Supplemental Table 4. Comparison of protein levels between adult and cord RBCs, and adult and cord reticulocytes.

Endogenous adult and cord RBCs and reticulocytes (retic) differentiated *in vitro* from adult peripheral blood and cord CD34$^+$ cells (RBCs and CD34$^+$ were pooled from 16 and 4 individuals respectively) were fractionated, the proteins subjected to trypsin digest and resultant peptides labelled with TMTs for nanoLC-MS/MS based quantitation. Values show the ratio of protein levels between adult and cord cells in membrane (A) and cytosol (B) fractions. All proteins were quantified from at least 2 unique peptides. Coverage; the percentage of the protein sequence covered by identified peptides. PSMs; the total number of identified peptide sequences for the protein. Peptides and unique peptides; the total number of peptide sequences and number of unique peptides identified for that protein. Score; the total score of the protein which is the sum of all peptide Xcorr values above the specified score threshold. Proteome Discoverer software v1.4 was used for analysis.

Supplemental Table 4A

Accession	Description	Score	Coverage	Unique Peptides	Peptides	PSMs	RBC adult/cord	Retic adult/cord
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	1.161	0.868
P62258	14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1 - [1433E_HUMAN]	77.85	38.82	9	12	22	0.708	0.935
Q04917	14-3-3 protein eta OS=Homo sapiens GN=YWHAH PE=1 SV=4 - [1433F_HUMAN]	43.88	29.27	4	8	13	0.807	0.655
P61981	14-3-3 protein gamma OS=Homo sapiens GN=YWHAG PE=1 SV=2 - [1433G_HUMAN]	65.13	40.49	7	11	19	0.803	0.724
P27348	14-3-3 protein theta OS=Homo sapiens GN=YWHAQ PE=1 SV=1 - [1433T_HUMAN]	49.95	30.61	2	7	14	0.648	0.802
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	0.488	0.838
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	1.531	1.280
P62333	26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1 - [PRS10_HUMAN]	69.71	27.76	11	11	22	1.180	0.773
P62191	26S protease regulatory subunit 4 OS=Homo sapiens GN=PSMC1 PE=1 SV=1 - [PRS4_HUMAN]	104.26	30.45	14	15	31	1.302	0.673
P17980	26S protease regulatory subunit 6A OS=Homo sapiens GN=PSMC3 PE=1 SV=3 - [PRS6A_HUMAN]	77.08	35.08	14	14	23	1.125	0.727
P43686	26S protease regulatory subunit 6B OS=Homo sapiens GN=PSMC4 PE=1 SV=2 - [PRS6B_HUMAN]	66.58	27.27	12	12	19	1.183	0.687
P35998	26S protease regulatory subunit 7 OS=Homo sapiens GN=PSMC2 PE=1 SV=3 - [PRS7_HUMAN]	173.63	47.34	20	20	49	1.143	0.680
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	1.130	0.720
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	1.143	0.678
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	0.845	0.692
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	1.039	0.701
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	0.729	0.656
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	1.305	0.727
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	1.166	0.702
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	0.983	0.669
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	0.503	0.886
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	0.850	0.922
P42765	3-ketoacyl-CoA thiolase, mitochondrial OS=Homo sapiens GN=ACAA2 PE=1 SV=2 - [THIM_HUMAN]	28.57	21.41	8	8	9	1.502	0.715
Q96RE3	36 kDa muscleblind protein EXP36 OS=Homo sapiens GN=MBNL1 PE=2 SV=1 - [Q96RE3_HUMAN]	5.74	7.01	2	2	2	0.534	0.725
P49189	4-trimethylaminobutyraldehyde dehydrogenase OS=Homo sapiens GN=ALDH9A1 PE=1 SV=3 - [AL9A1_HUMAN]	12.92	5.87	3	3	4	0.348	0.933
P46783	40S ribosomal protein S10 OS=Homo sapiens GN=RPS10 PE=1 SV=1 - [RS10_HUMAN]	25.40	24.24	4	4	8	0.564	0.553
P62280	40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=1 SV=3 - [RS11_HUMAN]	28.21	21.52	5	5	9	0.494	0.667
P25398	40S ribosomal protein S12 OS=Homo sapiens GN=RPS12 PE=1 SV=3 - [RS12_HUMAN]	16.43	21.97	3	3	5	0.618	0.629
P62277	40S ribosomal protein S13 OS=Homo sapiens GN=RPS13 PE=1 SV=2 - [RS13_HUMAN]	31.70	35.10	7	7	10	0.496	0.504
P62263	40S ribosomal protein S14 OS=Homo sapiens GN=RPS14 PE=1 SV=3 - [RS14_HUMAN]	24.03	23.84	4	4	7	0.426	0.511
P62249	40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=1 SV=2 - [RS16_HUMAN]	23.57	29.45	6	6	8	0.298	0.540
P0CW22	40S ribosomal protein S17-like OS=Homo sapiens GN=RPS17L PE=3 SV=1 - [RS17L_HUMAN]	13.40	8.89	2	2	4	0.663	0.729
P62269	40S ribosomal protein S18 OS=Homo sapiens GN=RPS18 PE=1 SV=3 - [RS18_HUMAN]	27.91	34.87	6	6	9	0.905	0.563
P39019	40S ribosomal protein S19 OS=Homo sapiens GN=RPS19 PE=1 SV=2 - [RS19_HUMAN]	59.36	41.38	8	8	16	0.225	0.520
P15880	40S ribosomal protein S2 OS=Homo sapiens GN=RPS2 PE=1 SV=2 - [RS2_HUMAN]	24.04	23.21	7	7	8	0.388	0.576
P60866	40S ribosomal protein S20 OS=Homo sapiens GN=RPS20 PE=1 SV=1 - [RS20_HUMAN]	25.74	30.25	4	4	9	1.232	0.589
Q8WVC2	40S ribosomal protein S21 OS=Homo sapiens GN=RPS21 PE=2 SV=1 - [Q8WVC2_HUMAN]	11.67	19.75	2	2	4	0.587	0.583
P62266	40S ribosomal protein S23 OS=Homo sapiens GN=RPS23 PE=1 SV=3 - [RS23_HUMAN]	39.86	20.98	3	3	11	1.012	0.633
P62851	40S ribosomal protein S25 OS=Homo sapiens GN=RPS25 PE=1 SV=1 - [RS25_HUMAN]	11.40	15.20	2	2	3	0.333	0.588
P62854	40S ribosomal protein S26 OS=Homo sapiens GN=RPS26 PE=1 SV=3 - [RS26_HUMAN]	22.48	20.87	2	2	7	0.890	0.607
P42677	40S ribosomal protein S27 OS=Homo sapiens GN=RPS27 PE=1 SV=3 - [RS27_HUMAN]	9.31	25.00	2	2	3	0.369	0.604
P62857	40S ribosomal protein S28 OS=Homo sapiens GN=RPS28 PE=1 SV=1 - [RS28_HUMAN]	7.63	30.43	2	2	2		0.459
P23396	40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2 - [RS3_HUMAN]	63.99	45.27	11	11	19	0.377	0.514
P61247	40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2 - [RS3A_HUMAN]	56.35	28.03	9	9	18	0.547	0.531
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	0.747	0.576
P46782	40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=4 - [RS5_HUMAN]	23.05	19.61	4	4	7	0.289	0.637
P62753	40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=1 SV=1 - [RS6_HUMAN]	40.96	20.48	7	7	12	0.253	0.535
P62081	40S ribosomal protein S7 OS=Homo sapiens GN=RPS7 PE=1 SV=1 - [RS7_HUMAN]	28.41	13.40	3	3	8	0.167	0.501
P46781	40S ribosomal protein S9 OS=Homo sapiens GN=RPS9 PE=1 SV=3 - [RS9_HUMAN]	27.73	45.36	9	9	9	0.193	0.525
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	0.158	0.671
P17858	6-phosphofructokinase, liver type OS=Homo sapiens GN=PFKL PE=1 SV=6 - [K6PL_HUMAN]	103.94	22.95	16	17	32	1.581	1.058
P08237	6-phosphofructokinase, muscle type OS=Homo sapiens GN=PFKM PE=1 SV=2 - [K6PF_HUMAN]	54.70	15.51	8	10	17	1.651	1.161
F5H7U0	6-phosphogluconate dehydrogenase, decarboxylating OS=Homo sapiens GN=PGD PE=3 SV=1 - [F5H7U0_HUMAN]	55.22	21.69	11	11	17	0.297	0.675
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	0.699	0.705
P05387	60S acidic ribosomal protein P2 OS=Homo sapiens GN=RPLP2 PE=1 SV=1 - [RLA2_HUMAN]	24.28	24.35	3	3	6	0.386	0.501

P27635	60S ribosomal protein L10 OS=Homo sapiens GN=RPL10 PE=1 SV=4 - [RL10_HUMAN]	5.74	7.94	2	2	2	0.425	0.534
P62906	60S ribosomal protein L10a OS=Homo sapiens GN=RPL10A PE=1 SV=2 - [RL10A_HUMAN]	19.53	27.19	5	5	6	0.632	0.465
P30050	60S ribosomal protein L12 OS=Homo sapiens GN=RPL12 PE=1 SV=1 - [RL12_HUMAN]	23.65	47.88	6	6	7	0.461	0.514
P26373	60S ribosomal protein L13 OS=Homo sapiens GN=RPL13 PE=1 SV=4 - [RL13_HUMAN]	62.25	36.02	9	9	16	0.378	0.404
P40429	60S ribosomal protein L13a OS=Homo sapiens GN=RPL13A PE=1 SV=2 - [RL13A_HUMAN]	30.33	19.70	5	5	10	0.160	0.425
P50914	60S ribosomal protein L14 OS=Homo sapiens GN=RPL14 PE=1 SV=4 - [RL14_HUMAN]	31.97	31.16	5	6	10	0.732	0.476
P18621	60S ribosomal protein L17 OS=Homo sapiens GN=RPL17 PE=1 SV=3 - [RL17_HUMAN]	18.68	19.57	4	4	6	0.596	0.492
Q07020	60S ribosomal protein L18 OS=Homo sapiens GN=RPL18 PE=1 SV=2 - [RL18_HUMAN]	10.49	20.21	3	3	3	0.577	0.538
P84098	60S ribosomal protein L19 OS=Homo sapiens GN=RPL19 PE=1 SV=1 - [RL19_HUMAN]	23.18	16.33	3	4	8	0.726	0.459
P46778	60S ribosomal protein L21 OS=Homo sapiens GN=RPL21 PE=1 SV=2 - [RL21_HUMAN]	8.26	13.75	3	3	3	0.627	0.423
P62829	60S ribosomal protein L23 OS=Homo sapiens GN=RPL23 PE=1 SV=1 - [RL23_HUMAN]	16.74	27.14	3	3	5	0.315	0.480
P62750	60S ribosomal protein L23a OS=Homo sapiens GN=RPL23A PE=1 SV=1 - [RL23A_HUMAN]	47.29	35.26	9	9	15	0.503	0.470
P61254	60S ribosomal protein L26 OS=Homo sapiens GN=RPL26 PE=1 SV=1 - [RL26_HUMAN]	23.62	33.10	6	6	8	0.588	0.455
P61353	60S ribosomal protein L27 OS=Homo sapiens GN=RPL27 PE=1 SV=2 - [RL27_HUMAN]	13.92	23.53	4	4	5	0.302	0.444
P46779	60S ribosomal protein L28 OS=Homo sapiens GN=RPL28 PE=1 SV=3 - [RL28_HUMAN]	19.78	19.71	4	4	5	0.211	0.408
P39023	60S ribosomal protein L3 OS=Homo sapiens GN=RPL3 PE=1 SV=2 - [RL3_HUMAN]	12.09	9.18	4	4	4	0.529	0.629
P62888	60S ribosomal protein L30 OS=Homo sapiens GN=RPL30 PE=1 SV=2 - [RL30_HUMAN]	18.61	44.35	5	5	6	0.494	0.411
P49207	60S ribosomal protein L34 OS=Homo sapiens GN=RPL34 PE=1 SV=3 - [RL34_HUMAN]	19.50	34.19	5	5	6	0.397	0.463
P42766	60S ribosomal protein L35 OS=Homo sapiens GN=RPL35 PE=1 SV=2 - [RL35_HUMAN]	29.35	32.52	5	6	10	0.646	0.430
Q9Y3U8	60S ribosomal protein L36 OS=Homo sapiens GN=RPL36 PE=1 SV=3 - [RL36_HUMAN]	6.69	19.05	2	2	2	0.533	0.517
P83881	60S ribosomal protein L36a OS=Homo sapiens GN=RPL36A PE=1 SV=2 - [RL36A_HUMAN]	15.62	25.47	4	4	5	0.789	0.605
P36578	60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5 - [RL4_HUMAN]	52.32	29.27	13	14	16	0.781	0.431
Q02878	60S ribosomal protein L6 OS=Homo sapiens GN=RPL6 PE=1 SV=3 - [RL6_HUMAN]	27.16	19.79	7	7	9	0.445	0.449
P18124	60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1 - [RL7_HUMAN]	39.74	26.61	7	7	11	0.399	0.454
P62424	60S ribosomal protein L7a OS=Homo sapiens GN=RPL7A PE=1 SV=2 - [RL7A_HUMAN]	41.66	23.31	8	8	12	0.348	0.429
P11021	78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2 - [GRP78_HUMAN]	257.37	46.33	29	32	76	1.198	0.910
D2K8Q1	AAA domain containing 3A protein OS=Homo sapiens GN=ATAD3A PE=2 SV=1 - [D2K8Q1_HUMAN]	40.78	10.92	7	7	12	0.409	0.831
Q2L6I2	ABC50 protein OS=Homo sapiens GN=ABCF1 PE=2 SV=1 - [Q2L6I2_HUMAN]	19.77	3.97	2	4	6	0.207	0.563
P24752	Acetyl-CoA acetyltransferase, mitochondrial OS=Homo sapiens GN=ACAT1 PE=1 SV=1 - [THIL_HUMAN]	48.08	19.67	8	8	16	0.573	0.804
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	0.405	0.560
P61160	Actin-related protein 2 OS=Homo sapiens GN=ACTR2 PE=1 SV=1 - [ARP2_HUMAN]	53.89	9.39	3	4	20	0.559	1.016
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	0.429	0.997
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	0.405	0.963
P60709	Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]	1033.91	61.60	8	19	316	1.440	1.292
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	0.442	0.688
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	1.200	2.089
P13798	Acylamino-acid-releasing enzyme OS=Homo sapiens GN=APEH PE=1 SV=4 - [ACPH_HUMAN]	220.03	25.14	20	20	64	0.867	0.871
F5H737	Adenosylhomocysteinase OS=Homo sapiens GN=AHCY PE=3 SV=1 - [F5H737_HUMAN]	22.09	17.08	7	7	7	0.274	1.037
P00568	Adenylate kinase isoenzyme 1 OS=Homo sapiens GN=AK1 PE=1 SV=3 - [KAD1_HUMAN]	7.07	10.31	2	2	2	0.622	0.717
P30566	Adenylosuccinate lyase OS=Homo sapiens GN=ADSL PE=1 SV=2 - [PUR8_HUMAN]	43.69	19.01	9	9	13	1.087	0.906
F5H6Z3	Adenylyl cyclase-associated protein OS=Homo sapiens GN=CAP1 PE=3 SV=1 - [F5H6Z3_HUMAN]	37.85	15.93	7	7	12	0.439	1.073
Q9HDC9	Adipocyte plasma membrane-associated protein OS=Homo sapiens GN=APMAP PE=1 SV=2 - [APMAP_HUMAN]	10.32	9.13	3	3	3	1.027	0.905
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	0.224	1.178
P05141	ADP/ATP translocase 2 OS=Homo sapiens GN=SLC25A5 PE=1 SV=7 - [ADT2_HUMAN]	77.37	32.89	4	12	25	0.146	0.726
P12236	ADP/ATP translocase 3 OS=Homo sapiens GN=SLC25A6 PE=1 SV=4 - [ADT3_HUMAN]	63.62	29.53	2	10	21	0.950	0.959
Q9Y4W6	AFG3-like protein 2 OS=Homo sapiens GN=AFG3L2 PE=1 SV=2 - [AFG32_HUMAN]	15.16	5.40	5	5	5	0.236	0.695
P49588	Alanyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=AARS PE=1 SV=2 - [SYAC_HUMAN]	57.66	12.60	13	13	18	1.033	0.645
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	1.642	1.128
P01023	Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3 - [A2MG_HUMAN]	40.35	7.80	11	11	13	0.617	1.026
P61163	Alpha-centractin OS=Homo sapiens GN=ACTR1A PE=1 SV=1 - [ACTZ_HUMAN]	118.48	34.04	13	14	40	0.927	0.795
P06733	Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2 - [ENOA_HUMAN]	19.53	13.13	5	5	6	0.313	0.813
Q9NZD4	Alpha-hemoglobin-stabilizing protein OS=Homo sapiens GN=AHSP PE=1 SV=1 - [AHSP_HUMAN]	19.47	30.39	3	3	6	0.380	0.526
P54920	Alpha-soluble NSF attachment protein OS=Homo sapiens GN=NAPA PE=1 SV=3 - [SNAA_HUMAN]	42.96	30.17	7	7	12	0.894	0.917
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	0.365	0.508
A8K6C4	Aminolevulinate, delta-, synthase 2 OS=Homo sapiens GN=ALAS2 PE=2 SV=1 - [A8K6C4_HUMAN]	10.59	5.09	3	3	3	0.091	0.732
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	0.716	0.780

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	0.832	0.881
P63010	AP-2 complex subunit beta OS=Homo sapiens GN=AP2B1 PE=1 SV=1 - [AP2B1_HUMAN]	139.41	22.95	12	24	42	1.013	0.899
Q2M2I8	AP2-associated protein kinase 1 OS=Homo sapiens GN=AAK1 PE=1 SV=3 - [AAK1_HUMAN]	12.50	3.75	3	3	4	0.767	1.169
O95831	Apoptosis-inducing factor 1, mitochondrial OS=Homo sapiens GN=AIFM1 PE=1 SV=1 - [AIFM1_HUMAN]	26.76	9.79	5	6	8	0.374	0.773
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	0.663	0.568
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	0.849	0.888
P05089	Arginase-1 OS=Homo sapiens GN=ARG1 PE=1 SV=2 - [ARGI1_HUMAN]	109.60	33.85	9	10	33	1.009	1.534
P78540	Arginase-2, mitochondrial OS=Homo sapiens GN=ARG2 PE=1 SV=1 - [ARGI2_HUMAN]	25.59	16.38	5	5	7	0.147	0.274
O43776	Asparaginyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=NARS PE=1 SV=1 - [SYNC_HUMAN]	19.32	13.14	6	6	6	0.640	0.598
P00505	Aspartate aminotransferase, mitochondrial OS=Homo sapiens GN=GOT2 PE=1 SV=3 - [AATM_HUMAN]	79.35	26.51	13	13	22	0.297	0.811
P14868	Aspartyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=DARS PE=1 SV=2 - [SYDC_HUMAN]	39.85	14.77	7	8	13	0.957	0.489
B4DL14	ATP synthase gamma chain OS=Homo sapiens GN=ATP5C1 PE=2 SV=1 - [B4DL14_HUMAN]	28.52	27.20	8	8	9	0.849	0.975
P25705	ATP synthase subunit alpha, mitochondrial OS=Homo sapiens GN=ATP5A1 PE=1 SV=1 - [ATPA_HUMAN]	158.19	36.89	20	20	46	0.301	0.837
P06576	ATP synthase subunit beta, mitochondrial OS=Homo sapiens GN=ATP5B PE=1 SV=3 - [ATPB_HUMAN]	136.58	37.24	16	16	40	0.773	0.860
O75947	ATP synthase subunit d, mitochondrial OS=Homo sapiens GN=ATP5H PE=1 SV=3 - [ATP5H_HUMAN]	29.71	37.89	7	7	10	0.114	0.896
P30049	ATP synthase subunit delta, mitochondrial OS=Homo sapiens GN=ATP5D PE=1 SV=2 - [ATPD_HUMAN]	21.87	13.69	2	2	5	0.219	0.838
P48047	ATP synthase subunit O, mitochondrial OS=Homo sapiens GN=ATP5O PE=1 SV=1 - [ATPO_HUMAN]	56.84	53.05	12	12	16	0.296	0.871
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	0.053	0.889
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	0.792	0.844
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	0.518	0.918
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	0.859	1.215
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	1.090	0.724
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	0.183	0.570
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	0.987	0.951
P53396	ATP-citrate synthase OS=Homo sapiens GN=ACLY PE=1 SV=3 - [ACLY_HUMAN]	357.14	33.51	12	37	109	0.685	1.228
Q08211	ATP-dependent RNA helicase A OS=Homo sapiens GN=DHX9 PE=1 SV=4 - [DHX9_HUMAN]	90.30	15.67	20	20	27	0.381	0.819
Q7Z478	ATP-dependent RNA helicase DHX29 OS=Homo sapiens GN=DHX29 PE=1 SV=2 - [DHX29_HUMAN]	5.95	1.39	2	2	2	0.750	0.668
Q9UII2	ATPase inhibitor, mitochondrial OS=Homo sapiens GN=ATPIF1 PE=1 SV=1 - [ATIF1_HUMAN]	88.19	24.53	5	5	24	0.596	1.376
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	0.869	0.726
P02730	Band 3 anion transport protein OS=Homo sapiens GN=SLC4A1 PE=1 SV=3 - [B3AT_HUMAN]	1578.29	32.05	27	27	481	1.750	1.648
P50895	Basal cell adhesion molecule OS=Homo sapiens GN=BCAM PE=1 SV=2 - [BCAM_HUMAN]	63.47	20.06	10	10	18	3.236	1.560
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	0.960	1.444
P35612	Beta-adducin OS=Homo sapiens GN=ADD2 PE=1 SV=3 - [ADDB_HUMAN]	440.34	41.74	10	32	135	1.775	1.413
P07686	Beta-hexosaminidase subunit beta OS=Homo sapiens GN=HEXB PE=1 SV=3 - [HEXB_HUMAN]	17.03	9.53	6	6	6	0.626	1.098
P53004	Biliverdin reductase A OS=Homo sapiens GN=BLVRA PE=1 SV=2 - [BIEA_HUMAN]	6.22	4.73	2	2	2	0.862	0.628
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	0.487	1.186
P07738	Bisphosphoglycerate mutase OS=Homo sapiens GN=BPGM PE=1 SV=2 - [PMGE_HUMAN]	39.66	27.03	6	6	13	0.198	0.859
Q13867	Bleomycin hydrolase OS=Homo sapiens GN=BLMH PE=1 SV=1 - [BLMH_HUMAN]	20.08	13.63	5	5	6	0.628	1.010
Q9NSY1	BMP-2-inducible protein kinase OS=Homo sapiens GN=BMP2K PE=1 SV=2 - [BMP2K_HUMAN]	30.48	9.22	8	8	8	1.179	0.766
P11586	C-1-tetrahydrofolate synthase, cytoplasmic OS=Homo sapiens GN=MTHFD1 PE=1 SV=3 - [C1TC_HUMAN]	299.99	32.19	33	33	91	1.538	1.496
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	1.503	1.149
P27708	CAD protein OS=Homo sapiens GN=CAD PE=1 SV=3 - [PYR1_HUMAN]	18.19	2.25	5	5	5	0.751	0.621
P62158	Calmodulin OS=Homo sapiens GN=CALM1 PE=1 SV=2 - [CALM_HUMAN]	45.04	38.26	7	7	14	0.940	1.040
P27824	Calnexin OS=Homo sapiens GN=CANX PE=1 SV=2 - [CALX_HUMAN]	75.29	21.11	15	15	23	0.711	0.908
P04632	Calpain small subunit 1 OS=Homo sapiens GN=CAPNS1 PE=1 SV=1 - [CPNS1_HUMAN]	5.48	4.85	2	2	2	0.379	0.816
P07384	Calpain-1 catalytic subunit OS=Homo sapiens GN=CAPN1 PE=1 SV=1 - [CAN1_HUMAN]	19.83	8.96	6	6	6	0.490	0.986
O15484	Calpain-5 OS=Homo sapiens GN=CAPN5 PE=1 SV=2 - [CAN5_HUMAN]	13.03	4.84	3	3	4	3.853	2.298
P27797	Calreticulin OS=Homo sapiens GN=CALR PE=1 SV=1 - [CALR_HUMAN]	193.71	42.93	19	19	60	1.052	1.157
O43852	Calumenin OS=Homo sapiens GN=CALU PE=1 SV=2 - [CALU_HUMAN]	14.08	9.52	3	3	5	1.038	1.274
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	0.931	1.407
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	1.027	1.398
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	0.924	0.890
P00918	Carbonic anhydrase 2 OS=Homo sapiens GN=CA2 PE=1 SV=2 - [CAH2_HUMAN]	10.09	11.92	3	3	3	4.133	1.201
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	1.814	0.865
P48729	Casein kinase I isoform alpha OS=Homo sapiens GN=CSNK1A1 PE=1 SV=2 - [KC1A_HUMAN]	6.16	8.90	2	2	2	1.108	1.642
P67870	Casein kinase II subunit beta OS=Homo sapiens GN=CSNK2B PE=1 SV=1 - [CSK2B_HUMAN]	13.81	15.81	3	3	4	0.788	0.812

P04040	Catalase OS=Homo sapiens GN=CAT PE=1 SV=3 - [CATA_HUMAN]	248.04	47.63	25	25	77	0.426	1.581
P07339	Cathepsin D OS=Homo sapiens GN=CTSD PE=1 SV=1 - [CATD_HUMAN]	37.38	15.29	6	6	12	0.600	1.052
P14091	Cathepsin E OS=Homo sapiens GN=CTSE PE=1 SV=2 - [CATE_HUMAN]	5.84	3.99	2	2	2	2.178	0.756
Q9Y5K6	CD2-associated protein OS=Homo sapiens GN=CD2AP PE=1 SV=1 - [CD2AP_HUMAN]	60.97	22.54	13	13	18	0.730	0.944
B6EAT9	CD44 OS=Homo sapiens PE=2 SV=1 - [B6EAT9_HUMAN]	58.48	18.82	6	6	17	1.274	0.771
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	1.752	1.394
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	0.652	1.068
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	0.813	0.857
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	0.831	1.041
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	0.489	0.569
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	0.819	0.534
B4DPJ6	cDNA FLJ53635, highly similar to Homo sapiens tumor protein D52-like 2 (TPD52L2), transcript variant 6, mRNA OS=Homo sapiens PE=2 SV=1 - [B4DPJ6_HUMAN]	7.99	11.04	2	2	2	0.285	0.636
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	0.363	0.469
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	1.114	1.200
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	0.798	0.998
Q9NV96	Cell cycle control protein 50A OS=Homo sapiens GN=TMEM30A PE=1 SV=1 - [CC50A_HUMAN]	6.09	7.48	2	2	2	1.142	0.970
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	1.356	1.709
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	0.611	0.893
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	0.689	0.960
Q7LBR1	Charged multivesicular body protein 1b OS=Homo sapiens GN=CHMP1B PE=1 SV=1 - [CHM1B_HUMAN]	11.23	15.58	4	4	4	0.707	0.915
O43633	Charged multivesicular body protein 2a OS=Homo sapiens GN=CHMP2A PE=1 SV=1 - [CHM2A_HUMAN]	22.99	22.97	6	6	6	0.864	0.933
Q96FZ7	Charged multivesicular body protein 6 OS=Homo sapiens GN=CHMP6 PE=1 SV=3 - [CHMP6_HUMAN]	9.68	13.43	3	3	3	1.168	1.449
Q9BWS9	Chitinase domain-containing protein 1 OS=Homo sapiens GN=CHID1 PE=1 SV=1 - [CHID1_HUMAN]	12.20	6.62	3	3	4	1.008	1.052
B4DJV2	Citrate synthase OS=Homo sapiens GN=CS PE=2 SV=1 - [B4DJV2_HUMAN]	57.93	20.09	9	9	18	0.654	0.861
Q00610	Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC PE=1 SV=5 - [CLH1_HUMAN]	479.20	30.75	50	50	141	0.876	0.795
P09497	Clathrin light chain B OS=Homo sapiens GN=CLTB PE=1 SV=1 - [CLCB_HUMAN]	27.27	22.27	7	7	9	1.184	0.863
P53621	Coatomer subunit alpha OS=Homo sapiens GN=COPA PE=1 SV=2 - [COPA_HUMAN]	14.61	3.10	4	4	5	0.524	0.796
P53618	Coatomer subunit beta OS=Homo sapiens GN=COPB1 PE=1 SV=3 - [COPB_HUMAN]	6.72	2.83	2	2	2	0.409	0.769
P48444	Coatomer subunit delta OS=Homo sapiens GN=ARCN1 PE=1 SV=1 - [COPD_HUMAN]	20.50	13.11	7	7	7	0.563	0.748
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	1.420	1.265
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	0.453	0.792
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	1.622	0.926
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	0.506	1.250
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	0.299	0.781
Q9BPX3	Condensin complex subunit 3 OS=Homo sapiens GN=NCAPG PE=1 SV=1 - [CND3_HUMAN]	6.54	1.58	2	2	2	0.291	0.465
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	0.748	1.015
Q13098	COP9 signalosome complex subunit 1 OS=Homo sapiens GN=GPS1 PE=1 SV=4 - [CSN1_HUMAN]	27.33	15.27	8	8	9	0.729	1.059
P61201	COP9 signalosome complex subunit 2 OS=Homo sapiens GN=COPS2 PE=1 SV=1 - [CSN2_HUMAN]	22.42	12.19	7	7	8	0.722	1.042
Q9BT78	COP9 signalosome complex subunit 4 OS=Homo sapiens GN=COPS4 PE=1 SV=1 - [CSN4_HUMAN]	36.26	25.37	9	9	11	0.792	0.968
Q92905	COP9 signalosome complex subunit 5 OS=Homo sapiens GN=COPS5 PE=1 SV=4 - [CSN5_HUMAN]	31.04	19.76	6	6	10	0.575	1.046
Q9H9Q2	COP9 signalosome complex subunit 7b OS=Homo sapiens GN=COPS7B PE=1 SV=1 - [CSN7B_HUMAN]	10.27	11.74	3	3	3	1.249	1.076
Q04656	Copper-transporting ATPase 1 OS=Homo sapiens GN=ATP7A PE=1 SV=3 - [ATP7A_HUMAN]	34.29	5.33	8	8	11	1.631	1.065
P36551	Coproporphyrinogen-III oxidase, mitochondrial OS=Homo sapiens GN=CPOX PE=1 SV=3 - [HEM6_HUMAN]	132.50	39.21	16	16	43	0.799	0.973
Q9ULV4	Coronin-1C OS=Homo sapiens GN=CORO1C PE=1 SV=1 - [COR1C_HUMAN]	70.45	22.78	14	14	21	0.581	0.763
Q9NRF8	CTP synthase 2 OS=Homo sapiens GN=CTPS2 PE=1 SV=1 - [PYRG2_HUMAN]	6.39	3.58	2	2	2	0.745	0.731
Q5T2B5	Cullin 2 OS=Homo sapiens GN=CUL2 PE=2 SV=1 - [Q5T2B5_HUMAN]	9.58	3.54	3	3	3	0.406	0.968
Q13618	Cullin-3 OS=Homo sapiens GN=CUL3 PE=1 SV=2 - [CUL3_HUMAN]	52.68	16.15	13	13	15	0.667	1.010
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	0.561	0.936
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	0.267	0.696
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	0.818	0.887
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	0.474	0.791
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	0.196	1.053
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	0.601	0.791
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	0.842	0.930
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	0.293	0.760
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	0.281	0.787

P09669	Cytochrome c oxidase subunit 6C OS=Homo sapiens GN=COX6C PE=1 SV=2 - [COX6C_HUMAN]	20.71	12.00	2	2	5	0.500	0.819
P08574	Cytochrome c1, heme protein, mitochondrial OS=Homo sapiens GN=CYC1 PE=1 SV=3 - [CY1_HUMAN]	6.10	6.15	2	2	2	0.229	1.000
Q8IUI8	Cytokine receptor-like factor 3 OS=Homo sapiens GN=CRLF3 PE=1 SV=2 - [CRLF3_HUMAN]	6.88	4.30	2	2	2	0.587	1.058
Q14008	Cytoskeleton-associated protein 5 OS=Homo sapiens GN=CKAP5 PE=1 SV=3 - [CKAP5_HUMAN]	18.22	3.00	5	5	5	1.146	0.640
P28838	Cytosol aminopeptidase OS=Homo sapiens GN=LAP3 PE=1 SV=3 - [AMPL_HUMAN]	17.75	10.21	5	5	5	0.949	0.884
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	0.454	0.863
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	1.400	1.298
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	0.929	0.988
B7Z3I9	Delta-aminolevulinic acid dehydratase OS=Homo sapiens PE=2 SV=1 - [B7Z3I9_HUMAN]	81.72	28.12	8	8	25	0.724	1.053
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	0.512	0.859
Q08495	Dematin OS=Homo sapiens GN=EPB49 PE=1 SV=3 - [DEMA_HUMAN]	551.59	54.57	20	20	170	1.490	1.513
Q96JH7	Deubiquitinating protein VCIP135 OS=Homo sapiens GN=VCPIP1 PE=1 SV=2 - [VCIP1_HUMAN]	6.52	1.80	2	2	2	0.583	0.644
F5H4I0	Dihydrolipoyl dehydrogenase OS=Homo sapiens GN=DLD PE=3 SV=1 - [F5H4I0_HUMAN]	31.95	14.60	6	6	10	0.460	0.798
P36957	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, OS=Homo sapiens GN=DLST PE=1 SV=4 - [ODO2_HUMAN]	55.30	22.52	10	10	16	0.360	0.883
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	1.457	1.485
Q16531	DNA damage-binding protein 1 OS=Homo sapiens GN=DDB1 PE=1 SV=1 - [DDB1_HUMAN]	63.63	17.19	18	18	21	0.661	0.807
Q92878	DNA repair protein RAD50 OS=Homo sapiens GN=RAD50 PE=1 SV=1 - [RAD50_HUMAN]	6.90	1.14	2	2	2	1.283	0.840
P16989	DNA-binding protein A OS=Homo sapiens GN=CSDA PE=1 SV=4 - [DBPA_HUMAN]	19.82	15.32	2	4	6	1.073	0.622
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	0.836	1.117
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	0.866	1.012
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	1.142	1.181
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	0.569	0.731
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	0.926	1.306
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	0.981	1.045
O60762	Dolichol-phosphate mannosyltransferase OS=Homo sapiens GN=DPM1 PE=1 SV=1 - [DPM1_HUMAN]	5.91	5.77	2	2	2	0.654	1.202
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	0.895	0.675
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	0.805	0.851
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	0.635	0.796
Q5T1I6	Dynactin 3 (P22) (Fragment) OS=Homo sapiens GN=DCTN3 PE=2 SV=1 - [Q5T1I6_HUMAN]	17.18	16.15	3	3	5	1.140	0.817
Q13561	Dynactin subunit 2 OS=Homo sapiens GN=DCTN2 PE=1 SV=4 - [DCTN2_HUMAN]	80.74	39.90	14	14	23	0.966	0.819
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	0.333	0.836
Q5XPI4	E3 ubiquitin-protein ligase RNF123 OS=Homo sapiens GN=RNF123 PE=1 SV=1 - [RN123_HUMAN]	52.11	7.84	11	11	17	0.404	0.929
Q5T4S7	E3 ubiquitin-protein ligase UBR4 OS=Homo sapiens GN=UBR4 PE=1 SV=1 - [UBR4_HUMAN]	244.45	11.02	56	56	74	0.976	0.826
Q14258	E3 ubiquitin/ISG15 ligase TRIM25 OS=Homo sapiens GN=TRIM25 PE=1 SV=2 - [TRI25_HUMAN]	17.68	8.89	5	5	5	1.082	0.641
Q15075	Early endosome antigen 1 OS=Homo sapiens GN=EEA1 PE=1 SV=2 - [EEA1_HUMAN]	9.49	2.91	2	3	3	1.114	0.844
Q93070	Ecto-ADP-ribosyltransferase 4 OS=Homo sapiens GN=ART4 PE=2 SV=2 - [NAR4_HUMAN]	9.46	7.96	3	3	3	1.442	1.331
Q4VBZ6	EEF1D protein OS=Homo sapiens GN=EEF1D PE=1 SV=1 - [Q4VBZ6_HUMAN]	47.62	25.68	6	7	15	0.810	0.667
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	1.167	0.723
Q9H4M9	EH domain-containing protein 1 OS=Homo sapiens GN=EHD1 PE=1 SV=2 - [EHD1_HUMAN]	70.58	27.72	16	16	22	1.155	0.713
P38117	Electron transfer flavoprotein subunit beta OS=Homo sapiens GN=ETFB PE=1 SV=3 - [ETFB_HUMAN]	54.60	32.94	9	9	16	0.634	0.780
P68104	Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 - [EF1A1_HUMAN]	183.28	32.47	16	16	58	0.366	0.619
P24534	Elongation factor 1-beta OS=Homo sapiens GN=EEF1B2 PE=1 SV=3 - [EF1B_HUMAN]	16.49	10.22	2	3	5	0.175	0.474
P26641	Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3 - [EF1G_HUMAN]	94.60	21.51	14	14	29	0.735	0.655
P13639	Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 - [EF2_HUMAN]	87.71	17.83	16	17	27	0.531	0.481
P49411	Elongation factor Tu, mitochondrial OS=Homo sapiens GN=TUFM PE=1 SV=2 - [EFTU_HUMAN]	72.10	32.52	13	13	20	0.623	0.711
P50402	Emerin OS=Homo sapiens GN=EMD PE=1 SV=1 - [EMD_HUMAN]	18.19	11.81	3	3	5	1.060	0.967
O94919	Endonuclease domain-containing 1 protein OS=Homo sapiens GN=ENDOD1 PE=1 SV=2 - [ENDD1_HUMAN]	44.87	16.20	7	7	14	1.528	1.533
P30040	Endoplasmic reticulum resident protein 29 OS=Homo sapiens GN=ERP29 PE=1 SV=4 - [ERP29_HUMAN]	45.80	29.89	8	8	14	1.108	1.168
Q9BS26	Endoplasmic reticulum resident protein 44 OS=Homo sapiens GN=ERP44 PE=1 SV=1 - [ERP44_HUMAN]	44.63	19.21	8	8	14	1.182	1.139
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	0.848	1.240
P14625	Endoplasmin OS=Homo sapiens GN=HSP90B1 PE=1 SV=1 - [ENPL_HUMAN]	182.71	29.89	28	29	55	1.052	1.161
O60869	Endothelial differentiation-related factor 1 OS=Homo sapiens GN=EDF1 PE=1 SV=1 - [EDF1_HUMAN]	10.40	11.49	2	2	3	0.758	0.657
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	0.446	0.886
Q4KKX0	EPB42 protein OS=Homo sapiens GN=EPB42 PE=2 SV=1 - [Q4KKX0_HUMAN]	798.90	41.20	31	31	247	1.693	1.488
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	0.840	0.810

P07099	Epoxide hydrolase 1 OS=Homo sapiens GN=EPHX1 PE=1 SV=1 - [HYEP_HUMAN]	6.02	3.96	2	2	2	1.241	1.095
A2RRF3	EPS15L1 protein OS=Homo sapiens GN=EPS15L1 PE=2 SV=1 - [A2RRF3_HUMAN]	13.87	4.77	4	4	4	0.901	0.817
Q9Y6I3	Epsin-1 OS=Homo sapiens GN=EPN1 PE=1 SV=2 - [EPN1_HUMAN]	8.66	4.51	3	3	3	1.010	1.269
Q99808	Equilibrative nucleoside transporter 1 OS=Homo sapiens GN=SLC29A1 PE=1 SV=3 - [S29A1_HUMAN]	96.18	15.35	9	9	26	0.699	0.658
O75477	Erlin-1 OS=Homo sapiens GN=ERLIN1 PE=1 SV=1 - [ERLN1_HUMAN]	22.55	17.92	3	6	7	0.825	1.005
Q96PL5	Erythroid membrane-associated protein OS=Homo sapiens GN=ERMAP PE=1 SV=1 - [ERMAP_HUMAN]	89.80	21.47	10	10	29	1.397	1.128
Q53GQ0	Estradiol 17-beta-dehydrogenase 12 OS=Homo sapiens GN=HSD17B12 PE=1 SV=2 - [DHB12_HUMAN]	24.12	15.06	4	4	6	0.900	1.132
P60842	Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=1 SV=1 - [IF4A1_HUMAN]	38.24	20.69	3	8	11	0.757	0.421
P38919	Eukaryotic initiation factor 4A-III OS=Homo sapiens GN=EIF4A3 PE=1 SV=4 - [IF4A3_HUMAN]	16.15	12.41	2	4	5	0.177	0.677
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	0.393	0.730
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	0.345	0.666
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	0.328	0.699
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	0.267	0.747
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	0.853	0.569
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	0.663	0.574
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	0.641	0.533
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	0.189	0.478
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	0.360	0.527
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	0.289	0.684
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	0.253	0.514
P06730	Eukaryotic translation initiation factor 4E OS=Homo sapiens GN=EIF4E PE=1 SV=2 - [IF4E_HUMAN]	16.61	18.43	4	4	5	0.491	0.732
P55010	Eukaryotic translation initiation factor 5 OS=Homo sapiens GN=EIF5 PE=1 SV=2 - [IF5_HUMAN]	19.43	12.76	5	5	6	0.301	0.527
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	0.202	0.519
O60841	Eukaryotic translation initiation factor 5B OS=Homo sapiens GN=EIF5B PE=1 SV=4 - [IF2P_HUMAN]	9.63	1.80	2	3	3	0.271	0.485
Q9BSJ8	Extended synaptotagmin-1 OS=Homo sapiens GN=ESYT1 PE=1 SV=1 - [ESYT1_HUMAN]	30.75	7.61	8	8	9	1.120	1.162
A0FGR8	Extended synaptotagmin-2 OS=Homo sapiens GN=ESYT2 PE=1 SV=1 - [ESYT2_HUMAN]	16.92	4.45	4	4	5	1.161	1.040
P15311	Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4 - [EZRI_HUMAN]	252.46	38.57	18	31	78	0.791	1.309
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	0.591	0.909
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	1.503	0.637
P49327	Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3 - [FAS_HUMAN]	299.76	23.62	54	54	92	0.394	1.189
Q86UX7	Fermitin family homolog 3 OS=Homo sapiens GN=FERMT3 PE=1 SV=1 - [URP2_HUMAN]	24.14	9.00	5	5	7	0.376	0.642
P02794	Ferritin heavy chain OS=Homo sapiens GN=FTH1 PE=1 SV=2 - [FRIH_HUMAN]	36.28	20.77	4	4	12	0.682	1.354
P02792	Ferritin light chain OS=Homo sapiens GN=FTL PE=1 SV=2 - [FRIL_HUMAN]	54.19	39.43	7	7	17	0.327	1.191
P22830	Ferrochelatase, mitochondrial OS=Homo sapiens GN=FECH PE=1 SV=2 - [HEMH_HUMAN]	69.22	29.08	10	10	23	0.818	0.692
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	0.726	1.075
Q5T1M5	FK506-binding protein 15 OS=Homo sapiens GN=FKBP15 PE=1 SV=2 - [FKB15_HUMAN]	15.96	4.18	4	4	4	0.844	0.833
P30043	Flavin reductase OS=Homo sapiens GN=BLVRB PE=1 SV=3 - [BLVRB_HUMAN]	42.80	22.33	4	4	12	0.952	0.745
O75955	Flotillin-1 OS=Homo sapiens GN=FLOT1 PE=1 SV=3 - [FLOT1_HUMAN]	342.48	70.49	29	29	105	1.491	1.184
Q14254	Flotillin-2 OS=Homo sapiens GN=FLOT2 PE=1 SV=2 - [FLOT2_HUMAN]	366.37	60.98	28	28	106	1.454	1.269
Q9H479	Fructosamine-3-kinase OS=Homo sapiens GN=FN3K PE=1 SV=1 - [FN3K_HUMAN]	25.24	21.36	6	6	7	1.133	1.376
P04075	Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2 - [ALDOA_HUMAN]	683.98	54.95	17	21	208	1.755	1.168
B7Z1N6	Fructose-bisphosphate aldolase OS=Homo sapiens GN=ALDOC PE=2 SV=1 - [B7Z1N6_HUMAN]	110.88	18.15	3	7	35	4.481	1.222
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	1.190	0.751
P07954	Fumarate hydratase, mitochondrial OS=Homo sapiens GN=FH PE=1 SV=3 - [FUMH_HUMAN]	49.87	15.88	8	8	15	0.514	1.110
Q9BWH2	FUN14 domain-containing protein 2 OS=Homo sapiens GN=FUNDC2 PE=1 SV=2 - [FUND2_HUMAN]	7.55	11.64	2	2	2	0.448	0.690
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	1.038	1.110
P17931	Galectin-3 OS=Homo sapiens GN=LGALS3 PE=1 SV=5 - [LEG3_HUMAN]	116.93	39.20	10	11	39	1.776	0.863
Q9UEY8	Gamma-adducin OS=Homo sapiens GN=ADD3 PE=1 SV=1 - [ADDG_HUMAN]	49.34	13.88	9	9	15	0.475	1.022
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	0.459	1.271
Q92820	Gamma-glutamyl hydrolase OS=Homo sapiens GN=GGH PE=1 SV=2 - [GGH_HUMAN]	5.97	6.29	2	2	2	0.521	1.122
Q99747	Gamma-soluble NSF attachment protein OS=Homo sapiens GN=NAPG PE=1 SV=1 - [SNAG_HUMAN]	7.67	8.65	2	3	3	0.727	1.010
P15104	Glutamine synthetase OS=Homo sapiens GN=GLUL PE=1 SV=4 - [GLNA_HUMAN]	8.83	5.63	3	3	3	0.398	0.935
Q86SX6	Glutaredoxin-related protein 5, mitochondrial OS=Homo sapiens GN=GLRX5 PE=1 SV=2 - [GLRX5_HUMAN]	25.18	20.38	4	4	9	0.414	0.561
Q92947	Glutaryl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=GCDH PE=1 SV=1 - [GCDH_HUMAN]	7.57	4.34	2	2	2	0.235	0.846
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	0.675	1.064
P07203	Glutathione peroxidase 1 OS=Homo sapiens GN=GPX1 PE=1 SV=4 - [GPX1_HUMAN]	13.17	14.29	3	3	4	0.633	0.736

P78417	Glutathione S-transferase omega-1 OS=Homo sapiens GN=GSTO1 PE=1 SV=2 - [GSTO1_HUMAN]	15.88	13.69	3	3	5	0.627	0.708
P04406	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3 - [G3P_HUMAN]	1215.74	68.06	10	22	420	1.162	1.274
B8Q185	Glycophorin A MNS blood group OS=Homo sapiens GN=GYPA PE=4 SV=1 - [B8Q185_HUMAN]	48.01	45.30	3	3	15	1.333	1.847
P04921	Glycophorin-C OS=Homo sapiens GN=GYPC PE=1 SV=1 - [GLPC_HUMAN]	170.74	29.69	4	4	52	1.646	1.432
P41250	Glycyl-tRNA synthetase OS=Homo sapiens GN=GARS PE=1 SV=3 - [SYG_HUMAN]	10.61	4.19	3	3	3	0.689	0.439
P36959	GMP reductase 1 OS=Homo sapiens GN=GMPR PE=1 SV=1 - [GMPR1_HUMAN]	25.91	14.49	4	4	7	0.421	1.170
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	1.269	1.480
P28799	Granulins OS=Homo sapiens GN=GRN PE=1 SV=2 - [GRN_HUMAN]	9.72	7.08	3	3	3	1.628	0.907
B4DWV5	GrpE protein homolog OS=Homo sapiens GN=GRPEL1 PE=2 SV=1 - [B4DWV5_HUMAN]	14.16	23.98	4	4	4	1.060	0.908
P62826	GTP-binding nuclear protein Ran OS=Homo sapiens GN=RAN PE=1 SV=3 - [RAN_HUMAN]	17.01	20.83	4	4	5	0.219	0.651
O00178	GTP-binding protein 1 OS=Homo sapiens GN=GTPBP1 PE=1 SV=3 - [GTPB1_HUMAN]	13.56	2.99	2	2	4	0.750	0.875
Q9BX10	GTP-binding protein 2 OS=Homo sapiens GN=GTPBP2 PE=2 SV=1 - [GTPB2_HUMAN]	5.70	3.65	2	2	2	0.472	0.464
P01116	GTPase KRas OS=Homo sapiens GN=KRAS PE=1 SV=1 - [RASK_HUMAN]	50.33	29.10	3	5	14	1.543	1.648
P01111	GTPase NRas OS=Homo sapiens GN=NRAS PE=1 SV=1 - [RASN_HUMAN]	35.83	31.22	3	5	10	1.358	1.288
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	0.880	0.754
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	1.108	1.382
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	1.239	1.295
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	1.147	1.381
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	1.127	1.654
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	0.980	1.419
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	0.594	1.285
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	2.033	1.626
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	1.222	1.430
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	1.265	0.995
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	1.283	1.521
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	0.346	0.437
B2RDM2	HCG1811539, isoform CRA_b OS=Homo sapiens GN=TXNDC5 PE=2 SV=1 - [B2RDM2_HUMAN]	30.48	20.37	5	6	9	1.671	1.356
A2A3U5	HCG20471, isoform CRA_d OS=Homo sapiens GN=OPRS1 PE=2 SV=1 - [A2A3U5_HUMAN]	5.28	7.29	2	2	2	0.553	0.868
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	0.263	0.837
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	0.921	0.625
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	0.720	0.977
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	0.716	0.779
P04792	Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2 - [HSPB1_HUMAN]	44.61	31.71	6	6	12	0.463	0.741
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	0.555	0.628
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	0.808	0.554
P09601	Heme oxygenase 1 OS=Homo sapiens GN=HMOX1 PE=1 SV=1 - [HMOX1_HUMAN]	18.66	10.42	3	3	6	1.242	0.389
Q9BXL5	Hemogen OS=Homo sapiens GN=HEMGN PE=1 SV=1 - [HEMGN_HUMAN]	50.22	17.77	9	9	16	0.279	0.362
P69905	Hemoglobin subunit alpha OS=Homo sapiens GN=HBA1 PE=1 SV=2 - [HBA_HUMAN]	351.10	67.61	6	7	100	1.189	0.744
P68871	Hemoglobin subunit beta OS=Homo sapiens GN=HBB PE=1 SV=2 - [HBB_HUMAN]	470.79	85.03	5	12	130	6.149	1.647
P02042	Hemoglobin subunit delta OS=Homo sapiens GN=HBD PE=1 SV=2 - [HBD_HUMAN]	240.15	76.19	4	11	66	17.337	2.459
P69892	Hemoglobin subunit gamma-2 OS=Homo sapiens GN=HBG2 PE=1 SV=2 - [HBG2_HUMAN]	601.36	77.55	3	12	161	0.120	0.085
Q6B0K9	Hemoglobin subunit mu OS=Homo sapiens GN=HBM PE=2 SV=1 - [HBM_HUMAN]	16.35	17.73	2	2	5	1.166	0.504
P02008	Hemoglobin subunit zeta OS=Homo sapiens GN=HBZ PE=1 SV=2 - [HBAZ_HUMAN]	67.95	36.62	4	5	23	0.330	0.146
D9YZU8	Hemoglobin, gamma A OS=Homo sapiens GN=HBG1 PE=3 SV=1 - [D9YZU8_HUMAN]	454.36	77.55	3	12	128	0.342	0.287
P51858	Hepatoma-derived growth factor OS=Homo sapiens GN=HDGF PE=1 SV=1 - [HDGF_HUMAN]	27.27	27.50	5	5	8	0.025	0.683
P09651	Heterogeneous nuclear ribonucleoprotein A1 OS=Homo sapiens GN=HNRNPA1 PE=1 SV=5 - [ROA1_HUMAN]	110.65	17.20	4	7	34	0.600	0.539
P31942	Heterogeneous nuclear ribonucleoprotein H3 OS=Homo sapiens GN=HNRNPH3 PE=1 SV=2 - [HNRH3_HUMAN]	8.09	8.67	2	2	2	0.227	0.611
Q5T6W5	Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK PE=2 SV=1 - [Q5T6W5_HUMAN]	75.89	27.34	11	11	21	0.351	0.525
P14866	Heterogeneous nuclear ribonucleoprotein L OS=Homo sapiens GN=HNRNPL PE=1 SV=2 - [HNRPL_HUMAN]	17.00	5.09	3	3	5	1.232	0.486
P52272	Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens GN=HNRNPM PE=1 SV=3 - [HNRPM_HUMAN]	39.15	11.51	9	9	12	0.424	0.420
P22626	Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens GN=HNRNPA2B1 PE=1 SV=2 - [ROA2_HUMAN]	131.98	34.56	10	13	41	0.672	0.576
P26583	High mobility group protein B2 OS=Homo sapiens GN=HMGB2 PE=1 SV=2 - [HMGB2_HUMAN]	8.19	7.66	2	2	3	0.118	0.161
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	0.873	0.875
P16402	Histone H1.3 OS=Homo sapiens GN=HIST1H1D PE=1 SV=2 - [H13_HUMAN]	86.09	36.20	4	11	27	0.634	0.043
P10412	Histone H1.4 OS=Homo sapiens GN=HIST1H1E PE=1 SV=2 - [H14_HUMAN]	76.32	37.44	2	10	24	0.350	0.069
P16401	Histone H1.5 OS=Homo sapiens GN=HIST1H1B PE=1 SV=3 - [H15_HUMAN]	72.68	35.40	7	11	24	0.149	0.037

O60814	Histone H2B type 1-K OS=Homo sapiens GN=HIST1H2BK PE=1 SV=3 - [H2B1K_HUMAN]	58.92	45.24	7	7	21	0.373	0.046
P68431	Histone H3.1 OS=Homo sapiens GN=HIST1H3A PE=1 SV=2 - [H31_HUMAN]	34.78	28.68	6	6	12	0.581	0.069
P62805	Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2 - [H4_HUMAN]	99.96	50.49	5	5	30	0.643	0.065
B0UX83	HLA-B associated transcript 3 OS=Homo sapiens GN=BAT3 PE=4 SV=1 - [B0UX83_HUMAN]	14.06	4.09	4	4	4	0.723	0.780
P51610	Host cell factor 1 OS=Homo sapiens GN=HCFC1 PE=1 SV=2 - [HCFC1_HUMAN]	7.20	0.98	2	2	2	0.827	1.020
P50502	Hsc70-interacting protein OS=Homo sapiens GN=ST13 PE=1 SV=2 - [F10A1_HUMAN]	75.99	27.64	11	11	24	0.467	0.903
Q16543	Hsp90 co-chaperone Cdc37 OS=Homo sapiens GN=CDC37 PE=1 SV=1 - [CDC37_HUMAN]	12.56	8.99	4	4	4	0.362	0.562
Q16836	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial OS=Homo sapiens GN=HADH PE=1 SV=3 - [HCDH_HUMAN]	22.67	16.88	6	6	7	0.197	0.814
Q16775	Hydroxyacylglutathione hydrolase, mitochondrial OS=Homo sapiens GN=HAGH PE=1 SV=2 - [GLO2_HUMAN]	40.41	18.51	5	5	14	1.295	0.870
Q6YN16	Hydroxysteroid dehydrogenase-like protein 2 OS=Homo sapiens GN=HSDL2 PE=1 SV=1 - [HSDL2_HUMAN]	12.63	6.94	3	3	4	0.846	0.746
Q9Y4L1	Hypoxia up-regulated protein 1 OS=Homo sapiens GN=HYOU1 PE=1 SV=1 - [HYOU1_HUMAN]	79.46	15.02	15	15	23	1.060	1.049
Q14974	Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2 - [IMB1_HUMAN]	104.21	15.41	14	14	30	0.475	0.816
O00410	Importin-5 OS=Homo sapiens GN=IPO5 PE=1 SV=4 - [IPO5_HUMAN]	42.67	6.56	7	7	12	0.539	0.903
O95373	Importin-7 OS=Homo sapiens GN=IPO7 PE=1 SV=1 - [IPO7_HUMAN]	33.02	6.74	6	6	9	1.059	0.984
P05556	Integrin beta-1 OS=Homo sapiens GN=ITGB1 PE=1 SV=2 - [ITB1_HUMAN]	24.57	10.40	7	7	7	0.861	0.663
Q14773	Intercellular adhesion molecule 4 OS=Homo sapiens GN=ICAM4 PE=2 SV=1 - [ICAM4_HUMAN]	18.22	19.93	5	5	6	0.510	0.832
Q12905	Interleukin enhancer-binding factor 2 OS=Homo sapiens GN=ILF2 PE=1 SV=2 - [ILF2_HUMAN]	12.12	9.49	3	3	3	0.464	0.521
P48735	Isocitrate dehydrogenase [NADP], mitochondrial OS=Homo sapiens GN=IDH2 PE=1 SV=2 - [IDHP_HUMAN]	115.62	34.73	16	16	38	0.534	1.057
P53990	IST1 homolog OS=Homo sapiens GN=KIAA0174 PE=1 SV=1 - [IST1_HUMAN]	16.50	11.54	5	5	5	0.673	1.002
Q9Y624	Junctional adhesion molecule A OS=Homo sapiens GN=F11R PE=1 SV=1 - [JAM1_HUMAN]	18.54	16.05	6	6	6	2.278	1.228
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	0.980	1.036
P23276	Kell blood group glycoprotein OS=Homo sapiens GN=KEL PE=1 SV=2 - [KELL_HUMAN]	53.63	10.52	8	8	18	1.594	1.121
P13645	Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6 - [K1C10_HUMAN]	20.74	8.56	4	5	6	0.463	0.603
P35527	Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3 - [K1C9_HUMAN]	13.05	6.90	2	3	3	0.193	0.327
P04264	Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6 - [K2C1_HUMAN]	36.47	14.91	11	11	12	0.410	0.430
Q17RZ5	Kinectin 1 (Kinesin receptor) OS=Homo sapiens GN=KTN1 PE=2 SV=1 - [Q17RZ5_HUMAN]	9.05	2.53	3	3	3	0.070	0.467
P33176	Kinesin-1 heavy chain OS=Homo sapiens GN=KIF5B PE=1 SV=1 - [KINH_HUMAN]	30.75	5.50	5	5	10	1.147	0.787
P07195	L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2 - [LDHB_HUMAN]	90.82	26.35	7	8	25	0.275	0.969
E9PH51	L-lactate dehydrogenase OS=Homo sapiens GN=LDHA PE=3 SV=2 - [E9PH51_HUMAN]	74.04	30.16	9	10	22	0.414	0.803
Q7Z4W1	L-xylulose reductase OS=Homo sapiens GN=DCXR PE=1 SV=2 - [DCXR_HUMAN]	9.85	7.38	2	2	3	0.407	0.985
Q6PKG0	La-related protein 1 OS=Homo sapiens GN=LARP1 PE=1 SV=2 - [LARP1_HUMAN]	15.73	3.92	4	5	5	0.543	0.451
Q9NS86	LanC-like protein 2 OS=Homo sapiens GN=LANCL2 PE=1 SV=1 - [LANC2_HUMAN]	22.82	12.22	5	5	7	0.992	1.005
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	0.891	0.376
Q14696	LDLR chaperone MESD OS=Homo sapiens GN=MESDC2 PE=1 SV=2 - [MESD_HUMAN]	5.83	8.97	2	2	2	1.262	1.140
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	0.381	0.770
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	1.199	1.081
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	0.738	0.758
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	1.017	1.279
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	0.416	1.136
P05455	Lupus La protein OS=Homo sapiens GN=SSB PE=1 SV=2 - [LA_HUMAN]	10.17	6.13	3	3	3	0.589	0.588
Q6ZWT7	Lysophospholipid acyltransferase 2 OS=Homo sapiens GN=MBOAT2 PE=2 SV=2 - [MBOA2_HUMAN]	14.41	6.54	3	3	4	1.053	1.025
Q14108	Lysosome membrane protein 2 OS=Homo sapiens GN=SCARB2 PE=1 SV=2 - [SCRB2_HUMAN]	9.36	5.44	3	3	3	0.742	1.576
P11279	Lysosome-associated membrane glycoprotein 1 OS=Homo sapiens GN=LAMP1 PE=1 SV=3 - [LAMP1_HUMAN]	21.32	8.39	4	4	6	1.472	1.305
P40925	Malate dehydrogenase, cytoplasmic OS=Homo sapiens GN=MDH1 PE=1 SV=4 - [MDHC_HUMAN]	18.40	15.87	5	5	5	0.228	0.685
P40926	Malate dehydrogenase, mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=3 - [MDHM_HUMAN]	108.11	50.89	14	14	30	0.207	0.749
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	1.716	1.464
P51811	Membrane transport protein XK OS=Homo sapiens GN=XK PE=1 SV=5 - [XK_HUMAN]	40.36	9.91	6	6	13	0.833	1.103
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	1.481	1.334
P35240	Merlin OS=Homo sapiens GN=NF2 PE=1 SV=1 - [MERL_HUMAN]	14.39	4.37	2	3	5	0.774	1.597
P50579	Methionine aminopeptidase 2 OS=Homo sapiens GN=METAP2 PE=1 SV=1 - [AMPM2_HUMAN]	8.66	6.90	2	2	2	0.137	0.403
Q9H8H3	Methyltransferase-like protein 7A OS=Homo sapiens GN=METTL7A PE=1 SV=1 - [MET7A_HUMAN]	12.95	17.21	3	3	4	0.843	0.777
Q8IY33	MICAL-like protein 2 OS=Homo sapiens GN=MICALL2 PE=1 SV=1 - [MILK2_HUMAN]	39.63	9.40	8	8	11	1.357	1.341
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	0.632	0.697
Q8TCT9	Minor histocompatibility antigen H13 OS=Homo sapiens GN=HM13 PE=1 SV=1 - [HM13_HUMAN]	6.64	4.77	2	2	2	0.350	0.517
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	0.399	0.778
Q9Y3D6	Mitochondrial fission 1 protein OS=Homo sapiens GN=FIS1 PE=1 SV=2 - [FIS1_HUMAN]	6.06	13.16	2	2	2	0.557	0.631

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	0.685	0.647
Q9NYZ2	Mitoferrin-1 OS=Homo sapiens GN=SLC25A37 PE=1 SV=2 - [MFRN1_HUMAN]	12.96	11.83	3	4	4	0.341	0.964
P26038	Moesin OS=Homo sapiens GN=MSN PE=1 SV=3 - [MOES_HUMAN]	245.89	40.73	23	33	75	0.533	1.122
P53985	Monocarboxylate transporter 1 OS=Homo sapiens GN=SLC16A1 PE=1 SV=3 - [MOT1_HUMAN]	61.04	9.60	6	6	18	0.666	1.517
O15439	Multidrug resistance-associated protein 4 OS=Homo sapiens GN=ABCC4 PE=1 SV=3 - [MRP4_HUMAN]	60.66	11.25	15	15	18	1.665	0.998
Q9UNW1	Multiple inositol polyphosphate phosphatase 1 OS=Homo sapiens GN=MINPP1 PE=1 SV=1 - [MINP1_HUMAN]	10.20	5.75	3	3	3	1.171	1.540
P12829	Myosin light chain 4 OS=Homo sapiens GN=MYL4 PE=1 SV=3 - [MYL4_HUMAN]	66.79	53.30	8	8	20	0.248	0.885
P60660	Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2 - [MYL6_HUMAN]	11.02	24.50	3	3	3	0.896	1.121
P19105	Myosin regulatory light chain 12A OS=Homo sapiens GN=MYL12A PE=1 SV=2 - [ML12A_HUMAN]	28.99	22.22	4	4	8	0.339	0.918
P35580	Myosin-10 OS=Homo sapiens GN=MYH10 PE=1 SV=3 - [MYH10_HUMAN]	667.07	39.27	74	88	200	0.199	0.858
P35579	Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4 - [MYH9_HUMAN]	740.90	45.36	83	96	229	0.392	0.921
Q13423	NAD(P) transhydrogenase, mitochondrial OS=Homo sapiens GN=NNT PE=1 SV=3 - [NNTM_HUMAN]	75.97	18.14	18	18	23	0.530	1.033
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	0.456	0.723
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	0.915	0.731
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	0.403	0.948
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	0.863	0.822
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		0.549
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	1.207	0.715
P00387	NADH-cytochrome b5 reductase 3 OS=Homo sapiens GN=CYB5R3 PE=1 SV=3 - [NB5R3_HUMAN]	24.28	16.61	4	4	7	1.098	1.054
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	0.033	0.506
A2RRP1	Neuroblastoma-amplified sequence OS=Homo sapiens GN=NBAS PE=1 SV=2 - [NBAS_HUMAN]	21.58	2.66	7	7	7	1.025	1.164
B2RAL7	Neuroplastin OS=Homo sapiens GN=NPTN PE=2 SV=1 - [B2RAL7_HUMAN]	17.41	8.51	2	2	5	1.563	1.359
Q14697	Neutral alpha-glucosidase AB OS=Homo sapiens GN=GANAB PE=1 SV=3 - [GANAB_HUMAN]	108.46	19.70	4	19	35	1.445	1.228
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	0.471	0.428
Q6PIU2	Neutral cholesterol ester hydrolase 1 OS=Homo sapiens GN=NCEH1 PE=1 SV=3 - [NCEH1_HUMAN]	44.61	20.83	7	7	12	1.059	1.006
Q49AL4	NMNAT3 protein OS=Homo sapiens GN=NMNAT3 PE=2 SV=1 - [Q49AL4_HUMAN]	10.81	11.97	2	2	3	1.496	0.773
P69849	Nodal modulator 3 OS=Homo sapiens GN=NOMO3 PE=2 SV=2 - [NOMO3_HUMAN]	6.01	1.72	2	2	2	0.840	0.647
Q9UNZ2	NSFL1 cofactor p47 OS=Homo sapiens GN=NSFL1C PE=1 SV=2 - [NSF1C_HUMAN]	62.35	38.92	11	11	19	0.695	0.925
Q14980	Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 PE=1 SV=2 - [NUMA1_HUMAN]	11.78	1.80	3	3	3	0.982	0.586
P61970	Nuclear transport factor 2 OS=Homo sapiens GN=NUTF2 PE=1 SV=1 - [NTF2_HUMAN]	6.15	11.02	2	2	2	0.358	0.839
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	0.294	0.576
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	0.486	0.520
P19338	Nucleolin OS=Homo sapiens GN=NCL PE=1 SV=3 - [NUCL_HUMAN]	30.89	8.73	9	9	10	0.333	0.374
Q9BYG9	Nucleophosmin (Nucleolar phosphoprotein B23, numatrin) OS=Homo sapiens GN=NPM1 PE=2 SV=1 - [Q9BYG9_HUMAN]	9.09	10.04	3	3	3	0.505	0.343
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	0.599	0.849
Q9NTK5	Obg-like ATPase 1 OS=Homo sapiens GN=OLA1 PE=1 SV=2 - [OLA1_HUMAN]	24.74	13.89	6	6	8	0.781	0.942
Q96CV9	Optineurin OS=Homo sapiens GN=OPTN PE=1 SV=2 - [OPTN_HUMAN]	42.95	12.48	7	7	13	0.718	1.044
P04181	Ornithine aminotransferase, mitochondrial OS=Homo sapiens GN=OAT PE=1 SV=1 - [OAT_HUMAN]	43.84	23.69	10	10	13	0.442	0.639
Q9BRP8	Partner of Y14 and mago OS=Homo sapiens GN=WIBG PE=1 SV=1 - [WIBG_HUMAN]	12.31	18.14	3	3	4	0.317	0.647
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	0.545	0.624
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	0.889	1.397
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	0.522	1.220
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	0.346	0.670
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	0.509	2.167
O60664	Perilipin-3 OS=Homo sapiens GN=PLIN3 PE=1 SV=3 - [PLIN3_HUMAN]	7.60	3.92	2	2	2	1.068	0.852
Q06830	Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1 - [PRDX1_HUMAN]	127.67	56.28	8	10	37	0.397	1.262
P32119	Peroxiredoxin-2 OS=Homo sapiens GN=PRDX2 PE=1 SV=5 - [PRDX2_HUMAN]	432.84	59.09	10	11	136	0.437	1.079
P30044	Peroxiredoxin-5, mitochondrial OS=Homo sapiens GN=PRDX5 PE=1 SV=4 - [PRDX5_HUMAN]	10.56	10.28	2	2	3	1.974	0.753
Q9Y285	Phenylalanyl-tRNA synthetase alpha chain OS=Homo sapiens GN=FARSA PE=1 SV=3 - [SYFA_HUMAN]	19.39	8.66	4	5	7	1.190	0.566
Q9NSD9	Phenylalanyl-tRNA synthetase beta chain OS=Homo sapiens GN=FARSB PE=1 SV=3 - [SYFB_HUMAN]	57.34	23.43	14	15	18	1.082	0.566
Q00325	Phosphate carrier protein, mitochondrial OS=Homo sapiens GN=SLC25A3 PE=1 SV=2 - [MPCP_HUMAN]	33.51	15.47	6	6	10	0.167	0.908
Q92539	Phosphatidate phosphatase LPIN2 OS=Homo sapiens GN=LPIN2 PE=1 SV=1 - [LPIN2_HUMAN]	17.87	4.69	4	4	5	0.672	0.686
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	0.763	1.237
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	1.243	1.078
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	0.961	0.438
Q13492	Phosphatidylinositol-binding clathrin assembly protein OS=Homo sapiens GN=PICALM PE=1 SV=2 - [PICAL_HUMAN]	64.67	13.96	9	11	21	1.071	0.752

Q16822	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=Homo sapiens GN=PCK2 PE=1 SV=3 - [PCKGM_HUMAN]	17.09	6.41	4	4	5	0.233	0.581
B7Z7A9	Phosphoglycerate kinase OS=Homo sapiens GN=PGK1 PE=2 SV=1 - [B7Z7A9_HUMAN]	38.93	18.77	8	8	12	0.224	0.780
Q9Y263	Phospholipase A-2-activating protein OS=Homo sapiens GN=PLAA PE=1 SV=2 - [PLAP_HUMAN]	8.86	2.39	2	2	2	0.439	0.916
P36969	Phospholipid hydroperoxide glutathione peroxidase, mitochondrial OS=Homo sapiens GN=GPX4 PE=1 SV=3 - [GPX4_HUMAN]	27.42	22.84	6	6	8	1.127	1.139
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	0.660	0.582
Q9GZP4	PITH domain-containing protein 1 OS=Homo sapiens GN=PITHD1 PE=1 SV=1 - [PITH1_HUMAN]	11.45	18.01	4	4	4	0.866	0.584
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	1.287	1.122
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	1.259	0.983
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	0.239	0.506
P13796	Plastin-2 OS=Homo sapiens GN=LCP1 PE=1 SV=6 - [PLSL_HUMAN]	5.43	4.31	2	2	2	0.568	0.739
Q68Y55	Poly(RC) binding protein 2 OS=Homo sapiens GN=PCBP2 PE=2 SV=1 - [Q68Y55_HUMAN]	38.24	21.75	2	6	12	1.166	0.701
Q15365	Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2 - [PCBP1_HUMAN]	49.40	30.90	5	9	15	0.290	0.427
P11940	Polyadenylate-binding protein 1 OS=Homo sapiens GN=PABPC1 PE=1 SV=2 - [PABP1_HUMAN]	39.37	18.71	11	11	12	0.594	0.414
P26599	Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 PE=1 SV=1 - [PTBP1_HUMAN]	32.78	9.60	6	6	10	1.226	0.635
Q9UHV9	Prefoldin subunit 2 OS=Homo sapiens GN=PFDN2 PE=1 SV=1 - [PFD2_HUMAN]	10.22	12.99	2	2	3	0.150	0.740
P07602	Proactivator polypeptide OS=Homo sapiens GN=PSAP PE=1 SV=2 - [SAP_HUMAN]	97.18	20.23	13	13	30	0.296	1.358
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	0.495	0.841
Q9H3G5	Probable serine carboxypeptidase CPVL OS=Homo sapiens GN=CPVL PE=1 SV=2 - [CPVL_HUMAN]	14.87	7.98	4	4	5	0.581	0.666
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	0.482	0.767
O14737	Programmed cell death protein 5 OS=Homo sapiens GN=PDCD5 PE=1 SV=3 - [PDCD5_HUMAN]	22.94	34.40	5	5	7	0.207	0.577
Q99623	Prohibitin-2 OS=Homo sapiens GN=PHB2 PE=1 SV=2 - [PHB2_HUMAN]	67.14	37.79	12	12	20	0.382	0.784
Q9UQ80	Proliferation-associated protein 2G4 OS=Homo sapiens GN=PA2G4 PE=1 SV=3 - [PA2G4_HUMAN]	96.44	37.82	14	14	31	0.388	0.577
Q16186	Proteasomal ubiquitin receptor ADRM1 OS=Homo sapiens GN=ADRM1 PE=1 SV=2 - [ADRM1_HUMAN]	16.06	8.11	3	3	5	0.922	0.607
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	1.136	0.655
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	0.951	0.646
Q06323	Proteasome activator complex subunit 1 OS=Homo sapiens GN=PSME1 PE=1 SV=1 - [PSME1_HUMAN]	102.94	46.99	13	13	33	1.730	0.789
Q9UL46	Proteasome activator complex subunit 2 OS=Homo sapiens GN=PSME2 PE=1 SV=4 - [PSME2_HUMAN]	76.44	26.36	8	8	21	1.356	0.849
P25786	Proteasome subunit alpha type-1 OS=Homo sapiens GN=PSMA1 PE=1 SV=1 - [PSA1_HUMAN]	200.52	49.81	15	15	62	1.219	0.750
P25787	Proteasome subunit alpha type-2 OS=Homo sapiens GN=PSMA2 PE=1 SV=2 - [PSA2_HUMAN]	47.08	30.77	7	7	15	1.251	0.659
P25788	Proteasome subunit alpha type-3 OS=Homo sapiens GN=PSMA3 PE=1 SV=2 - [PSA3_HUMAN]	180.21	38.82	12	12	55	1.236	0.726
P25789	Proteasome subunit alpha type-4 OS=Homo sapiens GN=PSMA4 PE=1 SV=1 - [PSA4_HUMAN]	92.59	39.08	11	11	29	1.073	0.751
P28066	Proteasome subunit alpha type-5 OS=Homo sapiens GN=PSMA5 PE=1 SV=3 - [PSA5_HUMAN]	119.13	34.02	7	7	37	1.222	0.722
P60900	Proteasome subunit alpha type-6 OS=Homo sapiens GN=PSMA6 PE=1 SV=1 - [PSA6_HUMAN]	110.91	51.63	13	13	32	1.251	0.729
O14818	Proteasome subunit alpha type-7 OS=Homo sapiens GN=PSMA7 PE=1 SV=1 - [PSA7_HUMAN]	93.15	38.31	10	10	28	1.142	0.717
P20618	Proteasome subunit beta type-1 OS=Homo sapiens GN=PSMB1 PE=1 SV=2 - [PSB1_HUMAN]	57.30	41.08	8	8	19	1.229	0.775
P49721	Proteasome subunit beta type-2 OS=Homo sapiens GN=PSMB2 PE=1 SV=1 - [PSB2_HUMAN]	55.52	17.91	6	6	18	1.064	0.770
P49720	Proteasome subunit beta type-3 OS=Homo sapiens GN=PSMB3 PE=1 SV=2 - [PSB3_HUMAN]	34.54	16.59	4	4	11	1.035	0.717
P28070	Proteasome subunit beta type-4 OS=Homo sapiens GN=PSMB4 PE=1 SV=4 - [PSB4_HUMAN]	50.08	20.45	4	4	14	1.209	0.745
P28074	Proteasome subunit beta type-5 OS=Homo sapiens GN=PSMB5 PE=1 SV=3 - [PSB5_HUMAN]	109.88	39.92	10	10	32	1.200	0.697
P28072	Proteasome subunit beta type-6 OS=Homo sapiens GN=PSMB6 PE=1 SV=4 - [PSB6_HUMAN]	59.06	17.57	5	5	17	1.224	0.708
Q99436	Proteasome subunit beta type-7 OS=Homo sapiens GN=PSMB7 PE=1 SV=1 - [PSB7_HUMAN]	70.67	21.30	8	8	21	1.280	0.692
Q5VYK3	Proteasome-associated protein ECM29 homolog OS=Homo sapiens GN=ECM29 PE=1 SV=2 - [ECM29_HUMAN]	11.84	1.84	4	4	4	1.136	0.654
P11171	Protein 4.1 OS=Homo sapiens GN=EPB41 PE=1 SV=4 - [41_HUMAN]	1234.38	44.44	8	44	389	1.216	1.553
O14744	Protein arginine N-methyltransferase 5 OS=Homo sapiens GN=PRMT5 PE=1 SV=4 - [ANM5_HUMAN]	20.48	10.83	7	7	7	0.744	0.861
Q9UKV8	Protein argonaute-2 OS=Homo sapiens GN=EIF2C2 PE=1 SV=3 - [AGO2_HUMAN]	279.08	42.49	31	31	88	1.669	1.258
Q9UKY7	Protein CDV3 homolog OS=Homo sapiens GN=CDV3 PE=1 SV=1 - [CDV3_HUMAN]	15.55	15.12	3	3	5	0.593	0.737
Q5TDH0	Protein DDI1 homolog 2 OS=Homo sapiens GN=DDI2 PE=1 SV=1 - [DDI2_HUMAN]	56.94	28.32	9	9	17	0.622	0.987
P13667	Protein disulfide-isomerase A4 OS=Homo sapiens GN=PDIA4 PE=1 SV=2 - [PDIA4_HUMAN]	44.23	18.29	10	10	14	1.082	1.283
P07237	Protein disulfide-isomerase OS=Homo sapiens GN=P4HB PE=1 SV=3 - [PDIA1_HUMAN]	201.00	41.54	25	25	62	1.430	1.203
Q99497	Protein DJ-1 OS=Homo sapiens GN=PARK7 PE=1 SV=2 - [PARK7_HUMAN]	12.46	15.34	3	3	4	0.267	0.793
P49257	Protein ERGIC-53 OS=Homo sapiens GN=LMAN1 PE=1 SV=2 - [LMAN1_HUMAN]	51.99	20.98	9	9	15	0.600	0.899
Q9NRY5	Protein FAM114A2 OS=Homo sapiens GN=FAM114A2 PE=1 SV=4 - [F1142_HUMAN]	7.75	5.15	2	2	2	0.297	1.047
Q96RT1	Protein LAP2 OS=Homo sapiens GN=ERBB2IP PE=1 SV=2 - [LAP2_HUMAN]	25.60	3.54	5	5	8	1.792	1.295
Q9NUP9	Protein lin-7 homolog C OS=Homo sapiens GN=LIN7C PE=1 SV=1 - [LIN7C_HUMAN]	12.65	12.18	3	3	4	1.812	1.316
Q92508	Protein PIEZO1 OS=Homo sapiens GN=FAM38A PE=1 SV=4 - [PIEZ1_HUMAN]	40.32	3.69	7	8	12	1.093	0.753
Q08AM6	Protein VAC14 homolog OS=Homo sapiens GN=VAC14 PE=1 SV=1 - [VAC14_HUMAN]	9.27	4.86	2	3	3	1.525	0.897

O75695	Protein XRP2 OS=Homo sapiens GN=RP2 PE=1 SV=4 - [XRP2_HUMAN]	35.38	14.86	6	6	11	1.303	1.162
P00491	Purine nucleoside phosphorylase OS=Homo sapiens GN=PNP PE=1 SV=2 - [PNPH_HUMAN]	15.75	9.69	3	3	5	0.283	0.949
Q9Y315	Putative deoxyribose-phosphate aldolase OS=Homo sapiens GN=DERA PE=1 SV=2 - [DEOC_HUMAN]	44.00	32.39	8	9	13	1.555	1.225
Q5HYI5	Putative uncharacterized protein DKFZp313C1541 OS=Homo sapiens GN=DKFZp313C1541 PE=2 SV=1 - [Q5HYI5_HUMAN]	25.48	28.71	2	5	7	1.099	0.823
P30613	Pyruvate kinase isozymes R/L OS=Homo sapiens GN=PKLR PE=1 SV=2 - [KPYR_HUMAN]	55.14	21.95	11	11	17	0.390	0.968
P50395	Rab GDP dissociation inhibitor beta OS=Homo sapiens GN=GDI2 PE=1 SV=2 - [GDIB_HUMAN]	12.49	8.99	3	4	4	0.590	1.016
Q96NA2	Rab-interacting lysosomal protein OS=Homo sapiens GN=RILP PE=1 SV=1 - [RILP_HUMAN]	10.98	7.48	3	3	3	0.359	0.803
P35241	Radixin OS=Homo sapiens GN=RDX PE=1 SV=1 - [RADI_HUMAN]	161.08	30.70	14	26	49	0.750	1.052
Q9UHA4	Ragulator complex protein LAMTOR3 OS=Homo sapiens GN=LAMTOR3 PE=1 SV=1 - [LTOR3_HUMAN]	7.62	20.97	2	2	2	0.608	1.129
P46060	Ran GTPase-activating protein 1 OS=Homo sapiens GN=RANGAP1 PE=1 SV=1 - [RAGP1_HUMAN]	14.48	7.67	4	4	4	0.533	0.904
P43487	Ran-specific GTPase-activating protein OS=Homo sapiens GN=RANBP1 PE=1 SV=1 - [RANG_HUMAN]	18.30	13.43	3	3	5	0.162	0.701
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	1.422	1.612
P61026	Ras-related protein Rab-10 OS=Homo sapiens GN=RAB10 PE=1 SV=1 - [RAB10_HUMAN]	103.38	34.00	5	8	32	1.096	1.054
P62491	Ras-related protein Rab-11A OS=Homo sapiens GN=RAB11A PE=1 SV=3 - [RB11A_HUMAN]	27.45	23.61	5	5	8	0.501	0.439
P61106	Ras-related protein Rab-14 OS=Homo sapiens GN=RAB14 PE=1 SV=4 - [RAB14_HUMAN]	41.33	20.00	3	4	12	0.670	0.861
P62820	Ras-related protein Rab-1A OS=Homo sapiens GN=RAB1A PE=1 SV=3 - [RAB1A_HUMAN]	95.66	35.61	4	9	28	0.614	0.946
Q9H0U4	Ras-related protein Rab-1B OS=Homo sapiens GN=RAB1B PE=1 SV=1 - [RAB1B_HUMAN]	107.07	34.33	3	8	31	0.823	0.795
Q9UL25	Ras-related protein Rab-21 OS=Homo sapiens GN=RAB21 PE=1 SV=3 - [RAB21_HUMAN]	19.46	14.67	3	3	6	1.161	1.106
P61019	Ras-related protein Rab-2A OS=Homo sapiens GN=RAB2A PE=1 SV=1 - [RAB2A_HUMAN]	27.38	28.30	2	5	8	1.176	0.937
Q15286	Ras-related protein Rab-35 OS=Homo sapiens GN=RAB35 PE=1 SV=1 - [RAB35_HUMAN]	83.01	32.34	5	7	23	1.252	1.232
P61020	Ras-related protein Rab-5B OS=Homo sapiens GN=RAB5B PE=1 SV=1 - [RAB5B_HUMAN]	48.85	33.02	3	6	14	0.956	1.002
P51148	Ras-related protein Rab-5C OS=Homo sapiens GN=RAB5C PE=1 SV=2 - [RAB5C_HUMAN]	74.42	36.57	4	6	19	0.958	1.127
P51149	Ras-related protein Rab-7a OS=Homo sapiens GN=RAB7A PE=1 SV=1 - [RAB7A_HUMAN]	69.26	58.45	12	12	20	0.825	0.927
P61006	Ras-related protein Rab-8A OS=Homo sapiens GN=RAB8A PE=1 SV=1 - [RAB8A_HUMAN]	97.86	51.69	6	13	28	1.317	1.391
Q92930	Ras-related protein Rab-8B OS=Homo sapiens GN=RAB8B PE=1 SV=2 - [RAB8B_HUMAN]	90.87	45.41	3	10	27	1.003	1.174
P11233	Ras-related protein Ral-A OS=Homo sapiens GN=RALA PE=1 SV=1 - [RALA_HUMAN]	60.07	24.27	5	5	17	1.277	1.239
P62834	Ras-related protein Rap-1A OS=Homo sapiens GN=RAP1A PE=1 SV=1 - [RAP1A_HUMAN]	105.47	36.96	2	7	32	1.120	1.652
P61225	Ras-related protein Rap-2b OS=Homo sapiens GN=RAP2B PE=1 SV=1 - [RAP2B_HUMAN]	67.67	33.33	4	6	21	1.766	1.503
Q00765	Receptor expression-enhancing protein 5 OS=Homo sapiens GN=REEP5 PE=1 SV=3 - [REEP5_HUMAN]	47.22	11.11	4	4	13	1.725	0.986
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	0.552	0.924
Q8TC12	Retinol dehydrogenase 11 OS=Homo sapiens GN=RDH11 PE=1 SV=2 - [RDH11_HUMAN]	19.85	17.92	5	5	6	1.017	0.917
O75116	Rho-associated protein kinase 2 OS=Homo sapiens GN=ROCK2 PE=1 SV=4 - [ROCK2_HUMAN]	11.66	2.88	3	4	4	1.025	1.054
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	1.152	1.149
P60891	Ribose-phosphate pyrophosphokinase 1 OS=Homo sapiens GN=PRPS1 PE=1 SV=2 - [PRPS1_HUMAN]	63.30	33.96	6	10	20	0.979	0.716
Q5VVC8	Ribosomal protein L11 (Fragment) OS=Homo sapiens GN=RPL11 PE=2 SV=1 - [Q5VVC8_HUMAN]	11.76	16.09	3	3	4	0.470	0.489
E7EQV9	Ribosomal protein L15 OS=Homo sapiens GN=RPL15 PE=3 SV=1 - [E7EQV9_HUMAN]	18.20	21.84	3	3	5	0.960	0.439
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	0.779	0.496
Q5JR95	Ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=4 SV=1 - [Q5JR95_HUMAN]	12.75	16.49	3	3	4	0.338	0.526
Q9Y3A5	Ribosome maturation protein SBDS OS=Homo sapiens GN=SBDS PE=1 SV=4 - [SBDS_HUMAN]	20.43	14.40	5	5	6	0.906	1.150
Q9P2E9	Ribosome-binding protein 1 OS=Homo sapiens GN=RRBP1 PE=1 SV=4 - [RRBP1_HUMAN]	36.27	18.44	6	7	10	0.495	0.746
O00442	RNA 3'-terminal phosphate cyclase OS=Homo sapiens GN=RTCD1 PE=1 SV=1 - [RTC1_HUMAN]	18.53	4.92	3	3	5	0.655	0.885
Q96PK6	RNA-binding protein 14 OS=Homo sapiens GN=RBM14 PE=1 SV=2 - [RBM14_HUMAN]	5.99	3.14	2	2	2	0.953	0.931
Q3B7A4	RPLP0 protein OS=Homo sapiens GN=RPLP0 PE=2 SV=1 - [Q3B7A4_HUMAN]	38.72	19.22	4	4	12	0.721	0.520
Q7L7Q6	RTN4 OS=Homo sapiens GN=RTN4 PE=2 SV=1 - [Q7L7Q6_HUMAN]	28.04	11.53	3	3	8	0.995	0.935
Q9Y265	RuvB-like 1 OS=Homo sapiens GN=RUVBL1 PE=1 SV=1 - [RUVB1_HUMAN]	33.86	16.67	7	7	9	0.440	0.732
Q9Y230	RuvB-like 2 OS=Homo sapiens GN=RUVBL2 PE=1 SV=3 - [RUVB2_HUMAN]	72.26	30.24	14	14	21	0.441	0.776
P0C7P3	Schlafen family member 14 OS=Homo sapiens GN=SLFN14 PE=2 SV=2 - [SLN14_HUMAN]	6.84	1.64	2	2	2	1.413	0.957
Q13228	Selenium-binding protein 1 OS=Homo sapiens GN=SELENBP1 PE=1 SV=2 - [SBP1_HUMAN]	9.24	6.36	3	3	3	0.392	0.583
O75326	Semaphorin-7A OS=Homo sapiens GN=SEMA7A PE=1 SV=1 - [SEM7A_HUMAN]	33.45	11.56	8	8	11	2.152	1.399
D6RGI3	Septin 11, isoform CRA_b OS=Homo sapiens GN=SEPT11 PE=3 SV=1 - [D6RGI3_HUMAN]	27.02	13.18	3	5	8	0.343	1.531
A8MYA6	Serine hydroxymethyltransferase OS=Homo sapiens GN=SHMT1 PE=3 SV=1 - [A8MYA6_HUMAN]	5.47	3.36	2	2	2	1.337	1.283
B7Z9F1	Serine hydroxymethyltransferase OS=Homo sapiens GN=SHMT2 PE=2 SV=1 - [B7Z9F1_HUMAN]	21.43	11.80	6	6	7	0.507	0.941
O95747	Serine/threonine-protein kinase OSR1 OS=Homo sapiens GN=OXSR1 PE=1 SV=1 - [OXSR1_HUMAN]	30.73	16.13	7	8	9	0.389	0.824
Q9H2K8	Serine/threonine-protein kinase TAO3 OS=Homo sapiens GN=TAOK3 PE=1 SV=2 - [TAOK3_HUMAN]	9.39	5.23	4	4	4	0.846	0.960
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	0.573	0.916
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	1.339	0.728

B4DDZ8	Serine/threonine-protein phosphatase OS=Homo sapiens GN=PPP5C PE=2 SV=1 - [B4DDZ8_HUMAN]	20.00	11.52	5	5	6	0.700	0.868
P02787	Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3 - [TRFE_HUMAN]	124.97	34.53	22	22	39	0.345	0.634
P02768	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2 - [ALBU_HUMAN]	113.54	33.33	19	19	31	1.092	0.681
P49591	Seryl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=SARS PE=1 SV=3 - [SYSC_HUMAN]	36.18	20.04	9	9	11	0.329	0.788
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	0.789	1.368
Q9H9B4	Sideroflexin-1 OS=Homo sapiens GN=SFXN1 PE=1 SV=4 - [SFXN1_HUMAN]	14.33	12.42	4	4	4	0.224	0.993
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	0.717	0.869
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	0.155	0.720
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	0.332	0.746
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	1.000	1.025
Q8NHG7	Small VCP/p97-interacting protein OS=Homo sapiens GN=SVIP PE=2 SV=1 - [SVIP_HUMAN]	29.54	41.56	3	3	8	1.832	1.452
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	0.785	0.483
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	1.012	1.276
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	1.335	1.104
Q00796	Sorbitol dehydrogenase OS=Homo sapiens GN=SORD PE=1 SV=4 - [DHSO_HUMAN]	97.24	32.49	12	12	32	2.862	0.414
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	0.591	0.847
P02549	Spectrin alpha chain, erythrocyte OS=Homo sapiens GN=SPTA1 PE=1 SV=5 - [SPTA1_HUMAN]	6080.81	61.35	164	165	1848	1.754	1.539
P11277	Spectrin beta chain, erythrocyte OS=Homo sapiens GN=SPTB PE=1 SV=5 - [SPTB1_HUMAN]	5690.80	69.21	153	154	1726	1.729	1.508
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	0.583	0.702
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	0.743	1.088
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	0.618	0.749
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	1.203	0.961
P31948	Stress-induced-phosphoprotein 1 OS=Homo sapiens GN=STIP1 PE=1 SV=1 - [STIP1_HUMAN]	237.02	45.12	33	33	74	0.544	0.830
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	0.573	0.492
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	0.677	0.816
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	0.250	0.871
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	1.225	0.969
Q9Y6N5	Sulfide:quinone oxidoreductase, mitochondrial OS=Homo sapiens GN=SQRDL PE=1 SV=1 - [SQRD_HUMAN]	41.16	20.89	9	9	12	0.253	0.936
P00441	Superoxide dismutase [Cu-Zn] OS=Homo sapiens GN=SOD1 PE=1 SV=2 - [SODC_HUMAN]	24.47	31.17	6	6	8	0.609	0.852
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	0.077	0.946
O00161	Synaptosomal-associated protein 23 OS=Homo sapiens GN=SNAP23 PE=1 SV=1 - [SNP23_HUMAN]	35.78	31.28	7	7	11	1.088	1.229
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	1.470	1.059
O15400	Syntaxin-7 OS=Homo sapiens GN=STX7 PE=1 SV=4 - [STX7_HUMAN]	73.02	29.89	8	8	22	0.991	1.030
O00186	Syntaxin-binding protein 3 OS=Homo sapiens GN=STXBP3 PE=1 SV=2 - [STXB3_HUMAN]	43.66	14.36	9	9	14	1.708	1.127
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	0.681	0.932
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	0.751	0.900
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	0.641	0.905
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	0.628	0.896
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	0.689	0.895
Q5TCU6	Talin 1 OS=Homo sapiens GN=TLN1 PE=2 SV=1 - [Q5TCU6_HUMAN]	164.22	17.09	40	40	50	0.504	0.721
Q9ULP9	TBC1 domain family member 24 OS=Homo sapiens GN=TBC1D24 PE=1 SV=2 - [TBC24_HUMAN]	15.95	9.12	5	5	5	1.097	2.241
Q59G71	Tensin variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59G71_HUMAN]	66.14	21.99	16	16	20	1.573	0.605
O43396	Thioredoxin-like protein 1 OS=Homo sapiens GN=TXNL1 PE=1 SV=3 - [TXNL1_HUMAN]	13.66	14.19	3	3	4	0.887	0.899
Q9H3N1	Thioredoxin-related transmembrane protein 1 OS=Homo sapiens GN=TMX1 PE=1 SV=1 - [TMX1_HUMAN]	25.00	14.64	5	5	7	1.178	0.952
P26639	Threonyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=TARS PE=1 SV=3 - [SYTC_HUMAN]	47.18	15.91	12	12	16	0.546	0.769
P23919	Thymidylate kinase OS=Homo sapiens GN=DTYMK PE=1 SV=4 - [KTHY_HUMAN]	10.71	9.91	2	2	3	1.368	0.839
P37837	Transaldolase OS=Homo sapiens GN=TALDO1 PE=1 SV=2 - [TALDO_HUMAN]	26.58	19.88	7	7	8	0.144	0.795
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	1.108	0.658
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	0.428	0.662
Q00059	Transcription factor A, mitochondrial OS=Homo sapiens GN=TFAM PE=1 SV=1 - [TFAM_HUMAN]	14.40	16.26	5	5	5	0.192	0.551
Q00577	Transcriptional activator protein Pur-alpha OS=Homo sapiens GN=PURA PE=1 SV=2 - [PURA_HUMAN]	16.35	10.56	4	4	5	1.129	0.922
P02786	Transferrin receptor protein 1 OS=Homo sapiens GN=TFRC PE=1 SV=2 - [TFR1_HUMAN]	256.20	38.68	27	27	79	0.485	0.196
P61586	Transforming protein RhoA OS=Homo sapiens GN=RHOA PE=1 SV=1 - [RHOA_HUMAN]	28.36	30.05	6	6	9	1.089	2.103
P55072	Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4 - [TERA_HUMAN]	568.95	44.79	35	35	175	0.964	0.901
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	0.650	0.739
Q92616	Translational activator GCN1 OS=Homo sapiens GN=GCN1L1 PE=1 SV=6 - [GCN1L_HUMAN]	6.18	0.60	2	2	2	0.352	0.396

Q99442	Translocation protein SEC62 OS=Homo sapiens GN=SEC62 PE=1 SV=1 - [SEC62_HUMAN]	10.99	5.26	2	2	3	0.686	0.518
Q9HD45	Transmembrane 9 superfamily member 3 OS=Homo sapiens GN=TM9SF3 PE=1 SV=2 - [TM9S3_HUMAN]	5.82	3.23	2	2	2	1.160	0.777
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	0.752	0.400
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	0.879	1.119
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	0.899	0.899
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	0.813	0.967
Q9BVC6	Transmembrane protein 109 OS=Homo sapiens GN=TMEM109 PE=1 SV=1 - [TM109_HUMAN]	15.28	8.64	2	2	4	0.646	0.802
Q5T3F8	Transmembrane protein 63B OS=Homo sapiens GN=TMEM63B PE=1 SV=1 - [TM63B_HUMAN]	9.83	3.13	3	3	3	1.104	0.924
Q92973	Transportin-1 OS=Homo sapiens GN=TNPO1 PE=1 SV=2 - [TNPO1_HUMAN]	10.16	2.90	3	3	3	0.413	0.772
P53007	Tricarboxylate transport protein, mitochondrial OS=Homo sapiens GN=SLC25A1 PE=1 SV=2 - [TXTP_HUMAN]	8.92	8.36	3	3	3	0.711	1.016
P40939	Trifunctional enzyme subunit alpha, mitochondrial OS=Homo sapiens GN=HADHA PE=1 SV=2 - [ECHA_HUMAN]	60.25	17.43	14	14	19	0.761	0.715
P55084	Trifunctional enzyme subunit beta, mitochondrial OS=Homo sapiens GN=HADHB PE=1 SV=3 - [ECHB_HUMAN]	36.72	14.35	7	7	11	0.463	0.702
P60174	Triosephosphate isomerase OS=Homo sapiens GN=TPI1 PE=1 SV=2 - [TPIS_HUMAN]	46.18	34.94	8	8	14	0.244	0.946
Q5SRJ5	Tripartite motif-containing 10 OS=Homo sapiens GN=TRIM10 PE=2 SV=1 - [Q5SRJ5_HUMAN]	12.31	8.86	3	3	3	0.544	1.519
Q8NG06	Tripartite motif-containing protein 58 OS=Homo sapiens GN=TRIM58 PE=2 SV=2 - [TRI58_HUMAN]	41.26	24.07	10	11	13	0.348	0.963
P29144	Tripeptidyl-peptidase 2 OS=Homo sapiens GN=TPP2 PE=1 SV=4 - [TPP2_HUMAN]	107.68	19.38	25	25	34	0.802	0.651
P28289	Tropomodulin-1 OS=Homo sapiens GN=TMOD1 PE=1 SV=1 - [TMOD1_HUMAN]	211.85	52.65	22	22	69	1.457	1.473
D9YZV7	Tropomyosin 1 (Alpha) isoform 6 OS=Homo sapiens GN=TPM1 PE=3 SV=1 - [D9YZV7_HUMAN]	260.23	47.76	2	15	76	1.347	1.350
Q5VU58	Tropomyosin 3 OS=Homo sapiens GN=TPM3 PE=2 SV=1 - [Q5VU58_HUMAN]	388.59	59.27	2	20	115	1.480	1.759
Q5VU59	Tropomyosin 3 OS=Homo sapiens GN=TPM3 PE=2 SV=1 - [Q5VU59_HUMAN]	403.59	63.79	4	22	120	2.028	1.464
Q5LJ98	TROVE domain family, member 2 OS=Homo sapiens GN=TROVE2 PE=2 SV=1 - [Q5LJ98_HUMAN]	28.32	11.39	7	7	9	0.389	0.749
P23381	Tryptophanyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=WARS PE=1 SV=2 - [SYWC_HUMAN]	8.71	7.01	3	3	3	0.476	0.513
Q9Y3Q8	TSC22 domain family protein 4 OS=Homo sapiens GN=TSC22D4 PE=1 SV=2 - [T22D4_HUMAN]	27.47	16.96	6	6	7	0.655	0.584
Q9BQE3	Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 - [TBA1C_HUMAN]	82.89	34.30	4	13	26	0.308	0.561
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	0.584	1.030
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	4.910	2.682
P54577	Tyrosyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=YARS PE=1 SV=4 - [SYYC_HUMAN]	77.02	33.52	19	19	24	0.395	0.663
P45974	Ubiquitin carboxyl-terminal hydrolase 5 OS=Homo sapiens GN=USP5 PE=1 SV=2 - [UBP5_HUMAN]	34.27	10.02	8	8	10	0.434	0.966
A6NJA2	Ubiquitin carboxyl-terminal hydrolase OS=Homo sapiens GN=USP14 PE=3 SV=1 - [A6NJA2_HUMAN]	58.45	25.27	12	12	17	0.508	0.903
E9PCQ3	Ubiquitin carboxyl-terminal hydrolase OS=Homo sapiens GN=USP15 PE=3 SV=2 - [E9PCQ3_HUMAN]	41.52	9.94	11	11	13	0.543	0.808
B7WPF4	Ubiquitin carboxyl-terminal hydrolase OS=Homo sapiens GN=USP24 PE=3 SV=2 - [B7WPF4_HUMAN]	6.81	0.65	2	2	2	0.375	0.690
Q9C0C9	Ubiquitin-conjugating enzyme E2 O OS=Homo sapiens GN=UBE2O PE=1 SV=3 - [UBE2O_HUMAN]	126.16	17.88	21	21	37	0.502	0.879
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	0.459	0.939
Q9NYU2	UDP-glucose:glycoprotein glucosyltransferase 1 OS=Homo sapiens GN=UGGT1 PE=1 SV=3 - [UGGG1_HUMAN]	73.25	13.31	20	20	23	1.154	1.085
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	0.702	0.695
Q5T446	Uncharacterized protein (Fragment) OS=Homo sapiens GN=UROD PE=2 SV=1 - [Q5T446_HUMAN]	6.74	13.47	2	2	2	0.294	0.690
E9PBW0	Uncharacterized protein OS=Homo sapiens GN=ABCC5 PE=3 SV=1 - [E9PBW0_HUMAN]	5.79	2.39	2	2	2	1.629	0.989
B7Z9I1	Uncharacterized protein OS=Homo sapiens GN=ACADM PE=2 SV=1 - [B7Z9I1_HUMAN]	38.60	18.70	7	7	11	0.730	0.731
E9PE82	Uncharacterized protein OS=Homo sapiens GN=ACADS PE=4 SV=1 - [E9PE82_HUMAN]	5.98	3.19	2	2	2	0.438	1.151
C9JGQ9	Uncharacterized protein OS=Homo sapiens GN=ACHE PE=4 SV=1 - [C9JGQ9_HUMAN]	19.30	9.98	5	5	6	2.313	1.200
F5H2A5	Uncharacterized protein OS=Homo sapiens GN=ACO2 PE=4 SV=1 - [F5H2A5_HUMAN]	11.92	6.18	4	4	4	0.398	0.565
E7ERD7	Uncharacterized protein OS=Homo sapiens GN=ACSL6 PE=4 SV=1 - [E7ERD7_HUMAN]	30.95	12.41	9	9	10	1.317	1.166
F5H6F4	Uncharacterized protein OS=Homo sapiens GN=ACSS1 PE=4 SV=1 - [F5H6F4_HUMAN]	10.25	4.40	2	3	3	0.202	0.807
F5GXS2	Uncharacterized protein OS=Homo sapiens GN=ACTN4 PE=4 SV=1 - [F5GXS2_HUMAN]	12.11	6.91	3	3	4	0.494	0.670
F5H3P5	Uncharacterized protein OS=Homo sapiens GN=ACTR3 PE=3 SV=1 - [F5H3P5_HUMAN]	23.39	17.42	5	5	7	0.481	0.985
E7ET30	Uncharacterized protein OS=Homo sapiens GN=AK3 PE=3 SV=1 - [E7ET30_HUMAN]	8.03	11.23	2	2	3	0.491	0.645
F5H328	Uncharacterized protein OS=Homo sapiens GN=ALDH5A1 PE=3 SV=1 - [F5H328_HUMAN]	12.34	6.26	3	3	4	0.958	1.031
E7EVE3	Uncharacterized protein OS=Homo sapiens GN=ANK1 PE=4 SV=1 - [E7EVE3_HUMAN]	2863.52	46.92	81	88	856	1.583	1.547
F5H754	Uncharacterized protein OS=Homo sapiens GN=ANKFY1 PE=4 SV=1 - [F5H754_HUMAN]	9.40	2.34	3	3	3	0.720	0.700
F5H0H0	Uncharacterized protein OS=Homo sapiens GN=AP2M1 PE=4 SV=1 - [F5H0H0_HUMAN]	44.86	18.57	9	9	14	1.001	0.874
E9PC21	Uncharacterized protein OS=Homo sapiens GN=AQP1 PE=3 SV=1 - [E9PC21_HUMAN]	33.28	17.53	2	2	11	2.104	1.565
B7ZB63	Uncharacterized protein OS=Homo sapiens GN=ARF3 PE=2 SV=1 - [B7ZB63_HUMAN]	7.00	13.19	2	2	2	0.689	0.651
F5GY14	Uncharacterized protein OS=Homo sapiens GN=ARL6IP1 PE=4 SV=1 - [F5GY14_HUMAN]	17.31	15.48	3	3	6	0.869	0.727
E9PER8	Uncharacterized protein OS=Homo sapiens GN=ARL6IP5 PE=4 SV=1 - [E9PER8_HUMAN]	11.82	15.06	3	3	4	0.886	0.762
B4DLQ7	Uncharacterized protein OS=Homo sapiens GN=ARPC1A PE=2 SV=1 - [B4DLQ7_HUMAN]	6.18	4.64	2	2	2	0.568	0.971
E7ERV9	Uncharacterized protein OS=Homo sapiens GN=ASAH1 PE=4 SV=1 - [E7ERV9_HUMAN]	8.56	8.52	3	3	3	0.798	0.998

C9JAL9	Uncharacterized protein OS=Homo sapiens GN=ASPSCR1 PE=4 SV=1 - [C9JAL9_HUMAN]	7.04	6.02	2	2	2	0.555	1.021
F5GWY2	Uncharacterized protein OS=Homo sapiens GN=ATIC PE=4 SV=1 - [F5GWY2_HUMAN]	6.09	3.38	2	2	2	0.549	0.810
F5H6I7	Uncharacterized protein OS=Homo sapiens GN=ATL3 PE=4 SV=1 - [F5H6I7_HUMAN]	39.88	9.94	6	6	13	1.876	1.459
F5H3A1	Uncharacterized protein OS=Homo sapiens GN=ATP1A1 PE=3 SV=1 - [F5H3A1_HUMAN]	84.03	19.35	19	19	23	1.539	0.681
E9PN17	Uncharacterized protein OS=Homo sapiens GN=ATP5L PE=4 SV=1 - [E9PN17_HUMAN]	33.73	60.53	4	5	9	0.404	0.851
F5H569	Uncharacterized protein OS=Homo sapiens GN=ATP6V0A1 PE=4 SV=1 - [F5H569_HUMAN]	29.15	6.69	6	6	8	1.185	1.025
B7Z1R5	Uncharacterized protein OS=Homo sapiens GN=ATP6V1A PE=2 SV=1 - [B7Z1R5_HUMAN]	93.34	25.51	15	15	28	0.451	0.935
A8MQ60	Uncharacterized protein OS=Homo sapiens GN=ATP6V1C1 PE=4 SV=1 - [A8MQ60_HUMAN]	13.12	10.16	4	4	4	0.648	0.695
A8MUN4	Uncharacterized protein OS=Homo sapiens GN=ATP6V1E1 PE=2 SV=1 - [A8MUN4_HUMAN]	42.58	28.06	7	7	14	0.510	0.940
E9PGE6	Uncharacterized protein OS=Homo sapiens GN=ATP6V1H PE=4 SV=1 - [E9PGE6_HUMAN]	16.29	9.15	4	4	5	0.360	0.992
B4DXE2	Uncharacterized protein OS=Homo sapiens GN=BAG2 PE=2 SV=1 - [B4DXE2_HUMAN]	28.28	32.58	5	5	7	0.676	0.768
A6NME1	Uncharacterized protein OS=Homo sapiens GN=BCAP29 PE=2 SV=2 - [A6NME1_HUMAN]	12.83	19.35	3	3	4	1.343	0.993
E9PL10	Uncharacterized protein OS=Homo sapiens GN=BTF3L4 PE=4 SV=1 - [E9PL10_HUMAN]	5.31	5.52	2	2	2	0.392	0.524
F5H2W0	Uncharacterized protein OS=Homo sapiens GN=C18orf8 PE=4 SV=1 - [F5H2W0_HUMAN]	6.06	3.28	2	2	2	0.572	1.197
E9PCW3	Uncharacterized protein OS=Homo sapiens GN=C22orf28 PE=4 SV=1 - [E9PCW3_HUMAN]	9.66	6.28	3	3	3	0.579	0.666
E7EWT6	Uncharacterized protein OS=Homo sapiens GN=CALCOCO1 PE=4 SV=2 - [E7EWT6_HUMAN]	22.71	10.49	6	6	6	0.279	0.616
E9PAQ6	Uncharacterized protein OS=Homo sapiens GN=CCT3 PE=3 SV=1 - [E9PAQ6_HUMAN]	239.56	38.60	24	24	67	0.677	0.904
E9PB22	Uncharacterized protein OS=Homo sapiens GN=CD47 PE=4 SV=1 - [E9PB22_HUMAN]	48.39	8.97	3	3	14	1.706	1.675
E9PNW4	Uncharacterized protein OS=Homo sapiens GN=CD59 PE=4 SV=1 - [E9PNW4_HUMAN]	41.39	27.78	3	3	12	0.983	2.022
E9PP50	Uncharacterized protein OS=Homo sapiens GN=CFL1 PE=4 SV=1 - [E9PP50_HUMAN]	13.10	14.37	3	3	4	0.508	0.539
E9PDB9	Uncharacterized protein OS=Homo sapiens GN=CLCN7 PE=4 SV=1 - [E9PDB9_HUMAN]	7.50	2.56	2	2	2	0.620	1.041
B4DIN1	Uncharacterized protein OS=Homo sapiens GN=CLTA PE=2 SV=1 - [B4DIN1_HUMAN]	101.53	23.91	3	8	31	1.261	0.836
F5GXH1	Uncharacterized protein OS=Homo sapiens GN=COPG PE=4 SV=1 - [F5GXH1_HUMAN]	8.25	3.93	3	3	3	0.863	0.706
E7EM64	Uncharacterized protein OS=Homo sapiens GN=COPS6 PE=4 SV=1 - [E7EM64_HUMAN]	13.13	9.20	3	3	4	0.618	0.911
A8MZ71	Uncharacterized protein OS=Homo sapiens GN=COX7A2 PE=4 SV=1 - [A8MZ71_HUMAN]	6.71	27.71	2	2	2	0.185	0.716
D6R9Z7	Uncharacterized protein OS=Homo sapiens GN=COX7C PE=4 SV=1 - [D6R9Z7_HUMAN]	13.91	32.14	2	2	4	0.653	1.031
E9PDY4	Uncharacterized protein OS=Homo sapiens GN=CR1 PE=4 SV=1 - [E9PDY4_HUMAN]	6.40	2.37	2	2	2	1.619	0.930
E7EU96	Uncharacterized protein OS=Homo sapiens GN=CSNK2A1 PE=4 SV=1 - [E7EU96_HUMAN]	8.40	10.39	3	3	3	0.951	0.937
E9PP21	Uncharacterized protein OS=Homo sapiens GN=CSRP1 PE=4 SV=1 - [E9PP21_HUMAN]	21.83	36.88	4	4	6	0.705	1.600
F5GWW0	Uncharacterized protein OS=Homo sapiens GN=CTSB PE=3 SV=1 - [F5GWW0_HUMAN]	22.93	20.88	5	5	7	0.293	1.236
B4E358	Uncharacterized protein OS=Homo sapiens GN=CTTN PE=2 SV=1 - [B4E358_HUMAN]	9.74	10.19	2	3	3	0.061	1.015
E7EWR0	Uncharacterized protein OS=Homo sapiens GN=CUL1 PE=3 SV=1 - [E7EWR0_HUMAN]	40.58	13.80	12	12	13	0.725	0.828
A8MSH7	Uncharacterized protein OS=Homo sapiens GN=CUL4A PE=3 SV=1 - [A8MSH7_HUMAN]	30.50	10.14	8	8	9	0.394	0.894
B4DWD7	Uncharacterized protein OS=Homo sapiens GN=CYBRD1 PE=2 SV=1 - [B4DWD7_HUMAN]	29.68	9.65	2	2	8	1.250	0.932
C9JFR7	Uncharacterized protein OS=Homo sapiens GN=CYCS PE=3 SV=1 - [C9JFR7_HUMAN]	43.19	47.52	6	6	13	0.200	0.921
E9PFS5	Uncharacterized protein OS=Homo sapiens GN=DCTN1 PE=4 SV=1 - [E9PFS5_HUMAN]	86.12	16.91	21	21	26	0.982	0.800
C9J8R4	Uncharacterized protein OS=Homo sapiens GN=DCUN1D1 PE=4 SV=1 - [C9J8R4_HUMAN]	7.68	16.41	2	2	2	0.318	1.021
E7EWT1	Uncharacterized protein OS=Homo sapiens GN=DDOST PE=4 SV=1 - [E7EWT1_HUMAN]	9.17	6.44	3	3	3	0.763	0.703
B4DME8	Uncharacterized protein OS=Homo sapiens GN=DDX1 PE=2 SV=1 - [B4DME8_HUMAN]	11.23	3.43	2	2	3	0.377	0.660
B7Z6B8	Uncharacterized protein OS=Homo sapiens GN=DECR1 PE=2 SV=1 - [B7Z6B8_HUMAN]	45.59	27.91	8	8	13	0.235	0.723
E7ERW8	Uncharacterized protein OS=Homo sapiens GN=DIAPH1 PE=4 SV=1 - [E7ERW8_HUMAN]	103.64	14.98	19	21	33	0.549	1.077
F5H7M3	Uncharacterized protein OS=Homo sapiens GN=DLAT PE=3 SV=1 - [F5H7M3_HUMAN]	10.30	6.22	3	3	3	0.758	0.834
E3W974	Uncharacterized protein OS=Homo sapiens GN=DNPEP PE=4 SV=2 - [E3W974_HUMAN]	12.07	19.15	2	2	3	0.761	0.954
E7ETW8	Uncharacterized protein OS=Homo sapiens GN=DYSF PE=4 SV=1 - [E7ETW8_HUMAN]	28.47	4.45	7	8	9	0.366	0.745
A6NJH9	Uncharacterized protein OS=Homo sapiens GN=EIF1AY PE=4 SV=1 - [A6NJH9_HUMAN]	20.80	23.62	3	3	7	0.189	0.462
B4DV79	Uncharacterized protein OS=Homo sapiens GN=EIF3B PE=2 SV=1 - [B4DV79_HUMAN]	34.30	11.38	8	8	10	0.562	0.526
B4DVQ5	Uncharacterized protein OS=Homo sapiens GN=EIF3C PE=2 SV=1 - [B4DVQ5_HUMAN]	42.54	13.81	12	12	13	0.356	0.540
B4DVY1	Uncharacterized protein OS=Homo sapiens GN=EIF3D PE=2 SV=1 - [B4DVY1_HUMAN]	12.64	7.01	3	3	4	0.303	0.544
B7ZAM9	Uncharacterized protein OS=Homo sapiens GN=EIF3K PE=2 SV=1 - [B7ZAM9_HUMAN]	15.94	15.17	3	3	5	0.316	0.493
E7EPC9	Uncharacterized protein OS=Homo sapiens GN=EIF4B PE=4 SV=1 - [E7EPC9_HUMAN]	51.15	18.06	10	10	15	0.487	0.727
E7EX73	Uncharacterized protein OS=Homo sapiens GN=EIF4G1 PE=4 SV=1 - [E7EX73_HUMAN]	85.06	14.90	22	22	26	0.257	0.537
E9PPD9	Uncharacterized protein OS=Homo sapiens GN=EPB41L2 PE=4 SV=1 - [E9PPD9_HUMAN]	29.86	9.62	9	9	9	1.534	1.716
B4DT43	Uncharacterized protein OS=Homo sapiens GN=ETFA PE=2 SV=1 - [B4DT43_HUMAN]	46.61	36.27	9	9	15	0.669	0.814
B4E0X8	Uncharacterized protein OS=Homo sapiens GN=FUBP1 PE=2 SV=1 - [B4E0X8_HUMAN]	9.66	4.29	2	3	3	0.570	0.657
B4DR70	Uncharacterized protein OS=Homo sapiens GN=FUS PE=2 SV=1 - [B4DR70_HUMAN]	25.50	13.29	3	5	7	0.434	0.871
F5H4D6	Uncharacterized protein OS=Homo sapiens GN=G3BP1 PE=4 SV=1 - [F5H4D6_HUMAN]	11.70	11.97	2	2	4	0.711	0.580

E7EQZ3	Uncharacterized protein OS=Homo sapiens GN=GSPT1 PE=4 SV=1 - [E7EQZ3_HUMAN]	26.06	9.28	8	8	8	0.290	0.611
F5H5Y5	Uncharacterized protein OS=Homo sapiens GN=HGS PE=4 SV=1 - [F5H5Y5_HUMAN]	18.94	8.17	5	6	6	0.929	0.912
E9PCK0	Uncharacterized protein OS=Homo sapiens GN=HK1 PE=3 SV=1 - [E9PCK0_HUMAN]	22.89	5.75	6	6	7	0.514	1.126
F5H345	Uncharacterized protein OS=Homo sapiens GN=HMBS PE=4 SV=1 - [F5H345_HUMAN]	23.75	14.24	5	5	7	0.696	0.655
A6NGP5	Uncharacterized protein OS=Homo sapiens GN=HN1L PE=2 SV=2 - [A6NGP5_HUMAN]	9.88	14.04	2	2	3	1.319	1.075
D6R9P3	Uncharacterized protein OS=Homo sapiens GN=HNRNPAB PE=4 SV=1 - [D6R9P3_HUMAN]	23.15	13.57	3	4	8	0.356	0.582
B2R603	Uncharacterized protein OS=Homo sapiens GN=HNRNPC PE=2 SV=1 - [B2R603_HUMAN]	24.40	17.16	5	5	6	0.334	0.280
B4DTC3	Uncharacterized protein OS=Homo sapiens GN=HNRNPD PE=2 SV=1 - [B4DTC3_HUMAN]	23.21	17.82	5	6	8	0.773	0.686
E9PCY7	Uncharacterized protein OS=Homo sapiens GN=HNRNPH1 PE=4 SV=1 - [E9PCY7_HUMAN]	30.66	21.21	7	7	9	0.667	0.578
B3KX72	Uncharacterized protein OS=Homo sapiens GN=HNRNPU PE=2 SV=1 - [B3KX72_HUMAN]	10.89	5.73	4	4	4	0.493	0.312
B7Z4V2	Uncharacterized protein OS=Homo sapiens GN=HSPA9 PE=2 SV=1 - [B7Z4V2_HUMAN]	163.05	35.79	23	24	48	0.500	0.727
B4DY72	Uncharacterized protein OS=Homo sapiens GN=HSPH1 PE=2 SV=1 - [B4DY72_HUMAN]	12.05	4.73	2	3	4	0.432	0.701
E9PD66	Uncharacterized protein OS=Homo sapiens GN=HUWE1 PE=4 SV=1 - [E9PD66_HUMAN]	104.10	5.85	25	25	31	0.938	0.807
B4DFG4	Uncharacterized protein OS=Homo sapiens GN=ILF3 PE=2 SV=1 - [B4DFG4_HUMAN]	13.32	5.93	3	3	4	0.562	0.539
C9J406	Uncharacterized protein OS=Homo sapiens GN=IMMT PE=4 SV=1 - [C9J406_HUMAN]	134.90	30.20	23	24	38	0.385	0.769
F5H153	Uncharacterized protein OS=Homo sapiens GN=ITSN1 PE=4 SV=1 - [F5H153_HUMAN]	17.78	3.80	4	4	5	0.511	0.702
F5H2Q7	Uncharacterized protein OS=Homo sapiens GN=KIAA1715 PE=4 SV=1 - [F5H2Q7_HUMAN]	9.25	6.81	2	2	3	0.706	0.855
C9JYI4	Uncharacterized protein OS=Homo sapiens GN=KPNA1 PE=4 SV=1 - [C9JYI4_HUMAN]	16.19	10.37	3	4	5	0.594	0.692
F5H479	Uncharacterized protein OS=Homo sapiens GN=LAMTOR1 PE=4 SV=1 - [F5H479_HUMAN]	20.55	12.12	2	2	6	0.760	1.279
E9PHS0	Uncharacterized protein OS=Homo sapiens GN=LANCL1 PE=4 SV=1 - [E9PHS0_HUMAN]	14.63	13.27	3	3	4	2.282	0.677
B4DWN1	Uncharacterized protein OS=Homo sapiens GN=LMAN2 PE=2 SV=1 - [B4DWN1_HUMAN]	23.15	14.04	4	4	7	0.965	0.800
B3KXS5	Uncharacterized protein OS=Homo sapiens GN=LONP1 PE=2 SV=1 - [B3KXS5_HUMAN]	55.11	14.41	13	13	17	0.559	0.691
B5MEG9	Uncharacterized protein OS=Homo sapiens GN=MAP4 PE=4 SV=2 - [B5MEG9_HUMAN]	7.37	2.81	2	2	2	1.098	0.699
E9PNT8	Uncharacterized protein OS=Homo sapiens GN=MTCH2 PE=3 SV=1 - [E9PNT8_HUMAN]	10.12	23.90	3	3	3	0.546	0.866
A8MZ22	Uncharacterized protein OS=Homo sapiens GN=NAP1L4 PE=3 SV=3 - [A8MZ22_HUMAN]	68.31	25.13	9	10	23	0.534	0.821
F5GZJ1	Uncharacterized protein OS=Homo sapiens GN=NCAPD2 PE=4 SV=1 - [F5GZJ1_HUMAN]	11.85	2.21	3	3	3	0.625	0.518
B4E189	Uncharacterized protein OS=Homo sapiens GN=NCAPH PE=2 SV=1 - [B4E189_HUMAN]	11.05	5.29	3	3	3	0.458	0.442
E9PC09	Uncharacterized protein OS=Homo sapiens GN=NCSTN PE=4 SV=1 - [E9PC09_HUMAN]	6.66	6.23	2	2	2	1.339	0.988
B4DJ81	Uncharacterized protein OS=Homo sapiens GN=NDUFS1 PE=2 SV=1 - [B4DJ81_HUMAN]	5.32	2.29	2	2	2	0.240	0.749
E9PMX3	Uncharacterized protein OS=Homo sapiens GN=NDUFV1 PE=4 SV=1 - [E9PMX3_HUMAN]	6.62	11.24	2	2	2	1.159	0.783
E9PGQ8	Uncharacterized protein OS=Homo sapiens GN=NECAP2 PE=4 SV=1 - [E9PGQ8_HUMAN]	32.73	33.33	6	6	10	0.989	1.009
E7ERL0	Uncharacterized protein OS=Homo sapiens GN=NME1 PE=3 SV=1 - [E7ERL0_HUMAN]	19.43	33.09	4	4	6	0.230	0.855
E9PFG7	Uncharacterized protein OS=Homo sapiens GN=OGDH PE=4 SV=1 - [E9PFG7_HUMAN]	44.68	9.16	9	9	14	0.598	0.842
E9PBS1	Uncharacterized protein OS=Homo sapiens GN=PAICS PE=4 SV=1 - [E9PBS1_HUMAN]	39.99	21.31	11	11	12	0.358	1.212
B7Z3X5	Uncharacterized protein OS=Homo sapiens GN=PDHA1 PE=2 SV=1 - [B7Z3X5_HUMAN]	18.96	12.81	5	5	6	0.442	0.672
B4DDD7	Uncharacterized protein OS=Homo sapiens GN=PDHB PE=2 SV=1 - [B4DDD7_HUMAN]	21.06	9.97	3	3	7	0.571	0.691
B3KQT9	Uncharacterized protein OS=Homo sapiens GN=PDIA3 PE=2 SV=1 - [B3KQT9_HUMAN]	144.81	38.96	20	20	43	1.424	1.239
B7Z254	Uncharacterized protein OS=Homo sapiens GN=PDIA6 PE=2 SV=1 - [B7Z254_HUMAN]	54.19	23.34	9	9	16	1.289	1.154
C9JW96	Uncharacterized protein OS=Homo sapiens GN=PHB PE=4 SV=2 - [C9JW96_HUMAN]	84.68	44.72	12	12	25	0.348	0.783
E9PBQ1	Uncharacterized protein OS=Homo sapiens GN=PIP5K1A PE=4 SV=1 - [E9PBQ1_HUMAN]	9.47	5.17	2	3	3	0.949	1.512
F5H0R5	Uncharacterized protein OS=Homo sapiens GN=PIP5K1C PE=4 SV=1 - [F5H0R5_HUMAN]	11.76	7.97	3	4	4	1.034	0.797
B4DTE8	Uncharacterized protein OS=Homo sapiens GN=PLSCR1 PE=2 SV=1 - [B4DTE8_HUMAN]	10.20	7.17	2	2	3	1.333	1.281
F5H5K9	Uncharacterized protein OS=Homo sapiens GN=PNPLA6 PE=4 SV=1 - [F5H5K9_HUMAN]	12.17	2.31	3	3	4	1.870	1.658
D6R967	Uncharacterized protein OS=Homo sapiens GN=PPA2 PE=4 SV=1 - [D6R967_HUMAN]	6.47	11.52	2	2	2	0.200	1.303
B4DY76	Uncharacterized protein OS=Homo sapiens GN=PPOX PE=2 SV=1 - [B4DY76_HUMAN]	29.60	12.61	5	5	8	0.364	0.688
F5H3X9	Uncharacterized protein OS=Homo sapiens GN=PPP2R1A PE=4 SV=1 - [F5H3X9_HUMAN]	23.91	9.36	6	6	8	0.283	0.752
E9PKF6	Uncharacterized protein OS=Homo sapiens GN=PPP6R3 PE=4 SV=1 - [E9PKF6_HUMAN]	8.98	3.10	3	3	3	0.848	0.877
E9PH29	Uncharacterized protein OS=Homo sapiens GN=PRDX3 PE=4 SV=1 - [E9PH29_HUMAN]	73.55	23.95	5	5	21	0.803	1.175
A8K318	Uncharacterized protein OS=Homo sapiens GN=PRKCSH PE=2 SV=1 - [A8K318_HUMAN]	71.70	20.95	13	13	21	1.394	1.250
E5RG77	Uncharacterized protein OS=Homo sapiens GN=PROSC PE=3 SV=1 - [E5RG77_HUMAN]	6.62	10.53	2	2	2	0.648	0.843
F5GZ16	Uncharacterized protein OS=Homo sapiens GN=PSMD2 PE=4 SV=1 - [F5GZ16_HUMAN]	176.03	28.78	26	26	54	1.154	0.672
F5H8K4	Uncharacterized protein OS=Homo sapiens GN=PSMD3 PE=4 SV=1 - [F5H8K4_HUMAN]	120.54	38.39	20	20	36	0.999	0.661
B4DZM8	Uncharacterized protein OS=Homo sapiens GN=PSMD5 PE=2 SV=1 - [B4DZM8_HUMAN]	6.18	3.47	2	2	2	1.234	0.813
B4DXI8	Uncharacterized protein OS=Homo sapiens GN=PSMD7 PE=2 SV=1 - [B4DXI8_HUMAN]	35.02	22.67	5	5	9	1.274	0.755
B8ZZI3	Uncharacterized protein OS=Homo sapiens GN=PTMA PE=4 SV=1 - [B8ZZI3_HUMAN]	14.48	22.58	2	2	4	0.148	0.629
A8MZH8	Uncharacterized protein OS=Homo sapiens GN=PTTG1IP PE=4 SV=1 - [A8MZH8_HUMAN]	14.17	23.36	2	2	5	0.261	1.717

B4DNN3	Uncharacterized protein OS=Homo sapiens GN=QARS PE=2 SV=1 - [B4DNN3_HUMAN]	14.60	3.86	3	3	5	1.438	1.314
E9PK89	Uncharacterized protein OS=Homo sapiens GN=RAB3IL1 PE=4 SV=1 - [E9PK89_HUMAN]	5.13	15.53	2	2	2	0.824	0.648
F5GZB1	Uncharacterized protein OS=Homo sapiens GN=RAB6A PE=3 SV=1 - [F5GZB1_HUMAN]	25.45	23.24	3	4	8	1.191	1.126
F5GZU7	Uncharacterized protein OS=Homo sapiens GN=RABEP1 PE=4 SV=1 - [F5GZU7_HUMAN]	11.37	3.21	4	4	4	0.865	0.813
B4DQI8	Uncharacterized protein OS=Homo sapiens GN=RAP1B PE=2 SV=1 - [B4DQI8_HUMAN]	129.65	45.45	3	8	42	0.964	1.115
Q8N8Y7	Uncharacterized protein OS=Homo sapiens GN=RBMX PE=2 SV=1 - [Q8N8Y7_HUMAN]	20.40	13.49	6	6	7	0.883	0.930
D6RBN9	Uncharacterized protein OS=Homo sapiens GN=RELL1 PE=4 SV=1 - [D6RBN9_HUMAN]	3.83	10.12	2	2	2	1.918	1.225
B4DM74	Uncharacterized protein OS=Homo sapiens GN=RPL18A PE=2 SV=1 - [B4DM74_HUMAN]	19.37	20.13	3	3	6	0.454	0.446
C9JXB8	Uncharacterized protein OS=Homo sapiens GN=RPL24 PE=4 SV=1 - [C9JXB8_HUMAN]	23.24	33.88	4	4	6	0.172	0.470
E9PLL6	Uncharacterized protein OS=Homo sapiens GN=RPL27A PE=3 SV=1 - [E9PLL6_HUMAN]	6.66	17.59	2	2	2	0.310	0.466
C9JU56	Uncharacterized protein OS=Homo sapiens GN=RPL31 PE=4 SV=1 - [C9JU56_HUMAN]	17.72	28.70	4	4	6	0.854	0.451
C9K025	Uncharacterized protein OS=Homo sapiens GN=RPL35A PE=4 SV=1 - [C9K025_HUMAN]	14.65	29.79	3	3	5	0.586	1.244
E9PEL3	Uncharacterized protein OS=Homo sapiens GN=RPL37A PE=4 SV=1 - [E9PEL3_HUMAN]	9.16	20.00	2	2	3	0.503	0.431
E9PIZ3	Uncharacterized protein OS=Homo sapiens GN=RPL8 PE=4 SV=1 - [E9PIZ3_HUMAN]	16.82	15.84	4	4	5	0.574	0.469
D6RAN4	Uncharacterized protein OS=Homo sapiens GN=RPL9 PE=4 SV=1 - [D6RAN4_HUMAN]	6.10	9.34	2	2	2	0.460	0.876
D6R910	Uncharacterized protein OS=Homo sapiens GN=RPS6KA2 PE=4 SV=1 - [D6R910_HUMAN]	7.43	19.20	2	2	2	0.868	0.840
C9J9K3	Uncharacterized protein OS=Homo sapiens GN=RPSA PE=3 SV=1 - [C9J9K3_HUMAN]	30.01	23.48	5	5	8	0.687	0.529
F5H774	Uncharacterized protein OS=Homo sapiens GN=RTN3 PE=4 SV=1 - [F5H774_HUMAN]	17.43	2.28	2	2	5	0.635	0.536
F5H3J5	Uncharacterized protein OS=Homo sapiens GN=S100A4 PE=4 SV=1 - [F5H3J5_HUMAN]	5.48	17.78	2	2	2	0.644	0.623
E9PGZ4	Uncharacterized protein OS=Homo sapiens GN=SACM1L PE=4 SV=1 - [E9PGZ4_HUMAN]	25.95	10.95	6	6	7	1.234	1.208
C9JPX0	Uncharacterized protein OS=Homo sapiens GN=SAFB2 PE=4 SV=2 - [C9JPX0_HUMAN]	7.16	5.67	2	2	2	0.762	0.457
E9PEA8	Uncharacterized protein OS=Homo sapiens GN=SCCPDH PE=4 SV=1 - [E9PEA8_HUMAN]	9.29	8.30	2	2	3	1.376	0.859
B7Z5N7	Uncharacterized protein OS=Homo sapiens GN=SCFD1 PE=2 SV=1 - [B7Z5N7_HUMAN]	19.04	14.66	5	5	6	1.100	0.923
E9PBJ5	Uncharacterized protein OS=Homo sapiens GN=SDHA PE=4 SV=1 - [E9PBJ5_HUMAN]	31.25	14.61	7	7	9	0.890	0.782
B5MCX3	Uncharacterized protein OS=Homo sapiens GN=SEPT2 PE=3 SV=1 - [B5MCX3_HUMAN]	24.17	17.13	5	5	8	0.369	1.527
B4DNE4	Uncharacterized protein OS=Homo sapiens GN=SEPT7 PE=2 SV=1 - [B4DNE4_HUMAN]	74.92	24.61	10	11	23	0.603	1.500
A6NMH6	Uncharacterized protein OS=Homo sapiens GN=SEPT8 PE=3 SV=1 - [A6NMH6_HUMAN]	38.57	16.28	5	7	11	0.453	1.674
B4DN87	Uncharacterized protein OS=Homo sapiens GN=SERPINH1 PE=2 SV=1 - [B4DN87_HUMAN]	27.80	12.85	5	5	8	0.930	0.769
E7EMJ6	Uncharacterized protein OS=Homo sapiens GN=SGTA PE=4 SV=1 - [E7EMJ6_HUMAN]	6.90	7.90	2	2	2	0.389	0.734
E5RJR5	Uncharacterized protein OS=Homo sapiens GN=SKP1 PE=4 SV=1 - [E5RJR5_HUMAN]	11.36	17.79	3	3	3	0.581	1.013
B7Z844	Uncharacterized protein OS=Homo sapiens GN=SLC2A14 PE=2 SV=1 - [B7Z844_HUMAN]	6.35	3.89	2	2	2	1.802	1.071
B4E2Z3	Uncharacterized protein OS=Homo sapiens GN=SLC3A2 PE=2 SV=1 - [B4E2Z3_HUMAN]	12.18	8.22	3	3	3	0.232	0.397
B7Z6X9	Uncharacterized protein OS=Homo sapiens GN=SLC43A2 PE=2 SV=1 - [B7Z6X9_HUMAN]	19.96	7.41	3	3	6	1.185	1.017
E9PS74	Uncharacterized protein OS=Homo sapiens GN=SLC43A3 PE=4 SV=1 - [E9PS74_HUMAN]	37.29	9.97	5	5	12	1.627	0.821
E9PD53	Uncharacterized protein OS=Homo sapiens GN=SMC4 PE=4 SV=1 - [E9PD53_HUMAN]	27.38	6.18	8	8	9	0.468	0.493
E7EPV7	Uncharacterized protein OS=Homo sapiens GN=SNCA PE=4 SV=1 - [E7EPV7_HUMAN]	43.17	69.57	7	7	12	0.340	0.439
E7ESM6	Uncharacterized protein OS=Homo sapiens GN=SND1 PE=4 SV=2 - [E7ESM6_HUMAN]	78.97	19.22	17	17	23	0.349	0.921
B4DEK4	Uncharacterized protein OS=Homo sapiens GN=SNX2 PE=2 SV=1 - [B4DEK4_HUMAN]	11.32	7.71	3	3	3	0.589	0.581
F5H3C5	Uncharacterized protein OS=Homo sapiens GN=SOD2 PE=3 SV=1 - [F5H3C5_HUMAN]	16.77	33.33	4	4	5	0.309	0.884
F5H7U6	Uncharacterized protein OS=Homo sapiens GN=SPAG9 PE=4 SV=1 - [F5H7U6_HUMAN]	7.15	2.50	2	2	2	0.818	0.843
E7EMJ8	Uncharacterized protein OS=Homo sapiens GN=SRSF4 PE=4 SV=2 - [E7EMJ8_HUMAN]	16.21	7.64	3	3	5	0.960	0.663
C9K0U8	Uncharacterized protein OS=Homo sapiens GN=SSBP1 PE=4 SV=1 - [C9K0U8_HUMAN]	5.33	11.57	2	2	2	0.397	0.836
A6NMU3	Uncharacterized protein OS=Homo sapiens GN=STAM PE=4 SV=1 - [A6NMU3_HUMAN]	9.97	12.30	3	3	3	0.880	0.893
B4E2V5	Uncharacterized protein OS=Homo sapiens GN=STOM PE=2 SV=1 - [B4E2V5_HUMAN]	415.36	54.43	14	14	127	1.571	1.905
B4E1K7	Uncharacterized protein OS=Homo sapiens GN=STOML2 PE=2 SV=1 - [B4E1K7_HUMAN]	42.51	27.65	8	8	12	0.409	0.879
D6RF48	Uncharacterized protein OS=Homo sapiens GN=STX18 PE=4 SV=1 - [D6RF48_HUMAN]	19.48	14.29	5	5	6	0.757	1.041
F5GXG3	Uncharacterized protein OS=Homo sapiens GN=STXBP2 PE=4 SV=1 - [F5GXG3_HUMAN]	13.62	6.04	4	4	4	1.605	1.350
F5GXC8	Uncharacterized protein OS=Homo sapiens GN=SUCLA2 PE=3 SV=1 - [F5GXC8_HUMAN]	6.35	6.67	2	2	2	1.432	0.992
F5GWQ7	Uncharacterized protein OS=Homo sapiens GN=TAF15 PE=4 SV=1 - [F5GWQ7_HUMAN]	12.97	16.96	2	4	4	0.162	0.927
B4DIT7	Uncharacterized protein OS=Homo sapiens GN=TGM2 PE=2 SV=1 - [B4DIT7_HUMAN]	28.62	11.06	6	6	9	0.168	0.600
F5GX39	Uncharacterized protein OS=Homo sapiens GN=TMED2 PE=3 SV=1 - [F5GX39_HUMAN]	21.36	31.90	4	4	7	0.567	0.888
E9PI90	Uncharacterized protein OS=Homo sapiens GN=TMEM126A PE=4 SV=1 - [E9PI90_HUMAN]	6.30	25.26	2	2	2	0.572	0.745
B4DZ87	Uncharacterized protein OS=Homo sapiens GN=TOMM70A PE=2 SV=1 - [B4DZ87_HUMAN]	7.52	11.58	3	3	3	0.871	0.576
B4DSE2	Uncharacterized protein OS=Homo sapiens GN=TPP1 PE=2 SV=1 - [B4DSE2_HUMAN]	6.78	7.27	2	2	2	1.205	1.304
F5H897	Uncharacterized protein OS=Homo sapiens GN=TRAP1 PE=3 SV=1 - [F5H897_HUMAN]	30.10	8.45	5	6	9	0.243	0.709
E9PGT1	Uncharacterized protein OS=Homo sapiens GN=TSN PE=4 SV=1 - [E9PGT1_HUMAN]	19.36	20.18	4	4	5	0.599	0.696

E9PLH9	Uncharacterized protein OS=Homo sapiens GN=TSTA3 PE=4 SV=1 - [E9PLH9_HUMAN]	14.81	19.33	2	2	4	0.277	0.755
F5H265	Uncharacterized protein OS=Homo sapiens GN=UBC PE=4 SV=1 - [F5H265_HUMAN]	186.73	87.25	8	8	61	1.351	1.046
E9PJ81	Uncharacterized protein OS=Homo sapiens GN=UBXN1 PE=4 SV=1 - [E9PJ81_HUMAN]	22.36	28.97	6	6	7	0.583	0.775
E9PGR0	Uncharacterized protein OS=Homo sapiens GN=UCHL5 PE=4 SV=1 - [E9PGR0_HUMAN]	19.20	15.14	5	5	6	1.156	0.707
C9JKD6	Uncharacterized protein OS=Homo sapiens GN=UGP2 PE=4 SV=1 - [C9JKD6_HUMAN]	19.16	10.04	5	5	6	0.818	1.067
E5RHG9	Uncharacterized protein OS=Homo sapiens GN=UQCRB PE=4 SV=1 - [E5RHG9_HUMAN]	23.27	32.89	3	3	6	0.944	0.894
F5GZ76	Uncharacterized protein OS=Homo sapiens GN=USO1 PE=4 SV=1 - [F5GZ76_HUMAN]	5.91	2.89	2	2	2	1.031	0.691
B7Z7T5	Uncharacterized protein OS=Homo sapiens GN=USP7 PE=2 SV=1 - [B7Z7T5_HUMAN]	14.98	6.76	5	5	5	0.698	0.792
B0V043	Uncharacterized protein OS=Homo sapiens GN=VARS PE=3 SV=1 - [B0V043_HUMAN]	27.83	7.52	9	9	9	0.991	0.758
F5H2A7	Uncharacterized protein OS=Homo sapiens GN=VBP1 PE=4 SV=1 - [F5H2A7_HUMAN]	5.70	10.94	2	2	2	0.229	0.796
B4DP38	Uncharacterized protein OS=Homo sapiens GN=WDR77 PE=2 SV=1 - [B4DP38_HUMAN]	14.30	7.19	3	3	4	0.848	0.829
B7Z6V3	Uncharacterized protein OS=Homo sapiens GN=WDR81 PE=2 SV=1 - [B7Z6V3_HUMAN]	5.92	3.67	2	2	2	1.060	0.962
F5GWT4	Uncharacterized protein OS=Homo sapiens GN=WNK1 PE=4 SV=1 - [F5GWT4_HUMAN]	71.50	9.51	19	19	23	1.275	0.915
E7ESC6	Uncharacterized protein OS=Homo sapiens GN=XPO7 PE=4 SV=1 - [E7ESC6_HUMAN]	156.55	25.18	26	26	47	0.335	0.715
B1AHC7	Uncharacterized protein OS=Homo sapiens GN=XRCC6 PE=4 SV=1 - [B1AHC7_HUMAN]	11.98	4.67	3	3	4	0.408	0.362
A1A528	Uncharacterized protein OS=Homo sapiens GN=ZW10 PE=2 SV=1 - [A1A528_HUMAN]	7.28	2.68	2	2	2	0.943	0.950
F5GYQ0	Uncharacterized protein OS=Homo sapiens PE=4 SV=1 - [F5GYQ0_HUMAN]	6.07	9.57	2	2	2	1.366	0.825
F6WSP1	Uncharacterized protein OS=Homo sapiens PE=4 SV=1 - [F6WSP1_HUMAN]	6.19	7.95	2	2	2	1.602	1.494
C4AM82	Uncharacterized protein OS=Homo sapiens PE=4 SV=3 - [C4AM82_HUMAN]	6.11	6.62	2	2	2	1.177	1.661
Q969H8	UPF0556 protein C19orf10 OS=Homo sapiens GN=C19orf10 PE=1 SV=1 - [CS010_HUMAN]	10.83	15.03	2	2	3	1.633	1.239
Q9Y224	UPF0568 protein C14orf166 OS=Homo sapiens GN=C14orf166 PE=1 SV=1 - [CN166_HUMAN]	6.57	6.15	2	2	2		0.611
Q13336	Urea transporter 1 OS=Homo sapiens GN=SLC14A1 PE=2 SV=2 - [UT1_HUMAN]	84.52	14.65	3	7	27	1.512	1.307
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	0.422	0.974
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	0.452	0.908
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	0.406	0.967
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	1.147	0.898
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	0.382	0.951
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	0.460	1.045
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	0.660	0.923
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	0.885	0.774
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	0.390	0.707
P50552	Vasodilator-stimulated phosphoprotein OS=Homo sapiens GN=VASP PE=1 SV=3 - [VASP_HUMAN]	34.74	11.58	6	6	9	2.298	1.286
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	0.594	0.706
Q12981	Vesicle transport protein SEC20 OS=Homo sapiens GN=BNIP1 PE=1 SV=3 - [SEC20_HUMAN]	6.85	8.33	2	2	2	0.883	1.055
Q9NZ43	Vesicle transport protein USE1 OS=Homo sapiens GN=USE1 PE=1 SV=2 - [USE1_HUMAN]	16.15	14.29	4	4	5	0.789	0.997
Q15836	Vesicle-associated membrane protein 3 OS=Homo sapiens GN=VAMP3 PE=1 SV=3 - [VAMP3_HUMAN]	12.39	33.00	2	2	4	0.603	0.920
P51809	Vesicle-associated membrane protein 7 OS=Homo sapiens GN=VAMP7 PE=1 SV=3 - [VAMP7_HUMAN]	20.20	16.82	4	4	7	0.767	0.943
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	1.104	0.937
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	1.104	1.077
P46459	Vesicle-fusing ATPase OS=Homo sapiens GN=NSF PE=1 SV=3 - [NSF_HUMAN]	116.38	28.90	23	23	34	0.793	1.485
O75396	Vesicle-trafficking protein SEC22b OS=Homo sapiens GN=SEC22B PE=1 SV=4 - [SC22B_HUMAN]	59.03	38.60	7	7	17	0.987	0.994
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	0.300	1.289
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	0.197	1.100
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	0.318	1.304
A4D1P6	WD repeat-containing protein 91 OS=Homo sapiens GN=WDR91 PE=1 SV=2 - [WDR91_HUMAN]	54.53	16.73	9	10	15	1.184	0.929
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	0.122	0.354
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	0.844	0.455
Q9Y6M5	Zinc transporter 1 OS=Homo sapiens GN=SLC30A1 PE=1 SV=3 - [ZNT1_HUMAN]	18.99	8.88	4	4	6	1.590	0.873

Supplemental Table 4B

Accession	Description	Score	Coverage	Unique Peptides	Peptides	PSMs	Retic adult/CB	RBC adult/CB
Q9NRX4	14 kDa phosphohistidine phosphatase OS=Homo sapiens GN=PHPT1 PE=1 SV=1 - [PHP14_HUMAN]	39.19	29.60	5	5	13	0.667	0.960
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	0.610	0.766
P62258	14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1 - [1433E_HUMAN]	175.35	52.94	11	14	57	0.644	0.818
Q04917	14-3-3 protein eta OS=Homo sapiens GN=YWHAH PE=1 SV=4 - [1433F_HUMAN]	117.70	41.46	6	11	40	0.279	0.440
P61981	14-3-3 protein gamma OS=Homo sapiens GN=YWHAG PE=1 SV=2 - [1433G_HUMAN]	147.38	46.56	8	14	49	0.467	0.753
P27348	14-3-3 protein theta OS=Homo sapiens GN=YWHAQ PE=1 SV=1 - [1433T_HUMAN]	171.10	54.29	8	17	56	0.562	0.866
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	0.640	0.782
P62333	26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1 - [PRS10_HUMAN]	30.86	16.45	8	8	10	0.551	1.175
P62191	26S protease regulatory subunit 4 OS=Homo sapiens GN=PSMC1 PE=1 SV=1 - [PRS4_HUMAN]	37.65	20.91	10	11	12	0.485	1.293
P17980	26S protease regulatory subunit 6A OS=Homo sapiens GN=PSMC3 PE=1 SV=3 - [PRS6A_HUMAN]	29.77	18.91	7	7	9	0.532	1.409
P43686	26S protease regulatory subunit 6B OS=Homo sapiens GN=PSMC4 PE=1 SV=2 - [PRS6B_HUMAN]	35.98	11.24	6	7	12	0.524	1.049
P35998	26S protease regulatory subunit 7 OS=Homo sapiens GN=PSMC2 PE=1 SV=3 - [PRS7_HUMAN]	49.36	22.86	10	10	15	0.521	1.202
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	0.491	1.156
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	0.494	1.143
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	0.523	1.076
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	0.509	1.094
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	0.501	1.054
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	0.680	1.063
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	0.912	1.214
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	1.043	0.539
P25325	3-mercaptopyruvate sulfurtransferase OS=Homo sapiens GN=MPST PE=1 SV=3 - [THTM_HUMAN]	25.72	20.88	6	7	9	0.838	1.220
P49189	4-trimethylaminobutyraldehyde dehydrogenase OS=Homo sapiens GN=ALDH9A1 PE=1 SV=3 - [AL9A1_HUMAN]	31.43	15.99	8	8	10	0.674	0.912
P46783	40S ribosomal protein S10 OS=Homo sapiens GN=RPS10 PE=1 SV=1 - [RS10_HUMAN]	20.64	26.67	6	6	8	0.375	0.544
P62280	40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=1 SV=3 - [RS11_HUMAN]	6.08	11.39	2	2	2	0.335	0.273
P25398	40S ribosomal protein S12 OS=Homo sapiens GN=RPS12 PE=1 SV=3 - [RS12_HUMAN]	7.10	14.39	2	2	2	0.566	0.673
P62249	40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=1 SV=2 - [RS16_HUMAN]	21.33	16.44	4	4	8	0.323	0.243
P0CW22	40S ribosomal protein S17-like OS=Homo sapiens GN=RPS17L PE=3 SV=1 - [RS17L_HUMAN]	12.33	9.63	2	3	5	0.469	0.839
P62269	40S ribosomal protein S18 OS=Homo sapiens GN=RPS18 PE=1 SV=3 - [RS18_HUMAN]	21.76	27.63	6	6	7	0.415	0.544
P39019	40S ribosomal protein S19 OS=Homo sapiens GN=RPS19 PE=1 SV=2 - [RS19_HUMAN]	19.31	26.90	4	4	6	0.363	0.474
P60866	40S ribosomal protein S20 OS=Homo sapiens GN=RPS20 PE=1 SV=1 - [RS20_HUMAN]	5.80	17.65	2	2	2	0.373	0.195
Q8WVC2	40S ribosomal protein S21 OS=Homo sapiens GN=RPS21 PE=2 SV=1 - [Q8WVC2_HUMAN]	14.67	32.10	3	3	5	0.416	0.880
P62857	40S ribosomal protein S28 OS=Homo sapiens GN=RPS28 PE=1 SV=1 - [RS28_HUMAN]	6.93	28.99	2	2	2	0.353	0.052
P23396	40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2 - [RS3_HUMAN]	20.80	22.63	5	5	6	0.335	0.301
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	0.343	0.290
P46782	40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=4 - [RS5_HUMAN]	5.92	8.82	2	2	2	0.460	0.428
P62753	40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=1 SV=1 - [RS6_HUMAN]	17.76	17.27	5	5	6	0.368	0.816
P62081	40S ribosomal protein S7 OS=Homo sapiens GN=RPS7 PE=1 SV=1 - [RS7_HUMAN]	18.46	17.53	4	4	6	0.365	0.472
P46781	40S ribosomal protein S9 OS=Homo sapiens GN=RPS9 PE=1 SV=3 - [RS9_HUMAN]	8.13	10.82	2	2	3	0.379	0.795
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	0.715	1.033
Q5JUV3	5'-nucleotidase, cytosolic II (Fragment) OS=Homo sapiens GN=NT5C2 PE=2 SV=1 - [Q5JUV3_HUMAN]	5.09	8.05	2	2	2	0.366	0.425
Q01813	6-phosphofructokinase type C OS=Homo sapiens GN=PFKP PE=1 SV=2 - [K6PP_HUMAN]	18.59	7.78	3	6	7	1.106	0.887
P17858	6-phosphofructokinase, liver type OS=Homo sapiens GN=PFKL PE=1 SV=6 - [K6PL_HUMAN]	26.65	11.03	5	8	9	0.987	1.209
P08237	6-phosphofructokinase, muscle type OS=Homo sapiens GN=PFKM PE=1 SV=2 - [K6PF_HUMAN]	36.80	8.59	6	7	12	0.997	1.216
F5H7U0	6-phosphogluconate dehydrogenase, decarboxylating OS=Homo sapiens GN=PGD PE=3 SV=1 - [F5H7U0_HUMAN]	136.83	33.41	16	16	45	0.795	0.921
O95336	6-phosphogluconolactonase OS=Homo sapiens GN=PGLS PE=1 SV=2 - [6PGL_HUMAN]	27.75	24.81	6	6	8	0.651	0.927
P05388	60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=1 SV=1 - [RLA0_HUMAN]	9.25	5.36	2	2	3	0.383	0.557
P62906	60S ribosomal protein L10a OS=Homo sapiens GN=RPL10A PE=1 SV=2 - [RL10A_HUMAN]	8.29	14.75	3	3	3	0.341	0.734
P30050	60S ribosomal protein L12 OS=Homo sapiens GN=RPL12 PE=1 SV=1 - [RL12_HUMAN]	8.35	13.94	3	3	3	0.270	0.465
P26373	60S ribosomal protein L13 OS=Homo sapiens GN=RPL13 PE=1 SV=4 - [RL13_HUMAN]	27.85	17.54	4	4	8	0.188	0.169
P40429	60S ribosomal protein L13a OS=Homo sapiens GN=RPL13A PE=1 SV=2 - [RL13A_HUMAN]	4.96	6.40	2	2	2	0.229	0.260
P18621	60S ribosomal protein L17 OS=Homo sapiens GN=RPL17 PE=1 SV=3 - [RL17_HUMAN]	16.26	21.74	4	4	5	0.276	0.256
P46778	60S ribosomal protein L21 OS=Homo sapiens GN=RPL21 PE=1 SV=2 - [RL21_HUMAN]	4.88	8.13	2	2	2	0.274	0.362
P35268	60S ribosomal protein L22 OS=Homo sapiens GN=RPL22 PE=1 SV=2 - [RL22_HUMAN]	7.52	17.97	3	3	3	0.322	0.661
P62750	60S ribosomal protein L23a OS=Homo sapiens GN=RPL23A PE=1 SV=1 - [RL23A_HUMAN]	5.48	5.13	2	2	2	0.258	0.335
P46779	60S ribosomal protein L28 OS=Homo sapiens GN=RPL28 PE=1 SV=3 - [RL28_HUMAN]	21.44	25.55	5	5	7	0.223	0.512

P62888	60S ribosomal protein L30 OS=Homo sapiens GN=RPL30 PE=1 SV=2 - [RL30_HUMAN]	13.00	14.78	2	2	5	0.266	0.672
P49207	60S ribosomal protein L34 OS=Homo sapiens GN=RPL34 PE=1 SV=3 - [RL34_HUMAN]	9.02	13.68	2	2	3	0.217	0.207
P42766	60S ribosomal protein L35 OS=Homo sapiens GN=RPL35 PE=1 SV=2 - [RL35_HUMAN]	10.92	18.70	3	4	4	0.217	0.288
P18077	60S ribosomal protein L35a OS=Homo sapiens GN=RPL35A PE=1 SV=2 - [RL35A_HUMAN]	8.16	23.64	3	3	3	0.326	0.660
Q02878	60S ribosomal protein L6 OS=Homo sapiens GN=RPL6 PE=1 SV=3 - [RL6_HUMAN]	11.13	13.19	4	4	4	0.259	0.795
P18124	60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1 - [RL7_HUMAN]	12.85	20.16	4	4	4	0.309	0.640
P11021	78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2 - [GRP78_HUMAN]	73.98	9.94	3	6	23	0.284	0.367
Q2L6I2	ABC50 protein OS=Homo sapiens GN=ABCF1 PE=2 SV=1 - [Q2L6I2_HUMAN]	15.17	4.21	4	4	5	0.756	0.259
Q9BWD1	Acetyl-CoA acetyltransferase, cytosolic OS=Homo sapiens GN=ACAT2 PE=1 SV=2 - [THIC_HUMAN]	24.71	12.59	7	7	9	0.889	0.793
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	0.273	0.369
P61160	Actin-related protein 2 OS=Homo sapiens GN=ACTR2 PE=1 SV=1 - [ARP2_HUMAN]	34.71	6.60	2	3	14	1.123	0.683
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	1.005	0.600
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	0.066	1.114
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	0.532	0.759
P07108	Acyl-CoA-binding protein OS=Homo sapiens GN=DBI PE=1 SV=2 - [ACBP_HUMAN]	10.03	41.38	2	2	3	0.603	0.403
P13798	Acylamino-acid-releasing enzyme OS=Homo sapiens GN=APEH PE=1 SV=4 - [ACPH_HUMAN]	162.91	28.01	21	21	49	0.916	1.190
P07311	Acylphosphatase-1 OS=Homo sapiens GN=ACYP1 PE=1 SV=2 - [ACYP1_HUMAN]	18.59	28.28	4	4	6	0.670	0.735
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	0.618	1.003
Q96D30	ADD1 protein OS=Homo sapiens GN=ADD1 PE=2 SV=1 - [Q96D30_HUMAN]	5.47	4.25	2	2	2	1.703	0.721
P07741	Adenine phosphoribosyltransferase OS=Homo sapiens GN=APRT PE=1 SV=2 - [APT_HUMAN]	35.69	32.78	7	7	13	0.717	0.795
F5H737	Adenosylhomocysteinase OS=Homo sapiens GN=AHCY PE=3 SV=1 - [F5H737_HUMAN]	46.43	24.26	10	10	15	0.724	0.742
P00568	Adenylate kinase isoenzyme 1 OS=Homo sapiens GN=AK1 PE=1 SV=3 - [KAD1_HUMAN]	136.77	45.36	11	12	43	0.865	1.633
P30566	Adenylosuccinate lyase OS=Homo sapiens GN=ADSL PE=1 SV=2 - [PUR8_HUMAN]	60.33	18.39	11	11	19	0.811	1.202
F5H6Z3	Adenylyl cyclase-associated protein OS=Homo sapiens GN=CAP1 PE=3 SV=1 - [F5H6Z3_HUMAN]	30.77	11.28	6	6	11	0.572	0.736
Q9UKK9	ADP-sugar pyrophosphatase OS=Homo sapiens GN=NUDT5 PE=1 SV=1 - [NUDT5_HUMAN]	13.15	16.89	4	4	4	0.694	0.786
P49588	Alanyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=AARS PE=1 SV=2 - [SYAC_HUMAN]	141.47	20.56	23	23	46	0.534	0.483
C9JKR2	Albumin, isoform CRA_k OS=Homo sapiens GN=ALB PE=4 SV=1 - [C9JKR2_HUMAN]	8.57	7.67	2	2	2	0.797	0.589
P14550	Alcohol dehydrogenase [NADP+] OS=Homo sapiens GN=AKR1A1 PE=1 SV=3 - [AK1A1_HUMAN]	20.01	10.15	4	4	7	0.775	0.825
P11766	Alcohol dehydrogenase class-3 OS=Homo sapiens GN=ADH5 PE=1 SV=4 - [ADHX_HUMAN]	25.06	13.10	6	6	9	0.634	0.794
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	1.741	1.533
P15121	Aldose reductase OS=Homo sapiens GN=AKR1B1 PE=1 SV=3 - [ALDR_HUMAN]	22.46	7.91	3	3	7	0.420	0.410
O43768	Alpha-endosulfine OS=Homo sapiens GN=ENSA PE=1 SV=1 - [ENSA_HUMAN]	23.94	52.89	6	6	9	1.072	0.684
P06733	Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2 - [ENOA_HUMAN]	292.07	35.48	15	17	98	0.657	0.307
Q9NZD4	Alpha-hemoglobin-stabilizing protein OS=Homo sapiens GN=AHSP PE=1 SV=1 - [AHSP_HUMAN]	326.31	56.86	7	7	103	0.555	0.306
P54920	Alpha-soluble NSF attachment protein OS=Homo sapiens GN=NAPA PE=1 SV=3 - [SNAA_HUMAN]	54.79	32.88	9	9	17	0.538	0.881
Q6FI81	Anamorsin OS=Homo sapiens GN=CIAPIN1 PE=1 SV=2 - [CPIN1_HUMAN]	6.39	7.05	2	2	2	0.620	0.812
P08758	Annexin A5 OS=Homo sapiens GN=ANXA5 PE=1 SV=2 - [ANXA5_HUMAN]	12.84	7.81	3	3	5	0.453	0.381
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	0.594	1.047
P05089	Arginase-1 OS=Homo sapiens GN=ARG1 PE=1 SV=2 - [ARGI1_HUMAN]	14.85	8.07	2	3	5	1.514	0.384
O43776	Asparaginyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=NARS PE=1 SV=1 - [SYNC_HUMAN]	26.51	9.67	5	6	9	0.587	0.593
P17174	Aspartate aminotransferase, cytoplasmic OS=Homo sapiens GN=GOT1 PE=1 SV=3 - [AATC_HUMAN]	54.91	17.68	7	7	16	0.622	0.877
P14868	Aspartyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=DARS PE=1 SV=2 - [SYDC_HUMAN]	41.93	20.96	11	11	14	0.836	0.663
P53396	ATP-citrate synthase OS=Homo sapiens GN=ACLY PE=1 SV=3 - [ACLY_HUMAN]	197.11	24.25	31	31	60	0.827	0.714
Q08211	ATP-dependent RNA helicase A OS=Homo sapiens GN=DHX9 PE=1 SV=4 - [DHX9_HUMAN]	25.35	5.98	7	7	9	0.472	0.465
P02730	Band 3 anion transport protein OS=Homo sapiens GN=SLC4A1 PE=1 SV=3 - [B3AT_HUMAN]	45.64	8.01	7	7	15	4.028	0.635
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	0.269	0.123
P07814	Bifunctional aminoacyl-tRNA synthetase OS=Homo sapiens GN=EPRS PE=1 SV=5 - [SYEP_HUMAN]	25.15	3.24	4	4	7	0.536	0.398
Q3LXA3	Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing) OS=Homo sapiens GN=DAK PE=1 SV=2 - [DHAK_HUMAN]	22.15	6.78	4	4	7	0.576	1.455
P53004	Biliverdin reductase A OS=Homo sapiens GN=BLVRA PE=1 SV=2 - [BIEA_HUMAN]	65.46	32.43	12	12	21	0.592	0.946
P07738	Bisphosphoglycerate mutase OS=Homo sapiens GN=BPGM PE=1 SV=2 - [PMGE_HUMAN]	334.23	49.42	14	14	102	0.703	0.615
Q13867	Bleomycin hydrolase OS=Homo sapiens GN=BLMH PE=1 SV=1 - [BLMH_HUMAN]	13.51	10.77	4	4	4	0.785	0.919
Q9H3K6	BolA-like protein 2 OS=Homo sapiens GN=BOLA2 PE=1 SV=1 - [BOLA2_HUMAN]	17.06	26.74	2	2	5	0.871	1.128
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	0.625	0.836
Q5VW32	BRO1 domain-containing protein BROX OS=Homo sapiens GN=BROX PE=1 SV=1 - [BROX_HUMAN]	35.09	13.63	8	8	12	0.735	1.080
P11586	C-1-tetrahydrofolate synthase, cytoplasmic OS=Homo sapiens GN=MTHFD1 PE=1 SV=3 - [C1TC_HUMAN]	122.17	23.21	26	26	40	0.836	1.160
P27708	CAD protein OS=Homo sapiens GN=CAD PE=1 SV=3 - [PYR1_HUMAN]	6.22	0.90	2	2	2	0.490	0.698

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	0.831	0.796
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	0.851	1.230
P62158	Calmodulin OS=Homo sapiens GN=CALM1 PE=1 SV=2 - [CALM_HUMAN]	153.79	23.49	6	6	46	0.724	1.183
P04632	Calpain small subunit 1 OS=Homo sapiens GN=CAPNS1 PE=1 SV=1 - [CPNS1_HUMAN]	23.52	21.27	6	6	9	0.804	1.456
P07384	Calpain-1 catalytic subunit OS=Homo sapiens GN=CAPN1 PE=1 SV=1 - [CAN1_HUMAN]	77.80	18.91	14	14	25	0.823	1.349
P27797	Calreticulin OS=Homo sapiens GN=CALR PE=1 SV=1 - [CALR_HUMAN]	19.77	18.47	6	6	7	0.625	0.524
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	0.629	0.982
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	0.765	0.933
P00915	Carbonic anhydrase 1 OS=Homo sapiens GN=CA1 PE=1 SV=2 - [CAH1_HUMAN]	421.71	55.56	11	11	130	1.075	8.706
P00918	Carbonic anhydrase 2 OS=Homo sapiens GN=CA2 PE=1 SV=2 - [CAH2_HUMAN]	220.55	47.69	11	11	70	1.470	4.976
P16152	Carbonyl reductase [NADPH] 1 OS=Homo sapiens GN=CBR1 PE=1 SV=3 - [CBR1_HUMAN]	8.38	5.78	2	2	3	0.759	1.578
Q96DG6	Carboxymethylenebutenolidase homolog OS=Homo sapiens GN=CMBL PE=1 SV=1 - [CMBL_HUMAN]	26.33	21.63	7	7	9	0.613	1.529
P04040	Catalase OS=Homo sapiens GN=CAT PE=1 SV=3 - [CATA_HUMAN]	549.08	53.70	30	30	180	0.903	1.135
Q9Y5K6	CD2-associated protein OS=Homo sapiens GN=CD2AP PE=1 SV=1 - [CD2AP_HUMAN]	13.81	5.48	4	4	5	0.926	0.801
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	0.624	1.410
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	0.467	0.638
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	0.737	0.821
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	0.241	0.264
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	0.532	0.420
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	0.627	0.846
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	1.505	0.812
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	0.968	1.042
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	0.683	1.117
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	0.770	0.965
O43633	Charged multivesicular body protein 2a OS=Homo sapiens GN=CHMP2A PE=1 SV=1 - [CHM2A_HUMAN]	14.42	14.41	4	4	5	1.300	1.001
Q9H444	Charged multivesicular body protein 4b OS=Homo sapiens GN=CHMP4B PE=1 SV=1 - [CHM4B_HUMAN]	13.57	15.63	4	4	4	0.823	0.856
O00299	Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4 - [CLIC1_HUMAN]	35.11	22.82	7	7	12	0.732	1.061
Q13185	Chromobox protein homolog 3 OS=Homo sapiens GN=CBX3 PE=1 SV=4 - [CBX3_HUMAN]	13.93	24.04	4	4	4	0.253	0.349
Q00610	Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC PE=1 SV=5 - [CLH1_HUMAN]	120.88	13.13	22	22	39	0.476	0.863
P09497	Clathrin light chain B OS=Homo sapiens GN=CLTB PE=1 SV=1 - [CLCB_HUMAN]	9.85	12.23	3	3	3	0.588	0.925
P48444	Coatomer subunit delta OS=Homo sapiens GN=ARCN1 PE=1 SV=1 - [COPD_HUMAN]	8.32	4.11	2	2	3	0.420	0.265
Q15021	Condensin complex subunit 1 OS=Homo sapiens GN=NCAPD2 PE=1 SV=3 - [CND1_HUMAN]	5.39	1.14	2	2	2	0.301	0.533
Q13098	COP9 signalosome complex subunit 1 OS=Homo sapiens GN=GPS1 PE=1 SV=4 - [CSN1_HUMAN]	15.51	8.35	5	5	6	0.656	1.283
Q9BT78	COP9 signalosome complex subunit 4 OS=Homo sapiens GN=COPS4 PE=1 SV=1 - [CSN4_HUMAN]	24.26	14.78	6	6	7	0.628	1.198
Q92905	COP9 signalosome complex subunit 5 OS=Homo sapiens GN=COPS5 PE=1 SV=4 - [CSN5_HUMAN]	16.14	6.89	3	3	5	0.743	1.091
Q9H9Q2	COP9 signalosome complex subunit 7b OS=Homo sapiens GN=COPS7B PE=1 SV=1 - [CSN7B_HUMAN]	5.52	8.71	2	2	2	0.675	1.060
Q5JX54	Copine I (Fragment) OS=Homo sapiens GN=CPNE1 PE=2 SV=1 - [Q5JX54_HUMAN]	6.27	13.24	2	2	2	0.646	1.383
O14618	Copper chaperone for superoxide dismutase OS=Homo sapiens GN=CCS PE=1 SV=1 - [CCS_HUMAN]	44.72	22.99	8	8	15	0.814	1.773
P36551	Coproporphyrinogen-III oxidase, mitochondrial OS=Homo sapiens GN=CPOX PE=1 SV=3 - [HEM6_HUMAN]	19.59	15.64	6	6	6	0.687	0.559
Q9ULV4	Coronin-1C OS=Homo sapiens GN=CORO1C PE=1 SV=1 - [COR1C_HUMAN]	37.25	11.81	9	9	12	0.483	0.510
P57737	Coronin-7 OS=Homo sapiens GN=CORO7 PE=1 SV=2 - [CORO7_HUMAN]	5.03	1.84	2	2	2	0.494	1.195
Q96H99	Cortactin OS=Homo sapiens GN=CTTN PE=2 SV=1 - [Q96H99_HUMAN]	11.36	8.38	4	4	4	0.815	0.882
P17812	CTP synthase 1 OS=Homo sapiens GN=CTPS PE=1 SV=2 - [PYRG1_HUMAN]	21.01	7.28	2	5	7	0.699	0.832
Q13617	Cullin-2 OS=Homo sapiens GN=CUL2 PE=1 SV=2 - [CUL2_HUMAN]	17.26	4.56	4	4	6	0.630	1.147
Q13618	Cullin-3 OS=Homo sapiens GN=CUL3 PE=1 SV=2 - [CUL3_HUMAN]	18.35	6.90	6	6	6	1.056	1.192
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	0.708	1.336
P04080	Cystatin-B OS=Homo sapiens GN=CSTB PE=1 SV=2 - [CYTB_HUMAN]	33.79	30.61	3	3	11	0.702	0.809
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	0.811	0.885
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	0.678	1.004
P00167	Cytochrome b5 OS=Homo sapiens GN=CYB5A PE=1 SV=2 - [CYB5_HUMAN]	13.39	27.61	4	4	5	0.625	0.759
Q8IUI8	Cytokine receptor-like factor 3 OS=Homo sapiens GN=CRLF3 PE=1 SV=2 - [CRLF3_HUMAN]	32.75	11.09	6	6	11	0.898	1.007
P28838	Cytosol aminopeptidase OS=Homo sapiens GN=LAP3 PE=1 SV=3 - [AMPL_HUMAN]	22.21	8.48	5	5	7	0.796	1.007
Q96KP4	Cytosolic non-specific dipeptidase OS=Homo sapiens GN=CNDP2 PE=1 SV=2 - [CNDP2_HUMAN]	16.49	5.05	3	3	6	0.881	1.161
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	0.754	0.937
P51397	Death-associated protein 1 OS=Homo sapiens GN=DAP PE=1 SV=3 - [DAP1_HUMAN]	9.95	23.53	3	3	4	1.205	0.643
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	0.541	0.817

B7Z3I9	Delta-aminolevulinic acid dehydratase OS=Homo sapiens PE=2 SV=1 - [B7Z3I9_HUMAN]	98.15	23.00	7	7	33	0.809	1.244
O43598	Deoxyribonucleoside 5'-monophosphate N-glycosidase OS=Homo sapiens GN=RCL PE=1 SV=1 - [RCL_HUMAN]	7.65	12.07	3	3	3	0.761	0.929
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	0.627	0.734
Q86TI2	Dipeptidyl peptidase 9 OS=Homo sapiens GN=DPP9 PE=1 SV=3 - [DPP9_HUMAN]	5.44	2.20	2	2	2	0.709	1.075
Q8NFP7	Diphosphoinositol polyphosphate phosphohydrolase 3-alpha OS=Homo sapiens GN=NUDT10 PE=1 SV=1 - [NUD10_HUMAN]	15.08	14.63	2	2	4	0.285	0.601
P53602	Diphosphomevalonate decarboxylase OS=Homo sapiens GN=MVD PE=1 SV=1 - [MVD1_HUMAN]	30.06	11.00	5	5	11	1.073	0.554
Q16531	DNA damage-binding protein 1 OS=Homo sapiens GN=DDB1 PE=1 SV=1 - [DDB1_HUMAN]	47.89	8.86	10	10	16	0.579	0.664
Q92878	DNA repair protein RAD50 OS=Homo sapiens GN=RAD50 PE=1 SV=1 - [RAD50_HUMAN]	5.34	1.07	2	2	2	0.634	0.930
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	0.799	1.100
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	0.525	0.894
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	1.127	1.015
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	0.771	0.809
Q9UJU6	Drebrin-like protein OS=Homo sapiens GN=DBNL PE=1 SV=1 - [DBNL_HUMAN]	10.45	7.67	3	3	3	0.874	0.884
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	0.661	1.433
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	0.917	0.830
Q9P0J7	E3 ubiquitin-protein ligase KCMF1 OS=Homo sapiens GN=KCMF1 PE=1 SV=2 - [KCMF1_HUMAN]	9.38	4.20	2	2	3	0.601	1.157
Q5XPI4	E3 ubiquitin-protein ligase RNF123 OS=Homo sapiens GN=RNF123 PE=1 SV=1 - [RN123_HUMAN]	33.91	6.24	9	9	11	0.574	1.285
Q5T4S7	E3 ubiquitin-protein ligase UBR4 OS=Homo sapiens GN=UBR4 PE=1 SV=1 - [UBR4_HUMAN]	29.46	1.16	9	9	11	0.566	1.004
Q4VBZ6	EEF1D protein OS=Homo sapiens GN=EEF1D PE=1 SV=1 - [Q4VBZ6_HUMAN]	12.59	13.62	3	4	4	0.560	0.764
P68104	Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 - [EF1A1_HUMAN]	163.46	21.65	15	15	57	0.616	0.331
P24534	Elongation factor 1-beta OS=Homo sapiens GN=EEF1B2 PE=1 SV=3 - [EF1B_HUMAN]	17.18	12.00	3	4	6	0.456	0.527
P26641	Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3 - [EF1G_HUMAN]	49.89	23.11	12	12	16	0.538	0.561
P13639	Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 - [EF2_HUMAN]	138.37	26.34	24	24	45	0.574	0.733
B7Z2X9	Enolase OS=Homo sapiens GN=ENO2 PE=2 SV=1 - [B7Z2X9_HUMAN]	85.35	17.65	5	8	31	0.698	0.811
Q96CG1	ETF1 protein OS=Homo sapiens GN=ETF1 PE=2 SV=1 - [Q96CG1_HUMAN]	13.82	8.91	4	4	5	0.608	0.371
Q99447	Ethanolamine-phosphate cytidylyltransferase OS=Homo sapiens GN=PCYT2 PE=1 SV=1 - [PCY2_HUMAN]	19.33	7.97	3	3	6	0.734	0.645
P60842	Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=1 SV=1 - [IF4A1_HUMAN]	83.30	33.25	6	12	23	0.538	0.355
P38919	Eukaryotic initiation factor 4A-III OS=Homo sapiens GN=EIF4A3 PE=1 SV=4 - [IF4A3_HUMAN]	22.93	13.63	3	5	7	0.536	0.651
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	0.443	0.362
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	0.797	0.540
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	0.804	0.413
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	0.816	0.500
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	0.235	0.261
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	0.360	0.330
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	0.375	0.287
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	0.762	0.700
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	0.402	0.525
P06730	Eukaryotic translation initiation factor 4E OS=Homo sapiens GN=EIF4E PE=1 SV=2 - [IF4E_HUMAN]	17.96	25.35	5	5	6	0.894	1.011
Q15056	Eukaryotic translation initiation factor 4H OS=Homo sapiens GN=EIF4H PE=1 SV=5 - [IF4H_HUMAN]	7.74	8.87	3	3	3	0.239	0.623
P55010	Eukaryotic translation initiation factor 5 OS=Homo sapiens GN=EIF5 PE=1 SV=2 - [IF5_HUMAN]	22.57	9.74	5	5	7	0.452	0.754
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	1.138	0.782
O60841	Eukaryotic translation initiation factor 5B OS=Homo sapiens GN=EIF5B PE=1 SV=4 - [IF2P_HUMAN]	13.38	3.03	5	5	5	0.425	0.426
O14980	Exportin-1 OS=Homo sapiens GN=XPO1 PE=1 SV=1 - [XPO1_HUMAN]	15.29	3.17	4	5	6	0.426	1.193
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	0.881	1.438
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	0.774	1.153
Q5TI86	F-box protein 7 OS=Homo sapiens GN=FBXO7 PE=2 SV=1 - [Q5TI86_HUMAN]	28.84	11.27	6	6	10	0.940	1.375
Q16658	Fascin OS=Homo sapiens GN=FSCN1 PE=1 SV=3 - [FSCN1_HUMAN]	37.64	15.82	10	10	14	0.589	0.831
P49327	Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3 - [FAS_HUMAN]	196.48	13.50	34	34	67	0.852	0.355
Q01469	Fatty acid-binding protein, epidermal OS=Homo sapiens GN=FABP5 PE=1 SV=3 - [FABP5_HUMAN]	26.35	31.11	5	5	9	0.354	0.486
A6NDY9	Filamin A OS=Homo sapiens GN=FLNA PE=2 SV=4 - [A6NDY9_HUMAN]	11.21	1.21	3	3	4	0.564	0.661
P30043	Flavin reductase OS=Homo sapiens GN=BLVRB PE=1 SV=3 - [BLVRB_HUMAN]	409.71	50.49	8	8	129	0.732	0.866
P04075	Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2 - [ALDOA_HUMAN]	313.08	36.81	15	20	92	1.038	0.485
P09972	Fructose-bisphosphate aldolase C OS=Homo sapiens GN=ALDOC PE=1 SV=2 - [ALDOC_HUMAN]	68.68	25.55	5	10	23	1.386	0.576
P07954	Fumarate hydratase, mitochondrial OS=Homo sapiens GN=FH PE=1 SV=3 - [FUMH_HUMAN]	18.61	6.47	4	4	6	0.772	0.852
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	0.533	0.493
P17931	Galectin-3 OS=Homo sapiens GN=LGALS3 PE=1 SV=5 - [LEG3_HUMAN]	25.07	25.20	7	7	9	1.944	1.106

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	0.414	0.462
Q13630	GDP-L-fucose synthase OS=Homo sapiens GN=TSTA3 PE=1 SV=1 - [FCL_HUMAN]	61.42	25.86	9	9	18	0.802	0.861
Q6PCE3	Glucose 1,6-bisphosphate synthase OS=Homo sapiens GN=PGM2L1 PE=1 SV=3 - [PGM2L_HUMAN]	34.66	9.49	5	6	11	0.905	1.318
P11413	Glucose-6-phosphate 1-dehydrogenase OS=Homo sapiens GN=G6PD PE=1 SV=4 - [G6PD_HUMAN]	74.35	20.97	13	13	26	0.641	0.575
P06744	Glucose-6-phosphate isomerase OS=Homo sapiens GN=GPI PE=1 SV=4 - [G6PI_HUMAN]	141.79	25.99	19	19	51	0.771	0.494
P48506	Glutamate--cysteine ligase catalytic subunit OS=Homo sapiens GN=GCLC PE=1 SV=2 - [GSH1_HUMAN]	98.03	21.04	14	14	31	0.735	0.979
P48507	Glutamate--cysteine ligase regulatory subunit OS=Homo sapiens GN=GCLM PE=1 SV=1 - [GSH0_HUMAN]	30.43	31.02	7	7	10	0.769	1.171
P15104	Glutamine synthetase OS=Homo sapiens GN=GLUL PE=1 SV=4 - [GLNA_HUMAN]	30.16	13.40	7	7	11	0.481	0.456
P35754	Glutaredoxin-1 OS=Homo sapiens GN=GLRX PE=1 SV=2 - [GLRX1_HUMAN]	8.00	28.30	3	3	3	0.759	0.470
O76003	Glutaredoxin-3 OS=Homo sapiens GN=GLRX3 PE=1 SV=2 - [GLRX3_HUMAN]	18.61	14.63	5	5	6	0.766	0.956
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	0.736	1.021
P07203	Glutathione peroxidase 1 OS=Homo sapiens GN=GPX1 PE=1 SV=4 - [GPX1_HUMAN]	9.87	9.36	2	2	3	0.695	1.358
P78417	Glutathione S-transferase omega-1 OS=Homo sapiens GN=GSTO1 PE=1 SV=2 - [GSTO1_HUMAN]	123.22	40.66	10	10	39	0.631	0.799
P48637	Glutathione synthetase OS=Homo sapiens GN=GSS PE=1 SV=1 - [GSHB_HUMAN]	33.98	15.61	8	8	12	0.966	1.235
P04406	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3 - [G3P_HUMAN]	278.89	42.99	16	16	100	1.322	0.538
P41250	Glycyl-tRNA synthetase OS=Homo sapiens GN=GARS PE=1 SV=3 - [SYG_HUMAN]	28.42	9.07	7	8	10	0.079	0.101
P36959	GMP reductase 1 OS=Homo sapiens GN=GMPR PE=1 SV=1 - [GMPR1_HUMAN]	52.16	19.71	6	7	17	0.816	1.205
Q14789	Golgin subfamily B member 1 OS=Homo sapiens GN=GOLGB1 PE=1 SV=2 - [GOGB1_HUMAN]	10.02	1.01	2	4	4	0.615	0.355
P62826	GTP-binding nuclear protein Ran OS=Homo sapiens GN=RAN PE=1 SV=3 - [RAN_HUMAN]	116.04	36.11	9	9	36	0.728	0.763
O00178	GTP-binding protein 1 OS=Homo sapiens GN=GTPBP1 PE=1 SV=3 - [GTPB1_HUMAN]	5.90	2.39	2	2	2	0.716	0.856
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	0.478	0.959
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	0.637	0.754
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	0.367	0.420
Q16774	Guanylate kinase OS=Homo sapiens GN=GUK1 PE=1 SV=2 - [KGUA_HUMAN]	11.74	9.64	2	2	4	0.714	1.011
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	0.390	0.473
Q9Y450	HBS1-like protein OS=Homo sapiens GN=HBS1L PE=1 SV=1 - [HBS1L_HUMAN]	9.03	3.65	3	3	3	0.593	0.603
Q7Z4H3	HD domain-containing protein 2 OS=Homo sapiens GN=HDDC2 PE=1 SV=1 - [HDDC2_HUMAN]	4.99	3.43	2	2	2	0.561	0.529
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	0.829	0.246
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	0.424	0.855
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	0.684	0.891
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	0.632	0.786
Q92598	Heat shock protein 105 kDa OS=Homo sapiens GN=HSPH1 PE=1 SV=1 - [HS105_HUMAN]	10.54	2.91	3	3	4	0.443	0.575
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	0.443	0.649
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	0.395	0.922
Q9NRV9	Heme-binding protein 1 OS=Homo sapiens GN=HEBP1 PE=1 SV=1 - [HEBP1_HUMAN]	51.14	33.33	6	6	15	0.799	1.183
Q9BXL5	Hemogen OS=Homo sapiens GN=HEMGN PE=1 SV=1 - [HEMGN_HUMAN]	32.83	15.29	8	8	12	0.266	0.307
P69905	Hemoglobin subunit alpha OS=Homo sapiens GN=HBA1 PE=1 SV=2 - [HBA_HUMAN]	4320.24	76.06	13	14	1324	0.951	1.115
P68871	Hemoglobin subunit beta OS=Homo sapiens GN=HBB PE=1 SV=2 - [HBB_HUMAN]	5787.45	100.00	8	16	1697	2.203	4.842
P02042	Hemoglobin subunit delta OS=Homo sapiens GN=HBD PE=1 SV=2 - [HBD_HUMAN]	2562.86	91.84	6	14	761	3.431	11.660
P02100	Hemoglobin subunit epsilon OS=Homo sapiens GN=HBE1 PE=1 SV=2 - [HBE_HUMAN]	895.47	39.46	3	6	310	0.281	0.044
P69892	Hemoglobin subunit gamma-2 OS=Homo sapiens GN=HBG2 PE=1 SV=2 - [HBG2_HUMAN]	7848.95	81.63	3	14	2305	0.106	0.015
Q6B0K9	Hemoglobin subunit mu OS=Homo sapiens GN=HBM PE=2 SV=1 - [HBM_HUMAN]	75.31	48.23	5	5	25	0.362	0.206
P09105	Hemoglobin subunit theta-1 OS=Homo sapiens GN=HBQ1 PE=1 SV=2 - [HBAT_HUMAN]	16.55	30.28	3	3	4	0.690	0.627
P02008	Hemoglobin subunit zeta OS=Homo sapiens GN=HBZ PE=1 SV=2 - [HBAZ_HUMAN]	1008.02	74.65	8	9	360	0.231	0.018
D9YZU8	Hemoglobin, gamma A OS=Homo sapiens GN=HBG1 PE=3 SV=1 - [D9YZU8_HUMAN]	6053.18	81.63	4	15	1857	0.328	0.085
P51858	Hepatoma-derived growth factor OS=Homo sapiens GN=HDGF PE=1 SV=1 - [HDGF_HUMAN]	56.32	35.42	8	8	17	0.545	0.349
P09651	Heterogeneous nuclear ribonucleoprotein A1 OS=Homo sapiens GN=HNRNPA1 PE=1 SV=5 - [ROA1_HUMAN]	34.94	15.32	3	7	12	0.364	0.382
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	0.207	0.563
P52272	Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens GN=HNRNPM PE=1 SV=3 - [HNRPM_HUMAN]	8.69	4.38	3	3	3	0.285	0.556
O60506	Heterogeneous nuclear ribonucleoprotein Q OS=Homo sapiens GN=SYNCRIP PE=1 SV=2 - [HNRPQ_HUMAN]	11.35	2.25	2	2	4	0.455	0.797
P22626	Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens GN=HNRNPA2B1 PE=1 SV=2 - [ROA2_HUMAN]	47.36	24.36	7	10	16	0.372	0.405
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	0.722	0.761
P16403	Histone H1.2 OS=Homo sapiens GN=HIST1H1C PE=1 SV=2 - [H12_HUMAN]	19.36	17.37	2	5	6	0.038	0.945
O60814	Histone H2B type 1-K OS=Homo sapiens GN=HIST1H2BK PE=1 SV=3 - [H2B1K_HUMAN]	15.92	24.60	4	4	6	0.040	0.493
P68431	Histone H3.1 OS=Homo sapiens GN=HIST1H3A PE=1 SV=2 - [H31_HUMAN]	5.78	13.24	2	2	2	0.129	0.884
P62805	Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2 - [H4_HUMAN]	11.07	21.36	2	2	3	0.027	0.656

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	0.446	0.738
B0UX83	HLA-B associated transcript 3 OS=Homo sapiens GN=BAT3 PE=4 SV=1 - [B0UX83_HUMAN]	4.61	1.95	2	2	2	0.507	0.905
P50502	Hsc70-interacting protein OS=Homo sapiens GN=ST13 PE=1 SV=2 - [F10A1_HUMAN]	52.44	24.12	11	11	18	0.808	1.053
Q16543	Hsp90 co-chaperone Cdc37 OS=Homo sapiens GN=CDC37 PE=1 SV=1 - [CDC37_HUMAN]	24.43	12.70	6	6	8	0.602	0.467
Q16775	Hydroxyacylglutathione hydrolase, mitochondrial OS=Homo sapiens GN=HAGH PE=1 SV=2 - [GLO2_HUMAN]	37.19	20.78	6	6	13	0.999	0.960
P00492	Hypoxanthine-guanine phosphoribosyltransferase OS=Homo sapiens GN=HPRT1 PE=1 SV=2 - [HPRT_HUMAN]	39.65	25.23	5	5	12	0.763	1.093
P78318	Immunoglobulin-binding protein 1 OS=Homo sapiens GN=IGBP1 PE=1 SV=1 - [IGBP1_HUMAN]	10.00	11.80	3	3	3	0.641	0.899
Q14974	Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2 - [IMB1_HUMAN]	47.55	10.05	8	8	16	0.553	0.790
O95373	Importin-7 OS=Homo sapiens GN=IPO7 PE=1 SV=1 - [IPO7_HUMAN]	9.60	1.54	2	2	3	0.486	1.502
Q96P70	Importin-9 OS=Homo sapiens GN=IPO9 PE=1 SV=3 - [IPO9_HUMAN]	9.87	2.40	3	3	3	0.529	1.079
Q15181	Inorganic pyrophosphatase OS=Homo sapiens GN=PPA1 PE=1 SV=2 - [IPYR_HUMAN]	26.28	24.57	7	7	8	0.681	0.978
P14735	Insulin-degrading enzyme OS=Homo sapiens GN=IDE PE=1 SV=4 - [IDE_HUMAN]	12.11	4.12	4	4	4	0.820	0.891
P80217	Interferon-induced 35 kDa protein OS=Homo sapiens GN=IFI35 PE=1 SV=5 - [IN35_HUMAN]	6.56	7.34	2	2	2	0.535	0.751
Q9HBB2	Iron regulatory protein 1 OS=Homo sapiens GN=IRP1 PE=2 SV=1 - [Q9HBB2_HUMAN]	21.96	6.33	6	6	8	0.630	0.672
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	0.810	1.181
O75874	Isocitrate dehydrogenase [NADP] cytoplasmic OS=Homo sapiens GN=IDH1 PE=1 SV=2 - [IDHC_HUMAN]	28.96	9.18	6	6	10	0.575	0.928
O76009	Keratin, type I cuticular Ha3-I OS=Homo sapiens GN=KRT33A PE=1 SV=2 - [KT33A_HUMAN]	11.77	4.70	2	2	4	0.618	0.010
P13645	Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6 - [K1C10_HUMAN]	22.70	8.05	5	5	7	1.991	0.077
P35527	Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3 - [K1C9_HUMAN]	48.75	14.93	9	9	14	1.115	0.140
Q9NSB4	Keratin, type II cuticular Hb2 OS=Homo sapiens GN=KRT82 PE=1 SV=3 - [KRT82_HUMAN]	14.13	3.70	2	2	5	0.664	0.010
P78385	Keratin, type II cuticular Hb3 OS=Homo sapiens GN=KRT83 PE=1 SV=2 - [KRT83_HUMAN]	46.92	17.65	10	11	16	0.783	0.027
P04264	Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6 - [K2C1_HUMAN]	60.86	15.53	11	12	18	1.097	0.067
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	2.060	0.015
Q9HA64	Ketosamine-3-kinase OS=Homo sapiens GN=FN3KRP PE=1 SV=2 - [KT3K_HUMAN]	31.55	13.59	6	6	11	0.871	1.264
P07195	L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2 - [LDHB_HUMAN]	243.80	38.02	13	15	72	0.694	0.905
E9PH51	L-lactate dehydrogenase OS=Homo sapiens GN=LDHA PE=3 SV=2 - [E9PH51_HUMAN]	280.99	38.03	11	13	85	0.789	0.543
Q7Z4W1	L-xylulose reductase OS=Homo sapiens GN=DCXR PE=1 SV=2 - [DCXR_HUMAN]	13.19	11.89	3	3	4	0.741	0.812
Q04760	Lactoylglutathione lyase OS=Homo sapiens GN=GLO1 PE=1 SV=4 - [LGUL_HUMAN]	28.37	20.65	4	4	9	0.901	1.280
Q9NS86	LanC-like protein 2 OS=Homo sapiens GN=LANCL2 PE=1 SV=1 - [LANC2_HUMAN]	5.67	4.67	2	2	2	0.903	1.205
Q9BS40	Latexin OS=Homo sapiens GN=LXN PE=1 SV=2 - [LXN_HUMAN]	52.70	27.03	6	6	17	0.654	0.800
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	0.608	0.876
P09960	Leukotriene A-4 hydrolase OS=Homo sapiens GN=LTA4H PE=1 SV=2 - [LKHA4_HUMAN]	27.50	11.29	8	8	10	0.541	0.946
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	0.711	0.915
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	0.699	0.955
P05455	Lupus La protein OS=Homo sapiens GN=SSB PE=1 SV=2 - [LA_HUMAN]	13.06	10.05	5	5	5	0.286	0.315
Q5QPQ1	Lysophospholipase II (Fragment) OS=Homo sapiens GN=LYPLA2 PE=2 SV=1 - [Q5QPQ1_HUMAN]	7.43	8.64	2	2	3	0.628	1.420
P40925	Malate dehydrogenase, cytoplasmic OS=Homo sapiens GN=MDH1 PE=1 SV=4 - [MDHC_HUMAN]	173.76	38.02	16	16	56	0.716	0.858
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	0.201	0.569
P50579	Methionine aminopeptidase 2 OS=Homo sapiens GN=METAP2 PE=1 SV=1 - [AMPM2_HUMAN]	12.99	7.74	3	3	4	0.783	1.060
P26038	Moesin OS=Homo sapiens GN=MSN PE=1 SV=3 - [MOES_HUMAN]	102.21	25.13	16	21	33	1.046	1.083
P60201	Myelin proteolipid protein OS=Homo sapiens GN=PLP1 PE=1 SV=2 - [MYPR_HUMAN]	19.73	14.08	4	4	6	1.441	0.617
P12829	Myosin light chain 4 OS=Homo sapiens GN=MYL4 PE=1 SV=3 - [MYL4_HUMAN]	22.67	26.40	4	4	6	0.673	0.259
P60660	Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2 - [MYL6_HUMAN]	5.87	13.25	2	2	2	0.847	0.873
P35580	Myosin-10 OS=Homo sapiens GN=MYH10 PE=1 SV=3 - [MYH10_HUMAN]	151.39	15.94	22	36	52	0.616	0.151
P35579	Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4 - [MYH9_HUMAN]	272.21	23.98	42	53	91	0.672	0.359
Q9BUF9	Myosin, light chain 9, regulatory OS=Homo sapiens GN=MYL9 PE=2 SV=1 - [Q9BUF9_HUMAN]	8.34	12.71	2	2	3	0.780	0.613
P58546	Myotrophin OS=Homo sapiens GN=MTPN PE=1 SV=2 - [MTPN_HUMAN]	26.51	22.03	2	2	9	0.904	1.309
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	0.600	0.402
Q15843	NEDD8 OS=Homo sapiens GN=NEDD8 PE=1 SV=1 - [NEDD8_HUMAN]	21.40	39.51	5	5	8	0.632	0.602
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	0.678	0.889
P61081	NEDD8-conjugating enzyme Ubc12 OS=Homo sapiens GN=UBE2M PE=1 SV=1 - [UBC12_HUMAN]	30.04	20.22	5	5	9	0.778	0.831
Q8NBF2	NHL repeat-containing protein 2 OS=Homo sapiens GN=NHLRC2 PE=1 SV=1 - [NHLC2_HUMAN]	6.67	2.62	2	2	2	0.723	0.889
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	0.780	1.121
Q9GZT8	NIF3-like protein 1 OS=Homo sapiens GN=NIF3L1 PE=1 SV=2 - [NIF3L_HUMAN]	8.63	4.77	2	2	3	0.845	1.003
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	0.863	1.048
Q9UNZ2	NSFL1 cofactor p47 OS=Homo sapiens GN=NSFL1C PE=1 SV=2 - [NSF1C_HUMAN]	42.32	23.51	8	8	12	0.723	1.392

Q9Y266	Nuclear migration protein nudC OS=Homo sapiens GN=NUDC PE=1 SV=1 - [NUDC_HUMAN]	29.13	12.99	5	5	9	0.315	0.227
P61970	Nuclear transport factor 2 OS=Homo sapiens GN=NUTF2 PE=1 SV=1 - [NTF2_HUMAN]	12.37	11.02	2	2	4	0.792	1.072
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	0.247	0.480
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	0.435	0.541
P19338	Nucleolin OS=Homo sapiens GN=NCL PE=1 SV=3 - [NUCL_HUMAN]	73.89	16.48	19	19	27	0.059	0.438
P06748	Nucleophosmin OS=Homo sapiens GN=NPM1 PE=1 SV=2 - [NPM_HUMAN]	17.54	10.88	4	4	6	0.012	0.317
Q32Q12	Nucleoside diphosphate kinase OS=Homo sapiens GN=NME1-NME2 PE=2 SV=1 - [Q32Q12_HUMAN]	83.57	40.75	7	7	24	0.755	0.879
Q7Z7N6	NUDT1 protein OS=Homo sapiens GN=NUDT1 PE=2 SV=2 - [Q7Z7N6_HUMAN]	8.06	17.31	2	2	2	0.556	0.425
Q9NTK5	Obg-like ATPase 1 OS=Homo sapiens GN=OLA1 PE=1 SV=2 - [OLA1_HUMAN]	26.78	16.92	7	7	9	0.705	0.938
Q9NQR4	Omega-amidase NIT2 OS=Homo sapiens GN=NIT2 PE=1 SV=1 - [NIT2_HUMAN]	11.33	11.23	3	3	4	0.587	0.728
Q96CV9	Optineurin OS=Homo sapiens GN=OPTN PE=1 SV=2 - [OPTN_HUMAN]	28.51	13.17	8	8	10	0.763	0.774
B4DTR3	Oxysterol-binding protein OS=Homo sapiens GN=OSBP2 PE=2 SV=1 - [B4DTR3_HUMAN]	9.12	4.35	2	2	2	0.665	1.758
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	0.377	0.602
P20962	Parathymosin OS=Homo sapiens GN=PTMS PE=1 SV=2 - [PTMS_HUMAN]	19.30	22.55	3	3	6	0.691	0.264
Q9UBV8	Peflin OS=Homo sapiens GN=PEF1 PE=1 SV=1 - [PEF1_HUMAN]	7.37	3.87	2	2	2	0.704	0.924
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	0.915	0.889
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	0.710	0.283
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	0.614	0.661
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	0.547	1.078
O60664	Perilipin-3 OS=Homo sapiens GN=PLIN3 PE=1 SV=3 - [PLIN3_HUMAN]	34.68	11.98	6	6	11	0.601	1.072
Q06830	Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1 - [PRDX1_HUMAN]	224.41	64.32	11	12	67	0.839	1.051
P32119	Peroxiredoxin-2 OS=Homo sapiens GN=PRDX2 PE=1 SV=5 - [PRDX2_HUMAN]	718.77	59.60	10	11	228	0.779	1.029
P30044	Peroxiredoxin-5, mitochondrial OS=Homo sapiens GN=PRDX5 PE=1 SV=4 - [PRDX5_HUMAN]	13.23	11.68	2	2	4	0.374	0.645
P30041	Peroxiredoxin-6 OS=Homo sapiens GN=PRDX6 PE=1 SV=3 - [PRDX6_HUMAN]	177.23	44.64	12	12	60	0.911	1.331
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	0.720	0.548
Q9NSD9	Phenylalanyl-tRNA synthetase beta chain OS=Homo sapiens GN=FARSB PE=1 SV=3 - [SYFB_HUMAN]	22.51	8.15	6	6	8	0.455	0.686
Q9UKL6	Phosphatidylcholine transfer protein OS=Homo sapiens GN=PCTP PE=1 SV=1 - [PPCT_HUMAN]	4.83	7.01	2	2	2	0.926	0.834
P30086	Phosphatidylethanolamine-binding protein 1 OS=Homo sapiens GN=PEBP1 PE=1 SV=3 - [PEBP1_HUMAN]	37.41	34.76	5	5	11	0.597	0.949
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	1.070	1.138
Q96G03	Phosphoglucomutase-2 OS=Homo sapiens GN=PGM2 PE=1 SV=4 - [PGM2_HUMAN]	33.18	11.44	7	8	12	0.903	1.100
P00558	Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 PE=1 SV=3 - [PGK1_HUMAN]	346.93	58.51	22	27	113	0.865	0.678
P07205	Phosphoglycerate kinase 2 OS=Homo sapiens GN=PGK2 PE=1 SV=3 - [PGK2_HUMAN]	63.25	19.66	2	9	23	0.808	0.564
P18669	Phosphoglycerate mutase 1 OS=Homo sapiens GN=PGAM1 PE=1 SV=2 - [PGAM1_HUMAN]	75.80	31.10	8	8	26	0.879	0.734
A6NDG6	Phosphoglycolate phosphatase OS=Homo sapiens GN=PGP PE=1 SV=1 - [PGP_HUMAN]	18.00	12.15	5	5	6	0.646	0.896
Q9HAB8	Phosphopantothenate--cysteine ligase OS=Homo sapiens GN=PPCS PE=1 SV=2 - [PPCS_HUMAN]	5.97	5.79	2	2	2	0.768	1.123
O15067	Phosphoribosylformylglycinamidine synthase OS=Homo sapiens GN=PFAS PE=1 SV=4 - [PUR4_HUMAN]	52.46	9.49	13	13	18	0.636	0.832
Q9Y617	Phosphoserine aminotransferase OS=Homo sapiens GN=PSAT1 PE=1 SV=2 - [SERC_HUMAN]	59.69	26.22	11	12	22	0.615	0.333
Q9GZP4	PITH domain-containing protein 1 OS=Homo sapiens GN=PITHD1 PE=1 SV=1 - [PITH1_HUMAN]	47.16	26.54	5	5	17	0.755	0.962
P13796	Plastin-2 OS=Homo sapiens GN=LCP1 PE=1 SV=6 - [PLSL_HUMAN]	42.49	14.99	10	10	14	0.436	0.380
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	0.796	0.840
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	0.767	1.020
Q68Y55	Poly(RC) binding protein 2 OS=Homo sapiens GN=PCBP2 PE=2 SV=1 - [Q68Y55_HUMAN]	30.03	15.71	2	5	9	0.619	0.666
Q15365	Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2 - [PCBP1_HUMAN]	33.09	15.45	3	6	10	0.701	0.981
P26599	Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 PE=1 SV=1 - [PTBP1_HUMAN]	12.55	4.71	3	3	4	0.340	1.036
O60925	Prefoldin subunit 1 OS=Homo sapiens GN=PFDN1 PE=1 SV=2 - [PFD1_HUMAN]	16.25	19.67	3	3	6	0.887	0.628
Q9UHV9	Prefoldin subunit 2 OS=Homo sapiens GN=PFDN2 PE=1 SV=1 - [PFD2_HUMAN]	21.85	27.27	4	4	7	0.771	0.484
Q9NQP4	Prefoldin subunit 4 OS=Homo sapiens GN=PFDN4 PE=1 SV=1 - [PFD4_HUMAN]	6.67	16.42	2	2	2	0.803	0.589
Q99471	Prefoldin subunit 5 OS=Homo sapiens GN=PFDN5 PE=1 SV=2 - [PFD5_HUMAN]	5.31	8.44	2	2	2	0.841	0.466
O15212	Prefoldin subunit 6 OS=Homo sapiens GN=PFDN6 PE=1 SV=1 - [PFD6_HUMAN]	13.91	17.05	4	4	5	0.787	0.405
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	0.501	0.733
P07737	Profilin-1 OS=Homo sapiens GN=PFN1 PE=1 SV=2 - [PROF1_HUMAN]	41.92	32.14	5	5	13	0.546	1.371
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	0.642	0.992
O14737	Programmed cell death protein 5 OS=Homo sapiens GN=PDCD5 PE=1 SV=3 - [PDCD5_HUMAN]	15.73	31.20	5	5	5	0.473	0.665
Q9UQ80	Proliferation-associated protein 2G4 OS=Homo sapiens GN=PA2G4 PE=1 SV=3 - [PA2G4_HUMAN]	59.33	29.19	12	12	19	1.077	0.379
P48147	Prolyl endopeptidase OS=Homo sapiens GN=PREP PE=1 SV=2 - [PPCE_HUMAN]	6.09	2.54	2	2	2	0.713	1.592
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	0.485	1.381

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	0.511	1.117
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	0.769	1.437
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	0.946	1.133
Q06323	Proteasome activator complex subunit 1 OS=Homo sapiens GN=PSME1 PE=1 SV=1 - [PSME1_HUMAN]	52.58	38.96	10	10	17	0.770	1.440
Q9UL46	Proteasome activator complex subunit 2 OS=Homo sapiens GN=PSME2 PE=1 SV=4 - [PSME2_HUMAN]	48.80	23.43	6	6	15	0.865	1.552
P25787	Proteasome subunit alpha type-2 OS=Homo sapiens GN=PSMA2 PE=1 SV=2 - [PSA2_HUMAN]	16.42	14.96	5	5	6	0.571	1.012
P25788	Proteasome subunit alpha type-3 OS=Homo sapiens GN=PSMA3 PE=1 SV=2 - [PSA3_HUMAN]	61.54	28.63	9	10	20	0.600	0.975
P28066	Proteasome subunit alpha type-5 OS=Homo sapiens GN=PSMA5 PE=1 SV=3 - [PSA5_HUMAN]	38.56	28.22	4	5	11	0.649	1.001
P60900	Proteasome subunit alpha type-6 OS=Homo sapiens GN=PSMA6 PE=1 SV=1 - [PSA6_HUMAN]	42.41	26.42	7	7	12	0.595	1.003
O14818	Proteasome subunit alpha type-7 OS=Homo sapiens GN=PSMA7 PE=1 SV=1 - [PSA7_HUMAN]	54.29	34.27	9	9	18	0.628	0.981
P20618	Proteasome subunit beta type-1 OS=Homo sapiens GN=PSMB1 PE=1 SV=2 - [PSB1_HUMAN]	24.42	19.92	4	4	8	0.761	1.034
P49721	Proteasome subunit beta type-2 OS=Homo sapiens GN=PSMB2 PE=1 SV=1 - [PSB2_HUMAN]	15.57	13.93	5	5	5	0.610	0.966
P28070	Proteasome subunit beta type-4 OS=Homo sapiens GN=PSMB4 PE=1 SV=4 - [PSB4_HUMAN]	24.21	7.20	2	2	7	0.638	0.936
P28074	Proteasome subunit beta type-5 OS=Homo sapiens GN=PSMB5 PE=1 SV=3 - [PSB5_HUMAN]	26.57	18.63	5	5	8	0.646	1.036
P28072	Proteasome subunit beta type-6 OS=Homo sapiens GN=PSMB6 PE=1 SV=4 - [PSB6_HUMAN]	27.42	19.67	5	5	9	0.577	1.021
Q5VYK3	Proteasome-associated protein ECM29 homolog OS=Homo sapiens GN=ECM29 PE=1 SV=2 - [ECM29_HUMAN]	5.31	0.81	2	2	2	0.494	1.096
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	0.760	0.897
Q9UKV8	Protein argonaute-2 OS=Homo sapiens GN=EIF2C2 PE=1 SV=3 - [AGO2_HUMAN]	13.45	5.59	5	5	5	0.825	0.621
Q5TDH0	Protein DDI1 homolog 2 OS=Homo sapiens GN=DDI2 PE=1 SV=1 - [DDI2_HUMAN]	56.82	20.05	9	9	19	0.796	1.300
Q99497	Protein DJ-1 OS=Homo sapiens GN=PARK7 PE=1 SV=2 - [PARK7_HUMAN]	89.59	44.97	9	9	29	0.819	1.268
Q9NRY5	Protein FAM114A2 OS=Homo sapiens GN=FAM114A2 PE=1 SV=4 - [F1142_HUMAN]	29.80	16.24	7	7	9	0.561	1.090
Q9NUQ9	Protein FAM49B OS=Homo sapiens GN=FAM49B PE=1 SV=1 - [FA49B_HUMAN]	8.35	7.41	3	3	3	0.487	0.939
Q8WZA0	Protein LZIC OS=Homo sapiens GN=LZIC PE=1 SV=1 - [LZIC_HUMAN]	18.02	16.32	4	4	6	0.821	1.209
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	0.744	0.801
P35813	Protein phosphatase 1A OS=Homo sapiens GN=PPM1A PE=1 SV=1 - [PPM1A_HUMAN]	21.61	16.23	5	6	7	0.720	1.383
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	0.670	1.235
Q9Y570	Protein phosphatase methylesterase 1 OS=Homo sapiens GN=PPME1 PE=1 SV=3 - [PPME1_HUMAN]	32.44	22.54	8	8	11	0.695	0.692
Q96M27	Protein PRRC1 OS=Homo sapiens GN=PRRC1 PE=1 SV=1 - [PRRC1_HUMAN]	5.71	3.15	2	2	2	0.679	0.981
P26447	Protein S100-A4 OS=Homo sapiens GN=S100A4 PE=1 SV=1 - [S10A4_HUMAN]	94.63	36.63	5	5	29	0.528	1.052
P06703	Protein S100-A6 OS=Homo sapiens GN=S100A6 PE=1 SV=1 - [S10A6_HUMAN]	120.91	40.00	5	6	42	0.687	1.186
B7Z972	Protein-L-isoaspartate O-methyltransferase OS=Homo sapiens GN=PCMT1 PE=2 SV=1 - [B7Z972_HUMAN]	26.51	18.23	4	4	9	0.870	1.063
Q567Q5	PSMA4 protein OS=Homo sapiens GN=PSMA4 PE=2 SV=1 - [Q567Q5_HUMAN]	49.23	31.05	8	8	16	0.592	1.013
P00491	Purine nucleoside phosphorylase OS=Homo sapiens GN=PNP PE=1 SV=2 - [PNPH_HUMAN]	194.95	45.33	12	12	62	0.716	0.951
Q53XA7	Putative uncharacterized protein DKFZp686F13224 OS=Homo sapiens GN=DKFZp686F13224 PE=2 SV=1 - [Q53XA7_HUMAN]	14.34	8.31	3	3	4	0.401	0.669
Q96GD0	Pyridoxal phosphate phosphatase OS=Homo sapiens GN=PDXP PE=1 SV=2 - [PLPP_HUMAN]	7.13	9.12	2	2	2	0.772	1.178
P14618	Pyruvate kinase isozymes M1/M2 OS=Homo sapiens GN=PKM2 PE=1 SV=4 - [KPYM_HUMAN]	54.68	13.18	8	9	19	0.470	0.415
P30613	Pyruvate kinase isozymes R/L OS=Homo sapiens GN=PKLR PE=1 SV=2 - [KPYR_HUMAN]	126.04	31.18	19	20	43	0.760	0.928
P50395	Rab GDP dissociation inhibitor beta OS=Homo sapiens GN=GDI2 PE=1 SV=2 - [GDIB_HUMAN]	111.07	33.71	11	15	36	0.769	0.938
P35241	Radixin OS=Homo sapiens GN=RDX PE=1 SV=1 - [RADI_HUMAN]	47.45	15.27	6	12	16	0.883	0.972
P46060	Ran GTPase-activating protein 1 OS=Homo sapiens GN=RANGAP1 PE=1 SV=1 - [RAGP1_HUMAN]	22.80	8.69	5	5	7	0.470	0.541
P43487	Ran-specific GTPase-activating protein OS=Homo sapiens GN=RANBP1 PE=1 SV=1 - [RANG_HUMAN]	24.47	23.38	5	5	8	0.827	0.801
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	0.459	1.332
P61026	Ras-related protein Rab-10 OS=Homo sapiens GN=RAB10 PE=1 SV=1 - [RAB10_HUMAN]	15.90	15.00	2	3	5	0.743	0.876
P62491	Ras-related protein Rab-11A OS=Homo sapiens GN=RAB11A PE=1 SV=3 - [RB11A_HUMAN]	15.16	7.41	2	2	5	0.421	1.213
P61106	Ras-related protein Rab-14 OS=Homo sapiens GN=RAB14 PE=1 SV=4 - [RAB14_HUMAN]	11.18	11.16	3	3	4	0.704	0.943
P62820	Ras-related protein Rab-1A OS=Homo sapiens GN=RAB1A PE=1 SV=3 - [RAB1A_HUMAN]	41.35	33.17	3	8	13	0.648	0.912
Q9H0U4	Ras-related protein Rab-1B OS=Homo sapiens GN=RAB1B PE=1 SV=1 - [RAB1B_HUMAN]	52.77	34.83	4	9	17	0.643	1.076
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	0.592	0.572
P00352	Retinal dehydrogenase 1 OS=Homo sapiens GN=ALDH1A1 PE=1 SV=2 - [AL1A1_HUMAN]	17.58	6.59	4	4	5	2.106	3.052
P52565	Rho GDP-dissociation inhibitor 1 OS=Homo sapiens GN=ARHGDIA PE=1 SV=3 - [GDIR1_HUMAN]	30.94	18.14	4	4	9	0.624	0.818
P13489	Ribonuclease inhibitor OS=Homo sapiens GN=RNH1 PE=1 SV=2 - [RINI_HUMAN]	74.25	28.42	13	13	22	0.666	1.288
P49247	Ribose-5-phosphate isomerase OS=Homo sapiens GN=RPIA PE=1 SV=3 - [RPIA_HUMAN]	28.97	13.83	5	5	9	0.832	0.984
P60891	Ribose-phosphate pyrophosphokinase 1 OS=Homo sapiens GN=PRPS1 PE=1 SV=2 - [PRPS1_HUMAN]	42.22	25.16	4	8	13	0.962	1.848
Q5VVC8	Ribosomal protein L11 (Fragment) OS=Homo sapiens GN=RPL11 PE=2 SV=1 - [Q5VVC8_HUMAN]	7.46	8.05	2	2	3	0.286	0.833
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	0.244	0.495
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	0.250	0.600

Q5T8U3	Ribosomal protein L7a (Fragment) OS=Homo sapiens GN=RPL7A PE=4 SV=1 - [Q5T8U3_HUMAN]	11.84	9.95	3	3	3	0.305	0.708
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	0.329	0.279
O00442	RNA 3'-terminal phosphate cyclase OS=Homo sapiens GN=RTCD1 PE=1 SV=1 - [RTC1_HUMAN]	6.99	2.73	2	2	2	0.982	1.022
Q9Y265	RuvB-like 1 OS=Homo sapiens GN=RUVBL1 PE=1 SV=1 - [RUVB1_HUMAN]	27.73	12.94	6	6	8	0.628	0.580
Q9Y230	RuvB-like 2 OS=Homo sapiens GN=RUVBL2 PE=1 SV=3 - [RUVB2_HUMAN]	42.37	19.44	9	9	13	0.577	0.589
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	0.433	0.935
P10768	S-formylglutathione hydrolase OS=Homo sapiens GN=ESD PE=1 SV=2 - [ESTD_HUMAN]	39.86	10.28	4	4	13	0.712	0.969
Q9UDX3	SEC14-like protein 4 OS=Homo sapiens GN=SEC14L4 PE=2 SV=1 - [S14L4_HUMAN]	13.08	10.34	5	5	5	0.915	0.970
Q13228	Selenium-binding protein 1 OS=Homo sapiens GN=SELENBP1 PE=1 SV=2 - [SBP1_HUMAN]	168.09	32.42	16	16	52	0.547	0.562
Q96GA7	Serine dehydratase-like OS=Homo sapiens GN=SDSL PE=1 SV=1 - [SDSL_HUMAN]	8.80	6.99	3	3	3	0.879	0.779
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	0.154	0.391
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	0.080	0.730
O95747	Serine/threonine-protein kinase OSR1 OS=Homo sapiens GN=OXSR1 PE=1 SV=1 - [OXSR1_HUMAN]	24.07	12.33	7	7	9	0.913	1.049
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	0.483	1.055
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	0.731	1.043
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	0.437	0.522
B4DDZ8	Serine/threonine-protein phosphatase OS=Homo sapiens GN=PPP5C PE=2 SV=1 - [B4DDZ8_HUMAN]	14.02	8.64	5	5	5	0.773	0.645
P02787	Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3 - [TRFE_HUMAN]	9.00	3.72	3	3	3	0.253	0.650
Q9BXP5	Serrate RNA effector molecule homolog OS=Homo sapiens GN=SRRT PE=1 SV=1 - [SRRT_HUMAN]	4.75	1.94	2	2	2	0.325	0.617
P49591	Seryl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=SARS PE=1 SV=3 - [SYSC_HUMAN]	28.41	9.34	6	6	10	0.737	0.335
B2REB8	SET nuclear oncogene OS=Homo sapiens GN=SET PE=3 SV=1 - [B2REB8_HUMAN]	5.34	6.42	2	2	2	0.134	
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	1.339	1.713
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	0.739	0.922
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	0.679	0.912
Q9NR45	Sialic acid synthase OS=Homo sapiens GN=NANS PE=1 SV=2 - [SIAS_HUMAN]	25.74	11.98	6	6	9	0.580	0.678
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	0.414	0.477
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	0.522	1.035
C0H5W9	SNX6 protein OS=Homo sapiens GN=SNX6 PE=2 SV=1 - [C0H5W9_HUMAN]	10.22	9.66	4	4	4	0.546	0.548
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	2.274	0.559
Q00796	Sorbitol dehydrogenase OS=Homo sapiens GN=SORD PE=1 SV=4 - [DHSO_HUMAN]	16.25	10.08	4	4	6	1.207	0.453
O60493	Sorting nexin-3 OS=Homo sapiens GN=SNX3 PE=1 SV=3 - [SNX3_HUMAN]	18.02	26.54	5	5	7	0.444	0.446
P02549	Spectrin alpha chain, erythrocyte OS=Homo sapiens GN=SPTA1 PE=1 SV=5 - [SPTA1_HUMAN]	153.09	15.71	35	36	48	1.589	0.821
P11277	Spectrin beta chain, erythrocyte OS=Homo sapiens GN=SPTB PE=1 SV=5 - [SPTB1_HUMAN]	53.88	6.27	16	17	19	1.422	0.831
P52788	Spermine synthase OS=Homo sapiens GN=SMS PE=1 SV=2 - [SPSY_HUMAN]	9.72	8.74	4	4	4	0.786	0.619
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	0.192	0.297
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	0.154	0.705
P16949	Stathmin OS=Homo sapiens GN=STMN1 PE=1 SV=3 - [STMN1_HUMAN]	89.12	61.74	14	14	29	0.560	0.611
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	0.779	0.935
P31948	Stress-induced-phosphoprotein 1 OS=Homo sapiens GN=STIP1 PE=1 SV=1 - [STIP1_HUMAN]	185.22	38.86	33	34	62	0.729	0.933
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	0.308	0.476
P00441	Superoxide dismutase [Cu-Zn] OS=Homo sapiens GN=SOD1 PE=1 SV=2 - [SODC_HUMAN]	248.78	49.35	11	11	92	0.647	0.970
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	0.684	0.787
O15498	Synaptobrevin homolog YKT6 OS=Homo sapiens GN=YKT6 PE=1 SV=1 - [YKT6_HUMAN]	7.86	13.64	3	3	3	0.789	0.865
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	0.777	0.844
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	0.763	0.891
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	0.766	0.884
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	0.785	0.869
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	0.762	0.856
Q5TCU6	Talin 1 OS=Homo sapiens GN=TLN1 PE=2 SV=1 - [Q5TCU6_HUMAN]	307.80	23.59	65	66	103	0.445	0.362
B1AKP7	TAR DNA binding protein OS=Homo sapiens GN=TARDBP PE=4 SV=1 - [B1AKP7_HUMAN]	6.96	6.44	2	2	2	0.477	0.796
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	0.413	0.465
Q59G71	Tensin variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59G71_HUMAN]	15.12	6.19	5	5	5	0.457	1.039
Q99614	Tetratricopeptide repeat protein 1 OS=Homo sapiens GN=TTC1 PE=1 SV=1 - [TTC1_HUMAN]	6.27	5.82	2	2	2	0.573	0.517
P52888	Thimet oligopeptidase OS=Homo sapiens GN=THOP1 PE=1 SV=2 - [THOP1_HUMAN]	29.45	7.98	6	6	9	0.621	0.973
B1ALW1	Thioredoxin OS=Homo sapiens GN=TXN PE=4 SV=1 - [B1ALW1_HUMAN]	69.66	36.47	3	3	20	0.512	0.972
O43396	Thioredoxin-like protein 1 OS=Homo sapiens GN=TXNL1 PE=1 SV=3 - [TXNL1_HUMAN]	33.76	18.69	5	5	10	0.781	1.240

P26639	Threonyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=TARS PE=1 SV=3 - [SYTC_HUMAN]	27.98	8.99	7	7	10	0.833	0.767
P23919	Thymidylate kinase OS=Homo sapiens GN=DTYMK PE=1 SV=4 - [KTHY_HUMAN]	9.78	6.60	2	2	4	0.785	0.870
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	0.223	0.246
O75663	TIP41-like protein OS=Homo sapiens GN=TIPRL PE=1 SV=2 - [TIPRL_HUMAN]	14.10	13.24	4	4	5	0.818	0.929
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	0.310	0.087
P37837	Transaldolase OS=Homo sapiens GN=TALDO1 PE=1 SV=2 - [TALDO_HUMAN]	161.93	44.81	19	19	54	0.568	0.889
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	0.468	0.310
Q13263	Transcription intermediary factor 1-beta OS=Homo sapiens GN=TRIM28 PE=1 SV=5 - [TIF1B_HUMAN]	14.37	3.11	3	3	6	0.149	0.053
P02786	Transferrin receptor protein 1 OS=Homo sapiens GN=TFRC PE=1 SV=2 - [TFR1_HUMAN]	23.61	7.37	6	6	8	0.074	0.528
P61586	Transforming protein RhoA OS=Homo sapiens GN=RHOA PE=1 SV=1 - [RHOA_HUMAN]	6.33	9.33	2	2	2	0.581	0.919
P37802	Transgelin-2 OS=Homo sapiens GN=TAGLN2 PE=1 SV=3 - [TAGL2_HUMAN]	58.47	41.71	10	10	17	0.919	0.866
P55072	Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4 - [TERA_HUMAN]	192.98	27.92	22	22	60	0.593	0.865
P13693	Translationally-controlled tumor protein OS=Homo sapiens GN=TPT1 PE=1 SV=1 - [TCTP_HUMAN]	30.04	29.65	6	6	10	0.878	0.803
Q92973	Transportin-1 OS=Homo sapiens GN=TNPO1 PE=1 SV=2 - [TNPO1_HUMAN]	21.56	4.34	3	3	7	0.519	0.591
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	0.492	0.832
P60174	Triosephosphate isomerase OS=Homo sapiens GN=TPI1 PE=1 SV=2 - [TPIS_HUMAN]	220.55	56.63	13	13	67	0.871	0.741
Q8NG06	Tripartite motif-containing protein 58 OS=Homo sapiens GN=TRIM58 PE=2 SV=2 - [TRI58_HUMAN]	26.03	13.79	8	8	9	0.563	0.782
P29144	Tripeptidyl-peptidase 2 OS=Homo sapiens GN=TPP2 PE=1 SV=4 - [TPP2_HUMAN]	20.50	4.08	6	6	7	0.789	0.978
D9YZV5	Tropomyosin 1 (Alpha) isoform 4 OS=Homo sapiens GN=TPM1 PE=3 SV=1 - [D9YZV5_HUMAN]	54.57	26.06	3	10	19	0.977	0.301
D9YZV7	Tropomyosin 1 (Alpha) isoform 6 OS=Homo sapiens GN=TPM1 PE=3 SV=1 - [D9YZV7_HUMAN]	73.95	31.02	2	9	23	1.196	0.434
Q5LJ98	TROVE domain family, member 2 OS=Homo sapiens GN=TROVE2 PE=2 SV=1 - [Q5LJ98_HUMAN]	17.00	4.83	3	3	6	0.468	0.546
P23381	Tryptophanyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=WARS PE=1 SV=2 - [SYWC_HUMAN]	38.93	13.16	7	7	13	0.292	0.588
Q9BQE3	Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 - [TBA1C_HUMAN]	108.25	22.27	3	9	35	0.577	0.824
P68371	Tubulin beta-2C chain OS=Homo sapiens GN=TUBB2C PE=1 SV=1 - [TBB2C_HUMAN]	129.74	25.84	12	12	45	0.571	0.841
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	0.697	0.667
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	0.745	0.926
Q15813	Tubulin-specific chaperone E OS=Homo sapiens GN=TBCE PE=1 SV=1 - [TBCE_HUMAN]	7.94	4.93	3	3	3	0.902	0.520
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	0.803	1.035
P54577	Tyrosyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=YARS PE=1 SV=4 - [SYYC_HUMAN]	91.66	29.55	19	19	30	0.646	0.538
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	0.623	0.807
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	0.698	1.181
P45974	Ubiquitin carboxyl-terminal hydrolase 5 OS=Homo sapiens GN=USP5 PE=1 SV=2 - [UBP5_HUMAN]	63.14	9.44	9	9	19	0.795	1.083
A6NJA2	Ubiquitin carboxyl-terminal hydrolase OS=Homo sapiens GN=USP14 PE=3 SV=1 - [A6NJA2_HUMAN]	84.40	23.09	14	14	27	0.742	1.155
E9PCQ3	Ubiquitin carboxyl-terminal hydrolase OS=Homo sapiens GN=USP15 PE=3 SV=2 - [E9PCQ3_HUMAN]	60.14	12.76	14	14	20	0.587	0.993
E9PM46	Ubiquitin carboxyl-terminal hydrolase OS=Homo sapiens GN=USP47 PE=3 SV=1 - [E9PM46_HUMAN]	7.84	2.21	3	3	3	0.463	0.610
F5GX52	Ubiquitin carrier protein OS=Homo sapiens PE=3 SV=1 - [F5GX52_HUMAN]	32.33	21.74	3	3	11	0.778	1.167
Q5VVQ6	Ubiquitin thioesterase OTU1 OS=Homo sapiens GN=YOD1 PE=1 SV=1 - [OTU1_HUMAN]	44.10	16.95	8	8	16	0.608	0.797
P62979	Ubiquitin-40S ribosomal protein S27a OS=Homo sapiens GN=RPS27A PE=1 SV=2 - [RS27A_HUMAN]	402.31	41.03	9	9	143	0.468	1.160
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	0.651	1.020
P61088	Ubiquitin-conjugating enzyme E2 N OS=Homo sapiens GN=UBE2N PE=1 SV=1 - [UBE2N_HUMAN]	55.31	36.18	7	7	17	0.753	1.008
Q9C0C9	Ubiquitin-conjugating enzyme E2 O OS=Homo sapiens GN=UBE2O PE=1 SV=3 - [UBE2O_HUMAN]	30.25	4.72	8	8	9	0.657	0.768
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	0.704	0.807
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	0.761	0.955
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	0.771	0.939
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	0.601	0.756
Q9NT62	Ubiquitin-like-conjugating enzyme ATG3 OS=Homo sapiens GN=ATG3 PE=1 SV=1 - [ATG3_HUMAN]	5.60	4.14	2	2	2	0.643	0.917
P30085	UMP-CMP kinase OS=Homo sapiens GN=CMPK1 PE=1 SV=3 - [KCY_HUMAN]	17.19	22.96	4	4	5	0.701	0.901
Q6ICL3	Uncharacterized protein C22orf25 OS=Homo sapiens GN=C22orf25 PE=2 SV=1 - [CV025_HUMAN]	24.51	14.13	5	5	9	0.720	0.866
Q8IXQ3	Uncharacterized protein C9orf40 OS=Homo sapiens GN=C9orf40 PE=1 SV=1 - [CI040_HUMAN]	13.85	12.89	2	2	5	0.609	0.885
B4DNR3	Uncharacterized protein OS=Homo sapiens GN=ABHD14B PE=2 SV=1 - [B4DNR3_HUMAN]	19.74	21.62	4	4	6	0.591	1.210
B4DUX0	Uncharacterized protein OS=Homo sapiens GN=ACOT7 PE=2 SV=1 - [B4DUX0_HUMAN]	6.07	5.66	2	2	2	0.585	0.597
F5H0N0	Uncharacterized protein OS=Homo sapiens GN=ACTG1 PE=3 SV=1 - [F5H0N0_HUMAN]	309.25	45.95	4	13	104	0.365	0.301
B4DXP9	Uncharacterized protein OS=Homo sapiens GN=ACTR1A PE=2 SV=1 - [B4DXP9_HUMAN]	53.48	11.85	5	6	21	0.571	0.868
B4DTI0	Uncharacterized protein OS=Homo sapiens GN=ACTR3 PE=2 SV=1 - [B4DTI0_HUMAN]	10.38	12.11	3	3	3	0.993	0.494
B7Z783	Uncharacterized protein OS=Homo sapiens GN=ADK PE=2 SV=1 - [B7Z783_HUMAN]	22.69	21.97	5	5	7	0.678	1.221
E9PEC0	Uncharacterized protein OS=Homo sapiens GN=ADRM1 PE=4 SV=2 - [E9PEC0_HUMAN]	9.30	10.73	3	3	3	0.472	0.935

C9J2I0	Uncharacterized protein OS=Homo sapiens GN=AGFG1 PE=4 SV=1 - [C9J2I0_HUMAN]	8.72	7.98	2	2	3	0.645	0.939
C9JSL3	Uncharacterized protein OS=Homo sapiens GN=AKR7A2 PE=4 SV=2 - [C9JSL3_HUMAN]	17.46	7.14	2	2	4	0.663	0.859
F5H4B6	Uncharacterized protein OS=Homo sapiens GN=ALDH16A1 PE=4 SV=1 - [F5H4B6_HUMAN]	18.48	8.92	5	5	6	0.678	1.503
E9PKC5	Uncharacterized protein OS=Homo sapiens GN=AMPD3 PE=4 SV=1 - [E9PKC5_HUMAN]	7.72	2.81	3	3	3	1.252	1.526
E7EVE3	Uncharacterized protein OS=Homo sapiens GN=ANK1 PE=4 SV=1 - [E7EVE3_HUMAN]	44.31	4.39	10	10	15	11.156	0.950
F5H754	Uncharacterized protein OS=Homo sapiens GN=ANKFY1 PE=4 SV=1 - [F5H754_HUMAN]	4.62	1.53	2	2	2	0.614	1.047
B4DT77	Uncharacterized protein OS=Homo sapiens GN=ANXA7 PE=2 SV=1 - [B4DT77_HUMAN]	74.20	38.69	13	13	23	0.771	0.900
F5H0H0	Uncharacterized protein OS=Homo sapiens GN=AP2M1 PE=4 SV=1 - [F5H0H0_HUMAN]	10.91	5.24	3	3	4	0.564	1.148
B7ZB63	Uncharacterized protein OS=Homo sapiens GN=ARF3 PE=2 SV=1 - [B7ZB63_HUMAN]	25.89	25.00	4	4	9	0.647	1.083
E9PNR6	Uncharacterized protein OS=Homo sapiens GN=ARHGAP1 PE=4 SV=1 - [E9PNR6_HUMAN]	6.20	10.94	2	2	2	0.676	1.307
F5H6Q0	Uncharacterized protein OS=Homo sapiens GN=ARHGDIB PE=4 SV=1 - [F5H6Q0_HUMAN]	23.70	59.82	6	6	8	0.730	0.993
E7EWX4	Uncharacterized protein OS=Homo sapiens GN=ARPC4 PE=4 SV=1 - [E7EWX4_HUMAN]	8.18	10.26	2	2	3	1.007	0.407
E9PBU3	Uncharacterized protein OS=Homo sapiens GN=ATIC PE=4 SV=1 - [E9PBU3_HUMAN]	57.78	19.97	11	11	18	0.730	1.010
B7Z1R5	Uncharacterized protein OS=Homo sapiens GN=ATP6V1A PE=2 SV=1 - [B7Z1R5_HUMAN]	55.45	16.27	11	11	17	0.671	0.760
A8MUN4	Uncharacterized protein OS=Homo sapiens GN=ATP6V1E1 PE=2 SV=1 - [A8MUN4_HUMAN]	29.22	26.02	6	6	10	0.639	0.669
E9PGE6	Uncharacterized protein OS=Homo sapiens GN=ATP6V1H PE=4 SV=1 - [E9PGE6_HUMAN]	10.64	4.36	2	2	3	0.569	0.753
C9JB13	Uncharacterized protein OS=Homo sapiens GN=BSDC1 PE=4 SV=1 - [C9JB13_HUMAN]	10.42	7.11	3	3	4	0.478	0.341
E9PL10	Uncharacterized protein OS=Homo sapiens GN=BTF3L4 PE=4 SV=1 - [E9PL10_HUMAN]	25.78	26.21	6	6	10	0.588	0.567
C9JXR7	Uncharacterized protein OS=Homo sapiens GN=CASP3 PE=4 SV=2 - [C9JXR7_HUMAN]	7.67	15.38	2	2	3	0.639	1.376
E9PAQ6	Uncharacterized protein OS=Homo sapiens GN=CCT3 PE=3 SV=1 - [E9PAQ6_HUMAN]	123.45	29.04	20	20	40	0.776	0.848
E7ENZ3	Uncharacterized protein OS=Homo sapiens GN=CCT5 PE=4 SV=1 - [E7ENZ3_HUMAN]	123.71	30.66	17	17	40	0.771	0.878
E9PP50	Uncharacterized protein OS=Homo sapiens GN=CFL1 PE=4 SV=1 - [E9PP50_HUMAN]	95.19	50.00	10	11	31	0.665	0.979
B4DIN1	Uncharacterized protein OS=Homo sapiens GN=CLTA PE=2 SV=1 - [B4DIN1_HUMAN]	27.96	13.48	5	5	9	0.456	0.699
B4DIH5	Uncharacterized protein OS=Homo sapiens GN=COPS2 PE=2 SV=1 - [B4DIH5_HUMAN]	6.14	3.96	2	2	2	0.647	1.220
B4DM67	Uncharacterized protein OS=Homo sapiens GN=CSE1L PE=2 SV=1 - [B4DM67_HUMAN]	5.86	2.84	2	2	2	0.519	1.502
F5GWW0	Uncharacterized protein OS=Homo sapiens GN=CTSB PE=3 SV=1 - [F5GWW0_HUMAN]	7.94	9.89	3	3	3	0.604	0.748
E7EWR0	Uncharacterized protein OS=Homo sapiens GN=CUL1 PE=3 SV=1 - [E7EWR0_HUMAN]	8.89	3.41	3	3	3	0.739	1.249
A8MSH7	Uncharacterized protein OS=Homo sapiens GN=CUL4A PE=3 SV=1 - [A8MSH7_HUMAN]	26.33	9.88	8	8	9	0.605	0.784
F2Z305	Uncharacterized protein OS=Homo sapiens GN=DCAF6 PE=4 SV=1 - [F2Z305_HUMAN]	5.60	3.60	2	2	2	1.154	0.758
E9PFS5	Uncharacterized protein OS=Homo sapiens GN=DCTN1 PE=4 SV=1 - [E9PFS5_HUMAN]	39.34	7.85	11	11	14	0.557	0.855
F5H223	Uncharacterized protein OS=Homo sapiens GN=DCTN2 PE=4 SV=1 - [F5H223_HUMAN]	24.49	12.70	6	6	8	0.569	0.923
C9J8R4	Uncharacterized protein OS=Homo sapiens GN=DCUN1D1 PE=4 SV=1 - [C9J8R4_HUMAN]	9.89	12.50	2	2	3	0.852	1.024
E9PML7	Uncharacterized protein OS=Homo sapiens GN=DERA PE=4 SV=1 - [E9PML7_HUMAN]	6.35	6.78	2	2	2	0.646	1.386
F5H6K0	Uncharacterized protein OS=Homo sapiens GN=DHX15 PE=4 SV=1 - [F5H6K0_HUMAN]	4.92	0.89	2	2	2	0.393	0.191
E7ERW8	Uncharacterized protein OS=Homo sapiens GN=DIAPH1 PE=4 SV=1 - [E7ERW8_HUMAN]	45.04	6.01	10	10	16	0.520	0.735
C9JXB9	Uncharacterized protein OS=Homo sapiens GN=DNAJB2 PE=4 SV=1 - [C9JXB9_HUMAN]	8.75	12.70	3	3	3	0.794	1.167
E7EPX3	Uncharacterized protein OS=Homo sapiens GN=DNPEP PE=3 SV=1 - [E7EPX3_HUMAN]	13.80	8.48	3	3	4	0.650	1.086
F5GXD5	Uncharacterized protein OS=Homo sapiens GN=DPP3 PE=4 SV=1 - [F5GXD5_HUMAN]	36.97	10.55	7	7	12	0.762	0.886
B4DR31	Uncharacterized protein OS=Homo sapiens GN=DPYSL2 PE=2 SV=1 - [B4DR31_HUMAN]	13.87	4.66	3	3	5	0.972	0.405
F5H335	Uncharacterized protein OS=Homo sapiens GN=EIF3A PE=4 SV=1 - [F5H335_HUMAN]	42.40	10.83	13	13	15	0.421	0.478
B4DV79	Uncharacterized protein OS=Homo sapiens GN=EIF3B PE=2 SV=1 - [B4DV79_HUMAN]	23.20	6.64	5	5	8	0.408	0.245
F5H1I1	Uncharacterized protein OS=Homo sapiens GN=EIF3C PE=4 SV=1 - [F5H1I1_HUMAN]	13.43	5.23	4	4	4	0.335	0.368
B7ZAM9	Uncharacterized protein OS=Homo sapiens GN=EIF3K PE=2 SV=1 - [B7ZAM9_HUMAN]	5.74	9.95	2	2	2	0.507	0.583
E7EQG2	Uncharacterized protein OS=Homo sapiens GN=EIF4A2 PE=3 SV=1 - [E7EQG2_HUMAN]	47.01	24.31	2	8	13	0.693	0.410
E7EPC9	Uncharacterized protein OS=Homo sapiens GN=EIF4B PE=4 SV=1 - [E7EPC9_HUMAN]	56.50	20.44	12	12	19	0.794	0.911
E7EX73	Uncharacterized protein OS=Homo sapiens GN=EIF4G1 PE=4 SV=1 - [E7EX73_HUMAN]	33.39	6.82	11	11	11	0.421	0.471
D6RA00	Uncharacterized protein OS=Homo sapiens GN=ENOPH1 PE=4 SV=1 - [D6RA00_HUMAN]	10.13	7.51	2	2	4	0.714	0.665
E9PEX0	Uncharacterized protein OS=Homo sapiens GN=EPB41 PE=4 SV=1 - [E9PEX0_HUMAN]	20.81	9.66	5	7	7	3.333	0.798
E5RJ56	Uncharacterized protein OS=Homo sapiens GN=EPB49 PE=4 SV=1 - [E5RJ56_HUMAN]	28.92	15.03	5	5	9	0.857	0.689
E7EQR4	Uncharacterized protein OS=Homo sapiens GN=EZR PE=4 SV=2 - [E7EQR4_HUMAN]	76.62	25.99	15	20	25	1.338	0.811
E9PCI9	Uncharacterized protein OS=Homo sapiens GN=FDPS PE=3 SV=1 - [E9PCI9_HUMAN]	18.29	14.73	5	5	6	0.648	0.949
B7Z7Z8	Uncharacterized protein OS=Homo sapiens GN=FKBP5 PE=2 SV=1 - [B7Z7Z8_HUMAN]	19.62	17.27	4	5	6	0.291	0.804
B3KNR9	Uncharacterized protein OS=Homo sapiens GN=FN3K PE=2 SV=1 - [B3KNR9_HUMAN]	13.82	16.95	3	3	4	1.350	1.345
B4E0X8	Uncharacterized protein OS=Homo sapiens GN=FUBP1 PE=2 SV=1 - [B4E0X8_HUMAN]	8.40	4.45	2	3	3	0.402	0.405
E9PGM4	Uncharacterized protein OS=Homo sapiens GN=GBE1 PE=4 SV=1 - [E9PGM4_HUMAN]	7.49	4.08	2	2	2	0.659	0.854
B4E192	Uncharacterized protein OS=Homo sapiens GN=GFAP PE=2 SV=1 - [B4E192_HUMAN]	37.91	21.87	8	9	13	1.289	0.418

B8ZZK2	Uncharacterized protein OS=Homo sapiens GN=GGCT PE=4 SV=1 - [B8ZZK2_HUMAN]	22.91	12.05	2	2	8	0.631	0.918
E7EMY5	Uncharacterized protein OS=Homo sapiens GN=GLOD4 PE=4 SV=1 - [E7EMY5_HUMAN]	42.38	16.37	9	9	14	0.652	0.896
C9JAH0	Uncharacterized protein OS=Homo sapiens GN=GMPPA PE=4 SV=1 - [C9JAH0_HUMAN]	5.76	7.23	2	2	2	0.747	0.700
B4DUT7	Uncharacterized protein OS=Homo sapiens GN=GMPS PE=2 SV=1 - [B4DUT7_HUMAN]	8.69	4.52	3	3	3	0.525	0.942
E9PDI1	Uncharacterized protein OS=Homo sapiens GN=GPCPD1 PE=4 SV=1 - [E9PDI1_HUMAN]	6.41	7.61	2	2	2	0.275	0.501
F5H8M4	Uncharacterized protein OS=Homo sapiens GN=GSN PE=4 SV=1 - [F5H8M4_HUMAN]	7.93	2.41	2	2	3	1.343	1.991
E7EQZ3	Uncharacterized protein OS=Homo sapiens GN=GSPT1 PE=4 SV=1 - [E7EQZ3_HUMAN]	54.56	16.67	13	13	19	0.595	0.528
A8MX94	Uncharacterized protein OS=Homo sapiens GN=GSTP1 PE=3 SV=1 - [A8MX94_HUMAN]	15.41	16.09	3	3	5	0.512	0.384
F5GZ06	Uncharacterized protein OS=Homo sapiens GN=HEATR7B2 PE=4 SV=1 - [F5GZ06_HUMAN]	5.17	2.54	2	2	2	0.762	1.150
F5H5Y5	Uncharacterized protein OS=Homo sapiens GN=HGS PE=4 SV=1 - [F5H5Y5_HUMAN]	16.67	6.05	5	5	6	0.569	1.140
E9PCK0	Uncharacterized protein OS=Homo sapiens GN=HK1 PE=3 SV=1 - [E9PCK0_HUMAN]	28.70	5.97	6	6	9	0.587	0.545
F5H345	Uncharacterized protein OS=Homo sapiens GN=HMBS PE=4 SV=1 - [F5H345_HUMAN]	89.60	25.76	9	9	30	0.621	0.603
B8ZZT7	Uncharacterized protein OS=Homo sapiens GN=HN1 PE=4 SV=1 - [B8ZZT7_HUMAN]	6.67	14.02	2	2	2	0.825	0.267
D6R9P3	Uncharacterized protein OS=Homo sapiens GN=HNRNPAB PE=4 SV=1 - [D6R9P3_HUMAN]	16.60	11.07	2	4	6	0.379	0.656
B4DTC3	Uncharacterized protein OS=Homo sapiens GN=HNRNPD PE=2 SV=1 - [B4DTC3_HUMAN]	21.23	13.20	3	5	8	0.414	0.591
B4DKS8	Uncharacterized protein OS=Homo sapiens GN=HNRNPF PE=2 SV=1 - [B4DKS8_HUMAN]	7.41	7.40	2	3	3	0.384	0.191
B4DPK8	Uncharacterized protein OS=Homo sapiens GN=HNRNPL PE=2 SV=1 - [B4DPK8_HUMAN]	8.69	13.75	3	3	3	0.291	0.536
B3KX72	Uncharacterized protein OS=Homo sapiens GN=HNRNPU PE=2 SV=1 - [B3KX72_HUMAN]	7.49	3.20	3	3	3	0.117	0.057
E9PDE8	Uncharacterized protein OS=Homo sapiens GN=HSPA4L PE=3 SV=1 - [E9PDE8_HUMAN]	7.60	2.71	2	3	3	0.598	0.413
B4DL87	Uncharacterized protein OS=Homo sapiens GN=HSPB1 PE=2 SV=1 - [B4DL87_HUMAN]	41.92	37.06	7	7	12	0.557	0.681
E9PD66	Uncharacterized protein OS=Homo sapiens GN=HUWE1 PE=4 SV=1 - [E9PD66_HUMAN]	56.51	3.19	16	16	19	0.526	1.146
B4E0R6	Uncharacterized protein OS=Homo sapiens GN=IPO5 PE=2 SV=1 - [B4E0R6_HUMAN]	36.78	7.51	7	7	12	0.484	0.637
E7EP96	Uncharacterized protein OS=Homo sapiens GN=KHSRP PE=4 SV=1 - [E7EP96_HUMAN]	7.46	6.59	2	3	3	0.314	0.155
F5H4G7	Uncharacterized protein OS=Homo sapiens GN=KPNA6 PE=4 SV=1 - [F5H4G7_HUMAN]	12.89	4.88	3	4	5	0.648	0.917
B4DJ10	Uncharacterized protein OS=Homo sapiens GN=LARS PE=2 SV=1 - [B4DJ10_HUMAN]	5.36	1.34	2	2	2	0.305	0.490
A8MUU4	Uncharacterized protein OS=Homo sapiens GN=MBP PE=4 SV=2 - [A8MUU4_HUMAN]	12.60	15.03	3	3	4	1.444	0.584
E9PGF9	Uncharacterized protein OS=Homo sapiens GN=MGEA5 PE=4 SV=1 - [E9PGF9_HUMAN]	13.45	3.48	3	4	5	0.262	0.163
A8MU28	Uncharacterized protein OS=Homo sapiens GN=NAE1 PE=4 SV=1 - [A8MU28_HUMAN]	9.96	4.72	3	3	3	0.637	0.658
C9JZI7	Uncharacterized protein OS=Homo sapiens GN=NAP1L4 PE=3 SV=1 - [C9JZI7_HUMAN]	32.06	17.99	5	6	11	0.485	0.520
B7Z463	Uncharacterized protein OS=Homo sapiens GN=NPEPPS PE=2 SV=1 - [B7Z463_HUMAN]	24.09	7.27	7	7	8	0.587	1.122
B9A035	Uncharacterized protein OS=Homo sapiens GN=NT5C3 PE=4 SV=1 - [B9A035_HUMAN]	10.81	12.68	3	3	4	0.609	0.964
E5RFP0	Uncharacterized protein OS=Homo sapiens GN=NUDCD2 PE=4 SV=1 - [E5RFP0_HUMAN]	5.56	15.15	2	2	2	0.844	1.162
F5GYN4	Uncharacterized protein OS=Homo sapiens GN=OTUB1 PE=4 SV=1 - [F5GYN4_HUMAN]	14.87	19.09	4	4	5	0.613	0.591
B4DUA5	Uncharacterized protein OS=Homo sapiens GN=P4HB PE=2 SV=1 - [B4DUA5_HUMAN]	5.89	3.54	2	2	2	0.643	0.763
E7EQV3	Uncharacterized protein OS=Homo sapiens GN=PABPC1 PE=4 SV=1 - [E7EQV3_HUMAN]	13.06	4.06	3	3	4	0.270	0.495
E9PBS1	Uncharacterized protein OS=Homo sapiens GN=PAICS PE=4 SV=1 - [E9PBS1_HUMAN]	89.96	22.52	12	12	30	0.755	0.778
E9PHT6	Uncharacterized protein OS=Homo sapiens GN=PANK4 PE=4 SV=1 - [E9PHT6_HUMAN]	5.05	2.72	2	2	2	0.424	0.817
F2Z2Y4	Uncharacterized protein OS=Homo sapiens GN=PDXK PE=4 SV=1 - [F2Z2Y4_HUMAN]	24.71	12.13	4	4	8	0.668	0.614
E9PCE8	Uncharacterized protein OS=Homo sapiens GN=PEPD PE=3 SV=1 - [E9PCE8_HUMAN]	34.19	19.11	7	7	10	0.754	0.892
F5GWE5	Uncharacterized protein OS=Homo sapiens GN=PITPNA PE=4 SV=1 - [F5GWE5_HUMAN]	30.22	24.07	7	9	11	0.656	0.984
E5RIM3	Uncharacterized protein OS=Homo sapiens GN=PLAA PE=4 SV=1 - [E5RIM3_HUMAN]	7.87	2.79	2	2	3	0.560	0.910
B4E0V0	Uncharacterized protein OS=Homo sapiens GN=PNPO PE=2 SV=1 - [B4E0V0_HUMAN]	5.00	9.04	2	2	2	0.658	0.456
D6RFZ8	Uncharacterized protein OS=Homo sapiens GN=PPIP5K2 PE=4 SV=1 - [D6RFZ8_HUMAN]	5.58	1.76	2	2	2	1.175	0.679
E7EPA1	Uncharacterized protein OS=Homo sapiens GN=PRPSAP2 PE=4 SV=1 - [E7EPA1_HUMAN]	19.02	13.81	4	5	6	0.737	0.812
F5GX11	Uncharacterized protein OS=Homo sapiens GN=PSMA1 PE=4 SV=1 - [F5GX11_HUMAN]	53.74	34.87	11	11	17	0.617	1.004
F5GZ16	Uncharacterized protein OS=Homo sapiens GN=PSMD2 PE=4 SV=1 - [F5GZ16_HUMAN]	41.60	12.78	10	10	13	0.484	1.313
F5H8K4	Uncharacterized protein OS=Homo sapiens GN=PSMD3 PE=4 SV=1 - [F5H8K4_HUMAN]	56.41	18.81	10	10	18	0.478	1.070
E9PHI9	Uncharacterized protein OS=Homo sapiens GN=PSMD6 PE=4 SV=1 - [E9PHI9_HUMAN]	21.70	11.43	5	5	7	0.526	1.046
B4DXI8	Uncharacterized protein OS=Homo sapiens GN=PSMD7 PE=2 SV=1 - [B4DXI8_HUMAN]	22.40	12.96	4	4	7	0.532	0.959
B8ZZQ6	Uncharacterized protein OS=Homo sapiens GN=PTMA PE=4 SV=1 - [B8ZZQ6_HUMAN]	29.47	23.36	4	4	9	0.412	0.229
B4DNN3	Uncharacterized protein OS=Homo sapiens GN=QARS PE=2 SV=1 - [B4DNN3_HUMAN]	12.70	5.10	4	4	4	0.457	0.775
C9J7D1	Uncharacterized protein OS=Homo sapiens GN=RAB7A PE=4 SV=1 - [C9J7D1_HUMAN]	4.85	14.29	2	2	2	0.679	0.965
B4DW94	Uncharacterized protein OS=Homo sapiens GN=RAP1B PE=2 SV=1 - [B4DW94_HUMAN]	5.64	13.14	2	2	2	1.335	1.683
F5H3T8	Uncharacterized protein OS=Homo sapiens GN=RARS PE=4 SV=1 - [F5H3T8_HUMAN]	5.57	3.52	2	2	2	0.445	0.880
E9PC52	Uncharacterized protein OS=Homo sapiens GN=RBBP7 PE=4 SV=1 - [E9PC52_HUMAN]	6.29	4.57	2	2	2	0.461	0.541
F5GX07	Uncharacterized protein OS=Homo sapiens GN=REXO2 PE=4 SV=1 - [F5GX07_HUMAN]	6.02	12.24	2	2	2	0.548	1.075

D6RJG8	Uncharacterized protein OS=Homo sapiens GN=RFESD PE=4 SV=1 - [D6RJG8_HUMAN]	16.27	50.00	4	4	5	0.792	0.790
E5RIT6	Uncharacterized protein OS=Homo sapiens GN=RPL26L1 PE=3 SV=1 - [E5RIT6_HUMAN]	5.09	10.94	2	2	2	0.364	0.720
F2Z3A5	Uncharacterized protein OS=Homo sapiens GN=RPL3 PE=3 SV=1 - [F2Z3A5_HUMAN]	7.85	6.50	3	3	3	0.302	0.677
B8ZZK4	Uncharacterized protein OS=Homo sapiens GN=RPL31 PE=4 SV=1 - [B8ZZK4_HUMAN]	5.34	20.25	2	2	2	0.319	0.455
E7EWF1	Uncharacterized protein OS=Homo sapiens GN=RPL4 PE=4 SV=1 - [E7EWF1_HUMAN]	19.85	10.10	6	6	7	0.285	0.720
E9PKZ0	Uncharacterized protein OS=Homo sapiens GN=RPL8 PE=4 SV=1 - [E9PKZ0_HUMAN]	8.72	16.10	3	3	3	0.259	0.378
E9PS50	Uncharacterized protein OS=Homo sapiens GN=RPS13 PE=4 SV=1 - [E9PS50_HUMAN]	11.42	22.41	3	3	4	0.342	0.291
E5RH77	Uncharacterized protein OS=Homo sapiens GN=RPS14 PE=4 SV=1 - [E5RH77_HUMAN]	8.04	9.70	2	2	3	0.508	0.596
E9PM36	Uncharacterized protein OS=Homo sapiens GN=RPS2 PE=3 SV=1 - [E9PM36_HUMAN]	10.90	8.13	2	2	4	0.359	0.469
C9J9K3	Uncharacterized protein OS=Homo sapiens GN=RPSA PE=3 SV=1 - [C9J9K3_HUMAN]	23.84	21.21	5	5	7	0.504	0.574
E5RJE3	Uncharacterized protein OS=Homo sapiens GN=RWDD1 PE=4 SV=1 - [E5RJE3_HUMAN]	6.23	17.65	2	2	2	0.591	0.728
B4DNE4	Uncharacterized protein OS=Homo sapiens GN=SEPT7 PE=2 SV=1 - [B4DNE4_HUMAN]	10.92	5.76	3	3	4	1.052	0.413
B4E3A8	Uncharacterized protein OS=Homo sapiens GN=SERPINB1 PE=2 SV=1 - [B4E3A8_HUMAN]	14.26	9.97	4	4	5	0.556	1.244
E7EMJ6	Uncharacterized protein OS=Homo sapiens GN=SGTA PE=4 SV=1 - [E7EMJ6_HUMAN]	29.61	13.40	5	5	10	0.727	0.925
E5RJR5	Uncharacterized protein OS=Homo sapiens GN=SKP1 PE=4 SV=1 - [E5RJR5_HUMAN]	43.83	34.36	7	7	13	0.866	1.447
E7EPV7	Uncharacterized protein OS=Homo sapiens GN=SNCA PE=4 SV=1 - [E7EPV7_HUMAN]	201.14	78.26	10	11	52	0.860	0.944
E7ESM6	Uncharacterized protein OS=Homo sapiens GN=SND1 PE=4 SV=2 - [E7ESM6_HUMAN]	28.88	6.33	6	6	9	0.438	0.121
B4DEK4	Uncharacterized protein OS=Homo sapiens GN=SNX2 PE=2 SV=1 - [B4DEK4_HUMAN]	17.13	7.46	3	3	6	0.552	0.570
E9PBC7	Uncharacterized protein OS=Homo sapiens GN=SNX5 PE=4 SV=1 - [E9PBC7_HUMAN]	6.01	5.45	2	2	2	0.460	0.455
C9J0K6	Uncharacterized protein OS=Homo sapiens GN=SRI PE=4 SV=1 - [C9J0K6_HUMAN]	46.76	43.23	7	7	16	0.757	0.888
E7ETK6	Uncharacterized protein OS=Homo sapiens GN=SRP68 PE=4 SV=1 - [E7ETK6_HUMAN]	6.11	4.36	2	2	2	0.381	0.442
B4E2V5	Uncharacterized protein OS=Homo sapiens GN=STOM PE=2 SV=1 - [B4E2V5_HUMAN]	12.50	12.24	3	3	4	4.556	0.639
F2Z3D0	Uncharacterized protein OS=Homo sapiens GN=SUMO2 PE=4 SV=1 - [F2Z3D0_HUMAN]	6.98	30.99	2	2	2	0.429	0.682
F5GWQ7	Uncharacterized protein OS=Homo sapiens GN=TAF15 PE=4 SV=1 - [F5GWQ7_HUMAN]	5.68	11.65	2	2	2	0.421	1.163
E5RIW3	Uncharacterized protein OS=Homo sapiens GN=TBCA PE=4 SV=1 - [E5RIW3_HUMAN]	45.58	50.00	6	6	14	0.755	0.769
A8MVD5	Uncharacterized protein OS=Homo sapiens GN=TBCB PE=4 SV=1 - [A8MVD5_HUMAN]	6.06	9.81	2	2	2	0.724	1.079
C9JJP5	Uncharacterized protein OS=Homo sapiens GN=TFG PE=4 SV=1 - [C9JJP5_HUMAN]	11.08	8.29	2	2	4	0.508	1.873
B4DIT7	Uncharacterized protein OS=Homo sapiens GN=TGM2 PE=2 SV=1 - [B4DIT7_HUMAN]	165.54	29.21	20	20	55	0.561	0.614
E9PGT1	Uncharacterized protein OS=Homo sapiens GN=TSN PE=4 SV=1 - [E9PGT1_HUMAN]	25.23	23.77	5	6	8	0.499	0.935
A6NKB1	Uncharacterized protein OS=Homo sapiens GN=TTN PE=4 SV=4 - [A6NKB1_HUMAN]	27.19	0.27	3	9	11	0.923	1.260
E9PIR7	Uncharacterized protein OS=Homo sapiens GN=TXNRD1 PE=3 SV=1 - [E9PIR7_HUMAN]	39.02	12.24	7	7	12	0.704	0.888
E7EWE1	Uncharacterized protein OS=Homo sapiens GN=UBA5 PE=4 SV=1 - [E7EWE1_HUMAN]	8.90	6.34	3	3	3	0.630	0.947
D6RDM7	Uncharacterized protein OS=Homo sapiens GN=UBE2K PE=4 SV=1 - [D6RDM7_HUMAN]	12.40	14.63	2	2	4	0.830	0.766
E9PJ81	Uncharacterized protein OS=Homo sapiens GN=UBXN1 PE=4 SV=1 - [E9PJ81_HUMAN]	8.60	7.24	3	3	3	0.696	0.750
A6NJ11	Uncharacterized protein OS=Homo sapiens GN=UFD1L PE=4 SV=1 - [A6NJ11_HUMAN]	9.29	11.82	2	3	3	0.746	0.276
C9JKD6	Uncharacterized protein OS=Homo sapiens GN=UGP2 PE=4 SV=1 - [C9JKD6_HUMAN]	18.59	11.02	6	6	6	0.727	1.322
E9PG85	Uncharacterized protein OS=Homo sapiens GN=UROS PE=4 SV=1 - [E9PG85_HUMAN]	28.83	29.11	6	6	10	0.525	0.721
B7Z7T5	Uncharacterized protein OS=Homo sapiens GN=USP7 PE=2 SV=1 - [B7Z7T5_HUMAN]	14.39	6.88	5	5	5	0.551	0.688
B0V043	Uncharacterized protein OS=Homo sapiens GN=VARS PE=3 SV=1 - [B0V043_HUMAN]	6.73	1.66	2	2	2	0.505	0.452
F5H2A7	Uncharacterized protein OS=Homo sapiens GN=VBP1 PE=4 SV=1 - [F5H2A7_HUMAN]	16.32	15.10	3	3	5	0.777	0.515
A6NG10	Uncharacterized protein OS=Homo sapiens GN=WBP2 PE=2 SV=2 - [A6NG10_HUMAN]	61.77	23.85	7	7	20	0.662	0.791
B4DP38	Uncharacterized protein OS=Homo sapiens GN=WDR77 PE=2 SV=1 - [B4DP38_HUMAN]	6.65	4.68	2	2	2	0.682	0.945
F5GWT4	Uncharacterized protein OS=Homo sapiens GN=WNK1 PE=4 SV=1 - [F5GWT4_HUMAN]	25.02	4.08	9	9	9	0.702	1.155
Q5T6H7	Uncharacterized protein OS=Homo sapiens GN=XPNPEP1 PE=2 SV=1 - [Q5T6H7_HUMAN]	24.46	6.34	4	4	8	0.713	0.913
E7ESC6	Uncharacterized protein OS=Homo sapiens GN=XPO7 PE=4 SV=1 - [E7ESC6_HUMAN]	96.16	15.44	18	18	32	0.378	0.651
E9PQI5	Uncharacterized protein OS=Homo sapiens PE=4 SV=1 - [E9PQI5_HUMAN]	19.05	17.47	3	3	5	0.858	0.755
Q9H7C9	UPF0366 protein C11orf67 OS=Homo sapiens GN=C11orf67 PE=1 SV=1 - [CK067_HUMAN]	5.93	18.85	2	2	2	0.695	1.044
Q5T6V5	UPF0553 protein C9orf64 OS=Homo sapiens GN=C9orf64 PE=1 SV=1 - [CI064_HUMAN]	8.48	4.40	2	2	3	0.600	0.696
Q9NWV4	UPF0587 protein C1orf123 OS=Homo sapiens GN=C1orf123 PE=1 SV=1 - [CA123_HUMAN]	14.04	23.75	4	4	5	0.699	0.868
P06132	Uroporphyrinogen decarboxylase OS=Homo sapiens GN=UROD PE=1 SV=2 - [DCUP_HUMAN]	43.35	19.35	7	7	15	0.509	0.750
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	0.836	1.103
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	0.816	0.983
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	0.655	0.547
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	0.644	0.714
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	0.654	0.687
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	0.844	0.966

P18206	Vinculin OS=Homo sapiens GN=VCL PE=1 SV=4 - [VINC_HUMAN]	147.27	24.34	28	28	48	0.925	0.473
O75083	WD repeat-containing protein 1 OS=Homo sapiens GN=WDR1 PE=1 SV=4 - [WDR1_HUMAN]	44.14	11.06	7	7	14	0.759	0.988
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	0.236	0.291
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	0.307	0.769