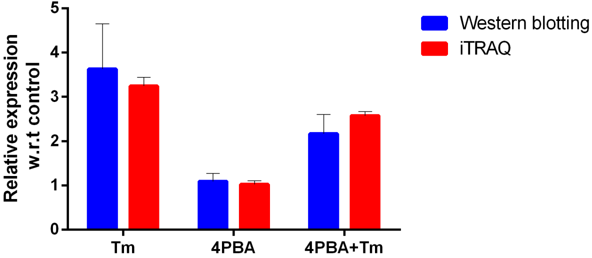
Supplementary Fig 1.

	Control	Tm	4-PBA	4-PBA+Tm
Experiment 1	114	115	116	117
Experiment 2	117	116	115	114
Experiment 3	115	114	117	116

Supplemantary Fig 2



Supplementary Table 1

		Biological Rep 1				Biological Rep 2				Biological Rep 3						
			Fold change w.r.t Control				Fold change w.r.t Control				Fold change w.r.t Control			% CV		
Acession ID	**Description**	**No. of peptides**	**Tm**	**4-PBA**	**4-PBA+Tm**	**No. of peptides**	**Tm**	**4-PBA**	**4-PBA+Tm**	**No. of peptides**	**Tm**	**4-PBA**	**4-PBA+Tm**	**Tm**	**4-PBA**	**4-PBA+Tm**
Q14204	Cytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens GN=DYNC1H1 PE=1 SV=5	195	1.04	1.01	1.04	171	0.96	0.98	0.97	165	1.03	1.02	1.03	4.27	2.06	3.81
P78527	DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=1 SV=3	185	0.93	1.01	0.96	149	0.93	0.99	0.94	139	0.93	0.97	0.95	0.48	2.03	0.92
Q60FE2	MYH9 variant protein OS=Homo sapiens GN=MYH9 PE=2 SV=1	151	1.16	0.99	1.17	138	1.19	1.01	1.20	137	1.15	1.00	1.19	1.49	0.97	1.46
Q60FE6	Filamin A OS=Homo sapiens GN=FLNA PE=2 SV=1	132	1.07	0.98	1.13	119	1.05	0.98	1.14	108	1.07	0.97	1.14	1.01	0.91	0.65
P49327	Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3	134	0.80	0.96	0.87	96	0.82	0.94	0.87	87	0.83	0.97	0.88	2.09	1.93	0.80
B2ZZ89	Spectrin beta non-erythrocytic 1 OS=Homo sapiens GN=SPTBN1 PE=2 SV=1	103	0.98	0.99	0.97	90	0.94	0.95	0.93	73	1.02	1.04	1.01	4.15	4.78	4.13
Q00610	Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC PE=1 SV=5	144	0.95	1.00	1.02	127	0.94	0.97	0.94	112	0.96	1.02	0.97	0.88	2.61	3.99
Q9Y490	Talin-1 OS=Homo sapiens GN=TLN1 PE=1 SV=3	114	1.03	0.96	1.08	121	0.96	0.91	0.99	81	1.03	1.02	1.03	3.98	5.81	4.13
E1NZA1	Peroxisome proliferator activated receptor interacting complex protein OS=Homo sapiens GN=PRIC295 PE=2 SV=1	85	0.94	1.02	0.95	65	0.96	1.03	0.98	67	0.93	0.97	0.94	1.53	3.19	2.52
P46821	Microtubule-associated protein 1B OS=Homo sapiens GN=MAP1B PE=1 SV=2	99	1.03	0.97	0.97	70	1.08	1.02	1.11	85	1.05	0.95	1.01	2.24	3.81	6.57
O75643	U5 small nuclear ribonucleoprotein 200 kDa helicase OS=Homo sapiens GN=SNRNP200 PE=1 SV=2	77	0.89	0.94	0.87	79	0.87	0.96	0.93	60	0.84	0.95	0.88	2.62	0.75	3.75
E5KNY5	Leucine-rich PPR-motif containing OS=Homo sapiens GN=LRPPRC PE=2 SV=1	93	0.94	1.02	0.98	91	0.93	1.00	0.94	82	0.93	0.98	0.97	0.62	2.01	2.07
Q6P2Q9	Pre-mRNA-processing-splicing factor 8 OS=Homo sapiens GN=PRPF8 PE=1 SV=2	72	0.88	0.95	0.94	61	0.92	0.97	0.94	64	0.92	1.01	0.95	2.63	3.01	1.13
Q09666	Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2	66	1.02	1.07	1.00	61	1.09	1.10	1.04	45	1.05	1.04	1.04	3.27	3.11	2.29
P08238	Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4	142	0.83	0.96	0.88	123	0.87	1.04	0.89	122	1.35	1.22	1.21	28.44	12.42	18.96
O75369	Filamin-B OS=Homo sapiens GN=FLNB PE=1 SV=2	73	1.02	1.01	1.02	67	1.04	1.02	1.09	57	1.03	1.04	1.13	0.61	1.73	5.36
P12814	Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 PE=1 SV=2	78	1.14	0.99	1.12	87	1.14	1.06	1.19	80	1.14	0.98	1.13	0.14	3.86	3.13
P13639	Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4	129	0.87	1.01	0.91	96	0.95	1.06	0.97	93	0.88	0.96	0.93	4.54	5.35	3.57
Q4LE64	NUMA1 variant protein (Fragment) OS=Homo sapiens GN=NUMA1 variant protein PE=2 SV=1	70	0.80	0.95	0.84	57	0.87	0.93	0.86	49	0.81	0.96	0.87	5.09	1.74	1.74
A4QPB0	IQ motif containing GTPase activating protein 1 OS=Homo sapiens GN=IQGAP1 PE=2 SV=1	65	1.03	1.00	1.10	57	0.95	0.93	0.99	50	0.99	1.03	1.01	4.18	5.34	5.85
P09874	Poly [ADP-ribose] polymerase 1 OS=Homo sapiens GN=PARP1 PE=1 SV=4	66	0.87	1.01	0.86	56	0.95	1.08	0.96	54	0.89	0.97	0.92	4.43	5.30	5.26

P14618	Pyruvate kinase PKM OS=Homo sapiens GN=PKM PE=1 SV=4	115	1.01	0.98	1.06	90	0.97	0.94	0.98	97	0.97	0.98	0.98	2.45	2.71	4.26
P07814	Bifunctional glutamate/proline--tRNA ligase OS=Homo sapiens GN=EPRS PE=1 SV=5	55	1.06	0.99	1.01	46	1.07	1.05	1.12	44	1.07	0.97	1.06	0.47	4.09	5.35
P22314	Ubiquitin-like modifier-activating enzyme 1 OS=Homo sapiens GN=UBA1 PE=1 SV=3	79	1.00	1.01	0.99	63	1.01	0.98	0.97	54	1.01	1.05	1.02	0.46	3.45	2.80
Q7Z6Z7	E3 ubiquitin-protein ligase HUWE1 OS=Homo sapiens GN=HUWE1 PE=1 SV=3	42	1.01	0.99	1.03	35	0.99	0.91	0.94	27	0.96	1.05	0.96	2.26	6.77	4.68
P11021	78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2	116	3.47	1.00	2.64	102	3.17	0.96	2.47	106	3.09	1.11	2.63	6.15	7.32	3.59
Q08211	ATP-dependent RNA helicase A OS=Homo sapiens GN=DHX9 PE=1 SV=4	63	0.89	0.96	0.97	61	0.91	0.94	0.95	59	0.94	0.96	0.95	2.91	1.34	1.03
B0V043	Valine--tRNA ligase OS=Homo sapiens GN=VARS PE=2 SV=1	50	0.93	1.04	0.99	31	1.01	1.05	0.98	27	0.93	1.00	0.93	5.08	2.87	3.22
P55072	Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4	66	1.03	1.03	1.05	66	1.02	0.97	1.01	57	1.03	1.03	1.06	0.60	3.41	2.65
Q9BQG0	Myb-binding protein 1A OS=Homo sapiens GN=MYBBP1A PE=1 SV=2	48	0.92	1.00	0.92	37	0.94	0.96	0.96	32	0.86	0.94	0.85	4.82	3.25	6.08
P30101	Protein disulfide-isomerase A3 OS=Homo sapiens GN=PDIA3 PE=1 SV=4	111	1.91	0.98	1.45	81	1.94	1.01	1.56	85	1.85	1.06	1.65	2.34	3.66	6.20
O00410	Importin-5 OS=Homo sapiens GN=IPO5 PE=1 SV=4	67	1.00	1.03	1.09	44	0.93	0.98	0.94	45	0.94	1.02	0.93	3.57	2.58	9.03
F8VPD4	DNA fragmentation factor subunit beta OS=Homo sapiens GN=CAD PE=2 SV=1	54	0.96	0.93	0.91	32	0.98	1.04	1.00	35	0.96	0.99	0.92	1.06	5.48	5.10
Q14315	Filamin-C OS=Homo sapiens GN=FLNC PE=1 SV=3	54	1.23	1.04	1.16	48	1.16	0.95	1.21	48	1.12	0.98	1.18	5.03	4.47	2.37
P53621	Coatomer subunit alpha OS=Homo sapiens GN=COPA PE=1 SV=2	43	1.02	1.03	1.03	46	1.04	1.07	1.06	40	1.05	0.96	1.04	1.16	5.60	1.45
P12270	Nucleoprotein TPR OS=Homo sapiens GN=TPR PE=1 SV=3	48	0.95	0.95	0.97	37	0.94	0.99	0.97	40	0.98	1.01	0.99	2.31	2.88	1.44
Q86UP2	Kinectin OS=Homo sapiens GN=KTN1 PE=1 SV=1	48	0.98	0.99	0.96	35	1.07	1.07	1.04	32	1.02	0.95	1.01	4.27	6.09	4.01
Q59G75	Isoleucyl-tRNA synthetase, cytoplasmic variant (Fragment) OS=Homo sapiens PE=2 SV=1	42	1.08	0.99	0.99	35	1.02	0.97	1.01	33	1.03	1.09	1.06	3.39	6.61	3.48
P11142	Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1	129	0.81	0.97	0.84	122	0.85	1.02	0.89	106	0.71	0.88	0.91	9.37	7.69	4.03
O75533	Splicing factor 3B subunit 1 OS=Homo sapiens GN=SF3B1 PE=1 SV=3	43	0.89	0.96	0.91	33	0.92	1.01	1.00	32	0.93	0.95	0.91	2.59	2.85	5.55
Q5SU16	Beta 5-tubulin OS=Homo sapiens GN=TUBB PE=2 SV=1	283	0.84	1.01	0.94	235	0.84	0.93	0.83	238	0.87	1.00	0.91	1.65	4.72	5.92
P08670	Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4	96	1.19	1.02	1.18	84	1.13	1.02	1.17	87	1.18	1.04	1.28	2.80	1.40	4.97
B3KX11	cDNA FLJ44436 fis, clone UTERU2019706, highly similar to T-complex protein 1 subunit gamma OS=Homo sapiens PE=2 SV=1	53	1.10	1.01	1.15	51	0.91	0.99	0.92	38	0.95	1.01	0.95	10.66	1.28	12.46
Q4LE58	EIF4G1 variant protein (Fragment) OS=Homo sapiens GN=EIF4G1 variant protein PE=2 SV=1	43	0.93	1.00	0.95	39	0.96	1.02	1.00	35	0.86	0.94	0.97	5.55	4.17	2.74
P34932	Heat shock 70 kDa protein 4 OS=Homo sapiens GN=HSPA4 PE=1 SV=4	56	0.93	0.99	0.98	43	0.93	0.98	0.95	33	0.92	1.03	0.97	0.61	2.62	1.89
O14980	Exportin-1 OS=Homo sapiens GN=XPO1 PE=1 SV=1	50	0.94	1.02	1.03	35	0.97	1.03	0.97	36	0.98	1.04	0.98	1.81	0.90	3.18

Q59EG8	Proteasome 26S non-ATPase subunit 2 variant (Fragment) OS=Homo sapiens PE=2 SV=1	54	0.93	0.96	0.98	40	1.02	1.01	1.02	34	0.98	0.96	0.96	4.89	2.73	3.29
Q4LE36	ACLY variant protein (Fragment) OS=Homo sapiens GN=ACLY variant protein PE=2 SV=1	39	0.91	0.93	0.92	35	1.00	1.01	0.98	47	0.92	0.99	0.96	5.29	3.99	3.39
Q6IAT1	GDI2 protein OS=Homo sapiens GN=GDI2 PE=2 SV=1	61	0.92	1.02	0.97	53	0.90	0.98	0.92	41	0.91	1.01	0.95	1.00	2.12	2.69
B4DLA6	cDNA FLJ54365, highly similar to DNA replication licensing factor MCM4 OS=Homo sapiens PE=2 SV=1	41	0.86	1.00	0.89	41	0.88	1.00	0.91	30	0.87	0.94	0.87	1.14	3.10	2.01
P13667	Protein disulfide-isomerase A4 OS=Homo sapiens GN=PDIA4 PE=1 SV=2	82	2.30	1.00	1.85	57	2.27	0.99	1.85	61	2.11	1.07	1.82	4.53	4.03	0.74
P53618	Coatomer subunit beta OS=Homo sapiens GN=COPB1 PE=1 SV=3	35	1.01	1.07	1.00	39	1.06	1.04	1.05	37	1.09	1.03	1.07	3.76	1.84	3.65
P13010	X-ray repair cross-complementing protein 5 OS=Homo sapiens GN=XRCC5 PE=1 SV=3	46	0.95	0.98	0.91	37	0.97	1.00	0.96	33	0.95	0.95	0.94	1.42	2.66	2.78
Q92598	Heat shock protein 105 kDa OS=Homo sapiens GN=HSPH1 PE=1 SV=1	55	0.86	0.97	0.87	43	0.86	1.02	0.90	37	0.91	1.01	0.92	3.31	2.93	2.98
P78371	T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=1 SV=4	55	0.93	1.05	0.94	55	0.98	1.00	0.94	51	0.98	1.00	0.99	2.86	3.27	3.02
Q6IBM8	U5-116KD protein OS=Homo sapiens GN=U5-116KD PE=2 SV=1	34	0.95	0.96	0.98	31	0.90	1.03	0.96	29	0.96	1.01	0.98	3.49	3.46	1.23
E7EX90	Dynactin subunit 1 OS=Homo sapiens GN=DCTN1 PE=2 SV=1	33	0.51	0.51	1.17	36	1.41	0.87	1.40	26	0.66	0.92	0.77	55.89	29.01	28.37
Q24JU4	Eukaryotic translation initiation factor 3 subunit A OS=Homo sapiens GN=EIF3A PE=2 SV=1	31	0.95	0.99	0.85	29	0.97	1.03	0.97	26	0.96	0.97	1.00	1.40	3.06	8.20
P55060	Exportin-2 OS=Homo sapiens GN=CSE1L PE=1 SV=3	42	0.93	1.01	1.01	40	0.91	0.99	0.94	37	0.93	1.08	0.97	1.42	4.61	3.57
B4DH52	cDNA FLJ55916, highly similar to General transcription factor II-I OS=Homo sapiens PE=2 SV=1	39	0.83	0.96	0.76	38	0.92	1.03	0.91	33	0.84	0.93	0.84	6.19	5.31	9.45
E9KL44	Epididymis tissue sperm binding protein Li 14m OS=Homo sapiens PE=2 SV=1	49	1.06	1.01	1.08	29	1.06	1.02	1.03	34	1.08	1.03	1.05	1.20	1.08	2.34
Q16531	DNA damage-binding protein 1 OS=Homo sapiens GN=DDB1 PE=1 SV=1	34	0.93	1.03	1.04	25	0.92	1.05	0.95	22	0.89	0.96	0.92	2.42	4.43	6.42
Q59GB4	Dihydropyrimidinase-like 2 variant (Fragment) OS=Homo sapiens PE=2 SV=1	70	0.86	0.98	0.87	56	0.93	0.92	0.98	55	0.92	0.95	0.94	4.17	3.11	5.87
P04406	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3	241	0.99	1.01	0.90	129	1.03	1.03	1.00	131	1.02	0.97	1.01	1.79	3.25	6.18
E9PDF6	Unconventional myosin-Ib OS=Homo sapiens GN=MYO1B PE=2 SV=1	37	0.91	0.94	0.81	29	0.92	0.97	0.92	25	0.96	0.98	0.95	2.81	2.16	8.36
Q92621	Nuclear pore complex protein Nup205 OS=Homo sapiens GN=NUP205 PE=1 SV=3	32	0.97	1.07	1.08	23	0.93	0.97	0.94	17	1.02	1.12	1.05	4.62	6.85	7.40
F8WCP6	Kinesin-like protein KIF21A OS=Homo sapiens GN=KIF21A PE=2 SV=1	38	0.90	0.93	0.91	33	0.90	0.98	0.93	19	0.88	1.04	0.93	1.72	5.64	0.95
O43707	Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2	89	1.11	0.96	1.11	79	1.08	0.94	1.07	89	1.10	1.02	1.10	1.30	4.05	2.10
P48643	T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=1 SV=1	53	0.91	0.98	0.87	52	1.05	1.12	1.03	36	0.96	0.99	0.97	7.37	7.33	7.99
P52701	DNA mismatch repair protein Msh6 OS=Homo sapiens GN=MSH6 PE=1 SV=2	31	0.89	0.98	0.95	27	0.84	0.95	0.85	29	0.86	1.10	0.91	2.56	7.93	5.79

P06733	Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2	140	0.97	1.03	0.95	126	1.01	1.01	1.00	108	0.99	1.01	1.04	1.94	1.22	4.49
P07237	Protein disulfide-isomerase OS=Homo sapiens GN=P4HB PE=1 SV=3	72	1.82	1.00	1.59	66	1.87	1.01	1.57	53	1.75	0.98	1.54	3.39	1.48	1.40
P17987	T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1 SV=1	44	0.94	1.02	1.02	41	0.86	0.93	0.92	36	0.92	1.01	0.96	4.59	5.34	5.60
Q14008	Cytoskeleton-associated protein 5 OS=Homo sapiens GN=CKAP5 PE=1 SV=3	30	0.89	1.01	0.87	23	1.07	1.12	1.08	27	0.92	0.97	0.97	9.97	7.48	10.52
P06576	ATP synthase subunit beta, mitochondrial OS=Homo sapiens GN=ATP5B PE=1 SV=3	82	1.42	1.02	1.33	74	1.39	0.91	1.15	79	1.40	1.05	1.27	1.26	7.45	7.27
E9PLK3	Puromycin-sensitive aminopeptidase OS=Homo sapiens GN=NPEPPS PE=2 SV=1	31	0.99	1.02	0.97	33	0.99	1.07	1.03	29	1.03	0.99	1.01	2.04	4.23	3.34
Q59HH3	Phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase isoform 1 variant (Fragment) OS=Homo sapiens PE=2 SV=1	36	0.96	1.01	0.93	33	0.97	1.03	0.94	30	0.96	0.95	0.98	0.82	3.90	3.05
P16615	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Homo sapiens GN=ATP2A2 PE=1 SV=1	33	1.18	0.96	1.10	33	1.22	1.08	1.17	23	1.12	0.98	1.09	4.49	6.30	4.11
D3DVC4	Nestin, isoform CRA_c OS=Homo sapiens GN=NES PE=3 SV=1	27	0.93	1.06	0.99	34	0.88	0.97	0.87	25	0.97	1.12	1.04	4.96	7.02	8.83
P33993	DNA replication licensing factor MCM7 OS=Homo sapiens GN=MCM7 PE=1 SV=4	33	0.86	1.08	0.83	32	0.91	1.15	0.91	32	0.84	1.00	0.90	4.04	6.99	4.88
Q59GX6	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3 variant (Fragment) OS=Homo sapiens PE=2 SV=1	34	0.88	0.95	0.86	26	0.81	0.88	0.87	32	0.91	0.96	0.94	5.78	4.46	5.29
P52272	Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens GN=HNRNPM PE=1 SV=3	50	0.85	0.96	0.90	45	0.86	0.95	0.88	39	0.85	0.98	0.91	0.43	1.29	1.74
P31939	Bifunctional purine biosynthesis protein PURH OS=Homo sapiens GN=ATIC PE=1 SV=3	34	0.95	1.02	1.02	42	0.88	0.97	0.93	33	0.97	1.03	1.02	5.00	3.30	5.46
Q5T4S7	E3 ubiquitin-protein ligase UBR4 OS=Homo sapiens GN=UBR4 PE=1 SV=1	27	1.19	1.01	1.19	22	0.93	0.96	1.00	16	1.05	1.03	1.02	12.44	3.62	9.76
Q00839	Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=6	56	0.94	0.98	0.89	43	1.01	1.03	1.02	45	0.94	0.96	0.99	4.15	3.79	7.36
P25705	ATP synthase subunit alpha, mitochondrial OS=Homo sapiens GN=ATP5A1 PE=1 SV=1	68	1.37	1.00	1.27	54	1.32	0.94	1.16	53	1.36	1.04	1.24	1.94	5.07	4.42
B4DGP8	Calnexin OS=Homo sapiens GN=CANX PE=2 SV=1	48	1.86	1.00	1.52	29	1.92	1.03	1.59	37	1.82	0.97	1.69	2.61	3.36	5.45
O43143	Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15 OS=Homo sapiens GN=DHX15 PE=1 SV=2	33	0.88	1.01	0.89	25	0.87	0.97	0.90	23	0.86	1.05	0.92	1.39	3.64	1.45
P49736	DNA replication licensing factor MCM2 OS=Homo sapiens GN=MCM2 PE=1 SV=4	36	0.79	1.01	0.85	31	0.74	0.95	0.80	29	0.85	1.00	0.87	6.81	3.79	4.45
B3KMC9	cDNA FLJ10711 fis, clone NT2RP3000917, highly similar to 5'-3' exoribonuclease 2 (EC 3.1.11.-) OS=Homo sapiens PE=2 SV=1	28	0.95	0.94	0.89	15	0.89	1.00	0.93	20	1.03	0.96	1.05	7.38	3.07	8.74

P49411	Elongation factor Tu, mitochondrial OS=Homo sapiens GN=TUFM PE=1 SV=2	36	0.99	1.00	0.98	31	0.96	0.96	0.97	28	0.94	0.96	0.98	2.46	2.20	0.57
Q53HS0	Glutaminyl-tRNA synthetase variant (Fragment) OS=Homo sapiens PE=2 SV=1	30	0.92	1.00	0.95	27	0.97	1.03	1.04	26	0.98	0.98	0.93	3.66	2.28	6.13
B3KMS0	Condensin complex subunit 1 OS=Homo sapiens PE=2 SV=1	26	0.87	0.87	0.84	24	1.00	1.06	0.98	17	1.00	0.95	0.89	7.72	9.95	7.56
P00338	L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2	67	0.90	1.02	0.98	36	0.97	1.02	1.00	53	0.93	0.95	0.97	3.77	3.92	1.71
H6VRG3	Keratin 1 OS=Homo sapiens GN=KRT1 PE=3 SV=1	54	1.52	1.47	2.53	32	6.05	0.94	2.59	14	1.60	1.23	1.74	84.85	22.08	20.75
P18206	Vinculin OS=Homo sapiens GN=VCL PE=1 SV=4	37	1.12	0.93	1.17	38	1.02	0.97	1.14	33	1.10	0.93	1.06	4.69	2.56	5.00
B7Z4V2	cDNA FLJ51907, highly similar to Stress-70 protein, mitochondrial OS=Homo sapiens PE=2 SV=1	40	0.97	0.99	1.01	41	0.97	0.93	0.94	38	0.99	1.02	1.04	1.08	4.97	4.94
P55884	Eukaryotic translation initiation factor 3 subunit B OS=Homo sapiens GN=EIF3B PE=1 SV=3	29	0.93	0.98	0.94	34	0.90	0.99	0.93	24	0.93	0.97	0.93	1.52	1.36	0.59
A8K492	cDNA FLJ76789, highly similar to Homo sapiens methionine-tRNA synthetase (MARS), mRNA OS=Homo sapiens PE=2 SV=1	31	1.00	0.99	0.98	28	1.01	0.94	0.97	23	0.91	0.98	0.95	5.52	2.29	1.33
B4DDF7	cDNA FLJ53296, highly similar to Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens PE=2 SV=1	40	0.95	1.07	1.01	33	0.99	1.02	0.96	33	0.94	0.99	0.98	2.86	3.84	2.58
B4DEM7	T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=2 SV=1	43	0.92	1.01	0.98	31	0.92	0.97	0.92	31	0.92	1.01	0.93	0.28	2.00	3.54
P12956	X-ray repair cross-complementing protein 6 OS=Homo sapiens GN=XRCC6 PE=1 SV=2	36	0.92	0.98	0.94	34	1.06	1.05	1.01	35	0.96	0.93	0.95	7.35	6.31	3.56
P29144	Tripeptidyl-peptidase 2 OS=Homo sapiens GN=TPP2 PE=1 SV=4	24	1.13	0.99	0.97	22	1.12	1.10	1.15	17	1.13	1.02	1.08	0.30	5.19	8.51
P00505	Aspartate aminotransferase, mitochondrial OS=Homo sapiens GN=GOT2 PE=1 SV=3	55	1.02	1.01	0.94	29	1.05	0.98	1.00	33	0.99	0.98	1.02	3.25	1.53	4.09
Q59FI4	Importin 4 variant (Fragment) OS=Homo sapiens PE=2 SV=1	30	1.03	1.06	1.15	25	0.82	0.92	0.83	19	1.02	1.09	0.97	12.46	8.48	16.31
J3KR97	Tubulin-specific chaperone D OS=Homo sapiens GN=TBCD PE=4 SV=1	30	0.96	1.01	1.08	20	0.95	1.04	0.97	19	0.96	1.01	0.89	1.06	1.65	9.72
D6REX3	Protein transport protein Sec31A OS=Homo sapiens GN=SEC31A PE=2 SV=1	33	1.08	1.02	1.09	18	1.08	1.02	1.07	24	1.06	0.96	1.08	1.17	3.34	1.05
Q96IH1	Fascin (Fragment) OS=Homo sapiens GN=FSCN1 PE=2 SV=1	56	0.88	1.02	0.90	47	0.85	0.93	0.85	43	0.89	1.04	0.89	2.51	6.17	3.33
Q53GX7	Threonyl-tRNA synthetase variant (Fragment) OS=Homo sapiens PE=2 SV=1	30	0.95	1.00	1.04	25	1.06	0.96	1.03	25	1.01	0.97	1.04	5.26	2.17	0.22
Q99460	26S proteasome non-ATPase regulatory subunit 1 OS=Homo sapiens GN=PSMD1 PE=1 SV=2	33	1.00	0.97	0.96	22	0.98	0.95	0.94	22	0.96	0.94	0.98	2.28	1.87	2.04
Q08J23	tRNA (cytosine(34)-C(5))-methyltransferase OS=Homo sapiens GN=NSUN2 PE=1 SV=2	30	1.01	0.99	1.06	22	0.93	0.99	0.92	23	0.96	1.08	0.99	3.82	5.21	6.95
P29401	Transketolase OS=Homo sapiens GN=TKT PE=1 SV=3	50	0.95	1.06	0.98	35	0.99	0.96	0.95	23	0.94	1.04	0.95	2.82	5.33	2.08
P35221	Catenin alpha-1 OS=Homo sapiens GN=CTNNA1 PE=1 SV=1	31	1.11	1.01	0.97	24	1.03	1.12	1.06	21	0.97	0.86	1.00	6.85	12.97	4.58

A3RJH1	ATP-dependent RNA helicase DDX1 OS=Homo sapiens GN=DDX1 PE=2 SV=1	32	0.88	0.99	0.90	27	0.91	0.99	0.93	24	0.94	0.98	0.94	2.91	0.53	2.50
Q5I6Y6	Lamin A/C transcript variant 1 OS=Homo sapiens GN=LMNA PE=2 SV=1	37	1.49	0.93	1.94	31	1.11	1.01	1.20	40	1.15	1.01	1.32	16.43	4.39	26.76
P54136	Arginine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=RARS PE=1 SV=2	30	0.93	0.97	0.91	30	0.98	1.03	0.97	27	0.98	1.01	1.07	2.64	2.95	8.44
J3KTA4	Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=3 SV=1	48	0.67	0.89	0.78	43	0.69	0.87	0.75	42	0.71	0.96	0.83	3.25	5.22	5.00
Q53HV2	Chaperonin containing TCP1, subunit 7 (Eta) variant (Fragment) OS=Homo sapiens PE=2 SV=1	33	0.93	0.99	0.96	34	0.97	0.97	0.94	32	0.92	1.00	0.95	3.03	1.62	1.07
P26038	Moesin OS=Homo sapiens GN=MSN PE=1 SV=3	26	1.16	0.98	1.01	32	1.00	0.91	1.00	25	1.12	0.97	1.12	7.65	4.07	6.65
P22626	Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens GN=HNRNPA2B1 PE=1 SV=2	44	1.17	1.01	1.10	40	1.15	0.98	1.05	30	1.11	0.96	1.14	2.86	2.61	3.88
O15240	Neurosecretory protein VGF OS=Homo sapiens GN=VGF PE=1 SV=2	61	1.24	1.09	1.49	30	1.25	1.01	1.38	37	1.31	1.17	1.13	2.95	7.33	13.63
F4ZW64	NF90a OS=Homo sapiens PE=2 SV=1	40	1.05	0.98	1.03	29	1.06	1.03	1.00	25	0.96	0.99	0.98	5.64	2.59	2.55
P20700	Lamin-B1 OS=Homo sapiens GN=LMNB1 PE=1 SV=2	30	0.84	0.96	0.84	21	0.93	0.99	0.91	20	0.87	1.00	0.95	4.92	2.21	6.26
Q9Y4G6	Talin-2 OS=Homo sapiens GN=TLN2 PE=1 SV=4	34	0.95	1.04	1.08	29	0.95	0.99	1.04	22	0.90	1.00	0.96	2.79	2.65	5.70
Q15046	Lysine--tRNA ligase OS=Homo sapiens GN=KARS PE=1 SV=3	34	0.98	1.01	0.98	31	1.08	1.08	1.09	28	0.95	0.99	0.98	6.56	4.40	6.14
O95373	Importin-7 OS=Homo sapiens GN=IPO7 PE=1 SV=1	26	0.94	1.00	1.00	26	0.97	0.98	0.95	19	0.90	0.98	0.92	3.73	1.10	4.43
Q8N5A0	Eukaryotic translation initiation factor 5B OS=Homo sapiens GN=EIF5B PE=2 SV=1	27	0.91	0.97	1.00	15	1.02	1.00	1.02	13	0.96	0.98	0.99	5.98	1.37	1.40
P49792	E3 SUMO-protein ligase RanBP2 OS=Homo sapiens GN=RANBP2 PE=1 SV=2	26	1.06	0.97	1.05	25	0.99	1.00	1.02	24	1.03	0.95	1.02	3.31	2.74	1.34
Q9Y678	Coatomer subunit gamma-1 OS=Homo sapiens GN=COPG1 PE=1 SV=1	25	1.12	1.04	1.08	20	1.13	1.09	1.13	16	1.14	1.05	1.06	0.83	2.59	3.35
E7EVA0	Microtubule-associated protein OS=Homo sapiens GN=MAP4 PE=2 SV=1	32	0.96	0.98	0.91	22	1.05	1.05	1.09	21	1.06	1.05	1.05	5.47	4.02	9.58
A8MXP9	Matrin-3 OS=Homo sapiens GN=MATR3 PE=2 SV=1	43	0.83	0.93	0.83	25	0.83	0.98	0.86	19	0.84	0.95	0.91	0.60	2.60	4.67
Q14566	DNA replication licensing factor MCM6 OS=Homo sapiens GN=MCM6 PE=1 SV=1	28	0.75	1.00	0.88	21	0.77	0.94	0.81	23	0.74	0.98	0.80	1.58	3.16	5.44
P35527	Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3	46	1.09	1.38	1.97	35	4.69	0.99	1.23	5	1.21	1.17	1.26	87.86	16.22	28.02
P00558	Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 PE=1 SV=3	41	0.97	1.05	0.97	38	1.04	1.07	1.01	44	0.99	1.00	1.03	3.90	3.36	2.81
Q14683	Structural maintenance of chromosomes protein 1A OS=Homo sapiens GN=SMC1A PE=1 SV=2	23	0.89	0.93	0.86	20	0.99	1.12	1.01	15	0.87	0.93	0.88	7.29	11.03	8.71
B3KTJ9	cDNA FLJ38393 fis, clone FEBRA2007212 OS=Homo sapiens PE=2 SV=1	23	0.89	0.94	1.04	21	0.90	0.89	0.93	21	0.98	1.04	1.00	5.25	7.93	5.71
Q16891-2	Isoform 2 of Mitochondrial inner membrane protein OS=Homo sapiens GN=IMMT	28	1.11	0.86	1.16	28	0.53	0.53	0.93	23	1.16	1.00	1.00	37.40	30.08	11.72

B1AHB0	MCM5 minichromosome maintenance deficient 5, cell division cycle 46 (S. cerevisiae), isoform CRA_a OS=Homo sapiens GN=MCM5 PE=2 SV=1	29	0.83	1.02	0.92	26	0.77	0.89	0.82	25	0.84	1.03	0.87	4.62	7.81	6.10
P41250	Glycine--tRNA ligase OS=Homo sapiens GN=GARS PE=1 SV=3	30	1.13	0.99	1.01	37	1.29	1.09	1.18	21	1.14	0.91	1.08	7.23	9.04	7.99
Q9NR30	Nucleolar RNA helicase 2 OS=Homo sapiens GN=DDX21 PE=1 SV=5	29	0.95	0.99	0.98	21	0.95	1.00	1.00	21	1.04	0.95	1.09	5.69	2.95	5.83
Q96QK1	Vacuolar protein sorting-associated protein 35 OS=Homo sapiens GN=VPS35 PE=1 SV=2	27	0.92	1.02	1.06	19	0.87	0.99	0.95	18	0.93	1.03	0.90	3.64	1.96	8.50
P11216	Glycogen phosphorylase, brain form OS=Homo sapiens GN=PYGB PE=1 SV=5	25	1.02	1.01	1.04	20	1.03	0.98	1.02	22	1.03	1.04	1.02	0.53	3.04	1.20
J3KN16	Proteasome-associated protein ECM29 homolog OS=Homo sapiens GN=KIAA0368 PE=4 SV=1	27	1.01	0.99	0.91	15	1.01	1.01	1.00	12	0.94	1.04	0.92	3.98	2.21	5.07
H7BXY3	Putative ATP-dependent RNA helicase DHX30 OS=Homo sapiens GN=DHX30 PE=2 SV=1	24	0.99	0.96	0.87	22	0.91	0.98	0.92	19	0.97	1.12	1.00	4.27	8.60	7.08
Q01813	6-phosphofructokinase type C OS=Homo sapiens GN=PFKP PE=1 SV=2	26	1.09	1.03	1.09	19	1.08	1.02	1.00	16	1.00	1.04	1.06	4.62	1.24	4.35
F8VQ10	Spliceosome RNA helicase DDX39B OS=Homo sapiens GN=DDX39B PE=2 SV=1	34	0.93	1.04	1.01	20	0.97	1.02	0.98	20	0.93	0.96	0.97	2.25	4.28	1.82
Q15393	Splicing factor 3B subunit 3 OS=Homo sapiens GN=SF3B3 PE=1 SV=4	22	0.92	0.91	1.02	23	0.86	0.88	0.86	20	0.89	0.96	0.92	3.52	4.40	8.64
B5BUB1	RuvB-like 1 (Fragment) OS=Homo sapiens GN=RUVBL1 PE=2 SV=1	31	1.00	1.00	0.94	24	0.94	0.99	0.94	26	1.04	0.97	0.99	5.33	1.89	2.73
P23528	Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3	73	0.91	1.05	0.91	63	1.01	1.15	1.00	71	0.91	0.90	0.94	6.09	12.07	5.00
Q59EC0	Adenosine deaminase, RNA-specific isoform ADAR-a variant (Fragment) OS=Homo sapiens PE=2 SV=1	27	0.93	0.88	1.05	27	1.03	1.04	1.00	19	0.96	0.95	1.01	5.18	8.28	2.75
Q53YD7	EEF1G protein OS=Homo sapiens GN=EEF1G PE=2 SV=1	43	1.04	1.02	1.10	33	1.08	0.96	1.03	29	1.12	1.03	1.15	3.56	3.56	5.47
Q86VX4	Structural maintenance of chromosomes 3 OS=Homo sapiens GN=SMC3 PE=2 SV=1	25	0.99	1.03	1.00	23	1.07	1.04	1.13	22	1.00	0.97	0.97	4.45	3.81	8.27
E7ESP9	Neurofilament medium polypeptide OS=Homo sapiens GN=NEFM PE=2 SV=1	29	0.82	0.95	0.84	25	0.88	0.93	0.90	19	0.92	1.01	0.97	5.24	4.53	7.13
G1UI16	SCC-112 protein, isoform CRA_b OS=Homo sapiens GN=PDS5A PE=2 SV=1	21	0.84	1.01	0.88	23	0.92	0.96	0.94	11	0.80	0.99	0.90	7.29	2.43	3.56
B7Z5S9	cDNA FLJ61359, highly similar to Adapter-relatedprotein complex 2 alpha- 2 subunit OS=Homo sapiens PE=2 SV=1	25	0.98	1.03	0.98	19	0.97	1.01	1.02	16	0.88	0.94	0.92	5.97	5.13	5.31
P04075	Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2	48	0.93	0.97	0.90	41	0.99	0.99	0.99	42	1.00	0.96	0.99	4.19	1.62	5.73
P62258	14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1	52	0.91	1.06	1.00	52	0.93	0.96	0.93	49	0.87	1.07	0.92	3.44	5.89	4.53
Q6IAW5	CALU protein OS=Homo sapiens GN=CALU PE=2 SV=1	43	1.49	0.99	1.32	31	1.73	1.10	1.48	32	1.57	1.02	1.44	7.64	5.75	5.75
Q92945	Far upstream element-binding protein 2 OS=Homo sapiens GN=KHSRP PE=1 SV=4	28	0.85	0.97	0.95	25	0.84	0.83	0.88	22	0.90	1.06	0.96	3.67	12.04	5.11
P36871	Phosphoglucomutase-1 OS=Homo sapiens GN=PGM1 PE=1 SV=3	25	0.96	1.08	1.09	25	1.00	1.05	1.06	15	0.99	1.07	1.02	2.09	1.34	3.43

P22234	Multifunctional protein ADE2 OS=Homo sapiens GN=PAICS PE=1 SV=3	38	0.96	1.06	0.99	32	0.92	0.97	0.92	29	0.96	1.02	0.96	2.09	4.25	3.81
B3KMR5	cDNA FLJ12434 fis, clone NT2RM1000037, highly similar to Homo sapiens KIAA0690 protein OS=Homo sapiens PE=2 SV=1	21	0.93	0.89	0.92	18	1.03	1.04	1.10	13	0.94	0.85	0.97	5.93	10.77	9.33
Q92878	DNA repair protein RAD50 OS=Homo sapiens GN=RAD50 PE=1 SV=1	22	0.91	0.94	0.87	21	0.97	1.02	0.97	9	1.04	0.91	0.95	6.79	6.12	5.61
J3KN36	Nodal modulator 3 OS=Homo sapiens GN=NOMO3 PE=4 SV=1	24	1.21	1.03	1.07	20	1.06	0.91	0.97	11	1.00	1.02	1.02	9.87	6.65	5.24
B4E2W0	3-ketoacyl-CoA thiolase OS=Homo sapiens GN=HADHB PE=2 SV=1	29	1.09	1.00	0.92	22	1.21	1.14	1.13	19	1.24	1.00	1.15	6.97	7.67	12.12
A8K5Y7	cDNA FLJ78655, highly similar to Homo sapiens exportin 5 (XPO5), mRNA OS=Homo sapiens PE=2 SV=1	25	1.09	0.99	1.24	19	0.98	0.97	0.99	23	0.92	0.98	0.98	8.52	1.13	13.88
B9EK54	RTL1 protein OS=Homo sapiens GN=RTL1 PE=2 SV=1	22	0.74	1.02	1.00	13	0.84	1.00	0.91	14	0.87	1.07	0.90	8.24	3.64	6.36
P50454	Serpin H1 OS=Homo sapiens GN=SERPINH1 PE=1 SV=2	40	1.45	0.94	1.31	32	1.49	1.02	1.41	36	1.40	0.95	1.32	3.02	4.52	4.24
Q14194-2	Isoform LCRMP-1 of Dihydropyrimidinase-related protein 1 OS=Homo sapiens GN=CRMP1	36	0.91	1.01	1.00	30	0.93	1.01	0.93	24	0.99	1.03	0.94	4.36	1.02	3.70
K7ELL7	Glucosidase 2 subunit beta OS=Homo sapiens GN=PRKCSH PE=4 SV=1	39	1.54	0.98	1.25	30	1.48	0.94	1.24	25	1.51	1.09	1.42	2.09	7.75	7.79
Q9BV61	TRAP1 protein (Fragment) OS=Homo sapiens GN=TRAP1 PE=2 SV=2	30	0.97	0.98	1.08	28	0.92	0.95	0.94	28	0.85	1.02	0.96	6.61	3.37	7.55
A8K639	Guanine monphosphate synthetase, isoform CRA_b OS=Homo sapiens GN=GMPS PE=2 SV=1	20	1.00	0.95	0.90	23	0.96	1.04	0.99	19	0.95	0.96	0.91	2.65	5.02	5.09
A8K6U7	cDNA FLJ78252, highly similar to Homo sapiens heterogeneous nuclear ribonucleoprotein U-like 1 (HNRPUL1), transcript variant 1, mRNA OS=Homo sapiens PE=2 SV=1	22	0.98	0.99	1.00	21	0.89	0.96	0.90	16	0.93	1.03	0.94	4.78	3.54	5.49
Q92900	Regulator of nonsense transcripts 1 OS=Homo sapiens GN=UPF1 PE=1 SV=2	20	0.99	1.05	1.12	18	0.99	0.96	1.00	15	1.01	0.95	1.07	1.22	5.53	5.61
P23381	Tryptophan--tRNA ligase, cytoplasmic OS=Homo sapiens GN=WARS PE=1 SV=2	30	1.25	0.95	1.09	24	1.31	0.98	1.17	24	1.18	0.97	1.11	5.31	1.47	3.92
O94906	Pre-mRNA-processing factor 6 OS=Homo sapiens GN=PRPF6 PE=1 SV=1	19	0.84	0.95	0.98	15	1.10	1.10	1.09	14	0.92	0.96	0.91	13.78	8.39	9.00
O95202	LETM1 and EF-hand domain-containing protein 1, mitochondrial OS=Homo sapiens GN=LETM1 PE=1 SV=1	35	1.08	0.94	0.98	16	1.05	0.98	1.00	20	1.05	0.96	1.06	1.82	2.41	4.25
P61978	Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK PE=1 SV=1	54	1.13	1.05	0.98	55	0.84	0.96	0.83	36	0.88	1.00	1.00	16.51	4.56	9.47
Q9HC35	Echinoderm microtubule-associated protein-like 4 OS=Homo sapiens GN=EML4 PE=1 SV=3	21	0.92	0.94	0.80	13	1.01	1.09	0.99	15	0.94	0.95	0.95	5.30	8.60	10.87
B2R5U3	EH-domain containing 1, isoform CRA_b OS=Homo sapiens GN=EHD1 PE=2 SV=1	22	1.20	1.04	1.07	20	0.98	0.99	1.03	17	1.09	0.96	1.06	10.20	4.41	2.05
P49321	Nuclear autoantigenic sperm protein OS=Homo sapiens GN=NASP PE=1 SV=2	36	0.79	1.03	0.87	27	0.93	1.07	0.89	25	0.84	0.96	0.91	8.77	5.55	2.42

P54578	Ubiquitin carboxyl-terminal hydrolase 14 OS=Homo sapiens GN=USP14 PE=1 SV=3	20	0.95	1.01	0.99	19	0.96	1.01	1.02	22	0.92	1.05	1.00	2.24	2.42	1.12
Q92973	Transportin-1 OS=Homo sapiens GN=TNPO1 PE=1 SV=2	24	0.98	1.03	1.00	21	0.94	1.04	0.98	19	1.04	0.98	1.07	5.28	2.79	4.95
P13645	Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6	30	1.65	1.09	1.92	25	1.36	1.00	1.89	12	1.08	1.19	1.35	20.71	8.87	18.51
P09960	Leukotriene A-4 hydrolase OS=Homo sapiens GN=LTA4H PE=1 SV=2	27	0.99	1.04	0.94	27	0.97	0.97	0.99	21	1.00	1.07	1.03	1.53	4.99	4.51
Q02952	A-kinase anchor protein 12 OS=Homo sapiens GN=AKAP12 PE=1 SV=4	23	1.07	1.05	0.97	12	1.33	1.20	1.32	10	1.05	0.94	0.92	13.67	12.13	20.57
P43246	DNA mismatch repair protein Msh2 OS=Homo sapiens GN=MSH2 PE=1 SV=1	23	0.83	1.01	0.91	19	0.83	0.89	0.86	20	0.87	1.06	0.90	3.05	8.60	2.81
Q9UBT2	SUMO-activating enzyme subunit 2 OS=Homo sapiens GN=UBA2 PE=1 SV=2	26	0.91	1.01	0.89	21	0.87	1.01	0.94	19	0.90	1.02	0.88	2.64	0.35	3.39
Q59G42	Eukaryotic translation initiation factor 4 gamma, 2 variant (Fragment) OS=Homo sapiens PE=2 SV=1	19	1.10	1.01	0.98	18	0.93	0.96	0.94	14	0.99	0.98	1.01	8.73	2.34	3.53
Q09161	Nuclear cap-binding protein subunit 1 OS=Homo sapiens GN=NCBP1 PE=1 SV=1	22	0.93	1.02	0.97	17	1.03	0.96	0.93	18	1.02	1.02	0.95	5.77	3.66	2.23
P12277	Creatine kinase B-type OS=Homo sapiens GN=CKB PE=1 SV=1	44	0.88	1.06	0.98	45	0.82	1.00	0.88	31	0.86	1.10	0.91	3.34	5.08	5.75
A0AVT1	Ubiquitin-like modifier-activating enzyme 6 OS=Homo sapiens GN=UBA6 PE=1 SV=1	22	1.14	1.07	1.00	16	1.01	1.09	1.06	9	1.07	1.08	0.99	6.23	0.72	4.02
O00231	26S proteasome non-ATPase regulatory subunit 11 OS=Homo sapiens GN=PSMD11 PE=1 SV=3	24	1.04	1.03	1.05	22	1.01	1.00	0.98	22	0.99	0.98	0.98	2.14	2.53	4.21
O43175	D-3-phosphoglycerate dehydrogenase OS=Homo sapiens GN=PHGDH PE=1 SV=4	31	1.07	0.98	1.00	23	1.04	1.06	1.03	18	1.12	1.13	1.05	4.08	7.37	2.42
P28838	Cytosol aminopeptidase OS=Homo sapiens GN=LAP3 PE=1 SV=3	25	1.04	1.01	1.03	16	1.02	0.95	1.01	20	1.04	1.03	1.05	1.32	4.15	1.93
Q9H4A4	Aminopeptidase B OS=Homo sapiens GN=RNPEP PE=1 SV=2	21	1.00	1.02	1.08	19	1.00	0.99	1.06	20	1.06	1.06	1.07	3.59	3.40	1.13
Q02790	Peptidyl-prolyl cis-trans isomerase FKBP4 OS=Homo sapiens GN=FKBP4 PE=1 SV=3	30	0.90	1.04	0.90	27	1.02	1.03	1.00	25	0.92	0.94	0.93	6.79	5.55	5.47
P54577	Tyrosine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=YARS PE=1 SV=4	25	1.14	1.06	1.09	22	1.17	0.98	1.10	21	1.14	0.99	1.07	1.41	4.48	1.45
Q9BSV4	SFPQ protein (Fragment) OS=Homo sapiens GN=SFPQ PE=2 SV=2	35	0.85	0.98	0.86	35	0.85	0.92	0.88	27	0.84	1.01	0.90	0.83	4.39	2.38
P52948	Nuclear pore complex protein Nup98-Nup96 OS=Homo sapiens GN=NUP98 PE=1 SV=4	19	0.87	0.91	0.78	15	0.95	1.06	0.98	12	0.97	0.91	1.01	5.96	8.96	13.47
P21281	V-type proton ATPase subunit B, brain isoform OS=Homo sapiens GN=ATP6V1B2 PE=1 SV=3	30	0.96	0.96	1.08	28	0.93	0.91	0.93	19	0.96	1.06	1.02	2.13	7.47	7.66
O94826	Mitochondrial import receptor subunit TOM70 OS=Homo sapiens GN=TOMM70A PE=1 SV=1	29	1.14	0.94	1.09	20	1.22	0.98	1.19	18	1.17	0.98	1.12	3.56	2.84	4.45
P61158	Actin-related protein 3 OS=Homo sapiens GN=ACTR3 PE=1 SV=3	30	1.05	1.04	1.12	18	1.00	1.03	1.01	17	0.98	0.98	1.00	3.98	3.08	6.21
P09172	Dopamine beta-hydroxylase OS=Homo sapiens GN=DBH PE=1 SV=3	30	0.91	0.96	1.10	19	0.94	0.96	1.00	24	0.91	0.93	1.00	2.18	2.01	5.48
Q92896	Golgi apparatus protein 1 OS=Homo sapiens GN=GLG1 PE=1 SV=2	21	1.21	1.00	1.17	16	1.09	0.95	1.04	15	1.12	1.10	1.09	5.21	7.47	6.26

Q5U077	L-lactate dehydrogenase OS=Homo sapiens GN=LDHB PE=2 SV=1	45	0.84	1.06	0.91	42	0.93	1.04	0.89	32	0.87	1.06	0.94	5.22	0.87	2.66
B4DZI8	Coatomer protein complex, subunit beta 2 (Beta prime), isoform CRA_b OS=Homo sapiens GN=COPB2 PE=2 SV=1	18	1.00	0.93	0.91	17	1.13	1.04	1.09	16	1.12	1.00	0.99	6.27	5.36	9.22
F4ZW62	NF45 OS=Homo sapiens PE=2 SV=1	23	0.97	0.99	0.94	22	1.02	1.05	0.97	22	0.94	0.99	0.98	3.93	3.26	2.41
Q9UBF2	Coatomer subunit gamma-2 OS=Homo sapiens GN=COPG2 PE=1 SV=1	23	1.00	1.06	0.95	18	1.00	1.07	1.01	18	0.98	0.94	0.93	0.92	7.43	4.37
P08758	Annexin A5 OS=Homo sapiens GN=ANXA5 PE=1 SV=2	32	1.44	1.03	1.23	24	1.40	1.00	1.31	24	1.34	0.93	1.26	3.69	4.82	2.98
P07355	Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2	44	1.50	1.13	1.44	33	1.43	1.02	1.29	27	1.44	1.15	1.42	2.52	6.28	6.01
Q2TB59	Nicotinamide nucleotide transhydrogenase OS=Homo sapiens GN=NNT PE=2 SV=1	21	1.20	0.96	1.18	13	1.09	0.93	1.10	9	1.07	1.06	1.04	6.27	7.03	6.60
Q63HR1	Putative uncharacterized protein DKFZp686P17171 OS=Homo sapiens GN=DKFZp686P17171 PE=2 SV=1	24	0.94	0.97	0.87	18	0.96	1.04	0.94	19	0.91	0.99	0.95	2.75	3.45	4.66
P48735	Isocitrate dehydrogenase [NADP], mitochondrial OS=Homo sapiens GN=IDH2 PE=1 SV=2	26	0.84	1.03	0.88	21	0.91	1.05	0.90	20	0.84	0.98	0.89	4.49	3.58	1.28
B3KWV6	cDNA FLJ43948 fis, clone TESTI4014924, highly similar to Homo sapiens cytoplasmic FMR1 interacting protein 1 (CYFIP1), transcript variant 1, mRNA OS=Homo sapiens PE=2 SV=1	20	1.02	1.11	0.93	14	0.93	0.98	0.94	20	1.00	1.08	0.92	4.80	6.65	0.74
Q9UIG0	Tyrosine-protein kinase BAZ1B OS=Homo sapiens GN=BAZ1B PE=1 SV=2	17	1.01	1.07	1.02	15	1.07	1.05	1.08	16	0.99	1.03	0.98	3.72	1.89	5.07
P54886	Delta-1-pyrroline-5-carboxylate synthase OS=Homo sapiens GN=ALDH18A1 PE=1 SV=2	22	0.86	0.95	1.10	20	0.87	0.93	0.89	18	0.98	1.22	0.99	7.25	15.47	10.26
G3XAI2	Laminin subunit beta-1 OS=Homo sapiens GN=LAMB1 PE=2 SV=1	18	1.40	0.92	1.26	21	1.40	0.95	1.33	12	1.32	1.01	1.24	3.28	4.63	3.86
P12081	Histidine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=HARS PE=1 SV=2	21	0.92	0.95	0.89	17	1.00	1.05	1.00	18	1.00	1.01	1.03	4.97	4.90	7.38
A8K525	cDNA FLJ76817, highly similar to Homo sapiens non-POU domain containing, octamer-binding (NONO), mRNA OS=Homo sapiens PE=2 SV=1	41	0.77	0.96	0.89	39	0.73	0.90	0.81	33	0.82	1.07	0.93	6.24	8.64	6.82
Q8N1F7	Nuclear pore complex protein Nup93 OS=Homo sapiens GN=NUP93 PE=1 SV=2	20	1.18	0.95	1.31	18	1.08	0.85	1.04	15	1.16	1.12	1.16	4.44	14.35	11.67
Q0D2N8	SARM1 protein (Fragment) OS=Homo sapiens GN=SARM1 PE=2 SV=1	18	1.00	0.97	1.05	19	1.05	1.00	1.02	16	0.92	0.95	0.91	6.50	2.79	7.54
P11498	Pyruvate carboxylase, mitochondrial OS=Homo sapiens GN=PC PE=1 SV=2	19	1.05	1.04	0.96	15	1.15	1.12	0.96	18	1.04	1.11	0.98	5.65	3.95	1.49
P26599	Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 PE=1 SV=1	61	1.44	1.69	0.94	46	0.91	1.04	0.96	31	0.86	0.90	0.92	29.79	34.78	1.69
J3KQ32	Obg-like ATPase 1 OS=Homo sapiens GN=OLA1 PE=4 SV=1	25	0.95	0.97	0.78	24	1.15	1.22	1.13	18	1.03	0.95	0.94	9.47	14.58	18.56
E9KL48	Epididymis tissue sperm binding protein Li 18mP OS=Homo sapiens GN=GLUD1 PE=2 SV=1	21	1.13	0.97	1.07	17	1.11	0.97	1.06	18	1.21	0.99	1.11	4.64	0.95	2.72

A8K2M0	Proteasome (Prosome, macropain) 26S subunit, ATPase, 4, isoform CRA_b OS=Homo sapiens GN=PSMC4 PE=2 SV=1	21	0.98	1.00	1.02	19	1.05	1.08	1.04	16	0.98	0.98	1.05	4.44	5.28	1.44
B0QY89	Eukaryotic translation initiation factor 3 subunit L OS=Homo sapiens GN=EIF3L PE=2 SV=1	17	0.91	0.99	0.91	19	1.01	1.08	0.96	18	0.92	0.99	0.89	6.15	5.27	3.87
G8JLB6	Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=2 SV=1	48	0.81	0.91	0.90	36	0.88	0.96	0.85	26	0.83	0.92	0.85	4.25	3.10	3.33
Q5HYG8	Putative uncharacterized protein DKFZp686P09201 OS=Homo sapiens GN=DKFZp686P09201 PE=2 SV=1	24	1.01	0.95	1.08	19	0.99	0.94	1.00	24	1.06	1.01	1.01	3.48	3.81	4.22
A8K6S3	cDNA FLJ77570, highly similar to Homo sapiens pleckstrin homology domain containing, family C (with FERM domain) member 1 (PLEKHC1), mRNA OS=Homo sapiens PE=2 SV=1	18	1.05	1.04	1.02	14	1.09	1.05	1.06	12	1.03	0.96	1.02	2.73	4.73	2.29
P62424	60S ribosomal protein L7a OS=Homo sapiens GN=RPL7A PE=1 SV=2	24	1.05	0.97	0.88	20	1.18	1.04	1.08	17	1.03	0.98	1.02	7.80	3.58	10.68
Q9UHD8-5	Isoform 5 of Septin-9 OS=Homo sapiens GN=SEPT9	22	0.96	0.97	0.94	21	0.85	0.97	0.88	23	0.90	1.04	0.92	6.28	4.32	3.43
P42285	Superkiller viralicidic activity 2-like 2 OS=Homo sapiens GN=SKIV2L2 PE=1 SV=3	21	0.90	0.94	0.90	19	0.97	1.07	1.01	17	0.86	0.92	0.89	6.19	8.35	7.11
P62195	26S protease regulatory subunit 8 OS=Homo sapiens GN=PSMC5 PE=1 SV=1	20	0.92	0.98	0.93	14	0.97	1.01	0.99	14	0.94	1.02	0.94	2.89	2.04	3.54
R4GNH3	26S protease regulatory subunit 6A OS=Homo sapiens GN=PSMC3 PE=4 SV=1	22	0.93	0.99	1.00	22	0.97	1.01	0.92	21	0.96	1.04	1.04	2.22	2.23	5.90
A8K401	Prohibitin, isoform CRA_a OS=Homo sapiens GN=PHB PE=2 SV=1	39	1.50	0.96	1.26	34	1.37	0.91	1.19	32	1.45	1.01	1.27	4.40	5.33	3.43
B2RB23	cDNA, FLJ95265, highly similar to Homo sapiens acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase) (ACAA2), nuclear gene encoding mitochondrial protein, mRNA OS=Homo sapiens PE=2 SV=1	25	1.03	1.09	1.13	28	0.94	0.99	0.99	18	0.95	0.95	1.02	4.83	7.30	7.18
A8MV58	Drebrin OS=Homo sapiens GN=DBN1 PE=2 SV=1	24	0.86	1.01	0.91	28	0.95	0.95	0.93	16	0.91	1.05	1.00	4.78	5.23	4.88
Q6MZS5	Putative uncharacterized protein DKFZp686A13234 (Fragment) OS=Homo sapiens GN=DKFZp686A13234 PE=2 SV=1	23	1.74	0.73	1.35	25	1.27	1.19	1.35	21	1.05	0.76	0.73	26.08	28.32	31.51
Q15459	Splicing factor 3A subunit 1 OS=Homo sapiens GN=SF3A1 PE=1 SV=1	18	0.99	1.06	0.97	18	0.94	1.08	0.98	21	1.03	0.97	0.99	4.30	5.79	0.86
P31150	Rab GDP dissociation inhibitor alpha OS=Homo sapiens GN=GDI1 PE=1 SV=2	54	0.95	0.98	1.08	49	1.00	1.00	0.97	37	0.91	0.97	0.92	4.53	1.68	8.39
Q9Y230	RuvB-like 2 OS=Homo sapiens GN=RUVBL2 PE=1 SV=3	32	0.93	1.00	0.99	23	0.89	0.92	0.86	19	0.95	1.11	0.94	3.27	9.25	7.17
B4DJV2	Citrate synthase OS=Homo sapiens GN=CS PE=2 SV=1	30	0.94	0.99	0.98	19	1.02	1.02	1.02	15	1.02	1.01	1.01	4.46	1.80	2.29
P14868	Aspartate--tRNA ligase, cytoplasmic OS=Homo sapiens GN=DARS PE=1 SV=2	19	0.94	1.00	1.09	19	0.91	0.97	0.96	18	0.97	1.09	0.97	3.16	5.75	7.24
O94925-3	Isoform 3 of Glutaminase kidney isoform, mitochondrial OS=Homo sapiens GN=GLS	23	0.93	1.02	1.13	19	0.88	0.99	0.97	15	0.89	1.28	1.05	3.10	14.75	7.81

Q59ER5	WD repeat-containing protein 1 isoform 1 variant (Fragment) OS=Homo sapiens PE=2 SV=1	25	0.98	0.96	1.04	15	1.15	1.08	1.09	22	1.04	0.97	1.12	7.98	6.75	3.86
D3DPU2	Adenylyl cyclase-associated protein OS=Homo sapiens GN=CAP1 PE=3 SV=1	30	1.00	1.08	1.04	21	1.01	1.00	1.01	22	1.03	1.08	1.05	1.83	4.54	1.89
Q8TEM1	Nuclear pore membrane glycoprotein 210 OS=Homo sapiens GN=NUP210 PE=1 SV=3	23	0.86	1.03	1.01	12	0.87	0.90	0.86	10	0.96	1.08	0.99	6.18	9.37	8.37
Q6IBS9	HADH2 protein OS=Homo sapiens GN=HADH2 PE=2 SV=1	31	0.96	0.99	0.96	17	0.84	0.84	0.88	23	1.02	1.01	0.96	9.45	10.09	5.16
Q9UQ35	Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2	17	1.03	0.94	0.96	10	0.84	0.85	0.93	8	0.90	1.09	1.01	10.19	12.75	4.37
P30041	Peroxiredoxin-6 OS=Homo sapiens GN=PRDX6 PE=1 SV=3	29	1.05	1.01	1.08	28	1.17	1.09	1.17	26	1.09	0.94	1.06	5.61	7.47	5.18
Q14103	Heterogeneous nuclear ribonucleoprotein D0 OS=Homo sapiens GN=HNRNPD PE=1 SV=1	26	0.95	0.99	0.77	15	1.12	1.19	1.07	23	0.97	0.86	0.95	9.14	16.10	15.96
B4DQJ8	6-phosphogluconate dehydrogenase, decarboxylating OS=Homo sapiens GN=PGD PE=2 SV=1	28	0.92	1.04	1.03	32	0.92	0.96	0.86	27	0.94	1.10	1.00	1.29	6.79	9.07
Q05193	Dynamin-1 OS=Homo sapiens GN=DNM1 PE=1 SV=2	18	1.08	1.30	1.25	18	0.83	0.85	0.90	15	0.90	0.92	0.94	13.56	23.78	18.30
A8K486	Peptidyl-prolyl cis-trans isomerase OS=Homo sapiens PE=2 SV=1	116	0.90	1.02	0.82	94	0.91	1.04	0.84	89	0.92	1.12	0.93	1.39	5.04	6.58
Q8WXH0	Nesprin-2 OS=Homo sapiens GN=SYNE2 PE=1 SV=3	19	0.96	0.97	0.97	21	0.98	1.03	0.94	25	0.86	0.97	0.93	7.01	3.34	2.12
O43776	Asparagine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=NARS PE=1 SV=1	18	1.00	1.02	1.26	23	1.01	0.88	0.98	20	1.01	1.09	0.98	0.52	10.46	15.25
F5H2S7	Dynactin subunit 2 OS=Homo sapiens GN=DCTN2 PE=2 SV=1	20	1.01	1.00	1.01	21	0.89	0.95	0.94	17	0.96	1.13	0.97	6.43	9.16	3.50
Q14166	Tubulin--tyrosine ligase-like protein 12 OS=Homo sapiens GN=TTLL12 PE=1 SV=2	20	0.95	0.97	0.98	11	1.08	1.03	0.96	14	1.11	0.96	1.03	7.99	3.55	3.46
B4DV28	cDNA FLJ54170, highly similar to Cytosolic nonspecific dipeptidase OS=Homo sapiens PE=2 SV=1	17	0.99	1.00	1.10	13	0.98	1.06	1.04	16	1.03	1.01	1.08	2.89	2.80	2.89
P60174	Triosephosphate isomerase OS=Homo sapiens GN=TPI1 PE=1 SV=3	64	0.97	1.06	0.92	45	1.09	1.08	1.02	45	0.99	0.94	0.99	6.10	7.79	5.54
P49756	RNA-binding protein 25 OS=Homo sapiens GN=RBM25 PE=1 SV=3	16	0.88	0.98	0.78	8	0.98	1.10	1.05	13	1.01	0.90	0.95	6.97	9.94	14.32
Q96P70	Importin-9 OS=Homo sapiens GN=IPO9 PE=1 SV=3	18	0.99	0.99	1.04	15	0.97	1.00	1.00	10	0.87	0.94	0.82	6.82	2.97	12.18
Q8WUM0	Nuclear pore complex protein Nup133 OS=Homo sapiens GN=NUP133 PE=1 SV=2	19	1.03	1.03	1.02	14	0.83	0.87	0.92	11	1.01	1.04	1.02	11.16	9.72	5.97
O60264	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5 OS=Homo sapiens GN=SMARCA5 PE=1 SV=1	17	0.94	1.05	0.89	19	0.97	1.00	0.99	20	0.99	1.04	1.05	2.96	2.31	7.94
P23526	Adenosylhomocysteinase OS=Homo sapiens GN=AHCY PE=1 SV=4	23	0.90	1.04	0.99	23	1.01	1.12	0.99	19	0.95	1.04	1.00	5.69	4.37	0.85
Q9Y2A7	Nck-associated protein 1 OS=Homo sapiens GN=NCKAP1 PE=1 SV=1	16	1.10	1.04	1.04	14	1.00	1.13	0.97	16	0.88	1.00	0.88	11.07	6.29	8.50
Q9Y3I0	tRNA-splicing ligase RtcB homolog OS=Homo sapiens GN=C22orf28 PE=1 SV=1	22	0.98	1.01	1.01	23	0.94	1.03	0.97	16	0.95	1.00	1.00	2.16	1.33	2.18
Q9UHB9	Signal recognition particle subunit SRP68 OS=Homo sapiens GN=SRP68 PE=1 SV=2	17	1.02	1.04	1.10	16	1.12	0.96	1.04	13	1.00	1.05	1.00	5.92	5.00	4.72

Q9NYF8	Bcl-2-associated transcription factor 1 OS=Homo sapiens GN=BCLAF1 PE=1 SV=2	23	0.88	0.95	0.91	14	0.97	1.01	0.96	9	0.96	0.97	0.95	4.98	3.49	3.07
P38919	Eukaryotic initiation factor 4A-III OS=Homo sapiens GN=EIF4A3 PE=1 SV=4	27	0.91	0.96	0.90	26	0.96	0.98	0.97	20	0.99	0.94	0.98	4.23	2.42	4.42
P23368	NAD-dependent malic enzyme, mitochondrial OS=Homo sapiens GN=ME2 PE=1 SV=1	24	0.92	0.99	1.11	18	0.99	0.98	1.02	14	0.92	0.98	0.97	3.84	0.79	7.02
Q53GX6	Nucleobindin 1 variant (Fragment) OS=Homo sapiens PE=2 SV=1	17	1.24	1.00	1.14	16	1.10	0.94	1.07	16	1.11	0.92	1.00	6.68	4.48	6.68
P49750-4	Isoform 4 of YLP motif-containing protein 1 OS=Homo sapiens GN=YLPM1	19	0.98	1.04	0.87	11	1.00	1.02	0.99	5	1.02	0.94	0.98	1.93	5.40	6.78
E5KRK5	Mitochondrial NADH-ubiquinone oxidoreductase 75 kDa subunit OS=Homo sapiens GN=NDUFS1 PE=2 SV=1	19	1.02	1.02	0.99	12	1.03	0.82	0.95	17	0.99	0.99	1.04	1.98	11.19	4.39
B4E0X8	cDNA FLJ61021, highly similar to Far upstream element-binding protein 1 OS=Homo sapiens PE=2 SV=1	24	0.92	0.95	0.95	21	0.83	0.94	0.86	22	0.89	1.03	0.90	5.03	4.70	4.54
B2RAQ8	cDNA, FLJ95058, highly similar to Homo sapiens carnitine palmitoyltransferase 1A (liver) (CPT1A),nuclear gene encoding mitochondrial protein, mRNA OS=Homo sapiens PE=2 SV=1	20	1.29	1.07	1.15	18	1.18	0.99	1.09	13	1.11	1.00	0.98	7.53	4.34	8.02
J3KPX7	Prohibitin-2 OS=Homo sapiens GN=PHB2 PE=4 SV=1	27	1.45	1.00	1.33	33	1.34	0.87	1.16	22	1.40	1.06	1.24	3.86	9.84	6.82
Q06210	Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 OS=Homo sapiens GN=GFPT1 PE=1 SV=3	20	1.19	1.15	1.22	13	1.03	0.95	0.97	10	1.04	0.90	1.00	8.45	13.12	12.96
P21796	Voltage-dependent anion-selective channel protein 1 OS=Homo sapiens GN=VDAC1 PE=1 SV=2	25	1.38	1.01	1.20	32	1.24	0.99	1.12	22	1.16	0.95	1.17	8.82	3.37	3.37
Q5TZZ9	Annexin OS=Homo sapiens GN=ANXA1 PE=2 SV=1	21	1.41	0.97	1.37	17	1.47	0.93	1.44	12	1.41	1.01	1.39	2.61	4.30	2.73
O00232	26S proteasome non-ATPase regulatory subunit 12 OS=Homo sapiens GN=PSMD12 PE=1 SV=3	17	1.02	1.01	1.06	15	0.95	0.90	0.89	15	0.96	1.08	0.95	4.17	9.17	8.85
Q6AHZ7	Putative uncharacterized protein DKFZp686A111 OS=Homo sapiens GN=DKFZp686A111 PE=2 SV=1	15	1.01	0.90	0.87	15	0.97	0.94	0.91	9	1.08	0.97	0.99	5.53	3.52	6.38
F5H4G7	Importin subunit alpha OS=Homo sapiens GN=KPNA6 PE=2 SV=1	17	1.02	1.18	1.04	7	0.74	0.83	0.97	10	1.01	1.24	0.96	17.44	20.63	4.17
A6NHR9	Structural maintenance of chromosomes flexible hinge domain-containing protein 1 OS=Homo sapiens GN=SMCHD1 PE=1 SV=2	18	1.05	0.91	0.87	16	1.15	1.07	1.11	13	1.03	1.08	1.00	6.26	9.00	11.99
J9JID7	Lamin B2, isoform CRA_a OS=Homo sapiens GN=LMNB2 PE=3 SV=1	15	0.94	0.94	1.04	17	0.95	0.99	0.95	13	1.06	1.01	1.07	6.70	3.79	6.10
Q6FHV6	ENO2 protein OS=Homo sapiens GN=ENO2 PE=2 SV=1	57	0.92	1.01	0.90	49	0.98	1.04	0.99	41	0.97	1.01	0.99	3.13	1.75	5.27
P30084	Enoyl-CoA hydratase, mitochondrial OS=Homo sapiens GN=ECHS1 PE=1 SV=4	19	0.97	1.08	1.11	20	0.93	0.97	0.92	21	0.94	0.95	1.02	2.35	6.73	9.46
Q9Y2L1	Exosome complex exonuclease RRP44 OS=Homo sapiens GN=DIS3 PE=1 SV=2	16	1.02	1.03	1.11	21	0.85	0.90	0.85	12	0.93	0.97	0.99	9.18	6.51	13.40
B4DNJ6	Serine-threonine kinase receptor-associated protein OS=Homo sapiens GN=STRAP PE=2 SV=1	22	0.86	1.01	0.98	18	0.91	1.01	0.95	15	0.89	0.97	1.00	2.67	2.05	2.70

P11137	Microtubule-associated protein 2 OS=Homo sapiens GN=MAP2 PE=1 SV=4	17	0.80	0.94	0.94	12	1.13	1.07	1.05	8	0.95	0.88	0.99	17.04	10.26	5.63
Q8N766	ER membrane protein complex subunit 1 OS=Homo sapiens GN=EMC1 PE=1 SV=1	17	1.08	0.98	1.02	7	1.02	1.03	1.17	11	0.95	0.84	0.96	5.98	10.35	10.52
P31930	Cytochrome b-c1 complex subunit 1, mitochondrial OS=Homo sapiens GN=UQCRC1 PE=1 SV=3	20	1.22	0.95	1.13	23	1.25	0.95	1.12	22	1.27	0.99	1.16	1.79	2.29	1.76
E9KL35	Epididymis tissue sperm binding protein Li 3a OS=Homo sapiens PE=2 SV=1	28	0.96	0.99	1.02	27	0.97	1.00	0.97	21	0.96	1.02	1.00	0.31	1.38	2.95
Q15181	Inorganic pyrophosphatase OS=Homo sapiens GN=PPA1 PE=1 SV=2	33	0.88	1.02	0.88	17	1.02	1.17	1.04	13	0.93	0.85	0.95	7.61	15.66	8.18
P26196	Probable ATP-dependent RNA helicase DDX6 OS=Homo sapiens GN=DDX6 PE=1 SV=2	16	0.91	0.98	0.91	12	0.81	0.93	0.86	14	0.99	1.06	0.91	9.64	6.49	2.83
P42224	Signal transducer and activator of transcription 1-alpha/beta OS=Homo sapiens GN=STAT1 PE=1 SV=2	16	1.19	0.99	1.18	12	1.06	0.85	1.02	10	1.08	1.10	1.04	6.25	12.70	8.24
P35237	Serpin B6 OS=Homo sapiens GN=SERPINB6 PE=1 SV=3	19	1.06	1.08	1.02	11	0.97	0.99	0.97	15	1.02	1.01	0.99	4.08	4.82	2.61
P09211	Glutathione S-transferase P OS=Homo sapiens GN=GSTP1 PE=1 SV=2	45	0.90	1.04	0.86	48	0.98	1.14	0.99	37	0.95	0.99	0.95	4.08	7.39	7.11
P53992	Protein transport protein Sec24C OS=Homo sapiens GN=SEC24C PE=1 SV=3	18	1.01	1.09	1.01	14	0.97	0.98	0.98	13	0.93	1.05	0.96	4.56	5.72	2.73
O14776	Transcription elongation regulator 1 OS=Homo sapiens GN=TCERG1 PE=1 SV=2	17	0.94	1.05	0.99	11	0.91	0.91	0.90	13	0.94	0.94	0.96	1.83	7.26	4.93
Q9NTI5	Sister chromatid cohesion protein PDS5 homolog B OS=Homo sapiens GN=PDS5B PE=1 SV=1	19	0.98	1.01	0.78	21	0.99	1.11	1.09	15	0.98	0.96	0.93	0.54	7.40	16.38
P15170-3	Isoform 3 of Eukaryotic peptide chain release factor GTP-binding subunit ERF3A OS=Homo sapiens GN=GSPT1	23	0.95	1.01	0.88	13	1.02	1.07	1.03	14	0.96	0.94	0.97	3.72	6.71	8.16
P24752	Acetyl-CoA acetyltransferase, mitochondrial OS=Homo sapiens GN=ACAT1 PE=1 SV=1	22	0.86	0.95	0.91	17	1.00	1.01	0.98	19	0.93	0.96	0.94	7.58	3.67	3.84
G3V1D3	Dipeptidyl peptidase 3 OS=Homo sapiens GN=DPP3 PE=2 SV=1	17	1.04	0.97	1.04	12	0.87	0.91	1.01	11	0.92	0.90	0.90	9.12	4.21	7.45
P21980	Protein-glutamine gamma-glutamyltransferase 2 OS=Homo sapiens GN=TGM2 PE=1 SV=2	32	1.24	0.99	1.39	32	1.25	0.99	1.31	25	1.17	1.01	1.28	3.35	1.22	4.32
P05091	Aldehyde dehydrogenase, mitochondrial OS=Homo sapiens GN=ALDH2 PE=1 SV=2	16	0.99	1.09	1.04	16	0.83	1.03	0.93	16	0.98	1.12	0.96	9.37	4.05	5.62
Q9BR63	FARSB protein (Fragment) OS=Homo sapiens GN=FARSB PE=2 SV=2	16	1.02	1.05	1.07	11	0.92	0.92	0.93	11	0.93	1.01	0.95	5.74	6.55	7.60
P16403	Histone H1.2 OS=Homo sapiens GN=HIST1H1C PE=1 SV=2	39	1.11	0.82	1.21	18	1.94	1.51	1.48	15	1.04	0.70	1.11	36.60	43.28	14.81
A7BI36	p180/ribosome receptor OS=Homo sapiens GN=RRBP1 PE=2 SV=2	15	1.04	0.94	1.10	19	1.02	0.95	1.06	12	1.04	0.93	1.05	1.52	1.06	2.75
P46063	ATP-dependent DNA helicase Q1 OS=Homo sapiens GN=RECQL PE=1 SV=3	15	0.98	0.96	0.95	13	1.08	1.07	1.11	11	0.95	0.93	0.92	6.65	7.30	9.86
Q9Y266	Nuclear migration protein nudC OS=Homo sapiens GN=NUDC PE=1 SV=1	19	0.83	0.96	0.92	18	0.95	1.01	0.98	18	0.93	1.09	1.01	6.96	6.06	4.43

A8K5M4	cDNA FLJ75088, highly similar to Homo sapiens p21 (CDKN1A)-activated kinase 2 (PAK2), mRNA OS=Homo sapiens PE=2 SV=1	18	1.10	1.04	0.96	17	1.13	1.13	1.10	13	0.95	0.91	0.99	9.27	10.81	7.36
Q9Y5B9	FACT complex subunit SPT16 OS=Homo sapiens GN=SUPT16H PE=1 SV=1	18	1.05	1.05	0.92	15	0.99	0.90	0.85	14	1.00	0.93	0.87	3.36	7.99	4.08
Q5TZP7	APEX nuclease (Multifunctional DNA repair enzyme) 1 OS=Homo sapiens GN=APEX1 PE=2 SV=1	27	0.90	1.00	0.82	24	0.94	1.02	0.92	20	0.90	0.99	0.94	2.67	1.58	7.57
Q59GY2	Ribosomal protein L4 variant (Fragment) OS=Homo sapiens PE=2 SV=1	22	0.92	0.98	0.91	28	0.98	0.98	0.95	24	0.95	0.98	0.99	3.35	0.40	4.24
P13591	Neural cell adhesion molecule 1 OS=Homo sapiens GN=NCAM1 PE=1 SV=3	15	1.08	1.00	1.03	8	0.97	0.97	0.93	10	1.09	0.95	1.09	6.15	2.54	7.70
P51991	Heterogeneous nuclear ribonucleoprotein A3 OS=Homo sapiens GN=HNRNPA3 PE=1 SV=2	22	1.10	1.02	1.06	21	1.06	0.96	1.00	16	1.11	1.05	1.11	2.34	4.54	5.36
Q08945	FACT complex subunit SSRP1 OS=Homo sapiens GN=SSRP1 PE=1 SV=1	18	1.03	0.94	0.87	17	1.01	0.87	0.82	14	1.04	0.95	0.80	1.65	4.61	3.97
Q12769	Nuclear pore complex protein Nup160 OS=Homo sapiens GN=NUP160 PE=1 SV=3	16	0.98	1.02	1.01	19	0.99	1.00	1.00	14	1.03	1.02	0.93	2.53	1.04	4.32
Q9HD20	Probable cation-transporting ATPase 13A1 OS=Homo sapiens GN=ATP13A1 PE=1 SV=2	15	1.09	1.01	1.06	19	0.99	0.98	1.03	15	0.88	0.94	0.85	10.72	3.98	11.90
Q99497	Protein DJ-1 OS=Homo sapiens GN=PARK7 PE=1 SV=2	25	0.95	1.02	0.86	22	1.09	1.18	1.04	18	1.01	0.95	0.95	7.21	11.47	9.74
Q14258	E3 ubiquitin/ISG15 ligase TRIM25 OS=Homo sapiens GN=TRIM25 PE=1 SV=2	19	0.93	1.11	0.87	14	1.16	1.21	1.17	13	0.97	1.00	0.99	12.30	9.50	15.03
P31689	DnaJ homolog subfamily A member 1 OS=Homo sapiens GN=DNAJA1 PE=1 SV=2	18	0.76	0.96	0.86	18	0.73	0.87	0.77	16	0.77	0.92	0.89	2.97	5.26	7.35
Q58EY4	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1 OS=Homo sapiens GN=SMARCC1 PE=2 SV=1	24	0.88	0.92	0.77	15	0.83	0.96	0.87	13	0.91	1.02	0.92	4.78	5.04	8.80
Q06323	Proteasome activator complex subunit 1 OS=Homo sapiens GN=PSME1 PE=1 SV=1	23	0.99	1.05	0.96	23	1.08	1.10	1.01	19	1.07	0.99	1.07	4.33	5.16	5.26
Q32Q12	Nucleoside diphosphate kinase OS=Homo sapiens GN=NME1-NME2 PE=2 SV=1	45	0.95	1.04	0.87	23	1.22	1.29	1.19	34	0.99	0.90	1.04	13.56	18.30	15.16
Q07960	Rho GTPase-activating protein 1 OS=Homo sapiens GN=ARHGAP1 PE=1 SV=1	24	1.07	0.99	1.23	18	0.99	0.82	0.97	13	1.10	1.13	1.10	5.37	16.12	11.92
P15121	Aldose reductase OS=Homo sapiens GN=AKR1B1 PE=1 SV=3	37	0.93	1.06	0.95	17	0.98	1.10	0.95	16	1.00	1.03	0.90	3.71	3.08	3.22
Q6FHU2	HCG2015269, isoform CRA_a (Fragment) OS=Homo sapiens GN=PGAM1 PE=2 SV=1	31	0.95	1.04	0.96	20	0.99	1.04	0.97	27	0.94	0.99	1.00	2.76	2.90	2.22
P42166	Lamina-associated polypeptide 2, isoform alpha OS=Homo sapiens GN=TMPO PE=1 SV=2	23	1.04	1.07	1.29	18	1.09	1.07	1.17	21	0.65	0.68	0.78	25.95	24.25	24.89
Q6IBR8	EIF2S2 protein OS=Homo sapiens GN=EIF2S2 PE=2 SV=1	21	1.01	0.94	1.06	10	1.08	1.07	1.14	10	1.12	1.04	1.19	5.23	7.02	5.91
A2A274	Aconitate hydratase, mitochondrial OS=Homo sapiens GN=ACO2 PE=2 SV=1	16	0.93	1.00	1.04	17	0.84	0.86	0.90	13	0.99	0.98	0.92	8.36	8.21	7.51
Q52LJ0-2	Isoform 2 of Protein FAM98B OS=Homo sapiens GN=FAM98B	16	1.02	1.09	0.94	11	0.83	0.94	0.88	13	0.96	1.18	1.08	10.79	11.09	10.55

Q8IY81	pre-rRNA processing protein FTSJ3 OS=Homo sapiens GN=FTSJ3 PE=1 SV=2	20	1.07	1.01	1.03	13	0.98	0.98	0.97	11	0.94	1.06	1.03	6.54	4.24	3.28
P13489	Ribonuclease inhibitor OS=Homo sapiens GN=RNH1 PE=1 SV=2	21	1.11	0.97	1.19	25	0.93	0.85	0.93	18	1.05	1.01	1.04	9.15	8.54	12.57
O75489	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial OS=Homo sapiens GN=NDUFS3 PE=1 SV=1	16	1.15	0.93	0.97	12	1.05	0.98	1.03	13	1.06	1.07	1.04	4.89	7.24	3.66
Q8N1G4	Leucine-rich repeat-containing protein 47 OS=Homo sapiens GN=LRRC47 PE=1 SV=1	14	1.02	0.95	0.97	20	0.96	0.94	0.92	13	1.03	1.05	1.05	3.90	6.33	6.50
Q6FIC5	CLIC4 protein OS=Homo sapiens GN=CLIC4 PE=2 SV=1	20	1.00	1.11	1.14	12	1.18	1.03	1.03	16	1.02	1.01	0.95	9.17	5.06	8.95
P09455	Retinol-binding protein 1 OS=Homo sapiens GN=RBP1 PE=1 SV=2	19	0.83	1.02	0.94	14	0.81	1.01	0.83	17	0.78	1.06	0.87	3.48	2.75	6.29
Q9BZQ8	Protein Niban OS=Homo sapiens GN=FAM129A PE=1 SV=1	15	1.22	0.92	1.19	17	1.32	1.03	1.36	14	1.28	0.89	1.22	3.83	8.20	7.08
B3KU60	cDNA FLJ39235 fis, clone OCBBF2007829, highly similar to Mus musculus fatso protein OS=Homo sapiens PE=2 SV=1	18	0.97	1.06	1.01	10	1.03	1.06	1.01	9	0.89	0.91	0.93	7.41	8.28	4.45
P52306	Rap1 GTPase-GDP dissociation stimulator 1 OS=Homo sapiens GN=RAP1GDS1 PE=1 SV=3	20	0.98	0.97	1.03	19	0.84	0.96	0.93	13	0.97	1.01	0.99	8.29	2.47	5.19
O15020	Spectrin beta chain, non-erythrocytic 2 OS=Homo sapiens GN=SPTBN2 PE=1 SV=3	19	0.91	0.97	1.00	13	1.08	1.00	1.04	12	0.86	0.99	0.97	12.33	1.56	3.60
P08243	Asparagine synthetase [glutamine-hydrolyzing] OS=Homo sapiens GN=ASNS PE=1 SV=4	16	1.32	1.07	1.44	12	1.15	1.01	1.21	10	1.14	1.02	1.12	8.19	3.39	13.17
P04181	Ornithine aminotransferase, mitochondrial OS=Homo sapiens GN=OAT PE=1 SV=1	18	0.78	1.03	0.85	15	0.92	1.14	0.95	13	0.95	1.06	0.97	9.87	5.40	7.12
P05556	Integrin beta-1 OS=Homo sapiens GN=ITGB1 PE=1 SV=2	19	1.00	1.06	1.00	12	0.98	0.97	0.99	13	1.12	1.16	1.04	7.48	9.08	2.54
D0PNI1	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein zeta polypeptide OS=Homo sapiens GN=YWHAZ PE=2 SV=1	40	0.98	1.08	1.12	33	1.01	0.99	1.01	38	0.93	1.00	1.03	4.59	4.84	5.46
Q7L2H7	Eukaryotic translation initiation factor 3 subunit M OS=Homo sapiens GN=EIF3M PE=1 SV=1	19	0.89	1.01	1.02	13	0.90	0.91	0.98	13	0.94	1.05	1.02	2.66	7.26	2.43
Q5T5C7	Serine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=SARS PE=2 SV=1	20	1.03	1.03	1.08	15	1.07	1.10	1.06	14	1.09	0.95	1.00	2.66	7.36	4.01
Q96ST3	Paired amphipathic helix protein Sin3a OS=Homo sapiens GN=SIN3A PE=1 SV=2	14	0.91	1.04	0.83	21	1.05	1.05	0.97	12	1.00	0.93	0.99	7.25	6.45	9.09
Q14157	Ubiquitin-associated protein 2-like OS=Homo sapiens GN=UBAP2L PE=1 SV=2	27	0.79	0.93	0.94	16	0.91	1.00	0.96	12	0.84	0.92	0.95	7.05	4.77	0.96
P05141	ADP/ATP translocase 2 OS=Homo sapiens GN=SLC25A5 PE=1 SV=7	25	1.33	1.04	1.17	26	1.31	0.97	1.16	25	1.26	0.95	1.20	2.59	4.69	2.02
I3L0N3	Vesicle-fusing ATPase OS=Homo sapiens GN=NSF PE=2 SV=1	15	0.98	0.97	1.07	14	1.03	1.04	1.01	11	1.05	0.99	1.10	3.81	3.86	4.43
Q6NTA2	HNRNPL protein (Fragment) OS=Homo sapiens GN=HNRNPL PE=2 SV=2	23	1.05	0.96	1.03	22	1.10	1.05	1.12	20	1.04	0.99	1.05	3.18	4.61	4.59
Q15019	Septin-2 OS=Homo sapiens GN=SEPT2 PE=1 SV=1	22	0.93	1.05	1.04	26	0.90	0.92	0.91	17	0.95	1.06	0.96	2.37	7.40	6.94
E9PAU2	Ribonucleoprotein PTB-binding 1 OS=Homo sapiens GN=RAVER1 PE=4 SV=1	20	0.83	0.90	0.99	12	1.09	1.02	1.05	8	0.87	0.93	0.84	15.31	6.33	11.35

Q6NXR8	40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=2 SV=1	23	0.99	0.96	0.93	27	1.02	0.99	1.00	20	1.00	0.97	0.97	1.64	1.38	3.60
O75131	Copine-3 OS=Homo sapiens GN=CPNE3 PE=1 SV=1	23	1.16	1.09	1.15	19	1.10	0.92	1.10	17	1.18	1.13	1.16	3.50	10.82	2.98
B7ZB41	cDNA, FLJ79405, highly similar to Homo sapiens solute carrier family 25, member 24, transcript variant 1, mRNA OS=Homo sapiens PE=2 SV=1	18	1.31	0.99	1.20	16	1.19	0.91	1.05	11	1.18	1.00	1.15	5.96	5.21	6.55
P35520	Cystathionine beta-synthase OS=Homo sapiens GN=CBS PE=1 SV=2	17	0.85	0.96	0.87	14	1.05	1.08	0.98	12	0.92	1.05	0.92	10.68	6.42	6.07
Q15691	Microtubule-associated protein RP/EB family member 1 OS=Homo sapiens GN=MAPRE1 PE=1 SV=3	16	0.94	1.06	0.88	14	0.99	1.08	0.99	16	0.89	1.00	1.00	5.74	3.73	6.73
Q9H845	Acyl-CoA dehydrogenase family member 9, mitochondrial OS=Homo sapiens GN=ACAD9 PE=1 SV=1	15	1.18	0.95	1.33	11	1.12	1.01	1.18	9	0.95	0.92	0.97	10.77	4.62	15.62
P09622	Dihydrolipoyl dehydrogenase, mitochondrial OS=Homo sapiens GN=DLD PE=1 SV=2	20	0.95	0.97	1.01	12	1.06	1.00	1.01	14	1.04	1.00	1.06	6.08	1.91	3.04
O60664	Perilipin-3 OS=Homo sapiens GN=PLIN3 PE=1 SV=3	23	1.09	1.10	1.15	11	1.14	1.02	1.08	12	1.06	1.05	1.01	3.86	3.73	6.44
P43490	Nicotinamide phosphoribosyltransferase OS=Homo sapiens GN=NAMPT PE=1 SV=1	14	1.10	0.93	1.11	10	1.02	1.03	1.04	14	1.03	1.04	0.97	4.09	5.82	6.87
O60763	General vesicular transport factor p115 OS=Homo sapiens GN=USO1 PE=1 SV=2	16	1.20	1.05	1.09	14	1.20	1.11	1.24	12	1.04	0.94	0.99	8.15	8.19	11.69
O75874	Isocitrate dehydrogenase [NADP] cytoplasmic OS=Homo sapiens GN=IDH1 PE=1 SV=2	26	1.07	1.09	1.08	13	1.07	1.06	1.03	14	1.03	1.09	1.11	2.35	1.67	3.36
Q9UKV3-5	Isoform 4 of Apoptotic chromatin condensation inducer in the nucleus OS=Homo sapiens GN=ACIN1	16	1.02	0.92	0.93	9	0.86	0.96	0.96	7	1.07	1.10	1.03	10.82	9.38	5.44
Q8TC62	Septin 7 OS=Homo sapiens GN=SEPT7 PE=2 SV=3	37	0.93	1.01	0.93	23	0.88	0.99	0.95	22	0.97	1.07	0.93	4.81	3.92	1.23
P07737	Profilin-1 OS=Homo sapiens GN=PFN1 PE=1 SV=2	44	1.02	1.05	1.05	34	1.05	0.99	1.00	43	0.99	1.02	1.07	3.22	3.05	3.77
Q9HCC0	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens GN=MCCC2 PE=1 SV=1	16	0.90	0.85	0.83	15	0.96	1.02	0.97	11	1.08	1.01	1.00	9.30	9.76	9.58
O60701	UDP-glucose 6-dehydrogenase OS=Homo sapiens GN=UGDH PE=1 SV=1	13	1.13	1.05	0.99	18	1.16	1.04	1.17	14	1.08	0.95	1.01	3.36	5.70	9.31
Q53SS8	Poly(RC) binding protein 1 OS=Homo sapiens GN=PCBP1 PE=2 SV=1	29	0.84	1.08	0.95	26	0.76	0.91	0.80	13	0.84	1.00	0.98	5.71	8.82	10.63
B1ANK7	Fumarate hydratase, isoform CRA_c OS=Homo sapiens GN=FH PE=2 SV=1	19	0.96	1.02	0.94	14	0.96	0.98	0.96	14	0.99	0.94	0.92	1.63	3.73	2.42
P49419-2	Isoform 2 of Alpha-aminoadipic semialdehyde dehydrogenase OS=Homo sapiens GN=ALDH7A1	15	1.13	1.10	1.18	10	1.12	1.10	1.05	10	1.19	1.00	1.10	3.43	5.64	5.69
P46060	Ran GTPase-activating protein 1 OS=Homo sapiens GN=RANGAP1 PE=1 SV=1	21	0.96	0.99	0.93	20	0.95	0.94	1.00	15	0.94	0.94	1.02	0.88	2.90	4.62
Q96A33	Coiled-coil domain-containing protein 47 OS=Homo sapiens GN=CCDC47 PE=1 SV=1	16	1.34	1.03	1.15	14	1.22	0.97	1.13	14	1.20	0.90	1.11	6.20	6.87	1.95
P37802	Transgelin-2 OS=Homo sapiens GN=TAGLN2 PE=1 SV=3	36	1.15	1.04	1.21	27	1.14	1.02	1.19	23	1.10	0.99	1.20	2.18	2.18	0.77

Q5SW79	Centrosomal protein of 170 kDa OS=Homo sapiens GN=CEP170 PE=1 SV=1	15	1.18	0.93	1.18	17	1.36	0.87	1.26	13	1.46	1.10	1.51	10.61	12.52	13.05
E9PAL9	5'-nucleotidase domain-containing protein 2 OS=Homo sapiens GN=NT5DC2 PE=2 SV=1	14	1.00	1.06	1.04	9	1.01	0.99	1.00	12	0.98	1.03	1.03	1.46	3.33	2.42
Q9BXP5	Serrate RNA effector molecule homolog OS=Homo sapiens GN=SRRT PE=1 SV=1	16	0.99	0.95	0.97	12	1.00	1.09	1.04	12	1.04	1.01	1.13	2.59	6.88	7.94
B0UX83	HLA-B associated transcript 3, isoform CRA_a OS=Homo sapiens GN=BAG6 PE=2 SV=1	14	0.94	1.03	1.08	15	0.90	0.92	0.96	12	0.95	1.03	1.02	2.80	6.62	6.20
Q9HBB3	60S ribosomal protein L6 OS=Homo sapiens PE=2 SV=1	23	0.99	1.02	1.08	20	0.96	0.93	0.93	23	0.96	1.04	0.98	1.97	5.95	7.79
P22695	Cytochrome b-c1 complex subunit 2, mitochondrial OS=Homo sapiens GN=UQCRC2 PE=1 SV=3	16	1.24	0.99	1.16	13	1.18	1.00	1.10	14	1.13	0.96	1.07	4.81	2.42	4.04
Q9HB71	Calcyclin-binding protein OS=Homo sapiens GN=CACYBP PE=1 SV=2	16	0.94	1.05	0.92	10	1.02	0.99	1.02	8	0.93	0.95	0.95	4.97	4.92	5.03
B2R6H7	cDNA, FLJ92955, highly similar to Homo sapiens transportin-SR (TRN-SR), mRNA OS=Homo sapiens PE=2 SV=1	21	0.91	0.95	1.04	11	0.95	0.94	0.98	9	0.92	1.07	0.95	1.76	7.39	4.34
Q9UBG0	C-type mannose receptor 2 OS=Homo sapiens GN=MRC2 PE=1 SV=2	14	1.13	1.03	1.26	7	0.92	0.85	1.04	8	1.01	1.10	1.06	10.04	12.69	10.82
P45880	Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2	23	1.26	1.00	1.23	23	1.16	0.89	1.07	23	1.16	1.00	1.14	4.73	6.80	6.95
Q86YI5	Dihydrolipoamide S-acetyltransferase OS=Homo sapiens GN=DLAT PE=2 SV=1	16	1.10	1.04	1.04	12	1.11	1.04	1.06	11	1.02	0.93	1.06	4.63	6.28	1.35
O60282	Kinesin heavy chain isoform 5C OS=Homo sapiens GN=KIF5C PE=1 SV=1	21	0.90	1.04	0.94	18	0.96	1.04	0.95	21	0.94	1.04	0.99	3.31	0.20	2.81
A8K4T6	cDNA FLJ76282, highly similar to Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 5 (PSMD5), mRNA OS=Homo sapiens PE=2 SV=1	15	1.04	0.98	1.24	15	0.90	0.88	0.92	8	1.10	1.07	1.07	10.22	9.97	14.82
P10253	Lysosomal alpha-glucosidase OS=Homo sapiens GN=GAA PE=1 SV=4	15	1.10	0.94	1.32	13	0.85	0.89	0.97	14	0.91	1.09	0.99	13.96	10.65	17.71
Q6NUR7	Ezrin OS=Homo sapiens GN=EZR PE=2 SV=1	25	1.15	1.01	1.04	25	1.02	1.16	1.24	21	1.01	0.89	0.89	7.04	13.33	16.67
P63241	Eukaryotic translation initiation factor 5A-1 OS=Homo sapiens GN=EIF5A PE=1 SV=2	44	0.93	1.05	0.81	29	1.11	1.13	0.93	29	1.00	1.02	0.70	9.03	5.42	14.02
B2RCX0	cDNA, FLJ96345, Homo sapiens SET translocation (myeloid leukemia-associated) (SET),mRNA OS=Homo sapiens PE=2 SV=1	36	0.85	1.04	0.92	17	0.83	0.89	0.81	18	0.88	1.07	0.95	2.92	9.53	8.14
Q53XC0	Eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa, isoform CRA_a OS=Homo sapiens GN=EIF2S1 PE=2 SV=1	14	1.01	0.96	0.97	9	1.07	1.08	1.08	9	1.04	1.08	1.08	3.00	6.57	6.12
Q53FN7	BZW1 protein variant (Fragment) OS=Homo sapiens PE=2 SV=1	18	0.73	0.95	0.79	19	0.96	1.13	0.99	14	0.87	0.93	0.94	14.01	10.95	11.33
P61221	ATP-binding cassette sub-family E member 1 OS=Homo sapiens GN=ABCE1 PE=1 SV=1	20	0.93	0.97	0.97	15	0.98	0.98	1.04	15	0.97	1.00	1.00	2.54	1.60	3.71
P61586	Transforming protein RhoA OS=Homo sapiens GN=RHOA PE=1 SV=1	22	0.87	1.03	0.73	18	0.99	1.21	0.95	17	0.90	0.87	0.90	6.76	16.45	13.31
O43681	ATPase ASNA1 OS=Homo sapiens GN=ASNA1 PE=1 SV=2	16	1.04	1.10	1.12	14	0.98	1.01	0.98	10	1.07	1.04	0.99	4.32	4.58	7.48

O95336	6-phosphogluconolactonase OS=Homo sapiens GN=PGLS PE=1 SV=2	17	1.01	1.05	1.09	15	0.92	0.85	0.94	10	1.04	1.18	1.07	6.41	16.09	7.78
O43290	U4/U6.U5 tri-snRNP-associated protein 1 OS=Homo sapiens GN=SART1 PE=1 SV=1	13	0.90	0.94	0.81	10	1.09	0.99	1.03	7	1.05	0.96	0.90	10.00	3.08	11.93
M0QZR4	Rho guanine nucleotide exchange factor 1 OS=Homo sapiens GN=ARHGEF1 PE=4 SV=1	16	0.95	1.01	0.93	11	1.07	1.07	0.99	13	1.02	0.98	0.92	5.70	4.37	4.21
Q8NCF7	cDNA FLJ90278 fis, clone NT2RP1000325, highly similar to Phosphate carrier protein, mitochondrialprecursor OS=Homo sapiens PE=2 SV=1	20	1.32	0.99	1.27	17	1.34	0.91	1.15	14	1.32	1.00	1.20	0.98	5.02	4.87
Q9C0C9	Ubiquitin-conjugating enzyme E2 O OS=Homo sapiens GN=UBE2O PE=1 SV=3	14	0.84	0.99	0.81	11	0.90	0.95	0.90	7	0.92	1.00	0.88	5.00	3.02	5.54
Q15942	Zyxin OS=Homo sapiens GN=ZYX PE=1 SV=1	19	1.20	1.02	1.09	14	1.05	1.04	1.20	11	1.12	1.09	1.21	6.32	3.83	5.91
P23284	Peptidyl-prolyl cis-trans isomerase B OS=Homo sapiens GN=PPIB PE=1 SV=2	23	1.97	1.04	1.45	19	2.22	1.13	1.77	18	1.92	0.91	1.75	7.82	11.08	10.71
H3BRN4	4-aminobutyrate aminotransferase, mitochondrial OS=Homo sapiens GN=ABAT PE=2 SV=1	13	0.88	0.98	0.96	13	0.99	1.02	0.99	8	0.94	0.98	0.90	5.49	2.53	4.67
F8WCY5	Reticulocalbin-2 OS=Homo sapiens GN=RCN2 PE=2 SV=1	16	1.16	0.91	1.09	14	1.08	0.94	0.98	11	1.09	1.07	1.07	3.74	8.69	5.28
G9I2H4	Aryl hydrocarbon receptor interacting protein OS=Homo sapiens GN=AIP PE=4 SV=1	18	0.89	0.96	0.82	8	1.16	1.06	0.99	7	0.87	0.86	0.99	16.52	10.46	10.69
P23396	40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2	21	0.96	1.00	1.05	23	0.96	0.94	0.97	21	0.97	1.03	1.05	0.82	4.53	4.55
P23258	Tubulin gamma-1 chain OS=Homo sapiens GN=TUBG1 PE=1 SV=2	12	1.05	1.15	0.96	15	1.07	1.14	1.03	7	0.97	0.90	0.95	5.29	13.07	4.21
C9J9K3	40S ribosomal protein SA (Fragment) OS=Homo sapiens GN=RPSA PE=2 SV=1	24	0.99	0.96	1.02	24	1.02	0.99	1.03	18	1.00	0.97	1.00	1.48	1.40	1.53
Q9BUF5	Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1	114	1.12	0.99	1.24	83	0.87	0.85	0.91	92	1.08	1.15	1.11	13.20	15.04	15.07
P27694	Replication protein A 70 kDa DNA-binding subunit OS=Homo sapiens GN=RPA1 PE=1 SV=2	14	0.86	0.83	0.89	12	1.06	1.03	1.00	6	0.91	0.97	0.91	11.00	10.59	6.38
Q53XL8	Proteasome (Prosome, macropain) 26S subunit, ATPase, 1 OS=Homo sapiens GN=PSMC1 PE=2 SV=1	16	0.93	1.02	0.88	13	0.93	0.99	0.95	16	0.95	1.03	0.95	1.10	2.33	4.17
P61163	Alpha-centractin OS=Homo sapiens GN=ACTR1A PE=1 SV=1	17	0.92	1.08	1.05	11	0.91	0.87	0.91	11	0.83	1.01	0.99	5.70	10.47	6.98
Q9NPQ8	Synembryn-A OS=Homo sapiens GN=RIC8A PE=1 SV=3	14	0.96	0.94	1.05	12	0.82	0.84	0.82	9	0.99	1.15	1.08	9.72	16.27	14.36
B1AKK2	Dimethylarginine dimethylaminohydrolase 1, isoform CRA_b OS=Homo sapiens GN=DDAH1 PE=2 SV=1	16	0.93	0.99	0.95	13	1.05	1.00	0.98	14	0.98	1.02	0.96	5.94	1.64	1.42
P51149	Ras-related protein Rab-7a OS=Homo sapiens GN=RAB7A PE=1 SV=1	17	1.02	0.99	1.03	16	1.07	0.96	1.00	14	1.00	0.95	1.02	3.61	2.08	1.60
Q9Y512	Sorting and assembly machinery component 50 homolog OS=Homo sapiens GN=SAMM50 PE=1 SV=3	13	1.16	1.01	1.11	11	1.27	1.05	1.24	11	1.20	0.95	1.12	4.97	5.48	6.14
Q9NQC3	Reticulon-4 OS=Homo sapiens GN=RTN4 PE=1 SV=2	17	1.12	1.03	1.06	23	1.17	0.99	1.05	12	0.94	1.00	0.65	11.49	2.50	25.80
Q6PKG0	La-related protein 1 OS=Homo sapiens GN=LARP1 PE=1 SV=2	15	1.11	0.98	1.13	13	0.94	0.96	0.88	10	1.08	1.05	0.92	8.38	4.69	13.85
Q6IBS0	Twinfilin-2 OS=Homo sapiens GN=TWF2 PE=1 SV=2	17	0.93	0.98	1.03	11	0.98	0.95	0.93	10	0.98	1.09	1.04	2.86	7.31	6.53

Q68CM6	STXBP1 protein OS=Homo sapiens GN=stxbp1 PE=2 SV=1	14	1.04	1.04	1.02	9	1.10	0.94	1.11	11	1.07	1.08	1.05	3.00	7.46	4.63
Q59F94	Ataxin-1 ubiquitin-like interacting protein variant (Fragment) OS=Homo sapiens PE=2 SV=1	17	0.99	0.95	1.05	13	0.79	0.86	0.80	12	1.30	1.12	1.16	24.85	13.38	18.11
P52788	Spermine synthase OS=Homo sapiens GN=SMS PE=1 SV=2	15	1.00	1.07	1.07	8	1.02	0.97	1.04	8	0.92	1.01	0.98	5.17	5.35	4.10
P35908	Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2	19	1.65	1.00	2.06	5	1.59	0.95	2.37	6	1.56	1.14	1.25	2.87	9.66	30.79
Q63HL4	NADPH--cytochrome P450 reductase OS=Homo sapiens GN=DKFZp686G04235 PE=2 SV=1	17	1.04	0.93	1.52	11	0.81	0.82	0.86	13	1.06	1.00	1.08	14.13	9.53	29.03
E7ET15	U2 snRNP-associated SURP motif-containing protein OS=Homo sapiens GN=U2SURP PE=2 SV=1	13	0.90	0.93	1.01	8	0.90	1.11	1.11	10	0.96	0.97	1.06	3.66	9.41	4.29
P32119	Peroxiredoxin-2 OS=Homo sapiens GN=PRDX2 PE=1 SV=5	32	0.88	1.00	0.81	17	1.12	1.13	1.03	14	0.99	0.93	0.98	12.05	9.44	12.60
O00425	Insulin-like growth factor 2 mRNA-binding protein 3 OS=Homo sapiens GN=IGF2BP3 PE=1 SV=2	16	0.90	0.97	0.92	15	1.12	1.00	1.07	14	1.04	1.00	1.09	10.90	1.71	8.86
B4DRS6	cDNA FLJ58980, highly similar to Sideroflexin-3 OS=Homo sapiens PE=2 SV=1	17	1.19	1.02	1.26	10	0.72	0.69	0.85	15	1.20	1.20	1.30	26.49	26.94	22.15
O00116	Alkyldihydroxyacetonephosphate synthase, peroxisomal OS=Homo sapiens GN=AGPS PE=1 SV=1	13	0.99	0.93	1.00	10	1.05	1.04	1.03	12	1.04	0.97	0.93	3.15	5.72	5.36
Q5U5J2	CSNK2A1 protein OS=Homo sapiens GN=CSNK2A1 PE=2 SV=1	18	0.99	0.95	0.96	18	1.08	1.02	0.98	14	1.00	1.09	1.01	4.96	7.00	2.95
J3KPF3	4F2 cell-surface antigen heavy chain OS=Homo sapiens GN=SLC3A2 PE=4 SV=1	14	1.45	1.03	1.38	14	1.46	0.99	1.29	16	1.43	1.06	1.35	1.17	3.42	3.75
Q99536	Synaptic vesicle membrane protein VAT-1 homolog OS=Homo sapiens GN=VAT1 PE=1 SV=2	12	0.95	0.93	0.90	13	0.96	0.99	0.96	9	1.06	1.05	1.03	6.27	6.01	7.04
P61160	Actin-related protein 2 OS=Homo sapiens GN=ACTR2 PE=1 SV=1	16	0.94	0.97	0.91	15	1.08	1.22	1.26	13	0.97	0.97	0.98	7.40	14.12	17.47
Q86UA3	Chromosome 12 open reading frame 10 OS=Homo sapiens GN=C12orf10 PE=2 SV=1	17	1.00	1.08	1.16	12	1.02	0.97	0.96	12	1.04	1.07	0.99	1.95	5.97	10.57
P06748	Nucleophosmin OS=Homo sapiens GN=NPM1 PE=1 SV=2	35	0.91	0.92	1.00	28	0.87	0.84	0.88	23	0.88	1.00	0.90	2.17	8.86	6.82
Q9UMS4	Pre-mRNA-processing factor 19 OS=Homo sapiens GN=PRPF19 PE=1 SV=1	17	0.88	1.00	0.90	13	0.94	1.05	0.97	10	0.85	0.87	0.85	5.17	9.67	6.69
O43809	Cleavage and polyadenylation specificity factor subunit 5 OS=Homo sapiens GN=NUDT21 PE=1 SV=1	16	0.84	0.98	0.86	16	0.91	1.03	0.90	10	0.99	1.08	0.91	8.31	4.90	2.92
Q9UKG1	DCC-interacting protein 13-alpha OS=Homo sapiens GN=APPL1 PE=1 SV=1	14	0.90	0.92	0.93	7	1.03	0.99	0.95	4	0.86	1.01	0.90	9.54	5.21	2.32
Q8N7G1	Purine nucleoside phosphorylase OS=Homo sapiens PE=2 SV=1	12	0.99	0.99	1.10	11	0.95	0.94	0.98	10	1.05	1.07	0.93	4.64	6.19	8.40
P62140	Serine/threonine-protein phosphatase PP1-beta catalytic subunit OS=Homo sapiens GN=PPP1CB PE=1 SV=3	24	0.99	0.99	1.00	16	0.89	1.07	0.89	17	0.97	1.11	1.03	5.92	5.98	7.60
Q6IAX5	Eukaryotic translation initiation factor 3 subunit E OS=Homo sapiens GN=EIF3S6 PE=2 SV=1	16	0.95	1.06	1.04	8	0.83	0.91	0.88	6	0.88	1.03	0.90	6.55	8.24	9.64
P28074	Proteasome subunit beta type-5 OS=Homo sapiens GN=PSMB5 PE=1 SV=3	12	0.93	0.95	0.92	11	0.92	1.07	0.98	13	1.03	0.99	1.04	6.13	6.11	6.14
E9PHK9	Treacle protein OS=Homo sapiens GN=TCOF1 PE=2 SV=1	15	1.06	1.03	1.08	13	1.23	1.12	1.30	5	1.05	0.90	0.98	9.32	10.77	14.37

Q9UJU6	Drebrin-like protein OS=Homo sapiens GN=DBNL PE=1 SV=1	16	1.04	1.10	1.13	12	0.83	0.85	0.99	11	0.99	1.17	0.99	11.14	16.15	7.97
Q6NVY1	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial OS=Homo sapiens GN=HIBCH PE=1 SV=2	13	0.84	0.97	0.87	12	0.89	1.08	0.96	12	0.94	1.00	0.93	5.59	5.70	5.14
B4DJ51	Calmodulin 1 (Phosphorylase kinase, delta), isoform CRA_a OS=Homo sapiens GN=CALM1 PE=2 SV=1	148	0.91	1.03	0.78	153	0.98	1.12	0.95	81	0.88	0.86	0.92	5.46	12.81	10.05
B2R7T8	cDNA, FLJ93598, highly similar to Homo sapiens capping protein (actin filament) muscle Z-line, beta (CAPZB), mRNA OS=Homo sapiens PE=2 SV=1	21	1.03	1.03	1.05	14	1.00	0.94	0.99	13	1.09	1.03	1.05	4.15	5.28	3.52
P61019	Ras-related protein Rab-2A OS=Homo sapiens GN=RAB2A PE=1 SV=1	13	0.94	0.92	1.13	12	1.17	0.95	0.94	14	0.97	1.04	1.00	12.17	6.48	9.31
Q5TZX1	Guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 3 OS=Homo sapiens GN=GNAI3 PE=2 SV=1	14	1.08	1.10	1.51	9	0.80	0.92	0.84	10	0.92	0.97	0.86	15.05	9.35	35.56
Q15417	Calponin-3 OS=Homo sapiens GN=CNN3 PE=1 SV=1	24	0.88	0.93	0.79	16	0.79	1.19	1.06	17	0.85	0.89	0.83	5.76	16.37	16.08
O76094	Signal recognition particle subunit SRP72 OS=Homo sapiens GN=SRP72 PE=1 SV=3	13	1.00	0.99	1.01	15	1.19	1.09	1.16	9	0.94	0.91	0.84	12.51	8.85	16.14
P18124	60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1	29	0.99	0.97	0.86	23	1.14	1.08	1.09	21	1.04	0.94	1.09	6.99	7.06	13.42
Q59EL2	COP9 constitutive photomorphogenic homolog subunit 2 variant (Fragment) OS=Homo sapiens PE=2 SV=1	14	1.03	1.09	1.04	11	0.98	1.05	1.03	14	0.97	0.98	0.90	3.20	5.44	7.68
Q53FV3	COP9 signalosome subunit 4 variant (Fragment) OS=Homo sapiens PE=2 SV=1	16	0.91	0.91	0.84	17	0.91	0.96	0.93	11	1.09	1.01	1.02	10.72	5.37	9.61
P27348	14-3-3 protein theta OS=Homo sapiens GN=YWHAQ PE=1 SV=1	58	0.88	1.04	1.11	36	0.89	0.93	0.87	35	0.81	1.03	0.88	5.42	5.82	14.17
P13521	Secretogranin-2 OS=Homo sapiens GN=SCG2 PE=1 SV=2	14	1.29	1.08	1.46	14	1.25	1.08	1.30	10	1.28	1.09	1.26	1.73	0.58	7.71
Q07954	Prolow-density lipoprotein receptor-related protein 1 OS=Homo sapiens GN=LRP1 PE=1 SV=2	14	1.20	1.01	1.04	7	0.97	0.93	1.03	12	1.21	1.09	1.26	11.90	7.77	11.85
Q96CS3	FAS-associated factor 2 OS=Homo sapiens GN=FAF2 PE=1 SV=2	13	1.14	1.08	1.12	9	1.00	0.95	0.95	10	1.08	1.04	1.11	6.40	6.79	9.35
Q13409-2	Isoform 2B of Cytoplasmic dynein 1 intermediate chain 2 OS=Homo sapiens GN=DYNC1I2	13	0.99	1.03	1.03	13	1.08	1.02	1.05	9	1.03	1.01	1.01	4.36	0.90	1.63
Q09028	Histone-binding protein RBBP4 OS=Homo sapiens GN=RBBP4 PE=1 SV=3	16	0.75	1.02	0.90	18	1.04	1.10	0.98	12	0.84	0.98	0.90	16.69	5.51	5.08
P30520	Adenylosuccinate synthetase isozyme 2 OS=Homo sapiens GN=ADSS PE=1 SV=3	16	1.11	1.01	1.12	12	0.97	0.92	1.05	12	1.08	1.08	1.05	7.04	7.97	3.74
P62333	26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1	13	0.96	1.03	1.02	12	0.86	0.97	0.91	14	0.94	1.02	0.97	5.68	3.24	5.61
B4DHQ3	cDNA FLJ56437, highly similar to Phosphoserine aminotransferase (EC 2.6.1.52) OS=Homo sapiens PE=2 SV=1	14	1.19	1.03	1.20	16	1.13	1.02	1.09	16	1.12	0.97	1.12	3.26	3.26	5.14
J3KTL2	Serine/arginine-rich-splicing factor 1 OS=Homo sapiens GN=SRSF1 PE=4 SV=1	13	1.06	0.94	1.05	13	1.10	1.08	1.08	12	1.00	1.00	0.95	4.71	6.83	7.00
Q53FN8	Aldehyde dehydrogenase 6A1 variant (Fragment) OS=Homo sapiens PE=2 SV=1	12	1.02	0.97	1.07	5	0.93	1.05	1.05	8	1.12	1.03	1.09	9.19	4.02	1.50

P29966	Myristoylated alanine-rich C-kinase substrate OS=Homo sapiens GN=MARCKS PE=1 SV=4	55	0.82	0.90	0.88	30	0.92	0.93	0.81	14	1.06	1.00	1.08	13.10	5.42	15.07
P10645	Chromogranin-A OS=Homo sapiens GN=CHGA PE=1 SV=7	13	1.10	1.12	1.13	10	1.11	1.03	1.04	8	1.00	1.17	1.05	5.34	6.25	4.41
Q9UBB4	Ataxin-10 OS=Homo sapiens GN=ATXN10 PE=1 SV=1	13	0.84	0.98	0.91	12	0.78	0.97	0.92	12	0.79	1.03	0.84	4.07	3.37	5.08
P10155	60 kDa SS-A/Ro ribonucleoprotein OS=Homo sapiens GN=TROVE2 PE=1 SV=2	16	1.10	0.98	1.06	7	0.93	0.97	0.99	8	1.05	0.98	0.96	8.39	0.55	5.10
Q96PK6	RNA-binding protein 14 OS=Homo sapiens GN=RBM14 PE=1 SV=2	15	0.94	0.97	0.92	9	0.86	0.92	0.87	11	0.94	0.91	0.93	5.22	3.84	3.82
Q5U0D2	Putative uncharacterized protein DKFZp686P11128 OS=Homo sapiens GN=TAGLN PE=2 SV=1	13	1.39	1.03	1.41	14	1.42	1.01	1.49	15	1.35	0.93	1.59	2.40	5.27	5.89
Q01780	Exosome component 10 OS=Homo sapiens GN=EXOSC10 PE=1 SV=2	11	1.05	1.02	0.90	11	1.09	1.08	1.09	9	1.05	0.92	0.97	2.34	7.83	9.53
P61011	Signal recognition particle 54 kDa protein OS=Homo sapiens GN=SRP54 PE=1 SV=1	12	1.27	1.01	1.19	12	1.20	0.97	1.08	12	0.95	1.02	1.08	14.88	2.80	5.38
Q6IAU5	PPM1G protein OS=Homo sapiens GN=PPM1G PE=2 SV=1	20	0.91	1.02	0.97	12	0.91	0.94	0.89	13	0.89	1.03	0.96	1.01	4.87	5.01
A8K878	cDNA FLJ77177, highly similar to Homo sapiens arginine-rich, mutated in early stage tumors (ARMET), mRNA OS=Homo sapiens PE=2 SV=1	16	2.00	0.99	1.34	15	1.85	1.05	1.62	17	1.87	1.01	1.71	4.21	3.19	12.51
P62750	60S ribosomal protein L23a OS=Homo sapiens GN=RPL23A PE=1 SV=1	15	1.06	1.01	0.95	11	1.25	1.15	1.15	13	1.10	0.99	1.09	8.50	8.58	9.57
Q9NZN4	EH domain-containing protein 2 OS=Homo sapiens GN=EHD2 PE=1 SV=2	16	1.03	1.03	0.96	12	1.04	0.96	1.05	12	1.22	0.93	1.30	9.51	5.15	16.32
P30040	Endoplasmic reticulum resident protein 29 OS=Homo sapiens GN=ERP29 PE=1 SV=4	16	1.41	0.96	1.23	17	1.36	0.91	1.17	11	1.42	1.02	1.28	2.22	5.74	4.38
D3DWL9	Cleavage and polyadenylation specific factor 1, 160kDa, isoform CRA_a OS=Homo sapiens GN=CPSF1 PE=2 SV=1	11	1.01	1.00	1.11	8	0.83	0.91	0.82	3	0.87	1.19	0.81	10.32	13.85	18.55
P42345	Serine/threonine-protein kinase mTOR OS=Homo sapiens GN=MTOR PE=1 SV=1	13	0.94	1.05	1.02	11	1.09	1.03	1.02	8	1.00	0.96	1.02	7.30	4.35	0.08
P16152	Carbonyl reductase [NADPH] 1 OS=Homo sapiens GN=CBR1 PE=1 SV=3	18	0.90	0.97	0.95	14	0.94	0.93	0.92	10	0.93	1.05	0.87	2.18	6.22	4.67
Q6FHX6	Flap endonuclease 1 OS=Homo sapiens GN=FEN1 PE=2 SV=1	16	0.87	1.03	0.89	15	0.89	0.95	0.90	13	0.94	1.01	0.95	3.99	4.08	3.40
Q9BS26	Endoplasmic reticulum resident protein 44 OS=Homo sapiens GN=ERP44 PE=1 SV=1	11	1.49	1.02	1.38	10	1.51	1.09	1.32	10	1.34	0.90	1.26	6.37	9.82	4.76
Q6FHM2	GNB2 protein OS=Homo sapiens GN=GNB2 PE=2 SV=1	19	1.05	0.97	1.11	14	0.94	0.90	0.96	14	0.94	1.06	1.02	6.32	8.33	7.41
Q5RLJ0	CLE OS=Homo sapiens PE=2 SV=1	15	1.00	1.03	1.00	17	1.08	1.13	1.05	13	0.98	1.02	1.01	5.01	5.92	2.56
Q10567	AP-1 complex subunit beta-1 OS=Homo sapiens GN=AP1B1 PE=1 SV=2	26	1.07	1.02	1.27	22	1.09	0.96	1.03	21	1.18	1.00	1.15	5.61	2.84	10.26
Q96HE7	ERO1-like protein alpha OS=Homo sapiens GN=ERO1L PE=1 SV=2	15	1.39	0.97	1.27	16	1.39	1.06	1.23	9	1.37	0.98	1.17	0.88	4.95	4.09
P37837	Transaldolase OS=Homo sapiens GN=TALDO1 PE=1 SV=2	13	0.87	1.02	0.86	12	0.96	1.11	0.91	16	0.88	1.03	0.90	5.38	4.65	2.92
B4DYK6	cDNA FLJ56887, highly similar to Homo sapiens guanine nucleotide binding protein-like 1 (GNL1), mRNA OS=Homo sapiens PE=2 SV=1	15	0.99	1.04	0.97	7	0.98	0.97	0.96	8	1.19	1.08	1.19	11.46	5.54	12.53

J3KPW7	Histone deacetylase 2 OS=Homo sapiens GN=HDAC2 PE=4 SV=1	20	0.83	1.03	0.80	9	0.94	1.05	0.94	13	0.81	0.84	0.89	8.40	12.08	7.88
P12532	Creatine kinase U-type, mitochondrial OS=Homo sapiens GN=CKMT1A PE=1 SV=1	13	1.00	1.03	1.05	14	0.87	0.96	0.92	11	0.97	1.00	0.96	7.48	3.36	6.82
Q6FGY1	HPCAL1 protein OS=Homo sapiens GN=HPCAL1 PE=2 SV=1	14	0.96	0.92	1.00	13	1.05	0.95	1.02	11	0.96	0.94	0.98	5.05	1.62	1.90
Q9UJZ1	Stomatin-like protein 2, mitochondrial OS=Homo sapiens GN=STOML2 PE=1 SV=1	27	1.28	0.96	1.27	17	1.11	0.85	1.04	14	1.14	0.99	1.08	7.66	7.97	10.75
Q53FT8	Proteasome subunit beta type (Fragment) OS=Homo sapiens PE=2 SV=1	14	0.96	0.96	1.11	12	0.92	0.91	0.91	12	1.06	1.06	1.01	7.30	7.71	10.01
P31937	3-hydroxyisobutyrate dehydrogenase, mitochondrial OS=Homo sapiens GN=HIBADH PE=1 SV=2	12	1.05	0.94	1.04	8	1.10	1.07	1.00	10	1.06	0.90	1.08	2.54	8.77	3.64
P35658	Nuclear pore complex protein Nup214 OS=Homo sapiens GN=NUP214 PE=1 SV=2	13	1.11	0.94	1.11	8	0.90	0.95	1.05	13	0.93	1.06	0.98	11.83	6.94	6.51
J3K000	PEPD protein OS=Homo sapiens GN=PEPD PE=2 SV=1	13	0.87	0.99	0.95	12	0.85	1.03	0.93	16	0.92	0.97	0.93	4.17	3.06	0.98
Q53Z07	NPC-A-16 OS=Homo sapiens GN=RPL9 PE=2 SV=1	22	0.95	0.97	0.89	22	1.00	1.01	0.99	15	0.99	0.97	1.01	2.24	2.48	6.36
O60443	Non-syndromic hearing impairment protein 5 OS=Homo sapiens GN=DFNA5 PE=1 SV=2	16	1.04	1.05	1.08	13	1.05	1.01	0.93	9	1.04	0.98	1.02	0.69	3.58	7.65
Q4LE60	TNPO2 variant protein (Fragment) OS=Homo sapiens GN=TNPO2 variant protein PE=2 SV=1	20	1.11	1.13	1.16	16	1.20	1.06	1.05	15	0.93	0.98	0.91	12.85	7.13	11.96
Q8N3C0	Activating signal cointegrator 1 complex subunit 3 OS=Homo sapiens GN=ASCC3 PE=1 SV=3	12	1.09	1.01	0.97	7	1.18	1.06	1.06	7	1.00	1.08	1.01	8.43	3.33	4.42
B3KY11	cDNA FLJ46571 fis, clone THYMU3041428, highly similar to Probable ATP-dependent RNA helicase DDX23 (EC 3.6.1.-) OS=Homo sapiens PE=2 SV=1	11	1.11	1.01	1.08	9	0.97	1.06	1.05	8	1.08	1.12	1.07	7.17	5.33	1.53
A4D2D2	Procollagen C-endopeptidase enhancer OS=Homo sapiens GN=PCOLCE PE=4 SV=1	11	0.97	0.99	1.05	10	1.00	0.82	0.90	6	0.92	1.11	1.02	3.78	14.69	8.26
Q15067-2	Isoform 2 of Peroxisomal acyl-coenzyme A oxidase 1 OS=Homo sapiens GN=ACOX1	13	1.05	1.11	0.85	13	0.90	0.78	0.91	7	1.10	1.01	1.02	10.25	17.33	8.97
Q6FG43	FLOT2 protein OS=Homo sapiens GN=FLOT2 PE=2 SV=1	11	1.31	0.98	1.08	8	1.19	1.20	1.16	8	0.96	1.03	0.98	15.47	10.44	8.77
P25786	Proteasome subunit alpha type-1 OS=Homo sapiens GN=PSMA1 PE=1 SV=1	13	0.99	1.01	0.96	12	1.02	1.04	0.98	13	1.00	1.02	0.89	1.52	1.55	4.67
P52597	Heterogeneous nuclear ribonucleoprotein F OS=Homo sapiens GN=HNRNPF PE=1 SV=3	37	0.92	0.97	0.96	27	0.86	0.92	0.89	20	0.85	1.01	0.96	4.11	4.58	4.52
O14531	Dihydropyrimidinase-related protein 4 OS=Homo sapiens GN=DPYSL4 PE=1 SV=2	15	0.85	0.95	0.80	18	1.01	1.06	0.99	12	0.97	0.92	0.94	8.91	7.26	10.64
Q8TA92	Similar to AFG3 ATPase family gene 3-like 2 (Yeast) (Fragment) OS=Homo sapiens PE=2 SV=1	11	1.09	0.93	0.79	11	1.03	1.05	1.08	8	1.07	1.05	1.04	2.97	6.97	16.24
Q6IBR2	FARSLA protein OS=Homo sapiens GN=FARSLA PE=2 SV=1	13	0.88	1.02	1.16	8	0.95	0.94	0.96	9	0.99	0.96	0.91	5.94	4.56	12.78
Q96T76	MMS19 nucleotide excision repair protein homolog OS=Homo sapiens GN=MMS19 PE=1 SV=2	14	0.82	0.95	0.96	11	0.89	0.92	0.95	10	0.97	1.04	0.93	8.34	6.39	1.72
O14744	Protein arginine N-methyltransferase 5 OS=Homo sapiens GN=PRMT5 PE=1 SV=4	12	0.87	0.97	1.05	13	1.01	1.08	0.99	9	1.11	1.09	1.06	12.09	6.62	3.46

P11177	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial OS=Homo sapiens GN=PDHB PE=1 SV=3	16	0.92	1.02	0.98	12	0.87	1.00	0.93	7	0.86	0.97	0.94	3.77	2.41	2.69
Q6P2E9	Enhancer of mRNA-decapping protein 4 OS=Homo sapiens GN=EDC4 PE=1 SV=1	13	0.95	1.00	0.94	22	1.00	1.02	1.02	16	0.94	0.98	0.99	3.44	1.90	4.16
P13674	Prolyl 4-hydroxylase subunit alpha-1 OS=Homo sapiens GN=P4HA1 PE=1 SV=2	15	1.17	0.89	0.94	10	1.51	1.10	1.34	8	1.13	0.89	1.05	16.39	12.64	18.79
O60884	DnaJ homolog subfamily A member 2 OS=Homo sapiens GN=DNAJA2 PE=1 SV=1	16	1.01	1.04	1.05	12	1.03	0.95	0.97	13	1.08	1.06	1.04	3.33	5.87	4.29
Q16352	Alpha-internexin OS=Homo sapiens GN=INA PE=1 SV=2	16	0.96	1.03	1.03	19	1.03	0.94	1.00	17	0.95	1.07	0.99	4.63	6.57	2.20
A5YKK6	CCR4-NOT transcription complex subunit 1 OS=Homo sapiens GN=CNOT1 PE=1 SV=2	10	0.97	1.00	0.98	11	0.86	1.06	0.96	9	0.99	1.03	0.94	7.31	2.81	1.91
P61106	Ras-related protein Rab-14 OS=Homo sapiens GN=RAB14 PE=1 SV=4	12	1.37	0.92	1.14	10	1.05	0.89	1.07	9	1.33	1.06	1.12	13.87	9.71	3.13
Q69YJ7	Putative uncharacterized protein DKFZp667H197 (Fragment) OS=Homo sapiens GN=DKFZp667H197 PE=2 SV=1	13	0.73	0.92	0.81	6	0.97	0.97	0.92	6	1.04	1.19	1.23	17.78	13.59	21.95
P19623	Spermidine synthase OS=Homo sapiens GN=SRM PE=1 SV=1	12	0.98	1.13	0.99	9	0.90	0.95	0.93	7	0.94	0.90	0.88	4.31	11.78	6.10
Q96N67	Dedicator of cytokinesis protein 7 OS=Homo sapiens GN=DOCK7 PE=1 SV=4	11	0.91	1.07	1.18	8	0.94	0.92	0.92	10	0.94	0.96	1.02	2.24	7.82	12.85
Q9UBE0	SUMO-activating enzyme subunit 1 OS=Homo sapiens GN=SAE1 PE=1 SV=1	16	0.94	1.06	0.91	13	0.92	1.05	0.97	12	0.87	0.93	0.95	4.05	7.10	3.76
Q7Z2W4	Zinc finger CCCH-type antiviral protein 1 OS=Homo sapiens GN=ZC3HAV1 PE=1 SV=3	13	0.93	0.98	1.10	8	1.01	0.97	1.06	8	1.09	1.08	1.10	8.09	5.62	2.22
Q07021	Complement component 1 Q subcomponent-binding protein, mitochondrial OS=Homo sapiens GN=C1QBP PE=1 SV=1	23	0.92	0.98	1.02	15	0.94	0.91	0.89	17	0.91	0.98	0.95	1.87	4.35	7.02
Q6IBS8	DDC protein OS=Homo sapiens GN=DDC PE=2 SV=1	11	0.81	1.07	0.99	7	0.77	0.95	0.83	10	0.84	1.06	0.90	4.33	6.66	8.86
O76003	Glutaredoxin-3 OS=Homo sapiens GN=GLRX3 PE=1 SV=2	11	1.08	1.01	1.16	10	1.03	1.02	1.06	8	1.04	0.94	0.95	2.64	4.51	9.80
B3KN06	Coronin OS=Homo sapiens PE=2 SV=1	18	1.14	1.11	0.99	7	0.98	1.11	1.06	9	0.99	1.04	0.98	8.42	3.82	4.38
O95831	Apoptosis-inducing factor 1, mitochondrial OS=Homo sapiens GN=AIFM1 PE=1 SV=1	11	1.06	1.02	1.09	13	1.09	1.05	1.06	10	1.07	0.98	1.02	1.54	3.57	3.17
P55010	Eukaryotic translation initiation factor 5 OS=Homo sapiens GN=EIF5 PE=1 SV=2	11	1.07	1.00	1.06	10	1.12	0.95	1.04	12	1.10	1.06	1.11	2.01	5.29	3.09
Q13308	Inactive tyrosine-protein kinase 7 OS=Homo sapiens GN=PTK7 PE=1 SV=2	11	1.03	1.02	1.12	9	0.81	0.86	0.91	8	0.94	0.95	0.94	11.78	8.79	11.17
Q9HDC9	Adipocyte plasma membrane-associated protein OS=Homo sapiens GN=APMAP PE=1 SV=2	13	1.12	0.99	0.99	8	1.17	0.95	1.05	12	1.05	0.99	1.03	5.10	2.38	3.09
Q5JR94	40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=2 SV=1	20	0.94	0.99	1.03	19	0.87	0.87	0.89	20	0.95	1.09	1.02	4.48	10.98	8.10
Q9UHD1	Cysteine and histidine-rich domain-containing protein 1 OS=Homo sapiens GN=CHORDC1 PE=1 SV=2	14	0.97	0.98	0.88	8	1.06	0.99	1.05	8	1.00	0.96	1.01	4.61	1.59	9.39
P05387	60S acidic ribosomal protein P2 OS=Homo sapiens GN=RPLP2 PE=1 SV=1	35	0.98	1.02	0.99	37	0.97	0.95	0.90	25	0.97	1.01	1.00	0.54	3.91	5.88

Q96ME1-4	Isoform 4 of F-box/LRR-repeat protein 18 OS=Homo sapiens GN=FBXL18	12	0.81	0.92	1.12	9	1.05	0.90	0.95	6	0.74	0.96	0.92	19.12	3.31	11.02
Q96AG4	Leucine-rich repeat-containing protein 59 OS=Homo sapiens GN=LRRC59 PE=1 SV=1	17	1.17	0.97	1.09	14	1.18	0.92	1.03	14	1.22	1.03	1.11	2.42	5.86	3.62
Q9NZL4	Hsp70-binding protein 1 OS=Homo sapiens GN=HSPBP1 PE=1 SV=1	14	0.86	0.96	0.95	12	0.93	0.93	0.85	8	0.85	1.02	0.94	4.78	5.06	5.83
P39656	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=Homo sapiens GN=DDOST PE=1 SV=4	22	1.11	1.01	1.17	13	1.00	0.86	0.97	11	1.03	1.02	1.02	5.29	9.07	10.18
P09936	Ubiquitin carboxyl-terminal hydrolase isozyme L1 OS=Homo sapiens GN=UCHL1 PE=1 SV=2	55	1.03	1.11	1.07	39	1.04	1.13	1.03	44	0.96	1.05	1.06	4.35	4.03	2.10
A7E2Y5	DnaJ (Hsp40) homolog, subfamily C, member 13 OS=Homo sapiens GN=DNAJC13 PE=2 SV=1	12	1.16	1.05	0.99	14	1.04	0.99	0.98	9	1.06	0.99	0.97	5.79	3.16	1.32
Q06830	Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1	23	0.95	0.98	0.79	14	1.09	1.16	1.04	17	0.96	0.83	0.95	7.77	16.82	13.64
B4DLN1	Mitochondrial dicarboxylate carrier OS=Homo sapiens GN=SLC25A10 PE=2 SV=1	14	0.88	0.92	0.75	12	1.13	1.04	1.04	13	0.96	0.91	0.88	13.12	7.65	16.34
Q9NVI7-2	Isoform 2 of ATPase family AAA domain-containing protein 3A OS=Homo sapiens GN=ATAD3A	11	0.90	0.82	1.03	9	0.93	0.87	0.93	10	0.98	0.92	1.02	4.25	5.64	5.95
G3V1C3	Apoptosis inhibitor 5 OS=Homo sapiens GN=API5 PE=2 SV=1	12	0.97	0.97	0.99	15	0.98	1.07	1.02	13	0.94	0.99	0.99	2.30	4.94	1.66
Q12756	Kinesin-like protein KIF1A OS=Homo sapiens GN=KIF1A PE=1 SV=2	9	1.02	0.99	0.93	8	1.00	1.05	0.99	7	0.91	0.97	0.87	5.84	3.82	6.42
B3KY12	cDNA FLJ46581 fis, clone THYMU3043200, highly similar to Splicing factor 3A subunit 3 OS=Homo sapiens PE=2 SV=1	12	0.93	0.99	0.86	10	1.02	1.04	0.96	16	0.86	0.95	0.91	8.64	4.74	5.63
Q9NXF1	Testis-expressed sequence 10 protein OS=Homo sapiens GN=TEX10 PE=1 SV=2	11	0.91	0.95	1.03	9	1.02	1.05	1.00	5	0.98	0.91	1.01	5.55	6.98	1.56
O60271	C-Jun-amino-terminal kinase-interacting protein 4 OS=Homo sapiens GN=SPAG9 PE=1 SV=4	12	0.93	0.99	1.03	6	1.10	1.05	1.09	8	1.06	1.15	1.20	8.39	7.81	8.02
P13804	Electron transfer flavoprotein subunit alpha, mitochondrial OS=Homo sapiens GN=ETFA PE=1 SV=1	11	0.83	0.98	0.99	9	0.78	0.83	0.78	9	0.85	0.98	0.88	4.29	9.24	11.81
P62249	40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=1 SV=2	14	1.03	1.02	1.00	14	1.09	1.02	0.99	10	0.99	0.99	0.87	4.84	1.69	7.49
Q53HW2	Ribosomal protein P0 variant (Fragment) OS=Homo sapiens PE=2 SV=1	18	1.03	1.02	1.04	22	1.04	0.96	1.03	15	1.03	0.94	1.03	0.63	4.32	0.61
D0PQI2	Enabled-like protein variant hMenaDv6 OS=Homo sapiens GN=ENAH PE=2 SV=1	13	0.96	1.00	0.89	11	1.22	1.20	1.13	7	1.12	1.01	1.12	12.36	10.51	12.81
Q53R19	Actin related protein 2/3 complex, subunit 2, 34kDa, isoform CRA_a OS=Homo sapiens GN=ARPC2 PE=2 SV=1	13	1.04	1.03	1.09	11	0.95	0.96	1.01	11	0.97	1.06	0.99	4.46	4.65	5.50
Q96I24	Far upstream element-binding protein 3 OS=Homo sapiens GN=FUBP3 PE=1 SV=2	15	1.13	0.90	0.89	10	0.92	0.97	0.97	11	1.21	1.09	0.98	13.67	9.66	5.35
P36507	Dual specificity mitogen-activated protein kinase kinase 2 OS=Homo sapiens GN=MAP2K2 PE=1 SV=1	13	0.93	0.83	0.96	11	1.13	1.10	1.04	10	1.03	1.00	0.99	9.53	14.07	4.35
Q5SRE5	Nucleoporin NUP188 homolog OS=Homo sapiens GN=NUP188 PE=1 SV=1	10	0.98	0.99	1.01	12	0.91	0.82	0.85	7	0.93	0.93	0.96	4.07	9.73	9.10

Q9NTJ5	Phosphatidylinositide phosphatase SAC1 OS=Homo sapiens GN=SACM1L PE=1 SV=2	11	1.06	0.99	0.96	11	0.97	0.93	0.94	9	0.97	1.00	1.05	5.46	3.99	5.99
Q5U058	Growth associated protein 43 OS=Homo sapiens GN=GAP43 PE=2 SV=1	13	0.92	1.11	0.89	7	0.93	1.19	0.92	7	1.09	1.29	1.24	9.94	7.68	19.10
A4LAA3	Alpha thalassemia/mental retardation syndrome X-linked OS=Homo sapiens GN=ATRX PE=4 SV=1	10	0.89	0.99	0.96	7	1.21	1.10	1.03	3	1.23	1.04	1.16	17.35	5.09	9.71
O60216	Double-strand-break repair protein rad21 homolog OS=Homo sapiens GN=RAD21 PE=1 SV=2	11	0.94	1.11	0.88	8	0.99	0.92	0.91	6	0.89	1.06	0.96	5.29	9.23	4.46
Q6IB58	FLOT1 protein OS=Homo sapiens GN=FLOT1 PE=2 SV=1	10	1.13	0.92	0.86	9	1.27	1.16	1.18	13	1.02	1.04	1.06	11.23	11.18	15.19
P57737-3	Isoform 3 of Coronin-7 OS=Homo sapiens GN=CORO7	12	1.11	0.90	0.96	9	1.03	1.02	1.01	9	1.09	1.04	1.05	4.04	7.23	4.47
Q9Y383	Putative RNA-binding protein Luc7-like 2 OS=Homo sapiens GN=LUC7L2 PE=1 SV=2	13	1.13	1.05	1.02	9	1.02	0.98	0.98	6	0.94	1.05	0.95	9.08	4.31	3.58
E9PEN8	Exportin-7 OS=Homo sapiens GN=XPO7 PE=2 SV=1	12	1.14	1.03	0.91	9	0.99	1.06	1.02	14	0.96	1.01	0.96	9.29	2.50	5.85
F1T0A5	PRP31 pre-mRNA processing factor 31 homolog (Yeast), isoform CRA_a OS=Homo sapiens GN=PRPF31 PE=2 SV=1	12	0.89	1.03	0.93	8	0.79	0.86	0.89	8	0.95	0.95	1.07	9.56	9.03	9.73
Q5SRT3	Chloride intracellular channel 1, isoform CRA_a OS=Homo sapiens GN=CLIC1 PE=2 SV=2	12	1.19	0.99	1.19	11	1.18	0.91	1.07	13	1.15	1.03	1.13	2.17	6.36	5.14
P53004	Biliverdin reductase A OS=Homo sapiens GN=BLVRA PE=1 SV=2	17	0.84	1.10	1.04	12	0.82	0.99	0.86	11	0.96	1.11	0.97	8.76	6.37	9.90
Q8N4P8	Nucleolar GTP-binding protein 1 (Fragment) OS=Homo sapiens GN=GTPBP4 PE=2 SV=1	11	0.95	1.02	0.78	8	0.96	0.97	0.98	8	0.97	1.02	0.96	1.08	2.49	12.35
P82933	28S ribosomal protein S9, mitochondrial OS=Homo sapiens GN=MRPS9 PE=1 SV=2	10	0.94	0.89	0.85	7	1.06	1.09	1.00	6	0.91	0.87	0.96	8.08	12.84	8.38
Q9BR76	Coronin-1B OS=Homo sapiens GN=CORO1B PE=1 SV=1	17	1.00	0.96	0.95	9	0.99	1.04	1.04	7	0.97	0.95	1.00	1.58	4.97	4.57
P04792	Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2	23	1.14	1.04	1.12	19	1.18	0.98	1.20	15	1.22	1.12	1.26	3.57	6.67	5.97
A6PVN5	Serine/threonine-protein phosphatase 2A activator OS=Homo sapiens GN=PPP2R4 PE=2 SV=1	10	0.96	1.09	1.16	7	1.02	1.00	0.95	8	0.92	0.99	1.02	5.30	5.43	10.51
Q9BWF3	RNA-binding protein 4 OS=Homo sapiens GN=RBM4 PE=1 SV=1	13	0.96	0.89	0.96	10	0.83	0.87	0.97	9	0.84	0.94	0.88	8.26	3.71	5.30
J3KQG4	Glucosylceramidase OS=Homo sapiens GN=GBA PE=4 SV=1	14	1.13	1.07	1.19	9	1.09	0.95	1.11	11	1.04	0.96	1.05	4.33	6.85	6.06
P67809	Nuclease-sensitive element-binding protein 1 OS=Homo sapiens GN=YBX1 PE=1 SV=3	31	0.90	0.99	0.98	23	0.99	1.03	0.97	31	0.98	0.98	0.99	5.09	2.97	1.31
Q9Y2Z0	Suppressor of G2 allele of SKP1 homolog OS=Homo sapiens GN=SUGT1 PE=1 SV=3	14	0.98	0.99	0.97	9	0.98	0.90	0.90	11	0.96	0.92	1.02	1.09	5.13	6.48
Q12904	Aminoacyl tRNA synthase complex-interacting multifunctional protein 1 OS=Homo sapiens GN=AIMP1 PE=1 SV=2	11	0.95	0.98	0.92	11	1.43	1.01	1.35	10	0.92	0.99	0.94	25.83	1.35	22.67
Q93034	Cullin-5 OS=Homo sapiens GN=CUL5 PE=1 SV=4	11	1.09	0.96	0.99	7	0.99	1.14	1.06	5	0.98	1.04	1.06	5.98	8.56	4.01
P62906	60S ribosomal protein L10a OS=Homo sapiens GN=RPL10A PE=1 SV=2	16	1.04	1.02	1.04	12	1.16	1.10	1.05	13	1.04	0.90	1.03	6.49	9.89	1.31

B7Z6H3	Peptidyl-prolyl cis-trans isomerase FKBP9 OS=Homo sapiens GN=FKBP9 PE=2 SV=1	11	0.98	1.00	1.03	13	0.92	0.84	0.94	11	1.00	0.90	0.98	4.33	8.63	4.83
K7ELJ7	Calpain small subunit 1 OS=Homo sapiens GN=CAPNS1 PE=4 SV=1	17	1.05	0.96	1.19	15	1.00	0.88	1.01	12	1.03	1.16	1.21	2.59	14.54	9.69
Q3LXA3	Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing) OS=Homo sapiens GN=DAK PE=1 SV=2	11	0.98	1.14	1.18	8	0.86	0.98	1.01	9	1.01	0.97	0.90	8.11	9.25	13.87
B1AVU8	Saposin-D OS=Homo sapiens GN=PSAP PE=2 SV=1	19	1.23	1.15	0.74	21	0.92	1.20	1.00	14	1.02	0.91	0.93	15.23	13.93	14.90
Q9UNF1	Melanoma-associated antigen D2 OS=Homo sapiens GN=MAGED2 PE=1 SV=2	13	0.80	0.96	0.92	7	0.76	0.96	0.82	7	0.66	1.07	0.90	10.03	6.47	6.36
P30044	Peroxiredoxin-5, mitochondrial OS=Homo sapiens GN=PRDX5 PE=1 SV=4	14	1.05	1.07	1.06	14	1.02	1.01	1.00	23	1.00	1.04	0.89	2.23	3.04	8.71
Q9UNM6	26S proteasome non-ATPase regulatory subunit 13 OS=Homo sapiens GN=PSMD13 PE=1 SV=2	18	0.94	1.00	1.02	20	0.87	0.89	0.88	19	1.00	1.07	1.00	7.09	9.06	7.87
P52907	F-actin-capping protein subunit alpha-1 OS=Homo sapiens GN=CAPZA1 PE=1 SV=3	16	1.03	1.02	1.10	11	0.96	1.05	0.98	12	0.97	1.05	1.02	3.88	1.51	5.86
Q8IXI1	Mitochondrial Rho GTPase 2 OS=Homo sapiens GN=RHOT2 PE=1 SV=2	14	0.97	0.84	1.09	13	1.15	1.01	1.23	7	1.06	1.13	1.00	8.88	14.70	10.43
A6NFX8	ADP-sugar pyrophosphatase OS=Homo sapiens GN=NUDT5 PE=2 SV=1	13	1.05	0.93	1.04	12	1.07	1.02	1.08	12	1.03	0.95	1.02	1.71	5.00	2.83
Q00796	Sorbitol dehydrogenase OS=Homo sapiens GN=SORD PE=1 SV=4	12	0.92	0.98	0.71	11	0.69	0.90	0.84	6	0.89	1.05	0.97	15.27	7.35	15.03
Q9H2M9	Rab3 GTPase-activating protein non-catalytic subunit OS=Homo sapiens GN=RAB3GAP2 PE=1 SV=1	11	1.15	1.11	1.10	8	1.20	1.13	1.19	6	0.93	0.90	0.93	12.96	12.57	12.47
O95433	Activator of 90 kDa heat shock protein ATPase homolog 1 OS=Homo sapiens GN=AHSA1 PE=1 SV=1	14	1.00	1.00	1.04	20	0.93	0.98	0.93	16	0.86	0.95	0.86	7.70	2.26	9.41
Q1HBJ4	Mitogen-activated protein kinase 1 OS=Homo sapiens GN=MAPK1 PE=2 SV=1	10	1.05	1.22	1.08	7	1.00	1.02	1.03	7	0.97	0.98	1.00	4.11	12.30	3.83
Q6FII1	Glutathione S-transferase kappa 1 OS=Homo sapiens GN=LOC51064 PE=2 SV=1	13	1.08	1.07	1.08	11	1.07	1.03	1.05	12	1.05	1.02	1.16	1.45	2.27	5.15
B4DXZ6	Fragile X mental retardation syndrome-related protein 1 OS=Homo sapiens GN=FXR1 PE=2 SV=1	14	0.92	0.85	0.90	9	0.88	0.93	0.94	6	0.93	1.01	0.93	2.59	8.46	2.60
O95782	AP-2 complex subunit alpha-1 OS=Homo sapiens GN=AP2A1 PE=1 SV=3	22	0.83	0.97	0.77	12	0.94	0.91	0.95	14	0.96	1.12	0.97	7.43	11.05	12.04
P62280	40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=1 SV=3	12	0.91	0.98	0.77	9	1.09	1.13	1.08	8	1.02	0.90	0.99	8.91	11.82	16.60
Q9BTV4	Transmembrane protein 43 OS=Homo sapiens GN=TMEM43 PE=1 SV=1	13	1.21	0.94	1.13	10	1.24	1.00	1.13	12	1.19	1.01	1.21	1.97	3.74	4.15
B2RDH6	cDNA, FLJ96613, highly similar to Homo sapiens vacuolar protein sorting 33A (yeast) (VPS33A), mRNA OS=Homo sapiens PE=2 SV=1	12	1.00	0.95	0.97	6	1.10	1.17	1.02	6	0.96	0.81	0.86	7.05	18.24	8.72
J3QK89	Calcium homeostasis endoplasmic reticulum protein OS=Homo sapiens GN=CHERP PE=4 SV=1	13	0.80	0.91	0.78	11	0.98	1.09	0.99	8	0.96	0.91	0.87	10.74	10.80	12.53

Q9NUU7	ATP-dependent RNA helicase DDX19A OS=Homo sapiens GN=DDX19A PE=1 SV=1	11	0.79	0.93	0.83	10	0.93	0.95	0.92	8	1.02	1.18	0.92	12.70	13.39	5.59
Q13616	Cullin-1 OS=Homo sapiens GN=CUL1 PE=1 SV=2	9	1.00	1.03	0.92	10	1.09	1.07	1.08	11	0.87	0.91	0.96	11.32	8.62	8.01
Q8NI27	THO complex subunit 2 OS=Homo sapiens GN=THOC2 PE=1 SV=2	9	1.05	1.12	1.04	7	0.86	1.02	0.95	7	0.97	1.02	1.07	9.86	5.46	5.98
Q53F02	Cleavage and polyadenylation specific factor 3, 73kDa variant (Fragment) OS=Homo sapiens PE=2 SV=1	11	0.85	0.95	1.04	8	0.83	0.89	0.80	9	0.99	1.04	0.96	9.63	8.13	13.12
Q9Y263	Phospholipase A-2-activating protein OS=Homo sapiens GN=PLAA PE=1 SV=2	10	1.15	1.14	0.99	8	0.98	1.12	1.03	10	1.01	0.95	0.98	8.32	9.88	2.56
Q7L0Y3	Mitochondrial ribonuclease P protein 1 OS=Homo sapiens GN=TRMT10C PE=1 SV=2	11	1.07	0.98	1.09	10	1.16	0.95	1.09	12	0.96	1.09	0.97	9.62	7.13	6.30
O00154	Cytosolic acyl coenzyme A thioester hydrolase OS=Homo sapiens GN=ACOT7 PE=1 SV=3	12	0.90	1.01	0.97	13	0.92	1.01	0.94	12	0.92	1.06	0.94	1.51	2.94	1.91
G3V5Z7	Proteasome subunit alpha type OS=Homo sapiens GN=PSMA6 PE=2 SV=1	11	0.97	1.01	1.17	11	0.96	0.96	0.95	11	0.97	1.05	1.00	0.58	4.64	10.85
G5EA30	CUG triplet repeat, RNA binding protein 1, isoform CRA_c OS=Homo sapiens GN=CELF1 PE=2 SV=1	12	1.00	0.92	0.83	10	1.14	1.14	1.07	9	0.94	0.92	1.03	9.95	12.85	13.46
Q6PKH8	ANP32A protein (Fragment) OS=Homo sapiens GN=ANP32A PE=2 SV=1	14	0.90	1.01	0.91	11	0.90	0.96	0.85	10	0.89	1.13	1.00	0.75	8.73	8.08
Q15293	Reticulocalbin-1 OS=Homo sapiens GN=RCN1 PE=1 SV=1	15	1.56	1.05	1.30	9	1.51	1.05	1.27	10	1.44	0.97	1.47	3.98	4.45	8.25
D6W4Z6	HCG23833, isoform CRA_b OS=Homo sapiens GN=hCG_23833 PE=4 SV=1	12	0.70	0.82	0.75	9	0.81	1.06	0.94	8	0.76	1.05	0.95	7.33	13.76	12.44
Q2NL82	Pre-rRNA-processing protein TSR1 homolog OS=Homo sapiens GN=TSR1 PE=1 SV=1	13	0.96	1.00	0.90	10	0.95	1.06	0.91	10	0.94	0.95	0.94	1.20	5.70	2.38
Q92823	Neuronal cell adhesion molecule OS=Homo sapiens GN=NRCAM PE=1 SV=3	9	1.12	1.02	1.05	10	0.91	1.00	0.98	7	1.13	1.25	0.91	11.91	13.08	6.90
Q6IB98	Eukaryotic translation initiation factor 3 subunit H OS=Homo sapiens GN=EIF3H PE=2 SV=1	10	0.94	0.98	0.78	8	1.43	1.21	1.25	9	1.07	0.82	1.06	22.38	19.58	23.21
B1AKJ5	Nardilysin OS=Homo sapiens GN=NRD1 PE=2 SV=1	12	0.99	1.01	1.02	12	0.93	0.92	0.92	11	0.95	0.95	0.90	3.17	5.06	6.37
A8K905	cDNA FLJ77615, highly similar to Homo sapiens nucleolar complex associated 3 homolog (S. cerevisiae) (NOC3L), mRNA OS=Homo sapiens PE=2 SV=1	10	1.01	0.87	0.83	9	1.08	1.07	0.97	6	0.99	0.97	1.06	4.63	10.15	11.97
K4DI93	Cullin 4B, isoform CRA_e OS=Homo sapiens GN=CUL4B PE=3 SV=1	11	1.05	0.71	0.99	7	1.47	1.26	1.24	6	0.95	0.91	0.85	24.24	28.67	19.26
P17812	CTP synthase 1 OS=Homo sapiens GN=CTPS1 PE=1 SV=2	12	1.02	1.09	1.05	13	1.04	0.99	1.08	9	1.14	0.98	1.01	5.82	6.25	3.23
Q96TA1	Niban-like protein 1 OS=Homo sapiens GN=FAM129B PE=1 SV=3	12	0.97	1.04	1.21	5	0.85	0.81	0.97	8	1.15	1.14	1.20	15.07	16.98	12.26
P04040	Catalase OS=Homo sapiens GN=CAT PE=1 SV=3	10	1.08	0.93	0.94	10	1.15	1.12	1.03	10	0.96	0.89	0.93	9.17	12.37	5.94
Q13315	Serine-protein kinase ATM OS=Homo sapiens GN=ATM PE=1 SV=3	9	0.83	0.93	0.90	7	0.86	1.03	0.95	6	0.90	0.98	0.92	4.13	5.41	2.82
P23786	Carnitine O-palmitoyltransferase 2, mitochondrial OS=Homo sapiens GN=CPT2 PE=1 SV=2	11	0.48	0.68	0.60	7	1.73	1.80	1.09	8	0.89	0.92	0.79	61.82	52.36	29.78

Q9BPW8	Protein NipSnap homolog 1 OS=Homo sapiens GN=NIPSNAP1 PE=1 SV=1	21	0.99	0.98	0.95	11	1.15	1.06	1.06	18	0.97	1.00	0.93	9.70	4.11	7.06
B4DR87	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1 OS=Homo sapiens GN=PLOD1 PE=2 SV=1	13	1.10	0.89	1.20	10	0.86	0.89	0.99	9	1.05	1.13	0.95	12.45	14.61	12.68
Q8TBR3	Fusion (Involved in t(1216) in malignant liposarcoma) OS=Homo sapiens GN=FUS PE=2 SV=1	15	0.92	0.96	0.93	11	1.11	1.14	1.05	12	1.02	0.96	1.05	9.27	10.09	6.44
Q9H2U1	Probable ATP-dependent RNA helicase DHX36 OS=Homo sapiens GN=DHX36 PE=1 SV=2	10	0.97	1.03	1.04	12	0.99	0.95	0.96	9	0.94	1.05	0.94	2.80	5.22	5.45
P09543	2',3'-cyclic-nucleotide 3'-phosphodiesterase OS=Homo sapiens GN=CNP PE=1 SV=2	10	1.06	1.01	1.00	8	1.05	1.07	0.92	9	0.98	0.92	1.14	4.43	7.55	10.89
Q5SSJ5	Heterochromatin protein 1-binding protein 3 OS=Homo sapiens GN=HP1BP3 PE=1 SV=1	13	0.99	0.94	1.09	8	0.99	0.96	1.00	9	1.02	0.97	1.00	1.75	1.75	5.58
P62081	40S ribosomal protein S7 OS=Homo sapiens GN=RPS7 PE=1 SV=1	26	0.88	1.05	0.95	11	0.92	0.95	0.94	16	0.92	0.97	0.99	2.53	5.07	2.58
Q05639	Elongation factor 1-alpha 2 OS=Homo sapiens GN=EEF1A2 PE=1 SV=1	78	0.99	1.12	1.13	51	1.08	1.12	1.15	45	1.06	1.05	0.95	4.68	3.93	10.23
P18085	ADP-ribosylation factor 4 OS=Homo sapiens GN=ARF4 PE=1 SV=3	15	1.08	1.03	1.23	15	1.08	0.98	1.02	9	0.95	1.03	0.95	7.32	2.60	13.66
P43034	Platelet-activating factor acetylhydrolase IB subunit alpha OS=Homo sapiens GN=PAFAH1B1 PE=1 SV=2	10	0.86	0.93	0.93	11	1.12	1.02	1.21	7	1.05	0.94	0.97	13.65	4.75	14.58
Q86UE4	Protein LYRIC OS=Homo sapiens GN=MTDH PE=1 SV=2	12	1.44	1.04	1.33	10	1.21	1.01	1.18	7	1.11	1.09	1.19	13.49	3.84	6.78
Q10713	Mitochondrial-processing peptidase subunit alpha OS=Homo sapiens GN=PMPCA PE=1 SV=2	10	0.83	0.91	0.86	8	0.96	1.05	0.93	5	0.92	0.96	0.96	7.63	7.06	5.58
Q9BRK5	45 kDa calcium-binding protein OS=Homo sapiens GN=SDF4 PE=1 SV=1	9	1.31	0.99	1.16	8	1.21	0.94	1.11	8	1.31	1.01	1.22	4.50	3.62	4.83
A4D1U5	Multiple substrate lipid kinase, isoform CRA_a OS=Homo sapiens GN=FLJ10842 PE=2 SV=1	17	1.19	1.02	1.04	13	1.18	0.94	1.11	7	1.10	1.01	0.99	4.23	4.20	5.55
Q5T081	CHC1 protein OS=Homo sapiens GN=RCC1 PE=2 SV=1	10	1.08	1.01	1.16	8	0.87	0.84	0.88	8	1.15	1.06	1.18	14.20	11.76	15.91
Q9UBQ7	Glyoxylate reductase/hydroxypyruvate reductase OS=Homo sapiens GN=GRHPR PE=1 SV=1	11	0.90	0.89	0.95	10	1.11	1.12	1.16	7	0.93	0.91	0.90	11.63	12.90	13.82
Q9H9B4	Sideroflexin-1 OS=Homo sapiens GN=SFXN1 PE=1 SV=4	22	1.37	0.92	1.27	17	1.12	0.95	1.20	15	1.16	1.03	1.02	10.72	6.29	11.05
Q92522	Histone H1x OS=Homo sapiens GN=H1FX PE=1 SV=1	21	1.39	1.00	1.19	7	1.15	0.95	1.17	8	1.30	1.08	1.23	9.46	6.94	2.26
B4DRT2	28S ribosomal protein S27, mitochondrial OS=Homo sapiens GN=MRPS27 PE=2 SV=1	11	0.92	1.02	0.81	10	1.06	1.08	1.05	10	0.97	0.92	0.96	7.41	8.03	12.39
Q14108	Lysosome membrane protein 2 OS=Homo sapiens GN=SCARB2 PE=1 SV=2	10	1.14	0.96	1.04	7	1.06	0.92	1.03	8	1.13	1.13	1.18	4.10	10.87	7.41
P54920	Alpha-soluble NSF attachment protein OS=Homo sapiens GN=NAPA PE=1 SV=3	10	1.08	0.99	1.02	11	1.03	0.91	0.92	11	1.02	0.94	0.93	3.00	4.19	5.88
B3KUN1	Serine/threonine-protein phosphatase OS=Homo sapiens GN=PPP2CA PE=2 SV=1	11	0.93	1.05	0.96	14	0.90	1.09	1.00	14	0.82	0.89	0.82	6.65	10.69	10.57
E7EM64	COP9 signalosome complex subunit 6 OS=Homo sapiens GN=COPS6 PE=2 SV=1	10	0.90	0.91	0.86	12	1.06	1.01	1.06	5	1.00	1.01	0.93	8.08	5.57	10.50

P63279	SUMO-conjugating enzyme UBC9 OS=Homo sapiens GN=UBE2I PE=1 SV=1	9	0.93	1.03	0.78	7	1.14	1.22	1.09	8	1.05	0.87	1.02	10.21	16.83	16.60
P25398	40S ribosomal protein S12 OS=Homo sapiens GN=RPS12 PE=1 SV=3	14	1.01	1.03	0.88	15	1.02	1.04	1.00	12	0.99	0.97	1.06	1.83	3.66	9.16
Q6FGJ9	GSTM3 protein OS=Homo sapiens GN=GSTM3 PE=2 SV=1	9	1.11	1.04	1.18	7	1.01	1.00	1.01	5	1.09	1.13	1.06	4.87	6.26	8.05
G3V4W0	Heterogeneous nuclear ribonucleoproteins C1/C2 (Fragment) OS=Homo sapiens GN=HNRNPC PE=2 SV=1	11	1.14	0.99	1.00	16	1.21	1.04	1.19	14	1.21	0.94	1.11	3.21	4.90	8.77
B4DP80	NAD(P)H-hydrate epimerase OS=Homo sapiens GN=APOA1BP PE=2 SV=1	10	0.98	1.05	0.89	10	1.09	1.09	1.12	7	1.12	1.01	1.11	7.33	4.01	12.45
Q96EY7	Pentatricopeptide repeat domain-containing protein 3, mitochondrial OS=Homo sapiens GN=PTCD3 PE=1 SV=3	10	1.08	1.15	0.90	8	1.03	1.15	1.20	9	1.04	0.90	1.02	2.93	13.12	14.52
E7EQ69	N-alpha-acetyltransferase 50 OS=Homo sapiens GN=NAA50 PE=2 SV=1	9	1.04	0.99	0.91	7	0.96	0.97	0.90	7	1.06	1.10	1.03	5.25	6.84	7.63
B3KQF0	cDNA FLJ90354 fis, clone NT2RP2003390, highly similar to Translocation protein SEC63 homolog OS=Homo sapiens PE=2 SV=1	10	1.10	0.96	1.14	7	1.09	0.91	1.11	8	1.17	0.93	1.15	3.88	2.66	1.78
E7EWR4	Cleavage stimulation factor subunit 2 OS=Homo sapiens GN=CSTF2 PE=2 SV=1	13	0.91	0.92	1.20	11	0.70	0.79	0.81	5	0.80	1.05	1.03	12.88	14.00	19.65
E7D7X9	Pyrroline-5-carboxylate reductase OS=Homo sapiens PE=2 SV=1	15	1.12	1.01	1.10	14	1.24	1.02	1.15	13	1.19	0.91	1.14	5.30	6.18	2.24
Q8WX92	Negative elongation factor B OS=Homo sapiens GN=NELFB PE=1 SV=1	10	1.01	0.84	1.03	9	1.15	1.17	1.05	9	0.93	1.08	0.98	10.54	16.62	3.58
Q96GM5	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 1 OS=Homo sapiens GN=SMARCD1 PE=1 SV=2	10	1.27	0.99	0.98	7	0.73	0.82	0.80	4	0.85	1.01	0.95	29.85	11.09	10.75
P61289	Proteasome activator complex subunit 3 OS=Homo sapiens GN=PSME3 PE=1 SV=1	10	0.85	1.02	0.97	12	0.84	0.95	0.85	10	0.88	1.06	0.90	2.59	5.53	6.63
P16401	Histone H1.5 OS=Homo sapiens GN=HIST1H1B PE=1 SV=3	26	1.77	1.08	1.24	16	2.18	1.28	1.81	12	1.83	1.04	1.85	11.41	11.12	20.89
O14818	Proteasome subunit alpha type-7 OS=Homo sapiens GN=PSMA7 PE=1 SV=1	13	0.92	0.97	1.02	14	0.95	0.99	0.98	14	0.98	1.09	0.97	3.30	6.10	2.74
Q12797	Aspartyl/asparaginyl beta-hydroxylase OS=Homo sapiens GN=ASPH PE=1 SV=3	9	1.07	0.97	0.99	8	1.38	1.15	1.26	10	1.12	1.05	1.04	13.92	8.47	13.28
P46781	40S ribosomal protein S9 OS=Homo sapiens GN=RPS9 PE=1 SV=3	11	0.93	0.99	1.01	11	0.93	0.95	0.93	12	0.97	1.04	1.02	2.60	4.54	5.00
B0FTY2	NudC-like protein OS=Homo sapiens PE=2 SV=1	10	0.80	1.04	0.93	9	0.95	0.98	0.93	8	0.99	1.03	1.03	11.38	3.25	5.78
Q6FGU2	DTYMK protein (Fragment) OS=Homo sapiens GN=DTYMK PE=2 SV=1	9	0.96	1.02	0.95	7	0.98	1.20	1.05	8	0.97	0.97	0.91	1.10	11.52	6.93
Q9NQR4	Omega-amidase NIT2 OS=Homo sapiens GN=NIT2 PE=1 SV=1	9	0.86	1.06	1.10	9	1.06	1.08	1.02	6	1.02	1.06	0.91	11.01	1.09	9.06
Q5U0F4	Eukaryotic translation initiation factor 3 subunit I OS=Homo sapiens GN=EIF3I PE=2 SV=1	15	0.88	0.99	0.88	11	0.99	1.07	0.95	11	1.02	1.01	0.98	7.57	3.92	5.87
Q12765	Secernin-1 OS=Homo sapiens GN=SCRN1 PE=1 SV=2	15	1.02	1.03	1.05	11	0.98	1.07	0.97	9	1.05	1.09	1.02	3.28	2.75	3.81

C9JFE4	COP9 signalosome complex subunit 1 OS=Homo sapiens GN=GPS1 PE=4 SV=2	11	0.96	0.94	1.14	6	0.93	0.87	0.78	6	0.95	1.10	1.04	1.49	12.38	18.84
G8JLC6	Melanoma inhibitory activity protein 3 OS=Homo sapiens GN=MIA3 PE=2 SV=1	9	1.24	1.06	1.20	9	1.02	0.96	1.07	6	1.28	1.11	1.20	11.77	7.55	6.44
A8K6X9	cDNA FLJ76427, highly similar to Homo sapiens SH2 domain binding protein 1 (tetratricopeptide repeat containing) (SH2BP1), mRNA OS=Homo sapiens PE=2 SV=1	9	1.04	1.14	0.94	6	0.94	0.87	0.98	6	1.04	0.85	0.89	5.54	16.63	4.85
Q53F64	Heterogeneous nuclear ribonucleoprotein AB isoform a variant (Fragment) OS=Homo sapiens PE=2 SV=1	11	1.05	1.08	0.92	10	1.20	1.16	1.15	9	1.07	0.90	1.17	7.32	12.61	12.93
Q9P2K5	Myelin expression factor 2 OS=Homo sapiens GN=MYEF2 PE=1 SV=3	14	0.95	0.92	0.81	12	0.95	1.00	1.02	14	0.93	1.04	1.00	1.00	6.34	12.11
M0R3D6	60S ribosomal protein L18a (Fragment) OS=Homo sapiens GN=RPL18A PE=4 SV=1	12	0.92	0.98	0.95	14	1.01	1.05	1.02	11	0.94	0.94	0.99	4.82	5.99	3.68
O95865	N(G),N(G)-dimethylarginine dimethylaminohydrolase 2 OS=Homo sapiens GN=DDAH2 PE=1 SV=1	12	0.98	1.00	1.07	9	0.80	0.97	0.88	9	0.91	1.01	0.89	9.96	1.99	11.32
P36957	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial OS=Homo sapiens GN=DLST PE=1 SV=4	12	1.19	1.03	1.11	11	1.21	0.95	1.10	10	1.17	0.97	1.19	1.39	4.32	4.42
Q6IB71	Proteasome subunit alpha type OS=Homo sapiens GN=PSMA3 PE=2 SV=1	10	0.87	0.94	0.90	9	1.07	1.16	1.07	6	0.92	1.00	0.95	11.12	11.02	8.99
P07741	Adenine phosphoribosyltransferase OS=Homo sapiens GN=APRT PE=1 SV=2	11	0.98	0.95	0.89	11	1.05	1.08	1.01	9	1.05	1.19	1.06	4.30	10.95	8.82
P07339	Cathepsin D OS=Homo sapiens GN=CTSD PE=1 SV=1	15	1.08	0.91	1.05	11	0.90	0.95	1.05	16	1.05	1.02	1.00	9.58	5.43	3.11
Q6DHZ8	Activity-dependent neuroprotector homeobox OS=Homo sapiens GN=ADNP PE=2 SV=1	9	0.95	1.00	0.90	7	1.09	1.14	1.10	6	0.89	0.91	1.01	10.53	11.41	10.33
Q53X45	Myosin regulatory light chain OS=Homo sapiens GN=MRLC3 PE=2 SV=1	16	1.10	1.02	1.17	19	1.11	0.97	1.19	17	1.14	1.00	1.20	1.57	2.51	1.53
Q96HI4	Glycylpeptide N-tetradecanoyltransferase (Fragment) OS=Homo sapiens GN=NMT1 PE=2 SV=2	12	1.04	0.99	0.98	8	0.94	0.92	0.97	8	1.01	0.91	1.09	5.13	4.60	6.73
P0CW22	40S ribosomal protein S17-like OS=Homo sapiens GN=RPS17L PE=1 SV=1	19	1.03	1.01	0.93	21	1.07	1.05	1.02	16	1.02	0.99	1.00	2.62	3.27	4.88
Q9BV57	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase OS=Homo sapiens GN=ADI1 PE=1 SV=1	10	0.91	1.06	0.84	8	0.97	1.17	0.98	9	1.26	1.02	1.27	18.15	6.85	21.32
Q8WUA4	General transcription factor 3C polypeptide 2 OS=Homo sapiens GN=GTF3C2 PE=1 SV=2	10	0.93	0.87	0.74	4	1.13	1.08	1.25	8	1.03	0.91	1.02	9.64	11.64	25.59
P24534	Elongation factor 1-beta OS=Homo sapiens GN=EEF1B2 PE=1 SV=3	22	0.94	0.99	0.99	8	0.98	1.04	1.02	11	0.97	0.99	0.99	1.97	2.87	1.59
Q92626	Peroxidasin homolog OS=Homo sapiens GN=PXDN PE=1 SV=2	8	1.00	0.85	0.92	10	1.19	1.05	1.17	11	1.44	1.06	1.46	18.40	12.17	23.01
P30048	Thioredoxin-dependent peroxide reductase, mitochondrial OS=Homo sapiens GN=PRDX3 PE=1 SV=3	15	0.94	1.01	1.04	15	1.36	0.96	1.26	12	0.93	0.97	0.99	22.79	2.86	13.18

Q9UBS4	DnaJ homolog subfamily B member 11 OS=Homo sapiens GN=DNAJB11 PE=1 SV=1	12	1.51	1.00	1.39	6	1.50	1.00	1.39	8	1.52	1.05	1.48	0.85	3.01	3.71
P41091	Eukaryotic translation initiation factor 2 subunit 3 OS=Homo sapiens GN=EIF2S3 PE=1 SV=3	13	0.96	0.95	0.96	10	1.11	1.03	1.07	13	0.98	1.00	1.05	8.29	4.25	5.65
Q5QPK2	Dolichol-phosphate mannosyltransferase OS=Homo sapiens GN=DPM1 PE=2 SV=1	10	1.43	0.98	1.42	8	1.12	0.79	0.97	6	1.17	1.07	1.14	13.66	15.09	19.25
Q14160	Protein scribble homolog OS=Homo sapiens GN=SCRIB PE=1 SV=4	12	1.14	1.17	0.85	9	1.00	1.13	1.04	6	1.05	1.08	1.04	6.61	3.72	11.02
B2RBP3	cDNA, FLJ95615, highly similar to Homo sapiens ubiquitin-activating enzyme E1C (UBA3 homolog, yeast)(UBE1C), mRNA OS=Homo sapiens PE=2 SV=1	10	0.94	0.94	0.96	8	0.99	0.94	0.99	7	0.96	1.08	0.89	2.68	7.91	5.27
B7ZLC9	GEMIN5 protein OS=Homo sapiens GN=GEMIN5 PE=2 SV=1	8	1.11	1.11	1.23	6	0.70	0.96	0.83	8	1.03	1.03	0.88	22.56	6.95	22.40
P14550	Alcohol dehydrogenase [NADP(+)] OS=Homo sapiens GN=AKR1A1 PE=1 SV=3	11	0.96	1.10	1.01	10	0.88	0.96	0.92	8	0.92	1.00	0.98	4.40	6.67	5.05
Q9Y2W1	Thyroid hormone receptor-associated protein 3 OS=Homo sapiens GN=THRAP3 PE=1 SV=2	10	0.93	0.97	0.89	9	1.06	0.99	1.00	8	1.01	1.07	0.98	6.20	5.34	6.04
Q12996	Cleavage stimulation factor subunit 3 OS=Homo sapiens GN=CSTF3 PE=1 SV=1	10	0.90	0.87	0.98	11	1.09	1.08	0.94	7	0.97	0.97	0.84	9.63	10.61	7.84
J3KP72	Protein-L-isoaspartate O-methyltransferase OS=Homo sapiens GN=PCMT1 PE=3 SV=1	15	1.18	1.13	0.96	11	1.10	1.17	1.04	6	1.13	1.12	1.01	3.67	2.37	3.70
P06132	Uroporphyrinogen decarboxylase OS=Homo sapiens GN=UROD PE=1 SV=2	11	1.01	0.98	0.91	12	1.04	1.03	1.07	7	0.86	1.00	0.87	10.07	2.81	10.94
Q99805	Transmembrane 9 superfamily member 2 OS=Homo sapiens GN=TM9SF2 PE=1 SV=1	14	1.30	1.09	1.27	10	1.11	0.96	1.09	9	1.22	1.05	1.23	7.83	6.35	7.76
P52565	Rho GDP-dissociation inhibitor 1 OS=Homo sapiens GN=ARHGDIA PE=1 SV=3	40	0.90	1.03	0.97	33	0.98	1.05	0.92	22	0.92	1.09	0.97	4.55	3.08	3.00
B7ZKT9	KIAA1033 protein OS=Homo sapiens GN=KIAA1033 PE=2 SV=1	9	0.91	0.84	0.68	9	0.90	0.84	0.91	7	0.94	1.03	0.87	2.18	12.23	15.39
E9PB61	THO complex subunit 4 OS=Homo sapiens GN=ALYREF PE=2 SV=1	25	0.83	0.91	0.84	12	0.86	0.92	0.86	13	0.82	1.02	0.91	2.76	6.67	3.95
Q7Z4H8	KDEL motif-containing protein 2 OS=Homo sapiens GN=KDELC2 PE=1 SV=2	9	1.22	1.18	1.17	6	1.22	1.10	1.23	6	1.10	1.05	1.21	6.17	6.22	2.72
Q9NU22	Midasin OS=Homo sapiens GN=MDN1 PE=1 SV=2	12	1.04	0.93	1.01	18	1.01	1.02	1.05	13	1.07	0.97	1.08	2.96	4.76	3.47
P46977	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A OS=Homo sapiens GN=STT3A PE=1 SV=2	9	1.07	0.96	0.95	9	1.05	1.00	1.02	9	1.02	0.97	0.87	2.50	2.30	7.88
Q9H3P7	Golgi resident protein GCP60 OS=Homo sapiens GN=ACBD3 PE=1 SV=4	9	0.97	1.05	1.17	8	1.18	1.20	1.34	4	1.08	1.05	1.10	9.78	7.71	10.48
Q6IAX6	3'-phosphoadenosine 5'-phosphosulfate synthase 1 OS=Homo sapiens GN=PAPSS1 PE=2 SV=1	8	0.94	1.12	0.96	9	0.93	1.01	0.97	8	0.96	1.01	1.00	1.78	6.07	2.06
P60981	Destrin OS=Homo sapiens GN=DSTN PE=1 SV=3	11	1.05	1.08	1.10	7	1.04	1.05	1.08	8	0.94	0.93	1.03	5.96	7.64	3.46
Q9UKX7	Nuclear pore complex protein Nup50 OS=Homo sapiens GN=NUP50 PE=1 SV=2	11	0.97	0.94	0.85	5	0.89	0.96	0.88	5	0.82	0.83	0.93	8.25	7.58	4.68

Q06124	Tyrosine-protein phosphatase non-receptor type 11 OS=Homo sapiens GN=PTPN11 PE=1 SV=2	11	1.00	1.10	0.93	11	0.98	1.06	0.92	9	0.93	0.95	0.97	3.72	7.30	3.15
P61981	14-3-3 protein gamma OS=Homo sapiens GN=YWHAG PE=1 SV=2	38	0.87	1.00	1.01	24	0.83	0.88	0.86	23	0.85	1.14	0.95	2.57	12.97	7.80
J3QT28	Mitotic checkpoint protein BUB3 (Fragment) OS=Homo sapiens GN=BUB3 PE=4 SV=1	12	0.92	0.96	1.10	11	0.79	0.85	0.83	10	0.92	1.20	0.83	9.02	17.47	17.01
P16949	Stathmin OS=Homo sapiens GN=STMN1 PE=1 SV=3	16	0.84	1.00	0.67	17	1.04	1.08	0.87	15	0.89	0.99	0.83	10.97	4.64	13.71
Q6FGM6	PPID protein OS=Homo sapiens GN=PPID PE=2 SV=1	10	0.97	1.06	1.05	9	0.98	1.01	1.03	7	1.01	0.99	0.97	1.81	3.72	4.36
Q9UHL4	Dipeptidyl peptidase 2 OS=Homo sapiens GN=DPP7 PE=1 SV=3	11	1.16	1.09	1.18	10	1.26	1.08	1.16	11	1.22	1.03	1.07	3.89	2.91	4.90
C9JIF9	Acylamino-acid-releasing enzyme OS=Homo sapiens GN=APEH PE=2 SV=1	8	0.86	1.06	1.07	12	0.93	0.86	0.90	8	1.06	1.13	0.98	10.75	13.95	8.72
Q0VAM0	Catenin, beta like 1 OS=Homo sapiens GN=CTNNBL1 PE=2 SV=1	8	0.92	1.09	0.95	8	0.98	1.05	0.92	7	1.03	0.98	1.12	5.44	5.53	10.82
J3KQU9	AP-1 complex subunit gamma-1 OS=Homo sapiens GN=AP1G1 PE=4 SV=1	9	0.95	0.99	0.93	8	1.07	1.06	1.00	7	1.01	1.04	0.92	5.80	3.38	4.72
P17858	6-phosphofructokinase, liver type OS=Homo sapiens GN=PFKL PE=1 SV=6	15	1.02	1.00	1.14	14	0.99	0.97	1.03	12	1.20	1.21	1.10	10.67	12.47	5.04
Q6NX51	Exocyst complex component 4 OS=Homo sapiens GN=EXOC4 PE=2 SV=1	12	0.90	0.98	0.84	14	0.99	1.13	0.94	12	0.98	1.27	0.99	5.25	12.91	8.67
Q6IBH0	SLC25A11 protein OS=Homo sapiens GN=SLC25A11 PE=2 SV=1	10	1.29	0.92	1.34	13	1.10	0.93	1.09	7	1.32	1.09	1.22	9.93	9.96	10.30
B3KUZ7	cDNA FLJ40986 fis, clone UTERU2014898, highly similar to Vacuolar ATP synthase subunit H (EC 3.6.3.14) OS=Homo sapiens PE=2 SV=1	10	1.05	1.10	1.10	6	0.94	0.95	1.08	7	1.08	0.95	1.12	7.36	8.49	1.70
P62917	60S ribosomal protein L8 OS=Homo sapiens GN=RPL8 PE=1 SV=2	29	0.93	0.99	0.95	12	0.99	0.95	0.95	15	0.95	1.08	1.01	3.27	6.40	3.60
B2ZZ90	Acetyl-Coenzyme A carboxylase alpha OS=Homo sapiens GN=ACACA PE=2 SV=1	9	0.85	0.92	0.94	13	0.98	0.95	1.06	6	0.96	0.90	0.89	7.86	3.03	9.08
Q13148	TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1	13	0.94	0.98	1.07	11	1.01	0.95	0.95	9	0.87	0.88	0.89	7.27	5.50	9.00
Q5RKT7	Ribosomal protein S27a OS=Homo sapiens GN=RPS27A PE=2 SV=1	23	0.94	1.01	0.78	21	1.07	1.21	1.27	20	0.98	0.83	0.99	6.54	18.69	23.91
Q59GJ0	Eukaryotic translation initiation factor 4 gamma, 3 variant (Fragment) OS=Homo sapiens PE=2 SV=1	13	1.02	1.05	1.01	10	0.98	1.17	1.14	11	0.98	1.20	0.98	2.55	7.08	7.92
P11171	Protein 4.1 OS=Homo sapiens GN=EPB41 PE=1 SV=4	10	0.95	0.95	0.82	6	0.73	0.91	0.79	7	0.90	0.87	0.80	13.68	4.44	1.53
O14497	AT-rich interactive domain-containing protein 1A OS=Homo sapiens GN=ARID1A PE=1 SV=3	9	0.82	0.90	0.81	7	0.95	1.11	1.07	7	0.89	0.75	1.00	7.00	19.83	13.89
Q96CV8	Thimet oligopeptidase 1 OS=Homo sapiens GN=THOP1 PE=2 SV=1	11	1.01	0.95	0.99	7	1.03	0.96	0.97	5	0.86	0.91	0.86	9.70	3.05	7.23
P55809	Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial OS=Homo sapiens GN=OXCT1 PE=1 SV=1	11	1.05	0.95	1.07	11	0.84	0.84	0.83	7	1.18	0.95	1.23	16.85	7.13	19.38
O75691	Small subunit processome component 20 homolog OS=Homo sapiens GN=UTP20 PE=1 SV=3	9	1.15	0.93	1.12	7	0.98	0.95	1.08	5	1.12	1.00	1.22	8.37	3.51	6.12
P49721	Proteasome subunit beta type-2 OS=Homo sapiens GN=PSMB2 PE=1 SV=1	8	1.02	1.08	0.99	7	0.85	0.89	0.81	8	0.99	1.12	1.00	9.46	11.80	11.31

P27635	60S ribosomal protein L10 OS=Homo sapiens GN=RPL10 PE=1 SV=4	15	0.88	1.00	1.03	9	0.81	0.86	0.88	8	0.95	1.06	0.93	8.01	10.54	7.71
F5H0L8	SEC23-interacting protein OS=Homo sapiens GN=SEC23IP PE=2 SV=1	12	1.17	1.07	0.97	10	1.02	1.06	1.15	9	1.02	0.96	0.97	8.00	5.53	9.79
Q9H2G0	CTCL tumor antigen se37-2 OS=Homo sapiens GN=UBE3A PE=2 SV=1	8	0.91	0.98	0.76	8	1.03	0.95	0.87	6	0.91	1.05	0.89	7.07	5.51	8.12
O00629	Importin subunit alpha-3 OS=Homo sapiens GN=KPNA4 PE=1 SV=1	12	0.95	0.98	1.08	13	0.98	0.92	1.01	11	0.88	1.07	1.01	5.39	7.67	4.08
Q9UPE4	Putative mitochondrial inner membrane protein import receptor OS=Homo sapiens GN=hTIM44 PE=2 SV=1	9	0.93	0.97	1.11	6	0.96	0.92	0.96	8	0.91	0.87	0.90	3.18	5.42	11.02
A1L0T0	Acetolactate synthase-like protein OS=Homo sapiens GN=ILVBL PE=1 SV=2	13	0.91	0.84	0.97	14	1.04	1.03	1.03	12	1.06	1.08	0.97	8.17	12.96	3.44
P61088	Ubiquitin-conjugating enzyme E2 N OS=Homo sapiens GN=UBE2N PE=1 SV=1	26	0.96	1.02	0.94	26	1.10	1.12	1.08	12	1.01	0.98	0.99	6.89	7.31	7.29
E5KND7	Mitochondrial elongation factor G OS=Homo sapiens PE=3 SV=1	11	0.87	0.95	1.01	10	0.95	0.95	0.92	11	0.90	1.06	0.96	4.43	6.47	4.49
P08559	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Homo sapiens GN=PDHA1 PE=1 SV=3	10	0.85	0.97	1.09	11	0.83	0.84	0.99	9	0.89	1.08	1.01	3.41	12.38	5.40
Q6LET3	HPRT1 protein (Fragment) OS=Homo sapiens GN=HPRT1 PE=2 SV=1	10	0.97	1.10	0.99	12	0.94	1.08	0.95	11	0.92	1.04	0.98	2.25	3.15	2.54
Q08ET0	Cell proliferation-inducing protein 47 OS=Homo sapiens GN=hCG_39985 PE=2 SV=1	18	1.29	0.93	1.19	17	1.48	1.07	1.31	10	1.21	0.91	1.20	10.35	9.11	5.68
Q6FGS1	TPD52L2 protein OS=Homo sapiens GN=TPD52L2 PE=2 SV=1	10	1.08	0.86	1.10	9	0.91	0.86	0.98	6	1.04	1.15	1.08	8.94	17.33	6.06
Q5LJA9	Ubiquitin carboxyl-terminal hydrolase isozyme L5 (Fragment) OS=Homo sapiens GN=UCHL5 PE=2 SV=1	9	1.02	1.08	1.04	7	0.93	0.95	1.01	8	1.06	0.98	1.03	6.80	6.86	1.16
J3QT22	Protein phosphatase methylesterase 1 OS=Homo sapiens GN=PPME1 PE=3 SV=1	8	0.92	0.97	0.98	9	0.90	0.98	0.96	10	0.88	0.98	0.98	2.45	0.53	1.19
Q9BVA1	Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1	232	0.76	0.94	1.17	203	0.83	0.85	0.71	189	0.63	0.91	0.92	13.99	4.98	24.94
Q8IX12	Cell division cycle and apoptosis regulator protein 1 OS=Homo sapiens GN=CCAR1 PE=1 SV=2	11	0.87	0.95	0.89	8	0.99	1.07	0.99	5	1.01	1.00	0.99	7.74	5.67	5.98
A8K335	cDNA FLJ76254, highly similar to Homo sapiens gamma-glutamyl hydrolase (GGH), mRNA OS=Homo sapiens PE=2 SV=1	12	1.39	1.09	1.09	11	1.41	1.12	1.23	12	1.19	0.82	1.07	9.07	16.81	7.36
B3KQI5	cDNA FLJ90522 fis, clone NT2RP4000108, highly similar to Neurofilament triplet L protein OS=Homo sapiens PE=2 SV=1	11	0.90	1.04	1.03	11	0.86	0.80	0.91	11	0.92	1.01	0.99	3.31	13.79	6.20
Q75MJ1	ATP-binding cassette sub-family F member 2 OS=Homo sapiens GN=ABCF2 PE=2 SV=1	9	0.96	0.99	1.03	7	1.08	1.09	1.02	6	0.96	0.86	0.90	6.70	11.55	7.36
P00390	Glutathione reductase, mitochondrial OS=Homo sapiens GN=GSR PE=1 SV=2	9	0.88	0.93	0.91	4	1.16	1.12	1.15	6	0.98	1.10	1.07	14.18	9.72	11.51
Q5U071	High-mobility group box 2 OS=Homo sapiens PE=2 SV=1	22	0.95	1.07	0.81	18	1.17	1.17	1.01	21	1.05	0.98	1.02	10.33	8.46	12.49
Q8TAS0	ATP synthase subunit gamma (Fragment) OS=Homo sapiens PE=2 SV=1	12	1.27	1.02	1.17	11	1.36	1.06	1.17	12	1.39	0.96	1.02	4.42	5.21	7.65

A8K787	cDNA FLJ75273, highly similar to Homo sapiens solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 4, mRNA OS=Homo sapiens PE=2 SV=1	28	1.30	1.07	1.00	29	1.28	0.95	1.19	28	1.08	1.37	0.85	10.14	18.79	16.97
Q5SQT9	SAR1 gene homolog A (S. cerevisiae), isoform CRA_a OS=Homo sapiens GN=SAR1A PE=2 SV=1	10	1.00	1.00	0.95	11	0.81	0.93	0.98	14	0.99	0.89	1.03	11.17	6.12	3.80
B2RDR4	cDNA, FLJ96732, highly similar to Homo sapiens testis derived transcript (3 LIM domains) (TES), transcript variant 1, mRNA OS=Homo sapiens PE=2 SV=1	9	1.09	0.91	0.77	4	1.03	1.07	1.04	6	0.93	0.99	0.98	7.94	7.96	14.94
Q9UKY7	Protein CDV3 homolog OS=Homo sapiens GN=CDV3 PE=1 SV=1	11	1.08	0.95	0.95	5	1.18	1.21	1.12	4	1.06	0.93	0.95	5.92	15.32	9.41
P46783	40S ribosomal protein S10 OS=Homo sapiens GN=RPS10 PE=1 SV=1	14	0.98	1.01	1.05	14	1.02	0.96	0.96	12	1.00	1.04	1.00	1.93	4.25	4.21
Q6FHN9	Sulfurtransferase (Fragment) OS=Homo sapiens GN=MPST PE=2 SV=1	9	0.94	0.95	0.90	9	1.02	1.06	1.00	11	1.05	1.06	1.00	5.39	6.13	6.10
Q92905	COP9 signalosome complex subunit 5 OS=Homo sapiens GN=COPS5 PE=1 SV=4	11	0.83	0.99	0.89	10	1.04	1.11	0.99	8	0.93	0.97	1.00	11.00	7.54	6.29
P29373	Cellular retinoic acid-binding protein 2 OS=Homo sapiens GN=CRABP2 PE=1 SV=2	10	1.08	1.09	1.18	7	1.09	1.11	1.21	9	1.15	1.15	1.31	3.07	3.03	5.28
O00487	26S proteasome non-ATPase regulatory subunit 14 OS=Homo sapiens GN=PSMD14 PE=1 SV=1	17	0.97	0.98	0.91	9	0.90	0.96	0.96	10	0.92	0.90	0.94	3.57	4.11	2.92
D9IAI1	Phosphatidylethanolamine-binding protein 1 OS=Homo sapiens PE=2 SV=1	20	0.92	1.06	0.93	12	0.87	1.02	0.90	13	0.90	1.03	0.89	2.41	2.05	2.16
Q86SZ7	Full-length cDNA clone CS0DJ015YJ12 of T cells (Jurkat cell line) of Homo sapiens (human) OS=Homo sapiens GN=PSME2 PE=2 SV=1	15	1.16	1.07	1.09	15	1.00	0.93	1.03	11	1.15	1.10	1.18	7.94	8.85	6.89
Q6IBP2	HMOX2 protein OS=Homo sapiens GN=HMOX2 PE=2 SV=1	9	1.15	0.93	0.86	7	1.01	1.05	1.14	8	1.16	0.92	1.08	7.60	7.47	14.61
P35251	Replication factor C subunit 1 OS=Homo sapiens GN=RFC1 PE=1 SV=4	8	0.90	0.92	0.88	9	0.85	0.91	0.81	4	0.84	1.13	0.90	3.52	12.38	5.41
P62277	40S ribosomal protein S13 OS=Homo sapiens GN=RPS13 PE=1 SV=2	18	1.13	1.01	0.98	10	1.25	1.13	1.12	9	1.11	0.98	1.09	6.59	7.36	7.16
Q2TU84	Aspartate aminotransferase OS=Homo sapiens GN=GIG18 PE=2 SV=1	9	0.94	0.91	0.96	10	1.06	1.07	1.06	10	1.04	1.07	1.05	5.99	9.34	5.35
Q9Y3P9	Rab GTPase-activating protein 1 OS=Homo sapiens GN=RABGAP1 PE=1 SV=3	8	0.79	0.88	0.99	3	1.06	1.59	1.34	4	0.92	0.86	1.01	14.83	37.77	17.31
Q12860	Contactin-1 OS=Homo sapiens GN=CNTN1 PE=1 SV=1	8	0.89	0.89	0.96	5	0.86	1.07	0.90	8	1.04	1.01	0.95	10.34	8.91	3.67
O95861	3'(2'),5'-bisphosphate nucleotidase 1 OS=Homo sapiens GN=BPNT1 PE=1 SV=1	10	1.10	0.99	1.13	9	1.09	1.06	1.08	9	1.06	1.03	1.06	1.89	3.50	3.40
P48047	ATP synthase subunit O, mitochondrial OS=Homo sapiens GN=ATP5O PE=1 SV=1	10	1.39	0.92	1.20	13	1.30	0.93	1.09	10	1.33	1.03	1.24	3.31	6.16	6.72
J3KR44	Ubiquitin thioesterase OTUB1 OS=Homo sapiens GN=OTUB1 PE=4 SV=1	11	0.95	0.99	1.00	10	1.03	1.07	0.96	6	0.93	1.04	0.94	5.13	3.85	3.27

Q7Z5K3	Syntaxin 1A (Brain), isoform CRA_b OS=Homo sapiens GN=stx1c PE=2 SV=1	9	1.25	1.02	0.90	5	1.35	1.15	1.18	4	1.16	0.99	1.38	7.39	8.17	20.58
Q5U0J2	Cysteine and glycine-rich protein 1 OS=Homo sapiens GN=CSRP1 PE=2 SV=1	13	1.34	1.00	1.33	9	1.36	0.97	1.29	8	1.19	0.92	1.35	7.08	3.96	2.34
B7Z592	cDNA FLJ61635, highly similar to Homo sapiens likely ortholog of mouse immediate early response, erythropoietin 4 (LEREPO4), mRNA OS=Homo sapiens PE=2 SV=1	9	0.80	0.97	0.81	7	0.89	1.06	0.95	6	0.87	0.86	0.92	5.08	10.27	8.52
Q14684	Ribosomal RNA processing protein 1 homolog B OS=Homo sapiens GN=RRP1B PE=1 SV=3	8	0.91	0.93	0.90	9	1.03	1.09	1.00	5	0.98	0.97	0.84	6.06	8.30	8.87
Q96FC7	Phytanoyl-CoA hydroxylase-interacting protein-like OS=Homo sapiens GN=PHYHIPL PE=1 SV=3	14	0.95	1.03	0.84	7	0.98	1.06	0.95	8	0.83	1.00	0.90	8.66	2.92	6.07
Q7L099-3	Isoform 3 of Protein RUFY3 OS=Homo sapiens GN=RUFY3	10	0.91	0.83	0.71	7	1.01	0.99	0.93	9	0.96	0.91	1.02	5.16	9.03	17.78
E5KLB5	DNA ligase OS=Homo sapiens PE=2 SV=1	7	0.93	0.93	0.96	8	1.08	1.06	1.16	7	0.98	0.77	0.81	7.45	15.64	17.77
Q53T76	Putative uncharacterized protein GPD2 (Fragment) OS=Homo sapiens GN=GPD2 PE=2 SV=1	8	1.21	0.98	1.17	9	1.42	1.17	1.19	6	1.15	1.06	1.16	11.53	8.56	1.21
P49720	Proteasome subunit beta type-3 OS=Homo sapiens GN=PSMB3 PE=1 SV=2	12	0.99	1.05	1.04	9	0.93	0.94	0.91	8	0.93	0.93	0.89	3.79	6.60	8.82
Q53X12	Vacuolar-type H(+)-ATPase OS=Homo sapiens PE=2 SV=1	9	1.17	1.07	1.41	4	0.85	0.84	0.93	4	0.96	1.07	0.99	16.24	13.34	23.18
Q53Y06	ATPase, H+ transporting, lysosomal 31kDa, V1 subunit E isoform 1 OS=Homo sapiens GN=ATP6V1E1 PE=2 SV=1	8	1.15	0.99	1.02	9	1.29	1.11	1.26	8	1.05	0.92	1.02	10.34	9.58	12.32
Q7Z5L9	Interferon regulatory factor 2-binding protein 2 OS=Homo sapiens GN=IRF2BP2 PE=1 SV=2	9	0.90	0.97	1.04	5	0.84	0.91	0.99	3	0.95	1.06	0.96	6.24	7.38	4.29
Q8TBT6	Putative uncharacterized protein (Fragment) OS=Homo sapiens PE=2 SV=1	14	1.10	0.96	1.14	12	1.05	1.07	1.04	11	1.24	1.00	1.02	8.97	5.15	6.21
Q13895	Bystin OS=Homo sapiens GN=BYSL PE=1 SV=3	12	0.92	1.06	0.81	12	0.96	1.04	0.97	12	0.88	1.03	0.89	4.62	1.63	9.11
Q59FE8	Epithelial protein lost in neoplasm beta variant (Fragment) OS=Homo sapiens PE=2 SV=1	8	0.95	0.88	0.94	10	1.26	1.17	1.18	7	1.11	0.96	1.02	13.85	15.21	12.02
Q9NZN3	EH domain-containing protein 3 OS=Homo sapiens GN=EHD3 PE=1 SV=2	19	0.92	0.93	0.96	14	1.14	1.32	1.09	12	1.18	1.17	1.08	12.81	17.14	6.93
Q6FHR0	RAB11B protein (Fragment) OS=Homo sapiens GN=RAB11B PE=2 SV=1	10	1.01	0.97	1.02	10	0.96	0.98	1.06	10	0.88	0.88	0.91	6.86	6.17	7.89
A8K6V6	cDNA FLJ75883, highly similar to Homo sapiens glucosamine (N-acetyl)-6-sulfatase (Sanfilippo disease IIID) (GNS), mRNA OS=Homo sapiens PE=2 SV=1	11	0.99	0.93	1.09	10	1.02	0.90	0.93	7	1.14	1.29	1.16	7.36	20.67	10.90
P10768	S-formylglutathione hydrolase OS=Homo sapiens GN=ESD PE=1 SV=2	13	0.98	0.93	0.96	13	1.13	0.92	1.06	12	1.05	1.00	0.96	7.12	4.39	6.05
Q9H6R4	Nucleolar protein 6 OS=Homo sapiens GN=NOL6 PE=1 SV=2	8	0.92	0.93	1.14	4	1.17	0.90	1.15	2	0.99	0.72	0.94	12.36	13.20	11.31
Q13769	THO complex subunit 5 homolog OS=Homo sapiens GN=THOC5 PE=1 SV=2	8	0.96	1.04	1.10	5	0.81	0.90	0.84	3	1.24	0.95	1.15	21.40	7.17	16.10
P40855	Peroxisomal biogenesis factor 19 OS=Homo sapiens GN=PEX19 PE=1 SV=1	9	0.80	0.97	0.79	5	0.69	0.89	0.91	4	0.88	0.86	0.87	11.71	6.64	7.13

Q6IAP9	PRPF4 protein OS=Homo sapiens GN=PRPF4 PE=2 SV=1	8	1.08	0.96	0.98	6	1.10	1.05	1.08	4	1.00	0.94	0.93	5.19	5.76	7.72
Q01970	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-3 OS=Homo sapiens GN=PLCB3 PE=1 SV=2	8	0.85	0.93	0.85	9	1.07	1.22	1.02	5	0.94	1.00	0.92	11.54	14.44	9.46
P09382	Galectin-1 OS=Homo sapiens GN=LGALS1 PE=1 SV=2	30	1.40	1.04	1.44	28	1.24	0.97	1.23	25	1.18	1.01	1.28	9.21	3.40	8.13
H3BN98	Uncharacterized protein (Fragment) OS=Homo sapiens PE=4 SV=2	12	1.31	1.02	1.24	11	1.03	0.92	0.96	8	1.23	1.09	0.64	12.27	8.28	31.54
Q14165	Malectin OS=Homo sapiens GN=MLEC PE=1 SV=1	9	1.27	1.16	1.22	5	1.18	0.92	1.06	6	1.24	1.06	1.36	3.41	11.60	12.70
D3DTC2	Acyltransferase like 2, isoform CRA_a OS=Homo sapiens GN=AYTL2 PE=2 SV=1	9	0.94	0.98	1.09	3	0.69	0.66	0.74	4	1.07	1.20	1.03	21.47	28.78	19.87
E7EQV9	Ribosomal protein L15 (Fragment) OS=Homo sapiens GN=RPL15 PE=2 SV=1	13	0.98	0.99	0.81	12	1.04	1.07	1.01	15	0.98	0.97	1.01	3.63	4.84	12.56
P23193	Transcription elongation factor A protein 1 OS=Homo sapiens GN=TCEA1 PE=1 SV=2	9	0.93	0.99	0.87	7	1.01	0.97	0.91	8	1.01	1.17	1.00	4.91	10.74	7.59
P08240	Signal recognition particle receptor subunit alpha OS=Homo sapiens GN=SRPR PE=1 SV=2	11	0.94	0.83	1.03	7	0.94	1.04	0.92	7	1.02	0.96	1.11	4.93	10.84	9.40
P07686	Beta-hexosaminidase subunit beta OS=Homo sapiens GN=HEXB PE=1 SV=3	8	1.30	1.08	1.44	10	1.18	1.04	1.06	10	0.98	1.14	1.02	13.78	4.41	19.90
Q96CN7	Isochorismatase domain-containing protein 1 OS=Homo sapiens GN=ISOC1 PE=1 SV=3	9	0.91	1.04	0.95	6	0.88	0.91	1.02	5	0.91	0.83	0.79	1.65	11.69	12.88
Q5VTR2	E3 ubiquitin-protein ligase BRE1A OS=Homo sapiens GN=RNF20 PE=1 SV=2	8	0.76	0.88	0.91	7	1.08	1.11	1.01	8	1.02	0.97	0.93	17.33	11.83	5.75
Q9H488	GDP-fucose protein O-fucosyltransferase 1 OS=Homo sapiens GN=POFUT1 PE=1 SV=1	8	1.32	1.02	1.01	5	1.12	1.13	1.13	4	1.19	0.98	1.28	8.52	7.49	11.59
E5RHW4	Erlin-2 (Fragment) OS=Homo sapiens GN=ERLIN2 PE=2 SV=1	9	1.17	1.14	1.20	10	1.17	0.94	1.03	9	1.11	1.06	1.05	3.08	9.87	8.60
Q8WYP5	Protein ELYS OS=Homo sapiens GN=AHCTF1 PE=1 SV=3	8	0.89	0.96	0.93	6	1.06	0.93	0.84	3	1.13	1.02	1.23	11.84	4.83	20.29
P67936	Tropomyosin alpha-4 chain OS=Homo sapiens GN=TPM4 PE=1 SV=3	16	1.06	0.98	1.04	17	1.17	1.06	1.09	16	0.99	0.89	1.08	8.07	9.17	2.47
E7ERK9	Translation initiation factor eIF-2B subunit delta OS=Homo sapiens GN=EIF2B4 PE=2 SV=1	8	1.63	0.83	1.06	8	0.89	0.92	0.87	3	0.97	1.10	1.01	34.80	14.48	10.17
P20290-2	Isoform 2 of Transcription factor BTF3 OS=Homo sapiens GN=BTF3	13	0.82	0.99	0.86	12	0.96	1.00	0.92	9	0.83	1.06	1.01	8.88	4.14	8.35
Q14997	Proteasome activator complex subunit 4 OS=Homo sapiens GN=PSME4 PE=1 SV=2	10	0.99	0.94	0.90	2	1.04	1.00	1.07	3	0.96	1.02	0.90	4.12	4.15	10.19
F8W1A4	Adenylate kinase 2, mitochondrial OS=Homo sapiens GN=AK2 PE=2 SV=1	8	0.99	1.01	0.90	10	0.90	0.93	0.91	10	0.95	1.00	0.98	4.59	4.16	4.77
Q9Y613	FH1/FH2 domain-containing protein 1 OS=Homo sapiens GN=FHOD1 PE=1 SV=3	10	1.06	1.04	0.86	12	0.78	0.94	1.04	5	0.91	1.01	0.96	15.60	4.97	9.21
Q6DHZ2	Protein kinase, cAMP-dependent, regulatory, type II, beta OS=Homo sapiens GN=PRKAR2B PE=2 SV=1	12	0.88	1.06	0.86	11	0.84	1.01	0.94	11	0.83	1.07	0.94	3.37	3.08	4.69
Q53H22	Amidophosphoribosyltransferase (Fragment) OS=Homo sapiens PE=2 SV=1	7	0.94	1.02	0.93	5	0.93	0.92	0.95	7	0.98	1.08	0.97	2.93	8.04	2.18
J3KNL3	Chitinase domain-containing protein 1 OS=Homo sapiens GN=CHID1 PE=3 SV=1	8	1.22	1.04	1.02	5	1.15	0.92	0.96	8	1.09	0.99	1.06	5.72	6.01	4.85

A9JR72	CDC42 binding protein kinase beta (DMPK-like) OS=Homo sapiens GN=CDC42BPB PE=2 SV=1	9	0.82	1.08	1.11	5	1.30	1.52	0.98	5	0.91	0.97	0.88	25.57	24.24	11.62
Q96T88	E3 ubiquitin-protein ligase UHRF1 OS=Homo sapiens GN=UHRF1 PE=1 SV=1	7	0.74	1.16	0.90	6	0.75	1.00	0.92	7	0.77	0.90	0.88	2.49	13.16	2.22
B7ZLP5	SAFB protein OS=Homo sapiens GN=SAFB PE=2 SV=1	10	0.99	1.11	1.22	8	0.96	1.00	0.96	7	0.76	1.14	0.89	13.92	6.75	17.34
Q14241	Transcription elongation factor B polypeptide 3 OS=Homo sapiens GN=TCEB3 PE=1 SV=2	11	0.80	1.09	1.01	5	1.13	1.02	1.16	6	0.77	0.85	0.92	22.16	12.66	12.00
Q14694	Ubiquitin carboxyl-terminal hydrolase 10 OS=Homo sapiens GN=USP10 PE=1 SV=2	9	0.96	1.17	1.03	10	0.94	1.01	0.87	6	0.84	1.07	1.05	6.78	7.16	10.04
Q9BXW7	Cat eye syndrome critical region protein 5 OS=Homo sapiens GN=CECR5 PE=1 SV=1	9	0.94	0.98	1.05	6	0.99	1.00	1.06	6	0.97	1.09	0.92	2.42	5.83	7.47
Q53GF9	Full-length cDNA 5-PRIME end of clone CS0DF013YM24 of Fetal brain of Homo sapiens (Human) variant (Fragment) OS=Homo sapiens PE=2 SV=1	12	1.58	0.98	1.43	12	1.53	0.96	1.33	9	1.43	1.06	1.30	5.16	5.44	5.08
Q59EK3	Adaptor-related protein complex 1, mu 1 subunit variant (Fragment) OS=Homo sapiens PE=2 SV=1	9	0.98	0.98	0.96	7	1.09	1.09	1.08	7	0.98	0.85	1.03	6.73	12.44	5.98
A8K9K6	cDNA FLJ76962, highly similar to Homo sapiens nucleolar protein 5A (56kDa with KKE/D repeat) (NOL5A), mRNA OS=Homo sapiens PE=2 SV=1	8	1.27	0.86	1.37	6	1.01	0.96	1.09	5	0.97	1.13	1.02	14.67	13.76	15.75
Q13867	Bleomycin hydrolase OS=Homo sapiens GN=BLMH PE=1 SV=1	8	1.05	0.97	0.91	7	1.24	1.26	1.20	6	1.02	1.00	0.91	10.70	14.60	16.81
B3KR50	cDNA FLJ33691 fis, clone BRAWH2002976, highly similar to GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2 OS=Homo sapiens PE=2 SV=1	9	1.02	1.02	0.89	10	1.26	1.22	1.14	8	0.92	0.92	1.00	16.62	14.63	12.20
P30837	Aldehyde dehydrogenase X, mitochondrial OS=Homo sapiens GN=ALDH1B1 PE=1 SV=3	8	0.96	0.96	0.81	6	0.92	0.94	1.01	5	1.05	0.80	0.86	7.22	9.71	11.38
E9PFW3	AP-2 complex subunit mu OS=Homo sapiens GN=AP2M1 PE=2 SV=1	8	0.90	1.09	1.05	9	0.91	0.95	0.95	9	0.86	0.92	0.95	2.53	9.12	6.07
B7ZKM8	Protein transport protein Sec24B OS=Homo sapiens GN=SEC24B PE=2 SV=1	8	1.03	1.01	0.92	7	1.04	0.91	0.80	13	1.00	1.06	1.13	2.25	7.69	17.48
O96008	Mitochondrial import receptor subunit TOM40 homolog OS=Homo sapiens GN=TOMM40 PE=1 SV=1	10	1.32	1.05	1.29	9	1.34	0.95	1.18	7	1.06	0.92	0.99	12.79	7.16	12.96
J3KNL6	Protein transport protein Sec16A OS=Homo sapiens GN=SEC16A PE=4 SV=1	8	1.03	1.13	1.03	7	1.04	1.05	1.07	2	0.88	1.08	1.16	9.18	3.75	6.44
B4E1U9	cDNA FLJ54776, highly similar to Cell division control protein 42 homolog OS=Homo sapiens PE=2 SV=1	15	1.04	1.03	1.05	9	1.00	1.01	1.04	8	1.00	0.98	0.99	2.48	2.57	3.06
Q9UNE7	E3 ubiquitin-protein ligase CHIP OS=Homo sapiens GN=STUB1 PE=1 SV=2	8	1.02	0.98	1.20	5	0.86	1.03	0.97	3	0.96	1.15	1.03	8.55	8.30	11.29
Q8WWM7	Ataxin-2-like protein OS=Homo sapiens GN=ATXN2L PE=1 SV=2	7	0.90	0.98	0.84	4	1.02	1.19	1.01	3	0.80	0.99	0.97	12.30	11.16	9.41
P80303	Nucleobindin-2 OS=Homo sapiens GN=NUCB2 PE=1 SV=2	7	1.53	0.95	1.32	5	1.32	1.08	1.38	8	1.32	0.93	1.05	8.64	8.22	14.27
Q6IBH6	RPL26 protein OS=Homo sapiens GN=RPL26 PE=2 SV=1	9	0.93	1.00	0.94	7	1.54	1.14	0.89	7	1.28	1.13	1.40	24.49	7.09	26.08

Q9NR12	PDZ and LIM domain protein 7 OS=Homo sapiens GN=PDLIM7 PE=1 SV=1	7	1.10	1.02	1.15	5	1.18	0.98	1.23	5	1.04	0.97	1.11	6.60	2.79	5.11
Q6LES2	Annexin (Fragment) OS=Homo sapiens GN=ANXA4 PE=2 SV=1	9	1.35	1.20	1.51	9	1.31	1.07	1.03	9	1.00	0.95	0.82	15.98	11.70	31.69
P28066	Proteasome subunit alpha type-5 OS=Homo sapiens GN=PSMA5 PE=1 SV=3	12	0.99	1.06	1.14	12	1.01	0.99	0.98	10	0.94	1.00	0.96	3.68	3.73	9.38
P33316-2	Isoform 2 of Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial OS=Homo sapiens GN=DUT	10	0.88	1.10	0.93	7	0.76	0.95	0.80	11	0.82	0.97	0.82	7.56	8.28	7.94
Q9Y3A5	Ribosome maturation protein SBDS OS=Homo sapiens GN=SBDS PE=1 SV=4	9	0.96	0.90	0.86	6	1.03	0.99	1.02	5	1.13	1.06	1.08	8.05	8.48	11.35
Q13162	Peroxiredoxin-4 OS=Homo sapiens GN=PRDX4 PE=1 SV=1	9	1.24	1.07	1.04	11	1.28	1.12	1.19	12	1.24	0.95	1.15	2.11	8.30	7.22
P51116	Fragile X mental retardation syndrome-related protein 2 OS=Homo sapiens GN=FXR2 PE=1 SV=2	10	1.07	1.00	0.82	6	1.10	0.94	1.19	7	0.97	1.09	1.07	6.29	7.32	18.60
Q6FHJ5	SCAMP3 protein (Fragment) OS=Homo sapiens GN=SCAMP3 PE=2 SV=1	10	1.25	1.21	1.12	14	1.01	0.75	0.96	8	1.24	0.92	1.07	11.91	24.12	7.82
Q6UXN9	WD repeat-containing protein 82 OS=Homo sapiens GN=WDR82 PE=1 SV=1	8	0.98	0.92	0.71	8	1.05	1.12	1.01	5	0.95	0.76	0.87	4.84	19.57	17.33
B2R7C2	cDNA, FLJ93375, highly similar to Homo sapiens ZW10, kinetochore associated, homolog (Drosophila) (ZW10), mRNA OS=Homo sapiens PE=2 SV=1	7	0.87	0.91	0.90	11	0.84	0.90	0.84	5	0.86	1.17	0.94	1.83	15.59	5.64
O14929	Histone acetyltransferase type B catalytic subunit OS=Homo sapiens GN=HAT1 PE=1 SV=1	10	1.12	0.99	1.18	7	0.96	0.85	0.90	5	1.05	1.00	1.16	7.65	9.02	14.46
R4GMR5	26S proteasome non-ATPase regulatory subunit 8 OS=Homo sapiens GN=PSMD8 PE=4 SV=1	10	1.11	1.03	1.15	9	1.02	1.09	1.08	7	1.16	0.95	1.05	6.48	7.18	4.68
B3KM97	cDNA FLJ10554 fis, clone NT2RP2002385, highly similar to Synaptic glycoprotein SC2 OS=Homo sapiens PE=2 SV=1	7	1.21	0.99	1.17	7	1.17	1.09	1.08	6	1.20	1.06	1.25	1.87	4.63	7.09
B2R761	cDNA, FLJ93299, highly similar to Homo sapiens sterol carrier protein 2 (SCP2), mRNA OS=Homo sapiens PE=2 SV=1	7	1.08	1.11	1.04	7	1.28	1.17	1.18	8	1.20	0.84	1.18	8.62	16.91	6.97
Q9P035	Very-long-chain (3R)-3-hydroxyacyl-[acyl-carrier protein] dehydratase 3 OS=Homo sapiens GN=PTPLAD1 PE=1 SV=2	10	1.20	1.05	1.22	8	1.13	0.97	1.05	7	1.07	0.95	1.07	5.84	5.63	8.23
Q8N129	Protein canopy homolog 4 OS=Homo sapiens GN=CNPY4 PE=2 SV=1	7	1.41	0.96	1.20	7	1.05	0.81	1.13	5	1.20	1.11	1.22	14.77	15.55	3.96
Q6ZSA3	cDNA FLJ45695 fis, clone FEBRA2013570, highly similar to 2-oxoisovalerate dehydrogenase alpha subunit, mitochondrial (EC 1.2.4.4) OS=Homo sapiens PE=2 SV=1	8	1.09	0.95	1.05	6	0.80	0.96	0.90	5	0.99	0.88	0.94	15.27	5.09	8.08
D3DR22	Hydroxysteroid (17-beta) dehydrogenase 12, isoform CRA_a OS=Homo sapiens GN=HSD17B12 PE=3 SV=1	11	1.09	1.01	0.99	6	1.46	1.14	1.30	7	1.05	0.97	1.10	19.14	8.82	13.82
P51148	Ras-related protein Rab-5C OS=Homo sapiens GN=RAB5C PE=1 SV=2	11	1.06	1.09	1.35	8	0.92	0.96	0.84	8	0.98	0.97	0.98	6.74	7.26	24.83

O75663	TIP41-like protein OS=Homo sapiens GN=TIPRL PE=1 SV=2	8	0.95	0.92	1.09	7	1.10	1.06	1.06	7	1.11	0.98	1.07	8.25	6.82	1.10
Q59EH3	Acid phosphatase 1 isoform c variant (Fragment) OS=Homo sapiens PE=2 SV=1	8	0.93	0.91	0.90	11	0.74	0.89	0.92	6	0.97	0.95	0.91	13.62	3.71	0.67
Q502X2	Diablo homolog (Drosophila) OS=Homo sapiens GN=DIABLO PE=2 SV=1	9	0.97	1.11	1.15	10	0.87	0.78	0.83	6	0.98	1.08	0.98	6.49	18.53	16.36
Q9H7Z7	Prostaglandin E synthase 2 OS=Homo sapiens GN=PTGES2 PE=1 SV=1	7	1.20	1.03	1.05	9	0.81	0.89	0.85	7	1.27	1.11	1.29	22.71	11.22	20.37
P37198	Nuclear pore glycoprotein p62 OS=Homo sapiens GN=NUP62 PE=1 SV=3	9	0.98	1.03	1.05	10	0.86	0.89	0.94	8	0.98	1.04	1.04	7.24	8.50	5.85
P21964	Catechol O-methyltransferase OS=Homo sapiens GN=COMT PE=1 SV=2	13	1.10	0.96	0.99	8	0.98	1.09	1.02	8	1.08	0.94	1.03	6.39	7.75	2.16
Q9BZE1	39S ribosomal protein L37, mitochondrial OS=Homo sapiens GN=MRPL37 PE=1 SV=2	8	0.91	1.01	0.79	8	0.92	1.05	0.95	8	0.83	0.97	0.78	5.75	3.85	11.19
Q59GW7	Replication factor C 5 isoform 1 variant (Fragment) OS=Homo sapiens PE=2 SV=1	8	0.90	0.91	0.84	3	0.69	0.78	0.74	8	0.96	0.98	0.97	16.94	11.43	13.69
B7Z6H4	DNA-directed RNA polymerase OS=Homo sapiens PE=2 SV=1	9	0.78	0.89	0.89	5	0.86	0.96	1.05	5	1.01	1.08	0.90	13.40	9.81	9.53
E7EUC7	UTP--glucose-1-phosphate uridylyltransferase OS=Homo sapiens GN=UGP2 PE=2 SV=1	10	1.10	1.04	1.23	12	0.96	0.81	0.99	7	1.06	0.97	1.06	6.90	12.40	11.38
Q9P287	BRCA2 and CDKN1A-interacting protein OS=Homo sapiens GN=BCCIP PE=1 SV=1	10	1.54	1.19	0.99	9	1.00	1.14	1.11	9	0.91	0.94	0.85	29.47	12.05	13.28
Q0QEY7	Succinate dehydrogenase complex subunit B (Fragment) OS=Homo sapiens GN=SDHB PE=2 SV=1	8	1.19	0.96	0.97	4	1.26	0.96	1.04	7	1.23	0.99	1.20	2.59	1.59	10.91
J3QLS3	28S ribosomal protein S7, mitochondrial OS=Homo sapiens GN=MRPS7 PE=4 SV=1	8	1.01	1.08	0.98	9	1.01	0.94	0.96	4	0.97	1.00	1.06	2.14	7.28	5.35
O75947	ATP synthase subunit d, mitochondrial OS=Homo sapiens GN=ATP5H PE=1 SV=3	14	1.29	0.99	1.31	16	1.31	0.96	1.20	16	1.31	1.08	1.30	0.96	6.28	4.77
B3KT21	cDNA FLJ37476 fis, clone BRAWH2012827, highly similar to Homo sapiens BH3 interacting domain death agonist (BID), transcript variant 1, mRNA OS=Homo sapiens PE=2 SV=1	11	1.08	1.07	1.19	6	1.25	0.93	1.14	7	1.06	1.05	1.10	9.34	7.64	4.11
D6RCD0	Estradiol 17-beta-dehydrogenase 11 OS=Homo sapiens GN=HSD17B11 PE=2 SV=1	7	1.18	1.03	0.98	6	1.16	0.95	0.98	5	1.00	1.03	1.00	9.04	4.30	1.29
Q53EX1	BCS1-like variant (Fragment) OS=Homo sapiens PE=2 SV=1	8	1.23	1.12	1.21	6	1.08	0.97	0.99	7	1.29	1.00	1.42	9.05	7.38	17.63
Q96C19	EF-hand domain-containing protein D2 OS=Homo sapiens GN=EFHD2 PE=1 SV=1	7	1.01	1.02	0.97	6	1.01	1.09	1.05	4	1.02	1.09	1.03	0.90	3.89	4.14
Q92665	28S ribosomal protein S31, mitochondrial OS=Homo sapiens GN=MRPS31 PE=1 SV=3	7	0.88	0.95	0.76	10	1.05	1.03	1.05	8	0.98	0.80	0.91	8.66	12.30	15.61
E7DVW5	Fatty acid binding protein 5 (Psoriasis-associated) OS=Homo sapiens GN=FABP5 PE=2 SV=1	10	0.92	1.09	0.82	8	1.02	1.09	0.95	7	0.86	0.96	0.86	8.81	6.93	7.64
P68402	Platelet-activating factor acetylhydrolase IB subunit beta OS=Homo sapiens GN=PAFAH1B2 PE=1 SV=1	15	0.97	1.16	1.16	11	0.86	0.93	0.79	11	0.91	1.22	0.91	6.23	13.94	19.67

Q5W0H4	Translationally-controlled tumor protein OS=Homo sapiens GN=TPT1 PE=2 SV=1	10	0.93	0.99	0.99	8	1.05	1.11	1.06	7	0.98	0.90	1.04	6.23	10.36	3.20
P14735	Insulin-degrading enzyme OS=Homo sapiens GN=IDE PE=1 SV=4	10	1.35	1.16	0.95	7	1.16	0.98	1.15	10	1.02	1.07	0.99	13.82	8.36	10.24
J3KNP2	Transducin beta-like protein 3 (Fragment) OS=Homo sapiens GN=TBL3 PE=4 SV=1	8	1.10	0.97	1.25	7	0.89	1.13	0.95	7	0.81	1.01	0.78	16.10	7.89	23.71
B9A018	U4/U6.U5 tri-snRNP-associated protein 2 OS=Homo sapiens GN=USP39 PE=2 SV=1	10	0.85	0.93	1.00	8	0.88	0.99	1.04	7	0.97	0.88	0.99	6.98	6.11	2.85
P49773	Histidine triad nucleotide-binding protein 1 OS=Homo sapiens GN=HINT1 PE=1 SV=2	12	1.09	1.03	0.88	6	1.14	1.19	1.03	4	1.03	1.08	0.92	4.96	7.46	7.81
Q6NZ55	60S ribosomal protein L13 OS=Homo sapiens GN=RPL13 PE=2 SV=1	10	0.93	0.97	1.09	7	0.90	0.87	0.87	7	0.91	1.12	1.00	1.85	12.67	11.37
E9PDC3	Armadillo repeat protein deleted in velo-cardio-facial syndrome OS=Homo sapiens GN=ARVCF PE=2 SV=1	7	0.70	0.96	0.76	3	0.96	0.87	0.82	4	0.85	0.90	0.91	15.73	5.13	9.25
P20674	Cytochrome c oxidase subunit 5A, mitochondrial OS=Homo sapiens GN=COX5A PE=1 SV=2	13	1.33	1.03	0.98	13	1.42	1.06	1.14	9	1.22	1.07	1.15	7.47	1.92	8.63
Q6IRT1	Alcohol dehydrogenase 5 (Class III), chi polypeptide OS=Homo sapiens GN=ADH5 PE=2 SV=2	7	1.03	1.10	1.03	9	1.10	1.06	1.07	7	0.99	1.01	1.04	5.31	4.26	2.14
B4DUX5	Methionine aminopeptidase OS=Homo sapiens GN=METAP2 PE=2 SV=1	7	0.94	1.00	0.99	6	0.91	0.80	0.88	5	1.51	1.44	1.17	30.12	30.22	14.46
B3KNC3	cDNA FLJ14222 fis, clone NT2RP3003992, highly similar to Nucleolar complex protein 2 homolog OS=Homo sapiens PE=2 SV=1	7	0.94	1.04	0.89	6	1.02	0.96	1.01	4	1.02	0.97	1.05	4.33	4.66	8.57
Q92747	Actin-related protein 2/3 complex subunit 1A OS=Homo sapiens GN=ARPC1A PE=1 SV=2	12	0.85	0.91	0.93	10	1.06	1.08	0.98	10	0.97	0.86	0.96	11.19	12.01	2.93
B2R7D2	cDNA, FLJ93389, highly similar to Homo sapiens multiple inositol polyphosphate histidine phosphatase, 1 (MINPP1), mRNA OS=Homo sapiens PE=2 SV=1	7	1.33	1.15	1.34	7	1.14	0.86	1.05	8	1.17	1.10	1.26	8.22	15.14	12.18
Q68E01	Integrator complex subunit 3 OS=Homo sapiens GN=INTS3 PE=1 SV=1	11	0.84	1.10	0.97	6	1.07	1.06	0.94	8	0.98	0.96	0.92	11.94	6.88	2.53
Q8TAT6	Nuclear protein localization protein 4 homolog OS=Homo sapiens GN=NPLOC4 PE=1 SV=3	8	0.90	1.02	0.96	8	0.88	0.95	0.89	7	0.97	1.05	0.95	4.69	5.29	4.02
Q8IV08	Phospholipase D3 OS=Homo sapiens GN=PLD3 PE=1 SV=1	8	0.69	1.03	0.93	8	0.67	0.82	0.74	9	0.74	1.09	0.86	5.45	14.72	11.19
P61353	60S ribosomal protein L27 OS=Homo sapiens GN=RPL27 PE=1 SV=2	15	0.94	0.95	0.91	10	0.94	0.96	0.95	16	0.98	1.02	1.03	2.51	4.16	6.84
P46109	Crk-like protein OS=Homo sapiens GN=CRKL PE=1 SV=1	7	0.86	0.98	0.82	8	1.00	1.14	1.00	10	0.97	0.94	0.86	7.40	10.33	10.56
Q9NPL8	Translocase of inner mitochondrial membrane domain-containing protein 1 OS=Homo sapiens GN=TIMMDC1 PE=1 SV=2	7	0.96	0.94	1.05	3	0.84	0.96	0.84	5	1.01	0.89	1.05	9.71	3.63	12.08
Q5T0G8	Annexin OS=Homo sapiens GN=ANXA11 PE=2 SV=1	8	1.40	1.08	1.55	5	1.36	0.86	1.07	6	1.48	1.18	1.41	4.36	16.10	18.66
Q8N1G2	Cap-specific mRNA (nucleoside-2'-O-)-methyltransferase 1 OS=Homo sapiens GN=FTSJD2 PE=1 SV=1	7	1.03	1.06	1.10	4	0.97	1.18	1.01	7	1.04	0.86	0.94	3.58	15.82	7.74

B7Z7Q0	Phosphatidylinositol transfer protein beta isoform OS=Homo sapiens GN=PITPNB PE=2 SV=1	9	1.05	1.03	0.96	9	1.02	1.02	0.99	11	1.16	1.16	0.99	6.77	7.28	1.68
A8K7A4	cDNA FLJ76904, highly similar to Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA OS=Homo sapiens PE=2 SV=1	8	1.06	1.01	0.94	6	0.92	0.98	0.90	6	0.87	1.05	0.92	10.70	3.26	2.02
Q15056	Eukaryotic translation initiation factor 4H OS=Homo sapiens GN=EIF4H PE=1 SV=5	12	0.87	1.02	1.01	12	0.87	0.90	0.89	10	0.90	1.05	1.00	1.88	8.08	7.08
Q9NQG5	Regulation of nuclear pre-mRNA domain-containing protein 1B OS=Homo sapiens GN=RPRD1B PE=1 SV=1	8	0.89	1.01	0.96	10	0.95	1.03	0.89	4	0.87	1.08	1.07	4.52	3.28	9.22
O43837	Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial OS=Homo sapiens GN=IDH3B PE=1 SV=2	10	0.97	1.05	1.08	7	0.99	1.02	1.03	9	0.96	0.91	0.88	1.45	7.47	10.15
B4DFD5	cDNA FLJ58528, highly similar to N-acetyltransferase 10 (EC 2.3.1.-) OS=Homo sapiens PE=2 SV=1	7	1.05	1.13	1.13	9	1.05	0.91	0.92	8	0.96	1.03	1.02	4.72	10.57	9.96
O95372	Acyl-protein thioesterase 2 OS=Homo sapiens GN=LYPLA2 PE=1 SV=1	15	0.83	0.94	0.88	7	0.83	1.11	0.94	8	0.95	1.00	0.93	7.75	8.62	3.51
Q9UKN8	General transcription factor 3C polypeptide 4 OS=Homo sapiens GN=GTF3C4 PE=1 SV=2	9	0.95	0.99	0.90	11	0.97	0.94	0.94	9	1.05	1.00	1.05	5.20	3.23	7.95
E9PGT1	Translin OS=Homo sapiens GN=TSN PE=2 SV=1	8	1.00	1.03	1.00	8	0.99	1.01	1.00	8	1.01	0.92	0.95	0.68	6.16	3.29
A8K517	Ribosomal protein S23, isoform CRA_a OS=Homo sapiens GN=RPS23 PE=2 SV=1	12	0.79	1.04	0.86	6	0.84	0.89	0.87	7	0.85	0.86	0.91	4.40	10.44	3.32
Q53GE2	Capping protein (Actin filament) muscle Z-line, alpha 2 variant (Fragment) OS=Homo sapiens PE=2 SV=1	11	1.01	1.15	1.08	11	0.86	0.94	0.88	8	1.00	1.03	0.95	8.68	9.79	10.27
Q9Y6G9	Cytoplasmic dynein 1 light intermediate chain 1 OS=Homo sapiens GN=DYNC1LI1 PE=1 SV=3	8	1.00	1.00	0.94	10	1.05	1.09	1.06	4	1.10	0.89	0.94	4.54	10.18	6.75
Q9UBB6	Neurochondrin OS=Homo sapiens GN=NCDN PE=1 SV=1	8	0.96	1.00	1.04	6	0.89	0.90	1.04	3	1.16	1.12	0.91	13.87	11.36	7.52
Q8TCS8	Polyribonucleotide nucleotidyltransferase 1, mitochondrial OS=Homo sapiens GN=PNPT1 PE=1 SV=2	7	1.00	1.06	1.03	7	1.00	0.94	1.03	7	1.08	1.08	1.04	4.64	7.52	0.56
Q6IBN6	CBX1 protein OS=Homo sapiens GN=CBX1 PE=2 SV=1	7	1.13	1.02	0.89	6	1.14	1.07	1.08	6	1.11	0.98	1.06	1.03	4.17	10.27
Q86Y56	HEAT repeat-containing protein 2 OS=Homo sapiens GN=HEATR2 PE=1 SV=4	7	0.80	0.80	0.77	9	0.91	0.94	0.95	9	0.92	1.01	0.94	7.44	11.45	11.29
Q9ULC4	Malignant T-cell-amplified sequence 1 OS=Homo sapiens GN=MCTS1 PE=1 SV=1	11	1.17	1.01	1.16	11	1.31	1.10	1.20	8	1.01	0.95	1.06	13.03	7.33	6.45
Q6PJG6	BRCA1-associated ATM activator 1 OS=Homo sapiens GN=BRAT1 PE=1 SV=2	8	0.98	1.15	1.03	5	0.92	0.94	0.89	5	0.83	1.00	0.96	8.34	10.55	7.11
Q32Q62	RSL1D1 protein (Fragment) OS=Homo sapiens GN=RSL1D1 PE=2 SV=1	7	1.05	0.90	0.97	6	1.22	1.12	1.23	6	1.20	1.01	1.21	8.27	10.87	12.83
P22059	Oxysterol-binding protein 1 OS=Homo sapiens GN=OSBP PE=1 SV=1	8	1.03	1.00	1.00	6	1.16	0.97	1.02	7	1.10	0.99	0.92	6.06	1.82	5.29

E7ETZ4	Basic leucine zipper and W2 domain-containing protein 2 (Fragment) OS=Homo sapiens GN=BZW2 PE=2 SV=1	11	0.76	1.00	0.91	10	0.88	0.95	0.94	9	0.86	0.97	0.82	7.49	2.31	7.15
Q8NBX0	Saccharopine dehydrogenase-like oxidoreductase OS=Homo sapiens GN=SCCPDH PE=1 SV=1	7	1.20	0.95	1.09	7	1.21	1.01	1.12	5	1.09	0.98	1.04	5.63	3.38	4.00
Q14353	Guanidinoacetate N-methyltransferase OS=Homo sapiens GN=GAMT PE=1 SV=1	10	0.86	1.03	0.88	4	0.86	0.98	0.87	2	0.82	0.99	1.00	2.78	2.41	7.97
Q6PGP7	Tetratricopeptide repeat protein 37 OS=Homo sapiens GN=TTC37 PE=1 SV=1	8	0.80	1.04	1.05	7	0.98	0.99	0.95	9	1.10	1.05	1.11	15.62	3.34	7.53
O00625	Pirin OS=Homo sapiens GN=PIR PE=1 SV=1	8	0.80	0.91	0.67	4	1.05	1.18	1.04	6	1.05	1.27	1.10	15.07	16.74	25.09
P49903	Selenide, water dikinase 1 OS=Homo sapiens GN=SEPHS1 PE=1 SV=2	10	0.91	0.95	0.83	6	0.91	0.93	0.97	7	1.06	1.11	0.97	8.93	9.49	8.83
B1B0M1	GRIP1-associated protein 1 OS=Homo sapiens GN=GRIPAP1 PE=2 SV=1	7	1.04	1.06	0.96	12	0.96	1.01	0.89	6	1.03	1.10	0.99	4.14	4.23	5.33
Q8NBJ5	Procollagen galactosyltransferase 1 OS=Homo sapiens GN=COLGALT1 PE=1 SV=1	7	1.00	1.00	0.83	6	0.99	1.14	1.04	8	1.02	1.24	1.00	1.28	10.89	11.26
B2R4D5	cDNA, FLJ92050, highly similar to Homo sapiens actin related protein 2/3 complex, subunit 3, 21kDa (ARPC3), mRNA OS=Homo sapiens PE=2 SV=1	11	0.99	1.07	1.08	14	1.05	1.05	1.03	12	0.98	1.07	1.06	3.91	1.16	2.59
Q99426	Tubulin-folding cofactor B OS=Homo sapiens GN=TBCB PE=1 SV=2	8	0.91	0.92	0.87	6	0.76	0.84	0.77	6	1.08	1.32	0.99	17.20	24.92	12.36
Q53S54	Putative uncharacterized protein CUL3 (Fragment) OS=Homo sapiens GN=CUL3 PE=2 SV=1	7	1.01	1.02	0.80	10	0.94	0.90	0.96	8	1.02	1.00	0.95	4.41	6.51	9.88
Q541A5	Ubiquitin fusion degradation 1 like (Yeast), isoform CRA_b OS=Homo sapiens GN=ufd1 PE=2 SV=1	8	0.93	1.00	0.97	5	1.01	0.89	0.93	6	0.99	1.13	1.09	4.21	11.92	8.36
B4DM85	cDNA FLJ56002, highly similar to Kinesin-like protein KIF2 OS=Homo sapiens PE=2 SV=1	7	0.94	1.07	0.87	5	0.82	0.85	0.81	4	0.84	0.93	1.11	7.25	11.68	17.12
Q53FW2	Ribose-phosphate pyrophosphokinase (Fragment) OS=Homo sapiens PE=2 SV=1	8	0.92	0.97	0.96	9	0.89	1.06	0.91	6	0.86	1.05	0.87	3.61	4.55	4.91
F5HFY4	Nucleosome assembly protein 1-like 4 OS=Homo sapiens GN=NAP1L4b PE=2 SV=1	15	0.90	1.07	0.90	17	0.97	0.99	0.95	15	1.00	0.96	1.02	5.71	5.79	6.21
P16930	Fumarylacetoacetase OS=Homo sapiens GN=FAH PE=1 SV=2	9	1.11	1.25	0.90	2	1.01	0.96	0.90	3	1.40	1.27	1.32	17.53	14.96	23.20
F8W727	60S ribosomal protein L32 OS=Homo sapiens GN=RPL32 PE=2 SV=1	11	0.89	1.01	0.81	11	1.05	1.10	1.03	8	0.94	0.89	0.94	8.59	10.54	11.80
Q14677	Clathrin interactor 1 OS=Homo sapiens GN=CLINT1 PE=1 SV=1	9	0.86	1.20	0.87	4	1.05	1.23	1.07	5	0.90	1.07	0.89	10.56	7.52	11.65
Q9Y4C2	Protein FAM115A OS=Homo sapiens GN=FAM115A PE=1 SV=3	8	0.89	1.00	1.02	6	0.64	0.89	0.82	8	0.73	1.02	0.87	16.67	7.32	11.36
Q5HYL6	Putative uncharacterized protein DKFZp686E1899 OS=Homo sapiens GN=DKFZp686E1899 PE=2 SV=1	13	0.82	1.04	0.90	6	0.90	0.94	0.98	2	0.87	0.81	0.83	4.71	12.73	7.81
Q54A51	Basigin (Ok blood group), isoform CRA_a OS=Homo sapiens GN=hEMMPRIN PE=2 SV=1	9	1.04	0.91	0.93	9	1.28	0.97	1.20	8	1.32	0.89	1.12	12.19	4.45	12.70
Q9Y6C9	Mitochondrial carrier homolog 2 OS=Homo sapiens GN=MTCH2 PE=1 SV=1	9	1.19	0.94	1.02	9	1.13	0.96	1.10	8	1.16	1.00	1.09	2.36	3.38	4.07

Q6MZU1	Putative uncharacterized protein DKFZp686A1195 OS=Homo sapiens GN=DKFZp686A1195 PE=2 SV=1	7	0.91	1.00	0.94	5	0.98	1.01	1.05	4	1.26	1.33	1.01	17.36	16.92	5.26
Q5SQH4	DBP2 protein OS=Homo sapiens GN=DHX16 PE=2 SV=1	8	0.98	0.88	1.08	8	0.95	1.01	1.01	5	1.11	1.04	1.14	8.63	8.45	6.07
Q12792	Twinfilin-1 OS=Homo sapiens GN=TWF1 PE=1 SV=3	9	1.07	1.15	1.17	8	0.99	1.02	0.99	7	1.04	0.89	0.99	4.08	12.83	9.76
Q9NRN7	L-aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase OS=Homo sapiens GN=AASDHPPT PE=1 SV=2	7	0.91	0.92	0.77	9	1.03	1.12	0.93	7	0.90	1.02	0.92	7.97	9.66	10.43
Q4LE43	PLCG1 variant protein (Fragment) OS=Homo sapiens GN=PLCG1 variant protein PE=2 SV=1	11	0.79	1.00	1.05	6	1.01	1.14	1.10	6	0.76	0.86	0.81	16.06	13.96	15.80
P37108	Signal recognition particle 14 kDa protein OS=Homo sapiens GN=SRP14 PE=1 SV=2	10	0.83	1.00	0.89	9	0.80	0.85	0.79	9	0.86	1.08	0.87	3.90	12.04	6.37
P62269	40S ribosomal protein S18 OS=Homo sapiens GN=RPS18 PE=1 SV=3	7	1.05	1.02	0.99	7	1.09	1.00	0.98	8	1.04	0.95	1.10	2.49	3.67	6.77
Q6FGV9	PMVK protein (Fragment) OS=Homo sapiens GN=PMVK PE=2 SV=1	7	0.85	0.91	1.14	9	0.98	0.92	0.93	6	0.86	1.21	0.95	8.31	16.56	11.72
Q5JTZ9	Alanine--tRNA ligase, mitochondrial OS=Homo sapiens GN=AARS2 PE=1 SV=1	9	0.98	1.10	1.27	6	0.75	0.81	0.88	5	1.03	1.00	1.04	16.08	15.04	18.34
Q5T4U5	Acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain, isoform CRA_a OS=Homo sapiens GN=ACADM PE=2 SV=1	18	0.99	0.99	1.12	10	0.88	0.78	0.86	6	0.94	1.06	0.94	6.14	14.99	13.76
P61970	Nuclear transport factor 2 OS=Homo sapiens GN=NUTF2 PE=1 SV=1	20	0.93	1.03	0.88	13	0.93	1.08	0.98	10	0.99	1.00	0.98	3.54	3.74	5.78
O95747	Serine/threonine-protein kinase OSR1 OS=Homo sapiens GN=OXSR1 PE=1 SV=1	8	0.77	0.87	1.04	5	0.65	0.78	1.14	6	0.91	1.19	0.82	16.55	22.89	16.23
Q9H078-2	Isoform 2 of Caseinolytic peptidase B protein homolog OS=Homo sapiens GN=CLPB	9	0.99	1.00	0.98	6	0.97	1.14	0.91	3	1.00	0.91	0.85	1.66	11.65	7.29
Q71SV8	Crn-related protein kim1 OS=Homo sapiens PE=2 SV=1	9	1.31	1.10	1.37	3	0.95	1.13	1.10	9	1.14	0.92	1.13	15.82	10.69	12.15
Q9UHY7	Enolase-phosphatase E1 OS=Homo sapiens GN=ENOPH1 PE=1 SV=1	7	1.04	1.10	1.29	5	0.89	0.91	0.88	3	0.88	0.89	0.88	9.50	11.78	23.25
Q9H4L7	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A containing DEAD/H box 1 OS=Homo sapiens GN=SMARCAD1 PE=1 SV=2	9	0.69	1.11	0.92	5	0.90	1.13	0.96	7	0.75	0.85	0.81	14.17	14.95	8.33
Q8NFF5	FAD synthase OS=Homo sapiens GN=FLAD1 PE=1 SV=1	11	0.89	0.88	0.93	11	0.84	0.87	0.93	8	1.48	1.28	1.17	33.12	23.02	13.98
Q6IB11	PGRMC1 protein OS=Homo sapiens GN=PGRMC1 PE=2 SV=1	15	1.22	0.90	1.12	4	0.87	0.96	1.09	4	1.32	1.16	1.17	20.97	13.72	3.45
Q9NWY4	UPF0609 protein C4orf27 OS=Homo sapiens GN=C4orf27 PE=1 SV=2	7	0.84	1.15	0.93	7	0.93	1.13	1.05	5	0.82	0.89	0.75	6.29	13.43	16.99
Q8TDN6	Ribosome biogenesis protein BRX1 homolog OS=Homo sapiens GN=BRIX1 PE=1 SV=2	7	1.12	0.96	0.93	2	1.26	1.16	1.27	2	0.92	0.84	0.81	15.35	16.13	23.80
D3DQU2	Tripeptidyl peptidase I, isoform CRA_a OS=Homo sapiens GN=TPP1 PE=2 SV=1	10	1.16	1.21	1.33	10	1.07	1.00	1.01	6	0.93	1.08	0.99	11.16	9.63	17.46
Q8WVY7	Ubiquitin-like domain-containing CTD phosphatase 1 OS=Homo sapiens GN=UBLCP1 PE=1 SV=2	7	0.94	1.08	0.94	5	1.00	1.11	1.08	6	0.93	0.93	0.94	3.57	9.28	8.21

J3KNH7	Sentrin-specific protease 3 OS=Homo sapiens GN=SENP3 PE=4 SV=1	7	0.94	1.06	0.90	7	0.97	1.01	1.02	7	0.96	0.95	0.90	1.63	5.46	7.32
B7ZAM9	Eukaryotic translation initiation factor 3 subunit K OS=Homo sapiens GN=EIF3K PE=2 SV=1	7	0.84	1.00	0.95	9	0.81	0.85	0.90	7	0.91	1.04	0.93	5.89	10.23	2.92
P28289	Tropomodulin-1 OS=Homo sapiens GN=TMOD1 PE=1 SV=1	6	0.80	1.01	0.90	8	0.94	1.12	0.88	9	0.84	0.91	0.80	8.40	10.18	6.26
Q13011	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial OS=Homo sapiens GN=ECH1 PE=1 SV=2	10	0.93	0.93	1.08	10	0.90	0.89	1.00	11	0.97	1.08	1.00	3.37	10.77	4.56
Q9H0U4	Ras-related protein Rab-1B OS=Homo sapiens GN=RAB1B PE=1 SV=1	10	0.97	1.02	1.05	11	0.80	0.97	0.82	15	0.81	0.91	0.97	11.47	5.80	12.78
Q14240	Eukaryotic initiation factor 4A-II OS=Homo sapiens GN=EIF4A2 PE=1 SV=2	28	0.90	0.93	0.83	25	0.98	1.13	0.94	23	0.98	1.01	1.00	4.90	9.86	9.45
B4DGM9	Torsin family 1, member A (Torsin A), isoform CRA_a OS=Homo sapiens GN=TOR1A PE=2 SV=1	8	1.09	1.03	1.20	8	1.02	0.99	1.05	6	1.05	0.97	1.10	3.42	2.72	7.04
Q53HS1	Achalasia, adrenocortical insufficiency, alacrimia (Allgrove, triple-A) variant (Fragment) OS=Homo sapiens PE=2 SV=1	7	0.98	0.93	1.18	9	0.75	0.94	0.90	5	1.15	1.39	0.98	20.75	24.31	13.87
O43865	Putative adenosylhomocysteinase 2 OS=Homo sapiens GN=AHCYL1 PE=1 SV=2	7	1.27	0.82	0.94	9	0.91	0.84	0.74	5	0.97	1.12	0.92	18.51	17.98	12.76
F5H365	Protein transport protein Sec23A OS=Homo sapiens GN=SEC23A PE=2 SV=1	10	1.05	1.07	0.94	11	0.95	0.94	0.96	11	0.91	0.88	0.94	7.58	10.37	1.10
Q13131	5'-AMP-activated protein kinase catalytic subunit alpha-1 OS=Homo sapiens GN=PRKAA1 PE=1 SV=4	7	1.29	1.15	1.13	8	1.05	1.06	1.01	2	0.84	0.79	0.91	21.53	18.49	10.62
P50897	Palmitoyl-protein thioesterase 1 OS=Homo sapiens GN=PPT1 PE=1 SV=1	9	0.96	1.10	0.92	5	0.75	0.96	0.86	5	0.81	1.02	0.90	12.74	6.79	3.55
Q08257	Quinone oxidoreductase OS=Homo sapiens GN=CRYZ PE=1 SV=1	10	1.07	0.96	1.07	11	1.09	0.96	1.04	8	0.96	1.10	1.07	6.62	8.26	1.56
D3DTX6	Protein phosphatase 1, regulatory subunit 9B, spinophilin, isoform CRA_b OS=Homo sapiens GN=PPP1R9B PE=4 SV=1	6	0.99	0.95	0.98	6	0.93	1.06	0.96	6	0.98	0.99	1.07	3.52	5.49	5.67
Q53HN4	DNAation factor, 45kDa, alpha polypeptide isoform 1 variant (Fragment) OS=Homo sapiens PE=2 SV=1	8	1.01	1.04	1.13	6	1.04	1.04	1.09	6	0.89	1.04	0.82	8.21	0.07	16.44
O94776	Metastasis-associated protein MTA2 OS=Homo sapiens GN=MTA2 PE=1 SV=1	9	1.07	0.96	0.88	4	0.87	0.87	0.97	4	1.07	1.14	1.11	11.76	13.44	11.96
Q9BTT5	Similar to NADH dehydrogenase (Ubiquinone) 1 alpha subcomplex, 9 (39kD) (Fragment) OS=Homo sapiens PE=2 SV=1	8	1.00	1.05	0.99	8	1.17	1.06	1.06	9	1.13	1.02	1.01	8.44	1.94	3.53
B4DUC8	S-methyl-5'-thioadenosine phosphorylase OS=Homo sapiens GN=MTAP PE=2 SV=1	7	0.83	1.01	1.00	14	0.88	0.98	0.86	8	0.89	1.07	0.93	3.33	4.72	7.77
G4XXL9	Cytochrome c OS=Homo sapiens GN=CYCS PE=2 SV=1	15	1.07	1.04	0.99	12	1.12	1.07	1.07	14	1.07	1.02	1.13	2.78	2.41	6.30
P40222	Alpha-taxilin OS=Homo sapiens GN=TXLNA PE=1 SV=3	7	0.98	0.86	0.87	5	0.84	0.94	0.82	3	0.93	0.98	0.95	8.17	6.68	7.27
O75962	Triple functional domain protein OS=Homo sapiens GN=TRIO PE=1 SV=2	6	1.07	1.01	0.93	8	1.09	1.08	1.15	8	1.02	0.92	0.96	3.45	7.96	11.58
O75400	Pre-mRNA-processing factor 40 homolog A OS=Homo sapiens GN=PRPF40A PE=1 SV=2	6	1.32	1.48	1.56	6	0.77	0.79	0.79	4	1.09	1.27	0.93	26.34	29.72	37.82

Q6IAX2	RPL21 protein OS=Homo sapiens GN=RPL21 PE=2 SV=1	7	0.91	1.03	0.90	8	1.11	1.10	1.07	6	1.00	0.94	0.89	9.66	7.82	10.41
Q9BQA1	Methylosome protein 50 OS=Homo sapiens GN=WDR77 PE=1 SV=1	7	1.19	1.17	1.27	5	0.95	0.88	1.01	6	0.83	0.91	0.82	18.50	16.14	21.84
A0MNN4	CDW3/SMU1 OS=Homo sapiens GN=SMU1 PE=2 SV=1	7	0.80	1.01	0.94	7	0.84	0.86	0.82	9	0.93	0.96	0.86	7.63	8.02	7.35
Q14696	LDLR chaperone MESD OS=Homo sapiens GN=MESDC2 PE=1 SV=2	6	1.22	0.98	0.92	8	1.63	1.14	1.27	5	1.36	0.96	1.29	14.81	9.85	18.13
Q6IBA2	PC4 protein OS=Homo sapiens GN=PC4 PE=2 SV=1	8	0.97	1.04	0.83	5	0.99	1.17	1.00	8	0.96	0.95	1.00	1.69	10.41	10.64
Q567R6	Single-stranded DNA-binding protein OS=Homo sapiens GN=SSBP1 PE=2 SV=1	10	1.13	1.00	1.01	6	0.95	0.82	0.96	8	1.02	0.99	1.07	8.93	10.63	5.39
A8KA83	cDNA FLJ78586, highly similar to Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa (VAPA), mRNA OS=Homo sapiens PE=2 SV=1	8	1.01	0.95	0.88	9	1.06	1.03	1.04	7	0.95	0.87	0.96	5.28	8.86	8.50
O75323	Protein NipSnap homolog 2 OS=Homo sapiens GN=GBAS PE=1 SV=1	7	1.19	1.07	0.93	3	1.07	1.19	1.05	5	0.98	0.90	0.98	10.06	13.88	6.06
Q96JZ5	SM-11044 binding protein, isoform CRA_b OS=Homo sapiens GN=SMBP PE=2 SV=1	7	1.42	0.99	1.24	3	1.21	0.91	1.08	5	1.27	0.98	1.19	8.26	4.81	7.28
Q13155	Aminoacyl tRNA synthase complex-interacting multifunctional protein 2 OS=Homo sapiens GN=AIMP2 PE=1 SV=2	8	1.04	1.02	0.94	9	0.92	0.86	0.88	6	0.84	0.98	0.93	10.90	8.90	3.17
A6QKW0	SHINC3 OS=Homo sapiens GN=SHINC3 PE=2 SV=1	7	0.96	0.96	1.02	6	1.02	0.96	1.05	7	1.09	0.89	0.88	6.19	4.20	9.43
P04899	Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 PE=1 SV=3	12	1.15	1.07	1.37	11	0.89	0.87	0.95	12	1.08	0.97	1.01	12.78	10.55	20.46
J3QQT2	60S ribosomal protein L17 (Fragment) OS=Homo sapiens GN=RPL17 PE=3 SV=1	20	0.95	1.01	0.96	13	1.06	1.10	1.10	15	0.96	0.92	0.95	5.95	8.80	8.38
K7ES61	39S ribosomal protein L4, mitochondrial (Fragment) OS=Homo sapiens GN=MRPL4 PE=3 SV=1	7	1.18	1.00	1.07	12	1.24	1.07	1.08	7	0.99	1.02	1.00	11.45	3.49	3.93
Q6YN16	Hydroxysteroid dehydrogenase-like protein 2 OS=Homo sapiens GN=HSDL2 PE=1 SV=1	7	0.89	1.04	0.87	9	1.12	1.17	0.99	10	0.87	0.96	0.93	14.51	9.86	6.54
H0YN81	WD repeat-containing protein 61 (Fragment) OS=Homo sapiens GN=WDR61 PE=2 SV=1	7	0.82	1.07	0.78	5	0.95	0.98	1.04	4	1.01	0.96	0.90	10.21	6.16	13.96
A8MWK3	Cadherin-2 OS=Homo sapiens GN=CDH2 PE=2 SV=1	8	0.99	0.96	0.98	8	1.01	1.07	1.03	7	1.12	0.92	1.00	6.46	7.96	2.59
B2R960	cDNA, FLJ94230, highly similar to Homo sapiens thioredoxin-like 1 (TXNL1), mRNA OS=Homo sapiens PE=2 SV=1	8	1.04	1.08	1.07	10	0.87	0.99	0.91	10	0.96	1.06	1.02	8.99	4.46	8.12
Q5VV89	Microsomal glutathione S-transferase 3 OS=Homo sapiens GN=MGST3 PE=2 SV=1	9	1.28	0.96	1.38	5	1.08	0.83	1.05	4	1.12	0.98	1.13	9.31	9.21	14.76
O75569	Interferon-inducible double stranded RNA-dependent protein kinase activator A OS=Homo sapiens GN=PRKRA PE=1 SV=1	9	0.95	0.90	0.80	9	0.91	0.97	0.99	6	0.92	0.88	0.98	2.37	5.26	11.48
Q13442	28 kDa heat- and acid-stable phosphoprotein OS=Homo sapiens GN=PDAP1 PE=1 SV=1	9	0.94	1.07	0.92	5	1.05	1.10	0.99	6	0.96	1.01	0.98	5.84	4.34	4.15
P31946	14-3-3 protein beta/alpha OS=Homo sapiens GN=YWHAB PE=1 SV=3	37	1.01	1.15	1.25	33	0.84	0.94	0.89	33	0.92	1.10	0.99	9.17	10.38	17.64
Q04917	14-3-3 protein eta OS=Homo sapiens GN=YWHAH PE=1 SV=4	18	0.82	1.00	1.11	19	0.78	0.88	0.94	18	0.89	1.06	0.97	6.80	9.51	9.42

P61224	Ras-related protein Rap-1b OS=Homo sapiens GN=RAP1B PE=1 SV=1	13	1.03	0.93	0.80	11	1.13	1.44	1.26	5	1.04	0.71	0.91	5.44	36.24	24.79
E9PRQ7	UBX domain-containing protein 1 OS=Homo sapiens GN=UBXN1 PE=2 SV=1	11	0.95	0.86	0.92	4	0.82	0.87	0.85	6	0.98	1.00	0.92	9.24	8.56	4.07
Q96Q11	CCA tRNA nucleotidyltransferase 1, mitochondrial OS=Homo sapiens GN=TRNT1 PE=1 SV=2	6	1.16	1.23	0.82	8	1.03	1.05	1.05	5	0.90	1.03	1.10	12.62	9.74	15.02
Q96M27	Protein PRRC1 OS=Homo sapiens GN=PRRC1 PE=1 SV=1	6	0.89	0.99	1.07	3	1.39	1.27	1.29	4	1.07	0.95	0.82	22.59	16.45	22.39
Q13144	Translation initiation factor eIF-2B subunit epsilon OS=Homo sapiens GN=EIF2B5 PE=1 SV=3	6	0.95	1.10	0.94	6	1.01	0.95	1.00	5	1.07	0.94	1.15	5.70	8.81	10.82
Q04760	Lactoylglutathione lyase OS=Homo sapiens GN=GLO1 PE=1 SV=4	10	0.91	1.16	0.92	8	1.01	1.17	1.02	14	0.94	0.99	0.91	5.42	9.18	6.61
O75844	CAAX prenyl protease 1 homolog OS=Homo sapiens GN=ZMPSTE24 PE=1 SV=2	6	1.16	0.85	0.89	6	1.37	1.14	1.23	6	1.26	0.92	1.17	8.44	15.71	16.40
Q38G75	UDP galactose 4'-epimerase OS=Homo sapiens GN=GALE PE=2 SV=1	6	1.13	0.92	1.13	10	1.03	1.02	1.14	5	1.17	1.23	1.19	6.66	14.96	2.80
B2RMW6	DnaJ (Hsp40) homolog, subfamily C, member 9 OS=Homo sapiens GN=DNAJC9 PE=2 SV=1	7	0.99	1.15	0.95	8	0.86	0.89	0.88	11	0.96	0.98	0.99	7.34	13.14	5.72
B1AQP2	Prefoldin subunit 2 OS=Homo sapiens GN=PFDN2 PE=2 SV=1	7	0.98	1.02	0.95	4	0.98	0.96	0.95	8	0.95	1.04	0.98	1.38	4.04	1.93
Q9UK76	Hematological and neurological expressed 1 protein OS=Homo sapiens GN=HN1 PE=1 SV=3	11	1.06	1.01	0.96	6	0.93	0.90	1.01	8	1.06	1.09	1.15	7.79	9.74	9.27
Q99598	Translin-associated protein X OS=Homo sapiens GN=TSNAX PE=1 SV=1	7	1.18	1.05	1.19	7	0.99	1.03	0.97	5	1.04	0.96	1.08	9.22	4.30	10.50
Q9UNM1	Chaperonin 10-related protein (Fragment) OS=Homo sapiens GN=EPFP1 PE=2 SV=1	10	0.91	1.00	0.93	8	0.97	0.95	0.91	9	0.96	1.02	1.01	3.46	3.46	5.73
Q5H9R2	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5 OS=Homo sapiens GN=DKFZp781K1356 PE=2 SV=1	7	1.01	1.04	1.08	4	1.09	1.11	1.16	8	1.13	0.90	1.04	5.61	10.59	5.31
Q0VDC6	Peptidyl-prolyl cis-trans isomerase OS=Homo sapiens GN=FKBP1A PE=2 SV=1	9	1.01	1.01	1.04	6	1.09	1.12	1.06	9	1.07	1.00	0.99	4.08	6.26	3.29
G5E9Q6	Profilin OS=Homo sapiens GN=PFN2 PE=2 SV=1	9	1.01	1.15	0.80	13	0.87	1.00	1.02	8	1.00	1.14	0.95	8.21	7.93	12.05
Q9BRF8	Calcineurin-like phosphoesterase domain-containing protein 1 OS=Homo sapiens GN=CPPED1 PE=1 SV=3	8	1.11	0.87	0.86	8	0.98	1.00	0.98	7	0.96	0.87	1.08	8.33	8.50	11.36
Q96CT7	Coiled-coil domain-containing protein 124 OS=Homo sapiens GN=CCDC124 PE=1 SV=1	6	0.85	0.93	0.84	7	0.90	1.03	0.88	5	0.87	0.95	0.79	2.47	5.66	5.39
Q8NBU5	ATPase family AAA domain-containing protein 1 OS=Homo sapiens GN=ATAD1 PE=1 SV=1	6	1.19	0.98	1.10	4	1.08	1.06	1.07	4	1.16	1.06	0.92	4.95	4.65	9.16
P56537	Eukaryotic translation initiation factor 6 OS=Homo sapiens GN=EIF6 PE=1 SV=1	9	0.84	0.89	1.07	13	1.08	1.06	1.05	11	1.06	1.04	1.08	13.46	9.24	1.38
J3KQ73	Peptidyl-prolyl cis-trans isomerase FKBP8 OS=Homo sapiens GN=FKBP8 PE=4 SV=1	6	0.96	1.00	1.29	5	0.84	0.82	0.92	4	0.93	1.31	1.06	6.83	23.51	17.47
Q6FHH6	LANCL1 protein (Fragment) OS=Homo sapiens GN=LANCL1 PE=2 SV=1	6	1.04	1.10	1.01	7	1.10	0.98	0.99	6	1.06	0.98	0.95	2.78	6.99	3.16

O75475	PC4 and SFRS1-interacting protein OS=Homo sapiens GN=PSIP1 PE=1 SV=1	10	0.95	0.91	0.86	11	1.31	1.04	1.12	8	1.08	0.86	0.94	16.17	9.80	13.51
Q53FN1	Cysteine-rich protein 2 variant (Fragment) OS=Homo sapiens PE=2 SV=1	7	1.06	1.05	1.00	4	0.97	0.90	0.98	4	0.87	0.97	0.98	9.49	7.98	1.32
Q96RS6	NudC domain-containing protein 1 OS=Homo sapiens GN=NUDCD1 PE=1 SV=2	11	1.23	0.98	1.13	7	1.18	0.90	0.98	6	1.00	0.91	1.01	10.49	4.54	7.50
Q7Z3D7	Putative uncharacterized protein DKFZp686E2459 OS=Homo sapiens GN=DKFZp686E2459 PE=2 SV=1	6	1.09	1.10	1.07	4	1.03	0.95	0.94	3	0.84	0.96	1.00	13.17	8.17	6.61
H0YAK1	G-rich sequence factor 1 (Fragment) OS=Homo sapiens GN=GRSF1 PE=2 SV=1	13	0.89	1.02	0.96	6	1.09	1.10	1.12	3	0.85	0.96	1.02	13.87	6.79	7.66
Q6MZT3	Putative uncharacterized protein DKFZp686C1054 OS=Homo sapiens GN=THUMPD1 PE=2 SV=1	7	1.04	1.10	1.01	4	0.82	0.87	1.09	3	0.91	0.86	0.96	12.22	14.01	6.94
B3KPN7	cDNA FLJ32002 fis, clone NT2RP7009394, highly similar to Exocyst complex component 2 OS=Homo sapiens PE=2 SV=1	7	0.82	1.60	1.09	3	0.85	0.96	0.93	6	0.98	1.06	0.94	9.18	28.61	9.50
Q63HN8	E3 ubiquitin-protein ligase RNF213 OS=Homo sapiens GN=RNF213 PE=1 SV=3	10	1.12	1.03	0.99	11	0.86	1.14	0.97	8	0.99	1.01	1.08	13.36	6.21	5.57
Q70J99	Protein unc-13 homolog D OS=Homo sapiens GN=UNC13D PE=1 SV=1	10	0.92	0.89	0.84	11	1.04	1.03	0.91	7	0.85	0.97	0.84	10.19	6.93	4.75
P62263	40S ribosomal protein S14 OS=Homo sapiens GN=RPS14 PE=1 SV=3	7	0.92	1.00	0.96	7	1.00	1.03	1.00	8	0.93	0.81	1.01	4.58	12.71	2.44
O15294	UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit OS=Homo sapiens GN=OGT PE=1 SV=3	6	0.87	1.03	0.80	6	0.95	0.92	0.97	8	0.77	0.91	0.86	10.39	7.03	10.22
Q8NBL9	cDNA PSEC0119 fis, clone PLACE1002376, highly similar to GPI transamidase component PIG-S OS=Homo sapiens PE=2 SV=1	6	1.00	1.31	1.14	6	0.94	0.80	0.86	6	0.99	1.13	1.04	3.24	23.97	14.23
Q15738	Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating OS=Homo sapiens GN=NSDHL PE=1 SV=2	9	1.10	1.04	1.03	7	0.94	0.93	0.97	7	1.23	1.06	1.23	13.48	6.88	12.63
J3KPP4	Cisplatin resistance-associated overexpressed protein, isoform CRA_b OS=Homo sapiens GN=LUC7L3 PE=4 SV=1	6	1.10	1.13	1.08	7	1.01	1.05	1.06	7	0.87	1.02	0.92	11.65	5.20	8.35
P11182	Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial OS=Homo sapiens GN=DBT PE=1 SV=3	7	1.03	0.99	0.92	5	1.05	1.10	1.06	3	1.07	1.11	1.10	1.73	6.31	9.18
Q9NYK5	39S ribosomal protein L39, mitochondrial OS=Homo sapiens GN=MRPL39 PE=1 SV=3	6	0.90	1.00	0.99	7	0.95	1.00	0.98	8	0.97	0.98	0.97	3.78	1.08	1.09
I6L9E8	Family with sequence similarity 98, member A OS=Homo sapiens GN=FAM98A PE=2 SV=1	11	0.72	1.09	0.85	4	0.93	1.16	0.96	4	0.79	0.80	0.85	13.18	18.86	7.20
Q15274	Nicotinate-nucleotide pyrophosphorylase [carboxylating] OS=Homo sapiens GN=QPRT PE=1 SV=3	6	1.01	1.10	1.17	5	0.87	1.06	0.89	5	0.80	0.92	0.88	11.99	9.27	16.98
Q6IAX1	FDFT1 protein OS=Homo sapiens GN=FDFT1 PE=2 SV=1	6	1.00	1.13	1.32	2	0.83	0.84	1.03	3	0.77	0.92	0.88	14.06	15.28	20.47
O15069	NAC-alpha domain-containing protein 1 OS=Homo sapiens GN=NACAD PE=1 SV=3	7	1.12	1.13	1.09	6	0.80	0.95	0.95	3	0.97	1.07	0.97	16.47	8.66	7.55

Q8N2K0	Monoacylglycerol lipase ABHD12 OS=Homo sapiens GN=ABHD12 PE=1 SV=2	7	1.25	1.16	1.30	3	1.03	0.81	0.89	4	1.23	1.05	1.10	10.48	17.89	18.73
F5GZ28	DNA ligase OS=Homo sapiens GN=LIG1 PE=2 SV=1	6	0.93	1.07	0.91	4	0.79	1.08	0.73	4	0.88	1.07	0.92	8.12	0.74	12.97
Q9NX46	Poly(ADP-ribose) glycohydrolase ARH3 OS=Homo sapiens GN=ADPRHL2 PE=1 SV=1	6	1.03	0.80	1.11	6	0.93	0.89	1.04	4	1.00	0.96	1.12	5.15	9.19	4.26
Q7KZ85	Transcription elongation factor SPT6 OS=Homo sapiens GN=SUPT6H PE=1 SV=2	7	0.94	0.98	0.99	7	0.82	0.96	0.93	6	0.87	1.01	0.98	6.71	2.70	3.07
Q15334	Lethal(2) giant larvae protein homolog 1 OS=Homo sapiens GN=LLGL1 PE=1 SV=3	6	0.87	1.16	1.08	4	1.22	1.14	1.03	4	1.21	1.43	1.51	17.87	13.05	22.13
C4B4C6	Antiapoptotic protein FEAT OS=Homo sapiens GN=feat PE=2 SV=1	7	1.37	1.07	1.14	8	0.76	0.69	0.80	6	0.84	0.85	0.88	33.65	21.95	19.02
Q8NC56	LEM domain-containing protein 2 OS=Homo sapiens GN=LEMD2 PE=1 SV=1	6	0.96	0.86	1.05	6	1.18	0.98	1.10	8	1.05	0.97	1.06	10.44	6.84	2.43
B4DR61	Protein transport protein Sec61 subunit alpha isoform 1 OS=Homo sapiens GN=SEC61A1 PE=2 SV=1	14	1.75	0.86	1.02	7	2.04	1.04	1.62	6	1.71	0.82	1.36	9.76	13.01	22.62
Q9H9J2	39S ribosomal protein L44, mitochondrial OS=Homo sapiens GN=MRPL44 PE=1 SV=1	7	1.00	0.99	1.06	8	1.14	1.14	1.08	5	0.90	1.02	0.96	11.81	7.26	6.16
Q16543	Hsp90 co-chaperone Cdc37 OS=Homo sapiens GN=CDC37 PE=1 SV=1	7	0.85	1.01	0.92	7	0.88	0.96	0.97	9	0.94	0.98	0.99	5.24	2.48	3.62
B4DG51	cDNA FLJ61110, highly similar to Hippocalcin-like protein 4 OS=Homo sapiens PE=2 SV=1	9	1.03	0.98	0.93	3	0.73	0.87	0.94	4	0.97	1.03	1.00	17.25	8.48	4.01
E5KS95	Elongation factor Ts, mitochondrial OS=Homo sapiens GN=TSFM PE=2 SV=1	7	0.87	0.80	0.86	11	0.95	0.95	0.93	2	1.17	0.95	1.10	15.53	9.34	13.04
Q9UK43	Chondrosarcoma-associated protein 2 OS=Homo sapiens GN=CSA2 PE=2 SV=1	6	0.99	0.96	0.84	5	0.94	1.06	0.95	5	1.03	1.12	1.02	4.55	7.51	9.75
Q96I99	Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial OS=Homo sapiens GN=SUCLG2 PE=1 SV=2	7	0.69	1.01	0.74	4	0.98	0.96	1.07	3	0.99	0.88	1.01	18.90	6.77	19.12
Q15059	Bromodomain-containing protein 3 OS=Homo sapiens GN=BRD3 PE=1 SV=1	7	1.16	0.88	0.99	7	1.38	1.19	1.33	2	0.84	0.66	0.86	24.22	29.27	22.88
Q14320	Protein FAM50A OS=Homo sapiens GN=FAM50A PE=1 SV=2	6	1.00	0.98	0.93	3	1.14	1.15	1.07	4	0.99	1.01	0.99	7.73	8.77	6.66
B7ZM99	MTHFD1L protein OS=Homo sapiens GN=MTHFD1L PE=2 SV=1	8	1.06	0.95	1.14	5	0.85	0.88	0.91	6	0.95	0.97	1.02	11.02	4.99	11.32
Q27J81	Inverted formin-2 OS=Homo sapiens GN=INF2 PE=1 SV=2	7	0.73	0.67	1.21	4	0.79	0.67	0.77	3	1.36	1.08	1.07	36.00	29.30	22.01
A4D177	Chromobox homolog 3 (HP1 gamma homolog, Drosophila) OS=Homo sapiens GN=CBX3 PE=2 SV=1	9	0.89	0.97	0.94	8	1.05	1.03	1.01	12	0.95	0.97	0.95	8.45	3.70	3.72
J3KMW7	E3 ubiquitin-protein ligase UBR5 OS=Homo sapiens GN=UBR5 PE=4 SV=1	7	1.01	1.05	1.06	7	0.74	0.98	0.72	4	0.94	1.08	1.07	15.86	4.87	21.13
G3V5T9	Cyclin-dependent kinase 2 OS=Homo sapiens GN=CDK2 PE=2 SV=1	6	0.95	1.03	0.85	4	0.94	1.20	1.01	4	0.94	1.00	0.94	1.10	9.98	8.43
Q9H3U1	Protein unc-45 homolog A OS=Homo sapiens GN=UNC45A PE=1 SV=1	7	1.36	1.17	1.12	5	0.96	1.05	0.92	4	0.82	1.03	0.73	26.80	6.60	21.06
O75396	Vesicle-trafficking protein SEC22b OS=Homo sapiens GN=SEC22B PE=1 SV=4	6	1.08	0.92	1.18	10	0.98	0.93	0.95	8	1.00	1.01	1.02	5.17	4.96	11.00

Q53H29	Nucleoporin 54kDa variant (Fragment) OS=Homo sapiens PE=2 SV=1	6	0.94	1.10	0.84	4	1.22	1.21	1.03	7	0.96	0.79	0.95	15.12	21.28	9.79
F5H442	Tumor susceptibility gene 101 protein OS=Homo sapiens GN=TSG101 PE=2 SV=1	6	1.10	0.91	0.87	4	1.05	1.16	1.01	7	1.03	0.98	1.10	3.70	12.93	11.35
Q6FHQ0	RBBP7 protein (Fragment) OS=Homo sapiens GN=RBBP7 PE=2 SV=1	16	0.81	0.97	0.85	19	0.92	1.05	0.92	14	0.87	1.09	1.00	6.14	5.98	8.03
Q71UA4	Adenylosuccinate lyase OS=Homo sapiens PE=4 SV=1	12	1.12	1.12	1.07	5	1.02	0.83	0.88	4	1.06	1.10	1.31	4.83	15.84	19.70
P54652	Heat shock-related 70 kDa protein 2 OS=Homo sapiens GN=HSPA2 PE=1 SV=1	42	0.92	0.98	1.00	37	1.00	1.21	0.98	32	1.04	1.26	1.12	6.09	12.98	7.53
Q9BY32	Inosine triphosphate pyrophosphatase OS=Homo sapiens GN=ITPA PE=1 SV=2	8	0.91	1.08	0.89	6	0.98	1.09	0.98	8	0.91	0.98	0.93	4.20	6.13	5.10
H0UI80	Negative elongation factor C/D OS=Homo sapiens GN=TH1L PE=2 SV=1	8	1.15	0.99	0.76	2	1.00	0.96	0.69	5	0.86	1.03	0.99	14.39	3.76	19.11
H9ZYJ2	Thioredoxin OS=Homo sapiens GN=TXN PE=2 SV=1	9	1.00	1.11	0.98	8	1.15	1.19	1.08	7	1.05	1.02	0.96	7.43	7.67	6.34
B4DRS4	cDNA FLJ60139, highly similar to Homo sapiens HIV TAT specific factor 1 (HTATSF1), mRNA OS=Homo sapiens PE=2 SV=1	10	0.76	0.85	0.89	6	0.90	0.96	0.93	6	1.01	1.00	0.86	13.78	8.09	4.19
Q16822	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=Homo sapiens GN=PCK2 PE=1 SV=3	6	1.31	0.97	1.23	12	0.95	0.98	0.99	8	1.05	1.06	1.06	16.54	4.56	11.36
Q9H2W6	39S ribosomal protein L46, mitochondrial OS=Homo sapiens GN=MRPL46 PE=1 SV=1	8	1.22	1.02	0.93	3	1.11	1.01	1.02	6	1.06	1.01	0.92	7.10	0.83	5.86
Q6FI51	DNAJB1 protein OS=Homo sapiens GN=DNAJB1 PE=2 SV=1	9	1.05	1.12	0.92	9	1.03	1.13	1.04	7	0.97	1.05	0.94	3.96	4.39	6.77
K7ENL3	Signal transducer and activator of transcription 3 OS=Homo sapiens GN=STAT3 PE=4 SV=1	7	0.83	0.97	0.82	6	0.76	0.93	0.81	8	1.08	1.13	0.90	18.42	10.51	6.31
B7ZMF2	Fanconi anemia, complementation group I OS=Homo sapiens GN=FANCI PE=2 SV=1	6	0.91	1.15	1.17	4	0.79	0.80	0.73	7	0.68	0.79	0.75	14.48	22.30	28.16
B4DYB4	Nucleoporin NUP53 OS=Homo sapiens GN=NUP35 PE=2 SV=1	6	1.05	0.93	1.02	3	1.16	0.94	0.90	4	0.90	0.93	0.69	12.82	0.25	18.88
Q9UFC0	Leucine-rich repeat and WD repeat-containing protein 1 OS=Homo sapiens GN=LRWD1 PE=1 SV=2	7	1.20	1.05	0.89	4	1.01	1.24	0.89	4	0.97	0.88	0.89	11.53	17.24	0.17
B2R7W3	Breast carcinoma amplified sequence 2 OS=Homo sapiens GN=BCAS2 PE=2 SV=1	10	0.95	0.92	0.97	6	1.22	1.07	1.13	7	1.10	0.92	1.06	12.43	8.76	7.61
I6L894	Ankyrin-2 OS=Homo sapiens GN=ANK2 PE=4 SV=1	7	0.90	0.98	1.03	3	0.96	0.82	1.07	5	0.81	1.03	1.34	8.49	11.51	15.04
Q9BT09	Protein canopy homolog 3 OS=Homo sapiens GN=CNPY3 PE=1 SV=1	7	1.16	0.96	1.12	5	1.34	1.03	1.12	5	1.12	0.96	1.20	9.89	4.32	4.02
A8K3M9	cDNA FLJ76387, highly similar to Homo sapiens splicing factor, arginine/serine-rich 9 (SFRS9), mRNA OS=Homo sapiens PE=2 SV=1	6	0.91	0.99	0.90	5	1.13	1.02	1.04	5	1.01	1.06	1.00	10.53	3.70	7.38
Q59G98	TIA1 protein variant (Fragment) OS=Homo sapiens PE=2 SV=1	6	1.19	0.95	0.72	7	0.81	0.80	0.87	3	0.97	0.82	0.93	18.94	9.77	12.79
Q9UBQ0	Vacuolar protein sorting-associated protein 29 OS=Homo sapiens GN=VPS29 PE=1 SV=1	6	0.94	0.99	0.90	7	1.06	1.17	1.09	6	1.14	1.03	1.14	9.74	8.96	12.31

P14324	Farnesyl pyrophosphate synthase OS=Homo sapiens GN=FDPS PE=1 SV=4	9	1.05	1.23	0.98	5	0.89	1.00	0.91	2	1.00	1.10	1.01	8.41	10.69	5.08
O95470	Sphingosine-1-phosphate lyase 1 OS=Homo sapiens GN=SGPL1 PE=1 SV=3	6	1.04	1.14	1.05	7	0.96	1.08	1.00	6	0.86	0.94	1.00	9.39	9.65	2.86
Q96F88	Processing of 1, ribonuclease P/MRP subunit (S. cerevisiae) OS=Homo sapiens GN=POP1 PE=2 SV=1	7	0.83	0.88	0.92	7	1.05	1.16	1.15	4	1.07	0.93	1.00	13.85	15.10	11.54
B7ZC38	Endophilin-B2 OS=Homo sapiens GN=SH3GLB2 PE=2 SV=1	6	0.92	0.96	1.20	6	1.07	1.04	1.11	6	1.00	1.01	1.01	7.38	3.99	8.43
Q53HM8	Annexin (Fragment) OS=Homo sapiens PE=2 SV=1	6	1.28	1.10	1.24	8	1.15	0.77	0.99	7	1.00	1.03	1.14	12.50	18.39	10.84
Q13617	Cullin-2 OS=Homo sapiens GN=CUL2 PE=1 SV=2	6	0.93	0.92	1.10	8	0.99	0.98	1.02	8	1.04	1.12	0.99	5.38	9.80	5.55
Q9BTE3	Mini-chromosome maintenance complex-binding protein OS=Homo sapiens GN=MCMBP PE=1 SV=2	6	0.94	1.19	1.01	4	0.82	1.06	0.94	3	1.07	0.94	0.92	13.09	12.10	5.21
Q9H3N1	Thioredoxin-related transmembrane protein 1 OS=Homo sapiens GN=TMX1 PE=1 SV=1	7	1.11	0.94	0.94	4	1.50	1.22	1.30	4	1.45	0.96	1.24	15.70	14.76	16.41
Q5SY16	Polynucleotide 5'-hydroxyl-kinase NOL9 OS=Homo sapiens GN=NOL9 PE=1 SV=1	7	0.73	0.85	0.84	5	0.80	0.92	0.87	6	1.06	1.01	1.01	20.18	8.75	10.25
P82663	28S ribosomal protein S25, mitochondrial OS=Homo sapiens GN=MRPS25 PE=1 SV=1	6	1.10	1.17	1.11	5	0.92	1.06	0.97	5	0.95	0.98	1.08	10.02	8.99	6.67
Q53XJ5	Peptidyl-prolyl cis-trans isomerase OS=Homo sapiens GN=FKBP2 PE=2 SV=1	6	1.39	0.90	1.15	9	1.44	0.97	1.29	15	1.37	1.04	1.27	2.58	7.50	6.39
Q6ICJ4	Em:AP000351.3 protein OS=Homo sapiens GN=Em:AP000351.3 PE=2 SV=1	5	0.94	1.04	0.90	5	0.90	1.06	0.88	2	1.11	1.08	1.07	11.16	1.87	10.77
J3QS36	L-xylulose reductase (Fragment) OS=Homo sapiens GN=DCXR PE=3 SV=1	6	1.04	1.03	1.13	4	1.04	0.76	0.91	3	0.98	1.07	0.91	3.37	17.31	13.07
B7Z5L4	cDNA FLJ61340, highly similar to Homo sapiens seizure related 6 homolog-like 2 (SEZ6L2), transcript variant 2, mRNA OS=Homo sapiens PE=2 SV=1	8	1.62	0.87	1.29	2	1.72	1.11	1.64	2	1.76	0.93	1.78	4.37	12.66	16.13
Q8NFH4	Nucleoporin Nup37 OS=Homo sapiens GN=NUP37 PE=1 SV=1	6	0.95	1.07	0.85	4	0.71	1.02	0.80	4	0.91	0.97	0.97	14.76	4.69	9.96
E9PHA2	Condensin complex subunit 2 OS=Homo sapiens GN=NCAPH PE=2 SV=1	7	0.90	0.88	1.00	8	0.87	0.85	0.83	7	0.99	1.21	1.04	6.81	20.16	11.26
J3KNQ4	Alpha-parvin OS=Homo sapiens GN=PARVA PE=4 SV=1	6	0.82	0.97	0.98	3	1.19	1.07	1.06	5	0.99	1.09	1.27	18.76	6.04	13.41
P36551	Coproporphyrinogen-III oxidase, mitochondrial OS=Homo sapiens GN=CPOX PE=1 SV=3	6	0.98	0.98	1.01	4	1.18	1.12	1.01	4	0.85	1.01	0.90	16.77	7.41	6.42
Q14558	Phosphoribosyl pyrophosphate synthase-associated protein 1 OS=Homo sapiens GN=PRPSAP1 PE=1 SV=2	8	0.92	1.21	0.99	9	0.82	0.89	0.88	11	1.04	0.97	1.03	11.98	16.03	7.80
P62851	40S ribosomal protein S25 OS=Homo sapiens GN=RPS25 PE=1 SV=1	8	1.00	1.08	0.96	7	1.32	1.17	1.21	8	1.08	0.84	1.16	14.80	16.81	11.72
P30626	Sorcin OS=Homo sapiens GN=SRI PE=1 SV=1	12	1.18	1.03	1.16	8	1.08	1.06	1.06	8	1.02	1.04	0.98	7.69	1.60	8.21
P19784	Casein kinase II subunit alpha' OS=Homo sapiens GN=CSNK2A2 PE=1 SV=1	7	1.06	1.03	0.90	10	0.94	0.95	0.96	9	1.01	1.08	1.02	6.16	6.30	6.00

B4DEH0	Mitochondrial ribosomal protein L10, isoform CRA_d OS=Homo sapiens GN=MRPL10 PE=2 SV=1	9	0.81	0.93	1.14	3	0.81	0.89	0.99	3	0.87	1.11	1.02	4.48	11.93	7.80
D3DSQ1	N-acylsphingosine amidohydrolase (Acid ceramidase) 1, isoform CRA_c OS=Homo sapiens GN=ASAH1 PE=4 SV=1	5	1.04	0.90	1.08	9	1.15	1.00	1.13	6	1.11	0.85	0.85	4.63	8.39	14.76
A2RRP1	Neuroblastoma-amplified sequence OS=Homo sapiens GN=NBAS PE=1 SV=2	6	0.92	0.93	0.91	4	1.02	1.00	0.92	3	1.02	1.04	1.04	5.72	5.76	7.67
P15927-3	Isoform 3 of Replication protein A 32 kDa subunit OS=Homo sapiens GN=RPA2	7	0.97	1.13	0.94	12	0.94	1.00	0.89	9	0.88	0.95	0.85	4.91	9.36	4.92
Q05DA4	P4HA2 protein OS=Homo sapiens GN=P4HA2 PE=2 SV=1	6	1.29	1.19	1.18	6	1.05	1.06	1.17	5	1.08	1.12	1.23	11.09	5.72	2.71
Q05DF2	SF3A2 protein (Fragment) OS=Homo sapiens GN=SF3A2 PE=2 SV=1	8	0.99	1.04	0.90	8	1.01	1.07	0.98	5	0.82	0.85	0.79	10.95	12.16	11.01
Q4TT34	Nucleoside diphosphate kinase, mitochondrial OS=Homo sapiens GN=NME4 PE=2 SV=1	7	0.89	1.04	0.93	5	0.98	1.10	1.06	4	1.00	1.00	1.08	6.44	5.01	7.81
P47985	Cytochrome b-c1 complex subunit Rieske, mitochondrial OS=Homo sapiens GN=UQCRFS1 PE=1 SV=2	7	1.29	1.02	1.18	5	1.16	0.98	1.16	4	1.20	1.06	1.07	5.14	4.00	5.20
A8K5J1	Uridine monophosphate synthetase (Orotate phosphoribosyl transferase and orotidine-5'-decarboxylase), isoform CRA_b OS=Homo sapiens GN=UMPS PE=2 SV=1	6	1.07	1.20	0.97	11	0.79	0.99	0.90	6	0.97	1.06	1.08	15.19	10.22	8.89
Q5T6V5	UPF0553 protein C9orf64 OS=Homo sapiens GN=C9orf64 PE=1 SV=1	7	1.12	1.10	1.20	5	0.96	1.06	1.01	6	1.03	1.17	0.97	7.88	5.37	11.61
B7Z382	Cytosolic purine 5'-nucleotidase OS=Homo sapiens GN=NT5C2 PE=2 SV=1	7	0.93	0.97	0.85	4	1.23	1.27	1.15	4	1.02	0.95	1.15	14.55	16.35	16.47
Q59H65	Aldehyde dehydrogenase (Fragment) OS=Homo sapiens PE=2 SV=1	6	1.19	1.01	1.05	6	0.93	0.96	0.93	7	1.02	1.23	0.98	12.46	13.70	5.88
Q9UFN0	Protein NipSnap homolog 3A OS=Homo sapiens GN=NIPSNAP3A PE=1 SV=2	6	1.19	1.08	1.13	6	1.20	0.97	1.15	5	0.89	1.01	0.99	16.35	5.40	8.13
Q9UQD4	SH3-containing Grb-2-like 1 protein OS=Homo sapiens PE=4 SV=1	6	1.19	0.90	1.27	3	1.00	1.00	0.95	4	0.89	1.05	0.83	14.83	7.56	22.28
Q548N1	Vacuolar protein sorting 28 (Yeast), isoform CRA_a OS=Homo sapiens GN=VPS28 PE=2 SV=1	7	0.76	1.03	0.93	4	1.00	0.95	0.91	4	0.93	1.01	1.08	13.57	4.25	9.24
Q86WA6	Valacyclovir hydrolase OS=Homo sapiens GN=BPHL PE=1 SV=1	6	1.00	0.95	0.75	5	1.00	0.97	0.91	5	0.97	0.99	1.08	1.56	2.30	18.23
K7ELC2	40S ribosomal protein S15 OS=Homo sapiens GN=RPS15 PE=3 SV=1	23	1.03	1.01	0.81	14	1.24	1.34	1.25	9	0.97	0.78	1.08	13.13	26.93	21.22
Q9NUQ9	Protein FAM49B OS=Homo sapiens GN=FAM49B PE=1 SV=1	7	0.93	0.82	0.99	9	0.96	0.98	1.04	6	1.20	1.42	1.10	14.46	28.91	5.13
Q6PJ77	BTF3L4 protein (Fragment) OS=Homo sapiens GN=BTF3L4 PE=2 SV=1	11	1.03	0.92	0.94	4	1.12	0.90	1.20	5	1.25	0.70	0.71	9.76	14.49	25.89
Q5T8U7	Surfeit 4 OS=Homo sapiens GN=SURF4 PE=2 SV=1	8	1.57	1.03	1.57	6	1.26	0.86	1.20	7	1.43	1.05	1.28	10.61	11.13	14.25
Q6IBK5	GTF2F1 protein OS=Homo sapiens GN=GTF2F1 PE=2 SV=1	7	0.92	1.03	0.96	4	0.92	0.99	0.94	4	0.90	1.07	0.89	1.51	4.20	4.26
F5H721	WW domain-binding protein 11 OS=Homo sapiens GN=WBP11 PE=2 SV=1	5	0.83	0.87	0.88	5	0.96	1.09	0.97	5	1.21	0.99	0.92	19.03	11.03	4.78
P62854	40S ribosomal protein S26 OS=Homo sapiens GN=RPS26 PE=1 SV=3	8	0.90	0.94	0.89	5	0.94	1.03	1.01	7	0.93	0.93	0.92	2.23	5.78	6.42

Q9NX40	OCIA domain-containing protein 1 OS=Homo sapiens GN=OCIAD1 PE=1 SV=1	9	1.36	1.10	1.06	8	1.23	0.92	1.14	9	1.17	0.95	1.09	7.62	10.09	3.66
Q8N516	Inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase complex-associated protein OS=Homo sapiens GN=IKBKAP PE=2 SV=1	6	1.12	1.02	0.99	6	1.08	0.94	1.04	3	0.92	0.88	0.90	10.05	7.40	7.47
D3DSW3	Proline synthetase co-transcribed homolog (Bacterial), isoform CRA_b OS=Homo sapiens GN=PROSC PE=2 SV=1	5	1.04	1.05	0.94	5	1.11	1.12	1.14	4	1.00	1.03	1.00	5.41	4.30	10.06
P36405	ADP-ribosylation factor-like protein 3 OS=Homo sapiens GN=ARL3 PE=1 SV=2	7	1.07	1.04	1.13	13	0.92	0.90	0.92	8	1.01	1.01	0.95	7.63	7.77	10.99
Q53GF8	Isocitrate dehydrogenase 3 (NAD+) alpha variant (Fragment) OS=Homo sapiens PE=2 SV=1	6	0.97	0.91	0.92	5	0.98	0.94	1.02	5	1.15	0.97	1.11	10.06	3.02	9.24
Q6P1J9	Parafibromin OS=Homo sapiens GN=CDC73 PE=1 SV=1	7	1.19	1.09	1.11	4	0.88	0.88	0.97	7	0.81	0.83	0.90	21.11	14.71	10.68
Q13363	C-terminal-binding protein 1 OS=Homo sapiens GN=CTBP1 PE=1 SV=2	7	1.09	1.11	0.99	7	1.05	1.12	0.97	4	1.12	1.21	1.05	2.82	4.78	4.15
Q53F20	Acidic (Leucine-rich) nuclear phosphoprotein 32 family, member E variant (Fragment) OS=Homo sapiens PE=2 SV=1	8	0.87	1.06	0.90	9	1.01	1.12	0.99	9	0.94	1.02	0.91	7.26	4.62	5.09
O95881	Thioredoxin domain-containing protein 12 OS=Homo sapiens GN=TXNDC12 PE=1 SV=1	12	1.29	1.02	1.18	9	1.42	1.13	1.25	6	1.15	0.94	0.97	10.64	9.51	12.88
A8MXV4	Nucleoside diphosphate-linked moiety X motif 19, mitochondrial OS=Homo sapiens GN=NUDT19 PE=1 SV=1	6	0.81	0.98	1.01	6	1.03	1.08	1.09	6	0.82	1.06	0.94	14.52	4.92	7.18
Q8TD19	Serine/threonine-protein kinase Nek9 OS=Homo sapiens GN=NEK9 PE=1 SV=2	6	1.57	0.94	0.95	4	1.19	1.07	1.16	4	1.55	1.18	1.39	14.79	11.67	19.01
Q96A35	39S ribosomal protein L24, mitochondrial OS=Homo sapiens GN=MRPL24 PE=1 SV=1	7	0.92	0.99	0.95	4	1.05	1.32	1.26	2	1.16	0.95	1.17	11.40	18.98	13.98
Q9H444	Charged multivesicular body protein 4b OS=Homo sapiens GN=CHMP4B PE=1 SV=1	6	1.07	0.96	0.78	5	1.15	1.13	1.23	4	1.01	0.94	0.96	6.46	9.95	22.70
Q5SZE1	Ceramide synthase 2 (Fragment) OS=Homo sapiens GN=CERS2 PE=2 SV=1	11	1.16	1.01	1.68	2	1.23	1.08	1.20	5	1.10	0.99	1.10	5.57	4.80	23.16
B4DXH2	cDNA FLJ51138, highly similar to Arfaptin-2 OS=Homo sapiens PE=2 SV=1	5	1.00	0.96	1.19	4	1.12	1.04	0.95	4	1.24	1.05	1.07	10.51	5.20	11.40
Q10471	Polypeptide N-acetylgalactosaminyltransferase 2 OS=Homo sapiens GN=GALNT2 PE=1 SV=1	6	1.03	0.97	1.09	4	1.09	0.92	1.19	6	1.09	1.02	1.09	3.37	5.10	4.98
Q07666	KH domain-containing, RNA-binding, signal transduction-associated protein 1 OS=Homo sapiens GN=KHDRBS1 PE=1 SV=1	9	0.76	0.94	0.77	10	0.97	1.11	1.00	11	0.83	0.84	0.95	12.95	13.98	13.54
Q9BWH6-2	Isoform 2 of RNA polymerase II-associated protein 1 OS=Homo sapiens GN=RPAP1	5	0.87	0.94	1.68	4	0.80	0.96	0.90	5	1.02	1.39	1.04	12.30	23.00	34.28
O43237	Cytoplasmic dynein 1 light intermediate chain 2 OS=Homo sapiens GN=DYNC1LI2 PE=1 SV=1	10	1.02	1.07	1.15	7	0.96	0.90	0.92	3	1.04	0.92	1.13	4.16	9.64	12.13
O15031	Plexin-B2 OS=Homo sapiens GN=PLXNB2 PE=1 SV=3	5	1.05	1.04	1.06	6	0.94	1.13	1.10	9	1.06	0.87	0.92	6.41	13.22	9.44

E7ESY4	Metastasis-associated protein MTA1 OS=Homo sapiens GN=MTA1 PE=2 SV=1	5	0.89	1.05	0.84	6	0.75	0.99	0.85	8	0.81	0.82	0.85	8.88	12.62	0.89
Q96C90	Protein phosphatase 1 regulatory subunit 14B OS=Homo sapiens GN=PPP1R14B PE=1 SV=3	7	0.97	0.99	0.85	4	1.04	1.08	1.03	4	0.92	0.87	0.94	6.39	10.78	9.21
Q69YP1	Putative uncharacterized protein DKFZp762M013 (Fragment) OS=Homo sapiens GN=DKFZp762M013 PE=2 SV=1	5	0.82	0.96	0.97	6	0.88	0.81	0.83	6	0.95	1.05	0.91	7.20	13.09	7.45
Q53G25	Ribosomal protein S5 variant (Fragment) OS=Homo sapiens PE=2 SV=1	13	0.99	0.93	1.04	13	0.96	0.92	0.95	13	1.04	1.03	1.04	4.37	6.40	5.34
Q3B874	STRN protein (Fragment) OS=Homo sapiens GN=STRN PE=2 SV=1	5	0.94	1.01	0.98	3	0.95	1.00	0.87	2	0.92	0.89	1.22	1.70	7.35	17.37
P30050	60S ribosomal protein L12 OS=Homo sapiens GN=RPL12 PE=1 SV=1	11	0.99	0.96	1.03	11	0.99	0.97	1.01	10	0.94	0.96	0.95	2.77	0.51	4.27
P20020	Plasma membrane calcium-transporting ATPase 1 OS=Homo sapiens GN=ATP2B1 PE=1 SV=3	5	1.11	1.20	1.07	4	0.86	1.05	1.03	5	1.15	0.93	1.16	14.80	12.74	6.13
Q9BVJ6	U3 small nucleolar RNA-associated protein 14 homolog A OS=Homo sapiens GN=UTP14A PE=1 SV=1	5	0.90	1.01	0.89	4	1.02	1.09	1.07	8	0.95	1.05	1.06	6.24	3.74	10.06
Q2UVF2	Kinesin-like protein KIF3Abeta OS=Homo sapiens GN=KIF3A PE=2 SV=1	5	1.04	0.76	0.87	5	1.23	1.24	1.17	6	0.99	0.76	0.82	11.70	29.88	19.65
E9PAV3	Nascent polypeptide-associated complex subunit alpha OS=Homo sapiens GN=NACA PE=2 SV=1	6	0.88	1.02	0.93	11	0.90	1.04	0.94	10	0.87	0.93	0.92	1.72	5.70	1.31
Q9H993	UPF0364 protein C6orf211 OS=Homo sapiens GN=C6orf211 PE=1 SV=1	8	1.10	1.22	1.28	6	1.14	1.08	1.02	5	0.88	0.81	1.00	13.77	20.06	13.99
B2R8K8	cDNA, FLJ93949, highly similar to Homo sapiens NIMA (never in mitosis gene a)-related kinase 7 (NEK7), mRNA OS=Homo sapiens PE=2 SV=1	6	1.25	0.98	0.94	4	0.97	0.93	1.20	5	1.04	0.93	1.00	13.64	3.11	12.82
B4DZ55	cDNA FLJ52097, weakly similar to Homo sapiens transmembrane and tetratricopeptide repeat containing 1 (TMTC1), mRNA OS=Homo sapiens PE=2 SV=1	7	0.93	0.83	0.96	5	0.92	0.91	0.94	4	1.12	1.16	1.12	11.39	17.75	10.11
O14813	Paired mesoderm homeobox protein 2A OS=Homo sapiens GN=PHOX2A PE=1 SV=2	5	0.79	1.03	0.82	4	0.89	1.11	0.84	4	0.83	0.94	0.91	5.95	8.31	5.38
Q7Z2Z2	Elongation factor Tu GTP-binding domain-containing protein 1 OS=Homo sapiens GN=EFTUD1 PE=1 SV=2	5	1.27	1.34	1.32	9	1.14	1.12	1.17	3	1.09	1.23	1.20	8.01	8.93	6.83
Q6LES8	TFAM protein (Fragment) OS=Homo sapiens GN=TFAM PE=2 SV=1	5	1.00	1.01	0.87	3	1.02	0.98	0.88	3	1.02	0.98	0.94	1.22	1.89	4.11
Q658J0	Putative uncharacterized protein DKFZp762L015 (Fragment) OS=Homo sapiens GN=DKFZp762L015 PE=2 SV=1	6	1.02	0.99	0.99	6	0.93	0.98	0.96	4	1.11	1.08	0.98	9.25	5.47	1.49
Q99471	Prefoldin subunit 5 OS=Homo sapiens GN=PFDN5 PE=1 SV=2	7	0.88	0.99	0.86	7	1.08	1.13	1.03	7	1.01	0.95	0.98	10.35	9.37	9.04
Q9Y3D9	28S ribosomal protein S23, mitochondrial OS=Homo sapiens GN=MRPS23 PE=1 SV=2	5	0.96	0.92	1.03	6	0.92	0.87	0.92	5	0.94	0.98	0.97	1.85	6.08	6.09
P52566	Rho GDP-dissociation inhibitor 2 OS=Homo sapiens GN=ARHGDIB PE=1 SV=3	9	1.19	0.91	1.31	8	0.91	0.88	1.05	5	0.91	0.90	1.17	16.24	2.09	11.38
Q8IWP6	Class IVb beta tubulin OS=Homo sapiens PE=2 SV=1	237	0.93	0.93	1.01	193	0.90	1.05	0.91	196	0.91	0.86	0.87	1.94	10.32	7.90

O94805	Actin-like protein 6B OS=Homo sapiens GN=ACTL6B PE=1 SV=1	6	0.93	1.09	0.99	7	0.96	1.01	0.95	6	0.81	0.86	0.86	8.88	11.65	6.70
Q6NUL6	PITPNA protein (Fragment) OS=Homo sapiens GN=PITPNA PE=2 SV=1	6	0.93	0.98	1.08	7	0.95	1.09	1.03	6	0.84	1.14	0.83	6.01	7.53	13.46
Q59EV6	Carrier family 6, member 8 variant (Fragment) OS=Homo sapiens GN=PPGB PE=2 SV=1	5	1.03	1.06	0.90	5	1.36	1.13	1.20	4	1.06	1.01	1.10	15.96	5.68	14.58
Q0QEW2	60S ribosomal protein L18 (Fragment) OS=Homo sapiens GN=RPL18 PE=2 SV=1	7	0.95	0.98	1.06	8	0.89	0.90	0.91	7	0.91	1.08	1.00	3.30	9.43	7.18
P00441	Superoxide dismutase [Cu-Zn] OS=Homo sapiens GN=SOD1 PE=1 SV=2	25	0.93	1.01	1.06	14	1.02	1.01	0.97	14	1.02	0.98	1.02	5.11	1.55	4.73
P30085	UMP-CMP kinase OS=Homo sapiens GN=CMPK1 PE=1 SV=3	7	1.10	1.12	0.98	6	1.04	1.16	1.09	4	0.95	0.86	0.96	7.07	15.74	7.05
Q59ET0	Glucan , branching enzyme 1 variant (Fragment) OS=Homo sapiens PE=2 SV=1	6	0.99	1.00	0.95	4	0.91	1.02	1.00	6	1.15	1.04	1.28	12.23	1.90	16.47
Q9Y6C2	EMILIN-1 OS=Homo sapiens GN=EMILIN1 PE=1 SV=2	6	1.56	1.13	1.05	2	0.80	0.82	0.81	3	1.28	1.10	1.03	32.05	16.62	13.60
H3BNV9	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial OS=Homo sapiens GN=COX4I1 PE=2 SV=1	5	1.33	1.04	1.04	5	1.15	0.91	0.97	5	1.16	1.10	1.13	8.34	9.25	7.46
B2R7I0	cDNA, FLJ93451, highly similar to Homo sapiens thioredoxin domain containing 14 (TXNDC14), mRNA OS=Homo sapiens PE=2 SV=1	5	1.10	0.96	1.08	3	1.05	1.06	1.35	4	1.15	0.95	1.13	4.18	6.31	12.00
A8K7N0	cDNA FLJ75556, highly similar to Homo sapiens ribosomal protein L14, mRNA OS=Homo sapiens PE=2 SV=1	7	0.97	1.03	1.14	5	0.93	0.89	0.90	6	0.97	1.11	1.01	2.61	11.11	11.72
Q8TCT9	Minor histocompatibility antigen H13 OS=Homo sapiens GN=HM13 PE=1 SV=1	5	1.54	0.95	1.35	2	1.20	1.09	1.09	2	1.25	1.04	1.12	13.72	6.85	11.66
Q8NHP8	Putative phospholipase B-like 2 OS=Homo sapiens GN=PLBD2 PE=1 SV=2	6	0.99	1.01	1.11	5	1.10	0.93	1.11	6	1.06	0.93	1.03	5.24	4.95	4.55
Q9NUF9	Nucleoside diphosphate kinase (Fragment) OS=Homo sapiens GN=c371H6.2 PE=2 SV=1	6	1.12	0.89	1.29	5	1.09	0.81	1.09	5	1.14	1.19	1.12	1.87	20.90	9.43
Q6LEU0	STX12 protein (Fragment) OS=Homo sapiens GN=STX12 PE=2 SV=1	5	0.94	1.02	1.24	2	0.68	0.68	0.89	2	1.02	1.08	0.84	19.99	23.24	22.10
Q6FGD7	TBCA protein OS=Homo sapiens GN=TBCA PE=2 SV=1	6	0.97	1.13	0.95	7	0.95	1.07	0.96	5	0.98	1.10	0.96	1.66	2.55	0.73
J3KQJ1	Sulfatase-modifying factor 2 OS=Homo sapiens GN=SUMF2 PE=4 SV=1	5	1.20	0.97	0.92	5	1.06	1.00	0.97	4	1.08	0.99	1.04	6.88	1.29	6.31
H0Y8X4	2'-deoxynucleoside 5'-phosphate N-hydrolase 1 (Fragment) OS=Homo sapiens GN=DNPH1 PE=2 SV=1	5	1.01	1.08	1.08	7	0.82	0.92	0.93	3	1.12	1.17	1.26	15.05	12.19	15.08
B4DYR5	cDNA FLJ61482, highly similar to Homo sapiens lysocardiolipin acyltransferase (LYCAT), transcript variant 1, mRNA OS=Homo sapiens PE=2 SV=1	5	1.07	1.00	0.99	4	0.90	1.11	1.03	3	0.93	0.89	0.98	9.34	11.49	2.68
A4D1K0	V-type proton ATPase subunit F OS=Homo sapiens GN=ATP6V1F PE=2 SV=1	9	0.98	1.05	0.91	3	1.06	1.12	1.15	4	1.28	1.10	1.17	14.26	3.32	13.62
Q9Y3D6	Mitochondrial fission 1 protein OS=Homo sapiens GN=FIS1 PE=1 SV=2	5	1.19	1.07	1.27	5	1.07	0.76	1.00	5	1.23	1.16	1.22	7.27	21.35	12.15
Q9Y3C6	Peptidyl-prolyl cis-trans isomerase-like 1 OS=Homo sapiens GN=PPIL1 PE=1 SV=1	12	1.03	1.01	1.03	6	0.83	0.87	1.02	5	0.94	1.00	0.95	10.62	8.43	4.35

P80723	Brain acid soluble protein 1 OS=Homo sapiens GN=BASP1 PE=1 SV=2	8	1.17	1.02	1.12	3	0.89	0.59	0.97	4	2.13	1.47	2.25	46.33	42.57	48.19
Q0IJ56	ST13 protein (Fragment) OS=Homo sapiens GN=ST13 PE=2 SV=1	6	0.88	0.98	0.89	7	0.92	0.97	0.93	6	0.99	1.05	1.03	6.19	4.21	7.33
Q549C5	HCG2010808, isoform CRA_a OS=Homo sapiens GN=MST065 PE=2 SV=1	5	1.37	0.93	1.34	4	1.14	0.78	1.07	8	1.46	1.21	1.27	12.39	22.72	11.54
Q6NUK7	LYN protein (Fragment) OS=Homo sapiens GN=LYN PE=2 SV=1	6	0.88	0.96	0.63	5	1.05	0.96	1.08	5	0.86	0.82	0.89	11.49	9.03	26.12
Q53F53	Atlastin variant (Fragment) OS=Homo sapiens PE=2 SV=1	6	1.01	1.08	1.13	4	0.81	1.02	1.00	3	0.97	0.82	0.97	11.42	14.16	7.98
Q9NPF4	Probable tRNA threonylcarbamoyladenosine biosynthesis protein OSGEP OS=Homo sapiens GN=OSGEP PE=1 SV=1	5	0.97	0.78	1.09	3	0.78	0.62	0.55	2	0.89	0.76	1.00	10.52	11.91	33.00
Q5STK2	Prefoldin subunit 6, isoform CRA_b OS=Homo sapiens GN=PFDN6 PE=2 SV=1	9	1.17	0.96	1.04	7	1.14	1.10	1.09	7	0.87	0.89	0.84	15.52	10.68	13.47
Q9H1I8	Activating signal cointegrator 1 complex subunit 2 OS=Homo sapiens GN=ASCC2 PE=1 SV=3	7	0.93	0.91	0.86	6	0.96	1.04	1.13	7	0.99	0.98	0.95	2.67	6.77	14.00
Q9Y6D6	Brefeldin A-inhibited guanine nucleotide-exchange protein 1 OS=Homo sapiens GN=ARFGEF1 PE=1 SV=2	6	1.02	0.99	0.82	4	1.04	1.18	1.01	4	1.36	1.01	1.14	16.42	9.78	16.51
Q8IY17	Neuropathy target esterase OS=Homo sapiens GN=PNPLA6 PE=1 SV=2	7	1.03	0.98	1.09	6	0.89	1.12	0.91	5	1.19	1.26	1.09	14.11	12.63	10.26
Q6DKJ4	Nucleoredoxin OS=Homo sapiens GN=NXN PE=1 SV=2	5	1.07	0.75	0.98	4	0.84	0.58	1.00	3	0.79	0.94	0.80	17.03	24.20	11.51
Q7Z612	Acidic ribosomal phosphoprotein P1 OS=Homo sapiens PE=2 SV=1	17	1.01	1.00	0.98	12	1.03	1.00	1.03	9	1.00	0.94	1.05	1.49	3.61	3.49
A8K3M3	Tyrosine-protein phosphatase non-receptor type OS=Homo sapiens GN=PTPN1 PE=2 SV=1	5	1.14	0.94	0.94	6	1.01	1.07	1.00	5	0.87	0.94	1.00	13.35	7.44	3.71
B3KXD1	cDNA FLJ45199 fis, clone BRCAN2003814, highly similar to Homo sapiens phosphatidylinositol-specific phospholipase C, X domain containing 3 (PLCXD3), mRNA OS=Homo sapiens PE=2 SV=1	5	0.90	1.04	0.96	5	0.86	1.14	0.97	3	0.89	1.05	0.94	2.56	5.37	1.63
Q9UBU9	Nuclear RNA export factor 1 OS=Homo sapiens GN=NXF1 PE=1 SV=1	6	0.93	0.93	1.00	8	1.01	1.08	1.12	6	0.83	0.84	1.00	9.85	12.38	6.43
Q9BQ69	O-acetyl-ADP-ribose deacetylase MACROD1 OS=Homo sapiens GN=MACROD1 PE=1 SV=2	6	0.88	1.00	0.79	3	0.88	1.14	0.95	5	0.84	0.90	0.83	2.16	11.62	9.85
P51970	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8 OS=Homo sapiens GN=NDUFA8 PE=1 SV=3	5	1.34	1.03	1.13	8	1.39	1.01	1.13	6	1.27	0.97	1.17	4.43	2.96	2.03
Q6IAA8	Ragulator complex protein LAMTOR1 OS=Homo sapiens GN=LAMTOR1 PE=1 SV=2	5	1.06	0.90	1.04	4	0.87	0.90	0.98	2	0.96	0.92	0.85	10.09	1.07	9.91
Q6FHT8	RNP24 protein OS=Homo sapiens GN=RNP24 PE=2 SV=1	7	1.37	0.96	1.34	4	1.37	1.09	1.35	3	1.26	1.01	1.25	4.73	6.21	3.96
Q53FP0	Pyridoxine 5'-phosphate oxidase variant (Fragment) OS=Homo sapiens PE=2 SV=1	5	1.01	1.17	0.98	4	0.70	0.76	0.76	5	0.89	0.83	0.89	17.88	23.98	12.48
P21283	V-type proton ATPase subunit C 1 OS=Homo sapiens GN=ATP6V1C1 PE=1 SV=4	6	1.11	0.91	0.76	5	0.78	1.01	1.00	9	1.04	0.93	0.98	17.92	5.64	14.07

Q8NBI6	Xyloside xylosyltransferase 1 OS=Homo sapiens GN=XXYLT1 PE=1 SV=1	5	1.18	0.89	0.88	3	1.30	1.15	1.26	2	1.25	0.97	1.00	4.95	13.57	18.33
Q6IAQ1	LYPLA1 protein OS=Homo sapiens GN=LYPLA1 PE=2 SV=1	8	1.04	1.14	1.10	3	0.59	0.57	0.82	2	1.09	1.25	1.00	30.20	37.46	14.47
O75367	Core histone macro-H2A.1 OS=Homo sapiens GN=H2AFY PE=1 SV=4	7	1.79	1.02	1.11	3	1.85	1.13	1.39	5	1.72	0.96	1.47	3.59	8.65	14.28
Q05519	Serine/arginine-rich splicing factor 11 OS=Homo sapiens GN=SRSF11 PE=1 SV=1	5	1.19	1.12	0.92	6	1.02	1.08	1.00	5	0.88	0.95	0.93	15.31	8.43	4.47
A4D2P1	Ras-related C3 botulinum toxin substrate 1 (Rho family, small GTP binding protein Rac1) OS=Homo sapiens GN=RAC1 PE=2 SV=1	7	0.93	0.91	0.65	9	1.23	1.32	1.15	7	1.10	1.01	0.90	13.81	19.65	27.45
Q9UK59	Lariat debranching enzyme OS=Homo sapiens GN=DBR1 PE=1 SV=2	6	1.01	1.05	1.03	2	0.93	1.07	0.94	5	1.07	1.10	1.03	7.29	2.16	5.09
D3DWY7	von Hippel-Lindau binding protein 1, isoform CRA_b OS=Homo sapiens GN=VBP1 PE=4 SV=1	5	0.81	0.94	0.88	4	0.90	0.95	0.86	6	0.90	1.16	0.81	5.75	12.26	4.21
P81605	Dermcidin OS=Homo sapiens GN=DCD PE=1 SV=2	9	1.06	0.69	1.80	4	0.94	0.66	1.04	4	1.50	1.81	2.26	25.14	62.07	36.04
P41227	N-alpha-acetyltransferase 10 OS=Homo sapiens GN=NAA10 PE=1 SV=1	6	1.17	0.73	0.85	4	0.93	1.14	0.93	3	1.14	0.80	0.97	11.91	24.53	6.61
B4DVE1	cDNA FLJ53478, highly similar to Galectin-3-binding protein OS=Homo sapiens PE=2 SV=1	5	1.37	0.95	1.01	8	1.39	0.97	1.33	9	1.25	1.01	1.23	5.77	3.26	13.71
B7Z3P1	Tubulin-specific chaperone E OS=Homo sapiens GN=TBCE PE=2 SV=1	22	1.05	0.89	0.86	4	0.90	1.13	0.97	4	0.84	0.91	1.01	11.59	13.70	8.24
P57105	Synaptojanin-2-binding protein OS=Homo sapiens GN=SYNJ2BP PE=1 SV=2	5	1.08	1.09	1.21	5	1.13	0.88	1.01	5	0.96	1.02	1.02	8.20	10.81	10.40
B4DEF8	cDNA FLJ61100, highly similar to 39S ribosomal protein L45, mitochondrial OS=Homo sapiens PE=2 SV=1	5	0.98	0.92	0.91	4	1.14	1.17	1.23	5	1.04	0.91	0.87	7.91	14.92	19.69
P82909	28S ribosomal protein S36, mitochondrial OS=Homo sapiens GN=MRPS36 PE=1 SV=2	5	0.97	0.84	0.75	4	1.16	1.26	1.16	5	1.01	1.00	1.08	9.42	20.16	21.66
Q7L4Q3	Glutathione peroxidase OS=Homo sapiens GN=GPX1 PE=2 SV=1	6	0.93	0.97	0.99	7	0.83	0.90	0.94	6	0.99	0.94	1.05	8.89	3.48	5.38
Q9Y2X3	Nucleolar protein 58 OS=Homo sapiens GN=NOP58 PE=1 SV=1	7	0.97	0.93	0.88	5	1.30	1.06	1.21	5	1.25	1.02	1.12	15.26	6.87	15.85
I4AY87	Macrophage migration inhibitory factor (Fragment) OS=Homo sapiens PE=2 SV=1	40	0.89	1.07	1.00	8	0.81	0.90	0.84	14	0.93	1.17	0.99	7.08	12.96	9.52
P35270	Sepiapterin reductase OS=Homo sapiens GN=SPR PE=1 SV=1	8	0.99	0.91	1.04	5	0.95	0.87	0.88	5	0.89	1.09	0.92	5.43	12.03	8.73
Q549N5	Signal recognition particle receptor beta subunit OS=Homo sapiens GN=SRPRB PE=2 SV=1	5	1.12	0.96	0.91	4	1.11	1.04	1.17	3	1.16	0.89	0.97	2.13	8.18	13.59
L7RT22	Integrin beta OS=Homo sapiens GN=ITGB5 PE=3 SV=1	6	1.06	1.17	1.33	3	0.88	0.94	1.14	4	1.25	1.00	1.02	17.79	11.60	13.18
Q6IAL5	Putative uncharacterized protein tmp_locus_1 OS=Homo sapiens GN=SUCLG1 PE=2 SV=1	7	1.15	0.96	1.00	8	1.24	1.08	1.21	5	1.36	1.03	1.10	8.41	5.59	9.16
O75368	SH3 domain-binding glutamic acid-rich-like protein OS=Homo sapiens GN=SH3BGRL PE=1 SV=1	5	1.19	1.48	1.34	7	0.88	1.06	0.95	7	0.87	1.03	0.92	18.45	21.00	21.71
H7BY84	General transcription factor 3C polypeptide 5 OS=Homo sapiens GN=GTF3C5 PE=2 SV=1	5	1.17	1.20	0.98	7	1.12	1.13	1.01	5	1.01	1.01	0.98	7.39	9.03	2.05

Q68D50	Putative uncharacterized protein DKFZp779I1858 OS=Homo sapiens GN=DKFZp779I1858 PE=2 SV=1	6	1.10	1.30	1.05	5	1.14	1.07	1.11	4	1.01	0.96	0.86	5.88	15.78	13.13
Q53T99	CDW7/WDR12 OS=Homo sapiens GN=WDR12 PE=2 SV=1	6	0.77	1.22	0.93	5	1.10	0.96	1.13	5	0.89	1.00	0.90	17.96	13.42	12.81
O75937	DnaJ homolog subfamily C member 8 OS=Homo sapiens GN=DNAJC8 PE=1 SV=2	5	0.88	0.82	0.74	6	0.94	1.27	1.08	6	1.00	0.80	0.97	6.55	27.56	18.76
Q9Y5P6	Mannose-1-phosphate guanyltransferase beta OS=Homo sapiens GN=GMPPB PE=1 SV=2	6	1.10	0.94	1.07	5	1.27	0.97	1.22	2	0.98	0.94	1.50	13.25	1.89	17.04
Q9NUJ1	Mycophenolic acid acyl-glucuronide esterase, mitochondrial OS=Homo sapiens GN=ABHD10 PE=1 SV=1	6	0.92	1.07	0.91	2	0.68	0.78	0.78	3	0.98	1.00	1.05	18.08	15.83	14.73
P54709	Sodium/potassium-transporting ATPase subunit beta-3 OS=Homo sapiens GN=ATP1B3 PE=1 SV=1	5	1.14	1.10	1.05	5	1.28	1.06	1.04	5	1.09	1.22	1.08	8.53	7.20	1.92
A8K0P8	cDNA FLJ78223 OS=Homo sapiens PE=2 SV=1	5	0.88	1.09	1.03	3	0.71	0.95	0.71	2	1.06	1.11	0.97	19.66	8.03	19.21
Q15370	Transcription elongation factor B polypeptide 2 OS=Homo sapiens GN=TCEB2 PE=1 SV=1	6	0.84	0.99	0.84	11	0.81	1.10	0.89	6	0.85	0.99	0.82	2.85	5.95	4.24
A8K946	mRNA cap guanine-N7 methyltransferase OS=Homo sapiens PE=2 SV=1	5	0.79	0.85	0.82	5	1.23	1.34	1.12	3	1.05	1.01	1.03	21.54	23.23	15.53
G5EA19	Putative deoxyribonuclease TATDN1 OS=Homo sapiens GN=TATDN1 PE=2 SV=1	6	1.00	1.02	0.89	6	0.99	1.02	1.08	6	1.13	0.97	1.05	7.83	2.79	9.99
O15173	Membrane-associated progesterone receptor component 2 OS=Homo sapiens GN=PGRMC2 PE=1 SV=1	7	1.32	1.15	1.27	5	1.34	1.08	1.10	5	1.29	1.11	1.05	1.77	2.93	10.29
Q16222	UDP-N-acetylhexosamine pyrophosphorylase OS=Homo sapiens GN=UAP1 PE=1 SV=3	9	1.68	1.05	1.52	5	1.58	1.17	1.47	5	1.40	0.87	1.21	9.26	14.80	12.20
G5E9W7	28S ribosomal protein S22, mitochondrial OS=Homo sapiens GN=MRPS22 PE=2 SV=1	8	1.03	0.96	0.93	9	1.03	1.10	0.95	3	1.27	1.27	1.18	12.59	13.88	13.65
O75976	Carboxypeptidase D OS=Homo sapiens GN=CPD PE=1 SV=2	5	1.19	1.18	0.99	7	1.14	1.18	1.13	3	1.13	0.99	1.13	3.06	9.55	7.82
Q59HH0	Retinoblastoma-associated protein variant (Fragment) OS=Homo sapiens PE=2 SV=1	5	0.68	0.87	0.85	4	0.63	0.50	0.88	3	1.07	0.97	1.09	30.65	31.70	14.22
Q9NV70	Exocyst complex component 1 OS=Homo sapiens GN=EXOC1 PE=1 SV=4	5	1.01	1.16	0.98	2	1.41	1.24	1.26	5	0.94	0.83	1.00	22.86	20.20	14.88
J3KN38	Methylosome subunit pICln OS=Homo sapiens GN=CLNS1A PE=4 SV=1	7	0.71	1.09	1.03	5	0.72	0.77	0.75	5	0.83	1.02	0.84	8.30	17.34	16.52
P54687	Branched-chain-amino-acid aminotransferase, cytosolic OS=Homo sapiens GN=BCAT1 PE=1 SV=3	6	1.19	1.05	1.02	4	0.81	0.97	0.87	4	1.03	1.00	1.26	18.45	4.15	18.83
E7ER68	Protein FAM91A1 OS=Homo sapiens GN=FAM91A1 PE=2 SV=1	5	0.96	1.13	0.96	3	0.91	1.08	1.08	5	0.99	1.11	1.05	4.32	2.06	6.13
O95400	CD2 antigen cytoplasmic tail-binding protein 2 OS=Homo sapiens GN=CD2BP2 PE=1 SV=1	5	0.76	1.05	0.94	4	0.84	0.91	0.79	6	0.91	0.96	0.97	9.31	7.49	10.54
Q96EE3	Nucleoporin SEH1 OS=Homo sapiens GN=SEH1L PE=1 SV=3	5	0.98	0.96	1.10	5	0.91	0.95	0.94	5	1.22	1.07	1.16	15.54	6.99	10.41
C9JJ19	28S ribosomal protein S34, mitochondrial OS=Homo sapiens GN=MRPS34 PE=2 SV=2	6	1.04	1.16	1.10	3	0.93	1.00	0.94	3	1.08	1.00	1.06	7.67	8.98	7.97
Q32P28-3	Isoform 3 of Prolyl 3-hydroxylase 1 OS=Homo sapiens GN=LEPRE1	5	1.05	0.96	1.13	7	1.10	0.86	1.05	7	1.03	1.01	1.19	3.69	8.11	6.04

P42574	Caspase-3 OS=Homo sapiens GN=CASP3 PE=1 SV=2	6	0.92	1.06	1.05	6	0.97	0.97	0.98	3	1.02	0.96	1.01	5.24	5.60	3.49
J3QQJ0	SAP30-binding protein (Fragment) OS=Homo sapiens GN=SAP30BP PE=4 SV=1	5	0.92	1.05	0.96	4	0.79	0.98	0.92	5	0.81	1.02	0.89	8.47	3.49	3.91
Q9UPT5	Exocyst complex component 7 OS=Homo sapiens GN=EXOC7 PE=1 SV=3	6	0.96	0.96	0.90	6	0.89	0.99	0.98	5	1.03	1.05	1.05	7.03	4.14	7.76
Q5TH30	NDRG family member 3, isoform CRA_c OS=Homo sapiens GN=NDRG3 PE=2 SV=1	5	0.87	0.89	1.00	2	1.42	1.41	1.08	3	1.34	0.99	0.99	24.82	25.22	4.81
D6RBL4	Methyltransferase-like protein 14 OS=Homo sapiens GN=METTL14 PE=2 SV=1	5	0.97	1.07	1.18	2	0.84	0.82	0.96	2	1.34	1.22	1.03	24.49	19.18	10.26
Q9P016	Thymocyte nuclear protein 1 OS=Homo sapiens GN=THYN1 PE=1 SV=1	5	1.09	1.03	0.95	5	1.08	1.01	1.06	5	1.22	1.33	1.14	7.14	16.21	8.80
O15270	Serine palmitoyltransferase 2 OS=Homo sapiens GN=SPTLC2 PE=1 SV=1	5	1.64	1.09	1.23	3	1.63	1.29	1.58	4	0.96	0.99	0.93	27.48	13.49	26.38
Q68CN5	Putative uncharacterized protein DKFZp686D17136 (Fragment) OS=Homo sapiens GN=DKFZp686D17136 PE=2 SV=2	8	0.89	1.06	1.04	9	0.91	1.06	1.04	6	1.08	0.99	0.92	10.86	3.76	6.72
Q96FX7	tRNA (adenine(58)-N(1))-methyltransferase catalytic subunit TRMT61A OS=Homo sapiens GN=TRMT61A PE=1 SV=1	5	0.99	1.10	0.91	6	1.08	0.96	1.08	4	1.14	1.02	1.19	7.02	6.96	13.29
F5GYQ1	V-type proton ATPase subunit d 1 OS=Homo sapiens GN=ATP6V0D1 PE=2 SV=1	5	0.95	1.00	0.96	6	0.82	0.79	0.76	3	0.94	0.92	0.98	7.65	11.65	13.47
Q86U44	N6-adenosine-methyltransferase 70 kDa subunit OS=Homo sapiens GN=METTL3 PE=1 SV=2	5	0.82	0.96	0.81	2	0.96	0.83	0.99	6	1.09	0.96	0.98	13.99	7.81	11.00
P48634	Protein PRRC2A OS=Homo sapiens GN=PRRC2A PE=1 SV=3	8	1.06	1.08	1.18	2	1.04	0.84	1.05	3	0.96	0.99	1.10	5.43	12.29	5.70
D3DPT8	Ras-related GTP binding C, isoform CRA_a OS=Homo sapiens GN=RRAGC PE=2 SV=1	5	0.98	0.95	0.93	2	0.99	1.12	0.93	2	1.34	1.38	0.98	18.64	19.09	3.03
M0R208	ATP-dependent Clp protease proteolytic subunit OS=Homo sapiens GN=CLPP PE=3 SV=1	5	1.10	0.92	1.09	3	1.48	0.88	1.28	4	1.31	1.34	1.21	14.67	24.09	7.70
Q53GS8	Wolf-Hirschhorn syndrome candidate 2 protein variant (Fragment) OS=Homo sapiens PE=2 SV=1	5	0.91	1.00	1.00	4	1.02	0.97	0.99	4	1.12	1.02	1.14	9.98	2.31	8.20
H0YJ66	Dehydrogenase/reductase SDR family member 7 (Fragment) OS=Homo sapiens GN=DHRS7 PE=3 SV=1	5	1.09	0.94	1.25	3	1.21	0.96	1.05	3	1.36	1.10	1.28	10.78	8.93	10.15
Q969S9	Ribosome-releasing factor 2, mitochondrial OS=Homo sapiens GN=GFM2 PE=1 SV=1	5	0.95	0.88	1.14	5	1.12	1.10	1.21	4	1.19	1.21	1.03	11.06	15.70	8.25
O96028	Histone-lysine N-methyltransferase NSD2 OS=Homo sapiens GN=WHSC1 PE=1 SV=1	5	0.88	0.81	0.77	3	0.65	0.89	0.68	5	0.94	0.81	0.83	18.77	5.70	9.89
E9PRI4	Ribosomal protein S6 kinase OS=Homo sapiens GN=RPS6KA1 PE=2 SV=1	5	1.03	0.88	0.74	5	0.98	1.10	1.12	5	1.01	1.04	1.07	2.33	11.45	21.42
Q8TAE8	Growth arrest and DNA damage-inducible proteins-interacting protein 1 OS=Homo sapiens GN=GADD45GIP1 PE=1 SV=1	5	0.92	1.07	1.39	7	0.99	0.86	0.96	5	0.97	1.28	0.88	3.67	19.58	25.69
Q7Z7H5	Transmembrane emp24 domain-containing protein 4 OS=Homo sapiens GN=TMED4 PE=1 SV=1	6	1.14	0.95	0.98	4	1.38	1.02	1.21	4	1.36	1.03	1.07	10.54	4.24	10.31

P55795	Heterogeneous nuclear ribonucleoprotein H2 OS=Homo sapiens GN=HNRNPH2 PE=1 SV=1	22	0.92	1.01	1.04	24	0.73	0.84	0.81	19	0.98	1.06	1.03	14.60	12.25	13.58
Q6NZX3	5'-nucleotidase, ecto (CD73) OS=Homo sapiens GN=NT5E PE=2 SV=1	7	0.94	0.99	0.86	8	1.11	1.25	1.15	7	1.18	1.10	1.08	11.44	11.82	14.59
P52735	Guanine nucleotide exchange factor VAV2 OS=Homo sapiens GN=VAV2 PE=1 SV=2	5	0.72	0.87	1.04	2	0.67	1.02	0.77	5	0.89	1.08	1.04	15.42	10.73	16.12
B3KPM8	cDNA FLJ31974 fis, clone NT2RP7008167, weakly similar to 85.1 kDa PROTEIN IN GREB-FEOA INTERGENIC REGION OS=Homo sapiens PE=2 SV=1	5	0.98	1.01	0.95	3	1.00	1.23	1.10	2	1.00	1.09	1.00	1.22	10.03	7.62
Q9NZM1	Myoferlin OS=Homo sapiens GN=MYOF PE=1 SV=1	6	1.19	1.06	1.22	7	1.16	0.85	1.08	5	0.97	1.03	0.94	10.71	11.52	13.33
Q8WU76	Sec1 family domain-containing protein 2 OS=Homo sapiens GN=SCFD2 PE=1 SV=2	5	0.85	0.83	0.84	3	1.21	1.20	1.08	3	1.01	0.91	0.94	17.69	19.85	12.50
A8KA82	DnaJ (Hsp40) homolog, subfamily C, member 3 OS=Homo sapiens GN=DNAJC3 PE=2 SV=1	8	1.51	1.08	1.58	6	1.52	0.98	1.20	3	1.39	1.11	1.26	4.74	6.61	15.28
B2RCD8	cDNA, FLJ96012, highly similar to Homo sapiens interferon regulatory factor 2 binding protein 1 (IRF2BP1), mRNA OS=Homo sapiens PE=2 SV=1	5	0.77	0.86	0.87	6	0.77	0.85	0.93	2	0.82	1.17	0.83	4.05	18.96	6.00
Q69YN4	Protein virilizer homolog OS=Homo sapiens GN=KIAA1429 PE=1 SV=2	6	1.00	1.06	1.27	4	0.52	0.66	0.74	4	1.05	1.28	1.10	34.11	31.36	26.02
A4D275	Actin related protein 2/3 complex, subunit 1B, 41kDa OS=Homo sapiens GN=ARPC1B PE=2 SV=1	9	1.11	1.20	1.05	7	1.13	1.03	1.13	3	1.13	1.11	1.07	0.92	7.91	3.59
P84090	Enhancer of rudimentary homolog OS=Homo sapiens GN=ERH PE=1 SV=1	7	0.83	0.93	0.65	4	0.84	0.84	0.84	8	0.87	0.98	0.86	2.25	7.65	15.26
H0YI09	Methyltransferase-like protein 7A (Fragment) OS=Homo sapiens GN=METTL7A PE=4 SV=1	5	0.97	0.95	0.87	5	1.14	1.04	1.04	3	0.90	1.03	0.97	12.17	4.67	9.20
Q5GJ64	Hypothetical rhabdomyosarcoma antigen MU-RMS-40.5 (Fragment) OS=Homo sapiens PE=2 SV=1	5	0.83	1.15	0.92	4	1.02	1.08	0.89	3	1.02	0.89	1.03	11.56	12.92	7.76
Q53GD8	Peptidyl-prolyl cis-trans isomerase (Fragment) OS=Homo sapiens PE=2 SV=1	7	0.96	1.01	0.77	5	0.99	1.12	0.98	3	0.88	0.92	0.88	6.03	10.10	11.57
P45973	Chromobox protein homolog 5 OS=Homo sapiens GN=CBX5 PE=1 SV=1	7	1.05	0.97	0.89	4	1.15	1.18	1.17	5	1.06	0.92	0.93	5.37	13.70	15.37
D6RBS5	ELMO domain-containing protein 2 (Fragment) OS=Homo sapiens GN=ELMOD2 PE=2 SV=1	6	1.28	1.09	0.76	5	0.99	1.02	0.86	5	1.14	1.08	1.13	12.99	3.53	20.66
Q9BRR6	ADP-dependent glucokinase OS=Homo sapiens GN=ADPGK PE=1 SV=1	7	1.32	1.05	1.30	4	1.43	1.11	1.20	5	1.22	0.99	1.11	7.95	5.95	8.02
Q53HT6	B-cell receptor-associated protein 31 variant (Fragment) OS=Homo sapiens PE=2 SV=1	10	1.14	0.96	1.01	7	1.29	1.11	1.28	5	1.12	0.93	1.16	7.82	10.06	11.89
Q14690	Protein RRP5 homolog OS=Homo sapiens GN=PDCD11 PE=1 SV=3	4	0.97	0.87	0.68	5	0.98	1.02	0.99	5	1.03	0.87	1.01	3.24	9.63	20.67
P43487	Ran-specific GTPase-activating protein OS=Homo sapiens GN=RANBP1 PE=1 SV=1	12	0.87	0.99	0.80	8	0.91	1.02	0.91	7	0.92	1.05	0.94	3.03	3.23	8.54
H3BRY6	von Willebrand factor A domain-containing protein 9 OS=Homo sapiens GN=VWA9 PE=2 SV=1	5	1.35	1.03	0.88	2	1.13	1.40	1.35	4	0.83	0.90	1.00	23.50	23.10	22.84

Q71TU5	Casein kinase 1, alpha 1, isoform CRA_g OS=Homo sapiens GN=CSNK1A1 PE=2 SV=1	7	0.91	1.12	0.87	7	0.85	0.85	0.93	5	0.88	1.02	0.88	3.61	13.67	3.81
Q8WXD2	Secretogranin-3 OS=Homo sapiens GN=SCG3 PE=1 SV=3	5	1.10	1.17	1.05	4	1.34	1.18	1.39	3	1.26	1.06	1.19	9.62	5.84	14.48
Q9UL25	Ras-related protein Rab-21 OS=Homo sapiens GN=RAB21 PE=1 SV=3	4	1.01	0.98	1.00	6	1.20	1.01	1.24	4	0.93	0.82	0.87	13.20	11.18	17.99
P82673	28S ribosomal protein S35, mitochondrial OS=Homo sapiens GN=MRPS35 PE=1 SV=1	4	0.99	0.94	1.03	3	1.04	1.22	1.18	7	0.98	0.98	1.06	3.22	14.69	7.26
Q13151	Heterogeneous nuclear ribonucleoprotein A0 OS=Homo sapiens GN=HNRNPA0 PE=1 SV=1	11	0.99	1.02	1.09	10	0.92	0.92	0.94	9	0.94	0.93	0.97	3.64	5.48	7.84
Q8IZ83	Aldehyde dehydrogenase family 16 member A1 OS=Homo sapiens GN=ALDH16A1 PE=1 SV=2	5	1.25	1.06	1.07	8	1.17	0.94	1.22	5	1.83	1.30	3.11	25.05	16.76	63.07
A0PJ79	MRPL1 protein (Fragment) OS=Homo sapiens GN=MRPL1 PE=2 SV=1	4	1.05	0.95	0.97	6	1.04	0.93	0.90	6	1.06	0.80	1.03	0.93	9.08	6.69
P61081	NEDD8-conjugating enzyme Ubc12 OS=Homo sapiens GN=UBE2M PE=1 SV=1	6	1.04	0.93	1.07	4	1.00	0.93	0.87	5	0.90	1.08	1.06	7.19	8.82	11.29
Q8WZ82	Ovarian cancer-associated gene 2 protein OS=Homo sapiens GN=OVCA2 PE=1 SV=1	8	1.10	0.84	0.96	2	0.71	0.72	0.69	2	1.42	1.60	1.14	33.21	45.43	24.59
P08727	Keratin, type I cytoskeletal 19 OS=Homo sapiens GN=KRT19 PE=1 SV=4	10	0.86	0.77	0.99	10	1.07	0.84	1.13	9	1.16	1.23	1.38	15.09	26.10	16.89
Q5UIP0	Telomere-associated protein RIF1 OS=Homo sapiens GN=RIF1 PE=1 SV=2	4	1.00	1.03	0.89	6	0.58	0.76	0.78	3	0.88	0.88	0.76	26.17	15.10	8.58
Q53Y51	D-dopachrome tautomerase OS=Homo sapiens GN=DDT PE=2 SV=1	6	1.14	1.09	1.41	6	1.00	1.02	1.12	3	1.07	0.98	1.04	6.36	5.30	16.25
Q9BRX8	Redox-regulatory protein FAM213A OS=Homo sapiens GN=FAM213A PE=1 SV=3	5	0.94	1.01	1.11	4	1.10	1.08	1.05	4	1.00	0.93	1.08	8.10	7.68	2.87
Q2M1V9	BTAF1 RNA polymerase II, B-TFIID transcription factor-associated, 170kDa OS=Homo sapiens GN=BTAF1 PE=2 SV=1	5	1.00	1.00	1.22	5	0.90	1.05	0.98	5	0.89	1.00	0.95	6.87	2.93	14.14
Q9Y3U8	60S ribosomal protein L36 OS=Homo sapiens GN=RPL36 PE=1 SV=3	6	1.00	0.95	0.95	5	1.05	1.04	1.04	6	0.98	0.92	0.99	3.33	6.36	4.75
O15511	Actin-related protein 2/3 complex subunit 5 OS=Homo sapiens GN=ARPC5 PE=1 SV=3	6	1.00	0.76	1.39	6	0.86	0.76	1.31	2	1.18	1.26	1.30	15.55	31.35	3.80
P50552	Vasodilator-stimulated phosphoprotein OS=Homo sapiens GN=VASP PE=1 SV=3	8	0.95	0.76	0.77	2	1.29	1.25	1.27	4	1.09	0.86	1.24	15.46	26.98	25.74
Q5R2V8	C2orf4 protein OS=Homo sapiens GN=C2orf4 PE=2 SV=1	6	1.07	0.95	0.85	5	0.84	0.90	0.86	3	1.11	0.82	0.87	14.66	7.67	0.83
P62314	Small nuclear ribonucleoprotein Sm D1 OS=Homo sapiens GN=SNRPD1 PE=1 SV=1	6	0.90	1.02	0.91	6	0.97	0.97	0.93	4	0.94	1.00	0.93	3.43	2.62	0.81
Q15785	Mitochondrial import receptor subunit TOM34 OS=Homo sapiens GN=TOMM34 PE=1 SV=2	5	1.05	0.76	0.73	7	0.95	1.55	1.52	4	0.90	0.99	1.09	7.55	36.65	35.64
Q6IT96	Histone deacetylase OS=Homo sapiens GN=HDAC1 PE=2 SV=1	9	1.07	0.95	1.00	5	1.03	1.20	1.10	7	0.86	1.12	0.94	11.18	11.94	8.17
Q9HD33	39S ribosomal protein L47, mitochondrial OS=Homo sapiens GN=MRPL47 PE=1 SV=2	5	0.90	0.93	0.86	5	0.96	1.07	0.90	5	0.83	0.98	0.90	7.20	6.91	2.90

O14561	Acyl carrier protein, mitochondrial OS=Homo sapiens GN=NDUFAB1 PE=1 SV=3	9	1.09	1.05	1.01	7	1.03	1.08	1.01	6	1.10	0.99	1.04	3.71	4.17	1.97
Q9H061	Transmembrane protein 126A OS=Homo sapiens GN=TMEM126A PE=1 SV=1	4	1.16	1.13	1.19	4	1.09	0.94	1.07	4	1.37	1.00	1.34	12.08	9.38	11.12
A4D105	Replication protein A3, 14kDa OS=Homo sapiens GN=RPA3 PE=2 SV=1	9	0.92	0.96	0.91	7	0.96	1.01	0.88	6	0.93	0.92	0.93	2.59	4.38	3.27
B7Z6D5	cDNA FLJ61659, highly similar to Probable ATP-dependent RNA helicase DDX27 (EC 3.6.1.-) OS=Homo sapiens PE=2 SV=1	5	1.14	0.95	1.39	4	1.06	0.97	1.01	2	1.31	1.29	1.23	11.06	17.48	15.48
Q9NR09	Baculoviral IAP repeat-containing protein 6 OS=Homo sapiens GN=BIRC6 PE=1 SV=2	6	1.15	1.06	1.02	9	1.07	0.94	0.93	8	1.16	0.99	0.95	4.22	6.04	5.11
C9JRZ6	Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial OS=Homo sapiens GN=CHCHD3 PE=2 SV=1	4	1.17	0.89	1.13	4	0.95	1.03	1.11	3	1.11	1.08	1.16	10.44	9.83	2.28
Q59FM5	Guanine nucleotide-binding protein G, alpha subunit variant (Fragment) OS=Homo sapiens PE=2 SV=1	4	1.01	0.95	0.96	7	1.09	0.65	0.99	3	1.02	1.10	0.96	4.58	25.17	1.81
F5H345	Porphobilinogen deaminase OS=Homo sapiens GN=HMBS PE=2 SV=1	6	0.97	0.99	0.82	4	1.03	1.06	1.05	4	1.12	0.97	1.06	6.99	4.77	14.09
A7E2F7	CAP-GLY domain containing linker protein 2 OS=Homo sapiens GN=CLIP2 PE=2 SV=1	5	0.73	0.95	0.74	5	1.06	1.14	0.94	2	1.22	1.14	1.03	25.03	9.83	16.37
B2R6X6	Peptidyl-prolyl cis-trans isomerase OS=Homo sapiens PE=2 SV=1	8	1.02	1.07	0.93	4	1.02	1.04	1.05	2	1.06	0.78	0.97	2.18	16.66	6.65
C9JQV0	Uncharacterized protein C7orf50 (Fragment) OS=Homo sapiens GN=C7orf50 PE=2 SV=1	4	0.90	0.91	1.03	4	0.82	0.88	0.87	4	0.89	1.24	1.02	5.20	19.66	9.20
H7C1U8	Apolipoprotein O (Fragment) OS=Homo sapiens GN=APOO PE=2 SV=1	6	1.33	1.09	1.25	4	1.19	1.11	1.26	2	1.42	0.96	1.27	8.75	8.01	0.68
P42766	60S ribosomal protein L35 OS=Homo sapiens GN=RPL35 PE=1 SV=2	5	0.96	1.04	0.73	3	1.25	1.29	1.18	3	0.99	0.93	1.04	15.32	16.99	23.85
B4DH44	cDNA FLJ52538, highly similar to Dual specificity mitogen-activated proteinkinase kinase 4 (EC 2.7.12.2) OS=Homo sapiens PE=2 SV=1	5	0.83	1.02	0.83	3	0.89	0.93	0.88	3	0.92	1.05	0.95	5.43	6.02	7.21
Q9UNW9	RNA-binding protein Nova-2 OS=Homo sapiens GN=NOVA2 PE=1 SV=1	6	1.31	1.64	1.06	5	1.19	1.25	1.03	3	0.92	0.87	0.97	17.69	30.52	4.50
H3BRL3	Ubiquitin domain-containing protein UBFD1 OS=Homo sapiens GN=UBFD1 PE=2 SV=1	5	0.87	0.91	0.89	2	0.99	1.04	0.88	4	0.97	1.14	0.85	7.08	11.51	2.15
Q6L8Q7	2',5'-phosphodiesterase 12 OS=Homo sapiens GN=PDE12 PE=1 SV=2	6	1.46	1.19	1.18	5	0.77	1.01	0.76	4	0.98	1.08	1.17	33.44	8.23	23.06
O75436	Vacuolar protein sorting-associated protein 26A OS=Homo sapiens GN=VPS26A PE=1 SV=2	4	1.08	1.00	1.12	3	1.01	0.97	0.97	2	1.02	1.05	1.04	3.35	4.07	7.26
Q9UJA5	tRNA (adenine(58)-N(1))-methyltransferase non-catalytic subunit TRM6 OS=Homo sapiens GN=TRMT6 PE=1 SV=1	4	0.99	1.00	1.06	5	0.91	1.00	0.99	7	0.98	1.09	0.96	4.40	5.06	5.14
Q9Y295	Developmentally-regulated GTP-binding protein 1 OS=Homo sapiens GN=DRG1 PE=1 SV=1	4	1.09	1.25	0.91	7	0.98	0.96	0.89	8	0.92	1.07	0.97	8.65	13.54	4.56
B4DXX1	cDNA FLJ56040 OS=Homo sapiens PE=2 SV=1	8	0.97	0.94	1.01	4	1.12	1.06	1.00	4	0.93	1.22	0.86	9.69	13.33	8.94

Q9H269	Vacuolar protein sorting-associated protein 16 homolog OS=Homo sapiens GN=VPS16 PE=1 SV=2	4	1.03	1.07	1.48	5	0.92	0.92	0.92	3	0.96	0.93	1.06	5.41	8.68	25.20
B3KMB9	cDNA FLJ10659 fis, clone NT2RP2006071, highly similar to DCC-interacting protein 13 beta OS=Homo sapiens PE=2 SV=1	5	1.00	1.00	1.08	3	0.89	0.93	1.04	2	1.21	1.05	1.05	15.74	6.44	2.32
Q53XM7	VAMP (Vesicle-associated membrane protein)-associated protein B and C OS=Homo sapiens GN=VAPB PE=2 SV=1	5	0.98	0.90	0.95	4	1.03	1.07	1.07	4	1.06	1.08	1.11	3.84	9.79	8.06
R4SBI6	EPHX1 OS=Homo sapiens GN=EPHX1 PE=2 SV=1	5	1.12	0.94	1.05	4	1.09	0.96	0.94	2	0.86	0.73	0.78	13.67	14.92	14.53
Q06587	E3 ubiquitin-protein ligase RING1 OS=Homo sapiens GN=RING1 PE=1 SV=2	4	0.97	0.86	0.98	4	0.69	0.88	0.89	4	1.22	1.22	1.10	27.46	21.05	10.52
Q6IAX4	RTN1 protein OS=Homo sapiens GN=RTN1 PE=2 SV=1	6	1.15	1.09	1.12	8	1.02	0.98	1.00	5	1.17	1.05	1.14	7.57	5.01	6.89
Q8NBL1	Protein O-glucosyltransferase 1 OS=Homo sapiens GN=POGLUT1 PE=1 SV=1	5	1.17	1.28	1.16	5	1.06	0.96	1.11	3	1.15	1.06	1.31	4.96	15.08	8.62
Q71UA6	Neutral amino acid transporter OS=Homo sapiens GN=SLC1A5 PE=2 SV=1	4	0.94	0.74	1.05	4	0.98	0.75	0.96	2	1.07	1.09	1.23	6.72	23.01	12.88
Q9Y3C8	Ubiquitin-fold modifier-conjugating enzyme 1 OS=Homo sapiens GN=UFC1 PE=1 SV=3	5	0.95	0.95	0.82	3	1.13	1.13	1.12	4	0.95	0.90	1.00	10.57	12.21	15.47
H7C0E5	Zinc finger protein ZPR1 (Fragment) OS=Homo sapiens GN=ZNF259 PE=4 SV=1	4	0.95	0.90	0.93	7	1.14	1.08	1.21	4	0.95	0.85	0.89	10.95	12.81	17.23
P61086	Ubiquitin-conjugating enzyme E2 K OS=Homo sapiens GN=UBE2K PE=1 SV=3	9	0.82	0.95	1.11	14	0.91	0.99	0.91	8	0.86	1.15	0.99	5.43	10.01	9.88
B2R6K1	cDNA, FLJ92992, highly similar to Homo sapiens methylmalonyl Coenzyme A mutase (MUT), nuclear gene encoding mitochondrial protein, mRNA OS=Homo sapiens PE=2 SV=1	5	1.02	1.36	1.07	4	0.99	1.20	0.92	5	1.02	1.02	1.04	1.77	14.07	7.69
A8K5Q1	cDNA FLJ77548, highly similar to Homo sapiens bin3, bicoid-interacting 3, homolog (Drosophila) (BCDIN3), mRNA OS=Homo sapiens PE=2 SV=1	4	1.16	1.15	1.09	2	1.02	1.05	1.03	2	0.80	0.93	0.84	17.95	10.25	13.13
P31949	Protein S100-A11 OS=Homo sapiens GN=S100A11 PE=1 SV=2	13	1.50	1.04	1.38	9	1.44	0.91	1.38	4	1.47	0.92	1.66	1.96	7.46	11.18
P61026	Ras-related protein Rab-10 OS=Homo sapiens GN=RAB10 PE=1 SV=1	6	1.00	1.01	1.01	6	0.97	1.03	1.05	6	1.01	0.95	0.99	2.14	4.25	2.93
B2RDZ9	cDNA, FLJ96850 OS=Homo sapiens PE=2 SV=1	4	0.96	0.99	0.92	7	0.84	0.99	0.85	3	0.87	0.90	0.91	7.22	5.68	4.55
Q9NP79	Vacuolar protein sorting-associated protein VTA1 homolog OS=Homo sapiens GN=VTA1 PE=1 SV=1	4	0.89	1.01	0.94	4	0.97	1.05	1.08	4	0.86	0.91	0.95	6.44	7.60	7.83
Q9BU23	Lipase maturation factor 2 OS=Homo sapiens GN=LMF2 PE=1 SV=2	4	1.03	0.99	1.05	6	1.05	1.06	1.02	5	0.96	0.96	0.92	4.66	5.16	6.58
B4DZF1	cDNA FLJ56541, highly similar to Ubiquilin-2 OS=Homo sapiens PE=2 SV=1	14	0.95	0.92	1.17	11	0.72	0.81	0.84	12	1.24	1.14	1.14	26.50	17.93	17.58
B3KN29	cDNA FLJ13371 fis, clone PLACE1000656, highly similar to PRA1 family protein 2 OS=Homo sapiens PE=2 SV=1	4	1.07	0.97	1.01	4	0.72	0.79	0.68	2	0.93	0.92	0.81	19.49	10.32	19.52

E9PCT1	Serine/arginine repetitive matrix protein 1 OS=Homo sapiens GN=SRRM1 PE=2 SV=2	5	1.00	0.95	0.74	5	1.20	1.24	1.13	4	0.99	0.89	0.93	11.00	18.49	21.31
Q7Z7M4	Superoxide dismutase (Fragment) OS=Homo sapiens GN=SOD2 PE=2 SV=1	7	1.09	0.88	0.78	5	0.82	0.86	0.94	5	0.97	1.02	0.93	13.74	9.62	10.38
Q9NRV9	Heme-binding protein 1 OS=Homo sapiens GN=HEBP1 PE=1 SV=1	4	0.85	1.08	1.14	4	1.07	1.03	0.98	4	0.94	0.91	0.95	11.71	9.01	9.97
B2R6S9	cDNA, FLJ93097, highly similar to Homo sapiens low density lipoprotein receptor-related protein associated protein 1 (LRPAP1), mRNA OS=Homo sapiens PE=2 SV=1	4	1.05	0.84	0.93	3	1.53	1.09	1.45	3	0.91	0.87	0.85	27.71	14.92	30.41
Q53HJ8	PKCI-1-related HIT protein variant (Fragment) OS=Homo sapiens PE=2 SV=1	4	0.89	1.05	0.94	3	0.90	0.97	0.97	3	1.00	1.06	0.99	6.48	4.58	2.81
B4DJP7	Small nuclear ribonucleoprotein Sm D3 OS=Homo sapiens GN=SNRPD3 PE=2 SV=1	7	0.96	0.97	0.98	7	0.88	0.86	0.87	4	0.95	1.05	0.93	4.65	10.35	5.72
Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13 OS=Homo sapiens GN=TIMM13 PE=1 SV=1	6	0.76	1.00	0.95	3	0.72	0.86	0.71	6	0.79	1.01	0.90	4.98	8.70	14.56
P83876	Thioredoxin-like protein 4A OS=Homo sapiens GN=TXNL4A PE=1 SV=1	4	0.92	0.96	0.80	2	0.73	0.79	0.94	3	0.75	0.97	0.81	12.95	11.00	8.93
P11233	Ras-related protein Ral-A OS=Homo sapiens GN=RALA PE=1 SV=1	4	1.10	0.98	0.82	5	1.18	1.19	1.10	4	0.98	0.85	0.95	9.29	16.88	14.39
P09417	Dihydropteridine reductase OS=Homo sapiens GN=QDPR PE=1 SV=2	5	0.88	0.97	0.91	5	1.05	1.21	1.24	6	0.90	1.03	0.90	10.01	11.64	19.11
P62136	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit OS=Homo sapiens GN=PPP1CA PE=1 SV=1	20	0.82	1.21	0.92	21	0.89	0.96	0.95	17	1.00	1.10	0.99	9.61	11.28	3.77
P09471-2	Isoform Alpha-2 of Guanine nucleotide-binding protein G(o) subunit alpha OS=Homo sapiens GN=GNAO1	8	1.00	1.09	1.21	10	0.96	0.96	0.94	10	1.09	1.12	1.02	6.78	8.38	12.83
Q1W6G4	LUC7-like (S. cerevisiae) OS=Homo sapiens GN=LUC7L PE=2 SV=1	8	1.02	1.10	0.90	8	1.06	1.00	0.82	9	0.95	0.96	0.76	5.52	7.22	8.45
B5BU72	Phosphatidylinositol-binding clathrin assembly protein isoform 2 OS=Homo sapiens GN=PICALM PE=2 SV=1	4	0.93	1.48	1.24	5	0.81	0.97	0.77	5	0.86	0.85	0.97	7.19	30.32	24.06
Q6PKC0	GMP reductase OS=Homo sapiens GN=GMPR2 PE=2 SV=1	4	0.93	1.25	1.03	3	1.39	1.33	1.18	3	0.99	0.93	0.96	22.62	18.17	10.73
A8K8X0	cDNA FLJ75187, highly similar to Homo sapiens nap1 P120 OS=Homo sapiens PE=2 SV=1	4	1.04	0.88	1.01	4	1.02	1.10	0.86	4	0.93	0.90	0.71	5.70	13.09	17.30
Q96FV9	THO complex subunit 1 OS=Homo sapiens GN=THOC1 PE=1 SV=1	4	1.06	0.90	0.55	2	1.02	1.06	0.84	3	2.43	1.00	1.81	53.33	8.18	62.20
Q69YG1	Myotrophin OS=Homo sapiens GN=DKFZp761E1322 PE=2 SV=1	7	0.86	1.06	1.04	6	0.99	1.15	1.05	7	0.86	0.90	0.92	7.91	12.63	7.31
Q9BYD2	39S ribosomal protein L9, mitochondrial OS=Homo sapiens GN=MRPL9 PE=1 SV=2	6	1.07	1.10	1.11	5	0.87	0.88	0.93	4	0.84	1.05	0.92	13.80	11.65	10.91
Q13526	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1 OS=Homo sapiens GN=PIN1 PE=1 SV=1	4	1.03	0.96	1.01	4	1.00	0.98	1.06	4	1.06	0.99	0.96	3.14	1.58	4.79
P41208	Centrin-2 OS=Homo sapiens GN=CETN2 PE=1 SV=1	4	1.05	1.03	1.04	2	0.91	1.01	1.04	2	1.04	1.01	1.22	7.80	1.09	9.26

Q6FHY4	N-ethylmaleimide-sensitive factor attachment protein, gamma, isoform CRA_b OS=Homo sapiens GN=NAPG PE=2 SV=1	4	1.30	1.11	1.02	4	0.97	1.05	1.01	3	0.88	1.02	1.02	21.24	4.04	0.66
Q6FGX9	AK1 protein OS=Homo sapiens GN=AK1 PE=2 SV=1	5	1.09	0.96	0.93	6	1.01	1.03	0.96	5	0.86	1.00	0.98	11.94	3.63	2.58
J3QL01	60S ribosomal protein L38 OS=Homo sapiens GN=RPL38 PE=3 SV=1	4	1.06	0.97	0.91	4	0.99	0.99	1.05	4	1.02	0.91	1.05	3.10	4.52	8.12
E5RI99	60S ribosomal protein L30 (Fragment) OS=Homo sapiens GN=RPL30 PE=2 SV=1	11	0.99	0.98	1.06	11	0.98	0.94	0.93	10	1.00	0.95	0.97	1.09	2.11	6.95
B2R4M6	cDNA, FLJ92148, highly similar to Homo sapiens S100 calcium binding protein A9 (calgranulin B) (S100A9), mRNA OS=Homo sapiens PE=4 SV=1	4	1.45	0.91	1.38	4	1.06	0.95	1.36	6	1.00	1.19	1.54	20.57	14.66	6.83
Q9BT22	Chitobiosyldiphosphodolichol beta-mannosyltransferase OS=Homo sapiens GN=ALG1 PE=1 SV=2	4	1.04	1.07	1.10	3	1.08	0.95	1.09	2	0.93	1.09	1.09	7.31	7.53	0.76
Q16186	Proteasomal ubiquitin receptor ADRM1 OS=Homo sapiens GN=ADRM1 PE=1 SV=2	5	1.00	1.07	0.96	4	0.86	1.03	0.89	5	1.04	1.18	1.02	9.59	6.71	6.64
P36639	7,8-dihydro-8-oxoguanine triphosphatase OS=Homo sapiens GN=NUDT1 PE=1 SV=3	4	1.17	1.12	1.35	5	1.00	1.20	1.13	4	1.09	0.96	1.03	7.54	11.47	13.84
O75607	Nucleoplasmin-3 OS=Homo sapiens GN=NPM3 PE=1 SV=3	5	0.84	0.82	0.81	5	1.00	1.16	0.98	3	1.42	1.24	1.15	28.00	20.44	17.74
Q9BS35	GMFB protein OS=Homo sapiens GN=GMFB PE=2 SV=1	4	1.01	0.93	0.93	2	0.81	0.93	0.92	5	0.89	1.00	1.01	11.65	4.45	4.97
Q86Z22	Putative uncharacterized protein OS=Homo sapiens PE=2 SV=1	18	0.91	0.92	1.35	9	0.87	0.87	0.97	8	1.05	1.08	1.10	10.08	11.49	17.27
Q7Z4Y4	GTP:AMP phosphotransferase OS=Homo sapiens PE=2 SV=1	4	0.79	1.01	1.13	3	0.98	0.95	0.98	5	0.78	0.91	0.91	13.64	5.08	11.41
Q59GA0	Thy-1 cell surface antigen variant (Fragment) OS=Homo sapiens PE=2 SV=1	4	1.08	0.99	0.89	3	1.29	1.03	1.08	4	1.31	0.96	1.18	10.41	3.33	13.97
B4DEA6	cDNA FLJ56566, highly similar to Small glutamine-rich tetratricopeptiderepeat-containing protein A OS=Homo sapiens PE=2 SV=1	4	0.84	0.94	0.84	4	0.78	0.91	0.76	5	0.96	1.08	0.94	10.83	9.02	10.62
Q9Y333	U6 snRNA-associated Sm-like protein LSm2 OS=Homo sapiens GN=LSM2 PE=1 SV=1	4	1.11	1.02	0.92	3	1.02	0.90	0.97	4	1.03	0.99	0.97	4.71	6.25	3.09
Q9HB40	Retinoid-inducible serine carboxypeptidase OS=Homo sapiens GN=SCPEP1 PE=1 SV=1	4	0.77	1.03	1.27	3	0.98	1.14	1.00	6	0.84	0.95	0.90	12.62	8.95	17.81
Q8NI22	Multiple coagulation factor deficiency protein 2 OS=Homo sapiens GN=MCFD2 PE=1 SV=1	9	1.33	0.91	1.05	4	1.23	1.16	1.30	4	1.20	1.08	1.12	5.59	12.26	10.92
Q8N5N7	39S ribosomal protein L50, mitochondrial OS=Homo sapiens GN=MRPL50 PE=1 SV=2	6	0.91	0.92	0.81	5	0.87	0.85	0.98	5	0.86	0.76	0.80	3.11	9.17	11.78
Q5RKV6	Exosome complex component MTR3 OS=Homo sapiens GN=EXOSC6 PE=1 SV=1	4	0.69	1.10	1.04	4	0.76	0.85	0.73	3	1.69	2.04	3.09	52.88	47.37	79.15
P51571	Translocon-associated protein subunit delta OS=Homo sapiens GN=SSR4 PE=1 SV=1	7	1.29	1.06	1.46	5	1.18	0.82	1.07	5	1.32	1.14	1.26	6.00	16.28	15.52
O95864	Fatty acid desaturase 2 OS=Homo sapiens GN=FADS2 PE=1 SV=1	4	0.66	0.86	0.65	5	0.95	1.03	1.04	3	0.80	0.80	0.83	17.86	13.46	22.82
O60493	Sorting nexin-3 OS=Homo sapiens GN=SNX3 PE=1 SV=3	4	0.99	1.10	0.99	4	0.84	1.00	0.91	4	0.92	0.97	0.83	8.22	6.51	8.46

O14933	Ubiquitin/ISG15-conjugating enzyme E2 L6 OS=Homo sapiens GN=UBE2L6 PE=1 SV=4	4	0.87	1.16	0.96	5	0.74	0.91	0.78	5	0.90	1.02	1.00	10.54	12.28	12.94
D5MQE1	RQCD1 protein OS=Homo sapiens GN=RQCD1 PE=2 SV=1	4	0.93	0.92	1.32	4	0.98	0.78	1.04	2	1.11	1.23	0.97	9.33	23.95	16.85
Q01081	Splicing factor U2AF 35 kDa subunit OS=Homo sapiens GN=U2AF1 PE=1 SV=3	8	0.71	0.81	0.74	8	1.44	1.09	1.30	8	1.11	0.83	0.96	33.73	16.93	28.11
Q9H773	dCTP pyrophosphatase 1 OS=Homo sapiens GN=DCTPP1 PE=1 SV=1	4	0.89	0.98	1.15	5	0.86	0.91	0.81	3	0.98	1.21	0.98	6.58	15.17	17.24
F1T0F7	Cellular retinoic acid binding protein 1 OS=Homo sapiens GN=CRABP1 PE=2 SV=1	6	0.95	1.24	1.09	5	1.02	1.15	0.93	5	0.74	1.22	0.86	15.83	4.00	12.45
Q53Y03	COX4 neighbor, isoform CRA_a OS=Homo sapiens GN=COX4NB PE=2 SV=1	4	1.74	1.06	1.24	3	0.88	0.83	0.84	2	1.41	1.11	1.19	32.29	14.48	20.13
B3KRY3	cDNA FLJ35079 fis, clone PLACE6005283, highly similar to Lysosome-associated membrane glycoprotein 1 OS=Homo sapiens PE=2 SV=1	5	0.97	0.80	1.16	5	1.09	0.89	1.18	5	0.94	0.91	0.85	8.12	6.90	17.30
Q92979	Ribosomal RNA small subunit methyltransferase NEP1 OS=Homo sapiens GN=EMG1 PE=1 SV=4	4	0.83	0.99	0.93	4	1.18	1.23	1.09	3	0.94	0.81	0.95	18.21	20.85	8.58
Q9NQT5	Exosome complex component RRP40 OS=Homo sapiens GN=EXOSC3 PE=1 SV=3	6	1.15	1.26	0.94	5	1.10	1.74	1.21	3	0.55	0.60	0.81	35.52	47.59	20.35
Q53EW7	Branched-chain-amino-acid aminotransferase (Fragment) OS=Homo sapiens PE=2 SV=1	5	0.94	0.87	0.74	3	1.12	1.21	1.11	4	1.11	1.03	1.09	9.70	16.35	21.32
P30049	ATP synthase subunit delta, mitochondrial OS=Homo sapiens GN=ATP5D PE=1 SV=2	9	1.30	0.91	1.21	7	1.61	0.99	1.17	8	1.62	1.04	1.25	11.93	6.82	3.15
Q76LA1	CSTB protein OS=Homo sapiens GN=CSTB PE=2 SV=1	5	0.99	0.97	0.96	5	1.24	1.09	1.09	3	1.06	1.05	0.95	12.07	5.62	7.73
A6NDU8	UPF0600 protein C5orf51 OS=Homo sapiens GN=C5orf51 PE=1 SV=1	4	1.05	1.07	0.95	2	1.01	1.09	1.01	3	0.93	0.91	0.87	6.06	9.49	7.31
Q9NPD3	Exosome complex component RRP41 OS=Homo sapiens GN=EXOSC4 PE=1 SV=3	5	1.61	1.12	1.39	2	1.03	1.11	1.17	3	2.27	1.31	2.02	37.92	9.63	28.98
B4E0N6	cDNA FLJ56280, highly similar to Endoplasmic reticulum-Golgi intermediate compartment protein 1 OS=Homo sapiens PE=2 SV=1	6	1.25	0.95	1.18	3	1.13	0.99	1.05	4	1.21	1.06	1.21	4.93	5.21	7.37
Q9UBV2	Protein sel-1 homolog 1 OS=Homo sapiens GN=SEL1L PE=1 SV=3	6	1.22	0.66	1.15	5	1.09	0.87	0.97	4	1.22	0.88	1.06	6.50	15.31	8.21
B3KVH4	cDNA FLJ16549 fis, clone PLACE7003657, highly similar to RAC-alpha serine/threonine-protein kinase (EC 2.7.11.1) OS=Homo sapiens PE=2 SV=1	5	0.93	0.91	0.80	2	1.08	1.07	0.89	6	0.91	0.92	1.01	9.54	9.32	11.61
B4DEM9	cDNA FLJ52257, highly similar to Polymerase delta-interacting protein 2 OS=Homo sapiens PE=2 SV=1	4	0.63	1.12	1.10	4	0.80	1.02	0.88	2	0.92	0.87	1.01	18.08	12.75	11.06
B3KUH0	cDNA FLJ39883 fis, clone SPLEN2016268, highly similar to Protein CHMP7 OS=Homo sapiens PE=2 SV=1	5	0.86	1.05	0.78	3	0.97	1.13	1.11	3	1.28	0.96	0.92	21.03	8.03	17.78
Q9NW13	RNA-binding protein 28 OS=Homo sapiens GN=RBM28 PE=1 SV=3	7	1.25	0.99	0.89	3	1.07	0.88	1.15	4	1.01	0.86	1.12	11.49	7.54	13.51
Q9NX20	39S ribosomal protein L16, mitochondrial OS=Homo sapiens GN=MRPL16 PE=1 SV=1	5	0.79	1.04	0.97	5	1.08	1.06	1.00	4	1.00	0.91	1.13	15.17	8.20	8.01
P20645	Cation-dependent mannose-6-phosphate receptor OS=Homo sapiens GN=M6PR PE=1 SV=1	5	1.35	1.11	1.24	4	0.91	0.84	0.93	3	0.89	0.99	0.94	24.38	13.92	16.96

Q9UMX5	Neudesin OS=Homo sapiens GN=NENF PE=1 SV=1	4	1.15	0.99	1.19	3	1.18	0.94	1.04	4	1.12	1.21	1.22	2.82	13.64	8.23
P82979	SAP domain-containing ribonucleoprotein OS=Homo sapiens GN=SARNP PE=1 SV=3	4	0.89	0.98	0.97	4	1.19	1.06	1.06	4	1.00	1.07	1.02	15.12	4.65	4.47
Q96HY6	DDRGK domain-containing protein 1 OS=Homo sapiens GN=DDRGK1 PE=1 SV=2	5	1.34	0.83	1.01	4	0.84	0.88	0.97	4	0.92	0.86	0.79	25.80	3.17	12.24
Q86TU7	Histone-lysine N-methyltransferase setd3 OS=Homo sapiens GN=SETD3 PE=1 SV=1	4	0.83	0.90	0.98	4	1.09	0.97	1.00	5	0.98	0.98	0.99	13.66	4.75	0.89
O00422	Histone deacetylase complex subunit SAP18 OS=Homo sapiens GN=SAP18 PE=1 SV=1	4	1.05	1.05	1.09	4	0.96	0.79	0.79	4	1.25	1.55	1.28	13.58	34.04	23.55
P50583	Bis(5'-nucleosyl)-tetraphosphatase [asymmetrical] OS=Homo sapiens GN=NUDT2 PE=1 SV=3	4	0.97	0.95	0.94	4	0.96	0.99	0.98	4	0.81	0.90	0.85	9.95	5.20	7.59
Q9H3K6	BolA-like protein 2 OS=Homo sapiens GN=BOLA2 PE=1 SV=1	8	0.93	1.04	0.94	5	0.98	1.05	1.01	6	1.00	1.00	1.01	3.44	2.96	4.12
O60869	Endothelial differentiation-related factor 1 OS=Homo sapiens GN=EDF1 PE=1 SV=1	5	0.91	0.96	0.80	2	0.97	1.20	1.02	3	0.88	0.94	0.97	5.11	14.13	12.25
Q9NZ45	CDGSH iron-sulfur domain-containing protein 1 OS=Homo sapiens GN=CISD1 PE=1 SV=1	4	1.32	0.97	1.17	4	1.30	1.07	1.19	4	1.27	1.01	1.28	2.22	5.11	5.08
Q15269	Periodic tryptophan protein 2 homolog OS=Homo sapiens GN=PWP2 PE=1 SV=2	5	1.21	1.14	1.23	7	0.84	0.82	0.87	5	1.06	1.15	0.99	18.10	18.18	17.67
Q8TD30	Alanine aminotransferase 2 OS=Homo sapiens GN=GPT2 PE=1 SV=1	4	1.04	0.83	0.68	6	0.86	0.96	1.00	3	1.00	1.02	1.11	9.89	10.07	24.09
Q96G95	BCKDK protein OS=Homo sapiens GN=BCKDK PE=2 SV=1	4	0.94	0.99	0.91	2	0.94	1.12	0.85	3	0.86	0.89	1.27	5.16	11.82	22.35
Q5SRQ6	Casein kinase 2, beta polypeptide, isoform CRA_d OS=Homo sapiens GN=CSNK2B PE=2 SV=2	6	1.00	1.02	1.03	4	0.89	0.93	0.90	6	0.99	1.11	0.93	6.22	8.81	7.36
A8MZF9	Developmentally-regulated GTP-binding protein 2 OS=Homo sapiens GN=DRG2 PE=2 SV=1	4	0.90	0.77	0.90	3	0.87	1.04	1.06	3	1.02	1.06	1.25	8.21	16.71	16.09
Q9UI26	Importin-11 OS=Homo sapiens GN=IPO11 PE=1 SV=1	5	0.93	1.09	1.38	4	1.04	1.11	0.92	5	0.97	0.94	1.16	5.71	9.14	19.83
Q70UQ0-4	Isoform 4 of Inhibitor of nuclear factor kappa-B kinase-interacting protein OS=Homo sapiens GN=IKBIP	6	1.16	1.06	1.18	5	1.36	1.21	1.34	6	1.38	1.08	1.30	9.37	7.01	6.45
A8K5D5	cDNA FLJ76832, highly similar to Homo sapiens mitochondrial ribosomal protein L19 (MRPL19), mRNA OS=Homo sapiens PE=2 SV=1	4	1.13	0.97	1.35	4	0.86	0.93	0.98	4	0.82	0.91	0.81	18.23	3.45	26.30
Q53GG3	Sorting nexin 2 variant (Fragment) OS=Homo sapiens PE=2 SV=1	5	1.01	1.05	1.33	4	0.97	1.02	0.98	3	0.78	1.09	0.83	13.08	3.69	24.36
Q0VDG5	SCRN3 protein OS=Homo sapiens GN=SCRN3 PE=2 SV=1	4	1.22	1.22	1.89	5	1.01	1.02	0.97	2	0.87	0.92	0.89	16.72	14.34	44.15
Q0VAB1	Translocase of inner mitochondrial membrane 50 homolog (S. cerevisiae) OS=Homo sapiens GN=TIMM50 PE=2 SV=1	4	1.10	1.06	1.21	4	1.09	0.92	0.96	4	1.19	1.10	1.12	4.62	8.95	11.58
E5RHG8	Transcription elongation factor B polypeptide 1 (Fragment) OS=Homo sapiens GN=TCEB1 PE=2 SV=1	7	0.81	0.99	0.94	8	0.93	0.95	0.90	5	0.93	1.09	0.94	7.59	6.72	2.66
A8K097	cDNA FLJ78373, highly similar to Homo sapiens PCI domain containing 2, mRNA OS=Homo sapiens PE=2 SV=1	4	0.93	1.06	0.92	5	1.11	1.14	1.09	3	0.94	0.91	0.76	10.22	11.26	17.90

O00743	Serine/threonine-protein phosphatase 6 catalytic subunit OS=Homo sapiens GN=PPP6C PE=1 SV=1	5	1.08	1.03	0.98	3	0.69	0.78	0.81	3	1.15	1.03	1.04	25.25	15.03	12.67
Q9NVH1	DnaJ homolog subfamily C member 11 OS=Homo sapiens GN=DNAJC11 PE=1 SV=2	5	1.16	1.01	0.86	6	0.90	1.05	1.14	10	1.42	1.04	1.25	22.36	2.02	18.20
Q59GX2	Solute carrier family 2 (Facilitated glucose transporter), member 1 variant (Fragment) OS=Homo sapiens PE=2 SV=1	4	1.14	1.00	1.17	5	1.25	0.86	1.13	4	1.27	0.91	1.23	5.78	7.22	4.34
Q59ET7	Thioredoxin reductase 2 isoform 1 variant (Fragment) OS=Homo sapiens PE=2 SV=1	6	1.09	0.91	1.07	2	0.85	0.72	0.81	3	0.73	0.85	0.72	20.87	11.56	20.89
O60502	Bifunctional protein NCOAT OS=Homo sapiens GN=MGEA5 PE=1 SV=2	5	1.31	0.83	1.30	5	1.12	1.00	1.09	3	1.06	1.00	1.13	11.34	10.67	9.75
Q59FC3	G protein-coupled receptor kinase interactor 1 variant (Fragment) OS=Homo sapiens PE=2 SV=1	7	0.91	1.22	0.85	7	0.98	0.94	1.04	2	1.32	1.43	1.51	20.59	20.32	30.12
Q9P0I2	ER membrane protein complex subunit 3 OS=Homo sapiens GN=EMC3 PE=1 SV=3	4	1.13	0.83	0.94	5	1.23	1.26	1.37	6	1.11	0.87	1.03	5.61	24.20	20.52
Q96GD0	Pyridoxal phosphate phosphatase OS=Homo sapiens GN=PDXP PE=1 SV=2	5	1.06	1.02	1.03	4	0.71	0.82	0.67	4	0.76	0.80	0.92	22.19	13.73	21.28
Q8N5K1	CDGSH iron-sulfur domain-containing protein 2 OS=Homo sapiens GN=CISD2 PE=1 SV=1	4	1.28	1.04	1.17	4	1.09	0.97	1.07	5	1.20	1.04	1.19	7.75	3.70	5.24
Q08209	Serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform OS=Homo sapiens GN=PPP3CA PE=1 SV=1	6	0.92	1.07	1.27	5	1.00	0.95	1.02	4	1.08	1.11	1.36	7.79	7.63	14.52
Q9UN37	Vacuolar protein sorting-associated protein 4A OS=Homo sapiens GN=VPS4A PE=1 SV=1	6	1.21	1.02	1.16	3	1.21	1.18	1.22	4	0.82	0.99	0.97	20.74	9.71	11.94
P49006	MARCKS-related protein OS=Homo sapiens GN=MARCKSL1 PE=1 SV=2	19	1.04	1.33	0.84	7	0.46	0.87	0.98	10	1.58	0.83	0.75	54.79	27.57	13.60
P28070	Proteasome subunit beta type-4 OS=Homo sapiens GN=PSMB4 PE=1 SV=4	10	0.92	0.88	1.07	7	0.79	0.95	1.00	6	0.90	0.92	1.03	7.98	3.68	3.35
Q53H56	Ubiquitin carboxyl-terminal hydrolase (Fragment) OS=Homo sapiens PE=2 SV=1	6	1.29	1.08	1.29	5	0.82	0.70	0.79	6	1.11	0.79	0.84	21.85	22.97	28.29
Q6UW63	KDEL motif-containing protein 1 OS=Homo sapiens GN=KDELC1 PE=1 SV=1	4	1.49	0.96	1.24	3	1.15	1.03	1.17	2	1.09	0.93	1.03	17.40	5.47	9.07
H7BYT1	Casein kinase I isoform delta OS=Homo sapiens GN=CSNK1D PE=2 SV=2	5	1.00	1.01	0.82	3	1.01	1.13	0.97	5	0.89	0.94	0.86	6.88	9.64	8.88
Q9UIU0	Dihydropyridine receptor alpha 2 subunit OS=Homo sapiens GN=CACNA2D1 PE=4 SV=1	4	1.19	0.97	1.05	3	1.06	1.04	1.05	2	1.03	1.20	1.15	7.72	11.13	5.16
Q8TDR3	DEAD-box corepressor DP103 OS=Homo sapiens GN=DDX20 PE=2 SV=1	5	1.06	1.10	1.11	4	0.69	0.78	0.87	3	0.87	0.98	0.89	21.01	16.99	14.28
B4DJQ8	cDNA FLJ55694, highly similar to Dipeptidyl-peptidase 1 (EC 3.4.14.1) OS=Homo sapiens PE=2 SV=1	6	1.23	1.06	1.24	8	1.18	1.04	1.01	5	1.14	1.18	1.03	3.67	6.70	11.95
Q12800	Alpha-globin transcription factor CP2 OS=Homo sapiens GN=TFCP2 PE=1 SV=2	4	1.04	0.90	1.31	5	1.15	1.09	1.20	4	1.06	1.15	1.05	5.51	12.34	11.21
Q96EK5	KIF1-binding protein OS=Homo sapiens GN=KIAA1279 PE=1 SV=1	4	0.96	0.86	0.94	4	0.93	0.93	1.02	5	0.94	1.05	0.86	1.40	10.55	8.34

Q9NPH2	Inositol-3-phosphate synthase 1 OS=Homo sapiens GN=ISYNA1 PE=1 SV=1	5	0.99	1.20	1.25	3	0.91	1.14	1.12	4	0.99	1.08	1.09	4.85	5.40	7.30
B3KM89	cDNA FLJ10528 fis, clone NT2RP2000943, highly similar to Protein transport protein Sec24D OS=Homo sapiens PE=2 SV=1	7	1.23	0.92	0.81	9	1.18	0.98	1.19	4	1.03	0.94	1.08	8.98	3.44	18.98
Q8N523	Tuftelin-interacting protein 11 OS=Homo sapiens GN=TFIP11 PE=2 SV=1	5	1.09	0.97	1.18	3	1.25	0.55	0.81	5	0.93	1.03	0.88	14.53	30.93	20.91
Q9UK61	Protein FAM208A OS=Homo sapiens GN=FAM208A PE=1 SV=3	4	0.89	1.18	0.91	5	1.09	1.11	1.02	3	0.94	1.01	0.94	10.63	7.71	5.54
B7Z475	cDNA FLJ55712, highly similar to F-box-like/WD repeat protein TBL1XR1 OS=Homo sapiens PE=2 SV=1	5	1.05	1.01	1.20	3	1.40	0.88	1.03	2	0.83	1.02	0.91	26.62	8.25	13.71
Q5TB52	3'-phosphoadenosine 5'-phosphosulfate synthase 2, isoform CRA_b OS=Homo sapiens GN=PAPSS2 PE=2 SV=1	4	1.10	0.86	0.81	3	1.11	1.14	1.13	3	1.20	1.07	1.02	4.67	14.44	16.36
O60888	Protein CutA OS=Homo sapiens GN=CUTA PE=1 SV=2	8	1.09	1.09	1.21	7	0.91	0.90	0.93	10	0.99	1.05	1.00	8.95	9.65	14.02
Q53FA7	Quinone oxidoreductase PIG3 OS=Homo sapiens GN=TP53I3 PE=1 SV=2	5	1.00	1.01	0.79	5	1.10	1.18	1.18	5	1.17	1.07	0.96	7.92	7.74	19.86
Q7L523	Ras-related GTP-binding protein A OS=Homo sapiens GN=RRAGA PE=1 SV=1	4	1.17	1.27	1.00	3	1.05	1.15	1.17	2	0.93	0.96	1.09	11.19	13.57	8.22
Q96HY7	Probable 2-oxoglutarate dehydrogenase E1 component DHKTD1, mitochondrial OS=Homo sapiens GN=DHTKD1 PE=1 SV=2	5	1.00	0.77	0.73	2	0.85	1.15	1.17	5	1.00	0.92	1.07	9.23	20.02	23.16
Q07812	Apoptosis regulator BAX OS=Homo sapiens GN=BAX PE=1 SV=1	5	1.15	0.98	1.35	5	0.91	0.79	0.95	5	1.10	1.23	1.14	12.15	21.72	17.39
B5MCF9	Pescadillo homolog OS=Homo sapiens GN=PES1 PE=2 SV=1	4	0.84	0.99	0.93	5	0.96	1.00	1.05	4	1.25	1.10	1.51	20.67	6.10	26.10
A1X283	SH3 and PX domain-containing protein 2B OS=Homo sapiens GN=SH3PXD2B PE=1 SV=3	3	0.92	1.16	1.02	4	0.78	0.97	0.79	3	0.99	0.96	0.94	11.87	11.38	12.66
P42858	Huntingtin OS=Homo sapiens GN=HTT PE=1 SV=2	5	1.20	1.07	0.92	4	0.91	1.04	0.98	4	0.92	0.97	0.93	16.59	5.15	3.29
F5H157	Ras-related protein Rab-35 (Fragment) OS=Homo sapiens GN=RAB35 PE=2 SV=1	6	0.76	0.92	0.80	4	0.95	0.88	0.96	4	0.89	0.93	0.95	11.15	2.64	9.75
Q8IW24	Exocyst complex component 5 OS=Homo sapiens GN=EXOC5 PE=2 SV=1	4	0.96	1.01	1.04	4	1.01	1.20	1.06	5	0.97	0.90	0.91	2.90	14.64	7.78
Q9BWJ5	Splicing factor 3B subunit 5 OS=Homo sapiens GN=SF3B5 PE=1 SV=1	4	1.00	0.99	0.87	2	0.98	0.98	0.95	5	1.10	1.08	0.98	6.27	5.57	6.10
Q9BQ95	Evolutionarily conserved signaling intermediate in Toll pathway, mitochondrial OS=Homo sapiens GN=ECSIT PE=1 SV=1	4	0.72	0.83	1.01	7	0.82	0.85	0.82	6	1.05	1.14	1.00	19.26	18.75	11.06
Q5TDG3	WD repeat domain 3, isoform CRA_b OS=Homo sapiens GN=WDR3 PE=2 SV=1	4	1.02	1.16	1.13	5	0.91	1.07	1.03	4	0.86	0.90	0.86	8.96	12.58	13.79
Q5VU08	Adducin 3 (Gamma), isoform CRA_a OS=Homo sapiens GN=ADD3 PE=2 SV=1	5	1.14	0.97	0.99	3	0.69	0.82	0.83	3	1.03	1.07	0.78	24.38	13.05	12.45
B2R823	cDNA, FLJ93703, highly similar to Homo sapiens putatative 28 kDa protein (LOC56902), mRNA OS=Homo sapiens PE=2 SV=1	4	1.23	1.33	1.16	3	0.90	1.02	0.90	4	0.46	0.96	0.76	44.68	17.92	22.11

Q4W5L2	Putative uncharacterized protein SNCA (Fragment) OS=Homo sapiens GN=SNCA PE=2 SV=1	4	1.17	0.73	0.92	3	0.99	1.20	1.03	2	1.25	0.90	1.04	11.45	25.34	6.83
Q6P587	Acylpyruvase FAHD1, mitochondrial OS=Homo sapiens GN=FAHD1 PE=1 SV=2	4	0.96	0.92	0.90	5	0.83	0.88	0.91	2	1.03	1.06	1.04	10.51	10.03	7.93
Q9UJW0	Dynactin subunit 4 OS=Homo sapiens GN=DCTN4 PE=1 SV=1	5	0.71	0.73	0.81	4	0.75	1.03	0.72	2	0.89	1.16	1.07	12.31	22.46	20.81
O75884	Putative hydrolase RBBP9 OS=Homo sapiens GN=RBBP9 PE=1 SV=2	4	1.06	1.08	0.84	2	0.94	1.08	1.00	2	0.97	1.06	1.09	5.98	1.03	12.57
J3QRN6	Unconventional myosin-Id OS=Homo sapiens GN=MYO1D PE=4 SV=1	5	1.27	1.01	1.07	8	1.16	0.83	1.28	7	1.09	0.88	1.16	7.54	10.01	8.95
Q5VIR6-4	Isoform 4 of Vacuolar protein sorting-associated protein 53 homolog OS=Homo sapiens GN=VPS53	4	1.03	0.84	0.99	2	0.91	1.09	1.03	4	0.96	1.00	0.96	6.22	12.82	3.55
P14927	Cytochrome b-c1 complex subunit 7 OS=Homo sapiens GN=UQCRB PE=1 SV=2	4	1.11	0.91	0.96	4	1.53	1.45	1.62	6	1.17	1.28	0.79	17.89	22.60	38.91
Q7Z7L8	Uncharacterized protein C11orf96 OS=Homo sapiens GN=C11orf96 PE=1 SV=3	6	0.76	0.93	1.04	4	0.61	0.87	0.71	4	0.53	0.94	0.64	18.24	3.92	26.87
F5CTF3	Deoxynucleoside kinase OS=Homo sapiens PE=2 SV=1	4	1.00	1.07	1.18	3	1.10	1.20	0.91	5	0.87	0.83	0.88	11.53	18.32	16.55
Q86YB2	DEAH (Asp-Glu-Ala-His) box polypeptide 8 OS=Homo sapiens GN=DHX8 PE=2 SV=2	5	0.71	1.04	0.77	2	0.67	0.91	0.66	2	1.80	0.79	1.26	60.35	13.86	35.87
Q9H7N4	Splicing factor, arginine/serine-rich 19 OS=Homo sapiens GN=SCAF1 PE=1 SV=3	5	0.50	0.81	0.72	3	0.81	0.77	0.73	4	0.85	0.86	0.77	26.83	5.34	3.84
Q969N2	GPI transamidase component PIG-T OS=Homo sapiens GN=PIGT PE=1 SV=1	4	0.94	0.87	0.96	4	1.18	1.13	1.14	4	1.10	0.94	0.98	10.95	13.61	9.59
E9PN17	ATP synthase subunit g, mitochondrial OS=Homo sapiens GN=ATP5L PE=2 SV=1	5	1.45	1.01	1.34	6	1.42	0.92	1.15	7	1.44	1.06	1.32	1.31	7.51	8.56
K7EQ03	RNA-binding protein 42 OS=Homo sapiens GN=RBM42 PE=4 SV=1	4	0.78	1.00	0.89	4	0.86	0.87	0.90	3	0.99	1.13	0.87	12.00	12.88	1.70
E9PH64	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9 OS=Homo sapiens GN=NDUFB9 PE=2 SV=1	4	1.28	0.90	1.19	4	1.03	0.90	0.96	3	1.29	1.04	1.06	12.38	8.68	10.84
Q6GMV3	Putative peptidyl-tRNA hydrolase PTRHD1 OS=Homo sapiens GN=PTRHD1 PE=1 SV=1	9	1.04	0.85	0.73	4	1.21	1.17	0.95	4	1.01	0.98	0.96	9.87	16.09	14.53
Q68DQ4	Putative uncharacterized protein DKFZp779L0468 OS=Homo sapiens GN=DKFZp779L0468 PE=2 SV=1	5	0.98	0.91	0.81	8	0.92	0.97	1.01	5	1.14	1.10	1.14	11.55	10.09	16.66
Q9Y5Q9	General transcription factor 3C polypeptide 3 OS=Homo sapiens GN=GTF3C3 PE=1 SV=1	6	0.75	0.83	0.81	4	0.89	0.97	0.99	3	1.03	0.96	0.91	15.77	8.89	9.86
Q8IY95	Transmembrane protein 192 OS=Homo sapiens GN=TMEM192 PE=1 SV=1	4	1.01	0.96	1.09	3	0.84	0.69	0.80	2	1.36	1.08	0.90	24.64	21.70	15.62
B2R9A0	cDNA, FLJ94294, highly similar to Homo sapiens cyclin-dependent kinase 4 (CDK4), mRNA OS=Homo sapiens PE=2 SV=1	4	0.91	1.11	0.94	3	0.94	0.97	0.87	2	0.98	1.03	0.79	3.58	6.71	8.34
Q9Y4R8	Telomere length regulation protein TEL2 homolog OS=Homo sapiens GN=TELO2 PE=1 SV=2	4	1.01	1.14	1.21	4	1.31	1.00	0.88	2	1.08	1.43	0.83	13.82	18.56	21.20
Q6FIA3	PACSIN2 protein OS=Homo sapiens GN=PACSIN2 PE=2 SV=1	4	0.99	0.83	0.91	3	1.09	1.15	1.66	2	0.93	0.23	0.19	8.03	62.97	79.79

B4DP11	Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 PE=2 SV=1	10	0.85	1.04	0.99	9	0.89	1.03	0.91	7	0.84	0.97	0.94	2.78	3.88	4.13
Q13619	Cullin-4A OS=Homo sapiens GN=CUL4A PE=1 SV=3	8	0.97	1.00	1.22	7	0.77	1.02	1.20	6	0.84	1.07	0.83	11.61	3.54	20.29
A8K8L7	Calcium binding protein 39, isoform CRA_a OS=Homo sapiens GN=CAB39 PE=2 SV=1	5	0.90	1.13	1.27	2	0.97	0.88	0.97	4	0.93	1.07	1.01	3.77	12.96	15.00
Q15031	Probable leucine--tRNA ligase, mitochondrial OS=Homo sapiens GN=LARS2 PE=1 SV=2	4	1.06	1.07	0.84	5	0.83	1.01	0.95	5	1.00	1.11	1.02	12.52	4.98	9.70
Q9BVP2	Guanine nucleotide-binding protein-like 3 OS=Homo sapiens GN=GNL3 PE=1 SV=2	5	1.05	1.16	0.93	4	0.85	1.19	1.13	3	0.92	0.77	0.97	10.81	22.47	10.41
Q6IB54	ATP synthase-coupling factor 6, mitochondrial OS=Homo sapiens GN=ATP5J PE=2 SV=1	4	1.57	1.00	1.26	6	1.24	0.81	1.11	3	1.19	0.96	1.08	15.69	10.89	8.60
Q9NZ32	Actin-related protein 10 OS=Homo sapiens GN=ACTR10 PE=1 SV=1	5	0.93	1.13	1.30	4	0.93	1.03	0.93	3	0.81	1.04	0.76	7.73	5.29	27.67
Q96HS1	Serine/threonine-protein phosphatase PGAM5, mitochondrial OS=Homo sapiens GN=PGAM5 PE=1 SV=2	3	0.88	0.73	0.78	5	1.23	1.16	1.16	2	1.09	1.02	0.98	16.35	22.79	19.52
Q8TBI1	Monoamine oxidase B OS=Homo sapiens GN=MAOB PE=2 SV=1	7	1.51	1.20	1.09	5	1.21	1.02	0.93	6	0.98	0.84	0.78	21.68	17.47	16.53
Q96JB5	CDK5 regulatory subunit-associated protein 3 OS=Homo sapiens GN=CDK5RAP3 PE=1 SV=2	6	0.86	0.96	1.02	6	0.96	0.98	1.01	6	1.01	1.10	1.06	8.49	7.90	2.69
Q9H8S9	MOB kinase activator 1A OS=Homo sapiens GN=MOB1A PE=1 SV=4	5	1.07	1.04	0.85	3	1.12	1.04	1.07	2	1.26	1.05	1.13	8.79	0.65	14.75
J3KN29	26S proteasome non-ATPase regulatory subunit 9 OS=Homo sapiens GN=PSMD9 PE=4 SV=1	4	0.79	0.97	1.12	4	1.02	0.88	1.11	3	1.03	1.16	1.12	14.37	14.58	0.34
K7EQZ6	Hepatoma-derived growth factor-related protein 2 OS=Homo sapiens GN=HDGFRP2 PE=4 SV=1	5	0.83	0.77	0.70	4	1.14	1.57	1.28	5	1.07	1.09	0.73	15.93	34.86	35.90
B0S7P4	cDNA, FLJ92156, Homo sapiens mitochondrial ribosomal protein S18B (MRPS18B),nuclear gene encoding mitochondrial protein, mRNA OS=Homo sapiens PE=2 SV=1	4	0.98	1.03	1.18	3	1.18	1.04	0.94	3	0.99	1.04	0.93	10.59	0.49	13.89
B2R7U5	cDNA, FLJ93607 OS=Homo sapiens PE=2 SV=1	5	1.17	0.96	0.56	5	0.94	0.82	1.27	6	0.77	0.92	0.88	21.16	8.14	39.37
P49366	Deoxyhypusine synthase OS=Homo sapiens GN=DHPS PE=1 SV=1	3	0.93	1.17	0.93	3	0.70	0.87	0.73	5	1.15	1.15	1.05	24.28	15.75	17.85
Q9BSH4	Translational activator of cytochrome c oxidase 1 OS=Homo sapiens GN=TACO1 PE=1 SV=1	5	1.04	1.10	1.13	2	1.69	1.28	1.45	2	0.83	0.94	0.83	37.74	15.18	27.07
B2R8W8	cDNA, FLJ94098, highly similar to Homo sapiens RAB3D, member RAS oncogene family (RAB3D), mRNA OS=Homo sapiens PE=2 SV=1	5	0.99	0.92	0.95	2	1.04	0.99	0.96	3	0.94	0.95	0.83	5.07	3.60	8.01
Q549N0	Cofilin 2 (Muscle), isoform CRA_a OS=Homo sapiens GN=CFL2 PE=2 SV=1	31	0.91	1.01	1.02	22	0.96	0.95	0.97	29	1.03	1.07	1.35	6.16	6.15	18.27
Q9NP97	Dynein light chain roadblock-type 1 OS=Homo sapiens GN=DYNLRB1 PE=1 SV=3	9	1.14	1.28	0.99	4	0.99	1.23	1.35	4	1.03	0.97	1.13	7.26	14.75	15.60
F8WBK5	39S ribosomal protein L40, mitochondrial OS=Homo sapiens GN=MRPL40 PE=2 SV=1	4	1.35	1.18	1.09	4	1.14	1.11	0.96	4	1.06	1.23	1.23	12.80	5.19	12.37
O43583	Density-regulated protein OS=Homo sapiens GN=DENR PE=1 SV=2	4	0.99	0.90	1.04	4	0.89	0.96	0.97	3	1.04	1.11	1.06	7.57	10.85	4.87

Q6ZRP7	Sulfhydryl oxidase 2 OS=Homo sapiens GN=QSOX2 PE=1 SV=3	3	0.86	0.75	0.81	5	0.95	0.80	1.05	4	0.95	0.95	1.02	5.56	12.06	13.99
Q8TCJ2	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B OS=Homo sapiens GN=STT3B PE=1 SV=1	4	1.40	0.97	1.23	4	1.30	0.77	1.25	4	1.15	0.96	0.89	9.68	12.83	17.72
Q9NVV4-2	Isoform 2 of Poly(A) RNA polymerase, mitochondrial OS=Homo sapiens GN=MTPAP	4	1.04	1.06	1.36	2	0.75	0.65	0.95	2	0.65	0.93	0.92	24.93	23.57	22.81
Q96FJ2	Dynein light chain 2, cytoplasmic OS=Homo sapiens GN=DYNLL2 PE=1 SV=1	6	0.80	1.05	0.88	6	0.83	0.98	0.82	4	1.04	1.12	1.05	14.60	6.51	13.04
P23378	Glycine dehydrogenase [decarboxylating], mitochondrial OS=Homo sapiens GN=GLDC PE=1 SV=2	5	1.15	1.19	1.09	7	0.81	1.02	0.92	3	0.75	0.90	0.69	23.57	14.02	22.23
B3KNK4	Phosphatidate cytidylyltransferase OS=Homo sapiens PE=2 SV=1	4	0.97	1.03	0.86	5	1.10	0.82	0.99	4	1.16	1.02	1.00	9.14	12.48	8.13
F5H0B0	Tumor protein D52 OS=Homo sapiens GN=TPD52 PE=2 SV=1	4	1.20	1.13	1.05	4	0.97	1.05	1.12	2	1.01	0.91	0.82	11.49	10.97	15.69
Q8NBF2	NHL repeat-containing protein 2 OS=Homo sapiens GN=NHLRC2 PE=1 SV=1	5	0.99	0.83	0.97	9	1.00	1.06	0.99	7	0.96	1.07	1.05	2.27	14.04	4.40
B2R6W1	cDNA, FLJ93143, highly similar to Homo sapiens complement component 7 (C7), mRNA OS=Homo sapiens PE=2 SV=1	4	1.04	0.99	1.18	2	0.89	0.98	0.94	4	1.40	0.94	1.24	23.72	2.88	14.14
F5H2U2	Serine/threonine-protein kinase PRP4 homolog OS=Homo sapiens GN=PRPF4B PE=2 SV=1	4	1.10	1.03	0.99	6	1.29	1.07	1.12	4	0.96	0.98	1.00	14.90	4.23	6.94
Q13505	Metaxin-1 OS=Homo sapiens GN=MTX1 PE=1 SV=2	4	1.30	0.85	1.11	6	1.13	0.93	1.23	3	1.25	0.88	1.01	6.92	4.42	10.01
Q9HBR0	Putative sodium-coupled neutral amino acid transporter 10 OS=Homo sapiens GN=SLC38A10 PE=1 SV=2	4	1.53	1.28	1.32	3	0.87	0.60	0.94	3	1.07	0.90	1.13	29.26	36.44	17.00
Q9BVJ7	Dual specificity protein phosphatase 23 OS=Homo sapiens GN=DUSP23 PE=1 SV=1	3	1.08	1.16	1.17	5	1.04	1.20	1.14	4	0.99	1.23	1.01	4.04	2.78	7.65
Q8IWA5	Choline transporter-like protein 2 OS=Homo sapiens GN=SLC44A2 PE=1 SV=3	4	1.16	1.09	0.80	3	1.41	1.18	1.24	3	1.20	0.96	1.22	10.73	10.34	22.91
R4GMU1	GDH/6PGL endoplasmic bifunctional protein OS=Homo sapiens GN=H6PD PE=4 SV=1	3	1.18	1.20	1.13	5	1.07	1.01	1.07	4	1.63	1.41	1.84	22.93	16.60	31.78
Q96HW7	Integrator complex subunit 4 OS=Homo sapiens GN=INTS4 PE=1 SV=2	3	1.87	0.82	1.65	6	1.14	0.88	1.22	3	0.70	0.54	0.68	47.56	24.21	41.16
Q9BYD1	39S ribosomal protein L13, mitochondrial OS=Homo sapiens GN=MRPL13 PE=1 SV=1	4	0.94	1.07	1.15	3	1.05	1.02	1.02	4	1.01	0.99	0.89	5.50	3.87	12.72
Q96A72	Protein mago nashi homolog 2 OS=Homo sapiens GN=MAGOHB PE=1 SV=1	4	0.83	0.94	0.48	4	1.08	1.06	1.07	4	0.91	0.97	0.84	13.43	6.08	37.31
B4DVZ5	cDNA FLJ53481, highly similar to Nucleolar autoantigen No55 OS=Homo sapiens PE=2 SV=1	3	1.23	0.96	1.15	3	1.15	1.10	1.08	5	0.95	1.16	1.11	12.83	9.53	3.01
Q96L92	Sorting nexin-27 OS=Homo sapiens GN=SNX27 PE=1 SV=2	4	1.04	1.09	1.02	3	1.08	1.02	1.05	3	0.93	0.91	1.06	7.48	9.06	2.16
P42126	Enoyl-CoA delta isomerase 1, mitochondrial OS=Homo sapiens GN=ECI1 PE=1 SV=1	4	0.82	1.05	1.06	4	0.93	0.96	0.97	5	0.99	1.22	1.35	9.85	12.34	17.37
B2RAY1	cDNA, FLJ95184, highly similar to Homo sapiens signal transducing adaptor molecule (SH3 domain and ITAM motif) 1 (STAM), mRNA OS=Homo sapiens PE=2 SV=1	3	1.32	0.85	0.95	5	1.18	1.08	1.02	2	1.05	0.99	1.03	11.55	12.10	4.62

Q6FGF7	AF1Q protein (Fragment) OS=Homo sapiens GN=AF1Q PE=2 SV=1	3	0.87	0.88	0.91	2	0.77	1.02	0.88	2	0.83	1.11	0.72	6.02	11.23	11.97
Q14739	Lamin-B receptor OS=Homo sapiens GN=LBR PE=1 SV=2	9	1.02	1.15	1.11	4	0.94	1.04	1.19	3	1.06	0.90	1.00	6.47	12.21	8.69
B4DZZ0	cDNA FLJ52128, highly similar to PRA1 family protein 3 OS=Homo sapiens PE=2 SV=1	5	1.12	0.94	1.08	10	1.06	0.99	0.94	6	1.01	1.04	1.05	5.00	4.80	7.15
Q96ER9	Coiled-coil domain-containing protein 51 OS=Homo sapiens GN=CCDC51 PE=1 SV=2	6	1.13	1.12	1.09	3	1.37	1.26	1.08	2	1.20	1.04	1.24	10.13	9.90	8.05
Q9Y3A6	Transmembrane emp24 domain-containing protein 5 OS=Homo sapiens GN=TMED5 PE=1 SV=1	3	1.59	1.84	1.61	3	1.63	1.26	1.36	4	1.73	1.30	1.44	4.29	22.29	8.74
Q6NS36	Ferritin (Fragment) OS=Homo sapiens GN=FTH1 PE=2 SV=1	3	0.82	0.85	0.79	3	0.93	1.08	0.98	3	0.86	0.95	0.82	6.25	12.07	11.81
B2RD09	cDNA, FLJ96406, highly similar to Homo sapiens NOL1/NOP2/Sun domain family, member 5 (NSUN5), transcript variant 1, mRNA OS=Homo sapiens PE=2 SV=1	3	0.57	0.75	0.81	4	0.70	0.72	0.82	3	0.94	0.98	0.93	25.24	17.18	7.96
B7Z4S9	BUD31 homolog (Yeast), isoform CRA_b OS=Homo sapiens GN=BUD31 PE=2 SV=1	4	0.90	0.99	1.02	4	1.11	1.06	0.96	3	0.95	1.07	0.98	10.76	4.05	2.98
P62316	Small nuclear ribonucleoprotein Sm D2 OS=Homo sapiens GN=SNRPD2 PE=1 SV=1	7	1.00	1.03	0.96	5	1.05	0.93	1.00	7	1.04	0.99	1.05	2.96	5.19	4.18
Q6QN92	Mitochondrial glycine cleavage system H-protein (Fragment) OS=Homo sapiens PE=2 SV=1	7	1.11	1.14	0.93	3	0.75	0.69	0.69	4	0.97	1.08	0.80	19.19	25.45	14.94
Q9NWU2	Glucose-induced degradation protein 8 homolog OS=Homo sapiens GN=GID8 PE=1 SV=1	3	0.91	0.78	0.57	6	0.38	0.58	0.58	5	1.17	0.81	0.93	48.96	17.52	29.46
Q92558	Wiskott-Aldrich syndrome protein family member 1 OS=Homo sapiens GN=WASF1 PE=1 SV=1	3	0.79	1.03	0.91	2	0.64	0.66	0.62	3	0.78	0.94	0.86	11.76	22.30	19.06
Q9NQ88	Fructose-2,6-bisphosphatase TIGAR OS=Homo sapiens GN=TIGAR PE=1 SV=1	3	0.63	0.79	1.39	2	0.68	0.98	1.18	2	1.03	1.18	1.05	27.85	19.62	14.38
P0CG38	POTE ankyrin domain family member I OS=Homo sapiens GN=POTEI PE=3 SV=1	77	1.14	1.16	1.31	58	0.60	0.93	0.86	47	0.96	0.97	1.04	30.62	12.02	21.46
Q9BV86	N-terminal Xaa-Pro-Lys N-methyltransferase 1 OS=Homo sapiens GN=NTMT1 PE=1 SV=3	3	0.64	1.02	1.26	3	0.78	0.89	0.76	2	0.93	1.24	0.92	18.26	16.79	25.96
Q92845	Kinesin-associated protein 3 OS=Homo sapiens GN=KIFAP3 PE=1 SV=2	3	1.04	1.19	1.18	3	0.80	0.71	0.77	3	0.97	1.02	1.08	13.52	25.23	21.07
Q6FH36	Peptidyl-prolyl cis-trans isomerase (Fragment) OS=Homo sapiens GN=PPIH PE=2 SV=1	4	0.81	0.92	0.73	7	1.01	0.94	0.99	4	0.93	0.95	0.93	10.70	1.60	15.10
P60866	40S ribosomal protein S20 OS=Homo sapiens GN=RPS20 PE=1 SV=1	4	0.95	0.95	1.05	6	0.96	0.93	0.91	2	0.96	1.07	1.07	0.49	7.74	8.85
Q59F44	Cytochrome b-5 isoform 1 variant (Fragment) OS=Homo sapiens PE=2 SV=1	3	1.23	1.01	1.18	4	1.32	1.21	1.51	2	1.05	0.97	0.96	11.36	12.18	22.72
Q96P16	Regulation of nuclear pre-mRNA domain-containing protein 1A OS=Homo sapiens GN=RPRD1A PE=1 SV=1	7	0.76	1.28	1.11	8	0.98	0.99	0.91	5	0.89	1.08	0.91	12.41	12.94	11.97
B4DJA5	Ras-related protein Rab-5A OS=Homo sapiens GN=RAB5A PE=2 SV=1	8	1.62	1.21	1.77	5	1.11	1.00	1.09	5	1.03	0.99	1.06	25.42	11.56	31.00
P07305	Histone H1.0 OS=Homo sapiens GN=H1F0 PE=1 SV=3	5	2.34	1.19	2.07	3	1.73	1.07	1.68	3	1.99	1.01	2.05	15.15	8.36	11.30

Q68D16	Putative uncharacterized protein DKFZp686D0638 (Fragment) OS=Homo sapiens GN=DKFZp686D0638 PE=2 SV=1	3	0.86	1.00	0.81	4	0.95	1.11	0.91	3	0.81	0.86	0.88	7.78	12.75	6.03
Q8NAK9	cDNA FLJ35170 fis, clone PLACE6012942, highly similar to SPLICING FACTOR, ARGININE/SERINE-RICH 2 OS=Homo sapiens PE=2 SV=1	8	0.96	0.94	0.98	7	0.82	0.92	0.88	4	0.94	1.18	0.98	8.50	14.43	5.98
O75223	Gamma-glutamylcyclotransferase OS=Homo sapiens GN=GGCT PE=1 SV=1	3	0.97	1.13	1.32	4	0.69	0.83	0.74	3	0.98	1.35	1.07	18.47	23.39	27.83
Q2TNI1	Caveolin OS=Homo sapiens GN=CAV1 PE=2 SV=1	4	1.31	0.91	1.22	4	1.36	0.98	1.35	5	1.09	0.84	1.14	11.22	7.45	8.63
H3BV80	RNA-binding protein with serine-rich domain 1 OS=Homo sapiens GN=RNPS1 PE=2 SV=2	4	0.90	1.08	0.73	4	1.20	1.07	1.10	3	1.05	0.94	0.98	14.03	7.68	20.22
E9PE51	Intraflagellar transport protein 27 homolog OS=Homo sapiens GN=IFT27 PE=2 SV=2	4	1.13	1.09	1.21	4	0.77	0.83	0.96	4	0.98	1.49	0.87	18.92	28.95	17.75
Q7Z4W8	Heparin-binding protein HBp15 OS=Homo sapiens PE=2 SV=1	7	0.96	1.05	1.11	7	0.93	0.92	0.89	8	0.98	1.01	1.03	2.62	6.79	11.36
Q6IBA0	NADH dehydrogenase (Ubiquinone) Fe-S protein 5, 15kDa (NADH-coenzyme Q reductase) OS=Homo sapiens GN=NDUFS5 PE=2 SV=1	4	1.08	0.93	1.18	3	1.26	0.97	1.00	2	1.40	1.04	1.35	12.79	5.76	14.98
O75243	R30783_1 OS=Homo sapiens PE=4 SV=1	3	0.69	1.04	0.91	2	0.68	0.77	1.11	2	0.80	1.18	0.99	9.45	21.12	10.06
D3DTW2	Ubiquitin-conjugating enzyme E2Z (Putative), isoform CRA_a OS=Homo sapiens GN=UBE2Z PE=4 SV=1	3	0.85	0.93	0.92	2	1.02	1.12	1.20	5	0.97	0.90	0.86	9.07	11.92	18.37
Q8NBM8	Prenylcysteine oxidase-like OS=Homo sapiens GN=PCYOX1L PE=1 SV=2	3	1.02	1.18	1.32	3	1.15	1.00	1.07	3	1.18	1.15	1.10	7.67	8.75	11.93
Q7Z7K6	Centromere protein V OS=Homo sapiens GN=CENPV PE=1 SV=1	3	0.80	1.04	0.87	2	0.44	1.06	1.25	2	0.28	0.50	0.90	53.48	37.01	21.18
Q13405	39S ribosomal protein L49, mitochondrial OS=Homo sapiens GN=MRPL49 PE=1 SV=1	4	1.12	0.95	0.85	4	1.13	0.97	1.11	3	1.02	1.02	0.95	5.52	3.76	13.57
O43324	Eukaryotic translation elongation factor 1 epsilon-1 OS=Homo sapiens GN=EEF1E1 PE=1 SV=1	3	1.04	1.17	1.28	6	1.11	1.08	0.95	2	0.99	1.05	0.89	5.91	5.54	19.82
O43181	NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial OS=Homo sapiens GN=NDUFS4 PE=1 SV=1	5	1.04	1.12	1.06	3	1.04	0.87	1.01	3	1.20	1.00	1.30	8.68	12.41	13.93
Q9H3H0	Vacuolar ATP synthase subunit D homolog OS=Homo sapiens GN=VATD PE=2 SV=1	3	1.18	0.99	1.02	5	0.93	1.12	0.99	4	1.08	1.03	1.15	11.98	6.43	8.30
Q6IBA3	ATOX1 protein OS=Homo sapiens GN=ATOX1 PE=4 SV=1	3	0.86	1.00	0.96	2	0.99	1.09	0.94	3	1.00	1.07	1.17	7.93	4.37	12.19
Q6IAT9	Proteasome subunit beta type OS=Homo sapiens GN=PSMB6 PE=2 SV=1	3	0.90	1.07	1.07	4	0.73	0.84	0.68	4	0.77	1.11	1.06	11.32	14.29	23.81
Q53HA5	CDP-diacylglycerol--inositol 3-phosphatidyltransferase isoform 1 variant (Fragment) OS=Homo sapiens PE=2 SV=1	3	1.36	1.04	1.46	3	1.26	1.03	1.26	3	1.08	1.09	1.06	11.37	2.99	15.86
I3L4Q0	HCG1818442, isoform CRA_a OS=Homo sapiens GN=FAM195B PE=2 SV=1	3	0.70	0.95	0.86	2	0.95	1.06	0.94	2	0.79	1.07	0.87	15.29	6.46	4.90
C9J4Z3	60S ribosomal protein L37a OS=Homo sapiens GN=RPL37A PE=2 SV=1	4	1.07	0.96	1.06	4	1.17	0.78	1.08	4	1.22	0.95	1.15	6.75	11.53	4.38

C9J0I9	Nuclear-interacting partner of ALK OS=Homo sapiens GN=ZC3HC1 PE=2 SV=1	3	1.03	1.04	0.98	3	1.20	1.06	0.93	3	1.05	0.75	0.94	8.55	18.10	2.70
B2RAR2	cDNA, FLJ95064, highly similar to Homo sapiens nin one binding protein (NOB1P), mRNA OS=Homo sapiens PE=2 SV=1	4	0.94	1.26	1.03	5	0.92	1.01	0.89	3	0.83	0.90	0.76	6.57	17.84	14.93
Q9Y4Z0	U6 snRNA-associated Sm-like protein LSm4 OS=Homo sapiens GN=LSM4 PE=1 SV=1	3	0.99	0.89	0.93	3	1.01	1.02	0.96	2	2.20	1.48	0.74	49.43	27.58	13.86
Q8WUY1	Protein THEM6 OS=Homo sapiens GN=THEM6 PE=1 SV=2	5	0.95	0.93	1.02	4	1.27	1.12	1.14	4	1.17	1.03	1.07	14.24	9.18	5.78
Q7L5D6	Golgi to ER traffic protein 4 homolog OS=Homo sapiens GN=GET4 PE=1 SV=1	3	1.08	1.21	0.94	2	0.97	1.00	0.92	5	1.02	1.07	1.01	5.27	9.91	4.43
Q56VL3	OCIA domain-containing protein 2 OS=Homo sapiens GN=OCIAD2 PE=1 SV=1	4	1.16	0.98	1.14	2	1.28	0.95	1.13	4	1.21	1.08	0.78	4.97	7.05	19.91
Q0VDF9	Heat shock 70 kDa protein 14 OS=Homo sapiens GN=HSPA14 PE=1 SV=1	3	0.87	0.99	0.97	4	0.86	1.01	0.98	2	0.72	0.90	0.96	10.08	6.23	0.85
P14854	Cytochrome c oxidase subunit 6B1 OS=Homo sapiens GN=COX6B1 PE=1 SV=2	7	0.98	1.02	0.99	4	0.85	0.90	0.84	4	0.92	1.08	0.99	6.71	9.26	9.33
O75531	Barrier-to-autointegration factor OS=Homo sapiens GN=BANF1 PE=1 SV=1	5	1.06	1.03	0.90	4	1.29	1.52	1.41	4	0.98	0.71	0.92	14.73	37.42	26.59
O60220	Mitochondrial import inner membrane translocase subunit Tim8 A OS=Homo sapiens GN=TIMM8A PE=1 SV=1	4	0.97	1.03	0.99	4	0.77	0.97	0.83	4	0.87	0.94	1.03	11.71	4.90	11.30
O75506	Heat shock factor-binding protein 1 OS=Homo sapiens GN=HSBP1 PE=1 SV=1	5	0.99	1.17	0.97	3	1.01	0.90	0.93	4	0.90	0.93	0.87	5.83	14.88	5.43
A8K8K1	cDNA FLJ76936, highly similar to Homo sapiens RNA terminal phosphate cyclase domain 1 (RTCD1), mRNA OS=Homo sapiens PE=2 SV=1	4	1.02	1.01	0.87	3	0.89	0.90	1.03	6	0.94	0.93	0.98	6.93	6.04	8.10
P49711	Transcriptional repressor CTCF OS=Homo sapiens GN=CTCF PE=1 SV=1	4	1.00	1.06	0.91	4	1.06	1.16	1.12	2	1.01	0.97	0.86	3.32	8.71	14.61
A8K3W7	cDNA FLJ76271, highly similar to Homo sapiens protein O-fucosyltransferase 2 (POFUT2), transcript variant 3, mRNA OS=Homo sapiens PE=2 SV=1	4	0.85	1.15	1.07	5	0.92	1.00	0.94	3	1.10	0.92	1.06	13.21	11.35	7.07
Q53EY1	Phosphoserine phosphatase variant (Fragment) OS=Homo sapiens PE=2 SV=1	4	1.12	1.10	1.36	4	0.86	0.81	0.93	5	1.14	1.12	1.28	15.22	17.48	19.21
A8K5J7	cDNA FLJ77290, highly similar to Homo sapiens BCL2-associated athanogene 5 (BAG5), mRNA OS=Homo sapiens PE=2 SV=1	4	0.77	1.14	1.20	5	1.10	0.98	0.93	3	1.21	1.57	0.87	22.44	24.72	17.42
Q6PUV4	Complexin-2 OS=Homo sapiens GN=CPLX2 PE=1 SV=2	3	0.94	0.90	1.05	4	1.10	1.00	0.98	3	1.00	1.12	1.14	8.01	11.00	7.51
Q9Y4W2	Ribosomal biogenesis protein LAS1L OS=Homo sapiens GN=LAS1L PE=1 SV=2	4	1.64	0.95	1.46	7	1.10	0.90	1.05	4	1.12	1.15	1.13	24.02	12.99	18.00
Q9H5Q4	Dimethyladenosine transferase 2, mitochondrial OS=Homo sapiens GN=TFB2M PE=1 SV=1	4	0.92	1.01	0.84	7	1.05	1.09	1.08	4	0.94	0.95	1.00	7.12	6.60	12.54

B4DET0	cDNA FLJ55900, highly similar to Pre-mRNA-splicing factor ATP-dependent RNA helicase PRP16 (EC 3.6.1.-) OS=Homo sapiens PE=2 SV=1	3	1.22	1.12	0.91	6	0.99	1.00	0.96	8	0.98	1.04	0.95	12.83	5.62	3.05
Q9NTX5	Ethylmalonyl-CoA decarboxylase OS=Homo sapiens GN=ECHDC1 PE=1 SV=2	3	1.09	1.06	0.84	7	1.15	1.12	1.26	3	1.05	0.86	1.02	4.55	13.11	20.23
Q15645	Pachytene checkpoint protein 2 homolog OS=Homo sapiens GN=TRIP13 PE=1 SV=2	3	0.89	0.96	1.09	5	1.10	1.13	1.04	7	1.02	1.01	1.15	10.89	8.21	4.91
H0UI15	Synaptosomal-associated protein, 91kDa homolog (Mouse), isoform CRA_a OS=Homo sapiens GN=SNAP91 PE=4 SV=1	4	1.15	1.00	1.19	3	0.77	0.92	0.90	3	1.10	1.02	0.96	20.34	5.23	14.97
B4DHC5	cDNA FLJ57927, highly similar to Nucleoporin-like protein RIP OS=Homo sapiens PE=2 SV=1	3	1.05	0.86	0.96	3	0.85	1.05	1.03	2	1.18	1.06	1.02	16.53	11.07	3.84
Q9Y237	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4 OS=Homo sapiens GN=PIN4 PE=1 SV=1	4	0.71	0.97	0.80	4	0.94	1.09	0.87	2	0.79	1.22	0.91	14.18	11.45	6.61
P35610	Sterol O-acyltransferase 1 OS=Homo sapiens GN=SOAT1 PE=1 SV=3	4	1.21	1.10	1.32	4	1.38	1.04	1.25	3	1.35	0.98	1.33	6.84	5.99	3.47
B7WPF4	Ubiquitin carboxyl-terminal hydrolase OS=Homo sapiens GN=USP24 PE=2 SV=2	4	0.76	0.97	1.27	4	0.87	1.06	1.13	2	1.07	0.99	0.79	17.40	4.63	22.91
B7ZLY0	PHC2 protein OS=Homo sapiens GN=PHC2 PE=2 SV=1	4	0.91	0.98	0.95	4	0.87	1.04	0.96	4	0.97	1.05	1.04	5.71	4.05	5.38
Q9NZ08	Endoplasmic reticulum aminopeptidase 1 OS=Homo sapiens GN=ERAP1 PE=1 SV=3	4	1.13	1.18	1.20	5	0.94	0.95	1.12	4	1.14	1.11	1.68	10.35	10.80	22.66
P09669	Cytochrome c oxidase subunit 6C OS=Homo sapiens GN=COX6C PE=1 SV=2	4	1.18	0.97	0.80	3	1.29	1.13	1.00	3	1.41	1.14	1.13	8.90	9.02	16.95
Q15050	Ribosome biogenesis regulatory protein homolog OS=Homo sapiens GN=RRS1 PE=1 SV=2	4	1.28	1.08	1.05	4	1.01	0.73	1.02	5	1.22	1.15	1.09	11.97	22.59	3.38
Q8WUV3	PRMT3 protein (Fragment) OS=Homo sapiens GN=PRMT3 PE=2 SV=1	5	0.99	1.20	1.36	5	1.18	1.17	1.03	4	0.99	0.93	0.98	10.50	13.33	18.13
J3KN32	REST corepressor 1 OS=Homo sapiens GN=RCOR1 PE=4 SV=1	5	1.07	0.94	1.05	5	1.25	1.16	1.14	3	0.80	0.77	0.69	21.91	20.26	24.91
Q9H2J4	Phosducin-like protein 3 OS=Homo sapiens GN=PDCL3 PE=1 SV=1	4	0.89	0.92	0.82	6	1.36	1.22	1.41	4	1.06	0.92	1.15	21.67	17.10	26.54
Q9C0H2	Protein tweety homolog 3 OS=Homo sapiens GN=TTYH3 PE=1 SV=3	4	0.86	1.30	1.26	2	0.77	0.71	0.83	2	1.24	1.14	1.12	25.76	29.11	20.37
B3KY04	cDNA FLJ46506 fis, clone THYMU3030752, highly similar to BTB/POZ domain-containing protein KCTD12 OS=Homo sapiens PE=2 SV=1	3	1.34	1.01	1.25	5	1.03	1.05	1.03	2	1.22	1.27	1.07	12.95	12.87	10.45
Q969S3	Zinc finger protein 622 OS=Homo sapiens GN=ZNF622 PE=1 SV=1	3	1.14	0.84	1.05	3	0.83	0.76	0.89	2	1.52	1.48	1.17	29.72	38.20	13.60
B4E2N0	Protein LZIC OS=Homo sapiens GN=LZIC PE=2 SV=1	5	1.12	1.12	1.04	4	0.88	1.00	1.02	3	0.90	0.90	1.01	14.20	10.90	1.69
Q9H4A6	Golgi phosphoprotein 3 OS=Homo sapiens GN=GOLPH3 PE=1 SV=1	4	1.09	0.99	1.02	3	1.19	0.97	1.18	2	0.69	0.61	0.60	26.61	24.75	32.52
Q9P265	Disco-interacting protein 2 homolog B OS=Homo sapiens GN=DIP2B PE=1 SV=3	3	0.96	0.94	0.77	3	0.93	1.00	0.96	3	0.81	1.08	0.93	8.57	7.18	11.40
Q9UBI1	COMM domain-containing protein 3 OS=Homo sapiens GN=COMMD3 PE=1 SV=1	3	0.95	1.20	1.17	2	0.93	0.91	1.15	2	0.83	0.85	0.73	6.82	18.58	24.39

Q53YD8	ADP-ribosylation factor-like 2 OS=Homo sapiens GN=hCG_23373 PE=2 SV=1	3	1.05	1.44	1.47	5	0.75	1.17	0.77	5	0.64	0.95	0.75	25.84	20.87	40.88
B1AJY7	26S proteasome non-ATPase regulatory subunit 10 OS=Homo sapiens GN=PSMD10 PE=2 SV=1	4	1.00	0.85	1.12	3	1.01	0.95	0.88	5	0.92	1.05	1.06	5.25	10.60	12.30
E5KTM5	Mitochondrial dimethyladenosine transferase 1 OS=Homo sapiens GN=TFB1M PE=2 SV=1	3	0.87	0.93	0.89	2	0.89	1.02	0.91	2	1.01	1.07	1.12	8.21	7.10	13.12
E9PJP2	Protein SOGA3 OS=Homo sapiens GN=SOGA3 PE=2 SV=1	5	0.90	0.89	1.10	3	0.80	0.73	0.79	4	1.17	1.05	0.99	19.83	18.29	16.33
B3KN59	cDNA FLJ13673 fis, clone PLACE1011858, highly similar to BAG family molecular chaperone regulator 2 OS=Homo sapiens PE=2 SV=1	4	0.86	1.11	0.97	4	0.96	0.99	0.92	3	0.98	1.18	1.32	6.83	8.96	20.01
Q9BPX4	Eukaryotic translation initiation factor 2B, subunit 2 beta, 39kDa OS=Homo sapiens GN=EIF2B2 PE=2 SV=1	3	1.11	1.19	1.09	4	0.97	0.95	1.06	4	1.09	1.01	0.89	7.47	11.88	10.58
Q86X94	TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 68kDa OS=Homo sapiens GN=TAF15 PE=2 SV=2	12	1.04	0.93	0.62	3	2.20	1.18	1.36	4	1.10	0.79	1.10	45.29	20.44	36.50
Q96GA3	Protein LTV1 homolog OS=Homo sapiens GN=LTV1 PE=1 SV=1	3	0.80	1.01	0.78	3	1.05	1.10	0.94	3	0.85	0.83	0.78	14.78	14.35	11.41
Q9Y4B6	Protein VPRBP OS=Homo sapiens GN=VPRBP PE=1 SV=3	4	0.66	0.80	0.83	2	1.13	1.00	0.86	3	0.90	0.78	0.93	25.95	13.95	5.41
Q9NUD5	Zinc finger CCHC domain-containing protein 3 OS=Homo sapiens GN=ZCCHC3 PE=1 SV=1	4	0.85	0.83	0.85	2	0.78	0.85	1.06	3	0.75	0.75	0.73	6.51	6.67	18.72
P50336	Protoporphyrinogen oxidase OS=Homo sapiens GN=PPOX PE=1 SV=1	3	0.91	0.94	0.95	4	0.87	0.88	0.86	2	1.04	1.12	1.07	9.74	13.05	10.92
Q8TBX8	Phosphatidylinositol 5-phosphate 4-kinase type-2 gamma OS=Homo sapiens GN=PIP4K2C PE=1 SV=3	3	0.98	0.98	1.24	4	0.89	0.83	0.87	3	0.85	0.95	0.86	7.36	9.19	21.74
H9KV45	Ubiquitin-conjugating enzyme E2 D3 OS=Homo sapiens GN=UBE2D3 PE=2 SV=1	6	0.83	0.95	0.97	7	1.10	0.85	0.95	5	0.75	0.77	0.87	20.08	10.10	5.77
Q6P1N1	PPM2C protein (Fragment) OS=Homo sapiens GN=PPM2C PE=2 SV=1	3	1.13	1.16	1.05	5	1.18	1.11	1.08	4	1.17	0.99	1.13	2.33	8.06	3.95
Q6FGR6	HCG2025883, isoform CRA_b OS=Homo sapiens GN=POLR2C PE=2 SV=1	5	0.83	0.76	1.11	3	1.03	0.88	0.82	2	0.88	1.11	0.95	11.30	19.19	14.87
B4DW13	HCG23341, isoform CRA_d OS=Homo sapiens GN=hCG_23341 PE=2 SV=1	3	0.95	1.12	0.93	6	0.90	0.86	0.98	6	0.95	1.06	0.99	3.32	13.47	3.46
L7RRS0	Phosphatidylinositol-4-phosphate 3-kinase, catalytic subunit type 2 alpha OS=Homo sapiens GN=PIK3C2A PE=4 SV=1	4	1.04	0.90	0.86	2	0.90	0.98	0.93	4	1.03	1.12	1.09	7.87	11.20	11.82
Q53XR6	MAD, mothers against decapentaplegic homolog 2 (Drosophila) OS=Homo sapiens GN=SMAD2 PE=2 SV=1	4	1.11	1.08	0.94	3	0.92	1.25	1.02	2	1.21	1.66	1.43	13.67	22.17	23.18
H0Y886	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 5, mitochondrial (Fragment) OS=Homo sapiens GN=NDUFB5 PE=4 SV=1	4	1.57	1.12	0.95	3	1.80	1.06	1.31	2	1.30	1.25	1.25	15.85	8.68	16.13
P21399	Cytoplasmic aconitate hydratase OS=Homo sapiens GN=ACO1 PE=1 SV=3	4	0.87	0.88	0.79	6	0.99	1.11	1.13	2	1.00	1.02	0.94	7.59	11.59	17.86
Q99622	Protein C10 OS=Homo sapiens GN=C12orf57 PE=1 SV=1	5	0.95	0.90	0.95	7	0.76	0.77	0.84	4	0.87	1.00	1.09	11.50	12.79	12.71

Q63HL5	Putative uncharacterized protein DKFZp686G12235 OS=Homo sapiens GN=DKFZp686G12235 PE=2 SV=1	5	0.87	0.95	0.85	3	0.98	1.26	1.06	3	0.97	0.86	1.01	6.07	20.65	11.16
D2D4A3	Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial OS=Homo sapiens GN=ALDH4A1 PE=2 SV=1	3	0.87	0.93	0.92	3	1.05	1.00	0.97	3	1.39	1.15	1.52	23.56	11.05	28.99
Q9UPZ6	Thrombospondin type-1 domain-containing protein 7A OS=Homo sapiens GN=THSD7A PE=1 SV=4	3	1.26	1.53	0.93	2	0.99	0.81	0.74	3	1.03	1.27	0.92	13.05	30.19	12.56
Q9Y3Z3	Deoxynucleoside triphosphate triphosphohydrolase SAMHD1 OS=Homo sapiens GN=SAMHD1 PE=1 SV=2	4	1.01	1.06	1.05	5	1.04	0.92	0.98	4	1.11	1.07	1.00	4.91	8.10	3.49
Q13057	Bifunctional coenzyme A synthase OS=Homo sapiens GN=COASY PE=1 SV=4	3	0.94	0.88	1.08	4	1.37	0.88	1.14	2	0.60	1.19	1.32	39.96	18.10	10.44
Q53F37	SAR1a gene homolog 2 variant (Fragment) OS=Homo sapiens PE=2 SV=1	5	0.92	0.95	0.87	7	0.78	0.85	0.78	5	1.01	0.83	1.07	12.74	7.72	16.00
Q2L6I0	FB19 protein OS=Homo sapiens GN=PPP1R10 PE=2 SV=1	3	0.80	0.78	0.89	4	0.80	1.08	0.98	2	0.78	0.90	1.02	1.11	16.59	6.50
D3DUE7	Cytokine-like nuclear factor n-pac, isoform CRA_a OS=Homo sapiens GN=N-PAC PE=4 SV=1	5	0.95	0.90	0.93	2	0.92	1.10	1.01	3	0.88	1.01	0.92	3.88	10.20	4.92
Q6VY07	Phosphofurin acidic cluster sorting protein 1 OS=Homo sapiens GN=PACS1 PE=1 SV=2	4	0.72	0.98	0.92	2	1.19	1.16	1.26	4	0.83	1.07	1.10	26.96	8.62	15.52
Q53HV6	Niemann-Pick disease, type C2 variant (Fragment) OS=Homo sapiens PE=2 SV=1	3	0.94	1.08	0.95	2	0.97	1.11	1.04	2	0.96	0.83	0.89	1.53	15.20	7.75
Q5TZX9	Vesicle transport through interaction with t-SNAREs homolog 1B (Yeast) OS=Homo sapiens PE=2 SV=1	4	1.16	0.87	1.17	4	0.71	0.90	0.84	2	0.99	1.16	0.97	23.67	16.55	16.87
P46087	Putative ribosomal RNA methyltransferase NOP2 OS=Homo sapiens GN=NOP2 PE=1 SV=2	4	0.97	1.11	1.03	3	1.04	1.05	1.12	3	0.91	0.97	1.00	6.68	6.64	5.87
O43504	Ragulator complex protein LAMTOR5 OS=Homo sapiens GN=LAMTOR5 PE=1 SV=1	5	1.29	0.78	0.74	5	0.94	1.05	1.02	4	1.18	1.00	1.11	15.63	15.02	19.97
H0YM23	Ankyrin repeat domain-containing protein 17 (Fragment) OS=Homo sapiens GN=ANKRD17 PE=4 SV=1	3	0.90	1.02	1.04	3	1.11	1.08	1.19	6	1.02	1.19	1.07	10.53	8.15	7.20
F5H8F7	Set1/Ash2 histone methyltransferase complex subunit ASH2 OS=Homo sapiens GN=ASH2L PE=2 SV=1	4	1.08	1.02	0.78	4	1.25	1.06	1.18	3	1.13	1.06	0.98	7.32	2.37	20.58
Q8TC12	Retinol dehydrogenase 11 OS=Homo sapiens GN=RDH11 PE=1 SV=2	4	1.15	0.62	0.88	3	1.24	1.36	1.53	3	0.90	0.83	0.76	16.35	40.67	39.28
Q9Y680	Peptidyl-prolyl cis-trans isomerase FKBP7 OS=Homo sapiens GN=FKBP7 PE=1 SV=1	3	0.90	0.98	1.11	4	1.57	1.51	1.26	3	1.31	1.07	1.40	26.62	24.07	11.78
A8K9X5	cDNA FLJ76472, highly similar to Homo sapiens Fas (TNFRSF6) associated factor 1 (FAF1), transcript variant 1, mRNA OS=Homo sapiens PE=2 SV=1	4	1.21	1.03	1.18	3	0.67	0.99	0.86	4	0.93	0.91	0.85	28.92	6.32	19.65
Q5BKZ1	DBIRD complex subunit ZNF326 OS=Homo sapiens GN=ZNF326 PE=1 SV=2	5	0.95	0.94	1.21	2	0.81	0.80	1.06	3	0.96	1.11	0.88	8.97	15.79	15.69
Q6P9B9	Integrator complex subunit 5 OS=Homo sapiens GN=INTS5 PE=1 SV=1	4	1.44	1.32	0.80	4	1.03	0.90	1.05	3	1.17	0.98	1.10	17.45	20.65	16.03

Q5JR04	Mov10, Moloney leukemia virus 10, homolog (Mouse), isoform CRA_a OS=Homo sapiens GN=MOV10 PE=2 SV=1	3	0.92	1.12	1.13	5	1.08	1.12	0.79	3	1.17	1.26	0.72	12.07	6.62	25.10
O75935	Dynactin subunit 3 OS=Homo sapiens GN=DCTN3 PE=1 SV=1	4	0.99	1.05	0.83	2	1.26	1.06	1.11	3	1.16	1.46	1.04	11.91	19.71	14.53
Q709C8	Vacuolar protein sorting-associated protein 13C OS=Homo sapiens GN=VPS13C PE=1 SV=1	4	1.15	0.93	0.82	5	1.22	1.23	1.14	3	1.16	1.08	1.08	3.36	13.92	17.26
Q9BTY2	Plasma alpha-L-fucosidase OS=Homo sapiens GN=FUCA2 PE=1 SV=2	5	0.76	0.91	0.77	5	0.74	0.60	0.72	2	1.05	1.08	1.09	20.65	28.30	23.31
G5E972	Thymopentin OS=Homo sapiens GN=TMPO PE=2 SV=1	18	1.14	0.94	1.08	19	0.76	0.86	0.78	19	1.11	0.96	0.83	21.18	5.62	17.65
Q9UFW8	CGG triplet repeat-binding protein 1 OS=Homo sapiens GN=CGGBP1 PE=1 SV=2	3	0.97	0.91	0.94	3	0.88	0.85	0.90	2	1.07	1.12	0.93	9.76	14.78	2.47
E7ERS3	Zinc finger CCCH domain-containing protein 18 OS=Homo sapiens GN=ZC3H18 PE=2 SV=1	5	0.84	0.95	0.81	4	0.91	0.84	0.90	2	1.03	1.25	1.05	10.47	20.82	13.13
Q9Y3D3	28S ribosomal protein S16, mitochondrial OS=Homo sapiens GN=MRPS16 PE=1 SV=1	4	0.97	0.88	1.12	4	1.03	0.86	0.97	4	1.01	1.17	1.08	3.24	18.08	7.03
Q7KZN9	Cytochrome c oxidase assembly protein COX15 homolog OS=Homo sapiens GN=COX15 PE=1 SV=1	3	1.02	0.92	1.12	5	1.08	1.01	0.96	2	1.04	1.03	1.22	2.91	6.32	12.21
E9PM92	Small acidic protein (Fragment) OS=Homo sapiens GN=C11orf58 PE=2 SV=1	3	0.96	0.69	0.74	3	1.17	1.00	1.05	3	0.93	1.03	0.86	12.42	20.60	18.09
B7ZLW0	LPP protein OS=Homo sapiens GN=LPP PE=2 SV=1	3	1.09	0.91	1.30	2	1.92	1.15	1.20	2	1.30	1.01	1.32	30.06	12.00	5.18
Q9H1B7	Interferon regulatory factor 2-binding protein-like OS=Homo sapiens GN=IRF2BPL PE=1 SV=1	5	1.15	1.11	1.08	4	0.70	0.78	0.90	2	0.97	1.05	1.22	23.78	17.94	15.21
Q9P0H9	RER1 protein OS=Homo sapiens GN=RER1 PE=2 SV=1	4	1.43	1.20	1.20	3	1.34	1.11	1.09	3	1.17	1.10	1.09	10.19	5.03	5.64
B4E164	cDNA FLJ56613, highly similar to Serine/threonine-protein kinase TBK1 (EC 2.7.11.1) OS=Homo sapiens PE=2 SV=1	4	0.71	1.11	1.08	2	0.82	0.84	0.72	2	1.39	1.34	1.05	37.37	22.73	21.04
A8KA84	cDNA FLJ78682, highly similar to Homo sapiens 2'-5'-oligoadenylate synthetase 3, 100kDa (OAS3), mRNA OS=Homo sapiens PE=2 SV=1	5	0.77	0.77	0.92	7	0.90	0.99	0.84	6	1.15	1.02	0.99	20.33	14.54	8.19
O60784-4	Isoform 4 of Target of Myb protein 1 OS=Homo sapiens GN=TOM1	4	0.86	0.99	0.94	3	0.23	0.45	0.47	2	0.91	0.79	1.20	56.37	36.42	42.34
P50402	Emerin OS=Homo sapiens GN=EMD PE=1 SV=1	3	1.12	0.99	1.07	5	0.97	0.98	0.96	2	1.04	0.97	1.06	7.14	0.81	6.13
B2R802	cDNA, FLJ93681, highly similar to Homo sapiens small nuclear ribonucleoprotein polypeptide A (SNRPA), mRNA OS=Homo sapiens PE=2 SV=1	3	0.96	0.89	1.19	6	0.74	0.95	0.88	4	1.04	1.09	0.99	17.06	10.41	15.16
G5E9P1	Inositol 1,4,5-triphosphate receptor, type 1, isoform CRA_d OS=Homo sapiens GN=ITPR1 PE=2 SV=1	5	1.14	1.01	1.38	4	0.97	0.95	1.05	4	1.17	1.07	1.19	9.78	5.64	13.78
B7ZLZ2	ER degradation-enhancing alpha-mannosidase-like protein 3 OS=Homo sapiens GN=EDEM3 PE=2 SV=1	3	0.71	0.74	0.74	3	0.99	0.89	0.97	2	1.14	0.86	0.97	23.09	10.11	15.05
Q9NX55	Huntingtin-interacting protein K OS=Homo sapiens GN=HYPK PE=1 SV=2	3	0.71	0.83	0.84	4	0.96	0.83	0.79	3	0.87	1.04	0.93	15.14	13.71	8.09

H0YBL1	Inositol monophosphatase 1 (Fragment) OS=Homo sapiens GN=IMPA1 PE=4 SV=1	4	1.02	1.02	1.01	4	0.78	1.01	0.93	2	0.88	1.20	0.95	13.30	9.87	4.50
B5BUK7	Protein kinase C iota type (Fragment) OS=Homo sapiens GN=PRKCI PE=2 SV=1	3	0.99	1.18	0.71	2	1.15	1.05	0.96	2	0.80	0.86	0.76	18.23	15.68	16.04
Q6NZY4	Zinc finger CCHC domain-containing protein 8 OS=Homo sapiens GN=ZCCHC8 PE=1 SV=2	5	0.92	1.02	0.87	3	0.90	0.94	0.93	3	1.02	0.84	0.87	6.46	9.51	4.38
Q6AI38	Putative uncharacterized protein DKFZp762F247 (Fragment) OS=Homo sapiens GN=DKFZp762F247 PE=2 SV=1	4	1.24	1.11	1.01	3	0.82	0.93	1.10	4	0.72	0.89	0.84	29.78	12.08	13.55
Q6AI08	HEAT repeat-containing protein 6 OS=Homo sapiens GN=HEATR6 PE=1 SV=1	4	1.12	1.18	1.55	4	0.73	0.74	0.91	5	0.78	0.98	1.23	24.08	22.73	26.30
B2RUU3	Dedicator of cytokinesis 1 OS=Homo sapiens GN=DOCK1 PE=2 SV=1	3	0.76	0.98	0.52	4	1.00	1.07	0.94	2	0.91	1.12	0.93	13.74	6.59	30.43
Q9NYB0	Telomeric repeat-binding factor 2-interacting protein 1 OS=Homo sapiens GN=TERF2IP PE=1 SV=1	2	1.27	0.94	1.07	2	1.66	1.03	1.42	3	2.73	0.79	1.68	39.90	13.02	22.20
A4D1G0	Cyclin-dependent kinase 6 OS=Homo sapiens GN=CDK6 PE=2 SV=1	4	1.05	0.87	1.16	3	1.10	0.87	0.91	5	1.12	1.06	1.00	3.55	11.68	12.46
Q9H6T3	RNA polymerase II-associated protein 3 OS=Homo sapiens GN=RPAP3 PE=1 SV=2	3	0.70	1.02	0.92	5	0.94	1.28	1.05	4	0.95	0.93	1.00	16.22	16.94	6.45
B4DX69	cDNA FLJ55158, highly similar to Thioredoxin, mitochondrial OS=Homo sapiens PE=2 SV=1	4	0.79	0.93	0.87	4	0.92	0.93	0.96	3	0.83	0.84	0.86	8.13	5.59	6.37
Q5U4P5	GAK protein OS=Homo sapiens GN=GAK PE=2 SV=1	3	1.09	0.95	1.17	2	0.88	1.01	1.13	2	0.92	1.36	1.06	11.77	20.28	4.83
Q8NE86	Calcium uniporter protein, mitochondrial OS=Homo sapiens GN=MCU PE=1 SV=1	3	1.10	0.95	0.94	4	1.21	1.06	1.15	4	0.97	0.87	1.01	10.69	9.92	10.41
G3V325	Pentatricopeptide repeat-containing protein 1, mitochondrial OS=Homo sapiens GN=ATP5J2-PTCD1 PE=4 SV=1	4	1.47	0.94	1.51	3	1.28	0.83	1.08	2	1.43	1.13	1.24	7.35	15.93	16.99
Q9NRF8	CTP synthase 2 OS=Homo sapiens GN=CTPS2 PE=1 SV=1	3	0.83	0.95	0.94	5	0.78	0.86	0.92	2	0.92	0.92	0.88	8.09	5.45	3.30
A8K6K1	cDNA FLJ78667, highly similar to Homo sapiens ring finger protein 40 (RNF40), transcript variant 1, mRNA OS=Homo sapiens PE=2 SV=1	3	0.74	0.94	0.77	3	0.87	0.79	0.91	6	1.00	1.16	1.08	15.19	19.56	16.91
O95218	Zinc finger Ran-binding domain-containing protein 2 OS=Homo sapiens GN=ZRANB2 PE=1 SV=2	6	1.15	0.96	0.87	4	0.89	0.88	0.88	4	0.96	1.09	0.96	13.28	10.50	5.92
Q8WW12	PEST proteolytic signal-containing nuclear protein OS=Homo sapiens GN=PCNP PE=1 SV=2	5	0.99	1.04	0.87	2	1.13	1.10	1.08	2	0.88	0.92	0.97	12.60	8.93	10.75
H7BXP1	NF-kappa-B inhibitor-interacting Ras-like protein 2 OS=Homo sapiens GN=NKIRAS2 PE=2 SV=1	2	1.19	1.16	0.74	4	1.37	1.20	1.15	3	0.83	0.93	0.92	24.74	13.05	22.22
Q6UWE0	E3 ubiquitin-protein ligase LRSAM1 OS=Homo sapiens GN=LRSAM1 PE=1 SV=1	2	0.90	1.06	0.88	2	0.84	0.94	0.97	3	1.17	0.94	1.08	17.96	7.38	10.39
A8K0F7	cDNA FLJ76587, highly similar to Homo sapiens vitamin K epoxide reductase complex, subunit 1-like 1 (VKORC1L1), mRNA OS=Homo sapiens PE=2 SV=1	2	1.33	1.40	1.46	3	1.36	0.86	1.12	3	1.24	0.98	1.29	4.75	26.11	12.98
Q9BYN8	28S ribosomal protein S26, mitochondrial OS=Homo sapiens GN=MRPS26 PE=1 SV=1	3	0.93	1.06	1.22	3	1.39	1.37	1.16	3	1.14	0.93	1.05	19.81	19.87	7.33

G0ZJH6	UFD2A-III/UBE4B-III splice isoform OS=Homo sapiens GN=Ube4B PE=2 SV=1	2	1.10	1.00	1.00	3	0.86	0.99	1.00	3	0.93	0.95	0.94	12.62	2.63	3.65
Q9Y2Q5	Ragulator complex protein LAMTOR2 OS=Homo sapiens GN=LAMTOR2 PE=1 SV=1	2	1.08	0.95	1.17	2	0.78	0.77	0.97	2	1.17	1.16	0.93	20.23	20.30	12.55
Q68D91	Metallo-beta-lactamase domain-containing protein 2 OS=Homo sapiens GN=MBLAC2 PE=1 SV=3	3	0.94	0.92	1.29	3	0.78	0.57	0.65	5	0.81	0.95	0.79	9.97	25.57	36.93
Q6UVY6	DBH-like monooxygenase protein 1 OS=Homo sapiens GN=MOXD1 PE=2 SV=1	3	0.95	0.79	0.89	5	1.16	0.98	1.04	4	0.87	0.94	0.91	15.37	10.88	8.83
J3KMZ8	Zinc finger protein ubi-d4 OS=Homo sapiens GN=DPF2 PE=4 SV=1	2	0.78	0.81	0.95	4	0.95	0.91	0.94	3	1.13	1.17	1.11	17.96	19.02	9.15
Q14966	Zinc finger protein 638 OS=Homo sapiens GN=ZNF638 PE=1 SV=2	3	1.08	0.96	1.07	3	0.65	0.80	0.59	2	1.00	1.19	1.02	25.16	19.65	29.47
J3KPA3	Oxysterol-binding protein OS=Homo sapiens GN=OSBPL9 PE=3 SV=1	2	1.35	1.09	1.10	2	1.11	1.46	1.29	2	0.97	0.82	0.59	16.67	28.48	36.41
A4D1E9	GTP-binding protein 10 OS=Homo sapiens GN=GTPBP10 PE=1 SV=1	2	0.79	0.95	1.18	6	1.12	1.18	0.96	3	0.80	0.72	0.89	20.73	24.48	15.01
H7C0G7	Non-homologous end-joining factor 1 (Fragment) OS=Homo sapiens GN=NHEJ1 PE=2 SV=1	3	0.87	1.01	0.94	2	1.40	1.16	1.04	3	0.83	0.92	0.89	30.66	11.87	8.11
A8MW61	Pleiotropic regulator 1 OS=Homo sapiens GN=PLRG1 PE=2 SV=1	2	0.77	1.15	1.41	3	1.14	1.26	1.07	2	0.83	1.01	0.91	21.88	10.88	22.35
B2R8A2	cDNA, FLJ93804, highly similar to Homo sapiens gp25L2 protein (HSGP25L2G), mRNA OS=Homo sapiens PE=2 SV=1	5	1.41	1.00	1.20	7	1.53	0.98	1.34	8	1.45	0.96	1.38	4.09	2.20	7.29
H3BSM7	UPF0420 protein C16orf58 OS=Homo sapiens GN=C16orf58 PE=2 SV=1	4	1.22	1.08	1.47	3	1.19	0.94	1.16	2	1.30	0.80	1.00	4.50	14.57	19.50
P15374	Ubiquitin carboxyl-terminal hydrolase isozyme L3 OS=Homo sapiens GN=UCHL3 PE=1 SV=1	3	1.21	0.98	0.96	3	0.80	0.82	0.85	3	1.17	0.90	1.18	21.56	8.83	16.88
Q15043	Zinc transporter ZIP14 OS=Homo sapiens GN=SLC39A14 PE=1 SV=3	6	1.05	0.96	1.02	4	1.04	0.99	1.03	4	1.71	0.97	1.35	30.35	1.66	16.46
Q53GX4	FK506 binding protein 5 variant (Fragment) OS=Homo sapiens PE=2 SV=1	2	1.09	1.10	1.25	3	0.91	0.98	0.89	5	0.93	0.95	0.96	10.58	7.68	18.73
A8K7G2	cDNA FLJ75762, highly similar to Homo sapiens protease, serine, 25 (PRSS25), nuclear gene encodingmitochondrial protein, transcript variant 1, mRNA OS=Homo sapiens PE=2 SV=1	2	0.84	1.04	1.36	3	0.89	0.67	0.72	2	1.29	1.08	1.00	24.46	24.29	31.51
Q96FT4	Papillary renal cell carcinoma (Translocation-associated) OS=Homo sapiens GN=PRCC PE=2 SV=1	3	1.06	1.01	0.75	2	1.11	1.26	1.13	2	0.94	0.92	0.96	8.50	16.64	20.20
Q59G94	Zinc finger protein 207 variant (Fragment) OS=Homo sapiens PE=2 SV=1	3	0.80	0.95	0.78	4	0.89	1.02	0.90	5	0.92	0.94	0.94	7.23	4.37	9.60
Q96JM3	Chromosome alignment-maintaining phosphoprotein 1 OS=Homo sapiens GN=CHAMP1 PE=1 SV=2	4	1.05	0.95	1.02	2	1.06	1.07	1.10	3	0.99	0.81	0.99	3.47	13.50	5.63
J3QTA6	Coiled-coil-helix-coiled-coil-helix domain-containing protein 6, mitochondrial OS=Homo sapiens GN=CHCHD6 PE=4 SV=1	4	1.05	1.19	1.13	4	0.83	1.03	0.94	4	1.02	0.82	0.91	12.19	18.02	11.89
A8K9L8	cDNA FLJ76964, highly similar to Homo sapiens tropomodulin 2 (neuronal) (TMOD2), mRNA OS=Homo sapiens PE=2 SV=1	2	1.10	1.05	1.07	4	0.71	0.91	0.83	2	1.42	1.59	1.81	33.25	30.74	41.43

B3KN49	cDNA FLJ13562 fis, clone PLACE1008080, highly similar to Homo sapiens hexamethylene bis-acetamide inducible 1 (HEXIM1), mRNA OS=Homo sapiens PE=2 SV=1	2	0.97	0.98	1.16	2	1.17	1.27	0.91	2	0.89	0.95	0.73	14.23	16.73	23.25
Q9NZZ3	Charged multivesicular body protein 5 OS=Homo sapiens GN=CHMP5 PE=1 SV=1	8	0.85	0.87	1.08	3	0.85	1.19	1.55	2	1.14	1.36	1.15	17.77	21.54	20.18
Q9HAV0	Guanine nucleotide-binding protein subunit beta-4 OS=Homo sapiens GN=GNB4 PE=1 SV=3	6	1.49	1.18	1.04	6	1.00	0.93	0.98	6	0.73	1.02	0.91	35.61	12.08	6.54
Q7Z3K3	Pogo transposable element with ZNF domain OS=Homo sapiens GN=POGZ PE=1 SV=2	4	0.75	0.85	0.72	6	0.72	0.82	0.71	4	1.01	1.20	0.82	19.57	21.93	7.89
Q8IVF2	Protein AHNAK2 OS=Homo sapiens GN=AHNAK2 PE=1 SV=2	2	0.97	0.96	1.00	2	0.98	1.02	1.10	2	1.08	1.01	1.07	5.81	3.56	5.21
Q6IAN0	Dehydrogenase/reductase SDR family member 7B OS=Homo sapiens GN=DHRS7B PE=1 SV=2	2	2.26	1.70	2.14	2	0.94	0.95	0.96	2	1.18	1.06	1.43	48.28	32.57	39.21
Q8IYI6	Exocyst complex component 8 OS=Homo sapiens GN=EXOC8 PE=1 SV=2	2	1.16	1.09	1.14	2	1.02	0.94	0.85	3	0.85	0.95	0.98	15.43	8.53	14.57
F8VY86	Tumor suppressor p53-binding protein 1 OS=Homo sapiens GN=TP53BP1 PE=2 SV=1	2	1.11	1.15	1.03	5	0.80	0.82	0.85	2	1.04	1.22	0.87	16.49	20.03	10.60
Q9P1U1	Actin-related protein 3B OS=Homo sapiens GN=ACTR3B PE=2 SV=1	3	1.24	1.06	0.93	4	1.03	1.18	1.02	4	1.00	1.11	0.95	11.99	5.04	4.80
M0QWZ7	Serine--tRNA ligase, mitochondrial OS=Homo sapiens GN=SARS2 PE=3 SV=1	3	0.82	0.68	0.74	4	1.21	1.04	1.01	3	0.98	0.95	1.07	19.77	21.46	18.78
B2RAH5	cDNA, FLJ94919, highly similar to Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 12A (PPP1R12A), mRNA OS=Homo sapiens PE=2 SV=1	4	0.96	0.94	0.88	4	0.97	1.25	1.25	5	0.92	0.77	0.95	3.00	24.59	19.20
Q96JB2	Conserved oligomeric Golgi complex subunit 3 OS=Homo sapiens GN=COG3 PE=1 SV=3	2	0.87	0.88	1.15	5	0.96	1.03	1.17	5	1.19	1.09	1.20	16.56	11.26	1.98
Q6IBU4	SDF2 protein OS=Homo sapiens GN=SDF2 PE=2 SV=1	8	1.36	1.02	0.90	2	1.23	1.10	1.32	4	1.68	1.06	1.44	16.44	4.03	23.43
E9PK47	Phosphorylase OS=Homo sapiens GN=PYGL PE=2 SV=1	4	0.93	0.63	0.98	5	1.37	1.28	1.36	5	1.17	1.06	1.03	18.80	33.30	18.47
Q53F98	DNA primase (Fragment) OS=Homo sapiens PE=2 SV=1	2	0.83	1.23	0.92	4	0.80	1.00	0.82	4	0.83	1.02	0.95	2.05	11.83	7.24
Q9BV44	THUMP domain-containing protein 3 OS=Homo sapiens GN=THUMPD3 PE=1 SV=1	2	1.27	0.92	1.48	4	1.01	1.08	1.36	2	0.99	1.23	0.93	14.46	14.26	23.22
B2R4W8	HCG1994130, isoform CRA_a OS=Homo sapiens GN=hCG_1994130 PE=2 SV=1	14	0.88	0.85	0.89	11	0.86	0.89	0.86	10	0.97	1.09	0.98	6.38	13.60	6.56
Q9NRY4	Rho GTPase-activating protein 35 OS=Homo sapiens GN=ARHGAP35 PE=1 SV=3	2	1.15	1.07	1.09	5	0.92	0.76	0.81	2	0.67	0.87	0.80	26.39	17.28	17.90
Q9UEW8	STE20/SPS1-related proline-alanine-rich protein kinase OS=Homo sapiens GN=STK39 PE=1 SV=3	5	0.83	1.04	0.79	6	0.87	0.96	0.91	6	1.34	1.18	1.14	27.79	10.31	18.82
E9PFK5	Nucleolar protein 14 OS=Homo sapiens GN=NOP14 PE=2 SV=1	2	0.93	0.91	0.96	3	1.21	1.21	0.90	2	0.78	0.90	0.67	22.38	17.21	18.10
Q8NI45	Placental protein KG-20 OS=Homo sapiens PE=2 SV=1	2	1.43	1.09	1.29	2	1.32	1.10	1.21	3	1.17	0.97	1.03	9.90	6.97	10.94
H0Y8C2	60S ribosomal protein L22-like 1 (Fragment) OS=Homo sapiens GN=RPL22L1 PE=2 SV=1	2	0.87	1.04	1.08	3	0.83	0.93	0.77	3	0.88	0.90	0.86	3.02	7.99	17.64

Q86W42	THO complex subunit 6 homolog OS=Homo sapiens GN=THOC6 PE=1 SV=1	3	0.86	0.80	1.25	3	0.79	1.01	0.86	3	1.17	1.07	0.95	20.98	14.40	19.86
O43149	Zinc finger ZZ-type and EF-hand domain-containing protein 1 OS=Homo sapiens GN=ZZEF1 PE=1 SV=6	2	1.12	1.04	1.00	3	0.87	0.82	1.74	5	0.93	0.97	0.79	13.29	11.47	42.37
P78356	Phosphatidylinositol 5-phosphate 4-kinase type-2 beta OS=Homo sapiens GN=PIP4K2B PE=1 SV=1	2	1.12	1.33	1.85	6	0.78	0.71	0.64	3	1.27	1.47	1.06	23.58	34.49	51.62
B2R4N3	cDNA, FLJ92155, highly similar to Homo sapiens ubiquitin-like 5 (UBL5), mRNA OS=Homo sapiens PE=4 SV=1	2	0.74	1.09	1.14	2	0.61	1.00	0.71	2	0.50	0.86	0.56	19.47	11.66	37.01
Q6NYC8	Phostensin OS=Homo sapiens GN=PPP1R18 PE=1 SV=1	2	1.06	1.06	1.12	2	1.58	1.50	2.19	3	1.05	0.71	0.82	24.55	36.46	51.92
P17600	Synapsin-1 OS=Homo sapiens GN=SYN1 PE=1 SV=3	2	0.81	1.11	0.94	2	0.99	1.27	1.00	2	1.08	1.05	0.99	14.18	10.18	3.15
F5H583	Cytoplasmic FMR1-interacting protein 2 OS=Homo sapiens GN=CYFIP2 PE=2 SV=1	10	1.11	1.23	1.41	6	1.16	0.99	0.91	9	0.74	1.02	0.68	23.13	12.26	37.63
C9JG97	Angio-associated migratory cell protein OS=Homo sapiens GN=AAMP PE=2 SV=1	2	1.18	1.11	1.08	3	0.95	1.17	1.03	5	0.85	0.87	0.97	17.13	15.39	5.19
Q9C0C2	182 kDa tankyrase-1-binding protein OS=Homo sapiens GN=TNKS1BP1 PE=1 SV=4	2	0.92	0.99	1.55	4	0.96	1.19	1.22	3	1.19	1.22	1.71	14.42	10.81	16.61
P62304	Small nuclear ribonucleoprotein E OS=Homo sapiens GN=SNRPE PE=1 SV=1	2	1.02	1.02	1.10	3	0.85	0.87	0.85	3	0.90	1.12	0.77	9.56	12.84	19.03
E5RGX5	Stathmin OS=Homo sapiens GN=STMN2 PE=2 SV=1	7	0.90	1.14	1.08	9	0.78	1.00	0.89	7	1.00	1.08	0.94	12.62	6.73	10.43
P09619	Platelet-derived growth factor receptor beta OS=Homo sapiens GN=PDGFRB PE=1 SV=1	3	1.13	0.88	1.01	3	1.12	1.59	1.51	2	0.99	0.54	0.60	7.09	53.50	43.75
Q9Y3Y2	Chromatin target of PRMT1 protein OS=Homo sapiens GN=CHTOP PE=1 SV=2	3	0.93	1.03	0.98	2	0.90	0.98	0.95	2	0.98	0.88	1.13	4.23	7.92	9.64
Q9BVQ7	Spermatogenesis-associated protein 5-like protein 1 OS=Homo sapiens GN=SPATA5L1 PE=1 SV=2	2	0.68	0.78	0.86	3	0.87	0.97	1.22	2	0.83	0.90	0.99	12.51	10.75	17.75
H0YLF2	Homeobox-containing protein 1 (Fragment) OS=Homo sapiens GN=HMBOX1 PE=2 SV=1	2	0.86	0.62	0.97	3	0.90	0.88	0.87	3	0.98	0.84	0.97	6.50	17.74	6.22
E9PGC1	Sodium bicarbonate cotransporter 3 OS=Homo sapiens GN=SLC4A7 PE=2 SV=1	2	1.41	1.39	0.76	2	0.60	0.63	0.62	3	0.91	0.80	0.76	42.27	42.73	11.48
Q86SX6	Glutaredoxin-related protein 5, mitochondrial OS=Homo sapiens GN=GLRX5 PE=1 SV=2	4	0.86	0.94	1.06	5	0.71	0.85	0.76	4	1.01	1.11	1.09	17.39	13.85	18.83
Q9H1E5	Thioredoxin-related transmembrane protein 4 OS=Homo sapiens GN=TMX4 PE=1 SV=1	4	1.02	0.99	0.94	2	0.94	0.94	1.03	2	1.10	0.97	1.03	7.89	2.46	5.24
Q8N2F6	Armadillo repeat-containing protein 10 OS=Homo sapiens GN=ARMC10 PE=1 SV=1	2	0.80	0.89	1.08	3	0.94	1.03	0.94	2	0.97	1.00	0.78	10.12	7.44	16.34
Q53F88	General transcription factor IIE, polypeptide 1 (Alpha subunit, 56kD) variant (Fragment) OS=Homo sapiens PE=2 SV=1	2	1.27	1.43	1.89	2	1.25	0.92	1.13	4	1.08	1.04	1.00	8.76	23.54	35.65
Q9Y2V2	Calcium-regulated heat stable protein 1 OS=Homo sapiens GN=CARHSP1 PE=1 SV=2	4	0.91	1.17	0.92	2	0.85	1.11	0.90	2	0.81	0.95	0.72	5.65	10.53	13.22
O15116	U6 snRNA-associated Sm-like protein LSm1 OS=Homo sapiens GN=LSM1 PE=1 SV=1	2	0.99	0.75	1.11	2	0.85	0.83	0.71	3	1.12	1.12	0.99	13.67	21.52	21.78

Q58FF7	Putative heat shock protein HSP 90-beta-3 OS=Homo sapiens GN=HSP90AB3P PE=5 SV=1	61	1.18	0.84	0.94	47	0.97	1.02	0.92	54	1.04	0.93	0.90	10.15	9.77	2.21
Q86U75	Dihydropyrimidinase-like 2 OS=Homo sapiens PE=2 SV=1	53	1.10	0.44	0.60	46	1.14	1.03	1.36	40	0.94	0.92	0.92	9.72	39.12	39.77
Q5JR08	Rho-related GTP-binding protein RhoC (Fragment) OS=Homo sapiens GN=RHOC PE=2 SV=1	18	1.26	0.99	0.89	14	1.06	1.45	1.50	15	0.85	0.77	0.83	19.28	32.43	34.84
P15531	Nucleoside diphosphate kinase A OS=Homo sapiens GN=NME1 PE=1 SV=1	27	1.06	1.17	1.46	19	0.80	0.84	0.76	27	0.94	1.03	1.07	14.33	16.37	31.76
K7EJH8	Alpha-actinin-4 (Fragment) OS=Homo sapiens GN=ACTN4 PE=4 SV=1	16	0.91	1.12	0.92	18	0.98	0.89	0.81	17	0.72	1.03	0.88	15.97	11.22	6.77
Q53F35	Acidic (Leucine-rich) nuclear phosphoprotein 32 family, member B variant (Fragment) OS=Homo sapiens PE=2 SV=1	11	0.89	1.09	1.08	13	0.90	0.98	0.82	13	0.94	1.14	0.98	2.87	7.68	13.35
Q8NFH9	MLL/SEPTIN6 fusion protein (Fragment) OS=Homo sapiens PE=2 SV=1	7	1.12	0.82	1.26	8	1.02	0.94	0.96	8	0.99	1.00	1.15	7.00	9.99	13.41
P01112	GTPase HRas OS=Homo sapiens GN=HRAS PE=1 SV=1	5	0.95	0.99	0.98	5	0.67	0.65	0.67	5	0.87	0.86	0.84	17.36	20.53	19.03
G9FP35	Guanine nucleotide binding protein OS=Homo sapiens GN=GNAQ PE=2 SV=1	4	1.25	1.59	1.73	6	0.83	0.94	0.93	4	1.01	1.18	1.25	20.69	26.48	31.02
Q71UI9	Histone H2A.V OS=Homo sapiens GN=H2AFV PE=1 SV=3	4	2.77	0.84	1.59	4	2.62	1.09	1.85	4	2.34	0.90	1.74	8.46	13.63	7.52
Q5U086	Serine/threonine-protein phosphatase OS=Homo sapiens PE=2 SV=1	4	0.97	0.95	1.35	5	1.00	0.81	0.97	5	1.08	0.97	1.26	5.36	9.46	16.83
O15397	Importin-8 OS=Homo sapiens GN=IPO8 PE=1 SV=2	3	1.19	0.90	1.15	5	0.79	0.88	0.84	6	0.97	1.11	1.06	20.54	13.16	15.65
Q9P032	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 4 OS=Homo sapiens GN=NDUFAF4 PE=1 SV=1	4	1.08	0.85	0.67	5	1.53	0.99	1.23	5	1.11	0.84	1.03	20.17	9.67	28.95
Q86YN1	Dolichyldiphosphatase 1 OS=Homo sapiens GN=DOLPP1 PE=1 SV=1	3	1.39	1.13	1.51	4	1.16	0.98	1.18	3	1.34	1.10	1.08	9.19	7.45	17.60
Q9P253	Vacuolar protein sorting-associated protein 18 homolog OS=Homo sapiens GN=VPS18 PE=1 SV=2	2	1.06	0.64	1.39	2	1.22	1.16	1.15	2	1.11	0.91	1.05	7.28	28.44	14.41
Q8WWI5	Choline transporter-like protein 1 OS=Homo sapiens GN=SLC44A1 PE=1 SV=1	3	1.20	1.47	0.94	2	1.07	0.95	1.17	3	0.73	0.94	0.85	24.13	27.47	17.07
Q6IAM7	SPC18 protein OS=Homo sapiens GN=SPC18 PE=2 SV=1	3	1.69	1.11	1.51	3	1.21	0.87	1.09	2	1.35	1.12	1.18	17.26	13.93	17.36
Q6FGB3	PCBD protein (Fragment) OS=Homo sapiens GN=PCBD1 PE=2 SV=1	3	0.96	1.00	0.77	3	1.09	1.15	1.03	2	0.86	1.05	0.92	11.76	7.13	14.32
Q53RG0	Eukaryotic translation initiation factor 4E member 2, isoform CRA_c OS=Homo sapiens GN=tmp_locus_9 PE=2 SV=1	2	0.70	0.75	0.58	4	1.18	1.25	1.14	3	1.19	0.99	1.06	27.63	25.39	32.30
Q9UBV8	Peflin OS=Homo sapiens GN=PEF1 PE=1 SV=1	2	0.75	1.01	0.97	2	0.74	0.77	0.97	4	1.20	1.25	1.13	29.77	23.74	8.98
O75348	V-type proton ATPase subunit G 1 OS=Homo sapiens GN=ATP6V1G1 PE=1 SV=3	2	0.86	1.05	0.95	2	1.01	0.86	0.94	3	0.98	1.12	1.03	8.59	13.40	4.89
Q6NUQ4	Transmembrane protein 214 OS=Homo sapiens GN=TMEM214 PE=1 SV=2	2	1.15	1.05	1.26	9	1.11	0.94	1.14	4	1.62	1.18	1.32	21.96	11.41	7.61
Q13425	Beta-2-syntrophin OS=Homo sapiens GN=SNTB2 PE=1 SV=1	2	1.37	1.03	1.55	2	1.49	0.78	1.35	2	1.21	0.76	1.20	10.31	17.24	13.04
Q9NY61	Protein AATF OS=Homo sapiens GN=AATF PE=1 SV=1	2	1.13	1.12	1.80	2	0.93	1.09	1.49	2	0.89	1.11	1.08	12.88	1.05	24.86

Q5XKP0	Protein QIL1 OS=Homo sapiens GN=QIL1 PE=1 SV=1	2	1.10	1.13	1.15	3	0.92	0.79	0.86	3	1.08	1.07	0.98	9.71	17.99	14.44
P63172	Dynein light chain Tctex-type 1 OS=Homo sapiens GN=DYNLT1 PE=1 SV=1	5	1.01	1.08	0.92	4	0.59	1.01	0.81	6	0.69	0.79	1.11	28.92	15.28	16.11
P47813	Eukaryotic translation initiation factor 1A, X-chromosomal OS=Homo sapiens GN=EIF1AX PE=1 SV=2	2	0.80	0.81	0.77	2	1.11	1.05	0.95	4	1.02	1.01	1.11	15.83	13.24	17.91
P29084	Transcription initiation factor IIE subunit beta OS=Homo sapiens GN=GTF2E2 PE=1 SV=1	3	0.76	1.14	0.74	2	0.78	0.97	0.79	3	0.96	1.06	1.05	13.54	7.64	19.12
Q6IPI1	Ribosomal protein L29 OS=Homo sapiens GN=RPL29 PE=2 SV=1	3	1.15	0.96	0.99	2	1.60	2.23	1.66	3	1.22	0.96	1.04	18.11	52.63	30.53
Q6IB68	MYCBP protein OS=Homo sapiens GN=MYCBP PE=4 SV=1	2	1.23	1.10	1.02	2	1.21	1.04	1.11	3	1.09	0.90	0.93	6.57	10.09	8.84
G8JLB3	tRNA pseudouridine synthase (Fragment) OS=Homo sapiens GN=PUS1 PE=2 SV=1	3	0.95	0.95	0.97	2	0.79	0.82	0.96	2	0.93	1.11	0.85	9.37	15.21	7.24
G3V3J9	Guanine nucleotide-binding protein subunit gamma OS=Homo sapiens GN=GNG2 PE=2 SV=1	2	1.00	1.05	1.08	2	1.04	0.97	1.03	2	1.16	0.99	1.07	7.97	4.42	2.46
C9JVE2	DCN1, defective in cullin neddylation 1, domain containing 1 (S. cerevisiae), isoform CRA_a OS=Homo sapiens GN=DCUN1D1 PE=2 SV=1	3	1.27	1.04	1.26	5	0.64	0.53	0.55	4	1.15	1.80	1.02	33.06	57.12	37.99
B3KM21	Family with sequence similarity 36, member A, isoform CRA_a OS=Homo sapiens GN=FAM36A PE=2 SV=1	2	1.28	1.10	1.30	3	0.81	0.61	0.78	2	1.09	1.18	1.21	22.16	32.16	25.45
Q9UK08	Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-8 OS=Homo sapiens GN=GNG8 PE=2 SV=1	3	0.95	1.13	1.04	2	1.04	1.10	0.98	2	1.02	0.92	0.95	4.62	10.76	4.82
Q9NYJ1	Cytochrome c oxidase assembly factor 4 homolog, mitochondrial OS=Homo sapiens GN=COA4 PE=1 SV=2	2	0.99	1.13	1.07	2	1.24	1.13	1.10	2	1.15	1.06	1.23	11.15	3.45	7.53
Q96DA6	Mitochondrial import inner membrane translocase subunit TIM14 OS=Homo sapiens GN=DNAJC19 PE=1 SV=3	3	1.16	1.12	1.09	2	1.28	1.16	1.11	2	1.32	1.08	1.38	6.59	3.47	13.60
Q69YL0	Uncharacterized protein DKFZp762I1415 OS=Homo sapiens PE=4 SV=1	2	1.09	1.13	0.85	2	0.81	0.84	0.76	2	1.09	1.01	0.85	16.00	14.66	5.79
P82921	28S ribosomal protein S21, mitochondrial OS=Homo sapiens GN=MRPS21 PE=1 SV=2	3	0.77	0.94	0.96	3	0.02	7.08	4.50	2	1.26	1.23	1.18	92.05	112.33	89.83
P49069	Calcium signal-modulating cyclophilin ligand OS=Homo sapiens GN=CAMLG PE=1 SV=1	2	1.47	0.96	1.15	2	0.88	1.59	0.89	3	0.70	0.84	0.99	39.79	35.55	13.01
O00483	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4 OS=Homo sapiens GN=NDUFA4 PE=1 SV=1	5	1.21	1.01	1.22	2	1.15	0.77	0.92	2	1.14	1.07	1.04	3.18	16.68	14.56
Q9BYK1	40S ribosomal protein S21 OS=Homo sapiens GN=RPS21 PE=2 SV=1	8	0.95	1.00	1.11	7	1.04	0.97	0.94	5	0.98	0.98	0.99	4.40	1.35	8.27
Q9BRV4	Vesicle-associated membrane protein 3 (Cellubrevin) OS=Homo sapiens GN=VAMP3 PE=4 SV=1	2	0.86	0.78	1.25	2	0.89	1.12	0.99	6	1.35	1.09	1.07	26.55	18.90	11.83
Q49AN9	SNRPG protein OS=Homo sapiens GN=SNRPG PE=2 SV=1	7	0.98	0.97	1.28	3	0.83	0.81	0.90	2	0.96	1.13	1.08	8.82	16.64	17.50

K7ERC8	3-ketodihydrosphingosine reductase (Fragment) OS=Homo sapiens GN=KDSR PE=3 SV=1	2	1.11	0.89	1.01	2	1.17	0.83	0.90	3	1.11	1.20	1.09	3.21	20.25	9.32
J3KS15	Peptidyl-tRNA hydrolase ICT1, mitochondrial (Fragment) OS=Homo sapiens GN=ICT1 PE=4 SV=1	2	1.13	1.10	1.39	2	1.07	0.95	0.93	2	1.10	1.20	1.02	2.68	11.44	21.82
H3BT58	Coactosin-like protein OS=Homo sapiens GN=COTL1 PE=2 SV=1	3	1.27	1.16	1.11	3	0.72	0.87	0.85	2	1.32	1.07	1.29	29.84	14.61	20.20
F5H577	Protein BRICK1 OS=Homo sapiens GN=BRK1 PE=2 SV=1	3	0.96	1.21	1.09	3	1.08	1.03	1.01	2	0.83	1.00	0.87	12.76	10.91	10.92
B7Z5Z2	Ras-related protein R-Ras2 OS=Homo sapiens GN=RRAS2 PE=2 SV=1	2	1.42	0.97	0.93	3	1.19	1.41	1.41	4	1.18	0.85	1.21	10.49	27.25	20.43
B1AH87	Putative peripheral benzodiazepine receptor-related protein (Fragment) OS=Homo sapiens GN=TSPO PE=2 SV=1	3	0.77	0.71	1.10	3	0.81	0.63	0.93	2	0.96	0.77	1.09	11.72	9.78	9.04
A4D158	Neuropeptide Y OS=Homo sapiens GN=NPY PE=2 SV=1	2	0.90	0.94	1.67	2	0.93	1.08	1.17	2	1.12	1.06	1.14	12.28	7.29	22.60
Q9Y2R0	Cytochrome c oxidase assembly protein 3 homolog, mitochondrial OS=Homo sapiens GN=COA3 PE=1 SV=1	2	1.23	1.14	1.17	2	1.06	0.81	0.92	2	1.04	0.84	1.00	9.69	19.42	12.37
Q9UNI6	Dual specificity protein phosphatase 12 OS=Homo sapiens GN=DUSP12 PE=1 SV=1	2	1.03	1.17	1.15	3	1.35	1.12	0.87	2	1.24	1.05	1.14	13.73	5.59	15.24
Q9GZP4	PITH domain-containing protein 1 OS=Homo sapiens GN=PITHD1 PE=1 SV=1	2	0.70	0.61	0.43	2	0.68	1.00	0.81	2	1.00	0.62	0.72	22.44	29.80	30.16
Q96EL3	39S ribosomal protein L53, mitochondrial OS=Homo sapiens GN=MRPL53 PE=1 SV=1	4	0.99	0.96	0.66	2	1.05	1.17	1.02	2	1.07	1.08	0.96	3.55	9.91	21.92
Q6NXE6	Armadillo repeat-containing protein 6 OS=Homo sapiens GN=ARMC6 PE=1 SV=2	2	1.55	1.23	1.05	4	0.98	0.86	0.72	2	1.73	0.88	1.93	27.36	21.32	50.71
P49458	Signal recognition particle 9 kDa protein OS=Homo sapiens GN=SRP9 PE=1 SV=2	2	0.85	0.95	0.83	4	0.98	0.94	0.93	3	0.87	1.01	0.91	7.79	4.17	5.58
H0YAV1	Ribonucleoside-diphosphate reductase subunit M2 B (Fragment) OS=Homo sapiens GN=RRM2B PE=4 SV=1	6	0.77	0.88	0.78	4	1.08	0.84	1.07	3	1.07	1.14	1.04	17.79	17.03	16.45
O15066	Kinesin-like protein KIF3B OS=Homo sapiens GN=KIF3B PE=1 SV=1	2	1.14	1.40	1.00	2	1.05	1.25	1.04	2	0.85	0.97	0.99	14.70	18.04	2.86
Q562R1	Beta-actin-like protein 2 OS=Homo sapiens GN=ACTBL2 PE=1 SV=2	65	1.16	0.96	1.08	51	0.96	0.98	0.96	49	1.13	0.86	0.87	10.04	6.93	10.86
B7Z5V6	cDNA FLJ57046, highly similar to Lysosomal alpha-glucosidase (EC 3.2.1.20) OS=Homo sapiens PE=2 SV=1	8	1.27	1.20	0.90	5	1.26	1.37	0.78	6	0.98	1.01	1.24	14.23	15.13	24.26
Q9UDW1	Cytochrome b-c1 complex subunit 9 OS=Homo sapiens GN=UQCR10 PE=1 SV=3	2	1.58	1.15	1.71	2	1.41	0.88	1.16	3	1.58	1.10	1.36	6.43	14.08	19.55
Q59FZ4	Serine/threonine kinase 4 variant (Fragment) OS=Homo sapiens PE=2 SV=1	3	0.85	1.04	0.95	2	1.23	1.05	0.99	2	0.88	0.60	1.25	20.86	28.59	15.11
H7C1E4	AP-1 complex subunit sigma-1A (Fragment) OS=Homo sapiens GN=AP1S1 PE=4 SV=1	2	0.71	0.96	1.68	4	0.99	0.86	0.96	3	0.99	0.91	0.91	17.92	5.65	36.55
E9PR30	40S ribosomal protein S30 OS=Homo sapiens GN=FAU PE=2 SV=1	2	0.91	0.95	0.74	2	1.09	1.04	0.97	2	0.92	1.00	0.97	10.15	4.22	14.43
Q53FG6	Splicing factor 3b, subunit 4 variant (Fragment) OS=Homo sapiens PE=2 SV=1	2	1.12	0.91	1.08	3	1.00	0.97	0.92	3	0.84	0.97	0.98	14.02	3.40	8.27

O75940	Survival of motor neuron-related-splicing factor 30 OS=Homo sapiens GN=SMNDC1 PE=1 SV=1	2	2.10	1.39	1.15	4	0.91	0.79	0.99	4	0.95	0.99	1.03	51.48	28.85	7.80
Q53HG5	KIAA0103 variant (Fragment) OS=Homo sapiens PE=2 SV=1	3	1.07	1.21	0.99	5	1.08	0.91	0.98	2	1.18	1.12	0.86	5.44	14.14	7.55
H7BZT4	Uncharacterized protein OS=Homo sapiens PE=4 SV=1	4	0.84	0.95	0.99	2	0.59	0.82	0.93	3	0.97	1.21	1.24	23.95	19.78	15.71
M0QX35	Paf1, RNA polymerase II associated factor, homolog (S. cerevisiae), isoform CRA_c OS=Homo sapiens GN=PAF1 PE=4 SV=1	3	0.96	0.85	0.95	3	1.04	1.01	0.86	4	1.01	1.03	1.06	3.93	10.21	10.54
Q8N995	cDNA FLJ38173 fis, clone FCBBF1000053, highly similar to HYDROXYMETHYLGLUTARYL-COA SYNTHASE, CYTOPLASMIC OS=Homo sapiens PE=2 SV=1	2	1.21	0.95	0.76	3	0.74	0.94	0.96	2	1.11	1.52	1.16	24.53	29.44	20.75
Q96E11	Ribosome-recycling factor, mitochondrial OS=Homo sapiens GN=MRRF PE=1 SV=1	2	0.83	0.72	1.18	2	0.65	0.55	0.92	2	1.19	1.14	1.05	30.73	38.25	12.56
Q96F85	CB1 cannabinoid receptor-interacting protein 1 OS=Homo sapiens GN=CNRIP1 PE=1 SV=1	3	0.98	1.02	0.85	3	0.99	0.99	0.98	3	0.92	0.90	1.02	4.24	6.73	9.17
Q8IXM3	39S ribosomal protein L41, mitochondrial OS=Homo sapiens GN=MRPL41 PE=1 SV=1	6	0.86	0.89	0.65	2	1.10	1.30	0.94	3	0.76	0.86	0.72	19.27	23.98	19.50
Q2NKX8	DNA excision repair protein ERCC-6-like OS=Homo sapiens GN=ERCC6L PE=1 SV=1	3	0.89	1.10	1.21	2	0.86	0.97	1.08	2	1.23	1.07	1.07	21.19	6.95	6.63
Q13501	Sequestosome-1 OS=Homo sapiens GN=SQSTM1 PE=1 SV=1	2	1.00	0.88	1.05	4	1.15	0.96	1.01	2	1.05	1.10	1.42	7.20	11.45	19.30
Q9BQC3	Diphthamide biosynthesis protein 2 OS=Homo sapiens GN=DPH2 PE=1 SV=1	2	1.04	1.18	1.33	3	0.97	1.09	1.03	2	1.55	2.09	1.82	26.47	38.08	28.59
Q5TDH0	Protein DDI1 homolog 2 OS=Homo sapiens GN=DDI2 PE=1 SV=1	2	0.73	1.00	1.15	2	1.14	0.96	1.16	3	0.98	0.97	0.82	21.80	1.73	18.49
A2A2Q9	Protein AAR2 homolog OS=Homo sapiens GN=AAR2 PE=2 SV=1	2	1.40	1.01	0.88	2	1.08	0.97	0.90	3	1.17	0.97	1.05	13.63	2.20	9.64
P22466	Galanin peptides OS=Homo sapiens GN=GAL PE=1 SV=3	2	1.12	0.87	1.03	3	1.05	0.99	1.02	3	1.16	0.92	1.18	4.83	6.46	8.18
Q7Z7F7	39S ribosomal protein L55, mitochondrial OS=Homo sapiens GN=MRPL55 PE=1 SV=1	2	0.90	0.86	0.83	2	0.98	1.17	0.94	2	0.80	0.87	0.98	10.11	18.38	9.00
B2R9X3	cDNA, FLJ94599, highly similar to Homo sapiens GDP-mannose 4,6-dehydratase (GMDS), mRNA OS=Homo sapiens PE=2 SV=1	2	1.03	0.78	0.95	3	0.74	1.23	0.64	3	0.96	1.14	0.85	16.72	22.36	19.80
P25490	Transcriptional repressor protein YY1 OS=Homo sapiens GN=YY1 PE=1 SV=2	2	1.08	1.35	0.82	2	0.85	0.95	0.99	8	1.23	1.17	1.20	18.46	17.42	18.63
B3KRQ2	cDNA FLJ34689 fis, clone MESAN2000815, highly similar to Homo sapiens leucine zipper protein 5 (LUZP5), mRNA OS=Homo sapiens PE=2 SV=1	3	0.82	1.00	0.85	10	0.73	0.85	0.82	4	0.88	1.00	1.10	8.84	9.01	16.57
O95197-3	Isoform 3 of Reticulon-3 OS=Homo sapiens GN=RTN3	4	1.28	1.05	1.31	5	1.15	1.02	1.11	5	1.13	1.19	1.02	7.13	8.56	13.02
J3KP76	RalBP1-associated Eps domain-containing protein 1 OS=Homo sapiens GN=REPS1 PE=4 SV=1	3	0.67	1.15	1.04	4	1.00	0.98	0.87	3	0.97	1.10	1.20	20.52	8.15	16.01
Q5BKZ2	Importin subunit alpha OS=Homo sapiens GN=KPNA1 PE=2 SV=1	10	0.74	1.09	1.06	8	0.74	0.81	0.82	9	1.01	1.23	1.00	18.50	20.37	12.92
Q9Y6H1	Coiled-coil-helix-coiled-coil-helix domain-containing protein 2, mitochondrial OS=Homo sapiens GN=CHCHD2 PE=1 SV=1	2	0.76	0.89	0.88	2	0.58	0.70	0.75	3	0.76	0.91	0.68	14.64	14.10	13.37

P05204	Non-histone chromosomal protein HMG-17 OS=Homo sapiens GN=HMGN2 PE=1 SV=3	5	1.76	0.91	0.25	3	4.21	2.63	2.61	5	1.29	1.12	0.96	64.80	60.60	94.97
Q9BQ61	Uncharacterized protein C19orf43 OS=Homo sapiens GN=C19orf43 PE=1 SV=1	4	0.91	0.80	0.67	2	1.55	1.04	1.44	2	1.62	0.96	1.24	28.98	13.44	36.08
M0QXA7	Protein Wiz OS=Homo sapiens GN=WIZ PE=4 SV=1	3	1.13	0.86	1.00	2	0.99	1.04	0.95	2	1.07	0.85	1.08	6.59	11.72	6.55
Q9H1A4	Anaphase-promoting complex subunit 1 OS=Homo sapiens GN=ANAPC1 PE=1 SV=1	2	1.23	1.26	1.28	3	0.91	1.03	1.01	3	1.01	0.90	1.03	15.57	17.31	13.91
P68431	Histone H3.1 OS=Homo sapiens GN=HIST1H3A PE=1 SV=2	19	6.10	1.01	3.43	8	3.90	1.16	3.09	9	9.30	1.35	6.60	42.18	14.55	44.30
Q9P1F3	Costars family protein ABRACL OS=Homo sapiens GN=ABRACL PE=1 SV=1	3	1.75	1.24	1.73	3	0.96	1.04	0.91	2	1.25	0.77	0.44	30.38	23.51	63.63
Q6QNY7	UDP-N-acetylglucosamine-2-epimerase / N-acetylmannosamine kinase OS=Homo sapiens GN=GNE PE=2 SV=1	3	0.96	1.37	1.09	4	1.12	1.16	1.29	3	0.95	0.95	1.10	9.11	18.32	9.91
Q7Z3R8	DNA-directed RNA polymerase OS=Homo sapiens GN=DKFZp686D10173 PE=2 SV=1	2	1.12	1.22	1.20	3	0.73	1.25	0.69	2	1.00	1.11	0.95	21.14	6.45	27.01
Q3ZCW2	Galectin-related protein OS=Homo sapiens GN=LGALSL PE=1 SV=2	3	0.78	1.09	1.91	3	1.07	1.10	1.20	2	1.03	0.96	0.92	16.07	7.60	37.88
D6RF48	Syntaxin-18 OS=Homo sapiens GN=STX18 PE=2 SV=1	2	0.70	0.71	0.84	2	1.20	1.01	0.69	2	1.91	1.41	1.26	47.70	33.37	31.93
F8W9S7	GTPase-activating protein and VPS9 domain-containing protein 1 OS=Homo sapiens GN=GAPVD1 PE=2 SV=1	2	1.07	0.87	0.97	4	0.98	1.00	1.04	4	1.01	1.00	1.20	4.49	7.76	11.07
P04350	Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2	205	0.96	0.84	1.13	161	0.86	0.88	0.85	173	1.02	0.94	0.88	8.68	5.63	16.40
B7Z6B8	2,4-dienoyl-CoA reductase, mitochondrial OS=Homo sapiens GN=DECR1 PE=2 SV=1	2	1.00	1.61	1.00	2	0.91	0.83	0.78	5	0.82	0.95	0.84	10.35	37.24	12.77
M0R300	Unconventional myosin-IXb (Fragment) OS=Homo sapiens GN=MYO9B PE=4 SV=1	2	0.72	0.82	0.87	4	0.81	0.86	0.92	4	0.94	0.97	1.00	13.27	8.77	6.88
Q9Y6D5	Brefeldin A-inhibited guanine nucleotide-exchange protein 2 OS=Homo sapiens GN=ARFGEF2 PE=1 SV=3	3	1.16	0.88	1.02	6	0.76	1.08	1.12	3	0.93	1.02	0.96	21.51	10.45	8.12
Q15554	Telomeric repeat-binding factor 2 OS=Homo sapiens GN=TERF2 PE=1 SV=2	3	1.01	1.04	0.73	3	0.86	1.27	1.05	3	0.99	0.95	0.78	8.63	15.13	20.16
A8K9U4	cDNA FLJ77205, highly similar to Homo sapiens hect domain and RLD 4 (HERC4), transcript variant 2, mRNA (Fragment) OS=Homo sapiens PE=2 SV=1	2	0.94	0.97	0.85	4	1.06	1.02	0.92	2	0.82	0.92	0.87	12.46	5.23	4.03
Q9H267	Vacuolar protein sorting-associated protein 33B OS=Homo sapiens GN=VPS33B PE=1 SV=2	3	0.79	0.74	0.75	5	1.11	1.02	1.01	4	0.89	0.91	0.80	17.81	16.08	16.08
Q53FU3	Coatomer protein complex, subunit zeta 1 variant (Fragment) OS=Homo sapiens PE=2 SV=1	2	0.72	1.01	1.14	3	0.79	0.98	1.13	2	0.89	1.01	0.83	10.68	1.91	16.74
B7Z4A1	cDNA FLJ50798, weakly similar to Ubiquinol-cytochrome c reductase complex ubiquinone-binding protein QP-C (EC 1.10.2.2) OS=Homo sapiens PE=4 SV=1	2	0.98	1.01	0.67	2	1.36	1.02	1.06	2	1.30	1.02	1.03	16.72	0.86	23.43
K7EJU9	Bifunctional arginine demethylase and lysyl-hydroxylase JMJD6 OS=Homo sapiens GN=JMJD6 PE=4 SV=1	3	1.02	1.01	1.74	2	0.77	0.88	0.92	3	0.87	1.12	0.99	13.93	12.00	37.60

F5GZ78	Paxillin OS=Homo sapiens GN=PXN PE=2 SV=1	2	0.98	1.13	1.07	4	1.26	1.24	1.21	2	0.87	0.98	1.10	19.41	11.48	6.43
R4GNA1	Neuroblastoma suppressor of tumorigenicity 1 (Fragment) OS=Homo sapiens GN=NBL1 PE=4 SV=1	6	1.32	1.06	1.16	2	1.35	1.10	1.15	2	1.11	0.65	0.85	10.33	26.34	16.46
E9PGC0	Ras GTPase-activating protein 1 OS=Homo sapiens GN=RASA1 PE=2 SV=1	2	0.96	1.17	1.19	4	1.07	0.96	1.08	4	0.86	0.90	0.83	11.27	14.06	17.78
B3KUH1	cDNA FLJ39884 fis, clone SPLEN2016304 OS=Homo sapiens PE=2 SV=1	3	1.21	0.71	1.30	2	1.89	1.16	1.07	2	1.17	1.02	1.00	28.29	23.76	14.20
P63096	Guanine nucleotide-binding protein G(i) subunit alpha-1 OS=Homo sapiens GN=GNAI1 PE=1 SV=2	10	1.19	1.13	1.86	7	0.91	0.71	0.79	9	0.84	1.23	0.88	18.81	26.92	50.33
Q86UU1	Pleckstrin homology-like domain family B member 1 OS=Homo sapiens GN=PHLDB1 PE=1 SV=1	3	0.75	0.91	0.96	4	0.60	0.80	0.66	2	0.91	1.40	1.23	20.41	31.07	30.10
D6RIZ4	Major facilitator superfamily domain-containing protein 10 OS=Homo sapiens GN=MFSD10 PE=2 SV=1	2	1.61	1.18	1.13	2	1.10	1.05	1.08	2	1.02	0.97	0.94	25.61	9.68	9.53
Q99496	E3 ubiquitin-protein ligase RING2 OS=Homo sapiens GN=RNF2 PE=1 SV=1	3	0.89	0.73	0.66	3	0.64	0.70	0.58	4	0.81	1.30	1.04	15.99	37.30	32.81
Q9H814	Phosphorylated adapter RNA export protein OS=Homo sapiens GN=PHAX PE=1 SV=1	2	1.33	0.78	3.21	2	1.05	1.08	1.06	2	1.04	0.88	0.93	14.56	17.10	73.67
D6RIY6	Exosome complex component RRP45 OS=Homo sapiens GN=EXOSC9 PE=2 SV=1	2	0.90	1.04	0.89	2	0.85	0.79	0.82	3	1.04	0.90	1.07	10.32	14.00	14.25
J3KT68	Transmembrane protein 97 OS=Homo sapiens GN=TMEM97 PE=4 SV=1	2	1.37	0.92	1.21	2	1.55	1.35	1.50	4	1.18	0.87	1.11	13.60	25.06	16.09
Q5T1M5	FK506-binding protein 15 OS=Homo sapiens GN=FKBP15 PE=1 SV=2	2	1.52	1.19	1.45	3	1.08	1.44	1.33	2	0.74	1.12	0.96	35.15	13.19	20.36
P61006	Ras-related protein Rab-8A OS=Homo sapiens GN=RAB8A PE=1 SV=1	5	1.17	1.25	1.27	6	0.68	0.70	1.01	6	0.60	0.71	1.28	38.02	35.02	12.98
Q86VR2	Protein FAM134C OS=Homo sapiens GN=FAM134C PE=1 SV=1	2	1.13	0.95	0.90	3	1.19	1.45	1.28	2	1.32	1.01	1.22	8.15	23.96	17.82
Q6ICQ8	ARHG protein (Fragment) OS=Homo sapiens GN=ARHG PE=2 SV=1	3	1.04	0.88	0.70	2	1.45	1.12	1.14	3	1.10	0.94	0.88	18.84	13.19	24.31
E7EV10	Metastasis-associated protein MTA3 OS=Homo sapiens GN=MTA3 PE=2 SV=1	5	1.04	1.55	1.31	2	0.80	0.95	0.99	4	0.96	0.95	1.18	13.48	30.04	13.69
A8K2Q6	Peptidyl-prolyl cis-trans isomerase OS=Homo sapiens PE=2 SV=1	2	1.57	1.12	1.40	3	1.37	0.92	1.20	2	1.37	1.40	1.69	8.11	21.03	17.38
Q9GZU8	Protein FAM192A OS=Homo sapiens GN=FAM192A PE=1 SV=1	4	0.98	1.11	0.92	2	0.59	0.86	0.83	4	0.68	1.00	0.87	27.29	12.69	5.18
K7ESP4	Dephospho-CoA kinase domain-containing protein (Fragment) OS=Homo sapiens GN=DCAKD PE=3 SV=1	2	0.91	1.11	1.09	4	0.68	0.87	0.76	3	1.00	0.96	1.30	19.20	12.06	25.72
Q9NRG1	Phosphoribosyltransferase domain-containing protein 1 OS=Homo sapiens GN=PRTFDC1 PE=1 SV=1	2	0.98	1.07	0.81	2	1.01	1.23	1.18	2	1.10	1.07	0.88	5.98	8.08	20.67
Q9BRX5	DNA replication complex GINS protein PSF3 OS=Homo sapiens GN=GINS3 PE=1 SV=1	2	0.62	1.15	0.92	2	0.93	1.13	1.10	2	0.85	1.01	0.98	20.42	6.64	9.44
Q9Y2D4	Exocyst complex component 6B OS=Homo sapiens GN=EXOC6B PE=1 SV=3	2	0.87	0.85	0.67	2	1.01	1.15	0.99	3	0.94	0.84	0.85	7.09	18.65	19.08
Q59GQ7	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin a3 variant (Fragment) OS=Homo sapiens PE=2 SV=1	3	1.06	1.07	0.57	3	1.01	1.16	1.04	2	0.70	0.73	1.03	20.99	22.75	30.30

B4E205	cDNA FLJ61651, highly similar to Protein transport protein Sec24A OS=Homo sapiens PE=2 SV=1	2	1.13	0.67	1.18	4	1.26	1.30	1.54	5	0.93	0.93	1.07	14.96	32.89	19.35
Q9P2N5	RNA-binding protein 27 OS=Homo sapiens GN=RBM27 PE=1 SV=2	2	0.67	0.88	0.75	5	0.98	0.96	0.88	2	0.91	0.97	1.00	18.99	5.46	14.21
Q02040	A-kinase anchor protein 17A OS=Homo sapiens GN=AKAP17A PE=1 SV=2	2	0.97	1.01	1.19	2	1.06	1.21	1.19	3	0.97	1.05	0.99	5.32	9.71	10.45
Q5W009	RNA binding motif protein 17, isoform CRA_a OS=Homo sapiens GN=RBM17 PE=2 SV=1	2	0.89	0.96	0.78	3	0.88	0.96	0.88	2	0.82	1.46	0.84	4.21	25.40	6.32
Q9Y3A3	MOB-like protein phocein OS=Homo sapiens GN=MOB4 PE=1 SV=1	2	0.98	1.11	1.19	2	0.97	0.96	1.10	2	1.02	0.86	1.49	2.53	12.80	16.26
Q9BXK5	Bcl-2-like protein 13 OS=Homo sapiens GN=BCL2L13 PE=1 SV=1	3	0.66	1.01	0.95	2	0.79	0.70	0.81	4	0.92	0.94	0.70	16.01	18.92	15.62
Q9NY93	Probable ATP-dependent RNA helicase DDX56 OS=Homo sapiens GN=DDX56 PE=1 SV=1	2	0.77	1.13	1.10	5	0.93	1.08	1.00	3	1.07	0.89	0.90	16.43	11.83	10.03
Q9UI15	Transgelin-3 OS=Homo sapiens GN=TAGLN3 PE=1 SV=2	5	0.93	0.81	0.86	4	1.35	0.93	1.12	6	0.87	0.83	1.04	24.96	7.28	13.45
Q9BVG4	Protein PBDC1 OS=Homo sapiens GN=PBDC1 PE=1 SV=1	2	0.83	1.25	0.80	6	0.88	0.93	0.68	2	1.08	0.92	0.80	14.28	18.17	9.46
C9J8P9	Clathrin light chain A OS=Homo sapiens GN=CLTA PE=2 SV=1	3	1.05	0.90	1.15	6	1.04	0.94	1.02	5	1.03	1.09	1.00	1.00	10.13	7.80
C9J5N1	Protein PTGES3L-AARSD1 OS=Homo sapiens GN=PTGES3L-AARSD1 PE=2 SV=1	2	0.97	0.83	1.46	3	0.87	0.94	0.90	2	0.98	0.95	1.26	6.55	7.01	23.72
H3BQV3	Conserved oligomeric Golgi complex subunit 8 OS=Homo sapiens GN=COG8 PE=2 SV=1	2	1.20	0.95	1.76	2	1.31	0.67	1.03	2	0.93	0.86	0.65	16.64	17.38	49.13
Q9NP58	ATP-binding cassette sub-family B member 6, mitochondrial OS=Homo sapiens GN=ABCB6 PE=1 SV=1	2	1.22	1.03	1.03	3	0.94	0.62	0.86	2	1.08	0.61	0.89	13.16	31.74	10.10
F5H5U2	ATP-dependent RNA helicase DDX55 OS=Homo sapiens GN=DDX55 PE=2 SV=1	2	1.43	0.93	0.75	2	0.73	0.99	0.79	3	0.96	1.07	0.83	33.89	7.17	4.59
Q9Y3C1	Nucleolar protein 16 OS=Homo sapiens GN=NOP16 PE=1 SV=2	3	0.96	1.03	1.08	2	0.81	0.78	0.95	2	1.09	1.12	0.99	14.34	17.91	7.00
Q1W6H1	DNA-3-methyladenine glycosylase OS=Homo sapiens GN=MPG PE=2 SV=1	2	0.41	0.79	0.83	2	0.39	0.44	0.51	2	1.22	1.06	1.02	69.96	40.17	32.29
B4DK44	Beta-soluble NSF attachment protein OS=Homo sapiens GN=NAPB PE=2 SV=1	3	0.88	1.10	0.74	5	1.02	1.00	0.98	3	1.12	0.93	1.07	11.64	8.65	18.33
A6NMQ1	DNA polymerase OS=Homo sapiens GN=POLA1 PE=2 SV=1	2	0.69	0.96	1.41	3	0.90	1.06	0.83	5	0.95	1.04	1.00	16.28	5.42	27.85
Q12873	Chromodomain-helicase-DNA-binding protein 3 OS=Homo sapiens GN=CHD3 PE=1 SV=3	9	1.62	0.93	1.97	12	1.35	0.62	1.22	16	1.00	1.02	0.93	23.24	24.13	39.11
Q6I9V5	SLC25A6 protein OS=Homo sapiens GN=SLC25A6 PE=2 SV=1	27	1.33	1.03	1.13	26	1.54	1.09	1.28	25	1.35	0.77	1.29	8.13	17.70	7.22
Q9BV79	Trans-2-enoyl-CoA reductase, mitochondrial OS=Homo sapiens GN=MECR PE=1 SV=2	3	0.82	0.96	1.03	2	0.95	0.78	1.00	3	1.15	1.23	0.86	16.78	22.84	9.53
A4D0Z3	ADP-ribosylation factor 5 OS=Homo sapiens GN=ARF5 PE=2 SV=1	9	1.14	1.50	1.23	11	0.89	0.90	0.88	6	0.90	1.00	0.87	14.43	28.44	20.72
Q00403	Transcription initiation factor IIB OS=Homo sapiens GN=GTF2B PE=1 SV=1	2	0.76	0.90	1.01	2	1.35	1.15	0.84	2	0.60	0.68	0.70	43.91	25.55	18.58
Q96SI9	Spermatid perinuclear RNA-binding protein OS=Homo sapiens GN=STRBP PE=1 SV=1	5	1.35	1.30	1.99	6	0.94	1.15	0.93	6	0.97	1.04	0.69	21.11	10.93	57.59
Q9ULT8	E3 ubiquitin-protein ligase HECTD1 OS=Homo sapiens GN=HECTD1 PE=1 SV=3	2	2.73	1.92	3.49	2	1.60	1.06	1.26	3	0.89	0.99	0.95	53.57	39.37	72.70

Q08379	Golgin subfamily A member 2 OS=Homo sapiens GN=GOLGA2 PE=1 SV=3	2	0.97	0.96	1.07	5	1.42	1.32	1.31	4	1.10	0.90	1.02	20.06	21.57	13.77
B4E1J8	cDNA FLJ56285, highly similar to ADP-ribosylation factor-like protein 8B OS=Homo sapiens PE=2 SV=1	3	0.86	0.78	0.95	4	1.04	0.96	1.13	6	0.92	0.96	0.76	9.78	11.34	19.76
Q5VW36	Focadhesin OS=Homo sapiens GN=FOCAD PE=1 SV=1	2	0.96	1.07	0.91	3	1.01	0.85	0.91	4	0.89	1.02	1.18	6.24	11.63	15.36
Q14964	Ras-related protein Rab-39A OS=Homo sapiens GN=RAB39A PE=2 SV=2	2	0.76	0.90	0.68	2	0.75	0.71	0.66	3	0.96	0.95	0.83	14.27	15.37	13.10
Q14692	Ribosome biogenesis protein BMS1 homolog OS=Homo sapiens GN=BMS1 PE=1 SV=1	2	1.54	1.08	0.68	4	1.00	1.21	1.27	4	0.94	0.93	0.95	28.27	12.90	30.64
K7EIG1	Clustered mitochondria protein homolog OS=Homo sapiens GN=CLUH PE=3 SV=1	3	0.67	0.79	0.41	4	0.84	1.11	0.68	2	0.69	0.94	1.11	12.72	17.07	48.33
B3KUD7	cDNA FLJ39640 fis, clone SMINT2003386, highly similar to DNA REPLICATION LICENSING FACTOR MCM7 OS=Homo sapiens PE=2 SV=1	27	0.74	0.77	0.70	27	1.11	1.14	1.19	27	1.17	0.82	1.06	23.42	22.18	26.08
Q0VGD6	HNRPR protein (Fragment) OS=Homo sapiens GN=HNRPR PE=2 SV=1	25	1.01	0.76	1.38	27	1.27	1.06	1.04	22	0.91	1.01	1.05	17.43	17.23	16.54
Q5T6W5	Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK PE=2 SV=1	48	1.02	0.92	1.04	47	1.07	0.94	1.07	35	0.92	0.86	0.90	7.19	4.47	8.88
A8K132	cDNA FLJ75476, highly similar to Homo sapiens glutaminase (GLS), mRNA OS=Homo sapiens PE=2 SV=1	22	1.13	1.09	0.96	17	1.56	1.30	1.25	13	0.97	0.79	1.15	24.91	23.99	13.01
Q5U0Q1	Putative uncharacterized protein DKFZp686L1159 OS=Homo sapiens GN=G3BP PE=2 SV=1	22	0.91	1.02	0.76	17	1.03	0.82	0.89	17	0.86	0.98	0.89	9.43	11.21	9.17
Q59EN5	Prosaposin variant (Fragment) OS=Homo sapiens PE=2 SV=1	22	0.75	1.22	0.60	21	0.51	1.04	0.63	15	0.50	0.88	0.59	24.38	16.51	3.28
Q14978-3	Isoform 3 of Nucleolar and coiled-body phosphoprotein 1 OS=Homo sapiens GN=NOLC1	11	0.64	0.92	0.97	9	0.68	0.88	0.75	5	1.02	1.15	0.99	26.78	14.71	14.64
A5A3E0	POTE ankyrin domain family member F OS=Homo sapiens GN=POTEF PE=1 SV=2	71	0.96	0.94	1.08	51	0.88	0.91	0.95	52	0.94	0.89	0.95	4.77	2.78	7.69
P61204	ADP-ribosylation factor 3 OS=Homo sapiens GN=ARF3 PE=1 SV=2	11	0.86	0.70	0.77	11	0.62	0.62	0.60	9	0.65	0.88	0.86	18.18	17.92	18.09
P0CG39	POTE ankyrin domain family member J OS=Homo sapiens GN=POTEJ PE=3 SV=1	42	0.90	1.01	1.12	40	1.11	0.74	0.75	36	0.96	0.89	1.08	10.56	15.66	20.90
P62633	Cellular nucleic acid-binding protein OS=Homo sapiens GN=CNBP PE=1 SV=1	9	1.15	0.80	0.67	7	0.79	0.62	0.85	7	0.87	1.00	0.78	20.19	23.57	11.80
P35080	Profilin-2 OS=Homo sapiens GN=PFN2 PE=1 SV=3	9	1.00	1.18	1.07	12	0.90	1.02	0.88	8	0.84	0.93	0.82	8.76	12.40	13.92
A8K4W8	cDNA FLJ77917, highly similar to Homo sapiens ubiquitin-conjugating enzyme E2L 3 (UBE2L3), transcript variant 1, mRNA OS=Homo sapiens PE=2 SV=1	11	0.96	0.94	0.92	7	0.85	1.00	0.89	8	1.01	0.98	1.08	8.59	3.09	10.17
Q5U0C3	RAP1A, member of RAS oncogene family OS=Homo sapiens PE=2 SV=1	7	1.25	1.21	0.92	7	1.49	1.37	1.44	4	1.25	0.90	0.98	10.27	20.68	25.40
F6U1T9	Calcineurin subunit B type 1 OS=Homo sapiens GN=PPP3R1 PE=2 SV=1	5	1.04	1.02	0.98	3	1.29	1.41	1.11	4	1.02	1.06	1.01	13.39	18.23	6.62
A9CQZ4	Dihydropyrimidinase-like 2 long form (Fragment) OS=Homo sapiens GN=DPYSL2 PE=2 SV=1	7	0.71	1.03	1.01	7	0.67	0.87	0.76	5	0.77	1.25	0.79	6.75	17.94	15.81

Q71DI3	Histone H3.2 OS=Homo sapiens GN=HIST2H3A PE=1 SV=3	12	5.06	1.22	2.73	8	4.58	0.85	2.78	9	4.16	1.65	2.99	9.82	32.25	4.88
Q6FGH9	DNCL1 protein OS=Homo sapiens GN=DNCL1 PE=2 SV=1	7	0.94	0.98	0.98	10	0.80	1.00	0.90	3	0.86	1.03	0.97	8.53	2.56	4.38
Q9UMZ1	Prothymosin a14 OS=Homo sapiens PE=1 SV=1	12	0.72	0.92	0.75	4	0.77	0.96	0.39	4	0.48	1.03	0.83	23.43	5.47	34.97
Q504R6	RAB13 protein (Fragment) OS=Homo sapiens GN=RAB13 PE=2 SV=1	2	0.69	0.81	0.93	3	0.81	0.95	0.80	4	1.10	1.09	1.20	23.82	14.75	21.13
H0YMV8	40S ribosomal protein S27 OS=Homo sapiens GN=RPS27L PE=2 SV=1	3	0.92	1.14	1.29	3	1.09	0.94	0.97	3	1.08	1.03	1.08	9.37	9.99	14.61
Q53EW8	Sulfurtransferase (Fragment) OS=Homo sapiens PE=2 SV=1	2	1.03	0.82	1.19	2	0.75	1.01	0.88	3	0.94	0.88	0.99	15.78	10.46	15.05
I1VE18	SEC22 vesicle trafficking protein B (Fragment) OS=Homo sapiens GN=SEC22B PE=4 SV=1	2	0.88	0.88	0.43	2	1.35	1.31	1.26	2	1.11	0.84	0.94	20.99	25.86	47.50
C9JAB2	Serine/arginine-rich-splicing factor 7 OS=Homo sapiens GN=SRSF7 PE=2 SV=1	2	1.15	1.27	0.79	4	1.02	1.01	0.92	4	1.06	1.08	1.01	6.24	11.89	12.43
B2R950	cDNA, FLJ94213, highly similar to Homo sapiens pregnancy-zone protein (PZP), mRNA OS=Homo sapiens PE=2 SV=1	4	0.87	0.74	1.21	2	1.27	0.96	1.46	2	1.07	1.06	1.26	19.03	17.94	10.06
Q5TAL4	U1 small nuclear ribonucleoprotein C OS=Homo sapiens GN=SNRPC PE=2 SV=1	2	0.92	1.13	1.16	3	0.92	1.01	0.91	3	0.84	1.08	1.03	5.48	5.60	12.24
R4IBW8	Cytochrome c oxidase subunit I OS=Homo sapiens GN=COX1 PE=4 SV=1	4	1.20	1.00	1.43	3	0.85	0.67	0.72	2	1.15	1.02	1.01	18.04	21.84	34.09
Q59GN2	Putative 60S ribosomal protein L39-like 5 OS=Homo sapiens GN=RPL39P5 PE=5 SV=2	2	1.12	1.11	1.09	2	0.89	0.96	0.87	2	1.10	1.03	1.09	12.25	7.53	12.58
F5H7R9	Parathymosin (Fragment) OS=Homo sapiens GN=PTMS PE=2 SV=1	5	0.87	1.10	0.97	3	0.88	0.93	0.77	3	0.77	1.07	0.93	6.93	8.71	11.96
Q13885	Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1	222	1.08	1.03	1.51	198	0.84	0.91	0.87	180	0.78	0.74	1.13	17.44	15.87	27.47
O60518	Ran-binding protein 6 OS=Homo sapiens GN=RANBP6 PE=1 SV=2	11	0.82	0.50	0.83	10	1.10	1.01	1.08	6	0.73	0.99	0.93	21.49	34.53	13.37
Q15843	NEDD8 OS=Homo sapiens GN=NEDD8 PE=1 SV=1	3	0.77	1.00	0.65	3	0.86	0.98	0.71	3	0.95	0.96	0.97	10.42	1.71	22.26
B5BU99	High glucose-regulated protein 8 OS=Homo sapiens GN=YTHDF2 PE=2 SV=1	3	1.05	1.19	0.81	4	0.81	1.09	0.93	2	0.90	1.01	0.86	13.23	8.37	7.41
Q562M3	Actin-like protein (Fragment) OS=Homo sapiens GN=ACT PE=3 SV=1	92	1.00	0.77	0.87	63	1.01	0.82	0.98	61	1.01	0.92	1.02	0.38	8.86	8.02
B2R769	cDNA, FLJ93308, highly similar to Homo sapiens leukocyte-derived arginine aminopeptidase (LRAP), mRNA OS=Homo sapiens PE=2 SV=1	2	1.05	0.95	0.82	2	1.47	1.24	1.36	2	1.18	1.60	1.34	17.38	25.91	26.02
E7ESP4	Integrin alpha-2 OS=Homo sapiens GN=ITGA2 PE=2 SV=1	3	0.76	0.77	1.00	6	1.19	0.99	1.03	5	1.06	1.00	0.98	22.14	14.60	2.70
Q9NZJ4	Sacsin OS=Homo sapiens GN=SACS PE=1 SV=2	2	0.87	0.74	0.74	2	1.15	1.14	1.28	3	0.94	1.04	0.98	14.69	21.77	27.20
Q9HC52	Chromobox protein homolog 8 OS=Homo sapiens GN=CBX8 PE=1 SV=3	2	1.10	0.97	1.06	2	1.04	0.81	0.94	2	0.99	0.86	0.75	5.06	9.48	16.88
Q86UA8	SMARCA1 protein (Fragment) OS=Homo sapiens GN=SMARCA1 PE=2 SV=2	9	0.90	0.83	0.56	12	0.76	1.20	0.95	9	0.73	0.97	1.13	11.55	18.40	33.05
Q3ZCM7	Tubulin beta-8 chain OS=Homo sapiens GN=TUBB8 PE=1 SV=2	72	0.98	0.95	0.86	53	0.93	1.17	0.96	52	0.94	0.85	0.89	3.03	16.30	5.59

Q71UH4	DNA topoisomerase 2 (Fragment) OS=Homo sapiens GN=TOP2B PE=3 SV=1	2	1.08	1.02	1.17	4	1.67	1.52	1.70	5	1.29	1.03	1.16	22.28	24.21	22.95
P12036	Neurofilament heavy polypeptide OS=Homo sapiens GN=NEFH PE=1 SV=4	5	0.81	1.20	0.94	4	0.83	1.00	0.91	6	1.22	1.29	1.24	24.17	13.09	17.78
Q68DH9	Putative uncharacterized protein DKFZp686M088 OS=Homo sapiens GN=DKFZp686M088 PE=2 SV=1	4	0.89	1.01	1.34	5	1.04	0.73	0.63	6	1.16	1.06	1.02	13.31	18.99	35.82
Q14151	Scaffold attachment factor B2 OS=Homo sapiens GN=SAFB2 PE=1 SV=1	7	0.91	0.77	0.85	7	1.02	1.13	1.09	6	1.93	1.35	1.39	43.35	26.99	24.70
Q08378	Golgin subfamily A member 3 OS=Homo sapiens GN=GOLGA3 PE=1 SV=2	2	1.46	1.26	1.40	3	1.02	1.07	1.09	4	1.07	0.93	1.12	20.44	15.09	14.13

Supplemantary Table 2

Biological Process

Term	Count	%	PValue	Genes
GO:0042776~mitochondrial ATP synthesis coupled proton transport	8	9.52	3.56E-12	P06576, Q8TAS0, P48047, E9PN17, Q08ET0, P30049, P25705, O75947
GO:0015986~ATP synthesis coupled proton transport	8	9.52	5.20E-12	P06576, Q8TAS0, P48047, E9PN17, Q08ET0, P30049, P25705, O75947
GO:0006754~ATP biosynthetic process	8	9.52	4.64E-11	P06576, Q8TAS0, P48047, E9PN17, Q08ET0, P30049, P25705, O75947
GO:0006457~protein folding	11	13.10	9.20E-09	P13667, P30101, P31689, P27824, Q96HE7, Q14696, Q9UBS4, Q53XJ5, P30040, K7ELL7, Q9BS26
GO:0034976~response to endoplasmic reticulum stress	6	7.14	2.39E-05	P13667, P30101, Q96HE7, P07237, Q9BZQ8, Q9BS26
GO:0034975~protein folding in endoplasmic reticulum	4	4.76	2.57E-05	P30101, P27824, Q96HE7, P11021
GO:0045454~cell redox homeostasis	6	7.14	2.71E-05	P13667, P30101, Q96HE7, P07237, Q13162, Q9BS26
GO:0009306~protein secretion	4	4.76	4.18E-04	P13667, P27824, P13521, P30040
GO:0061077~chaperone-mediated protein folding	4	4.76	6.44E-04	P13667, P27824, P23284, Q53XJ5
GO:0006986~response to unfolded protein	4	4.76	9.36E-04	P31689, P50454, A8K878, Q9BS26
GO:0006119~oxidative phosphorylation	3	3.57	1.57E-03	P31930, Q8TAS0, P30049
GO:0006334~nucleosome assembly	5	5.95	2.18E-03	O75367, P16401, P68431, P07305, Q71DI3
GO:0036498~IRE1-mediated unfolded protein response	4	4.76	2.51E-03	A8KA82, B4DR61, Q9UBS4, P11021
GO:0007005~mitochondrion organization	4	4.76	5.32E-03	P06576, J3KPX7, Q9Y6H1, A8K401
GO:0019471~4-hydroxyproline metabolic process	2	2.38	1.37E-02	Q96HE7, Q13162
GO:0015853~adenine transport	2	2.38	1.82E-02	Q6I9V5, P05141
GO:0045814~negative regulation of gene expression, epigenetic	3	3.57	2.21E-02	O75367, P68431, Q71DI3
GO:0050821~protein stabilization	4	4.76	2.46E-02	J3KPX7, P23284, P16401, A8K401
GO:0016049~cell growth	3	3.57	2.72E-02	J3KTA4, B4DR61, J3KPF3
GO:0071169~establishment of protein localization to chromatin	2	2.38	3.17E-02	O75367, P16401
GO:0031340~positive regulation of vesicle fusion	2	2.38	3.17E-02	P07355, Q5TZZ9
GO:1902600~hydrogen ion transmembrane transport	3	3.57	3.19E-02	P31930, P20674, Q9UDW1
GO:0045815~positive regulation of gene expression, epigenetic	3	3.57	3.29E-02	O75367, P68431, Q71DI3
GO:0098609~cell-cell adhesion	5	5.95	3.59E-02	P07355, P68431, P31949, J3KPF3, P11021
GO:0022417~protein maturation by protein folding	2	2.38	4.05E-02	Q96HE7, Q13162
GO:0043086~negative regulation of catalytic activity	3	3.57	4.64E-02	P07355, P08758, Q2L6I0
GO:0021680~cerebellar Purkinje cell layer development	2	2.38	4.93E-02	B7Z5L4, P11021

Cellular Localization

Term	Count	%	PValue	Genes
GO:0070062~extracellular exosome	45	54.22	2.71E-16	P07355, Q8IV08, P31689, Q71UI9, J3KTA4, Q5TZZ9, Q08ET0, J3KPF3, Q71DI3, Q13162, Q9UDW1, P05141, A9CQZ4, Q5T0G8, P31949, Q13425, P11021, P08758, P30101, O75367, Q8TAS0, Q9BZQ8, P20674, Q53XJ5, P80303, P50454, G3XAI2, P30040, Q9BRK5, P06576, H6VRG3, J3KPX7, P23284, A8KA82, P48047, E9PN17, P16401, P68431, P07237, P35908, P25705, A8K401, O75947, Q9NZ45, Q9BS26
GO:0005753~mitochondrial proton-transporting ATP synthase complex	8	9.64	2.66E-12	P06576, Q8TAS0, P48047, E9PN17, Q08ET0, P30049, P25705, O75947
GO:0005743~mitochondrial inner membrane	18	21.69	6.17E-12	Q8TAS0, Q08ET0, P51970, P20674, H0Y886, Q9Y5L4, Q9UDW1, Q6I9V5, P05141, P06576, P31930, J3KPX7, P48047, E9PN17, P30049, A8K401, P25705, O75947
GO:0005788~endoplasmic reticulum lumen	13	15.66	4.27E-11	P13667, P30101, Q96HE7, A8KA82, P23284, P07237, Q15293, Q9UBS4, P11021, P50454, P30040, K7ELL7, Q9BS26
GO:0042470~melanosome	10	12.05	5.75E-10	P07355, P13667, P30101, Q5T0G8, P23284, P07237, J3KPF3, P11021, P30040, Q6IAW5
GO:0016020~membrane	32	38.55	1.01E-09	P07355, P31689, J3KTA4, Q08ET0, J3KPF3, P05141, A9CQZ4, Q5T0G8, Q13425, P11021, P08758, Q9BRR6, O15173, Q6IAW5, P35610, Q8TAS0, Q9BZQ8, P30040, Q9BRK5, P06576, H6VRG3, J3KPX7, P23284, Q96HE7, A8KA82, B4DR61, P68431, P35908, Q9UBS4, A8K401, P25705, Q6IBU4
GO:0043209~myelin sheath	11	13.25	1.21E-09	P30101, P05141, A9CQZ4, P06576, P31930, Q8TAS0, Q08ET0, P25705, A8K401, P20674, P11021
GO:0005783~endoplasmic reticulum	20	24.10	2.13E-09	P30101, P35610, Q14696, Q15293, P80303, Q53XJ5, Q6FHT8, P50454, P30040, B7Z5L4, A8KA82, P23284, Q96HE7, P07237, Q9UBS4, P11021, Q9BRR6, Q6IAW5, K7ELL7, A8K878
GO:0005793~endoplasmic reticulum-Golgi intermediate compartment	8	9.64	1.88E-08	P07237, P11021, P80303, Q9Y3A6, Q6FHT8, P50454, Q9BS26, Q5T8U7
GO:0005739~mitochondrion	22	26.51	1.81E-07	P31689, Q8TAS0, Q08ET0, P51970, H0Y886, Q13162, Q9Y5L4, Q6I9V5, P05141, P06576, A9CQZ4, P31930, J3KPX7, P48047, E9PN17, Q9Y6H1, P30049, A8K401, P25705, P11021, O75947, Q9NZ45
GO:0045261~proton-transporting ATP synthase complex, catalytic core F(1)	4	4.82	3.25E-07	P06576, Q8TAS0, P30049, P25705
GO:0031012~extracellular matrix	11	13.25	6.63E-07	P07355, Q6I9V5, P05141, H6VRG3, P06576, J3KTA4, P48047, P07237, P25705, P11021, G3XAI2
GO:0005790~smooth endoplasmic reticulum	5	6.02	4.78E-06	A8KA82, P23284, P11021, P30040, Q13162
GO:0034663~endoplasmic reticulum chaperone complex	4	4.82	1.31E-05	P23284, P07237, Q9UBS4, P11021
GO:0000786~nucleosome	6	7.23	5.81E-05	O75367, Q71UI9, P16401, P68431, P07305, Q71DI3
GO:0009986~cell surface	11	13.25	1.27E-04	P07355, P13667, P30101, P06576, J3KPX7, Q5TZZ9, A8K401, J3KPF3, P11021, P30040, Q9BS26
GO:0005789~endoplasmic reticulum membrane	13	15.66	3.61E-04	Q8IV08, P35610, Q53XJ5, Q6FHT8, B7Z5L4, Q96HE7, Q9Y3A6, P11021, Q6IBU4, A8K0F7, Q6IAW5, Q9BS26, Q5T8U7
GO:0000276~mitochondrial proton-transporting ATP synthase complex, coup	3	3.61	1.22E-03	E9PN17, Q08ET0, O75947
GO:0005925~focal adhesion	8	9.64	1.64E-03	P30101, Q92558, P23284, Q5TZZ9, P07237, Q13425, P11021, P08758
GO:0000784~nuclear chromosome, telomeric region	5	6.02	2.57E-03	O75367, P68431, Q9NYB0, Q2L6I0, Q14566
GO:0030133~transport vesicle	4	4.82	8.44E-03	Q6FHT8, P30040, O15240, Q5T8U7
GO:0005623~cell	4	4.82	9.71E-03	P13667, P30101, P07237, Q13162
GO:0000790~nuclear chromatin	5	6.02	1.03E-02	Q96T88, O75367, Q71UI9, P16401, P07305
GO:0005913~cell-cell adherens junction	6	7.23	1.38E-02	P07355, Q5TZZ9, P68431, P31949, J3KPF3, P11021
GO:0005615~extracellular space	13	15.66	1.41E-02	P07355, H6VRG3, Q5TZZ9, P31949, P35908, Q6IBU4, P80303, P13521, P50454, G3XAI2, O15240, Q13162, A8K878
GO:0000275~mitochondrial proton-transporting ATP synthase complex, catal	2	2.41	1.74E-02	Q8TAS0, P30049
GO:0000228~nuclear chromosome	3	3.61	2.27E-02	O75367, P68431, Q9NYB0
GO:0033116~endoplasmic reticulum-Golgi intermediate compartment membr	3	3.61	3.22E-02	Q9Y3A6, Q6FHT8, Q5T8U7
GO:0005635~nuclear envelope	4	4.82	3.29E-02	Q5T0G8, P80303, Q9NYB0, O15173