Accession	Description	Score A	Coverage A	# Peptides A	# PSM A	Score B	Coverage B	# Peptides B	# PSM B	Score C	Coverage C	# Peptides C	# PSM C
P05387	60S acidic ribosomal prot	35.67	69.57	4	7	30.65	59.13	3	6	15.23	16.52	1	3
P01966	Hemoglobin subunit alpha	35.18	46.10	4	7	37.72	54.61	4	7	46.19	57.45	4	9
P04406	Glyceraldehyde-3-phosph	297.69	56.12	10	55	191.59	31.64	5	36	270.05	40.60	8	47
P00921	Carbonic anhydrase 2 - B	82.93	41.70	6	16	71.91	50.19	7	14	60.83	25.10	4	11
P05787	Keratin, type II cytoskele	92.33	45.76	13	18	93.42	39.13	11	17	145.80	39.96	11	27
P02070	Hemoglobin subunit beta	116.45	30.34	3	23	117.81	30.34	3	24	128.32	30.34	3	25
P02662	Alpha-S1-casein - Bos tau	73.62	45.79	5	14	46.37	35.51	3	9	32.94	22.43	3	7
Q13268	Dehydrogenase/reductas	52.47	32.86	4	11	65.49	33.21	4	14	99.83	33.21	4	21
P06576	ATP synthase subunit bet	64.31	37.05	11	13	61.41	34.03	10	13	39.64	17.39	6	8
O43852	Calumenin OS=Homo sap	29.77	35.24	5	6	25.09	28.89	4	5	20.62	15.56	2	4
P06733	Alpha-enolase OS=Homo	219.44	38.02	9	45	173.97	37.10	9	36	316.58	22.12	6	65
P30086	Phosphatidylethanolamin	9.50	24.60	2	2	18.00	14.97	3	4	16.25	35.29	3	3
P60842	Eukaryotic initiation facto	30.75	30.54	6	6	14.71	14.78	3	3	42.22	33.00	8	9
Q15847	Adipogenesis regulatory factor OS=Ho	0.00					0.00			6.02	40.79	1	1
Q8IUE6	Histone H2A type 2-B OS	11.10	40.00	2	2	5.49	17.69	1	1	5.62	17.69	1	1
P21796	Voltage-dependent anion	24.50	33.22	5	5	24.49	33.22	5	5	30.06	27.92	4	6
Q9UK76	Hematological and neuro	3.97	11.69	1	1	4.24	11.69	1	1	5.32	27.27	1	1
P08727	Keratin, type I cytoskelet	305.42	26.75	7	58	205.65	31.00	8	41	349.78	21.25	5	65
P05783	Keratin, type I cytoskelet	94.77	37.44	10	17	78.74	37.67	10	14	90.60	34.65	7	16
P10809	60 kDa heat shock protei	89.71	37.35	12	17	73.92	29.32	9	13	99.89	32.11	11	18
Q96KK5	Histone H2A type 1-H OS	14.07	37.50	2	3	14.17	14.84	1	3	9.72	14.84	1	2
P62158	Calmodulin OS=Homo sa	24.46	36.91	4	5	13.07	34.23	3	3	14.11	36.91	3	3
P22626	Heterogeneous nuclear ri	29.75	19.83	4	6	39.57	36.26	6	8	37.31	24.08	4	8
P55327	Tumor protein D52 OS=H	38.94	36.16	6	8	40.73	29.02	4	8	18.52	29.02	3	4
P11142	Heat shock cognate 71 kI	36.97	23.53	8	8	34.02	13.62	5	7	79.47	26.78	8	15
P23528	Cofilin-1 OS=Homo sapie	42.02	35.54	4	8	23.71	35.54	4	5	42.66	35.54	4	8
P12763	Alpha-2-HS-glycoprotein	599.23	30.64	5	102	653.17	30.64	5	110	659.70	35.38	6	111
O43707	Alpha-actinin-4 OS=Hom	69.26	23.82	13	14	55.13	20.31	10	11	73.04	25.36	13	15
O75223	Gamma-glutamylcyclotra	14.32	21.28	2	3	9.61	22.87	2	2	8.93	21.28	2	2
Q8WXC6	Myeloma-overexpressed gene 2 protein OS=Homo sapiens GN=MYEOV2 PE					4.14	35.09	1	1	4.19	35.09	1	1
P04075	Fructose-bisphosphate al	166.31	34.89	7	33	126.24	34.89	7	26	141.40	24.73	4	27
P07437	Tubulin beta chain OS=H	44.31	29.05	7	9	36.04	25.90	6	7	42.08	22.97	5	8
P04264	Keratin, type II cytoskele	26.34	12.58	6	6	56.09	24.07	10	12	42.36	25.00	8	9
P68371	Tubulin beta-4B chain OS	24.65	19.10	5	5	36.34	28.54	6	7	36.19	16.85	4	7
P08758	Annexin A5 OS=Homo sa	27.11	26.25	5	6	24.13	21.56	4	5	20.61	17.50	3	4
P0CW22	40S ribosomal protein S1	9.87	32.59	2	2	5.04	16.30	1	1	19.70	32.59	2	4
P16152	Carbonyl reductase [NAD	24.14	21.30	4	5	19.76	21.30	4	4	21.19	28.16	4	4
P14618	Pyruvate kinase PKM OS=	81.12	29.38	10	17	43.95	13.94	4	9	66.03	26.93	10	14

P68363	Tubulin alpha-1B chain O	49.87	23.95	6	10	44.74	23.95	6	9	56.97	32.15	8	12
Q13011	Delta(3,5)-Delta(2,4)-dier	10.31	12.80	2	2	13.75	19.51	3	3	20.84	25.30	4	4
P62894	Cytochrome c - Bos tauru	19.63	30.77	2	4	5.30	16.35	1	1	8.53	30.77	2	2
P31937	3-hydroxyisobutyrate deh	22.93	26.19	5	5	14.21	14.88	3	3	13.85	15.77	3	3
P07737	Profilin-1 OS=Homo sapie	17.54	20.00	2	4	12.80	31.43	3	3	23.01	20.00	2	5
P04792	Heat shock protein beta-1	18.81	31.22	4	4	19.28	31.22	4	4	14.86	31.22	3	3
P06703	Protein S100-A6 OS=Hon	9.98	31.11	2	2		0.00				0.00		
P68036	Ubiquitin-conjugating enz	6.27	16.23	1	1	10.65	16.23	1	2	10.10	30.52	2	2
P07237	Protein disulfide-isomeras	39.29	28.15	6	8	32.17	13.78	4	7	43.12	26.97	6	8
P78371	T-complex protein 1 subu	49.58	26.73	10	10	56.03	25.98	9	11	44.77	23.93	8	9
P31946	14-3-3 protein beta/alpha	26.13	21.14	3	5	29.61	21.14	3	6	9.87	16.67	2	2
P20674	Cytochrome c oxidase sul	9.60	30.00	2	2		0.00			4.24	10.00	1	1
P29401	Transketolase OS=Homo	38.07	23.92	7	8	43.80	18.14	5	8	42.63	22.15	5	7
O95994	Anterior gradient protein	19.43	29.71	3	4	8.98	20.00	2	2	5.12	9.71	1	1
P51858	Hepatoma-derived growth	15.91	29.58	3	3	16.57	18.33	3	3	20.77	18.33	4	4
P26599	Polypyrimidine tract-bindi	19.76	17.14	4	4	15.48	13.18	3	3	11.55	11.68	2	2
P37802	Transgelin-2 OS=Homo s	8.71	16.08	2	2	13.83	22.11	3	3	13.77	22.11	3	3
P09211	Glutathione S-transferase	16.38	20.00	2	3	21.46	29.05	3	4	6.53	9.05	1	1
P35527	Keratin, type I cytoskelet	28.79	17.82	4	5	50.45	26.48	6	9	31.79	13.96	4	6
P67809	Nuclease-sensitive eleme	18.15	9.88	2	4	14.97	18.21	3	3	28.39	29.01	5	6
O14548	Cytochrome c oxidase subunit 7A-rela	0.00			5.43	28.95	1	1		0.00			
P62841	40S ribosomal protein S1	11.62	28.28	2	2	10.23	13.10	1	2	5.02	13.10	1	1
P08865	40S ribosomal protein SA	14.22	17.97	3	3	18.80	15.93	3	4	16.84	13.56	2	3
Q16698	2,4-dienoyl-CoA reductas	18.86	23.58	4	4	12.69	16.12	3	3	19.68	15.82	4	4
P02769	Serum albumin - Bos tau	535.66	24.88	12	122	525.64	20.76	10	118	424.37	18.29	8	94
P61204	ADP-ribosylation factor 3	24.15	27.62	3	5	8.14	17.68	2	2	4.56	7.73	1	1
P47755	F-actin-capping protein su	10.83	14.69	2	2	14.07	18.53	3	3	4.19	5.59	1	1
Q02790	Peptidyl-prolyl cis-trans is	37.69	20.26	5	8	27.87	24.18	6	6	20.78	17.43	4	4
P61978	Heterogeneous nuclear ri	39.99	18.14	5	8	29.99	15.33	4	6	46.12	24.19	6	9
P60709	Actin, cytoplasmic 1 OS=	114.87	27.20	6	23	65.17	18.93	4	13	149.20	27.20	6	29
Q9UL46	Proteasome activator con	30.46	27.20	4	6	20.47	27.20	4	4	25.95	21.34	3	5
Q15181	Inorganic pyrophosphatas	24.74	20.42	4	5	18.19	13.15	3	4	30.59	21.45	4	6
P61106	Ras-related protein Rab-1	13.01	26.98	3	3		0.00				0.00		
P38646	Stress-70 protein, mitoch	57.72	20.32	10	13	45.95	16.35	8	10	47.10	16.35	7	10
Q9Y316	Protein MEMO1 OS=Hom	13.34	16.50	3	3	4.84	6.40	1	1	13.81	22.56	3	3
Q13228	Selenium-binding protein	24.54	19.07	5	6	21.57	9.11	3	5	18.03	12.29	4	4
Q16881	Thioredoxin reductase 1,	35.52	15.72	6	7	17.67	11.86	3	3	25.82	13.71	5	5
P62081	40S ribosomal protein S7	11.10	26.80	2	2	4.61	11.34	1	1	5.90	11.34	1	1
P27348	14-3-3 protein theta OS=	30.58	26.53	6	6	34.72	21.63	5	7	9.91	13.47	2	2

P20339	Ras-related protein Rab-5	8.80	15.35	2	2		0.00			9.20	17.67	2	2
P50151	Guanine nucleotide-binding protein G(	0.00			4.40	26.47	1	1		0.00			
P51148	Ras-related protein Rab-5	16.53	26.39	3	3	21.24	26.39	3	4	15.25	26.39	3	3
O60361	Putative nucleoside diphc	25.66	26.28	2	5	15.95	13.87	1	3	10.99	13.87	1	2
O00264	Membrane-associated prc	9.38	26.15	2	2	4.63	10.26	1	1	5.22	10.26	1	1
Q9NS69	Mitochondrial import rece	3.86	8.45	1	1	12.74	17.61	1	2	5.47	17.61	1	1
Q9H0U4	Ras-related protein Rab-1	13.47	17.41	2	3	23.86	25.87	3	5	17.49	25.87	3	4
P21266	Glutathione S-transferase	13.68	19.56	3	3	4.47	6.67	1	1	8.71	12.00	2	2
P02655	Apolipoprotein C-II OS=Homo sapiens	0.00								5.24	25.74	1	1
P50395	Rab GDP dissociation inhi	41.49	21.12	6	8	35.96	21.12	6	7	30.03	13.26	5	6
P09972	Fructose-bisphosphate al	51.95	19.51	5	10	21.12	10.71	2	4	34.17	17.03	4	7
P61604	10 kDa heat shock protei	9.19	25.49	2	2	9.39	13.73	1	2	4.76	13.73	1	1
P00167	Cytochrome b5 OS=Hom	9.00	25.37	2	2	10.58	15.67	1	2	5.75	15.67	1	1
P62820	Ras-related protein Rab-1	22.67	25.37	3	5	23.50	25.37	3	5	22.17	25.37	3	5
P63104	14-3-3 protein zeta/delta	17.22	19.59	3	3	35.28	20.82	3	7	21.87	15.10	2	4
P08133	Annexin A6 OS=Homo sa	26.94	13.52	6	6	38.12	18.28	7	8	33.95	17.09	6	7
P14927	Cytochrome b-c1 complex	3.83	13.51	1	1		0.00			9.37	25.23	2	2
Q13404	Ubiquitin-conjugating enz	4.37	10.88	1	1	4.23	14.29	1	1		0.00		
Q12905	Interleukin enhancer-binc	14.15	18.21	3	3	14.35	20.00	3	3	24.99	20.00	3	5
P09110	3-ketoacyl-CoA thiolase, p	12.82	15.09	3	3	20.27	20.05	4	4	25.29	25.00	5	5
Q16836	Hydroxyacyl-coenzyme A	6.88	9.55	1	1	21.04	24.84	3	4		0.00		
P06744	Glucose-6-phosphate isor	39.87	15.95	5	8	27.74	16.49	5	6	24.65	14.52	5	5
P40926	Malate dehydrogenase, m	39.07	24.56	5	8	54.81	24.56	5	11	52.96	24.56	5	10
P0CG06	Ig lambda-3 chain C regi	4.85	24.53	1	1		0.00				0.00		
P52943	Cysteine-rich protein 2 OS=Homo sap	0.00			6.99	15.38	1	1	11.63	24.52	2	2	
Q9Y2V2	Calcium-regulated heat stable protein	0.00				0.00			5.84	24.49	1	1	
P11021	78 kDa glucose-regulatec	49.50	20.34	8	10	59.38	17.28	8	12	29.15	9.79	5	6
Q9UKY7	Protein CDV3 homolog O	11.28	24.42	2	2	12.03	18.99	1	2		0.00		
Q9Y5U9	Immediate early response	4.68	24.39	1	1		0.00						
Q96QR8	Transcriptional activator p	9.40	14.10	2	2	6.36	9.94	1	1	12.05	20.19	2	2
P24752	Acetyl-CoA acetyltransfer	20.08	17.56	4	4	19.37	18.03	4	4	4.61	3.04	1	1
Q9UNZ2	NSFL1 cofactor p47 OS=I	9.39	10.54	2	2	13.30	15.41	3	3	9.52	10.81	2	2
P28070	Proteasome subunit beta	16.41	24.24	3	3	14.59	15.15	2	3	11.02	16.67	2	2
P27797	Calreticulin OS=Homo sa	19.98	23.98	4	4	9.40	10.31	2	2	13.94	17.27	3	3
P00558	Phosphoglycerate kinase	39.29	24.22	6	8	32.97	17.27	4	6	39.89	17.27	4	8
P22314	Ubiquitin-like modifier-act	51.36	16.82	10	11	47.62	17.77	10	10	50.28	16.16	9	10
Q99714	3-hydroxyacyl-CoA dehyd	10.81	16.48	2	2	16.18	16.48	2	3	12.02	16.48	2	2
P25705	ATP synthase subunit alp	32.87	17.90	6	7	31.90	21.70	7	7	28.77	16.46	5	6
P40939	Trifunctional enzyme sub	26.35	12.71	5	6	21.58	9.96	5	5	38.31	13.50	6	8

P17987	T-complex protein 1 subu	28.96	17.09	5	6	25.43	13.13	4	5	30.34	16.37	5	6
P15531	Nucleoside diphosphate k	9.62	23.68	2	2		0.00				0.00		
P25713	Metallothionein-3 OS=Homo sapiens (	0.00			3.94	23.53	1	1		0.00			
Q13185	Chromobox protein homo	8.66	15.85	2	2	9.46	16.39	2	2	15.35	23.50	3	3
Q13405	39S ribosomal protein L4	9.34	16.27	2	2	13.76	23.49	3	3	4.93	7.83	1	1
P42765	3-ketoacyl-CoA thiolase, r	9.22	11.08	2	2	4.85	7.05	1	1	4.98	5.04	1	1
P62258	14-3-3 protein epsilon OS	14.84	23.14	3	3	5.22	7.45	1	1	17.01	14.90	2	3
Q13263	Transcription intermediar	33.30	13.77	6	7	19.95	12.57	4	4	19.69	10.90	4	4
P05388	60S acidic ribosomal prot	23.34	23.03	4	5	10.75	9.78	1	2	17.09	15.14	2	3
P07355	Annexin A2 OS=Homo sa	19.89	13.86	4	4	23.23	22.71	5	5	25.32	14.75	4	5
P10599	Thioredoxin OS=Homo sa	8.02	22.86	2	2	3.93	12.38	1	1		0.00		
P62263	40S ribosomal protein S1	8.47	22.52	2	2	4.37	8.61	1	1	14.25	22.52	3	3
P35579	Myosin-9 OS=Homo sapi	166.33	18.47	26	33	130.17	14.95	21	27	143.59	17.96	23	28
Q16718	NADH dehydrogenase [ubiquinone] 1	0.00			5.37	22.41	1	1		0.00			
Q04837	Single-stranded DNA-binc	8.88	22.30	2	2	9.43	22.30	2	2	9.62	22.30	2	2
Q9Y281	Cofilin-2 OS=Homo sapie	5.49	10.24	1	1	4.50	10.24	1	1	14.06	22.29	2	3
P47985	Cytochrome b-c1 complex	15.28	12.77	2	3	10.80	7.66	1	2	9.16	17.15	2	2
P09661	U2 small nuclear ribonucl	10.05	15.29	2	2	9.88	15.29	2	2	10.12	12.16	2	2
Q9UJZ1	Stomatin-like protein 2, m	15.30	17.70	3	3	14.24	17.13	3	3	10.18	8.99	2	2
P29692	Elongation factor 1-delta	16.15	21.71	4	4	18.10	21.71	4	4	10.25	13.17	2	2
Q99497	Protein DJ-1 OS=Homo s	14.11	21.69	2	3	9.24	21.69	2	2	10.20	21.69	2	2
P63220	40S ribosomal protein S21 OS=Homo	0.00			5.30	21.69	1	1		0.00			
O75363	Breast carcinoma-amplifie	23.93	17.12	5	5	30.94	15.41	4	6	13.93	7.53	3	3
P13674	Prolyl 4-hydroxylase subu	28.43	18.91	5	6	20.40	9.93	3	4	4.17	2.62	1	1
P06748	Nucleophosmin OS=Hom	19.05	21.43	4	4	26.86	16.67	3	5	15.15	21.43	3	3
P52907	F-actin-capping protein su	8.22	12.24	2	2	15.53	15.73	2	3	9.60	14.69	2	2
O00193	Small acidic protein OS=H	14.81	8.74	1	3	4.34	8.74	1	1	10.38	21.31	2	2
P51149	Ras-related protein Rab-7	4.33	7.73	1	1	4.44	6.76	1	1	8.92	13.53	2	2
P61586	Transforming protein Rhc	10.66	21.24	2	2	5.52	8.81	1	1	15.77	21.24	2	3
O43678	NADH dehydrogenase [ul	4.25	21.21	1	1	3.94	21.21	1	1	4.47	21.21	1	1
P12004	Proliferating cell nuclear a	8.70	16.09	2	2	9.93	12.26	2	2	5.11	7.28	1	1
P0CG48	Polyubiquitin-C OS=Homo	8.68	21.02	1	2	4.79	21.02	1	1	4.79	21.02	1	1
P60174	Triosephosphate isomera	22.45	15.38	5	5	21.17	20.98	5	5	14.12	15.38	3	3
O75340	Programmed cell death p	4.74	14.14	1	1	5.16	14.14	1	1	8.68	20.94	2	2
P13693	Translationally-controlled	5.02	12.79	1	1	9.25	20.93	2	2	15.62	12.79	1	3
P08729	Keratin, type II cytoskele	37.75	18.55	6	8	28.08	15.99	5	6	30.30	18.55	6	6
P48643	T-complex protein 1 subu	11.04	8.69	2	2	8.21	6.84	2	2	19.24	11.65	3	4
O43399	Tumor protein D54 OS=H	9.62	20.87	2	2	9.29	20.87	2	2	5.14	9.22	1	1
P49327	Fatty acid synthase OS=H	202.63	13.94	20	41	171.15	16.61	26	36	127.40	13.14	22	26

P49915	GMP synthase [glutamine	24.05	15.87	4	5	11.38	7.07	2	2	18.72	9.96	4	4
P07900	Heat shock protein HSP 9	49.00	18.58	8	11	26.72	7.79	4	6	45.65	17.21	7	9
P46778	60S ribosomal protein L2	9.12	20.63	2	2	4.94	9.38	1	1	10.11	20.63	2	2
O95292	Vesicle-associated memb	4.47	8.23	1	1	12.28	20.58	3	3	4.68	6.58	1	1
O14818	Proteasome subunit alpha	9.11	11.69	2	2	9.13	6.05	1	2	9.54	14.92	2	2
P60660	Myosin light polypeptide (	9.54	20.53	2	2	18.15	20.53	2	4	8.85	20.53	2	2
P24534	Elongation factor 1-beta OS=Homo sa	0.00				9.43	12.44	2	2	10.02	14.67	2	2
Q15233	Non-POU domain-contain	15.17	15.50	3	3	5.52	4.67	1	1	11.42	9.55	2	2
P98179	Putative RNA-binding protein 3 OS=H	0.00				4.81	20.38	1	1		0.00		
P61019	Ras-related protein Rab-2	4.09	6.13	1	1	4.23	6.60	1	1	5.74	7.55	1	1
P50991	T-complex protein 1 subu	17.12	14.47	4	4	12.77	9.65	3	3	23.45	17.63	5	5
P42167	Lamina-associated polype	15.70	16.08	3	3		0.00			9.43	3.96	2	2
Q99798	Aconitate hydratase, mitc	22.20	14.10	5	5	17.92	8.08	4	4	17.04	7.69	4	4
P60981	Destrin OS=Homo sapien	13.32	20.00	2	3	9.52	9.70	1	2	4.68	9.70	1	1
Q9Y333	U6 snRNA-associated Sm-like protein	0.00					0.00			4.18	20.00	1	1
Q9NVJ2	ADP-ribosylation factor-lik	4.14	7.53	1	1	3.94	7.53	1	1	5.09	12.37	1	1
P14866	Heterogeneous nuclear ri	18.51	13.92	4	4	9.69	7.13	2	2	11.10	8.66	2	2
P55072	Transitional endoplasmic	37.22	15.63	7	8	27.57	10.67	5	6	29.64	14.89	6	6
P30101	Protein disulfide-isomeras	9.45	7.13	2	2	10.08	6.14	2	2	28.59	19.80	6	6
Q16891	MICOS complex subunit M	13.56	6.60	3	3	12.18	6.07	3	3	14.94	10.82	3	3
Q7KZF4	Staphylococcal nuclease (	61.64	19.78	9	12	41.77	12.86	6	8	27.07	10.55	4	5
P26885	Peptidyl-prolyl cis-trans isomerase FKB	0.00					0.00			5.22	19.72	1	1
Q9BUP0	EF-hand domain-containi	11.35	12.55	2	2	4.33	7.11	1	1	4.56	7.11	1	1
P12532	Creatine kinase U-type, m	25.70	19.66	4	5	5.88	5.04	1	1	16.51	11.27	2	3
P61513	60S ribosomal protein L37	9.26	19.57	1	2		0.00			4.16	19.57	1	1
Q6DRA6	Putative histone H2B type	4.46	9.15	1	1		0.00			4.13	10.37	1	1
P58107	Epiplakin OS=Homo sapie	107.82	19.51	17	21	64.15	12.73	9	12	60.72	9.63	9	12
P45880	Voltage-dependent anion	11.61	7.82	1	2	9.62	12.59	2	2	15.08	14.63	2	3
O75874	Isocitrate dehydrogenase	9.20	7.97	2	2	8.53	6.76	2	2	13.62	12.80	3	3
Q9HB71	Calcyclin-binding protein	8.59	19.30	2	2	6.08	10.53	1	1	16.28	19.30	2	3
P29966	Myristoylated alanine-rich	11.52	19.28	2	2		0.00			12.30	19.28	2	2
Q06323	Proteasome activator con	20.39	19.28	3	4	9.64	13.65	2	2	10.30	13.65	2	2
P41208	Centrin-2 OS=Homo sapiens GN=CET	0.00					0.00			5.41	19.19	1	1
Q15084	Protein disulfide-isomeras	8.86	6.82	2	2	23.41	16.14	4	5	26.34	19.09	5	5
Q13155	Aminoacyl tRNA synthase complex-int	0.00				4.81	7.81	1	1	6.74	11.25	1	1
P28074	Proteasome subunit beta	13.85	19.01	3	3		0.00			8.34	11.03	2	2
Q8N6T3	ADP-ribosylation factor G	10.27	14.04	2	2	4.47	3.69	1	1	16.50	8.62	2	3
O43598	2'-deoxynucleoside 5'-pho	5.34	18.97	1	1		0.00				0.00		
Q9UBW8	COP9 signalosome compl	9.41	10.91	2	2		0.00			5.19	8.00	1	1

P08195	4F2 cell-surface antigen h	10.32	6.83	2	2	12.73	8.10	3	3	26.60	11.59	4	5
P08107	Heat shock 70 kDa protei	20.64	12.32	4	4	43.14	18.56	6	8	46.84	18.88	7	9
P02545	Prelamin-A/C OS=Homo s	32.18	17.17	7	7	33.57	15.21	6	7	38.63	16.87	7	8
P35270	Sepiapterin reductase OS	9.62	13.03	2	2	9.41	13.03	2	2	9.32	13.03	2	2
P35232	Prohibitin OS=Homo sapi	3.91	5.15	1	1	15.96	13.60	2	3	8.94	11.40	2	2
P15374	Ubiquitin carboxyl-termin	7.74	13.04	2	2	12.69	11.74	2	3	4.33	6.96	1	1
P07339	Cathepsin D OS=Homo s	17.76	15.53	4	4	17.46	16.02	4	4	13.84	11.89	3	3
O00299	Chloride intracellular char	10.97	18.67	2	2	10.70	18.67	2	2	10.47	18.67	2	2
O75947	ATP synthase subunit d,	10.19	9.94	1	2	4.41	9.94	1	1	9.30	18.63	2	2
Q9H3K6	BolA-like protein 2 OS=H	3.88	18.60	1	1	4.77	18.60	1	1	5.13	18.60	1	1
P31939	Bifunctional purine biosyr	17.92	13.18	4	4	19.49	11.15	4	4	14.63	9.63	3	3
P63173	60S ribosomal protein L38 OS=Homo	0.00				9.02	18.57	1	2		0.00		
P13645	Keratin, type I cytoskelet	56.32	18.49	7	10	37.13	17.47	6	7	21.49	11.13	3	4
Q99653	Calcineurin B homologous	3.95	8.21	1	1	9.63	10.26	1	2		0.00		
Q96FQ6	Protein S100-A16 OS=Ho	4.91	18.45	1	1	4.36	18.45	1	1	8.75	18.45	1	2
Q9Y3D7	Mitochondrial import inne	5.02	18.40	1	1	4.63	18.40	1	1		0.00		
P18754	Regulator of chromosome	10.71	11.40	2	2		0.00			17.83	18.29	3	3
P14174	Macrophage migration inl	4.16	18.26	1	1	4.72	18.26	1	1	4.34	18.26	1	1
O95336	6-phosphogluconolactona	5.83	8.14	1	1		0.00			9.70	18.22	2	2
O95833	Chloride intracellular channel protein 3	0.00				8.88	18.22	2	2		0.00		
P43490	Nicotinamide phosphoribo	30.87	18.13	5	6	11.84	7.13	2	2	27.19	15.07	4	5
Q8WXX5	DnaJ homolog subfamily	4.73	7.69	1	1	5.26	10.38	1	1	10.73	18.08	2	2
Q99623	Prohibitin-2 OS=Homo sa	19.08	18.06	4	4	14.15	14.72	3	3	10.69	10.70	2	2
O43752	Syntaxin-6 OS=Homo sap	5.14	9.80	1	1		0.00			4.96	8.24	1	1
P16435	NADPH--cytochrome P45	21.63	9.01	3	4	9.64	5.91	2	2	24.61	11.82	4	5
Q92597	Protein NDRG1 OS=Hom	9.42	8.12	2	2	8.41	7.61	2	2	9.82	10.41	2	2
P25787	Proteasome subunit alpha type-2 OS=	0.00				9.48	17.95	2	2	10.25	17.95	2	2
Q15369	Transcription elongation f	5.17	17.86	1	1	9.95	17.86	1	2	10.73	17.86	1	2
P34932	Heat shock 70 kDa protei	38.45	13.81	7	8	24.65	11.90	5	5	17.62	6.79	3	3
P83916	Chromobox protein homo	4.42	8.65	1	1	4.53	8.65	1	1	9.09	17.84	2	2
O00429	Dynamin-1-like protein O	26.43	14.81	5	5	24.26	10.46	4	5	10.22	5.16	2	2
P05091	Aldehyde dehydrogenase	14.85	9.86	3	3	18.08	11.80	4	4	24.69	12.77	4	5
Q07021	Complement component	9.93	17.73	2	2	4.49	7.09	1	1	4.67	7.09	1	1
P18669	Phosphoglycerate mutase	15.78	17.72	2	3		0.00			10.90	7.09	1	2
P31942	Heterogeneous nuclear ri	4.40	4.91	1	1	14.07	17.63	3	3	4.96	4.91	1	1
Q08257	Quinone oxidoreductase OS=Homo sa	0.00				5.02	8.21	1	1	5.93	9.42	1	1
P27695	DNA-(apurinic or apyrimic	9.03	10.69	2	2	9.57	12.26	2	2	19.64	17.61	3	4
P18859	ATP synthase-coupling fa	4.39	17.59	1	1	5.12	17.59	1	1	9.56	17.59	1	2
P12814	Alpha-actinin-1 OS=Hom	33.48	10.76	6	7	13.89	4.93	3	3	40.22	12.67	7	8

P00966	Argininosuccinate synthase OS=Homo		0.00			40.37	17.48	4	8	19.36	11.89	3	4
P82909	28S ribosomal protein S3	4.65	17.48	1	1	4.16	17.48	1	1	4.49	17.48	1	1
Q96KP4	Cytosolic non-specific dip	4.07	2.95	1	1	13.53	9.89	3	3	13.74	10.53	3	3
P09651	Heterogeneous nuclear ri	10.44	4.57	2	2	18.21	12.90	4	4	28.00	17.20	4	6
Q9NRV9	Heme-binding protein 1 O	8.51	17.46	2	2	5.17	8.99	1	1	5.40	8.99	1	1
O75369	Filamin-B OS=Homo sapi	73.58	11.53	16	16	60.79	8.22	12	13	62.33	9.92	11	12
P00761	Trypsin OS=Sus scrofa PI	31.68	17.32	2	6	24.00	8.66	1	4	16.11	17.32	2	3
P46940	Ras GTPase-activating-lik	55.10	11.59	11	11	32.11	7.18	6	6	50.80	9.72	9	10
P99999	Cytochrome c OS=Homo sapiens GN=		0.00				0.00			4.26	17.14	1	1
P20042	Eukaryotic translation init	4.38	6.61	1	1	4.05	4.50	1	1	5.50	6.01	1	1
Q9Y6U3	Adseverin OS=Homo sap	19.70	9.51	4	4	25.03	11.33	5	5	20.06	10.49	4	4
Q8NCW5	NAD(P)H-hydrate epimer	12.16	17.01	3	3	4.35	6.25	1	1	4.41	6.60	1	1
Q15836	Vesicle-associated memb	5.49	17.00	1	1	4.58	17.00	1	1	4.42	17.00	1	1
P62937	Peptidyl-prolyl cis-trans is	13.90	16.97	2	3	8.70	16.97	2	2	4.24	9.09	1	1
Q8N4Q1	Mitochondrial intermembrane space in		0.00				0.00			4.86	16.90	1	1
P08238	Heat shock protein HSP 9	61.46	16.71	8	14	36.94	10.50	5	8	26.95	10.77	6	6
Q9Y5J7	Mitochondrial import inner membrane		0.00				0.00			4.91	16.85	1	1
P63244	Guanine nucleotide-bindi	4.94	5.05	1	1	14.71	16.72	3	3	10.03	12.62	2	2
Q9Y4L1	Hypoxia up-regulated pro	34.26	11.11	6	7	34.87	9.81	5	6	25.05	9.21	5	5
O75347	Tubulin-specific chaperon	11.04	16.67	2	2	4.10	13.89	1	1	11.06	16.67	2	2
P01767	Ig heavy chain V-III region BUT OS=H		0.00				0.00			4.57	16.52	1	1
P36873	Serine/threonine-protein	8.17	11.15	2	2	13.24	9.60	2	3	4.86	5.26	1	1
P30044	Peroxiredoxin-5, mitocho	4.64	8.41	1	1	9.17	16.36	2	2		0.00		
Q9BPX5	Actin-related protein 2/3	3.89	7.84	1	1	4.26	8.50	1	1	4.13	8.50	1	1
Q15019	Septin-2 OS=Homo sapie	4.67	4.43	1	1	9.05	11.63	2	2	8.36	9.14	2	2
Q9H910	Hematological and neuro	4.34	8.95	1	1	4.20	7.37	1	1		0.00		
P28072	Proteasome subunit beta	6.12	16.32	1	1		0.00				0.00		
P12956	X-ray repair cross-comple	9.42	5.42	2	2	5.13	2.30	1	1	22.17	13.14	5	5
P07476	Involucrin OS=Homo sapiens GN=IVL		0.00			4.88	3.42	1	1	29.05	16.24	5	6
P62140	Serine/threonine-protein	8.78	11.01	2	2	13.24	9.48	2	3	4.86	5.20	1	1
P02656	Apolipoprotein C-III OS=	5.07	16.16	1	1	4.72	16.16	1	1	5.32	16.16	1	1
Q04323	UBX domain-containing protein 1 OS=		0.00			4.78	9.76	1	1	5.31	6.40	1	1
Q9H299	SH3 domain-binding glut	5.23	16.13	1	1	4.70	16.13	1	1	5.02	16.13	1	1
P62316	Small nuclear ribonucleoprotein Sm D2		0.00			4.29	15.25	1	1	4.44	16.10	1	1
P48735	Isocitrate dehydrogenase	25.13	15.93	5	5	14.77	9.73	3	3	9.70	6.64	2	2
P13804	Electron transfer flavopro	4.67	5.71	1	1	4.63	5.41	1	1	4.15	4.80	1	1
P06396	Gelsolin OS=Homo sapie	26.95	13.55	6	6	15.53	7.29	3	3	20.12	10.36	4	4
P09429	High mobility group prote	5.68	8.84	1	1	9.27	15.81	2	2	4.54	6.98	1	1
A8MWD9	Putative small nuclear rib	4.36	15.79	1	1	4.01	15.79	1	1		0.00		

Q6IBS0	Twinfilin-2 OS=Homo sap	13.62	15.76	3	3	5.01	5.44	1	1	9.59	10.89	2	2
P13010	X-ray repair cross-comple	14.83	9.70	3	3	19.05	9.02	3	4	4.11	3.28	1	1
P42166	Lamina-associated polype	15.07	10.23	3	3		0.00			13.78	5.48	3	3
P60953	Cell division control prote	14.16	15.71	2	3	9.55	8.90	1	2	10.68	8.90	1	2
P14550	Alcohol dehydrogenase [I	13.69	11.38	3	3	18.78	15.69	4	4	4.85	5.85	1	1
P52565	Rho GDP-dissociation inh	14.37	15.69	3	3	4.44	7.35	1	1	9.91	15.20	2	2
Q9Y2T7	Y-box-binding protein 2 C	22.33	15.66	3	5	3.93	4.67	1	1	13.91	8.79	2	3
P02666	Beta-casein - Bos taurus	20.92	15.63	2	4	26.04	15.63	2	5	20.53	15.63	2	4
Q15907	Ras-related protein Rab-1	4.20	5.96	1	1	9.32	15.60	2	2	5.19	9.63	1	1
P63241	Eukaryotic translation init	21.92	15.58	2	4	17.05	15.58	2	3	27.94	15.58	2	5
Q00169	Phosphatidylinositol trans	4.78	7.04	1	1	4.35	7.04	1	1	10.36	8.52	1	2
Q9H6S3	Epidermal growth factor r	20.35	10.49	3	4	19.26	10.21	3	4	30.26	15.52	5	6
P42677	40S ribosomal protein S2	3.86	15.48	1	1		0.00				0.00		
P22695	Cytochrome b-c1 complex	15.26	11.70	3	3	17.42	11.48	3	4	10.97	7.51	2	2
P61457	Pterin-4-alpha-carbinolamine dehydrat	0.00			4.51	15.38	1	1	4.90	15.38	1	1	
O75396	Vesicle-trafficking protein	9.37	15.35	2	2	4.56	8.84	1	1	13.93	15.35	2	3
Q9NYL9	Tropomodulin-3 OS=Hom	5.10	5.97	1	1	8.14	9.94	2	2	5.53	5.40	1	1
P31949	Protein S100-A11 OS=Homo sapiens (	0.00			10.88	15.24	1	2		0.00			
Q08380	Galectin-3-binding protein	27.28	15.21	5	6	4.35	2.39	1	1	5.85	3.25	1	1
P62306	Small nuclear ribonucleoprotein F OS=	0.00								4.76	15.12	1	1
O76003	Glutaredoxin-3 OS=Homo	8.63	7.46	2	2		0.00			5.15	7.46	1	1
P09960	Leukotriene A-4 hydrolase	17.99	10.31	4	4	8.72	4.42	2	2	23.37	10.47	4	5
P40227	T-complex protein 1 subu	24.00	14.88	4	5	28.64	14.88	4	6	14.58	7.91	2	3
P02663	Alpha-S2-casein [Contain	20.38	14.86	2	4	11.63	9.91	1	2	18.09	9.91	1	3
Q01105	Protein SET OS=Homo sa	19.19	11.03	2	4	11.03	10.00	2	2	10.39	10.00	2	2
Q99807	Ubiquinone biosynthesis protein COQ7	0.00			4.79	14.75	1	1		0.00			
Q9Y5L4	Mitochondrial import inne	5.21	14.74	1	1		0.00			5.32	14.74	1	1
P09525	Annexin A4 OS=Homo sa	14.13	14.73	3	3	8.98	10.03	2	2	4.91	5.02	1	1
Q86U42	Polyadenylate-binding protein 2 OS=H	0.00				0.00			5.25	14.71	1	1	
Q15121	Astrocytic phosphoprotein PEA-15 OS=	0.00				0.00			4.58	14.62	1	1	
Q15691	Microtubule-associated pr	4.09	4.48	1	1	5.42	10.07	1	1		0.00		
P25325	3-mercaptopyruvate sulfurtransferase	0.00			9.97	14.48	2	2	5.10	9.09	1	1	
P00338	L-lactate dehydrogenase	30.77	9.64	2	6	25.56	9.64	2	5	20.70	14.46	3	4
P32322	Pyrroline-5-carboxylate re	12.27	9.09	2	3	8.52	10.97	2	2		0.00		
Q9HCY8	Protein S100-A14 OS=Ho	5.01	14.42	1	1	5.53	14.42	1	1	4.55	14.42	1	1
P58546	Myotrophin OS=Homo sa	6.24	14.41	1	1	10.75	14.41	1	2	5.01	14.41	1	1
P23396	40S ribosomal protein S3	8.96	14.40	2	2	13.33	14.40	2	3	4.98	9.05	1	1
Q14103	Heterogeneous nuclear ri	9.68	9.01	2	2	14.46	9.30	2	3	9.15	9.30	2	2
Q15365	Poly(rC)-binding protein 1	9.58	5.62	1	2	10.22	14.33	2	2	9.93	5.62	1	2

P13995	Bifunctional methylenetet	8.85	14.29	2	2		0.00				0.00		
P21281	V-type proton ATPase sul	5.16	2.74	1	1	4.57	4.31	1	1	14.79	11.55	3	3
P15559	NAD(P)H dehydrogenase	5.22	6.57	1	1	16.24	14.23	2	3	21.67	14.23	2	4
O00629	Importin subunit alpha-3 OS=Homo s	0.00				15.28	11.52	3	3	21.12	10.94	3	4
P50402	Emerin OS=Homo sapien	8.85	14.17	2	2		0.00			4.81	5.91	1	1
Q13283	Ras GTPase-activating pr	14.60	10.94	3	3	16.30	7.08	2	3	19.43	14.16	4	4
P62333	26S protease regulatory s	10.23	10.54	2	2	5.24	7.71	1	1	4.18	3.60	1	1
Q9P2E9	Ribosome-binding protein	52.44	11.91	9	11	43.53	10.07	8	9	41.67	7.73	5	8
Q92905	COP9 signalosome compl	5.88	8.38	1	1		0.00			10.91	5.69	1	2
O95139	NADH dehydrogenase [ubiquinone] 1	0.00					0.00			4.18	14.06	1	1
P05386	60S acidic ribosomal prot	3.94	14.04	1	1		0.00				0.00		
P51991	Heterogeneous nuclear ri	5.06	5.82	1	1	3.91	4.23	1	1	15.12	9.79	2	3
Q9Y5M8	Signal recognition particle	9.45	14.02	2	2	9.28	14.02	2	2	5.57	7.01	1	1
Q9Y3F4	Serine-threonine kinase r	9.78	8.86	2	2	14.87	10.29	2	3	5.32	5.14	1	1
P05023	Sodium/potassium-transp	34.47	10.75	6	7	13.95	5.28	3	3	25.90	5.87	3	5
P05198	Eukaryotic translation init	3.92	3.81	1	1		0.00			9.53	10.16	2	2
O75390	Citrate synthase, mitocho	13.37	6.65	2	3	4.17	3.43	1	1	14.14	13.95	3	3
O95168	NADH dehydrogenase [ul	4.13	13.95	1	1		0.00				0.00		
Q9NZ45	CDGSH iron-sulfur domai	4.39	13.89	1	1		0.00			4.53	13.89	1	1
P28331	NADH-ubiquinone oxidore	23.43	11.55	5	5	8.21	4.54	2	2	24.57	11.28	5	5
Q07020	60S ribosomal protein L1	8.63	13.83	2	2	4.69	6.91	1	1	8.64	13.83	2	2
P55209	Nucleosome assembly pr	9.39	9.21	2	2	4.67	4.35	1	1	9.49	8.95	2	2
Q15388	Mitochondrial import rece	11.46	13.79	1	2	5.65	13.79	1	1	5.24	13.79	1	1
P07954	Fumarate hydratase, mito	15.82	10.78	3	3	13.47	9.22	3	3	15.88	8.04	2	3
P16989	Y-box-binding protein 3 O	23.05	13.71	3	5	3.93	4.57	1	1	18.74	13.71	3	4
O14907	Tax1-binding protein 3 OS=Homo sap	0.00				3.95	13.71	1	1	4.41	13.71	1	1
P25815	Protein S100-P OS=Homo	4.27	13.68	1	1	4.19	13.68	1	1		0.00		
Q9Y5Z4	Heme-binding protein 2 O	4.33	7.32	1	1	8.90	13.66	2	2	4.31	6.34	1	1
P31943	Heterogeneous nuclear ri	28.74	13.59	4	6	8.24	9.58	2	2	16.12	9.80	3	3
Q9NP72	Ras-related protein Rab-1	4.08	6.31	1	1	4.06	7.28	1	1	4.31	6.31	1	1
O96008	Mitochondrial import rece	8.68	13.57	2	2		0.00			4.36	4.16	1	1
Q13509	Tubulin beta-3 chain OS=	24.36	13.56	4	5	20.11	10.89	3	4	14.71	10.89	3	3
Q16204	Coiled-coil domain-contai	13.82	10.55	3	3	5.52	4.01	1	1	15.39	6.96	3	3
O75531	Barrier-to-autointegration factor OS=H	0.00				4.27	13.48	1	1		0.00		
P62241	40S ribosomal protein S8	8.84	13.46	2	2	4.76	6.25	1	1	4.82	6.25	1	1
P35908	Keratin, type II cytoskele	4.88	1.88	1	1	27.73	7.82	4	6	18.49	7.51	4	4
Q00796	Sorbitol dehydrogenase O	13.11	13.45	3	3		0.00				0.00		
Q04917	14-3-3 protein eta OS=H	9.85	7.72	1	2	5.10	7.72	1	1	14.77	13.41	2	3
P41250	Glycine--tRNA ligase OS=	30.01	13.40	5	6	10.21	5.55	2	2	19.86	11.64	4	4

Q9H444	Charged multivesicular bo	4.25	6.25	1	1	4.71	7.14	1	1		0.00		
P11177	Pyruvate dehydrogenase	8.03	8.91	2	2	9.29	8.91	2	2	5.11	4.46	1	1
P61981	14-3-3 protein gamma OS	10.99	13.36	2	2	10.51	13.36	2	2	8.87	13.36	2	2
P62993	Growth factor receptor-bo	4.77	13.36	1	1		0.00				0.00		
Q9UJS0	Calcium-binding mitochon	20.95	10.81	4	4	19.76	10.52	4	4	9.93	5.19	2	2
P18124	60S ribosomal protein L7	4.64	5.65	1	1		0.00			4.58	7.66	1	1
P49411	Elongation factor Tu, mito	4.91	3.98	1	1	13.31	10.62	3	3	17.29	10.18	3	4
Q9Y2Q3	Glutathione S-transferase	8.87	13.27	2	2	8.89	13.27	2	2	9.49	13.27	2	2
Q14257	Reticulocalbin-2 OS=Hom	10.26	7.26	1	2	5.61	5.99	1	1	5.43	7.26	1	1
P05455	Lupus La protein OS=Hor	17.99	13.24	4	4	8.20	6.86	2	2	4.35	3.43	1	1
P19338	Nucleolin OS=Homo sapi	44.44	13.24	7	9	41.70	11.27	6	8	36.85	10.85	4	7
P35244	Replication protein A 14 kDa subunit C		0.00							4.57	13.22	1	1
Q9BWF3	RNA-binding protein 4 OS	4.89	4.40	1	1	4.32	4.40	1	1	5.32	8.79	1	1
Q9NX55	Huntingtin-interacting pro	4.76	13.18	1	1	4.23	13.18	1	1		0.00		
P06702	Protein S100-A9 OS=Hon	8.22	13.16	1	2		0.00				0.00		
Q9Y224	UPF0568 protein C14orf1	3.84	6.56	1	1		0.00			5.14	6.56	1	1
Q8IY81	pre-rRNA processing prot	9.57	5.08	2	2	18.83	10.04	4	4	15.89	8.03	3	3
Q6P1L8	39S ribosomal protein L1	4.94	13.10	1	1	5.20	13.10	1	1		0.00		
Q8N5G0	Small integral membrane protein 20 C		0.00			5.04	13.10	1	1		0.00		
Q9NR45	Sialic acid synthase OS=H	8.84	5.01	1	2	4.21	3.90	1	1	4.69	4.18	1	1
P54105	Methylosome subunit pICln OS=Homo		0.00			5.79	13.08	1	1		0.00		
P62854	40S ribosomal protein S2	3.92	13.04	1	1		0.00						
P31150	Rab GDP dissociation inhi	28.89	12.98	4	5	27.41	12.98	4	5	25.61	12.98	4	5
P62942	Peptidyl-prolyl cis-trans is	9.76	12.96	1	2		0.00			4.25	12.96	1	1
O43390	Heterogeneous nuclear ri	12.52	7.90	3	3	8.95	4.42	2	2	8.86	4.74	2	2
P53396	ATP-citrate synthase OS=	32.14	10.17	7	7	34.01	8.81	6	7	18.84	5.81	4	4
P28066	Proteasome subunit alpha	4.50	4.98	1	1	4.62	4.98	1	1	4.97	7.88	1	1
Q9GZT3	SRA stem-loop-interacting RNA-bindin		0.00			4.92	12.84	1	1		0.00		
Q9Y2Q9	28S ribosomal protein S2	5.14	12.83	1	1	5.22	12.83	1	1		0.00		
P43686	26S protease regulatory s	4.78	4.78	1	1	5.77	7.89	1	1	11.87	7.89	1	2
Q8N5N7	39S ribosomal protein L5	4.31	12.66	1	1	4.02	12.66	1	1		0.00		
Q9H3Z4	DnaJ homolog subfamily C member 5		0.00			5.32	12.63	1	1		0.00		
P62805	Histone H4 OS=Homo sa	9.54	12.62	2	2		0.00			5.36	12.62	1	1
O76070	Gamma-synuclein OS=Ho	4.67	12.60	1	1	3.95	12.60	1	1				
O43776	Asparagine--tRNA ligase,	17.79	9.31	3	4		0.00			18.56	10.40	3	4
O96005	Cleft lip and palate transr	4.93	3.29	1	1	5.34	3.29	1	1	10.98	9.27	2	2
Q14247	Src substrate cortactin OS	16.79	12.55	3	3	9.46	6.73	2	2	19.53	6.73	2	4
Q13158	FAS-associated death domain protein		0.00			5.44	12.50	1	1		0.00		
Q8TCD5	5'(3')-deoxyribonucleotidase, cytosolic		0.00			4.76	12.44	1	1	5.22	12.44	1	1

Q9NX24	H/ACA ribonucleoprotein	5.50	12.42	1	1	9.29	12.42	1	2	5.44	12.42	1	1
O75312	Zinc finger protein ZPR1 OS=Homo sa	0.00				4.43	3.05	1	1	10.09	9.37	2	2
O60739	Eukaryotic translation init	4.02	12.39	1	1		0.00				0.00		
Q96LD1	Zeta-sarcoglycan OS=Ho	5.61	12.37	1	1		0.00				0.00		
P13639	Elongation factor 2 OS=H	30.37	8.62	4	6	29.80	9.09	4	6	50.82	11.31	6	10
P68104	Elongation factor 1-alpha	11.82	7.14	2	2	9.99	12.12	2	2	6.12	6.93	1	1
P04040	Catalase OS=Homo sapiens GN=CAT	0.00				9.87	8.35	2	2	4.12	3.98	1	1
P00387	NADH-cytochrome b5 rec	5.40	5.98	1	1	9.42	12.29	2	2	9.29	12.29	2	2
P49368	T-complex protein 1 subu	13.90	10.09	3	3	9.04	5.87	2	2		0.00		
Q9NRF9	DNA polymerase epsilon subunit 3 OS	0.00					0.00			4.70	12.24	1	1
P50990	T-complex protein 1 subu	17.14	10.04	4	4	8.91	4.93	2	2	13.59	7.48	3	3
P28482	Mitogen-activated protein	9.34	12.22	2	2		0.00			5.10	4.17	1	1
Q13561	Dynactin subunit 2 OS=H	9.39	8.23	2	2	3.93	3.99	1	1	5.39	4.49	1	1
Q14011	Cold-inducible RNA-bindi	4.81	12.21	1	1	4.07	12.21	1	1	5.26	12.21	1	1
Q96FW1	Ubiquitin thioesterase OTUB1 OS=Hor	0.00				9.64	5.54	1	2	12.80	12.18	2	3
Q9UQ80	Proliferation-associated p	4.25	3.30	1	1	8.64	7.87	2	2	14.38	8.88	2	3
Q9H4A4	Aminopeptidase B OS=Ho	8.76	4.62	2	2	9.06	4.77	2	2	4.43	2.77	1	1
P20290	Transcription factor BTF3 OS=Homo s	0.00					0.00			4.60	12.14	1	1
P06493	Cyclin-dependent kinase	4.83	6.73	1	1	4.25	5.39	1	1	9.02	12.12	2	2
P48147	Prolyl endopeptidase OS=	18.73	9.86	4	4	4.92	2.39	1	1	15.04	7.75	3	3
P04181	Ornithine aminotransferas	9.90	4.56	1	2	5.67	4.56	1	1	10.92	12.07	2	2
Q96DA6	Mitochondrial import inner membrane	0.00					0.00			4.17	12.07	1	1
P52597	Heterogeneous nuclear ri	15.29	12.05	3	3	15.33	12.05	3	3	15.92	7.95	2	3
P04844	Dolichyl-diphosphooligosa	22.39	9.35	4	5	13.52	7.13	3	3	13.60	7.61	3	3
P62330	ADP-ribosylation factor 6	4.09	12.00	1	1		0.00				0.00		
Q99733	Nucleosome assembly pr	16.22	12.00	2	3		0.00			10.64	12.00	2	2
Q9NRX4	14 kDa phosphohistidine phosphatase	0.00				4.15	12.00	1	1		0.00		
Q15717	ELAV-like protein 1 OS=Homo sapiens	0.00				3.96	4.29	1	1	10.11	11.96	2	2
Q14116	Interleukin-18 OS=Homo sapiens GN=	0.00					0.00			5.79	11.92	1	1
P39023	60S ribosomal protein L3	5.12	5.96	1	1	10.82	6.45	2	2	15.30	11.91	3	3
O60814	Histone H2B type 1-K OS	5.10	11.90	1	1	5.13	11.90	1	1	5.20	11.90	1	1
P05026	Sodium/potassium-transp	10.00	8.25	1	2	9.73	11.88	2	2	16.64	8.25	1	3
P49591	Serine--tRNA ligase, cytoplasmic OS=I	0.00				4.77	5.45	1	1	9.35	6.42	2	2
Q9UJU6	Drebrin-like protein OS=H	10.31	8.37	2	2	4.95	3.72	1	1	9.32	7.21	2	2
P09382	Galectin-1 OS=Homo sap	4.34	11.85	1	1	4.09	11.85	1	1		0.00		
P61289	Proteasome activator con	3.90	5.91	1	1	4.97	5.91	1	1	4.81	5.91	1	1
P31040	Succinate dehydrogenase	15.07	11.75	3	3	14.42	11.75	3	3	11.02	6.63	2	2
P16403	Histone H1.2 OS=Homo s	4.35	5.63	1	1	8.05	11.74	2	2	13.95	11.74	2	3
Q96AG4	Leucine-rich repeat-containing protein	0.00					0.00			11.57	11.73	2	2

Q9UI09	NADH dehydrogenase [ul	4.23	11.72	1	1		0.00				0.00		
Q15056	Eukaryotic translation init	5.63	11.69	1	1		0.00				0.00		
Q96QK1	Vacuolar protein sorting-a	16.67	5.65	3	4	18.44	5.65	3	4	15.29	6.16	3	3
P17858	ATP-dependent 6-phosph	19.44	7.18	3	4	13.56	7.56	3	3	18.74	9.36	4	4
Q92598	Heat shock protein 105 k	24.98	7.93	4	5	18.34	7.58	4	4	26.58	8.04	4	5
P17980	26S protease regulatory s	12.93	11.62	3	3	4.93	4.33	1	1	18.60	11.62	3	4
Q9NR31	GTP-binding protein SAR1	4.70	11.62	1	1		0.00			4.30	11.62	1	1
P23434	Glycine cleavage system	5.32	11.56	1	1	4.01	11.56	1	1	5.17	11.56	1	1
Q12931	Heat shock protein 75 kD	13.70	9.66	3	3	12.72	3.84	2	3	9.76	3.84	2	2
P30040	Endoplasmic reticulum re	12.68	11.49	2	3	4.27	5.75	1	1	4.64	5.75	1	1
Q14376	UDP-glucose 4-epimerase	17.58	11.49	2	3	5.64	5.46	1	1	11.31	11.49	2	2
Q7Z4W1	L-xylulose reductase OS=	5.90	11.48	1	1		0.00			6.92	11.48	1	1
O75937	DnaJ homolog subfamily C member 8	0.00					0.00			5.53	11.46	1	1
Q9NX63	MICOS complex subunit M	8.37	11.45	2	2		0.00			4.39	6.61	1	1
Q9H4M9	EH domain-containing pro	13.71	11.42	3	3	9.68	8.99	2	2	4.93	2.81	1	1
Q9NQ55	Suppressor of SWI4 1 ho	5.10	7.82	1	1	4.29	3.59	1	1		0.00		
P10109	Adrenodoxin, mitochondrial OS=Homo	0.00					0.00			4.42	11.41	1	1
P21291	Cysteine and glycine-rich	4.54	11.40	1	1	4.59	11.40	1	1	4.64	11.40	1	1
P24666	Low molecular weight ph	9.40	11.39	1	2	5.57	11.39	1	1	8.88	11.39	1	2
O75489	NADH dehydrogenase [ul	3.93	4.92	1	1	4.39	6.44	1	1	4.48	4.92	1	1
Q9NTK5	Obg-like ATPase 1 OS=H	12.94	11.36	3	3	4.24	3.79	1	1	4.23	3.79	1	1
Q14166	Tubulin--tyrosine ligase-li	3.93	2.02	1	1		0.00			15.11	9.32	3	3
O75367	Core histone macro-H2A.	5.57	5.91	1	1	5.28	5.91	1	1	15.20	11.29	2	3
Q96C86	m7GpppX diphosphatase	4.21	5.64	1	1	5.07	5.64	1	1	5.63	5.64	1	1
P20839	Inosine-5'-monophosphat	11.19	5.06	1	2	4.20	2.33	1	1	12.29	8.95	2	2
P62847	40S ribosomal protein S2	4.07	11.28	1	1		0.00				0.00		
Q15366	Poly(rC)-binding protein 2	9.58	5.48	1	2	4.99	5.48	1	1	14.10	11.23	2	3
Q5JTJ3	Cytochrome c oxidase ass	4.07	11.20	1	1		0.00				0.00		
P62899	60S ribosomal protein L31 OS=Homo	0.00				3.97	11.20	1	1		0.00		
Q9UI30	Multifunctional methyltransferase subu	0.00				4.54	11.20	1	1	5.29	11.20	1	1
Q9NQP4	Prefoldin subunit 4 OS=H	4.17	11.19	1	1	4.41	11.19	1	1		0.00		
P38606	V-type proton ATPase cat	18.46	7.78	3	4	10.44	6.32	2	2	12.21	6.32	2	2
Q9Y6M9	NADH dehydrogenase [ubiquinone] 1	0.00					0.00			4.13	11.17	1	1
O14745	Na(+)/H(+) exchange re	16.63	7.26	1	3	13.98	11.17	2	3	10.36	7.26	1	2
Q01518	Adenylyl cyclase-associat	13.89	11.16	3	3	5.06	3.79	1	1	4.34	3.79	1	1
Q13501	Sequestosome-1 OS=Homo sapiens G	0.00				5.29	3.41	1	1	11.39	11.14	2	2
Q14157	Ubiquitin-associated prot	19.09	8.28	4	4	4.55	1.75	1	1	17.88	6.44	4	4
O14602	Eukaryotic translation init	4.07	11.11	1	1		0.00				0.00		
P00491	Purine nucleoside phosph	7.95	11.07	2	2	4.54	5.88	1	1	4.20	5.88	1	1

Q99832	T-complex protein 1 subu	21.60	11.05	3	4	16.59	8.47	2	3	16.74	6.63	2	3
P36578	60S ribosomal protein L4	7.87	8.43	2	2	8.37	5.85	2	2	4.35	5.15	1	1
Q7L5L3	Glycerophosphodiester ph	11.14	6.60	1	2	6.10	6.60	1	1	10.16	11.01	2	2
P52209	6-phosphogluconate dehy	9.00	8.07	2	2	10.36	7.04	2	2	6.13	3.93	1	1
P0C0S5	Histone H2A.Z OS=Homo sapiens GN=	0.00				4.08	10.94	1	1	4.19	10.94	1	1
Q9Y5S9	RNA-binding protein 8A OS=Homo sa	0.00					0.00			4.13	10.92	1	1
P62424	60S ribosomal protein L7	8.98	10.90	2	2	9.33	10.90	2	2		0.00		
Q04760	Lactoylglutathione lyase (	5.14	10.87	1	1	5.92	10.87	1	1	5.90	10.87	1	1
Q9HCN8	Stromal cell-derived factor 2-like prote	0.00					0.00			5.26	10.86	1	1
O15212	Prefoldin subunit 6 OS=Homo sapiens	0.00					0.00			4.77	10.85	1	1
P18206	Vinculin OS=Homo sapien	27.52	8.47	5	5	20.43	6.17	4	4	25.41	6.79	4	5
P50897	Palmitoyl-protein thioeste	8.40	10.78	2	2	4.92	5.88	1	1	5.07	5.88	1	1
P61923	Coatomer subunit zeta-1 OS=Homo sa	0.00					0.00			4.72	10.73	1	1
O75817	Ribonuclease P protein su	4.20	10.71	1	1								
P62829	60S ribosomal protein L2	4.13	10.71	1	1		0.00			4.58	10.71	1	1
O95433	Activator of 90 kDa heat	4.23	4.14	1	1		0.00			4.82	6.51	1	1
P61803	Dolichyl-diphosphooligosa	4.06	10.62	1	1		0.00						
P15170	Eukaryotic peptide chain	8.57	5.61	2	2	8.94	7.41	2	2		0.00		
Q13630	GDP-L-fucose synthase O	4.11	4.67	1	1	3.99	5.92	1	1		0.00		
P20700	Lamin-B1 OS=Homo sapi	18.85	10.58	4	4	9.52	4.95	2	2	9.09	5.12	2	2
Q14444	Caprin-1 OS=Homo sapiens GN=CAPF	0.00					0.00			13.43	10.58	3	3
P00390	Glutathione reductase, m	9.40	10.54	2	2		0.00			6.00	6.51	1	1
P19105	Myosin regulatory light ch	4.97	10.53	1	1	5.07	10.53	1	1	5.28	10.53	1	1
P12268	Inosine-5'-monophosphat	4.70	2.92	1	1		0.00			13.55	10.51	3	3
O00422	Histone deacetylase comp	4.39	10.46	1	1		0.00			4.85	10.46	1	1
Q9P2J5	Leucine--tRNA ligase, cyt	26.25	9.18	6	6	12.77	4.00	3	3	25.76	6.80	4	5
P62888	60S ribosomal protein L3	4.28	10.43	1	1		0.00				0.00		
Q16851	UTP--glucose-1-phosphat	9.78	6.89	2	2	5.12	3.94	1	1	9.81	7.48	2	2
Q07812	Apoptosis regulator BAX (	4.71	10.42	1	1		0.00			4.54	10.42	1	1
Q02878	60S ribosomal protein L6	4.03	4.51	1	1		0.00			4.49	5.90	1	1
P62995	Transformer-2 protein ho	9.31	4.86	1	2		0.00			5.23	5.56	1	1
P36542	ATP synthase subunit ga	5.27	10.40	1	1		0.00				0.00		
Q9GZL7	Ribosome biogenesis pro	4.94	4.49	1	1		0.00			5.16	5.91	1	1
P05452	Tetranectin OS=Homo sa	4.84	10.40	1	1	4.56	10.40	1	1	4.16	10.40	1	1
P35998	26S protease regulatory s	4.67	4.39	1	1	8.68	6.00	2	2	9.55	4.39	1	2
O14828	Secretory carrier-associat	9.71	4.61	1	2	10.09	4.61	1	2	19.37	10.37	2	4
P17900	Ganglioside GM2 activator OS=Homo	0.00				4.67	10.36	1	1		0.00		
Q86X59	Putative uncharacterized protein C17o	0.00				4.94	10.36	1	1		0.00		
P39019	40S ribosomal protein S1	5.07	10.34	1	1		0.00				0.00		

Q9BRT2	Ubiquinol-cytochrome-c reductase con	0.00				0.00			4.54	10.32	1	1
P00568	Adenylate kinase isoenzyme 1 OS=Ho	0.00				0.00			4.62	10.31	1	1
Q99426	Tubulin-folding cofactor B	4.57	10.25	1	1		0.00				0.00		
Q7Z2W9	39S ribosomal protein L21, mitochond	0.00				0.00			4.10	10.24	1	1
P49748	Very long-chain specific a	14.32	10.23	3	3	3.94	3.66	1	1	4.46	3.66	1	1
O75439	Mitochondrial-processing	10.59	10.22	2	2		0.00			11.22	10.22	2	2
O95169	NADH dehydrogenase [ul	4.48	10.22	1	1		0.00			4.57	10.22	1	1
Q6XQN6	Nicotinate phosphoribosy	9.57	7.62	2	2	4.52	2.60	1	1		0.00		
Q15370	Transcription elongation factor B polyp	0.00				4.16	10.17	1	1		0.00		
P11766	Alcohol dehydrogenase cl	4.72	4.28	1	1	5.08	5.88	1	1	4.51	4.28	1	1
P60900	Proteasome subunit alpha	3.85	4.88	1	1	4.15	5.28	1	1		0.00		
P35268	60S ribosomal protein L22 OS=Homo	0.00				3.93	10.16	1	1		0.00		
O60869	Endothelial differentiation	4.74	10.14	1	1	9.13	10.14	1	2		0.00		
P61966	AP-1 complex subunit sigma-1A OS=H	0.00				4.64	10.13	1	1	5.19	10.13	1	1
P40763	Signal transducer and act	24.98	8.44	4	5	10.61	3.77	2	2	14.53	5.45	3	3
Q00610	Clathrin heavy chain 1 OS	47.42	8.48	8	9	41.21	5.97	5	8	37.30	7.46	6	7
O75436	Vacuolar protein sorting-a	8.70	10.09	2	2		0.00				0.00		
Q9Y508	E3 ubiquitin-protein ligas	9.37	10.09	1	2		0.00			9.49	10.09	1	2
O43684	Mitotic checkpoint protein	4.00	5.79	1	1	3.95	4.27	1	1	4.29	4.27	1	1
O95747	Serine/threonine-protein	9.02	6.26	2	2	15.47	10.06	3	3	11.45	7.40	2	2
Q03154	Aminoacylase-1 OS=Hom	4.46	4.41	1	1	4.70	5.64	1	1		0.00		
P00367	Glutamate dehydrogenas	4.45	3.41	1	1	13.46	10.04	3	3	4.37	3.41	1	1
P20810	Calpastatin OS=Homo sa	14.76	10.03	3	3	9.54	6.64	2	2	5.80	3.39	1	1
Q6GMV3	Putative peptidyl-tRNA hydrolase PTRI	0.00				3.95	10.00	1	1	4.36	10.00	1	1
Q12849	G-rich sequence factor 1	5.59	4.17	1	1	6.01	4.17	1	1	4.96	5.83	1	1
O60506	Heterogeneous nuclear ri	9.88	5.14	2	2	9.82	3.37	2	2	25.75	8.99	3	5
P26440	Isovaleryl-CoA dehydroge	4.30	4.02	1	1		0.00			5.12	5.91	1	1
P19013	Keratin, type II cytoskele	13.37	7.68	3	3	13.79	7.30	3	3	9.46	3.00	1	2
P35249	Replication factor C subu	3.84	4.41	1	1		0.00			6.03	5.51	1	1
P11413	Glucose-6-phosphate 1-d	9.54	6.02	2	2	4.19	2.91	1	1	9.40	6.99	2	2
P32969	60S ribosomal protein L9 OS=Homo s	0.00				5.48	9.90	1	1	5.24	9.90	1	1
P61088	Ubiquitin-conjugating enzyme E2 N OS	0.00				4.05	9.87	1	1		0.00		
P00711	Alpha-lactalbumin - Bos t	5.20	9.86	1	1		0.00			5.55	9.86	1	1
P14314	Glucosidase 2 subunit bet	8.61	6.25	2	2	8.23	6.25	2	2	14.48	9.85	3	3
Q96EY4	Translation machinery-as	9.13	9.85	1	2	4.36	9.85	1	1	4.19	9.85	1	1
Q9BX68	Histidine triad nucleotide-	3.85	9.82	1	1		0.00				0.00		
P56537	Eukaryotic translation init	4.76	9.80	1	1		0.00			4.26	9.80	1	1
P46782	40S ribosomal protein S5	4.48	9.80	1	1	10.27	9.80	1	2	5.50	9.80	1	1
Q96EK6	Glucosamine 6-phosphate N-acetyltrar	0.00					0.00			4.57	9.78	1	1

Q99471	Prefoldin subunit 5 OS=H	4.33	9.74	1	1	4.45	9.74	1	1	4.24	9.74	1	1
P25685	DnaJ homolog subfamily B member 1	0.00				8.51	9.71	2	2		0.00		
P14625	Endoplasmin OS=Homo s	22.42	7.35	4	5	19.76	8.34	4	4	24.36	8.34	4	5
P11233	Ras-related protein Ral-A	5.83	9.71	1	1	4.95	9.71	1	1	5.25	9.71	1	1
P00374	Dihydrofolate reductase (	5.56	9.63	1	1		0.00			5.47	9.63	1	1
P23921	Ribonucleoside-diphospha	12.22	7.70	2	2	15.62	9.60	3	3	27.23	9.60	3	5
P42704	Leucine-rich PPR motif-co	27.59	7.39	6	6	14.45	3.59	3	3	10.12	2.15	2	2
Q15149	Plectin OS=Homo sapiens	59.02	4.53	12	12	55.35	4.21	11	11	87.35	6.30	16	18
Q9NQG5	Regulation of nuclear pre	8.22	9.51	2	2	4.08	4.60	1	1	9.18	9.51	2	2
O00762	Ubiquitin-conjugating enz	4.29	9.50	1	1	4.70	9.50	1	1		0.00		
Q9Y490	Talin-1 OS=Homo sapien	49.59	6.14	8	10	31.26	4.88	6	6	48.40	6.45	8	9
P02668	Kappa-casein [Contains: (	5.30	9.47	1	1	5.56	9.47	1	1	5.06	9.47	1	1
O43488	Aflatoxin B1 aldehyde rec	4.89	4.18	1	1	7.97	9.47	2	2	9.06	9.47	2	2
P53004	Biliverdin reductase A OS	8.21	9.46	2	2		0.00				0.00		
Q8WUM4	Programmed cell death 6	18.87	6.80	4	4	25.52	5.99	3	5	13.83	6.34	3	3
P47914	60S ribosomal protein L29 OS=Homo	0.00					0.00			4.15	9.43	1	1
Q92552	28S ribosomal protein S27, mitochond	0.00				9.60	9.42	2	2	4.43	3.62	1	1
Q16576	Histone-binding protein R	9.50	9.41	2	2	9.96	9.41	2	2		0.00		
P57735	Ras-related protein Rab-25 OS=Homo	0.00					0.00			4.91	9.39	1	1
Q9ULC4	Malignant T-cell-amplified sequence 1	0.00					0.00			4.23	9.39	1	1
Q9Y3B7	39S ribosomal protein L1	4.15	9.38	1	1		0.00			5.36	9.38	1	1
O14980	Exportin-1 OS=Homo sap	14.08	4.20	3	3	9.01	2.71	2	2	16.15	5.70	3	3
P30042	ES1 protein homolog, mitochondrial O	0.00				4.72	9.33	1	1		0.00		
O75348	V-type proton ATPase sul	3.98	9.32	1	1		0.00				0.00		
Q9UNM6	26S proteasome non-ATPase regulato	0.00					0.00			9.14	9.31	2	2
Q9H1Z9	Tetraspanin-10 OS=Hom	4.79	9.30	1	1		0.00				0.00		
Q12906	Interleukin enhancer-binc	4.98	2.01	1	1	10.25	5.48	2	2	5.92	3.80	1	1
P07195	L-lactate dehydrogenase	5.13	4.49	1	1	4.03	4.79	1	1	9.73	9.28	2	2
Q9UGI8	Testin OS=Homo sapiens	9.44	9.26	2	2		0.00			5.27	5.23	1	1
O43708	Maleylacetoacetate isome	4.04	9.26	1	1		0.00				0.00		
P55786	Puromycin-sensitive amin	5.11	2.94	1	1	13.41	6.31	3	3	4.33	1.85	1	1
Q9HCC0	Methylcrotonoyl-CoA carb	12.33	9.24	3	3	8.19	6.04	2	2	4.24	3.20	1	1
O60682	Musculin OS=Homo sapie	3.87	9.22	1	1		0.00				0.00		
Q8N163	Cell cycle and apoptosis r	16.45	9.21	3	3	11.41	5.96	2	2	5.11	3.58	1	1
P31948	Stress-induced-phosphop	15.43	3.68	1	3	8.50	6.81	2	2	19.83	9.21	3	4
O15258	Protein RER1 OS=Homo sapiens GN=	0.00				4.22	9.18	1	1		0.00		
P13798	Acylamino-acid-releasing	4.95	3.14	1	1	4.21	2.05	1	1	13.92	7.10	3	3
Q9Y678	Coatomer subunit gamma	14.25	6.86	3	3	13.52	4.35	2	3	4.18	2.06	1	1
Q13555	Calcium/calmodulin-depe	8.69	5.73	2	2	4.43	3.41	1	1	9.46	6.81	2	2

Q12792	Twinfilin-1 OS=Homo sap	9.05	9.14	2	2	4.81	5.43	1	1	4.91	5.43	1	1
Q92945	Far upstream element-bir	13.34	6.61	3	3	13.04	5.06	2	3	9.25	5.63	2	2
O43583	Density-regulated protein OS=Homo s	0.00				4.17	9.09	1	1		0.00		
Q9UHV9	Prefoldin subunit 2 OS=Homo sapiens	0.00				3.93	9.09	1	1	4.13	9.09	1	1
P30050	60S ribosomal protein L12 OS=Homo	0.00					0.00			9.55	9.09	1	2
P46783	40S ribosomal protein S1	3.95	8.48	1	1		0.00			5.04	9.09	1	1
P00441	Superoxide dismutase [Cu-Zn] OS=Ho	0.00				4.06	9.09	1	1	4.26	9.09	1	1
P82979	SAP domain-containing ri	4.62	9.05	1	1		0.00				0.00		
P14651	Homeobox protein Hox-B3 OS=Homo	0.00				4.78	9.05	1	1		0.00		
Q9BY77	Polymerase delta-interact	4.08	4.51	1	1	5.12	4.51	1	1		0.00		
O00410	Importin-5 OS=Homo sap	24.11	7.75	4	5	9.69	3.74	2	2	19.04	4.38	3	4
Q7Z406	Myosin-14 OS=Homo sap	28.12	4.81	6	6	19.35	3.31	4	4	34.57	5.06	7	7
Q5TFE4	5'-nucleotidase domain-c	4.08	4.62	1	1	8.87	9.01	2	2	5.50	4.40	1	1
O95782	AP-2 complex subunit alp	5.10	2.76	1	1	14.77	6.24	3	3	15.36	6.24	3	3
Q13084	39S ribosomal protein L2	12.23	8.98	1	2	5.80	8.98	1	1	5.06	8.98	1	1
Q9BZE1	39S ribosomal protein L37, mitochond	0.00				4.17	3.78	1	1	5.02	5.20	1	1
P04632	Calpain small subunit 1 C	5.60	8.96	1	1		0.00			10.27	8.96	1	2
P51570	Galactokinase OS=Homo	4.92	4.08	1	1	11.03	8.93	2	2		0.00		
Q86SX6	Glutaredoxin-related protein 5, mitoch	0.00					0.00			5.25	8.92	1	1
P84095	Rho-related GTP-binding	5.63	8.90	1	1		0.00			5.45	8.90	1	1
O75934	Pre-mRNA-splicing factor	4.42	8.89	1	1		0.00				0.00		
Q13442	28 kDa heat- and acid-sta	4.55	8.84	1	1	4.76	8.84	1	1		0.00		
P07910	Heterogeneous nuclear ri	5.44	5.23	1	1	9.43	8.82	2	2	9.66	8.82	2	2
Q9Y6A4	Cilia- and flagella-associa	4.03	8.81	1	1		0.00				0.00		
Q13907	Isopentenyl-diphosphate	3.86	8.81	1	1		0.00				0.00		
Q9Y2B0	Protein canopy homolog	4.00	8.79	1	1	4.34	8.79	1	1	4.44	8.79	1	1
P51398	28S ribosomal protein S29, mitochond	0.00					0.00			10.96	8.79	2	2
Q9BY32	Inosine triphosphate pyro	4.81	8.76	1	1	4.69	8.76	1	1	8.38	8.76	1	2
P34949	Mannose-6-phosphate iso	4.08	4.96	1	1	4.09	3.78	1	1	4.21	3.78	1	1
P18621	60S ribosomal protein L1	5.14	8.70	1	1	4.40	8.70	1	1	10.46	8.70	1	2
O60936	Nucleolar protein 3 OS=Homo sapiens	0.00				4.73	8.68	1	1		0.00		
P04083	Annexin A1 OS=Homo sapiens GN=AI	0.00					0.00			8.42	8.67	2	2
P84098	60S ribosomal protein L1	5.66	8.67	1	1	5.12	8.67	1	1	4.73	8.67	1	1
P12277	Creatine kinase B-type OS	10.54	8.66	2	2	4.55	4.20	1	1	4.49	4.20	1	1
Q15404	Ras suppressor protein 1	5.41	8.66	1	1	7.16	8.66	1	1	5.96	8.66	1	1
Q92499	ATP-dependent RNA helic	10.13	5.27	2	2	17.88	8.65	4	4	9.44	5.27	2	2
Q8NBT2	Kinetochore protein Spc24 OS=Homo	0.00				4.11	8.63	1	1	5.25	8.63	1	1
Q9UEU0	Vesicle transport through	4.55	8.62	1	1		0.00				0.00		
O15498	Synaptobrevin homolog Y	4.06	8.59	1	1	4.14	8.59	1	1		0.00		

Q14974	Importin subunit beta-1 (	24.76	8.56	5	5	12.95	4.91	3	3	11.23	3.88	2	2
Q96HC4	PDZ and LIM domain pro	14.43	8.56	2	3	5.51	5.37	1	1		0.00		
Q9BY43	Charged multivesicular body protein 4	0.00					0.00			4.22	8.56	1	1
P84103	Serine/arginine-rich splici	3.99	8.54	1	1		0.00				0.00		
P38919	Eukaryotic initiation facto	10.43	8.52	2	2	5.35	3.89	1	1	9.79	8.52	2	2
P63267	Actin, gamma-enteric sm	13.87	8.51	2	3	13.95	8.51	2	3	18.72	8.51	2	4
O00151	PDZ and LIM domain protein 1 OS=H	0.00				4.99	8.51	1	1		0.00		
P53618	Coatomer subunit beta O	19.46	6.61	3	4	9.82	3.78	2	2	5.29	1.89	1	1
P54578	Ubiquitin carboxyl-termin	5.74	4.86	1	1	14.05	8.50	3	3	6.21	4.86	1	1
Q8WVQ1	Soluble calcium-activated	9.08	8.48	2	2	5.23	4.49	1	1	5.73	4.49	1	1
Q9BQA1	Methylosome protein 50 OS=Homo sa	0.00				4.45	4.09	1	1	9.59	8.48	2	2
P60033	CD81 antigen OS=Homo	6.16	8.47	1	1		0.00				0.00		
Q14749	Glycine N-methyltransfera	4.87	8.47	1	1		0.00				0.00		
Q9HD15	Steroid receptor RNA acti	4.02	8.47	1	1		0.00				0.00		
P52566	Rho GDP-dissociation inhibitor 2 OS=H	0.00					0.00			5.10	8.46	1	1
Q9UL25	Ras-related protein Rab-21 OS=Homo	0.00					0.00			4.27	8.44	1	1
A6NKF9	Putative Golgi pH regulator C OS=Hor	0.00					0.00			5.39	8.44	1	1
O00148	ATP-dependent RNA helic	4.44	3.28	1	1	4.35	3.28	1	1	5.06	5.15	1	1
Q9UHY7	Enolase-phosphatase E1 OS=Homo sa	0.00					0.00			5.43	8.43	1	1
P11388	DNA topoisomerase 2-alp	29.26	4.51	5	6	23.00	4.25	5	5	31.46	6.60	5	6
Q9Y3C1	Nucleolar protein 16 OS=Homo sapier	0.00				4.06	8.43	1	1		0.00		
P78347	General transcription fact	13.67	3.91	2	3	14.52	4.21	2	3	9.91	3.71	2	2
P13861	cAMP-dependent protein	15.78	8.42	2	3		0.00			5.39	4.21	1	1
P22087	rRNA 2'-O-methyltransfer	3.86	8.41	1	1		0.00				0.00		
Q96E11	Ribosome-recycling facto	5.38	8.40	1	1		0.00				0.00		
O00487	26S proteasome non-ATPase regulato	0.00				5.00	8.39	1	1		0.00		
P62195	26S protease regulatory s	10.02	8.37	2	2		0.00			10.67	8.37	2	2
P22061	Protein-L-isoaspartate(D-	4.28	8.37	1	1		0.00				0.00		
Q00839	Heterogeneous nuclear ri	11.29	5.70	2	2	15.46	8.36	3	3	11.62	5.70	2	2
P30049	ATP synthase subunit delta, mitochon	0.00				4.22	8.33	1	1	4.24	8.33	1	1
P06133	UDP-glucuronosyltransfer	5.58	8.33	1	1		0.00				0.00		
P40121	Macrophage-capping prot	8.76	8.33	2	2	4.01	4.60	1	1	4.17	4.60	1	1
P60228	Eukaryotic translation init	19.05	8.31	2	4	15.16	8.31	2	3	15.65	8.31	2	3
Q96S44	TP53-regulating kinase OS=Homo sap	0.00					0.00			10.56	8.30	1	2
Q8IYU8	Calcium uptake protein 2	7.98	8.29	2	2	4.03	3.92	1	1		0.00		
P83731	60S ribosomal protein L2	4.30	8.28	1	1	8.59	8.28	1	2	4.48	8.28	1	1
Q9NXV6	CDKN2A-interacting protein OS=Homo	0.00				5.56	3.62	1	1	10.40	8.28	2	2
Q5T2N8	ATPase family AAA doma	5.31	4.87	1	1		0.00			4.59	3.41	1	1
P54725	UV excision repair protein	6.14	8.26	1	1	5.04	8.26	1	1		0.00		

Q02818	Nucleobindin-1 OS=Homo	4.85	5.42	1	1	4.70	2.82	1	1		0.00		
Q9H2W6	39S ribosomal protein L4	4.91	8.24	1	1		0.00				0.00		
P17174	Aspartate aminotransfera	9.03	8.23	2	2		0.00			9.28	8.23	2	2
O95757	Heat shock 70 kDa protei	14.24	4.17	2	3	18.90	5.96	3	4		0.00		
Q8TF63	Dendritic cell nuclear protein 1 OS=Ho	0.00					0.00			4.29	8.20	1	1
Q15287	RNA-binding protein with	5.61	4.92	1	1	9.55	8.20	2	2	4.68	4.92	1	1
P23246	Splicing factor, proline- a	13.67	8.20	3	3	4.46	3.25	1	1	14.14	8.20	3	3
Q16643	Drebrin OS=Homo sapien	5.41	2.77	1	1	4.31	3.08	1	1	5.15	2.31	1	1
P10768	S-formylglutathione hydro	6.69	8.16	1	1	5.28	8.16	1	1	4.29	8.16	1	1
Q9BT78	COP9 signalosome compl	5.43	4.19	1	1	9.20	8.13	2	2	4.85	4.19	1	1
Q16401	26S proteasome non-ATP	10.65	8.13	2	2	10.45	8.13	2	2	5.42	4.37	1	1
Q92804	TATA-binding protein-ass	9.33	8.11	2	2	4.99	5.74	1	1		0.00		
Q15257	Serine/threonine-protein	4.85	8.10	1	1		0.00				0.00		
P19388	DNA-directed RNA polym	4.36	8.10	1	1		0.00			4.61	8.10	1	1
Q96I99	Succinyl-CoA ligase [GDP	4.84	4.63	1	1		0.00			9.72	8.10	2	2
P07477	Trypsin-1 OS=Homo sapi	4.07	8.10	1	1	9.69	8.10	1	2	5.37	8.10	1	1
O15173	Membrane-associated progesterone re	0.00					0.00			5.18	8.07	1	1
O00231	26S proteasome non-ATP	4.22	3.32	1	1	3.92	4.74	1	1		0.00		
Q9P2T1	GMP reductase 2 OS=Ho	5.09	8.05	1	1		0.00			5.20	8.05	1	1
Q9Y263	Phospholipase A-2-activa	8.71	5.53	2	2	4.26	2.39	1	1	5.13	2.52	1	1
Q06830	Peroxiredoxin-1 OS=Homo sapiens GN	0.00					0.00			4.35	8.04	1	1
P11586	C-1-tetrahydrofolate synt	18.33	6.31	4	4	14.37	5.13	3	3	14.57	5.13	3	3
P33991	DNA replication licensing factor MCM4	0.00				4.10	2.20	1	1	15.17	8.00	3	3
P09874	Poly [ADP-ribose] polyme	4.96	3.06	1	1	10.10	3.16	2	2	17.65	7.89	4	4
P48047	ATP synthase subunit O,	5.17	7.98	1	1	9.92	7.98	1	2		0.00		
P13796	Plastin-2 OS=Homo sapie	3.85	2.55	1	1	9.16	5.58	2	2	4.15	2.39	1	1
Q15005	Signal peptidase complex	3.91	7.96	1	1		0.00			4.47	7.96	1	1
Q15363	Transmembrane emp24 d	4.94	7.96	1	1		0.00				0.00		
P62191	26S protease regulatory s	15.78	7.95	2	3	5.33	4.55	1	1	4.99	3.41	1	1
P19623	Spermidine synthase OS=	10.11	7.95	1	2	4.28	7.95	1	1	4.70	7.95	1	1
Q14697	Neutral alpha-glucosidase	8.74	4.66	2	2		0.00			17.55	5.08	3	4
Q15029	116 kDa U5 small nuclear	24.50	6.07	3	5	5.18	1.75	1	1	19.92	7.92	4	4
Q9Y383	Putative RNA-binding pro	12.78	7.91	2	3	4.38	3.83	1	1		0.00		
P51553	Isocitrate dehydrogenase	6.27	7.89	1	1	6.95	7.89	1	1	6.70	7.89	1	1
Q8N6H7	ADP-ribosylation factor G	5.89	3.45	1	1	9.43	3.45	1	2	4.95	4.41	1	1
O95232	Luc7-like protein 3 OS=H	8.95	7.87	2	2	4.44	4.17	1	1	4.56	4.17	1	1
P62913	60S ribosomal protein L1	3.89	7.87	1	1		0.00				0.00		
P61221	ATP-binding cassette sub	8.48	5.34	2	2	4.00	2.50	1	1	4.99	2.67	1	1
Q8NC51	Plasminogen activator inh	12.45	7.84	2	3	5.00	3.92	1	1	9.98	7.84	2	2

A6NCN2	Putative keratin-87 protei	5.81	7.84	1	1		0.00			5.36	7.84	1	1
O60934	Nibrin OS=Homo sapiens	4.74	2.25	1	1	4.79	2.25	1	1	5.16	3.32	1	1
Q9H1E3	Nuclear ubiquitous casein and cyclin-d	0.00				5.90	7.82	1	1	5.71	7.82	1	1
Q13257	Mitotic spindle assembly checkpoint pr	0.00				4.08	7.80	1	1		0.00		
P49720	Proteasome subunit beta type-3 OS=H	0.00				4.27	7.80	1	1	4.14	7.80	1	1
Q9Y446	Plakophilin-3 OS=Homo s	13.77	5.90	3	3	8.89	3.89	2	2	18.43	7.78	4	4
Q12874	Splicing factor 3A subunit	9.03	4.19	1	2	9.07	7.78	2	2	11.44	4.19	1	2
P02786	Transferrin receptor prote	12.35	5.66	3	3	9.19	3.95	2	2		0.00		
O75822	Eukaryotic translation init	4.39	7.75	1	1		0.00			4.96	7.75	1	1
P19367	Hexokinase-1 OS=Homo	14.05	5.23	3	3	17.69	6.43	4	4	15.30	3.93	2	3
P07814	Bifunctional glutamate/pr	19.94	5.29	4	4	16.52	4.17	3	3	14.76	4.76	3	3
Q9NY33	Dipeptidyl peptidase 3 OS	5.63	3.26	1	1	5.17	3.26	1	1	9.72	4.48	2	2
P36957	Dihydrolipoyllysine-residu	4.51	3.09	1	1	11.77	7.73	2	2	6.61	4.64	1	1
Q09666	Neuroblast differentiation	77.83	4.74	15	16	40.44	2.70	7	9	75.07	5.74	15	16
Q9HC07	Transmembrane protein	5.26	7.72	1	1		0.00				0.00		
Q70J99	Protein unc-13 homolog D	13.62	4.68	3	3	13.46	5.14	3	3	13.74	4.68	3	3
Q8NE71	ATP-binding cassette sub	12.60	3.43	2	3	13.03	5.68	3	3	18.06	5.92	3	4
Q96S94	Cyclin-L2 OS=Homo sapiens GN=CCN	0.00					0.00			4.99	7.69	1	1
Q9GZZ1	N-alpha-acetyltransferase 50 OS=Hom	0.00					0.00			4.55	7.69	1	1
Q08J23	tRNA (cytosine(34)-C(5))	8.21	4.43	2	2	4.90	3.26	1	1	5.12	2.35	1	1
Q01130	Serine/arginine-rich splici	4.93	7.69	1	1	9.62	7.69	1	2	5.40	7.69	1	1
P31947	14-3-3 protein sigma OS=Homo sapie	0.00					0.00			11.32	7.66	1	2
Q8TEA8	D-tyrosyl-tRNA(Tyr) deac	5.08	7.66	1	1	4.90	7.66	1	1	9.48	7.66	1	2
Q9NQT5	Exosome complex compo	5.96	7.64	1	1	4.12	7.64	1	1		0.00		
P19404	NADH dehydrogenase [ul	4.27	7.63	1	1		0.00				0.00		
P55795	Heterogeneous nuclear ri	13.36	3.79	1	3		0.00			10.03	7.57	2	2
Q32MZ4	Leucine-rich repeat flightl	14.41	7.55	3	3	4.67	1.73	1	1	4.38	1.73	1	1
Q14498	RNA-binding protein 39 C	5.54	3.21	1	1	4.68	3.21	1	1	10.54	7.55	2	2
P09234	U1 small nuclear ribonucl	3.88	7.55	1	1		0.00				0.00		
Q01813	ATP-dependent 6-phosph	11.46	5.10	2	2	15.19	7.53	3	3	9.51	5.10	2	2
Q13409	Cytoplasmic dynein 1 inte	4.76	4.23	1	1		0.00			4.29	3.29	1	1
P15311	Ezrin OS=Homo sapiens	13.36	7.51	3	3	5.53	2.56	1	1	5.80	2.56	1	1
O43809	Cleavage and polyadenyl	4.47	7.49	1	1		0.00				0.00		
O95861	3'(2'),5'-bisphosphate nu	4.86	7.47	1	1	10.24	7.47	1	2		0.00		
Q6ZRV2	Protein FAM83H OS=Hon	13.59	4.58	3	3	4.17	1.53	1	1	10.05	2.88	2	2
P27824	Calnexin OS=Homo sapie	4.05	2.70	1	1	4.00	2.70	1	1	9.42	4.73	2	2
Q86UE4	Protein LYRIC OS=Homo sapiens GN=	0.00					0.00			9.89	7.39	2	2
Q8WVX9	Fatty acyl-CoA reductase	16.62	7.38	3	4		0.00				0.00		
O60664	Perilipin-3 OS=Homo sapiens GN=PLI	0.00				9.93	7.37	2	2	9.77	7.37	2	2

P11310	Medium-chain specific ac	4.44	3.09	1	1	4.16	4.28	1	1	4.31	3.09	1	1
Q15102	Platelet-activating factor acetylhydrola	0.00				4.03	7.36	1	1		0.00		
P63208	S-phase kinase-associated protein 1 C	0.00				4.23	7.36	1	1		0.00		
Q9Y294	Histone chaperone ASF1A	4.47	7.35	1	1					4.90	7.35	1	1
O00287	Regulatory factor X-associated protein	0.00				4.46	7.35	1	1		0.00		
Q96S19	UPF0585 protein C16orf13 OS=Homo	0.00					0.00			4.12	7.35	1	1
Q9UBQ5	Eukaryotic translation initiation factor	0.00				5.71	7.34	1	1	5.08	7.34	1	1
Q86VQ1	Glucocorticoid-induced tra	4.86	7.31	1	1		0.00				0.00		
O15145	Actin-related protein 2/3	4.87	7.30	1	1	3.96	7.30	1	1		0.00		
P23786	Carnitine O-palmitoyltransferase 2, mi	0.00				4.78	3.34	1	1	10.46	7.29	2	2
P22234	Multifunctional protein AD	3.81	3.06	1	1	3.93	3.06	1	1	4.78	4.24	1	1
P30043	Flavin reductase (NADPH	4.17	7.28	1	1	4.09	7.28	1	1	5.16	7.28	1	1
P30519	Heme oxygenase 2 OS=Homo sapiens	0.00					0.00			4.31	7.28	1	1
P25789	Proteasome subunit alpha type-4 OS=	0.00				4.04	7.28	1	1		0.00		
Q96MX6	WD repeat-containing protein 92 OS=	0.00					0.00			4.80	7.28	1	1
O75083	WD repeat-containing pro	5.33	2.64	1	1	5.25	2.64	1	1	10.49	7.26	2	2
Q96A33	Coiled-coil domain-contai	9.02	7.25	2	2		0.00			4.99	3.52	1	1
P30084	Enoyl-CoA hydratase, mit	5.03	7.24	1	1	5.75	7.24	1	1	5.14	7.24	1	1
P11216	Glycogen phosphorylase,	16.23	7.24	3	3	5.17	1.90	1	1	9.63	4.27	2	2
O75431	Metaxin-2 OS=Homo sapiens GN=MTX2 PE=1 SV=1 - [MTX2_HUMAN]						0.00			4.42	7.22	1	1
Q99848	Probable rRNA-processing protein EBF	0.00					0.00			5.09	7.19	1	1
P49407	Beta-arrestin-1 OS=Homo sapiens GN	0.00					0.00			5.76	7.18	1	1
Q9UGT4	Sushi domain-containing	14.38	4.14	2	3	9.77	4.74	2	2	19.69	7.18	3	4
Q9BQ67	Glutamate-rich WD repea	4.34	3.59	1	1		0.00			9.75	7.17	2	2
O00159	Unconventional myosin-Ic	24.27	7.15	4	5	9.83	3.48	2	2	8.55	1.79	1	2
Q9Y2C2	Uronyl 2-sulfotransferase	4.73	7.14	1	1		0.00				0.00		
P13667	Protein disulfide-isomeras	19.06	7.13	3	4	14.72	7.13	3	3	4.58	2.33	1	1
P55060	Exportin-2 OS=Homo sap	10.43	1.75	1	2	18.75	5.66	3	4	19.99	4.84	3	4
Q02252	Methylmalonate-semialdehyde dehydr	0.00					0.00			8.81	7.10	2	2
Q58FF8	Putative heat shock prote	13.02	7.09	2	3	4.82	3.94	1	1	5.02	3.94	1	1
P00403	Cytochrome c oxidase subunit 2 OS=H	0.00					0.00			4.75	7.05	1	1
Q15437	Protein transport protein	15.81	7.04	3	3	4.02	1.83	1	1	10.30	4.17	2	2
Q13435	Splicing factor 3B subunit	15.30	4.92	2	3	5.75	2.12	1	1	5.00	1.68	1	1
Q96C23	Aldose 1-epimerase OS=I	4.79	7.02	1	1		0.00			5.49	7.02	1	1
P30520	Adenylosuccinate synthet	8.85	7.02	2	2	4.72	4.61	1	1	4.51	4.61	1	1
Q86V81	THO complex subunit 4 C	5.60	7.00	1	1	5.31	7.00	1	1	5.25	7.00	1	1
O96019	Actin-like protein 6A OS=Homo sapier	0.00				4.94	6.99	1	1	5.29	6.99	1	1
Q9H7E9	UPF0488 protein C8orf33 OS=Homo s	0.00					0.00			4.30	6.99	1	1
Q9BUF5	Tubulin beta-6 chain OS=	10.18	6.95	2	2	4.47	3.14	1	1	4.79	3.14	1	1

Q9C0K7	STE20-related kinase adapter protein	0.00				0.00			5.07	6.94	1	1
O43175	D-3-phosphoglycerate de	4.12	2.81	1	1		0.00			5.00	4.13	1	1
P16930	Fumarylacetoacetase OS=Homo sapie	0.00					0.00			8.88	6.92	2	2
Q96E39	RNA binding motif protein, X-linked-lik	0.00				4.11	3.33	1	1	4.14	3.59	1	1
Q9Y230	RuvB-like 2 OS=Homo sa	8.98	6.91	2	2	4.68	3.46	1	1	4.21	3.46	1	1
Q6ZVX7	F-box only protein 50 OS=Homo sapie	0.00				5.21	6.91	1	1	5.20	6.91	1	1
P40925	Malate dehydrogenase, c	8.18	6.89	2	2		0.00				0.00		
Q9GZS3	WD repeat-containing pro	4.81	6.89	1	1	4.13	6.89	1	1	4.61	6.89	1	1
P82930	28S ribosomal protein S3	4.91	6.88	1	1		0.00				0.00		
Q6UW68	Transmembrane protein	4.26	6.88	1	1		0.00				0.00		
P45974	Ubiquitin carboxyl-termin	9.13	3.96	2	2	12.13	5.13	2	3	8.68	5.13	2	2
Q99436	Proteasome subunit beta	4.98	6.86	1	1	4.90	6.86	1	1	5.09	6.86	1	1
P61313	60S ribosomal protein L15 OS=Homo	0.00				4.68	6.86	1	1		0.00		
Q9UKL4	Gap junction delta-2 protein OS=Hom	0.00				3.95	6.85	1	1		0.00		
O95716	Ras-related protein Rab-3D OS=Homo	0.00					0.00			4.55	6.85	1	1
Q99614	Tetratricopeptide repeat	5.10	6.85	1	1	5.09	6.85	1	1	5.24	6.85	1	1
P17612	cAMP-dependent protein	5.15	6.84	1	1		0.00			5.23	6.84	1	1
Q13813	Spectrin alpha chain, non	13.97	2.22	3	3	20.60	3.11	4	4	19.58	3.07	4	4
P37837	Transaldolase OS=Homo	3.92	3.56	1	1		0.00			4.25	3.26	1	1
Q8WXS5	Voltage-dependent calcium channel ga	0.00					0.00			5.64	6.82	1	1
P31327	Carbamoyl-phosphate syn	23.19	6.80	5	5	14.24	3.60	3	3	13.84	3.27	3	3
Q9UHX1	Poly(U)-binding-splicing f	4.65	3.94	1	1		0.00			4.61	2.86	1	1
Q13838	Spliceosome RNA helicase	8.93	6.78	2	2	4.35	3.27	1	1		0.00		
P33316	Deoxyuridine 5'-triphosph	4.17	6.75	1	1		0.00			4.64	6.75	1	1
Q00688	Peptidyl-prolyl cis-trans isomerase FKB	0.00					0.00			4.71	6.70	1	1
P07305	Histone H1.0 OS=Homo s	4.68	6.70	1	1	4.34	6.70	1	1		0.00		
Q9Y6G9	Cytoplasmic dynein 1 light intermediat	0.00				8.43	6.69	2	2	4.11	3.25	1	1
P54819	Adenylate kinase 2, mitochondrial OS=	0.00					0.00			5.01	6.69	1	1
Q96IU4	Alpha/beta hydrolase domain-containi	0.00				3.93	6.67	1	1		0.00		
Q9NRR5	Ubiquilin-4 OS=Homo sapiens GN=UB	0.00				4.22	2.66	1	1	9.03	6.66	2	2
A1L0T0	Acetolactate synthase-like	6.03	3.64	1	1	18.22	6.65	2	3	11.51	6.65	2	2
Q8TCS8	Polyribonucleotide nucleo	19.38	4.60	2	4	8.70	4.34	2	2	5.01	2.30	1	1
P30085	UMP-CMP kinase OS=Homo sapiens G	0.00					0.00			4.30	6.63	1	1
P52292	Importin subunit alpha-1	10.10	6.62	2	2	10.45	6.62	2	2	9.23	6.62	2	2
Q3LXA3	Bifunctional ATP-depende	9.06	6.61	2	2	4.65	2.96	1	1		0.00		
O75208	Ubiquinone biosynthesis protein COQ9	0.00				4.92	6.60	1	1		0.00		
Q53H82	Beta-lactamase-like protein 2 OS=Hor	0.00				4.91	6.60	1	1		0.00		
P27105	Erythrocyte band 7 integral membrane	0.00				6.58	6.60	1	1	5.98	6.60	1	1
P36639	7,8-dihydro-8-oxoguanine	3.88	6.60	1	1		0.00				0.00		

O75251	NADH dehydrogenase [ul	3.97	6.57	1	1		0.00				0.00		
Q96TA1	Niban-like protein 1 OS=I	14.65	4.42	2	3	5.45	2.28	1	1	5.09	2.14	1	1
P17655	Calpain-2 catalytic subuni	16.32	6.57	3	3	10.67	6.57	2	2	9.42	2.14	1	2
Q96GG9	DCN1-like protein 1 OS=I	5.18	6.56	1	1	4.84	6.56	1	1	4.32	6.56	1	1
Q13151	Heterogeneous nuclear ribonucleoprot	0.00					0.00			5.74	6.56	1	1
P04259	Keratin, type II cytoskeletal 6B OS=H	0.00				12.67	4.43	2	3	4.42	2.13	1	1
Q9BRX8	Redox-regulatory protein	4.02	6.55	1	1		0.00			4.34	6.55	1	1
Q99598	Translin-associated prote	4.55	6.55	1	1		0.00				0.00		
Q9NUJ1	Mycophenolic acid acyl-gl	4.93	6.54	1	1	5.45	6.54	1	1	5.05	6.54	1	1
A6NIZ1	Ras-related protein Rap-1	8.67	6.52	1	2	4.13	6.52	1	1		0.00		
O60716	Catenin delta-1 OS=Hom	9.74	4.96	2	2		0.00			9.57	4.55	2	2
O15266	Short stature homeobox protein OS=H	0.00				3.92	6.51	1	1		0.00		
Q9NP79	Vacuolar protein sorting-a	5.95	6.51	1	1	5.42	6.51	1	1		0.00		
A0MZ66	Shootin-1 OS=Homo sapi	4.62	3.17	1	1	9.93	6.50	2	2	8.46	6.50	2	2
P27694	Replication protein A 70 kDa DNA-binc	0.00				4.64	3.08	1	1	4.34	3.41	1	1
Q9BZZ5	Apoptosis inhibitor 5 OS=Homo sapier	0.00				4.72	3.05	1	1	10.04	3.44	1	2
Q9Y5K8	V-type proton ATPase subunit D OS=H	0.00					0.00			5.43	6.48	1	1
Q15785	Mitochondrial import rece	5.44	6.47	1	1	9.70	6.47	1	2	4.76	6.47	1	1
P62701	40S ribosomal protein S4	3.97	6.46	1	1	4.07	6.46	1	1	4.28	6.46	1	1
P36955	Pigment epithelium-derive	9.12	6.46	2	2	4.53	3.35	1	1	4.59	3.35	1	1
Q587J8	KHDC3-like protein OS=H	4.01	6.45	1	1		0.00				0.00		
P06730	Eukaryotic translation init	3.90	6.45	1	1		0.00				0.00		
Q9BXR0	Queuine tRNA-ribosyltran	5.21	6.45	1	1		0.00				0.00		
P33176	Kinesin-1 heavy chain OS	4.17	1.56	1	1	3.96	1.56	1	1	13.52	4.88	3	3
P61247	40S ribosomal protein S3	10.40	6.44	1	2	5.24	6.44	1	1	15.06	6.44	1	3
P53041	Serine/threonine-protein phosphatase	0.00				5.05	3.81	1	1	9.24	6.41	2	2
O00567	Nucleolar protein 56 OS=	9.75	6.40	2	2		0.00			10.07	3.20	1	2
Q9HC38	Glyoxalase domain-contai	4.49	6.39	1	1		0.00				0.00		
P41227	N-alpha-acetyltransferase 10 OS=Hon	0.00				4.23	6.38	1	1		0.00		
Q13144	Translation initiation factc	5.24	3.88	1	1		0.00			4.39	2.50	1	1
P39656	Dolichyl-diphosphooligosa	4.83	6.36	1	1		0.00				0.00		
Q9HBA9	Putative N-acetylated-alp	4.76	6.33	1	1		0.00				0.00		
P04179	Superoxide dismutase [M	3.82	6.31	1	1		0.00				0.00		
Q9Y2Z0	Suppressor of G2 allele o	5.57	6.30	1	1		0.00			11.51	6.30	1	2
P31146	Coronin-1A OS=Homo sapiens GN=CC	0.00				5.17	6.29	1	1	5.04	6.29	1	1
P04626	Receptor tyrosine-protein	21.00	5.10	3	4	4.78	1.51	1	1	10.19	3.11	2	2
P30153	Serine/threonine-protein	9.43	6.28	2	2	10.28	3.06	1	2	9.28	6.28	2	2
P50213	Isocitrate dehydrogenase [NAD] subu	0.00					0.00			4.60	6.28	1	1
P00505	Aspartate aminotransfera	8.11	6.28	2	2	3.91	3.49	1	1		0.00		

P48444	Coatomer subunit delta C	5.29	6.26	1	1		0.00			5.68	6.26	1	1
P41252	Isoleucine--tRNA ligase, c	8.66	3.41	2	2	9.46	2.93	2	2	14.62	4.28	3	3
P30041	Peroxiredoxin-6 OS=Homo sapiens GN	0.00				3.91	6.25	1	1	4.82	6.25	1	1
P14678	Small nuclear ribonucleop	3.96	6.25	1	1		0.00				0.00		
P23526	Adenosylhomocysteinase	8.80	6.25	2	2	4.72	3.01	1	1		0.00		
P62917	60S ribosomal protein L8 OS=Homo s	0.00					0.00			4.34	6.23	1	1
P30038	Delta-1-pyrroline-5-carbo	13.82	6.22	2	3	9.69	6.22	2	2	9.12	6.22	2	2
P37235	Hippocalcin-like protein 1	4.20	6.22	1	1		0.00				0.00		
Q9Y262	Eukaryotic translation init	9.34	6.21	2	2		0.00			4.74	3.55	1	1
O95299	NADH dehydrogenase [ul	4.91	6.20	1	1	6.09	6.20	1	1	5.26	6.20	1	1
P60510	Serine/threonine-protein	6.04	6.19	1	1		0.00			4.97	6.19	1	1
O75534	Cold shock domain-conta	5.45	2.26	1	1	4.53	2.26	1	1	8.56	3.88	2	2
P42566	Epidermal growth factor r	9.40	3.91	2	2	4.82	2.23	1	1	5.55	2.12	1	1
O00505	Importin subunit alpha-4	4.09	3.45	1	1	4.10	2.69	1	1	4.91	2.69	1	1
P21333	Filamin-A OS=Homo sapi	33.80	4.61	7	7	23.20	3.59	5	5	39.09	4.23	6	8
O75494	Serine/arginine-rich splicing factor 10	0.00					0.00			4.42	6.11	1	1
Q16473	Putative tenascin-XA OS=Homo sapier	0.00				4.76	6.11	1	1		0.00		
P61758	Prefoldin subunit 3 OS=H	3.86	6.09	1	1		0.00				0.00		
Q68D91	Metallo-beta-lactamase d	3.82	6.09	1	1		0.00				0.00		
P27635	60S ribosomal protein L10 OS=Homo	0.00				4.61	6.07	1	1		0.00		
O15160	DNA-directed RNA polym	4.87	6.07	1	1		0.00				0.00		
Q96DB5	Regulator of microtubule	5.85	6.05	1	1		0.00			5.78	6.05	1	1
P67936	Tropomyosin alpha-4 chain OS=Homo	0.00					0.00			10.09	6.05	1	2
Q92841	Probable ATP-dependent	8.71	3.70	2	2	5.27	2.06	1	1	13.52	4.39	2	3
P62753	40S ribosomal protein S6	4.91	6.02	1	1	4.35	6.02	1	1	4.28	6.02	1	1
Q9NVA1	Ubiquinol-cytochrome-c reductase con	0.00				4.07	6.02	1	1		0.00		
Q9NYP9	Protein Mis18-alpha OS=Homo sapien	0.00				4.08	6.01	1	1		0.00		
Q13126	S-methyl-5'-thioadenosine	4.32	6.01	1	1	4.46	6.01	1	1		0.00		
P26196	Probable ATP-dependent RNA helicase	0.00				5.87	6.00	1	1	5.42	6.00	1	1
Q92734	Protein TFG OS=Homo sapiens GN=T	0.00					0.00			4.39	6.00	1	1
P02647	Apolipoprotein A-I OS=H	4.23	5.99	1	1		0.00				0.00		
Q12972	Nuclear inhibitor of protei	4.44	5.98	1	1	4.47	5.98	1	1		0.00		
Q96JY6	PDZ and LIM domain pro	4.00	5.97	1	1	3.93	5.97	1	1		0.00		
Q8NC56	LEM domain-containing p	3.97	2.58	1	1	3.91	3.38	1	1		0.00		
Q13217	DnaJ homolog subfamily	5.54	5.95	1	1		0.00			5.95	5.95	1	1
Q9Y3I0	tRNA-splicing ligase RtcB	6.55	5.94	1	1	6.75	5.94	1	1		0.00		
Q9BR76	Coronin-1B OS=Homo sapiens GN=C0	0.00				5.46	5.93	1	1	5.40	5.93	1	1
Q8TAT6	Nuclear protein localizatic	14.10	5.92	2	3	15.11	5.92	2	3	11.30	2.96	1	2
O00232	26S proteasome non-ATP	4.95	2.85	1	1	12.61	5.92	2	3	4.52	2.85	1	1

Q9Y285	Phenylalanine--tRNA ligas	9.04	5.91	2	2	8.51	5.91	2	2	5.37	2.76	1	1
P21964	Catechol O-methyltransfe	9.15	5.90	2	2	5.27	5.90	1	1	5.03	5.90	1	1
P43246	DNA mismatch repair protein Msh2 OS		0.00				0.00			14.63	5.89	3	3
Q6PID8	Kelch domain-containing protein 10 O		0.00				0.00			4.40	5.88	1	1
P24539	ATP synthase F(0) complex subunit B		0.00			3.96	5.86	1	1		0.00		
Q9NUQ9	Protein FAM49B OS=Hom	4.33	5.86	1	1		0.00			4.72	5.86	1	1
P35606	Coatomer subunit beta' C	8.19	3.97	2	2	3.94	1.88	1	1		0.00		
Q96GM1	Lipid phosphate phosphatase-related		0.00				0.00			4.18	5.83	1	1
Q14764	Major vault protein OS=H	7.75	3.92	2	2	4.51	1.79	1	1	4.15	1.90	1	1
P20618	Proteasome subunit beta	4.77	5.81	1	1		0.00				0.00		
Q13564	NEDD8-activating enzyme E1 regulato		0.00			4.81	5.81	1	1	6.51	5.81	1	1
O95678	Keratin, type II cytoskeletal 75 OS=H		0.00				0.00			8.68	5.81	2	2
Q13148	TAR DNA-binding protein 43 OS=Hom		0.00			6.24	5.80	1	1		0.00		
Q9BWD1	Acetyl-CoA acetyltransferase, cytosolic		0.00				0.00			4.95	5.79	1	1
Q9Y2R9	28S ribosomal protein S7	4.25	5.79	1	1	4.32	5.79	1	1	4.33	5.79	1	1
Q52LJ0	Protein FAM98B OS=Hom	4.73	5.76	1	1		0.00			4.96	5.76	1	1
P16401	Histone H1.5 OS=Homo s	4.28	5.75	1	1		0.00			4.19	5.75	1	1
P17812	CTP synthase 1 OS=Hom	6.03	3.05	1	1	10.45	5.75	2	2	11.26	5.75	2	2
Q309B1	Tripartite motif-containing protein 16-		0.00			4.23	5.75	1	1		0.00		
Q7Z434	Mitochondrial antiviral-signaling protei		0.00			4.85	5.74	1	1		0.00		
P52788	Spermine synthase OS=H	5.92	5.74	1	1	5.41	5.74	1	1	5.31	5.74	1	1
Q6PID6	Tetratricopeptide repeat protein 33 OS		0.00				0.00			4.44	5.73	1	1
Q9H9J2	39S ribosomal protein L4	4.08	5.72	1	1		0.00			4.17	5.72	1	1
Q99729	Heterogeneous nuclear ri	5.59	5.72	1	1	4.82	5.72	1	1		0.00		
Q6P1N9	Putative deoxyribonuclease TATDN1 C		0.00				0.00			4.57	5.72	1	1
P21912	Succinate dehydrogenase	5.14	5.71	1	1		0.00				0.00		
P13797	Plastin-3 OS=Homo sapie	4.88	2.22	1	1		0.00			10.20	3.49	1	2
Q9Y570	Protein phosphatase met	4.87	5.70	1	1		0.00				0.00		
P25786	Proteasome subunit alpha type-1 OS=		0.00				0.00			4.26	5.70	1	1
O43709	Probable 18S rRNA (guanine-N(7))-m		0.00			4.01	5.69	1	1		0.00		
Q99674	Cell growth regulator with	3.91	5.65	1	1		0.00				0.00		
Q15124	Phosphoglucomutase-like	13.08	5.64	2	3	8.77	5.64	2	2	4.49	2.82	1	1
P07996	Thrombospondin-1 OS=H	13.67	4.19	3	3	10.54	3.25	2	2		0.00		
Q9P0L0	Vesicle-associated membrane protein-		0.00			4.80	5.62	1	1	4.45	5.62	1	1
Q92882	Osteoclast-stimulating fac	4.25	5.61	1	1		0.00			4.25	5.61	1	1
Q8TAQ2	SWI/SNF complex subuni	9.08	2.97	2	2	4.05	1.24	1	1	5.66	2.64	1	1
P46108	Adapter molecule crk OS=	4.49	5.59	1	1		0.00			4.82	5.59	1	1
Q9HB07	UPF0160 protein MYG1, m	4.96	5.59	1	1		0.00			5.52	5.59	1	1
Q16543	Hsp90 co-chaperone Cdc37 OS=Homo		0.00			4.72	5.56	1	1	9.69	5.56	1	2

P04183	Thymidine kinase, cytoso	4.77	5.56	1	1		0.00				0.00		
Q9UKM9	RNA-binding protein Raly OS=Homo s		0.00				0.00			4.53	5.56	1	1
Q92530	Proteasome inhibitor PI31 subunit OS		0.00				0.00			4.22	5.54	1	1
P55263	Adenosine kinase OS=Ho	10.11	5.52	1	2	10.20	5.52	1	2	5.05	5.52	1	1
O95571	Persulfide dioxygenase E	4.20	5.51	1	1		0.00			4.12	5.51	1	1
P61026	Ras-related protein Rab-1	4.21	5.50	1	1	3.96	5.50	1	1	4.28	5.50	1	1
P43304	Glycerol-3-phosphate deh	4.78	2.48	1	1	9.67	5.50	2	2		0.00		
P55039	Developmentally-regulated GTP-bindir		0.00				0.00			5.10	5.49	1	1
Q5TC12	ATP synthase mitochondr	5.52	5.49	1	1	4.93	5.49	1	1		0.00		
P37058	Testosterone 17-beta-deh	3.89	5.48	1	1		0.00				0.00		
P48507	Glutamate--cysteine ligase regulatory		0.00				0.00			4.38	5.47	1	1
P30048	Thioredoxin-dependent p	4.27	5.47	1	1		0.00				0.00		
O00764	Pyridoxal kinase OS=Hon	5.37	5.45	1	1	5.19	5.45	1	1	4.45	5.45	1	1
Q9H993	UPF0364 protein C6orf211 OS=Homo		0.00				0.00			5.06	5.44	1	1
Q99961	Endophilin-A2 OS=Homo sapiens GN=		0.00				0.00			5.86	5.43	1	1
Q9UMX0	Ubiquilin-1 OS=Homo sapiens GN=UB		0.00			4.22	2.72	1	1	10.16	5.43	2	2
Q9NQR4	Omega-amidase NIT2 OS=Homo sapi		0.00				0.00			4.85	5.43	1	1
Q15393	Splicing factor 3B subunit	9.27	2.63	2	2	4.60	1.40	1	1	13.67	4.19	3	3
Q9P015	39S ribosomal protein L15, mitochond		0.00			3.97	5.41	1	1		0.00		
Q8NBF2	NHL repeat-containing pr	8.85	5.37	2	2	9.95	3.44	1	2	10.35	3.44	1	2
Q14847	LIM and SH3 domain pro	4.07	5.36	1	1		0.00				0.00		
P49903	Selenide, water dikinase	5.23	5.36	1	1		0.00				0.00		
Q8IVW6	AT-rich interactive domain-containing		0.00				0.00			5.01	5.35	1	1
P52272	Heterogeneous nuclear ri	4.53	2.19	1	1		0.00			5.32	3.15	1	1
P51884	Lumican OS=Homo sapie	4.52	5.33	1	1	4.62	5.33	1	1	9.91	5.33	1	2
Q7Z6J2	General receptor for phos	3.88	5.32	1	1		0.00				0.00		
P07858	Cathepsin B OS=Homo sapiens GN=C		0.00			4.99	5.31	1	1	4.26	5.31	1	1
Q9H7Z7	Prostaglandin E synthase	4.69	5.31	1	1		0.00			9.80	5.31	1	2
P41091	Eukaryotic translation initiation factor		0.00				0.00			4.25	5.30	1	1
P02533	Keratin, type I cytoskelet	7.76	5.08	2	2	8.63	5.30	2	2	4.18	3.18	1	1
P55735	Protein SEC13 homolog C	4.35	5.28	1	1	4.95	5.28	1	1		0.00		
Q8ND83	SLAIN motif-containing p	4.80	5.28	1	1		0.00				0.00		
P18615	Negative elongation factor E OS=Hom		0.00			5.49	5.26	1	1	10.27	5.26	1	2
Q99442	Translocation protein SEC	3.83	5.26	1	1		0.00				0.00		
Q16181	Septin-7 OS=Homo sapiens GN=SEPT		0.00			4.99	5.26	1	1		0.00		
Q14204	Cytoplasmic dynein 1 hea	38.77	3.16	8	8	32.77	2.48	6	7	38.11	2.91	8	8
P49841	Glycogen synthase kinase-3 beta OS=		0.00				0.00			4.36	5.24	1	1
P43897	Elongation factor Ts, mitc	4.70	5.23	1	1	4.86	5.23	1	1	4.91	5.23	1	1
P53990	IST1 homolog OS=Homo sapiens GN=		0.00			5.04	5.22	1	1		0.00		

P26373	60S ribosomal protein L1	4.01	5.21	1	1	3.93	5.21	1	1	4.22	5.21	1	1
O95793	Double-stranded RNA-bin	4.01	2.43	1	1		0.00			5.35	2.77	1	1
O43396	Thioredoxin-like protein 1	3.91	5.19	1	1		0.00			5.12	5.19	1	1
Q9UBQ7	Glyoxylate reductase/hyd	5.45	5.18	1	1		0.00				0.00		
Q9H0A0	N-acetyltransferase 10 O	9.95	3.71	2	2	9.41	3.51	2	2	10.01	2.05	1	2
P36871	Phosphoglucomutase-1 C	9.04	5.16	2	2	9.27	5.16	2	2	4.50	2.85	1	1
O95983	Methyl-CpG-binding dom	3.89	5.15	1	1		0.00				0.00		
Q15424	Scaffold attachment facto	4.90	2.84	1	1		0.00			10.21	2.30	2	2
P29144	Tripeptidyl-peptidase 2 O	10.44	2.88	2	2	20.31	5.12	3	4	16.25	5.12	3	3
P50895	Basal cell adhesion molecule OS=Hom	0.00					0.00			5.01	5.10	1	1
P16422	Epithelial cell adhesion m	4.36	5.10	1	1	4.47	5.10	1	1		0.00		
O94776	Metastasis-associated protein MTA2 O	0.00				8.58	5.09	2	2		0.00		
Q15738	Sterol-4-alpha-carboxylat	4.04	5.09	1	1		0.00				0.00		
Q8NFV4	Alpha/beta hydrolase dor	4.49	5.08	1	1		0.00			5.20	5.08	1	1
P08779	Keratin, type I cytoskelet	8.17	4.86	2	2	4.14	2.11	1	1		0.00		
Q9NPF4	Probable tRNA N6-adenosine threonyl	0.00				3.99	5.07	1	1		0.00		
O75533	Splicing factor 3B subunit	12.80	5.06	3	3		0.00			9.39	2.76	2	2
Q9Y6Z7	Collectin-10 OS=Homo sapiens GN=C	0.00					0.00			4.18	5.05	1	1
Q9H4A6	Golgi phosphoprotein 3 OS=Homo sap	0.00				4.36	5.03	1	1	5.18	5.03	1	1
P11940	Polyadenylate-binding pro	9.45	5.03	2	2	9.47	5.03	2	2	5.62	2.67	1	1
O14734	Acyl-coenzyme A thioeste	4.28	5.02	1	1		0.00				0.00		
P54709	Sodium/potassium-transporting ATPas	0.00				4.13	5.02	1	1		0.00		
P28288	ATP-binding cassette sub	6.22	2.88	1	1	10.04	5.01	2	2		0.00		
Q14722	Voltage-gated potassium	3.99	5.01	1	1		0.00				0.00		
P33993	DNA replication licensing	4.81	3.06	1	1	4.42	1.95	1	1	4.30	1.95	1	1
Q06430	N-acetyllactosaminide be	4.98	5.00	1	1		0.00				0.00		
Q15435	Protein phosphatase 1 re	5.04	5.00	1	1		0.00				0.00		
P80303	Nucleobindin-2 OS=Homo sapiens GN	0.00				4.81	5.00	1	1		0.00		
Q8IZ26	Zinc finger protein 34 OS=Homo sapie	0.00					0.00			5.18	5.00	1	1
Q8NBJ4	Golgi membrane protein 1 OS=Homo	0.00					0.00			4.85	4.99	1	1
O60763	General vesicular transpo	4.64	1.87	1	1	4.28	1.87	1	1	8.88	3.12	2	2
Q8N2F6	Armadillo repeat-containi	4.43	4.96	1	1		0.00				0.00		
P12429	Annexin A3 OS=Homo sapiens GN=AI	0.00					0.00			4.24	4.95	1	1
P09758	Tumor-associated calcium signal trans	0.00				4.20	4.95	1	1	4.36	4.95	1	1
P78527	DNA-dependent protein k	57.01	3.95	11	13	32.51	2.69	7	7	27.38	2.33	6	6
Q12824	SWI/SNF-related matrix-associated ac	0.00					0.00			4.27	4.94	1	1
Q92979	Ribosomal RNA small sub	3.94	4.92	1	1		0.00				0.00		
Q9UBE0	SUMO-activating enzyme subunit 1 OS	0.00				5.39	4.91	1	1	5.01	4.91	1	1
Q9NUE0	Palmitoyltransferase ZDHHC18 OS=Ho	0.00				3.97	4.90	1	1		0.00		

Q04637	Eukaryotic translation init	18.09	4.88	4	4	5.25	2.13	1	1	4.66	1.06	1	1
Q7L266	Isoaspartyl peptidase/L-a	4.16	4.87	1	1		0.00				0.00		
Q5VW32	BRO1 domain-containing protein BRO	0.00					0.00			4.98	4.87	1	1
O95218	Zinc finger Ran-binding domain-contai	0.00					0.00			4.29	4.85	1	1
O00515	Ladinin-1 OS=Homo sapi	4.02	2.32	1	1		0.00			4.44	2.51	1	1
Q9BYV8	Centrosomal protein of 41 kDa OS=Hc	0.00					0.00			5.85	4.83	1	1
Q9BTE3	Mini-chromosome mainte	5.18	4.83	1	1		0.00				0.00		
O00273	DNA fragmentation factor subunit alpl	0.00					0.00			4.33	4.83	1	1
Q9NWS0	PIH1 domain-containing p	4.10	4.83	1	1		0.00				0.00		
Q99460	26S proteasome non-ATP	6.68	2.73	1	1	9.96	4.83	2	2	5.24	2.10	1	1
Q9Y4P1	Cysteine protease ATG4B OS=Homo s	0.00					0.00			4.24	4.83	1	1
Q53GQ0	Estradiol 17-beta-dehydrogenase 12 C	0.00				4.15	4.81	1	1	4.63	4.81	1	1
Q12904	Aminoacyl tRNA synthase	3.84	4.81	1	1		0.00				0.00		
Q7KZ85	Transcription elongation f	6.13	1.33	1	1	4.73	1.10	1	1	15.36	3.71	3	3
A8MU46	Smoothelin-like protein 1 OS=Homo s	0.00				4.12	4.81	1	1		0.00		
P55265	Double-stranded RNA-spe	18.63	3.59	3	4	9.49	2.69	2	2	4.27	1.22	1	1
Q9H2U2	Inorganic pyrophosphata	5.51	4.79	1	1		0.00				0.00		
O00541	Pescadillo homolog OS=Homo sapiens	0.00					0.00			5.06	4.76	1	1
Q9UMS4	Pre-mRNA-processing factor 19 OS=H	0.00				4.35	4.76	1	1		0.00		
Q9NW64	Pre-mRNA-splicing factor	4.66	4.76	1	1		0.00				0.00		
Q86TX2	Acyl-coenzyme A thioeste	5.01	4.75	1	1	3.92	4.75	1	1	5.36	4.75	1	1
P49354	Protein farnesyltransferas	5.04	4.75	1	1	9.27	4.75	1	2	9.47	4.75	1	2
Q2M2Z5	Centrosomal protein kizuna OS=Homc	0.00				5.56	4.75	1	1		0.00		
Q16531	DNA damage-binding pro	6.47	2.11	1	1		0.00			11.63	4.74	2	2
P50219	Motor neuron and pancre	3.81	4.74	1	1		0.00				0.00		
Q86VP6	Cullin-associated NEDD8-	12.97	3.50	3	3	13.00	2.36	2	3		0.00		
Q86SH2	Zygote arrest protein 1 OS=Homo sap	0.00				4.19	4.72	1	1		0.00		
P25788	Proteasome subunit alpha	4.07	4.71	1	1		0.00				0.00		
P46777	60S ribosomal protein L5	4.31	4.71	1	1	4.74	4.71	1	1	4.54	4.71	1	1
P25205	DNA replication licensing	4.84	2.48	1	1		0.00			5.89	2.23	1	1
Q02218	2-oxoglutarate dehydroge	13.34	4.69	3	3		0.00				0.00		
Q96PZ0	Pseudouridylate synthase	4.66	2.57	1	1	4.35	2.57	1	1	9.19	4.69	2	2
O15144	Actin-related protein 2/3 complex sub	0.00				4.44	4.67	1	1		0.00		
A6NDG6	Phosphoglycolate phosph	3.90	4.67	1	1	4.47	4.67	1	1	4.40	4.67	1	1
Q7Z4P5	Growth/differentiation factor 7 OS=Hc	0.00				3.91	4.67	1	1		0.00		
Q9H8Y8	Golgi reassembly-stacking protein 2 O	0.00				8.34	4.65	1	2		0.00		
Q8N3X6	Ligand-dependent nuclear receptor co	0.00				4.87	4.65	1	1		0.00		
P54727	UV excision repair protein	9.13	4.65	1	2	8.95	4.65	1	2		0.00		
P49585	Choline-phosphate cytidy	4.39	4.63	1	1		0.00			5.74	4.63	1	1

P31350	Ribonucleoside-diphospha	4.12	4.63	1	1	4.11	4.63	1	1	4.37	4.63	1	1
O95365	Zinc finger and BTB domain-containing	0.00					0.00			5.13	4.62	1	1
Q8IZA3	Histone H1oo OS=Homo	4.00	4.62	1	1		0.00				0.00		
Q14161	ARF GTPase-activating protein GIT2 C	0.00				4.80	4.61	1	1		0.00		
Q6P9A2	Polypeptide N-acetylgalactosaminyltra	0.00					0.00			5.01	4.61	1	1
Q6ZN04	RNA-binding protein MEX	5.20	4.57	1	1		0.00				0.00		
Q07960	Rho GTPase-activating protein 1 OS=I	0.00					0.00			4.38	4.56	1	1
Q9NP92	28S ribosomal protein S3	4.46	4.56	1	1	4.72	4.56	1	1		0.00		
O14579	Coatomer subunit epsilon	3.97	4.55	1	1	4.03	4.55	1	1	4.47	4.55	1	1
Q9H3P7	Golgi resident protein GCP60 OS=Hon	0.00					0.00			11.88	4.55	1	2
Q9Y276	Mitochondrial chaperone BCS1 OS=Ho	0.00					0.00			4.15	4.53	1	1
Q9Y6E2	Basic leucine zipper and W	5.30	4.53	1	1	5.16	4.53	1	1	4.45	4.53	1	1
Q9Y266	Nuclear migration protein	4.03	4.53	1	1		0.00				0.00		
Q3ZCQ8	Mitochondrial import inner membrane	0.00				8.31	4.53	1	2		0.00		
Q06124	Tyrosine-protein phospha	4.00	2.01	1	1	4.02	2.51	1	1	4.23	2.51	1	1
Q15165	Serum paraoxonase/arylesterase 2 OS	0.00					0.00			4.18	4.52	1	1
Q9C0C2	182 kDa tankyrase-1-bind	8.68	2.20	2	2	8.24	1.97	2	2	5.28	1.45	1	1
O14908	PDZ domain-containing p	4.25	4.50	1	1		0.00				0.00		
O15231	Zinc finger protein 185 O	4.81	4.50	1	1	5.79	4.50	1	1		0.00		
O00300	Tumor necrosis factor receptor superf	0.00					0.00			4.39	4.49	1	1
Q8IXZ3	Transcription factor Sp8 OS=Homo sa	0.00					0.00			4.48	4.49	1	1
P10515	Dihydrolipoyllysine-residu	8.99	4.48	2	2		0.00			4.87	2.32	1	1
Q9UBS4	DnaJ homolog subfamily B member 1	0.00					0.00			4.27	4.47	1	1
Q9Y365	PCTP-like protein OS=Ho	3.99	4.47	1	1	4.77	4.47	1	1	4.56	4.47	1	1
Q9UHB9	Signal recognition particle	3.95	2.07	1	1	8.29	4.47	2	2	4.20	2.07	1	1
Q7L0Y3	Mitochondrial ribonucleas	4.32	4.47	1	1		0.00				0.00		
P10644	cAMP-dependent protein	4.34	4.46	1	1		0.00			4.43	4.46	1	1
P31321	cAMP-dependent protein kinase type I	0.00				4.22	4.46	1	1	5.06	4.46	1	1
Q9BST9	Rhotekin OS=Homo sapie	4.95	4.44	1	1		0.00			4.99	4.44	1	1
Q05655	Protein kinase C delta typ	8.89	4.44	2	2		0.00				0.00		
Q9NYK5	39S ribosomal protein L39, mitochond	0.00				3.95	4.44	1	1		0.00		
Q9NVA2	Septin-11 OS=Homo sapiens GN=SEP	0.00					0.00			5.07	4.43	1	1
Q9NW68	BSD domain-containing p	3.94	4.42	1	1		0.00			4.80	4.42	1	1
O43837	Isocitrate dehydrogenase [NAD] subu	0.00					0.00			5.04	4.42	1	1
Q6P9B9	Integrator complex subur	5.53	4.42	1	1		0.00				0.00		
Q00325	Phosphate carrier protein, mitochondr	0.00					0.00			4.19	4.42	1	1
P26368	Splicing factor U2AF 65 k	5.02	4.42	1	1		0.00			5.67	4.42	1	1
Q14151	Scaffold attachment factc	4.90	2.73	1	1		0.00			4.20	1.68	1	1
Q92820	Gamma-glutamyl hydrola	9.76	4.40	1	2	4.80	4.40	1	1	4.96	4.40	1	1

Q8TC12	Retinol dehydrogenase 11 OS=Homo	0.00				0.00			4.53	4.40	1	1
O00571	ATP-dependent RNA helic	8.91	4.38	2	2	4.50	1.81	1	1	9.08	4.38	2	2
P12236	ADP/ATP translocase 3 OS=Homo sap	0.00					0.00			4.41	4.36	1	1
P05141	ADP/ATP translocase 2 O	4.80	4.36	1	1	4.79	4.36	1	1	4.48	4.36	1	1
P22059	Oxysterol-binding protein	3.92	2.35	1	1		0.00			9.15	4.34	2	2
P53621	Coatomer subunit alpha (	10.19	3.10	2	2	4.98	1.31	1	1	14.57	3.02	2	3
P12081	Histidine--tRNA ligase, cytoplasmic OS	0.00					0.00			5.32	4.32	1	1
P04424	Argininosuccinate lyase OS=Homo sap	0.00				4.31	4.31	1	1	4.53	4.31	1	1
Q6YN16	Hydroxysteroid dehydrog	4.80	4.31	1	1		0.00			4.22	4.31	1	1
P42126	Enoyl-CoA delta isomeras	4.34	4.30	1	1		0.00			4.19	4.30	1	1
O75907	Diacylglycerol O-acyltrans	4.13	4.30	1	1	9.17	4.30	1	2		0.00		
O14929	Histone acetyltransferase	4.61	4.30	1	1		0.00				0.00		
Q9NVD7	Alpha-parvin OS=Homo s	3.93	4.30	1	1		0.00				0.00		
P14324	Farnesyl pyrophosphate s	3.84	4.30	1	1	7.96	4.30	1	2	4.30	4.30	1	1
P33908	Mannosyl-oligosaccharide 1,2-alpha-m	0.00				5.25	4.29	1	1		0.00		
Q9H3N1	Thioredoxin-related transmembrane p	0.00					0.00			4.20	4.29	1	1
Q92733	Proline-rich protein PRCC OS=Homo s	0.00				4.42	4.28	1	1		0.00		
P16278	Beta-galactosidase OS=H	7.75	2.22	1	2	4.30	2.22	1	1	8.57	4.28	2	2
Q8N2K0	Monoacylglycerol lipase ABHD12 OS=I	0.00				4.56	4.27	1	1	4.13	4.27	1	1
Q96A49	Synapse-associated prote	4.30	4.26	1	1		0.00				0.00		
P47897	Glutamine--tRNA ligase C	8.81	4.26	2	2	4.99	2.06	1	1		0.00		
Q58FF3	Putative endoplasmin-like protein OS=	0.00				4.05	4.26	1	1		0.00		
Q00341	Vigilin OS=Homo sapiens	15.39	2.84	2	3	9.20	2.84	2	2	9.70	3.00	2	2
Q9NUQ7	Ufm1-specific protease 2 OS=Homo s	0.00					0.00			4.25	4.26	1	1
Q9NXG2	THUMP domain-containing protein 1 C	0.00				4.78	4.25	1	1	4.69	4.25	1	1
P08754	Guanine nucleotide-bindi	4.15	4.24	1	1	4.54	4.24	1	1		0.00		
Q9NR30	Nucleolar RNA helicase 2	10.27	4.21	2	2	4.74	2.17	1	1	4.43	2.17	1	1
P39748	Flap endonuclease 1 OS=	3.98	4.21	1	1		0.00			4.38	4.21	1	1
P21283	V-type proton ATPase sul	4.11	4.19	1	1		0.00				0.00		
P61964	WD repeat-containing protein 5 OS=H	0.00					0.00			4.20	4.19	1	1
P34897	Serine hydroxymethyltrar	5.09	4.17	1	1	5.00	4.17	1	1	4.80	4.17	1	1
Q8IVD9	NudC domain-containing	4.47	4.16	1	1		0.00			9.04	4.16	1	2
P46926	Glucosamine-6-phosphate	4.08	4.15	1	1		0.00				0.00		
Q15061	WD repeat-containing protein 43 OS=	0.00				6.28	4.14	1	1		0.00		
Q92575	UBX domain-containing protein 4 OS=	0.00				4.42	4.13	1	1		0.00		
Q9Y2X9	Zinc finger protein 281 O	4.75	4.13	1	1		0.00				0.00		
P08621	U1 small nuclear ribonucleoprotein 70	0.00				4.36	4.12	1	1	4.99	4.12	1	1
Q9Y371	Endophilin-B1 OS=Homo	3.92	4.11	1	1	3.93	4.11	1	1		0.00		
O75306	NADH dehydrogenase [ul	3.94	4.10	1	1	4.75	4.10	1	1	4.18	4.10	1	1

A8MVM7	Putative uncharacterized protein ENSF		0.00			5.07	4.10	1	1		0.00		
O43602	Neuronal migration protein doublecort		0.00			4.29	4.08	1	1		0.00		
Q02750	Dual specificity mitogen-activated prot		0.00			4.37	4.07	1	1	4.50	4.07	1	1
P09543	2',3'-cyclic-nucleotide 3'-p	4.77	4.04	1	1	4.53	4.04	1	1	5.24	4.04	1	1
Q9NQ29	Putative RNA-binding pro	4.53	4.04	1	1		0.00				0.00		
P26640	Valine--tRNA ligase OS=H	8.53	2.77	2	2		0.00			8.91	2.85	2	2
P14923	Junction plakoglobin OS=Homo sapier		0.00			5.13	4.03	1	1		0.00		
P51114	Fragile X mental retardati	12.17	4.03	1	2	4.72	4.03	1	1	6.14	4.03	1	1
Q96GQ7	Probable ATP-dependent RNA helicase		0.00				0.00			9.22	4.02	2	2
P11117	Lysosomal acid phosphat	4.15	4.02	1	1		0.00				0.00		
Q9Y2P8	RNA 3'-terminal phosphat	4.33	4.02	1	1		0.00				0.00		
Q96GA3	Protein LTV1 homolog OS	3.96	4.00	1	1		0.00				0.00		
Q9UGV2	Protein NDRG3 OS=Homo sapiens GN		0.00			4.46	4.00	1	1		0.00		
Q9BW91	ADP-ribose pyrophosphat	4.09	4.00	1	1		0.00				0.00		
Q9BPX6	Calcium uptake protein 1, mitochondri		0.00				0.00			4.30	3.99	1	1
Q8IVT2	Mitotic interactor and substrate of PLK		0.00			9.86	3.98	1	2		0.00		
P04278	Sex hormone-binding glo	4.07	3.98	1	1		0.00			4.62	3.98	1	1
P61011	Signal recognition particle 54 kDa prot		0.00				0.00			5.37	3.97	1	1
Q8WUA8	Tsukushin OS=Homo sap	4.31	3.97	1	1								
P07099	Epoxide hydrolase 1 OS=	5.02	3.96	1	1		0.00				0.00		
Q96C03	Mitochondrial dynamics p	4.01	3.96	1	1		0.00				0.00		
Q9BZE4	Nucleolar GTP-binding protein 1 OS=H		0.00			5.19	3.94	1	1	11.48	3.94	1	2
P19971	Thymidine phosphorylase OS=Homo s		0.00				0.00			4.47	3.94	1	1
Q96EP5	DAZ-associated protein 1	5.36	3.93	1	1	5.71	3.93	1	1	4.84	3.93	1	1
P37287	Phosphatidylinositol N-acetylglucosam		0.00				0.00			4.85	3.93	1	1
Q9UI12	V-type proton ATPase sul	4.89	3.93	1	1	4.65	3.93	1	1	4.65	3.93	1	1
O95202	LETM1 and EF-hand dom	4.31	1.62	1	1	4.66	1.62	1	1	8.85	3.92	2	2
P49257	Protein ERGIC-53 OS=Homo sapiens (		0.00				0.00			5.00	3.92	1	1
Q96K80	Zinc finger CCCH domain-containing p		0.00				0.00			4.11	3.92	1	1
Q8N4J0	UPF0586 protein C9orf41	3.93	3.91	1	1		0.00				0.00		
Q9H490	Phosphatidylinositol glyca	5.13	3.91	1	1		0.00			4.36	3.91	1	1
Q92890	Ubiquitin fusion degradation protein 1		0.00				0.00			4.10	3.91	1	1
Q14566	DNA replication licensing	4.36	1.83	1	1	4.86	2.07	1	1		0.00		
P06737	Glycogen phosphorylase,	8.79	2.13	1	2	4.07	1.77	1	1		0.00		
Q8N336	ELMO domain-containing protein 1 OS		0.00				0.00			4.26	3.89	1	1
O76021	Ribosomal L1 domain-containing prote		0.00				0.00			4.97	3.88	1	1
Q15599	Na(+)/H(+) exchange regulatory cofa		0.00			4.25	3.86	1	1		0.00		
Q9NYU2	UDP-glucose:glycoproteir	10.71	2.89	2	2		0.00			4.80	0.96	1	1
Q9NUG4	Cerebral cavernous malfc	3.84	3.85	1	1		0.00				0.00		

P12270	Nucleoprotein TPR OS=H	14.28	2.16	3	3	4.07	0.63	1	1	5.11	1.06	1	1
Q9Y2R4	Probable ATP-dependent RNA helicase	0.00					0.00			5.16	3.84	1	1
Q9P287	BRCA2 and CDKN1A-inter	3.82	3.82	1	1		0.00			4.12	3.82	1	1
P61160	Actin-related protein 2 OS=Homo sapi	0.00					0.00			4.53	3.81	1	1
O14979	Heterogeneous nuclear ri	4.87	3.81	1	1		0.00			4.64	3.81	1	1
A6NHL2	Tubulin alpha chain-like 3	4.05	3.81	1	1		0.00				0.00		
O14983	Sarcoplasmic/endoplasmi	5.04	2.30	1	1	4.28	1.50	1	1	4.83	2.30	1	1
P31153	S-adenosylmethionine syı	4.63	3.80	1	1	4.88	3.80	1	1	4.38	3.80	1	1
Q8TE77	Protein phosphatase Slingshot homolo	0.00				4.98	3.79	1	1		0.00		
O75643	U5 small nuclear ribonucl	9.16	1.92	2	2	14.42	2.81	3	3		0.00		
Q8IYB3	Serine/arginine repetitive matrix prote	0.00				5.10	3.76	1	1	5.19	3.76	1	1
P36269	Gamma-glutamyltransferase 5 OS=Ho	0.00				5.01	3.75	1	1		0.00		
Q7Z5L9	Interferon regulatory fact	5.21	3.75	1	1		0.00				0.00		
Q01082	Spectrin beta chain, non-	15.19	2.16	3	3	9.82	1.44	2	2	15.59	2.37	3	3
Q14344	Guanine nucleotide-bindi	3.90	3.71	1	1		0.00				0.00		
O95396	Adenylyltransferase and s	5.41	3.70	1	1		0.00			5.41	3.70	1	1
Q92769	Histone deacetylase 2 OS	3.89	3.69	1	1		0.00				0.00		
Q9BS26	Endoplasmic reticulum re	4.48	3.69	1	1	4.64	3.69	1	1	5.15	3.69	1	1
Q15075	Early endosome antigen	4.74	1.13	1	1	5.68	1.20	1	1	15.84	3.69	3	3
Q27J81	Inverted formin-2 OS=Homo sapiens	0.00				4.90	2.16	1	1	5.73	1.52	1	1
P49321	Nuclear autoantigenic spe	9.82	3.68	2	2	5.60	2.03	1	1	9.86	3.68	2	2
Q8NFH3	Nucleoporin Nup43 OS=Homo sapiens	0.00				4.01	3.68	1	1		0.00		
P35250	Replication factor C subu	4.45	3.67	1	1		0.00				0.00		
Q01844	RNA-binding protein EWS	5.22	3.66	1	1		0.00				0.00		
P43034	Platelet-activating factor	8.22	3.66	1	2		0.00			4.40	3.66	1	1
P49356	Protein farnesyltransferase subunit be	0.00					0.00			4.58	3.66	1	1
Q9NSE4	Isoleucine--tRNA ligase, r	9.63	3.66	2	2		0.00			5.26	1.98	1	1
Q7Z2W4	Zinc finger CCCH-type antiviral protein	0.00				9.62	2.00	1	2	9.74	3.66	2	2
Q01970	1-phosphatidylinositol 4,5	10.41	3.65	2	2	5.47	1.46	1	1	4.96	1.46	1	1
Q6P2Q9	Pre-mRNA-processing-spl	19.71	3.64	4	4		0.00			5.58	0.99	1	1
P08686	Steroid 21-hydroxylase O	4.14	3.64	1	1		0.00				0.00		
O75530	Polycomb protein EED OS	4.42	3.63	1	1		0.00				0.00		
P41219	Peripherin OS=Homo sap	4.18	3.62	1	1		0.00				0.00		
Q9NYV4	Cyclin-dependent kinase 12 OS=Homo	0.00					0.00			10.92	3.62	2	2
Q9P289	Serine/threonine-protein	4.25	3.61	1	1		0.00				0.00		
O15213	WD repeat-containing protein 46 OS=	0.00					0.00			4.42	3.61	1	1
A2A3N6	Putative PIP5K1A and PS	4.65	1.97	1	1	4.10	1.62	1	1		0.00		
P48637	Glutathione synthetase O	4.17	3.59	1	1		0.00				0.00		
Q96PK6	RNA-binding protein 14 OS=Homo sap	0.00				4.71	3.59	1	1		0.00		

Q9NVH1	DnaJ homolog subfamily	4.55	3.58	1	1	4.37	3.58	1	1	4.65	3.58	1	1
Q8NFF5	FAD synthase OS=Homo sapiens GN=	0.00				4.62	3.58	1	1	4.62	3.58	1	1
O15382	Branched-chain-amino-ac	3.90	3.57	1	1		0.00				0.00		
P51116	Fragile X mental retardation syndrome	0.00					0.00			5.51	3.57	1	1
Q92917	G patch domain and KOW	3.88	3.57	1	1		0.00				0.00		
Q96SK2	Transmembrane protein 209 OS=Hom	0.00					0.00			4.92	3.57	1	1
Q96NJ3	Zinc finger protein 285 OS=Homo sap	0.00				4.74	3.56	1	1		0.00		
Q9UNS2	COP9 signalosome complex subunit 3	0.00				4.49	3.55	1	1	4.43	3.55	1	1
Q8N8S7	Protein enabled homolog	4.03	3.55	1	1		0.00				0.00		
Q01650	Large neutral amino acids transporter	0.00				3.98	3.55	1	1	4.24	3.55	1	1
O96013	Serine/threonine-protein	3.88	3.55	1	1		0.00				0.00		
P11172	Uridine 5'-monophosphat	3.90	3.54	1	1		0.00			4.17	3.54	1	1
A1A5D9	Bicaudal D-related protein 2 OS=Hom	0.00					0.00			4.26	3.54	1	1
Q9UN86	Ras GTPase-activating protein-binding	0.00				4.43	3.53	1	1		0.00		
P52294	Importin subunit alpha-5	4.05	3.53	1	1		0.00				0.00		
P51648	Fatty aldehyde dehydroge	4.13	3.51	1	1	3.93	3.51	1	1	4.22	3.51	1	1
Q6DD88	Atlastin-3 OS=Homo sapi	6.31	3.51	1	1	4.01	3.51	1	1	5.55	3.51	1	1
Q5TDH0	Protein DDI1 homolog 2 (	3.84	3.51	1	1		0.00				0.00		
Q05519	Serine/arginine-rich splici	4.31	3.51	1	1		0.00				0.00		
Q01831	DNA repair protein complementing XP	0.00				5.99	3.51	1	1		0.00		
Q15172	Serine/threonine-protein phosphatase	0.00				4.29	3.50	1	1	4.31	3.09	1	1
Q15067	Peroxisomal acyl-coenzyn	4.63	3.48	1	1		0.00			5.16	3.48	1	1
P55010	Eukaryotic translation init	4.96	3.48	1	1	9.78	3.48	1	2	5.13	3.48	1	1
Q9GZM8	Nuclear distribution protein nudE-like	0.00				4.07	3.48	1	1		0.00		
P35269	General transcription factor IIF subuni	0.00					0.00			4.24	3.48	1	1
P40222	Alpha-taxilin OS=Homo s	4.45	3.48	1	1	5.24	3.48	1	1	5.60	3.48	1	1
P35659	Protein DEK OS=Homo sa	4.36	3.47	1	1		0.00				0.00		
Q01085	Nucleolysin TIAR OS=Hor	3.93	3.47	1	1		0.00				0.00		
P26639	Threonine--tRNA ligase, cytoplasmic C	0.00				3.91	1.80	1	1	4.15	1.66	1	1
O60784	Target of Myb protein 1 OS=Homo sa	0.00					0.00			4.65	3.46	1	1
Q13177	Serine/threonine-protein kinase PAK 2	0.00					0.00			5.24	3.44	1	1
Q9H1V8	Sodium-dependent neutral amino acid	0.00				4.73	3.44	1	1		0.00		
O60701	UDP-glucose 6-dehydroge	4.05	3.44	1	1	4.02	3.44	1	1	9.56	3.44	1	2
P23588	Eukaryotic translation initiation factor	0.00				9.71	3.44	1	2	15.02	3.44	1	3
Q9Y2X3	Nucleolar protein 58 OS=	8.76	3.40	1	2	4.63	3.40	1	1	5.43	3.40	1	1
O75475	PC4 and SFRS1-interactir	4.32	3.40	1	1		0.00			5.63	3.40	1	1
Q86WB0	Nuclear-interacting partn	3.89	3.39	1	1		0.00				0.00		
Q08945	FACT complex subunit SSRP1 OS=Hor	0.00				5.67	3.39	1	1		0.00		
Q9Y6E0	Serine/threonine-protein	5.69	3.39	1	1		0.00				0.00		

Q5FYA8	Arylsulfatase H OS=Homo sapiens GN		0.00			4.85	3.38	1	1		0.00		
P15924	Desmoplakin OS=Homo s	26.01	1.95	3	5	24.25	2.61	4	5	26.43	3.38	5	5
P55084	Trifunctional enzyme sub	9.98	3.38	1	2	15.65	3.38	1	3	5.16	3.38	1	1
O75844	CAAX prenyl protease 1 h	5.38	3.37	1	1	8.62	3.37	1	2	5.94	3.37	1	1
Q96M27	Protein PRRC1 OS=Homc	3.89	3.37	1	1		0.00				0.00		
Q15833	Syntaxin-binding protein 2 OS=Homo		0.00			3.98	3.37	1	1		0.00		
Q7Z3B4	Nucleoporin p54 OS=Homo sapiens G		0.00				0.00			4.86	3.35	1	1
Q14152	Eukaryotic translation init	8.16	2.03	2	2	9.75	2.17	2	2		0.00		
Q86TD4	Sarcalumenin OS=Homo sapiens GN=		0.00				0.00			5.49	3.33	1	1
Q96EY1	DnaJ homolog subfamily A member 3,		0.00			4.46	3.33	1	1	4.82	3.33	1	1
Q9UHI8	A disintegrin and metallo	5.26	3.31	1	1		0.00				0.00		
P78352	Disks large homolog 4 OS=Homo sapi		0.00				0.00			4.65	3.31	1	1
Q92879	CUGBP Elav-like family member 1 OS=		0.00			3.98	3.29	1	1	4.43	3.29	1	1
Q5K4L6	Long-chain fatty acid trar	5.46	3.29	1	1	5.07	3.29	1	1		0.00		
O75153	Clustered mitochondria p	3.87	1.53	1	1		0.00			4.84	1.76	1	1
P20073	Annexin A7 OS=Homo sa	9.60	3.28	1	2	5.32	3.28	1	1		0.00		
P18858	DNA ligase 1 OS=Homo s	9.51	3.26	2	2	9.37	3.26	2	2	4.95	1.52	1	1
P41214	Eukaryotic translation initiation factor		0.00			4.13	3.25	1	1		0.00		
P13489	Ribonuclease inhibitor OS	4.78	3.25	1	1		0.00				0.00		
Q8TEX9	Importin-4 OS=Homo sap	7.85	3.24	2	2	4.26	1.57	1	1	5.08	1.57	1	1
Q2M2I5	Keratin, type I cytoskeletal 24 OS=Ho		0.00				0.00			4.44	3.24	1	1
Q8IXI1	Mitochondrial Rho GTPas	5.96	3.24	1	1		0.00				0.00		
P49821	NADH dehydrogenase [ul	3.93	3.23	1	1		0.00				0.00		
Q1KMD3	Heterogeneous nuclear ribonucleoprot		0.00			5.82	3.21	1	1	5.19	3.21	1	1
Q9UHD9	Ubiquilin-2 OS=Homo sap	4.50	3.21	1	1		0.00				0.00		
P63010	AP-2 complex subunit bet	8.69	3.20	2	2		0.00				0.00		
Q6P1J9	Parafibromin OS=Homo sapiens GN=(		0.00				0.00			4.31	3.20	1	1
Q6UN15	Pre-mRNA 3'-end-processing factor FI		0.00			4.53	3.20	1	1	5.08	3.20	1	1
Q53GS9	U4/U6.U5 tri-snRNP-associated protei		0.00			4.38	3.19	1	1		0.00		
P50995	Annexin A11 OS=Homo s	4.74	3.17	1	1		0.00				0.00		
O60825	6-phosphofructo-2-kinase	4.39	3.17	1	1		0.00			4.57	3.17	1	1
Q07065	Cytoskeleton-associated p	4.73	3.16	1	1	4.93	3.16	1	1	5.49	3.16	1	1
Q9H0D6	5'-3' exoribonuclease 2 O	9.73	3.16	2	2	9.46	3.16	2	2	4.87	1.58	1	1
Q10567	AP-1 complex subunit bet	4.83	1.58	1	1	4.07	1.58	1	1		0.00		
O14744	Protein arginine N-methyltransferase 5		0.00			3.98	3.14	1	1	4.57	3.14	1	1
P04004	Vitronectin OS=Homo sap	4.54	3.14	1	1	4.34	3.14	1	1	4.56	3.14	1	1
Q96AE4	Far upstream element-binding protein		0.00			9.65	3.11	1	2	4.56	3.11	1	1
Q6P1M0	Long-chain fatty acid transport protein		0.00				0.00			5.44	3.11	1	1
P56192	Methionine--tRNA ligase,	4.79	1.89	1	1	8.08	3.11	2	2		0.00		

P49736	DNA replication licensing factor MCM2	0.00				0.00			5.09	3.10	1	1
Q9NP81	Serine--tRNA ligase, mitochondrial OS	0.00				0.00			5.53	3.09	1	1
Q13867	Bleomycin hydrolase OS=Homo sapier	0.00				0.00			4.83	3.08	1	1
P23368	NAD-dependent malic en:	4.29	3.08	1	1	5.00	3.08	1	1		0.00		
Q13492	Phosphatidylinositol-bindi	4.42	3.07	1	1		0.00			5.01	3.07	1	1
Q9Y265	RuvB-like 1 OS=Homo sa	4.40	3.07	1	1	9.03	3.07	1	2	5.00	3.07	1	1
P50851	Lipopolysaccharide-respo	9.81	1.96	2	2		0.00			5.07	1.12	1	1
Q9C0E8	Protein lunapark OS=Hor	3.85	3.04	1	1		0.00				0.00		
Q494U1	Pleckstrin homology dom	4.02	3.02	1	1		0.00				0.00		
Q7Z5R6	Amyloid beta A4 precursor protein-bin	0.00				0.00			4.21	3.00	1	1
Q9HC77	Centromere protein J OS=	4.73	1.57	1	1		0.00			4.24	1.42	1	1
Q13618	Cullin-3 OS=Homo sapiens GN=CUL3	0.00				0.00			5.23	2.99	1	1
Q96HE7	ERO1-like protein alpha (	3.87	2.99	1	1		0.00				0.00		
P18031	Tyrosine-protein phospha	4.14	2.99	1	1		0.00				0.00		
O15075	Serine/threonine-protein kinase DCLK:	0.00				4.25	2.97	1	1		0.00		
P26641	Elongation factor 1-gamn	3.90	2.97	1	1		0.00				0.00		
P05166	Propionyl-CoA carboxylas	9.83	2.97	1	2		0.00			4.32	2.97	1	1
P11217	Glycogen phosphorylase,	5.51	2.97	1	1		0.00				0.00		
Q9NRY5	Protein FAM114A2 OS=Homo sapiens	0.00				0.00			4.20	2.97	1	1
Q8WVM8	Sec1 family domain-containing protein	0.00				8.98	2.96	1	2		0.00		
Q9Y305	Acyl-coenzyme A thioeste	3.95	2.96	1	1		0.00				0.00		
P28329	Choline O-acetyltransfera	3.90	2.94	1	1		0.00				0.00		
P61201	COP9 signalosome compl	3.98	2.93	1	1		0.00				0.00		
P31930	Cytochrome b-c1 comple:	4.52	2.92	1	1	4.34	2.92	1	1		0.00		
Q9UPT8	Zinc finger CCCH domain-containing p	0.00				8.28	2.92	2	2		0.00		
Q9Y4P3	Transducin beta-like protein 2 OS=Ho	0.00					0.00			4.14	2.91	1	1
Q9HAV4	Exportin-5 OS=Homo sap	4.04	1.66	1	1	4.30	1.66	1	1	4.88	1.25	1	1
P55196	Afadin OS=Homo sapiens	9.84	1.92	2	2	4.09	0.99	1	1	4.78	0.93	1	1
Q7Z6Z7	E3 ubiquitin-protein ligas	10.30	0.94	2	2	18.62	1.97	4	4	5.49	0.73	1	1
Q04206	Transcription factor p65 (	4.65	2.90	1	1		0.00				0.00		
Q92973	Transportin-1 OS=Homo sapiens GN=	0.00					0.00			5.22	2.90	1	1
Q8NCA5	Protein FAM98A OS=Hon	4.28	2.89	1	1	4.19	2.89	1	1		0.00		
P05165	Propionyl-CoA carboxylas	4.77	2.88	1	1		0.00				0.00		
Q9P258	Protein RCC2 OS=Homo sapiens GN=	0.00				4.79	2.87	1	1		0.00		
Q14728	Major facilitator superfamily domain-c	0.00				3.99	2.86	1	1		0.00		
Q9NNW7	Thioredoxin reductase 2,	5.06	2.86	1	1	8.35	2.86	1	2	4.27	2.86	1	1
Q9UP83	Conserved oligomeric Gol	5.27	2.86	1	1		0.00				0.00		
Q8N6L0	Protein KASH5 OS=Homo sapiens GN=	0.00				4.10	2.85	1	1		0.00		
Q9NW75	G patch domain-containir	4.28	2.84	1	1		0.00				0.00		

Q03252	Lamin-B2 OS=Homo sapiens GN=LMN		0.00				0.00			4.63	2.83	1	1
Q8NF37	Lysophosphatidylcholine acyltransfera		0.00			4.38	2.81	1	1		0.00		
Q4KMQ1	Taperin OS=Homo sapier	4.34	2.53	1	1		0.00			10.01	2.81	2	2
P36915	Guanine nucleotide-bindi	4.66	2.80	1	1		0.00				0.00		
Q13573	SNW domain-containing protein 1 OS=		0.00				0.00			4.32	2.80	1	1
P52306	Rap1 GTPase-GDP dissociation stimula		0.00				0.00			5.02	2.80	1	1
Q16850	Lanosterol 14-alpha dem	5.12	2.78	1	1	4.82	2.78	1	1	4.31	2.78	1	1
P01024	Complement C3 OS=Hom	14.38	2.77	2	3	4.89	1.44	1	1	5.42	1.44	1	1
Q9H223	EH domain-containing protein 4 OS=H		0.00			4.26	2.77	1	1	4.78	2.77	1	1
Q9UDY2	Tight junction protein ZO	5.80	2.77	1	1		0.00				0.00		
Q3KQV9	UDP-N-acetylhexosamine	4.20	2.76	1	1		0.00			4.33	2.76	1	1
A6NLF2	RNA polymerase II transcription factor		0.00				0.00			4.41	2.75	1	1
P09622	Dihydrolipoyl dehydrogenase, mitocho		0.00			4.03	2.75	1	1		0.00		
Q17RY0	Cytoplasmic polyadenylation element-		0.00				0.00			4.16	2.74	1	1
P46060	Ran GTPase-activating pr	5.08	2.73	1	1		0.00			4.95	2.73	1	1
Q9H6R4	Nucleolar protein 6 OS=H	5.28	2.71	1	1		0.00				0.00		
Q14980	Nuclear mitotic apparatus protein 1 O		0.00				0.00			14.25	2.70	3	3
O43815	Striatin OS=Homo sapien	4.96	2.69	1	1		0.00				0.00		
E9PAV3	Nascent polypeptide-assc	9.15	1.35	2	2	17.22	2.02	3	4	17.45	2.69	4	4
Q92800	Histone-lysine N-methyltransferase EZ		0.00			3.92	2.68	1	1		0.00		
Q9NZB2	Constitutive coactivator o	8.44	2.68	2	2		0.00				0.00		
Q68E01	Integrator complex subunit 3 OS=Hor		0.00				0.00			4.69	2.68	1	1
P37198	Nuclear pore glycoprotein	4.41	2.68	1	1		0.00				0.00		
Q96AX1	Vacuolar protein sorting-associated pr		0.00			5.14	2.68	1	1		0.00		
Q99767	Amyloid beta A4 precursor protein-bin		0.00			4.68	2.67	1	1	4.43	2.67	1	1
P10909	Clusterin OS=Homo sapie	3.88	2.67	1	1		0.00				0.00		
O75027	ATP-binding cassette sub-family B me		0.00			4.87	2.66	1	1	4.80	2.66	1	1
Q8IUR6	CREB3 regulatory factor OS=Homo sa		0.00			3.92	2.66	1	1		0.00		
O95453	Poly(A)-specific ribonucle	3.84	2.66	1	1		0.00				0.00		
Q9H270	Vacuolar protein sorting-a	5.22	2.66	1	1		0.00				0.00		
Q6P1M3	Lethal(2) giant larvae protein homolog		0.00				0.00			5.78	2.65	1	1
O43615	Mitochondrial import inne	4.06	2.65	1	1		0.00			4.18	2.65	1	1
O00533	Neural cell adhesion molecule L1-like		0.00				0.00			5.23	2.65	1	1
Q92731	Estrogen receptor beta OS=Homo sap		0.00			4.05	2.64	1	1		0.00		
P49790	Nuclear pore complex pro	4.00	1.42	1	1		0.00			5.50	1.22	1	1
Q5T0N5	Formin-binding protein 1-like OS=Hon		0.00				0.00			4.27	2.64	1	1
P02771	Alpha-fetoprotein OS=Ho	10.35	2.63	1	2	10.68	2.63	1	2	10.69	2.63	1	2
O94826	Mitochondrial import rece	3.86	2.63	1	1		0.00				0.00		
Q9BSC4	Nucleolar protein 10 OS=	4.59	2.62	1	1		0.00				0.00		

Q14839	Chromodomain-helicase-I	9.76	1.94	2	2	8.26	1.78	2	2	5.52	1.10	1	1
Q9H4G0	Band 4.1-like protein 1 OS=Homo sap	0.00					0.00			4.35	2.61	1	1
Q70EK8	Inactive ubiquitin carboxy	5.24	2.61	1	1		0.00				0.00		
Q9Y6W5	Wiskott-Aldrich syndrome	4.05	2.61	1	1		0.00			4.23	2.61	1	1
P49419	Alpha-aminoadipic semial	4.30	2.60	1	1		0.00				0.00		
Q9UMF0	Intercellular adhesion mo	4.86	2.60	1	1		0.00				0.00		
Q9C0B0	RING finger protein unkempt homolog	0.00					0.00			4.28	2.59	1	1
P55884	Eukaryotic translation initiation factor	0.00				4.68	2.58	1	1		0.00		
P35241	Radixin OS=Homo sapiens GN=RDX P	0.00					0.00			4.70	2.57	1	1
Q9Y2J8	Protein-arginine deiminas	4.83	2.56	1	1	5.35	2.56	1	1	4.60	2.56	1	1
Q9H6T3	RNA polymerase II-assoc	4.48	2.56	1	1	4.89	2.56	1	1		0.00		
Q2TB10	Zinc finger protein 800 OS=Homo sap	0.00					0.00			4.70	2.56	1	1
O15371	Eukaryotic translation init	4.40	2.55	1	1		0.00				0.00		
P04745	Alpha-amylase 1 OS=Hor	3.99	2.54	1	1		0.00				0.00		
Q6P995	Protein FAM171B OS=Homo sapiens C	0.00				5.18	2.54	1	1		0.00		
Q9P265	Disco-interacting protein	4.01	1.14	1	1	3.93	1.40	1	1	4.41	1.40	1	1
Q9UFB7	Zinc finger and BTB domain-containing	0.00				4.02	2.54	1	1		0.00		
O60488	Long-chain-fatty-acid--Co	4.42	2.53	1	1	4.07	2.53	1	1		0.00		
O76094	Signal recognition particle subunit SRP	0.00				9.34	2.53	1	2	4.85	2.53	1	1
P08243	Asparagine synthetase [glutamine-hyd	0.00					0.00			4.24	2.50	1	1
Q08379	Golgin subfamily A memb	5.03	2.50	1	1		0.00				0.00		
Q9UKW4	Guanine nucleotide exchange factor V	0.00					0.00			4.29	2.48	1	1
P04843	Dolichyl-diphosphooligosaccharide--pr	0.00				4.11	2.47	1	1		0.00		
P02461	Collagen alpha-1(III) chain OS=Homo	0.00				4.70	2.46	1	1		0.00		
Q13219	Pappalysin-1 OS=Homo s	5.31	2.46	1	1		0.00				0.00		
O95831	Apoptosis-inducing factor 1, mitochon	0.00					0.00			4.22	2.45	1	1
P08237	ATP-dependent 6-phosph	8.84	2.44	1	2		0.00			4.15	2.44	1	1
O95644	Nuclear factor of activate	4.73	2.44	1	1		0.00				0.00		
O75694	Nuclear pore complex pro	8.59	2.44	2	2	4.27	1.22	1	1	4.73	1.22	1	1
Q99615	DnaJ homolog subfamily C member 7	0.00					0.00			4.19	2.43	1	1
Q9H845	Acyl-CoA dehydrogenase family memb	0.00				4.26	2.42	1	1	4.47	2.42	1	1
P10155	60 kDa SS-A/Ro ribonucle	4.09	2.42	1	1		0.00				0.00		
Q8NCL4	Polypeptide N-acetylgalactosaminyltra	0.00					0.00			4.97	2.41	1	1
Q4G0J3	La-related protein 7 OS=	3.97	2.41	1	1		0.00				0.00		
Q6P996	Pyridoxal-dependent deca	5.75	2.41	1	1	5.54	2.41	1	1	5.61	2.41	1	1
P49589	Cysteine--tRNA ligase, cytoplasmic OS	0.00					0.00			4.78	2.41	1	1
Q9GZY0	Nuclear RNA export facto	4.23	2.40	1	1		0.00				0.00		
Q9Y3Z3	Deoxynucleoside triphosp	4.73	2.40	1	1	4.09	2.40	1	1		0.00		
Q15063	Periostin OS=Homo sapie	10.61	2.39	1	2	4.34	2.39	1	1		0.00		

A6NFQ2	Protein FAM115C OS=Homo sapiens C		0.00				0.00			4.13	2.39	1	1
Q15849	Urea transporter 2 OS=Homo sapiens		0.00				0.00			4.64	2.39	1	1
Q12797	Aspartyl/asparaginyl beta	5.19	2.37	1	1		0.00			5.70	2.37	1	1
P06400	Retinoblastoma-associated protein OS		0.00				0.00			4.27	2.37	1	1
P41743	Protein kinase C iota type OS=Homo s		0.00				0.00			4.10	2.35	1	1
Q9UJC3	Protein Hook homolog 1 (	4.47	2.34	1	1		0.00			4.94	2.34	1	1
Q7L804	Rab11 family-interacting protein 2 OS		0.00			4.34	2.34	1	1	4.32	2.34	1	1
Q9UBT2	SUMO-activating enzyme	4.10	2.34	1	1		0.00				0.00		
Q86Y56	Dynein assembly factor 5, axonemal C		0.00			5.34	2.34	1	1	5.75	2.34	1	1
Q9NY61	Protein AATF OS=Homo s	4.41	2.32	1	1		0.00			4.25	2.32	1	1
Q96ST2	Protein IWS1 homolog OS	4.50	2.32	1	1		0.00				0.00		
Q96EY7	Pentatricopeptide repeat	4.70	2.32	1	1	10.53	2.32	1	2		0.00		
Q6P4Q7	Metal transporter CNNM4 OS=Homo s		0.00				0.00			4.92	2.32	1	1
Q9NQX3	Gephyrin OS=Homo sapie	3.91	2.31	1	1		0.00			4.63	2.31	1	1
O43264	Centromere/kinetochore	4.80	2.31	1	1		0.00			4.20	2.31	1	1
A6NDK9	Putative golgin subfamily A member 6		0.00				0.00			4.15	2.31	1	1
Q9H0M4	Zinc finger CW-type PWWP domain pr		0.00				0.00			4.67	2.31	1	1
Q05209	Tyrosine-protein phospha	4.31	2.31	1	1	4.40	2.31	1	1		0.00		
Q92615	La-related protein 4B OS=Homo sapie		0.00				0.00			4.33	2.30	1	1
Q9NVC6	Mediator of RNA polymerase II transc		0.00			4.23	2.30	1	1		0.00		
Q06210	Glutamine--fructose-6-phosphate amir		0.00			4.62	2.29	1	1	5.05	2.29	1	1
Q8IVT5	Kinase suppressor of Ras 1 OS=Homo		0.00				0.00			4.61	2.28	1	1
O00139	Kinesin-like protein KIF2A OS=Homo s		0.00				0.00			4.44	2.27	1	1
O95359	Transforming acidic coile	9.36	1.32	2	2	9.34	1.56	2	2	4.55	0.61	1	1
Q8NBJ5	Procollagen galactosyltransferase 1 OS		0.00				0.00			8.25	2.25	1	2
O43719	HIV Tat-specific factor 1 OS=Homo sa		0.00				0.00			4.63	2.25	1	1
O43290	U4/U6.U5 tri-snRNP-associated protei		0.00				0.00			5.33	2.25	1	1
Q9UBY0	Sodium/hydrogen exchanger 2 OS=H		0.00			4.07	2.22	1	1		0.00		
Q93084	Sarcoplasmic/endoplasmic reticulum c		0.00				0.00			5.90	2.21	1	1
P52701	DNA mismatch repair protein Msh6 OS		0.00			8.92	2.21	2	2	4.28	0.88	1	1
P50416	Carnitine O-palmitoyltrans	5.08	2.20	1	1	5.93	2.20	1	1	5.52	2.20	1	1
Q5T7W0	Zinc finger protein 618 OS=Homo sap		0.00				0.00			4.12	2.20	1	1
P49023	Paxillin OS=Homo sapien	4.46	2.20	1	1		0.00				0.00		
P33402	Guanylate cyclase soluble subunit alph		0.00				0.00			4.13	2.19	1	1
Q16822	Phosphoenolpyruvate car	3.98	2.19	1	1		0.00				0.00		
Q92621	Nuclear pore complex protein Nup205		0.00			5.27	1.39	1	1	4.30	0.80	1	1
Q6ZVT6	Uncharacterized protein C3orf67 OS=I		0.00			3.94	2.18	1	1		0.00		
P84550	SKI family transcriptional corepressor		0.00				0.00			4.10	2.18	1	1
Q6PJT7	Zinc finger CCCH domain-containing p		0.00				0.00			4.18	2.17	1	1

Q9Y592	Centrosomal protein of 83 kDa OS=Hc		0.00				0.00			4.10	2.16	1	1
Q96KP1	Exocyst complex component 2 OS=Hc		0.00			4.57	2.16	1	1		0.00		
O75382	Tripartite motif-containing	4.30	2.15	1	1		0.00				0.00		
P13671	Complement component C6 OS=Hom		0.00			3.93	2.14	1	1		0.00		
Q8IXB1	DnaJ homolog subfamily C member 1(		0.00			4.11	2.14	1	1		0.00		
Q13214	Semaphorin-3B OS=Homo sapiens GN		0.00			3.96	2.14	1	1		0.00		
Q5T4S7	E3 ubiquitin-protein ligas	9.74	1.00	2	2	4.82	0.56	1	1	5.22	0.58	1	1
P43243	Matrin-3 OS=Homo sapiens GN=MATI		0.00			4.46	2.13	1	1		0.00		
P23229	Integrin alpha-6 OS=Homo sapiens GI		0.00				0.00			5.17	2.12	1	1
Q14008	Cytoskeleton-associated p	4.24	0.69	1	1		0.00			5.19	1.43	1	1
P02751	Fibronectin OS=Homo sa	9.67	1.38	2	2	4.45	0.71	1	1		0.00		
P17480	Nucleolar transcription factor 1 OS=H		0.00				0.00			4.50	2.09	1	1
Q86Y38	Xylosyltransferase 1 OS=	4.09	2.09	1	1		0.00				0.00		
P54577	Tyrosine--tRNA ligase, cy	3.94	2.08	1	1		0.00				0.00		
Q9NQI0	Probable ATP-dependent RNA helicase		0.00				0.00			4.31	2.07	1	1
Q9NZT2	Opioid growth factor rece	3.86	2.07	1	1		0.00				0.00		
O75182	Paired amphipathic helix	4.85	2.07	1	1		0.00				0.00		
Q14258	E3 ubiquitin/ISG15 ligase	4.61	2.06	1	1		0.00				0.00		
Q9H7Z3	Protein NRDE2 homolog OS=Homo sa		0.00			4.72	2.06	1	1		0.00		
Q8IYB8	ATP-dependent RNA helicase SUPV3L1		0.00			4.16	2.04	1	1		0.00		
O60242	Brain-specific angiogenesis inhibitor 3		0.00			5.19	2.04	1	1		0.00		
Q6PL18	ATPase family AAA domain-containing		0.00			9.10	2.01	2	2	4.61	1.08	1	1
Q8IW93	Rho guanine nucleotide exchange fact		0.00			4.05	2.00	1	1		0.00		
Q99459	Cell division cycle 5-like p	4.07	2.00	1	1		0.00				0.00		
Q8IZ83	Aldehyde dehydrogenase family 16 m		0.00				0.00			4.91	2.00	1	1
Q9Y6T7	Diacylglycerol kinase beta	4.11	1.99	1	1		0.00				0.00		
Q86YT6	E3 ubiquitin-protein ligase MIB1 OS=H		0.00			4.17	1.99	1	1		0.00		
Q6WCQ1	Myosin phosphatase Rho-	3.88	1.95	1	1		0.00				0.00		
P52735	Guanine nucleotide exchange factor V		0.00				0.00			4.48	1.94	1	1
P35658	Nuclear pore complex pro	4.11	1.05	1	1	4.03	1.05	1	1	5.09	0.86	1	1
P35221	Catenin alpha-1 OS=Hom	4.36	1.88	1	1		0.00				0.00		
Q8IZL8	Proline-, glutamic acid- a	4.34	1.86	1	1	4.00	1.86	1	1		0.00		
P12109	Collagen alpha-1(VI) chai	5.32	1.85	1	1	10.87	1.85	1	2	11.52	1.85	1	2
O75152	Zinc finger CCCH domain-containing p		0.00			4.13	1.85	1	1		0.00		
P57740	Nuclear pore complex pro	4.98	1.84	1	1		0.00				0.00		
P28290	Sperm-specific antigen 2	4.02	1.83	1	1		0.00				0.00		
P07384	Calpain-1 catalytic subuni	4.02	1.82	1	1		0.00				0.00		
P55011	Solute carrier family 12 member 2 OS		0.00				0.00			4.30	1.82	1	1
Q86XP3	ATP-dependent RNA helic	3.90	1.81	1	1		0.00				0.00		

Q8TCU6	Phosphatidylinositol 3,4,5	4.84	1.81	1	1		0.00				0.00		
O94906	Pre-mRNA-processing factor 6 OS=Ho		0.00			4.85	1.81	1	1		0.00		
P52732	Kinesin-like protein KIF11 OS=Homo s		0.00				0.00			4.35	1.80	1	1
P17844	Probable ATP-dependent RNA helicase		0.00				0.00			4.11	1.79	1	1
Q96RQ3	Methylcrotonoyl-CoA carb	4.65	1.79	1	1	4.26	1.79	1	1	4.40	1.79	1	1
Q7Z410	Transmembrane protease serine 9 OS		0.00				0.00			4.29	1.79	1	1
Q658Y4	Protein FAM91A1 OS=Homo sapiens (		0.00			4.60	1.79	1	1		0.00		
Q6VY07	Phosphofurin acidic cluster sorting pro		0.00				0.00			4.38	1.77	1	1
Q5JTH9	RRP12-like protein OS=Homo sapiens		0.00				0.00			5.55	1.77	1	1
Q9NSV4	Protein diaphanous homo	3.86	1.76	1	1		0.00				0.00		
Q13563	Polycystin-2 OS=Homo sa	4.22	1.76	1	1		0.00				0.00		
Q15003	Condensin complex subunit 2 OS=Hor		0.00				0.00			4.70	1.75	1	1
Q99613	Eukaryotic translation init	5.49	1.75	1	1	8.72	1.75	1	2	5.54	1.75	1	1
Q9BUJ2	Heterogeneous nuclear ri	5.37	1.75	1	1	4.76	1.75	1	1		0.00		
O15381	Nuclear valosin-containin	3.93	1.75	1	1	4.50	1.75	1	1		0.00		
P46459	Vesicle-fusing ATPase OS	4.77	1.75	1	1	4.37	1.75	1	1		0.00		
P52789	Hexokinase-2 OS=Homo sapiens GN=		0.00			5.38	1.74	1	1		0.00		
Q96P70	Importin-9 OS=Homo sap	5.16	1.73	1	1	4.75	1.73	1	1	5.59	1.73	1	1
Q9H2P0	Activity-dependent neuro	3.90	1.72	1	1		0.00			4.59	1.72	1	1
Q6P3W7	SCY1-like protein 2 OS=H	3.85	1.72	1	1		0.00				0.00		
P49747	Cartilage oligomeric matr	3.95	1.72	1	1		0.00				0.00		
Q6NSJ2	Pleckstrin homology-like	3.84	1.72	1	1		0.00				0.00		
Q01804	OTU domain-containing p	3.99	1.71	1	1		0.00				0.00		
Q9Y4F5	Centrosomal protein of 1	4.94	1.70	1	1		0.00				0.00		
Q6Y7W6	PERQ amino acid-rich with GYF domai		0.00				0.00			5.23	1.69	1	1
Q8IX07	Zinc finger protein ZFPM1 OS=Homo s		0.00				0.00			4.15	1.69	1	1
Q5JTC6	APC membrane recruitment protein 1		0.00			3.93	1.67	1	1		0.00		
P78524	Suppression of tumoriger	3.82	1.67	1	1		0.00				0.00		
Q9NYA4	Myotubularin-related protein 4 OS=Ho		0.00			3.98	1.67	1	1		0.00		
Q13200	26S proteasome non-ATPase regulato		0.00			4.05	1.65	1	1	5.18	1.65	1	1
P53992	Protein transport protein	4.17	1.65	1	1		0.00				0.00		
O95373	Importin-7 OS=Homo sapiens GN=IP(		0.00				0.00			5.08	1.64	1	1
Q15459	Splicing factor 3A subunit 1 OS=Homo		0.00				0.00			4.42	1.64	1	1
Q6UB35	Monofunctional C1-tetrahydrofolate sy		0.00				0.00			4.28	1.64	1	1
A0FGR8	Extended synaptotagmin-	4.16	1.63	1	1		0.00				0.00		
Q14676	Mediator of DNA damage checkpoint p		0.00			4.74	1.63	1	1		0.00		
Q9Y4E8	Ubiquitin carboxyl-termin	4.26	1.63	1	1		0.00				0.00		
O15020	Spectrin beta chain, non-	4.45	0.84	1	1	5.11	0.84	1	1	4.59	0.79	1	1
Q9Y6D5	Brefeldin A-inhibited guar	8.16	1.62	2	2		0.00			5.27	0.84	1	1

Q12788	Transducin beta-like protein 3 OS=Ho		0.00				0.00			4.54	1.61	1	1
Q9NQW6	Actin-binding protein anillin OS=Homc		0.00				0.00			4.53	1.60	1	1
Q5SNT6	WASH complex subunit FAM21B OS=H		0.00				0.00			5.03	1.60	1	1
Q9Y3P9	Rab GTPase-activating pr	4.36	1.59	1	1		0.00				0.00		
Q9NPG3	Ubinuclein-1 OS=Homo sapiens GN=U		0.00				0.00			4.15	1.59	1	1
Q9H3U1	Protein unc-45 homolog A	3.88	1.59	1	1		0.00				0.00		
Q5JRA6	Melanoma inhibitory activ	4.99	0.89	1	1	4.10	0.68	1	1		0.00		
Q9BZH6	WD repeat-containing protein 11 OS=		0.00				0.00			5.42	1.55	1	1
Q6PKG0	La-related protein 1 OS=	4.99	1.55	1	1		0.00			5.05	1.55	1	1
Q9BYX2	TBC1 domain family member 2A OS=I		0.00				0.00			4.31	1.51	1	1
Q9UPN9	E3 ubiquitin-protein ligase TRIM33 OS		0.00			4.13	1.51	1	1		0.00		
Q29RF7	Sister chromatid cohesion protein PDS		0.00			4.16	1.50	1	1	10.43	1.50	1	2
Q14324	Myosin-binding protein C, fast-type OS		0.00			3.91	1.49	1	1		0.00		
Q8IX12	Cell division cycle and ap	3.98	1.48	1	1		0.00				0.00		
Q9UHF7	Zinc finger transcription f	5.26	1.48	1	1		0.00			4.74	1.48	1	1
P27816	Microtubule-associated pı	3.95	1.48	1	1	3.95	1.48	1	1		0.00		
Q8N1F7	Nuclear pore complex protein Nup93 (		0.00			4.22	1.47	1	1		0.00		
P36776	Lon protease homolog, m	4.18	1.46	1	1		0.00				0.00		
O14974	Protein phosphatase 1 re	4.78	1.46	1	1		0.00				0.00		
O43592	Exportin-T OS=Homo sap	3.88	1.46	1	1		0.00				0.00		
Q9BSJ8	Extended synaptotagmin-	4.88	1.45	1	1		0.00			5.29	1.45	1	1
P30876	DNA-directed RNA polymerase II subu		0.00				0.00			4.65	1.45	1	1
P49588	Alanine--tRNA ligase, cytoplasmic OS=		0.00			4.01	1.45	1	1		0.00		
P11498	Pyruvate carboxylase, mit	4.86	1.44	1	1		0.00				0.00		
Q86VH2	Kinesin-like protein KIF27 OS=Homo s		0.00				0.00			4.54	1.43	1	1
O60264	SWI/SNF-related matrix-associated ac		0.00			4.10	1.43	1	1	4.15	1.43	1	1
Q8TDI7	Transmembrane channel-like protein 2		0.00				0.00			4.29	1.43	1	1
P82279	Protein crumbs homolog	4.00	1.42	1	1		0.00				0.00		
O15067	Phosphoribosylformylglyc	4.11	1.42	1	1		0.00				0.00		
O60610	Protein diaphanous homc	4.99	1.42	1	1	10.47	1.42	1	2		0.00		
Q6ZTY8	Putative uncharacterized protein C12o		0.00			4.23	1.42	1	1		0.00		
Q96KR1	Zinc finger RNA-binding protein OS=H		0.00				0.00			4.15	1.40	1	1
P49916	DNA ligase 3 OS=Homo s	4.41	1.39	1	1		0.00				0.00		
P69849	Nodal modulator 3 OS=Homo sapiens		0.00				0.00			4.49	1.39	1	1
Q9NTI5	Sister chromatid cohesion protein PDS		0.00				0.00			4.36	1.38	1	1
Q13009	T-lymphoma invasion and	3.98	1.38	1	1		0.00				0.00		
Q9Y2L1	Exosome complex exonuclease RRP44		0.00			4.06	1.36	1	1	4.37	1.36	1	1
P49746	Thrombospondin-3 OS=H	3.91	1.36	1	1		0.00				0.00		
Q15021	Condensin complex subunit 1 OS=Hor		0.00				0.00			4.35	1.36	1	1

Q9P217	Zinc finger SWIM domain-containing p		0.00				0.00			4.19	1.35	1	1
Q5JV73	FERM and PDZ domain-containing pro		0.00			5.15	1.33	1	1		0.00		
P51610	Host cell factor 1 OS=Homo sapiens G		0.00				0.00			5.52	1.33	1	1
Q9UGU0	Transcription factor 20 O	4.04	1.33	1	1		0.00				0.00		
O15084	Serine/threonine-protein phosphatase		0.00			4.08	1.33	1	1		0.00		
P08183	Multidrug resistance protein 1 OS=Ho		0.00			4.22	1.33	1	1		0.00		
Q5T1H1	Protein eyes shut homolo	4.90	0.76	1	1	4.00	0.57	1	1		0.00		
P19827	Inter-alpha-trypsin inhibit	3.93	1.32	1	1		0.00				0.00		
P20908	Collagen alpha-1(V) chair	3.88	1.31	1	1		0.00				0.00		
Q92614	Unconventional myosin-X	4.05	0.73	1	1	3.93	0.58	1	1		0.00		
Q96J66	ATP-binding cassette sub	3.90	1.30	1	1		0.00				0.00		
O95239	Chromosome-associated kinesin KIF4A		0.00			4.01	1.30	1	1		0.00		
P22102	Trifunctional purine biosy	5.07	1.29	1	1	4.70	1.29	1	1		0.00		
O60292	Signal-induced proliferati	4.05	1.29	1	1		0.00				0.00		
Q7Z3K3	Pogo transposable element with ZNF		0.00				0.00			4.83	1.28	1	1
Q93009	Ubiquitin carboxyl-terminal hydrolase		0.00				0.00			4.20	1.27	1	1
Q08211	ATP-dependent RNA helic	3.87	1.26	1	1		0.00			4.70	1.26	1	1
Q14126	Desmoglein-2 OS=Homo sapiens GN=		0.00			4.37	1.25	1	1	4.97	1.25	1	1
Q96KQ7	Histone-lysine N-methyltr	3.95	1.24	1	1		0.00				0.00		
A0AVT1	Ubiquitin-like modifier-activating enzy		0.00			3.97	1.24	1	1		0.00		
Q92616	Translational activator GC	8.86	1.24	2	2	4.32	0.60	1	1	4.35	0.64	1	1
Q9C0C9	E2/E3 hybrid ubiquitin-pr	4.91	1.24	1	1		0.00				0.00		
Q8IZH2	5'-3' exoribonuclease 1 OS=Homo sap		0.00				0.00			5.01	1.23	1	1
Q99700	Ataxin-2 OS=Homo sapie	3.82	1.22	1	1		0.00				0.00		
Q9Y4F4	Protein FAM179B OS=Ho	4.97	1.22	1	1		0.00				0.00		
O60271	C-Jun-amino-terminal kin	3.89	1.21	1	1		0.00				0.00		
O60486	Plexin-C1 OS=Homo sapi	3.88	1.21	1	1		0.00				0.00		
Q08378	Golgin subfamily A memb	4.51	1.20	1	1		0.00				0.00		
Q8TEQ6	Gem-associated protein 5	3.99	1.19	1	1	4.02	1.19	1	1	4.59	1.19	1	1
Q10570	Cleavage and polyadenyla	4.50	1.18	1	1		0.00				0.00		
Q9UM54	Unconventional myosin-V	4.72	1.16	1	1		0.00				0.00		
P12107	Collagen alpha-1(XI) chain OS=Homo		0.00			8.24	1.16	1	2		0.00		
P46379	Large proline-rich protein BAG6 OS=H		0.00				0.00			4.55	1.15	1	1
P41229	Lysine-specific demethyla	3.85	1.15	1	1		0.00				0.00		
O60313	Dynamin-like 120 kDa protein, mitoch		0.00			3.98	1.15	1	1		0.00		
O60841	Eukaryotic translation initiation factor		0.00				0.00			9.48	1.15	1	2
P25940	Collagen alpha-3(V) chain OS=Homo		0.00			4.03	1.15	1	1		0.00		
Q15648	Mediator of RNA polymer	4.10	1.14	1	1		0.00				0.00		
Q9Y4C1	Lysine-specific demethyla	3.81	1.14	1	1		0.00				0.00		

Q7L576	Cytoplasmic FMR1-intera	3.93	1.12	1	1		0.00				0.00		
Q9C0I4	Thrombospondin type-1 d	3.83	1.12	1	1		0.00				0.00		
P26358	DNA (cytosine-5)-methylt	4.56	1.11	1	1		0.00				0.00		
Q8WWZ4	ATP-binding cassette sub-family A me	0.00					0.00			4.14	1.10	1	1
Q8IZD2	Histone-lysine N-methyltransferase 2E	0.00					0.00			5.08	1.08	1	1
Q63HN8	E3 ubiquitin-protein ligas	6.25	0.42	1	1	8.61	0.61	2	2	4.68	0.33	1	1
Q9NSI6	Bromodomain and WD re	4.80	1.03	1	1		0.00			4.97	1.03	1	1
Q7Z4S6	Kinesin-like protein KIF21A OS=Homo	0.00				4.46	1.02	1	1		0.00		
Q5VU43	Myomegalin OS=Homo s	4.83	1.02	1	1		0.00				0.00		
A6NMZ7	Collagen alpha-6(VI) chai	4.29	1.02	1	1		0.00				0.00		
Q99250	Sodium channel protein type 2 subuni	0.00					0.00			4.15	1.00	1	1
Q9P260	LisH domain and HEAT repeat-contain	0.00					0.00			4.18	0.99	1	1
Q8WWQ0	PH-interacting protein OS	4.90	0.99	1	1		0.00			4.52	0.99	1	1
O15031	Plexin-B2 OS=Homo sapi	4.42	0.98	1	1		0.00				0.00		
Q9P1Z9	Coiled-coil domain-contai	4.00	0.91	1	1		0.00				0.00		
Q9H583	HEAT repeat-containing p	4.20	0.89	1	1		0.00				0.00		
P49792	E3 SUMO-protein ligase R	3.84	0.40	1	1		0.00			4.33	0.47	1	1
Q7Z6E9	E3 ubiquitin-protein ligas	3.85	0.84	1	1		0.00				0.00		
O75165	DnaJ homolog subfamily C member 1	0.00					0.00			4.37	0.80	1	1
Q8IWZ3	Ankyrin repeat and KH domain-contair	0.00					0.00			9.16	0.79	1	2
P42694	Probable helicase with zir	3.83	0.77	1	1		0.00				0.00		
P12259	Coagulation factor V OS=	5.51	0.76	1	1	5.38	0.76	1	1		0.00		
Q4AC94	C2 domain-containing protein 3 OS=H	0.00				3.94	0.76	1	1		0.00		
Q8TEM1	Nuclear pore membrane g	4.12	0.74	1	1		0.00				0.00		
Q15154	Pericentriolar material 1 protein OS=H	0.00				4.00	0.74	1	1		0.00		
Q96L96	Alpha-protein kinase 3 OS	3.92	0.73	1	1		0.00				0.00		
P49750	YLP motif-containing protein 1 OS=Ho	0.00					0.00			4.25	0.72	1	1
P42345	Serine/threonine-protein	4.27	0.71	1	1		0.00				0.00		
Q9UQ35	Serine/arginine repetitive matrix prote	0.00					0.00			4.63	0.65	1	1
Q9NYQ7	Cadherin EGF LAG seven-pass G-type	0.00					0.00			4.66	0.63	1	1
O60229	Kalirin OS=Homo sapiens GN=KALRN	0.00				3.93	0.60	1	1		0.00		
Q9NZJ4	Sacsin OS=Homo sapiens	5.37	0.59	1	1		0.00				0.00		
Q12955	Ankyrin-3 OS=Homo sapiens GN=ANK	0.00					0.00			5.31	0.59	1	1
P27708	CAD protein OS=Homo s	4.04	0.58	1	1		0.00				0.00		
P18583	Protein SON OS=Homo sapiens GN=S	0.00				4.23	0.58	1	1		0.00		
Q14789	Golgin subfamily B memb	5.44	0.55	1	1		0.00				0.00		
A2VEC9	SCO-spondin OS=Homo s	4.90	0.52	1	1		0.00				0.00		
Q96DT5	Dynein heavy chain 11, axonemal OS=	0.00				4.73	0.49	1	1		0.00		
P13611	Versican core protein OS=	4.07	0.47	1	1		0.00				0.00		

A5YKK6	CCR4-NOT transcription c	3.90	0.42	1	1		0.00				0.00		
Q07954	Prolow-density lipoprotein receptor-re	0.00			4.04	0.37	1	1		0.00		
Q9UPN3	Microtubule-actin cross-li	3.83	0.22	1	1		0.00				0.00		
Q8WZ42	Titin OS=Homo sapiens (	3.89	0.06	1	1		0.00				0.00		
					3031				2454				2769