

Table S2 MGUS Patients

accession	name	c_expcount	s_expcount	n_expcount	Peptides	c_empai	s_empai	n_empai	coverage	score
Q14874	[3-methyl-2-oxobutanoate dehydrogenase [lipoamide]	0 3	0 3	1 3	1	0.000	0.000	0.080	4.13	16.94
Q9BV57	1,2-dihydroxy-3-keto-5-methylthiopentene dioxigenase	1 3	0 3	0 3	2	0.311	0.000	0.000	21.79	22.31
Q04446	1,4-alpha-glucan-branching enzyme (Glycogen-branching	3 3	0 3	0 3	9	0.236	0.000	0.000	22.65	375.75
P61604	10 kDa heat shock protein, mitochondrial (Hsp10) (10	3 3	1 3	0 3	12	2.509	0.233	0.000	80.39	465.10
Q15029	116 kDa U5 small nuclear ribonucleoprotein component	0 3	0 3	1 3	1	0.000	0.000	0.038	1.65	11.02
Q9NRX4	14 kDa phosphohistidine phosphatase (Phosphohistidine	2 3	0 3	0 3	2	0.329	0.000	0.000	28.80	66.41
P31946	14-3-3 protein beta/alpha (Protein kinase C inhibitor	3 3	3 3	0 3	12	0.700	0.410	0.000	52.85	561.41
P62258	14-3-3 protein epsilon (14-3-3E)	3 3	3 3	3 3	19	1.270	0.518	0.439	55.69	1083.85
Q04917	14-3-3 protein eta (Protein AS1)	3 3	1 3	2 3	11	0.600	0.233	0.520	40.24	325.85
P61981	14-3-3 protein gamma (Protein kinase C inhibitor protein	3 3	3 3	3 3	14	1.056	0.389	0.377	66.40	924.84
P31947	14-3-3 protein sigma (Stratifin) (Epithelial cell marker	0 3	0 3	1 3	1	0.000	0.000	0.105	9.68	16.98
P27348	14-3-3 protein theta (14-3-3 protein tau) (14-3-3 protein	3 3	1 3	2 3	12	0.932	0.369	0.520	45.31	616.47
P63104	14-3-3 protein zeta/delta (Protein kinase C inhibitor protein	3 3	3 3	3 3	17	1.190	0.817	0.619	61.63	1305.25
O60613	15 kDa selenoprotein	3 3	0 3	2 3	4	0.537	0.000	0.233	35.19	127.03
P51178	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase	1 3	0 3	0 3	1	0.044	0.000	0.000	1.32	14.29
P09543	2',3'-cyclic-nucleotide 3'-phosphodiesterase (CNPase)	3 3	0 3	0 3	2	0.079	0.000	0.000	9.03	73.44
Q16698	2,4-dienoyl-CoA reductase, mitochondrial (2,4-dienoyl-CoA	0 3	0 3	3 3	7	0.000	0.000	0.479	24.48	143.62
P62191	26S protease regulatory subunit 4 (P26s4) (Proteasome	3 3	0 3	0 3	1	0.072	0.000	0.000	3.41	90.45
P17980	26S protease regulatory subunit 6A (Proteasome 26S	3 3	0 3	2 3	4	0.070	0.000	0.145	10.93	77.33
P43686	26S protease regulatory subunit 6B (Proteasome 26S	2 3	0 3	3 3	3	0.119	0.000	0.077	12.44	65.29
P35998	26S protease regulatory subunit 7 (Proteasome 26S	3 3	0 3	1 3	1	0.061	0.000	0.061	3.46	82.46
P62195	26S protease regulatory subunit 8 (Proteasome 26S	2 3	0 3	3 3	4	0.152	0.000	0.096	22.17	158.68
P62333	26S protease regulatory subunit S10B (Proteasome 26S	3 3	0 3	3 3	3	0.127	0.000	0.093	10.28	190.96
Q99460	26S proteasome non-ATPase regulatory subunit 1 (26S	2 3	0 3	0 3	4	0.078	0.000	0.000	7.45	77.81
O00231	26S proteasome non-ATPase regulatory subunit 11 (26S	3 3	0 3	0 3	5	0.132	0.000	0.000	18.25	134.83
O00232	26S proteasome non-ATPase regulatory subunit 12 (26S	3 3	0 3	3 3	2	0.109	0.000	0.061	5.48	177.73
Q9UNM6	26S proteasome non-ATPase regulatory subunit 13 (26S	3 3	0 3	0 3	4	0.229	0.000	0.000	17.82	136.97
O00487	26S proteasome non-ATPase regulatory subunit 14 (26S	2 3	0 3	0 3	4	0.294	0.000	0.000	24.84	77.97
Q13200	26S proteasome non-ATPase regulatory subunit 2 (26S	3 3	0 3	2 3	5	0.107	0.000	0.037	9.69	188.69
O43242	26S proteasome non-ATPase regulatory subunit 3 (26S	2 3	0 3	0 3	4	0.100	0.000	0.000	12.17	80.53
Q16401	26S proteasome non-ATPase regulatory subunit 5 (26S	1 3	0 3	0 3	1	0.066	0.000	0.000	3.77	14.80
P51665	26S proteasome non-ATPase regulatory subunit 7 (26S	2 3	0 3	2 3	3	0.159	0.000	0.116	16.05	85.26
P48556	26S proteasome non-ATPase regulatory subunit 8 (26S	3 3	0 3	1 3	1	0.101	0.000	0.101	5.84	101.23
O00233	26S proteasome non-ATPase regulatory subunit 9 (26S	1 3	0 3	0 3	1	0.179	0.000	0.000	5.38	9.04
Q13442	28 kDa heat- and acid-stable phosphoprotein (PDGF-alpha	1 3	0 3	0 3	1	0.145	0.000	0.000	7.18	12.67
O60783	28S ribosomal protein S14, mitochondrial (S14mt)	1 3	0 3	0 3	1	0.233	0.000	0.000	11.72	12.06
P82921	28S ribosomal protein S21, mitochondrial (S21mt)	1 3	0 3	0 3	1	0.292	0.000	0.000	16.09	17.88
P82930	28S ribosomal protein S34, mitochondrial (S34mt)	1 3	0 3	0 3	1	0.145	0.000	0.000	6.88	13.98
P82909	28S ribosomal protein S36, mitochondrial (S36mt)	1 3	0 3	0 3	1	0.292	0.000	0.000	15.53	14.35
Q02218	2-oxoglutarate dehydrogenase E1 component, mitochondrial	3 3	0 3	2 3	5	0.058	0.000	0.036	9.29	141.85
P42126	3,2-trans-enoyl-CoA isomerase, mitochondrial (Dodecanoyl	1 3	0 3	0 3	2	0.259	0.000	0.000	14.90	21.97
Q727H8	39S ribosomal protein L10, mitochondrial (L10mt) (M	2 3	0 3	0 3	1	0.155	0.000	0.000	7.28	40.50
P52815	39S ribosomal protein L12, mitochondrial (L12mt) (5c	3 3	0 3	0 3	3	0.367	0.000	0.000	17.68	101.07
Q9NRX2	39S ribosomal protein L17, mitochondrial (L17mt) (LY	1 3	0 3	0 3	2	0.274	0.000	0.000	13.71	30.52
Q16540	39S ribosomal protein L23, mitochondrial (L23mt) (L2	3 3	0 3	0 3	2	0.276	0.000	0.000	24.18	71.32
Q8N983	39S ribosomal protein L43, mitochondrial (L43mt) (M	2 3	0 3	0 3	1	0.166	0.000	0.000	5.12	27.96
Q9H912	39S ribosomal protein L44, mitochondrial (L44mt)	2 3	0 3	0 3	2	0.096	0.000	0.000	9.64	26.13
Q13405	39S ribosomal protein L49, mitochondrial (L49mt) (Pr	2 3	0 3	0 3	2	0.145	0.000	0.000	15.66	27.67
Q8N5N7	39S ribosomal protein L50, mitochondrial (L50mt)	1 3	0 3	0 3	1	0.194	0.000	0.000	12.03	16.95
Q96EL3	39S ribosomal protein L53, mitochondrial (L53mt)	2 3	0 3	0 3	2	0.368	0.000	0.000	25.00	50.64
Q99714	3-hydroxyacyl-CoA dehydrogenase type-2 (3-hydroxyacyl	3 3	0 3	2 3	13	1.447	0.000	0.145	75.10	511.19
Q9BUT1	3-hydroxybutyrate dehydrogenase type 2 (R-beta-hydroxy	3 3	0 3	0 3	4	0.229	0.000	0.000	28.98	119.54
P31937	3-hydroxyisobutyrate dehydrogenase, mitochondrial	2 3	0 3	0 3	6	0.439	0.000	0.000	31.55	143.13
P42765	3-ketoacyl-CoA thiolase, mitochondrial (Beta-ketothiolase	2 3	0 3	0 3	3	0.190	0.000	0.000	14.36	60.03
P09110	3-ketoacyl-CoA thiolase, peroxisomal (Beta-ketothiolase	2 3	0 3	0 3	1	0.101	0.000	0.000	4.95	43.64
P25325	3-mercaptopyruvate sulfurtransferase (MST)	2 3	0 3	0 3	2	0.116	0.000	0.000	9.76	45.32
P46783	40S ribosomal protein S10	3 3	0 3	3 3	10	0.646	0.000	1.676	47.88	557.14
P62280	40S ribosomal protein S11	3 3	0 3	3 3	9	0.673	0.000	2.445	63.29	474.56
P25398	40S ribosomal protein S12	3 3	0 3	3 3	13	1.017	0.000	6.943	67.42	624.45
P62277	40S ribosomal protein S13	3 3	0 3	3 3	13	1.092	0.000	3.916	52.98	761.95
P62263	40S ribosomal protein S14	3 3	0 3	3 3	12	2.228	0.000	8.756	70.20	591.24
P62841	40S ribosomal protein S15 (RIG protein)	2 3	0 3	3 3	7	0.894	0.000	0.627	40.00	206.64
P62244	40S ribosomal protein S15a	3 3	0 3	3 3	12	1.645	0.000	5.218	61.54	874.79
P62249	40S ribosomal protein S16	3 3	1 3	3 3	10	1.683	0.179	2.538	52.05	737.03
P08708	40S ribosomal protein S17	3 3	0 3	3 3	10	1.069	0.000	4.145	55.56	528.16
P62269	40S ribosomal protein S18 (Ke-3) (Ke3)	3 3	1 3	3 3	14	0.891	0.389	3.564	51.32	638.57
P39019	40S ribosomal protein S19	3 3	0 3	3 3	9	0.639	0.000	2.012	46.21	569.99
P15880	40S ribosomal protein S2 (S4) (LLRep3 protein)	3 3	0 3	3 3	9	0.160	0.000	0.822	25.26	362.67
P60866	40S ribosomal protein S20	3 3	0 3	3 3	6	1.045	0.000	2.294	32.77	387.73
P63220	40S ribosomal protein S21	3 3	0 3	3 3	6	0.907	0.000	3.393	62.65	342.22
P62266	40S ribosomal protein S23	3 3	0 3	3 3	3	0.233	0.000	0.553	19.58	238.01
P62847	40S ribosomal protein S24	3 3	0 3	3 3	6	0.476	0.000	1.911	31.58	422.14
P62851	40S ribosomal protein S25	3 3	0 3	3 3	6	1.151	0.000	2.594	30.40	493.38
P62854	40S ribosomal protein S26	3 3	0 3	3 3	4	0.690	0.000	1.225	44.35	391.89
P42677	40S ribosomal protein S27 (Metallopan-stimulin 1) (M	3 3	0 3	3 3	5	1.240	0.000	4.727	30.95	348.10
P62979	40S ribosomal protein S27a	0 3	0 3	1 3	2	0.000	0.000	1.154	31.25	22.40
Q71UM5	40S ribosomal protein S27-like protein	0 3	0 3	3 3	5	0.000	0.000	4.727	30.95	170.23
P62857	40S ribosomal protein S28	3 3	0 3	3 3	7	2.230	0.000	8.723	60.87	326.61
P62273	40S ribosomal protein S29	2 3	0 3	3 3	3	0.334	0.000	0.852	33.93	107.91
P23396	40S ribosomal protein S3	3 3	1 3	3 3	22	1.025	0.116	2.750	69.96	960.61
P62861	40S ribosomal protein S30	1 3	0 3	3 3	2	1.512	0.000	1.048	18.64	65.06

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P61247	40S ribosomal protein S3a	1 3	0 3	3 3	11	0.194	0.000	0.960	38.26	318.28
P62701	40S ribosomal protein S4, X isoform (Single copy abun	2 3	0 3	3 3	17	0.333	0.000	2.723	52.85	494.54
P22090	40S ribosomal protein S4, Y isoform 1	0 3	0 3	3 3	9	0.000	0.000	0.964	28.14	181.96
P46782	40S ribosomal protein S5	3 3	1 3	3 3	7	0.327	0.166	1.001	43.63	356.94
P62753	40S ribosomal protein S6 (Phosphoprotein NP33)	1 3	0 3	3 3	8	0.369	0.000	0.874	24.90	215.20
P62081	40S ribosomal protein S7	3 3	1 3	3 3	14	1.014	0.155	3.616	63.40	874.45
P62241	40S ribosomal protein S8	3 3	0 3	3 3	13	1.122	0.000	3.311	54.33	803.30
P46781	40S ribosomal protein S9	3 3	0 3	3 3	17	0.480	0.000	2.012	44.33	455.07
P08865	40S ribosomal protein SA (Laminin receptor 1) (LamR)	3 3	1 3	3 3	11	0.216	0.129	1.405	51.86	393.66
Q9BRK5	45 kDa calcium-binding protein (Cab45) (Stromal cell-	2 3	0 3	0 3	2	0.132	0.000	0.000	13.54	48.59
P49189	4-trimethylaminobutylaldehyde dehydrogenase (TM/	1 3	0 3	0 3	1	0.068	0.000	0.000	2.02	14.36
Q8TCD5	5'(3')-deoxyribonucleotidase, cytosolic type (Cytosolic	3 3	0 3	0 3	3	0.244	0.000	0.000	25.87	89.90
P21589	5'-nucleotidase (Ecto-5'-nucleotidase) (5'-NT)	2 3	0 3	3 3	4	0.074	0.000	0.144	10.98	159.48
P10809	60 kDa heat shock protein, mitochondrial (Heat shock	3 3	0 3	3 3	30	1.585	0.000	0.116	50.79	1470.46
P10155	60 kDa SS-A/Ro ribonucleoprotein (60 kDa ribonucleo	2 3	0 3	0 3	2	0.061	0.000	0.000	4.46	25.82
P05388	60S acidic ribosomal protein P0 (L10E)	3 3	0 3	3 3	8	0.320	0.000	1.092	42.27	497.78
P05386	60S acidic ribosomal protein P1	3 3	1 3	3 3	1	0.585	0.585	0.585	14.04	133.87
P05387	60S acidic ribosomal protein P2 (Renal carcinoma ant	3 3	0 3	3 3	6	3.717	0.000	4.727	72.17	720.51
P27635	60S ribosomal protein L10 (Protein QM) (Tumor supp	2 3	0 3	3 3	12	0.168	0.000	1.663	34.58	362.28
P62906	60S ribosomal protein L10a (CSA-19) (Neural precursor	2 3	0 3	3 3	6	0.129	0.000	0.636	32.26	180.53
P62913	60S ribosomal protein L11 (CLL-associated antigen KV	3 3	0 3	3 3	7	0.456	0.000	1.720	25.28	514.36
P30050	60S ribosomal protein L12	3 3	1 3	3 3	8	1.261	0.468	2.902	60.61	770.19
P26373	60S ribosomal protein L13 (Breast basic conserved pr	3 3	0 3	3 3	10	0.345	0.000	1.254	40.76	335.22
P40429	60S ribosomal protein L13a (23 kDa highly basic prote	2 3	0 3	3 3	5	0.110	0.000	0.520	17.24	190.83
P50914	60S ribosomal protein L14 (CAG-ISL 7)	3 3	0 3	3 3	6	0.149	0.000	0.682	21.40	432.58
P61313	60S ribosomal protein L15	3 3	0 3	3 3	5	0.165	0.000	0.376	30.88	188.05
P18621	60S ribosomal protein L17 (60S ribosomal protein L23	3 3	0 3	3 3	13	0.737	0.000	3.311	47.28	492.43
Q07020	60S ribosomal protein L18	3 3	0 3	3 3	8	0.425	0.000	2.175	35.11	480.80
Q02543	60S ribosomal protein L18a	3 3	0 3	3 3	17	0.442	0.000	4.203	55.11	587.52
P84098	60S ribosomal protein L19	0 3	0 3	2 3	3	0.000	0.000	0.501	9.69	58.11
P46778	60S ribosomal protein L21	2 3	0 3	3 3	11	0.214	0.000	1.371	43.75	229.77
P35268	60S ribosomal protein L22 (Epstein-Barr virus small R	3 3	0 3	3 3	9	0.919	0.000	4.145	69.53	637.00
Q6P5R6	60S ribosomal protein L22-like 1	1 3	0 3	3 3	5	0.212	0.000	1.194	48.36	164.52
P62829	60S ribosomal protein L23 (Ribosomal protein L17)	3 3	0 3	3 3	10	0.766	0.000	6.126	35.00	655.87
P62750	60S ribosomal protein L23a	3 3	0 3	3 3	6	0.418	0.000	1.848	30.13	336.84
P83731	60S ribosomal protein L24 (Ribosomal protein L30)	3 3	0 3	3 3	9	0.592	0.000	3.236	29.94	457.87
P61254	60S ribosomal protein L26	2 3	0 3	3 3	7	0.638	0.000	1.276	33.79	211.20
P61353	60S ribosomal protein L27	3 3	0 3	3 3	8	0.678	0.000	2.398	48.53	357.18
P46776	60S ribosomal protein L27a	3 3	0 3	3 3	7	0.405	0.000	1.479	33.11	401.13
P46779	60S ribosomal protein L28	0 3	0 3	2 3	3	0.000	0.000	0.540	19.71	63.60
P47914	60S ribosomal protein L29 (Cell surface heparin-bindin	2 3	0 3	3 3	2	0.212	0.000	0.468	10.06	123.42
P39023	60S ribosomal protein L3 (HIV-1 TAR RNA-binding pro	0 3	0 3	3 3	7	0.000	0.000	0.314	22.08	117.44
P62888	60S ribosomal protein L30	3 3	2 3	3 3	8	1.141	0.627	4.145	53.04	791.87
P62899	60S ribosomal protein L31	2 3	0 3	3 3	4	0.233	0.000	0.771	34.40	154.20
P62910	60S ribosomal protein L32	3 3	0 3	3 3	8	0.212	0.000	1.805	34.81	295.57
P49207	60S ribosomal protein L34	2 3	0 3	3 3	2	0.233	0.000	0.376	10.26	98.20
P42766	60S ribosomal protein L35	3 3	0 3	3 3	5	0.386	0.000	1.443	34.15	265.73
P18077	60S ribosomal protein L35a (Cell growth-inhibiting ge	2 3	0 3	3 3	3	0.212	0.000	0.623	24.55	138.43
Q9Y3U8	60S ribosomal protein L36	2 3	0 3	3 3	8	0.931	0.000	6.590	31.43	260.44
P83881	60S ribosomal protein L36a (60S ribosomal protein L4	0 3	0 3	1 3	2	0.000	0.000	0.668	13.21	21.84
P61513	60S ribosomal protein L37a	2 3	0 3	1 3	2	0.468	0.000	1.154	32.61	79.45
P63173	60S ribosomal protein L38	3 3	0 3	3 3	6	3.526	0.000	8.771	54.29	412.85
Q92901	60S ribosomal protein L3-like	0 3	0 3	1 3	1	0.000	0.000	0.064	3.93	14.77
P36578	60S ribosomal protein L4 (L1)	2 3	0 3	3 3	11	0.068	0.000	0.646	30.91	350.23
P46777	60S ribosomal protein L5	2 3	0 3	3 3	9	0.132	0.000	0.743	31.31	257.58
Q02878	60S ribosomal protein L6 (TAX-responsive enhancer e	3 3	0 3	3 3	5	0.113	0.000	0.532	22.92	377.85
P18124	60S ribosomal protein L7	3 3	0 3	3 3	14	0.312	0.000	2.045	45.97	477.52
P62424	60S ribosomal protein L7a (Surfeit locus protein 3) (P	3 3	0 3	3 3	16	0.358	0.000	2.504	50.00	542.67
P62917	60S ribosomal protein L8	2 3	0 3	3 3	6	0.122	0.000	0.422	26.07	139.92
P32969	60S ribosomal protein L9	2 3	0 3	3 3	12	1.228	0.000	4.001	34.90	432.55
Q01813	6-phosphofructokinase type C (Phosphofructokinase	3 3	0 3	0 3	12	0.296	0.000	0.000	20.03	367.21
P17858	6-phosphofructokinase, liver type (Phosphofructokinase	2 3	0 3	0 3	3	0.113	0.000	0.000	4.62	64.94
P52209	6-phosphogluconate dehydrogenase, decarboxylating	3 3	0 3	0 3	11	0.427	0.000	0.000	29.19	398.20
Q95336	6-phosphogluconolactonase (6PGL)	3 3	0 3	0 3	9	1.112	0.000	0.000	53.10	346.60
P08253	72 kDa type IV collagenase (72 kDa gelatinase) (Matri	1 3	3 3	0 3	3	0.051	0.139	0.000	9.39	220.29
P11021	78 kDa glucose-regulated protein (GRP 78) (Heat shock	3 3	1 3	3 3	35	1.576	0.054	0.985	46.64	1818.85
Q9NUJ1	Abhydrolase domain-containing protein 10, mitochondr	2 3	0 3	0 3	2	0.101	0.000	0.000	8.82	30.92
Q96IU4	Abhydrolase domain-containing protein 14B (CCG1-in	3 3	0 3	0 3	5	0.844	0.000	0.000	40.48	216.39
Q8IZT6	Abnormal spindle-like microcephaly-associated prote	0 3	0 3	1 3	2	0.000	0.000	0.015	0.98	26.16
P24752	Acetyl-CoA acetyltransferase, mitochondrial (Acetoac	3 3	0 3	0 3	7	0.312	0.000	0.000	21.78	282.11
Q13510	Acid ceramidase (AC) (Acylsphingosine deacylase) (N-	3 3	0 3	0 3	4	0.155	0.000	0.000	11.90	104.99
P39687	Acidic leucine-rich nuclear phosphoprotein 32 family	2 3	0 3	0 3	3	0.375	0.000	0.000	12.05	54.58
Q92688	Acidic leucine-rich nuclear phosphoprotein 32 family	3 3	0 3	0 3	4	0.472	0.000	0.000	24.70	146.73
Q9BTT0	Acidic leucine-rich nuclear phosphoprotein 32 family	1 3	0 3	0 3	2	0.520	0.000	0.000	10.45	33.95
Q99798	Aconitate hydratase, mitochondrial (Aconitase) (Citra	2 3	0 3	0 3	8	0.164	0.000	0.000	20.90	145.31
P68133	Actin, alpha skeletal muscle (Alpha-actin-1)	2 3	0 3	0 3	19	2.097	0.000	0.000	36.34	663.75
P60709	Actin, cytoplasmic 1 (Beta-actin)	3 3	3 3	3 3	35	3.328	0.582	8.699	70.67	4040.21
P63261	Actin, cytoplasmic 2 (Gamma-actin)	3 3	3 3	3 3	35	3.328	0.582	8.686	70.67	4040.21
P61160	Actin-related protein 2 (Actin-like protein 2)	3 3	0 3	2 3	3	0.156	0.000	0.086	13.71	115.86
Q92747	Actin-related protein 2/3 complex subunit 1A (SOP2-I	1 3	0 3	0 3	1	0.080	0.000	0.000	4.59	12.70
O15143	Actin-related protein 2/3 complex subunit 1B (Arp2/3	1 3	0 3	0 3	1	0.101	0.000	0.000	4.84	18.53
O15144	Actin-related protein 2/3 complex subunit 2 (Arp2/3 c	3 3	0 3	3 3	10	0.328	0.000	0.089	43.00	250.18

accession	name	c_expcount	s_expcount	n_expcount	Peptides	c_empai	s_empai	n_empai	coverage	score
O15145	Actin-related protein 2/3 complex subunit 3 (Arp2/3 c	3 3	0 3	3 3	6	0.595	0.000	0.501	29.21	437.92
P59998	Actin-related protein 2/3 complex subunit 4 (Arp2/3 c	3 3	0 3	3 3	7	0.759	0.000	0.604	50.00	448.25
O15511	Actin-related protein 2/3 complex subunit 5 (Arp2/3 c	3 3	1 3	0 3	4	0.288	0.166	0.000	31.79	128.85
Q9BPX5	Actin-related protein 2/3 complex subunit 5-like prot	3 3	0 3	3 3	2	0.205	0.000	0.166	16.34	166.25
P61158	Actin-related protein 3 (Actin-like protein 3)	3 3	2 3	2 3	10	0.309	0.086	0.179	35.41	328.01
P53999	Activated RNA polymerase II transcriptional coactivat	1 3	0 3	0 3	1	0.233	0.000	0.000	18.90	16.10
O95433	Activator of 90 kDa heat shock protein ATPase homol	1 3	0 3	0 3	1	0.083	0.000	0.000	6.51	10.33
P13798	Acylamino-acid-releasing enzyme (AARE) (Acyl-peptid	2 3	0 3	0 3	4	0.123	0.000	0.000	6.97	75.58
P07108	Acyl-CoA-binding protein (ACBP) (Diazepam-binding i	2 3	0 3	0 3	4	1.025	0.000	0.000	44.83	87.79
Q9NPJ3	Acyl-coenzyme A thioesterase 13 (Acyl-CoA thioester	3 3	0 3	0 3	4	1.068	0.000	0.000	37.86	192.05
O75608	Acyl-protein thioesterase 1 (Lysophospholipase 1) (Ly	2 3	0 3	0 3	4	0.716	0.000	0.000	34.78	84.14
O95372	Acyl-protein thioesterase 2 (Lysophospholipase II) (LP	2 3	0 3	0 3	1	0.136	0.000	0.000	11.26	27.25
P07741	Adenine phosphoribosyltransferase (APRT)	3 3	0 3	3 3	9	2.019	0.000	0.389	70.56	643.21
P55263	Adenosine kinase (AK) (Adenosine 5'-phosphotransfe	3 3	0 3	0 3	5	0.218	0.000	0.000	20.44	160.74
P23526	Adenosylhomocysteinase (AdoHcyase) (S-adenosyl-L-	3 3	0 3	0 3	5	0.198	0.000	0.000	14.81	138.89
P54819	Adenylate kinase 2, mitochondrial (AK 2) (ATP-AMP tr	3 3	0 3	3 3	7	0.530	0.000	0.202	41.00	306.72
P00568	Adenylate kinase isoenzyme 1 (AK 1) (ATP-AMP trans	3 3	0 3	3 3	7	0.923	0.000	0.145	34.54	352.01
P27144	Adenylate kinase isoenzyme 4, mitochondrial (Adenyl	2 3	0 3	0 3	1	0.145	0.000	0.000	16.14	28.47
P30566	Adenylosuccinate lyase (ASL) (Adenylosuccinase) (AS	1 3	0 3	0 3	1	0.066	0.000	0.000	3.93	12.05
Q01518	Adenylyl cyclase-associated protein 1 (CAP 1)	3 3	0 3	3 3	11	0.412	0.000	0.070	34.32	471.27
Q9HDC9	Adipocyte plasma membrane-associated protein (Pro	1 3	0 3	0 3	2	0.186	0.000	0.000	13.46	30.48
P12235	ADP/ATP translocase 1 (Adenine nucleotide transloca	1 3	0 3	0 3	1	0.093	0.000	0.000	4.03	18.14
P05141	ADP/ATP translocase 2 (Adenine nucleotide transloca	3 3	0 3	2 3	5	0.196	0.000	0.194	18.46	164.37
P12236	ADP/ATP translocase 3 (Adenine nucleotide transloca	2 3	0 3	0 3	4	0.267	0.000	0.000	12.75	129.57
Q9BRR6	ADP-dependent glucokinase (ADP-GK) (RbBP-35)	2 3	0 3	0 3	1	0.101	0.000	0.000	3.22	70.58
P84077	ADP-ribosylation factor 1	3 3	0 3	0 3	15	2.578	0.000	0.000	61.88	809.67
P18085	ADP-ribosylation factor 4	3 3	0 3	0 3	13	2.621	0.000	0.000	64.44	776.28
P62330	ADP-ribosylation factor 6	3 3	0 3	0 3	8	0.829	0.000	0.000	43.43	208.22
P40616	ADP-ribosylation factor-like protein 1	3 3	0 3	0 3	6	0.621	0.000	0.000	38.12	196.64
P36404	ADP-ribosylation factor-like protein 2	2 3	0 3	0 3	2	0.166	0.000	0.000	11.41	33.52
Q9Y2Y0	ADP-ribosylation factor-like protein 2-binding protein	1 3	0 3	0 3	1	0.292	0.000	0.000	9.20	15.57
P36405	ADP-ribosylation factor-like protein 3	2 3	0 3	0 3	3	0.402	0.000	0.000	21.98	82.86
Q9NVJ2	ADP-ribosylation factor-like protein 8B (ADP-ribosylat	3 3	0 3	0 3	7	0.400	0.000	0.000	38.17	113.32
Q43488	Aflatoxin B1 aldehyde reductase member 2 (AFB1-AR	1 3	0 3	0 3	2	0.222	0.000	0.000	9.47	27.46
O00170	AH receptor-interacting protein (AIP) (Aryl-hydrocarb	1 3	0 3	0 3	1	0.086	0.000	0.000	4.24	13.27
Q02952	A-kinase anchor protein 12 (A-kinase anchor protein 2	3 3	0 3	0 3	11	0.067	0.000	0.000	12.01	254.53
Q9Y2D5	A-kinase anchor protein 2 (AKAP-2) (Protein kinase A	0 3	0 3	1 3	1	0.000	0.000	0.048	2.21	18.04
Q5JQC9	A-kinase anchor protein 4 (Protein kinase A-anchoring	1 3	0 3	0 3	1	0.037	0.000	0.000	2.46	12.52
P49588	Alanyl-tRNA synthetase, cytoplasmic (Alanine--tRNA I	3 3	0 3	0 3	15	0.235	0.000	0.000	25.31	468.15
P14550	Alcohol dehydrogenase [NADP+] (Aldehyde reductase	3 3	0 3	0 3	4	0.137	0.000	0.000	16.62	82.43
P07327	Alcohol dehydrogenase 1A (Alcohol dehydrogenase si	3 3	0 3	0 3	6	0.324	0.000	0.000	17.07	248.39
P00325	Alcohol dehydrogenase 1B (Alcohol dehydrogenase si	2 3	0 3	0 3	10	0.672	0.000	0.000	40.80	374.20
P00326	Alcohol dehydrogenase 1C (Alcohol dehydrogenase si	1 3	0 3	0 3	1	0.093	0.000	0.000	10.93	27.27
P11766	Alcohol dehydrogenase class-3 (Alcohol dehydrogenase	2 3	0 3	0 3	1	0.105	0.000	0.000	7.22	37.49
Q8IZ83	Aldehyde dehydrogenase family 16 member A1	3 3	0 3	0 3	4	0.112	0.000	0.000	4.61	100.23
P30837	Aldehyde dehydrogenase X, mitochondrial (Aldehyde	3 3	0 3	0 3	2	0.105	0.000	0.000	5.42	113.98
Q04828	Aldo-keto reductase family 1 member C1 (20-alpha-h	3 3	0 3	0 3	9	0.465	0.000	0.000	43.96	360.14
P52895	Aldo-keto reductase family 1 member C2 (Trans-1,2-c	1 3	0 3	0 3	4	0.468	0.000	0.000	21.36	81.65
P42330	Aldo-keto reductase family 1 member C3 (Trans-1,2-c	2 3	0 3	0 3	6	0.542	0.000	0.000	29.41	154.38
P15121	Aldose reductase (AR) (Aldehyde reductase)	3 3	0 3	0 3	8	0.401	0.000	0.000	41.46	250.26
P05186	Alkaline phosphatase, tissue-nonspecific isozyme (AP	2 3	0 3	0 3	4	0.152	0.000	0.000	13.74	81.54
P08697	Alpha-2-antiplasmin (Alpha-2-AP) (Alpha-2-plasmin in	0 3	1 3	0 3	1	0.000	0.093	0.000	2.24	13.11
P01023	Alpha-2-macroglobulin (Alpha-2-M) (C3 and PZP-like a	2 3	1 3	0 3	2	0.025	0.025	0.000	1.29	36.37
P30533	Alpha-2-macroglobulin receptor-associated protein (A	1 3	0 3	0 3	2	0.150	0.000	0.000	7.28	21.51
P12814	Alpha-actinin-1 (Alpha-actinin cytoskeletal isoform) (A	3 3	2 3	3 3	47	0.788	0.069	1.551	55.38	2562.46
Q43707	Alpha-actinin-4 (Non-muscle alpha-actinin 4) (F-actin	3 3	0 3	3 3	45	0.563	0.000	1.281	59.39	1992.44
P35611	Alpha-adducin (Erythrocyte adducin subunit alpha)	0 3	0 3	1 3	1	0.000	0.000	0.056	2.44	16.26
P49419	Alpha-aminoacidic semialdehyde dehydrogenase (Alp	2 3	0 3	0 3	4	0.092	0.000	0.000	12.24	63.98
P61163	Alpha-contractin (Contractin) (Centrosome-associated	3 3	0 3	0 3	2	0.104	0.000	0.000	12.23	99.95
P02511	Alpha-crystallin B chain (Alpha(B)-crystallin) (Rosent	3 3	0 3	2 3	11	1.234	0.000	0.389	61.71	331.04
P06733	Alpha-enolase (2-phospho-D-glycerate hydro-lyase) (E	3 3	3 3	3 3	34	2.457	0.382	0.469	73.50	2374.20
P02771	Alpha-fetoprotein (Alpha-1-fetoprotein) (Alpha-fetog	2 3	3 3	0 3	4	0.054	0.113	0.000	9.20	325.51
P17050	Alpha-N-acetylgalactosaminidase (Alpha-galactosidas	0 3	0 3	1 3	1	0.000	0.000	0.096	5.35	13.02
P54802	Alpha-N-acetylglucosaminidase (N-acetyl-alpha-glucos	1 3	0 3	0 3	1	0.053	0.000	0.000	4.44	12.79
P54920	Alpha-soluble NSF attachment protein (SNAP-alpha) (E	3 3	0 3	0 3	8	0.335	0.000	0.000	38.31	188.12
Q12904	Aminoacyl tRNA synthetase complex-interacting mult	0 3	0 3	1 3	1	0.000	0.000	0.101	3.85	14.48
Q9H4A4	Aminopeptidase B (Ap-B) (Arginine aminopeptidase) (	2 3	0 3	0 3	8	0.295	0.000	0.000	18.15	159.50
P15144	Aminopeptidase N (hAPN) (Alanyl aminopeptidase) (M	3 3	0 3	3 3	20	0.354	0.000	0.223	25.34	809.74
Q8N302	Angiogenic factor with G patch and FHA domains 1 (A	0 3	1 3	0 3	1	0.000	0.054	0.000	3.64	10.79
Q9POK7	Ankyrin repeat and coiled-coil structure-1 (Ankyrin	0 3	0 3	3 3	2	0.000	0.000	0.042	2.76	44.11
P04083	Annexin A1 (Annexin-1) (Annexin I) (Lipocortin I) (Calp	3 3	2 3	3 3	23	2.205	0.323	0.486	60.12	1913.80
P50995	Annexin A11 (Annexin-11) (Annexin XI) (Calcylin-assc	3 3	0 3	0 3	6	0.210	0.000	0.000	17.62	127.31
P07355	Annexin A2 (Annexin-2) (Annexin II) (Lipocortin II) (Ca	3 3	3 3	3 3	35	3.853	0.658	3.330	75.81	3858.16
P09525	Annexin A4 (Annexin-4) (Annexin IV) (Lipocortin IV) (E	3 3	0 3	0 3	9	0.451	0.000	0.000	40.13	342.48
P08758	Annexin A5 (Annexin-5) (Annexin V) (Lipocortin V) (Er	3 3	1 3	3 3	28	3.368	0.166	0.535	78.13	2041.25
P08133	Annexin A6 (Annexin-6) (Annexin VI) (Lipocortin VI) (p	3 3	0 3	3 3	36	0.772	0.000	1.645	54.38	2277.43
P20073	Annexin A7 (Annexin-7) (Annexin VII) (Synexin)	2 3	0 3	0 3	3	0.181	0.000	0.000	8.61	77.82
Q9H6X2	Anthrax toxin receptor 1 (Tumor endothelial marker 8	0 3	1 3	0 3	2	0.000	0.122	0.000	4.61	19.75
P01008	Antithrombin-III (ATIII)	0 3	1 3	0 3	2	0.000	0.136	0.000	6.90	25.39
Q10567	AP-1 complex subunit beta-1 (Adapter-related protein	3 3	0 3	0 3	11	0.162	0.000	0.000	11.59	303.83
O95782	AP-2 complex subunit alpha-1 (Adapter-related prote	1 3	0 3	0 3	3	0.102	0.000	0.000	5.73	48.04
P63010	AP-2 complex subunit beta (Adapter-related protein c	3 3	0 3	2 3	10	0.166	0.000	0.084	11.74	259.47

accession	name	c_expcount	s_expcount	n_expcount	Peptides	c_empai	s_empai	n_empai	coverage	score
Q96CW1	AP-2 complex subunit mu (Adapter-related protein c	1 3	0 3	0 3	1	0.064	0.000	0.000	4.60	15.65
O00203	AP-3 complex subunit beta-1 (Adapter-related protei	0 3	0 3	1 3	1	0.000	0.000	0.032	1.74	14.83
Q8NCW5	Apolipoprotein A-I-binding protein (AI-BP) (YjeF N-ter	1 3	0 3	0 3	3	0.468	0.000	0.000	17.01	36.25
P02649	Apolipoprotein E (Apo-E)	3 3	1 3	0 3	12	0.511	0.638	0.000	41.96	396.16
Q9BUR5	Apolipoprotein O (Protein FAM121B)	1 3	0 3	0 3	1	0.166	0.000	0.000	8.08	12.88
Q9BZ25	Apoptosis inhibitor 5 (API-5) (Fibroblast growth factor	0 3	0 3	3 3	1	0.000	0.000	0.059	3.53	54.05
Q07812	Apoptosis regulator BAX (Bcl-2-like protein 4) (Bcl2-L	1 3	0 3	0 3	1	0.194	0.000	0.000	6.77	15.32
Q9ULZ3	Apoptosis-associated speck-like protein containing a	3 3	0 3	0 3	2	0.276	0.000	0.000	11.28	79.19
P52594	Arf-GAP domain and FG repeats-containing protein 1	1 3	0 3	0 3	1	0.116	0.000	0.000	4.80	14.56
Q15027	Arf-GAP with coiled-coil, ANK repeat and PH domain-	0 3	0 3	1 3	1	0.000	0.000	0.046	2.16	14.34
P05089	Arginase-1 (Type I arginase) (Liver-type arginase)	0 3	1 3	2 3	4	0.000	0.245	0.389	19.25	82.06
P54136	Arginyl-tRNA synthetase, cytoplasmic (Arginine--tRNA	2 3	0 3	3 3	7	0.070	0.000	0.174	13.48	128.29
O43681	Arsenical pump-driving ATPase (Arsenite-translocatin	2 3	0 3	0 3	2	0.129	0.000	0.000	9.20	40.94
P15289	Arylsulfatase A (ASA) (Cerebroside-sulfatase)	3 3	0 3	0 3	2	0.175	0.000	0.000	6.51	85.33
O43776	Asparaginyl-tRNA synthetase, cytoplasmic (Asparagin	2 3	0 3	0 3	4	0.136	0.000	0.000	9.85	83.47
P17174	Aspartate aminotransferase, cytoplasmic (Transamina	2 3	0 3	0 3	2	0.150	0.000	0.000	9.93	42.43
P00505	Aspartate aminotransferase, mitochondrial (mAspAT)	3 3	0 3	0 3	3	0.151	0.000	0.000	9.53	139.18
Q12797	Aspartyl/asparaginyl beta-hydroxylase (Aspartate bet	1 3	0 3	2 3	3	0.113	0.000	0.055	7.26	44.11
P14868	Aspartyl-tRNA synthetase, cytoplasmic (Aspartate--tR	2 3	0 3	3 3	8	0.108	0.000	0.269	23.35	195.67
Q15121	Astrocytic phosphoprotein PEA-15 (Phosphoprotein e	3 3	0 3	0 3	4	0.422	0.000	0.000	36.92	113.79
Q6DD88	Atlastin-3	3 3	0 3	0 3	3	0.072	0.000	0.000	7.02	81.60
P25705	ATP synthase subunit alpha, mitochondrial	3 3	0 3	3 3	19	0.829	0.000	0.181	43.04	1074.35
P24539	ATP synthase subunit b, mitochondrial	3 3	0 3	0 3	7	0.296	0.000	0.000	40.23	148.96
P06576	ATP synthase subunit beta, mitochondrial	3 3	0 3	3 3	24	1.373	0.000	0.541	61.44	1622.35
O75947	ATP synthase subunit d, mitochondrial	3 3	0 3	0 3	11	1.173	0.000	0.000	75.16	287.89
P30049	ATP synthase subunit delta, mitochondrial (F-ATPase	2 3	0 3	0 3	3	0.723	0.000	0.000	17.26	51.60
P56385	ATP synthase subunit e, mitochondrial	3 3	0 3	0 3	3	0.865	0.000	0.000	52.17	119.86
P56134	ATP synthase subunit f, mitochondrial	3 3	0 3	0 3	2	0.667	0.000	0.000	25.53	100.94
O75964	ATP synthase subunit g, mitochondrial (ATPase subun	3 3	0 3	0 3	5	1.141	0.000	0.000	39.81	251.60
P36542	ATP synthase subunit gamma, mitochondrial (F-ATPase	3 3	0 3	0 3	6	0.278	0.000	0.000	24.16	182.17
P48047	ATP synthase subunit O, mitochondrial (Oligomycin se	3 3	0 3	3 3	9	1.417	0.000	0.263	46.48	573.13
P18859	ATP synthase-coupling factor 6, mitochondrial (ATPas	1 3	0 3	0 3	1	0.233	0.000	0.000	6.48	11.83
Q9UII2	ATPase inhibitor, mitochondrial	2 3	0 3	0 3	2	0.376	0.000	0.000	17.92	44.81
P61221	ATP-binding cassette sub-family E member 1 (RNase l	1 3	0 3	0 3	1	0.050	0.000	0.000	2.67	14.69
P53396	ATP-citrate synthase (ATP-citrate (pro-S)-lyase) (Citra	3 3	0 3	2 3	23	0.345	0.000	0.098	27.43	788.13
P12956	ATP-dependent DNA helicase 2 subunit 1 (ATP-depen	2 3	0 3	3 3	14	0.103	0.000	0.547	26.60	374.47
P13010	ATP-dependent DNA helicase 2 subunit 2 (ATP-depen	2 3	0 3	3 3	10	0.113	0.000	0.158	21.31	174.55
P46063	ATP-dependent DNA helicase Q1 (DNA-dependent AT	0 3	0 3	1 3	2	0.000	0.000	0.099	5.86	24.40
Q08211	ATP-dependent RNA helicase A (Nuclear DNA helicase	0 3	0 3	3 3	14	0.000	0.000	0.244	15.51	246.88
Q92499	ATP-dependent RNA helicase DDX1 (DEAD box protei	0 3	0 3	3 3	10	0.000	0.000	0.334	20.41	200.20
Q9NVP1	ATP-dependent RNA helicase DDX18 (DEAD box prote	0 3	0 3	1 3	1	0.000	0.000	0.053	2.09	14.08
O00148	ATP-dependent RNA helicase DDX39 (DEAD box prote	1 3	0 3	3 3	5	0.075	0.000	0.287	18.27	135.24
O00571	ATP-dependent RNA helicase DDX3X (DEAD box prote	2 3	0 3	3 3	8	0.049	0.000	0.244	16.62	184.18
O15523	ATP-dependent RNA helicase DDX3Y (DEAD box prote	0 3	0 3	3 3	7	0.000	0.000	0.178	14.85	103.32
Q86XP3	ATP-dependent RNA helicase DDX42 (DEAD box prote	1 3	0 3	0 3	1	0.033	0.000	0.000	1.60	12.91
P17342	Atrial natriuretic peptide receptor 3 (Atrial natriuret	1 3	0 3	0 3	2	0.122	0.000	0.000	6.28	23.16
O95816	BAG family molecular chaperone regulator 2 (BAG-2)	3 3	0 3	3 3	6	0.279	0.000	0.481	37.91	234.90
O75531	Barrier-to-autointegration factor (Breakpoint cluster	2 3	0 3	3 3	4	0.480	0.000	0.911	42.70	174.24
P98160	Basement membrane-specific heparan sulfate proteo	0 3	3 3	0 3	9	0.000	0.050	0.000	2.48	328.89
Q7L1Q6	Basic leucine zipper and W2 domain-containing prote	2 3	0 3	0 3	1	0.066	0.000	0.000	2.39	37.66
P35613	Basigin (Leukocyte activation antigen M6) (Collagenas	2 3	0 3	0 3	3	0.181	0.000	0.000	8.83	46.80
P61769	Beta-2-microglobulin	2 3	3 3	2 3	5	0.630	0.815	0.334	44.54	200.33
Q562R1	Beta-actin-like protein 2 (Kappa-actin)	2 3	3 3	2 3	7	0.484	0.221	0.194	25.00	464.20
Q8WYA6	Beta-catenin-like protein 1 (Nuclear-associated prote	0 3	0 3	1 3	1	0.000	0.000	0.068	3.73	13.65
P13929	Beta-enolase (2-phospho-D-glycerate hydro-lyase) (M	3 3	2 3	2 3	4	0.298	0.160	0.160	16.13	501.26
P16278	Beta-galactosidase (Acid beta-galactosidase) (Lactase	2 3	0 3	0 3	4	0.104	0.000	0.000	7.68	55.02
P06865	Beta-hexosaminidase subunit alpha (N-acetyl-beta-glu	2 3	0 3	0 3	2	0.111	0.000	0.000	5.67	44.10
P07686	Beta-hexosaminidase subunit beta (N-acetyl-beta-glu	3 3	0 3	0 3	6	0.171	0.000	0.000	18.88	158.42
P09619	Beta-type platelet-derived growth factor receptor (PD	2 3	0 3	0 3	4	0.070	0.000	0.000	4.70	64.90
P55957	BH3-interacting domain death agonist (p22 BID) (BID)	3 3	0 3	0 3	3	0.263	0.000	0.000	21.03	115.98
Q95340	Bifunctional 3'-phosphoadenosine 5'-phosphosulfate	2 3	0 3	0 3	2	0.051	0.000	0.000	5.86	41.94
P07814	Bifunctional aminoacyl-tRNA synthetase (Proliferator	3 3	0 3	3 3	8	0.051	0.000	0.041	7.74	207.00
P31939	Bifunctional purine biosynthesis protein PURH	3 3	0 3	2 3	9	0.186	0.000	0.054	25.00	237.87
P21810	Biglycan (Bone/cartilage proteoglycan I) (PG-S1)	0 3	2 3	0 3	2	0.000	0.137	0.000	7.07	42.12
P53004	Biliverdin reductase A (BVR A) (Biliverdin-IX alpha-red	2 3	0 3	0 3	2	0.172	0.000	0.000	7.77	33.93
Q9H3K6	BoA-like protein 2	3 3	0 3	0 3	3	1.171	0.000	0.000	51.16	152.75
Q96CX2	BTB/POZ domain-containing protein KCTD12 (Pfetin)	1 3	0 3	0 3	1	0.101	0.000	0.000	4.00	13.59
P11586	C-1-tetrahydrofolate synthase, cytoplasmic (C1-THF s	3 3	0 3	2 3	8	0.064	0.000	0.035	16.68	132.20
P05937	Calbindin (Vitamin D-dependent calcium-binding prot	2 3	0 3	1 3	1	0.110	0.000	0.110	7.28	38.31
O43745	Calcineurin B homologous protein 2 (Hepatocellular c	1 3	0 3	1 3	1	0.166	0.000	0.166	5.10	26.95
Q9BRF8	Calcineurin-like phosphoesterase domain-containing	1 3	0 3	0 3	1	0.110	0.000	0.000	5.73	18.68
Q13557	Calcium/calmodulin-dependent protein kinase type II	3 3	0 3	1 3	2	0.066	0.000	0.136	7.62	100.45
Q9BPX6	Calcium-binding atopy-related autoantigen 1 (Atopy-r	0 3	0 3	3 3	1	0.000	0.000	0.066	3.15	37.62
O75746	Calcium-binding mitochondrial carrier protein Aralar1	2 3	0 3	0 3	1	0.054	0.000	0.000	1.77	40.90
Q6NUK1	Calcium-binding mitochondrial carrier protein SCA1	2 3	0 3	0 3	2	0.108	0.000	0.000	6.08	47.05
Q9Y2V2	Calcium-regulated heat stable protein 1 (Calcium-reg	1 3	0 3	0 3	1	0.259	0.000	0.000	10.88	12.80
Q9HB71	Calcyclin-binding protein (CacyBP) (Siah-interacting p	1 3	0 3	0 3	1	0.129	0.000	0.000	10.09	10.60
Q05682	Caldesmon (CDM)	3 3	0 3	3 3	23	0.060	0.000	0.586	29.26	662.36
P62158	Calmodulin (CaM)	3 3	0 3	0 3	6	0.758	0.000	0.000	71.81	202.80
P27824	Calnexin (Major histocompatibility complex class I an	3 3	0 3	0 3	6	0.201	0.000	0.000	10.64	203.77
P04632	Calpain small subunit 1 (CSS1) (Calcium-dependent p	3 3	0 3	2 3	9	1.023	0.000	0.155	55.97	535.29
P07384	Calpain-1 catalytic subunit (Calpain-1 large subunit) (C	3 3	0 3	0 3	7	0.118	0.000	0.000	14.71	119.61

accession	name	c_expcount	s_expcount	n_expcount	Peptides	c_empai	s_empai	n_empai	coverage	score
P17655	Calpain-2 catalytic subunit (Calpain-2 large subunit) (C	3 3	0 3	0 3	12	0.240	0.000	0.000	29.29	316.41
Q9Y6W3	Calpain-7 (PalB homolog) (PalBH)	0 3	0 3	1 3	1	0.000	0.000	0.036	2.71	13.06
Q99439	Calponin-2 (Calponin H2, smooth muscle) (Neutral cal	3 3	0 3	0 3	10	0.702	0.000	0.000	38.51	471.76
Q15417	Calponin-3 (Calponin, acidic isoform)	3 3	0 3	0 3	5	0.290	0.000	0.000	20.67	157.65
P27797	Calreticulin (CRP55) (Calregulin) (HACBP) (ERP60) (grp	3 3	0 3	2 3	10	0.421	0.000	0.179	39.33	306.97
O43852	Calumenin (Crocalbin) (IEF SSP 9302)	3 3	1 3	0 3	4	0.154	0.105	0.000	25.40	120.36
P10644	cAMP-dependent protein kinase type I-alpha regulato	3 3	0 3	0 3	3	0.163	0.000	0.000	15.49	78.66
P30622	CAP-Gly domain-containing linker protein 1 (Restin) (C	1 3	0 3	0 3	1	0.018	0.000	0.000	0.90	17.13
Q14444	Caprin-1 (Cytoplasmic activation- and proliferation-as	0 3	0 3	3 3	3	0.000	0.000	0.127	7.19	41.74
P16152	Carbonyl reductase [NADPH] 1 (NADPH-dependent ca	3 3	1 3	0 3	10	0.761	0.105	0.000	47.29	511.07
O75828	Carbonyl reductase [NADPH] 3 (NADPH-dependent ca	2 3	0 3	0 3	4	0.318	0.000	0.000	17.33	109.55
Q96DG6	Carboxymethylenebutenolidase homolog	1 3	0 3	0 3	5	0.778	0.000	0.000	27.76	56.30
P43155	Carnitine O-acetyltransferase (Carnitine acetylase) (C	1 3	0 3	0 3	1	0.053	0.000	0.000	2.40	17.74
O75718	Cartilage-associated protein	2 3	0 3	0 3	1	0.066	0.000	0.000	3.24	53.81
P68400	Casein kinase II subunit alpha (CK II)	0 3	0 3	3 3	1	0.000	0.000	0.110	4.60	35.03
P19784	Casein kinase II subunit alpha' (CK II)	0 3	0 3	3 3	1	0.000	0.000	0.096	4.57	42.78
P67870	Casein kinase II subunit beta (CK II beta) (Phosvitin) (C	0 3	0 3	3 3	1	0.000	0.000	0.179	5.12	35.03
P42574	Caspase-3 (CASP-3) (Apopain) (Cysteine protease CPP	1 3	0 3	0 3	1	0.101	0.000	0.000	5.05	11.94
P04040	Catalase	2 3	0 3	0 3	5	0.126	0.000	0.000	16.70	87.51
P21964	Catechol O-methyltransferase	3 3	0 3	0 3	5	0.609	0.000	0.000	35.79	249.53
P35221	Catenin alpha-1 (Cadherin-associated protein) (Alpha	0 3	0 3	1 3	1	0.000	0.000	0.033	2.87	16.92
P35222	Catenin beta-1 (Beta-catenin)	1 3	0 3	1 3	2	0.050	0.000	0.050	6.27	25.84
O60716	Catenin delta-1 (p120 catenin) (p120(ctn)) (Cadherin-	1 3	0 3	0 3	1	0.032	0.000	0.000	2.27	15.27
P07858	Cathepsin B (Cathepsin B1) (APP secretase) (APPS)	3 3	3 3	0 3	18	1.662	0.860	0.000	41.30	1110.01
P07339	Cathepsin D	3 3	1 3	2 3	14	0.764	0.179	0.086	36.89	528.71
P07711	Cathepsin L1 (Major excreted protein) (MEP)	2 3	3 3	0 3	3	0.214	0.175	0.000	14.71	151.78
Q9UBR2	Cathepsin Z (Cathepsin X) (Cathepsin P)	0 3	2 3	0 3	2	0.000	0.136	0.000	9.24	41.56
Q03135	Caveolin-1	1 3	0 3	3 3	4	0.389	0.000	0.284	32.58	84.75
Q96F85	CB1 cannabinoid receptor-interacting protein 1 (CRIP-	1 3	0 3	0 3	3	0.701	0.000	0.000	38.41	36.90
Q6YHK3	CD109 antigen (C3 and PZP-like alpha-2-macroglobuli	1 3	0 3	0 3	1	0.027	0.000	0.000	1.18	12.71
Q13740	CD166 antigen (Activated leukocyte cell adhesion mo	2 3	0 3	0 3	2	0.116	0.000	0.000	4.97	73.58
Q5ZPR3	CD276 antigen (Costimulatory molecule) (B7 homolog	1 3	0 3	0 3	1	0.122	0.000	0.000	4.87	18.69
P16070	CD44 antigen (Phagocytic glycoprotein I) (PGP-I) (HUT	3 3	0 3	3 3	2	0.116	0.000	0.062	2.96	177.92
P13987	CD59 glycoprotein (Membrane attack complex inhibit	3 3	0 3	3 3	4	1.532	0.000	2.205	21.88	367.00
P08962	CD63 antigen (Melanoma-associated antigen ME491)	1 3	0 3	0 3	1	0.194	0.000	0.000	5.04	14.98
P60033	CD81 antigen (26 kDa cell surface protein TAPA-1) (Ta	1 3	0 3	0 3	1	0.259	0.000	0.000	8.47	13.14
P48960	CD97 antigen (Leukocyte antigen CD97)	1 3	0 3	0 3	1	0.054	0.000	0.000	1.92	15.68
P14209	CD99 antigen (T-cell surface glycoprotein E2) (E2 anti	2 3	0 3	0 3	3	1.075	0.000	0.000	29.73	66.53
Q8NSK1	CDGSH iron sulfur domain-containing protein 2 (Endo	2 3	0 3	0 3	1	0.259	0.000	0.000	10.37	29.97
Q92600	Cell differentiation protein RCD1 homolog (Rcd-1)	0 3	0 3	3 3	1	0.000	0.000	0.105	7.02	34.96
P60953	Cell division control protein 42 homolog (G25K GTP-b	3 3	0 3	3 3	2	0.462	0.000	0.233	10.99	242.74
Q99459	Cell division cycle 5-like protein (Cdc5-like protein) (P	0 3	0 3	1 3	1	0.000	0.000	0.038	2.24	17.16
P62633	Cellular nucleic acid-binding protein (CNBP) (Zinc fing	2 3	0 3	0 3	3	0.359	0.000	0.000	23.16	64.54
O94986	Centrosomal protein of 152 kDa (Cep152)	0 3	1 3	0 3	1	0.000	0.018	0.000	1.63	13.77
Q1MSJ5	Centrosome and spindle pole-associated protein 1	2 3	0 3	0 3	1	0.025	0.000	0.000	1.31	26.56
Q96F27	Charged multivesicular body protein 6 (Chromatin-mc	1 3	0 3	0 3	1	0.194	0.000	0.000	6.47	16.02
P36222	Chitinase-3-like protein 1 (Cartilage glycoprotein 39) (	0 3	3 3	0 3	9	0.000	0.369	0.000	29.77	198.47
O00299	Chloride intracellular channel protein 1 (Nuclear chlo	3 3	1 3	2 3	8	0.789	0.145	0.719	36.10	414.10
Q9Y696	Chloride intracellular channel protein 4 (Intracellular	3 3	0 3	3 3	12	0.772	0.000	0.635	60.87	518.10
Q8WWI5	Choline transporter-like protein 1 (Solute carrier fami	2 3	0 3	0 3	1	0.068	0.000	0.000	2.13	31.56
P83916	Chromobox protein homolog 1 (Heterochromatin pro	1 3	0 3	0 3	1	0.179	0.000	0.000	8.65	16.91
Q13185	Chromobox protein homolog 3 (Heterochromatin pro	1 3	0 3	0 3	3	0.585	0.000	0.000	22.40	39.04
O75390	Citrate synthase, mitochondrial	3 3	0 3	0 3	3	0.127	0.000	0.000	6.44	111.79
O60271	C-jun-amino-terminal kinase-interacting protein 4 (JN	1 3	0 3	0 3	1	0.024	0.000	0.000	0.83	11.51
Q00610	Clathrin heavy chain 1 (CLH-17)	3 3	0 3	3 3	54	0.651	0.000	0.221	44.24	2426.14
P53675	Clathrin heavy chain 2 (CLH-22)	3 3	0 3	2 3	10	0.123	0.000	0.080	6.04	397.49
Q9P210	Cleavage and polyadenylation specificity factor subun	0 3	0 3	1 3	1	0.000	0.000	0.043	1.66	14.34
Q9UKF6	Cleavage and polyadenylation specificity factor subun	1 3	0 3	0 3	1	0.056	0.000	0.000	2.19	23.01
O43809	Cleavage and polyadenylation specificity factor subun	2 3	0 3	2 3	4	0.214	0.000	0.334	23.35	94.40
Q12996	Cleavage stimulation factor subunit 3 (Cleavage stimu	0 3	0 3	1 3	1	0.000	0.000	0.040	1.67	12.80
P10909	Clusterin (Complement-associated protein SP-40,40) (	0 3	2 3	0 3	3	0.000	0.115	0.000	14.70	35.69
Q99417	C-Myc-binding protein (Associate of Myc 1) (AMY-1)	1 3	0 3	0 3	1	0.292	0.000	0.000	10.68	11.61
Q14019	Coactosin-like protein	3 3	2 3	3 3	8	1.734	0.376	0.376	41.55	621.93
P12259	Coagulation factor V (Activated protein C cofactor) (P	0 3	0 3	3 3	1	0.000	0.000	0.019	0.63	27.22
P53621	Coatomer subunit alpha (Alpha-coat protein) (Alpha-C	3 3	0 3	0 3	11	0.116	0.000	0.000	13.73	273.00
P53618	Coatomer subunit beta (Beta-coat protein) (Beta-COF	3 3	0 3	0 3	12	0.182	0.000	0.000	20.57	421.52
P35606	Coatomer subunit beta' (Beta'-coat protein) (Beta'-CC	2 3	0 3	0 3	6	0.110	0.000	0.000	11.48	111.87
P48444	Coatomer subunit delta (Delta-coat protein) (Delta-CC	2 3	0 3	0 3	1	0.062	0.000	0.000	2.35	65.54
O14579	Coatomer subunit epsilon (Epsilon-coat protein) (Epsi	2 3	0 3	0 3	2	0.105	0.000	0.000	15.26	45.91
Q9Y678	Coatomer subunit gamma (Gamma-coat protein) (Ga	3 3	0 3	2 3	10	0.168	0.000	0.122	17.85	361.23
P61923	Coatomer subunit zeta-1 (Zeta-1-coat protein) (Zeta-1	3 3	0 3	2 3	6	0.787	0.000	0.585	37.85	170.43
Q9P299	Coatomer subunit zeta-2 (Zeta-2-coat protein) (Zeta-2	2 3	0 3	0 3	2	0.179	0.000	0.000	13.81	25.00
P23528	Cofilin-1 (Cofilin, non-muscle isoform) (18 kDa phosph	3 3	2 3	3 3	16	5.575	0.402	2.778	69.28	1865.50
Q9Y281	Cofilin-2 (Cofilin, muscle isoform)	3 3	2 3	2 3	11	2.248	0.514	1.683	53.01	772.61
Q76M96	Coiled-coil domain-containing protein 80 (Down-regu	0 3	1 3	0 3	1	0.000	0.036	0.000	1.37	10.45
Q9Y6H1	Coiled-coil-helix-coiled-coil-helix domain-containing p	1 3	0 3	0 3	1	0.468	0.000	0.000	18.54	21.83
O75534	Cold shock domain-containing protein E1 (UNR protei	1 3	0 3	0 3	1	0.037	0.000	0.000	1.75	14.66
Q14011	Cold-inducible RNA-binding protein (Glycine-rich RNA	0 3	0 3	3 3	3	0.000	0.000	0.214	25.00	50.42
P02452	Collagen alpha-1(I) chain (Alpha-1 type I collagen)	3 3	3 3	3 3	20	0.052	0.232	0.052	15.92	1061.11
P02461	Collagen alpha-1(III) chain	0 3	3 3	0 3	9	0.000	0.080	0.000	9.14	211.83
P20908	Collagen alpha-1(V) chain	0 3	2 3	0 3	4	0.000	0.038	0.000	5.71	58.98
P12109	Collagen alpha-1(VI) chain	3 3	3 3	3 3	20	0.159	0.391	0.160	25.00	1551.20

accession	name	c_expcount	s_expcount	n_expcount	Peptides	c_emptai	s_emptai	n_emptai	coverage	score
P27658	Collagen alpha-1(VIII) chain (Endothelial collagen)	3 3	0 3	3 3	4	0.183	0.000	0.160	5.78	318.99
P08123	Collagen alpha-2(I) chain (Alpha-2 type I collagen)	0 3	3 3	2 3	26	0.000	0.389	0.027	25.04	1239.88
P05997	Collagen alpha-2(V) chain	0 3	1 3	0 3	1	0.000	0.026	0.000	0.67	11.51
P12110	Collagen alpha-2(VI) chain	2 3	3 3	2 3	11	0.067	0.118	0.066	13.35	344.82
P12111	Collagen alpha-3(VI) chain	3 3	3 3	3 3	61	0.237	0.253	0.233	28.49	4058.00
Q96CG8	Collagen triple helix repeat-containing protein 1 (NM)	0 3	2 3	0 3	3	0.000	0.472	0.000	16.05	59.29
Q9UBI1	COMM domain-containing protein 3 (Protein Bup) (Pr	2 3	0 3	0 3	2	0.284	0.000	0.000	12.31	42.86
P00736	Complement C1r subcomponent (Complement compo	0 3	1 3	0 3	3	0.000	0.170	0.000	7.09	42.47
P09871	Complement C1s subcomponent (Complement compo	0 3	2 3	0 3	2	0.000	0.090	0.000	4.36	62.08
Q07021	Complement component 1 Q subcomponent-binding	2 3	0 3	0 3	3	0.136	0.000	0.000	14.89	37.99
P00746	Complement factor D (C3 convertase activator) (Prop	0 3	3 3	0 3	9	0.000	1.402	0.000	54.15	547.75
P29279	Connective tissue growth factor (Hypertrophic chond	0 3	2 3	0 3	2	0.000	0.132	0.000	6.59	41.63
P61201	COP9 signalosome complex subunit 2 (Signalosome s	1 3	0 3	0 3	1	0.066	0.000	0.000	4.51	10.70
Q9BT78	COP9 signalosome complex subunit 4 (Signalosome s	3 3	0 3	0 3	3	0.066	0.000	0.000	11.58	51.77
Q9UBW8	COP9 signalosome complex subunit 7a (Signalosome	2 3	0 3	0 3	2	0.122	0.000	0.000	10.91	28.93
Q99627	COP9 signalosome complex subunit 8 (Signalosome s	3 3	0 3	0 3	4	0.519	0.000	0.000	36.36	113.94
Q99829	Copine-1 (Copine I)	3 3	0 3	0 3	4	0.156	0.000	0.000	12.29	162.30
O75131	Copine-3 (Copine III)	0 3	0 3	3 3	4	0.000	0.000	0.191	11.55	72.21
Q9BR76	Coronin-1B (Coronin-2)	0 3	0 3	3 3	6	0.000	0.000	0.350	17.59	125.85
Q9ULV4	Coronin-1C (Coronin-3) (hCRNN4)	1 3	0 3	3 3	7	0.166	0.000	0.485	18.78	192.29
P17812	CTP synthase 1 (UTP--ammonia ligase 1) (CTP synthet	2 3	0 3	0 3	3	0.123	0.000	0.000	7.78	81.69
Q9Y240	C-type lectin domain family 11 member A (Stem cell g	1 3	0 3	0 3	1	0.129	0.000	0.000	3.41	11.82
Q9UBG0	C-type mannose receptor 2 (Macrophage mannose re	2 3	0 3	0 3	2	0.040	0.000	0.000	1.83	76.64
Q13620	Cullin-4B (CUL-4B)	2 3	0 3	0 3	4	0.101	0.000	0.000	6.35	142.48
Q93034	Cullin-5 (CUL-5) (Vasopressin-activated calcium-mobil	0 3	0 3	1 3	1	0.000	0.000	0.034	2.31	12.63
Q86VP6	Cullin-associated NEDD8-dissociated protein 1 (Cullin	3 3	0 3	2 3	14	0.199	0.000	0.028	17.56	571.02
P42771	Cyclin-dependent kinase inhibitor 2A, isoforms 1/2/3	1 3	0 3	0 3	2	0.468	0.000	0.000	18.59	29.83
P01040	Cystatin-A (Cystatin-AS) (Stefin-A)	0 3	1 3	0 3	1	0.000	0.292	0.000	12.24	13.36
P04080	Cystatin-B (Stefin-B) (Liver thiol proteinase inhibitor)	3 3	2 3	0 3	4	1.174	0.334	0.000	55.10	301.95
P01034	Cystatin-C (Cystatin-3) (Neuroendocrine basic polypep	1 3	3 3	0 3	8	0.233	1.766	0.000	36.99	342.72
P21291	Cysteine and glycine-rich protein 1 (Cysteine-rich prot	3 3	0 3	3 3	6	0.448	0.000	0.668	50.26	268.06
P52943	Cysteine-rich protein 2 (CRP2) (Protein ESP1)	0 3	0 3	3 3	2	0.000	0.000	0.166	16.83	41.83
P49589	Cysteinyl-tRNA synthetase, cytoplasmic (Cysteine--tRNA	1 3	0 3	0 3	1	0.043	0.000	0.000	2.01	12.63
P00167	Cytochrome b5	3 3	0 3	0 3	3	0.606	0.000	0.000	35.82	105.27
O43169	Cytochrome b5 type B (Cytochrome b5 outer mitochr	2 3	0 3	0 3	2	0.329	0.000	0.000	8.90	63.10
P31930	Cytochrome b-c1 complex subunit 1, mitochondrial (U	2 3	0 3	2 3	7	0.166	0.000	0.259	28.75	90.41
P22695	Cytochrome b-c1 complex subunit 2, mitochondrial (U	1 3	0 3	1 3	3	0.083	0.000	0.172	8.39	36.23
P14927	Cytochrome b-c1 complex subunit 7 (Ubiquinol-cytoc	2 3	0 3	0 3	2	0.340	0.000	0.000	28.83	34.17
P47985	Cytochrome b-c1 complex subunit Rieske, mitochond	1 3	0 3	3 3	4	0.129	0.000	0.438	15.69	162.98
P99999	Cytochrome c	3 3	0 3	0 3	6	1.499	0.000	0.000	49.52	351.32
P14406	Cytochrome c oxidase polypeptide 7A2, mitochondria	2 3	0 3	1 3	2	0.697	0.000	0.468	27.71	69.32
P00403	Cytochrome c oxidase subunit 2 (Cytochrome c oxidase	2 3	0 3	3 3	6	1.040	0.000	0.668	23.35	214.38
P13073	Cytochrome c oxidase subunit 4 isoform 1, mitochond	1 3	0 3	0 3	1	0.136	0.000	0.000	6.51	15.03
P20674	Cytochrome c oxidase subunit 5A, mitochondrial (Cyt	3 3	0 3	2 3	6	0.565	0.000	0.468	28.00	191.68
P10606	Cytochrome c oxidase subunit 5B, mitochondrial (Cyt	3 3	0 3	2 3	4	0.547	0.000	0.233	24.03	151.32
P14854	Cytochrome c oxidase subunit 6B1 (Cytochrome c oxid	1 3	0 3	0 3	1	0.334	0.000	0.000	13.95	11.68
P09669	Cytochrome c oxidase subunit 6C (Cytochrome c oxid	0 3	0 3	2 3	5	0.000	0.000	3.217	38.67	119.07
P08574	Cytochrome c1, heme protein, mitochondrial (Ubiquin	1 3	0 3	2 3	4	0.116	0.000	0.551	20.00	77.06
Q16678	Cytochrome P450 1B1 (CYPIB1)	0 3	0 3	1 3	1	0.000	0.000	0.062	2.03	9.40
Q8WWM	Cytoglobin (Histoglobin) (HGb) (Stellate cell activator	1 3	0 3	0 3	2	0.359	0.000	0.000	17.37	25.54
P21399	Cytoplasmic aconitate hydratase (Aconitase) (Citrate	3 3	0 3	0 3	8	0.117	0.000	0.000	14.96	169.01
Q07065	Cytoskeleton-associated protein 4 (63 kDa membrane	3 3	0 3	3 3	27	0.068	0.000	1.550	55.15	1114.78
P28838	Cytosol aminopeptidase (Leucine aminopeptidase) (Le	3 3	0 3	0 3	6	0.130	0.000	0.000	21.97	126.80
O00154	Cytosolic acyl coenzyme A thioester hydrolase (Long c	3 3	0 3	0 3	4	0.196	0.000	0.000	14.47	111.87
Q9Y5Y2	Cytosolic Fe-S cluster assembly factor NUBP2 (Nucleo	1 3	0 3	0 3	2	0.389	0.000	0.000	19.56	36.21
Q96KP4	Cytosolic non-specific dipeptidase (CNDP dipeptidase	1 3	0 3	0 3	1	0.070	0.000	0.000	4.42	11.56
P49902	Cytosolic purine 5'-nucleotidase (Cytosolic 5'-nucleoti	1 3	0 3	0 3	1	0.058	0.000	0.000	2.32	14.84
O43175	D-3-phosphoglycerate dehydrogenase (3-PGDH)	3 3	0 3	0 3	3	0.174	0.000	0.000	12.01	113.45
Q02338	D-beta-hydroxybutyrate dehydrogenase, mitochondr	0 3	2 3	0 3	1	0.000	0.089	0.000	5.25	28.17
P30046	D-dopachrome decarboxylase (D-dopachrome tauton	3 3	0 3	0 3	4	1.154	0.000	0.000	33.05	233.80
P78560	Death domain-containing protein CRADD (Caspase an	1 3	0 3	0 3	2	0.468	0.000	0.000	15.08	31.13
P07585	Decorin (Bone proteoglycan II) (PG-S2) (PG40)	0 3	1 3	3 3	4	0.000	0.179	0.132	14.76	63.48
Q13011	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochr	2 3	0 3	3 3	5	0.086	0.000	0.183	24.70	95.69
P30038	Delta-1-pyrroline-5-carboxylate dehydrogenase, mito	1 3	0 3	0 3	3	0.189	0.000	0.000	8.17	41.17
P54886	Delta-1-pyrroline-5-carboxylate synthetase (P5CS) (Al	3 3	0 3	1 3	3	0.052	0.000	0.087	4.53	124.65
P32321	Deoxycytidylate deaminase (dCMP deaminase)	3 3	0 3	0 3	3	0.294	0.000	0.000	24.72	101.86
O43598	Deoxyribonucleoside 5'-monophosphate N-glycosidas	1 3	0 3	0 3	2	0.425	0.000	0.000	16.09	27.26
Q8WVC6	Dephospho-CoA kinase domain-containing protein	1 3	0 3	0 3	1	0.129	0.000	0.000	5.63	13.01
P60981	Destrin (Actin-depolymerizing factor) (ADF)	3 3	2 3	3 3	14	3.305	0.284	0.389	67.88	915.53
Q9Y295	Developmentally-regulated GTP-binding protein 1 (Df	0 3	0 3	3 3	2	0.000	0.000	0.132	8.72	43.90
P55039	Developmentally-regulated GTP-binding protein 2 (Df	1 3	0 3	0 3	1	0.083	0.000	0.000	5.49	13.09
Q9NR28	Diablo homolog, mitochondrial (Second mitochondria	3 3	0 3	0 3	3	0.315	0.000	0.000	12.97	131.38
P09622	Dihydropolpyol dehydrogenase, mitochondrial (Dihydro	3 3	0 3	0 3	5	0.178	0.000	0.000	9.82	169.78
P10515	Dihydropolpyllsine-residue acetyltransferase compo	1 3	0 3	0 3	3	0.199	0.000	0.000	7.11	33.92
P36957	Dihydropolpyllsine-residue succinyltransferase comp	1 3	0 3	0 3	2	0.172	0.000	0.000	3.75	34.10
Q16555	Dihydropyrimidinase-related protein 2 (DRP-2) (Colla	3 3	0 3	0 3	11	0.378	0.000	0.000	37.59	434.06
P53634	Dipeptidyl-peptidase 1 (Dipeptidyl-peptidase I) (DPP-I	1 3	0 3	0 3	2	0.172	0.000	0.000	9.50	31.51
Q9UHL4	Dipeptidyl-peptidase 2 (Dipeptidyl-peptidase II) (DPP	2 3	0 3	0 3	2	0.108	0.000	0.000	10.37	36.65
O95989	Diphosphoinositol polyphosphate phosphohydrolase	1 3	0 3	0 3	2	0.389	0.000	0.000	15.70	20.96
Q9UKF2	Disintegrin and metalloproteinase domain-containing	2 3	3 3	0 3	1	0.047	0.047	0.000	2.03	181.91
Q16531	DNA damage-binding protein 1 (Damage-specific DNA	2 3	0 3	0 3	3	0.035	0.000	0.000	4.56	35.36
Q8IUX4	DNA dC->dU-editing enzyme APOBEC-3F (Apolipoprotei	0 3	0 3	1 3	2	0.000	0.000	0.222	8.04	23.95

accession	name	c_expcount	s_expcount	n_expcount	Peptides	c_empai	s_empai	n_empai	coverage	score
Q02880	DNA topoisomerase 2-beta (DNA topoisomerase II, beta)	0 3	0 3	1 3	1	0.000	0.000	0.019	0.74	12.52
P27695	DNA-(apurinic or apyrimidinic site) lyase (Apurinic-ap	2 3	0 3	1 3	2	0.212	0.000	0.101	11.01	60.60
P52434	DNA-directed RNA polymerases I, II, and III subunit R	1 3	0 3	0 3	1	0.259	0.000	0.000	10.67	13.08
Q9UBS4	DnaJ homolog subfamily B member 11 (ER-associated	2 3	0 3	0 3	1	0.086	0.000	0.000	3.07	25.43
O60762	Dolichol-phosphate mannosyltransferase (Dolichol-ph	2 3	0 3	0 3	1	0.116	0.000	0.000	8.46	47.05
Q9P2X0	Dolichol-phosphate mannosyltransferase subunit 3 (C	1 3	0 3	0 3	1	1.154	0.000	0.000	10.87	11.69
P39656	Dolichyl-diphosphooligosaccharide--protein glycosylt	2 3	0 3	3 3	8	0.142	0.000	0.615	24.56	304.29
P04843	Dolichyl-diphosphooligosaccharide--protein glycosylt	2 3	0 3	3 3	13	0.235	0.000	0.469	31.96	403.77
P04844	Dolichyl-diphosphooligosaccharide--protein glycosylt	3 3	0 3	3 3	7	0.102	0.000	0.292	20.13	288.86
P46977	Dolichyl-diphosphooligosaccharide--protein glycosylt	0 3	0 3	1 3	2	0.000	0.000	0.110	3.40	25.14
O95793	Double-stranded RNA-binding protein Stauflen homol	0 3	0 3	1 3	1	0.000	0.000	0.062	1.91	15.12
P55265	Double-stranded RNA-specific adenosine deaminase (	0 3	0 3	3 3	2	0.000	0.000	0.038	2.94	61.65
O60469	Down syndrome cell adhesion molecule (CHD2)	0 3	1 3	0 3	2	0.000	0.034	0.000	0.75	22.08
Q9BVJ7	Dual specificity protein phosphatase 23 (Low molecu	2 3	0 3	0 3	3	0.340	0.000	0.000	20.67	39.72
P51452	Dual specificity protein phosphatase 3 (Dual specifici	2 3	0 3	0 3	4	0.589	0.000	0.000	25.95	98.21
Q14203	Dynactin subunit 1 (150 kDa dynein-associated polype	2 3	0 3	0 3	2	0.025	0.000	0.000	2.74	37.21
Q13561	Dynactin subunit 2 (Dynactin complex 50 kDa subunit	1 3	0 3	0 3	2	0.186	0.000	0.000	6.23	22.57
O00429	Dynamamin-1-like protein (Dynamamin-like protein) (Dnm1	2 3	0 3	3 3	3	0.040	0.000	0.060	6.52	73.93
P63167	Dynein light chain 1, cytoplasmic (Dynein light chain L	3 3	0 3	1 3	3	0.815	0.000	0.778	25.84	142.50
Q96FJ2	Dynein light chain 2, cytoplasmic (Dynein light chain L	2 3	0 3	0 3	2	0.556	0.000	0.000	13.48	40.10
Q9NP97	Dynein light chain roadblock-type 1 (Dynein light chain	3 3	0 3	0 3	3	0.973	0.000	0.000	33.33	182.69
P31712	Dynein light chain Tctex-type 1 (T-complex testis-spec	3 3	0 3	0 3	3	0.593	0.000	0.000	38.94	84.22
Q14118	Dystroglycan (Dystrophin-associated glycoprotein 1)	1 3	0 3	0 3	1	0.043	0.000	0.000	1.45	14.49
Q14258	E3 ubiquitin/ISG15 ligase TRIM25 (Ubiquitin/ISG15-co	0 3	0 3	1 3	1	0.000	0.000	0.050	2.86	20.81
Q8NC42	E3 ubiquitin-protein ligase RNF149 (RING finger prote	1 3	1 3	1 3	1	0.086	0.086	0.086	2.50	57.76
Q15075	Early endosome antigen 1 (Endosome-associated prote	2 3	0 3	0 3	7	0.054	0.000	0.000	6.17	113.97
Q96C19	EF-hand domain-containing protein D2 (Swiprosin-1)	2 3	0 3	0 3	1	0.110	0.000	0.000	5.00	27.25
Q12805	EGF-containing fibulin-like extracellular matrix protei	0 3	1 3	0 3	1	0.000	0.083	0.000	1.83	24.33
Q9H4M9	EH domain-containing protein 1 (Testilin) (hPAST1)	2 3	0 3	0 3	3	0.099	0.000	0.000	9.93	63.17
Q9NZN4	EH domain-containing protein 2	3 3	0 3	3 3	10	0.222	0.000	0.317	30.20	468.42
Q15717	ELAV-like protein 1 (Hu-antigen R) (HuR)	0 3	0 3	3 3	2	0.000	0.000	0.259	8.28	79.77
P13804	Electron transfer flavoprotein subunit alpha, mitoch	3 3	0 3	2 3	13	0.750	0.000	0.096	53.45	478.60
P38117	Electron transfer flavoprotein subunit beta (Beta-ETF)	3 3	0 3	0 3	10	0.789	0.000	0.000	49.41	329.89
P68104	Elongation factor 1-alpha 1 (EF-1-alpha-1) (eEF1A-1) (	3 3	1 3	3 3	18	0.834	0.083	1.304	44.59	1563.90
P24534	Elongation factor 1-beta (EF-1-beta)	3 3	0 3	3 3	4	0.392	0.000	0.467	23.11	238.26
P29692	Elongation factor 1-delta (EF-1-delta) (Antigen NY-CO	3 3	0 3	3 3	6	0.356	0.000	0.500	25.62	401.26
P26641	Elongation factor 1-gamma (EF-1-gamma) (eEF-1B gai	3 3	0 3	3 3	9	0.242	0.000	0.790	27.00	507.28
P13639	Elongation factor 2 (EF-2)	3 3	0 3	3 3	26	0.704	0.000	0.477	38.81	1915.94
Q96RP9	Elongation factor G 1, mitochondrial (mEF-G 1) (Elong	1 3	0 3	0 3	1	0.044	0.000	0.000	1.60	14.57
P49411	Elongation factor Tu, mitochondrial (EF-Tu) (P43)	3 3	0 3	0 3	7	0.293	0.000	0.000	20.35	313.33
Q9NZ08	Endoplasmic reticulum aminopeptidase 1 (Adipocyte-	2 3	0 3	0 3	3	0.047	0.000	0.000	3.72	49.20
P30040	Endoplasmic reticulum protein ERp29 (Erp31) (Erp28	3 3	0 3	0 3	9	0.587	0.000	0.000	41.00	328.87
Q9BS26	Endoplasmic reticulum resident protein Erp44 (Thiore	2 3	0 3	0 3	2	0.089	0.000	0.000	13.05	28.88
P14625	Endoplasmic reticulum (Heat shock protein 90 kDa beta membe	3 3	0 3	3 3	31	0.873	0.000	0.174	46.08	1709.72
O60869	Endothelial differentiation-related factor 1 (EDF-1) (M	0 3	0 3	3 3	1	0.000	0.000	0.166	10.14	36.02
Q9UNN8	Endothelial protein C receptor (Endothelial cell protei	0 3	1 3	0 3	2	0.000	0.425	0.000	9.24	21.88
Q9UHY7	Enolase-phosphatase E1 (2,3-diketo-5-methylthio-1-p	2 3	0 3	0 3	2	0.319	0.000	0.000	13.41	70.10
Q9NTX5	Enoyl-CoA hydratase domain-containing protein 1	1 3	0 3	2 3	4	0.233	0.000	0.369	19.22	75.48
P30084	Enoyl-CoA hydratase, mitochondrial (Short chain eno	3 3	0 3	3 3	9	0.514	0.000	0.181	42.76	405.03
Q12929	Epidermal growth factor receptor kinase substrate 8	1 3	0 3	1 3	1	0.041	0.000	0.041	2.43	28.03
P61916	Epididymal secretory protein E1 (Niemann-Pick diseas	3 3	2 3	0 3	4	0.471	0.677	0.000	40.40	226.36
P07099	Epoxide hydrolase 1 (Microsomal epoxide hydrolase)	2 3	0 3	0 3	5	0.150	0.000	0.000	14.51	74.26
O75477	Erlin-1 (Endoplasmic reticulum lipid raft-associated pr	0 3	0 3	3 3	1	0.000	0.000	0.077	3.47	36.68
Q96HE7	ERO1-like protein alpha (ERO1-L-alpha) (Oxidoreducti	2 3	0 3	0 3	6	0.293	0.000	0.000	21.79	96.96
P27105	Erythrocyte band 7 integral membrane protein (Stom	2 3	0 3	2 3	5	0.226	0.000	0.222	20.83	115.19
P60842	Eukaryotic initiation factor 4A-I (eIF-4A-I) (ATP-depen	3 3	0 3	3 3	10	0.403	0.000	0.321	33.50	542.49
Q14240	Eukaryotic initiation factor 4A-II (eIF-4A-II) (ATP-depe	1 3	0 3	2 3	8	0.585	0.000	0.259	24.82	145.46
P15170	Eukaryotic peptide chain release factor GTP-binding s	2 3	0 3	0 3	1	0.066	0.000	0.000	3.21	37.35
O43324	Eukaryotic translation elongation factor 1 epsilon-1 (M	3 3	0 3	3 3	2	0.166	0.000	0.263	11.49	103.88
P41567	Eukaryotic translation initiation factor 1 (eIF1) (Protei	1 3	0 3	0 3	2	0.931	0.000	0.000	15.93	30.59
P47813	Eukaryotic translation initiation factor 1A, X-chromos	3 3	0 3	1 3	3	0.340	0.000	0.212	29.17	99.04
P05198	Eukaryotic translation initiation factor 2 subunit 1 (Eu	1 3	0 3	1 3	2	0.096	0.000	0.096	12.06	38.32
P20042	Eukaryotic translation initiation factor 2 subunit 2 (Eu	0 3	0 3	2 3	5	0.000	0.000	0.616	20.42	62.85
P41091	Eukaryotic translation initiation factor 2 subunit 3 (Eu	0 3	0 3	3 3	4	0.000	0.000	0.179	13.77	82.70
Q14152	Eukaryotic translation initiation factor 3 subunit A (eIF	2 3	0 3	3 3	9	0.026	0.000	0.099	8.76	213.25
P55884	Eukaryotic translation initiation factor 3 subunit B (eIF	1 3	0 3	3 3	3	0.083	0.000	0.083	7.37	108.54
Q99613	Eukaryotic translation initiation factor 3 subunit C (eIF	0 3	0 3	3 3	3	0.000	0.000	0.075	3.83	53.31
O15371	Eukaryotic translation initiation factor 3 subunit D (eIF	0 3	0 3	3 3	4	0.000	0.000	0.119	9.67	48.44
P60228	Eukaryotic translation initiation factor 3 subunit E (eIF	0 3	0 3	1 3	2	0.000	0.000	0.145	4.94	29.75
O00303	Eukaryotic translation initiation factor 3 subunit F (eIF	3 3	0 3	3 3	4	0.187	0.000	0.515	17.37	217.42
O75821	Eukaryotic translation initiation factor 3 subunit G (eIF	0 3	0 3	3 3	3	0.000	0.000	0.194	11.88	50.08
Q15372	Eukaryotic translation initiation factor 3 subunit H (eIF	0 3	0 3	3 3	1	0.000	0.000	0.096	5.68	28.40
Q13347	Eukaryotic translation initiation factor 3 subunit I (eIF	0 3	0 3	1 3	1	0.000	0.000	0.093	7.38	20.77
Q9UBQ5	Eukaryotic translation initiation factor 3 subunit K (eIF	2 3	0 3	3 3	7	0.271	0.000	1.063	33.49	198.10
Q9Y262	Eukaryotic translation initiation factor 3 subunit L (eIF	0 3	0 3	1 3	2	0.000	0.000	0.113	5.32	26.39
Q7L2H7	Eukaryotic translation initiation factor 3 subunit M (eIF	1 3	0 3	3 3	5	0.083	0.000	0.269	20.59	102.92
Q04637	Eukaryotic translation initiation factor 4 gamma 1 (eIF	3 3	0 3	3 3	3	0.036	0.000	0.065	2.75	186.43
P78344	Eukaryotic translation initiation factor 4 gamma 2 (eIF	0 3	0 3	1 3	1	0.000	0.000	0.031	2.54	11.61
O43432	Eukaryotic translation initiation factor 4 gamma 3 (eIF	1 3	0 3	0 3	1	0.020	0.000	0.000	0.63	12.36
P06730	Eukaryotic translation initiation factor 4E (eIF-4E) (mF	2 3	0 3	0 3	1	0.166	0.000	0.000	6.45	20.50
Q15056	Eukaryotic translation initiation factor 4H (eIF-4H) (W	1 3	0 3	0 3	1	0.105	0.000	0.000	5.24	21.53
P55010	Eukaryotic translation initiation factor 5 (eIF-5)	3 3	0 3	0 3	1	0.077	0.000	0.000	3.48	66.50

accession	name	c_expcount	s_expcount	n_expcount	Peptides	c_empai	s_empai	n_empai	coverage	score
P63241	Eukaryotic translation initiation factor 5A-1 (eIF-5A-1)	3/3	0/3	3/3	13	2.967	0.000	1.154	46.10	836.48
O60841	Eukaryotic translation initiation factor 5B (eIF-5B) (Tra	0/3	0/3	3/3	2	0.000	0.000	0.027	3.03	31.58
P56537	Eukaryotic translation initiation factor 6 (eIF-6) (B4 in	3/3	0/3	2/3	5	0.513	0.000	0.179	38.78	197.61
Q86V11	Exocyst complex component 3-like protein (Protein J)	0/3	0/3	1/3	1	0.000	0.000	0.056	3.89	14.67
Q9NVH0	Exonuclease 3'-5' domain-containing protein 2 (Exonu	0/3	0/3	1/3	1	0.000	0.000	0.061	3.83	11.84
O14980	Exportin-1 (Exp1) (Chromosome region maintenance	2/3	0/3	0/3	1	0.033	0.000	0.000	1.12	28.44
P55060	Exportin-2 (Exp2) (Importin-alpha re-exporter) (Chro	3/3	0/3	0/3	6	0.061	0.000	0.000	13.59	108.08
Q9BSJ8	Extended synaptotagmin-1 (E-Syt1) (Membrane-bou	2/3	0/3	0/3	3	0.086	0.000	0.000	3.71	112.99
P15311	Ezrin (p81) (Cyto villin) (Villin-2)	2/3	0/3	2/3	5	0.062	0.000	0.198	9.04	113.41
Q08945	FACT complex subunit SSRP1 (Facilitates chromatin tr	0/3	0/3	1/3	2	0.000	0.000	0.089	3.67	26.75
P52907	F-actin-capping protein subunit alpha-1 (CapZ alpha-1	3/3	2/3	3/3	7	0.439	0.163	0.286	45.45	408.61
P47755	F-actin-capping protein subunit alpha-2 (CapZ alpha-2	2/3	0/3	0/3	4	0.269	0.000	0.000	20.63	88.55
P47756	F-actin-capping protein subunit beta (CapZ beta)	3/3	0/3	2/3	10	0.790	0.000	0.492	52.35	456.54
Q92945	Far upstream element-binding protein 2 (FUSE-binding	2/3	0/3	0/3	3	0.069	0.000	0.000	6.20	52.39
P14324	Farnesyl pyrophosphate synthetase (FPP synthetase)	1/3	0/3	0/3	1	0.096	0.000	0.000	4.30	12.18
Q16658	Fascin (Singed-like protein) (55 kDa actin-bundling pr	3/3	0/3	2/3	4	0.120	0.000	0.066	12.58	111.03
P49327	Fatty acid synthase	3/3	0/3	0/3	44	0.321	0.000	0.000	26.05	1316.94
P15090	Fatty acid-binding protein, adipocyte (A-FABP) (AFABP	2/3	0/3	0/3	6	0.883	0.000	0.000	36.36	141.36
Q01469	Fatty acid-binding protein, epidermal (E-FABP) (Fatty	3/3	1/3	0/3	6	0.342	0.701	0.000	48.89	165.04
Q96AC1	Fermitin family homolog 2 (Pleckstrin homology dom	3/3	0/3	0/3	4	0.097	0.000	0.000	10.29	195.32
P02794	Ferritin heavy chain (Ferritin H subunit) (Cell prolifera	3/3	0/3	0/3	7	0.555	0.000	0.000	50.27	163.66
P02792	Ferritin light chain (Ferritin L subunit)	3/3	0/3	0/3	6	1.033	0.000	0.000	41.14	415.46
P35555	Fibrillin-1	0/3	3/3	0/3	4	0.000	0.027	0.000	2.16	164.74
P21802	Fibroblast growth factor receptor 2 (FGFR-2) (Keratin	2/3	1/3	1/3	1	0.046	0.046	0.046	1.34	56.68
P02751	Fibronectin (FN) (Cold-insoluble globulin) (CIG)	3/3	3/3	3/3	86	0.243	1.285	0.491	49.75	6230.11
P23142	Fibulin-1 (FIBL-1)	2/3	1/3	1/3	2	0.084	0.055	0.113	4.98	98.41
P21333	Filamin-A (Alpha-filamin) (Filamin-1) (Endothelial acti	3/3	1/3	3/3	66	0.371	0.014	0.463	37.51	2377.13
Q75369	Filamin-B (FLN-B) (Beta-filamin) (Actin-binding-like pr	1/3	0/3	2/3	8	0.071	0.000	0.071	4.65	121.47
Q14315	Filamin-C (Gamma-filamin) (Filamin-2) (Protein FLNC)	3/3	0/3	3/3	41	0.196	0.000	0.039	23.56	1065.99
Q96AY3	FK506-binding protein 10 (Peptidyl-prolyl cis-trans isc	3/3	0/3	0/3	9	0.229	0.000	0.000	23.88	258.39
Q9NYL4	FK506-binding protein 11 (Peptidyl-prolyl cis-trans isc	2/3	0/3	3/3	2	0.376	0.000	0.520	17.91	120.48
P26885	FK506-binding protein 2 (Peptidyl-prolyl cis-trans isom	3/3	0/3	0/3	3	0.668	0.000	0.000	23.24	185.61
Q00688	FK506-binding protein 3 (Peptidyl-prolyl cis-trans isom	1/3	0/3	1/3	3	0.136	0.000	0.468	15.18	50.17
Q02790	FK506-binding protein 4 (Peptidyl-prolyl cis-trans isom	2/3	0/3	0/3	1	0.062	0.000	0.000	2.83	25.61
Q13451	FK506-binding protein 5 (Peptidyl-prolyl cis-trans isom	2/3	0/3	0/3	4	0.164	0.000	0.000	10.50	69.82
Q9Y680	FK506-binding protein 7 (Peptidyl-prolyl cis-trans isom	1/3	0/3	0/3	2	0.233	0.000	0.000	7.72	30.31
P30043	Flavin reductase (FR) (NADPH-dependent diaphorase)	3/3	0/3	0/3	4	0.481	0.000	0.000	36.89	143.35
Q12841	Follistatin-related protein 1 (Follistatin-like 1)	0/3	3/3	0/3	6	0.000	0.324	0.000	20.13	197.14
Q13642	Four and a half LIM domains protein 1 (FHL-1) (Skelet	2/3	0/3	0/3	2	0.105	0.000	0.000	7.74	72.11
Q14192	Four and a half LIM domains protein 2 (FHL-2) (Skelet	2/3	0/3	1/3	3	0.154	0.000	0.186	10.75	116.66
P51114	Fragile X mental retardation syndrome-related protei	0/3	0/3	3/3	2	0.000	0.000	0.103	5.15	73.01
P04075	Fructose-bisphosphate aldolase A (Muscle-type aldolase	3/3	3/3	0/3	14	1.072	0.206	0.000	47.80	821.12
P09972	Fructose-bisphosphate aldolase C (Brain-type aldolase	3/3	0/3	1/3	2	0.118	0.000	0.093	7.14	88.15
P07954	Fumarate hydratase, mitochondrial (Fumarase)	3/3	0/3	0/3	2	0.086	0.000	0.000	7.25	80.01
P16930	Fumarylacetoacetase (FAA) (Fumarylacetoacetate hydrol	2/3	0/3	0/3	1	0.101	0.000	0.000	3.10	28.47
Q6P587	Fumarylacetoacetate hydrolase domain-containing pr	2/3	0/3	0/3	1	0.136	0.000	0.000	7.14	47.90
P51570	Galactokinase (Galactose kinase)	1/3	0/3	0/3	1	0.096	0.000	0.000	5.61	14.43
P09382	Galectin-1 (Lectin galactoside-binding soluble 1) (Beta	3/3	2/3	3/3	11	4.019	0.542	2.511	55.56	1293.58
P17931	Galectin-3 (Galactose-specific lectin 3) (Mac-2 antigen	3/3	1/3	2/3	6	0.792	0.520	1.848	28.40	340.11
Q08380	Galectin-3-binding protein (Lectin galactoside-binding	2/3	3/3	0/3	6	0.096	0.145	0.000	13.50	195.19
P47929	Galectin-7 (Gal-7) (HKL-14) (P17) (p53-induced gene 1	0/3	1/3	0/3	1	0.000	0.233	0.000	8.09	12.92
Q9UEY8	Gamma-adducin (Adducin-like protein 70)	0/3	0/3	3/3	1	0.000	0.000	0.055	2.27	23.68
P09104	Gamma-enolase (2-phospho-D-glycerate hydro-lyase)	0/3	1/3	0/3	3	0.000	0.241	0.000	15.44	39.51
O75223	Gamma-glutamylcyclotransferase (Cytochrome c-rele	1/3	0/3	0/3	1	0.145	0.000	0.000	5.32	10.09
P36269	Gamma-glutamyltransferase 5 (GGT 5) (Gamma-gluta	3/3	0/3	0/3	6	0.257	0.000	0.000	14.85	259.96
Q16666	Gamma-interferon-inducible protein 16 (Ifi-16) (Interf	0/3	0/3	1/3	1	0.000	0.000	0.040	2.17	29.61
P17900	Ganglioside GM2 activator (GM2-AP) (Cerebroside su	2/3	0/3	0/3	1	0.194	0.000	0.000	10.36	34.40
Q95479	GDH/6PGL endoplasmic bifunctional protein	3/3	0/3	0/3	4	0.110	0.000	0.000	7.84	177.10
Q9H488	GDP-fucose protein O-fucosyltransferase 1 (Peptide-C	3/3	0/3	0/3	3	0.167	0.000	0.000	17.27	85.36
O60547	GDP-mannose 4,6 dehydratase (GDP-D-mannose dehyd	2/3	0/3	0/3	2	0.150	0.000	0.000	6.99	50.77
P06396	Gelsolin (Actin-depolymerizing factor) (ADF) (Brevin)	3/3	0/3	3/3	8	0.190	0.000	0.120	19.82	382.53
O60763	General vesicular transport factor p115 (Protein USO)	2/3	0/3	0/3	5	0.060	0.000	0.000	8.21	67.94
P60983	Glia maturation factor beta (GMF-beta)	2/3	0/3	2/3	4	0.783	0.000	0.233	32.39	150.85
P07093	Glia-derived nexin (GDN) (Protease nexin I) (PN-1) (Pr	3/3	3/3	3/3	13	0.249	0.632	0.260	43.97	745.58
Q96EK6	Glucosamine 6-phosphate N-acetyltransferase (Phosph	2/3	0/3	0/3	4	0.688	0.000	0.000	30.43	110.65
P46926	Glucosamine-6-phosphate isomerase 1 (Glucosamine	2/3	0/3	0/3	3	0.253	0.000	0.000	18.34	55.93
Q06210	Glucosamine--fructose-6-phosphate aminotransferase	1/3	0/3	0/3	1	0.042	0.000	0.000	2.00	15.38
P11413	Glucose-6-phosphate 1-dehydrogenase (G6PD)	3/3	0/3	0/3	14	0.385	0.000	0.000	34.17	438.45
P06744	Glucose-6-phosphate isomerase (GPI) (Phosphoglucose	3/3	2/3	2/3	10	0.313	0.086	0.116	23.12	619.99
P14314	Glucosidase 2 subunit beta (Glucosidase II subunit be	1/3	0/3	0/3	2	0.179	0.000	0.000	6.82	31.51
P04062	Glucosylceramidase (Beta-glucocerebrosidase) (Acid l	1/3	0/3	0/3	1	0.066	0.000	0.000	4.29	11.89
P00367	Glutamate dehydrogenase 1, mitochondrial (GDH)	1/3	0/3	0/3	2	0.119	0.000	0.000	5.38	21.92
O94925	Glutaminase kidney isoform, mitochondrial (GLS) (L-gl	2/3	0/3	0/3	1	0.048	0.000	0.000	3.89	26.90
P47897	Glutamyl-tRNA synthetase (Glutamine--tRNA ligase)	2/3	0/3	0/3	5	0.038	0.000	0.119	13.03	117.13
P35754	Glutaredoxin-1 (Thioltransferase-1) (TTase-1)	3/3	1/3	0/3	6	1.569	0.334	0.000	55.66	263.52
Q86SX6	Glutaredoxin-related protein 5	3/3	0/3	0/3	3	0.393	0.000	0.000	31.85	98.37
P07203	Glutathione peroxidase 1 (GSHPx-1) (GPx-1) (Cellular	3/3	0/3	0/3	11	1.701	0.000	0.000	80.10	375.15
Q96SL4	Glutathione peroxidase 7 (GSHPx-7) (CL683)	1/3	0/3	0/3	1	0.179	0.000	0.000	6.95	12.22
P00390	Glutathione reductase, mitochondrial (GRase)	3/3	0/3	0/3	5	0.113	0.000	0.000	16.09	133.88
Q9Y2Q3	Glutathione S-transferase kappa 1 (Glutathione S-tran	3/3	0/3	3/3	8	0.571	0.000	0.129	50.88	347.37
P09488	Glutathione S-transferase Mu 1 (GSTM1-1) (GST class	2/3	0/3	0/3	1	0.122	0.000	0.000	5.96	45.25
P28161	Glutathione S-transferase Mu 2 (GSTM2-2) (GST class	3/3	0/3	0/3	4	0.225	0.000	0.000	24.31	125.23

accession	name	c_expcount	s_expcount	n_expcount	Peptides	c_empai	s_empai	n_empai	coverage	score
P21266	Glutathione S-transferase Mu 3 (GSTM3-3) (GST class	3 3	0 3	0 3	8	0.526	0.000	0.000	35.56	283.57
Q03013	Glutathione S-transferase Mu 4 (GSTM4-4) (GST class	2 3	0 3	0 3	1	0.129	0.000	0.000	5.96	28.55
P78417	Glutathione S-transferase omega-1 (GSTO 1-1)	3 3	1 3	2 3	7	0.574	0.122	0.122	23.65	378.56
P09211	Glutathione S-transferase P (GST class-pi) (GSTP1-1)	3 3	2 3	3 3	10	2.014	0.609	0.612	60.95	781.10
P30711	Glutathione S-transferase theta-1 (GST class-theta-1)	1 3	0 3	0 3	1	0.145	0.000	0.000	4.17	10.88
P0CG29	Glutathione S-transferase theta-2 (GST class-theta-2)	1 3	0 3	0 3	1	0.166	0.000	0.000	6.15	15.92
P48637	Glutathione synthetase (Glutathione synthase) (GSH s	2 3	0 3	0 3	1	0.064	0.000	0.000	2.74	21.74
P04406	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH	3 3	2 3	3 3	24	3.506	0.226	0.571	74.63	2169.42
P43304	Glycerol-3-phosphate dehydrogenase, mitochondrial	2 3	0 3	0 3	5	0.176	0.000	0.000	11.14	172.02
P11216	Glycogen phosphorylase, brain form	3 3	0 3	0 3	21	0.362	0.000	0.000	30.37	697.82
P06737	Glycogen phosphorylase, liver form	2 3	0 3	0 3	8	0.115	0.000	0.000	10.86	121.05
P11217	Glycogen phosphorylase, muscle form (Myophosphor	1 3	0 3	0 3	2	0.064	0.000	0.000	4.39	19.73
P41250	Glycyl-tRNA synthetase (Glycine--tRNA ligase) (GlyRS)	3 3	0 3	0 3	8	0.193	0.000	0.000	16.51	373.19
Q9HC38	Glyoxalase domain-containing protein 4	2 3	0 3	0 3	1	0.089	0.000	0.000	4.15	26.43
Q9UBQ7	Glyoxylate reductase/hydroxypruvate reductase	2 3	0 3	0 3	2	0.151	0.000	0.000	12.50	57.47
P49915	GMP synthase [glutamine-hydrolyzing] (Glutamine an	1 3	0 3	0 3	1	0.046	0.000	0.000	2.74	12.13
Q9H3P7	Golgi resident protein GCP60 (Acyl-CoA-binding dom	2 3	0 3	0 3	1	0.068	0.000	0.000	2.46	42.13
Q9HAV7	GrpE protein homolog 1, mitochondrial (Mt-GrpE#1) (	3 3	0 3	0 3	2	0.116	0.000	0.000	9.22	84.60
Q9UIJ7	GTP-AMP phosphotransferase mitochondrial (Adenylk	3 3	0 3	0 3	5	0.281	0.000	0.000	36.56	176.21
P01112	GTPase HRas (Transforming protein p21) (p21ras) (H-	2 3	0 3	0 3	4	0.359	0.000	0.000	33.86	47.08
P62826	GTP-binding nuclear protein Ran (GTPase Ran) (Ras-r	3 3	0 3	3 3	9	1.103	0.000	0.604	35.65	488.75
P36406	GTP-binding protein ARD-1 (ADP-ribosylation factor d	1 3	0 3	0 3	1	0.055	0.000	0.000	1.74	17.17
Q9NR31	GTP-binding protein SAR1a (COPII-associated small G	3 3	0 3	0 3	6	0.657	0.000	0.000	59.09	210.66
P04899	Guanine nucleotide-binding protein G(i), alpha-2 subu	2 3	0 3	3 3	3	0.181	0.000	0.280	12.68	156.97
Q9UBI6	Guanine nucleotide-binding protein G(i)/G(s)/G(o) su	3 3	0 3	3 3	3	1.406	0.000	1.658	45.83	215.52
P62873	Guanine nucleotide-binding protein G(i)/G(s)/G(t) su	3 3	0 3	2 3	8	0.373	0.000	0.110	23.82	211.15
P62879	Guanine nucleotide-binding protein G(i)/G(s)/G(t) su	2 3	0 3	2 3	6	0.374	0.000	0.110	17.65	128.27
P50148	Guanine nucleotide-binding protein G(q) subunit alph	0 3	0 3	1 3	1	0.000	0.000	0.077	5.85	14.51
P29992	Guanine nucleotide-binding protein subunit alpha-11	2 3	0 3	0 3	1	0.077	0.000	0.000	5.85	36.08
P63244	Guanine nucleotide-binding protein subunit beta-2-li	3 3	0 3	3 3	14	0.842	0.000	2.373	67.51	866.52
Q16774	Guanylate kinase (GMP kinase)	2 3	0 3	0 3	3	0.249	0.000	0.000	22.84	60.17
Q9NY12	H/ACA ribonucleoprotein complex subunit 1 (snoRNP	0 3	0 3	3 3	2	0.000	0.000	0.202	14.29	45.89
Q9NX24	H/ACA ribonucleoprotein complex subunit 2 (snoRNP	0 3	0 3	1 3	2	0.000	0.000	0.778	18.95	26.37
O60832	H/ACA ribonucleoprotein complex subunit 4 (Dyskeri	0 3	0 3	3 3	2	0.000	0.000	0.093	8.56	44.62
P08107	Heat shock 70 kDa protein 1 (HSP70.1) (HSP70-1/HSP	3 3	0 3	0 3	9	0.287	0.000	0.000	19.03	312.95
P34932	Heat shock 70 kDa protein 4 (Heat shock 70-related p	3 3	0 3	0 3	15	0.226	0.000	0.000	25.00	426.85
P17066	Heat shock 70 kDa protein 6 (Heat shock 70 kDa prote	1 3	0 3	0 3	3	0.162	0.000	0.000	6.22	41.65
P11142	Heat shock cognate 71 kDa protein (Heat shock 70 kD	3 3	0 3	3 3	25	0.880	0.000	0.716	39.78	1228.27
Q92598	Heat shock protein 105 kDa (Heat shock 110 kDa prot	2 3	0 3	0 3	3	0.064	0.000	0.000	5.01	62.75
Q12931	Heat shock protein 75 kDa, mitochondrial (HSP 75) (T	3 3	0 3	3 3	5	0.084	0.000	0.040	12.07	239.19
P04792	Heat shock protein beta-1 (HspB1) (Heat shock 27 kDa	3 3	2 3	3 3	12	1.521	0.406	0.311	67.32	758.39
Q9Y547	Heat shock protein beta-11 (HspB11) (Placental prote	2 3	0 3	0 3	1	0.468	0.000	0.000	8.33	23.77
O14558	Heat shock protein beta-6 (HspB6) (Heat shock 20 kDa	3 3	0 3	0 3	5	0.640	0.000	0.000	56.88	141.01
P07900	Heat shock protein HSP 90-alpha (HSP 86) (Renal carc	3 3	0 3	3 3	27	0.831	0.000	0.089	40.30	1330.29
P08238	Heat shock protein HSP 90-beta (HSP 90) (HSP 84)	3 3	0 3	3 3	23	0.650	0.000	0.111	39.09	1204.93
Q9NRV9	Heme-binding protein 1 (p22HBP)	2 3	0 3	0 3	4	0.402	0.000	0.000	30.16	94.92
Q9Y5Z4	Heme-binding protein 2 (Placental protein 23) (PP23)	1 3	0 3	0 3	2	0.425	0.000	0.000	12.20	31.66
P69905	Hemoglobin subunit alpha (Hemoglobin alpha chain)	1 3	0 3	0 3	4	1.783	0.000	0.000	34.51	58.20
P68871	Hemoglobin subunit beta (Hemoglobin beta chain) (B	1 3	0 3	0 3	1	0.233	0.000	0.000	6.80	12.59
P02042	Hemoglobin subunit delta (Hemoglobin delta chain) (	1 3	0 3	0 3	1	0.233	0.000	0.000	6.80	12.59
P20823	Hepatocyte nuclear factor 1-alpha (HNF-1A) (Liver-sp	0 3	1 3	0 3	1	0.000	0.122	0.000	3.80	30.15
Q55J55	Heterochromatin protein 1-binding protein 3 (Protein	0 3	0 3	3 3	12	0.000	0.000	0.567	25.68	236.47
Q99729	Heterogeneous nuclear ribonucleoprotein A/B (hnRN	0 3	0 3	3 3	2	0.000	0.000	0.190	5.42	36.99
Q13151	Heterogeneous nuclear ribonucleoprotein A0 (hnRNP	0 3	0 3	3 3	2	0.000	0.000	0.263	14.10	54.48
P09651	Heterogeneous nuclear ribonucleoprotein A1 (hnRNP	0 3	0 3	3 3	10	0.000	0.000	1.164	30.38	302.19
P51991	Heterogeneous nuclear ribonucleoprotein A3 (hnRNP	0 3	0 3	3 3	10	0.000	0.000	0.661	33.33	174.58
Q14103	Heterogeneous nuclear ribonucleoprotein D0 (hnRNP	1 3	0 3	3 3	5	0.110	0.000	0.444	14.65	190.37
O14979	Heterogeneous nuclear ribonucleoprotein D-like (hnR	0 3	0 3	3 3	2	0.000	0.000	0.119	5.95	46.49
P52597	Heterogeneous nuclear ribonucleoprotein F (hnRNP F	3 3	0 3	1 3	3	0.156	0.000	0.212	12.05	114.00
P38159	Heterogeneous nuclear ribonucleoprotein G (hnRNP G	0 3	0 3	3 3	2	0.000	0.000	0.119	6.91	55.29
P31943	Heterogeneous nuclear ribonucleoprotein H (hnRNP H	2 3	0 3	2 3	4	0.190	0.000	0.186	16.48	98.58
P55795	Heterogeneous nuclear ribonucleoprotein H2 (hnRNP	1 3	0 3	0 3	1	0.089	0.000	0.000	4.68	14.15
P31942	Heterogeneous nuclear ribonucleoprotein H3 (hnRNP	0 3	0 3	1 3	1	0.000	0.000	0.110	4.91	15.57
P61978	Heterogeneous nuclear ribonucleoprotein K (hnRNP K	3 3	0 3	3 3	10	0.310	0.000	0.682	31.75	665.05
P14866	Heterogeneous nuclear ribonucleoprotein L (hnRNP L	0 3	0 3	3 3	10	0.000	0.000	0.554	27.50	218.49
P52272	Heterogeneous nuclear ribonucleoprotein M (hnRNP	0 3	0 3	1 3	2	0.000	0.000	0.078	3.56	24.54
O60506	Heterogeneous nuclear ribonucleoprotein Q (hnRNP Q	2 3	0 3	3 3	20	0.115	0.000	1.144	35.47	494.04
O43390	Heterogeneous nuclear ribonucleoprotein R (hnRNP R	0 3	0 3	3 3	16	0.000	0.000	0.924	28.12	357.25
Q00839	Heterogeneous nuclear ribonucleoprotein U (hnRNP U	2 3	0 3	3 3	6	0.100	0.000	0.200	12.48	317.63
Q9BUJ2	Heterogeneous nuclear ribonucleoprotein U-like prot	0 3	0 3	1 3	1	0.000	0.000	0.039	2.57	12.87
P22626	Heterogeneous nuclear ribonucleoproteins A2/B1 (hr	2 3	0 3	3 3	8	0.105	0.000	0.919	18.41	257.49
P07910	Heterogeneous nuclear ribonucleoproteins C1/C2 (hn	0 3	0 3	3 3	4	0.000	0.000	0.249	12.75	85.40
P19367	Hexokinase-1 (Hexokinase type I) (HK I) (Brain form h	3 3	0 3	3 3	19	0.153	0.000	0.477	23.88	700.23
P09429	High mobility group protein B1 (High mobility group p	3 3	0 3	0 3	4	0.346	0.000	0.000	28.37	112.90
P17096	High mobility group protein HMG-I/HMG-Y (HMG-I(Y)	0 3	0 3	3 3	2	0.000	0.000	0.660	23.36	43.58
P50135	Histamine N-methyltransferase (HMT)	1 3	0 3	0 3	1	0.110	0.000	0.000	8.22	15.51
P49773	Histidine triad nucleotide-binding protein 1 (Adenosin	3 3	0 3	0 3	7	1.010	0.000	0.000	72.22	207.66
Q9BX68	Histidine triad nucleotide-binding protein 2 (HINT-2) (	2 3	0 3	0 3	2	0.309	0.000	0.000	22.09	41.94
P12081	Histidyl-tRNA synthetase, cytoplasmic (Histidine--trN	1 3	0 3	0 3	1	0.050	0.000	0.000	2.36	13.60
P16403	Histone H1.2 (Histone H1d)	0 3	0 3	2 3	4	0.000	0.000	0.668	15.96	58.89
P16401	Histone H1.5 (Histone H1a)	0 3	0 3	2 3	4	0.000	0.000	0.668	14.60	44.28
Q92522	Histone H1x	0 3	0 3	3 3	1	0.000	0.000	0.145	5.63	31.88

accession	name	c_expcount	s_expcount	n_expcount	Peptides	c_empai	s_empai	n_empai	coverage	score
P0C0S8	Histone H2A type 1 (H2A.1)	0 3	0 3	3 3	8	0.000	0.000	8.537	36.15	437.87
P04908	Histone H2A type 1-B/E (H2A/m) (H2A.2) (H2A/a)	3 3	0 3	0 3	2	0.714	0.000	0.000	21.54	133.51
Q71UI9	Histone H2A.V (H2A.F/Z)	1 3	0 3	0 3	1	0.389	0.000	0.000	7.03	11.21
P16104	Histone H2A.x (H2a/x)	0 3	0 3	3 3	4	0.000	0.000	1.468	32.17	172.13
P33778	Histone H2B type 1-B (H2B.f) (H2B/f) (H2B.1)	1 3	0 3	3 3	5	0.212	0.000	1.382	19.84	278.98
P68431	Histone H3.1 (H3/a) (H3/b) (H3/c) (H3/d) (H3/f) (H3/h)	0 3	0 3	1 3	2	0.000	0.000	0.520	13.24	26.45
P84243	Histone H3.3	0 3	0 3	1 3	1	0.000	0.000	0.233	23.53	19.10
P62805	Histone H4	2 3	1 3	3 3	13	0.926	1.154	8.805	58.25	640.49
P30443	HLA class I histocompatibility antigen, A-1 alpha chain	2 3	0 3	0 3	2	0.143	0.000	0.000	9.32	44.91
Q16543	Hsp90 co-chaperone Cdc37 (Hsp90 chaperone protein 1)	3 3	0 3	0 3	2	0.139	0.000	0.000	4.23	114.22
Q9NX55	Huntingtin-interacting protein K (Huntingtin yeast partner)	2 3	0 3	0 3	2	0.212	0.000	0.000	23.43	29.56
Q16836	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	3 3	0 3	0 3	7	0.300	0.000	0.000	47.13	155.66
P35914	Hydroxymethylglutaryl-CoA lyase, mitochondrial (HMG-CoA lyase)	3 3	0 3	0 3	6	0.388	0.000	0.000	20.00	151.52
Q6YN16	Hydroxysteroid dehydrogenase-like protein 2	2 3	0 3	0 3	2	0.123	0.000	0.000	6.70	34.89
P00492	Hypoxanthine-guanine phosphoribosyltransferase (HGPRT)	2 3	0 3	0 3	5	0.727	0.000	0.000	27.52	87.04
Q9Y4L1	Hypoxia up-regulated protein 1 (150 kDa oxygen-regulated protein)	3 3	0 3	0 3	9	0.130	0.000	0.000	16.92	230.38
Q14197	Immature colon carcinoma transcript 1 protein (Digestion product)	1 3	0 3	0 3	1	0.136	0.000	0.000	5.83	11.41
O14498	Immunoglobulin superfamily containing leucine-rich repeats	0 3	2 3	0 3	4	0.000	0.342	0.000	12.62	106.49
O00505	Importin subunit alpha-3 (Karyopherin subunit alpha-3)	0 3	0 3	1 3	1	0.000	0.000	0.101	6.33	17.53
O00629	Importin subunit alpha-4 (Karyopherin subunit alpha-4)	3 3	0 3	3 3	3	0.175	0.000	0.105	11.71	231.49
O60684	Importin subunit alpha-7 (Karyopherin subunit alpha-7)	3 3	0 3	0 3	3	0.098	0.000	0.000	9.89	78.34
Q14974	Importin subunit beta-1 (Karyopherin subunit beta-1)	3 3	0 3	3 3	11	0.380	0.000	0.182	19.06	692.86
Q8TEX9	Importin-4 (Imp4) (Importin-4b) (Imp4b) (Ran-binding protein 4)	2 3	0 3	0 3	2	0.039	0.000	0.000	3.24	36.61
O00410	Importin-5 (Imp5) (Importin subunit beta-3) (Karyopherin subunit beta-3)	3 3	0 3	0 3	16	0.319	0.000	0.000	22.33	619.01
O95373	Importin-7 (Imp7) (Ran-binding protein 7) (RanBP7)	2 3	0 3	0 3	2	0.039	0.000	0.000	2.41	29.89
Q96P70	Importin-9 (Imp9) (Ran-binding protein 9) (RanBP9)	2 3	0 3	0 3	1	0.045	0.000	0.000	2.69	26.97
O14920	Inhibitor of nuclear factor kappa-B kinase subunit beta	1 3	0 3	0 3	1	0.041	0.000	0.000	2.12	15.22
Q70UQ0	Inhibitor of nuclear factor kappa-B kinase-interacting protein	1 3	0 3	1 3	3	0.070	0.000	0.225	14.57	64.53
Q15181	Inorganic pyrophosphatase (Pyrophosphate phosphatase)	3 3	0 3	0 3	10	0.368	0.000	0.000	48.44	218.80
Q9H2U2	Inorganic pyrophosphatase 2, mitochondrial (PPase 2)	2 3	0 3	0 3	4	0.145	0.000	0.000	14.97	71.13
Q9BY32	Inosine triphosphate pyrophosphatase (ITPase) (Putative)	3 3	0 3	0 3	3	0.346	0.000	0.000	26.80	112.50
P12268	Inosine-5'-monophosphate dehydrogenase 2 (IMP dehydrogenase 2)	2 3	0 3	0 3	5	0.292	0.000	0.000	14.59	82.57
P29218	Inositol monophosphatase (Inositol-1(or 4)-monophosphatase)	2 3	0 3	0 3	1	0.129	0.000	0.000	3.97	40.79
Q9Y6M1	Insulin-like growth factor 2 mRNA-binding protein 2 (IGF2BP2)	1 3	0 3	3 3	6	0.113	0.000	0.207	13.69	143.67
O00425	Insulin-like growth factor 2 mRNA-binding protein 3 (IGF2BP3)	0 3	0 3	3 3	1	0.000	0.000	0.056	2.42	34.85
P01344	Insulin-like growth factor II (IGF-II) (Somatomedin-A)	0 3	2 3	0 3	5	0.000	1.063	0.000	21.11	154.69
P18065	Insulin-like growth factor-binding protein 2 (IGF-binding protein 2)	3 3	3 3	0 3	13	0.096	0.891	0.000	51.08	909.12
P22692	Insulin-like growth factor-binding protein 4 (IGF-binding protein 4)	3 3	3 3	0 3	8	0.136	0.875	0.000	31.78	409.97
P24592	Insulin-like growth factor-binding protein 6 (IGF-binding protein 6)	0 3	3 3	0 3	3	0.000	0.317	0.000	23.75	125.63
Q16270	Insulin-like growth factor-binding protein 7 (IGF-binding protein 7)	1 3	3 3	0 3	10	0.145	1.145	0.000	49.29	582.26
P08648	Integrin alpha-5 (Fibronectin receptor subunit alpha-5)	2 3	0 3	0 3	4	0.072	0.000	0.000	7.82	76.45
P06756	Integrin alpha-V (Vitronectin receptor subunit alpha-V)	2 3	0 3	2 3	6	0.065	0.000	0.032	7.63	88.67
P05556	Integrin beta-1 (Fibronectin receptor subunit beta-1) (Irbeta-1)	3 3	0 3	0 3	8	0.170	0.000	0.000	13.53	235.10
P18084	Integrin beta-5	2 3	0 3	0 3	2	0.056	0.000	0.000	4.26	57.92
Q13418	Integrin-linked protein kinase (ILK-1) (ILK-2) (59 kDa subunit)	2 3	0 3	0 3	1	0.066	0.000	0.000	2.43	26.14
P13164	Interferon-induced transmembrane protein 1 (Interferon-induced protein 1)	3 3	0 3	1 3	2	3.144	0.000	3.642	12.80	338.67
P19525	Interferon-induced, double-stranded RNA-activated protein kinase	0 3	0 3	1 3	2	0.000	0.000	0.145	4.72	34.32
Q12905	Interleukin enhancer-binding factor 2 (Nuclear factor 1)	0 3	0 3	3 3	7	0.000	0.000	0.660	25.64	153.10
Q12906	Interleukin enhancer-binding factor 3 (Nuclear factor 2)	0 3	0 3	3 3	12	0.000	0.000	0.460	15.32	244.96
Q27J81	Inverted formin-2 (HBEBP2-binding protein C)	2 3	0 3	1 3	2	0.051	0.000	0.030	3.12	78.73
Q96AB3	Isochorismatase domain-containing protein 2, mitochondrial	3 3	0 3	0 3	5	0.559	0.000	0.000	47.32	137.20
P50213	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	3 3	0 3	0 3	5	0.295	0.000	0.000	20.49	140.30
O75874	Isocitrate dehydrogenase [NADP] cytoplasmic (IDH) (Citrate isomerase)	3 3	0 3	0 3	8	0.225	0.000	0.000	29.47	187.85
P48735	Isocitrate dehydrogenase [NADP], mitochondrial (IDH) (Citrate isomerase)	3 3	0 3	0 3	6	0.213	0.000	0.000	18.81	181.66
P41252	Isoleucyl-tRNA synthetase, cytoplasmic (Isoleucine--tRNA synthetase)	3 3	0 3	2 3	12	0.080	0.000	0.086	12.52	169.05
Q9NSE4	Isoleucyl-tRNA synthetase, mitochondrial (Isoleucine--tRNA synthetase)	3 3	0 3	0 3	6	0.089	0.000	0.000	9.58	150.04
Q13907	Isopentenyl-diphosphate Delta-isomerase 1 (Isopentenyl diphosphate isomerase 1)	1 3	0 3	0 3	3	0.438	0.000	0.000	20.26	35.64
P26440	Isovaleryl-CoA dehydrogenase, mitochondrial (IVD)	2 3	0 3	0 3	1	0.070	0.000	0.000	5.91	29.84
Q07666	KH domain-containing, RNA-binding, signal transducing protein	0 3	0 3	1 3	2	0.000	0.000	0.160	7.67	31.05
Q86UP2	Kinectin (Kinesin receptor) (CG-1 antigen)	0 3	1 3	1 3	2	0.000	0.020	0.020	2.14	31.29
Q07866	Kinesin light chain 1 (KLC 1)	2 3	0 3	0 3	1	0.054	0.000	0.000	2.27	28.03
P33176	Kinesin-1 heavy chain (Ubiquitous kinesin heavy chain)	3 3	0 3	0 3	7	0.048	0.000	0.000	13.29	109.51
Q86Y91	Kinesin-like protein KIF18B	0 3	1 3	3 3	1	0.000	0.042	0.042	1.90	36.12
Q632Y3	KN motif and ankyrin repeat domain-containing protein	1 3	0 3	0 3	1	0.040	0.000	0.000	1.88	13.40
Q16719	Kynureninase (L-kynurenine hydrolase)	2 3	0 3	0 3	1	0.070	0.000	0.000	2.58	27.09
Q14657	L antigen family member 3 (Protein ITBA2) (Protein E5)	1 3	0 3	0 3	2	0.520	0.000	0.000	39.86	24.33
Q08431	Lactadherin (Milk fat globule-EGF factor 8) (MFG-E8) (Lactadherin)	2 3	1 3	0 3	2	0.143	0.093	0.000	7.24	59.00
P02788	Lactotransferrin (Lactoferrin) (Tala lactoferrin)	0 3	1 3	0 3	1	0.000	0.044	0.000	1.69	11.11
Q04760	Lactoylglyoxalase lyase (Methylglyoxalase) (Aldoketolase)	3 3	0 3	0 3	8	1.338	0.000	0.000	38.59	371.10
O00515	Ladinin-1 (Lad-1) (Linear IgA disease antigen) (LADA)	0 3	0 3	3 3	1	0.000	0.000	0.043	3.48	28.58
P02545	Lamin A/C (70 kDa lamin) (Renal carcinoma antigen NCA)	0 3	1 3	3 3	18	0.000	0.040	0.677	28.01	527.61
Q16363	Laminin subunit alpha-4	0 3	2 3	0 3	6	0.000	0.062	0.000	5.43	215.10
P07942	Laminin subunit beta-1 (Laminin B1 chain)	0 3	2 3	0 3	4	0.000	0.036	0.000	4.65	80.53
P55268	Laminin subunit beta-2 (S-laminin) (Laminin B1s chain)	1 3	1 3	0 3	3	0.019	0.038	0.000	3.23	33.12
P11047	Laminin subunit gamma-1 (Laminin B2 chain)	3 3	3 3	0 3	9	0.058	0.057	0.000	10.01	347.51
Q6PKG0	La-related protein 1 (La ribonucleoprotein domain factor)	0 3	0 3	1 3	1	0.000	0.000	0.028	1.73	12.76
Q14767	Latent-transforming growth factor beta-binding protein	1 3	1 3	0 3	2	0.028	0.028	0.000	1.87	25.37
P29536	Leiomodin-1 (64 kDa autoantigen 1D) (64 kDa autoantigen 1D)	0 3	0 3	1 3	1	0.000	0.000	0.046	2.00	14.29
O95202	LETM1 and EF-hand domain-containing protein 1, mitochondrial	1 3	0 3	0 3	1	0.041	0.000	0.000	2.44	15.51
P42704	Leucine-rich PPR motif-containing protein, mitochondrial	3 3	0 3	3 3	10	0.052	0.000	0.040	10.40	239.03
Q96AG4	Leucine-rich repeat-containing protein 59	1 3	0 3	3 3	5	0.194	0.000	0.491	24.76	213.85
Q9P2J5	Leucyl-tRNA synthetase, cytoplasmic (Leucine--tRNA synthetase)	2 3	0 3	0 3	2	0.028	0.000	0.000	2.30	28.98

accession	name	c_expcount	s_expcount	n_expcount	Peptides	c_emptai	s_emptai	n_emptai	coverage	score
P30740	Leukocyte elastase inhibitor (LEI) (Monocyte/neutrop	2 3	0 3	0 3	2	0.167	0.000	0.000	6.07	54.22
P09960	Leukotriene A-4 hydrolase (Leukotriene A(4) hydrolas	2 3	0 3	0 3	3	0.073	0.000	0.000	5.40	55.50
P48059	LIM and senescent cell antigen-like-containing domai	2 3	0 3	0 3	1	0.096	0.000	0.000	3.69	22.30
Q14847	LIM and SH3 domain protein 1 (LASP-1) (MLN 50)	3 3	0 3	3 3	3	0.262	0.000	0.122	14.94	262.47
Q9UHB6	LIM domain and actin-binding protein 1 (Epithelial pro	0 3	0 3	3 3	4	0.000	0.000	0.093	6.46	59.71
Q8WW11	LIM domain only protein 7 (LMO-7) (LOMP) (F-box on	0 3	0 3	3 3	10	0.000	0.000	0.102	9.27	164.92
P23141	Liver carboxylesterase 1 (Acyl coenzyme A:cholesterol	2 3	0 3	0 3	7	0.336	0.000	0.000	20.81	201.20
P00338	L-lactate dehydrogenase A chain (LDH-A) (LDH muscle	3 3	2 3	3 3	22	2.026	0.437	0.212	66.27	1906.60
Q9BY22	L-lactate dehydrogenase A-like 6B	3 3	0 3	1 3	1	0.089	0.000	0.089	4.46	210.99
P07195	L-lactate dehydrogenase B chain (LDH-B) (LDH heart s	3 3	3 3	0 3	19	1.660	0.789	0.000	56.59	1191.02
P36776	Lon protease homolog, mitochondrial (Lon protease-l	2 3	0 3	0 3	5	0.104	0.000	0.000	7.40	105.28
P24666	Low molecular weight phosphotyrosine protein phosph	3 3	0 3	0 3	5	0.791	0.000	0.000	39.24	226.23
P51884	Lumican (Keratan sulfate proteoglycan lumican) (KSPC	0 3	2 3	0 3	2	0.000	0.226	0.000	9.47	101.07
P05455	Lupus La protein (Sjogren syndrome type B antigen)	2 3	0 3	0 3	2	0.104	0.000	0.000	10.05	38.60
Q7Z4W1	L-xylulose reductase (XR) (Dicarbonyl/L-xylulose redu	3 3	0 3	0 3	4	0.238	0.000	0.000	27.46	110.86
P10253	Lysosomal alpha-glucosidase (Acid maltase) (Aglucosi	2 3	0 3	0 3	6	0.263	0.000	0.000	10.50	135.93
O00754	Lysosomal alpha-mannosidase (Laman) (Lysosomal ac	1 3	0 3	0 3	1	0.037	0.000	0.000	1.19	13.81
P10619	Lysosomal protective protein (Cathepsin A) (Carboxype	3 3	0 3	2 3	7	0.325	0.000	0.202	16.88	241.89
P42785	Lysosomal Pro-X carboxypeptidase (Prolylcarboxypep	2 3	0 3	0 3	2	0.126	0.000	0.000	8.06	55.53
Q14108	Lysosome membrane protein 2 (Lysosome membrane	2 3	0 3	0 3	2	0.119	0.000	0.000	5.23	34.50
P11279	Lysosome-associated membrane glycoprotein 1 (LAM	3 3	0 3	0 3	4	0.209	0.000	0.000	9.83	202.85
P13473	Lysosome-associated membrane glycoprotein 2 (LAM	2 3	0 3	0 3	4	0.213	0.000	0.000	11.46	77.07
Q15046	Lysyl-tRNA synthetase (Lysine--tRNA ligase) (LysRS)	2 3	0 3	3 3	6	0.096	0.000	0.129	17.59	80.94
P09603	Macrophage colony-stimulating factor 1 (CSF-1) (Lan	0 3	1 3	0 3	1	0.000	0.086	0.000	2.17	12.15
P14174	Macrophage migration inhibitory factor (MIF) (Phenyl	3 3	2 3	1 3	2	0.770	0.585	0.585	11.30	190.23
P40121	Macrophage-capping protein (Actin regulatory protei	1 3	0 3	0 3	1	0.122	0.000	0.000	6.32	12.16
Q14764	Major vault protein (MVP) (Lung resistance-related pr	3 3	0 3	3 3	33	0.565	0.000	0.493	49.16	1141.10
P40925	Malate dehydrogenase, cytoplasmic (Cytosolic malate	3 3	2 3	0 3	9	0.516	0.249	0.000	37.43	450.58
P40926	Malate dehydrogenase, mitochondrial	3 3	2 3	3 3	17	1.607	0.273	0.101	55.62	965.90
Q14165	Malectin	1 3	0 3	0 3	1	0.110	0.000	0.000	5.48	13.25
Q9ULC4	Malignant T cell amplified sequence 1 (MCT-1) (Multi	3 3	0 3	0 3	6	0.748	0.000	0.000	51.38	244.12
Q9UM22	Mammalian ependymin-related protein 1 (MERP-1) (L	2 3	2 3	0 3	3	0.486	0.212	0.000	14.29	138.04
O60664	Mannose-6-phosphate receptor-binding protein 1 (Ca	3 3	0 3	0 3	12	0.622	0.000	0.000	56.91	597.78
P43243	Matrin-3	0 3	0 3	3 3	6	0.000	0.000	0.144	12.63	117.06
P50281	Matrix metalloproteinase-14 (MMP-14) (Membrane-t	2 3	0 3	0 3	2	0.098	0.000	0.000	3.95	46.59
O00264	Membrane-associated progesterone receptor compo	3 3	0 3	0 3	4	0.762	0.000	0.000	29.74	217.52
O15173	Membrane-associated progesterone receptor compo	3 3	0 3	0 3	4	0.555	0.000	0.000	18.83	258.09
P55145	Mesencephalic astrocyte-derived neurotrophic factor	3 3	0 3	0 3	4	0.654	0.000	0.000	26.82	192.99
P01033	Metalloproteinase inhibitor 1 (Tissue inhibitor of met	3 3	3 3	0 3	14	0.271	3.740	0.000	64.73	1075.03
P16035	Metalloproteinase inhibitor 2 (Tissue inhibitor of met	1 3	3 3	2 3	10	0.145	0.840	0.145	39.09	301.15
P35625	Metalloproteinase inhibitor 3 (Tissue inhibitor of met	0 3	0 3	1 3	1	0.000	0.000	0.166	4.27	10.56
O75431	Metaxin-2 (Mitochondrial outer membrane import co	0 3	0 3	1 3	1	0.000	0.000	0.179	7.22	19.55
Q2M296	Methenyltetrahydrofolate synthetase domain-contain	1 3	0 3	0 3	1	0.075	0.000	0.000	4.18	12.17
P56192	Methionyl-tRNA synthetase, cytoplasmic (Methionine	1 3	0 3	2 3	6	0.047	0.000	0.318	12.33	97.34
Q9HCC0	Methylcrotonoyl-CoA carboxylase beta chain, mitoch	2 3	0 3	0 3	3	0.076	0.000	0.000	9.77	48.64
Q9BQA1	Methylosome protein 50 (MEP-50) (WD repeat-conta	1 3	0 3	0 3	1	0.155	0.000	0.000	7.89	15.98
P10620	Microsomal glutathione S-transferase 1 (Microsomal	3 3	0 3	2 3	5	0.758	0.000	0.292	22.58	109.11
O14880	Microsomal glutathione S-transferase 3 (Microsomal	0 3	0 3	3 3	1	0.000	0.000	0.334	8.55	40.15
P78559	Microtubule-associated protein 1A (MAP-1A) (Prolife	3 3	0 3	2 3	6	0.024	0.000	0.013	2.82	174.94
P46821	Microtubule-associated protein 1B (MAP-1B)	2 3	0 3	0 3	4	0.022	0.000	0.000	3.12	48.89
P27816	Microtubule-associated protein 4 (MAP-4)	3 3	0 3	3 3	5	0.052	0.000	0.029	7.99	141.85
Q15691	Microtubule-associated protein RP/EB family membe	1 3	0 3	0 3	2	0.274	0.000	0.000	12.69	25.71
Q02978	Mitochondrial 2-oxoglutarate/malate carrier protein	1 3	0 3	0 3	1	0.101	0.000	0.000	3.82	12.83
Q9Y6C9	Mitochondrial carrier homolog 2 (Met-induced mitoc	1 3	0 3	1 3	2	0.122	0.000	0.122	9.90	27.28
Q9Y3D6	Mitochondrial fission 1 protein (Fis1 homolog) (hFis1	3 3	0 3	0 3	4	0.627	0.000	0.000	24.34	211.69
Q9Y5L4	Mitochondrial import inner membrane translocase su	2 3	0 3	0 3	1	0.389	0.000	0.000	14.74	56.06
O60220	Mitochondrial import inner membrane translocase su	1 3	0 3	0 3	1	0.389	0.000	0.000	17.53	13.06
Q15388	Mitochondrial import receptor subunit TOM20 homo	0 3	0 3	1 3	1	0.000	0.000	0.334	8.97	15.36
Q9N569	Mitochondrial import receptor subunit TOM22 homo	3 3	0 3	2 3	4	0.714	0.000	1.683	51.41	160.19
O96008	Mitochondrial import receptor subunit TOM40 homo	1 3	0 3	1 3	3	0.166	0.000	0.359	5.26	43.00
O94826	Mitochondrial import receptor subunit TOM70 (Mito	2 3	0 3	0 3	1	0.053	0.000	0.000	2.96	54.09
Q10713	Mitochondrial-processing peptidase subunit alpha (Al	2 3	0 3	0 3	1	0.070	0.000	0.000	3.24	25.44
P27361	Mitogen-activated protein kinase 3 (Extracellular sign	0 3	1 3	0 3	1	0.000	0.093	0.000	8.44	12.59
Q9UHA4	Mitogen-activated protein kinase scaffold protein 1 (f	3 3	0 3	1 3	3	0.667	0.000	0.259	49.19	184.31
Q9Y2Q5	Mitogen-activated protein-binding protein-interactin	3 3	0 3	2 3	6	0.925	0.000	0.292	52.00	176.69
P26038	Moesin (Membrane-organizing extension spike prote	3 3	0 3	3 3	14	0.476	0.000	0.265	28.25	774.20
Q7L9L4	Mps one binder kinase activator-like 1A (Mob1 homo	2 3	0 3	0 3	1	0.212	0.000	0.000	5.09	35.67
P22234	Multifunctional protein ADE2	3 3	0 3	0 3	6	0.292	0.000	0.000	20.71	253.28
Q9NZM1	Myoferlin (Fer-1-like protein 3)	3 3	0 3	3 3	14	0.031	0.000	0.080	11.50	241.66
P08590	Myosin light chain 3 (Myosin light chain 1, slow-twitc	1 3	0 3	0 3	1	0.136	0.000	0.000	8.21	16.62
Q15746	Myosin light chain kinase, smooth muscle (MLCK) (Te	0 3	0 3	1 3	1	0.000	0.000	0.018	1.36	16.56
P60660	Myosin light polypeptide 6 (Smooth muscle and nonm	3 3	0 3	3 3	11	3.043	0.000	1.743	61.59	1219.19
P19105	Myosin regulatory light chain 12A (Myosin regulatory	3 3	0 3	3 3	10	1.699	0.000	2.497	62.57	795.67
P24844	Myosin regulatory light polypeptide 9 (Myosin regula	3 3	0 3	3 3	10	1.417	0.000	1.886	62.21	600.43
P35580	Myosin-10 (Myosin heavy chain 10) (Myosin heavy ch	0 3	0 3	3 3	6	0.000	0.000	0.050	6.17	114.73
Q7Z406	Myosin-14 (Myosin heavy chain 14) (Myosin heavy ch	3 3	0 3	1 3	2	0.021	0.000	0.028	1.40	124.94
P35579	Myosin-9 (Myosin heavy chain 9) (Myosin heavy chain	3 3	0 3	3 3	67	0.374	0.000	0.338	41.33	2633.34
O43795	Myosin-Ib (Myosin I alpha) (MMI-alpha) (MYH-1c)	1 3	0 3	0 3	2	0.053	0.000	0.000	2.29	26.70
O00159	Myosin-Ic (Myosin I beta) (MMI-beta) (MMIb)	3 3	0 3	2 3	11	0.100	0.000	0.027	13.92	308.22
Q9UM54	Myosin-VI (Unconventional myosin VI)	2 3	0 3	0 3	1	0.022	0.000	0.000	0.85	35.12
P58546	Myotrophin (Protein V-1)	3 3	0 3	0 3	7	1.332	0.000	0.000	77.97	306.96
Q9UJ70	N-acetyl-D-glucosamine kinase (N-acetylglucosamine	3 3	0 3	0 3	4	0.230	0.000	0.000	19.19	158.51

accession	name	c_expcount	s_expcount	n_expcount	Peptides	c_empai	s_empai	n_empai	coverage	score
P15586	N-acetylglucosamine-6-sulfatase (G6S)	3 3	0 3	0 3	3	0.126	0.000	0.000	6.70	86.08
O95671	N-acetylserotonin O-methyltransferase-like protein (NAT10)	1 3	0 3	0 3	1	0.059	0.000	0.000	1.93	11.07
Q9GZ21	N-acetyltransferase 13 (N-acetyltransferase 5) (hNAT13)	3 3	0 3	0 3	4	0.252	0.000	0.000	32.54	64.02
P15559	NAD(P)H dehydrogenase [quinone] 1 (Quinone reductase 1)	3 3	0 3	0 3	6	0.319	0.000	0.000	32.12	100.22
O95299	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex 1	3 3	0 3	1 3	2	0.101	0.000	0.080	9.58	88.27
Q86Y39	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex 2	2 3	1 3	3 3	3	0.750	0.389	0.931	42.55	143.00
Q9P0J0	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex 3	2 3	0 3	3 3	4	0.376	0.000	0.376	25.00	68.97
O43678	NADH dehydrogenase [ubiquinone] 1 beta subcomplex 1	3 3	0 3	3 3	3	0.406	0.000	0.259	41.41	111.25
O00483	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex 4	3 3	0 3	1 3	2	0.606	0.000	0.931	27.16	104.71
Q16718	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex 5	3 3	0 3	3 3	3	0.525	0.000	0.259	35.34	138.28
P56556	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex 6	2 3	0 3	0 3	2	0.179	0.000	0.000	14.84	25.72
O95182	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex 7	1 3	0 3	0 3	1	0.212	0.000	0.000	16.81	11.18
P51970	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex 8	0 3	0 3	1 3	1	0.000	0.000	0.194	12.21	18.95
Q16795	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex 9	0 3	0 3	1 3	1	0.000	0.000	0.077	3.45	10.80
O96000	NADH dehydrogenase [ubiquinone] 1 beta subcomplex 1	3 3	0 3	3 3	4	0.155	0.000	0.437	33.14	147.46
O95168	NADH dehydrogenase [ubiquinone] 1 beta subcomplex 2	3 3	0 3	1 3	3	0.376	0.000	0.520	31.01	141.92
O43674	NADH dehydrogenase [ubiquinone] 1 beta subcomplex 3	0 3	0 3	1 3	1	0.000	0.000	0.145	7.94	14.67
P19404	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial	3 3	0 3	3 3	2	0.156	0.000	0.122	9.24	106.63
O75489	NADH dehydrogenase [ubiquinone] iron-sulfur protein 1	3 3	0 3	3 3	7	0.225	0.000	0.523	38.26	259.04
O43920	NADH dehydrogenase [ubiquinone] iron-sulfur protein 2	2 3	0 3	2 3	4	0.480	0.000	0.668	32.08	66.02
O75380	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3	0 3	0 3	1 3	1	0.000	0.000	0.212	19.35	15.95
O00217	NADH dehydrogenase [ubiquinone] iron-sulfur protein 4	2 3	0 3	3 3	2	0.129	0.000	0.202	9.52	109.73
P00387	NADH-cytochrome b5 reductase 3 (Cytochrome b5 reductase 3)	3 3	0 3	0 3	6	0.399	0.000	0.000	37.54	284.35
P28331	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	1 3	0 3	3 3	5	0.145	0.000	0.096	11.69	82.25
P48163	NADP-dependent malic enzyme (NADP-ME) (Malic enzyme 1)	2 3	0 3	0 3	3	0.131	0.000	0.000	9.97	62.13
P16435	NADPH--cytochrome P450 reductase (CPR)	1 3	0 3	0 3	2	0.110	0.000	0.000	7.24	27.39
Q13765	Nascent polypeptide-associated complex subunit alpha	3 3	0 3	3 3	6	1.842	0.000	2.205	33.95	416.51
Q9NV92	NEDD4 family-interacting protein 2 (NEDD4 WW domain)	1 3	0 3	0 3	1	0.155	0.000	0.000	4.76	12.37
Q15843	NEDD8 (Ubiquitin-like protein Nedd8) (Neddylin) (Nedd8)	2 3	0 3	0 3	3	0.585	0.000	0.000	40.74	82.39
Q13564	NEDD8-activating enzyme E1 regulatory subunit (Amyloidosis)	1 3	0 3	0 3	1	0.072	0.000	0.000	3.00	11.59
P61081	NEDD8-conjugating enzyme Ubc12 (Ubiquitin-conjugating enzyme E2)	3 3	0 3	0 3	4	0.797	0.000	0.000	25.68	159.54
P08473	Neprilysin (Neutral endopeptidase 24.11) (Neutral endopeptidase)	0 3	1 3	0 3	1	0.000	0.047	0.000	5.07	11.28
Q09666	Neuroblast differentiation associated protein AHNAK	3 3	0 3	3 3	56	0.083	0.000	0.044	14.60	1125.42
O14786	Neuropilin-1 (Vascular endothelial cell growth factor receptor 1)	1 3	0 3	0 3	1	0.045	0.000	0.000	3.14	13.24
Q9Y639	Neuroplastin (Stromal cell-derived receptor 1) (SDR-1)	1 3	0 3	0 3	1	0.145	0.000	0.000	3.55	15.81
Q14697	Neutral alpha-glucosidase AB (Glucosidase II subunit alpha)	3 3	0 3	0 3	32	0.714	0.000	0.000	53.07	1080.72
Q15758	Neutral amino acid transporter B(0) (ATB(0)) (Sodium-dependent)	1 3	0 3	0 3	3	0.334	0.000	0.000	8.13	34.62
P55769	NHP2-like protein 1 (High mobility group-like nuclear protein 1)	0 3	0 3	3 3	5	0.000	0.000	0.915	45.31	115.17
Q96TA1	Niban-like protein 1 (Protein FAM129B) (Meg-3)	3 3	0 3	0 3	9	0.181	0.000	0.000	20.05	248.23
Q9HAN9	Nicotinamide mononucleotide adenylyltransferase 1 (NAMP1)	0 3	0 3	3 3	2	0.000	0.000	0.105	11.11	28.26
P40261	Nicotinamide N-methyltransferase	3 3	0 3	3 3	12	1.554	0.000	0.323	50.76	833.73
P43490	Nicotinamide phosphoribosyltransferase (NAMPTase)	2 3	0 3	0 3	2	0.066	0.000	0.000	7.13	23.99
P14543	Nidogen-1 (NID-1) (Entactin)	0 3	2 3	0 3	10	0.000	0.159	0.000	12.83	171.64
Q14112	Nidogen-2 (NID-2) (Osteonidogen)	0 3	2 3	0 3	8	0.000	0.116	0.000	7.85	136.10
Q86X76	Nitrilase homolog 1	1 3	0 3	0 3	1	0.105	0.000	0.000	9.79	12.77
Q9NQ44	Nitrilase homolog 2	1 3	0 3	0 3	4	0.492	0.000	0.000	22.83	55.32
Q15155	Nodal modulator 1 (pM5)	1 3	0 3	0 3	2	0.062	0.000	0.000	3.03	23.93
Q15233	Non-POU domain-containing octamer-binding protein 1	0 3	0 3	3 3	11	0.000	0.000	0.658	26.54	300.13
P22307	Non-specific lipid-transfer protein (Propanoyl-CoA C-acyltransferase)	3 3	0 3	0 3	12	0.538	0.000	0.000	14.99	520.05
O60443	Non-syndromic hearing impairment protein 5 (Inverse)	2 3	0 3	0 3	1	0.075	0.000	0.000	2.82	43.10
P61970	Nuclear transport factor 2 (NTF-2) (Placental protein 1)	3 3	0 3	0 3	6	1.114	0.000	0.000	55.91	215.33
P67809	Nuclease-sensitive element-binding protein 1 (Y-box-1)	2 3	0 3	1 3	3	0.110	0.000	0.233	17.28	64.63
Q02818	Nucleobindin-1 (CALNUC)	1 3	1 3	0 3	1	0.055	0.055	0.000	3.47	26.19
Q9Y2X3	Nucleolar protein 58 (Nucleolar protein 5)	0 3	0 3	3 3	2	0.000	0.000	0.062	6.24	30.59
Q9NR30	Nucleolar RNA helicase 2 (Nucleolar RNA helicase II) (NHP2)	0 3	0 3	1 3	1	0.000	0.000	0.044	2.81	11.22
P17480	Nucleolar transcription factor 1 (Upstream-binding factor)	0 3	0 3	1 3	1	0.000	0.000	0.036	2.36	14.23
P19338	Nucleolin (Protein C23)	1 3	0 3	3 3	16	0.039	0.000	0.590	27.04	415.43
P06748	Nucleophosmin (NPM) (Nucleolar phosphoprotein B2)	1 3	0 3	3 3	7	0.116	0.000	0.730	28.57	307.10
P12270	Nucleoprotein TPR	0 3	0 3	1 3	1	0.000	0.000	0.012	0.76	13.97
P15531	Nucleoside diphosphate kinase A (NDP kinase A) (TunA)	3 3	2 3	3 3	11	2.643	0.701	0.448	70.39	851.75
P22392	Nucleoside diphosphate kinase B (NDP kinase B) (nm2)	3 3	2 3	0 3	12	3.373	0.784	0.000	68.42	906.04
P55209	Nucleosome assembly protein 1-like 1 (NAP-1-related)	3 3	0 3	1 3	2	0.198	0.000	0.136	7.16	126.92
Q99733	Nucleosome assembly protein 1-like 4 (Nucleosome assembly protein 4)	3 3	0 3	0 3	1	0.105	0.000	0.000	2.93	74.34
Q9H173	Nucleotide exchange factor SIL1 (BiP-associated protein)	2 3	0 3	0 3	1	0.083	0.000	0.000	2.82	29.37
Q9NTK5	Obg-like ATPase 1 (GTP-binding protein 9)	3 3	0 3	1 3	1	0.077	0.000	0.077	3.79	130.89
Q9Y3B8	Oligoribonuclease, mitochondrial (Small fragment nuclease)	3 3	0 3	0 3	4	0.192	0.000	0.000	22.78	115.49
Q92882	Osteoclast-stimulating factor 1	3 3	0 3	0 3	2	0.226	0.000	0.000	17.76	111.99
Q8WX93	Palladin (Sarcoma antigen NY-SAR-77) (SIH002)	1 3	0 3	3 3	5	0.055	0.000	0.099	5.42	135.18
Q8WXF1	Paraspeckle component 1 (Paraspeckle protein 1)	0 3	0 3	3 3	3	0.000	0.000	0.091	10.33	41.99
P20962	Parathyroid hormone-related protein	2 3	0 3	0 3	1	0.778	0.000	0.000	10.78	47.09
O00151	PDZ and LIM domain protein 1 (Elfin) (LIM domain protein 1)	1 3	0 3	0 3	1	0.105	0.000	0.000	4.26	11.27
Q96JY6	PDZ and LIM domain protein 2 (PDZ-LIM protein myosin)	1 3	0 3	1 3	1	0.089	0.000	0.089	3.13	27.86
P50479	PDZ and LIM domain protein 4 (LIM protein RIL) (Reverend)	0 3	0 3	3 3	3	0.000	0.000	0.163	17.88	45.77
Q96HC4	PDZ and LIM domain protein 5 (Enigma homolog) (Enigma)	3 3	0 3	3 3	7	0.097	0.000	0.179	17.62	177.74
Q9NR12	PDZ and LIM domain protein 7 (LIM mineralization protein)	0 3	0 3	3 3	6	0.000	0.000	0.267	17.94	101.38
Q9UBV8	Peflin (PEF protein with a long N-terminal hydrophobic region)	1 3	0 3	0 3	1	0.233	0.000	0.000	3.87	13.70
P26022	Pentraxin-related protein PTX3 (Pentaxin-related protein 3)	0 3	3 3	0 3	11	0.000	0.815	0.000	37.53	580.10
P62937	Peptidyl-prolyl cis-trans isomerase A (PPIase A) (Cyclophilin A)	3 3	3 3	2 3	15	3.494	0.594	0.359	70.91	1070.26
P23284	Peptidyl-prolyl cis-trans isomerase B (PPIase) (Cyclophilin B)	3 3	2 3	3 3	23	3.863	0.361	3.221	67.13	1900.37
P45877	Peptidyl-prolyl cis-trans isomerase C (PPIase) (Cyclophilin C)	1 3	1 3	0 3	2	0.212	0.468	0.000	10.85	37.96
P62942	Peptidyl-prolyl cis-trans isomerase FKBP1A (PPIase FKBP1A)	3 3	1 3	0 3	4	0.815	0.334	0.000	37.96	191.47
O95302	Peptidyl-prolyl cis-trans isomerase FKBP9 (PPIase FKBP9)	1 3	0 3	0 3	1	0.077	0.000	0.000	2.98	13.07

accession	name	c_expcount	s_expcount	n_expcount	Peptides	c_empai	s_empai	n_empai	coverage	score
Q13526	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1 (PPIase)	1/3	0/3	0/3	1	0.212	0.000	0.000	9.20	16.81
Q9Y3C6	Peptidyl-prolyl cis-trans isomerase-like 1 (PPIase)	1/3	0/3	0/3	2	0.585	0.000	0.000	16.27	22.35
Q9H2H8	Peptidyl-prolyl cis-trans isomerase-like 3 (PPIase) (Cyclophilin B)	2/3	0/3	0/3	2	0.284	0.000	0.000	20.50	38.63
Q9Y3E5	Peptidyl-tRNA hydrolase 2, mitochondrial (PTH 2) (Bcl-2)	2/3	0/3	0/3	1	0.212	0.000	0.000	8.38	69.21
Q15063	Periostin (PN) (Osteoblast-specific factor 2) (OSF-2)	0/3	2/3	0/3	1	0.000	0.040	0.000	1.67	29.62
Q92626	Peroxidasin homolog (Vascular peroxidase 1) (Melanocyte peroxidase)	0/3	0/3	3/3	4	0.000	0.000	0.064	4.06	64.85
Q06830	Peroxiredoxin-1 (Thioredoxin peroxidase 2) (Thioredoxin-dependent peroxidoreductase)	3/3	3/3	3/3	17	2.684	0.645	0.956	67.34	1056.30
P32119	Peroxiredoxin-2 (Thioredoxin peroxidase 1) (Thioredoxin-dependent peroxidoreductase)	3/3	1/3	3/3	12	2.156	0.166	0.359	46.97	166.11
Q13162	Peroxiredoxin-4 (Prx-IV) (Thioredoxin peroxidase AO3)	3/3	0/3	0/3	12	1.235	0.000	0.000	49.82	554.07
P30044	Peroxiredoxin-5, mitochondrial (Prx-V) (Peroxisomal acyl-CoA oxidase)	3/3	0/3	0/3	14	3.718	0.000	0.000	57.01	700.36
P30041	Peroxiredoxin-6 (Antioxidant protein 2) (1-Cys peroxidase)	3/3	1/3	0/3	19	2.883	0.129	0.000	70.09	1026.61
P40855	Peroxisomal biogenesis factor 19 (Peroxin-19) (Peroxin)	1/3	0/3	0/3	1	0.122	0.000	0.000	10.03	12.59
P51659	Peroxisomal multifunctional enzyme type 2 (MFE-2) (Pexophagy)	3/3	0/3	3/3	13	0.061	0.000	0.556	24.05	375.97
Q7RTV0	PHD finger-like domain-containing protein 5A (PHD finger-like domain)	0/3	0/3	1/3	1	0.000	0.000	0.259	11.82	17.72
Q9Y285	Phenylalanyl-tRNA synthetase alpha chain (Phenylalanyl-tRNA synthetase)	1/3	0/3	3/3	4	0.059	0.000	0.159	13.98	105.45
Q9NSD9	Phenylalanyl-tRNA synthetase beta chain (Phenylalanyl-tRNA synthetase)	0/3	0/3	3/3	8	0.000	0.000	0.195	17.83	111.31
Q00325	Phosphate carrier protein, mitochondrial (Phosphate carrier)	1/3	0/3	0/3	1	0.086	0.000	0.000	3.31	10.33
P30086	Phosphatidylethanolamine-binding protein 1 (PEBP-1)	3/3	2/3	0/3	12	1.629	0.166	0.000	78.07	555.95
P48739	Phosphatidylinositol transfer protein beta isoform (PTP-beta)	1/3	0/3	0/3	2	0.194	0.000	0.000	9.96	25.36
O00329	Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit	2/3	0/3	0/3	1	0.031	0.000	0.000	1.15	24.02
Q13492	Phosphatidylinositol-binding clathrin assembly protein	0/3	0/3	1/3	1	0.000	0.000	0.070	5.52	20.75
O95394	Phosphoacetylglucosamine mutase (PAGM) (Acetylglucosaminidase)	2/3	0/3	0/3	2	0.141	0.000	0.000	8.30	50.47
Q16822	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	2/3	0/3	0/3	4	0.207	0.000	0.000	10.63	96.42
P36871	Phosphoglucosyltransferase-1 (PGM 1) (Glucose phosphomutase)	3/3	0/3	0/3	7	0.156	0.000	0.000	18.51	243.48
Q96G03	Phosphoglucosyltransferase-2 (PGM 2) (Glucose phosphomutase)	2/3	0/3	0/3	1	0.048	0.000	0.000	2.94	56.13
P00558	Phosphoglycerate kinase 1 (Primer recognition protein)	3/3	3/3	0/3	17	0.896	0.153	0.000	59.47	928.55
P18669	Phosphoglycerate mutase 1 (Phosphoglycerate mutase)	3/3	3/3	0/3	18	1.547	0.516	0.000	77.56	881.43
Q15126	Phosphomevalonate kinase (PMKase)	3/3	0/3	0/3	3	0.228	0.000	0.000	20.83	88.90
O15067	Phosphoribosylformylglycinamidine synthase (FGAM synthase)	2/3	0/3	0/3	3	0.045	0.000	0.000	3.51	45.79
Q9Y617	Phosphoserine aminotransferase (Phosphohydroxytransferase)	1/3	0/3	0/3	1	0.075	0.000	0.000	3.51	15.83
P78330	Phosphoserine phosphatase (PSPase) (O-phosphoserine phosphatase)	1/3	0/3	0/3	2	0.274	0.000	0.000	11.56	23.22
Q96BW5	Phosphotriesterase-related protein (Parathion hydrolase)	2/3	0/3	0/3	1	0.093	0.000	0.000	3.15	24.42
P36955	Pigment epithelium-derived factor (PEDF) (Serpine-F1)	0/3	3/3	0/3	19	0.000	1.154	0.000	47.13	655.24
P05155	Plasma protease C1 inhibitor (C1 Inh) (C1 esterase inhibitor)	1/3	3/3	0/3	8	0.080	0.312	0.000	18.60	253.21
P05121	Plasminogen activator inhibitor 1 (PAI-1) (Endothelial plasminogen activator inhibitor)	2/3	3/3	0/3	13	0.093	0.777	0.000	47.76	498.47
Q8NC51	Plasminogen activator inhibitor 1 RNA-binding protein	0/3	0/3	1/3	3	0.000	0.000	0.233	10.29	50.41
P13797	Plastin-3 (T-plastin)	3/3	0/3	0/3	7	0.132	0.000	0.000	15.56	170.57
P43034	Platelet-activating factor acetylhydrolase IB subunit a	3/3	0/3	0/3	4	0.132	0.000	0.000	12.44	96.14
P68402	Platelet-activating factor acetylhydrolase IB subunit b	3/3	0/3	0/3	3	0.298	0.000	0.000	20.96	133.81
Q15149	Plectin-1 (PLTN) (Hemidesmosomal protein 1) (HD1)	0/3	1/3	3/3	58	0.000	0.011	0.220	17.85	1154.94
P09874	Poly [ADP-ribose] polymerase 1 (PARP-1) (ADPRT) (NAD+ glycohydrolase)	0/3	0/3	1/3	1	0.000	0.000	0.030	1.87	20.15
Q15365	Poly(rC)-binding protein 1 (Alpha-CP1) (hnRNP-E1) (Nucleolar protein)	2/3	0/3	3/3	4	0.307	0.000	0.286	17.70	176.14
Q15366	Poly(rC)-binding protein 2 (Alpha-CP2) (hnRNP-E2) (Nucleolar protein)	3/3	0/3	3/3	6	0.338	0.000	0.181	23.29	254.76
Q9UHX1	Poly(U)-binding-splicing factor PUF60 (60 kDa poly(U) binding protein)	0/3	0/3	3/3	2	0.000	0.000	0.070	8.23	43.97
P11940	Polyadenylate-binding protein 1 (Poly(A)-binding protein)	2/3	0/3	3/3	9	0.062	0.000	0.312	17.14	256.20
Q6NZ12	Polymerase I and transcript release factor	3/3	0/3	3/3	17	0.356	0.000	1.655	32.56	754.34
P26599	Polypyrimidine tract-binding protein 1 (PTB) (Heterogeneous nuclear protein)	1/3	0/3	3/3	11	0.072	0.000	0.666	38.42	272.25
Q9UKA9	Polypyrimidine tract-binding protein 2 (Neurally-enriched protein)	0/3	0/3	1/3	1	0.000	0.000	0.072	1.51	15.48
P08397	Porphobilinogen deaminase (PBG-D) (Pre-uroporphyrinogen decarboxylase)	1/3	0/3	0/3	1	0.096	0.000	0.000	5.54	14.97
O60925	Prefoldin subunit 1	2/3	0/3	0/3	2	0.340	0.000	0.000	14.75	44.07
Q9UHV9	Prefoldin subunit 2	3/3	0/3	0/3	4	0.404	0.000	0.000	32.47	176.45
P61758	Prefoldin subunit 3 (Von Hippel-Lindau-binding protein)	2/3	0/3	0/3	3	0.274	0.000	0.000	27.41	91.97
Q9NQP4	Prefoldin subunit 4 (Protein C-1)	2/3	0/3	0/3	1	0.292	0.000	0.000	8.96	43.01
Q99471	Prefoldin subunit 5 (C-myc-binding protein Mm-1) (Myc-binding protein)	2/3	0/3	0/3	2	0.166	0.000	0.000	24.03	49.74
O15212	Prefoldin subunit 6 (Protein Ke2)	2/3	0/3	0/3	4	0.425	0.000	0.000	50.39	73.91
Q9Y3B4	Pre-mRNA branch site protein p14 (SF3b 14 kDa subunit)	0/3	0/3	3/3	2	0.000	0.000	0.468	20.00	57.89
Q9UM54	Pre-mRNA-processing factor 19 (PRP19/PSO4 homolog)	0/3	0/3	3/3	4	0.000	0.000	0.248	10.71	63.03
O75400	Pre-mRNA-processing factor 40 homolog A (Formin-binding protein)	0/3	0/3	3/3	4	0.000	0.000	0.096	7.42	51.65
Q9HCG8	Pre-mRNA-splicing factor CWC22 homolog (Nucamphorin)	0/3	1/3	0/3	1	0.000	0.033	0.000	1.54	15.01
O75934	Pre-mRNA-splicing factor SPF27 (Spliceosome-associated protein)	0/3	0/3	3/3	1	0.000	0.000	0.136	5.78	31.61
Q9UHG3	Prenylcysteine oxidase 1 (Prenylcysteine lyase)	3/3	0/3	0/3	9	0.271	0.000	0.000	24.36	162.82
P07602	Proactivator polypeptide	3/3	1/3	2/3	11	0.497	0.062	0.062	16.22	669.83
Q3SY69	Probable 10-formyltetrahydrofolate dehydrogenase A	3/3	0/3	0/3	5	0.066	0.000	0.000	12.13	172.52
Q92841	Probable ATP-dependent RNA helicase DDX17 (DEAD box protein)	0/3	0/3	3/3	11	0.000	0.000	0.389	18.92	181.76
Q9BUQ8	Probable ATP-dependent RNA helicase DDX23 (DEAD box protein)	0/3	0/3	1/3	1	0.000	0.000	0.038	2.07	15.89
Q7L014	Probable ATP-dependent RNA helicase DDX46 (DEAD box protein)	0/3	0/3	1/3	1	0.000	0.000	0.030	0.97	15.44
P17844	Probable ATP-dependent RNA helicase DDX5 (DEAD box protein)	0/3	0/3	3/3	10	0.000	0.000	0.325	17.10	159.22
P26196	Probable ATP-dependent RNA helicase DDX6 (DEAD box protein)	0/3	0/3	1/3	1	0.000	0.000	0.068	3.93	14.73
Q9HA77	Probable cysteinyl-tRNA synthetase, mitochondrial (Cys-tRNA synthetase)	3/3	0/3	0/3	2	0.089	0.000	0.000	8.16	75.28
Q9NRW3	Probable DNA dC->dU-editing enzyme APOBEC-3C (A3C)	0/3	0/3	3/3	4	0.000	0.000	0.660	28.42	90.70
Q9NQ88	Probable fructose-2,6-bisphosphatase TIGAR (TP53-inducible)	3/3	0/3	0/3	1	0.122	0.000	0.000	4.07	77.96
Q6N021	Probable methylcytosine dioxygenase TET2	0/3	1/3	1/3	1	0.000	0.018	0.018	0.85	27.41
Q15113	Procollagen C-endopeptidase enhancer 1 (Procollagenase enhancer)	0/3	3/3	2/3	13	0.000	0.621	0.194	40.98	403.83
Q02809	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1 (Lysyl oxidase)	3/3	0/3	3/3	7	0.118	0.000	0.259	14.17	299.31
O00469	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 2 (Lysyl oxidase)	3/3	0/3	2/3	12	0.260	0.000	0.044	25.64	404.91
O60568	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3 (Lysyl oxidase)	0/3	0/3	1/3	1	0.000	0.000	0.046	2.17	14.14
P07737	Profilin-1 (Profilin I)	3/3	3/3	3/3	19	8.521	2.987	1.579	71.43	1827.55
P35080	Profilin-2 (Profilin II)	3/3	0/3	0/3	5	0.838	0.000	0.000	32.14	268.70
Q8WUM4	Programmed cell death 6-interacting protein (PDCD6-interacting protein)	3/3	0/3	0/3	8	0.127	0.000	0.000	13.82	300.35
Q9BUL8	Programmed cell death protein 10 (TF-1 cell apoptosis-inducing factor)	1/3	0/3	0/3	1	0.122	0.000	0.000	6.13	11.84
O14737	Programmed cell death protein 5 (TF-1 cell apoptosis-inducing factor)	3/3	0/3	0/3	3	0.427	0.000	0.000	28.00	196.84
O75340	Programmed cell death protein 6 (Apoptosis-linked gene 1)	2/3	0/3	0/3	5	0.758	0.000	0.000	30.89	113.54

accession	name	c_expcount	s_expcount	n_expcount	Peptides	c_empai	s_empai	n_empai	coverage	score
P35232	Prohibitin	3 3	0 3	3 3	11	1.194	0.000	0.842	68.38	818.64
Q99623	Prohibitin-2 (B-cell receptor-associated protein BAP3)	3 3	0 3	3 3	10	0.497	0.000	0.169	43.14	441.15
P12273	Prolactin-inducible protein (Prolactin-induced protein 1)	0 3	1 3	0 3	1	0.000	0.212	0.000	6.85	13.32
Q9UQ80	Proliferation-associated protein 2G4 (Cell cycle protein 1)	0 3	0 3	1 3	2	0.000	0.000	0.166	7.61	26.70
O94903	Proline synthetase co-transcribed bacterial homolog	3 3	0 3	0 3	3	0.167	0.000	0.000	15.64	109.91
Q07954	Prolow-density lipoprotein receptor-related protein 1	1 3	0 3	0 3	11	0.090	0.000	0.000	3.59	140.88
Q32P28	Prolyl 3-hydroxylase 1 (Leucine- and proline-enriched)	2 3	0 3	1 3	3	0.074	0.000	0.055	6.25	75.04
P13674	Prolyl 4-hydroxylase subunit alpha-1 (4-PH alpha-1) (F)	2 3	0 3	1 3	2	0.071	0.000	0.053	6.37	87.21
P48147	Prolyl endopeptidase (PE) (Post-proline cleaving enzyme)	2 3	0 3	0 3	2	0.061	0.000	0.000	3.94	62.69
P05166	Propionyl-CoA carboxylase beta chain, mitochondrial	1 3	0 3	0 3	1	0.062	0.000	0.000	2.41	14.00
Q9H727	Prostaglandin E synthase 2 (Microsomal prostaglandin synthase)	2 3	0 3	0 3	4	0.221	0.000	0.000	22.28	57.82
Q15185	Prostaglandin E synthase 3 (Cytosolic prostaglandin synthase)	3 3	0 3	0 3	5	0.623	0.000	0.000	31.88	142.42
P23219	Prostaglandin G/H synthase 1 (Cyclooxygenase-1) (CCO)	2 3	0 3	0 3	3	0.093	0.000	0.000	8.85	32.39
Q14914	Prostaglandin reductase 1 (PRG-1) (NADP-dependent)	3 3	0 3	0 3	5	0.240	0.000	0.000	22.49	150.47
P41222	Prostaglandin-H2 D-isomerase (Lipocalin-type prostaglandin synthase)	1 3	3 3	0 3	5	0.194	0.767	0.000	28.42	326.56
Q06323	Proteasome activator complex subunit 1 (Proteasome activator complex subunit 1)	3 3	0 3	0 3	9	0.500	0.000	0.000	39.76	361.34
Q9UL46	Proteasome activator complex subunit 2 (Proteasome activator complex subunit 2)	3 3	0 3	0 3	10	0.568	0.000	0.000	56.49	430.59
P61289	Proteasome activator complex subunit 3 (Proteasome activator complex subunit 3)	2 3	0 3	0 3	2	0.222	0.000	0.000	9.45	47.92
Q9BT73	Proteasome assembly chaperone 3 (PAC-3)	2 3	0 3	0 3	2	0.417	0.000	0.000	22.95	55.74
P25786	Proteasome subunit alpha type-1 (Proteasome subunit alpha type-1)	3 3	0 3	2 3	6	0.370	0.000	0.116	31.56	161.62
P25787	Proteasome subunit alpha type-2 (Proteasome subunit alpha type-2)	3 3	0 3	3 3	6	0.464	0.000	0.437	35.47	323.49
P25788	Proteasome subunit alpha type-3 (Proteasome subunit alpha type-3)	3 3	0 3	2 3	5	0.393	0.000	0.122	23.14	229.05
P25789	Proteasome subunit alpha type-4 (Proteasome subunit alpha type-4)	3 3	0 3	3 3	4	0.297	0.000	0.190	27.59	222.00
P28066	Proteasome subunit alpha type-5 (Proteasome zeta class)	3 3	0 3	1 3	3	0.450	0.000	0.166	18.26	232.02
P60900	Proteasome subunit alpha type-6 (Proteasome iota class)	3 3	2 3	3 3	7	0.857	0.155	0.916	31.71	536.16
Q14818	Proteasome subunit alpha type-7 (Proteasome subunit alpha type-7)	3 3	0 3	3 3	10	0.649	0.000	0.399	50.40	465.11
P20618	Proteasome subunit beta type-1 (Proteasome component beta type-1)	3 3	0 3	3 3	10	1.583	0.000	0.844	46.89	726.22
P40306	Proteasome subunit beta type-10 (Proteasome subunit beta type-10)	1 3	0 3	0 3	1	0.136	0.000	0.000	7.33	12.55
P49721	Proteasome subunit beta type-2 (Proteasome component beta type-2)	3 3	1 3	3 3	5	0.587	0.179	0.179	41.79	218.94
P49720	Proteasome subunit beta type-3 (Proteasome component beta type-3)	3 3	1 3	3 3	6	1.183	0.668	2.188	36.10	426.19
P28070	Proteasome subunit beta type-4 (Proteasome beta class)	2 3	0 3	0 3	6	0.319	0.000	0.000	39.77	73.57
P28074	Proteasome subunit beta type-5 (Proteasome epsilon class)	3 3	0 3	3 3	11	0.909	0.000	0.214	47.53	395.53
P28072	Proteasome subunit beta type-6 (Proteasome delta class)	3 3	1 3	3 3	4	0.244	0.155	0.155	34.31	146.81
Q99436	Proteasome subunit beta type-7 (Proteasome subunit beta type-7)	2 3	0 3	0 3	2	0.230	0.000	0.000	12.27	57.97
P28062	Proteasome subunit beta type-8 (Proteasome subunit beta type-8)	2 3	0 3	2 3	5	0.335	0.000	0.129	23.19	112.21
P28065	Proteasome subunit beta type-9 (Proteasome subunit beta type-9)	2 3	0 3	0 3	4	0.563	0.000	0.000	18.26	54.06
Q5VYK3	Proteasome-associated protein ECM29 homolog (Ecm29)	1 3	0 3	0 3	3	0.054	0.000	0.000	2.98	47.32
Q8IVF2	Protein AHNK2	1 3	0 3	0 3	1	0.006	0.000	0.000	0.50	12.23
Q99873	Protein arginine N-methyltransferase 1 (Interferon regulated)	3 3	0 3	0 3	1	0.096	0.000	0.000	3.05	67.24
Q99622	Protein C10	2 3	0 3	0 3	3	0.852	0.000	0.000	40.48	56.88
Q9Y2B0	Protein canopy homolog 2 (MIR-interacting saposin-like)	3 3	0 3	2 3	7	0.951	0.000	0.425	51.65	329.99
O60888	Protein CutA (Brain acetylcholinesterase putative member)	3 3	1 3	0 3	2	0.520	0.259	0.000	17.88	166.25
P35659	Protein DEK	0 3	0 3	1 3	1	0.000	0.000	0.077	3.20	12.25
O60610	Protein diaphanous homolog 1 (Diaphanous-related family)	1 3	0 3	0 3	1	0.027	0.000	0.000	1.26	12.35
P07237	Protein disulfide-isomerase (PDI) (Prolyl 4-hydroxylase)	3 3	0 3	3 3	17	0.687	0.000	0.307	46.46	953.53
P30101	Protein disulfide-isomerase A3 (Disulfide isomerase E)	3 3	0 3	3 3	18	0.467	0.000	0.121	42.97	566.00
P13667	Protein disulfide-isomerase A4 (Protein ERp-72) (ERp72)	3 3	0 3	0 3	8	0.125	0.000	0.000	18.14	181.61
Q15084	Protein disulfide-isomerase A6 (Protein disulfide isomerase A6)	3 3	0 3	3 3	11	0.697	0.000	0.398	37.27	1000.96
Q96JJ7	Protein disulfide-isomerase TMX3 (Thioredoxin-related)	1 3	0 3	0 3	1	0.083	0.000	0.000	2.86	13.69
Q99497	Protein DJ-1 (Oncogene DJ1) (Parkinson disease protein)	3 3	2 3	0 3	12	1.720	0.359	0.000	72.49	614.45
Q9C005	Protein dpy-30 homolog (Dpy-30-like protein)	3 3	0 3	0 3	2	0.525	0.000	0.000	36.36	113.63
Q8N8S7	Protein enabled homolog	1 3	0 3	3 3	3	0.083	0.000	0.127	11.17	56.42
P49257	Protein ERGIC-53 (ER-Golgi intermediate compartment)	1 3	0 3	0 3	3	0.218	0.000	0.000	7.45	35.12
O95571	Protein ETHE1, mitochondrial (Ethylmalonic encephalopathy)	1 3	0 3	0 3	3	0.438	0.000	0.000	23.23	43.63
Q92520	Protein FAM3C	0 3	2 3	0 3	5	0.000	0.276	0.000	22.47	90.01
Q8NCA5	Protein FAM98A	0 3	0 3	3 3	6	0.000	0.000	0.361	13.29	127.95
P0CAP2	Protein GRINL1A (Glutamate receptor-like protein 1A)	0 3	0 3	1 3	1	0.000	0.000	0.089	7.88	12.23
Q8N163	Protein KIAA1967 (Deleted in breast cancer gene 1 protein)	0 3	0 3	1 3	1	0.000	0.000	0.036	1.52	12.20
P17252	Protein kinase C alpha type (PKC-alpha)	1 3	0 3	0 3	1	0.051	0.000	0.000	1.93	13.71
Q969G5	Protein kinase C delta-binding protein (Serum deprivation)	0 3	0 3	3 3	3	0.000	0.000	0.437	17.24	76.06
Q3MHD2	Protein LSM12 homolog	0 3	0 3	1 3	1	0.000	0.000	0.179	6.67	13.97
Q86UE4	Protein LYRIC (Lysine-rich CEACAM1 co-isolated protein)	0 3	0 3	1 3	1	0.000	0.000	0.062	2.23	11.50
P39210	Protein Mpv17	1 3	0 3	0 3	1	0.212	0.000	0.000	13.07	17.99
Q9UFN0	Protein NipSnap homolog 3A (NipSnap3A) (NipSnap4)	2 3	0 3	0 3	2	0.110	0.000	0.000	10.53	23.65
Q8IWE2	Protein NOXP20 (Nervous system over-expressed protein)	2 3	0 3	0 3	3	0.148	0.000	0.000	10.48	84.31
O14974	Protein phosphatase 1 regulatory subunit 12A (Myosin)	0 3	0 3	1 3	2	0.000	0.000	0.068	2.23	35.84
Q96C90	Protein phosphatase 1 regulatory subunit 14B (Phosphatase)	3 3	0 3	0 3	4	0.811	0.000	0.000	42.18	87.20
Q15435	Protein phosphatase 1 regulatory subunit 7 (Protein phosphatase)	3 3	0 3	0 3	1	0.089	0.000	0.000	5.00	107.52
P49593	Protein phosphatase 1F (Ca(2+)/calmodulin-dependent)	1 3	0 3	0 3	2	0.179	0.000	0.000	8.15	23.95
Q96M27	Protein PRRC1	3 3	0 3	0 3	2	0.199	0.000	0.000	3.60	72.06
P60903	Protein S100-A10 (S100 calcium-binding protein A10)	3 3	0 3	3 3	8	1.233	0.000	1.874	40.21	354.08
P31949	Protein S100-A11 (S100 calcium-binding protein A11)	3 3	1 3	3 3	9	3.294	0.389	1.829	77.14	554.48
Q99584	Protein S100-A13 (S100 calcium-binding protein A13)	3 3	0 3	3 3	7	1.608	0.000	1.683	39.80	308.00
Q96FQ6	Protein S100-A16 (S100 calcium-binding protein A16)	3 3	0 3	3 3	4	0.704	0.000	0.556	38.83	169.51
P06703	Protein S100-A6 (S100 calcium-binding protein A6) (Cal)	3 3	1 3	2 3	6	2.245	0.389	2.728	30.00	250.21
P05109	Protein S100-A8 (S100 calcium-binding protein A8) (Cal)	0 3	0 3	1 3	1	0.000	0.000	0.292	11.83	15.14
P06702	Protein S100-A9 (S100 calcium-binding protein A9) (Cal)	0 3	1 3	0 3	2	0.000	0.668	0.000	24.56	29.21
P55735	Protein SEC13 homolog (SEC13-related protein) (SEC13)	3 3	0 3	0 3	1	0.129	0.000	0.000	5.28	98.28
Q01105	Protein SET (Phosphatase 2A inhibitor I2PP2A) (I-2PP2A)	2 3	0 3	0 3	3	0.249	0.000	0.000	19.31	47.92
Q9BRJ7	Protein syndesmos (NUDT16-like protein 1)	1 3	0 3	0 3	1	0.129	0.000	0.000	10.43	25.34
Q15436	Protein transport protein Sec23A (SEC23-related protein)	3 3	0 3	0 3	8	0.154	0.000	0.000	15.16	173.18
O95486	Protein transport protein Sec24A (SEC24-related protein)	1 3	0 3	0 3	1	0.053	0.000	0.000	1.01	16.21

accession	name	c_expcount	s_expcount	n_expcount	Peptides	c_empai	s_empai	n_empai	coverage	score
P53992	Protein transport protein Sec24C (SEC24-related prot	1 3	0 3	0 3	1	0.043	0.000	0.000	1.65	15.23
O94855	Protein transport protein Sec24D (SEC24-related prot	2 3	0 3	0 3	2	0.075	0.000	0.000	2.71	35.41
O94979	Protein transport protein Sec31A (SEC31-related prot	3 3	0 3	0 3	10	0.144	0.000	0.000	13.52	278.04
P61619	Protein transport protein Sec61 subunit alpha isoform	1 3	0 3	3 3	5	0.122	0.000	0.336	18.07	93.83
Q12974	Protein tyrosine phosphatase type IVA 2 (Protein-tyro	1 3	0 3	0 3	1	0.179	0.000	0.000	8.98	11.86
Q9H3U1	Protein unc-45 homolog A (UNC-45A) (GCUNC-45) (Sr	2 3	0 3	0 3	1	0.034	0.000	0.000	2.12	26.87
P21980	Protein-glutamine gamma-glutamyltransferase 2 (Tiss	1 3	0 3	3 3	3	0.056	0.000	0.116	6.26	78.96
P22061	Protein-L-isaspartate(D-aspartate) O-methyltransfer	3 3	1 3	0 3	3	0.211	0.145	0.000	33.92	131.71
P46108	Proto-oncogene C-crk (p38) (Adapter molecule crk)	3 3	0 3	0 3	1	0.129	0.000	0.000	5.59	63.47
P08922	Proto-oncogene tyrosine-protein kinase ROS (Proto-o	0 3	1 3	0 3	1	0.000	0.018	0.000	1.07	20.84
P61457	Pterin-4-alpha-carbinolamine dehydratase (PHS) (4-al	2 3	0 3	0 3	2	0.329	0.000	0.000	28.85	59.14
P00491	Purine nucleoside phosphorylase (PNP) (Inosine phos	3 3	0 3	0 3	13	0.740	0.000	0.000	60.90	412.04
P55786	Puromycin-sensitive aminopeptidase (PSA)	3 3	0 3	0 3	8	0.125	0.000	0.000	10.01	209.87
Q58FF8	Putative heat shock protein HSP 90-beta 2 (Heat shoc	3 3	0 3	0 3	4	0.191	0.000	0.000	11.81	165.04
P0C7M2	Putative heterogeneous nuclear ribonucleoprotein A1	0 3	0 3	2 3	9	0.000	0.000	1.462	34.06	180.89
O43143	Putative pre-mRNA-splicing factor ATP-dependent RN	2 3	0 3	0 3	1	0.043	0.000	0.000	1.51	25.28
P46087	Putative ribosomal RNA methyltransferase NOP2 (Nu	0 3	0 3	1 3	1	0.000	0.000	0.043	2.46	15.13
P98179	Putative RNA-binding protein 3 (RNA-binding motif pr	2 3	0 3	3 3	3	0.179	0.000	0.408	21.02	105.42
A6NL28	Putative tropomyosin alpha-3 chain-like protein	2 3	0 3	0 3	3	0.156	0.000	0.000	11.66	43.38
O00764	Pyridoxal kinase (Pyridoxine kinase)	3 3	0 3	0 3	3	0.169	0.000	0.000	11.86	130.91
Q9NXJ5	Pyroglutamyl-peptidase 1 (Pyroglutamyl-peptidase I)	1 3	1 3	0 3	2	0.194	0.194	0.000	18.18	23.07
P11498	Pyruvate carboxylase, mitochondrial (Pyruvic carboxy	3 3	0 3	0 3	9	0.096	0.000	0.000	12.05	268.71
P11177	Pyruvate dehydrogenase E1 component subunit beta	2 3	0 3	0 3	4	0.368	0.000	0.000	19.78	112.21
P14618	Pyruvate kinase isozymes M1/M2 (Pyruvate kinase m	3 3	1 3	3 3	40	2.247	0.054	0.429	72.69	2527.22
Q08257	Quinone oxidoreductase (NADPH:quinone reductase)	1 3	0 3	0 3	1	0.093	0.000	0.000	3.34	12.16
P31150	Rab GDP dissociation inhibitor alpha (Rab GDI alpha)	2 3	0 3	0 3	4	0.298	0.000	0.000	13.65	152.69
P50395	Rab GDP dissociation inhibitor beta (Rab GDI beta) (G	3 3	1 3	0 3	18	0.854	0.301	0.000	51.24	862.45
Q15276	Rab GTPase-binding effector protein 1 (Rabaptin-5) (F	2 3	0 3	0 3	2	0.031	0.000	0.000	2.44	26.31
Q9H5N1	Rab GTPase-binding effector protein 2 (Rabaptin-5-be	2 3	0 3	0 3	1	0.058	0.000	0.000	2.28	30.65
P35241	Radixin	2 3	0 3	3 3	6	0.158	0.000	0.196	11.32	185.18
P46060	Ran GTPase-activating protein 1 (RanGAP1)	0 3	0 3	1 3	1	0.000	0.000	0.066	4.09	17.44
O60518	Ran-binding protein 6 (RanBP6)	2 3	0 3	0 3	1	0.033	0.000	0.000	1.18	51.14
P43487	Ran-specific GTPase-activating protein (Ran-binding p	2 3	0 3	0 3	4	0.389	0.000	0.000	32.84	80.38
P52306	Rap1 GTPase-GDP dissociation stimulator 1 (SMG GDS	2 3	0 3	0 3	3	0.078	0.000	0.000	9.72	35.60
Q13283	Ras GTPase-activating protein-binding protein 1 (G3B	0 3	0 3	3 3	8	0.000	0.000	0.529	29.83	137.32
Q9UN86	Ras GTPase-activating protein-binding protein 2 (G3B	0 3	0 3	1 3	1	0.000	0.000	0.070	3.53	17.50
P46940	Ras GTPase-activating-like protein IQGAP1 (p195)	3 3	0 3	3 3	27	0.314	0.000	0.089	25.41	1501.96
Q15404	Ras suppressor protein 1 (Rsu-1)	3 3	0 3	0 3	8	0.331	0.000	0.000	42.60	155.35
P63000	Ras-related C3 botulinum toxin substrate 1 (p21-Rac1	3 3	0 3	2 3	8	1.622	0.000	0.212	35.42	325.07
P15153	Ras-related C3 botulinum toxin substrate 2 (p21-Rac2	2 3	0 3	0 3	4	0.866	0.000	0.000	22.92	86.44
Q7L523	Ras-related GTP-binding protein A (Rag A) (Adenoviru	1 3	0 3	0 3	1	0.093	0.000	0.000	6.71	16.21
P61026	Ras-related protein Rab-10	3 3	0 3	2 3	5	0.430	0.000	0.468	24.00	231.24
P62491	Ras-related protein Rab-11A (Rab-11) (YL8)	3 3	0 3	0 3	6	0.533	0.000	0.000	32.87	226.23
Q15907	Ras-related protein Rab-11B (GTP-binding protein YPT	2 3	0 3	0 3	4	0.500	0.000	0.000	19.27	130.28
P51153	Ras-related protein Rab-13 (Cell growth-inhibiting ge	2 3	0 3	0 3	3	0.292	0.000	0.000	16.75	83.37
P61106	Ras-related protein Rab-14	3 3	0 3	0 3	10	0.916	0.000	0.000	58.14	247.33
P59190	Ras-related protein Rab-15	3 3	0 3	1 3	2	0.259	0.000	0.259	10.38	246.05
Q9NP72	Ras-related protein Rab-18	2 3	0 3	0 3	3	0.299	0.000	0.000	19.90	70.09
P62820	Ras-related protein Rab-1A (YPT1-related protein)	3 3	0 3	2 3	9	1.161	0.000	0.468	58.54	627.27
Q9H0U4	Ras-related protein Rab-1B	2 3	0 3	2 3	9	1.417	0.000	0.719	59.70	236.65
Q9UL25	Ras-related protein Rab-21	1 3	0 3	0 3	1	0.122	0.000	0.000	4.44	12.17
Q9UL26	Ras-related protein Rab-22A (Rab-22)	1 3	0 3	0 3	2	0.334	0.000	0.000	12.89	30.38
Q9ULC3	Ras-related protein Rab-23	1 3	0 3	0 3	1	0.129	0.000	0.000	6.75	18.46
P61019	Ras-related protein Rab-2A	3 3	0 3	2 3	9	1.120	0.000	0.311	49.53	407.86
Q13636	Ras-related protein Rab-31 (Rab-22B)	2 3	0 3	0 3	3	0.370	0.000	0.000	18.56	88.53
Q9H082	Ras-related protein Rab-33B	3 3	0 3	1 3	1	0.145	0.000	0.145	4.80	131.94
Q15286	Ras-related protein Rab-35 (Rab-1C) (GTP-binding pro	3 3	0 3	1 3	3	0.416	0.000	0.334	19.90	287.09
P20339	Ras-related protein Rab-5A	2 3	0 3	3 3	4	0.375	0.000	0.145	21.86	160.97
P61020	Ras-related protein Rab-5B	3 3	0 3	0 3	3	0.316	0.000	0.000	16.28	152.25
P51148	Ras-related protein Rab-5C (RAB5L) (L1880)	3 3	0 3	2 3	5	0.676	0.000	0.311	31.48	363.56
P20340	Ras-related protein Rab-6A (Rab-6)	3 3	0 3	2 3	5	0.482	0.000	0.136	26.44	298.59
P51149	Ras-related protein Rab-7a	3 3	0 3	3 3	12	1.769	0.000	0.782	67.63	771.76
P61006	Ras-related protein Rab-8A (Oncogene c-mel)	3 3	0 3	0 3	4	0.438	0.000	0.000	23.19	230.33
P62834	Ras-related protein Rap-1A (GTP-binding protein smg	3 3	0 3	3 3	9	1.020	0.000	0.716	45.11	490.37
P61224	Ras-related protein Rap-1b (GTP-binding protein smg	2 3	0 3	2 3	10	2.068	0.000	1.512	57.07	284.72
P10114	Ras-related protein Rap-2a (RbBP-30)	2 3	0 3	0 3	1	0.179	0.000	0.000	6.56	31.77
P61225	Ras-related protein Rap-2b	2 3	0 3	0 3	1	0.194	0.000	0.000	6.56	30.38
Q9Y3L5	Ras-related protein Rap-2c	1 3	0 3	0 3	1	0.179	0.000	0.000	6.56	15.60
P10301	Ras-related protein R-Ras (p23)	3 3	0 3	3 3	7	0.901	0.000	0.244	39.45	442.18
P62070	Ras-related protein R-Ras2 (Ras-like protein TC21) (Te	1 3	0 3	0 3	4	0.719	0.000	0.000	21.08	76.74
P18754	Regulator of chromosome condensation (Chromosome	0 3	0 3	1 3	2	0.000	0.000	0.212	8.08	31.83
Q96DB5	Regulator of microtubule dynamics protein 1 (RMD-1	2 3	0 3	0 3	1	0.086	0.000	0.000	3.50	26.41
Q92900	Regulator of nonsense transcripts 1 (ATP-dependent l	1 3	0 3	0 3	1	0.036	0.000	0.000	1.42	12.29
P35244	Replication protein A 14 kDa subunit (RP-A p14) (Repl	2 3	0 3	0 3	1	0.334	0.000	0.000	14.05	34.35
P15927	Replication protein A 32 kDa subunit (RP-A p32) (RP-A	1 3	0 3	0 3	1	0.145	0.000	0.000	8.52	14.38
Q15293	Reticulocalbin-1	2 3	0 3	0 3	2	0.151	0.000	0.000	10.57	57.80
Q96D15	Reticulocalbin-3 (EF-hand calcium-binding protein RL	3 3	0 3	0 3	6	0.448	0.000	0.000	23.78	143.92
Q9NQC3	Reticulon-4 (Neurite outgrowth inhibitor) (Nogo prote	2 3	0 3	0 3	1	0.034	0.000	0.000	1.34	25.53
Q9HB40	Retinoid-inducible serine carboxypeptidase (Serine ca	2 3	0 3	0 3	5	0.248	0.000	0.000	12.83	70.93
P02753	Retinol-binding protein 4 (Plasma retinol-binding pro	0 3	1 3	0 3	1	0.000	0.212	0.000	4.98	12.33
P52565	Rho GDP-dissociation inhibitor 1 (Rho GDI 1) (Rho-GD	3 3	0 3	2 3	5	0.588	0.000	0.155	31.37	295.24
Q07960	Rho GTPase-activating protein 1 (Rho-type GTPase-ac	3 3	0 3	0 3	4	0.107	0.000	0.000	18.91	92.72

accession	name	c_expcount	s_expcount	n_expcount	Peptides	c_empai	s_empai	n_empai	coverage	score
Q13464	Rho-associated protein kinase 1 (Rho-associated, coil	0 3	1 3	0 3	1	0.000	0.020	0.000	1.03	11.90
P08134	Rho-related GTP-binding protein RhoC (H9)	3 3	0 3	2 3	7	1.080	0.000	0.334	39.38	422.93
P84095	Rho-related GTP-binding protein RhoG	2 3	0 3	0 3	3	0.249	0.000	0.000	32.46	46.57
P13489	Ribonuclease inhibitor (Ribonuclease/angiogenin inh	3 3	0 3	0 3	10	0.409	0.000	0.000	39.91	355.49
O75817	Ribonuclease P protein subunit p20 (RNaseP protein p	0 3	0 3	1 3	1	0.000	0.000	0.259	10.71	17.04
P52758	Ribonuclease UK114 (14.5 kDa translational inhibitor	3 3	0 3	0 3	3	0.537	0.000	0.000	31.39	107.43
P60891	Ribose-phosphate pyrophosphokinase 1 (Phosphoribo	1 3	0 3	0 3	1	0.122	0.000	0.000	7.23	10.30
O76021	Ribosomal L1 domain-containing protein 1 (Cellular se	0 3	0 3	3 3	4	0.000	0.000	0.116	12.65	54.45
Q9P2E9	Ribosome-binding protein 1 (Ribosome receptor prot	3 3	0 3	3 3	20	0.038	0.000	0.285	18.87	660.05
P16083	Ribosylidihydronicotinamide dehydrogenase [quinone	1 3	0 3	0 3	2	0.334	0.000	0.000	16.88	25.07
Q96AT9	Ribulose-phosphate 3-epimerase (Ribulose-5-phosph	2 3	0 3	0 3	1	0.212	0.000	0.000	8.33	45.28
Q96PK6	RNA-binding protein 14 (RNA-binding motif protein 1	0 3	0 3	3 3	2	0.000	0.000	0.115	4.63	52.33
Q14498	RNA-binding protein 39 (RNA-binding motif protein 3	0 3	0 3	3 3	2	0.000	0.000	0.111	4.91	36.92
Q9Y5S9	RNA-binding protein 8A (RNA-binding motif protein 8	1 3	0 3	0 3	1	0.292	0.000	0.000	10.92	18.84
Q01844	RNA-binding protein EWS (EWS oncogene) (Ewing sar	1 3	0 3	0 3	1	0.089	0.000	0.000	3.66	15.19
P35637	RNA-binding protein FUS (Oncogene FUS) (Oncogene	3 3	0 3	0 3	2	0.093	0.000	0.000	5.51	68.69
P22087	rRNA 2'-O-methyltransferase fibrillarin (34 kDa nucle	0 3	0 3	1 3	1	0.000	0.000	0.096	5.92	16.08
Q9Y265	RuvB-like 1 (49 kDa TATA box-binding protein-interac	0 3	0 3	1 3	3	0.000	0.000	0.250	8.55	46.65
Q9Y230	RuvB-like 2 (48 kDa TATA box-binding protein-interac	2 3	0 3	1 3	3	0.108	0.000	0.070	7.13	54.43
P31153	S-adenosylmethionine synthetase isoform type-2 (Ad	2 3	0 3	0 3	2	0.127	0.000	0.000	2.78	47.73
Q9Y323	SAM domain and HD domain-containing protein 1 (De	3 3	0 3	0 3	3	0.075	0.000	0.000	7.99	78.70
P16615	Sarcoplasmic/endoplasmic reticulum calcium ATPase	2 3	0 3	2 3	5	0.093	0.000	0.036	8.25	70.24
Q8WVM8	Sec1 family domain-containing protein 1 (Syntaxin-bi	2 3	0 3	0 3	2	0.056	0.000	0.000	5.92	26.19
Q12765	Secernin-1	1 3	0 3	0 3	1	0.086	0.000	0.000	3.86	12.16
Q13228	Selenium-binding protein 1 (56 kDa selenium-binding	2 3	0 3	0 3	2	0.072	0.000	0.000	8.26	29.02
Q8WWX9	Selenoprotein M (SelM)	1 3	0 3	0 3	1	0.292	0.000	0.000	11.03	18.23
P35270	Sepiapterin reductase (SPR)	3 3	0 3	0 3	5	0.358	0.000	0.000	27.97	167.34
Q9NVA2	Septin-11	1 3	0 3	0 3	1	0.077	0.000	0.000	4.66	15.50
Q15019	Septin-2 (Neural precursor cell expressed developme	3 3	0 3	2 3	4	0.295	0.000	0.096	16.34	183.00
Q9UHD8	Septin-9 (MLL septin-like fusion protein MSF-A) (MLL	2 3	0 3	0 3	2	0.103	0.000	0.000	3.58	94.60
P83111	Serine beta-lactamase-like protein LACTB, mitochond	0 3	0 3	3 3	1	0.000	0.000	0.062	2.74	27.15
P34897	Serine hydroxymethyltransferase, mitochondrial (SHM	3 3	0 3	2 3	5	0.124	0.000	0.189	14.68	176.05
O95084	Serine protease 23 (Putative secreted protein ZS1G13	0 3	1 3	0 3	1	0.000	0.080	0.000	3.39	9.36
Q92743	Serine protease HTRA1 (L56) (Serine protease 11)	0 3	1 3	3 3	2	0.000	0.083	0.083	5.21	40.35
Q8IYB3	Serine/arginine repetitive matrix protein 1 (Ser/Arg-r	0 3	0 3	1 3	1	0.000	0.000	0.034	3.76	13.02
P42345	Serine/threonine-protein kinase mTOR (Mammalian t	0 3	1 3	1 3	1	0.000	0.013	0.013	1.22	28.67
O95747	Serine/threonine-protein kinase OSR1 (Oxidative stre	1 3	0 3	0 3	1	0.064	0.000	0.000	5.12	16.80
Q13177	Serine/threonine-protein kinase PAK 2 (p21-activated	1 3	0 3	0 3	1	0.077	0.000	0.000	3.05	12.27
P63151	Serine/threonine-protein phosphatase 2A 55 kDa reg	3 3	0 3	0 3	1	0.070	0.000	0.000	3.13	70.32
P30153	Serine/threonine-protein phosphatase 2A 65 kDa reg	3 3	0 3	2 3	9	0.334	0.000	0.179	22.41	406.81
P67775	Serine/threonine-protein phosphatase 2A catalytic su	2 3	0 3	0 3	2	0.163	0.000	0.000	8.09	34.07
Q96HS1	Serine/threonine-protein phosphatase PGAM5, mitoc	0 3	0 3	1 3	1	0.000	0.000	0.105	5.88	13.81
P62136	Serine/threonine-protein phosphatase PP1-alpha cata	2 3	0 3	2 3	6	0.286	0.000	0.650	24.24	149.00
P62140	Serine/threonine-protein phosphatase PP1-beta catal	2 3	0 3	3 3	8	0.178	0.000	0.778	30.58	251.56
Q9Y3F4	Serine-threonine kinase receptor-associated protein (	2 3	0 3	0 3	1	0.101	0.000	0.000	5.14	37.65
Q96P63	Serpin B12	1 3	1 3	1 3	1	0.093	0.093	0.093	4.20	52.53
P35237	Serpin B6 (Placental thrombin inhibitor) (Cytoplasmic	3 3	0 3	0 3	6	0.331	0.000	0.000	19.41	381.09
P50454	Serpin H1 (Collagen-binding protein) (Colligin) (47 kDa	3 3	2 3	3 3	16	0.845	0.223	0.513	46.41	1625.62
O75830	Serpin I2 (Myoepithelium-derived serine protease inh	0 3	1 3	0 3	1	0.000	0.086	0.000	3.46	10.08
Q9BXP5	Serrate RNA effector molecule homolog (Arsenite-res	0 3	0 3	1 3	1	0.000	0.000	0.036	1.48	13.77
Q15165	Serum paraoxonase/arylesterase 2 (PON 2) (Serum ar	1 3	0 3	0 3	1	0.122	0.000	0.000	4.52	15.70
P49591	Seryl-tRNA synthetase, cytoplasmic (Seryl-tRNA(Ser/S	2 3	0 3	0 3	5	0.181	0.000	0.000	14.59	80.08
P10768	S-formylglutathione hydrolase (FGH) (Esterase D)	3 3	0 3	0 3	6	0.437	0.000	0.000	40.78	213.36
O75368	SH3 domain-binding glutamic acid-rich-like protein	3 3	0 3	0 3	6	1.531	0.000	0.000	52.63	305.21
Q9H299	SH3 domain-binding glutamic acid-rich-like protein 3	3 3	1 3	2 3	6	0.719	0.334	0.778	21.51	219.40
Q9UIL1	Short coiled-coil protein	1 3	0 3	0 3	1	0.233	0.000	0.000	11.32	14.92
P16219	Short-chain specific acyl-CoA dehydrogenase, mitoch	2 3	0 3	0 3	2	0.127	0.000	0.000	9.22	53.39
Q9H9B4	Sideroflexin-1 (Tricarboxylate carrier protein) (TCC)	1 3	0 3	0 3	1	0.116	0.000	0.000	5.90	12.88
Q9BWM7	Sideroflexin-3	1 3	0 3	0 3	1	0.110	0.000	0.000	5.30	14.80
P37108	Signal recognition particle 14 kDa protein (SRP14) (18	1 3	0 3	1 3	1	0.233	0.000	0.233	10.29	27.08
Q9UHB9	Signal recognition particle 68 kDa protein (SRP68)	0 3	0 3	1 3	2	0.000	0.000	0.094	4.15	27.58
O76094	Signal recognition particle 72 kDa protein (SRP72)	1 3	0 3	1 3	3	0.048	0.000	0.099	9.84	52.54
P49458	Signal recognition particle 9 kDa protein (SRP9)	1 3	0 3	3 3	2	0.334	0.000	0.556	25.58	68.18
P08240	Signal recognition particle receptor subunit alpha (SR	0 3	0 3	1 3	1	0.000	0.000	0.050	4.39	12.14
Q9Y5M8	Signal recognition particle receptor subunit beta (SR-I	0 3	0 3	1 3	2	0.000	0.000	0.245	9.23	25.18
P42224	Signal transducer and activator of transcription 1-alph	3 3	0 3	0 3	11	0.195	0.000	0.000	20.13	253.59
P40763	Signal transducer and activator of transcription 3 (Act	3 3	0 3	0 3	2	0.045	0.000	0.000	5.71	69.85
Q04837	Single-stranded DNA-binding protein, mitochondrial (	3 3	0 3	2 3	6	0.584	0.000	0.166	44.59	320.25
Q9NTI5	Sister chromatid cohesion protein PDS5 homolog B (A	0 3	0 3	1 3	2	0.000	0.000	0.040	3.11	28.82
P62304	Small nuclear ribonucleoprotein E (snRNP-E)	2 3	0 3	3 3	5	0.334	0.000	2.162	29.35	207.04
P62306	Small nuclear ribonucleoprotein F (snRNP-F)	2 3	0 3	3 3	2	0.585	0.000	1.048	24.42	122.57
P62308	Small nuclear ribonucleoprotein G (snRNP-G)	0 3	0 3	1 3	2	0.000	0.000	1.154	17.11	44.10
P62314	Small nuclear ribonucleoprotein Sm D1 (Sm-D1) (snRN	2 3	0 3	3 3	4	0.389	0.000	2.728	36.97	224.61
P62316	Small nuclear ribonucleoprotein Sm D2 (Sm-D2) (snRN	0 3	0 3	3 3	4	0.000	0.000	0.495	38.14	73.05
P62318	Small nuclear ribonucleoprotein Sm D3 (Sm-D3) (snRN	0 3	0 3	3 3	2	0.000	0.000	0.422	24.60	75.41
P14678	Small nuclear ribonucleoprotein-associated proteins f	0 3	0 3	3 3	5	0.000	0.000	0.501	12.50	75.14
P61956	Small ubiquitin-related modifier 2 (SUMO-2) (Ubiquiti	3 3	0 3	0 3	1	0.389	0.000	0.000	12.63	92.27
Q13126	S-methyl-5'-thioadenosine phosphorylase (5'-methylt	2 3	0 3	0 3	4	0.281	0.000	0.000	22.97	85.51
O95295	SNARE-associated protein Snapin (Synaptosomal-assc	1 3	0 3	0 3	1	0.259	0.000	0.000	19.12	16.91
P05023	Sodium/potassium-transporting ATPase subunit alpha	2 3	0 3	0 3	10	0.207	0.000	0.000	11.44	212.48
P54709	Sodium/potassium-transporting ATPase subunit beta-	1 3	0 3	0 3	1	0.145	0.000	0.000	5.02	12.63
O94875	Sorbin and SH3 domain-containing protein 2 (Arg/Abl	0 3	0 3	2 3	5	0.000	0.000	0.161	7.09	59.86

accession	name	c_expcount	s_expcount	n_expcount	Peptides	c_empai	s_empai	n_empai	coverage	score
P30626	Sorcin (22 kDa protein) (CP-22) (V19)	2 3	0 3	0 3	5	0.763	0.000	0.000	21.21	105.48
Q99523	Sortilin (Neurotensin receptor 3) (NTR3) (Glycoprotein)	2 3	0 3	0 3	1	0.045	0.000	0.000	1.44	30.93
Q9UMY4	Sorting nexin-12	2 3	0 3	0 3	5	0.585	0.000	0.000	25.00	74.40
O60493	Sorting nexin-3 (Protein SDP3)	3 3	0 3	0 3	8	0.714	0.000	0.000	38.27	218.30
Q9Y5X2	Sorting nexin-8	1 3	0 3	0 3	1	0.072	0.000	0.000	3.44	11.97
P09486	SPARC (Secreted protein acidic and rich in cysteine) (C	0 3	3 3	0 3	13	0.000	1.184	0.000	39.93	435.90
Q9NUQ6	SPATS2-like protein (DNA polymerase-transactivated	0 3	0 3	3 3	3	0.000	0.000	0.109	9.14	56.89
Q13813	Spectrin alpha chain, brain (Spectrin, non-erythroid al	1 3	0 3	3 3	37	0.033	0.000	0.250	21.12	693.46
Q01082	Spectrin beta chain, brain 1 (Spectrin, non-erythroid b	1 3	0 3	3 3	34	0.024	0.000	0.311	20.77	722.39
P19623	Spermidine synthase (SPDSY) (Putrescine aminopropyl	3 3	0 3	0 3	9	0.513	0.000	0.000	35.43	205.71
P63208	S-phase kinase-associated protein 1 (Cyclin A/CDK2-a	2 3	0 3	0 3	1	0.179	0.000	0.000	7.36	26.99
Q13838	Spliceosome RNA helicase BAT1 (DEAD box protein U	0 3	0 3	2 3	6	0.000	0.000	0.520	24.53	92.38
Q15459	Splicing factor 3A subunit 1 (Spliceosome-associated p	0 3	0 3	1 3	1	0.000	0.000	0.044	3.03	12.42
Q12874	Splicing factor 3A subunit 3 (Spliceosome-associated p	0 3	0 3	1 3	3	0.000	0.000	0.199	7.98	45.40
O75533	Splicing factor 3B subunit 1 (Pre-mRNA-splicing factor	0 3	0 3	2 3	4	0.000	0.000	0.107	4.83	51.73
Q9BWJ5	Splicing factor 3B subunit 5 (SF3b5) (Pre-mRNA-splicin	0 3	0 3	1 3	1	0.000	0.000	0.389	17.44	14.79
P26368	Splicing factor U2AF 65 kDa subunit (U2 auxiliary fact	0 3	0 3	1 3	1	0.000	0.000	0.093	3.37	13.66
Q07955	Splicing factor, arginine/serine-rich 1 (pre-mRNA-splic	0 3	0 3	3 3	5	0.000	0.000	0.334	26.61	76.40
Q01130	Splicing factor, arginine/serine-rich 2 (Splicing factor S	0 3	0 3	3 3	2	0.000	0.000	0.166	11.31	31.69
P84103	Splicing factor, arginine/serine-rich 3 (Pre-mRNA-splic	0 3	0 3	3 3	4	0.000	0.000	0.472	28.66	70.36
Q16629	Splicing factor, arginine/serine-rich 7 (Splicing factor S	0 3	0 3	3 3	2	0.000	0.000	0.245	15.97	44.58
Q13242	Splicing factor, arginine/serine-rich 9 (Pre-mRNA-splic	0 3	0 3	1 3	1	0.000	0.000	0.096	4.98	16.53
P23246	Splicing factor, proline- and glutamine-rich (Polypyrim	0 3	0 3	3 3	11	0.000	0.000	0.537	21.64	302.47
Q8WW59	SPRY domain-containing protein 4	2 3	0 3	0 3	2	0.129	0.000	0.000	9.66	24.66
Q9GZT3	SRA stem-loop-interacting RNA-binding protein, mito	2 3	0 3	0 3	6	0.874	0.000	0.000	66.97	69.40
Q14247	Src substrate cortactin (Amplixin) (Oncogene EMS1)	2 3	0 3	2 3	4	0.078	0.000	0.058	9.09	65.34
O76061	Stanniocalcin-2 (STC-2) (Stanniocalcin-related protein	0 3	3 3	0 3	3	0.000	0.122	0.000	9.27	51.60
Q7KZF4	Staphylococcal nuclease domain-containing protein 1	3 3	0 3	3 3	26	0.122	0.000	0.883	34.29	1057.74
P16949	Stathmin (Phosphoprotein p19) (pp19) (Leukemia-ass	3 3	0 3	0 3	4	0.464	0.000	0.000	24.16	188.98
Q9UEW8	STE20/SPS1-related proline-alanine-rich protein kinas	1 3	0 3	0 3	1	0.066	0.000	0.000	4.94	13.47
Q9H2G2	STE20-like serine/threonine-protein kinase (STE20-like	1 3	0 3	0 3	1	0.023	0.000	0.000	1.70	17.27
Q9UJZ1	Stomatin-like protein 2 (SLP-2) (EPB72-like 2)	3 3	0 3	3 3	5	0.167	0.000	0.273	18.26	181.91
P38646	Stress-70 protein, mitochondrial (75 kDa glucose-regu	3 3	0 3	2 3	14	0.333	0.000	0.045	25.04	454.91
P31948	Stress-induced-phosphoprotein 1 (STI1) (Hsc70/Hsp90	2 3	0 3	0 3	2	0.059	0.000	0.000	4.24	54.36
P31040	Succinate dehydrogenase [ubiquinone] flavoprotein s	3 3	0 3	0 3	1	0.045	0.000	0.000	2.11	95.02
P21912	Succinate dehydrogenase [ubiquinone] iron-sulfur sul	2 3	0 3	0 3	2	0.138	0.000	0.000	8.21	52.21
Q9P2R7	Succinyl-CoA ligase [ADP-forming] subunit beta, mito	1 3	0 3	0 3	1	0.062	0.000	0.000	2.16	12.50
P53597	Succinyl-CoA ligase [GDP-forming] subunit alpha, mito	2 3	0 3	0 3	1	0.166	0.000	0.000	4.62	31.79
P55809	Succinyl-CoA:3-ketoadid-coenzyme A transferase 1, m	1 3	0 3	0 3	1	0.072	0.000	0.000	2.69	16.00
Q8NBJ7	Sulfatase-modifying factor 2 (C-alpha-formylglycine-g	2 3	0 3	0 3	3	0.226	0.000	0.000	13.62	66.60
O00391	Sulphydryl oxidase 1 (hQSOX) (Quiescin Q6)	0 3	2 3	0 3	3	0.000	0.066	0.000	6.29	44.88
Q9Y6N5	Sulfide:quinone oxidoreductase, mitochondrial	3 3	0 3	0 3	6	0.173	0.000	0.000	22.89	174.84
Q9BYN0	Sulfiredoxin-1	1 3	0 3	0 3	1	0.259	0.000	0.000	6.57	10.25
P51687	Sulfite oxidase, mitochondrial	1 3	0 3	0 3	1	0.061	0.000	0.000	2.39	17.73
P50225	Sulfotransferase 1A1 (Aryl sulfotransferase 1) (Pheno	2 3	0 3	0 3	2	0.172	0.000	0.000	12.54	57.31
Q9UBT2	SUMO-activating enzyme subunit 2 (Ubiquitin-like 1-ε	2 3	0 3	0 3	1	0.049	0.000	0.000	2.34	32.43
P63279	SUMO-conjugating enzyme UBC9 (SUMO-protein liga	2 3	0 3	0 3	3	0.520	0.000	0.000	22.78	49.76
P00441	Superoxide dismutase [Cu-Zn]	3 3	2 3	0 3	7	1.084	0.194	0.000	79.87	457.18
P04179	Superoxide dismutase [Mn], mitochondrial	3 3	1 3	3 3	10	1.474	0.359	0.359	54.05	616.41
O15260	Surfeit locus protein 4	1 3	0 3	0 3	2	0.389	0.000	0.000	10.78	26.13
Q9UH65	Switch-associated protein 70 (SWAP-70)	1 3	0 3	0 3	1	0.049	0.000	0.000	1.71	10.05
Q99536	Synaptic vesicle membrane protein VAT-1 homolog	3 3	0 3	0 3	5	0.268	0.000	0.000	21.12	178.99
O15498	Synaptobrevin homolog YKT6	1 3	0 3	0 3	1	0.136	0.000	0.000	6.57	14.24
O00161	Synaptosomal-associated protein 23 (SNAP-23) (Vesic	1 3	0 3	0 3	1	0.145	0.000	0.000	6.64	17.26
P34741	Syndecan-2 (SYND2) (Fibroglycan) (Heparan sulfate p	2 3	0 3	0 3	1	0.194	0.000	0.000	9.95	21.60
Q9Y490	Talin-1	3 3	0 3	3 3	69	0.489	0.000	0.056	38.02	2533.92
Q9Y4G6	Talin-2	1 3	0 3	2 3	7	0.098	0.000	0.013	3.46	102.70
O60784	Target of Myb protein 1	2 3	0 3	0 3	2	0.137	0.000	0.000	7.93	54.11
Q6SJ96	TATA box-binding protein-like protein 2 (TBP-like prot	2 3	0 3	0 3	1	0.105	0.000	0.000	5.07	21.02
O14907	Tax1-binding protein 3 (Tax interaction protein 1) (TIF	2 3	0 3	0 3	1	0.259	0.000	0.000	13.71	47.33
P17987	T-complex protein 1 subunit alpha (TCP-1-alpha) (CCT	3 3	0 3	0 3	11	0.283	0.000	0.000	25.54	298.12
P78371	T-complex protein 1 subunit beta (TCP-1-beta) (CCT-b	3 3	0 3	2 3	9	0.199	0.000	0.184	24.11	296.16
P50991	T-complex protein 1 subunit delta (TCP-1-delta) (CCT-	3 3	0 3	3 3	4	0.184	0.000	0.151	11.50	311.45
P48643	T-complex protein 1 subunit epsilon (TCP-1-epsilon) (	3 3	0 3	2 3	5	0.178	0.000	0.053	14.23	277.88
Q99832	T-complex protein 1 subunit eta (TCP-1-eta) (CCT-eta)	2 3	0 3	0 3	8	0.241	0.000	0.000	16.57	178.93
P49368	T-complex protein 1 subunit gamma (TCP-1-gamma) (	3 3	0 3	2 3	7	0.260	0.000	0.059	20.92	317.52
P50990	T-complex protein 1 subunit theta (TCP-1-theta) (CCT	3 3	0 3	2 3	11	0.265	0.000	0.174	28.10	405.02
P40227	T-complex protein 1 subunit zeta (TCP-1-zeta) (CCT-zε	3 3	0 3	3 3	13	0.430	0.000	0.088	35.40	532.01
P24821	Tenascin (TN) (Tenascin-C) (TN-C) (Hexabrachion) (Cy	0 3	2 3	0 3	4	0.000	0.045	0.000	2.32	64.59
P05452	Tetranectin (TN) (C-type lectin domain family 3 memb	0 3	2 3	0 3	7	0.000	0.950	0.000	35.64	183.22
Q8N5M4	Tetratricopeptide repeat protein 9C (TPR repeat prote	1 3	0 3	0 3	1	0.194	0.000	0.000	8.19	13.07
Q9BU02	Thiamine-triphosphatase (ThTPase)	2 3	0 3	0 3	2	0.155	0.000	0.000	23.48	25.58
P52888	Thimet oligopeptidase (Endopeptidase 24.15) (MP78)	1 3	0 3	0 3	1	0.048	0.000	0.000	2.76	13.27
P10599	Thioredoxin (Trx) (ATL-derived factor) (ADF) (Surface-	3 3	2 3	0 3	4	1.174	0.679	0.000	42.86	307.59
O95881	Thioredoxin domain-containing protein 12 (Thioredox	3 3	0 3	0 3	3	0.456	0.000	0.000	22.09	164.21
Q9BRA2	Thioredoxin domain-containing protein 17 (Thioredox	3 3	0 3	0 3	6	1.633	0.000	0.000	65.04	297.62
Q8NBS9	Thioredoxin domain-containing protein 5 (Thioredoxin	3 3	0 3	0 3	7	0.245	0.000	0.000	26.85	208.30
Q16881	Thioredoxin reductase 1, cytoplasmic (TR) (Thioredoxi	2 3	0 3	0 3	6	0.097	0.000	0.000	19.57	88.01
P30048	Thioredoxin-dependent peroxide reductase, mitochon	3 3	1 3	3 3	8	0.594	0.145	0.844	26.95	498.88
Q43396	Thioredoxin-like protein 1 (32 kDa thioredoxin-relate	2 3	0 3	0 3	2	0.177	0.000	0.000	11.76	63.01
Q86V81	THO complex subunit 4 (Tho4) (Ally of AML-1 and LEF	0 3	0 3	1 3	1	0.000	0.000	0.136	4.28	18.02
P26639	Threonyl-tRNA synthetase, cytoplasmic (Threonine--t	3 3	0 3	0 3	5	0.085	0.000	0.000	9.41	139.51

accession	name	c_expcount	s_expcount	n_expcount	Peptides	c_empai	s_empai	n_empai	coverage	score
P07996	Thrombospondin-1	3 3	3 3	3 3	13	0.180	0.108	0.197	13.76	818.34
P35442	Thrombospondin-2	0 3	1 3	1 3	3	0.000	0.112	0.036	5.29	51.86
P04216	Thy-1 membrane glycoprotein (Thy-1 antigen) (CDw9	3 3	0 3	3 3	4	0.602	0.000	1.254	24.84	256.83
P19971	Thymidine phosphorylase (TdRPase) (TP) (Platelet-de	1 3	0 3	0 3	1	0.083	0.000	0.000	3.11	13.33
P62328	Thymosin beta-4 (T beta-4) (Fx)	1 3	0 3	0 3	2	2.162	0.000	0.000	43.18	23.24
P05543	Thyroxine-binding globulin (T4-binding globulin) (Serp	0 3	1 3	0 3	1	0.000	0.096	0.000	2.41	12.46
Q07157	Tight junction protein ZO-1 (Zonula occludens protein	0 3	0 3	1 3	1	0.000	0.000	0.019	1.09	13.80
Q9H0E2	Toll-interacting protein	2 3	0 3	0 3	2	0.200	0.000	0.000	9.85	51.23
O14656	Torsin-1A (Torsin family 1 member A) (Dystonia 1 pro	2 3	0 3	0 3	1	0.096	0.000	0.000	4.52	27.47
Q9Y3C4	TP53RK-binding protein (PRPK-binding protein)	2 3	0 3	0 3	2	0.422	0.000	0.000	26.29	41.67
O43617	Trafficking protein particle complex subunit 3 (BET3 h	3 3	0 3	0 3	4	0.536	0.000	0.000	26.11	154.39
P37837	Transaldolase	3 3	2 3	0 3	10	0.489	0.086	0.000	29.38	393.51
Q15369	Transcription elongation factor B polypeptide 1 (RNA	3 3	0 3	0 3	5	0.704	0.000	0.000	50.00	104.35
Q15370	Transcription elongation factor B polypeptide 2 (RNA	2 3	0 3	0 3	2	0.556	0.000	0.000	31.36	58.84
Q00059	Transcription factor A, mitochondrial (mtTFA) (Mitoch	0 3	0 3	1 3	1	0.000	0.000	0.089	4.88	11.69
P20290	Transcription factor BTF3 (RNA polymerase B transcri	3 3	0 3	3 3	3	0.346	0.000	0.408	20.39	183.76
Q13263	Transcription intermediary factor 1-beta (TIF1-beta) (	0 3	0 3	1 3	1	0.000	0.000	0.048	2.40	13.99
P11308	Transcriptional regulator ERG (Transforming protein E	0 3	1 3	0 3	1	0.000	0.075	0.000	4.12	11.05
Q9Y4P3	Transducin beta-like protein 2 (WS beta-transducin re	0 3	0 3	1 3	1	0.000	0.000	0.062	2.91	16.03
P02786	Transferrin receptor protein 1 (TfR1) (T9) (p90)	1 3	0 3	0 3	3	0.124	0.000	0.000	4.74	35.39
Q15582	Transforming growth factor-beta-induced protein ig-f	1 3	3 3	3 3	6	0.049	0.155	0.075	15.81	370.74
P61586	Transforming protein RhoA (H12)	3 3	0 3	2 3	9	1.510	0.000	0.166	54.40	570.66
Q01995	Transgelin (Smooth muscle protein 22-alpha) (SM22-a	3 3	3 3	3 3	32	8.478	0.608	1.998	89.05	2978.90
P37802	Transgelin-2 (SM22-alpha homolog)	3 3	2 3	3 3	21	5.936	0.334	1.212	83.42	1660.02
P55072	Transitional endoplasmic reticulum ATPase (TER ATPa	3 3	0 3	3 3	34	0.756	0.000	0.419	52.98	1428.58
P29401	Transketolase (TK)	3 3	0 3	0 3	17	0.524	0.000	0.000	47.67	781.86
Q92616	Translational activator GCN1 (GCN1-like protein 1) (H	1 3	0 3	0 3	1	0.011	0.000	0.000	0.75	15.71
P13693	Translationally-controlled tumor protein (TCTP) (p23)	3 3	1 3	2 3	7	1.335	0.520	0.233	28.49	420.45
Q15631	Translin	2 3	0 3	0 3	2	0.129	0.000	0.000	12.28	26.34
Q99598	Translin-associated protein X (Translin-associated fac	2 3	0 3	0 3	1	0.105	0.000	0.000	6.55	33.69
P43307	Translocon-associated protein subunit alpha (TRAP-al	0 3	0 3	3 3	1	0.000	0.000	0.212	5.24	38.99
P51571	Translocon-associated protein subunit delta (TRAP-de	3 3	0 3	3 3	7	0.591	0.000	2.588	32.37	449.91
P49755	Transmembrane emp24 domain-containing protein 1	3 3	0 3	2 3	4	0.244	0.000	0.155	12.79	89.82
Q15363	Transmembrane emp24 domain-containing protein 2	3 3	0 3	2 3	4	0.294	0.000	0.389	20.40	149.24
Q7Z7H5	Transmembrane emp24 domain-containing protein 4	0 3	0 3	1 3	1	0.000	0.000	0.145	7.49	13.64
Q9Y3A6	Transmembrane emp24 domain-containing protein 5	1 3	0 3	0 3	1	0.194	0.000	0.000	10.04	12.11
Q9Y3B3	Transmembrane emp24 domain-containing protein 7	0 3	0 3	1 3	1	0.000	0.000	0.129	5.80	13.80
Q9BVK6	Transmembrane emp24 domain-containing protein 9	3 3	0 3	3 3	4	0.424	0.000	0.302	16.17	249.67
Q9BVC6	Transmembrane protein 109 (Mitsugumin-23) (Mg23	2 3	0 3	1 3	1	0.179	0.000	0.179	4.94	95.53
Q9H061	Transmembrane protein 126A	2 3	0 3	0 3	1	0.194	0.000	0.000	10.26	47.23
Q92973	Transportin-1 (Importin beta-2) (Karyopherin beta-2)	2 3	0 3	1 3	3	0.073	0.000	0.043	4.01	102.76
P53007	Tricarboxylate transport protein, mitochondrial (Citra	2 3	0 3	1 3	1	0.086	0.000	0.086	3.86	40.42
P40939	Trifunctional enzyme subunit alpha, mitochondrial (T	3 3	0 3	3 3	24	0.378	0.000	0.657	38.79	831.91
P55084	Trifunctional enzyme subunit beta, mitochondrial (T	3 3	0 3	3 3	7	0.086	0.000	0.304	18.35	195.32
P22102	Trifunctional purine biosynthetic protein adenosine-3	2 3	0 3	0 3	3	0.051	0.000	0.000	5.15	37.47
P60174	Triosephosphate isomerase (TIM) (Triose-phosphate i	3 3	3 3	2 3	19	3.477	1.110	0.122	77.11	1830.78
O14773	Tripeptidyl-peptidase 1 (TPP-1) (Tripeptidyl-peptidase	3 3	0 3	1 3	2	0.118	0.000	0.093	7.28	97.65
Q9UI30	TRM112-like protein	3 3	0 3	0 3	2	0.422	0.000	0.000	21.60	76.16
Q9NYL9	Tropomodulin-3 (Ubiquitous tropomodulin) (U-Tmod	0 3	0 3	3 3	2	0.000	0.000	0.132	11.65	35.47
P09493	Tropomyosin alpha-1 chain (Tropomyosin-1) (Alpha-t	1 3	0 3	3 3	16	0.225	0.000	1.344	38.03	559.62
P06753	Tropomyosin alpha-3 chain (Tropomyosin-3) (Gamma	3 3	1 3	3 3	21	0.369	0.311	1.612	48.59	989.71
P67936	Tropomyosin alpha-4 chain (Tropomyosin-4) (TM30p	3 3	3 3	3 3	28	0.918	0.358	3.649	78.23	1805.69
P07951	Tropomyosin beta chain (Tropomyosin-2) (Beta-tropo	3 3	2 3	3 3	16	0.367	0.152	1.333	44.37	1037.17
P23381	Tryptophanyl-tRNA synthetase, cytoplasmic (Tryptopl	3 3	0 3	0 3	6	0.161	0.000	0.000	21.87	132.24
Q71U36	Tubulin alpha-1A chain (Tubulin B-alpha-1) (Tubulin a	3 3	1 3	0 3	22	2.383	0.089	0.000	60.98	1611.60
P68363	Tubulin alpha-1B chain (Tubulin alpha-ubiquitous cha	3 3	0 3	3 3	21	1.785	0.000	0.600	57.87	1449.17
Q9BQE3	Tubulin alpha-1C chain (Tubulin alpha-6 chain) (Alph	3 3	0 3	0 3	19	2.046	0.000	0.000	55.90	1030.71
P07437	Tubulin beta chain (Tubulin beta-5 chain)	3 3	0 3	3 3	35	6.314	0.000	1.993	69.37	2522.54
Q13885	Tubulin beta-2A chain	3 3	0 3	0 3	31	4.376	0.000	0.000	53.26	1422.67
P68371	Tubulin beta-2C chain (Tubulin beta-2 chain)	3 3	0 3	0 3	34	6.096	0.000	0.000	68.31	1509.26
Q13509	Tubulin beta-3 chain (Tubulin beta-III) (Tubulin beta-4	3 3	0 3	0 3	23	3.390	0.000	0.000	43.78	1092.41
P04350	Tubulin beta-4 chain (Tubulin 5 beta)	2 3	0 3	0 3	20	3.392	0.000	0.000	49.10	474.93
Q9BUF5	Tubulin beta-6 chain	3 3	0 3	0 3	23	2.193	0.000	0.000	57.17	957.27
Q3ZCM7	Tubulin beta-8 chain	1 3	0 3	0 3	5	0.585	0.000	0.000	10.81	96.22
O75347	Tubulin-specific chaperone A (Tubulin-folding cofacto	3 3	1 3	0 3	7	1.019	0.233	0.000	55.56	336.61
O43399	Tumor protein D54 (hD54) (Tumor protein D52-like 2)	3 3	0 3	0 3	7	0.541	0.000	0.000	44.66	285.34
Q12792	Twinfilin-1 (Protein A6) (Protein tyrosine kinase 9)	3 3	0 3	0 3	1	0.093	0.000	0.000	3.71	90.89
Q6IBS0	Twinfilin-2 (Twinfilin-1-like protein) (A6-related prote	3 3	0 3	1 3	2	0.137	0.000	0.089	8.60	111.30
P54577	Tyrosyl-tRNA synthetase, cytoplasmic (Tyrosyl--tRNA	3 3	0 3	1 3	3	0.049	0.000	0.049	12.88	84.69
P09234	U1 small nuclear ribonucleoprotein C (U1 snRNP C)	0 3	0 3	1 3	2	0.000	0.000	1.512	13.21	29.60
P09661	U2 small nuclear ribonucleoprotein A' (U2 snRNP-A')	0 3	0 3	2 3	4	0.000	0.000	0.668	20.00	69.35
P08579	U2 small nuclear ribonucleoprotein B''	0 3	0 3	1 3	1	0.000	0.000	0.166	10.22	14.95
O15042	U2-associated protein SR140 (140 kDa Ser/Arg-rich do	0 3	0 3	1 3	1	0.000	0.000	0.032	1.46	15.97
O75643	U5 small nuclear ribonucleoprotein 200 kDa helicase	0 3	0 3	3 3	4	0.000	0.000	0.039	3.75	66.94
Q9Y333	U6 snRNA-associated Sm-like protein Lsm2 (snRNP co	2 3	0 3	2 3	4	0.504	0.000	0.259	68.42	98.30
P62312	U6 snRNA-associated Sm-like protein Lsm6	0 3	0 3	1 3	1	0.000	0.000	0.389	13.75	11.56
O95777	U6 snRNA-associated Sm-like protein Lsm8	0 3	0 3	1 3	1	0.000	0.000	0.389	23.96	17.52
P54578	Ubiquitin carboxyl-terminal hydrolase 14 (Ubiquitin th	2 3	0 3	0 3	4	0.134	0.000	0.000	9.92	101.90
P45974	Ubiquitin carboxyl-terminal hydrolase 5 (Ubiquitin thi	2 3	0 3	0 3	2	0.044	0.000	0.000	3.50	56.71
Q93009	Ubiquitin carboxyl-terminal hydrolase 7 (Ubiquitin thi	0 3	0 3	1 3	1	0.000	0.000	0.027	1.00	11.16
P09936	Ubiquitin carboxyl-terminal hydrolase isozyme L1 (UC	3 3	0 3	0 3	8	0.744	0.000	0.000	45.29	243.15
P15374	Ubiquitin carboxyl-terminal hydrolase isozyme L3 (UC	3 3	0 3	0 3	3	0.319	0.000	0.000	16.52	112.67

accession	name	c_expcount	s_expcount	n_expcount	Peptides	c_empai	s_empai	n_empai	coverage	score
Q92890	Ubiquitin fusion degradation protein 1 homolog (UB f	1 3	0 3	0 3	1	0.110	0.000	0.000	7.82	13.94
Q96FW1	Ubiquitin thioesterase OTUB1 (Otubain-1) (OTU doma	2 3	0 3	0 3	2	0.188	0.000	0.000	12.55	62.55
O14933	Ubiquitin/ISG15-conjugating enzyme E2 L6 (Ubiquitin	2 3	0 3	0 3	3	0.495	0.000	0.000	39.22	79.68
P62987	Ubiquitin-60S ribosomal protein L40 (Ubiquitin A-52 r	3 3	2 3	3 3	8	1.105	0.392	0.515	47.66	815.02
P51668	Ubiquitin-conjugating enzyme E2 D1 (Ubiquitin-prote	1 3	0 3	0 3	1	0.468	0.000	0.000	7.48	12.74
P62837	Ubiquitin-conjugating enzyme E2 D2 (Ubiquitin-prote	3 3	0 3	0 3	3	0.880	0.000	0.000	30.61	116.42
P61086	Ubiquitin-conjugating enzyme E2 K (Ubiquitin-conjug	3 3	0 3	0 3	4	0.232	0.000	0.000	35.50	102.73
P68036	Ubiquitin-conjugating enzyme E2 L3 (Ubiquitin-protei	3 3	0 3	0 3	6	0.999	0.000	0.000	48.70	210.25
P61088	Ubiquitin-conjugating enzyme E2 N (Ubiquitin-protein	3 3	1 3	0 3	8	1.042	0.179	0.000	61.18	310.97
Q13404	Ubiquitin-conjugating enzyme E2 variant 1 (UEV-1) (C	3 3	0 3	0 3	5	0.751	0.000	0.000	28.57	229.86
Q15819	Ubiquitin-conjugating enzyme E2 variant 2 (MMS2) (E	3 3	0 3	0 3	5	0.706	0.000	0.000	33.10	210.73
P61960	Ubiquitin-fold modifier 1	2 3	0 3	0 3	2	0.811	0.000	0.000	58.82	39.60
P22314	Ubiquitin-like modifier-activating enzyme 1 (Ubiquitin	3 3	0 3	0 3	24	0.424	0.000	0.000	35.92	959.02
P41226	Ubiquitin-like modifier-activating enzyme 7 (Ubiquitin	2 3	0 3	0 3	2	0.060	0.000	0.000	5.24	50.25
O60701	UDP-glucose 6-dehydrogenase (UDP-Glc dehydrogenase	3 3	0 3	0 3	15	0.441	0.000	0.000	47.37	404.03
Q9NYU2	UDP-glucose:glycoprotein glucosyltransferase 1 (UDP	3 3	0 3	2 3	11	0.100	0.000	0.048	10.03	342.68
Q16222	UDP-N-acetylhexosamine pyrophosphorylase (Antigen	3 3	0 3	0 3	3	0.082	0.000	0.000	8.05	86.56
Q9Y3C8	Ufm1-conjugating enzyme 1 (Ubiquitin-fold modifier-	2 3	0 3	0 3	2	0.179	0.000	0.000	20.96	29.65
P30085	UMP-CMP kinase (Cytidylate kinase) (Deoxycytidylate	3 3	0 3	3 3	10	1.174	0.000	0.155	53.57	372.41
Q6PIY5	Uncharacterized protein C1orf228 (p40)	1 3	0 3	0 3	1	0.077	0.000	0.000	5.45	12.01
Q9BUH6	Uncharacterized protein C9orf142	1 3	0 3	0 3	1	0.179	0.000	0.000	5.88	12.47
Q9Y3I0	UPF0027 protein C22orf28	1 3	0 3	3 3	8	0.072	0.000	0.535	21.98	185.66
Q5TGZ0	UPF0327 protein C1orf151	1 3	0 3	0 3	1	0.585	0.000	0.000	10.26	12.25
Q9H7C9	UPF0366 protein C11orf67	1 3	0 3	0 3	2	0.425	0.000	0.000	16.39	29.72
Q6IAA8	UPF0404 protein C11orf59	3 3	0 3	3 3	4	0.995	0.000	0.259	42.86	289.42
Q8WUH6	UPF0444 transmembrane protein C12orf23	2 3	0 3	0 3	1	0.292	0.000	0.000	22.41	31.96
Q969H8	UPF0556 protein C19orf10 (Stromal cell-derived grow	3 3	2 3	0 3	6	2.215	0.334	0.000	32.95	430.75
Q9Y224	UPF0568 protein C14orf166	2 3	0 3	3 3	13	0.138	0.000	1.075	58.20	317.48
Q9NWW4	UPF0587 protein C1orf123	3 3	0 3	0 3	1	0.212	0.000	0.000	10.63	57.28
Q6P1X6	UPF0598 protein C8orf82	2 3	0 3	0 3	1	0.145	0.000	0.000	6.94	43.72
Q9P1F3	UPF0727 protein C6orf115	1 3	0 3	0 3	1	0.585	0.000	0.000	16.05	12.59
P06132	Uroporphyrinogen decarboxylase (URO-D)	2 3	0 3	0 3	2	0.122	0.000	0.000	16.35	28.30
Q16851	UTP--glucose-1-phosphate uridylyltransferase (UDP-g	3 3	0 3	0 3	8	0.250	0.000	0.000	26.97	252.01
P54727	UV excision repair protein RAD23 homolog B (hHR23E	2 3	0 3	0 3	1	0.129	0.000	0.000	4.65	25.43
Q9BZF9	Uveal autoantigen with coiled-coil domains and ankyr	0 3	1 3	3 3	3	0.000	0.017	0.026	2.68	46.86
Q9UBQ0	Vacuolar protein sorting-associated protein 29 (Vesicle	3 3	0 3	0 3	3	0.495	0.000	0.000	25.27	118.12
Q96QK1	Vacuolar protein sorting-associated protein 35 (Vesicle	3 3	0 3	0 3	7	0.116	0.000	0.000	10.05	165.37
Q9BRG1	Vacuolar protein-sorting-associated protein 25 (hVps)	2 3	0 3	0 3	4	0.382	0.000	0.000	25.00	65.53
P26640	Valyl-tRNA synthetase (Valine--tRNA ligase) (ValRS) (P	3 3	0 3	3 3	8	0.087	0.000	0.043	9.49	230.09
P19320	Vascular cell adhesion protein 1 (V-CAM 1) (INCAM-1)	2 3	0 3	0 3	9	0.230	0.000	0.000	18.00	182.01
P50552	Vasodilator-stimulated phosphoprotein (VASP)	0 3	0 3	1 3	1	0.000	0.000	0.122	3.68	17.71
Q6EMK4	Vasorin (Protein slit-like 2)	3 3	2 3	0 3	3	0.151	0.098	0.000	8.77	198.90
P49748	Very long-chain specific acyl-CoA dehydrogenase, mit	3 3	0 3	0 3	5	0.115	0.000	0.000	14.66	126.82
P63027	Vesicle-associated membrane protein 2 (VAMP-2) (Syn	3 3	0 3	0 3	3	0.927	0.000	0.000	28.45	264.88
Q15836	Vesicle-associated membrane protein 3 (VAMP-3) (Syn	3 3	0 3	0 3	4	1.273	0.000	0.000	50.00	249.42
Q9POL0	Vesicle-associated membrane protein-associated pro	0 3	0 3	1 3	1	0.000	0.000	0.136	5.62	11.11
P46459	Vesicle-fusing ATPase (N-ethylmaleimide-sensitive fus	3 3	0 3	0 3	5	0.094	0.000	0.000	9.68	171.69
O75396	Vesicle-trafficking protein SEC22b (SEC22 vesicle-traf	2 3	0 3	0 3	6	0.420	0.000	0.000	31.16	113.69
Q00341	Vigilin (High density lipoprotein-binding protein) (HDL	3 3	0 3	3 3	20	0.037	0.000	0.297	27.84	491.08
P08670	Vimentin	3 3	3 3	3 3	63	0.477	1.449	8.701	84.33	4226.48
P18206	Vinculin (Metavinculin)	3 3	2 3	2 3	36	0.420	0.037	0.050	40.04	1284.78
Q7Z5L0	Vitelline membrane outer layer protein 1 homolog	2 3	2 3	0 3	3	0.194	0.609	0.000	19.80	203.04
P04004	Vitronectin (Serum-spreading factor) (S-protein) (V75	1 3	0 3	1 3	1	0.083	0.000	0.083	3.14	31.03
P21796	Voltage-dependent anion-selective channel protein 1	3 3	0 3	3 3	15	0.846	0.000	2.793	68.55	660.20
P45880	Voltage-dependent anion-selective channel protein 2	3 3	0 3	3 3	9	0.446	0.000	1.154	39.80	403.36
Q9Y277	Voltage-dependent anion-selective channel protein 3	1 3	0 3	3 3	8	0.122	0.000	0.778	28.62	160.11
Q9NY47	Voltage-dependent calcium channel subunit alpha-2/	1 3	0 3	0 3	1	0.035	0.000	0.000	2.35	20.51
P38606	V-type proton ATPase catalytic subunit A (V-ATPase s	2 3	0 3	0 3	5	0.130	0.000	0.000	13.13	88.68
P21281	V-type proton ATPase subunit B, brain isoform (V-ATP	3 3	0 3	3 3	5	0.127	0.000	0.143	18.59	197.21
P36543	V-type proton ATPase subunit E 1 (V-ATPase subunit E	1 3	0 3	0 3	2	0.292	0.000	0.000	11.95	21.19
Q16864	V-type proton ATPase subunit F (V-ATPase subunit F)	1 3	0 3	0 3	2	0.668	0.000	0.000	23.53	21.34
O75083	WD repeat-containing protein 1 (Actin-interacting pro	3 3	0 3	3 3	11	0.293	0.000	0.212	34.65	519.59
Q9BZH6	WD repeat-containing protein 11 (Bromodomain and	0 3	0 3	1 3	1	0.000	0.000	0.027	1.47	12.65
Q9GZS3	WD repeat-containing protein 61 (Meiotic recombina	1 3	0 3	1 3	1	0.145	0.000	0.145	6.56	25.76
Q969T9	WW domain-binding protein 2 (WBP-2)	1 3	0 3	0 3	1	0.212	0.000	0.000	5.36	13.62
Q9NQW7	Xaa-Pro aminopeptidase 1 (X-Pro aminopeptidase 1) (	2 3	0 3	0 3	2	0.080	0.000	0.000	4.33	39.52
P12955	Xaa-Pro dipeptidase (X-Pro dipeptidase) (Proline dipe	3 3	0 3	0 3	5	0.141	0.000	0.000	18.05	108.50
O75191	Xylulose kinase (Xylulokinase)	0 3	0 3	3 3	1	0.000	0.000	0.075	2.43	25.09
Q9UPT8	Zinc finger CCCH domain-containing protein 4	0 3	0 3	1 3	1	0.000	0.000	0.040	1.23	14.21
Q15942	Zyxin (Zyxin-2)	2 3	0 3	0 3	3	0.108	0.000	0.000	14.69	55.09