No.	Accession	Description	Sum PEP Score	Coverage [%]	# Peptides	# PSMs	# Unique Peptides	Score Mascot: A5 Mascot	Score Sequest HT: A2 Sequest HT	# Peptides (by Search Engine): A2 Sequest HT	# Peptides (by Search Engine): A5 Mascot	# Razor Peptides	ctrl Abundances_1	ctrl Abundances_2	ctrl Abundances_3	ctrl Abundances_4	JAM-A KO Abundances_1	JAM-A KO Abundances_2	JAM-A KO Abundances_3	JAM-A KO Abundances_4
1	Q15149-1	plectin [OS=Homo sapiens]	2088.5	54	208	9145	4	130257	12847	206	207	201	1.50.E+10	1.50.E+10	1.54.E+10	1.51.E+10	1.26.E+10	1.31.E+10	1.31.E+10	1.31.E+10
2	Q09666-1	Neuroblast differentiation-associated protein AHNAK [OS=Homo sapiens]	2086.0	65	199	8536	199	89526	10776	199	194	0	1.37.E+10	1.34.E+10	1.40.E+10	1.31.E+10	1.26.E+10	1.26.E+10	1.31.E+10	1.26.E+10
3	Q15149-4	Isoform 4 of Plectin [OS=Homo sapiens]	1636.7	55	207	4611	2		12917	207		0	1.44.E+08	1.44.E+08	1.45.E+08	1.52.E+08	1.19.E+08	1.33.E+08	1.32.E+08	1.13.E+08
4	P49327	Fatty acid synthase [OS=Homo sapiens]	1436.3	60	106	7224	105	118921	11958	106	105	1	1.48.E+10	1.51.E+10	1.50.E+10	1.48.E+10	1.08.E+10	1.09.E+10	1.07.E+10	1.06.E+10
5	P21333	Filamin-A [OS=Homo sapiens]	1392.4	57	108	6121	101	94126	9209	108	108	7	6.45.E+09	6.53.E+09	6.48.E+09	6.40.E+09	1.16.E+10	1.15.E+10	1.16.E+10	1.16.E+10
6	Q9Y490	Talin-1 [OS=Homo sapiens]	1279.4	58	95	5375	88	109118	8687	95	95	8	8.19.E+09	8.13.E+09	7.83.E+09	8.10.E+09	9.82.E+09	9.72.E+09	9.66.E+09	9.89.E+09
7	P35579-1	Myosin-9 [OS=Homo sapiens]	1229.4	53	97	5159	81	93256	8017	96	96	15	7.18.E+09	7.13.E+09	7.24.E+09	6.80.E+09	9.53.E+09	9.57.E+09	9.17.E+09	9.41.E+09
8	P05783	Keratin, type I cytoskeletal 18 [OS=Homo sapiens]	1110.7	81	47	10535	44	209848	16983	47	45	4	8.39.E+10	8.32.E+10	8.42.E+10	8.72.E+10	4.37.E+10	4.44.E+10	4.49.E+10	4.40.E+10
9	Q13813	Spectrin alpha chain, non-erythrocytic 1 [OS=Homo sapiens]	1078.1	54	101	3621	101	58038	5203	101	97	0	4.43.E+09	4.33.E+09	4.40.E+09	4.39.E+09	4.90.E+09	4.86.E+09	4.80.E+09	4.94.E+09
10	Q14204	Cytoplasmic dynein 1 heavy chain 1 [OS=Homo sapiens]	1069.0	41	131	4252	131	52296	5907	131	131	0	4.69.E+09	5.05.E+09	5.00.E+09	5.27.E+09	6.15.E+09	6.15.E+09	5.78.E+09	5.95.E+09
11	P55072	Transitional endoplasmic reticulum ATPase [OS=Homo sapiens]	1065.9	85	68	9027	68	151749	14363	67	66	0	2.67.E+10	2.75.E+10	2.62.E+10	2.59.E+10	2.98.E+10	3.04.E+10	2.93.E+10	2.95.E+10
12	O43707	Alpha-actinin-4 [OS=Homo sapiens]	1028.6	76	67	6793	45	101498	10378	66	66	22	1.62.E+10	1.67.E+10	1.55.E+10	1.61.E+10	1.59.E+10	1.62.E+10	1.60.E+10	1.60.E+10
13	P07900	Heat shock protein HSP 90-alpha [OS=Homo sapiens]	1024.4	75	67	10382	43	163720	16657	65	65	25	3.92.E+10	3.90.E+10	4.06.E+10	3.82.E+10	4.32.E+10	4.37.E+10	4.53.E+10	4.28.E+10
14	P13639	Elongation factor 2 [OS=Homo sapiens]	979.4	77	61	9101	60	144100	14619	60	58	1	2.17.E+10	2.15.E+10	2.03.E+10	2.24.E+10	1.96.E+10	1.82.E+10	1.87.E+10	1.83.E+10
15	Q00610-1	Clathrin heavy chain 1 [OS=Homo sapiens]	933.0	60	74	3970	74	66736	6197	73	73	0	5.23.E+09	5.45.E+09	5.26.E+09	5.27.E+09	9.33.E+09	9.40.E+09	9.21.E+09	9.30.E+09
16	P08238	Heat shock protein HSP 90-beta [OS=Homo sapiens]	888.5	73	61	7686	36	122279	12255	60	58	2	1.33.E+10	1.34.E+10	1.36.E+10	1.32.E+10	1.24.E+10	1.24.E+10	1.16.E+10	1.24.E+10
17	P14618	Pyruvate kinase PKM [OS=Homo sapiens]	838.7	78	40	7881	40	159852	14026	39	39	0	4.29.E+10	4.31.E+10	4.23.E+10	4.26.E+10	4.17.E+10	4.26.E+10	4.05.E+10	4.31.E+10
18	P63261	Actin, cytoplasmic 2 [OS=Homo sapiens]	800.5	90	34	13892	1	288263	21966	32	33	0	5.09.E+08	5.65.E+08	4.45.E+08	5.62.E+08	6.18.E+08	6.06.E+08	5.39.E+08	6.25.E+08
19	Q01082-1	Spectrin beta chain, non-erythrocytic 1 [OS=Homo sapiens]	783.5	44	72	2286	7	27921	3121	72	69	60	2.54.E+09	2.53.E+09	2.54.E+09	2.55.E+09	3.14.E+09	3.03.E+09	2.95.E+09	3.14.E+09
20	P21980	Protein-glutamine gamma-glutamyltransferase 2 [OS=Homo sapiens]	773.3	71	47	7076	47	146906	11700	46	47	0	2.08.E+10	2.12.E+10	2.10.E+10	2.10.E+10	2.64.E+10	2.71.E+10	2.67.E+10	2.70.E+10
21	P06733-1	alpha-enolase [OS=Homo sapiens]	757.8	79	37	10199	33	222051	16699	37	37	4	4.49.E+10	4.58.E+10	4.43.E+10	4.56.E+10	4.81.E+10	4.86.E+10	4.63.E+10	4.81.E+10
22	P46940	Ras GTPase-activating-like protein IQGAP1 [OS=Homo sapiens]	737.0	59	75	2789	71	44940	4322	74	74	3	3.35.E+09	3.50.E+09	3.31.E+09	3.28.E+09	4.13.E+09	4.07.E+09	3.83.E+09	3.94.E+09
23	P78527	DNA-dependent protein kinase catalytic subunit [OS=Homo sapiens]	725.2	31	91	2625	91	33537	2976	90	89	0	3.22.E+09	3.11.E+09	3.22.E+09	3.04.E+09	3.58.E+09	3.60.E+09	3.65.E+09	3.56.E+09
24	P07355	Annexin A2 [OS=Homo sapiens]	724.2	85	46	10272	46	192605	16560	45	44	0	6.13.E+10	6.54.E+10	6.38.E+10	6.53.E+10	5.89.E+10	5.82.E+10	5.79.E+10	5.80.E+10
25	P07437	tubulin beta chain [OS=Homo sapiens]	719.8	82	30	8476	6	153867	14254	30	30	2	5.16.E+09	5.52.E+09	5.17.E+09	5.23.E+09	7.02.E+09	6.88.E+09	5.71.E+09	6.76.E+09
26	P68371	Tubulin beta-4B chain [OS=Homo sapiens]	703.7	82	31	7878	1	140525	13114	31	31	41	2.65.E+10	2.77.E+10	2.63.E+10	2.74.E+10	3.11.E+10	3.12.E+10	3.01.E+10	3.01.E+10
27	P11142-1	Heat shock cognate 71 kDa protein [OS=Homo sapiens]	698.2	70	45	5152	41	88940	7681	44	45	4	1.91.E+10	1.91.E+10	1.93.E+10	1.84.E+10	1.85.E+10	1.98.E+10	2.01.E+10	1.96.E+10
28	P29401	Transketolase [OS=Homo sapiens]	686.0	81	39	5153	39	92099	8295	39	39	0	1.22.E+10	1.26.E+10	1.22.E+10	1.25.E+10	1.24.E+10	1.30.E+10	1.29.E+10	1.28.E+10
29	P12814-1	Alpha-actinin-1 [OS=Homo sapiens]	682.4	70	53	4719	31	71435	6751	53	52	0	2.71.E+09	2.82.E+09	2.82.E+09	2.65.E+09	4.63.E+09	4.87.E+09	4.77.E+09	4.61.E+09
30	O75369-1	Filamin-B [OS=Homo sapiens]	676.8	44	77	2387	70	27281	2935	76	77	0	2.53.E+09	2.58.E+09	2.70.E+09	2.23.E+09	2.75.E+09	2.80.E+09	2.97.E+09	2.94.E+09
31	P42704	Leucine-rich PPR motif-containing protein, mitochondrial [OS=Homo sapiens]	664.7	57	58	3078	58	42255	3947	58	58	0	3.47.E+09	3.57.E+09	3.54.E+09	3.73.E+09	4.33.E+09	4.32.E+09	3.96.E+09	4.24.E+09
32	P22314	Ubiquitin-like modifier-activating enzyme 1 [OS=Homo sapiens]	652.3	69	48	3848	48	68422	6117	47	48	0	6.02.E+09	6.03.E+09	5.94.E+09	5.95.E+09	7.32.E+09	7.35.E+09	7.22.E+09	7.25.E+09
33	Q9NZM1	Myoferlin [OS=Homo sapiens]	635.4	45	69	2289	69	23093	2893	69	69	0	4.53.E+09	4.37.E+09	4.47.E+09	4.52.E+09	2.56.E+09	2.59.E+09	2.46.E+09	2.64.E+09
34	P04406-1	glyceraldehyde-3-phosphate dehydrogenase [OS=Homo sapiens]	620.7	85	27	8652	27	157026	16002	27	27	0	4.87.E+10	5.04.E+10	4.87.E+10	4.68.E+10	4.41.E+10	4.34.E+10	4.35.E+10	4.41.E+10
35	P10809	60 kDa heat shock protein, mitochondrial [OS=Homo sapiens]	611.1	74	38	4411	38	86617	7133	38	37	0	1.03.E+10	1.05.E+10	1.01.E+10	1.05.E+10	1.14.E+10	1.14.E+10	1.13.E+10	1.17.E+10
36	Q9BQE3	Tubulin alpha-1C chain [OS=Homo sapiens]	606.0	77	32	5918	2	118909	9877	32	32	34	2.08.E+10	2.16.E+10	2.07.E+10	1.99.E+10	3.11.E+10	3.17.E+10	3.03.E+10	3.11.E+10
37	P68104	Elongation factor 1-alpha 1 [OS=Homo sapiens]	587.2	70	26	7346	15	98018	12491	26	25	14	3.68.E+10	3.58.E+10	3.72.E+10	3.72.E+10	3.63.E+10	3.59.E+10	3.75.E+10	3.64.E+10
38	Q14697-1	Neutral alpha-glucosidase AB [OS=Homo sapiens]	585.2	62	42	2877	42	33502	3908	42	42	0	5.28.E+09	5.15.E+09	5.05.E+09	4.94.E+09	5.82.E+09	5.91.E+09	5.85.E+09	5.86.E+09
39	Q71U36	tubulin alpha-1A chain [OS=Homo sapiens]	581.7	76	31	5135	1	100856	9066	31	31	3	9.02.E+08	8.94.E+08	8.17.E+08	8.22.E+08	1.14.E+09	1.16.E+09	1.03.E+09	1.09.E+09
40	P04350	Tubulin beta-4A chain [OS=Homo sapiens]	576.5	71	26	6559	4	114288	10871	26	25	0	6.88.E+07	1.79.E+08	1.15.E+08	7.79.E+07	2.36.E+08	2.42.E+08	2.36.E+08	2.38.E+08
41	P02545	Prelamin-A/C [OS=Homo sapiens]	567.0	66	45	3894	5	68422	5838	45	45	47	1.30.E+10	1.25.E+10	1.31.E+10	1.34.E+10	9.73.E+09	9.44.E+09	9.93.E+09	9.42.E+09
42	P13010	X-ray repair cross-complementing protein 5 [OS=Homo sapiens]	566.5	73	44	3203	43	40967	4602	44	42	1	6.09.E+09	6.09.E+09	6.00.E+09	5.89.E+09	6.60.E+09	6.51.E+09	6.75.E+09	6.55.E+09
43	Q01082-3	Isoform 2 of Spectrin beta chain, non-erythrocytic 1 [OS=Homo sapiens]	561.0	46	66	1050	1		2750	66		0								3.82.E+06
44	Q9BVA1	Tubulin beta-2B chain [OS=Homo sapiens]	542.3	66	27	6658	3	116888	10889	27	27	0	4.58.E+07	4.43.E+07	4.01.E+07	4.80.E+07	8.16.E+07	7.66.E+07	8.20.E+07	9.10.E+07
45	P30101	Protein disulfide-isomerase A3 [OS=Homo sapiens]	529.2	67	36	3231	36	46485	5043	36	36	0	7.61.E+09	7.54.E+09	7.18.E+09	7.83.E+09	9.56.E+09	1.00.E+10	9.61.E+09	9.91.E+09
46	P68366	Tubulin alpha-4A chain [OS=Homo sapiens]	526.8	66	26	5182	8	97467	8480	26	26	0	2.08.E+09	2.18.E+09	2.09.E+09	2.06.E+09	2.95.E+09	3.16.E+09	1.84.E+09	2.97.E+09
47	P11021	78 kDa glucose-regulated protein [OS=Homo sapiens]	498.9	53	33	3485	31	58674	5541	33	33	0	7.10.E+09	7.35.E+09	7.47.E+09	7.05.E+09	7.79.E+09	7.41.E+09	7.45.E+09	7.53.E+09
48	P04075	fructose-bisphosphate aldolase A [OS=Homo sapiens]	490.0	89	32	3181	30	48453	5086	30	32	2	8.84.E+09	8.71.E+09	8.43.E+09	9.25.E+09	9.56.E+09	1.00.E+10	9.88.E+09	1.03.E+10
49	P07237	Protein disulfide-isomerase [OS=Homo sapiens]	489.9	75	37	4950	37	75694	6857	37	37	0	1.29.E+10	1.25.E+10	1.31.E+10	1.28.E+10	1.19.E+10	1.21.E+10	1.14.E+10	1.22.E+10
50	P14625	Endoplasmin [OS=Homo sapiens]	488.2	58	46	2806	44	39336	3789	46	45	0	4.46.E+09	4.37.E+09	4.27.E+09	4.40.E+09	6.22.E+09	6.27.E+09	6.44.E+09	6.29.E+09
51	O60701	UDP-glucose 6-dehydrogenase [OS=Homo sapiens]	487.6	80	35	2659	35	50680	4167	35	35	0	5.51.E+09	5.52.E+09	5.58.E+09	5.60.E+09	5.94.E+09	5.94.E+09	5.75.E+09	5.91.E+09
52	P07814	Bifunctional glutamate/proline--tRNA ligase [OS=Homo sapiens]	483.3	54	57	1840	57	23813	2397	56	55	0	1.71.E+09	1.83.E+09	1.70.E+09	1.87.E+09	1.79.E+09	1.86.E+09	1.60.E+09	1.70.E+09
53	P27708	CAD protein [OS=Homo sapiens]	482.1	43	55	1773	55	18663	2195	54	54	0	2.24.E+09	2.18.E+09	2.14.E+09	2.37.E+09	2.75.E+09	2.74.E+09	2.39.E+09	2.74.E+09
54	P00338-1	L-lactate dehydrogenase A chain [OS=Homo sapiens]	481.5	86	30	4104	29	71432	5636	28	29	1	1.78.E+10	1.84.E+10	1.79.E+10	1.82.E+10	2.22.E+10	2.22.E+10	2.26.E+10	2.21.E+10
55	P49588	Alanine--tRNA ligase, cytoplasmic [OS=Homo sapiens]	471.0	63	38	1987	38	33016	2776	37	37	0	2.64.E+09	2.77.E+09	2.62.E+09	2.77.E+09	2.63.E+09	2.54.E+09	2.48.E+09	2.50.E+09
56	P11413-1	Glucose-6-phosphate 1-dehydrogenase [OS=Homo sapiens]	465.8	86	40	3035	40	37201	4084	39	40	0	6.81.E+09	6.83.E+09	6.83.E+09	6.84.E+09	7.97.E+09	7.94.E+09	7.75.E+09	7.81.E+09

No.	Accession	Description	Sum PEP Score	Coverage [%]	# Peptides	# PSMs	# Unique Peptides	Score Mascot: A5 Mascot	Score Sequest HT: A2 Sequest HT	# Peptides (by Search Engine): A2 Sequest HT	# Peptides (by Search Engine): A5 Mascot	# Razor Peptides	ctrl Abundances_1	ctrl Abundances_2	ctrl Abundances_3	ctrl Abundances_4	JAM-A KO Abundances_1	JAM-A KO Abundances_2	JAM-A KO Abundances_3	JAM-A KO Abundances_4
57	P06576	ATP synthase subunit beta, mitochondrial [OS=Homo sapiens]	461.4	71	25	2852	25	53974	4833	25	25	0	6.76.E+09	6.82.E+09	6.34.E+09	6.55.E+09	6.83.E+09	6.90.E+09	6.53.E+09	6.74.E+09
58	P15311	Ezrin [OS=Homo sapiens]	461.0	62	45	4342	32	48130	5252	45	45	15	1.05.E+10	1.05.E+10	1.07.E+10	1.03.E+10	8.27.E+09	8.52.E+09	8.70.E+09	8.31.E+09
59	P04083	annexin A1 [OS=Homo sapiens]	458.7	77	29	3530	29	66338	5452	28	29	0	9.71.E+09	9.82.E+09	9.78.E+09	9.98.E+09	8.45.E+09	8.38.E+09	8.40.E+09	8.58.E+09
60	Q13509	tubulin beta-3 chain [OS=Homo sapiens]	454.7	69	24	4033	7	72252	6442	24	24	2	1.01.E+09	1.07.E+09	9.98.E+08	9.69.E+08	8.88.E+08	8.37.E+08	7.81.E+08	8.18.E+08
61	P12956	X-ray repair cross-complementing protein 6 [OS=Homo sapiens]	433.7	55	37	2850	37	35068	3690	37	37	0	4.52.E+09	4.62.E+09	4.49.E+09	4.33.E+09	4.95.E+09	4.96.E+09	5.07.E+09	5.19.E+09
62	P43490	nicotinamide phosphoribosyltransferase [OS=Homo sapiens]	431.5	77	33	1988	33	28309	2796	33	33	0	2.02.E+09	2.05.E+09	2.01.E+09	1.94.E+09	1.59.E+09	1.62.E+09	1.60.E+09	1.52.E+09
63	P31939	bifunctional purine biosynthesis protein purH [OS=Homo sapiens]	429.1	77	36	2069	36	29862	3052	33	36	0	3.48.E+09	3.42.E+09	3.38.E+09	3.27.E+09	3.98.E+09	4.04.E+09	4.15.E+09	4.20.E+09
64	Q08211	Atp-dependent rna helicase a [OS=Homo sapiens]	424.9	41	38	1748	38	23643	2483	38	38	0	2.87.E+09	2.91.E+09	2.91.E+09	2.87.E+09	3.14.E+09	3.17.E+09	3.20.E+09	3.14.E+09
65	P52895	Aldo-keto reductase family 1 member C2 [OS=Homo sapiens]	421.6	81	24	3031	5	31324	4554	24	23	0	1.25.E+09	1.09.E+09	1.19.E+09	1.19.E+09	3.97.E+09	4.09.E+09	4.43.E+09	4.19.E+09
66	P61978	Heterogeneous nuclear ribonucleoprotein K [OS=Homo sapiens]	409.7	56	27	3019	2	48369	4386	27	26	25	6.18.E+09	6.18.E+09	6.31.E+09	6.46.E+09	7.23.E+09	7.17.E+09	7.33.E+09	7.20.E+09
67	Q05639	Elongation factor 1-alpha 2 [OS=Homo sapiens]	401.6	66	21	5124	10	71382	8254	21	21	0	7.28.E+08	8.14.E+08	6.00.E+08	8.51.E+08	1.46.E+09	1.38.E+09	1.21.E+09	1.32.E+09
68	P07195	L-lactate dehydrogenase B chain [OS=Homo sapiens]	399.8	71	24	3071	23	52632	3739	24	24	0	7.10.E+09	6.95.E+09	7.05.E+09	6.99.E+09	8.43.E+09	8.56.E+09	8.99.E+09	8.67.E+09
69	P22626	heterogeneous nuclear ribonucleoproteins A2/B1 [OS=Homo sapiens]	399.1	63	25	2870	21	42483	4095	25	25	4	8.18.E+09	8.04.E+09	7.91.E+09	8.65.E+09	9.50.E+09	8.92.E+09	8.92.E+09	9.02.E+09
70	P78371-1	T-complex protein 1 subunit beta [OS=Homo sapiens]	399.0	73	30	1571	30	27507	2262	29	30	0	3.96.E+09	3.95.E+09	3.82.E+09	3.81.E+09	3.93.E+09	3.81.E+09	3.81.E+09	3.93.E+09
71	P02545-2	Isoform C of Prelamin-A/C [OS=Homo sapiens]	398.2	65	41	1803	1		5331	41		0	2.18.E+08	2.30.E+08	1.89.E+08	2.21.E+08	2.12.E+08	2.03.E+08	2.01.E+08	1.94.E+08
72	P22234	multifunctional protein ADE2 [OS=Homo sapiens]	395.9	77	35	1797	35	27254	2584	33	34	0	3.42.E+09	3.52.E+09	3.14.E+09	3.27.E+09	3.94.E+09	3.92.E+09	3.85.E+09	3.84.E+09
73	P15924-1	Desmoplakin [OS=Homo sapiens]	395.3	26	47	1279	47	15918	1714	47	46	0	1.41.E+09	1.44.E+09	1.41.E+09	1.42.E+09	1.21.E+09	1.19.E+09	1.11.E+09	1.13.E+09
74	P0DMV8	heat shock 70 kDa protein 1A [OS=Homo sapiens]	393.8	54	26	1900	23	30208	2994	26	26	0	3.42.E+09	3.56.E+09	3.57.E+09	3.45.E+09	2.90.E+09	2.82.E+09	2.90.E+09	2.94.E+09
75	P09651-1	Heterogeneous nuclear ribonucleoprotein A1 [OS=Homo sapiens]	392.9	51	24	3091	20	49499	4437	24	24	0	4.68.E+09	4.72.E+09	4.50.E+09	4.67.E+09	4.22.E+09	4.45.E+09	4.33.E+09	4.43.E+09
76	Q14974	Importin subunit beta-1 [OS=Homo sapiens]	382.3	54	32	1817	32	27892	2370	32	32	0	1.58.E+09	1.64.E+09	1.50.E+09	1.66.E+09	2.36.E+09	2.25.E+09	2.16.E+09	2.27.E+09
77	P19338	Nucleolin [OS=Homo sapiens]	376.0	37	30	2815	30	56653	4084	30	30	0	7.45.E+09	7.52.E+09	7.22.E+09	7.35.E+09	7.04.E+09	7.46.E+09	7.40.E+09	7.45.E+09
78	P23528	Cofilin-1 [OS=Homo sapiens]	375.2	78	18	3220	12	66841	5401	17	17	6	1.50.E+10	1.48.E+10	1.46.E+10	1.47.E+10	1.80.E+10	1.88.E+10	1.78.E+10	1.80.E+10
79	Q04828	aldo-keto reductase family 1 member C1 [OS=Homo sapiens]	373.7	81	26	2358	2	23703	3612	26	25	27	2.95.E+09	2.93.E+09	2.92.E+09	3.06.E+09	9.31.E+09	9.31.E+09	1.00.E+10	9.21.E+09
80	Q16881-1	Thioredoxin reductase 1, cytoplasmic [OS=Homo sapiens]	366.6	54	22	1256	22	19005	2086	22	22	0	1.82.E+09	1.86.E+09	2.03.E+09	1.89.E+09	2.14.E+09	2.42.E+09	2.08.E+09	2.07.E+09
81	P13797	Plastin-3 [OS=Homo sapiens]	365.8	55	31	1566	27	19458	2336	31	31	4	2.25.E+09	2.29.E+09	2.27.E+09	2.20.E+09	3.06.E+09	3.19.E+09	3.14.E+09	2.96.E+09
82	Q00839	Heterogeneous nuclear ribonucleoprotein U [OS=Homo sapiens]	362.1	46	30	2519	30	36410	3635	30	30	0	5.90.E+09	6.17.E+09	5.81.E+09	6.07.E+09	6.28.E+09	6.22.E+09	6.29.E+09	6.19.E+09
83	P67936	Tropomyosin alpha-4 chain [OS=Homo sapiens]	361.8	74	27	1827	19	24735	2662	26	27	8	2.59.E+09	2.63.E+09	2.65.E+09	2.55.E+09	3.84.E+09	3.76.E+09	3.99.E+09	3.80.E+09
84	P60842	Eukaryotic initiation factor 4A-I [OS=Homo sapiens]	359.4	77	28	2326	16	40832	3227	28	28	12	6.33.E+09	6.06.E+09	6.11.E+09	6.11.E+09	4.60.E+09	4.72.E+09	5.06.E+09	4.69.E+09
85	P06744	glucose-6-phosphate isomerase [OS=Homo sapiens]	357.7	62	29	2477	29	36923	3530	28	27	0	4.76.E+09	4.75.E+09	4.74.E+09	4.90.E+09	4.10.E+09	4.22.E+09	4.27.E+09	4.07.E+09
86	O75643-1	U5 small nuclear ribonucleoprotein 200 kDa helicase [OS=Homo sapiens]	351.6	27	35	1044	35	15500	1373	35	35	0	8.20.E+08	8.73.E+08	8.10.E+08	9.30.E+08	8.57.E+08	8.11.E+08	7.42.E+08	7.96.E+08
87	P11586	C-1-tetrahydrofolate synthase, cytoplasmic [OS=Homo sapiens]	351.2	55	37	1828	37	25773	2586	37	37	0	3.56.E+09	3.53.E+09	3.52.E+09	3.39.E+09	4.43.E+09	4.37.E+09	4.29.E+09	4.34.E+09
88	P55060-1	Exportin-2 [OS=Homo sapiens]	338.5	46	32	1651	32	23424	2051	32	32	0	1.36.E+09	1.33.E+09	1.32.E+09	1.28.E+09	1.63.E+09	1.58.E+09	1.63.E+09	1.55.E+09
89	P25705-1	ATP synthase subunit alpha, mitochondrial [OS=Homo sapiens]	334.6	63	29	2555	29	51755	4084	29	28	0	6.97.E+09	6.80.E+09	6.99.E+09	6.80.E+09	7.75.E+09	7.64.E+09	7.76.E+09	7.77.E+09
90	P48643	T-complex protein 1 subunit epsilon [OS=Homo sapiens]	334.4	68	26	1311	25	20492	1774	24	26	1	2.87.E+09	2.95.E+09	3.46.E+09	3.28.E+09	2.78.E+09	3.09.E+09	3.20.E+09	3.25.E+09
91	Q01813	ATP-dependent 6-phosphofructokinase, platelet type [OS=Homo sapiens]	332.5	52	31	1469	29	20218	1828	31	31	2	2.59.E+09	2.54.E+09	2.53.E+09	2.58.E+09	2.52.E+09	2.54.E+09	2.54.E+09	2.57.E+09
92	P18669	Phosphoglycerate mutase 1 [OS=Homo sapiens]	331.1	70	17	1800	17	26495	3078	17	17	0	3.57.E+09	3.76.E+09	3.60.E+09	3.78.E+09	4.33.E+09	4.25.E+09	4.40.E+09	4.23.E+09
93	P36578	60S ribosomal protein L4 [OS=Homo sapiens]	329.4	51	26	1578	26	19768	2590	24	26	0	4.50.E+09	4.49.E+09	4.45.E+09	4.20.E+09	3.81.E+09	3.92.E+09	3.91.E+09	3.90.E+09
94	P27797	Calreticulin [OS=Homo sapiens]	327.1	62	18	1705	18	24169	2480	18	18	0	3.02.E+09	2.97.E+09	3.01.E+09	3.20.E+09	4.06.E+09	4.06.E+09	3.98.E+09	4.09.E+09
95	P31947-1	14-3-3 protein sigma [OS=Homo sapiens]	326.4	82	19	3344	15	52984	4644	19	19	0	6.21.E+09	6.20.E+09	6.12.E+09	6.43.E+09	3.90.E+09	3.65.E+09	3.71.E+09	3.71.E+09
96	P35580	Myosin-10 [OS=Homo sapiens]	326.2	21	31	1083	17	14581	1428	31	30	0	5.02.E+08	5.19.E+08	5.13.E+08	4.85.E+08	4.97.E+08	4.85.E+08	4.62.E+08	4.41.E+08
97	P06748	Nucleophosmin [OS=Homo sapiens]	325.8	63	14	1692	13	44680	3346	14	14	1	3.77.E+09	3.99.E+09	3.93.E+09	4.46.E+09	3.87.E+09	3.87.E+09	3.89.E+09	3.99.E+09
98	P00558	phosphoglycerate kinase 1 [OS=Homo sapiens]	325.5	73	22	1650	22	29423	2778	22	22	0	3.59.E+09	3.58.E+09	3.58.E+09	3.63.E+09	4.46.E+09	4.52.E+09	3.92.E+09	4.40.E+09
99	O00151	PDZ and LIM domain protein 1 [OS=Homo sapiens]	324.6	84	20	1329	20	18559	2166	19	20	0	1.60.E+09	1.60.E+09	1.60.E+09	1.50.E+09	2.29.E+09	2.34.E+09	2.38.E+09	2.24.E+09
100	P38646	Stress-70 protein, mitochondrial [OS=Homo sapiens]	323.7	54	28	1625	28	30151	2299	28	28	0	3.31.E+09	3.42.E+09	3.27.E+09	3.28.E+09	3.51.E+09	3.71.E+09	3.40.E+09	3.51.E+09
101	Q99832	T-complex protein 1 subunit eta [OS=Homo sapiens]	310.6	68	27	1630	27	35617	2557	27	27	0	2.74.E+09	2.79.E+09	2.71.E+09	2.70.E+09	2.78.E+09	2.79.E+09	2.81.E+09	2.74.E+09
102	P26038	Moesin [OS=Homo sapiens]	308.8	51	30	2302	18	22784	2427	30	30	1	9.63.E+08	9.86.E+08	8.86.E+08	9.36.E+08	9.70.E+08	8.83.E+08	9.06.E+08	8.68.E+08
103	P26641	elongation factor 1-gamma [OS=Homo sapiens]	306.7	69	24	2567	24	36985	3535	23	23	0	8.99.E+09	8.63.E+09	8.96.E+09	9.01.E+09	7.77.E+09	7.77.E+09	7.96.E+09	7.27.E+09
104	P09936	Ubiquitin carboxyl-terminal hydrolase isozyme L1 [OS=Homo sapiens]	305.5	78	16	1581	16	23243	2666	16	16	0	4.08.E+09	3.85.E+09	3.98.E+09	4.16.E+09	5.79.E+09	5.34.E+09	5.68.E+09	5.38.E+09
105	P60174	Triosephosphate isomerase [OS=Homo sapiens]	303.0	72	17	2480	17	44927	4485	17	17	0	7.75.E+09	7.87.E+09	7.78.E+09	8.03.E+09	8.30.E+09	8.29.E+09	7.53.E+09	8.31.E+09
106	P41250	Glycine--tRNA ligase [OS=Homo sapiens]	302.9	45	24	1167	24	19982	1672	24	24	0	1.31.E+09	1.29.E+09	1.26.E+09	1.35.E+09	1.37.E+09	1.40.E+09	1.37.E+09	1.42.E+09
107	P08195	4F2 cell-surface antigen heavy chain [OS=Homo sapiens]	302.3	40	22	1895	22	26308	2948	22	22	0	4.95.E+09	5.12.E+09	4.90.E+09	4.82.E+09	7.39.E+09	7.48.E+09	7.48.E+09	7.48.E+09
108	Q04637	eukaryotic translation initiation factor 4 gamma 1 [OS=Homo sapiens]	302.3	29	35	1390	35	17736	1599	35	35	0	1.63.E+09	1.69.E+09	1.68.E+09	1.83.E+09	1.70.E+09	1.66.E+09	1.61.E+09	1.74.E+09
109	P50991	T-complex protein 1 subunit delta [OS=Homo sapiens]	298.5	58	23	1289	22	18290	1835	23	23	0	2.13.E+09	2.17.E+09	2.11.E+09	2.15.E+09	2.38.E+09	2.27.E+09	2.09.E+09	2.25.E+09
110	P26640	Valine--tRNA ligase [OS=Homo sapiens]	297.8	37	27	1138	27	14701	1358	26	27	0	1.35.E+09	1.33.E+09	1.28.E+09	1.31.E+09	1.52.E+09	1.57.E+09	1.49.E+09	1.55.E+09
111	P62258-1	14-3-3 protein epsilon [OS=Homo sapiens]	296.7	78	23	2280	21	29970	2829	23	23	3	8.28.E+09	8.41.E+09	8.36.E+09	8.21.E+09	6.82.E+09	6.85.E+09	6.83.E+09	6.96.E+09

No.	Accession	Description	Sum PEP Score	Coverage [%]	# Peptides	# PSMs	# Unique Peptides	Score Mascot: A5 Mascot	Score Sequest HT: A2 Sequest HT	# Peptides (by Search Engine): A2 Sequest HT	# Peptides (by Search Engine): A5 Mascot	# Razor Peptides	ctrl Abundances_1	ctrl Abundances_2	ctrl Abundances_3	ctrl Abundances_4	JAM-A KO Abundances_1	JAM-A KO Abundances_2	JAM-A KO Abundances_3	JAM-A KO Abundances_4
112	Q9UQ80	proliferation-associated protein 2G4 [OS=Homo sapiens]	294.5	67	24	1513	24	16855	2415	23	24	0	2.93.E+09	2.96.E+09	2.96.E+09	2.82.E+09	2.48.E+09	2.44.E+09	2.52.E+09	2.46.E+09
113	P26599	Polypyrimidine tract-binding protein 1 [OS=Homo sapiens]	293.1	60	20	1600	18	31061	2571	19	20	2	2.26.E+09	2.22.E+09	2.13.E+09	2.17.E+09	2.43.E+09	2.46.E+09	2.18.E+09	2.31.E+09
114	P52209	6-phosphogluconate dehydrogenase, decarboxylating [OS=Homo sapiens]	292.9	67	25	1423	25	19707	2022	24	25	0	2.19.E+09	2.19.E+09	2.11.E+09	2.17.E+09	1.81.E+09	1.82.E+09	1.72.E+09	1.73.E+09
115	P50395-1	Rab GDP dissociation inhibitor beta [OS=Homo sapiens]	291.9	64	23	1277	17	20710	1902	23	22	6	1.96.E+09	2.09.E+09	1.81.E+09	1.99.E+09	2.04.E+09	2.12.E+09	1.94.E+09	2.12.E+09
116	Q13200	26S proteasome non-ATPase regulatory subunit 2 [OS=Homo sapiens]	290.9	48	29	1102	29	13561	1213	29	28	0	9.80.E+08	1.02.E+09	9.89.E+08	1.04.E+09	1.06.E+09	1.08.E+09	1.04.E+09	1.09.E+09
117	P41252	isoleucine--tRNA ligase, cytoplasmic [OS=Homo sapiens]	288.0	39	38	961	38	7761	1044	38	36	0	1.17.E+09	1.22.E+09	1.15.E+09	1.26.E+09	1.52.E+09	1.45.E+09	1.35.E+09	1.39.E+09
118	P31946	14-3-3 protein beta/alpha [OS=Homo sapiens]	285.9	63	19	1737	11	26032	2029	19	19	2	8.04.E+08	8.35.E+08	7.72.E+08	8.09.E+08	8.50.E+08	8.65.E+08	8.42.E+08	8.43.E+08
119	P09874	Poly [ADP-ribose] polymerase 1 [OS=Homo sapiens]	285.0	41	28	976	28	11435	1291	27	28	0	1.56.E+09	1.60.E+09	1.58.E+09	1.60.E+09	1.77.E+09	1.74.E+09	1.78.E+09	1.77.E+09
120	P11940-1	Polyadenylate-binding protein 1 [OS=Homo sapiens]	283.5	46	23	1473	15	21647	2093	23	23	10	2.74.E+09	2.79.E+09	2.78.E+09	2.68.E+09	2.40.E+09	2.47.E+09	2.50.E+09	2.43.E+09
121	P06753-2	Isoform 2 of Tropomyosin alpha-3 chain [OS=Homo sapiens]	283.5	61	24	972	16		2720	24		0	2.06.E+09	1.87.E+09	2.11.E+09	2.00.E+09	2.03.E+09	2.01.E+09	2.25.E+09	2.09.E+09
122	P30153	serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform [OS=Homo sapiens]	281.3	53	23	1096	19	22963	1864	21	23	4	1.38.E+09	1.24.E+09	1.31.E+09	1.36.E+09	1.47.E+09	1.32.E+09	1.40.E+09	1.40.E+09
123	Q7Z6Z7	E3 ubiquitin-protein ligase HUWE1 [OS=Homo sapiens]	277.6	15	34	789	34	11299	998	33	34	0	6.92.E+08	7.01.E+08	7.12.E+08	7.40.E+08	7.96.E+08	7.25.E+08	7.24.E+08	7.27.E+08
124	P34897-1	Serine hydroxymethyltransferase, mitochondrial [OS=Homo sapiens]	276.8	56	21	1404	20	23761	2236	21	21	1	2.60.E+09	2.66.E+09	2.65.E+09	2.58.E+09	2.61.E+09	2.61.E+09	2.61.E+09	2.63.E+09
125	Q86VP6-1	cullin-associated nedd8-dissociated protein 1 [OS=Homo sapiens]	276.2	35	28	1435	28	18815	1763	27	28	0	1.16.E+09	1.26.E+09	1.20.E+09	1.28.E+09	1.33.E+09	1.29.E+09	1.20.E+09	1.25.E+09
126	P63241-1	Eukaryotic translation initiation factor 5A-1 [OS=Homo sapiens]	273.2	83	16	1559	16	31088	2512	15	16	0	4.40.E+09	4.53.E+09	4.46.E+09	4.12.E+09	3.00.E+09	3.13.E+09	3.11.E+09	3.04.E+09
127	P31948	stress-induced-phosphoprotein 1 [OS=Homo sapiens]	272.7	51	27	1280	27	12990	1506	27	27	0	2.37.E+09	2.28.E+09	2.34.E+09	2.44.E+09	2.43.E+09	2.34.E+09	2.54.E+09	2.35.E+09
128	O95373	Importin-7 [OS=Homo sapiens]	272.1	35	25	1051	25	12585	1314	25	25	0	6.74.E+08	7.84.E+08	7.41.E+08	7.83.E+08	8.35.E+08	8.28.E+08	8.28.E+08	8.71.E+08
129	P51991-1	Heterogeneous nuclear ribonucleoprotein A3 [OS=Homo sapiens]	269.0	50	24	1404	6	13435	1755	23	24	16	1.65.E+09	1.78.E+09	1.62.E+09	1.65.E+09	1.81.E+09	1.91.E+09	1.80.E+09	1.88.E+09
130	P18206	Vinculin [OS=Homo sapiens]	269.0	38	27	923	27	14506	1307	27	27	0	8.41.E+08	9.11.E+08	8.53.E+08	8.73.E+08	1.17.E+09	1.08.E+09	1.06.E+09	1.09.E+09
131	P27348	14-3-3 protein theta [OS=Homo sapiens]	268.9	63	20	1846	14	31026	2331	19	20	6	1.68.E+09	1.70.E+09	1.57.E+09	1.73.E+09	1.59.E+09	1.61.E+09	1.58.E+09	1.57.E+09
132	P35241-1	radixin [OS=Homo sapiens]	267.9	49	29	2364	15	21579	2229	29	29	0	5.37.E+08	5.84.E+08	5.95.E+08	6.01.E+08	8.44.E+08	8.34.E+08	6.62.E+08	8.10.E+08
133	P61978-3	Isoform 3 of Heterogeneous nuclear ribonucleoprotein K [OS=Homo sapiens]	266.9	53	26	1305	1		3730	26		0	1.79.E+07	1.58.E+07	1.59.E+07	1.36.E+07	2.66.E+07	2.27.E+07	2.63.E+07	2.73.E+07
134	P23381	Tryptophan--tRNA ligase, cytoplasmic [OS=Homo sapiens]	266.5	69	23	1530	23	24830	2050	22	23	0	1.60.E+09	1.66.E+09	1.61.E+09	1.63.E+09	1.62.E+09	1.61.E+09	1.42.E+09	1.64.E+09
135	Q12906-1	Interleukin enhancer-binding factor 3 [OS=Homo sapiens]	265.5	46	25	1031	22	12503	1333	24	25	3	2.36.E+09	2.30.E+09	2.15.E+09	2.30.E+09	2.06.E+09	2.24.E+09	2.36.E+09	2.20.E+09
136	P12429	annexin A3 [OS=Homo sapiens]	264.1	74	25	1492	25	20782	2030	24	25	0	3.32.E+09	3.43.E+09	3.31.E+09	3.17.E+09	3.06.E+09	3.03.E+09	3.04.E+09	3.12.E+09
137	P63244	Receptor of activated protein C kinase 1 [OS=Homo sapiens]	263.3	79	18	1444	18	26751	2287	18	18	0	5.25.E+09	4.99.E+09	5.34.E+09	5.04.E+09	4.67.E+09	4.97.E+09	5.15.E+09	4.78.E+09
138	P27695	DNA-(apurinic or apyrimidinic site) lyase [OS=Homo sapiens]	262.6	72	18	1149	18	17875	1828	18	18	0	1.70.E+09	1.73.E+09	1.64.E+09	1.67.E+09	1.85.E+09	1.90.E+09	1.76.E+09	1.81.E+09
139	P37802	Transgelin-2 [OS=Homo sapiens]	259.8	91	20	3158	20	59662	5011	19	20	0	8.60.E+09	8.89.E+09	8.35.E+09	8.63.E+09	1.02.E+10	1.03.E+10	9.52.E+09	9.92.E+09
140	P40227-1	T-complex protein 1 subunit zeta [OS=Homo sapiens]	259.2	57	25	1630	25	22119	2119	25	25	0	3.02.E+09	2.98.E+09	3.00.E+09	2.87.E+09	2.79.E+09	2.96.E+09	3.09.E+09	2.93.E+09
141	P08865	40S ribosomal protein SA [OS=Homo sapiens]	258.0	64	18	1365	18	28296	2454	16	18	0	4.53.E+09	4.61.E+09	4.57.E+09	4.73.E+09	4.65.E+09	4.62.E+09	4.00.E+09	4.32.E+09
142	Q9Y4L1	Hypoxia up-regulated protein 1 [OS=Homo sapiens]	257.3	36	26	896	26	11678	1173	26	26	0	1.07.E+09	1.07.E+09	9.91.E+08	1.11.E+09	1.41.E+09	1.34.E+09	1.37.E+09	1.39.E+09
143	P22102-1	trifunctional purine biosynthetic protein adenosine-3 [OS=Homo sapiens]	256.8	42	30	1040	30	15363	1583	30	29	0	1.49.E+09	1.59.E+09	1.55.E+09	1.63.E+09	1.70.E+09	1.72.E+09	1.72.E+09	1.73.E+09
144	Q06210-1	glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 [OS=Homo sapiens]	256.6	48	27	767	27	7844	910	27	26	0	7.91.E+08	8.43.E+08	7.91.E+08	8.91.E+08	7.10.E+08	8.32.E+08	7.09.E+08	6.60.E+08
145	P63104-1	14-3-3 protein zeta/delta [OS=Homo sapiens]	255.8	63	19	2394	14	41022	3199	19	19	1	3.90.E+09	4.07.E+09	3.89.E+09	4.17.E+09	3.99.E+09	4.03.E+09	3.93.E+09	4.08.E+09
146	P50990	T-complex protein 1 subunit theta [OS=Homo sapiens]	254.3	51	24	1301	24	18745	1854	24	24	0	2.78.E+09	2.77.E+09	2.80.E+09	2.60.E+09	2.88.E+09	2.88.E+09	2.93.E+09	2.87.E+09
147	P35221	Catenin alpha-1 [OS=Homo sapiens]	253.6	43	24	760	24	14544	1049	23	24	0	1.02.E+09	1.05.E+09	1.08.E+09	1.09.E+09	1.45.E+09	1.43.E+09	1.44.E+09	1.49.E+09
148	P14866	Heterogeneous nuclear ribonucleoprotein L [OS=Homo sapiens]	252.6	64	18	814	18	11085	1323	18	18	0	1.14.E+09	1.21.E+09	1.13.E+09	1.24.E+09	1.19.E+09	1.22.E+09	1.11.E+09	1.21.E+09
149	P13489	Ribonuclease inhibitor [OS=Homo sapiens]	252.5	67	19	1071	19	22133	1779	19	19	0	9.96.E+08	1.03.E+09	9.76.E+08	9.77.E+08	9.70.E+08	9.63.E+08	9.00.E+08	9.67.E+08
150	O15067	Phosphoribosylformylglycinamidine synthase [OS=Homo sapiens]	251.3	33	25	733	25	8561	1108	24	25	0	8.70.E+08	8.85.E+08	8.76.E+08	8.72.E+08	6.61.E+08	7.05.E+08	6.41.E+08	6.66.E+08
151	O43175	D-3-phosphoglycerate dehydrogenase [OS=Homo sapiens]	250.7	52	19	1464	19	21834	1916	19	19	0	2.67.E+09	2.72.E+09	2.60.E+09	2.67.E+09	2.89.E+09	2.82.E+09	2.76.E+09	2.85.E+09
152	Q15084-1	Protein disulfide-isomerase A6 [OS=Homo sapiens]	249.7	51	17	1548	17	23987	2458	17	17	0	2.46.E+09	2.75.E+09	2.51.E+09	2.52.E+09	3.50.E+09	3.51.E+09	3.12.E+09	3.46.E+09
153	Q9UJZ1	Stomatin-like protein 2, mitochondrial [OS=Homo sapiens]	248.5	61	15	1484	15	40783	2593	15	15	0	1.80.E+09	1.88.E+09	1.73.E+09	1.94.E+09	1.80.E+09	1.79.E+09	1.67.E+09	1.73.E+09
154	P68032	Actin, alpha cardiac muscle 1 [OS=Homo sapiens]	248.1	47	18	5344	3	57518	5864	17	18	0	5.53.E+09	5.61.E+09	5.34.E+09	4.95.E+09	4.77.E+09	4.82.E+09	4.84.E+09	4.52.E+09
155	Q7KZF4	staphylococcal nuclease domain-containing protein 1 [OS=Homo sapiens]	247.7	42	23	770	23	8531	1069	23	22	0	7.21.E+08	7.34.E+08	7.28.E+08	8.04.E+08	7.83.E+08	8.03.E+08	8.01.E+08	7.63.E+08
156	Q7Z406-6	Isoform 6 of Myosin-14 [OS=Homo sapiens]	247.0	26	37	406	30		1172	37		1	8.47.E+08	8.21.E+08	7.91.E+08	7.66.E+08	3.90.E+08	3.92.E+08	4.05.E+08	4.07.E+08
157	Q9BSJ8	Extended synaptotagmin-1 [OS=Homo sapiens]	245.4	35	23	666	23	10891	916	23	23	0	5.39.E+08	5.50.E+08	4.95.E+08	5.12.E+08	8.24.E+08	8.11.E+08	7.98.E+08	8.03.E+08
158	P30041	Peroxiredoxin-6 [OS=Homo sapiens]	243.8	85	19	2004	19	31322	2488	18	19	0	3.90.E+09	3.90.E+09	3.82.E+09	3.74.E+09	4.68.E+09	4.79.E+09	4.45.E+09	4.86.E+09
159	P12268	inosine-5'-monophosphate dehydrogenase 2 [OS=Homo sapiens]	243.5	49	19	649	19	8556	1038	19	19	0	1.65.E+09	1.66.E+09	1.65.E+09	1.61.E+09	1.62.E+09	1.61.E+09	1.62.E+09	1.60.E+09
160	Q6DD88	Atlastin-3 [OS=Homo sapiens]	242.4	54	18	1214	17	16943	1733	18	18	1	1.04.E+09	1.15.E+09	1.12.E+09	1.16.E+09	1.26.E+09	1.27.E+09	1.15.E+09	1.23.E+09
161	P53621-1	coatomer subunit alpha [OS=Homo sapiens]	241.1	31	31	729	31	5692	875	31	29	0	1.03.E+09	1.01.E+09	9.79.E+08	1.05.E+09	1.27.E+09	1.28.E+09	1.21.E+09	1.22.E+09
162	P17987	T-complex protein 1 subunit alpha [OS=Homo sapiens]	241.0	62	24	1242	24	14692	1574	24	24	0	2.03.E+09	2.03.E+09	2.07.E+09	2.01.E+09	1.90.E+09	1.94.E+09	2.07.E+09	2.01.E+09
163	Q9BUF5	Tubulin beta-6 chain [OS=Homo sapiens]	240.0	54	17	3113	7	47789	4406	17	17	0	1.03.E+08	1.03.E+08	6.18.E+07	1.19.E+08	1.50.E+08	1.66.E+08	1.28.E+08	1.64.E+08
164	P05455	Lupus La protein [OS=Homo sapiens]	240.0	60	22	1099	22	15615	1427	22	20	0	1.65.E+09	1.66.E+09	1.58.E+09	1.71.E+09	1.83.E+09	1.86.E+09	1.67.E+09	1.86.E+09
165	Q9Y617-1	phosphoserine aminotransferase [OS=Homo sapiens]	239.2	74	23	1843	23	25566	2618	23	23	0	4.62.E+09	4.47.E+09	4.54.E+09	4.36.E+09	4.26.E+09	3.97.E+09	4.11.E+09	4.16.E+09
166	P05387	60S acidic ribosomal protein P2 [OS=Homo sapiens]	238.8	76	9	1089	9	23170	2238	9	9	0	3.38.E+09	3.56.E+09	3.22.E+09	3.24.E+09	3.52.E+09	3.86.E+09	3.52.E+09	3.80.E+09

No.	Accession	Description	Sum PEP Score	Coverage [%]	# Peptides	# PSMs	# Unique Peptides	Score Mascot: A5 Mascot	Score Sequest HT: A2 Sequest HT	# Peptides (by Search Engine): A2 Sequest HT	# Peptides (by Search Engine): A5 Mascot	# Razor Peptides	ctrl Abundances_1	ctrl Abundances_2	ctrl Abundances_3	ctrl Abundances_4	JAM-A KO Abundances_1	JAM-A KO Abundances_2	JAM-A KO Abundances_3	JAM-A KO Abundances_4
167	P58107	Epiplakin OS=Homo sapiens OX=9606 GN=EPPK1 PE=1 SV=3	236.7	26	17	368	10	13575			17	0	2.88.E+08	2.97.E+08	2.71.E+08	3.04.E+08	2.11.E+08	1.46.E+08	1.35.E+08	1.53.E+08
168	P62701	40S ribosomal protein S4, X isoform [OS=Homo sapiens]	236.1	67	22	1987	22	15246	2472	22	21	0	4.78.E+09	4.58.E+09	4.91.E+09	4.77.E+09	4.24.E+09	4.26.E+09	4.74.E+09	4.44.E+09
169	P00390	Glutathione reductase, mitochondrial [OS=Homo sapiens]	235.7	64	19	769	19	12588	1252	19	19	0	1.29.E+09	1.31.E+09	1.33.E+09	1.33.E+09	1.83.E+09	1.89.E+09	1.99.E+09	1.95.E+09
170	P49591	Serine--tRNA ligase, cytoplasmic [OS=Homo sapiens]	235.3	54	21	1444	21	16539	1859	20	21	0	2.06.E+09	2.06.E+09	1.99.E+09	1.97.E+09	2.15.E+09	2.16.E+09	2.08.E+09	2.21.E+09
171	P04844-1	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 [OS=Homo sapiens]	235.0	46	15	988	15	21179	1854	15	15	0	8.30.E+08	8.60.E+08	7.94.E+08	8.54.E+08	1.12.E+09	1.00.E+09	9.26.E+08	9.92.E+08
172	P55786	puromycin-sensitive aminopeptidase [OS=Homo sapiens]	234.9	36	23	771	23	6775	984	23	23	0	9.38.E+08	9.95.E+08	9.87.E+08	9.99.E+08	1.91.E+09	2.02.E+09	1.64.E+09	1.84.E+09
173	P55209	Nucleosome assembly protein 1-like 1 [OS=Homo sapiens]	233.2	57	17	1004	15	15567	1592	15	17	2	1.85.E+09	1.94.E+09	1.74.E+09	1.96.E+09	2.41.E+09	2.42.E+09	2.11.E+09	2.35.E+09
174	Q13263	Transcription intermediary factor 1-beta [OS=Homo sapiens]	232.5	47	20	716	20	13723	1063	19	20	0	1.12.E+09	1.19.E+09	1.08.E+09	1.09.E+09	7.46.E+08	6.30.E+08	5.72.E+08	6.70.E+08
175	P07099	epoxide hydrolase 1 [OS=Homo sapiens]	232.2	50	22	1171	22	14057	1786	22	20	0	2.55.E+09	2.54.E+09	2.52.E+09	2.48.E+09	2.78.E+09	2.71.E+09	2.78.E+09	2.75.E+09
176	P07737	profilin-1 [OS=Homo sapiens]	229.5	91	14	1930	14	37067	2328	12	14	0	9.36.E+09	9.39.E+09	8.47.E+09	9.02.E+09	6.47.E+09	6.63.E+09	5.73.E+09	6.49.E+09
177	P26639-1	Threonine--tRNA ligase, cytoplasmic [OS=Homo sapiens]	229.4	46	29	1258	29	12605	1612	29	29	0	2.01.E+09	2.05.E+09	2.01.E+09	2.02.E+09	1.98.E+09	2.12.E+09	1.89.E+09	2.06.E+09
178	P11166	Solute carrier family 2, facilitated glucose transporter member 1 [OS=Homo sapiens]	228.3	37	18	1444	17	17317	1975	18	17	1	1.14.E+10	1.07.E+10	1.07.E+10	9.72.E+09	9.20.E+09	9.29.E+09	1.01.E+10	9.36.E+09
179	O00159-1	Unconventional myosin-Ic [OS=Homo sapiens]	227.5	34	26	758	25	9107	1004	26	26	1	1.03.E+09	1.11.E+09	1.03.E+09	1.12.E+09	6.70.E+08	7.69.E+08	6.17.E+08	7.60.E+08
180	Q92616	eIF-2-alpha kinase activator GCN1 [OS=Homo sapiens]	227.4	18	33	811	33	8895	806	33	32	0	5.83.E+08	6.25.E+08	5.90.E+08	5.76.E+08	5.72.E+08	6.29.E+08	5.21.E+08	6.45.E+08
181	P62805	histone H4 [OS=Homo sapiens]	227.2	58	13	3192	13	48786	4460	13	12	0	5.50.E+10	5.28.E+10	5.63.E+10	5.25.E+10	4.80.E+10	4.84.E+10	5.22.E+10	4.96.E+10
182	Q16555-1	Dihydropyrimidinase-related protein 2 [OS=Homo sapiens]	226.2	53	19	642	19	8989	947	19	19	0	4.71.E+08	4.73.E+08	4.48.E+08	4.24.E+08	9.53.E+08	9.41.E+08	9.35.E+08	9.44.E+08
183	O75533-1	splicing factor 3B subunit 1 [OS=Homo sapiens]	223.7	24	21	782	21	8741	887	21	21	0	5.95.E+08	5.98.E+08	6.08.E+08	5.38.E+08	5.82.E+08	5.94.E+08	5.60.E+08	6.34.E+08
184	P30043	flavin reductase (NADPH) [OS=Homo sapiens]	223.4	87	14	1011	14	15357	1849	14	14	0	1.55.E+09	1.67.E+09	1.40.E+09	1.58.E+09	1.76.E+09	1.79.E+09	1.53.E+09	1.76.E+09
185	P36871-1	Phosphoglucomutase-1 [OS=Homo sapiens]	223.4	53	19	975	19	14991	1238	19	18	0	1.12.E+09	1.14.E+09	1.09.E+09	1.13.E+09	9.88.E+08	9.83.E+08	8.80.E+08	9.53.E+08
186	Q14152	Eukaryotic translation initiation factor 3 subunit A [OS=Homo sapiens]	223.3	35	37	947	37	6186	920	36	35	0	9.64.E+08	9.58.E+08	9.31.E+08	9.46.E+08	9.18.E+08	9.40.E+08	9.54.E+08	9.39.E+08
187	O60716-1	Catenin delta-1 [OS=Homo sapiens]	221.5	29	19	684	19	9287	876	19	18	0	7.29.E+08	7.24.E+08	7.24.E+08	7.84.E+08	7.88.E+08	7.55.E+08	7.42.E+08	7.62.E+08
188	P09429	High mobility group protein B1 [OS=Homo sapiens]	221.3	49	15	1430	13	12675	1702	15	15	2	3.89.E+09	3.80.E+09	3.91.E+09	4.03.E+09	3.90.E+09	3.94.E+09	4.28.E+09	3.82.E+09
189	P08243-1	Asparagine synthetase [glutamine-hydrolyzing] [OS=Homo sapiens]	221.3	51	23	1212	23	15907	1306	23	23	0	1.93.E+09	1.87.E+09	1.90.E+09	2.01.E+09	2.08.E+09	2.02.E+09	2.14.E+09	2.07.E+09
190	P49411	elongation factor Tu, mitochondrial [OS=Homo sapiens]	220.3	55	20	1058	20	11557	1486	20	18	0	1.41.E+09	1.41.E+09	1.37.E+09	1.38.E+09	1.34.E+09	1.33.E+09	1.36.E+09	1.32.E+09
191	Q3ZCM7	tubulin beta-8 chain [OS=Homo sapiens]	219.5	29	12	3112	1	43563	4361	11	12	0	4.59.E+07	3.80.E+07	2.96.E+07	3.66.E+07	6.85.E+07	5.15.E+07	6.08.E+07	4.87.E+07
192	Q6P2Q9	Pre-mRNA-processing-splicing factor 8 [OS=Homo sapiens]	219.3	19	32	778	32	8439	672	32	32	0	6.93.E+08	6.75.E+08	6.88.E+08	6.72.E+08	6.54.E+08	6.49.E+08	6.28.E+08	6.50.E+08
193	P62424	60S ribosomal protein L7a [OS=Homo sapiens]	218.2	62	19	1164	19	12978	1704	19	18	0	3.18.E+09	2.91.E+09	3.19.E+09	3.30.E+09	2.52.E+09	2.48.E+09	2.79.E+09	2.60.E+09
194	O43776	Asparagine--tRNA ligase, cytoplasmic [OS=Homo sapiens]	217.5	47	22	684	22	7619	847	21	19	0	1.33.E+09	1.15.E+09	1.18.E+09	1.13.E+09	1.49.E+09	1.50.E+09	1.47.E+09	1.53.E+09
195	P67809	Nuclease-sensitive element-binding protein 1 [OS=Homo sapiens]	217.4	64	12	962	7	13565	1290	11	12	5	1.36.E+09	1.37.E+09	1.39.E+09	1.59.E+09	1.51.E+09	1.48.E+09	1.56.E+09	1.57.E+09
196	P52597	Heterogeneous nuclear ribonucleoprotein F [OS=Homo sapiens]	217.1	58	15	1179	13	18349	1689	15	15	2	2.20.E+09	2.19.E+09	2.16.E+09	2.43.E+09	2.12.E+09	2.10.E+09	2.13.E+09	2.09.E+09
197	Q12905	Interleukin enhancer-binding factor 2 [OS=Homo sapiens]	216.9	73	19	932	19	12930	1338	19	19	0	1.93.E+09	1.87.E+09	1.95.E+09	1.74.E+09	1.95.E+09	1.97.E+09	1.75.E+09	1.95.E+09
198	P61981	14-3-3 protein gamma [OS=Homo sapiens]	216.3	71	18	1808	12	26655	2347	17	17	0	1.51.E+09	1.44.E+09	1.39.E+09	1.56.E+09	1.40.E+09	1.39.E+09	1.42.E+09	1.42.E+09
199	Q14566	DNA replication licensing factor MCM6 [OS=Homo sapiens]	216.0	42	26	716	26	6703	850	26	26	0	1.21.E+09	1.36.E+09	1.36.E+09	1.22.E+09	1.51.E+09	1.57.E+09	1.49.E+09	1.41.E+09
200	P49368-1	T-complex protein 1 subunit gamma [OS=Homo sapiens]	214.5	56	22	1304	22	15927	1881	22	21	0	2.92.E+09	2.91.E+09	2.92.E+09	2.90.E+09	2.75.E+09	2.87.E+09	2.91.E+09	2.88.E+09
201	P46821	microtubule-associated protein 1B [OS=Homo sapiens]	213.3	17	25	321	25	4909	427	25	25	0	1.55.E+08	1.37.E+08	1.80.E+08	1.62.E+08	3.24.E+08	3.21.E+08	2.94.E+08	3.45.E+08
202	P14923	Junction plakoglobin [OS=Homo sapiens]	213.0	41	19	699	15	13279	1002	19	19	0	4.85.E+08	5.30.E+08	4.89.E+08	4.85.E+08	5.04.E+08	5.11.E+08	5.18.E+08	5.40.E+08
203	P34932	Heat shock 70 kDa protein 4 [OS=Homo sapiens]	212.8	37	22	780	21	12676	1052	22	22	1	9.17.E+08	9.17.E+08	8.80.E+08	8.47.E+08	1.00.E+09	9.80.E+08	9.39.E+08	9.75.E+08
204	P35222	Catenin beta-1 [OS=Homo sapiens]	212.6	35	19	757	15	11055	965	19	19	3	8.63.E+08	8.58.E+08	8.48.E+08	8.28.E+08	1.09.E+09	1.05.E+09	1.10.E+09	1.09.E+09
205	Q9Y678	Coatomer subunit gamma-1 [OS=Homo sapiens]	212.4	46	25	1131	24	13782	1212	25	25	1	6.69.E+08	7.61.E+08	6.72.E+08	7.22.E+08	9.41.E+08	8.71.E+08	8.33.E+08	8.95.E+08
206	P33991	DNA replication licensing factor MCM4 [OS=Homo sapiens]	212.0	35	22	883	22	9552	1072	22	22	0	7.28.E+08	6.95.E+08	7.40.E+08	7.81.E+08	8.56.E+08	8.79.E+08	8.13.E+08	8.66.E+08
207	O75083	WD repeat-containing protein 1 [OS=Homo sapiens]	210.2	59	20	706	20	7354	1040	20	20	0	1.01.E+09	1.10.E+09	1.10.E+09	1.16.E+09	1.73.E+09	1.79.E+09	1.66.E+09	1.69.E+09
208	P19367-1	Hexokinase-1 [OS=Homo sapiens]	209.4	33	25	620	25	8847	770	25	25	0	6.76.E+08	6.55.E+08	6.53.E+08	6.79.E+08	6.62.E+08	6.37.E+08	6.17.E+08	6.34.E+08
209	P43243	Matrin-3 [OS=Homo sapiens]	208.9	33	20	1157	20	15624	1689	20	20	0	1.30.E+09	1.35.E+09	1.29.E+09	1.31.E+09	1.46.E+09	1.45.E+09	1.39.E+09	1.46.E+09
210	P48506	glutamate--cysteine ligase catalytic subunit [OS=Homo sapiens]	208.7	45	23	648	23	8034	917	21	23	0	7.92.E+08	8.02.E+08	8.02.E+08	7.48.E+08	7.75.E+08	8.23.E+08	7.86.E+08	7.82.E+08
211	Q13501-1	sequestosome-1 [OS=Homo sapiens]	208.0	54	15	697	15	11205	981	15	15	0	8.22.E+08	8.35.E+08	8.29.E+08	8.13.E+08	9.75.E+08	9.30.E+08	8.00.E+08	1.06.E+09
212	Q9NR30-1	Nucleolar RNA helicase 2 [OS=Homo sapiens]	208.0	37	23	752	21	11245	1136	23	22	2	1.02.E+09	1.06.E+09	1.06.E+09	1.14.E+09	1.14.E+09	1.13.E+09	1.03.E+09	1.11.E+09
213	P02786	Transferrin receptor protein 1 [OS=Homo sapiens]	207.6	35	21	1308	21	14115	1905	21	21	0	1.94.E+09	2.02.E+09	1.88.E+09	1.96.E+09	2.64.E+09	2.63.E+09	2.46.E+09	2.54.E+09
214	P40926	Malate dehydrogenase, mitochondrial [OS=Homo sapiens]	205.9	61	17	1808	17	33654	2720	16	17	0	6.54.E+09	6.74.E+09	6.59.E+09	6.57.E+09	5.84.E+09	5.92.E+09	5.36.E+09	5.95.E+09
215	P05388	60S acidic ribosomal protein P0 [OS=Homo sapiens]	205.6	55	16	1287	16	22885	2146	16	15	0	4.09.E+09	4.16.E+09	3.81.E+09	4.23.E+09	4.08.E+09	4.20.E+09	3.95.E+09	4.05.E+09
216	P27824	Calnexin [OS=Homo sapiens]	205.4	47	19	1252	19	17855	1827	18	18	0	2.04.E+09	2.13.E+09	2.08.E+09	1.96.E+09	2.52.E+09	2.38.E+09	2.43.E+09	2.50.E+09
217	P09493-3	Isoform 3 of Tropomyosin alpha-1 chain [OS=Homo sapiens]	205.3	66	22	603	11		1669	22		4	5.56.E+08	5.29.E+08	5.82.E+08	5.49.E+08	1.11.E+09	1.12.E+09	1.14.E+09	1.11.E+09
218	Q9BQG0	Myb-binding protein 1A [OS=Homo sapiens]	205.2	33	28	756	28	8387	848	28	27	0	5.81.E+08	6.02.E+08	5.67.E+08	6.03.E+08	3.72.E+08	3.45.E+08	2.97.E+08	3.52.E+08
219	P48735	Isocitrate dehydrogenase [NADP], mitochondrial [OS=Homo sapiens]	204.9	54	23	1279	22	12852	1402	23	23	1	1.84.E+09	1.86.E+09	1.87.E+09	1.77.E+09	3.42.E+09	3.55.E+09	3.41.E+09	3.53.E+09
220	P25205	DNA replication licensing factor mcm3 [OS=Homo sapiens]	203.2	33	20	741	20	12197	841	19	20	0	8.42.E+08	9.02.E+08	8.04.E+08	8.57.E+08	1.02.E+09	1.07.E+09	9.43.E+08	1.01.E+09
221	P39023	60S ribosomal protein L3 [OS=Homo sapiens]	202.7	45	21	1073	21	10650	1358	19	20	0	2.15.E+09	2.64.E+09	2.61.E+09	2.84.E+09	2.17.E+09	2.17.E+09	2.40.E+09	2.08.E+09
222	O14980	Exportin-1 [OS=Homo sapiens]	202.5	30	23	770	23	10070	896	22	23	0	4.71.E+08	5.01.E+08	5.04.E+08	5.17.E+08	6.77.E+08	6.87.E+08	6.34.E+08	6.95.E+08
223	P46782	40S ribosomal protein S5 [OS=Homo sapiens]	201.1	68	14	937	14	20242	1423	13	14	0	1.74.E+09	2.11.E+09	1.66.E+09	1.94.E+09	1.92.E+09	1.91.E+09	1.76.E+09	1.77.E+09
224	P04843	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 [OS=Homo sapiens]	201.0	43	17	927	17	11251	1401	17	17	0	1.32.E+09	1.36.E+09	1.35.E+09	1.34.E+09	1.53.E+09	1.56.E+09	1.37.E+09	1.51.E+09
225	Q15365	Poly(RC)-binding protein 1 [OS=Homo sapiens]	200.2	80	15	1147	12	22245	1845	15	15	3	2.50.E+09	2.57.E+09	2.45.E+09	2.57.E+09	2.50.E+09	2.46.E+09	2.41.E+09	2.49.E+09

No.	Accession	Description	Sum PEP Score	Coverage [%]	# Peptides	# PSMs	# Unique Peptides	Score Mascot: A5 Mascot	Score Sequest HT: A2 Sequest HT	# Peptides (by Search Engine): A2 Sequest HT	# Peptides (by Search Engine): A5 Mascot	# Razor Peptides	ctrl Abundances_1	ctrl Abundances_2	ctrl Abundances_3	ctrl Abundances_4	JAM-A KO Abundances_1	JAM-A KO Abundances_2	JAM-A KO Abundances_3	JAM-A KO Abundances_4
226	P20700	Lamin-B1 [OS=Homo sapiens]	199.2	37	19	628	18	7815	709	19	19	0	8.88.E+08	8.97.E+08	8.97.E+08	9.26.E+08	8.55.E+08	8.55.E+08	8.91.E+08	8.89.E+08
227	P31040	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial [OS=Homo sapiens]	199.2	48	20	783	20	14250	1150	20	20	0	1.26.E+09	1.22.E+09	1.21.E+09	1.29.E+09	1.41.E+09	1.34.E+09	1.38.E+09	1.31.E+09
228	P23284	peptidyl-prolyl cis-trans isomerase B [OS=Homo sapiens]	198.2	62	17	1812	17	16778	1866	17	16	0	8.16.E+09	7.84.E+09	8.18.E+09	7.52.E+09	8.22.E+09	8.27.E+09	8.89.E+09	8.40.E+09
229	P51991-2	Isoform 2 of Heterogeneous nuclear ribonucleoprotein A3 [OS=Homo sapiens]	195.4	47	19	610	1		1600	19		0	2.62.E+07	2.79.E+07	2.73.E+07	3.11.E+07	3.36.E+07	3.03.E+07	3.48.E+07	3.51.E+07
230	Q00341-1	Vigilin [OS=Homo sapiens]	195.2	30	24	498	24	6566	599	23	24	0	7.42.E+08	7.69.E+08	7.47.E+08	7.48.E+08	9.03.E+08	9.24.E+08	9.19.E+08	9.47.E+08
231	Q13838-1	spliceosome RNA helicase DDX39B [OS=Homo sapiens]	194.7	66	18	1201	9	15236	1574	17	18	9	2.20.E+09	2.29.E+09	2.30.E+09	2.16.E+09	2.22.E+09	2.32.E+09	2.26.E+09	2.29.E+09
232	P17655-1	Calpain-2 catalytic subunit [OS=Homo sapiens]	194.6	42	20	520	20	7092	718	20	20	0	5.60.E+08	6.41.E+08	5.28.E+08	6.75.E+08	7.17.E+08	6.16.E+08	6.67.E+08	6.69.E+08
233	P56192	Methionine--tRNA ligase, cytoplasmic [OS=Homo sapiens]	194.5	44	25	489	25	5497	684	25	25	0	6.89.E+08	6.57.E+08	6.59.E+08	6.77.E+08	7.18.E+08	8.00.E+08	6.58.E+08	6.84.E+08
234	P84077	ADP-ribosylation factor 1 [OS=Homo sapiens]	193.7	90	17	1029	11	10713	1422	15	17	6	2.34.E+09	2.38.E+09	2.36.E+09	2.31.E+09	2.29.E+09	2.35.E+09	2.30.E+09	2.37.E+09
235	P51858	hepatoma-derived growth factor [OS=Homo sapiens]	192.7	64	15	891	15	10849	1453	15	14	0	1.32.E+09	1.31.E+09	1.30.E+09	1.31.E+09	1.29.E+09	1.29.E+09	1.26.E+09	1.24.E+09
236	P52272	Heterogeneous nuclear ribonucleoprotein M [OS=Homo sapiens]	192.2	36	24	796	24	13034	1088	23	24	0	1.30.E+09	1.20.E+09	1.14.E+09	1.29.E+09	1.47.E+09	1.63.E+09	1.53.E+09	1.65.E+09
237	P21964-1	Catechol O-methyltransferase [OS=Homo sapiens]	191.7	67	13	816	13	14402	1545	13	13	0	1.28.E+09	1.31.E+09	1.25.E+09	1.29.E+09	1.11.E+09	1.07.E+09	1.08.E+09	1.08.E+09
238	Q99714-1	3-hydroxyacyl-CoA dehydrogenase type-2 [OS=Homo sapiens]	191.7	85	13	801	13	13356	1157	13	13	0	6.39.E+08	7.85.E+08	6.75.E+08	7.43.E+08	6.82.E+08	7.60.E+08	7.03.E+08	7.78.E+08
239	P09104	Gamma-enolase [OS=Homo sapiens]	191.1	49	12	3291	8	74649	5361	12	12	0	1.40.E+09	1.28.E+09	1.36.E+09	1.53.E+09	1.62.E+09	1.62.E+09	1.80.E+09	1.71.E+09
240	P62826	GTP-binding nuclear protein RAN [OS=Homo sapiens]	189.2	53	15	1271	15	16147	1855	14	15	0	4.52.E+09	4.50.E+09	4.71.E+09	4.25.E+09	4.63.E+09	4.74.E+09	4.61.E+09	4.54.E+09
241	P33993-1	DNA replication licensing factor MCM7 [OS=Homo sapiens]	187.4	46	24	762	24	5501	771	23	24	0	1.13.E+09	1.13.E+09	1.12.E+09	1.08.E+09	1.32.E+09	1.30.E+09	1.27.E+09	1.33.E+09
242	P62136-1	serine/threonine-protein phosphatase PP1-alpha catalytic subunit [OS=Homo sapiens]	187.4	65	17	890	6	14988	1141	16	16	10	9.94.E+08	1.06.E+09	9.96.E+08	1.01.E+09	1.06.E+09	1.03.E+09	1.02.E+09	1.02.E+09
243	O00571	ATP-dependent RNA helicase DDX3X [OS=Homo sapiens]	187.2	41	19	1105	19	17163	1767	18	19	0	1.60.E+09	1.71.E+09	1.60.E+09	1.67.E+09	1.71.E+09	1.90.E+09	1.54.E+09	1.80.E+09
244	P16403	Histone H1.2 [OS=Homo sapiens]	186.9	31	13	1070	3	17650	1129	9	13	0	5.26.E+08	5.01.E+08	5.67.E+08	6.29.E+08	6.78.E+08	6.52.E+08	6.95.E+08	7.10.E+08
245	P09960-1	leukotriene A-4 hydrolase [OS=Homo sapiens]	186.1	49	20	544	20	6146	643	19	20	0	8.79.E+08	8.85.E+08	8.15.E+08	8.89.E+08	8.15.E+08	8.44.E+08	8.91.E+08	8.68.E+08
246	P52565-1	rho GDP-dissociation inhibitor 1 [OS=Homo sapiens]	186.0	75	9	1013	9	16602	1665	8	9	0	2.54.E+09	2.55.E+09	2.46.E+09	2.28.E+09	1.73.E+09	1.76.E+09	1.75.E+09	1.75.E+09
247	P52292	Importin subunit alpha-1 [OS=Homo sapiens]	184.7	50	14	948	14	16919	1421	14	14	0	9.99.E+08	1.12.E+09	1.07.E+09	1.06.E+09	9.21.E+08	9.41.E+08	7.42.E+08	9.15.E+08
248	Q8IVF2-1	Protein AHNAK2 [OS=Homo sapiens]	184.6	17	25	455	25	4310	453	25	24	0	7.65.E+08	8.09.E+08	8.39.E+08	9.17.E+08	2.40.E+08	3.32.E+08	3.75.E+08	2.78.E+08
249	Q15181	Inorganic pyrophosphatase [OS=Homo sapiens]	183.3	63	12	793	11	13330	1200	12	12	1	1.60.E+09	1.67.E+09	1.58.E+09	1.50.E+09	1.85.E+09	1.88.E+09	1.63.E+09	1.86.E+09
250	P23246-1	splicing factor, proline- and glutamine-rich [OS=Homo sapiens]	182.7	38	19	1047	18	13103	1399	19	19	1	4.40.E+09	4.07.E+09	4.62.E+09	5.21.E+09	4.62.E+09	4.64.E+09	5.58.E+09	4.97.E+09
251	Q8WUM4	Programmed cell death 6-interacting protein [OS=Homo sapiens]	182.5	41	23	672	23	7123	761	21	23	0	7.35.E+08	7.28.E+08	7.47.E+08	6.87.E+08	8.11.E+08	8.06.E+08	7.82.E+08	8.70.E+08
252	P54577	Tyrosine--tRNA ligase, cytoplasmic [OS=Homo sapiens]	182.4	57	23	876	23	10275	1167	23	22	0	1.03.E+09	1.12.E+09	1.07.E+09	1.26.E+09	1.18.E+09	1.10.E+09	1.39.E+09	1.11.E+09
253	P10412	Histone H1.4 [OS=Homo sapiens]	182.3	31	13	1022	3	16918	1129	9	13	12	6.70.E+09	6.14.E+09	6.60.E+09	7.11.E+09	7.50.E+09	6.90.E+09	7.85.E+09	7.16.E+09
254	P16435	NADPH--cytochrome P450 reductase [OS=Homo sapiens]	182.2	39	20	571	20	8743	722	20	20	0	7.01.E+08	7.57.E+08	7.92.E+08	7.33.E+08	8.56.E+08	7.49.E+08	7.28.E+08	7.86.E+08
255	P17844	probable ATP-dependent RNA helicase DDX5 [OS=Homo sapiens]	181.7	48	20	1129	15	13445	1489	20	20	0	1.59.E+09	1.64.E+09	1.61.E+09	1.59.E+09	1.09.E+09	1.15.E+09	1.13.E+09	1.15.E+09
256	O60506	Heterogeneous nuclear ribonucleoprotein Q [OS=Homo sapiens]	181.4	46	20	992	14	13326	1194	20	20	0	8.19.E+08	9.04.E+08	8.34.E+08	8.67.E+08	9.44.E+08	9.03.E+08	8.72.E+08	9.61.E+08
257	P47897	glutamine--tRNA ligase [OS=Homo sapiens]	181.1	40	22	513	22	6378	734	20	21	0	9.09.E+08	9.34.E+08	8.87.E+08	8.41.E+08	9.57.E+08	9.62.E+08	9.78.E+08	9.64.E+08
258	P41091	eukaryotic translation initiation factor 2 subunit 3 [OS=Homo sapiens]	180.5	48	16	889	16	9206	1263	15	16	0	1.39.E+09	1.31.E+09	1.35.E+09	1.43.E+09	1.46.E+09	1.42.E+09	1.44.E+09	1.43.E+09
259	Q02878	60S ribosomal protein L6 [OS=Homo sapiens]	179.3	52	22	1363	22	24824	1778	22	22	0	3.02.E+09	3.02.E+09	3.06.E+09	3.19.E+09	2.18.E+09	2.12.E+09	2.25.E+09	2.14.E+09
260	O00567	Nucleolar protein 56 [OS=Homo sapiens]	178.9	52	21	514	21	5467	542	21	21	0	7.39.E+08	7.66.E+08	7.56.E+08	7.91.E+08	6.57.E+08	6.18.E+08	6.43.E+08	6.43.E+08
261	O75874	Isocitrate dehydrogenase [NADP] cytoplasmic [OS=Homo sapiens]	178.6	50	19	831	18	6225	821	19	19	0	1.36.E+09	1.39.E+09	1.39.E+09	1.39.E+09	1.34.E+09	1.39.E+09	1.42.E+09	1.56.E+09
262	Q99623	Prohibitin-2 [OS=Homo sapiens]	178.1	58	14	993	14	15277	1378	14	14	0	1.82.E+09	1.89.E+09	1.87.E+09	1.85.E+09	1.66.E+09	1.66.E+09	1.76.E+09	1.67.E+09
263	P35606	Coatomer subunit beta' [OS=Homo sapiens]	177.8	40	22	709	22	6020	717	22	21	0	6.45.E+08	6.22.E+08	6.26.E+08	5.80.E+08	7.50.E+08	7.27.E+08	7.31.E+08	7.31.E+08
264	P32322	Pyrroline-5-carboxylate reductase 1, mitochondrial [OS=Homo sapiens]	176.6	63	14	519	13	9615	578	12	14	1	8.24.E+08	8.55.E+08	8.53.E+08	8.81.E+08	7.85.E+08	7.83.E+08	7.84.E+08	7.95.E+08
265	P50454	Serpin H1 [OS=Homo sapiens]	176.4	51	15	730	15	13866	1192	15	15	0	7.30.E+08	8.07.E+08	7.78.E+08	7.97.E+08	8.69.E+08	7.63.E+08	7.43.E+08	7.55.E+08
266	P49736	DNA replication licensing factor mcm2 [OS=Homo sapiens]	176.2	27	18	811	18	12418	1138	18	18	0	9.36.E+08	9.50.E+08	9.23.E+08	9.30.E+08	1.08.E+09	1.08.E+09	1.09.E+09	1.09.E+09
267	Q27J81	Inverted formin-2 [OS=Homo sapiens]	175.5	26	20	294	20	5503	399	20	20	0	2.36.E+08	2.52.E+08	2.34.E+08	2.41.E+08	2.57.E+08	2.58.E+08	2.08.E+08	2.37.E+08
268	P62140	Serine/threonine-protein phosphatase PP1-beta catalytic subunit [OS=Homo sapiens]	175.5	58	16	748	5	13467	1020	15	15	0	1.60.E+08	1.53.E+08	1.49.E+08	1.41.E+08	1.41.E+08	1.48.E+08	1.37.E+08	1.30.E+08
269	P22392-2	Isoform 3 of Nucleoside diphosphate kinase B [OS=Homo sapiens]	174.8	82	16	944	6		2297	16		11	6.03.E+09	5.64.E+09	5.94.E+09	5.95.E+09	9.25.E+09	8.76.E+09	9.48.E+09	8.99.E+09
270	P53618	Coatomer subunit beta [OS=Homo sapiens]	174.1	35	22	548	22	4753	736	21	21	0	7.53.E+08	7.80.E+08	7.44.E+08	7.60.E+08	1.00.E+09	9.96.E+08	8.79.E+08	9.72.E+08
271	O43390-1	heterogeneous nuclear ribonucleoprotein r [OS=Homo sapiens]	173.3	35	20	1215	14	13212	1323	20	20	6	2.72.E+09	2.62.E+09	2.74.E+09	2.68.E+09	2.80.E+09	2.90.E+09	2.92.E+09	2.89.E+09
272	O60664-1	Perilipin-3 [OS=Homo sapiens]	172.9	52	13	465	13	7646	759	13	12	0	4.27.E+08	4.19.E+08	4.06.E+08	4.45.E+08	4.76.E+08	4.38.E+08	4.32.E+08	4.41.E+08
273	P45880	Voltage-dependent anion-selective channel protein 2 [OS=Homo sapiens]	171.8	68	13	959	13	16319	1405	12	13	0	1.94.E+09	2.01.E+09	2.07.E+09	1.91.E+09	1.50.E+09	1.56.E+09	1.62.E+09	1.61.E+09
274	P33176	Kinesin-1 heavy chain [OS=Homo sapiens]	170.1	31	18	517	18	8658	666	18	18	0	3.95.E+08	3.08.E+08	3.84.E+08	3.24.E+08	3.79.E+08	3.61.E+08	3.64.E+08	3.89.E+08
275	Q14980-1	nuclear mitotic apparatus protein 1 [OS=Homo sapiens]	170.1	20	24	333	24	5105	384	24	23	0	3.03.E+08	3.39.E+08	2.82.E+08	2.98.E+08	4.15.E+08	3.54.E+08	3.98.E+08	4.12.E+08
276	P23396-1	40S ribosomal protein S3 [OS=Homo sapiens]	169.8	77	21	1481	21	14107	1792	21	21	0	4.87.E+09	4.74.E+09	4.80.E+09	4.56.E+09	4.23.E+09	4.29.E+09	4.47.E+09	4.18.E+09
277	P31943	Heterogeneous nuclear ribonucleoprotein H [OS=Homo sapiens]	169.7	37	11	955	5	17276	1404	11	10	4	1.36.E+09	1.33.E+09	1.39.E+09	1.35.E+09	1.62.E+09	1.62.E+09	1.54.E+09	1.64.E+09
278	P15121	aldose reductase [OS=Homo sapiens]	168.0	75	16	687	15	4219	670	16	16	2	1.13.E+09	1.10.E+09	1.15.E+09	1.20.E+09	1.72.E+09	1.66.E+09	1.79.E+09	1.69.E+09

No.	Accession	Description	Sum PEP Score	Coverage [%]	# Peptides	# PSMs	# Unique Peptides	Score Mascot: A5 Mascot	Score Sequest HT: A2 Sequest HT	# Peptides (by Search Engine): A2 Sequest HT	# Peptides (by Search Engine): A5 Mascot	# Razor Peptides	ctrl Abundances_1	ctrl Abundances_2	ctrl Abundances_3	ctrl Abundances_4	JAM-A KO Abundances_1	JAM-A KO Abundances_2	JAM-A KO Abundances_3	JAM-A KO Abundances_4
279	Q9NYL9	tropomodulin-3 [OS=Homo sapiens]	165.2	61	14	568	14	8169	833	14	14	0	7.83.E+08	8.08.E+08	8.45.E+08	7.17.E+08	7.75.E+08	7.54.E+08	8.42.E+08	7.75.E+08
280	Q5T4S7-1	e3 ubiquitin-protein ligase UBR4 [OS=Homo sapiens]	165.0	8	21	517	21	6668	431	21	20	0	2.14.E+08	2.36.E+08	2.26.E+08	2.44.E+08	2.97.E+08	2.69.E+08	2.56.E+08	3.13.E+08
281	P18124	60S ribosomal protein L7 [OS=Homo sapiens]	164.7	53	15	1355	15	11402	1760	15	14	0	3.24.E+09	3.16.E+09	3.34.E+09	3.27.E+09	2.63.E+09	2.57.E+09	2.60.E+09	2.59.E+09
282	Q13310	Polyadenylate-binding protein 4 [OS=Homo sapiens]	164.6	29	14	641	6	12121	1033	14	12	0	1.95.E+08	2.01.E+08	1.90.E+08	1.81.E+08	1.63.E+08	1.59.E+08	1.66.E+08	1.71.E+08
283	O00764-1	Pyridoxal kinase [OS=Homo sapiens]	163.9	55	10	639	10	14699	888	10	10	0	6.35.E+08	6.19.E+08	6.18.E+08	6.84.E+08	8.17.E+08	7.35.E+08	8.23.E+08	7.64.E+08
284	P15531	Nucleoside diphosphate kinase A [OS=Homo sapiens]	163.4	91	12	1185	2	11854	1439	12	12	1	2.11.E+08	2.11.E+08	1.85.E+08	2.53.E+08	1.64.E+08	1.66.E+08	1.97.E+08	1.72.E+08
285	Q8TEX9-1	Importin-4 [OS=Homo sapiens]	163.4	24	16	341	16	6438	510	16	16	0	2.11.E+08	2.46.E+08	2.13.E+08	2.38.E+08	2.32.E+08	2.10.E+08	1.99.E+08	2.03.E+08
286	P17812	CTP synthase 1 [OS=Homo sapiens]	161.8	40	18	704	18	8159	917	18	17	0	8.82.E+08	9.64.E+08	9.98.E+08	9.89.E+08	1.22.E+09	1.37.E+09	1.43.E+09	1.38.E+09
287	Q92841	Probable ATP-dependent RNA helicase DDX17 [OS=Homo sapiens]	161.4	37	22	875	17	7347	1055	22	22	4	2.11.E+09	2.13.E+09	2.17.E+09	2.02.E+09	2.27.E+09	2.34.E+09	2.28.E+09	2.33.E+09
288	O14818-1	Proteasome subunit alpha type-7 [OS=Homo sapiens]	160.9	61	14	716	14	9115	1085	14	14	0	1.06.E+09	1.05.E+09	1.03.E+09	1.07.E+09	1.22.E+09	1.21.E+09	1.15.E+09	1.22.E+09
289	P35232	Prohibitin [OS=Homo sapiens]	159.4	79	15	1037	15	17805	1610	15	15	0	1.90.E+09	1.99.E+09	1.96.E+09	1.83.E+09	2.04.E+09	2.02.E+09	2.04.E+09	1.97.E+09
290	P29692	Elongation factor 1-delta [OS=Homo sapiens]	159.3	76	14	561	14	13468	935	11	14	0	1.72.E+09	1.73.E+09	1.68.E+09	1.64.E+09	2.05.E+09	2.13.E+09	2.13.E+09	2.13.E+09
291	P16615	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [OS=Homo sapiens]	159.1	21	15	434	15	4589	550	15	15	0	4.17.E+08	4.61.E+08	4.27.E+08	4.27.E+08	7.66.E+08	8.21.E+08	5.92.E+08	8.06.E+08
292	Q99497	protein DJ-1 [OS=Homo sapiens]	158.7	68	9	805	9	14129	1481	9	9	0	1.47.E+09	1.37.E+09	1.46.E+09	1.60.E+09	1.74.E+09	1.67.E+09	1.77.E+09	1.72.E+09
293	Q99613	Eukaryotic translation initiation factor 3 subunit C [OS=Homo sapiens]	158.7	25	16	559	16	7045	671	16	16	0	7.22.E+08	7.27.E+08	7.21.E+08	6.64.E+08	5.64.E+08	6.08.E+08	5.62.E+08	5.66.E+08
294	P05187	alkaline phosphatase, placental type [OS=Homo sapiens]	158.6	39	13	363	4	4646	553	13	12	9	1.05.E+09	1.05.E+09	1.05.E+09	1.04.E+09	7.03.E+07	1.08.E+08	7.59.E+07	1.09.E+08
295	Q01518-1	adenylyl cyclase-associated protein 1 [OS=Homo sapiens]	157.8	39	15	1097	15	15431	1475	15	15	0	7.07.E+08	7.46.E+08	7.11.E+08	7.36.E+08	8.75.E+08	8.65.E+08	8.66.E+08	8.67.E+08
296	Q15233	Non-POU domain-containing octamer-binding protein [OS=Homo sapiens]	157.5	45	18	731	17	9189	887	18	18	0	1.10.E+09	1.00.E+09	1.03.E+09	1.07.E+09	8.29.E+08	8.93.E+08	9.38.E+08	7.31.E+08
297	O95573	long-chain-fatty-acid--CoA ligase 3 [OS=Homo sapiens]	157.1	31	16	438	14	5774	627	16	16	2	8.55.E+08	8.88.E+08	8.20.E+08	8.36.E+08	1.17.E+09	1.04.E+09	8.17.E+08	1.14.E+09
298	P01892	HLA class I histocompatibility antigen, A-2 alpha chain [OS=Homo sapiens]	156.1	51	12	573	5	8584	933	12	12	7	9.18.E+08	9.47.E+08	9.18.E+08	9.17.E+08	9.47.E+08	9.65.E+08	1.01.E+09	9.43.E+08
299	P05198	Eukaryotic translation initiation factor 2 subunit 1 [OS=Homo sapiens]	155.9	53	13	625	13	9620	971	13	13	0	1.25.E+09	1.31.E+09	1.31.E+09	1.27.E+09	1.31.E+09	1.34.E+09	1.34.E+09	1.30.E+09
300	P16152	Carbonyl reductase [NADPH] 1 [OS=Homo sapiens]	155.6	65	14	1002	11	16734	1557	14	14	3	1.63.E+09	1.65.E+09	1.76.E+09	1.61.E+09	2.28.E+09	2.27.E+09	2.19.E+09	2.37.E+09
301	P09382	Galectin-1 [OS=Homo sapiens]	155.5	81	8	1368	8	27637	1691	7	8	0	2.59.E+09	2.65.E+09	2.64.E+09	2.43.E+09	3.54.E+09	3.78.E+09	3.84.E+09	3.75.E+09
302	P55884	Eukaryotic translation initiation factor 3 subunit B [OS=Homo sapiens]	155.0	29	16	566	16	6992	833	16	16	0	8.70.E+08	8.74.E+08	8.40.E+08	8.49.E+08	8.06.E+08	8.63.E+08	8.62.E+08	7.97.E+08
303	P25398	40S ribosomal protein S12 [OS=Homo sapiens]	154.2	75	10	1049	10	19753	1162	9	10	0	2.98.E+09	2.89.E+09	3.05.E+09	2.80.E+09	2.71.E+09	2.74.E+09	2.95.E+09	2.76.E+09
304	Q9H4A4	aminopeptidase B [OS=Homo sapiens]	153.8	47	17	538	17	6216	742	16	17	0	7.64.E+08	7.80.E+08	7.73.E+08	7.34.E+08	7.89.E+08	7.69.E+08	7.17.E+08	7.58.E+08
305	Q92945	Far upstream element-binding protein 2 [OS=Homo sapiens]	153.8	34	19	484	17	7258	594	19	19	2	7.53.E+08	7.58.E+08	6.65.E+08	7.46.E+08	8.24.E+08	8.44.E+08	8.70.E+08	7.89.E+08
306	O95336	6-phosphogluconolactonase [OS=Homo sapiens]	153.0	81	12	478	12	4469	694	11	12	0	8.97.E+08	9.02.E+08	9.01.E+08	8.88.E+08	1.06.E+09	1.03.E+09	1.01.E+09	1.03.E+09
307	P16402	Histone H1.3 [OS=Homo sapiens]	152.5	30	12	937	2	14962	1129	9	12	0	1.49.E+08	1.65.E+08	1.62.E+08	1.56.E+08	2.30.E+08	2.03.E+08	2.06.E+08	2.20.E+08
308	P23526-1	Adenosylhomocysteinase [OS=Homo sapiens]	151.9	46	17	1158	16	17902	1568	16	17	1	2.87.E+09	2.75.E+09	2.97.E+09	2.95.E+09	2.49.E+09	2.44.E+09	2.64.E+09	2.50.E+09
309	Q14103	heterogeneous nuclear ribonucleoprotein D0 [OS=Homo sapiens]	150.1	33	15	1071	12	8264	990	15	15	3	2.97.E+09	2.94.E+09	2.91.E+09	2.77.E+09	3.19.E+09	3.12.E+09	2.67.E+09	3.07.E+09
310	Q9UL46	proteasome activator complex subunit 2 [OS=Homo sapiens]	150.1	58	11	781	11	13360	983	11	10	0	4.13.E+08	4.60.E+08	4.43.E+08	4.76.E+08	4.55.E+08	4.43.E+08	4.35.E+08	4.32.E+08
311	P19971	thymidine phosphorylase [OS=Homo sapiens]	150.0	37	13	585	13	9783	874	13	13	0	7.61.E+08	7.36.E+08	7.30.E+08	7.22.E+08	1.25.E+09	1.22.E+09	1.20.E+09	1.20.E+09
312	Q15393-1	Splicing factor 3B subunit 3 [OS=Homo sapiens]	150.0	23	16	536	16	6980	771	15	16	0	7.12.E+08	6.80.E+08	7.29.E+08	6.96.E+08	6.44.E+08	6.24.E+08	6.69.E+08	6.48.E+08
313	P30044-1	Peroxiredoxin-5, mitochondrial [OS=Homo sapiens]	149.5	56	12	1152	12	12119	1475	12	12	0	1.64.E+09	1.70.E+09	1.97.E+09	1.53.E+09	1.69.E+09	1.64.E+09	1.70.E+09	1.68.E+09
314	P52788-1	Spermine synthase [OS=Homo sapiens]	149.0	60	14	338	14	4478	467	14	14	0	4.42.E+08	4.53.E+08	4.11.E+08	4.47.E+08	5.46.E+08	5.57.E+08	5.05.E+08	5.33.E+08
315	P00352	Retinal dehydrogenase 1 [OS=Homo sapiens]	148.4	54	18	361	16	2793	461	18	16	2	1.83.E+09	1.82.E+09	1.79.E+09	1.48.E+09	1.99.E+09	2.17.E+09	1.95.E+09	2.11.E+09
316	Q9P2J5	Leucine--tRNA ligase, cytoplasmic [OS=Homo sapiens]	148.3	22	17	589	17	6704	583	17	17	0	3.79.E+08	4.12.E+08	3.44.E+08	3.83.E+08	4.34.E+08	4.37.E+08	3.50.E+08	4.19.E+08
317	Q9NY33	dipeptidyl peptidase 3 [OS=Homo sapiens]	148.2	38	14	321	14	5276	465	14	14	0	6.46.E+08	6.14.E+08	7.68.E+08	6.62.E+08	7.52.E+08	8.24.E+08	1.04.E+09	3.23.E+08
318	P61221	ATP-binding cassette sub-family E member 1 [OS=Homo sapiens]	147.9	42	18	569	18	7513	789	18	17	0	8.59.E+08	8.72.E+08	8.66.E+08	8.43.E+08	9.91.E+08	9.04.E+08	9.40.E+08	9.33.E+08
319	P32969	60S ribosomal protein L9 [OS=Homo sapiens]	147.7	66	12	885	12	10664	1395	12	12	0	1.83.E+09	1.78.E+09	1.84.E+09	2.04.E+09	1.70.E+09	1.64.E+09	1.63.E+09	1.65.E+09
320	P61247	40S ribosomal protein S3a [OS=Homo sapiens]	147.5	56	16	853	16	13134	1051	16	16	0	3.59.E+09	3.57.E+09	3.57.E+09	3.36.E+09	2.99.E+09	2.99.E+09	3.20.E+09	2.98.E+09
321	Q96QK1	Vacuolar protein sorting-associated protein 35 [OS=Homo sapiens]	147.3	28	16	476	16	5943	560	15	16	0	4.62.E+08	4.65.E+08	4.33.E+08	4.43.E+08	6.67.E+08	6.48.E+08	6.31.E+08	6.31.E+08
322	P21796	voltage-dependent anion-selective channel protein 1 [OS=Homo sapiens]	147.0	66	13	848	12	13656	1121	13	13	1	2.38.E+09	2.36.E+09	2.32.E+09	2.26.E+09	1.76.E+09	1.84.E+09	1.90.E+09	1.86.E+09
323	P30086	phosphatidylethanolamine-binding protein 1 [OS=Homo sapiens]	146.4	76	10	662	10	14966	1300	10	10	0	1.18.E+09	1.25.E+09	1.21.E+09	1.16.E+09	1.23.E+09	1.32.E+09	1.20.E+09	1.28.E+09
324	P61158	actin-related protein 3 [OS=Homo sapiens]	146.1	57	13	509	13	7686	804	12	13	0	5.78.E+08	6.01.E+08	5.36.E+08	5.98.E+08	6.80.E+08	6.72.E+08	5.74.E+08	6.05.E+08
325	P42330	Aldo-keto reductase family 1 member C3 [OS=Homo sapiens]	146.1	58	17	792	7	6983	1007	17	16	0	1.40.E+08	1.78.E+08	1.42.E+08	1.58.E+08	4.14.E+08	4.36.E+08	3.90.E+08	4.01.E+08
326	P24534	Elongation factor 1-beta [OS=Homo sapiens]	146.1	79	9	632	9	13748	1333	8	9	0	2.16.E+09	2.24.E+09	1.94.E+09	2.10.E+09	2.08.E+09	2.13.E+09	1.83.E+09	2.18.E+09
327	O00410	Importin-5 [OS=Homo sapiens]	145.5	29	18	405	18	5882	515	17	18	0	3.30.E+08	3.12.E+08	3.31.E+08	3.18.E+08	4.39.E+08	3.94.E+08	4.12.E+08	4.44.E+08
328	P40939	Trifunctional enzyme subunit alpha, mitochondrial [OS=Homo sapiens]	145.4	34	19	477	19	6439	629	19	19	0	6.53.E+08	6.67.E+08	6.60.E+08	6.30.E+08	8.00.E+08	6.54.E+08	7.02.E+08	7.00.E+08
329	P43686	26S proteasome regulatory subunit 6B [OS=Homo sapiens]	145.1	52	13	496	13	5903	581	13	13	0	4.06.E+08	4.14.E+08	3.98.E+08	3.92.E+08	4.30.E+08	4.21.E+08	3.83.E+08	3.83.E+08
330	Q9Y262	eukaryotic translation initiation factor 3 subunit L [OS=Homo sapiens]	144.7	34	17	719	17	9604	777	17	17	0	5.02.E+08	5.39.E+08	5.06.E+08	5.05.E+08	5.17.E+08	5.34.E+08	5.23.E+08	5.06.E+08
331	P62081	40S ribosomal protein S7 [OS=Homo sapiens]	144.7	57	11	1115	11	13415	1576	11	11	0	2.33.E+09	2.34.E+09	2.23.E+09	2.54.E+09	2.20.E+09	2.19.E+09	2.11.E+09	2.24.E+09
332	Q96HC4	PDZ and LIM domain protein 5 [OS=Homo sapiens]	143.6	39	17	490	17	3766	480	16	17	0	5.06.E+08	4.84.E+08	4.86.E+08	5.06.E+08	7.63.E+08	7.97.E+08	7.64.E+08	7.66.E+08

No.	Accession	Description	Sum PEP Score	Coverage [%]	# Peptides	# PSMs	# Unique Peptides	Score Mascot: A5 Mascot	Score Sequest HT: A2 Sequest HT	# Peptides (by Search Engine): A2 Sequest HT	# Peptides (by Search Engine): A5 Mascot	# Razor Peptides	ctrl Abundances_1	ctrl Abundances_2	ctrl Abundances_3	ctrl Abundances_4	JAM-A KO Abundances_1	JAM-A KO Abundances_2	JAM-A KO Abundances_3	JAM-A KO Abundances_4
333	P17858-1	ATP-dependent 6-phosphofructokinase, liver type [OS=Homo sapiens]	143.0	29	12	307	10	4882	419	12	12	0	1.93.E+08	2.12.E+08	2.06.E+08	1.99.E+08	2.07.E+08	2.07.E+08	1.87.E+08	2.17.E+08
334	P14868	Aspartate--tRNA ligase, cytoplasmic [OS=Homo sapiens]	142.9	50	21	607	21	4598	633	21	21	0	1.17.E+09	1.14.E+09	1.19.E+09	1.13.E+09	1.24.E+09	1.27.E+09	1.39.E+09	1.26.E+09
335	O00299	chloride intracellular channel protein 1 [OS=Homo sapiens]	142.1	84	16	741	15	12395	1059	15	15	1	1.09.E+09	1.08.E+09	1.14.E+09	1.27.E+09	1.22.E+09	1.25.E+09	1.17.E+09	1.25.E+09
336	P62328	Thymosin beta-4 [OS=Homo sapiens]	141.2	89	9	825	9	9198	991	7	9	0	1.95.E+09	1.84.E+09	1.95.E+09	1.99.E+09	2.35.E+09	2.37.E+09	2.62.E+09	2.60.E+09
337	P38919	Eukaryotic initiation factor 4A-III [OS=Homo sapiens]	140.9	39	13	826	10	15177	1266	12	13	0	7.54.E+08	8.24.E+08	6.76.E+08	7.80.E+08	8.67.E+08	8.46.E+08	8.73.E+08	7.27.E+08
338	P63010-1	AP-2 complex subunit beta [OS=Homo sapiens]	140.9	23	20	457	10	5944	509	20	19	10	5.64.E+08	4.89.E+08	5.23.E+08	5.50.E+08	6.62.E+08	6.04.E+08	6.35.E+08	5.99.E+08
339	P11388-1	DNA topoisomerase 2-alpha [OS=Homo sapiens]	140.1	14	18	401	18	4143	439	18	18	0	4.68.E+08	4.71.E+08	4.50.E+08	4.47.E+08	7.60.E+08	7.73.E+08	7.73.E+08	7.86.E+08
340	P17174	Aspartate aminotransferase, cytoplasmic [OS=Homo sapiens]	138.4	57	13	686	13	9911	836	12	13	0	6.36.E+08	7.51.E+08	7.35.E+08	7.75.E+08	7.80.E+08	7.89.E+08	7.53.E+08	7.68.E+08
341	P31949	protein S100-A11 [OS=Homo sapiens]	138.3	87	7	1406	7	26215	1945	7	7	0	2.57.E+09	2.61.E+09	2.29.E+09	2.59.E+09	2.12.E+09	2.06.E+09	1.86.E+09	2.08.E+09
342	P04632	Calpain small subunit 1 [OS=Homo sapiens]	138.0	56	12	602	12	9133	722	12	10	0	5.75.E+08	5.67.E+08	5.59.E+08	6.07.E+08	5.57.E+08	5.20.E+08	5.57.E+08	5.47.E+08
343	P37837	Transaldolase [OS=Homo sapiens]	137.8	51	16	861	16	7871	768	16	15	0	1.91.E+09	1.88.E+09	1.91.E+09	1.98.E+09	2.34.E+09	2.24.E+09	2.34.E+09	2.31.E+09
344	P10696	Alkaline phosphatase, placental-like [OS=Homo sapiens]	137.7	33	11	357	2	4474	541	11	11	0	3.85.E+07	3.62.E+07	4.21.E+07	3.39.E+07	3.18.E+06	3.40.E+06	4.22.E+06	3.66.E+06
345	P13804-1	Electron transfer flavoprotein subunit alpha, mitochondrial [OS=Homo sapiens]	137.1	60	13	617	13	10297	910	13	13	0	6.15.E+08	6.52.E+08	6.04.E+08	5.75.E+08	5.61.E+08	5.55.E+08	5.49.E+08	5.43.E+08
346	P39687	Acidic leucine-rich nuclear phosphoprotein 32 family member A [OS=Homo sapiens]	136.1	45	10	787	5	18706	1184	10	10	0	1.40.E+09	1.37.E+09	1.34.E+09	1.35.E+09	1.36.E+09	1.30.E+09	1.37.E+09	1.32.E+09
347	Q08945	FACT complex subunit SSRP1 [OS=Homo sapiens]	136.0	38	21	416	21	4050	410	20	21	0	9.09.E+08	8.61.E+08	9.30.E+08	8.62.E+08	9.18.E+08	9.24.E+08	8.44.E+08	9.68.E+08
348	P40925	Malate dehydrogenase, cytoplasmic [OS=Homo sapiens]	136.0	48	12	851	12	14919	1240	12	12	0	1.54.E+09	1.58.E+09	1.55.E+09	1.58.E+09	2.15.E+09	2.13.E+09	2.13.E+09	2.17.E+09
349	Q14240-1	eukaryotic initiation factor 4A-II [OS=Homo sapiens]	135.9	33	14	1314	2	23730	1705	14	14	0	3.43.E+07	3.32.E+07	3.55.E+07	4.41.E+07	6.53.E+07	5.90.E+07	6.09.E+07	5.67.E+07
350	P49748-1	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial [OS=Homo sapiens]	135.5	36	14	346	14	5139	490	14	14	0	5.23.E+08	5.40.E+08	5.33.E+08	4.96.E+08	4.01.E+08	4.27.E+08	3.90.E+08	4.08.E+08
351	P09493-5	Isoform 5 of Tropomyosin alpha-1 chain [OS=Homo sapiens]	135.2	38	12	473	1		1321	12		0	1.41.E+07	1.26.E+07	1.39.E+07	1.58.E+07	1.15.E+07	1.20.E+07	1.46.E+07	1.29.E+07
352	Q96DG6	Carboxymethylenebutenolidase homolog [OS=Homo sapiens]	134.8	58	14	583	14	8123	562	13	12	0	6.53.E+08	6.78.E+08	6.68.E+08	6.78.E+08	5.98.E+08	5.88.E+08	6.34.E+08	5.92.E+08
353	P31150	Rab GDP dissociation inhibitor alpha [OS=Homo sapiens]	134.6	28	8	506	2	12220	945	8	8	0	3.76.E+07	4.39.E+07	3.78.E+07	3.95.E+07	4.85.E+07	4.92.E+07	4.64.E+07	5.56.E+07
354	Q13162	Peroxiredoxin-4 [OS=Homo sapiens]	133.9	60	12	866	9	8885	1079	12	12	0	5.31.E+08	4.95.E+08	5.07.E+08	4.76.E+08	7.36.E+08	7.41.E+08	7.38.E+08	6.93.E+08
355	P22087	rRNA 2'-O-methyltransferase fibrillarin [OS=Homo sapiens]	133.4	44	13	431	13	3993	586	13	12	0	1.09.E+09	1.01.E+09	1.10.E+09	1.04.E+09	7.51.E+08	7.33.E+08	7.65.E+08	7.44.E+08
356	Q99798	Aconitate hydratase, mitochondrial [OS=Homo sapiens]	133.3	30	14	349	14	4845	475	14	14	0	3.41.E+08	3.27.E+08	3.51.E+08	3.26.E+08	3.69.E+08	3.73.E+08	3.62.E+08	4.64.E+08
357	Q16822	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=Homo sapiens OX=9606 GN=PCK2 PE=1 SV=4	133.3	41	18	196	18	5469			18	0	5.93.E+08	6.05.E+08	6.05.E+08	6.19.E+08	6.19.E+08	6.25.E+08	5.70.E+08	5.99.E+08
358	P07910-1	Heterogeneous nuclear ribonucleoproteins C1/C2 [OS=Homo sapiens]	133.2	39	14	1133	1	13117	1339	14	13	0	1.18.E+07	2.63.E+07	1.53.E+07	1.81.E+07	2.96.E+07	2.45.E+07		2.97.E+07
359	P61586	Transforming protein RhoA [OS=Homo sapiens]	133.1	69	10	851	2	15454	1293	10	10	8	1.47.E+09	1.46.E+09	1.52.E+09	1.43.E+09	1.14.E+09	1.17.E+09	1.16.E+09	1.12.E+09
360	P62158	Calmodulin [OS=Homo sapiens]	133.0	85	9	587	9	14323	657	7	9	0	1.36.E+09	1.35.E+09	1.40.E+09	1.35.E+09	1.58.E+09	1.60.E+09	1.61.E+09	1.85.E+09
361	P12236	ADP/ATP translocase 3 [OS=Homo sapiens]	132.7	55	19	894	4	10785	973	18	17	13	2.99.E+09	2.91.E+09	2.70.E+09	3.06.E+09	2.58.E+09	2.83.E+09	2.71.E+09	2.85.E+09
362	P42167	Lamina-associated polypeptide 2, isoforms beta/gamma [OS=Homo sapiens]	132.3	38	10	521	5	8067	721	10	10	6	6.17.E+08	5.33.E+08	6.12.E+08	6.26.E+08	7.76.E+08	7.00.E+08	7.08.E+08	7.47.E+08
363	Q9UHD8-1	Septin-9 [OS=Homo sapiens]	132.2	34	14	593	14	6934	772	14	14	0	6.57.E+08	6.48.E+08	6.79.E+08	6.88.E+08	5.17.E+08	5.11.E+08	5.10.E+08	4.96.E+08
364	Q9UNM6	26S proteasome non-ATPase regulatory subunit 13 [OS=Homo sapiens]	132.2	48	15	373	15	3924	396	15	15	0	5.92.E+08	6.00.E+08	6.05.E+08	5.80.E+08	6.64.E+08	6.80.E+08	7.12.E+08	6.85.E+08
365	P49321	Nuclear autoantigenic sperm protein [OS=Homo sapiens]	131.9	28	12	326	12	6044	523	11	12	0	5.32.E+08	5.35.E+08	5.52.E+08	5.15.E+08	7.69.E+08	6.81.E+08	6.84.E+08	7.67.E+08
366	Q15019	septin-2 [OS=Homo sapiens]	131.8	60	13	496	13	6718	688	13	13	0	6.97.E+08	7.07.E+08	6.49.E+08	7.21.E+08	8.27.E+08	9.06.E+08	6.88.E+08	8.39.E+08
367	O94925-3	Isoform 3 of Glutaminase kidney isoform, mitochondrial [OS=Homo sapiens]	130.9	37	14	236	14		613	14		0	3.59.E+08	3.27.E+08	3.40.E+08	3.50.E+08	4.28.E+08	4.14.E+08	3.64.E+08	3.76.E+08
368	Q15029	116 kDa U5 small nuclear ribonucleoprotein component [OS=Homo sapiens]	130.8	25	16	535	15	5532	553	16	15	0	5.93.E+08	6.80.E+08	5.77.E+08	5.79.E+08	5.38.E+08	5.25.E+08	5.39.E+08	6.05.E+08
369	P46777	60S ribosomal protein L5 [OS=Homo sapiens]	130.7	53	13	762	13	10251	1008	13	13	0	1.48.E+09	1.45.E+09	1.39.E+09	1.58.E+09	1.27.E+09	1.32.E+09	1.26.E+09	1.29.E+09
370	Q16576-1	Histone-binding protein RBBP7 [OS=Homo sapiens]	130.3	73	15	428	11	4802	460	14	15	4	1.86.E+09	2.04.E+09	1.95.E+09	1.86.E+09	1.58.E+09	1.79.E+09	1.68.E+09	1.57.E+09
371	O75390	citrate synthase, mitochondrial [OS=Homo sapiens]	129.5	48	14	829	14	10588	984	14	14	0	1.35.E+09	1.37.E+09	1.34.E+09	1.31.E+09	1.17.E+09	1.17.E+09	1.16.E+09	1.20.E+09
372	P23588	eukaryotic translation initiation factor 4B [OS=Homo sapiens]	129.5	34	16	644	16	6834	809	16	16	0	6.98.E+08	6.71.E+08	7.45.E+08	7.73.E+08	5.68.E+08	5.19.E+08	5.55.E+08	5.28.E+08
373	P11387	DNA topoisomerase 1 [OS=Homo sapiens]	129.0	28	15	311	15	3070	442	14	15	0	9.96.E+08	1.00.E+09	9.92.E+08	9.87.E+08	8.55.E+08	8.03.E+08	8.98.E+08	8.12.E+08
374	Q9NZL4	Hsp70-binding protein 1 OS=Homo sapiens OX=9606 GN=HSPBP1 PE=1 SV=2	128.9	62	13	127	13	4035			13	0	5.79.E+08	6.81.E+08	6.75.E+08	6.32.E+08	4.80.E+08	5.08.E+08	4.59.E+08	4.61.E+08
375	Q02790	Peptidyl-prolyl cis-trans isomerase FKBP4 [OS=Homo sapiens]	128.7	46	16	367	16	4212	528	15	16	0	7.62.E+08	7.56.E+08	7.49.E+08	7.52.E+08	5.91.E+08	6.38.E+08	5.89.E+08	5.67.E+08
376	P00505	Aspartate aminotransferase, mitochondrial [OS=Homo sapiens]	128.2	43	12	436	12	6364	766	12	12	0	7.37.E+08	7.23.E+08	7.77.E+08	7.49.E+08	7.70.E+08	7.39.E+08	7.87.E+08	7.39.E+08
377	P21291	Cysteine and glycine-rich protein 1 [OS=Homo sapiens]	128.1	59	7	407	7	8215	706	7	7	0	5.44.E+08	5.68.E+08	5.68.E+08	5.51.E+08	8.98.E+08	9.17.E+08	9.45.E+08	9.16.E+08
378	P60953	Cell division control protein 42 homolog [OS=Homo sapiens]	128.0	63	9	1094	8	14655	1551	9	9	1	1.16.E+09	1.20.E+09	1.03.E+09	1.31.E+09	1.21.E+09	1.29.E+09	1.16.E+09	1.25.E+09
379	Q07021	Complement component 1 Q subcomponent-binding protein, mitochondrial [OS=Homo sapiens]	127.9	48	7	618	7	14596	1335	7	7	0	1.03.E+09	1.03.E+09	9.69.E+08	1.03.E+09	8.23.E+08	8.09.E+08	5.90.E+08	7.11.E+08
380	Q92499	ATP-dependent RNA helicase DDX1 [OS=Homo sapiens]	127.7	22	13	626	13	6765	704	13	13	0	4.26.E+08	4.39.E+08	4.28.E+08	4.52.E+08	5.00.E+08	4.64.E+08	3.83.E+08	4.71.E+08
381	P62906	60S ribosomal protein L10A [OS=Homo sapiens]	127.5	47	10	835	10	7088	1052	10	10	0	2.46.E+09	2.35.E+09	2.53.E+09	2.32.E+09	2.12.E+09	2.12.E+09	2.35.E+09	2.16.E+09
382	Q9Y5B9	FACT complex subunit SPT16 [OS=Homo sapiens]	127.1	23	17	287	17	3176	299	16	16	0	4.68.E+08	4.93.E+08	4.44.E+08	4.39.E+08	4.77.E+08	4.19.E+08	4.22.E+08	5.02.E+08
383	Q00796	Sorbitol dehydrogenase [OS=Homo sapiens]	127.0	52	13	372	13	5820	416	12	13	0	6.00.E+08	5.68.E+08	5.73.E+08	5.79.E+08	7.82.E+08	7.70.E+08	7.70.E+08	7.87.E+08
384	P12235	ADP/ATP translocase 1 [OS=Homo sapiens]	126.8	48	16	771	4	10810	866	14	16	0	9.83.E+07	6.67.E+07	6.32.E+07	8.02.E+07	1.35.E+08	1.32.E+08	9.92.E+07	1.16.E+08
385	O00148	ATP-dependent RNA helicase DDX39A [OS=Homo sapiens]	126.5	41	14	944	5	10489	1089	14	14	0	1.50.E+08	1.12.E+08	1.49.E+08	1.63.E+08	1.65.E+08	1.70.E+08	1.05.E+08	1.63.E+08
386	P48163	NADP-dependent malic enzyme [OS=Homo sapiens]	126.5	42	14	460	14	7888	582	14	14	0	2.24.E+08	2.54.E+08	2.22.E+08	2.37.E+08	2.44.E+08	2.34.E+08	2.50.E+08	2.42.E+08

No.	Accession	Description	Sum PEP Score	Coverage [%]	# Peptides	# PSMs	# Unique Peptides	Score Mascot: A5 Mascot	Score Sequest HT: A2 Sequest HT	# Peptides (by Search Engine): A2 Sequest HT	# Peptides (by Search Engine): A5 Mascot	# Razor Peptides	ctrl Abundances_1	ctrl Abundances_2	ctrl Abundances_3	ctrl Abundances_4	JAM-A KO Abundances_1	JAM-A KO Abundances_2	JAM-A KO Abundances_3	JAM-A KO Abundances_4
387	O43143	Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15 [OS=Homo sapiens]	126.5	27	15	490	15	5758	646	15	15	0	7.59.E+08	7.08.E+08	7.46.E+08	7.02.E+08	7.60.E+08	7.12.E+08	7.75.E+08	7.40.E+08
388	Q6PIU2	Neutral cholesterol ester hydrolase 1 [OS=Homo sapiens]	126.5	40	12	350	12	4105	434	12	12	0	3.89.E+08	4.13.E+08	3.73.E+08	3.90.E+08	4.95.E+08	4.75.E+08	4.53.E+08	4.90.E+08
389	P62241	40S ribosomal protein S8 [OS=Homo sapiens]	125.5	59	13	1080	13	15365	1508	13	13	0	3.43.E+09	3.46.E+09	3.51.E+09	3.31.E+09	2.78.E+09	2.85.E+09	2.92.E+09	2.89.E+09
390	P30838	Aldehyde dehydrogenase, dimeric NADP-preferring [OS=Homo sapiens]	125.3	37	13	191	12	1999	248	13	13	1	1.44.E+08	1.36.E+08	1.50.E+08	1.14.E+08	1.79.E+08	1.68.E+08	2.05.E+08	1.75.E+08
391	P25786-1	Proteasome subunit alpha type-1 [OS=Homo sapiens]	125.2	64	14	528	14	6654	707	14	14	0	6.39.E+08	7.21.E+08	6.47.E+08	6.75.E+08	7.87.E+08	8.24.E+08	7.29.E+08	7.99.E+08
392	Q9HB71	Calcyclin-binding protein [OS=Homo sapiens]	124.9	62	10	433	10	5204	624	9	10	0	9.50.E+08	9.86.E+08	9.66.E+08	8.59.E+08	9.55.E+08	9.88.E+08	9.96.E+08	9.70.E+08
393	P18085	ADP-ribosylation factor 4 [OS=Homo sapiens]	124.7	71	11	613	5	8203	1032	10	11	0	3.96.E+08	3.66.E+08	3.79.E+08	4.43.E+08	5.59.E+08	5.24.E+08	4.63.E+08	5.27.E+08
394	P55795	heterogeneous nuclear ribonucleoprotein H2 [OS=Homo sapiens]	124.4	27	9	770	4	12549	1068	9	8	0	2.31.E+08	2.79.E+08	2.04.E+08	2.11.E+08	2.02.E+08	2.04.E+08	1.86.E+08	2.52.E+08
395	Q8NC51-1	Plasminogen activator inhibitor 1 RNA-binding protein [OS=Homo sapiens]	123.5	39	14	449	14	6213	258	12	14	0	9.21.E+08	9.15.E+08	8.57.E+08	9.51.E+08	9.20.E+08	8.67.E+08	9.15.E+08	8.75.E+08
396	Q1KMD3	heterogeneous nuclear ribonucleoprotein U-like protein 2 [OS=Homo sapiens]	123.4	31	13	328	13	4212	449	13	13	0	6.07.E+08	5.90.E+08	5.55.E+08	6.03.E+08	4.71.E+08	4.64.E+08	4.26.E+08	4.30.E+08
397	Q9H0U4	ras-related protein Rab-1B [OS=Homo sapiens]	123.3	72	11	894	4	14182	1210	11	11	7	2.20.E+09	2.07.E+09	2.11.E+09	2.06.E+09	2.23.E+09	2.33.E+09	2.31.E+09	2.31.E+09
398	Q99460	26S proteasome non-ATPase regulatory subunit 1 [OS=Homo sapiens]	123.2	32	17	420	17	2882	396	17	17	0	4.90.E+08	5.00.E+08	4.65.E+08	5.19.E+08	4.74.E+08	5.44.E+08	4.97.E+08	5.37.E+08
399	P16989-1	Y-box-binding protein 3 [OS=Homo sapiens]	122.9	39	10	456	5	4512	541	10	10	0	6.26.E+07	6.71.E+07	5.04.E+07	6.56.E+07	8.03.E+07	7.71.E+07	7.24.E+07	7.81.E+07
400	P07954	fumarate hydratase, mitochondrial [OS=Homo sapiens]	122.5	50	14	513	14	7751	644	14	14	0	6.72.E+08	6.63.E+08	6.37.E+08	6.82.E+08	7.47.E+08	7.30.E+08	6.73.E+08	6.18.E+08
401	Q9H3U1	Protein unc-45 homolog A [OS=Homo sapiens]	122.3	22	12	431	12	7308	495	12	12	0	2.87.E+08	2.76.E+08	2.82.E+08	2.69.E+08	2.60.E+08	2.55.E+08	2.59.E+08	2.27.E+08
402	O75531	Barrier-to-autointegration factor [OS=Homo sapiens]	122.3	76	9	607	9	4910	757	9	9	0	1.19.E+09	1.21.E+09	1.14.E+09	1.27.E+09	1.21.E+09	1.13.E+09	1.14.E+09	1.05.E+09
403	A1L0T0	Acetolactate synthase-like protein [OS=Homo sapiens]	122.1	40	12	220	12	4696	348	12	12	0	2.12.E+08	2.13.E+08	3.25.E+08	3.10.E+08	2.60.E+08	2.51.E+08	2.13.E+08	2.52.E+08
404	P12004	proliferating cell nuclear antigen [OS=Homo sapiens]	122.0	61	10	640	10	11097	959	10	10	0	1.00.E+09	8.91.E+08	8.42.E+08	8.41.E+08	1.19.E+09	1.12.E+09	1.16.E+09	1.05.E+09
405	Q71DI3	histone H3.2 [OS=Homo sapiens]	121.8	48	6	1830	1	34476	2608	6	5	0	1.71.E+09	1.72.E+09	1.49.E+09	1.67.E+09	6.80.E+08	6.03.E+08	5.19.E+08	5.93.E+08
406	P45974-1	Ubiquitin carboxyl-terminal hydrolase 5 [OS=Homo sapiens]	121.7	26	13	518	13	4855	656	13	13	0	3.21.E+08	3.09.E+08	2.65.E+08	3.46.E+08	3.77.E+08	3.67.E+08	3.68.E+08	3.73.E+08
407	Q9Y2X3	Nucleolar protein 58 [OS=Homo sapiens]	121.7	37	13	508	13	6531	551	13	13	0	5.40.E+08	5.13.E+08	4.91.E+08	5.01.E+08	3.72.E+08	3.78.E+08	3.74.E+08	3.80.E+08
408	Q15691	Microtubule-associated protein RP/EB family member 1 [OS=Homo sapiens]	121.6	65	12	424	12	5600	489	11	12	0	3.58.E+08	3.51.E+08	3.68.E+08	3.36.E+08	5.28.E+08	5.19.E+08	5.50.E+08	5.26.E+08
409	Q9Y265	RuvB-like 1 [OS=Homo sapiens]	121.4	35	12	568	12	7656	804	12	12	0	7.46.E+08	7.29.E+08	6.47.E+08	7.73.E+08	8.22.E+08	8.34.E+08	7.03.E+08	8.10.E+08
410	P68036	Ubiquitin-conjugating enzyme E2 L3 [OS=Homo sapiens]	121.3	68	8	463	8	5658	749	8	8	0	7.64.E+08	8.19.E+08	6.65.E+08	8.19.E+08	1.02.E+09	1.07.E+09	1.00.E+09	1.03.E+09
411	Q9UMS4	Pre-mRNA-processing factor 19 [OS=Homo sapiens]	120.9	44	12	349	12	3985	497	11	11	0	8.15.E+08	8.12.E+08	8.17.E+08	7.76.E+08	7.99.E+08	8.57.E+08	8.64.E+08	8.41.E+08
412	P32119	Peroxiredoxin-2 [OS=Homo sapiens]	120.6	66	11	748	10	9181	1029	11	11	0	1.02.E+09	1.07.E+09	1.11.E+09	1.16.E+09	1.40.E+09	1.44.E+09	1.48.E+09	1.45.E+09
413	P27635	60S ribosomal protein L10 [OS=Homo sapiens]	120.2	46	12	734	12	7813	950	12	11	0	1.82.E+09	1.67.E+09	1.81.E+09	1.67.E+09	1.53.E+09	1.54.E+09	1.74.E+09	1.60.E+09
414	Q14444-1	Caprin-1 [OS=Homo sapiens]	119.6	21	9	451	9	8116	643	9	9	0	4.99.E+08	5.36.E+08	4.64.E+08	5.39.E+08	5.33.E+08	5.34.E+08	4.89.E+08	5.29.E+08
415	Q9HBI6	Phylloquinone omega-hydroxylase CYP4F11 [OS=Homo sapiens]	119.4	39	15	440	15	3057	539	15	15	0	3.46.E+08	3.56.E+08	3.20.E+08	2.90.E+08	4.87.E+08	4.87.E+08	4.20.E+08	4.55.E+08
416	P13667	Protein disulfide-isomerase A4 [OS=Homo sapiens]	119.3	33	20	277	20	1931	274	20	19	0	6.60.E+08	6.28.E+08	6.81.E+08	6.80.E+08	9.67.E+08	9.77.E+08	1.02.E+09	9.65.E+08
417	Q16531	DNA damage-binding protein 1 [OS=Homo sapiens]	119.2	20	17	229	17	2012	242	17	16	0	4.75.E+08	4.99.E+08	5.20.E+08	4.59.E+08	6.16.E+08	6.58.E+08	6.67.E+08	6.34.E+08
418	Q08J23	tRNA (Cytosine(34)-C(5))-methyltransferase [OS=Homo sapiens]	119.2	33	16	483	16	4886	623	16	16	0	5.04.E+08	5.25.E+08	4.99.E+08	5.09.E+08	5.31.E+08	5.21.E+08	4.55.E+08	5.05.E+08
419	O15371	Eukaryotic translation initiation factor 3 subunit D [OS=Homo sapiens]	119.2	39	13	304	13	3649	340	13	13	0	3.60.E+08	3.34.E+08	3.26.E+08	3.57.E+08	2.90.E+08	3.08.E+08	3.13.E+08	3.20.E+08
420	P06493	Cyclin-dependent kinase 1 [OS=Homo sapiens]	118.9	50	12	287	11	2490	360	12	12	1	9.83.E+08	9.39.E+08	9.76.E+08	8.61.E+08	1.11.E+09	1.10.E+09	1.20.E+09	1.14.E+09
421	P17980	26S proteasome regulatory subunit 6A [OS=Homo sapiens]	118.2	45	13	460	13	6353	591	13	13	0	4.08.E+08	4.32.E+08	3.98.E+08	4.08.E+08	4.44.E+08	4.43.E+08	4.27.E+08	4.31.E+08
422	P62277	40S ribosomal protein S13 [OS=Homo sapiens]	117.9	50	11	1188	11	9173	1143	11	11	0	3.45.E+09	3.36.E+09	3.57.E+09	3.34.E+09	3.23.E+09	3.12.E+09	3.34.E+09	3.22.E+09
423	Q99873	protein arginine N-methyltransferase 1 [OS=Homo sapiens]	117.1	44	14	298	14		824	14		0	9.66.E+08	9.51.E+08	9.53.E+08	9.01.E+08	7.36.E+08	7.65.E+08	7.65.E+08	7.29.E+08
424	Q16181	Septin-7 [OS=Homo sapiens]	117.1	32	10	578	9	7868	767	10	10	0	4.13.E+08	4.22.E+08	3.84.E+08	4.30.E+08	4.65.E+08	4.53.E+08	4.20.E+08	4.56.E+08
425	P54136-1	arginine--tRNA ligase, cytoplasmic [OS=Homo sapiens]	116.3	34	17	559	17	5962	617	17	17	0	6.39.E+08	5.98.E+08	6.48.E+08	6.51.E+08	6.48.E+08	7.13.E+08	7.72.E+08	8.69.E+08
426	P35637-1	RNA-binding protein FUS [OS=Homo sapiens]	116.1	20	7	503	5	6804	725	7	7	2	7.46.E+08	7.26.E+08	6.12.E+08	6.52.E+08	8.67.E+08	7.97.E+08	8.19.E+08	7.86.E+08
427	O75367-1	Core histone macro-H2A.1 [OS=Homo sapiens]	115.8	41	11	406	11	3859	571	11	11	0	7.02.E+08	7.14.E+08	7.13.E+08	6.57.E+08	7.62.E+08	7.71.E+08	6.76.E+08	7.89.E+08
428	P56537-1	eukaryotic translation initiation factor 6 [OS=Homo sapiens]	115.8	57	8	551	8	11336	917	8	8	0	9.60.E+08	9.53.E+08	9.27.E+08	1.01.E+09	9.75.E+08	9.14.E+08	8.77.E+08	9.16.E+08
429	P51665	26S proteasome non-ATPase regulatory subunit 7 [OS=Homo sapiens]	115.8	40	7	469	7	7795	743	7	7	0	4.13.E+08	3.70.E+08	3.82.E+08	4.05.E+08	4.37.E+08	4.21.E+08	4.44.E+08	4.49.E+08
430	Q9UM47	Neurogenic locus notch homolog protein 3 [OS=Homo sapiens]	115.0	10	14	326	14	5366	444	14	14	0	1.43.E+08	1.56.E+08	1.50.E+08	1.56.E+08	2.95.E+08	2.90.E+08	2.77.E+08	2.91.E+08
431	P15880	40S ribosomal protein S2 [OS=Homo sapiens]	115.0	51	14	966	14	10818	1195	14	14	0	2.49.E+09	2.44.E+09	2.56.E+09	2.54.E+09	2.35.E+09	2.34.E+09	2.50.E+09	2.38.E+09
432	P27816-1	Microtubule-associated protein 4 [OS=Homo sapiens]	114.8	15	12	286	12	2697	280	11	12	0	2.24.E+08	1.88.E+08	2.30.E+08	2.42.E+08	3.07.E+08	2.90.E+08	2.92.E+08	2.99.E+08
433	P18621	60S ribosomal protein L17 [OS=Homo sapiens]	114.7	52	11	632	11	5321	720	11	10	0	1.81.E+09	1.63.E+09	1.76.E+09	1.76.E+09	1.69.E+09	1.68.E+09	1.81.E+09	1.72.E+09
434	P41567	eukaryotic translation initiation factor 1 [OS=Homo sapiens]	114.7	82	10	349	5	8889	253	8	10	5	4.75.E+08	5.50.E+08	4.23.E+08	5.28.E+08	6.32.E+08	6.28.E+08	5.66.E+08	6.40.E+08
435	P62263	40S ribosomal protein S14 [OS=Homo sapiens]	114.3	72	11	476	11	4804	472	11	11	0	1.08.E+09	1.04.E+09	1.12.E+09	1.10.E+09	9.68.E+08	9.59.E+08	1.05.E+09	9.42.E+08
436	Q96T76-1	MMS19 nucleotide excision repair protein homolog [OS=Homo sapiens]	114.2	18	11	306	11	5092	388	11	11	0	2.20.E+08	2.08.E+08	1.92.E+08	1.88.E+08	2.36.E+08	2.06.E+08	1.94.E+08	2.09.E+08
437	P30566	adenylosuccinate lyase [OS=Homo sapiens]	113.6	45	13	397	13	3459	393	12	12	0	3.12.E+08	3.17.E+08	2.97.E+08	3.10.E+08	4.94.E+08	4.54.E+08	4.05.E+08	4.45.E+08
438	Q10471	Polypeptide N-acetylgalactosaminyltransferase 2 [OS=Homo sapiens]	113.6	32	13	465	13	5039	522	13	12	0	2.86.E+08	2.68.E+08	2.76.E+08	3.18.E+08	4.15.E+08	4.27.E+08	3.16.E+08	4.26.E+08
439	Q15293	Reticulocalbin-1 [OS=Homo sapiens]	113.6	47	11	388	11	4095	447	11	11	0	8.12.E+08	8.03.E+08	7.88.E+08	8.12.E+08	9.84.E+08	9.97.E+08	1.03.E+09	1.00.E+09
440	Q9UGI8	Testin [OS=Homo sapiens]	113.2	40	12	219	12	1913	270	12	12	0	2.91.E+08	2.63.E+08	2.91.E+08	3.01.E+08	1.98.E+08	2.28.E+08	2.27.E+08	2.36.E+08
441	P16401	Histone H1.5 [OS=Homo sapiens]	113.1	27	10	812	10	13558	837	7	10	0	3.62.E+09	3.36.E+09	3.63.E+09	3.81.E+09	4.03.E+09	3.75.E+09	4.27.E+09	4.00.E+09
442	Q15046	Lysine--tRNA ligase [OS=Homo sapiens]	113.0	35	14	339	14	2898	362	13	14	0	5.28.E+08	5.78.E+08	5.34.E+08	5.27.E+08	4.89.E+08	4.63.E+08	4.50.E+08	4.85.E+08

No.	Accession	Description	Sum PEP Score	Coverage [%]	# Peptides	# PSMs	# Unique Peptides	Score Mascot: A5 Mascot	Score Sequest HT: A2 Sequest HT	# Peptides (by Search Engine): A2 Sequest HT	# Peptides (by Search Engine): A5 Mascot	# Razor Peptides	ctrl Abundances_1	ctrl Abundances_2	ctrl Abundances_3	ctrl Abundances_4	JAM-A KO Abundances_1	JAM-A KO Abundances_2	JAM-A KO Abundances_3	JAM-A KO Abundances_4
443	P05534	HLA class I histocompatibility antigen, A-24 alpha chain [OS=Homo sapiens]	112.1	35	7	360	0	5715	660	7	7	0								
444	Q92598	Heat shock protein 105 kDa [OS=Homo sapiens]	111.8	30	16	312	14	3687	377	16	16	1	3.39.E+08	3.52.E+08	3.63.E+08	3.40.E+08	3.78.E+08	4.14.E+08	3.07.E+08	3.71.E+08
445	Q6FI13	Histone H2A type 2-A [OS=Homo sapiens]	111.8	58	7	2281	3	25618	3203	7	7	0	4.80.E+09	4.57.E+09	4.92.E+09	4.01.E+09	3.76.E+09	3.68.E+09	4.18.E+09	3.87.E+09
446	P08708	40S ribosomal protein S17 [OS=Homo sapiens]	111.6	63	9	680	9	9290	922	9	9	0	1.05.E+09	1.04.E+09	1.02.E+09	1.11.E+09	9.89.E+08	9.45.E+08	9.29.E+08	9.63.E+08
447	Q96FW1	Ubiquitin thioesterase otub1 [OS=Homo sapiens]	111.2	45	10	458	10	5828	514	10	10	0	5.97.E+08	6.13.E+08	6.25.E+08	6.98.E+08	7.10.E+08	8.28.E+08	7.38.E+08	7.02.E+08
448	Q01469	Fatty acid-binding protein, epidermal [OS=Homo sapiens]	110.9	72	10	398	10	6720	588	8	10	0	1.16.E+09	1.17.E+09	1.17.E+09	1.07.E+09	1.10.E+09	1.11.E+09	1.16.E+09	1.12.E+09
449	P11216	Glycogen phosphorylase, brain form [OS=Homo sapiens]	110.8	23	15	278	13	4520	318	15	15	2	3.28.E+08	3.41.E+08	3.23.E+08	3.20.E+08	2.65.E+08	2.53.E+08	2.38.E+08	2.63.E+08
450	P07741-1	Adenine phosphoribosyltransferase [OS=Homo sapiens]	110.7	64	9	418	9	9593	608	8	9	0	7.86.E+08	8.02.E+08	6.70.E+08	7.23.E+08	9.38.E+08	9.27.E+08	8.34.E+08	9.01.E+08
451	P62873	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1 [OS=Homo sapiens]	110.5	58	13	219	9	2892	249	11	13	4	4.56.E+08	2.83.E+08	3.03.E+08	3.30.E+08	5.67.E+08	5.80.E+08	5.27.E+08	5.23.E+08
452	P00387	NADH-cytochrome b5 reductase 3 [OS=Homo sapiens]	110.3	43	9	348	9	4500	645	9	9	0	4.63.E+08	4.78.E+08	3.99.E+08	4.34.E+08	4.46.E+08	4.76.E+08	3.87.E+08	4.61.E+08
453	P98179	RNA-binding protein 3 [OS=Homo sapiens]	109.8	54	6	649	6	10888	1008	5	6	0	1.01.E+09	1.04.E+09	9.75.E+08	1.03.E+09	8.52.E+08	8.31.E+08	8.06.E+08	7.90.E+08
454	P25789	Proteasome subunit alpha type-4 [OS=Homo sapiens]	109.8	51	9	427	9	7689	627	9	9	0	6.28.E+08	6.32.E+08	6.08.E+08	6.02.E+08	7.11.E+08	7.13.E+08	7.25.E+08	7.52.E+08
455	Q9NSD9	Phenylalanine--tRNA ligase beta subunit [OS=Homo	109.8	31	13	454	13	3342	573	13	13	0	7.43.E+08	7.34.E+08	7.50.E+08	7.28.E+08	7.87.E+08	8.12.E+08	7.46.E+08	7.86.E+08
456	A0MZ66	Shootin-1 [OS=Homo sapiens]	109.7	32	15	263	15	2319	257	15	15	0	3.27.E+08	3.24.E+08	3.12.E+08	3.22.E+08	5.12.E+08	5.02.E+08	5.07.E+08	4.90.E+08
457	Q9BUJ2-1	Heterogeneous nuclear ribonucleoprotein U-like protein 1 [OS=Homo sapiens]	109.6	21	12	354	12	4245	425	12	11	0	3.30.E+08	2.86.E+08	3.22.E+08	3.21.E+08	2.04.E+08	2.48.E+08	2.51.E+08	2.13.E+08
458	Q92688	Acidic leucine-rich nuclear phosphoprotein 32 family member B [OS=Homo sapiens]	109.4	32	10	616	5	12330	796	10	10	5	9.11.E+08	9.75.E+08	9.86.E+08	9.23.E+08	1.18.E+09	1.13.E+09	1.05.E+09	1.08.E+09
459	O43813	LanC-like protein 1 [OS=Homo sapiens]	109.4	42	10	321	10	4440	493	10	10	0	5.54.E+08	6.18.E+08	6.30.E+08	6.10.E+08	6.75.E+08	6.79.E+08	6.41.E+08	7.47.E+08
460	P55327	Tumor protein D52 [OS=Homo sapiens]	109.2	60	9	455	9	7266	663	9	9	0	3.71.E+08	4.29.E+08	4.19.E+08	4.33.E+08	6.35.E+08	6.25.E+08	6.13.E+08	6.44.E+08
461	P25787	Proteasome subunit alpha type-2 [OS=Homo sapiens]	108.6	36	7	453	7	6692	608	7	7	0	4.53.E+08	4.72.E+08	4.30.E+08	4.46.E+08	5.02.E+08	5.17.E+08	5.09.E+08	5.12.E+08
462	Q86V81	THO complex subunit 4 [OS=Homo sapiens]	108.6	42	6	383	6	8201	624	6	6	0	8.81.E+08	7.93.E+08	8.26.E+08	8.71.E+08	7.85.E+08	7.29.E+08	7.81.E+08	7.49.E+08
463	P30040-1	Endoplasmic reticulum resident protein 29 [OS=Homo sapiens]	108.5	52	10	786	10	11146	1018	10	10	0	1.30.E+09	1.31.E+09	1.30.E+09	1.33.E+09	1.50.E+09	1.44.E+09	1.39.E+09	1.45.E+09
464	Q92973-1	transportin-1 [OS=Homo sapiens]	108.5	30	18	443	18	3230	372	17	16	0	6.35.E+08	6.53.E+08	6.30.E+08	6.04.E+08	6.38.E+08	6.53.E+08	6.34.E+08	6.63.E+08
465	Q3LXA3	Triokinase/FMN cyclase [OS=Homo sapiens]	108.4	41	14	207	14	2371	213	14	12	0	3.32.E+08	3.49.E+08	3.29.E+08	3.25.E+08	3.89.E+08	4.24.E+08	2.85.E+08	4.00.E+08
466	P61313-1	60S ribosomal protein L15 [OS=Homo sapiens]	108.2	43	10	889	10	7698	899	10	10	0	1.66.E+09	1.73.E+09	1.79.E+09	1.76.E+09	1.38.E+09	1.47.E+09	1.53.E+09	1.44.E+09
467	Q9UBT2	SUMO-activating enzyme subunit 2 [OS=Homo sapiens]	108.2	36	14	302	14	1755	292	14	14	0	3.74.E+08	4.09.E+08	3.82.E+08	3.73.E+08	2.62.E+08	2.58.E+08	2.34.E+08	2.38.E+08
468	O14979-1	Heterogeneous nuclear ribonucleoprotein D-like [OS=Homo sapiens]	107.1	27	12	797	9	6657	774	12	12	0	6.09.E+08	6.24.E+08	6.36.E+08	5.70.E+08	5.68.E+08	5.85.E+08	5.82.E+08	5.72.E+08
469	P80723	Brain acid soluble protein 1 [OS=Homo sapiens]	107.1	70	11	499	11	4953	671	11	11	0	3.38.E+08	3.28.E+08	3.44.E+08	3.94.E+08	8.46.E+08	8.49.E+08	9.07.E+08	8.60.E+08
470	P42166	Lamina-associated polypeptide 2, isoform alpha [OS=Homo sapiens]	107.0	24	8	407	3	5349	488	8	8	0	2.96.E+07	3.35.E+07	4.53.E+07	2.57.E+07	2.53.E+07	3.26.E+07	2.55.E+07	3.44.E+07
471	P05023	Sodium/potassium-transporting ATPase subunit alpha-1 [OS=Homo sapiens]	106.8	20	14	267	14	2883	349	14	14	0	5.79.E+08	6.15.E+08	6.10.E+08	6.23.E+08	6.05.E+08	5.20.E+08	6.11.E+08	5.36.E+08
472	P46776	60S ribosomal protein L27a [OS=Homo sapiens]	106.8	33	9	561	9	11689	815	9	9	0	1.38.E+09	1.91.E+09	1.42.E+09	1.77.E+09	1.29.E+09	1.29.E+09	1.35.E+09	1.28.E+09
473	Q15366-6	Isoform 6 of Poly(rC)-binding protein 2 [OS=Homo sapiens]	106.6	61	12	429	2		1243	12		7	1.38.E+09	1.40.E+09	1.38.E+09	1.34.E+09	1.33.E+09	1.35.E+09	1.34.E+09	1.38.E+09
474	P68431	Histone H3.1 [OS=Homo sapiens]	106.0	48	6	1649	1	28822	2186	6	5	5	2.11.E+10	1.87.E+10	2.02.E+10	2.34.E+10	1.63.E+10	1.51.E+10	1.80.E+10	1.55.E+10
475	P11766	alcohol dehydrogenase class-3 [OS=Homo sapiens]	106.0	45	13	242	13	2760	320	13	11	0	4.47.E+08	4.54.E+08	4.54.E+08	4.74.E+08	5.66.E+08	6.05.E+08	6.03.E+08	5.91.E+08
476	P53992	Protein transport protein sec24c [OS=Homo sapiens]	106.0	18	14	311	13	3400	299	14	13	0	3.05.E+08	2.90.E+08	2.75.E+08	2.89.E+08	3.58.E+08	3.37.E+08	3.06.E+08	3.58.E+08
477	P08134	Rho-related GTP-binding protein RhoC [OS=Homo sapiens]	105.8	63	9	625	1	10036	914	9	9	0	1.88.E+07	2.17.E+07	1.72.E+07	1.94.E+07	9.96.E+06	9.85.E+06	8.18.E+06	9.15.E+06
478	P33316-3	Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial [OS=Homo sapiens]	105.6	38	8	652	8	11499	1042	8	8	0	1.36.E+09	1.40.E+09	1.46.E+09	1.37.E+09	1.81.E+09	1.81.E+09	1.66.E+09	1.81.E+09
479	Q9UK76	Jupiter microtubule associated homolog 1 [OS=Homo sapiens]	105.4	65	5	359	5	5479	760	5	5	0	6.06.E+08	6.25.E+08	6.35.E+08	6.04.E+08	4.36.E+08	4.50.E+08	4.54.E+08	4.84.E+08
480	P05091	Aldehyde dehydrogenase, mitochondrial [OS=Homo sapiens]	105.1	39	14	383	12	4148	467	14	13	0	3.99.E+08	4.11.E+08	3.86.E+08	4.16.E+08	4.75.E+08	4.74.E+08	4.31.E+08	4.62.E+08
481	Q96TA1	Niban-like protein 1 [OS=Homo sapiens]	105.1	23	11	382	11	4753	478	11	10	0	3.47.E+08	4.02.E+08	3.26.E+08	3.68.E+08	2.77.E+08	2.67.E+08	2.27.E+08	2.69.E+08
482	O00625	Pirin [OS=Homo sapiens]	104.9	61	10	505	10	4068	607	10	10	0	6.32.E+08	6.46.E+08	6.29.E+08	6.35.E+08	8.66.E+08	8.25.E+08	8.35.E+08	8.48.E+08
483	P14550	alcohol dehydrogenase [NADP(+)] [OS=Homo sapiens]	104.8	54	12	256	11	3855	381	11	12	0	5.41.E+08	5.64.E+08	5.65.E+08	5.45.E+08	5.63.E+08	5.70.E+08	5.96.E+08	6.03.E+08
484	Q96AE4	Far upstream element-binding protein 1 [OS=Homo sapiens]	104.7	27	15	537	11	6481	606	15	15	2	1.01.E+09	9.67.E+08	9.99.E+08	9.97.E+08	9.41.E+08	9.81.E+08	9.84.E+08	9.52.E+08
485	O60763-1	General vesicular transport factor p115 [OS=Homo sapiens]	104.3	17	12	278	12	2908	271	12	12	0	1.77.E+08	2.95.E+08	1.73.E+08	3.01.E+08	4.01.E+08	2.64.E+08	4.01.E+08	3.79.E+08
486	Q14166	Tubulin--tyrosine ligase-like protein 12 [OS=Homo sapiens]	104.0	34	12	274	12	3227	406	12	12	0	2.99.E+08	2.65.E+08	2.77.E+08	3.18.E+08	3.05.E+08	3.37.E+08	2.81.E+08	3.21.E+08
487	P60660	Myosin light polypeptide 6 [OS=Homo sapiens]	104.0	56	8	796	8	10534	948	6	8	0	2.06.E+09	2.35.E+09	2.37.E+09	2.39.E+09	2.53.E+09	2.54.E+09	2.60.E+09	2.53.E+09
488	P00491	purine nucleoside phosphorylase [OS=Homo sapiens]	103.8	48	11	338	11	4977	433	11	11	0	3.94.E+08	4.15.E+08	3.71.E+08	3.91.E+08	3.62.E+08	3.95.E+08	3.61.E+08	3.89.E+08
489	P07910-2	Isoform C1 of Heterogeneous nuclear ribonucleoproteins C1/C2 [OS=Homo sapiens]	103.6	36	14	567	1		1381	14		13	4.08.E+09	4.08.E+09	4.20.E+09	4.12.E+09	4.18.E+09	4.34.E+09	4.55.E+09	4.39.E+09
490	O00264	Membrane-associated progesterone receptor component 1 [OS=Homo sapiens]	103.4	57	9	267	8	4885	430	9	8	1	3.75.E+08	3.78.E+08	3.84.E+08	3.55.E+08	4.06.E+08	4.02.E+08	4.12.E+08	4.09.E+08
491	Q70J99-1	Protein unc-13 homolog D [OS=Homo sapiens]	103.1	18	10	338	10	4803	425	10	10	0	2.19.E+08	2.22.E+08	1.45.E+08	2.61.E+08	1.58.E+08	1.40.E+08	1.37.E+08	1.78.E+08
492	Q15185	Prostaglandin E synthase 3 [OS=Homo sapiens]	103.0	39	7	510	7	7081	711	7	7	0	2.34.E+09	2.33.E+09	2.35.E+09	2.10.E+09	2.65.E+09	2.50.E+09	2.81.E+09	2.77.E+09
493	P20290-1	transcription factor BTF3 [OS=Homo sapiens]	102.7	49	6	412	6	8102	706	6	6	0	4.64.E+08	4.71.E+08	4.61.E+08	4.43.E+08	4.06.E+08	4.02.E+08	3.95.E+08	3.79.E+08
494	Q13283	Ras GTPase-activating protein-binding protein 1 [OS=Homo sapiens]	102.7	41	11	417	10	3431	379	10	10	0	4.41.E+08	5.45.E+08	4.96.E+08	4.66.E+08	4.75.E+08	5.18.E+08	4.75.E+08	5.63.E+08
495	Q15366-4	Isoform 4 of Poly(rC)-binding protein 2 [OS=Homo sapiens]	102.6	71	12	433	2		1304	12		0	1.54.E+08	1.69.E+08	1.49.E+08	1.80.E+08	1.46.E+08	1.44.E+08	1.20.E+08	1.45.E+08
496	P60900	Proteasome subunit alpha type-6 [OS=Homo sapiens]	102.6	50	11	385	11	4512	475	11	11	0	6.59.E+08	6.69.E+08	6.75.E+08	6.80.E+08	7.86.E+08	7.69.E+08	7.98.E+08	7.69.E+08
497	P62917	60S ribosomal protein L8 [OS=Homo sapiens]	102.3	50	11	700	11	7870	821	11	11	0	1.35.E+09	1.21.E+09	1.37.E+09	1.46.E+09	1.02.E+09	1.05.E+09	1.14.E+09	1.06.E+09
498	P05141	ADP/ATP translocase 2 [OS=Homo sapiens]	101.8	45	16	758	5	6552	651	15	16	0	4.88.E+08	4.20.E+08	5.00.E+08	4.91.E+08	4.47.E+08	4.30.E+08	4.82.E+08	4.16.E+08
499	P06899	Histone H2B type 1-J [OS=Homo sapiens]	101.7	41	6	2455	2	40546	2003	6	6	0	2.56.E+09	2.41.E+09	2.61.E+09	2.66.E+09	2.79.E+09	2.54.E+09	2.85.E+09	2.67.E+09

No.	Accession	Description	Sum PEP Score	Coverage [%]	# Peptides	# PSMs	# Unique Peptides	Score Mascot: A5 Mascot	Score Sequest HT: A2 Sequest HT	# Peptides (by Search Engine): A2 Sequest HT	# Peptides (by Search Engine): A5 Mascot	# Razor Peptides	ctrl Abundances_1	ctrl Abundances_2	ctrl Abundances_3	ctrl Abundances_4	JAM-A KO Abundances_1	JAM-A KO Abundances_2	JAM-A KO Abundances_3	JAM-A KO Abundances_4
500	P05556-1	Integrin beta-1 [OS=Homo sapiens]	101.7	21	10	381	10	3862	477	10	9	0	3.46.E+08	4.49.E+08	3.64.E+08	3.92.E+08	5.54.E+08	5.86.E+08	4.91.E+08	4.93.E+08
501	P04181-1	Ornithine aminotransferase, mitochondrial [OS=Homo sapiens]	101.4	38	10	179	10	3065	268	10	10	0	3.00.E+08	3.08.E+08	3.03.E+08	2.99.E+08	3.16.E+08	3.12.E+08	3.15.E+08	3.11.E+08
502	Q9UBB4-1	Ataxin-10 [OS=Homo sapiens]	101.3	39	10	324	10	3808	362	10	10	0	2.30.E+08	2.03.E+08	1.91.E+08	1.79.E+08	2.55.E+08	2.44.E+08	2.61.E+08	2.60.E+08
503	P30084	Enoyl-CoA hydratase, mitochondrial [OS=Homo sapiens]	101.2	42	10	324	10	5458	457	10	10	0	5.19.E+08	5.04.E+08	5.38.E+08	5.84.E+08	4.75.E+08	4.59.E+08	4.73.E+08	4.77.E+08
504	O96008	Mitochondrial import receptor subunit TOM40 homolog [OS=Homo sapiens]	101.2	40	9	412	9	6235	481	9	9	0	3.69.E+08	4.04.E+08	3.79.E+08	3.98.E+08	2.06.E+08	1.69.E+08	1.62.E+08	1.63.E+08
505	O60814	Histone H2B type 1-K [OS=Homo sapiens]	101.1	41	6	2653	2	43470	2266	6	6	7	3.12.E+10	3.05.E+10	3.23.E+10	2.94.E+10	3.03.E+10	3.00.E+10	3.24.E+10	3.03.E+10
506	P0C0S5	Histone H2A.Z [OS=Homo sapiens]	101.0	54	6	1091	4	7358	1218	6	6	0	1.75.E+09	1.69.E+09	1.78.E+09	1.79.E+09	1.76.E+09	1.71.E+09	1.85.E+09	1.69.E+09
507	P18465	HLA class I histocompatibility antigen, B-57 alpha chain [OS=Homo sapiens]	100.7	33	8	385	1	5504	549	8	8	1	1.59.E+08	1.42.E+08	1.57.E+08	1.48.E+08	1.95.E+08	1.76.E+08	1.85.E+08	1.87.E+08
508	Q6NZI2-1	caveolae-associated protein 1 [OS=Homo sapiens]	100.6	29	9	296	9	3931	300	9	9	0	3.13.E+08	2.86.E+08	3.30.E+08	2.60.E+08	3.60.E+08	3.45.E+08	3.98.E+08	3.97.E+08
509	P60228	Eukaryotic translation initiation factor 3 subunit E [OS=Homo sapiens]	100.3	38	11	367	11	3170	402	11	11	0	4.00.E+08	3.79.E+08	3.43.E+08	3.84.E+08	3.44.E+08	3.51.E+08	3.52.E+08	3.68.E+08
510	P60981-1	Destrin [OS=Homo sapiens]	100.2	64	10	402	9	4457	347	9	10	0	6.67.E+08	6.44.E+08	6.33.E+08	6.20.E+08	7.38.E+08	7.37.E+08	7.88.E+08	7.65.E+08
511	P43487	Ran-specific GTPase-activating protein [OS=Homo sapiens]	99.9	60	7	408	7	7675	903	7	7	0	1.27.E+09	1.30.E+09	1.28.E+09	1.22.E+09	1.35.E+09	1.41.E+09	1.20.E+09	1.34.E+09
512	Q9BT78	COP9 signalosome complex subunit 4 [OS=Homo sapiens]	99.8	39	11	303	11	2898	341	11	11	0	1.92.E+08	2.12.E+08	2.01.E+08	2.00.E+08	2.49.E+08	3.08.E+08	2.94.E+08	2.22.E+08
513	P52306-1	Rap1 GTPase-GDP dissociation stimulator 1 [OS=Homo sapiens]	99.7	28	9	160	9	2641	182	9	9	0	5.74.E+07	6.18.E+07	5.85.E+07	7.01.E+07	7.65.E+07	5.99.E+07	5.27.E+07	5.85.E+07
514	Q9BTT0	Acidic leucine-rich nuclear phosphoprotein 32 family member E [OS=Homo sapiens]	99.4	41	7	364	7	7827	612	7	7	0	4.15.E+08	4.36.E+08	3.99.E+08	4.04.E+08	7.24.E+08	7.42.E+08	6.83.E+08	7.14.E+08
515	P84085	ADP-ribosylation factor 5 [OS=Homo sapiens]	99.1	42	8	577	1	6847	882	7	8	0	1.46.E+08	1.35.E+08	6.46.E+07	6.86.E+07	1.33.E+08	1.19.E+08	1.16.E+08	1.13.E+08
516	Q8IUE6	Histone H2A type 2-B [OS=Homo sapiens]	99.1	58	5	1256	3	18757	1997	5	5	0	1.89.E+09	2.04.E+09	1.94.E+09	2.16.E+09	2.59.E+09	2.38.E+09	2.35.E+09	2.43.E+09
517	Q9H0A0	RNA cytidine acetyltransferase [OS=Homo sapiens]	99.0	17	9	263	9	3929	272	9	9	0	1.56.E+08	1.88.E+08	1.48.E+08	1.54.E+08	1.31.E+08	2.00.E+08	1.23.E+08	1.66.E+08
518	O76094	Signal recognition particle subunit SRP72 [OS=Homo sapiens]	98.9	25	11	365	11	3960	487	11	11	0	2.12.E+08	2.30.E+08	1.99.E+08	2.19.E+08	2.47.E+08	1.82.E+08	1.64.E+08	2.04.E+08
519	P62841	40S ribosomal protein S15 [OS=Homo sapiens]	98.9	56	5	366	5	4722	471	5	5	0	4.41.E+08	4.11.E+08	3.73.E+08	4.32.E+08	2.92.E+08	2.89.E+08	2.94.E+08	2.78.E+08
520	P55265-1	Double-stranded RNA-specific adenosine deaminase [OS=Homo sapiens]	98.7	17	16	242	16	1516	199	16	16	0	4.38.E+08	3.74.E+08	3.88.E+08	4.26.E+08	4.41.E+08	4.45.E+08	4.32.E+08	3.98.E+08
521	Q14914	Prostaglandin reductase 1 [OS=Homo sapiens]	98.7	45	9	348	9	5391	539	9	9	0	4.22.E+08	3.99.E+08	3.99.E+08	3.90.E+08	7.04.E+08	6.75.E+08	6.26.E+08	7.18.E+08
522	P14314	Glucosidase 2 subunit beta [OS=Homo sapiens]	98.4	28	11	382	11	5950	467	11	11	0	9.73.E+08	8.57.E+08	8.75.E+08	8.78.E+08	1.01.E+09	1.02.E+09	1.04.E+09	1.01.E+09
523	Q01105	Protein SET [OS=Homo sapiens]	98.3	45	9	669	9	7843	975	9	9	0	1.87.E+09	1.83.E+09	1.87.E+09	1.96.E+09	1.69.E+09	1.68.E+09	1.75.E+09	1.64.E+09
524	P36776	Lon protease homolog, mitochondrial [OS=Homo sapiens]	97.4	22	11	422	11	3509	440	11	11	0	1.82.E+08	1.98.E+08	1.78.E+08	2.02.E+08	1.64.E+08	1.64.E+08	1.56.E+08	1.62.E+08
525	P26368	Splicing factor U2AF 65 kDa subunit [OS=Homo sapiens]	97.4	27	9	362	9	5293	645	9	9	0	5.85.E+08	5.17.E+08	5.33.E+08	4.96.E+08	3.89.E+08	3.84.E+08	3.02.E+08	3.61.E+08
526	P31930	Cytochrome b-c1 complex subunit 1, mitochondrial [OS=Homo sapiens]	97.3	30	9	325	9	4210	432	9	9	0	4.09.E+08	4.05.E+08	4.24.E+08	3.95.E+08	4.37.E+08	4.42.E+08	3.96.E+08	3.83.E+08
527	P49720	proteasome subunit beta type-3 [OS=Homo sapiens]	97.0	45	8	328	8	6174	398	8	8	0	4.19.E+08	3.74.E+08	3.86.E+08	3.79.E+08	3.84.E+08	3.99.E+08	3.68.E+08	4.04.E+08
528	Q15437	protein transport protein Sec23B [OS=Homo sapiens]	96.9	21	12	260	10	2656	210	11	12	2	2.31.E+08	2.44.E+08	2.14.E+08	2.42.E+08	2.61.E+08	2.59.E+08	2.58.E+08	2.36.E+08
529	P06132	Uroporphyrinogen decarboxylase [OS=Homo sapiens]	96.9	51	10	180	10	3051	225	10	9	0	2.51.E+08	2.49.E+08	2.48.E+08	2.23.E+08	2.23.E+08	2.30.E+08	2.31.E+08	2.36.E+08
530	P04908	histone H2A type 1-B/E [OS=Homo sapiens]	96.8	58	7	2068	2	22620	2870	7	7	5	4.00.E+10	3.88.E+10	4.09.E+10	4.06.E+10	4.09.E+10	4.12.E+10	4.44.E+10	4.28.E+10
531	P62753	40S RIBOSOMAL PROTEIN S6 [OS=Homo sapiens]	96.7	26	9	400	9	5334	521	9	8	0	1.54.E+09	1.46.E+09	1.52.E+09	1.55.E+09	1.32.E+09	1.28.E+09	1.37.E+09	1.29.E+09
532	P54886	delta-1-pyrroline-5-carboxylate synthase [OS=Homo sapiens]	96.5	23	12	354	12	3885	454	12	12	0	3.16.E+08	3.51.E+08	3.07.E+08	3.49.E+08	3.76.E+08	4.09.E+08	3.32.E+08	3.70.E+08
533	Q9Y281-1	Cofilin-2 [OS=Homo sapiens]	96.2	43	8	858	2	14255	1286	8	7	0	3.79.E+07	4.45.E+07	2.01.E+07	4.51.E+07	6.26.E+07	3.23.E+07	2.14.E+07	5.68.E+07
534	P54727	UV excision repair protein RAD23 homolog B [OS=Homo sapiens]	96.2	29	8	336	8	5902	434	8	8	0	2.51.E+08	2.31.E+08	2.50.E+08	2.80.E+08	3.20.E+08	3.12.E+08	3.31.E+08	3.16.E+08
535	P30046	D-dopachrome decarboxylase [OS=Homo sapiens]	96.2	50	7	432	7	7491	443	4	7	0	1.27.E+09	1.22.E+09	1.25.E+09	1.17.E+09	1.18.E+09	1.24.E+09	1.26.E+09	1.22.E+09
536	P48047	ATP synthase subunit O, mitochondrial [OS=Homo sapiens]	96.2	45	8	401	8	7561	628	8	8	0	7.39.E+08	6.80.E+08	7.50.E+08	7.24.E+08	8.87.E+08	8.80.E+08	9.78.E+08	9.19.E+08
537	P26583	High mobility group protein B2 [OS=Homo sapiens]	96.1	41	9	543	7	6340	665	9	9	0	4.73.E+08	4.15.E+08	4.74.E+08	4.35.E+08	6.10.E+08	5.82.E+08	6.29.E+08	6.07.E+08
538	Q53GQ0	Very-long-chain 3-oxoacyl-CoA reductase [OS=Homo sapiens]	96.0	37	9	283	9	4668	329	9	9	0	2.44.E+08	2.66.E+08	2.52.E+08	2.78.E+08	3.46.E+08	3.37.E+08	3.15.E+08	3.37.E+08
539	P17931	Galectin-3 [OS=Homo sapiens]	95.9	32	7	537	7	4436	675	7	7	0	1.36.E+09	1.27.E+09	1.42.E+09	1.39.E+09	1.29.E+09	1.24.E+09	1.41.E+09	1.30.E+09
540	Q9UHB9	Signal recognition particle subunit SRP68 [OS=Homo sapiens]	95.2	31	10	252	10	3626	313	10	10	0	2.55.E+08	2.96.E+08	2.27.E+08	2.41.E+08	3.87.E+08	3.59.E+08	3.05.E+08	3.31.E+08
541	P13693	Translationally-controlled tumor protein [OS=Homo sapiens]	94.7	73	10	467	10	4873	740	10	10	0	5.65.E+08	6.17.E+08	5.79.E+08	5.86.E+08	5.74.E+08	6.20.E+08	5.98.E+08	5.88.E+08
542	P50502	Hsc70-interacting protein [OS=Homo sapiens]	94.1	23	7	415	7	5126	607	7	7	0	1.01.E+09	1.02.E+09	1.03.E+09	9.52.E+08	1.31.E+09	1.33.E+09	1.36.E+09	1.32.E+09
543	Q96KP4	cytosolic non-specific dipeptidase [OS=Homo sapiens]	93.9	44	12	387	12	5386	555	12	11	0	2.63.E+08	3.43.E+08	2.74.E+08	3.30.E+08	3.89.E+08	3.71.E+08	3.11.E+08	3.43.E+08
544	Q9Y230	RuvB-like 2 [OS=Homo sapiens]	93.4	34	12	310	12	3331	422	11	12	0	4.57.E+08	5.88.E+08	5.25.E+08	6.00.E+08	5.06.E+08	4.99.E+08	5.04.E+08	4.65.E+08
545	P20618	proteasome subunit beta type-1 [OS=Homo sapiens]	93.3	49	9	342	9	3860	373	9	8	0	5.92.E+08	5.55.E+08	5.98.E+08	6.22.E+08	6.33.E+08	6.24.E+08	6.64.E+08	6.33.E+08
546	Q13620	Cullin-4B [OS=Homo sapiens]	92.7	22	16	196	16	2115	155	16	16	0	1.30.E+08	1.57.E+08	1.09.E+08	1.38.E+08	2.49.E+08	2.57.E+08	1.68.E+08	2.52.E+08
547	P54920	alpha-soluble nsf attachment protein [OS=Homo sapiens]	92.7	48	9	153	9	1296	167	9	9	0	3.01.E+08	3.07.E+08	3.10.E+08	3.01.E+08	2.36.E+08	2.17.E+08	2.56.E+08	1.88.E+08
548	Q07960	rho GTPase-activating protein 1 [OS=Homo sapiens]	92.5	36	9	303	9	4340	465	9	8	0	1.66.E+08	1.88.E+08	1.65.E+08	2.08.E+08	2.20.E+08	2.10.E+08	2.26.E+08	2.24.E+08
549	Q9Y3I0	tRNA-splicing ligase RtcB homolog [OS=Homo sapiens]	92.4	26	9	281	9	3825	371	9	8	0	2.93.E+08	3.10.E+08	2.91.E+08	2.86.E+08	2.95.E+08	2.95.E+08	2.95.E+08	2.89.E+08
550	Q86VI3	Ras GTPase-activating-like protein IQGAP3 [OS=Homo sapiens]	92.3	12	14	138	10	1470	101	14	14	0	2.84.E+07	4.14.E+07	2.68.E+07	4.23.E+07	6.89.E+07	6.05.E+07	5.65.E+07	7.76.E+07
551	P30048	Thioredoxin-dependent peroxide reductase, mitochondrial [OS=Homo sapiens]	92.1	53	9	516	9	4892	743	9	9	0	1.26.E+09	1.21.E+09	1.26.E+09	1.29.E+09	1.77.E+09	1.71.E+09	1.34.E+09	1.67.E+09
552	Q14247-1	Src substrate cortactin [OS=Homo sapiens]	92.0	30	12	206	12	4254	311	12	12	0	2.23.E+08	2.39.E+08	2.31.E+08	2.53.E+08	3.75.E+08	3.88.E+08	3.36.E+08	3.72.E+08
553	Q9H6S3	epidermal growth factor receptor kinase substrate 8-like protein 2 [OS=Homo sapiens]	92.0	25	8	187	8	4036	287	8	8	0	9.51.E+07	9.32.E+07	8.50.E+07	9.63.E+07	1.24.E+08	1.13.E+08	1.20.E+08	1.23.E+08

No.	Accession	Description	Sum PEP Score	Coverage [%]	# Peptides	# PSMs	# Unique Peptides	Score Mascot: A5 Mascot	Score Sequest HT: A2 Sequest HT	# Peptides (by Search Engine): A2 Sequest HT	# Peptides (by Search Engine): A5 Mascot	# Razor Peptides	ctrl Abundance s_1	ctrl Abundance s_2	ctrl Abundance s_3	ctrl Abundance s_4	JAM-A KO Abundance s_1	JAM-A KO Abundance s_2	JAM-A KO Abundance s_3	JAM-A KO Abundance s_4
554	P62191	26S proteasome regulatory subunit 4 [OS=Homo sapiens]	91.9	37	13	425	12	5613	601	13	13	1	6.26.E+08	6.45.E+08	6.50.E+08	6.52.E+08	6.04.E+08	6.34.E+08	6.69.E+08	6.66.E+08
555	Q99829	Copine-1 [OS=Homo sapiens]	91.6	20	7	569	7	13168	943	6	7	0	3.76.E+08	4.01.E+08	3.71.E+08	3.97.E+08	3.64.E+08	3.71.E+08	3.19.E+08	3.72.E+08
556	P28482	mitogen-activated protein kinase 1 [OS=Homo sapiens]	91.5	43	11	303	11	1589	325	10	11	0	5.66.E+08	5.46.E+08	6.39.E+08	5.09.E+08	7.60.E+08	7.67.E+08	8.47.E+08	8.22.E+08
557	Q13185	chromobox protein homolog 3 [OS=Homo sapiens]	91.1	54	7	454	5	6401	693	7	7	1	7.88.E+08	7.74.E+08	7.74.E+08	8.07.E+08	7.25.E+08	6.83.E+08	7.14.E+08	7.11.E+08
558	P46783	40S ribosomal protein S10 [OS=Homo sapiens]	90.9	42	7	745	7	11330	1117	7	7	0	1.01.E+09	1.06.E+09	9.99.E+08	1.12.E+09	1.74.E+09	1.69.E+09	1.09.E+09	1.64.E+09
559	P07384	Calpain-1 catalytic subunit [OS=Homo sapiens]	90.7	25	12	238	12	1685	288	12	12	0	4.41.E+08	4.45.E+08	4.51.E+08	4.01.E+08	3.01.E+08	3.36.E+08	2.60.E+08	3.00.E+08
560	O14579-1	coatomer subunit epsilon [OS=Homo sapiens]	90.5	51	8	105	8	2759	184	8	8	0	9.86.E+07	1.14.E+08	9.79.E+07	1.27.E+08	1.34.E+08	1.28.E+08	1.22.E+08	1.41.E+08
561	Q31612	HLA class I histocompatibility antigen, B-73 alpha chain [OS=Homo sapiens]	90.2	31	8	334	3	4943	455	8	8	3	1.64.E+08	1.75.E+08	1.84.E+08	1.54.E+08	1.90.E+08	1.97.E+08	2.08.E+08	1.88.E+08
562	P07858	Cathepsin B [OS=Homo sapiens]	90.0	32	9	499	9	7961	699	9	9	0	9.16.E+08	9.04.E+08	9.75.E+08	8.86.E+08	8.54.E+08	9.04.E+08	9.65.E+08	8.85.E+08
563	P04080	Cystatin-B [OS=Homo sapiens]	89.8	70	4	465	4	6398	696	4	4	0	1.91.E+09	1.80.E+09	1.93.E+09	1.62.E+09	1.39.E+09	1.40.E+09	1.55.E+09	1.51.E+09
564	P62333	26S proteasome regulatory subunit 10B [OS=Homo sapiens]	89.7	38	10	184	10	2594	249	10	10	0	2.54.E+08	2.52.E+08	2.44.E+08	2.75.E+08	3.28.E+08	2.94.E+08	3.23.E+08	3.02.E+08
565	P78347	General transcription factor II-I [OS=Homo sapiens]	89.6	17	10	188	10	1832	256	10	10	0	2.28.E+08	2.35.E+08	2.36.E+08	2.43.E+08	2.83.E+08	2.99.E+08	2.68.E+08	2.81.E+08
566	P50238	Cysteine-rich protein 1 [OS=Homo sapiens]	89.3	68	5	662	5	3112	755	5	5	0	4.79.E+09	4.22.E+09	4.75.E+09	5.51.E+09	1.75.E+09	1.79.E+09	2.11.E+09	1.85.E+09
567	P0CG39	POTE ankyrin domain family member J [OS=Homo sapiens]	89.2	8	6	1629	2	23637	1967	6	5	0	4.00.E+08	4.20.E+08	4.43.E+08	3.83.E+08	5.64.E+08	5.44.E+08	4.90.E+08	5.51.E+08
568	P39748	Flap endonuclease 1 [OS=Homo sapiens]	89.1	37	9	416	9	4474	616	9	8	0	6.51.E+08	6.76.E+08	6.52.E+08	6.27.E+08	7.34.E+08	7.39.E+08	6.85.E+08	6.57.E+08
569	O95571	Persulfide dioxygenase ETHE1, mitochondrial [OS=Homo sapiens]	88.9	54	7	190	7	3585	316	7	7	0	3.07.E+08	3.27.E+08	2.88.E+08	2.94.E+08	2.97.E+08	2.98.E+08	2.63.E+08	2.60.E+08
570	P38159-1	RNA-binding motif protein, X chromosome [OS=Homo sapiens]	88.6	26	10	575	10	5987	524	10	10	0	8.94.E+08	8.75.E+08	9.21.E+08	9.04.E+08	8.66.E+08	8.46.E+08	9.01.E+08	8.86.E+08
571	P51149	ras-related protein Rab-7a [OS=Homo sapiens]	88.6	66	11	317	11	2380	451	11	11	0	6.90.E+08	7.08.E+08	7.09.E+08	6.63.E+08	7.41.E+08	7.76.E+08	6.19.E+08	7.41.E+08
572	Q04917	14-3-3 protein eta [OS=Homo sapiens]	88.5	40	12	928	8	9044	909	12	12	0	2.11.E+08	2.17.E+08	2.13.E+08	2.28.E+08	2.27.E+08	2.24.E+08	2.20.E+08	2.28.E+08
573	Q13045-1	protein flightless-1 homolog [OS=Homo sapiens]	88.5	18	13	288	13	3072	317	13	13	0	2.30.E+08	2.40.E+08	2.13.E+08	2.41.E+08	2.02.E+08	2.05.E+08	1.46.E+08	1.82.E+08
574	Q9GZT3-1	SRA stem-loop-interacting RNA-binding protein, mitochondrial [OS=Homo sapiens]	88.4	78	8	345	8	2701	443	8	8	0	4.60.E+08	4.24.E+08	4.53.E+08	4.83.E+08	5.70.E+08	5.47.E+08	6.07.E+08	5.67.E+08
575	Q96HE7	ERO1-like protein alpha [OS=Homo sapiens]	88.4	37	12	280	12	3339	276	12	12	0	2.56.E+08	2.64.E+08	2.52.E+08	2.45.E+08	3.68.E+08	3.01.E+08	3.09.E+08	3.04.E+08
576	Q13155	aminoacyl tRNA synthase complex-interacting multifunctional protein 2 [OS=Homo sapiens]	88.4	52	10	332	10	4042	399	10	10	0	3.02.E+08	3.20.E+08	3.05.E+08	3.24.E+08	3.92.E+08	3.66.E+08	3.35.E+08	3.86.E+08
577	P20042	Eukaryotic translation initiation factor 2 subunit 2 [OS=Homo sapiens]	88.4	42	13	354	13	3999	469	13	12	0	7.35.E+08	7.06.E+08	7.60.E+08	6.91.E+08	7.10.E+08	7.07.E+08	7.35.E+08	7.23.E+08
578	O75116	Rho-associated protein kinase 2 [OS=Homo sapiens]	87.7	16	15	200	15	1470	196	13	15	0	2.19.E+08	2.55.E+08	2.41.E+08	2.43.E+08	3.51.E+08	3.55.E+08	3.03.E+08	3.48.E+08
579	O75694	nuclear pore complex protein nup155 [OS=Homo sapiens]	87.6	12	9	295	9	3209	301	9	9	0	1.03.E+08	1.04.E+08	1.37.E+08	1.09.E+08	1.41.E+08	1.84.E+08	1.22.E+08	1.58.E+08
580	P24752	Acetyl-CoA acetyltransferase, mitochondrial [OS=Homo sapiens]	87.3	30	8	378	8	5098	478	8	8	0	2.59.E+08	2.57.E+08	2.56.E+08	2.66.E+08	3.18.E+08	3.15.E+08	3.13.E+08	3.23.E+08
581	Q14651	Plastin-1 [OS=Homo sapiens]	87.1	18	8	539	4	8881	768	8	8	0	1.04.E+08	1.06.E+08	1.05.E+08	1.05.E+08	1.24.E+08	1.15.E+08	1.28.E+08	1.23.E+08
582	Q10567-3	Isoform C of AP-1 complex subunit beta-1 [OS=Homo sapiens]	87.0	18	15	198	5		433	15		0	1.09.E+08	1.16.E+08	1.06.E+08	1.12.E+08	1.09.E+08	1.07.E+08	9.62.E+07	1.04.E+08
583	Q8N1F7-1	Nuclear pore complex protein Nup93 [OS=Homo sapiens]	86.8	24	10	191	10	4108	279	9	10	0	1.23.E+08	1.29.E+08	1.22.E+08	1.42.E+08	1.74.E+08	1.65.E+08	1.67.E+08	1.74.E+08
584	Q9BZZ5-4	Apoptosis inhibitor 5 [OS=Homo sapiens]	86.8	24	8	269	1	6033	398	7	8	6	2.88.E+08	2.76.E+08	2.64.E+08	2.20.E+08	3.07.E+08	3.33.E+08	3.32.E+08	2.94.E+08
585	P62244	40S ribosomal protein S15a [OS=Homo sapiens]	86.7	67	9	592	9	6342	694	9	9	0	2.00.E+09	1.96.E+09	2.12.E+09	1.92.E+09	1.79.E+09	1.68.E+09	1.96.E+09	1.82.E+09
586	Q9NQC3	Reticulon-4 [OS=Homo sapiens]	86.6	9	5	304	5	6406	564	5	5	0	6.08.E+08	5.78.E+08	6.04.E+08	6.18.E+08	6.52.E+08	6.80.E+08	7.62.E+08	6.90.E+08
587	P30050-1	60S ribosomal protein L12 [OS=Homo sapiens]	86.0	55	6	766	6	15694	1288	6	6	0	1.95.E+09	1.88.E+09	1.92.E+09	1.76.E+09	1.79.E+09	1.91.E+09	1.97.E+09	1.94.E+09
588	P08754	Guanine nucleotide-binding protein G(k) subunit alpha [OS=Homo sapiens]	86.0	47	11	225	8	3084	305	11	11	2	2.56.E+08	2.64.E+08	2.62.E+08	2.54.E+08	2.62.E+08	2.82.E+08	2.76.E+08	2.62.E+08
589	P47756-2	Isoform 2 of F-actin-capping protein subunit beta [OS=Homo sapiens]	85.7	48	10	127	10		421	10		0	3.72.E+08	3.67.E+08	3.71.E+08	3.25.E+08	4.43.E+08	4.57.E+08	4.85.E+08	4.33.E+08
590	Q96A72	protein mago nashi homolog 2 [OS=Homo sapiens]	85.5	53	6	250	6	1524	373	5	6	0	4.26.E+08	4.62.E+08	3.91.E+08	3.69.E+08	4.33.E+08	4.46.E+08	5.10.E+08	4.21.E+08
591	Q15813	Tubulin-specific chaperone E [OS=Homo sapiens]	85.5	29	8	281	8	4727	301	8	8	0	2.15.E+08	2.12.E+08	2.01.E+08	2.26.E+08	2.72.E+08	2.64.E+08	2.34.E+08	2.66.E+08
592	Q09028	Histone-binding protein RBBP4 [OS=Homo sapiens]	85.3	45	10	382	6	4755	236	9	10	0	2.80.E+08	3.14.E+08	2.88.E+08	3.07.E+08	3.70.E+08	3.55.E+08	3.37.E+08	3.59.E+08
593	Q15102	Platelet-activating factor acetylhydrolase IB subunit gamma [OS=Homo sapiens]	85.2	56	8	285	8	3989	305	7	8	0	4.74.E+08	4.79.E+08	3.80.E+08	4.77.E+08	3.53.E+08	2.98.E+08	3.30.E+08	2.88.E+08
594	P36957	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial [OS=Homo sapiens]	84.8	26	11	450	11	6222	534	11	10	0	1.24.E+09	1.25.E+09	1.23.E+09	1.08.E+09	1.40.E+09	1.41.E+09	1.50.E+09	1.43.E+09
595	Q9ULV4	coronin-1C [OS=Homo sapiens]	84.6	38	11	365	11	4879	530	11	11	0	3.65.E+08	3.77.E+08	3.71.E+08	4.53.E+08	4.22.E+08	4.55.E+08	3.95.E+08	4.48.E+08
596	Q9UNZ2	NSFL1 cofactor p47 [OS=Homo sapiens]	84.4	29	7	138	7	3139	214	7	7	0	1.38.E+08	1.44.E+08	1.38.E+08	1.49.E+08	1.65.E+08	1.73.E+08	1.64.E+08	1.58.E+08
597	Q96C36	Pyrroline-5-carboxylate reductase 2 [OS=Homo sapiens]	84.0	39	7	140	6	2868	218	6	7	0	1.51.E+08	1.43.E+08	1.56.E+08	1.50.E+08	1.65.E+08	1.46.E+08	1.66.E+08	1.64.E+08
598	Q5JWF2-1	Guanine nucleotide-binding protein G(S) subunit alpha isoforms XLas [OS=Homo sapiens]	83.9	15	11	385	9	4040	361	11	11	2	5.07.E+08	5.09.E+08	4.97.E+08	4.71.E+08	6.59.E+08	6.40.E+08	6.27.E+08	6.53.E+08
599	P24666-1	Low molecular weight phosphotyrosine protein phosphatase [OS=Homo sapiens]	83.9	61	8	319	8	4620	407	8	8	0	4.44.E+08	4.84.E+08	4.77.E+08	3.29.E+08	5.10.E+08	5.04.E+08	5.61.E+08	5.01.E+08
600	P35998	26S proteasome regulatory subunit 7 [OS=Homo sapiens]	83.7	40	13	313	13	2765	331	13	13	0	2.71.E+08	2.67.E+08	3.84.E+08	2.91.E+08	5.87.E+08	4.07.E+08	4.07.E+08	2.97.E+08
601	P05386	60S acidic ribosomal protein P1 [OS=Homo sapiens]	83.7	80	4	458	4	9699	808	2	4	0	1.95.E+09	2.15.E+09	1.96.E+09	2.13.E+09	1.79.E+09	1.72.E+09	1.59.E+09	1.72.E+09
602	P50579	methionine aminopeptidase 2 [OS=Homo sapiens]	83.6	38	10	160	10	1599	184	9	10	0	1.90.E+08	1.91.E+08	1.88.E+08	1.89.E+08	1.69.E+08	1.75.E+08	1.64.E+08	1.54.E+08
603	Q9BWD1	Acetyl-CoA acetyltransferase, cytosolic [OS=Homo sapiens]	83.3	41	7	304	7	3687	417	7	7	0	3.01.E+08	3.12.E+08	3.10.E+08	2.96.E+08	3.45.E+08	3.52.E+08	3.28.E+08	3.49.E+08
604	P49589-1	Cysteine--tRNA ligase, cytoplasmic [OS=Homo sapiens]	83.2	22	13	288	13	1597	357	13	13	0	3.60.E+08	3.44.E+08	3.20.E+08	3.61.E+08	3.53.E+08	3.79.E+08	2.88.E+08	3.62.E+08
605	O76021	Ribosomal L1 domain-containing protein 1 [OS=Homo sapiens]	83.2	29	12	287	12	3030	324	12	12	0	4.36.E+08	4.43.E+08	4.39.E+08	4.40.E+08	4.12.E+08	4.33.E+08	3.93.E+08	4.26.E+08
606	O43242	26S proteasome non-ATPase regulatory subunit 3 [OS=Homo sapiens]	83.1	28	11	345	11	4900	520	11	10	0	2.89.E+08	3.97.E+08	2.86.E+08	2.94.E+08	3.95.E+08	3.95.E+08	3.38.E+08	3.89.E+08

No.	Accession	Description	Sum PEP Score	Coverage [%]	# Peptides	# PSMs	# Unique Peptides	Score Mascot: A5 Mascot	Score Sequest HT: A2 Sequest HT	# Peptides (by Search Engine): A2 Sequest HT	# Peptides (by Search Engine): A5 Mascot	# Razor Peptides	ctrl Abundances_1	ctrl Abundances_2	ctrl Abundances_3	ctrl Abundances_4	JAM-A KO Abundances_1	JAM-A KO Abundances_2	JAM-A KO Abundances_3	JAM-A KO Abundances_4
607	Q9BX68	Histidine triad nucleotide-binding protein 2, mitochondrial [OS=Homo sapiens]	82.5	58	6	435	6	7251	631	6	6	0	5.64.E+08	5.99.E+08	5.59.E+08	5.67.E+08	8.10.E+08	8.27.E+08	7.95.E+08	7.96.E+08
608	P62879	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 [OS=Homo sapiens]	82.5	54	11	187	7	1805	208	10	11	0	2.59.E+08	2.45.E+08	2.51.E+08	2.82.E+08	3.08.E+08	2.69.E+08	2.56.E+08	2.77.E+08
609	Q9P258	Protein RCC2 [OS=Homo sapiens]	82.4	23	10	208	10	1539	181	10	9	0	4.66.E+08	4.61.E+08	4.28.E+08	3.76.E+08	3.69.E+08	3.66.E+08	4.04.E+08	4.06.E+08
610	P54819	Adenylate kinase 2, mitochondrial [OS=Homo sapiens]	82.4	38	6	356	6	8235	598	5	5	0	3.23.E+08	3.44.E+08	3.61.E+08	4.16.E+08	2.62.E+08	2.47.E+08	2.36.E+08	2.41.E+08
611	P18031	Tyrosine-protein phosphatase non-receptor type 1 [OS=Homo sapiens]	82.1	29	10	171	10	1454	226	10	10	0	2.62.E+08	2.64.E+08	2.86.E+08	2.62.E+08	4.64.E+08	4.31.E+08	4.67.E+08	4.57.E+08
612	O15144	Actin-related protein 2/3 complex subunit 2 [OS=Homo sapiens]	82.1	27	6	239	6	2959	347	6	6	0	2.79.E+08	2.47.E+08	2.26.E+08	2.63.E+08	2.81.E+08	2.47.E+08	2.70.E+08	2.99.E+08
613	P30740	Leukocyte elastase inhibitor [OS=Homo sapiens]	82.0	31	7	129	7	1534	158	7	7	0	1.76.E+08	1.73.E+08	1.91.E+08	1.94.E+08	1.18.E+08	1.12.E+08	9.89.E+07	1.13.E+08
614	Q9H9B4	Sideroflexin-1 [OS=Homo sapiens]	81.9	41	9	254	7	3278	279	9	8	2	3.94.E+08	3.79.E+08	3.88.E+08	3.78.E+08	3.59.E+08	3.43.E+08	3.38.E+08	3.58.E+08
615	Q9H2U2	Inorganic pyrophosphatase 2, mitochondrial [OS=Homo sapiens]	81.7	31	8	400	7	5158	359	8	8	0	2.19.E+08	2.65.E+08	1.65.E+08	2.12.E+08	3.17.E+08	3.08.E+08	2.78.E+08	3.01.E+08
616	Q9BR76	Coronin-1B [OS=Homo sapiens]	81.6	31	10	346	10	6025	555	10	10	0	5.24.E+08	5.05.E+08	5.18.E+08	4.95.E+08	5.88.E+08	5.83.E+08	5.33.E+08	5.61.E+08
617	P62195-1	26S proteasome regulatory subunit 8 [OS=Homo sapiens]	81.6	31	9	384	8	3279	484	9	9	0	3.95.E+08	4.23.E+08	3.76.E+08	3.51.E+08	4.15.E+08	4.25.E+08	3.72.E+08	4.04.E+08
618	P62888	60S ribosomal protein L30 [OS=Homo sapiens]	81.5	57	5	439	4	8801	793	5	4	0	1.03.E+09	1.02.E+09	1.06.E+09	1.03.E+09	9.22.E+08	9.25.E+08	9.49.E+08	8.97.E+08
619	O43809	Cleavage and polyadenylation specificity factor subunit 5 [OS=Homo sapiens]	81.4	52	8	429	8	4381	530	8	8	0	3.78.E+08	4.02.E+08	3.83.E+08	3.89.E+08	4.77.E+08	4.95.E+08	4.81.E+08	4.94.E+08
620	Q12904-1	aminoacyl tRNA synthase complex-interacting multifunctional protein 1 [OS=Homo sapiens]	81.4	37	9	220	9	1764	258	9	9	0	3.38.E+08	4.43.E+08	3.76.E+08	4.62.E+08	4.07.E+08	5.21.E+08	5.47.E+08	5.25.E+08
621	P39019	40S ribosomal protein S19 [OS=Homo sapiens]	80.6	50	11	741	11	7331	831	10	11	0	2.65.E+09	2.53.E+09	2.70.E+09	2.34.E+09	2.30.E+09	2.34.E+09	2.62.E+09	2.47.E+09
622	E9PAV3	Nascent polypeptide-associated complex subunit alpha, muscle-specific form [OS=Homo sapiens]	80.4	3	6	476	6	8117	763	6	6	0	1.04.E+09	1.10.E+09	1.05.E+09	9.95.E+08	9.73.E+08	9.85.E+08	9.94.E+08	9.78.E+08
623	P49915	GMP synthase [glutamine-hydrolyzing] [OS=Homo sapiens]	80.4	23	9	189	9	2540	225	9	9	0	1.72.E+08	1.87.E+08	1.78.E+08	2.03.E+08	2.06.E+08	1.81.E+08	1.81.E+08	1.86.E+08
624	P00533-1	epidermal growth factor receptor [OS=Homo sapiens]	80.4	14	13	200	13	2497	244	13	13	0	3.57.E+08	3.72.E+08	3.71.E+08	3.55.E+08	3.37.E+08	3.60.E+08	3.47.E+08	3.65.E+08
625	Q9Y446	Plakophilin-3 [OS=Homo sapiens]	80.2	21	11	172	11	1242	130	11	11	0	2.64.E+08	2.34.E+08	2.57.E+08	2.58.E+08	8.73.E+07	1.14.E+08	9.50.E+07	1.08.E+08
626	P55263-1	Adenosine kinase [OS=Homo sapiens]	79.8	53	11	239	11	3608	303	11	11	0	3.41.E+08	3.11.E+08	2.32.E+08	2.37.E+08	3.21.E+08	3.41.E+08	4.11.E+08	2.92.E+08
627	P62269	40S ribosomal protein S18 [OS=Homo sapiens]	79.7	59	13	771	13	7403	733	12	11	0	3.20.E+09	3.12.E+09	3.19.E+09	3.16.E+09	2.56.E+09	2.58.E+09	2.71.E+09	2.60.E+09
628	Q6DKJ4	nucleoredoxin [OS=Homo sapiens]	79.5	36	9	239	9	3028	241	7	9	0	2.72.E+08	2.68.E+08	2.45.E+08	2.25.E+08	1.65.E+08	1.67.E+08	1.61.E+08	1.72.E+08
629	Q15165-1	Isoform 1 of Serum paraoxonase/arylesterase 2 [OS=Homo sapiens]	79.4	51	8	246	8		679	8		0	4.77.E+08	5.00.E+08	4.80.E+08	4.17.E+08	9.29.E+08	9.13.E+08	9.41.E+08	9.25.E+08
630	O00303	Eukaryotic translation initiation factor 3 subunit F [OS=Homo sapiens]	79.1	23	6	236	6	4605	394	6	6	0	2.31.E+08	2.33.E+08	2.30.E+08	2.58.E+08	2.82.E+08	2.62.E+08	2.38.E+08	2.93.E+08
631	Q13435	Splicing factor 3b subunit 2 [OS=Homo sapiens]	79.1	17	11	183	11	1784	171	10	10	0	3.66.E+08	3.67.E+08	3.71.E+08	3.74.E+08	3.80.E+08	3.75.E+08	3.57.E+08	3.88.E+08
632	P39656	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit [OS=Homo sapiens]	79.1	39	11	314	11	1682	340	11	11	0	2.53.E+09	8.78.E+08	2.72.E+09	7.61.E+08	2.94.E+09	2.89.E+09	3.00.E+09	2.94.E+09
633	P09622	Dihydrolipoyl dehydrogenase, mitochondrial [OS=Homo sapiens]	78.9	23	7	303	7	5116	409	7	7	0	3.57.E+08	3.31.E+08	3.59.E+08	3.59.E+08	3.68.E+08	4.00.E+08	3.87.E+08	3.78.E+08
634	P62820	Ras-related protein Rab-1A [OS=Homo sapiens]	78.6	58	9	642	2	10053	873	9	9	0	6.48.E+07	4.79.E+07	5.43.E+07	5.89.E+07	8.37.E+07	6.91.E+07	5.91.E+07	8.25.E+07
635	P43034	Platelet-activating factor acetylhydrolase IB subunit alpha [OS=Homo sapiens]	78.6	29	9	185	8	1867	202	9	9	1	3.36.E+08	3.29.E+08	2.99.E+08	3.56.E+08	2.50.E+08	2.47.E+08	2.41.E+08	2.48.E+08
636	O43399	Tumor protein D54 [OS=Homo sapiens]	78.4	54	6	358	6	4038	715	6	6	0	7.10.E+08	7.20.E+08	6.82.E+08	6.72.E+08	6.08.E+08	5.89.E+08	5.66.E+08	5.64.E+08
637	P16422	Epithelial cell adhesion molecule [OS=Homo sapiens]	77.7	34	7	321	7	7057	550	7	6	0	2.04.E+08	2.27.E+08	2.12.E+08	2.05.E+08	1.70.E+08	2.00.E+08	1.80.E+08	2.03.E+08
638	P28074-1	proteasome subunit beta type-5 [OS=Homo sapiens]	77.3	40	8	224	8	2738	325	8	8	0	8.27.E+08	8.65.E+08	8.19.E+08	7.71.E+08	8.33.E+08	7.68.E+08	9.58.E+08	7.07.E+08
639	P35520-1	Cystathionine beta-synthase [OS=Homo sapiens]	77.1	35	11	218	11	1168	224	10	11	0	3.77.E+08	3.26.E+08	3.28.E+08	3.38.E+08	3.57.E+08	2.82.E+08	3.53.E+08	2.88.E+08
640	Q13347	Eukaryotic translation initiation factor 3 subunit I [OS=Homo sapiens]	77.1	51	11	339	11	3392	409	11	11	0	5.04.E+08	5.05.E+08	4.75.E+08	5.06.E+08	4.97.E+08	5.24.E+08	4.91.E+08	5.01.E+08
641	Q9NVP1	ATP-dependent RNA helicase DDX18 [OS=Homo sapiens]	76.4	23	9	218	9	1554	227	9	9	0	1.75.E+08	2.07.E+08	2.98.E+08	1.66.E+08	1.85.E+08	2.08.E+08	1.47.E+08	2.10.E+08
642	Q9Y4G6	Talin-2 [OS=Homo sapiens]	76.4	4	9	370	2	3739	597	9	9	0	3.50.E+06	2.66.E+06	4.13.E+06	3.84.E+06	3.69.E+06	3.31.E+06	2.39.E+06	1.81.E+06
643	P11498	pyruvate carboxylase, mitochondrial [OS=Homo sapiens]	76.3	16	13	242	13	2176	261	13	13	0	4.29.E+08	4.04.E+08	3.86.E+08	4.33.E+08	3.95.E+08	3.76.E+08	4.00.E+08	3.78.E+08
644	P50995	annexin A11 [OS=Homo sapiens]	75.7	18	8	245	8	2642	299	8	8	0	2.47.E+08	3.03.E+08	2.06.E+08	2.75.E+08	1.44.E+08	1.76.E+08	1.45.E+08	1.77.E+08
645	P20674	Cytochrome c oxidase subunit 5A, mitochondrial [OS=Homo sapiens]	75.6	58	7	431	7	3714	688	7	7	0	8.01.E+08	8.20.E+08	8.12.E+08	8.64.E+08	6.09.E+08	6.06.E+08	6.05.E+08	6.92.E+08
646	Q07955-1	Serine/arginine-rich splicing factor 1 [OS=Homo sapiens]	75.5	40	9	483	9	3554	629	9	9	0	8.08.E+08	7.74.E+08	8.79.E+08	7.77.E+08	1.02.E+09	9.00.E+08	8.99.E+08	8.26.E+08
647	P53396-1	ATP-citrate synthase [OS=Homo sapiens]	75.2	12	10	303	10	4358	326	10	9	0	3.22.E+08	3.13.E+08	3.05.E+08	3.46.E+08	6.29.E+08	5.92.E+08	6.09.E+08	5.92.E+08
648	P49773	Histidine triad nucleotide-binding protein 1 [OS=Homo sapiens]	74.5	71	5	203	5	604	265	5	5	0	5.59.E+08	5.58.E+08	5.41.E+08	5.40.E+08	5.10.E+08	5.22.E+08	5.21.E+08	5.33.E+08
649	P42224-1	Signal transducer and activator of transcription 1-alpha/beta [OS=Homo sapiens]	74.5	18	10	123	10	1290	158	10	10	0	1.89.E+08	2.08.E+08	2.08.E+08	2.22.E+08	3.12.E+08	3.26.E+08	2.49.E+08	3.10.E+08
650	Q9NTK5-1	obg-like ATPase 1 [OS=Homo sapiens]	74.4	43	9	347	9	5399	475	9	9	0	4.11.E+08	4.63.E+08	4.27.E+08	4.63.E+08	5.49.E+08	5.03.E+08	4.27.E+08	5.23.E+08
651	P61604	10 kDa heat shock protein, mitochondrial [OS=Homo sapiens]	74.3	67	9	934	9	11794	1058	9	9	0	3.79.E+09	3.82.E+09	3.87.E+09	3.60.E+09	4.32.E+09	4.42.E+09	4.51.E+09	4.44.E+09
652	P30154	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform [OS=Homo sapiens]	74.3	11	5	392	1	9782	677	5	5	0								
653	O14773	Tripeptidyl-peptidase 1 [OS=Homo sapiens]	74.0	25	7	230	7	3304	353	6	7	0	1.92.E+08	2.07.E+08	2.15.E+08	1.99.E+08	4.14.E+08	4.57.E+08	4.68.E+08	4.14.E+08
654	P50897	Palmitoyl-protein thioesterase 1 [OS=Homo sapiens]	74.0	42	7	185	7	3226	260	7	7	0	2.90.E+08	3.03.E+08	2.64.E+08	2.65.E+08	3.31.E+08	3.51.E+08	2.68.E+08	3.27.E+08
655	Q16836-1	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial [OS=Homo sapiens]	73.7	46	8	414	8	6026	516	8	7	0	4.77.E+08	4.99.E+08	4.89.E+08	4.92.E+08	4.53.E+08	4.67.E+08	4.26.E+08	4.73.E+08
656	P53582	Methionine aminopeptidase 1 [OS=Homo sapiens]	73.5	41	8	176	8	1193	202	8	8	0	2.53.E+08	2.37.E+08	2.21.E+08	2.45.E+08	2.67.E+08	2.88.E+08	2.80.E+08	3.02.E+08

No.	Accession	Description	Sum PEP Score	Coverage [%]	# Peptides	# PSMs	# Unique Peptides	Score Mascot: A5 Mascot	Score Sequest HT: A2 Sequest HT	# Peptides (by Search Engine): A2 Sequest HT	# Peptides (by Search Engine): A5 Mascot	# Razor Peptides	ctrl Abundances_1	ctrl Abundances_2	ctrl Abundances_3	ctrl Abundances_4	JAM-A KO Abundances_1	JAM-A KO Abundances_2	JAM-A KO Abundances_3	JAM-A KO Abundances_4
657	Q9Y2W1	Thyroid hormone receptor-associated protein 3 [OS=Homo sapiens]	73.3	12	9	183	9	1714	211	9	9	0	2.37.E+08	2.26.E+08	2.41.E+08	2.55.E+08	3.31.E+08	2.89.E+08	3.41.E+08	3.15.E+08
658	P35268	60S ribosomal protein L22 [OS=Homo sapiens]	73.1	48	6	369	6	8113	678	6	6	0	1.27.E+09	1.24.E+09	1.26.E+09	1.31.E+09	1.00.E+09	9.56.E+08	1.01.E+09	9.72.E+08
659	Q9H3K6-1	bola-like protein 2 [OS=Homo sapiens]	73.0	80	6	306	6	2620	412	6	6	0	4.78.E+08	5.50.E+08	5.78.E+08	5.75.E+08	4.34.E+08	4.33.E+08	4.66.E+08	5.12.E+08
660	O00629	Importin subunit alpha-3 [OS=Homo sapiens]	72.9	25	7	181	4	2754	238	7	6	2	8.53.E+07	9.24.E+07	7.26.E+07	7.44.E+07	9.45.E+07	9.13.E+07	8.25.E+07	8.37.E+07
661	Q12931	heat shock protein 75 kDa, mitochondrial [OS=Homo sapiens]	72.7	17	9	293	8	5906	452	9	9	0	2.09.E+08	1.37.E+08	1.32.E+08	1.58.E+08	1.04.E+08	1.72.E+08	1.79.E+08	1.06.E+08
662	Q96AG4	Leucine-rich repeat-containing protein 59 [OS=Homo sapiens]	72.7	39	8	357	8	2125	475	8	8	0	6.29.E+08	6.39.E+08	6.55.E+08	5.95.E+08	9.63.E+08	1.05.E+09	6.27.E+08	9.76.E+08
663	Q8WX93-1	palladin [OS=Homo sapiens]	72.6	17	12	258	12	1529	336	12	12	0	3.00.E+08	3.10.E+08	2.58.E+08	3.06.E+08	3.63.E+08	3.92.E+08	3.34.E+08	4.04.E+08
664	P14324	Farnesyl pyrophosphate synthase [OS=Homo sapiens]	72.5	29	8	215	8	1692	263	8	8	0	3.41.E+08	3.54.E+08	3.38.E+08	3.16.E+08	2.96.E+08	2.85.E+08	2.92.E+08	2.99.E+08
665	P62913	60S ribosomal protein L11 [OS=Homo sapiens]	72.3	51	10	456	10	5348	478	9	10	0	1.48.E+09	1.48.E+09	1.51.E+09	1.38.E+09	1.45.E+09	1.45.E+09	1.51.E+09	1.48.E+09
666	P31689-1	DnaJ homolog subfamily A member 1 [OS=Homo sapiens]	72.3	35	8	180	8	2412	244	7	8	0	1.89.E+08	2.00.E+08	1.86.E+08	1.95.E+08	2.10.E+08	2.20.E+08	2.05.E+08	2.03.E+08
667	O60684	Importin subunit alpha-7 [OS=Homo sapiens]	72.3	27	7	236	4	3010	233	7	7	3	1.41.E+08	1.45.E+08	1.35.E+08	1.48.E+08	1.76.E+08	1.78.E+08	1.50.E+08	1.57.E+08
668	Q15758-1	Neutral amino acid transporter B(0) [OS=Homo sapiens]	71.9	26	10	446	10	7922	603	10	10	0	5.03.E+08	7.29.E+08	6.86.E+08	8.51.E+08	5.73.E+08	3.78.E+08	5.74.E+08	5.85.E+08
669	Q8N163-1	Cell cycle and apoptosis regulator protein 2 [OS=Homo sapiens]	71.9	22	11	227	11	1841	222	11	11	0	2.38.E+08	2.60.E+08	2.26.E+08	2.59.E+08	2.94.E+08	3.05.E+08	2.58.E+08	2.93.E+08
670	P84098	60S ribosomal protein L19 [OS=Homo sapiens]	71.8	27	7	396	7	6971	504	7	7	0	5.88.E+08	5.20.E+08	5.97.E+08	6.13.E+08	4.13.E+08	4.24.E+08	4.92.E+08	4.50.E+08
671	Q15907	Ras-related protein Rab-11B [OS=Homo sapiens]	71.8	54	10	391	10	5556	547	9	10	0	1.29.E+09	1.30.E+09	1.33.E+09	1.36.E+09	1.51.E+09	1.62.E+09	1.63.E+09	1.62.E+09
672	P23919	thymidylate kinase [OS=Homo sapiens]	71.7	59	10	305	10	2774	388	10	10	0	6.25.E+08	5.94.E+08	6.48.E+08	6.22.E+08	7.67.E+08	6.58.E+08	7.01.E+08	6.91.E+08
673	Q15436	protein transport protein Sec23A [OS=Homo sapiens]	71.6	19	8	101	6	2111	160	7	8	0	6.58.E+07	7.35.E+07	6.52.E+07	5.22.E+07	9.81.E+07	1.02.E+08	8.65.E+07	1.11.E+08
674	Q96PK6-1	RNA-binding protein 14 [OS=Homo sapiens]	71.6	20	10	335	10	4143	436	10	10	0	3.66.E+08	3.47.E+08	4.00.E+08	3.80.E+08	3.86.E+08	4.51.E+08	3.94.E+08	3.76.E+08
675	P28288	ATP-binding cassette sub-family D member 3 [OS=Homo sapiens]	71.6	19	8	210	8	1825	212	8	8	0	1.37.E+08	1.50.E+08	1.26.E+08	1.41.E+08	2.51.E+08	2.40.E+08	2.26.E+08	2.40.E+08
676	O95994	Anterior gradient protein 2 homolog [OS=Homo sapiens]	71.5	43	7	204	7	1880	253	7	7	0	2.64.E+08	2.99.E+08	2.75.E+08	2.63.E+08	2.76.E+08	3.08.E+08	2.97.E+08	2.89.E+08
677	Q99439	Calponin-2 [OS=Homo sapiens]	71.3	35	9	221	8	1927	226	8	9	1	3.94.E+08	3.84.E+08	4.05.E+08	4.19.E+08	7.85.E+08	7.52.E+08	7.53.E+08	7.63.E+08
678	P00367	Glutamate dehydrogenase 1, mitochondrial [OS=Homo sapiens]	71.3	25	9	192	9	2002	250	9	8	0	2.95.E+08	3.18.E+08	3.03.E+08	2.85.E+08	2.56.E+08	2.46.E+08	2.57.E+08	2.38.E+08
679	P62280	40S ribosomal protein S11 [OS=Homo sapiens]	71.2	58	13	593	13	4207	622	13	13	0	2.23.E+09	1.99.E+09	2.16.E+09	2.29.E+09	1.82.E+09	1.82.E+09	1.94.E+09	1.85.E+09
680	O75947-1	ATP synthase subunit d, mitochondrial [OS=Homo sapiens]	71.2	73	8	465	8	5259	543	8	8	0	6.11.E+08	6.31.E+08	5.95.E+08	6.43.E+08	5.99.E+08	6.34.E+08	5.30.E+08	5.93.E+08
681	O60832-1	H/ACA ribonucleoprotein complex subunit 4 [OS=Homo sapiens]	71.0	23	8	222	8	1486	261	8	8	0	1.82.E+08	2.27.E+08	1.77.E+08	1.92.E+08	1.91.E+08	1.82.E+08	1.91.E+08	1.89.E+08
682	O00232-1	26s proteasome non-atpase regulatory subunit 12 [OS=Homo sapiens]	70.8	34	10	285	9	3887	368	10	9	1	4.48.E+08	4.78.E+08	4.29.E+08	4.96.E+08	4.33.E+08	4.66.E+08	4.28.E+08	4.01.E+08
683	O43852	Calumenin [OS=Homo sapiens]	70.5	40	9	259	9	1770	291	8	9	0	2.18.E+08	2.21.E+08	2.17.E+08	2.11.E+08	3.36.E+08	3.23.E+08	3.33.E+08	2.95.E+08
684	P51659-1	peroxisomal multifunctional enzyme type 2 [OS=Homo sapiens]	70.3	25	9	122	9	1662	153	9	9	0	1.80.E+08	1.45.E+08	1.53.E+08	1.83.E+08	2.34.E+08	2.19.E+08	1.67.E+08	2.28.E+08
685	O00231	26S proteasome non-ATPase regulatory subunit 11 [OS=Homo sapiens]	70.3	32	13	369	13	3351	411	12	13	0	6.26.E+08	6.23.E+08	6.55.E+08	5.90.E+08	6.89.E+08	6.76.E+08	6.16.E+08	6.86.E+08
686	P06737-1	Glycogen phosphorylase, liver form [OS=Homo sapiens]	70.2	18	11	147	9	2413	161	11	10	0	2.68.E+08	2.69.E+08	2.53.E+08	2.62.E+08	4.13.E+08	4.06.E+08	4.01.E+08	4.13.E+08
687	Q92817	Envoplakin [OS=Homo sapiens]	70.1	8	10	107	10	798	73	10	10	0	1.06.E+08	1.71.E+08	1.81.E+08	1.64.E+08	1.72.E+08	1.65.E+08	1.98.E+08	1.62.E+08
688	P28066-1	Proteasome subunit alpha type-5 [OS=Homo sapiens]	70.1	37	7	363	7	6717	513	7	7	0	6.92.E+08	7.18.E+08	6.81.E+08	7.25.E+08	8.73.E+08	8.33.E+08	8.45.E+08	8.43.E+08
689	Q8NBS9-1	Thioredoxin domain-containing protein 5 [OS=Homo sapiens]	70.0	27	10	481	10	4496	479	10	10	0	4.97.E+08	5.27.E+08	4.64.E+08	5.19.E+08	6.07.E+08	6.11.E+08	5.21.E+08	6.12.E+08
690	Q7L2H7	Eukaryotic translation initiation factor 3 subunit M [OS=Homo sapiens]	69.7	30	7	189	7	1948	200	6	7	0	2.97.E+08	2.73.E+08	2.47.E+08	3.10.E+08	3.10.E+08	2.68.E+08	1.78.E+08	3.20.E+08
691	Q13151	Heterogeneous nuclear ribonucleoprotein A0 [OS=Homo sapiens]	69.7	33	8	539	6	4796	570	8	8	0	3.27.E+08	3.38.E+08	3.37.E+08	3.41.E+08	3.84.E+08	3.98.E+08	3.77.E+08	4.01.E+08
692	Q99733	Nucleosome assembly protein 1-like 4 [OS=Homo sapiens]	69.6	27	8	231	6	2702	229	7	8	0	1.08.E+08	1.11.E+08	1.11.E+08	1.00.E+08	1.70.E+08	2.00.E+08	1.64.E+08	1.60.E+08
693	Q14978-1	nucleolar and coiled-body phosphoprotein 1 [OS=Homo sapiens]	69.6	12	7	483	1	5139	443	7	7	5	2.42.E+08	2.45.E+08	2.46.E+08	2.74.E+08	1.99.E+08	1.91.E+08	2.08.E+08	1.90.E+08
694	Q8IVT2	Mitotic interactor and substrate of PLK1 [OS=Homo sapiens]	69.2	28	10	141	10	1022	113	10	10	0	2.04.E+08	2.06.E+08	2.13.E+08	1.96.E+08	1.71.E+08	1.88.E+08	1.95.E+08	1.62.E+08
695	P62750	60S ribosomal protein L23a [OS=Homo sapiens]	69.2	38	6	536	6	4599	603	6	6	0	1.13.E+09	9.24.E+08	1.19.E+09	1.13.E+09	1.01.E+09	1.05.E+09	1.14.E+09	1.08.E+09
696	Q15459	splicing factor 3A subunit 1 [OS=Homo sapiens]	69.1	18	9	190	9	1491	234	9	9	0	2.17.E+08	2.57.E+08	2.53.E+08	2.40.E+08	2.84.E+08	2.24.E+08	2.44.E+08	2.43.E+08
697	P61289-1	Proteasome activator complex subunit 3 [OS=Homo sapiens]	69.0	33	7	224	7	3720	262	7	7	0	1.74.E+08	1.68.E+08	1.74.E+08	2.05.E+08	4.51.E+08	4.48.E+08	4.13.E+08	4.96.E+08
698	P46060	Ran GTPase-activating protein 1 [OS=Homo sapiens]	69.0	23	8	188	8	2184	291	8	8	0	1.26.E+08	1.45.E+08	1.17.E+08	1.37.E+08	1.98.E+08	2.03.E+08	1.80.E+08	2.12.E+08
699	Q6KB66	Keratin, type II cytoskeletal 80 [OS=Homo sapiens]	69.0	17	8	1096	6	17703	1523	8	7	0	8.00.E+07	7.24.E+07	7.89.E+07	8.09.E+07	1.13.E+08	1.13.E+08	1.05.E+08	1.17.E+08
700	O76003	glutaredoxin-3 [OS=Homo sapiens]	68.9	39	7	221	7	2509	233	6	6	0	2.27.E+08	2.30.E+08	2.15.E+08	2.12.E+08	2.24.E+08	2.29.E+08	2.16.E+08	2.20.E+08
701	Q9Y5S2	Serine/threonine-protein kinase MRCK beta [OS=Homo sapiens]	68.9	10	11	239	11	2345	154	11	11	0	4.57.E+08	4.96.E+08	5.14.E+08	4.98.E+08	5.29.E+08	5.33.E+08	5.34.E+08	5.68.E+08
702	P20810-1	Calpastatin [OS=Homo sapiens]	68.7	28	9	109	9	1057	129	9	9	0	1.87.E+08	1.99.E+08	1.96.E+08	2.08.E+08	2.06.E+08	2.03.E+08	1.54.E+08	1.93.E+08
703	P61163	Alpha-centractin [OS=Homo sapiens]	68.7	34	8	268	8	3186	322	7	7	0	2.75.E+08	3.02.E+08	2.80.E+08	3.02.E+08	4.01.E+08	3.95.E+08	3.91.E+08	3.18.E+08
704	P60903	Protein S100-A10 [OS=Homo sapiens]	68.6	45	4	816	4	14411	1069	3	4	0	5.87.E+09	5.96.E+09	6.10.E+09	5.84.E+09	4.42.E+09	4.74.E+09	4.81.E+09	4.51.E+09
705	Q9BZZ5-2	Isoform 2 of Apoptosis inhibitor 5 [OS=Homo sapiens]	68.5	25	8	148	1		429	8		0	1.66.E+07	1.87.E+07	1.83.E+07	1.74.E+07	2.12.E+07	2.05.E+07	2.09.E+07	2.10.E+07
706	P78417	Glutathione S-transferase omega-1 [OS=Homo sapiens]	68.5	39	12	492	12	2968	370	12	12	0	9.74.E+08	9.49.E+08	9.78.E+08	9.97.E+08	8.70.E+08	8.79.E+08	9.11.E+08	8.83.E+08
707	Q07020	60S ribosomal protein L18 [OS=Homo sapiens]	68.4	38	6	528	6	7908	634	6	6	0	1.90.E+09	1.80.E+09	1.93.E+09	2.04.E+09	1.61.E+09	1.55.E+09	1.73.E+09	1.60.E+09
708	P62249	40S ribosomal protein S16 [OS=Homo sapiens]	68.3	44	9	746	9	9248	803	8	9	0	2.61.E+09	2.54.E+09	2.65.E+09	2.52.E+09	2.30.E+09	2.32.E+09	1.92.E+09	2.34.E+09
709	Q9BPW8	Protein NipSnap homolog 1 [OS=Homo sapiens]	68.3	40	7	199	6	2151	265	7	6	1	3.10.E+08	3.05.E+08	3.05.E+08	2.46.E+08	3.06.E+08	2.99.E+08	2.50.E+08	2.77.E+08
710	Q14257	Reticulocalbin-2 [OS=Homo sapiens]	68.2	24	6	145	6	4339	236	6	6	0	1.03.E+08	1.07.E+08	9.17.E+07	1.12.E+08	1.59.E+08	1.60.E+08	1.51.E+08	1.66.E+08

No.	Accession	Description	Sum PEP Score	Coverage [%]	# Peptides	# PSMs	# Unique Peptides	Score Mascot: A5 Mascot	Score Sequest HT: A2 Sequest HT	# Peptides (by Search Engine): A2 Sequest HT	# Peptides (by Search Engine): A5 Mascot	# Razor Peptides	ctrl Abundances_1	ctrl Abundances_2	ctrl Abundances_3	ctrl Abundances_4	JAM-A KO Abundances_1	JAM-A KO Abundances_2	JAM-A KO Abundances_3	JAM-A KO Abundances_4
711	O00425	Insulin-like growth factor 2 mRNA-binding protein 3 [OS=Homo sapiens]	68.2	19	8	104	7	2135	154	8	8	1	1.52.E+08	1.67.E+08	1.57.E+08	1.55.E+08	2.08.E+08	2.15.E+08	2.10.E+08	2.11.E+08
712	P08621-1	U1 small nuclear ribonucleoprotein 70 kDa [OS=Homo sapiens]	68.0	26	10	267	10	1622	247	8	10	0	4.04.E+08	4.29.E+08	4.71.E+08	5.00.E+08	4.76.E+08	4.22.E+08	4.98.E+08	4.07.E+08
713	Q13011	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial [OS=Homo sapiens]	68.0	40	9	561	9	7936	764	9	8	0	7.46.E+08	7.73.E+08	7.86.E+08	7.11.E+08	4.51.E+08	4.32.E+08	4.58.E+08	4.66.E+08
714	Q9Y570	Protein phosphatase methylesterase 1 [OS=Homo sapiens]	68.0	42	10	156	10	1033	175	10	10	0	1.71.E+08	1.43.E+08	1.74.E+08	1.78.E+08	2.60.E+08	2.27.E+08	2.53.E+08	2.79.E+08
715	Q9Y224	UPF0568 protein C14orf166 [OS=Homo sapiens]	67.9	36	6	154	6	2025	192	6	6	0	1.14.E+08	1.41.E+08	1.20.E+08	1.45.E+08	1.78.E+08	1.69.E+08	1.67.E+08	1.82.E+08
716	Q9BWF3-1	RNA-binding protein 4 [OS=Homo sapiens]	67.3	29	6	184	6	2967	296	6	6	0	1.69.E+08	1.66.E+08	1.77.E+08	1.79.E+08	2.14.E+08	2.11.E+08	2.15.E+08	2.15.E+08
717	P61224-1	Ras-related protein Rap-1b [OS=Homo sapiens]	67.3	43	8	357	8	5986	407	8	7	0	3.67.E+08	3.65.E+08	3.67.E+08	4.00.E+08	5.66.E+08	5.45.E+08	5.56.E+08	5.47.E+08
718	Q7Z4W1	L-xylulose reductase [OS=Homo sapiens]	67.3	50	9	145	9	1318	133	9	9	0	2.52.E+08	2.32.E+08	2.41.E+08	2.15.E+08	1.29.E+08	1.10.E+08	1.37.E+08	1.26.E+08
719	P62899	60S ribosomal protein L31 [OS=Homo sapiens]	67.3	34	5	316	5	4334	559	5	5	0	7.63.E+08	7.54.E+08	7.69.E+08	8.40.E+08	7.35.E+08	7.38.E+08	7.30.E+08	7.22.E+08
720	Q02218	2-oxoglutarate dehydrogenase, mitochondrial [OS=Homo sapiens]	67.1	16	8	208	8	1938	229	8	8	0	1.31.E+08	1.27.E+08	1.28.E+08	1.48.E+08	1.32.E+08	1.23.E+08	1.22.E+08	1.18.E+08
721	Q15056-1	Eukaryotic translation initiation factor 4H [OS=Homo sapiens]	67.0	37	6	341	6	3388	436	6	6	0	4.76.E+08	4.74.E+08	4.84.E+08	5.09.E+08	5.23.E+08	5.06.E+08	5.14.E+08	5.38.E+08
722	P26196	Probable ATP-dependent RNA helicase DDX6 [OS=Homo sapiens]	66.8	28	9	164	8	1293	239	9	8	1	3.30.E+08	3.22.E+08	3.21.E+08	3.15.E+08	3.46.E+08	3.41.E+08	2.87.E+08	3.50.E+08
723	Q5JTH9-1	RRP12-like protein [OS=Homo sapiens]	66.5	10	9	124	9	1173	95	9	9	0	1.20.E+08	1.15.E+08	1.06.E+08	1.16.E+08	1.16.E+08	1.34.E+08	9.99.E+07	1.28.E+08
724	Q15126	phosphomevalonate kinase [OS=Homo sapiens]	66.3	57	9	324	9	4736	380	9	9	0	2.79.E+08	3.12.E+08	3.12.E+08	3.06.E+08	3.93.E+08	3.81.E+08	3.94.E+08	3.77.E+08
725	Q01650	large neutral amino acids transporter small subunit 1 [OS=Homo sapiens]	66.2	17	6	259	6	4327	310	6	6	0	3.02.E+08	3.00.E+08	3.33.E+08	2.93.E+08	4.67.E+08	4.81.E+08	5.58.E+08	4.89.E+08
726	P30520	adenylosuccinate synthetase isozyme 2 [OS=Homo sapiens]	66.2	21	6	158	6	3641	264	6	6	0	2.49.E+08	2.82.E+08	1.87.E+08	2.62.E+08	2.93.E+08	3.04.E+08	2.85.E+08	3.14.E+08
727	P55010	Eukaryotic translation initiation factor 5 [OS=Homo sapiens]	65.9	28	11	484	11	2453	451	11	11	0	5.69.E+08	5.33.E+08	5.21.E+08	5.39.E+08	8.09.E+08	8.08.E+08	8.78.E+08	7.22.E+08
728	P25325	3-mercaptopyruvate sulfurtransferase [OS=Homo sapiens]	65.8	37	7	222	7	2494	332	7	7	0	1.96.E+08	1.98.E+08	1.42.E+08	2.22.E+08	2.58.E+08	2.61.E+08	2.16.E+08	2.52.E+08
729	P26373-1	60S ribosomal protein L13 [OS=Homo sapiens]	65.7	45	10	591	10	5850	516	9	8	0	2.22.E+09	2.19.E+09	2.33.E+09	2.15.E+09	1.86.E+09	1.83.E+09	1.92.E+09	1.87.E+09
730	P68402-1	platelet-activating factor acetylhydrolase IB subunit beta [OS=Homo sapiens]	65.6	48	5	316	5	6341	575	4	5	0	5.07.E+08	5.23.E+08	4.75.E+08	5.26.E+08	5.21.E+08	5.25.E+08	2.69.E+08	5.30.E+08
731	P78344-1	Eukaryotic translation initiation factor 4 gamma 2 [OS=Homo sapiens]	65.5	18	13	259	13	1569	225	13	13	0	2.13.E+08	2.61.E+08	2.63.E+08	2.62.E+08	3.30.E+08	3.20.E+08	2.85.E+08	3.10.E+08
732	P61088	ubiquitin-conjugating enzyme E2 N [OS=Homo sapiens]	65.5	66	8	453	8	4826	669	8	8	0	6.48.E+08	6.41.E+08	6.88.E+08	6.00.E+08	6.94.E+08	7.02.E+08	7.52.E+08	7.12.E+08
733	Q93052	Lipoma-preferred partner [OS=Homo sapiens]	65.5	21	7	195	7	1228	279	7	7	0	1.33.E+08	1.30.E+08	1.20.E+08	1.24.E+08	2.03.E+08	1.94.E+08	1.74.E+08	1.96.E+08
734	Q9H4M9	EH domain-containing protein 1 [OS=Homo sapiens]	65.2	39	12	230	10	867	207	12	12	2	3.21.E+08	3.73.E+08	3.44.E+08	3.98.E+08	2.44.E+08	2.49.E+08	2.67.E+08	2.59.E+08
735	Q14498-1	RNA-binding protein 39 [OS=Homo sapiens]	64.9	29	9	172	9	3886	293	9	9	0	2.81.E+08	3.01.E+08	2.20.E+08	2.66.E+08	2.65.E+08	2.90.E+08	2.20.E+08	2.76.E+08
736	Q16630	Cleavage and polyadenylation specificity factor subunit 6 [OS=Homo sapiens]	64.9	13	4	110	4	1536	146	4	4	0	9.07.E+07	7.67.E+07	8.21.E+07	8.14.E+07	9.60.E+07	7.28.E+07	9.25.E+07	9.48.E+07
737	P06703	protein S100-A6 [OS=Homo sapiens]	64.8	57	6	116	6	1441	70	4	6	0	3.85.E+08	3.45.E+08	3.64.E+08	3.86.E+08	8.13.E+07	9.61.E+07	9.68.E+07	8.26.E+07
738	O94973	AP-2 complex subunit alpha-2 [OS=Homo sapiens]	64.6	17	9	215	5	2501	267	9	9	4	2.15.E+08	2.29.E+08	2.17.E+08	2.17.E+08	2.58.E+08	2.62.E+08	2.43.E+08	2.46.E+08
739	O95361-1	Tripartite motif-containing protein 16 [OS=Homo sapiens]	64.6	18	7	142	7	1333	140	7	7	0	1.19.E+08	1.44.E+08	1.22.E+08	1.26.E+08	6.11.E+07	6.26.E+07	4.58.E+07	6.20.E+07
740	O15143	Actin-related protein 2/3 complex subunit 1B [OS=Homo sapiens]	64.5	28	7	211	6	2091	262	7	7	1	2.84.E+08	2.88.E+08	2.70.E+08	2.62.E+08	2.30.E+08	2.31.E+08	2.48.E+08	2.50.E+08
741	P63313	thymosin beta-10 [OS=Homo sapiens]	64.4	64	3	297	3	5440	230	2	3	0	1.44.E+09	1.39.E+09	1.43.E+09	1.36.E+09	1.00.E+09	1.03.E+09	1.02.E+09	1.04.E+09
742	Q13409-1	cytoplasmic dynein 1 intermediate chain 2 [OS=Homo sapiens]	64.4	14	6	167	6	3590	194	5	6	0	1.13.E+08	1.13.E+08	1.16.E+08	1.32.E+08	1.28.E+08	1.33.E+08	1.34.E+08	1.38.E+08
743	P38606	V-type proton ATPase catalytic subunit A [OS=Homo sapiens]	64.3	28	8	178	8	1973	274	8	8	0	3.11.E+08	4.34.E+08	3.66.E+08	4.19.E+08	3.29.E+08	3.37.E+08	3.18.E+08	3.26.E+08
744	Q16629	serine/arginine-rich splicing factor 7 [OS=Homo sapiens]	64.1	27	7	360	6	1947	349	7	7	1	5.72.E+08	5.74.E+08	5.79.E+08	5.71.E+08	5.59.E+08	5.60.E+08	5.16.E+08	5.39.E+08
745	P52907	F-actin-capping protein subunit alpha-1 [OS=Homo sapiens]	64.0	41	10	349	8	2585	393	8	9	2	5.08.E+08	5.22.E+08	5.02.E+08	4.90.E+08	6.80.E+08	6.89.E+08	7.03.E+08	7.05.E+08
746	P61353	60S ribosomal protein L27 [OS=Homo sapiens]	64.0	49	9	576	9	2176	579	9	9	0	1.80.E+09	1.65.E+09	1.77.E+09	1.70.E+09	1.50.E+09	1.46.E+09	1.65.E+09	1.51.E+09
747	Q14847	LIM and SH3 domain protein 1 [OS=Homo sapiens]	64.0	39	6	133	5	756	114	6	6	1	1.00.E+08	1.02.E+08	9.79.E+07	8.98.E+07	3.48.E+08	3.76.E+08	3.86.E+08	3.58.E+08
748	P50213-1	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial [OS=Homo sapiens]	64.0	29	8	227	8	3214	348	8	8	0	3.80.E+08	4.06.E+08	3.84.E+08	3.89.E+08	4.09.E+08	4.30.E+08	3.91.E+08	3.87.E+08
749	Q9UBQ0	Vacuolar protein sorting-associated protein 29 [OS=Homo sapiens]	63.7	40	6	212	6	1835	224	5	6	0	2.45.E+08	2.36.E+08	2.26.E+08	2.56.E+08	2.49.E+08	2.46.E+08	2.64.E+08	2.50.E+08
750	Q9UI30	Multifunctional methyltransferase subunit TRM112-like protein [OS=Homo sapiens]	63.7	50	4	230	4	4249	273	4	4	0	1.95.E+08	1.65.E+08	1.72.E+08	2.23.E+08	1.81.E+08	1.82.E+08	1.69.E+08	1.74.E+08
751	Q9UBE0-1	SUMO-activating enzyme subunit 1 [OS=Homo sapiens]	63.7	27	6	193	6	5788	306	6	6	0	1.90.E+08	1.71.E+08	1.83.E+08	2.03.E+08	1.46.E+08	1.25.E+08	1.26.E+08	1.08.E+08
752	P33992	DNA replication licensing factor mcm5 [OS=Homo sapiens]	63.5	21	10	344	10	2982	442	10	9	0	4.18.E+08	4.56.E+08	4.32.E+08	4.13.E+08	4.84.E+08	4.90.E+08	4.89.E+08	4.65.E+08
753	P09972	Fructose-bisphosphate aldolase C [OS=Homo sapiens]	63.5	17	4	432	2	11322	902	4	4	0	6.17.E+08	6.88.E+08	6.15.E+08	6.38.E+08	7.78.E+08	8.00.E+08	7.11.E+08	7.75.E+08
754	O95433	activator of 90 kDa heat shock protein ATPase homolog 1 [OS=Homo sapiens]	63.3	37	8	180	8	2333	256	8	6	0	3.90.E+08	4.05.E+08	3.92.E+08	3.90.E+08	3.53.E+08	3.39.E+08	3.52.E+08	3.61.E+08
755	P63220	40S ribosomal protein S21 [OS=Homo sapiens]	63.3	46	4	233	4	4241	410	4	4	0	7.64.E+08	7.29.E+08	7.42.E+08	8.30.E+08	6.68.E+08	6.19.E+08	6.84.E+08	6.55.E+08
756	O94906-1	Pre-mRNA-processing factor 6 [OS=Homo sapiens]	63.2	20	12	120	12	1724	121	12	11	0	2.07.E+08	1.73.E+08	1.77.E+08	2.19.E+08	1.89.E+08	1.91.E+08	1.86.E+08	1.85.E+08
757	P09661	U2 small nuclear ribonucleoprotein A' [OS=Homo sapiens]	63.2	45	7	139	7	1994	144	6	7	0	1.65.E+08	1.68.E+08	1.67.E+08	1.33.E+08	1.67.E+08	1.79.E+08	1.78.E+08	1.80.E+08
758	P36542-1	ATP synthase subunit gamma, mitochondrial [OS=Homo sapiens]	63.0	34	7	298	7	2471	311	7	7	0	6.45.E+08	6.12.E+08	6.61.E+08	6.72.E+08	5.91.E+08	5.85.E+08	6.64.E+08	6.24.E+08
759	O15231-3	Isoform 3 of Zinc finger protein 185 [OS=Homo sapiens]	62.9	30	12	93	12		186	12		0	1.83.E+08	1.80.E+08	1.66.E+08	1.81.E+08	1.47.E+08	1.55.E+08	1.56.E+08	1.41.E+08
760	P47813	Eukaryotic translation initiation factor 1A, X-chromosomal [OS=Homo sapiens]	62.7	44	8	273	8	1892	242	8	8	0	4.39.E+08	4.08.E+08	4.43.E+08	4.70.E+08	4.28.E+08	4.16.E+08	4.50.E+08	4.21.E+08
761	P61019-1	Ras-related protein Rab-2A [OS=Homo sapiens]	62.7	42	7	168	7	2621	244	6	7	0	3.11.E+08	3.14.E+08	3.17.E+08	2.98.E+08	3.27.E+08	3.46.E+08	2.98.E+08	3.39.E+08

No.	Accession	Description	Sum PEP Score	Coverage [%]	# Peptides	# PSMs	# Unique Peptides	Score Mascot: A5 Mascot	Score Sequest HT: A2 Sequest HT	# Peptides (by Search Engine): A2 Sequest HT	# Peptides (by Search Engine): A5 Mascot	# Razor Peptides	ctrl Abundances_1	ctrl Abundances_2	ctrl Abundances_3	ctrl Abundances_4	JAM-A KO Abundances_1	JAM-A KO Abundances_2	JAM-A KO Abundances_3	JAM-A KO Abundances_4
762	Q13724-1	Mannosyl-oligosaccharide glucosidase [OS=Homo sapiens]	62.5	14	6	132	6	1846	193	6	6	0	6.64.E+07	8.23.E+07	5.89.E+07	6.94.E+07	6.94.E+07	6.80.E+07	5.40.E+07	7.76.E+07
763	Q96P70	Importin-9 [OS=Homo sapiens]	62.5	13	6	157	6	3031	230	6	6	0	7.06.E+07	7.90.E+07	5.86.E+07	7.16.E+07	8.43.E+07	8.44.E+07	6.91.E+07	8.11.E+07
764	Q9BQ52-1	Zinc phosphodiesterase ELAC protein 2 [OS=Homo sapiens]	62.5	22	10	165	10	1582	207	9	10	0	1.90.E+08	2.06.E+08	2.18.E+08	2.14.E+08	1.20.E+08	1.41.E+08	1.44.E+08	1.45.E+08
765	P61026	ras-related protein rab-10 [OS=Homo sapiens]	62.3	48	10	790	7	10204	799	10	10	0	4.09.E+08	4.54.E+08	3.61.E+08	4.35.E+08	4.68.E+08	4.69.E+08	4.19.E+08	4.14.E+08
766	Q8TC12	Retinol dehydrogenase 11 [OS=Homo sapiens]	62.2	32	7	207	7	2431	258	7	7	0	1.81.E+08	2.40.E+08	2.47.E+08	2.21.E+08	2.10.E+08	2.81.E+08	2.80.E+08	2.95.E+08
767	P42766	60S ribosomal protein L35 [OS=Homo sapiens]	61.9	37	6	278	6	2499	355	6	6	0	1.12.E+09	1.10.E+09	1.12.E+09	1.17.E+09	9.76.E+08	9.93.E+08	1.05.E+09	9.65.E+08
768	Q8WXX5	dnaJ homolog subfamily C member 9 [OS=Homo sapiens]	61.6	45	9	160	9	1098	174	8	9	0	2.30.E+08	2.05.E+08	1.90.E+08	2.10.E+08	2.35.E+08	2.65.E+08	2.16.E+08	2.23.E+08
769	P56545	c-terminal-binding protein 2 [OS=Homo sapiens]	61.6	22	5	154	5	2370	246	5	5	0	1.18.E+08	1.32.E+08	1.06.E+08	1.12.E+08	1.13.E+08	9.95.E+07	9.70.E+07	1.11.E+08
770	P60866	40S ribosomal protein S20 [OS=Homo sapiens]	61.5	24	4	491	4	5196	721	4	4	0	1.40.E+09	1.16.E+09	1.42.E+09	1.32.E+09	1.18.E+09	1.19.E+09	1.40.E+09	1.24.E+09
771	Q14126	Desmoglein-2 [OS=Homo sapiens]	61.4	14	10	216	10	1381	230	10	9	0	1.86.E+08	1.81.E+08	1.27.E+08	1.49.E+08	2.85.E+08	2.77.E+08	2.90.E+08	2.98.E+08
772	Q06323-1	Proteasome activator complex subunit 1 [OS=Homo sapiens]	61.2	52	8	152	8	1978	111	8	8	0	3.27.E+08	3.12.E+08	3.01.E+08	2.96.E+08	3.00.E+08	2.97.E+08	3.04.E+08	2.94.E+08
773	P67775	Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform [OS=Homo sapiens]	61.2	37	7	206	6	2982	317	7	7	1	3.06.E+08	3.52.E+08	3.12.E+08	3.07.E+08	3.81.E+08	4.07.E+08	3.19.E+08	4.11.E+08
774	Q7L1Q6-1	Basic leucine zipper and W2 domain-containing protein 1 [OS=Homo sapiens]	61.2	21	7	464	6	5854	536	7	6	1	3.63.E+08	3.56.E+08	3.73.E+08	3.37.E+08	3.45.E+08	3.53.E+08	3.29.E+08	3.45.E+08
775	Q9Y3F4	Serine-threonine kinase receptor-associated protein [OS=Homo sapiens]	60.9	47	9	144	9	1444	167	9	9	0	2.26.E+08	1.82.E+08	2.20.E+08	1.25.E+08	1.88.E+08	2.92.E+08	1.61.E+08	2.26.E+08
776	Q02543	60S ribosomal protein L18a [OS=Homo sapiens]	60.8	38	9	627	9	5845	812	9	9	0	1.26.E+09	1.23.E+09	1.34.E+09	1.22.E+09	9.78.E+08	9.84.E+08	1.12.E+09	1.03.E+09
777	O94992	Protein HEXIM1 [OS=Homo sapiens]	60.8	32	6	146	6	2570	228	6	6	0	1.71.E+08	1.87.E+08	1.06.E+08	1.79.E+08	3.52.E+08	3.42.E+08	3.36.E+08	3.36.E+08
778	P46781	40S ribosomal protein S9 [OS=Homo sapiens]	60.8	40	13	670	13	3067	533	13	13	0	3.52.E+09	3.41.E+09	3.61.E+09	3.35.E+09	2.86.E+09	2.88.E+09	3.16.E+09	3.01.E+09
779	O94979	Protein transport protein Sec31A [OS=Homo sapiens]	60.8	13	10	132	10	1024	146	10	10	0	2.11.E+08	2.04.E+08	1.93.E+08	1.50.E+08	1.86.E+08	2.35.E+08	2.42.E+08	2.24.E+08
780	Q6PKG0-1	La-related protein 1 [OS=Homo sapiens]	60.6	8	7	163	7	2191	112	6	6	0	1.08.E+08	1.30.E+08	1.24.E+08	1.03.E+08	1.20.E+08	1.28.E+08	9.94.E+07	1.30.E+08
781	P13798	Acylamino-acid-releasing enzyme [OS=Homo sapiens]	60.6	19	10	124	10	691	126	10	10	0	2.84.E+08	2.77.E+08	2.86.E+08	3.09.E+08	2.81.E+08	2.56.E+08	2.88.E+08	2.54.E+08
782	O15355	Protein phosphatase 1G [OS=Homo sapiens]	60.6	24	7	163	7	2697	218	7	7	0	1.74.E+08	1.64.E+08	1.50.E+08	1.73.E+08	2.00.E+08	1.99.E+08	1.83.E+08	1.99.E+08
783	P13995	Bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase, mitochondrial [OS=Homo sapiens]	60.4	39	7	234	7	2599	333	7	7	0	2.52.E+08	2.22.E+08	2.10.E+08	1.65.E+08	2.50.E+08	2.06.E+08	2.14.E+08	1.12.E+08
784	Q9H583	HEAT repeat-containing protein 1 [OS=Homo sapiens]	60.4	7	10	160	10	1205	83	10	10	0	8.02.E+07	8.68.E+07	8.32.E+07	8.60.E+07	1.02.E+08	9.83.E+07	9.33.E+07	9.53.E+07
785	P40261	Nicotinamide N-methyltransferase [OS=Homo sapiens]	60.3	43	6	134	6	1500	133	6	6	0	2.35.E+08	3.33.E+07	2.25.E+08	2.02.E+08	3.06.E+08	3.27.E+08	3.62.E+08	3.36.E+08
786	P62266	40S ribosomal protein S23 [OS=Homo sapiens]	60.3	43	5	360	5	4319	484	5	5	0	6.70.E+08	7.13.E+08	7.47.E+08	7.01.E+08	5.14.E+08	5.51.E+08	5.32.E+08	5.30.E+08
787	P16070	CD44 antigen [OS=Homo sapiens]	60.1	9	6	227	6	3586	309	6	6	0	5.21.E+08	5.23.E+08	5.13.E+08	4.73.E+08	3.62.E+08	3.44.E+08	3.74.E+08	3.46.E+08
788	O14975	very long-chain acyl-CoA synthetase [OS=Homo sapiens]	60.0	17	7	301	7	4086	253	7	7	0	1.24.E+08	1.37.E+08	1.19.E+08	1.34.E+08	1.51.E+08	1.43.E+08	1.40.E+08	1.49.E+08
789	Q00688	peptidyl-prolyl cis-trans isomerase FKBP3 [OS=Homo sapiens]	59.9	46	7	200	7	696	221	7	7	0	2.64.E+08	2.55.E+08	2.86.E+08	2.59.E+08	4.10.E+08	4.05.E+08	3.55.E+08	4.14.E+08
790	P49419	Alpha-aminoadipic semialdehyde dehydrogenase [OS=Homo sapiens]	59.8	22	7	127	7	3048	203	7	7	0	3.38.E+08	3.56.E+08	3.21.E+08	3.18.E+08	4.19.E+08	4.35.E+08	4.30.E+08	4.17.E+08
791	P46459	Vesicle-fusing ATPase [OS=Homo sapiens]	59.6	20	10	256	10	1952	198	10	9	0	1.54.E+08	1.75.E+08	1.18.E+08	1.41.E+08	2.10.E+08	2.06.E+08	2.05.E+08	2.65.E+08
792	O14880	Microsomal glutathione S-transferase 3 [OS=Homo sapiens]	59.6	60	5	38	5	861	65	4	5	0	1.19.E+08	1.16.E+08	7.00.E+07	1.12.E+08	5.38.E+07	5.06.E+07	3.45.E+07	4.73.E+07
793	P63000-1	Ras-related C3 botulinum toxin substrate 1 [OS=Homo sapiens]	59.3	55	8	238	7	1330	216	8	8	0	8.35.E+08	7.53.E+08	8.23.E+08	9.08.E+08	6.15.E+08	6.31.E+08	7.59.E+08	6.73.E+08
794	Q14978-3	Isoform 3 of Nucleolar and coiled-body phosphoprotein 1 [OS=Homo sapiens]	59.0	12	7	237	1		470	7		0								
795	P12270	Nucleoprotein TPR [OS=Homo sapiens]	58.9	6	9	186	9	2632	125	8	9	0	1.40.E+08	1.44.E+08	1.37.E+08	1.35.E+08	1.87.E+08	1.68.E+08	1.50.E+08	1.63.E+08
796	Q5VT79	annexin A8-like protein 1 [OS=Homo sapiens]	58.8	30	7	112	7	910	138	7	7	0	1.66.E+08	1.57.E+08	1.77.E+08	1.64.E+08	1.65.E+08	1.62.E+08	1.74.E+08	1.63.E+08
797	P63173	60s ribosomal protein l38 [OS=Homo sapiens]	58.7	53	4	452	4	7726	652	4	4	0	1.05.E+09	1.05.E+09	1.11.E+09	9.61.E+08	8.67.E+08	9.37.E+08	9.77.E+08	8.94.E+08
798	Q53FA7-1	Quinone oxidoreductase PIG3 [OS=Homo sapiens]	58.6	30	6	205	6	1596	228	6	6	0	2.02.E+08	2.21.E+08	2.15.E+08	2.23.E+08	2.71.E+08	2.64.E+08	2.79.E+08	2.75.E+08
799	O95757	Heat shock 70 kDa protein 4L [OS=Homo sapiens]	58.6	17	11	165	8	1815	180	11	10	1	2.30.E+08	2.15.E+08	2.11.E+08	2.26.E+08	2.16.E+08	1.86.E+08	1.94.E+08	1.92.E+08
800	Q9Y285	Phenylalanine--tRNA ligase alpha subunit [OS=Homo sapiens]	58.6	22	8	161	8	1746	188	7	8	0	1.93.E+08	2.81.E+08	2.01.E+08	3.23.E+08	3.66.E+08	3.54.E+08	3.42.E+08	3.68.E+08
801	P52888	thimet oligopeptidase [OS=Homo sapiens]	58.5	19	9	86	9	496	68	9	9	0	1.24.E+08	1.16.E+08	1.03.E+08	1.06.E+08	1.08.E+08	9.95.E+07	1.19.E+08	1.16.E+08
802	P48507	Glutamate--cysteine ligase regulatory subunit [OS=Homo sapiens]	58.4	38	6	191	6	2517	294	6	6	0	4.07.E+08	4.23.E+08	4.06.E+08	3.90.E+08	4.48.E+08	4.87.E+08	4.53.E+08	4.88.E+08
803	Q8WXF1	Paraspeckle component 1 [OS=Homo sapiens]	58.3	16	6	268	6	4055	372	6	6	0	1.69.E+08	1.72.E+08	1.76.E+08	1.63.E+08	1.67.E+08	1.69.E+08	1.69.E+08	1.67.E+08
804	P84243	histone H3.3 [OS=Homo sapiens]	58.3	48	6	1353	1	18692	1781	6	5	0	8.65.E+08	8.98.E+08	8.06.E+08	8.01.E+08	4.75.E+08	4.38.E+08	3.77.E+08	4.26.E+08
805	P55769	NHP2-like protein 1 [OS=Homo sapiens]	58.2	47	6	286	6	3349	382	6	5	0	4.94.E+08	4.49.E+08	4.71.E+08	5.09.E+08	4.06.E+08	3.64.E+08	4.08.E+08	3.86.E+08
806	Q9NVA2-1	Septin-11 [OS=Homo sapiens]	58.2	28	10	281	7	2940	260	9	9	3	6.08.E+08	6.05.E+08	6.16.E+08	6.02.E+08	6.95.E+08	7.42.E+08	7.25.E+08	7.38.E+08
807	Q14108-1	Lysosome membrane protein 2 [OS=Homo sapiens]	58.2	18	6	176	6	911	216	5	6	0	2.68.E+08	2.62.E+08	2.83.E+08	2.60.E+08	3.95.E+08	3.33.E+08	3.52.E+08	3.57.E+08
808	Q9BUP3	Oxidoreductase htatip2 [OS=Homo sapiens]	58.0	47	8	141	8	659	187	8	8	0	2.43.E+08	2.48.E+08	2.11.E+08	2.13.E+08	3.76.E+08	3.66.E+08	3.57.E+08	3.74.E+08
809	Q9Y266	nuclear migration protein nudC [OS=Homo sapiens]	57.6	18	4	176	4	1164	180	4	4	0	1.92.E+08	1.87.E+08	1.87.E+08	2.22.E+08	2.04.E+08	2.06.E+08	2.29.E+08	2.18.E+08
810	P62829	60S ribosomal protein L23 [OS=Homo sapiens]	57.6	51	6	394	6	7043	510	6	6	0	1.54.E+09	1.57.E+09	1.57.E+09	1.44.E+09	1.48.E+09	1.50.E+09	1.35.E+09	1.47.E+09
811	P16949-1	Stathmin [OS=Homo sapiens]	57.6	32	7	438	7	4978	584	7	7	0	9.54.E+08	9.31.E+08	9.42.E+08	8.17.E+08	1.16.E+09	1.22.E+09	1.23.E+09	1.19.E+09
812	P52294	Importin subunit alpha-5 [OS=Homo sapiens]	57.5	21	6	225	3	1820	210	6	6	0	4.82.E+07	5.25.E+07	4.65.E+07	7.51.E+07	3.46.E+07	5.12.E+07	2.28.E+07	3.47.E+07
813	Q9UBQ5	Eukaryotic translation initiation factor 3 subunit K [OS=Homo sapiens]	57.4	53	7	148	7	1311	182	7	7	0	2.12.E+08	2.29.E+08	2.24.E+08	1.93.E+08	1.77.E+08	1.82.E+08	1.75.E+08	1.73.E+08
814	O43795	Unconventional myosin-Ib [OS=Homo sapiens]	57.4	12	8	78	7	588	74	8	8	0	4.99.E+07	4.75.E+07	4.47.E+07	6.30.E+07	7.91.E+07	1.13.E+08	8.61.E+07	9.80.E+07
815	P10768	S-formylglutathione hydrolase [OS=Homo sapiens]	57.1	50	7	200	7	1808	201	7	7	0	2.70.E+08	2.58.E+08	2.23.E+08	2.75.E+08	2.96.E+08	2.87.E+08	2.66.E+08	2.65.E+08
816	Q13561-1	dynactin subunit 2 [OS=Homo sapiens]	57.0	18	5	90	5	1003	132	5	5	0	1.48.E+08	1.56.E+08	1.49.E+08	1.74.E+08	2.21.E+08	2.09.E+08	2.15.E+08	2.06.E+08
817	Q9Y696	Chloride intracellular channel protein 4 [OS=Homo sapiens]	57.0	43	8	411	7	5759	476	8	7	0	1.98.E+08	2.04.E+08	1.89.E+08	2.03.E+08	3.19.E+08	3.17.E+08	3.03.E+08	3.25.E+08
818	Q07065	Cytoskeleton-associated protein 4 [OS=Homo sapiens]	56.9	23	7	49	7	1195	67	7	7	0	3.41.E+07	3.08.E+07	3.01.E+07	3.76.E+07	6.99.E+07	6.24.E+07	6.73.E+07	6.64.E+07
819	P09525	annexin A4 [OS=Homo sapiens]	56.8	35	9	162	9	1383	202	9	9	0	3.58.E+08	3.67.E+08	3.61.E+08	3.69.E+08	4.18.E+08	4.27.E+08	4.18.E+08	4.17.E+08

No.	Accession	Description	Sum PEP Score	Coverage [%]	# Peptides	# PSMs	# Unique Peptides	Score Mascot: A5 Mascot	Score Sequest HT: A2 Sequest HT	# Peptides (by Search Engine): A2 Sequest HT	# Peptides (by Search Engine): A5 Mascot	# Razor Peptides	ctrl Abundance s_1	ctrl Abundance s_2	ctrl Abundance s_3	ctrl Abundance s_4	JAM-A KO Abundance s_1	JAM-A KO Abundance s_2	JAM-A KO Abundance s_3	JAM-A KO Abundance s_4
820	P35270	Sepiapterin reductase [OS=Homo sapiens]	56.8	27	4	248	4	3787	262	4	4	0	5.87.E+07	5.48.E+07	5.49.E+07	5.22.E+07	5.40.E+07	5.01.E+07	4.69.E+07	4.82.E+07
821	P20073-1	Annexin A7 [OS=Homo sapiens]	56.5	20	8	302	8	3614	402	8	8	0	4.05.E+08	4.15.E+08	4.08.E+08	3.71.E+08	4.90.E+08	4.92.E+08	4.85.E+08	4.78.E+08
822	Q16851	UTP--glucose-1-phosphate uridylyltransferase [OS=Homo sapiens]	56.4	22	7	143	7	1876	185	7	7	0	1.15.E+08	1.37.E+08	1.37.E+08	1.14.E+08	1.98.E+08	2.04.E+08	1.80.E+08	2.23.E+08
823	P61106	Ras-related protein Rab-14 [OS=Homo sapiens]	56.2	42	7	329	5	4355	452	6	7	0	1.68.E+08	1.72.E+08	1.65.E+08	1.69.E+08	1.77.E+08	1.68.E+08	1.75.E+08	1.74.E+08
824	P51398-1	28S ribosomal protein S29, mitochondrial [OS=Homo sapiens]	56.0	35	9	148	9	1333	159	9	9	0	1.60.E+08	1.66.E+08	1.51.E+08	1.57.E+08	1.41.E+08	1.37.E+08	1.41.E+08	1.36.E+08
825	P28340	DNA polymerase delta catalytic subunit [OS=Homo sapiens]	55.9	13	9	198	8	2057	175	9	9	0	6.68.E+07	1.04.E+08	9.48.E+07	8.99.E+07	9.33.E+07	8.25.E+07	8.24.E+07	6.80.E+07
826	Q9P035	Very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase 3 [OS=Homo sapiens]	55.8	25	6	235	6	4549	314	6	6	0	2.81.E+08	2.92.E+08	2.26.E+08	3.04.E+08	4.11.E+08	4.13.E+08	3.12.E+08	3.97.E+08
827	P08240-1	signal recognition particle receptor subunit alpha [OS=Homo sapiens]	55.8	20	8	100	8	989	74	8	8	0	8.66.E+07	1.40.E+08	1.14.E+08	1.36.E+08	1.31.E+08	1.33.E+08	1.23.E+08	1.37.E+08
828	Q9UHX1-1	poly(U)-binding-splicing factor PUF60 [OS=Homo sapiens]	55.7	23	9	223	9	1153	198	9	9	0	2.28.E+08	2.16.E+08	2.19.E+08	2.01.E+08	2.13.E+08	2.21.E+08	2.21.E+08	2.19.E+08
829	Q12849	G-rich sequence factor 1 [OS=Homo sapiens]	55.7	20	5	224	5	4174	317	5	5	0	1.49.E+08	1.74.E+08	2.39.E+08	2.19.E+08	1.34.E+08	1.73.E+08	1.34.E+08	1.76.E+08
830	P55735-1	protein SEC13 homolog [OS=Homo sapiens]	55.6	29	4	117	4	4038	204	3	4	0	1.17.E+08	1.22.E+08	1.03.E+08	1.29.E+08	1.20.E+08	1.13.E+08	9.81.E+07	1.10.E+08
831	Q12965	unconventional myosin-Ie [OS=Homo sapiens]	55.6	15	10	88	9	1001	96	10	10	0	1.56.E+08	1.32.E+08	1.22.E+08	1.43.E+08	1.82.E+08	1.68.E+08	1.45.E+08	1.81.E+08
832	Q9Y383	Putative RNA-binding protein Luc7-like 2 [OS=Homo sapiens]	55.6	17	5	194	5	1902	198	5	5	0	1.76.E+08	1.62.E+08	1.83.E+08	1.63.E+08	1.91.E+08	1.89.E+08	2.04.E+08	1.85.E+08
833	Q16891	MICOS complex subunit Mic60 [OS=Homo sapiens]	55.4	16	7	128	7	876	179	7	7	0	1.65.E+08	1.66.E+08	1.75.E+08	1.78.E+08	1.57.E+08	1.62.E+08	1.68.E+08	2.13.E+08
834	P48637	glutathione synthetase [OS=Homo sapiens]	55.4	26	8	188	8	2093	196	7	8	0	2.72.E+08	2.83.E+08	2.63.E+08	2.75.E+08	3.33.E+08	3.32.E+08	3.00.E+08	3.31.E+08
835	Q96I99-1	Succinate--CoA ligase [GDP-forming] subunit beta, mitochondrial [OS=Homo sapiens]	55.4	27	9	193	9	986	156	9	8	0	2.60.E+08	2.62.E+08	2.65.E+08	2.57.E+08	3.63.E+08	3.61.E+08	3.51.E+08	3.61.E+08
836	Q9UNS2	COP9 signalosome complex subunit 3 [OS=Homo sapiens]	55.3	24	5	101	5	2495	69	4	5	0	1.42.E+08	1.61.E+08	1.16.E+08	1.38.E+08	1.51.E+08	1.49.E+08	1.46.E+08	1.49.E+08
837	P62318	small nuclear ribonucleoprotein sm d3 [OS=Homo sapiens]	55.2	32	3	392	3	5324	631	3	3	0	5.29.E+08	5.32.E+08	5.10.E+08	5.90.E+08	5.48.E+08	5.20.E+08	5.46.E+08	5.62.E+08
838	P04792	Heat shock protein beta-1 [OS=Homo sapiens]	55.1	62	8	114	8	1576	179	8	8	0	4.70.E+07	6.53.E+07	5.43.E+07	5.32.E+07	2.25.E+08	2.33.E+08	2.20.E+08	2.32.E+08
839	O14744	Protein arginine N-methyltransferase 5 [OS=Homo sapiens]	55.0	24	9	142	9	971	145	9	9	0	1.85.E+08	1.64.E+08	2.05.E+08	2.06.E+08	1.90.E+08	2.30.E+08	1.85.E+08	1.73.E+08
840	P55084	Trifunctional enzyme subunit beta, mitochondrial [OS=Homo sapiens]	54.9	19	7	206	7	1915	246	7	7	0	2.49.E+08	2.42.E+08	2.56.E+08	2.44.E+08	2.90.E+08	2.73.E+08	2.95.E+08	2.83.E+08
841	P51648	Fatty aldehyde dehydrogenase [OS=Homo sapiens]	54.8	15	5	119	4	982	156	5	5	0	1.08.E+08	1.07.E+08	9.57.E+07	1.02.E+08	1.87.E+07	2.45.E+07	1.84.E+07	3.44.E+07
842	P48739	Phosphatidylinositol transfer protein beta isoform [OS=Homo sapiens]	54.7	42	8	170	5	877	194	8	8	3	2.59.E+08	2.76.E+08	2.85.E+08	2.77.E+08	2.89.E+08	2.87.E+08	2.79.E+08	2.88.E+08
843	O60739	eukaryotic translation initiation factor 1b [OS=Homo sapiens]	54.7	65	6	94	1	1227	115	5	6	0		6.61.E+06		4.81.E+06	1.42.E+07	9.91.E+05		1.54.E+07
844	Q99536	Synaptic vesicle membrane protein VAT-1 homolog [OS=Homo sapiens]	54.6	22	5	110	5	1092	167	5	5	0	1.22.E+08	1.29.E+08	8.87.E+07	6.65.E+07	1.35.E+08	1.34.E+08	1.35.E+08	1.22.E+08
845	P49721	proteasome subunit beta type-2 [OS=Homo sapiens]	54.3	48	8	144	8	1601	168	8	8	0	1.94.E+08	2.06.E+08	1.76.E+08	2.07.E+08	2.86.E+08	3.00.E+08	2.76.E+08	2.89.E+08
846	P40121	Macrophage-capping protein [OS=Homo sapiens]	54.3	34	8	107	8	868	124	8	8	0	1.35.E+08	1.32.E+08	1.07.E+08	1.22.E+08	7.47.E+07	7.16.E+07	8.57.E+07	8.40.E+07
847	P28070	Proteasome subunit beta type-4 [OS=Homo sapiens]	54.2	43	7	231	7	2466	269	7	7	0	3.06.E+08	3.14.E+08	2.95.E+08	3.48.E+08	3.15.E+08	2.88.E+08	2.91.E+08	2.97.E+08
848	P10620	Microsomal glutathione S-transferase 1 [OS=Homo sapiens]	54.2	23	4	168	4	1922	264	4	4	0	3.46.E+08	3.21.E+08	3.46.E+08	3.08.E+08	5.36.E+08	5.49.E+08	5.94.E+08	5.21.E+08
849	Q9UQB8	Brain-specific angiogenesis inhibitor 1-associated protein 2 [OS=Homo sapiens]	54.1	24	10	133	10	1116	160	10	10	0	2.24.E+08	2.77.E+08	2.24.E+08	2.30.E+08	2.07.E+08	2.16.E+08	1.62.E+08	1.85.E+08
850	Q9BQ67	Glutamate-rich WD repeat-containing protein 1 [OS=Homo sapiens]	54.0	21	6	127	6	1181	170	6	5	0	2.42.E+08	2.83.E+08	2.11.E+08	2.67.E+08	1.29.E+08	1.44.E+08	1.12.E+08	1.42.E+08
851	Q03135	Caveolin-1 [OS=Homo sapiens]	53.9	44	6	168	6	1006	234	6	5	0	1.87.E+08	1.93.E+08	1.93.E+08	2.05.E+08	1.55.E+08	1.50.E+08	1.61.E+08	1.51.E+08
852	P07686	Beta-hexosaminidase subunit beta [OS=Homo sapiens]	53.9	15	5	116	5	580	150	5	5	0	9.50.E+07	7.78.E+07	7.38.E+07	8.81.E+07	3.56.E+08	3.64.E+08	2.84.E+08	3.45.E+08
853	P30085-1	UMP-CMP kinase [OS=Homo sapiens]	53.8	51	7	452	7	3423	266	7	7	0	3.22.E+08	3.35.E+08	3.20.E+08	3.13.E+08	4.21.E+08	4.23.E+08	4.19.E+08	4.13.E+08
854	P34896-1	Serine hydroxymethyltransferase, cytosolic [OS=Homo sapiens]	53.6	22	6	118	5	2989	187	6	6	0	6.21.E+07	6.71.E+07	4.89.E+07	5.75.E+07	5.90.E+07	5.38.E+07	4.43.E+07	5.46.E+07
855	P68400	Casein kinase II subunit alpha [OS=Homo sapiens]	53.5	32	8	139	8	1800	222	7	7	0	2.68.E+08	3.08.E+08	2.60.E+08	3.32.E+08	3.04.E+08	3.27.E+08	2.89.E+08	3.26.E+08
856	Q9P0L0	vesicle-associated membrane protein-associated protein A [OS=Homo sapiens]	53.5	35	6	202	6	1018	150	6	6	0	2.03.E+08	2.04.E+08	2.11.E+08	1.78.E+08	2.08.E+08	2.30.E+08	2.36.E+08	2.17.E+08
857	Q01844	RNA-binding protein EWS [OS=Homo sapiens]	53.5	7	4	124	4	1944	188	4	3	0	2.17.E+08	2.35.E+08	2.30.E+08	2.03.E+08	2.34.E+08	2.39.E+08	2.42.E+08	2.31.E+08
858	P18754-1	Regulator of chromosome condensation [OS=Homo sapiens]	53.4	19	5	166	5	2669	189	5	5	0	1.88.E+08	1.87.E+08	1.90.E+08	1.83.E+08	1.94.E+08	1.87.E+08	1.80.E+08	1.93.E+08
859	Q15942	Zyxin [OS=Homo sapiens]	53.4	22	7	178	7	2382	207	7	7	0	8.92.E+07	7.34.E+07	8.21.E+07	9.11.E+07	1.85.E+08	1.74.E+08	1.75.E+08	1.74.E+08
860	P48444	Coatomer subunit delta [OS=Homo sapiens]	53.3	23	9	251	9	2030	271	7	9	0	2.26.E+08	2.28.E+08	2.21.E+08	2.37.E+08	3.04.E+08	2.79.E+08	2.32.E+08	2.83.E+08
861	Q99471-1	prefoldin subunit 5 [OS=Homo sapiens]	53.2	43	4	224	4	5572	284	3	4	0	9.85.E+07	1.13.E+08	1.00.E+08	1.07.E+08	1.46.E+08	1.37.E+08	1.27.E+08	1.33.E+08
862	O00469-1	procollagen-lysine,2-oxoglutarate 5-dioxygenase 2 [OS=Homo sapiens]	53.2	15	8	150	8	1411	103	8	8	0	2.56.E+07	2.32.E+07	1.28.E+07	1.80.E+07	1.25.E+08	1.20.E+08	1.16.E+08	1.23.E+08
863	Q16718	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5 [OS=Homo sapiens]	53.0	58	4	172	4	1809	286	4	4	0	1.49.E+08	1.49.E+08	1.49.E+08	1.49.E+08	1.99.E+08	1.97.E+08	1.65.E+08	1.89.E+08
864	Q9NR31	GTP-binding protein SAR1a [OS=Homo sapiens]	52.6	56	7	261	4	2625	337	7	6	3	4.64.E+08	4.88.E+08	4.46.E+08	4.58.E+08	4.58.E+08	4.68.E+08	4.38.E+08	3.82.E+08
865	P61916	Epididymal secretory protein E1 [OS=Homo sapiens]	52.6	41	4	292	4	2832	432	4	4	0	3.28.E+08	3.44.E+08	3.31.E+08	3.70.E+08	4.09.E+08	3.96.E+08	3.57.E+08	3.29.E+08
866	Q9UQ35	serine/arginine repetitive matrix protein 2 [OS=Homo sapiens]	52.5	5	9	137	9	771	161	9	9	0	3.92.E+08	3.72.E+08	4.16.E+08	3.52.E+08	3.85.E+08	3.92.E+08	4.58.E+08	4.11.E+08
867	P42126	Enoyl-CoA delta isomerase 1, mitochondrial [OS=Homo sapiens]	52.2	30	7	104	7	941	109	7	7	0	1.85.E+08	2.05.E+08	1.39.E+08	1.88.E+08	1.28.E+08	1.61.E+08	1.29.E+08	1.58.E+08
868	P61254	60S ribosomal protein L26 [OS=Homo sapiens]	52.0	43	10	400	10	1931	315	10	10	0	6.92.E+08	6.54.E+08	7.18.E+08	6.16.E+08	5.49.E+08	5.70.E+08	6.25.E+08	5.66.E+08
869	Q9P2E9-1	Ribosome-binding protein 1 [OS=Homo sapiens]	51.9	11	9	68	9		150	9		0	8.01.E+07	8.26.E+07	7.76.E+07	7.59.E+07	1.10.E+08	1.03.E+08	9.60.E+07	9.26.E+07
870	Q9NQR4	Omega-amidase NIT2 [OS=Homo sapiens]	51.8	37	6	140	6	1616	203	6	6	0	1.02.E+08	1.09.E+08	9.44.E+07	1.06.E+08	9.78.E+07	9.82.E+07	8.65.E+07	1.00.E+08
871	Q9Y6C9	Mitochondrial carrier homolog 2 [OS=Homo sapiens]	51.7	31	5	82	5	1288	133	4	5	0	1.23.E+08	1.09.E+08	1.12.E+08	1.23.E+08	1.02.E+08	9.99.E+07	1.05.E+08	9.79.E+07

No.	Accession	Description	Sum PEP Score	Coverage [%]	# Peptides	# PSMs	# Unique Peptides	Score Mascot: A5 Mascot	Score Sequest HT: A2 Sequest HT	# Peptides (by Search Engine): A2 Sequest HT	# Peptides (by Search Engine): A5 Mascot	# Razor Peptides	ctrl Abundance s_1	ctrl Abundance s_2	ctrl Abundance s_3	ctrl Abundance s_4	JAM-A KO Abundance s_1	JAM-A KO Abundance s_2	JAM-A KO Abundance s_3	JAM-A KO Abundance s_4
872	P52815	39S ribosomal protein L12, mitochondrial [OS=Homo sapiens]	51.6	24	5	132	5	2313	220	5	5	0	2.05.E+08	1.89.E+08	2.16.E+08	2.19.E+08	2.32.E+08	2.23.E+08	2.36.E+08	2.28.E+08
873	O00429	Dynamin-1-like protein [OS=Homo sapiens]	51.6	15	6	144	6	2860	144	6	6	0	6.01.E+07	6.96.E+07	5.44.E+07	7.16.E+07	1.01.E+08	9.07.E+07	8.21.E+07	9.15.E+07
874	Q8N6T3-1	ADP-ribosylation factor GTPase-activating protein 1 [OS=Homo sapiens]	51.4	35	7	103	7	1089	99	7	7	0	1.30.E+08	1.43.E+08	9.49.E+07	1.13.E+08	1.88.E+08	1.92.E+08	1.74.E+08	1.90.E+08
875	P49753-1	Acyl-coenzyme A thioesterase 2, mitochondrial [OS=Homo sapiens]	51.4	27	8	132	1	1942	162	8	7	7	2.59.E+08	2.14.E+08	2.25.E+08	2.42.E+08	2.58.E+08	2.46.E+08	2.50.E+08	2.61.E+08
876	O75822	Eukaryotic translation initiation factor 3 subunit J [OS=Homo sapiens]	51.4	29	8	90	8	2012	146	8	8	0	2.95.E+08	3.31.E+08	2.95.E+08	3.20.E+08	3.45.E+08	3.44.E+08	3.64.E+08	3.46.E+08
877	P62995	transformer-2 protein homolog beta [OS=Homo sapiens]	51.4	33	7	219	6	2434	243	7	7	1	2.51.E+08	2.94.E+08	2.73.E+08	2.80.E+08	2.33.E+08	2.45.E+08	2.62.E+08	2.61.E+08
878	P63151	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform [OS=Homo sapiens]	51.4	24	7	297	7	4635	328	7	7	0	1.74.E+08	1.82.E+08	1.74.E+08	1.82.E+08	1.58.E+08	1.57.E+08	1.56.E+08	1.71.E+08
879	Q9BZE9	tether containing UBX domain for GLUT4 [OS=Homo sapiens]	51.4	19	6	106	6	1961	125	6	5	0	1.03.E+08	9.50.E+07	9.48.E+07	9.31.E+07	8.72.E+07	8.19.E+07	6.40.E+07	8.20.E+07
880	Q13895	Bystin [OS=Homo sapiens]	51.3	21	7	207	7	2594	190	7	7	0	1.56.E+08	1.69.E+08	1.44.E+08	1.62.E+08	1.72.E+08	1.68.E+08	1.72.E+08	1.76.E+08
881	Q8TAT6-1	Nuclear protein localization protein 4 homolog [OS=Homo sapiens]	51.3	22	8	162	8	1999	175	7	6	0	1.08.E+08	1.15.E+08	9.20.E+07	9.88.E+07	8.85.E+07	8.36.E+07	8.35.E+07	1.01.E+08
882	P46108-1	Adapter molecule crk [OS=Homo sapiens]	51.2	36	8	175	8	1630	205	8	8	0	2.21.E+08	1.95.E+08	2.00.E+08	2.08.E+08	1.78.E+08	1.43.E+08	1.71.E+08	1.44.E+08
883	P0DMM9	Sulfotransferase 1A3 [OS=Homo sapiens]	51.1	38	7	231	7	502	295	7	7	0	2.52.E+08	2.33.E+08	2.22.E+08	2.38.E+08	4.12.E+08	4.18.E+08	3.80.E+08	4.10.E+08
884	Q9BYN0	sulfiredoxin-1 [OS=Homo sapiens]	51.0	61	6	255	6	1017	426	6	6	0	5.11.E+08	5.31.E+08	4.50.E+08	5.98.E+08	5.26.E+08	5.34.E+08	4.88.E+08	5.21.E+08
885	P31350-1	ribonucleoside-diphosphate reductase subunit M2 [OS=Homo sapiens]	50.9	18	5	122	5	2037	181	5	5	0	1.82.E+08	2.53.E+08	2.52.E+08	2.49.E+08	2.40.E+08	2.34.E+08	2.26.E+08	1.64.E+08
886	Q8TDN6	Ribosome biogenesis protein BRX1 homolog [OS=Homo sapiens]	50.8	37	9	222	9	1679	132	9	7	0	1.76.E+08	1.87.E+08	1.79.E+08	1.88.E+08	1.90.E+08	2.17.E+08	1.61.E+08	1.75.E+08
887	Q14376	UDP-glucose 4-epimerase [OS=Homo sapiens]	50.8	32	6	60	6	583	82	6	6	0	9.26.E+07	9.08.E+07	8.86.E+07	9.76.E+07	1.10.E+08	7.63.E+07	1.09.E+08	9.82.E+07
888	P25788-1	Proteasome subunit alpha type-3 [OS=Homo sapiens]	50.7	24	6	108	6	1082	94	5	5	0	2.36.E+08	2.22.E+08	2.51.E+08	2.59.E+08	3.08.E+08	2.97.E+08	3.41.E+08	3.07.E+08
889	Q08257	Quinone oxidoreductase [OS=Homo sapiens]	50.7	30	6	191	6	2673	334	6	6	0	1.97.E+08	2.10.E+08	2.00.E+08	2.06.E+08	4.21.E+08	4.30.E+08	4.07.E+08	4.26.E+08
890	Q96FQ6	Protein S100-A16 [OS=Homo sapiens]	50.6	57	6	152	6	2436	178	6	6	0	2.01.E+08	1.97.E+08	2.01.E+08	2.10.E+08	9.34.E+07	8.59.E+07	4.19.E+07	8.83.E+07
891	P12830	Cadherin-1 [OS=Homo sapiens]	50.6	15	6	96	6	2343	148	6	6	0	5.36.E+07	6.19.E+07	8.76.E+07	6.36.E+07	1.35.E+08	1.82.E+08	1.41.E+08	1.37.E+08
892	P49902	Cytosolic purine 5'-nucleotidase [OS=Homo sapiens]	50.5	19	6	122	6	1209	123	6	6	0	5.22.E+07	6.80.E+07	6.18.E+07	7.05.E+07	8.89.E+07	6.64.E+07	7.48.E+07	8.32.E+07
893	O00204	Sulfotransferase family cytosolic 2B member 1 [OS=Homo sapiens]	50.5	25	5	93	5	468	75	5	4	0	1.31.E+08	1.28.E+08	1.44.E+08	1.39.E+08	7.44.E+07	7.18.E+07	7.24.E+07	7.15.E+07
894	P49755	Transmembrane emp24 domain-containing protein 10 [OS=Homo sapiens]	50.5	27	5	187	5	1764	167	5	5	0	4.14.E+08	4.30.E+08	4.40.E+08	4.14.E+08	4.09.E+08	4.40.E+08	5.09.E+08	4.66.E+08
895	P29966	Myristoylated alanine-rich C-kinase substrate [OS=Homo sapiens]	50.4	24	5	114	5	535	73	5	5	0	6.55.E+07	6.77.E+07	7.36.E+07	6.24.E+07	1.50.E+08	1.54.E+08	1.59.E+08	1.52.E+08
896	Q9BZQ8	Protein Niban [OS=Homo sapiens]	50.3	8	5	107	5	1037	129	5	5	0	6.31.E+07	7.01.E+07	5.38.E+07	7.63.E+07	3.84.E+07	3.65.E+07	4.18.E+07	3.11.E+07
897	P62910	60S ribosomal protein L32 [OS=Homo sapiens]	50.3	49	6	351	6	3118	332	5	6	0	8.87.E+08	8.43.E+08	8.93.E+08	8.70.E+08	5.75.E+08	5.81.E+08	6.68.E+08	6.05.E+08
898	Q96C90	Protein phosphatase 1 regulatory subunit 14B [OS=Homo sapiens]	50.2	43	6	116	6	1206	92	6	6	0	5.69.E+07	6.30.E+07	5.39.E+07	5.99.E+07	1.28.E+08	2.99.E+07	2.77.E+07	3.11.E+07
899	P42677	40S ribosomal protein S27 [OS=Homo sapiens]	50.1	40	5	433	5	3404	466	5	5	0	6.92.E+08	6.65.E+08	6.13.E+08	7.15.E+08	4.91.E+08	5.24.E+08	5.41.E+08	5.26.E+08
900	Q13492-1	Phosphatidylinositol-binding clathrin assembly protein [OS=Homo sapiens]	50.0	17	6	105	6	1315	108	6	6	0	6.31.E+07	7.67.E+07	5.98.E+07	7.21.E+07	8.49.E+07	7.76.E+07	6.91.E+07	6.50.E+07
901	Q86TX2	acyl-coenzyme A thioesterase 1 [OS=Homo sapiens]	49.8	28	8	124	1	1953	162	7	7	0	3.97.E+07	3.73.E+07	4.06.E+07	3.62.E+07	4.86.E+07	4.96.E+07	5.65.E+07	5.22.E+07
902	P38117	electron transfer flavoprotein subunit beta [OS=Homo sapiens]	49.8	29	6	253	6	3529	305	6	6	0	3.13.E+08	3.17.E+08	3.25.E+08	2.87.E+08	2.87.E+08	2.93.E+08	3.03.E+08	2.99.E+08
903	P04062	glucosylceramidase [OS=Homo sapiens]	49.8	18	4	144	4	1831	248	4	4	0	8.75.E+07	9.53.E+07	8.25.E+07	6.50.E+07	1.39.E+08	1.43.E+08	9.63.E+07	1.21.E+08
904	Q9UHD1	cysteine and histidine-rich domain-containing protein 1 [OS=Homo sapiens]	49.6	29	7	138	7	379	132	7	6	0	1.68.E+08	1.75.E+08	1.70.E+08	1.53.E+08	1.93.E+08	1.93.E+08	2.02.E+08	1.94.E+08
905	O43598-1	2'-deoxynucleoside 5'-phosphate N-hydrolase 1 [OS=Homo sapiens]	49.6	54	5	210	5	3213	334	5	5	0	3.29.E+08	3.50.E+08	3.46.E+08	3.05.E+08	3.72.E+08	4.09.E+08	3.86.E+08	4.31.E+08
906	Q8NCW5	NAD(P)H-hydrate epimerase [OS=Homo sapiens]	49.6	35	8	269	8	1002	268	8	8	0	2.46.E+08	3.37.E+08	3.35.E+08	3.77.E+08	2.76.E+08	3.99.E+08	2.75.E+08	4.14.E+08
907	Q709C8	Vacuolar protein sorting-associated protein 13C [OS=Homo sapiens]	49.6	4	8	119	8	984	107	8	8	0	8.44.E+07	1.10.E+08	9.75.E+07	8.92.E+07	8.78.E+07	5.61.E+07	6.46.E+07	1.14.E+08
908	P55036-1	26S proteasome non-ATPase regulatory subunit 4 [OS=Homo sapiens]	49.4	23	5	68	5	609	90	5	5	0	2.74.E+08	2.32.E+08	2.48.E+08	2.34.E+08	1.97.E+08	2.67.E+08	3.23.E+08	3.61.E+08
909	Q9H3P7	Golgi resident protein GCP60 [OS=Homo sapiens]	49.4	13	4	79	4	1463	122	4	4	0	4.62.E+07	4.78.E+07	4.60.E+07	5.13.E+07	6.25.E+07	4.10.E+07	6.05.E+07	6.08.E+07
910	Q92621	Nuclear pore complex protein Nup205 [OS=Homo sapiens]	49.3	4	5	80	5	1849	110	5	5	0	5.35.E+07	4.28.E+07	4.03.E+07	4.68.E+07	4.94.E+07	8.33.E+07	6.77.E+07	6.97.E+07
911	Q9NYF8-1	Bcl-2-associated transcription factor 1 [OS=Homo sapiens]	49.3	13	10	149	10	527	135	10	8	0	2.01.E+08	1.69.E+08	2.06.E+08	1.59.E+08	2.32.E+08	2.16.E+08	2.20.E+08	2.16.E+08
912	O14828	Secretory carrier-associated membrane protein 3 [OS=Homo sapiens]	49.3	27	5	67	5	1328	91	5	5	0	1.54.E+08	2.05.E+08	1.75.E+08	1.85.E+08	2.47.E+08	2.19.E+08	2.27.E+08	2.13.E+08
913	Q9NR45	sialic acid synthase [OS=Homo sapiens]	49.1	39	8	115	8	1264	110	7	8	0	1.23.E+08	1.47.E+08	1.35.E+08	1.12.E+08	1.41.E+08	1.54.E+08	1.43.E+08	1.33.E+08
914	P28838	cytosol aminopeptidase [OS=Homo sapiens]	48.8	22	8	224	8	1503	246	8	8	0	1.47.E+08	1.63.E+08	1.36.E+08	1.59.E+08	2.20.E+08	2.02.E+08	1.73.E+08	2.03.E+08
915	O60841	Eukaryotic translation initiation factor 5B [OS=Homo sapiens]	48.8	14	8	105	8	872	76	7	8	0	1.15.E+08	1.34.E+08	1.09.E+08	8.70.E+07	1.04.E+08	1.30.E+08	1.44.E+08	1.49.E+08
916	P49756-1	RNA-binding protein 25 [OS=Homo sapiens]	48.6	15	8	157	8	740	150	8	8	0	2.53.E+08	1.92.E+08	1.78.E+08	2.47.E+08	1.73.E+08	1.73.E+08	1.82.E+08	1.52.E+08
917	Q14764	major vault protein [OS=Homo sapiens]	48.5	17	8	72	8	753	53	7	8	0	7.19.E+07	6.53.E+07	6.69.E+07	6.92.E+07	2.61.E+07	2.60.E+07	2.69.E+07	2.75.E+07
918	Q13148-1	TAR DNA-binding protein 43 [OS=Homo sapiens]	48.4	21	4	271	4	5596	488	4	4	0	2.27.E+08	2.41.E+08	2.28.E+08	2.45.E+08	2.49.E+08	2.33.E+08	2.25.E+08	2.45.E+08
919	Q13362	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit gamma isoform [OS=Homo sapiens]	48.4	19	7	137	4	1758	137	7	7	3	1.19.E+08	1.26.E+08	1.27.E+08	1.43.E+08	1.72.E+08	1.67.E+08	1.60.E+08	1.59.E+08

No.	Accession	Description	Sum PEP Score	Coverage [%]	# Peptides	# PSMs	# Unique Peptides	Score Mascot: A5 Mascot	Score Sequest HT: A2 Sequest HT	# Peptides (by Search Engine): A2 Sequest HT	# Peptides (by Search Engine): A5 Mascot	# Razor Peptides	ctrl Abundances_1	ctrl Abundances_2	ctrl Abundances_3	ctrl Abundances_4	JAM-A KO Abundances_1	JAM-A KO Abundances_2	JAM-A KO Abundances_3	JAM-A KO Abundances_4
920	Q02978	Mitochondrial 2-oxoglutarate/malate carrier protein [OS=Homo sapiens]	48.4	22	6	197	6	3211	149	5	6	0	2.05.E+08	2.13.E+08	1.87.E+08	2.17.E+08	1.36.E+08	1.58.E+08	1.47.E+08	1.60.E+08
921	P10155-1	60 kDa SS-A/Ro ribonucleoprotein [OS=Homo sapiens]	48.4	15	6	156	6	1509	108	6	6	0	1.34.E+08	1.53.E+08	1.50.E+08	1.61.E+08	1.44.E+08	1.76.E+08	9.40.E+07	1.54.E+08
922	Q01130	serine/arginine-rich splicing factor 2 [OS=Homo sapiens]	48.3	22	5	137	5	2968	85	3	5	0	4.88.E+08	4.18.E+08	4.94.E+08	5.25.E+08	4.72.E+08	4.34.E+08	4.93.E+08	4.40.E+08
923	P51812	Ribosomal protein S6 kinase alpha-3 [OS=Homo sapiens]	48.0	14	9	117	6	678	133	9	8	3	1.81.E+08	2.49.E+08	1.87.E+08	2.00.E+08	2.66.E+08	2.03.E+08	2.93.E+08	2.66.E+08
924	Q9UN86	Ras GTPase-activating protein-binding protein 2 [OS=Homo sapiens]	48.0	17	5	212	4	2290	185	4	5	0	9.33.E+07	9.42.E+07	8.98.E+07	8.99.E+07	9.45.E+07	9.33.E+07	8.59.E+07	8.35.E+07
925	P62314	Small nuclear ribonucleoprotein Sm D1 [OS=Homo sapiens]	47.8	28	2	302	2	5431	399	2	2	0	3.81.E+08	3.72.E+08	3.85.E+08	3.31.E+08	3.30.E+08	3.17.E+08	3.45.E+08	3.25.E+08
926	O75828	Carbonyl reductase [NADPH] 3 [OS=Homo sapiens]	47.8	21	5	320	2	7374	515	5	5	0	1.71.E+07	1.54.E+07	2.45.E+07	1.81.E+07	3.03.E+07	2.62.E+07	2.94.E+07	3.26.E+07
927	Q92538	Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1 [OS=Homo sapiens]	47.7	7	8	189	7	666	199	8	7	0	5.56.E+07	6.11.E+07	5.96.E+07	5.90.E+07	6.86.E+07	6.54.E+07	6.13.E+07	5.91.E+07
928	Q6P1M3-1	Lethal(2) giant larvae protein homolog 2 [OS=Homo sapiens]	47.6	11	5	38	5	315	44	5	5	0	7.68.E+07	8.29.E+07	8.24.E+07	9.40.E+07	2.67.E+07	3.06.E+07	3.15.E+07	1.85.E+07
929	P14854	Cytochrome c oxidase subunit 6B1 [OS=Homo sapiens]	47.6	58	4	208	4	1854	259	4	4	0	3.39.E+08	3.54.E+08	3.36.E+08	3.23.E+08	2.66.E+08	2.94.E+08	2.69.E+08	2.81.E+08
930	Q15417	Calponin-3 [OS=Homo sapiens]	47.5	31	8	72	7	1140	89	8	8	0	1.43.E+08	1.51.E+08	1.25.E+08	1.31.E+08	1.43.E+08	1.35.E+08	1.43.E+08	1.34.E+08
931	Q04760-1	lactoylglutathione lyase [OS=Homo sapiens]	47.5	43	7	257	7	3472	321	7	7	0	2.55.E+08	2.66.E+08	2.62.E+08	2.39.E+08	3.94.E+08	3.89.E+08	4.02.E+08	3.91.E+08
932	P50914	60S ribosomal protein L14 [OS=Homo sapiens]	47.5	24	6	443	6	6102	495	6	5	0	1.69.E+09	1.66.E+09	1.72.E+09	1.75.E+09	1.39.E+09	1.36.E+09	1.35.E+09	1.37.E+09
933	Q99729-2	Isoform 2 of Heterogeneous nuclear ribonucleoprotein A/B [OS=Homo sapiens]	47.4	25	8	232	7		442	8		0	5.41.E+08	5.46.E+08	5.64.E+08	5.29.E+08	5.48.E+08	5.46.E+08	4.93.E+08	5.55.E+08
934	Q96C86	M7GpppX diphosphatase [OS=Homo sapiens]	47.4	29	7	142	7	1357	158	7	7	0	1.27.E+08	1.41.E+08	1.30.E+08	1.34.E+08	1.42.E+08	1.61.E+08	1.19.E+08	1.51.E+08
935	P50570-1	Dynamin-2 [OS=Homo sapiens]	47.3	12	8	145	8	683	101	8	8	0	5.14.E+07	4.76.E+07	3.91.E+07	5.17.E+07	6.73.E+07	6.76.E+07	5.69.E+07	6.59.E+07
936	P61160-1	Actin-related protein 2 [OS=Homo sapiens]	47.3	27	7	176	7	1654	200	7	7	0	3.61.E+08	3.44.E+08	3.27.E+08	3.16.E+08	3.64.E+08	3.51.E+08	3.21.E+08	3.55.E+08
937	P49257	Protein ERGIC-53 [OS=Homo sapiens]	47.3	13	4	65	4	627	103	4	4	0	2.05.E+08	1.57.E+08	1.53.E+08	1.09.E+08	2.80.E+08	2.66.E+08	2.91.E+08	2.70.E+08
938	Q9BV57	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase [OS=Homo sapiens]	47.0	47	6	208	6	503	187	5	6	0	2.63.E+08	2.72.E+08	2.66.E+08	2.68.E+08	2.30.E+08	1.91.E+08	2.06.E+08	2.37.E+08
939	Q9BS26	Endoplasmic reticulum resident protein 44 [OS=Homo sapiens]	46.9	19	5	78	4	985	107	5	5	0	3.75.E+07	4.08.E+07	3.94.E+07	4.00.E+07	6.17.E+07	5.71.E+07	4.99.E+07	5.31.E+07
940	Q14696	LDLR chaperone MESD [OS=Homo sapiens]	46.9	26	4	168	4	2020	208	4	4	0	1.65.E+08	1.53.E+08	1.65.E+08	1.75.E+08	2.10.E+08	1.97.E+08	2.07.E+08	1.85.E+08
941	P36952-1	Serpin B5 [OS=Homo sapiens]	46.8	24	6	123	6	1800	149	6	6	0	1.46.E+08	2.09.E+08	1.49.E+08	1.99.E+08	5.97.E+07	6.04.E+07	4.75.E+07	6.20.E+07
942	O15173	Membrane-associated progesterone receptor component 2 [OS=Homo sapiens]	46.7	49	7	228	6	2020	211	7	6	0	2.53.E+08	2.62.E+08	2.55.E+08	2.64.E+08	3.58.E+08	3.80.E+08	3.71.E+08	3.51.E+08
943	Q12874	splicing factor 3a subunit 3 [OS=Homo sapiens]	46.6	21	6	70	6	770	94	6	5	0	1.79.E+08	1.93.E+08	1.87.E+08	1.86.E+08	2.11.E+08	2.10.E+08	2.11.E+08	9.07.E+07
944	O75340	programmed cell death protein 6 [OS=Homo sapiens]	46.6	49	6	298	6	4317	226	5	6	0	6.45.E+08	6.55.E+08	6.77.E+08	6.21.E+08	6.67.E+08	6.52.E+08	5.91.E+08	6.33.E+08
945	Q68CZ2-1	Tensin-3 [OS=Homo sapiens]	46.5	8	6	122	6	1632	177	6	5	0	1.16.E+08	1.09.E+08	1.22.E+08	1.12.E+08	1.06.E+08	9.96.E+07	9.28.E+07	9.95.E+07
946	P53634-1	Dipeptidyl peptidase 1 [OS=Homo sapiens]	46.4	14	5	86	5	702	70	5	5	0	7.61.E+07	8.13.E+07	8.11.E+07	6.75.E+07	1.11.E+08	1.27.E+08	1.29.E+08	1.21.E+08
947	P30419	glycylpeptide N-tetradecanoyltransferase 1 [OS=Homo sapiens]	46.3	21	6	143	6	1112	144	6	6	0	9.69.E+07	1.10.E+08	6.95.E+07	8.76.E+07	1.73.E+08	1.67.E+08	1.54.E+08	1.71.E+08
948	Q14739	Lamin-B receptor [OS=Homo sapiens]	46.3	11	6	140	6	2549	212	6	6	0	2.01.E+08	3.06.E+08	3.16.E+08	2.92.E+08	3.47.E+08	3.51.E+08	3.65.E+08	3.53.E+08
949	O75477	erlin-1 [OS=Homo sapiens]	46.3	35	7	88	7	1148	102	7	7	0	1.01.E+08	9.18.E+07	9.01.E+07	1.06.E+08	1.16.E+08	1.31.E+08	1.37.E+08	1.33.E+08
950	O43169	Cytochrome b5 type B [OS=Homo sapiens]	46.0	45	4	126	4	595	157	4	4	0	1.33.E+08	1.35.E+08	1.26.E+08	1.15.E+08	1.23.E+08	1.22.E+08	1.21.E+08	1.33.E+08
951	O60936-2	Nucleolar protein 3 [OS=Homo sapiens]	46.0	35	4	130	4	2142	125	4	4	0	8.78.E+07	8.86.E+07	8.60.E+07	8.51.E+07	9.60.E+07	9.97.E+07	8.81.E+07	9.38.E+07
952	Q9C005	Protein dpy-30 homolog [OS=Homo sapiens]	45.8	36	2	186	2	2493	335	2	2	0	9.98.E+07	1.07.E+08	1.10.E+08	9.81.E+07	1.22.E+08	1.28.E+08	1.13.E+08	1.19.E+08
953	P40429	60S ribosomal protein L13a [OS=Homo sapiens]	45.8	31	8	398	8	4425	247	7	5	0	1.74.E+09	1.52.E+09	1.71.E+09	1.74.E+09	1.45.E+09	1.43.E+09	1.23.E+09	1.39.E+09
954	Q12769	nuclear pore complex protein Nup160 [OS=Homo sapiens]	45.8	5	4	82	4	908	39	4	4	0	5.49.E+07	5.58.E+07	5.18.E+07	4.68.E+07	5.13.E+07	3.47.E+07	4.93.E+07	4.96.E+07
955	P42765	3-ketoacyl-CoA thiolase, mitochondrial [OS=Homo sapiens]	45.7	22	6	70	6	328	51	6	6	0	8.15.E+07	8.46.E+07	1.22.E+08	8.95.E+07	1.13.E+08	1.14.E+08	6.95.E+07	1.20.E+08
956	Q14258	E3 ubiquitin/ISG15 ligase TRIM25 [OS=Homo sapiens]	45.6	12	6	197	6	4518	253	6	6	0	9.14.E+07	9.22.E+07	9.64.E+07	1.10.E+08	1.53.E+08	1.48.E+08	1.32.E+08	1.42.E+08
957	P50416	Carnitine O-palmitoyltransferase 1, liver isoform [OS=Homo sapiens]	45.6	12	7	188	7	2128	186	7	7	0	7.93.E+07	8.35.E+07	8.32.E+07	8.53.E+07	1.44.E+08	1.41.E+08	1.48.E+08	1.45.E+08
958	Q12756	Kinesin-like protein KIF1A [OS=Homo sapiens]	45.6	7	9	65	9	475	26	8	8	0	1.19.E+08	1.14.E+08	1.14.E+08	1.11.E+08	1.97.E+08	1.89.E+08	1.91.E+08	1.81.E+08
959	O14950	Myosin regulatory light chain 12B [OS=Homo sapiens]	45.5	51	6	218	6	5585	332	6	6	0	4.15.E+08	4.37.E+08	3.98.E+08	3.95.E+08	5.11.E+08	4.95.E+08	5.15.E+08	5.28.E+08
960	Q13057	Bifunctional coenzyme A synthase [OS=Homo sapiens]	45.4	27	7	176	7	1081	133	7	7	0	9.44.E+07	9.85.E+07	7.63.E+07	1.03.E+08	1.16.E+08	1.45.E+08	1.11.E+08	1.36.E+08
961	Q16658	Fascin [OS=Homo sapiens]	45.4	15	5	40	5	579	44	5	5	0	1.74.E+07	1.89.E+07	1.07.E+07	2.22.E+07	5.64.E+07	1.01.E+08	1.07.E+08	4.17.E+07
962	P63172	Dynein light chain Tctex-type 1 [OS=Homo sapiens]	45.4	30	2	172	2	4376	274	2	2	0	5.62.E+07	7.25.E+07	6.73.E+07	7.31.E+07	9.29.E+07	1.02.E+08	9.31.E+07	9.71.E+07
963	P51570	galactokinase [OS=Homo sapiens]	45.2	29	6	78	6	1649	140	6	6	0	3.04.E+07	4.85.E+07	4.54.E+07	4.71.E+07	8.12.E+07	4.29.E+07	7.28.E+07	3.56.E+07
964	Q9Y5K5-1	Ubiquitin carboxyl-terminal hydrolase isozyme L5 [OS=Homo sapiens]	45.2	36	7	120	7	1368	119	7	7	0	9.62.E+07	1.02.E+08	1.02.E+08	9.95.E+07	1.41.E+08	1.27.E+08	1.25.E+08	1.21.E+08
965	Q8IZ83	Aldehyde dehydrogenase family 16 member A1 [OS=Homo sapiens]	45.2	11	5	96	5	1983	107	5	5	0	6.12.E+07	5.02.E+07	3.59.E+07	6.04.E+07	2.15.E+07	2.27.E+07	3.98.E+07	2.29.E+07
966	O15347	High mobility group protein B3 [OS=Homo sapiens]	44.9	37	5	146	5	1190	241	5	5	0	3.31.E+08	3.53.E+08	3.15.E+08	2.79.E+08	4.56.E+08	4.90.E+08	6.14.E+08	4.69.E+08
967	O43252	bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 1 [OS=Homo sapiens]	44.9	18	6	73	6	933	97	6	6	0	6.40.E+07	7.00.E+07	7.05.E+07	7.10.E+07	9.64.E+07	9.01.E+07	8.61.E+07	9.34.E+07
968	O43765	Small glutamine-rich tetratricopeptide repeat-containing protein alpha [OS=Homo sapiens]	44.9	20	5	243	5	3085	279	5	5	0	7.84.E+07	7.79.E+07	7.57.E+07	8.98.E+07	1.11.E+08	1.18.E+08	1.14.E+08	1.13.E+08
969	Q9Y2B0	Protein canopy homolog 2 [OS=Homo sapiens]	44.8	35	4	195	4	2667	302	4	4	0	2.46.E+08	2.41.E+08	2.46.E+08	2.50.E+08	4.23.E+08	4.19.E+08	3.81.E+08	3.99.E+08
970	P53004	Biliverdin reductase A [OS=Homo sapiens]	44.7	24	5	238	5	4304	366	5	5	0	1.23.E+08	1.17.E+08	1.30.E+08	1.15.E+08	2.39.E+08	2.06.E+08	2.06.E+08	2.24.E+08
971	Q5JPE7	NODAL modulator 2 [OS=Homo sapiens]	44.7	8	5	186	5	2872	240	5	5	0	5.88.E+07	4.24.E+07	5.35.E+07	6.57.E+07	7.45.E+07	7.36.E+07	5.48.E+07	6.17.E+07
972	P84103	Serine/arginine-rich splicing factor 3 [OS=Homo sapiens]	44.4	35	6	453	5	2007	517	6	6	0	9.44.E+08	9.74.E+08	9.75.E+08	8.60.E+08	8.95.E+08	9.28.E+08	8.46.E+08	9.04.E+08
973	P06280	alpha-galactosidase A [OS=Homo sapiens]	44.3	22	7	55	7	787	58	7	6	0	1.19.E+08	1.17.E+08	8.91.E+07	1.13.E+08	2.41.E+08	2.48.E+08	2.37.E+08	2.49.E+08
974	O75607	Nucleoplasmin-3 [OS=Homo sapiens]	44.3	32	3	18	3	364	30	3	3	0	2.54.E+07	1.55.E+07	1.66.E+07	1.84.E+07	9.02.E+06	9.11.E+06	1.43.E+07	1.27.E+07
975	P06730	Eukaryotic translation initiation factor 4E [OS=Homo sapiens]	44.3	38	6	260	6	3517	306	5	6	0	4.39.E+08	4.63.E+08	4.46.E+08	4.55.E+08	5.05.E+08	5.18.E+08	4.91.E+08	5.16.E+08

No.	Accession	Description	Sum PEP Score	Coverage [%]	# Peptides	# PSMs	# Unique Peptides	Score Mascot: A5 Mascot	Score Sequest HT: A2 Sequest HT	# Peptides (by Search Engine): A2 Sequest HT	# Peptides (by Search Engine): A5 Mascot	# Razor Peptides	ctrl Abundances_1	ctrl Abundances_2	ctrl Abundances_3	ctrl Abundances_4	JAM−A KO Abundances_1	JAM−A KO Abundances_2	JAM−A KO Abundances_3	JAM−A KO Abundances_4
976	P50552	Vasodilator−stimulated phosphoprotein [OS=Homo sapiens]	44.3	17	5	142	5	1090	142	5	5	0	1.51.E+08	1.62.E+08	1.54.E+08	1.78.E+08	1.30.E+08	1.31.E+08	1.36.E+08	1.54.E+08
977	Q14137	Ribosome biogenesis protein BOP1 [OS=Homo sapiens]	44.3	13	6	67	6	959	77	6	6	0	1.13.E+08	8.41.E+07	7.12.E+07	1.28.E+08	1.28.E+08	9.20.E+07	9.47.E+07	1.02.E+08
978	P84090	Enhancer of rudimentary homolog [OS=Homo sapiens]	44.2	49	5	201	5	4206	182	4	5	0	5.35.E+08	5.16.E+08	5.35.E+08	4.86.E+08	6.66.E+08	6.49.E+08	6.84.E+08	6.75.E+08
979	Q9NZ01−1	Very−long−chain enoyl−CoA reductase [OS=Homo sapiens]	44.0	23	7	170	7	867	144	7	7	0	3.14.E+08	2.99.E+08	3.13.E+08	3.43.E+08	3.45.E+08	3.74.E+08	4.01.E+08	3.65.E+08
980	P30042−1	ES1 protein homolog, mitochondrial [OS=Homo sapiens]	43.7	48	6	104	6	691	138	6	4	0	1.48.E+08	1.61.E+08	1.47.E+08	1.65.E+08	1.62.E+08	1.75.E+08	1.43.E+08	1.57.E+08
981	Q9UJS0	Calcium−binding mitochondrial carrier protein Aralar2 [OS=Homo sapiens]	43.5	21	8	93	5	681	87	8	8	3	1.29.E+08	1.49.E+08	1.36.E+08	1.44.E+08	1.45.E+08	1.41.E+08	1.42.E+08	1.18.E+08
982	Q12788	Transducin beta−like protein 3 [OS=Homo sapiens]	43.5	10	5	52	5	572	50	5	5	0	5.79.E+07	6.79.E+07	4.94.E+07	6.95.E+07	5.62.E+07	5.07.E+07	3.18.E+07	5.72.E+07
983	P00492	Hypoxanthine−guanine phosphoribosyltransferase [OS=Homo sapiens]	43.3	40	6	134	6	1573	156	6	6	0	2.03.E+08	1.94.E+08	1.98.E+08	1.91.E+08	2.21.E+08	2.12.E+08	2.18.E+08	2.23.E+08
984	Q8N8S7	Protein enabled homolog [OS=Homo sapiens]	43.3	14	5	189	5	1749	121	5	5	0	2.22.E+08	2.18.E+08	2.28.E+08	2.47.E+08	2.70.E+08	2.39.E+08	2.46.E+08	2.23.E+08
985	Q9Y4P3	Transducin beta−like protein 2 [OS=Homo sapiens]	43.3	18	6	109	6	981	117	5	6	0	1.80.E+08	1.50.E+08	1.74.E+08	1.83.E+08	1.74.E+08	1.79.E+08	1.85.E+08	1.46.E+08
986	Q16543	Hsp90 co−chaperone Cdc37 [OS=Homo sapiens]	43.2	28	8	148	8	1309	163	8	8	0	1.87.E+08	2.02.E+08	1.82.E+08	1.80.E+08	2.00.E+08	2.29.E+08	2.06.E+08	2.03.E+08
987	P12955	xaa−Pro dipeptidase [OS=Homo sapiens]	43.1	19	4	78	4	980	97	4	4	0	5.41.E+07	6.69.E+07	5.27.E+07	5.48.E+07	3.82.E+07	2.99.E+07	2.90.E+07	3.19.E+07
988	Q13177	Serine/threonine−protein kinase PAK 2 [OS=Homo sapiens]	43.1	24	8	58	8	290	44	7	8	0	8.11.E+07	1.16.E+08	9.29.E+07	9.41.E+07	1.77.E+08	1.74.E+08	1.81.E+08	2.05.E+08
989	Q92747	Actin−related protein 2/3 complex subunit 1A [OS=Homo sapiens]	43.1	15	3	100	2	2171	96	2	3	0	4.99.E+07	4.64.E+07	4.74.E+07	5.64.E+07	8.82.E+07	8.22.E+07	7.30.E+07	7.78.E+07
990	Q03252	Lamin−B2 [OS=Homo sapiens]	43.1	13	7	184	6	1678	134	7	7	0	1.13.E+08	1.14.E+08	1.25.E+08	1.18.E+08	1.31.E+08	1.33.E+08	1.33.E+08	1.34.E+08
991	P28072	Proteasome subunit beta type−6 [OS=Homo sapiens]	42.9	34	5	343	5	2788	483	5	5	0	3.31.E+08	3.20.E+08	3.44.E+08	3.35.E+08	3.33.E+08	3.37.E+08	3.57.E+08	3.49.E+08
992	P22695	Cytochrome b−c1 complex subunit 2, mitochondrial [OS=Homo sapiens]	42.9	18	5	118	5	2016	208	5	5	0	1.31.E+08	1.30.E+08	1.44.E+08	1.31.E+08	1.38.E+08	1.34.E+08	1.60.E+08	1.45.E+08
993	P59998	Actin−related protein 2/3 complex subunit 4 [OS=Homo sapiens]	42.8	41	6	175	6	1965	165	5	6	0	5.19.E+08	5.33.E+08	5.48.E+08	4.97.E+08	5.52.E+08	5.94.E+08	5.94.E+08	5.48.E+08
994	P23258	tubulin gamma−1 chain [OS=Homo sapiens]	42.7	27	6	89	6	398	55	6	6	0	1.10.E+08	1.31.E+08	1.43.E+08	1.37.E+08	1.19.E+08	1.07.E+08	1.01.E+08	1.34.E+08
995	P61201−1	COP9 signalosome complex subunit 2 [OS=Homo sapiens]	42.6	20	6	170	1	2656	181	6	6	5	1.52.E+08	1.46.E+08	1.45.E+08	1.38.E+08	1.07.E+08	1.09.E+08	1.40.E+08	8.88.E+07
996	Q9NZI8	Insulin−like growth factor 2 mRNA−binding protein 1 [OS=Homo sapiens]	42.4	15	6	67	5	587	82	6	5	0	7.22.E+07	7.40.E+07	6.32.E+07	7.85.E+07	9.33.E+07	1.03.E+08	7.35.E+07	9.86.E+07
997	O43684	Mitotic checkpoint protein BUB3 [OS=Homo sapiens]	42.4	25	6	229	6	2784	198	6	6	0	1.45.E+08	1.50.E+08	1.46.E+08	1.46.E+08	1.67.E+08	1.68.E+08	1.61.E+08	1.65.E+08
998	O75937	DnaJ homolog subfamily C member 8 [OS=Homo sapiens]	42.4	28	4	162	4	960	200	4	4	0	1.19.E+08	1.19.E+08	1.21.E+08	1.19.E+08	1.69.E+08	1.65.E+08	1.38.E+08	1.69.E+08
999	P20340−1	Ras−related protein Rab−6A [OS=Homo sapiens]	42.4	42	8	398	1	4557	381	7	7	6	7.21.E+08	6.97.E+08	7.04.E+08	6.54.E+08	8.06.E+08	7.06.E+08	8.04.E+08	7.62.E+08
1000	Q14116	Interleukin−18 [OS=Homo sapiens]	42.1	47	6	93	6	689	92	5	5	0	1.13.E+08	1.06.E+08	7.60.E+07	1.14.E+08	3.37.E+08	3.38.E+08	3.10.E+08	3.45.E+08
1001	Q99436	Proteasome subunit beta type−7 [OS=Homo sapiens]	42.1	37	5	147	5	1898	214	5	5	0	1.56.E+08	1.70.E+08	1.62.E+08	1.58.E+08	1.50.E+08	1.51.E+08	1.46.E+08	1.46.E+08
1002	Q02750	Dual specificity mitogen−activated protein kinase kinase 1 [OS=Homo sapiens]	42.1	12	3	150	1	2764	179	3	3	0	1.76.E+07	1.61.E+07	1.63.E+07	1.39.E+07	1.49.E+07	1.49.E+07	1.50.E+07	1.45.E+07
1003	P04183	Thymidine kinase, cytosolic [OS=Homo sapiens]	42.0	35	6	218	6	1206	208	6	6	0	1.18.E+08	1.64.E+08	1.42.E+08	1.84.E+08	1.08.E+08	7.52.E+07	1.25.E+08	1.38.E+08
1004	Q96IU4	Protein ABHD14B [OS=Homo sapiens]	41.8	47	6	129	6	823	131	6	5	0	1.56.E+08	1.63.E+08	1.62.E+08	1.56.E+08	2.25.E+08	2.31.E+08	2.39.E+08	2.46.E+08
1005	Q8WUM0	Nuclear pore complex protein Nup133 [OS=Homo sapiens]	41.8	11	6	121	6	1449	143	6	6	0	8.38.E+07	8.70.E+07	7.24.E+07	8.99.E+07	8.61.E+07	8.20.E+07	5.89.E+07	7.41.E+07
1006	P09758	Tumor−associated calcium signal transducer 2 [OS=Homo sapiens]	41.7	22	4	81	4	1086	124	4	4	0	8.82.E+07	8.24.E+07	8.02.E+07	8.82.E+07	1.38.E+08	1.46.E+08	1.35.E+08	1.37.E+08
1007	Q9NP72	Ras−related protein Rab−18 [OS=Homo sapiens]	41.7	40	6	93	6	782	115	6	5	0	5.50.E+07	8.12.E+07	7.35.E+07	8.01.E+07	2.35.E+08	1.97.E+08	1.98.E+08	2.19.E+08
1008	O00116	Alkyldihydroxyacetonephosphate synthase, peroxisomal [OS=Homo sapiens]	41.6	16	6	69	6	337	50	6	6	0	8.24.E+07	7.16.E+07	7.91.E+07	8.65.E+07	1.06.E+08	7.92.E+07	8.25.E+07	9.97.E+07
1009	P46379−1	Large proline−rich protein BAG6 [OS=Homo sapiens]	41.6	9	5	124	5	1039	160	5	5	0	1.09.E+08	9.41.E+07	7.10.E+07	8.13.E+07	9.68.E+07	8.09.E+07	1.04.E+08	9.63.E+07
1010	P49023	Paxillin [OS=Homo sapiens]	41.6	15	5	105	5	779	92	5	5	0	5.91.E+07	6.25.E+07	6.29.E+07	6.69.E+07	6.49.E+07	6.55.E+07	3.84.E+07	6.42.E+07
1011	Q15631−1	Translin [OS=Homo sapiens]	41.5	25	5	142	5	1022	170	5	5	0	9.77.E+07	1.07.E+08	1.10.E+08	9.39.E+07	1.91.E+08	1.94.E+08	1.70.E+08	1.86.E+08
1012	Q7Z2W4	zinc finger CCCH−type antiviral protein 1 [OS=Homo sapiens]	41.4	13	8	58	8	428	50	8	8	0	1.47.E+08	1.42.E+08	1.33.E+08	1.98.E+08	1.52.E+08	1.52.E+08	1.48.E+08	1.32.E+08
1013	Q00325−2	Isoform B of Phosphate carrier protein, mitochondrial [OS=Homo sapiens]	41.2	24	7	136	7		291	7		0	8.13.E+08	7.95.E+08	7.83.E+08	8.50.E+08	7.50.E+08	7.47.E+08	7.76.E+08	7.29.E+08
1014	P07602−1	Prosaposin [OS=Homo sapiens]	41.2	10	6	509	6	4973	560	6	6	0	6.68.E+08	6.75.E+08	6.12.E+08	6.90.E+08	5.95.E+08	6.16.E+08	5.82.E+08	6.08.E+08
1015	Q9UL25	Ras−related protein Rab−21 [OS=Homo sapiens]	41.2	13	3	146	3	2049	147	3	3	0	6.67.E+07	6.24.E+07	5.82.E+07	5.39.E+07	6.24.E+07	6.88.E+07	7.01.E+07	7.04.E+07
1016	P20340−2	Isoform 2 of Ras−related protein Rab−6A [OS=Homo sapiens]	41.2	47	8	204	1		402	8		0	1.73.E+07	1.83.E+07	1.50.E+07	9.68.E+06	3.86.E+07	2.74.E+07	2.45.E+07	3.38.E+07
1017	P31153	S−adenosylmethionine synthase isoform type−2 [OS=Homo sapiens]	41.1	13	4	198	4	2874	220	4	4	0	2.58.E+08	2.51.E+08	2.61.E+08	2.25.E+08	2.20.E+08	2.13.E+08	2.34.E+08	2.14.E+08
1018	P04899−1	guanine nucleotide−binding protein G(i) subunit alpha−2 [OS=Homo sapiens]	41.1	18	5	120	2	943	154	5	5	0	2.12.E+07	2.26.E+07	2.24.E+07	2.47.E+07	2.42.E+07	2.53.E+07	2.39.E+07	2.09.E+07
1019	Q9UKV3−1	Apoptotic chromatin condensation inducer in the nucleus [OS=Homo sapiens]	41.1	9	8	98	8	257	85	8	8	0	1.17.E+08	1.17.E+08	1.23.E+08	1.30.E+08	1.30.E+08	1.25.E+08	1.13.E+08	1.20.E+08
1020	Q9NYU2−1	UDP−glucose:glycoprotein glucosyltransferase 1 [OS=Homo sapiens]	41.0	8	7	100	7	453	47	7	7	0	8.87.E+07	9.85.E+07	9.16.E+07	9.27.E+07	1.16.E+08	1.30.E+08	1.49.E+08	1.17.E+08
1021	Q13098	COP9 signalosome complex subunit 1 [OS=Homo sapiens]	40.9	20	7	108	7	509	79	7	7	0	3.20.E+08	2.83.E+08	2.99.E+08	2.62.E+08	2.99.E+08	3.24.E+08	3.35.E+08	3.23.E+08
1022	Q01081	Splicing factor U2AF 35 kDa subunit [OS=Homo sapiens]	40.8	15	4	138	4	2769	86	2	4	0	1.62.E+08	1.70.E+08	1.68.E+08	1.58.E+08	1.70.E+08	1.64.E+08	1.65.E+08	1.68.E+08
1023	P17096−1	High mobility group protein HMG−I/HMG−Y [OS=Homo sapiens]	40.8	23	2	181	2	1518	328	2	2	0	2.27.E+08	2.13.E+08	2.29.E+08	2.74.E+08	1.73.E+08	1.50.E+08	1.69.E+08	1.76.E+08
1024	Q969Z0−1	Protein TBRG4 [OS=Homo sapiens]	40.8	16	4	68	4	991	97	4	4	0	5.57.E+07	7.19.E+07	5.87.E+07	7.07.E+07	5.77.E+07	5.19.E+07	4.52.E+07	5.28.E+07
1025	Q96EP5	DAZ−associated protein 1 [OS=Homo sapiens]	40.8	19	5	138	5	2132	183	5	5	0	1.41.E+08	1.46.E+08	1.53.E+08	1.48.E+08	1.79.E+08	1.75.E+08	1.39.E+08	1.77.E+08
1026	O95782	AP−2 complex subunit alpha−1 [OS=Homo sapiens]	40.6	12	8	126	4	1518	142	7	8	0	5.98.E+07	5.95.E+07	6.11.E+07	5.75.E+07	5.32.E+07	3.97.E+07	5.82.E+07	5.05.E+07
1027	P53999	Activated RNA polymerase II transcriptional coactivator p15 [OS=Homo sapiens]	40.6	20	4	330	4	6274	536	4	4	0	4.36.E+08	4.48.E+08	4.46.E+08	4.70.E+08	5.07.E+08	4.95.E+08	4.94.E+08	5.05.E+08

No.	Accession	Description	Sum PEP Score	Coverage [%]	# Peptides	# PSMs	# Unique Peptides	Score Mascot: A5 Mascot	Score Sequest HT: A2 Sequest HT	# Peptides (by Search Engine): A2 Sequest HT	# Peptides (by Search Engine): A5 Mascot	# Razor Peptides	ctrl Abundances_1	ctrl Abundances_2	ctrl Abundances_3	ctrl Abundances_4	JAM-A KO Abundances_1	JAM-A KO Abundances_2	JAM-A KO Abundances_3	JAM-A KO Abundances_4
1028	P24539	ATP synthase F(0) complex subunit B1, mitochondrial [OS=Homo sapiens]	40.5	16	3	202	3	2160	262	3	3	0	2.39.E+08	2.35.E+08	2.53.E+08	2.79.E+08	2.52.E+08	2.31.E+08	2.68.E+08	2.51.E+08
1029	Q8TDB8-1	Solute carrier family 2, facilitated glucose transporter member 14 [OS=Homo sapiens]	40.5	10	5	306	4	2415	212	5	4	0	5.52.E+08	5.41.E+08	5.20.E+08	5.39.E+08	4.39.E+08	4.54.E+08	1.59.E+08	4.80.E+08
1030	Q9BZX2-1	Uridine-cytidine kinase 2 [OS=Homo sapiens]	40.5	26	4	48	4	391	62	4	4	0	5.77.E+07	6.66.E+07	6.24.E+07	6.06.E+07	2.74.E+07	2.32.E+07	5.07.E+06	2.16.E+07
1031	Q8NF37	Lysophosphatidylcholine acyltransferase 1 [OS=Homo sapiens]	40.4	12	5	186	5	3081	210	4	5	0	1.10.E+08	1.20.E+08	1.06.E+08	1.10.E+08	1.32.E+08	1.36.E+08	1.25.E+08	1.51.E+08
1032	P53041	Serine/threonine-protein phosphatase 5 [OS=Homo sapiens]	40.2	11	4	82	4	1939	127	4	4	0	1.19.E+08	1.26.E+08	1.17.E+08	1.12.E+08	7.96.E+07	8.86.E+07	5.93.E+07	7.59.E+07
1033	Q14CN4-1	Keratin, type II cytoskeletal 72 [OS=Homo sapiens]	40.1	4	5	747	1	6040	765	5	5	0	2.07.E+07	1.97.E+07	2.08.E+07	2.40.E+07	8.06.E+06	7.71.E+06	8.14.E+06	8.20.E+06
1034	P14735	insulin-degrading enzyme [OS=Homo sapiens]	40.0	13	9	127	9	830	139	9	8	0	1.52.E+08	1.67.E+08	1.43.E+08	1.64.E+08	2.08.E+08	2.45.E+08	2.06.E+08	1.98.E+08
1035	Q8NE71-1	ATP-binding cassette sub-family F member 1 [OS=Homo sapiens]	39.9	17	7	156	7	1092	197	7	7	0	1.42.E+08	9.51.E+07	1.26.E+08	8.53.E+07	1.12.E+08	1.06.E+08	1.44.E+08	1.65.E+08
1036	Q04837	Single-stranded DNA-binding protein, mitochondrial [OS=Homo sapiens]	39.9	41	4	119	4	2155	174	4	4	0	1.33.E+08	1.36.E+08	1.24.E+08	1.31.E+08	1.33.E+08	1.41.E+08	1.35.E+08	1.29.E+08
1037	Q9H8Y8-1	Golgi reassembly-stacking protein 2 [OS=Homo sapiens]	39.8	13	3	114	3	3323	187	3	3	0	1.08.E+08	1.08.E+08	9.58.E+07	1.00.E+08	1.36.E+08	1.32.E+08	1.03.E+08	1.21.E+08
1038	P22061	protein-L-isoaspartate(D-aspartate) O-methyltransferase [OS=Homo sapiens]	39.8	43	5	98	5	1240	149	5	5	0	1.22.E+08	1.21.E+08	1.23.E+08	1.24.E+08	1.21.E+08	1.21.E+08	1.23.E+08	1.27.E+08
1039	Q13363-1	C-terminal-binding protein 1 [OS=Homo sapiens]	39.8	20	4	116	4	2267	188	4	4	0	8.54.E+07	8.64.E+07	7.81.E+07	8.00.E+07	7.33.E+07	7.37.E+07	7.24.E+07	7.75.E+07
1040	P36507	Dual specificity mitogen-activated protein kinase kinase 2 [OS=Homo sapiens]	39.7	12	3	129	1	2667	177	3	3	2	9.98.E+07	9.65.E+07	1.01.E+08	1.14.E+08	1.20.E+08	1.02.E+08	1.04.E+08	1.08.E+08
1041	Q12797	Aspartyl/Asparaginyl beta-hydroxylase [OS=Homo sapiens]	39.6	14	5	119	5	741	132	5	5	0	1.11.E+08	5.53.E+07	4.72.E+07	5.90.E+07	1.00.E+08	1.61.E+08	1.34.E+08	8.71.E+07
1042	P20020-3	Isoform B of Plasma membrane calcium-transporting ATPase 1 [OS=Homo sapiens]	39.5	8	6	74	6	599	77	6	6	0	5.20.E+07	5.90.E+07	4.36.E+07	5.96.E+07	6.50.E+07	6.31.E+07	5.57.E+07	5.38.E+07
1043	O60888-1	Protein CutA [OS=Homo sapiens]	39.5	33	3	316	3	6657	661	3	3	0	2.61.E+08	2.97.E+08	2.70.E+08	2.92.E+08	4.42.E+08	4.24.E+08	3.74.E+08	4.03.E+08
1044	Q7Z7H8	39S ribosomal protein L10, mitochondrial [OS=Homo sapiens]	39.4	23	2	84	2	2195	122	2	2	0	3.74.E+07	3.13.E+07	3.22.E+07	3.42.E+07	2.94.E+07	2.06.E+07	2.20.E+07	2.47.E+07
1045	Q9Y5M8	signal recognition particle receptor subunit beta [OS=Homo sapiens]	39.4	29	6	131	6	525	88	5	6	0	1.05.E+08	1.03.E+08	9.97.E+07	1.00.E+08	7.40.E+07	9.88.E+07	1.00.E+08	1.00.E+08
1046	Q9BVK6	Transmembrane emp24 domain-containing protein 9 [OS=Homo sapiens]	39.4	20	5	237	4	2547	273	5	5	1	3.00.E+08	2.86.E+08	2.88.E+08	3.02.E+08	3.11.E+08	2.96.E+08	2.89.E+08	2.93.E+08
1047	P62633-1	Cellular nucleic acid-binding protein [OS=Homo sapiens]	39.4	23	3	146	1	1447	105	3	3	2	1.13.E+08	1.02.E+08	1.05.E+08	1.24.E+08	6.62.E+07	7.63.E+07	7.64.E+07	6.85.E+07
1048	Q5SSJ5-1	Heterochromatin protein 1-binding protein 3 [OS=Homo sapiens]	39.4	17	5	121	5	1840	88	4	5	0	8.35.E+07	1.08.E+08	9.61.E+07	1.30.E+08	9.88.E+07	9.38.E+07	1.02.E+08	1.15.E+08
1049	Q9UNF0	Protein kinase C and casein kinase substrate in neurons protein 2 [OS=Homo sapiens]	39.3	18	7	97	7	300	113	7	6	0	2.47.E+08	2.31.E+08	2.46.E+08	2.35.E+08	2.61.E+08	2.66.E+08	2.99.E+08	2.75.E+08
1050	O75964	ATP synthase subunit g, mitochondrial [OS=Homo sapiens]	39.3	48	4	183	4	1850	251	4	4	0	4.16.E+08	4.33.E+08	4.33.E+08	3.77.E+08	4.11.E+08	4.30.E+08	4.32.E+08	4.44.E+08
1051	Q9Y2Q3-1	Glutathione S-transferase kappa 1 [OS=Homo sapiens]	39.1	32	5	82	5	572	57	5	5	0	9.55.E+07	1.09.E+08	7.14.E+07	1.05.E+08	6.44.E+07	1.13.E+08	8.55.E+07	9.76.E+07
1052	P49821	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial [OS=Homo sapiens]	39.1	23	5	127	5	1113	130	5	5	0	8.57.E+07	9.62.E+07	8.38.E+07	1.12.E+08	1.08.E+08	1.03.E+08	9.61.E+07	1.17.E+08
1053	P13861	cAMP-dependent protein kinase type II-alpha regulatory subunit [OS=Homo sapiens]	39.0	17	4	64	4	1250	56	3	4	0	4.63.E+07	4.80.E+07	4.90.E+07	4.69.E+07	5.34.E+07	5.24.E+07	5.03.E+07	5.10.E+07
1054	P62854	40S ribosomal protein S26 [OS=Homo sapiens]	38.9	44	4	432	4	4984	468	4	4	0	8.53.E+08	8.12.E+08	8.10.E+08	9.73.E+08	6.48.E+08	6.71.E+08	6.58.E+08	7.11.E+08
1055	P48556	26S proteasome non-ATPase regulatory subunit 8 [OS=Homo sapiens]	38.9	24	7	150	7	1090	121	7	7	0	2.61.E+08	2.79.E+08	2.58.E+08	2.94.E+08	2.92.E+08	2.86.E+08	2.84.E+08	2.95.E+08
1056	Q9BRA2	Thioredoxin domain-containing protein 17 [OS=Homo sapiens]	38.9	38	4	180	4	2500	229	4	4	0	3.82.E+08	3.82.E+08	4.10.E+08	3.37.E+08	2.69.E+08	2.80.E+08	2.87.E+08	2.80.E+08
1057	Q9UDY4	DnaJ homolog subfamily B member 4 [OS=Homo sapiens]	38.9	21	4	167	3	1332	222	4	4	0	6.07.E+07	6.69.E+07	6.02.E+07	6.63.E+07	6.86.E+07	7.20.E+07	6.22.E+07	6.90.E+07
1058	P16144-1	Integrin beta-4 [OS=Homo sapiens]	38.9	5	6	74	6	629	85	6	6	0	8.57.E+07	9.49.E+07	5.49.E+07	8.62.E+07	7.61.E+07	7.79.E+07	7.67.E+07	3.84.E+07
1059	Q96AC1	Fermitin family homolog 2 [OS=Homo sapiens]	38.9	19	5	110	5	1800	165	5	5	0	5.00.E+07	5.12.E+07	4.23.E+07	5.50.E+07	6.27.E+07	7.46.E+07	6.51.E+07	6.74.E+07
1060	Q9GZS3	WD repeat-containing protein 61 [OS=Homo sapiens]	38.9	23	3	57	3	1082	64	3	3	0	8.49.E+07	8.86.E+07	6.20.E+07	8.45.E+07	1.10.E+08	1.07.E+08	7.13.E+07	1.00.E+08
1061	Q7RTV0	PHD finger-like domain-containing protein 5A [OS=Homo sapiens]	38.8	48	4	155	4	2573	194	4	4	0	1.50.E+08	1.41.E+08	1.42.E+08	1.56.E+08	1.25.E+08	1.28.E+08	1.38.E+08	1.23.E+08
1062	P61457	Pterin-4-alpha-carbinolamine dehydratase [OS=Homo sapiens]	38.8	70	5	218	5	1266	267	5	5	0	3.79.E+08	3.60.E+08	3.68.E+08	3.30.E+08	3.09.E+08	3.04.E+08	3.23.E+08	3.02.E+08
1063	Q9NQW6	Anillin [OS=Homo sapiens]	38.8	13	9	80	9	243	32	9	8	0	7.30.E+07	8.24.E+07	7.65.E+07	7.59.E+07	8.49.E+07	8.67.E+07	8.62.E+07	8.51.E+07
1064	Q9UHY7	Enolase-phosphatase E1 [OS=Homo sapiens]	38.7	25	4	167	4	993	155	4	4	0	1.65.E+08	1.75.E+08	1.53.E+08	1.79.E+08	1.65.E+08	1.41.E+08	1.05.E+08	1.45.E+08
1065	O43865	S-adenosylhomocysteine hydrolase-like protein 1 [OS=Homo sapiens]	38.6	13	5	79	4	367	53	5	5	0	5.97.E+07	5.76.E+07	5.86.E+07	6.63.E+07	9.89.E+07	9.14.E+07	9.67.E+07	9.95.E+07
1066	Q9UL15-1	BAG family molecular chaperone regulator 5 [OS=Homo sapiens]	38.5	13	3	58	3	1065	80	3	3	0	3.11.E+07	3.18.E+07	3.24.E+07	3.25.E+07	3.02.E+07	3.23.E+07	2.71.E+07	2.51.E+07
1067	O00461	Golgi integral membrane protein 4 [OS=Homo sapiens]	38.3	10	4	74	4	751	81	4	4	0	4.22.E+07	4.66.E+07	3.71.E+07	3.87.E+07	6.95.E+07	5.93.E+07	5.69.E+07	5.22.E+07
1068	Q14008	Cytoskeleton-associated protein 5 [OS=Homo sapiens]	38.3	7	8	101	8	610	43	8	8	0	5.70.E+07	5.68.E+07	5.43.E+07	5.52.E+07	7.69.E+07	7.37.E+07	7.35.E+07	7.57.E+07
1069	P46778	60S ribosomal protein L21 [OS=Homo sapiens]	38.2	26	4	268	4	3210	333	4	4	0	8.78.E+08	7.64.E+08	8.15.E+08	7.10.E+08	6.31.E+08	6.29.E+08	7.11.E+08	6.58.E+08
1070	P83916	Chromobox protein homolog 1 [OS=Homo sapiens]	38.2	56	8	84	7	496	80	7	8	1	9.22.E+07	9.07.E+07	7.88.E+07	8.87.E+07	1.10.E+08	6.99.E+07	7.85.E+07	9.16.E+07
1071	Q15717	ELAV-like protein 1 [OS=Homo sapiens]	38.0	21	5	169	5	2496	231	5	5	0	3.67.E+08	4.07.E+08	3.89.E+08	2.72.E+08	3.57.E+08	3.27.E+08	3.80.E+08	3.56.E+08
1072	Q9BXJ9	N-alpha-acetyltransferase 15, NatA auxiliary subunit [OS=Homo sapiens]	37.9	10	9	79	9	156	32	8	9	0	1.37.E+08	1.40.E+08	1.35.E+08	1.56.E+08	1.57.E+08	1.55.E+08	1.21.E+08	1.56.E+08
1073	O15260-1	surfeit locus protein 4 [OS=Homo sapiens]	37.9	14	3	91	3	3835	35	2	3	0	9.37.E+07	9.68.E+07	8.90.E+07	1.02.E+08	1.22.E+08	1.19.E+08	9.99.E+07	1.20.E+08
1074	P61923	Coatomer subunit zeta-1 [OS=Homo sapiens]	37.8	27	4	42	4	683	101	4	4	0	1.67.E+08	1.74.E+08	1.69.E+08	1.71.E+08	2.13.E+08	2.18.E+08	1.83.E+08	2.14.E+08
1075	P61077-1	Ubiquitin-conjugating enzyme E2 D3 [OS=Homo sapiens]	37.8	29	2	204	2	3943	312	2	2	0	1.03.E+08	1.14.E+08	1.13.E+08	1.16.E+08	1.28.E+08	1.09.E+08	1.07.E+08	1.21.E+08

No.	Accession	Description	Sum PEP Score	Coverage [%]	# Peptides	# PSMs	# Unique Peptides	Score Mascot: A5 Mascot	Score Sequest HT: A2 Sequest HT	# Peptides (by Search Engine): A2 Sequest HT	# Peptides (by Search Engine): A5 Mascot	# Razor Peptides	ctrl Abundances_1	ctrl Abundances_2	ctrl Abundances_3	ctrl Abundances_4	JAM-A KO Abundances_1	JAM-A KO Abundances_2	JAM-A KO Abundances_3	JAM-A KO Abundances_4
1076	O95197	Reticulon-3 [OS=Homo sapiens]	37.7	5	2	88	1	1458	40	1	2	1	1.03.E+08	9.64.E+07	1.11.E+08	1.15.E+08	1.52.E+08	1.22.E+08	1.39.E+08	1.39.E+08
1077	Q9ULC4-1	Malignant T-cell-amplified sequence 1 [OS=Homo sapiens]	37.6	36	4	225	4	2676	146	4	4	0	8.39.E+07	9.69.E+07	8.78.E+07	7.55.E+07	8.89.E+07	8.67.E+07	8.89.E+07	8.56.E+07
1078	Q96EY1-1	DnaJ homolog subfamily A member 3, mitochondrial [OS=Homo sapiens]	37.6	14	5	136	5	2139	165	5	5	0	9.66.E+07	9.22.E+07	9.72.E+07	1.03.E+08	7.81.E+07	7.41.E+07	8.35.E+07	9.17.E+07
1079	Q14839	Chromodomain-helicase-DNA-binding protein 4 [OS=Homo sapiens]	37.6	4	5	124	5	1191	149	5	5	0	5.89.E+07	6.71.E+07	6.73.E+07	6.02.E+07	6.78.E+07	6.64.E+07	5.80.E+07	6.43.E+07
1080	P62316	Small nuclear ribonucleoprotein Sm D2 [OS=Homo sapiens]	37.5	46	7	121	7	774	109	6	7	0	3.63.E+08	3.90.E+08	3.71.E+08	4.35.E+08	3.33.E+08	3.85.E+08	3.76.E+08	3.54.E+08
1081	O15382	Branched-chain-amino-acid aminotransferase, mitochondrial [OS=Homo sapiens]	37.4	25	5	56	5	940	74	5	5	0	7.95.E+07	7.20.E+07	7.41.E+07	7.78.E+07	4.43.E+07	4.13.E+07	4.35.E+07	4.07.E+07
1082	Q07666	KH domain-containing, RNA-binding, signal transduction-associated protein 1 [OS=Homo sapiens]	37.4	12	5	197	5	1565	154	5	5	0	1.91.E+08	1.96.E+08	1.97.E+08	2.15.E+08	2.25.E+08	2.40.E+08	2.36.E+08	2.40.E+08
1083	O00743	Serine/threonine-protein phosphatase 6 catalytic subunit [OS=Homo sapiens]	37.4	22	5	58	5	606	36	4	5	0	7.82.E+07	6.41.E+07	7.79.E+07	6.01.E+07	7.59.E+07	7.79.E+07	8.44.E+07	7.93.E+07
1084	Q5TFE4	5'-nucleotidase domain-containing protein 1 [OS=Homo sapiens]	37.3	23	5	101	5	772	44	4	4	0	7.85.E+07	7.25.E+07	6.74.E+07	6.59.E+07	8.97.E+07	6.97.E+07	4.30.E+07	8.18.E+07
1085	P10515	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial [OS=Homo sapiens]	37.1	18	7	101	7	454	68	7	7	0	1.33.E+08	1.37.E+08	1.32.E+08	1.63.E+08	1.36.E+08	1.34.E+08	1.45.E+08	1.43.E+08
1086	O75436-1	Vacuolar protein sorting-associated protein 26A [OS=Homo sapiens]	37.1	19	4	96	4	1326	120	4	4	0	9.90.E+07	9.54.E+07	9.23.E+07	9.62.E+07	1.23.E+08	1.24.E+08	1.04.E+08	1.17.E+08
1087	Q3ZCQ8	Mitochondrial import inner membrane translocase subunit TIM50 [OS=Homo sapiens]	37.0	17	4	68	4	1344	82	4	4	0	5.78.E+07	6.78.E+07	4.52.E+07	5.50.E+07	5.83.E+07	5.01.E+07	4.82.E+07	5.05.E+07
1088	P82979	SAP domain-containing ribonucleoprotein [OS=Homo sapiens]	37.0	33	6	108	6	1995	113	6	6	0	1.62.E+08	1.60.E+08	1.61.E+08	1.64.E+08	1.71.E+08	1.82.E+08	1.77.E+08	1.69.E+08
1089	P83731	60S ribosomal protein L24 [OS=Homo sapiens]	36.9	29	6	384	6	5481	475	6	6	0	1.24.E+09	1.26.E+09	1.26.E+09	1.11.E+09	1.06.E+09	1.14.E+09	1.13.E+09	1.07.E+09
1090	Q9GZR7	ATP-dependent RNA helicase DDX24 [OS=Homo sapiens]	36.9	12	8	122	8	201	61	8	7	0	1.02.E+08	9.42.E+07	1.07.E+08	1.06.E+08	1.21.E+08	1.15.E+08	1.22.E+08	1.10.E+08
1091	P51572	B-cell receptor-associated protein 31 [OS=Homo sapiens]	36.9	12	2	152	2	1687	181	2	2	0	2.54.E+08	2.46.E+08	2.60.E+08	2.52.E+08	2.35.E+08	2.51.E+08	2.73.E+08	2.51.E+08
1092	P25685	dnaJ homolog subfamily B member 1 [OS=Homo sapiens]	36.8	19	5	164	4	2128	191	5	5	1	1.58.E+08	1.63.E+08	1.31.E+08	1.50.E+08	9.83.E+07	1.04.E+08	9.86.E+07	1.07.E+08
1093	Q9UBN7-1	histone deacetylase 6 [OS=Homo sapiens]	36.8	4	2	58	2	648	93	2	2	0	3.04.E+07	2.90.E+07	2.40.E+07	2.49.E+07	2.75.E+07	2.31.E+07	2.21.E+07	2.56.E+07
1094	O00487	26S proteasome non-ATPase regulatory subunit 14 [OS=Homo sapiens]	36.7	27	5	170	5	1589	195	5	5	0	8.56.E+07	2.02.E+08	2.11.E+08	1.70.E+08	6.93.E+07	1.00.E+08	1.11.E+08	1.74.E+08
1095	Q6DKI1	60S ribosomal protein L7-like 1 [OS=Homo sapiens]	36.7	29	5	121	5	568	80	5	5	0	1.13.E+08	9.99.E+07	1.05.E+08	1.13.E+08	8.28.E+07	7.95.E+07	7.30.E+07	7.22.E+07
1096	Q13867	bleomycin hydrolase [OS=Homo sapiens]	36.7	13	4	54	4	539	64	4	4	0	6.69.E+07	6.38.E+07	6.79.E+07	7.04.E+07	1.54.E+08	1.35.E+08	1.56.E+08	1.56.E+08
1097	O43592	Exportin-T [OS=Homo sapiens]	36.5	11	6	79	6	182	65	6	6	0	7.57.E+07	7.72.E+07	7.37.E+07	8.26.E+07	1.08.E+08	1.05.E+08	6.79.E+07	9.42.E+07
1098	Q32MZ4-2	Isoform 2 of Leucine-rich repeat flightless-interacting protein 1 [OS=Homo sapiens]	36.3	16	6	36	6		83	6		0	5.18.E+07	8.29.E+07	5.84.E+07	9.43.E+07	6.37.E+07	5.54.E+07	5.90.E+07	5.87.E+07
1099	Q6IAA8	ragulator complex protein LAMTOR1 [OS=Homo sapiens]	36.2	45	4	76	4	535	112	4	4	0	1.56.E+08	1.53.E+08	1.56.E+08	1.39.E+08	1.75.E+08	1.88.E+08	1.74.E+08	1.76.E+08
1100	O95274	Ly6/PLAUR domain-containing protein 3 [OS=Homo sapiens]	36.2	14	3	210	3	5735	377	3	3	0	1.56.E+08	1.63.E+08	1.55.E+08	1.68.E+08	1.92.E+08	1.82.E+08	1.76.E+08	1.76.E+08
1101	Q8N1G4	Leucine-rich repeat-containing protein 47 [OS=Homo sapiens]	36.0	17	5	155	5	1504	209	5	5	0	6.40.E+07	7.31.E+07	9.02.E+07	1.08.E+08	7.37.E+07	6.54.E+07	8.22.E+07	7.64.E+07
1102	Q13573	SNW domain-containing protein 1 [OS=Homo sapiens]	35.9	16	5	34	5	498	41	4	5	0	4.14.E+07	2.03.E+07	5.03.E+07	3.13.E+07	6.43.E+07	8.41.E+07	6.18.E+07	6.04.E+07
1103	Q9NQX3	Gephyrin [OS=Homo sapiens]	35.8	13	5	77	5	1566	118	5	4	0	4.56.E+07	5.21.E+07	5.05.E+07	5.78.E+07	5.83.E+07	5.02.E+07	4.20.E+07	4.90.E+07
1104	Q53EL6-1	Programmed cell death protein 4 [OS=Homo sapiens]	35.8	17	5	42	5	619	62	5	5	0	8.90.E+07	6.76.E+07	1.05.E+08	9.13.E+07	8.94.E+07	1.05.E+08	5.64.E+07	6.69.E+07
1105	Q16222-1	UDP-N-acetylhexosamine pyrophosphorylase [OS=Homo sapiens]	35.8	15	6	127	5	1413	134	6	5	1	1.06.E+08	1.04.E+08	1.11.E+08	9.71.E+07	1.08.E+08	1.08.E+08	1.01.E+08	9.06.E+07
1106	P15927-1	Replication protein A 32 kDa subunit [OS=Homo sapiens]	35.7	26	4	138	4	2513	229	4	4	0	1.36.E+08	1.40.E+08	1.39.E+08	1.32.E+08	1.42.E+08	1.52.E+08	1.44.E+08	1.53.E+08
1107	O15020	Spectrin beta chain, non-erythrocytic 2 [OS=Homo sapiens]	35.6	3	6	132	1	318	105	5	6	0	2.30.E+06	2.28.E+06	2.68.E+06	1.84.E+06	3.27.E+06	3.41.E+06	3.71.E+06	3.61.E+06
1108	O60264	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5 [OS=Homo sapiens]	35.5	8	8	103	8	314	66	8	7	0	1.91.E+08	1.61.E+08	1.61.E+08	1.85.E+08	1.78.E+08	1.88.E+08	1.69.E+08	1.38.E+08
1109	Q13158	FAS-associated death domain protein [OS=Homo sapiens]	35.5	24	3	78	3	956	61	3	2	0	4.84.E+07	4.39.E+07	4.71.E+07	5.41.E+07	6.29.E+07	5.40.E+07	4.57.E+07	5.45.E+07
1110	P08574	Cytochrome c1, heme protein, mitochondrial [OS=Homo sapiens]	35.4	18	4	137	4	2554	242	4	4	0	9.72.E+07	1.00.E+08	9.88.E+07	9.52.E+07	1.05.E+08	9.06.E+07	1.03.E+08	1.04.E+08
1111	O43818	U3 small nucleolar RNA-interacting protein 2 [OS=Homo sapiens]	35.4	17	3	60	3	886	71	3	3	0	2.79.E+07	3.39.E+07	2.72.E+07	3.31.E+07	1.96.E+07	1.97.E+07	1.63.E+07	1.72.E+07
1112	Q12907	Vesicular integral-membrane protein VIP36 [OS=Homo sapiens]	35.3	26	6	73	6	432	95	6	5	0	2.26.E+08	2.38.E+08	2.31.E+08	2.22.E+08	3.45.E+08	3.83.E+08	3.37.E+08	3.51.E+08
1113	Q96TA2-1	ATP-dependent zinc metalloprotease YME1L1 [OS=Homo sapiens]	35.2	11	6	50	6	271	59	6	6	0	9.66.E+07	9.38.E+07	9.83.E+07	8.95.E+07	1.05.E+08	1.06.E+08	1.05.E+08	1.06.E+08
1114	Q15645	Pachytene checkpoint protein 2 homolog [OS=Homo sapiens]	35.1	19	6	60	6	523	71	6	6	0	7.03.E+07	7.58.E+07	7.82.E+07	7.53.E+07	6.98.E+07	9.09.E+07	9.43.E+07	8.29.E+07
1115	Q96N66-1	Lysophospholipid acyltransferase 7 [OS=Homo sapiens]	35.0	13	4	124	4	1361	161	4	4	0	1.26.E+08	1.29.E+08	1.30.E+08	1.32.E+08	7.76.E+07	7.55.E+07	7.35.E+07	7.69.E+07
1116	P61970	nuclear transport factor 2 [OS=Homo sapiens]	35.0	43	3	71	3	2225	41	2	3	0	9.00.E+07	9.47.E+07	7.69.E+07	8.43.E+07	7.90.E+07	7.78.E+07	6.66.E+07	7.47.E+07
1117	O43396	Thioredoxin-like protein 1 [OS=Homo sapiens]	35.0	23	5	148	5	1053	94	4	5	0	1.36.E+08	1.91.E+08	1.98.E+08	1.77.E+08	2.30.E+08	2.28.E+08	2.44.E+08	2.26.E+08
1118	O95372	acyl-protein thioesterase 2 [OS=Homo sapiens]	34.9	28	2	59	2	814	76	2	2	0	4.89.E+07	7.55.E+07	5.66.E+07	4.39.E+07	7.29.E+07	7.53.E+07	6.36.E+07	7.06.E+07
1119	Q6YHK3-1	CD109 antigen [OS=Homo sapiens]	34.8	7	6	45	6	628	30	6	6	0	4.67.E+07	5.46.E+07	5.31.E+07	5.24.E+07	8.12.E+07	8.05.E+07	7.80.E+07	7.52.E+07
1120	P35237	serpin B6 [OS=Homo sapiens]	34.8	13	3	84	3	579	105	3	3	0	5.57.E+07	6.60.E+07	6.35.E+07	7.13.E+07	9.86.E+07	8.94.E+07	9.87.E+07	8.05.E+07
1121	P43357	Melanoma-associated antigen 3 [OS=Homo sapiens]	34.8	19	4	117	4	1158	117	4	4	0	8.69.E+07	8.84.E+07	8.51.E+07	8.08.E+07	9.51.E+07	7.23.E+07	6.43.E+07	8.88.E+07

No.	Accession	Description	Sum PEP Score	Coverage [%]	# Peptides	# PSMs	# Unique Peptides	Score Mascot: A5 Mascot	Score Sequest HT: A2 Sequest HT	# Peptides (by Search Engine): A2 Sequest HT	# Peptides (by Search Engine): A5 Mascot	# Razor Peptides	ctrl Abundances_1	ctrl Abundances_2	ctrl Abundances_3	ctrl Abundances_4	JAM-A KO Abundances_1	JAM-A KO Abundances_2	JAM-A KO Abundances_3	JAM-A KO Abundances_4
1122	Q9H9J2	39S ribosomal protein L44, mitochondrial [OS=Homo sapiens]	34.8	21	5	39	5	356	44	5	5	0	6.15.E+07	6.23.E+07	5.63.E+07	5.63.E+07	6.26.E+07	5.95.E+07	5.17.E+07	5.46.E+07
1123	P08397-1	porphobilinogen deaminase [OS=Homo sapiens]	34.7	14	3	196	3	2307	223	3	3	0	7.97.E+07	8.37.E+07	7.49.E+07	9.53.E+07	1.01.E+08	9.63.E+07	9.37.E+07	1.01.E+08
1124	O15372	Eukaryotic translation initiation factor 3 subunit H [OS=Homo sapiens]	34.7	26	7	147	7	621	118	7	6	0	2.53.E+08	2.31.E+08	2.51.E+08	2.74.E+08	2.23.E+08	2.06.E+08	2.06.E+08	2.27.E+08
1125	Q8N684-1	Cleavage and polyadenylation specificity factor subunit 7 [OS=Homo sapiens]	34.5	10	3	40	3	616	49	3	3	0	3.28.E+07	3.26.E+07	3.74.E+07	3.14.E+07	3.26.E+07	3.41.E+07	3.29.E+07	3.56.E+07
1126	O60232	Sjoegren syndrome/scleroderma autoantigen 1 [OS=Homo sapiens]	34.5	46	4	58	4	769	85	4	3	0	8.68.E+07	9.25.E+07	7.97.E+07	8.15.E+07	6.58.E+07	8.05.E+07	6.49.E+07	7.06.E+07
1127	O75352	Mannose-P-dolichol utilization defect 1 protein [OS=Homo sapiens]	34.5	21	3	158	3	1356	151	3	3	0	1.50.E+08	1.50.E+08	1.50.E+08	1.46.E+08	1.02.E+08	1.04.E+08	2.02.E+07	9.16.E+07
1128	O15269	serine palmitoyltransferase 1 [OS=Homo sapiens]	34.5	19	5	22	5	208	29	5	5	0	4.59.E+07	1.55.E+07	5.01.E+07	1.13.E+08	8.66.E+07	5.96.E+07	1.34.E+08	4.04.E+07
1129	O75534	cold shock domain-containing protein E1 [OS=Homo sapiens]	34.4	8	5	81	5	1243	102	5	5	0	1.30.E+08	1.35.E+08	1.48.E+08	1.25.E+08	1.34.E+08	1.44.E+08	1.28.E+08	1.51.E+08
1130	Q15637	Splicing factor 1 [OS=Homo sapiens]	34.4	10	4	139	4	1594	147	4	4	0	1.04.E+08	1.18.E+08	9.81.E+07	1.05.E+08	6.53.E+07	6.94.E+07	3.64.E+07	6.48.E+07
1131	Q92542-1	Nicastrin [OS=Homo sapiens]	34.4	13	4	72	4	574	47	4	4	0	2.42.E+07	6.23.E+07	2.34.E+07	3.24.E+07	9.80.E+07	9.39.E+07	7.85.E+07	1.01.E+08
1132	Q9NSE4	Isoleucine--tRNA ligase, mitochondrial [OS=Homo sapiens]	34.3	11	8	163	8	148	31	8	8	0	9.54.E+07	1.15.E+08	8.76.E+07	1.05.E+08	1.32.E+08	1.46.E+08	1.61.E+08	1.34.E+08
1133	Q9UBX3	Mitochondrial dicarboxylate carrier [OS=Homo sapiens]	34.2	22	4	72	4	1228	92	4	4	0	8.27.E+07	8.76.E+07	8.76.E+07	8.63.E+07	5.45.E+07	4.79.E+07	5.00.E+07	5.57.E+07
1134	O60884	DnaJ homolog subfamily A member 2 [OS=Homo sapiens]	34.1	15	4	84	4	481	65	4	4	0	4.28.E+07	5.09.E+07	4.48.E+07	4.62.E+07	4.65.E+07	2.91.E+07	4.26.E+07	4.69.E+07
1135	O75821	Eukaryotic translation initiation factor 3 subunit G [OS=Homo sapiens]	34.1	17	5	157	5	828	155	5	5	0	2.39.E+08	2.09.E+08	2.39.E+08	2.53.E+08	2.74.E+08	2.58.E+08	3.19.E+08	2.59.E+08
1136	Q9UKY7	Protein CDV3 homolog [OS=Homo sapiens]	34.1	40	3	66	3	501	95	3	3	0	8.90.E+07	1.00.E+08	6.94.E+07	9.05.E+07	1.02.E+08	1.02.E+08	7.91.E+07	7.98.E+07
1137	Q969H8	Myeloid-derived growth factor [OS=Homo sapiens]	34.1	20	3	158	3	1584	168	3	3	0	1.46.E+08	1.51.E+08	1.51.E+08	1.28.E+08	1.45.E+08	1.57.E+08	1.70.E+08	1.61.E+08
1138	P49189	4-trimethylaminobutyraldehyde dehydrogenase [OS=Homo sapiens]	34.1	15	4	114	4	1512	196	4	4	0	9.34.E+07	1.11.E+08	1.12.E+08	1.12.E+08	1.06.E+08	9.73.E+07	9.98.E+07	9.89.E+07
1139	P28331-1	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial [OS=Homo sapiens]	34.0	15	6	44	6	348	56	6	6	0	3.62.E+07	9.24.E+07	4.30.E+07	4.43.E+07	6.89.E+07	1.47.E+08	1.39.E+08	1.56.E+08
1140	Q9BXL6-1	Caspase recruitment domain-containing protein 14 [OS=Homo sapiens]	33.9	7	4	52	4	1382	79	4	4	0	2.18.E+07	2.96.E+07	4.47.E+07	2.56.E+07	3.60.E+07	2.95.E+07	2.40.E+07	2.69.E+07
1141	P15586	N-acetylglucosamine-6-sulfatase [OS=Homo sapiens]	33.9	14	5	103	5	884	126	5	5	0	8.99.E+07	1.31.E+08	1.11.E+08	1.19.E+08	2.09.E+08	2.09.E+08	1.87.E+08	2.06.E+08
1142	O75569-1	Interferon-inducible double-stranded RNA-dependent protein kinase activator A [OS=Homo sapiens]	33.7	28	5	92	5	1380	136	5	4	0	6.99.E+07	7.27.E+07	6.79.E+07	6.71.E+07	9.56.E+07	8.31.E+07	6.79.E+07	9.00.E+07
1143	Q9Y5S9	RNA-binding protein 8A [OS=Homo sapiens]	33.7	22	4	99	4	1457	141	4	4	0	1.90.E+08	1.91.E+08	1.89.E+08	1.92.E+08	1.93.E+08	2.03.E+08	2.14.E+08	1.98.E+08
1144	Q8IY67-2	Isoform 2 of Ribonucleoprotein PTB-binding 1 [OS=Homo sapiens]	33.6	19	6	41	6		74	6		0	3.94.E+07	3.04.E+07	4.48.E+07	4.86.E+07	4.60.E+07	4.53.E+07	5.20.E+07	4.86.E+07
1145	P23368-1	NAD-dependent malic enzyme, mitochondrial [OS=Homo sapiens]	33.6	21	5	88	5	588	62	5	5	0	9.48.E+07	9.83.E+07	7.94.E+07	8.74.E+07	7.50.E+07	7.41.E+07	6.83.E+07	6.37.E+07
1146	Q9NVJ2	ADP-ribosylation factor-like protein 8B [OS=Homo sapiens]	33.6	33	5	141	5	777	126	5	5	0	1.33.E+08	1.33.E+08	1.33.E+08	1.52.E+08	9.61.E+07	8.36.E+07	1.04.E+08	1.03.E+08
1147	Q9UBS4	DnaJ homolog subfamily B member 11 [OS=Homo sapiens]	33.6	15	4	90	4	1543	104	4	4	0	1.10.E+08	1.18.E+08	1.23.E+08	1.40.E+08	1.52.E+08	1.46.E+08	1.54.E+08	1.57.E+08
1148	Q14134-1	Tripartite motif-containing protein 29 [OS=Homo sapiens]	33.5	15	6	71	6	459	62	6	6	0	1.43.E+08	1.39.E+08	1.35.E+08	1.51.E+08	8.32.E+07	9.00.E+07	8.02.E+07	7.65.E+07
1149	Q8N766-1	ER membrane protein complex subunit 1 [OS=Homo sapiens]	33.4	7	4	112	4	1442	121	4	4	0	3.91.E+07	4.22.E+07	3.07.E+07	4.26.E+07	4.41.E+07	4.07.E+07	3.70.E+07	4.20.E+07
1150	Q08209-1	Serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform [OS=Homo sapiens]	33.3	21	7	51	7	326	38	7	7	0	2.31.E+08	2.37.E+08	2.38.E+08	2.43.E+08	2.06.E+08	1.94.E+08	2.16.E+08	2.00.E+08
1151	Q96BS2-1	calcineurin B homologous protein 3 [OS=Homo sapiens]	33.3	25	4	120	4	827	148	4	4	0	1.75.E+08	1.67.E+08	1.83.E+08	1.98.E+08	2.58.E+08	2.00.E+08	2.44.E+08	2.60.E+08
1152	Q96EK5	KIF1-binding protein [OS=Homo sapiens]	33.3	17	6	19	6	91	12	6	5	0	1.72.E+07	6.00.E+07	1.61.E+07	5.40.E+07	6.03.E+07	2.29.E+07	2.47.E+07	5.47.E+07
1153	O60784	Target of Myb protein 1 [OS=Homo sapiens]	33.3	15	4	100	4	1951	161	4	4	0	4.71.E+07	5.50.E+07	5.14.E+07	5.06.E+07	6.53.E+07	6.65.E+07	7.08.E+07	6.46.E+07
1154	Q9UHG3	prenylcysteine oxidase 1 [OS=Homo sapiens]	33.3	15	5	79	5	681	56	5	5	0	1.37.E+08	1.34.E+08	1.31.E+08	1.39.E+08	1.45.E+08	1.59.E+08	1.36.E+08	1.50.E+08
1155	Q9Y2Z0-1	Protein SGT1 homolog [OS=Homo sapiens]	33.2	18	4	60	4	691	76	4	4	0	6.75.E+07	6.81.E+07	6.70.E+07	6.79.E+07	5.75.E+07	7.87.E+07	7.17.E+07	7.98.E+07
1156	Q92804-1	TATA-binding protein-associated factor 2N [OS=Homo sapiens]	33.2	8	4	164	2	1214	186	4	4	0	9.16.E+07	9.53.E+07	9.23.E+07	7.68.E+07	1.15.E+08	1.28.E+08	1.17.E+08	1.23.E+08
1157	P62847-1	40S ribosomal protein S24 [OS=Homo sapiens]	33.2	29	4	278	4	4070	394	4	4	0	6.21.E+08	6.62.E+08	5.61.E+08	6.66.E+08	5.42.E+08	5.31.E+08	4.19.E+08	5.01.E+08
1158	O15247	Chloride intracellular channel protein 2 [OS=Homo sapiens]	33.2	32	6	79	5	957	22	5	5	0	4.90.E+07	3.34.E+07	2.93.E+07	2.88.E+07				
1159	O75306-1	NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial [OS=Homo sapiens]	33.2	14	4	24	4	102	30	4	4	0	5.07.E+07	5.91.E+07	4.51.E+07	4.18.E+07	5.68.E+07	6.51.E+07	6.43.E+07	6.49.E+07
1160	O43278	Kunitz-type protease inhibitor 1 [OS=Homo sapiens]	33.1	9	4	56	4	251	57	4	4	0	7.46.E+07	6.80.E+07	7.25.E+07	6.58.E+07	7.23.E+07	7.24.E+07	7.37.E+07	6.77.E+07
1161	Q8TD19	Serine/threonine-protein kinase Nek9 [OS=Homo sapiens]	33.1	7	4	15	4	222	21	4	3	0	3.99.E+07	2.45.E+07	3.74.E+07	3.34.E+07	6.39.E+07	6.34.E+07	3.35.E+07	8.75.E+07
1162	P49354	protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha [OS=Homo sapiens]	33.1	13	3	65	3	864	40	3	3	0	2.96.E+07	3.37.E+07	3.24.E+07	3.00.E+07	3.49.E+07	3.23.E+07	3.04.E+07	3.36.E+07
1163	P07919	Cytochrome b-c1 complex subunit 6, mitochondrial [OS=Homo sapiens]	33.0	30	2	130	2	2009	239	2	2	0	1.41.E+08	1.45.E+08	1.54.E+08	1.55.E+08	1.30.E+08	1.42.E+08	1.07.E+08	1.26.E+08
1164	O00170	AH receptor-interacting protein [OS=Homo sapiens]	32.9	22	5	77	5	987	80	5	5	0	8.68.E+07	8.44.E+07	8.74.E+07	9.25.E+07	1.34.E+08	1.28.E+08	1.30.E+08	1.44.E+08
1165	Q06203	amidophosphoribosyltransferase [OS=Homo sapiens]	32.9	14	5	63	5	888	78	5	5	0	1.57.E+08	1.69.E+08	1.65.E+08	1.61.E+08	2.03.E+08	2.03.E+08	2.05.E+08	2.05.E+08
1166	O43708	maleylacetoacetate isomerase [OS=Homo sapiens]	32.7	24	3	80	3	966	129	3	3	0	7.21.E+07	8.51.E+07	7.62.E+07	7.08.E+07	8.14.E+07	8.77.E+07	8.16.E+07	8.08.E+07
1167	Q13572-1	Inositol-tetrakisphosphate 1-kinase [OS=Homo sapiens]	32.7	18	4	58	4	418	92	4	4	0	1.83.E+08	1.88.E+08	1.40.E+08	1.83.E+08	1.37.E+08	1.16.E+08	8.22.E+07	8.41.E+07
1168	P35659-1	Protein DEK [OS=Homo sapiens]	32.7	22	7	120	7	495	68	7	7	0	1.04.E+08	1.04.E+08	1.01.E+08	9.74.E+07	1.00.E+08	9.89.E+07	1.04.E+08	1.02.E+08
1169	O94826	Mitochondrial import receptor subunit TOM70 [OS=Homo sapiens]	32.6	12	6	177	6	1246	148	6	5	0	1.59.E+08	1.61.E+08	1.64.E+08	1.60.E+08	1.62.E+08	9.12.E+07	1.41.E+08	1.55.E+08
1170	Q6GMV3	Putative peptidyl-tRNA hydrolase PTRHD1 [OS=Homo sapiens]	32.5	50	4	34	4	246	61	4	4	0	7.12.E+07	7.57.E+07	7.09.E+07	7.00.E+07	8.85.E+07	8.31.E+07	8.07.E+07	8.61.E+07
1171	P42285	Superkiller viralicidic activity 2-like 2 [OS=Homo sapiens]	32.4	6	4	40	4	581	26	4	4	0	2.45.E+07	2.25.E+07	1.73.E+07	1.88.E+07	1.27.E+07	9.21.E+06	1.01.E+07	8.27.E+06
1172	P61081	NEDD8-conjugating enzyme Ubc12 [OS=Homo sapiens]	32.4	34	7	168	7	1330	140	7	6	0	3.85.E+08	3.92.E+08	4.09.E+08	3.77.E+08	2.16.E+08	2.31.E+08	2.23.E+08	2.34.E+08

No.	Accession	Description	Sum PEP Score	Coverage [%]	# Peptides	# PSMs	# Unique Peptides	Score Mascot: A5 Mascot	Score Sequest HT: A2 Sequest HT	# Peptides (by Search Engine): A2 Sequest HT	# Peptides (by Search Engine): A5 Mascot	# Razor Peptides	ctrl Abundances_1	ctrl Abundances_2	ctrl Abundances_3	ctrl Abundances_4	JAM-A KO Abundances_1	JAM-A KO Abundances_2	JAM-A KO Abundances_3	JAM-A KO Abundances_4
1173	Q9H2W6	39S ribosomal protein L46, mitochondrial [OS=Homo sapiens]	32.3	24	3	87	3	1582	152	3	3	0	7.47.E+07	6.23.E+07	7.05.E+07	8.21.E+07	6.11.E+07	6.22.E+07	6.51.E+07	6.82.E+07
1174	Q8N5N7	39S ribosomal protein L50, mitochondrial [OS=Homo sapiens]	32.3	32	3	57	3	253	18	3	3	0	4.70.E+07	5.22.E+07	4.73.E+07	3.94.E+07	4.98.E+07	5.48.E+07	4.37.E+07	4.79.E+07
1175	P23229-1	integrin alpha-6 [OS=Homo sapiens]	32.3	5	4	25	4	462	34	3	4	0	3.03.E+07	3.17.E+07	3.20.E+07	3.08.E+07	3.56.E+07	3.63.E+07	2.32.E+07	2.95.E+07
1176	P15170-3	Isoform 3 of Eukaryotic peptide chain release factor GTP-binding subunit ERF3A [OS=Homo sapiens]	32.1	14	6	68	6		154	6		0	1.44.E+08	1.42.E+08	1.51.E+08	1.62.E+08	1.45.E+08	1.33.E+08	1.54.E+08	1.44.E+08
1177	Q9Y3D6	mitochondrial fission 1 protein [OS=Homo sapiens]	32.1	34	4	163	4	1367	133	4	4	0	7.75.E+07	8.74.E+07	7.17.E+07	9.00.E+07	8.17.E+07	8.22.E+07	6.92.E+07	7.85.E+07
1178	Q9Y316-1	Protein MEMO1 [OS=Homo sapiens]	32.0	29	5	52	5	474	48	5	5	0	2.78.E+07	2.90.E+07	3.02.E+07	3.06.E+07	4.46.E+07	4.35.E+07	3.96.E+07	4.38.E+07
1179	P11717	Cation-independent mannose-6-phosphate receptor [OS=Homo sapiens]	32.0	5	8	88	8	362	65	8	8	0	2.72.E+07	2.89.E+07	2.92.E+07	3.29.E+07	9.70.E+07	1.05.E+08	8.10.E+07	8.66.E+07
1180	P61006	Ras-related protein Rab-8A [OS=Homo sapiens]	31.9	18	4	369	1	5491	482	4	4	0	2.42.E+07	1.84.E+07	1.40.E+07	2.14.E+07	1.87.E+07	2.20.E+07	2.29.E+07	2.77.E+07
1181	Q12765	Secernin-1 [OS=Homo sapiens]	31.9	18	5	62	5	272	58	5	5	0	8.67.E+07	1.25.E+08	3.95.E+07	4.21.E+07	1.26.E+08	1.86.E+08	1.12.E+08	1.39.E+08
1182	P78330	phosphoserine phosphatase [OS=Homo sapiens]	31.9	43	7	70	7	488	63	6	7	0	1.44.E+08	1.24.E+08	1.52.E+08	1.57.E+08	2.34.E+08	2.20.E+08	2.43.E+08	2.37.E+08
1183	O00505	Importin subunit alpha-4 [OS=Homo sapiens]	31.9	20	6	47	3	541	57	6	5	0	1.52.E+07	1.72.E+07	2.01.E+07	1.92.E+07	2.60.E+07	8.15.E+06	2.44.E+07	2.61.E+07
1184	A0AVT1-1	Ubiquitin-like modifier-activating enzyme 6 [OS=Homo sapiens]	31.9	8	6	74	6	593	69	6	6	0	2.02.E+08	1.80.E+08	2.16.E+08	1.77.E+08	1.20.E+08	1.14.E+08	1.30.E+08	1.16.E+08
1185	Q9BWM7	Sideroflexin-3 [OS=Homo sapiens]	31.8	13	3	87	1	941	82	3	3	0	5.71.E+07	4.99.E+07	3.76.E+07	3.21.E+07	6.18.E+07	4.40.E+07	2.88.E+07	2.58.E+07
1186	Q9NRX4	14 kDa phosphohistidine phosphatase [OS=Homo sapiens]	31.8	45	3	56	3	1466	0	2	2	0	1.72.E+08	1.78.E+08	1.78.E+08	1.79.E+08	2.13.E+08	1.93.E+08	2.02.E+08	2.00.E+08
1187	Q15121	Astrocytic phosphoprotein PEA-15 [OS=Homo sapiens]	31.6	40	3	63	3	1338	55	2	3	0	4.31.E+07	3.16.E+07	3.36.E+07	3.56.E+07	3.50.E+07	3.73.E+07	3.58.E+07	3.89.E+07
1188	P23921	Ribonucleoside-diphosphate reductase large subunit [OS=Homo sapiens]	31.6	11	4	44	4	810	60	4	3	0	2.45.E+07	2.16.E+07	1.68.E+07	2.91.E+07	2.19.E+07	2.27.E+07	2.19.E+07	1.90.E+07
1189	Q07157	Tight junction protein ZO-1 [OS=Homo sapiens]	31.6	4	5	66	5	454	47	5	5	0	3.10.E+07	3.97.E+07	3.35.E+07	3.41.E+07	6.10.E+07	6.49.E+07	6.16.E+07	5.65.E+07
1190	Q9Y6B6	GTP-binding protein SAR1b [OS=Homo sapiens]	31.6	47	6	112	3	685	89	6	6	0	3.37.E+07	3.72.E+07	3.33.E+07	2.45.E+07	4.68.E+07	4.13.E+07	2.98.E+07	4.23.E+07
1191	P10253	lysosomal alpha-glucosidase [OS=Homo sapiens]	31.5	11	5	54	5	398	54	5	5	0	6.94.E+07	6.75.E+07	6.35.E+07	6.80.E+07	1.07.E+08	1.20.E+08	7.43.E+07	1.25.E+08
1192	O95197-3	Isoform 3 of Reticulon-3 [OS=Homo sapiens]	31.5	11	2	76	1		217	2		0	1.81.E+08	1.87.E+08	1.79.E+08	1.62.E+08	1.97.E+08	2.03.E+08	2.08.E+08	1.94.E+08
1193	Q15397	Pumilio homolog 3 [OS=Homo sapiens]	31.5	15	5	84	5	1306	123	5	5	0	3.96.E+07	5.16.E+07	3.85.E+07	4.37.E+07	4.55.E+07	3.79.E+07	3.42.E+07	3.67.E+07
1194	Q5VYK3	Proteasome-associated protein ECM29 homolog [OS=Homo sapiens]	31.5	3	5	110	5	1115	63	5	5	0	3.48.E+07	4.75.E+07	4.05.E+07	4.28.E+07	5.07.E+07	4.57.E+07	4.63.E+07	4.75.E+07
1195	P63208	s-phase kinase-associated protein 1 [OS=Homo sapiens]	31.5	47	6	143	6	1757	128	6	6	0	2.20.E+08	8.77.E+07	1.52.E+08	1.67.E+08	1.26.E+08	1.26.E+08	2.95.E+08	1.20.E+08
1196	Q9Y5K6	CD2-associated protein [OS=Homo sapiens]	31.4	18	8	67	8	184	58	8	7	0	8.06.E+07	7.72.E+07	8.10.E+07	1.04.E+08	8.74.E+07	1.14.E+08	9.76.E+07	1.33.E+08
1197	O15145	Actin-related protein 2/3 complex subunit 3 [OS=Homo sapiens]	31.3	33	7	121	7	578	93	6	6	0	7.98.E+07	9.04.E+07	7.81.E+07	8.52.E+07	1.07.E+08	1.11.E+08	1.13.E+08	1.01.E+08
1198	Q93009	Ubiquitin carboxyl-terminal hydrolase 7 [OS=Homo sapiens]	31.3	6	5	76	5	687	78	5	5	0	4.73.E+07	5.15.E+07	4.16.E+07	5.37.E+07	3.93.E+07	3.27.E+07	3.55.E+07	3.31.E+07
1199	Q13442	28 kDa heat- and acid-stable phosphoprotein [OS=Homo sapiens]	31.2	23	3	110	3	2829	194	3	3	0	1.34.E+08	1.40.E+08	1.35.E+08	1.41.E+08	1.57.E+08	1.55.E+08	1.64.E+08	1.36.E+08
1200	P53597	Succinate--CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial [OS=Homo sapiens]	31.2	22	6	162	6	943	147	6	6	0	2.40.E+08	2.45.E+08	2.40.E+08	2.52.E+08	3.03.E+08	2.47.E+08	2.53.E+08	2.60.E+08
1201	Q96K17-1	transcription factor BTF3 homolog 4 [OS=Homo sapiens]	31.2	50	3	132	3	1834	213	3	3	0	1.19.E+08	1.27.E+08	1.22.E+08	1.36.E+08	1.49.E+08	1.33.E+08	1.36.E+08	1.39.E+08
1202	Q96EL3	39S ribosomal protein L53, mitochondrial [OS=Homo sapiens]	31.2	28	2	88	2	1813	140	2	2	0	3.86.E+07	4.31.E+07	3.17.E+07	4.28.E+07	3.41.E+07	3.74.E+07	3.13.E+07	3.65.E+07
1203	P54105	Methylosome subunit pICln [OS=Homo sapiens]	31.1	22	2	78	2	2077	136	2	2	0	6.52.E+07	7.54.E+07	6.23.E+07	6.93.E+07	6.07.E+07	6.45.E+07	5.19.E+07	6.15.E+07
1204	Q9NS69	Mitochondrial import receptor subunit TOM22 homolog [OS=Homo sapiens]	31.1	49	4	68	4	1416	81	3	4	0	1.23.E+08	1.19.E+08	1.06.E+08	1.46.E+08	9.70.E+07	7.53.E+07	8.42.E+07	9.99.E+07
1205	P61619	Protein transport protein Sec61 subunit alpha isoform 1 [OS=Homo sapiens]	31.1	9	2	98	2	652	88	2	2	0	7.81.E+07	8.04.E+07	6.34.E+07	8.94.E+07	9.22.E+07	9.42.E+07	8.06.E+07	8.40.E+07
1206	P27694	Replication protein A 70 kDa DNA-binding subunit [OS=Homo sapiens]	31.0	14	5	78	5	1067	92	5	5	0	1.16.E+08	1.19.E+08	1.11.E+08	1.22.E+08	1.13.E+08	1.25.E+08	9.77.E+07	1.18.E+08
1207	Q9NTJ3-1	Structural maintenance of chromosomes protein 4 [OS=Homo sapiens]	31.0	6	4	66	4	704	100	4	4	0	6.80.E+07	7.09.E+07	7.03.E+07	7.39.E+07	8.01.E+07	7.94.E+07	7.99.E+07	8.01.E+07
1208	Q5JTV8	Torsin-1A-interacting protein 1 [OS=Homo sapiens]	31.0	9	4	66	4	520	92	4	4	0	6.59.E+07	6.92.E+07	6.20.E+07	5.75.E+07	9.50.E+07	9.25.E+07	7.88.E+07	9.52.E+07
1209	O95816	BAG family molecular chaperone regulator 2 [OS=Homo sapiens]	31.0	47	6	114	6	1083	121	6	5	0	1.14.E+08	1.30.E+08	1.25.E+08	1.25.E+08	1.63.E+08	1.63.E+08	1.54.E+08	1.69.E+08
1210	Q9BXP5	serrate RNA effector molecule homolog [OS=Homo sapiens]	30.9	13	7	91	7	255	71	7	6	0	8.58.E+07	9.03.E+07	8.34.E+07	9.24.E+07	1.04.E+08	9.68.E+07	9.78.E+07	1.03.E+08
1211	Q99426	tubulin-folding cofactor B [OS=Homo sapiens]	30.9	30	5	118	5	859	79	5	5	0	1.10.E+08	1.00.E+08	9.18.E+07	1.05.E+08	9.12.E+07	9.24.E+07	7.93.E+07	9.06.E+07
1212	P62633-4	Isoform 4 of Cellular nucleic acid-binding protein [OS=Homo sapiens]	30.8	24	3	61	1		67	3		0								
1213	Q96SI9	spermatid perinuclear RNA-binding protein [OS=Homo sapiens]	30.8	9	4	43	1	145	38	4	4	0	1.02.E+07	1.12.E+07	7.57.E+06	4.25.E+06		8.78.E+06		7.75.E+05
1214	Q9P000-1	COMM domain-containing protein 9 [OS=Homo sapiens]	30.7	31	3	46	3	1354	28	2	3	0	4.80.E+07	4.74.E+07	3.75.E+07	4.43.E+07	4.11.E+07	3.90.E+07	3.26.E+07	2.98.E+07
1215	Q15369-1	elongin-C [OS=Homo sapiens]	30.7	49	4	55	4	430	31	4	4	0	1.39.E+08	1.61.E+08	1.23.E+08	7.41.E+07	1.74.E+08	1.63.E+08	1.41.E+08	1.38.E+08
1216	Q9Y277	Voltage-dependent anion-selective channel protein 3 [OS=Homo sapiens]	30.7	30	6	199	5	3163	221	5	6	0	1.33.E+08	1.50.E+08	1.73.E+08	1.58.E+08	9.37.E+07	1.04.E+08	1.03.E+08	9.61.E+07
1217	P46109	Crk-like protein [OS=Homo sapiens]	30.7	15	3	49	3	178	55	3	3	0	2.66.E+08	2.73.E+08	2.77.E+08	2.44.E+08	3.42.E+08	3.49.E+08	3.67.E+08	3.41.E+08
1218	Q9HB07	UPF0160 protein MYG1, mitochondrial [OS=Homo sapiens]	30.6	20	6	112	6	1030	141	6	6	0	2.36.E+08	2.29.E+08	2.34.E+08	2.13.E+08	2.23.E+08	2.39.E+08	2.39.E+08	2.40.E+08
1219	O75489	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial [OS=Homo sapiens]	30.6	27	5	80	5	961	119	5	5	0	1.09.E+08	1.20.E+08	1.05.E+08	1.12.E+08	1.31.E+08	1.49.E+08	1.26.E+08	1.41.E+08
1220	P13987	CD59 glycoprotein [OS=Homo sapiens]	30.6	20	3	224	3	1426	332	3	3	0	7.18.E+08	6.39.E+08	7.04.E+08	7.73.E+08	4.74.E+08	4.35.E+08	5.18.E+08	4.64.E+08
1221	Q8TCT9-1	Minor histocompatibility antigen H13 [OS=Homo sapiens]	30.6	22	4	184	4	1553	237	4	4	0	1.90.E+08	1.36.E+08	1.82.E+08	1.46.E+08	2.19.E+08	1.43.E+08	2.01.E+08	2.02.E+08
1222	P43246-1	DNA mismatch repair protein MSH2 [OS=Homo sapiens]	30.6	7	6	82	6	1117	63	6	6	0	3.82.E+08	4.19.E+08	3.45.E+08	4.39.E+08	5.01.E+08	4.44.E+08	4.38.E+08	4.78.E+08

No.	Accession	Description	Sum PEP Score	Coverage [%]	# Peptides	# PSMs	# Unique Peptides	Score Mascot: A5 Mascot	Score Sequest HT: A2 Sequest HT	# Peptides (by Search Engine): A2 Sequest HT	# Peptides (by Search Engine): A5 Mascot	# Razor Peptides	ctrl Abundances_1	ctrl Abundances_2	ctrl Abundances_3	ctrl Abundances_4	JAM−A KO Abundances_1	JAM−A KO Abundances_2	JAM−A KO Abundances_3	JAM−A KO Abundances_4
1223	P43307	Translocon−associated protein subunit alpha [OS=Homo sapiens]	30.5	22	4	149	4	2260	156	4	4	0	1.18.E+08	1.12.E+08	1.06.E+08	1.12.E+08	1.49.E+08	1.67.E+08	1.58.E+08	1.59.E+08
1224	P29373	Cellular retinoic acid−binding protein 2 [OS=Homo sapiens]	30.4	18	2	40	2	591	64	2	2	0	9.39.E+07	8.83.E+07	8.54.E+07	8.64.E+07	2.24.E+07	2.37.E+07	2.23.E+07	2.30.E+07
1225	Q9NUU7	ATP−dependent RNA helicase DDX19A [OS=Homo sapiens]	30.4	13	4	19	4	185	21	4	3	0	5.70.E+07	5.90.E+07	4.16.E+07	5.54.E+07	5.01.E+07	6.41.E+07	4.67.E+07	5.81.E+07
1226	O75347	Tubulin−specific chaperone A [OS=Homo sapiens]	30.3	35	4	70	4	1415	132	4	4	0	2.01.E+08	1.83.E+08	2.04.E+08	1.89.E+08	2.47.E+08	2.43.E+08	2.56.E+08	2.41.E+08
1227	Q9Y3C8	ubiquitin−fold modifier−conjugating enzyme 1 [OS=Homo sapiens]	30.2	34	4	108	4	317	66	4	4	0	1.12.E+08	1.14.E+08	1.20.E+08	9.52.E+07	1.19.E+08	1.27.E+08	1.35.E+08	1.27.E+08
1228	P62851	40S ribosomal protein S25 [OS=Homo sapiens]	30.2	26	5	471	5	4922	539	5	5	0	2.29.E+09	2.24.E+09	2.35.E+09	2.04.E+09	2.33.E+09	2.28.E+09	2.46.E+09	2.27.E+09
1229	Q96KB5	Lymphokine−activated killer T−cell−originated protein kinase [OS=Homo sapiens]	30.2	27	6	125	6	419	81	6	6	0	7.78.E+07	5.65.E+07	6.32.E+07	7.41.E+07	8.49.E+07	9.21.E+07	8.59.E+07	9.14.E+07
1230	Q6Y7W6−1	GRB10−interacting GYF protein 2 [OS=Homo sapiens]	30.1	7	4	104	4	385	116	4	4	0	2.83.E+08	7.58.E+07	7.26.E+07	8.06.E+07	7.52.E+07	6.58.E+07	6.73.E+07	7.16.E+07
1231	P07108	acyl−CoA−binding protein [OS=Homo sapiens]	30.1	41	4	186	4	1019	135	4	4	0	1.30.E+08	2.32.E+08	2.32.E+08	2.25.E+08	3.61.E+08	3.47.E+08	3.64.E+08	3.40.E+08
1232	Q9P0V9	septin−10 [OS=Homo sapiens]	30.0	15	5	91	3	650	103	5	4	0	4.69.E+07	5.45.E+07	4.77.E+07	4.93.E+07	6.03.E+07	6.33.E+07	5.33.E+07	5.70.E+07
1233	P61758	Prefoldin subunit 3 [OS=Homo sapiens]	29.9	28	3	104	3	1984	166	3	3	0	4.81.E+07	5.16.E+07	4.49.E+07	5.21.E+07	3.61.E+07	3.63.E+07	3.44.E+07	3.51.E+07
1234	Q9HD45	Transmembrane 9 superfamily member 3 [OS=Homo sapiens]	29.8	10	4	122	4	731	116	4	4	0	1.69.E+08	1.77.E+08	1.70.E+08	1.26.E+08	2.25.E+08	2.02.E+08	1.63.E+08	1.99.E+08
1235	Q96AT9	ribulose−phosphate 3−epimerase [OS=Homo sapiens]	29.8	21	3	110	3	1423	151	3	3	0	1.66.E+08	2.19.E+08	1.75.E+08	1.47.E+08	2.30.E+08	2.41.E+08	2.04.E+08	1.77.E+08
1236	Q96JY6−1	PDZ and LIM domain protein 2 [OS=Homo sapiens]	29.8	21	5	37	5	387	41	4	5	0	4.25.E+07	4.38.E+07	4.20.E+07	3.83.E+07	3.40.E+07	2.48.E+07	2.39.E+07	2.98.E+07
1237	Q9Y223−1	bifunctional UDP−N−acetylglucosamine 2−epimerase/N−acetylmannosamine kinase [OS=Homo sapiens]	29.7	10	6	51	6	522	54	6	5	0	7.94.E+07	9.36.E+07	8.13.E+07	8.23.E+07	1.17.E+08	1.13.E+08	1.30.E+08	1.21.E+08
1238	Q5RI15−1	Cytochrome c oxidase protein 20 homolog [OS=Homo sapiens]	29.7	53	5	49	5	423	40	3	5	0	5.44.E+07	5.55.E+07	4.69.E+07	5.25.E+07	6.56.E+07	6.06.E+07	6.29.E+07	6.42.E+07
1239	Q9BVP2	Guanine nucleotide−binding protein−like 3 [OS=Homo sapiens]	29.7	14	5	32	5	275	27	5	4	0	1.08.E+08	1.15.E+08	1.16.E+08	1.20.E+08	9.63.E+07	6.91.E+07	7.90.E+07	7.60.E+07
1240	P62993	Growth factor receptor−bound protein 2 [OS=Homo sapiens]	29.7	32	5	91	5	584	83	5	5	0	7.70.E+07	7.91.E+07	8.14.E+07	8.16.E+07	6.86.E+07	6.99.E+07	6.32.E+07	6.91.E+07
1241	P62942	Peptidyl−prolyl cis−trans isomerase FKBP1A [OS=Homo sapiens]	29.6	41	3	48	3	1202	37	2	3	0	1.95.E+08	1.84.E+08	1.95.E+08	2.06.E+08	1.69.E+08	1.65.E+08	1.83.E+08	1.64.E+08
1242	Q9Y3U8	60S ribosomal protein L36 [OS=Homo sapiens]	29.4	30	4	293	4	2787	350	4	4	0	8.86.E+08	8.46.E+08	8.30.E+08	8.74.E+08	7.32.E+08	7.08.E+08	7.46.E+08	6.85.E+08
1243	Q8WWI1−3	Isoform 3 of LIM domain only protein 7 [OS=Homo sapiens]	29.4	7	6	16	6		26	6		0	5.29.E+07	5.17.E+07	4.86.E+07	3.43.E+07	5.93.E+07	4.07.E+07	4.69.E+07	4.05.E+07
1244	P36405	ADP−ribosylation factor−like protein 3 [OS=Homo sapiens]	29.4	38	5	51	5	580	43	4	5	0	8.22.E+07	9.13.E+07	9.10.E+07	9.46.E+07	1.36.E+08	1.37.E+08	1.28.E+08	1.35.E+08
1245	Q15008	26S proteasome non−ATPase regulatory subunit 6 [OS=Homo sapiens]	29.3	17	6	71	6	393	40	6	5	0	1.40.E+08	1.17.E+08	1.41.E+08	1.51.E+08	1.60.E+08	1.64.E+08	1.58.E+08	1.75.E+08
1246	O43847−2	Isoform 2 of Nardilysin [OS=Homo sapiens]	29.3	6	7	47	7		71	7		0	1.26.E+08	1.35.E+08	1.35.E+08	1.18.E+08	1.70.E+08	1.73.E+08	1.92.E+08	1.79.E+08
1247	O43768	alpha−endosulfine [OS=Homo sapiens]	29.2	34	3	68	2	1166	31	1	3	1	8.17.E+07	7.78.E+07	7.16.E+07	8.63.E+07	7.21.E+07	6.81.E+07	6.79.E+07	6.74.E+07
1248	P61201−2	Isoform 2 of COP9 signalosome complex subunit 2 [OS=Homo sapiens]	29.2	21	6	69	1		150	6		0								
1249	O95299	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial [OS=Homo sapiens]	29.2	19	4	94	4	1985	149	4	4	0	5.94.E+07	8.44.E+07	6.36.E+07	6.87.E+07	6.81.E+07	6.75.E+07	6.40.E+07	7.29.E+07
1250	Q15257−1	Serine/threonine−protein phosphatase 2A activator [OS=Homo sapiens]	29.2	18	3	112	3	1647	177	3	3	0	7.14.E+07	7.46.E+07	6.73.E+07	7.62.E+07	9.94.E+07	9.65.E+07	8.19.E+07	9.04.E+07
1251	Q9Y6E2	Basic leucine zipper and W2 domain−containing protein 2 [OS=Homo sapiens]	29.2	12	4	210	3	2713	229	4	4	0	1.15.E+08	1.26.E+08	1.25.E+08	1.27.E+08	1.53.E+08	1.56.E+08	1.40.E+08	1.55.E+08
1252	O43290	U4/U6.U5 tri−snRNP−associated protein 1 [OS=Homo sapiens]	29.2	9	5	43	5	193	39	5	5	0	5.86.E+07	4.05.E+07	4.01.E+07	5.85.E+07	6.71.E+07	6.92.E+07	6.58.E+07	6.39.E+07
1253	Q7L2E3−1	Putative ATP−dependent RNA helicase DHX30 [OS=Homo sapiens]	29.1	6	4	96	4	551	57	4	4	0	4.78.E+07	4.73.E+07	3.83.E+07	4.61.E+07	3.78.E+07	3.55.E+07	2.30.E+07	3.58.E+07
1254	O43837−1	isocitrate dehydrogenase [NAD] subunit beta, mitochondrial [OS=Homo sapiens]	29.1	14	4	46	4	348	43	4	4	0	7.17.E+07	8.10.E+07	7.14.E+07	7.49.E+07	8.69.E+07	8.46.E+07	8.47.E+07	8.48.E+07
1255	Q96CW1	AP−2 complex subunit mu [OS=Homo sapiens]	29.1	13	4	138	4	933	172	4	4	0	7.28.E+07	7.41.E+07	7.47.E+07	6.78.E+07	6.94.E+07	8.00.E+07	7.65.E+07	7.30.E+07
1256	Q14738−1	Serine/threonine−protein phosphatase 2A 56 kDa regulatory subunit delta isoform [OS=Homo sapiens]	29.1	10	4	104	1	1467	121	4	3	0								
1257	P30626−1	Sorcin [OS=Homo sapiens]	29.0	33	4	38	4	472	39	4	4	0	1.10.E+08	1.11.E+08	1.10.E+08	1.15.E+08	1.34.E+08	1.38.E+08	1.45.E+08	1.35.E+08
1258	Q9HAV4	exportin−5 [OS=Homo sapiens]	29.0	8	7	159	7	960	113	7	7	0	8.48.E+07	9.44.E+07	9.20.E+07	9.75.E+07	1.14.E+08	1.18.E+08	1.18.E+08	1.23.E+08
1259	Q9BYD3	39S ribosomal protein L4, mitochondrial [OS=Homo sapiens]	28.9	24	4	53	4	321	54	4	4	0	6.28.E+07	7.05.E+07	6.39.E+07	7.09.E+07	6.79.E+07	7.49.E+07	6.95.E+07	7.77.E+07
1260	O15031	Plexin−B2 [OS=Homo sapiens]	28.9	6	5	96	5	302	15	5	5	0	4.56.E+07	4.82.E+07	4.19.E+07	4.12.E+07	6.28.E+07	5.63.E+07	4.23.E+07	6.00.E+07
1261	Q9UG63	ATP−binding cassette sub−family F member 2 [OS=Homo sapiens]	28.9	10	5	78	5	419	87	5	5	0	9.22.E+07	1.07.E+08	1.08.E+08	9.71.E+07	9.51.E+07	9.84.E+07	1.03.E+08	1.20.E+08
1262	Q86X76	Nitrilase homolog 1 [OS=Homo sapiens]	28.9	16	4	126	4	845	128	4	4	0	6.13.E+07	6.82.E+07	6.79.E+07	6.65.E+07	6.54.E+07	6.44.E+07	6.03.E+07	6.13.E+07
1263	O43747−1	AP−1 complex subunit gamma−1 [OS=Homo sapiens]	28.8	9	4	84	4	344	57	4	4	0	2.49.E+08	2.69.E+08	2.35.E+08	2.42.E+08	1.51.E+08	1.44.E+08	1.35.E+08	1.44.E+08
1264	P51148	Ras−related protein Rab−5C [OS=Homo sapiens]	28.6	22	4	125	2	1076	157	4	4	2	1.79.E+08	1.67.E+08	1.71.E+08	1.63.E+08	1.82.E+08	1.71.E+08	2.24.E+08	1.72.E+08
1265	P18859	ATP synthase−coupling factor 6, mitochondrial [OS=Homo sapiens]	28.6	34	3	176	3	3695	299	3	3	0	2.24.E+08	2.20.E+08	2.30.E+08	1.91.E+08	2.55.E+08	2.58.E+08	2.56.E+08	2.38.E+08
1266	O14745	Na(+)/H(+) exchange regulatory cofactor NHE−RF1 [OS=Homo sapiens]	28.6	18	4	91	4	877	95	4	4	0	1.07.E+08	1.07.E+08	1.13.E+08	1.06.E+08	8.99.E+07	8.77.E+07	9.42.E+07	8.65.E+07
1267	Q9H6R4−1	Nucleolar protein 6 [OS=Homo sapiens]	28.4	7	4	49	4	327	55	4	4	0	7.03.E+07	6.64.E+07	7.12.E+07	7.72.E+07	6.04.E+07	6.86.E+07	6.84.E+07	6.71.E+07
1268	Q96I24−1	Far upstream element−binding protein 3 [OS=Homo sapiens]	28.4	12	5	119	3	702	115	5	5	0	1.43.E+08	1.35.E+08	1.49.E+08	1.71.E+08	1.32.E+08	1.41.E+08	1.56.E+08	1.43.E+08
1269	O43324−1	Eukaryotic translation elongation factor 1 epsilon−1 [OS=Homo sapiens]	28.4	42	5	107	5	1517	114	4	5	0	2.03.E+08	2.03.E+08	2.05.E+08	1.96.E+08	2.78.E+08	2.80.E+08	2.19.E+08	2.33.E+08
1270	Q9UBP6	tRNA (guanine−N(7)−)−methyltransferase [OS=Homo sapiens]	28.4	17	4	66	4	439	33	4	4	0	7.75.E+07	8.81.E+07	8.39.E+07	8.37.E+07	8.93.E+07	9.03.E+07	9.29.E+07	8.35.E+07

No.	Accession	Description	Sum PEP Score	Coverage [%]	# Peptides	# PSMs	# Unique Peptides	Score Mascot: A5 Mascot	Score Sequest HT: A2 Sequest HT	# Peptides (by Search Engine): A2 Sequest HT	# Peptides (by Search Engine): A5 Mascot	# Razor Peptides	ctrl Abundances_1	ctrl Abundances_2	ctrl Abundances_3	ctrl Abundances_4	JAM-A KO Abundances_1	JAM-A KO Abundances_2	JAM-A KO Abundances_3	JAM-A KO Abundances_4
1271	Q99538	Legumain [OS=Homo sapiens]	28.4	12	3	110	3	2501	175	3	3	0	5.64.E+07	6.12.E+07	5.78.E+07	6.84.E+07	8.67.E+07	8.36.E+07	8.37.E+07	8.82.E+07
1272	Q92734-1	Protein TFG [OS=Homo sapiens]	28.4	14	3	97	3	489	147	3	3	0	1.57.E+08	1.56.E+08	1.51.E+08	1.74.E+08	1.91.E+08	1.88.E+08	1.87.E+08	1.88.E+08
1273	Q9P1F3	Costars family protein ABRACL [OS=Homo sapiens]	28.3	40	3	110	3	1440	130	3	3	0	6.55.E+07	7.60.E+07	5.77.E+07	7.48.E+07	9.17.E+07	8.81.E+07	7.17.E+07	7.92.E+07
1274	Q9NRX2	39S ribosomal protein L17, mitochondrial [OS=Homo sapiens]	28.3	14	2	78	2	1188	117	2	2	0	5.43.E+07	6.02.E+07	5.01.E+07	5.44.E+07	5.63.E+07	5.71.E+07	5.99.E+07	6.08.E+07
1275	O75915	PRA1 family protein 3 [OS=Homo sapiens]	28.3	16	2	82	2	1510	81	2	2	0	1.24.E+08	1.32.E+08	1.63.E+08	1.55.E+08	1.65.E+08	1.25.E+08	1.21.E+08	1.84.E+08
1276	Q8IY81	pre-rRNA processing protein FTSJ3 [OS=Homo sapiens]	28.3	14	6	53	6	419	26	6	5	0	3.00.E+07	3.54.E+07	3.05.E+07	3.11.E+07	2.31.E+07	3.04.E+07	2.56.E+07	1.28.E+07
1277	P52434	DNA-directed RNA polymerases I, II, and III subunit RPABC3 [OS=Homo sapiens]	28.2	23	3	52	3	1709	0	1	2	0	6.43.E+07	6.47.E+07	5.65.E+07	6.73.E+07	4.31.E+07	4.02.E+07	3.64.E+07	3.96.E+07
1278	Q14203	Dynactin subunit 1 [OS=Homo sapiens]	28.2	8	6	62	6	453	70	6	5	0	8.67.E+07	6.62.E+07	9.60.E+07	8.57.E+07	1.18.E+08	1.19.E+08	7.82.E+07	1.19.E+08
1279	Q9Y3A5	Ribosome maturation protein SBDS [OS=Homo sapiens]	28.1	31	8	166	8	451	189	7	8	0	2.94.E+08	2.74.E+08	2.98.E+08	3.10.E+08	2.89.E+08	2.82.E+08	3.15.E+08	2.86.E+08
1280	P43897	Elongation factor Ts, mitochondrial [OS=Homo sapiens]	28.0	18	3	36	3	292	48	3	3	0	2.28.E+06	5.05.E+07	2.40.E+06	4.66.E+07		3.77.E+07	4.04.E+05	3.62.E+07
1281	O43681	ATPase ASNA1 [OS=Homo sapiens]	28.0	20	6	186	6	681	127	6	6	0	4.39.E+08	4.77.E+08	5.04.E+08	4.91.E+08	5.83.E+08	5.99.E+08	6.02.E+08	6.44.E+08
1282	P08237	ATP-dependent 6-phosphofructokinase, muscle type [OS=Homo sapiens]	27.9	9	4	143	3	758	161	3	4	0	1.53.E+07	1.98.E+07	1.30.E+07	1.26.E+07	2.64.E+07	2.57.E+07	1.70.E+07	2.29.E+07
1283	Q2NL82	Pre-rRNA-processing protein TSR1 homolog [OS=Homo sapiens]	27.9	10	5	76	5	113	65	5	5	0	7.78.E+07	8.82.E+07	8.41.E+07	8.95.E+07	6.60.E+07	5.78.E+07	6.35.E+07	5.82.E+07
1284	Q9UJU6-1	Drebrin-like protein [OS=Homo sapiens]	27.9	10	3	60	3	1194	87	3	3	0	2.27.E+07	2.74.E+07	2.53.E+07	3.35.E+07	3.52.E+07	3.20.E+07	2.83.E+07	3.27.E+07
1285	Q13596	Sorting nexin-1 [OS=Homo sapiens]	27.9	12	5	81	4	317	89	5	5	1	1.86.E+08	1.58.E+08	1.66.E+08	1.73.E+08	1.39.E+08	1.94.E+08	1.60.E+08	1.37.E+08
1286	Q9BYT8	Neurolysin, mitochondrial [OS=Homo sapiens]	27.8	10	5	54	5	321	54	5	5	0	5.96.E+07	6.88.E+07	5.11.E+07	5.37.E+07	8.98.E+07	8.03.E+07	8.39.E+07	8.75.E+07
1287	Q8N5K1	CDGSH iron-sulfur domain-containing protein 2 [OS=Homo sapiens]	27.8	26	4	128	4	1088	153	4	4	0	1.24.E+08	1.32.E+08	1.33.E+08	1.20.E+08	1.52.E+08	1.76.E+08	1.60.E+08	1.70.E+08
1288	O43272	Proline dehydrogenase 1, mitochondrial [OS=Homo sapiens]	27.8	15	5	26	5	133	38	5	5	0	1.28.E+08	1.67.E+08	1.38.E+08	1.62.E+08	5.90.E+07	6.51.E+07	5.70.E+07	5.95.E+07
1289	Q9BYD6	39S ribosomal protein L1, mitochondrial [OS=Homo sapiens]	27.7	20	4	81	4	715	75	4	4	0	8.66.E+07	1.41.E+08	9.38.E+07	2.18.E+08	1.50.E+08	1.43.E+08	1.60.E+08	1.42.E+08
1290	O15127	Secretory carrier-associated membrane protein 2 [OS=Homo sapiens]	27.7	10	2	120	2	2566	195	2	2	0	1.30.E+08	1.28.E+08	1.28.E+08	1.65.E+08	1.65.E+08	1.47.E+08	1.70.E+08	1.72.E+08
1291	P61024	cyclin-dependent kinases regulatory subunit 1 [OS=Homo sapiens]	27.7	53	2	78	2	1257	135	2	2	0	9.75.E+07	1.01.E+08	9.44.E+07	9.67.E+07	1.08.E+08	9.52.E+07	8.51.E+07	7.45.E+07
1292	Q9Y3B8-1	Oligoribonuclease, mitochondrial [OS=Homo sapiens]	27.7	17	3	66	3	1586	89	3	3	0	5.01.E+07	4.82.E+07	4.59.E+07	4.81.E+07	6.99.E+07	7.21.E+07	7.97.E+07	7.81.E+07
1293	P21926	CD9 antigen [OS=Homo sapiens]	27.6	15	2	188	2	4230	412	2	2	0	2.52.E+08	2.73.E+08	2.94.E+08	2.67.E+08	2.52.E+08	2.42.E+08	2.56.E+08	2.51.E+08
1294	Q02241-1	Kinesin-like protein KIF23 [OS=Homo sapiens]	27.6	7	4	68	4	710	29	4	4	0	5.05.E+07	6.20.E+07	5.07.E+07	6.84.E+07	3.61.E+07	7.45.E+07	3.01.E+07	7.48.E+07
1295	Q16795	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial [OS=Homo sapiens]	27.5	17	5	102	5	407	88	5	5	0	6.38.E+07	7.53.E+07	5.93.E+07	6.64.E+07	7.70.E+07	6.75.E+07	6.18.E+07	7.25.E+07
1296	Q13243-1	Serine/arginine-rich splicing factor 5 [OS=Homo sapiens]	27.5	23	4	72	4	576	112	4	4	0	6.99.E+07	7.16.E+07	6.95.E+07	7.37.E+07	8.18.E+07	8.77.E+07	8.85.E+07	9.42.E+07
1297	P10909-1	Clusterin [OS=Homo sapiens]	27.4	13	4	93	4	168	50	4	4	0	5.61.E+07	5.39.E+07	5.45.E+07	5.67.E+07	7.23.E+07	6.21.E+07	6.95.E+07	6.48.E+07
1298	Q06124	tyrosine-protein phosphatase non-receptor type 11 [OS=Homo sapiens]	27.3	12	5	38	5	593	57	5	5	0	2.29.E+07	2.96.E+07	2.86.E+07	3.53.E+07	4.03.E+07	4.01.E+07	3.83.E+07	4.63.E+07
1299	P14174	Macrophage Migration inhibitory factor [OS=Homo sapiens]	27.3	17	2	294	2	6188	171	1	2	0	7.35.E+09	7.43.E+09	7.44.E+09	6.56.E+09	6.61.E+09	6.47.E+09	6.62.E+09	6.66.E+09
1300	Q13126-1	S-methyl-5'-thioadenosine phosphorylase [OS=Homo sapiens]	27.2	14	2	144	2	3086	236	2	2	0	4.53.E+07	8.29.E+07	6.48.E+07	8.01.E+07	9.43.E+07	9.52.E+07	7.09.E+07	9.23.E+07
1301	P53367	Arfaptin-1 [OS=Homo sapiens]	27.1	20	4	97	4	722	123	4	4	0	3.65.E+07	3.40.E+07	3.29.E+07	3.64.E+07	3.33.E+07	3.69.E+07	3.45.E+07	3.19.E+07
1302	P54709	sodium/potassium-transporting ATPase subunit beta-3 [OS=Homo sapiens]	27.0	18	4	52	4	407	40	4	3	0	1.74.E+08	1.65.E+08	1.76.E+08	1.68.E+08	2.36.E+08	2.26.E+08	2.23.E+08	1.89.E+08
1303	P62495	Eukaryotic peptide chain release factor subunit 1 [OS=Homo sapiens]	27.0	18	5	63	5	554	46	4	4	0	1.49.E+08	1.43.E+08	1.49.E+08	1.30.E+08	1.46.E+08	1.53.E+08	1.64.E+08	1.53.E+08
1304	O15212	Prefoldin subunit 6 [OS=Homo sapiens]	27.0	46	4	171	4	1556	151	4	4	0	1.60.E+08	1.69.E+08	1.66.E+08	1.41.E+08	1.79.E+08	1.71.E+08	1.75.E+08	1.73.E+08
1305	Q96F86	Enhancer of mRNA-decapping protein 3 [OS=Homo sapiens]	27.0	10	2	60	2	345	45	2	2	0	2.80.E+07	2.84.E+07	1.82.E+07	2.73.E+07	2.81.E+07	2.43.E+07	2.27.E+07	2.38.E+07
1306	O75494-1	Serine/arginine-rich splicing factor 10 [OS=Homo sapiens]	27.0	19	4	115	4	1496	154	4	3	0	9.70.E+07	9.16.E+07	7.36.E+07	8.39.E+07	9.12.E+07	9.00.E+07	8.47.E+07	8.59.E+07
1307	P80297	metallothionein-1X [OS=Homo sapiens]	26.8	54	3	106	3	1199	51	3	3	0	4.08.E+07	4.35.E+07	3.58.E+07	3.56.E+07	9.44.E+06	1.07.E+07	9.81.E+06	9.51.E+06
1308	Q9Y6A9	Signal peptidase complex subunit 1 [OS=Homo sapiens]	26.8	17	1	64	1	663	88	1	1	0	6.08.E+07	5.63.E+07	5.77.E+07	6.90.E+07	5.61.E+07	5.76.E+07	6.70.E+07	6.37.E+07
1309	Q9UHL4	Dipeptidyl peptidase 2 [OS=Homo sapiens]	26.8	9	3	33	3	289	33	3	3	0	2.94.E+07	2.90.E+07	3.19.E+07	3.83.E+07	2.07.E+07	1.81.E+07	1.90.E+07	1.67.E+07
1310	Q5T1J5	Putative coiled-coil-helix-coiled-coil-helix domain-containing protein CHCHD2P9, mitochondrial [OS=Homo	26.8	27	2	70	2	1564	149	2	2	0	5.39.E+07	5.21.E+07	5.46.E+07	5.64.E+07	7.93.E+07	7.30.E+07	7.44.E+07	7.06.E+07
1311	O60488-1	Long-chain-fatty-acid--CoA ligase 4 [OS=Homo sapiens]	26.7	8	3	57	1	697	64	3	3	0	4.49.E+06	2.74.E+06	1.92.E+06	3.02.E+06	7.77.E+06	3.52.E+06	3.17.E+06	8.17.E+06
1312	Q9BXW7	Haloacid dehalogenase-like hydrolase domain-containing 5 [OS=Homo sapiens]	26.7	17	3	12	3	149	14	3	3	0	2.18.E+07	2.33.E+07	1.61.E+07	2.00.E+07	1.86.E+07	2.01.E+07	1.31.E+07	1.27.E+07
1313	Q07866-1	Kinesin light chain 1 [OS=Homo sapiens]	26.6	17	6	81	6	456	19	6	5	0	5.94.E+07	6.51.E+07	6.43.E+07	6.91.E+07	1.32.E+08	9.01.E+07	1.18.E+08	1.26.E+08
1314	Q6UN15-1	Pre-mRNA 3'-end-processing factor FIP1 [OS=Homo sapiens]	26.6	17	5	56	5	768	55	5	5	0	3.77.E+07	7.46.E+07	4.60.E+07	1.09.E+08	8.73.E+07	7.61.E+07	5.21.E+07	9.77.E+07
1315	P10644	cAMP-dependent protein kinase type I-alpha regulatory subunit [OS=Homo sapiens]	26.6	15	5	61	5	539	65	5	5	0	1.10.E+08	1.06.E+08	1.17.E+08	1.20.E+08	1.13.E+08	9.57.E+07	1.08.E+08	1.11.E+08
1316	O14929	histone acetyltransferase type B catalytic subunit [OS=Homo sapiens]	26.6	16	3	48	3	839	62	3	3	0	5.25.E+07	4.96.E+07	3.64.E+07	5.26.E+07	7.03.E+07	7.36.E+07	5.70.E+07	5.93.E+07
1317	Q9UKK9	ADP-sugar pyrophosphatase [OS=Homo sapiens]	26.5	31	4	83	4	544	122	4	4	0	1.71.E+08	1.57.E+08	1.51.E+08	1.56.E+08	1.70.E+08	1.67.E+08	1.59.E+08	1.73.E+08
1318	P30038	Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial [OS=Homo sapiens]	26.5	11	4	102	4	977	117	4	4	0	8.57.E+07	8.41.E+07	8.25.E+07	8.86.E+07	1.02.E+08	9.34.E+07	8.70.E+07	8.66.E+07
1319	Q9H910-1	Jupiter microtubule associated homolog 2 [OS=Homo sapiens]	26.5	44	5	96	5	1049	131	5	4	0	1.13.E+08	8.91.E+07	1.09.E+08	8.37.E+07	2.17.E+08	2.14.E+08	2.38.E+08	2.22.E+08
1320	Q9NP81-1	Serine--tRNA ligase, mitochondrial [OS=Homo sapiens]	26.4	12	4	38	4	433	51	4	4	0	4.69.E+07	4.00.E+07	3.93.E+07	4.68.E+07	3.81.E+07	2.75.E+07	2.94.E+07	2.18.E+07
1321	Q9H7Z7	Prostaglandin E synthase 2 [OS=Homo sapiens]	26.3	23	4	108	4	820	147	4	4	0	7.12.E+07	7.36.E+07	7.14.E+07	6.03.E+07	6.96.E+07	6.80.E+07	5.79.E+07	6.60.E+07

No.	Accession	Description	Sum PEP Score	Coverage [%]	# Peptides	# PSMs	# Unique Peptides	Score Mascot: A5 Mascot	Score Sequest HT: A2 Sequest HT	# Peptides (by Search Engine): A2 Sequest HT	# Peptides (by Search Engine): A5 Mascot	# Razor Peptides	ctrl Abundance s_1	ctrl Abundance s_2	ctrl Abundance s_3	ctrl Abundance s_4	JAM-A KO Abundance s_1	JAM-A KO Abundance s_2	JAM-A KO Abundance s_3	JAM-A KO Abundance s_4
1322	P40616	ADP-ribosylation factor-like protein 1 [OS=Homo sapiens]	26.3	36	4	104	4	1686	133	4	4	0	8.02.E+07	8.11.E+07	7.47.E+07	7.59.E+07	8.44.E+07	8.54.E+07	6.64.E+07	7.85.E+07
1323	Q9UBF2	Coatomer subunit gamma-2 [OS=Homo sapiens]	26.3	7	3	190	2	2298	224	3	3	0	1.53.E+07	1.18.E+07	1.49.E+07	1.46.E+07	1.61.E+07	1.43.E+07	1.72.E+07	1.38.E+07
1324	Q63HN8-3	E3 ubiquitin-protein ligase RNF213 [OS=Homo sapiens]	26.3	2	5	65	5	1062	91	5	5	0	3.95.E+07	4.06.E+07	3.80.E+07	3.74.E+07	6.26.E+07	5.15.E+07	4.20.E+07	4.03.E+07
1325	O95810	caveolae-associated protein 2 [OS=Homo sapiens]	26.2	8	2	86	2	1462	117	2	2	0	2.24.E+07	2.59.E+07	2.23.E+07	4.31.E+07	3.09.E+07	5.84.E+07	4.86.E+07	2.80.E+07
1326	O60437	periplakin [OS=Homo sapiens]	26.2	4	4	34	4	138	42	4	4	0	5.51.E+07	5.98.E+07	4.37.E+07	5.98.E+07	7.39.E+07	7.27.E+07	6.21.E+07	7.71.E+07
1327	P46977	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A [OS=Homo sapiens]	26.2	6	3	82	3	350	53	3	3	0	8.98.E+07	8.26.E+07	8.41.E+07	7.86.E+07	8.23.E+07	7.70.E+07	8.40.E+07	8.38.E+07
1328	Q15370	Elongin-B [OS=Homo sapiens]	26.1	46	4	114	4	148	130	4	4	0	1.70.E+08	1.59.E+08	1.46.E+08	1.63.E+08	2.18.E+08	2.07.E+08	1.88.E+08	1.92.E+08
1329	P50402	Emerin [OS=Homo sapiens]	26.1	22	4	65	4	214	53	4	4	0	5.42.E+07	5.66.E+07	4.61.E+07	5.89.E+07	6.10.E+07	5.85.E+07	4.73.E+07	6.51.E+07
1330	P61960	Ubiquitin-fold modifier 1 [OS=Homo sapiens]	26.1	59	2	144	2	2808	258	2	2	0	1.24.E+08	1.35.E+08	1.29.E+08	1.36.E+08	1.78.E+08	1.71.E+08	1.39.E+08	1.79.E+08
1331	Q8NBJ7-1	Sulfatase-modifying factor 2 [OS=Homo sapiens]	26.1	19	4	146	4	577	171	4	3	0	9.94.E+07	8.19.E+07	1.20.E+08	8.80.E+07	1.35.E+08	1.34.E+08	1.37.E+08	1.45.E+08
1332	P07203	Glutathione peroxidase 1 [OS=Homo sapiens]	26.1	33	3	57	3	419	72	3	3	0	4.82.E+07	4.48.E+07	7.07.E+07	4.37.E+07	8.72.E+07	7.72.E+07	6.80.E+07	5.29.E+07
1333	Q5T0N5-1	Formin-binding protein 1-like [OS=Homo sapiens]	26.0	4	2	18	2	756	25	2	1	0	2.70.E+07	2.65.E+07	2.38.E+07	2.49.E+07	2.07.E+07	2.38.E+07	2.34.E+07	2.44.E+07
1334	Q13595-1	Transformer-2 protein homolog alpha [OS=Homo sapiens]	26.0	19	4	78	3	1069	98	4	4	0	6.24.E+07	1.04.E+08	7.34.E+07	9.75.E+07	6.74.E+07	7.47.E+07	7.17.E+07	7.99.E+07
1335	Q8WTT2	Nucleolar complex protein 3 homolog [OS=Homo sapiens]	25.9	3	1	24	1	162	51	1	1	0	2.21.E+07	2.11.E+07	2.49.E+07	2.19.E+07	1.83.E+07	2.06.E+07	2.41.E+07	1.80.E+07
1336	P52594-1	Arf-GAP domain and FG repeat-containing protein 1 [OS=Homo sapiens]	25.9	10	2	6	2	138	9	2	2	0	1.39.E+07	1.62.E+07	1.51.E+07	1.68.E+07	2.27.E+07	1.95.E+07	1.61.E+07	2.42.E+07
1337	O95470	sphingosine-1-phosphate lyase 1 [OS=Homo sapiens]	25.8	8	3	56	3	565	73	3	3	0	5.98.E+07	6.25.E+07	6.10.E+07	5.86.E+07	7.20.E+07	6.67.E+07	6.96.E+07	7.04.E+07
1338	Q9NWH9-1	SAFB-like transcription modulator [OS=Homo sapiens]	25.8	6	4	39	4	145	26	3	4	0	1.44.E+07	1.49.E+07	1.47.E+07	1.72.E+07	1.92.E+07	1.83.E+07	1.85.E+07	1.85.E+07
1339	O75312	Zinc finger protein ZPR1 [OS=Homo sapiens]	25.7	11	4	31	4	393	30	4	4	0	4.79.E+07	5.46.E+07	5.03.E+07	4.84.E+07	2.61.E+07	2.98.E+07	2.20.E+07	2.80.E+07
1340	Q96C19	EF-hand domain-containing protein D2 [OS=Homo sapiens]	25.7	28	6	64	6	475	38	6	6	0	8.96.E+07	8.30.E+07	6.71.E+07	9.40.E+07	5.16.E+07	6.19.E+07	5.68.E+07	6.17.E+07
1341	Q9BZE4	Nucleolar GTP-binding protein 1 [OS=Homo sapiens]	25.6	9	4	22	4	149	23	4	3	0	1.04.E+08	9.30.E+07	1.03.E+08	9.66.E+07	8.75.E+07	1.02.E+08	1.07.E+08	9.75.E+07
1342	Q9NX24	H/ACA ribonucleoprotein complex subunit 2 [OS=Homo sapiens]	25.6	41	3	26	3	257	36	3	3	0	5.79.E+07	5.67.E+07	3.53.E+07	5.15.E+07	3.52.E+07	3.88.E+07	4.54.E+07	3.54.E+07
1343	Q9Y6G9	Cytoplasmic dynein 1 light intermediate chain 1 [OS=Homo sapiens]	25.6	16	4	116	4	1463	122	4	4	0	5.86.E+07	5.61.E+07	5.93.E+07	5.58.E+07	5.62.E+07	6.30.E+07	7.18.E+07	8.10.E+07
1344	Q9Y295	developmentally-regulated GTP-binding protein 1 [OS=Homo sapiens]	25.5	22	5	70	5	802	64	5	5	0	4.30.E+07	4.82.E+07	4.20.E+07	4.64.E+07	7.18.E+07	7.00.E+07	6.37.E+07	7.17.E+07
1345	Q92974	Rho guanine nucleotide exchange factor 2 [OS=Homo sapiens]	25.5	6	4	68	4	1013	35	4	4	0	1.77.E+07	1.55.E+07	1.91.E+07	3.05.E+07	1.49.E+07	1.20.E+07	1.01.E+07	1.38.E+07
1346	Q92979	Ribosomal RNA small subunit methyltransferase Nep1 [OS=Homo sapiens]	25.5	26	4	66	4	308	47	3	4	0	5.44.E+07	7.57.E+07	7.35.E+07	6.79.E+07	6.04.E+07	5.84.E+07	5.27.E+07	5.70.E+07
1347	P37108	Signal recognition particle 14 kDa protein [OS=Homo sapiens]	25.5	20	2	90	2	2788	38	1	2	0	1.64.E+08	1.82.E+08	1.63.E+08	1.98.E+08	2.72.E+08	2.83.E+08	2.52.E+08	2.67.E+08
1348	Q13510	Acid ceramidase [OS=Homo sapiens]	25.4	12	3	105	3	808	105	3	3	0	1.14.E+08	1.20.E+08	1.15.E+08	1.09.E+08	1.35.E+08	1.49.E+08	1.31.E+08	1.41.E+08
1349	P23193	Transcription elongation factor A protein 1 [OS=Homo sapiens]	25.4	25	5	59	5	1107	66	5	5	0	9.94.E+07	6.24.E+07	9.62.E+07	1.01.E+08	4.96.E+07	4.09.E+07	4.96.E+07	4.28.E+07
1350	P19623	spermidine synthase [OS=Homo sapiens]	25.4	23	4	121	4	1618	192	4	4	0	1.28.E+08	1.49.E+08	1.26.E+08	1.31.E+08	9.08.E+07	8.94.E+07	8.43.E+07	9.39.E+07
1351	P30049	ATP synthase subunit delta, mitochondrial [OS=Homo sapiens]	25.4	38	3	128	3	428	195	3	3	0	1.72.E+08	1.64.E+08	1.63.E+08	1.79.E+08	1.71.E+08	1.65.E+08	1.78.E+08	1.58.E+08
1352	P61513	60S ribosomal protein L37a [OS=Homo sapiens]	25.4	41	3	126	3	3291	200	3	3	0	1.44.E+08	1.43.E+08	1.45.E+08	1.55.E+08	1.13.E+08	1.22.E+08	1.18.E+08	1.17.E+08
1353	Q13685	angio-associated migratory cell protein [OS=Homo sapiens]	25.4	10	3	48	3	681	36	3	3	0	3.14.E+07	3.32.E+07	3.34.E+07	3.33.E+07	3.12.E+07	3.35.E+07	3.80.E+07	3.55.E+07
1354	Q9NX58	Cell growth-regulating nucleolar protein [OS=Homo sapiens]	25.4	15	3	17	3	290	26	3	2	0	2.42.E+07	1.76.E+07	2.51.E+07	1.98.E+07	2.31.E+07	2.17.E+07	1.86.E+07	2.46.E+07
1355	P21912	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial [OS=Homo sapiens]	25.3	20	5	86	5	749	98	5	5	0	2.92.E+08	2.93.E+08	2.80.E+08	2.81.E+08	3.19.E+08	3.15.E+08	3.20.E+08	3.05.E+08
1356	Q9C0D9	Ethanolaminephosphotransferase 1 [OS=Homo sapiens]	25.3	14	3	60	3	1144	12	2	3	0	8.88.E+07	9.86.E+07	8.99.E+07	9.56.E+07	9.75.E+07	9.50.E+07	6.06.E+07	8.69.E+07
1357	P16278	Beta-galactosidase [OS=Homo sapiens]	25.3	13	5	64	5	307	32	5	5	0	4.79.E+07	5.24.E+07	5.36.E+07	5.14.E+07	6.01.E+07	6.27.E+07	6.08.E+07	6.49.E+07
1358	Q9BQ39	ATP-dependent RNA helicase DDX50 [OS=Homo sapiens]	25.2	10	4	102	2	1534	160	4	4	0	1.40.E+07	1.84.E+07	1.29.E+07	2.98.E+07	3.42.E+07	3.13.E+07	2.60.E+07	2.87.E+07
1359	Q9HCY8	protein S100-A14 [OS=Homo sapiens]	25.2	29	2	36	2	706	55	2	2	0	1.80.E+08	1.70.E+08	1.67.E+08	1.66.E+08	1.17.E+08	1.25.E+08	1.13.E+08	1.11.E+08
1360	Q96A33-1	Coiled-coil domain-containing protein 47 [OS=Homo sapiens]	25.2	9	3	52	3	355	51	3	3	0	1.16.E+08	9.08.E+07	1.24.E+08	1.43.E+08	1.32.E+08	1.28.E+08	1.35.E+08	1.09.E+08
1361	Q9GZZ1-1	N-alpha-acetyltransferase 50 [OS=Homo sapiens]	25.2	37	5	34	5	128	38	5	4	0	7.27.E+07	8.30.E+07	8.49.E+07	8.28.E+07	9.46.E+07	8.48.E+07	9.10.E+07	9.07.E+07
1362	P63167	Dynein light chain 1, cytoplasmic [OS=Homo sapiens]	25.1	21	3	204	3	1645	252	3	2	0	3.92.E+08	3.51.E+08	4.02.E+08	3.05.E+08	3.32.E+08	3.97.E+08	4.07.E+08	3.73.E+08
1363	O96005-1	Cleft lip and palate transmembrane protein 1 [OS=Homo sapiens]	25.1	10	3	44	3	322	44	3	3	0	1.86.E+07	3.06.E+07	2.62.E+07	2.52.E+07	2.73.E+07	2.26.E+07	2.98.E+07	3.35.E+07
1364	Q9UKX7	Nuclear pore complex protein Nup50 [OS=Homo sapiens]	25.0	16	4	41	4	530	56	4	4	0	3.65.E+07	3.98.E+07	3.31.E+07	3.82.E+07	7.63.E+07	6.14.E+07	5.47.E+07	5.74.E+07
1365	Q9BY44-1	Eukaryotic translation initiation factor 2A [OS=Homo sapiens]	25.0	13	5	72	5	262	55	5	5	0	5.26.E+07	5.24.E+07	4.94.E+07	4.81.E+07	5.40.E+07	5.43.E+07	5.38.E+07	5.65.E+07
1366	P35244	Replication protein A 14 kDa subunit [OS=Homo sapiens]	24.9	30	2	120	2	1296	200	2	2	0	6.95.E+07	6.98.E+07	4.51.E+07	7.83.E+07	7.49.E+07	8.52.E+07	6.07.E+07	9.16.E+07
1367	O75608	Acyl-protein thioesterase 1 [OS=Homo sapiens]	24.9	27	3	79	3	1084	94	2	3	0	3.40.E+07	6.02.E+07	2.17.E+07	5.76.E+07	5.56.E+07	4.83.E+07	3.99.E+07	4.57.E+07
1368	O43504	Ragulator complex protein LAMTOR5 [OS=Homo sapiens]	24.8	59	2	16	2	223	30	2	2	0	5.51.E+07	5.67.E+07	5.43.E+07	1.15.E+07	4.88.E+07	5.61.E+07	4.75.E+07	5.20.E+07
1369	P26885	Peptidyl-prolyl cis-trans isomerase FKBP2 [OS=Homo sapiens]	24.8	39	3	62	3	364	71	3	3	0	9.36.E+07	8.67.E+07	9.32.E+07	9.06.E+07	1.20.E+08	1.16.E+08	1.06.E+08	1.18.E+08
1370	Q02818	Nucleobindin-1 [OS=Homo sapiens]	24.8	13	5	73	5	580	70	5	5	0	5.70.E+07	5.09.E+07	5.11.E+07	6.20.E+07	5.45.E+07	5.09.E+07	2.99.E+07	3.52.E+07
1371	Q09161	Nuclear cap-binding protein subunit 1 [OS=Homo sapiens]	24.8	12	6	47	6	222	23	6	5	0	3.73.E+07	4.14.E+07	4.45.E+07	3.77.E+07	5.36.E+07	5.78.E+07	5.69.E+07	5.95.E+07
1372	Q86U42-1	polyadenylate-binding protein 2 [OS=Homo sapiens]	24.7	13	2	90	2	1152	148	2	2	0	1.15.E+08	1.31.E+08	1.23.E+08	1.18.E+08	2.05.E+08	1.53.E+08	1.53.E+08	1.69.E+08
1373	Q15021	condensin complex subunit 1 [OS=Homo sapiens]	24.7	5	5	65	5	683	45	5	5	0	3.96.E+07	4.48.E+07	3.53.E+07	3.77.E+07	6.34.E+07	7.05.E+07	5.06.E+07	7.48.E+07
1374	O60762	Dolichol-phosphate mannosyltransferase subunit 1 [OS=Homo sapiens]	24.7	19	3	90	3	592	140	3	3	0	5.91.E+07	6.07.E+07	5.32.E+07	5.98.E+07	9.52.E+07	9.64.E+07	8.59.E+07	9.43.E+07
1375	Q8NFU3-1	Thiosulfate sulfurtransferase/rhodanese-like domain-containing protein 1 [OS=Homo sapiens]	24.6	55	3	83	3	1060	168	2	3	0	1.19.E+08	1.15.E+08	1.06.E+08	1.22.E+08	9.90.E+07	9.13.E+07	9.66.E+07	1.11.E+08

No.	Accession	Description	Sum PEP Score	Coverage [%]	# Peptides	# PSMs	# Unique Peptides	Score Mascot: A5 Mascot	Score Sequest HT: A2 Sequest HT	# Peptides (by Search Engine): A2 Sequest HT	# Peptides (by Search Engine): A5 Mascot	# Razor Peptides	ctrl Abundances_1	ctrl Abundances_2	ctrl Abundances_3	ctrl Abundances_4	JAM-A KO Abundances_1	JAM-A KO Abundances_2	JAM-A KO Abundances_3	JAM-A KO Abundances_4
1376	Q56VL3	OCIA domain-containing protein 2 [OS=Homo sapiens]	24.6	21	3	198	3	2120	195	3	3	0	8.90.E+07	9.72.E+07	9.12.E+07	9.54.E+07	9.75.E+07	9.76.E+07	9.46.E+07	9.61.E+07
1377	P11137	microtubule-associated protein 2 [OS=Homo sapiens]	24.6	5	5	44	5	146	29	5	4	0	5.43.E+07	5.04.E+07	5.43.E+07	4.94.E+07	6.09.E+07	5.14.E+07	9.91.E+07	9.26.E+07
1378	P00403	Cytochrome c oxidase subunit 2 [OS=Homo sapiens]	24.5	37	4	210	4	1746	178	4	4	0	3.08.E+08	3.09.E+08	2.94.E+08	2.97.E+08	2.50.E+08	2.61.E+08	2.59.E+08	2.53.E+08
1379	O14672	Disintegrin and metalloproteinase domain-containing protein 10 [OS=Homo sapiens]	24.5	7	4	39	4	195	43	4	4	0	1.33.E+08	1.25.E+08	6.97.E+07	1.22.E+08	1.12.E+08	1.21.E+08	1.16.E+08	1.27.E+08
1380	P52701	DNA mismatch repair protein MSH6 [OS=Homo sapiens]	24.5	6	5	78	5	1255	72	5	4	0	4.92.E+07	5.21.E+07	4.87.E+07	4.82.E+07	5.01.E+07	3.91.E+07	3.85.E+07	4.40.E+07
1381	P47985	cytochrome b-c1 complex subunit Rieske, mitochondrial [OS=Homo sapiens]	24.4	25	3	71	1	624	80	3	2	0			1.70.E+07		1.63.E+07	1.91.E+07		
1382	Q01085	Nucleolysin TIAR [OS=Homo sapiens]	24.4	14	4	31	2	130	24	4	4	2	7.87.E+07	7.25.E+07	6.78.E+07	8.38.E+07	7.07.E+07	7.95.E+07	8.39.E+07	7.54.E+07
1383	O00541-1	Pescadillo homolog [OS=Homo sapiens]	24.4	13	5	92	5	388	62	5	5	0	1.61.E+08	1.61.E+08	1.58.E+08	1.63.E+08	1.40.E+08	1.43.E+08	1.65.E+08	1.30.E+08
1384	Q9NTI5	Sister chromatid cohesion protein PDS5 homolog B [OS=Homo sapiens]	24.3	5	3	50	3	487	7	3	3	0	1.37.E+07	1.36.E+07	1.30.E+07	1.27.E+07	2.49.E+07	2.17.E+07	2.15.E+07	2.32.E+07
1385	P30519	Heme oxygenase 2 [OS=Homo sapiens]	24.3	25	4	17	4	211	28	3	4	0	6.47.E+07	6.81.E+07	5.77.E+07	4.28.E+07	5.81.E+07	5.73.E+07	3.85.E+07	5.97.E+07
1386	Q04206	Transcription factor p65 [OS=Homo sapiens]	24.1	10	4	10	4	147	13	4	4	0	7.38.E+07	7.75.E+07	6.49.E+07	5.85.E+07	7.33.E+07	7.83.E+07	8.04.E+07	8.08.E+07
1387	Q9UKM9-1	RNA-binding protein Raly [OS=Homo sapiens]	24.1	13	4	64	4	469	49	4	4	0	1.97.E+08	1.96.E+08	2.01.E+08	1.94.E+08	1.72.E+08	1.76.E+08	1.83.E+08	1.78.E+08
1388	Q96AB3	isochorismatase domain-containing protein 2 [OS=Homo sapiens]	24.0	31	3	128	3	1462	115	3	3	0	4.82.E+07	5.14.E+07	4.35.E+07	4.46.E+07	3.35.E+07	3.00.E+07	2.60.E+07	3.05.E+07
1389	Q9UNH7-1	Sorting nexin-6 [OS=Homo sapiens]	24.0	10	2	32	2	695	27	2	2	0	1.38.E+07	1.54.E+07	1.59.E+07	1.78.E+07	3.13.E+07	2.52.E+07	3.08.E+07	3.14.E+07
1390	Q969V3	Nicalin [OS=Homo sapiens]	24.0	11	4	26	4	90	25	4	4	0	3.82.E+07	4.50.E+07	4.20.E+07	4.71.E+07	1.95.E+07	5.71.E+07	3.74.E+07	1.72.E+07
1391	P51116	Fragile X mental retardation syndrome-related protein 2 [OS=Homo sapiens]	24.0	8	4	22	4	239	24	4	4	0	6.18.E+07	6.46.E+07	7.61.E+07	6.60.E+07	4.59.E+07	2.27.E+07	4.09.E+07	2.54.E+07
1392	Q12792-2	Twinfilin-1 [OS=Homo sapiens]	23.9	11	2	27	2	1225	49	1	2	0	2.63.E+07	3.77.E+07	3.46.E+07	3.40.E+07	3.32.E+07	4.64.E+07	4.43.E+07	2.08.E+07
1393	P09496-2	Isoform Non-brain of Clathrin light chain A [OS=Homo sapiens]	23.9	21	5	49	5		161	5		0	2.11.E+08	2.14.E+08	2.14.E+08	2.05.E+08	4.65.E+08	4.61.E+08	4.85.E+08	4.94.E+08
1394	O75475-1	PC4 and SFRS1-interacting protein [OS=Homo sapiens]	23.9	7	3	85	3	364	32	3	3	0	4.86.E+07	5.64.E+07	5.57.E+07	5.04.E+07	8.12.E+07	8.88.E+07	7.80.E+07	6.36.E+07
1395	P45973	chromobox protein homolog 5 [OS=Homo sapiens]	23.8	21	3	100	2	1275	147	3	3	0	4.86.E+07	4.56.E+07	4.13.E+07	3.97.E+07	1.70.E+07	4.48.E+07	3.96.E+07	1.74.E+07
1396	Q15404-1	Ras suppressor protein 1 [OS=Homo sapiens]	23.7	21	3	26	3	316	28	3	3	0	3.33.E+07	2.60.E+07	3.46.E+07	3.56.E+07	5.41.E+07	4.45.E+07	4.29.E+07	4.80.E+07
1397	P60983	glia maturation factor beta [OS=Homo sapiens]	23.6	27	2	15	2	88	21	1	2	0	8.84.E+06	8.34.E+06	7.31.E+06	6.77.E+06	1.40.E+07	1.72.E+07	1.08.E+07	1.62.E+07
1398	P04179	Superoxide dismutase [Mn], mitochondrial [OS=Homo sapiens]	23.5	40	4	24	4		67	4		0	1.09.E+08	7.68.E+07	1.26.E+08	1.24.E+08	1.15.E+08	1.06.E+08	1.14.E+08	1.18.E+08
1399	Q96G03	Phosphoglucomutase-2 [OS=Homo sapiens]	23.5	9	3	112	2	881	99	3	2	0	1.45.E+07	4.76.E+07	4.74.E+07	1.64.E+07	5.87.E+07	5.54.E+07	4.73.E+07	5.41.E+07
1400	P10606	Cytochrome c oxidase subunit 5B, mitochondrial [OS=Homo sapiens]	23.4	30	4	172	4	1418	206	4	4	0	3.23.E+08	3.00.E+08	3.28.E+08	3.36.E+08	2.71.E+08	2.84.E+08	3.36.E+08	3.10.E+08
1401	Q99627-1	COP9 signalosome complex subunit 8 [OS=Homo sapiens]	23.4	33	3	51	3	333	60	3	3	0	2.87.E+07	3.38.E+07	3.76.E+07	3.35.E+07	3.30.E+07	4.16.E+07	3.51.E+07	3.27.E+07
1402	P31483	nucleolysin TIA-1 isoform p40 [OS=Homo sapiens]	23.3	11	3	64	1	529	32	3	3	0	5.55.E+06	1.39.E+07	1.33.E+07	1.42.E+07	8.89.E+06	5.02.E+06	5.97.E+06	8.84.E+06
1403	Q9UBV8	Peflin [OS=Homo sapiens]	23.3	17	2	40	2	962	30	2	2	0	9.99.E+06	1.09.E+07	9.91.E+06	1.03.E+07	9.56.E+06	8.00.E+06	7.07.E+06	6.57.E+06
1404	Q14232	Translation initiation factor eIF-2B subunit alpha [OS=Homo sapiens]	23.3	18	4	53	4	533	48	4	4	0	4.19.E+07	4.40.E+07	4.55.E+07	4.51.E+07	5.42.E+07	5.24.E+07	5.13.E+07	4.90.E+07
1405	Q9BW27	nuclear pore complex protein Nup85 [OS=Homo sapiens]	23.2	4	2	52	2	600	44	2	2	0	2.00.E+07	2.02.E+07	1.72.E+07	2.13.E+07	1.62.E+07	1.45.E+07	1.28.E+07	1.45.E+07
1406	Q14019	coactosin-like protein [OS=Homo sapiens]	23.2	32	2	74	2	1171	90	2	2	0	3.18.E+07	3.50.E+07	2.92.E+07	3.90.E+07	6.96.E+07	7.37.E+07	6.39.E+07	7.35.E+07
1407	Q9NPF4	Probable tRNA N6-adenosine threonylcarbamoyltransferase [OS=Homo sapiens]	23.1	14	2	16	2	488	25	2	2	0	1.15.E+07	4.25.E+06	1.06.E+07	1.00.E+07	1.05.E+05		5.68.E+05	1.18.E+05
1408	Q9C0C9	(E3-independent) E2 ubiquitin-conjugating enzyme [OS=Homo sapiens]	23.1	5	3	12	3	108	15	3	3	0	3.53.E+07	3.33.E+07	2.94.E+07	2.13.E+07	3.14.E+07	3.05.E+07	2.36.E+07	2.74.E+07
1409	P54619-1	5'-AMP-activated protein kinase subunit gamma-1 [OS=Homo sapiens]	23.1	15	2	68	2	1513	75	2	2	0	1.39.E+07	1.58.E+07	1.65.E+07	1.89.E+07	1.69.E+07	1.51.E+07	1.24.E+07	1.57.E+07
1410	P48147	prolyl endopeptidase [OS=Homo sapiens]	23.1	7	3	46	3	905	57	3	3	0	3.66.E+07	3.56.E+07	3.84.E+07	3.91.E+07	3.70.E+07	3.22.E+07	2.57.E+07	3.30.E+07
1411	Q14690	Protein RRP5 homolog [OS=Homo sapiens]	23.1	4	6	50	6	177	17	6	6	0	1.64.E+08	1.70.E+08	1.85.E+08	1.06.E+08	1.18.E+08	1.52.E+08	1.88.E+08	1.13.E+08
1412	P19525	interferon-induced, double-stranded RNA-activated protein kinase [OS=Homo sapiens]	23.1	9	4	96	4	1341	120	4	4	0	6.07.E+07	8.02.E+07	7.82.E+07	6.44.E+07	8.14.E+07	8.06.E+07	7.88.E+07	8.08.E+07
1413	Q9Y3T9	Nucleolar complex protein 2 homolog [OS=Homo sapiens]	23.0	7	3	35	3	108	32	3	3	0	6.34.E+07	5.88.E+07	6.10.E+07	5.89.E+07	3.87.E+07	5.10.E+07	5.21.E+07	5.56.E+07
1414	P05204	Non-histone chromosomal protein HMG-17 [OS=Homo sapiens]	23.0	17	1	213	1	707	89	1	1	0	8.16.E+07	7.81.E+07	8.62.E+07	6.41.E+07	7.06.E+07	8.40.E+07	8.21.E+07	7.85.E+07
1415	O14925	Mitochondrial import inner membrane translocase subunit tim23 [OS=Homo sapiens]	23.0	38	3	75	3	836	86	3	3	0	6.04.E+07	6.95.E+07	5.90.E+07	6.69.E+07	2.97.E+07	3.03.E+07	2.46.E+07	3.18.E+07
1416	Q92888-1	Rho guanine nucleotide exchange factor 1 [OS=Homo sapiens]	23.0	8	5	38	5	131	25	5	5	0	2.89.E+07	3.24.E+07	2.85.E+07	2.77.E+07	1.48.E+07	1.49.E+07	1.56.E+07	1.24.E+07
1417	P46779	60S ribosomal protein L28 [OS=Homo sapiens]	23.0	36	6	201	6	1562	80	5	6	0	7.52.E+08	7.08.E+08	7.37.E+08	7.68.E+08	5.47.E+08	5.49.E+08	5.96.E+08	5.50.E+08
1418	Q96PZ0	pseudouridylate synthase 7 homolog [OS=Homo sapiens]	22.9	7	2	28	2	611	29	2	2	0	1.39.E+07	1.14.E+07	1.21.E+07	1.37.E+07	2.30.E+07	2.08.E+07	1.82.E+07	2.37.E+07
1419	Q9BRR6-1	ADP-dependent glucokinase [OS=Homo sapiens]	22.9	16	3	31	3	161	37	3	3	0	1.94.E+07	1.20.E+07	1.13.E+07	1.21.E+07	2.02.E+07	1.85.E+07	1.60.E+07	1.81.E+07
1420	P0C7P4	Putative cytochrome b-c1 complex subunit Rieske-like protein 1 [OS=Homo sapiens]	22.9	22	3	71	1	624	80	3	2	2	6.61.E+07	7.10.E+07	6.69.E+07	6.65.E+07	7.40.E+07	7.22.E+07	6.24.E+07	7.50.E+07
1421	O95292	Vesicle-associated membrane protein-associated protein B/C [OS=Homo sapiens]	22.8	16	3	87	3	753	108	3	3	0	8.58.E+07	8.94.E+07	9.40.E+07	7.71.E+07	1.08.E+08	1.06.E+08	1.15.E+08	1.10.E+08
1422	O75223-1	gamma-glutamylcyclotransferase [OS=Homo sapiens]	22.8	32	4	39	4	204	39	4	4	0	1.64.E+08	8.34.E+07	1.56.E+08	1.40.E+08	2.20.E+08	1.68.E+08	1.71.E+08	1.67.E+08
1423	O95232-1	Luc7-like protein 3 [OS=Homo sapiens]	22.8	11	3	66	3	1406	76	3	3	0	3.05.E+07	3.54.E+07	3.35.E+07	3.24.E+07	3.55.E+07	3.62.E+07	3.33.E+07	3.83.E+07
1424	P52943	Cysteine-rich protein 2 [OS=Homo sapiens]	22.8	32	3	32	3	512	47	3	3	0	4.64.E+07	4.90.E+07	4.23.E+07	4.75.E+07	3.10.E+07	2.95.E+07	2.75.E+07	2.97.E+07
1425	Q5H9R7-1	Serine/threonine-protein phosphatase 6 regulatory subunit 3 [OS=Homo sapiens]	22.7	5	3	74	3	1090	82	3	3	0	2.35.E+07	2.18.E+07	2.32.E+07	2.80.E+07	3.56.E+07	3.58.E+07	6.79.E+07	2.44.E+07

No.	Accession	Description	Sum PEP Score	Coverage [%]	# Peptides	# PSMs	# Unique Peptides	Score Mascot: A5 Mascot	Score Sequest HT: A2 Sequest HT	# Peptides (by Search Engine): A2 Sequest HT	# Peptides (by Search Engine): A5 Mascot	# Razor Peptides	ctrl Abundances_1	ctrl Abundances_2	ctrl Abundances_3	ctrl Abundances_4	JAM-A KO Abundances_1	JAM-A KO Abundances_2	JAM-A KO Abundances_3	JAM-A KO Abundances_4
1426	Q9BW72	HIG1 domain family member 2A, mitochondrial [OS=Homo sapiens]	22.7	51	2	70	2	1327	144	1	2	0	6.71.E+07	7.78.E+07	6.74.E+07	7.86.E+07	8.40.E+07	7.65.E+07	6.78.E+07	8.03.E+07
1427	Q6ZNJ1-1	Neurobeachin-like protein 2 [OS=Homo sapiens]	22.6	2	3	60	3	896	79	3	3	0	2.08.E+07	1.81.E+07	1.72.E+07	1.88.E+07	1.11.E+07	6.85.E+06	8.56.E+06	1.07.E+07
1428	Q9HDC9	Adipocyte plasma membrane-associated protein [OS=Homo sapiens]	22.6	21	4	58	4	265	55	4	4	0	7.87.E+07	7.68.E+07	7.08.E+07	4.98.E+07	8.18.E+07	1.03.E+08	1.05.E+08	1.08.E+08
1429	P40763	Signal transducer and activator of transcription 3 [OS=Homo sapiens]	22.6	16	6	65	5	326	24	6	5	1	5.41.E+07	5.76.E+07	5.38.E+07	5.36.E+07	6.61.E+07	6.76.E+07	6.52.E+07	6.84.E+07
1430	Q9NYL4	Peptidyl-prolyl cis-trans isomerase FKBP11 [OS=Homo sapiens]	22.5	27	2	46	2	99	73	2	2	0	6.00.E+07	9.98.E+07	7.54.E+07	6.46.E+07	1.02.E+08	1.30.E+08	1.08.E+08	8.35.E+07
1431	Q9BXY0	Protein MAK16 homolog [OS=Homo sapiens]	22.5	11	3	26	3	313	23	3	3	0	1.42.E+07	1.58.E+07	4.55.E+06	5.94.E+06	3.65.E+06	1.46.E+07	1.00.E+07	1.47.E+07
1432	P38405	Guanine nucleotide-binding protein G(olf) subunit alpha [OS=Homo sapiens]	22.5	14	3	47	1	638	60	2	3	0								
1433	Q9H9Q2	COP9 signalosome complex subunit 7b [OS=Homo sapiens]	22.5	20	3	30	3	299	15	2	3	0	3.20.E+07	3.20.E+07	3.33.E+07	3.47.E+07	4.38.E+07	3.79.E+07	4.15.E+07	4.20.E+07
1434	Q9BPX5	actin-related protein 2/3 complex subunit 5-like protein [OS=Homo sapiens]	22.5	33	2	24	2	283	40	2	2	0	6.23.E+07	7.01.E+07	6.47.E+07	6.40.E+07	5.71.E+07	6.20.E+07	5.54.E+07	4.43.E+07
1435	Q92544	Transmembrane 9 superfamily member 4 [OS=Homo sapiens]	22.5	12	5	49	5	640	64	5	4	0	3.42.E+08	3.22.E+08	3.40.E+08	2.62.E+08	5.86.E+08	5.34.E+08	5.14.E+08	5.46.E+08
1436	Q14683	structural maintenance of chromosomes protein 1a [OS=Homo sapiens]	22.5	6	5	64	5	894	45	4	5	0	3.29.E+07	3.65.E+07	3.52.E+07	3.44.E+07	3.65.E+07	3.87.E+07	3.05.E+07	3.80.E+07
1437	Q15418-1	Ribosomal protein S6 kinase alpha-1 [OS=Homo sapiens]	22.4	9	5	49	2	276	60	5	4	0	1.16.E+07	1.13.E+07	1.34.E+07	9.94.E+06	1.67.E+07	1.57.E+07	1.36.E+07	1.41.E+07
1438	P13073	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial [OS=Homo sapiens]	22.3	20	4	178	4	685	222	4	4	0	3.41.E+08	3.31.E+08	3.53.E+08	3.88.E+08	2.94.E+08	2.97.E+08	3.22.E+08	3.03.E+08
1439	Q9Y5Z4-1	Heme-binding protein 2 [OS=Homo sapiens]	22.3	24	4	36	4	199	40	4	4	0	4.09.E+07	5.05.E+07	4.14.E+07	4.88.E+07	6.60.E+07	6.37.E+07	5.30.E+07	6.30.E+07
1440	Q9HC38-2	Isoform 2 of Glyoxalase domain-containing protein 4 [OS=Homo sapiens]	22.3	20	4	21	4		35	4		0	2.18.E+07	1.82.E+07	2.33.E+07	1.63.E+07	4.52.E+06	8.50.E+06	5.68.E+06	1.05.E+07
1441	Q9NP97	Dynein light chain roadblock-type 1 [OS=Homo sapiens]	22.3	39	3	83	3	1580	105	2	3	0	1.69.E+08	1.79.E+08	1.75.E+08	1.76.E+08	2.13.E+08	2.07.E+08	2.01.E+08	2.15.E+08
1442	P62304	small nuclear ribonucleoprotein E [OS=Homo sapiens]	22.2	39	2	132	2	2117	160	2	2	0	1.35.E+08	9.68.E+07	7.48.E+07	1.10.E+08	6.61.E+07	7.20.E+07	7.97.E+07	8.53.E+07
1443	Q9UM00-1	Calcium load-activated calcium channel [OS=Homo sapiens]	22.2	20	3	147	3	2357	189	3	3	0	1.24.E+08	1.34.E+08	1.16.E+08	1.23.E+08	1.67.E+08	1.63.E+08	1.67.E+08	1.56.E+08
1444	Q13740-1	CD166 antigen [OS=Homo sapiens]	22.2	15	4	55	4	625	55	4	4	0	3.46.E+07	3.27.E+07	1.74.E+07	3.16.E+07	6.59.E+07	7.48.E+07	5.68.E+07	6.41.E+07
1445	O75131	Copine-3 [OS=Homo sapiens]	22.2	8	3	110	3	971	143	3	3	0	8.01.E+07	8.44.E+07	1.05.E+08	8.20.E+07	9.57.E+07	8.26.E+07	8.40.E+07	1.10.E+08
1446	Q9Y333	U6 snRNA-associated Sm-like protein LSm2 [OS=Homo sapiens]	22.2	40	2	77	2	2221	119	2	2	0	5.75.E+07	6.54.E+07	7.03.E+07	6.52.E+07	1.17.E+08	1.10.E+08	8.90.E+07	1.06.E+08
1447	P55145	Mesencephalic astrocyte-derived neurotrophic factor [OS=Homo sapiens]	22.1	29	5	88	5	238	75	5	4	0	8.90.E+07	8.24.E+07	9.42.E+07	9.31.E+07	1.15.E+08	1.11.E+08	8.14.E+07	1.11.E+08
1448	O94760-1	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1 [OS=Homo sapiens]	22.1	22	5	68	5	244	39	4	5	0	1.38.E+08	1.47.E+08	1.45.E+08	1.51.E+08	1.26.E+08	1.12.E+08	1.23.E+08	1.17.E+08
1449	P52732	Kinesin-like protein KIF11 [OS=Homo sapiens]	22.1	6	3	7	3	122	6	3	2	0	2.69.E+07	3.25.E+07	3.01.E+07	3.32.E+07	1.57.E+07	3.79.E+07	1.37.E+07	1.38.E+07
1450	O43237	Cytoplasmic dynein 1 light intermediate chain 2 [OS=Homo sapiens]	22.1	7	2	90	2	2001	102	2	2	0	3.62.E+07	3.88.E+07	3.08.E+07	4.04.E+07	4.22.E+07	3.97.E+07	3.69.E+07	4.03.E+07
1451	O15230	Laminin subunit alpha-5 [OS=Homo sapiens]	22.1	1	2	36	2	689	55	2	2	0	1.54.E+07	2.04.E+07	1.23.E+07	1.31.E+07	2.85.E+07	2.20.E+07	1.46.E+07	1.74.E+07
1452	Q00059	Transcription factor A, mitochondrial [OS=Homo sapiens]	22.0	19	4	110	4	269	72	4	4	0	1.53.E+08	1.42.E+08	1.45.E+08	1.25.E+08	1.36.E+08	1.36.E+08	1.48.E+08	1.45.E+08
1453	Q52LJ0	Protein Fam98b [OS=Homo sapiens]	21.9	24	4	24	4	303	24	4	4	0	2.51.E+07	3.51.E+07	2.02.E+07	3.93.E+07	3.75.E+07	3.10.E+07	3.42.E+07	4.20.E+07
1454	O14737	Programmed cell death protein 5 [OS=Homo sapiens]	21.9	35	5	83	5	112	34	4	5	0	2.53.E+08	2.84.E+08	2.97.E+08	2.21.E+08	1.49.E+08	1.60.E+08	2.07.E+08	1.96.E+08
1455	O00203-1	AP-3 complex subunit beta-1 [OS=Homo sapiens]	21.9	8	6	64	6	146	24	6	6	0	1.15.E+08	1.18.E+08	1.15.E+08	1.21.E+08	1.32.E+08	1.45.E+08	1.17.E+08	1.32.E+08
1456	P30536	translocator protein [OS=Homo sapiens]	21.9	14	1	9	1	244			1	0								
1457	Q9NRW7	Vacuolar protein sorting-associated protein 45 [OS=Homo sapiens]	21.8	8	4	48	4	323	16	4	4	0	1.67.E+07	2.29.E+07	1.95.E+07	2.85.E+07	2.70.E+07	2.68.E+07	2.04.E+07	2.73.E+07
1458	P04637	Cellular tumor antigen p53 [OS=Homo sapiens]	21.8	8	2	58	2	1547	129	2	2	0	3.46.E+07	3.79.E+07	2.68.E+07	3.71.E+07	2.46.E+07	2.88.E+07	1.89.E+07	2.80.E+07
1459	P32320	cytidine deaminase [OS=Homo sapiens]	21.8	26	2	36	2	949	55	2	2	0	1.32.E+07	7.85.E+06	1.64.E+07	1.03.E+07	3.52.E+07	3.44.E+07	3.10.E+07	2.83.E+07
1460	Q9H0C8	Integrin-linked kinase-associated serine/threonine phosphatase 2C [OS=Homo sapiens]	21.8	9	2	97	2	2433	114	2	2	0	4.95.E+07	4.96.E+07	4.33.E+07	5.55.E+07	1.41.E+07	1.56.E+07	3.80.E+07	1.17.E+07
1461	O75380	NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial [OS=Homo sapiens]	21.7	33	3	72	3	386	12	3	3	0	3.70.E+07	3.74.E+07	3.77.E+07	3.42.E+07	3.24.E+07	3.12.E+07	3.35.E+07	3.34.E+07
1462	Q86TU7	Histone-lysine N-methyltransferase setd3 [OS=Homo sapiens]	21.7	13	4	46	4	443	39	4	4	0	2.90.E+07	2.89.E+07	3.04.E+07	2.84.E+07	1.24.E+07	1.38.E+07	7.80.E+06	1.53.E+07
1463	Q9Y5X3	sorting nexin-5 [OS=Homo sapiens]	21.6	19	4	45	4	334	25	3	4	0	5.42.E+07	6.50.E+07	5.16.E+07	5.45.E+07	8.63.E+07	8.42.E+07	7.29.E+07	8.26.E+07
1464	P11279	Lysosome-associated membrane glycoprotein 1 [OS=Homo sapiens]	21.6	7	3	30	3	423	26	3	3	0	8.85.E+07	8.53.E+07	8.73.E+07	9.49.E+07	1.78.E+08	1.45.E+08	1.50.E+08	1.70.E+08
1465	Q7Z7H5	Transmembrane emp24 domain-containing protein 4 [OS=Homo sapiens]	21.5	21	3	53	2	1234	77	3	2	0	4.67.E+07	4.61.E+07	3.34.E+07	4.78.E+07	5.19.E+07	5.97.E+07	5.12.E+07	5.38.E+07
1466	P30876	DNA-directed RNA polymerase II subunit RPB2 [OS=Homo sapiens]	21.5	7	6	51	6	234	42	5	6	0	7.74.E+07	6.63.E+07	8.49.E+07	7.14.E+07	8.68.E+07	9.19.E+07	8.88.E+07	8.88.E+07
1467	O75153	Clustered mitochondria protein homolog [OS=Homo sapiens]	21.4	5	4	67	4	201	51	4	3	0	8.65.E+07	8.65.E+07	8.81.E+07	8.48.E+07	4.95.E+07	5.55.E+07	5.09.E+07	3.39.E+07
1468	Q9UI10-1	translation initiation factor eIF-2B subunit delta [OS=Homo sapiens]	21.4	9	3	76	3	833	116	3	3	0	8.22.E+07	8.28.E+07	8.29.E+07	7.49.E+07	8.34.E+07	8.66.E+07	8.92.E+07	7.60.E+07
1469	P62306	Small nuclear ribonucleoprotein F [OS=Homo sapiens]	21.4	34	3	104	3	1299	118	3	3	0	2.06.E+08	1.88.E+08	1.79.E+08	2.11.E+08	1.71.E+08	1.43.E+08	1.60.E+08	1.39.E+08
1470	Q9UNF1	Melanoma-associated antigen D2 [OS=Homo sapiens]	21.4	15	5	46	5	269	34	5	5	0	4.12.E+07	6.42.E+07	6.98.E+07	5.64.E+07	9.51.E+07	1.04.E+08	1.02.E+08	1.03.E+08
1471	Q99653	Calcineurin B homologous protein 1 [OS=Homo sapiens]	21.3	17	3	21	3	196	22	3	3	0	4.50.E+07	4.97.E+07	4.13.E+07	4.91.E+07	2.06.E+07	2.04.E+07	2.61.E+07	2.82.E+07
1472	Q8WVM8	Sec1 family domain-containing protein 1 [OS=Homo sapiens]	21.3	9	3	42	3	323	15	2	3	0	1.97.E+07	2.08.E+07	1.80.E+07	5.19.E+07	6.51.E+07	6.91.E+07	2.18.E+07	7.51.E+07
1473	P35052	Glypican-1 [OS=Homo sapiens]	21.2	13	5	33	5	71	33	5	5	0	5.82.E+06	6.13.E+06	2.58.E+06	4.94.E+06	3.36.E+07	2.79.E+07	2.64.E+07	3.04.E+07

No.	Accession	Description	Sum PEP Score	Coverage [%]	# Peptides	# PSMs	# Unique Peptides	Score Mascot: A5 Mascot	Score Sequest HT: A2 Sequest HT	# Peptides (by Search Engine): A2 Sequest HT	# Peptides (by Search Engine): A5 Mascot	# Razor Peptides	ctrl Abundances_1	ctrl Abundances_2	ctrl Abundances_3	ctrl Abundances_4	JAM-A KO Abundances_1	JAM-A KO Abundances_2	JAM-A KO Abundances_3	JAM-A KO Abundances_4
1474	O95394	phosphoacetylglucosamine mutase [OS=Homo sapiens]	21.2	11	3	26	3	179	31	3	3	0	2.72.E+07	3.52.E+07	3.71.E+07	3.39.E+07	3.75.E+07	6.85.E+07	3.38.E+07	3.71.E+07
1475	O75746	Calcium-binding mitochondrial carrier protein Aralar1 [OS=Homo sapiens]	21.1	8	4	21	1	81	22	4	4	0	4.12.E+06	1.03.E+07	2.86.E+06	4.37.E+06	7.15.E+06	3.09.E+06	1.90.E+06	2.68.E+06
1476	Q68E01	Integrator complex subunit 3 [OS=Homo sapiens]	21.1	4	2	84	2	1713	84	2	2	0	2.75.E+07	3.03.E+07	2.46.E+07	3.16.E+07	3.18.E+07	2.63.E+07	2.65.E+07	2.75.E+07
1477	Q9BPX3	Condensin complex subunit 3 [OS=Homo sapiens]	21.1	4	3	52	3	794	44	3	3	0	9.67.E+06	3.01.E+07	2.93.E+07	3.18.E+07	2.78.E+07	3.41.E+07	1.54.E+07	2.88.E+07
1478	Q9NVI7	ATPase family AAA domain-containing protein 3A [OS=Homo sapiens]	21.1	8	5	100	5	638	105	4	5	0	8.76.E+07	9.91.E+07	1.19.E+08	9.22.E+07	9.30.E+07	1.06.E+08	1.04.E+08	9.46.E+07
1479	P21281	V-type proton ATPase subunit B, brain isoform [OS=Homo sapiens]	21.1	9	3	33	3	224	56	3	3	0	8.02.E+07	7.91.E+07	8.15.E+07	8.29.E+07	1.12.E+08	9.88.E+07	1.03.E+08	1.12.E+08
1480	P32929	Cystathionine gamma-lyase [OS=Homo sapiens]	21.1	12	2	70	2	2815	108	2	2	0	3.65.E+07	3.90.E+07	3.36.E+07	3.76.E+07	3.89.E+07	3.48.E+07	3.07.E+07	3.36.E+07
1481	O00422	Histone deacetylase complex subunit SAP18 [OS=Homo sapiens]	21.0	24	3	92	3	1691	96	3	3	0	1.24.E+08	1.23.E+08	1.23.E+08	1.42.E+08	1.28.E+08	1.21.E+08	1.05.E+08	1.22.E+08
1482	Q53GS9	U4/U6.U5 tri-snRNP-associated protein 2 [OS=Homo sapiens]	21.0	10	3	24	3	176	26	3	3	0	3.51.E+07	3.77.E+07	2.97.E+07	3.73.E+07	4.68.E+07	4.78.E+07	3.57.E+07	4.48.E+07
1483	Q9H0S4	Probable ATP-dependent RNA helicase DDX47 [OS=Homo sapiens]	21.0	11	3	43	3	272	37	3	3	0	5.27.E+07	5.53.E+07	5.32.E+07	4.90.E+07	7.07.E+07	6.97.E+07	5.97.E+07	5.74.E+07
1484	P51571	translocon-associated protein subunit delta [OS=Homo sapiens]	20.9	23	3	159	3	2248	250	3	3	0	2.22.E+08	2.35.E+08	2.25.E+08	2.20.E+08	3.75.E+08	2.84.E+08	2.64.E+08	3.60.E+08
1485	Q96HV5	Transmembrane protein 41A [OS=Homo sapiens]	20.9	11	2	28	2	258	18	2	2	0	2.57.E+07	1.94.E+07	1.85.E+07	2.17.E+07	2.08.E+07	2.10.E+07	2.78.E+07	1.93.E+07
1486	Q96KR1	Zinc finger RNA-binding protein [OS=Homo sapiens]	20.9	4	3	16	3	264	16	3	3	0	1.60.E+07	1.52.E+07	1.22.E+07	1.70.E+07	1.73.E+07	1.77.E+07	2.23.E+07	1.78.E+07
1487	Q96EK6	glucosamine 6-phosphate N-acetyltransferase [OS=Homo sapiens]	20.8	26	2	74	2	179	90	2	2	0	6.05.E+07	6.21.E+07	5.15.E+07	6.05.E+07	9.13.E+07	9.72.E+07	4.58.E+07	8.42.E+07
1488	O14548	Cytochrome c oxidase subunit 7A-related protein, mitochondrial [OS=Homo sapiens]	20.7	40	2	42	2	330	53	2	2	0	2.31.E+07	1.91.E+07	1.65.E+07	2.11.E+07	1.86.E+07	2.00.E+07	8.34.E+06	1.95.E+07
1489	P78310-1	Coxsackievirus and adenovirus receptor [OS=Homo sapiens]	20.7	10	2	47	2	1016	61	2	2	0	2.20.E+07	3.65.E+07	2.44.E+07	3.60.E+07	6.54.E+07	5.46.E+07	6.27.E+07	6.72.E+07
1490	P43353-1	Aldehyde dehydrogenase family 3 member B1 [OS=Homo sapiens]	20.6	6	2	47	1	230	58	2	2	0	8.67.E+06	7.54.E+06	9.02.E+06		1.61.E+07	1.25.E+07	1.26.E+07	1.41.E+07
1491	O75629	Protein CREG1 [OS=Homo sapiens]	20.5	18	3	36	3	420	52	3	2	0	6.87.E+07	6.73.E+07	6.09.E+07	6.66.E+07	9.61.E+07	1.03.E+08	1.10.E+08	1.07.E+08
1492	Q9UBQ7	Glyoxylate reductase/hydroxypyruvate reductase [OS=Homo sapiens]	20.5	16	3	59	3	187	93	3	3	0	5.27.E+07	5.93.E+07	7.42.E+07	6.75.E+07	7.51.E+07	7.18.E+07	7.13.E+07	5.90.E+07
1493	P62273-1	40S ribosomal protein S29 [OS=Homo sapiens]	20.4	34	2	139	2	711	12	1	2	0	5.05.E+08	4.51.E+08	5.23.E+08	6.02.E+08	4.04.E+08	4.30.E+08	4.94.E+08	4.34.E+08
1494	Q9Y320	Thioredoxin-related transmembrane protein 2 [OS=Homo sapiens]	20.4	18	4	67	4	1923	5	3	4	0	4.55.E+07	4.55.E+07	5.00.E+07	4.61.E+07	6.70.E+07	6.75.E+07	4.09.E+07	6.43.E+07
1495	P14678-1	Small nuclear ribonucleoprotein-associated proteins B and B' [OS=Homo sapiens]	20.4	15	4	172	4	1544	97	4	4	0	4.29.E+08	4.28.E+08	4.34.E+08	3.86.E+08	3.70.E+08	3.81.E+08	3.96.E+08	3.92.E+08
1496	Q15435	Protein phosphatase 1 regulatory subunit 7 [OS=Homo sapiens]	20.4	10	3	80	3	817	95	3	3	0	5.45.E+07	5.52.E+07	5.69.E+07	5.46.E+07	6.93.E+07	7.23.E+07	4.68.E+07	4.95.E+07
1497	P11177	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial [OS=Homo sapiens]	20.4	13	3	84	3	553	72	3	3	0	1.63.E+08	1.65.E+08	1.54.E+08	1.68.E+08	3.69.E+08	2.09.E+08	3.37.E+08	3.68.E+08
1498	Q92600	CCR4-NOT transcription complex subunit 9 [OS=Homo sapiens]	20.3	11	2	60	2	466	59	2	2	0	3.57.E+07	3.76.E+07	3.36.E+07	3.24.E+07	2.97.E+07	2.80.E+07	1.19.E+07	2.76.E+07
1499	P21399	Cytoplasmic aconitate hydratase [OS=Homo sapiens]	20.3	8	4	18	4	142	24	4	4	0	2.49.E+07	2.18.E+07	3.29.E+07	2.09.E+07	5.45.E+07	5.50.E+07	5.46.E+07	5.96.E+07
1500	Q92530	proteasome inhibitor PI31 subunit [OS=Homo sapiens]	20.3	12	2	45	2	1504	22	1	2	0	4.51.E+07	4.18.E+07	3.98.E+07	4.01.E+07	4.16.E+07	3.92.E+07	3.83.E+07	4.34.E+07
1501	O75431	Metaxin-2 [OS=Homo sapiens]	20.3	19	2	18	2	79	18	1	2	0	1.60.E+07	2.99.E+07	1.21.E+07	3.18.E+07	3.35.E+07	2.05.E+07	3.07.E+07	2.09.E+07
1502	Q14011	Cold-inducible RNA-binding protein [OS=Homo sapiens]	20.2	20	3	81	3	1662	116	2	3	0	5.08.E+07	5.98.E+07	4.46.E+07	6.21.E+07	5.91.E+07	5.40.E+07	4.78.E+07	6.23.E+07
1503	Q86UP2-1	Kinectin [OS=Homo sapiens]	20.2	4	4	41	4	319	44	3	4	0	1.99.E+07	2.67.E+07	3.77.E+07	3.71.E+07	5.74.E+07	6.11.E+07	5.40.E+07	5.68.E+07
1504	Q9NW13-1	RNA-binding protein 28 [OS=Homo sapiens]	20.1	6	4	33	4	211	4	3	4	0	4.16.E+07	2.78.E+07	4.02.E+07	2.91.E+07	1.14.E+07	3.09.E+07	2.65.E+07	2.95.E+07
1505	P61011-1	signal recognition particle 54 kDa protein [OS=Homo	20.1	11	4	42	4	186	19	4	4	0	4.50.E+07	5.14.E+07	4.90.E+07	4.64.E+07	6.24.E+07	6.20.E+07	6.80.E+07	5.66.E+07
1506	P35613	Basigin [OS=Homo sapiens]	20.0	8	2	49	2	272	56	2	2	0	6.81.E+07	6.97.E+07	7.47.E+07	7.60.E+07	9.86.E+07	9.41.E+07	1.08.E+08	1.05.E+08
1507	Q9BTE6-1	Alanyl-tRNA editing protein Aarsd1 [OS=Homo sapiens]	20.0	15	4	18	4	108	20	4	4	0	3.64.E+07	3.27.E+07	2.78.E+07	3.29.E+07	7.96.E+07	8.43.E+07	7.29.E+07	7.88.E+07
1508	P34949	mannose-6-phosphate isomerase [OS=Homo sapiens]	20.0	13	3	20	3	138	27	3	3	0	2.40.E+07	2.91.E+07	2.80.E+07	3.23.E+07	4.69.E+07	5.15.E+07	4.00.E+07	6.59.E+07
1509	Q03701	CCAAT/enhancer-binding protein zeta [OS=Homo sapiens]	19.8	5	3	23	3	155	10	3	2	0	3.08.E+07	3.75.E+07	2.83.E+07	4.14.E+07	2.88.E+07	4.52.E+07	2.52.E+07	3.70.E+07
1510	P24941-1	cyclin-dependent kinase 2 [OS=Homo sapiens]	19.8	12	3	45	2	695	57	3	3	0	4.08.E+07	1.61.E+07	4.23.E+07	3.93.E+07	5.12.E+07	1.64.E+07	1.97.E+07	4.82.E+07
1511	Q9C0B1-1	alpha-ketoglutarate-dependent dioxygenase FTO [OS=Homo sapiens]	19.7	8	3	63	3	1299	57	3	3	0	2.53.E+07	2.93.E+07	2.75.E+07	2.51.E+07	3.71.E+07	3.76.E+07	2.05.E+07	3.23.E+07
1512	Q9UHV9	Prefoldin subunit 2 [OS=Homo sapiens]	19.6	17	2	88	2	1336	130	2	2	0	1.41.E+08	1.52.E+08	1.45.E+08	1.38.E+08	1.01.E+08	1.66.E+08	1.57.E+08	8.36.E+07
1513	Q9UNW1	Multiple inositol polyphosphate phosphatase 1 [OS=Homo sapiens]	19.6	10	2	35	2	251	32	2	2	0	6.07.E+06	1.80.E+07	1.60.E+07	5.95.E+06	2.76.E+07	2.24.E+07	1.39.E+07	1.79.E+07
1514	O43488	aflatoxin B1 aldehyde reductase member 2 [OS=Homo sapiens]	19.6	9	2	32	2	265	43	2	2	0	3.86.E+07	4.30.E+07	4.26.E+07	4.17.E+07	5.17.E+07	4.75.E+07	3.02.E+07	4.42.E+07
1515	Q15125	3-beta-hydroxysteroid-delta(8),delta(7)-isomerase [OS=Homo sapiens]	19.5	7	1	18	1	349			1	0	1.22.E+08	1.29.E+08	1.37.E+08	1.05.E+08	1.90.E+08	1.92.E+08	2.05.E+08	1.96.E+08
1516	P53007	Tricarboxylate transport protein, mitochondrial [OS=Homo sapiens]	19.5	17	5	32	5	116	20	5	5	0	6.95.E+07	6.75.E+07	6.51.E+07	7.40.E+07	6.26.E+07	6.69.E+07	6.66.E+07	6.86.E+07
1517	O75396	Vesicle-trafficking protein SEC22b [OS=Homo sapiens]	19.4	25	3	18	3	241	19	3	3	0	2.80.E+07	2.66.E+07		2.34.E+07	4.71.E+07	4.58.E+07	4.50.E+07	3.71.E+07
1518	P24468	COUP transcription factor 2 [OS=Homo sapiens]	19.4	8	2	18	2	389	22	2	2	0	9.06.E+06	1.58.E+07	1.06.E+07	1.53.E+07	3.49.E+07	3.06.E+07	3.02.E+07	2.93.E+07
1519	Q9Y6N5	Sulfide:quinone oxidoreductase, mitochondrial [OS=Homo sapiens]	19.4	9	3	10	3	87	12	3	3	0	6.76.E+07	1.04.E+08	7.83.E+07	8.08.E+07	3.97.E+07	3.90.E+07	4.59.E+07	4.78.E+07
1520	Q53T59	HCLS1-binding protein 3 [OS=Homo sapiens]	19.4	9	2	8	2	176	11	2	2	0	1.51.E+07	1.71.E+07	1.31.E+07	1.74.E+07	4.04.E+07	3.89.E+07	2.70.E+07	3.57.E+07

No.	Accession	Description	Sum PEP Score	Coverage [%]	# Peptides	# PSMs	# Unique Peptides	Score Mascot: A5 Mascot	Score Sequest HT: A2 Sequest HT	# Peptides (by Search Engine): A2 Sequest HT	# Peptides (by Search Engine): A5 Mascot	# Razor Peptides	ctrl Abundances_1	ctrl Abundances_2	ctrl Abundances_3	ctrl Abundances_4	JAM-A KO Abundances_1	JAM-A KO Abundances_2	JAM-A KO Abundances_3	JAM-A KO Abundances_4
1521	O00217	NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial [OS=Homo sapiens]	19.3	13	2	28	2	280	23	2	2	0	1.95.E+07	2.37.E+07	1.49.E+07	2.05.E+07	3.40.E+07	3.68.E+07	2.79.E+07	3.95.E+07
1522	P26006	Integrin alpha-3 [OS=Homo sapiens]	19.3	4	5	39	5	184	42	5	5	0	1.55.E+08	1.28.E+08	1.39.E+08	1.24.E+08	1.72.E+08	1.64.E+08	1.82.E+08	1.77.E+08
1523	Q9NPQ8	Synembryn-A [OS=Homo sapiens]	19.3	9	4	62	4	493	51	4	4	0	5.27.E+07	5.52.E+07	5.42.E+07	5.39.E+07	7.36.E+07	7.83.E+07	7.72.E+07	7.22.E+07
1524	Q9UPY5	Cystine/glutamate transporter [OS=Homo sapiens]	19.2	8	3	66	3	714	80	2	3	0	4.80.E+07	5.06.E+07	4.83.E+07	5.13.E+07	6.82.E+07	6.81.E+07	6.28.E+07	6.64.E+07
1525	Q8NBT2	kinetochore protein SPC24 [OS=Homo sapiens]	19.2	9	1	20	1	393	20	1	1	0	2.32.E+06	5.46.E+06	7.68.E+06	9.59.E+06	1.40.E+07	1.16.E+07	1.02.E+07	9.75.E+06
1526	P58546	Myotrophin [OS=Homo sapiens]	19.2	32	2	70	2	1571	123	2	2	0	7.24.E+07	8.02.E+07	7.83.E+07	7.50.E+07	8.77.E+07	8.04.E+07	8.33.E+07	8.76.E+07
1527	P60510	Serine/threonine-protein phosphatase 4 catalytic subunit [OS=Homo sapiens]	19.1	21	4	32	3	620	51	4	2	0					3.36.E+07	3.39.E+07	3.56.E+07	3.60.E+07
1528	Q9BW60	Elongation of very long chain fatty acids protein 1 [OS=Homo sapiens]	19.1	10	2	96	2	1575	109	2	2	0	3.92.E+07	3.86.E+07	3.53.E+07	3.47.E+07	2.49.E+07	2.39.E+07	2.24.E+07	2.31.E+07
1529	P35250-1	Replication factor C subunit 2 [OS=Homo sapiens]	19.1	10	2	28	2	244	31	2	2	0	1.99.E+07	2.33.E+07	2.12.E+07	2.06.E+07	2.40.E+07	2.43.E+07	2.54.E+07	2.41.E+07
1530	Q9NP79	Vacuolar protein sorting-associated protein VTA1 homolog [OS=Homo sapiens]	19.0	14	2	10	2	90	13	2	2	0	3.93.E+07	4.11.E+07	4.76.E+07	4.47.E+07	6.60.E+07	6.32.E+07	3.52.E+07	5.76.E+07
1531	Q15061	WD repeat-containing protein 43 [OS=Homo sapiens]	19.0	9	3	19	3	149	15	2	3	0	3.98.E+07	4.17.E+07	5.82.E+07	4.56.E+07	4.01.E+07	4.69.E+07	4.13.E+07	4.57.E+07
1532	Q13405	39S ribosomal protein L49, mitochondrial [OS=Homo sapiens]	18.9	15	2	68	2	1380	69	2	2	0	2.98.E+07	3.38.E+07	2.66.E+07	3.25.E+07	4.11.E+07	4.46.E+07	3.45.E+07	4.43.E+07
1533	P17480-1	Nucleolar transcription factor 1 [OS=Homo sapiens]	18.9	5	3	48	3	276	65	3	3	0	4.82.E+07	5.95.E+07	4.96.E+07	5.98.E+07	6.22.E+07	5.85.E+07	5.98.E+07	6.80.E+07
1534	O14974	Protein phosphatase 1 regulatory subunit 12A [OS=Homo sapiens]	18.9	3	3	57	3	508	23	3	3	0	3.50.E+07	2.16.E+07	3.64.E+07	2.63.E+07	2.29.E+07	2.97.E+07	2.95.E+07	3.19.E+07
1535	Q92900	Regulator of nonsense transcripts 1 [OS=Homo sapiens]	18.8	6	6	66	6	135	17	6	6	0	8.08.E+07	8.61.E+07	7.80.E+07	7.57.E+07	9.26.E+07	9.26.E+07	8.34.E+07	8.86.E+07
1536	Q9Y5L4	mitochondrial import inner membrane translocase subunit TIM13 [OS=Homo sapiens]	18.8	41	3	63	3	1061	80	3	3	0	8.94.E+07	9.40.E+07	9.48.E+07	8.44.E+07	6.47.E+07	7.34.E+07	8.04.E+07	6.66.E+07
1537	P57735	ras-related protein Rab-25 [OS=Homo sapiens]	18.6	20	3	20	3	85	23	3	3	0	1.27.E+08	1.21.E+08	1.24.E+08	9.59.E+07	2.00.E+07	4.05.E+07	5.77.E+07	1.86.E+07
1538	Q15286	Ras-related protein Rab-35 [OS=Homo sapiens]	18.6	18	3	328	1	4659	417	3	3	0								
1539	Q7L576-1	cytoplasmic FMR1-interacting protein 1 [OS=Homo sapiens]	18.6	3	3	48	3	279	34	3	3	0	2.06.E+07	2.14.E+07	2.93.E+07	2.88.E+07	3.87.E+07	4.05.E+07	3.55.E+07	2.93.E+07
1540	Q9Y624	Junctional adhesion molecule A [OS=Homo sapiens]	18.5	14	2	34	2	242	60	2	2	0	9.29.E+07	1.03.E+08	9.67.E+07	8.76.E+07				
1541	P41240	tyrosine-protein kinase CSK [OS=Homo sapiens]	18.5	9	3	50	3	336	30	3	3	0	2.70.E+07	2.75.E+07	2.58.E+07	2.68.E+07	2.58.E+07	2.68.E+07	2.20.E+07	2.91.E+07
1542	P18827	syndecan-1 [OS=Homo sapiens]	18.5	12	2	30	2	375	48	2	2	0	3.56.E+07	3.89.E+07	3.46.E+07	3.22.E+07	5.54.E+07	4.48.E+07	4.68.E+07	8.72.E+07
1543	Q9UK22	F-box only protein 2 [OS=Homo sapiens]	18.5	14	3	67	3	597	62	3	3	0	3.12.E+07	3.42.E+07	2.91.E+07	3.25.E+07	4.23.E+07	3.72.E+07	3.60.E+07	3.66.E+07
1544	P54725-1	UV excision repair protein RAD23 homolog A [OS=Homo sapiens]	18.5	11	2	64	2	1708	141	2	2	0	2.49.E+07	2.83.E+07	2.71.E+07	3.06.E+07	3.82.E+07	2.82.E+07	2.53.E+07	3.15.E+07
1545	Q9NR12-1	PDZ and LIM domain protein 7 [OS=Homo sapiens]	18.4	12	4	27	4	104	21	4	4	0	6.12.E+07	3.41.E+07	6.37.E+07	2.76.E+07	1.25.E+07	6.89.E+07	9.32.E+07	8.52.E+07
1546	O60907	F-box-like/WD repeat-containing protein TBL1X [OS=Homo sapiens]	18.4	7	2	36	2	711	48	2	2	0	1.17.E+07	1.43.E+07	1.34.E+07	1.66.E+07	1.84.E+07	8.50.E+06	1.75.E+07	1.91.E+07
1547	O95777	U6 snRNA-associated Sm-like protein LSm8 [OS=Homo sapiens]	18.4	38	3	41	3	238	36	2	3	0	6.25.E+07	8.04.E+07	5.53.E+07	7.78.E+07	6.38.E+07	9.27.E+07	8.17.E+07	9.52.E+07
1548	Q9P2R7	Succinate--CoA ligase [ADP-forming] subunit beta, mitochondrial [OS=Homo sapiens]	18.4	10	5	64	5	267	23	5	5	0	5.25.E+07	4.99.E+07	5.43.E+07	5.28.E+07	5.38.E+07	5.25.E+07	5.59.E+07	5.22.E+07
1549	P53985	Monocarboxylate transporter 1 [OS=Homo sapiens]	18.3	11	4	35	4	132	27	4	3	0	3.43.E+07	2.01.E+07	2.09.E+07	3.31.E+07	3.64.E+07	3.81.E+07	4.34.E+07	2.20.E+07
1550	Q96CS3	FAS-associated factor 2 [OS=Homo sapiens]	18.3	7	2	44	2	630	61	2	2	0	3.85.E+07	3.80.E+07	3.65.E+07	3.61.E+07	4.90.E+07	4.67.E+07	3.79.E+07	4.13.E+07
1551	Q00653-1	Nuclear factor NF-kappa-B p100 subunit [OS=Homo sapiens]	18.3	8	3	42	3	130	45	3	3	0	6.52.E+07	6.93.E+07	4.02.E+07	5.83.E+07	5.95.E+07	6.27.E+07	4.98.E+07	5.01.E+07
1552	P22059	Oxysterol-binding protein 1 [OS=Homo sapiens]	18.3	8	4	42	4	63	22	4	4	0	2.00.E+07	1.72.E+07	2.57.E+07	1.69.E+07	2.17.E+07	2.20.E+07	2.05.E+07	2.33.E+07
1553	Q92890	Ubiquitin recognition factor in ER-associated degradation protein 1 [OS=Homo sapiens]	18.2	17	3	37	3	966	49	3	3	0	1.03.E+08	1.05.E+08	1.14.E+08	1.13.E+08	1.03.E+08	1.09.E+08	1.05.E+08	1.02.E+08
1554	Q15796-1	Mothers against decapentaplegic homolog 2 [OS=Homo sapiens]	18.2	10	4	90	4	318	83	4	4	0	1.47.E+08	1.38.E+08	1.39.E+08	1.18.E+08	1.19.E+08	1.58.E+08	1.02.E+08	1.21.E+08
1555	Q7L014	probable ATP-dependent RNA helicase DDX46 [OS=Homo sapiens]	18.1	4	3	62	3	604	61	3	3	0	5.54.E+07	4.54.E+07	5.46.E+07	4.84.E+07	5.27.E+07	4.38.E+07	5.41.E+07	4.52.E+07
1556	Q04323-1	UBX domain-containing protein 1 [OS=Homo sapiens]	18.1	31	3	37	3	138	9	3	3	0	5.58.E+07	5.52.E+07	5.77.E+07	5.68.E+07	4.60.E+07	2.92.E+07	2.29.E+07	3.51.E+07
1557	P15328	Folate receptor alpha [OS=Homo sapiens]	18.0	17	2	6	2	72	11	2	1	0	1.12.E+07	1.97.E+07	1.06.E+07	1.35.E+07				
1558	P15291	Beta-1,4-galactosyltransferase 1 [OS=Homo sapiens]	18.0	12	3	71	3	751	77	3	3	0	5.21.E+07	5.86.E+07	4.73.E+07	5.06.E+07	7.59.E+07	7.02.E+07	6.53.E+07	7.41.E+07
1559	Q5SRE5	Nucleoporin NUP188 homolog [OS=Homo sapiens]	18.0	3	3	46	3	925	28	3	3	0	8.40.E+06	1.16.E+07	8.49.E+06	1.05.E+07	1.37.E+07	1.10.E+07	1.01.E+07	1.01.E+07
1560	Q969X5	Endoplasmic reticulum-Golgi intermediate compartment protein 1 [OS=Homo sapiens]	17.9	11	2	28	2	305	30	2	2	0	2.98.E+07	2.65.E+07	2.82.E+07	3.00.E+07	5.78.E+07	5.62.E+07	2.71.E+07	4.80.E+07
1561	P09543-1	2',3'-cyclic-nucleotide 3'-phosphodiesterase [OS=Homo sapiens]	17.9	9	2	33	2	472	25	2	2	0	1.45.E+07	1.41.E+07	1.39.E+07	1.39.E+07	1.56.E+07	1.53.E+07	1.38.E+07	1.51.E+07
1562	P57076	UPF0769 protein C21orf59 [OS=Homo sapiens]	17.9	15	2	43	2	849	88	2	2	0	1.92.E+07	2.15.E+07	1.86.E+07	1.97.E+07	2.44.E+07	2.60.E+07	2.08.E+07	2.50.E+07
1563	Q9UKD2	mRNA turnover protein 4 homolog [OS=Homo sapiens]	17.9	24	4	91	4	323	72	4	4	0	5.59.E+08	6.18.E+08	5.11.E+08	5.61.E+08	7.99.E+08	8.24.E+08	6.11.E+08	6.75.E+08
1564	Q9NRR5-1	Ubiquilin-4 [OS=Homo sapiens]	17.9	4	3	22	3	323	37	3	2	0	6.62.E+07	8.82.E+07	6.19.E+07	7.95.E+07	7.37.E+07	8.21.E+07	5.51.E+07	8.99.E+07
1565	Q8N3R9-1	MAGUK p55 subfamily member 5 [OS=Homo sapiens]	17.9	9	4	17	4	90	11	3	4	0	2.94.E+07	3.65.E+07	2.97.E+07	3.12.E+07	4.13.E+07	3.72.E+07	3.73.E+07	3.97.E+07
1566	Q9BTV4	Transmembrane protein 43 [OS=Homo sapiens]	17.8	9	2	41	2	150	63	2	2	0	2.76.E+07	3.11.E+07	2.84.E+07	2.33.E+07	3.44.E+07	3.33.E+07	1.93.E+07	2.72.E+07
1567	Q8N668	COMM domain-containing protein 1 [OS=Homo sapiens]	17.7	18	1	22	1	499			1	0	1.72.E+07	2.15.E+07	1.87.E+07	1.99.E+07	2.13.E+07	2.11.E+07	1.75.E+07	1.56.E+07
1568	Q6NUK1	Calcium-binding mitochondrial carrier protein SCaMC-1 [OS=Homo sapiens]	17.6	9	3	32	3	107	29	3	3	0	1.64.E+07	1.64.E+07	2.02.E+07	1.55.E+07	5.54.E+07	7.72.E+07	6.24.E+07	7.17.E+07
1569	Q9BQA1	Methylosome protein 50 [OS=Homo sapiens]	17.6	25	5	90	5	473	71	5	4	0	1.56.E+08	1.46.E+08	1.42.E+08	1.44.E+08	1.73.E+08	1.79.E+08	1.73.E+08	1.59.E+08
1570	Q8IXM3	39S ribosomal protein L41, mitochondrial [OS=Homo sapiens]	17.6	31	2	84	2	1364	107	2	2	0	4.43.E+07	4.71.E+07	4.08.E+07	4.71.E+07	5.17.E+07	5.16.E+07	4.89.E+07	4.78.E+07
1571	O60341	Lysine-specific histone demethylase 1A [OS=Homo sapiens]	17.5	4	2	22	2	173	23	2	2	0	3.22.E+07	2.98.E+07	3.25.E+07	2.68.E+07	2.86.E+07	2.23.E+07	2.45.E+07	2.23.E+07

No.	Accession	Description	Sum PEP Score	Coverage [%]	# Peptides	# PSMs	# Unique Peptides	Score Mascot: A5 Mascot	Score Sequest HT: A2 Sequest HT	# Peptides (by Search Engine): A2 Sequest HT	# Peptides (by Search Engine): A5 Mascot	# Razor Peptides	ctrl Abundances_1	ctrl Abundances_2	ctrl Abundances_3	ctrl Abundances_4	JAM-A KO Abundances_1	JAM-A KO Abundances_2	JAM-A KO Abundances_3	JAM-A KO Abundances_4
1572	Q9Y3E5	Peptidyl-tRNA hydrolase 2, mitochondrial [OS=Homo sapiens]	17.5	25	2	89	2	442	83	2	2	0	6.39.E+07	6.71.E+07	4.31.E+07	6.73.E+07	9.25.E+07	9.36.E+07	7.30.E+07	7.54.E+07
1573	Q96GG9	DCN1-like protein 1 [OS=Homo sapiens]	17.4	11	2	68	2	2047	89	2	2	0	3.32.E+07	3.45.E+07	2.92.E+07	3.52.E+07	3.93.E+07	4.35.E+07	3.37.E+07	3.66.E+07
1574	Q14157-2	Ubiquitin-associated protein 2-like [OS=Homo sapiens]	17.4	4	3	94	3	966	89	3	3	0	8.03.E+07	9.01.E+07	7.73.E+07	8.91.E+07	8.30.E+07	7.74.E+07	2.47.E+07	8.10.E+07
1575	Q96RT1	Erbin [OS=Homo sapiens]	17.4	3	3	24	3	246	9	3	3	0	2.44.E+07	2.15.E+07	2.03.E+07	2.15.E+07	3.33.E+07	3.11.E+07	2.93.E+07	4.00.E+07
1576	P46926	glucosamine-6-phosphate isomerase 1 [OS=Homo sapiens]	17.4	10	2	48	2	828	66	2	2	0	4.78.E+07	4.80.E+07	4.83.E+07	4.49.E+07	7.78.E+07	7.56.E+07	6.29.E+07	7.51.E+07
1577	Q96IX5	Up-regulated during skeletal muscle growth protein 5 [OS=Homo sapiens]	17.4	28	2	44	2	2661			2	0	1.20.E+08	1.17.E+08	1.27.E+08	1.28.E+08	1.01.E+08	1.45.E+08	1.42.E+08	9.55.E+07
1578	Q6IBS0	Twinfilin-2 [OS=Homo sapiens]	17.4	11	2	16	2	179	15	2	2	0	2.81.E+07	1.29.E+07	2.03.E+07	3.71.E+07	2.64.E+07	2.80.E+07	3.08.E+07	2.55.E+07
1579	P47914	60S ribosomal protein L29 [OS=Homo sapiens]	17.3	14	2	194	2	2230	207	2	2	0	1.66.E+08	1.48.E+08	1.66.E+08	1.70.E+08	1.23.E+08	1.33.E+08	1.55.E+08	1.33.E+08
1580	Q9NP73-1	Putative bifunctional UDP-N-acetylglucosamine transferase and deubiquitinase ALG13 [OS=Homo sapiens]	17.3	2	2	31	2	299	13	2	2	0	2.42.E+07	2.22.E+07	2.19.E+07	2.08.E+07	2.80.E+07	2.81.E+07	2.67.E+07	2.94.E+07
1581	Q9P015	39S ribosomal protein L15, mitochondrial [OS=Homo sapiens]	17.3	14	3	22	3	146	26	3	3	0	7.00.E+07	7.60.E+07	7.87.E+07	7.47.E+07	6.70.E+07	5.93.E+07	5.72.E+07	7.10.E+07
1582	Q99459	Cell division cycle 5-like protein [OS=Homo sapiens]	17.3	6	3	44	3	418	42	3	3	0	4.93.E+07	5.61.E+07	5.06.E+07	4.93.E+07	5.39.E+07	5.53.E+07	4.66.E+07	5.47.E+07
1583	Q92769	Histone deacetylase 2 [OS=Homo sapiens]	17.3	9	4	92	3	499	89	4	3	1	2.10.E+08	2.11.E+08	2.08.E+08	2.14.E+08	2.15.E+08	2.08.E+08	2.21.E+08	2.03.E+08
1584	O75663	TIP41-like protein [OS=Homo sapiens]	17.3	16	3	52	3	535	52	3	3	0	3.47.E+07	3.51.E+07	3.35.E+07	3.29.E+07	3.80.E+07	3.91.E+07	4.11.E+07	4.21.E+07
1585	O00165	HCLS1-associated protein X-1 [OS=Homo sapiens]	17.2	16	3	92	3	977	70	3	3	0	5.71.E+07	5.65.E+07	5.41.E+07	5.71.E+07	3.55.E+07	3.88.E+07	4.04.E+07	4.07.E+07
1586	O43660-1	Pleiotropic regulator 1 [OS=Homo sapiens]	17.1	7	2	50	2	234	72	2	2	0	4.41.E+07	4.93.E+07	5.17.E+07	5.46.E+07	4.90.E+07	5.14.E+07	5.08.E+07	5.69.E+07
1587	Q9BUK6	Protein misato homolog 1 [OS=Homo sapiens]	17.1	9	2	18	2	117	15	2	2	0	2.11.E+07	2.12.E+07	1.45.E+07	2.69.E+07	2.61.E+06	8.14.E+06	2.63.E+06	3.49.E+06
1588	Q9BTW9	Tubulin-specific chaperone D [OS=Homo sapiens]	17.1	5	3	13	3	164	10	3	2	0	1.72.E+07	7.02.E+06	1.16.E+07	1.03.E+07	2.97.E+06	1.73.E+06	7.28.E+06	1.11.E+07
1589	O14617-1	AP-3 complex subunit delta-1 [OS=Homo sapiens]	17.0	3	2	54	2	455	49	2	2	0	8.20.E+06	9.99.E+06	6.06.E+06	2.11.E+07	2.49.E+07	2.57.E+07	2.22.E+07	2.38.E+07
1590	P33240	cleavage stimulation factor subunit 2 [OS=Homo sapiens]	17.0	7	2	52	2	744	63	2	2	0	4.66.E+07	4.39.E+07	4.53.E+07	4.56.E+07	4.64.E+07	4.29.E+07	4.00.E+07	4.40.E+07
1591	P18077	60S ribosomal protein L35a [OS=Homo sapiens]	17.0	24	5	100	5	115	31	5	5	0	6.94.E+08	6.30.E+08	5.67.E+08	7.02.E+08	4.48.E+08	4.48.E+08	4.45.E+08	4.00.E+08
1592	Q15041	ADP-ribosylation factor-like protein 6-interacting protein 1 [OS=Homo sapiens]	17.0	19	2	82	2	185	91	2	2	0	1.15.E+08	9.73.E+07	1.10.E+08	1.22.E+08	1.03.E+08	1.03.E+08	1.30.E+08	1.07.E+08
1593	Q8WUF5	RelA-associated inhibitor [OS=Homo sapiens]	16.9	7	3	10	3	54	13	3	3	0	2.44.E+07	3.64.E+07	3.41.E+07	3.66.E+07	2.24.E+07	1.21.E+07	2.00.E+06	9.65.E+06
1594	P61020	Ras-related protein Rab-5B [OS=Homo sapiens]	16.9	16	3	94	1	637	124	3	3	0	4.89.E+07	4.58.E+07	6.48.E+07	3.19.E+07	2.54.E+07	4.09.E+07	1.44.E+07	3.16.E+07
1595	O94919	endonuclease domain-containing 1 protein [OS=Homo sapiens]	16.9	9	4	15	4	72	5	4	4	0	5.88.E+07	5.55.E+07	5.17.E+07	6.20.E+07	5.79.E+07	5.54.E+07	5.42.E+07	5.58.E+07
1596	Q9H4A6	Golgi phosphoprotein 3 [OS=Homo sapiens]	16.9	13	2	60	2	550	13	2	2	0	1.26.E+07	1.62.E+07	1.68.E+07	1.39.E+07	1.01.E+07	1.20.E+07	2.13.E+07	1.22.E+07
1597	P50336	protoporphyrinogen oxidase [OS=Homo sapiens]	16.8	10	2	54	2	758	78	2	2	0	2.86.E+07	2.63.E+07	1.48.E+07	2.70.E+07	3.13.E+07	3.01.E+07	2.73.E+07	3.16.E+07
1598	Q5BJD5-1	Transmembrane protein 41B [OS=Homo sapiens]	16.8	7	1	43	1	183	15	1	1	0	5.89.E+06	5.53.E+06	6.83.E+06	5.20.E+06	4.34.E+06	5.20.E+06	5.30.E+06	5.07.E+06
1599	Q9Y2W2	WW domain-binding protein 11 [OS=Homo sapiens]	16.8	10	3	34	3	214	21	3	3	0	3.49.E+07	3.99.E+07	3.80.E+07	3.37.E+07	4.46.E+07	4.13.E+07	4.43.E+07	4.51.E+07
1600	Q9GZP4	PITH domain-containing protein 1 [OS=Homo sapiens]	16.8	29	4	32	4	195	34	4	4	0	4.14.E+07	4.08.E+07	4.33.E+07	3.56.E+07	4.01.E+07	4.63.E+07	4.99.E+07	4.55.E+07
1601	P21589-1	5'-nucleotidase [OS=Homo sapiens]	16.7	8	2	16	2	157	16	2	2	0	1.10.E+07	1.93.E+07	1.07.E+07	1.31.E+07	1.54.E+07	6.49.E+06	3.03.E+06	4.23.E+06
1602	Q16401	26S proteasome non-ATPase regulatory subunit 5 [OS=Homo sapiens]	16.7	13	5	15	5	259	5	4	5	0	2.42.E+07	3.08.E+07	2.84.E+07	2.58.E+07	5.78.E+07	5.32.E+07	5.01.E+07	5.36.E+07
1603	Q96HY6-1	DDRGK domain-containing protein 1 [OS=Homo sapiens]	16.7	17	3	8	3	97	9	3	3	0	9.47.E+06	1.21.E+07	1.29.E+07	1.13.E+07	1.79.E+07	1.78.E+07	1.85.E+07	2.00.E+07
1604	Q14320	Protein FAM50A [OS=Homo sapiens]	16.7	9	2	43	2	369	40	2	2	0	3.17.E+07	2.47.E+07	3.24.E+07	1.91.E+07	3.45.E+07	3.68.E+07	3.44.E+07	3.68.E+07
1605	Q9Y3B4	Splicing factor 3B subunit 6 [OS=Homo sapiens]	16.7	11	1	48	1	376	55	1	1	0	3.35.E+07	3.12.E+07	3.37.E+07	3.93.E+07	3.87.E+07	3.56.E+07	3.68.E+07	3.42.E+07
1606	O75351	Vacuolar protein sorting-associated protein 4B [OS=Homo sapiens]	16.6	9	2	94	2	1010	67	2	2	0	2.75.E+07	2.44.E+07	2.23.E+07	2.48.E+07	4.12.E+07	3.57.E+07	4.18.E+07	3.80.E+07
1607	O60869-1	Endothelial differentiation-related factor 1 [OS=Homo sapiens]	16.6	10	1	50	1	615	68	1	1	0	6.66.E+07	6.02.E+07	6.72.E+07	7.57.E+07	8.04.E+07	7.00.E+07	7.68.E+07	7.45.E+07
1608	P47755	F-actin-capping protein subunit alpha-2 [OS=Homo sapiens]	16.6	12	3	81	1	1042	114	3	2	0	3.36.E+07	2.03.E+07	2.97.E+07	3.25.E+07	3.97.E+07	3.52.E+07	1.50.E+07	3.50.E+07
1609	P09110-1	3-ketoacyl-CoA thiolase, peroxisomal [OS=Homo sapiens]	16.6	9	2	80	2	905	18	2	2	0	8.97.E+06	1.58.E+07	1.46.E+07	1.57.E+07	1.09.E+07	1.05.E+07	9.17.E+06	8.65.E+06
1610	Q9UDW1	cytochrome b-c1 complex subunit 9 [OS=Homo sapiens]	16.6	25	2	78	2	591	10	1	2	0	6.07.E+07	4.58.E+07	3.79.E+07	4.49.E+07	3.20.E+07	4.21.E+07	4.12.E+07	3.36.E+07
1611	Q96T88	E3 ubiquitin-protein ligase UHRF1 [OS=Homo sapiens]	16.5	6	4	70	4	569	28	4	4	0	6.02.E+07	6.15.E+07	6.29.E+07	6.50.E+07	6.33.E+07	5.97.E+07	5.47.E+07	5.87.E+07
1612	Q9ULA0	Aspartyl aminopeptidase [OS=Homo sapiens]	16.5	12	3	19	3	57	9	3	3	0	2.05.E+07	9.18.E+06	1.36.E+07	1.17.E+07	2.35.E+06	2.12.E+07	2.10.E+07	
1613	P08559	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial [OS=Homo sapiens]	16.5	20	5	24	5	54	14	5	5	0	3.33.E+07	3.90.E+07	3.34.E+07	2.92.E+07	5.10.E+07	3.79.E+07	1.01.E+08	3.45.E+07
1614	Q15050	Ribosome biogenesis regulatory protein homolog [OS=Homo sapiens]	16.5	17	3	50	3	189	47	3	2	0	6.23.E+07	8.19.E+07	8.15.E+07	7.78.E+07	1.14.E+08	8.47.E+07	9.43.E+07	8.78.E+07
1615	Q99447-1	ethanolamine-phosphate cytidylyltransferase [OS=Homo sapiens]	16.5	9	2	80	2	950	68	2	2	0	2.80.E+07	2.87.E+07	2.85.E+07	2.75.E+07	1.71.E+07	1.71.E+07	1.56.E+07	1.63.E+07
1616	O95456	Proteasome assembly chaperone 1 [OS=Homo sapiens]	16.4	19	3	26	3	189	13	2	3	0	1.09.E+07	7.31.E+06	9.91.E+06	1.35.E+07	3.13.E+07	2.10.E+07	2.59.E+07	2.33.E+07
1617	Q96DI7	U5 small nuclear ribonucleoprotein 40 kDa protein [OS=Homo sapiens]	16.4	15	3	45	3	80	9	3	3	0	4.44.E+07	3.82.E+07	4.54.E+07	4.41.E+07	4.23.E+07	4.35.E+07	4.69.E+07	4.50.E+07
1618	Q15003	Condensin complex subunit 2 [OS=Homo sapiens]	16.4	6	2	68	2	1172	103	2	2	0	3.09.E+07	1.53.E+07	1.39.E+07	2.74.E+07	3.15.E+07	1.24.E+07	1.14.E+07	2.99.E+07
1619	Q9P0J7	E3 ubiquitin-protein ligase KCMF1 [OS=Homo sapiens]	16.4	4	1	47	1	1035	57	1	1	0	8.83.E+06	9.26.E+06	7.61.E+06	8.38.E+06	1.59.E+07	1.29.E+07	1.17.E+07	1.42.E+07
1620	Q96CT7	Coiled-coil domain-containing protein 124 [OS=Homo sapiens]	16.4	16	2	37	2	298	50	2	2	0	4.27.E+06	7.68.E+07	6.16.E+07	6.31.E+07	9.04.E+07	8.99.E+07	8.03.E+07	1.28.E+07
1621	Q15785	Mitochondrial import receptor subunit TOM34 [OS=Homo sapiens]	16.3	11	2	49	2	567	30	2	2	0	3.26.E+07	3.21.E+07	2.87.E+07	3.25.E+07	4.36.E+07	3.31.E+07	3.59.E+07	4.11.E+07
1622	Q86XP3-1	ATP-dependent RNA helicase DDX42 [OS=Homo sapiens]	16.3	7	5	39	5	88	10	5	5	0	2.23.E+07	6.71.E+07	6.76.E+07	2.68.E+07	5.94.E+07	1.84.E+07	2.45.E+07	2.14.E+07
1623	P49750-4	Isoform 4 of YLP motif-containing protein 1 [OS=Homo sapiens]	16.3	4	5	53	5	139	11	5	5	0	5.81.E+07	7.07.E+07	6.93.E+07	7.44.E+07	7.46.E+07	9.64.E+07	9.77.E+07	9.13.E+07
1624	Q9UJ70	N-acetyl-D-glucosamine kinase [OS=Homo sapiens]	16.2	14	3	20	3	119	28	3	2	0	3.28.E+07	3.34.E+07	4.96.E+07	3.34.E+07	1.73.E+07	2.27.E+07	2.79.E+07	1.81.E+07
1625	Q13618	Cullin-3 [OS=Homo sapiens]	16.1	6	3	34	3	337	30	3	3	0	3.25.E+07	3.55.E+07	3.19.E+07	2.94.E+07	2.67.E+07	3.62.E+07	3.35.E+07	3.49.E+07

No.	Accession	Description	Sum PEP Score	Coverage [%]	# Peptides	# PSMs	# Unique Peptides	Score Mascot: A5 Mascot	Score Sequest HT: A2 Sequest HT	# Peptides (by Search Engine): A2 Sequest HT	# Peptides (by Search Engine): A5 Mascot	# Razor Peptides	ctrl Abundances_1	ctrl Abundances_2	ctrl Abundances_3	ctrl Abundances_4	JAM-A KO Abundances_1	JAM-A KO Abundances_2	JAM-A KO Abundances_3	JAM-A KO Abundances_4
1626	Q8TDD1	ATP-dependent RNA helicase DDX54 [OS=Homo sapiens]	16.1	7	3	50	3	115	15	3	3	0	2.99.E+07	3.05.E+07	2.15.E+07	3.14.E+07	1.09.E+07	1.40.E+07	1.81.E+07	1.40.E+07
1627	O00483	Cytochrome c oxidase subunit NDUFA4 [OS=Homo sapiens]	16.1	53	3	47	3	223	40	3	3	0	1.61.E+08	1.58.E+08	1.58.E+08	1.56.E+08	1.35.E+08	1.30.E+08	1.45.E+08	1.40.E+08
1628	Q9NX14-1	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11, mitochondrial [OS=Homo sapiens]	16.1	22	2	24	2	169	42	2	2	0	4.20.E+07	4.21.E+07	4.42.E+07	5.65.E+07	6.47.E+07	6.33.E+07	6.12.E+07	6.09.E+07
1629	Q9HCN8	Stromal cell-derived factor 2-like protein 1 [OS=Homo sapiens]	16.0	22	2	34	2	69	43	2	2	0	7.93.E+07	5.86.E+07	7.22.E+07	3.64.E+07	6.26.E+07	4.32.E+07	4.42.E+07	6.23.E+07
1630	Q13428-1	Treacle protein [OS=Homo sapiens]	16.0	3	3	20	3	107	14	3	3	0	1.93.E+07	3.64.E+07	2.69.E+07	1.99.E+07	2.48.E+07	1.18.E+07	6.75.E+07	1.24.E+07
1631	P62857	40S ribosomal protein S28 [OS=Homo sapiens]	16.0	30	2	214	2	4559	326	2	2	0	6.97.E+08	7.44.E+08	6.87.E+08	7.67.E+08	7.13.E+08	6.96.E+08	5.67.E+08	6.86.E+08
1632	Q13557	Calcium/calmodulin-dependent protein kinase type II subunit delta [OS=Homo sapiens]	16.0	10	4	29	4	247	27	4	3	0	7.72.E+07	6.72.E+07	6.92.E+07	8.90.E+07	6.80.E+07	8.69.E+07	6.48.E+07	9.51.E+07
1633	P09012	U1 SMALL NUCLEAR RIBONUCLEOPROTEIN A [OS=Homo sapiens]	16.0	13	3	156	2	1127	115	2	3	1	2.35.E+08	2.42.E+08	2.50.E+08	2.12.E+08	2.45.E+08	2.47.E+08	2.56.E+08	2.39.E+08
1634	Q00765	Receptor expression-enhancing protein 5 [OS=Homo sapiens]	15.9	15	4	71	4	165	42	4	4	0	2.39.E+08	1.87.E+08	2.32.E+08	2.07.E+08	1.61.E+08	1.96.E+08	2.25.E+08	1.88.E+08
1635	P42785-1	lysosomal Pro-X carboxypeptidase [OS=Homo sapiens]	15.9	8	2	26	2	159	3	2	2	0	1.32.E+07	1.55.E+07	1.38.E+07	1.52.E+07	2.26.E+07	1.96.E+07	1.67.E+07	1.86.E+07
1636	Q9H074	Polyadenylate-binding protein-interacting protein 1 [OS=Homo sapiens]	15.9	10	3	11	3	44	13	2	3	0	8.84.E+06	6.57.E+06	8.82.E+06	1.02.E+07	9.03.E+06	8.42.E+06	4.97.E+06	7.52.E+06
1637	Q9BZE1	39S ribosomal protein L37, mitochondrial [OS=Homo sapiens]	15.8	6	2	28	2	639	32	2	2	0	4.80.E+07	5.29.E+07	5.04.E+07	4.90.E+07	5.57.E+07	5.51.E+07	6.12.E+07	6.27.E+07
1638	P41227-1	N-alpha-acetyltransferase 10 [OS=Homo sapiens]	15.8	14	2	36	2	328	57	2	2	0	7.02.E+07	3.96.E+07	6.62.E+07	7.93.E+07	7.17.E+07	6.03.E+07	6.46.E+07	6.36.E+07
1639	Q6P1J9	Parafibromin [OS=Homo sapiens]	15.8	7	3	43	3	299	41	2	3	0	2.07.E+07	1.99.E+07	1.19.E+07	2.88.E+07	2.26.E+07	2.60.E+07	1.87.E+07	2.82.E+07
1640	Q9Y5L0-2	transportin-3 [OS=Homo sapiens]	15.7	7	3	54	3	845	73	3	2	0	5.60.E+07	1.86.E+07	3.16.E+07	1.64.E+07	1.38.E+07	2.28.E+07	2.83.E+07	2.95.E+07
1641	P06454-1	Prothymosin alpha [OS=Homo sapiens]	15.7	24	2	181	2	8224	0	1	2	0	3.75.E+08	4.54.E+08	4.31.E+08	3.65.E+08	5.39.E+08	4.60.E+08	4.11.E+08	3.44.E+08
1642	Q13630	GDP-L-fucose synthase [OS=Homo sapiens]	15.7	13	3	14	3	57	13	3	3	0	7.81.E+07	7.01.E+07	6.70.E+07	6.71.E+07	6.82.E+07	7.36.E+07	6.88.E+07	6.18.E+07
1643	Q16643	drebrin [OS=Homo sapiens]	15.6	8	3	29	3	291	18	3	3	0	2.57.E+07	2.36.E+07	2.56.E+07	3.23.E+07	2.41.E+07	2.81.E+07	2.14.E+07	2.82.E+07
1644	Q9NVM6	DnaJ homolog subfamily C member 17 [OS=Homo sapiens]	15.6	7	1	56	1	1477	93	1	1	0	1.45.E+07	1.48.E+07	1.36.E+07	1.47.E+07	1.45.E+07	1.41.E+07	1.16.E+07	1.26.E+07
1645	Q7Z7E8-1	Ubiquitin-conjugating enzyme E2 Q1 [OS=Homo sapiens]	15.6	7	1	32	1	616	46	1	1	0	1.87.E+07	2.26.E+07	1.85.E+07	2.38.E+07	2.79.E+07	2.76.E+07	2.36.E+07	2.74.E+07
1646	P29353	SHC-transforming protein 1 [OS=Homo sapiens]	15.6	4	1	90	1	2751	166	1	1	0	3.27.E+07	1.97.E+07	2.90.E+07	2.30.E+07	1.70.E+07	1.61.E+07	1.38.E+07	1.63.E+07
1647	Q96GC9	Vacuole membrane protein 1 [OS=Homo sapiens]	15.6	7	1	40	1	640	60	1	1	0	1.44.E+07	1.60.E+07	1.19.E+07	1.38.E+07	3.09.E+07	2.73.E+07	2.57.E+07	3.07.E+07
1648	Q15651-1	High mobility group nucleosome-binding domain-containing protein 3 [OS=Homo sapiens]	15.6	15	1	63	1	54	40	1	1	0	2.65.E+07	2.57.E+07	2.82.E+07	2.33.E+07	1.47.E+07	1.62.E+07	1.62.E+07	1.54.E+07
1649	P17676	CCAAT/enhancer-binding protein beta [OS=Homo sapiens]	15.6	5	1	34	1	636	50	1	1	0	7.58.E+06	7.67.E+06	7.06.E+06	7.31.E+06	1.44.E+07	1.33.E+07	1.29.E+07	1.43.E+07
1650	P60602-1	Reactive oxygen species modulator 1 [OS=Homo sapiens]	15.6	22	1	39	1	2796			1	0	8.91.E+07	9.36.E+07	8.69.E+07	9.20.E+07	1.06.E+08	1.08.E+08	9.79.E+07	9.91.E+07
1651	O76071	Probable cytosolic iron-sulfur protein assembly protein Ciao1 [OS=Homo sapiens]	15.5	14	3	25	3	386	30	3	2	0	7.73.E+07	5.65.E+07	3.85.E+07	7.59.E+07	3.00.E+07	4.63.E+07	4.10.E+07	3.90.E+07
1652	P36954	DNA-directed RNA polymerase II subunit RPB9 [OS=Homo sapiens]	15.5	18	1	26	1	835	51	1	1	0	2.40.E+07	1.93.E+07	1.92.E+07	2.53.E+07	2.22.E+07	2.36.E+07	1.86.E+07	2.24.E+07
1653	Q15643	Thyroid receptor-interacting protein 11 [OS=Homo sapiens]	15.4	3	2	14	2	54	14	2	2	0	1.35.E+06	2.12.E+07	1.89.E+06	2.02.E+07	2.88.E+07	1.79.E+07	1.89.E+07	2.60.E+07
1654	Q8WVC0-1	RNA polymerase-associated protein LEO1 [OS=Homo sapiens]	15.4	6	3	47	3	258	4	3	3	0	2.43.E+07	2.47.E+07	2.42.E+07	2.34.E+07	3.00.E+07	2.71.E+07	2.52.E+07	2.91.E+07
1655	Q9H3N1	Thioredoxin-related transmembrane protein 1 [OS=Homo sapiens]	15.3	17	4	84	4	102	36	4	4	0	8.36.E+07	9.43.E+07	8.97.E+07	8.78.E+07	1.17.E+08	1.38.E+08	1.02.E+08	1.28.E+08
1656	Q8WVJ2	NudC domain-containing protein 2 [OS=Homo sapiens]	15.3	11	1	4	1	144	6	1	1	0	3.43.E+06	5.10.E+06	6.34.E+06	6.28.E+06	5.95.E+06	1.09.E+07	1.20.E+07	8.62.E+06
1657	P56134	ATP synthase subunit f, mitochondrial [OS=Homo sapiens]	15.3	26	2	114	2	1204	119	2	2	0	9.63.E+07	1.24.E+08	8.20.E+07	1.09.E+08	1.23.E+08	1.30.E+08	9.88.E+07	1.17.E+08
1658	Q92504	Zinc transporter SLC39A7 [OS=Homo sapiens]	15.3	10	2	47	2	681	65	2	1	0	2.81.E+07	2.62.E+07	2.42.E+07	1.71.E+07	3.58.E+07	2.96.E+07	2.47.E+07	2.97.E+07
1659	Q96HQ2-1	CDKN2AIP N-terminal-like protein [OS=Homo sapiens]	15.3	16	1	6	1	164	10	1	1	0								
1660	Q13404	Ubiquitin-conjugating enzyme E2 variant 1 [OS=Homo sapiens]	15.3	28	5	116	5	638	95	5	5	0	3.26.E+08	3.17.E+08	3.45.E+08	2.98.E+08	4.63.E+08	4.55.E+08	4.98.E+08	4.47.E+08
1661	Q16831	uridine phosphorylase 1 [OS=Homo sapiens]	15.2	13	3	21	3	166	6	2	3	0	5.36.E+06	2.49.E+07	2.51.E+07	6.12.E+06	2.38.E+07	2.37.E+07	2.47.E+07	4.30.E+06
1662	Q9BV86-1	N-terminal Xaa-Pro-Lys N-methyltransferase 1 [OS=Homo sapiens]	15.2	16	3	25	3	255	10	2	3	0	2.16.E+07	2.69.E+07	2.48.E+07	2.01.E+07	2.57.E+07	2.88.E+07	2.04.E+07	2.22.E+07
1663	P46087	Probable 28S rRNA (cytosine(4447)-C(5))-methyltransferase [OS=Homo sapiens]	15.1	9	3	65	3	110	79	3	3	0	1.18.E+07	8.96.E+06	1.41.E+07	1.66.E+07	1.05.E+06	4.38.E+06	7.59.E+06	4.53.E+06
1664	Q8WW12	PEST proteolytic signal-containing nuclear protein [OS=Homo sapiens]	15.1	21	3	39	3	586	36	3	3	0	2.87.E+07	2.67.E+07	3.05.E+07	3.21.E+07	2.98.E+07	3.30.E+07	3.69.E+07	3.17.E+07
1665	Q9NUQ9	protein FAM49B [OS=Homo sapiens]	15.1	21	3	42	3	194	33	3	3	0	2.13.E+07	3.46.E+07	2.35.E+07	1.83.E+07	5.47.E+07	5.36.E+07	5.61.E+07	5.65.E+07
1666	Q8NFF5	FAD synthase [OS=Homo sapiens]	15.0	7	2	30	2	507	16	2	2	0	2.36.E+07	2.37.E+07	2.32.E+07	2.85.E+07	1.32.E+07	1.15.E+07	1.32.E+07	1.47.E+07
1667	P46939	Utrophin [OS=Homo sapiens]	15.0	2	3	42	3	444	46	3	3	0	1.25.E+07	1.91.E+07	1.26.E+07	1.47.E+07	2.21.E+07	1.59.E+07	1.15.E+07	1.68.E+07
1668	Q96HR8	H/ACA ribonucleoprotein complex non-core subunit NAF1 [OS=Homo sapiens]	15.0	6	2	39	2	253	12	2	2	0	1.12.E+07	1.30.E+07	1.01.E+07	1.27.E+07	1.06.E+07	9.50.E+06	7.48.E+06	1.01.E+07
1669	P09234	U1 small nuclear ribonucleoprotein C [OS=Homo sapiens]	15.0	11	1	22	1	537	33	1	1	0	4.57.E+07	4.81.E+07	4.31.E+07	4.43.E+07	5.68.E+07	5.45.E+07	5.60.E+07	5.65.E+07
1670	Q8N122	Regulatory-associated protein of mTOR [OS=Homo sapiens]	15.0	2	2	42	2	901	42	2	2	0	1.16.E+07	1.85.E+07	1.29.E+07	1.78.E+07	1.24.E+07	9.90.E+06	9.16.E+06	7.94.E+06
1671	O00411	DNA-directed RNA polymerase, mitochondrial [OS=Homo sapiens]	15.0	2	2	34	2	267	29	2	2	0	2.00.E+07	2.32.E+07	2.01.E+07	2.01.E+07	1.01.E+07	7.38.E+06	6.02.E+06	9.47.E+06
1672	P15374	Ubiquitin carboxyl-terminal hydrolase isozyme L3 [OS=Homo sapiens]	14.9	16	2	32	2	415	35	2	2	0	2.33.E+07	1.94.E+07	1.67.E+07	1.87.E+07	2.62.E+07	2.71.E+07	2.81.E+07	2.61.E+07
1673	O60610-1	Protein diaphanous homolog 1 [OS=Homo sapiens]	14.9	2	2	18	2	175	10	2	2	0	2.37.E+07	1.95.E+07	1.99.E+07	1.91.E+07	1.37.E+07	1.91.E+07	1.87.E+07	1.75.E+07
1674	Q15424-1	Scaffold attachment factor B1 [OS=Homo sapiens]	14.9	3	3	96	3	484	83	3	3	0	9.00.E+07	1.32.E+08	1.19.E+08	1.20.E+08	1.47.E+08	1.35.E+08	1.92.E+08	1.51.E+08
1675	O43678	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2 [OS=Homo sapiens]	14.9	21	1	2	1	93	4	1	1	0	9.92.E+06	1.25.E+07	8.75.E+06	8.92.E+06	1.13.E+07	1.10.E+07	1.14.E+07	1.01.E+07

No.	Accession	Description	Sum PEP Score	Coverage [%]	# Peptides	# PSMs	# Unique Peptides	Score Mascot: A5 Mascot	Score Sequest HT: A2 Sequest HT	# Peptides (by Search Engine): A2 Sequest HT	# Peptides (by Search Engine): A5 Mascot	# Razor Peptides	ctrl Abundances_1	ctrl Abundances_2	ctrl Abundances_3	ctrl Abundances_4	JAM-A KO Abundances_1	JAM-A KO Abundances_2	JAM-A KO Abundances_3	JAM-A KO Abundances_4
1676	Q96A49	Synapse-associated protein 1 [OS=Homo sapiens]	14.9	9	2	30	2	239	34	2	2	0	8.89.E+06	1.69.E+07	8.85.E+06	1.03.E+07	4.27.E+07	4.04.E+07	3.74.E+07	4.18.E+07
1677	P26358-1	DNA (cytosine-5)-methyltransferase 1 [OS=Homo sapiens]	14.9	4	4	20	4	62	24	4	4	0	3.93.E+07	4.35.E+07	2.04.E+07	4.06.E+07	2.50.E+07	2.30.E+07	4.44.E+07	2.32.E+07
1678	P13674-1	prolyl 4-hydroxylase subunit alpha-1 [OS=Homo sapiens]	14.8	7	3	16	3	157	12	3	3	0	1.32.E+07	1.33.E+07	1.51.E+07	1.02.E+07	3.04.E+07	2.83.E+07	2.86.E+07	2.62.E+07
1679	Q9Y4Z0	U6 snRNA-associated Sm-like protein LSm4 [OS=Homo sapiens]	14.8	17	2	36	2	90	28	2	2	0	2.20.E+07	2.66.E+07	9.22.E+06	2.68.E+07	1.49.E+07	3.68.E+07	2.24.E+07	1.59.E+07
1680	P49792	E3 SUMO-protein ligase RanBP2 [OS=Homo sapiens]	14.7	2	4	10	4	76	6	4	4	0	2.30.E+07	3.15.E+07	2.45.E+07	2.70.E+07	2.86.E+07	3.51.E+07	2.19.E+07	3.29.E+07
1681	P40222	alpha-taxilin [OS=Homo sapiens]	14.7	10	2	10	2	100	13	2	2	0	1.49.E+07	2.10.E+07	1.25.E+07	1.53.E+07	1.80.E+07	3.73.E+07	1.62.E+07	2.52.E+07
1682	Q5JTZ9	alanine--tRNA ligase, mitochondrial [OS=Homo sapiens]	14.7	4	2	18	2	229	25	2	2	0	1.14.E+07	1.05.E+07	6.02.E+06	9.19.E+06	2.21.E+06	4.31.E+06	1.08.E+06	3.75.E+06
1683	Q9Y6Y8	SEC23-interacting protein [OS=Homo sapiens]	14.7	5	2	34	2	133	51	2	2	0	3.44.E+07	4.11.E+07	3.86.E+07	4.03.E+07	5.72.E+07	6.04.E+07	5.10.E+07	5.87.E+07
1684	O75844	caax prenyl protease 1 homolog [OS=Homo sapiens]	14.6	5	2	22	2	122	25	2	2	0	2.68.E+07	2.74.E+07	2.64.E+07	2.67.E+07	3.29.E+07	3.04.E+07	2.01.E+07	3.17.E+07
1685	Q01970-1	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-3 [OS=Homo sapiens]	14.6	3	2	12	2	284	12	2	2	0	5.95.E+06	4.85.E+06	6.74.E+06	5.01.E+06	8.00.E+06	3.16.E+06	1.75.E+07	7.92.E+06
1686	Q9NZN4	EH domain-containing protein 2 [OS=Homo sapiens]	14.6	6	3	44	2	384	31	3	3	0	1.79.E+07	1.77.E+07	1.88.E+07	1.61.E+07	4.03.E+06	9.76.E+06	1.10.E+07	7.69.E+06
1687	Q8NCG7	Sn1-specific diacylglycerol lipase beta [OS=Homo sapiens]	14.6	8	3	8	3	94	6	3	3	0	6.31.E+06	8.74.E+06	5.71.E+06	8.13.E+06	1.20.E+07	8.60.E+06	7.98.E+06	8.49.E+06
1688	P14927	Cytochrome b-c1 complex subunit 7 [OS=Homo sapiens]	14.6	52	3	22	3	46	33	3	3	0	6.69.E+07	7.62.E+07	6.53.E+07	6.69.E+07	3.29.E+07	2.28.E+07	1.88.E+07	2.72.E+07
1689	Q8WX92	Negative elongation factor B [OS=Homo sapiens]	14.5	5	2	44	2	564	37	2	2	0	1.91.E+07	1.71.E+07	1.63.E+07	1.99.E+07	2.04.E+07	1.86.E+07	1.76.E+07	1.77.E+07
1690	Q9UI26	Importin-11 [OS=Homo sapiens]	14.5	6	3	80	3	408	13	3	3	0	1.32.E+07	4.63.E+06	1.25.E+07	7.39.E+06	2.38.E+07	2.59.E+07	2.29.E+07	2.20.E+07
1691	Q9Y3C6	Peptidyl-prolyl cis-trans isomerase-like 1 [OS=Homo sapiens]	14.5	37	3	15	3	41	8	2	3	0	6.96.E+07	6.28.E+07	6.40.E+07	5.85.E+07	7.47.E+07	7.39.E+07	8.03.E+07	7.53.E+07
1692	Q8NDC0	MAPK-interacting and spindle-stabilizing protein-like OS=Homo sapiens OX=9606 GN=MAPK1IP1L PE=1 SV=4	14.5	7	1	30	1	1448			1	0	3.58.E+07	3.97.E+07	3.50.E+07	3.25.E+07	4.72.E+07	5.17.E+07	4.48.E+07	4.58.E+07
1693	Q15738	sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating [OS=Homo sapiens]	14.5	11	2	30	2	358	3	2	2	0	1.41.E+07	1.24.E+07	1.49.E+07	1.43.E+07	2.03.E+07	1.64.E+07	1.50.E+07	1.59.E+07
1694	Q6ZXV5	Transmembrane and TPR repeat-containing protein 3 [OS=Homo sapiens]	14.4	3	2	32	2	340	10	2	2	0	7.98.E+06	1.21.E+07	1.30.E+07	1.40.E+07	1.68.E+07	1.54.E+07	1.29.E+07	1.67.E+07
1695	Q6UW68	Transmembrane protein 205 [OS=Homo sapiens]	14.4	24	2	8	2	88	8	2	2	0	2.74.E+07	3.25.E+07	2.48.E+07	3.55.E+07	2.63.E+07	2.56.E+07	2.75.E+07	2.82.E+07
1696	Q7Z4V5	Hepatoma-derived growth factor-related protein 2 [OS=Homo sapiens]	14.4	4	2	28	2	323	25	1	2	0	3.55.E+07	3.52.E+07	3.93.E+07	3.63.E+07	4.89.E+07	4.84.E+07	5.00.E+07	5.08.E+07
1697	Q04941-1	proteolipid protein 2 [OS=Homo sapiens]	14.4	18	2	113	2	1854	163	2	2	0	8.89.E+07	9.57.E+07	9.08.E+07	8.39.E+07	5.39.E+07	5.35.E+07	5.22.E+07	5.40.E+07
1698	Q05519	serine/arginine-rich splicing factor 11 [OS=Homo sapiens]	14.3	5	2	98	2	625	91	2	2	0	7.60.E+07	7.58.E+07	7.98.E+07	7.65.E+07	7.97.E+07	8.69.E+07	6.56.E+07	8.00.E+07
1699	Q5UIP0	Telomere-associated protein RIF1 [OS=Homo sapiens]	14.3	2	3	11	3	80	3	3	2	0	1.33.E+07	1.57.E+07	1.27.E+07	1.54.E+07	1.11.E+07	9.60.E+06	8.45.E+06	1.13.E+07
1700	Q9Y512	sorting and assembly machinery component 50 homolog [OS=Homo sapiens]	14.3	7	3	46	3	313	50	3	3	0	5.23.E+07	4.81.E+07	4.80.E+07	4.41.E+07	5.42.E+07	6.47.E+07	5.91.E+07	5.57.E+07
1701	Q9NXH9-1	tRNA (guanine(26)-N(2))-dimethyltransferase [OS=Homo sapiens]	14.3	4	1	48	1	910	69	1	1	0	2.29.E+07	1.84.E+07	1.92.E+07	2.27.E+07	1.60.E+07	1.36.E+07	2.06.E+07	1.11.E+07
1702	Q9H307	Pinin [OS=Homo sapiens]	14.3	5	3	38	3		93	3		0	5.37.E+07	5.55.E+07	4.98.E+07	5.35.E+07	5.77.E+07	5.61.E+07	3.77.E+07	5.03.E+07
1703	Q9Y2A7-1	Nck-associated protein 1 [OS=Homo sapiens]	14.3	2	1	54	1	510	73	1	1	0	3.60.E+07	2.12.E+07	3.83.E+07	1.75.E+07	1.78.E+07	1.99.E+07	8.13.E+06	3.05.E+07
1704	Q8TCD5	5'(3')-deoxyribonucleotidase, cytosolic type [OS=Homo sapiens]	14.3	19	2	36	2	285	32	2	2	0	3.21.E+07	3.33.E+07	2.87.E+07	2.87.E+07	2.87.E+07	2.92.E+07	2.93.E+07	2.64.E+07
1705	Q99986	Serine/threonine-protein kinase VRK1 [OS=Homo sapiens]	14.2	9	3	6	3	30	6	3	3	0	3.63.E+07	3.63.E+07	6.15.E+07	5.67.E+07	9.82.E+07	6.03.E+07	9.61.E+07	9.11.E+07
1706	Q9H7B2	Ribosome production factor 2 homolog [OS=Homo sapiens]	14.2	15	4	24	4	85	8	4	4	0	3.22.E+07	3.41.E+07	2.88.E+07	2.41.E+07	1.68.E+07	2.87.E+07	1.25.E+07	1.99.E+07
1707	O95202-1	mitochondrial proton/calcium exchanger protein [OS=Homo sapiens]	14.1	9	4	51	4	80	23	4	4	0	7.82.E+07	8.82.E+07	5.83.E+07	7.93.E+07	6.64.E+07	6.47.E+07	5.60.E+07	6.46.E+07
1708	Q13751	Laminin subunit beta-3 [OS=Homo sapiens]	14.1	2	1	60	1	1760	91	1	1	0	1.19.E+07	9.29.E+06	1.02.E+07	1.03.E+07	8.15.E+06	7.46.E+06	7.10.E+06	7.78.E+06
1709	Q9Y2U8	inner nuclear membrane protein Man1 [OS=Homo sapiens]	14.1	7	4	10	4	51	5	4	3	0	5.12.E+07	4.89.E+07	4.96.E+07	4.23.E+07	3.82.E+07	4.08.E+07	4.89.E+07	3.49.E+07
1710	O43172-1	U4/U6 small nuclear ribonucleoprotein Prp4 [OS=Homo sapiens]	14.1	8	3	6	3	44	5	3	2	0	4.54.E+07	3.03.E+07	3.30.E+07	3.05.E+07	2.65.E+07	2.46.E+07	2.93.E+07	2.39.E+07
1711	Q9Y241	HIG1 domain family member 1A, mitochondrial [OS=Homo sapiens]	14.0	47	2	8	2	162	0	1	2	0	1.55.E+07	1.45.E+07	1.34.E+07	1.62.E+07	1.50.E+07	1.29.E+07	1.37.E+07	1.70.E+07
1712	Q9Y2V2	Calcium-regulated heat-stable protein 1 [OS=Homo sapiens]	14.0	11	1	46	1	621	84	1	1	0	4.88.E+07	5.08.E+07	5.59.E+07	4.71.E+07	7.98.E+07	8.50.E+07	8.27.E+07	8.15.E+07
1713	Q9Y5Y2	Cytosolic Fe-S cluster assembly factor NUBP2 [OS=Homo sapiens]	14.0	20	2	30	2	184	37	2	2	0	3.27.E+07	3.42.E+07	2.07.E+07	3.05.E+07	4.83.E+07	4.72.E+07	3.95.E+07	4.25.E+07
1714	Q9H0D6-1	5'-3' exoribonuclease 2 [OS=Homo sapiens]	14.0	7	4	15	4	24	14	3	4	0	3.85.E+07	5.54.E+07	5.31.E+07	4.85.E+07	6.52.E+07	6.25.E+07	5.54.E+07	5.82.E+07
1715	P61421	V-type proton ATPase subunit d 1 [OS=Homo sapiens]	14.0	15	3	13	3	68	9	3	2	0	1.73.E+08	1.71.E+08	1.67.E+08	1.94.E+08	2.61.E+08	2.23.E+08	2.41.E+08	2.33.E+08
1716	Q8NE86	Calcium uniporter protein, mitochondrial [OS=Homo sapiens]	14.0	10	2	36	2	607	33	2	2	0	1.90.E+07	2.11.E+07	1.81.E+07	2.16.E+07	1.89.E+07	1.91.E+07	1.55.E+07	1.87.E+07
1717	Q9NPJ3-1	Acyl-coenzyme A thioesterase 13 [OS=Homo sapiens]	14.0	31	3	74	3	907	95	3	1	0	2.08.E+08	2.30.E+08	2.78.E+08	2.26.E+08	2.99.E+08	3.88.E+08	3.65.E+08	3.81.E+08
1718	Q9NX40	OCIA domain-containing protein 1 [OS=Homo sapiens]	13.9	11	2	26	2	375	26	2	2	0	6.17.E+07	6.35.E+07	5.99.E+07	6.74.E+07	8.09.E+07	6.60.E+07	7.34.E+07	7.15.E+07
1719	P49959	Double-strand break repair protein MRE11 [OS=Homo sapiens]	13.9	5	2	10	2	46	11	2	2	0	1.35.E+07	1.09.E+07	1.07.E+07	1.92.E+07	1.90.E+07	2.31.E+07	1.76.E+07	2.01.E+07
1720	Q13247	Serine/arginine-rich splicing factor 6 [OS=Homo sapiens]	13.9	8	3	112	3	781	75	3	3	0	2.68.E+08	2.55.E+08	2.71.E+08	2.66.E+08	2.73.E+08	2.65.E+08	2.73.E+08	2.67.E+08
1721	Q9Y305-1	Acyl-coenzyme A thioesterase 9, mitochondrial [OS=Homo sapiens]	13.9	10	3	26	3	36	7	3	3	0	3.67.E+07	3.66.E+07	4.06.E+07	2.03.E+07	3.83.E+07	4.03.E+07	4.35.E+07	4.02.E+07
1722	Q15363	Transmembrane emp24 domain-containing protein 2 [OS=Homo sapiens]	13.9	11	2	40	2	341	38	2	2	0	8.44.E+07	8.32.E+07	8.10.E+07	8.56.E+07	8.65.E+07	8.25.E+07	6.44.E+07	7.59.E+07
1723	P82912-1	28S ribosomal protein S11, mitochondrial [OS=Homo sapiens]	13.8	28	3	12	3	72	9	3	3	0	6.64.E+07	3.47.E+07	4.69.E+07	6.90.E+07	3.63.E+07	3.54.E+07	3.66.E+07	6.34.E+07
1724	P01116	GTPase KRas [OS=Homo sapiens]	13.8	24	3	25	3	87	17	3	3	0	3.29.E+07	4.45.E+07	3.64.E+07	2.74.E+07	5.29.E+07	5.53.E+07	5.00.E+07	4.42.E+07
1725	Q13144	Translation initiation factor eIF-2B subunit epsilon [OS=Homo sapiens]	13.8	5	2	28	2	104	22	2	2	0	9.29.E+06	8.76.E+06	2.87.E+06	4.55.E+06	8.89.E+06	8.69.E+06	1.31.E+07	1.01.E+07
1726	O95758	polypyrimidine tract-binding protein 3 [OS=Homo sapiens]	13.8	10	4	107	2	439	103	3	4	0	1.94.E+07	1.78.E+07	1.79.E+07	1.36.E+07	1.67.E+07	1.81.E+07	2.07.E+07	1.60.E+07

No.	Accession	Description	Sum PEP Score	Coverage [%]	# Peptides	# PSMs	# Unique Peptides	Score Mascot: A5 Mascot	Score Sequest HT: A2 Sequest HT	# Peptides (by Search Engine): A2 Sequest HT	# Peptides (by Search Engine): A5 Mascot	# Razor Peptides	ctrl Abundances_1	ctrl Abundances_2	ctrl Abundances_3	ctrl Abundances_4	JAM-A KO Abundances_1	JAM-A KO Abundances_2	JAM-A KO Abundances_3	JAM-A KO Abundances_4
1727	Q9HAB8-1	phosphopantothenate--cysteine ligase [OS=Homo sapiens]	13.8	17	3	76	3	311	10	3	3	0	9.41.E+07	8.28.E+07	8.46.E+07	7.39.E+07	7.72.E+07	7.70.E+07	7.85.E+07	8.18.E+07
1728	P41223	Protein BUD31 homolog [OS=Homo sapiens]	13.7	21	2	89	2	418	44	2	2	0	2.40.E+07	2.17.E+07	2.78.E+07	2.22.E+07	1.85.E+07	2.01.E+07	5.48.E+07	5.65.E+07
1729	P30405	Peptidyl-prolyl cis-trans isomerase F, mitochondrial [OS=Homo sapiens]	13.7	30	4	83	4	49	14	3	3	0	8.18.E+07	7.47.E+07	7.90.E+07	8.44.E+07	1.06.E+08	9.49.E+07	8.94.E+07	9.90.E+07
1730	P55268	laminin subunit beta-2 [OS=Homo sapiens]	13.6	1	1	2	1	63	3	1	1	0	5.83.E+06	6.60.E+06	4.53.E+06	1.32.E+06	8.41.E+06	1.04.E+07	7.41.E+06	8.14.E+06
1731	O15160	DNA-directed RNA polymerases I and III subunit RPAC1 [OS=Homo sapiens]	13.6	9	2	23	2	298	25	2	2	0	4.36.E+07	4.59.E+07	4.34.E+07	3.90.E+07	4.77.E+07	4.89.E+07	5.33.E+07	5.64.E+07
1732	P20339	Ras-related protein Rab-5A [OS=Homo sapiens]	13.6	16	3	92	1	613	120	3	3	0								
1733	Q9P2I0	Cleavage and polyadenylation specificity factor subunit 2 [OS=Homo sapiens]	13.6	2	1	66	1	1773	75	1	1	0	9.04.E+06	8.99.E+06	7.93.E+06	9.11.E+06	5.15.E+06	4.79.E+06	4.06.E+06	5.60.E+06
1734	Q9NP58	ATP-binding cassette sub-family B member 6, mitochondrial [OS=Homo sapiens]	13.6	4	2	29	2	403	34	2	2	0	3.53.E+07	3.76.E+07	3.41.E+07	3.42.E+07	3.26.E+07	3.52.E+07	3.04.E+07	3.15.E+07
1735	Q04446	1,4-alpha-glucan-branching enzyme [OS=Homo sapiens]	13.6	6	3	36	3	285	25	3	3	0	3.64.E+07	4.37.E+07	4.42.E+07	4.59.E+07	3.20.E+07	5.32.E+07	2.74.E+07	2.95.E+07
1736	Q9UMS0	NFU1 iron-sulfur cluster scaffold homolog, mitochondrial [OS=Homo sapiens]	13.6	17	3	12	3	153	12	3	3	0	3.78.E+07	3.64.E+07	3.65.E+07	3.59.E+07	5.34.E+07	5.50.E+07	2.78.E+07	5.64.E+07
1737	Q14684	Ribosomal RNA processing protein 1 homolog B [OS=Homo sapiens]	13.5	3	2	30	2	205	14	2	2	0	1.10.E+07	1.04.E+07	8.70.E+06	9.64.E+06	9.79.E+06	1.05.E+07	8.77.E+06	9.44.E+06
1738	Q14160	protein scribble homolog [OS=Homo sapiens]	13.5	3	2	8	2	79	8	2	2	0	1.14.E+07	1.55.E+07	1.22.E+07	1.68.E+07	6.29.E+06	1.18.E+07	1.08.E+07	1.25.E+07
1739	P49593	Protein phosphatase 1F [OS=Homo sapiens]	13.4	8	2	44	2	389	20	2	2	0	1.13.E+07	1.54.E+07	9.33.E+06	1.22.E+07	2.01.E+07	1.26.E+07	1.43.E+07	1.36.E+07
1740	Q9Y2T2	ap-3 complex subunit mu-1 [OS=Homo sapiens]	13.4	8	2	24	2	216	37	2	2	0	2.80.E+07	2.89.E+07	2.27.E+07	2.72.E+07	3.51.E+07	3.56.E+07	3.25.E+07	3.72.E+07
1741	P18583-1	Protein SON [OS=Homo sapiens]	13.4	1	2	7	1	140	6	1	2	1	2.46.E+07	2.38.E+07	2.43.E+07	2.48.E+07	2.48.E+07	2.32.E+07	1.19.E+07	2.32.E+07
1742	Q08752	peptidyl-prolyl cis-trans isomerase D [OS=Homo sapiens]	13.4	7	2	11	2	223	16	2	1	0	4.16.E+07	4.16.E+07	4.11.E+07	4.80.E+07	4.97.E+07	5.05.E+07	4.85.E+07	4.79.E+07
1743	Q6RW13	Type-1 angiotensin II receptor-associated protein [OS=Homo sapiens]	13.4	14	1	8	1	224	13	1	1	0	9.49.E+06	1.16.E+07	8.92.E+06	1.24.E+07	1.59.E+07	1.87.E+07	1.60.E+07	1.60.E+07
1744	O75348	V-type proton ATPase subunit G 1 [OS=Homo sapiens]	13.4	31	2	16	2	121	23	2	2	0	2.56.E+07	3.05.E+07	2.48.E+07	3.20.E+07	3.73.E+07	2.35.E+07	2.68.E+07	1.79.E+07
1745	P40937-1	Replication factor C subunit 5 [OS=Homo sapiens]	13.3	9	2	37	2	647	45	2	1	0	2.33.E+07	2.83.E+07	2.34.E+07	3.21.E+07	3.79.E+07	3.41.E+07	3.34.E+07	3.63.E+07
1746	O43156	TELO2-interacting protein 1 homolog [OS=Homo sapiens]	13.3	3	2	44	2	504	5	2	2	0	7.00.E+06	1.13.E+07	1.09.E+07	1.08.E+07	1.01.E+07	8.01.E+06	1.55.E+07	8.75.E+06
1747	Q99808	Equilibrative nucleoside transporter 1 [OS=Homo sapiens]	13.3	3	1	86	1	1394	71	1	1	0	1.23.E+07	1.23.E+07	1.13.E+07	1.20.E+07	9.69.E+06	8.49.E+06	8.21.E+06	9.12.E+06
1748	Q6IN85	Serine/threonine-protein phosphatase 4 regulatory subunit 3A [OS=Homo sapiens]	13.2	4	2	8	2	121	8	2	2	0	1.95.E+07	2.28.E+07	1.62.E+07	2.28.E+07	1.92.E+07	1.40.E+07	1.22.E+07	1.93.E+07
1749	Q96IJ6	Mannose-1-phosphate guanyltransferase alpha [OS=Homo sapiens]	13.2	10	3	33	3	81	25	3	3	0	2.98.E+07	2.94.E+07	2.87.E+07	3.36.E+07	3.76.E+07	3.51.E+07	3.77.E+07	3.57.E+07
1750	Q9NWV4	UPF0587 protein C1orf123 [OS=Homo sapiens]	13.2	25	2	44	2	108	60	2	2	0	4.97.E+07	6.50.E+07	5.64.E+07	5.88.E+07	6.51.E+07	7.39.E+07	6.74.E+07	7.28.E+07
1751	Q86U38	Nucleolar protein 9 [OS=Homo sapiens]	13.2	8	2	16	2	252	17	2	2	0	9.36.E+06	9.89.E+06	1.46.E+07	1.46.E+07	2.54.E+07	8.37.E+06	9.76.E+06	9.90.E+05
1752	Q8NFJ5	Retinoic acid-induced protein 3 [OS=Homo sapiens]	13.2	10	1	18	1	250	36	1	1	0	2.66.E+07	3.29.E+07	2.38.E+07	3.26.E+07	4.57.E+07	4.49.E+07	3.25.E+07	3.88.E+07
1753	O00161	Synaptosomal-associated protein 23 [OS=Homo sapiens]	13.1	13	2	18	2	334	16	2	2	0	8.49.E+06	7.43.E+06	6.59.E+06	9.09.E+06	1.47.E+07	1.46.E+07	1.37.E+07	3.48.E+07
1754	Q9Y679-2	Isoform Short of Ancient ubiquitous protein 1 [OS=Homo sapiens]	13.1	9	1	40	1	362	62	1	1	0	2.05.E+07	2.08.E+07	2.03.E+07	2.53.E+07	2.53.E+07	2.19.E+07	1.45.E+07	2.18.E+07
1755	P40938	replication factor C subunit 3 [OS=Homo sapiens]	13.1	12	3	24	3	141	16	3	3	0	2.64.E+07	2.41.E+07	2.41.E+07	2.48.E+07	3.72.E+07	3.59.E+07	2.54.E+07	3.57.E+07
1756	Q9P287	BRCA2 and CDKN1A-interacting protein [OS=Homo sapiens]	13.1	12	2	14	2	24	39	2	1	0								
1757	O15511-1	Actin-related protein 2/3 complex subunit 5 [OS=Homo sapiens]	13.1	23	1	6	1	85	12	1	1	0	1.58.E+07	1.74.E+07	1.53.E+07	1.41.E+07	2.88.E+07	2.44.E+07	2.70.E+07	3.20.E+07
1758	Q14669-1	E3 ubiquitin-protein ligase TRIP12 [OS=Homo sapiens]	13.0	2	2	26	2	282	11	2	2	0	1.07.E+07	1.29.E+07	8.28.E+06	1.21.E+07	1.49.E+07	1.45.E+07	1.26.E+07	1.54.E+07
1759	Q92896	Golgi apparatus protein 1 [OS=Homo sapiens]	13.0	3	2	28	2	432	28	2	2	0	1.57.E+07	9.61.E+06	1.58.E+07	1.40.E+07	2.44.E+07	1.40.E+07	2.27.E+07	2.40.E+07
1760	P51114-1	Fragile X mental retardation syndrome-related protein 1 [OS=Homo sapiens]	13.0	2	1	42	1	929	42	1	1	0	9.98.E+06	1.05.E+07	8.34.E+06	8.69.E+06	3.11.E+06	4.73.E+06	3.71.E+06	3.92.E+06
1761	Q8TF42	ubiquitin-associated and SH3 domain-containing protein B [OS=Homo sapiens]	13.0	6	2	16	2	195	14	2	2	0	1.29.E+07	1.22.E+07	1.07.E+07	1.26.E+07	2.32.E+07	2.15.E+07	1.95.E+07	2.11.E+07
1762	O94822	E3 ubiquitin-protein ligase listerin [OS=Homo sapiens]	13.0	4	4	22	4	64	6	4	4	0	5.03.E+07	5.61.E+07	5.31.E+07	6.17.E+07	5.48.E+07	5.86.E+07	5.25.E+07	6.60.E+07
1763	Q2TAY7	WD40 repeat-containing protein SMU1 [OS=Homo sapiens]	12.9	9	3	12	3	43	6	3	3	0	5.30.E+06	3.76.E+06	5.36.E+06	1.95.E+07	2.15.E+07	2.04.E+07	2.15.E+07	1.90.E+07
1764	O15027-1	Protein transport protein Sec16A [OS=Homo sapiens]	12.9	1	1	34	1	745	46	1	1	0	9.41.E+06	8.66.E+06	8.66.E+06	9.20.E+06	7.63.E+06	7.05.E+06	6.96.E+06	6.77.E+06
1765	Q9BY32-1	Inosine triphosphate pyrophosphatase [OS=Homo sapiens]	12.8	17	2	42	2	559	51	2	2	0	3.79.E+07	4.38.E+07	3.69.E+07	4.07.E+07	6.36.E+07	6.29.E+07	5.88.E+07	6.01.E+07
1766	Q9NQP4	Prefoldin subunit 4 [OS=Homo sapiens]	12.8	20	2	58	2	729	74	2	2	0	6.14.E+07	6.76.E+07	5.69.E+07	5.85.E+07	8.06.E+07	8.14.E+07	7.69.E+07	8.35.E+07
1767	Q9Y3B7-1	39S ribosomal protein L11, mitochondrial [OS=Homo sapiens]	12.8	16	2	22	2	128	27	2	2	0	3.34.E+07	3.64.E+07	3.58.E+07	3.37.E+07	2.58.E+07	2.92.E+07	2.89.E+07	2.74.E+07
1768	Q8N183	Mimitin, mitochondrial [OS=Homo sapiens]	12.8	11	1	12	1	262	16	1	1	0	7.79.E+06	6.97.E+06	6.94.E+06	8.57.E+06	9.66.E+06	9.46.E+06	6.27.E+06	8.55.E+06
1769	Q9Y276	Mitochondrial chaperone BCS1 [OS=Homo sapiens]	12.8	9	2	28	2	302	13	2	2	0	1.31.E+07	2.06.E+07	2.50.E+07	4.32.E+06		1.22.E+07	1.05.E+07	1.36.E+07
1770	Q01658	Protein Dr1 [OS=Homo sapiens]	12.8	27	2	8	2	63	9	2	2	0	2.42.E+07	3.16.E+07	1.99.E+07	3.09.E+07	2.70.E+07	3.01.E+07	2.48.E+07	3.51.E+07
1771	P05114	Non-histone chromosomal protein HMG-14 [OS=Homo sapiens]	12.8	48	2	14	2	169	6	2	2	0	1.31.E+07	1.32.E+07	1.44.E+07	8.18.E+06	1.92.E+07	2.03.E+07	2.04.E+07	2.14.E+07
1772	O95487-1	Protein transport protein Sec24B [OS=Homo sapiens]	12.7	2	3	33	3	204	2	3	3	0	1.08.E+07	1.09.E+07	1.08.E+07	1.12.E+07	1.42.E+07	1.12.E+07	1.16.E+07	1.35.E+07
1773	P39210	Protein Mpv17 [OS=Homo sapiens]	12.7	13	1	13	1	184	14	1	1	0	1.18.E+07	3.70.E+06	5.95.E+06	5.74.E+06	5.26.E+06	1.23.E+07	9.29.E+06	
1774	Q9NVS9	Pyridoxine-5'-phosphate oxidase [OS=Homo sapiens]	12.7	16	2	12	2	204	14	2	2	0	1.51.E+07	1.69.E+07	1.36.E+07	6.55.E+06	2.11.E+07	2.52.E+07	1.86.E+07	1.88.E+07
1775	Q9H3Z4	DnaJ homolog subfamily C member 5 [OS=Homo sapiens]	12.7	16	2	67	2	184	5	2	2	0	3.72.E+07	3.48.E+07	3.82.E+07	3.74.E+07	2.94.E+07	3.11.E+07	3.23.E+07	2.93.E+07
1776	P00374	dihydrofolate reductase [OS=Homo sapiens]	12.7	12	2	44	2	410	33	2	2	0	9.13.E+07	8.71.E+07	8.73.E+07	7.67.E+07	8.87.E+07	9.36.E+07	9.27.E+07	9.42.E+07
1777	O00560-1	Syntenin-1 [OS=Homo sapiens]	12.6	11	1	4	1	99	8	1	1	0					1.72.E+07	1.67.E+07	1.20.E+07	1.90.E+07
1778	Q92696	geranylgeranyl transferase type-2 subunit alpha [OS=Homo sapiens]	12.6	8	2	20	2	145	8	2	2	0	7.21.E+06	8.16.E+06	7.17.E+06	8.59.E+06	5.62.E+06	4.67.E+06	4.37.E+06	5.49.E+06
1779	P00568	Adenylate kinase isoenzyme 1 [OS=Homo sapiens]	12.6	7	1	72	1	1021	42	1	1	0	1.57.E+07	1.59.E+07	1.30.E+07	1.66.E+07	1.14.E+07	1.05.E+07	9.20.E+06	1.06.E+07

No.	Accession	Description	Sum PEP Score	Coverage [%]	# Peptides	# PSMs	# Unique Peptides	Score Mascot: A5 Mascot	Score Sequest HT: A2 Sequest HT	# Peptides (by Search Engine): A2 Sequest HT	# Peptides (by Search Engine): A5 Mascot	# Razor Peptides	ctrl Abundance s_1	ctrl Abundance s_2	ctrl Abundance s_3	ctrl Abundance s_4	JAM-A KO Abundance s_1	JAM-A KO Abundance s_2	JAM-A KO Abundance s_3	JAM-A KO Abundance s_4
1780	Q9BV44	THUMP domain-containing protein 3 [OS=Homo sapiens]	12.6	7	2	46	2	514	50	2	2	0	3.41.E+07	3.60.E+07	2.55.E+07	3.36.E+07	3.67.E+07	4.00.E+07	3.06.E+07	3.58.E+07
1781	Q6WCQ1	Myosin phosphatase Rho-interacting protein [OS=Homo sapiens]	12.6	3	2	10	2	147	12	2	2	0	3.88.E+07	3.99.E+07	3.22.E+07	3.70.E+07		3.41.E+06	6.30.E+06	
1782	Q96A65	Exocyst complex component 4 [OS=Homo sapiens]	12.6	5	3	26	3	54	2	3	3	0	1.10.E+07	9.85.E+06	1.07.E+07	8.74.E+06	1.78.E+07	1.76.E+07	1.54.E+07	1.49.E+07
1783	Q15067	Peroxisomal acyl-coenzyme A oxidase 1 [OS=Homo sapiens]	12.6	8	3	32	3	111	33	3	3	0	2.26.E+07	2.12.E+07	1.74.E+07	2.37.E+07	1.38.E+07	1.18.E+07	1.03.E+07	1.10.E+07
1784	P35080-2	Isoform IIb of Profilin-2 [OS=Homo sapiens]	12.6	16	2	46	2		144	2		0	8.42.E+07	1.08.E+08	1.15.E+08	1.20.E+08	1.37.E+08	1.40.E+08	1.46.E+08	1.37.E+08
1785	P51784	Ubiquitin carboxyl-terminal hydrolase 11 [OS=Homo sapiens]	12.6	5	2	36	2	469	31	2	2	0	1.67.E+07	2.14.E+07	9.42.E+06	1.42.E+07	2.88.E+07	9.96.E+06		3.18.E+07
1786	O75323-1	Protein NipSnap homolog 2 [OS=Homo sapiens]	12.5	14	3	73	2	617	43	3	2	0	1.14.E+07	1.33.E+07	9.80.E+06	1.42.E+07	1.41.E+07	1.30.E+07	1.01.E+07	1.28.E+07
1787	Q9NY12-1	H/ACA ribonucleoprotein complex subunit 1 [OS=Homo sapiens]	12.5	16	3	57	3	23	45	3	3	0	1.28.E+08	1.28.E+08	1.35.E+08	1.28.E+08	1.39.E+08	1.35.E+08	1.04.E+08	1.29.E+08
1788	P52948-1	nuclear pore complex protein Nup98-Nup96 [OS=Homo sapiens]	12.5	2	2	6	2	57	8	2	2	0	1.19.E+07	1.40.E+07	1.22.E+07	2.20.E+07	1.54.E+07	2.22.E+07	1.42.E+07	1.49.E+07
1789	O95747	Serine/threonine-protein kinase OSR1 [OS=Homo sapiens]	12.5	4	2	22	2	352	17	2	2	0	4.62.E+07	4.94.E+07	4.80.E+07	4.64.E+07	3.96.E+07	4.01.E+07	3.68.E+07	3.47.E+07
1790	Q9NUJ1	Mycophenolic acid acyl-glucuronide esterase, mitochondrial [OS=Homo sapiens]	12.5	7	1	6	1	202	8	1	1	0	5.37.E+06	7.60.E+06	5.46.E+06	7.33.E+06	6.43.E+06	9.38.E+06	6.48.E+06	7.70.E+06
1791	Q96JJ7-1	Protein disulfide-isomerase TMX3 [OS=Homo sapiens]	12.5	6	1	2	1	42	4	1	1	0								
1792	Q9P0M9	39S ribosomal protein L27, mitochondrial [OS=Homo sapiens]	12.5	10	1	32	1	38	34	1	1	0	3.74.E+07	3.57.E+07	4.13.E+07	4.21.E+07	3.41.E+07	3.16.E+07	3.61.E+07	3.33.E+07
1793	O15498	Synaptobrevin homolog YKT6 [OS=Homo sapiens]	12.5	13	2	10	2	214	12	2	2	0	5.06.E+07	4.97.E+07	4.90.E+07	4.59.E+07	4.79.E+07	4.78.E+07	4.38.E+07	4.94.E+07
1794	Q9Y3D0	Mitotic spindle-associated MMXD complex subunit MIP18 [OS=Homo sapiens]	12.4	13	1	12	1	157	26	1	1	0	1.88.E+07	1.90.E+07	1.90.E+07	2.12.E+07	2.31.E+07	2.29.E+07	2.10.E+07	2.42.E+07
1795	Q13564-1	NEDD8-activating enzyme E1 regulatory subunit [OS=Homo sapiens]	12.4	6	2	8	2	133	12	2	2	0	2.05.E+07	2.44.E+07	2.18.E+07	2.63.E+07	2.97.E+07	2.57.E+07	2.76.E+07	3.20.E+07
1796	Q12824-1	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily B member 1 [OS=Homo sapiens]	12.3	8	2	24	2	242	28	2	2	0	3.64.E+07	3.70.E+07	3.30.E+07	3.26.E+07	3.64.E+07	4.10.E+07	3.67.E+07	4.06.E+07
1797	Q9NZB2-1	Constitutive coactivator of PPAR-gamma-like protein 1 [OS=Homo sapiens]	12.3	4	3	17	3	35	7	2	3	0	4.53.E+07	4.62.E+07	2.98.E+07	3.58.E+07	4.74.E+07	4.28.E+07	3.70.E+07	4.37.E+07
1798	P49770	Translation initiation factor eIF-2B subunit beta [OS=Homo sapiens]	12.3	9	1	10	1	187	17	1	1	0	1.05.E+07	1.15.E+07	1.00.E+07	1.03.E+07	1.23.E+06			
1799	Q6PI48	Aspartate--tRNA ligase, mitochondrial [OS=Homo sapiens]	12.3	9	4	42	4	304	35	4	3	0	3.34.E+07	3.18.E+07	3.62.E+07	3.16.E+07	6.70.E+07	6.14.E+07	4.03.E+07	6.13.E+07
1800	Q7Z5K2-1	Wings apart-like protein homolog [OS=Homo sapiens]	12.3	2	1	50	1	771	48	1	1	0	8.93.E+06	8.27.E+06	8.45.E+06	9.36.E+06	8.28.E+06	7.47.E+06	7.29.E+06	7.44.E+06
1801	Q13084	39S ribosomal protein L28, mitochondrial [OS=Homo sapiens]	12.3	20	3	44	3	401	45	3	3	0	2.43.E+07	2.55.E+07	2.21.E+07	1.83.E+07	3.10.E+07	2.62.E+07	2.63.E+07	2.61.E+07
1802	O75400	pre-mRNA-processing factor 40 homolog A [OS=Homo sapiens]	12.3	3	2	34	2	350	43	2	2	0	8.00.E+07	7.89.E+07	8.59.E+07	7.01.E+07	6.64.E+07	7.66.E+07	7.13.E+07	7.52.E+07
1803	Q9UHN6-1	Cell surface hyaluronidase [OS=Homo sapiens]	12.3	4	3	12	3	100	8	2	3	0	7.93.E+05	9.23.E+05	9.30.E+05	7.38.E+05	3.30.E+06	6.64.E+06	2.44.E+06	9.00.E+05
1804	P22830-1	Ferrochelatase, mitochondrial [OS=Homo sapiens]	12.2	8	3	41	3	124	15	3	3	0	7.13.E+07	6.53.E+07	7.20.E+07	7.99.E+07	9.64.E+07	9.57.E+07	1.09.E+08	1.02.E+08
1805	Q93008-3	Probable ubiquitin carboxyl-terminal hydrolase FAF-X [OS=Homo sapiens]	12.2	2	2	32	2	483	31	1	2	0	5.74.E+06	5.09.E+06	3.74.E+06	4.30.E+06	4.12.E+06	3.87.E+06	3.47.E+06	3.28.E+06
1806	Q12789-2	General transcription factor 3C polypeptide 1 [OS=Homo sapiens]	12.2	1	1	2	1	40	3	1	1	0	1.77.E+06	1.83.E+06	1.62.E+06	1.79.E+06				
1807	Q9NR50-1	Translation initiation factor eIF-2B subunit gamma [OS=Homo sapiens]	12.2	13	3	26	3	67	15	3	3	0	2.47.E+07	2.75.E+07	2.47.E+07	2.29.E+07	3.96.E+07	4.63.E+07	2.10.E+07	3.70.E+07
1808	P43304	Glycerol-3-phosphate dehydrogenase, mitochondrial [OS=Homo sapiens]	12.2	9	4	78	4	94	23	4	4	0	4.50.E+07	5.62.E+07	4.15.E+07	4.92.E+07	4.43.E+07	4.87.E+07	4.06.E+07	3.91.E+07
1809	Q9BY77	Polymerase delta-interacting protein 3 [OS=Homo sapiens]	12.2	9	2	14	2	287	19	2	2	0	1.10.E+07	1.36.E+07	1.20.E+07	1.13.E+07	1.59.E+07	1.71.E+07	1.28.E+07	1.65.E+07
1810	Q9BRP1	Programmed cell death protein 2-like [OS=Homo sapiens]	12.1	6	2	32	2	366	6	1	2	0	3.81.E+07	3.53.E+07	2.66.E+07	3.42.E+07	1.54.E+07	2.01.E+07	1.32.E+07	1.72.E+07
1811	Q6NUQ4	Transmembrane protein 214 [OS=Homo sapiens]	12.0	5	2	66	2	245	23	2	2	0	2.16.E+07	2.76.E+07	2.80.E+07	2.82.E+07	1.53.E+07	2.88.E+07	2.18.E+07	2.56.E+07
1812	Q8NHH9	Atlastin-2 [OS=Homo sapiens]	12.0	3	2	38	1	85	3	2	2	0	8.14.E+06	8.08.E+06	7.61.E+06	8.76.E+06	9.25.E+06	9.80.E+06	8.93.E+06	8.73.E+06
1813	P61966	AP-1 complex subunit sigma-1A [OS=Homo sapiens]	12.0	10	1	6	1	186	8	1	1	0	5.06.E+06	7.83.E+06	4.97.E+06	6.96.E+06	5.20.E+06	8.08.E+06	5.15.E+06	2.88.E+06
1814	Q6P2E9-1	Enhancer of mRNA-decapping protein 4 [OS=Homo sapiens]	12.0	3	2	18	2	88	7	2	2	0	9.23.E+07	6.99.E+07	7.65.E+07	4.64.E+07	6.11.E+07	7.45.E+07	6.81.E+07	7.71.E+07
1815	Q9Y520	Protein Prrc2c [OS=Homo sapiens]	12.0	3	4	28	4	27	0	4	4	0	7.65.E+06	6.88.E+06	7.21.E+06	8.32.E+06	8.44.E+06	9.09.E+06	8.66.E+06	8.70.E+06
1816	P62891	60S ribosomal protein L39 [OS=Homo sapiens]	12.0	20	1	128	1	502	159	1	1	0	4.07.E+08	3.46.E+08	3.93.E+08	2.99.E+08	3.35.E+08	3.55.E+08	4.26.E+08	3.71.E+08
1817	Q9BVJ6-1	U3 small nucleolar RNA-associated protein 14 homolog A [OS=Homo sapiens]	11.9	5	3	39	3	145	15	3	3	0	2.03.E+07	2.30.E+07	1.95.E+07	2.22.E+07	1.83.E+07	1.79.E+07	5.99.E+07	1.85.E+07
1818	Q9H223	EH domain-containing protein 4 [OS=Homo sapiens]	11.9	7	3	28	2	61	23	3	3	0	1.18.E+07	5.48.E+07	5.85.E+07	5.66.E+07	6.25.E+07	6.73.E+07	6.74.E+07	5.77.E+07
1819	Q8NEJ9	neuroguidin [OS=Homo sapiens]	11.9	6	1	34	1	1198			1	0	8.93.E+06	8.96.E+06	8.71.E+06	9.33.E+06	9.67.E+06	8.26.E+06	7.74.E+06	8.70.E+06
1820	Q9UNL2	Translocon-associated protein subunit gamma [OS=Homo sapiens]	11.9	8	1	52	1	2079	103	1	1	0	5.69.E+07	5.98.E+07	5.57.E+07	5.81.E+07	7.50.E+07	7.53.E+07	6.85.E+07	8.84.E+07
1821	O14907	Tax1-binding protein 3 [OS=Homo sapiens]	11.8	14	1	32	1	699	53	1	1	0	3.28.E+07	4.05.E+07	3.60.E+07	3.79.E+07	3.58.E+07	2.93.E+07	2.52.E+07	3.67.E+07
1822	Q86WQ0	nuclear receptor 2C2-associated protein [OS=Homo sapiens]	11.8	41	3	22	3	87	0	2	3	0	9.23.E+06	5.99.E+07	5.55.E+07	6.50.E+07	9.33.E+06	5.08.E+07	2.43.E+07	5.35.E+07
1823	P17612	cAMP-dependent protein kinase catalytic subunit alpha [OS=Homo sapiens]	11.8	10	2	58	2	655	49	2	2	0	2.39.E+07	2.65.E+07	3.98.E+07	3.92.E+07	3.05.E+07	4.20.E+07	2.51.E+07	4.12.E+07
1824	O95168-1	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4 [OS=Homo sapiens]	11.8	22	2	18	2	49	19	2	2	0	4.54.E+07	4.04.E+07	4.51.E+07	3.37.E+07	4.12.E+07	4.13.E+07	4.03.E+07	4.15.E+07
1825	Q6UB35-1	Monofunctional C1-tetrahydrofolate synthase, mitochondrial [OS=Homo sapiens]	11.8	4	2	10	2	88	8	2	2	0	9.45.E+06	7.96.E+06	4.65.E+06	1.26.E+07	1.01.E+07	9.87.E+06	8.39.E+06	5.16.E+06

No.	Accession	Description	Sum PEP Score	Coverage [%]	# Peptides	# PSMs	# Unique Peptides	Score Mascot: A5 Mascot	Score Sequest HT: A2 Sequest HT	# Peptides (by Search Engine): A2 Sequest HT	# Peptides (by Search Engine): A5 Mascot	# Razor Peptides	ctrl Abundances_1	ctrl Abundances_2	ctrl Abundances_3	ctrl Abundances_4	JAM-A KO Abundances_1	JAM-A KO Abundances_2	JAM-A KO Abundances_3	JAM-A KO Abundances_4
1826	Q16740	ATP-dependent Clp protease proteolytic subunit, mitochondrial [OS=Homo sapiens]	11.8	18	2	37	2	136	34	2	2	0	2.20.E+07	2.40.E+07	1.78.E+07	2.06.E+07	2.49.E+07	2.62.E+07	2.14.E+07	2.50.E+07
1827	P37198	nuclear pore glycoprotein p62 [OS=Homo sapiens]	11.7	6	2	20	2	169	12	2	2	0	2.11.E+07	2.34.E+07	1.92.E+07	2.20.E+07	2.68.E+07	2.67.E+07	2.38.E+07	2.48.E+07
1828	P62877	E3 ubiquitin-protein ligase RBX1 [OS=Homo sapiens]	11.7	18	1	2	1	116			1	0	9.03.E+06	9.81.E+06	1.20.E+07	1.49.E+07	6.91.E+06	8.29.E+06	7.09.E+06	6.42.E+06
1829	Q9H444	Charged multivesicular body protein 4b [OS=Homo sapiens]	11.7	16	3	20	3	69	6	3	2	0	4.13.E+07	3.98.E+07	4.31.E+07	4.21.E+07	3.41.E+07	3.60.E+07	4.32.E+07	3.58.E+07
1830	Q8TE77	Protein phosphatase Slingshot homolog 3 [OS=Homo sapiens]	11.7	5	2	8	2	40	6	2	2	0	1.58.E+07	1.68.E+07	1.27.E+07	1.29.E+07	1.87.E+07	1.82.E+07	1.08.E+07	1.50.E+07
1831	Q99961	Endophilin-A2 [OS=Homo sapiens]	11.7	9	3	49	3	237	44	3	3	0	8.04.E+07	7.62.E+07	8.01.E+07	8.89.E+07	8.09.E+07	6.24.E+07	8.43.E+07	8.37.E+07
1832	Q9NS86	lanC-like protein 2 [OS=Homo sapiens]	11.7	4	1	4	1	192	7	1	1	0	5.21.E+06	8.76.E+06	7.48.E+06	1.12.E+07	1.11.E+07	7.57.E+06	1.73.E+06	1.12.E+07
1833	P29992	guanine nucleotide-binding protein subunit alpha-11 [OS=Homo sapiens]	11.7	6	1	26	1	512	48	1	1	0	1.39.E+07	1.39.E+07	1.19.E+07	1.32.E+07	1.34.E+07	1.14.E+07	9.08.E+06	1.21.E+07
1834	Q9NZL9	Methionine adenosyltransferase 2 subunit beta [OS=Homo sapiens]	11.7	10	3	9	3	53	4	3	3	0	4.44.E+07	4.34.E+07	4.61.E+07	3.79.E+07	4.68.E+07	4.49.E+07	4.49.E+07	4.93.E+07
1835	Q15388	Mitochondrial import receptor subunit TOM20 homolog [OS=Homo sapiens]	11.7	30	1	26	1	179	39	1	1	0	2.70.E+07	2.92.E+07	2.00.E+07	2.53.E+07				7.28.E+05
1836	Q86X55	Histone-arginine methyltransferase CARM1 [OS=Homo sapiens]	11.6	3	1	25	1	256	41	1	1	0								
1837	O14964	Hepatocyte growth factor-regulated tyrosine kinase substrate [OS=Homo sapiens]	11.6	4	2	62	2	383	48	2	2	0	2.60.E+07	2.65.E+07	2.27.E+07	2.75.E+07	3.09.E+07	2.48.E+07	2.55.E+07	2.46.E+07
1838	P07305	Histone H1.0 [OS=Homo sapiens]	11.6	11	2	89	2	468	107	2	2	0	2.28.E+08	2.20.E+08	2.21.E+08	2.41.E+08	2.30.E+08	2.25.E+08	2.45.E+08	2.33.E+08
1839	Q12962	transcription initiation factor TFIID subunit 10 [OS=Homo sapiens]	11.6	11	1	4	1	147	5	1	1	0	2.89.E+06	4.39.E+06	1.49.E+06	4.91.E+06	6.34.E+06	6.24.E+06	6.01.E+06	5.26.E+06
1840	Q9NSP4-1	Centromere protein M [OS=Homo sapiens]	11.6	12	1	24	1	559	35	1	1	0	9.99.E+06	1.09.E+07	9.68.E+06	1.08.E+07	1.20.E+07	1.04.E+07	8.85.E+06	1.00.E+07
1841	O14949	Cytochrome b-c1 complex subunit 8 [OS=Homo sapiens]	11.6	35	3	80	3	392	12	2	3	0	8.93.E+07	8.15.E+07	9.71.E+07	9.99.E+07	8.46.E+07	7.57.E+07	9.22.E+07	7.75.E+07
1842	P62861	40S ribosomal protein S30 [OS=Homo sapiens]	11.6	19	2	149	2	1106	171	2	2	0	3.92.E+08	3.96.E+08	4.34.E+08	3.56.E+08	4.29.E+08	4.30.E+08	4.70.E+08	4.33.E+08
1843	Q9NYK5-1	39S ribosomal protein L39, mitochondrial [OS=Homo sapiens]	11.5	8	2	38	2	266	26	2	2	0	3.56.E+07	2.96.E+07	3.58.E+07	3.25.E+07	1.16.E+07	1.02.E+07	2.06.E+07	4.53.E+07
1844	Q9UIQ6-1	Leucyl-cystinyl aminopeptidase [OS=Homo sapiens]	11.5	2	2	13	2	155	9	2	1	0	4.34.E+06	4.95.E+06	5.24.E+06	5.10.E+06	9.19.E+06	8.05.E+06	8.65.E+06	8.90.E+06
1845	Q9Y6M9	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9 [OS=Homo sapiens]	11.5	22	3	32	3	219	2	2	3	0	3.61.E+07	9.41.E+07	7.93.E+07	8.06.E+07	9.26.E+07	9.69.E+07	8.32.E+07	8.80.E+07
1846	Q8NBF2-1	NHL repeat-containing protein 2 [OS=Homo sapiens]	11.5	9	3	19	3	47	7	3	3	0	1.21.E+07	1.09.E+07	9.81.E+06	1.03.E+07	4.89.E+06	5.81.E+06	4.72.E+06	2.20.E+06
1847	Q92905	COP9 signalosome complex subunit 5 [OS=Homo sapiens]	11.5	7	2	42	2	157	42	2	2	0	3.98.E+07	3.74.E+07	4.09.E+07	3.62.E+07	3.81.E+07	4.41.E+07	3.25.E+07	4.34.E+07
1848	P67812	Signal peptidase complex catalytic subunit SEC11A [OS=Homo sapiens]	11.5	11	2	100	2	975	95	2	2	0	1.15.E+08	1.12.E+08	1.12.E+08	1.03.E+08	1.08.E+08	1.10.E+08	9.67.E+07	1.08.E+08
1849	O14976	Cyclin-G-associated kinase [OS=Homo sapiens]	11.4	1	1	44	1	422	16	1	1	0	6.36.E+06	6.15.E+06	7.13.E+06	6.58.E+06	6.79.E+06	5.16.E+06	5.68.E+06	6.17.E+06
1850	Q9NQW7-1	xaa-Pro aminopeptidase 1 [OS=Homo sapiens]	11.4	4	2	35	2	279	24	2	2	0	1.79.E+07	1.73.E+07	8.58.E+06	7.80.E+06	2.36.E+07	2.05.E+07	1.63.E+07	2.17.E+07
1851	P24821	Tenascin [OS=Homo sapiens]	11.4	2	2	8	2	63	6	2	2	0	5.04.E+06	7.04.E+05	4.35.E+06	3.34.E+06	2.49.E+06	4.51.E+06	3.29.E+06	1.83.E+06
1852	O43583	density-regulated protein [OS=Homo sapiens]	11.4	21	3	49	3	203	23	2	3	0	1.55.E+08	1.23.E+08	1.19.E+08	1.38.E+08	1.43.E+08	1.44.E+08	1.47.E+08	1.38.E+08
1853	Q96S52	GPI transamidase component PIG-S [OS=Homo sapiens]	11.4	9	2	28	2	243	19	2	2	0	9.61.E+06	7.45.E+06	8.84.E+06	9.82.E+06	1.53.E+07	1.06.E+07	1.31.E+07	1.25.E+07
1854	Q15427	Splicing factor 3b subunit 4 [OS=Homo sapiens]	11.4	7	2	105	2	701	93	2	2	0	4.24.E+07	4.62.E+07	4.15.E+07	4.37.E+07	3.33.E+07	2.98.E+07	1.90.E+07	3.10.E+07
1855	Q9UKN8	General transcription factor 3C polypeptide 4 [OS=Homo sapiens]	11.4	3	2	12	2	236	12	2	2	0	4.58.E+06	2.45.E+06	2.06.E+06	1.70.E+06	1.55.E+06	1.21.E+06	1.16.E+06	1.08.E+06
1856	P19387	DNA-directed RNA polymerase II subunit RPB3 [OS=Homo sapiens]	11.4	13	2	42	2	200	32	2	2	0	2.03.E+07	2.19.E+07	2.06.E+07	2.32.E+07	2.30.E+07	2.31.E+07	1.91.E+07	1.98.E+07
1857	Q9UNE7-1	E3 ubiquitin-protein ligase CHIP [OS=Homo sapiens]	11.4	12	3	21	3	166	18	3	3	0	1.71.E+07	2.74.E+07	2.03.E+07	2.71.E+07	2.45.E+07	1.40.E+07	1.69.E+07	2.28.E+07
1858	Q9UHY1	Nuclear receptor-binding protein [OS=Homo sapiens]	11.4	5	2	16	2	79	4	2	2	0	6.45.E+06	8.77.E+06	8.11.E+06	9.02.E+06			5.10.E+06	
1859	Q15042-1	Rab3 GTPase-activating protein catalytic subunit [OS=Homo sapiens]	11.4	3	2	6	2	31	5	2	2	0	1.75.E+07	1.68.E+07	1.80.E+07	1.60.E+07	2.27.E+07	2.32.E+07	2.11.E+07	2.37.E+07
1860	O15344-1	E3 ubiquitin-protein ligase Midline-1 [OS=Homo sapiens]	11.4	6	3	30	3	101	4	3	3	0	1.31.E+07	1.32.E+07	1.19.E+07	1.42.E+07	2.43.E+07	9.07.E+06	1.81.E+07	1.83.E+07
1861	Q9NRP0-1	oligosaccharyltransferase complex subunit OSTC [OS=Homo sapiens]	11.4	8	1	64	1	1051	103	1	1	0	8.12.E+07	8.46.E+07	8.52.E+07	8.56.E+07	9.92.E+07	9.35.E+07	4.79.E+07	9.55.E+07
1862	Q9Y3B3-1	Transmembrane emp24 domain-containing protein 7 [OS=Homo sapiens]	11.3	10	2	64	2	225	79	2	2	0	6.07.E+07	5.56.E+07	5.64.E+07	5.87.E+07	5.77.E+07	5.46.E+07	6.55.E+07	6.44.E+07
1863	Q16698	2,4-dienoyl-CoA reductase, mitochondrial [OS=Homo sapiens]	11.3	9	3	29	3	13	15	3	3	0	1.03.E+08	7.54.E+07	1.05.E+08	6.72.E+07	9.30.E+07	8.43.E+07	1.26.E+08	1.21.E+08
1864	Q9BRG1	Vacuolar protein-sorting-associated protein 25 [OS=Homo sapiens]	11.3	21	3	64	3	706	69	3	3	0	3.56.E+07	4.16.E+07	3.86.E+07	3.68.E+07	6.26.E+07	5.78.E+07	5.35.E+07	5.84.E+07
1865	C9JLW8	Mapk-regulated corepressor-interacting protein 1 [OS=Homo sapiens]	11.3	23	2	34	2	81	10	2	2	0	7.09.E+07	8.52.E+07	2.26.E+07	6.84.E+07	7.86.E+07	8.38.E+07	5.39.E+07	7.78.E+07
1866	P57088	Transmembrane protein 33 [OS=Homo sapiens]	11.3	8	2	52	2	1070	81	2	2	0	9.76.E+07	1.63.E+08	9.91.E+07	1.52.E+08	1.01.E+08	1.01.E+08	9.86.E+07	1.08.E+08
1867	O43291	Kunitz-type protease inhibitor 2 [OS=Homo sapiens]	11.2	8	2	18	2	122	11	2	2	0	3.73.E+07	4.34.E+07	6.04.E+07	4.28.E+07	2.98.E+06	4.94.E+06	5.10.E+06	1.92.E+06
1868	Q96I59	probable asparagine--tRNA ligase, mitochondrial [OS=Homo sapiens]	11.2	4	1	20	1	289	24	1	1	0	2.08.E+07	3.89.E+07	4.23.E+07	4.56.E+07	3.10.E+07	3.14.E+07	2.97.E+07	2.93.E+07
1869	O75251	NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial [OS=Homo sapiens]	11.2	13	1	28	1	339	23	1	1	0	1.13.E+07	1.01.E+07	1.09.E+07	1.19.E+07	6.78.E+06	5.21.E+06	5.30.E+06	7.20.E+06
1870	Q15004-1	PCNA-associated factor [OS=Homo sapiens]	11.2	30	2	47	2	32	16	2	2	0	3.50.E+07	2.96.E+07	4.00.E+07	3.92.E+07	4.02.E+07	4.07.E+07	4.28.E+07	4.05.E+07
1871	Q8IWX8	Calcium homeostasis endoplasmic reticulum protein [OS=Homo sapiens]	11.2	4	2	18	2	145	12	2	2	0	3.45.E+07	3.38.E+07	3.60.E+07	3.23.E+07	3.71.E+07	2.92.E+07	3.11.E+07	3.81.E+07
1872	Q15654-1	thyroid receptor-interacting protein 6 [OS=Homo sapiens]	11.2	6	2	4	2	46	4	2	2	0	1.46.E+07	1.42.E+07	1.43.E+07	1.52.E+07	1.47.E+07	1.49.E+07	1.84.E+07	1.55.E+07

No.	Accession	Description	Sum PEP Score	Coverage [%]	# Peptides	# PSMs	# Unique Peptides	Score Mascot: A5 Mascot	Score Sequest HT: A2 Sequest HT	# Peptides (by Search Engine): A2 Sequest HT	# Peptides (by Search Engine): A5 Mascot	# Razor Peptides	ctrl Abundances_1	ctrl Abundances_2	ctrl Abundances_3	ctrl Abundances_4	JAM-A KO Abundances_1	JAM-A KO Abundances_2	JAM-A KO Abundances_3	JAM-A KO Abundances_4
1873	Q8N3C0	Activating signal cointegrator 1 complex subunit 3 [OS=Homo sapiens]	11.2	1	1	2	1	55	4	1	1	0	7.81.E+06	1.00.E+07	8.67.E+06	1.04.E+07				5.73.E+05
1874	P49458	Signal recognition particle 9 kDa protein [OS=Homo sapiens]	11.1	22	2	45	2	520	7	1	2	0	1.80.E+08	1.81.E+08	1.90.E+08	1.50.E+08	1.72.E+08	1.75.E+08	2.01.E+08	1.72.E+08
1875	Q96B26	Exosome complex component RRP43 [OS=Homo sapiens]	11.1	10	1	49	1	436	19	1	1	0	1.29.E+07	1.36.E+07	8.02.E+06	1.10.E+07	1.23.E+07	1.11.E+07	1.41.E+07	1.14.E+07
1876	P61803	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1 [OS=Homo sapiens]	11.1	19	2	10	2	116	12	2	2	0	1.00.E+08	1.22.E+08	1.06.E+08	1.06.E+08	1.38.E+08	1.35.E+08	1.31.E+08	1.34.E+08
1877	P16219	Short-chain specific acyl-CoA dehydrogenase, mitochondrial [OS=Homo sapiens]	11.1	6	1	24	1	556	24	1	1	0	9.26.E+06	7.84.E+06	7.45.E+06	6.45.E+06	4.14.E+06	5.67.E+06	4.72.E+06	5.36.E+06
1878	P05026	Sodium/potassium-transporting ATPase subunit beta-1 [OS=Homo sapiens]	11.1	8	2	98	2	761	95	2	2	0	9.50.E+07	8.96.E+07	9.94.E+07	1.00.E+08	9.21.E+07	9.00.E+07	9.46.E+07	8.91.E+07
1879	O00479	High mobility group nucleosome-binding domain-containing protein 4 [OS=Homo sapiens]	11.1	17	1	3	1	0			1	0								
1880	P11908	ribose-phosphate pyrophosphokinase 2 [OS=Homo sapiens]	11.1	7	2	44	2	191	18	2	2	0	3.16.E+07	1.86.E+07	3.27.E+07	1.62.E+07	3.87.E+07	4.42.E+07	4.48.E+07	4.08.E+07
1881	Q14061	cytochrome C oxidase copper chaperone [OS=Homo sapiens]	11.1	46	2	20	2	512	0	1	2	0	1.65.E+07	1.56.E+07	1.74.E+07	1.91.E+07	1.45.E+07	1.49.E+07	1.66.E+07	1.36.E+07
1882	Q9NZZ3	Charged multivesicular body protein 5 [OS=Homo sapiens]	11.1	16	2	38	2	250	38	2	2	0	1.75.E+07	3.53.E+07	3.14.E+07	3.61.E+07	4.99.E+07	6.05.E+07	4.71.E+07	4.98.E+07
1883	Q8NI36	WD repeat-containing protein 36 [OS=Homo sapiens]	11.0	8	4	18	4	39	8	4	4	0	2.76.E+07	2.70.E+07	2.42.E+07	2.88.E+07	2.71.E+07	2.46.E+07	2.45.E+07	2.79.E+07
1884	Q9NRF9	DNA polymerase epsilon subunit 3 [OS=Homo sapiens]	11.0	15	2	31	2	483	0	1	1	0	3.03.E+07	3.26.E+07	3.29.E+07	3.69.E+07	3.64.E+07	3.62.E+07	3.72.E+07	3.72.E+07
1885	Q9Y639-2	Neuroplastin [OS=Homo sapiens]	11.0	8	2	33	2	85	7	2	2	0	5.60.E+07	5.45.E+07	5.62.E+07	4.87.E+07	5.35.E+07	5.85.E+07	5.92.E+07	5.67.E+07
1886	P61964	WD repeat-containing protein 5 [OS=Homo sapiens]	11.0	8	2	15	2	51	13	2	2	0	7.51.E+06	2.09.E+07	2.29.E+07	2.35.E+07	2.75.E+07	2.08.E+07	2.24.E+07	2.62.E+07
1887	Q00577	Transcriptional activator protein Pur-alpha [OS=Homo sapiens]	11.0	8	1	14	1	193	22	1	1	0	6.67.E+06	1.22.E+07	1.47.E+07	1.30.E+07	1.20.E+07	1.84.E+07	9.55.E+06	9.58.E+06
1888	P35249	replication factor C subunit 4 [OS=Homo sapiens]	11.0	11	3	12	3	55	11	3	3	0	6.00.E+07	3.92.E+07	4.77.E+07	4.16.E+07	4.99.E+07	6.13.E+07	5.28.E+07	5.73.E+07
1889	O60306	Intron-binding protein aquarius [OS=Homo sapiens]	11.0	2	2	4	2	65	3	2	2	0	1.04.E+07	1.23.E+07	8.92.E+06	1.44.E+07	1.50.E+07	1.26.E+07	1.19.E+07	1.43.E+07
1890	Q86Y56	Dynein assembly factor 5, axonemal [OS=Homo sapiens]	10.9	3	2	6	2	99	5	2	2	0	1.96.E+07	1.20.E+07	1.07.E+07	1.55.E+07	1.74.E+07	9.71.E+06	2.57.E+07	2.15.E+07
1891	Q9NTZ6	RNA-binding protein 12 [OS=Homo sapiens]	10.9	4	4	22	4	0	3	4	4	0	1.92.E+08	1.73.E+08	1.94.E+08	1.81.E+08	4.04.E+08	4.11.E+08	4.10.E+08	4.01.E+08
1892	Q96LD4	Tripartite motif-containing protein 47 [OS=Homo sapiens]	10.9	3	1	15	1	258	9	1	1	0	6.27.E+06	4.85.E+06	5.63.E+06	4.19.E+06	4.68.E+06	3.49.E+06	4.18.E+06	3.46.E+06
1893	Q16537	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit epsilon isoform [OS=Homo sapiens]	10.9	7	3	16	2	35	6	3	3	0	1.59.E+07	1.44.E+07	1.60.E+07	1.34.E+07	1.43.E+07	1.61.E+07	1.96.E+07	1.37.E+07
1894	Q14657	EKC/KEOPS complex subunit LAGE3 [OS=Homo sapiens]	10.9	16	1	36	1	390	50	1	1	0	1.94.E+07	1.72.E+07	2.09.E+07	2.21.E+07	1.87.E+07	1.88.E+07	2.23.E+07	2.09.E+07
1895	Q96EY7-1	pentatricopeptide repeat domain-containing protein 3, mitochondrial [OS=Homo sapiens]	10.8	6	2	9	2	39	2	2	2	0	2.02.E+07	1.55.E+07	1.83.E+07	2.68.E+07	1.75.E+07	1.93.E+07	2.14.E+07	2.41.E+07
1896	P62875	DNA-directed RNA polymerases I, II, and III subunit RPABC5 [OS=Homo sapiens]	10.8	45	1	10	1	128	16	1	1	0	7.34.E+06	9.27.E+06	8.02.E+06	7.71.E+06			2.76.E+06	3.69.E+06
1897	Q9Y2Q5	Ragulator complex protein LAMTOR2 [OS=Homo sapiens]	10.8	12	1	2	1	76	4	1	1	0								
1898	Q14192	Four and a half LIM domains protein 2 [OS=Homo sapiens]	10.8	24	4	27	4	37	2	4	3	0	1.50.E+07	1.76.E+07	1.66.E+07	1.31.E+07	2.49.E+07	2.44.E+07	2.49.E+07	2.57.E+07
1899	P10398-1	serine/threonine-protein kinase A-Raf [OS=Homo sapiens]	10.7	3	1	24	1	425	35	1	1	0	1.34.E+07	1.43.E+07	1.36.E+07	6.92.E+06	1.89.E+07	1.67.E+07	1.39.E+07	1.51.E+07
1900	P54687	Branched-chain-amino-acid aminotransferase, cytosolic [OS=Homo sapiens]	10.7	13	2	62	2	550	37	2	2	0	1.80.E+07	1.99.E+07	1.62.E+07	1.85.E+07	2.34.E+07	2.18.E+07	1.91.E+07	2.16.E+07
1901	P57740	Nuclear pore complex protein Nup107 [OS=Homo sapiens]	10.7	5	3	34	3	121	5	2	3	0	7.65.E+06	1.54.E+07	6.90.E+06	1.64.E+07	2.18.E+07	2.05.E+07	1.95.E+07	5.56.E+06
1902	O00267	Transcription elongation factor Spt5 [OS=Homo sapiens]	10.7	2	2	24	2	48	20	2	2	0	1.74.E+07	1.35.E+07	1.51.E+07	1.69.E+07	9.90.E+06	1.17.E+07	9.55.E+06	1.42.E+07
1903	Q9NUP9	Protein lin-7 homolog C [OS=Homo sapiens]	10.6	11	2	46	2	347	50	2	2	0	8.78.E+07	8.40.E+07	6.36.E+07	6.27.E+07	9.39.E+07	6.23.E+07	1.02.E+08	5.74.E+07
1904	Q9H2M9	Rab3 GTPase-activating protein non-catalytic subunit [OS=Homo sapiens]	10.6	2	2	18	2	63	9	2	2	0	9.04.E+06	8.67.E+06	1.08.E+07	1.38.E+07	2.12.E+07	1.64.E+07	1.46.E+07	2.05.E+07
1905	P46937-1	Transcriptional coactivator YAP1 [OS=Homo sapiens]	10.6	7	2	39	2	162	41	2	2	0	5.64.E+07	4.27.E+07	3.45.E+07	4.38.E+07	4.59.E+07	4.60.E+07	4.49.E+07	4.29.E+07
1906	P51553-1	isocitrate dehydrogenase [NAD] subunit gamma, mitochondrial [OS=Homo sapiens]	10.6	5	2	36	2	96	47	2	2	0	5.37.E+07	5.63.E+07	5.54.E+07	5.51.E+07	5.49.E+07	5.23.E+07	5.97.E+07	5.82.E+07
1907	P31937	3-hydroxyisobutyrate dehydrogenase, mitochondrial [OS=Homo sapiens]	10.6	4	1	6	1	106	11	1	1	0	1.62.E+07	1.97.E+07	1.64.E+07	1.68.E+07	2.13.E+07	2.68.E+07	1.89.E+07	2.06.E+07
1908	Q07812	Apoptosis regulator BAX [OS=Homo sapiens]	10.6	7	1	44	1	987	82	1	1	0	3.89.E+07	4.44.E+07	4.38.E+07	4.61.E+07	4.61.E+07	3.86.E+07	1.25.E+07	3.30.E+07
1909	O60493-1	sorting nexin-3 [OS=Homo sapiens]	10.6	15	3	110	2	100	49	3	3	1	1.00.E+08	9.72.E+07	1.07.E+08	8.54.E+07	9.37.E+07	1.02.E+08	1.15.E+08	1.04.E+08
1910	P84095	Rho-related GTP-binding protein RhoG [OS=Homo sapiens]	10.6	13	2	20	1	130	23	2	2	0								
1911	O60344-4	Isoform D of Endothelin-converting enzyme 2 [OS=Homo sapiens]	10.6	13	1	22	1	217	25	1	1	0	9.40.E+06	1.07.E+07	9.02.E+06	1.09.E+07	1.14.E+07	1.02.E+07	9.98.E+06	1.12.E+07
1912	Q14CX7-1	N-alpha-acetyltransferase 25, NatB auxiliary subunit [OS=Homo sapiens]	10.6	2	2	12	2	140	7	2	2	0	1.62.E+07	1.96.E+07	1.57.E+07	1.81.E+07	1.71.E+07	1.80.E+07	1.36.E+07	1.83.E+07
1913	O60573	eukaryotic translation initiation factor 4E type 2 [OS=Homo sapiens]	10.6	11	2	28	2	217	2	2	2	0	1.86.E+07	1.86.E+07	2.05.E+07	1.61.E+07	1.51.E+07	1.56.E+07	1.49.E+07	1.70.E+07
1914	P82930	28S ribosomal protein S34, mitochondrial [OS=Homo sapiens]	10.5	11	2	52	2	441	30	2	2	0	2.75.E+07	2.85.E+07	2.79.E+07	2.62.E+07	1.61.E+07	1.63.E+07	1.69.E+07	1.51.E+07
1915	Q9NVI1-3	Fanconi anemia group I protein [OS=Homo sapiens]	10.5	2	3	58	2	335	11	3	2	0	4.86.E+06	6.10.E+06	4.61.E+06	7.79.E+06	1.69.E+07	1.53.E+07	1.27.E+07	1.41.E+07
1916	O60925	prefoldin subunit 1 [OS=Homo sapiens]	10.5	17	2	42	2	308	29	2	2	0	9.73.E+07	8.82.E+07	9.75.E+07	1.08.E+08	8.55.E+07	8.34.E+07	8.22.E+07	8.24.E+07
1917	P53801	pituitary tumor-transforming gene 1 protein-interacting protein [OS=Homo sapiens]	10.5	10	1	56	1	725	75	1	1	0	5.14.E+07	1.91.E+07	6.22.E+07	4.01.E+07	8.96.E+07	5.84.E+07	8.63.E+07	3.71.E+07
1918	A0FGR8-1	Extended synaptotagmin-2 [OS=Homo sapiens]	10.5	6	3	22	3	38	11	3	3	0	2.52.E+07	1.72.E+07	1.17.E+07	1.61.E+07	2.90.E+07	2.61.E+07	2.51.E+07	3.97.E+07
1919	Q9UBI6	guanine nucleotide-binding protein g(i)/g(s)/g(o) subunit gamma-12 [OS=Homo sapiens]	10.5	22	1	24	1	230	46	1	1	0	6.52.E+07	5.83.E+07	5.78.E+07	6.93.E+07	5.12.E+07	5.42.E+07	3.55.E+07	5.56.E+07
1920	A5YKK6	CCR4-NOT transcription complex subunit 1 [OS=Homo sapiens]	10.5	1	2	8	2	95	10	2	2	0	1.55.E+07	1.64.E+07	1.49.E+07	2.07.E+07	2.17.E+07	2.25.E+07	1.83.E+07	2.04.E+07
1921	Q05D32	CTD small phosphatase-like protein 2 [OS=Homo sapiens]	10.5	6	2	20	2	60	2	2	2	0	1.74.E+07	1.82.E+07	1.70.E+07	1.73.E+07	1.64.E+07	1.78.E+07	1.91.E+07	1.98.E+07

No.	Accession	Description	Sum PEP Score	Coverage [%]	# Peptides	# PSMs	# Unique Peptides	Score Mascot: A5 Mascot	Score Sequest HT: A2 Sequest HT	# Peptides (by Search Engine): A2 Sequest HT	# Peptides (by Search Engine): A5 Mascot	# Razor Peptides	ctrl Abundances_1	ctrl Abundances_2	ctrl Abundances_3	ctrl Abundances_4	JAM-A KO Abundances_1	JAM-A KO Abundances_2	JAM-A KO Abundances_3	JAM-A KO Abundances_4
1922	Q9NX62	Inositol monophosphatase 3 [OS=Homo sapiens]	10.4	7	1	20	1	182	24	1	1	0	1.05.E+07	1.12.E+07	9.53.E+06	1.06.E+07	1.43.E+07	1.57.E+07	1.24.E+07	8.55.E+06
1923	Q9Y4Y9	U6 snRNA-associated Sm-like protein LSm5 OS=Homo sapiens OX=9606 GN=LSM5 PE=1 SV=3	10.4	21	1	21	1	315			1	0	1.92.E+07	2.34.E+07	1.84.E+07	2.26.E+07	3.90.E+07	4.01.E+07	3.40.E+07	3.51.E+07
1924	P55039	Developmentally-regulated GTP-binding protein 2 [OS=Homo sapiens]	10.4	8	2	14	2	108	11	2	2	0	9.86.E+06	9.44.E+06	1.07.E+07	9.19.E+06	1.25.E+07	1.14.E+07	1.16.E+07	1.09.E+07
1925	Q3MHD2	Protein LSM12 homolog [OS=Homo sapiens]	10.4	12	1	48	1	686	37	1	1	0	1.38.E+07	1.61.E+07	1.26.E+07	1.64.E+07	1.37.E+07	2.21.E+07	2.17.E+07	2.41.E+07
1926	Q9Y221-1	60S ribosome subunit biogenesis protein NIP7 homolog [OS=Homo sapiens]	10.3	21	2	17	2	114	24	2	1	0	4.14.E+07	4.45.E+07	4.55.E+07	3.87.E+07	3.29.E+07	4.43.E+07	4.60.E+07	4.46.E+07
1927	P57081-1	tRNA (guanine-N(7)-)-methyltransferase non-catalytic subunit WDR4 [OS=Homo sapiens]	10.3	8	2	8	2	169	9	2	2	0	2.32.E+07	2.76.E+07	2.47.E+07	2.56.E+07	2.43.E+07	2.95.E+07	2.56.E+07	2.42.E+07
1928	Q86X29	Lipolysis-stimulated lipoprotein receptor [OS=Homo sapiens]	10.3	4	2	39	2	463	35	2	2	0	2.70.E+07	2.89.E+07	2.84.E+07	2.44.E+07	2.46.E+07	4.71.E+06	2.31.E+07	2.83.E+07
1929	Q9NR56-1	Muscleblind-like protein 1 [OS=Homo sapiens]	10.3	8	2	13	2	34	15	2	2	0	2.97.E+07	3.03.E+07	3.08.E+07	3.04.E+07	2.54.E+07	2.70.E+07	2.02.E+07	2.57.E+07
1930	Q9Y3A6-1	Transmembrane emp24 domain-containing protein 5 [OS=Homo sapiens]	10.3	10	1	16	1	247	4	1	1	0	1.06.E+07	1.05.E+07	9.91.E+06	9.65.E+06	4.86.E+06	3.30.E+06	2.97.E+06	3.75.E+06
1931	Q9NWW5	ceroid-lipofuscinosis neuronal protein 6 [OS=Homo sapiens]	10.3	7	1	18	1	110	38	1	1	0	2.27.E+07	2.76.E+07	2.32.E+07	2.09.E+07	3.29.E+07	3.41.E+07	3.68.E+07	3.28.E+07
1932	Q969S3	Zinc finger protein 622 [OS=Homo sapiens]	10.3	3	1	36	1	713	52	1	1	0	4.92.E+06	5.46.E+06	3.61.E+06	5.30.E+06	9.11.E+06	7.94.E+06	6.40.E+06	9.27.E+06
1933	Q13242	serine/arginine-rich splicing factor 9 [OS=Homo sapiens]	10.3	15	3	46	3	105	37	3	3	0	5.49.E+07	5.40.E+07	5.48.E+07	5.10.E+07	5.87.E+07	6.83.E+07	6.58.E+07	6.47.E+07
1934	Q9H9Q4-1	non-homologous end-joining factor 1 [OS=Homo sapiens]	10.2	7	1	46	1	243	21	1	1	0	1.72.E+07	1.92.E+07	1.73.E+07	2.06.E+07	1.10.E+07	1.28.E+07	1.23.E+07	1.01.E+07
1935	P35269	General transcription factor iif subunit 1 [OS=Homo sapiens]	10.2	3	1	2	1	91			1	0	6.93.E+06	8.26.E+06	7.72.E+06	8.59.E+06	1.36.E+07	1.25.E+07	1.14.E+07	1.27.E+07
1936	Q8WWY3	U4/U6 small nuclear ribonucleoprotein Prp31 [OS=Homo sapiens]	10.2	3	1	36	1	443	41	1	1	0	2.14.E+07	2.58.E+07	2.03.E+07	4.14.E+06	2.35.E+07	2.26.E+07	1.13.E+07	1.54.E+07
1937	Q8NFH5	Nucleoporin NUP53 [OS=Homo sapiens]	10.2	6	1	4	1	99	6	1	1	0	5.26.E+06	5.76.E+06	1.57.E+06	5.94.E+06	9.68.E+06	1.03.E+07	5.94.E+06	1.25.E+07
1938	Q9UIG0	Tyrosine-protein kinase BAZ1B [OS=Homo sapiens]	10.1	3	3	16	3	21	2	3	3	0	3.47.E+07	3.28.E+07	3.49.E+07	2.94.E+07	3.10.E+07	2.83.E+07	2.66.E+07	3.14.E+07
1939	P48960-1	CD97 antigen [OS=Homo sapiens]	10.1	2	1	46	1	712	13	1	1	0	1.21.E+07	1.34.E+07	1.09.E+07	1.54.E+07	1.29.E+07	1.21.E+07	9.09.E+06	1.18.E+07
1940	Q08499-1	cAMP-specific 3',5'-cyclic phosphodiesterase 4D [OS=Homo sapiens]	10.1	3	1	14	1	189	27	1	1	0	1.15.E+07	1.31.E+07	1.14.E+07	1.46.E+07	1.05.E+07	2.21.E+07	1.06.E+07	1.19.E+07
1941	Q9H299	SH3 domain-binding glutamic acid-rich-like protein 3 [OS=Homo sapiens]	10.1	31	2	36	2	187	52	2	2	0	3.55.E+07	3.76.E+07	4.41.E+07	3.19.E+06	3.59.E+07	3.46.E+07	4.11.E+07	3.91.E+07
1942	Q8WZA0	Protein LZIC [OS=Homo sapiens]	10.1	12	1	12	1	254	9	1	1	0	7.18.E+06	6.12.E+06	5.74.E+06	4.21.E+06	1.47.E+07	1.09.E+07	1.11.E+07	1.25.E+07
1943	P37235	Hippocalcin-like protein 1 [OS=Homo sapiens]	10.0	9	2	78	2	334	71	2	2	0	6.83.E+07	6.59.E+07	6.84.E+07	6.21.E+07	1.22.E+08	1.26.E+08	1.36.E+08	1.38.E+08
1944	Q9NWS0-1	PIH1 domain-containing protein 1 [OS=Homo sapiens]	10.0	18	2	6	2	39	3	2	2	0	2.15.E+07	2.11.E+07	2.13.E+07	2.30.E+07	2.89.E+07	2.75.E+07	2.20.E+07	2.64.E+07
1945	Q96P48-6	Arf-GAP with Rho-GAP domain, ANK repeat and PH domain-containing protein 1 [OS=Homo sapiens]	10.0	1	1	3	1	116			1	0		7.97.E+06	5.31.E+06	5.74.E+06	3.72.E+06	2.93.E+06	2.55.E+06	1.91.E+06
1946	Q9P253	Vacuolar protein sorting-associated protein 18 homolog [OS=Homo sapiens]	10.0	4	2	38	2	126	14	2	2	0	1.54.E+07	1.98.E+07	1.62.E+07	1.42.E+07	1.44.E+07	1.16.E+07	2.48.E+07	1.83.E+07
1947	Q9Y5J7	Mitochondrial import inner membrane translocase subunit Tim9 [OS=Homo sapiens]	10.0	30	2	28	2	160	20	2	2	0	3.03.E+07	3.14.E+07	3.08.E+07	2.59.E+07	2.66.E+07	3.07.E+07	2.94.E+07	3.10.E+07
1948	O95159	Zinc finger protein-like 1 [OS=Homo sapiens]	10.0	10	3	22	3	31	8	3	3	0	7.10.E+07	6.54.E+07	6.91.E+07	7.74.E+07	7.80.E+07	6.82.E+07	7.72.E+07	6.79.E+07
1949	Q14643-1	Inositol 1,4,5-trisphosphate receptor type 1 [OS=Homo sapiens]	10.0	1	2	16	2	163	7	2	2	0	9.03.E+06	6.78.E+06	9.04.E+06	6.90.E+06	1.71.E+07	1.92.E+07	1.58.E+07	1.65.E+07
1950	Q00169	Phosphatidylinositol transfer protein alpha isoform [OS=Homo sapiens]	10.0	11	4	86	1	158	72	4	3	0	7.83.E+07	5.21.E+07	6.96.E+07	8.77.E+07	5.13.E+07	5.84.E+07	7.17.E+07	6.38.E+07
1951	P83881	60S ribosomal protein L36a [OS=Homo sapiens]	9.9	18	2	49	2	114	41	2	2	0	7.11.E+07	6.72.E+07	8.32.E+07	8.19.E+07	4.65.E+07	4.95.E+07	5.68.E+07	4.99.E+07
1952	P80303	Nucleobindin-2 [OS=Homo sapiens]	9.9	7	2	21	2		21	2		0	2.14.E+07	2.14.E+07	2.06.E+07	2.23.E+07	4.62.E+07	4.06.E+07	3.78.E+07	4.06.E+07
1953	O15305	Phosphomannomutase 2 [OS=Homo sapiens]	9.9	8	1	4	1	103			1	0	6.37.E+06	1.16.E+07	8.89.E+06	1.22.E+07		3.90.E+06		
1954	P18858	DNA ligase 1 [OS=Homo sapiens]	9.9	2	1	43	1	635	39	1	1	0	9.58.E+06	1.11.E+07	1.04.E+07	1.12.E+07	9.55.E+06	9.06.E+06	6.28.E+06	8.11.E+06
1955	O00154	cytosolic acyl coenzyme A thioester hydrolase [OS=Homo sapiens]	9.9	6	2	52	2	284	59	2	2	0	4.78.E+07	5.92.E+07	5.15.E+07	7.38.E+07	1.30.E+07	4.51.E+07	4.22.E+07	5.19.E+07
1956	Q9GZP9	Derlin-2 [OS=Homo sapiens]	9.9	13	1	12	1	72	16	1	1	0	1.91.E+07	2.44.E+07	2.10.E+07	2.36.E+07	1.38.E+07	1.85.E+07	1.20.E+07	1.59.E+07
1957	Q13586	stromal interaction molecule 1 [OS=Homo sapiens]	9.9	5	2	14	2	74	10	2	2	0	6.68.E+06	6.92.E+06	7.50.E+06	7.12.E+06	4.78.E+06	4.60.E+06	5.87.E+06	5.35.E+06
1958	Q7L5N1	COP9 signalosome complex subunit 6 [OS=Homo sapiens]	9.9	20	4	34	4	21	51	3	4	0	1.08.E+08	1.09.E+08	1.10.E+08	9.53.E+07	9.96.E+07	1.13.E+08	1.12.E+08	9.75.E+07
1959	P35754	Glutaredoxin-1 [OS=Homo sapiens]	9.9	27	1	4	1	110	6	1	1	0	1.05.E+06	2.21.E+06	6.86.E+05	2.13.E+06	2.31.E+06	5.87.E+06	4.56.E+06	2.17.E+06
1960	Q8TEQ8-1	GPI ethanolamine phosphate transferase 3 [OS=Homo sapiens]	9.9	2	1	36	1	460	2	1	1	0	3.85.E+06	3.32.E+06	3.60.E+06	3.01.E+06	3.80.E+06	2.97.E+06	2.93.E+06	3.71.E+06
1961	Q9BY43	Charged multivesicular body protein 4a [OS=Homo sapiens]	9.9	6	1	14	1	297	19	1	1	0	1.21.E+07	1.59.E+07	1.24.E+07	1.57.E+07	1.54.E+07	1.47.E+07	1.80.E+07	1.50.E+07
1962	Q92882	osteoclast-stimulating factor 1 [OS=Homo sapiens]	9.8	6	1	38	1	707	43	1	1	0	1.45.E+07	2.05.E+07	1.48.E+07	1.88.E+07	2.20.E+07	2.11.E+07	1.86.E+07	2.00.E+07
1963	O14561	Acyl carrier protein, mitochondrial [OS=Homo sapiens]	9.8	12	2	20	2	85	19	2	2	0	6.75.E+07	8.62.E+07	4.06.E+07	8.08.E+07	5.51.E+07	4.99.E+07	3.91.E+07	5.48.E+07
1964	P24928	DNA-directed RNA polymerase II subunit RPB1 [OS=Homo sapiens]	9.8	3	2	16	2	151	3	2	2	0	7.32.E+06	5.06.E+06	6.12.E+06	7.51.E+06	5.34.E+06	5.78.E+06	5.94.E+06	4.91.E+06
1965	P55854	Small ubiquitin-related modifier 3 [OS=Homo sapiens]	9.8	12	1	88	1	2142	126	1	1	0	4.42.E+08	3.50.E+08	4.48.E+08	4.34.E+08	3.87.E+08	3.52.E+08	3.91.E+08	3.57.E+08
1966	Q8NDI1	EH domain-binding protein 1 [OS=Homo sapiens]	9.7	1	1	48	1	660	25	1	1	0	6.46.E+06	6.67.E+06	5.86.E+06	6.35.E+06	1.01.E+07	7.55.E+06	7.32.E+06	8.00.E+06
1967	Q16850-1	lanosterol 14-alpha demethylase [OS=Homo sapiens]	9.7	4	1	30	1	260	36	1	1	0	9.56.E+06	1.08.E+07	1.21.E+07	1.06.E+07	1.22.E+07	1.00.E+07	8.67.E+06	8.91.E+06
1968	Q15287-1	RNA-binding protein with serine-rich domain 1 [OS=Homo sapiens]	9.7	5	1	32	1	655	48	1	1	0	4.08.E+07	3.86.E+07	4.36.E+07	4.04.E+07	4.31.E+07	4.13.E+07	3.71.E+07	3.88.E+07
1969	P14635	G2/mitotic-specific cyclin-B1 [OS=Homo sapiens]	9.7	4	1	18	1	163	18	1	1	0	1.25.E+07	1.11.E+07	1.20.E+07	1.04.E+07	7.17.E+06	7.79.E+06	4.76.E+06	8.16.E+06
1970	Q9BUQ8	Probable ATP-dependent RNA helicase DDX23 [OS=Homo sapiens]	9.7	3	2	9	2	34	10	2	2	0	1.93.E+07	1.86.E+07	2.09.E+07	1.98.E+07	2.07.E+07	1.95.E+07	2.42.E+07	2.17.E+07
1971	P29317	Ephrin type-A receptor 2 [OS=Homo sapiens]	9.7	4	3	11	3	29	5	3	3	0		1.82.E+07	1.94.E+07	1.63.E+07			7.11.E+06	1.09.E+07
1972	Q9UIA9	exportin-7 [OS=Homo sapiens]	9.7	1	1	47	1	501	35	1	1	0	1.69.E+07	1.61.E+07	9.77.E+06	1.49.E+07	6.44.E+06	1.17.E+07	5.55.E+06	1.13.E+07
1973	O95297-1	Myelin protein zero-like protein 1 [OS=Homo sapiens]	9.7	6	1	14	1	360	16	1	1	0	4.51.E+06	4.80.E+06	5.45.E+06	4.76.E+06	9.21.E+06	9.41.E+06	9.54.E+06	1.02.E+07

No.	Accession	Description	Sum PEP Score	Coverage [%]	# Peptides	# PSMs	# Unique Peptides	Score Mascot: A5 Mascot	Score Sequest HT: A2 Sequest HT	# Peptides (by Search Engine): A2 Sequest HT	# Peptides (by Search Engine): A5 Mascot	# Razor Peptides	ctrl Abundance s_1	ctrl Abundance s_2	ctrl Abundance s_3	ctrl Abundance s_4	JAM-A KO Abundance s_1	JAM-A KO Abundance s_2	JAM-A KO Abundance s_3	JAM-A KO Abundance s_4
1974	Q6P1X6	UPF0598 protein C8orf82 [OS=Homo sapiens]	9.7	8	1	14	1	379	17	1	1	0	1.06.E+07	8.56.E+06	7.05.E+06	8.89.E+06				
1975	Q9UBH6	Xenotropic and polytropic retrovirus receptor 1 [OS=Homo sapiens]	9.7	4	2	12	2	46	3	2	2	0	3.77.E+06	3.79.E+06	4.33.E+06	3.25.E+06	5.18.E+06	5.57.E+06	5.86.E+06	5.31.E+06
1976	Q9BZH6	WD repeat-containing protein 11 [OS=Homo sapiens]	9.6	1	1	28	1	517	29	1	1	0	7.10.E+06	7.41.E+06	6.34.E+06	6.53.E+06	8.04.E+06	7.29.E+06	6.51.E+06	6.98.E+06
1977	Q8NEZ5-1	F-box only protein 22 [OS=Homo sapiens]	9.6	5	1	6	1	56	10	1	1	0	8.47.E+06	6.96.E+06		5.37.E+06	1.52.E+07	1.41.E+07	9.29.E+06	1.38.E+07
1978	Q9UGV2	protein NDRG3 [OS=Homo sapiens]	9.6	6	1	44	1	392	61	1	1	0	1.17.E+07	9.56.E+06	1.28.E+07	1.19.E+07	2.50.E+07	2.39.E+07	2.26.E+07	2.68.E+07
1979	Q8WWM7-1	ataxin-2-like protein [OS=Homo sapiens]	9.6	3	2	14	2	38	16	2	2	0	5.26.E+07	4.77.E+07	4.87.E+07	5.21.E+07	6.45.E+07	6.98.E+07	7.97.E+07	7.76.E+07
1980	Q9H0E2	Toll-interacting protein [OS=Homo sapiens]	9.6	5	1	20	1	131	23	1	1	0	1.14.E+07	1.39.E+07	1.21.E+07	1.14.E+07	1.20.E+07	1.18.E+07	1.19.E+07	1.38.E+07
1981	Q9H078-2	Isoform 2 of Caseinolytic peptidase B protein homolog [OS=Homo sapiens]	9.6	7	3	24	3		23	3		0	9.61.E+07	8.85.E+07	6.52.E+07	5.16.E+07	6.33.E+07	6.86.E+07	1.29.E+07	6.70.E+07
1982	Q3KQV9	UDP-N-acetylhexosamine pyrophosphorylase-like protein 1 [OS=Homo sapiens]	9.5	6	2	8	1	45	6	2	2	0	1.13.E+06	1.45.E+06	1.70.E+06	1.31.E+06	3.26.E+06	1.35.E+06	3.16.E+06	
1983	P28799	Granulins [OS=Homo sapiens]	9.5	6	1	4	1	45	7	1	1	0					2.16.E+07	2.23.E+07	2.81.E+06	5.70.E+06
1984	Q6P996-1	Pyridoxal-dependent decarboxylase domain-containing protein 1 [OS=Homo sapiens]	9.5	5	2	14	2	118	10	2	2	0	1.50.E+07	1.84.E+07	1.49.E+07	1.41.E+07	1.81.E+07	2.04.E+07	9.66.E+06	1.73.E+07
1985	Q9P2R3	Rabankyrin-5 [OS=Homo sapiens]	9.5	2	2	22	2	115	24	2	2	0	4.02.E+07	4.21.E+07	4.12.E+07	4.07.E+07	3.40.E+07	3.98.E+07	3.69.E+07	3.60.E+07
1986	O43159	ribosomal rna-processing protein 8 [OS=Homo sapiens]	9.5	7	2	9	2	27	0	2	2	0	3.60.E+06	1.36.E+07	1.37.E+07	4.48.E+06	2.41.E+06	2.54.E+06	3.09.E+06	2.91.E+06
1987	Q969N2	GPI transamidase component PIG-T [OS=Homo sapiens]	9.5	4	2	16	2	44	13	2	2	0	6.04.E+06	1.77.E+07	7.13.E+06	7.46.E+06	2.94.E+07	2.39.E+07	2.07.E+07	2.76.E+07
1988	Q14146	Unhealthy ribosome biogenesis protein 2 homolog [OS=Homo sapiens]	9.4	2	1	2	1	75	3	1	1	0	3.42.E+05							
1989	Q13136	Liprin-alpha-1 [OS=Homo sapiens]	9.4	2	3	30	1	45	4	3	1	1	6.67.E+07	7.07.E+07	6.93.E+07	6.30.E+07	6.10.E+07	6.38.E+07	4.94.E+07	6.37.E+07
1990	Q9H2J4	phosducin-like protein 3 [OS=Homo sapiens]	9.4	11	2	18	2	65	4	2	2	0	1.07.E+07	1.14.E+07	1.21.E+07	1.28.E+07	1.67.E+07	1.19.E+07	1.17.E+07	1.50.E+07
1991	P42892	Endothelin-converting enzyme 1 [OS=Homo sapiens]	9.4	3	1	2	1	31	0	1	1	0	8.51.E+06	1.06.E+07	9.17.E+06	1.06.E+07	1.54.E+07	1.26.E+07	1.15.E+07	1.49.E+07
1992	P08579	U2 small nuclear ribonucleoprotein B'' [OS=Homo sapiens]	9.4	12	2	151	1	989	110	2	2	0	9.96.E+06	8.72.E+06	9.07.E+06	9.46.E+06	7.22.E+06	7.68.E+06	5.72.E+06	6.60.E+06
1993	O96013-1	serine/threonine-protein kinase PAK 4 [OS=Homo sapiens]	9.4	3	1	10	1	144	5	1	1	0	1.63.E+06	2.12.E+06	3.59.E+05	2.64.E+06	3.32.E+05	2.52.E+05		1.07.E+06
1994	Q9UGP8	Translocation protein SEC63 homolog [OS=Homo sapiens]	9.4	3	2	12	2	52	12	2	2	0	3.26.E+07	2.99.E+07	3.19.E+07	3.15.E+07	4.18.E+07	4.35.E+07	4.86.E+07	2.90.E+07
1995	P19404	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial [OS=Homo sapiens]	9.4	9	2	38	2	128	24	2	2	0	5.00.E+07	5.17.E+07	5.02.E+07	4.97.E+07	6.35.E+07	5.89.E+07	5.47.E+07	6.48.E+07
1996	P05161	Ubiquitin-like protein ISG15 [OS=Homo sapiens]	9.4	18	1	2	1	33	4	1	1	0	5.02.E+06		4.30.E+06	6.81.E+06	1.19.E+07	1.11.E+07	4.31.E+06	1.03.E+07
1997	Q6PCE3	glucose 1,6-bisphosphate synthase [OS=Homo sapiens]	9.3	8	2	11	2	54	2	1	2	0	2.06.E+07	2.29.E+07	2.19.E+07	2.57.E+07	2.33.E+07	3.54.E+07	2.56.E+07	2.94.E+07
1998	P82932	28S ribosomal protein S6, mitochondrial [OS=Homo sapiens]	9.3	19	1	10	1	149	9	1	1	0	8.65.E+06	6.63.E+06	7.02.E+06	6.55.E+06	3.13.E+06	1.63.E+06	3.05.E+06	3.20.E+06
1999	P31751	RAC-beta serine/threonine-protein kinase [OS=Homo sapiens]	9.3	5	2	8	2	69	2	2	2	0	6.55.E+06	1.10.E+07	8.78.E+06	4.75.E+06	5.52.E+06	6.37.E+06	4.60.E+06	3.49.E+06
2000	Q9BXV9	EKC/KEOPS complex subunit GON7 [OS=Homo sapiens]	9.3	16	1	14	1	116	18	1	1	0	1.80.E+07	2.23.E+07		1.76.E+07	2.11.E+07	2.56.E+07	1.66.E+07	2.24.E+07
2001	Q16186	Proteasomal ubiquitin receptor ADRM1 [OS=Homo sapiens]	9.3	13	3	9	3	44	3	2	3	0	2.93.E+07	3.15.E+07	1.78.E+07	3.37.E+07	3.04.E+07	2.70.E+07	2.15.E+07	4.12.E+07
2002	Q9BU23-1	Lipase maturation factor 2 [OS=Homo sapiens]	9.2	2	1	10	1	195	12	1	1	0		4.77.E+06		5.02.E+06	8.76.E+06	9.13.E+06	6.53.E+06	6.96.E+06
2003	Q15428	splicing factor 3a subunit 2 [OS=Homo sapiens]	9.2	4	2	38	2	25	2	2	2	0	1.53.E+07	1.21.E+07	1.47.E+07	1.31.E+07	1.34.E+07	1.37.E+07	1.25.E+07	1.28.E+07
2004	Q14790-1	Caspase-8 [OS=Homo sapiens]	9.2	4	1	4	1	107	6	1	1	0	5.37.E+06	1.08.E+07	7.04.E+06	9.95.E+06	1.32.E+07	1.51.E+07	9.54.E+06	1.35.E+07
2005	O60749	Sorting nexin-2 [OS=Homo sapiens]	9.2	5	2	47	1	101	66	2	2	0								
2006	Q8NFV4	Protein Abhd11 [OS=Homo sapiens]	9.2	7	1	95	1	685	49	1	1	0	1.64.E+07	1.71.E+07	1.75.E+07	1.90.E+07	1.40.E+07	1.29.E+07	1.23.E+07	1.33.E+07
2007	Q13617-1	Cullin-2 [OS=Homo sapiens]	9.2	6	4	52	3	13	22	4	2	0	9.45.E+06	9.32.E+06	9.13.E+06	1.05.E+07	8.16.E+06	8.47.E+06	5.99.E+06	9.08.E+06
2008	P13284	Gamma-interferon-inducible lysosomal thiol reductase [OS=Homo sapiens]	9.1	15	1	6	1	78	5	1	1	0	1.06.E+07	1.38.E+07	1.22.E+07	1.23.E+07		8.04.E+06	7.20.E+05	5.57.E+05
2009	Q6FI81-1	Anamorsin [OS=Homo sapiens]	9.1	9	2	15	2	38	17	2	2	0	2.58.E+07	2.62.E+07	2.27.E+07	2.34.E+07	3.25.E+07	9.24.E+06	3.25.E+07	2.83.E+07
2010	O14618	copper chaperone for superoxide dismutase [OS=Homo sapiens]	9.1	8	2	38	2	56	26	2	2	0	3.45.E+08	3.78.E+08	3.61.E+08	3.39.E+08	4.95.E+08	5.36.E+08	5.07.E+08	5.24.E+08
2011	Q9GZT9-1	Egl nine homolog 1 [OS=Homo sapiens]	9.1	6	1	4	1	49	6	1	1	0	1.29.E+07	1.05.E+07	1.19.E+07	1.27.E+07	9.06.E+06	8.68.E+06	1.08.E+07	1.02.E+07
2012	Q8N806	Putative E3 ubiquitin-protein ligase UBR7 [OS=Homo sapiens]	9.1	8	1	6	1	160	8	1	1	0	5.03.E+06		3.72.E+06	4.70.E+06				
2013	Q969X6	U3 small nucleolar RNA-associated protein 4 homolog [OS=Homo sapiens]	9.1	3	2	14	2	77	2	2	2	0	1.88.E+07	2.15.E+07	2.98.E+07	2.10.E+07	1.80.E+07	1.92.E+07	1.78.E+07	1.52.E+07
2014	Q9BTC0	Death-inducer obliterator 1 [OS=Homo sapiens]	9.1	3	3	41	3	103	0	2	3	0	1.73.E+07	1.44.E+07	1.45.E+07	1.57.E+07	1.80.E+07	1.77.E+07	1.58.E+07	1.03.E+07
2015	P17568	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7 [OS=Homo sapiens]	9.1	20	3	49	3	78	27	3	2	0	4.80.E+07	5.03.E+07	5.27.E+07	4.42.E+07	5.16.E+07	5.14.E+07	5.40.E+07	5.04.E+07
2016	P43007-1	neutral amino acid transporter A [OS=Homo sapiens]	9.1	4	1	8	1	41	16	1	1	0	8.49.E+06	8.69.E+06	9.50.E+06	8.03.E+06	1.06.E+07	1.11.E+07	1.13.E+07	1.25.E+07
2017	P08651	Nuclear factor 1 C-type [OS=Homo sapiens]	9.0	6	1	2	1	33	2	1	1	0	4.97.E+06		6.53.E+05			9.38.E+06	2.38.E+06	
2018	Q8TCT8	Signal peptide peptidase-like 2A [OS=Homo sapiens]	9.0	3	1	62	1	322	79	1	1	0	7.61.E+07	7.71.E+07	8.18.E+07	7.10.E+07	8.76.E+07	9.86.E+07	9.54.E+07	9.27.E+07
2019	Q8IX12	Cell division cycle and apoptosis regulator protein 1 [OS=Homo sapiens]	9.0	3	2	15	2	53	8	2	2	0	4.14.E+08	4.37.E+08	3.93.E+08	3.89.E+08	3.41.E+08	3.74.E+08	3.35.E+08	3.46.E+08
2020	O00273-1	DNA fragmentation factor subunit alpha [OS=Homo sapiens]	9.0	8	2	26	2	248	24	2	2	0	1.56.E+07	1.91.E+07	1.40.E+07	1.67.E+07	2.40.E+07	2.37.E+07	2.20.E+07	1.95.E+07
2021	Q5JS54-1	Proteasome assembly chaperone 4 [OS=Homo sapiens]	8.9	23	2	10	2	54	2	2	2	0	6.10.E+06	5.69.E+06	1.04.E+07	3.40.E+06	3.03.E+06	2.87.E+06	2.96.E+06	3.24.E+06
2022	P48729-1	Casein kinase I isoform alpha [OS=Homo sapiens]	8.9	6	2	54	2	365	14	2	2	0	2.23.E+07	1.95.E+07	2.11.E+07	2.44.E+07	1.71.E+07	1.50.E+07	1.69.E+07	1.47.E+07
2023	P49366-1	deoxyhypusine synthase [OS=Homo sapiens]	8.9	9	2	20	2	90	9	2	2	0	1.39.E+07	1.42.E+07	1.22.E+07	1.64.E+07	1.29.E+07	1.35.E+07	1.01.E+07	1.39.E+07
2024	Q92552	28S ribosomal protein S27, mitochondrial [OS=Homo sapiens]	8.9	5	2	44	2	100	18	2	2	0	2.53.E+07	3.03.E+07	2.97.E+07	2.68.E+07	2.83.E+07	2.95.E+07	1.46.E+07	3.00.E+07
2025	O95347-1	structural maintenance of chromosomes protein 2 [OS=Homo sapiens]	8.9	6	4	6	4	0	0	2	4	0	8.78.E+06	6.31.E+06	2.79.E+06	1.41.E+07	3.15.E+07	1.89.E+07	2.76.E+07	2.98.E+07
2026	Q9Y676	28S ribosomal protein S18b, mitochondrial [OS=Homo sapiens]	8.8	13	1	18	1	116	22	1	1	0	1.10.E+07	1.36.E+07	4.30.E+06	1.23.E+07	1.11.E+07	1.11.E+07	8.70.E+06	4.34.E+06
2027	O76041-2	Isoform 2 of Nebulette [OS=Homo sapiens]	8.8	9	2	19	1		8	2		0	1.85.E+07	1.46.E+07	1.57.E+07	1.79.E+07	3.20.E+07	3.49.E+07		3.56.E+07

No.	Accession	Description	Sum PEP Score	Coverage [%]	# Peptides	# PSMs	# Unique Peptides	Score Mascot: A5 Mascot	Score Sequest HT: A2 Sequest HT	# Peptides (by Search Engine): A2 Sequest HT	# Peptides (by Search Engine): A5 Mascot	# Razor Peptides	ctrl Abundances_1	ctrl Abundances_2	ctrl Abundances_3	ctrl Abundances_4	JAM-A KO Abundances_1	JAM-A KO Abundances_2	JAM-A KO Abundances_3	JAM-A KO Abundances_4
2028	Q6P1L8	39S ribosomal protein L14, mitochondrial [OS=Homo sapiens]	8.8	17	2	10	2	52	2	2	2	0	2.36.E+07	2.30.E+07	2.29.E+07	2.76.E+07	2.09.E+07	1.56.E+07	2.18.E+07	2.24.E+07
2029	Q14318	peptidyl-prolyl cis-trans isomerase FKBP8 [OS=Homo sapiens]	8.8	4	1	4	1	58	6	1	1	0								
2030	Q86TB9	Protein PAT1 homolog 1 [OS=Homo sapiens]	8.8	3	2	4	2	34	0	2	2	0	4.53.E+06	5.05.E+06	5.94.E+06	3.97.E+06	7.95.E+06	9.33.E+06	9.35.E+06	8.86.E+06
2031	O14908-1	PDZ domain-containing protein GIPC1 [OS=Homo sapiens]	8.8	14	3	20	3	0	0	2	3	0	9.99.E+07	1.08.E+08	8.98.E+07	1.16.E+08	1.36.E+08	1.13.E+08	1.06.E+08	1.30.E+08
2032	Q2TAA2	Isoamyl acetate-hydrolyzing esterase 1 homolog [OS=Homo sapiens]	8.8	11	2	42	2	119	14	2	2	0	1.01.E+07	1.33.E+07	8.17.E+06	1.30.E+07	1.58.E+07	1.57.E+07	1.59.E+07	1.80.E+07
2033	Q9NZT2-1	opioid growth factor receptor [OS=Homo sapiens]	8.8	5	2	12	2	51	5	2	2	0	1.18.E+07	1.39.E+07	1.24.E+07	1.36.E+07	1.14.E+07	1.35.E+07	1.08.E+07	1.15.E+07
2034	Q8TCS8	Polyribonucleotide nucleotidyltransferase 1, mitochondrial [OS=Homo sapiens]	8.8	4	3	29	3	93	0	3	3	0	8.16.E+07	7.56.E+07	8.06.E+07	9.31.E+07	7.62.E+07	7.54.E+07	8.57.E+07	7.86.E+07
2035	Q6ICB0	Desumoylating isopeptidase 1 [OS=Homo sapiens]	8.7	15	1	26	1	523	38	1	1	0	1.21.E+07	1.24.E+07	1.15.E+07	1.28.E+07	1.05.E+07	4.42.E+06	8.01.E+06	4.76.E+06
2036	Q7Z2W9	39S ribosomal protein L21, mitochondrial [OS=Homo sapiens]	8.7	14	2	7	2	18	2	2	2	0	2.75.E+07	3.00.E+07	2.80.E+07	2.93.E+07	2.65.E+07	2.64.E+07	3.05.E+07	3.03.E+07
2037	O95295	SNARE-associated protein Snapin [OS=Homo sapiens]	8.7	19	1	34	1	109	16	1	1	0	1.35.E+07	1.67.E+07	1.23.E+07	1.52.E+07	1.12.E+07	9.07.E+06	7.28.E+06	5.03.E+06
2038	P17900	Ganglioside GM2 activator [OS=Homo sapiens]	8.7	10	1	12	1	225	15	1	1	0	1.25.E+07	1.35.E+07	1.06.E+07	1.21.E+07			9.30.E+06	
2039	P50750	Cyclin-dependent kinase 9 [OS=Homo sapiens]	8.7	6	2	17	1	55	17	2	2	0	1.32.E+07	1.51.E+07	5.40.E+06	1.37.E+07	1.01.E+07	1.18.E+07	8.37.E+06	9.35.E+06
2040	P04004	Vitronectin [OS=Homo sapiens]	8.7	3	1	34	1	349	39	1	1	0	2.29.E+07	2.65.E+07	2.10.E+07	2.48.E+07	1.20.E+07	1.17.E+07	9.83.E+06	1.10.E+07
2041	Q96KG9	N-terminal kinase-like protein [OS=Homo sapiens]	8.6	5	1	4	1	19	7	1	1	0								
2042	Q96RP9	Elongation factor G, mitochondrial [OS=Homo sapiens]	8.6	4	1	6	1	58	7	1	1	0	4.09.E+06	1.06.E+07	8.66.E+06	1.01.E+07	1.15.E+07	1.20.E+07	8.95.E+06	1.05.E+07
2043	O95466	formin-like protein 1 [OS=Homo sapiens]	8.6	2	1	6	1	131	8	1	1	0	4.22.E+06	3.35.E+06	3.08.E+06	3.48.E+06	9.26.E+06	8.90.E+06	9.23.E+06	9.11.E+06
2044	Q96CP7	Calfacilitin [OS=Homo sapiens]	8.6	7	1	16	1	126	17	1	1	0	6.12.E+06	7.23.E+06	7.13.E+06	6.05.E+06	1.01.E+07	8.51.E+06	7.69.E+06	7.64.E+06
2045	P56211	cAMP-regulated phosphoprotein 19 [OS=Homo sapiens]	8.6	37	2	44	1	104	31	1	2	0	2.18.E+07	2.53.E+07	7.89.E+06	1.80.E+07	9.97.E+06	8.72.E+06	3.09.E+07	2.96.E+07
2046	Q9NTJ5	Phosphatidylinositide phosphatase SAC1 [OS=Homo sapiens]	8.6	4	2	14	2	59	14	2	1	0	3.06.E+07	3.40.E+07	2.90.E+07	2.75.E+07	2.88.E+07	3.40.E+07	3.10.E+07	3.34.E+07
2047	Q9BXK5-1	Bcl-2-like protein 13 [OS=Homo sapiens]	8.5	5	1	26	1	83	32	1	1	0	9.25.E+06	8.54.E+06	8.11.E+06	1.05.E+07		1.66.E+07	1.46.E+07	
2048	Q9UHR4	Brain-specific angiogenesis inhibitor 1-associated protein 2-like protein 1 [OS=Homo sapiens]	8.5	5	1	30	1	130	5	1	1	0	2.15.E+07	1.78.E+07	1.74.E+07	2.16.E+07	2.30.E+07	2.02.E+07	1.76.E+07	2.06.E+07
2049	Q9NZM5	ribosome biogenesis protein NOP53 [OS=Homo sapiens]	8.5	4	1	28	1	380	26	1	1	0	9.19.E+06	9.96.E+06	8.86.E+06	9.09.E+06	1.09.E+07	7.64.E+06	6.47.E+06	6.38.E+06
2050	Q9Y6E0	Serine/threonine-protein kinase 24 [OS=Homo sapiens]	8.5	6	2	32	1	30	6	2	2	0	4.78.E+06	3.30.E+05	6.11.E+06		8.65.E+06	8.61.E+06	6.28.E+06	1.02.E+07
2051	P46736	Lys-63-specific deubiquitinase BRCC36 [OS=Homo sapiens]	8.5	5	1	10	1	74	3	1	1	0	9.00.E+06	8.61.E+06	1.05.E+07	9.34.E+06	1.18.E+07	1.39.E+07	1.45.E+07	1.52.E+07
2052	Q8IZL8	Proline-, glutamic acid- and leucine-rich protein 1 [OS=Homo sapiens]	8.5	2	2	18	2	84	0	2	2	0	2.18.E+07	2.06.E+07	2.58.E+07	2.09.E+07	2.22.E+07	2.21.E+07	2.25.E+07	2.30.E+07
2053	P18084	Integrin beta-5 [OS=Homo sapiens]	8.4	4	2	3	2	47	3	2	1	0			3.56.E+07		5.09.E+07	4.63.E+07	6.10.E+07	4.95.E+07
2054	Q9H2V7	Protein spinster homolog 1 [OS=Homo sapiens]	8.4	3	1	6	1	58	5	1	1	0	2.87.E+06	5.09.E+06	3.25.E+06	4.00.E+06	8.16.E+06	8.24.E+06	6.90.E+06	6.78.E+06
2055	Q8NB90-1	Spermatogenesis-associated protein 5 [OS=Homo sapiens]	8.4	3	2	66	1	213	81	2	2	0								
2056	Q99848	Probable rRNA-processing protein EBP2 [OS=Homo	8.4	10	2	10	2	87	11	2	2	0	4.76.E+07	4.47.E+07	3.69.E+07	5.13.E+07	5.43.E+07	5.91.E+07	5.35.E+07	5.03.E+07
2057	O60828	Polyglutamine-binding protein 1 [OS=Homo sapiens]	8.4	12	1	32	1	171	13	1	1	0	2.17.E+07	2.89.E+07	2.37.E+07	2.82.E+07	2.41.E+07	2.16.E+07	5.23.E+06	2.26.E+07
2058	P36969	Phospholipid hydroperoxide glutathione peroxidase, mitochondrial [OS=Homo sapiens]	8.4	7	1	24	1	272	35	1	1	0	2.22.E+07	2.51.E+07	2.21.E+07		4.70.E+07	4.40.E+07	4.76.E+07	4.67.E+07
2059	Q13425-1	Beta-2-syntrophin [OS=Homo sapiens]	8.3	4	2	34	2	525	24	2	2	0	2.66.E+07	2.77.E+07	2.50.E+07	2.49.E+07	2.48.E+07	2.27.E+07	2.40.E+07	2.21.E+07
2060	Q9NP61-1	ADP-ribosylation factor GTPase-activating protein 3 [OS=Homo sapiens]	8.3	5	2	64	2	163	0	2	2	0	2.97.E+07	3.27.E+07	3.47.E+07	3.04.E+07	3.25.E+07	2.67.E+07	3.20.E+07	3.19.E+07
2061	P49406	39S ribosomal protein L19, mitochondrial [OS=Homo sapiens]	8.3	8	2	37	2	210	40	2	2	0	4.03.E+07	4.46.E+07	3.98.E+07	4.31.E+07	3.87.E+07	3.51.E+07	3.43.E+07	2.71.E+07
2062	Q00535	Cyclin-dependent-like kinase 5 [OS=Homo sapiens]	8.3	8	3	19	2	65	7	3	3	0	7.12.E+06	8.88.E+06	8.43.E+06	8.81.E+06	1.39.E+07	1.59.E+07	3.56.E+06	1.61.E+07
2063	P62072	Mitochondrial import inner membrane translocase subunit Tim10 [OS=Homo sapiens]	8.3	16	1	14	1	149	10	1	1	0	2.07.E+07	1.86.E+07	2.02.E+07	2.34.E+07	1.56.E+07	1.69.E+07	2.06.E+07	1.77.E+07
2064	Q9H3S7	Tyrosine-protein phosphatase non-receptor type 23 [OS=Homo sapiens]	8.3	2	2	5	2	51	7	2	2	0	2.24.E+06		8.16.E+06	1.12.E+06		7.92.E+06	6.55.E+06	6.09.E+06
2065	Q92685-1	Dol-P-Man:Man(5)GlcNAc(2)-PP-Dol alpha-1,3-mannosyltransferase [OS=Homo sapiens]	8.3	2	1	28	1	320	30	1	1	0	8.77.E+06	9.32.E+06	8.37.E+06	9.51.E+06	1.53.E+07	1.73.E+07	1.27.E+06	1.62.E+07
2066	Q6NUM9-1	all-trans-retinol 13,14-reductase [OS=Homo sapiens]	8.3	5	2	24	2	95	18	2	2	0	1.78.E+07	2.19.E+07	1.58.E+07	1.95.E+07	2.73.E+07	2.74.E+07	2.42.E+07	2.62.E+07
2067	Q53FV1	ORM1-like protein 2 [OS=Homo sapiens]	8.3	10	1	6	1	90	8	1	1	0	1.92.E+07	1.56.E+07	1.60.E+07	2.00.E+07	1.95.E+07	1.84.E+07	1.40.E+07	1.71.E+07
2068	Q9H974-1	Queuine tRNA-ribosyltransferase accessory subunit 2 [OS=Homo sapiens]	8.3	4	1	10	1	89	10	1	1	0	7.28.E+06	7.85.E+06	6.15.E+06	7.57.E+06	6.54.E+06	6.70.E+06	5.29.E+06	6.38.E+06
2069	Q13421	mesothelin [OS=Homo sapiens]	8.3	6	2	4	2	0	0	2	1	0	5.99.E+06	1.21.E+07	1.72.E+07	1.24.E+07	1.05.E+07	3.31.E+07	3.30.E+07	3.53.E+07
2070	Q9BTE3-1	Mini-chromosome maintenance complex-binding protein [OS=Homo sapiens]	8.3	4	2	19	2	51	16	2	2	0	1.97.E+07	1.93.E+07	2.06.E+07	1.74.E+07	2.15.E+07	2.26.E+07	2.38.E+07	2.20.E+07
2071	P35658-1	Nuclear pore complex protein Nup214 [OS=Homo sapiens]	8.3	1	1	6	1	116	7	1	1	0	8.76.E+06	1.04.E+07	8.75.E+06	5.47.E+06	8.63.E+06	4.42.E+06	6.05.E+06	7.51.E+06
2072	Q9Y2S7	Polymerase delta-interacting protein 2 [OS=Homo sapiens]	8.2	3	1	8	1	142	11	1	1	0	1.65.E+07	1.73.E+07	1.79.E+07	1.75.E+07	2.34.E+07	1.76.E+07	2.33.E+07	1.57.E+07
2073	Q14181	DNA polymerase alpha subunit B [OS=Homo sapiens]	8.2	3	1	35	1	168	21	1	1	0	2.28.E+07		2.28.E+07				1.94.E+07	1.57.E+07
2074	Q9Y5J9	mitochondrial import inner membrane translocase subunit Tim8 B [OS=Homo sapiens]	8.2	13	1	26	1	216	24	1	1	0	8.21.E+06	7.90.E+06	8.69.E+06	9.07.E+06	5.54.E+06	6.18.E+06	6.36.E+06	5.72.E+06
2075	Q9NYP7-1	elongation of very long chain fatty acids protein 5 [OS=Homo sapiens]	8.2	7	2	4	2	17	2	2	2	0	1.24.E+07	1.24.E+07	8.77.E+06	1.25.E+07	2.14.E+07	2.36.E+07	2.63.E+07	2.22.E+07
2076	A8MWD9	Putative small nuclear ribonucleoprotein G-like protein 15 [OS=Homo sapiens]	8.2	26	2	99	2	288	49	2	2	0	1.10.E+08	8.23.E+07	1.17.E+08	7.27.E+07	1.17.E+08	1.14.E+08	1.02.E+08	1.15.E+08
2077	O43615	Mitochondrial import inner membrane translocase subunit TIM44 [OS=Homo sapiens]	8.2	6	2	16	2	97	9	2	2	0	1.24.E+07	1.85.E+07	1.80.E+07	1.31.E+07	1.52.E+07	1.75.E+07	3.28.E+06	2.67.E+07
2078	O00442	RNA 3'-terminal phosphate cyclase [OS=Homo sapiens]	8.2	5	1	10	1	220	7	1	1	0	4.81.E+06	4.96.E+06	4.32.E+06	4.72.E+06	3.21.E+06	1.80.E+06	2.51.E+06	2.27.E+06

No.	Accession	Description	Sum PEP Score	Coverage [%]	# Peptides	# PSMs	# Unique Peptides	Score Mascot: A5 Mascot	Score Sequest HT: A2 Sequest HT	# Peptides (by Search Engine): A2 Sequest HT	# Peptides (by Search Engine): A5 Mascot	# Razor Peptides	ctrl Abundances_1	ctrl Abundances_2	ctrl Abundances_3	ctrl Abundances_4	JAM-A KO Abundances_1	JAM-A KO Abundances_2	JAM-A KO Abundances_3	JAM-A KO Abundances_4
2079	Q9Y314	nitric oxide synthase-interacting protein [OS=Homo sapiens]	8.2	9	2	44	2	103	11	2	2	0	2.16.E+07	2.89.E+07	2.98.E+07	3.19.E+07	2.51.E+07	2.76.E+07	1.82.E+07	2.82.E+07
2080	P46934	E3 ubiquitin-protein ligase NEDD4 [OS=Homo sapiens]	8.2	2	2	34	2	62	15	2	2	0	1.82.E+07	2.05.E+07	1.64.E+07	2.12.E+07	2.05.E+07	2.18.E+07	1.95.E+07	2.27.E+07
2081	Q9HD33-1	39S ribosomal protein L47, mitochondrial [OS=Homo sapiens]	8.1	5	1	36	1	355	15	1	1	0	1.12.E+07	1.41.E+07	1.03.E+07	1.39.E+07	1.63.E+07	1.56.E+07	1.11.E+07	1.73.E+07
2082	Q14527	Helicase-like transcription factor [OS=Homo sapiens]	8.1	2	1	2	1	50	3	1	1	0								
2083	Q6YN16	Hydroxysteroid dehydrogenase-like protein 2 [OS=Homo sapiens]	8.1	7	2	12	2	46	14	2	2	0	3.92.E+07	3.62.E+07	3.58.E+07	3.31.E+07	4.79.E+07	4.65.E+07	4.70.E+07	4.50.E+07
2084	P02794	Ferritin heavy chain [OS=Homo sapiens]	8.1	15	3	21	3	24	0	3	2	0	4.13.E+07	4.14.E+07	4.81.E+07	4.17.E+07	5.16.E+07	4.50.E+07	4.85.E+07	5.34.E+07
2085	Q8IY17-4	Isoform 4 of Neuropathy target esterase [OS=Homo sapiens]	8.1	2	1	8	1	89	0	1	1	0	4.13.E+06	6.25.E+06	5.65.E+06	7.47.E+06	7.60.E+06	4.79.E+06	3.13.E+06	3.89.E+06
2086	Q9UIL1-1	Short coiled-coil protein [OS=Homo sapiens]	8.1	18	1	18	1	150	9	1	1	0	4.72.E+06	1.04.E+07	9.75.E+06	4.89.E+06	2.14.E+07	1.06.E+07	9.00.E+06	1.08.E+07
2087	Q8WUY1	Protein THEM6 [OS=Homo sapiens]	8.0	16	2	16	2	49	5	2	2	0	3.94.E+07	4.42.E+07	3.96.E+07	4.16.E+07	3.88.E+07	3.82.E+07	3.68.E+07	3.78.E+07
2088	Q86VS8	Protein Hook homolog 3 [OS=Homo sapiens]	8.0	2	1	2	1	72	2	1	1	0	3.54.E+06	4.86.E+06	4.03.E+06	4.44.E+06	6.92.E+06	6.62.E+06	4.71.E+06	5.44.E+06
2089	Q9C0D5	Protein TANC1 [OS=Homo sapiens]	8.0	2	1	12	1	146	0	1	1	0	8.22.E+06	9.83.E+06	8.94.E+06	8.61.E+06	3.40.E+06	2.96.E+06	3.63.E+06	2.37.E+06
2090	Q9BW83-1	Intraflagellar transport protein 27 homolog [OS=Homo sapiens]	8.0	9	1	4	1	63	5	1	1	0	6.06.E+06					2.06.E+07	1.29.E+07	2.13.E+07
2091	Q96H20-1	Vacuolar-sorting protein SNF8 [OS=Homo sapiens]	8.0	5	1	2	1	55	2	1	1	0	3.63.E+06	6.47.E+06	3.10.E+06	5.55.E+06	1.18.E+07	1.45.E+07	1.58.E+07	1.35.E+07
2092	Q86WJ1	Chromodomain-helicase-DNA-binding protein 1-like OS=Homo sapiens OX=9606 GN=CHD1L PE=1 SV=3	8.0	2	1	3	1	16			1	0	4.88.E+06		5.51.E+06	4.09.E+06	1.15.E+07	8.36.E+06	1.26.E+07	1.03.E+07
2093	P09669	Cytochrome c oxidase subunit 6C [OS=Homo sapiens]	7.9	33	3	60	3	29	7	2	3	0	9.11.E+07	8.13.E+07	9.28.E+07	1.02.E+08	8.23.E+07	7.46.E+07	8.75.E+07	7.78.E+07
2094	Q9BWJ5	Splicing factor 3B subunit 5 [OS=Homo sapiens]	7.9	28	2	66	2	476	36	2	2	0	2.65.E+07	2.49.E+07	2.20.E+07	2.53.E+07	2.90.E+07	2.95.E+07	3.05.E+07	3.29.E+07
2095	Q9UK45	U6 snRNA-associated Sm-like protein LSm7 [OS=Homo sapiens]	7.9	30	2	8	2	22	5	2	2	0	3.45.E+07	3.63.E+07	3.25.E+07	3.73.E+07	4.52.E+06	1.71.E+07	1.17.E+07	1.40.E+07
2096	Q8IWA5	Choline transporter-like protein 2 [OS=Homo sapiens]	7.9	5	2	8	2	57	6	2	2	0	4.46.E+07	5.29.E+07	2.60.E+07	4.56.E+07	5.01.E+07	5.09.E+07	4.81.E+07	5.27.E+07
2097	Q6DD87	Zinc finger protein 787 [OS=Homo sapiens]	7.9	7	2	6	2		7	2		0	6.04.E+06	5.21.E+06	6.42.E+06	6.55.E+06	3.23.E+06	2.95.E+06	3.69.E+06	3.45.E+06
2098	P16930	Fumarylacetoacetase [OS=Homo sapiens]	7.9	9	2	8	2	58	8	1	2	0	3.87.E+06	8.99.E+06	4.01.E+06	7.89.E+06	7.21.E+06	6.52.E+06		7.07.E+06
2099	Q99549	M-phase phosphoprotein 8 [OS=Homo sapiens]	7.9	2	1	38	1	382	11	1	1	0	8.69.E+06	5.31.E+06	4.86.E+06	1.01.E+07	1.08.E+07	8.84.E+06	8.32.E+06	9.28.E+06
2100	Q9BW91-1	ADP-ribose pyrophosphatase, mitochondrial [OS=Homo sapiens]	7.9	7	1	2	1	43	3	1	1	0	4.86.E+06	1.01.E+07	8.51.E+06	9.42.E+06	6.52.E+06	5.76.E+06	5.05.E+06	7.84.E+06
2101	Q69YN2-1	CWF19-like protein 1 [OS=Homo sapiens]	7.8	3	1	2	1	41	2	1	1	0	3.52.E+06	3.60.E+06	3.83.E+06	3.50.E+06	3.80.E+06	4.53.E+06	4.41.E+06	4.58.E+06
2102	P61009	Signal peptidase complex subunit 3 [OS=Homo sapiens]	7.8	7	1	60	1	589	78	1	1	0	5.10.E+07	5.70.E+07	4.57.E+07	5.40.E+07	5.06.E+07	6.73.E+07	5.51.E+07	5.44.E+07
2103	P18583-5	Isoform D of Protein SON [OS=Homo sapiens]	7.8	2	2	7	1		6	2		0	5.73.E+06	8.38.E+06	6.15.E+06	7.98.E+06	8.15.E+06	6.43.E+06	5.75.E+06	6.74.E+06
2104	Q86TG7-1	Retrotransposon-derived protein PEG10 [OS=Homo sapiens]	7.8	2	1	14	1	84	19	1	1	0	6.84.E+06	6.15.E+06	9.50.E+06	6.97.E+06	1.73.E+07	1.92.E+07	2.31.E+07	1.57.E+07
2105	Q12959	Disks large homolog 1 [OS=Homo sapiens]	7.8	3	2	30	2	116	6	2	2	0	1.63.E+07	2.00.E+07	1.70.E+07	2.18.E+07	2.56.E+07	2.61.E+07	2.30.E+07	2.35.E+07
2106	Q8WYA6	Beta-catenin-like protein 1 [OS=Homo sapiens]	7.8	3	2	30	2	274	26	2	2	0	4.50.E+07	4.82.E+07	4.34.E+07	4.17.E+07	3.98.E+07	4.33.E+07	3.26.E+07	4.22.E+07
2107	Q9BRJ2	39S ribosomal protein L45, mitochondrial [OS=Homo sapiens]	7.8	5	1	8	1	20	5	1	1	0	3.19.E+07	3.54.E+07	4.24.E+07	3.53.E+07	5.41.E+07	5.39.E+07	3.57.E+07	4.04.E+07
2108	Q15833-1	Syntaxin-binding protein 2 [OS=Homo sapiens]	7.8	6	2	5	2	30	3	2	2	0	7.95.E+07	4.27.E+06	5.52.E+06	4.30.E+06	4.58.E+07	3.99.E+06	3.80.E+07	4.36.E+06
2109	Q9BSD7	Cancer-related nucleoside-triphosphatase [OS=Homo sapiens]	7.8	18	2	10	2	80	9	2	2	0	1.14.E+07	1.11.E+07	7.64.E+06	1.06.E+07	2.24.E+07	2.61.E+07	2.17.E+07	2.29.E+07
2110	P56182	Ribosomal RNA processing protein 1 homolog A [OS=Homo sapiens]	7.8	3	1	10	1	82	12	1	1	0	2.50.E+07	2.59.E+07	2.57.E+07	2.76.E+07	3.14.E+07	2.77.E+07	3.09.E+07	2.77.E+07
2111	Q8WUK0	Phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1 [OS=Homo sapiens]	7.8	6	1	8	1	87	9	1	1	0	4.29.E+06	8.19.E+06	4.54.E+06	7.39.E+06	9.99.E+06	8.52.E+06	7.70.E+06	7.59.E+06
2112	Q92878	DNA repair protein Rad50 [OS=Homo sapiens]	7.8	2	2	4	2	43	2	2	2	0		1.25.E+06	2.73.E+06	4.50.E+06	5.78.E+06	6.06.E+06	6.51.E+06	6.25.E+06
2113	P52756	RNA-binding protein 5 [OS=Homo sapiens]	7.7	3	1	10	1	148	11	1	1	0	9.18.E+06	8.74.E+06	5.13.E+06	8.87.E+06	6.65.E+06	6.74.E+06	3.10.E+06	3.22.E+06
2114	Q9H1B7	interferon regulatory factor 2-binding protein-like [OS=Homo sapiens]	7.7	3	1	4	1	42	5	1	1	0	1.31.E+06		4.17.E+05	1.35.E+06	4.50.E+06	3.14.E+06	3.75.E+06	4.08.E+06
2115	P49757	Protein numb homolog [OS=Homo sapiens]	7.7	4	1	10	1	40	14	1	1	0	3.36.E+07	2.09.E+07	3.57.E+07	1.87.E+07	3.64.E+07	4.03.E+07	2.93.E+07	3.45.E+07
2116	Q9H2G2-1	STE20-like serine/threonine-protein kinase [OS=Homo sapiens]	7.7	4	3	9	3	19	5	3	3	0	3.43.E+07	1.88.E+07	3.26.E+07	3.00.E+07	2.32.E+07	1.96.E+07	2.85.E+07	2.81.E+07
2117	Q96ST3	Paired amphipathic helix protein Sin3a [OS=Homo sapiens]	7.7	2	2	23	2	23	2	2	2	0	1.15.E+08	1.18.E+08	1.36.E+08	1.12.E+08	1.14.E+08	1.12.E+08	1.09.E+08	1.06.E+08
2118	Q13217	DnaJ homolog subfamily C member 3 [OS=Homo sapiens]	7.7	6	1	2	1	32	3	1	1	0	1.40.E+07	1.80.E+07	1.20.E+07	1.39.E+07	1.65.E+07	1.34.E+07	1.25.E+07	1.59.E+07
2119	Q99595	Mitochondrial import inner membrane translocase subunit Tim17-A [OS=Homo sapiens]	7.7	13	1	2	1	34	3	1	1	0								
2120	P57678	Gem-associated protein 4 [OS=Homo sapiens]	7.7	2	1	20	1	185	0	1	1	0	6.77.E+06	7.20.E+06	6.39.E+06	7.54.E+06	5.69.E+06	4.99.E+06	4.83.E+06	4.35.E+06
2121	Q8N0U8	Vitamin K epoxide reductase complex subunit 1-like protein 1 [OS=Homo sapiens]	7.7	6	1	104	1	1410	116	1	1	0	2.68.E+07	3.11.E+07	2.72.E+07	2.90.E+07	4.88.E+07	4.67.E+07	2.77.E+07	4.78.E+07
2122	Q00534	Cyclin-dependent kinase 6 [OS=Homo sapiens]	7.7	7	2	23	1	96	12	2	2	0	5.02.E+06	6.76.E+06	4.45.E+06	6.55.E+06	7.21.E+06	7.52.E+06	6.02.E+06	7.70.E+06
2123	Q9H3P2-1	Negative elongation factor A [OS=Homo sapiens]	7.6	2	1	8	1	116	8	1	1	0	6.14.E+06	5.57.E+06	6.54.E+06	4.56.E+06	9.28.E+06	9.66.E+06	8.51.E+06	9.06.E+06
2124	Q9NRY5	Protein FAM114A2 [OS=Homo sapiens]	7.6	4	1	6	1	29	4	1	1	0	6.42.E+06	7.14.E+06	6.49.E+06	7.73.E+06	6.55.E+06	5.13.E+06	7.01.E+06	6.20.E+06
2125	Q9NVH1-1	DnaJ homolog subfamily C member 11 [OS=Homo sapiens]	7.6	4	1	4	1	26	4	1	1	0	7.27.E+06	7.51.E+06	5.78.E+06		1.03.E+07	9.62.E+06	2.19.E+06	8.93.E+06
2126	P49903-1	Selenide, water dikinase 1 [OS=Homo sapiens]	7.6	8	2	36	2	123	38	2	2	0	1.89.E+07	5.80.E+07	1.66.E+07	1.56.E+07	1.99.E+07	8.40.E+07	3.92.E+06	1.93.E+07
2127	Q7Z2Z2	Elongation factor-like GTPase 1 [OS=Homo sapiens]	7.6	3	3	8	3	26	2	3	3	0	4.02.E+07	4.21.E+07	4.83.E+07	3.92.E+07	3.67.E+07	4.16.E+07	4.34.E+07	3.90.E+07
2128	Q8TCJ2	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B [OS=Homo sapiens]	7.6	2	2	30	2	202	25	2	2	0	5.43.E+07	6.06.E+07	5.61.E+07	5.19.E+07	8.08.E+07	8.84.E+07	8.59.E+07	7.87.E+07
2129	Q9BVI4	Nucleolar complex protein 4 homolog [OS=Homo sapiens]	7.6	5	1	16	1	85	17	1	1	0								
2130	Q9NPA8-1	Transcription and mRNA export factor ENY2 [OS=Homo sapiens]	7.5	17	1	12	1	39	18	1	1	0	2.52.E+07	2.68.E+07	1.21.E+07	2.68.E+07	2.92.E+07	3.68.E+07	2.43.E+07	3.81.E+07
2131	Q9NRV9	Heme-binding protein 1 [OS=Homo sapiens]	7.5	8	1	8	1	39	10	1	1	0	1.17.E+07	1.27.E+07	1.36.E+07	1.17.E+07	1.63.E+07	1.56.E+07	1.97.E+07	1.71.E+07

No.	Accession	Description	Sum PEP Score	Coverage [%]	# Peptides	# PSMs	# Unique Peptides	Score Mascot: A5 Mascot	Score Sequest HT: A2 Sequest HT	# Peptides (by Search Engine): A2 Sequest HT	# Peptides (by Search Engine): A5 Mascot	# Razor Peptides	ctrl Abundances_1	ctrl Abundances_2	ctrl Abundances_3	ctrl Abundances_4	JAM-A KO Abundances_1	JAM-A KO Abundances_2	JAM-A KO Abundances_3	JAM-A KO Abundances_4
2132	Q13427	peptidyl-prolyl cis-trans isomerase g [OS=Homo sapiens]	7.5	2	1	4	1	64	5	1	1	0	4.31.E+07	3.68.E+07	4.37.E+07	4.13.E+07	3.50.E+07	4.41.E+07	2.27.E+07	3.77.E+07
2133	Q99797	Mitochondrial intermediate peptidase [OS=Homo sapiens]	7.5	5	2	6	2	35	0	1	2	0	2.20.E+06	2.43.E+06	2.85.E+06	2.55.E+06	2.46.E+06	2.27.E+06	2.59.E+06	3.13.E+06
2134	Q9Y580	RNA-binding protein 7 [OS=Homo sapiens]	7.5	7	1	4	1	70	5	1	1	0		8.90.E+06		8.53.E+06	1.09.E+07	9.10.E+06	9.64.E+06	1.03.E+07
2135	Q8WZ82	Esterase OVCA2 [OS=Homo sapiens]	7.5	6	1	22	1	380	16	1	1	0	1.01.E+07	1.02.E+07	9.71.E+06	1.08.E+07	7.73.E+06	8.23.E+06	8.35.E+06	8.76.E+06
2136	Q9P0J0	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13 [OS=Homo sapiens]	7.4	19	2	8	2	86	6	2	2	0	7.97.E+07	8.36.E+07	7.59.E+07	8.00.E+07	7.12.E+07	7.19.E+07	4.19.E+07	6.99.E+07
2137	Q92665	28S ribosomal protein S31, mitochondrial [OS=Homo sapiens]	7.4	6	1	17	1	105	5	1	1	0	4.41.E+06	3.56.E+06	3.67.E+06	2.83.E+06	5.10.E+06	4.04.E+06	4.50.E+06	5.50.E+06
2138	P13807	glycogen [starch] synthase, muscle [OS=Homo sapiens]	7.4	3	1	10	1	0	7	1	1	0		4.46.E+07	4.86.E+07	3.60.E+07	2.50.E+07	8.02.E+06	1.76.E+07	2.77.E+07
2139	Q0VDG4-1	secernin-3 [OS=Homo sapiens]	7.4	7	1	2	1	0	0	1	1	0	3.16.E+06	3.76.E+06	2.26.E+06	4.05.E+06	5.34.E+06	3.34.E+06	2.56.E+06	4.35.E+06
2140	Q7Z2T5-1	TRMT1-like protein [OS=Homo sapiens]	7.3	2	1	2	1	51	2	1	1	0								
2141	Q9UH65	Switch-associated protein 70 [OS=Homo sapiens]	7.3	3	2	8	2	46	5	2	2	0	2.62.E+07	2.26.E+07	3.51.E+07	1.88.E+07		1.90.E+07		
2142	Q9NZD2	Glycolipid transfer protein OS=Homo sapiens OX=9606 GN=GLTP PE=1 SV=3	7.3	7	1	2	1	33			1	0	1.11.E+07	1.13.E+07	1.13.E+07	1.14.E+07	1.54.E+07	1.48.E+07	5.91.E+06	1.39.E+07
2143	Q9H9C1-1	Spermatogenesis-defective protein 39 homolog [OS=Homo sapiens]	7.3	5	1	14	1	97	2	1	1	0	7.33.E+06	7.84.E+06	6.20.E+06	5.84.E+06	3.37.E+06	3.53.E+06	2.16.E+06	3.67.E+06
2144	O15270	Serine palmitoyltransferase 2 [OS=Homo sapiens]	7.3	4	1	44	1	631	24	1	1	0	2.14.E+07	1.31.E+07		1.70.E+07	3.55.E+07	2.91.E+07		1.10.E+07
2145	P36639	7,8-dihydro-8-oxoguanine triphosphatase [OS=Homo sapiens]	7.2	7	1	18	1	161	27	1	1	0	2.22.E+07	2.00.E+07	3.23.E+07	2.80.E+07	3.16.E+07	4.08.E+07	3.51.E+07	2.82.E+07
2146	Q9H0W8	protein SMG9 [OS=Homo sapiens]	7.2	8	2	8	2	77	6	2	2	0	8.03.E+06	1.04.E+07	9.32.E+06	8.95.E+06	9.01.E+06	1.10.E+07	9.28.E+06	7.84.E+06
2147	Q9NY93	Probable ATP-dependent RNA helicase DDX56 [OS=Homo sapiens]	7.2	3	1	6	1	29	8	1	1	0	1.34.E+07	1.09.E+07	1.42.E+07	1.44.E+07	1.30.E+07	1.22.E+07	1.18.E+07	6.00.E+06
2148	Q9BTZ2	dehydrogenase/reductase sdr family member 4 [OS=Homo sapiens]	7.2	6	2	27	2	226	28	2	2	0	3.65.E+07	3.28.E+07	3.59.E+07	3.37.E+07	3.01.E+07	2.61.E+07	2.81.E+07	2.79.E+07
2149	Q96CU9	FAD-dependent oxidoreductase domain-containing protein 1 [OS=Homo sapiens]	7.2	6	2	16	2	114	15	2	2	0	5.37.E+06	6.36.E+06	5.34.E+06	7.83.E+06	1.00.E+07	8.86.E+06	8.62.E+06	9.95.E+06
2150	Q9UMY4-1	Sorting nexin-12 [OS=Homo sapiens]	7.2	8	2	78	1	47	18	2	2	0	8.59.E+06		9.20.E+06	1.14.E+07	1.23.E+07	1.12.E+07	1.30.E+07	1.29.E+07
2151	P22307-1	Non-specific lipid-transfer protein [OS=Homo sapiens]	7.2	3	2	39	2	106	12	2	2	0	7.36.E+07	7.43.E+07	7.95.E+07	6.50.E+07	8.40.E+07	8.93.E+07	9.23.E+07	8.21.E+07
2152	Q96QC0	Serine/threonine-protein phosphatase 1 regulatory subunit 10 [OS=Homo sapiens]	7.2	4	2	30	2	74	6	2	2	0	1.40.E+07	1.48.E+07	7.91.E+06	1.44.E+07	1.31.E+07	1.37.E+07	1.08.E+07	1.25.E+07
2153	Q8WU90	Zinc finger CCCH domain-containing protein 15 [OS=Homo sapiens]	7.2	4	2	16	2	30	2	2	2	0	3.24.E+07	3.65.E+07	3.25.E+07	3.10.E+07	5.10.E+07	4.63.E+07	3.95.E+07	4.85.E+07
2154	O94776	Metastasis-associated protein MTA2 [OS=Homo sapiens]	7.2	3	1	4	1	75	6	1	1	0	1.98.E+07				1.39.E+07	1.23.E+07	5.50.E+06	1.44.E+07
2155	Q9NQG5	regulation of nuclear pre-mRNA domain-containing protein 1B [OS=Homo sapiens]	7.2	13	2	10	2	66	2	2	2	0	1.03.E+07	1.39.E+07	1.39.E+07		1.69.E+07	1.19.E+07	3.75.E+06	5.28.E+06
2156	Q6NXG1-1	epithelial splicing regulatory protein 1 [OS=Homo sapiens]	7.2	5	2	45	2	111	4	2	1	0	1.25.E+08	1.24.E+08	1.35.E+08	1.10.E+08	1.15.E+08	1.15.E+08	1.23.E+08	1.23.E+08
2157	P57105	Synaptojanin-2-binding protein [OS=Homo sapiens]	7.2	8	1	26	1	342	27	1	1	0	2.38.E+07	2.51.E+07	2.42.E+07	2.40.E+07	3.65.E+07	3.68.E+07	3.59.E+07	3.99.E+07
2158	Q8IVT5-1	kinase suppressor of Ras 1 [OS=Homo sapiens]	7.2	4	2	4	2	29	4	2	2	0	2.05.E+06	1.34.E+06	1.55.E+06	1.22.E+06	1.19.E+07	4.38.E+06	3.68.E+06	1.07.E+07
2159	O94874-1	E3 UFM1-protein ligase 1 [OS=Homo sapiens]	7.1	3	1	20	1	150	2	1	1	0								
2160	Q9NX63	MICOS complex subunit MIC19 [OS=Homo sapiens]	7.1	5	1	16	1	80	17	1	1	0	1.08.E+07	1.03.E+07	1.15.E+07	1.42.E+07	1.58.E+07	1.61.E+07	1.46.E+07	1.56.E+07
2161	Q9UQE7	Structural maintenance of chromosomes protein 3 [OS=Homo sapiens]	7.1	2	2	6	2	37	4	2	2	0	2.22.E+07	2.22.E+07	2.39.E+07	2.32.E+07	2.90.E+07	2.72.E+07	3.15.E+07	2.63.E+07
2162	Q9UHB6	LIM domain and actin-binding protein 1 [OS=Homo sapiens]	7.1	2	1	4	1	58	2	1	1	0	1.72.E+07	1.69.E+07	1.44.E+07	1.50.E+07	1.43.E+07	1.42.E+07	1.62.E+07	1.56.E+07
2163	Q15269	Periodic tryptophan protein 2 homolog [OS=Homo sapiens]	7.1	3	2	23	2	44	25	2	2	0	2.52.E+07	3.13.E+07	2.48.E+07	2.13.E+07	4.12.E+07	3.43.E+07	2.41.E+07	3.66.E+07
2164	Q9H2U1	ATP-dependent RNA helicase DHX36 [OS=Homo sapiens]	7.1	3	2	16	2	35	4	2	2	0	3.23.E+06	3.46.E+06	3.21.E+06	2.83.E+06	2.92.E+06	3.37.E+06	2.91.E+06	3.59.E+06
2165	Q14671-1	Pumilio homolog 1 [OS=Homo sapiens]	7.1	3	3	7	3	17	4	3	2	0	8.93.E+06	8.63.E+06	1.01.E+07	1.10.E+07	9.23.E+06	8.95.E+06	1.03.E+07	9.30.E+06
2166	Q96JP5-1	E3 ubiquitin-protein ligase ZFP91 [OS=Homo sapiens]	7.1	4	1	4	1	28	6	1	1	0								
2167	P22570	NADPH:adrenodoxin oxidoreductase, mitochondrial [OS=Homo sapiens]	7.1	4	1	46	1	115	32	1	1	0	1.18.E+07	1.42.E+07	1.21.E+07	1.28.E+07	1.47.E+07	1.45.E+07	1.15.E+07	1.38.E+07
2168	Q5T3I0	G patch domain-containing protein 4 [OS=Homo sapiens]	7.1	4	1	4	1	70	6	1	1	0								
2169	Q9NT62	ubiquitin-like-conjugating enzyme ATG3 [OS=Homo sapiens]	7.1	9	2	30	2	20	25	2	2	0	3.64.E+07	4.52.E+07	4.42.E+07	3.88.E+07	5.56.E+07	5.81.E+07	5.56.E+07	4.93.E+07
2170	Q9Y3E7	Charged multivesicular body protein 3 [OS=Homo sapiens]	7.0	5	1	2	1	32	3	1	1	0	1.62.E+07	1.54.E+07	1.81.E+07	1.72.E+07	1.89.E+07	2.01.E+07	1.95.E+07	2.01.E+07
2171	Q96HR9	Receptor expression-enhancing protein 6 [OS=Homo sapiens]	7.0	6	1	34	1	406	16	1	1	0	8.53.E+06	9.39.E+06	7.64.E+06	7.91.E+06	1.14.E+07	1.05.E+07	8.51.E+06	9.11.E+06
2172	Q9Y3C4	EKC/KEOPS complex subunit TPRKB [OS=Homo sapiens]	7.0	14	2	28	2	175	4	2	2	0	2.19.E+07	2.52.E+07	2.29.E+07	1.96.E+07	2.32.E+07	2.24.E+07	2.27.E+07	2.39.E+07
2173	Q9NRG7-2	Isoform 2 of Epimerase family protein SDR39U1 [OS=Homo sapiens]	7.0	13	2	8	2		0	2		0	1.50.E+06	1.41.E+06	1.65.E+06	1.28.E+06	1.74.E+06	1.56.E+06	1.79.E+06	1.90.E+06
2174	Q5W0V3	Protein FAM160B1 [OS=Homo sapiens]	7.0	4	1	8	1	43	12	1	1	0	8.80.E+06	8.44.E+06	1.07.E+07	9.00.E+06		4.64.E+06	4.98.E+06	5.73.E+06
2175	P20645	Cation-dependent mannose-6-phosphate receptor [OS=Homo sapiens]	7.0	5	1	4	1	41	5	1	1	0								
2176	P82650	28S ribosomal protein S22, mitochondrial [OS=Homo sapiens]	6.9	13	2	9	2	20	0	2	2	0	2.12.E+07	2.79.E+07	3.33.E+07	2.19.E+07	4.53.E+07	3.76.E+07	2.83.E+07	4.66.E+07
2177	Q96QD8	sodium-coupled neutral amino acid transporter 2 [OS=Homo sapiens]	6.9	4	1	8	1	81	12	1	1	0	1.21.E+07	1.19.E+07	1.40.E+07	1.37.E+07	8.50.E+06		5.33.E+06	7.76.E+06
2178	Q96AY3	Peptidyl-prolyl cis-trans isomerase FKBP10 [OS=Homo sapiens]	6.8	6	2	22	2	140	14	2	2	0	8.63.E+06	7.69.E+06	5.97.E+06	1.16.E+07	2.98.E+07	1.92.E+07	1.61.E+07	2.67.E+07
2179	O75718	Cartilage-associated protein [OS=Homo sapiens]	6.8	5	2	10	2	34	2	2	2	0	6.64.E+06	7.80.E+06	4.62.E+06	8.03.E+06	1.28.E+07	1.36.E+07	9.60.E+06	1.57.E+07
2180	Q06265-1	Exosome complex component RRP45 [OS=Homo sapiens]	6.8	3	1	6	1	71	8	1	1	0	1.82.E+07	2.10.E+07	2.29.E+07	2.23.E+07	2.43.E+07	2.40.E+07	2.58.E+07	3.04.E+07
2181	Q9UI09	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12 [OS=Homo sapiens]	6.8	8	1	6	1	33	8	1	1	0	2.97.E+07	2.72.E+07	2.99.E+07	3.15.E+07	1.46.E+07	1.36.E+07	1.62.E+07	1.47.E+07

No.	Accession	Description	Sum PEP Score	Coverage [%]	# Peptides	# PSMs	# Unique Peptides	Score Mascot: A5 Mascot	Score Sequest HT: A2 Sequest HT	# Peptides (by Search Engine): A2 Sequest HT	# Peptides (by Search Engine): A5 Mascot	# Razor Peptides	ctrl Abundances_1	ctrl Abundances_2	ctrl Abundances_3	ctrl Abundances_4	JAM-A KO Abundances_1	JAM-A KO Abundances_2	JAM-A KO Abundances_3	JAM-A KO Abundances_4
2182	P07311	Acylphosphatase-1 [OS=Homo sapiens]	6.7	22	2	14	2	30	10	2	2	0	3.49.E+07	3.22.E+07	3.83.E+07	4.49.E+07	4.03.E+07	3.65.E+07	4.35.E+07	4.02.E+07
2183	Q9Y5P6	Mannose-1-phosphate guanyltransferase beta [OS=Homo sapiens]	6.7	7	2	31	2	0	2	2	2	0	2.14.E+07	2.06.E+07	2.14.E+07	2.14.E+07	2.35.E+07	1.90.E+07	4.36.E+06	2.13.E+07
2184	Q9Y5U8	Mitochondrial pyruvate carrier 1 [OS=Homo sapiens]	6.7	19	1	4	1	86	5	1	1	0	4.40.E+06	5.13.E+06	4.16.E+06	5.40.E+06	2.57.E+06	3.49.E+06	2.38.E+06	3.04.E+06
2185	O00233-1	26S proteasome non-ATPase regulatory subunit 9 [OS=Homo sapiens]	6.7	9	2	15	2	18	12	2	2	0	2.95.E+07	3.10.E+07	2.89.E+07	9.87.E+06	3.50.E+07	4.01.E+07	2.93.E+07	8.78.E+06
2186	P11233	Ras-related protein Ral-A [OS=Homo sapiens]	6.7	6	1	20	1	250	4	1	1	0	1.61.E+07	1.43.E+07	1.47.E+07	1.40.E+07	7.30.E+06	7.86.E+06	4.66.E+06	8.04.E+06
2187	Q8NI22	Multiple coagulation factor deficiency protein 2 [OS=Homo sapiens]	6.7	12	1	12	1	118	16	1	1	0	1.14.E+07	1.53.E+07	1.28.E+07	1.32.E+07	2.60.E+07	2.53.E+07	2.60.E+07	2.77.E+07
2188	Q96DV4	39S ribosomal protein L38, mitochondrial [OS=Homo sapiens]	6.7	8	2	68	2	306	19	2	2	0	3.93.E+07	4.07.E+07	3.72.E+07	4.05.E+07	4.12.E+07	3.84.E+07	3.08.E+07	3.74.E+07
2189	O75145-1	Liprin-alpha-3 [OS=Homo sapiens]	6.7	3	2	15	1	45	4	2	2	0								
2190	P53779	mitogen-activated protein kinase 10 [OS=Homo sapiens]	6.7	4	2	71	1	272	30	2	2	1	4.38.E+07	4.37.E+07	4.62.E+07	3.82.E+07	3.83.E+07	4.19.E+07	4.18.E+07	4.20.E+07
2191	P30622-3	CAP-Gly domain-containing linker protein 1 [OS=Homo sapiens]	6.6	2	2	4	2	15	2	2	2	0	1.74.E+07	1.77.E+07	1.72.E+07	1.64.E+07	2.00.E+07	2.14.E+07	1.13.E+07	1.92.E+07
2192	Q9BTE7	DCN1-like protein 5 [OS=Homo sapiens]	6.6	18	2	10	2	0	5	2	2	0		1.19.E+07	4.41.E+06	1.32.E+07	9.80.E+06	3.37.E+06		8.09.E+06
2193	Q9NRG9-1	Aladin [OS=Homo sapiens]	6.6	2	1	25	1	84	20	1	1	0	6.96.E+06	8.18.E+06	6.39.E+06	7.98.E+06	1.10.E+07	1.05.E+07	9.17.E+06	1.06.E+07
2194	P18615	Negative elongation factor E [OS=Homo sapiens]	6.6	5	1	2	1	58	2	1	1	0	4.02.E+06	3.84.E+06	3.28.E+06	3.70.E+06	6.13.E+06	5.19.E+06	3.99.E+06	4.40.E+06
2195	Q9BT73	Proteasome assembly chaperone 3 [OS=Homo sapiens]	6.6	12	1	30	1	197	30	1	1	0	1.17.E+07	1.26.E+07	1.38.E+07	1.17.E+07				
2196	P09417	dihydropteridine reductase [OS=Homo sapiens]	6.6	5	1	8	1	63	7	1	1	0	8.80.E+06	6.54.E+06	6.75.E+06	8.88.E+06	4.01.E+06	5.05.E+06	8.38.E+06	4.85.E+06
2197	Q6WKZ4-4	Rab11 family-interacting protein 1 [OS=Homo sapiens]	6.6	2	1	2	1	0	3	1	1	0								
2198	Q9Y5J1	U3 small nucleolar RNA-associated protein 18 homolog [OS=Homo sapiens]	6.5	6	2	14	2	0	2	2	2	0	7.73.E+05	8.31.E+05	8.66.E+05	7.64.E+05	8.08.E+05	8.91.E+05	8.64.E+05	9.70.E+05
2199	Q9NQX4	Unconventional myosin-Vc [OS=Homo sapiens]	6.5	1	1	12	1	111	5	1	1	0	1.46.E+07	1.54.E+07	1.72.E+07	1.44.E+07	1.18.E+07	1.29.E+07	1.17.E+07	1.35.E+07
2200	Q14165	Malectin [OS=Homo sapiens]	6.5	12	2	6	2	38	6	2	2	0	1.47.E+07	4.64.E+06	1.68.E+07		1.81.E+07	6.32.E+06	1.18.E+07	1.71.E+07
2201	Q9Y3B2	Exosome complex component csl4 [OS=Homo sapiens]	6.5	8	1	6	1	103	7	1	1	0	7.65.E+06	7.81.E+06	8.73.E+06	6.61.E+06	8.12.E+06	7.46.E+06	6.77.E+06	7.86.E+06
2202	Q9NP66	High mobility group protein 20A [OS=Homo sapiens]	6.5	5	1	14	1	109	2	1	1	0	4.89.E+06	7.00.E+06	9.22.E+06	8.08.E+06	1.18.E+07	9.92.E+06	9.49.E+06	1.01.E+07
2203	Q8N8N7-1	Prostaglandin reductase 2 [OS=Homo sapiens]	6.5	13	2	16	2	38	2	2	2	0	6.47.E+06	6.78.E+06	5.66.E+06	7.40.E+06	1.35.E+07	1.18.E+07	1.01.E+07	1.14.E+07
2204	P49459-1	Ubiquitin-conjugating enzyme E2 A [OS=Homo sapiens]	6.5	11	1	24	1	195	26	1	1	0	1.88.E+07	2.08.E+07	2.09.E+07	1.80.E+07	2.26.E+07	2.05.E+07	2.32.E+07	2.13.E+07
2205	P56556	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6 [OS=Homo sapiens]	6.4	10	1	1	1		3	1		0					2.70.E+07	3.20.E+07	3.10.E+07	3.25.E+07
2206	Q15345-2	Leucine-rich repeat-containing protein 41 [OS=Homo sapiens]	6.4	2	1	8	1	91	0	1	1	0	5.28.E+06	6.03.E+06	3.61.E+06	5.82.E+06	4.38.E+06	4.15.E+06	3.18.E+06	4.36.E+06
2207	Q8WXA9-2	Isoform 2 of Splicing regulatory glutamine/lysine-rich protein 1 [OS=Homo sapiens]	6.4	2	1	5	1		10	1		0	1.09.E+07	1.16.E+07	1.04.E+07	1.30.E+07		1.00.E+07	7.92.E+06	
2208	P40123	Adenylyl cyclase-associated protein 2 [OS=Homo sapiens]	6.4	3	1	4	1	47	5	1	1	0	2.25.E+06	5.14.E+06	2.01.E+06	3.16.E+06	7.00.E+06	7.23.E+06	5.57.E+06	9.29.E+06
2209	O75691	Small subunit processome component 20 homolog [OS=Homo sapiens]	6.4	1	2	23	2	30	0	2	2	0	1.09.E+07	1.24.E+07	8.49.E+06	1.31.E+07	1.43.E+07	1.36.E+07	1.08.E+07	1.28.E+07
2210	Q16539	Mitogen-activated protein kinase 14 [OS=Homo sapiens]	6.4	6	2	68	1	284	30	2	2	0	5.98.E+06	5.43.E+06	5.64.E+06	5.86.E+06	6.46.E+06	7.94.E+06	5.02.E+06	8.00.E+06
2211	Q96JB5	CDK5 regulatory subunit-associated protein 3 [OS=Homo sapiens]	6.4	4	3	13	2	0	3	3	2	0	2.50.E+07	2.29.E+07	2.48.E+07	5.51.E+06	3.10.E+07	2.58.E+07	3.11.E+07	2.81.E+07
2212	Q9NY27	Serine/threonine-protein phosphatase 4 regulatory subunit 2 [OS=Homo sapiens]	6.3	4	1	13	1	37	0	1	1	0	1.26.E+07	1.48.E+07	3.91.E+06	1.84.E+07	1.15.E+07	1.56.E+07	9.84.E+06	1.41.E+07
2213	Q5XKP0	MICOS complex subunit MIC13 [OS=Homo sapiens]	6.3	32	2	30	2	103	10	2	1	0	1.81.E+07	2.00.E+07	1.70.E+07	1.90.E+07	7.07.E+07	5.01.E+07	7.07.E+07	6.82.E+07
2214	Q5TBC7-1	Bcl-2-like protein 15 [OS=Homo sapiens]	6.3	8	1	2	1	36	2	1	1	0	4.54.E+06	5.99.E+06	4.13.E+06	4.46.E+06	1.40.E+07	1.31.E+07	1.14.E+07	1.12.E+07
2215	Q9NX20	39S ribosomal protein L16, mitochondrial [OS=Homo sapiens]	6.2	6	1	4	1	24	5	1	1	0	8.93.E+06	7.68.E+06	5.92.E+06	6.36.E+06	1.03.E+07	9.55.E+06	8.41.E+06	1.09.E+07
2216	Q5RKV6	Exosome complex component MTR3 [OS=Homo sapiens]	6.2	6	1	28	1	384	23	1	1	0	1.05.E+07	9.22.E+06	9.40.E+06	1.06.E+07	1.01.E+07	1.06.E+07	1.15.E+07	1.09.E+07
2217	O15400	Syntaxin-7 [OS=Homo sapiens]	6.2	6	1	20	1	251	25	1	1	0	1.42.E+07	1.28.E+07	1.37.E+07	1.31.E+07	1.54.E+07	1.64.E+07	1.59.E+07	1.76.E+07
2218	Q92990	Glomulin [OS=Homo sapiens]	6.2	4	2	5	2	28	2	1	2	0	8.92.E+06	8.77.E+06	9.08.E+06	1.08.E+07	1.07.E+07	9.87.E+06	8.06.E+06	8.62.E+06
2219	Q92643	GPI-anchor transamidase [OS=Homo sapiens]	6.2	3	1	8	1	150	10	1	1	0	1.65.E+07	2.59.E+07	1.94.E+07	2.33.E+07	2.47.E+07	2.72.E+07	2.47.E+07	2.63.E+07
2220	P60033	CD81 antigen [OS=Homo sapiens]	6.2	7	1	4	1	32	4	1	1	0		3.54.E+07		3.09.E+07	4.71.E+07		2.36.E+07	7.07.E+07
2221	Q9GZT8-1	NIF3-like protein 1 [OS=Homo sapiens]	6.2	6	1	32	1	43	52	1	1	0	2.24.E+07	3.46.E+07	2.65.E+07	3.14.E+07	3.05.E+07	2.89.E+07	3.05.E+07	3.31.E+07
2222	Q9HC07	Transmembrane protein 165 [OS=Homo sapiens]	6.2	8	1	4	1	62	3	1	1	0	1.10.E+07	9.99.E+06	8.54.E+06	1.05.E+07	2.23.E+07	2.32.E+07	1.95.E+07	2.06.E+07
2223	Q92620	Pre-mRNA-splicing factor ATP-dependent RNA helicase PRP16 [OS=Homo sapiens]	6.1	1	1	22	1	157	19	1	1	0	4.51.E+06	5.57.E+06	3.94.E+06	3.88.E+06	8.28.E+06	7.69.E+06	5.93.E+06	7.34.E+06
2224	P19838	Nuclear factor NF-kappa-B p105 subunit [OS=Homo sapiens]	6.1	2	1	15	1	37	2	1	1	0	7.44.E+06	8.02.E+06	7.91.E+06	8.25.E+06	7.93.E+06	7.19.E+06	1.06.E+07	9.76.E+06
2225	Q14677-1	Clathrin interactor 1 [OS=Homo sapiens]	6.1	4	2	8	2	51	2	2	2	0	1.29.E+07	1.34.E+07	1.05.E+07	8.61.E+06	9.81.E+06	9.93.E+06	1.29.E+07	1.20.E+07
2226	Q9NVS2	39S ribosomal protein S18a, mitochondrial [OS=Homo sapiens]	6.1	8	1	30	1	282	5	1	1	0	6.83.E+06	9.07.E+06	6.21.E+06	7.29.E+06	9.94.E+06	9.23.E+06	7.49.E+06	8.44.E+06
2227	Q9H336	Cysteine-rich secretory protein LCCL domain-containing 1 [OS=Homo sapiens]	6.1	3	1	12	1	21	15	1	1	0	4.29.E+06	3.37.E+06	4.71.E+06	5.43.E+06	4.10.E+06	3.48.E+06		4.13.E+06
2228	Q9P032	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 4 [OS=Homo sapiens]	6.0	8	1	12	1	59	0	1	1	0	1.02.E+06	2.19.E+06	1.81.E+06	1.85.E+06	1.05.E+07	8.50.E+06	7.81.E+06	1.07.E+07
2229	O95793	double-stranded RNA-binding protein Staufen homolog 1 [OS=Homo sapiens]	6.0	6	2	17	2	14	15	2	2	0	3.34.E+07	3.63.E+07	3.69.E+07	3.03.E+07	4.53.E+07	4.83.E+07	4.44.E+07	4.46.E+07
2230	Q96KP1	exocyst complex component 2 [OS=Homo sapiens]	6.0	3	2	6	2	25	4	2	2	0	1.01.E+06	2.05.E+06	1.12.E+06	1.32.E+06	5.71.E+06	4.95.E+06	4.27.E+06	5.54.E+06
2231	O00515	Ladinin-1 [OS=Homo sapiens]	6.0	5	2	4	2	0	4	2	2	0	1.34.E+07	1.34.E+07	1.43.E+07	1.04.E+07	6.78.E+06	6.96.E+06	8.09.E+06	6.35.E+06
2232	Q92783	signal transducing adapter molecule 1 [OS=Homo sapiens]	5.9	4	2	54	2	0	15	1	2	0	4.46.E+07	4.37.E+07	3.09.E+07	3.69.E+07	3.60.E+07	2.42.E+07	3.97.E+07	3.67.E+07

No.	Accession	Description	Sum PEP Score	Coverage [%]	# Peptides	# PSMs	# Unique Peptides	Score Mascot: A5 Mascot	Score Sequest HT: A2 Sequest HT	# Peptides (by Search Engine): A2 Sequest HT	# Peptides (by Search Engine): A5 Mascot	# Razor Peptides	ctrl Abundances_1	ctrl Abundances_2	ctrl Abundances_3	ctrl Abundances_4	JAM-A KO Abundances_1	JAM-A KO Abundances_2	JAM-A KO Abundances_3	JAM-A KO Abundances_4
2233	Q9UKF6	Cleavage and polyadenylation specificity factor subunit 3 [OS=Homo sapiens]	5.9	3	2	9	2	32	0	2	1	0	2.75.E+07	2.90.E+07	2.67.E+07	2.57.E+07	3.15.E+07	3.27.E+07	1.19.E+07	2.90.E+07
2234	Q9Y2Z4	Tyrosine--tRNA ligase, mitochondrial [OS=Homo sapiens]	5.9	7	2	6	2	26	2	2	2	0	9.97.E+06	1.17.E+07	9.46.E+06	1.20.E+07	1.31.E+07	1.20.E+07	1.05.E+07	1.29.E+07
2235	Q9Y2K7	Lysine-specific demethylase 2A [OS=Homo sapiens]	5.9	2	2	6	2	28	4	2	2	0	1.27.E+07	1.32.E+07	1.35.E+07	1.52.E+07	1.25.E+07	9.24.E+06	1.19.E+07	1.24.E+07
2236	Q9BWU0	kanadaptin [OS=Homo sapiens]	5.9	1	1	10	1	93	7	1	1	0	1.48.E+07	1.54.E+07	1.45.E+07	1.42.E+07	1.49.E+07		1.49.E+07	1.76.E+07
2237	Q9HD15	Steroid receptor RNA activator 1 [OS=Homo sapiens]	5.9	5	1	6	1	44	6	1	1	0	7.83.E+06	8.05.E+06	9.12.E+06	9.47.E+06	1.11.E+07	1.02.E+07	1.03.E+07	9.14.E+06
2238	Q14517	Protocadherin Fat 1 [OS=Homo sapiens]	5.9	1	2	11	2	67	0	2	2	0	5.93.E+06	5.60.E+06	5.18.E+06	6.51.E+06	8.67.E+06	7.87.E+06	8.67.E+06	7.87.E+06
2239	Q9UPN6	Protein SCAF8 [OS=Homo sapiens]	5.9	1	1	2	1	36	3	1	1	0	2.59.E+07	2.57.E+07	3.90.E+06	2.64.E+07	1.56.E+07	2.53.E+07	1.12.E+07	2.35.E+07
2240	P67870	Casein kinase II subunit beta [OS=Homo sapiens]	5.9	4	1	41	1	33	16	1	1	0	3.43.E+07	3.34.E+07	3.54.E+07	2.79.E+07	2.45.E+07	2.70.E+07	3.16.E+07	2.71.E+07
2241	Q9NPA0	ER membrane protein complex subunit 7 [OS=Homo sapiens]	5.9	16	2	5	2	14	5	1	2	0	1.68.E+07	2.40.E+07	3.23.E+07	2.55.E+07	5.15.E+07	2.29.E+07	2.87.E+07	3.42.E+07
2242	Q02952-1	A-kinase anchor protein 12 [OS=Homo sapiens]	5.9	1	1	6	1	35	5	1	1	0	3.86.E+06	3.91.E+06	7.14.E+05		1.24.E+07	5.06.E+06	4.10.E+06	1.10.E+07
2243	Q8IUR7-1	Armadillo repeat-containing protein 8 [OS=Homo sapiens]	5.8	3	1	16	1	96	10	1	1	0	4.70.E+06	5.58.E+06	5.25.E+06	5.40.E+06	4.64.E+06	4.24.E+06	2.95.E+06	4.62.E+06
2244	Q9UBU9-1	nuclear RNA export factor 1 [OS=Homo sapiens]	5.8	2	1	16	1	42	9	1	1	0	7.90.E+06	1.29.E+07	1.04.E+07	9.03.E+06	9.23.E+06	9.28.E+06	9.04.E+06	1.01.E+07
2245	Q9UNX4	WD repeat-containing protein 3 [OS=Homo sapiens]	5.8	4	2	7	2	21	2	1	2	0	1.21.E+07	1.46.E+07		1.32.E+07	9.11.E+06	4.58.E+06		
2246	O75832	26S proteasome non-ATPase regulatory subunit 10 [OS=Homo sapiens]	5.8	15	2	6	2	14	0	2	2	0	3.03.E+07	3.05.E+07	3.44.E+07	2.51.E+07	4.90.E+07	4.41.E+07	5.01.E+07	4.94.E+07
2247	Q9Y3D7	Mitochondrial import inner membrane translocase subunit TIM16 [OS=Homo sapiens]	5.8	18	1	4	1	52	4	1	1	0	4.50.E+06	4.47.E+06	3.75.E+06		4.02.E+06	4.73.E+06	8.35.E+05	4.06.E+06
2248	Q6GMV2	SET and MYND domain-containing protein 5 [OS=Homo sapiens]	5.7	6	1	2	1	40	2	1	1	0								
2249	O43670-1	BUB3-interacting and GLEBS motif-containing protein ZNF207 [OS=Homo sapiens]	5.7	3	1	10	1	107	12	1	1	0	2.37.E+07	2.39.E+07	2.41.E+07	2.51.E+07	3.71.E+07	3.37.E+07	3.69.E+07	3.06.E+07
2250	P82673-1	28S ribosomal protein S35, mitochondrial [OS=Homo sapiens]	5.7	3	1	28	1	138	5	1	1	0	6.92.E+06	1.03.E+07	4.36.E+06	1.33.E+07	1.11.E+07	1.12.E+07	8.59.E+06	1.11.E+07
2251	Q16763	ubiquitin-conjugating enzyme E2 S [OS=Homo sapiens]	5.7	13	2	9	2	14	4	2	2	0	3.52.E+07	1.08.E+07	3.06.E+07	3.82.E+07	7.29.E+06	6.50.E+06	8.76.E+06	5.57.E+06
2252	Q5QJE6	Deoxynucleotidyltransferase terminal-interacting protein 2 [OS=Homo sapiens]	5.7	4	2	14	2	32	2	2	2	0	1.01.E+08	1.02.E+08	2.74.E+07	1.08.E+08	1.00.E+08	1.28.E+08	6.79.E+07	1.15.E+08
2253	Q7Z739	YTH domain-containing family protein 3 [OS=Homo sapiens]	5.7	4	2	12	2	13	9	2	1	0	3.52.E+07	3.86.E+07	3.69.E+07	3.56.E+07	4.12.E+07	4.58.E+07	4.13.E+07	4.27.E+07
2254	Q99735	microsomal glutathione S-transferase 2 [OS=Homo sapiens]	5.7	10	1	16	1	155	18	1	1	0	3.11.E+07	2.77.E+07	3.04.E+07	2.78.E+07	2.42.E+07	2.37.E+07	2.48.E+07	2.76.E+07
2255	P82933	28S ribosomal protein S9, mitochondrial [OS=Homo sapiens]	5.7	3	1	10	1	99	13	1	1	0	1.01.E+07	2.02.E+07	9.52.E+06	1.31.E+07	1.99.E+07	1.78.E+07	1.50.E+07	1.91.E+07
2256	P00846	ATP synthase subunit A [OS=Homo sapiens]	5.6	4	1	62	1	214	74	1	1	0	1.04.E+08	1.13.E+08	1.09.E+08	9.82.E+07	1.10.E+08	1.17.E+08	1.13.E+08	1.18.E+08
2257	Q9BSH4	Translational activator of cytochrome c oxidase 1 [OS=Homo sapiens]	5.6	4	1	2	1	22	2	1	1	0	2.59.E+07	2.35.E+07	2.50.E+07	2.73.E+07	1.62.E+07	1.25.E+07	1.79.E+07	1.62.E+07
2258	P60059	Protein transport protein Sec61 subunit gamma [OS=Homo sapiens]	5.6	18	1	4	1	59	5	1	1	0	1.24.E+07	1.40.E+07	1.12.E+07	1.41.E+07	1.14.E+07	1.07.E+07	9.52.E+06	1.08.E+07
2259	P51159-1	Ras-related protein Rab-27A [OS=Homo sapiens]	5.6	10	2	45	2	14	21	2	2	0	3.14.E+07	3.10.E+07	3.14.E+07	3.06.E+07	3.10.E+07	2.95.E+07	1.96.E+07	2.07.E+07
2260	O95249-1	Golgi SNAP receptor complex member 1 [OS=Homo sapiens]	5.6	5	1	1	1	32			1	0		2.33.E+07		2.09.E+07	4.03.E+07	4.54.E+07	3.59.E+07	3.91.E+07
2261	Q9NX55-2	Huntingtin-interacting protein K [OS=Homo sapiens]	5.6	12	1	84	1	1705	73	1	1	0	3.00.E+07	3.28.E+07	2.82.E+07	3.59.E+07	3.32.E+07	2.91.E+07	2.75.E+07	2.89.E+07
2262	P61086	Ubiquitin-conjugating enzyme E2 K [OS=Homo sapiens]	5.6	14	2	4	2	19	0	2	2	0	9.13.E+06	8.30.E+06	1.16.E+07	1.39.E+07	1.23.E+07	1.26.E+07	1.95.E+07	7.34.E+07
2263	Q9BY42	protein RTF2 homolog [OS=Homo sapiens]	5.6	6	1	4	1	42	5	1	1	0	5.37.E+06	4.49.E+06	7.47.E+06	6.58.E+06	4.54.E+06	5.61.E+06	5.58.E+06	6.63.E+06
2264	Q9HA64	Ketosamine-3-kinase [OS=Homo sapiens]	5.6	6	2	34	2	0	0	2	1	0	3.88.E+07	3.59.E+07	3.88.E+07	3.18.E+07	2.25.E+07	2.77.E+07	3.20.E+07	2.87.E+07
2265	Q8NFH4	Nucleoporin Nup37 [OS=Homo sapiens]	5.5	4	1	4	1	52	2	1	1	0								
2266	Q9UPQ0-1	LIM and calponin homology domains-containing protein 1 [OS=Homo sapiens]	5.5	2	2	10	2	62	2	2	2	0	8.53.E+06	1.16.E+07	1.17.E+07	9.90.E+06	7.92.E+06		8.21.E+06	1.05.E+07
2267	O75438	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 1 [OS=Homo sapiens]	5.5	19	1	18	1	139	21	1	1	0	4.05.E+07	3.64.E+07	3.98.E+07	3.60.E+07	3.60.E+07	4.08.E+07	4.49.E+07	3.87.E+07
2268	Q9H0H5	Rac GTPase-activating protein 1 [OS=Homo sapiens]	5.5	3	2	22	2	58	2	2	2	0	3.93.E+07	3.71.E+07	4.17.E+07	2.96.E+07	3.80.E+07	4.83.E+07	5.97.E+07	4.10.E+07
2269	Q13131	5'-AMP-activated protein kinase catalytic subunit alpha-1 [OS=Homo sapiens]	5.5	3	1	4	1	95	5	1	1	0	8.92.E+06	9.76.E+06	7.52.E+06	8.78.E+06	1.28.E+07	1.27.E+07	1.39.E+07	1.14.E+07
2270	Q9UJY5-1	ADP-ribosylation factor-binding protein GGA1 [OS=Homo sapiens]	5.5	10	2	21	2	0	0	2	2	0	1.79.E+07	2.07.E+07	1.78.E+07	2.17.E+07	2.63.E+07	2.03.E+07	2.22.E+07	2.47.E+07
2271	Q9BQB6-1	vitamin K epoxide reductase complex subunit 1 [OS=Homo sapiens]	5.5	8	1	13	1	26	11	1	1	0	5.18.E+07	3.01.E+07	4.96.E+07	3.98.E+07	4.51.E+07	3.94.E+07	5.65.E+07	4.51.E+07
2272	P49207	60S ribosomal protein L34 [OS=Homo sapiens]	5.5	13	2	154	2	670	106	2	2	0	5.74.E+08	5.48.E+08	5.73.E+08	6.34.E+08	5.75.E+08	4.89.E+08	5.47.E+08	5.37.E+08
2273	Q96FX7	tRNA (adenine(58)-N(1))-methyltransferase catalytic subunit TRMT61A [OS=Homo sapiens]	5.5	13	2	29	2	194	16	1	2	0	1.88.E+08	2.01.E+08	1.62.E+08	6.57.E+06	1.92.E+08	2.05.E+08	1.70.E+08	1.86.E+08
2274	O00506	serine/threonine-protein kinase 25 [OS=Homo sapiens]	5.5	5	2	36	1	39	2	2	2	1	2.88.E+07	3.10.E+07	3.19.E+07	2.91.E+07	2.75.E+07	3.20.E+07	3.21.E+07	2.78.E+07
2275	Q99584	Protein S100-A13 [OS=Homo sapiens]	5.4	12	1	2	1	24	3	1	1	0	2.65.E+07	2.55.E+07	2.25.E+07	2.17.E+07	1.89.E+07	1.97.E+07	1.90.E+07	1.77.E+07
2276	Q4G0F5	Vacuolar protein sorting-associated protein 26B [OS=Homo sapiens]	5.4	3	1	17	1	152	16	1	1	0	1.81.E+07	1.55.E+07	1.87.E+07	1.82.E+07	1.91.E+07	2.03.E+07	2.41.E+07	2.47.E+07
2277	Q9Y6K5	2'-5'-oligoadenylate synthase 3 [OS=Homo sapiens]	5.4	3	1	6	1	43	2	1	1	0	1.00.E+07	9.35.E+06	2.01.E+06	1.03.E+07	1.44.E+07	1.18.E+07	1.04.E+07	1.22.E+07
2278	Q7Z417	Nuclear fragile X mental retardation-interacting protein 2 [OS=Homo sapiens]	5.4	2	1	8	1	62	4	1	1	0	1.07.E+07	1.11.E+07	9.76.E+06	1.18.E+07	1.20.E+07	1.07.E+07	1.50.E+07	9.96.E+06
2279	P36543	V-type proton ATPase subunit E 1 [OS=Homo sapiens]	5.4	6	1	2	1	29	3	1	1	0	1.28.E+07	1.94.E+07	1.42.E+07	1.25.E+07	2.68.E+07	2.40.E+07	2.07.E+07	2.80.E+07
2280	Q969T9	WW domain-binding protein 2 [OS=Homo sapiens]	5.4	4	1	8	1	21	9	1	1	0	7.30.E+06	2.33.E+07	8.51.E+06	8.66.E+06	6.81.E+06	2.44.E+07	7.12.E+06	2.56.E+07
2281	O00244	Copper transport protein ATOX1 [OS=Homo sapiens]	5.4	25	1	10	1	27	4	1	1	0	1.57.E+07	1.91.E+07	1.32.E+07	1.71.E+07	1.66.E+07	1.49.E+07	1.50.E+07	1.64.E+07
2282	Q6NVY1	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial [OS=Homo sapiens]	5.3	5	2	28	2	66	2	2	2	0	3.82.E+07	3.45.E+07	3.81.E+07	3.85.E+07	4.00.E+07	3.86.E+07	4.31.E+07	3.94.E+07
2283	P52655-1	Transcription initiation factor IIA subunit 1 [OS=Homo sapiens]	5.3	3	1	2	1	33	3	1	1	0	4.27.E+07	3.04.E+07	4.21.E+07	4.60.E+07	4.46.E+07	4.59.E+07	1.95.E+07	3.29.E+07

No.	Accession	Description	Sum PEP Score	Coverage [%]	# Peptides	# PSMs	# Unique Peptides	Score Mascot: A5 Mascot	Score Sequest HT: A2 Sequest HT	# Peptides (by Search Engine): A2 Sequest HT	# Peptides (by Search Engine): A5 Mascot	# Razor Peptides	ctrl Abundances_1	ctrl Abundances_2	ctrl Abundances_3	ctrl Abundances_4	JAM-A KO Abundances_1	JAM-A KO Abundances_2	JAM-A KO Abundances_3	JAM-A KO Abundances_4
2284	O60313	Dynamin-like 120 kDa protein, mitochondrial [OS=Homo sapiens]	5.3	4	2	8	2	27	2	2	2	0	6.14.E+06	8.04.E+06	6.79.E+06	1.25.E+07	1.75.E+07	1.55.E+07	1.45.E+07	1.58.E+07
2285	Q8TBX8-1	Phosphatidylinositol 5-phosphate 4-kinase type-2 gamma [OS=Homo sapiens]	5.3	4	1	6	1	33	0	1	1	0	5.10.E+06	5.02.E+06	3.22.E+06	4.94.E+06	2.88.E+06	2.23.E+06	2.24.E+06	2.11.E+06
2286	P78406	mRNA export factor [OS=Homo sapiens]	5.3	4	1	32	1	203	32	1	1	0	2.11.E+07	2.41.E+07	2.16.E+07	1.86.E+07	2.62.E+07	2.81.E+07	2.28.E+07	2.21.E+07
2287	P09497-1	clathrin light chain B [OS=Homo sapiens]	5.3	9	2	14	2	37	14	2	2	0	2.85.E+07	2.48.E+07	3.18.E+07	3.47.E+07	2.84.E+07	2.80.E+07	3.27.E+07	3.05.E+07
2288	Q4G0J3	La-related protein 7 [OS=Homo sapiens]	5.3	2	1	6	1	70	8	1	1	0	1.84.E+07	1.36.E+07	1.14.E+07	1.55.E+07	1.88.E+07	2.43.E+07	1.60.E+07	1.72.E+07
2289	Q9BRP4	Proteasomal ATPase-associated factor 1 [OS=Homo sapiens]	5.3	3	1	6	1	46	7	1	1	0	1.21.E+07	1.49.E+07	1.33.E+07	1.45.E+07	1.41.E+07	1.32.E+07	6.67.E+06	1.27.E+07
2290	P15428-1	15-hydroxyprostaglandin dehydrogenase [NAD(+)] [OS=Homo sapiens]	5.3	8	2	15	2	22	8	2	2	0	1.38.E+07	1.71.E+07	1.44.E+07	1.59.E+07	1.54.E+07	4.19.E+06	2.50.E+06	2.74.E+06
2291	Q03001-7	dystonin [OS=Homo sapiens]	5.3	0	2	6	2	0	2	2	2	0	2.58.E+06			2.35.E+06				
2292	Q9HAV7	GrpE protein homolog 1, mitochondrial [OS=Homo sapiens]	5.3	9	2	25	2	67	29	2	2	0	7.77.E+07	7.25.E+07	8.72.E+07	8.10.E+07	7.52.E+07	6.43.E+07	7.71.E+07	6.31.E+07
2293	Q16513	Serine/threonine-protein kinase N2 [OS=Homo sapiens]	5.2	3	1	6	1	56	8	1	1	0	7.32.E+06	5.73.E+06	4.82.E+06	4.40.E+06	4.75.E+06	7.40.E+06	7.63.E+06	7.34.E+06
2294	O94855	Protein transport protein Sec24D [OS=Homo sapiens]	5.2	2	2	7	1	17	5	2	2	0	1.52.E+07	1.35.E+07	1.35.E+07	1.42.E+07	1.89.E+07	1.99.E+07	1.67.E+07	2.00.E+07
2295	Q9C0E8-1	Protein lunapark [OS=Homo sapiens]	5.2	3	1	2	1	30	3	1	1	0			8.59.E+06	7.55.E+06	1.46.E+07		1.31.E+07	1.43.E+07
2296	O76031	ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial [OS=Homo sapiens]	5.2	2	1	16	1	0	0	1	1	0	9.96.E+06	1.11.E+07	1.76.E+07	1.07.E+07	1.68.E+07	1.19.E+07	1.58.E+07	1.34.E+07
2297	Q9BQ61	Uncharacterized protein C19orf43 [OS=Homo sapiens]	5.2	15	1	12	1	22	0	1	1	0	9.72.E+06	8.25.E+06	7.10.E+06	9.96.E+06	1.45.E+07	1.36.E+07	1.28.E+07	1.36.E+07
2298	P14406	Cytochrome c oxidase subunit 7A2, mitochondrial [OS=Homo sapiens]	5.2	12	1	10	1	175	11	1	1	0	9.49.E+07	9.43.E+07	1.01.E+08	8.25.E+07	7.55.E+07	7.78.E+07	8.40.E+07	7.17.E+07
2299	P50148	Guanine nucleotide-binding protein G(Q) subunit alpha [OS=Homo sapiens]	5.2	6	1	2	1	19	3	1	1	0				5.62.E+06				
2300	Q9Y606	tRNA pseudouridine synthase A, mitochondrial [OS=Homo sapiens]	5.1	3	1	4	1	53	4	1	1	0		5.67.E+06	4.38.E+06	7.02.E+06	9.47.E+06	9.34.E+06	1.03.E+07	9.18.E+06
2301	Q9BYG3	MKI67 FHA domain-interacting nucleolar phosphoprotein [OS=Homo sapiens]	5.1	6	1	8	1	35	9	1	1	0	1.00.E+07	1.18.E+07	1.05.E+07	1.12.E+07	1.20.E+07	1.46.E+07	1.32.E+07	1.22.E+07
2302	Q9UH99	SUN domain-containing protein 2 [OS=Homo sapiens]	5.1	3	1	6	1	51	2	1	1	0	7.13.E+06	7.75.E+06	7.14.E+06	8.48.E+06	1.01.E+07	9.07.E+06	8.67.E+06	8.26.E+06
2303	Q00613	heat shock factor protein 1 [OS=Homo sapiens]	5.1	3	1	4	1	72	0	1	1	0	2.33.E+06	2.69.E+06	1.76.E+06	2.50.E+06	1.64.E+06	1.18.E+06	1.47.E+06	
2304	Q9H788	SH2 domain-containing protein 4A [OS=Homo sapiens]	5.1	4	1	12	1	13	2	1	1	0	6.49.E+06	6.44.E+06	6.68.E+06	6.40.E+06	1.41.E+07	1.35.E+07	1.12.E+07	1.29.E+07
2305	Q29RF7-1	Sister chromatid cohesion protein PDS5 homolog A [OS=Homo sapiens]	5.1	2	2	55	2	247	3	1	2	0	1.16.E+07	9.90.E+06	1.01.E+07	1.05.E+07	1.37.E+07	1.21.E+07	1.35.E+07	1.45.E+07
2306	Q9UEW8	STE20/SPS1-related proline-alanine-rich protein kinase [OS=Homo sapiens]	5.1	5	1	10	1	79	4	1	1	0	3.91.E+06	5.61.E+06	4.72.E+06	8.55.E+06	9.14.E+06	9.06.E+06	6.96.E+06	8.14.E+06
2307	Q96TC7	Regulator of microtubule dynamics protein 3 [OS=Homo sapiens]	5.1	5	1	2	1	62	3	1	1	0	3.73.E+06	1.58.E+06	1.12.E+05	3.46.E+06	1.63.E+05		2.33.E+06	7.01.E+06
2308	P42356	phosphatidylinositol 4-kinase alpha [OS=Homo sapiens]	5.1	2	3	36	3	67	0	3	3	0	3.32.E+07	3.22.E+07	3.36.E+07	2.84.E+07	3.20.E+07	3.24.E+07	3.17.E+07	3.26.E+07
2309	Q9BSC4-1	Nucleolar protein 10 [OS=Homo sapiens]	5.1	2	1	10	1	87	9	1	1	0	4.99.E+06	5.00.E+06	4.47.E+06	6.23.E+06	9.15.E+06	8.85.E+06	4.89.E+06	9.09.E+06
2310	O95674-1	phosphatidate cytidylyltransferase 2 [OS=Homo sapiens]	5.0	5	1	7	1	0	8	1	1	0	6.69.E+06	6.59.E+06	6.39.E+06	6.73.E+06	1.01.E+07	9.39.E+06	8.90.E+06	9.71.E+06
2311	Q9BYD1	39S ribosomal protein L13, mitochondrial [OS=Homo sapiens]	5.0	13	2	19	2	28	3	2	2	0	3.55.E+07	3.55.E+07	3.57.E+07	3.60.E+07	3.84.E+07	3.28.E+07	3.63.E+07	3.85.E+07
2312	Q9Y376	Calcium-binding protein 39 [OS=Homo sapiens]	5.0	3	1	13	1	21	9	1	1	0	1.27.E+08	1.06.E+08	1.20.E+08	1.11.E+08	5.65.E+07	1.32.E+08	8.10.E+07	8.11.E+07
2313	Q9BTD8-1	RNA-binding protein 42 [OS=Homo sapiens]	5.0	4	1	12	1	19	12	1	1	0	2.57.E+07	2.63.E+07	2.10.E+07	3.07.E+07	2.98.E+07	3.28.E+07	1.76.E+07	
2314	Q9Y6I4-1	Ubiquitin carboxyl-terminal hydrolase 3 [OS=Homo sapiens]	5.0	3	1	28	1	377	11	1	1	0	3.72.E+06	1.05.E+07	9.78.E+06	1.29.E+07	2.12.E+07	2.46.E+07	2.02.E+07	2.35.E+07
2315	Q99598	Translin-associated protein X [OS=Homo sapiens]	4.9	7	1	10	1	14	7	1	1	0								
2316	P20962	Parathymosin [OS=Homo sapiens]	4.9	11	1	10	1	23	10	1	1	0	1.16.E+08	1.07.E+08	1.15.E+08	1.38.E+08	1.10.E+08	1.11.E+08	1.26.E+08	1.12.E+08
2317	Q96GQ7	Probable ATP-dependent RNA helicase DDX27 [OS=Homo sapiens]	4.9	1	1	14	1	196	17	1	1	0	2.84.E+07	3.12.E+07	2.58.E+07	2.53.E+07	2.69.E+07	3.23.E+07	2.76.E+07	2.72.E+07
2318	P80404	4-aminobutyrate aminotransferase, mitochondrial [OS=Homo sapiens]	4.9	2	1	2	1	34	2	1	1	0	2.13.E+06	2.41.E+06		4.15.E+06	1.68.E+06	3.06.E+06	1.96.E+06	2.62.E+06
2319	Q9UQ88-1	Cyclin-dependent kinase 11A [OS=Homo sapiens]	4.9	1	1	10	1	63	5	1	1	0	7.23.E+06	7.03.E+06	7.51.E+06	6.42.E+06	1.20.E+07	1.06.E+07	9.28.E+06	1.10.E+07
2320	Q9UHD2	Serine/threonine-protein kinase TBK1 [OS=Homo sapiens]	4.9	4	2	31	2	28	7	2	2	0								
2321	P33981	Dual specificity protein kinase TTK [OS=Homo sapiens]	4.9	2	1	2	1	33	0	1	1	0	2.75.E+06	3.20.E+06	2.88.E+06	3.41.E+06	3.10.E+06	2.11.E+06	2.75.E+06	2.80.E+06
2322	P42345	Serine/threonine-protein kinase mTOR [OS=Homo sapiens]	4.9	2	2	4	2	21	0	2	2	0	1.06.E+07	1.29.E+07	1.28.E+07	8.61.E+06	1.15.E+06	6.71.E+06	3.17.E+06	1.33.E+07
2323	Q53EU6	Glycerol-3-phosphate acyltransferase 3 [OS=Homo sapiens]	4.9	3	1	22	1	50	19	1	1	0	8.04.E+07	8.03.E+07	7.81.E+07	8.72.E+07	5.27.E+07	5.99.E+07	5.30.E+07	4.05.E+07
2324	Q15054	DNA polymerase delta subunit 3 [OS=Homo sapiens]	4.9	3	1	10	1	103	10	1	1	0	7.61.E+06	7.92.E+06	8.69.E+06	8.91.E+06	9.75.E+06	7.87.E+06	1.03.E+07	9.16.E+06
2325	O95218-1	Zinc finger Ran-binding domain-containing protein 2 [OS=Homo sapiens]	4.9	3	1	12	1	42	5	1	1	0	2.46.E+07	2.59.E+07	2.50.E+07	2.12.E+07	2.11.E+07	2.25.E+07	2.09.E+07	2.09.E+07
2326	P49841-1	Glycogen synthase kinase-3 beta [OS=Homo sapiens]	4.9	7	1	6	1	55	4	1	1	0			8.18.E+06	9.86.E+05	1.18.E+07	1.21.E+07	9.58.E+06	1.18.E+07
2327	Q96GC5-1	39S ribosomal protein L48, mitochondrial [OS=Homo sapiens]	4.9	6	1	2	1	19	3	1	1	0		3.36.E+07						
2328	Q13505-1	Metaxin-1 [OS=Homo sapiens]	4.9	3	1	11	1		9	1		0	1.53.E+07	9.57.E+06	1.06.E+07	8.24.E+06	9.75.E+06	1.06.E+07	9.55.E+06	9.17.E+06
2329	O95831-1	Apoptosis-inducing factor 1, mitochondrial [OS=Homo sapiens]	4.9	2	1	14	1	54	16	1	1	0	2.26.E+07	2.38.E+07	2.37.E+07	2.69.E+07	2.74.E+07	2.72.E+07	1.97.E+07	3.01.E+07
2330	Q9Y4X5	E3 ubiquitin-protein ligase ARIH1 [OS=Homo sapiens]	4.9	2	1	6	1	18	0	1	1	0	1.17.E+07	8.83.E+06	1.07.E+07	7.61.E+06	8.16.E+06	8.84.E+06	1.13.E+07	1.17.E+07
2331	Q9H0Q0	Protein FAM49A [OS=Homo sapiens]	4.9	4	1	4	1	37	2	1	1	0								
2332	Q9GZL7	ribosome biogenesis protein WDR12 [OS=Homo sapiens]	4.9	6	1	2	1	23	2	1	1	0	3.81.E+06	3.64.E+06	2.38.E+07	3.36.E+06	6.33.E+06	9.21.E+06	4.02.E+06	9.70.E+06
2333	O75955	Flotillin-1 [OS=Homo sapiens]	4.9	3	1	12	1	85	16	1	1	0	2.09.E+07	2.64.E+07	2.25.E+07	2.34.E+07	3.58.E+07	3.73.E+07	3.70.E+07	3.76.E+07
2334	Q9BRJ6	Uncharacterized protein C7orf50 [OS=Homo sapiens]	4.8	7	1	4	1	44	4	1	1	0	9.75.E+06	1.01.E+07	8.94.E+06	1.14.E+07	1.10.E+07	1.14.E+07	9.65.E+06	1.08.E+07

No.	Accession	Description	Sum PEP Score	Coverage [%]	# Peptides	# PSMs	# Unique Peptides	Score Mascot: A5 Mascot	Score Sequest HT: A2 Sequest HT	# Peptides (by Search Engine): A2 Sequest HT	# Peptides (by Search Engine): A5 Mascot	# Razor Peptides	ctrl Abundances_1	ctrl Abundances_2	ctrl Abundances_3	ctrl Abundances_4	JAM-A KO Abundances_1	JAM-A KO Abundances_2	JAM-A KO Abundances_3	JAM-A KO Abundances_4
2335	Q9H2H8-1	peptidyl-prolyl cis-trans isomerase-like 3 [OS=Homo sapiens]	4.8	7	1	6	1	48	4	1	1	0	6.80.E+06	6.75.E+06	7.41.E+06	5.13.E+06	8.89.E+06	1.00.E+07	1.01.E+07	5.97.E+06
2336	Q9NP92	39S ribosomal protein S30, mitochondrial [OS=Homo sapiens]	4.8	7	2	8	2	0	6	2	2	0	2.30.E+07	2.11.E+07	2.10.E+07	2.15.E+07	2.11.E+07	1.93.E+07	1.57.E+07	1.95.E+07
2337	Q8TED0	U3 small nucleolar RNA-associated protein 15 homolog [OS=Homo sapiens]	4.8	6	1	2	1	24	0	1	1	0	1.13.E+07	2.55.E+06	1.18.E+07	1.19.E+07	1.34.E+06	1.26.E+07	1.06.E+07	
2338	Q7LGA3-1	Heparan sulfate 2-O-sulfotransferase 1 [OS=Homo sapiens]	4.8	5	1	2	1	41	2	1	1	0	9.30.E+05	1.61.E+06	1.13.E+06	5.03.E+05	3.77.E+06	4.27.E+06	2.54.E+06	3.25.E+06
2339	Q7Z4H8	KDEL motif-containing protein 2 [OS=Homo sapiens]	4.8	2	1	4	1	0	2	1	1	0	9.46.E+06	1.90.E+07	9.45.E+06	1.71.E+07	1.76.E+07	3.39.E+07	2.06.E+07	3.07.E+07
2340	Q9NXF1	Testis-expressed protein 10 [OS=Homo sapiens]	4.8	3	2	4	2	26	0	2	2	0	3.87.E+06	4.69.E+06	1.69.E+06	3.14.E+06	1.68.E+07	1.55.E+07	1.36.E+07	1.52.E+07
2341	P51452	dual specificity protein phosphatase 3 [OS=Homo sapiens]	4.8	8	1	2	1	35	2	1	1	0	2.31.E+07	2.64.E+07	2.88.E+07	2.39.E+07	5.49.E+07	5.25.E+07	5.54.E+07	5.54.E+07
2342	Q96S44	TP53-regulating kinase [OS=Homo sapiens]	4.8	8	1	2	1	35	2	1	1	0	7.36.E+06	7.50.E+06	7.43.E+06	1.12.E+07	7.84.E+06	6.69.E+06	5.91.E+06	5.64.E+06
2343	Q14197	Peptidyl-tRNA hydrolase ICT1, mitochondrial [OS=Homo sapiens]	4.8	7	1	12	1	102	18	1	1	0	2.26.E+07	2.55.E+07	2.47.E+07	2.15.E+07	2.32.E+07	2.18.E+07	2.33.E+07	2.55.E+07
2344	Q9Y315	deoxyribose-phosphate aldolase [OS=Homo sapiens]	4.8	7	1	20	1	52	25	1	1	0	1.58.E+07	1.63.E+07	1.61.E+07	9.94.E+06	1.64.E+07	1.62.E+07	1.30.E+07	1.41.E+07
2345	O75792	Ribonuclease H2 subunit A [OS=Homo sapiens]	4.8	5	1	4	1	20	4	1	1	0		1.03.E+07	5.94.E+06	7.63.E+06	1.10.E+07	9.67.E+06	8.70.E+06	1.12.E+07
2346	P54802	alpha-N-acetylglucosaminidase [OS=Homo sapiens]	4.8	2	1	4	1	51	5	1	1	0	4.45.E+06	4.39.E+06	3.89.E+06	4.97.E+06	6.58.E+06	7.11.E+06	6.74.E+06	7.38.E+06
2347	Q9UHR5-1	SAP30-binding protein [OS=Homo sapiens]	4.7	5	1	2	1	36	2	1	1	0								
2348	Q14919-1	Dr1-associated corepressor [OS=Homo sapiens]	4.7	6	2	16	2	28	0	2	2	0	6.82.E+05	4.92.E+06	5.36.E+06	4.55.E+06				
2349	Q99615-1	DnaJ homolog subfamily C member 7 [OS=Homo sapiens]	4.7	2	1	10	1	68	12	1	1	0	2.51.E+07	2.98.E+07	2.60.E+07	2.93.E+07	4.34.E+07	4.00.E+07	3.85.E+07	4.33.E+07
2350	P15151-1	Poliovirus receptor [OS=Homo sapiens]	4.7	5	2	18	2	39	22	2	2	0	3.81.E+07	3.67.E+07	4.36.E+07	4.64.E+07	2.38.E+07	2.81.E+07	2.81.E+07	2.76.E+07
2351	A4D1E9-1	GTP-binding protein 10 [OS=Homo sapiens]	4.7	7	1	4	1	22	0	1	1	0	2.93.E+06	7.24.E+06	6.50.E+06	1.25.E+06	7.87.E+06	8.49.E+06	2.68.E+06	7.92.E+06
2352	O94915-1	protein furry homolog-like [OS=Homo sapiens]	4.7	1	2	49	2	61	0	1	2	0				2.20.E+05	3.19.E+06	2.51.E+06	2.48.E+06	2.35.E+06
2353	Q8NI27-1	THO complex subunit 2 [OS=Homo sapiens]	4.7	2	2	12	2	20	0	2	2	0	7.20.E+06	7.22.E+06	5.93.E+06	6.32.E+06	1.26.E+07	1.12.E+07	8.96.E+06	1.24.E+07
2354	Q9BST9	Rhotekin [OS=Homo sapiens]	4.7	3	1	2	1	21	3	1	1	0								
2355	Q96Q11-1	CCA tRNA nucleotidyltransferase 1, mitochondrial [OS=Homo sapiens]	4.7	4	1	10	1	36	0	1	1	0	4.75.E+06	7.40.E+06	3.95.E+06	7.92.E+06	8.32.E+06	7.87.E+06	7.37.E+06	8.77.E+06
2356	Q96G21	U3 small nucleolar ribonucleoprotein protein IMP4 [OS=Homo sapiens]	4.7	3	1	12	1	54	2	1	1	0	4.09.E+06	4.31.E+06	4.70.E+06	3.87.E+06	2.93.E+06	3.29.E+06	3.34.E+06	3.01.E+06
2357	O95049-1	Tight junction protein ZO-3 [OS=Homo sapiens]	4.7	2	2	9	2	71	0	1	2	0	9.31.E+06	8.75.E+06	1.01.E+07	7.85.E+06	8.97.E+06	9.97.E+06	7.16.E+06	9.45.E+06
2358	Q9NVU7	Protein SDA1 homolog [OS=Homo sapiens]	4.6	4	2	3	2	33	3	1	2	0								
2359	Q9UGJ1	gamma-tubulin complex component 4 [OS=Homo sapiens]	4.6	3	1	8	1	26	0	1	1	0	5.54.E+06	8.03.E+06	5.14.E+06	7.53.E+06	6.01.E+06	3.59.E+06	4.40.E+06	5.09.E+06
2360	Q13308-1	Inactive tyrosine-protein kinase 7 [OS=Homo sapiens]	4.6	1	1	8	1	29	8	1	1	0	8.02.E+06	6.45.E+06	9.24.E+06	7.36.E+06	1.50.E+07	1.35.E+07	1.67.E+07	1.64.E+07
2361	Q9H1E3	Nuclear ubiquitous casein and cyclin-dependent kinase substrate 1 [OS=Homo sapiens]	4.6	12	2	49	2	90	11	2	2	0	8.82.E+06	7.99.E+06	9.09.E+06	6.91.E+06	7.04.E+06	8.01.E+06	8.86.E+06	7.26.E+06
2362	Q07817-1	bcl-2-like protein 1 [OS=Homo sapiens]	4.6	4	1	16	1	138	17	1	1	0	9.93.E+06	1.08.E+07	9.42.E+06	1.13.E+07	9.84.E+06	7.85.E+06	1.90.E+06	7.73.E+06
2363	P49407-1	Beta-arrestin-1 [OS=Homo sapiens]	4.6	10	2	5	2	20	0	2	2	0	1.35.E+07	1.51.E+07	3.30.E+06	3.92.E+06	2.38.E+07	2.13.E+06	1.47.E+07	2.30.E+06
2364	Q9NVP2	Histone chaperone ASF1B [OS=Homo sapiens]	4.6	10	1	14	1	22	7	1	1	0	1.30.E+07	1.38.E+07	1.24.E+07	2.06.E+07	1.10.E+07	1.20.E+07	1.06.E+07	1.22.E+07
2365	Q9UKS6	Protein kinase C and casein kinase substrate in neurons protein 3 [OS=Homo sapiens]	4.6	5	2	10	2	0	4	2	2	0	3.58.E+07	3.79.E+07	3.23.E+07	3.40.E+07	2.61.E+07	2.64.E+07	2.75.E+07	2.86.E+07
2366	A0AV96	RNA-binding protein 47 [OS=Homo sapiens]	4.6	2	1	4	1	20	2	1	1	0	1.10.E+07	1.09.E+07	1.04.E+07	1.39.E+07	1.40.E+07	1.25.E+07	1.34.E+07	1.36.E+07
2367	Q9BRT3	migration and invasion enhancer 1 [OS=Homo sapiens]	4.6	10	1	23	1	13	23	1	1	0	3.57.E+07	3.14.E+07	3.26.E+07	3.07.E+07	5.62.E+07	5.77.E+07	6.07.E+07	6.02.E+07
2368	Q7KZ85	transcription elongation factor spt6 [OS=Homo sapiens]	4.6	2	2	22	2	19	0	1	2	0	1.67.E+07	1.07.E+07	1.79.E+07	2.18.E+07	1.43.E+07	1.52.E+07	1.73.E+07	1.56.E+07
2369	Q9Y3E0	vesicle transport protein GOT1B [OS=Homo sapiens]	4.6	11	1	14	1	98	22	1	1	0	1.17.E+07	7.56.E+06	6.76.E+06	1.55.E+07	1.74.E+07	1.89.E+07	1.89.E+07	2.23.E+07
2370	Q9BUL9	Ribonuclease P protein subunit p25 [OS=Homo sapiens]	4.5	6	1	17	1	35	2	1	1	0	1.70.E+07	1.67.E+07	1.70.E+07	1.66.E+07	2.05.E+07	2.08.E+07	1.87.E+06	2.29.E+07
2371	Q8NC56-1	LEM domain-containing protein 2 [OS=Homo sapiens]	4.5	3	1	2	1	25	2	1	1	0								
2372	P02765	Alpha-2-HS-glycoprotein [OS=Homo sapiens]	4.5	4	2	7	2		0	2		0	2.72.E+05	4.01.E+05	3.71.E+05	3.60.E+05	1.29.E+06	3.66.E+05	1.15.E+06	1.45.E+06
2373	O43760	Synaptogyrin-2 [OS=Homo sapiens]	4.5	8	2	29	2	73	22	2	2	0	5.07.E+07	4.56.E+07	5.24.E+07	5.44.E+07	2.78.E+07	2.53.E+07	2.93.E+07	2.40.E+07
2374	O96000	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10 [OS=Homo sapiens]	4.5	8	1	28	1	41	37	1	1	0	1.59.E+08	1.76.E+08	1.52.E+08	1.50.E+08	2.21.E+08	2.36.E+08	2.13.E+08	2.20.E+08
2375	P46976-1	Glycogenin-1 [OS=Homo sapiens]	4.5	6	2	8	2	24	2	2	2	0	2.48.E+07	2.22.E+07	2.43.E+07	2.76.E+07	2.17.E+07	2.12.E+07	2.51.E+07	2.26.E+07
2376	O14965	Aurora kinase A [OS=Homo sapiens]	4.5	3	1	8	1	34	4	1	1	0								
2377	Q9C0A0-1	Contactin-associated protein-like 4 [OS=Homo sapiens]	4.5	1	2	23	1	68	2	1	2	0	7.18.E+06	6.80.E+06	9.14.E+06	9.05.E+06	1.33.E+07	1.28.E+07	1.66.E+07	1.35.E+07
2378	Q9Y3D9	28S ribosomal protein S23, mitochondrial [OS=Homo sapiens]	4.5	5	1	20	1	114	23	1	1	0	3.12.E+07	2.31.E+07	2.23.E+07	1.83.E+07	1.79.E+07	2.42.E+07	2.40.E+07	2.30.E+07
2379	Q92597	Protein NDRG1 [OS=Homo sapiens]	4.5	5	1	10	1	23	2	1	1	0	9.08.E+06	9.05.E+06	9.73.E+06	9.11.E+06	1.11.E+07	1.04.E+07	2.19.E+06	1.09.E+07
2380	Q9GZP8-1	Immortalization up-regulated protein [OS=Homo sapiens]	4.5	25	1	4	1	17	6	1	1	0	2.73.E+07	2.73.E+07	2.46.E+07	2.64.E+07	1.81.E+07	1.61.E+07	1.12.E+07	
2381	Q05682-1	Caldesmon [OS=Homo sapiens]	4.5	4	2	13	2	0	2	2	2	0	4.79.E+06	9.94.E+06	1.27.E+07	1.57.E+07	1.57.E+06	2.98.E+06	1.29.E+06	1.44.E+07
2382	P82909	28S ribosomal protein S36, mitochondrial [OS=Homo sapiens]	4.5	16	1	12	1	18	2	1	1	0	9.80.E+06	9.44.E+06	9.78.E+06	7.82.E+06	6.73.E+06	7.69.E+06	8.06.E+06	7.24.E+06
2383	P62310	U6 snRNA-associated Sm-like protein LSm3 [OS=Homo sapiens]	4.4	12	1	50	1	281	66	1	1	0	5.84.E+07	5.89.E+07	5.82.E+07	5.08.E+07	6.52.E+07	6.53.E+07	6.80.E+07	6.72.E+07
2384	P13473-1	Lysosome-associated membrane glycoprotein 2 [OS=Homo sapiens]	4.4	2	1	10	1	130	11	1	1	0	3.56.E+07	3.93.E+07	3.70.E+07	3.36.E+07	3.29.E+07	3.38.E+07	3.43.E+07	3.37.E+07
2385	Q5K4L6-1	Long-chain fatty acid transport protein 3 [OS=Homo sapiens]	4.4	3	1	2	1	25	2	1	1	0	1.23.E+07	7.02.E+06	5.87.E+06	5.96.E+06	3.54.E+06	1.77.E+07		4.26.E+06
2386	P49356	protein farnesyltransferase subunit beta [OS=Homo sapiens]	4.4	4	1	2	1	42	2	1	1	0	9.14.E+06	5.18.E+06	4.62.E+06	1.63.E+07	1.01.E+07	1.31.E+07	4.88.E+06	1.00.E+07
2387	Q8IXH7	Negative elongation factor C/D [OS=Homo sapiens]	4.4	3	1	2	1	53	0	1	1	0	2.60.E+06	2.84.E+06	2.87.E+06	4.45.E+06	3.21.E+06	2.84.E+06	3.12.E+06	2.31.E+06
2388	O75521	Enoyl-CoA delta isomerase 2, mitochondrial [OS=Homo sapiens]	4.4	4	1	2	1	19	0	1	1	0	8.51.E+06	3.81.E+06	2.99.E+06	3.92.E+06	3.35.E+06	3.58.E+06	1.97.E+06	7.12.E+06

No.	Accession	Description	Sum PEP Score	Coverage [%]	# Peptides	# PSMs	# Unique Peptides	Score Mascot: A5 Mascot	Score Sequest HT: A2 Sequest HT	# Peptides (by Search Engine): A2 Sequest HT	# Peptides (by Search Engine): A5 Mascot	# Razor Peptides	ctrl Abundances_1	ctrl Abundances_2	ctrl Abundances_3	ctrl Abundances_4	JAM-A KO Abundances_1	JAM-A KO Abundances_2	JAM-A KO Abundances_3	JAM-A KO Abundances_4
2389	Q9BV10	Dol-P-Man:Man(7)GlcNAc(2)-PP-Dol alpha-1,6-mannosyltransferase [OS=Homo sapiens]	4.4	3	1	4	1	35	2	1	1	0	2.17.E+06	1.72.E+06	1.80.E+06	2.50.E+06	1.48.E+06			1.29.E+06
2390	Q9NZ45	CDGSH iron-sulfur domain-containing protein 1 [OS=Homo sapiens]	4.4	14	1	22	1	31	25	1	1	0	1.99.E+07	2.47.E+07	2.65.E+07	2.36.E+07	3.57.E+07	3.83.E+07	4.13.E+07	3.61.E+07
2391	Q9NXG2	THUMP domain-containing protein 1 [OS=Homo sapiens]	4.4	3	1	4	1	16	4	1	1	0	2.08.E+06	2.95.E+06	1.95.E+06	2.52.E+05	6.12.E+06	5.49.E+06	7.86.E+06	8.58.E+06
2392	Q15714-1	TSC22 domain family protein 1 [OS=Homo sapiens]	4.4	1	1	8	1	31	10	1	1	0	2.64.E+07	2.49.E+07	2.97.E+07	3.66.E+07	1.25.E+07			
2393	Q7L0Y3	Mitochondrial ribonuclease P protein 1 [OS=Homo sapiens]	4.4	3	1	7	1	0	2	1	1	0	8.23.E+06	1.09.E+07	9.70.E+06	1.15.E+07	1.04.E+07	9.17.E+06	9.22.E+06	9.95.E+06
2394	O96019-1	Actin-like protein 6A [OS=Homo sapiens]	4.4	2	1	22	1	84	2	1	1	0	5.91.E+06	5.52.E+06	6.75.E+06	7.57.E+06	4.48.E+06	4.85.E+06	5.78.E+06	4.94.E+06
2395	Q96CD2-1	phosphopantothenoylcysteine decarboxylase [OS=Homo sapiens]	4.3	8	1	2	1	18	2	1	1	0	4.53.E+06	5.47.E+06	4.25.E+06	4.60.E+06	7.15.E+06	7.19.E+06	5.89.E+06	7.68.E+06
2396	Q14692	ribosome biogenesis protein BMS1 homolog [OS=Homo sapiens]	4.3	2	1	12	1	68	5	1	1	0	1.08.E+07	1.17.E+07	9.76.E+06	1.12.E+07	9.48.E+06	4.92.E+05	8.64.E+06	4.18.E+06
2397	P58511	Small integral membrane protein 11A [OS=Homo sapiens]	4.3	26	1	14	1	27	2	1	1	0		5.78.E+06			4.49.E+06		4.94.E+06	
2398	Q6UWP7-1	Lysocardiolipin acyltransferase 1 [OS=Homo sapiens]	4.3	2	1	30	1	0	0	1	1	0	8.26.E+06	8.59.E+06	9.36.E+06	7.54.E+06	8.25.E+06	7.80.E+06	8.51.E+06	8.44.E+06
2399	Q9Y6V7	Probable ATP-dependent RNA helicase ddx49 [OS=Homo sapiens]	4.3	4	1	2	1	52	2	1	1	0								
2400	Q8IZP0	abl interactor 1 [OS=Homo sapiens]	4.3	3	1	2	1	50			1	0	7.06.E+06	1.10.E+07	2.86.E+06		8.95.E+06	9.22.E+06	8.25.E+06	1.06.E+07
2401	Q96KA5-1	cleft lip and palate transmembrane protein 1-like protein [OS=Homo sapiens]	4.3	4	1	4	1	0	2	1	1	0		1.78.E+07	1.19.E+07	1.66.E+07			1.28.E+06	9.47.E+05
2402	Q9UBW8	COP9 signalosome complex subunit 7a [OS=Homo sapiens]	4.3	5	1	4	1	22	5	1	1	0								
2403	Q9H6T3	RNA polymerase II-associated protein 3 [OS=Homo sapiens]	4.3	2	1	28	1	129	6	1	1	0	4.05.E+06	4.33.E+06	2.88.E+06	4.47.E+06	1.29.E+07	1.04.E+07	8.94.E+06	1.08.E+07
2404	Q2LD37-1	Uncharacterized protein KIAA1109 [OS=Homo sapiens]	4.3	0	1	143	1	0	0	1	1	0	1.14.E+07	1.04.E+07	1.22.E+07	1.01.E+07	1.65.E+07	1.70.E+07	1.92.E+07	1.83.E+07
2405	Q96T60	Bifunctional polynucleotide phosphatase/kinase [OS=Homo sapiens]	4.3	2	1	8	1	0	7	1	1	0								
2406	P12074	Cytochrome c oxidase subunit 6A1, mitochondrial [OS=Homo sapiens]	4.3	43	2	10	2	0	11	2	1	0	9.74.E+07	1.10.E+08	9.59.E+07	1.07.E+08	1.11.E+08	1.11.E+08	1.07.E+08	1.01.E+08
2407	Q9H061-1	Transmembrane protein 126A [OS=Homo sapiens]	4.3	5	1	34	1	89	33	1	1	0	1.43.E+07	1.85.E+07	1.53.E+07	2.45.E+07	2.17.E+07	2.04.E+07	1.34.E+07	2.37.E+07
2408	Q9NUW8	tyrosyl-DNA phosphodiesterase 1 [OS=Homo sapiens]	4.2	2	1	33	1	23	0	1	1	0	1.91.E+06	1.91.E+06	2.24.E+06	1.39.E+06	1.89.E+06	2.26.E+06	2.44.E+06	1.99.E+06
2409	P36406-1	E3 ubiquitin-protein ligase TRIM23 [OS=Homo sapiens]	4.2	2	1	18	1	79	21	1	1	0	3.02.E+07	2.79.E+07	2.94.E+07	2.77.E+07	3.03.E+07	3.54.E+07	3.29.E+06	2.93.E+07
2410	Q5JRX3-2	Isoform 2 of Presequence protease, mitochondrial [OS=Homo sapiens]	4.2	3	1	2	1		0	1		0	5.91.E+06	6.34.E+06	6.11.E+06	6.62.E+06	5.68.E+06	6.35.E+06	5.99.E+06	5.86.E+06
2411	Q6P9B6	TLD domain-containing protein 1 [OS=Homo sapiens]	4.2	4	1	2	1	35	0	1	1	0	6.74.E+06	6.02.E+06	8.02.E+06	6.16.E+06	7.13.E+06	5.30.E+06	3.92.E+06	6.80.E+06
2412	Q9BV40	vesicle-associated membrane protein 8 [OS=Homo sapiens]	4.2	14	1	24	1	16	23	1	1	0	7.30.E+06	1.15.E+07	1.08.E+07	1.18.E+07	9.22.E+06	8.23.E+06	9.02.E+06	1.02.E+07
2413	Q96B49	Mitochondrial import receptor subunit TOM6 homolog OS=Homo sapiens OX=9606 GN=TOMM6 PE=1 SV=1	4.2	38	1	4	1	36			1	0	1.31.E+07	1.64.E+07	1.27.E+07	1.47.E+07	1.45.E+07	1.52.E+07	1.47.E+07	2.05.E+07
2414	P49840	Glycogen synthase kinase-3 alpha [OS=Homo sapiens]	4.2	3	1	3	1	0	5	1	1	0								
2415	Q01581	hydroxymethylglutaryl-CoA synthase, cytoplasmic [OS=Homo sapiens]	4.2	4	1	6	1	15	2	1	1	0	1.34.E+07	2.31.E+07	9.97.E+06	1.17.E+07	2.06.E+07	2.94.E+07	2.63.E+07	2.17.E+07
2416	Q92947-1	Glutaryl-CoA dehydrogenase, mitochondrial [OS=Homo sapiens]	4.2	6	1	2	1	16	2	1	1	0	6.53.E+06	3.12.E+06	5.22.E+06	6.36.E+06	5.01.E+05	3.48.E+06	2.68.E+06	2.24.E+06
2417	P51690	Arylsulfatase E [OS=Homo sapiens]	4.2	2	1	6	1	51	2	1	1	0			1.92.E+05	3.22.E+05	7.83.E+06	6.56.E+06	6.66.E+06	6.26.E+06
2418	O75976	Carboxypeptidase D [OS=Homo sapiens]	4.2	1	1	7	1	62	0	1	1	0		9.70.E+06	8.06.E+06	5.94.E+06	1.24.E+07	1.01.E+07	6.32.E+06	8.99.E+06
2419	P23434	Glycine cleavage system H protein, mitochondrial [OS=Homo sapiens]	4.1	6	1	32	1	19	18	1	1	0	3.58.E+07	4.35.E+07	4.22.E+07	3.44.E+07	4.25.E+07	4.15.E+07	4.00.E+07	3.98.E+07
2420	Q96A35	39S ribosomal protein L24, mitochondrial [OS=Homo sapiens]	4.1	6	1	6	1	0	6	1	1	0								1.18.E+07
2421	Q9H5V8-1	CUB domain-containing protein 1 [OS=Homo sapiens]	4.1	2	1	2	1	13	3	1	1	0	6.79.E+06	6.35.E+06	6.17.E+06	4.92.E+06	7.40.E+06	9.26.E+06	1.36.E+07	5.73.E+06
2422	Q8TBC4-1	NEDD8-activating enzyme E1 catalytic subunit [OS=Homo sapiens]	4.1	5	1	14	1	0	4	1	1	0	1.13.E+07	1.41.E+07	1.32.E+07	1.71.E+07	1.83.E+07	1.82.E+07	1.74.E+07	1.25.E+07
2423	Q9H267	Vacuolar protein sorting-associated protein 33B [OS=Homo sapiens]	4.1	2	1	6	1	76	5	1	1	0	6.82.E+06	6.89.E+06	4.74.E+06	6.41.E+06	7.19.E+06	4.88.E+06	3.62.E+06	5.75.E+06
2424	Q96C23	aldose 1-epimerase [OS=Homo sapiens]	4.1	7	1	8	1	89	5	1	1	0	4.92.E+06	7.03.E+06	2.98.E+06	6.20.E+06				
2425	P09848	Lactase-phlorizin hydrolase [OS=Homo sapiens]	4.1	2	2	6	2	0	7	2	1	0	2.61.E+07	3.15.E+07	3.69.E+07	3.36.E+07	4.32.E+07	3.79.E+07	5.54.E+07	3.64.E+07
2426	Q9BRP8	Partner of Y14 and mago [OS=Homo sapiens]	4.1	7	1	4	1	43	4	1	1	0	1.46.E+07	1.07.E+07	9.53.E+06	1.16.E+07	1.45.E+07	1.50.E+07	1.42.E+07	1.23.E+07
2427	Q96S97	myeloid-associated differentiation marker [OS=Homo sapiens]	4.1	5	2	20	2	14	0	2	1	0	4.06.E+07	2.37.E+07	1.74.E+07	2.15.E+07	6.71.E+06		6.00.E+06	1.81.E+07
2428	P21246	Pleiotrophin [OS=Homo sapiens]	4.1	14	1	2	1	19	2	1	1	0								
2429	Q96MW1	Coiled-coil domain-containing protein 43 [OS=Homo sapiens]	4.0	5	1	4	1	23	4	1	1	0		1.83.E+07	1.98.E+07	1.69.E+07	2.42.E+07	2.27.E+07	2.74.E+07	3.02.E+07
2430	P35610	sterol O-acyltransferase 1 [OS=Homo sapiens]	4.0	3	1	35	1	112	13	1	1	0	1.39.E+07	1.33.E+07	1.25.E+07	1.09.E+07	2.21.E+07	2.37.E+07	1.99.E+07	2.12.E+07
2431	Q8IV08	Phospholipase D3 [OS=Homo sapiens]	4.0	2	1	10	1	87	12	1	1	0	4.60.E+07	3.14.E+07	2.98.E+07	2.66.E+07				
2432	Q6PD74	Alpha- and gamma-adaptin-binding protein p34 [OS=Homo sapiens]	4.0	4	1	4	1	52	2	1	1	0	8.35.E+06	7.02.E+06	2.95.E+06	1.03.E+07	2.18.E+07	1.82.E+07	2.29.E+07	1.78.E+07
2433	Q9Y3A3	MOB-like protein phocein [OS=Homo sapiens]	4.0	4	1	14	1	13	2	1	1	0	9.40.E+06	8.63.E+06	8.75.E+06	8.99.E+06	7.53.E+06	8.09.E+06	9.84.E+06	8.43.E+06
2434	Q9Y4A5	Transformation/transcription domain-associated protein [OS=Homo sapiens]	4.0	1	2	10	2	0	0	1	2	0	1.15.E+07	9.60.E+06	1.25.E+07	1.09.E+07	1.39.E+07	1.49.E+07	1.69.E+07	1.39.E+07
2435	Q9NWU2	Glucose-induced degradation protein 8 homolog [OS=Homo sapiens]	4.0	10	1	8	1	57	9	1	1	0		1.98.E+06			1.13.E+07	9.32.E+06	8.95.E+06	8.98.E+06
2436	Q8TEQ6	gem-associated protein 5 [OS=Homo sapiens]	3.9	2	1	10	1	18	0	1	1	0	5.35.E+06	7.16.E+06	5.67.E+06	6.93.E+06	6.16.E+06	6.11.E+06	4.59.E+06	6.59.E+06
2437	P51451	Tyrosine-protein kinase Blk [OS=Homo sapiens]	3.9	3	2	45	1	207	7	1	2	0	2.70.E+08	2.48.E+08	2.64.E+08	2.93.E+08	2.96.E+08	2.66.E+08	3.00.E+08	2.81.E+08
2438	Q9NQZ2	Something about silencing protein 10 [OS=Homo sapiens]	3.9	5	1	26	1	67	15	1	1	0	1.77.E+07	2.71.E+07		2.72.E+07		1.87.E+07	1.12.E+07	2.14.E+07

No.	Accession	Description	Sum PEP Score	Coverage [%]	# Peptides	# PSMs	# Unique Peptides	Score Mascot: A5 Mascot	Score Sequest HT: A2 Sequest HT	# Peptides (by Search Engine): A2 Sequest HT	# Peptides (by Search Engine): A5 Mascot	# Razor Peptides	ctrl Abundances_1	ctrl Abundances_2	ctrl Abundances_3	ctrl Abundances_4	JAM-A KO Abundances_1	JAM-A KO Abundances_2	JAM-A KO Abundances_3	JAM-A KO Abundances_4
2439	Q9UIJ7-1	GTP:AMP phosphotransferase AK3, mitochondrial [OS=Homo sapiens]	3.9	7	1	2	1	26	2	1	1	0	6.14.E+06	6.87.E+06	4.27.E+06	5.36.E+06	9.60.E+06	8.60.E+06	1.00.E+07	1.05.E+07
2440	P29084	transcription initiation factor iie subunit beta [OS=Homo sapiens]	3.9	7	1	9	1	16	8	1	1	0	6.44.E+06	8.13.E+06	6.41.E+06	8.36.E+06	7.19.E+06	6.16.E+06	4.42.E+06	7.87.E+06
2441	Q5T440	Putative transferase CAF17, mitochondrial [OS=Homo sapiens]	3.9	9	1	4	1	46	5	1	1	0			1.64.E+06	4.45.E+06	3.54.E+06	3.15.E+06	3.23.E+06	3.66.E+06
2442	Q96G23	Ceramide synthase 2 [OS=Homo sapiens]	3.9	2	1	8	1	33	7	1	1	0	5.90.E+07	5.19.E+07	5.30.E+07	4.75.E+07	5.75.E+07	5.03.E+07	5.71.E+07	5.35.E+07
2443	Q9GZM5	protein YIPF3 [OS=Homo sapiens]	3.9	7	1	6	1	17	9	1	1	0	7.37.E+06	1.02.E+07	7.29.E+06	7.93.E+06	1.07.E+06			
2444	Q9C0C2	182 kDa tankyrase-1-binding protein [OS=Homo sapiens]	3.9	1	1	2	1	42	2	1	1	0								
2445	Q9NRN7	L-aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase [OS=Homo sapiens]	3.9	4	1	2	1	18	2	1	1	0	1.81.E+07		2.27.E+07	2.11.E+07	2.73.E+07	2.46.E+07	2.03.E+07	3.11.E+07
2446	Q7L5D6	Golgi to ER traffic protein 4 homolog [OS=Homo sapiens]	3.9	4	1	4	1	16			1	0	2.32.E+07	2.62.E+07	2.62.E+07	2.12.E+07	2.68.E+07	2.25.E+07	2.72.E+07	2.50.E+07
2447	Q3KQU3	MAP7 domain-containing protein 1 [OS=Homo sapiens]	3.8	2	1	12	1	54	4	1	1	0								
2448	Q13523	Serine/threonine-protein kinase PRP4 homolog [OS=Homo sapiens]	3.8	1	1	4	1	35	4	1	1	0	6.85.E+06	5.62.E+06	4.20.E+06	6.25.E+06	1.25.E+07	7.78.E+06	6.34.E+06	9.10.E+06
2449	Q9NQH7-1	Probable Xaa-Pro aminopeptidase 3 [OS=Homo sapiens]	3.8	7	2	293	1	1103	12	2	2	0	9.29.E+06	1.12.E+07	5.92.E+06	1.12.E+07	1.28.E+07	1.15.E+07	1.04.E+07	
2450	Q8TEA8	D-tyrosyl-tRNA(Tyr) deacylase 1 [OS=Homo sapiens]	3.8	13	2	17	2	19	2	2	1	0	5.03.E+06	5.44.E+06	5.06.E+06	4.20.E+06	4.61.E+06	5.65.E+06	5.47.E+06	4.97.E+06
2451	Q9H5Q4	Dimethyladenosine transferase 2, mitochondrial [OS=Homo sapiens]	3.8	4	1	8	1	15	8	1	1	0	8.06.E+06	1.06.E+07	7.70.E+06	7.82.E+06	1.25.E+07	1.18.E+07	9.49.E+06	9.91.E+06
2452	Q8IWA0	WD repeat-containing protein 75 [OS=Homo sapiens]	3.8	2	1	12	1	76	10	1	1	0	9.73.E+06	9.24.E+06	6.93.E+06	9.29.E+06	9.64.E+06	9.59.E+06	6.31.E+06	9.19.E+06
2453	P42566-1	epidermal growth factor receptor substrate 15 [OS=Homo sapiens]	3.8	2	1	9	1	39	0	1	1	0	5.82.E+06	6.00.E+06	4.73.E+06	6.88.E+06	8.51.E+06	8.24.E+06	7.13.E+06	7.95.E+06
2454	Q9UHI6	Probable ATP-dependent RNA helicase DDX20 [OS=Homo sapiens]	3.8	3	1	2	1	0	3	1	1	0	1.03.E+07	1.13.E+07	9.52.E+06	1.14.E+07	1.11.E+07	5.32.E+06	1.12.E+07	1.06.E+07
2455	O43299	AP-5 complex subunit zeta-1 [OS=Homo sapiens]	3.8	2	1	15	1	23			1	0	1.69.E+07	2.52.E+07	1.97.E+07	2.60.E+07	2.19.E+07	2.48.E+07	2.95.E+07	2.61.E+07
2456	Q96T23	remodeling and spacing factor 1 [OS=Homo sapiens]	3.8	1	1	10	1	31	9	1	1	0	4.22.E+06	5.82.E+06	6.45.E+06	6.24.E+06	6.98.E+06	5.33.E+06	4.30.E+06	5.21.E+06
2457	Q9NYC9-1	Dynein heavy chain 9, axonemal [OS=Homo sapiens]	3.8	0	1	5	1	23	5	1	1	0	3.46.E+07	3.27.E+07	3.21.E+07	2.95.E+07	2.82.E+07	2.89.E+07	3.07.E+07	2.91.E+07
2458	Q9BXB5	Oxysterol-binding protein-related protein 10 [OS=Homo sapiens]	3.8	1	1	6	1	22	2	1	1	0	7.99.E+06	6.94.E+06	6.93.E+06	7.92.E+06	7.19.E+06	6.73.E+06	7.82.E+05	7.25.E+06
2459	Q9GZY8-1	Mitochondrial fission factor [OS=Homo sapiens]	3.8	9	1	25	1	13	2	1	1	0		1.33.E+07		1.25.E+07	1.64.E+07	1.95.E+07	1.60.E+07	1.93.E+07
2460	Q70Z35-1	Phosphatidylinositol 3,4,5-trisphosphate-dependent Rac exchanger 2 protein [OS=Homo sapiens]	3.8	1	1	66	1	0	0	1	1	0	2.22.E+07	1.48.E+07	1.91.E+07	1.46.E+07	1.09.E+07	1.19.E+07	1.15.E+07	8.98.E+06
2461	Q9GZZ9-1	Ubiquitin-like modifier-activating enzyme 5 [OS=Homo sapiens]	3.8	5	1	14	1	0	2	1	1	0	6.55.E+06	7.92.E+06	5.93.E+06	6.19.E+06	8.92.E+06	8.92.E+06	8.31.E+06	9.82.E+06
2462	Q9BV20-1	methylthioribose-1-phosphate isomerase [OS=Homo sapiens]	3.8	4	1	21	1	65	5	1	1	0	5.89.E+06	7.53.E+06	4.47.E+06	5.06.E+06	1.24.E+07	1.09.E+07	9.51.E+06	1.11.E+07
2463	Q8NBQ5	Estradiol 17-beta-dehydrogenase 11 [OS=Homo sapiens]	3.7	5	1	3	1	20	0	1	1	0	4.72.E+06	4.54.E+06	2.73.E+06	5.20.E+06	7.66.E+06	6.64.E+06	6.75.E+06	5.47.E+06
2464	Q9P0R6	GSK3-beta interaction protein [OS=Homo sapiens]	3.7	24	1	4	1	55	2	1	1	0	8.40.E+06	9.71.E+06	8.60.E+06	2.20.E+06	1.50.E+07	4.71.E+06	1.18.E+07	1.43.E+07
2465	O43264	Centromere/kinetochore protein zw10 homolog [OS=Homo sapiens]	3.7	2	1	4	1	48	4	1	1	0		5.40.E+06		4.68.E+06	7.46.E+06	3.34.E+06	6.10.E+06	6.11.E+06
2466	Q15020	Squamous cell carcinoma antigen recognized by T-cells 3 [OS=Homo sapiens]	3.7	1	1	2	1	18	2	1	1	0	6.22.E+06		1.13.E+07		7.57.E+06		8.43.E+06	1.00.E+07
2467	P00395	Cytochrome c oxidase subunit 1 [OS=Homo sapiens]	3.7	6	1	2	1	0	0	1	1	0	1.13.E+07	8.28.E+06	2.25.E+06	2.75.E+06	4.14.E+06	2.03.E+06		5.04.E+06
2468	Q8WTS6	Histone-lysine N-methyltransferase SETD7 [OS=Homo sapiens]	3.7	4	1	6	1	26	6	1	1	0	2.15.E+07	2.30.E+07	2.23.E+07	3.28.E+07	3.88.E+07		5.08.E+07	4.16.E+07
2469	Q8WXC6-2	COP9 signalosome complex subunit 9 [OS=Homo sapiens]	3.7	35	1	40	1	745	45	1	1	0	1.39.E+07	1.64.E+07	1.41.E+07	1.57.E+07	9.93.E+06	1.27.E+07	7.31.E+06	1.05.E+07
2470	Q96RQ1	Endoplasmic reticulum-Golgi intermediate compartment protein 2 [OS=Homo sapiens]	3.7	6	1	4	1	29	5	1	1	0								
2471	Q14435	Polypeptide N-acetylgalactosaminyltransferase 3 [OS=Homo sapiens]	3.7	2	1	8	1	14	5	1	1	0	8.73.E+06	7.66.E+06	7.74.E+06	9.46.E+06	7.50.E+06	7.56.E+06	7.21.E+06	7.26.E+06
2472	Q9H8H0	nucleolar protein 11 [OS=Homo sapiens]	3.6	3	1	4	1	35	0	1	1	0	3.95.E+06	2.69.E+06	3.63.E+06	2.31.E+06	5.16.E+06	3.96.E+06	4.38.E+06	2.64.E+06
2473	Q86YP4	Transcriptional repressor p66-alpha [OS=Homo sapiens]	3.6	2	1	4	1	53	2	1	1	0	5.45.E+06	6.08.E+06	5.66.E+06	6.53.E+06	2.88.E+06	2.53.E+06	3.65.E+06	3.88.E+06
2474	Q86SX6	Glutaredoxin-related protein 5, mitochondrial [OS=Homo sapiens]	3.6	11	1	8	1	0	9	1	1	0	9.30.E+06	1.10.E+07	1.33.E+07	1.38.E+07				
2475	Q9NWU5	39S ribosomal protein L22, mitochondrial [OS=Homo sapiens]	3.6	4	1	27	1	13	0	1	1	0	1.59.E+06	1.72.E+06	1.92.E+06	1.43.E+06	1.10.E+06	1.22.E+06	9.03.E+05	1.12.E+06
2476	P60468	protein transport protein Sec61 subunit beta [OS=Homo sapiens]	3.6	11	1	34	1	77	25	1	1	0	1.99.E+07	1.73.E+07	1.69.E+07	2.09.E+07	1.35.E+07	1.59.E+07	1.55.E+07	1.31.E+07
2477	Q16762	thiosulfate sulfurtransferase [OS=Homo sapiens]	3.6	6	1	14	1	23	9	1	1	0	1.54.E+07	1.39.E+07	1.54.E+07	1.77.E+07	1.86.E+07	2.25.E+07	2.39.E+07	2.12.E+07
2478	O75439	mitochondrial-processing peptidase subunit beta [OS=Homo sapiens]	3.6	2	1	10	1	0	10	1	1	0	1.98.E+07	1.87.E+07	2.03.E+07	1.24.E+07				
2479	Q86WB0	Nuclear-interacting partner of ALK [OS=Homo sapiens]	3.6	2	1	4	1	15	0	1	1	0	4.71.E+06	4.76.E+06	7.33.E+06	3.03.E+06	4.24.E+06	4.40.E+06	8.55.E+06	5.09.E+06
2480	P10619	lysosomal protective protein [OS=Homo sapiens]	3.6	2	1	71	1	63	0	1	1	0	3.97.E+07	3.93.E+07	4.22.E+07	3.68.E+07	5.10.E+07	5.65.E+07	5.28.E+07	4.98.E+07
2481	Q92692-1	Nectin-2 [OS=Homo sapiens]	3.6	2	1	6	1	26	0	1	1	0					6.72.E+06	5.86.E+06	2.68.E+06	1.12.E+07
2482	Q96B97-1	SH3 domain-containing kinase-binding protein 1 [OS=Homo sapiens]	3.6	2	1	39	1	14	0	1	1	0	5.77.E+06	5.44.E+06	6.10.E+06	4.86.E+06	2.98.E+06	3.36.E+06	3.43.E+06	2.97.E+06
2483	Q13601	KRR1 small subunit processome component homolog [OS=Homo sapiens]	3.6	2	1	8	1	14	4	1	1	0	1.26.E+07	2.89.E+07	1.33.E+07	9.28.E+06	9.44.E+06	1.77.E+07	2.34.E+07	1.45.E+07
2484	Q14241	Elongin-A [OS=Homo sapiens]	3.6	5	1	16	1	18	3	1	1	0	1.12.E+07	1.20.E+07	1.05.E+07	1.14.E+07	1.03.E+07	8.63.E+06	7.36.E+06	2.70.E+06

No.	Accession	Description	Sum PEP Score	Coverage [%]	# Peptides	# PSMs	# Unique Peptides	Score Mascot: A5 Mascot	Score Sequest HT: A2 Sequest HT	# Peptides (by Search Engine): A2 Sequest HT	# Peptides (by Search Engine): A5 Mascot	# Razor Peptides	ctrl Abundances_1	ctrl Abundances_2	ctrl Abundances_3	ctrl Abundances_4	JAM-A KO Abundances_1	JAM-A KO Abundances_2	JAM-A KO Abundances_3	JAM-A KO Abundances_4
2485	P78560	Death domain-containing protein CRADD [OS=Homo sapiens]	3.5	8	1	4	1	35	2	1	1	0	3.86.E+06	3.15.E+06	2.70.E+06	4.05.E+06	2.17.E+06	1.88.E+06	2.11.E+06	2.93.E+06
2486	P25490	Transcriptional repressor protein YY1 [OS=Homo sapiens]	3.5	2	1	20	1	66	15	1	1	0	4.09.E+07	3.93.E+07	3.82.E+07	3.57.E+07	3.51.E+07	3.31.E+07	3.32.E+07	3.33.E+07
2487	Q9P0V3-1	SH3 domain-binding protein 4 [OS=Homo sapiens]	3.5	2	1	14	1	104	4	1	1	0	8.33.E+06	7.99.E+06	5.43.E+06	6.79.E+06	8.32.E+06	7.03.E+06	6.33.E+06	6.44.E+06
2488	Q96EY4	translation machinery-associated protein 16 [OS=Homo sapiens]	3.5	13	2	3	2	15	0	1	2	0	9.60.E+06	7.23.E+06	8.89.E+06	8.65.E+06	9.79.E+06	1.05.E+07	1.11.E+07	1.07.E+07
2489	Q8NI35	InaD-like protein [OS=Homo sapiens]	3.5	1	2	23	1		15	2		0								
2490	Q9Y2R4	Probable ATP-dependent RNA helicase DDX52 [OS=Homo sapiens]	3.5	2	1	10	1	30	2	1	1	0								
2491	Q16563	Synaptophysin-like protein 1 [OS=Homo sapiens]	3.5	4	1	42	1	188	41	1	1	0								
2492	Q9BX40	protein LSM14 homolog B [OS=Homo sapiens]	3.5	3	1	4	1	19	3	1	1	0	1.97.E+07	1.40.E+07	1.87.E+07	1.22.E+07	1.76.E+07	1.88.E+07	1.99.E+07	1.51.E+07
2493	Q96SU4	Oxysterol-binding protein-related protein 9 [OS=Homo sapiens]	3.5	1	1	6	1	71	6	1	1	0	1.45.E+07	1.49.E+07	1.49.E+07	1.49.E+07	1.96.E+07	1.74.E+07	3.96.E+06	1.45.E+07
2494	Q9UIV1-1	CCR4-NOT transcription complex subunit 7 [OS=Homo sapiens]	3.5	5	1	2	1	0	2	1	1	0								
2495	Q969G6	Riboflavin kinase [OS=Homo sapiens]	3.5	14	1	10	1	99	2	1	1	0	6.98.E+06	7.20.E+06	6.54.E+06	6.68.E+06	6.65.E+06	4.48.E+06	5.57.E+06	4.96.E+06
2496	P14209	CD99 antigen [OS=Homo sapiens]	3.5	18	1	6	1	27	0	1	1	0	2.99.E+05	6.15.E+05	5.76.E+05	6.28.E+05				
2497	Q9UNN8	Endothelial protein C receptor [OS=Homo sapiens]	3.4	4	1	4	1	23	2	1	1	0	7.57.E+06	5.61.E+06	5.13.E+06	5.01.E+06	1.72.E+07	2.19.E+07	1.95.E+07	2.02.E+07
2498	Q96EL2	28S ribosomal protein S24, mitochondrial [OS=Homo sapiens]	3.4	12	1	2	1	16	3	1	1	0	9.62.E+06	9.03.E+06	3.98.E+06		1.03.E+07	8.62.E+06	1.06.E+07	
2499	Q9Y3Y2	Chromatin target of PRMT1 protein [OS=Homo sapiens]	3.4	5	1	4	1	51	2	1	1	0	3.31.E+06	3.01.E+06	2.77.E+06		1.88.E+06			1.56.E+06
2500	P56385	ATP synthase subunit e, mitochondrial [OS=Homo sapiens]	3.4	10	1	6	1	57	6	1	1	0	1.19.E+07	1.03.E+07	1.06.E+07	1.31.E+07	9.52.E+06	1.13.E+07	1.18.E+07	9.14.E+06
2501	Q12996-1	Cleavage stimulation factor subunit 3 [OS=Homo sapiens]	3.4	2	1	2	1	23	2	1	1	0								
2502	Q02224	Centromere-associated protein E [OS=Homo sapiens]	3.4	1	2	35	2	0	9	1	2	0	6.06.E+07	5.54.E+07	7.14.E+07	4.73.E+07	5.57.E+07	5.54.E+07	5.38.E+07	5.31.E+07
2503	Q8WUA2	Peptidyl-prolyl cis-trans isomerase-like 4 [OS=Homo sapiens]	3.4	6	1	2	1	0	2	1	1	0	1.63.E+07	2.04.E+07	1.82.E+07	1.84.E+07	2.12.E+07	1.91.E+07	1.86.E+07	1.81.E+07
2504	O95298-1	NADH dehydrogenase [ubiquinone] 1 subunit C2 [OS=Homo sapiens]	3.4	10	1	19	1	17	0	1	1	0	8.45.E+06	8.39.E+06	1.28.E+07	1.01.E+07	1.06.E+07	1.22.E+07	1.07.E+07	1.15.E+07
2505	Q05048	Cleavage stimulation factor subunit 1 [OS=Homo sapiens]	3.4	6	1	2	1	18	3	1	1	0	3.29.E+06	3.89.E+06	8.24.E+06	6.63.E+06	6.32.E+06	6.01.E+06	8.00.E+06	1.06.E+07
2506	Q86V88	Magnesium-dependent phosphatase 1 [OS=Homo sapiens]	3.4	10	1	2	1	43	0	1	1	0	4.81.E+06		3.54.E+06	4.66.E+06	2.46.E+05		5.29.E+05	1.16.E+06
2507	Q9UHQ9	NADH-cytochrome b5 reductase 1 [OS=Homo sapiens]	3.4	4	1	2	1	0	2	1	1	0			1.12.E+08		1.16.E+07			1.28.E+08
2508	Q9H098	Protein FAM107B [OS=Homo sapiens]	3.4	14	1	1	1	43			1	0	1.06.E+07	1.19.E+07	7.85.E+06	1.19.E+07	2.37.E+07	3.08.E+07	2.33.E+07	1.63.E+07
2509	Q15006	ER membrane protein complex subunit 2 [OS=Homo sapiens]	3.4	6	1	5	1	0	0	1	1	0	2.49.E+06	3.14.E+06	2.85.E+06	2.02.E+06		2.98.E+06	2.25.E+06	2.79.E+06
2510	O94901-1	SUN domain-containing protein 1 [OS=Homo sapiens]	3.3	2	1	2	1	0	2	1	1	0	5.60.E+06	6.35.E+06	6.65.E+06	7.22.E+06	6.01.E+06	6.71.E+06	6.32.E+06	6.82.E+06
2511	P49005	DNA polymerase delta subunit 2 [OS=Homo sapiens]	3.3	5	1	1	1		0	1		0	3.52.E+06	8.86.E+06	3.31.E+06	1.02.E+07	8.20.E+06	1.01.E+07	3.90.E+06	8.89.E+06
2512	P11172	uridine 5'-monophosphate synthase [OS=Homo sapiens]	3.3	2	1	4	1	14	5	1	1	0	3.84.E+07	3.69.E+07	4.02.E+07	3.36.E+07	1.37.E+07		2.43.E+07	2.12.E+07
2513	O43719	HIV Tat-specific factor 1 [OS=Homo sapiens]	3.3	2	1	2	1	16	3	1	1	0	3.58.E+06	3.85.E+06	4.23.E+06	3.27.E+06	3.30.E+06	4.26.E+06		5.17.E+06
2514	Q15642	Cdc42-interacting protein 4 [OS=Homo sapiens]	3.3	4	1	4	1	18	0	1	1	0	1.94.E+06	2.41.E+06	2.75.E+06	1.87.E+06	3.54.E+06	3.63.E+06	4.82.E+06	3.51.E+06
2515	O43402	ER membrane protein complex subunit 8 [OS=Homo sapiens]	3.3	4	1	2	1	16	2	1	1	0	4.20.E+07	3.79.E+07	3.92.E+07	4.64.E+07	2.34.E+07	3.24.E+07	3.31.E+07	3.01.E+07
2516	P78346-1	ribonuclease P protein subunit p30 [OS=Homo sapiens]	3.3	3	1	5	1	154			1	0	7.09.E+06	7.46.E+06	7.81.E+06	6.29.E+06	8.10.E+06	7.15.E+06	9.16.E+06	4.88.E+06
2517	Q9UKL0	REST corepressor 1 [OS=Homo sapiens]	3.3	3	1	2	1	18	2	1	1	0								
2518	Q14676	Mediator of DNA damage checkpoint protein 1 [OS=Homo sapiens]	3.2	1	1	14	1	43	2	1	1	0	4.91.E+06	5.41.E+06	4.98.E+06	4.40.E+06	5.18.E+06	3.50.E+06	3.76.E+06	5.57.E+06
2519	Q9H0U3	Magnesium transporter protein 1 [OS=Homo sapiens]	3.2	3	1	15	1	72	4	1	1	0	1.31.E+07	1.08.E+07	1.31.E+07	1.44.E+07	1.17.E+07	1.50.E+07	1.73.E+07	1.29.E+07
2520	Q8N726	Tumor suppressor ARF [OS=Homo sapiens]	3.2	14	1	2	1	0	0	1	1	0	1.89.E+05	2.17.E+05	2.42.E+05	1.70.E+05	2.65.E+05	1.37.E+05	1.54.E+05	2.16.E+05
2521	Q5TDH0	Protein DDI1 homolog 2 [OS=Homo sapiens]	3.2	4	1	2	1	0	2	1	1	0	2.16.E+07						2.14.E+07	2.73.E+07
2522	Q9P2X0-1	Dolichol-phosphate mannosyltransferase subunit 3 [OS=Homo sapiens]	3.2	11	1	7	1	0	2	1	1	0								
2523	Q8N7R7-1	Cyclin-Y-like protein 1 [OS=Homo sapiens]	3.2	5	1	4	1	25	3	1	1	0		2.54.E+06	1.34.E+06	2.52.E+06	5.90.E+06	4.35.E+06		
2524	Q12899	Tripartite motif-containing protein 26 [OS=Homo sapiens]	3.2	3	1	2	1	0	0	1	1	0	1.30.E+06	2.26.E+06	6.47.E+05	2.12.E+06	2.43.E+06	1.82.E+06	1.89.E+06	2.53.E+06
2525	Q9UHQ4	B-cell receptor-associated protein 29 [OS=Homo sapiens]	3.2	4	1	8	1	31	2	1	1	0	7.12.E+06	8.13.E+06	8.07.E+06	6.90.E+06	8.26.E+06	4.59.E+06	1.97.E+06	
2526	Q96S66	chloride channel CLIC-like protein 1 [OS=Homo sapiens]	3.2	3	1	8	1	64	0	1	1	0	6.69.E+05	9.81.E+05	8.79.E+05	8.74.E+05	2.14.E+06	2.14.E+06	2.29.E+06	1.97.E+06
2527	Q06481	Amyloid-like protein 2 [OS=Homo sapiens]	3.2	2	1	2	1	0	3	1	1	0					2.64.E+07	1.24.E+07	1.67.E+07	2.68.E+07
2528	P56270-1	Myc-associated zinc finger protein [OS=Homo sapiens]	3.1	3	1	3	1	0	0	1	1	0	7.63.E+05	6.79.E+05	8.59.E+05	4.88.E+05	5.61.E+05	6.23.E+05	6.31.E+05	5.26.E+05
2529	P55212	Caspase-6 [OS=Homo sapiens]	3.1	3	1	25	1	51	25	1	1	0								
2530	Q99614	tetratricopeptide repeat protein 1 [OS=Homo sapiens]	3.1	6	1	2	1	26	0	1	1	0	2.13.E+06	5.28.E+06	4.27.E+06	4.84.E+06	6.95.E+06	6.70.E+06	5.09.E+06	6.66.E+06
2531	Q12800-1	Alpha-globin transcription factor CP2 [OS=Homo sapiens]	3.1	2	1	2	1	0	2	1	1	0	1.24.E+07		1.39.E+07	1.38.E+07	1.41.E+07			1.41.E+07
2532	Q15075	Early endosome antigen 1 [OS=Homo sapiens]	3.1	1	1	4	1	15	6	1	1	0	3.11.E+06	1.03.E+06	1.61.E+06		5.71.E+06	5.90.E+06		4.92.E+06
2533	Q16204	coiled-coil domain-containing protein 6 [OS=Homo sapiens]	3.1	3	1	2	1	38	2	1	1	0	5.68.E+06	4.82.E+06	6.45.E+06	7.76.E+06	8.62.E+06	1.18.E+07	8.66.E+06	9.88.E+06
2534	Q9UHC6-1	Contactin-associated protein-like 2 [OS=Homo sapiens]	3.1	1	1	20	1	0	0	1	1	0	2.98.E+07	2.74.E+07	3.22.E+07	3.75.E+07	2.25.E+07	2.57.E+07	3.15.E+07	2.85.E+07
2535	P09001	39S ribosomal protein L3, mitochondrial [OS=Homo sapiens]	3.1	5	1	4	1		2	1		0					7.99.E+07	7.21.E+07	4.00.E+07	
2536	Q9BSR8	protein YIPF4 [OS=Homo sapiens]	3.1	4	1	4	1	0	4	1	1	0	2.28.E+07	2.55.E+07	2.55.E+07					
2537	O76095-1	Protein JTB [OS=Homo sapiens]	3.1	9	1	8	1	16	0	1	1	0	5.71.E+06	5.30.E+06	4.69.E+06	6.16.E+06	7.68.E+06	8.88.E+06		7.62.E+06
2538	Q9UPT8	Zinc finger CCCH domain-containing protein 4 [OS=Homo sapiens]	3.1	1	1	20	1	91	17	1	1	0	6.05.E+06		5.98.E+06	8.94.E+06	5.44.E+06	5.50.E+06	4.68.E+06	7.01.E+06
2539	Q8IZ21-1	Phosphatase and actin regulator 4 [OS=Homo sapiens]	3.1	1	1	2	1	14	0	1	1	0	3.48.E+06	2.92.E+06	3.90.E+06	3.21.E+06	3.34.E+06	4.04.E+06	3.18.E+06	4.60.E+06
2540	Q5JTJ3-1	Cytochrome c oxidase assembly factor 6 homolog [OS=Homo sapiens]	3.1	11	1	2	1	0	0	1	1	0								
2541	Q8TBA6	Golgin subfamily A member 5 [OS=Homo sapiens]	3.1	2	1	15	1	25	9	1	1	0	1.40.E+07	1.10.E+07	1.20.E+07	1.04.E+07	1.69.E+07	1.74.E+07	1.84.E+07	2.01.E+07
2542	Q9Y371	Endophilin-B1 [OS=Homo sapiens]	3.1	4	1	2	1	18	2	1	1	0	1.01.E+07	8.46.E+06	7.53.E+06	1.04.E+07	1.08.E+07	1.11.E+07	1.17.E+07	1.04.E+07

No.	Accession	Description	Sum PEP Score	Coverage [%]	# Peptides	# PSMs	# Unique Peptides	Score Mascot: A5 Mascot	Score Sequest HT: A2 Sequest HT	# Peptides (by Search Engine): A2 Sequest HT	# Peptides (by Search Engine): A5 Mascot	# Razor Peptides	ctrl Abundances_1	ctrl Abundances_2	ctrl Abundances_3	ctrl Abundances_4	JAM-A KO Abundances_1	JAM-A KO Abundances_2	JAM-A KO Abundances_3	JAM-A KO Abundances_4
2543	Q7L2J0-1	7SK snRNA methylphosphate capping enzyme [OS=Homo sapiens]	3.0	1	1	20	1	38	0	1	1	0	1.70.E+07	1.78.E+07	1.92.E+07	1.41.E+07	1.42.E+07	1.24.E+07	1.69.E+07	1.39.E+07
2544	Q99523	Sortilin [OS=Homo sapiens]	3.0	2	1	2	1	15	2	1	1	0			1.16.E+07					2.03.E+07
2545	Q96T37-1	Putative RNA-binding protein 15 [OS=Homo sapiens]	3.0	2	1	2	1	0	0	1	1	0			6.10.E+06	1.13.E+07	5.60.E+06	6.12.E+06	4.48.E+06	
2546	Q9Y3E2	BolA-like protein 1 [OS=Homo sapiens]	3.0	11	1	2	1	0	0	1	1	0	8.24.E+06	9.38.E+06	8.40.E+06	7.87.E+06	1.00.E+07	1.26.E+07	1.19.E+07	9.20.E+06
2547	O60287	nucleolar pre-ribosomal-associated protein 1 [OS=Homo sapiens]	3.0	1	1	2	1	41	0	1	1	0	3.29.E+06	1.06.E+06	3.00.E+06	2.25.E+06	1.48.E+06			
2548	Q6ZRV2	Protein FAM83H [OS=Homo sapiens]	3.0	1	1	1	1		0	1		0	8.35.E+06	7.06.E+06	8.68.E+06	9.11.E+06	4.91.E+06	5.08.E+06	6.02.E+06	5.36.E+06
2549	O14530	Thioredoxin domain-containing protein 9 [OS=Homo sapiens]	3.0	4	1	16	1	55	7	1	1	0	1.56.E+07	1.70.E+07	1.58.E+07	1.22.E+07	1.65.E+07	1.70.E+07	1.59.E+07	1.72.E+07
2550	P0CG08	Golgi pH regulator B [OS=Homo sapiens]	3.0	6	1	10	1	38	0	1	1	0	4.19.E+07	3.42.E+07	4.17.E+07	4.74.E+07	7.00.E+07	3.65.E+07		6.27.E+07
2551	Q96AZ6-1	Interferon-stimulated gene 20 kDa protein [OS=Homo sapiens]	3.0	4	1	8	1	50	2	1	1	0	9.91.E+06	9.49.E+06	8.13.E+06	9.60.E+06	3.67.E+06	3.61.E+06	3.25.E+06	3.43.E+06
2552	P23141	Liver carboxylesterase 1 [OS=Homo sapiens]	3.0	5	1	8	1	24	2	1	1	0						2.91.E+05	2.72.E+06	3.73.E+05
2553	Q9UGT4	Sushi domain-containing protein 2 [OS=Homo sapiens]	3.0	4	1	4	1	35	0	1	1	0						3.76.E+06		3.16.E+06
2554	P42696	RNA-binding protein 34 [OS=Homo sapiens]	3.0	2	1	4	1	40	4	1	1	0	2.02.E+07		2.34.E+07					
2555	Q9Y394	Dehydrogenase/reductase SDR family member 7 [OS=Homo sapiens]	3.0	7	1	14	1	71	0	1	1	0	5.53.E+06	3.07.E+06	5.48.E+06	4.32.E+06	3.73.E+06	3.19.E+06	2.92.E+06	3.62.E+06
2556	Q8IY22-1	C-Maf-inducing protein [OS=Homo sapiens]	3.0	4	1	6	1	64	0	1	1	0	1.04.E+07	1.07.E+07	1.01.E+07	1.15.E+07	2.52.E+06	1.04.E+07	2.66.E+06	3.26.E+06
2557	Q96AX1	Vacuolar protein sorting-associated protein 33A [OS=Homo sapiens]	3.0	2	1	4	1	37	0	1	1	0	6.06.E+06	5.30.E+06	6.31.E+06	5.33.E+06	4.78.E+06	6.75.E+06	6.87.E+06	6.78.E+06
2558	Q9BV79	Enoyl-[acyl-carrier-protein] reductase, mitochondrial [OS=Homo sapiens]	3.0	3	1	2	1	18	2	1	1	0	2.18.E+06	1.96.E+06	1.69.E+06	1.71.E+06	2.83.E+06	2.46.E+06	2.05.E+06	3.01.E+06
2559	O75934	Pre-mRNA-splicing factor spf27 [OS=Homo sapiens]	2.9	6	1	5	1	14	7	1	1	0		9.85.E+06	1.48.E+07	1.30.E+07			6.61.E+07	1.63.E+07
2560	Q9H2P0	Activity-dependent neuroprotector homeobox protein [OS=Homo sapiens]	2.9	1	1	2	1	0	0	1	1	0	1.61.E+07	1.44.E+07	1.45.E+07	1.62.E+07	1.63.E+07	1.61.E+07	1.78.E+07	1.64.E+07
2561	Q6P4A7-1	Sideroflexin-4 [OS=Homo sapiens]	2.9	4	1	2	1	17	0	1	1	0								
2562	O96011-1	Peroxisomal membrane protein 11B [OS=Homo sapiens]	2.9	4	1	2	1	0	0	1	1	0	9.14.E+06	8.74.E+06	8.37.E+06	6.53.E+06	7.71.E+06	1.13.E+07	9.48.E+06	8.28.E+06
2563	A6NIH7	Protein unc-119 homolog B [OS=Homo sapiens]	2.9	4	1	2	1	0	2	1	1	0				5.53.E+06	1.77.E+06	9.08.E+06		6.31.E+06
2564	Q9Y3Q3	Transmembrane emp24 domain-containing protein 3 [OS=Homo sapiens]	2.9	6	1	4	1	0	0	1	1	0	8.73.E+06	9.16.E+06	1.03.E+07	1.16.E+07	1.26.E+07	1.16.E+07	1.43.E+07	1.18.E+07
2565	Q2NL68-1	Proline and serine-rich protein 3 [OS=Homo sapiens]	2.9	4	1	48	1	0	0	1	1	0	1.41.E+08	1.54.E+08	1.23.E+08	1.38.E+08	2.13.E+08	2.20.E+08	1.96.E+08	2.21.E+08
2566	O60830-1	Mitochondrial import inner membrane translocase subunit Tim17-B [OS=Homo sapiens]	2.9	13	1	2	1	14	3	1	1	0	1.35.E+07	1.26.E+07		1.54.E+07	1.51.E+07	1.38.E+07	1.22.E+07	1.25.E+07
2567	Q12768	WASH complex subunit 5 [OS=Homo sapiens]	2.9	2	1	2	1	29	0	1	1	0	4.18.E+06	4.26.E+06			3.30.E+06	2.35.E+06	2.24.E+06	2.48.E+06
2568	Q9UNN5-1	fas-associated factor 1 [OS=Homo sapiens]	2.9	2	1	4	1	0	0	1	1	0	1.11.E+07	1.33.E+07	9.54.E+06	1.10.E+07	8.58.E+06	7.19.E+06	6.96.E+06	7.60.E+06
2569	Q3ZAQ7	Vacuolar ATPase assembly integral membrane protein vma21 [OS=Homo sapiens]	2.8	12	1	2	1	32	2	1	1	0								
2570	O94903	Pyridoxal phosphate homeostasis protein [OS=Homo sapiens]	2.8	5	1	2	1	0	2	1	1	0								
2571	A8MXV4	nucleoside diphosphate-linked moiety X motif 19 [OS=Homo sapiens]	2.8	3	1	2	1	0	0	1	1	0	8.28.E+06	7.72.E+06	1.26.E+07	9.61.E+06	3.38.E+06	6.37.E+06	5.23.E+06	
2572	P41743	Protein kinase c iota type [OS=Homo sapiens]	2.8	5	1	8	1	18	0	1	1	0	1.29.E+07	1.80.E+07	1.18.E+07	1.66.E+07	1.91.E+07	1.14.E+07	1.14.E+07	1.30.E+07
2573	O15213	WD repeat-containing protein 46 [OS=Homo sapiens]	2.8	3	1	3	1	0	2	1	1	0	1.50.E+07	1.67.E+07	1.56.E+07	1.68.E+07	2.76.E+07	2.89.E+07	2.55.E+07	2.56.E+07
2574	Q8WW59	SPRY domain-containing protein 4 [OS=Homo sapiens]	2.8	5	1	10	1	0	0	1	1	0	1.10.E+07	9.97.E+06	1.23.E+07	1.16.E+07	9.42.E+06	8.64.E+06	1.02.E+07	9.55.E+06
2575	P82663	28S ribosomal protein S25, mitochondrial [OS=Homo sapiens]	2.8	8	1	4	1	14	0	1	1	0	1.28.E+07	1.29.E+07	1.13.E+07	1.35.E+07	1.51.E+07	1.19.E+07	1.47.E+07	9.34.E+06
2576	Q9UI42-1	Carboxypeptidase A4 [OS=Homo sapiens]	2.8	6	1	8	1	20	0	1	1	0	2.90.E+06	9.67.E+05	2.44.E+06	3.10.E+05		1.62.E+06		
2577	Q5T8D3-1	Acyl-CoA-binding domain-containing protein 5 [OS=Homo sapiens]	2.8	2	1	4	1	0	2	1	1	0	1.86.E+07	2.20.E+07	1.27.E+07	1.27.E+07	2.30.E+07	1.66.E+07	1.87.E+07	1.58.E+07
2578	O95972	Bone morphogenetic protein 15 [OS=Homo sapiens]	2.8	2	1	44	1	728	0	1	1	0	8.87.E+07	7.32.E+07	8.85.E+07	1.04.E+08	6.94.E+07	7.43.E+07	1.00.E+08	7.34.E+07
2579	Q12929	Epidermal growth factor receptor kinase substrate 8 [OS=Homo sapiens]	2.8	2	1	4	1	35	0	1	1	0	4.42.E+06	5.89.E+06	4.83.E+06		4.70.E+06	6.04.E+06	3.66.E+06	4.25.E+06
2580	Q15392	Delta(24)-sterol reductase [OS=Homo sapiens]	2.8	2	1	6	1	14	6	1	1	0	4.20.E+07	4.59.E+07	5.08.E+07	3.93.E+07	5.63.E+07	5.80.E+07	6.51.E+07	5.93.E+07
2581	Q99570	Phosphoinositide 3-kinase regulatory subunit 4 [OS=Homo sapiens]	2.8	1	1	2	1	20	0	1	1	0	1.54.E+06	1.72.E+06	9.92.E+05	1.54.E+06	1.62.E+06	1.33.E+06	1.03.E+06	1.45.E+06
2582	Q02338	D-beta-hydroxybutyrate dehydrogenase, mitochondrial [OS=Homo sapiens]	2.8	2	1	10	1	49	0	1	1	0	1.61.E+07	1.76.E+07	1.62.E+07	1.44.E+07	7.19.E+06	7.41.E+06	6.41.E+06	6.66.E+06
2583	Q02083	N-acylethanolamine-hydrolyzing acid amidase [OS=Homo sapiens]	2.8	5	1	7	1	16	0	1	1	0	4.33.E+06	3.23.E+06	1.07.E+08	2.24.E+06	5.45.E+07	5.88.E+06	4.95.E+07	3.07.E+07
2584	P45877	peptidyl-prolyl cis-trans isomerase C [OS=Homo sapiens]	2.8	4	1	56	1	296	26	1	1	0	8.97.E+07	9.46.E+07	9.29.E+07	7.76.E+07	8.61.E+07	9.50.E+07	9.16.E+07	8.79.E+07
2585	O15427	Monocarboxylate transporter 4 [OS=Homo sapiens]	2.8	3	1	4	1	18	0	1	1	0					7.58.E+06	7.50.E+06	7.64.E+06	7.51.E+06
2586	Q96ER3	protein saal1 [OS=Homo sapiens]	2.8	2	1	4	1	41	0	1	1	0	2.59.E+06	3.05.E+06		3.91.E+06	1.15.E+07	9.40.E+06	8.57.E+06	9.29.E+06
2587	Q30201-1	Hereditary hemochromatosis protein [OS=Homo sapiens]	2.8	4	1	2	1	13	0	1	1	0	1.24.E+06	1.10.E+06	1.28.E+06	9.36.E+05	2.51.E+06	2.85.E+06	3.21.E+06	3.06.E+06
2588	Q13671	ras and Rab interactor 1 [OS=Homo sapiens]	2.8	1	1	4	1	37	0	1	1	0	5.06.E+06	5.77.E+06	4.34.E+06	5.29.E+06	6.20.E+06	7.49.E+06	6.27.E+06	6.92.E+06
2589	O15294	UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit [OS=Homo sapiens]	2.8	2	1	2	1	32	0	1	1	0	4.52.E+06	4.79.E+06	1.83.E+06	5.03.E+06	3.86.E+06	4.16.E+06	2.54.E+06	4.57.E+06
2590	O43541-1	mothers against decapentaplegic homolog 6 [OS=Homo sapiens]	2.8	3	1	6	1	0	0	1	1	0								
2591	Q9H6Z4	Ran-binding protein 3 [OS=Homo sapiens]	2.8	4	1	1	1	0			1	0	2.65.E+06	5.77.E+06	5.04.E+06	9.34.E+06	7.17.E+06	8.01.E+06	1.18.E+07	1.30.E+07

No.	Accession	Description	Sum PEP Score	Coverage [%]	# Peptides	# PSMs	# Unique Peptides	Score Mascot: A5 Mascot	Score Sequest HT: A2 Sequest HT	# Peptides (by Search Engine): A2 Sequest HT	# Peptides (by Search Engine): A5 Mascot	# Razor Peptides	ctrl Abundances_1	ctrl Abundances_2	ctrl Abundances_3	ctrl Abundances_4	JAM-A KO Abundances_1	JAM-A KO Abundances_2	JAM-A KO Abundances_3	JAM-A KO Abundances_4
2592	Q9Y263	Phospholipase A-2-activating protein [OS=Homo sapiens]	2.8	2	1	2	1	31	0	1	1	0								
2593	Q92733	proline-rich protein PRCC [OS=Homo sapiens]	2.8	2	1	26	1	14	0	1	1	0	1.99.E+07	1.93.E+07	2.16.E+07	1.74.E+07	1.75.E+07	1.67.E+07	1.90.E+07	1.76.E+07
2594	Q6ZNW5	GDP-D-glucose phosphorylase 1 [OS=Homo sapiens]	2.7	4	1	2	1	21	0	1	1	0	1.54.E+06	7.68.E+05			3.03.E+06	2.22.E+06	2.07.E+06	2.10.E+06
2595	P38571	lysosomal acid lipase/cholesteryl ester hydrolase [OS=Homo sapiens]	2.7	4	1	4	1	0	0	1	1	0	2.83.E+05	4.28.E+05	2.64.E+05	5.83.E+05	9.72.E+06	6.66.E+06	9.35.E+06	1.03.E+07
2596	Q8N543	prolyl 3-hydroxylase OGFOD1 [OS=Homo sapiens]	2.7	4	1	2	1	0	0	1	1	0	1.34.E+07			1.21.E+07				
2597	Q9Y5X1	Sorting nexin-9 [OS=Homo sapiens]	2.7	2	1	2	1	0	0	1	1	0	5.32.E+06	6.46.E+06	6.63.E+06	6.10.E+06	8.87.E+06	8.23.E+06	4.46.E+06	8.08.E+06
2598	Q9H9A6	Leucine-rich repeat-containing protein 40 [OS=Homo sapiens]	2.7	1	1	4	1	45	0	1	1	0	7.27.E+06	5.82.E+06	7.03.E+06	5.54.E+06	9.90.E+06	9.40.E+06	8.82.E+06	9.97.E+06
2599	P51948-1	CDK-activating kinase assembly factor MAT1 [OS=Homo sapiens]	2.7	7	1	2	1	15	0	1	1	0	3.27.E+06	2.95.E+06	2.75.E+06	2.48.E+06	5.19.E+06	4.35.E+06	3.66.E+06	3.39.E+06
2600	Q8N3D4	EH domain-binding protein 1-like protein 1 [OS=Homo sapiens]	2.7	1	1	2	1	18	0	1	1	0	2.49.E+06	2.05.E+06	2.11.E+06	2.44.E+06	1.58.E+06	1.46.E+06	1.35.E+06	1.24.E+06
2601	Q15005	Signal peptidase complex subunit 2 [OS=Homo sapiens]	2.7	3	1	40	1	69	22	1	1	0	7.37.E+07	6.32.E+07	8.09.E+07	7.90.E+07	8.96.E+07	7.17.E+07	8.09.E+07	7.63.E+07
2602	Q9P016	Thymocyte nuclear protein 1 [OS=Homo sapiens]	2.7	3	1	2	1	0	0	1	1	0	1.33.E+07	1.45.E+07	1.36.E+07	1.38.E+07	1.88.E+07	1.83.E+07	2.08.E+07	1.74.E+07
2603	A6NCW0	Ubiquitin carboxyl-terminal hydrolase 17-like protein 3 [OS=Homo sapiens]	2.7	1	1	13	1	0	0	1	1	0								
2604	O60645	exocyst complex component 3 [OS=Homo sapiens]	2.7	2	1	2	1	16	0	1	1	0								
2605	O95801	Tetratricopeptide repeat protein 4 [OS=Homo sapiens]	2.7	6	1	2	1	0	0	1	1	0	7.08.E+06	1.02.E+07		1.15.E+07			2.97.E+06	
2606	P29558-1	RNA-binding motif, single-stranded-interacting protein 1 [OS=Homo sapiens]	2.7	4	1	4	1	15	4	1	1	0	1.38.E+07	1.30.E+07	1.18.E+07	1.15.E+07	1.08.E+07	9.41.E+06	1.33.E+07	1.34.E+07
2607	Q9UM54-3	Unconventional myosin-VI [OS=Homo sapiens]	2.7	2	1	5	1	15			1	0						6.91.E+05	1.41.E+07	7.44.E+05
2608	Q9NX46	Poly(ADP-ribose) glycohydrolase ARH3 [OS=Homo sapiens]	2.7	2	1	1	1		0	1		0	1.48.E+07	1.53.E+07	1.49.E+07	1.25.E+07	1.75.E+07	1.73.E+07	1.85.E+07	1.66.E+07
2609	Q9UBM7	7-dehydrocholesterol reductase [OS=Homo sapiens]	2.7	1	1	2	1	0	0	1	1	0	3.36.E+07	3.06.E+07	3.32.E+07	3.91.E+07	3.65.E+07	3.19.E+07	3.34.E+07	3.69.E+07
2610	Q3ZCW2	Galectin-related protein [OS=Homo sapiens]	2.7	6	1	1	1		0	1		0	1.04.E+07	8.27.E+06	8.79.E+06	7.75.E+06	8.55.E+06	9.53.E+06	9.18.E+06	7.89.E+06
2611	P31749	RAC-alpha serine/threonine-protein kinase [OS=Homo sapiens]	2.7	4	1	2	1	0	0	1	1	0	2.44.E+06	6.15.E+06	5.79.E+06	3.75.E+06	4.24.E+06	4.02.E+06	4.46.E+06	7.16.E+06
2612	Q32P28-1	Prolyl 3-hydroxylase 1 [OS=Homo sapiens]	2.7	1	1	5	1	26	0	1	1	0	5.38.E+06	2.98.E+06	4.45.E+06	2.11.E+06			3.30.E+06	3.43.E+05
2613	P25098	Beta-adrenergic receptor kinase 1 [OS=Homo sapiens]	2.7	1	1	6	1	26	2	1	1	0	1.06.E+07	9.57.E+06	1.03.E+07	7.43.E+06	9.28.E+06	1.13.E+07	8.47.E+06	1.04.E+07
2614	Q9P2W9	Syntaxin-18 [OS=Homo sapiens]	2.7	4	1	2	1	22	0	1	1	0	2.38.E+06	2.52.E+06	2.52.E+06	2.06.E+06	2.46.E+06	2.30.E+06	2.07.E+06	2.82.E+06
2615	Q9H4L7	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A containing DEAD/H box 1 [OS=Homo sapiens]	2.7	1	1	2	1	14	0	1	1	0	5.90.E+06	5.96.E+06	5.13.E+06	6.64.E+06	6.23.E+06	5.34.E+06	5.48.E+06	5.68.E+06
2616	O60783	28S ribosomal protein S14, mitochondrial [OS=Homo sapiens]	2.7	10	1	2	1	16	0	1	1	0	8.16.E+06	7.68.E+06	9.59.E+06	9.69.E+06	7.65.E+06	7.15.E+06	7.82.E+06	7.13.E+06
2617	Q9NUQ7	Ufm1-specific protease 2 [OS=Homo sapiens]	2.7	4	1	2	1	0	2	1	1	0								
2618	Q15024	Exosome complex component RRP42 [OS=Homo sapiens]	2.6	4	1	5	1	0	0	1	1	0	1.09.E+07	8.72.E+06	9.99.E+06	1.14.E+07	1.14.E+07	1.03.E+07	1.34.E+07	1.31.E+07
2619	O95563	Mitochondrial pyruvate carrier 2 [OS=Homo sapiens]	2.6	9	1	10	1	0	2	1	1	0	1.09.E+07	9.13.E+06	1.10.E+07	1.07.E+07	7.67.E+06	7.89.E+06	1.03.E+07	7.52.E+06
2620	L0R6Q1	SLC35A4 upstream open reading frame protein [OS=Homo sapiens]	2.6	10	1	8	1	15	4	1	1	0	1.30.E+07	1.51.E+07	1.31.E+07	1.55.E+07	6.19.E+06	7.99.E+06	8.20.E+06	1.05.E+07
2621	Q8NBX0	saccharopine dehydrogenase-like oxidoreductase [OS=Homo sapiens]	2.6	3	1	4	1	0	2	1	1	0	1.63.E+07	1.59.E+07	1.63.E+07		2.72.E+07	2.86.E+07	3.24.E+07	3.27.E+07
2622	P54578	Ubiquitin carboxyl-terminal hydrolase 14 [OS=Homo sapiens]	2.6	2	1	5	1	0	0	1	1	0								
2623	Q9H0W9	Ester hydrolase C11orf54 [OS=Homo sapiens]	2.6	5	1	6	1	23	7	1	1	0	1.09.E+07	1.43.E+07	1.02.E+07	1.32.E+07	2.13.E+07	2.11.E+07	1.97.E+07	2.09.E+07
2624	O75127	pentatricopeptide repeat-containing protein 1, mitochondrial [OS=Homo sapiens]	2.6	2	1	6	1	20	0	1	1	0		3.10.E+06		4.09.E+06	3.71.E+06	3.75.E+06	2.52.E+06	1.62.E+06
2625	Q99417	C-Myc-binding protein [OS=Homo sapiens]	2.6	11	1	23	1	28	9	1	1	0	1.00.E+07	9.13.E+06	8.95.E+06	1.01.E+07	1.16.E+07	1.02.E+07	1.21.E+07	1.18.E+07
2626	Q96GA7	serine dehydratase-like [OS=Homo sapiens]	2.6	8	1	2	1	20	0	1	1	0								
2627	Q14118	Dystroglycan [OS=Homo sapiens]	2.6	3	1	2	1	19	0	1	1	0	2.61.E+06	2.53.E+06	3.12.E+06	2.84.E+06	7.58.E+06	5.69.E+06		6.21.E+06
2628	O15235	28S ribosomal protein S12, mitochondrial [OS=Homo sapiens]	2.6	9	1	14	1	15	0	1	1	0	3.61.E+06	4.13.E+06	3.55.E+06	3.60.E+06	2.74.E+06	2.47.E+06	2.38.E+06	2.11.E+06
2629	Q8N8E3	Centrosomal protein of 112 kDa [OS=Homo sapiens]	2.6	2	1	8	1		0	1		0	1.40.E+06	1.88.E+06	1.58.E+06	1.23.E+06	1.89.E+06	2.51.E+06	2.05.E+06	2.06.E+06
2630	Q9BX95	Sphingosine-1-phosphate phosphatase 1 [OS=Homo sapiens]	2.6	4	1	15	1	0	0	1	1	0	4.50.E+06	4.41.E+06	5.14.E+06	3.86.E+06	5.50.E+06	6.01.E+06	5.75.E+06	5.90.E+06
2631	Q92797-1	Symplekin [OS=Homo sapiens]	2.6	3	1	2	1	0	0	1	1	0								
2632	Q9H4H8	Protein FAM83D [OS=Homo sapiens]	2.5	2	1	4	1	0	0	1	1	0								
2633	Q9H6F5	Coiled-coil domain-containing protein 86 [OS=Homo sapiens]	2.5	6	1	2	1	15	0	1	1	0	8.01.E+06	5.19.E+06	8.60.E+06	8.35.E+06	4.32.E+06	5.02.E+06	7.58.E+06	3.50.E+06
2634	O15050	TPR and ankyrin repeat-containing protein 1 [OS=Homo sapiens]	2.5	0	1	26	1	101	5	1	1	0	1.25.E+08	1.26.E+08	1.11.E+08	1.00.E+08	1.02.E+08	8.37.E+07	1.14.E+08	1.12.E+08
2635	Q9NTM9	Copper homeostasis protein cutC homolog [OS=Homo sapiens]	2.5	4	1	11	1	0	12	1	1	0		1.44.E+07	1.55.E+07		1.32.E+07	1.28.E+07	1.05.E+07	1.55.E+07
2636	Q14966-1	Zinc finger protein 638 [OS=Homo sapiens]	2.5	1	1	2	1	0	0	1	1	0	3.81.E+06	3.39.E+06	3.24.E+06	3.31.E+06	3.03.E+06	2.96.E+06	3.61.E+06	3.41.E+06
2637	O95721	Synaptosomal-associated protein 29 [OS=Homo sapiens]	2.5	5	1	2	1	0	0	1	1	0	7.34.E+06	5.85.E+06	7.42.E+06	9.74.E+06			5.99.E+06	
2638	O75165	DnaJ homolog subfamily C member 13 [OS=Homo sapiens]	2.5	1	1	6	1	0	4	1	1	0	5.50.E+06	6.43.E+06	2.03.E+07	7.44.E+06	6.69.E+06	2.06.E+07	1.62.E+07	1.59.E+07
2639	Q9H490	Phosphatidylinositol glycan anchor biosynthesis class U protein [OS=Homo sapiens]	2.5	4	1	4	1	32	0	1	1	0	3.15.E+06	2.81.E+06	5.06.E+06	3.67.E+06	1.80.E+06	1.40.E+06	5.15.E+06	
2640	O75665	Oral-facial-digital syndrome 1 protein [OS=Homo sapiens]	2.5	1	1	6	1	39			1	0								
2641	Q9C0J8	pre-mRNA 3' end processing protein WDR33 [OS=Homo sapiens]	2.5	1	1	13	1	0	0	1	1	0	8.14.E+05	1.21.E+06	9.67.E+05	7.25.E+05	9.81.E+05	1.30.E+06	1.02.E+06	9.63.E+05
2642	Q9BVG4	Protein PBDC1 [OS=Homo sapiens]	2.4	4	1	2	1	15	2	1	1	0	1.16.E+07	9.47.E+06	1.11.E+07	1.05.E+07	1.20.E+07	1.23.E+07	9.09.E+06	9.05.E+06

No.	Accession	Description	Sum PEP Score	Coverage [%]	# Peptides	# PSMs	# Unique Peptides	Score Mascot: A5 Mascot	Score Sequest HT: A2 Sequest HT	# Peptides (by Search Engine): A2 Sequest HT	# Peptides (by Search Engine): A5 Mascot	# Razor Peptides	ctrl Abundances_1	ctrl Abundances_2	ctrl Abundances_3	ctrl Abundances_4	JAM-A KO Abundances_1	JAM-A KO Abundances_2	JAM-A KO Abundances_3	JAM-A KO Abundances_4
2643	Q13257-1	Mitotic spindle assembly checkpoint protein MAD2A [OS=Homo sapiens]	2.4	5	1	17	1	0	2	1	1	0	3.06.E+07	3.16.E+07	3.20.E+07	2.74.E+07	3.11.E+07	3.13.E+07	3.45.E+07	3.38.E+07
2644	Q9Y324	rRNA-processing protein FCF1 homolog [OS=Homo sapiens]	2.4	6	1	2	1	0	0	1	1	0	4.28.E+06	5.18.E+06	5.73.E+06	6.65.E+06	4.76.E+06	5.29.E+06	5.22.E+06	5.65.E+06
2645	Q96GM8	Target of EGR1 protein 1 [OS=Homo sapiens]	2.4	4	1	4	1	21	4	1	1	0	1.77.E+07	1.85.E+07	1.59.E+07	2.06.E+07	3.01.E+07	2.92.E+07	2.59.E+07	2.16.E+07
2646	P17735	tyrosine aminotransferase [OS=Homo sapiens]	2.4	2	1	35	1	14	0	1	1	0	3.70.E+07	3.17.E+07	3.71.E+07	4.33.E+07	3.71.E+07	3.62.E+07	4.38.E+07	3.93.E+07
2647	Q8WUA4-1	General transcription factor 3C polypeptide 2 [OS=Homo sapiens]	2.4	1	1	2	1	0	0	1	1	0	5.16.E+05	4.89.E+05	4.85.E+05	3.91.E+05	3.13.E+05	4.46.E+05	3.54.E+05	3.85.E+05
2648	Q2Q1W2	E3 ubiquitin-protein ligase TRIM71 [OS=Homo sapiens]	2.4	1	1	3	1	0	0	1	1	0								
2649	Q9NR28-1	Diablo homolog, mitochondrial [OS=Homo sapiens]	2.4	5	1	2	1	0	2	1	1	0	6.76.E+06	5.90.E+06	8.24.E+06	7.86.E+06	3.16.E+06	4.39.E+06	5.13.E+06	4.60.E+06
2650	Q9BUI4	DNA-directed RNA polymerase III subunit RPC3 [OS=Homo sapiens]	2.4	3	1	2	1	0	0	1	1	0	1.19.E+06	1.46.E+06	9.02.E+05	1.37.E+06	2.46.E+06	2.42.E+06	2.69.E+06	3.33.E+06
2651	Q9GZU1	Mucolipin-1 [OS=Homo sapiens]	2.4	4	1	2	1	20	0	1	1	0	6.17.E+06	1.52.E+06	6.59.E+06	1.72.E+06		1.38.E+06		
2652	Q96EE3	nucleoporin Seh1 [OS=Homo sapiens]	2.3	3	1	5	1	0	3	1	1	0								
2653	P00813	adenosine deaminase [OS=Homo sapiens]	2.3	10	1	2	1	18	0	1	1	0	5.64.E+06	4.83.E+06	5.34.E+06	6.07.E+06	3.36.E+06		4.59.E+05	2.08.E+06
2654	Q9NQR7	Coiled-coil domain-containing protein 177 [OS=Homo sapiens]	2.3	1	1	24	1	22	17	1	1	0	1.18.E+07	1.05.E+07	1.33.E+07	1.56.E+07	1.55.E+07	1.90.E+07	2.44.E+07	1.70.E+07
2655	Q96HS1-1	Serine/threonine-protein phosphatase Pgam5, mitochondrial [OS=Homo sapiens]	2.3	2	1	18	1		0	1		0	6.42.E+07	6.22.E+07	6.60.E+07	7.49.E+07	6.63.E+07	5.79.E+07	6.48.E+07	5.70.E+07
2656	Q8TB61	Adenosine 3'-phospho 5'-phosphosulfate transporter 1 [OS=Homo sapiens]	2.3	5	1	7	1	20	0	1	1	0								
2657	O94850	Dendrin [OS=Homo sapiens]	2.3	3	1	10	1	0			1	0	9.33.E+05	9.14.E+05	9.39.E+05	7.68.E+05	8.77.E+05	1.01.E+06	7.95.E+05	1.01.E+06
2658	Q8IUD2-1	ELKS/Rab6-interacting/CAST family member 1 [OS=Homo sapiens]	2.3	1	1	15	1	0	2	1	1	0	1.67.E+08	1.62.E+08	1.73.E+08	1.50.E+08	2.35.E+08	2.39.E+08	2.51.E+08	2.48.E+08
2659	O43511	pendrin [OS=Homo sapiens]	2.3	2	1	4	1	0	0	1	1	0	1.58.E+06	2.02.E+06	2.70.E+06	1.55.E+06	1.03.E+07	9.83.E+06	9.30.E+06	1.12.E+07
2660	Q9BYN8	28S ribosomal protein S26, mitochondrial [OS=Homo sapiens]	2.3	5	1	6	1	15	0	1	1	0	9.87.E+06	1.00.E+07	9.08.E+06	2.03.E+07	8.37.E+06	9.04.E+06	1.47.E+07	8.93.E+06
2661	P06756	Integrin alpha-V [OS=Homo sapiens]	2.3	2	1	2	1	23	0	1	1	0					3.69.E+06	8.36.E+06	6.42.E+06	5.90.E+06
2662	Q9H488-1	GDP-fucose protein O-fucosyltransferase 1 [OS=Homo sapiens]	2.3	4	1	9	1	0	0	1	1	0								
2663	Q99496	E3 ubiquitin-protein ligase RING2 [OS=Homo sapiens]	2.3	3	1	1	1	0			1	0			1.13.E+07		1.14.E+07		1.43.E+07	1.34.E+07
2664	Q8WWB7	Glycosylated lysosomal membrane protein [OS=Homo sapiens]	2.3	5	1	2	1	0	0	1	1	0	2.39.E+06	4.42.E+06	3.77.E+06	1.74.E+06	1.52.E+06	2.06.E+06	2.00.E+05	2.20.E+05
2665	Q17RC7	Exocyst complex component 3-like protein 4 [OS=Homo sapiens]	2.3	1	1	96	1	26	20	1	1	0	1.70.E+08	1.70.E+08	1.78.E+08	1.47.E+08	2.15.E+08	2.15.E+08	2.31.E+08	2.18.E+08
2666	Q8N5M9	Protein jagunal homolog 1 [OS=Homo sapiens]	2.2	7	1	1	1		0	1		0	2.04.E+07	3.04.E+07			2.91.E+07		3.05.E+07	3.07.E+07
2667	Q5VY09	immediate early response gene 5 protein [OS=Homo sapiens]	2.2	3	1	14	1	0	5	1	1	0	3.49.E+07	5.03.E+07	5.37.E+07	5.07.E+07	6.67.E+07		9.32.E+07	8.51.E+07
2668	Q9H9T3	elongator complex protein 3 [OS=Homo sapiens]	2.2	3	1	2	1	19	0	1	1	0	3.84.E+06	3.00.E+06	3.31.E+06	3.58.E+06	2.58.E+06	2.52.E+06	1.85.E+06	
2669	Q9H9Y2	Ribosome production factor 1 [OS=Homo sapiens]	2.2	3	1	4	1	0	0	1	1	0	2.47.E+06	2.87.E+06	3.06.E+06	2.83.E+06	1.85.E+06		2.24.E+06	1.70.E+06
2670	Q9H0U6	39S ribosomal protein L18, mitochondrial [OS=Homo sapiens]	2.2	5	1	2	1	0	2	1	1	0	2.01.E+07	2.39.E+07	2.16.E+07	2.05.E+07	2.10.E+07	2.11.E+07	1.94.E+07	2.00.E+07
2671	Q9H993	protein-glutamate O-methyltransferase [OS=Homo sapiens]	2.2	4	1	2	1	0	0	1	1	0		1.40.E+07	1.48.E+07		2.28.E+07	2.20.E+07	6.79.E+06	2.53.E+07
2672	B1ANS9	WD repeat-containing protein 64 [OS=Homo sapiens]	2.2	1	1	10	1	0	0	1	1	0	6.82.E+07	5.73.E+07	7.11.E+07	8.40.E+07	5.50.E+07	5.57.E+07	6.65.E+07	5.82.E+07
2673	Q9H9S4	Calcium-binding protein 39-like [OS=Homo sapiens]	2.2	3	1	1	1	0			1	0								
2674	O00468	Agrin OS=Homo sapiens OX=9606 GN=AGRN PE=1 SV=6	2.2	0	1	1	1	24			1	0	4.55.E+06	5.76.E+06	5.49.E+06	5.12.E+06	6.00.E+06	7.16.E+06	5.78.E+06	7.21.E+06
2675	Q8WXE9-1	Stonin-2 [OS=Homo sapiens]	2.2	2	1	2	1	15	0	1	1	0		1.79.E+06	1.46.E+06	1.84.E+06	2.73.E+06	1.64.E+06	2.32.E+06	2.26.E+06
2676	Q9BTY7	Protein HGH1 homolog [OS=Homo sapiens]	2.2	3	1	2	1	16	2	1	1	0	2.97.E+07	3.16.E+07	2.91.E+07	2.12.E+07	1.24.E+07	1.00.E+07	1.65.E+07	7.84.E+06
2677	P49790	Nuclear pore complex protein Nup153 [OS=Homo sapiens]	2.2	2	1	1	1	0			1	0	3.62.E+06	9.68.E+06	3.16.E+06	3.34.E+06		5.34.E+06	1.32.E+06	
2678	Q96QH2-2	Isoform 2 of PML-RARA-regulated adapter molecule 1 [OS=Homo sapiens]	2.1	1	1	1	1	0			1	0	7.08.E+06	6.29.E+06	6.28.E+06	8.01.E+06	3.90.E+06	3.94.E+06	3.97.E+06	3.77.E+06
2679	Q8WUX9	Charged multivesicular body protein 7 [OS=Homo sapiens]	2.1	4	1	4	1	33	0	1	1	0	2.18.E+06	2.58.E+06	2.27.E+06	2.19.E+06	1.80.E+06	1.31.E+06	1.52.E+06	1.38.E+06
2680	P78316	Nucleolar protein 14 [OS=Homo sapiens]	2.1	2	1	2	1	0	2	1	1	0	2.42.E+07	2.59.E+07	2.36.E+07	2.04.E+07	2.59.E+07	2.66.E+07	2.42.E+07	2.93.E+07
2681	P17050	alpha-N-acetylgalactosaminidase [OS=Homo sapiens]	2.1	3	1	2	1	23	0	1	1	0								
2682	P10721-1	Mast/stem cell growth factor receptor Kit [OS=Homo sapiens]	2.1	1	1	13	1		0	1		0	2.07.E+07	1.94.E+07	2.27.E+07	1.84.E+07	2.26.E+07	2.49.E+07	2.78.E+07	2.74.E+07
2683	Q08AM6	Protein VAC14 homolog [OS=Homo sapiens]	2.1	2	1	7	1	0	0	1	1	0	2.26.E+07	1.87.E+07	2.36.E+07	1.97.E+07	1.83.E+07	1.70.E+07	1.79.E+07	1.59.E+07
2684	Q86XA9	HEAT repeat-containing protein 5A [OS=Homo sapiens]	2.1	1	1	4	1	17	0	1	1	0	1.69.E+06	2.19.E+06	1.82.E+06	1.96.E+06	2.82.E+06	2.28.E+06	2.31.E+06	2.23.E+06
2685	Q93034	Cullin-5 [OS=Homo sapiens]	2.1	1	1	2	1	15	0	1	1	0	2.27.E+06		9.20.E+05	2.12.E+06	5.28.E+06	3.00.E+06	3.65.E+06	4.53.E+06
2686	O94900	Thymocyte selection-associated high mobility group box protein TOX [OS=Homo sapiens]	2.1	4	1	15	1		0	1		0	3.17.E+06	4.14.E+06	3.13.E+06	3.31.E+06	7.25.E+06	9.24.E+06	4.35.E+06	6.30.E+06
2687	Q86VU5	Catechol O-methyltransferase domain-containing protein 1 [OS=Homo sapiens]	2.1	6	1	2	1	0	2	1	1	0	4.80.E+06	4.64.E+06	5.03.E+06	5.99.E+06	4.58.E+06	3.79.E+06	3.49.E+06	3.41.E+06
2688	Q32P41	tRNA (guanine(37)-N1)-methyltransferase [OS=Homo sapiens]	2.1	3	1	11	1	0	3	1	1	0								
2689	Q8ND56	protein LSM14 homolog A [OS=Homo sapiens]	2.1	2	1	2	1	0	0	1	1	0	1.19.E+07	1.32.E+07	1.27.E+07	1.12.E+07	1.24.E+07	1.16.E+07	1.20.E+07	1.23.E+07
2690	Q7Z3B4	Nucleoporin p54 [OS=Homo sapiens]	2.1	1	1	5	1	0	0	1	1	0	1.19.E+07	1.03.E+07	1.15.E+07	1.02.E+07	1.23.E+07	1.20.E+07	1.01.E+07	1.21.E+07
2691	P35251-1	Replication factor C subunit 1 [OS=Homo sapiens]	2.1	1	1	8	1	19	0	1	1	0	1.02.E+06	1.82.E+06	1.44.E+06	1.19.E+06	6.25.E+06	4.34.E+06	4.00.E+06	5.73.E+06
2692	P42336	Phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic subunit alpha isoform [OS=Homo sapiens]	2.1	1	1	101	1	13	0	1	1	0	2.19.E+08	1.98.E+08	2.66.E+08	1.67.E+08	3.06.E+08	2.75.E+08	3.52.E+08	3.38.E+08
2693	P57772	selenocysteine-specific elongation factor [OS=Homo sapiens]	2.1	3	1	3	1	0	4	1	1	0	6.23.E+07	6.88.E+07	7.26.E+07	6.32.E+07	1.01.E+08	7.93.E+07	7.46.E+07	1.09.E+08

No.	Accession	Description	Sum PEP Score	Coverage [%]	# Peptides	# PSMs	# Unique Peptides	Score Mascot: A5 Mascot	Score Sequest HT: A2 Sequest HT	# Peptides (by Search Engine): A2 Sequest HT	# Peptides (by Search Engine): A5 Mascot	# Razor Peptides	ctrl Abundances_1	ctrl Abundances_2	ctrl Abundances_3	ctrl Abundances_4	JAM-A KO Abundances_1	JAM-A KO Abundances_2	JAM-A KO Abundances_3	JAM-A KO Abundances_4
2694	Q9NNW7-1	thioredoxin reductase 2, mitochondrial [OS=Homo sapiens]	2.1	5	1	2	1	0	0	1	1	0	6.51.E+06	2.98.E+06	6.51.E+06		6.33.E+06	8.81.E+06	4.67.E+06	5.08.E+06
2695	P32321	deoxycytidylate deaminase [OS=Homo sapiens]	2.1	4	1	15	1	0	0	1	1	0	2.11.E+07	1.94.E+07	2.21.E+07	2.43.E+07	2.74.E+07	2.28.E+07	2.65.E+07	2.36.E+07
2696	Q92485-1	acid sphingomyelinase-like phosphodiesterase 3B [OS=Homo sapiens]	2.1	5	1	2	1	0	0	1	1	0	1.52.E+07	1.45.E+07	1.41.E+07	1.50.E+07	1.50.E+07	1.82.E+06	6.05.E+06	1.10.E+07
2697	Q9NPL8	Complex I assembly factor TIMMDC1, mitochondrial [OS=Homo sapiens]	2.1	8	1	2	1	0	0	1	1	0	3.73.E+06	3.97.E+06	4.03.E+06	4.30.E+06	1.81.E+06	2.73.E+06	2.20.E+06	3.89.E+06
2698	P48509	CD151 antigen [OS=Homo sapiens]	2.1	4	1	2	1	15	2	1	1	0		4.32.E+07	4.00.E+07			5.54.E+07	7.55.E+07	6.98.E+07
2699	P49914	5-formyltetrahydrofolate cyclo-ligase [OS=Homo sapiens]	2.1	3	1	13	1		0	1		0	3.63.E+07	3.22.E+07	3.31.E+07	2.90.E+07	3.21.E+07	2.85.E+07	3.16.E+07	3.18.E+07
2700	Q86YN1-1	Dolichyldiphosphatase 1 [OS=Homo sapiens]	2.1	5	1	11	1	18	0	1	1	0	5.35.E+06	5.68.E+06	5.04.E+06	4.82.E+06	5.34.E+06	4.50.E+06	4.87.E+06	3.73.E+06
2701	O15116	U6 snRNA-associated Sm-like protein LSm1 [OS=Homo sapiens]	2.0	5	1	10	1	39	0	1	1	0	1.63.E+07	1.57.E+07	1.87.E+07	1.49.E+07	1.35.E+07	1.85.E+07	1.72.E+07	1.59.E+07
2702	Q9Y4K1	beta/gamma crystallin domain-containing protein 1 [OS=Homo sapiens]	2.0	1	1	6	1	19	0	1	1	0	2.86.E+07	3.81.E+07		5.34.E+07	3.59.E+07	4.91.E+07		8.72.E+07
2703	P15498-1	Proto-oncogene vav [OS=Homo sapiens]	2.0	2	1	3	1	0	0	1	1	0								
2704	P11310-1	medium-chain specific acyl-CoA dehydrogenase, mitochondrial [OS=Homo sapiens]	2.0	2	1	8	1	0	0	1	1	0	7.71.E+06	7.54.E+06	1.02.E+07	6.72.E+06	1.19.E+07	1.26.E+07	1.31.E+07	1.15.E+07
2705	P10243-1	Myb-related protein A [OS=Homo sapiens]	2.0	1	1	20	1		0	1		0	6.20.E+07	6.33.E+07	6.67.E+07	5.50.E+07	4.59.E+07	4.66.E+07	5.11.E+07	4.95.E+07
2706	Q15629	Translocating chain-associated membrane protein 1 [OS=Homo sapiens]	2.0	2	1	6	1	0	0	1	1	0	4.10.E+06	3.22.E+06		3.59.E+06	7.75.E+06	9.87.E+06	8.99.E+06	9.48.E+06
2707	O75530	Polycomb protein EED [OS=Homo sapiens]	2.0	5	1	3	1	0	0	1	1	0	1.86.E+07	2.13.E+07	2.16.E+07	1.72.E+07	2.21.E+07	2.46.E+07	2.06.E+07	2.21.E+07
2708	Q13496	Myotubularin [OS=Homo sapiens]	2.0	1	1	6	1		0	1		0								
2709	Q92785	Zinc finger protein ubi-d4 [OS=Homo sapiens]	2.0	4	1	2	1	0	0	1	1	0	1.13.E+07	1.36.E+07	5.23.E+06	4.70.E+06	1.06.E+07	1.41.E+07	6.81.E+06	9.79.E+06
2710	Q6JEL2	Kelch-like protein 10 [OS=Homo sapiens]	2.0	2	1	6	1	0	0	1	1	0	2.65.E+05	3.25.E+05	2.58.E+05	1.48.E+05	5.30.E+05	7.03.E+05	6.16.E+05	4.25.E+05
2711	Q92615	la-related protein 4B [OS=Homo sapiens]	2.0	2	1	4	1	0			1	0	1.18.E+07	5.93.E+06	1.07.E+07	1.29.E+07	5.53.E+06	5.61.E+06	6.26.E+06	1.02.E+07
2712	Q9HCJ6	Synaptic vesicle membrane protein VAT-1 homolog-like [OS=Homo sapiens]	2.0	3	1	7	1	54	5	1	1	0	6.79.E+06	8.76.E+06	1.08.E+07	1.30.E+07	1.96.E+07	1.53.E+07	1.89.E+07	1.66.E+07
2713	P14616	Insulin receptor-related protein [OS=Homo sapiens]	2.0	1	1	25	1	0	0	1	1	0	3.80.E+07	3.54.E+07	3.64.E+07	3.24.E+07	5.74.E+07	5.49.E+07	5.80.E+07	5.90.E+07
2714	Q6NW29	RWD domain-containing protein 4 [OS=Homo sapiens]	2.0	5	1	1	1		0	1		0	6.49.E+06	7.35.E+06	6.74.E+06	5.85.E+06	5.39.E+06	8.47.E+06	6.32.E+06	7.53.E+06
2715	Q7Z6K5-2	Isoform C15orf38-AP3S2 of Arpin [OS=Homo sapiens]	2.0	3	1	1	1		0	1		0	1.20.E+07	1.12.E+07	9.59.E+06	1.38.E+07	1.53.E+07	1.15.E+07	1.36.E+07	1.17.E+07
2716	Q9UPQ3-1	Arf-GAP with GTPase, ANK repeat and PH domain-containing protein 1 [OS=Homo sapiens]	2.0	2	1	2	1	0	0	1	1	0	2.73.E+06	3.63.E+06	2.72.E+06	2.68.E+06	2.88.E+06	3.28.E+06	2.81.E+06	3.36.E+06
2717	O75695	Protein XRP2 [OS=Homo sapiens]	2.0	2	1	3	1	0	0	1	1	0	2.26.E+07	1.97.E+07	2.21.E+07	2.54.E+07	2.43.E+07	2.96.E+07	2.80.E+07	2.80.E+07
2718	Q9UJ41-1	Rab5 GDP/GTP exchange factor [OS=Homo sapiens]	2.0	2	1	2	1	0	2	1	1	0		1.84.E+07						
2719	Q9Y6Q5-2	Isoform 2 of AP-1 complex subunit mu-2 [OS=Homo sapiens]	2.0	5	1	1	1		0	1		0	1.35.E+06	8.19.E+06	1.14.E+06	2.98.E+06	4.28.E+05	6.84.E+05		7.26.E+05
2720	Q6AI08	HEAT repeat-containing protein 6 [OS=Homo sapiens]	2.0	1	1	6	1	40	0	1	1	0	2.83.E+06	3.71.E+06	3.27.E+06	3.50.E+06	6.36.E+06	5.42.E+06	5.26.E+06	5.21.E+06
2721	O75368	SH3 domain-binding glutamic acid-rich-like protein [OS=Homo sapiens]	2.0	16	1	4	1	24	0	1	1	0	1.11.E+06					8.33.E+06	6.63.E+06	8.33.E+06
2722	Q86UQ4	ATP-binding cassette sub-family A member 13 [OS=Homo sapiens]	2.0	0	1	5	1	0			1	0	3.82.E+08	3.99.E+08	4.09.E+08	3.55.E+08	3.25.E+08	3.58.E+08	3.53.E+08	3.49.E+08
2723	Q6BDS2	UHRF1-binding protein 1 [OS=Homo sapiens]	2.0	1	1	9	1	15	0	1	1	0	4.42.E+07	2.49.E+07	4.06.E+07	4.75.E+07	1.17.E+08	1.18.E+08	1.45.E+08	1.32.E+08
2724	Q06546	GA-binding protein alpha chain [OS=Homo sapiens]	1.9	3	1	1	1	0			1	0	8.11.E+06	4.20.E+06	9.22.E+06	3.61.E+06	8.42.E+06	1.18.E+07	4.40.E+06	9.49.E+06
2725	A6NK44	Glyoxalase domain-containing protein 5 [OS=Homo sapiens]	1.9	8	1	13	1	0	0	1	1	0	3.58.E+07	3.00.E+07	3.47.E+07	2.94.E+07	4.31.E+07	4.77.E+07	4.70.E+07	4.86.E+07
2726	O95881	Thioredoxin domain-containing protein 12 [OS=Homo sapiens]	1.9	8	1	3	1	0	0	1	1	0	2.88.E+07	2.99.E+07			2.92.E+07	3.41.E+07		3.70.E+07
2727	P54278	Mismatch repair endonuclease PMS2 [OS=Homo sapiens]	1.9	2	1	1	1	0			1	0	3.97.E+06	3.68.E+06	3.29.E+06	2.90.E+06	4.94.E+06	6.22.E+06	6.09.E+06	4.81.E+06
2728	O00178	GTP-binding protein 1 [OS=Homo sapiens]	1.9	3	1	2	1	0	0	1	1	0	2.26.E+06	2.74.E+06	3.72.E+06	2.72.E+06	2.35.E+06	1.09.E+06	2.47.E+06	2.17.E+06
2729	P49006	MARCKS-related protein [OS=Homo sapiens]	1.9	8	1	4	1	18	0	1	1	0								
2730	Q9Y619	mitochondrial ornithine transporter 1 [OS=Homo sapiens]	1.9	9	1	4	1	0	0	1	1	0	3.59.E+06		1.08.E+06		5.65.E+06	4.96.E+06	1.87.E+06	5.54.E+06
2731	O60502	protein O-GlcNAcase [OS=Homo sapiens]	1.9	2	1	1	1		0	1		0								
2732	Q9UKG1	DCC-interacting protein 13-alpha [OS=Homo sapiens]	1.9	2	1	4	1		0	1		0	3.18.E+06	2.85.E+06	3.15.E+06	2.69.E+06	3.44.E+06	3.57.E+06	3.74.E+06	3.70.E+06
2733	Q8NG06	E3 ubiquitin-protein ligase TRIM58 [OS=Homo sapiens]	1.9	3	1	3	1		0	1		0	5.05.E+06	3.43.E+06	5.04.E+06	4.78.E+06	7.42.E+06	7.09.E+06	6.72.E+06	6.83.E+06
2734	Q9NZU0	Leucine-rich repeat transmembrane protein FLRT3 [OS=Homo sapiens]	1.9	1	1	3	1		0	1		0	1.30.E+07	1.31.E+07	1.30.E+07	1.15.E+07	1.42.E+07	1.37.E+07	1.36.E+07	1.38.E+07
2735	Q9UKW6-1	ETS-related transcription factor Elf-5 [OS=Homo sapiens]	1.9	7	1	17	1	0			1	0	1.45.E+07	1.48.E+07	1.41.E+07	1.17.E+07	1.89.E+07	2.02.E+07	1.83.E+07	1.77.E+07
2736	Q6P9G9-1	zinc finger protein 449 [OS=Homo sapiens]	1.9	3	1	1	1		0	1		0								
2737	Q9P0U1	Mitochondrial import receptor subunit TOM7 homolog [OS=Homo sapiens]	1.9	11	1	5	1		5	1		0	5.04.E+07	4.30.E+07	5.29.E+07	4.95.E+07	3.39.E+07	2.75.E+07	3.50.E+07	3.43.E+07
2738	O95983-1	methyl-CpG-binding domain protein 3 [OS=Homo sapiens]	1.9	5	1	4	1	26	0	1	1	0	2.62.E+06	1.03.E+06			4.00.E+06	4.06.E+06		5.10.E+06
2739	O75884-1	Putative hydrolase RBBP9 [OS=Homo sapiens]	1.8	11	1	2	1	0	0	1	1	0								
2740	O43815	striatin [OS=Homo sapiens]	1.8	2	1	2	1	0	0	1	1	0	5.06.E+06	4.80.E+06	4.81.E+06	5.30.E+06	4.48.E+06	2.96.E+06	4.18.E+06	3.39.E+06
2741	Q9NSU2-3	Isoform 3 of Three-prime repair exonuclease 1 [OS=Homo sapiens]	1.8	6	1	2	1	0	0	1	1	0	9.90.E+05	2.07.E+06	2.33.E+06	2.13.E+06	6.12.E+05	5.25.E+05	1.22.E+06	6.50.E+05
2742	Q7L9L4	mob kinase activator 1b [OS=Homo sapiens]	1.8	3	1	30	1	28	0	1	1	0	4.44.E+07	3.89.E+07	4.32.E+07	3.44.E+07	5.03.E+07	5.06.E+07	5.68.E+07	5.44.E+07
2743	Q8TAQ2	SWI/SNF complex subunit SMARCC2 [OS=Homo sapiens]	1.8	2	1	1	1		0	1		0	5.10.E+06	4.80.E+06	3.84.E+06	3.70.E+06	6.54.E+06	6.53.E+06	6.79.E+06	5.63.E+06
2744	Q9BQF6	Sentrin-specific protease 7 [OS=Homo sapiens]	1.8	1	1	30	1	0	0	1	1	0	1.67.E+08	1.57.E+08	1.74.E+08	1.99.E+08	1.19.E+08	1.18.E+08	1.41.E+08	1.28.E+08
2745	P49642	DNA primase small subunit [OS=Homo sapiens]	1.8	5	1	1	1		0	1		0								
2746	Q6UWE0	E3 ubiquitin-protein ligase LRSAM1 [OS=Homo sapiens]	1.8	2	1	2	1	0	0	1	1	0	2.72.E+06	2.88.E+06	2.92.E+06	2.71.E+06	1.66.E+06	1.67.E+06	1.55.E+06	1.68.E+06
2747	O14981	TATA-binding protein-associated factor 172 [OS=Homo sapiens]	1.8	1	1	2	1	15	0	1	1	0	2.28.E+06		1.83.E+06	2.20.E+06	4.80.E+06	3.28.E+06	3.09.E+06	4.21.E+06

No.	Accession	Description	Sum PEP Score	Coverage [%]	# Peptides	# PSMs	# Unique Peptides	Score Mascot: A5 Mascot	Score Sequest HT: A2 Sequest HT	# Peptides (by Search Engine): A2 Sequest HT	# Peptides (by Search Engine): A5 Mascot	# Razor Peptides	ctrl Abundances_1	ctrl Abundances_2	ctrl Abundances_3	ctrl Abundances_4	JAM-A KO Abundances_1	JAM-A KO Abundances_2	JAM-A KO Abundances_3	JAM-A KO Abundances_4
2748	Q8N944	APC membrane recruitment protein 3 [OS=Homo sapiens]	1.8	2	1	9	1	0	0	1	1	0								
2749	Q8NDH2	Coiled-coil domain-containing protein 168 [OS=Homo sapiens]	1.8	0	1	2	1	0	0	1	1	0	1.64.E+06	1.70.E+06	2.54.E+06	1.61.E+06	3.02.E+06	3.60.E+06	3.75.E+06	3.34.E+06
2750	Q9BXS5-1	AP-1 complex subunit mu-1 [OS=Homo sapiens]	1.8	4	1	2	1	0	0	1	1	0	4.37.E+06	2.14.E+06	1.99.E+06	1.78.E+06	3.23.E+06	2.75.E+06	3.51.E+06	3.20.E+06
2751	0A1B0GUW	Uncharacterized protein SPEM3 OS=Homo sapiens OX=9606 GN=SPEM3 PE=3 SV=1	1.8	2	1	1	1	0			1	0	6.14.E+05	7.36.E+05	8.36.E+05	7.52.E+05	1.16.E+06	1.26.E+06	1.33.E+06	9.83.E+05
2752	Q8N1G1	RNA exonuclease 1 homolog [OS=Homo sapiens]	1.8	2	1	1	1	0			1	0								
2753	Q8NAF0	Zinc finger protein 579 [OS=Homo sapiens]	1.8	3	1	1	1		0	1		0	5.18.E+05	5.69.E+05	5.82.E+05	4.26.E+05	3.63.E+05	3.78.E+05	3.92.E+05	4.05.E+05
2754	Q8NFW8	N-acylneuraminate cytidylyltransferase [OS=Homo sapiens]	1.7	3	1	2	1	0	0	1	1	0	2.56.E+06	2.32.E+06	2.42.E+06	2.34.E+06	2.86.E+06	3.55.E+06	2.71.E+06	2.30.E+06
2755	A3KMH1	von Willebrand factor A domain-containing protein 8 [OS=Homo sapiens]	1.7	1	1	2	1	16	0	1	1	0	3.10.E+06	3.63.E+06	4.00.E+06	3.89.E+06	5.91.E+06	4.12.E+06		6.04.E+06
2756	Q9UK61	Protein TASOR [OS=Homo sapiens]	1.7	1	1	4	1	0	0	1	1	0	3.52.E+06	3.90.E+06		4.80.E+06	3.97.E+06	3.86.E+06	3.35.E+06	3.18.E+06
2757	Q86Y97	Histone-lysine N-methyltransferase KMT5C [OS=Homo sapiens]	1.7	3	1	18	1	0	0	1	1	0	8.00.E+06	9.64.E+06	5.75.E+06	8.82.E+06	8.22.E+06	8.14.E+06	5.85.E+06	8.29.E+06
2758	Q8IXJ9	Putative Polycomb group protein ASXL1 [OS=Homo sapiens]	1.7	1	1	18	1		0	1		0	1.58.E+08	1.49.E+08	1.59.E+08	1.73.E+08	1.38.E+08	1.43.E+08	1.48.E+08	1.47.E+08
2759	Q9H1D0	Transient receptor potential cation channel subfamily V member 6 [OS=Homo sapiens]	1.7	1	1	1	1	0			1	0	1.11.E+07	1.23.E+07	2.12.E+07	1.37.E+07	1.53.E+07	1.61.E+07	1.97.E+07	1.91.E+07
2760	P08069	Insulin-like growth factor 1 receptor [OS=Homo sapiens]	1.7	1	1	1	1	0			1	0								
2761	Q96AE7	Tetratricopeptide repeat protein 17 [OS=Homo sapiens]	1.7	1	1	62	1	0	0	1	1	0	3.99.E+07	2.59.E+07	4.45.E+07	2.26.E+07	4.86.E+07	4.14.E+07	6.58.E+07	6.04.E+07
2762	Q9UKN7	Unconventional myosin-XV [OS=Homo sapiens]	1.7	1	1	8	1	0			1	0	3.24.E+06	2.61.E+06	2.89.E+06	2.03.E+06	4.68.E+06	6.00.E+06	4.60.E+06	4.52.E+06
2763	Q96JQ0	Protocadherin-16 [OS=Homo sapiens]	1.7	1	1	2	1	0	0	1	1	0								
2764	Q9BPX6-1	Calcium uptake protein 1, mitochondrial [OS=Homo sapiens]	1.7	1	1	2	1	0	0	1	1	0	6.11.E+06	6.08.E+06	4.81.E+06	5.51.E+06	3.83.E+06	4.97.E+06	1.95.E+06	4.38.E+06
2765	Q8NGC3	Olfactory receptor 10G2 OS=Homo sapiens OX=9606 GN=OR10G2 PE=2 SV=1	1.7	5	1	4	1	0			1	0	6.19.E+05	6.99.E+05	7.11.E+05	8.78.E+05	3.55.E+05	3.95.E+05	3.80.E+05	2.59.E+05
2766	Q9NRK6	ATP-binding cassette sub-family B member 10, mitochondrial [OS=Homo sapiens]	1.7	1	1	2	1	22	0	1	1	0	5.25.E+06	5.60.E+06	9.85.E+05	6.38.E+06	4.83.E+06	5.45.E+06	2.31.E+06	6.89.E+06
2767	A6NFR6-1	Putative uncharacterized protein C5orf60 [OS=Homo sapiens]	1.7	4	1	1	1	0			1	0	4.15.E+05	4.63.E+05	3.77.E+05	3.03.E+05	5.08.E+05	7.05.E+05	4.47.E+05	5.47.E+05
2768	Q9P013	spliceosome-associated protein CWC15 homolog [OS=Homo sapiens]	1.7	5	1	3	1	0			1	0	3.08.E+07	2.91.E+07	3.12.E+07	3.55.E+07	2.65.E+07	3.03.E+07	2.88.E+07	2.90.E+07
2769	Q86XI6	Protein phosphatase 1 regulatory subunit 3B [OS=Homo sapiens]	1.7	4	1	2	1	0	0	1	1	0	2.05.E+07	3.39.E+07	3.78.E+07	2.72.E+07	3.09.E+07	2.84.E+07	3.64.E+07	3.41.E+07
2770	Q8WVV9	Heterogeneous nuclear ribonucleoprotein L-like [OS=Homo sapiens]	1.7	5	1	5	1	0	0	1	1	0	8.98.E+06	2.07.E+07	1.49.E+07	1.74.E+07	1.97.E+07	2.63.E+07	1.78.E+07	2.04.E+07
2771	Q504Q3	PAB-dependent poly(A)-specific ribonuclease subunit PAN2 [OS=Homo sapiens]	1.7	1	1	9	1	0	0	1	1	0								
2772	Q641Q2	WASH complex subunit 2A [OS=Homo sapiens]	1.6	1	1	2	1	0	0	1	1	0	8.68.E+06	9.48.E+06	8.86.E+06	1.25.E+07	1.51.E+07	1.15.E+07	7.29.E+06	3.39.E+06
2773	Q96F83	Uncharacterized protein C14orf79 [OS=Homo sapiens]	1.6	3	1	4	1	0	0	1	1	0	4.12.E+06	6.46.E+06	5.43.E+06	7.44.E+06	1.95.E+07	1.74.E+07	2.06.E+07	2.03.E+07
2774	O75592	E3 ubiquitin-protein ligase MYCBP2 OS=Homo sapiens OX=9606 GN=MYCBP2 PE=1 SV=4	1.6	0	1	22	1	0			1	0								
2775	Q9UBR2	Cathepsin Z [OS=Homo sapiens]	1.6	4	1	5	1	0	2	1	1	0								
2776	P49279	natural resistance-associated macrophage protein 1 [OS=Homo sapiens]	1.6	1	1	6	1	0			1	0								
2777	Q8N4H5	mitochondrial import receptor subunit TOM5 homolog [OS=Homo sapiens]	1.6	14	1	15	1	0	3	1	1	0	7.33.E+07	6.72.E+07	7.24.E+07	5.94.E+07	4.27.E+07	4.52.E+07	5.10.E+07	4.47.E+07
2778	O14776-1	Transcription elongation regulator 1 [OS=Homo sapiens]	1.6	1	1	4	1	0	0	1	1	0		1.07.E+07	1.45.E+07	1.01.E+07	1.36.E+07	1.26.E+07	1.42.E+07	1.21.E+07
2779	Q10587	thyrotroph embryonic factor [OS=Homo sapiens]	1.6	4	1	5	1	0	0	1	1	0	4.87.E+07	5.43.E+07	5.16.E+07	5.33.E+07	5.46.E+07	6.39.E+07	5.79.E+07	5.80.E+07
2780	Q71RC2	La-related protein 4 [OS=Homo sapiens]	1.6	3	1	2	1	0	0	1	1	0	9.29.E+06	7.80.E+06	7.59.E+06	1.07.E+07	7.94.E+06	8.55.E+06	1.19.E+07	8.83.E+06
2781	Q9BX84	Transient receptor potential cation channel subfamily M member 6 [OS=Homo sapiens]	1.6	1	1	16	1	0	0	1	1	0	1.66.E+06	1.25.E+06				1.32.E+06	1.15.E+06	1.23.E+06
2782	Q9NV70-1	exocyst complex component 1 [OS=Homo sapiens]	1.6	2	1	1	1	0			1	0								
2783	Q13393-1	Phospholipase D1 [OS=Homo sapiens]	1.6	1	1	55	1	0	0	1	1	0	5.39.E+07	5.09.E+07	5.36.E+07	4.43.E+07	4.42.E+07	4.82.E+07	4.72.E+07	4.54.E+07
2784	P52758	2-iminobutanoate/2-iminopropanoate deaminase [OS=Homo sapiens]	1.6	12	1	1	1	0			1	0								
2785	Q8NI08	Nuclear receptor coactivator 7 [OS=Homo sapiens]	1.6	1	1	3	1	0	0	1	1	0	3.85.E+06	3.90.E+06		4.42.E+06	4.34.E+06	4.54.E+06		4.83.E+06
2786	Q9BZF1-1	Oxysterol-binding protein-related protein 8 [OS=Homo sapiens]	1.6	1	1	2	1	0	0	1	1	0	4.25.E+06	3.75.E+06	3.64.E+06	3.72.E+06	3.82.E+06	4.84.E+06	3.78.E+06	4.74.E+06
2787	Q16706	Alpha-mannosidase 2 [OS=Homo sapiens]	1.6	1	1	2	1	0	0	1	1	0								
2788	Q9BSJ6	Protein PIMREG [OS=Homo sapiens]	1.6	3	1	2	1	0	2	1	1	0	4.72.E+07	4.15.E+07	5.13.E+07	5.96.E+07	5.92.E+07	6.15.E+07	7.12.E+07	6.83.E+07
2789	Q6ZS17	RHO family-interacting cell polarization regulator 1 [OS=Homo sapiens]	1.5	1	1	7	1	0	0	1	1	0	1.96.E+06	2.03.E+06	2.43.E+06	2.14.E+06	1.78.E+06	2.57.E+06	3.25.E+06	2.41.E+06
2790	Q8WW01	tRNA-splicing endonuclease subunit Sen15 [OS=Homo sapiens]	1.5	11	1	14	1	18	0	1	1	0								
2791	O95163	Elongator complex protein 1 [OS=Homo sapiens]	1.5	1	1	2	1	0	0	1	1	0						1.27.E+07		9.49.E+06
2792	Q86UD0	Suppressor APC domain-containing protein 2 [OS=Homo sapiens]	1.5	4	1	61	1	0	39	1	1	0	4.06.E+07	3.69.E+07	4.39.E+07	2.93.E+07	2.48.E+07	2.90.E+07	3.71.E+07	2.67.E+07
2793	Q9NZJ9-2	Isoform 2 of Diphosphoinositol polyphosphate phosphohydrolase 2 [OS=Homo sapiens]	1.5	8	1	6	1	0	0	1	1	0	3.68.E+06	3.14.E+06	4.44.E+06	2.37.E+06	1.78.E+06	2.19.E+06	3.97.E+06	2.67.E+06

No.	Accession	Description	Sum PEP Score	Coverage [%]	# Peptides	# PSMs	# Unique Peptides	Score Mascot: A5 Mascot	Score Sequest HT: A2 Sequest HT	# Peptides (by Search Engine): A2 Sequest HT	# Peptides (by Search Engine): A5 Mascot	# Razor Peptides	ctrl Abundances_1	ctrl Abundances_2	ctrl Abundances_3	ctrl Abundances_4	JAM-A KO Abundances_1	JAM-A KO Abundances_2	JAM-A KO Abundances_3	JAM-A KO Abundances_4
2794	Q6P2M8-1	Calcium/calmodulin-dependent protein kinase type 1B [OS=Homo sapiens]	1.5	3	1	24	1	0	0	1	1	0	2.26.E+06	2.15.E+06	2.60.E+06	2.01.E+06	2.86.E+06	4.26.E+06	4.21.E+06	3.24.E+06
2795	Q9C0D3	Protein zyg-11 homolog B [OS=Homo sapiens]	1.5	1	1	1	1	0			1	0								
2796	Q9P1Z9-2	Isoform 2 of Coiled-coil domain-containing protein 180 [OS=Homo sapiens]	1.5	0	1	29	1	22	0	1	1	0	3.08.E+07	2.64.E+07	2.86.E+07	3.12.E+07	3.12.E+07	2.80.E+07	3.32.E+07	2.89.E+07
2797	O60487	Myelin protein zero-like protein 2 [OS=Homo sapiens]	1.5	4	1	2	1	0	0	1	1	0	9.12.E+06	9.97.E+06	1.08.E+07	1.07.E+07	2.81.E+06	2.66.E+06	3.07.E+06	
2798	Q9NPI6	mRNA-decapping enzyme 1A [OS=Homo sapiens]	1.5	3	1	1	1		0	1		0								
2799	Q8NHA6	Putative olfactory receptor 2W6 [OS=Homo sapiens]	1.5	5	1	1	1	0			1	0								
2800	Q86W42	THO complex subunit 6 homolog [OS=Homo sapiens]	1.5	3	1	2	1	0	0	1	1	0	4.53.E+06	3.08.E+06	4.42.E+06	5.49.E+06		4.51.E+06	4.10.E+06	3.48.E+06
2801	P18074-1	Tfiih basal transcription factor complex helicase xpd subunit [OS=Homo sapiens]	1.5	1	1	7	1	0	0	1	1	0	3.15.E+07	2.42.E+07	3.27.E+07	3.30.E+07	3.13.E+07	3.44.E+07	3.85.E+07	3.52.E+07
2802	O75764	Transcription elongation factor A protein 3 [OS=Homo sapiens]	1.5	3	1	5	1	0	0	1	1	0								
2803	Q86XN6	Zinc finger protein 761 OS=Homo sapiens OX=9606 GN=ZNF761 PE=1 SV=3	1.5	1	1	1	1	0			1	0	3.98.E+08	3.47.E+08	3.96.E+08	3.27.E+08	2.32.E+08	2.42.E+08	2.71.E+08	2.68.E+08
2804	O95602	DNA-directed RNA polymerase I subunit RPA1 [OS=Homo sapiens]	1.5	1	1	4	1	0	0	1	1	0	3.99.E+06	5.00.E+06	5.28.E+06	5.44.E+06	4.73.E+06	4.57.E+06	4.99.E+06	4.49.E+06
2805	Q96JM2	zinc finger protein 462 [OS=Homo sapiens]	1.4	1	1	10	1	0			1	0	7.45.E+07	7.45.E+07	7.86.E+07	7.20.E+07	6.28.E+07	1.17.E+08	1.24.E+08	1.23.E+08
2806	Q8IUH4	Palmitoyltransferase ZDHHC13 [OS=Homo sapiens]	1.4	1	1	18	1	0			1	0	1.06.E+08	1.12.E+08	1.05.E+08	9.08.E+07	1.18.E+08	1.35.E+08	1.27.E+08	1.27.E+08
2807	P50613	Cyclin-dependent kinase 7 [OS=Homo sapiens]	1.4	6	1	4	1	0	0	1	1	0	1.89.E+06	2.73.E+06	1.82.E+06	2.26.E+06	3.94.E+06	3.02.E+06	2.06.E+06	2.38.E+06
2808	P46063	ATP-dependent DNA helicase Q1 [OS=Homo sapiens]	1.4	2	1	3	1	0	0	1	1	0	6.16.E+06	4.36.E+06	6.72.E+06	3.92.E+06	1.26.E+07	1.05.E+07	1.32.E+07	1.24.E+07
2809	Q9H0I9	Transketolase-like protein 2 [OS=Homo sapiens]	1.4	3	1	1	1	0			1	0	1.38.E+06	1.44.E+06	8.26.E+05	8.47.E+05	1.80.E+06	1.76.E+06	3.37.E+06	1.66.E+06
2810	Q8NB78-1	Lysine-specific histone demethylase 1B [OS=Homo sapiens]	1.4	2	1	2	1	0	0	1	1	0	7.75.E+05	1.39.E+06	1.03.E+06	7.23.E+05	5.14.E+05	6.87.E+05	6.18.E+05	3.90.E+05
2811	Q96J65-1	Multidrug resistance-associated protein 9 [OS=Homo sapiens]	1.4	1	1	3	1	0			1	0	1.99.E+07	1.84.E+07	1.91.E+07	1.72.E+07	2.85.E+07	2.77.E+07	2.90.E+07	3.21.E+07
2812	Q8NFD2	ankyrin repeat and protein kinase domain-containing protein 1 [OS=Homo sapiens]	1.4	2	1	1	1	0			1	0	3.91.E+05	4.34.E+05	4.84.E+05	4.23.E+05	2.58.E+05		2.74.E+05	3.09.E+05
2813	Q9BZQ4	Nicotinamide/nicotinic acid mononucleotide adenylyltransferase 2 [OS=Homo sapiens]	1.4	5	1	6	1	0	0	1	1	0								
2814	Q5C9Z4	nucleolar MIF4G domain-containing protein 1 [OS=Homo sapiens]	1.4	2	1	7	1	0	0	1	1	0	7.11.E+05	6.17.E+05	8.72.E+05	4.67.E+05	5.89.E+05	9.25.E+05	7.30.E+05	6.88.E+05
2815	Q9UIF9-1	Bromodomain adjacent to zinc finger domain protein 2A [OS=Homo sapiens]	1.4	1	1	10	1	0	0	1	1	0	5.27.E+05	3.86.E+05	5.07.E+05	1.32.E+05	4.50.E+05	8.40.E+05	8.78.E+05	5.27.E+05
2816	Q5T8P6	RNA-binding protein 26 [OS=Homo sapiens]	1.4	1	1	10	1	15	0	1	1	0	3.55.E+06	3.68.E+06	3.55.E+06	3.45.E+06		2.91.E+06	2.71.E+06	2.79.E+06
2817	Q9UG01	Intraflagellar transport protein 172 homolog [OS=Homo sapiens]	1.3	0	1	7	1	54			1	0	5.79.E+07	3.96.E+07	5.30.E+07	5.22.E+07	6.01.E+07	3.85.E+07	5.96.E+07	4.85.E+07
2818	P40126-1	L-dopachrome tautomerase [OS=Homo sapiens]	1.3	3	1	2	1	0			1	0								
2819	A6NK06	cis-aconitate decarboxylase [OS=Homo sapiens]	1.3	2	1	2	1	0	0	1	1	0	7.26.E+05		2.14.E+06	8.76.E+05	9.43.E+05	1.16.E+06	1.33.E+06	1.12.E+06
2820	Q8TD43-1	Transient receptor potential cation channel subfamily M member 4 [OS=Homo sapiens]	1.3	1	1	7	1	0	2	1	1	0	2.45.E+07	2.28.E+07	2.10.E+07	2.08.E+07	2.47.E+07	2.22.E+07	2.38.E+07	2.35.E+07
2821	A6NKB5	Pecanex-like protein 2 [OS=Homo sapiens]	1.3	0	1	1	1	0			1	0								
2822	Q07352	mRNA decay activator protein ZFP36L1 [OS=Homo sapiens]	1.3	5	1	1	1	0			1	0								
2823	O43292-1	Glycosylphosphatidylinositol anchor attachment 1 protein [OS=Homo sapiens]	1.3	2	1	1	1	0			1	0	2.26.E+06	3.12.E+06				3.48.E+06	3.18.E+06	
2824	P16452-1	Erythrocyte membrane protein band 4.2 [OS=Homo sapiens]	1.3	2	1	5	1	0			1	0								
2825	Q5TEJ8	protein THEMIS2 [OS=Homo sapiens]	1.3	3	1	7	1	0			1	0								
2826	Q5TEU4	Arginine-hydroxylase NDUFAF5, mitochondrial [OS=Homo sapiens]	1.3	4	1	36	1	16			1	0								
2827	Q9ULH0-1	Kinase D-interacting substrate of 220 kDa [OS=Homo sapiens]	1.3	1	1	4	1	0			1	0	9.78.E+05	1.15.E+06	9.25.E+05	7.35.E+05	2.37.E+06	2.38.E+06	1.92.E+06	2.03.E+06
2828	Q5VV63-1	Attractin-like protein 1 [OS=Homo sapiens]	1.2	1	1	1	1	0			1	0								
2829	Q9UQ53-1	Alpha-1,3-mannosyl-glycoprotein 4-beta-N-acetylglucosaminyltransferase B [OS=Homo sapiens]	1.2	2	1	4	1	0			1	0			1.13.E+07	5.09.E+06	5.07.E+06	9.41.E+06	8.37.E+06	8.65.E+06
2830	Q5VST9	Obscurin [OS=Homo sapiens]	1.2	0	1	42	1	13	0	1	1	0	5.49.E+07	4.49.E+07	6.52.E+07	3.88.E+07	5.78.E+07	5.26.E+07	8.37.E+07	7.47.E+07
2831	Q92508	Piezo-type mechanosensitive ion channel component 1 [OS=Homo sapiens]	1.2	0	1	17	1	18	0	1	1	0	9.57.E+07	1.11.E+08	8.10.E+07	8.68.E+07	1.19.E+08	1.24.E+08	1.14.E+08	1.10.E+08
2832	Q3SXM5	Inactive hydroxysteroid dehydrogenase-like protein 1 [OS=Homo sapiens]	1.2	4	1	2	1	0	0	1	1	0	2.13.E+06	2.20.E+06	1.95.E+06	1.85.E+06	4.26.E+06	4.46.E+06	4.58.E+06	5.49.E+06
2833	Q8IYM2	Schlafen family member 12 [OS=Homo sapiens]	1.2	3	1	1	1	0			1	0	1.03.E+07	7.61.E+06	1.19.E+07	9.88.E+06	3.71.E+06	4.01.E+06	4.30.E+06	4.20.E+06
2834	Q8WVY7	Ubiquitin-like domain-containing CTD phosphatase 1 [OS=Homo sapiens]	1.2	4	1	2	1	0	0	1	1	0	3.35.E+06	3.20.E+06	2.89.E+06	3.68.E+06	6.86.E+06	6.19.E+06	2.50.E+06	7.62.E+06
2835	Q14997	Proteasome activator complex subunit 4 [OS=Homo sapiens]	1.2	1	1	4	1	0	0	1	1	0								
2836	Q9HBA9	putative N-acetylated-alpha-linked acidic dipeptidase [OS=Homo sapiens]	1.2	2	1	13	1	0	0	1	1	0	1.29.E+07	1.05.E+07	1.40.E+07	1.60.E+07	1.38.E+07	1.38.E+07	1.69.E+07	1.46.E+07
2837	Q96I15-1	selenocysteine lyase [OS=Homo sapiens]	1.2	4	1	4	1	0	0	1	1	0								
2838	Q9UJA5-1	tRNA (adenine(58)-N(1))-methyltransferase non-catalytic subunit TRM6 [OS=Homo sapiens]	1.2	2	1	2	1	0	0	1	1	0	8.71.E+06	9.78.E+06	1.17.E+07	8.31.E+06	7.29.E+06	8.74.E+06	1.12.E+07	1.06.E+07
2839	Q8IYH5-1	ZZ-type zinc finger-containing protein 3 [OS=Homo sapiens]	1.2	2	1	5	1	0	0	1	1	0	1.93.E+07	1.76.E+07	1.92.E+07	2.24.E+07	2.38.E+07	2.56.E+07	3.02.E+07	2.99.E+07
2840	Q7Z4G4	tRNA (guanine(10)-N2)-methyltransferase homolog [OS=Homo sapiens]	1.2	3	1	10	1	0			1	0	1.29.E+09	1.34.E+09	1.25.E+09	1.22.E+09	1.39.E+09	1.46.E+09	1.35.E+09	1.46.E+09

No.	Accession	Description	Sum PEP Score	Coverage [%]	# Peptides	# PSMs	# Unique Peptides	Score Mascot: A5 Mascot	Score Sequest HT: A2 Sequest HT	# Peptides (by Search Engine): A2 Sequest HT	# Peptides (by Search Engine): A5 Mascot	# Razor Peptides	ctrl Abundances_1	ctrl Abundances_2	ctrl Abundances_3	ctrl Abundances_4	JAM-A KO Abundances_1	JAM-A KO Abundances_2	JAM-A KO Abundances_3	JAM-A KO Abundances_4
2841	Q8TBB1-1	E3 ubiquitin-protein ligase LNX [OS=Homo sapiens]	1.2	2	1	2	1	0			1	0	3.63.E+06	4.49.E+06	4.90.E+06	4.34.E+06	6.32.E+06	5.97.E+06	6.96.E+06	6.58.E+06
2842	Q96EZ4	Myeloma-overexpressed gene protein [OS=Homo sapiens]	1.2	5	1	1	1	0			1	0	1.15.E+08	1.54.E+08	2.16.E+08	1.65.E+08	1.21.E+08	1.51.E+08	2.14.E+08	2.11.E+08
2843	Q6ZT62	Bargin OS=Homo sapiens OX=9606 GN=BARGIN PE=1 SV=2	1.2	5	1	8	1	0			1	0	8.35.E+06	4.94.E+06	3.73.E+06	4.34.E+06	1.72.E+07	1.93.E+07	2.16.E+07	1.05.E+07
2844	Q8TAQ5	Zinc finger protein 420 [OS=Homo sapiens]	1.1	2	1	1	1	0			1	0								
2845	A6NMB1	Sialic acid-binding Ig-like lectin 16 [OS=Homo sapiens]	1.1	1	1	7	1	0	0	1	1	0	8.33.E+06	7.73.E+06	1.04.E+07	7.59.E+06	3.35.E+06	3.95.E+06	4.24.E+06	4.36.E+06
2846	Q9BXT2	voltage-dependent calcium channel gamma-6 subunit [OS=Homo sapiens]	1.1	3	1	63	1	193	0	1	1	0								
2847	P02675	Fibrinogen beta chain [OS=Homo sapiens]	1.1	1	1	7	1	0	0	1	1	0								
2848	Q969F9-1	Hermansky-pudlak syndrome 3 protein [OS=Homo sapiens]	1.1	1	1	1	1	0			1	0	2.63.E+05	1.86.E+05	2.98.E+05	1.96.E+05	2.12.E+05	3.82.E+05	2.70.E+05	
2849	Q9UPR3	Protein SMG5 [OS=Homo sapiens]	1.1	1	1	3	1	0			1	0	5.89.E+07	6.03.E+07	5.94.E+07	6.92.E+07	6.04.E+07	6.28.E+07	6.42.E+07	6.16.E+07