Supplemental Table 6. Comparison of protein levels between adult RBCs and reticulocytes, and cord RBCs and reticulocytes. See legend for Supplemental Table 4 for experimental details. Values show the ratio of protein levels between RBCs and reticulocytes in membrane (A) and cytosol (B) fractions.

Supplemental Table 6A

Accession	Description	Score	Coverage	Unique Peptides	Peptides	PSMs	membrane fraction Adult RBC/retic	membrane fraction cord RBC/retic
P31946	14-3-3 protein beta/alpha OS=Homo sapiens GN=YWHAB PE=1 SV=3 - [1433B_HUMAN]	50.55	34.96	3	8	15	1.173	0.855
P62258	14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1 - [1433E_HUMAN]	77.85	38.82	9	12	22	0.700	1.044
Q04917	14-3-3 protein eta OS=Homo sapiens GN=YWHAH PE=1 SV=4 - [1433F_HUMAN]	43.88	29.27	4	8	13	0.405	0.294
P61981	14-3-3 protein gamma OS=Homo sapiens GN=YWHAG PE=1 SV=2 - [1433G_HUMAN]	65.13	40.49	7	11	19	0.548	0.559
P27348	14-3-3 protein theta OS=Homo sapiens GN=YWHAQ PE=1 SV=1 - [1433T_HUMAN]	49.95	30.61	2	7	14	0.332	0.391
P63104	14-3-3 protein zeta/delta OS=Homo sapiens GN=YWHAZ PE=1 SV=1 - [1433Z_HUMAN]	54.47	35.10	4	8	15	0.469	0.772
P09543	2',3'-cyclic-nucleotide 3'-phosphodiesterase OS=Homo sapiens GN=CNP PE=1 SV=2 - [CN37_HUMAN]	107.23	36.82	18	19	34	2.099	1.759
P62333	26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1 - [PRS10_HUMAN]	69.71	27.76	11	11	22	1.395	0.922
P62191	26S protease regulatory subunit 4 OS=Homo sapiens GN=PSMC1 PE=1 SV=1 - [PRS4_HUMAN]	104.26	30.45	14	15	31	1.708	0.892
P17980	26S protease regulatory subunit 6A OS=Homo sapiens GN=PSMC3 PE=1 SV=3 - [PRS6A_HUMAN]	77.08	35.08	14	14	23	1.303	0.835
P43686	26S protease regulatory subunit 6B OS=Homo sapiens GN=PSMC4 PE=1 SV=2 - [PRS6B_HUMAN]	66.58	27.27	12	12	19	1.399	0.817
P35998	26S protease regulatory subunit 7 OS=Homo sapiens GN=PSMC2 PE=1 SV=3 - [PRS7_HUMAN]	173.63	47.34	20	20	49	1.480	0.847
Q99460	26S proteasome non-ATPase regulatory subunit 1 OS=Homo sapiens GN=PSMD1 PE=1 SV=2 - [PSMD1_HUMAN]	144.55	29.17	25	25	44	1.271	0.779
O00231	26S proteasome non-ATPase regulatory subunit 11 OS=Homo sapiens GN=PSMD11 PE=1 SV=3 - [PSD11_HUMAN]	79.96	34.60	14	14	25	1.219	0.734
O00232	26S proteasome non-ATPase regulatory subunit 12 OS=Homo sapiens GN=PSMD12 PE=1 SV=3 - [PSD12_HUMAN]	89.37	28.73	15	15	27	0.833	0.701
Q9UNM6	26S proteasome non-ATPase regulatory subunit 13 OS=Homo sapiens GN=PSMD13 PE=1 SV=2 - [PSD13_HUMAN]	84.10	31.91	13	13	26	1.135	0.740
O00487	26S proteasome non-ATPase regulatory subunit 14 OS=Homo sapiens GN=PSMD14 PE=1 SV=1 - [PSDE_HUMAN]	46.17	15.81	6	6	15	0.851	0.735
P55036	26S proteasome non-ATPase regulatory subunit 4 OS=Homo sapiens GN=PSMD4 PE=1 SV=1 - [PSMD4_HUMAN]	33.77	19.63	6	6	10	1.331	0.749
Q15008	26S proteasome non-ATPase regulatory subunit 6 OS=Homo sapiens GN=PSMD6 PE=1 SV=1 - [PSMD6_HUMAN]	81.35	27.76	14	14	24	1.230	0.732
P48556	26S proteasome non-ATPase regulatory subunit 8 OS=Homo sapiens GN=PSMD8 PE=1 SV=2 - [PSMD8_HUMAN]	38.56	14.29	7	7	13	1.021	0.742
Q13442	28 kDa heat- and acid-stable phosphoprotein OS=Homo sapiens GN=PDAP1 PE=1 SV=1 - [HAP28_HUMAN]	54.27	50.28	8	8	15	0.115	0.204
Q99714	3-hydroxyacyl-CoA dehydrogenase type-2 OS=Homo sapiens GN=HSD17B10 PE=1 SV=3 - [HCD2_HUMAN]	31.97	27.97	5	5	9	0.234	0.138
P42765	3-ketoacyl-CoA thiolase, mitochondrial OS=Homo sapiens GN=ACAA2 PE=1 SV=2 - [THIM_HUMAN]	28.57	21.41	8	8	9	0.376	0.171
Q96RE3	36 kDa muscleblind protein EXP36 OS=Homo sapiens GN=MBNL1 PE=2 SV=1 - [Q96RE3_HUMAN]	5.74	7.01	2	2	2	0.114	0.154
P49189	4-trimethylaminobutyraldehyde dehydrogenase OS=Homo sapiens GN=ALDH9A1 PE=1 SV=3 - [AL9A1_HUMAN]	12.92	5.87	3	3	4	0.186	0.490
P46783	40S ribosomal protein S10 OS=Homo sapiens GN=RPS10 PE=1 SV=1 - [RS10_HUMAN]	25.40	24.24	4	4	8	0.157	0.156
P62280	40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=1 SV=3 - [RS11_HUMAN]	28.21	21.52	5	5	9	0.112	0.158
P25398	40S ribosomal protein S12 OS=Homo sapiens GN=RPS12 PE=1 SV=3 - [RS12_HUMAN]	16.43	21.97	3	3	5	0.223	0.233
P62277	40S ribosomal protein S13 OS=Homo sapiens GN=RPS13 PE=1 SV=2 - [RS13_HUMAN]	31.70	35.10	7	7	10	0.146	0.116
P62263	40S ribosomal protein S14 OS=Homo sapiens GN=RPS14 PE=1 SV=3 - [RS14_HUMAN]	24.03	23.84	4	4	7	0.222	0.142
P62249	40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=1 SV=2 - [RS16_HUMAN]	23.57	29.45	6	6	8	0.050	0.093
P0CW22	40S ribosomal protein S17-like OS=Homo sapiens GN=RPS17L PE=3 SV=1 - [RS17L_HUMAN]	13.40	8.89	2	2	4	0.245	0.262
P62269	40S ribosomal protein S18 OS=Homo sapiens GN=RPS18 PE=1 SV=3 - [RS18_HUMAN]	27.91	34.87	6	6	9	0.304	0.159
P39019	40S ribosomal protein S19 OS=Homo sapiens GN=RPS19 PE=1 SV=2 - [RS19_HUMAN]	59.36	41.38	8	8	16	0.045	0.099
P15880	40S ribosomal protein S2 OS=Homo sapiens GN=RPS2 PE=1 SV=2 - [RS2_HUMAN]	24.04	23.21	7	7	8	0.096	0.129
P60866	40S ribosomal protein S20 OS=Homo sapiens GN=RPS20 PE=1 SV=1 - [RS20_HUMAN]	25.74	30.25	4	4	9	0.660	0.303
Q8WVC2	40S ribosomal protein S21 OS=Homo sapiens GN=RPS21 PE=2 SV=1 - [Q8WVC2_HUMAN]	11.67	19.75	2	2	4	0.193	0.175
P62266	40S ribosomal protein S23 OS=Homo sapiens GN=RPS23 PE=1 SV=3 - [RS23_HUMAN]	39.86	20.98	3	3	11	0.383	0.248
P62851	40S ribosomal protein S25 OS=Homo sapiens GN=RPS25 PE=1 SV=1 - [RS25_HUMAN]	11.40	15.20	2	2	3	0.063	0.113
P62854	40S ribosomal protein S26 OS=Homo sapiens GN=RPS26 PE=1 SV=3 - [RS26_HUMAN]	22.48	20.87	2	2	7	0.361	0.229
P42677	40S ribosomal protein S27 OS=Homo sapiens GN=RPS27 PE=1 SV=3 - [RS27_HUMAN]	9.31	25.00	2	2	3	0.082	0.132
P62857	40S ribosomal protein S28 OS=Homo sapiens GN=RPS28 PE=1 SV=1 - [RS28_HUMAN]	7.63	30.43	2	2	2		0.086
P23396	40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2 - [RS3_HUMAN]	63.99	45.27	11	11	19	0.119	0.133
P61247	40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2 - [RS3A_HUMAN]	56.35	28.03	9	9	18	0.175	0.121
P62701	40S ribosomal protein S4, X isoform OS=Homo sapiens GN=RPS4X PE=1 SV=2 - [RS4X_HUMAN]	71.84	28.14	11	11	23	0.253	0.176
P46782	40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=4 - [RS5_HUMAN]	23.05	19.61	4	4	7	0.058	0.129
P62753	40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=1 SV=1 - [RS6_HUMAN]	40.96	20.48	7	7	12	0.053	0.122
P62081	40S ribosomal protein S7 OS=Homo sapiens GN=RPS7 PE=1 SV=1 - [RS7_HUMAN]	28.41	13.40	3	3	8	0.044	0.109
P46781	40S ribosomal protein S9 OS=Homo sapiens GN=RPS9 PE=1 SV=3 - [RS9_HUMAN]	27.73	45.36	9	9	9	0.041	0.108
Q13131	5'-AMP-activated protein kinase catalytic subunit alpha-1 OS=Homo sapiens GN=PRKAA1 PE=1 SV=4 - [AAPK1_HUMAN]	7.63	3.58	2	2	2	0.053	0.226
P17858	6-phosphofructokinase, liver type OS=Homo sapiens GN=PFKL PE=1 SV=6 - [K6PL_HUMAN]	103.94	22.95	16	17	32	1.902	1.204
P08237	6-phosphofructokinase, muscle type OS=Homo sapiens GN=PFKM PE=1 SV=2 - [K6PF_HUMAN]	54.70	15.51	8	10	17	3.024	2.147
F5H7U0	6-phosphogluconate dehydrogenase, decarboxylating OS=Homo sapiens GN=PGD PE=3 SV=1 - [F5H7U0_HUMAN]	55.22	21.69	11	11	17	0.138	0.331
P10809	60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 - [CH60_HUMAN]	219.85	37.00	22	22	70	0.206	0.131
P05387	60S acidic ribosomal protein P2 OS=Homo sapiens GN=RPLP2 PE=1 SV=1 - [RLA2_HUMAN]	24.28	24.35	3	3	6	0.123	0.146

P27635	60S ribosomal protein L10 OS=Homo sapiens GN=RPL10 PE=1 SV=4 - [RL10_HUMAN]	5.74	7.94	2	2	2	0.135	0.170
P62906	60S ribosomal protein L10a OS=Homo sapiens GN=RPL10A PE=1 SV=2 - [RL10A_HUMAN]	19.53	27.19	5	5	6	0.228	0.148
P30050	60S ribosomal protein L12 OS=Homo sapiens GN=RPL12 PE=1 SV=1 - [RL12_HUMAN]	23.65	47.88	6	6	7	0.132	0.147
P26373	60S ribosomal protein L13 OS=Homo sapiens GN=RPL13 PE=1 SV=4 - [RL13_HUMAN]	62.25	36.02	9	9	16	0.111	0.119
P40429	60S ribosomal protein L13a OS=Homo sapiens GN=RPL13A PE=1 SV=2 - [RL13A_HUMAN]	30.33	19.70	5	5	10	0.044	0.120
P50914	60S ribosomal protein L14 OS=Homo sapiens GN=RPL14 PE=1 SV=4 - [RL14_HUMAN]	31.97	31.16	5	6	10	0.306	0.187
P18621	60S ribosomal protein L17 OS=Homo sapiens GN=RPL17 PE=1 SV=3 - [RL17_HUMAN]	18.68	19.57	4	4	6	0.341	0.175
Q07020	60S ribosomal protein L18 OS=Homo sapiens GN=RPL18 PE=1 SV=2 - [RL18_HUMAN]	10.49	20.21	3	3	3	0.208	0.223
P84098	60S ribosomal protein L19 OS=Homo sapiens GN=RPL19 PE=1 SV=1 - [RL19_HUMAN]	23.18	16.33	3	4	8	0.332	0.177
P46778	60S ribosomal protein L21 OS=Homo sapiens GN=RPL21 PE=1 SV=2 - [RL21_HUMAN]	8.26	13.75	3	3	3	0.305	0.193
P62829	60S ribosomal protein L23 OS=Homo sapiens GN=RPL23 PE=1 SV=1 - [RL23_HUMAN]	16.74	27.14	3	3	5	0.083	0.116
P62750	60S ribosomal protein L23a OS=Homo sapiens GN=RPL23A PE=1 SV=1 - [RL23A_HUMAN]	47.29	35.26	9	9	15	0.158	0.140
P61254	60S ribosomal protein L26 OS=Homo sapiens GN=RPL26 PE=1 SV=1 - [RL26_HUMAN]	23.62	33.10	6	6	8	0.217	0.178
P61353	60S ribosomal protein L27 OS=Homo sapiens GN=RPL27 PE=1 SV=2 - [RL27_HUMAN]	13.92	23.53	4	4	5	0.070	0.121
P46779	60S ribosomal protein L28 OS=Homo sapiens GN=RPL28 PE=1 SV=3 - [RL28_HUMAN]	19.78	19.71	4	4	5	0.053	0.114
P39023	60S ribosomal protein L3 OS=Homo sapiens GN=RPL3 PE=1 SV=2 - [RL3_HUMAN]	12.09	9.18	4	4	4	0.151	0.180
P62888	60S ribosomal protein L30 OS=Homo sapiens GN=RPL30 PE=1 SV=2 - [RL30_HUMAN]	18.61	44.35	5	5	6	0.149	0.122
P49207	60S ribosomal protein L34 OS=Homo sapiens GN=RPL34 PE=1 SV=3 - [RL34_HUMAN]	19.50	34.19	5	5	6	0.124	0.146
P42766	60S ribosomal protein L35 OS=Homo sapiens GN=RPL35 PE=1 SV=2 - [RL35_HUMAN]	29.35	32.52	5	6	10	0.250	0.159
Q9Y3U8	60S ribosomal protein L36 OS=Homo sapiens GN=RPL36 PE=1 SV=3 - [RL36_HUMAN]	6.69	19.05	2	2	2	0.322	0.313
P83881	60S ribosomal protein L36a OS=Homo sapiens GN=RPL36A PE=1 SV=2 - [RL36A_HUMAN]	15.62	25.47	4	4	5	0.202	0.147
P36578	60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5 - [RL4_HUMAN]	52.32	29.27	13	14	16	0.298	0.158
Q02878	60S ribosomal protein L6 OS=Homo sapiens GN=RPL6 PE=1 SV=3 - [RL6_HUMAN]	27.16	19.79	7	7	9	0.188	0.154
P18124	60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1 - [RL7_HUMAN]	39.74	26.61	7	7	11	0.109	0.128
P62424	60S ribosomal protein L7a OS=Homo sapiens GN=RPL7A PE=1 SV=2 - [RL7A_HUMAN]	41.66	23.31	8	8	12	0.112	0.120
P11021	78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2 - [GRP78_HUMAN]	257.37	46.33	29	32	76	0.958	0.731
D2K8Q1	AAA domain containing 3A protein OS=Homo sapiens GN=ATAD3A PE=2 SV=1 - [D2K8Q1_HUMAN]	40.78	10.92	7	7	12	0.095	0.141
Q2L6I2	ABC50 protein OS=Homo sapiens GN=ABCF1 PE=2 SV=1 - [Q2L6I2_HUMAN]	19.77	3.97	2	4	6	0.098	0.276
P24752	Acetyl-CoA acetyltransferase, mitochondrial OS=Homo sapiens GN=ACAT1 PE=1 SV=1 - [THIL_HUMAN]	48.08	19.67	8	8	16	0.102	0.144
Q92688	Acidic leucine-rich nuclear phosphoprotein 32 family member B OS=Homo sapiens GN=ANP32B PE=1 SV=1 - [AN32B_HUMAN]	33.92	15.54	3	5	10	0.240	0.340
P61160	Actin-related protein 2 OS=Homo sapiens GN=ACTR2 PE=1 SV=1 - [ARP2_HUMAN]	53.89	9.39	3	4	20	0.327	0.639
O15144	Actin-related protein 2/3 complex subunit 2 OS=Homo sapiens GN=ARPC2 PE=1 SV=1 - [ARPC2_HUMAN]	35.47	22.33	7	7	11	0.249	0.576
P59998	Actin-related protein 2/3 complex subunit 4 OS=Homo sapiens GN=ARPC4 PE=1 SV=3 - [ARPC4_HUMAN]	16.58	21.43	4	4	5	0.239	0.558
P60709	Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]	1033.91	61.60	8	19	316	3.062	2.862
Q9H845	Acyl-CoA dehydrogenase family member 9, mitochondrial OS=Homo sapiens GN=ACAD9 PE=1 SV=1 - [ACAD9_HUMAN]	15.45	8.21	5	5	5	0.081	0.116
Q5JWV8	Acyl-CoA synthetase long-chain family member 4 OS=Homo sapiens GN=ACSL4 PE=2 SV=1 - [Q5JWV8_HUMAN]	47.09	17.16	9	10	14	1.297	2.011
P13798	Acylamino-acid-releasing enzyme OS=Homo sapiens GN=APEH PE=1 SV=4 - [ACPH_HUMAN]	220.03	25.14	20	20	64	2.444	2.618
F5H737	Adenosylhomocysteinase OS=Homo sapiens GN=AHCY PE=3 SV=1 - [F5H737_HUMAN]	22.09	17.08	7	7	7	0.405	1.415
P00568	Adenylate kinase isoenzyme 1 OS=Homo sapiens GN=AK1 PE=1 SV=3 - [KAD1_HUMAN]	7.07	10.31	2	2	2	0.322	0.371
P30566	Adenylosuccinate lyase OS=Homo sapiens GN=ADSL PE=1 SV=2 - [PUR8_HUMAN]	43.69	19.01	9	9	13	6.929	5.910
F5H6Z3	Adenylyl cyclase-associated protein OS=Homo sapiens GN=CAP1 PE=3 SV=1 - [F5H6Z3_HUMAN]	37.85	15.93	7	7	12	0.379	0.904
Q9HDC9	Adipocyte plasma membrane-associated protein OS=Homo sapiens GN=APMAP PE=1 SV=2 - [APMAP_HUMAN]	10.32	9.13	3	3	3	0.782	0.616
Q9NVJ2	ADP-ribosylation factor-like protein 8B OS=Homo sapiens GN=ARL8B PE=1 SV=1 - [ARL8B_HUMAN]	24.44	19.89	4	4	7	0.034	0.197
P05141	ADP/ATP translocase 2 OS=Homo sapiens GN=SLC25A5 PE=1 SV=7 - [ADT2_HUMAN]	77.37	32.89	4	12	25	0.018	0.099
P12236	ADP/ATP translocase 3 OS=Homo sapiens GN=SLC25A6 PE=1 SV=4 - [ADT3_HUMAN]	63.62	29.53	2	10	21	0.283	0.175
Q9Y4W6	AFG3-like protein 2 OS=Homo sapiens GN=AFG3L2 PE=1 SV=2 - [AFG32_HUMAN]	15.16	5.40	5	5	5	0.052	0.119
P49588	Alanyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=AARS PE=1 SV=2 - [SYAC_HUMAN]	57.66	12.60	13	13	18	0.276	0.122
Q8IZ83	Aldehyde dehydrogenase family 16 member A1 OS=Homo sapiens GN=ALDH16A1 PE=1 SV=2 - [A16A1_HUMAN]	62.69	15.84	11	11	17	4.559	2.774
P01023	Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3 - [A2MG_HUMAN]	40.35	7.80	11	11	13	0.066	0.101
P61163	Alpha-centractin OS=Homo sapiens GN=ACTR1A PE=1 SV=1 - [ACTZ_HUMAN]	118.48	34.04	13	14	40	0.957	0.806
P06733	Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2 - [ENOA_HUMAN]	19.53	13.13	5	5	6	0.113	0.307
Q9NZD4	Alpha-hemoglobin-stabilizing protein OS=Homo sapiens GN=AHSP PE=1 SV=1 - [AHSP_HUMAN]	19.47	30.39	3	3	6	0.073	0.101
P54920	Alpha-soluble NSF attachment protein OS=Homo sapiens GN=NAPA PE=1 SV=3 - [SNAA_HUMAN]	42.96	30.17	7	7	12	0.658	0.609
Q12904	Aminoacyl tRNA synthase complex-interacting multifunctional protein 1 OS=Homo sapiens GN=AIMP1 PE=1 SV=2 - [AIMP1_HUMAN]	8.62	9.62	2	2	2	0.100	0.123
A8K6C4	Aminolevulinate, delta-, synthase 2 OS=Homo sapiens GN=ALAS2 PE=2 SV=1 - [A8K6C4_HUMAN]	10.59	5.09	3	3	3	0.014	0.116
Q10567	AP-1 complex subunit beta-1 OS=Homo sapiens GN=AP1B1 PE=1 SV=2 - [AP1B1_HUMAN]	109.87	14.54	4	16	31	0.575	0.639

O95782	AP-2 complex subunit alpha-1 OS=Homo sapiens GN=AP2A1 PE=1 SV=3 - [AP2A1_HUMAN]	267.81	37.36	38	38	84	0.501	0.544
P63010	AP-2 complex subunit beta OS=Homo sapiens GN=AP2B1 PE=1 SV=1 - [AP2B1_HUMAN]	139.41	22.95	12	24	42	0.665	0.596
Q2M2I8	AP2-associated protein kinase 1 OS=Homo sapiens GN=AAK1 PE=1 SV=3 - [AAK1_HUMAN]	12.50	3.75	3	3	4	0.173	0.239
O95831	Apoptosis-inducing factor 1, mitochondrial OS=Homo sapiens GN=AIFM1 PE=1 SV=1 - [AIFM1_HUMAN]	26.76	9.79	5	6	8	0.080	0.091
P52594	Arf-GAP domain and FG repeats-containing protein 1 OS=Homo sapiens GN=AGFG1 PE=1 SV=2 - [AGFG1_HUMAN]	24.28	11.39	4	6	8	0.309	0.279
Q9ULH1	Arf-GAP with SH3 domain, ANK repeat and PH domain-containing protein 1 OS=Homo sapiens GN=ASAP1 PE=1 SV=4 - [ASAP1_HUMAN]	21.20	4.69	7	7	7	0.899	1.124
P05089	Arginase-1 OS=Homo sapiens GN=ARG1 PE=1 SV=2 - [ARGI1_HUMAN]	109.60	33.85	9	10	33	1.163	1.785
P78540	Arginase-2, mitochondrial OS=Homo sapiens GN=ARG2 PE=1 SV=1 - [ARGI2_HUMAN]	25.59	16.38	5	5	7	0.025	0.016
O43776	Asparaginyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=NARS PE=1 SV=1 - [SYNC_HUMAN]	19.32	13.14	6	6	6	0.233	0.230
P00505	Aspartate aminotransferase, mitochondrial OS=Homo sapiens GN=GOT2 PE=1 SV=3 - [AATM_HUMAN]	79.35	26.51	13	13	22	0.062	0.143
P14868	Aspartyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=DARS PE=1 SV=2 - [SYDC_HUMAN]	39.85	14.77	7	8	13	0.746	0.334
B4DL14	ATP synthase gamma chain OS=Homo sapiens GN=ATP5C1 PE=2 SV=1 - [B4DL14_HUMAN]	28.52	27.20	8	8	9	0.239	0.203
P25705	ATP synthase subunit alpha, mitochondrial OS=Homo sapiens GN=ATP5A1 PE=1 SV=1 - [ATPA_HUMAN]	158.19	36.89	20	20	46	0.042	0.117
P06576	ATP synthase subunit beta, mitochondrial OS=Homo sapiens GN=ATP5B PE=1 SV=3 - [ATPB_HUMAN]	136.58	37.24	16	16	40	0.202	0.160
O75947	ATP synthase subunit d, mitochondrial OS=Homo sapiens GN=ATP5H PE=1 SV=3 - [ATP5H_HUMAN]	29.71	37.89	7	7	10	0.020	0.148
P30049	ATP synthase subunit delta, mitochondrial OS=Homo sapiens GN=ATP5D PE=1 SV=2 - [ATPD_HUMAN]	21.87	13.69	2	2	5	0.037	0.133
P48047	ATP synthase subunit O, mitochondrial OS=Homo sapiens GN=ATP5O PE=1 SV=1 - [ATPO_HUMAN]	56.84	53.05	12	12	16	0.051	0.146
P18859	ATP synthase-coupling factor 6, mitochondrial OS=Homo sapiens GN=ATP5J PE=1 SV=1 - [ATP5J_HUMAN]	6.54	24.07	2	2	2	0.010	0.114
Q5QNZ2	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit B1 OS=Homo sapiens GN=ATP5F1 PE=2 SV=1 - [Q5QNZ2_HUMAN]	16.27	14.36	3	3	5	0.230	0.226
Q9NRK6	ATP-binding cassette sub-family B member 10, mitochondrial OS=Homo sapiens GN=ABCB10 PE=1 SV=2 - [ABCBA_HUMAN]	77.57	18.29	14	14	21	0.175	0.203
Q9NP58	ATP-binding cassette sub-family B member 6, mitochondrial OS=Homo sapiens GN=ABCB6 PE=1 SV=1 - [ABCB6_HUMAN]	157.61	19.00	14	15	46	0.816	1.166
P61221	ATP-binding cassette sub-family E member 1 OS=Homo sapiens GN=ABCE1 PE=1 SV=1 - [ABCE1_HUMAN]	35.09	12.69	8	8	10	0.578	0.401
Q5STZ8	ATP-binding cassette sub-family F (GCN20) member 1 (Fragment) OS=Homo sapiens GN=ABCF1 PE=2 SV=2 - [Q5STZ8_HUMAN]	19.46	9.71	2	4	6	0.084	0.273
Q9UNQ0	ATP-binding cassette sub-family G member 2 OS=Homo sapiens GN=ABCG2 PE=1 SV=3 - [ABCG2_HUMAN]	23.83	4.27	3	3	7	2.204	2.023
P53396	ATP-citrate synthase OS=Homo sapiens GN=ACLY PE=1 SV=3 - [ACLY_HUMAN]	357.14	33.51	12	37	109	1.350	2.482
Q08211	ATP-dependent RNA helicase A OS=Homo sapiens GN=DHX9 PE=1 SV=4 - [DHX9_HUMAN]	90.30	15.67	20	20	27	0.154	0.285
Q7Z478	ATP-dependent RNA helicase DHX29 OS=Homo sapiens GN=DHX29 PE=1 SV=2 - [DHX29_HUMAN]	5.95	1.39	2	2	2	0.575	0.512
Q9UII2	ATPase inhibitor, mitochondrial OS=Homo sapiens GN=ATPIF1 PE=1 SV=1 - [ATIF1_HUMAN]	88.19	24.53	5	5	24	0.113	0.262
P51572	B-cell receptor-associated protein 31 OS=Homo sapiens GN=BCAP31 PE=1 SV=3 - [BAP31_HUMAN]	12.56	10.57	3	3	4	0.164	0.138
P02730	Band 3 anion transport protein OS=Homo sapiens GN=SLC4A1 PE=1 SV=3 - [B3AT_HUMAN]	1578.29	32.05	27	27	481	3.826	3.604
P50895	Basal cell adhesion molecule OS=Homo sapiens GN=BCAM PE=1 SV=2 - [BCAM_HUMAN]	63.47	20.06	10	10	18	2.373	1.155
Q54A51	Basigin (Ok blood group), isoform CRA_a OS=Homo sapiens GN=hEMMPRIN PE=2 SV=1 - [Q54A51_HUMAN]	80.31	43.49	11	11	26	0.954	1.260
P35612	Beta-adducin OS=Homo sapiens GN=ADD2 PE=1 SV=3 - [ADDB_HUMAN]	440.34	41.74	10	32	135	4.433	3.571
P07686	Beta-hexosaminidase subunit beta OS=Homo sapiens GN=HEXB PE=1 SV=3 - [HEXB_HUMAN]	17.03	9.53	6	6	6	0.097	0.118
P53004	Biliverdin reductase A OS=Homo sapiens GN=BLVRA PE=1 SV=2 - [BIEA_HUMAN]	6.22	4.73	2	2	2	1.807	1.315
P78537	Biogenesis of lysosome-related organelles complex 1 subunit 1 OS=Homo sapiens GN=BLOC1S1 PE=1 SV=2 - [BL1S1_HUMAN]	8.73	11.11	2	2	3	0.101	0.302
P07738	Bisphosphoglycerate mutase OS=Homo sapiens GN=BPGM PE=1 SV=2 - [PMGE_HUMAN]	39.66	27.03	6	6	13	0.436	1.850
Q13867	Bleomycin hydrolase OS=Homo sapiens GN=BLMH PE=1 SV=1 - [BLMH_HUMAN]	20.08	13.63	5	5	6	1.040	1.722
Q9NSY1	BMP-2-inducible protein kinase OS=Homo sapiens GN=BMP2K PE=1 SV=2 - [BMP2K_HUMAN]	30.48	9.22	8	8	8	0.592	0.377
P11586	C-1-tetrahydrofolate synthase, cytoplasmic OS=Homo sapiens GN=MTHFD1 PE=1 SV=3 - [C1TC_HUMAN]	299.99	32.19	33	33	91	0.531	0.475
O14523	C2 domain-containing protein 2-like OS=Homo sapiens GN=C2CD2L PE=1 SV=3 - [C2C2L_HUMAN]	15.93	3.97	3	3	5	2.247	1.979
P27708	CAD protein OS=Homo sapiens GN=CAD PE=1 SV=3 - [PYR1_HUMAN]	18.19	2.25	5	5	5	0.386	0.329
P62158	Calmodulin OS=Homo sapiens GN=CALM1 PE=1 SV=2 - [CALM_HUMAN]	45.04	38.26	7	7	14	0.690	0.737
P27824	Calnexin OS=Homo sapiens GN=CANX PE=1 SV=2 - [CALX_HUMAN]	75.29	21.11	15	15	23	0.633	0.814
P04632	Calpain small subunit 1 OS=Homo sapiens GN=CAPNS1 PE=1 SV=1 - [CPNS1_HUMAN]	5.48	4.85	2	2	2	0.557	1.199
P07384	Calpain-1 catalytic subunit OS=Homo sapiens GN=CAPN1 PE=1 SV=1 - [CAN1_HUMAN]	19.83	8.96	6	6	6	0.714	1.524
O15484	Calpain-5 OS=Homo sapiens GN=CAPN5 PE=1 SV=2 - [CAN5_HUMAN]	13.03	4.84	3	3	4	2.957	1.726
P27797	Calreticulin OS=Homo sapiens GN=CALR PE=1 SV=1 - [CALR_HUMAN]	193.71	42.93	19	19	60	0.537	0.601
O43852	Calumenin OS=Homo sapiens GN=CALU PE=1 SV=2 - [CALU_HUMAN]	14.08	9.52	3	3	5	0.766	0.906
P17612	cAMP-dependent protein kinase catalytic subunit alpha OS=Homo sapiens GN=PRKACA PE=1 SV=2 - [KAPCA_HUMAN]	75.54	21.94	9	9	22	1.676	2.908
P10644	cAMP-dependent protein kinase type I-alpha regulatory subunit OS=Homo sapiens GN=PRKAR1A PE=1 SV=1 - [KAP0_HUMAN]	96.02	37.01	15	15	27	2.008	3.164
B1AK87	Capping protein (Actin filament) muscle Z-line, beta OS=Homo sapiens GN=CAPZB PE=4 SV=1 - [B1AK87_HUMAN]	31.87	19.62	6	6	10	0.982	0.819
P00918	Carbonic anhydrase 2 OS=Homo sapiens GN=CA2 PE=1 SV=2 - [CAH2_HUMAN]	10.09	11.92	3	3	3	1.465	0.398
P50416	Carnitine O-palmitoyltransferase 1, liver isoform OS=Homo sapiens GN=CPT1A PE=1 SV=2 - [CPT1A_HUMAN]	12.40	4.01	3	3	4	0.464	0.167
P48729	Casein kinase I isoform alpha OS=Homo sapiens GN=CSNK1A1 PE=1 SV=2 - [KC1A_HUMAN]	6.16	8.90	2	2	2	1.337	1.980
P67870	Casein kinase II subunit beta OS=Homo sapiens GN=CSNK2B PE=1 SV=1 - [CSK2B_HUMAN]	13.81	15.81	3	3	4	0.832	0.766

P04040	Catalase OS=Homo sapiens GN=CAT PE=1 SV=3 - [CATA_HUMAN]	248.04	47.63	25	25	77	0.711	2.535
P07339	Cathepsin D OS=Homo sapiens GN=CTSD PE=1 SV=1 - [CATD_HUMAN]	37.38	15.29	6	6	12	0.110	0.146
P14091	Cathepsin E OS=Homo sapiens GN=CTSE PE=1 SV=2 - [CATE_HUMAN]	5.84	3.99	2	2	2	17.672	6.129
Q9Y5K6	CD2-associated protein OS=Homo sapiens GN=CD2AP PE=1 SV=1 - [CD2AP_HUMAN]	60.97	22.54	13	13	18	0.373	0.495
B6EAT9	CD44 OS=Homo sapiens PE=2 SV=1 - [B6EAT9_HUMAN]	58.48	18.82	6	6	17	1.946	1.188
B1AMW1	CD58 antigen, (Lymphocyte function-associated antigen 3), isoform CRA_c OS=Homo sapiens GN=CD58 PE=4 SV=1 - [B1AMW1_HUMAN]	14.55	7.50	2	2	4	1.477	1.175
Q8N5K1	CDGSH iron-sulfur domain-containing protein 2 OS=Homo sapiens GN=CISD2 PE=1 SV=1 - [CISD2_HUMAN]	69.48	40.00	6	6	18	0.943	1.517
B7Z3E2	cDNA FLJ50777, highly similar to Serine/threonine-protein phosphatase 6 (EC 3.1.3.16) OS=Homo sapiens PE=2 SV=1 - [B7Z3E2_HUMAN]	15.94	19.62	3	3	5	0.993	0.989
B4DM63	cDNA FLJ51245, highly similar to Actin-related protein 2/3 complex subunit 3 OS=Homo sapiens PE=2 SV=1 - [B4DM63_HUMAN]	8.99	14.37	3	3	3	0.477	0.498
B4DEW9	cDNA FLJ52478, highly similar to Eukaryotic translation initiation factor 3 subunit 5 OS=Homo sapiens PE=2 SV=1 - [B4DEW9_HUMAN]	16.21	19.71	4	4	5	0.162	0.125
B4DS57	cDNA FLJ53176, highly similar to Nuclear autoantigenic sperm protein OS=Homo sapiens PE=2 SV=1 - [B4DS57_HUMAN]	10.14	2.76	3	3	3	0.621	0.425
B4DPJ6	cDNA FLJ53635, highly similar to Homo sapiens tumor protein D52-like 2, transcript variant 6, mRNA OS=Homo sapiens PE=2 SV=1 - [B4DPJ6_HUMAN]	7.99	11.04	2	2	2	0.676	1.507
B4DW31	cDNA FLJ54186, highly similar to Nuclear receptor-binding protein OS=Homo sapiens PE=2 SV=1 - [B4DW31_HUMAN]	5.97	5.63	2	2	2	0.500	0.647
B4DZV5	cDNA FLJ58820, highly similar to 55 kDa erythrocyte membrane protein (p55) OS=Homo sapiens PE=2 SV=1 - [B4DZV5_HUMAN]	280.15	45.41	19	19	88	1.528	1.643
Q8NBU8	cDNA FLJ90737 fis, clone PLACE1010827, moderately similar to Membrane protein p24B OS=Homo sapiens PE=2 SV=1 - [Q8NBU8_HUMAN]	6.14	9.04	2	2	2	0.925	1.156
Q9NV96	Cell cycle control protein 50A OS=Homo sapiens GN=TMEM30A PE=1 SV=1 - [CC50A_HUMAN]	6.09	7.48	2	2	2	0.899	0.763
P60953	Cell division control protein 42 homolog OS=Homo sapiens GN=CDC42 PE=1 SV=2 - [CDC42_HUMAN]	51.07	26.70	4	5	14	1.839	2.245
B7ZAT2	Chaperonin containing TCP1, subunit 2 (Beta), isoform CRA_c OS=Homo sapiens GN=CCT2 PE=2 SV=1 - [B7ZAT2_HUMAN]	142.07	40.37	21	21	43	0.497	0.754
B7Z4T9	Chaperonin containing TCP1, subunit 7 (Eta), isoform CRA_c OS=Homo sapiens GN=CCT7 PE=2 SV=1 - [B7Z4T9_HUMAN]	209.47	51.50	26	26	64	0.626	0.849
Q7LBR1	Charged multivesicular body protein 1b OS=Homo sapiens GN=CHMP1B PE=1 SV=1 - [CHM1B_HUMAN]	11.23	15.58	4	4	4	0.974	1.289
O43633	Charged multivesicular body protein 2a OS=Homo sapiens GN=CHMP2A PE=1 SV=1 - [CHM2A_HUMAN]	22.99	22.97	6	6	6	0.775	0.855
Q96FZ7	Charged multivesicular body protein 6 OS=Homo sapiens GN=CHMP6 PE=1 SV=3 - [CHMP6_HUMAN]	9.68	13.43	3	3	3	1.039	1.245
Q9BWS9	Chitinase domain-containing protein 1 OS=Homo sapiens GN=CHID1 PE=1 SV=1 - [CHID1_HUMAN]	12.20	6.62	3	3	4	0.610	0.612
B4DJV2	Citrate synthase OS=Homo sapiens GN=CS PE=2 SV=1 - [B4DJV2_HUMAN]	57.93	20.09	9	9	18	0.157	0.183
Q00610	Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC PE=1 SV=5 - [CLH1_HUMAN]	479.20	30.75	50	50	141	0.546	0.495
P09497	Clathrin light chain B OS=Homo sapiens GN=CLTB PE=1 SV=1 - [CLCB_HUMAN]	27.27	22.27	7	7	9	0.581	0.452
P53621	Coatomer subunit alpha OS=Homo sapiens GN=COPA PE=1 SV=2 - [COPA_HUMAN]	14.61	3.10	4	4	5	0.201	0.302
P53618	Coatomer subunit beta OS=Homo sapiens GN=COPB1 PE=1 SV=3 - [COPB_HUMAN]	6.72	2.83	2	2	2	0.203	0.382
P48444	Coatomer subunit delta OS=Homo sapiens GN=ARCN1 PE=1 SV=1 - [COPD_HUMAN]	20.50	13.11	7	7	7	0.415	0.526
Q6P1N0	Coiled-coil and C2 domain-containing protein 1A OS=Homo sapiens GN=CC2D1A PE=1 SV=1 - [C2D1A_HUMAN]	28.73	9.78	8	8	8	1.335	1.097
Q96CT7	Coiled-coil domain-containing protein 124 OS=Homo sapiens GN=CCDC124 PE=1 SV=1 - [CC124_HUMAN]	23.44	23.77	6	6	7	0.424	0.618
Q2TAC2	Coiled-coil domain-containing protein 57 OS=Homo sapiens GN=CCDC57 PE=2 SV=2 - [CCD57_HUMAN]	5.24	1.64	2	2	2	5.260	3.003
Q9Y2S6	Coiled-coil domain-containing protein 72 OS=Homo sapiens GN=CCDC72 PE=1 SV=1 - [CCD72_HUMAN]	10.19	25.00	2	2	3	0.162	0.407
Q9NX63	Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial OS=Homo sapiens GN=CHCHD3 PE=1 SV=1 - [CHCH3_HUMAN]	33.70	31.72	8	8	10	0.050	0.112
Q9BPX3	Condensin complex subunit 3 OS=Homo sapiens GN=NCAPG PE=1 SV=1 - [CND3_HUMAN]	6.54	1.58	2	2	2	0.265	0.424
A8K1H6	COP9 constitutive photomorphogenic homolog subunit 8 (Arabidopsis), isoform CRA_b OS=Homo sapiens GN=COPS8 PE=2 SV=1 - [A8K1H6_HUMAN]	33.04	39.38	4	4	8	1.015	1.532
Q13098	COP9 signalosome complex subunit 1 OS=Homo sapiens GN=GPS1 PE=1 SV=4 - [CSN1_HUMAN]	27.33	15.27	8	8	9	1.373	1.818
P61201	COP9 signalosome complex subunit 2 OS=Homo sapiens GN=COPS2 PE=1 SV=1 - [CSN2_HUMAN]	22.42	12.19	7	7	8	0.990	1.706
Q9BT78	COP9 signalosome complex subunit 4 OS=Homo sapiens GN=COPS4 PE=1 SV=1 - [CSN4_HUMAN]	36.26	25.37	9	9	11	1.344	1.800
Q92905	COP9 signalosome complex subunit 5 OS=Homo sapiens GN=COPS5 PE=1 SV=4 - [CSN5_HUMAN]	31.04	19.76	6	6	10	0.840	1.693
Q9H9Q2	COP9 signalosome complex subunit 7b OS=Homo sapiens GN=COPS7B PE=1 SV=1 - [CSN7B_HUMAN]	10.27	11.74	3	3	3	1.171	1.491
Q04656	Copper-transporting ATPase 1 OS=Homo sapiens GN=ATP7A PE=1 SV=3 - [ATP7A_HUMAN]	34.29	5.33	8	8	11	1.103	0.754
P36551	Coproporphyrinogen-III oxidase, mitochondrial OS=Homo sapiens GN=CPOX PE=1 SV=3 - [HEM6_HUMAN]	132.50	39.21	16	16	43	0.125	0.153
Q9ULV4	Coronin-1C OS=Homo sapiens GN=CORO1C PE=1 SV=1 - [COR1C_HUMAN]	70.45	22.78	14	14	21	0.080	0.085
Q9NRF8	CTP synthase 2 OS=Homo sapiens GN=CTPS2 PE=1 SV=1 - [PYRG2_HUMAN]	6.39	3.58	2	2	2	0.646	0.635
Q5T2B5	Cullin 2 OS=Homo sapiens GN=CUL2 PE=2 SV=1 - [Q5T2B5_HUMAN]	9.58	3.54	3	3	3	0.596	1.201
Q13618	Cullin-3 OS=Homo sapiens GN=CUL3 PE=1 SV=2 - [CUL3_HUMAN]	52.68	16.15	13	13	15	0.630	1.095
Q86VP6	Cullin-associated NEDD8-dissociated protein 1 OS=Homo sapiens GN=CAND1 PE=1 SV=2 - [CAND1_HUMAN]	107.64	17.32	21	21	33	0.985	1.764
A8MVQ3	Cysteinyl-tRNA synthetase, isoform CRA_b OS=Homo sapiens GN=CARS PE=2 SV=1 - [A8MVQ3_HUMAN]	7.75	2.44	2	2	2	0.079	0.206
P31930	Cytochrome b-c1 complex subunit 1, mitochondrial OS=Homo sapiens GN=UQCRC1 PE=1 SV=3 - [QCR1_HUMAN]	33.19	14.58	6	6	9	0.212	0.252
P22695	Cytochrome b-c1 complex subunit 2, mitochondrial OS=Homo sapiens GN=UQCRC2 PE=1 SV=3 - [QCR2_HUMAN]	63.53	28.48	11	11	20	0.108	0.157
P07919	Cytochrome b-c1 complex subunit 6, mitochondrial OS=Homo sapiens GN=UQCRH PE=1 SV=2 - [QCR6_HUMAN]	6.37	16.48	2	2	2	0.033	0.178
P47985	Cytochrome b-c1 complex subunit Rieske, mitochondrial OS=Homo sapiens GN=UQCRFS1 PE=1 SV=2 - [UCRI_HUMAN]	13.54	11.31	3	3	4	0.161	0.218
P13073	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial OS=Homo sapiens GN=COX4I1 PE=1 SV=1 - [COX41_HUMAN]	21.24	21.30	4	4	6	0.235	0.251
P20674	Cytochrome c oxidase subunit 5A, mitochondrial OS=Homo sapiens GN=COX5A PE=1 SV=2 - [COX5A_HUMAN]	11.99	14.67	3	3	4	0.061	0.158
P10606	Cytochrome c oxidase subunit 5B, mitochondrial OS=Homo sapiens GN=COX5B PE=1 SV=2 - [COX5B_HUMAN]	15.23	24.03	4	4	5	0.055	0.126

P09669	Cytochrome c oxidase subunit 6C OS=Homo sapiens GN=COX6C PE=1 SV=2 - [COX6C_HUMAN]	20.71	12.00	2	2	5	0.141	0.199
P08574	Cytochrome c1, heme protein, mitochondrial OS=Homo sapiens GN=CYC1 PE=1 SV=3 - [CY1_HUMAN]	6.10	6.15	2	2	2	0.040	0.159
Q8IUI8	Cytokine receptor-like factor 3 OS=Homo sapiens GN=CRLF3 PE=1 SV=2 - [CRLF3_HUMAN]	6.88	4.30	2	2	2	0.921	1.660
Q14008	Cytoskeleton-associated protein 5 OS=Homo sapiens GN=CKAP5 PE=1 SV=3 - [CKAP5_HUMAN]	18.22	3.00	5	5	5	2.164	1.202
P28838	Cytosol aminopeptidase OS=Homo sapiens GN=LAP3 PE=1 SV=3 - [AMPL_HUMAN]	17.75	10.21	5	5	5	0.208	0.222
Q58WW2	DDB1- and CUL4-associated factor 6 OS=Homo sapiens GN=DCAF6 PE=1 SV=1 - [DCAF6_HUMAN]	6.47	2.21	2	2	2	0.588	1.118
Q14UF5	Decay-accelerating factor splicing variant 2 OS=Homo sapiens GN=DAF PE=2 SV=1 - [Q14UF5_HUMAN]	68.26	22.25	11	11	22	2.113	2.026
P54886	Delta-1-pyrroline-5-carboxylate synthase OS=Homo sapiens GN=ALDH18A1 PE=1 SV=2 - [P5CS_HUMAN]	12.26	6.67	4	4	4	0.446	0.350
B7Z3I9	Delta-aminolevulinic acid dehydratase OS=Homo sapiens PE=2 SV=1 - [B7Z3I9_HUMAN]	81.72	28.12	8	8	25	1.867	3.188
Q13011	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial OS=Homo sapiens GN=ECH1 PE=1 SV=2 - [ECH1_HUMAN]	50.81	25.61	9	9	15	0.060	0.107
Q08495	Dematin OS=Homo sapiens GN=EPB49 PE=1 SV=3 - [DEMA_HUMAN]	551.59	54.57	20	20	170	2.988	3.044
Q96JH7	Deubiquitinating protein VCIP135 OS=Homo sapiens GN=VCPIP1 PE=1 SV=2 - [VCIP1_HUMAN]	6.52	1.80	2	2	2	0.163	0.180
F5H4I0	Dihydrolipoyl dehydrogenase OS=Homo sapiens GN=DLD PE=3 SV=1 - [F5H4I0_HUMAN]	31.95	14.60	6	6	10	0.178	0.106
P36957	Dihydrolipoyllysine-residue succinyltransferase OS=Homo sapiens GN=DLST PE=1 SV=4 - [ODO2_HUMAN]	55.30	22.52	10	10	16	0.068	0.162
Q9P265	Disco-interacting protein 2 homolog B OS=Homo sapiens GN=DIP2B PE=1 SV=3 - [DIP2B_HUMAN]	6.46	1.14	2	2	2	1.268	0.780
Q9Y4D1	Disheveled-associated activator of morphogenesis 1 OS=Homo sapiens GN=DAAM1 PE=1 SV=2 - [DAAM1_HUMAN]	9.80	2.60	3	3	3	2.362	2.697
Q16531	DNA damage-binding protein 1 OS=Homo sapiens GN=DDB1 PE=1 SV=1 - [DDB1_HUMAN]	63.63	17.19	18	18	21	0.506	0.719
Q92878	DNA repair protein RAD50 OS=Homo sapiens GN=RAD50 PE=1 SV=1 - [RAD50_HUMAN]	6.90	1.14	2	2	2	0.394	0.258
P16989	DNA-binding protein A OS=Homo sapiens GN=CSDA PE=1 SV=4 - [DBPA_HUMAN]	19.82	15.32	2	4	6	0.883	0.511
P25685	DnaJ homolog subfamily B member 1 OS=Homo sapiens GN=DNAJB1 PE=1 SV=4 - [DNJB1_HUMAN]	37.89	25.00	8	9	12	0.758	0.997
Q9UBS4	DnaJ homolog subfamily B member 11 OS=Homo sapiens GN=DNAJB11 PE=1 SV=1 - [DJB11_HUMAN]	8.76	9.22	3	3	3	0.592	0.641
Q9UDY4	DnaJ homolog subfamily B member 4 OS=Homo sapiens GN=DNAJB4 PE=1 SV=1 - [DNJB4_HUMAN]	8.90	9.79	2	3	3	1.091	1.129
Q9NVH1	DnaJ homolog subfamily C member 11 OS=Homo sapiens GN=DNAJC11 PE=1 SV=2 - [DJC11_HUMAN]	9.66	4.83	3	3	3	0.137	0.155
Q9H3Z4	DnaJ homolog subfamily C member 5 OS=Homo sapiens GN=DNAJC5 PE=1 SV=1 - [DNJC5_HUMAN]	16.68	19.19	3	3	5	0.370	0.566
O75937	DnaJ homolog subfamily C member 8 OS=Homo sapiens GN=DNAJC8 PE=1 SV=2 - [DNJC8_HUMAN]	5.94	6.32	2	2	2	0.205	0.219
O60762	Dolichol-phosphate mannosyltransferase OS=Homo sapiens GN=DPM1 PE=1 SV=1 - [DPM1_HUMAN]	5.91	5.77	2	2	2	0.159	0.292
P04843	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Homo sapiens GN=RPN1 PE=1 SV=1 - [RPN1_HUMAN]	29.12	12.52	8	8	9	0.392	0.296
P49959	Double-strand break repair protein MRE11A OS=Homo sapiens GN=MRE11A PE=1 SV=3 - [MRE11_HUMAN]	9.34	4.52	3	3	3	0.162	0.178
P46734	Dual specificity mitogen-activated protein kinase kinase 3 OS=Homo sapiens GN=MAP2K3 PE=1 SV=2 - [MP2K3_HUMAN]	34.68	20.17	7	7	10	0.276	0.352
Q5T1I6	Dynactin 3 (P22) (Fragment) OS=Homo sapiens GN=DCTN3 PE=2 SV=1 - [Q5T1I6_HUMAN]	17.18	16.15	3	3	5	1.146	0.821
Q13561	Dynactin subunit 2 OS=Homo sapiens GN=DCTN2 PE=1 SV=4 - [DCTN2_HUMAN]	80.74	39.90	14	14	23	1.111	0.905
O60313	Dynamin-like 120 kDa protein, mitochondrial OS=Homo sapiens GN=OPA1 PE=1 SV=3 - [OPA1_HUMAN]	23.45	6.56	7	7	7	0.055	0.130
Q5XPI4	E3 ubiquitin-protein ligase RNF123 OS=Homo sapiens GN=RNF123 PE=1 SV=1 - [RN123_HUMAN]	52.11	7.84	11	11	17	0.542	1.194
Q5T4S7	E3 ubiquitin-protein ligase UBR4 OS=Homo sapiens GN=UBR4 PE=1 SV=1 - [UBR4_HUMAN]	244.45	11.02	56	56	74	1.028	0.879
Q14258	E3 ubiquitin/ISG15 ligase TRIM25 OS=Homo sapiens GN=TRIM25 PE=1 SV=2 - [TRI25_HUMAN]	17.68	8.89	5	5	5	0.858	0.539
Q15075	Early endosome antigen 1 OS=Homo sapiens GN=EEA1 PE=1 SV=2 - [EEA1_HUMAN]	9.49	2.91	2	3	3	1.266	0.959
Q93070	Ecto-ADP-ribosyltransferase 4 OS=Homo sapiens GN=ART4 PE=2 SV=2 - [NAR4_HUMAN]	9.46	7.96	3	3	3	3.086	3.262
Q4VBZ6	EEF1D protein OS=Homo sapiens GN=EEF1D PE=1 SV=1 - [Q4VBZ6_HUMAN]	47.62	25.68	6	7	15	0.218	0.186
Q8N3D4	EH domain-binding protein 1-like protein 1 OS=Homo sapiens GN=EHBP1L1 PE=1 SV=2 - [EH1L1_HUMAN]	37.16	6.17	6	6	10	1.851	1.183
Q9H4M9	EH domain-containing protein 1 OS=Homo sapiens GN=EHD1 PE=1 SV=2 - [EHD1_HUMAN]	70.58	27.72	16	16	22	0.763	0.472
P38117	Electron transfer flavoprotein subunit beta OS=Homo sapiens GN=ETFB PE=1 SV=3 - [ETFB_HUMAN]	54.60	32.94	9	9	16	0.077	0.086
P68104	Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 - [EF1A1_HUMAN]	183.28	32.47	16	16	58	0.096	0.168
P24534	Elongation factor 1-beta OS=Homo sapiens GN=EEF1B2 PE=1 SV=3 - [EF1B_HUMAN]	16.49	10.22	2	3	5	0.039	0.076
P26641	Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3 - [EF1G_HUMAN]	94.60	21.51	14	14	29	0.189	0.140
P13639	Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 - [EF2_HUMAN]	87.71	17.83	16	17	27	0.256	0.241
P49411	Elongation factor Tu, mitochondrial OS=Homo sapiens GN=TUFM PE=1 SV=2 - [EFTU_HUMAN]	72.10	32.52	13	13	20	0.234	0.216
P50402	Emerin OS=Homo sapiens GN=EMD PE=1 SV=1 - [EMD_HUMAN]	18.19	11.81	3	3	5	0.613	0.546
O94919	Endonuclease domain-containing 1 protein OS=Homo sapiens GN=ENDOD1 PE=1 SV=2 - [ENDD1_HUMAN]	44.87	16.20	7	7	14	1.540	1.475
P30040	Endoplasmic reticulum resident protein 29 OS=Homo sapiens GN=ERP29 PE=1 SV=4 - [ERP29_HUMAN]	45.80	29.89	8	8	14	0.688	0.688
Q9BS26	Endoplasmic reticulum resident protein 44 OS=Homo sapiens GN=ERP44 PE=1 SV=1 - [ERP44_HUMAN]	44.63	19.21	8	8	14	1.467	1.327
Q9Y282	Endoplasmic reticulum-Golgi intermediate compartment protein 3 OS=Homo sapiens GN=ERGIC3 PE=1 SV=1 - [ERGI3_HUMAN]	15.07	11.23	4	4	5	0.720	0.994
P14625	Endoplasmin OS=Homo sapiens GN=HSP90B1 PE=1 SV=1 - [ENPL_HUMAN]	182.71	29.89	28	29	55	0.723	0.804
O60869	Endothelial differentiation-related factor 1 OS=Homo sapiens GN=EDF1 PE=1 SV=1 - [EDF1_HUMAN]	10.40	11.49	2	2	3	0.235	0.204
P42126	Enoyl-CoA delta isomerase 1, mitochondrial OS=Homo sapiens GN=ECI1 PE=1 SV=1 - [ECI1_HUMAN]	8.32	10.93	3	3	3	0.084	0.169
Q4KKX0	EPB42 protein OS=Homo sapiens GN=EPB42 PE=2 SV=1 - [Q4KKX0_HUMAN]	798.90	41.20	31	31	247	4.086	4.011
B1AUU8	Epidermal growth factor receptor pathway substrate 15 OS=Homo sapiens GN=EPS15 PE=4 SV=1 - [B1AUU8_HUMAN]	18.14	5.64	5	5	6	0.634	0.617

P07099	Epoxide hydrolase 1 OS=Homo sapiens GN=EPHX1 PE=1 SV=1 - [HYEP_HUMAN]	6.02	3.96	2	2	2	0.541	0.477
A2RRF3	EPS15L1 protein OS=Homo sapiens GN=EPS15L1 PE=2 SV=1 - [A2RRF3_HUMAN]	13.87	4.77	4	4	4	0.703	0.642
Q9Y6I3	Epsin-1 OS=Homo sapiens GN=EPN1 PE=1 SV=2 - [EPN1_HUMAN]	8.66	4.51	3	3	3	0.552	0.761
Q99808	Equilibrative nucleoside transporter 1 OS=Homo sapiens GN=SLC29A1 PE=1 SV=3 - [S29A1_HUMAN]	96.18	15.35	9	9	26	1.651	1.596
O75477	Erlin-1 OS=Homo sapiens GN=ERLIN1 PE=1 SV=1 - [ERLN1_HUMAN]	22.55	17.92	3	6	7	0.452	0.557
Q96PL5	Erythroid membrane-associated protein OS=Homo sapiens GN=ERMAP PE=1 SV=1 - [ERMAP_HUMAN]	89.80	21.47	10	10	29	3.127	2.423
Q53GQ0	Estradiol 17-beta-dehydrogenase 12 OS=Homo sapiens GN=HSD17B12 PE=1 SV=2 - [DHB12_HUMAN]	24.12	15.06	4	4	6	0.729	0.887
P60842	Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=1 SV=1 - [IF4A1_HUMAN]	38.24	20.69	3	8	11	0.748	0.416
P38919	Eukaryotic initiation factor 4A-III OS=Homo sapiens GN=EIF4A3 PE=1 SV=4 - [IF4A3_HUMAN]	16.15	12.41	2	4	5	0.166	0.634
P62495	Eukaryotic peptide chain release factor subunit 1 OS=Homo sapiens GN=ETF1 PE=1 SV=3 - [ERF1_HUMAN]	46.25	20.59	9	9	16	0.182	0.401
P05198	Eukaryotic translation initiation factor 2 subunit 1 OS=Homo sapiens GN=EIF2S1 PE=1 SV=3 - [IF2A_HUMAN]	46.34	33.33	11	11	14	0.255	0.486
P20042	Eukaryotic translation initiation factor 2 subunit 2 OS=Homo sapiens GN=EIF2S2 PE=1 SV=2 - [IF2B_HUMAN]	52.47	35.44	11	12	16	0.284	0.648
P41091	Eukaryotic translation initiation factor 2 subunit 3 OS=Homo sapiens GN=EIF2S3 PE=1 SV=3 - [IF2G_HUMAN]	55.15	27.75	11	11	17	0.208	0.617
Q14152	Eukaryotic translation initiation factor 3 subunit A OS=Homo sapiens GN=EIF3A PE=1 SV=1 - [EIF3A_HUMAN]	71.84	13.31	20	20	24	0.276	0.176
P60228	Eukaryotic translation initiation factor 3 subunit E OS=Homo sapiens GN=EIF3E PE=1 SV=1 - [EIF3E_HUMAN]	12.64	5.62	3	3	4	0.184	0.148
O75821	Eukaryotic translation initiation factor 3 subunit G OS=Homo sapiens GN=EIF3G PE=1 SV=2 - [EIF3G_HUMAN]	11.81	7.81	2	2	3	0.191	0.156
O15372	Eukaryotic translation initiation factor 3 subunit H OS=Homo sapiens GN=EIF3H PE=1 SV=1 - [EIF3H_HUMAN]	29.80	17.05	6	6	8	0.054	0.076
Q13347	Eukaryotic translation initiation factor 3 subunit I OS=Homo sapiens GN=EIF3I PE=1 SV=1 - [EIF3I_HUMAN]	26.59	14.15	5	5	8	0.122	0.122
O75822	Eukaryotic translation initiation factor 3 subunit J OS=Homo sapiens GN=EIF3J PE=1 SV=2 - [EIF3J_HUMAN]	72.51	24.03	9	9	21	0.184	0.435
Q9Y262	Eukaryotic translation initiation factor 3 subunit L OS=Homo sapiens GN=EIF3L PE=1 SV=1 - [EIF3L_HUMAN]	21.81	9.22	5	6	7	0.072	0.132
P06730	Eukaryotic translation initiation factor 4E OS=Homo sapiens GN=EIF4E PE=1 SV=2 - [IF4E_HUMAN]	16.61	18.43	4	4	5	0.227	0.365
P55010	Eukaryotic translation initiation factor 5 OS=Homo sapiens GN=EIF5 PE=1 SV=2 - [IF5_HUMAN]	19.43	12.76	5	5	6	0.274	0.484
P63241	Eukaryotic translation initiation factor 5A-1 OS=Homo sapiens GN=EIF5A PE=1 SV=2 - [IF5A1_HUMAN]	25.18	35.71	6	6	8	0.168	0.405
O60841	Eukaryotic translation initiation factor 5B OS=Homo sapiens GN=EIF5B PE=1 SV=4 - [IF2P_HUMAN]	9.63	1.80	2	3	3	0.090	0.161
Q9BSJ8	Extended synaptotagmin-1 OS=Homo sapiens GN=ESYT1 PE=1 SV=1 - [ESYT1_HUMAN]	30.75	7.61	8	8	9	0.347	0.356
A0FGR8	Extended synaptotagmin-2 OS=Homo sapiens GN=ESYT2 PE=1 SV=1 - [ESYT2_HUMAN]	16.92	4.45	4	4	5	0.748	0.734
P15311	Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4 - [EZRI_HUMAN]	252.46	38.57	18	31	78	0.390	0.644
P52907	F-actin-capping protein subunit alpha-1 OS=Homo sapiens GN=CAPZA1 PE=1 SV=3 - [CAZA1_HUMAN]	30.88	22.03	5	6	10	0.725	0.998
Q92945	Far upstream element-binding protein 2 OS=Homo sapiens GN=KHSRP PE=1 SV=4 - [FUBP2_HUMAN]	10.07	4.64	2	3	3	0.375	0.110
P49327	Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3 - [FAS_HUMAN]	299.76	23.62	54	54	92	0.230	0.766
Q86UX7	Fermitin family homolog 3 OS=Homo sapiens GN=FERMT3 PE=1 SV=1 - [URP2_HUMAN]	24.14	9.00	5	5	7	0.238	0.442
P02794	Ferritin heavy chain OS=Homo sapiens GN=FTH1 PE=1 SV=2 - [FRIH_HUMAN]	36.28	20.77	4	4	12	0.106	0.189
P02792	Ferritin light chain OS=Homo sapiens GN=FTL PE=1 SV=2 - [FRIL_HUMAN]	54.19	39.43	7	7	17	0.041	0.167
P22830	Ferrochelatase, mitochondrial OS=Homo sapiens GN=FECH PE=1 SV=2 - [HEMH_HUMAN]	69.22	29.08	10	10	23	0.345	0.154
Q5HY54	Filamin A, alpha (Actin binding protein 280) OS=Homo sapiens GN=FLNA PE=2 SV=1 - [Q5HY54_HUMAN]	52.94	5.10	13	13	16	0.207	0.287
Q5T1M5	FK506-binding protein 15 OS=Homo sapiens GN=FKBP15 PE=1 SV=2 - [FKB15_HUMAN]	15.96	4.18	4	4	4	0.381	0.348
P30043	Flavin reductase OS=Homo sapiens GN=BLVRB PE=1 SV=3 - [BLVRB_HUMAN]	42.80	22.33	4	4	12	0.982	0.798
O75955	Flotillin-1 OS=Homo sapiens GN=FLOT1 PE=1 SV=3 - [FLOT1_HUMAN]	342.48	70.49	29	29	105	2.899	2.200
Q14254	Flotillin-2 OS=Homo sapiens GN=FLOT2 PE=1 SV=2 - [FLOT2_HUMAN]	366.37	60.98	28	28	106	2.982	2.809
Q9H479	Fructosamine-3-kinase OS=Homo sapiens GN=FN3K PE=1 SV=1 - [FN3K_HUMAN]	25.24	21.36	6	6	7	1.104	1.266
P04075	Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2 - [ALDOA_HUMAN]	683.98	54.95	17	21	208	1.536	1.028
B7Z1N6	Fructose-bisphosphate aldolase OS=Homo sapiens GN=ALDOC PE=2 SV=1 - [B7Z1N6_HUMAN]	110.88	18.15	3	7	35	4.309	1.181
Q86TT8	Full-length cDNA clone CS0DC011YL17 of Neuroblastoma of Homo sapiens (human) OS=Homo sapiens GN=MARK3 PE=2 SV=1 - [Q86TT8_HUMAN]	47.03	15.63	8	11	13	0.989	0.561
P07954	Fumarate hydratase, mitochondrial OS=Homo sapiens GN=FH PE=1 SV=3 - [FUMH_HUMAN]	49.87	15.88	8	8	15	0.140	0.311
Q9BWH2	FUN14 domain-containing protein 2 OS=Homo sapiens GN=FUNDC2 PE=1 SV=2 - [FUND2_HUMAN]	7.55	11.64	2	2	2	0.091	0.141
P43250	G protein-coupled receptor kinase 6 OS=Homo sapiens GN=GRK6 PE=1 SV=2 - [GRK6_HUMAN]	20.44	10.24	6	6	7	1.249	1.463
P17931	Galectin-3 OS=Homo sapiens GN=LGALS3 PE=1 SV=5 - [LEG3_HUMAN]	116.93	39.20	10	11	39	0.361	0.171
Q9UEY8	Gamma-adducin OS=Homo sapiens GN=ADD3 PE=1 SV=1 - [ADDG_HUMAN]	49.34	13.88	9	9	15	0.825	1.895
P60520	Gamma-aminobutyric acid receptor-associated protein-like 2 OS=Homo sapiens GN=GABARAPL2 PE=1 SV=1 - [GBRL2_HUMAN]	24.57	41.03	4	5	8	0.701	1.623
Q92820	Gamma-glutamyl hydrolase OS=Homo sapiens GN=GGH PE=1 SV=2 - [GGH_HUMAN]	5.97	6.29	2	2	2	0.046	0.100
Q99747	Gamma-soluble NSF attachment protein OS=Homo sapiens GN=NAPG PE=1 SV=1 - [SNAG_HUMAN]	7.67	8.65	2	3	3	0.279	0.387
P15104	Glutamine synthetase OS=Homo sapiens GN=GLUL PE=1 SV=4 - [GLNA_HUMAN]	8.83	5.63	3	3	3	0.095	0.219
Q86SX6	Glutaredoxin-related protein 5, mitochondrial OS=Homo sapiens GN=GLRX5 PE=1 SV=2 - [GLRX5_HUMAN]	25.18	20.38	4	4	9	0.093	0.078
Q92947	Glutaryl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=GCDH PE=1 SV=1 - [GCDH_HUMAN]	7.57	4.34	2	2	2	0.057	0.172
C8KIM0	Glutathion reductase delta8+9 alternative splicing variant OS=Homo sapiens GN=GSR PE=2 SV=1 - [C8KIM0_HUMAN]	10.40	7.05	3	3	3	1.044	1.746
P07203	Glutathione peroxidase 1 OS=Homo sapiens GN=GPX1 PE=1 SV=4 - [GPX1_HUMAN]	13.17	14.29	3	3	4	0.544	0.632

P78417	Glutathione S-transferase omega-1 OS=Homo sapiens GN=GSTO1 PE=1 SV=2 - [GSTO1_HUMAN]	15.88	13.69	3	3	5	0.315	0.452
P04406	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3 - [G3P_HUMAN]	1215.74	68.06	10	22	420	1.015	1.167
B8Q185	Glycophorin A MNS blood group OS=Homo sapiens GN=GYPA PE=4 SV=1 - [B8Q185_HUMAN]	48.01	45.30	3	3	15	10.251	11.878
P04921	Glycophorin-C OS=Homo sapiens GN=GYPC PE=1 SV=1 - [GLPC_HUMAN]	170.74	29.69	4	4	52	2.684	2.892
P41250	Glycyl-tRNA synthetase OS=Homo sapiens GN=GARS PE=1 SV=3 - [SYG_HUMAN]	10.61	4.19	3	3	3	0.237	0.162
P36959	GMP reductase 1 OS=Homo sapiens GN=GMPR PE=1 SV=1 - [GMPR1_HUMAN]	25.91	14.49	4	4	7	0.445	1.343
Q9H4G4	Golgi-associated plant pathogenesis-related protein 1 OS=Homo sapiens GN=GLIPR2 PE=1 SV=3 - [GAPR1_HUMAN]	70.40	40.26	6	6	18	4.382	5.674
P28799	Granulins OS=Homo sapiens GN=GRN PE=1 SV=2 - [GRN_HUMAN]	9.72	7.08	3	3	3	1.068	0.534
B4DWV5	GrpE protein homolog OS=Homo sapiens GN=GRPEL1 PE=2 SV=1 - [B4DWV5_HUMAN]	14.16	23.98	4	4	4	0.192	0.138
P62826	GTP-binding nuclear protein Ran OS=Homo sapiens GN=RAN PE=1 SV=3 - [RAN_HUMAN]	17.01	20.83	4	4	5	0.337	1.051
O00178	GTP-binding protein 1 OS=Homo sapiens GN=GTPBP1 PE=1 SV=3 - [GTPB1_HUMAN]	13.56	2.99	2	2	4	0.436	0.476
Q9BX10	GTP-binding protein 2 OS=Homo sapiens GN=GTPBP2 PE=2 SV=1 - [GTPB2_HUMAN]	5.70	3.65	2	2	2	0.141	0.138
P01116	GTPase KRas OS=Homo sapiens GN=KRAS PE=1 SV=1 - [RASK_HUMAN]	50.33	29.10	3	5	14	2.097	2.059
P01111	GTPase NRas OS=Homo sapiens GN=NRAS PE=1 SV=1 - [RASN_HUMAN]	35.83	31.22	3	5	10	0.776	0.764
Q14C86	GTPase-activating protein and VPS9 domain-containing protein 1 OS=Homo sapiens GN=GAPVD1 PE=1 SV=2 - [GAPD1_HUMAN]	108.64	15.49	21	22	32	1.496	1.387
P04899	Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 PE=1 SV=3 - [GNAI2_HUMAN]	84.95	32.11	5	12	26	0.644	0.860
P59768	Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2 OS=Homo sapiens GN=GNG2 PE=1 SV=2 - [GBG2_HUMAN]	46.21	61.97	4	4	14	0.757	0.784
P63218	Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-5 OS=Homo sapiens GN=GNG5 PE=1 SV=3 - [GBG5_HUMAN]	55.36	33.82	3	3	19	0.895	1.057
P62873	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1 OS=Homo sapiens GN=GNB1 PE=1 SV=3 - [GBB1_HUMAN]	69.86	24.41	5	8	20	1.134	1.638
P62879	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 OS=Homo sapiens GN=GNB2 PE=1 SV=3 - [GBB2_HUMAN]	71.63	24.41	5	8	21	0.518	0.659
P08754	Guanine nucleotide-binding protein G(k) subunit alpha OS=Homo sapiens GN=GNAI3 PE=1 SV=3 - [GNAI3_HUMAN]	86.25	33.62	5	12	27	0.546	1.087
P50148	Guanine nucleotide-binding protein G(q) subunit alpha OS=Homo sapiens GN=GNAQ PE=1 SV=4 - [GNAQ_HUMAN]	25.30	16.16	3	6	8	0.887	0.683
P63092	Guanine nucleotide-binding protein G(s) subunit alpha isoforms short OS=Homo sapiens GN=GNAS PE=1 SV=1 - [GNAS2_HUMAN]	70.93	18.02	5	7	20	0.967	1.168
P29992	Guanine nucleotide-binding protein subunit alpha-11 OS=Homo sapiens GN=GNA11 PE=1 SV=2 - [GNA11_HUMAN]	14.14	10.31	2	5	5	0.389	0.306
Q14344	Guanine nucleotide-binding protein subunit alpha-13 OS=Homo sapiens GN=GNA13 PE=1 SV=2 - [GNA13_HUMAN]	76.81	32.89	11	13	23	0.396	0.448
P63244	Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Homo sapiens GN=GNB2L1 PE=1 SV=3 - [GBLP_HUMAN]	40.55	23.97	9	9	13	0.092	0.116
B2RDM2	HCG1811539, isoform CRA_b OS=Homo sapiens GN=TXNDC5 PE=2 SV=1 - [B2RDM2_HUMAN]	30.48	20.37	5	6	9	1.107	0.904
A2A3U5	HCG20471, isoform CRA_d OS=Homo sapiens GN=OPRS1 PE=2 SV=1 - [A2A3U5_HUMAN]	5.28	7.29	2	2	2	0.111	0.175
B8ZZL8	Heat shock 10kDa protein 1 (Chaperonin 10), isoform CRA_b OS=Homo sapiens GN=HSPE1 PE=3 SV=1 - [B8ZZL8_HUMAN]	79.07	59.41	8	8	24	0.037	0.067
P08107	Heat shock 70 kDa protein 1A/1B OS=Homo sapiens GN=HSPA1A PE=1 SV=5 - [HSP71_HUMAN]	244.67	33.85	15	21	74	1.045	0.697
P34932	Heat shock 70 kDa protein 4 OS=Homo sapiens GN=HSPA4 PE=1 SV=4 - [HSP74_HUMAN]	106.68	24.88	19	20	33	0.830	1.188
P11142	Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1 - [HSP7C_HUMAN]	415.84	48.30	27	35	126	1.143	1.249
P04792	Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2 - [HSPB1_HUMAN]	44.61	31.71	6	6	12	0.323	0.512
P07900	Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5 - [HS90A_HUMAN]	220.18	35.66	16	28	68	0.557	0.621
P08238	Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4 - [HS90B_HUMAN]	123.98	26.93	6	19	38	0.609	0.404
P09601	Heme oxygenase 1 OS=Homo sapiens GN=HMOX1 PE=1 SV=1 - [HMOX1_HUMAN]	18.66	10.42	3	3	6	0.667	0.218
Q9BXL5	Hemogen OS=Homo sapiens GN=HEMGN PE=1 SV=1 - [HEMGN_HUMAN]	50.22	17.77	9	9	16	0.111	0.140
P69905	Hemoglobin subunit alpha OS=Homo sapiens GN=HBA1 PE=1 SV=2 - [HBA_HUMAN]	351.10	67.61	6	7	100	0.796	0.447
P68871	Hemoglobin subunit beta OS=Homo sapiens GN=HBB PE=1 SV=2 - [HBB_HUMAN]	470.79	85.03	5	12	130	1.018	0.283
P02042	Hemoglobin subunit delta OS=Homo sapiens GN=HBD PE=1 SV=2 - [HBD_HUMAN]	240.15	76.19	4	11	66	2.447	0.371
P69892	Hemoglobin subunit gamma-2 OS=Homo sapiens GN=HBG2 PE=1 SV=2 - [HBG2_HUMAN]	601.36	77.55	3	12	161	0.520	0.590
Q6B0K9	Hemoglobin subunit mu OS=Homo sapiens GN=HBM PE=2 SV=1 - [HBM_HUMAN]	16.35	17.73	2	2	5	0.583	0.515
P02008	Hemoglobin subunit zeta OS=Homo sapiens GN=HBZ PE=1 SV=2 - [HBAZ_HUMAN]	67.95	36.62	4	5	23	1.114	0.997
D9YZU8	Hemoglobin, gamma A OS=Homo sapiens GN=HBG1 PE=3 SV=1 - [D9YZU8_HUMAN]	454.36	77.55	3	12	128	0.617	0.493
P51858	Hepatoma-derived growth factor OS=Homo sapiens GN=HDGF PE=1 SV=1 - [HDGF_HUMAN]	27.27	27.50	5	5	8	0.010	0.211
P09651	Heterogeneous nuclear ribonucleoprotein A1 OS=Homo sapiens GN=HNRNPA1 PE=1 SV=5 - [ROA1_HUMAN]	110.65	17.20	4	7	34	0.108	0.086
P31942	Heterogeneous nuclear ribonucleoprotein H3 OS=Homo sapiens GN=HNRNPH3 PE=1 SV=2 - [HNRH3_HUMAN]	8.09	8.67	2	2	2	0.029	0.082
Q5T6W5	Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK PE=2 SV=1 - [Q5T6W5_HUMAN]	75.89	27.34	11	11	21	0.105	0.175
P14866	Heterogeneous nuclear ribonucleoprotein L OS=Homo sapiens GN=HNRNPL PE=1 SV=2 - [HNRPL_HUMAN]	17.00	5.09	3	3	5	0.717	0.217
P52272	Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens GN=HNRNPM PE=1 SV=3 - [HNRPM_HUMAN]	39.15	11.51	9	9	12	0.068	0.057
P22626	Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens GN=HNRNPA2B1 PE=1 SV=2 - [ROA2_HUMAN]	131.98	34.56	10	13	41	0.113	0.066
P26583	High mobility group protein B2 OS=Homo sapiens GN=HMGB2 PE=1 SV=2 - [HMGB2_HUMAN]	8.19	7.66	2	2	3	0.029	0.028
Q9BX68	Histidine triad nucleotide-binding protein 2, mitochondrial OS=Homo sapiens GN=HINT2 PE=1 SV=1 - [HINT2_HUMAN]	15.90	14.72	2	2	5	0.199	0.187
P16402	Histone H1.3 OS=Homo sapiens GN=HIST1H1D PE=1 SV=2 - [H13_HUMAN]	86.09	36.20	4	11	27	0.593	0.039
P10412	Histone H1.4 OS=Homo sapiens GN=HIST1H1E PE=1 SV=2 - [H14_HUMAN]	76.32	37.44	2	10	24	0.391	0.054
P16401	Histone H1.5 OS=Homo sapiens GN=HIST1H1B PE=1 SV=3 - [H15_HUMAN]	72.68	35.40	7	11	24	0.163	0.022

O60814	Histone H2B type 1-K OS=Homo sapiens GN=HIST1H2BK PE=1 SV=3 - [H2B1K_HUMAN]	58.92	45.24	7	7	21	0.154	0.017
P68431	Histone H3.1 OS=Homo sapiens GN=HIST1H3A PE=1 SV=2 - [H31_HUMAN]	34.78	28.68	6	6	12	0.553	0.036
P62805	Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2 - [H4_HUMAN]	99.96	50.49	5	5	30	0.388	0.022
B0UX83	HLA-B associated transcript 3 OS=Homo sapiens GN=BAT3 PE=4 SV=1 - [B0UX83_HUMAN]	14.06	4.09	4	4	4	0.432	0.456
P51610	Host cell factor 1 OS=Homo sapiens GN=HCFC1 PE=1 SV=2 - [HCFC1_HUMAN]	7.20	0.98	2	2	2	0.315	0.388
P50502	Hsc70-interacting protein OS=Homo sapiens GN=ST13 PE=1 SV=2 - [F10A1_HUMAN]	75.99	27.64	11	11	24	0.961	1.827
Q16543	Hsp90 co-chaperone Cdc37 OS=Homo sapiens GN=CDC37 PE=1 SV=1 - [CDC37_HUMAN]	12.56	8.99	4	4	4	0.254	0.401
Q16836	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial OS=Homo sapiens GN=HADH PE=1 SV=3 - [HCDH_HUMAN]	22.67	16.88	6	6	7	0.028	0.128
Q16775	Hydroxyacylglutathione hydrolase, mitochondrial OS=Homo sapiens GN=HAGH PE=1 SV=2 - [GLO2_HUMAN]	40.41	18.51	5	5	14	1.394	1.013
Q6YN16	Hydroxysteroid dehydrogenase-like protein 2 OS=Homo sapiens GN=HSDL2 PE=1 SV=1 - [HSDL2_HUMAN]	12.63	6.94	3	3	4	0.180	0.167
Q9Y4L1	Hypoxia up-regulated protein 1 OS=Homo sapiens GN=HYOU1 PE=1 SV=1 - [HYOU1_HUMAN]	79.46	15.02	15	15	23	0.621	0.592
Q14974	Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2 - [IMB1_HUMAN]	104.21	15.41	14	14	30	0.462	0.837
O00410	Importin-5 OS=Homo sapiens GN=IPO5 PE=1 SV=4 - [IPO5_HUMAN]	42.67	6.56	7	7	12	0.783	1.506
O95373	Importin-7 OS=Homo sapiens GN=IPO7 PE=1 SV=1 - [IPO7_HUMAN]	33.02	6.74	6	6	9	2.597	2.677
P05556	Integrin beta-1 OS=Homo sapiens GN=ITGB1 PE=1 SV=2 - [ITB1_HUMAN]	24.57	10.40	7	7	7	0.224	0.176
Q14773	Intercellular adhesion molecule 4 OS=Homo sapiens GN=ICAM4 PE=2 SV=1 - [ICAM4_HUMAN]	18.22	19.93	5	5	6	2.414	4.418
Q12905	Interleukin enhancer-binding factor 2 OS=Homo sapiens GN=ILF2 PE=1 SV=2 - [ILF2_HUMAN]	12.12	9.49	3	3	3	0.214	0.242
P48735	Isocitrate dehydrogenase [NADP], mitochondrial OS=Homo sapiens GN=IDH2 PE=1 SV=2 - [IDHP_HUMAN]	115.62	34.73	16	16	38	0.103	0.216
P53990	IST1 homolog OS=Homo sapiens GN=KIAA0174 PE=1 SV=1 - [IST1_HUMAN]	16.50	11.54	5	5	5	0.774	1.196
Q9Y624	Junctional adhesion molecule A OS=Homo sapiens GN=F11R PE=1 SV=1 - [JAM1_HUMAN]	18.54	16.05	6	6	6	3.475	1.624
Q5TFJ7	Karyopherin alpha 6 (Importin alpha 7) (Fragment) OS=Homo sapiens GN=KPNA6 PE=2 SV=1 - [Q5TFJ7_HUMAN]	12.74	9.35	2	3	4	1.351	1.710
P23276	Kell blood group glycoprotein OS=Homo sapiens GN=KEL PE=1 SV=2 - [KELL_HUMAN]	53.63	10.52	8	8	18	3.245	2.189
P13645	Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6 - [K1C10_HUMAN]	20.74	8.56	4	5	6	0.313	0.406
P35527	Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3 - [K1C9_HUMAN]	13.05	6.90	2	3	3	0.275	0.466
P04264	Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6 - [K2C1_HUMAN]	36.47	14.91	11	11	12	0.463	0.460
Q17RZ5	Kinectin 1 (Kinesin receptor) OS=Homo sapiens GN=KTN1 PE=2 SV=1 - [Q17RZ5_HUMAN]	9.05	2.53	3	3	3	0.014	0.106
P33176	Kinesin-1 heavy chain OS=Homo sapiens GN=KIF5B PE=1 SV=1 - [KINH_HUMAN]	30.75	5.50	5	5	10	1.284	0.901
P07195	L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2 - [LDHB_HUMAN]	90.82	26.35	7	8	25	0.429	1.664
E9PH51	L-lactate dehydrogenase OS=Homo sapiens GN=LDHA PE=3 SV=2 - [E9PH51_HUMAN]	74.04	30.16	9	10	22	0.134	0.237
Q7Z4W1	L-xylulose reductase OS=Homo sapiens GN=DCXR PE=1 SV=2 - [DCXR_HUMAN]	9.85	7.38	2	2	3	0.220	0.622
Q6PKG0	La-related protein 1 OS=Homo sapiens GN=LARP1 PE=1 SV=2 - [LARP1_HUMAN]	15.73	3.92	4	5	5	0.191	0.152
Q9NS86	LanC-like protein 2 OS=Homo sapiens GN=LANCL2 PE=1 SV=1 - [LANC2_HUMAN]	22.82	12.22	5	5	7	2.886	2.943
Q01650	Large neutral amino acids transporter small subunit 1 OS=Homo sapiens GN=SLC7A5 PE=1 SV=2 - [LAT1_HUMAN]	18.41	6.31	3	3	5	0.821	0.052
Q14696	LDLR chaperone MESD OS=Homo sapiens GN=MESDC2 PE=1 SV=2 - [MESD_HUMAN]	5.83	8.97	2	2	2	1.009	0.912
O95202	LETM1 and EF-hand domain-containing protein 1, mitochondrial OS=Homo sapiens GN=LETM1 PE=1 SV=1 - [LETM1_HUMAN]	15.51	5.82	4	4	5	0.077	0.143
Q8N9N7	Leucine-rich repeat-containing protein 57 OS=Homo sapiens GN=LRRC57 PE=1 SV=1 - [LRC57_HUMAN]	44.66	32.64	8	8	14	1.527	1.386
Q96AG4	Leucine-rich repeat-containing protein 59 OS=Homo sapiens GN=LRRC59 PE=1 SV=1 - [LRC59_HUMAN]	18.71	11.07	4	4	6	0.337	0.354
O95573	Long-chain-fatty-acid--CoA ligase 3 OS=Homo sapiens GN=ACSL3 PE=1 SV=3 - [ACSL3_HUMAN]	14.74	5.14	2	3	4	0.380	0.477
Q969J3	Loss of heterozygosity 12 chromosomal region 1 protein OS=Homo sapiens GN=LOH12CR1 PE=1 SV=1 - [L12R1_HUMAN]	6.15	8.67	2	2	2	0.088	0.241
P05455	Lupus La protein OS=Homo sapiens GN=SSB PE=1 SV=2 - [LA_HUMAN]	10.17	6.13	3	3	3	0.439	0.438
Q6ZWT7	Lysophospholipid acyltransferase 2 OS=Homo sapiens GN=MBOAT2 PE=2 SV=2 - [MBOA2_HUMAN]	14.41	6.54	3	3	4	1.151	1.168
Q14108	Lysosome membrane protein 2 OS=Homo sapiens GN=SCARB2 PE=1 SV=2 - [SCRB2_HUMAN]	9.36	5.44	3	3	3	0.149	0.141
P11279	Lysosome-associated membrane glycoprotein 1 OS=Homo sapiens GN=LAMP1 PE=1 SV=3 - [LAMP1_HUMAN]	21.32	8.39	4	4	6	0.269	0.073
P40925	Malate dehydrogenase, cytoplasmic OS=Homo sapiens GN=MDH1 PE=1 SV=4 - [MDHC_HUMAN]	18.40	15.87	5	5	5	0.185	0.516
P40926	Malate dehydrogenase, mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=3 - [MDHM_HUMAN]	108.11	50.89	14	14	30	0.064	0.136
B8ZZG1	Membrane protein, palmitoylated 6 (MAGUK p55 subfamily member 6), isoform CRA_a OS=Homo sapiens GN=MPP6 PE=4 SV=1 - [B8ZZG1_HUMAN]	18.11	8.88	4	4	6	1.872	1.552
P51811	Membrane transport protein XK OS=Homo sapiens GN=XK PE=1 SV=5 - [XK_HUMAN]	40.36	9.91	6	6	13	2.411	2.520
O15173	Membrane-associated progesterone receptor component 2 OS=Homo sapiens GN=PGRMC2 PE=1 SV=1 - [PGRC2_HUMAN]	20.86	24.22	5	5	6	0.643	0.556
P35240	Merlin OS=Homo sapiens GN=NF2 PE=1 SV=1 - [MERL_HUMAN]	14.39	4.37	2	3	5	1.024	2.050
P50579	Methionine aminopeptidase 2 OS=Homo sapiens GN=METAP2 PE=1 SV=1 - [AMPM2_HUMAN]	8.66	6.90	2	2	2	0.107	0.162
Q9H8H3	Methyltransferase-like protein 7A OS=Homo sapiens GN=METTL7A PE=1 SV=1 - [MET7A_HUMAN]	12.95	17.21	3	3	4	1.487	1.273
Q8IY33	MICAL-like protein 2 OS=Homo sapiens GN=MICALL2 PE=1 SV=1 - [MILK2_HUMAN]	39.63	9.40	8	8	11	0.673	0.701
Q15691	Microtubule-associated protein RP/EB family member 1 OS=Homo sapiens GN=MAPRE1 PE=1 SV=3 - [MARE1_HUMAN]	5.69	10.07	2	2	2	1.264	1.394
Q8TCT9	Minor histocompatibility antigen H13 OS=Homo sapiens GN=HM13 PE=1 SV=1 - [HM13_HUMAN]	6.64	4.77	2	2	2	0.423	0.625
Q02978	Mitochondrial 2-oxoglutarate/malate carrier protein OS=Homo sapiens GN=SLC25A11 PE=1 SV=3 - [M2OM_HUMAN]	18.03	18.79	4	5	5	0.081	0.175
Q9Y3D6	Mitochondrial fission 1 protein OS=Homo sapiens GN=FIS1 PE=1 SV=2 - [FIS1_HUMAN]	6.06	13.16	2	2	2	0.231	0.261

O43615	Mitochondrial import inner membrane translocase subunit TIM44 OS=Homo sapiens GN=TIMM44 PE=1 SV=2 - [TIM44_HUMAN]	9.19	5.97	3	3	3	0.106	0.051
Q9NYZ2	Mitoferrin-1 OS=Homo sapiens GN=SLC25A37 PE=1 SV=2 - [MFRN1_HUMAN]	12.96	11.83	3	4	4	0.075	0.211
P26038	Moesin OS=Homo sapiens GN=MSN PE=1 SV=3 - [MOES_HUMAN]	245.89	40.73	23	33	75	0.428	1.023
P53985	Monocarboxylate transporter 1 OS=Homo sapiens GN=SLC16A1 PE=1 SV=3 - [MOT1_HUMAN]	61.04	9.60	6	6	18	0.241	0.866
O15439	Multidrug resistance-associated protein 4 OS=Homo sapiens GN=ABCC4 PE=1 SV=3 - [MRP4_HUMAN]	60.66	11.25	15	15	18	1.213	0.769
Q9UNW1	Multiple inositol polyphosphate phosphatase 1 OS=Homo sapiens GN=MINPP1 PE=1 SV=1 - [MINP1_HUMAN]	10.20	5.75	3	3	3	0.729	0.928
P12829	Myosin light chain 4 OS=Homo sapiens GN=MYL4 PE=1 SV=3 - [MYL4_HUMAN]	66.79	53.30	8	8	20	0.226	0.777
P60660	Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2 - [MYL6_HUMAN]	11.02	24.50	3	3	3	0.279	0.323
P19105	Myosin regulatory light chain 12A OS=Homo sapiens GN=MYL12A PE=1 SV=2 - [ML12A_HUMAN]	28.99	22.22	4	4	8	0.287	0.741
P35580	Myosin-10 OS=Homo sapiens GN=MYH10 PE=1 SV=3 - [MYH10_HUMAN]	667.07	39.27	74	88	200	0.180	0.766
P35579	Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4 - [MYH9_HUMAN]	740.90	45.36	83	96	229	0.292	0.710
Q13423	NAD(P) transhydrogenase, mitochondrial OS=Homo sapiens GN=NNT PE=1 SV=3 - [NNTM_HUMAN]	75.97	18.14	18	18	23	0.124	0.196
O00483	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4 OS=Homo sapiens GN=NDUFA4 PE=1 SV=1 - [NDUA4_HUMAN]	8.05	18.52	2	2	3	0.086	0.155
O95182	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 7 OS=Homo sapiens GN=NDUFA7 PE=1 SV=3 - [NDUA7_HUMAN]	6.29	8.85	2	2	2	0.382	0.169
O96000	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10 OS=Homo sapiens GN=NDUFB10 PE=1 SV=3 - [NDUBA_HUMAN]	6.35	12.21	2	2	2	0.111	0.262
P17568	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7 OS=Homo sapiens GN=NDUFB7 PE=1 SV=4 - [NDUB7_HUMAN]	5.17	13.87	2	2	2	0.265	0.253
P19404	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial OS=Homo sapiens GN=NDUFV2 PE=1 SV=2 - [NDUV2_HUMAN]	6.56	7.63	2	2	2		0.080
O75489	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial OS=Homo sapiens GN=NDUFS3 PE=1 SV=1 - [NDUS3_HUMAN]	9.48	15.15	3	3	3	0.298	0.152
P00387	NADH-cytochrome b5 reductase 3 OS=Homo sapiens GN=CYB5R3 PE=1 SV=3 - [NB5R3_HUMAN]	24.28	16.61	4	4	7	1.134	0.931
Q13765	Nascent polypeptide-associated complex subunit alpha OS=Homo sapiens GN=NACA PE=1 SV=1 - [NACA_HUMAN]	7.50	13.49	2	2	2	0.020	0.297
A2RRP1	Neuroblastoma-amplified sequence OS=Homo sapiens GN=NBAS PE=1 SV=2 - [NBAS_HUMAN]	21.58	2.66	7	7	7	0.690	0.693
B2RAL7	Neuroplastin OS=Homo sapiens GN=NPTN PE=2 SV=1 - [B2RAL7_HUMAN]	17.41	8.51	2	2	5	2.937	2.552
Q14697	Neutral alpha-glucosidase AB OS=Homo sapiens GN=GANAB PE=1 SV=3 - [GANAB_HUMAN]	108.46	19.70	4	19	35	0.873	0.787
Q15758	Neutral amino acid transporter B(0) OS=Homo sapiens GN=SLC1A5 PE=1 SV=2 - [AAAT_HUMAN]	23.22	5.73	3	3	6	0.204	0.100
Q6PIU2	Neutral cholesterol ester hydrolase 1 OS=Homo sapiens GN=NCEH1 PE=1 SV=3 - [NCEH1_HUMAN]	44.61	20.83	7	7	12	0.715	0.717
Q49AL4	NMNAT3 protein OS=Homo sapiens GN=NMNAT3 PE=2 SV=1 - [Q49AL4_HUMAN]	10.81	11.97	2	2	3	0.703	0.350
P69849	Nodal modulator 3 OS=Homo sapiens GN=NOMO3 PE=2 SV=2 - [NOMO3_HUMAN]	6.01	1.72	2	2	2	0.848	0.653
Q9UNZ2	NSFL1 cofactor p47 OS=Homo sapiens GN=NSFL1C PE=1 SV=2 - [NSF1C_HUMAN]	62.35	38.92	11	11	19	1.156	1.728
Q14980	Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 PE=1 SV=2 - [NUMA1_HUMAN]	11.78	1.80	3	3	3	0.428	0.235
P61970	Nuclear transport factor 2 OS=Homo sapiens GN=NUTF2 PE=1 SV=1 - [NTF2_HUMAN]	6.15	11.02	2	2	2	0.188	0.440
Q9H1E3	Nuclear ubiquitous casein and cyclin-dependent kinases substrate OS=Homo sapiens GN=NUCKS1 PE=1 SV=1 - [NUCKS_HUMAN]	6.19	6.58	2	2	2	0.086	0.169
P67809	Nuclease-sensitive element-binding protein 1 OS=Homo sapiens GN=YBX1 PE=1 SV=3 - [YBOX1_HUMAN]	83.79	41.98	7	9	26	0.122	0.160
P19338	Nucleolin OS=Homo sapiens GN=NCL PE=1 SV=3 - [NUCL_HUMAN]	30.89	8.73	9	9	10	0.116	0.115
Q9BYG9	Nucleophosmin (Nucleolar phosphoprotein B23, numatrin) OS=Homo sapiens GN=NPM1 PE=2 SV=1 - [Q9BYG9_HUMAN]	9.09	10.04	3	3	3	0.274	0.200
B3KV44	Nucleosome assembly protein 1-like 1, isoform CRA_c OS=Homo sapiens GN=NAP1L1 PE=2 SV=1 - [B3KV44_HUMAN]	22.89	13.93	2	3	7	1.772	2.595
Q9NTK5	Obg-like ATPase 1 OS=Homo sapiens GN=OLA1 PE=1 SV=2 - [OLA1_HUMAN]	24.74	13.89	6	6	8	0.814	1.007
Q96CV9	Optineurin OS=Homo sapiens GN=OPTN PE=1 SV=2 - [OPTN_HUMAN]	42.95	12.48	7	7	13	0.626	0.898
P04181	Ornithine aminotransferase, mitochondrial OS=Homo sapiens GN=OAT PE=1 SV=1 - [OAT_HUMAN]	43.84	23.69	10	10	13	0.081	0.081
Q9BRP8	Partner of Y14 and mago OS=Homo sapiens GN=WIBG PE=1 SV=1 - [WIBG_HUMAN]	12.31	18.14	3	3	4	0.071	0.141
P62937	Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2 - [PPIA_HUMAN]	14.56	22.42	4	4	5	0.156	0.176
P23284	Peptidyl-prolyl cis-trans isomerase B OS=Homo sapiens GN=PPIB PE=1 SV=2 - [PPIB_HUMAN]	37.08	27.31	7	7	12	0.602	0.986
Q00688	Peptidyl-prolyl cis-trans isomerase FKBP3 OS=Homo sapiens GN=FKBP3 PE=1 SV=1 - [FKBP3_HUMAN]	80.75	53.13	14	14	25	0.637	1.621
Q02790	Peptidyl-prolyl cis-trans isomerase FKBP4 OS=Homo sapiens GN=FKBP4 PE=1 SV=3 - [FKBP4_HUMAN]	6.14	3.49	2	2	2	0.452	0.876
Q9Y237	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4 OS=Homo sapiens GN=PIN4 PE=1 SV=1 - [PIN4_HUMAN]	21.87	19.08	3	3	6	0.908	3.833
O60664	Perilipin-3 OS=Homo sapiens GN=PLIN3 PE=1 SV=3 - [PLIN3_HUMAN]	7.60	3.92	2	2	2	1.664	1.327
Q06830	Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1 - [PRDX1_HUMAN]	127.67	56.28	8	10	37	0.693	2.303
P32119	Peroxiredoxin-2 OS=Homo sapiens GN=PRDX2 PE=1 SV=5 - [PRDX2_HUMAN]	432.84	59.09	10	11	136	1.282	3.425
P30044	Peroxiredoxin-5, mitochondrial OS=Homo sapiens GN=PRDX5 PE=1 SV=4 - [PRDX5_HUMAN]	10.56	10.28	2	2	3	0.713	0.240
Q9Y285	Phenylalanyl-tRNA synthetase alpha chain OS=Homo sapiens GN=FARSA PE=1 SV=3 - [SYFA_HUMAN]	19.39	8.66	4	5	7	0.412	0.188
Q9NSD9	Phenylalanyl-tRNA synthetase beta chain OS=Homo sapiens GN=FARSB PE=1 SV=3 - [SYFB_HUMAN]	57.34	23.43	14	15	18	0.353	0.197
Q00325	Phosphate carrier protein, mitochondrial OS=Homo sapiens GN=SLC25A3 PE=1 SV=2 - [MPCP_HUMAN]	33.51	15.47	6	6	10	0.021	0.107
Q92539	Phosphatidate phosphatase LPIN2 OS=Homo sapiens GN=LPIN2 PE=1 SV=1 - [LPIN2_HUMAN]	17.87	4.69	4	4	5	0.981	0.941
Q9BTU6	Phosphatidylinositol 4-kinase type 2-alpha OS=Homo sapiens GN=PI4K2A PE=1 SV=1 - [P4K2A_HUMAN]	80.24	41.54	16	16	26	0.171	0.235
Q92835	Phosphatidylinositol-3,4,5-trisphosphate 5-phosphatase 1 OS=Homo sapiens GN=INPP5D PE=1 SV=2 - [SHIP1_HUMAN]	26.74	5.63	7	7	9	0.559	0.520
P48426	Phosphatidylinositol-5-phosphate 4-kinase type-2 alpha OS=Homo sapiens GN=PIP4K2A PE=1 SV=2 - [PI42A_HUMAN]	60.49	29.80	12	13	19	2.069	0.963
Q13492	Phosphatidylinositol-binding clathrin assembly protein OS=Homo sapiens GN=PICALM PE=1 SV=2 - [PICAL_HUMAN]	64.67	13.96	9	11	21	0.467	0.341

Q16822	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=Homo sapiens GN=PCK2 PE=1 SV=3 - [PCKGM_HUMAN]	17.09	6.41	4	4	5	0.039	0.068
B7Z7A9	Phosphoglycerate kinase OS=Homo sapiens GN=PGK1 PE=2 SV=1 - [B7Z7A9_HUMAN]	38.93	18.77	8	8	12	0.265	0.890
Q9Y263	Phospholipase A-2-activating protein OS=Homo sapiens GN=PLAA PE=1 SV=2 - [PLAP_HUMAN]	8.86	2.39	2	2	2	0.238	0.496
P36969	Phospholipid hydroperoxide glutathione peroxidase, mitochondrial OS=Homo sapiens GN=GPX4 PE=1 SV=3 - [GPX4_HUMAN]	27.42	22.84	6	6	8	1.306	1.299
O60256	Phosphoribosyl pyrophosphate synthase-associated protein 2 OS=Homo sapiens GN=PRPSAP2 PE=1 SV=1 - [KPRB_HUMAN]	59.43	21.41	5	7	17	1.633	1.274
Q9GZP4	PITH domain-containing protein 1 OS=Homo sapiens GN=PITHD1 PE=1 SV=1 - [PITH1_HUMAN]	11.45	18.01	4	4	4	1.470	0.849
P20020	Plasma membrane calcium-transporting ATPase 1 OS=Homo sapiens GN=ATP2B1 PE=1 SV=3 - [AT2B1_HUMAN]	97.19	17.33	9	19	28	1.149	1.048
P23634	Plasma membrane calcium-transporting ATPase 4 OS=Homo sapiens GN=ATP2B4 PE=1 SV=2 - [AT2B4_HUMAN]	154.95	21.11	16	26	46	2.245	2.066
Q8NC51	Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2 - [PAIRB_HUMAN]	51.35	22.30	10	10	15	0.068	0.122
P13796	Plastin-2 OS=Homo sapiens GN=LCP1 PE=1 SV=6 - [PLSL_HUMAN]	5.43	4.31	2	2	2	0.495	0.644
Q68Y55	Poly(RC) binding protein 2 OS=Homo sapiens GN=PCBP2 PE=2 SV=1 - [Q68Y55_HUMAN]	38.24	21.75	2	6	12	0.431	0.236
Q15365	Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2 - [PCBP1_HUMAN]	49.40	30.90	5	9	15	0.095	0.141
P11940	Polyadenylate-binding protein 1 OS=Homo sapiens GN=PABPC1 PE=1 SV=2 - [PABP1_HUMAN]	39.37	18.71	11	11	12	0.484	0.346
P26599	Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 PE=1 SV=1 - [PTBP1_HUMAN]	32.78	9.60	6	6	10	1.272	0.558
Q9UHV9	Prefoldin subunit 2 OS=Homo sapiens GN=PFDN2 PE=1 SV=1 - [PFD2_HUMAN]	10.22	12.99	2	2	3	0.084	0.334
P07602	Proactivator polypeptide OS=Homo sapiens GN=PSAP PE=1 SV=2 - [SAP_HUMAN]	97.18	20.23	13	13	30	0.075	0.164
Q9Y4D8	Probable E3 ubiquitin-protein ligase C12orf51 OS=Homo sapiens GN=C12orf51 PE=1 SV=5 - [K0614_HUMAN]	42.37	2.80	11	11	13	0.180	0.282
Q9H3G5	Probable serine carboxypeptidase CPVL OS=Homo sapiens GN=CPVL PE=1 SV=2 - [CPVL_HUMAN]	14.87	7.98	4	4	5	0.127	0.152
Q93008	Probable ubiquitin carboxyl-terminal hydrolase FAF-X OS=Homo sapiens GN=USP9X PE=1 SV=3 - [USP9X_HUMAN]	120.29	9.49	27	27	38	0.548	0.845
O14737	Programmed cell death protein 5 OS=Homo sapiens GN=PDCD5 PE=1 SV=3 - [PDCD5_HUMAN]	22.94	34.40	5	5	7	0.281	0.812
Q99623	Prohibitin-2 OS=Homo sapiens GN=PHB2 PE=1 SV=2 - [PHB2_HUMAN]	67.14	37.79	12	12	20	0.109	0.156
Q9UQ80	Proliferation-associated protein 2G4 OS=Homo sapiens GN=PA2G4 PE=1 SV=3 - [PA2G4_HUMAN]	96.44	37.82	14	14	31	0.214	0.348
Q16186	Proteasomal ubiquitin receptor ADRM1 OS=Homo sapiens GN=ADRM1 PE=1 SV=2 - [ADRM1_HUMAN]	16.06	8.11	3	3	5	0.368	0.250
A8K3Z3	Proteasome (Prosome, macropain) 26S subunit, ATPase, 5, isoform CRA_b OS=Homo sapiens GN=PSMC5 PE=2 SV=1 - [A8K3Z3_HUMAN]	66.99	23.87	9	10	19	1.318	0.756
B1AJY5	Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 10 OS=Homo sapiens GN=PSMD10 PE=4 SV=1 - [B1AJY5_HUMAN]	6.25	8.11	2	2	2	0.590	0.401
Q06323	Proteasome activator complex subunit 1 OS=Homo sapiens GN=PSME1 PE=1 SV=1 - [PSME1_HUMAN]	102.94	46.99	13	13	33	3.067	1.364
Q9UL46	Proteasome activator complex subunit 2 OS=Homo sapiens GN=PSME2 PE=1 SV=4 - [PSME2_HUMAN]	76.44	26.36	8	8	21	2.151	1.336
P25786	Proteasome subunit alpha type-1 OS=Homo sapiens GN=PSMA1 PE=1 SV=1 - [PSA1_HUMAN]	200.52	49.81	15	15	62	2.716	1.815
P25787	Proteasome subunit alpha type-2 OS=Homo sapiens GN=PSMA2 PE=1 SV=2 - [PSA2_HUMAN]	47.08	30.77	7	7	15	2.287	1.732
P25788	Proteasome subunit alpha type-3 OS=Homo sapiens GN=PSMA3 PE=1 SV=2 - [PSA3_HUMAN]	180.21	38.82	12	12	55	2.712	1.638
P25789	Proteasome subunit alpha type-4 OS=Homo sapiens GN=PSMA4 PE=1 SV=1 - [PSA4_HUMAN]	92.59	39.08	11	11	29	2.055	1.741
P28066	Proteasome subunit alpha type-5 OS=Homo sapiens GN=PSMA5 PE=1 SV=3 - [PSA5_HUMAN]	119.13	34.02	7	7	37	2.803	1.661
P60900	Proteasome subunit alpha type-6 OS=Homo sapiens GN=PSMA6 PE=1 SV=1 - [PSA6_HUMAN]	110.91	51.63	13	13	32	3.356	1.954
O14818	Proteasome subunit alpha type-7 OS=Homo sapiens GN=PSMA7 PE=1 SV=1 - [PSA7_HUMAN]	93.15	38.31	10	10	28	2.921	1.817
P20618	Proteasome subunit beta type-1 OS=Homo sapiens GN=PSMB1 PE=1 SV=2 - [PSB1_HUMAN]	57.30	41.08	8	8	19	2.764	1.859
P49721	Proteasome subunit beta type-2 OS=Homo sapiens GN=PSMB2 PE=1 SV=1 - [PSB2_HUMAN]	55.52	17.91	6	6	18	2.327	1.644
P49720	Proteasome subunit beta type-3 OS=Homo sapiens GN=PSMB3 PE=1 SV=2 - [PSB3_HUMAN]	34.54	16.59	4	4	11	2.797	1.937
P28070	Proteasome subunit beta type-4 OS=Homo sapiens GN=PSMB4 PE=1 SV=4 - [PSB4_HUMAN]	50.08	20.45	4	4	14	3.065	1.836
P28074	Proteasome subunit beta type-5 OS=Homo sapiens GN=PSMB5 PE=1 SV=3 - [PSB5_HUMAN]	109.88	39.92	10	10	32	2.875	1.594
P28072	Proteasome subunit beta type-6 OS=Homo sapiens GN=PSMB6 PE=1 SV=4 - [PSB6_HUMAN]	59.06	17.57	5	5	17	2.764	1.773
Q99436	Proteasome subunit beta type-7 OS=Homo sapiens GN=PSMB7 PE=1 SV=1 - [PSB7_HUMAN]	70.67	21.30	8	8	21	3.496	1.928
Q5VYK3	Proteasome-associated protein ECM29 homolog OS=Homo sapiens GN=ECM29 PE=1 SV=2 - [ECM29_HUMAN]	11.84	1.84	4	4	4	0.860	0.484
P11171	Protein 4.1 OS=Homo sapiens GN=EPB41 PE=1 SV=4 - [41_HUMAN]	1234.38	44.44	8	44	389	3.289	3.928
O14744	Protein arginine N-methyltransferase 5 OS=Homo sapiens GN=PRMT5 PE=1 SV=4 - [ANM5_HUMAN]	20.48	10.83	7	7	7	1.372	1.590
Q9UKV8	Protein argonaute-2 OS=Homo sapiens GN=EIF2C2 PE=1 SV=3 - [AGO2_HUMAN]	279.08	42.49	31	31	88	4.027	3.638
Q9UKY7	Protein CDV3 homolog OS=Homo sapiens GN=CDV3 PE=1 SV=1 - [CDV3_HUMAN]	15.55	15.12	3	3	5	0.200	0.248
Q5TDH0	Protein DDI1 homolog 2 OS=Homo sapiens GN=DDI2 PE=1 SV=1 - [DDI2_HUMAN]	56.94	28.32	9	9	17	1.169	1.695
P13667	Protein disulfide-isomerase A4 OS=Homo sapiens GN=PDIA4 PE=1 SV=2 - [PDIA4_HUMAN]	44.23	18.29	10	10	14	0.959	1.098
P07237	Protein disulfide-isomerase OS=Homo sapiens GN=P4HB PE=1 SV=3 - [PDIA1_HUMAN]	201.00	41.54	25	25	62	1.034	0.874
Q99497	Protein DJ-1 OS=Homo sapiens GN=PARK7 PE=1 SV=2 - [PARK7_HUMAN]	12.46	15.34	3	3	4	0.086	0.270
P49257	Protein ERGIC-53 OS=Homo sapiens GN=LMAN1 PE=1 SV=2 - [LMAN1_HUMAN]	51.99	20.98	9	9	15	0.785	1.030
Q9NRY5	Protein FAM114A2 OS=Homo sapiens GN=FAM114A2 PE=1 SV=4 - [F1142_HUMAN]	7.75	5.15	2	2	2	0.296	1.043
Q96RT1	Protein LAP2 OS=Homo sapiens GN=ERBB2IP PE=1 SV=2 - [LAP2_HUMAN]	25.60	3.54	5	5	8	0.757	0.502
Q9NUP9	Protein lin-7 homolog C OS=Homo sapiens GN=LIN7C PE=1 SV=1 - [LIN7C_HUMAN]	12.65	12.18	3	3	4	1.525	1.108
Q92508	Protein PIEZO1 OS=Homo sapiens GN=FAM38A PE=1 SV=4 - [PIEZ1_HUMAN]	40.32	3.69	7	8	12	4.326	3.870
Q08AM6	Protein VAC14 homolog OS=Homo sapiens GN=VAC14 PE=1 SV=1 - [VAC14_HUMAN]	9.27	4.86	2	3	3	1.566	0.921

O75695	Protein XRP2 OS=Homo sapiens GN=RP2 PE=1 SV=4 - [XRP2_HUMAN]	35.38	14.86	6	6	11	1.607	1.388
P00491	Purine nucleoside phosphorylase OS=Homo sapiens GN=PNP PE=1 SV=2 - [PNPH_HUMAN]	15.75	9.69	3	3	5	0.250	0.795
Q9Y315	Putative deoxyribose-phosphate aldolase OS=Homo sapiens GN=DERA PE=1 SV=2 - [DEOC_HUMAN]	44.00	32.39	8	9	13	3.774	3.128
Q5HYI5	Putative uncharacterized protein DKFZp313C1541 OS=Homo sapiens GN=DKFZp313C1541 PE=2 SV=1 - [Q5HYI5_HUMAN]	25.48	28.71	2	5	7	1.544	1.159
P30613	Pyruvate kinase isozymes R/L OS=Homo sapiens GN=PKLR PE=1 SV=2 - [KPYR_HUMAN]	55.14	21.95	11	11	17	0.287	0.786
P50395	Rab GDP dissociation inhibitor beta OS=Homo sapiens GN=GDI2 PE=1 SV=2 - [GDIB_HUMAN]	12.49	8.99	3	4	4	0.328	0.629
Q96NA2	Rab-interacting lysosomal protein OS=Homo sapiens GN=RILP PE=1 SV=1 - [RILP_HUMAN]	10.98	7.48	3	3	3	0.181	0.403
P35241	Radixin OS=Homo sapiens GN=RDX PE=1 SV=1 - [RADI_HUMAN]	161.08	30.70	14	26	49	1.886	2.414
Q9UHA4	Ragulator complex protein LAMTOR3 OS=Homo sapiens GN=LAMTOR3 PE=1 SV=1 - [LTOR3_HUMAN]	7.62	20.97	2	2	2	0.180	0.335
P46060	Ran GTPase-activating protein 1 OS=Homo sapiens GN=RANGAP1 PE=1 SV=1 - [RAGP1_HUMAN]	14.48	7.67	4	4	4	0.739	1.082
P43487	Ran-specific GTPase-activating protein OS=Homo sapiens GN=RANBP1 PE=1 SV=1 - [RANG_HUMAN]	18.30	13.43	3	3	5	0.256	1.105
P63000	Ras-related C3 botulinum toxin substrate 1 OS=Homo sapiens GN=RAC1 PE=1 SV=1 - [RAC1_HUMAN]	132.59	42.71	9	10	40	2.099	2.215
P61026	Ras-related protein Rab-10 OS=Homo sapiens GN=RAB10 PE=1 SV=1 - [RAB10_HUMAN]	103.38	34.00	5	8	32	0.630	0.641
P62491	Ras-related protein Rab-11A OS=Homo sapiens GN=RAB11A PE=1 SV=3 - [RB11A_HUMAN]	27.45	23.61	5	5	8	0.203	0.201
P61106	Ras-related protein Rab-14 OS=Homo sapiens GN=RAB14 PE=1 SV=4 - [RAB14_HUMAN]	41.33	20.00	3	4	12	0.356	0.477
P62820	Ras-related protein Rab-1A OS=Homo sapiens GN=RAB1A PE=1 SV=3 - [RAB1A_HUMAN]	95.66	35.61	4	9	28	0.674	1.030
Q9H0U4	Ras-related protein Rab-1B OS=Homo sapiens GN=RAB1B PE=1 SV=1 - [RAB1B_HUMAN]	107.07	34.33	3	8	31	0.596	0.557
Q9UL25	Ras-related protein Rab-21 OS=Homo sapiens GN=RAB21 PE=1 SV=3 - [RAB21_HUMAN]	19.46	14.67	3	3	6	0.911	0.905
P61019	Ras-related protein Rab-2A OS=Homo sapiens GN=RAB2A PE=1 SV=1 - [RAB2A_HUMAN]	27.38	28.30	2	5	8	1.258	0.916
Q15286	Ras-related protein Rab-35 OS=Homo sapiens GN=RAB35 PE=1 SV=1 - [RAB35_HUMAN]	83.01	32.34	5	7	23	1.432	1.578
P61020	Ras-related protein Rab-5B OS=Homo sapiens GN=RAB5B PE=1 SV=1 - [RAB5B_HUMAN]	48.85	33.02	3	6	14	1.058	1.072
P51148	Ras-related protein Rab-5C OS=Homo sapiens GN=RAB5C PE=1 SV=2 - [RAB5C_HUMAN]	74.42	36.57	4	6	19	0.727	0.807
P51149	Ras-related protein Rab-7a OS=Homo sapiens GN=RAB7A PE=1 SV=1 - [RAB7A_HUMAN]	69.26	58.45	12	12	20	0.142	0.143
P61006	Ras-related protein Rab-8A OS=Homo sapiens GN=RAB8A PE=1 SV=1 - [RAB8A_HUMAN]	97.86	51.69	6	13	28	1.096	1.103
Q92930	Ras-related protein Rab-8B OS=Homo sapiens GN=RAB8B PE=1 SV=2 - [RAB8B_HUMAN]	90.87	45.41	3	10	27	0.582	0.729
P11233	Ras-related protein Ral-A OS=Homo sapiens GN=RALA PE=1 SV=1 - [RALA_HUMAN]	60.07	24.27	5	5	17	1.590	1.790
P62834	Ras-related protein Rap-1A OS=Homo sapiens GN=RAP1A PE=1 SV=1 - [RAP1A_HUMAN]	105.47	36.96	2	7	32	1.230	1.754
P61225	Ras-related protein Rap-2b OS=Homo sapiens GN=RAP2B PE=1 SV=1 - [RAP2B_HUMAN]	67.67	33.33	4	6	21	1.119	0.961
Q00765	Receptor expression-enhancing protein 5 OS=Homo sapiens GN=REEP5 PE=1 SV=3 - [REEP5_HUMAN]	47.22	11.11	4	4	13	1.895	1.118
Q96TC7	Regulator of microtubule dynamics protein 3 OS=Homo sapiens GN=FAM82A2 PE=1 SV=2 - [RMD3_HUMAN]	27.69	11.49	5	5	8	0.122	0.174
Q8TC12	Retinol dehydrogenase 11 OS=Homo sapiens GN=RDH11 PE=1 SV=2 - [RDH11_HUMAN]	19.85	17.92	5	5	6	0.355	0.312
O75116	Rho-associated protein kinase 2 OS=Homo sapiens GN=ROCK2 PE=1 SV=4 - [ROCK2_HUMAN]	11.66	2.88	3	4	4	0.994	0.924
P84095	Rho-related GTP-binding protein RhoG OS=Homo sapiens GN=RHOG PE=1 SV=1 - [RHOG_HUMAN]	34.17	28.80	6	7	10	0.170	0.146
P60891	Ribose-phosphate pyrophosphokinase 1 OS=Homo sapiens GN=PRPS1 PE=1 SV=2 - [PRPS1_HUMAN]	63.30	33.96	6	10	20	2.459	1.719
Q5VVC8	Ribosomal protein L11 (Fragment) OS=Homo sapiens GN=RPL11 PE=2 SV=1 - [Q5VVC8_HUMAN]	11.76	16.09	3	3	4	0.170	0.183
E7EQV9	Ribosomal protein L15 OS=Homo sapiens GN=RPL15 PE=3 SV=1 - [E7EQV9_HUMAN]	18.20	21.84	3	3	5	0.344	0.177
B3KTM6	Ribosomal protein L5, isoform CRA_b OS=Homo sapiens GN=RPL5 PE=2 SV=1 - [B3KTM6_HUMAN]	21.72	12.96	4	4	7	0.321	0.156
Q5JR95	Ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=4 SV=1 - [Q5JR95_HUMAN]	12.75	16.49	3	3	4	0.076	0.118
Q9Y3A5	Ribosome maturation protein SBDS OS=Homo sapiens GN=SBDS PE=1 SV=4 - [SBDS_HUMAN]	20.43	14.40	5	5	6	1.134	1.646
Q9P2E9	Ribosome-binding protein 1 OS=Homo sapiens GN=RRBP1 PE=1 SV=4 - [RRBP1_HUMAN]	36.27	18.44	6	7	10	0.097	0.152
O00442	RNA 3'-terminal phosphate cyclase OS=Homo sapiens GN=RTCD1 PE=1 SV=1 - [RTC1_HUMAN]	18.53	4.92	3	3	5	0.698	0.939
Q96PK6	RNA-binding protein 14 OS=Homo sapiens GN=RBM14 PE=1 SV=2 - [RBM14_HUMAN]	5.99	3.14	2	2	2	0.438	0.428
Q3B7A4	RPLP0 protein OS=Homo sapiens GN=RPLP0 PE=2 SV=1 - [Q3B7A4_HUMAN]	38.72	19.22	4	4	12	0.293	0.200
Q7L7Q6	RTN4 OS=Homo sapiens GN=RTN4 PE=2 SV=1 - [Q7L7Q6_HUMAN]	28.04	11.53	3	3	8	0.339	0.316
Q9Y265	RuvB-like 1 OS=Homo sapiens GN=RUVBL1 PE=1 SV=1 - [RUVB1_HUMAN]	33.86	16.67	7	7	9	0.777	1.318
Q9Y230	RuvB-like 2 OS=Homo sapiens GN=RUVBL2 PE=1 SV=3 - [RUVB2_HUMAN]	72.26	30.24	14	14	21	0.770	1.261
P0C7P3	Schlafen family member 14 OS=Homo sapiens GN=SLFN14 PE=2 SV=2 - [SLN14_HUMAN]	6.84	1.64	2	2	2	0.410	0.277
Q13228	Selenium-binding protein 1 OS=Homo sapiens GN=SELENBP1 PE=1 SV=2 - [SBP1_HUMAN]	9.24	6.36	3	3	3	0.615	0.593
O75326	Semaphorin-7A OS=Homo sapiens GN=SEMA7A PE=1 SV=1 - [SEM7A_HUMAN]	33.45	11.56	8	8	11	5.814	3.986
D6RGI3	Septin 11, isoform CRA_b OS=Homo sapiens GN=SEPT11 PE=3 SV=1 - [D6RGI3_HUMAN]	27.02	13.18	3	5	8	0.050	0.213
A8MYA6	Serine hydroxymethyltransferase OS=Homo sapiens GN=SHMT1 PE=3 SV=1 - [A8MYA6_HUMAN]	5.47	3.36	2	2	2	1.944	1.866
B7Z9F1	Serine hydroxymethyltransferase OS=Homo sapiens GN=SHMT2 PE=2 SV=1 - [B7Z9F1_HUMAN]	21.43	11.80	6	6	7	0.153	0.223
O95747	Serine/threonine-protein kinase OSR1 OS=Homo sapiens GN=OXSR1 PE=1 SV=1 - [OXSR1_HUMAN]	30.73	16.13	7	8	9	0.330	0.700
Q9H2K8	Serine/threonine-protein kinase TAO3 OS=Homo sapiens GN=TAOK3 PE=1 SV=2 - [TAOK3_HUMAN]	9.39	5.23	4	4	4	0.550	0.602
P67775	Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform OS=Homo sapiens GN=PPP2CA PE=1 SV=1 - [PP2AA_HUMAN]	12.47	10.03	4	4	4	0.826	1.357
Q9UPN7	Serine/threonine-protein phosphatase 6 regulatory subunit 1 OS=Homo sapiens GN=PPP6R1 PE=1 SV=5 - [PP6R1_HUMAN]	5.20	2.95	2	2	2	2.107	1.146

B4DDZ8	Serine/threonine-protein phosphatase OS=Homo sapiens GN=PPP5C PE=2 SV=1 - [B4DDZ8_HUMAN]	20.00	11.52	5	5	6	1.549	1.921
P02787	Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3 - [TRFE_HUMAN]	124.97	34.53	22	22	39	0.095	0.174
P02768	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2 - [ALBU_HUMAN]	113.54	33.33	19	19	31	6.604	4.214
P49591	Seryl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=SARS PE=1 SV=3 - [SYSC_HUMAN]	36.18	20.04	9	9	11	0.130	0.361
O75368	SH3 domain-binding glutamic acid-rich-like protein OS=Homo sapiens GN=SH3BGRL PE=1 SV=1 - [SH3L1_HUMAN]	25.42	45.61	5	5	8	1.476	2.649
Q9H9B4	Sideroflexin-1 OS=Homo sapiens GN=SFXN1 PE=1 SV=4 - [SFXN1_HUMAN]	14.33	12.42	4	4	4	0.100	0.292
O76094	Signal recognition particle 72 kDa protein OS=Homo sapiens GN=SRP72 PE=1 SV=3 - [SRP72_HUMAN]	9.48	4.17	2	2	3	0.333	0.318
P49458	Signal recognition particle 9 kDa protein OS=Homo sapiens GN=SRP9 PE=1 SV=2 - [SRP09_HUMAN]	6.38	22.09	2	2	2	0.029	0.135
Q9Y5M8	Signal recognition particle receptor subunit beta OS=Homo sapiens GN=SRPRB PE=1 SV=3 - [SRPRB_HUMAN]	8.83	11.81	2	2	3	0.068	0.169
Q8N3X5	Similar to ATPase, Ca++ transporting, cardiac muscle, fast twitch 1 (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q8N3X5_HUMAN]	5.45	2.01	2	2	2	0.368	0.377
Q8NHG7	Small VCP/p97-interacting protein OS=Homo sapiens GN=SVIP PE=2 SV=1 - [SVIP_HUMAN]	29.54	41.56	3	3	8	1.017	0.862
P54709	Sodium/potassium-transporting ATPase subunit beta-3 OS=Homo sapiens GN=ATP1B3 PE=1 SV=1 - [AT1B3_HUMAN]	22.88	14.70	4	4	7	0.115	0.100
P11166	Solute carrier family 2, facilitated glucose transporter member 1 OS=Homo sapiens GN=SLC2A1 PE=1 SV=2 - [GTR1_HUMAN]	375.01	14.02	8	8	111	1.803	2.627
Q9NP59	Solute carrier family 40 member 1 OS=Homo sapiens GN=SLC40A1 PE=1 SV=1 - [S40A1_HUMAN]	26.03	7.53	4	4	8	6.283	5.448
Q00796	Sorbitol dehydrogenase OS=Homo sapiens GN=SORD PE=1 SV=4 - [DHSO_HUMAN]	97.24	32.49	12	12	32	12.996	2.030
Q9Y512	Sorting and assembly machinery component 50 homolog OS=Homo sapiens GN=SAMM50 PE=1 SV=3 - [SAM50_HUMAN]	11.79	6.82	3	3	4	0.191	0.211
P02549	Spectrin alpha chain, erythrocyte OS=Homo sapiens GN=SPTA1 PE=1 SV=5 - [SPTA1_HUMAN]	6080.81	61.35	164	165	1848	4.681	4.164
P11277	Spectrin beta chain, erythrocyte OS=Homo sapiens GN=SPTB PE=1 SV=5 - [SPTB1_HUMAN]	5690.80	69.21	153	154	1726	4.470	4.109
B4E241	Splicing factor, arginine/serine-rich 3, isoform CRA_a OS=Homo sapiens GN=SRSF3 PE=2 SV=1 - [B4E241_HUMAN]	8.68	20.16	3	3	3	0.138	0.222
P23246	Splicing factor, proline- and glutamine-rich OS=Homo sapiens GN=SFPQ PE=1 SV=2 - [SFPQ_HUMAN]	21.68	10.33	6	6	7	0.210	0.230
Q9H2G2	STE20-like serine/threonine-protein kinase OS=Homo sapiens GN=SLK PE=1 SV=1 - [SLK_HUMAN]	28.52	7.04	8	9	9	0.448	0.511
Q9C0K7	STE20-related kinase adapter protein beta OS=Homo sapiens GN=STRADB PE=1 SV=1 - [STRAB_HUMAN]	5.56	4.31	2	2	2	1.405	1.121
P31948	Stress-induced-phosphoprotein 1 OS=Homo sapiens GN=STIP1 PE=1 SV=1 - [STIP1_HUMAN]	237.02	45.12	33	33	74	0.593	0.939
O95347	Structural maintenance of chromosomes protein 2 OS=Homo sapiens GN=SMC2 PE=1 SV=2 - [SMC2_HUMAN]	27.67	6.43	8	8	8	0.387	0.343
P53597	Succinyl-CoA ligase [GDP-forming] subunit alpha, mitochondrial OS=Homo sapiens GN=SUCLG1 PE=1 SV=4 - [SUCA_HUMAN]	6.44	6.94	2	2	2	0.120	0.144
Q96I99	Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial OS=Homo sapiens GN=SUCLG2 PE=1 SV=2 - [SUCB2_HUMAN]	13.17	6.25	4	4	4	0.043	0.150
P55809	Succinyl-CoA:3-ketoacid-coenzyme A transferase 1, mitochondrial OS=Homo sapiens GN=OXCT1 PE=1 SV=1 - [SCOT1_HUMAN]	23.84	9.62	5	5	7	0.242	0.176
Q9Y6N5	Sulfide:quinone oxidoreductase, mitochondrial OS=Homo sapiens GN=SQRDL PE=1 SV=1 - [SQRD_HUMAN]	41.16	20.89	9	9	12	0.027	0.105
P00441	Superoxide dismutase [Cu-Zn] OS=Homo sapiens GN=SOD1 PE=1 SV=2 - [SODC_HUMAN]	24.47	31.17	6	6	8	0.116	0.145
Q99536	Synaptic vesicle membrane protein VAT-1 homolog OS=Homo sapiens GN=VAT1 PE=1 SV=2 - [VAT1_HUMAN]	11.82	10.69	3	3	4	0.024	0.192
O00161	Synaptosomal-associated protein 23 OS=Homo sapiens GN=SNAP23 PE=1 SV=1 - [SNP23_HUMAN]	35.78	31.28	7	7	11	0.655	1.022
A8MXY0	Syntaxin 4A (Placental), isoform CRA_c OS=Homo sapiens GN=STX4 PE=2 SV=1 - [A8MXY0_HUMAN]	18.83	13.22	3	3	5	1.161	0.867
O15400	Syntaxin-7 OS=Homo sapiens GN=STX7 PE=1 SV=4 - [STX7_HUMAN]	73.02	29.89	8	8	22	0.829	0.859
O00186	Syntaxin-binding protein 3 OS=Homo sapiens GN=STXBP3 PE=1 SV=2 - [STXB3_HUMAN]	43.66	14.36	9	9	14	1.142	0.729
P17987	T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1 SV=1 - [TCPA_HUMAN]	189.39	38.31	21	21	58	0.532	0.755
P50991	T-complex protein 1 subunit delta OS=Homo sapiens GN=CCT4 PE=1 SV=4 - [TCPD_HUMAN]	207.77	45.45	21	22	64	0.627	0.799
P48643	T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=1 SV=1 - [TCPE_HUMAN]	218.83	44.55	25	26	68	0.531	0.755
P50990	T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=1 SV=4 - [TCPQ_HUMAN]	320.72	56.20	30	30	94	0.510	0.724
P40227	T-complex protein 1 subunit zeta OS=Homo sapiens GN=CCT6A PE=1 SV=3 - [TCPZ_HUMAN]	211.12	33.90	21	21	65	0.579	0.783
Q5TCU6	Talin 1 OS=Homo sapiens GN=TLN1 PE=2 SV=1 - [Q5TCU6_HUMAN]	164.22	17.09	40	40	50	0.250	0.283
Q9ULP9	TBC1 domain family member 24 OS=Homo sapiens GN=TBC1D24 PE=1 SV=2 - [TBC24_HUMAN]	15.95	9.12	5	5	5	2.451	6.044
Q59G71	Tensin variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59G71_HUMAN]	66.14	21.99	16	16	20	1.159	0.405
O43396	Thioredoxin-like protein 1 OS=Homo sapiens GN=TXNL1 PE=1 SV=3 - [TXNL1_HUMAN]	13.66	14.19	3	3	4	0.518	0.525
Q9H3N1	Thioredoxin-related transmembrane protein 1 OS=Homo sapiens GN=TMX1 PE=1 SV=1 - [TMX1_HUMAN]	25.00	14.64	5	5	7	0.870	0.704
P26639	Threonyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=TARS PE=1 SV=3 - [SYTC_HUMAN]	47.18	15.91	12	12	16	0.137	0.157
P23919	Thymidylate kinase OS=Homo sapiens GN=DTYMK PE=1 SV=4 - [KTHY_HUMAN]	10.71	9.91	2	2	3	0.500	0.307
P37837	Transaldolase OS=Homo sapiens GN=TALDO1 PE=1 SV=2 - [TALDO_HUMAN]	26.58	19.88	7	7	8	0.076	0.420
P23193	Transcription elongation factor A protein 1 OS=Homo sapiens GN=TCEA1 PE=1 SV=2 - [TCEA1_HUMAN]	13.71	7.31	2	2	4	1.965	1.064
B8ZZU8	Transcription elongation factor B (SIII), polypeptide 2 (18kDa, elongin B), isoform CRA_b OS=Homo sapiens GN=TCEB2 PE=4 SV=1 - [B8ZZU8_HUMAN]	13.31	25.66	3	3	4	0.410	0.589
Q00059	Transcription factor A, mitochondrial OS=Homo sapiens GN=TFAM PE=1 SV=1 - [TFAM_HUMAN]	14.40	16.26	5	5	5	0.039	0.117
Q00577	Transcriptional activator protein Pur-alpha OS=Homo sapiens GN=PURA PE=1 SV=2 - [PURA_HUMAN]	16.35	10.56	4	4	5	0.818	0.667
P02786	Transferrin receptor protein 1 OS=Homo sapiens GN=TFRC PE=1 SV=2 - [TFR1_HUMAN]	256.20	38.68	27	27	79	0.295	0.088
P61586	Transforming protein RhoA OS=Homo sapiens GN=RHOA PE=1 SV=1 - [RHOA_HUMAN]	28.36	30.05	6	6	9	1.018	2.277
P55072	Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4 - [TERA_HUMAN]	568.95	44.79	35	35	175	1.797	1.742
P49770	Translation initiation factor eIF-2B subunit beta OS=Homo sapiens GN=EIF2B2 PE=1 SV=3 - [EI2BB_HUMAN]	11.16	10.54	4	4	4	0.371	0.408
Q92616	Translational activator GCN1 OS=Homo sapiens GN=GCN1L1 PE=1 SV=6 - [GCN1L_HUMAN]	6.18	0.60	2	2	2	0.090	0.081

Q99442	Translocation protein SEC62 OS=Homo sapiens GN=SEC62 PE=1 SV=1 - [SEC62_HUMAN]	10.99	5.26	2	2	3	0.338	0.255
Q9HD45	Transmembrane 9 superfamily member 3 OS=Homo sapiens GN=TM9SF3 PE=1 SV=2 - [TM9S3_HUMAN]	5.82	3.23	2	2	2	1.335	0.894
B7Z1P7	Transmembrane and coiled-coil domain family 2, isoform CRA_d OS=Homo sapiens GN=TMCC2 PE=2 SV=1 - [B7Z1P7_HUMAN]	157.62	29.48	7	17	52	0.546	0.211
Q13445	Transmembrane emp24 domain-containing protein 1 OS=Homo sapiens GN=TMED1 PE=1 SV=1 - [TMED1_HUMAN]	8.17	11.45	2	2	2	1.000	1.273
P49755	Transmembrane emp24 domain-containing protein 10 OS=Homo sapiens GN=TMED10 PE=1 SV=2 - [TMEDA_HUMAN]	20.92	22.37	4	4	7	1.122	1.131
Q9BVK6	Transmembrane emp24 domain-containing protein 9 OS=Homo sapiens GN=TMED9 PE=1 SV=2 - [TMED9_HUMAN]	23.18	16.60	4	6	8	1.027	1.163
Q9BVC6	Transmembrane protein 109 OS=Homo sapiens GN=TMEM109 PE=1 SV=1 - [TM109_HUMAN]	15.28	8.64	2	2	4	0.312	0.401
Q5T3F8	Transmembrane protein 63B OS=Homo sapiens GN=TMEM63B PE=1 SV=1 - [TM63B_HUMAN]	9.83	3.13	3	3	3	1.117	0.793
Q92973	Transportin-1 OS=Homo sapiens GN=TNPO1 PE=1 SV=2 - [TNPO1_HUMAN]	10.16	2.90	3	3	3	0.336	0.675
P53007	Tricarboxylate transport protein, mitochondrial OS=Homo sapiens GN=SLC25A1 PE=1 SV=2 - [TXTP_HUMAN]	8.92	8.36	3	3	3	0.162	0.256
P40939	Trifunctional enzyme subunit alpha, mitochondrial OS=Homo sapiens GN=HADHA PE=1 SV=2 - [ECHA_HUMAN]	60.25	17.43	14	14	19	0.247	0.146
P55084	Trifunctional enzyme subunit beta, mitochondrial OS=Homo sapiens GN=HADHB PE=1 SV=3 - [ECHB_HUMAN]	36.72	14.35	7	7	11	0.106	0.112
P60174	Triosephosphate isomerase OS=Homo sapiens GN=TPI1 PE=1 SV=2 - [TPIS_HUMAN]	46.18	34.94	8	8	14	0.069	0.250
Q5SRJ5	Tripartite motif-containing 10 OS=Homo sapiens GN=TRIM10 PE=2 SV=1 - [Q5SRJ5_HUMAN]	12.31	8.86	3	3	3	0.151	0.421
Q8NG06	Tripartite motif-containing protein 58 OS=Homo sapiens GN=TRIM58 PE=2 SV=2 - [TRI58_HUMAN]	41.26	24.07	10	11	13	0.077	0.202
P29144	Tripeptidyl-peptidase 2 OS=Homo sapiens GN=TPP2 PE=1 SV=4 - [TPP2_HUMAN]	107.68	19.38	25	25	34	1.353	1.231
P28289	Tropomodulin-1 OS=Homo sapiens GN=TMOD1 PE=1 SV=1 - [TMOD1_HUMAN]	211.85	52.65	22	22	69	3.518	3.770
D9YZV7	Tropomyosin 1 (Alpha) isoform 6 OS=Homo sapiens GN=TPM1 PE=3 SV=1 - [D9YZV7_HUMAN]	260.23	47.76	2	15	76	2.520	2.409
Q5VU58	Tropomyosin 3 OS=Homo sapiens GN=TPM3 PE=2 SV=1 - [Q5VU58_HUMAN]	388.59	59.27	2	20	115	2.842	3.021
Q5VU59	Tropomyosin 3 OS=Homo sapiens GN=TPM3 PE=2 SV=1 - [Q5VU59_HUMAN]	403.59	63.79	4	22	120	3.198	2.880
Q5LJ98	TROVE domain family, member 2 OS=Homo sapiens GN=TROVE2 PE=2 SV=1 - [Q5LJ98_HUMAN]	28.32	11.39	7	7	9	0.118	0.228
P23381	Tryptophanyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=WARS PE=1 SV=2 - [SYWC_HUMAN]	8.71	7.01	3	3	3	0.404	0.436
Q9Y3Q8	TSC22 domain family protein 4 OS=Homo sapiens GN=TSC22D4 PE=1 SV=2 - [T22D4_HUMAN]	27.47	16.96	6	6	7	0.949	0.932
Q9BQE3	Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 - [TBA1C_HUMAN]	82.89	34.30	4	13	26	0.074	0.102
B1AH89	Tubulin tyrosine ligase-like family, member 12 OS=Homo sapiens GN=TTLL12 PE=4 SV=1 - [B1AH89_HUMAN]	10.52	5.50	3	3	3	0.514	0.993
P25445	Tumor necrosis factor receptor superfamily member 6 OS=Homo sapiens GN=FAS PE=1 SV=1 - [TNR6_HUMAN]	11.92	6.27	2	2	3	1.518	0.750
P54577	Tyrosyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=YARS PE=1 SV=4 - [SYYC_HUMAN]	77.02	33.52	19	19	24	0.294	0.554
P45974	Ubiquitin carboxyl-terminal hydrolase 5 OS=Homo sapiens GN=USP5 PE=1 SV=2 - [UBP5_HUMAN]	34.27	10.02	8	8	10	0.830	1.812
A6NJA2	Ubiquitin carboxyl-terminal hydrolase OS=Homo sapiens GN=USP14 PE=3 SV=1 - [A6NJA2_HUMAN]	58.45	25.27	12	12	17	0.520	0.847
E9PCQ3	Ubiquitin carboxyl-terminal hydrolase OS=Homo sapiens GN=USP15 PE=3 SV=2 - [E9PCQ3_HUMAN]	41.52	9.94	11	11	13	0.942	1.245
B7WPF4	Ubiquitin carboxyl-terminal hydrolase OS=Homo sapiens GN=USP24 PE=3 SV=2 - [B7WPF4_HUMAN]	6.81	0.65	2	2	2	0.314	0.579
Q9C0C9	Ubiquitin-conjugating enzyme E2 O OS=Homo sapiens GN=UBE2O PE=1 SV=3 - [UBE2O_HUMAN]	126.16	17.88	21	21	37	2.200	3.904
P22314	Ubiquitin-like modifier-activating enzyme 1 OS=Homo sapiens GN=UBA1 PE=1 SV=3 - [UBA1_HUMAN]	44.04	9.55	9	9	13	0.464	1.381
Q9NYU2	UDP-glucose:glycoprotein glucosyltransferase 1 OS=Homo sapiens GN=UGGT1 PE=1 SV=3 - [UGGG1_HUMAN]	73.25	13.31	20	20	23	0.846	0.812
O15294	UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit OS=Homo sapiens GN=OGT PE=1 SV=3 - [OGT1_HUMAN]	9.76	2.87	3	3	3	0.382	0.373
Q5T446	Uncharacterized protein (Fragment) OS=Homo sapiens GN=UROD PE=2 SV=1 - [Q5T446_HUMAN]	6.74	13.47	2	2	2	0.386	0.908
E9PBW0	Uncharacterized protein OS=Homo sapiens GN=ABCC5 PE=3 SV=1 - [E9PBW0_HUMAN]	5.79	2.39	2	2	2	1.371	0.832
B7Z9I1	Uncharacterized protein OS=Homo sapiens GN=ACADM PE=2 SV=1 - [B7Z9I1_HUMAN]	38.60	18.70	7	7	11	0.295	0.218
E9PE82	Uncharacterized protein OS=Homo sapiens GN=ACADS PE=4 SV=1 - [E9PE82_HUMAN]	5.98	3.19	2	2	2	0.075	0.197
C9JGQ9	Uncharacterized protein OS=Homo sapiens GN=ACHE PE=4 SV=1 - [C9JGQ9_HUMAN]	19.30	9.98	5	5	6	2.742	1.406
F5H2A5	Uncharacterized protein OS=Homo sapiens GN=ACO2 PE=4 SV=1 - [F5H2A5_HUMAN]	11.92	6.18	4	4	4	0.117	0.176
E7ERD7	Uncharacterized protein OS=Homo sapiens GN=ACSL6 PE=4 SV=1 - [E7ERD7_HUMAN]	30.95	12.41	9	9	10	1.079	1.118
F5H6F4	Uncharacterized protein OS=Homo sapiens GN=ACSS1 PE=4 SV=1 - [F5H6F4_HUMAN]	10.25	4.40	2	3	3	0.040	0.160
F5GXS2	Uncharacterized protein OS=Homo sapiens GN=ACTN4 PE=4 SV=1 - [F5GXS2_HUMAN]	12.11	6.91	3	3	4	0.695	0.862
F5H3P5	Uncharacterized protein OS=Homo sapiens GN=ACTR3 PE=3 SV=1 - [F5H3P5_HUMAN]	23.39	17.42	5	5	7	0.335	0.683
E7ET30	Uncharacterized protein OS=Homo sapiens GN=AK3 PE=3 SV=1 - [E7ET30_HUMAN]	8.03	11.23	2	2	3	0.167	0.218
F5H328	Uncharacterized protein OS=Homo sapiens GN=ALDH5A1 PE=3 SV=1 - [F5H328_HUMAN]	12.34	6.26	3	3	4	0.246	0.216
E7EVE3	Uncharacterized protein OS=Homo sapiens GN=ANK1 PE=4 SV=1 - [E7EVE3_HUMAN]	2863.52	46.92	81	88	856	3.627	3.927
F5H754	Uncharacterized protein OS=Homo sapiens GN=ANKFY1 PE=4 SV=1 - [F5H754_HUMAN]	9.40	2.34	3	3	3	1.305	1.241
F5H0H0	Uncharacterized protein OS=Homo sapiens GN=AP2M1 PE=4 SV=1 - [F5H0H0_HUMAN]	44.86	18.57	9	9	14	0.744	0.647
E9PC21	Uncharacterized protein OS=Homo sapiens GN=AQP1 PE=3 SV=1 - [E9PC21_HUMAN]	33.28	17.53	2	2	11	5.165	3.412
B7ZB63	Uncharacterized protein OS=Homo sapiens GN=ARF3 PE=2 SV=1 - [B7ZB63_HUMAN]	7.00	13.19	2	2	2	0.298	0.282
F5GY14	Uncharacterized protein OS=Homo sapiens GN=ARL6IP1 PE=4 SV=1 - [F5GY14_HUMAN]	17.31	15.48	3	3	6	0.618	0.534
E9PER8	Uncharacterized protein OS=Homo sapiens GN=ARL6IP5 PE=4 SV=1 - [E9PER8_HUMAN]	11.82	15.06	3	3	4	0.675	0.568
B4DLQ7	Uncharacterized protein OS=Homo sapiens GN=ARPC1A PE=2 SV=1 - [B4DLQ7_HUMAN]	6.18	4.64	2	2	2	0.452	0.773
E7ERV9	Uncharacterized protein OS=Homo sapiens GN=ASAH1 PE=4 SV=1 - [E7ERV9_HUMAN]	8.56	8.52	3	3	3	0.173	0.139

C9JAL9	Uncharacterized protein OS=Homo sapiens GN=ASPSCR1 PE=4 SV=1 - [C9JAL9_HUMAN]	7.04	6.02	2	2	2	0.589	1.084
F5GWY2	Uncharacterized protein OS=Homo sapiens GN=ATIC PE=4 SV=1 - [F5GWY2_HUMAN]	6.09	3.38	2	2	2	0.652	0.962
F5H6I7	Uncharacterized protein OS=Homo sapiens GN=ATL3 PE=4 SV=1 - [F5H6I7_HUMAN]	39.88	9.94	6	6	13	1.398	1.057
F5H3A1	Uncharacterized protein OS=Homo sapiens GN=ATP1A1 PE=3 SV=1 - [F5H3A1_HUMAN]	84.03	19.35	19	19	23	0.527	0.218
E9PN17	Uncharacterized protein OS=Homo sapiens GN=ATP5L PE=4 SV=1 - [E9PN17_HUMAN]	33.73	60.53	4	5	9	0.052	0.113
F5H569	Uncharacterized protein OS=Homo sapiens GN=ATP6V0A1 PE=4 SV=1 - [F5H569_HUMAN]	29.15	6.69	6	6	8	0.319	0.308
B7Z1R5	Uncharacterized protein OS=Homo sapiens GN=ATP6V1A PE=2 SV=1 - [B7Z1R5_HUMAN]	93.34	25.51	15	15	28	0.207	0.442
A8MQ60	Uncharacterized protein OS=Homo sapiens GN=ATP6V1C1 PE=4 SV=1 - [A8MQ60_HUMAN]	13.12	10.16	4	4	4	0.139	0.129
A8MUN4	Uncharacterized protein OS=Homo sapiens GN=ATP6V1E1 PE=2 SV=1 - [A8MUN4_HUMAN]	42.58	28.06	7	7	14	0.265	0.486
E9PGE6	Uncharacterized protein OS=Homo sapiens GN=ATP6V1H PE=4 SV=1 - [E9PGE6_HUMAN]	16.29	9.15	4	4	5	0.174	0.517
B4DXE2	Uncharacterized protein OS=Homo sapiens GN=BAG2 PE=2 SV=1 - [B4DXE2_HUMAN]	28.28	32.58	5	5	7	0.574	0.655
A6NME1	Uncharacterized protein OS=Homo sapiens GN=BCAP29 PE=2 SV=2 - [A6NME1_HUMAN]	12.83	19.35	3	3	4	1.032	0.775
E9PL10	Uncharacterized protein OS=Homo sapiens GN=BTF3L4 PE=4 SV=1 - [E9PL10_HUMAN]	5.31	5.52	2	2	2	0.152	0.203
F5H2W0	Uncharacterized protein OS=Homo sapiens GN=C18orf8 PE=4 SV=1 - [F5H2W0_HUMAN]	6.06	3.28	2	2	2	0.089	0.187
E9PCW3	Uncharacterized protein OS=Homo sapiens GN=C22orf28 PE=4 SV=1 - [E9PCW3_HUMAN]	9.66	6.28	3	3	3	0.224	0.178
E7EWT6	Uncharacterized protein OS=Homo sapiens GN=CALCOCO1 PE=4 SV=2 - [E7EWT6_HUMAN]	22.71	10.49	6	6	6	0.362	0.985
E9PAQ6	Uncharacterized protein OS=Homo sapiens GN=CCT3 PE=3 SV=1 - [E9PAQ6_HUMAN]	239.56	38.60	24	24	67	0.569	0.742
E9PB22	Uncharacterized protein OS=Homo sapiens GN=CD47 PE=4 SV=1 - [E9PB22_HUMAN]	48.39	8.97	3	3	14	5.260	5.309
E9PNW4	Uncharacterized protein OS=Homo sapiens GN=CD59 PE=4 SV=1 - [E9PNW4_HUMAN]	41.39	27.78	3	3	12	1.259	2.748
E9PP50	Uncharacterized protein OS=Homo sapiens GN=CFL1 PE=4 SV=1 - [E9PP50_HUMAN]	13.10	14.37	3	3	4	0.207	0.149
E9PDB9	Uncharacterized protein OS=Homo sapiens GN=CLCN7 PE=4 SV=1 - [E9PDB9_HUMAN]	7.50	2.56	2	2	2	0.165	0.276
B4DIN1	Uncharacterized protein OS=Homo sapiens GN=CLTA PE=2 SV=1 - [B4DIN1_HUMAN]	101.53	23.91	3	8	31	1.010	0.678
F5GXH1	Uncharacterized protein OS=Homo sapiens GN=COPG PE=4 SV=1 - [F5GXH1_HUMAN]	8.25	3.93	3	3	3	0.401	0.328
E7EM64	Uncharacterized protein OS=Homo sapiens GN=COPS6 PE=4 SV=1 - [E7EM64_HUMAN]	13.13	9.20	3	3	4	1.018	1.549
A8MZ71	Uncharacterized protein OS=Homo sapiens GN=COX7A2 PE=4 SV=1 - [A8MZ71_HUMAN]	6.71	27.71	2	2	2	0.027	0.092
D6R9Z7	Uncharacterized protein OS=Homo sapiens GN=COX7C PE=4 SV=1 - [D6R9Z7_HUMAN]	13.91	32.14	2	2	4	0.272	0.307
E9PDY4	Uncharacterized protein OS=Homo sapiens GN=CR1 PE=4 SV=1 - [E9PDY4_HUMAN]	6.40	2.37	2	2	2	1.885	1.083
E7EU96	Uncharacterized protein OS=Homo sapiens GN=CSNK2A1 PE=4 SV=1 - [E7EU96_HUMAN]	8.40	10.39	3	3	3	1.266	1.373
E9PP21	Uncharacterized protein OS=Homo sapiens GN=CSRP1 PE=4 SV=1 - [E9PP21_HUMAN]	21.83	36.88	4	4	6	0.143	0.383
F5GWW0	Uncharacterized protein OS=Homo sapiens GN=CTSB PE=3 SV=1 - [F5GWW0_HUMAN]	22.93	20.88	5	5	7	0.243	0.433
B4E358	Uncharacterized protein OS=Homo sapiens GN=CTTN PE=2 SV=1 - [B4E358_HUMAN]	9.74	10.19	2	3	3	0.029	0.202
E7EWR0	Uncharacterized protein OS=Homo sapiens GN=CUL1 PE=3 SV=1 - [E7EWR0_HUMAN]	40.58	13.80	12	12	13	1.407	1.548
A8MSH7	Uncharacterized protein OS=Homo sapiens GN=CUL4A PE=3 SV=1 - [A8MSH7_HUMAN]	30.50	10.14	8	8	9	0.496	1.169
B4DWD7	Uncharacterized protein OS=Homo sapiens GN=CYBRD1 PE=2 SV=1 - [B4DWD7_HUMAN]	29.68	9.65	2	2	8	2.132	1.578
C9JFR7	Uncharacterized protein OS=Homo sapiens GN=CYCS PE=3 SV=1 - [C9JFR7_HUMAN]	43.19	47.52	6	6	13	0.045	0.211
E9PFS5	Uncharacterized protein OS=Homo sapiens GN=DCTN1 PE=4 SV=1 - [E9PFS5_HUMAN]	86.12	16.91	21	21	26	0.973	0.834
C9J8R4	Uncharacterized protein OS=Homo sapiens GN=DCUN1D1 PE=4 SV=1 - [C9J8R4_HUMAN]	7.68	16.41	2	2	2	0.418	1.341
E7EWT1	Uncharacterized protein OS=Homo sapiens GN=DDOST PE=4 SV=1 - [E7EWT1_HUMAN]	9.17	6.44	3	3	3	0.454	0.297
B4DME8	Uncharacterized protein OS=Homo sapiens GN=DDX1 PE=2 SV=1 - [B4DME8_HUMAN]	11.23	3.43	2	2	3	0.056	0.090
B7Z6B8	Uncharacterized protein OS=Homo sapiens GN=DECR1 PE=2 SV=1 - [B7Z6B8_HUMAN]	45.59	27.91	8	8	13	0.186	0.102
E7ERW8	Uncharacterized protein OS=Homo sapiens GN=DIAPH1 PE=4 SV=1 - [E7ERW8_HUMAN]	103.64	14.98	19	21	33	0.649	1.268
F5H7M3	Uncharacterized protein OS=Homo sapiens GN=DLAT PE=3 SV=1 - [F5H7M3_HUMAN]	10.30	6.22	3	3	3	0.257	0.273
E3W974	Uncharacterized protein OS=Homo sapiens GN=DNPEP PE=4 SV=2 - [E3W974_HUMAN]	12.07	19.15	2	2	3	1.416	1.560
E7ETW8	Uncharacterized protein OS=Homo sapiens GN=DYSF PE=4 SV=1 - [E7ETW8_HUMAN]	28.47	4.45	7	8	9	0.172	0.314
A6NJH9	Uncharacterized protein OS=Homo sapiens GN=EIF1AY PE=4 SV=1 - [A6NJH9_HUMAN]	20.80	23.62	3	3	7	0.060	0.140
B4DV79	Uncharacterized protein OS=Homo sapiens GN=EIF3B PE=2 SV=1 - [B4DV79_HUMAN]	34.30	11.38	8	8	10	0.131	0.092
B4DVQ5	Uncharacterized protein OS=Homo sapiens GN=EIF3C PE=2 SV=1 - [B4DVQ5_HUMAN]	42.54	13.81	12	12	13	0.105	0.154
B4DVY1	Uncharacterized protein OS=Homo sapiens GN=EIF3D PE=2 SV=1 - [B4DVY1_HUMAN]	12.64	7.01	3	3	4	0.074	0.141
B7ZAM9	Uncharacterized protein OS=Homo sapiens GN=EIF3K PE=2 SV=1 - [B7ZAM9_HUMAN]	15.94	15.17	3	3	5	0.063	0.103
E7EPC9	Uncharacterized protein OS=Homo sapiens GN=EIF4B PE=4 SV=1 - [E7EPC9_HUMAN]	51.15	18.06	10	10	15	0.408	0.596
E7EX73	Uncharacterized protein OS=Homo sapiens GN=EIF4G1 PE=4 SV=1 - [E7EX73_HUMAN]	85.06	14.90	22	22	26	0.157	0.390
E9PPD9	Uncharacterized protein OS=Homo sapiens GN=EPB41L2 PE=4 SV=1 - [E9PPD9_HUMAN]	29.86	9.62	9	9	9	1.309	1.498
B4DT43	Uncharacterized protein OS=Homo sapiens GN=ETFA PE=2 SV=1 - [B4DT43_HUMAN]	46.61	36.27	9	9	15	0.160	0.099
B4E0X8	Uncharacterized protein OS=Homo sapiens GN=FUBP1 PE=2 SV=1 - [B4E0X8_HUMAN]	9.66	4.29	2	3	3	0.103	0.119
B4DR70	Uncharacterized protein OS=Homo sapiens GN=FUS PE=2 SV=1 - [B4DR70_HUMAN]	25.50	13.29	3	5	7	0.064	0.104
F5H4D6	Uncharacterized protein OS=Homo sapiens GN=G3BP1 PE=4 SV=1 - [F5H4D6_HUMAN]	11.70	11.97	2	2	4	0.404	0.369

E7EQZ3	Uncharacterized protein OS=Homo sapiens GN=GSPT1 PE=4 SV=1 - [E7EQZ3_HUMAN]	26.06	9.28	8	8	8	0.188	0.418
F5H5Y5	Uncharacterized protein OS=Homo sapiens GN=HGS PE=4 SV=1 - [F5H5Y5_HUMAN]	18.94	8.17	5	6	6	0.733	0.687
E9PCK0	Uncharacterized protein OS=Homo sapiens GN=HK1 PE=3 SV=1 - [E9PCK0_HUMAN]	22.89	5.75	6	6	7	0.081	0.157
F5H345	Uncharacterized protein OS=Homo sapiens GN=HMBS PE=4 SV=1 - [F5H345_HUMAN]	23.75	14.24	5	5	7	0.354	0.320
A6NGP5	Uncharacterized protein OS=Homo sapiens GN=HN1L PE=2 SV=2 - [A6NGP5_HUMAN]	9.88	14.04	2	2	3	0.499	0.396
D6R9P3	Uncharacterized protein OS=Homo sapiens GN=HNRNPAB PE=4 SV=1 - [D6R9P3_HUMAN]	23.15	13.57	3	4	8	0.113	0.194
B2R603	Uncharacterized protein OS=Homo sapiens GN=HNRNPC PE=2 SV=1 - [B2R603_HUMAN]	24.40	17.16	5	5	6	0.259	0.208
B4DTC3	Uncharacterized protein OS=Homo sapiens GN=HNRNPD PE=2 SV=1 - [B4DTC3_HUMAN]	23.21	17.82	5	6	8	0.302	0.217
E9PCY7	Uncharacterized protein OS=Homo sapiens GN=HNRNPH1 PE=4 SV=1 - [E9PCY7_HUMAN]	30.66	21.21	7	7	9	0.245	0.201
B3KX72	Uncharacterized protein OS=Homo sapiens GN=HNRNPU PE=2 SV=1 - [B3KX72_HUMAN]	10.89	5.73	4	4	4	0.224	0.121
B7Z4V2	Uncharacterized protein OS=Homo sapiens GN=HSPA9 PE=2 SV=1 - [B7Z4V2_HUMAN]	163.05	35.79	23	24	48	0.088	0.112
B4DY72	Uncharacterized protein OS=Homo sapiens GN=HSPH1 PE=2 SV=1 - [B4DY72_HUMAN]	12.05	4.73	2	3	4	0.224	0.360
E9PD66	Uncharacterized protein OS=Homo sapiens GN=HUWE1 PE=4 SV=1 - [E9PD66_HUMAN]	104.10	5.85	25	25	31	0.806	0.708
B4DFG4	Uncharacterized protein OS=Homo sapiens GN=ILF3 PE=2 SV=1 - [B4DFG4_HUMAN]	13.32	5.93	3	3	4	0.311	0.287
C9J406	Uncharacterized protein OS=Homo sapiens GN=IMMT PE=4 SV=1 - [C9J406_HUMAN]	134.90	30.20	23	24	38	0.076	0.124
F5H153	Uncharacterized protein OS=Homo sapiens GN=ITSN1 PE=4 SV=1 - [F5H153_HUMAN]	17.78	3.80	4	4	5	0.287	0.388
F5H2Q7	Uncharacterized protein OS=Homo sapiens GN=KIAA1715 PE=4 SV=1 - [F5H2Q7_HUMAN]	9.25	6.81	2	2	3	0.344	0.439
C9JYI4	Uncharacterized protein OS=Homo sapiens GN=KPNA1 PE=4 SV=1 - [C9JYI4_HUMAN]	16.19	10.37	3	4	5	0.520	0.607
F5H479	Uncharacterized protein OS=Homo sapiens GN=LAMTOR1 PE=4 SV=1 - [F5H479_HUMAN]	20.55	12.12	2	2	6	0.101	0.139
E9PHS0	Uncharacterized protein OS=Homo sapiens GN=LANCL1 PE=4 SV=1 - [E9PHS0_HUMAN]	14.63	13.27	3	3	4	4.795	1.355
B4DWN1	Uncharacterized protein OS=Homo sapiens GN=LMAN2 PE=2 SV=1 - [B4DWN1_HUMAN]	23.15	14.04	4	4	7	1.459	1.382
B3KXS5	Uncharacterized protein OS=Homo sapiens GN=LONP1 PE=2 SV=1 - [B3KXS5_HUMAN]	55.11	14.41	13	13	17	0.105	0.111
B5MEG9	Uncharacterized protein OS=Homo sapiens GN=MAP4 PE=4 SV=2 - [B5MEG9_HUMAN]	7.37	2.81	2	2	2	0.321	0.205
E9PNT8	Uncharacterized protein OS=Homo sapiens GN=MTCH2 PE=3 SV=1 - [E9PNT8_HUMAN]	10.12	23.90	3	3	3	0.107	0.170
A8MZ22	Uncharacterized protein OS=Homo sapiens GN=NAP1L4 PE=3 SV=3 - [A8MZ22_HUMAN]	68.31	25.13	9	10	23	1.482	2.285
F5GZJ1	Uncharacterized protein OS=Homo sapiens GN=NCAPD2 PE=4 SV=1 - [F5GZJ1_HUMAN]	11.85	2.21	3	3	3	0.571	0.466
B4E189	Uncharacterized protein OS=Homo sapiens GN=NCAPH PE=2 SV=1 - [B4E189_HUMAN]	11.05	5.29	3	3	3	0.370	0.420
E9PC09	Uncharacterized protein OS=Homo sapiens GN=NCSTN PE=4 SV=1 - [E9PC09_HUMAN]	6.66	6.23	2	2	2	1.013	0.747
B4DJ81	Uncharacterized protein OS=Homo sapiens GN=NDUFS1 PE=2 SV=1 - [B4DJ81_HUMAN]	5.32	2.29	2	2	2	0.058	0.182
E9PMX3	Uncharacterized protein OS=Homo sapiens GN=NDUFV1 PE=4 SV=1 - [E9PMX3_HUMAN]	6.62	11.24	2	2	2	0.434	0.293
E9PGQ8	Uncharacterized protein OS=Homo sapiens GN=NECAP2 PE=4 SV=1 - [E9PGQ8_HUMAN]	32.73	33.33	6	6	10	0.494	0.528
E7ERL0	Uncharacterized protein OS=Homo sapiens GN=NME1 PE=3 SV=1 - [E7ERL0_HUMAN]	19.43	33.09	4	4	6	0.220	0.840
E9PFG7	Uncharacterized protein OS=Homo sapiens GN=OGDH PE=4 SV=1 - [E9PFG7_HUMAN]	44.68	9.16	9	9	14	0.123	0.138
E9PBS1	Uncharacterized protein OS=Homo sapiens GN=PAICS PE=4 SV=1 - [E9PBS1_HUMAN]	39.99	21.31	11	11	12	0.236	0.814
B7Z3X5	Uncharacterized protein OS=Homo sapiens GN=PDHA1 PE=2 SV=1 - [B7Z3X5_HUMAN]	18.96	12.81	5	5	6	0.103	0.102
B4DDD7	Uncharacterized protein OS=Homo sapiens GN=PDHB PE=2 SV=1 - [B4DDD7_HUMAN]	21.06	9.97	3	3	7	0.124	0.116
B3KQT9	Uncharacterized protein OS=Homo sapiens GN=PDIA3 PE=2 SV=1 - [B3KQT9_HUMAN]	144.81	38.96	20	20	43	0.927	0.829
B7Z254	Uncharacterized protein OS=Homo sapiens GN=PDIA6 PE=2 SV=1 - [B7Z254_HUMAN]	54.19	23.34	9	9	16	0.788	0.738
C9JW96	Uncharacterized protein OS=Homo sapiens GN=PHB PE=4 SV=2 - [C9JW96_HUMAN]	84.68	44.72	12	12	25	0.070	0.131
E9PBQ1	Uncharacterized protein OS=Homo sapiens GN=PIP5K1A PE=4 SV=1 - [E9PBQ1_HUMAN]	9.47	5.17	2	3	3	2.586	4.123
F5H0R5	Uncharacterized protein OS=Homo sapiens GN=PIP5K1C PE=4 SV=1 - [F5H0R5_HUMAN]	11.76	7.97	3	4	4	1.438	1.020
B4DTE8	Uncharacterized protein OS=Homo sapiens GN=PLSCR1 PE=2 SV=1 - [B4DTE8_HUMAN]	10.20	7.17	2	2	3	2.482	2.451
F5H5K9	Uncharacterized protein OS=Homo sapiens GN=PNPLA6 PE=4 SV=1 - [F5H5K9_HUMAN]	12.17	2.31	3	3	4	1.080	0.796
D6R967	Uncharacterized protein OS=Homo sapiens GN=PPA2 PE=4 SV=1 - [D6R967_HUMAN]	6.47	11.52	2	2	2	0.023	0.150
B4DY76	Uncharacterized protein OS=Homo sapiens GN=PPOX PE=2 SV=1 - [B4DY76_HUMAN]	29.60	12.61	5	5	8	0.074	0.132
F5H3X9	Uncharacterized protein OS=Homo sapiens GN=PPP2R1A PE=4 SV=1 - [F5H3X9_HUMAN]	23.91	9.36	6	6	8	0.406	1.060
E9PKF6	Uncharacterized protein OS=Homo sapiens GN=PPP6R3 PE=4 SV=1 - [E9PKF6_HUMAN]	8.98	3.10	3	3	3	0.708	0.854
E9PH29	Uncharacterized protein OS=Homo sapiens GN=PRDX3 PE=4 SV=1 - [E9PH29_HUMAN]	73.55	23.95	5	5	21	0.212	0.245
A8K318	Uncharacterized protein OS=Homo sapiens GN=PRKCSH PE=2 SV=1 - [A8K318_HUMAN]	71.70	20.95	13	13	21	0.883	0.799
E5RG77	Uncharacterized protein OS=Homo sapiens GN=PROSC PE=3 SV=1 - [E5RG77_HUMAN]	6.62	10.53	2	2	2	1.508	1.962
F5GZ16	Uncharacterized protein OS=Homo sapiens GN=PSMD2 PE=4 SV=1 - [F5GZ16_HUMAN]	176.03	28.78	26	26	54	1.572	0.868
F5H8K4	Uncharacterized protein OS=Homo sapiens GN=PSMD3 PE=4 SV=1 - [F5H8K4_HUMAN]	120.54	38.39	20	20	36	0.867	0.631
B4DZM8	Uncharacterized protein OS=Homo sapiens GN=PSMD5 PE=2 SV=1 - [B4DZM8_HUMAN]	6.18	3.47	2	2	2	1.186	0.781
B4DXI8	Uncharacterized protein OS=Homo sapiens GN=PSMD7 PE=2 SV=1 - [B4DXI8_HUMAN]	35.02	22.67	5	5	9	1.498	0.745
B8ZZI3	Uncharacterized protein OS=Homo sapiens GN=PTMA PE=4 SV=1 - [B8ZZI3_HUMAN]	14.48	22.58	2	2	4	0.051	0.212
A8MZH8	Uncharacterized protein OS=Homo sapiens GN=PTTG1IP PE=4 SV=1 - [A8MZH8_HUMAN]	14.17	23.36	2	2	5	0.010	0.079

B4DNN3	Uncharacterized protein OS=Homo sapiens GN=QARS PE=2 SV=1 - [B4DNN3_HUMAN]	14.60	3.86	3	3	5	3.987	3.643
E9PK89	Uncharacterized protein OS=Homo sapiens GN=RAB3IL1 PE=4 SV=1 - [E9PK89_HUMAN]	5.13	15.53	2	2	2	0.685	0.539
F5GZB1	Uncharacterized protein OS=Homo sapiens GN=RAB6A PE=3 SV=1 - [F5GZB1_HUMAN]	25.45	23.24	3	4	8	0.320	0.373
F5GZU7	Uncharacterized protein OS=Homo sapiens GN=RABEP1 PE=4 SV=1 - [F5GZU7_HUMAN]	11.37	3.21	4	4	4	0.827	1.009
B4DQI8	Uncharacterized protein OS=Homo sapiens GN=RAP1B PE=2 SV=1 - [B4DQI8_HUMAN]	129.65	45.45	3	8	42	0.898	1.077
Q8N8Y7	Uncharacterized protein OS=Homo sapiens GN=RBMX PE=2 SV=1 - [Q8N8Y7_HUMAN]	20.40	13.49	6	6	7	0.293	0.314
D6RBN9	Uncharacterized protein OS=Homo sapiens GN=RELL1 PE=4 SV=1 - [D6RBN9_HUMAN]	3.83	10.12	2	2	2	2.695	1.722
B4DM74	Uncharacterized protein OS=Homo sapiens GN=RPL18A PE=2 SV=1 - [B4DM74_HUMAN]	19.37	20.13	3	3	6	0.176	0.162
C9JXB8	Uncharacterized protein OS=Homo sapiens GN=RPL24 PE=4 SV=1 - [C9JXB8_HUMAN]	23.24	33.88	4	4	6	0.044	0.131
E9PLL6	Uncharacterized protein OS=Homo sapiens GN=RPL27A PE=3 SV=1 - [E9PLL6_HUMAN]	6.66	17.59	2	2	2	0.108	0.162
C9JU56	Uncharacterized protein OS=Homo sapiens GN=RPL31 PE=4 SV=1 - [C9JU56_HUMAN]	17.72	28.70	4	4	6	0.471	0.170
C9K025	Uncharacterized protein OS=Homo sapiens GN=RPL35A PE=4 SV=1 - [C9K025_HUMAN]	14.65	29.79	3	3	5	0.096	0.208
E9PEL3	Uncharacterized protein OS=Homo sapiens GN=RPL37A PE=4 SV=1 - [E9PEL3_HUMAN]	9.16	20.00	2	2	3	0.140	0.120
E9PIZ3	Uncharacterized protein OS=Homo sapiens GN=RPL8 PE=4 SV=1 - [E9PIZ3_HUMAN]	16.82	15.84	4	4	5	0.206	0.109
D6RAN4	Uncharacterized protein OS=Homo sapiens GN=RPL9 PE=4 SV=1 - [D6RAN4_HUMAN]	6.10	9.34	2	2	2	0.418	0.795
D6R910	Uncharacterized protein OS=Homo sapiens GN=RPS6KA2 PE=4 SV=1 - [D6R910_HUMAN]	7.43	19.20	2	2	2	0.423	0.409
C9J9K3	Uncharacterized protein OS=Homo sapiens GN=RPSA PE=3 SV=1 - [C9J9K3_HUMAN]	30.01	23.48	5	5	8	0.153	0.106
F5H774	Uncharacterized protein OS=Homo sapiens GN=RTN3 PE=4 SV=1 - [F5H774_HUMAN]	17.43	2.28	2	2	5	0.554	0.452
F5H3J5	Uncharacterized protein OS=Homo sapiens GN=S100A4 PE=4 SV=1 - [F5H3J5_HUMAN]	5.48	17.78	2	2	2	0.651	0.630
E9PGZ4	Uncharacterized protein OS=Homo sapiens GN=SACM1L PE=4 SV=1 - [E9PGZ4_HUMAN]	25.95	10.95	6	6	7	1.052	1.049
C9JPX0	Uncharacterized protein OS=Homo sapiens GN=SAFB2 PE=4 SV=2 - [C9JPX0_HUMAN]	7.16	5.67	2	2	2	0.300	0.180
E9PEA8	Uncharacterized protein OS=Homo sapiens GN=SCCPDH PE=4 SV=1 - [E9PEA8_HUMAN]	9.29	8.30	2	2	3	0.932	0.581
B7Z5N7	Uncharacterized protein OS=Homo sapiens GN=SCFD1 PE=2 SV=1 - [B7Z5N7_HUMAN]	19.04	14.66	5	5	6	0.380	0.380
E9PBJ5	Uncharacterized protein OS=Homo sapiens GN=SDHA PE=4 SV=1 - [E9PBJ5_HUMAN]	31.25	14.61	7	7	9	0.281	0.186
B5MCX3	Uncharacterized protein OS=Homo sapiens GN=SEPT2 PE=3 SV=1 - [B5MCX3_HUMAN]	24.17	17.13	5	5	8	0.053	0.219
B4DNE4	Uncharacterized protein OS=Homo sapiens GN=SEPT7 PE=2 SV=1 - [B4DNE4_HUMAN]	74.92	24.61	10	11	23	0.150	0.399
A6NMH6	Uncharacterized protein OS=Homo sapiens GN=SEPT8 PE=3 SV=1 - [A6NMH6_HUMAN]	38.57	16.28	5	7	11	0.114	0.360
B4DN87	Uncharacterized protein OS=Homo sapiens GN=SERPINH1 PE=2 SV=1 - [B4DN87_HUMAN]	27.80	12.85	5	5	8	0.325	0.209
E7EMJ6	Uncharacterized protein OS=Homo sapiens GN=SGTA PE=4 SV=1 - [E7EMJ6_HUMAN]	6.90	7.90	2	2	2	0.473	0.893
E5RJR5	Uncharacterized protein OS=Homo sapiens GN=SKP1 PE=4 SV=1 - [E5RJR5_HUMAN]	11.36	17.79	3	3	3	0.626	1.269
B7Z844	Uncharacterized protein OS=Homo sapiens GN=SLC2A14 PE=2 SV=1 - [B7Z844_HUMAN]	6.35	3.89	2	2	2	2.713	1.613
B4E2Z3	Uncharacterized protein OS=Homo sapiens GN=SLC3A2 PE=2 SV=1 - [B4E2Z3_HUMAN]	12.18	8.22	3	3	3	0.058	0.090
B7Z6X9	Uncharacterized protein OS=Homo sapiens GN=SLC43A2 PE=2 SV=1 - [B7Z6X9_HUMAN]	19.96	7.41	3	3	6	1.959	1.925
E9PS74	Uncharacterized protein OS=Homo sapiens GN=SLC43A3 PE=4 SV=1 - [E9PS74_HUMAN]	37.29	9.97	5	5	12	0.876	0.443
E9PD53	Uncharacterized protein OS=Homo sapiens GN=SMC4 PE=4 SV=1 - [E9PD53_HUMAN]	27.38	6.18	8	8	9	0.325	0.349
E7EPV7	Uncharacterized protein OS=Homo sapiens GN=SNCA PE=4 SV=1 - [E7EPV7_HUMAN]	43.17	69.57	7	7	12	0.396	0.479
E7ESM6	Uncharacterized protein OS=Homo sapiens GN=SND1 PE=4 SV=2 - [E7ESM6_HUMAN]	78.97	19.22	17	17	23	0.216	0.619
B4DEK4	Uncharacterized protein OS=Homo sapiens GN=SNX2 PE=2 SV=1 - [B4DEK4_HUMAN]	11.32	7.71	3	3	3	0.753	0.801
F5H3C5	Uncharacterized protein OS=Homo sapiens GN=SOD2 PE=3 SV=1 - [F5H3C5_HUMAN]	16.77	33.33	4	4	5	0.069	0.107
F5H7U6	Uncharacterized protein OS=Homo sapiens GN=SPAG9 PE=4 SV=1 - [F5H7U6_HUMAN]	7.15	2.50	2	2	2	0.575	0.593
E7EMJ8	Uncharacterized protein OS=Homo sapiens GN=SRSF4 PE=4 SV=2 - [E7EMJ8_HUMAN]	16.21	7.64	3	3	5	0.701	0.393
C9K0U8	Uncharacterized protein OS=Homo sapiens GN=SSBP1 PE=4 SV=1 - [C9K0U8_HUMAN]	5.33	11.57	2	2	2	0.139	0.292
A6NMU3	Uncharacterized protein OS=Homo sapiens GN=STAM PE=4 SV=1 - [A6NMU3_HUMAN]	9.97	12.30	3	3	3	0.647	0.737
B4E2V5	Uncharacterized protein OS=Homo sapiens GN=STOM PE=2 SV=1 - [B4E2V5_HUMAN]	415.36	54.43	14	14	127	1.911	2.484
B4E1K7	Uncharacterized protein OS=Homo sapiens GN=STOML2 PE=2 SV=1 - [B4E1K7_HUMAN]	42.51	27.65	8	8	12	0.076	0.143
D6RF48	Uncharacterized protein OS=Homo sapiens GN=STX18 PE=4 SV=1 - [D6RF48_HUMAN]	19.48	14.29	5	5	6	0.293	0.421
F5GXG3	Uncharacterized protein OS=Homo sapiens GN=STXBP2 PE=4 SV=1 - [F5GXG3_HUMAN]	13.62	6.04	4	4	4	0.786	0.678
F5GXC8	Uncharacterized protein OS=Homo sapiens GN=SUCLA2 PE=3 SV=1 - [F5GXC8_HUMAN]	6.35	6.67	2	2	2	1.313	0.910
F5GWQ7	Uncharacterized protein OS=Homo sapiens GN=TAF15 PE=4 SV=1 - [F5GWQ7_HUMAN]	12.97	16.96	2	4	4	0.034	0.134
B4DIT7	Uncharacterized protein OS=Homo sapiens GN=TGM2 PE=2 SV=1 - [B4DIT7_HUMAN]	28.62	11.06	6	6	9	0.436	1.343
F5GX39	Uncharacterized protein OS=Homo sapiens GN=TMED2 PE=3 SV=1 - [F5GX39_HUMAN]	21.36	31.90	4	4	7	0.598	0.956
E9PI90	Uncharacterized protein OS=Homo sapiens GN=TMEM126A PE=4 SV=1 - [E9PI90_HUMAN]	6.30	25.26	2	2	2	0.115	0.150
B4DZ87	Uncharacterized protein OS=Homo sapiens GN=TOMM70A PE=2 SV=1 - [B4DZ87_HUMAN]	7.52	11.58	3	3	3	0.745	0.147
B4DSE2	Uncharacterized protein OS=Homo sapiens GN=TPP1 PE=2 SV=1 - [B4DSE2_HUMAN]	6.78	7.27	2	2	2	0.379	0.410
F5H897	Uncharacterized protein OS=Homo sapiens GN=TRAP1 PE=3 SV=1 - [F5H897_HUMAN]	30.10	8.45	5	6	9	0.034	0.117
E9PGT1	Uncharacterized protein OS=Homo sapiens GN=TSN PE=4 SV=1 - [E9PGT1_HUMAN]	19.36	20.18	4	4	5	0.909	1.205

E9PLH9	Uncharacterized protein OS=Homo sapiens GN=TSTA3 PE=4 SV=1 - [E9PLH9_HUMAN]	14.81	19.33	2	2	4	0.239	0.773
F5H265	Uncharacterized protein OS=Homo sapiens GN=UBC PE=4 SV=1 - [F5H265_HUMAN]	186.73	87.25	8	8	61	1.400	0.954
E9PJ81	Uncharacterized protein OS=Homo sapiens GN=UBXN1 PE=4 SV=1 - [E9PJ81_HUMAN]	22.36	28.97	6	6	7	0.560	0.761
E9PGR0	Uncharacterized protein OS=Homo sapiens GN=UCHL5 PE=4 SV=1 - [E9PGR0_HUMAN]	19.20	15.14	5	5	6	0.642	0.347
C9JKD6	Uncharacterized protein OS=Homo sapiens GN=UGP2 PE=4 SV=1 - [C9JKD6_HUMAN]	19.16	10.04	5	5	6	0.847	1.130
E5RHG9	Uncharacterized protein OS=Homo sapiens GN=UQCRB PE=4 SV=1 - [E5RHG9_HUMAN]	23.27	32.89	3	3	6	0.366	0.231
F5GZ76	Uncharacterized protein OS=Homo sapiens GN=USO1 PE=4 SV=1 - [F5GZ76_HUMAN]	5.91	2.89	2	2	2	1.308	0.877
B7Z7T5	Uncharacterized protein OS=Homo sapiens GN=USP7 PE=2 SV=1 - [B7Z7T5_HUMAN]	14.98	6.76	5	5	5	0.706	0.761
B0V043	Uncharacterized protein OS=Homo sapiens GN=VARS PE=3 SV=1 - [B0V043_HUMAN]	27.83	7.52	9	9	9	0.644	0.356
F5H2A7	Uncharacterized protein OS=Homo sapiens GN=VBP1 PE=4 SV=1 - [F5H2A7_HUMAN]	5.70	10.94	2	2	2	0.150	0.523
B4DP38	Uncharacterized protein OS=Homo sapiens GN=WDR77 PE=2 SV=1 - [B4DP38_HUMAN]	14.30	7.19	3	3	4	1.884	1.898
B7Z6V3	Uncharacterized protein OS=Homo sapiens GN=WDR81 PE=2 SV=1 - [B7Z6V3_HUMAN]	5.92	3.67	2	2	2	0.878	0.796
F5GWT4	Uncharacterized protein OS=Homo sapiens GN=WNK1 PE=4 SV=1 - [F5GWT4_HUMAN]	71.50	9.51	19	19	23	0.897	0.698
E7ESC6	Uncharacterized protein OS=Homo sapiens GN=XPO7 PE=4 SV=1 - [E7ESC6_HUMAN]	156.55	25.18	26	26	47	0.202	0.429
B1AHC7	Uncharacterized protein OS=Homo sapiens GN=XRCC6 PE=4 SV=1 - [B1AHC7_HUMAN]	11.98	4.67	3	3	4	0.201	0.092
A1A528	Uncharacterized protein OS=Homo sapiens GN=ZW10 PE=2 SV=1 - [A1A528_HUMAN]	7.28	2.68	2	2	2	0.611	0.616
F5GYQ0	Uncharacterized protein OS=Homo sapiens PE=4 SV=1 - [F5GYQ0_HUMAN]	6.07	9.57	2	2	2	1.610	0.972
F6WSP1	Uncharacterized protein OS=Homo sapiens PE=4 SV=1 - [F6WSP1_HUMAN]	6.19	7.95	2	2	2	0.891	0.830
C4AM82	Uncharacterized protein OS=Homo sapiens PE=4 SV=3 - [C4AM82_HUMAN]	6.11	6.62	2	2	2	0.796	1.123
Q969H8	UPF0556 protein C19orf10 OS=Homo sapiens GN=C19orf10 PE=1 SV=1 - [CS010_HUMAN]	10.83	15.03	2	2	3	1.388	1.009
Q9Y224	UPF0568 protein C14orf166 OS=Homo sapiens GN=C14orf166 PE=1 SV=1 - [CN166_HUMAN]	6.57	6.15	2	2	2		0.108
Q13336	Urea transporter 1 OS=Homo sapiens GN=SLC14A1 PE=2 SV=2 - [UT1_HUMAN]	84.52	14.65	3	7	27	2.844	2.518
P54725	UV excision repair protein RAD23 homolog A OS=Homo sapiens GN=RAD23A PE=1 SV=1 - [RD23A_HUMAN]	24.09	17.91	4	5	8	0.604	1.309
P54727	UV excision repair protein RAD23 homolog B OS=Homo sapiens GN=RAD23B PE=1 SV=1 - [RD23B_HUMAN]	17.68	14.18	4	5	5	0.204	0.471
P21281	V-type proton ATPase subunit B, brain isoform OS=Homo sapiens GN=ATP6V1B2 PE=1 SV=3 - [VATB2_HUMAN]	34.09	13.50	6	6	10	0.196	0.410
P61421	V-type proton ATPase subunit d 1 OS=Homo sapiens GN=ATP6V0D1 PE=1 SV=1 - [VA0D1_HUMAN]	19.96	9.69	4	4	6	0.397	0.295
Q9Y5K8	V-type proton ATPase subunit D OS=Homo sapiens GN=ATP6V1D PE=1 SV=1 - [VATD_HUMAN]	11.20	14.98	3	3	3	0.207	0.542
O75348	V-type proton ATPase subunit G 1 OS=Homo sapiens GN=ATP6V1G1 PE=1 SV=3 - [VATG1_HUMAN]	22.83	28.81	4	4	6	0.172	0.452
Q96RL7	Vacuolar protein sorting-associated protein 13A OS=Homo sapiens GN=VPS13A PE=1 SV=2 - [VP13A_HUMAN]	27.50	2.52	7	7	8	0.748	1.110
Q9UBQ0	Vacuolar protein sorting-associated protein 29 OS=Homo sapiens GN=VPS29 PE=1 SV=1 - [VPS29_HUMAN]	9.33	14.84	3	3	3	0.167	0.176
Q96QK1	Vacuolar protein sorting-associated protein 35 OS=Homo sapiens GN=VPS35 PE=1 SV=2 - [VPS35_HUMAN]	23.06	7.54	6	6	7	0.089	0.170
P50552	Vasodilator-stimulated phosphoprotein OS=Homo sapiens GN=VASP PE=1 SV=3 - [VASP_HUMAN]	34.74	11.58	6	6	9	1.637	0.776
P49748	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADVL PE=1 SV=1 - [ACADV_HUMAN]	46.38	12.98	9	9	13	0.129	0.096
Q12981	Vesicle transport protein SEC20 OS=Homo sapiens GN=BNIP1 PE=1 SV=3 - [SEC20_HUMAN]	6.85	8.33	2	2	2	0.955	1.141
Q9NZ43	Vesicle transport protein USE1 OS=Homo sapiens GN=USE1 PE=1 SV=2 - [USE1_HUMAN]	16.15	14.29	4	4	5	0.505	0.660
Q15836	Vesicle-associated membrane protein 3 OS=Homo sapiens GN=VAMP3 PE=1 SV=3 - [VAMP3_HUMAN]	12.39	33.00	2	2	4	0.475	0.655
P51809	Vesicle-associated membrane protein 7 OS=Homo sapiens GN=VAMP7 PE=1 SV=3 - [VAMP7_HUMAN]	20.20	16.82	4	4	7	0.234	0.269
Q9P0L0	Vesicle-associated membrane protein-associated protein A OS=Homo sapiens GN=VAPA PE=1 SV=3 - [VAPA_HUMAN]	63.24	36.14	8	9	20	0.758	0.673
O95292	Vesicle-associated membrane protein-associated protein B/C OS=Homo sapiens GN=VAPB PE=1 SV=3 - [VAPB_HUMAN]	35.06	27.16	4	6	11	0.706	0.723
P46459	Vesicle-fusing ATPase OS=Homo sapiens GN=NSF PE=1 SV=3 - [NSF_HUMAN]	116.38	28.90	23	23	34	0.411	0.783
O75396	Vesicle-trafficking protein SEC22b OS=Homo sapiens GN=SEC22B PE=1 SV=4 - [SC22B_HUMAN]	59.03	38.60	7	7	17	0.547	0.553
P21796	Voltage-dependent anion-selective channel protein 1 OS=Homo sapiens GN=VDAC1 PE=1 SV=2 - [VDAC1_HUMAN]	142.54	38.16	9	11	43	0.025	0.066
P45880	Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2 - [VDAC2_HUMAN]	134.91	42.18	11	12	40	0.014	0.066
Q9Y277	Voltage-dependent anion-selective channel protein 3 OS=Homo sapiens GN=VDAC3 PE=1 SV=1 - [VDAC3_HUMAN]	159.01	51.24	13	15	46	0.032	0.095
A4D1P6	WD repeat-containing protein 91 OS=Homo sapiens GN=WDR91 PE=1 SV=2 - [WDR91_HUMAN]	54.53	16.73	9	10	15	1.065	0.824
P13010	X-ray repair cross-complementing protein 5 OS=Homo sapiens GN=XRCC5 PE=1 SV=3 - [XRCC5_HUMAN]	14.04	5.87	4	4	4	0.031	0.100
Q7Z2W4	Zinc finger CCCH-type antiviral protein 1 OS=Homo sapiens GN=ZC3HAV1 PE=1 SV=3 - [ZCCHV_HUMAN]	20.45	9.20	6	6	6	0.667	0.279
Q9Y6M5	Zinc transporter 1 OS=Homo sapiens GN=SLC30A1 PE=1 SV=3 - [ZNT1_HUMAN]	18.99	8.88	4	4	6	1.355	0.761

Supplemental Table 6B

Accession	Description	Score	Coverage	Unique Peptides	Peptides	PSMs	Cytosol fraction Adult RBC/retic	Cytosol fraction cord RBC/retic
Q9NRX4	14 kDa phosphohistidine phosphatase OS=Homo sapiens GN=PHPT1 PE=1 SV=1 - [PHP14_HUMAN]	39.19	29.60	5	5	13	0.546	0.438
P31946	14-3-3 protein beta/alpha OS=Homo sapiens GN=YWHAB PE=1 SV=3 - [1433B_HUMAN]	166.33	43.09	4	13	57	0.310	0.251
P62258	14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1 - [1433E_HUMAN]	175.35	52.94	11	14	57	0.359	0.288
Q04917	14-3-3 protein eta OS=Homo sapiens GN=YWHAH PE=1 SV=4 - [1433F_HUMAN]	117.70	41.46	6	11	40	0.078	0.060
P61981	14-3-3 protein gamma OS=Homo sapiens GN=YWHAG PE=1 SV=2 - [1433G_HUMAN]	147.38	46.56	8	14	49	0.264	0.180
P27348	14-3-3 protein theta OS=Homo sapiens GN=YWHAQ PE=1 SV=1 - [1433T_HUMAN]	171.10	54.29	8	17	56	0.173	0.113
P63104	14-3-3 protein zeta/delta OS=Homo sapiens GN=YWHAZ PE=1 SV=1 - [1433Z_HUMAN]	164.93	38.78	5	12	54	0.261	0.209
P62333	26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1 - [PRS10_HUMAN]	30.86	16.45	8	8	10	0.488	0.213
P62191	26S protease regulatory subunit 4 OS=Homo sapiens GN=PSMC1 PE=1 SV=1 - [PRS4_HUMAN]	37.65	20.91	10	11	12	0.489	0.181
P17980	26S protease regulatory subunit 6A OS=Homo sapiens GN=PSMC3 PE=1 SV=3 - [PRS6A_HUMAN]	29.77	18.91	7	7	9	0.489	0.203
P43686	26S protease regulatory subunit 6B OS=Homo sapiens GN=PSMC4 PE=1 SV=2 - [PRS6B_HUMAN]	35.98	11.24	6	7	12	0.337	0.177
P35998	26S protease regulatory subunit 7 OS=Homo sapiens GN=PSMC2 PE=1 SV=3 - [PRS7_HUMAN]	49.36	22.86	10	10	15	0.437	0.193
Q99460	26S proteasome non-ATPase regulatory subunit 1 OS=Homo sapiens GN=PSMD1 PE=1 SV=2 - [PSMD1_HUMAN]	36.24	8.60	9	9	12	0.366	0.188
O00231	26S proteasome non-ATPase regulatory subunit 11 OS=Homo sapiens GN=PSMD11 PE=1 SV=3 - [PSD11_HUMAN]	27.89	14.69	7	7	10	0.329	0.143
O00232	26S proteasome non-ATPase regulatory subunit 12 OS=Homo sapiens GN=PSMD12 PE=1 SV=3 - [PSD12_HUMAN]	38.87	17.98	9	9	13	0.311	0.175
Q9UNM6	26S proteasome non-ATPase regulatory subunit 13 OS=Homo sapiens GN=PSMD13 PE=1 SV=2 - [PSD13_HUMAN]	34.43	15.16	7	7	11	0.294	0.143
O00487	26S proteasome non-ATPase regulatory subunit 14 OS=Homo sapiens GN=PSMD14 PE=1 SV=1 - [PSDE_HUMAN]	13.13	9.03	4	4	5	0.374	0.143
P55036	26S proteasome non-ATPase regulatory subunit 4 OS=Homo sapiens GN=PSMD4 PE=1 SV=1 - [PSMD4_HUMAN]	15.18	10.34	4	4	5	0.290	0.244
O00233	26S proteasome non-ATPase regulatory subunit 9 OS=Homo sapiens GN=PSMD9 PE=1 SV=3 - [PSMD9_HUMAN]	43.88	27.80	7	7	13	0.663	0.498
Q13442	28 kDa heat- and acid-stable phosphoprotein OS=Homo sapiens GN=PDAP1 PE=1 SV=1 - [HAP28_HUMAN]	36.22	29.28	7	7	12	0.063	0.117
P25325	3-mercaptopyruvate sulfurtransferase OS=Homo sapiens GN=MPST PE=1 SV=3 - [THTM_HUMAN]	25.72	20.88	6	7	9	0.759	0.536
P49189	4-trimethylaminobutyraldehyde dehydrogenase OS=Homo sapiens GN=ALDH9A1 PE=1 SV=3 - [AL9A1_HUMAN]	31.43	15.99	8	8	10	0.448	0.317
P46783	40S ribosomal protein S10 OS=Homo sapiens GN=RPS10 PE=1 SV=1 - [RS10_HUMAN]	20.64	26.67	6	6	8	0.173	0.102
P62280	40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=1 SV=3 - [RS11_HUMAN]	6.08	11.39	2	2	2	0.047	0.057
P25398	40S ribosomal protein S12 OS=Homo sapiens GN=RPS12 PE=1 SV=3 - [RS12_HUMAN]	7.10	14.39	2	2	2	0.088	0.074
P62249	40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=1 SV=2 - [RS16_HUMAN]	21.33	16.44	4	4	8	0.054	0.097
P0CW22	40S ribosomal protein S17-like OS=Homo sapiens GN=RPS17L PE=3 SV=1 - [RS17L_HUMAN]	12.33	9.63	2	3	5	0.282	0.150
P62269	40S ribosomal protein S18 OS=Homo sapiens GN=RPS18 PE=1 SV=3 - [RS18_HUMAN]	21.76	27.63	6	6	7	0.099	0.103
P39019	40S ribosomal protein S19 OS=Homo sapiens GN=RPS19 PE=1 SV=2 - [RS19_HUMAN]	19.31	26.90	4	4	6	0.112	0.094
P60866	40S ribosomal protein S20 OS=Homo sapiens GN=RPS20 PE=1 SV=1 - [RS20_HUMAN]	5.80	17.65	2	2	2	0.038	0.055
Q8WVC2	40S ribosomal protein S21 OS=Homo sapiens GN=RPS21 PE=2 SV=1 - [Q8WVC2_HUMAN]	14.67	32.10	3	3	5	0.128	0.063
P62857	40S ribosomal protein S28 OS=Homo sapiens GN=RPS28 PE=1 SV=1 - [RS28_HUMAN]	6.93	28.99	2	2	2	0.013	0.032
P23396	40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2 - [RS3_HUMAN]	20.80	22.63	5	5	6	0.046	0.050
P62701	40S ribosomal protein S4, X isoform OS=Homo sapiens GN=RPS4X PE=1 SV=2 - [RS4X_HUMAN]	21.17	10.65	3	3	7	0.067	0.078
P46782	40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=4 - [RS5_HUMAN]	5.92	8.82	2	2	2	0.074	0.080
P62753	40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=1 SV=1 - [RS6_HUMAN]	17.76	17.27	5	5	6	0.178	0.051
P62081	40S ribosomal protein S7 OS=Homo sapiens GN=RPS7 PE=1 SV=1 - [RS7_HUMAN]	18.46	17.53	4	4	6	0.076	0.045
P46781	40S ribosomal protein S9 OS=Homo sapiens GN=RPS9 PE=1 SV=3 - [RS9_HUMAN]	8.13	10.82	2	2	3	0.274	0.090
Q13131	5'-AMP-activated protein kinase catalytic subunit alpha-1 OS=Homo sapiens GN=PRKAA1 PE=1 SV=4 - [AAPK1_HUMAN]	8.97	5.01	3	3	3	0.153	0.153
Q5JUV3	5'-nucleotidase, cytosolic II (Fragment) OS=Homo sapiens GN=NT5C2 PE=2 SV=1 - [Q5JUV3_HUMAN]	5.09	8.05	2	2	2	0.145	0.125
Q01813	6-phosphofructokinase type C OS=Homo sapiens GN=PFKP PE=1 SV=2 - [K6PP_HUMAN]	18.59	7.78	3	6	7	0.169	0.211
P17858	6-phosphofructokinase, liver type OS=Homo sapiens GN=PFKL PE=1 SV=6 - [K6PL_HUMAN]	26.65	11.03	5	8	9	0.339	0.387
P08237	6-phosphofructokinase, muscle type OS=Homo sapiens GN=PFKM PE=1 SV=2 - [K6PF_HUMAN]	36.80	8.59	6	7	12	0.383	0.319
F5H7U0	6-phosphogluconate dehydrogenase, decarboxylating OS=Homo sapiens GN=PGD PE=3 SV=1 - [F5H7U0_HUMAN]	136.83	33.41	16	16	45	0.226	0.195
O95336	6-phosphogluconolactonase OS=Homo sapiens GN=PGLS PE=1 SV=2 - [6PGL_HUMAN]	27.75	24.81	6	6	8	0.584	0.415
P05388	60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=1 SV=1 - [RLA0_HUMAN]	9.25	5.36	2	2	3	0.105	0.072
P62906	60S ribosomal protein L10a OS=Homo sapiens GN=RPL10A PE=1 SV=2 - [RL10A_HUMAN]	8.29	14.75	3	3	3	0.111	0.070
P30050	60S ribosomal protein L12 OS=Homo sapiens GN=RPL12 PE=1 SV=1 - [RL12_HUMAN]	8.35	13.94	3	3	3	0.109	0.069
P26373	60S ribosomal protein L13 OS=Homo sapiens GN=RPL13 PE=1 SV=4 - [RL13_HUMAN]	27.85	17.54	4	4	8	0.044	0.031
P40429	60S ribosomal protein L13a OS=Homo sapiens GN=RPL13A PE=1 SV=2 - [RL13A_HUMAN]	4.96	6.40	2	2	2	0.064	0.056
P18621	60S ribosomal protein L17 OS=Homo sapiens GN=RPL17 PE=1 SV=3 - [RL17_HUMAN]	16.26	21.74	4	4	5	0.034	0.037
P46778	60S ribosomal protein L21 OS=Homo sapiens GN=RPL21 PE=1 SV=2 - [RL21_HUMAN]	4.88	8.13	2	2	2	0.146	0.110
P35268	60S ribosomal protein L22 OS=Homo sapiens GN=RPL22 PE=1 SV=2 - [RL22_HUMAN]	7.52	17.97	3	3	3	0.252	0.075
P62750	60S ribosomal protein L23a OS=Homo sapiens GN=RPL23A PE=1 SV=1 - [RL23A_HUMAN]	5.48	5.13	2	2	2	0.092	0.071
P46779	60S ribosomal protein L28 OS=Homo sapiens GN=RPL28 PE=1 SV=3 - [RL28_HUMAN]	21.44	25.55	5	5	7	0.160	0.075

P62888	60S ribosomal protein L30 OS=Homo sapiens GN=RPL30 PE=1 SV=2 - [RL30_HUMAN]	13.00	14.78	2	2	5	0.218	0.056
P49207	60S ribosomal protein L34 OS=Homo sapiens GN=RPL34 PE=1 SV=3 - [RL34_HUMAN]	9.02	13.68	2	2	3	0.034	0.037
P42766	60S ribosomal protein L35 OS=Homo sapiens GN=RPL35 PE=1 SV=2 - [RL35_HUMAN]	10.92	18.70	3	4	4	0.136	0.082
P18077	60S ribosomal protein L35a OS=Homo sapiens GN=RPL35A PE=1 SV=2 - [RL35A_HUMAN]	8.16	23.64	3	3	3	0.223	0.110
Q02878	60S ribosomal protein L6 OS=Homo sapiens GN=RPL6 PE=1 SV=3 - [RL6_HUMAN]	11.13	13.19	4	4	4	0.201	0.069
P18124	60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1 - [RL7_HUMAN]	12.85	20.16	4	4	4	0.211	0.112
P11021	78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2 - [GRP78_HUMAN]	73.98	9.94	3	6	23	0.174	0.097
Q2L6I2	ABC50 protein OS=Homo sapiens GN=ABCF1 PE=2 SV=1 - [Q2L6I2_HUMAN]	15.17	4.21	4	4	5	0.047	0.149
Q9BWD1	Acetyl-CoA acetyltransferase, cytosolic OS=Homo sapiens GN=ACAT2 PE=1 SV=2 - [THIC_HUMAN]	24.71	12.59	7	7	9	0.283	0.353
Q92688	Acidic leucine-rich nuclear phosphoprotein 32 family member B OS=Homo sapiens GN=ANP32B PE=1 SV=1 - [AN32B_HUMAN]	36.09	15.94	3	5	11	0.062	0.051
P61160	Actin-related protein 2 OS=Homo sapiens GN=ACTR2 PE=1 SV=1 - [ARP2_HUMAN]	34.71	6.60	2	3	14	0.185	0.309
O15144	Actin-related protein 2/3 complex subunit 2 OS=Homo sapiens GN=ARPC2 PE=1 SV=1 - [ARPC2_HUMAN]	10.90	11.67	4	4	4	0.126	0.228
P53999	Activated RNA polymerase II transcriptional coactivator p15 OS=Homo sapiens GN=SUB1 PE=1 SV=3 - [TCP4_HUMAN]	6.36	15.75	2	2	2	0.545	0.032
O95433	Activator of 90 kDa heat shock protein ATPase homolog 1 OS=Homo sapiens GN=AHSA1 PE=1 SV=1 - [AHSA1_HUMAN]	13.72	10.65	4	4	5	0.185	0.152
P07108	Acyl-CoA-binding protein OS=Homo sapiens GN=DBI PE=1 SV=2 - [ACBP_HUMAN]	10.03	41.38	2	2	3	0.122	0.197
P13798	Acylamino-acid-releasing enzyme OS=Homo sapiens GN=APEH PE=1 SV=4 - [ACPH_HUMAN]	162.91	28.01	21	21	49	0.510	0.376
P07311	Acylphosphatase-1 OS=Homo sapiens GN=ACYP1 PE=1 SV=2 - [ACYP1_HUMAN]	18.59	28.28	4	4	6	0.435	0.410
Q7Z451	Adaptor-related protein complex 2, beta 1 subunit, isoform CRA_f OS=Homo sapiens GN=AP2B1 PE=2 SV=1 - [Q7Z451_HUMAN]	21.68	5.00	6	6	7	0.341	0.181
Q96D30	ADD1 protein OS=Homo sapiens GN=ADD1 PE=2 SV=1 - [Q96D30_HUMAN]	5.47	4.25	2	2	2	0.148	0.349
P07741	Adenine phosphoribosyltransferase OS=Homo sapiens GN=APRT PE=1 SV=2 - [APT_HUMAN]	35.69	32.78	7	7	13	0.294	0.262
F5H737	Adenosylhomocysteinase OS=Homo sapiens GN=AHCY PE=3 SV=1 - [F5H737_HUMAN]	46.43	24.26	10	10	15	0.487	0.493
P00568	Adenylate kinase isoenzyme 1 OS=Homo sapiens GN=AK1 PE=1 SV=3 - [KAD1_HUMAN]	136.77	45.36	11	12	43	0.780	0.428
P30566	Adenylosuccinate lyase OS=Homo sapiens GN=ADSL PE=1 SV=2 - [PUR8_HUMAN]	60.33	18.39	11	11	19	0.685	0.470
F5H6Z3	Adenylyl cyclase-associated protein OS=Homo sapiens GN=CAP1 PE=3 SV=1 - [F5H6Z3_HUMAN]	30.77	11.28	6	6	11	0.237	0.186
Q9UKK9	ADP-sugar pyrophosphatase OS=Homo sapiens GN=NUDT5 PE=1 SV=1 - [NUDT5_HUMAN]	13.15	16.89	4	4	4	0.408	0.327
P49588	Alanyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=AARS PE=1 SV=2 - [SYAC_HUMAN]	141.47	20.56	23	23	46	0.038	0.047
C9JKR2	Albumin, isoform CRA_k OS=Homo sapiens GN=ALB PE=4 SV=1 - [C9JKR2_HUMAN]	8.57	7.67	2	2	2	0.662	0.895
P14550	Alcohol dehydrogenase [NADP+] OS=Homo sapiens GN=AKR1A1 PE=1 SV=3 - [AK1A1_HUMAN]	20.01	10.15	4	4	7	0.432	0.421
P11766	Alcohol dehydrogenase class-3 OS=Homo sapiens GN=ADH5 PE=1 SV=4 - [ADHX_HUMAN]	25.06	13.10	6	6	9	0.210	0.172
P42330	Aldo-keto reductase family 1 member C3 OS=Homo sapiens GN=AKR1C3 PE=1 SV=4 - [AK1C3_HUMAN]	14.00	9.91	4	4	5	0.147	0.169
P15121	Aldose reductase OS=Homo sapiens GN=AKR1B1 PE=1 SV=3 - [ALDR_HUMAN]	22.46	7.91	3	3	7	0.221	0.210
O43768	Alpha-endosulfine OS=Homo sapiens GN=ENSA PE=1 SV=1 - [ENSA_HUMAN]	23.94	52.89	6	6	9	0.120	0.180
P06733	Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2 - [ENOA_HUMAN]	292.07	35.48	15	17	98	0.080	0.171
Q9NZD4	Alpha-hemoglobin-stabilizing protein OS=Homo sapiens GN=AHSP PE=1 SV=1 - [AHSP_HUMAN]	326.31	56.86	7	7	103	0.051	0.094
P54920	Alpha-soluble NSF attachment protein OS=Homo sapiens GN=NAPA PE=1 SV=3 - [SNAA_HUMAN]	54.79	32.88	9	9	17	0.775	0.458
Q6FI81	Anamorsin OS=Homo sapiens GN=CIAPIN1 PE=1 SV=2 - [CPIN1_HUMAN]	6.39	7.05	2	2	2	0.252	0.192
P08758	Annexin A5 OS=Homo sapiens GN=ANXA5 PE=1 SV=2 - [ANXA5_HUMAN]	12.84	7.81	3	3	5	0.236	0.249
O95782	AP-2 complex subunit alpha-1 OS=Homo sapiens GN=AP2A1 PE=1 SV=3 - [AP2A1_HUMAN]	36.69	7.16	9	9	12	0.314	0.177
P05089	Arginase-1 OS=Homo sapiens GN=ARG1 PE=1 SV=2 - [ARGI1_HUMAN]	14.85	8.07	2	3	5	0.168	0.558
O43776	Asparaginyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=NARS PE=1 SV=1 - [SYNC_HUMAN]	26.51	9.67	5	6	9	0.109	0.092
P17174	Aspartate aminotransferase, cytoplasmic OS=Homo sapiens GN=GOT1 PE=1 SV=3 - [AATC_HUMAN]	54.91	17.68	7	7	16	0.362	0.261
P14868	Aspartyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=DARS PE=1 SV=2 - [SYDC_HUMAN]	41.93	20.96	11	11	14	0.227	0.258
P53396	ATP-citrate synthase OS=Homo sapiens GN=ACLY PE=1 SV=3 - [ACLY_HUMAN]	197.11	24.25	31	31	60	0.272	0.300
Q08211	ATP-dependent RNA helicase A OS=Homo sapiens GN=DHX9 PE=1 SV=4 - [DHX9_HUMAN]	25.35	5.98	7	7	9	0.128	0.118
P02730	Band 3 anion transport protein OS=Homo sapiens GN=SLC4A1 PE=1 SV=3 - [B3AT_HUMAN]	45.64	8.01	7	7	15	0.050	0.480
O43491	Band 4.1-like protein 2 OS=Homo sapiens GN=EPB41L2 PE=1 SV=1 - [E41L2_HUMAN]	8.05	4.48	2	3	3	0.228	0.499
P07814	Bifunctional aminoacyl-tRNA synthetase OS=Homo sapiens GN=EPRS PE=1 SV=5 - [SYEP_HUMAN]	25.15	3.24	4	4	7	0.060	0.053
Q3LXA3	Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase OS=Homo sapiens GN=DAK PE=1 SV=2 - [DHAK_HUMAN]	22.15	6.78	4	4	7	0.890	0.420
P53004	Biliverdin reductase A OS=Homo sapiens GN=BLVRA PE=1 SV=2 - [BIEA_HUMAN]	65.46	32.43	12	12	21	0.408	0.250
P07738	Bisphosphoglycerate mutase OS=Homo sapiens GN=BPGM PE=1 SV=2 - [PMGE_HUMAN]	334.23	49.42	14	14	102	0.673	0.755
Q13867	Bleomycin hydrolase OS=Homo sapiens GN=BLMH PE=1 SV=1 - [BLMH_HUMAN]	13.51	10.77	4	4	4	0.455	0.389
Q9H3K6	BolA-like protein 2 OS=Homo sapiens GN=BOLA2 PE=1 SV=1 - [BOLA2_HUMAN]	17.06	26.74	2	2	5	0.517	0.414
Q9NWV8	BRISC and BRCA1-A complex member 1 OS=Homo sapiens GN=BABAM1 PE=1 SV=1 - [BABA1_HUMAN]	11.88	6.08	2	2	4	0.182	0.136
Q5VW32	BRO1 domain-containing protein BROX OS=Homo sapiens GN=BROX PE=1 SV=1 - [BROX_HUMAN]	35.09	13.63	8	8	12	0.481	0.337
P11586	C-1-tetrahydrofolate synthase, cytoplasmic OS=Homo sapiens GN=MTHFD1 PE=1 SV=3 - [C1TC_HUMAN]	122.17	23.21	26	26	40	0.118	0.096
P27708	CAD protein OS=Homo sapiens GN=CAD PE=1 SV=3 - [PYR1_HUMAN]	6.22	0.90	2	2	2	0.154	0.108

Q9BRF8	Calcineurin-like phosphoesterase domain-containing protein 1 OS=Homo sapiens GN=CPPED1 PE=1 SV=3 - [CPPED_HUMAN]	6.38	5.41	2	2	2	0.203	0.212
Q9Y2V2	Calcium-regulated heat stable protein 1 OS=Homo sapiens GN=CARHSP1 PE=1 SV=2 - [CHSP1_HUMAN]	19.72	12.93	2	2	6	0.443	0.301
P62158	Calmodulin OS=Homo sapiens GN=CALM1 PE=1 SV=2 - [CALM_HUMAN]	153.79	23.49	6	6	46	0.253	0.162
P04632	Calpain small subunit 1 OS=Homo sapiens GN=CAPNS1 PE=1 SV=1 - [CPNS1_HUMAN]	23.52	21.27	6	6	9	0.527	0.298
P07384	Calpain-1 catalytic subunit OS=Homo sapiens GN=CAPN1 PE=1 SV=1 - [CAN1_HUMAN]	77.80	18.91	14	14	25	0.591	0.359
P27797	Calreticulin OS=Homo sapiens GN=CALR PE=1 SV=1 - [CALR_HUMAN]	19.77	18.47	6	6	7	0.037	0.046
P17612	cAMP-dependent protein kinase catalytic subunit alpha OS=Homo sapiens GN=PRKACA PE=1 SV=2 - [KAPCA_HUMAN]	12.88	7.69	4	4	4	0.212	0.114
B1AK87	Capping protein (Actin filament) muscle Z-line, beta OS=Homo sapiens GN=CAPZB PE=4 SV=1 - [B1AK87_HUMAN]	25.57	21.92	6	6	8	0.307	0.252
P00915	Carbonic anhydrase 1 OS=Homo sapiens GN=CA1 PE=1 SV=2 - [CAH1_HUMAN]	421.71	55.56	11	11	130	13.615	1.656
P00918	Carbonic anhydrase 2 OS=Homo sapiens GN=CA2 PE=1 SV=2 - [CAH2_HUMAN]	220.55	47.69	11	11	70	2.712	0.830
P16152	Carbonyl reductase [NADPH] 1 OS=Homo sapiens GN=CBR1 PE=1 SV=3 - [CBR1_HUMAN]	8.38	5.78	2	2	3	0.696	0.319
Q96DG6	Carboxymethylenebutenolidase homolog OS=Homo sapiens GN=CMBL PE=1 SV=1 - [CMBL_HUMAN]	26.33	21.63	7	7	9	0.572	0.225
P04040	Catalase OS=Homo sapiens GN=CAT PE=1 SV=3 - [CATA_HUMAN]	549.08	53.70	30	30	180	0.792	0.623
Q9Y5K6	CD2-associated protein OS=Homo sapiens GN=CD2AP PE=1 SV=1 - [CD2AP_HUMAN]	13.81	5.48	4	4	5	0.235	0.264
B7Z3E2	cDNA FLJ50777, highly similar to Serine/threonine-protein phosphatase 6 (EC 3.1.3.16) OS=Homo sapiens PE=2 SV=1 - [B7Z3E2_HUMAN]	4.81	8.86	2	2	2	0.569	0.252
B4DEW9	cDNA FLJ52478, highly similar to Eukaryotic translation initiation factor 3 subunit 5 OS=Homo sapiens PE=2 SV=1 - [B4DEW9_HUMAN]	16.03	11.54	3	3	6	0.084	0.057
B4DHX4	cDNA FLJ52902, highly similar to Rab GDP dissociation inhibitor alpha OS=Homo sapiens PE=2 SV=1 - [B4DHX4_HUMAN]	24.55	13.91	2	6	8	0.368	0.330
B4DS57	cDNA FLJ53176, highly similar to Nuclear autoantigenic sperm protein OS=Homo sapiens PE=2 SV=1 - [B4DS57_HUMAN]	27.86	8.87	5	6	9	0.043	0.042
B4DFF1	cDNA FLJ53312, highly similar to Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens PE=2 SV=1 - [B4DFF1_HUMAN]	80.66	18.74	10	10	25	0.093	0.112
B4E022	cDNA FLJ56274, highly similar to Transketolase (EC 2.2.1.1) OS=Homo sapiens PE=2 SV=1 - [B4E022_HUMAN]	108.97	28.65	16	16	34	0.151	0.107
B4DZV5	cDNA FLJ58820, highly similar to 55 kDa erythrocyte membrane protein (p55) OS=Homo sapiens PE=2 SV=1 - [B4DZV5_HUMAN]	5.39	3.44	2	2	2	0.177	0.329
A8K1B6	cDNA FLJ78533, highly similar to Homo sapiens dynamin 2 (DNM2), transcript variant 4, mRNA OS=Homo sapiens PE=2 SV=1 - [A8K1B6_HUMAN]	17.30	5.43	5	5	6	0.329	0.280
P60953	Cell division control protein 42 homolog OS=Homo sapiens GN=CDC42 PE=1 SV=2 - [CDC42_HUMAN]	27.52	20.94	3	4	8	0.544	0.325
B7Z4T9	Chaperonin containing TCP1, subunit 7 (Eta), isoform CRA_c OS=Homo sapiens GN=CCT7 PE=2 SV=1 - [B7Z4T9_HUMAN]	102.85	25.05	14	14	33	0.205	0.168
O43633	Charged multivesicular body protein 2a OS=Homo sapiens GN=CHMP2A PE=1 SV=1 - [CHM2A_HUMAN]	14.42	14.41	4	4	5	0.300	0.449
Q9H444	Charged multivesicular body protein 4b OS=Homo sapiens GN=CHMP4B PE=1 SV=1 - [CHM4B_HUMAN]	13.57	15.63	4	4	4	0.168	0.183
O00299	Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4 - [CLIC1_HUMAN]	35.11	22.82	7	7	12	0.306	0.212
Q13185	Chromobox protein homolog 3 OS=Homo sapiens GN=CBX3 PE=1 SV=4 - [CBX3_HUMAN]	13.93	24.04	4	4	4	0.195	0.129
Q00610	Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC PE=1 SV=5 - [CLH1_HUMAN]	120.88	13.13	22	22	39	0.209	0.107
P09497	Clathrin light chain B OS=Homo sapiens GN=CLTB PE=1 SV=1 - [CLCB_HUMAN]	9.85	12.23	3	3	3	0.154	0.081
P48444	Coatomer subunit delta OS=Homo sapiens GN=ARCN1 PE=1 SV=1 - [COPD_HUMAN]	8.32	4.11	2	2	3	0.140	0.197
Q15021	Condensin complex subunit 1 OS=Homo sapiens GN=NCAPD2 PE=1 SV=3 - [CND1_HUMAN]	5.39	1.14	2	2	2	0.167	0.095
Q13098	COP9 signalosome complex subunit 1 OS=Homo sapiens GN=GPS1 PE=1 SV=4 - [CSN1_HUMAN]	15.51	8.35	5	5	6	0.649	0.356
Q9BT78	COP9 signalosome complex subunit 4 OS=Homo sapiens GN=COPS4 PE=1 SV=1 - [CSN4_HUMAN]	24.26	14.78	6	6	7	0.626	0.326
Q92905	COP9 signalosome complex subunit 5 OS=Homo sapiens GN=COPS5 PE=1 SV=4 - [CSN5_HUMAN]	16.14	6.89	3	3	5	0.531	0.355
Q9H9Q2	COP9 signalosome complex subunit 7b OS=Homo sapiens GN=COPS7B PE=1 SV=1 - [CSN7B_HUMAN]	5.52	8.71	2	2	2	0.504	0.321
Q5JX54	Copine I (Fragment) OS=Homo sapiens GN=CPNE1 PE=2 SV=1 - [Q5JX54_HUMAN]	6.27	13.24	2	2	2	0.361	0.169
O14618	Copper chaperone for superoxide dismutase OS=Homo sapiens GN=CCS PE=1 SV=1 - [CCS_HUMAN]	44.72	22.99	8	8	15	0.420	0.207
P36551	Coproporphyrinogen-III oxidase, mitochondrial OS=Homo sapiens GN=CPOX PE=1 SV=3 - [HEM6_HUMAN]	19.59	15.64	6	6	6	0.276	0.100
Q9ULV4	Coronin-1C OS=Homo sapiens GN=CORO1C PE=1 SV=1 - [COR1C_HUMAN]	37.25	11.81	9	9	12	0.071	0.034
P57737	Coronin-7 OS=Homo sapiens GN=CORO7 PE=1 SV=2 - [CORO7_HUMAN]	5.03	1.84	2	2	2	0.249	0.103
Q96H99	Cortactin OS=Homo sapiens GN=CTTN PE=2 SV=1 - [Q96H99_HUMAN]	11.36	8.38	4	4	4	0.223	0.163
P17812	CTP synthase 1 OS=Homo sapiens GN=CTPS PE=1 SV=2 - [PYRG1_HUMAN]	21.01	7.28	2	5	7	0.340	0.286
Q13617	Cullin-2 OS=Homo sapiens GN=CUL2 PE=1 SV=2 - [CUL2_HUMAN]	17.26	4.56	4	4	6	0.733	0.402
Q13618	Cullin-3 OS=Homo sapiens GN=CUL3 PE=1 SV=2 - [CUL3_HUMAN]	18.35	6.90	6	6	6	0.727	0.665
Q86VP6	Cullin-associated NEDD8-dissociated protein 1 OS=Homo sapiens GN=CAND1 PE=1 SV=2 - [CAND1_HUMAN]	89.90	12.11	19	19	30	0.915	0.492
P04080	Cystatin-B OS=Homo sapiens GN=CSTB PE=1 SV=2 - [CYTB_HUMAN]	33.79	30.61	3	3	11	0.215	0.183
Q9UHD1	Cysteine and histidine-rich domain-containing protein 1 OS=Homo sapiens GN=CHORDC1 PE=1 SV=2 - [CHRD1_HUMAN]	9.79	6.93	2	2	3	0.217	0.249
A8MVQ3	Cysteinyl-tRNA synthetase, isoform CRA_b OS=Homo sapiens GN=CARS PE=2 SV=1 - [A8MVQ3_HUMAN]	19.95	7.45	6	6	7	0.155	0.108
P00167	Cytochrome b5 OS=Homo sapiens GN=CYB5A PE=1 SV=2 - [CYB5_HUMAN]	13.39	27.61	4	4	5	0.502	0.436
Q8IUI8	Cytokine receptor-like factor 3 OS=Homo sapiens GN=CRLF3 PE=1 SV=2 - [CRLF3_HUMAN]	32.75	11.09	6	6	11	0.361	0.320
P28838	Cytosol aminopeptidase OS=Homo sapiens GN=LAP3 PE=1 SV=3 - [AMPL_HUMAN]	22.21	8.48	5	5	7	0.090	0.125
Q96KP4	Cytosolic non-specific dipeptidase OS=Homo sapiens GN=CNDP2 PE=1 SV=2 - [CNDP2_HUMAN]	16.49	5.05	3	3	6	0.154	0.111
B7Z522	D-dopachrome tautomerase, isoform CRA_a OS=Homo sapiens GN=DDT PE=4 SV=1 - [B7Z522_HUMAN]	46.58	21.50	2	2	15	0.787	0.648
P51397	Death-associated protein 1 OS=Homo sapiens GN=DAP PE=1 SV=3 - [DAP1_HUMAN]	9.95	23.53	3	3	4	0.166	0.251
Q6UWP2	Dehydrogenase/reductase SDR family member 11 OS=Homo sapiens GN=DHRS11 PE=1 SV=1 - [DHR11_HUMAN]	6.90	6.15	2	2	2	0.454	0.300

B7Z3I9	Delta-aminolevulinic acid dehydratase OS=Homo sapiens PE=2 SV=1 - [B7Z3I9_HUMAN]	98.15	23.00	7	7	33	0.727	0.474
O43598	Deoxyribonucleoside 5'-monophosphate N-glycosidase OS=Homo sapiens GN=RCL PE=1 SV=1 - [RCL_HUMAN]	7.65	12.07	3	3	3	0.621	0.660
B4DYA6	Destrin (Actin depolymerizing factor), isoform CRA_a OS=Homo sapiens GN=DSTN PE=2 SV=1 - [B4DYA6_HUMAN]	14.83	14.86	2	3	5	0.163	0.139
Q86TI2	Dipeptidyl peptidase 9 OS=Homo sapiens GN=DPP9 PE=1 SV=3 - [DPP9_HUMAN]	5.44	2.20	2	2	2	0.203	0.134
Q8NFP7	Diphosphoinositol polyphosphate phosphohydrolase 3-alpha OS=Homo sapiens GN=NUDT10 PE=1 SV=1 - [NUD10_HUMAN]	15.08	14.63	2	2	4	0.074	0.035
P53602	Diphosphomevalonate decarboxylase OS=Homo sapiens GN=MVD PE=1 SV=1 - [MVD1_HUMAN]	30.06	11.00	5	5	11	0.118	0.237
Q16531	DNA damage-binding protein 1 OS=Homo sapiens GN=DDB1 PE=1 SV=1 - [DDB1_HUMAN]	47.89	8.86	10	10	16	0.232	0.199
Q92878	DNA repair protein RAD50 OS=Homo sapiens GN=RAD50 PE=1 SV=1 - [RAD50_HUMAN]	5.34	1.07	2	2	2	0.110	0.075
Q8WW22	DnaJ homolog subfamily A member 4 OS=Homo sapiens GN=DNAJA4 PE=1 SV=1 - [DNJA4_HUMAN]	10.42	9.07	3	4	4	0.516	0.383
P25685	DnaJ homolog subfamily B member 1 OS=Homo sapiens GN=DNAJB1 PE=1 SV=4 - [DNJB1_HUMAN]	14.09	13.24	5	5	5	0.508	0.315
Q8WXX5	DnaJ homolog subfamily C member 9 OS=Homo sapiens GN=DNAJC9 PE=1 SV=1 - [DNJC9_HUMAN]	19.27	13.85	5	5	7	0.259	0.252
P49959	Double-strand break repair protein MRE11A OS=Homo sapiens GN=MRE11A PE=1 SV=3 - [MRE11_HUMAN]	5.11	2.82	2	2	2	0.079	0.076
Q9UJU6	Drebrin-like protein OS=Homo sapiens GN=DBNL PE=1 SV=1 - [DBNL_HUMAN]	10.45	7.67	3	3	3	0.234	0.310
P36507	Dual specificity mitogen-activated protein kinase kinase 2 OS=Homo sapiens GN=MAP2K2 PE=1 SV=1 - [MP2K2_HUMAN]	11.64	11.00	4	4	4	0.382	0.175
P46734	Dual specificity mitogen-activated protein kinase kinase 3 OS=Homo sapiens GN=MAP2K3 PE=1 SV=2 - [MP2K3_HUMAN]	42.77	23.92	8	8	13	0.120	0.137
Q9P0J7	E3 ubiquitin-protein ligase KCMF1 OS=Homo sapiens GN=KCMF1 PE=1 SV=2 - [KCMF1_HUMAN]	9.38	4.20	2	2	3	0.424	0.204
Q5XPI4	E3 ubiquitin-protein ligase RNF123 OS=Homo sapiens GN=RNF123 PE=1 SV=1 - [RN123_HUMAN]	33.91	6.24	9	9	11	0.723	0.312
Q5T4S7	E3 ubiquitin-protein ligase UBR4 OS=Homo sapiens GN=UBR4 PE=1 SV=1 - [UBR4_HUMAN]	29.46	1.16	9	9	11	0.323	0.182
Q4VBZ6	EEF1D protein OS=Homo sapiens GN=EEF1D PE=1 SV=1 - [Q4VBZ6_HUMAN]	12.59	13.62	3	4	4	0.070	0.051
P68104	Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 - [EF1A1_HUMAN]	163.46	21.65	15	15	57	0.026	0.049
P24534	Elongation factor 1-beta OS=Homo sapiens GN=EEF1B2 PE=1 SV=3 - [EF1B_HUMAN]	17.18	12.00	3	4	6	0.050	0.039
P26641	Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3 - [EF1G_HUMAN]	49.89	23.11	12	12	16	0.059	0.051
P13639	Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 - [EF2_HUMAN]	138.37	26.34	24	24	45	0.115	0.079
B7Z2X9	Enolase OS=Homo sapiens GN=ENO2 PE=2 SV=1 - [B7Z2X9_HUMAN]	85.35	17.65	5	8	31	0.266	0.284
Q96CG1	ETF1 protein OS=Homo sapiens GN=ETF1 PE=2 SV=1 - [Q96CG1_HUMAN]	13.82	8.91	4	4	5	0.065	0.111
Q99447	Ethanolamine-phosphate cytidylyltransferase OS=Homo sapiens GN=PCYT2 PE=1 SV=1 - [PCY2_HUMAN]	19.33	7.97	3	3	6	0.085	0.102
P60842	Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=1 SV=1 - [IF4A1_HUMAN]	83.30	33.25	6	12	23	0.233	0.338
P38919	Eukaryotic initiation factor 4A-III OS=Homo sapiens GN=EIF4A3 PE=1 SV=4 - [IF4A3_HUMAN]	22.93	13.63	3	5	7	0.245	0.211
O14602	Eukaryotic translation initiation factor 1A, Y-chromosomal OS=Homo sapiens GN=EIF1AY PE=1 SV=4 - [IF1AY_HUMAN]	35.17	41.67	9	9	13	0.163	0.202
P05198	Eukaryotic translation initiation factor 2 subunit 1 OS=Homo sapiens GN=EIF2S1 PE=1 SV=3 - [IF2A_HUMAN]	25.32	22.86	7	7	8	0.127	0.191
P20042	Eukaryotic translation initiation factor 2 subunit 2 OS=Homo sapiens GN=EIF2S2 PE=1 SV=2 - [IF2B_HUMAN]	22.38	14.71	4	4	7	0.073	0.140
P41091	Eukaryotic translation initiation factor 2 subunit 3 OS=Homo sapiens GN=EIF2S3 PE=1 SV=3 - [IF2G_HUMAN]	26.95	17.37	7	7	9	0.105	0.178
Q9BQI3	Eukaryotic translation initiation factor 2-alpha kinase 1 OS=Homo sapiens GN=EIF2AK1 PE=1 SV=2 - [E2AK1_HUMAN]	4.91	2.54	2	2	2	0.127	0.114
O75821	Eukaryotic translation initiation factor 3 subunit G OS=Homo sapiens GN=EIF3G PE=1 SV=2 - [EIF3G_HUMAN]	25.62	14.37	6	6	8	0.054	0.043
Q13347	Eukaryotic translation initiation factor 3 subunit I OS=Homo sapiens GN=EIF3I PE=1 SV=1 - [EIF3I_HUMAN]	10.16	7.08	2	2	3	0.038	0.051
O75822	Eukaryotic translation initiation factor 3 subunit J OS=Homo sapiens GN=EIF3J PE=1 SV=2 - [EIF3J_HUMAN]	34.40	19.38	7	7	10	0.173	0.191
E2QC29	Eukaryotic translation initiation factor 3, subunit E interacting protein (Fragment) OS=Homo sapiens GN=EIF3EIP PE=4 SV=1 - [E2QC29_HUMAN]	5.29	12.00	2	2	2	0.117	0.090
P06730	Eukaryotic translation initiation factor 4E OS=Homo sapiens GN=EIF4E PE=1 SV=2 - [IF4E_HUMAN]	17.96	25.35	5	5	6	0.268	0.237
Q15056	Eukaryotic translation initiation factor 4H OS=Homo sapiens GN=EIF4H PE=1 SV=5 - [IF4H_HUMAN]	7.74	8.87	3	3	3	0.370	0.110
P55010	Eukaryotic translation initiation factor 5 OS=Homo sapiens GN=EIF5 PE=1 SV=2 - [IF5_HUMAN]	22.57	9.74	5	5	7	0.498	0.280
P63241	Eukaryotic translation initiation factor 5A-1 OS=Homo sapiens GN=EIF5A PE=1 SV=2 - [IF5A1_HUMAN]	45.49	16.23	4	4	15	0.309	0.461
O60841	Eukaryotic translation initiation factor 5B OS=Homo sapiens GN=EIF5B PE=1 SV=4 - [IF2P_HUMAN]	13.38	3.03	5	5	5	0.077	0.068
O14980	Exportin-1 OS=Homo sapiens GN=XPO1 PE=1 SV=1 - [XPO1_HUMAN]	15.29	3.17	4	5	6	0.577	0.199
A8CZ64	Extracellular signal-regulated kinase-2 splice variant OS=Homo sapiens GN=MAPK1 PE=2 SV=1 - [A8CZ64_HUMAN]	9.35	11.39	3	3	3	0.300	0.184
P52907	F-actin-capping protein subunit alpha-1 OS=Homo sapiens GN=CAPZA1 PE=1 SV=3 - [CAZA1_HUMAN]	35.89	24.13	5	7	13	0.273	0.194
Q5TI86	F-box protein 7 OS=Homo sapiens GN=FBXO7 PE=2 SV=1 - [Q5TI86_HUMAN]	28.84	11.27	6	6	10	0.788	0.537
Q16658	Fascin OS=Homo sapiens GN=FSCN1 PE=1 SV=3 - [FSCN1_HUMAN]	37.64	15.82	10	10	14	0.519	0.374
P49327	Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3 - [FAS_HUMAN]	196.48	13.50	34	34	67	0.065	0.163
Q01469	Fatty acid-binding protein, epidermal OS=Homo sapiens GN=FABP5 PE=1 SV=3 - [FABP5_HUMAN]	26.35	31.11	5	5	9	0.377	0.275
A6NDY9	Filamin A OS=Homo sapiens GN=FLNA PE=2 SV=4 - [A6NDY9_HUMAN]	11.21	1.21	3	3	4	0.161	0.142
P30043	Flavin reductase OS=Homo sapiens GN=BLVRB PE=1 SV=3 - [BLVRB_HUMAN]	409.71	50.49	8	8	129	0.424	0.359
P04075	Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2 - [ALDOA_HUMAN]	313.08	36.81	15	20	92	0.083	0.163
P09972	Fructose-bisphosphate aldolase C OS=Homo sapiens GN=ALDOC PE=1 SV=2 - [ALDOC_HUMAN]	68.68	25.55	5	10	23	0.108	0.150
P07954	Fumarate hydratase, mitochondrial OS=Homo sapiens GN=FH PE=1 SV=3 - [FUMH_HUMAN]	18.61	6.47	4	4	6	0.425	0.377
Q96GK7	Fumarylacetoacetate hydrolase domain-containing protein 2A OS=Homo sapiens GN=FAHD2A PE=1 SV=1 - [FAH2A_HUMAN]	5.23	6.69	2	2	2	0.170	0.184
P17931	Galectin-3 OS=Homo sapiens GN=LGALS3 PE=1 SV=5 - [LEG3_HUMAN]	25.07	25.20	7	7	9	0.064	0.118

P60520	Gamma-aminobutyric acid receptor-associated protein-like 2 OS=Homo sapiens GN=GABARAPL2 PE=1 SV=1 - [GBRL2_HUMAN]	6.87	16.24	2	2	2	0.152	0.136
Q13630	GDP-L-fucose synthase OS=Homo sapiens GN=TSTA3 PE=1 SV=1 - [FCL_HUMAN]	61.42	25.86	9	9	18	0.284	0.259
Q6PCE3	Glucose 1,6-bisphosphate synthase OS=Homo sapiens GN=PGM2L1 PE=1 SV=3 - [PGM2L_HUMAN]	34.66	9.49	5	6	11	0.449	0.278
P11413	Glucose-6-phosphate 1-dehydrogenase OS=Homo sapiens GN=G6PD PE=1 SV=4 - [G6PD_HUMAN]	74.35	20.97	13	13	26	0.215	0.226
P06744	Glucose-6-phosphate isomerase OS=Homo sapiens GN=GPI PE=1 SV=4 - [G6PI_HUMAN]	141.79	25.99	19	19	51	0.065	0.107
P48506	Glutamate--cysteine ligase catalytic subunit OS=Homo sapiens GN=GCLC PE=1 SV=2 - [GSH1_HUMAN]	98.03	21.04	14	14	31	0.473	0.345
P48507	Glutamate--cysteine ligase regulatory subunit OS=Homo sapiens GN=GCLM PE=1 SV=1 - [GSH0_HUMAN]	30.43	31.02	7	7	10	0.519	0.346
P15104	Glutamine synthetase OS=Homo sapiens GN=GLUL PE=1 SV=4 - [GLNA_HUMAN]	30.16	13.40	7	7	11	0.052	0.073
P35754	Glutaredoxin-1 OS=Homo sapiens GN=GLRX PE=1 SV=2 - [GLRX1_HUMAN]	8.00	28.30	3	3	3	0.340	0.549
O76003	Glutaredoxin-3 OS=Homo sapiens GN=GLRX3 PE=1 SV=2 - [GLRX3_HUMAN]	18.61	14.63	5	5	6	0.514	0.409
C8KIL8	Glutathion reductase delta8 alternative splicing variant OS=Homo sapiens GN=GSR PE=2 SV=1 - [C8KIL8_HUMAN]	35.14	13.18	7	7	13	0.429	0.303
P07203	Glutathione peroxidase 1 OS=Homo sapiens GN=GPX1 PE=1 SV=4 - [GPX1_HUMAN]	9.87	9.36	2	2	3	1.208	0.615
P78417	Glutathione S-transferase omega-1 OS=Homo sapiens GN=GSTO1 PE=1 SV=2 - [GSTO1_HUMAN]	123.22	40.66	10	10	39	0.335	0.262
P48637	Glutathione synthetase OS=Homo sapiens GN=GSS PE=1 SV=1 - [GSHB_HUMAN]	33.98	15.61	8	8	12	0.499	0.401
P04406	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3 - [G3P_HUMAN]	278.89	42.99	16	16	100	0.115	0.294
P41250	Glycyl-tRNA synthetase OS=Homo sapiens GN=GARS PE=1 SV=3 - [SYG_HUMAN]	28.42	9.07	7	8	10	0.068	0.046
P36959	GMP reductase 1 OS=Homo sapiens GN=GMPR PE=1 SV=1 - [GMPR1_HUMAN]	52.16	19.71	6	7	17	0.318	0.238
Q14789	Golgin subfamily B member 1 OS=Homo sapiens GN=GOLGB1 PE=1 SV=2 - [GOGB1_HUMAN]	10.02	1.01	2	4	4	0.160	0.278
P62826	GTP-binding nuclear protein Ran OS=Homo sapiens GN=RAN PE=1 SV=3 - [RAN_HUMAN]	116.04	36.11	9	9	36	0.406	0.377
O00178	GTP-binding protein 1 OS=Homo sapiens GN=GTPBP1 PE=1 SV=3 - [GTPB1_HUMAN]	5.90	2.39	2	2	2	0.169	0.141
Q14C86	GTPase-activating protein and VPS9 domain-containing protein 1 OS=Homo sapiens GN=GAPVD1 PE=1 SV=2 - [GAPD1_HUMAN]	27.18	4.80	7	7	9	0.499	0.207
Q8TBN0	Guanine nucleotide exchange factor for Rab-3A OS=Homo sapiens GN=RAB3IL1 PE=1 SV=1 - [R3GEF_HUMAN]	5.04	4.71	2	2	2	0.256	0.216
P63244	Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Homo sapiens GN=GNB2L1 PE=1 SV=3 - [GBLP_HUMAN]	24.04	13.25	4	4	8	0.064	0.063
Q16774	Guanylate kinase OS=Homo sapiens GN=GUK1 PE=1 SV=2 - [KGUA_HUMAN]	11.74	9.64	2	2	4	0.212	0.151
Q9H0R4	Haloacid dehalogenase-like hydrolase domain-containing protein 2 OS=Homo sapiens GN=HDHD2 PE=1 SV=1 - [HDHD2_HUMAN]	7.89	10.81	3	3	3	0.446	0.368
Q9Y450	HBS1-like protein OS=Homo sapiens GN=HBS1L PE=1 SV=1 - [HBS1L_HUMAN]	9.03	3.65	3	3	3	0.157	0.154
Q7Z4H3	HD domain-containing protein 2 OS=Homo sapiens GN=HDDC2 PE=1 SV=1 - [HDDC2_HUMAN]	4.99	3.43	2	2	2	0.291	0.309
B8ZZL8	Heat shock 10kDa protein 1 (Chaperonin 10), isoform CRA_b OS=Homo sapiens GN=HSPE1 PE=3 SV=1 - [B8ZZL8_HUMAN]	12.91	19.80	3	3	4	0.013	0.049
P08107	Heat shock 70 kDa protein 1A/1B OS=Homo sapiens GN=HSPA1A PE=1 SV=5 - [HSP71_HUMAN]	201.64	31.20	16	21	63	0.238	0.120
P34932	Heat shock 70 kDa protein 4 OS=Homo sapiens GN=HSPA4 PE=1 SV=4 - [HSP74_HUMAN]	107.97	28.21	22	23	34	0.300	0.227
P11142	Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1 - [HSP7C_HUMAN]	282.82	39.32	23	29	91	0.343	0.273
Q92598	Heat shock protein 105 kDa OS=Homo sapiens GN=HSPH1 PE=1 SV=1 - [HS105_HUMAN]	10.54	2.91	3	3	4	0.136	0.110
P07900	Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5 - [HS90A_HUMAN]	276.27	38.80	15	28	88	0.139	0.092
P08238	Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4 - [HS90B_HUMAN]	143.13	31.22	8	22	45	0.298	0.102
Q9NRV9	Heme-binding protein 1 OS=Homo sapiens GN=HEBP1 PE=1 SV=1 - [HEBP1_HUMAN]	51.14	33.33	6	6	15	0.599	0.415
Q9BXL5	Hemogen OS=Homo sapiens GN=HEMGN PE=1 SV=1 - [HEMGN_HUMAN]	32.83	15.29	8	8	12	0.086	0.050
P69905	Hemoglobin subunit alpha OS=Homo sapiens GN=HBA1 PE=1 SV=2 - [HBA_HUMAN]	4320.24	76.06	13	14	1324	0.894	0.725
P68871	Hemoglobin subunit beta OS=Homo sapiens GN=HBB PE=1 SV=2 - [HBB_HUMAN]	5787.45	100.00	8	16	1697	0.970	0.450
P02042	Hemoglobin subunit delta OS=Homo sapiens GN=HBD PE=1 SV=2 - [HBD_HUMAN]	2562.86	91.84	6	14	761	0.901	0.268
P02100	Hemoglobin subunit epsilon OS=Homo sapiens GN=HBE1 PE=1 SV=2 - [HBE_HUMAN]	895.47	39.46	3	6	310	0.123	0.968
P69892	Hemoglobin subunit gamma-2 OS=Homo sapiens GN=HBG2 PE=1 SV=2 - [HBG2_HUMAN]	7848.95	81.63	3	14	2305	0.174	1.171
Q6B0K9	Hemoglobin subunit mu OS=Homo sapiens GN=HBM PE=2 SV=1 - [HBM_HUMAN]	75.31	48.23	5	5	25	0.161	0.496
P09105	Hemoglobin subunit theta-1 OS=Homo sapiens GN=HBQ1 PE=1 SV=2 - [HBAT_HUMAN]	16.55	30.28	3	3	4	0.720	0.652
P02008	Hemoglobin subunit zeta OS=Homo sapiens GN=HBZ PE=1 SV=2 - [HBAZ_HUMAN]	1008.02	74.65	8	9	360	0.119	1.291
D9YZU8	Hemoglobin, gamma A OS=Homo sapiens GN=HBG1 PE=3 SV=1 - [D9YZU8_HUMAN]	6053.18	81.63	4	15	1857	0.253	0.933
P51858	Hepatoma-derived growth factor OS=Homo sapiens GN=HDGF PE=1 SV=1 - [HDGF_HUMAN]	56.32	35.42	8	8	17	0.036	0.058
P09651	Heterogeneous nuclear ribonucleoprotein A1 OS=Homo sapiens GN=HNRNPA1 PE=1 SV=5 - [ROA1_HUMAN]	34.94	15.32	3	7	12	0.069	0.098
O60812	Heterogeneous nuclear ribonucleoprotein C-like 1 OS=Homo sapiens GN=HNRNPCL1 PE=1 SV=1 - [HNRCL_HUMAN]	5.88	6.83	2	2	2	0.342	0.126
P52272	Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens GN=HNRNPM PE=1 SV=3 - [HNRPM_HUMAN]	8.69	4.38	3	3	3	0.044	0.047
O60506	Heterogeneous nuclear ribonucleoprotein Q OS=Homo sapiens GN=SYNCRIP PE=1 SV=2 - [HNRPQ_HUMAN]	11.35	2.25	2	2	4	0.189	0.106
P22626	Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens GN=HNRNPA2B1 PE=1 SV=2 - [ROA2_HUMAN]	47.36	24.36	7	10	16	0.063	0.045
P49773	Histidine triad nucleotide-binding protein 1 OS=Homo sapiens GN=HINT1 PE=1 SV=2 - [HINT1_HUMAN]	40.95	29.37	5	5	14	0.275	0.246
P16403	Histone H1.2 OS=Homo sapiens GN=HIST1H1C PE=1 SV=2 - [H12_HUMAN]	19.36	17.37	2	5	6	1.359	0.044
O60814	Histone H2B type 1-K OS=Homo sapiens GN=HIST1H2BK PE=1 SV=3 - [H2B1K_HUMAN]	15.92	24.60	4	4	6	1.186	0.154
P68431	Histone H3.1 OS=Homo sapiens GN=HIST1H3A PE=1 SV=2 - [H31_HUMAN]	5.78	13.24	2	2	2	0.450	0.066
P62805	Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2 - [H4_HUMAN]	11.07	21.36	2	2	3	2.858	0.098

B0V2L0	HLA-B associated transcript 1 (Fragment) OS=Homo sapiens GN=BAT1 PE=4 SV=1 - [B0V2L0_HUMAN]	7.78	7.82	3	3	3	0.146	0.088
B0UX83	HLA-B associated transcript 3 OS=Homo sapiens GN=BAT3 PE=4 SV=1 - [B0UX83_HUMAN]	4.61	1.95	2	2	2	0.180	0.101
P50502	Hsc70-interacting protein OS=Homo sapiens GN=ST13 PE=1 SV=2 - [F10A1_HUMAN]	52.44	24.12	11	11	18	0.403	0.315
Q16543	Hsp90 co-chaperone Cdc37 OS=Homo sapiens GN=CDC37 PE=1 SV=1 - [CDC37_HUMAN]	24.43	12.70	6	6	8	0.146	0.165
Q16775	Hydroxyacylglutathione hydrolase, mitochondrial OS=Homo sapiens GN=HAGH PE=1 SV=2 - [GLO2_HUMAN]	37.19	20.78	6	6	13	0.442	0.397
P00492	Hypoxanthine-guanine phosphoribosyltransferase OS=Homo sapiens GN=HPRT1 PE=1 SV=2 - [HPRT_HUMAN]	39.65	25.23	5	5	12	0.536	0.371
P78318	Immunoglobulin-binding protein 1 OS=Homo sapiens GN=IGBP1 PE=1 SV=1 - [IGBP1_HUMAN]	10.00	11.80	3	3	3	0.383	0.267
Q14974	Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2 - [IMB1_HUMAN]	47.55	10.05	8	8	16	0.351	0.254
O95373	Importin-7 OS=Homo sapiens GN=IPO7 PE=1 SV=1 - [IPO7_HUMAN]	9.60	1.54	2	2	3	0.508	0.164
Q96P70	Importin-9 OS=Homo sapiens GN=IPO9 PE=1 SV=3 - [IPO9_HUMAN]	9.87	2.40	3	3	3	0.603	0.336
Q15181	Inorganic pyrophosphatase OS=Homo sapiens GN=PPA1 PE=1 SV=2 - [IPYR_HUMAN]	26.28	24.57	7	7	8	0.243	0.159
P14735	Insulin-degrading enzyme OS=Homo sapiens GN=IDE PE=1 SV=4 - [IDE_HUMAN]	12.11	4.12	4	4	4	0.355	0.339
P80217	Interferon-induced 35 kDa protein OS=Homo sapiens GN=IFI35 PE=1 SV=5 - [IN35_HUMAN]	6.56	7.34	2	2	2	0.214	0.152
Q9HBB2	Iron regulatory protein 1 OS=Homo sapiens GN=IRP1 PE=2 SV=1 - [Q9HBB2_HUMAN]	21.96	6.33	6	6	8	0.226	0.226
Q2TAA2	Isoamyl acetate-hydrolyzing esterase 1 homolog OS=Homo sapiens GN=IAH1 PE=1 SV=1 - [IAH1_HUMAN]	5.62	10.08	2	2	2	0.405	0.278
O75874	Isocitrate dehydrogenase [NADP] cytoplasmic OS=Homo sapiens GN=IDH1 PE=1 SV=2 - [IDHC_HUMAN]	28.96	9.18	6	6	10	0.128	0.087
P13645	Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6 - [K1C10_HUMAN]	22.70	8.05	5	5	7	0.067	1.832
P35527	Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3 - [K1C9_HUMAN]	48.75	14.93	9	9	14	0.052	0.575
P04264	Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6 - [K2C1_HUMAN]	60.86	15.53	11	12	18	0.042	0.631
P35908	Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2 - [K22E_HUMAN]	7.24	4.23	2	2	2	0.017	2.814
Q9HA64	Ketosamine-3-kinase OS=Homo sapiens GN=FN3KRP PE=1 SV=2 - [KT3K_HUMAN]	31.55	13.59	6	6	11	0.625	0.433
P07195	L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2 - [LDHB_HUMAN]	243.80	38.02	13	15	72	0.396	0.313
E9PH51	L-lactate dehydrogenase OS=Homo sapiens GN=LDHA PE=3 SV=2 - [E9PH51_HUMAN]	280.99	38.03	11	13	85	0.081	0.119
Q7Z4W1	L-xylulose reductase OS=Homo sapiens GN=DCXR PE=1 SV=2 - [DCXR_HUMAN]	13.19	11.89	3	3	4	0.438	0.409
Q04760	Lactoylglutathione lyase OS=Homo sapiens GN=GLO1 PE=1 SV=4 - [LGUL_HUMAN]	28.37	20.65	4	4	9	0.601	0.400
Q9NS86	LanC-like protein 2 OS=Homo sapiens GN=LANCL2 PE=1 SV=1 - [LANC2_HUMAN]	5.67	4.67	2	2	2	0.711	0.532
Q9BS40	Latexin OS=Homo sapiens GN=LXN PE=1 SV=2 - [LXN_HUMAN]	52.70	27.03	6	6	17	0.286	0.229
Q8N1G4	Leucine-rich repeat-containing protein 47 OS=Homo sapiens GN=LRRC47 PE=1 SV=1 - [LRC47_HUMAN]	8.81	4.46	3	3	3	0.140	0.099
P09960	Leukotriene A-4 hydrolase OS=Homo sapiens GN=LTA4H PE=1 SV=2 - [LKHA4_HUMAN]	27.50	11.29	8	8	10	0.635	0.354
Q14847	LIM and SH3 domain protein 1 OS=Homo sapiens GN=LASP1 PE=1 SV=2 - [LASP1_HUMAN]	61.35	30.27	9	9	20	0.267	0.210
P24666	Low molecular weight phosphotyrosine protein phosphatase OS=Homo sapiens GN=ACP1 PE=1 SV=3 - [PPAC_HUMAN]	51.40	41.77	6	6	17	0.562	0.408
P05455	Lupus La protein OS=Homo sapiens GN=SSB PE=1 SV=2 - [LA_HUMAN]	13.06	10.05	5	5	5	0.065	0.071
Q5QPQ1	Lysophospholipase II (Fragment) OS=Homo sapiens GN=LYPLA2 PE=2 SV=1 - [Q5QPQ1_HUMAN]	7.43	8.64	2	2	3	0.421	0.204
P40925	Malate dehydrogenase, cytoplasmic OS=Homo sapiens GN=MDH1 PE=1 SV=4 - [MDHC_HUMAN]	173.76	38.02	16	16	56	0.390	0.323
A4D2A2	MCM7 minichromosome maintenance deficient 7 (S. cerevisiae) OS=Homo sapiens GN=MCM7 PE=2 SV=1 - [A4D2A2_HUMAN]	8.89	4.97	3	3	3	0.180	0.047
P50579	Methionine aminopeptidase 2 OS=Homo sapiens GN=METAP2 PE=1 SV=1 - [AMPM2_HUMAN]	12.99	7.74	3	3	4	0.134	0.101
P26038	Moesin OS=Homo sapiens GN=MSN PE=1 SV=3 - [MOES_HUMAN]	102.21	25.13	16	21	33	0.317	0.313
P60201	Myelin proteolipid protein OS=Homo sapiens GN=PLP1 PE=1 SV=2 - [MYPR_HUMAN]	19.73	14.08	4	4	6	0.585	1.280
P12829	Myosin light chain 4 OS=Homo sapiens GN=MYL4 PE=1 SV=3 - [MYL4_HUMAN]	22.67	26.40	4	4	6	0.065	0.186
P60660	Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2 - [MYL6_HUMAN]	5.87	13.25	2	2	2	0.086	0.084
P35580	Myosin-10 OS=Homo sapiens GN=MYH10 PE=1 SV=3 - [MYH10_HUMAN]	151.39	15.94	22	36	52	0.044	0.210
P35579	Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4 - [MYH9_HUMAN]	272.21	23.98	42	53	91	0.099	0.178
Q9BUF9	Myosin, light chain 9, regulatory OS=Homo sapiens GN=MYL9 PE=2 SV=1 - [Q9BUF9_HUMAN]	8.34	12.71	2	2	3	0.172	0.219
P58546	Myotrophin OS=Homo sapiens GN=MTPN PE=1 SV=2 - [MTPN_HUMAN]	26.51	22.03	2	2	9	0.538	0.381
Q13765	Nascent polypeptide-associated complex subunit alpha OS=Homo sapiens GN=NACA PE=1 SV=1 - [NACA_HUMAN]	9.99	18.60	3	3	4	0.082	0.151
Q15843	NEDD8 OS=Homo sapiens GN=NEDD8 PE=1 SV=1 - [NEDD8_HUMAN]	21.40	39.51	5	5	8	0.170	0.178
Q8TBC4	NEDD8-activating enzyme E1 catalytic subunit OS=Homo sapiens GN=UBA3 PE=1 SV=2 - [UBA3_HUMAN]	5.94	4.10	2	2	2	0.284	0.216
P61081	NEDD8-conjugating enzyme Ubc12 OS=Homo sapiens GN=UBE2M PE=1 SV=1 - [UBC12_HUMAN]	30.04	20.22	5	5	9	0.173	0.168
Q8NBF2	NHL repeat-containing protein 2 OS=Homo sapiens GN=NHLRC2 PE=1 SV=1 - [NHLC2_HUMAN]	6.67	2.62	2	2	2	0.244	0.199
C9J8U2	Nicotinate phosphoribosyltransferase domain containing 1, isoform CRA_e OS=Homo sapiens GN=NAPRT1 PE=4 SV=1 - [C9J8U2_HUMAN]	27.39	9.59	5	5	8	0.456	0.306
Q9GZT8	NIF3-like protein 1 OS=Homo sapiens GN=NIF3L1 PE=1 SV=2 - [NIF3L_HUMAN]	8.63	4.77	2	2	3	0.512	0.435
Q5SYT8	Novel protein similar to Pre-B cell enhancing factor (PBEF) (Fragment) OS=Homo sapiens GN=RP11-92J19.4 PE=1 SV=1 - [Q5SYT8_HUMAN]	4.67	4.24	2	2	2	0.333	0.274
Q9UNZ2	NSFL1 cofactor p47 OS=Homo sapiens GN=NSFL1C PE=1 SV=2 - [NSF1C_HUMAN]	42.32	23.51	8	8	12	0.575	0.297
Q9Y266	Nuclear migration protein nudC OS=Homo sapiens GN=NUDC PE=1 SV=1 - [NUDC_HUMAN]	29.13	12.99	5	5	9	0.049	0.066
P61970	Nuclear transport factor 2 OS=Homo sapiens GN=NUTF2 PE=1 SV=1 - [NTF2_HUMAN]	12.37	11.02	2	2	4	0.592	0.437
Q9H1E3	Nuclear ubiquitous casein and cyclin-dependent kinases substrate OS=Homo sapiens GN=NUCKS1 PE=1 SV=1 - [NUCKS_HUMAN]	16.70	6.58	2	2	6	0.095	0.041

P67809	Nuclease-sensitive element-binding protein 1 OS=Homo sapiens GN=YBX1 PE=1 SV=3 - [YBOX1_HUMAN]	22.83	24.38	4	4	7	0.086	0.072
P19338	Nucleolin OS=Homo sapiens GN=NCL PE=1 SV=3 - [NUCL_HUMAN]	73.89	16.48	19	19	27	0.292	0.027
P06748	Nucleophosmin OS=Homo sapiens GN=NPM1 PE=1 SV=2 - [NPM_HUMAN]	17.54	10.88	4	4	6	0.225	0.017
Q32Q12	Nucleoside diphosphate kinase OS=Homo sapiens GN=NME1-NME2 PE=2 SV=1 - [Q32Q12_HUMAN]	83.57	40.75	7	7	24	0.450	0.394
Q7Z7N6	NUDT1 protein OS=Homo sapiens GN=NUDT1 PE=2 SV=2 - [Q7Z7N6_HUMAN]	8.06	17.31	2	2	2	0.040	0.053
Q9NTK5	Obg-like ATPase 1 OS=Homo sapiens GN=OLA1 PE=1 SV=2 - [OLA1_HUMAN]	26.78	16.92	7	7	9	0.747	0.548
Q9NQR4	Omega-amidase NIT2 OS=Homo sapiens GN=NIT2 PE=1 SV=1 - [NIT2_HUMAN]	11.33	11.23	3	3	4	0.239	0.233
Q96CV9	Optineurin OS=Homo sapiens GN=OPTN PE=1 SV=2 - [OPTN_HUMAN]	28.51	13.17	8	8	10	0.131	0.171
B4DTR3	Oxysterol-binding protein OS=Homo sapiens GN=OSBP2 PE=2 SV=1 - [B4DTR3_HUMAN]	9.12	4.35	2	2	2	0.183	0.069
Q5VU21	PAI-1 mRNA-binding protein variant OS=Homo sapiens GN=SERBP1 PE=2 SV=1 - [Q5VU21_HUMAN]	20.68	11.89	4	4	7	0.195	0.128
P20962	Parathymosin OS=Homo sapiens GN=PTMS PE=1 SV=2 - [PTMS_HUMAN]	19.30	22.55	3	3	6	0.037	0.050
Q9UBV8	Peflin OS=Homo sapiens GN=PEF1 PE=1 SV=1 - [PEF1_HUMAN]	7.37	3.87	2	2	2	0.339	0.258
P62937	Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2 - [PPIA_HUMAN]	189.39	49.70	3	10	69	0.271	0.273
Q00688	Peptidyl-prolyl cis-trans isomerase FKBP3 OS=Homo sapiens GN=FKBP3 PE=1 SV=1 - [FKBP3_HUMAN]	22.01	13.84	4	4	8	0.058	0.145
Q02790	Peptidyl-prolyl cis-trans isomerase FKBP4 OS=Homo sapiens GN=FKBP4 PE=1 SV=3 - [FKBP4_HUMAN]	27.14	8.06	4	5	9	0.269	0.258
Q9Y3C6	Peptidyl-prolyl cis-trans isomerase-like 1 OS=Homo sapiens GN=PPIL1 PE=1 SV=1 - [PPIL1_HUMAN]	15.83	27.71	4	4	5	0.304	0.139
O60664	Perilipin-3 OS=Homo sapiens GN=PLIN3 PE=1 SV=3 - [PLIN3_HUMAN]	34.68	11.98	6	6	11	0.429	0.243
Q06830	Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1 - [PRDX1_HUMAN]	224.41	64.32	11	12	67	0.493	0.404
P32119	Peroxiredoxin-2 OS=Homo sapiens GN=PRDX2 PE=1 SV=5 - [PRDX2_HUMAN]	718.77	59.60	10	11	228	0.781	0.580
P30044	Peroxiredoxin-5, mitochondrial OS=Homo sapiens GN=PRDX5 PE=1 SV=4 - [PRDX5_HUMAN]	13.23	11.68	2	2	4	0.080	0.046
P30041	Peroxiredoxin-6 OS=Homo sapiens GN=PRDX6 PE=1 SV=3 - [PRDX6_HUMAN]	177.23	44.64	12	12	60	0.758	0.531
Q8WW12	PEST proteolytic signal-containing nuclear protein OS=Homo sapiens GN=PCNP PE=1 SV=2 - [PCNP_HUMAN]	13.40	19.66	3	3	4	0.167	0.226
Q9NSD9	Phenylalanyl-tRNA synthetase beta chain OS=Homo sapiens GN=FARSB PE=1 SV=3 - [SYFB_HUMAN]	22.51	8.15	6	6	8	0.124	0.055
Q9UKL6	Phosphatidylcholine transfer protein OS=Homo sapiens GN=PCTP PE=1 SV=1 - [PPCT_HUMAN]	4.83	7.01	2	2	2	0.262	0.292
P30086	Phosphatidylethanolamine-binding protein 1 OS=Homo sapiens GN=PEBP1 PE=1 SV=3 - [PEBP1_HUMAN]	37.41	34.76	5	5	11	0.667	0.435
P48426	Phosphatidylinositol-5-phosphate 4-kinase type-2 alpha OS=Homo sapiens GN=PIP4K2A PE=1 SV=2 - [PI42A_HUMAN]	21.14	9.61	4	4	7	0.433	0.383
Q96G03	Phosphoglucomutase-2 OS=Homo sapiens GN=PGM2 PE=1 SV=4 - [PGM2_HUMAN]	33.18	11.44	7	8	12	0.439	0.358
P00558	Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 PE=1 SV=3 - [PGK1_HUMAN]	346.93	58.51	22	27	113	0.140	0.186
P07205	Phosphoglycerate kinase 2 OS=Homo sapiens GN=PGK2 PE=1 SV=3 - [PGK2_HUMAN]	63.25	19.66	2	9	23	0.132	0.189
P18669	Phosphoglycerate mutase 1 OS=Homo sapiens GN=PGAM1 PE=1 SV=2 - [PGAM1_HUMAN]	75.80	31.10	8	8	26	0.140	0.170
A6NDG6	Phosphoglycolate phosphatase OS=Homo sapiens GN=PGP PE=1 SV=1 - [PGP_HUMAN]	18.00	12.15	5	5	6	0.415	0.320
Q9HAB8	Phosphopantothenate--cysteine ligase OS=Homo sapiens GN=PPCS PE=1 SV=2 - [PPCS_HUMAN]	5.97	5.79	2	2	2	0.461	0.315
O15067	Phosphoribosylformylglycinamidine synthase OS=Homo sapiens GN=PFAS PE=1 SV=4 - [PUR4_HUMAN]	52.46	9.49	13	13	18	0.374	0.286
Q9Y617	Phosphoserine aminotransferase OS=Homo sapiens GN=PSAT1 PE=1 SV=2 - [SERC_HUMAN]	59.69	26.22	11	12	22	0.041	0.043
Q9GZP4	PITH domain-containing protein 1 OS=Homo sapiens GN=PITHD1 PE=1 SV=1 - [PITH1_HUMAN]	47.16	26.54	5	5	17	0.364	0.294
P13796	Plastin-2 OS=Homo sapiens GN=LCP1 PE=1 SV=6 - [PLSL_HUMAN]	42.49	14.99	10	10	14	0.171	0.224
P43034	Platelet-activating factor acetylhydrolase IB subunit alpha OS=Homo sapiens GN=PAFAH1B1 PE=1 SV=2 - [LIS1_HUMAN]	17.21	10.24	4	4	5	0.319	0.303
Q15102	Platelet-activating factor acetylhydrolase IB subunit gamma OS=Homo sapiens GN=PAFAH1B3 PE=1 SV=1 - [PA1B3_HUMAN]	10.98	15.15	3	4	4	0.765	0.576
Q68Y55	Poly(RC) binding protein 2 OS=Homo sapiens GN=PCBP2 PE=2 SV=1 - [Q68Y55_HUMAN]	30.03	15.71	2	5	9	0.131	0.121
Q15365	Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2 - [PCBP1_HUMAN]	33.09	15.45	3	6	10	0.171	0.137
P26599	Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 PE=1 SV=1 - [PTBP1_HUMAN]	12.55	4.71	3	3	4	0.179	0.078
O60925	Prefoldin subunit 1 OS=Homo sapiens GN=PFDN1 PE=1 SV=2 - [PFD1_HUMAN]	16.25	19.67	3	3	6	0.153	0.232
Q9UHV9	Prefoldin subunit 2 OS=Homo sapiens GN=PFDN2 PE=1 SV=1 - [PFD2_HUMAN]	21.85	27.27	4	4	7	0.098	0.156
Q9NQP4	Prefoldin subunit 4 OS=Homo sapiens GN=PFDN4 PE=1 SV=1 - [PFD4_HUMAN]	6.67	16.42	2	2	2	0.164	0.223
Q99471	Prefoldin subunit 5 OS=Homo sapiens GN=PFDN5 PE=1 SV=2 - [PFD5_HUMAN]	5.31	8.44	2	2	2	0.087	0.157
O15212	Prefoldin subunit 6 OS=Homo sapiens GN=PFDN6 PE=1 SV=1 - [PFD6_HUMAN]	13.91	17.05	4	4	5	0.108	0.214
Q93008	Probable ubiquitin carboxyl-terminal hydrolase FAF-X OS=Homo sapiens GN=USP9X PE=1 SV=3 - [USP9X_HUMAN]	56.17	5.60	15	15	19	0.276	0.190
P07737	Profilin-1 OS=Homo sapiens GN=PFN1 PE=1 SV=2 - [PROF1_HUMAN]	41.92	32.14	5	5	13	0.232	0.105
Q8WUM4	Programmed cell death 6-interacting protein OS=Homo sapiens GN=PDCD6IP PE=1 SV=1 - [PDC6I_HUMAN]	52.29	11.75	12	12	17	0.527	0.350
O14737	Programmed cell death protein 5 OS=Homo sapiens GN=PDCD5 PE=1 SV=3 - [PDCD5_HUMAN]	15.73	31.20	5	5	5	0.283	0.174
Q9UQ80	Proliferation-associated protein 2G4 OS=Homo sapiens GN=PA2G4 PE=1 SV=3 - [PA2G4_HUMAN]	59.33	29.19	12	12	19	0.268	0.729
P48147	Prolyl endopeptidase OS=Homo sapiens GN=PREP PE=1 SV=2 - [PPCE_HUMAN]	6.09	2.54	2	2	2	0.315	0.141
B4DP21	Prostaglandin E synthase 3 (Cytosolic), isoform CRA_d OS=Homo sapiens GN=PTGES3 PE=2 SV=1 - [B4DP21_HUMAN]	19.70	28.46	5	5	7	0.245	0.124
A8K3Z3	Proteasome (Prosome, macropain) 26S subunit, ATPase, 5, isoform CRA_b OS=Homo sapiens GN=PSMC5 PE=2 SV=1 - [A8K3Z3_HUMAN]	26.49	8.04	3	4	8	0.331	0.151
B1AJY5	Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 10 OS=Homo sapiens GN=PSMD10 PE=4 SV=1 - [B1AJY5_HUMAN]	12.50	21.08	3	3	4	0.653	0.399
Q5QPM7	Proteasome (Prosome, macropain) inhibitor subunit 1 (PI31) OS=Homo sapiens GN=PSMF1 PE=2 SV=2 - [Q5QPM7_HUMAN]	14.81	11.79	4	4	6	0.390	0.332

Q06323	Proteasome activator complex subunit 1 OS=Homo sapiens GN=PSME1 PE=1 SV=1 - [PSME1_HUMAN]	52.58	38.96	10	10	17	0.388	0.201
Q9UL46	Proteasome activator complex subunit 2 OS=Homo sapiens GN=PSME2 PE=1 SV=4 - [PSME2_HUMAN]	48.80	23.43	6	6	15	0.485	0.269
P25787	Proteasome subunit alpha type-2 OS=Homo sapiens GN=PSMA2 PE=1 SV=2 - [PSA2_HUMAN]	16.42	14.96	5	5	6	0.522	0.327
P25788	Proteasome subunit alpha type-3 OS=Homo sapiens GN=PSMA3 PE=1 SV=2 - [PSA3_HUMAN]	61.54	28.63	9	10	20	0.478	0.298
P28066	Proteasome subunit alpha type-5 OS=Homo sapiens GN=PSMA5 PE=1 SV=3 - [PSA5_HUMAN]	38.56	28.22	4	5	11	0.518	0.325
P60900	Proteasome subunit alpha type-6 OS=Homo sapiens GN=PSMA6 PE=1 SV=1 - [PSA6_HUMAN]	42.41	26.42	7	7	12	0.484	0.308
O14818	Proteasome subunit alpha type-7 OS=Homo sapiens GN=PSMA7 PE=1 SV=1 - [PSA7_HUMAN]	54.29	34.27	9	9	18	0.484	0.306
P20618	Proteasome subunit beta type-1 OS=Homo sapiens GN=PSMB1 PE=1 SV=2 - [PSB1_HUMAN]	24.42	19.92	4	4	8	0.513	0.396
P49721	Proteasome subunit beta type-2 OS=Homo sapiens GN=PSMB2 PE=1 SV=1 - [PSB2_HUMAN]	15.57	13.93	5	5	5	0.508	0.328
P28070	Proteasome subunit beta type-4 OS=Homo sapiens GN=PSMB4 PE=1 SV=4 - [PSB4_HUMAN]	24.21	7.20	2	2	7	0.462	0.327
P28074	Proteasome subunit beta type-5 OS=Homo sapiens GN=PSMB5 PE=1 SV=3 - [PSB5_HUMAN]	26.57	18.63	5	5	8	0.564	0.372
P28072	Proteasome subunit beta type-6 OS=Homo sapiens GN=PSMB6 PE=1 SV=4 - [PSB6_HUMAN]	27.42	19.67	5	5	9	0.499	0.299
Q5VYK3	Proteasome-associated protein ECM29 homolog OS=Homo sapiens GN=ECM29 PE=1 SV=2 - [ECM29_HUMAN]	5.31	0.81	2	2	2	0.307	0.138
A8MTP3	Protein arginine methyltransferase 5, isoform CRA_c OS=Homo sapiens GN=PRMT5 PE=4 SV=1 - [A8MTP3_HUMAN]	13.66	7.73	5	5	5	0.403	0.322
Q9UKV8	Protein argonaute-2 OS=Homo sapiens GN=EIF2C2 PE=1 SV=3 - [AGO2_HUMAN]	13.45	5.59	5	5	5	0.221	0.360
Q5TDH0	Protein DDI1 homolog 2 OS=Homo sapiens GN=DDI2 PE=1 SV=1 - [DDI2_HUMAN]	56.82	20.05	9	9	19	0.696	0.402
Q99497	Protein DJ-1 OS=Homo sapiens GN=PARK7 PE=1 SV=2 - [PARK7_HUMAN]	89.59	44.97	9	9	29	0.533	0.343
Q9NRY5	Protein FAM114A2 OS=Homo sapiens GN=FAM114A2 PE=1 SV=4 - [F1142_HUMAN]	29.80	16.24	7	7	9	0.427	0.278
Q9NUQ9	Protein FAM49B OS=Homo sapiens GN=FAM49B PE=1 SV=1 - [FA49B_HUMAN]	8.35	7.41	3	3	3	0.542	0.290
Q8WZA0	Protein LZIC OS=Homo sapiens GN=LZIC PE=1 SV=1 - [LZIC_HUMAN]	18.02	16.32	4	4	6	0.532	0.363
Q15435	Protein phosphatase 1 regulatory subunit 7 OS=Homo sapiens GN=PPP1R7 PE=1 SV=1 - [PP1R7_HUMAN]	17.44	6.94	3	3	6	0.350	0.313
P35813	Protein phosphatase 1A OS=Homo sapiens GN=PPM1A PE=1 SV=1 - [PPM1A_HUMAN]	21.61	16.23	5	6	7	0.407	0.241
A6PVN5	Protein phosphatase 2A activator, regulatory subunit 4 OS=Homo sapiens GN=PPP2R4 PE=4 SV=1 - [A6PVN5_HUMAN]	17.18	10.03	4	4	6	0.647	0.312
Q9Y570	Protein phosphatase methylesterase 1 OS=Homo sapiens GN=PPME1 PE=1 SV=3 - [PPME1_HUMAN]	32.44	22.54	8	8	11	0.215	0.210
Q96M27	Protein PRRC1 OS=Homo sapiens GN=PRRC1 PE=1 SV=1 - [PRRC1_HUMAN]	5.71	3.15	2	2	2	0.162	0.112
P26447	Protein S100-A4 OS=Homo sapiens GN=S100A4 PE=1 SV=1 - [S10A4_HUMAN]	94.63	36.63	5	5	29	0.952	0.483
P06703	Protein S100-A6 OS=Homo sapiens GN=S100A6 PE=1 SV=1 - [S10A6_HUMAN]	120.91	40.00	5	6	42	0.514	0.303
B7Z972	Protein-L-isoaspartate O-methyltransferase OS=Homo sapiens GN=PCMT1 PE=2 SV=1 - [B7Z972_HUMAN]	26.51	18.23	4	4	9	0.708	0.569
Q567Q5	PSMA4 protein OS=Homo sapiens GN=PSMA4 PE=2 SV=1 - [Q567Q5_HUMAN]	49.23	31.05	8	8	16	0.483	0.294
P00491	Purine nucleoside phosphorylase OS=Homo sapiens GN=PNP PE=1 SV=2 - [PNPH_HUMAN]	194.95	45.33	12	12	62	0.391	0.263
Q53XA7	Putative uncharacterized protein DKFZp686F13224 OS=Homo sapiens GN=DKFZp686F13224 PE=2 SV=1 - [Q53XA7_HUMAN]	14.34	8.31	3	3	4	0.527	0.337
Q96GD0	Pyridoxal phosphate phosphatase OS=Homo sapiens GN=PDXP PE=1 SV=2 - [PLPP_HUMAN]	7.13	9.12	2	2	2	0.610	0.400
P14618	Pyruvate kinase isozymes M1/M2 OS=Homo sapiens GN=PKM2 PE=1 SV=4 - [KPYM_HUMAN]	54.68	13.18	8	9	19	0.085	0.076
P30613	Pyruvate kinase isozymes R/L OS=Homo sapiens GN=PKLR PE=1 SV=2 - [KPYR_HUMAN]	126.04	31.18	19	20	43	0.302	0.254
P50395	Rab GDP dissociation inhibitor beta OS=Homo sapiens GN=GDI2 PE=1 SV=2 - [GDIB_HUMAN]	111.07	33.71	11	15	36	0.522	0.438
P35241	Radixin OS=Homo sapiens GN=RDX PE=1 SV=1 - [RADI_HUMAN]	47.45	15.27	6	12	16	0.512	0.474
P46060	Ran GTPase-activating protein 1 OS=Homo sapiens GN=RANGAP1 PE=1 SV=1 - [RAGP1_HUMAN]	22.80	8.69	5	5	7	0.301	0.240
P43487	Ran-specific GTPase-activating protein OS=Homo sapiens GN=RANBP1 PE=1 SV=1 - [RANG_HUMAN]	24.47	23.38	5	5	8	0.388	0.330
P15153	Ras-related C3 botulinum toxin substrate 2 OS=Homo sapiens GN=RAC2 PE=1 SV=1 - [RAC2_HUMAN]	15.33	19.27	3	4	5	0.614	0.231
P61026	Ras-related protein Rab-10 OS=Homo sapiens GN=RAB10 PE=1 SV=1 - [RAB10_HUMAN]	15.90	15.00	2	3	5	0.275	0.224
P62491	Ras-related protein Rab-11A OS=Homo sapiens GN=RAB11A PE=1 SV=3 - [RB11A_HUMAN]	15.16	7.41	2	2	5	0.568	0.203
P61106	Ras-related protein Rab-14 OS=Homo sapiens GN=RAB14 PE=1 SV=4 - [RAB14_HUMAN]	11.18	11.16	3	3	4	0.559	0.391
P62820	Ras-related protein Rab-1A OS=Homo sapiens GN=RAB1A PE=1 SV=3 - [RAB1A_HUMAN]	41.35	33.17	3	8	13	0.642	0.455
Q9H0U4	Ras-related protein Rab-1B OS=Homo sapiens GN=RAB1B PE=1 SV=1 - [RAB1B_HUMAN]	52.77	34.83	4	9	17	0.583	0.355
O43665	Regulator of G-protein signaling 10 OS=Homo sapiens GN=RGS10 PE=1 SV=2 - [RGS10_HUMAN]	16.16	10.40	2	2	5	0.408	0.431
P00352	Retinal dehydrogenase 1 OS=Homo sapiens GN=ALDH1A1 PE=1 SV=2 - [AL1A1_HUMAN]	17.58	6.59	4	4	5	3.310	2.621
P52565	Rho GDP-dissociation inhibitor 1 OS=Homo sapiens GN=ARHGDIA PE=1 SV=3 - [GDIR1_HUMAN]	30.94	18.14	4	4	9	0.391	0.283
P13489	Ribonuclease inhibitor OS=Homo sapiens GN=RNH1 PE=1 SV=2 - [RINI_HUMAN]	74.25	28.42	13	13	22	0.474	0.245
P49247	Ribose-5-phosphate isomerase OS=Homo sapiens GN=RPIA PE=1 SV=3 - [RPIA_HUMAN]	28.97	13.83	5	5	9	0.591	0.552
P60891	Ribose-phosphate pyrophosphokinase 1 OS=Homo sapiens GN=PRPS1 PE=1 SV=2 - [PRPS1_HUMAN]	42.22	25.16	4	8	13	0.846	0.445
Q5VVC8	Ribosomal protein L11 (Fragment) OS=Homo sapiens GN=RPL11 PE=2 SV=1 - [Q5VVC8_HUMAN]	7.46	8.05	2	2	3	0.191	0.093
C9JNW5	Ribosomal protein L24, isoform CRA_e OS=Homo sapiens GN=RPL24 PE=4 SV=1 - [C9JNW5_HUMAN]	16.72	16.00	5	5	5	0.075	0.036
B3KTM6	Ribosomal protein L5, isoform CRA_b OS=Homo sapiens GN=RPL5 PE=2 SV=1 - [B3KTM6_HUMAN]	8.56	10.93	3	3	3	0.143	0.043
Q5T8U3	Ribosomal protein L7a (Fragment) OS=Homo sapiens GN=RPL7A PE=4 SV=1 - [Q5T8U3_HUMAN]	11.84	9.95	3	3	3	0.262	0.101
D6R9B6	Ribosomal protein S3A, isoform CRA_e OS=Homo sapiens GN=RPS3A PE=4 SV=1 - [D6R9B6_HUMAN]	23.79	19.31	4	4	8	0.047	0.035
O00442	RNA 3'-terminal phosphate cyclase OS=Homo sapiens GN=RTCD1 PE=1 SV=1 - [RTC1_HUMAN]	6.99	2.73	2	2	2	0.441	0.424

Q9Y265	RuvB-like 1 OS=Homo sapiens GN=RUVBL1 PE=1 SV=1 - [RUVB1_HUMAN]	27.73	12.94	6	6	8	0.261	0.272
Q9Y230	RuvB-like 2 OS=Homo sapiens GN=RUVBL2 PE=1 SV=3 - [RUVB2_HUMAN]	42.37	19.44	9	9	13	0.265	0.278
P31153	S-adenosylmethionine synthase isoform type-2 OS=Homo sapiens GN=MAT2A PE=1 SV=1 - [METK2_HUMAN]	9.17	3.80	2	2	3	0.407	0.184
P10768	S-formylglutathione hydrolase OS=Homo sapiens GN=ESD PE=1 SV=2 - [ESTD_HUMAN]	39.86	10.28	4	4	13	0.538	0.401
Q9UDX3	SEC14-like protein 4 OS=Homo sapiens GN=SEC14L4 PE=2 SV=1 - [S14L4_HUMAN]	13.08	10.34	5	5	5	0.430	0.405
Q13228	Selenium-binding protein 1 OS=Homo sapiens GN=SELENBP1 PE=1 SV=2 - [SBP1_HUMAN]	168.09	32.42	16	16	52	0.517	0.485
Q96GA7	Serine dehydratase-like OS=Homo sapiens GN=SDSL PE=1 SV=1 - [SDSL_HUMAN]	8.80	6.99	3	3	3	0.133	0.163
Q07955	Serine/arginine-rich splicing factor 1 OS=Homo sapiens GN=SRSF1 PE=1 SV=2 - [SRSF1_HUMAN]	5.69	7.66	2	2	2	0.131	0.051
Q08170	Serine/arginine-rich splicing factor 4 OS=Homo sapiens GN=SRSF4 PE=1 SV=2 - [SRSF4_HUMAN]	4.85	4.05	2	2	2	0.558	0.049
O95747	Serine/threonine-protein kinase OSR1 OS=Homo sapiens GN=OXSR1 PE=1 SV=1 - [OXSR1_HUMAN]	24.07	12.33	7	7	9	0.433	0.365
P30153	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=4 - [2AAA_HUMAN]	93.94	19.69	12	16	32	0.781	0.363
P67775	Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform OS=Homo sapiens GN=PPP2CA PE=1 SV=1 - [PP2AA_HUMAN]	15.67	5.18	2	2	5	0.436	0.310
O15084	Serine/threonine-protein phosphatase 6 regulatory ankyrin repeat subunit A OS=Homo sapiens GN=ANKRD28 PE=1 SV=5 - [ANR28_HUMAN]	6.34	3.23	2	2	2	0.211	0.176
B4DDZ8	Serine/threonine-protein phosphatase OS=Homo sapiens GN=PPP5C PE=2 SV=1 - [B4DDZ8_HUMAN]	14.02	8.64	5	5	5	0.299	0.355
P02787	Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3 - [TRFE_HUMAN]	9.00	3.72	3	3	3	0.188	0.073
Q9BXP5	Serrate RNA effector molecule homolog OS=Homo sapiens GN=SRRT PE=1 SV=1 - [SRRT_HUMAN]	4.75	1.94	2	2	2	0.234	0.124
P49591	Seryl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=SARS PE=1 SV=3 - [SYSC_HUMAN]	28.41	9.34	6	6	10	0.030	0.078
B2REB8	SET nuclear oncogene OS=Homo sapiens GN=SET PE=3 SV=1 - [B2REB8_HUMAN]	5.34	6.42	2	2	2		0.030
Q5T123	SH3 domain binding glutamic acid-rich protein like 3 OS=Homo sapiens GN=SH3BGRL3 PE=2 SV=1 - [Q5T123_HUMAN]	28.30	28.41	3	3	10	0.132	0.105
O75368	SH3 domain-binding glutamic acid-rich-like protein OS=Homo sapiens GN=SH3BGRL PE=1 SV=1 - [SH3L1_HUMAN]	67.16	58.77	7	7	21	0.372	0.275
B7ZC39	SH3-domain GRB2-like endophilin B2 OS=Homo sapiens GN=SH3GLB2 PE=4 SV=1 - [B7ZC39_HUMAN]	7.51	5.61	3	3	3	0.298	0.229
Q9NR45	Sialic acid synthase OS=Homo sapiens GN=NANS PE=1 SV=2 - [SIAS_HUMAN]	25.74	11.98	6	6	9	0.271	0.258
O76094	Signal recognition particle 72 kDa protein OS=Homo sapiens GN=SRP72 PE=1 SV=3 - [SRP72_HUMAN]	10.57	6.26	3	4	4	0.203	0.106
Q1KLZ6	Signal transducer and activator of transcription 5A variant delta5 OS=Homo sapiens GN=STAT5A PE=2 SV=1 - [Q1KLZ6_HUMAN]	12.46	3.93	3	3	4	0.423	0.206
C0H5W9	SNX6 protein OS=Homo sapiens GN=SNX6 PE=2 SV=1 - [C0H5W9_HUMAN]	10.22	9.66	4	4	4	0.137	0.141
P11166	Solute carrier family 2, facilitated glucose transporter member 1 OS=Homo sapiens GN=SLC2A1 PE=1 SV=2 - [GTR1_HUMAN]	22.94	7.32	4	4	7	0.075	0.246
Q00796	Sorbitol dehydrogenase OS=Homo sapiens GN=SORD PE=1 SV=4 - [DHSO_HUMAN]	16.25	10.08	4	4	6	0.151	0.387
O60493	Sorting nexin-3 OS=Homo sapiens GN=SNX3 PE=1 SV=3 - [SNX3_HUMAN]	18.02	26.54	5	5	7	0.111	0.073
P02549	Spectrin alpha chain, erythrocyte OS=Homo sapiens GN=SPTA1 PE=1 SV=5 - [SPTA1_HUMAN]	153.09	15.71	35	36	48	0.106	0.221
P11277	Spectrin beta chain, erythrocyte OS=Homo sapiens GN=SPTB PE=1 SV=5 - [SPTB1_HUMAN]	53.88	6.27	16	17	19	0.083	0.577
P52788	Spermine synthase OS=Homo sapiens GN=SMS PE=1 SV=2 - [SPSY_HUMAN]	9.72	8.74	4	4	4	0.152	0.154
P26368	Splicing factor U2AF 65 kDa subunit OS=Homo sapiens GN=U2AF2 PE=1 SV=4 - [U2AF2_HUMAN]	4.78	2.95	2	2	2	0.129	0.083
B3KUY1	Splicing factor, arginine/serine-rich 2, isoform CRA_d OS=Homo sapiens GN=SFRS2 PE=2 SV=1 - [B3KUY1_HUMAN]	5.16	7.66	2	2	2	0.269	0.059
P16949	Stathmin OS=Homo sapiens GN=STMN1 PE=1 SV=3 - [STMN1_HUMAN]	89.12	61.74	14	14	29	0.060	0.084
Q9H2G2	STE20-like serine/threonine-protein kinase OS=Homo sapiens GN=SLK PE=1 SV=1 - [SLK_HUMAN]	5.31	1.13	2	2	2	0.198	0.165
P31948	Stress-induced-phosphoprotein 1 OS=Homo sapiens GN=STIP1 PE=1 SV=1 - [STIP1_HUMAN]	185.22	38.86	33	34	62	0.295	0.220
O95347	Structural maintenance of chromosomes protein 2 OS=Homo sapiens GN=SMC2 PE=1 SV=2 - [SMC2_HUMAN]	4.97	1.17	2	2	2	0.139	0.090
P00441	Superoxide dismutase [Cu-Zn] OS=Homo sapiens GN=SOD1 PE=1 SV=2 - [SODC_HUMAN]	248.78	49.35	11	11	92	0.643	0.444
Q9Y2Z0	Suppressor of G2 allele of SKP1 homolog OS=Homo sapiens GN=SUGT1 PE=1 SV=3 - [SUGT1_HUMAN]	13.36	6.58	2	2	4	0.229	0.218
O15498	Synaptobrevin homolog YKT6 OS=Homo sapiens GN=YKT6 PE=1 SV=1 - [YKT6_HUMAN]	7.86	13.64	3	3	3	0.511	0.508
P17987	T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1 SV=1 - [TCPA_HUMAN]	104.78	23.38	15	15	35	0.157	0.166
P78371	T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=1 SV=4 - [TCPB_HUMAN]	134.05	34.02	21	21	43	0.178	0.157
P50991	T-complex protein 1 subunit delta OS=Homo sapiens GN=CCT4 PE=1 SV=4 - [TCPD_HUMAN]	129.49	34.69	20	20	43	0.178	0.155
P50990	T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=1 SV=4 - [TCPQ_HUMAN]	165.26	47.08	26	26	51	0.169	0.151
P40227	T-complex protein 1 subunit zeta OS=Homo sapiens GN=CCT6A PE=1 SV=3 - [TCPZ_HUMAN]	118.77	27.68	19	19	39	0.162	0.165
Q5TCU6	Talin 1 OS=Homo sapiens GN=TLN1 PE=2 SV=1 - [Q5TCU6_HUMAN]	307.80	23.59	65	66	103	0.053	0.062
B1AKP7	TAR DNA binding protein OS=Homo sapiens GN=TARDBP PE=4 SV=1 - [B1AKP7_HUMAN]	6.96	6.44	2	2	2	0.327	0.196
A8K8E1	TBC1 domain family, member 15, isoform CRA_d OS=Homo sapiens GN=TBC1D15 PE=2 SV=1 - [A8K8E1_HUMAN]	5.83	3.60	2	2	2	0.221	0.196
Q59G71	Tensin variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59G71_HUMAN]	15.12	6.19	5	5	5	0.226	0.115
Q99614	Tetratricopeptide repeat protein 1 OS=Homo sapiens GN=TTC1 PE=1 SV=1 - [TTC1_HUMAN]	6.27	5.82	2	2	2	0.078	0.086
P52888	Thimet oligopeptidase OS=Homo sapiens GN=THOP1 PE=1 SV=2 - [THOP1_HUMAN]	29.45	7.98	6	6	9	0.304	0.190
B1ALW1	Thioredoxin OS=Homo sapiens GN=TXN PE=4 SV=1 - [B1ALW1_HUMAN]	69.66	36.47	3	3	20	0.401	0.206
O43396	Thioredoxin-like protein 1 OS=Homo sapiens GN=TXNL1 PE=1 SV=3 - [TXNL1_HUMAN]	33.76	18.69	5	5	10	0.242	0.162
P26639	Threonyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=TARS PE=1 SV=3 - [SYTC_HUMAN]	27.98	8.99	7	7	10	0.072	0.067
P23919	Thymidylate kinase OS=Homo sapiens GN=DTYMK PE=1 SV=4 - [KTHY_HUMAN]	9.78	6.60	2	2	4	0.277	0.254
A8MW06	Thymosin beta-4-like protein 3 OS=Homo sapiens GN=TMSL3 PE=2 SV=1 - [TMSL3_HUMAN]	48.21	45.45	4	4	17	0.024	0.019

O75663	TIP41-like protein OS=Homo sapiens GN=TIPRL PE=1 SV=2 - [TIPRL_HUMAN]	14.10	13.24	4	4	5	0.222	0.185
A6NDN0	Trafficking protein particle complex 3, isoform CRA_a OS=Homo sapiens GN=TRAPPC3 PE=4 SV=1 - [A6NDN0_HUMAN]	5.06	11.19	2	2	2	0.104	0.604
P37837	Transaldolase OS=Homo sapiens GN=TALDO1 PE=1 SV=2 - [TALDO_HUMAN]	161.93	44.81	19	19	54	0.238	0.156
P23193	Transcription elongation factor A protein 1 OS=Homo sapiens GN=TCEA1 PE=1 SV=2 - [TCEA1_HUMAN]	20.05	14.62	4	4	6	0.051	0.062
Q13263	Transcription intermediary factor 1-beta OS=Homo sapiens GN=TRIM28 PE=1 SV=5 - [TIF1B_HUMAN]	14.37	3.11	3	3	6	0.240	1.201
P02786	Transferrin receptor protein 1 OS=Homo sapiens GN=TFRC PE=1 SV=2 - [TFR1_HUMAN]	23.61	7.37	6	6	8	0.291	0.031
P61586	Transforming protein RhoA OS=Homo sapiens GN=RHOA PE=1 SV=1 - [RHOA_HUMAN]	6.33	9.33	2	2	2	0.585	0.370
P37802	Transgelin-2 OS=Homo sapiens GN=TAGLN2 PE=1 SV=3 - [TAGL2_HUMAN]	58.47	41.71	10	10	17	0.172	0.148
P55072	Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4 - [TERA_HUMAN]	192.98	27.92	22	22	60	0.391	0.278
P13693	Translationally-controlled tumor protein OS=Homo sapiens GN=TPT1 PE=1 SV=1 - [TCTP_HUMAN]	30.04	29.65	6	6	10	0.173	0.183
Q92973	Transportin-1 OS=Homo sapiens GN=TNPO1 PE=1 SV=2 - [TNPO1_HUMAN]	21.56	4.34	3	3	7	0.199	0.187
P22102	Trifunctional purine biosynthetic protein adenosine-3 OS=Homo sapiens GN=GART PE=1 SV=1 - [PUR2_HUMAN]	26.03	5.94	6	7	9	0.173	0.079
P60174	Triosephosphate isomerase OS=Homo sapiens GN=TPI1 PE=1 SV=2 - [TPIS_HUMAN]	220.55	56.63	13	13	67	0.139	0.169
Q8NG06	Tripartite motif-containing protein 58 OS=Homo sapiens GN=TRIM58 PE=2 SV=2 - [TRI58_HUMAN]	26.03	13.79	8	8	9	0.145	0.100
P29144	Tripeptidyl-peptidase 2 OS=Homo sapiens GN=TPP2 PE=1 SV=4 - [TPP2_HUMAN]	20.50	4.08	6	6	7	0.460	0.357
D9YZV5	Tropomyosin 1 (Alpha) isoform 4 OS=Homo sapiens GN=TPM1 PE=3 SV=1 - [D9YZV5_HUMAN]	54.57	26.06	3	10	19	0.059	0.279
D9YZV7	Tropomyosin 1 (Alpha) isoform 6 OS=Homo sapiens GN=TPM1 PE=3 SV=1 - [D9YZV7_HUMAN]	73.95	31.02	2	9	23	0.043	0.116
Q5LJ98	TROVE domain family, member 2 OS=Homo sapiens GN=TROVE2 PE=2 SV=1 - [Q5LJ98_HUMAN]	17.00	4.83	3	3	6	0.064	0.073
P23381	Tryptophanyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=WARS PE=1 SV=2 - [SYWC_HUMAN]	38.93	13.16	7	7	13	0.151	0.083
Q9BQE3	Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 - [TBA1C_HUMAN]	108.25	22.27	3	9	35	0.121	0.076
P68371	Tubulin beta-2C chain OS=Homo sapiens GN=TUBB2C PE=1 SV=1 - [TBB2C_HUMAN]	129.74	25.84	12	12	45	0.119	0.083
B1AH89	Tubulin tyrosine ligase-like family, member 12 OS=Homo sapiens GN=TTLL12 PE=4 SV=1 - [B1AH89_HUMAN]	36.59	13.21	7	7	11	0.170	0.175
Q5QJ74	Tubulin-specific chaperone cofactor E-like protein OS=Homo sapiens GN=TBCEL PE=2 SV=2 - [TBCEL_HUMAN]	9.60	8.25	3	3	3	0.303	0.229
Q15813	Tubulin-specific chaperone E OS=Homo sapiens GN=TBCE PE=1 SV=1 - [TBCE_HUMAN]	7.94	4.93	3	3	3	0.036	0.060
Q06124	Tyrosine-protein phosphatase non-receptor type 11 OS=Homo sapiens GN=PTPN11 PE=1 SV=2 - [PTN11_HUMAN]	13.78	7.20	5	5	5	0.342	0.298
P54577	Tyrosyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=YARS PE=1 SV=4 - [SYYC_HUMAN]	91.66	29.55	19	19	30	0.094	0.111
P62312	U6 snRNA-associated Sm-like protein LSm6 OS=Homo sapiens GN=LSM6 PE=1 SV=1 - [LSM6_HUMAN]	5.93	21.25	2	2	2	0.146	0.113
Q5TBK7	Ubiquitin carboxyl-terminal esterase L3 (Ubiquitin thiolesterase) (Fragment) OS=Homo sapiens GN=UCHL3 PE=2 SV=1 - [Q5TBK7_HUMAN]	7.96	5.26	2	2	3	0.613	0.355
P45974	Ubiquitin carboxyl-terminal hydrolase 5 OS=Homo sapiens GN=USP5 PE=1 SV=2 - [UBP5_HUMAN]	63.14	9.44	9	9	19	0.477	0.359
A6NJA2	Ubiquitin carboxyl-terminal hydrolase OS=Homo sapiens GN=USP14 PE=3 SV=1 - [A6NJA2_HUMAN]	84.40	23.09	14	14	27	0.646	0.401
E9PCQ3	Ubiquitin carboxyl-terminal hydrolase OS=Homo sapiens GN=USP15 PE=3 SV=2 - [E9PCQ3_HUMAN]	60.14	12.76	14	14	20	0.449	0.253
E9PM46	Ubiquitin carboxyl-terminal hydrolase OS=Homo sapiens GN=USP47 PE=3 SV=1 - [E9PM46_HUMAN]	7.84	2.21	3	3	3	0.287	0.073
F5GX52	Ubiquitin carrier protein OS=Homo sapiens PE=3 SV=1 - [F5GX52_HUMAN]	32.33	21.74	3	3	11	0.535	0.364
Q5VVQ6	Ubiquitin thioesterase OTU1 OS=Homo sapiens GN=YOD1 PE=1 SV=1 - [OTU1_HUMAN]	44.10	16.95	8	8	16	0.510	0.432
P62979	Ubiquitin-40S ribosomal protein S27a OS=Homo sapiens GN=RPS27A PE=1 SV=2 - [RS27A_HUMAN]	402.31	41.03	9	9	143	0.602	0.262
Q9BSL1	Ubiquitin-associated domain-containing protein 1 OS=Homo sapiens GN=UBAC1 PE=1 SV=1 - [UBAC1_HUMAN]	35.59	16.30	6	6	10	0.453	0.300
P61088	Ubiquitin-conjugating enzyme E2 N OS=Homo sapiens GN=UBE2N PE=1 SV=1 - [UBE2N_HUMAN]	55.31	36.18	7	7	17	0.667	0.476
Q9C0C9	Ubiquitin-conjugating enzyme E2 O OS=Homo sapiens GN=UBE2O PE=1 SV=3 - [UBE2O_HUMAN]	30.25	4.72	8	8	9	0.649	0.571
Q13404	Ubiquitin-conjugating enzyme E2 variant 1 OS=Homo sapiens GN=UBE2V1 PE=1 SV=2 - [UB2V1_HUMAN]	35.58	40.82	4	8	13	0.340	0.298
Q15819	Ubiquitin-conjugating enzyme E2 variant 2 OS=Homo sapiens GN=UBE2V2 PE=1 SV=4 - [UB2V2_HUMAN]	24.75	36.55	3	7	9	0.494	0.408
P22314	Ubiquitin-like modifier-activating enzyme 1 OS=Homo sapiens GN=UBA1 PE=1 SV=3 - [UBA1_HUMAN]	105.88	14.08	16	16	34	0.389	0.325
A0AVT1	Ubiquitin-like modifier-activating enzyme 6 OS=Homo sapiens GN=UBA6 PE=1 SV=1 - [UBA6_HUMAN]	23.37	3.61	4	4	7	0.127	0.108
Q9NT62	Ubiquitin-like-conjugating enzyme ATG3 OS=Homo sapiens GN=ATG3 PE=1 SV=1 - [ATG3_HUMAN]	5.60	4.14	2	2	2	0.268	0.188
P30085	UMP-CMP kinase OS=Homo sapiens GN=CMPK1 PE=1 SV=3 - [KCY_HUMAN]	17.19	22.96	4	4	5	0.309	0.244
Q6ICL3	Uncharacterized protein C22orf25 OS=Homo sapiens GN=C22orf25 PE=2 SV=1 - [CV025_HUMAN]	24.51	14.13	5	5	9	0.445	0.392
Q8IXQ3	Uncharacterized protein C9orf40 OS=Homo sapiens GN=C9orf40 PE=1 SV=1 - [CI040_HUMAN]	13.85	12.89	2	2	5	0.616	0.477
B4DNR3	Uncharacterized protein OS=Homo sapiens GN=ABHD14B PE=2 SV=1 - [B4DNR3_HUMAN]	19.74	21.62	4	4	6	0.941	0.462
B4DUX0	Uncharacterized protein OS=Homo sapiens GN=ACOT7 PE=2 SV=1 - [B4DUX0_HUMAN]	6.07	5.66	2	2	2	0.364	0.357
F5H0N0	Uncharacterized protein OS=Homo sapiens GN=ACTG1 PE=3 SV=1 - [F5H0N0_HUMAN]	309.25	45.95	4	13	104	0.053	0.060
B4DXP9	Uncharacterized protein OS=Homo sapiens GN=ACTR1A PE=2 SV=1 - [B4DXP9_HUMAN]	53.48	11.85	5	6	21	0.259	0.177
B4DTI0	Uncharacterized protein OS=Homo sapiens GN=ACTR3 PE=2 SV=1 - [B4DTI0_HUMAN]	10.38	12.11	3	3	3	0.077	0.149
B7Z783	Uncharacterized protein OS=Homo sapiens GN=ADK PE=2 SV=1 - [B7Z783_HUMAN]	22.69	21.97	5	5	7	0.356	0.195
E9PEC0	Uncharacterized protein OS=Homo sapiens GN=ADRM1 PE=4 SV=2 - [E9PEC0_HUMAN]	9.30	10.73	3	3	3	0.148	0.062
C9J2I0	Uncharacterized protein OS=Homo sapiens GN=AGFG1 PE=4 SV=1 - [C9J2I0_HUMAN]	8.72	7.98	2	2	3	0.295	0.203
C9JSL3	Uncharacterized protein OS=Homo sapiens GN=AKR7A2 PE=4 SV=2 - [C9JSL3_HUMAN]	17.46	7.14	2	2	4	0.478	0.352
F5H4B6	Uncharacterized protein OS=Homo sapiens GN=ALDH16A1 PE=4 SV=1 - [F5H4B6_HUMAN]	18.48	8.92	5	5	6	0.866	0.387

E9PKC5	Uncharacterized protein OS=Homo sapiens GN=AMPD3 PE=4 SV=1 - [E9PKC5_HUMAN]	7.72	2.81	3	3	3	0.399	0.351
E7EVE3	Uncharacterized protein OS=Homo sapiens GN=ANK1 PE=4 SV=1 - [E7EVE3_HUMAN]	44.31	4.39	10	10	15	0.041	0.391
F5H754	Uncharacterized protein OS=Homo sapiens GN=ANKFY1 PE=4 SV=1 - [F5H754_HUMAN]	4.62	1.53	2	2	2	0.753	0.442
B4DT77	Uncharacterized protein OS=Homo sapiens GN=ANXA7 PE=2 SV=1 - [B4DT77_HUMAN]	74.20	38.69	13	13	23	0.349	0.301
F5H0H0	Uncharacterized protein OS=Homo sapiens GN=AP2M1 PE=4 SV=1 - [F5H0H0_HUMAN]	10.91	5.24	3	3	4	0.334	0.149
B7ZB63	Uncharacterized protein OS=Homo sapiens GN=ARF3 PE=2 SV=1 - [B7ZB63_HUMAN]	25.89	25.00	4	4	9	0.457	0.275
E9PNR6	Uncharacterized protein OS=Homo sapiens GN=ARHGAP1 PE=4 SV=1 - [E9PNR6_HUMAN]	6.20	10.94	2	2	2	0.735	0.380
F5H6Q0	Uncharacterized protein OS=Homo sapiens GN=ARHGDIB PE=4 SV=1 - [F5H6Q0_HUMAN]	23.70	59.82	6	6	8	0.572	0.429
E7EWX4	Uncharacterized protein OS=Homo sapiens GN=ARPC4 PE=4 SV=1 - [E7EWX4_HUMAN]	8.18	10.26	2	2	3	0.072	0.194
E9PBU3	Uncharacterized protein OS=Homo sapiens GN=ATIC PE=4 SV=1 - [E9PBU3_HUMAN]	57.78	19.97	11	11	18	0.315	0.239
B7Z1R5	Uncharacterized protein OS=Homo sapiens GN=ATP6V1A PE=2 SV=1 - [B7Z1R5_HUMAN]	55.45	16.27	11	11	17	0.153	0.142
A8MUN4	Uncharacterized protein OS=Homo sapiens GN=ATP6V1E1 PE=2 SV=1 - [A8MUN4_HUMAN]	29.22	26.02	6	6	10	0.139	0.142
E9PGE6	Uncharacterized protein OS=Homo sapiens GN=ATP6V1H PE=4 SV=1 - [E9PGE6_HUMAN]	10.64	4.36	2	2	3	0.176	0.134
C9JB13	Uncharacterized protein OS=Homo sapiens GN=BSDC1 PE=4 SV=1 - [C9JB13_HUMAN]	10.42	7.11	3	3	4	0.046	0.152
E9PL10	Uncharacterized protein OS=Homo sapiens GN=BTF3L4 PE=4 SV=1 - [E9PL10_HUMAN]	25.78	26.21	6	6	10	0.075	0.068
C9JXR7	Uncharacterized protein OS=Homo sapiens GN=CASP3 PE=4 SV=2 - [C9JXR7_HUMAN]	7.67	15.38	2	2	3	0.201	0.093
E9PAQ6	Uncharacterized protein OS=Homo sapiens GN=CCT3 PE=3 SV=1 - [E9PAQ6_HUMAN]	123.45	29.04	20	20	40	0.190	0.170
E7ENZ3	Uncharacterized protein OS=Homo sapiens GN=CCT5 PE=4 SV=1 - [E7ENZ3_HUMAN]	123.71	30.66	17	17	40	0.215	0.202
E9PP50	Uncharacterized protein OS=Homo sapiens GN=CFL1 PE=4 SV=1 - [E9PP50_HUMAN]	95.19	50.00	10	11	31	0.419	0.282
B4DIN1	Uncharacterized protein OS=Homo sapiens GN=CLTA PE=2 SV=1 - [B4DIN1_HUMAN]	27.96	13.48	5	5	9	0.143	0.099
B4DIH5	Uncharacterized protein OS=Homo sapiens GN=COPS2 PE=2 SV=1 - [B4DIH5_HUMAN]	6.14	3.96	2	2	2	0.669	0.355
B4DM67	Uncharacterized protein OS=Homo sapiens GN=CSE1L PE=2 SV=1 - [B4DM67_HUMAN]	5.86	2.84	2	2	2	0.493	0.170
F5GWW0	Uncharacterized protein OS=Homo sapiens GN=CTSB PE=3 SV=1 - [F5GWW0_HUMAN]	7.94	9.89	3	3	3	0.098	0.095
E7EWR0	Uncharacterized protein OS=Homo sapiens GN=CUL1 PE=3 SV=1 - [E7EWR0_HUMAN]	8.89	3.41	3	3	3	0.624	0.384
A8MSH7	Uncharacterized protein OS=Homo sapiens GN=CUL4A PE=3 SV=1 - [A8MSH7_HUMAN]	26.33	9.88	8	8	9	0.383	0.276
F2Z305	Uncharacterized protein OS=Homo sapiens GN=DCAF6 PE=4 SV=1 - [F2Z305_HUMAN]	5.60	3.60	2	2	2	0.239	0.364
E9PFS5	Uncharacterized protein OS=Homo sapiens GN=DCTN1 PE=4 SV=1 - [E9PFS5_HUMAN]	39.34	7.85	11	11	14	0.252	0.160
F5H223	Uncharacterized protein OS=Homo sapiens GN=DCTN2 PE=4 SV=1 - [F5H223_HUMAN]	24.49	12.70	6	6	8	0.266	0.157
C9J8R4	Uncharacterized protein OS=Homo sapiens GN=DCUN1D1 PE=4 SV=1 - [C9J8R4_HUMAN]	9.89	12.50	2	2	3	0.350	0.295
E9PML7	Uncharacterized protein OS=Homo sapiens GN=DERA PE=4 SV=1 - [E9PML7_HUMAN]	6.35	6.78	2	2	2	0.819	0.381
F5H6K0	Uncharacterized protein OS=Homo sapiens GN=DHX15 PE=4 SV=1 - [F5H6K0_HUMAN]	4.92	0.89	2	2	2	0.061	0.125
E7ERW8	Uncharacterized protein OS=Homo sapiens GN=DIAPH1 PE=4 SV=1 - [E7ERW8_HUMAN]	45.04	6.01	10	10	16	0.328	0.232
C9JXB9	Uncharacterized protein OS=Homo sapiens GN=DNAJB2 PE=4 SV=1 - [C9JXB9_HUMAN]	8.75	12.70	3	3	3	1.355	0.679
E7EPX3	Uncharacterized protein OS=Homo sapiens GN=DNPEP PE=3 SV=1 - [E7EPX3_HUMAN]	13.80	8.48	3	3	4	0.524	0.308
F5GXD5	Uncharacterized protein OS=Homo sapiens GN=DPP3 PE=4 SV=1 - [F5GXD5_HUMAN]	36.97	10.55	7	7	12	0.472	0.400
B4DR31	Uncharacterized protein OS=Homo sapiens GN=DPYSL2 PE=2 SV=1 - [B4DR31_HUMAN]	13.87	4.66	3	3	5	0.175	0.320
F5H335	Uncharacterized protein OS=Homo sapiens GN=EIF3A PE=4 SV=1 - [F5H335_HUMAN]	42.40	10.83	13	13	15	0.169	0.106
B4DV79	Uncharacterized protein OS=Homo sapiens GN=EIF3B PE=2 SV=1 - [B4DV79_HUMAN]	23.20	6.64	5	5	8	0.056	0.030
F5H1I1	Uncharacterized protein OS=Homo sapiens GN=EIF3C PE=4 SV=1 - [F5H1I1_HUMAN]	13.43	5.23	4	4	4	0.047	0.033
B7ZAM9	Uncharacterized protein OS=Homo sapiens GN=EIF3K PE=2 SV=1 - [B7ZAM9_HUMAN]	5.74	9.95	2	2	2	0.413	0.112
E7EQG2	Uncharacterized protein OS=Homo sapiens GN=EIF4A2 PE=3 SV=1 - [E7EQG2_HUMAN]	47.01	24.31	2	8	13	0.321	0.542
E7EPC9	Uncharacterized protein OS=Homo sapiens GN=EIF4B PE=4 SV=1 - [E7EPC9_HUMAN]	56.50	20.44	12	12	19	0.352	0.271
E7EX73	Uncharacterized protein OS=Homo sapiens GN=EIF4G1 PE=4 SV=1 - [E7EX73_HUMAN]	33.39	6.82	11	11	11	0.165	0.134
D6RA00	Uncharacterized protein OS=Homo sapiens GN=ENOPH1 PE=4 SV=1 - [D6RA00_HUMAN]	10.13	7.51	2	2	4	0.189	0.191
E9PEX0	Uncharacterized protein OS=Homo sapiens GN=EPB41 PE=4 SV=1 - [E9PEX0_HUMAN]	20.81	9.66	5	7	7	0.143	0.614
E5RJ56	Uncharacterized protein OS=Homo sapiens GN=EPB49 PE=4 SV=1 - [E5RJ56_HUMAN]	28.92	15.03	5	5	9	0.081	0.095
E7EQR4	Uncharacterized protein OS=Homo sapiens GN=EZR PE=4 SV=2 - [E7EQR4_HUMAN]	76.62	25.99	15	20	25	0.089	0.169
E9PCI9	Uncharacterized protein OS=Homo sapiens GN=FDPS PE=3 SV=1 - [E9PCI9_HUMAN]	18.29	14.73	5	5	6	0.272	0.162
B7Z7Z8	Uncharacterized protein OS=Homo sapiens GN=FKBP5 PE=2 SV=1 - [B7Z7Z8_HUMAN]	19.62	17.27	4	5	6	0.110	0.041
B3KNR9	Uncharacterized protein OS=Homo sapiens GN=FN3K PE=2 SV=1 - [B3KNR9_HUMAN]	13.82	16.95	3	3	4	0.588	0.481
B4E0X8	Uncharacterized protein OS=Homo sapiens GN=FUBP1 PE=2 SV=1 - [B4E0X8_HUMAN]	8.40	4.45	2	3	3	0.067	0.067
E9PGM4	Uncharacterized protein OS=Homo sapiens GN=GBE1 PE=4 SV=1 - [E9PGM4_HUMAN]	7.49	4.08	2	2	2	0.210	0.162
B4E192	Uncharacterized protein OS=Homo sapiens GN=GFAP PE=2 SV=1 - [B4E192_HUMAN]	37.91	21.87	8	9	13	0.581	1.753
B8ZZK2	Uncharacterized protein OS=Homo sapiens GN=GGCT PE=4 SV=1 - [B8ZZK2_HUMAN]	22.91	12.05	2	2	8	0.523	0.377
E7EMY5	Uncharacterized protein OS=Homo sapiens GN=GLOD4 PE=4 SV=1 - [E7EMY5_HUMAN]	42.38	16.37	9	9	14	0.469	0.341
C9JAH0	Uncharacterized protein OS=Homo sapiens GN=GMPPA PE=4 SV=1 - [C9JAH0_HUMAN]	5.76	7.23	2	2	2	0.308	0.329

B4DUT7	Uncharacterized protein OS=Homo sapiens GN=GMPS PE=2 SV=1 - [B4DUT7_HUMAN]	8.69	4.52	3	3	3	0.226	0.126
E9PDI1	Uncharacterized protein OS=Homo sapiens GN=GPCPD1 PE=4 SV=1 - [E9PDI1_HUMAN]	6.41	7.61	2	2	2	0.063	0.035
F5H8M4	Uncharacterized protein OS=Homo sapiens GN=GSN PE=4 SV=1 - [F5H8M4_HUMAN]	7.93	2.41	2	2	3	0.344	0.268
E7EQZ3	Uncharacterized protein OS=Homo sapiens GN=GSPT1 PE=4 SV=1 - [E7EQZ3_HUMAN]	54.56	16.67	13	13	19	0.115	0.133
A8MX94	Uncharacterized protein OS=Homo sapiens GN=GSTP1 PE=3 SV=1 - [A8MX94_HUMAN]	15.41	16.09	3	3	5	0.349	0.420
F5GZ06	Uncharacterized protein OS=Homo sapiens GN=HEATR7B2 PE=4 SV=1 - [F5GZ06_HUMAN]	5.17	2.54	2	2	2	0.469	0.311
F5H5Y5	Uncharacterized protein OS=Homo sapiens GN=HGS PE=4 SV=1 - [F5H5Y5_HUMAN]	16.67	6.05	5	5	6	0.381	0.140
E9PCK0	Uncharacterized protein OS=Homo sapiens GN=HK1 PE=3 SV=1 - [E9PCK0_HUMAN]	28.70	5.97	6	6	9	0.108	0.121
F5H345	Uncharacterized protein OS=Homo sapiens GN=HMBS PE=4 SV=1 - [F5H345_HUMAN]	89.60	25.76	9	9	30	0.132	0.157
B8ZZT7	Uncharacterized protein OS=Homo sapiens GN=HN1 PE=4 SV=1 - [B8ZZT7_HUMAN]	6.67	14.02	2	2	2	0.166	0.513
D6R9P3	Uncharacterized protein OS=Homo sapiens GN=HNRNPAB PE=4 SV=1 - [D6R9P3_HUMAN]	16.60	11.07	2	4	6	0.228	0.125
B4DTC3	Uncharacterized protein OS=Homo sapiens GN=HNRNPD PE=2 SV=1 - [B4DTC3_HUMAN]	21.23	13.20	3	5	8	0.162	0.044
B4DKS8	Uncharacterized protein OS=Homo sapiens GN=HNRNPF PE=2 SV=1 - [B4DKS8_HUMAN]	7.41	7.40	2	3	3	0.117	0.234
B4DPK8	Uncharacterized protein OS=Homo sapiens GN=HNRNPL PE=2 SV=1 - [B4DPK8_HUMAN]	8.69	13.75	3	3	3	0.091	0.038
B3KX72	Uncharacterized protein OS=Homo sapiens GN=HNRNPU PE=2 SV=1 - [B3KX72_HUMAN]	7.49	3.20	3	3	3	0.036	0.044
E9PDE8	Uncharacterized protein OS=Homo sapiens GN=HSPA4L PE=3 SV=1 - [E9PDE8_HUMAN]	7.60	2.71	2	3	3	0.059	0.086
B4DL87	Uncharacterized protein OS=Homo sapiens GN=HSPB1 PE=2 SV=1 - [B4DL87_HUMAN]	41.92	37.06	7	7	12	0.132	0.106
E9PD66	Uncharacterized protein OS=Homo sapiens GN=HUWE1 PE=4 SV=1 - [E9PD66_HUMAN]	56.51	3.19	16	16	19	0.283	0.129
B4E0R6	Uncharacterized protein OS=Homo sapiens GN=IPO5 PE=2 SV=1 - [B4E0R6_HUMAN]	36.78	7.51	7	7	12	0.331	0.272
E7EP96	Uncharacterized protein OS=Homo sapiens GN=KHSRP PE=4 SV=1 - [E7EP96_HUMAN]	7.46	6.59	2	3	3	0.023	0.034
F5H4G7	Uncharacterized protein OS=Homo sapiens GN=KPNA6 PE=4 SV=1 - [F5H4G7_HUMAN]	12.89	4.88	3	4	5	0.340	0.252
B4DJ10	Uncharacterized protein OS=Homo sapiens GN=LARS PE=2 SV=1 - [B4DJ10_HUMAN]	5.36	1.34	2	2	2	0.122	0.049
A8MUU4	Uncharacterized protein OS=Homo sapiens GN=MBP PE=4 SV=2 - [A8MUU4_HUMAN]	12.60	15.03	3	3	4	0.617	1.497
E9PGF9	Uncharacterized protein OS=Homo sapiens GN=MGEA5 PE=4 SV=1 - [E9PGF9_HUMAN]	13.45	3.48	3	4	5	0.030	0.037
A8MU28	Uncharacterized protein OS=Homo sapiens GN=NAE1 PE=4 SV=1 - [A8MU28_HUMAN]	9.96	4.72	3	3	3	0.322	0.332
C9JZI7	Uncharacterized protein OS=Homo sapiens GN=NAP1L4 PE=3 SV=1 - [C9JZI7_HUMAN]	32.06	17.99	5	6	11	0.238	0.209
B7Z463	Uncharacterized protein OS=Homo sapiens GN=NPEPPS PE=2 SV=1 - [B7Z463_HUMAN]	24.09	7.27	7	7	8	0.497	0.253
B9A035	Uncharacterized protein OS=Homo sapiens GN=NT5C3 PE=4 SV=1 - [B9A035_HUMAN]	10.81	12.68	3	3	4	0.196	0.145
E5RFP0	Uncharacterized protein OS=Homo sapiens GN=NUDCD2 PE=4 SV=1 - [E5RFP0_HUMAN]	5.56	15.15	2	2	2	0.387	0.281
F5GYN4	Uncharacterized protein OS=Homo sapiens GN=OTUB1 PE=4 SV=1 - [F5GYN4_HUMAN]	14.87	19.09	4	4	5	0.196	0.218
B4DUA5	Uncharacterized protein OS=Homo sapiens GN=P4HB PE=2 SV=1 - [B4DUA5_HUMAN]	5.89	3.54	2	2	2	0.115	0.097
E7EQV3	Uncharacterized protein OS=Homo sapiens GN=PABPC1 PE=4 SV=1 - [E7EQV3_HUMAN]	13.06	4.06	3	3	4	0.185	0.101
E9PBS1	Uncharacterized protein OS=Homo sapiens GN=PAICS PE=4 SV=1 - [E9PBS1_HUMAN]	89.96	22.52	12	12	30	0.154	0.149
E9PHT6	Uncharacterized protein OS=Homo sapiens GN=PANK4 PE=4 SV=1 - [E9PHT6_HUMAN]	5.05	2.72	2	2	2	0.124	0.065
F2Z2Y4	Uncharacterized protein OS=Homo sapiens GN=PDXK PE=4 SV=1 - [F2Z2Y4_HUMAN]	24.71	12.13	4	4	8	0.077	0.142
E9PCE8	Uncharacterized protein OS=Homo sapiens GN=PEPD PE=3 SV=1 - [E9PCE8_HUMAN]	34.19	19.11	7	7	10	0.343	0.291
F5GWE5	Uncharacterized protein OS=Homo sapiens GN=PITPNA PE=4 SV=1 - [F5GWE5_HUMAN]	30.22	24.07	7	9	11	0.652	0.445
E5RIM3	Uncharacterized protein OS=Homo sapiens GN=PLAA PE=4 SV=1 - [E5RIM3_HUMAN]	7.87	2.79	2	2	3	0.213	0.143
B4E0V0	Uncharacterized protein OS=Homo sapiens GN=PNPO PE=2 SV=1 - [B4E0V0_HUMAN]	5.00	9.04	2	2	2	0.137	0.198
D6RFZ8	Uncharacterized protein OS=Homo sapiens GN=PPIP5K2 PE=4 SV=1 - [D6RFZ8_HUMAN]	5.58	1.76	2	2	2	0.078	0.135
E7EPA1	Uncharacterized protein OS=Homo sapiens GN=PRPSAP2 PE=4 SV=1 - [E7EPA1_HUMAN]	19.02	13.81	4	5	6	0.512	0.440
F5GX11	Uncharacterized protein OS=Homo sapiens GN=PSMA1 PE=4 SV=1 - [F5GX11_HUMAN]	53.74	34.87	11	11	17	0.519	0.306
F5GZ16	Uncharacterized protein OS=Homo sapiens GN=PSMD2 PE=4 SV=1 - [F5GZ16_HUMAN]	41.60	12.78	10	10	13	0.506	0.181
F5H8K4	Uncharacterized protein OS=Homo sapiens GN=PSMD3 PE=4 SV=1 - [F5H8K4_HUMAN]	56.41	18.81	10	10	18	0.281	0.142
E9PHI9	Uncharacterized protein OS=Homo sapiens GN=PSMD6 PE=4 SV=1 - [E9PHI9_HUMAN]	21.70	11.43	5	5	7	0.299	0.148
B4DXI8	Uncharacterized protein OS=Homo sapiens GN=PSMD7 PE=2 SV=1 - [B4DXI8_HUMAN]	22.40	12.96	4	4	7	0.291	0.166
B8ZZQ6	Uncharacterized protein OS=Homo sapiens GN=PTMA PE=4 SV=1 - [B8ZZQ6_HUMAN]	29.47	23.36	4	4	9	0.015	0.032
B4DNN3	Uncharacterized protein OS=Homo sapiens GN=QARS PE=2 SV=1 - [B4DNN3_HUMAN]	12.70	5.10	4	4	4	0.142	0.108
C9J7D1	Uncharacterized protein OS=Homo sapiens GN=RAB7A PE=4 SV=1 - [C9J7D1_HUMAN]	4.85	14.29	2	2	2	0.225	0.158
B4DW94	Uncharacterized protein OS=Homo sapiens GN=RAP1B PE=2 SV=1 - [B4DW94_HUMAN]	5.64	13.14	2	2	2	0.544	0.432
F5H3T8	Uncharacterized protein OS=Homo sapiens GN=RARS PE=4 SV=1 - [F5H3T8_HUMAN]	5.57	3.52	2	2	2	0.242	0.123
E9PC52	Uncharacterized protein OS=Homo sapiens GN=RBBP7 PE=4 SV=1 - [E9PC52_HUMAN]	6.29	4.57	2	2	2	0.142	0.121
F5GX07	Uncharacterized protein OS=Homo sapiens GN=REXO2 PE=4 SV=1 - [F5GX07_HUMAN]	6.02	12.24	2	2	2	0.505	0.257
D6RJG8	Uncharacterized protein OS=Homo sapiens GN=RFESD PE=4 SV=1 - [D6RJG8_HUMAN]	16.27	50.00	4	4	5	0.401	0.451
E5RIT6	Uncharacterized protein OS=Homo sapiens GN=RPL26L1 PE=3 SV=1 - [E5RIT6_HUMAN]	5.09	10.94	2	2	2	0.221	0.112
F2Z3A5	Uncharacterized protein OS=Homo sapiens GN=RPL3 PE=3 SV=1 - [F2Z3A5_HUMAN]	7.85	6.50	3	3	3	0.187	0.081

B8ZZK4	Uncharacterized protein OS=Homo sapiens GN=RPL31 PE=4 SV=1 - [B8ZZK4_HUMAN]	5.34	20.25	2	2	2	0.113	0.079
E7EWF1	Uncharacterized protein OS=Homo sapiens GN=RPL4 PE=4 SV=1 - [E7EWF1_HUMAN]	19.85	10.10	6	6	7	0.229	0.104
E9PKZ0	Uncharacterized protein OS=Homo sapiens GN=RPL8 PE=4 SV=1 - [E9PKZ0_HUMAN]	8.72	16.10	3	3	3	0.094	0.064
E9PS50	Uncharacterized protein OS=Homo sapiens GN=RPS13 PE=4 SV=1 - [E9PS50_HUMAN]	11.42	22.41	3	3	4	0.042	0.053
E5RH77	Uncharacterized protein OS=Homo sapiens GN=RPS14 PE=4 SV=1 - [E5RH77_HUMAN]	8.04	9.70	2	2	3	0.158	0.135
E9PM36	Uncharacterized protein OS=Homo sapiens GN=RPS2 PE=3 SV=1 - [E9PM36_HUMAN]	10.90	8.13	2	2	4	0.077	0.057
C9J9K3	Uncharacterized protein OS=Homo sapiens GN=RPSA PE=3 SV=1 - [C9J9K3_HUMAN]	23.84	21.21	5	5	7	0.123	0.163
E5RJE3	Uncharacterized protein OS=Homo sapiens GN=RWDD1 PE=4 SV=1 - [E5RJE3_HUMAN]	6.23	17.65	2	2	2	0.329	0.267
B4DNE4	Uncharacterized protein OS=Homo sapiens GN=SEPT7 PE=2 SV=1 - [B4DNE4_HUMAN]	10.92	5.76	3	3	4	0.117	0.247
B4E3A8	Uncharacterized protein OS=Homo sapiens GN=SERPINB1 PE=2 SV=1 - [B4E3A8_HUMAN]	14.26	9.97	4	4	5	0.540	0.273
E7EMJ6	Uncharacterized protein OS=Homo sapiens GN=SGTA PE=4 SV=1 - [E7EMJ6_HUMAN]	29.61	13.40	5	5	10	0.262	0.198
E5RJR5	Uncharacterized protein OS=Homo sapiens GN=SKP1 PE=4 SV=1 - [E5RJR5_HUMAN]	43.83	34.36	7	7	13	0.696	0.413
E7EPV7	Uncharacterized protein OS=Homo sapiens GN=SNCA PE=4 SV=1 - [E7EPV7_HUMAN]	201.14	78.26	10	11	52	0.684	0.671
E7ESM6	Uncharacterized protein OS=Homo sapiens GN=SND1 PE=4 SV=2 - [E7ESM6_HUMAN]	28.88	6.33	6	6	9	0.017	0.051
B4DEK4	Uncharacterized protein OS=Homo sapiens GN=SNX2 PE=2 SV=1 - [B4DEK4_HUMAN]	17.13	7.46	3	3	6	0.188	0.162
E9PBC7	Uncharacterized protein OS=Homo sapiens GN=SNX5 PE=4 SV=1 - [E9PBC7_HUMAN]	6.01	5.45	2	2	2	0.135	0.137
C9J0K6	Uncharacterized protein OS=Homo sapiens GN=SRI PE=4 SV=1 - [C9J0K6_HUMAN]	46.76	43.23	7	7	16	0.351	0.274
E7ETK6	Uncharacterized protein OS=Homo sapiens GN=SRP68 PE=4 SV=1 - [E7ETK6_HUMAN]	6.11	4.36	2	2	2	0.049	0.043
B4E2V5	Uncharacterized protein OS=Homo sapiens GN=STOM PE=2 SV=1 - [B4E2V5_HUMAN]	12.50	12.24	3	3	4	0.056	0.470
F2Z3D0	Uncharacterized protein OS=Homo sapiens GN=SUMO2 PE=4 SV=1 - [F2Z3D0_HUMAN]	6.98	30.99	2	2	2	0.355	0.223
F5GWQ7	Uncharacterized protein OS=Homo sapiens GN=TAF15 PE=4 SV=1 - [F5GWQ7_HUMAN]	5.68	11.65	2	2	2	0.247	0.069
E5RIW3	Uncharacterized protein OS=Homo sapiens GN=TBCA PE=4 SV=1 - [E5RIW3_HUMAN]	45.58	50.00	6	6	14	0.272	0.291
A8MVD5	Uncharacterized protein OS=Homo sapiens GN=TBCB PE=4 SV=1 - [A8MVD5_HUMAN]	6.06	9.81	2	2	2	0.396	0.266
C9JJP5	Uncharacterized protein OS=Homo sapiens GN=TFG PE=4 SV=1 - [C9JJP5_HUMAN]	11.08	8.29	2	2	4	0.371	0.101
B4DIT7	Uncharacterized protein OS=Homo sapiens GN=TGM2 PE=2 SV=1 - [B4DIT7_HUMAN]	165.54	29.21	20	20	55	0.375	0.338
E9PGT1	Uncharacterized protein OS=Homo sapiens GN=TSN PE=4 SV=1 - [E9PGT1_HUMAN]	25.23	23.77	5	6	8	0.523	0.286
A6NKB1	Uncharacterized protein OS=Homo sapiens GN=TTN PE=4 SV=4 - [A6NKB1_HUMAN]	27.19	0.27	3	9	11	0.865	0.631
E9PIR7	Uncharacterized protein OS=Homo sapiens GN=TXNRD1 PE=3 SV=1 - [E9PIR7_HUMAN]	39.02	12.24	7	7	12	0.292	0.214
E7EWE1	Uncharacterized protein OS=Homo sapiens GN=UBA5 PE=4 SV=1 - [E7EWE1_HUMAN]	8.90	6.34	3	3	3	0.521	0.308
D6RDM7	Uncharacterized protein OS=Homo sapiens GN=UBE2K PE=4 SV=1 - [D6RDM7_HUMAN]	12.40	14.63	2	2	4	0.267	0.282
E9PJ81	Uncharacterized protein OS=Homo sapiens GN=UBXN1 PE=4 SV=1 - [E9PJ81_HUMAN]	8.60	7.24	3	3	3	0.190	0.172
A6NJ11	Uncharacterized protein OS=Homo sapiens GN=UFD1L PE=4 SV=1 - [A6NJ11_HUMAN]	9.29	11.82	2	3	3	0.045	0.123
C9JKD6	Uncharacterized protein OS=Homo sapiens GN=UGP2 PE=4 SV=1 - [C9JKD6_HUMAN]	18.59	11.02	6	6	6	0.471	0.247
E9PG85	Uncharacterized protein OS=Homo sapiens GN=UROS PE=4 SV=1 - [E9PG85_HUMAN]	28.83	29.11	6	6	10	0.143	0.122
B7Z7T5	Uncharacterized protein OS=Homo sapiens GN=USP7 PE=2 SV=1 - [B7Z7T5_HUMAN]	14.39	6.88	5	5	5	0.250	0.198
B0V043	Uncharacterized protein OS=Homo sapiens GN=VARS PE=3 SV=1 - [B0V043_HUMAN]	6.73	1.66	2	2	2	0.095	0.106
F5H2A7	Uncharacterized protein OS=Homo sapiens GN=VBP1 PE=4 SV=1 - [F5H2A7_HUMAN]	16.32	15.10	3	3	5	0.147	0.217
A6NG10	Uncharacterized protein OS=Homo sapiens GN=WBP2 PE=2 SV=2 - [A6NG10_HUMAN]	61.77	23.85	7	7	20	0.412	0.345
B4DP38	Uncharacterized protein OS=Homo sapiens GN=WDR77 PE=2 SV=1 - [B4DP38_HUMAN]	6.65	4.68	2	2	2	0.396	0.286
F5GWT4	Uncharacterized protein OS=Homo sapiens GN=WNK1 PE=4 SV=1 - [F5GWT4_HUMAN]	25.02	4.08	9	9	9	0.330	0.220
Q5T6H7	Uncharacterized protein OS=Homo sapiens GN=XPNPEP1 PE=2 SV=1 - [Q5T6H7_HUMAN]	24.46	6.34	4	4	8	0.154	0.121
E7ESC6	Uncharacterized protein OS=Homo sapiens GN=XPO7 PE=4 SV=1 - [E7ESC6_HUMAN]	96.16	15.44	18	18	32	0.199	0.115
E9PQI5	Uncharacterized protein OS=Homo sapiens PE=4 SV=1 - [E9PQI5_HUMAN]	19.05	17.47	3	3	5	0.258	0.309
Q9H7C9	UPF0366 protein C11orf67 OS=Homo sapiens GN=C11orf67 PE=1 SV=1 - [CK067_HUMAN]	5.93	18.85	2	2	2	0.516	0.343
Q5T6V5	UPF0553 protein C9orf64 OS=Homo sapiens GN=C9orf64 PE=1 SV=1 - [CI064_HUMAN]	8.48	4.40	2	2	3	0.290	0.233
Q9NWV4	UPF0587 protein C1orf123 OS=Homo sapiens GN=C1orf123 PE=1 SV=1 - [CA123_HUMAN]	14.04	23.75	4	4	5	0.602	0.437
P06132	Uroporphyrinogen decarboxylase OS=Homo sapiens GN=UROD PE=1 SV=2 - [DCUP_HUMAN]	43.35	19.35	7	7	15	0.284	0.185
P54725	UV excision repair protein RAD23 homolog A OS=Homo sapiens GN=RAD23A PE=1 SV=1 - [RD23A_HUMAN]	61.61	23.97	5	8	19	0.656	0.470
P54727	UV excision repair protein RAD23 homolog B OS=Homo sapiens GN=RAD23B PE=1 SV=1 - [RD23B_HUMAN]	44.91	15.16	5	8	14	0.241	0.204
P21281	V-type proton ATPase subunit B, brain isoform OS=Homo sapiens GN=ATP6V1B2 PE=1 SV=3 - [VATB2_HUMAN]	36.27	16.24	9	9	12	0.141	0.125
Q9Y5K8	V-type proton ATPase subunit D OS=Homo sapiens GN=ATP6V1D PE=1 SV=1 - [VATD_HUMAN]	8.15	9.72	3	3	3	0.203	0.179
O75348	V-type proton ATPase subunit G 1 OS=Homo sapiens GN=ATP6V1G1 PE=1 SV=3 - [VATG1_HUMAN]	14.82	16.95	2	2	4	0.123	0.127
Q9NP79	Vacuolar protein sorting-associated protein VTA1 homolog OS=Homo sapiens GN=VTA1 PE=1 SV=1 - [VTA1_HUMAN]	5.84	2.61	2	2	2	0.311	0.272
P18206	Vinculin OS=Homo sapiens GN=VCL PE=1 SV=4 - [VINC_HUMAN]	147.27	24.34	28	28	48	0.048	0.080
O75083	WD repeat-containing protein 1 OS=Homo sapiens GN=WDR1 PE=1 SV=4 - [WDR1_HUMAN]	44.14	11.06	7	7	14	0.348	0.269
P13010	X-ray repair cross-complementing protein 5 OS=Homo sapiens GN=XRCC5 PE=1 SV=3 - [XRCC5_HUMAN]	11.15	5.60	4	4	4	0.136	0.126

Q7Z2W4	Zinc finger CCCH-type antiviral protein 1 OS=Homo sapiens GN=ZC3HAV1 PE=1 SV=3 - [ZCCHV_HUMAN]	14.15	4.88	4	4	5	0.275	0.110