase-4 precursor (EC 3.4.22.57) (CASP-4) (ICH-2 protease) (TX protease) (ICE(rel)-II) [Contains: Caspase-4 subunit 1; Caspase-4 subunit 2]
3075	Q13371	2	2	7.6	301	34282	4.7	Phosducin-like protein
3076	Q53T37	2	4	7.6	262	29844	7.8	Hypothetical protein FLJ21820
3076	Q9H6V9	2	4	6.2	325	37319	6.5	Uncharacterized protein C2orf43
3077	Q92665	2	2	7.6	395	45319	9.3	28S ribosomal protein S31, mitochondrial precursor
3077	UPI0000167B37	2	2	7.6	395	45318	9.4	mitochondrial ribosomal protein S31
3078	Q96E11-3	2	2	9.2	218	24115	9.6	Isoform 3 of Q96E11
3078	Q96E11	2	2	7.6	262	29277	9.8	Ribosome recycling factor, mitochondrial precursor
3079	Q96G23	2	5	7.6	380	44876	9	LAG1 longevity assurance homolog 2
3080	Q9Y312	2	2	7.8	384	43472	6	Uncharacterized protein C20orf4
3080	A2A2Q9	2	2	7.5	398	45034	7.5	Chromosome 20 open reading frame 4
3081	Q5JTE4	2	3	8.3	314	35838	5.7	OTTHUMP00000016471
3081	O15160-2	2	3	7.6	342	38647	6	Isoform 2 of O15160
3081	O15160	2	3	7.5	346	39250	5.5	DNA-directed RNA polymerase I 40 kDa polypeptide
3082	UPI000041C169	2	24	10.7	159	17764	6.3	CD9 antigen (p24) (Leukocyte antigen MIC3) (Motility-related protein) (MRP-1) (Tetraspanin-29) (Tspan-29).
3082	P21926	2	24	7.5	228	25416	7.1	CD9 antigen
3083	Q8IVD9	2	2	7.5	361	40822	5.3	NudC domain-containing protein 3
3084	O95639-3	2	4	8.2	243	27419	8.2	Isoform 3 of O95639
3084	O95639-2	2	4	8.2	244	27547	8.2	Isoform 2 of O95639
3084	O95639	2	4	7.4	269	30255	8.3	Cleavage and polyadenylation specificity factor subunit 4
3085	Q53GB1	2	4	7.4	338	38124	9.5	Solute carrier family 25 member 40
3085	Q8TBP6	2	4	7.4	338	38125	9.4	Solute carrier family 25, member 40
3086	Q8TBX8	2	3	7.4	421	47328	6.8	Phosphatidylinositol-4-phosphate 5-kinase type II gamma
3086	UPI000003F553	2	3	7.4	421	47300	6.8	phosphatidylinositol-4-phosphate 5-kinase, type II, gamma
3087	Q9BY49	2	2	7.3	303	32544	8.8	Peroxisomal trans-2-enoyl-CoA reductase
3087	UPI0000D612AC	2	2	7.3	302	32380	8.8	Peroxisomal trans-2-enoyl-CoA reductase (EC 1.3.1.38) (TERP) (HPDHase) (pVI-ARL) (2,4-dienoyl-CoA reductase-related protein) (DCR-RP).
3088	Q9NTM9	2	2	7.3	273	29341	8.2	Copper homeostasis protein cutC homolog
3088	UPI0000070B78	2	2	7.3	273	29311	7.9	cutC copper transporter homolog
3089	UPI0000367289	2	2	7.3	288	30752	11.2	Heparin-binding growth factor 2 precursor (HBGF-2) (Basic fibroblast growth factor) (BFGF) (Prostatropin).
3090	Q9BSP1	2	2	7.4	378	41969	9.2	GTPBP10 protein
3090	A4D1E9	2	2	7.2	387	42933	9	Hypothetical protein LOC85865
3090	Q8N982	2	2	7.2	387	43016	9.1	CDNA FLJ38242 fis, clone FCBBF2006781, weakly similar to SPO0B- ASSOCIATED GTP-BINDING PROTEIN
3090	Q3B7A6	2	2	7.2	387	42917	9	GTP-binding protein 10
3091	O75525-2	2	2	9.2	271	30250	9.5	Isoform 2 of O75525
3091	O75525	2	2	7.2	346	38800	7.6	KH domain-containing, RNA-binding, signal transduction-associated protein 3

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
3092	Q86YA9	2	2	7.2	552	61379	6	Golgi associated, gamma adaptin ear containing, ARF binding protein 1
3092	Q9UJY5	2	2	6.3	639	70384	5.3	ADP-ribosylation factor-binding protein GGA1
3093	Q96AZ0	2	20	7.2	373	43759	8.8	CLPTM1L protein
3093	Q96KA5	2	20	5	538	62229	8.6	CLPTM1-like protein
3094	Q9BXK5	2	2	7.2	485	52723	4.4	Bcl-2-like 13 protein
3095	Q9UBP6	2	3	7.2	276	31471	7.6	tRNA (guanine-N(7)-)-methyltransferase (EC 2.1.1.33) (tRNA(m7G46)- methyltransferase)
3096	UPI0000D61CD4	2	5	7.9	430	47710	5.1	Nuclear-interacting partner of ALK (Nuclear-interacting partner of anaplastic lymphoma kinase) (hNIPA) (Zinc finger C3HC-type protein 1).
3096	Q86WB0-3	2	5	7.9	431	47771	5.2	Isoform 3 of Q86WB0
3096	A4D1L4	2	5	7.1	481	53603	6.2	Nuclear interacting partner of anaplastic lymphoma kinase
3096	UPI0000457601	2	5	7.1	480	53498	6.2	Nuclear-interacting partner of ALK (Nuclear-interacting partner of anaplastic lymphoma kinase) (hNIPA) (Zinc finger C3HC-type protein 1).
3096	Q86WB0-2	2	5	7.1	481	53559	6.4	Isoform 2 of Q86WB0
3096	UPI0000457602	2	5	6.8	501	55200	5.5	Nuclear-interacting partner of ALK (Nuclear-interacting partner of anaplastic lymphoma kinase) (hNIPA) (Zinc finger C3HC-type protein 1).
3096	Q86WB0	2	5	6.8	502	55262	5.6	Nuclear-interacting partner of ALK
3097	UPI0000470117	2	6	13.1	183	21384	4.9	Cell division cycle protein 123 homolog (Protein D123) (HT-1080) (PZ32).
3097	UPI0000470118	2	6	8.1	295	33891	4.6	Cell division cycle protein 123 homolog (Protein D123) (HT-1080) (PZ32).
3097	O75794	2	6	7.1	336	39135	4.8	Cell division cycle protein 123 homolog
3097	UPI0000072E2F	2	6	7.1	336	39188	4.9	D123 gene product
3097	UPI0000D60F09	2	6	6.7	359	41283	6	Cell division cycle protein 123 homolog (Protein D123) (HT-1080) (PZ32).
3098	P82673	2	6	7.1	323	36844	8.2	28S ribosomal protein S35, mitochondrial precursor
3099	Q5SW96	2	2	7.1	308	33885	6.7	Low density lipoprotein receptor adapter protein 1
3100	Q96EM0	2	2	7.1	354	38168	6.6	Uncharacterized protein C14orf149
3100	Q96LJ5	2	2	7.1	354	38138	6.7	CDNA FLJ25436 fis, clone TST08261
3101	Q9BX67	2	2	7.1	310	35020	7.6	Junctional adhesion molecule C precursor
3102	Q9Y371	2	3	7.1	365	40796	6	SH3 domain GRB2-like protein B1
3102	Q9Y371-2	2	3	6.7	386	43196	5.7	Isoform 2 of Q9Y371
3103	O43772	2	2	7	301	32944	9.4	Mitochondrial carnitine/acylcarnitine carrier protein
3104	UPI0000EDA44A	2	3	12.1	173	19704	5.1	SCO1 protein homolog, mitochondrial
3104	O75880	2	3	7	301	33814	8.9	SCO1 protein homolog, mitochondrial precursor
3105	P61962	2	2	7	342	38926	5.5	WD repeat protein 68
3105	UPI000013D01D	2	2	7	341	38855	5.5	WD repeat protein 68 (WD repeat protein An11 homolog).
3106	Q9Y2G5-2	2	3	7.9	380	44083	6.5	Isoform B of Q9Y2G5
3106	Q9Y2G5-1	2	3	7.1	424	48896	6.8	Isoform A of Q9Y2G5
3106	Q9Y2G5	2	3	7	429	49976	6.6	GDP-fucose protein O-fucosyltransferase 2 precursor
3107	Q8IUB6	2	2	21.1	109	12386	8.1	CD95 antigen
3107	Q5T9P2	2	2	7.3	314	35386	7.9	Fas
3107	P25445	2	2	6.9	335	37732	7.9	Tumor necrosis factor receptor superfamily member 6 precursor
3107	Q6ICT6	2	2	6.9	335	37702	7.9	TNFRSF6 protein
3107	UPI0000D60F8D	2	2	6.4	362	40667	8.2	Tumor necrosis factor receptor superfamily member 6 precursor (FASLG receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen) (CD95 antigen).
3107	Q59FU8	2	2	6.4	362	40494	8.1	Tumor necrosis factor receptor superfamily, member 6 isoform 1 variant
3108	P50579	2	2	6.9	478	52892	5.8	Methionine aminopeptidase 2
3109	Q53EZ4-2	2	2	8	400	46803	7.9	Isoform 2 of Q53EZ4
3109	Q53EZ4	2	2	6.9	464	54124	7	Centrosomal protein of 55 kDa
3110	Q92575	2	3	6.9	508	56778	6.4	UBX domain-containing protein 2
3111	O43819	2	5	6.8	266	29810	8.9	SCO2 protein homolog, mitochondrial precursor
3111	UPI0000167B35	2	5	6.8	266	29751	8.6	cytochrome oxidase deficient homolog 2
3112	Q8WU61	2	2	6.8	442	49967	4.8	Uncharacterized protein C5orf22
3112	Q9NUR1	2	2	6.8	442	49977	4.8	CDNA FLJ11193 fis, clone PLACE1007621
3113	Q5U622	2	3	6.7	537	60492	5.1	Adenylate kinase 5
3113	UPI0000167E21	2	3	6.7	536	60315	5.1	adenylate kinase 5 isoform 2
3113	Q86YS0	2	3	6.7	536	60277	5.1	Adenylate kinase 6
3113	UPI0000D61F49	2	3	6.4	564	63535	5.1	Adenylate kinase isoenzyme 5 (EC 2.7.4.3) (ATP-AMP transphosphorylase).
3113	UPI0000167E20	2	3	6.4	562	63333	5.1	adenylate kinase 5 isoform 1
3113	Q8N464	2	3	6.4	562	63279	5.1	Adenylate kinase 5
3113	Q7Z4T5	2	3	6.4	563	63446	5.1	Hypothetical protein
3114	Q8NEJ9-2	2	3	6.8	311	35250	9.3	Isoform 2 of Q8NEJ9
3114	Q8NEJ9	2	3	6.7	315	35894	9.6	Neuroguidin
3115	Q96NA3	2	3	6.7	434	48705	8.9	CDNA FLJ31187 fis, clone KIDNE2000349, moderately similar to Mus musculus putative lysophosphatidic acid acyltransferase mRNA

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
3116	Q96SI1	2	3	6.7	283	31942	7.4	BTB/POZ domain-containing protein KCTD15
3117	Q9H425	2	3	6.7	327	36346	5.7	Uncharacterized protein C1orf198
3118	Q9Y639-3	2	7	6.8	278	30835	7.8	Isoform 3 of Q9Y639
3118	Q9Y639	2	7	6.7	282	31291	6.9	Neuroplastin precursor
3118	Q9Y639-4	2	7	5.6	337	37792	7.4	Isoform 4 of Q9Y639
3118	UPI0000D6136C	2	7	4.8	392	43385	7.8	Neuroplastin precursor (Stromal cell-derived receptor 1) (SDR-1).
3118	Q9Y639-2	2	7	4.8	398	44387	8	Isoform 2 of Q9Y639
3119	Q5T4U8	2	6	14.5	152	17318	5.5	Rab geranylgeranyltransferase, beta subunit
3119	UPI0000D61F47	2	6	6.9	321	35983	5.5	Geranylgeranyl transferase type-2 subunit beta (EC 2.5.1.60) (Geranylgeranyl transferase type II subunit beta) (Rab geranylgeranyltransferase subunit beta) (Rab geranyl- geranyltransferase subunit beta) (Rab GG transferase beta) (Rab GGTase beta).
3119	Q59GT6	2	6	6.9	320	35915	5.4	Rab geranylgeranyltransferase, beta subunit variant
3119	P53611	2	6	6.6	331	36924	5	Geranylgeranyl transferase type-2 subunit beta
3119	UPI0000D61F46	2	6	6.6	332	36992	5.1	Geranylgeranyl transferase type-2 subunit beta (EC 2.5.1.60) (Geranylgeranyl transferase type II subunit beta) (Rab geranylgeranyltransferase subunit beta) (Rab geranyl- geranyltransferase subunit beta) (Rab GG transferase beta) (Rab GGTase beta).
3120	P53985	2	4	6.6	500	53958	8.7	Monocarboxylate transporter 1
3121	UPI0000072D91	2	2	8.8	274	31404	4.9	hypothetical protein LOC55148 isoform 1
3121	Q05DA8	2	2	6.6	361	41243	5.1	C14orf130 protein
3121	UPI000006DD14	2	2	5.6	425	47996	4.9	hypothetical protein LOC55148 isoform 2
3121	Q8N806	2	2	5.6	425	47999	4.8	Uncharacterized protein C14orf130
3122	Q5TCL9	2	3	17.2	151	17801	5.5	Wilms tumor 1 associated protein
3122	Q15007	2	3	6.6	396	44244	5.2	Wilms' tumor 1-associating protein (WT1-associated protein) (Putative pre-mRNA-splicing regulator female-lethal(2D) homolog)
3123	Q8WUX9	2	7	6.6	453	50911	5.3	Protein CHMP7
3124	UPI0000F24436	2	2	7.2	400	45523	6.8	2-OXOISOVALERATE DEHYDROGENASE ALPHA SUBUNIT
3124	P12694	2	2	6.5	445	50471	8.3	2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial precursor
3124	Q59EI3	2	2	6.5	444	50400	8.3	Branched chain keto acid dehydrogenase E1, alpha polypeptide variant
3124	UPI0000D617AD	2	2	6.1	479	54203	6.4	Transmembrane protein 91.
3124	Q6ZSA3	2	2	6.1	479	54131	6.5	CDNA FLJ45695 fis, clone FEBRA2013570, highly similar to 2- oxoisovalerate dehydrogenase alpha subunit, mitochondrial
3125	Q59FW7	2	4	7.7	272	31652	8.5	Cyclin H variant
3125	P51946	2	4	6.5	323	37643	7.2	Cyclin-H
3125	Q53X72	2	4	6.5	323	37615	7.2	CCNH protein
3126	Q53YP0	2	2	6.5	478	54417	10.4	PreS1 binding protein
3126	Q9NZM5	2	2	6.5	478	54389	10.3	Glioma tumor suppressor candidate region gene 2 protein
3126	Q96CS0	2	2	6.5	476	54215	10.4	GLTSCR2 protein
3126	Q7L4X7	2	2	6.5	474	54087	10.4	Glioma tumor suppressor candidate region gene 2
3127	Q9H0E2	2	4	8.4	274	30282	6	Toll-interacting protein
3127	Q59FB9	2	4	6.5	352	38895	8.5	Toll interacting protein variant
3127	UPI0000D6257D	2	4	6.5	355	39151	8.8	Toll-interacting protein.
3128	Q86TV2	2	2	7.5	372	42008	6.2	Full-length cDNA clone CS0DI002YH20 of Placenta of Homo sapiens
3128	Q86TV3	2	2	7.4	376	42948	6.4	Full-length cDNA clone CS0DB001YK19 of Neuroblastoma of Homo sapiens
3128	Q6I9U9	2	2	6.5	433	49353	6.6	LGMN protein
3128	Q99538	2	2	6.5	433	49411	6.6	Legumain precursor
3129	Q8NFF5	2	3	6.5	587	65266	6.9	FAD1 flavin adenine dinucleotide synthetase homolog
3130	Q9C0B1	2	3	6.5	507	58456	5.2	KIAA1752 protein
3130	UPI000013D7B3	2	3	6.5	505	58282	5.2	fatso
3131	O75381	2	2	6.4	377	41237	4.9	Peroxisomal membrane protein PEX14
3132	Q5TAA8	2	2	6.4	326	36433	6.6	Hermansky-Pudlak syndrome 1
3132	Q658M9	2	2	6.2	338	38870	9.4	Hypothetical protein DKFZp666K145
3132	UPI000049DD09	2	2	5.6	376	42880	9.1	Hermansky-Pudlak syndrome 1 protein.
3132	Q92902-4	2	2	3.1	680	76937	5.8	Isoform IV of Q92902
3132	Q92902-2	2	2	3.1	667	75877	5.7	Isoform II of Q92902
3132	Q92902	2	2	3	700	79292	5.9	Hermansky-Pudlak syndrome 1 protein
3133	Q5XKR6	2	7	6.4	373	41385	7.9	AUP1 protein
3133	UPI0000D611C1	2	7	6.4	375	41670	8.3	Ancient ubiquitous protein 1 precursor.
3133	Q68CX8	2	7	6.4	375	41587	8.3	Hypothetical protein DKFZp686P12272
3133	Q9Y679-2	2	7	5.9	410	45787	8.6	Isoform Short of Q9Y679
3133	UPI000013CFAF	2	7	5.1	474	52751	7.9	Ancient ubiquitous protein 1 precursor.
3133	Q9Y679	2	7	5	476	53028	8.1	Ancient ubiquitous protein 1 precursor
3134	Q8WYI2	2	2	10.9	221	24997	5.4	MSTP024
3134	Q96CT6	2	2	7.5	322	36363	8.1	C12orf10 protein
3134	UPI000049DD6D	2	2	7.4	325	36629	7.6	UPF0160 protein MYG1.
3134	Q86UA3	2	2	6.4	376	42508	6.8	Chromosome 12 open reading frame 10

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
3134	UPI000013D729	2	2	6.4	376	42449	6.7	UPF0160 protein MYG1.
3134	Q9HB07	2	2	6.4	376	42445	6.7	UPF0160 protein MYG1
3135	Q96GC9	2	11	6.4	406	46238	6.9	Transmembrane protein 49
3136	Q9NQ48	2	2	6.4	299	34592	5.4	Leucine zipper transcription factor-like 1
3136	UPI00004570F2	2	2	6.4	298	34461	5.4	leucine zipper transcription factor-like 1
3136	Q9NQ56	2	2	6.4	299	34591	5.4	Leucine zipper transcription factor-like 1
3137	Q8TCM0	2	3	9.5	262	28494	5.6	Hypothetical protein DKFZp547L059
3137	Q59HD3	2	3	8.3	303	33161	5.8	Ataxin 2-binding protein 1 isoform 4 variant
3137	UPI0000F54B2B	2	3	6.8	370	39783	6.7	RNA binding motif protein 9 isoform 4
3137	UPI000013F818	2	3	6.8	367	39515	6.7	RNA binding motif protein 9 isoform 2
3137	Q7Z7I7	2	3	6.8	370	40005	7.1	Ataxin 2-binding protein variant 1
3137	Q0VH35	2	3	6.8	370	39753	6.7	RNA binding motif protein 9
3137	O43251-4	2	3	6.8	366	39386	6.7	Isoform 4 of O43251
3137	O43251-5	2	3	6.6	376	39954	8.6	Isoform 5 of O43251
3137	O43251-2	2	3	6.6	380	40351	8.6	Isoform 2 of O43251
3137	UPI0000D62145	2	3	6.4	390	41453	7.7	RNA-binding protein 9 (RNA-binding motif protein 9) (Hexaribonucleotide-binding protein 2) (Repressor of tamoxifen transcriptional activity).
3137	UPI000045690E	2	3	6.4	388	41624	6.9	Ataxin-2-binding protein 1.
3137	Q8TAE3	2	3	6.4	392	42084	7.7	Hexaribonucleotide binding protein 1 isoform alpha
3137	O43251	2	3	6.4	390	41374	7.2	RNA-binding protein 9
3137	A4F5G8	2	3	6.3	398	42920	6	RNA binding motif protein 9
3137	UPI0000163C0C	2	3	6.3	397	42784	6.9	ataxin 2-binding protein 1 isoform 4
3137	Q9NWB1	2	3	6.3	397	42754	6.9	Ataxin-2-binding protein 1
3137	Q8TAF2	2	3	6.3	395	42402	6.4	Hexaribonucleotide binding protein 1 isoform beta
3137	Q8WYB2	2	3	6	418	44793	7.4	Hexaribonucleotide binding protein 1 isoform gamma
3137	UPI0000D9C931	2	3	5.6	450	47206	6.6	RNA binding motif protein 9 isoform 6
3137	Q0PRL5	2	3	5.5	451	47334	6.6	Hypothetical protein
3138	O75695	2	3	6.3	350	39641	5.1	Protein XRP2
3138	UPI0000139021	2	3	6.3	350	39642	5.1	XRP2 protein
3139	P07711	2	6	6.3	333	37564	5.4	Cathepsin L precursor (EC 3.4.22.15) (Major excreted protein) (MEP) [Contains: Cathepsin L heavy chain; Cathepsin L light chain]
3140	Q9H6A6	2	2	7.2	373	42030	5.9	CDNA: FLJ22433 fis, clone HRC09172
3140	Q19CC6	2	2	6.3	431	48410	5.6	TTG1A
3140	UPI0000D62063	2	2	5.9	456	51333	6	Putative LAG1-interacting protein
3140	Q5SWX8	2	2	5.9	454	51103	5.9	Uncharacterized protein C1orf27
3141	O60256	2	2	6.2	369	40926	7.4	Phosphoribosyl pyrophosphate synthetase-associated protein 2
3141	UPI0000F51D5E	2	2	6.1	379	42102	7.4	PHOSPHORIBOSYL PYROPHOSPHATE SYNTHETASE-ASSOC
3142	P35269	2	3	6.2	517	58241	7.5	Transcription initiation factor IIF subunit alpha
3142	UPI00001367FB	2	3	6.2	517	58275	7.5	general transcription factor IIF, polypeptide 1, 74kDa
3142	Q6IBK5	2	3	6.2	517	58226	7.5	GTF2F1 protein
3143	Q13449	2	2	6.2	338	37394	7	Limbic system-associated membrane protein precursor
3144	UPI000006F931	2	2	8.3	217	23468	5.2	B-cell CLL/lymphoma 7C
3144	Q8WUZ0	2	2	8.3	217	23365	5.3	B-cell CLL/lymphoma 7 protein family member C
3144	UPI00001D6EEE	2	2	7.4	242	26422	10.7	B-cell CLL/lymphoma 7 protein family member C.
3144	Q8WUZ0-2	2	2	7.4	242	26391	10.7	Isoform 2 of Q8WUZ0
3144	Q6PJY5	2	2	6.2	292	32726	6.5	Hypothetical protein
3145	Q86U42-2	2	4	6.4	296	31497	5	Isoform 2 of Q86U42
3145	Q86U42	2	4	6.2	306	32749	5.1	Polyadenylate-binding protein 2 (Poly(A)-binding protein 2) (Poly(A)- binding protein II) (PABII) (Polyadenylate-binding nuclear protein 1) (Nuclear poly(A)-binding protein 1)
3146	Q96G21	2	5	6.2	291	33757	9.5	U3 small nucleolar ribonucleoprotein protein IMP4
3147	UPI00000473F8	2	2	6.2	321	34006	6.1	hypothetical protein LOC283871
3148	UPI0000DD7A4B	2	15	6.2	1038	117390	6	PREDICTED: similar to Prostate, ovary, testis expressed protein on chromosome 2
3149	Q14254	2	2	6.1	379	41685	5.3	Flotillin-2
3149	Q9BTI6	2	2	6	385	42566	5.3	FLOT2 protein
3149	UPI00001AE777	2	2	5.4	428	47064	5.3	flotillin 2
3150	Q9BXW7-2	2	2	6.6	393	43588	6.9	Isoform 1 of Q9BXW7
3150	Q9BXW7	2	2	6.1	423	46321	8.1	Cat eye syndrome critical region protein 5 precursor
3151	UPI00004561E0	2	3	7.4	353	40347	9	39S ribosomal protein L37, mitochondrial precursor (L37mt) (MRP-L37).
3151	UPI0000D61F21	2	3	6.2	416	47647	7.7	39S ribosomal protein L37, mitochondrial precursor (L37mt) (MRP-L37).
3151	Q9BZE1	2	3	6.1	423	48101	8.6	39S ribosomal protein L37, mitochondrial precursor
3151	UPI000006CF76	2	3	6.1	423	48118	8.6	mitochondrial ribosomal protein L37
3152	Q9H6F5	2	3	6.1	360	40236	10.3	Coiled-coil domain-containing protein 86
3153	Q53F51	2	2	6.2	357	41238	6.9	FGF intracellular binding protein isoform b variant
3153	O46431	2	2	6.2	357	41210	6.8	Acidic fibroblast growth factor intracellular-binding protein
3153	O43427	2	2	6	364	41878	6.5	Acidic fibroblast growth factor intracellular-binding protein
3154	UPI0000456D2D	2	14	7.1	340	37965	9.5	leukocyte receptor cluster (LRC) member 4 protein

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
3154	Q99908	2	14	7	342	38164	9.5	BB1 protein
3154	Q05DF0	2	14	6	399	44733	8.9	LENG4 protein
3154	Q9BPV2	2	14	5.1	472	52765	9	Leukocyte receptor cluster (LRC) member 4
3154	Q96N66	2	14	5.1	472	52775	9	Leukocyte receptor cluster member 4
3154	Q7L5N2	2	14	5.1	471	52634	9	LENG4 protein
3155	Q15036	2	2	6	470	52901	7.5	Sorting nexin-17
3156	UPI00001D6A08	2	5	6.8	338	38012	8.5	3-hydroxyisobutyryl-Coenzyme A hydrolase isoform 2
3156	Q9BS94	2	5	6.4	362	40418	8.6	HIBCH protein
3156	Q53GA8	2	5	6	385	43321	8.2	3-hydroxyisobutyryl-Coenzyme A hydrolase isoform 1 variant
3156	UPI000013F16E	2	5	6	386	43482	8.2	3-hydroxyisobutyryl-Coenzyme A hydrolase isoform 1
3156	Q6NVY1	2	5	6	386	43410	8.4	3-hydroxyisobutyryl-CoA hydrolase
3156	Q53GF2	2	5	6	385	43348	8.6	3-hydroxyisobutyryl-Coenzyme A hydrolase isoform 1 variant
3157	Q8IXS6	2	3	6.9	379	42185	5.1	Paralemmin-2
3157	Q8IXS6-2	2	3	6.3	411	45438	5.1	Isoform 2 of Q8IXS6
3157	Q5T719	2	3	6	433	47627	4.9	Paralemmin-2 (A kinase (PRKA) anchor protein 2)
3158	Q6ZNR2	2	8	6	316	35381	11.1	CDNA FLJ27308 fis, clone TMS06173
3158	UPI0000D6217D	2	8	6	319	36177	10.3	transmembrane protein 153 (TMEM153), mRNA
3158	Q96C62	2	8	2.8	682	76915	10	Transmembrane protein 112B
3158	Q9BU23	2	8	2.7	707	79698	10.1	Transmembrane protein 153
3159	Q8TDR2	2	3	6	401	44573	9	Serine/threonine-protein kinase 35
3160	O95251	2	2	5.9	611	70642	8.8	Histone acetyltransferase MYST2
3161	P35659	2	5	5.9	375	42674	8.6	Protein DEK
3162	P55347-2	2	2	5.9	405	44629	6.7	Isoform 2 of P55347
3163	Q15738	2	2	5.9	373	41900	8.1	Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating
3164	Q17RS0	2	2	5.9	1105	122867	5.8	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1
3164	UPI0000167B18	2	2	5.9	1105	122721	5.8	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin c1
3164	Q58EY4	2	2	5.9	1105	122911	5.7	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1
3165	Q6NSW5	2	2	5.9	357	40514	6.5	Protein FAM45B
3166	Q969N2-2	2	2	8.9	384	43616	6.9	Isoform 2 of Q969N2
3166	Q969N2-4	2	2	7.1	476	54118	8.2	Isoform 4 of Q969N2
3166	Q969N2	2	2	5.9	578	65700	8.4	GPI transamidase component PIG-T precursor
3167	Q9H832-2	2	3	8.5	246	28075	6.1	Isoform 2 of Q9H832
3167	UPI0000DBEF08	2	3	6.1	347	38506	9.4	ubiquitin-conjugating enzyme E2Z (putative)
3167	Q9H832	2	3	5.9	354	38210	5.6	Ubiquitin-conjugating enzyme E2 Z
3168	Q9Y4G6	2	2	5.9	2542	271553	5.6	Talin-2
3168	UPI0000D6134E	2	2	5.9	2544	271795	5.6	Talin-2.
3168	UPI00001FE5FC	2	2	5.9	2542	271611	5.6	Talin-2.
3169	P43897	2	4	5.8	325	35391	8.4	Elongation factor Ts, mitochondrial precursor
3169	Q561V7	2	4	5.8	325	35378	8.4	TSFM protein
3169	P43897-2	2	4	5.5	346	37656	7.7	Isoform 2 of P43897
3170	Q9BYB4-2	2	2	9	212	22896	7.2	Isoform 2 of Q9BYB4
3170	Q9BYB4	2	2	5.8	327	35618	8	Guanine nucleotide-binding protein subunit beta-like protein 1
3171	O75787	2	9	5.7	350	39008	6.1	Renin receptor precursor (Renin/prorenin receptor) (ATPase H(+)- transporting lysosomal accessory protein 2) (ATPase H(+)-transporting lysosomal-interacting protein 2)
3172	Q13641	2	7	5.7	420	46032	6.8	Trophoblast glycoprotein precursor
3173	Q15035	2	4	5.7	370	43328	9.2	Translocation-associated membrane protein 2
3174	Q5QP19	2	2	6.5	397	44017	7.1	NFS1 nitrogen fixation 1
3174	Q53FP3	2	2	5.7	457	50186	8.3	NFS1 nitrogen fixation 1 isoform a variant
3174	Q9Y697	2	2	5.7	457	50196	8.3	Cysteine desulfurase, mitochondrial precursor
3175	Q9H0W9	2	2	5.7	315	35117	6.7	Ester hydrolase C11orf54
3176	UPI0000D61B7E	2	4	5.7	420	48535	7.2	Prostatic acid phosphatase precursor (EC 3.1.3.2).
3177	O95905	2	7	5.6	644	72758	4.9	SGT1 protein
3177	Q6I9U8	2	7	5.6	644	72710	4.9	HSGT1 protein
3178	P57081	2	2	5.6	412	45490	7.1	WD repeat protein 4
3179	Q6PKB3	2	2	10.4	222	25023	5	MRPS27 protein
3179	Q6P1S1	2	2	5.6	414	47611	6.2	Mitochondrial ribosomal protein S27
3180	Q9H173	2	3	5.6	461	52085	5.4	Nucleotide exchange factor SIL1 precursor
3181	O43464-2	2	2	6.9	361	38493	10.7	Isoform 2 of O43464
3181	O43464-4	2	2	6.6	377	39914	10.6	Isoform 4 of O43464
3181	O43464-3	2	2	5.7	436	46382	10.2	Isoform 3 of O43464
3181	O43464	2	2	5.5	458	48841	10.1	Serine protease HTRA2, mitochondrial precursor
3182	O95684-2	2	2	5.8	379	40907	4.6	Isoform 2 of O95684
3182	O95684	2	2	5.5	399	43065	4.8	FGFR1 oncogene partner
3183	Q13454	2	8	5.5	348	39676	9.9	Tumor suppressor candidate 3
3183	Q13454-2	2	8	5.5	347	39558	10.1	Isoform 2 of Q13454

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
3184	Q6NVW6	2	2	7.9	151	16479	9.4	Similar to hepatitis C virus core-binding protein 6; cervical cancer oncogene 3
3184	UPI00001615C6	2	2	6.3	189	20678	9.7	UPI00001615C6 UniRef100 entry
3184	Q9BWH2	2	2	6.3	189	20676	9.7	FUN14 domain-containing protein 2
3184	Q5HYP8	2	2	5.5	218	23339	10.4	FUN14 domain containing 2
3185	Q92917	2	2	5.5	476	52229	6.2	G patch domain and KOW motifs-containing protein
3185	UPI000059DB1D	2	2	5.5	475	52115	6.3	G patch domain and KOW motifs-containing protein (Protein T54).
3186	Q8WV24	2	3	6.6	259	29524	9.2	Pleckstrin homology-like domain family A member 1
3186	A2BDE7	2	3	5.4	312	34897	9.3	PHLDA1 protein
3186	UPI000013D704	2	3	4.2	401	45016	9.9	pleckstrin homology-like domain, family A, member 1
3187	UPI0000D612CF	2	2	9.1	309	34862	6.3	Autophagy-related protein 16-1 (APG16-like 1).
3187	Q676U5-3	2	2	6	470	53220	5.9	Isoform 3 of Q676U5
3187	Q53SV2	2	2	5.4	523	58272	6.3	Hypothetical protein FLJ10035
3187	Q676U5	2	2	4.6	607	68265	6.6	Autophagy-related protein 16-1
3188	UPI0000D60EDC	2	2	6.4	342	36977	5.1	Uncharacterized protein C18orf25.
3188	Q96B23-2	2	2	6.4	343	37048	5.1	Isoform 2 of Q96B23
3188	UPI000013DCB6	2	2	5.5	403	43324	4.9	Uncharacterized protein C18orf25.
3188	Q96B23	2	2	5.4	404	43395	4.9	Uncharacterized protein C18orf25
3189	Q9UKM7	2	3	5.4	699	79580	7.7	Endoplasmic reticulum mannosyl-oligosaccharide 1,2-alpha-mannosidase
3189	UPI0000036A6B	2	3	5.4	699	79553	7.7	alpha 1,2-mannosidase
3190	UPI00004577B7	2	2	5.4	404	44731	6	SH3 domain GRB2-like protein B2 (Endophilin-B2).
3191	O95359-2	2	2	5.3	571	64156	5.3	Isoform 2 of O95359
3191	Q4VXL4	2	2	5.2	575	64676	5.3	Transforming, acidic coiled-coil containing protein 2
3191	Q4VXL5	2	2	3.6	832	91585	5.5	Transforming, acidic coiled-coil containing protein 2
3191	UPI000002B4B3	2	2	3.2	949	103741	5	Transforming acidic coiled-coil-containing protein 2 (Anti Zuai-1) (AZU-1).
3192	Q9UHS8	2	2	6.1	393	44147	9	PRO1975
3192	Q53HW7	2	2	5.3	450	49950	9	Sulfide dehydrogenase like
3193	Q6YP21	2	2	5.3	454	51400	8.2	Kynurenine aminotransferase III
3194	Q9NXG7	2	27	5.3	525	55145	4.9	CDNA FLJ20261 fis, clone COLF7630
3195	Q5TD05	2	2	8.6	139	15645	5.3	NAD(P)H dehydrogenase, quinone 2
3195	Q59EN2	2	2	7.5	160	17996	8	NAD(P)H dehydrogenase, quinone 2 variant
3195	Q5TD07	2	2	6.2	193	21537	6.5	NAD(P)H dehydrogenase, quinone 2
3195	P16083	2	2	5.2	231	25953	6.3	Ribosyldihydronicotinamide dehydrogenase [quinone]
3195	Q5TD04	2	2	5.2	231	25919	6.3	NAD(P)H dehydrogenase, quinone 2
3196	Q16850	2	6	5.2	503	56806	8.5	Cytochrome P450 51A1
3197	Q05BI1	2	2	5.6	392	41979	9.1	Hypothetical protein
3197	A0JLT1	2	2	5.1	429	46024	8.8	Hypothetical protein
3197	O15446-2	2	2	4.3	512	55172	8.4	Isoform 2 of O15446
3197	O15446	2	2	4.3	510	54986	8.5	RNA polymerase I-associated factor PAF49
3198	Q5SY40	2	2	6.5	460	51013	8.9	Ligatin
3198	P41214-2	2	2	6.5	460	51040	8.9	Isoform 2 of P41214
3198	P41214	2	2	5.1	584	64734	7.6	Ligatin
3198	Q96DG3	2	2	5.1	584	64707	7.6	Ligatin
3199	P48651	2	19	5.1	473	55528	8.4	Phosphatidylserine synthase 1
3200	P49810	2	2	5.1	448	50140	4.6	Presenilin-2 (EC 3.4.23.-) (PS-2) (STM-2) (E5-1) (AD3LP) (AD5) [Contains: Presenilin-2 NTF subunit; Presenilin-2 CTF subunit]
3200	UPI00001616FE	2	2	5.1	447	50015	4.6	presenilin 2 isoform 2
3200	UPI000003F060	2	2	5.1	448	50144	4.6	presenilin 2 isoform 1
3201	Q12972	2	2	5.1	351	38479	7.4	Nuclear inhibitor of protein phosphatase 1 (NIPP-1) (Protein phosphatase 1 regulatory inhibitor subunit 8) [Includes: Activator of RNA decay (EC 3.1.4.-) (ARD-1)]
3201	Q561W4	2	2	5.1	351	38478	7.4	Protein phosphatase 1, regulatory (Inhibitor) subunit 8
3202	Q16566	2	2	5.1	473	51926	5.8	Calcium/calmodulin-dependent protein kinase type IV
3203	Q8NBJ4-2	2	2	5.4	391	44273	4.9	Isoform 2 of Q8NBJ4
3203	Q8NBJ4	2	2	5.2	401	45333	5	Golgi phosphoprotein 2
3203	Q5VZE3	2	2	5.1	410	46273	5	Golgi phosphoprotein 2
3204	UPI0000D6136D	2	6	5.5	492	52720	5.5	CD276 antigen precursor (Costimulatory molecule) (B7 homolog 3) (B7- H3) (4Ig-B7-H3).
3204	Q5ZPR3-3	2	6	5.5	493	52762	5.5	Isoform 3 of Q5ZPR3
3204	Q5ZPR3	2	6	5.1	534	57235	4.9	CD276 antigen precursor
3204	Q5ZPR3-4	2	6	5.1	533	57165	5	Isoform 4 of Q5ZPR3
3205	Q9P2K3-2	2	2	5.7	436	47760	6.7	Isoform 2 of Q9P2K3
3205	Q9P2K3	2	2	5.1	495	55581	8.3	REST corepressor 3
3206	Q9Y302-2	2	3	6.9	335	38484	9.4	Isoform 2 of Q9Y302
3206	UPI0000D4C36B	2	3	6.1	379	43772	9.4	PREDICTED: similar to G protein-coupled receptor 89
3206	Q9Y302	2	3	5.1	455	52917	9.3	Protein GPR89A
3206	UPI0000D61FC4	2	3	5	458	53279	9.3	Protein GPR89A (Putative MAPK-activating protein PM01) (Putative NF- kappa-B-activating protein 90).
3207	Q14194	2	3	5.9	572	62184	7	Dihydropyrimidinase-related protein 1

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3207	A0EJG6	2	3	5	686	74262	6.9	Long form collapsin response mediator protein 1
3208	A0PJ71	2	3	5	478	53226	9.1	Hypothetical protein
3208	O60934	2	3	3.2	754	84959	6.9	Nibrin
3209	P29083	2	3	5	439	49452	4.8	Transcription initiation factor IIE subunit alpha
3209	UPI00001367F2	2	3	5	439	49480	4.8	general transcription factor IIE, polypeptide 1 (alpha subunit, 56kD)
3210	UPI00001AED12	2	2	5.4	355	38659	5.2	vacuolar protein sorting 37C
3210	Q8N3K4	2	2	5	377	41650	7.3	Vacuolar protein sorting-associated protein 37 homolog C
3211	Q9NSG8	2	2	9.3	258	30204	9.2	Hypothetical protein DKFZp761G1923
3211	Q9BTU6	2	2	5	479	54022	8.3	Phosphatidylinositol 4-kinase type II
3212	Q9NV88	2	3	5	658	73815	6.3	Integrator complex subunit 9
3212	UPI0000070FF9	2	3	5	658	73786	6.3	integrator complex subunit 9
3213	Q5T7V6	2	2	4.9	350	39927	6.8	Protein prenyltransferase alpha subunit repeat containing 1
3214	Q5TDF7	2	3	4.9	384	43089	8.2	NOL1/NOP2/Sun domain family, member 4
3214	Q96CB9	2	3	4.9	384	43059	8.2	NOL1/NOP2/Sun domain family, member 4
3215	Q68D27	2	2	4.9	575	63967	6.9	Hypothetical protein DKFZp686B20267
3215	Q96RQ3	2	2	3.9	725	80473	7.8	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial precursor
3216	Q8IVX4	2	2	4.9	509	57063	5.6	T-complex 11-like protein 1
3216	Q9NUJ3	2	2	4.9	509	57035	5.6	CDNA FLJ11336 fis, clone PLACE1010661, weakly similar to TESTIS- SPECIFIC PROTEIN PBS13
3217	UPI000045631B	2	2	5.2	404	43603	8.5	Egl nine homolog 1 (EC 1.14.11.-) (Hypoxia-inducible factor prolyl hydroxylase 2) (HIF-prolyl hydroxylase 2) (HIF-PH2) (HPH-2) (Prolyl hydroxylase domain-containing protein 2) (PHD2) (SM-20).
3217	Q9GZT9-2	2	2	5.2	404	43666	8.5	Isoform 2 of Q9GZT9
3217	Q9GZT9	2	2	4.9	426	46021	8.5	Egl nine homolog 1
3218	Q9NRX5	2	3	4.9	453	50495	5.8	Serine incorporator 1
3219	Q9NWQ8	2	3	4.9	432	46981	4.6	Phosphoprotein associated with glycosphingolipid-enriched microdomains 1
3220	P04049	2	2	4.8	648	73052	9.2	RAF proto-oncogene serine/threonine-protein kinase
3221	P15291	2	3	4.8	398	43920	8.6	Beta-1,4-galactosyltransferase 1 (EC 2.4.1.-) (Beta-1,4-GalTase 1) (Beta4Gal-T1) (b4Gal-T1) (UDP-galactose:beta-N-acetylglucosamine beta- 1,4-galactosyltransferase 1) (UDP-Gal:beta-GlcNAc beta-1,4- galactosyltransferase 1) [Includes: Lactose synthase A protein (EC 2.4.1.22); N-acetyllactosamine synthase (EC 2.4.1.90) (Nal synthetase); Beta-N-acetylglucosaminylglycopeptide beta-1,4- galactosyltransferase (EC 2.4.1.38); Beta-N-acetylglucosaminyl- glycolipid beta-1,4-galactosyltransferase (EC 2.4.1.-)]
3222	P30837	2	4	4.8	517	57238	6.8	Aldehyde dehydrogenase X, mitochondrial precursor
3223	Q9BPW0	2	5	5	484	55096	6.2	PPP5C protein
3223	P53041	2	5	4.8	499	56879	6.3	Serine/threonine-protein phosphatase 5
3223	Q53FR0	2	5	4.8	499	56907	6.3	Protein phosphatase 5, catalytic subunit variant
3224	Q15629	2	18	4.8	374	43072	9.6	Translocation-associated membrane protein 1
3225	UPI000013E464	2	2	6.7	596	65586	6	family with sequence similarity 91, member A1 (FAM91A1), mRNA
3225	Q658Y4	2	2	4.8	838	93969	6.4	Protein FAM91A1
3226	Q9HAB1	2	2	5.3	438	47170	6.8	CDNA FLJ11863 fis, clone HEMBA1006926
3226	UPI000045716A	2	2	5.2	439	47299	6.8	solute carrier family 41, member 3 isoform 4
3226	UPI000013FC30	2	2	5	461	49916	7.9	solute carrier family 41, member 3 isoform 4
3226	Q8NB27	2	2	4.8	478	51507	7.2	CDNA FLJ34352 fis, clone FEBRA2011593
3226	UPI00003D2133	2	2	4.7	487	52449	6.9	solute carrier family 41, member 3 isoform 2
3226	UPI00001AF113	2	2	4.6	496	53923	7.2	solute carrier family 41, member 3 isoform 4
3226	UPI000013D523	2	2	4.5	507	54767	7.8	solute carrier family 41, member 3 isoform 4
3226	Q96GZ6	2	2	4.5	507	54737	7.8	Solute carrier family 41 member 3
3227	Q8NI20	2	2	5.4	790	86067	5.7	Spermatogenesis associated factor protein
3227	Q8NB90	2	2	4.8	893	97934	5.7	Spermatogenesis-associated protein 5
3227	UPI000013D9E6	2	2	4.8	893	97904	5.7	spermatogenesis associated factor SPAF
3227	Q8TDL7	2	2	4.8	893	97920	5.7	Spermatogenesis associated factor
3228	Q96HC3	2	2	4.8	538	60647	7.2	CWF19-like protein 1
3228	Q9NV13	2	2	4.8	538	60619	7.2	CDNA FLJ10998 fis, clone PLACE1002465
3229	A2VDI4	2	9	4.7	674	76138	6.5	KIAA0143 protein
3229	UPI000041A085	2	9	4.1	785	88802	6.5	hypothetical protein LOC23167
3229	Q14156-3	2	9	4.1	777	87580	6.6	Isoform 3 of Q14156
3229	Q14156	2	9	3.9	821	92924	6.7	Protein EFR3-like
3230	Q8TD12	2	3	6.8	265	29370	8.4	Decay-accelerating factor 3
3230	Q5VW88	2	3	6.1	293	32190	5.5	CD55 molecule, decay accelerating factor for complement
3230	UPI0000D6209C	2	3	5	358	38991	7.4	Complement decay-accelerating factor precursor (CD55 antigen).
3230	Q14UF5	2	3	4.9	364	39759	7.6	Decay-accelerating factor splicing variant 2
3230	P08174	2	3	4.7	381	41400	7.6	Complement decay-accelerating factor precursor

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
3230	UPI0000D6209A	2	3	4.7	381	41574	7.4	Complement decay-accelerating factor precursor (CD55 antigen).
3230	Q14UF4	2	3	4.7	384	41900	7.9	Decay-accelerating factor splicing variant 3
3230	Q8TD13	2	3	4.3	422	44850	9.6	Decay-accelerating factor 1 ab
3230	Q8TD11	2	3	4.3	419	44797	9.7	Decay-accelerating factor 4ab
3230	UPI00004562EE	2	3	4.1	440	48744	8.4	Complement decay-accelerating factor precursor (CD55 antigen).
3230	Q5VW91	2	3	4.1	444	49338	8.8	CD55 molecule, decay accelerating factor for complement
3230	Q14UF6	2	3	4.1	439	48513	7.9	Decay-accelerating factor splicing variant 1
3230	P08174-2	2	3	4.1	440	48717	8.4	Isoform 1 of P08174
3230	Q14UF3	2	3	3.4	525	56218	8.5	Decay-accelerating factor splicing variant 4
3230	Q14UF2	2	3	3.3	551	59038	8.8	Decay-accelerating factor splicing variant 5
3231	Q06587	2	4	4.7	406	42429	5.6	E3 ubiquitin-protein ligase RING1
3232	Q6P1Q2	2	2	5.4	484	52550	8.8	N-PAC protein
3232	Q9BTI1	2	2	5	523	57215	9.2	Similar to RIKEN cDNA 3930401K13 gene
3232	UPI000059D307	2	2	4.9	536	58637	9.2	cytokine-like nuclear factor n-pac
3232	Q9BXK2	2	2	4.8	547	59828	9.3	Cytokine-like nuclear factor n-pac
3232	Q49A26	2	2	4.7	553	60606	9.2	Cytokine-like nuclear factor n-pac
3232	UPI00001FF8EE	2	2	4.7	553	60556	9.2	cytokine-like nuclear factor n-pac
3232	Q6V3W7	2	2	4.7	553	60547	9.2	Cytokine-like nuclear factor n-pac-like protein
3232	Q5U632	2	2	4.7	553	60548	9.1	Cytokine-like nuclear factor n-pac
3233	UPI00006C18D5	2	3	6.5	403	43994	6.2	PREDICTED: similar to alveolar soft part sarcoma chromosome region, candidate 1
3233	Q9BZE9	2	3	4.7	553	60183	6.6	Tether containing UBX domain for GLUT4
3233	Q9BZE9-2	2	3	4	647	69990	8.1	Isoform 2 of Q9BZE9
3234	UPI0000D610A8	2	4	8.5	316	36720	6.7	Nuclear receptor coactivator 5 (NCoA-5) (Coactivator independent of AF-2) (CIA).
3234	Q9HCD5	2	4	4.7	579	65536	9.6	Nuclear receptor coactivator 5
3235	Q9NVH1-3	2	6	5.1	507	57197	7.5	Isoform 3 of Q9NVH1
3235	UPI0000D61E3A	2	6	5	523	59173	7.6	DnaJ homolog subfamily C member 11.
3235	Q9NVH1-2	2	6	5	521	58947	7.6	Isoform 2 of Q9NVH1
3235	Q9NVH1	2	6	4.7	559	63278	8.4	DnaJ homolog subfamily C member 11
3235	UPI000006D6B2	2	6	4.7	559	63336	8.4	DnaJ (Hsp40) homolog, subfamily C, member 11
3236	Q9UQB8-3	2	3	5.1	512	56626	9	Isoform 3 of Q9UQB8
3236	Q9UQB8-6	2	3	5	522	57430	8.9	Isoform 6 of Q9UQB8
3236	Q9UQB8-5	2	3	5	520	57445	8.8	Isoform 5 of Q9UQB8
3236	Q9UQB8-4	2	3	5	521	57359	8.9	Isoform 4 of Q9UQB8
3236	Q9UQB8-2	2	3	4.9	534	59014	9	Isoform 2 of Q9UQB8
3236	Q9UQB8	2	3	4.7	552	60868	8.9	Brain-specific angiogenesis inhibitor 1-associated protein 2
3237	A0AV58	2	2	4.6	713	77718	5.3	Striatin, calmodulin binding protein 3
3237	UPI0000456764	2	2	4.6	716	78195	5.3	Striatin-3 (Cell-cycle autoantigen SG2NA) (S/G2 antigen).
3237	UPI00001B09B8	2	2	4.6	713	77696	5.3	nuclear autoantigen
3237	Q13033-2	2	2	4.6	713	77669	5.3	Isoform Alpha of Q13033
3237	A2RTX7	2	2	4.6	713	77745	5.3	Striatin, calmodulin binding protein 3
3238	A0S2X6	2	8	4.6	603	67055	9	NADH dehydrogenase subunit 5
3238	Q4F4F8	2	8	4.6	603	67011	9	NADH dehydrogenase subunit 5
3238	Q4F454	2	8	4.6	603	67087	9	NADH dehydrogenase subunit 5
3238	Q4F3W3	2	8	4.6	603	67029	9	NADH dehydrogenase subunit 5
3238	Q4F340	2	8	4.6	603	66984	9	NADH dehydrogenase subunit 5
3238	Q4F2Y8	2	8	4.6	603	66963	9	NADH dehydrogenase subunit 5
3238	Q4F2K8	2	8	4.6	603	67012	9	NADH dehydrogenase subunit 5
3238	Q4F2F6	2	8	4.6	603	67027	9	NADH dehydrogenase subunit 5
3238	Q4F200	2	8	4.6	603	67043	9	NADH dehydrogenase subunit 5
3238	Q4F1S2	2	8	4.6	603	67069	9	NADH dehydrogenase subunit 5
3238	Q4F0F4	2	8	4.6	603	67011	9	NADH dehydrogenase subunit 5
3238	Q4F050	2	8	4.6	603	67039	9	NADH dehydrogenase subunit 5
3238	Q4EZT3	2	8	4.6	603	67013	9	NADH dehydrogenase subunit 5
3238	Q4EZS0	2	8	4.6	603	67027	9	NADH dehydrogenase subunit 5
3238	Q4EZP4	2	8	4.6	603	67041	9	NADH dehydrogenase subunit 5
3238	Q4EZ36	2	8	4.6	603	67023	9	NADH dehydrogenase subunit 5
3238	Q4EYP3	2	8	4.6	603	67000	9	NADH dehydrogenase subunit 5
3238	Q4EY48	2	8	4.6	603	66981	9	NADH dehydrogenase subunit 5
3238	Q4EXY9	2	8	4.6	603	66971	9	NADH dehydrogenase subunit 5
3238	Q4EXW4	2	8	4.6	603	67018	9	NADH dehydrogenase subunit 5
3238	Q4EXU5	2	8	4.6	603	67004	9	NADH dehydrogenase subunit 5
3238	Q4EXP2	2	8	4.6	603	67040	9	NADH dehydrogenase subunit 5
3238	Q4EXM9	2	8	4.6	603	67043	9.1	NADH dehydrogenase subunit 5
3238	Q4EWD7	2	8	4.6	603	67023	9	NADH dehydrogenase subunit 5
3238	Q3S9H4	2	8	4.6	603	67057	9	NADH dehydrogenase subunit 5
3238	Q306C1	2	8	4.6	603	67013	9	NADH dehydrogenase subunit 5
3238	Q305W9	2	8	4.6	603	67000	9	NADH dehydrogenase subunit 5
3238	Q2LHU9	2	8	4.6	603	66997	9	NADH dehydrogenase subunit 5
3238	Q2LHB7	2	8	4.6	603	67017	9	NADH dehydrogenase subunit 5
3238	Q2LH26	2	8	4.6	603	67057	9	NADH dehydrogenase subunit 5
3238	Q2L743	2	8	4.6	603	67057	9	NADH dehydrogenase subunit 5
3238	Q2HKQ7	2	8	4.6	603	67025	9	NADH dehydrogenase subunit 5

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
3238	Q2HKK5	2	8	4.6	603	67012	9	NADH dehydrogenase subunit 5
3238	Q2HJQ6	2	8	4.6	603	66967	9	NADH dehydrogenase subunit 5
3238	Q27H51	2	8	4.6	603	67057	9	NADH dehydrogenase subunit 5
3238	Q27H25	2	8	4.6	603	67043	9	NADH dehydrogenase subunit 5
3238	Q1ZY31	2	8	4.6	603	67072	9	NADH dehydrogenase subunit 5
3238	Q1W0U7	2	8	4.6	603	67042	9	NADH dehydrogenase subunit 5
3238	Q1ADM1	2	8	4.6	603	66998	9	NADH dehydrogenase subunit 5
3238	Q1ADK8	2	8	4.6	603	67040	9	NADH dehydrogenase subunit 5
3238	Q15II4	2	8	4.6	603	67013	9	NADH dehydrogenase subunit 5
3238	Q15ID2	2	8	4.6	603	67051	9	NADH dehydrogenase subunit 5
3238	Q15HM4	2	8	4.6	603	66986	9	NADH dehydrogenase subunit 5
3238	Q15HL1	2	8	4.6	603	67000	9	NADH dehydrogenase subunit 5
3238	Q15HH2	2	8	4.6	603	67042	9	NADH dehydrogenase subunit 5
3238	Q15HE6	2	8	4.6	603	67027	9	NADH dehydrogenase subunit 5
3238	Q15H42	2	8	4.6	603	66983	9	NADH dehydrogenase subunit 5
3238	Q15GZ0	2	8	4.6	603	67013	9	NADH dehydrogenase subunit 5
3238	Q15GW4	2	8	4.6	603	67013	9	NADH dehydrogenase subunit 5
3238	Q0ZK24	2	8	4.6	603	66997	9	NADH dehydrogenase subunit 5
3238	Q0ZFK3	2	8	4.6	603	67039	9	NADH dehydrogenase subunit 5
3238	Q0ZFC5	2	8	4.6	603	66999	9	NADH dehydrogenase subunit 5
3238	Q0Z7P8	2	8	4.6	603	66967	9	NADH dehydrogenase subunit 5
3238	Q0Z7K9	2	8	4.6	603	66971	9	NADH dehydrogenase subunit 5
3238	Q06V50	2	8	4.6	603	67000	9	NADH dehydrogenase subunit 5
3238	Q06UH9	2	8	4.6	603	67031	9	NADH dehydrogenase subunit 5
3238	Q06UC7	2	8	4.6	603	67000	9	NADH dehydrogenase subunit 5
3238	P03915	2	8	4.6	603	67027	9	NADH-ubiquinone oxidoreductase chain 5
3238	A4GYN5	2	8	4.6	603	67016	9	NADH dehydrogenase subunit 5
3238	A3R0P4	2	8	4.6	603	67027	9	NADH dehydrogenase subunit 5
3238	A3R0N1	2	8	4.6	603	67069	9	NADH dehydrogenase subunit 5
3238	A3R0L8	2	8	4.6	603	67026	9.1	NADH dehydrogenase subunit 5
3238	A1Z550	2	8	4.6	603	67007	9	NADH dehydrogenase subunit 5
3238	A1Z4K5	2	8	4.6	603	67027	9	NADH dehydrogenase subunit 5
3238	A1Z4H9	2	8	4.6	603	67083	9	NADH dehydrogenase subunit 5
3238	A1Z4G6	2	8	4.6	603	66997	9	NADH dehydrogenase subunit 5
3238	A1E1L3	2	8	4.6	603	67005	9	NADH dehydrogenase subunit 5
3238	A1DVU9	2	8	4.6	603	67051	9	NADH dehydrogenase subunit 5
3238	A1DVT6	2	8	4.6	603	67054	9	NADH dehydrogenase subunit 5
3238	A1DVN4	2	8	4.6	603	67054	9	NADH dehydrogenase subunit 5
3238	A1DV00	2	8	4.6	603	67011	9	NADH dehydrogenase subunit 5
3238	A1DTY1	2	8	4.6	603	67044	9	NADH dehydrogenase subunit 5
3238	A1DTP0	2	8	4.6	603	67028	9	NADH dehydrogenase subunit 5
3238	A1DTE9	2	8	4.6	603	67000	9	NADH dehydrogenase subunit 5
3238	A1DTD6	2	8	4.6	603	67000	9	NADH dehydrogenase subunit 5
3238	A1DT71	2	8	4.6	603	67014	9	NADH dehydrogenase subunit 5
3238	A1DSY0	2	8	4.6	603	67070	9	NADH dehydrogenase subunit 5
3238	A1DSV4	2	8	4.6	603	67070	9	NADH dehydrogenase subunit 5
3238	A1DSU1	2	8	4.6	603	67026	9	NADH dehydrogenase subunit 5
3238	A1DSK0	2	8	4.6	603	67010	9	NADH dehydrogenase subunit 5
3238	A1DSD5	2	8	4.6	603	67010	9	NADH dehydrogenase subunit 5
3238	A0SBQ0	2	8	4.6	603	66953	8.9	NADH dehydrogenase subunit 5
3238	A0SBN6	2	8	4.6	603	66983	9	NADH dehydrogenase subunit 5
3238	A0SBJ7	2	8	4.6	603	67043	9	NADH dehydrogenase subunit 5
3238	A0SBH1	2	8	4.6	603	67017	9	NADH dehydrogenase subunit 5
3238	A0SB29	2	8	4.6	603	67087	9	NADH dehydrogenase subunit 5
3238	A0S952	2	8	4.6	603	67033	9	NADH dehydrogenase subunit 5
3238	A0S939	2	8	4.6	603	67033	9	NADH dehydrogenase subunit 5
3238	A0S8Q9	2	8	4.6	603	67081	9	NADH dehydrogenase subunit 5
3238	A0S8I1	2	8	4.6	603	67033	9	NADH dehydrogenase subunit 5
3238	A0S4F9	2	8	4.6	603	67015	9	NADH dehydrogenase subunit 5
3238	A0S481	2	8	4.6	603	66979	9	NADH dehydrogenase subunit 5
3238	A0S302	2	8	4.6	603	67041	9	NADH dehydrogenase subunit 5
3239	O43264	2	4	4.6	779	88830	6.3	Centromere/kinetochore protein zw10 homolog
3240	Q7Z7E9	2	2	6.8	384	40283	9.1	BLOM7 gamma
3240	O94981	2	2	4.6	569	59608	8.4	KIAA0907 protein
3240	Q7Z7F0	2	2	4.2	614	64845	8.7	Protein KIAA0907
3241	P09960-2	2	2	5.2	537	60704	5.6	Isoform 2 of P09960
3241	P09960	2	2	4.6	611	69285	6.2	Leukotriene A-4 hydrolase (EC 3.3.2.6) (LTA-4 hydrolase) (Leukotriene A(4) hydrolase)
3242	UPI0000D615AF	2	6	6.7	344	38821	8.5	Calcium/calmodulin-dependent protein kinase type II delta chain (EC 2.7.11.17) (CaM-kinase II delta chain) (CaM kinase II subunit delta) (CaMK-II subunit delta).
3242	Q4G1A8	2	6	6.7	344	38880	9	CAMK2D protein
3242	Q13557-8	2	6	4.8	478	54128	7.3	Isoform Delta 6 of Q13557
3242	UPI0000D615AE	2	6	4.7	489	55378	7.7	Calcium/calmodulin-dependent protein kinase type II delta chain (EC 2.7.11.17) (CaM-kinase II delta chain) (CaM kinase II subunit delta) (CaMK-II subunit delta).
3242	Q13557-9	2	6	4.7	488	55250	7.6	Isoform Delta 7 of Q13557

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
3242	Q13557	2	6	4.6	499	56369	7.2	Calcium/calmodulin-dependent protein kinase type II delta chain
3242	Q13557-5	2	6	4.6	497	56102	7.3	Isoform Delta 8 of Q13557
3242	Q13557-11	2	6	4.6	498	56298	7.2	Isoform Delta 11 of Q13557
3242	Q13557-6	2	6	4.5	512	57773	7	Isoform Delta 9 of Q13557
3242	Q13557-3	2	6	4.5	509	57492	7.5	Isoform Delta 3 of Q13557
3242	Q13557-4	2	6	4.4	518	58344	7.2	Isoform Delta 4 of Q13557
3243	UPI000006F0A2	2	2	6.1	311	34819	5.9	hypothetical protein LOC23172
3243	Q15018	2	2	4.6	415	46901	6.2	Uncharacterized protein KIAA0157
3244	Q15554	2	2	4.6	500	55551	9.2	Telomeric repeat-binding factor 2
3245	Q9NQX3	2	2	4.6	736	79748	5.4	Gephyrin
3245	Q9NQX3-2	2	2	4.4	769	83447	5.6	Isoform 2 of Q9NQX3
3246	Q5TCW7	2	2	5	541	61804	7.9	RNA guanylyltransferase and 5'-phosphatase
3246	O60942-4	2	2	5	541	61705	7.7	Isoform 4 of O60942
3246	O60942-2	2	2	4.7	574	66042	8.4	Isoform 2 of O60942
3246	O60942	2	2	4.5	597	68557	8.1	mRNA-capping enzyme (HCE) (HCAP1) [Includes: Polynucleotide 5'- triphosphatase (EC 3.1.3.33) (mRNA 5'-triphosphatase) (TPase); mRNA guanylyltransferase (EC 2.7.7.50) (GTP--RNA guanylyltransferase) (GTase)]
3246	Q8WUM8	2	2	4.5	597	68542	8	RNA guanylyltransferase and 5'-phosphatase
3247	P43007	2	4	4.5	532	55723	6.3	Neutral amino acid transporter A
3247	Q53F03	2	4	4.5	532	55723	6.3	Solute carrier family 1, member 4 variant
3248	UPI000013F63F	2	2	4.7	491	55217	9.7	ATP-dependent RNA helicase ROK1 isoform b
3248	Q59H21	2	2	4.5	512	57758	9.4	ATP-dependent RNA helicase ROK1 isoform a variant
3248	UPI0000046805	2	2	3.8	599	67498	9.7	ATP-dependent RNA helicase ROK1 isoform a
3248	Q9Y2R4	2	2	3.8	599	67466	9.7	Probable ATP-dependent RNA helicase DDX52
3249	Q6UN15-4	2	5	7.1	378	40835	4.7	Isoform 4 of Q6UN15
3249	Q6UN15-3	2	5	5.2	520	58376	5.6	Isoform 3 of Q6UN15
3249	Q6UN15-2	2	5	4.8	559	63048	6.5	Isoform 2 of Q6UN15
3249	Q6UN15	2	5	4.5	594	66526	5.6	Pre-mRNA 3'-end-processing factor FIP1
3250	Q9P0J1	2	4	4.5	537	61054	6.7	[Pyruvate dehydrogenase [lipoamide]]-phosphatase 1, mitochondrial precursor
3251	Q9HCH4	2	2	4.5	446	51474	5.5	KIAA1598 protein
3251	A0MZ66	2	2	4.4	456	52636	5.4	Shootin1
3251	Q68DG1	2	2	3.1	649	73609	5.4	Protein KIAA1598
3252	A2A2V2	2	2	4.4	408	45918	10.1	Novel protein
3252	P42696	2	2	4.2	430	48565	10.1	RNA-binding protein 34
3253	Q4AEJ5	2	4	4.4	523	59249	6.6	KIAA0488 protein
3253	Q5VWB2	2	4	4.4	528	59811	6.3	Sorting nexin family member 27
3253	Q5VWB1	2	4	4.3	541	61265	6.5	Sorting nexin family member 27
3254	Q96J85	2	4	7.7	375	42505	6.1	C-Mpl binding protein
3254	Q6ZV14	2	4	4.4	654	73149	7.8	CDNA FLJ43123 fis, clone CTONG3003972
3254	UPI000045660C	2	4	4.4	653	72382	6.2	La-related protein 4 (La ribonucleoprotein domain family member 4).
3254	UPI0000231CB7	2	4	4.4	653	72400	6.3	c-Mpl binding protein isoform c
3254	UPI000045660B	2	4	4	730	81226	6.5	La-related protein 4 (La ribonucleoprotein domain family member 4).
3254	UPI0000231CB8	2	4	4	730	81244	6.6	c-Mpl binding protein isoform b
3254	UPI0000141A27	2	4	4	724	80624	6.6	c-Mpl binding protein isoform a
3254	Q71RC2	2	4	4	723	80468	6.6	La-related protein 4
3255	Q96NJ5	2	2	4.4	620	70363	6.4	Kelch-like protein 32
3255	UPI000006D428	2	2	4.4	620	70352	6.4	KIAA1900
3255	UPI0000D6149D	2	2	4.3	622	70594	6.5	BTB and kelch domain-containing protein 5.
3256	Q9HCW0	2	6	6.5	340	39829	8.4	Primase, polypeptide 2A, 58kDa
3256	P49643	2	6	4.3	509	58806	7.9	DNA primase large subunit
3257	Q08AM6	2	5	4.3	782	87973	6.1	Vac14 homolog
3257	UPI0000DD83A9	2	5	2.7	1240	135879	8.6	PREDICTED: similar to Vac14 homolog
3258	Q13144	2	4	4.3	721	80366	5.1	Translation initiation factor eIF-2B subunit epsilon
3258	UPI000013D9CF	2	4	4.3	721	80380	5.1	eukaryotic translation initiation factor 2B, subunit 5 epsilon, 82kDa
3259	Q14680	2	2	4.3	651	74642	8.7	Maternal embryonic leucine zipper kinase
3259	Q53GX0	2	2	4.3	651	74642	8.7	Maternal embryonic leucine zipper kinase variant
3260	Q8ND56	2	2	4.3	463	50530	9.5	LSM14 protein homolog A
3260	UPI000006F08C	2	2	4.3	463	50526	9.4	LSM14 homolog A
3260	Q8ND56-2	2	2	4.3	463	50554	9.5	Isoform 2 of Q8ND56
3261	Q9H943	2	3	4.3	628	71506	9.3	Uncharacterized protein C10orf68
3261	Q9H943-2	2	3	3.9	692	78463	9.1	Isoform 2 of Q9H943
3262	Q8IZW2	2	2	4.5	462	49917	5.6	TAB1-like protein
3262	Q15750	2	2	4.2	504	54644	5.5	Mitogen-activated protein kinase kinase kinase 7-interacting protein 1
3262	Q59FT7	2	2	3.2	648	70265	5.3	Mitogen-activated protein kinase kinase kinase 7 interacting protein 1 isoform alpha variant
3263	UPI0000D62393	2	2	4.5	573	65651	6.5	Exocyst complex component 7 (Exocyst complex component Exo70).
3263	Q63HP7	2	2	4.5	573	65663	6.6	Hypothetical protein DKFZp686P1551
3263	Q5G0E1	2	2	4.2	616	70201	7	2-5-3p
3263	Q9UPT5-2	2	2	4	653	74713	6.4	Isoform 2 of Q9UPT5

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
3263	Q9UPT5-1	2	2	3.8	684	78060	6.7	Isoform 1 of Q9UPT5
3263	Q9UPT5	2	2	3.5	735	83382	6.8	Exocyst complex component 7
3264	Q5JUA8	2	2	4.2	525	59347	7.5	Vacuolar protein sorting 16
3264	Q9H269-2	2	2	3.2	695	78300	7.9	Isoform 2 of Q9H269
3264	UPI0000D6101F	2	2	2.6	839	94679	6.8	Vacuolar protein sorting-associated protein 16 (hVPS16).
3264	Q9H269	2	2	2.6	839	94694	6.8	Vacuolar protein sorting-associated protein 16 homolog
3265	Q6PEW1	2	2	4.2	402	45370	6.2	Zinc finger CCHC domain-containing protein 12
3265	UPI0000072244	2	2	4.2	403	45160	7.4	UPI0000072244 UniRef100 entry
3266	Q86YA8	2	2	4.2	520	56757	6.6	YLPM1 protein
3266	UPI00006C1433	2	2	1	2146	241643	6.6	PREDICTED: similar to YLP motif-containing protein 1 (Nuclear protein ZAP3) (ZAP113) isoform 2
3267	UPI000045613B	2	2	4.9	634	69185	8.2	KIAA2013 (KIAA2013), mRNA
3267	Q8IYS2	2	2	4.9	634	69157	8.2	KIAA2013
3267	Q8IVF8	2	2	4.2	730	79352	9.6	Protein KIAA2013
3268	Q96CV9	2	4	4.2	577	65922	5.2	Optineurin
3268	UPI000046FEE5	2	4	4.2	571	65202	5.2	Optineurin (Optic neuropathy-inducing protein) (E3-14.7K-interacting protein) (FIP-2) (Huntingtin-interacting protein HYPL) (NEMO-related protein) (Transcription factor IIIA-interacting protein) (TFIIIA-IntP).
3268	UPI000013D38D	2	4	4.2	577	65921	5.2	Optineurin (Optic neuropathy-inducing protein) (E3-14.7K-interacting protein) (FIP-2) (Huntingtin-interacting protein HYPL) (NEMO-related protein) (Transcription factor IIIA-interacting protein) (TFIIIA-IntP).
3268	Q96CV9-2	2	4	4.2	571	65203	5.1	Isoform 2 of Q96CV9
3269	Q9HA87	2	4	4.2	542	63216	5.1	CDNA FLJ12068 fis, clone HEMBB1002329
3269	Q9HCG0	2	4	4.2	550	64187	5.1	2-oxoglutarate and iron-dependent oxygenase domain-containing protein 1
3270	Q9Y450	2	7	4.2	684	75473	6.6	HBS1-like protein
3271	O00566	2	2	4.1	681	78864	4.9	U3 small nucleolar ribonucleoprotein protein MPP10
3272	O15091	2	3	4.1	567	65486	8.5	Uncharacterized protein KIAA0391
3272	Q8N5L5	2	3	3.9	583	67315	8.8	KIAA0391
3272	Q86YB5	2	3	3.9	583	67288	8.8	KIAA0391
3273	O60826	2	4	4.1	627	70756	6.8	Coiled-coil domain-containing protein 22
3274	UPI0000456358	2	3	4.2	578	66787	5.6	Regulator of nonsense transcripts 2 (Nonsense mRNA reducing factor 2) (Up-frameshift suppressor 2 homolog) (hUpf2).
3274	Q5W0J4	2	3	4.1	579	66842	5.7	UPF2 regulator of nonsense transcripts homolog
3274	Q9HAU5	2	3	1.9	1272	147810	5.7	Regulator of nonsense transcripts 2
3275	Q85KV2	2	8	4.1	459	51623	9.4	NADH dehydrogenase subunit 4
3276	Q8NA66	2	2	4.1	436	50224	9.1	Cyclic nucleotide-binding domain-containing protein 1
3276	UPI00004576C7	2	2	4.1	436	50239	9.1	cyclic nucleotide binding domain containing 1
3277	Q96K12	2	2	4.1	515	59439	9.4	Fatty acyl-CoA reductase 2
3277	Q9NUX8	2	2	4.1	515	59339	9.3	CDNA FLJ11065 fis, clone PLACE1004868, weakly similar to MALE STERILITY PROTEIN 2
3278	Q9BQD0	2	10	4.1	607	70305	8.1	NLN protein
3278	Q9BYT8	2	10	3.6	704	80652	6.6	Neurolysin, mitochondrial precursor
3279	Q9NVM9	2	2	4.1	706	80225	6.7	Uncharacterized protein C12orf11
3279	UPI0000073AB1	2	2	4.1	706	80103	6.8	hypothetical protein LOC55726
3280	Q5TBH6	2	3	12.2	222	25225	8.7	Glyceronephosphate O-acyltransferase
3280	Q5TBH8	2	3	4.6	587	67046	6.3	Glyceronephosphate O-acyltransferase
3280	O15228	2	3	4	680	77188	6.6	Dihydroxyacetone phosphate acyltransferase
3280	Q53H08	2	3	4	680	77162	6.6	Glyceronephosphate O-acyltransferase variant
3280	Q53FI2	2	3	4	680	77089	6.4	Glyceronephosphate O-acyltransferase variant
3280	Q59EC9	2	3	3.9	693	78595	6.8	Glyceronephosphate O-acyltransferase variant
3281	UPI0000456A75	2	6	4.8	395	41554	10	Zinc finger protein 207.
3281	Q53XS9	2	6	4.8	395	41559	9.9	Zinc finger protein 207
3281	O43670-2	2	6	4.1	463	49692	9.1	Isoform 2 of O43670
3281	O43670	2	6	4	478	50751	9.1	Zinc finger protein 207
3281	Q59G94	2	6	3.8	496	52856	9	Zinc finger protein 207 variant
3282	P36406-3	2	9	4.2	546	61068	6.4	Isoform Gamma of P36406
3282	P36406	2	9	4	574	64067	6.4	GTP-binding protein ARD-1
3282	P36406-2	2	9	4	569	63690	6.4	Isoform Beta of P36406
3283	Q5JPC7	2	2	4	471	53610	7.2	Hypothetical protein DKFZp667E137
3283	Q86U73	2	2	4	471	53644	7.2	Flavin containing monooxygenase 2
3283	Q99518	2	2	3.6	535	60907	8.3	Dimethylaniline monooxygenase [N-oxide-forming] 2
3284	Q8IYI6	2	2	4	725	81799	5.5	Exocyst complex component 8
3285	Q8IZ52	2	5	4	775	85495	7	Chondroitin sulfate synthase 2
3285	UPI00001AE6D6	2	5	4	775	85467	6.9	Chondroitin sulfate synthase 2 (EC 2.4.1.175) (Glucuronosyl-N- acetylgalactosaminyl-proteoglycan 4-beta-N- acetylgalactosaminyltransferase II) (N-acetylgalactosaminyl- proteoglycan 3-beta-glucuronosyltransferase II) (EC 2.4.1.226) (Chondroitin glucuronylt
3286	Q96EB6	2	3	4	747	81681	4.7	NAD-dependent deacetylase sirtuin-1

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
3287	Q9BYH2	2	12	4	494	54424	9.2	Cystine/glutamate exchanger
3287	Q9UPY5	2	12	4	501	55423	9.2	Cystine/glutamate transporter
3288	A2CEE0	2	3	3.9	698	77529	7.7	Quiescin Q6-like 1
3288	UPI0000D6194B	2	3	3.9	698	77420	7.4	Sulfhydryl oxidase 2 precursor (EC 1.8.3.2) (Quiescin Q6-like protein 1) (Neuroblastoma-derived sulfhydryl oxidase).
3288	UPI0000D6194A	2	3	3.9	700	77756	7.7	Sulfhydryl oxidase 2 precursor (EC 1.8.3.2) (Quiescin Q6-like protein 1) (Neuroblastoma-derived sulfhydryl oxidase).
3288	Q6ZRP7	2	3	3.9	698	77543	7.7	Sulfhydryl oxidase 2 precursor
3289	Q8NDZ7	2	3	4.2	500	55072	5	RBBP5 protein
3289	Q15291	2	3	3.9	538	59082	5.1	Retinoblastoma-binding protein 5
3289	Q7Z6D8	2	3	3.9	538	59153	5.1	Retinoblastoma binding protein 5
3290	Q8TED0	2	2	3.9	518	58355	9.1	U3 small nucleolar RNA-associated protein 15 homolog
3290	UPI000020CADC	2	2	3.9	518	58415	9.1	UTP15, U3 small nucleolar ribonucleoprotein, homolog
3291	Q9UK59	2	2	3.9	544	61555	5.5	Lariat debranching enzyme
3292	Q2Y122	2	6	3.8	764	85884	8.2	Transient receptor potencial vanilloid 4 channel variant E
3292	Q9HBA0-2	2	6	3.6	811	91261	8.2	Isoform 2 of Q9HBA0
3292	Q2Y124	2	6	3.5	824	92904	7.6	Transient receptor potencial vanilloid 4 channel variant C
3292	Q2Y123	2	6	3.5	837	94998	8.2	Transient receptor potencial vanilloid 4 channel variant D
3292	Q9HBA0-3	2	6	3.4	853	96449	8.4	Isoform 3 of Q9HBA0
3292	Q9HBA0	2	6	3.3	871	98281	7.8	Transient receptor potential cation channel subfamily V member 4
3293	Q68E02	2	4	3.8	710	78418	6.8	Hypothetical protein DKFZp686I1650
3293	Q8NI36	2	4	2.8	951	105322	7.5	WD repeat protein 36
3294	Q86YR5	2	2	3.8	652	72136	6.5	G-protein-signaling modulator 1
3295	Q9H1I8	2	2	3.8	757	86360	5.2	Activating signal cointegrator 1 complex subunit 2
3296	A2BEX3	2	5	4.1	467	51803	5.5	MutS homolog 5
3296	Q59EC5	2	5	3.9	489	54471	5.7	MSH5 protein variant
3296	A2BEX2	2	5	3.8	497	54787	5.9	MutS homolog 5
3296	A2ABF0	2	5	3.7	508	56121	5.9	MutS homolog 5
3296	Q5SSQ8	2	5	2.3	821	91734	6.2	MutS homolog 5
3296	O43196-2	2	5	2.3	835	93004	6.4	Isoform 2 of O43196
3296	O43196	2	5	2.3	834	92875	6.4	MutS protein homolog 5
3296	Q9UMP2	2	5	2.2	851	94669	6.3	G7 protein
3296	O43196-3	2	5	2.2	851	94719	6.4	Isoform 3 of O43196
3297	Q14662	2	3	4.2	669	77129	4.7	Binding protein
3297	UPI000036684D	2	3	4	707	80707	4.7	Amyloid-like protein 2 precursor (Amyloid protein homolog) (APPH) (CDEI box-binding protein) (CDEBP).
3297	Q13861	2	3	4	695	79238	4.7	Binding protein
3297	Q06481-2	2	3	4	707	80721	4.7	Isoform 2 of Q06481
3297	Q06481	2	3	3.7	763	86956	4.8	Amyloid-like protein 2 precursor
3297	Q71U10	2	3	3.7	763	86942	4.8	Amyloid protein homolog HSD-2
3297	Q06481-3	2	3	3.7	751	85487	4.8	Isoform 3 of Q06481
3298	Q49AT7	2	2	6	416	45414	6.7	TGFBI protein
3298	Q15582	2	2	3.7	683	74681	7.7	Transforming growth factor-beta-induced protein ig-h3 precursor
3298	UPI000045734C	2	2	3.7	682	74591	7.3	Transforming growth factor-beta-induced protein ig-h3 precursor (Beta ig-h3) (Kerato-epithelin) (RGD-containing collagen-associated protein) (RGD-CAP).
3298	Q53GU8	2	2	3.7	683	74651	7.7	Transforming growth factor, beta-induced, 68kDa variant
3299	Q53HB9	2	4	3.7	547	61566	9.3	DEAD (Asp-Glu-Ala-Asp) box polypeptide 56 variant
3299	Q9NY93	2	4	3.7	547	61590	9.3	Probable ATP-dependent RNA helicase DDX56
3299	Q6IAE2	2	4	3.7	547	61640	9.3	DDX56 protein
3300	Q66K25	2	4	3.9	664	72501	7.3	SAMD4B protein
3300	Q5PRF9	2	4	3.7	694	75483	6.8	Sterile alpha motif domain-containing protein 4B
3301	Q8IWZ8	2	2	3.7	645	72471	7.6	Splicing factor 4
3302	UPI0000456AAE	2	2	3.9	1166	126691	5.4	Serine/threonine-protein kinase WNK4 (EC 2.7.11.1) (Protein kinase with no lysine 4) (Protein kinase, lysine-deficient 4).
3302	Q96J92-3	2	2	3.9	1165	126577	5.4	Isoform 3 of Q96J92
3302	Q96J92	2	2	3.7	1243	134739	5.5	Serine/threonine-protein kinase WNK4
3303	Q13322-2	2	5	3.8	548	62026	7.1	Isoform 1 of Q13322
3303	A4D258	2	5	3.6	588	66487	8.2	Growth factor receptor-bound protein 10
3303	Q13322	2	5	3.5	594	67231	7.9	Growth factor receptor-bound protein 10
3304	O15269	2	3	3.6	473	52744	6	Serine palmitoyltransferase 1
3304	Q6NUL7	2	3	3.3	513	57396	7.5	SPTLC1 protein
3305	P28288	2	26	3.6	659	75476	9.4	ATP-binding cassette sub-family D member 3
3306	Q08AF3	2	6	3.6	891	101055	8.2	Schlafen family member 5
3307	Q5T8D9	2	6	3.6	716	79832	8.6	YME1-like 1
3307	Q96TA2	2	6	3.4	773	86455	8.8	ATP-dependent metalloprotease YME1L1
3308	Q68CQ4	2	2	3.6	756	87055	5.9	Digestive organ expansion factor homolog

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
3309	Q9P134	2	8	26.5	68	7722	7.1	PRO3078
3309	UPI0000F2443B	2	8	6.8	265	30483	5.4	Proto-oncogene tyrosine-protein kinase LCK
3309	UPI0000F24456	2	8	6.6	273	31536	5.4	Proto-oncogene tyrosine-protein kinase LCK
3309	UPI0000F2443A	2	8	6.5	277	32023	5.4	Proto-oncogene tyrosine-protein kinase LCK
3309	UPI0000D614B3	2	8	3.7	489	55126	7	Proto-oncogene tyrosine-protein kinase Fyn (EC 2.7.10.2) (p59-Fyn) (Protooncogene Syn) (SLK).
3309	Q5R3A8	2	8	3.7	485	54669	7	FYN oncogene related to SRC, FGR, YES
3309	P06241-3	2	8	3.7	482	54514	6.2	Isoform 3 of P06241
3309	P06239	2	8	3.5	509	58001	5.4	Proto-oncogene tyrosine-protein kinase LCK
3309	UPI0000D61EBE	2	8	3.5	516	58303	5.8	Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.10.2) (p56-LCK) (Lymphocyte cell-specific protein-tyrosine kinase) (LSK) (T cell- specific protein-tyrosine kinase).
3309	Q573B4	2	8	3.5	516	58333	5.8	Proto-oncogene tyrosine-protein kinase LCK
3309	P06241-2	2	8	3.4	534	60159	6.2	Isoform 2 of P06241
3309	P06241	2	8	3.4	537	60762	6.7	Proto-oncogene tyrosine-protein kinase Fyn
3309	UPI0000456B50	2	8	3.3	543	60827	6.7	Proto-oncogene tyrosine-protein kinase Yes (EC 2.7.10.2) (p61-Yes) (c- Yes).
3309	P07947	2	8	3.3	543	60801	6.7	Proto-oncogene tyrosine-protein kinase Yes
3309	P06239-3	2	8	3.3	539	61190	5.2	Isoform 3 of P06239
3310	Q4JCQ8	2	2	3.8	497	55149	9	Glutamate transporter variant EAAT1ex9skip
3310	P43003	2	2	3.5	542	59572	8.4	Excitatory amino acid transporter 1
3310	Q8N169	2	2	3.5	542	59503	8.2	Solute carrier family 1 (Glial high affinity glutamate transporter), member 3
3311	Q6FHF7	2	2	3.5	567	65042	5.7	RABGGTA protein
3311	UPI00003669A8	2	2	3.5	570	65317	5.7	Geranylgeranyl transferase type-2 alpha subunit (EC 2.5.1.60) (Geranylgeranyl transferase type II alpha subunit) (Rab geranylgeranyltransferase alpha subunit) (Rab geranyl- geranyltransferase alpha subunit) (Rab GG transferase alpha) (Rab GGTase alpha).
3311	Q92696	2	2	3.5	567	65072	5.7	Geranylgeranyl transferase type-2 alpha subunit
3312	Q8NDI4	2	3	3.5	657	75091	5.6	85 kDa nucleoporin
3312	Q9H9U1	2	3	3.5	656	75003	5.6	CDNA FLJ12549 fis, clone NT2RM4000689
3313	Q8WVC0	2	2	3.5	666	75404	4.5	RNA polymerase-associated protein LEO1
3314	UPI0000D616BF	2	3	4.5	557	61741	5.5	Retinoid X receptor-interacting protein 110 (Receptor-associated protein 80) (Nuclear zinc finger protein RAP80).
3314	Q96RL1-2	2	3	4.5	553	61325	5.6	Isoform 2 of Q96RL1
3314	Q96RL1	2	3	3.5	719	79728	5.4	Ubiquitin interaction motif-containing protein 1
3314	UPI0000D616BD	2	3	3.5	721	79928	5.4	Retinoid X receptor-interacting protein 110 (Receptor-associated protein 80) (Nuclear zinc finger protein RAP80).
3315	A1KY36	2	5	3.4	745	73453	9.6	Cell proliferation-inducing protein 41
3315	P27658	2	5	3.4	744	73364	9.6	Collagen alpha-1(VIII) chain precursor
3316	O43164-2	2	2	3.5	688	76119	4.4	Isoform 2 of O43164
3316	O43164	2	2	3.4	708	78242	4.4	E3 ubiquitin-protein ligase Praja2
3316	UPI000013D192	2	2	3.4	708	78214	4.4	praja 2, RING-H2 motif containing
3316	UPI0000070696	2	2	3.4	708	78242	4.4	praja 2, RING-H2 motif containing
3317	UPI0000DD868E	2	2	5.4	388	42732	5.9	PREDICTED: similar to N-acetylserotonin O-methyltransferase-like protein (ASMTL)
3317	UPI00004577F8	2	2	3.5	605	67102	6.1	N-acetylserotonin O-methyltransferase-like protein (ASMTL).
3317	Q5JQ52	2	2	3.5	605	67193	6.1	Acetylserotonin O-methyltransferase-like
3317	O95671	2	2	3.4	621	68857	6.1	N-acetylserotonin O-methyltransferase-like protein
3317	UPI00004577F9	2	2	3.3	629	69791	6	N-acetylserotonin O-methyltransferase-like protein (ASMTL).
3318	Q0WX56	2	2	3.4	530	59557	8	Deubiquitinating enzyme DUB2
3319	Q15139	2	2	3.4	912	101888	6.7	Serine/threonine-protein kinase D1
3319	UPI0000D623E9	2	2	3.4	914	101889	6.6	Serine/threonine-protein kinase D1 (EC 2.7.11.13) (nPKC-D1) (Protein kinase D) (Protein kinase C mu type) (nPKC-mu).
3319	UPI0000456761	2	2	3.4	912	101704	6.6	protein kinase D1
3319	Q1KKQ2	2	2	3.4	914	101848	6.6	Protein kinase D1
3320	UPI000015D94C	2	2	3.7	464	53306	7.2	serum/glucocorticoid regulated kinase 3 isoform 2
3320	Q53EW6	2	2	3.4	496	57048	6.9	Serum/glucocorticoid regulated kinase-like isoform 1 variant
3320	Q96BR1	2	2	3.4	496	57108	6.9	Serine/threonine-protein kinase Sgk3
3320	Q5H9Q5	2	2	3.4	496	57094	6.8	Hypothetical protein DKFZp781N0293
3321	Q5JPE5	2	2	3.4	738	83566	6.1	Hypothetical protein DKFZp667L062
3321	Q99549	2	2	2.9	860	97182	6.1	M-phase phosphoprotein 8
3322	Q5MIZ7-3	2	6	3.8	764	87377	4.8	Isoform 3 of Q5MIZ7
3322	Q5MIZ7-2	2	6	3.5	817	93718	4.9	Isoform 2 of Q5MIZ7
3322	Q5MIZ7	2	6	3.4	849	97444	5	SMEK homolog 2
3322	UPI00001C1DBA	2	6	3.4	849	97458	5	SMEK homolog 2.
3323	Q8TAS8	2	2	3.8	558	62528	6.4	Oxysterol binding protein-like 9
3323	Q8NB17	2	2	3.7	571	63892	6.3	CDNA FLJ34384 fis, clone HCHON1000131, weakly similar to KES1 PROTEIN
3323	Q6IA67	2	2	3.7	571	63926	6.3	Oxysterol-binding protein

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
3323	Q5TFC0	2	2	3.4	626	70237	6.1	Oxysterol-binding protein
3323	Q96SK4	2	2	3.4	626	70265	6.1	CDNA FLJ14801 fis, clone NT2RP4001389, weakly similar to KES1 PROTEIN
3323	UPI000049DC8D	2	2	3.3	628	70465	6.1	Oxysterol-binding protein-related protein 9 (OSBP-related protein 9) (ORP-9).
3323	UPI0000D61F19	2	2	2.9	721	81394	5.8	Oxysterol-binding protein-related protein 9 (OSBP-related protein 9) (ORP-9).
3323	Q96SU4-2	2	2	2.9	723	81787	6.2	Isoform 2 of Q96SU4
3323	Q96SU4	2	2	2.9	736	83185	6.2	Oxysterol-binding protein-related protein 9
3323	Q86YQ3	2	2	2.9	719	81166	5.8	Oxysterol-binding protein-like protein 9
3323	UPI0000D61F18	2	2	2.8	743	84013	6.5	Oxysterol-binding protein-related protein 9 (OSBP-related protein 9) (ORP-9).
3323	UPI0000167BAD	2	2	2.8	746	84255	6.2	oxysterol-binding protein-like protein 9 isoform f
3323	UPI000013E7D3	2	2	2.8	738	83412	6.2	Oxysterol-binding protein-related protein 9 (OSBP-related protein 9) (ORP-9).
3323	Q5VSM6	2	2	2.8	752	84823	6.3	Oxysterol-binding protein
3323	Q5VSM3	2	2	2.8	741	83786	6.5	Oxysterol-binding protein
3323	UPI0000D61F17	2	2	2.7	766	86481	6.5	Oxysterol-binding protein-related protein 9 (OSBP-related protein 9) (ORP-9).
3324	O95470	2	2	3.3	568	63524	9.2	Sphingosine-1-phosphate lyase 1
3325	O60518	2	12	3.2	1105	124713	5	Ran-binding protein 6
3326	Q8WYA6-3	2	2	5.8	311	36103	6.7	Isoform 3 of Q8WYA6
3326	Q8WYA6-2	2	2	4.8	376	43392	6.2	Isoform 2 of Q8WYA6
3326	Q0VAM0	2	2	3.2	563	65145	5	Catenin, beta like 1
3326	UPI0000D61088	2	2	3.2	568	65751	5	Beta-catenin-like protein 1 (Nuclear-associated protein) (NAP) (Testis development protein NYD-SP19).
3326	Q8WYA6	2	2	3.2	563	65173	5	Beta-catenin-like protein 1
3327	Q53HI2	2	2	3.2	622	69839	6.8	DEAD-box protein abstrakt variant
3327	Q9UJV9	2	2	3.2	622	69838	6.8	Probable ATP-dependent RNA helicase DDX41
3328	Q86X55	2	4	3.2	585	63460	6.6	Histone-arginine methyltransferase CARM1
3328	UPI000004B825	2	4	3.1	608	65854	6.7	coactivator-associated arginine methyltransferase 1
3329	Q8IXI1	2	5	3.2	618	68118	5.9	Mitochondrial Rho GTPase 2
3330	Q96PU4	2	3	3.2	802	89985	8.2	E3 ubiquitin-protein ligase UHRF2
3331	Q9ULH1	2	5	3.2	1129	125471	7.3	130 kDa phosphatidylinositol 4,5-biphosphate-dependent ARF1 GTPase- activating protein
3331	UPI0000D62501	2	5	3.2	1132	125759	7.3	130 kDa phosphatidylinositol 4,5-biphosphate-dependent ARF1 GTPase- activating protein (PIP2-dependent ARF1 GAP) (ADP-ribosylation factor-directed GTPase-activating protein 1) (ARF GTPase-activating protein 1) (Development and differentiation-enhancing f
3331	UPI0000351D6E	2	5	3.2	1129	125498	7.3	development and differentiation enhancing factor 1
3331	Q9ULH1-2	2	5	3.2	1132	125870	7.5	Isoform 1 of Q9ULH1
3332	Q86TN5	2	4	3.3	676	78276	7.8	Similar to Origin recognition complex subunit 3
3332	A2A2T5	2	4	3.1	712	82325	7.6	Origin recognition complex, subunit 3-like
3332	Q9UBD5	2	4	3.1	711	82254	7.6	Origin recognition complex subunit 3
3332	Q53GY6	2	4	3.1	711	82332	7.6	Origin recognition complex, subunit 3 isoform 2 variant
3333	Q3SYP6	2	3	4.6	482	53480	9	PTCD1 protein
3333	O75127	2	3	3.1	700	78856	8.6	Pentatricopeptide repeat protein 1
3333	Q3ZB84	2	3	3.1	700	78886	8.5	Pentatricopeptide repeat domain 1
3334	O95834	2	3	3.1	649	70679	6.3	Echinoderm microtubule-associated protein-like 2
3335	P51116	2	2	3.1	673	74223	6.2	Fragile X mental retardation syndrome-related protein 2
3335	UPI000012ADF3	2	2	3.1	673	74128	6.1	fragile X mental retardation syndrome related protein 2
3335	Q86V09	2	2	3.1	673	74232	6.3	Fragile X mental retardation, autosomal homolog 2
3335	UPI0000D622B8	2	2	3	698	77072	6.6	Fragile X mental retardation syndrome-related protein 2.
3336	Q8IX18-2	2	3	3.3	732	83320	8.7	Isoform 2 of Q8IX18
3336	Q8IX18	2	3	3.1	779	88560	8.6	Probable ATP-dependent RNA helicase DHX40
3336	UPI00006C189F	2	3	3.1	779	88385	8.8	PREDICTED: similar to DEAH (Asp-Glu-Ala-His) box polypeptide 40 isoform 2
3336	UPI0000061E1D	2	3	3.1	779	88529	8.5	DEAH (Asp-Glu-Ala-His) box polypeptide 40
3337	Q8IY81	2	5	3.1	847	96576	8.2	Putative rRNA methyltransferase 3 (EC 2.1.1.-) (rRNA (uridine-2'-O-)- methyltransferase 3)
3337	UPI000013C87B	2	5	3.1	847	96558	8.4	Putative rRNA methyltransferase 3 (EC 2.1.1.-) (rRNA (uridine-2'-O-)- methyltransferase 3).
3338	Q9Y613	2	3	3.1	1164	126551	6.4	FH1/FH2 domain-containing protein 1
3339	P49756	2	11	3.2	784	94122	6.2	Probable RNA-binding protein 25
3339	A0PJL9	2	11	3	839	99723	6.3	RBM25 protein
3339	UPI0000373D58	2	11	3	843	100186	6.3	RNA binding motif protein 25
3340	UPI00006C06FA	2	3	4.1	512	56162	6.8	PREDICTED: similar to lactotransferrin
3340	P02788	2	3	3	710	78182	8.1	Lactotransferrin precursor (EC 3.4.21.-) (Lactoferrin) (Talalactoferrin alfa) [Contains: Kaliocin-1; Lactoferroxin A; Lactoferroxin B; Lactoferroxin C]
3340	Q5EK51	2	3	3	711	78322	8.2	Lactoferrin
3340	Q5DSM0	2	3	3	711	78384	8.2	Growth-inhibiting protein 12

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3340	Q2TUW9	2	3	3	709	77981	8.1	Lactoferrin
3341	P27986	2	2	3	724	83598	6.2	Phosphatidylinositol 3-kinase regulatory subunit alpha
3341	P27986-4	2	2	3	732	84474	6.2	Isoform 4 of P27986
3342	Q9H2G0	2	2	3.1	852	97968	5.2	CTCL tumor antigen se37-2
3342	Q5W7F7	2	2	3.1	852	97958	5.3	Ubiquitin ligase E3A isoform 1
3342	Q05086	2	2	3	875	100646	5.2	Ubiquitin-protein ligase E3A
3342	UPI0000161F3B	2	2	3	875	100688	5.2	ubiquitin protein ligase E3A isoform 2
3342	UPI00001605CC	2	2	3	872	100102	5.2	ubiquitin protein ligase E3A isoform 3
3342	Q9BUI6	2	2	3	872	100044	5.2	Ubiquitin protein ligase E3A
3342	Q05086-3	2	2	3	872	100060	5.2	Isoform III of Q05086
3343	Q5VU09	2	2	3.1	674	75671	6.8	Adducin 3
3343	Q59EK1	2	2	3	698	78214	6.2	Adducin 3 isoform a variant
3343	Q9UEY8	2	2	3	706	79155	6.3	Gamma-adducin
3344	Q5T447	2	2	3	861	97113	5.6	Probable E3 ubiquitin-protein ligase HECTD3
3345	Q8TC07-2	2	4	3.1	674	77395	5.4	Isoform 2 of Q8TC07
3345	Q8TC07	2	4	3	691	79491	5.7	TBC1 domain family member 15
3346	UPI000021D19B	2	2	3	739	78505	9.2	G2 and S phase expressed protein 1 (B99 homolog).
3347	Q3B768	2	5	4	803	90317	6.4	Hypothetical protein
3347	O43156	2	5	2.9	1089	122069	6	Uncharacterized protein KIAA0406
3348	Q08174	2	2	2.9	1026	111270	5	Protocadherin-1 precursor
3348	UPI000045735F	2	2	2.9	1031	111812	5	Protocadherin-1 precursor (Protocadherin-42) (PC42) (Cadherin-like protein 1).
3348	Q08174-2	2	2	2.9	1030	111704	5	Isoform 2 of Q08174
3348	Q8IUP2	2	2	2.8	1060	114743	5	Protocadherin 1
3348	UPI000016158F	2	2	2.4	1237	133722	5.1	protocadherin 1 isoform 2 precursor
3349	Q13671-2	2	3	3.2	721	77500	7.2	Isoform RIN1
3349	Q13671	2	3	2.9	783	84099	8	Ras and Rab interactor 1
3350	Q13823	2	2	2.9	731	83655	9.2	Nucleolar GTP-binding protein 2
3351	UPI000046FF02	2	3	4.3	484	53859	7.9	transmembrane protein 141
3351	UPI0000D61953	2	3	4	520	57379	8.3	transmembrane protein 141
3351	Q5T5R6	2	3	4	520	57397	8.3	Chromosome 9 open reading frame 86
3351	Q3YEC7	2	3	2.9	729	79549	5.2	Putative GTP-binding protein Parf
3351	Q3YEC7-2	2	3	2.9	730	79636	5.2	Isoform 2 of Q3YEC7
3352	Q59EB3	2	2	2.9	712	79524	7	Met proto-oncogene variant
3353	Q9BUQ8	2	3	2.9	820	95647	9.6	Probable ATP-dependent RNA helicase DDX23
3353	UPI0000073875	2	3	2.9	820	95583	9.6	DEAD (Asp-Glu-Ala-Asp) box polypeptide 23
3354	Q9NV70-2	2	3	3	879	100283	6.6	Isoform 2 of Q9NV70
3354	Q9NV70	2	3	2.9	894	101982	6.6	Exocyst complex component 1
3355	Q9UF55	2	2	2.9	990	115956	7.5	WD repeat protein 52
3356	Q504Z1	2	25	3.4	1305	146870	6.1	EIF4G3 protein
3356	O43432	2	25	2.8	1585	176651	5.4	Eukaryotic translation initiation factor 4 gamma 3
3356	Q59GJ0	2	25	2.5	1780	195956	5.6	Eukaryotic translation initiation factor 4 gamma, 3 variant
3357	Q5H9P4	2	3	2.8	924	99824	6.3	Hypothetical protein DKFZp686M19106
3357	UPI0000D4BE3E	2	3	2.2	1170	128486	6.1	ankyrin repeat and FYVE domain containing 1 isoform 1
3357	UPI00004569F8	2	3	2.2	1168	128295	6.1	Ankyrin repeat and FYVE domain-containing protein 1 (Ankyrin repeats hooked to a zinc finger motif).
3357	Q9P2R3	2	3	2.2	1169	128399	6.1	Ankyrin repeat and FYVE domain-containing protein 1
3358	UPI00006C1A6E	2	2	2.9	661	75741	9.3	PREDICTED: similar to zinc finger protein 528 isoform 4
3358	Q76KX9	2	2	2.9	661	75792	9.3	Kruppel-like zinc finger protein isoform 1
3358	Q76KX8	2	2	2.8	674	77167	9.3	Zinc finger protein 534
3358	UPI0000D61806	2	2	2.8	673	77037	9.3	Kruppel-like zinc finger protein isoform 1
3359	Q8N8A2	2	3	2.8	944	102557	6.3	Ankyrin repeat domain-containing protein 44
3359	UPI000049DF2F	2	3	2.8	919	99788	6.3	Ankyrin repeat domain-containing protein 44.
3359	UPI0000073B9C	2	3	2.8	919	99819	6.4	ankyrin repeat domain 44
3359	Q8N8A2-4	2	3	2.8	919	99807	6.4	Isoform 4 of Q8N8A2
3360	Q05CN5	2	2	2.9	441	49185	5.7	Hypothetical protein
3360	A2VCS9	2	2	2.7	488	54695	5.6	MAP9 protein
3360	Q49MG5	2	2	2	647	74234	7.8	Microtubule-associated protein 9
3361	UPI000013E40F	2	6	3.2	822	91113	7.2	Sad1/unc-84 protein-like 1 (Unc-84 homolog A).
3361	O94901	2	6	3.2	812	90064	7.1	Sad1/unc-84 protein-like 1
3361	A4D2Q0	2	6	2.7	974	108455	8	Unc-84 homolog A
3362	Q5T693	2	3	3.2	760	88198	6.2	Adenosine monophosphate deaminase 2
3362	Q5T695	2	3	3	798	92071	6.3	Adenosine monophosphate deaminase 2
3362	Q01433-4	2	3	3	804	92918	6.4	Isoform Ex1B
3362	Q01433	2	3	2.7	879	100688	6.9	AMP deaminase 2
3362	Q5T694	2	3	2.7	890	101853	7.1	Adenosine monophosphate deaminase 2
3363	Q59FC4	2	2	3.5	687	75961	6.5	Presynaptic protein SAP97 variant
3363	UPI0000D61BDD	2	2	2.8	853	95166	6	Disks large homolog 1 (Synapse-associated protein 97) (SAP-97) (hDlg).
3363	Q12959-5	2	2	2.8	853	95066	6	Isoform 5 of Q12959
3363	Q12959-3	2	2	2.8	871	96976	5.9	Isoform 3 of Q12959
3363	Q12959	2	2	2.7	904	100355	5.7	Disks large homolog 1

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3363	UPI0000D61BDC	2	2	2.7	890	98892	5.7	Disks large homolog 1 (Synapse-associated protein 97) (SAP-97) (hDlg).
3363	UPI00004DF217	2	2	2.7	893	99942	6	Disks large homolog 1 (Synapse-associated protein 97) (SAP-97) (hDlg).
3363	Q12959-6	2	2	2.7	891	98990	5.8	Isoform 6 of Q12959
3363	Q12959-4	2	2	2.7	893	99842	6	Isoform 4 of Q12959
3363	UPI0000D61BDB	2	2	2.6	916	101692	5.7	Disks large homolog 1 (Synapse-associated protein 97) (SAP-97) (hDlg).
3363	UPI000013CD24	2	2	2.6	926	103321	5.9	Disks large homolog 1 (Synapse-associated protein 97) (SAP-97) (hDlg).
3363	Q12959-7	2	2	2.6	917	101748	5.7	Isoform 7 of Q12959
3363	Q12959-2	2	2	2.6	926	103221	5.9	Isoform 2 of Q12959
3364	Q4V328-3	2	2	3.9	594	68188	5.5	Isoform 3 of Q4V328
3364	UPI0000457834	2	2	3.7	624	71806	5.3	GRIP1-associated protein 1 (GRASP-1).
3364	Q4V328-2	2	2	3.7	625	71878	5.4	Isoform 2 of Q4V328
3364	UPI0000D61D63	2	2	2.9	798	90999	5.1	GRIP1-associated protein 1 (GRASP-1).
3364	Q4V329	2	2	2.9	796	90841	5.1	GRIP1 associated protein 1
3364	UPI0000D61D62	2	2	2.8	811	92825	5.1	GRIP1-associated protein 1 (GRASP-1).
3364	Q4V328-4	2	2	2.8	810	92738	5.2	Isoform 4 of Q4V328
3364	Q4V328	2	2	2.7	841	95989	5.1	GRIP1-associated protein 1
3364	UPI0000457833	2	2	2.7	842	96076	5.1	GRIP1-associated protein 1 (GRASP-1).
3365	Q7RTP6	2	2	2.7	976	109911	8.4	Protein MICAL-3
3365	UPI0000DD85C8	2	2	2.7	963	108956	8.4	PREDICTED: similar to Protein MICAL-3
3365	Q7RTP6-2	2	2	2.7	948	106837	8.2	Isoform 2 of Q7RTP6
3366	Q8N596	2	2	2.7	811	90794	6.8	Oxysterol binding protein-like 5
3366	UPI0000366761	2	2	2.7	821	91898	6.9	Oxysterol-binding protein-related protein 5 (OSBP-related protein 5) (ORP-5).
3366	UPI00001AF3AD	2	2	2.5	889	99721	7.6	Oxysterol-binding protein-related protein 5 (OSBP-related protein 5) (ORP-5).
3366	Q9H0X9	2	2	2.5	879	98617	7.5	Oxysterol-binding protein-related protein 5
3367	Q99567	2	3	2.7	741	83542	5.7	Nuclear pore complex protein Nup88
3368	Q9NXH9-2	2	3	2.9	630	69306	7.2	Isoform 2 of Q9NXH9
3368	Q9NXH9	2	3	2.7	659	72234	7.6	N(2),N(2)-dimethylguanosine tRNA methyltransferase (EC 2.1.1.32) (tRNA(guanine-26,N(2)-N(2)) methyltransferase) (tRNA 2,2-dimethylguanosine-26 methyltransferase) (tRNA(m(2,2)G26)dimethyltransferase)
3369	Q9Y3E9	2	2	5.2	404	45005	8.5	CGI-151 protein
3369	Q9Y2J6	2	2	2.7	772	83643	7.7	KIAA0992 protein
3370	A1KY35	2	6	2.6	900	104190	6	Cell proliferation-inducing protein 53
3370	UPI00001C1F92	2	6	2.6	900	104217	6	neural precursor cell expressed, developmentally down-regulated 4 isoform 1
3370	UPI000045685E	2	6	2.3	1000	114992	7	E3 ubiquitin-protein ligase NEDD4 (EC 6.3.2.-).
3370	P46934	2	6	2.3	1000	114936	6.9	E3 ubiquitin-protein ligase NEDD4
3370	UPI00001418FE	2	6	1.8	1247	140696	6.6	neural precursor cell expressed, developmentally down-regulated 4 isoform 2
3371	O60645-2	2	3	3.1	641	73797	7.1	Isoform 2 of O60645
3371	O60645	2	3	2.6	756	86845	6.1	Exocyst complex component 3
3372	P20594-2	2	3	2.7	995	111208	6.8	Isoform Short of P20594
3372	P20594	2	3	2.6	1047	117022	6.9	Atrial natriuretic peptide receptor B precursor
3372	P20594-3	2	3	2.6	1023	114113	7.1	Isoform 3 of P20594
3373	UPI0000D62299	2	3	6.3	347	39626	6.5	Active breakpoint cluster region-related protein.
3373	Q6ZT60	2	3	6.1	362	41155	6.7	CDNA FLJ44934 fis, clone BRAMY3017920, highly similar to Active breakpoint cluster region-related protein
3373	Q12979-2	2	3	2.7	822	93707	6.4	Isoform Short of Q12979
3373	Q12979	2	3	2.6	859	97697	6.6	Active breakpoint cluster region-related protein
3373	UPI00001AED3D	2	3	2.6	859	97598	6.6	active breakpoint cluster region-related protein isoform a
3374	Q14118	2	3	2.6	895	97581	8.6	Dystroglycan precursor (Dystrophin-associated glycoprotein 1) [Contains: Alpha-dystroglycan (Alpha-DG); Beta-dystroglycan (Beta- DG)]
3374	UPI000013EDAE	2	3	2.6	895	97441	8.6	Dystroglycan precursor (Dystrophin-associated glycoprotein 1) [Contains: Alpha-dystroglycan (Alpha-DG); Beta-dystroglycan (Beta- DG)].
3374	Q969J9	2	3	2.6	895	97541	8.6	Dystroglycan 1
3375	UPI0000D61F63	2	2	2.9	543	63041	6.3	Formin-binding protein 1-like (Transducer of Cdc42-dependent actin assembly protein 1) (Toca-1).
3375	Q5T0N5-4	2	2	2.9	551	64033	6.2	Isoform 4 of Q5T0N5
3375	Q5T0N5-3	2	2	2.9	547	63572	6.2	Isoform 3 of Q5T0N5
3375	UPI0000D61F62	2	2	2.7	596	68903	6.6	Formin-binding protein 1-like (Transducer of Cdc42-dependent actin assembly protein 1) (Toca-1).
3375	Q5T0N5-2	2	2	2.7	600	69434	6.6	Isoform 2 of Q5T0N5
3375	Q5T0N5	2	2	2.6	605	69977	6.6	Formin-binding protein 1-like
3375	Q5T0N5-5	2	2	2.6	604	69894	6.6	Isoform 5 of Q5T0N5
3376	Q6NUQ2	2	5	2.6	1002	111640	4.9	Calmin
3376	Q96JQ2	2	5	2.6	1002	111651	4.9	Calmin
3377	Q6PD62	2	3	2.6	1173	133502	6.8	RNA polymerase-associated protein CTR9 homolog
3378	O15037	2	2	2.5	678	74461	7	Protein KIAA0323

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3378	UPI000000CC1F	2	2	2.5	678	74534	7	hypothetical protein LOC23351
3379	O94799	2	3	2.5	486	56526	4.4	HRIHFB2216 protein
3379	Q9BZW6	2	3	1.9	633	72788	4.6	Differentially expressed nucleolar TGF-beta1 target protein
3379	UPI0000DD86A4	2	3	1.7	695	79700	4.6	PREDICTED: similar to TSPY-like 2
3379	Q9H2G4	2	3	1.7	693	79435	4.6	TSPY-like protein 2
3380	P50416	2	5	2.5	773	88368	8.7	Carnitine O-palmitoyltransferase I, liver isoform
3380	P50416-2	2	5	2.5	756	86239	8.4	Isoform 2 of P50416
3381	Q1RLN5	2	7	2.5	799	90874	8.5	ARHGAP12 protein
3381	Q5T2Y2	2	7	2.5	816	93114	7.8	Rho GTPase activating protein 12
3381	Q5T2Y0	2	7	2.5	794	90403	8.4	Rho GTPase activating protein 12
3381	Q8IWW6	2	7	2.4	846	96254	7.6	Rho GTPase-activating protein 12
3381	Q504X1	2	7	2.4	841	95784	7.4	ARHGAP12 protein
3382	Q8IVU2	2	2	2.6	705	76392	6.2	ESPNL protein
3382	Q6ZVG1	2	2	2.5	722	78412	6.1	CDNA FLJ42621 fis, clone BRACE3015262
3382	UPI000022BC90	2	2	1.8	1005	108132	6.5	espin-like
3382	Q6ZVH7	2	2	1.8	1005	108176	6.5	Espin-like protein
3383	Q86TI2-3	2	3	3.3	674	76702	6.5	Isoform 3 of Q86TI2
3383	UPI000043F349	2	3	2.6	850	96613	6.5	dipeptidylpeptidase 9
3383	Q86TI2-4	2	3	2.6	836	95013	6.5	Isoform 4 of Q86TI2
3383	Q86TI2	2	3	2.5	863	98263	6.5	Dipeptidyl peptidase 9
3384	Q8IVL5	2	6	2.5	708	80985	5.7	Prolyl 3-hydroxylase 2 precursor
3385	P06400	2	2	2.4	928	106159	7.9	Retinoblastoma-associated protein
3385	Q59HH0	2	2	2.3	960	109774	8.2	Retinoblastoma-associated protein variant
3386	Q13563	2	4	2.4	968	109691	5.7	Polycystin-2
3387	Q8TDD1	2	3	2.4	881	98595	10	ATP-dependent RNA helicase DDX54
3388	Q9UPZ3	2	2	2.4	1129	127449	5.5	Hermansky-Pudlak syndrome 5 protein
3389	P11498	2	2	2.3	1178	129634	6.8	Pyruvate carboxylase, mitochondrial precursor
3390	Q14527	2	2	2.3	1009	113928	8.6	Helicase-like transcription factor
3390	Q59GQ7	2	2	2.3	992	111966	8.7	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin a3 variant
3391	Q9H9Z1	2	2	10.6	170	19571	9.3	CDNA FLJ12462 fis, clone NT2RM1000770, weakly similar to DXS6673E PROTEIN
3391	Q9NXG9	2	2	4.3	416	47549	6.1	CDNA FLJ20259 fis, clone COLF7443
3391	Q2TAL8	2	2	2.3	776	86436	5.9	Glutamine-rich protein 1
3392	Q7Z3G5	2	2	2.4	890	100704	6.3	Hypothetical protein DKFZp686O12114
3392	Q5CZB1	2	2	2.3	910	102937	6.7	Hypothetical protein DKFZp686A01247
3392	UPI0000D61553	2	2	2.3	910	103010	6.6	UPI0000D61553 UniRef100 entry
3392	Q6PJ44	2	2	2.3	897	101434	6.3	DKFZP686A01247 protein
3392	Q68E07	2	2	2.3	902	101990	6.1	Hypothetical protein DKFZp686B2470
3392	Q5CZB6	2	2	2	1069	120484	6.7	Hypothetical protein DKFZp686G18243
3392	UPI0000D61554	2	2	1.9	1083	121867	6.5	UPI0000D61554 UniRef100 entry
3392	Q9UPQ0	2	2	1.9	1101	123942	7.1	KIAA1102 protein
3392	UPI00001C1E0E	2	2	1.4	1467	164438	6.4	UPI00001C1E0E UniRef100 entry
3393	Q9H6M7	2	7	3.5	774	84408	7.6	CDNA: FLJ22087 fis, clone HEP15918
3393	Q9H6B3	2	7	3.5	774	84378	7.6	CDNA: FLJ22417 fis, clone HRC08579
3393	Q8TDM9	2	7	2.7	1013	110352	7.3	Amplified in breast cancer 1
3393	Q6AI08	2	7	2.3	1181	128781	7	Hypothetical protein DKFZp686D22141
3393	Q6MZX1	2	7	2.3	1181	128707	7.1	Hypothetical protein DKFZp686B03209
3394	Q6P1N0	2	2	2.3	951	104062	8.1	Coiled-coil and C2 domain-containing protein 1A
3394	Q6P1N0-2	2	2	2.3	950	103934	8.1	Isoform 2 of Q6P1N0
3395	Q8IY37	2	2	2.3	1157	129545	8.1	Probable ATP-dependent RNA helicase DHX37
3396	Q96KP1	2	3	2.3	924	104066	6.9	Exocyst complex component 2
3396	UPI00004573AB	2	3	2.3	925	104238	6.9	Exocyst complex component 2 (Exocyst complex component Sec5).
3397	Q96QC0	2	4	2.3	940	99058	9.2	Serine/threonine-protein phosphatase 1 regulatory subunit 10
3398	A0JLU5	2	8	2.2	552	63457	4.7	Hypothetical protein
3398	Q05C10	2	8	2	595	68611	4.9	Hypothetical protein
3398	Q9H501	2	8	1.4	851	98796	5.1	ESF1 homolog
3399	A1L3A9	2	5	2.2	1232	138540	5.3	TBC1 domain family, member 9B
3399	UPI000034ECFF	2	5	2.2	1250	140525	5.3	TBC1 domain family, member 9B (with GRAM domain) isoform a
3399	UPI000020CCFB	2	5	2.2	1233	138670	5.3	TBC1 domain family, member 9B (with GRAM domain) isoform b
3399	UPI000013D22E	2	5	2.1	1261	141519	5.3	TBC1 domain family, member 9B (with GRAM domain) isoform b
3399	O75163	2	5	2.1	1262	141589	5.3	TBC1 domain family member 9B
3400	Q59F15	2	4	3.4	847	82980	8.7	COL4A1 protein variant
3400	A2A373	2	4	2.2	1318	127981	7.9	Collagen type IV alpha 1
3400	UPI0000D61AA3	2	4	1.7	1670	160743	8.3	Collagen alpha-1(IV) chain precursor.
3400	UPI000004981D	2	4	1.7	1669	160611	8.3	alpha 1 type IV collagen preproprotein
3400	P02462	2	4	1.7	1669	160615	8.3	Collagen alpha-1(IV) chain precursor
3401	Q548W1	2	2	2.5	920	103012	6.9	HRNT1
3401	O15294	2	2	2.2	1046	116924	6.7	UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit
3401	O15294-3	2	2	2.2	1036	115706	6.7	Isoform 1 of O15294
3402	Q02156	2	2	2.2	737	83674	7.1	Protein kinase C epsilon type
3403	Q9Y3Z1	2	3	3.4	529	60751	7.3	Hypothetical protein DKFZp564L2123

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
3403	Q3MJA4	2	3	2.2	831	94132	6.8	Solute carrier family 39 (Zinc transporter), member 10
3403	Q9ULF5	2	3	2.2	835	94559	6.8	Solute carrier family 39 member 10
3403	Q68CR5	2	3	2.2	831	94120	6.8	Hypothetical protein DKFZp781L10106
3404	Q8TD19	2	3	2.2	979	107168	5.7	Serine/threonine-protein kinase Nek9
3404	UPI0000070F8F	2	3	2.2	979	107034	5.7	NIMA related kinase 9
3405	UPI0000D61AD9	2	2	2.2	1053	112884	6.3	Ankyrin repeat domain-containing protein 28.
3405	UPI00004120FF	2	2	2.2	1053	112966	6.3	ankyrin repeat domain 28
3405	O15084	2	2	2.1	1086	116543	6.2	Ankyrin repeat domain-containing protein 28
3406	Q13577	2	2	2.3	1149	126809	8.9	51C protein
3406	O15357	2	2	2.1	1258	138585	6.5	Inositol polyphosphate phosphatase-like protein 1
3406	UPI000013E4AF	2	2	2.1	1258	138599	6.5	inositol polyphosphate phosphatase-like 1
3407	O95155-3	2	3	2.5	1061	121820	6.2	Isoform 3 of O95155
3407	UPI0000D61E44	2	3	2.3	1175	133468	6.2	Ubiquitin conjugation factor E4 B (Ubiquitin fusion degradation protein 2) (Homozygously deleted in neuroblastoma 1).
3407	O95155-2	2	3	2.3	1173	133275	6.1	Isoform 2 of O95155
3407	O95155	2	3	2.1	1302	146184	6.6	Ubiquitin conjugation factor E4 B
3408	Q2TAJ0	2	2	4.3	397	45229	9.2	Cell division cycle 2-like 2
3408	Q9UQ88-10	2	2	3.9	439	49624	5.7	Isoform 4 of Q9UQ88
3408	P21127-12	2	2	3.9	439	49555	5.8	Isoform 7 of P21127
3408	Q96CA8	2	2	3.7	464	52406	5.1	CDC2L2 protein
3408	P21127-4	2	2	3.7	461	51925	5.2	Isoform 3 of P21127
3408	Q6P5Y5	2	2	3.6	475	53688	4.8	CDC2L1 protein
3408	Q4VBY6	2	2	3.6	475	53757	4.8	CDC2L2 protein
3408	P21127-10	2	2	3	565	63937	4.7	Isoform SV11 of P21127
3408	UPI0000DD7877	2	2	2.9	593	67740	4.9	PREDICTED: similar to cell division cycle 2-like 1 (PITSLRE proteins) isoform 1
3408	UPI0000D61E1B	2	2	2.3	750	86357	5.3	cell division cycle 2-like 1 (PITSLRE proteins) isoform 3
3408	UPI000006CC9E	2	2	2.3	737	85906	5.3	cell division cycle 2-like 1 (PITSLRE proteins) isoform 4
3408	Q5QPR4	2	2	2.3	746	86824	5.3	Cell division cycle 2-like 2
3408	P21127-9	2	2	2.3	748	87138	5.4	Isoform SV10 of P21127
3408	P21127-6	2	2	2.3	738	86063	5.3	Isoform SV5 of P21127
3408	UPI0000D61E1A	2	2	2.2	785	90626	5.2	cell division cycle 2-like 1 (PITSLRE proteins) isoform 3
3408	UPI0000470904	2	2	2.2	770	90045	5.3	PITSLRE serine/threonine-protein kinase CDC2L2 (EC 2.7.11.22) (Galactosyltransferase-associated protein kinase p58/GTA) (Cell division cycle 2-like protein kinase 2) (CDK11).
3408	UPI00003664B8	2	2	2.2	783	91362	5.4	PITSLRE serine/threonine-protein kinase CDC2L2 (EC 2.7.11.22) (Galactosyltransferase-associated protein kinase p58/GTA) (Cell division cycle 2-like protein kinase 2) (CDK11).
3408	UPI000022B1E1	2	2	2.2	780	91018	5.4	PITSLRE serine/threonine-protein kinase CDC2L2 (EC 2.7.11.22) (Galactosyltransferase-associated protein kinase p58/GTA) (Cell division cycle 2-like protein kinase 2) (CDK11).
3408	UPI0000163C11	2	2	2.2	777	90663	5.5	cell division cycle 2-like 2 isoform 1
3408	UPI00001613C8	2	2	2.2	775	90394	5.4	cell division cycle 2-like 2 isoform 9
3408	UPI0000160F88	2	2	2.2	771	90047	5.4	cell division cycle 2-like 1 (PITSLRE proteins) isoform 9
3408	UPI0000160F86	2	2	2.2	780	91009	5.4	cell division cycle 2-like 1 (PITSLRE proteins) isoform 8
3408	UPI0000072148	2	2	2.2	776	90698	5.4	cell division cycle 2-like 2 isoform 3
3408	UPI0000071930	2	2	2.2	767	89688	5.4	cell division cycle 2-like 2 isoform 4
3408	UPI000006F867	2	2	2.2	777	90661	5.5	cell division cycle 2-like 2 isoform 1
3408	UPI000006EE37	2	2	2.2	780	91063	5.4	cell division cycle 2-like 2 isoform 5
3408	Q9UQ88-4	2	2	2.2	767	89658	5.4	Isoform SV3 of Q9UQ88
3408	Q9UQ88-3	2	2	2.2	776	90668	5.4	Isoform SV2 of Q9UQ88
3408	Q9UQ88-2	2	2	2.2	777	90631	5.5	Isoform SV1 of Q9UQ88
3408	Q9UQ88	2	2	2.2	780	90974	5.4	PITSLRE serine/threonine-protein kinase CDC2L2
3408	Q5QPR3	2	2	2.2	779	91007	5.3	Cell division cycle 2-like 2
3408	P21127-8	2	2	2.2	772	90256	5.4	Isoform 8 of P21127
3408	P21127-3	2	2	2.2	781	91219	5.4	Isoform 2 of P21127
3408	P21127-2	2	2	2.2	782	91332	5.5	Isoform SV1 of P21127
3408	P21127	2	2	2.1	795	92707	5.6	PITSLRE serine/threonine-protein kinase CDC2L1
3408	UPI0000D61E19	2	2	2.1	797	91867	5.4	cell division cycle 2-like 1 (PITSLRE proteins) isoform 3
3409	UPI0000DD7E29	2	2	2.5	746	83454	8.1	PREDICTED: hypothetical protein
3409	Q75KM8	2	2	2.1	919	101892	6.5	Hypothetical protein KIAA0738
3409	Q75KM9	2	2	2.1	921	102126	6.5	Hypothetical protein KIAA0738
3409	Q9Y4C2	2	2	2	941	104377	6.4	KIAA0738 protein
3410	Q8NAP3	2	3	2.1	1195	134257	8	Zinc finger and BTB domain-containing protein 38
3411	UPI0000457488	2	7	2.2	981	108579	6.5	NEDD9-interacting protein with calponin homology and LIM domains (Molecule interacting with CasL protein 1).
3411	Q8TDZ2-2	2	7	2.2	981	108552	6.5	Isoform 2 of Q8TDZ2

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3411	Q8TDZ2	2	7	2.1	1067	117875	6.4	NEDD9-interacting protein with calponin homology and LIM domains
3411	UPI0000457487	2	7	2.1	1067	117902	6.4	NEDD9-interacting protein with calponin homology and LIM domains (Molecule interacting with CasL protein 1).
3411	UPI000012F0E5	2	7	2.1	1067	117932	6.5	microtubule associated monoxygenase, calponin and LIM domain containing 1
3412	UPI000045678E	2	2	2.6	884	100957	7.7	Disheveled-associated activator of morphogenesis 1.
3412	Q9Y4D1-3	2	2	2.6	882	100745	7.7	Isoform 3 of Q9Y4D1
3412	Q9Y4D1-2	2	2	2.2	1068	122306	7.2	Isoform 2 of Q9Y4D1
3412	Q9Y4D1	2	2	2.1	1078	123473	7.2	Disheveled-associated activator of morphogenesis 1
3413	A4D228	2	2	2	1156	132195	6.8	More than blood homolog
3413	Q86XI2	2	2	2	1143	130960	6.9	Condensin-II complex subunit G2
3414	P35251	2	6	2	1148	128254	9.4	Replication factor C subunit 1
3414	P35251-2	2	6	2	1147	128183	9.4	Isoform 2 of P35251
3415	UPI0000D6164B	2	2	3	1077	123611	6.7	Ras GTPase-activating-like protein IQGAP2.
3415	Q13576-2	2	2	3	1071	122840	6.7	Isoform 2 of Q13576
3415	Q59HA3	2	2	2.8	1155	132687	5.9	IQ motif containing GTPase activating protein 2 variant
3415	Q13576	2	2	2	1575	180612	5.6	Ras GTPase-activating-like protein IQGAP2
3415	UPI0000E56ECC	2	2	2	1575	180578	5.6	IQ motif containing GTPase activating protein 2
3415	UPI000020CB2C	2	2	2	1575	180577	5.6	Ras GTPase-activating-like protein IQGAP2.
3416	Q587J1	2	2	2	1336	145891	9.2	Hypothetical protein FLJ11294
3416	Q9C0J8	2	2	2	1336	145921	9.2	WD repeat protein 33
3417	Q69YQ0	2	2	2	1117	124592	5.8	Cytospin-A
3417	UPI00001B64E9	2	2	2	1117	124602	5.7	Cytospin-A (SPECC1-like protein) (Renal carcinoma antigen NY-REN-22).
3418	Q86V48	2	2	2	1076	120275	8.5	Leucine zipper protein 1
3418	UPI0000445E0E	2	2	2	1076	120304	8.6	leucine zipper protein 1
3418	Q86V48-3	2	2	2	1053	117555	8.9	Isoform 3 of Q86V48
3418	Q86V48-2	2	2	2	1026	114588	8.9	Isoform 2 of Q86V48
3419	Q86W91	2	3	2	1149	127382	8.9	Plakophilin 4
3420	Q9H7F0	2	5	2	1130	127139	6.5	Probable cation-transporting ATPase 13A3
3420	UPI00006C0765	2	5	1.8	1256	141717	6.7	PREDICTED: similar to Probable cation-transporting ATPase 13A3 (ATPase family homolog up-regulated in senescence cells 1) isoform 3
3421	Q6DHZ8	2	5	1.9	1102	123447	7.4	Activity-dependent neuroprotector
3421	Q9H2P0	2	5	1.9	1102	123563	7.3	Activity-dependent neuroprotector
3422	Q7LBC6	2	5	1.9	1761	191610	7.2	JmjC domain-containing histone demethylation protein 2B
3422	UPI000020C6A8	2	5	1.9	1761	191580	7.2	JmjC domain-containing histone demethylation protein 2B (EC 1.14.11.-) (Jumonji domain-containing protein 1B) (Nuclear protein 5qNCA).
3423	Q8TEQ8	2	2	1.9	1089	118699	8.1	GPI ethanolamine phosphate transferase 3
3424	Q9UM54	2	7	1.9	1294	149691	8.5	Myosin-VI
3424	UPI000020D228	2	7	1.9	1253	145015	8.6	Myosin-6 (Myosin VI) (Unconventional myosin VI).
3424	Q9UM54-5	2	7	1.9	1253	145041	8.6	Isoform 5 of Q9UM54
3424	Q9UM54-4	2	7	1.9	1285	148684	8.6	Isoform 4 of Q9UM54
3424	Q9UM54-2	2	7	1.9	1262	146047	8.5	Isoform 2 of Q9UM54
3424	Q9UM54-1	2	7	1.9	1285	148713	8.5	Isoform 1 of Q9UM54
3425	Q9UQL6	2	2	1.9	1122	121992	6.2	Histone deacetylase 5
3425	UPI0000508BBA	2	2	1.9	1123	122049	6.2	histone deacetylase 5 isoform 3
3425	UPI0000201355	2	2	1.9	1122	121978	6.2	histone deacetylase 5 isoform 1
3426	A3KN83	2	2	1.8	1393	154312	7.9	Strawberry notch homolog 1
3426	UPI00001AE90E	2	2	1.8	1392	154183	7.9	sno, strawberry notch homolog 1
3426	Q9H3T8	2	2	1.8	1392	154156	7.9	Strawberry notch homolog 1
3427	UPI00001413ED	2	4	2	1163	132464	6.5	Apoptotic protease-activating factor 1 (Apaf-1).
3427	O14727-5	2	4	2	1171	133355	6.5	Isoform 5 of O14727
3427	O14727-4	2	4	1.9	1205	137075	6.4	Isoform 4 of O14727
3427	O14727-3	2	4	1.9	1194	135980	6.4	Isoform 3 of O14727
3427	O14727-2	2	4	1.9	1237	140744	6.4	Isoform 2 of O14727
3427	O14727	2	4	1.8	1248	141840	6.4	Apoptotic protease-activating factor 1
3428	O15013-3	2	4	3.9	610	68223	4.7	Isoform 3 of O15013
3428	O15013-2	2	4	3.6	661	75449	6.9	Isoform 2 of O15013
3428	O15013	2	4	1.8	1369	151611	5.7	Rho guanine nucleotide exchange factor 10
3428	UPI0000D6247C	2	4	1.8	1315	145585	5.7	Rho guanine nucleotide exchange factor 10.
3428	UPI00005054FE	2	4	1.8	1344	148869	5.6	Rho guanine nucleotide exchange factor 10
3428	Q2KHR8	2	4	1.8	1306	144303	5.4	ARHGEF10 protein
3428	O15013-4	2	4	1.8	1340	148328	5.8	Isoform 4 of O15013
3429	O94854	2	2	1.8	1174	122340	4.2	KIAA0754 protein
3430	O94885	2	4	1.8	1247	136653	6.1	SAM and SH3 domain-containing protein 1
3430	Q6P4R9	2	4	1.8	1228	134825	6.4	SASH1 protein
3431	Q14185	2	2	1.8	1865	215374	7.6	Dedicator of cytokinesis protein 1
3431	Q5VXF6	2	2	1.8	1865	215344	7.6	Dedicator of cytokinesis 1
3432	Q6UWR4	2	2	5.5	363	38825	9.6	UBAP2
3432	UPI0000457732	2	2	1.9	1066	111703	7.5	Ubiquitin-associated protein 2.
3432	Q5T6F2	2	2	1.8	1119	117115	7.3	Ubiquitin-associated protein 2

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3432	UPI0000457731	2	2	1.8	1119	117130	7.3	Ubiquitin-associated protein 2.
3433	Q86WZ4	2	5	1.8	899	100842	7.2	WDFY4 protein
3433	Q9HCG5	2	5	1.3	1270	143019	6.9	KIAA1607 protein
3433	UPI000045639A	2	5	0.8	1887	210629	6.8	Uncharacterized protein C10orf64.
3433	Q8TEN7	2	5	0.8	1887	210611	6.8	WD repeat and FYVE domain-containing protein 4
3434	Q9UMZ2-4	2	2	2	1224	131222	5.1	Isoform 3 of Q9UMZ2
3434	Q9UMZ2-3	2	2	1.9	1236	132653	5.1	Isoform 2 of Q9UMZ2
3434	Q9UMZ2	2	2	1.8	1314	140654	5	AP1 subunit gamma-binding protein 1
3434	UPI0000225CBB	2	2	1.8	1302	139222	5	AP1 gamma subunit binding protein 1 isoform 2
3435	A0JP11	2	2	1.7	1358	153158	7.2	Phosphoinositide-3-kinase, regulatory subunit 4, p150
3435	Q99570	2	2	1.7	1358	153103	7.2	Phosphoinositide 3-kinase regulatory subunit 4
3436	A0JP15	2	2	1.7	1381	154958	7	KIAA1012 protein
3436	UPI0000D60ECC	2	2	1.7	1359	152868	6.8	Protein TRS85 homolog.
3436	Q9Y2L5-2	2	2	1.7	1359	152973	6.8	Isoform 2 of Q9Y2L5
3436	UPI000034ECB4	2	2	1.6	1435	160970	6.9	hypothetical protein LOC22878
3436	UPI0000052E22	2	2	1.6	1435	160996	6.9	Protein TRS85 homolog.
3436	Q9Y2L5	2	2	1.6	1435	160940	6.9	Protein TRS85 homolog
3437	A1L4N8	2	2	1.7	1265	140469	5.6	5-methyltetrahydrofolate-homocysteine methyltransferase
3437	UPI0000D620E0	2	2	1.7	1267	140685	5.6	Methionine synthase (EC 2.1.1.13) (5-methyltetrahydrofolate-- homocysteine methyltransferase) (Methionine synthase, vitamin-B12 dependent) (MS).
3437	UPI0000036BC3	2	2	1.7	1265	140587	5.6	5-methyltetrahydrofolate-homocysteine methyltransferase
3437	Q99707	2	2	1.7	1265	140527	5.6	Methionine synthase
3438	Q86XZ1	2	2	2.6	1102	125730	6.7	JARID1A protein
3438	UPI00001FBD40	2	2	1.8	1641	186837	6.8	retinoblastoma binding protein 2 isoform 2
3438	P29375	2	2	1.7	1722	195815	6.8	Jumonji/ARID domain-containing protein 1A
3438	UPI0000D62185	2	2	1.7	1722	195723	6.8	Jumonji/ARID domain-containing protein 1A (Retinoblastoma-binding protein 2) (RBBP-2).
3438	UPI0000D62184	2	2	1.7	1730	196284	6.5	Jumonji/ARID domain-containing protein 1A (Retinoblastoma-binding protein 2) (RBBP-2).
3438	Q4LE72	2	2	1.7	1731	196355	6.5	JARID1A variant protein
3439	P78559	2	2	1.7	2805	306530	4.9	Microtubule-associated protein 1A (MAP 1A) (Proliferation-related protein p80) [Contains: MAP1 light chain LC2]
3439	UPI0000456839	2	2	1.7	2805	305697	4.9	Microtubule-associated protein 1A (MAP 1A) (Proliferation-related protein p80) [Contains: MAP1 light chain LC2].
3439	UPI000066D92C	2	2	1.5	3041	331259	4.9	Microtubule-associated protein 1A (MAP 1A) (Proliferation-related protein p80) [Contains: MAP1 light chain LC2].
3440	Q59ER0	2	5	2.2	1138	130427	6.4	Rho GTPase activating protein 5 variant
3440	Q05BU8	2	5	2.1	1189	136660	6.7	Hypothetical protein
3440	Q05BE8	2	5	1.7	1502	172429	6.7	ARHGAP5 protein
3440	UPI000057B85C	2	5	1.7	1502	172459	6.6	Rho GTPase activating protein 5 isoform a
3440	UPI000057B85B	2	5	1.7	1501	172331	6.6	Rho GTPase activating protein 5 isoform b
3440	Q13017	2	5	1.7	1499	171568	6.6	Rho GTPase-activating protein 5
3441	Q14139	2	2	1.7	1066	122560	5.2	Ubiquitin conjugation factor E4 A
3441	Q14139-2	2	2	1.7	1073	123522	5.2	Isoform 2 of Q14139
3442	Q76L82	2	2	1.7	1536	164641	5.9	Polycomb group protein
3442	UPI0000D61064	2	2	1.7	1539	165119	6	Putative Polycomb group protein ASXL1 (Additional sex combs-like protein 1).
3443	Q9H9N7	2	2	2	938	104155	7.8	CDNA FLJ12634 fis, clone NT2RM4001858, weakly similar to T-BOX CONTAINING PROTEIN TBX6L
3443	Q8IWI9	2	2	1.7	1139	126801	8.3	MAX gene-associated protein
3443	UPI0000DD82F4	2	2	0.6	3033	332646	6.8	PREDICTED: similar to MAX-interacting protein isoform 5
3443	UPI0000DD82F3	2	2	0.6	3114	341349	7.1	PREDICTED: similar to MAX-interacting protein isoform 6
3443	UPI0000DD82A0	2	2	0.6	3033	332660	6.8	PREDICTED: similar to MAX-interacting protein isoform 4
3443	UPI0000DBEE61	2	2	0.6	3026	331836	6.8	MAX gene associated (MGA), mRNA
3443	UPI00001D7772	2	2	0.6	3114	341363	7.1	MAX dimerization protein 5
3444	A2A3B8	2	3	1.6	1123	128993	7.2	Diaphanous homolog 3
3444	UPI0000D61A7B	2	3	1.6	1110	127642	6.9	Protein diaphanous homolog 3 (Diaphanous-related formin-3) (DRF3).
3444	UPI0000D61A7A	2	3	1.6	1112	127857	6.9	Protein diaphanous homolog 3 (Diaphanous-related formin-3) (DRF3).
3444	Q9NSV4	2	3	1.6	1110	127594	6.9	Protein diaphanous homolog 3
3444	Q3ZK23	2	3	1.6	1152	132402	6.8	Diaphanous homolog 3
3444	Q2KPB6	2	3	1.6	1112	127856	6.9	Diaphanous-related formin 3
3444	Q18P99	2	3	1.6	1123	128921	7.3	Mammalian diaphanous homologue 2_splice_variant2
3444	A2A3B9	2	3	1.6	1147	131486	7.1	Diaphanous homolog 3
3444	Q5JTP8	2	3	1.5	1182	135615	7.1	Diaphanous homolog 3
3444	A2A3C0	2	3	1.5	1193	136926	7	Diaphanous homolog 3

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
3445	P01023	2	2	1.6	1474	163277	6.4	Alpha-2-macroglobulin precursor
3445	UPI00004565D0	2	2	1.6	1474	163237	6.5	Alpha-2-macroglobulin precursor (Alpha-2-M).
3445	UPI0000155718	2	2	1.6	1474	163291	6.4	alpha-2-macroglobulin precursor
3446	P39880-5	2	3	1.7	1449	157980	5.8	Isoform 6 of P39880
3446	P39880	2	3	1.6	1505	164272	6	Homeobox protein cut-like 1
3446	UPI00004575CB	2	3	1.6	1494	163149	5.8	Protein CASP.
3446	UPI0000246CDF	2	3	1.6	1505	164187	5.9	Protein CASP.
3446	UPI00001A95D7	2	3	1.6	1505	164312	6	CCAAT displacement protein isoform a
3446	P39880-3	2	3	1.6	1516	165687	5.9	Isoform 3 of P39880
3446	P39880-2	2	3	1.6	1483	161734	5.9	Isoform 2 of P39880
3447	Q5JPV5	2	6	1.9	1501	169350	6.3	Myeloid/lymphoid or mixed-lineage leukemia (Trithorax homolog, Drosophila); translocated to, 4
3447	UPI0000711FD9	2	6	1.8	1651	187671	6.5	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 4 isoform 2
3447	Q5TIG7	2	6	1.8	1612	181998	6.5	Myeloid/lymphoid or mixed-lineage leukemia (Trithorax homolog, Drosophila); translocated to, 4
3447	Q59FP0	2	6	1.8	1639	186298	6.5	Afadin variant
3447	P55196-2	2	6	1.8	1611	181899	6.5	Isoform 1 of P55196
3447	UPI0000D61519	2	6	1.7	1665	189138	6.5	Afadin (Protein AF-6).
3447	Q5TIG5	2	6	1.7	1665	189153	6.5	Myeloid/lymphoid or mixed-lineage leukemia (Trithorax homolog, Drosophila); translocated to, 4
3447	P55196-3	2	6	1.7	1743	197652	6.5	Isoform 3 of P55196
3447	P55196	2	6	1.6	1816	205604	6.8	Afadin
3447	UPI0000D61518	2	6	1.6	1824	206788	6.5	Afadin (Protein AF-6).
3447	UPI00004574E7	2	6	1.6	1816	205589	6.8	Afadin (Protein AF-6).
3447	P55196-4	2	6	1.6	1824	206803	6.5	Isoform 4 of P55196
3448	Q5QD01	2	3	1.6	1581	180550	5.9	SP-A receptor subunit SP-R210 alphaS
3448	Q92614-5	2	3	1.6	1581	180494	5.9	Isoform 5 of Q92614
3448	Q92614-2	2	3	1.5	1723	196436	5.9	Isoform 2 of Q92614
3448	UPI0000456A6A	2	3	1.3	2005	227119	6.2	TGFB1-induced anti-apoptotic factor 1 (12 kDa TGF-beta1-induced antiapoptotic factor).
3448	UPI0000456A69	2	3	1.3	2057	233545	6.4	TGFB1-induced anti-apoptotic factor 1 (12 kDa TGF-beta1-induced antiapoptotic factor).
3448	UPI0000456A68	2	3	1.3	2042	231669	6.2	TGFB1-induced anti-apoptotic factor 1 (12 kDa TGF-beta1-induced antiapoptotic factor).
3448	Q92614-4	2	3	1.3	2039	231238	6.2	Isoform 4 of Q92614
3448	Q92614-3	2	3	1.3	2002	226688	6.2	Isoform 3 of Q92614
3448	Q92614	2	3	1.3	2054	233113	6.3	Myosin-XVIIIa
3449	Q6WKZ4	2	2	1.6	1283	137195	5.5	Rab11 family-interacting protein 1
3449	UPI0000D624B1	2	2	1.6	1283	137167	5.4	Rab11 family-interacting protein 1 (Rab11-FIP1) (Rab-coupling protein).
3449	UPI00003FF22E	2	2	1.6	1283	137165	5.4	RAB11 family interacting protein 1 isoform 3
3450	Q8WY21	2	2	1.6	1168	129635	7.6	VPS10 domain-containing receptor SorCS1 precursor
3450	Q8WY21-4	2	2	1.6	1159	129141	7.1	Isoform 4 of Q8WY21
3450	Q8WY21-3	2	2	1.6	1179	131327	7.1	Isoform 3 of Q8WY21
3450	Q8WY21-2	2	2	1.6	1198	133373	7	Isoform 2 of Q8WY21
3451	Q9Y2H0	2	2	1.6	989	107567	7.3	Disks large-associated protein 4
3451	Q9Y2H0-2	2	2	1.6	992	108012	7.1	Isoform 2 of Q9Y2H0
3452	O94822	2	2	1.5	1766	200533	6.3	Zinc finger protein 294
3452	UPI0000D62531	2	2	1.5	1769	200863	6.3	Zinc finger protein 294 (RING finger protein 160).
3452	UPI00001A95E0	2	2	1.5	1766	200550	6.3	zinc finger protein 294
3453	Q6AHX6	2	9	1.5	1365	152964	7.9	Structural maintenance of chromosomes flexible hinge domain-containing protein 1
3453	UPI0000D60EB0	2	9	1.5	1365	152892	7.9	CDNA FLJ44350 fis, clone TRACH3006228.
3454	P55268	2	2	1.4	1798	196079	6.5	Laminin subunit beta-2 precursor
3454	UPI000013EA62	2	2	1.4	1798	195980	6.5	laminin, beta 2 precursor
3455	Q8NCI1	2	6	1.5	1106	124720	5.4	CDNA FLJ90238 fis, clone NT2RM2000632, weakly similar to EXCISION REPAIR PROTEIN ERCC-6
3455	Q2NKX8	2	6	1.4	1250	141103	5.3	FLJ20105 protein
3456	Q9P2K8	2	3	1.4	1649	186837	6.3	Eukaryotic translation initiation factor 2-alpha kinase 4
3456	UPI0000D61316	2	3	1.4	1621	183744	6.4	Eukaryotic translation initiation factor 2-alpha kinase 4 (EC 2.7.11.1) (GCN2-like protein).
3456	UPI0000D61315	2	3	1.4	1649	186937	6.3	Eukaryotic translation initiation factor 2-alpha kinase 4 (EC 2.7.11.1) (GCN2-like protein).
3456	UPI0000160791	2	3	1.4	1649	186909	6.3	eukaryotic translation initiation factor 2 alpha kinase 4
3456	Q9P2K8-2	2	3	1.4	1621	183644	6.5	Isoform 2 of Q9P2K8
3457	A1L0R6	2	8	1.3	1553	176565	6.9	FRYL protein
3457	O94915	2	8	0.7	3013	339598	5.6	Protein furry homolog-like
3458	Q9UF42	2	16	2	1031	115311	7.7	Hypothetical protein DKFZp434F0621
3458	A1L4N4	2	16	1.3	1672	185545	6.8	KIDINS220 protein
3458	Q9ULH0	2	16	1.2	1777	197210	6.7	KIAA1250 protein
3459	O15031	2	2	1.3	1838	205126	6.2	Plexin-B2 precursor
3460	O60885-2	2	3	2.5	722	80463	8.6	Isoform 2 of O60885
3460	Q4G0X8	2	3	2.3	794	88289	8.4	BRD4 protein
3460	O60885	2	3	1.3	1362	152218	9.2	Bromodomain-containing protein 4

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
3460	Q86YS8	2	3	1	1846	200087	6.4	BRD4-NUT fusion oncoprotein
3461	Q4G1H2	2	2	1.7	1062	124482	10.4	Abnormal spindle-like microcephaly associated splice variant 3
3461	Q5VYL4	2	2	1.6	1142	133558	9.9	Asp (Abnormal spindle) homolog, microcephaly associated
3461	Q4G1H0	2	2	1.3	1389	164947	10.9	Abnormal spindle-like microcephaly associated splice variant 2
3461	UPI0000D6206D	2	2	1.3	1389	164902	10.8	Abnormal spindle-like microcephaly-associated protein (Abnormal spindle protein homolog) (Asp homolog).
3461	Q4G1H1	2	2	1	1892	217792	9.8	Abnormal spindle-like microcephaly associated splice variant 1
3461	UPI0000D6206B	2	2	0.5	3479	409972	10.4	Abnormal spindle-like microcephaly-associated protein (Abnormal spindle protein homolog) (Asp homolog).
3461	Q8IZT6	2	2	0.5	3477	409803	10.4	Abnormal spindle-like microcephaly-associated protein
3461	Q5VYL3	2	2	0.5	3477	409801	10.4	Asp (Abnormal spindle) homolog, microcephaly associated
3462	Q8IWV8	2	2	1.3	1755	200537	6.2	E3 ubiquitin-protein ligase UBR2
3462	Q8IWV8-4	2	2	1.3	1755	200539	6.2	Isoform 4 of Q8IWV8
3463	Q68CP7	2	3	1.5	1215	134927	6.6	Hypothetical protein DKFZp781G125
3463	UPI000059D323	2	3	1.3	1416	158948	7.4	ATP-binding cassette, sub-family C, member 1 isoform 4
3463	UPI000013D386	2	3	1.3	1400	157240	7.5	Multidrug resistance-associated protein 1 (ATP-binding cassette sub- family C member 1) (Leukotriene C(4) transporter) (LTC4 transporter).
3463	Q9UQ98	2	3	1.3	1400	157210	7.5	Multidrug resistance protein
3463	P33527-8	2	3	1.3	1351	151631	7.6	Isoform 8 of P33527
3463	P33527-7	2	3	1.3	1410	158251	7.1	Isoform 7 of P33527
3463	P33527-6	2	3	1.3	1407	157652	7.8	Isoform 6 of P33527
3463	A3RJX2	2	3	1.2	1531	171590	7.1	ATP-binding cassette, sub-family C (CFTR/MRP), member 1
3463	UPI000059D326	2	3	1.2	1472	164970	7.6	ATP-binding cassette, sub-family C, member 1 isoform 2
3463	UPI000059D325	2	3	1.2	1466	164303	7.3	ATP-binding cassette, sub-family C, member 1 isoform 5
3463	UPI00004091AF	2	3	1.2	1475	165569	6.9	ATP-binding cassette, sub-family C, member 1 isoform 3
3463	UPI00001604C7	2	3	1.2	1482	166166	7.3	ATP-binding cassette, sub-family C, member 1 isoform 7
3463	UPI00001604C6	2	3	1.2	1489	166653	7.4	ATP-binding cassette, sub-family C, member 1 isoform 6
3463	UPI000013D385	2	3	1.2	1473	164975	7.6	Multidrug resistance-associated protein 1 (ATP-binding cassette sub- family C member 1) (Leukotriene C(4) transporter) (LTC4 transporter).
3463	UPI000013D384	2	3	1.2	1456	163262	7.7	Multidrug resistance-associated protein 1 (ATP-binding cassette sub- family C member 1) (Leukotriene C(4) transporter) (LTC4 transporter).
3463	UPI000013D383	2	3	1.2	1459	163861	7	Multidrug resistance-associated protein 1 (ATP-binding cassette sub- family C member 1) (Leukotriene C(4) transporter) (LTC4 transporter).
3463	UPI000013D382	2	3	1.2	1466	164488	7.4	Multidrug resistance-associated protein 1 (ATP-binding cassette sub- family C member 1) (Leukotriene C(4) transporter) (LTC4 transporter).
3463	UPI000013D381	2	3	1.2	1450	162595	7.4	Multidrug resistance-associated protein 1 (ATP-binding cassette sub- family C member 1) (Leukotriene C(4) transporter) (LTC4 transporter).
3463	UPI000013D380	2	3	1.2	1515	169882	7.2	Multidrug resistance-associated protein 1 (ATP-binding cassette sub- family C member 1) (Leukotriene C(4) transporter) (LTC4 transporter).
3463	P33527-9	2	3	1.2	1541	172609	6.8	Isoform 9 of P33527
3463	P33527-4	2	3	1.2	1466	164273	7.3	Isoform 4 of P33527
3463	P33527-3	2	3	1.2	1475	165538	6.9	Isoform 3 of P33527
3463	P33527-2	2	3	1.2	1472	164940	7.6	Isoform 2 of P33527
3463	P33527	2	3	1.2	1531	171560	7.1	Multidrug resistance-associated protein 1 (ATP-binding cassette sub- family C member 1) (Leukotriene C(4) transporter)
3464	Q7Z3Z5	2	2	1.2	2027	226321	6.8	TNRC11 protein
3464	UPI0000457852	2	2	1.1	2188	244357	7.2	Mediator of RNA polymerase II transcription subunit 12 (Thyroid hormone receptor-associated protein complex 230 kDa component) (Trap230) (Activator-recruited cofactor 240 kDa component) (ARC240) (CAG repeat protein 45) (OPA-containing protein) (Trinucleot
3464	UPI00004257E2	2	2	1.1	2177	243079	7.1	mediator of RNA polymerase II transcription, subunit 12 homolog

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
3464	UPI000021230F	2	2	1.1	2176	242950	7.1	Mediator of RNA polymerase II transcription subunit 12 (Thyroid hormone receptor-associated protein complex 230 kDa component) (Trap230) (Activator-recruited cofactor 240 kDa component) (ARC240) (CAG repeat protein 45) (OPA-containing protein) (Trinucleot
3464	Q93074	2	2	1.1	2212	247331	7.4	Mediator of RNA polymerase II transcription subunit 12
3465	Q8IWY7	2	3	1.2	1649	182466	7	Tau-tubulin kinase
3465	UPI000049DDD9	2	3	1.2	1651	182794	7	Tau-tubulin kinase 2 (EC 2.7.11.1).
3466	Q96BY6	2	6	1.2	2183	249310	6.9	Dedicator of cytokinesis protein 10
3467	Q6NX41	2	2	3.7	566	63641	9.1	POLR2A protein
3467	P24928	2	2	1.1	1970	217204	7.4	DNA-directed RNA polymerase II largest subunit
3467	UPI0000D622B7	2	2	1.1	1972	217430	7.4	DNA-directed RNA polymerase II largest subunit (EC 2.7.7.6) (RPB1).
3467	UPI0000140EB9	2	2	1.1	1970	217174	7.4	DNA-directed RNA polymerase II largest subunit (EC 2.7.7.6) (RPB1).
3468	Q86XA9	2	2	1.1	1778	193180	6.3	Uncharacterized protein C14orf125
3469	UPI0000D61577	2	2	3.4	741	76632	4.8	ankyrin repeat domain protein 17 isoform b
3469	Q86XI3	2	2	3.3	751	77825	4.8	ANKRD17 protein
3469	UPI0000457229	2	2	2.2	1161	122340	4.9	ankyrin repeat domain protein 17 isoform b
3469	Q9H288	2	2	2.1	1188	125431	5	Serologically defined breast cancer antigen NY-BR-16
3469	UPI0000D61576	2	2	1.7	1500	159042	5.3	ankyrin repeat domain protein 17 isoform b
3469	Q6PKA2	2	2	1.7	1500	158854	5.5	ANKRD17 protein
3469	UPI0000D61575	2	2	1.1	2358	247568	6.8	ankyrin repeat domain protein 17 isoform b
3469	UPI00002263B1	2	2	1.1	2352	246748	6.7	ankyrin repeat domain protein 17 isoform b
3469	O75179	2	2	1	2486	263242	6.4	Ankyrin repeat domain-containing protein 17
3469	UPI0000D61574	2	2	1	2609	275076	6.6	ankyrin repeat domain protein 17 isoform b
3469	UPI00002263B0	2	2	1	2603	274256	6.5	ankyrin repeat domain protein 17 isoform a
3470	Q04721	2	2	1	2471	265403	5.1	Neurogenic locus notch homolog protein 2 precursor (Notch 2) (hN2) [Contains: Notch 2 extracellular truncation; Notch 2 intracellular domain]
3471	UPI0000DD79AC	2	7	1.3	1797	186653	7.9	PREDICTED: similar to filaggrin 2
3471	Q5D862	2	7	1	2391	248072	8.3	Ifapsoriasin
3472	Q2TAZ4	2	2	2.4	788	85874	5	MDC1 protein
3472	UPI0000D6113B	2	2	1	1825	197569	5.7	UPI0000D6113B UniRef100 entry
3472	A2BF04	2	2	0.9	2089	226606	5.5	Mediator of DNA damage checkpoint 1
3472	UPI00004A3B34	2	2	0.9	2089	226636	5.5	UPI00004A3B34 UniRef100 entry
3472	Q14676	2	2	0.9	2089	226664	5.5	Mediator of DNA damage checkpoint protein 1
3472	Q0EFC2	2	2	0.9	2089	226680	5.5	KIAA0170 protein
3473	UPI0000D60F33	2	3	1.2	1788	200772	7.1	Supervillin (Archvillin) (p205/p250).
3473	UPI0000366679	2	3	1.2	1788	200846	6.9	Supervillin (Archvillin) (p205/p250).
3473	UPI000006D31C	2	3	1.2	1788	200820	6.9	supervillin isoform 1
3473	O95425-2	2	3	1.2	1788	200792	6.9	Isoform 2 of O95425
3473	O95425	2	3	0.9	2214	247704	7	Supervillin
3473	UPI0000D60F34	2	3	0.9	2214	247670	7.1	Supervillin (Archvillin) (p205/p250).
3473	UPI0000366678	2	3	0.9	2214	247744	7	Supervillin (Archvillin) (p205/p250).
3474	UPI0000D6265A	2	2	1.7	1200	138256	8.7	Myosin-7A (Myosin VIIa).
3474	Q13402-4	2	2	1.7	1203	138689	8.6	Isoform 4 of Q13402
3474	Q13402-3	2	2	1.7	1200	138349	8.6	Isoform 3 of Q13402
3474	UPI000045654F	2	2	1	2095	240949	8.8	Myosin-7A (Myosin VIIa).
3474	Q13402-5	2	2	1	2092	240654	8.7	Isoform 5 of Q13402
3474	Q13402	2	2	0.9	2215	254404	8.6	Myosin-VIIa
3474	UPI0000E445E2	2	2	0.9	2175	250243	8.6	myosin VIIA
3474	UPI000045654E	2	2	0.9	2179	250212	8.5	Myosin-7A (Myosin VIIa).
3474	UPI000045654D	2	2	0.9	2186	251059	8.5	Myosin-7A (Myosin VIIa).
3474	UPI000045654C	2	2	0.9	2216	254483	8.6	Myosin-7A (Myosin VIIa).
3474	Q13402-7	2	2	0.9	2177	249975	8.4	Isoform 7 of Q13402
3474	Q13402-6	2	2	0.9	2185	250980	8.4	Isoform 6 of Q13402
3474	Q13402-2	2	2	0.9	2177	250486	8.6	Isoform 2 of Q13402
3475	UPI0000DD7998	2	2	0.9	2454	276735	6.3	PREDICTED: similar to Ubiquitin carboxyl-terminal hydrolase 24 (Ubiquitin thioesterase 24) (Ubiquitin-specific-processing protease 24) (Deubiquitinating enzyme 24) isoform 5
3475	UPI0000DD78C2	2	2	0.9	2460	277414	6.3	PREDICTED: similar to Ubiquitin carboxyl-terminal hydrolase 24 (Ubiquitin thioesterase 24) (Ubiquitin-specific-processing protease 24) (Deubiquitinating enzyme 24) isoform 1
3475	UPI000059CFDE	2	2	0.8	2620	294364	6.1	Ubiquitin carboxyl-terminal hydrolase 24 (EC 3.1.2.15) (Ubiquitin thioesterase 24) (Ubiquitin-specific-processing protease 24) (Deubiquitinating enzyme 24).
3476	P21359	2	2	0.7	2839	319372	7.4	Neurofibromin (Neurofibromatosis-related protein NF-1) [Contains: Neurofibromin truncated]
3476	P21359-2	2	2	0.7	2818	317032	7.3	Isoform 1 of P21359
3477	P42858	2	2	0.7	3144	347859	6.2	Huntingtin
3477	UPI0000D61535	2	2	0.7	3142	347775	6.2	Huntingtin (Huntington disease protein) (HD protein).
3477	UPI000013D567	2	2	0.7	3142	347603	6.2	Huntingtin (Huntington disease protein) (HD protein).

No.	Accession Number	Unique Peptide Count	Spectrum Count	Sequence Coverage (%)	Length	MolWt	pI	Descriptive Name
3478	Q7Z6C1	2	2	1.1	1553	170081	7.5	Hypothetical protein
3478	Q09472	2	2	0.7	2414	264140	8.5	Histone acetyltransferase p300
3478	Q5W1B6	2	2	0.7	2414	264158	8.5	E1A binding protein p300
3479	UPI0000DD847C	2	2	0.7	2769	295312	10	PREDICTED: similar to BAH domain and coiled-coil containing 1
3480	Q5MJ67	2	2	0.6	3345	379235	6.4	Cardiomyopathy-associated protein 3
3481	P04114	2	3	0.5	4563	515569	7.1	Apolipoprotein B-100 precursor (Apo B-100) [Contains: Apolipoprotein B-48 (Apo B-48)]
3481	UPI0000D820D0	2	3	0.5	4563	515537	7	apolipoprotein B precursor
3481	UPI0000141B94	2	3	0.5	4563	515611	7	Apolipoprotein B-100 precursor (Apo B-100) [Contains: Apolipoprotein B-48 (Apo B-48)].
3481	Q4ZG63	2	3	0.5	3929	441771	7.5	Hypothetical protein APOB
3482	Q9NR09	2	4	0.5	4829	527615	6	Baculoviral IAP repeat-containing protein 6
3482	UPI0000DBEF4D	2	4	0.5	4829	527615	6	Baculoviral IAP repeat-containing protein 6 (Ubiquitin-conjugating BIR domain enzyme apollon).
3482	UPI00004EC29E	2	4	0.5	4829	527629	6	baculoviral IAP repeat-containing 6
3482	UPI00004578FF	2	4	0.5	4829	527683	6.1	Baculoviral IAP repeat-containing protein 6 (Ubiquitin-conjugating BIR domain enzyme apollon).
3483	Q9NZJ4	2	2	0.5	4579	521131	7	Sacsin
3483	UPI0000D626BD	2	2	0.5	4576	520845	7	Sacsin.
3484	Q96JB1	2	3	0.4	4490	514668	6.3	Ciliary dynein heavy chain 8
3484	UPI0000D626B6	2	3	0.4	4699	537743	6.2	Ciliary dynein heavy chain 8 (Axonemal beta dynein heavy chain 8).
3484	Q96JB1-2	2	3	0.4	4454	510452	6.3	Isoform 2 of Q96JB1
3485	Q9Y6V0	2	2	0.4	5183	566666	6.5	Protein piccolo
3485	UPI0000DD87B8	2	2	0.4	5021	547665	6.3	PREDICTED: similar to Protein piccolo (Aczonin) isoform 7
3485	UPI0000DD87B7	2	2	0.4	5011	546724	6.3	PREDICTED: similar to Protein piccolo (Aczonin) isoform 12
3485	UPI0000DD87B6	2	2	0.4	5010	546565	6.3	PREDICTED: similar to Protein piccolo (Aczonin) isoform 2
3485	UPI0000DBEF4F	2	2	0.4	5039	550261	6.4	PCLO_HUMAN Isoform 3 of Q9Y6V0 - Homo sapiens (Human)
3485	UPI0000DBEF4E	2	2	0.4	5048	550881	6.4	PCLO_HUMAN Isoform 3 of Q9Y6V0 - Homo sapiens (Human)
3485	Q9Y6V0-2	2	2	0.4	4866	530973	6.3	Isoform 2 of Q9Y6V0
3486	UPI0000DD87BC	2	34	0.3	5048	534427	5.3	PREDICTED: similar to AHNAK nucleoprotein isoform 1 isoform 1