Supplementary Table S1 The results of proteomic analysis

Protein ID	Protein names	Gene names	Unique peptides	Sequence coverage [%]	Q-value	Score	Ratio of TGF-β 1+SFN	Ratio of TGF-β 1+SFN	Ratio of TGF-β 1+SFN	Ratio of SFN / Con_1	Ratio of SFN / Con_2	Ratio of SFN / Con_3	Ratio of TGF-β1/ Con_1	Ratio of TGF-β1/ Con_2	Ratio of TGF-β1/ Con_3
A0A2R8YD12	Serpin B6	SERPINB6	9	38.6	0	77.31	1.23	1.36	1.18	1.15	0.92	1.19	1.11	1.24	1.13
A0A024R4E5	Vigilin	HDLBP	15	16.7	0	33.19	1.00	1.25	NaN	NaN	0.85	0.93	NaN	0.97	0.79
A0A024R4M0	40S ribosomal protein S9	RPS9	15	57.7	0	32.79	0.74	0.75	0.73	0.77	0.95	0.80	0.85	0.68	0.75
A0A024RA52	Proteasome subunit alpha type;Proteasome subunit alpha type-2	PSMA2	10	53.4	0	39.83	0.95	1.12	1.03	1.06	0.88	1.04	1.05	0.93	0.89
E9PKG6	Nucleobindin-2;Nesfatin-1	NUCB2	4	15.1	0	3.55	0.92	0.85	0.93	0.77	0.77	0.91	0.79	0.89	NaN
A0A087WSW9	Thioredoxin reductase 1, cytoplasmic	TXNRD1	15	51.1	0	322.7	1.42	1.38	1.38	1.24	1.65	1.45	1.02	1.01	0.88
A0A087WT44	Heme oxygenase 2	HMOX2	3	11.6	0	6.981	NaN	NaN	NaN	0.80	NaN	0.61	NaN	0.51	0.63
A0A087WTP3	Far upstream element-binding protein 2	KHSRP	22	40.2	0	323.3	1.16	1.19	1.11	1.00	1.17	1.27	1.14	0.84	1.07
A0A087WU07	MICOS complex subunit MIC10	MINOS1	2	24.2	0.009	1.412	1.33	1.33	1.09	NaN	NaN	1.12	NaN	NaN	0.91
A0A087WUB9	Beta-catenin-like protein 1	CTNNBL1	4	6.5	0	3.143	0.91	1.10	1.04	NaN	1.13	0.96	1.14	1.25	0.54
E9PL01	Signal peptidase complex subunit 2	SPCS2	3	26.1	0	112.1	1.13	1.27	1.23	1.14	1.12	NaN	NaN	1.35	1.22
A0A087WUD3	Oligosaccharyltransferase complex subunit OSTC	OSTC	1	14.5	0.002	1.956	1.05	1.06	0.94	0.91	NaN	0.93	0.98	NaN	0.99
A0A087WUK2	Heterogeneous nuclear ribonucleoprotein D-like	HNRNPDL	7	23.7	0	185.9	0.79	0.83	0.82	NaN	0.77	0.81	0.94	0.95	0.78
A0A087WZG9	Retrotransposon-derived protein PEG10	PEG10	2	6.7	1E-03	2.249	1.68	1.72	1.69	1.46	1.53	2.05	NaN	1.48	1.38
A0A087WUN7	SRA stem-loop-interacting RNA-binding protein, mitochondrial	SLIRP	4	55.4	0	24.8	0.90	1.49	0.79	0.64	0.77	0.80	0.69	0.68	NaN
A0A087WUQ6	Glutathione peroxidase;Glutathione peroxidase 1	GPX1	3	22.8	0	5.291	1.17	NaN	0.96	NaN	NaN	NaN	NaN	NaN	NaN
E7ETK0	40S ribosomal protein S24	RPS24	4	26.7	0	49.47	0.74	0.78	0.90	0.94	0.82	0.74	0.74	0.74	0.67
A0A087WUT6	Eukaryotic translation initiation factor 5B	EIF5B	18	21.7	0	38.88	1.31	0.93	1.03	1.16	0.77	0.91	NaN	0.98	0.99
A0A087WV05	C-Myc-binding protein	MYCBP	2	28.2	0	7.662	NaN	NaN	0.75	NaN	1.17	NaN	NaN	0.99	1.18
A0A087WVQ6	Clathrin heavy chain;Clathrin heavy chain 1	CLTC	58	51.7	0	323.3	1.05	1.01	1.06	1.01	1.01	1.05	0.97	0.99	1.00
A0A087WW4	Endophilin-B1	SH3GLB1	7	28.4	0	28.76	1.16	NaN	1.80	2.06	0.71	0.77	0.91	2.76	0.98
A0A087WWJ1	DNA mismatch repair protein	MSH6	4	4.6	0	3.205	NaN	NaN	NaN	0.73	0.67	0.59	0.76	0.77	NaN
A0A087WWU		TPM3	0	81.1	0	323.3	1.03	1.00	1.02	0.99	1.08	0.97	0.99	1.07	0.98
Q8IXW7	Fragile X mental retardation protein 1	FMR1	1	7.4	1E-03	2.234	1.13	1.76	1.32	NaN	NaN	NaN	NaN	NaN	NaN
A0A087WXM	60S ribosomal protein L17	RPL17	7	37.9	0	97.17	0.81	0.68	0.88	0.89	0.83	0.83	0.79	0.86	1.12

A0A087WXR5	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	NDUFA5	1	33.8	0	54.98	0.97	1.01	1.05	NaN	NaN	0.86	NaN	NaN	1.18
A0A087WY55	Vacuolar protein sorting-associated protein VTA1	VTA1	5	27.9	0	10.58	NaN	0.94	0.70	1.11	NaN	0.93	1.09	NaN	0.90
A0A087WY71	AP-2 complex subunit mu	AP2M1	6	15.2	0	27.73	0.76	0.86	0.83	0.96	NaN	0.91	1.23	1.12	1.16
A0A087WYN9	ATP-dependent RNA helicase DHX29	DHX29	1	1.1	5E-04	2.859	0.63	0.58	NaN	NaN	NaN	NaN	NaN	NaN	NaN
A0A087WYS1	UTP--glucose-1-phosphate uridylyltransferase	UGP2	9	38	0	145	0.90	0.96	0.85	0.97	0.94	0.95	0.92	1.34	1.05
A0A087WZF1	Lipoma-preferred partner	LPP	6	19.8	0	92.35	1.11	NaN	1.35	1.12	1.32	1.00	0.99	0.97	1.62
A0A087X020	Ribosome maturation protein SBDS	SBDS	11	39.6	0	30.45	1.00	0.99	1.09	1.49	1.08	1.15	1.59	1.12	0.90
J3KN36	Nodal modulator 1;Nodal modulator 3;Nodal modulator 2	NOMO3	5	5.6	0	4.633	NaN	NaN	0.54	0.50	0.36	0.83	0.71	0.79	0.55
J3QT73	COP9 signalosome complex subunit 7b	COPS7B	1	5.2	0.006	1.706	1.00	1.43	0.60	1.43	NaN	NaN	NaN	1.14	0.13
A0A087X1Z3	Proteasome activator complex subunit 2	PSME2	13	61	0	142	1.11	1.15	1.25	1.12	1.03	1.24	1.08	1.17	1.11
A0A087X2D8	C-Jun-amino-terminal kinase-interacting protein 4	SPAG9	7	8.1	0	6.925	NaN	0.77	0.74	NaN	NaN	NaN	NaN	NaN	NaN
F1T0B3	ATP-dependent RNA helicase DDX1	DDX1	11	23.1	0	42.57	0.89	0.72	0.89	0.87	0.52	0.63	1.22	0.82	0.75
A0A087X2I1	26S protease regulatory subunit 10B	PSMC6	15	48.6	0	79.13	1.16	1.10	1.15	1.05	1.22	1.03	1.07	1.09	1.03
A0A0A0MR02	Voltage-dependent anion-selective channel protein 2	VDAC2	12	51.1	0	323.3	1.08	1.22	1.02	1.00	1.06	1.03	1.05	1.03	1.24
B9ZVX7	Glutathione S-transferase Mu 4;Glutathione S-transferase Mu 1;Glutathione S-transferase Mu 5	GSTM1	2	28.2	0	8.262	0.49	0.60	0.43	NaN	0.62	0.77	NaN	1.25	0.77
A0A0A0MRA5	Heterogeneous nuclear ribonucleoprotein U-like protein 1	HNRNPUL	14	22.3	0	33.05	0.82	0.94	0.96	1.04	0.91	0.79	0.98	1.08	0.96
A0A0A0MRF9	Phosphoinositide phospholipase C;1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-2	PLCG2	1	1	0.008	1.522	1.38	1.32	1.26	NaN	1.26	1.20	NaN	1.88	1.54
A0A0A0MRI2	Sorting nexin-6;Sorting nexin-6, N-terminally processed	SNX6	5	11.7	0	5.436	NaN	0.90	0.91	0.70	1.33	NaN	NaN	0.92	1.03
F6S8N6	Protein-L-isoaspartate O-methyltransferase;Protein-L-isoaspartate(D-aspartate) O-methyltransferase	PCMT1	8	54	0	98.42	1.02	1.09	1.13	1.22	1.13	0.99	1.61	1.78	1.02
A0A0A0MRM	Unconventional myosin-VI	MYO6	15	18.8	0	43.09	2.03	0.97	1.89	1.42	1.43	1.03	0.63	0.95	0.76
A0A0A0MRR7	U1 small nuclear ribonucleoprotein C	SNRPC	3	21.7	0	34.23	1.08	0.96	1.16	0.96	0.96	0.90	1.08	1.09	0.99
J3KNW4	Four and a half LIM domains protein 2	FHL2	7	21.3	0	32.29	1.06	1.10	0.96	1.24	0.89	1.49	1.13	0.87	NaN

A0A0G2JKZ1	Tapasin	TAPBP	5	16.7	0	7.431	0.74	0.72	0.80	0.98	0.99	1.19	0.90	NaN	0.89
B3KYB6	Phosphatidylinositol transfer protein beta isoform	PITPNB	4	38.3	0	5.232	1.02	0.94	NaN	NaN	NaN	1.44	NaN	NaN	1.28
A0A0A0MTH3	Integrin-linked protein kinase	ILK	9	23.6	0	15.01	NaN	NaN	1.94	NaN	0.83	0.80	NaN	NaN	1.21
A0A0R4J2G3	Neutral cholesterol ester hydrolase 1	NCEH1	6	21.4	0	69.66	1.04	0.75	0.95	1.07	1.10	0.78	0.75	0.88	0.84
Q5T2B5	Cullin-2	CUL2	3	5.7	0.008	1.484	NaN	0.68	NaN	0.69	1.06	NaN	NaN	NaN	NaN
F6UJY9	Hydroxypyruvate isomerase;Putative hydroxypyruvate isomerase	HYI	4	38.5	0	23.56	1.27	NaN	NaN	0.64	0.39	NaN	0.95	1.22	0.81
A0A0A0MTS2	Glucose-6-phosphate isomerase	GPI	22	44.9	0	323.3	0.94	0.98	0.98	1.04	1.01	1.08	0.95	1.01	1.06
A0A0A0MTS7	Titin	TTN	7	0.3	5E-04	2.855	2.48	1.85	1.48	NaN	1.37	NaN	NaN	1.45	1.08
A0A0A6YYL4	Coronin;Coronin-7	CORO7-PA	4	7.8	0	4.627	0.85	NaN	NaN	0.49	0.88	0.95	NaN	NaN	NaN
A0A0B4J1Z1	Serine/arginine-rich splicing factor 7	SRSF7	7	54.7	0	12.37	1.11	1.03	1.02	0.74	0.77	1.16	NaN	0.79	1.04
A0A0C4DFT3	Disks large homolog 1	DLG1	6	10.1	0	16.77	1.73	0.77	1.43	0.88	NaN	1.01	NaN	NaN	1.06
A0A0C4DFV9	Protein SET;Protein SETSIP	SET	6	27.8	0	323.3	1.11	1.08	1.04	1.14	1.07	1.10	1.05	1.09	1.07
C9J9K3	40S ribosomal protein SA	RPSA	6	65.8	0	323.3	1.05	1.11	1.23	0.95	1.03	1.02	1.14	0.96	1.05
E7ENN3	Nesprin-1	SYNE1	3	0.6	0.008	1.526	0.88	1.10	1.77	NaN	NaN	1.03	NaN	NaN	NaN
A0A0C4DG44	Serine protease HTRA2, mitochondrial	HTRA2	1	5.7	0	5.089	1.65	1.58	1.34	NaN	1.10	NaN	NaN	NaN	1.21
A0A0C4DG49	Poliovirus receptor	PVR	1	3.4	0	64.55	1.47	1.59	1.38	0.99	1.13	NaN	NaN	1.06	1.06
A0A0C4DG89	Probable ATP-dependent RNA helicase DDX46	DDX46	8	10.1	0	10.61	1.38	0.80	1.33	0.56	0.72	1.94	NaN	NaN	0.83
A0A0C4DGA2	Enoyl-CoA delta isomerase 2, mitochondrial	ECI2	8	30.2	0	14.07	1.03	0.51	NaN	0.60	0.72	1.12	NaN	NaN	NaN
A0A0C4DGB0	Short coiled-coil protein	SCOC	1	22	0	22.86	0.97	1.31	1.09	NaN	NaN	1.13	NaN	NaN	1.10
A0A0C4DGB5	Calpastatin	CAST	16	54	0	323.3	0.88	0.90	0.88	1.11	1.12	1.07	1.01	1.00	0.91
A0A2R8Y8B3	Chromodomain-helicase-DNA-binding protein 4	CHD4	3	4.9	0	7.371	0.67	0.93	0.87	NaN	NaN	NaN	1.55	NaN	1.28
A0A0C4DGQ	Calpain small subunit 1	CAPNS1	8	51.9	0	323.3	1.00	0.93	0.98	1.02	1.10	1.07	1.16	1.36	1.09
A0A0C4DGS1	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	DDOST	7	24.4	0	36.77	1.08	0.92	1.13	1.04	0.90	1.15	0.99	0.99	0.99
F6S8Q4	ATP-dependent RNA helicase DDX3X;ATP-dependent RNA helicase DDX3Y	DDX3X	19	40.1	0	70.33	1.00	1.09	1.08	0.78	1.08	0.97	1.02	0.92	0.96
A0A0D9SFK2	Unconventional myosin-XVIIIa	MYO18A	5	3	0	17.1	0.93	1.06	0.95	1.07	0.78	0.92	NaN	1.02	0.98
A0A0D9SFM0	E3 ubiquitin-protein ligase	SHPRH	3	2.3	0.008	1.521	1.21	NaN	1.22	1.54	NaN	1.07	NaN	NaN	1.11
A0A1W2PNM1	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	HADH	5	26.2	0	43.04	0.81	0.91	NaN	1.14	1.18	0.96	1.14	0.85	NaN
A0A1B0GWF	Syntaxin-binding protein 1	STXBP1	3	12.2	0	4.767	NaN	1.68	1.11	NaN	NaN	0.95	NaN	NaN	NaN
A0A140T8Z0	Protein diaphanous homolog 1	DIAPH1	16	16.6	0	18.03	0.91	0.75	0.96	1.00	NaN	0.77	0.99	0.75	1.03
A0A0G2JHC2	Phostensin	PPP1R18	2	4.2	0	14.06	0.78	NaN	1.21	NaN	NaN	NaN	NaN	NaN	NaN
A0A0G2JIW1	Heat shock 70 kDa protein 1B;Heat shock 70 kDa protein 1A	HSPA1B	19	68.7	0	323.3	2.70	3.13	2.66	2.64	2.57	2.59	0.91	0.92	0.91

A0A0J9YYL3	Poly(U)-binding-splicing factor PUF60	PUF60	10	30.9	0	18.7	1.11	1.24	NaN	0.82	NaN	1.17	NaN	2.57	NaN
C9JB42	DnaJ homolog subfamily B member 3;DnaJ homolog subfamily B member 6	DNAJB6	1	19.7	0	28.37	2.28	NaN	2.53	NaN	NaN	NaN	NaN	NaN	NaN
A0A0R4J2E8	Matrin-3	MATR3	26	37.8	0	207.3	1.08	0.86	1.00	1.06	1.01	1.04	0.94	0.77	0.69
A0A0R4J2F3			1	18.1	5E-04	2.832	0.90	NaN	0.61	NaN	NaN	NaN	NaN	NaN	NaN
A0A0U1RQC9	Cellular tumor antigen p53	TP53	6	19.5	0	25.15	0.34	NaN	0.30	NaN	NaN	NaN	NaN	NaN	1.40
A0A0U1RR32	Histone H2A type 1-J;Histone H2A type 1-H;Histone H2A.J;Histone H2A type 2-C;Histone H2A type 2-A;Histone H2A type 1-D;Histone H2A type 1;Histone H2A;Histone H2A type 1-C;Histone H2A type 3;Histone	HIST1H2A	2	27.2	0	246.9	0.63	0.61	0.68	1.14	0.94	0.74	0.43	NaN	NaN
A0A0U1RRL7			3	87.3	0	40.97	1.32	1.16	1.13	1.18	0.91	1.30	1.43	1.32	1.38
A0A0U1RRM4	Polypyrimidine tract-binding protein 1	PTBP1	2	52.2	0	323.3	0.99	1.06	1.08	0.94	1.00	0.94	0.77	0.91	0.95
A0A0U1RRM	Fermitin family homolog 2	FERMT2	3	8.8	0	61	NaN	NaN	1.44	NaN	1.41	1.33	NaN	NaN	1.06
A0A140T9I0	HLA class I histocompatibility antigen, A-2 alpha chain;HLA class I histocompatibility antigen, A-74 alpha chain	HLA-A	0	54	0	323.3	0.97	0.97	1.04	1.06	1.08	1.15	1.00	0.95	0.98
Q5JNW7	Proteasome subunit beta type;Proteasome subunit beta type-8	PSMB8	2	10.3	0	4.054	1.08	NaN	1.03	1.03	NaN	0.75	1.07	NaN	0.77
A0A140T9R1	Flotillin-1	FLOT1	6	21.6	0	61.35	0.91	0.75	1.39	0.82	0.75	NaN	0.91	1.01	NaN
A0A1B0GTG2	Alpha-aminoadipic semialdehyde dehydrogenase	ALDH7A1	16	43.3	0	69.66	0.94	0.83	1.04	0.64	0.97	0.95	0.81	0.76	0.95
A0A1B0GWJ0	Adenylosuccinate lyase	ADSL	10	34.6	0	57.49	1.31	0.90	0.91	0.82	1.00	1.25	0.84	1.03	1.13
F5GZ78	Paxillin	PXN	9	21.2	0	159.8	1.29	1.76	1.72	1.32	1.33	1.36	1.30	0.99	1.73
A0A1B0GUA3	KIF1-binding protein	KIAA1279	1	2.9	0	8.056	1.75	1.54	NaN	NaN	NaN	1.47	NaN	NaN	1.71
A0A1B0GVD5	Cathepsin D;Cathepsin D light chain;Cathepsin D heavy chain	CTSD	18	50.4	0	236.5	0.92	0.94	0.87	1.11	1.06	1.15	0.93	0.87	0.96
A0A1C7CYX9	Dihydropyrimidinase-related protein 2	DPYSL2	24	52.4	0	323.3	0.88	0.68	0.74	0.94	0.96	0.76	0.61	0.75	0.74
C9J4M6	DNA-directed RNA polymerase;DNA-directed RNA polymerase II subunit RPB2	POLR2B	4	5.5	0	5.379	NaN	NaN	NaN	NaN	NaN	NaN	0.19	0.18	NaN
A0A1W2PPZ5	Transcription elongation factor A protein 1	TCEA1	3	12	0	4.836	0.91	0.82	1.25	NaN	NaN	1.25	1.08	1.24	1.04
E9PJA7	Bcl-2-associated transcription factor 1	BCLAF1	4	12.8	0	48.17	1.10	0.99	1.22	0.71	1.02	1.11	1.07	0.81	1.03
A0A1X7SBZ2	Probable ATP-dependent RNA helicase DDX17	DDX17	15	36.6	0	134.6	0.85	0.91	0.83	0.68	0.79	0.90	0.83	0.79	1.19
C9JP51	Protein FAM131A	FAM131A	1	6.1	0	2.987	1.44	1.98	1.63	NaN	2.02	1.61	NaN	NaN	NaN

A0A1W2PQV2	Glycine cleavage system H protein, mitochondrial	GCSH	2	30	0	3.652	NaN	NaN	NaN	1.25	1.29	NaN	1.55	0.86	NaN
A8MYT4	Phosphatidylinositol 3-kinase;Phosphatidylinositol 3-kinase catalytic subunit type 3	PIK3C3	1	1	0.009	1.455	1.04	1.14	1.10	1.07	0.98	1.13	1.11	1.12	1.37
A0A2R8Y3X5	Dynamin-like 120 kDa protein, mitochondrial;Dynamin-like 120 kDa protein, form S1	OPA1	8	13.7	0	19.31	0.30	0.95	NaN	NaN	NaN	1.46	NaN	NaN	NaN
A0A2R8Y430	Glutathione synthetase	GSS	15	45.1	0	80.66	1.15	0.94	0.97	1.01	1.10	0.96	1.07	1.08	0.99
A6NNI4	Tetraspanin;CD9 antigen	CD9	5	34	0	11.58	1.09	1.04	1.13	1.00	1.07	0.79	0.66	0.88	1.47
A0A2R8Y484	Leukocyte surface antigen CD47	CD47	3	15.3	0	3.662	0.85	1.55	1.73	1.06	1.61	0.85	0.90	1.39	0.94
H7C048	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1	SMARCE1	1	8.3	0.009	1.431	0.96	NaN	1.14	NaN	NaN	NaN	NaN	NaN	0.77
A0A2R8YEZ4	DNA-directed RNA polymerases I and III subunit RPAC1	POLR1C	2	10.1	0	15.31	0.98	1.29	NaN	NaN	1.02	NaN	0.95	1.13	NaN
A0A2R8Y7E7	Tubulin-specific chaperone E	TBCE	5	11.1	0	4.228	0.74	0.86	1.43	NaN	1.03	NaN	NaN	NaN	0.77
A0A2R8Y5S7	Radixin	RDX	13	45.9	0	67.06	NaN	1.25	1.39	1.20	1.89	NaN	0.97	0.75	0.91
A0A2R8Y793			1	90	0.003	1.862	NaN	0.85	NaN	NaN	NaN	0.91	0.70	0.92	0.91
B1ALA9	Ribose-phosphate pyrophosphokinase 1	PRPS1	2	35.4	0	15.4	0.71	0.84	1.00	0.53	0.98	1.05	0.86	0.75	0.90
A0A2R8Y811	40S ribosomal protein S14	RPS14	8	41.3	0	55.93	0.95	0.91	0.98	0.86	0.97	0.82	0.95	1.02	0.90
A0A2R8YGD1	Tripeptidyl-peptidase 1	TPP1	3	9.8	0	5.059	0.81	NaN	NaN	NaN	0.84	1.10	NaN	NaN	0.73
A0A2R8YD50	Peroxisomal multifunctional enzyme type 2;(3R)-hydroxyacyl-CoA dehydrogenase;Enoyl-CoA hydratase 2	HSD17B4	7	14.8	0	12.18	1.06	1.01	1.49	NaN	NaN	NaN	NaN	NaN	NaN
A0A2R8YF43	Casein kinase II subunit alpha 3;Casein kinase II subunit alpha	CSNK2A1	5	23.1	0	23.85	1.27	1.04	1.04	1.16	1.22	1.40	0.84	0.80	1.38
A0A2R8YEA7			2	76.4	0	92.95	1.76	1.63	1.69	1.66	1.73	1.88	1.90	1.89	1.37
A0A2R8YEP4	Flavin reductase (NADPH)	BLVRB	5	31.4	0	54.92	1.25	1.38	0.94	1.03	1.24	1.17	1.20	1.20	0.83
A0A2R8YFH5	Protein transport protein Sec23B	SEC23B	4	12.1	0	6.65	NaN	0.91	1.07	0.90	NaN	NaN	NaN	1.27	1.15
A0A2U3TZH3	Elongation factor 1-alpha 2	EEF1A2	3	44	0	11	0.28	0.29	NaN	0.94	NaN	0.44	NaN	NaN	0.20
E9PNW4	CD59 glycoprotein	CD59	4	29.6	0	55.51	1.06	1.04	1.09	1.07	0.96	1.03	1.16	1.19	1.05
V9GYY3	C-1-tetrahydrofolate synthase, cytoplasmic;Methylenetetrahydrofolate dehydrogenase;Methenyltetrahydrofolate cyclohydrolase;Formyltetrahydrofolate synthetase;C-1-tetrahydrofolate synthase, cytoplasmic, N-terminally	MTHFD1	35	46.4	0	140.7	0.67	0.72	0.76	0.73	0.87	0.79	0.79	0.78	0.67
A0A3B3IRI2	CTP synthase 1;CTP synthase	CTPS1	11	25.2	0	31.69	1.03	1.16	1.09	1.03	0.84	0.90	1.21	1.16	1.10

A0A3B3IRK6	Mannosyl-oligosaccharide glucosidase	MOGS	11	20.6	0	27.05	1.20	1.06	1.11	1.14	0.82	1.07	0.91	1.02	0.97
A0A3B3IRT8	Translocon-associated protein subunit alpha	SSR1	4	20.8	0	46.35	0.79	0.88	0.91	0.92	0.90	0.86	1.02	1.03	1.11
A0A3B3IS06	Treacle protein	TCOF1	5	4.1	0	6.04	1.18	1.08	0.92	0.81	NaN	1.58	0.94	0.82	1.08
A0A3B3IS84	Coatomer subunit alpha;Xenin;Proxenin	COPA	32	35.9	0	323.3	0.82	0.75	0.81	0.73	0.77	0.78	0.97	0.84	0.90
B4DKB2	Endothelin-converting enzyme 1	ECE1	3	7.3	0	40.4	0.80	NaN	0.68	NaN	NaN	NaN	NaN	NaN	0.92
A0A3B3ISG5	Insulin-degrading enzyme	IDE	3	5.7	0	5.832	0.48	NaN	NaN	NaN	NaN	0.77	NaN	0.75	0.89
A0A3B3ISV4	Vitamin K epoxide reductase complex subunit 1-like protein 1	VKORC1L´	1	4.9	0.001	2.745	1.05	1.02	0.99	1.23	0.98	2.02	0.78	1.44	1.08
A0A3B3IUC9	Acylglycerol kinase,	AGK	2	27.6	0.007	1.613	0.89	NaN	1.15	0.73	NaN	0.99	NaN	NaN	0.62
A0A3B3IT92	DNA replication licensing factor MCM4	MCM4	10	17.7	0	20.16	NaN	0.63	NaN	NaN	1.03	0.72	NaN	NaN	0.67
A0A3B3ITF0	m7GpppX diphosphatase	DCPS	3	17.2	0	3.726	0.91	0.92	1.02	0.57	0.71	NaN	1.00	0.60	3.48
A0A3B3ITN8	Retinoic acid-induced protein 3	GPRC5A	4	12.4	0	7.827	NaN	NaN	NaN	0.80	0.82	0.66	NaN	NaN	0.81
A0A3B3ITT5	60S ribosomal protein L29	RPL29	2	13.8	0	36.32	1.24	1.59	1.18	1.14	1.32	1.28	1.18	1.11	1.20
E9PN17	ATP synthase subunit g, mitochondrial	ATP5L	2	31.6	0	4.062	1.54	1.19	1.16	0.94	1.54	1.69	1.10	0.76	1.94
A0A3B3ITZ9	Thyroid hormone receptor-associated protein 3	THRAP3	9	13.8	0	17.51	1.25	NaN	1.11	1.27	0.98	0.90	1.31	1.33	1.33
A0A3B3IUA2		NHP2L1	2	16.9	0	77.82	0.94	1.06	0.97	1.30	1.15	1.24	0.89	1.04	1.09
A0A3B3IUB1	Translation initiation factor eIF-2B subunit epsilon	EIF2B5	2	3	0	3.485	1.13	1.00	0.85	1.32	1.13	0.89	1.09	NaN	0.96
A0A3B3IUB5	Minor histocompatibility antigen H13	HM13	7	20.7	0	111.4	1.02	0.91	0.91	1.36	1.15	1.04	1.28	NaN	1.66
A0A3F2YNY6	Pre-mRNA-processing factor 40 homolog A	PRPF40A	6	8.4	0	14.71	0.51	0.80	0.49	0.91	2.07	NaN	NaN	0.83	0.71
A0A494C017	Myeloid-associated differentiation marker	MYADM	2	27	0	323.3	1.12	0.94	0.89	0.87	1.27	0.87	3.59	3.89	1.04
H0Y993	Protein DEK	DEK	9	24.2	0	26.45	0.66	0.79	1.01	0.75	0.76	1.08	0.91	0.82	0.65
A0A494C039	Hypoxia up-regulated protein 1	HYOU1	28	36.9	0	209.8	0.84	0.88	0.83	0.95	0.90	0.98	0.97	0.91	0.85
A0A494C0B4	UV excision repair protein RAD23 homolog A	RAD23A	4	20.9	0	3.135	0.90	1.02	NaN	1.15	0.84	0.97	1.17	NaN	NaN
A0A494C128	Nucleolar protein 56	NOP56	3	8.6	0	9.37	NaN	NaN	0.82	1.33	1.12	NaN	1.18	1.22	1.06
A0A494C1F2	Nuclear pore complex protein Nup214	NUP214	4	2.3	0	3.742	1.60	1.64	1.92	1.46	NaN	NaN	NaN	NaN	1.47
A0A494C1K3	General transcription factor II-I	GTF2I	8	9.5	0	9.474	NaN	NaN	NaN	NaN	1.00	1.01	NaN	NaN	NaN
A0A494C1L1	Lamin-B receptor	LBR	5	14.4	0	41.92	0.99	0.84	NaN	NaN	0.94	0.87	0.84	NaN	NaN
A0A494C1N0	Peptidyl-prolyl cis-trans isomerase FKBP2	FKBP2	2	15.8	0	3.199	NaN	NaN	NaN	1.79	0.98	NaN	NaN	NaN	NaN
A0A499FIX8	Extended synaptotagmin-2	ESYT2	15	25.6	0	111.8	0.93	0.87	1.01	0.67	0.86	0.99	0.91	0.78	1.02
H3BUX2	Cytochrome b5 type B	CYB5B	3	22.9	0	9.274	0.71	1.07	0.89	NaN	NaN	0.97	NaN	NaN	NaN
A0AVT1	Ubiquitin-like modifier-activating enzyme 6	UBA6	15	18.4	0	19.74	NaN	NaN	0.69	NaN	0.66	0.56	NaN	1.84	NaN
M0R026	Acetolactate synthase-like	ILVBL	4	14.5	0	28.02	NaN	1.60	1.37	NaN	0.69	NaN	NaN	NaN	NaN
A2A274	Aconitate hydratase,	ACO2	12	24.2	0	44.06	0.74	0.52	0.84	NaN	0.81	0.82	NaN	NaN	NaN

A2A2V1	Major prion protein	PRNP	1	4.8	0	6.304	1.48	1.17	1.02	NaN	NaN	1.02	NaN	NaN	0.95
H3BTL1	Microtubule-associated proteins 1A/1B light chain 3B;Microtubule-associated proteins 1A/1B light chain 3 beta 2	MAP1LC3E	1	18.7	0	7.386	1.00	1.54	NaN	NaN	NaN	NaN	NaN	NaN	0.56
A6NEM2	Host cell factor 1;HCF N-terminal chain 1;HCF N-terminal chain 2;HCF N-terminal chain 3;HCF N-terminal chain 4;HCF N-terminal chain 5;HCF N-terminal chain 6;HCF C-terminal chain 1;HCF C-terminal chain 2;HCF C-terminal chain 3;HCF C-terminal chain 4;HCF C-terminal	HCFC1	2	1.6	0	3.005	NaN	NaN	NaN	NaN	1.54	NaN	0.78	0.88	NaN
A6NFX8	ADP-sugar pyrophosphatase	NUDT5	8	33.2	0	59.09	0.91	0.92	0.72	1.50	1.29	1.20	NaN	NaN	NaN
A6NGP5	Hematological and neurological expressed 1-like protein	HN1L	7	61.2	0	77.31	1.17	1.46	1.42	0.95	1.03	1.09	1.06	1.81	1.38
A6NHQ2	rRNA/tRNA 2-O-methyltransferase fibrillarin-like	FBLL1	1	6.6	0.001	2.363	NaN	0.98	NaN	0.79	1.04	NaN	0.75	0.97	NaN
J3KTL8	Structural maintenance of chromosomes flexible hinge domain-containing protein 1	SMCHD1	1	0.7	0.002	1.953	0.78	0.85	0.75	NaN	NaN	0.77	NaN	NaN	0.97
A6NLH6	Protein cornichon homolog 4	CNIH4	1	14.6	0	15.56	NaN	0.68	NaN	1.24	1.09	1.17	NaN	NaN	NaN
E9PJK1	Tetraspanin;CD81 antigen	CD81	3	35.8	0	40.33	1.09	1.02	1.07	NaN	NaN	1.26	0.85	0.74	1.19
A6NMQ3	Alpha-endosulfine	ENSA	3	32.9	0	180	NaN	NaN	1.27	NaN	NaN	1.54	NaN	1.62	4.03
Q5T949	Serine/threonine-protein phosphatase 2A activator	PPP2R4	3	17.6	0.001	2.754	1.18	NaN	NaN	NaN	1.59	1.13	1.04	1.41	0.94
A8K878	Mesencephalic astrocyte-derived neurotrophic factor	MANF	7	41.1	0	11.72	1.71	1.19	2.74	1.15	1.02	1.31	0.88	NaN	1.59
A8MUA9	Small ubiquitin-related modifier 3	SUMO3	1	15.6	1E-03	2.3	NaN	0.91	1.12	0.85	1.06	0.74	0.89	0.96	1.13
P62308	Small nuclear ribonucleoprotein G;Putative small nuclear ribonucleoprotein G-like protein	SNRPG	3	35.5	0	24.09	0.97	1.08	0.98	1.17	1.08	1.27	1.20	0.85	1.06
J3QRI9	Developmentally-regulated GTP-binding protein 2	DRG2	3	25.6	0	7.428	0.91	1.00	1.08	NaN	1.12	0.82	NaN	NaN	1.00
A8MZH8	Pituitary tumor-transforming gene 1 protein-interacting protein	PTTG1IP	2	23.4	0	3.994	1.14	1.53	1.30	1.10	1.53	1.35	NaN	1.00	1.38
B0QY89	Eukaryotic translation initiation factor 3 subunit L	EIF3L	15	31.3	0	184.3	1.09	1.13	0.98	1.06	1.03	0.96	NaN	0.78	0.96
B0QYK0	RNA-binding protein EWS	EWSR1	6	14.6	0	44.06	0.94	0.98	1.01	1.07	1.03	1.00	0.73	0.99	0.93
H3BQQ9	SUMO-conjugating enzyme	UBE2I	5	51.1	0	11.52	0.73	0.74	NaN	NaN	0.85	0.71	0.79	NaN	0.50
B0QZ36	mRNA export factor	RAE1	3	38.7	0	7.664	1.18	1.20	NaN	NaN	NaN	1.41	NaN	NaN	1.49
B0YIW6	Coatomer subunit delta	ARCN1	21	43.7	0	114.8	0.89	0.93	1.00	0.96	1.02	0.90	1.04	1.03	0.86
B1AHB1	DNA helicase;DNA replication licensing factor MCM5	MCM5	9	16.6	0	6.905	0.62	0.72	0.67	1.01	0.85	0.86	NaN	0.83	0.77

B1AJY7	26S proteasome non-ATPase regulatory subunit 10	PSMD10	4	32.6	0	170.7	NaN	NaN	NaN	NaN	1.09	NaN	NaN	1.15	3.07
B1AK87		CAPZB	3	56.5	0	158.2	1.07	1.09	1.03	0.99	0.92	1.04	1.10	0.85	1.00
B1AKD8	Rootletin	CROCC	1	0.6	0.009	1.407	1.03	0.97	1.02	0.99	0.96	1.02	0.93	0.06	0.95
B1AKJ5	Nardilysin	NRD1	3	3.3	0	3.554	NaN	0.54	0.47	NaN	0.55	NaN	NaN	NaN	NaN
B3KT28	FAS-associated factor 1	FAF1	1	1.9	0.004	1.774	0.63	1.30	NaN	NaN	NaN	NaN	NaN	NaN	NaN
B1ANR0	Polyadenylate-binding protein;Polyadenylate-binding protein 4	PABPC4	6	28.9	0	8.143	NaN	1.08	0.56	0.86	NaN	1.95	NaN	0.81	2.04
H3BLV0	Complement decay-accelerating factor	CD55	9	31.9	0	30.26	NaN	1.21	1.10	0.99	1.11	1.24	0.90	0.98	1.00
B4DG22	Ribosomal protein S6 kinase alpha-3;Ribosomal protein S6 kinase;Ribosomal protein S6 kinase alpha-2;Ribosomal protein S6 kinase alpha-1	RPS6KA3	3	5.5	0.001	2.448	1.62	1.03	0.83	NaN	NaN	0.92	NaN	NaN	1.54
G3V4W0	Heterogeneous nuclear ribonucleoproteins C1/C2;Heterogeneous nuclear ribonucleoprotein C-like 1;Heterogeneous nuclear ribonucleoprotein C-like 2	HNRNPC	22	55	0	323.3	0.80	0.82	0.79	0.75	0.83	0.82	0.89	0.94	0.89
B3KS98	Eukaryotic translation initiation factor 3 subunit H	EIF3H	6	34.4	0	323.3	1.20	1.10	1.09	1.12	1.19	0.92	0.91	1.14	0.66
M0QZP4	Branched-chain-amino-acid aminotransferase;Branched-chain-amino-acid aminotransferase, mitochondrial	BCAT2	4	17.9	0	17.89	1.28	0.86	1.12	0.90	1.00	0.89	1.19	1.02	1.27
B4DDD8	Histidine--tRNA ligase,	HARS	12	33.8	0	30.35	0.79	0.68	0.63	NaN	0.74	0.68	NaN	NaN	0.76
B4DDF4	Calponin;Calponin-2	CNN2	12	55.4	0	323.3	1.16	1.03	1.16	1.07	1.14	1.08	1.14	1.01	1.12
U3KQP3	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13	NDUFA13	1	18.7	0.008	1.546	0.56	0.56	0.66	NaN	0.57	0.56	0.82	1.06	0.64
H0YKU5	COP9 signalosome complex subunit 2	COPS2	3	12.5	0	3.914	NaN	NaN	NaN	NaN	1.78	0.68	NaN	1.25	0.88
B4DJ81	NADH-ubiquinone oxidoreductase 75 kDa subunit,	NDUFS1	9	24.5	0	13.34	1.12	0.83	0.72	NaN	0.63	NaN	NaN	NaN	NaN
B4DJV2	Citrate synthase;Citrate synthase, mitochondrial	CS	11	41.1	0	306.5	1.14	1.06	1.14	0.97	1.10	1.05	0.95	0.95	0.99
B4DKY1	Cysteine--tRNA ligase, cytoplasmic	CARS	6	10.1	0	6.645	0.69	0.69	1.00	NaN	NaN	NaN	NaN	NaN	NaN
B4DLN1	39S ribosomal protein L12, mitochondrial	MRPL12	7	22.2	0	56.66	0.80	0.90	0.84	1.08	1.16	0.84	1.04	0.95	0.97
B4DR61	Protein transport protein Sec61 subunit alpha isoform 1	SEC61A1	5	10.4	0	7.812	NaN	0.67	NaN	1.20	0.85	1.21	0.89	0.58	NaN

H0Y630	Serine/threonine-protein kinase 24;Serine/threonine-protein kinase 24 36 kDa subunit;Serine/threonine-protein kinase 24 12 kDa subunit	STK24	5	22	0	7.651	1.00	1.06	0.87	0.91	0.82	0.79	0.76	0.68	1.13
B4DY09	Interleukin enhancer-binding factor 2	ILF2	17	66.8	0	121.4	0.95	0.90	0.96	0.90	0.89	0.96	1.00	1.00	0.94
B4E0K5	Mitogen-activated protein kinase 14	MAPK14	4	15.5	0	5.133	0.94	NaN	0.73	NaN	NaN	0.99	0.69	NaN	1.14
B5MBZ0	Echinoderm microtubule-associated protein-like 4	EML4	2	2.8	1E-03	2.285	NaN	NaN	NaN	0.60	NaN	NaN	0.97	0.60	NaN
B5MBZ8	Protein phosphatase 1 regulatory subunit 7	PPP1R7	3	17.9	0	19.14	NaN	NaN	NaN	NaN	NaN	NaN	1.37	NaN	0.78
B5MC59	Replication protein A 14 kDa subunit	RPA3	3	52.4	0	5.935	1.17	1.26	1.30	1.65	NaN	1.59	NaN	0.51	1.07
B5MDF5	GTP-binding nuclear protein Ran	RAN	10	41.2	0	151.3	1.03	0.93	0.94	0.93	0.94	0.92	0.92	0.97	0.90
E7EW69	Septin-10	SEPT10	5	24.4	0	70.93	NaN	1.29	0.93	1.10	0.94	1.21	0.80	0.77	1.49
B7Z4M1	Reticulon	RTN3	1	12.2	0	67.28	0.98	1.29	1.02	NaN	1.26	1.15	NaN	NaN	1.36
B7Z7F3	Ran-binding protein 3	RANBP3	3	9.9	0	2.945	1.15	1.26	NaN	NaN	NaN	0.88	NaN	NaN	NaN
B7Z7P8	Eukaryotic peptide chain release factor subunit 1	ETF1	9	25.8	0	16.54	1.26	0.83	1.11	0.92	1.18	0.94	0.99	0.99	0.92
B7ZC38	Endophilin-B2	SH3GLB2	6	22.8	0	20.72	1.01	NaN	0.99	0.97	1.09	1.08	1.14	1.01	NaN
B8ZZN6	Small ubiquitin-related modifier 1	SUMO1	3	25.3	0	7.793	0.60	NaN	0.67	0.60	NaN	0.65	0.74	0.88	0.81
B8ZZQ6	Prothymosin alpha;Prothymosin alpha, N-terminally processed;Thymosin alpha-1	PTMA	7	37.4	0	323.3	0.97	1.06	1.01	0.97	0.99	0.91	1.00	1.06	0.98
B8ZZU8	Transcription elongation factor B polypeptide 2	TCEB2	5	79.6	0	51.56	1.08	0.83	1.12	1.01	1.13	1.06	0.86	0.97	1.01
C9J0K6	Sorcin	SRI	7	55.5	0	43.71	1.01	1.15	1.03	1.17	1.24	1.40	NaN	1.08	1.10
D6RBD7	Eukaryotic translation elongation factor 1 epsilon-1	EEF1E1	3	30.7	0	41.23	NaN	1.08	0.93	NaN	NaN	0.88	NaN	0.54	0.84
C9J1Z8	ADP-ribosylation factor 5	ARF5	3	67.3	0	4.913	0.81	0.89	0.87	0.62	0.79	0.80	0.93	0.99	1.17
C9J4Z3	60S ribosomal protein L37a	RPL37A	4	69.1	0	18.85	0.82	0.73	0.73	0.80	0.92	0.78	0.91	0.63	0.83
C9JA28	Translocon-associated protein subunit gamma	SSR3	1	8	0	29.45	NaN	NaN	1.16	0.69	NaN	0.98	NaN	0.76	1.19
C9JAF7	Synaptosomal-associated protein;Synaptosomal-associated protein 29	SNAP29	2	15	0	2.948	NaN	NaN	NaN	0.88	0.70	NaN	NaN	NaN	NaN
C9JBI3	Phosphoserine phosphatase	PSPH	2	12.3	1E-03	2.167	1.32	1.31	1.33	1.65	1.52	1.46	0.78	0.96	0.91
E9PNC7	Dr1-associated corepressor	DRAP1	2	14.8	0.001	2.632	0.97	0.98	1.12	NaN	1.13	0.89	NaN	NaN	1.00
C9JCD9	Protein BUD31 homolog	BUD31	2	29.1	0.008	1.526	1.01	1.30	0.89	1.15	1.61	1.05	0.92	0.98	1.21
C9JFE4	COP9 signalosome complex subunit 1	GPS1	6	18	0	25.62	0.73	1.11	0.89	0.90	0.70	0.75	1.12	NaN	0.95
C9JFM5	Syntaxin-4	STX4	2	17.1	0	14.69	1.21	1.17	NaN	NaN	1.22	1.64	NaN	NaN	0.99
C9JFR7	Cytochrome c	CYCS	6	57.4	0	39.05	1.01	1.05	0.92	0.95	1.21	1.11	0.81	0.59	0.69
C9JG08			2	0.6	0.008	1.485	1.29	1.02	1.14	NaN	1.31	1.21	NaN	NaN	NaN

C9JJT5	ATP synthase subunit f, mitochondrial	ATP5J2-PT	2	44.4	0	4.72	0.98	NaN	1.08	1.07	1.01	1.04	NaN	0.89	0.93
C9JXB8	60S ribosomal protein L24	RPL24	6	44.6	0	35.58	0.83	0.91	0.85	1.06	0.96	0.99	0.86	1.04	0.78
C9JRR5	Protein PTHB1	BBS9	1	15.8	1E-03	2.311	0.76	0.76	0.77	0.95	0.95	0.93	0.66	0.63	0.63
C9JRZ6	MICOS complex subunit MIC19	CHCHD3	9	28.9	0	34.38	1.01	1.08	1.13	1.03	1.11	0.98	0.94	0.91	0.89
C9JSF2	Heat shock factor 2-binding protein	HSF2BP	1	4.4	0.002	1.993	1.29	1.29	1.15	1.20	1.10	1.17	1.45	1.26	1.35
C9K055	Prenylcysteine oxidase 1	PCYOX1	3	15.3	0	3.014	0.79	0.97	0.95	0.74	0.86	1.18	0.64	0.55	0.77
C9K0J5	Ras-associated and pleckstrin homology domains-containing protein 1	RAPH1	4	4.8	0	6.37	NaN	1.72	1.46	0.70	0.61	NaN	0.98	NaN	0.87
F6U1T9	Calcineurin subunit B type 1	PPP3R1	5	55.6	0	42.48	0.89	0.96	1.20	0.96	0.73	0.97	0.97	NaN	0.77
D3YTB1	60S ribosomal protein L32	RPL32	7	45.1	0	55.43	0.75	0.77	0.89	1.00	0.90	0.85	1.08	1.04	0.91
D6R967	Inorganic pyrophosphatase 2, mitochondrial	PPA2	4	28.3	0	10.14	0.76	0.59	NaN	1.32	1.18	1.02	NaN	NaN	1.15
D6R9P3	Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB	8	31.8	0	236.2	0.89	0.89	0.84	1.28	0.94	1.01	1.32	0.88	0.84
D6RBQ9		HNRNPD	1	40	0	35.16	0.96	0.81	0.79	0.97	0.91	1.16	0.93	0.84	0.94
D6RBT3	NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial	NDUFS6	1	8.7	0.004	1.782	1.32	NaN	0.91	NaN	NaN	1.84	NaN	NaN	1.35
D6RBV2	Vesicular integral-membrane protein VIP36	LMAN2	5	26.2	0	5.502	NaN	1.08	0.96	NaN	1.12	1.04	1.00	1.24	1.14
D6REM1	Golgi phosphoprotein 3	GOLPH3	1	17.2	0	203.9	0.87	1.05	0.74	0.91	NaN	NaN	NaN	0.89	1.02
D6RGI3	Septin-11	SEPT11	10	35.5	0	139.3	1.03	1.32	1.06	1.05	1.14	0.94	1.24	1.01	1.35
D6REX3	Protein transport protein Sec31A	SEC31A	8	8	0	15.66	0.80	0.79	NaN	NaN	0.56	0.48	0.57	0.94	0.91
D6RFI1	Drebrin	DBN1	3	33.1	0	3.437	1.03	1.13	0.99	0.72	NaN	NaN	NaN	0.81	NaN
D6RFM5	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	SDHA	10	27.6	0	122.6	0.79	1.00	0.89	0.68	0.84	0.84	0.83	0.76	1.05
D6RG15	Twinfilin-2	TWF2	3	24	0	4.087	NaN	NaN	0.91	NaN	NaN	NaN	1.12	0.86	1.67
E5RFP0	NudC domain-containing protein	NUDCD2	1	8.3	5E-04	2.834	NaN	1.32	NaN	1.23	1.36	1.17	NaN	NaN	NaN
E5RGN3	Copper transport protein ATOX1	ATOX1	4	45.8	0	33.52	1.14	0.77	1.18	NaN	0.92	0.88	1.70	NaN	0.93
E5RGS4	Prefoldin subunit 1	PFDN1	3	23.9	0	3.332	NaN	0.29	NaN	NaN	0.93	0.84	1.49	1.63	NaN
E5RGX5	Stathmin;Stathmin-2	STMN2	1	16.7	0	70.07	0.83	0.87	0.85	0.86	0.91	0.86	0.94	0.90	0.97
E5RHG8	Transcription elongation factor B polypeptide 1	TCEB1	4	62.9	0	126.9	0.98	1.08	1.15	0.95	1.04	0.95	0.97	NaN	0.91
E5RHT6	ADP-ribosylation factor GTPase-activating protein 1	ARFGAP1	3	19.7	0	4.239	1.07	0.85	NaN	NaN	NaN	NaN	NaN	NaN	NaN
E5RIW3	Tubulin-specific chaperone A	TBCA	10	76.2	0	88.15	1.03	1.11	1.23	0.91	0.98	1.01	0.73	0.61	0.94
E5RJR5	S-phase kinase-associated protein 1	SKP1	5	38.7	0	73.37	1.20	1.37	1.47	0.96	1.12	1.08	0.99	0.77	2.10
E7EM64	COP9 signalosome complex subunit 6	COPS6	3	13.8	0	3.158	NaN	NaN	NaN	NaN	1.00	1.84	NaN	NaN	0.90
J3QLD9	Flotillin-2	FLOT2	10	29.7	0	27.28	0.66	0.70	0.71	0.73	0.77	0.98	0.81	0.73	0.73
J3KMY5	Epididymal secretory protein E1	NPC2	5	43.9	0	80.67	1.36	1.37	1.38	1.06	1.05	1.06	1.38	1.40	1.51
K7EJL1	AP-1 complex subunit mu-1	AP1M1	5	19.1	0	3.592	0.83	0.69	0.76	NaN	NaN	0.77	NaN	NaN	0.57

I3L4G9	Phosphoribosyl pyrophosphate synthase-associated protein 2	PRPSAP2	1	21.7	0.008	1.493	0.83	0.83	NaN	NaN	NaN	NaN	NaN	NaN	0.68
E7ES33	Septin-7	SEPT7	15	43.6	0	168.6	1.07	1.12	1.08	1.00	0.97	0.95	1.06	0.95	0.97
E7EPN9	Protein PRRC2C	PRRC2C	5	3.2	0	16.21	1.23	NaN	1.35	1.00	1.10	1.00	NaN	0.99	1.30
E7EPT4	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial	NDUFV2	2	9.1	1E-03	2.259	NaN	1.25	1.09	NaN	NaN	0.98	NaN	NaN	NaN
E7EQ69	N-alpha-acetyltransferase 50	NAA50	3	20.2	0	3.046	1.14	1.29	1.11	0.81	NaN	NaN	0.77	1.16	1.04
E7EQR4	Ezrin	EZR	31	64	0	323.3	0.90	0.88	0.87	0.92	0.97	0.93	0.81	0.96	0.83
S4R3H4	Apoptotic chromatin condensation inducer in the	ACIN1	9	10.1	0	28.77	1.20	0.96	1.02	1.12	0.65	0.70	1.78	1.01	1.33
E7EQY1	Protein FAM136A	FAM136A	4	19.6	0	132.3	NaN	0.64	NaN	NaN	1.31	1.16	NaN	NaN	NaN
E7ESI2	Cyclin-dependent kinase 2;Cyclin-dependent kinase 3	CDK2	2	20.6	0	4.727	NaN	NaN	NaN	0.91	0.69	NaN	NaN	NaN	NaN
E7ETU9	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 2	PLOD2	16	30.3	0	82.36	1.63	1.50	1.37	1.19	1.60	1.32	2.03	1.54	1.02
E7ETZ4	Basic leucine zipper and W2 domain-containing protein 2	BZW2	2	10	0	63.02	NaN	0.97	1.20	0.92	0.97	0.85	0.93	0.90	0.87
E7EUU4	Eukaryotic translation initiation factor 4 gamma 1	EIF4G1	30	29.4	0	323.3	1.04	1.04	0.99	1.04	0.87	1.03	0.89	0.97	0.90
G5E9S8	Kinesin light chain 1	KLC1	6	17.1	0	6.55	NaN	0.57	0.94	NaN	NaN	0.70	0.75	0.72	NaN
E7EWB4	Dihydropyrimidinase-related protein 5	DPYSL5	1	3.7	0.007	1.655	NaN	0.97	0.96	0.63	NaN	0.71	0.91	0.87	0.94
E7EWR4	Cleavage stimulation factor subunit 2;Cleavage stimulation factor subunit 2 tau variant	CSTF2	6	14.4	0	5.016	0.67	1.24	1.02	NaN	NaN	1.21	NaN	NaN	0.64
E7EX17	Eukaryotic translation initiation factor 4B	EIF4B	16	31.5	0	323.3	1.24	1.22	1.24	0.98	1.08	1.18	1.04	0.98	1.06
E7EX90	Dynactin subunit 1	DCTN1	18	19.8	0	76.36	0.83	0.73	1.17	0.98	0.71	0.87	0.94	0.98	0.77
E7EXA3	NIF3-like protein 1	NIF3L1	1	5.3	1E-03	2.115	NaN	NaN	NaN	1.17	NaN	0.76	NaN	NaN	0.60
F8VZJ2	Nascent polypeptide-associated complex subunit alpha;Nascent polypeptide-associated complex subunit alpha, muscle-specific form	NACA	5	45.6	0	122.3	1.22	1.16	1.21	1.05	0.96	1.07	1.04	1.11	1.12
E9PBT8	Sulfatase-modifying factor 2	SUMF2	3	17.2	0	16.87	0.94	1.05	0.97	NaN	1.73	NaN	1.15	NaN	0.60
E9PC52	Histone-binding protein RBBP7	RBBP7	6	35.8	0	54.82	0.67	0.64	0.90	0.77	0.80	0.86	0.91	0.87	0.99
E9PCR7	2-oxoglutarate dehydrogenase, mitochondrial	OGDH	8	17.3	0	21.72	NaN	1.00	0.81	1.01	0.57	0.92	0.65	0.83	1.15
E9PCY7	Heterogeneous nuclear ribonucleoprotein H;Heterogeneous nuclear ribonucleoprotein H, N-terminally processed	HNRNPH1	8	47.8	0	323.3	0.88	0.88	0.91	0.85	0.85	0.87	0.97	0.99	0.96

E9PD53	Structural maintenance of chromosomes protein;Structural maintenance of chromosomes protein 4	SMC4	8	7.4	0	14.87	NaN	0.83	0.76	0.73	NaN	0.80	NaN	0.89	NaN
E9PDF6	Unconventional myosin-Ib	MYO1B	5	7.1	0	6.527	NaN	0.71	0.94	NaN	1.06	0.83	0.96	NaN	0.88
E9PEB5	Far upstream element-binding protein 1	FUBP1	11	22.7	0	50.74	1.01	0.88	0.95	0.98	1.04	0.93	0.88	0.84	1.16
E9PF10	Nuclear pore complex protein Nup155	NUP155	4	3.8	0	5.073	0.59	NaN	0.65	0.84	NaN	1.12	1.05	1.13	0.81
E9PF63	Rho-associated protein kinase 2	ROCK2	4	5.5	0	13.93	1.55	2.01	1.55	NaN	NaN	0.50	0.85	0.62	1.09
E9PFH4	Transportin-3	TNPO3	3	5.3	0	13.85	1.22	1.34	NaN	NaN	0.96	NaN	NaN	NaN	NaN
E9PFP8	Poly(rC)-binding protein 3	PCBP3	0	20.2	0	20.36	NaN	1.40	NaN	1.18	1.13	NaN	NaN	NaN	0.88
E9PFR3	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform	PPP2R5D	10	22.7	0	53.85	0.94	0.69	1.03	1.00	1.12	0.99	1.02	1.05	0.86
E9PGC0	Ras GTPase-activating protein 1	RASA1	4	8.2	0	8.536	0.51	NaN	NaN	0.74	0.73	NaN	0.93	1.04	NaN
E9PGT1	Translin	TSN	6	42.6	0	19.55	0.99	0.88	0.97	0.83	0.90	0.86	0.69	0.79	0.72
E9PGZ1	Caldesmon	CALD1	19	38.1	0	174.1	1.08	0.90	1.20	0.79	0.96	0.62	1.12	1.11	1.31
E9PHI4	SUN domain-containing protein 1	SUN1	3	5.7	5E-04	2.766	1.09	0.89	1.22	NaN	NaN	NaN	NaN	NaN	0.83
E9PHY5	Band 4.1-like protein 2	EPB41L2	13	20.2	0	14.33	0.86	0.99	0.89	1.15	0.99	0.66	3.08	0.83	0.83
E9PIQ8	Stromal interaction molecule 1	STIM1	2	16.5	0.001	2.726	NaN	NaN	NaN	0.93	0.98	NaN	NaN	NaN	NaN
E9PK01	Elongation factor 1-delta	EEF1D	4	57.9	0	323.3	1.19	1.16	1.09	1.18	1.12	1.10	0.83	0.93	1.03
E9PK54		HSPA8	1	88	0	6.235	1.62	1.61	1.56	1.53	1.48	1.42	1.11	1.03	1.06
E9PKG1	Protein arginine N-methyltransferase 1	PRMT1	13	45.8	0	109.6	1.04	1.09	0.92	1.14	1.07	1.29	1.03	1.01	0.96
E9PN51	NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial	NDUFS8	1	8.2	0.001	2.11	1.09	1.13	1.00	1.12	NaN	1.04	NaN	1.03	1.13
E9PKZ0	60S ribosomal protein L8	RPL8	6	32.7	0	176.2	0.98	0.97	0.93	0.86	0.94	0.81	1.03	NaN	0.73
F8VSA6	NEDD8	NEDD8	2	46	0	18.88	0.79	0.91	0.90	NaN	0.83	0.92	NaN	NaN	0.75
E9PL71		EEF1D	1	54	0	136.5	NaN	NaN	1.49	1.28	1.21	NaN	NaN	1.31	1.40
E9PLK3	Puromycin-sensitive aminopeptidase	NPEPPS	27	36.7	0	168.3	1.08	1.09	1.12	1.11	1.08	1.14	1.03	1.00	1.04
E9PLL6	60S ribosomal protein L27a	RPL27A	4	42.6	0	18.76	0.75	1.10	0.72	0.76	1.12	0.84	1.02	1.02	0.75
I3L3B4	Vitamin K epoxide reductase complex subunit 1	VKORC1	1	12.5	0	5.325	NaN	NaN	NaN	1.50	NaN	NaN	2.30	1.48	NaN
K4DIA7	Tetraspanin;CD151 antigen	CD151	4	15.7	0	9.393	0.94	1.17	1.04	1.32	1.20	1.00	1.21	1.20	1.11
E9PR30	40S ribosomal protein S30	FAU	2	11.2	0	3.659	1.11	1.20	1.20	1.39	1.23	1.39	1.40	1.42	1.79
E9PS97	Alpha-parvin	PARVA	4	27.8	0	17.42	1.08	1.39	1.15	NaN	NaN	1.07	0.64	NaN	1.30
F2Z2E2	Ras GTPase-activating-like protein IQGAP3	IQGAP3	5	6.5	1E-03	2.284	NaN	1.10	0.58	NaN	NaN	NaN	NaN	NaN	NaN
F2Z2Y8	Toll-interacting protein	TOLLIP	2	12.7	0	5.787	0.62	0.71	NaN	NaN	NaN	0.98	NaN	NaN	NaN
F5GWX2	Heme-binding protein 1	HEBP1	5	62.4	0	78.33	1.17	0.93	NaN	1.19	1.06	1.18	0.85	0.67	1.01
F5H5V4	26S proteasome non-ATPase regulatory subunit 9	PSMD9	5	39.9	0	17.75	NaN	0.84	NaN	NaN	0.84	NaN	0.92	0.80	NaN
H0YLY7	Calcineurin B homologous protein 1	CHP1	1	17.6	0.002	1.971	NaN	NaN	1.27	1.63	NaN	NaN	1.06	1.36	NaN

F5GX77	Multifunctional methyltransferase subunit TRM112-like protein	TRMT112	3	38.7	0	3.864	0.97	1.49	NaN	0.97	NaN	1.48	NaN	NaN	1.61
F5GXJ9	CD166 antigen	ALCAM	15	45.3	0	283.8	1.06	1.01	1.00	1.33	1.19	1.15	0.90	1.02	1.23
F5GXX5	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase	DAD1	3	37.6	0	13.26	NaN	1.29	NaN	0.79	1.06	0.96	0.90	0.97	NaN
H0YG54	Oligoribonuclease, mitochondrial	REXO2	8	45.7	0	10.66	1.09	1.19	1.05	0.95	0.98	0.87	1.17	1.28	1.11
F5GZS6	4F2 cell-surface antigen heavy chain	SLC3A2	17	34.2	0	323.3	1.12	1.07	1.10	0.94	1.06	0.99	1.13	1.10	1.12
F5H157	Ras-related protein Rab-35	RAB35	1	5.9	0	208.8	1.40	1.22	1.01	0.98	1.39	1.33	NaN	1.01	1.07
F5H2U8	High mobility group protein HMGI-C	HMGA2	2	36.4	0	18.51	NaN	NaN	0.72	1.22	NaN	NaN	0.71	1.02	NaN
F5H365	Protein transport protein Sec23A	SEC23A	7	18.9	0	26.35	0.74	0.67	0.83	0.93	2.07	0.85	0.90	0.93	0.97
F5H442	Tumor susceptibility gene 101 protein	TSG101	4	15.6	0	6.658	NaN	NaN	1.00	0.86	NaN	1.07	NaN	NaN	NaN
F8VY35	Nucleosome assembly protein 1-like 1	NAP1L1	3	75.4	0	323.3	1.09	1.05	1.03	1.08	1.04	1.02	1.13	1.09	1.07
F5H5D3	Tubulin alpha-1C chain	TUBA1C	4	69.7	0	323.3	0.53	0.56	0.53	0.56	0.58	0.59	0.96	0.89	0.94
F5H6E2	Unconventional myosin-Ic	MYO1C	20	25.1	0	85.7	0.84	0.79	0.97	0.92	1.18	1.00	1.06	0.92	1.02
F5H7F6	Microsomal glutathione S-transferase 1	MGST1	2	18.2	0	11.02	NaN	NaN	NaN	NaN	0.94	0.64	NaN	NaN	NaN
H0Y3C5	Non-specific protein-tyrosine kinase;Tyrosine-protein kinase Lyn;Tyrosine-protein kinase HCK;Proto-oncogene tyrosine-protein kinase Src;Tyrosine-protein kinase Fyn;Tyrosine-protein kinase Yes	HCK	1	1.5	0	5.689	0.89	0.78	NaN	0.84	NaN	0.66	NaN	0.76	0.89
F6TLX2	Glyoxalase domain-containing protein 4	GLOD4	11	26.5	0	25.02	1.02	1.05	1.00	0.93	1.14	1.08	0.90	0.92	0.91
F6TR53	HCLS1-binding protein 3	HS1BP3	2	11.7	0.008	1.561	1.09	NaN	1.07	NaN	NaN	0.92	NaN	NaN	NaN
F8VNT9	Tetraspanin;CD63 antigen	CD63	1	6	0	4.749	0.83	0.96	0.93	2.00	1.62	1.18	0.98	1.19	0.95
F8VPD4	CAD protein;Glutamine-dependent carbamoyl-phosphate synthase;Aspartate carbamoyltransferase;Dihydroorotase	CAD	32	20.8	0	242.8	0.79	0.76	0.76	0.74	0.74	0.77	1.02	1.02	0.96
F8VQE1	LIM domain and actin-binding protein 1	LIMA1	14	32.1	0	82.95	0.97	0.84	0.75	0.74	0.90	1.09	0.69	0.64	0.88
F8VVA7	Coatomer subunit zeta-1	COPZ1	6	31.3	0	26.73	0.99	NaN	1.08	1.08	1.32	1.11	0.86	NaN	1.00
F8VVL1	Density-regulated protein	DENR	5	36.2	0	156.7	NaN	NaN	0.84	1.48	NaN	NaN	1.33	1.25	0.89
F8VVM2		SLC25A3	1	38.9	0	231.3	0.86	0.91	1.06	1.07	1.06	1.05	0.77	1.04	0.83
F8VXC8	SWI/SNF complex subunit SMARCC2;SWI/SNF complex subunit SMARCC1	SMARCC2	4	4.6	0	12.4	1.06	1.52	0.99	1.30	1.00	NaN	NaN	0.61	0.66
F8VXU5	Vacuolar protein sorting-associated protein 29	VPS29	3	15.9	0	149	1.08	1.19	0.93	1.18	0.85	1.30	1.15	NaN	1.16

F8VYE8	Serine/threonine-protein phosphatase;Serine/threonine-protein phosphatase PP1-gamma catalytic subunit	PPP1CC	3	70.4	0	45.99	1.20	1.14	1.14	NaN	1.62	1.38	NaN	NaN	NaN
F8VZQ9	SAP domain-containing ribonucleoprotein	SARNP	4	17.4	0	3.912	0.92	0.91	0.91	NaN	NaN	NaN	NaN	NaN	0.86
F8W031	Protein canopy homolog 2	CNPY2	3	19	0	10.07	1.26	1.21	1.22	1.13	NaN	0.99	NaN	1.03	0.84
F8W1A4	Adenylate kinase 2, mitochondrial;Adenylate kinase 2, mitochondrial;Adenylate kinase 2, mitochondrial, N-terminally processed	AK2	9	42.2	0	12.19	0.89	1.07	1.56	NaN	1.72	1.52	NaN	NaN	0.77
F8W6G1	Nuclear receptor-binding protein	NRBP1	5	12.3	0	18.78	0.71	0.94	0.79	1.08	0.74	1.12	NaN	NaN	NaN
F8W6I7	Heterogeneous nuclear ribonucleoprotein A1;Heterogeneous nuclear ribonucleoprotein A1, N-terminally processed;Heterogeneous	HNRNPA1	9	58.6	0	323.3	0.88	0.85	0.92	0.88	0.90	0.92	0.95	0.91	0.94
F8W726	Ubiquitin-associated protein 2-	UBAP2L	12	17.4	0	230.3	1.26	1.07	1.27	0.85	1.00	1.27	1.11	0.94	1.02
F8W7U8	Double-strand break repair protein MRE11A	MRE11A	4	8.1	0	5.058	0.82	1.35	NaN	0.98	NaN	0.88	NaN	0.89	NaN
F8W930	Insulin-like growth factor 2 mRNA-binding protein 2	IGF2BP2	9	22	0	63.12	1.45	1.16	1.26	0.54	0.78	0.63	0.85	NaN	1.69
F8WCF6	Actin-related protein 2/3 complex subunit 4	ARPC4-TT	8	48.6	0	13.86	0.95	0.88	1.20	0.92	1.04	0.92	1.01	0.86	1.07
G3V0I5	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	NDUFV1	2	8.1	0	4.215	1.04	NaN	0.82	NaN	NaN	NaN	NaN	NaN	1.81
G3V1D3	Dipeptidyl peptidase 3	DPP3	13	27.6	0	147.3	0.72	0.88	0.86	NaN	0.76	0.89	NaN	1.08	0.91
G3V1C3	Apoptosis inhibitor 5	API5	9	24.7	0	231.8	0.93	0.93	0.99	1.26	1.28	0.80	1.33	1.46	0.91
G3V1D4	Protein lin-7 homolog C	LIN7C	5	24.9	0	3.92	NaN	0.80	0.59	NaN	NaN	NaN	NaN	NaN	NaN
G3V1U3	Methionine aminopeptidase 2	METAP2	7	32.9	0	140.6	0.89	0.62	NaN	NaN	NaN	0.79	1.20	1.12	0.85
G3V2U7	Acylphosphatase;Acylphosphatase-1	ACYP1	2	17.8	0	14.98	NaN	1.33	NaN	1.08	1.13	1.34	1.08	0.95	NaN
G3V4P8	Glia maturation factor beta	GMFB	5	46	0	168.3	1.09	1.12	1.11	0.93	0.98	1.02	1.02	0.83	1.13
G3V5Z7	Proteasome subunit alpha type;Proteasome subunit alpha type-6	PSMA6	12	49.6	0	122.2	1.00	0.82	0.99	0.98	1.02	0.97	0.99	0.94	0.81
G5EA06	28S ribosomal protein S27, mitochondrial	MRPS27	2	7.3	0	2.895	0.89	NaN	1.15	NaN	NaN	NaN	NaN	NaN	0.66
G5EA30	CUGBP Elav-like family member	CELF1	4	10.3	0.001	2.655	0.87	0.57	NaN	NaN	NaN	0.80	NaN	NaN	NaN
G8JLA2		MYL6	1	69.7	0	323.3	0.98	0.97	0.96	0.95	1.01	0.99	1.09	1.01	1.04
G8JLD5	Dynamin-1-like protein	DNM1L	14	28.1	0	88.27	1.19	0.98	1.21	0.99	1.22	1.11	0.80	0.82	1.02
H0Y2V6	Centrosomal protein of 170 kDa	CEP170	5	4.5	0	10.16	NaN	NaN	NaN	NaN	NaN	0.86	0.95	1.48	NaN
H0Y2Y8	Zyxin	ZYX	11	30.6	0	152.9	1.72	1.56	1.45	1.37	1.37	1.38	1.32	1.37	1.46

Q5QPK2	Dolichol-phosphate mannosyltransferase subunit 1	DPM1	6	23.7	0	10.71	1.19	0.94	1.30	1.34	0.95	0.99	NaN	1.68	1.29
H0Y4E0	Ubiquitin carboxyl-terminal hydrolase;Ubiquitin carboxyl-terminal hydrolase isozyme L5	UCHL5	2	20.8	0	8.369	0.93	0.87	1.11	0.76	0.85	1.13	NaN	0.99	NaN
H0Y5B4	60S ribosomal protein L36a;60S ribosomal protein L36a-like	RPL36A	5	35.7	0	17.39	0.99	1.68	1.20	1.00	NaN	1.28	1.17	1.11	1.14
P0DP25		CALM2	11	60.4	0	323.3	1.01	0.97	0.98	0.99	0.96	0.94	1.01	1.02	1.01
H0Y8E6	DNA replication licensing factor MCM2	MCM2	11	18.5	0	29	0.72	0.76	NaN	0.98	0.91	1.00	0.66	0.89	0.61
H0Y8Z9	Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	2	7	0.001	2.755	0.84	0.72	0.98	NaN	NaN	0.79	NaN	NaN	0.90
H0Y987	Phosphoacetylglucosamine mutase	PGM3	15	33.6	0	121	0.99	0.93	0.97	1.01	1.01	0.89	1.06	1.15	1.06
H0YBL1	Inositol monophosphatase 1	IMPA1	4	20.8	0	6.095	0.89	0.69	1.31	1.02	0.80	NaN	NaN	1.12	0.81
H0YC42	Tumor protein D52	TPD52	6	34.9	0	36.81	1.28	1.30	1.21	1.11	1.13	NaN	1.18	1.24	NaN
H0YD13	CD44 antigen	CD44	8	47.6	0	322.3	1.22	1.24	1.18	1.06	1.04	1.08	1.21	0.95	0.97
H0YDU8	Serine/threonine-protein phosphatase;Serine/threonine-protein phosphatase 5	PPP5C	6	14.4	0	10.67	1.26	NaN	2.19	0.71	0.97	0.77	0.96	0.70	1.09
H0YFD6	Trifunctional enzyme subunit alpha, mitochondrial;Long-chain enoyl-CoA hydratase;Long chain 3-hydroxyacyl-CoA dehydrogenase	HADHA	27	50.5	0	323.3	1.04	0.76	1.04	1.07	0.95	0.85	0.87	0.87	0.91
H0YHA7	60S ribosomal protein L18	RPL18	7	46.7	0	161.9	0.98	0.99	1.05	0.84	0.92	1.02	0.91	0.96	1.05
H0YMV8	40S ribosomal protein S27;40S ribosomal protein S27-like	RPS27L	1	32	1E-03	2.141	NaN	NaN	NaN	0.67	NaN	NaN	1.16	1.03	NaN
H0YNW5	Deoxyuridine 5-triphosphate nucleotidohydrolase,	DUT	5	37.1	0	26.77	1.09	1.25	1.20	0.88	0.87	1.06	0.71	NaN	0.87
H3BLV9	SRSF protein kinase 1	SRPK1	5	12.1	0	26.41	0.88	0.94	1.10	0.66	0.79	0.94	NaN	0.79	0.66
H3BM14	NEDD8 ultimate buster 1	NUB1	2	3.7	0	3.501	0.77	0.86	0.89	NaN	0.47	NaN	NaN	NaN	1.67
H3BN50	Na(+)/H(+) exchange regulatory cofactor NHE-RF2	SLC9A3R2	4	23.3	0	2.892	1.08	0.77	1.20	NaN	0.66	NaN	NaN	NaN	0.75
H3BN98			2	23.6	0.002	1.984	0.89	1.35	1.04	1.17	1.07	NaN	0.94	0.74	1.04
H3BNC9	40S ribosomal protein S17	RPS17	6	14	0	323.3	0.77	0.84	0.76	0.82	0.89	0.81	0.73	0.83	0.77
H3BPE1	Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5	MACF1	11	2.6	0	9.739	0.77	NaN	0.70	0.83	1.15	0.86	1.22	1.11	1.31
H3BPK3	Hydroxyacylglutathione hydrolase, mitochondrial	HAGH	3	14.2	0.001	2.585	NaN	1.23	1.06	NaN	1.06	0.86	NaN	NaN	0.93
H3BUU8		VAC14	1	14.4	0	5.888	0.66	0.66	0.67	NaN	NaN	0.72	NaN	NaN	1.50
H7BYN3	Transcription factor A, mitochondrial	TFAM	2	10	0.009	1.449	NaN	NaN	1.04	0.87	0.94	NaN	NaN	NaN	NaN
H7BYY1		TPM1	7	65.3	0	86.32	1.23	1.17	1.37	0.98	1.15	0.97	1.88	1.92	1.93
H7BZI1	Nucleobindin-1	NUCB1	4	17.3	0	7.564	1.41	0.99	1.37	NaN	NaN	0.94	NaN	1.24	NaN
H7BZJ3		PDIA3	1	53.7	0	127.7	1.32	1.28	1.72	1.18	1.16	1.24	1.20	1.25	1.34
H7C0E5	Zinc finger protein ZPR1	ZPR1	4	12.2	0	6.483	1.26	0.96	1.17	1.12	1.38	0.98	1.00	NaN	0.99

H7C2Q8	Probable rRNA-processing protein EBP2	EBNA1BP2	4	15	0	3.79	1.91	NaN	NaN	1.43	0.83	1.05	NaN	NaN	1.43
H7C4H2	Signal recognition particle receptor subunit beta	SRPRB	1	8.1	0	4.804	1.24	0.87	0.93	NaN	1.01	1.03	NaN	NaN	1.17
H7C4T5	Muscleblind-like protein 1;Muscleblind-like protein 2	MBNL1	5	20.7	0	3.455	NaN	0.73	NaN	NaN	1.24	1.62	NaN	NaN	0.59
H7C5G1	Isoamyl acetate-hydrolyzing esterase 1 homolog	IAH1	2	17.1	0	48.11	2.42	2.32	NaN	1.80	NaN	NaN	NaN	1.40	2.20
I1E4Y6	PERQ amino acid-rich with GYF domain-containing protein 2	GIGYF2	3	3.6	0	2.904	NaN	NaN	NaN	1.38	1.41	NaN	NaN	NaN	NaN
I3L0H8	ATP-dependent RNA helicase DDX19A;ATP-dependent RNA helicase DDX19B	DDX19A	2	5.8	0	7.61	NaN	NaN	NaN	0.80	NaN	NaN	1.50	0.85	NaN
I3L0N3	Vesicle-fusing ATPase	NSF	6	8.5	0	5.778	0.60	0.72	0.90	0.90	NaN	NaN	NaN	NaN	NaN
I3L1P8	Mitochondrial 2-oxoglutarate/malate carrier	SLC25A11	3	11.8	0	153.1	0.65	1.09	NaN	NaN	1.55	NaN	NaN	NaN	0.81
I3L294	Monoacylglycerol lipase ABHD12	ABHD12	2	19.5	0.001	2.084	0.68	NaN	0.95	1.01	NaN	1.16	NaN	1.07	1.01
I3L397	Eukaryotic translation initiation factor 5A;Eukaryotic translation initiation factor 5A-1;Eukaryotic translation initiation factor 5A-1-like;Eukaryotic translation initiation factor 5A-2	EIF5A	14	76.7	0	296.5	0.98	1.01	0.92	1.06	0.98	0.97	0.86	0.95	0.94
J3KMZ9	Low-density lipoprotein receptor	LDLR	13	20.1	0	108.5	1.29	1.03	0.94	1.53	1.76	1.73	0.95	1.32	0.94
J3KN16	Proteasome-associated protein ECM29 homolog	KIAA0368	6	4.3	0	5.975	NaN	NaN	NaN	0.93	NaN	1.19	1.04	1.20	0.72
J3KN66		TOR1AIP1	1	15.9	0	30.88	1.35	1.30	1.07	0.98	0.81	1.43	NaN	1.35	1.36
J3KN67		TPM3	0	62.8	0	15.42	1.03	0.95	1.00	NaN	1.65	0.76	NaN	NaN	1.13
J3QL05	Serine/arginine-rich splicing factor 2	SRSF2	5	45.4	0	93.49	0.85	1.80	1.23	1.02	0.96	0.95	0.51	0.46	0.44
J3KPX7	Prohibitin-2	PHB2	16	58.1	0	105.3	1.00	0.91	0.94	1.03	0.95	0.95	0.78	1.21	0.77
J3KQ18	D-dopachrome decarboxylase;D-dopachrome decarboxylase-like protein	DDT	5	40.9	0	22.72	1.10	1.10	0.99	0.90	1.14	1.04	NaN	0.91	0.97
J3KQ32	Obg-like ATPase 1	OLA1	16	55.8	0	102.5	0.83	0.91	0.89	1.00	1.10	0.89	0.81	1.06	0.90
J3KQ48	Peptidyl-tRNA hydrolase 2, mitochondrial	PTRH2	3	26.7	0	8.885	1.46	1.60	0.80	0.86	0.93	1.44	NaN	NaN	0.86
J3KR44	Ubiquitin thioesterase OTUB1	OTUB1	11	55.1	0	119.5	0.84	0.97	0.80	1.20	0.81	0.74	1.24	1.05	0.80
J3KR97	Tubulin-specific chaperone D	TBCD	3	4.2	0	9.811	NaN	NaN	0.40	0.89	0.71	0.70	NaN	NaN	0.77
J3QR09	Ribosomal protein L19;60S ribosomal protein L19	RPL19	8	31.6	0	44.42	1.05	1.05	0.99	1.07	1.10	1.09	1.16	1.02	1.10
J3KTI2	Migration and invasion enhancer	MIEN1	2	29.3	0	5.034	0.84	0.78	0.91	NaN	NaN	1.18	NaN	NaN	NaN
J3KTL2	Serine/arginine-rich splicing factor 1	SRSF1	13	46.2	0	107.5	1.04	0.95	1.11	0.97	0.95	0.92	1.04	1.01	1.01

J3QLE5	Small nuclear ribonucleoprotein-associated protein N;Small nuclear ribonucleoprotein-associated proteins B and B	SNRPN	7	38.5	0	15.84	0.84	0.85	0.86	0.86	0.89	0.85	1.02	0.99	0.96
J3QRS3	Myosin regulatory light chain 12A;Myosin regulatory light chain 12B	MYL12A	4	64.4	0	323.3	0.90	0.96	0.86	0.99	1.05	0.98	0.95	0.94	0.79
K4DI93	Cullin-4B	CUL4B	6	13.7	0	61.68	0.96	1.07	1.09	1.04	1.16	1.10	0.73	0.75	0.92
K7EM02	Katanin p60 ATPase-containing subunit A-like 2	KATNAL2	1	9.4	0	4.338	0.94	NaN	0.90	1.01	1.01	NaN	0.90	0.84	NaN
K7EJE8	Lon protease homolog, mitochondrial	LONP1	11	21.4	0	170.2	0.90	0.86	1.00	NaN	0.83	0.97	0.63	NaN	1.05
K7EK07	Histone H3;Histone H3.3	H3F3B	1	40.9	0.001	2.751	0.33	0.52	NaN	NaN	NaN	NaN	NaN	NaN	NaN
K7EQ02	DAZ-associated protein 1	DAZAP1	5	22.6	0	25.6	1.34	1.14	1.34	1.93	1.15	1.11	NaN	1.37	1.05
K7EKL3	Granulins;Acrogranin;Paragranulin;Granulin-1;Granulin-2;Granulin-3;Granulin-4;Granulin-5;Granulin-6;Granulin-7	GRN	3	10.8	0	69.04	NaN	NaN	NaN	NaN	0.57	0.66	NaN	NaN	2.13
K7EL20	Eukaryotic translation initiation factor 3 subunit G	EIF3G	1	43.5	0	182.9	1.07	1.10	1.07	0.94	1.16	0.86	1.01	1.02	0.88
K7ELD9	Synaptogyrin-2	SYNGR2	2	30.8	0.001	2.671	NaN	NaN	NaN	1.03	0.84	NaN	NaN	NaN	NaN
K7ELL7	Glucosidase 2 subunit beta	PRKCSH	23	48	0	323.3	1.13	1.03	1.02	1.11	1.12	1.15	0.99	0.97	0.96
K7ELP0		TPM4	1	15.9	0	24.89	0.88	0.97	0.74	NaN	NaN	0.82	1.60	1.49	1.33
K7ELS0	Uncharacterized protein	C19orf43	1	10.6	0	3.023	0.98	1.26	NaN	0.98	1.85	2.93	NaN	0.91	1.14
K7EM18	Eukaryotic translation initiation factor 1;Eukaryotic translation initiation factor 1b	EIF1	6	62	0	49.15	0.86	1.03	1.09	1.72	1.01	1.07	1.01	NaN	NaN
K7ENT6		TPM4	2	63.6	0	40.36	1.27	1.27	1.18	1.21	0.94	1.18	1.44	1.63	1.49
Q08E86	Protein KIAA0100	KIAA0100	1	0.4	0.009	1.414	NaN	NaN	NaN	NaN	1.03	0.68	NaN	NaN	1.33
K7EQX8		MXRA7	1	73.3	0	24.03	1.16	1.84	NaN	2.12	NaN	NaN	NaN	NaN	1.50
K7ER90		EIF3G	1	48.9	0	33.35	1.18	1.27	1.25	1.13	1.06	1.07	0.98	0.98	0.99
K7ER96	Thioredoxin-like protein 1	TXNL1	4	19.2	0	9.479	0.75	0.65	0.86	0.87	1.52	0.89	1.06	0.84	1.11
K7ERF1	Eukaryotic translation initiation factor 3 subunit K	EIF3K	7	42.2	0	24.88	1.18	0.96	1.27	1.13	1.13	0.97	NaN	0.59	NaN
K7ERV3	Thymidine kinase;Thymidine kinase, cytosolic	TK1	2	11.2	0.007	1.635	NaN	NaN	NaN	0.86	1.20	NaN	NaN	NaN	NaN
M0QXB4	Coatomer subunit epsilon	COPE	8	32.9	0	21.94	0.72	0.73	0.98	0.90	1.10	0.92	0.87	0.75	0.91
M0QXN5	Nuclear pore glycoprotein p62	NUP62	4	17.9	0	27.4	NaN	NaN	0.87	0.90	0.98	NaN	0.87	NaN	NaN
M0QYT0			0	42.7	0	5.035	1.21	1.10	1.20	0.96	1.53	1.18	0.77	0.81	1.01
M0R0N4	AP-2 complex subunit sigma	AP2S1	2	11.1	0.003	1.883	0.75	0.85	NaN	0.73	1.00	0.95	NaN	0.77	1.04
M0R0F0	40S ribosomal protein S5;40S ribosomal protein S5, N-terminally processed	RPS5	12	50	0	248.9	0.88	0.89	0.78	0.78	0.75	1.13	0.94	0.90	0.93
M0R117	60S ribosomal protein L18a	RPL18A	9	53.9	0	84.35	0.82	0.81	0.79	0.83	0.73	0.80	0.72	0.70	1.01

M0R208	ATP-dependent Clp protease proteolytic subunit;ATP-dependent Clp protease proteolytic subunit, mitochondrial	CLPP	2	12.1	0.003	1.862	1.46	1.50	NaN	NaN	1.71	NaN	NaN	NaN	NaN
O00116	Alkyldihydroxyacetonephosphate synthase, peroxisomal	AGPS	7	16.9	0	30.57	0.73	0.62	0.58	NaN	NaN	0.78	1.16	2.46	0.82
O00148	ATP-dependent RNA helicase DDX39A	DDX39A	3	48.7	0	61.82	0.74	0.80	0.69	NaN	NaN	0.99	0.71	NaN	0.83
O00151	PDZ and LIM domain protein 1	PDLIM1	18	82.7	0	323.3	0.87	0.91	0.91	0.93	0.99	0.96	0.86	0.97	1.06
O00154	Cytosolic acyl coenzyme A thioester hydrolase	ACOT7	5	15.5	0	23.3	1.28	NaN	1.11	NaN	NaN	1.18	NaN	NaN	1.29
O00170	AH receptor-interacting protein	AIP	11	41.8	0	14.15	0.96	1.29	1.09	0.83	1.03	0.97	0.93	1.00	1.26
O00203	AP-3 complex subunit beta-1	AP3B1	5	8	0	6.681	2.06	NaN	NaN	1.18	NaN	NaN	1.04	1.05	NaN
O00231	26S proteasome non-ATPase regulatory subunit 11	PSMD11	17	48.6	0	61.35	1.05	1.11	1.03	1.04	0.94	1.13	1.03	1.00	0.99
O00232	26S proteasome non-ATPase regulatory subunit 12	PSMD12	10	27.6	0	17.33	1.34	1.07	1.07	0.91	0.95	0.91	NaN	1.46	1.00
O00273	DNA fragmentation factor subunit alpha	DFFA	1	5.1	0.002	2.021	1.17	1.19	NaN	NaN	NaN	NaN	NaN	NaN	0.95
O00299	Chloride intracellular channel protein 1	CLIC1	17	87.1	0	323.3	1.00	0.93	1.01	1.02	1.00	0.99	0.96	0.93	0.97
O00303	Eukaryotic translation initiation factor 3 subunit F	EIF3F	11	38.9	0	73.51	1.14	1.22	1.23	1.08	1.20	0.99	1.18	0.73	1.05
O00410	Importin-5	IPO5	38	47.7	0	323.3	1.11	1.07	0.99	1.01	1.04	0.98	0.73	0.79	1.01
O00422	Histone deacetylase complex subunit SAP18	SAP18	5	40.5	0	3.092	0.60	NaN	1.44	NaN	1.15	1.17	1.17	NaN	1.37
O00483	Cytochrome c oxidase subunit NDUFA4	NDUFA4	3	37	0	6.352	1.13	0.92	0.98	1.08	1.24	1.14	1.15	1.17	NaN
O00487	26S proteasome non-ATPase regulatory subunit 14	PSMD14	6	34.8	0	89.9	0.86	0.88	1.11	0.92	0.98	1.09	0.89	0.79	1.20
O00499	Myc box-dependent-interacting protein 1	BIN1	6	18.9	0	24.63	1.42	0.96	0.90	NaN	3.51	0.73	NaN	0.95	0.93
O00505	Importin subunit alpha-4	KPNA3	6	23.6	0	62.26	0.82	0.79	0.48	1.01	0.91	0.86	1.26	1.06	0.89
O00560	Syntenin-1	SDCBP	2	13.8	0	18.49	0.82	0.87	0.78	NaN	NaN	0.85	NaN	NaN	0.81
O00592	Podocalyxin	PODXL	7	17.4	0	99.48	2.17	2.51	2.14	1.15	1.18	1.06	1.95	1.98	2.85
O00622	Protein CYR61	CYR61	21	68.2	0	234.2	2.49	2.33	2.61	1.27	1.34	1.20	1.39	1.38	1.25
O00629	Importin subunit alpha-3	KPNA4	7	29.2	0	54.42	1.37	0.91	0.93	0.95	1.43	0.63	NaN	0.97	0.77
O00743	Serine/threonine-protein phosphatase 6 catalytic subunit;Serine/threonine-protein phosphatase 6 catalytic subunit, N-terminally processed	PPP6C	3	11.1	0.008	1.48	NaN	0.48	NaN	0.69	0.95	0.45	NaN	NaN	NaN
O00764	Pyridoxal kinase	PDXK	8	41.7	0	264.8	1.18	1.31	1.10	0.78	0.93	1.17	1.12	NaN	1.20
O14493	Claudin-4;Claudin-9;Claudin-6;Claudin-3	CLDN4	2	12.9	0	15.07	1.52	0.79	NaN	NaN	NaN	0.98	1.39	1.45	NaN
O14561	Acyl carrier protein, mitochondrial;Acyl carrier protein	NDUFAB1	3	21.2	0	9.133	0.98	1.09	1.01	1.19	1.07	1.09	0.93	0.93	1.04

O14617	AP-3 complex subunit delta-1	AP3D1	6	9	0	21.65	0.79	0.66	NaN	NaN	0.52	1.00	NaN	NaN	0.58
O14737	Programmed cell death protein 5	PDCD5	7	56	0	218.2	1.20	1.11	1.31	1.21	1.13	1.06	1.51	1.19	1.15
O14744	Protein arginine N-methyltransferase 5;Protein arginine N-methyltransferase 5, N-terminally processed	PRMT5	6	11.9	0	35.91	1.07	0.94	1.27	NaN	0.80	0.95	NaN	1.40	0.88
O14745	Na(+)/H(+) exchange regulatory cofactor NHE-RF1	SLC9A3R1	7	28.5	0	35.57	NaN	0.79	1.08	1.13	0.67	NaN	NaN	0.48	0.78
O14763	Tumor necrosis factor receptor superfamily member 10B	TNFRSF10	1	3.9	0.009	1.457	NaN	1.85	1.21	NaN	NaN	NaN	NaN	NaN	NaN
O14818	Proteasome subunit alpha type-7	PSMA7	14	66.5	0	323.3	0.98	1.10	0.97	0.94	1.00	0.99	0.92	0.92	0.97
O14828	Secretory carrier-associated membrane protein 3	SCAMP3	3	12.4	0	6.226	0.89	1.43	NaN	2.16	NaN	1.41	NaN	1.43	NaN
O14907	Tax1-binding protein 3	TAX1BP3	3	39.5	0	14.17	1.18	1.45	NaN	NaN	NaN	NaN	NaN	NaN	NaN
O14929	Histone acetyltransferase type B catalytic subunit	HAT1	3	12.9	0.001	2.618	NaN	0.64	0.84	NaN	0.94	NaN	1.35	NaN	NaN
O14964	Hepatocyte growth factor-regulated tyrosine kinase substrate	HGS	7	10.7	0	6.788	0.96	1.11	0.86	0.98	0.86	0.95	NaN	1.14	1.27
O14974	Protein phosphatase 1 regulatory subunit 12A	PPP1R12A	11	12.9	0	91.9	NaN	1.32	NaN	NaN	2.78	0.61	NaN	NaN	1.86
O14980	Exportin-1	XPO1	26	31.6	0	173.3	0.95	0.96	0.95	0.93	1.04	0.93	0.88	1.00	0.94
O15067	Phosphoribosylformylglycinamidine synthase	PFAS	6	7.2	0	9.764	NaN	0.89	NaN	0.72	0.85	NaN	NaN	0.84	1.14
O15131	Importin subunit alpha-6;Importin subunit alpha-5;Importin subunit alpha-5, N-terminally processed;Importin subunit alpha-7	KPNA5	3	6	0	8.008	NaN	0.88	0.93	1.10	0.99	0.77	0.95	0.98	0.97
O15143	Actin-related protein 2/3 complex subunit 1B	ARPC1B	4	55.1	0	319.7	0.87	1.08	0.91	0.95	0.91	0.96	0.84	0.98	0.90
O15144	Actin-related protein 2/3 complex subunit 2	ARPC2	13	40.3	0	66.77	0.82	0.95	0.87	1.16	1.02	0.90	1.08	1.06	0.69
O15145	Actin-related protein 2/3 complex subunit 3	ARPC3	8	42.1	0	33.33	0.97	0.95	0.99	1.13	1.00	0.97	0.96	1.12	1.06
O15173	Membrane-associated progesterone receptor component 2	PGRMC2	5	29.6	0	35.45	NaN	NaN	NaN	0.86	0.91	0.84	1.02	2.17	1.26
O15212	Prefoldin subunit 6	PFDN6	5	32.6	0	27.76	0.87	NaN	0.89	1.19	NaN	NaN	0.97	1.17	NaN
O15231	Zinc finger protein 185	ZNF185	12	27.4	0	90.95	1.03	0.96	NaN	1.19	1.00	1.04	1.22	1.85	1.78
Q5T8U5	Surfeit locus protein 4	SURF4	4	26.9	0	29.83	1.04	0.95	0.84	1.05	1.16	1.02	0.78	0.65	0.78
O15355	Protein phosphatase 1G	PPM1G	13	33.3	0	234.5	1.08	1.11	1.28	0.98	1.14	1.00	0.95	1.03	0.99
O15371	Eukaryotic translation initiation factor 3 subunit D	EIF3D	15	43.1	0	88.33	1.09	0.96	1.08	1.36	0.92	1.01	0.89	0.91	0.93
O15400	Syntaxin-7	STX7	5	25.7	0	17.37	1.41	NaN	NaN	NaN	0.88	1.00	0.67	0.87	NaN
O15427	Monocarboxylate transporter 4	SLC16A3	6	15.3	0	38.68	1.11	1.02	0.99	0.93	0.97	1.21	1.17	1.20	1.32

O15460	Prolyl 4-hydroxylase subunit alpha-2	P4HA2	5	15.3	0	13.19	NaN	1.28	NaN	NaN	NaN	NaN	1.23	NaN	1.38
O15498	Synaptobrevin homolog YKT6	YKT6	2	11.1	0.001	2.54	0.80	NaN	0.82	NaN	0.71	1.22	NaN	NaN	NaN
O15511	Actin-related protein 2/3 complex subunit 5	ARPC5	3	40.4	0	60.31	1.17	1.05	1.09	0.90	0.96	1.01	NaN	0.96	1.14
O43143	Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15	14	20.4	0	33.13	0.99	0.70	0.64	0.97	1.26	0.95	0.78	0.61	0.94
O43172	U4/U6 small nuclear ribonucleoprotein Prp4	PRPF4	3	7.1	0	7.048	1.12	NaN	1.21	NaN	NaN	NaN	NaN	NaN	1.18
O43237	Cytoplasmic dynein 1 light intermediate chain 2	DYNC1LI2	6	30.1	0	24.86	1.50	1.15	0.67	0.73	NaN	NaN	0.71	0.44	0.80
O43242	26S proteasome non-ATPase regulatory subunit 3	PSMD3	13	28.1	0	259.4	1.16	1.27	1.14	1.00	1.03	1.07	0.95	1.01	0.95
O43264	Centromere/kinetochore protein zw10 homolog	ZW10	3	6.2	0	24.3	0.83	0.84	0.80	NaN	0.77	NaN	NaN	NaN	0.89
O43291	Kunitz-type protease inhibitor 2	SPINT2	2	9.5	0.001	2.599	1.08	1.31	1.54	NaN	NaN	NaN	NaN	NaN	1.08
O43294	Transforming growth factor beta-1-induced transcript 1 protein	TGFB1I1	2	5.4	0	10.06	NaN	1.32	0.88	NaN	NaN	1.00	NaN	NaN	0.97
O43390	Heterogeneous nuclear ribonucleoprotein R	HNRNPR	17	43.4	0	58.51	0.79	0.82	0.92	0.76	0.84	0.91	1.05	1.10	0.87
O43399	Tumor protein D54	TPD52L2	12	68.9	0	323.3	1.18	1.06	1.11	1.09	1.37	1.02	0.98	1.04	0.97
O43447	Peptidyl-prolyl cis-trans isomerase H;Peptidyl-prolyl cis-trans isomerase	PPIH	4	38.4	0	5.263	0.80	NaN	NaN	NaN	0.80	0.90	NaN	NaN	NaN
O43493	Trans-Golgi network integral membrane protein 2	TGOLN2	4	14	0	119.3	1.53	1.85	1.31	NaN	1.50	1.30	0.63	NaN	1.21
O43592	Exportin-T	XPOT	5	7.8	0	9.218	0.89	0.78	0.88	NaN	1.10	1.08	NaN	NaN	NaN
O43615	Mitochondrial import inner membrane translocase subunit TIM44	TIMM44	6	15.3	0	15.14	0.95	1.09	1.29	0.96	NaN	1.07	0.90	1.13	1.04
O43684	Mitotic checkpoint protein BUB3	BUB3	8	35.4	0	27.91	1.05	0.95	1.03	0.73	1.04	0.96	0.81	1.04	1.04
O43707	Alpha-actinin-4	ACTN4	45	74.2	0	323.3	1.05	1.04	1.02	1.05	0.99	1.00	1.01	1.02	1.03
O43719	HIV Tat-specific factor 1	HTATSF1	2	3	0.003	1.822	1.07	1.61	NaN	NaN	NaN	1.12	NaN	NaN	NaN
O43765	Small glutamine-rich tetratricopeptide repeat-containing protein alpha	SGTA	8	29.4	0	77.26	1.19	1.22	1.32	0.98	1.23	1.13	1.18	0.80	1.23
O43776	Asparagine--tRNA ligase, cytoplasmic	NARS	8	19.5	0	13.35	0.72	0.75	0.72	1.79	0.71	1.04	NaN	NaN	1.40
O43852	Calumenin	CALU	20	72.4	0	323.3	1.16	1.09	1.19	1.17	1.09	1.11	1.17	1.17	0.97
O60361	Putative nucleoside diphosphate kinase	NME2P1	1	66.4	0.001	2.415	1.32	1.36	1.41	1.40	1.22	1.26	1.61	1.49	1.57
O60488	Long-chain-fatty-acid--CoA ligase 4	ACSL4	11	29.3	0	55.16	0.85	0.89	0.61	1.24	0.75	0.63	1.24	1.14	1.08
O60493	Sorting nexin-3	SNX3	9	67.3	0	31.17	1.56	1.38	1.52	1.27	1.57	1.36	1.13	1.13	1.25
O60502	Protein O-GlcNAcase	MGEA5	2	3.8	0	3.574	NaN	NaN	0.77	NaN	0.64	0.58	NaN	NaN	NaN
O60506	Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	5	47.8	0	323.3	0.86	0.82	0.84	0.86	0.91	0.95	0.75	0.81	0.90

O60568	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3	PLOD3	10	18.8	0	29.07	1.19	1.44	1.19	NaN	0.97	1.07	NaN	1.06	1.26
O60664	Perilipin-3	PLIN3	21	66.4	0	323.3	0.96	0.89	0.94	1.00	0.98	0.91	1.05	1.10	1.04
O60701	UDP-glucose 6-dehydrogenase	UGDH	7	19.8	0	11.05	1.22	1.21	1.12	1.56	1.33	1.42	NaN	1.00	NaN
O60749	Sorting nexin-2	SNX2	4	13.9	0	6.876	NaN	0.96	NaN	NaN	NaN	0.71	0.87	1.06	NaN
O60763	General vesicular transport factor p115	USO1	14	21.3	0	323.3	1.07	1.02	1.18	0.98	0.93	0.88	NaN	1.30	1.11
U3KQK0	Histone H2B;Histone H2B type 1-L;Histone H2B type 1-M;Histone H2B type 1-N;Histone H2B type 1-H;Histone H2B type 2-F;Histone H2B type 1-C/E/F/G/I;Histone H2B type 1-D;Histone H2B type 1-K;Histone H2B type F-S;Histone H2B type	HIST1H2BI	2	42.8	0	11.52	0.47	0.43	0.44	0.46	0.46	0.45	0.49	0.33	0.33
O60869	Endothelial differentiation-related factor 1	EDF1	6	43.2	0	37.4	0.99	1.04	0.92	0.97	0.90	1.02	0.96	0.98	0.81
O60884	DnaJ homolog subfamily A member 2	DNAJA2	6	24.5	0	28.64	1.31	1.06	1.40	NaN	0.91	1.10	NaN	NaN	0.83
O60888	Protein CutA	CUTA	4	40.8	0	92.14	0.90	1.03	1.07	0.89	0.86	0.94	0.91	1.00	0.86
O75083	WD repeat-containing protein 1	WDR1	33	67	0	323.3	0.85	0.82	0.80	0.86	0.86	0.82	1.08	0.94	0.99
O75131	Copine-3	CPNE3	11	26.1	0	79.9	0.84	0.82	0.83	0.73	0.86	0.92	0.73	1.22	1.10
O75223	Gamma-glutamylcyclotransferase	GGCT	4	31.9	0	86.19	0.69	0.89	1.37	0.60	NaN	0.77	1.35	0.98	0.83
O75340	Programmed cell death protein 6	PDCD6	5	39.3	0	61.98	0.71	0.78	0.85	0.77	0.83	0.90	NaN	NaN	0.98
O75348	V-type proton ATPase subunit G	ATP6V1G1	2	21.2	0	4.913	1.71	1.52	NaN	NaN	1.22	NaN	NaN	NaN	1.74
O75351	Vacuolar protein sorting-associated protein 4B	VPS4B	2	9.9	5E-04	2.856	1.16	1.07	1.05	NaN	NaN	1.00	NaN	NaN	0.93
O75367	Core histone macro-H2A.1;Histone H2A	H2AFY	11	41.9	0	195.8	1.21	1.11	1.11	1.03	1.03	1.21	1.11	1.17	1.26
O75368	SH3 domain-binding glutamic acid-rich-like protein	SH3BGRL	4	51.8	0	12.22	1.04	1.06	1.12	1.06	NaN	1.06	1.12	1.09	1.25
O75369	Filamin-B	FLNB	129	73.6	0	323.3	1.12	1.09	1.10	1.03	1.01	1.01	1.11	1.08	1.09
O75396	Vesicle-trafficking protein	SEC22B	8	42.3	0	89.19	0.99	1.05	1.06	1.04	1.03	1.07	0.97	1.01	0.95
O75436	Vacuolar protein sorting-associated protein 26A	VPS26A	10	38.5	0	64.05	0.92	1.19	1.27	0.93	0.77	1.15	NaN	NaN	0.69
O75475	PC4 and SFRS1-interacting protein	PSIP1	3	10.8	0	6.28	0.60	0.47	NaN	NaN	NaN	NaN	NaN	NaN	0.75
O75477	Erlin-1	ERLIN1	3	14.7	0	75.84	0.94	1.02	1.05	0.98	1.05	1.03	0.74	0.80	0.78
Q5JRI1	Serine/arginine-rich splicing factor 10	SRSF10	3	22.7	0	15.21	NaN	NaN	0.71	NaN	0.67	0.84	NaN	NaN	NaN
O75531	Barrier-to-autointegration factor;Barrier-to-autointegration factor, N-terminally processed	BANF1	8	67.4	0	128	1.21	1.26	1.23	1.11	1.15	1.18	1.26	1.26	1.31
O75533	Splicing factor 3B subunit 1	SF3B1	27	30.9	0	249.8	0.95	0.94	0.91	0.98	0.97	0.97	0.93	0.98	0.91
O75534	Cold shock domain-containing protein E1	CSDE1	9	14	0	8.572	1.50	1.32	1.17	0.59	1.05	1.33	0.86	0.93	1.06
O75607	Nucleoplasmin-3	NPM3	2	20.8	0	31.32	0.90	NaN	1.20	NaN	NaN	NaN	NaN	NaN	NaN

O75643	U5 small nuclear ribonucleoprotein 200 kDa	SNRNP20(	18	10.9	0	38.16	0.75	0.97	1.00	NaN	0.94	1.11	1.29	1.18	1.10
O75663	TIP41-like protein	TIPRL	5	28.3	0	6.936	1.36	1.42	1.26	NaN	NaN	1.02	1.27	NaN	1.66
O75695	Protein XRP2	RP2	3	8.3	0.008	1.547	1.28	0.90	0.82	0.98	0.65	NaN	NaN	0.96	1.00
O75822	Eukaryotic translation initiation factor 3 subunit J	EIF3J	5	20.5	0	5.276	1.51	NaN	NaN	1.06	0.76	NaN	1.01	0.88	NaN
O75844	CAAX prenyl protease 1 homolog	ZMPSTE24	5	13.9	0	18.89	1.10	1.62	1.90	1.05	1.01	NaN	0.84	1.03	1.06
O75874	Isocitrate dehydrogenase [NADP] cytoplasmic	IDH1	14	35	0	27.31	0.67	0.65	0.80	0.66	0.74	0.69	0.71	0.69	0.74
O75915	PRA1 family protein 3	ARL6IP5	3	20.7	0	26.66	0.72	0.96	0.93	0.87	0.78	1.02	0.83	0.66	0.81
O75934	Pre-mRNA-splicing factor SPF27	BCAS2	3	29.8	0	9.632	1.00	0.76	NaN	NaN	NaN	NaN	NaN	NaN	NaN
O75937	DnaJ homolog subfamily C member 8	DNAJC8	5	32	0	32.58	0.91	0.85	1.23	0.76	NaN	0.81	NaN	NaN	1.03
O75947	ATP synthase subunit d, mitochondrial	ATP5H	6	51.6	0	23.52	0.97	1.00	1.03	1.09	1.05	1.17	1.17	1.25	0.96
O75976	Carboxypeptidase D	CPD	12	11.4	0	131.6	1.21	1.26	0.98	1.00	1.35	1.18	0.95	1.29	0.67
O76003	Glutaredoxin-3	GLRX3	10	41.5	0	65.54	1.02	1.03	1.07	0.96	0.79	0.86	0.92	1.15	0.85
O76021	Ribosomal L1 domain-containing protein 1	RSL1D1	7	16.1	0	14.99	NaN	0.75	1.18	NaN	1.01	1.41	NaN	NaN	NaN
O76094	Signal recognition particle subunit SRP72	SRP72	9	24.1	0	19.14	0.83	1.05	NaN	0.84	1.20	NaN	NaN	NaN	0.58
O94760	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1	DDAH1	11	50.9	0	44.43	1.17	0.96	1.12	1.23	0.98	1.07	1.28	1.30	1.27
O94804	Serine/threonine-protein kinase	STK10	5	6.3	0	14.27	NaN	NaN	NaN	1.09	1.06	NaN	0.97	NaN	NaN
O94826	Mitochondrial import receptor subunit TOM70	TOMM70A	12	29.1	0	113.1	1.08	1.16	1.05	1.27	1.18	1.26	1.13	1.00	0.80
O94919	Endonuclease domain-containing 1 protein	ENDOD1	2	6.8	0	4.182	0.97	1.22	NaN	NaN	NaN	NaN	1.60	NaN	NaN
O94925	Glutaminase kidney isoform, mitochondrial	GLS	11	24.7	0	82.57	1.19	1.94	1.49	1.33	1.09	1.20	1.26	1.32	1.22
O94973	AP-2 complex subunit alpha-2	AP2A2	6	19.4	0	14.13	0.80	1.05	0.80	NaN	0.86	0.76	NaN	NaN	0.87
O95197	Reticulon-3	RTN3	1	1.1	0	6.785	NaN	1.13	0.95	0.79	0.81	1.00	0.91	0.83	NaN
O95202	LETM1 and EF-hand domain-containing protein 1,	LETM1	7	15.2	0	27.07	0.82	0.86	0.91	NaN	0.80	NaN	NaN	NaN	0.98
O95292	Vesicle-associated membrane protein-associated protein B/C	VAPB	7	38.3	0	12.01	1.49	0.87	1.57	NaN	1.38	NaN	NaN	0.71	1.83
O95336	6-phosphogluconolactonase	PGLS	12	67.4	0	42.15	1.06	1.04	1.19	1.10	1.30	1.00	1.04	1.06	NaN
O95340	Bifunctional 3-phosphoadenosine 5-phosphosulfate synthase 2;Sulfate adenylyltransferase;Adenylyl-sulfate kinase	PAPSS2	5	13.4	0	13.66	0.81	0.91	0.82	NaN	1.04	1.13	1.37	0.58	0.67
O95347	Structural maintenance of chromosomes protein 2	SMC2	14	17.5	0	22.98	0.73	NaN	0.73	0.83	0.97	0.94	0.81	NaN	0.81
O95372	Acyl-protein thioesterase 2	LYPLA2	3	29.9	0	42.73	0.78	0.91	NaN	NaN	NaN	1.29	NaN	NaN	0.71
O95373	Importin-7	IPO7	23	28.4	0	323.3	1.13	1.16	1.11	0.97	0.98	1.16	0.86	0.89	1.14
Q5H8X8	Urotensin-2	UTS2	1	5.8	0	8.813	0.98	1.03	1.04	0.98	0.90	0.89	1.08	1.11	1.02

O95433	Activator of 90 kDa heat shock protein ATPase homolog 1	AHSA1	9	37.6	0	52.89	1.19	1.39	1.02	NaN	1.13	1.09	NaN	1.09	0.91
O95456	Proteasome assembly chaperone 1	PSMG1	5	22.6	0	10.29	0.71	1.07	0.77	1.22	0.70	0.91	0.98	1.36	0.87
O95573	Long-chain-fatty-acid--CoA ligase 3	ACSL3	8	18.2	0	69.32	0.84	NaN	0.90	NaN	NaN	1.15	1.08	1.69	1.47
O95630	STAM-binding protein	STAMBP	3	8.5	0.007	1.652	0.91	NaN	1.05	NaN	NaN	1.03	NaN	NaN	0.76
O95747	Serine/threonine-protein kinase OSR1	OXSR1	10	23.3	0	117.9	1.16	1.06	1.14	1.05	1.08	1.12	1.41	1.03	1.12
O95777	U6 snRNA-associated Sm-like protein LSm8	LSM8	5	71.9	0	18.16	1.10	1.04	1.09	0.92	1.13	1.00	1.02	NaN	1.15
O95782	AP-2 complex subunit alpha-1	AP2A1	19	37.6	0	124.9	0.89	0.99	0.92	0.97	0.92	0.96	0.85	0.88	1.13
O95793	Double-stranded RNA-binding protein Staufen homolog 1	STAU1	7	16.6	0	33.45	1.20	1.43	1.15	1.10	0.85	1.21	1.14	NaN	0.96
O95810	Serum deprivation-response protein	SDPR	6	18.6	0	9.281	0.76	0.87	0.70	0.89	0.85	0.44	0.80	0.60	1.14
O95816	BAG family molecular chaperone regulator 2	BAG2	10	50.2	0	53.65	0.88	0.93	0.88	0.88	0.81	1.02	0.99	NaN	0.85
O95817	BAG family molecular chaperone regulator 3	BAG3	13	26.3	0	46.83	1.30	1.70	1.59	1.51	1.55	1.53	NaN	1.26	NaN
O95833	Chloride intracellular channel protein 3	CLIC3	3	18.2	0	4.488	0.90	0.84	0.72	NaN	NaN	0.46	1.44	1.47	1.50
O95864	Fatty acid desaturase 2	FADS2	3	7.4	0	3.182	1.04	NaN	1.27	NaN	NaN	NaN	NaN	NaN	NaN
O95865	N(G),N(G)-dimethylarginine dimethylaminohydrolase 2	DDAH2	3	17.5	0	14.37	NaN	1.02	1.32	0.90	NaN	NaN	1.20	0.97	1.15
O95881	Thioredoxin domain-containing protein 12	TXNDC12	3	22.7	0	3.612	1.02	1.02	1.01	NaN	NaN	1.05	NaN	NaN	1.04
O96008	Mitochondrial import receptor subunit TOM40 homolog	TOMM40	6	26	0	69.93	1.00	0.75	0.79	0.76	0.94	0.74	NaN	0.98	0.78
O96019	Actin-like protein 6A	ACTL6A	2	6.8	0	3.043	NaN	NaN	0.82	NaN	0.69	0.52	NaN	NaN	0.86
P00338	L-lactate dehydrogenase A chain	LDHA	30	81.6	0	323.3	0.94	0.96	0.92	1.03	1.03	0.97	1.11	1.07	1.06
P00367	Glutamate dehydrogenase 1, mitochondrial;Glutamate dehydrogenase 2, mitochondrial	GLUD1	20	43.4	0	244.1	0.97	0.93	1.03	0.86	1.02	0.93	0.84	0.86	1.00
P00387	NADH-cytochrome b5 reductase 3;NADH-cytochrome b5 reductase 3 membrane-bound form;NADH-cytochrome b5 reductase 3 soluble form	CYB5R3	10	52.2	0	189.4	1.04	1.09	0.97	0.91	0.99	1.04	0.85	0.98	1.07
P00390	Glutathione reductase, mitochondrial	GSR	2	4.8	0	3.402	0.93	0.81	0.92	1.18	1.10	1.05	0.89	0.78	0.82
P00403	Cytochrome c oxidase subunit 2	MT-CO2	4	24.7	0	58.59	1.07	1.02	0.95	1.18	1.08	1.08	0.96	0.93	0.98
P00441	Superoxide dismutase [Cu-Zn]	SOD1	8	77.9	0	323.3	1.32	1.26	1.27	1.14	1.12	1.14	1.07	1.03	1.07
P00491	Purine nucleoside phosphorylase	PNP	6	31.5	0	10.55	0.82	0.86	0.91	1.07	0.54	0.70	NaN	NaN	0.72
P00492	Hypoxanthine-guanine phosphoribosyltransferase	HPRT1	8	45	0	137.5	1.01	1.29	1.04	1.08	1.09	1.11	1.09	1.14	1.00

P00505	Aspartate aminotransferase, mitochondrial	GOT2	16	39.5	0	139	1.16	1.14	1.12	1.08	1.07	1.14	1.08	0.90	1.07
P00533	Epidermal growth factor receptor;Receptor protein-tyrosine kinase	EGFR	14	17.9	0	41.73	1.24	0.95	1.13	1.13	NaN	1.15	1.17	1.28	1.11
P00558	Phosphoglycerate kinase 1	PGK1	35	82.5	0	323.3	1.18	1.20	1.18	1.21	1.21	1.21	1.12	1.17	1.20
Q5T9B7	Adenylate kinase isoenzyme 1	AK1	5	31.9	0	10.95	0.86	1.07	0.67	0.90	NaN	0.66	1.00	0.74	0.74
P00846	ATP synthase subunit a	MT-ATP6	1	4.4	0.008	1.537	0.98	0.93	NaN	1.18	NaN	NaN	NaN	1.46	NaN
P01111	GTPase NRas;GTPase KRas;GTPase KRas, N-terminally processed;GTPase HRas;GTPase HRas, N-	NRAS	4	33.3	0.001	2.441	0.69	0.45	0.62	0.72	NaN	0.81	0.30	0.50	0.41
P02545	Prelamin-A/C;Lamin-A/C	LMNA	3	69.4	0	323.3	0.94	0.94	0.92	1.03	1.03	0.99	0.99	1.04	0.98
P02786	Transferrin receptor protein 1;Transferrin receptor protein 1, serum form	TFRC	30	44.2	0	323.3	1.27	1.30	1.31	1.30	1.40	1.50	1.12	1.08	1.25
P02795	Metallothionein-2;Metallothionein-	MT2A	2	67.2	0	151.4	1.91	1.94	1.80	1.58	1.58	1.52	1.08	1.22	1.30
P04040	Catalase	CAT	16	40.8	0	60.08	1.10	1.08	1.02	0.96	0.99	1.24	1.03	1.02	0.96
P04075	Fructose-bisphosphate aldolase A;Fructose-bisphosphate	ALDOA	27	84.1	0	323.3	1.03	1.06	1.05	1.07	1.10	1.05	1.11	1.09	1.09
P04080	Cystatin-B	CSTB	7	88.8	0	323.3	1.16	1.35	1.09	1.01	1.19	1.20	0.67	0.58	1.11
P04083	Annexin A1	ANXA1	25	71.1	0	323.3	0.94	0.95	0.92	0.99	0.99	0.99	0.86	0.86	0.86
P04179	Superoxide dismutase [Mn], mitochondrial	SOD2	6	30.6	0	31.37	0.99	0.75	0.90	0.82	1.08	1.13	0.58	1.00	0.66
P04181	Ornithine aminotransferase, mitochondrial;Ornithine aminotransferase, hepatic form;Ornithine aminotransferase, renal form	OAT	15	48.7	0	210.1	0.71	0.59	0.65	0.74	0.78	0.77	0.92	1.00	1.11
P04406	Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	27	80.9	0	323.3	0.93	0.90	0.92	0.98	0.99	0.96	0.95	0.95	0.93
P04792	Heat shock protein beta-1	HSPB1	11	78	0	323.3	0.86	0.82	0.86	0.82	0.82	0.84	1.00	0.90	0.89
P04843	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase	RPN1	23	44.8	0	263.3	1.10	0.97	1.06	0.97	0.98	1.08	1.05	1.00	0.98
P04844	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase	RPN2	13	31.2	0	204.6	0.98	0.96	0.97	1.16	1.11	1.06	1.20	1.17	0.99
P04899	Guanine nucleotide-binding protein G(i) subunit alpha-2;Guanine nucleotide-binding protein G(i) subunit alpha-1	GNAI2	5	34.9	0	43.46	0.72	0.76	0.82	0.77	0.89	0.96	0.87	0.77	0.96
P05023	Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	32	36	0	323.3	0.94	0.99	1.01	1.26	1.31	1.30	0.77	0.75	0.86
P05026	Sodium/potassium-transporting ATPase subunit beta-1	ATP1B1	10	36.3	0	26.75	1.04	0.78	0.83	1.16	1.14	1.63	1.41	0.85	NaN

P05091	Aldehyde dehydrogenase, mitochondrial	ALDH2	8	23	0	33.59	1.21	NaN	NaN	NaN	0.55	0.95	NaN	NaN	0.72
P05114	Non-histone chromosomal protein HMG-14	HMGN1	7	50	0	195.2	0.69	0.76	0.73	0.52	0.80	0.71	0.77	0.60	0.86
P05121	Plasminogen activator inhibitor 1	SERPINE1	12	40	0	241.6	13.08	8.99	10.74	NaN	NaN	1.76	NaN	16.26	13.89
P05141	ADP/ATP translocase 2;ADP/ATP translocase 2, N-terminally processed	SLC25A5	5	44.6	0	39.26	1.05	1.12	1.11	0.96	1.11	1.07	0.98	0.99	1.05
P05198	Eukaryotic translation initiation factor 2 subunit 1	EIF2S1	16	54.6	0	323.3	0.98	0.82	0.94	1.07	0.92	1.02	0.80	0.90	0.75
P05204	Non-histone chromosomal protein HMG-17	HMGN2	4	45.6	0	215.3	0.76	0.76	NaN	0.95	0.61	0.49	NaN	0.66	0.68
P05386	60S acidic ribosomal protein P1	RPLP1	2	51.8	0	234.9	0.94	1.01	0.98	0.88	1.03	0.89	0.99	0.94	1.01
P05387	60S acidic ribosomal protein P2	RPLP2	8	78.3	0	323.3	0.98	1.11	1.02	0.94	0.98	0.91	0.99	0.96	0.98
P05388	60S acidic ribosomal protein P0;60S acidic ribosomal protein P0-like	RPLP0	18	65.6	0	323.3	0.86	0.85	0.87	0.85	0.81	0.85	0.88	0.82	0.79
P05455	Lupus La protein	SSB	26	57.4	0	154.1	0.82	0.87	0.89	0.86	0.94	0.86	0.92	0.93	0.82
P05556	Integrin beta-1	ITGB1	25	36.8	0	323.3	1.37	1.33	1.31	1.16	1.17	1.21	1.28	1.24	1.39
P05783	Keratin, type I cytoskeletal 18	KRT18	33	76.5	0	323.3	1.21	1.21	1.02	0.97	0.93	0.96	1.48	1.26	1.16
P05976	Myosin light chain 1/3, skeletal muscle isoform;Myosin light chain 3	MYL1	2	8.2	0	190.4	0.93	0.81	0.82	1.05	1.04	0.99	0.67	0.63	0.76
P06493	Cyclin-dependent kinase 1	CDK1	14	62	0	45.21	0.95	1.04	0.85	1.05	1.12	0.98	1.03	0.95	0.84
P06576	ATP synthase subunit beta, mitochondrial;ATP synthase subunit beta	ATP5B	21	57.5	0	323.3	0.98	1.02	1.02	1.07	1.06	1.03	0.84	0.78	0.87
R4GN98	Protein S100;Protein S100-A6	S100A6	7	60	0	67.15	0.98	0.96	0.87	0.98	0.94	0.98	0.89	0.84	0.74
P06733	Alpha-enolase	ENO1	33	79.5	0	323.3	0.96	0.95	0.97	1.03	0.99	1.03	0.97	0.91	0.95
P06737	Glycogen phosphorylase, liver form;Alpha-1,4 glucan phosphorylase	PYGL	25	44.2	0	253.5	0.72	0.89	0.93	0.94	0.68	0.99	0.73	1.01	1.04
P06748	Nucleophosmin	NPM1	18	56.1	0	323.3	0.94	0.96	0.92	0.96	1.01	0.98	0.91	0.91	0.85
Q16778	Histone H2B type 2-E;Histone H2B type 1-B;Histone H2B type 1-O;Histone H2B type 1-J	HIST2H2BI	0	56.3	0	323.3	0.79	0.78	0.77	0.79	0.77	0.80	0.66	0.74	0.67
P07108	Acyl-CoA-binding protein	DBI	7	73.6	0	323.3	0.83	0.76	0.85	0.96	1.07	0.88	0.87	0.78	0.90
P07195	L-lactate dehydrogenase B chain;L-lactate dehydrogenase	LDHB	16	52.4	0	323.3	0.96	0.95	0.94	0.92	0.96	0.98	0.94	0.88	0.92
P07237	Protein disulfide-isomerase	P4HB	39	78	0	323.3	1.07	1.08	1.09	1.06	1.08	1.11	1.04	1.03	1.05
P07355	Annexin A2;Annexin;Putative annexin A2-like protein	ANXA2	16	79.9	0	323.3	0.82	0.82	0.81	0.86	0.83	0.84	0.98	0.94	0.91
P07384	Calpain-1 catalytic subunit	CAPN1	12	20.7	0	37.55	0.72	0.74	0.81	0.85	0.88	0.73	1.02	1.25	0.81
Q5JP53	Tubulin beta chain	TUBB	5	66	0	323.3	0.41	0.40	0.41	0.49	0.47	0.47	0.85	0.81	0.83
P07602	Prosaposin;Saposin-A;Saposin-B-Val;Saposin-B;Saposin-C;Saposin-D	PSAP	13	26.1	0	56.57	1.55	1.47	1.52	1.55	1.26	1.46	1.36	1.63	1.37

Q5URX0	Beta-hexosaminidase subunit beta;Beta-hexosaminidase subunit beta chain B;Beta-hexosaminidase subunit beta	HEXB	4	15.7	0	6.247	1.01	NaN	NaN	1.20	1.18	1.27	NaN	NaN	NaN
P07737	Profilin-1	PFN1	12	89.3	0	323.3	1.10	1.15	1.15	1.16	1.11	1.08	1.10	1.01	0.97
P07741	Adenine phosphoribosyltransferase	APRT	9	58.9	0	43.54	1.49	1.30	2.18	NaN	1.60	0.96	1.25	1.10	1.21
P07814	Bifunctional glutamate/proline--tRNA ligase;Glutamate--tRNA ligase;Proline--tRNA ligase	EPRS	34	32.8	0	211.2	0.96	0.78	0.97	0.89	0.84	0.89	0.74	0.80	0.92
P07858	Cathepsin B;Cathepsin B light chain;Cathepsin B heavy chain	CTSB	6	24.2	0	36.75	1.44	0.98	1.33	1.32	1.23	1.60	1.36	1.24	1.31
P07900	Heat shock protein HSP 90-alpha	HSP90AA1	33	61.3	0	323.3	1.14	1.17	1.15	1.17	1.22	1.20	0.88	0.83	0.84
P07919	Cytochrome b-c1 complex subunit 6, mitochondrial;Cytochrome b-c1	UQCRH	2	28.6	0	7.431	1.78	1.69	1.10	NaN	1.11	1.20	1.73	NaN	NaN
P07954	Fumarate hydratase,	FH	15	48.4	0	59.62	0.98	1.06	NaN	NaN	0.90	1.23	1.36	0.95	0.60
P08133	Annexin A6;Annexin	ANXA6	15	63	0	323.3	0.88	0.84	0.91	0.89	0.87	0.92	1.12	1.01	0.94
Q5JR08	Rho-related GTP-binding protein RhoC	RHOC	2	45.2	0	3.774	1.13	1.05	1.09	NaN	1.06	1.09	NaN	NaN	1.09
P08238	Heat shock protein HSP 90-beta	HSP90AB1	28	64.4	0	323.3	1.16	1.15	1.16	1.08	1.08	1.11	0.92	0.89	0.94
P08240	Signal recognition particle receptor subunit alpha	SRPR	5	12.1	0	18.94	0.68	0.77	0.68	NaN	NaN	0.69	NaN	NaN	NaN
P08243	Asparagine synthetase [glutamine-hydrolyzing]	ASNS	5	14.1	0	5.348	NaN	0.81	NaN	0.49	0.69	0.85	NaN	0.76	0.82
P08559	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	11	29	0	38.17	0.67	0.72	0.81	1.03	0.82	0.87	0.98	0.96	1.16
P08574	Cytochrome c1, heme protein, mitochondrial	CYC1	2	8.6	0	3.586	1.05	0.94	1.10	1.06	1.12	1.18	NaN	1.16	1.21
P08579	U2 small nuclear ribonucleoprotein B	SNRPB2	1	11.6	0	70.84	1.00	1.02	1.33	NaN	1.43	1.16	NaN	NaN	1.15
P08582	Melanotransferrin	MFI2	8	15.3	0	29.24	0.91	1.07	0.90	NaN	NaN	1.07	NaN	1.03	1.19
P08621	U1 small nuclear ribonucleoprotein 70 kDa	SNRNP70	12	30.7	0	233.4	0.90	1.03	0.89	0.91	0.85	1.06	0.76	0.64	0.81
P08670	Vimentin	VIM	47	88.8	0	323.3	1.02	1.00	1.00	0.94	0.96	0.95	1.14	1.10	1.10
P08754	Guanine nucleotide-binding protein G(k) subunit alpha	GNAI3	2	25.7	0	31.42	0.51	0.67	0.56	0.58	NaN	0.73	0.81	NaN	0.78
P08758	Annexin A5;Annexin	ANXA5	27	80.6	0	323.3	1.07	1.08	1.13	1.00	1.06	1.02	0.96	0.97	0.95
P09012	U1 small nuclear ribonucleoprotein A	SNRPA	5	21.3	0	9.592	0.74	0.75	0.81	0.77	0.74	0.73	0.69	0.81	0.73
P09104	Gamma-enolase;Enolase	ENO2	13	63.1	0	323.3	1.11	1.09	1.20	1.15	1.27	1.15	1.11	1.20	1.17
P09211	Glutathione S-transferase P	GSTP1	12	69.5	0	323.3	0.99	0.90	1.01	1.00	1.14	0.96	1.05	1.01	1.04
P09382	Galectin-1	LGALS1	9	77.8	0	323.3	1.10	1.03	1.07	1.06	1.09	1.07	1.18	1.14	1.12
Q5T7C4	High mobility group protein B1;Putative high mobility group protein B1-like 1	HMGB1	9	48.7	0	120.7	0.88	0.86	0.88	0.95	0.94	0.98	0.92	0.84	0.81

P09496	Clathrin light chain A	CLTA	7	19.4	0	9.796	1.27	1.01	1.12	0.93	1.08	0.95	1.02	1.05	0.98
P09497	Clathrin light chain B	CLTB	8	24.9	0	8.794	0.88	1.31	0.85	1.10	1.04	1.68	0.82	0.92	1.46
P09525	Annexin A4;Annexin	ANXA4	12	40.1	0	323.3	0.83	0.90	0.99	1.56	1.09	1.07	0.90	0.98	0.94
P09543	2,3-cyclic-nucleotide 3-phosphodiesterase	CNP	5	20	0	152.2	0.83	0.98	1.33	1.18	0.96	1.04	1.16	NaN	0.64
P09622	Dihydrolipoyl dehydrogenase, mitochondrial;Dihydrolipoyl dehydrogenase	DLD	14	35.8	0	238.7	1.02	1.01	1.05	0.97	0.93	0.97	1.01	1.07	1.02
P09874	Poly [ADP-ribose] polymerase 1	PARP1	26	32.7	0	86.42	0.78	0.75	0.77	0.81	0.97	0.82	0.90	0.84	1.05
P09960	Leukotriene A-4 hydrolase	LTA4H	16	34.7	0	52.5	0.65	0.74	0.77	1.05	0.89	1.04	1.49	0.93	0.71
P09972	Fructose-bisphosphate aldolase C;Fructose-bisphosphate	ALDOC	4	28.3	0	237.3	1.23	1.14	1.06	1.25	1.14	1.20	1.17	1.23	1.15
Q71UI9	Histone H2A.V;Histone H2A.Z;Histone H2A	H2AFV	2	31.2	0	13.49	NaN	0.83	NaN	0.64	NaN	NaN	0.54	NaN	1.10
P0DN76	Splicing factor U2AF 35 kDa subunit	U2AF1	7	32.9	0	42.96	1.46	1.23	1.02	1.04	NaN	0.79	1.01	1.03	0.88
P10155	60 kDa SS-A/Ro	TROVE2	2	4.1	0	4.793	0.69	0.86	0.86	NaN	NaN	0.83	NaN	NaN	0.72
P10301	Ras-related protein R-Ras	RRAS	1	19.7	0.008	1.476	1.06	0.98	1.08	0.86	NaN	0.53	NaN	0.73	1.12
P10515	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial;Acetyltransferase component of pyruvate	DLAT	12	25.7	0	54.78	1.00	0.89	0.88	0.97	0.91	0.93	0.88	0.73	0.89
P10599	Thioredoxin	TXN	9	88.6	0	135.8	1.22	1.18	1.16	1.17	1.17	1.16	1.11	0.95	0.97
P10606	Cytochrome c oxidase subunit 5B, mitochondrial	COX5B	6	31	0	7.049	1.06	0.90	1.14	0.93	1.19	1.15	1.26	1.14	1.17
X6R5C5	Carboxypeptidase;Lysosomal protective protein;Lysosomal protective protein 32 kDa chain;Lysosomal protective protein 20 kDa chain	CTSA	6	16.8	0	25.66	1.44	1.34	1.44	1.17	1.30	1.21	2.04	1.51	1.54
P10644	cAMP-dependent protein kinase type I-alpha regulatory subunit;cAMP-dependent protein kinase type I-alpha regulatory subunit, N-terminally processed	PRKAR1A	6	19.2	0	41.88	0.86	1.14	1.30	0.79	1.45	0.92	NaN	0.92	1.27
P10768	S-formylglutathione hydrolase	ESD	8	52.5	0	97.23	NaN	0.95	1.00	0.89	0.86	0.85	0.78	0.76	0.67
P10809	60 kDa heat shock protein, mitochondrial	HSPD1	38	72.3	0	323.3	1.19	1.19	1.18	1.19	1.21	1.19	1.00	1.00	1.01
P11021	78 kDa glucose-regulated protein	HSPA5	39	57.3	0	323.3	0.93	1.00	1.04	0.91	0.94	0.98	0.98	1.00	1.01
P11047	Laminin subunit gamma-1	LAMC1	1	1.4	0	3.372	8.86	1.98	1.49	NaN	NaN	NaN	NaN	NaN	1.39
P11142	Heat shock cognate 71 kDa protein	HSPA8	27	72.3	0	323.3	1.30	1.31	1.31	1.27	1.26	1.25	0.93	0.91	0.93
P11166	Solute carrier family 2, facilitated glucose transporter member 1	SLC2A1	8	15.2	0	299.8	1.15	1.22	1.30	1.00	1.06	1.01	1.21	0.92	1.26

P11177	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	11	42.9	0	109.2	1.08	0.52	0.95	1.00	1.13	1.06	1.05	1.14	1.27
P11216	Glycogen phosphorylase, brain form	PYGB	27	48.2	0	166.4	0.89	0.79	0.79	0.87	0.77	0.89	0.95	0.85	0.94
P11233	Ras-related protein Ral-A	RALA	2	21.8	0	43.17	0.89	1.08	0.83	1.19	1.05	0.93	1.24	1.17	0.72
P11279	Lysosome-associated membrane glycoprotein 1	LAMP1	3	8.6	0	98.51	1.07	1.10	1.05	1.11	0.91	1.32	0.81	0.98	0.96
P11388	DNA topoisomerase 2-alpha	TOP2A	3	5.3	0	6.997	NaN	NaN	NaN	NaN	1.87	1.80	NaN	NaN	NaN
P11413	Glucose-6-phosphate 1-dehydrogenase	G6PD	28	64.7	0	323.3	0.94	0.89	1.01	1.08	1.07	1.10	0.83	0.92	0.96
P11498	Pyruvate carboxylase, mitochondrial	PC	22	26.1	0	72.31	0.90	0.85	0.81	0.88	1.00	0.90	0.84	0.99	0.94
P11717	Cation-independent mannose-6-phosphate receptor	IGF2R	7	3.2	0	5.257	1.39	0.60	0.89	0.96	NaN	NaN	NaN	NaN	NaN
P11766	Alcohol dehydrogenase class-3	ADH5	10	40.1	0	57.47	0.85	NaN	0.73	0.86	0.47	0.84	0.85	1.05	0.97
P11908	Ribose-phosphate pyrophosphokinase 2	PRPS2	1	27.7	0	5.664	0.74	0.76	0.50	NaN	NaN	NaN	NaN	NaN	0.76
P11940	Polyadenylate-binding protein 1;Polyadenylate-binding protein	PABPC1	20	53.6	0	323.3	0.91	1.00	0.86	1.09	1.05	1.07	0.98	0.87	0.73
P12004	Proliferating cell nuclear antigen	PCNA	12	56.3	0	323.3	1.00	0.99	0.98	1.06	0.97	1.03	0.97	0.89	0.92
P12235	ADP/ATP translocase 1	SLC25A4	2	47.7	0.004	1.802	0.97	NaN	0.74	NaN	NaN	0.66	NaN	NaN	NaN
P12236	ADP/ATP translocase 3;ADP/ATP translocase 3, N-terminally processed	SLC25A6	6	66.8	0	265.3	1.04	1.02	1.03	1.06	1.00	1.08	0.95	0.93	0.95
P12268	Inosine-5-monophosphate dehydrogenase 2	IMPDH2	24	51.6	0	229.5	0.92	0.99	0.95	0.98	0.99	0.93	0.88	0.84	0.94
P12270	Nucleoprotein TPR	TPR	20	11.2	0	53.14	0.94	1.24	0.99	0.74	0.88	1.69	NaN	1.35	0.89
P12277	Creatine kinase B-type	CKB	4	12.3	0	26.41	2.08	2.01	0.94	NaN	1.00	NaN	NaN	NaN	NaN
P12429	Annexin A3;Annexin	ANXA3	18	59.1	0	309.1	0.99	0.86	0.87	0.99	0.93	0.99	1.02	1.01	0.94
P12814	Alpha-actinin-1	ACTN1	41	73.2	0	323.3	1.19	1.16	1.17	1.10	1.04	1.08	1.12	1.22	1.18
P12955	Xaa-Pro dipeptidase	PEPD	9	21.7	0	39.74	NaN	1.10	NaN	NaN	NaN	1.16	0.86	1.24	NaN
P12956	X-ray repair cross-complementing protein 6	XRCC6	27	47.3	0	311.8	0.89	0.88	0.90	0.83	0.85	0.98	0.83	0.89	0.86
P13010	X-ray repair cross-complementing protein 5	XRCC5	28	45.1	0	323.3	0.98	0.92	0.92	0.90	0.97	0.99	0.97	0.89	0.89
P13073	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial	COX4I1	6	31.4	0	10.17	1.01	0.97	0.93	1.19	NaN	0.98	0.98	0.75	0.80
P13473	Lysosome-associated membrane glycoprotein 2	LAMP2	3	7.3	0	34.14	1.00	0.98	1.22	NaN	0.74	1.11	NaN	NaN	1.00
P13489	Ribonuclease inhibitor	RNH1	22	64.9	0	323.3	0.91	0.86	0.92	0.92	0.91	0.93	1.14	1.14	1.14
P13639	Elongation factor 2	EEF2	50	69.9	0	323.3	0.79	0.78	0.82	0.88	0.84	0.85	0.84	0.89	0.90
P13667	Protein disulfide-isomerase A4	PDIA4	37	53.2	0	323.3	0.84	0.88	0.83	0.96	0.95	0.84	0.85	0.96	0.91
P13674	Prolyl 4-hydroxylase subunit alpha-1	P4HA1	13	34.1	0	122.7	1.67	1.21	1.56	1.47	1.12	1.51	0.93	1.60	1.50
P13693	Translationally-controlled tumor protein	TPT1	9	39	0	114.2	1.13	1.34	1.17	1.32	1.22	1.30	0.94	0.95	1.01

P13726	Tissue factor	F3	9	37.3	0	323.3	1.14	1.18	0.97	1.18	1.19	1.20	1.08	1.04	0.99
P13797	Plastin-3	PLS3	32	59.5	0	231.7	1.00	0.99	1.03	0.98	0.92	0.90	0.98	1.00	0.97
P13804	Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	10	43.2	0	24.17	1.07	NaN	1.28	0.82	1.11	1.31	1.13	NaN	2.25
P13807	Glycogen [starch] synthase, muscle	GYS1	1	3.3	0	6.875	0.89	0.86	NaN	NaN	NaN	1.14	NaN	NaN	1.28
P13861	cAMP-dependent protein kinase type II-alpha regulatory subunit	PRKAR2A	8	24.5	0	41.73	0.90	1.27	0.93	1.20	0.90	0.84	1.53	NaN	1.40
P14174	Macrophage migration inhibitory factor	MIF	2	26.1	0	46.08	1.34	1.27	1.29	1.19	1.11	1.34	1.34	1.16	1.18
P14324	Farnesyl pyrophosphate	FDPS	6	17.4	0	37.34	0.70	0.72	0.76	0.90	0.79	0.83	1.22	0.86	0.86
V9GYG2	Alcohol dehydrogenase	AKR1A1	2	18.5	0	4.092	0.64	0.66	NaN	0.83	0.78	0.87	NaN	NaN	NaN
P14618	Pyruvate kinase PKM;Pyruvate kinase	PKM	5	83.8	0	323.3	0.90	0.92	0.89	0.99	0.98	1.00	0.99	0.94	0.89
P14625	Endoplasmin	HSP90B1	53	58.8	0	323.3	1.05	1.03	1.04	1.08	1.10	1.10	0.86	1.00	0.99
P14854	Cytochrome c oxidase subunit	COX6B1	4	58.1	0	65.81	0.97	1.01	1.08	1.14	1.12	1.02	1.57	1.70	1.08
P14866	Heterogeneous nuclear ribonucleoprotein L	HNRNPL	8	49.9	0	323.3	0.94	0.91	1.03	1.06	0.97	0.99	0.82	1.00	0.95
P14868	Aspartate--tRNA ligase, cytoplasmic	DARS	27	57.5	0	311	1.03	1.09	0.99	1.14	0.99	1.00	1.05	0.98	0.99
P15121	Aldose reductase	AKR1B1	15	59.5	0	123.5	0.86	0.98	0.94	0.92	0.90	1.03	0.93	0.88	0.77
P15170	Eukaryotic peptide chain release factor GTP-binding subunit ERF3A;Eukaryotic peptide chain release factor GTP-binding subunit ERF3B	GSPT1	11	27.5	0	22.46	1.07	0.99	0.95	0.90	1.24	1.36	NaN	0.87	1.16
P15374	Ubiquitin carboxyl-terminal hydrolase isozyme L3;Ubiquitin carboxyl-terminal hydrolase	UCHL3	8	60.4	0	99.72	0.91	1.08	0.95	0.98	0.99	0.91	0.58	1.17	0.88
P15531	Nucleoside diphosphate kinase A	NME1	1	70.4	0	13.27	1.11	1.00	0.96	0.99	0.94	0.95	1.05	1.01	1.07
P15586	N-acetylglucosamine-6-sulfatase	GNS	6	13.4	0	5.204	0.84	0.69	NaN	0.66	NaN	0.77	NaN	NaN	0.69
P15880	40S ribosomal protein S2	RPS2	16	54.3	0	130.7	0.85	0.81	0.76	0.83	0.79	0.82	0.87	0.84	0.84
P15927	Replication protein A 32 kDa subunit	RPA2	5	39.6	0	65.78	0.78	0.74	0.77	NaN	1.01	0.83	1.10	NaN	0.49
P16104	Histone H2AX;Histone H2A type 1-A	H2AFX	2	38.5	0	243	0.88	0.83	0.95	0.83	0.82	0.88	0.90	0.86	0.94
P16144	Integrin beta-4	ITGB4	12	8.8	0	30.47	NaN	0.56	0.58	NaN	0.94	0.92	NaN	0.91	0.83
P16152	Carbonyl reductase [NADPH] 1	CBR1	11	59.2	0	290.4	0.93	0.92	0.94	0.95	0.89	0.98	1.91	1.13	0.96
P16403	Histone H1.2	HIST1H1C	1	26.8	0	14.56	1.69	1.19	1.28	1.38	1.50	1.44	1.28	1.27	1.39
P16615	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	27	32	0	177.8	0.86	0.83	0.91	1.10	0.95	0.90	1.07	1.07	0.92
P16930	Fumarylacetoacetase	FAH	4	14.1	0	8.331	NaN	0.82	0.50	NaN	0.70	1.01	0.97	NaN	NaN
P16949	Stathmin	STMN1	11	63.1	0	155.5	0.81	0.78	0.78	0.83	0.84	0.83	0.91	0.90	0.91
P17066	Heat shock 70 kDa protein 6;Putative heat shock 70 kDa protein 7	HSPA6	1	17.4	0	58.27	1.48	1.42	1.40	1.35	1.30	1.33	1.04	1.01	0.98

P17096	High mobility group protein HMG-I/HMG-Y	HMGA1	5	40.2	0	119.9	1.03	1.07	1.12	0.90	0.96	0.84	0.96	0.98	1.10
P17174	Aspartate aminotransferase, cytoplasmic	GOT1	13	42.9	0	181.3	0.82	0.88	1.04	0.90	1.07	0.84	0.95	0.97	0.95
P17252	Protein kinase C alpha type	PRKCA	8	16.8	0	25.31	NaN	0.40	0.36	0.89	1.73	0.71	0.67	0.80	0.41
P17301	Integrin alpha-2	ITGA2	9	9.9	0	27.14	1.32	1.15	1.65	NaN	0.69	0.91	NaN	1.52	0.96
P17612	cAMP-dependent protein kinase catalytic subunit alpha;cAMP-dependent protein kinase catalytic subunit beta	PRKACA	2	14	0	3.949	0.90	0.88	0.97	NaN	NaN	NaN	NaN	0.84	1.33
P17655	Calpain-2 catalytic subunit	CAPN2	29	53.3	0	323.3	0.98	0.95	0.92	0.99	1.08	0.98	0.91	1.10	1.02
P17844	Probable ATP-dependent RNA helicase DDX5	DDX5	16	45.6	0	168.7	0.79	0.85	0.88	0.88	0.87	0.89	0.79	0.93	0.78
P17858	ATP-dependent 6-phosphofructokinase, liver type	PFKL	16	31.9	0	182	0.90	0.86	0.97	1.01	0.88	1.02	0.88	1.01	1.10
P17931	Galectin-3;Galectin	LGALS3	8	34	0	29.68	0.73	0.84	0.87	0.94	0.87	0.92	1.17	0.88	0.98
P17987	T-complex protein 1 subunit	TCP1	27	53.8	0	323.3	1.18	1.07	1.08	1.05	1.05	1.04	0.82	0.90	0.97
P18031	Tyrosine-protein phosphatase non-receptor type 1;Tyrosine-protein phosphatase non-receptor type	PTPN1	18	55.9	0	98.77	0.73	0.93	1.61	1.18	0.96	1.04	0.83	1.77	1.00
P18077	60S ribosomal protein L35a	RPL35A	6	39.1	0	31.03	0.80	0.81	0.81	0.87	0.80	0.90	0.87	0.95	0.89
P18085	ADP-ribosylation factor 4	ARF4	6	64.4	0	250.5	0.92	1.05	0.95	0.90	0.96	1.03	0.77	0.77	0.83
P18124	60S ribosomal protein L7	RPL7	16	46.4	0	323.3	0.77	0.80	0.76	0.73	0.78	0.74	0.83	0.84	0.82
P18206	Vinculin	VCL	59	63.5	0	323.3	1.04	1.04	1.07	1.05	1.05	1.01	1.08	1.00	1.10
P18669	Phosphoglycerate mutase 1	PGAM1	17	70.9	0	323.3	1.08	0.98	1.06	1.08	1.09	1.06	1.03	0.95	1.04
P18754	Regulator of chromosome condensation	RCC1	6	21.9	0	20.91	0.99	0.80	0.73	0.80	0.52	0.79	NaN	0.68	0.81
P18827	Syndecan-1	SDC1	2	10.3	0	3.499	0.81	NaN	0.64	NaN	0.53	NaN	NaN	1.33	1.21
P18859	ATP synthase-coupling factor 6, mitochondrial	ATP5J	3	44.4	0	168.7	1.35	1.00	1.23	1.11	1.26	1.12	1.35	1.25	NaN
P19338	Nucleolin	NCL	33	40	0	323.3	0.96	0.96	0.94	1.00	0.96	0.97	0.87	0.82	0.84
P19367	Hexokinase-1	HK1	24	34.8	0	92.56	1.08	NaN	1.21	0.98	1.23	0.99	1.03	1.01	0.97
P19525	Interferon-induced, double-stranded RNA-activated protein kinase	EIF2AK2	5	10	0	4.583	NaN	1.43	NaN	NaN	1.11	0.99	NaN	NaN	0.86
P19623	Spermidine synthase	SRM	9	50.3	0	59.04	0.76	0.96	0.95	0.90	0.74	0.77	0.81	0.86	0.98
P20042	Eukaryotic translation initiation factor 2 subunit 2	EIF2S2	16	44.4	0	166.9	1.13	1.09	0.97	0.96	1.06	1.00	1.10	0.84	0.91
P20073	Annexin A7	ANXA7	12	26.6	0	20.76	0.95	1.05	0.96	1.09	1.01	0.82	1.35	1.39	1.00
P20290	Transcription factor BTF3	BTF3	9	60.2	0	200.3	0.89	0.73	0.88	0.97	1.17	0.87	1.21	1.01	0.83
P20339	Ras-related protein Rab-5A	RAB5A	4	39.5	0	26.2	1.03	1.13	1.23	1.24	1.35	1.13	0.70	1.54	0.94
P20340	Ras-related protein Rab-6A	RAB6A	7	37	0	36.49	0.69	0.79	0.87	1.10	1.03	0.85	0.96	0.76	0.99
P20618	Proteasome subunit beta type-1	PSMB1	9	45.6	0	178.3	0.87	0.80	0.94	0.79	0.97	1.01	1.38	0.70	0.95
P20700	Lamin-B1	LMNB1	24	52.7	0	323.3	0.98	0.86	1.12	0.90	0.99	0.90	0.97	0.89	1.04
P20962	Parathymosin	PTMS	2	11.8	0	88.24	1.07	1.18	1.12	1.04	1.23	1.01	NaN	NaN	1.08
P21266	Glutathione S-transferase Mu 3	GSTM3	14	65.3	0	56.38	1.09	1.02	0.96	0.96	0.94	0.90	1.02	1.18	0.95

P21281	V-type proton ATPase subunit B, brain isoform	ATP6V1B2	6	17.6	0	11.61	NaN	NaN	NaN	NaN	1.39	0.74	NaN	NaN	NaN
P21283	V-type proton ATPase subunit C	ATP6V1C1	3	9.2	0	4.809	0.84	1.90	1.18	NaN	NaN	1.34	1.10	NaN	1.11
P21291	Cysteine and glycine-rich protein	CSRP1	7	59.6	0	294.3	0.95	0.85	0.90	1.00	0.99	1.06	0.83	1.18	0.89
P21333	Filamin-A	FLNA	112	62.6	0	323.3	1.06	1.02	1.06	0.99	0.99	0.97	1.04	1.00	1.05
P21399	Cytoplasmic aconitate hydratase	ACO1	16	27.1	0	76.11	0.83	0.70	0.79	0.77	0.61	0.79	0.76	0.99	1.00
P21589	5-nucleotidase	NT5E	21	40.4	0	323.3	1.14	1.18	1.16	1.18	1.04	1.25	1.13	1.00	0.95
P21796	Voltage-dependent anion-selective channel protein 1	VDAC1	18	83.4	0	323.3	1.03	1.01	1.02	1.03	0.99	1.08	1.06	0.95	1.00
P21964	Catechol O-methyltransferase	COMT	9	49.1	0	23.85	1.01	0.73	0.95	NaN	NaN	1.22	NaN	1.11	1.08
P21980	Protein-glutamine gamma-glutamyltransferase 2	TGM2	32	53.6	0	323.3	1.14	1.21	1.19	1.16	1.13	1.15	1.30	1.29	1.31
P22087	rRNA 2-O-methyltransferase fibrillarin	FBL	4	44.9	0	14.99	0.57	0.99	0.90	0.78	0.85	0.93	0.65	0.75	0.61
P22102	Trifunctional purine biosynthetic protein adenosine-3;Phosphoribosylamine--glycine ligase;Phosphoribosylformylglycinamidine cyclo-ligase;Phosphoribosylglycinamide formyltransferase	GART	22	40.1	0	303.3	1.01	0.91	0.89	0.82	0.90	0.86	0.82	0.78	0.97
P22234	Multifunctional protein ADE2;Phosphoribosylaminoimidazole-succinocarboxamide synthase;Phosphoribosylaminoimidazole carboxylase	PAICS	19	51.5	0	177.3	0.83	0.89	0.81	0.94	0.95	0.98	0.90	1.04	0.94
P22307	Non-specific lipid-transfer protein	SCP2	15	24.9	0	39.27	0.76	0.70	0.78	0.94	0.90	0.94	0.71	0.70	0.75
P22314	Ubiquitin-like modifier-activating enzyme 1	UBA1	43	54.2	0	323.3	1.02	1.02	1.05	0.94	0.97	0.96	1.13	1.07	1.15
P22413	Ectonucleotide pyrophosphatase/phosphodiesterase family member 1;Alkaline phosphodiesterase I;Nucleotide pyrophosphatase	ENPP1	4	6.7	0	4.262	NaN	NaN	1.18	NaN	1.10	0.73	NaN	NaN	NaN
P22626	Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2I	23	69.1	0	323.3	0.92	0.91	0.91	0.91	0.92	0.94	0.79	0.92	0.94
P22695	Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	8	32.9	0	79.28	1.30	1.13	1.22	0.99	1.02	0.95	0.99	0.81	0.97
P23229	Integrin alpha-6;Integrin alpha-6 heavy chain;Integrin alpha-6 light chain;Processed integrin alpha-6	ITGA6	10	12.4	0	162.4	0.73	0.83	0.93	0.73	NaN	0.83	0.56	NaN	1.54
P23246	Splicing factor, proline- and glutamine-rich	SFPQ	23	38	0	206.4	1.15	1.19	1.08	1.13	1.15	1.09	1.17	1.12	0.88
P23284	Peptidyl-prolyl cis-trans isomerase B	PPIB	14	61.1	0	232.1	1.13	1.11	1.04	0.99	1.01	1.06	0.93	1.01	0.99
P23381	Tryptophan--tRNA ligase, cytoplasmic;T1-TrpRS;T2-TrpRS	WARS	9	27.2	0	86.23	0.96	0.80	0.97	0.69	0.73	0.94	0.97	0.94	0.95

P23396	40S ribosomal protein S3	RPS3	18	79.8	0	146.8	0.85	0.86	0.86	0.87	0.86	0.91	0.88	0.94	0.90
P23526	Adenosylhomocysteinase	AHCY	20	46.3	0	323.3	0.87	0.85	0.87	0.86	0.90	0.80	0.91	0.82	0.76
P23528	Cofilin-1	CFL1	16	89.8	0	323.3	0.93	0.91	0.88	0.93	0.95	1.02	1.00	0.97	0.90
P23634	Plasma membrane calcium-transporting ATPase 4	ATP2B4	2	7.4	0	15.08	NaN	0.67	1.06	0.99	0.52	0.71	0.88	NaN	NaN
P23919	Thymidylate kinase	DTYMK	9	38.2	0	9.826	0.97	1.05	1.25	0.91	1.39	0.96	1.23	1.26	1.11
P24534	Elongation factor 1-beta	EEF1B2	8	47.6	0	323.3	1.01	1.01	0.91	1.03	1.15	1.05	0.92	0.95	1.03
Q5QNZ2	ATP synthase F(0) complex subunit B1, mitochondrial	ATP5F1	6	27.7	0	127.3	1.18	1.06	1.02	0.99	1.19	1.46	1.59	0.74	0.99
P24666	Low molecular weight phosphotyrosine protein phosphatase	ACP1	4	41.1	0	6.582	0.78	NaN	0.60	NaN	NaN	NaN	NaN	NaN	NaN
P24752	Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	18	55.3	0	264.1	0.83	0.80	0.94	0.87	0.94	1.10	0.80	0.75	0.93
P24844	Myosin regulatory light polypeptide 9	MYL9	3	66.3	0	19.32	1.28	1.06	1.14	1.05	0.90	1.08	1.13	1.29	1.16
P25205	DNA replication licensing factor MCM3	MCM3	11	15	0	17.6	0.89	0.78	0.54	0.82	0.68	0.85	0.72	0.73	0.73
P25398	40S ribosomal protein S12	RPS12	8	71.2	0	262.6	0.95	1.01	0.99	0.89	0.97	1.01	1.01	1.06	1.00
P25685	DnaJ homolog subfamily B member 1	DNAJB1	11	36.5	0	106.8	1.71	1.55	1.84	1.50	1.82	1.43	1.45	1.03	1.02
P25705	ATP synthase subunit alpha, mitochondrial	ATP5A1	29	61.7	0	323.3	1.06	1.06	1.09	0.97	0.93	0.97	0.95	0.93	0.93
P25786	Proteasome subunit alpha type-1	PSMA1	17	75.3	0	153.5	1.03	0.98	1.01	0.96	1.04	0.99	1.11	1.09	1.03
P25788	Proteasome subunit alpha type-3	PSMA3	11	42.7	0	63.51	1.13	1.11	1.08	0.91	1.06	1.00	0.93	0.77	1.06
P25789	Proteasome subunit alpha type-4;Proteasome subunit alpha type;Proteasome subunit beta	PSMA4	13	58.2	0	306.2	1.08	1.02	1.12	1.05	0.97	1.02	0.91	0.95	0.95
P26006	Integrin alpha-3;Integrin alpha-3 heavy chain;Integrin alpha-3 light chain	ITGA3	18	19	0	174.2	0.85	1.00	0.95	0.99	0.95	0.95	0.89	0.97	0.93
P26038	Moesin	MSN	44	76.8	0	323.3	0.95	0.95	0.97	0.99	1.01	1.01	0.94	0.92	0.90
P26196	Probable ATP-dependent RNA helicase DDX6	DDX6	7	25.5	0	100.3	1.05	0.99	0.99	1.20	1.06	0.89	0.72	0.79	0.83
P26368	Splicing factor U2AF 65 kDa subunit	U2AF2	12	42.5	0	79.94	0.93	0.93	0.80	0.96	1.09	0.89	1.10	0.98	0.92
P26373	60S ribosomal protein L13	RPL13	9	35.5	0	150.9	0.98	0.94	0.95	0.96	0.96	0.98	1.04	0.97	1.00
P26447	Protein S100-A4	S100A4	5	36.6	0	96.57	0.76	0.93	0.86	0.83	0.84	0.87	0.80	0.86	0.81
P26583	High mobility group protein B2	HMGB2	9	28.7	0	50.5	0.93	1.09	0.82	0.81	1.09	0.74	0.72	0.76	0.67
P26639	Threonine--tRNA ligase, cytoplasmic	TARS	32	49.8	0	323.3	1.05	1.02	1.08	0.99	1.11	0.97	1.03	0.94	0.89
P26640	Valine--tRNA ligase	VARS	20	21.8	0	86.93	0.88	0.89	0.96	0.92	0.84	0.83	1.01	0.94	0.89
P26641	Elongation factor 1-gamma	EEF1G	27	61.1	0	323.3	1.03	1.07	1.05	1.01	1.00	1.03	0.96	0.94	0.93
P27144	Adenylate kinase 4,	AK4	5	25.1	0	13.66	1.30	1.10	1.32	1.38	1.41	1.60	1.29	1.31	1.11
P27348	14-3-3 protein theta	YWHAQ	14	59.2	0	323.3	1.02	1.02	1.00	0.96	1.02	1.00	0.91	0.97	1.00
X1WI28	60S ribosomal protein L10	RPL10	3	49.5	0	233.6	0.67	0.80	0.70	0.79	0.78	0.82	0.73	0.69	0.65

P27658	Collagen alpha-1(VIII) chain;Vastatin	COL8A1	1	1.3	0.001	2.085	0.95	1.10	1.13	1.83	1.44	1.39	NaN	NaN	NaN
P27694	Replication protein A 70 kDa DNA-binding subunit;Replication protein A 70 kDa DNA-binding subunit, N-terminally processed	RPA1	9	21.8	0	15.03	0.88	0.59	0.66	1.02	0.88	0.75	0.81	1.01	NaN
P27695	DNA-(apurinic or apyrimidinic site) lyase;DNA-(apurinic or apyrimidinic site) lyase, mitochondrial	APEX1	11	44.7	0	87.77	1.01	0.88	0.89	0.93	0.99	0.99	0.89	0.92	0.97
P27701	CD82 antigen;Tetraspanin	CD82	2	9.7	0	3.613	0.79	NaN	1.32	NaN	NaN	NaN	1.80	1.08	NaN
P27797	Calreticulin	CALR	28	71.5	0	323.3	1.07	1.03	1.07	1.04	1.09	1.06	1.09	1.14	1.09
P27816	Microtubule-associated protein 4;Microtubule-associated protein	MAP4	39	49	0	323.3	0.82	0.85	0.90	0.89	0.95	0.97	0.91	0.90	1.06
P27824	Calnexin	CANX	27	45.6	0	323.3	1.04	1.05	1.04	1.02	1.04	1.06	1.04	0.93	1.10
P28066	Proteasome subunit alpha type-5	PSMA5	12	57.3	0	130.1	0.93	0.81	0.88	0.99	0.81	1.01	1.13	0.86	0.76
P28070	Proteasome subunit beta type-4	PSMB4	8	48.5	0	132.8	0.97	1.08	1.12	1.02	0.96	1.11	0.90	1.03	1.11
P28072	Proteasome subunit beta type-6	PSMB6	4	16.7	0	15.63	1.18	1.22	1.20	1.22	1.10	1.01	1.14	1.28	1.05
P28074	Proteasome subunit beta type-5	PSMB5	7	36.5	0	25.96	0.79	0.88	1.04	0.79	0.97	0.96	0.62	0.80	1.09
P28288	ATP-binding cassette sub-family D member 3	ABCD3	5	10.3	0	8.774	1.26	1.15	1.19	0.84	1.01	1.17	1.03	0.84	1.23
P28482	Mitogen-activated protein kinase	MAPK1	8	38.9	0	80.56	0.99	0.84	0.82	1.11	1.05	0.89	1.20	1.13	1.09
P28838	Cytosol aminopeptidase	LAP3	16	45.1	0	62.52	0.96	0.84	0.87	NaN	0.71	1.09	1.22	0.63	0.98
P29317	Ephrin type-A receptor 2	EPHA2	8	11.3	0	23.66	1.35	1.37	1.47	1.29	1.04	1.20	NaN	1.10	1.10
P29353	SHC-transforming protein 1	SHC1	2	4.6	0	3.337	0.95	1.01	NaN	NaN	NaN	1.35	NaN	NaN	NaN
P29401	Transketolase	TKT	35	68.2	0	323.3	1.01	1.01	1.02	1.03	1.09	1.02	0.89	0.89	0.92
P29966	Myristoylated alanine-rich C-kinase substrate	MARCKS	10	50.3	0	323.3	0.77	0.69	0.68	0.71	0.68	0.79	1.20	1.23	1.19
P29992	Guanine nucleotide-binding protein subunit alpha-11;Guanine nucleotide-binding protein subunit alpha-14;Guanine nucleotide-binding protein G(q)	GNA11	2	7.2	0	5.236	0.94	0.58	0.84	NaN	0.91	1.16	NaN	NaN	0.93
P30040	Endoplasmic reticulum resident protein 29	ERP29	5	21.8	0	34.05	0.96	1.04	1.02	0.91	1.04	1.05	1.08	1.00	0.97
P30041	Peroxiredoxin-6	PRDX6	18	66.1	0	323.3	1.01	0.95	1.08	1.08	1.01	1.02	1.07	1.04	0.91
P30044	Peroxiredoxin-5, mitochondrial	PRDX5	9	55.1	0	50.49	0.92	1.01	1.02	0.89	1.10	1.07	1.33	1.49	1.41
P30048	Thioredoxin-dependent peroxide reductase, mitochondrial	PRDX3	9	43.4	0	181.4	0.91	0.86	0.92	1.05	1.09	1.04	1.09	0.90	0.90
P30049	ATP synthase subunit delta, mitochondrial	ATP5D	2	13.7	0	6.676	NaN	NaN	NaN	0.99	NaN	NaN	0.93	0.76	NaN
P30050	60S ribosomal protein L12	RPL12	8	63	0	299	0.77	0.76	0.77	0.73	0.75	0.82	0.88	0.88	0.86
P30084	Enoyl-CoA hydratase, mitochondrial	ECHS1	8	36.6	0	104.3	1.00	0.87	1.17	1.09	1.03	1.10	1.13	0.99	0.99
P30085	UMP-CMP kinase	CMPK1	7	47.4	0	36.19	0.95	1.05	1.07	0.95	0.88	1.04	1.12	1.04	1.15

P30086	Phosphatidylethanolamine-binding protein 1;Hippocampal cholinergic neurostimulating	PEBP1	11	79.7	0	323.3	0.98	1.01	0.96	0.98	1.02	1.10	0.98	1.04	0.98
P30101	Protein disulfide-isomerase A3	PDIA3	29	68.3	0	323.3	1.02	0.99	1.00	0.99	1.05	1.06	0.93	1.07	0.96
P30153	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha	PPP2R1A	25	54.5	0	323.3	1.14	1.16	1.20	1.29	1.23	1.23	0.96	1.06	0.89
P30405	Peptidyl-prolyl cis-trans isomerase F, mitochondrial;Peptidyl-prolyl cis-	PPIF	5	49.8	0	45.81	0.78	0.72	NaN	1.41	NaN	1.38	NaN	NaN	NaN
P30419	Glycylpeptide N-tetradecanoyltransferase 1	NMT1	9	20.8	0	284.4	0.88	0.81	0.86	0.87	1.02	0.88	0.63	0.60	0.82
P30479	HLA class I histocompatibility antigen, B-41 alpha chain;HLA class I histocompatibility antigen, B-42 alpha chain;HLA class I histocompatibility antigen, B-8 alpha chain;HLA class I histocompatibility antigen, B-18 alpha chain	HLA-B	1	37.3	0	246	1.07	1.02	1.03	1.14	1.15	1.13	1.02	1.10	1.04
P30520	Adenylosuccinate synthetase isozyme 2	ADSS	12	37.3	0	60.86	0.81	0.84	0.87	0.99	0.94	1.04	1.09	0.87	0.91
P30740	Leukocyte elastase inhibitor	SERPINB1	15	51.2	0	70.14	0.81	0.85	0.86	1.01	0.88	0.92	0.82	0.94	0.83
P30825	High affinity cationic amino acid transporter 1	SLC7A1	1	3	0	4.961	1.07	0.93	1.22	NaN	NaN	0.88	NaN	NaN	0.89
P30837	Aldehyde dehydrogenase X, mitochondrial	ALDH1B1	8	23.4	0	16.85	0.86	0.92	0.73	0.81	0.81	0.88	0.71	0.86	0.95
P31150	Rab GDP dissociation inhibitor alpha	GDI1	12	60.4	0	190.1	0.86	0.76	0.70	1.40	1.01	1.07	0.80	1.65	0.94
P31153	S-adenosylmethionine synthase isoform type-2	MAT2A	8	22.8	0	27.98	1.23	0.88	1.05	1.20	0.93	0.97	0.91	1.20	0.94
P31689	DnaJ homolog subfamily A member 1	DNAJA1	9	39.8	0	43.53	1.87	1.98	1.94	1.59	1.50	1.56	0.81	0.72	0.93
P31930	Cytochrome b-c1 complex subunit 1, mitochondrial	UQCRC1	10	34.8	0	29.99	1.21	1.06	1.22	1.14	0.94	1.20	NaN	1.41	0.99
P31937	3-hydroxyisobutyrate dehydrogenase, mitochondrial	HIBADH	8	40.5	0	48.33	0.95	0.70	0.82	NaN	0.96	1.09	1.11	NaN	0.57
P31939	Bifunctional purine biosynthesis protein PURH;Phosphoribosylaminoimid azolecarboxamide formyltransferase;IMP cyclohydrolase	ATIC	21	50.3	0	210	0.88	0.80	0.85	0.81	0.95	0.81	0.76	0.76	0.86
P31942	Heterogeneous nuclear ribonucleoprotein H3	HNRNPH3	7	34.7	0	233.9	0.85	0.77	0.87	0.85	0.88	0.91	0.95	0.97	1.07

P31946	14-3-3 protein beta/alpha;14-3-3 protein beta/alpha, N-terminally processed	YWHAB	9	52.8	0	323.3	0.97	0.95	0.97	1.00	0.91	0.97	1.01	0.99	1.00
P31947	14-3-3 protein sigma	SFN	11	61.3	0	323.3	0.91	0.88	0.90	0.92	0.96	0.98	0.95	0.98	1.11
P31948	Stress-induced-phosphoprotein 1	STIP1	44	65	0	323.3	1.08	1.12	1.18	1.29	1.32	1.16	0.86	0.92	0.90
P31949	Protein S100-A11;Protein S100-A11, N-terminally processed	S100A11	6	52.4	0	283.2	1.02	0.95	1.01	0.92	1.01	0.91	0.92	0.96	1.06
P32119	Peroxiredoxin-2	PRDX2	12	60.6	0	182.6	0.97	1.00	1.01	0.94	1.02	0.93	1.01	0.96	1.07
P32320	Cytidine deaminase	CDA	4	45.2	0	123	0.97	0.85	0.67	1.06	1.13	1.10	1.77	1.60	1.14
P32321	Deoxycytidylate deaminase	DCTD	2	18.5	0	4.252	NaN	NaN	1.30	NaN	1.33	0.71	NaN	NaN	0.77
P32969	60S ribosomal protein L9	RPL9	8	65.1	0	323.3	0.79	0.71	0.79	0.69	0.73	0.68	0.80	0.73	0.87
P33176	Kinesin-1 heavy chain	KIF5B	38	49.1	0	323.3	0.89	0.94	0.72	0.95	0.87	0.85	0.92	0.85	0.81
P33993	DNA replication licensing factor MCM7	MCM7	15	28.1	0	47.29	0.90	0.54	0.69	0.96	0.96	0.74	NaN	NaN	0.94
P34897	Serine hydroxymethyltransferase, mitochondrial;Serine hydroxymethyltransferase	SHMT2	15	42.5	0	152.3	0.80	0.66	0.74	0.87	0.85	0.88	NaN	0.87	1.00
P34932	Heat shock 70 kDa protein 4	HSPA4	39	56.7	0	323.3	1.10	1.17	1.11	1.20	1.15	1.07	1.02	0.94	0.96
P35221	Catenin alpha-1	CTNNA1	13	23.5	0	23.62	1.46	1.53	1.25	0.64	0.83	0.75	NaN	NaN	NaN
P35232	Prohibitin	PHB	16	72.8	0	189.3	1.12	0.97	1.09	1.04	1.02	1.09	1.11	0.96	1.12
P35268	60S ribosomal protein L22	RPL22	4	39.8	0	231.1	0.93	0.78	0.81	0.74	0.66	0.98	0.98	0.70	0.65
P35269	General transcription factor IIF subunit 1	GTF2F1	5	13.5	0	22.42	0.76	1.18	0.95	0.71	1.01	0.97	NaN	1.21	0.98
P35270	Sepiapterin reductase	SPR	10	51	0	88.06	0.84	0.96	0.97	1.10	1.09	0.94	0.92	0.88	1.06
P35579	Myosin-9	MYH9	147	69.3	0	323.3	0.90	0.94	0.91	0.94	0.97	0.96	0.95	0.95	0.99
P35580	Myosin-10	MYH10	15	21.9	0	62.77	0.92	0.58	0.58	0.89	1.10	0.52	NaN	0.73	NaN
P35606	Coatomer subunit beta	COPB2	23	35	0	136	0.92	0.87	0.90	1.15	0.90	0.92	1.01	0.78	1.22
P35610	Sterol O-acyltransferase 1	SOAT1	5	11.3	0	11.41	1.17	1.14	1.14	0.94	1.38	1.17	NaN	NaN	1.12
P35613	Basigin	BSG	9	25.7	0	148.2	0.95	1.07	1.20	0.97	1.01	0.98	0.62	0.64	1.06
P35637	RNA-binding protein FUS	FUS	7	20	0	141.5	0.82	0.70	0.85	0.77	0.83	0.77	0.60	0.72	0.69
P35998	26S protease regulatory subunit	PSMC2	22	61.7	0	323.3	1.10	1.08	1.05	1.09	1.01	1.02	1.02	1.07	1.04
P36405	ADP-ribosylation factor-like protein 3	ARL3	7	47.8	0	25.45	0.89	1.13	0.85	1.02	1.07	0.92	0.99	0.99	1.10
P36406	E3 ubiquitin-protein ligase	TRIM23	1	1.7	0	3.773	0.62	0.61	0.71	NaN	0.92	0.73	NaN	NaN	0.50
P36507	Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	3	19.2	0	36.46	0.93	1.17	0.94	0.90	0.89	0.94	1.16	1.03	1.03
P36542	ATP synthase subunit gamma, mitochondrial	ATP5C1	6	21.8	0	5.852	0.93	0.84	0.85	NaN	1.29	1.11	0.85	1.35	0.68
P36543	V-type proton ATPase subunit E 1;V-type proton ATPase subunit E 2	ATP6V1E1	2	10.2	0	6.45	NaN	NaN	1.50	NaN	0.63	0.86	NaN	NaN	1.14
P36551	Oxygen-dependent coproporphyrinogen-III oxidase, mitochondrial	CPOX	13	36.3	0	141.9	1.13	1.16	1.03	1.04	1.01	1.06	0.97	1.08	1.18
P36578	60S ribosomal protein L4	RPL4	18	48.5	0	182.8	0.82	0.86	0.78	0.92	0.83	0.90	0.77	0.76	0.82
P36871	Phosphoglucomutase-1	PGM1	22	47.7	0	305.2	1.12	0.96	1.10	1.04	1.09	1.11	1.03	1.16	1.16

P36957	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial	DLST	8	18.8	0	16.23	0.94	0.99	0.94	1.10	0.96	1.03	1.07	0.86	0.83
P37108	Signal recognition particle 14 kDa protein	SRP14	4	47.1	0	31.51	0.92	1.00	0.86	0.63	0.74	0.85	0.93	0.92	1.01
P37235	Hippocalcin-like protein 1;Neuron-specific calcium-binding protein hippocalcin	HPCAL1	12	59.6	0	193.9	1.23	1.20	1.22	1.32	1.41	1.42	0.99	1.04	1.24
X6RJP6	Transgelin-2	TAGLN2	16	77.5	0	323.3	1.02	1.06	1.02	0.96	0.97	0.98	1.30	1.13	1.39
P37837	Transaldolase	TALDO1	22	52.8	0	183	1.15	1.12	1.13	1.18	1.22	1.23	0.95	1.01	1.01
P38117	Electron transfer flavoprotein subunit beta	ETFB	7	32.9	0	6.24	1.08	0.96	0.93	1.48	1.25	1.02	NaN	0.86	NaN
P38159	RNA-binding motif protein, X chromosome;RNA-binding motif protein, X chromosome, N-terminally processed;RNA binding motif protein, X-linked-	RBMX	17	40.4	0	98.15	0.72	0.75	0.82	0.68	0.72	0.85	0.65	0.70	0.74
P38606	V-type proton ATPase catalytic subunit A	ATP6V1A	10	24.6	0	204.4	0.88	0.94	0.96	1.20	0.88	0.97	1.10	1.29	1.15
P38646	Stress-70 protein, mitochondrial	HSPA9	41	58.9	0	323.3	0.92	1.03	0.97	1.07	1.13	1.09	0.93	0.87	0.89
P38919	Eukaryotic initiation factor 4A-III;Eukaryotic initiation factor 4A-III, N-terminally processed	EIF4A3	12	44	0	66.13	0.80	0.92	0.80	0.98	0.82	0.95	0.85	1.00	0.93
P39019	40S ribosomal protein S19	RPS19	12	67.6	0	53.31	0.86	0.79	0.78	0.79	0.81	0.80	0.77	0.75	0.80
P39023	60S ribosomal protein L3	RPL3	19	47.6	0	180.1	0.79	0.77	0.80	0.88	0.83	0.78	0.79	0.84	0.77
P39687	Acidic leucine-rich nuclear phosphoprotein 32 family member A	ANP32A	6	34.1	0	216	1.16	1.08	1.02	0.87	0.89	1.11	1.21	1.17	0.92
P39748	Flap endonuclease 1	FEN1	9	36.8	0	323.3	0.74	0.74	0.81	0.93	0.81	0.77	0.85	0.85	0.91
P40121	Macrophage-capping protein	CAPG	16	56.6	0	323.3	0.93	0.97	1.01	0.90	0.94	1.04	1.07	0.80	0.98
P40227	T-complex protein 1 subunit zeta	CCT6A	22	56.9	0	274	0.97	0.93	1.03	1.02	0.95	1.00	0.95	0.87	0.82
P40306	Proteasome subunit beta type-10	PSMB10	2	11	0	34.47	0.70	0.61	0.81	NaN	NaN	1.07	NaN	NaN	0.88
P40429	60S ribosomal protein L13a	RPL13A	11	44.8	0	28.09	0.83	0.82	0.79	0.79	0.80	0.88	0.88	0.77	0.82
P40616	ADP-ribosylation factor-like protein 1	ARL1	4	35.4	0	4.354	0.71	0.93	1.06	0.89	0.94	1.07	0.87	0.74	0.92
P40763	Signal transducer and activator of transcription 3;Signal transducer and activator of transcription	STAT3	12	21.4	0	192.8	NaN	0.78	0.74	0.95	0.92	1.15	NaN	NaN	0.74
P40925	Malate dehydrogenase, cytoplasmic;Malate dehydrogenase	MDH1	15	46.4	0	323.3	0.88	0.94	0.86	0.92	1.01	0.99	0.94	0.96	0.97
P40926	Malate dehydrogenase, mitochondrial;Malate dehydrogenase	MDH2	18	64.8	0	323.3	1.00	1.00	0.95	1.03	1.04	1.07	0.85	0.88	0.89

P41091	Eukaryotic translation initiation factor 2 subunit 3;Putative eukaryotic translation initiation factor 2 subunit 3-like protein	EIF2S3	21	52.3	0	323.3	0.88	0.96	0.94	0.96	0.93	0.87	0.88	0.99	0.75
P41219	Peripherin	PRPH	1	9.1	0	17.17	1.19	1.23	1.10	NaN	NaN	1.00	NaN	NaN	1.15
P41227	N-alpha-acetyltransferase 10	NAA10	6	32.3	0	47.69	1.06	1.15	1.09	1.22	1.16	0.97	0.96	1.14	1.26
P41250	Glycine--tRNA ligase	GARS	18	34.9	0	176.7	1.07	0.92	1.05	1.02	0.83	0.95	0.82	1.21	0.86
P41252	Isoleucine--tRNA ligase, cytoplasmic	IARS	27	29	0	87.13	0.98	1.00	0.94	0.80	0.97	0.97	1.09	0.94	0.89
P42126	Enoyl-CoA delta isomerase 1, mitochondrial	ECI1	4	20.5	0	11.94	0.82	0.87	NaN	NaN	NaN	1.14	NaN	NaN	NaN
P42166	Lamina-associated polypeptide 2, isoform alpha;Thymopoietin;Thymopentin	TMPO	7	28.8	0	21.56	NaN	NaN	NaN	NaN	0.88	0.61	0.82	1.52	NaN
P42167	Lamina-associated polypeptide 2, isoforms beta/gamma;Thymopoietin;Thymopentin	TMPO	7	39.6	0	287.4	1.03	1.06	1.12	1.01	1.00	1.03	1.01	1.03	0.98
P42224	Signal transducer and activator of transcription 1-alpha/beta;Signal transducer and activator of transcription	STAT1	11	18.3	0	26.33	NaN	0.68	NaN	0.89	0.40	0.24	1.68	NaN	0.48
P42677	40S ribosomal protein S27	RPS27	2	39.3	0	23.07	0.90	0.97	0.85	0.99	0.77	0.85	1.14	1.04	0.93
P42704	Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	51	49.1	0	323.3	0.85	0.86	0.75	0.83	0.92	0.90	1.11	0.85	0.86
P42765	3-ketoacyl-CoA thiolase, mitochondrial	ACAA2	6	23.4	0	47.21	3.66	4.52	NaN	NaN	NaN	1.07	1.41	1.29	NaN
P42766	60S ribosomal protein L35	RPL35	3	26	0	8.24	0.99	1.00	0.96	1.02	1.09	0.97	1.02	0.89	0.90
P43034	Platelet-activating factor acetylhydrolase IB subunit alpha	PAFAH1B1	9	27.6	0	35.14	0.99	1.02	0.72	NaN	1.56	0.81	NaN	NaN	0.85
P43304	Glycerol-3-phosphate dehydrogenase, mitochondrial;Glycerol-3-phosphate dehydrogenase	GPD2	4	8	0	14.55	NaN	NaN	0.84	0.70	0.92	1.14	0.63	0.63	0.72
P43487	Ran-specific GTPase-activating protein	RANBP1	7	54.7	0	177.2	0.96	1.12	1.09	1.06	1.02	0.91	1.21	1.12	1.03
P43490	Nicotinamide phosphoribosyltransferase	NAMPT	27	71.5	0	323.3	1.14	1.26	1.12	1.23	1.20	1.27	0.96	0.93	0.97
P43686	26S protease regulatory subunit 6B	PSMC4	14	45.7	0	137.4	1.01	1.06	0.91	1.00	1.25	0.99	1.34	1.00	0.91
P45974	Ubiquitin carboxyl-terminal hydrolase 5	USP5	15	30.9	0	134	0.91	1.09	1.13	1.14	0.86	1.05	0.75	0.53	1.06
P46013	Antigen KI-67	MKI67	4	1.7	0.001	2.654	NaN	NaN	NaN	1.99	NaN	0.90	NaN	0.80	NaN
P46060	Ran GTPase-activating protein 1	RANGAP1	15	32.5	0	105.5	0.78	1.06	1.33	0.82	0.85	0.93	0.93	0.74	0.74
P46108	Adapter molecule crk	CRK	6	26	0	22.05	1.76	1.91	NaN	NaN	1.18	1.33	NaN	NaN	1.06
P46777	60S ribosomal protein L5	RPL5	12	42.4	0	61.84	0.93	0.89	0.87	0.96	0.90	0.99	0.94	0.91	0.92
P46778	60S ribosomal protein L21	RPL21	5	31.2	0	73.61	0.79	0.75	0.73	0.82	0.73	0.89	0.72	0.81	0.86

P46779	60S ribosomal protein L28	RPL28	6	32.8	0	73.49	0.68	0.76	0.66	0.85	0.78	0.92	0.92	0.98	0.69
P46783	40S ribosomal protein S10;Putative 40S ribosomal protein S10-like	RPS10	12	58.8	0	24.65	1.02	0.96	0.96	0.94	0.92	0.95	1.05	1.10	0.98
P46821	Microtubule-associated protein 1B;MAP1B heavy chain;MAP1 light chain LC1	MAP1B	24	16.1	0	221.9	0.72	0.79	0.88	0.60	0.80	0.78	0.85	0.83	0.92
P46939	Utrophin	UTRN	7	3.5	0	11.54	NaN	NaN	NaN	NaN	0.59	2.09	NaN	NaN	NaN
P46940	Ras GTPase-activating-like protein IQGAP1	IQGAP1	67	56	0	323.3	0.84	0.78	0.83	0.88	0.92	0.92	0.94	0.95	0.92
P46977	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A	STT3A	4	7.7	0	6.068	NaN	1.18	NaN	0.75	1.15	1.05	NaN	0.82	NaN
P47755	F-actin-capping protein subunit alpha-2	CAPZA2	5	43.4	0	55.95	1.10	1.03	1.37	1.42	1.08	1.08	1.17	1.11	1.45
P47813	Eukaryotic translation initiation factor 1A, X-chromosomal;Eukaryotic translation initiation factor 1A, Y-chromosomal	EIF1AX	5	35.4	0	5.237	0.75	NaN	1.36	1.20	NaN	0.87	NaN	NaN	NaN
P47897	Glutamine--tRNA ligase	QARS	5	36.1	0	34.15	0.72	0.81	0.73	1.17	0.95	0.91	0.83	NaN	0.92
P47985	Cytochrome b-c1 complex subunit Rieske, mitochondrial;Cytochrome b-c1 complex subunit 11;Putative cytochrome b-c1 complex subunit	UQCRFS1	2	8	0	3.381	0.77	1.31	NaN	1.26	NaN	0.77	NaN	NaN	NaN
P48047	ATP synthase subunit O, mitochondrial	ATP5O	8	48.4	0	106.6	1.12	1.08	1.34	1.03	1.04	1.02	0.77	0.84	0.88
P48059	LIM and senescent cell antigen-like-containing domain protein 1	LIMS1	2	13.8	0	11.98	1.04	1.55	1.08	1.38	NaN	0.96	0.93	NaN	1.04
P48147	Prolyl endopeptidase	PREP	7	12.8	0	15.33	1.52	1.01	1.29	1.17	0.79	1.23	0.78	1.32	1.39
P48449	Lanosterol synthase	LSS	4	6.3	0	2.993	NaN	1.13	1.11	NaN	2.28	NaN	NaN	NaN	NaN
P48507	Glutamate--cysteine ligase regulatory subunit	GCLM	4	20.8	0	52.89	1.81	1.82	1.75	1.34	2.10	1.18	NaN	NaN	1.15
R4GMR5	26S proteasome non-ATPase regulatory subunit 8	PSMD8	8	35.9	0	8.603	1.04	0.91	1.28	1.35	0.92	1.14	1.07	0.92	1.15
P48643	T-complex protein 1 subunit epsilon	CCT5	30	60.3	0	323.3	1.00	1.07	1.07	0.88	1.09	1.03	0.59	0.64	0.95
P48735	Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	6	15.5	0	9.779	0.73	0.85	0.93	1.23	1.14	0.99	NaN	NaN	1.09
P48960	CD97 antigen;CD97 antigen subunit alpha;CD97 antigen subunit beta	CD97	10	19.5	0	138	1.11	1.14	1.04	0.90	0.97	1.08	0.72	0.74	0.93
P49189	4-trimethylaminobutyraldehyde dehydrogenase	ALDH9A1	10	23.1	0	49.82	0.65	0.64	0.90	NaN	0.87	0.73	0.87	0.90	0.99
P49207	60S ribosomal protein L34	RPL34	4	29.9	0	7.227	1.12	1.10	0.98	0.83	0.99	1.01	0.73	0.85	0.91

P49257	Protein ERGIC-53	LMAN1	10	31.8	0	52.31	1.21	1.11	1.13	0.87	1.24	1.21	0.71	1.20	0.94
P49321	Nuclear autoantigenic sperm protein	NASP	13	21.1	0	53.19	1.19	0.95	1.10	0.91	1.05	1.12	0.92	1.16	0.74
P49327	Fatty acid synthase;[Acyl-carrier-protein] S-acetyltransferase;[Acyl-carrier-protein] S-malonyltransferase;3-oxoacyl-[acyl-carrier-protein] synthase;3-oxoacyl-[acyl-carrier-protein] reductase;3-hydroxyacyl-[acyl-carrier-protein] dehydratase;Enoyl-[acyl-carrier-protein] reductase;Oleoyl-[acyl-	FASN	88	48.1	0	323.3	0.62	0.58	0.52	0.67	0.67	0.67	0.81	0.78	0.84
Q5J8M5	Deoxyhypusine synthase	DHPS	2	9	0.009	1.409	NaN	0.75	NaN	NaN	1.00	0.61	0.79	0.83	NaN
P49368	T-complex protein 1 subunit gamma	CCT3	33	66.8	0	290.2	1.01	0.99	1.05	0.92	1.06	0.94	0.88	0.89	0.88
P49411	Elongation factor Tu,	TUFM	21	54.6	0	323.3	1.17	1.08	1.08	1.08	1.02	1.07	0.99	0.99	1.05
P49458	Signal recognition particle 9 kDa protein	SRP9	3	32.6	0	6.256	0.81	0.91	0.81	1.00	1.32	0.91	1.00	1.07	0.91
P49588	Alanine--tRNA ligase,	AARS	18	25.9	0	81.5	0.68	0.59	0.94	0.83	1.06	0.86	1.02	1.14	0.90
Q5T5C7	Serine--tRNA ligase, cytoplasmic	SARS	12	30.6	0	42.16	0.71	0.82	0.52	0.63	0.79	0.79	0.92	0.95	0.96
P49593	Protein phosphatase 1F	PPM1F	5	20.7	0	27.08	NaN	1.10	1.28	NaN	NaN	0.73	NaN	NaN	1.50
P49720	Proteasome subunit beta type-3	PSMB3	8	46.8	0	143.2	0.88	0.92	0.95	1.10	1.13	0.92	0.98	1.07	0.59
P49721	Proteasome subunit beta type-2	PSMB2	10	50.2	0	28.24	0.91	0.97	1.01	0.90	0.98	1.09	0.85	0.70	0.87
P49748	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial	ACADVL	23	47.3	0	323.3	1.12	1.07	1.18	1.15	1.18	1.15	1.32	1.24	1.20
P49755	Transmembrane emp24 domain-containing protein 10	TMED10	4	19.6	0	16.78	0.87	0.73	0.74	1.19	1.07	0.99	0.97	0.95	0.51
P49756	RNA-binding protein 25	RBM25	3	5.6	0	10.3	1.05	1.31	0.81	1.23	NaN	1.40	NaN	1.00	1.24
P49773	Histidine triad nucleotide-binding protein 1	HINT1	6	78.6	0	187.4	1.33	1.30	1.31	1.09	1.28	1.26	1.12	1.16	1.08
P49792	E3 SUMO-protein ligase RanBP2	RANBP2	4	2.1	0	4.926	1.06	NaN	NaN	NaN	NaN	NaN	1.11	NaN	0.75
P49915	GMP synthase [glutamine-hydrolyzing]	GMPS	13	30	0	33.75	0.80	0.94	0.79	NaN	0.74	1.01	NaN	0.91	0.96
P50213	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A	4	16.1	0	5.695	NaN	1.34	1.17	1.20	1.10	1.36	NaN	NaN	1.05
P50395	Rab GDP dissociation inhibitor beta	GDI2	21	72.4	0	323.3	0.96	0.96	0.98	0.98	1.00	1.01	0.95	1.02	1.00
P50402	Emerin	EMD	6	31.1	0	66.91	NaN	1.31	1.25	NaN	1.12	0.93	NaN	NaN	1.74
P50416	Carnitine O-palmitoyltransferase 1, liver isoform	CPT1A	8	13.2	0	17.54	0.98	0.95	0.91	0.83	1.26	0.96	1.38	NaN	0.99
P50453	Serpin B9	SERPINB9	10	37.2	0	29.11	1.25	NaN	1.43	0.66	1.03	NaN	NaN	NaN	1.43
P50454	Serpin H1	SERPINH1	17	47.6	0	307.8	1.06	1.01	1.04	0.98	1.07	0.95	0.96	1.01	1.03
P50502	Hsc70-interacting protein;Putative protein FAM10A5;Putative protein	ST13	9	29	0	121.4	1.05	1.04	1.11	1.04	1.00	1.00	0.87	0.84	0.99

P50552	Vasodilator-stimulated phosphoprotein	VASP	11	36.6	0	73.08	1.09	1.21	1.21	1.61	1.08	0.69	2.01	0.93	1.06
P50570	Dynamin-2	DNM2	13	30.8	0	97.16	1.25	1.01	0.99	0.66	0.98	1.13	1.29	1.16	0.86
P50583	Bis(5-nucleosyl)-tetraphosphatase [asymmetrical]	NUDT2	1	16.3	0	10.78	0.77	0.80	0.74	NaN	NaN	0.82	NaN	NaN	NaN
P50914	60S ribosomal protein L14	RPL14	5	26	0	21.07	0.80	0.84	0.88	0.88	0.61	0.82	0.74	NaN	0.72
P50990	T-complex protein 1 subunit theta	CCT8	39	73.9	0	323.3	1.06	1.02	1.07	1.10	0.99	1.10	0.96	0.87	0.92
P50991	T-complex protein 1 subunit delta	CCT4	27	61.2	0	323.3	1.05	0.98	1.09	0.99	1.03	1.11	0.85	0.85	0.91
P50995	Annexin A11	ANXA11	15	31.5	0	110.2	0.72	0.67	0.88	0.79	0.90	1.01	0.91	1.10	0.88
P51114	Fragile X mental retardation syndrome-related protein 1	FXR1	7	21.7	0	67.08	1.08	1.00	1.27	0.82	1.33	1.28	2.11	0.89	1.16
P51116	Fragile X mental retardation syndrome-related protein 2	FXR2	3	8.8	0	5.968	0.99	0.95	NaN	NaN	NaN	NaN	0.73	NaN	NaN
P51148	Ras-related protein Rab-5C	RAB5C	7	65.3	0	271.2	0.96	1.00	0.97	0.95	1.01	1.03	1.02	1.08	0.90
P51149	Ras-related protein Rab-7a	RAB7A	11	69.6	0	71.23	0.93	0.90	0.84	0.96	0.87	0.91	1.17	1.52	1.04
P51397	Death-associated protein 1	DAP	2	19.6	5E-04	2.767	NaN	NaN	NaN	0.97	NaN	1.13	NaN	0.58	NaN
P51571	Translocon-associated protein subunit delta	SSR4	3	24.3	0	25.4	0.99	1.13	NaN	NaN	0.93	NaN	NaN	NaN	1.06
P51572	B-cell receptor-associated protein 31	BCAP31	14	48	0	35.45	0.75	0.72	0.66	1.16	0.96	1.10	1.11	1.16	0.69
P51665	26S proteasome non-ATPase regulatory subunit 7	PSMD7	8	36.4	0	150	1.11	1.03	1.13	1.34	1.02	0.98	0.56	1.13	0.89
P51858	Hepatoma-derived growth factor	HDGF	13	65	0	323.3	0.89	0.72	0.79	1.04	1.08	0.83	0.96	1.33	0.79
P51970	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8	NDUFA8	3	20.3	0	5.947	1.02	1.17	1.11	1.57	1.31	1.27	NaN	1.14	1.20
P51991	Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	19	49.7	0	323.3	0.84	0.83	0.81	0.82	0.93	0.84	0.99	0.94	0.92
P52209	6-phosphogluconate dehydrogenase, decarboxylating	PGD	19	44.9	0	184.5	0.86	0.93	0.89	0.94	0.94	1.01	0.95	0.82	1.00
P52272	Heterogeneous nuclear ribonucleoprotein M	HNRNPM	38	61.2	0	323.3	0.88	0.88	0.83	1.04	0.99	0.96	0.80	1.10	0.78
P52292	Importin subunit alpha-1	KPNA2	9	21.7	0	265.6	1.33	1.11	1.19	1.37	1.45	1.39	0.76	0.64	1.22
P52306	Rap1 GTPase-GDP dissociation stimulator 1	RAP1GDS	7	16.5	0	9.593	NaN	0.66	0.69	1.09	NaN	NaN	1.13	1.01	1.39
P52565	Rho GDP-dissociation inhibitor 1	ARHGDIA	11	60.3	0	323.3	0.93	0.97	1.05	0.95	1.02	0.94	0.91	1.02	0.94
P52566	Rho GDP-dissociation inhibitor 2	ARHGDIB	6	50.7	0	49.38	0.88	1.14	0.92	NaN	NaN	0.93	NaN	1.38	0.91
P52597	Heterogeneous nuclear ribonucleoprotein F;Heterogeneous nuclear ribonucleoprotein F, N-terminally processed	HNRNPF	13	54.7	0	112.2	0.99	1.16	1.00	1.09	0.98	1.02	0.94	0.97	0.90
P52788	Spermine synthase	SMS	21	73	0	323.3	0.92	1.04	0.98	1.02	1.00	1.04	1.05	0.98	1.01
P52888	Thimet oligopeptidase	THOP1	4	8.9	0	16.69	0.90	0.82	1.09	NaN	0.97	NaN	2.18	1.23	1.17
P52907	F-actin-capping protein subunit alpha-1	CAPZA1	11	64.7	0	323.3	0.98	1.16	1.17	0.99	1.04	1.05	1.03	0.92	1.08
P53004	Biliverdin reductase A	BLVRA	8	32.4	0	153.2	0.85	0.71	0.72	0.96	0.92	0.77	0.69	0.72	0.76

P53007	Tricarboxylate transport protein, mitochondrial	SLC25A1	6	26.4	0	31.7	0.82	0.80	0.95	0.77	1.15	0.84	0.95	0.67	0.85
P53396	ATP-citrate synthase	ACLY	36	38.1	0	308.1	0.95	0.91	0.92	0.94	0.91	0.82	1.04	1.04	1.02
P53582	Methionine aminopeptidase 1	METAP1	2	8.5	0	2.872	1.09	0.93	1.24	NaN	NaN	NaN	NaN	NaN	1.44
P53597	Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	SUCLG1	5	22.8	0	11.53	NaN	0.75	1.14	NaN	0.47	0.46	0.63	1.91	0.81
P53618	Coatomer subunit beta	COPB1	37	49.3	0	281.2	0.95	0.87	0.98	0.95	0.99	0.91	1.02	1.03	0.90
P53992	Protein transport protein Sec24C	SEC24C	8	9.7	0	26.82	0.84	0.66	0.82	0.78	1.01	0.81	0.71	NaN	0.80
P53999	Activated RNA polymerase II transcriptional coactivator p15	SUB1	8	46.5	0	60.41	1.01	1.02	1.00	1.14	NaN	1.31	NaN	1.81	1.22
P54136	Arginine--tRNA ligase,	RARS	24	43.5	0	102.6	0.99	0.94	0.94	0.96	0.98	0.95	0.86	0.77	0.89
P54577	Tyrosine--tRNA ligase, cytoplasmic;Tyrosine--tRNA ligase, cytoplasmic, N-terminally processed;Tyrosine--tRNA ligase	YARS	16	41.1	0	63.11	1.01	1.06	1.00	0.95	0.79	0.92	0.86	1.00	1.31
P54578	Ubiquitin carboxyl-terminal hydrolase 14;Ubiquitin carboxyl-terminal hydrolase	USP14	18	38.7	0	302.2	1.00	0.79	0.79	1.04	0.95	1.20	0.62	1.10	1.06
P54709	Sodium/potassium-transporting ATPase subunit beta-3	ATP1B3	7	29.4	0	11.58	1.13	1.33	1.24	1.17	1.24	0.95	1.03	1.15	0.86
P54727	UV excision repair protein RAD23 homolog B	RAD23B	9	32	0	323.3	0.96	0.96	0.61	1.07	0.94	0.82	1.07	1.13	1.00
P54886	Delta-1-pyrroline-5-carboxylate synthase;Glutamate 5-kinase;Gamma-glutamyl phosphate reductase	ALDH18A1	14	26.8	0	26.55	0.73	0.76	0.75	0.91	NaN	0.73	0.78	0.73	0.83
P54920	Alpha-soluble NSF attachment protein	NAPA	6	25.8	0	9.499	NaN	NaN	1.06	0.63	0.71	0.93	NaN	NaN	0.60
P55010	Eukaryotic translation initiation factor 5	EIF5	9	26.5	0	37.49	1.20	1.23	1.34	1.07	0.93	0.91	0.99	0.93	0.92
P55036	26S proteasome non-ATPase regulatory subunit 4	PSMD4	6	36.1	0	56.78	0.86	0.90	1.43	1.30	1.05	0.91	0.86	0.79	NaN
P55060	Exportin-2	CSE1L	34	37.5	0	323.3	0.92	0.91	0.94	0.92	0.93	0.90	0.84	0.83	0.92
P55072	Transitional endoplasmic reticulum ATPase	VCP	40	58.6	0	323.3	0.96	1.02	1.01	1.04	1.02	1.07	0.99	0.96	0.93
P55084	Trifunctional enzyme subunit beta, mitochondrial;3-ketoacyl-CoA thiolase	HADHB	11	31	0	30.96	1.09	0.95	1.10	1.23	0.68	1.28	0.64	1.07	0.65
P55263	Adenosine kinase	ADK	11	35.9	0	49.97	0.98	0.97	0.84	0.62	0.80	0.63	0.95	1.40	1.17
P55735	Protein SEC13 homolog	SEC13	6	31.4	0	167.9	NaN	NaN	1.68	1.35	1.00	1.30	1.42	NaN	NaN
P55795	Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	4	31.6	0	11.62	1.08	0.67	1.01	1.34	1.27	0.85	NaN	0.88	0.75
P55884	Eukaryotic translation initiation factor 3 subunit B	EIF3B	25	39.4	0	323.3	1.18	1.10	1.19	0.91	1.23	1.02	0.97	1.18	0.94

P55957	BH3-interacting domain death agonist;BH3-interacting domain death agonist p15;BH3-interacting domain death agonist p13;BH3-interacting domain death agonist p11	BID	4	36.4	0	19.15	0.90	NaN	1.38	NaN	NaN	1.23	NaN	NaN	0.89
P56182	Ribosomal RNA processing protein 1 homolog A	RRP1	1	2.6	0.001	2.732	1.07	NaN	1.21	NaN	NaN	NaN	NaN	NaN	NaN
P56192	Methionine--tRNA ligase, cytoplasmic	MARS	12	20.4	0	46.39	0.89	1.01	1.02	0.77	0.95	0.87	0.93	0.81	0.93
P56385	ATP synthase subunit e, mitochondrial	ATP5I	2	31.9	5E-04	2.788	1.05	1.16	1.17	1.14	1.09	1.94	NaN	NaN	1.09
P56537	Eukaryotic translation initiation factor 6	EIF6	7	40.8	0	269.5	0.78	0.80	0.59	0.85	0.82	0.96	0.90	1.08	0.69
P58546	Myotrophin	MTPN	4	57.6	0	195.7	1.14	1.15	0.92	1.26	0.85	1.10	0.96	1.04	0.97
P60174	Triosephosphate isomerase	TPI1	18	74.1	0	323.3	1.18	1.19	1.16	1.23	1.15	1.17	1.14	1.11	1.15
P60228	Eukaryotic translation initiation factor 3 subunit E	EIF3E	17	45.4	0	109.6	1.03	1.10	1.09	0.94	1.23	1.17	0.83	0.79	0.93
P60842	Eukaryotic initiation factor 4A-I	EIF4A1	13	59.9	0	323.3	1.02	1.05	1.01	1.17	1.11	1.08	0.83	0.89	0.80
P60866	40S ribosomal protein S20	RPS20	4	28.6	0	18.36	0.86	0.88	0.89	0.83	0.95	0.94	0.80	0.87	0.84
P60903	Protein S100-A10	S100A10	5	37.1	0	95.7	0.87	0.82	0.80	0.93	0.93	0.91	0.87	0.90	0.94
P60953	Cell division control protein 42 homolog	CDC42	6	42.4	0	56.09	1.12	1.04	1.01	0.99	0.95	0.99	0.87	0.91	0.89
P60981	Destrin	DSTN	14	66.1	0	226.9	0.82	0.89	0.94	1.03	1.04	1.02	1.04	1.04	0.96
P61006	Ras-related protein Rab-8A	RAB8A	5	35.7	0	36.55	1.06	1.05	1.07	1.15	0.95	0.85	1.12	0.86	0.82
P61009	Signal peptidase complex subunit 3	SPCS3	2	11.1	0.005	1.709	1.42	NaN	1.28	0.75	NaN	1.03	NaN	2.03	1.53
P61011	Signal recognition particle 54 kDa protein	SRP54	8	21.8	0	39.59	0.84	0.60	0.88	NaN	0.72	0.75	NaN	NaN	0.84
P61019	Ras-related protein Rab-2A;Ras-related protein Rab-2B	RAB2A	10	60.4	0	65.63	1.11	0.95	0.67	NaN	0.91	0.81	NaN	1.14	0.67
P61020	Ras-related protein Rab-5B	RAB5B	5	45.1	0	30.39	NaN	0.91	0.44	0.86	NaN	1.30	NaN	1.11	1.36
Q5T179	Cyclin-dependent kinases regulatory subunit;Cyclin-dependent kinases regulatory subunit 1	CKS1B	2	38.8	0	10.59	1.21	1.20	1.19	NaN	0.98	1.70	NaN	NaN	NaN
P61026	Ras-related protein Rab-10	RAB10	6	43	0	46.05	0.99	0.95	1.04	1.18	1.07	1.02	1.24	0.97	0.96
P61081	NEDD8-conjugating enzyme Ubc12	UBE2M	8	39.3	0	100.6	0.69	0.96	1.50	0.81	0.84	1.10	0.91	0.88	0.68
P61086	Ubiquitin-conjugating enzyme E2	UBE2K	7	44	0	17.9	1.14	0.92	1.19	NaN	1.04	1.13	NaN	NaN	1.03
P61088	Ubiquitin-conjugating enzyme E2 N;Putative ubiquitin-conjugating enzyme E2 N-like	UBE2N	8	59.2	0	70.22	1.03	0.93	1.01	1.09	0.98	1.01	1.08	1.10	0.91
P61106	Ras-related protein Rab-14	RAB14	13	70.7	0	95.77	1.00	1.02	1.09	1.02	0.96	1.05	0.88	0.93	0.90
P61158	Actin-related protein 3	ACTR3	18	57.2	0	267.7	1.01	1.09	0.90	1.02	1.02	1.04	1.06	1.12	1.16
P61160	Actin-related protein 2	ACTR2	13	36.3	0	92.17	1.18	1.00	1.12	1.03	1.20	0.97	NaN	NaN	1.06
P61163	Alpha-centractin	ACTR1A	5	32.2	0	75.76	0.94	0.85	0.85	1.24	0.98	0.99	1.73	1.33	1.18

P61221	ATP-binding cassette sub-family E member 1	ABCE1	15	30.7	0	43.66	0.72	0.62	0.84	0.80	0.86	0.69	0.94	0.76	0.86
P61224	Ras-related protein Rap-1b;Ras-related protein Rap-1b-like	RAP1B	3	65.2	0	90.52	1.14	0.99	1.06	0.97	0.90	0.97	1.12	1.05	0.80
P61247	40S ribosomal protein S3a	RPS3A	15	51.9	0	212.1	0.84	0.81	0.87	0.81	0.82	0.81	0.78	0.82	0.82
P61254	60S ribosomal protein L26;60S ribosomal protein L26-like 1	RPL26	6	36.6	0	5.751	0.83	0.87	0.88	1.53	0.84	0.79	0.95	0.66	0.79
P61289	Proteasome activator complex subunit 3	PSME3	6	28.7	0	26.4	1.04	1.13	1.18	1.31	1.18	1.05	1.17	1.00	1.13
P61313	60S ribosomal protein L15;Ribosomal protein L15	RPL15	11	51	0	166.2	0.67	0.70	0.67	0.75	0.66	0.81	0.81	0.78	0.78
P61326	Protein mago nashi homolog	MAGOH	1	42.5	0	11.13	0.94	0.91	1.09	1.21	1.07	1.05	0.83	0.97	1.07
P61353	60S ribosomal protein L27	RPL27	6	50.7	0	7.782	0.80	0.71	0.78	0.88	0.81	0.79	0.93	0.93	0.86
P61586	Transforming protein RhoA	RHOA	4	56.5	0	285.2	0.97	0.92	0.93	1.00	1.01	1.03	0.88	0.85	0.89
P61604	10 kDa heat shock protein, mitochondrial	HSPE1	11	83.3	0	120.3	1.22	1.24	1.32	1.23	1.21	1.21	0.99	0.98	1.00
P61758	Prefoldin subunit 3	VBP1	8	43.7	0	5.424	0.77	0.91	NaN	1.09	NaN	NaN	0.93	1.01	1.23
P61769	Beta-2-microglobulin;Beta-2-microglobulin form pI 5.3	B2M	4	37.8	0	80.95	0.97	1.02	0.99	1.09	1.18	1.08	0.93	1.01	0.98
P61956	Small ubiquitin-related modifier 2;Small ubiquitin-related modifier	SUMO2	1	23.2	0	108.4	1.00	1.00	0.99	0.87	1.10	1.14	0.91	0.95	1.02
P61970	Nuclear transport factor 2	NUTF2	5	62.2	0	32.49	1.43	1.18	1.48	1.54	1.89	1.45	1.22	1.29	1.06
P61978	Heterogeneous nuclear ribonucleoprotein K	HNRNPK	4	61.6	0	323.3	0.89	0.90	0.92	0.92	0.95	0.95	0.88	0.91	0.99
P61981	14-3-3 protein gamma;14-3-3 protein gamma, N-terminally processed	YWHAG	13	72.5	0	323.3	1.14	1.20	1.13	1.09	1.15	1.09	1.08	1.01	1.05
P62070	Ras-related protein R-Ras2	RRAS2	2	25	0	10.48	1.08	1.01	0.93	1.17	1.06	1.00	0.72	1.00	0.84
P62081	40S ribosomal protein S7	RPS7	3	60.3	0	323.3	0.99	0.93	0.94	0.83	0.96	0.89	0.96	0.93	1.06
P62136	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit;Serine/threonine-protein phosphatase	PPP1CA	6	73.6	0	319.7	1.17	1.03	1.09	1.20	1.16	1.02	1.12	1.26	1.17
P62140	Serine/threonine-protein phosphatase PP1-beta catalytic subunit;Serine/threonine-protein phosphatase	PPP1CB	5	63.3	0	59.66	0.93	1.09	1.14	1.07	NaN	0.80	NaN	1.12	1.12
P62191	26S protease regulatory subunit	PSMC1	15	45	0	133.6	1.04	1.04	1.03	0.99	1.12	1.13	1.09	0.95	0.86
P62195	26S protease regulatory subunit	PSMC5	14	47	0	182.3	1.06	0.95	1.08	0.85	0.96	1.11	0.93	1.10	0.86
P62241	40S ribosomal protein S8	RPS8	8	45.7	0	143.2	0.91	0.95	1.03	0.78	0.91	0.91	0.85	0.74	0.73
P62244	40S ribosomal protein S15a	RPS15A	3	54.6	0	54.12	0.88	0.89	0.80	0.85	0.82	0.90	0.66	0.64	0.96
P62249	40S ribosomal protein S16	RPS16	8	50	0	23.09	0.51	0.61	0.74	0.87	0.73	0.72	0.48	0.31	0.65
P62258	14-3-3 protein epsilon	YWHAE	24	78.4	0	323.3	0.91	0.94	0.96	0.94	0.90	0.97	0.85	0.92	0.93
P62266	40S ribosomal protein S23	RPS23	6	43.4	0	24.33	0.64	0.64	0.66	0.62	0.56	0.67	0.57	0.79	0.73
P62269	40S ribosomal protein S18	RPS18	10	48.7	0	41.95	0.77	0.81	0.78	0.75	0.74	0.86	0.89	0.91	0.82
P62277	40S ribosomal protein S13	RPS13	10	57	0	58.17	0.80	0.75	0.72	0.62	0.72	0.83	0.57	0.82	0.75
P62280	40S ribosomal protein S11	RPS11	9	51.9	0	192.8	0.90	0.88	0.92	0.78	0.79	0.86	0.84	0.84	0.87

P62304	Small nuclear ribonucleoprotein	SNRPE	2	25	0	14.2	0.80	0.79	0.88	1.06	0.92	0.95	0.67	0.69	0.70
P62306	Small nuclear ribonucleoprotein F	SNRPF	2	24.4	0	77.87	1.25	1.18	0.95	1.06	1.01	1.09	0.72	0.71	1.05
P62310	U6 snRNA-associated Sm-like protein LSm3	LSM3	2	32.4	0	135.4	1.24	1.06	1.37	1.07	NaN	1.13	NaN	NaN	1.05
P62314	Small nuclear ribonucleoprotein Sm D1	SNRPD1	3	37	0	8.623	0.82	1.01	0.75	0.76	4.06	1.26	0.67	0.90	1.27
P62316	Small nuclear ribonucleoprotein Sm D2	SNRPD2	8	61.9	0	97.68	0.75	0.91	0.93	0.84	0.92	0.99	0.71	0.89	0.85
P62318	Small nuclear ribonucleoprotein Sm D3	SNRPD3	5	53.2	0	23.21	0.75	0.78	0.90	1.09	0.92	0.92	0.81	0.74	0.76
P62328	Thymosin beta-4;Hematopoietic system regulatory peptide	TMSB4X	11	88.6	0	323.3	0.97	0.96	0.95	1.03	1.00	1.01	0.91	0.86	0.90
P62330	ADP-ribosylation factor 6	ARF6	5	48.6	0	60.36	1.01	0.73	0.88	0.71	1.09	0.84	0.57	0.87	0.72
P62424	60S ribosomal protein L7a	RPL7A	12	37.6	0	195.1	0.77	0.77	0.73	0.78	0.83	0.81	0.74	0.71	0.69
P62633	Cellular nucleic acid-binding protein	CNBP	6	40.1	0	82.73	0.95	0.78	0.89	1.03	0.87	0.88	1.00	0.98	1.06
P62701	40S ribosomal protein S4, X isoform	RPS4X	18	63.5	0	238.5	0.81	0.68	0.83	0.69	0.73	0.71	0.69	0.65	0.75
P62750	60S ribosomal protein L23a	RPL23A	9	42.3	0	8.203	0.85	0.87	0.95	0.80	0.88	0.83	0.87	0.87	0.95
P62753	40S ribosomal protein S6	RPS6	6	27.3	0	110	1.02	1.16	1.09	0.97	1.02	0.91	0.80	0.91	1.16
P62805	Histone H4	HIST1H4A	9	59.2	0	135.4	0.84	0.84	0.83	0.65	0.66	0.66	0.90	0.86	0.91
P62820	Ras-related protein Rab-1A	RAB1A	7	78.5	0	194.3	1.04	0.94	0.97	0.93	0.97	1.02	0.92	0.89	0.96
P62829	60S ribosomal protein L23	RPL23	7	52.1	0	101	0.72	0.73	0.66	0.72	0.83	0.77	0.82	0.91	0.90
P62841	40S ribosomal protein S15	RPS15	6	54.5	0	124.1	0.76	0.88	0.78	0.82	0.80	0.96	0.66	0.50	0.71
P62851	40S ribosomal protein S25	RPS25	6	37.6	0	12.05	0.87	0.85	0.86	0.84	0.77	0.86	0.82	0.85	0.91
P62854	40S ribosomal protein S26;Putative 40S ribosomal protein S26-like 1	RPS26	4	44.3	0	17.45	0.50	0.74	0.86	0.78	0.88	0.76	0.58	0.54	NaN
P62857	40S ribosomal protein S28	RPS28	3	46.4	0	323.3	1.13	1.20	1.03	1.12	1.11	1.21	1.09	1.05	0.88
P62873	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1	GNB1	9	50	0	240	0.88	0.73	0.83	0.72	0.88	0.96	0.81	0.88	0.72
P62877	E3 ubiquitin-protein ligase RBX1;E3 ubiquitin-protein ligase RBX1, N-terminally processed	RBX1	3	29.6	0	40.71	NaN	1.12	0.93	NaN	NaN	1.03	NaN	NaN	0.84
P62879	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	GNB2	5	50	0	151.4	0.86	0.85	1.02	NaN	0.96	0.96	0.44	1.39	0.79
P62888	60S ribosomal protein L30	RPL30	6	66.1	0	109.7	1.04	0.89	0.93	1.03	1.08	0.90	1.03	1.08	0.99
Q59GN2	Putative 60S ribosomal protein L39-like 5;60S ribosomal protein L39	RPL39P5	1	19.6	0	3.923	1.33	1.33	1.36	NaN	0.98	1.15	NaN	NaN	1.48
P62899	60S ribosomal protein L31	RPL31	5	40	0	91.88	0.78	0.91	NaN	0.78	0.69	0.76	0.87	0.91	0.75
P62906	60S ribosomal protein L10a	RPL10A	12	48.4	0	53.56	0.87	0.82	0.90	0.88	0.74	0.80	0.72	0.90	1.01
Q5VVC8	60S ribosomal protein L11	RPL11	4	22.2	0	80.59	0.78	0.75	0.76	0.81	0.82	NaN	0.92	0.88	0.86

P62937	Peptidyl-prolyl cis-trans isomerase A;Peptidyl-prolyl cis-trans isomerase A, N-terminally processed;Peptidyl-prolyl cis-trans isomerase	PPIA	11	78.8	0	323.3	1.08	1.14	1.10	1.20	1.14	1.14	1.07	1.08	1.13
P62942	Peptidyl-prolyl cis-trans isomerase FKBP1A;Peptidyl-prolyl cis-trans isomerase	FKBP1A	7	73.1	0	184.9	0.99	1.10	1.18	1.69	1.14	1.17	1.39	1.42	0.93
P62979	Ubiquitin-40S ribosomal protein S27a;Ubiquitin;40S ribosomal protein S27a;Polyubiquitin-B;Ubiquitin;Polyubiquitin-C;Ubiquitin	RPS27A	3	57.1	0	323.3	0.93	1.06	1.25	0.81	0.81	0.90	0.98	0.90	1.14
P62993	Growth factor receptor-bound protein 2	GRB2	7	41.5	0	16.31	NaN	1.44	1.72	1.16	NaN	1.16	1.02	NaN	0.98
P62995	Transformer-2 protein homolog beta	TRA2B	7	28.1	0	18.21	0.97	0.97	0.96	NaN	1.24	1.14	NaN	NaN	0.90
P63000	Ras-related C3 botulinum toxin substrate 1	RAC1	4	41.1	0	52.44	0.96	0.98	0.96	1.01	1.05	0.97	0.71	0.80	0.85
P63010	AP-2 complex subunit beta	AP2B1	18	39.8	0	207.7	1.12	1.00	1.01	0.87	0.94	0.95	0.95	0.97	1.03
P63092	Guanine nucleotide-binding protein G(s) subunit alpha isoforms short;Guanine nucleotide-binding protein G(s) subunit alpha isoforms XL as	GNAS	4	17.5	0	27	1.40	0.89	1.00	NaN	1.04	NaN	NaN	1.64	1.14
P63104	14-3-3 protein zeta/delta	YWHAZ	16	75.9	0	323.3	0.97	0.93	0.92	0.95	0.93	0.92	0.90	0.93	0.96
P63167	Dynein light chain 1, cytoplasmic	DYNLL1	3	58.4	0	311.6	0.70	0.82	0.77	0.87	0.96	0.75	0.44	0.89	0.91
P63172	Dynein light chain Tctex-type 1	DYNLT1	3	38.9	0	40.08	0.76	1.28	0.75	0.80	NaN	0.75	0.80	NaN	0.76
P63173	60S ribosomal protein L38	RPL38	4	50	0	6.379	0.59	0.56	0.77	NaN	NaN	0.48	0.61	0.63	0.71
Q8WVC2	40S ribosomal protein S21	RPS21	6	74.1	0	105.1	0.96	0.97	1.04	0.95	0.98	1.05	NaN	0.99	0.80
P63244	Guanine nucleotide-binding protein subunit beta-2-like 1;Guanine nucleotide-binding protein subunit beta-2-like 1, N-terminally processed	GNB2L1	20	79.5	0	193.2	0.98	0.94	0.91	0.87	1.00	0.81	0.95	0.92	0.95
P63261	Actin, cytoplasmic 2;Actin, cytoplasmic 2, N-terminally processed	ACTG1	3	80.5	0	323.3	0.98	0.96	0.98	0.95	0.95	0.94	1.05	1.03	1.06
P63313	Thymosin beta-10	TMSB10	3	54.5	0	90.42	0.58	0.69	0.77	0.94	1.02	1.08	NaN	NaN	0.80
P67775	Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform;Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform	PPP2CA	9	53.1	0	131.7	1.13	1.21	1.20	0.90	1.13	1.16	1.15	0.90	0.98
P67809	Nuclease-sensitive element-binding protein 1	YBX1	10	54	0	323.3	1.25	1.22	1.19	1.11	1.09	1.09	0.98	1.03	1.01
Q5SRQ6	Casein kinase II subunit beta	CSNK2B	6	38	0	8.063	1.77	1.25	1.43	NaN	0.86	0.90	NaN	3.09	1.11

P67936	Tropomyosin alpha-4 chain	TPM4	8	73	0	323.3	1.20	1.11	1.08	0.94	0.97	0.93	1.19	1.11	1.16
P68032	Actin, alpha cardiac muscle 1;Actin, gamma-enteric smooth muscle;Actin, alpha skeletal muscle;Actin, aortic smooth	ACTC1	4	45.6	0	22.92	0.91	NaN	NaN	0.91	NaN	0.99	0.62	0.64	0.84
P68036	Ubiquitin-conjugating enzyme E2 L3	UBE2L3	7	63.6	0	173.7	1.01	1.18	1.09	1.13	1.11	1.09	1.16	1.34	0.96
P68104	Elongation factor 1-alpha 1;Putative elongation factor 1-alpha-like 3;Elongation factor 1-alpha	EEF1A1	17	74.9	0	323.3	0.82	0.79	0.82	0.94	0.90	0.92	0.77	0.87	0.85
P68363	Tubulin alpha-1B chain	TUBA1B	0	80.7	0	323.3	0.67	0.61	0.60	0.67	0.71	0.69	1.03	0.87	0.89
P68366	Tubulin alpha-4A chain	TUBA4A	3	56.5	0	17.53	1.00	0.99	1.23	NaN	1.01	0.97	NaN	1.95	2.09
P68371	Tubulin beta-4B chain	TUBB4B	1	67	0	323.3	0.55	0.52	0.53	0.61	0.61	0.60	0.94	0.86	0.87
P68402	Platelet-activating factor acetylhydrolase IB subunit beta	PAFAH1B2	8	58.1	0	143.5	1.11	1.01	0.96	1.01	1.07	1.04	1.08	1.04	1.10
Q71DI3	Histone H3.2;Histone H3.1t;Histone H3.1;Histone H3	HIST2H3A	3	39.7	0	45.61	0.79	0.77	0.76	0.67	0.67	0.63	0.88	0.82	0.68
P78318	Immunoglobulin-binding protein 1	IGBP1	3	11.5	0	48.45	NaN	0.72	1.12	NaN	NaN	1.26	NaN	0.87	1.26
P78344	Eukaryotic translation initiation factor 4 gamma 2	EIF4G2	10	14.6	0	25.93	1.06	0.99	1.21	1.21	1.02	0.89	1.02	0.81	1.01
P78346	Ribonuclease P protein subunit p30	RPP30	2	9.7	0.002	1.9	0.99	1.00	1.12	NaN	0.85	1.01	NaN	NaN	NaN
P78371	T-complex protein 1 subunit beta	CCT2	35	80	0	323.3	1.07	1.06	1.06	1.01	1.00	1.06	0.96	1.08	0.97
P78417	Glutathione S-transferase omega-1	GSTO1	20	66.4	0	227.5	1.22	1.17	1.22	1.22	1.17	1.21	1.08	1.01	1.16
P78527	DNA-dependent protein kinase catalytic subunit	PRKDC	69	20.6	0	226.7	0.88	0.76	0.79	1.06	0.90	0.91	0.90	1.01	0.94
P80723	Brain acid soluble protein 1	BASP1	14	89.9	0	323.3	0.93	0.98	0.95	0.90	0.88	0.91	1.02	1.09	1.15
P82673	28S ribosomal protein S35, mitochondrial	MRPS35	3	11.1	0	3.985	0.69	0.54	0.56	NaN	1.16	0.49	NaN	NaN	NaN
P83111	Serine beta-lactamase-like protein LACTB, mitochondrial	LACTB	4	10.6	0	7.36	1.05	1.02	0.97	NaN	NaN	0.91	NaN	NaN	NaN
P83916	Chromobox protein homolog 1	CBX1	5	55.7	0	51.41	NaN	0.55	NaN	0.70	NaN	0.58	0.72	0.81	0.72
P84022	Mothers against decapentaplegic homolog 3;Mothers against decapentaplegic homolog;Mothers against decapentaplegic homolog 2;Mothers against	SMAD3	3	8	0	3.479	0.48	NaN	NaN	0.55	NaN	0.72	NaN	NaN	NaN
P84077	ADP-ribosylation factor 1;ADP-ribosylation factor 3	ARF1	4	59.7	0	60.34	0.75	0.77	0.88	1.03	0.95	0.92	0.66	0.71	0.67
P84090	Enhancer of rudimentary	ERH	5	51	0	323.3	0.95	1.10	1.03	1.13	0.87	1.01	0.91	0.98	1.35
P84095	Rho-related GTP-binding protein RhoG	RHOG	6	47.6	0	14.04	1.17	1.01	1.13	0.69	NaN	1.19	4.43	5.19	1.01
P84103	Serine/arginine-rich splicing factor 3	SRSF3	8	47	0	23.35	1.06	1.08	1.04	1.01	0.96	0.96	1.18	1.07	1.16

P98179	RNA-binding protein 3	RBM3	4	47.8	0	323.3	0.80	0.75	0.80	0.94	0.85	0.92	0.81	0.85	0.88
Q00688	Peptidyl-prolyl cis-trans isomerase FKBP3	FKBP3	11	52.7	0	47.91	0.81	1.06	NaN	1.19	1.11	1.15	NaN	3.06	1.01
Q00765	Receptor expression-enhancing protein 5	REEP5	5	20.1	0	4.783	1.20	1.15	1.04	1.23	NaN	1.27	1.06	0.94	0.90
Q00839	Heterogeneous nuclear ribonucleoprotein U	HNRNPU	4	41.9	0	323.3	0.73	0.80	0.76	0.80	0.82	0.86	0.80	0.86	0.87
Q01082	Spectrin beta chain, non-erythrocytic 1	SPTBN1	3	60.5	0	323.3	0.72	0.73	0.74	0.77	0.76	0.77	0.92	0.92	0.92
Q01085	Nucleolysin TIAR	TIAL1	4	11.7	0	11.16	0.95	NaN	1.10	NaN	0.78	NaN	NaN	NaN	NaN
Q01518	Adenylyl cyclase-associated protein 1	CAP1	23	60.2	0	323.3	1.06	1.06	1.05	1.07	1.01	1.06	1.04	1.03	1.01
Q01650	Large neutral amino acids transporter small subunit 1	SLC7A5	3	9.5	0	89.18	1.58	0.90	0.94	0.88	1.18	0.71	1.00	1.01	1.74
Q01813	ATP-dependent 6-phosphofructokinase, platelet	PFKP	33	56.1	0	323.3	0.97	0.98	0.96	1.02	1.01	1.05	0.98	1.08	1.03
Q01970	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-3	PLCB3	7	8.1	0	11.51	NaN	NaN	0.95	0.42	0.92	NaN	0.85	0.86	NaN
Q02790	Peptidyl-prolyl cis-trans isomerase FKBP4;Peptidyl-prolyl cis-trans isomerase FKBP4, N-terminally processed	FKBP4	15	46	0	70.57	0.81	0.83	1.21	1.09	1.07	1.17	0.69	0.84	0.51
Q02809	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1	PLOD1	11	22.3	0	14.53	0.58	0.70	0.68	NaN	0.62	NaN	NaN	1.06	1.12
Q02878	60S ribosomal protein L6	RPL6	13	45.1	0	139.6	0.99	1.00	0.96	0.99	0.97	0.97	0.99	0.95	0.98
Q03135	Caveolin-1;Caveolin	CAV1	3	39.9	0	167.3	1.08	1.11	1.08	1.15	1.01	1.17	0.86	0.89	0.90
Q03252	Lamin-B2	LMNB2	19	35.3	0	112.4	1.07	1.10	1.45	1.11	1.10	1.26	1.29	1.11	1.21
Q04446	1,4-alpha-glucan-branching enzyme	GBE1	17	32.1	0	126.4	1.09	1.09	0.95	0.96	1.36	1.59	1.00	0.85	1.04
Q04760	Lactoylglutathione lyase	GLO1	11	66.3	0	279.5	0.85	0.82	0.92	0.94	0.95	0.93	0.82	0.84	0.80
Q04837	Single-stranded DNA-binding protein, mitochondrial	SSBP1	6	47.3	0	113	1.13	1.17	1.22	1.37	1.15	1.16	0.73	0.74	0.81
Q04917	14-3-3 protein eta	YWHAH	13	61.4	0	323.3	0.77	0.86	0.90	0.85	0.87	0.94	0.80	0.83	0.84
Q04941	Proteolipid protein 2	PLP2	2	18.4	0	31.59	1.16	1.20	1.23	1.00	1.03	1.02	0.71	0.88	1.11
Q5T760	Serine/arginine-rich splicing factor 11	SRSF11	2	6.4	0	7.365	1.11	1.03	1.13	1.03	1.05	1.11	0.52	0.75	1.08
Q06124	Tyrosine-protein phosphatase non-receptor type 11	PTPN11	5	14.4	0	26.15	1.10	0.90	0.93	NaN	NaN	1.41	NaN	NaN	NaN
Q06210	Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1	GFPT1	19	37.1	0	175.3	0.76	0.94	0.97	0.84	0.88	0.85	0.92	0.93	1.07
Q06323	Proteasome activator complex subunit 1	PSME1	17	67.5	0	126.8	1.17	1.12	1.04	1.12	1.10	1.20	1.17	1.14	1.16
Q06481	Amyloid-like protein 2	APLP2	2	3.7	0	21.22	NaN	1.19	0.53	NaN	1.06	NaN	NaN	NaN	NaN
Q06830	Peroxiredoxin-1	PRDX1	15	77.4	0	323.3	0.96	0.95	0.98	1.03	1.02	1.02	0.98	0.94	0.95

Q07021	Complement component 1 Q subcomponent-binding protein, mitochondrial	C1QBP	4	22	0	202.1	1.09	1.24	1.02	1.07	1.00	1.03	0.99	1.05	1.15
Q07065	Cytoskeleton-associated protein	CKAP4	25	53	0	323.3	1.09	1.08	1.08	1.10	1.06	1.01	1.00	1.03	1.11
Q07666	KH domain-containing, RNA-binding, signal transduction-associated protein 1	KHDRBS1	6	16.7	0	124.2	0.92	0.99	0.92	1.38	0.93	1.02	NaN	NaN	0.84
Q07812	Apoptosis regulator BAX	BAX	6	40.6	0	42.87	1.04	NaN	0.68	1.03	1.63	0.96	0.54	NaN	0.76
Q5QP56	Bcl-2-like protein 1	BCL2L1	2	10.5	1E-03	2.21	0.96	1.33	NaN	NaN	NaN	1.39	NaN	NaN	0.89
Q07960	Rho GTPase-activating protein 1	ARHGAP1	9	33.5	0	50.74	0.97	0.97	1.04	0.77	0.85	0.89	1.88	1.02	1.08
Q08170	Serine/arginine-rich splicing factor 4	SRSF4	2	11.3	0	323.3	0.96	1.22	1.20	1.31	1.10	1.25	1.59	1.33	1.24
Q08209	Serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform;Serine/threonine-protein phosphatase	PPP3CA	7	18	0	16.17	0.44	NaN	0.49	0.64	0.88	NaN	1.06	NaN	0.53
Q08211	ATP-dependent RNA helicase A	DHX9	31	32.3	0	323.3	0.90	0.85	0.86	0.90	0.88	0.98	0.95	0.88	0.97
Q08380	Galectin-3-binding protein	LGALS3BP	7	15.9	0	15.55	0.78	0.73	0.93	0.84	0.92	0.86	0.82	0.71	1.53
Q08752	Peptidyl-prolyl cis-trans isomerase D	PPID	3	13.5	0	5.036	0.98	1.23	1.03	1.26	0.93	1.18	NaN	0.81	1.00
Q08945	FACT complex subunit SSRP1	SSRP1	15	29.3	0	116.6	0.73	0.55	0.84	0.98	0.99	0.74	0.98	1.20	0.92
Q08J23	tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	10	17.5	0	30.1	NaN	NaN	0.71	NaN	0.64	0.66	3.39	NaN	0.94
Q09161	Nuclear cap-binding protein subunit 1	NCBP1	3	5.6	5E-04	2.832	1.11	NaN	NaN	NaN	1.43	0.79	NaN	NaN	1.22
Q09666	Neuroblast differentiation-associated protein AHNAK	AHNAK	300	74.4	0	323.3	0.71	0.74	0.74	0.88	0.89	0.88	0.82	0.77	0.83
Q0VF96	Cingulin-like protein 1	CGNL1	3	2.2	0	3.818	1.16	1.01	1.06	0.94	1.05	0.86	1.32	1.26	1.23
Q10471	Polypeptide N-acetylgalactosaminyltransferase 2;Polypeptide N-acetylgalactosaminyltransferase 2 soluble form	GALNT2	4	11.4	0	13.76	1.12	1.03	1.59	NaN	1.23	1.16	NaN	NaN	1.17
Q10567	AP-1 complex subunit beta-1	AP1B1	3	21.4	0.007	1.649	NaN	NaN	NaN	1.00	NaN	NaN	1.65	1.39	NaN
Q12765	Secernin-1	SCRN1	12	34.3	0	33.96	0.85	0.87	0.94	0.98	1.14	1.09	0.94	0.71	0.85
Q12792	Twinfilin-1	TWF1	5	18	0	75.56	1.22	1.13	1.24	NaN	NaN	0.67	NaN	NaN	NaN
Q12797	Aspartyl/asparaginyl beta-hydroxylase	ASPH	5	13.3	0	203.2	0.98	0.91	1.27	0.88	1.01	0.94	0.89	0.92	1.33
Q12874	Splicing factor 3A subunit 3	SF3A3	9	21	0	25.11	0.88	1.06	0.99	0.90	0.90	1.13	1.38	0.86	0.98
Q12904	Aminoacyl tRNA synthase complex-interacting multifunctional protein 1;Endothelial monocyte-	AIMP1	13	54.2	0	124.1	1.04	0.94	0.98	1.06	0.99	1.07	0.48	NaN	0.83
Q12906	Interleukin enhancer-binding factor 3	ILF3	25	37.9	0	323.3	0.83	0.85	0.79	0.93	0.93	0.93	0.80	0.89	0.91
Q12931	Heat shock protein 75 kDa, mitochondrial	TRAP1	7	14.6	0	17.92	0.85	1.02	0.75	NaN	NaN	0.85	NaN	NaN	0.67

Q13011	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial	ECH1	6	36	0	34.88	0.99	1.06	1.10	0.90	1.00	1.12	NaN	1.01	1.13
Q13045	Protein flightless-1 homolog	FLII	8	9.2	0	18.21	1.13	1.20	1.18	1.04	0.97	0.71	2.09	2.31	1.24
Q13148	TAR DNA-binding protein 43	TARDBP	9	36.2	0	45.36	0.78	0.81	0.99	1.14	1.03	1.08	NaN	NaN	0.97
Q13151	Heterogeneous nuclear ribonucleoprotein A0	HNRNPA0	6	28.2	0	50.73	0.84	0.82	0.66	0.95	0.62	0.92	1.03	1.06	1.09
Q13155	Aminoacyl tRNA synthase complex-interacting multifunctional protein 2	AIMP2	7	28.8	0	45.71	NaN	0.82	1.32	NaN	0.87	1.20	NaN	NaN	0.96
Q13158	FAS-associated death domain protein	FADD	1	8.7	0	3.118	1.09	1.15	1.13	1.51	1.26	1.40	NaN	2.37	0.91
Q13162	Peroxiredoxin-4	PRDX4	9	53.9	0	85.96	1.01	0.97	0.98	1.03	1.07	1.09	1.18	1.09	1.09
Q13177	Serine/threonine-protein kinase PAK 2;PAK-2p27;PAK-2p34	PAK2	19	53.8	0	237.5	1.06	1.03	0.89	1.08	0.97	0.95	0.85	0.96	0.84
Q13185	Chromobox protein homolog 3	CBX3	5	58.5	0	309.9	0.86	0.80	0.81	1.06	0.89	0.86	1.05	0.81	0.77
Q13200	26S proteasome non-ATPase regulatory subunit 2	PSMD2	31	44.9	0	260.8	1.15	1.21	1.39	1.04	1.07	1.02	1.09	1.18	1.06
Q13242	Serine/arginine-rich splicing factor 9	SRSF9	5	23.5	0	31.28	1.61	1.10	1.02	1.07	1.26	0.89	1.60	1.07	1.40
Q13243	Serine/arginine-rich splicing factor 5	SRSF5	2	12.9	0.002	1.893	NaN	NaN	NaN	NaN	NaN	NaN	1.34	1.22	NaN
Q13247	Serine/arginine-rich splicing factor 6	SRSF6	2	18	1E-03	2.154	2.23	2.57	2.12	NaN	1.01	NaN	NaN	NaN	2.10
Q13263	Transcription intermediary factor 1-beta	TRIM28	16	33.4	0	127.3	1.02	1.08	1.00	0.90	1.01	1.12	0.69	0.76	0.92
Q13283	Ras GTPase-activating protein-binding protein 1	G3BP1	13	46.6	0	148.4	1.38	1.23	1.23	0.98	0.92	1.03	0.90	1.06	1.04
Q13347	Eukaryotic translation initiation factor 3 subunit I	EIF3I	10	55.4	0	172.7	1.08	1.00	1.01	1.24	1.01	1.02	1.39	1.00	0.91
Q13404	Ubiquitin-conjugating enzyme E2 variant 1	UBE2V1	6	58.5	0	46.56	1.19	1.12	1.19	1.02	1.04	1.12	1.02	1.02	1.05
Q13409	Cytoplasmic dynein 1 intermediate chain 2	DYNC1I2	6	31.2	0	323.3	0.89	1.04	0.68	0.82	0.67	0.82	0.83	0.90	1.06
Q13423	NAD(P) transhydrogenase, mitochondrial	NNT	15	18.8	0	98.23	0.90	0.86	0.80	0.83	0.74	0.93	0.90	0.79	0.90
Q13435	Splicing factor 3B subunit 2	SF3B2	18	25.7	0	91.05	1.21	0.73	0.90	1.05	1.02	1.04	1.07	0.95	0.68
Q13442	28 kDa heat- and acid-stable phosphoprotein	PDAP1	10	38.7	0	178.3	0.99	0.96	0.99	1.01	1.14	0.97	0.80	0.89	0.96
Q13492	Phosphatidylinositol-binding clathrin assembly protein	PICALM	7	16.4	0	25.95	1.07	0.94	0.90	1.07	1.19	0.89	1.56	1.08	0.69
Q13501	Sequestosome-1	SQSTM1	10	38.9	0	254.7	1.22	1.35	1.30	1.63	1.41	1.42	NaN	NaN	0.81
Q13526	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1	PIN1	5	55.8	0	12.33	0.67	0.64	0.71	0.82	0.94	0.68	0.78	0.89	0.66
Q13547	Histone deacetylase 1	HDAC1	4	19.9	0	8.918	0.27	0.79	0.66	0.87	0.94	0.97	NaN	NaN	0.81
Q13561	Dynactin subunit 2	DCTN2	13	47.1	0	194.5	0.90	0.95	0.95	1.05	0.95	0.98	0.96	1.12	1.04
Q13564	NEDD8-activating enzyme E1 regulatory subunit	NAE1	5	14	0	17.11	NaN	0.76	NaN	NaN	NaN	0.79	0.96	1.14	NaN

Q13573	SNW domain-containing protein	SNW1	4	15.1	0	5.545	0.84	NaN	0.67	NaN	NaN	NaN	NaN	NaN	NaN
Q13596	Sorting nexin-1	SNX1	4	13.6	0	45.19	1.10	1.02	1.21	0.92	0.86	1.00	0.77	1.18	1.20
Q13630	GDP-L-fucose synthase	TSTA3	4	15.3	0	6.267	NaN	0.88	1.21	NaN	0.79	0.91	NaN	1.44	1.29
Q13813	Spectrin alpha chain, non-erythrocytic 1	SPTAN1	3	66	0	323.3	0.74	0.75	0.77	0.79	0.82	0.78	0.93	0.92	0.94
Q13838	Spliceosome RNA helicase DDX39B	DDX39B	7	53.3	0	323.3	0.90	0.86	0.89	0.81	0.89	0.90	0.95	0.86	0.96
Q9BVA1	Tubulin beta-2B chain;Tubulin beta-2A chain	TUBB2B	3	57.8	0	16.04	0.72	0.56	0.59	0.75	0.65	0.74	NaN	NaN	0.82
Q13907	Isopentenyl-diphosphate Delta-isomerase 1	IDI1	6	45.8	0	21.18	0.67	NaN	0.53	NaN	1.47	NaN	NaN	NaN	NaN
Q14008	Cytoskeleton-associated protein	CKAP5	18	11.2	0	29.52	1.01	1.10	0.91	0.94	1.02	1.22	NaN	0.56	1.13
Q14011	Cold-inducible RNA-binding protein	CIRBP	3	26.7	0	47.97	2.31	1.57	0.62	NaN	NaN	1.05	NaN	NaN	1.48
Q14019	Coactosin-like protein	COTL1	11	66.2	0	167.5	1.08	1.04	1.04	1.00	0.99	1.00	1.01	1.00	0.99
Q14103	Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	3	39.7	0	323.3	0.91	0.92	0.86	0.91	0.90	0.91	0.77	0.82	0.86
Q14152	Eukaryotic translation initiation factor 3 subunit A	EIF3A	44	36.2	0	289.6	1.08	1.26	1.26	1.26	1.20	1.18	0.88	0.86	0.98
Q14204	Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	140	38.8	0	323.3	0.91	0.92	0.92	0.91	0.89	0.96	0.96	0.93	0.86
Q14232	Translation initiation factor eIF-2B subunit alpha	EIF2B1	4	16.1	0	2.982	0.69	0.58	0.56	NaN	0.59	NaN	0.87	NaN	1.56
Q14240	Eukaryotic initiation factor 4A-II;Eukaryotic initiation factor 4A-II, N-terminally processed	EIF4A2	7	44	0	15.29	0.83	NaN	NaN	1.06	0.53	NaN	NaN	NaN	NaN
Q14247	Src substrate cortactin	CTTN	23	49.5	0	207.8	1.03	0.89	1.04	0.99	1.12	1.07	1.33	1.16	1.04
Q14258	E3 ubiquitin/ISG15 ligase	TRIM25	19	37.6	0	89.08	0.79	0.93	1.03	0.86	0.69	1.01	1.23	1.04	0.90
Q14315	Filamin-C	FLNC	74	45.6	0	323.3	1.06	1.11	1.01	0.97	0.94	0.94	1.11	1.22	1.05
Q14320	Protein FAM50A;Protein	FAM50A	4	16.5	0	15.28	0.91	0.92	1.12	NaN	NaN	1.63	NaN	NaN	1.66
Q14344	Guanine nucleotide-binding protein subunit alpha-13	GNA13	2	5.3	0.008	1.589	NaN	1.02	1.38	NaN	NaN	NaN	NaN	NaN	NaN
Q5QPP3	UDP-glucose 4-epimerase	GALE	5	28.6	0	23.84	0.81	1.32	0.90	0.87	0.93	1.42	1.05	NaN	0.56
Q14444	Caprin-1	CAPRIN1	11	22.8	0	284.6	0.99	1.01	1.30	0.99	1.01	1.06	0.83	0.83	0.73
Q14498	RNA-binding protein 39	RBM39	11	30.8	0	124.6	1.25	1.42	1.46	0.78	1.31	1.24	0.78	0.74	0.89
Q14566	DNA replication licensing factor MCM6	MCM6	6	8.6	0	7.33	NaN	1.07	NaN	6.73	0.84	0.65	NaN	NaN	0.79
Q14573	Inositol 1,4,5-trisphosphate receptor type 3	ITPR3	13	8.9	0	35.28	0.80	0.97	0.81	0.67	0.75	0.70	NaN	0.85	0.95
Q14677	Clathrin interactor 1	CLINT1	2	4.8	0	6.117	NaN	NaN	NaN	NaN	NaN	0.75	2.04	NaN	1.29
Q14697	Neutral alpha-glucosidase AB	GANAB	38	47.6	0	323.3	1.01	0.96	1.00	0.94	1.06	0.98	1.00	0.97	1.02
Q14764	Major vault protein	MVP	24	37.4	0	126.8	0.74	0.66	0.67	0.72	0.84	0.94	0.81	0.69	1.03
Q14847	LIM and SH3 domain protein 1	LASP1	17	57.5	0	323.3	0.94	1.01	0.96	1.09	1.04	1.01	0.94	0.91	0.96
Q14974	Importin subunit beta-1	KPNB1	29	42.2	0	323.3	0.96	0.96	0.96	0.94	1.00	0.95	0.93	0.89	0.97
Q14978	Nucleolar and coiled-body phosphoprotein 1	NOLC1	9	13.3	0	25.46	0.95	0.85	0.89	0.79	1.22	1.06	0.79	0.75	0.89
Q14980	Nuclear mitotic apparatus protein	NUMA1	36	24.3	0	323.3	0.76	0.78	0.59	0.78	0.72	0.73	0.66	0.66	0.81

Q14CX7	N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	3	3.5	0.009	1.406	NaN	NaN	0.67	NaN	0.71	1.02	NaN	NaN	NaN
Q15008	26S proteasome non-ATPase regulatory subunit 6	PSMD6	10	29.3	0	136.8	1.10	1.00	1.15	1.11	0.93	1.09	1.06	1.09	1.00
Q15019	Septin-2	SEPT2	12	47.9	0	323.3	1.04	0.99	1.02	1.03	1.08	1.04	1.03	1.01	1.06
Q15021	Condensin complex subunit 1	NCAPD2	8	8.1	0	11	1.13	1.30	NaN	NaN	NaN	1.15	NaN	NaN	1.26
Q15029	116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	14	23.4	0	47.84	0.81	0.78	0.74	NaN	1.01	0.86	0.94	0.76	0.93
Q15046	Lysine--tRNA ligase	KARS	15	29	0	35.21	1.26	1.03	1.08	0.88	1.11	1.00	1.05	1.05	1.62
Q15056	Eukaryotic translation initiation factor 4H	EIF4H	13	45.6	0	284.7	1.17	1.05	1.23	1.12	1.10	1.14	1.11	0.98	0.87
Q15075	Early endosome antigen 1	EEA1	21	21.2	0	113.3	1.07	1.34	1.11	1.13	0.93	1.09	0.87	1.02	1.24
Q15084	Protein disulfide-isomerase A6	PDIA6	17	51.4	0	323.3	1.12	1.17	1.11	1.00	1.05	1.09	1.14	1.09	1.14
Q15102	Platelet-activating factor acetylhydrolase IB subunit	PAFAH1B3	7	49.8	0	323.3	1.03	0.93	0.93	1.05	0.91	0.87	1.00	1.02	0.89
Q15121	Astrocytic phosphoprotein PEA-15	PEA15	7	45.4	0	35.98	1.30	1.28	1.41	NaN	1.22	1.17	1.12	NaN	1.06
Q15125	3-beta-hydroxysteroid-Delta(8),Delta(7)-isomerase	EBP	3	16.5	0	196.3	0.90	1.11	1.25	0.86	0.82	0.78	0.91	1.05	1.20
Q15149	Plectin	PLEC	259	59	0	323.3	0.92	0.90	0.90	0.90	0.86	0.89	1.12	1.12	1.09
Q15181	Inorganic pyrophosphatase	PPA1	18	82	0	293.9	0.97	0.93	0.97	1.05	0.97	0.97	0.95	0.94	0.94
Q15185	Prostaglandin E synthase 3	PTGES3	7	46.2	0	186.2	1.31	1.29	1.30	1.24	1.01	1.42	1.06	1.23	1.17
Q15233	Non-POU domain-containing octamer-binding protein	NONO	21	53.9	0	122.4	0.90	0.88	0.90	0.92	0.97	1.00	0.88	0.88	0.83
Q15293	Reticulocalbin-1	RCN1	19	61.3	0	323.3	0.90	0.98	1.00	1.11	1.06	1.01	0.96	1.08	0.88
Q15363	Transmembrane emp24 domain-containing protein 2	TMED2	4	24.4	0	2.92	1.12	0.78	NaN	NaN	1.09	NaN	0.49	NaN	NaN
Q15365	Poly(rC)-binding protein 1	PCBP1	13	87.1	0	323.3	0.92	0.90	0.83	0.91	0.95	0.99	0.93	0.88	0.94
Q15366	Poly(rC)-binding protein 2	PCBP2	2	41.9	0	94	0.93	0.98	0.92	0.90	0.88	0.91	0.95	0.96	0.90
Q15382	GTP-binding protein Rheb	RHEB	6	28.8	0	40.27	0.79	0.76	0.78	0.89	0.89	0.88	0.61	0.88	0.69
Q15393	Splicing factor 3B subunit 3	SF3B3	9	8.4	0	9.23	0.88	0.85	0.96	0.96	0.87	1.17	1.10	0.97	0.88
Q15417	Calponin-3	CNN3	7	61.7	0	323.3	1.17	1.12	1.15	1.06	1.02	1.04	1.16	1.18	1.20
Q15424	Scaffold attachment factor B1	SAFB	9	24.3	0	223.6	1.02	0.93	1.03	0.93	1.12	1.17	0.83	2.66	1.09
Q15427	Splicing factor 3B subunit 4	SF3B4	5	20.3	0	31.36	0.66	0.87	NaN	NaN	NaN	0.88	NaN	NaN	1.04
Q15428	Splicing factor 3A subunit 2	SF3A2	5	16.8	0	323.3	0.83	0.91	0.99	1.06	0.96	0.89	NaN	1.39	1.03
Q15459	Splicing factor 3A subunit 1	SF3A1	14	23.8	0	159.5	0.90	1.00	0.92	1.69	1.15	0.90	0.85	1.58	0.85
Q15637	Splicing factor 1	SF1	10	20.2	0	51.5	1.12	1.17	1.19	1.03	1.17	1.06	1.01	1.07	0.88
Q15642	Cdc42-interacting protein 4	TRIP10	12	31.3	0	79.14	1.25	1.21	1.26	1.75	1.16	1.51	NaN	1.64	1.05
Q15645	Pachytene checkpoint protein 2 homolog	TRIP13	4	12	0	4.034	NaN	NaN	NaN	0.95	0.83	NaN	NaN	NaN	NaN
Q15691	Microtubule-associated protein RP/EB family member 1	MAPRE1	18	76.5	0	285.3	1.20	1.19	1.08	1.05	1.21	1.02	0.98	1.00	1.04
Q15717	ELAV-like protein 1	ELAVL1	12	45.7	0	255.3	1.00	0.92	0.99	0.84	0.92	0.94	1.02	0.80	0.94
Q15738	Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating	NSDHL	6	27.6	0	17.21	NaN	NaN	0.61	NaN	0.92	NaN	0.83	NaN	0.65
Q15758	Neutral amino acid transporter B(0);Amino acid transporter	SLC1A5	6	13.3	0	39.9	0.70	0.84	0.71	0.92	0.85	NaN	0.92	0.93	0.97

Q15785	Mitochondrial import receptor subunit TOM34	TOMM34	3	14.2	0	23.12	0.91	NaN	1.09	NaN	0.75	NaN	NaN	NaN	NaN
Q15819	Ubiquitin-conjugating enzyme E2 variant 2	UBE2V2	3	36.6	0.006	1.693	1.20	0.97	0.92	1.06	0.99	0.86	NaN	NaN	NaN
Q15836	Vesicle-associated membrane protein 3	VAMP3	3	46	0	214.8	NaN	1.07	NaN	1.25	NaN	1.07	0.88	0.94	1.42
Q15907	Ras-related protein Rab-11B	RAB11B	2	58.7	0	223.5	1.27	1.19	1.15	1.22	1.19	1.12	1.38	1.26	1.30
Q16186	Proteasomal ubiquitin receptor ADRM1	ADRM1	7	21.4	0	179.9	1.25	1.17	1.01	1.17	1.07	1.18	0.80	NaN	1.00
Q16222	UDP-N-acetylhexosamine pyrophosphorylase;UDP-N-acetylgalactosamine pyrophosphorylase;UDP-N-acetylglucosamine pyrophosphorylase	UAP1	9	25.9	0	23.39	1.23	1.23	1.42	1.17	0.90	1.36	NaN	1.23	1.24
Q16270	Insulin-like growth factor-binding protein 7	IGFBP7	7	39.7	0	223.2	1.98	1.93	2.34	1.06	1.29	1.55	2.16	2.56	2.62
Q16401	26S proteasome non-ATPase regulatory subunit 5	PSMD5	10	28.2	0	41.15	NaN	NaN	NaN	1.43	0.86	NaN	0.71	0.74	0.74
Q16531	DNA damage-binding protein 1	DDB1	20	22.5	0	227.3	0.83	0.71	0.84	0.86	0.89	0.90	0.98	0.85	0.99
Q16543	Hsp90 co-chaperone Cdc37;Hsp90 co-chaperone	CDC37	12	34.9	0	302.1	0.89	0.91	0.87	0.92	0.90	0.87	0.86	0.86	0.86
Q16658	Cdc37, N-terminally processed Fascin	FSCN1	5	14.6	0	5.275	0.60	1.09	0.72	NaN	0.97	0.59	NaN	0.90	0.87
Q16666	Gamma-interferon-inducible protein 16	IFI16	3	5.9	0	4.128	0.43	NaN	0.71	NaN	0.96	0.97	NaN	NaN	0.74
Q16698	2,4-dienoyl-CoA reductase, mitochondrial	DECR1	7	28.4	0	40.33	0.86	1.15	0.65	NaN	0.97	0.91	0.58	NaN	0.85
Q16706	Alpha-mannosidase 2	MAN2A1	2	3	0.001	2.695	1.02	1.02	0.90	NaN	NaN	1.29	NaN	NaN	NaN
Q16891	MICOS complex subunit MIC60	IMMT	24	43.1	0	236.6	1.01	0.91	1.05	1.00	0.93	0.94	0.91	1.09	0.99
Q1KMD3	Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	13	24.1	0	178	0.78	0.90	0.99	0.82	0.83	0.98	0.90	0.57	1.05
Q27J81	Inverted formin-2	INF2	7	10.1	0	35.48	NaN	0.92	1.18	NaN	1.36	NaN	NaN	1.10	NaN
Q2NKX8	DNA excision repair protein ERCC-6-like	ERCC6L	3	3.8	0.001	2.641	0.78	0.81	1.24	0.89	0.87	0.88	0.70	0.67	1.48
Q2TAY7	WD40 repeat-containing protein SMU1;WD40 repeat-containing protein SMU1, N-terminally processed	SMU1	2	3.9	0	4.617	0.97	1.04	0.92	0.73	0.99	0.99	0.76	0.85	1.17
Q32MZ4	Leucine-rich repeat flightless-interacting protein 1	LRRFIP1	10	19.3	0	100.6	1.20	1.00	0.97	0.75	1.05	0.75	0.91	NaN	1.52
Q32P28	Prolyl 3-hydroxylase 1	LEPRE1	9	17.7	0	14.09	NaN	1.12	1.09	1.05	0.86	0.92	NaN	0.98	0.72
Q32Q12	Nucleoside diphosphate kinase;Nucleoside diphosphate kinase B	NME1-NME2	1	71.9	0	323.3	0.97	0.98	0.98	1.00	1.00	1.00	1.02	1.03	1.01
Q3BDU5		LMNA	0	72.7	0	144.9	1.31	1.19	1.12	NaN	0.95	0.95	NaN	NaN	1.12
Q3ZCM7	Tubulin beta-8 chain	TUBB8	2	25.9	0	323.3	0.39	0.38	0.43	0.54	0.51	0.45	0.59	0.53	0.50

Q3ZCQ8	Mitochondrial import inner membrane translocase subunit TIM50	TIMM50	4	15.3	0	12.29	0.96	1.23	1.04	NaN	NaN	1.07	1.38	1.40	1.14
Q52LW3	Rho GTPase-activating protein	ARHGAP2	7	7.1	0	7.896	NaN	NaN	0.54	1.06	0.84	0.89	0.71	NaN	0.68
Q53GQ0	Very-long-chain 3-oxoacyl-CoA reductase	HSD17B12	7	34.6	0	87.16	0.75	0.85	1.14	NaN	1.00	0.70	NaN	0.52	0.81
Q562R1	Beta-actin-like protein 2	ACTBL2	2	25.3	0	14.68	1.04	0.99	NaN	1.00	0.99	0.89	1.09	1.08	1.13
Q56VL3	OCIA domain-containing protein	OCIAD2	3	19.5	0	4.814	0.67	0.87	0.67	NaN	NaN	0.68	NaN	NaN	1.21
Q58FF6	Putative heat shock protein HSP 90-beta 4	HSP90AB4	1	10.1	0	34	0.93	0.90	0.95	0.92	0.95	0.91	0.52	0.54	0.57
Q58FF8	Putative heat shock protein HSP 90-beta 2	HSP90AB2	1	27	0	56.76	0.92	0.87	0.91	0.88	0.98	0.91	0.70	NaN	0.70
Q5HYB6		DKFZp686	0	78.9	0	126	1.07	1.07	1.05	1.01	0.98	1.11	1.14	1.04	1.11
Q5JPT2	SH3 domain-containing kinase-binding protein 1	SH3KBP1	13	27.4	0	141.4	2.43	2.36	2.56	1.54	1.18	1.05	0.87	1.22	1.31
Q5QPL9	RNA-binding protein Raly	RALY	13	54.9	0	28.45	0.86	0.88	0.81	0.94	0.85	0.88	0.87	0.81	0.88
Q5R3I4	Tetratricopeptide repeat protein	TTC38	6	18.8	0	6.508	0.54	0.59	0.52	0.56	0.63	0.81	0.72	0.98	0.89
Q5STZ8		ABCF1	1	12.7	0	21.82	NaN	NaN	NaN	NaN	0.65	0.71	NaN	NaN	NaN
Q5T123	SH3 domain-binding glutamic acid-rich-like protein 3	SH3BGRL3	4	42	0	47.52	1.07	0.93	1.00	0.86	0.73	1.04	1.10	0.86	0.81
Q9Y6H1	Coiled-coil-helix-coiled-coil-helix domain-containing protein 2;Putative coiled-coil-helix-coiled-coil-helix domain-containing protein CHCHD2P9	CHCHD2	2	27.2	0	36.59	1.05	0.86	0.91	1.00	1.00	1.46	1.09	1.15	0.87
Q5T4S7	E3 ubiquitin-protein ligase UBR4	UBR4	8	2.7	0	37.88	1.03	0.85	1.06	NaN	NaN	0.96	NaN	NaN	0.78
Q5T6H7	Xaa-Pro aminopeptidase 1	XPNPEP1	6	19.9	0	18.73	0.57	0.75	0.80	0.85	0.91	0.66	0.74	0.91	0.90
Q5T6W2		HNRNPK	1	57.5	0	3.313	0.82	0.66	0.79	NaN	NaN	NaN	1.01	0.97	0.79
Q5TH30	Protein NDRG3	NDRG3	4	15.5	0	6.676	NaN	0.54	NaN	0.63	0.79	1.07	0.95	0.73	NaN
Q6DD88	Atlastin-3	ATL3	11	28.5	0	270.9	0.97	1.00	0.98	0.89	0.92	1.07	0.60	0.73	1.03
Q6DKJ4	Nucleoredoxin	NXN	10	31	0	21.56	0.82	0.80	NaN	NaN	0.87	NaN	NaN	0.71	NaN
Q6NUK1	Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24	24	53.7	0	126.5	1.57	1.71	1.67	1.19	1.20	1.20	1.64	1.20	1.41
Q6NZI2	Polymerase I and transcript release factor	PTRF	11	34.1	0	323.3	1.00	0.98	1.05	0.97	1.04	1.06	0.84	0.96	0.94
Q6P2Q9	Pre-mRNA-processing-splicing factor 8	PRPF8	23	13.1	0	39.36	0.64	0.77	0.92	0.78	0.85	0.90	0.80	0.95	1.07
Q6PKG0	La-related protein 1	LARP1	2	1.9	1E-03	2.148	0.97	0.78	0.73	0.70	NaN	NaN	0.67	0.75	0.46
Q6WKZ4	Rab11 family-interacting protein	RAB11FIP	1	0.6	0.009	1.431	1.36	1.41	1.54	1.19	1.29	1.37	NaN	1.87	1.92
Q6YN16	Hydroxysteroid dehydrogenase-like protein 2	HSDL2	8	25.1	0	74.97	1.39	1.17	1.33	NaN	1.17	1.27	0.98	1.72	1.52
Q6ZN40	Tropomyosin alpha-1 chain	TPM1	1	33.4	0	7.568	1.41	1.25	NaN	NaN	NaN	1.20	NaN	NaN	1.39
Q70J99	Protein unc-13 homolog D	UNC13D	5	8.3	0	24.62	NaN	0.45	0.49	NaN	NaN	0.65	0.95	NaN	1.36
Q70UQ0	Inhibitor of nuclear factor kappa-B kinase-interacting protein	IKBIP	4	12.3	0	7.237	NaN	NaN	1.61	0.58	1.50	1.31	NaN	NaN	NaN
Q71U36	Tubulin alpha-1A chain;Tubulin alpha-3E chain	TUBA1A	1	80.7	0	4.532	0.28	0.40	0.42	NaN	NaN	0.46	NaN	NaN	0.95

Q7KZF4	Staphylococcal nuclease domain-containing protein 1	SND1	34	50.7	0	323.3	0.91	0.95	0.85	0.88	0.89	0.85	1.08	0.98	0.97
Q7L1Q6	Basic leucine zipper and W2 domain-containing protein 1	BZW1	6	28.2	0	20.36	1.34	1.29	1.27	1.39	1.12	1.25	1.05	1.03	1.07
Q7L2H7	Eukaryotic translation initiation factor 3 subunit M	EIF3M	15	47.1	0	120	1.03	0.83	0.89	1.10	0.95	0.90	0.54	1.10	0.87
Q7L576	Cytoplasmic FMR1-interacting protein 1	CYFIP1	7	11.2	0	15.7	1.16	0.85	0.73	0.84	0.90	0.89	NaN	1.25	0.83
Q9H8S9	MOB kinase activator 1A;MOB kinase activator 1B	MOB1A	2	10.6	0	3.127	1.07	1.17	NaN	NaN	1.21	NaN	NaN	0.75	NaN
Q7RTV0	PHD finger-like domain-containing protein 5A	PHF5A	2	26.4	0	58.28	1.27	0.89	NaN	NaN	0.88	NaN	NaN	NaN	0.93
Q7Z406	Myosin-14	MYH14	3	6.1	0	7.572	1.08	0.96	0.91	1.13	1.19	1.53	1.11	1.30	1.23
Q7Z6Z7	E3 ubiquitin-protein ligase	HUWE1	41	13.3	0	245.6	0.97	0.97	0.94	1.00	0.99	0.98	0.90	0.96	0.82
Q7Z7H5	Transmembrane emp24 domain-containing protein 4	TMED4	3	20.3	0	18.54	0.87	0.99	1.07	1.37	0.98	0.97	NaN	NaN	0.93
Q86TI2	Dipeptidyl peptidase 9	DPP9	6	8.7	0	25.64	NaN	NaN	NaN	NaN	0.76	0.77	NaN	NaN	0.90
Q86UE4	Protein LYRIC	MTDH	10	21	0	164.3	0.75	0.98	1.26	0.97	1.04	1.00	0.97	0.89	0.86
Q86UP2	Kinectin	KTN1	32	27.7	0	142.3	1.09	1.17	1.14	1.20	1.15	1.33	0.82	1.01	1.34
Q86V81	THO complex subunit 4	ALYREF	5	36.2	0	41.14	0.92	0.90	NaN	1.00	0.86	NaN	0.86	0.87	0.81
Q86VP6	Cullin-associated NEDD8-dissociated protein 1	CAND1	19	18.3	0	39.33	1.03	0.96	0.99	0.96	1.02	1.01	0.91	0.91	1.09
Q86X55	Histone-arginine methyltransferase CARM1	CARM1	5	17.8	0	22.55	NaN	0.56	0.61	NaN	0.48	0.68	NaN	NaN	NaN
Q86Y56	Dynein assembly factor 5, axonemal	DNAAF5	3	4.4	0.001	2.085	NaN	NaN	0.92	0.76	0.68	NaN	NaN	NaN	1.00
Q8IUE6	Histone H2A type 2-B	HIST2H2AI	1	35.4	0	6.544	1.11	0.97	0.82	1.14	1.22	0.99	NaN	NaN	0.85
Q8IVD9	NudC domain-containing protein	NUDCD3	3	17.2	0	2.885	NaN	NaN	NaN	0.63	0.75	0.95	NaN	NaN	NaN
Q8IVF2	Protein AHNAK2	AHNAK2	4	5.3	0	5.874	0.91	0.82	0.99	0.44	NaN	0.77	1.17	1.37	0.99
Q8IVM0	Coiled-coil domain-containing protein 50	CCDC50	3	11.8	0	8.379	NaN	1.36	1.29	NaN	NaN	NaN	NaN	NaN	1.58
Q8IW52	SLIT and NTRK-like protein 4	SLITRK4	2	2.7	0.007	1.624	0.84	0.82	0.85	0.98	NaN	0.79	0.98	NaN	0.93
Q8IWE2	Protein NOXP20	FAM114A1	9	23.8	0	102	0.93	0.82	1.11	0.97	1.04	0.79	NaN	1.01	1.06
Q8IY81	pre-rRNA processing protein FTSJ3	FTSJ3	6	12.5	0	15.97	1.16	1.00	1.35	NaN	1.04	0.96	NaN	1.09	0.95
Q8N0X7	Spartin	SPG20	3	6.5	0	5.031	NaN	1.99	1.02	NaN	NaN	0.79	NaN	NaN	0.75
Q8N163	Cell cycle and apoptosis regulator protein 2	CCAR2	5	9	0	11.4	0.77	0.78	0.78	1.01	0.95	0.62	1.11	0.96	0.91
Q8N1F7	Nuclear pore complex protein Nup93	NUP93	10	19.4	0	43.76	NaN	NaN	NaN	0.60	0.92	0.87	0.93	0.87	1.07
Q8N1G4	Leucine-rich repeat-containing protein 47	LRRC47	9	19.7	0	30.36	0.68	1.09	0.73	1.07	1.12	0.73	1.26	1.28	0.91
Q8N3U4	Cohesin subunit SA-2	STAG2	2	3.2	0.001	2.673	NaN	NaN	0.76	NaN	0.93	1.06	NaN	NaN	0.76
Q8N4X5	Actin filament-associated protein 1-like 2	AFAP1L2	4	9.2	0	8.154	1.22	1.07	1.28	1.26	NaN	1.12	1.39	NaN	NaN
Q8N999	Uncharacterized protein	C12orf29	1	3.1	5E-04	2.843	1.26	1.19	1.34	1.03	1.18	1.15	1.17	NaN	1.15
Q8NBF2	NHL repeat-containing protein 2	NHLRC2	2	4.5	0	5.7	NaN	NaN	0.39	0.66	NaN	NaN	0.60	NaN	0.38

Q8NBJ5	Procollagen galactosyltransferase 1	COLGALT1	7	13.7	0	9.849	0.72	0.74	1.78	0.95	1.13	0.85	NaN	1.16	0.84
Q8NBS9	Thioredoxin domain-containing protein 5	TXNDC5	17	45.1	0	322.1	1.12	1.27	1.23	1.05	1.09	1.16	1.32	1.26	1.26
Q8NBX0	Saccharopine dehydrogenase-like oxidoreductase	SCCPDH	6	20.7	0	9.15	NaN	NaN	NaN	0.98	0.95	NaN	1.34	0.21	NaN
Q8NC51	Plasminogen activator inhibitor 1 RNA-binding protein	SERBP1	16	47.8	0	323.3	0.95	0.90	0.89	1.02	0.96	0.91	0.76	0.86	0.82
Q8NCW5	NAD(P)H-hydrate epimerase	APOA1BP	5	27.8	0	12.04	0.69	0.78	0.82	0.81	NaN	0.75	NaN	NaN	1.21
Q8NE71	ATP-binding cassette sub-family F member 1	ABCF1	9	17.2	0	26.38	0.90	0.80	0.93	0.89	0.89	0.80	NaN	0.62	0.83
Q8NE73	Ectonucleoside triphosphate diphosphohydrolase 4	ENTPD4	2	6.1	0.008	1.488	1.01	0.88	0.87	1.08	1.01	1.10	NaN	NaN	NaN
Q8NF37	Lysophosphatidylcholine acyltransferase 1	LPCAT1	4	11.4	0	10.86	0.75	NaN	NaN	0.78	1.95	0.92	NaN	1.03	1.05
Q8NFQ8	Torsin-1A-interacting protein 2	TOR1AIP2	1	5.3	5E-04	2.814	1.18	0.94	1.37	NaN	NaN	NaN	NaN	NaN	0.97
Q8NI27	THO complex subunit 2	THOC2	3	2.6	0	3.139	0.78	NaN	0.53	NaN	NaN	NaN	NaN	NaN	NaN
Q8TAT6	Nuclear protein localization protein 4 homolog	NPLOC4	8	17.6	0	23.4	1.07	1.32	1.24	0.76	0.84	0.92	1.65	1.25	1.15
Q8TBC4	NEDD8-activating enzyme E1 catalytic subunit	UBA3	6	25.3	0	12.9	NaN	1.74	NaN	NaN	0.97	0.88	NaN	NaN	NaN
Q8TBQ9	Protein kish-A	TMEM167A	1	12.5	0.002	1.914	1.15	1.14	1.11	NaN	1.24	1.10	NaN	1.35	1.36
Q8TCJ2	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B	STT3B	3	5.7	0	5.267	1.75	NaN	1.42	1.57	1.19	1.24	NaN	NaN	1.40
Q8TDN6	Ribosome biogenesis protein BRX1 homolog	BRIX1	2	5.9	1E-03	2.243	1.15	0.96	1.26	1.07	0.90	1.23	1.17	0.77	0.92
Q8TEA8	D-tyrosyl-tRNA(Tyr) deacylase 1;D-tyrosyl-tRNA(Tyr) deacylase	DTD1	2	20.6	0	109.7	0.94	0.86	0.97	0.81	0.88	0.88	NaN	NaN	0.87
Q8TEX9	Importin-4	IPO4	6	8	0	12.98	NaN	0.89	NaN	0.61	NaN	0.73	0.81	0.84	NaN
Q8TF65	PDZ domain-containing protein GIPC2	GIPC2	1	5.4	0	5.025	1.30	2.05	1.68	NaN	NaN	1.10	NaN	NaN	1.16
Q8WUH6	Transmembrane protein 263	TMEM263	2	35.3	0	11.01	NaN	NaN	1.68	1.00	0.96	1.07	NaN	NaN	NaN
Q8WUM4	Programmed cell death 6-interacting protein	PDCD6IP	33	46.4	0	252.7	0.95	0.92	0.92	0.87	0.91	0.94	0.87	0.90	1.00
Q8WVM8	Sec1 family domain-containing protein 1	SCFD1	5	11.4	0	10.06	NaN	0.96	0.98	NaN	NaN	0.93	NaN	NaN	0.68
Q8WW12	PEST proteolytic signal-containing nuclear protein	PCNP	6	42.1	0	43.13	1.24	1.18	1.09	0.83	1.20	1.08	1.19	1.10	1.26
Q8WWM7	Ataxin-2-like protein	ATXN2L	6	7.3	0	6.696	1.06	1.15	1.10	NaN	NaN	NaN	1.15	NaN	0.96
Q8WX92	Negative elongation factor B	NELFB	3	7.6	0	9.645	NaN	NaN	NaN	NaN	0.84	0.79	NaN	NaN	NaN
Q8WX93	Palladin	PALLD	8	8	0	7.941	0.74	0.26	0.96	NaN	0.94	0.38	NaN	NaN	0.55
Q8WXF1	Paraspeckle component 1	PSPC1	7	21.8	0	26.02	2.62	NaN	NaN	0.79	0.94	NaN	0.84	0.90	NaN
Q8WXX5	DnaJ homolog subfamily C member 9	DNAJC9	9	45.8	0	32.93	0.71	0.93	0.82	0.93	0.90	0.62	NaN	0.80	0.88
Q92504	Zinc transporter SLC39A7	SLC39A7	2	5.3	0	6.335	1.06	1.02	NaN	0.84	1.01	0.46	NaN	1.02	1.10

Q92520	Protein FAM3C	FAM3C	7	34.8	0	24.79	0.98	0.79	0.96	0.95	0.98	1.14	0.90	0.55	0.71
Q92597	Protein NDRG1	NDRG1	9	44.7	0	226.7	1.00	0.90	0.93	1.18	1.40	1.40	0.65	1.04	1.14
Q92598	Heat shock protein 105 kDa	HSPH1	32	51.9	0	277.9	1.97	1.66	1.92	1.68	1.93	1.93	0.94	0.75	0.83
Q92616	Translational activator GCN1	GCN1L1	30	15	0	52.27	0.91	0.92	0.87	0.89	0.86	0.89	1.06	0.94	0.89
Q92688	Acidic leucine-rich nuclear phosphoprotein 32 family member B	ANP32B	6	31.9	0	22.2	0.82	0.99	0.91	0.81	0.95	0.98	0.95	0.89	0.97
Q92734	Protein TFG	TFG	6	29.5	0	16.8	NaN	NaN	NaN	1.44	1.23	1.37	NaN	NaN	NaN
Q92743	Serine protease HTRA1	HTRA1	6	17.3	0	99.7	1.16	2.14	1.12	NaN	1.52	1.21	1.40	NaN	0.59
Q92769	Histone deacetylase 2	HDAC2	2	10.9	0.001	2.742	0.80	0.67	0.78	NaN	NaN	NaN	NaN	NaN	0.75
Q92804	TATA-binding protein-associated factor 2N	TAF15	7	23.6	0	323.3	0.95	0.95	1.02	1.06	0.93	0.85	1.06	0.94	0.97
Q92890	Ubiquitin fusion degradation protein 1 homolog	UFD1L	3	12.4	0	6.623	NaN	NaN	NaN	NaN	0.82	0.99	NaN	NaN	NaN
Q92900	Regulator of nonsense transcripts 1	UPF1	14	15.2	0	35.09	1.18	1.17	1.24	1.13	1.12	1.15	0.96	1.02	0.99
Q92905	COP9 signalosome complex subunit 5	COPS5	1	4.5	0	3.54	0.54	0.54	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Q92973	Transportin-1	TNPO1	14	27.6	0	162.2	1.23	1.07	1.05	1.03	0.99	1.01	1.07	1.05	0.89
Q93008	Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	9	5.1	0	10.16	0.64	0.96	1.63	1.08	1.18	1.12	NaN	1.43	0.86
Q969E4	Transcription elongation factor A protein-like 3	TCEAL3	1	12	0	22.63	0.99	0.83	1.05	NaN	NaN	NaN	0.89	NaN	1.00
Q969G5	Protein kinase C delta-binding protein	PRKCDBP	4	18.8	0	5.618	1.33	NaN	1.09	NaN	1.22	1.58	NaN	NaN	0.80
Q969H8	Myeloid-derived growth factor	MYDGF	4	27.2	0	51.99	1.07	1.07	1.10	1.02	0.97	0.88	1.15	1.06	0.84
Q969U7	Proteasome assembly chaperone 2	PSMG2	4	17.4	0	3.592	0.74	NaN	0.74	0.88	0.63	0.87	1.64	0.65	1.07
Q96A49	Synapse-associated protein 1	SYAP1	3	11.1	0	20.85	NaN	NaN	0.87	0.61	3.60	0.94	1.02	0.64	0.90
Q96AG4	Leucine-rich repeat-containing protein 59	LRRC59	10	42.7	0	146.5	1.10	1.05	1.06	1.06	0.95	1.03	0.98	0.89	1.07
Q96B36	Proline-rich AKT1 substrate 1	AKT1S1	2	11.7	0	3.99	NaN	NaN	1.04	0.57	NaN	0.86	0.84	0.74	0.85
Q9NVJ2	ADP-ribosylation factor-like protein 8B;ADP-ribosylation factor-like protein 8A	ARL8B	2	14	0	9.157	1.21	0.96	0.92	NaN	NaN	1.03	NaN	NaN	0.78
Q96C19	EF-hand domain-containing protein D2	EFHD2	11	42.5	0	124.5	1.18	0.98	1.15	1.26	1.20	1.01	1.24	1.06	1.04
Q96C90	Protein phosphatase 1 regulatory subunit 14B	PPP1R14B	3	48.3	0	51.71	1.14	1.07	1.12	0.75	0.87	0.86	1.35	1.13	1.22
Q96CT7	Coiled-coil domain-containing protein 124	CCDC124	6	30	0	16.77	1.07	1.56	0.95	NaN	1.37	1.18	0.63	NaN	0.92
Q96CV9	Optineurin	OPTN	5	14.6	0	29.42	NaN	0.97	0.98	NaN	1.06	1.01	NaN	NaN	0.93
Q96CX2	BTB/POZ domain-containing protein KCTD12	KCTD12	3	11.4	0	14.39	NaN	NaN	NaN	0.83	NaN	0.99	NaN	NaN	NaN
Q96D71	RalBP1-associated Eps domain-containing protein 1	REPS1	4	5.5	0.001	2.366	1.27	NaN	NaN	NaN	1.43	NaN	0.50	1.62	1.28

Q96DG6	Carboxymethylenebutenolidase homolog	CMBL	4	20.8	0	5.456	1.06	0.92	0.71	NaN	0.90	0.78	0.73	0.72	0.50
Q96EL3	39S ribosomal protein L53, mitochondrial	MRPL53	1	13.4	1E-03	2.269	1.08	0.72	1.08	NaN	NaN	NaN	NaN	NaN	1.03
Q96FJ2	Dynein light chain 2, cytoplasmic	DYNLL2	1	49.4	0	14.34	0.83	NaN	NaN	1.01	0.78	0.90	NaN	NaN	NaN
Q96FQ6	Protein S100-A16	S100A16	6	54.4	0	14.67	1.83	1.70	1.72	NaN	NaN	1.39	NaN	0.33	1.70
Q96G03	Phosphoglucomutase-2	PGM2	9	20.1	0	118.8	0.98	0.90	1.46	1.13	0.77	0.91	NaN	1.48	0.84
Q96HC4	PDZ and LIM domain protein 5	PDLIM5	8	19.5	0	17.45	1.15	1.16	1.25	1.43	1.40	1.34	1.08	1.07	0.98
Q96HE7	ERO1-like protein alpha	ERO1L	16	50.2	0	199.2	1.27	1.09	1.22	1.04	1.30	1.28	1.23	1.19	1.19
Q96HS1	Serine/threonine-protein phosphatase PGAM5, mitochondrial	PGAM5	2	6.6	0	6.559	0.95	1.05	1.29	1.13	NaN	1.12	1.16	1.09	0.95
Q96I24	Far upstream element-binding protein 3	FUBP3	6	14.5	0	5.955	0.86	NaN	NaN	3.55	NaN	0.80	NaN	1.99	NaN
Q96I99	Succinyl-CoA ligase [GDP-forming] subunit beta,	SUCLG2	12	39.4	0	41.82	0.96	0.96	1.08	NaN	0.99	0.94	NaN	NaN	0.93
Q96IU4	Alpha/beta hydrolase domain-containing protein 14B	ABHD14B	5	31.4	0	10.08	0.88	NaN	0.80	1.47	1.00	0.75	0.97	2.10	1.15
Q96IZ0	PRKC apoptosis WT1 regulator protein	PAWR	8	41.2	0	183.4	1.42	1.17	1.30	1.23	1.05	0.89	1.04	0.92	1.14
Q96K17	Transcription factor BTF3 homolog 4;Transcription factor	BTF3L4	2	36.7	0	41.8	0.58	0.86	0.45	1.22	1.40	1.33	1.00	0.97	NaN
Q96KP4	Cytosolic non-specific	CNDP2	12	39.6	0	73.86	0.90	0.94	0.88	0.71	1.00	0.88	NaN	0.71	0.88
Q96N66	Lysophospholipid acyltransferase 7	MBOAT7	8	21.2	0	217.8	0.81	0.87	0.98	0.87	0.88	0.86	1.33	1.00	0.94
Q96P70	Importin-9	IPO9	7	9.6	0	34.6	1.03	0.92	NaN	NaN	1.04	NaN	NaN	NaN	1.01
Q96PK6	RNA-binding protein 14	RBM14	3	5.7	0	7.67	1.47	NaN	NaN	0.82	NaN	0.84	NaN	NaN	1.05
Q96QK1	Vacuolar protein sorting-associated protein 35	VPS35	17	26.6	0	92.16	1.21	1.20	1.16	1.02	1.05	1.00	1.06	1.41	1.21
Q96RS6	NudC domain-containing protein	NUDCD1	11	24.4	0	41.26	1.06	0.84	0.91	0.93	0.95	0.92	NaN	NaN	0.92
Q96T51	RUN and FYVE domain-containing protein 1	RUFY1	4	11.7	0	21.31	NaN	0.90	1.10	NaN	1.35	0.91	1.52	1.54	1.47
Q96T76	MMS19 nucleotide excision repair protein homolog	MMS19	5	7.1	0	5.006	0.39	NaN	2.36	NaN	NaN	NaN	NaN	NaN	NaN
Q96TA1	Niban-like protein 1	FAM129B	22	42	0	171	1.07	1.16	1.09	0.93	1.11	0.96	1.19	1.12	0.96
Q99426	Tubulin-folding cofactor B	TBCB	7	38.9	0	26.2	0.93	0.94	0.95	NaN	0.93	0.88	1.19	NaN	0.92
Q99436	Proteasome subunit beta type-7;Proteasome subunit beta type	PSMB7	6	22.7	0	23.52	1.14	1.34	NaN	1.21	1.34	1.37	1.42	1.15	0.98
Q99447	Ethanolamine-phosphate cytidylyltransferase	PCYT2	3	10.3	0	42.53	0.61	0.59	0.78	0.79	NaN	NaN	NaN	0.68	0.70
Q99459	Cell division cycle 5-like protein	CDC5L	6	11.1	0	5.361	NaN	0.80	1.22	0.60	0.69	NaN	NaN	NaN	NaN
Q99460	26S proteasome non-ATPase regulatory subunit 1	PSMD1	21	29.4	0	178.6	0.99	0.96	1.08	1.14	1.06	1.37	0.81	0.96	0.93
Q99471	Prefoldin subunit 5	PFDN5	7	59.7	0	267.6	0.96	0.80	0.90	0.74	0.99	0.93	0.62	0.78	0.83
Q99497	Protein deglycase DJ-1	PARK7	14	79.9	0	323.3	1.02	1.04	0.99	1.08	1.07	1.07	1.00	1.02	1.05
Q99536	Synaptic vesicle membrane protein VAT-1 homolog	VAT1	12	43.3	0	108.8	0.67	0.75	0.79	0.88	0.95	0.80	0.77	0.73	0.71

Q99584	Protein S100-A13	S100A13	7	55.1	0	45.64	1.13	1.11	1.07	1.06	1.07	1.22	1.09	1.12	1.30
Q99613	Eukaryotic translation initiation factor 3 subunit C;Eukaryotic translation initiation factor 3 subunit C-like protein	EIF3C	21	27.5	0	120.2	1.17	1.24	1.05	0.93	1.03	1.38	0.86	0.96	1.03
Q99614	Tetratricopeptide repeat protein 1	TTC1	4	14.7	0	3.972	NaN	NaN	NaN	1.09	NaN	0.85	NaN	NaN	0.85
Q99615	DnaJ homolog subfamily C member 7	DNAJC7	5	12.8	0	5.994	1.51	1.31	1.66	NaN	1.01	1.33	NaN	NaN	1.40
Q99714	3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	8	49.4	0	111.2	0.98	0.96	0.98	1.18	0.97	1.11	1.22	0.98	0.93
Q99733	Nucleosome assembly protein 1-like 4	NAP1L4	7	32	0	146.5	0.84	1.07	1.02	1.06	0.85	0.99	0.85	0.88	1.11
Q99805	Transmembrane 9 superfamily member 2	TM9SF2	1	2.1	0.009	1.413	NaN	1.08	NaN	NaN	0.66	1.03	NaN	NaN	0.97
Q99829	Copine-1	CPNE1	18	37.1	0	86.01	1.02	0.92	0.92	0.91	0.91	0.89	1.03	1.13	1.09
Q99832	T-complex protein 1 subunit eta	CCT7	24	58.7	0	323.3	1.04	1.07	1.08	1.04	1.03	1.08	0.93	0.99	0.93
Q99961	Endophilin-A2	SH3GL1	10	32.6	0	27.16	NaN	NaN	1.14	0.86	0.84	0.95	0.89	0.93	NaN
Q9BPX3	Condensin complex subunit 3	NCAPG	5	6.6	0	4.415	NaN	1.02	0.89	NaN	1.09	NaN	NaN	NaN	0.59
Q9BPX5	Actin-related protein 2/3 complex subunit 5-like protein	ARPC5L	4	58.8	0	13.7	1.19	1.07	1.29	1.05	0.97	1.26	0.96	0.95	1.06
Q9BQG0	Myb-binding protein 1A	MYBBP1A	14	16	0	46.76	0.97	1.05	0.96	0.78	0.91	1.15	1.17	0.71	1.13
Q9BR76	Coronin-1B	CORO1B	9	27.4	0	40.08	1.16	NaN	0.78	0.71	1.03	1.19	1.05	0.72	0.81
Q9BRA2	Thioredoxin domain-containing protein 17	TXNDC17	5	43.1	0	39.19	1.18	1.11	1.19	1.11	1.08	1.02	1.23	1.18	1.20
Q9BRX8	Redox-regulatory protein FAM213A	FAM213A	3	15.7	0.004	1.755	0.97	0.89	0.88	0.86	0.67	1.06	NaN	NaN	NaN
Q9BS26	Endoplasmic reticulum resident protein 44	ERP44	7	20.9	0	39.01	1.38	1.96	1.49	NaN	1.17	1.36	NaN	NaN	1.19
Q9BSJ8	Extended synaptotagmin-1	ESYT1	18	22.1	0	154.8	0.83	0.83	0.92	0.90	0.96	0.91	0.91	0.92	1.00
Q9BT78	COP9 signalosome complex subunit 4	COPS4	5	18.7	0	5.045	NaN	1.01	NaN	6.46	0.56	1.13	NaN	NaN	NaN
Q9BTT0	Acidic leucine-rich nuclear phosphoprotein 32 family member E	ANP32E	5	24.6	0	162.2	1.04	1.23	0.81	0.73	0.85	1.08	NaN	1.20	1.17
Q9BTV4	Transmembrane protein 43	TMEM43	7	23.8	0	62.33	0.99	0.85	NaN	1.00	0.89	1.06	NaN	NaN	1.10
Q9BUF5	Tubulin beta-6 chain	TUBB6	8	59.9	0	304.9	0.60	1.01	0.76	0.75	0.67	0.63	NaN	1.07	1.15
Q9BV40	Vesicle-associated membrane protein 8	VAMP8	4	45	0	12.99	0.72	0.68	0.76	0.69	0.90	0.77	0.58	0.58	0.87
Q9BV86	N-terminal Xaa-Pro-Lys N-methyltransferase 1;N-terminal Xaa-Pro-Lys N-methyltransferase 1, N-terminally processed	NTMT1	2	9.4	1E-03	2.167	0.94	1.08	1.22	0.99	0.93	0.80	1.03	0.96	1.05
Q9BVC6	Transmembrane protein 109	TMEM109	3	12.3	0	5.785	0.97	1.08	0.98	0.99	1.26	1.31	1.60	1.23	0.90
Q9BVG4	Protein PBDC1	PBDC1	4	21.9	0	3.377	0.70	0.97	NaN	NaN	1.05	0.57	1.16	1.03	0.77
Q9BVK6	Transmembrane emp24 domain-containing protein 9	TMED9	3	15.7	0	96.99	1.46	1.17	1.06	1.03	1.39	1.27	1.77	1.37	1.36

Q9BW60	Elongation of very long chain fatty acids protein 1	ELOVL1	1	4.3	0	13.64	0.72	NaN	NaN	0.79	0.71	0.99	NaN	NaN	NaN
Q9BWD1	Acetyl-CoA acetyltransferase, cytosolic	ACAT2	12	50.6	0	323.3	0.74	0.74	0.66	0.80	0.87	0.82	0.98	0.99	0.98
Q9BX68	Histidine triad nucleotide-binding protein 2, mitochondrial	HINT2	2	21.5	0	4.774	0.98	NaN	1.19	0.73	1.01	NaN	NaN	NaN	NaN
Q9BXJ9	N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	6	8.3	0	24.1	0.48	NaN	NaN	0.93	1.12	0.94	NaN	0.82	0.66
Q9BXP5	Serrate RNA effector molecule homolog	SRRT	6	10.4	0	9.477	0.87	0.89	NaN	1.25	0.90	1.02	0.68	1.31	1.04
Q9BY32	Inosine triphosphate pyrophosphatase	ITPA	5	38.7	0	20.73	1.12	0.83	0.82	NaN	0.68	0.98	NaN	NaN	1.36
Q9BZE4	Nucleolar GTP-binding protein 1	GTPBP4	3	7.4	0	5.088	NaN	0.51	0.50	NaN	NaN	NaN	NaN	NaN	NaN
Q9BZL1	Ubiquitin-like protein 5	UBL5	2	28.8	0.002	1.903	0.74	NaN	0.61	NaN	1.38	2.74	NaN	NaN	0.85
Q9BZQ8	Protein Niban	FAM129A	5	7.8	0	4.743	1.11	NaN	1.07	NaN	NaN	1.15	NaN	NaN	0.99
Q9C002	Normal mucosa of esophagus-specific gene 1 protein	NMES1	2	32.5	0	4.77	1.05	0.92	0.87	1.00	0.59	0.84	1.98	1.52	1.09
Q9C0C2	182 kDa tankyrase-1-binding protein	TNKS1BP1	6	5.1	0	6.961	0.80	1.22	NaN	1.11	NaN	NaN	NaN	1.23	NaN
Q9GZN8	UPF0687 protein C20orf27	C20orf27	2	13.8	0.008	1.517	1.11	0.93	NaN	1.05	NaN	1.22	NaN	NaN	0.87
Q9GZP8	Immortalization up-regulated protein	IMUP	2	17	0	12.69	0.82	NaN	1.03	NaN	NaN	0.87	NaN	NaN	NaN
Q9H074	Polyadenylate-binding protein-interacting protein 1	PAIP1	3	13.4	0	4.676	1.32	NaN	1.27	1.12	1.48	1.06	NaN	NaN	NaN
Q9H0B6	Kinesin light chain 2;Kinesin light chain 4	KLC2	2	7.7	0	3.969	0.93	1.31	1.11	NaN	1.82	1.27	NaN	NaN	1.29
Q9H0D6	5-3 exoribonuclease 2	XRN2	7	12.4	0	13.64	1.26	NaN	0.92	NaN	1.27	1.52	1.27	1.68	1.36
Q9H0U4	Ras-related protein Rab-1B	RAB1B	3	67.7	0	42.7	0.73	0.84	0.82	1.02	1.12	0.99	0.56	0.62	0.67
Q9H1E3	Nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	NUCKS1	3	13.2	0	8.121	0.55	0.58	0.59	0.69	0.88	0.69	0.97	1.14	1.10
Q9H223	EH domain-containing protein 4	EHD4	5	14	0	14.2	0.79	NaN	NaN	NaN	NaN	NaN	1.32	1.48	NaN
Q9H307	Pinin	PNN	7	14.1	0	10.58	NaN	NaN	NaN	1.14	NaN	NaN	1.00	1.38	NaN
Q9H3H3	UPF0696 protein C11orf68	C11orf68	5	19.5	0	6.508	1.06	NaN	NaN	0.75	NaN	1.01	0.79	1.68	0.69
Q9H3K6	BolA-like protein 2	BOLA2	5	72.1	0	23.71	1.22	1.18	1.19	1.25	1.20	1.04	1.14	NaN	1.20
Q9H3N1	Thioredoxin-related transmembrane protein 1	TMX1	6	23.6	0	13.87	1.18	1.21	1.41	1.24	1.21	1.26	1.72	1.12	1.17
Q9H3P7	Golgi resident protein GCP60	ACBD3	4	14	0	15.6	NaN	1.73	NaN	NaN	1.17	1.35	0.76	NaN	0.89
Q9H444	Charged multivesicular body protein 4b	CHMP4B	6	33.9	0	244.6	1.47	1.26	1.26	1.19	1.21	1.01	1.26	0.97	1.07
Q9H488	GDP-fucose protein O-fucosyltransferase 1	POFUT1	5	23.7	0	18.73	1.13	1.33	1.22	1.01	1.34	1.31	NaN	NaN	0.90
Q9H4A4	Aminopeptidase B	RNPEP	14	28.8	0	186.1	0.97	1.31	1.28	NaN	NaN	NaN	1.21	1.11	1.42
Q9H4L5	Oxysterol-binding protein-related protein 3	OSBPL3	10	16	0	41.37	0.93	1.00	1.06	NaN	NaN	0.96	0.80	NaN	0.91
Q9H4M9	EH domain-containing protein 1	EHD1	17	51.3	0	258	0.92	0.98	0.89	0.96	0.97	1.05	1.03	0.92	0.93

Q9H6S3	Epidermal growth factor receptor kinase substrate 8-like protein 2	EPS8L2	15	36.6	0	307.5	1.05	0.87	0.85	0.89	0.78	0.93	NaN	NaN	1.10
Q9H993	Protein-glutamate O-methyltransferase	ARMT1	6	21.8	0	30.22	1.05	1.12	0.96	NaN	0.99	1.18	NaN	1.12	1.13
Q9H9B4	Sideroflexin-1	SFXN1	7	36.6	0	19.15	0.80	0.98	0.67	0.99	1.66	0.91	0.49	0.53	1.02
Q9H9H4	Vacuolar protein sorting-associated protein 37B	VPS37B	2	10.9	0	4.058	NaN	0.40	0.61	NaN	NaN	NaN	NaN	NaN	NaN
Q9HAV4	Exportin-5	XPO5	9	10.6	0	26.49	0.86	0.80	0.77	1.14	NaN	0.97	1.03	1.01	1.12
Q9HAV7	GrpE protein homolog 1, mitochondrial	GRPEL1	3	15.2	0	5.862	1.72	1.46	1.24	NaN	0.82	1.11	0.77	NaN	0.97
Q9HB71	Calcyclin-binding protein	CACYBP	20	76.3	0	206.3	1.20	1.33	1.24	1.26	1.13	1.17	0.81	0.84	1.06
Q9HC07	Transmembrane protein 165	TMEM165	4	20.4	0	6.481	1.02	0.75	0.99	NaN	NaN	1.06	NaN	NaN	NaN
Q9HDC9	Adipocyte plasma membrane-associated protein	APMAP	12	40.6	0	84.43	0.92	0.88	0.96	1.00	1.06	0.95	0.96	0.89	0.78
Q9NP97	Dynein light chain roadblock-type 1;Dynein light chain roadblock-type 2	DYNLRB1	6	83.3	0	32.15	1.01	1.23	0.90	0.61	NaN	1.12	NaN	NaN	1.19
Q9NPQ8	Synembryn-A	RIC8A	6	13.9	0	20.89	0.81	1.01	NaN	NaN	NaN	0.94	NaN	NaN	0.60
Q9NQ50	39S ribosomal protein L40, mitochondrial	MRPL40	1	7.8	0.002	1.983	NaN	0.81	1.13	NaN	NaN	NaN	NaN	NaN	NaN
Q9NQC3	Reticulon-4	RTN4	2	14.8	0	323.3	1.12	0.97	0.98	0.98	1.25	1.10	0.87	1.06	1.02
Q9NQG5	Regulation of nuclear pre-mRNA domain-containing protein 1B	RPRD1B	5	22.7	0	36.25	1.22	1.03	NaN	NaN	1.21	1.09	NaN	NaN	0.95
Q9NQR4	Omega-amidase NIT2	NIT2	5	21	0	19.37	1.81	NaN	NaN	NaN	NaN	NaN	1.51	NaN	1.69
Q9NQW6	Actin-binding protein anillin	ANLN	15	16.5	0	104.1	0.81	0.99	1.03	NaN	1.53	1.50	NaN	NaN	0.72
Q9NR12	PDZ and LIM domain protein 7	PDLIM7	7	17.3	0	6.777	NaN	NaN	3.16	NaN	0.99	0.89	NaN	NaN	2.03
Q9NR30	Nucleolar RNA helicase 2	DDX21	6	12.4	0	53.19	NaN	NaN	NaN	NaN	1.39	1.01	NaN	0.60	0.96
Q9NR31	GTP-binding protein SAR1a	SAR1A	7	42.9	0	47.6	1.11	0.69	0.79	1.05	1.18	1.02	0.97	1.07	0.92
Q9NR45	Sialic acid synthase	NANS	9	36.5	0	99.79	0.95	0.84	0.80	1.41	1.25	1.11	1.00	0.97	0.87
Q9NRN7	L-aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase	AASDHPP	3	12.6	0	37.1	0.80	NaN	0.43	0.74	0.91	0.91	0.87	0.94	0.83
Q9NRX4	14 kDa phosphohistidine phosphatase	PHPT1	3	37.6	0	59.16	1.16	1.15	1.19	1.10	1.12	1.04	1.20	0.96	1.01
Q9NS69	Mitochondrial import receptor subunit TOM22 homolog	TOMM22	5	66.2	0	31.81	0.90	0.75	0.94	0.68	1.02	0.97	NaN	0.40	0.72
Q9NSD9	Phenylalanine--tRNA ligase beta subunit	FARSB	9	15.4	0	21.1	0.81	0.94	0.98	0.93	1.03	0.93	0.64	0.92	0.99
Q9NSE4	Isoleucine--tRNA ligase, mitochondrial	IARS2	15	20.3	0	26.7	0.95	0.76	0.70	1.04	0.88	0.85	NaN	NaN	0.92
Q9NTZ6	RNA-binding protein 12	RBM12	2	2.4	0.008	1.531	NaN	2.03	NaN	1.01	0.97	1.12	2.03	NaN	0.70
Q9NUQ6	SPATS2-like protein	SPATS2L	9	25.8	0	31.94	1.08	0.56	0.65	0.59	0.54	0.41	0.96	0.81	0.77
Q9NUQ9	Protein FAM49B	FAM49B	9	45.4	0	53.41	1.22	1.11	1.25	1.00	0.98	1.14	0.72	0.78	1.24
Q9NVI7	ATPase family AAA domain-containing protein 3A	ATAD3A	9	18.5	0	49.45	1.30	0.89	1.67	1.32	1.22	1.16	1.10	1.12	0.62
Q9NVZ3	Adaptin ear-binding coat-associated protein 2	NECAP2	4	26.6	0	11.47	1.45	1.00	NaN	NaN	1.03	1.26	NaN	NaN	0.87

Q9NWV4	UPF0587 protein C1orf123	C1orf123	4	40	0	17.26	1.14	0.82	1.14	0.61	0.95	NaN	NaN	1.05	1.50
Q9NX40	OCIA domain-containing protein	OCIAD1	2	11.4	0	8.876	NaN	0.77	NaN	NaN	1.01	1.32	NaN	NaN	NaN
Q9NXG2	THUMP domain-containing protein 1	THUMPD1	1	4.5	0	4.405	0.73	0.94	1.09	0.76	NaN	NaN	0.77	NaN	1.07
Q9NY12	H/ACA ribonucleoprotein complex subunit 1	GAR1	1	8.3	0	5.417	NaN	0.97	0.98	NaN	0.95	0.92	0.95	1.00	NaN
Q9NYL9	Tropomodulin-3	TMOD3	12	52	0	116.8	1.09	0.89	0.96	1.19	0.91	1.15	NaN	1.29	1.16
Q9NYU2	UDP-glucose:glycoprotein glucosyltransferase 1	UGGT1	4	3.7	0	3.096	0.85	1.08	0.99	NaN	NaN	0.98	NaN	NaN	0.58
Q9NZ01	Very-long-chain enoyl-CoA reductase	TECR	5	14.9	0	23.66	0.80	0.82	0.88	0.95	0.82	0.89	0.74	NaN	0.75
Q9NZB2	Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	9	11.9	0	56.65	0.99	1.11	1.25	1.11	1.09	1.02	1.17	NaN	1.02
Q9NZL4	Hsp70-binding protein 1	HSPBP1	2	11.7	0	26.28	NaN	NaN	NaN	NaN	1.11	1.14	NaN	NaN	NaN
Q9NZL9	Methionine adenosyltransferase 2 subunit beta	MAT2B	2	6.9	0.003	1.879	NaN	NaN	0.85	0.67	0.47	NaN	0.95	NaN	0.92
Q9NZM1	Myoferlin	MYOF	84	52.6	0	323.3	0.72	0.75	0.83	0.90	0.89	0.89	0.70	0.88	1.02
Q9NZN4	EH domain-containing protein 2	EHD2	12	35.7	0	42.68	0.70	0.89	0.59	0.94	0.85	0.78	1.08	0.70	0.94
Q9P035	Very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase 3	HACD3	4	18.8	0	10.81	0.69	0.54	NaN	1.14	0.71	0.76	1.20	0.84	1.06
Q9P0L0	Vesicle-associated membrane protein-associated protein A	VAPA	13	61	0	144.2	0.97	0.85	1.00	0.90	1.07	0.98	0.65	0.81	0.62
Q9P1F3	Costars family protein ABRACL	ABRACL	3	43.2	0	15.93	0.89	1.03	NaN	NaN	1.03	1.05	1.19	1.19	1.25
Q9P258	Protein RCC2	RCC2	2	6.1	0	2.925	NaN	NaN	1.41	NaN	NaN	NaN	0.98	0.83	NaN
Q9P287	BRCA2 and CDKN1A-interacting protein	BCCIP	3	18.2	0	11.54	NaN	0.98	NaN	NaN	NaN	0.81	0.84	NaN	1.47
Q9P2E9	Ribosome-binding protein 1	RRBP1	42	36	0	323.3	0.92	0.87	0.92	0.93	0.81	0.86	0.63	0.90	0.86
Q9P2J5	Leucine--tRNA ligase,	LARS	23	27.7	0	142.2	1.02	0.92	0.93	0.67	0.82	0.96	NaN	0.85	1.10
Q9P2X0	Dolichol-phosphate mannosyltransferase subunit 3	DPM3	2	23.9	0.002	2.029	1.34	1.36	0.85	NaN	NaN	NaN	NaN	NaN	1.00
Q9UBB4	Ataxin-10	ATXN10	7	17.5	0	106.2	NaN	0.90	1.03	1.08	1.20	1.04	NaN	0.61	0.76
Q9UBE0	SUMO-activating enzyme subunit 1;SUMO-activating enzyme subunit 1, N-terminally processed	SAE1	10	29.8	0	27.25	1.28	1.98	1.08	0.98	1.31	1.06	1.10	1.00	1.03
Q9UBF2	Coatomer subunit gamma-2	COPG2	8	18.9	0	19.74	NaN	NaN	1.18	NaN	0.83	0.85	NaN	NaN	NaN
Q9UBI6	Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-12	GNG12	3	56.9	0	96.94	0.93	1.03	0.80	1.08	1.02	0.99	1.07	0.94	1.18
Q9UBM7	7-dehydrocholesterol reductase	DHCR7	4	10.5	0	8.396	NaN	NaN	NaN	0.98	1.09	0.86	1.86	1.43	NaN
Q9UBQ7	Glyoxylate reductase/hydroxypyruvate reductase	GRHPR	8	40.2	0	100.4	0.85	0.62	0.79	NaN	0.94	0.71	NaN	NaN	0.82
Q9UBR2	Cathepsin Z	CTSZ	3	12.9	0	67.04	1.38	1.05	1.49	1.14	1.97	1.21	1.26	1.15	1.04
Q9UBS4	DnaJ homolog subfamily B member 11	DNAJB11	4	17.6	0	4.818	NaN	NaN	1.17	NaN	NaN	NaN	1.05	0.97	NaN
Q9UBT2	SUMO-activating enzyme subunit 2	UBA2	9	22.8	0	13.46	0.78	0.79	0.71	0.79	1.33	1.10	1.10	0.73	0.90

Q9UDY2	Tight junction protein ZO-2	TJP2	13	16.6	0	93.64	1.69	1.37	NaN	1.29	1.13	NaN	1.20	NaN	NaN
Q9UG63	ATP-binding cassette sub-family F member 2	ABCF2	4	7.4	0	6.417	1.26	1.16	1.11	NaN	0.74	1.46	NaN	0.89	1.07
Q9UGI8	Testin	TES	18	51.5	0	78.51	1.10	1.35	1.10	NaN	0.97	1.24	1.30	NaN	1.01
Q9UH65	Switch-associated protein 70	SWAP70	12	20.5	0	16.95	0.89	0.97	0.83	1.27	1.18	1.02	1.12	1.30	1.05
Q9UH99	SUN domain-containing protein 2	SUN2	3	8.6	0	5.686	NaN	1.92	1.77	NaN	NaN	1.42	NaN	NaN	1.41
Q9UHB9	Signal recognition particle subunit SRP68	SRP68	11	25.2	0	116.8	0.89	0.78	0.98	0.98	0.90	0.85	0.96	0.78	0.56
Q9UHD1	Cysteine and histidine-rich domain-containing protein 1	CHORDC1	9	47.9	0	52.51	1.64	1.86	1.65	1.42	1.70	1.65	0.88	0.69	0.82
Q9UHD8	Septin-9	9-Sep	16	43.3	0	323.3	1.01	1.06	1.04	1.03	1.05	1.00	1.10	1.03	1.05
Q9UHD9	Ubiquilin-2	UBQLN2	3	14.7	0	126.8	1.18	0.76	0.71	0.83	1.09	1.12	NaN	NaN	0.56
Q9UHV9	Prefoldin subunit 2	PFDN2	7	51.9	0	74.29	1.04	1.11	1.19	1.06	1.01	1.17	1.32	0.93	1.09
Q9UHY7	Enolase-phosphatase E1	ENOPH1	2	13	0	22.77	0.63	0.75	0.82	NaN	NaN	1.23	0.97	NaN	1.51
Q9UI47	Catenin alpha-3	CTNNA3	1	3.5	0	4.184	0.93	0.95	0.94	NaN	1.06	1.02	0.97	NaN	1.00
Q9UJS0	Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	4	7.9	5E-04	2.831	1.02	1.09	0.91	NaN	NaN	NaN	NaN	NaN	NaN
Q9UJU6	Drebrin-like protein	DBNL	10	32.3	0	134.9	0.95	0.86	0.89	0.93	0.92	1.02	1.25	NaN	1.14
Q9UJZ1	Stomatin-like protein 2, mitochondrial	STOML2	9	49.4	0	41.07	1.47	0.93	0.97	1.35	1.06	0.93	1.61	1.08	1.30
Q9UK76	Hematological and neurological expressed 1 protein;Hematological and neurological expressed 1 protein.	HN1	5	64.9	0	290.3	1.28	1.29	1.44	0.76	1.13	0.93	1.46	1.55	1.53
Q9UKY7	Protein CDV3 homolog	CDV3	7	54.3	0	202.5	1.24	1.20	1.27	1.52	1.17	1.00	1.13	1.06	0.81
Q9UL25	Ras-related protein Rab-21	RAB21	7	39.1	0	33.53	1.22	1.36	1.20	NaN	1.08	2.39	NaN	NaN	0.76
Q9ULC4	Malignant T-cell-amplified sequence 1	MCTS1	4	40.9	0	23.36	NaN	0.70	0.68	0.67	0.81	0.66	0.92	0.50	NaN
Q9ULC5	Long-chain-fatty-acid--CoA ligase 5	ACSL5	2	3.4	0	3.279	0.59	NaN	NaN	NaN	1.16	1.21	NaN	NaN	NaN
Q9ULV4	Coronin-1C	CORO1C	3	47.9	0	225.9	0.80	0.82	0.83	0.81	0.87	0.90	0.85	0.95	0.89
Q9ULW0	Targeting protein for Xklp2	TPX2	1	2.1	0	17.33	NaN	NaN	0.33	1.03	0.85	1.48	0.33	0.39	0.12
Q9UM22	Mammalian ependymin-related protein 1	EPDR1	1	4.9	0.008	1.495	NaN	0.50	0.44	0.40	NaN	0.58	NaN	NaN	NaN
Q9UMS4	Pre-mRNA-processing factor 19	PRPF19	12	35.1	0	163.5	1.24	1.00	1.09	0.95	0.87	0.87	1.01	0.97	0.90
Q9UMX0	Ubiquilin-1	UBQLN1	2	16.3	0	10.82	NaN	NaN	NaN	1.18	1.17	1.03	NaN	NaN	NaN
Q9UMX5	Neudesin	NENF	4	27.9	0	3.428	NaN	NaN	NaN	1.03	NaN	1.78	0.72	NaN	NaN
Q9UN86	Ras GTPase-activating protein-binding protein 2	G3BP2	7	20.7	0	8.231	1.40	1.20	1.27	1.20	1.28	1.13	1.07	0.87	0.88
Q9UNF0	Protein kinase C and casein kinase substrate in neurons protein 2	PACSIN2	9	21	0	6.422	1.14	1.13	0.91	1.15	1.00	1.20	1.01	1.37	0.94
Q9UNF1	Melanoma-associated antigen D2	MAGED2	10	23.8	0	33.29	1.08	NaN	0.94	NaN	NaN	0.83	0.72	NaN	1.44
Q9UNM6	26S proteasome non-ATPase regulatory subunit 13	PSMD13	16	55.9	0	98.97	0.97	0.91	1.03	0.95	1.31	1.02	1.53	1.09	1.02
Q9UNS2	COP9 signalosome complex subunit 3	COPS3	4	14.2	0	49.5	1.02	NaN	1.26	NaN	1.09	1.52	NaN	0.76	1.10

Q9UNW1	Multiple inositol polyphosphate phosphatase 1	MINPP1	1	3.1	0.001	2.717	NaN	1.26	1.20	NaN	1.28	NaN	NaN	NaN	NaN
Q9UNZ2	NSFL1 cofactor p47	NSFL1C	11	40.5	0	80.02	1.06	1.23	1.19	1.06	0.94	0.98	1.18	0.99	1.11
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	8	4.3	0	15.96	1.69	1.32	1.41	0.84	1.09	NaN	0.85	0.88	1.45
Q9UQ80	Proliferation-associated protein 2G4	PA2G4	23	60.4	0	198.1	0.89	0.92	0.80	1.06	0.87	0.92	0.84	1.04	0.90
Q9UQE7	Structural maintenance of chromosomes protein 3	SMC3	14	16.3	0	22.14	NaN	NaN	NaN	0.96	1.29	NaN	NaN	NaN	NaN
Q9Y224	UPF0568 protein C14orf166	C14orf166	9	44.7	0	33.88	1.07	1.05	1.10	0.98	0.94	1.12	0.84	0.77	1.01
Q9Y230	RuvB-like 2	RUVBL2	17	44.3	0	81.45	1.01	0.83	0.77	0.98	1.07	0.94	0.82	0.83	0.77
Q9Y237	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4	PIN4	2	17.6	0	4.809	1.16	1.03	1.14	0.99	1.25	1.51	1.12	NaN	NaN
Q9Y265	RuvB-like 1	RUVBL1	13	39.3	0	64.7	0.85	0.89	0.85	0.91	0.78	0.77	0.82	0.88	0.85
Q9Y266	Nuclear migration protein nudC	NUDC	15	52.6	0	42.05	1.27	1.13	1.21	1.14	0.99	1.30	1.04	1.16	1.23
Q9Y281	Cofilin-2	CFL2	5	62	0	15.19	0.80	0.85	NaN	0.80	NaN	0.91	NaN	NaN	NaN
Q9Y285	Phenylalanine--tRNA ligase alpha subunit	FARSA	6	19.3	0	16.57	1.06	0.95	1.01	NaN	0.93	1.02	NaN	NaN	0.92
Q9Y295	Developmentally-regulated GTP-binding protein 1	DRG1	3	11.2	0	8.405	0.97	1.03	1.06	NaN	NaN	0.97	1.33	1.21	0.95
Q9Y2A7	Nck-associated protein 1	NCKAP1	11	15	0	28.87	0.87	0.97	0.79	0.95	0.99	0.84	NaN	0.84	0.99
Q9Y2D5	A-kinase anchor protein 2	AKAP2	5	8.5	0	3.645	NaN	NaN	NaN	NaN	2.38	4.45	0.86	NaN	NaN
S6FW71	GDP-fucose protein O-fucosyltransferase 2	POFUT2	1	6.6	0.008	1.543	1.35	0.98	0.85	NaN	0.95	NaN	NaN	NaN	1.12
Q9Y2Q3	Glutathione S-transferase kappa	GSTK1	5	28.8	0	97.45	0.64	0.35	NaN	0.26	0.74	0.87	NaN	0.67	0.72
Q9Y2R0	Cytochrome c oxidase assembly factor 3 homolog, mitochondrial	COA3	2	17.9	0.001	2.758	1.63	1.38	1.32	NaN	NaN	1.40	NaN	NaN	NaN
Q9Y2S6	Translation machinery-associated protein 7	TMA7	1	15.6	0.001	2.087	1.18	1.30	1.26	1.40	1.13	1.19	0.85	0.94	NaN
Q9Y2T2	AP-3 complex subunit mu-1	AP3M1	2	12.9	0	6.401	0.88	NaN	1.00	NaN	NaN	1.37	NaN	NaN	0.92
Q9Y2V2	Calcium-regulated heat stable protein 1	CARHSP1	3	42.9	0	14.44	1.01	0.81	0.94	0.91	1.07	0.94	NaN	0.98	0.96
Q9Y2X3	Nucleolar protein 58	NOP58	6	16.3	0	8.944	1.11	1.16	NaN	NaN	NaN	NaN	NaN	NaN	1.46
Q9Y2Z0	Suppressor of G2 allele of SKP1 homolog	SUGT1	7	28.5	0	46.75	NaN	1.04	1.25	0.67	1.05	NaN	NaN	0.86	NaN
Q9Y305	Acyl-coenzyme A thioesterase 9, mitochondrial	ACOT9	14	33.9	0	44.3	0.78	0.79	0.91	0.87	1.02	0.99	1.13	0.74	0.97
Q9Y333	U6 snRNA-associated Sm-like protein LSm2	LSM2	4	67.4	0	25.05	1.17	1.36	1.31	NaN	NaN	NaN	NaN	NaN	1.31
Q9Y376	Calcium-binding protein 39	CAB39	4	14.7	0	6.151	1.53	NaN	NaN	NaN	0.98	0.80	NaN	NaN	0.81
Q9Y383	Putative RNA-binding protein Luc7-like 2;Putative RNA-binding protein Luc7-like 1	LUC7L2	10	28.8	0	56.28	0.81	0.91	0.82	0.88	0.76	0.94	0.76	0.82	0.77
Q9Y3A6	Transmembrane emp24 domain-containing protein 5	TMED5	2	10	5E-04	2.87	NaN	NaN	NaN	1.04	NaN	NaN	0.99	0.88	NaN
Q9Y3B4	Splicing factor 3B subunit 6	SF3B6	4	38.4	0	4.67	NaN	NaN	0.66	0.98	0.99	1.02	NaN	0.47	NaN
Q9Y3C1	Nucleolar protein 16	NOP16	1	8.4	0.007	1.672	1.30	1.17	NaN	NaN	1.64	1.39	NaN	NaN	NaN

Q9Y3C6	Peptidyl-prolyl cis-trans isomerase-like 1	PPIL1	5	35.5	0	12.29	1.02	0.95	1.01	1.31	0.99	0.88	0.98	1.31	0.78
Q9Y3D0	Mitotic spindle-associated MMXD complex subunit MIP18	FAM96B	3	39.3	0	20.23	NaN	NaN	0.83	NaN	NaN	1.28	2.19	NaN	1.71
Q9Y3D6	Mitochondrial fission 1 protein	FIS1	2	15.8	0	37.27	NaN	NaN	1.03	NaN	1.15	0.83	1.01	0.96	NaN
Q9Y3F4	Serine-threonine kinase receptor-associated protein	STRAP	17	63.4	0	56.24	0.97	1.03	0.93	NaN	1.20	1.22	1.03	1.01	0.98
Q9Y3I0	tRNA-splicing ligase RtcB	RTCB	18	46.3	0	110.9	0.87	0.66	0.97	NaN	1.11	0.61	1.60	0.95	0.65
Q9Y3U8	60S ribosomal protein L36	RPL36	4	27.6	0	8.096	0.71	0.81	0.85	0.86	0.85	0.86	NaN	1.16	0.72
Q9Y490	Talin-1	TLN1	107	63.3	0	323.3	1.05	1.05	1.06	1.07	1.02	1.04	1.01	0.99	1.00
V9GZ56	U6 snRNA-associated Sm-like protein LSm4	LSM4	2	11.8	0	3.31	0.61	0.69	0.69	1.08	0.69	0.92	NaN	NaN	0.49
Q9Y512	Sorting and assembly machinery component 50 homolog	SAMM50	3	8.3	0.001	2.451	NaN	1.17	0.97	NaN	1.66	1.13	NaN	NaN	1.51
Q9Y570	Protein phosphatase methylesterase 1	PPME1	13	44.6	0	102.6	1.28	1.00	1.26	1.20	1.13	1.20	0.88	0.73	NaN
Q9Y5B9	FACT complex subunit SPT16	SUPT16H	20	23	0	32.52	0.85	1.10	0.87	0.69	0.99	0.88	1.36	0.94	0.90
Q9Y5J1	U3 small nucleolar RNA-associated protein 18 homolog	UTP18	3	9	0	2.962	NaN	1.41	NaN	NaN	0.99	NaN	0.77	NaN	1.84
Q9Y5K6	CD2-associated protein	CD2AP	7	16.6	0	17.97	NaN	1.00	1.26	0.55	0.61	0.90	1.05	0.65	1.21
Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13	TIMM13	4	52.6	0	12.83	1.56	1.05	0.85	1.15	1.27	NaN	0.99	0.85	0.39
Q9Y5S9	RNA-binding protein 8A	RBM8A	4	27.6	0	37.23	1.05	1.13	1.17	1.08	0.97	1.17	0.81	0.86	1.15
Q9Y5X3	Sorting nexin-5	SNX5	2	6.7	0.008	1.559	1.18	1.03	1.05	NaN	0.92	1.05	NaN	NaN	0.88
Q9Y617	Phosphoserine aminotransferase	PSAT1	8	25.9	0	7.437	NaN	NaN	0.71	0.72	0.39	0.52	0.52	0.62	0.69
Q9Y678	Coatomer subunit gamma-1	COPG1	20	35.5	0	112.3	1.05	1.03	1.08	0.95	1.01	1.11	1.13	1.08	1.00
Q9Y696	Chloride intracellular channel protein 4	CLIC4	12	62.5	0	228.5	1.02	0.88	1.23	0.96	0.95	1.01	0.97	1.00	1.16
Q9Y6C9	Mitochondrial carrier homolog 2	MTCH2	6	25.4	0	30.75	1.54	1.32	1.07	0.82	1.03	1.09	0.75	0.90	NaN
Q9Y6G9	Cytoplasmic dynein 1 light intermediate chain 1	DYNC1LI1	7	23.9	0	15.48	1.15	0.94	1.24	0.65	0.90	0.91	1.05	1.07	0.93
Q9Y6N5	Sulfide:quinone oxidoreductase, mitochondrial	SQRDL	8	22.4	0	13.52	NaN	NaN	NaN	0.96	NaN	1.06	NaN	NaN	NaN
R4GNH3	26S protease regulatory subunit 6A	PSMC3	17	51.8	0	310.2	0.97	1.00	1.17	0.95	0.97	1.01	1.05	0.99	0.78

Supplementary Table S2 The results of phosphoproteomic analysis

Protein ID	Protein names	Gene names	Phospho-site positions	Amino acid	Localization prob	Score	Ratio of TGF-β1+SFN / Con_1	Ratio of TGF-β1+SFN / Con_2	Ratio of TGF-β1+SFN / Con_3	Ratio of SFN / Con_1	Ratio of SFN / Con_2	Ratio of SFN / Con_3	Ratio of TGF-β1/ Con_1	Ratio of TGF-β1/ Con_2	Ratio of TGF-β1/ Con_3
A0A1B0GWH8	Battenin	CLN3	12	S	1	112	0.79	NaN	NaN	NaN	NaN	0.90	1.50	1.06	1.88
A0A024R4E5	Vigilin	HDLBP	31	S	1	228.5	1.41	1.32	1.48	1.73	1.36	1.24	1.28	1.42	1.17
A0A0G2JL47	Large proline-rich protein	BAT3	113	S	0.997	149.4	NaN	0.73	NaN	0.92	0.96	NaN	1.05	0.82	0.90
A0A0G2JL47	Large proline-rich protein	BAT3	958	S	1	123.1	NaN	0.85	0.72	0.98	NaN	NaN	0.94	NaN	0.59
A0A0G2JL47	Large proline-rich protein	BAT3	967	S	1	261	0.80	0.90	0.99	1.13	1.21	1.10	0.88	0.87	0.73
A0A075B784	Ubiquitin carboxyl-terminal hydrolase;Ubiquitin carboxyl-terminal hydrolase 36	USP36	742	S	0.998	47.06	1.36	1.32	1.04	0.67	1.03	1.01	NaN	1.19	1.00
A0A075B784	Ubiquitin carboxyl-terminal hydrolase;Ubiquitin carboxyl-terminal hydrolase 36	USP36	807	S	0.838	122.7	0.64	0.72	NaN	NaN	NaN	NaN	NaN	NaN	NaN
A0A087WXA6	GRIP1-associated protein 1	GRIPAP1	271	S	0.968	181.6	1.75	1.47	1.30	1.52	NaN	0.98	1.01	NaN	0.80
H0YL34	Synemin	SYNM	758	S	1	78.91	1.35	0.99	1.43	0.81	1.67	0.49	1.90	NaN	NaN
H0YL34	Synemin	SYNM	763	S	1	78.91	1.35	1.95	1.43	1.14	0.87	NaN	0.65	0.76	NaN
G3V2E8	Alpha-actinin-1;Alpha-actinin-2;Alpha-actinin-3;Alpha-actinin-4	ACTN1	75	S	0.996	98.63	0.35	0.36	NaN	0.88	0.91	0.79	1.33	1.29	1.41
A0A087WT18	Putative monooxygenase p33MONOX	KIAA1191	102	S	0.633	95.52	NaN	NaN	NaN	NaN	0.63	0.59	NaN	NaN	NaN
A0A087WTB8	Ubiquitin carboxyl-terminal hydrolase;Ubiquitin carboxyl-terminal hydrolase isozyme L3	UCHL3	90	S	0.666	60.35	NaN	NaN	NaN	1.22	NaN	1.56	NaN	NaN	NaN
A0A087WTB8	Ubiquitin carboxyl-terminal hydrolase;Ubiquitin carboxyl-terminal hydrolase isozyme L3	UCHL3	94	S	0.883	108.7	0.96	0.87	NaN	NaN	NaN	NaN	NaN	NaN	NaN
A0A087WTP3	Far upstream element-binding protein 2	KHSRP	480	S	1	105.1	1.78	1.47	1.67	2.73	2.38	2.67	NaN	0.62	0.83
A0A087WTP3	Far upstream element-binding protein 2	KHSRP	181	S	0.998	121.4	NaN	NaN	1.46	1.79	1.85	1.69	0.95	1.11	0.96
A0A087WTQ7	DNA damage-binding protein	DDB2	26	S	0.851	73.27	NaN	NaN	0.57	0.83	0.46	NaN	1.72	1.62	NaN
Q1JUQ3	Peptidyl-prolyl cis-trans isomerase;Peptidyl-prolyl cis-trans isomerase FKBP1A	FKBP12-Exin	9	S	0.999	153.9	NaN	1.58	NaN	2.63	2.17	2.53	0.84	NaN	NaN
A0A087WTS8	Heat shock 70 kDa protein 4	HSPA4	76	S	1	61.42	1.32	1.09	1.38	1.34	1.23	NaN	NaN	NaN	NaN
Q5JWB9	Transmembrane protein 230	TMEM230	24	S	0.758	75.02	NaN	3.61	NaN	NaN	NaN	NaN	2.24	3.27	NaN
A0A087WTU3	Testis-expressed sequence 264 protein	TEX264	170	S	0.993	172.6	NaN	NaN	0.36	0.68	0.63	NaN	0.33	0.33	0.32
A0A087WVR3	E3 ubiquitin-protein ligase UHRF1	UHRF1	104	S	0.856	126.4	0.68	NaN	0.38	NaN	NaN	NaN	0.59	NaN	NaN

E9PS08	UBX domain-containing protein 1	UBXN1	58	S	0.703	163.7	NaN	NaN	1.50	NaN	NaN	1.70	1.11	1.29	1.18
E7ER32	MKL/myocardin-like protein 1	MKL1	454	S	0.994	172.9	1.26	1.45	NaN	NaN	NaN	NaN	NaN	NaN	NaN
A0A0G2JNN3	Leukocyte receptor cluster member 8	LENG8	203	S	1	79.71	NaN	0.94	0.87	1.12	1.24	1.20	0.74	0.71	0.74
A0A087WUT6	Eukaryotic translation initiation factor 5B	EIF5B	1168	S	1	83.05	1.11	1.12	NaN	2.18	1.34	1.56	NaN	0.85	0.61
A0A087WUT6	Eukaryotic translation initiation factor 5B	EIF5B	107	S	1	122.2	0.63	0.72	0.71	1.07	0.93	0.76	0.85	0.81	0.84
A0A087WUT6	Eukaryotic translation initiation factor 5B	EIF5B	113	S	1	430.8	1.01	0.98	0.90	0.96	0.86	0.94	1.08	1.00	1.07
A0A087WUT6	Eukaryotic translation initiation factor 5B	EIF5B	164	S	1	113.7	0.77	0.76	1.05	0.93	0.95	0.98	0.73	0.85	NaN
A0A087WUT6	Eukaryotic translation initiation factor 5B	EIF5B	214	S	1	202.2	1.28	1.34	1.31	1.30	1.33	1.27	1.46	1.38	1.35
A0A087WUT6	Eukaryotic translation initiation factor 5B	EIF5B	135	S	0.999	186.9	0.70	0.71	0.68	0.35	0.44	0.36	0.43	0.62	0.61
A0A087WUT6	Eukaryotic translation initiation factor 5B	EIF5B	137	S	1	186.9	0.70	0.71	0.68	0.97	1.02	0.94	0.64	0.47	0.61
A0A087X0G7	NF-kappa-B essential modulator	IKBKG	379	S	1	99.53	2.27	NaN	1.29	1.97	NaN	1.45	NaN	NaN	NaN
A0A087WUZ3	Spectrin beta chain, non-erythrocytic 1	SPTBN1	2342	S	0.77	240.2	1.12	NaN	NaN	NaN	NaN	NaN	1.15	NaN	1.11
A0A087WUZ3	Spectrin beta chain, non-erythrocytic 1	SPTBN1	2343	S	0.973	268.1	0.81	1.02	1.10	1.62	1.20	1.60	NaN	NaN	NaN
A0A087WUZ3	Spectrin beta chain, non-erythrocytic 1	SPTBN1	2166	S	0.993	118.2	NaN	0.65	NaN	0.79	0.65	0.76	0.97	1.00	0.96
A0A087WUZ3	Spectrin beta chain, non-erythrocytic 1	SPTBN1	2167	S	0.993	181.2	0.92	0.76	0.75	0.76	0.78	0.75	0.63	0.67	0.64
A0A087WUZ3	Spectrin beta chain, non-erythrocytic 1	SPTBN1	2171	S	1	168.8	0.80	0.76	0.77	0.76	0.78	0.75	0.61	0.61	0.64
A0A087WUZ3	Spectrin beta chain, non-erythrocytic 1	SPTBN1	2162	S	0.851	143.3	NaN	0.63	NaN	0.70	0.75	0.70	1.12	1.11	0.96
A0A087WUZ3	Spectrin beta chain, non-erythrocytic 1	SPTBN1	2163	S	0.971	181.2	0.63	0.61	0.60	0.70	0.63	0.76	1.07	1.02	0.96
A0A087WUZ3	Spectrin beta chain, non-erythrocytic 1	SPTBN1	2104	S	1	174.7	0.67	0.72	0.61	0.72	0.73	0.70	0.89	0.86	0.91
A0A087WVA8	Testis-expressed sequence 2 protein	TEX2	266	S	0.992	116.8	NaN	NaN	1.22	1.39	NaN	1.35	0.83	0.90	NaN
K7EK53	Eukaryotic translation initiation factor 3 subunit K	EIF3K	130	S	0.989	124.3	1.24	1.50	NaN	0.96	1.36	NaN	0.71	0.90	NaN
A0A087WVF1	Uncharacterized protein C18orf25	C18orf25	66	S	0.985	88.29	1.35	1.38	1.33	1.04	1.01	1.00	1.85	1.74	1.99
A0A087WVF1	Uncharacterized protein C18orf25	C18orf25	145	S	0.919	49.07	NaN	NaN	2.28	2.00	NaN	NaN	1.91	2.04	1.93
A0A087WVF7	Intersectin-2	ITSN2	867	S	0.988	69.58	NaN	NaN	1.39	1.70	NaN	1.49	NaN	1.33	NaN
A0A087WVF7	Intersectin-2	ITSN2	872	S	0.955	139.2	1.06	1.05	0.95	0.94	1.00	0.70	0.96	1.12	NaN

H7C4X9	Protein kinase C-binding protein 1	ZMYND8	595	S	1	60.03	NaN	0.70	0.53	NaN	NaN	NaN	1.01	NaN	0.89
H7C4X9	Protein kinase C-binding protein 1	ZMYND8	474	S	1	78.84	1.01	1.33	1.16	NaN	1.35	2.10	0.87	0.87	0.98
H7C4X9	Protein kinase C-binding protein 1	ZMYND8	417	S	0.973	111.6	0.45	0.46	0.48	0.57	NaN	0.56	0.97	1.19	1.13
H7C4X9	Protein kinase C-binding protein 1	ZMYND8	683	S	0.991	82.87	0.72	0.65	NaN	0.81	NaN	0.83	0.97	0.96	0.98
E7ET14	Lysine-specific demethylase PHF2	PHF2	95	S	0.998	76.21	1.02	0.81	NaN	1.05	1.55	NaN	0.89	1.30	0.97
E7ET14	Lysine-specific demethylase PHF2	PHF2	269	S	0.667	75.51	NaN	NaN	0.23	0.72	0.93	0.76	0.78	0.38	NaN
E7ET14	Lysine-specific demethylase PHF2	PHF2	271	S	0.667	75.51	NaN	NaN	0.23	0.72	0.93	0.76	0.78	0.38	NaN
E7ET14	Lysine-specific demethylase PHF2	PHF2	272	S	0.667	75.51	NaN	NaN	0.23	0.72	0.93	0.76	0.78	0.38	NaN
A0A087WW66	26S proteasome non-ATPase regulatory subunit 1	PSMD1	315	S	1	84.95	NaN	0.95	0.95	1.04	1.08	1.22	1.01	0.98	1.26
A0A087WWA3	Kinesin-like protein;Kinesin-like protein KIF1B	KIF1B	1428	S	0.94	71.56	0.48	NaN	NaN	0.75	0.79	1.06	0.51	0.54	NaN
A0A087WWA3	Kinesin-like protein;Kinesin-like protein KIF1B	KIF1B	1031	S	1	102.4	1.19	0.94	NaN	NaN	NaN	NaN	1.67	1.20	1.38
A0A087WWC8	Myelin expression factor 2	MYEF2	17	S	0.986	152.1	0.85	1.03	0.93	1.09	NaN	1.00	1.20	1.37	1.14
A0A087WWF4	Kanadaptin	SLC4A1AP	82	S	1	238	0.54	0.88	0.57	0.98	0.86	0.87	0.35	0.43	0.47
M0R2H0	Leucine-rich repeat-containing protein C10orf11	C10orf11	9	S	1	66.54	NaN	NaN	1.21	1.66	1.61	1.92	1.52	1.41	1.65
M0R2H0	Leucine-rich repeat-containing protein C10orf11	C10orf11	10	S	1	66.54	NaN	NaN	1.21	1.66	1.61	1.92	1.52	1.41	1.65
A0A087WWJ1	DNA mismatch repair protein Msh6	MSH6	251	S	0.996	129.6	NaN	0.40	0.28	0.49	0.53	0.45	0.63	0.63	0.61
A0A499FJY3	Putative RNA-binding protein 15	RBM15	626	S	1	189.6	NaN	0.87	1.08	0.84	0.91	NaN	1.11	1.10	0.97
A0A499FJY3	Putative RNA-binding protein 15	RBM15	630	S	1	189.6	NaN	0.87	1.08	0.84	0.91	NaN	1.11	1.10	0.97
A0A499FJY3	Putative RNA-binding protein 15	RBM15	656	S	1	77.32	1.11	0.91	1.03	0.83	0.89	0.57	0.76	1.27	0.69
A0A499FJY3	Putative RNA-binding protein 15	RBM15	250	S	1	126.7	0.87	0.88	0.90	NaN	NaN	0.78	1.04	1.05	1.05
A0A499FJY3	Putative RNA-binding protein 15	RBM15	213	S	0.985	82.41	0.80	0.77	NaN	NaN	NaN	NaN	NaN	NaN	NaN
A0A499FJY3	Putative RNA-binding protein 15	RBM15	215	S	0.986	82.41	0.80	0.77	NaN	NaN	NaN	NaN	NaN	NaN	NaN
A0A499FJY3	Putative RNA-binding protein 15	RBM15	697	S	0.998	56.29	0.67	0.62	NaN	0.59	0.65	0.96	0.66	NaN	0.87
A0A087WWW	B-cell lymphoma/leukemia 10	BCL10	127	S	1	151.2	NaN	NaN	1.60	1.60	NaN	NaN	1.13	0.74	1.64
A0A087WWY2		FOLR2	139	S	0.999	48.11	0.80	0.67	NaN	NaN	0.73	NaN	0.81	0.98	NaN

A0A087WXE2	RNA pseudouridylate synthase domain-containing	RPUSD2	35	S	1	60.92	0.89	0.74	0.82	1.06	1.05	1.31	0.93	1.09	0.91
A0A087WXN9	MTSS1-like protein	MTSS1L	611	S	1	90.88	1.00	1.02	1.06	0.92	0.96	0.87	1.03	1.02	1.44
A0A499FIX8	Extended synaptotagmin-2	ESYT2	615	S	0.997	160.6	0.45	0.56	NaN	0.84	1.00	0.84	0.50	NaN	0.32
A0A499FIX8	Extended synaptotagmin-2	ESYT2	617	S	1	160.6	0.45	0.56	NaN	0.84	1.00	0.81	0.50	NaN	0.32
A0A499FIX8	Extended synaptotagmin-2	ESYT2	667	S	1	156.7	2.35	2.76	2.59	3.31	2.87	2.53	0.98	0.86	0.95
A0A087WXZ7	HEAT repeat-containing protein 6	HEATR6	490	S	0.917	101.9	NaN	NaN	NaN	NaN	NaN	NaN	0.98	2.48	0.74
A0A087WY28	Optineurin	OPTN	64	S	0.996	51.14	1.19	NaN	1.23	1.10	1.39	NaN	1.18	1.28	1.26
A0A087WY61	Nuclear mitotic apparatus protein 1	NUMA1	169	S	0.999	241.2	0.87	0.79	0.86	1.10	1.14	1.14	0.86	0.90	0.92
A0A087WY61	Nuclear mitotic apparatus protein 1	NUMA1	1225	S	0.78	62.66	0.71	0.69	NaN	0.99	1.07	NaN	NaN	NaN	NaN
A0A087WY61	Nuclear mitotic apparatus protein 1	NUMA1	271	S	1	69.34	2.49	NaN	NaN	NaN	NaN	NaN	1.90	1.47	NaN
A0A087WY61	Nuclear mitotic apparatus protein 1	NUMA1	1741	S	1	239.8	1.08	1.03	1.12	1.09	1.11	1.21	1.06	1.03	1.04
A0A087WYN9	ATP-dependent RNA helicase DHX29	DHX29	200	S	1	114.4	0.95	0.88	0.90	0.83	0.74	0.81	0.94	1.10	1.13
A0A087WYW3	NK-tumor recognition protein;Putative peptidyl-prolyl cis-trans isomerase	NKTR	163	S	0.958	62.45	1.41	NaN	NaN	1.19	1.09	NaN	1.90	2.17	1.95
A0A087WZ06	Serine/threonine-protein kinase 3;Serine/threonine-protein kinase 3 36kDa subunit;Serine/threonine-protein kinase 3 20kDa	STK3	274	S	0.717	40.99	0.66	0.52	NaN	NaN	NaN	NaN	NaN	1.15	NaN
A0A087WZ13		RAVER1	617	S	1	67.45	0.68	NaN	0.79	0.96	0.93	0.99	0.77	0.65	0.64
A0A087WZ13		RAVER1	567	S	1	96.11	2.75	3.42	2.77	3.99	3.29	3.39	1.51	1.55	NaN
B7Z385	Adenylyl cyclase-associated protein;Adenylyl cyclase-associated protein 2	CAP2	197	S	0.998	116.8	0.72	0.48	0.48	0.35	0.66	0.41	0.68	0.54	0.66
B7Z385	Adenylyl cyclase-associated protein;Adenylyl cyclase-associated protein 2	CAP2	200	S	0.854	139.8	0.96	NaN	0.92	0.88	0.87	0.64	0.81	1.02	1.09
M0QZS0	Rho guanine nucleotide exchange factor 18	ARHGEF 18	405	S	1	53.6	NaN	1.41	1.88	1.89	2.31	1.63	1.13	2.86	1.03
M0QZS0	Rho guanine nucleotide exchange factor 18	ARHGEF 18	742	S	1	150.1	1.92	1.75	1.71	1.03	1.06	1.12	1.86	2.04	1.80
A0A087WZU8	Cellular tumor antigen p53	TP53	304	S	0.917	174.4	0.34	0.36	0.34	0.60	0.64	0.63	0.82	0.83	0.79
F8VQD8	CCR4-NOT transcription complex subunit 2	CNOT2	80	S	0.999	143	0.87	0.67	NaN	0.82	NaN	0.29	NaN	0.73	0.68
A0A087X055	Ras-responsive element-binding protein 1	RREB1	288	S	0.861	83.11	0.82	1.19	NaN	NaN	NaN	NaN	NaN	NaN	NaN
A0A087X055	Ras-responsive element-binding protein 1	RREB1	389	S	0.804	70.54	0.58	NaN	0.49	NaN	NaN	NaN	NaN	0.58	0.64
G3V2W9	E2F-associated	EAPP	88	S	0.999	134.4	0.69	0.83	NaN	NaN	NaN	NaN	NaN	NaN	NaN

G3V2W9	E2F-associated	EAPP	90	S	1	134.4	0.69	0.83	NaN	NaN	NaN	NaN	NaN	NaN	NaN
A0A087X0H9	RNA-binding protein 26	RBM26	127	S	0.974	58.75	0.85	1.20	NaN	1.29	NaN	NaN	NaN	1.26	NaN
A0A087X0K9	Tight junction protein ZO-1	TJP1	1525;161	S	0.996	173	3.08	3.16	2.60	2.08	1.82	2.12	1.28	1.12	1.20
A0A087X0K9	Tight junction protein ZO-1	TJP1	113;125	S	0.999	104.5	1.88	1.13	1.92	0.73	1.42	1.44	1.52	NaN	1.11
A0A087X0K9	Tight junction protein ZO-1	TJP1	119;131	S	0.974	93.66	1.88	NaN	1.92	NaN	NaN	1.50	NaN	NaN	NaN
C9JZJ7	E3 ubiquitin-protein ligase Midline-1	MID1	96	S	0.992	135.9	1.03	0.86	0.96	0.98	1.06	0.88	1.01	1.23	NaN
A0A087X1M6	Fibronectin type-III domain-containing protein 3A	FNDC3A	203	S	0.961	84.31	0.57	NaN	0.57	0.68	NaN	0.62	NaN	0.59	0.52
A0A087X1N7	Nebulin	NEB	308	S	0.855	60.44	1.07	1.21	NaN	NaN	1.44	NaN	NaN	NaN	NaN
E9PL71	Elongation factor 1-delta	EEF1D	109	S	1	238.1	0.87	0.88	0.80	1.02	1.10	1.04	0.77	0.75	0.75
E9PL71	Elongation factor 1-delta	EEF1D	138	S	1	407.8	1.02	1.05	1.05	0.97	1.04	1.04	0.94	0.91	1.03
A0A087X2B6	Cell cycle and apoptosis regulator protein 2	CCAR2	138	S	0.994	100.3	NaN	1.96	NaN	NaN	NaN	1.75	1.57	2.08	NaN
A0A087X2B6	Cell cycle and apoptosis regulator protein 2	CCAR2	141	S	0.962	100.3	NaN	1.96	NaN	NaN	NaN	1.75	3.68	2.15	NaN
G3V4V5	E3 ubiquitin-protein ligase HECTD1	HECTD1	632	S	0.828	164.3	0.88	0.90	0.87	0.95	NaN	0.89	0.90	NaN	0.96
A0A088AWL3	Nuclear receptor corepressor	NCOR1	115	S	1	145	NaN	0.73	0.70	0.87	0.95	0.83	0.99	0.89	0.91
A0A088AWL3	Nuclear receptor corepressor	NCOR1	2088	S	0.995	115.7	1.04	0.82	0.92	1.03	0.91	0.80	0.88	0.91	0.87
A0A088AWL3	Nuclear receptor corepressor	NCOR1	2024	S	1	83.05	0.76	0.69	0.79	NaN	0.83	0.83	1.03	0.87	1.16
A0A088AWL3	Nuclear receptor corepressor	NCOR1	1881	S	1	94.19	0.87	NaN	0.92	0.64	NaN	0.74	1.23	NaN	NaN
A0A088AWL3	Nuclear receptor corepressor	NCOR1	1884	S	0.702	94.19	0.87	NaN	0.92	0.64	NaN	0.74	NaN	NaN	NaN
A0A494C0S2	DNA repair protein complementing XP-G cells	ERCC5-201	384	S	0.759	129.1	0.81	NaN	NaN	0.77	0.65	0.86	NaN	1.02	1.02
A0A096LP07	COP9 signalosome complex subunit 1	GPS1	469	S	1	187.6	1.01	0.92	0.90	0.98	1.22	1.11	1.01	1.04	0.87
A0A096LP07		GPS1	212	S	0.742	47.13	NaN	NaN	1.60	1.42	1.41	1.36	1.54	1.52	NaN
A0A096LP07		GPS1	219	S	0.719	47.13	NaN	NaN	1.60	1.42	1.41	1.36	1.54	1.52	NaN
A0A096LP25	Uncharacterized protein FLJ45252	AAK1	249	S	1	105	0.58	0.48	0.57	0.86	0.88	0.82	0.97	1.00	0.81
F8W7U3	WASH complex subunit FAM21C;WASH complex subunit FAM21A	FAM21C	498;410	S	1	131	0.85	1.15	0.67	1.53	1.22	1.74	0.74	0.78	0.58
F8W7U3	WASH complex subunit FAM21C;WASH complex subunit FAM21A	FAM21C	333;245	S	1	117.8	1.17	1.09	NaN	0.87	NaN	NaN	1.12	0.97	1.10
F8W7U3	WASH complex subunit FAM21C;WASH complex subunit FAM21A	FAM21C	728;640	S	1	115.5	NaN	NaN	1.74	1.65	NaN	NaN	0.83	0.89	0.93
A0A0A0MR88	WASH complex subunit FAM21C	FAM21C	539	S	1	158.4	1.17	1.26	1.15	1.24	NaN	1.18	1.12	1.07	1.05
F5H0Q6	CLK4-associating serine/arginine rich protein	CLASRP	285	S	0.996	49.08	0.87	NaN	NaN	0.92	0.88	NaN	NaN	0.91	0.96
Q5JSD2	Voltage-dependent anion-selective channel protein 2	VDAC2	115	S	0.973	104.9	0.85	0.72	0.86	1.02	1.15	NaN	1.04	0.88	NaN
C9JW01	Pumilio homolog 2	PUM2	136	S	1	111.1	1.16	NaN	1.15	1.14	1.07	0.99	NaN	NaN	0.92

C9JW01	Pumilio homolog 2	PUM2	182	S	1	130.2	1.34	1.25	1.27	1.14	1.12	1.06	1.03	1.03	1.16
A0A0A0MSK4	G-protein-signaling modulator	GPSM1	492	S	0.5	111.8	0.80	0.96	NaN	1.21	0.96	1.16	NaN	1.44	1.31
A0A0A0MSK4	G-protein-signaling modulator	GPSM1	493	S	0.545	111.8	0.80	0.96	NaN	1.21	0.96	1.16	1.00	1.44	1.31
H0YBF7	Arf-GAP with SH3 domain, ANK repeat and PH domain-containing protein 1	ASAP1	949	S	1	115.1	1.23	1.19	NaN	1.03	1.25	NaN	1.07	0.86	NaN
H0YBF7	Arf-GAP with SH3 domain, ANK repeat and PH domain-containing protein 1	ASAP1	538	S	1	221.3	0.74	0.83	0.88	0.79	0.76	0.70	0.95	1.04	0.95
H0YBF7	Arf-GAP with SH3 domain, ANK repeat and PH domain-containing protein 1	ASAP1	547	S	1	144.4	0.78	0.95	0.93	1.59	1.57	1.28	0.75	NaN	0.61
H0YBF7	Arf-GAP with SH3 domain, ANK repeat and PH domain-containing protein 1	ASAP1	829	S	1	95.09	1.61	1.41	1.35	1.32	1.44	1.39	1.31	NaN	1.19
H0YBF7	Arf-GAP with SH3 domain, ANK repeat and PH domain-containing protein 1	ASAP1	660	S	0.998	107.2	3.41	NaN	2.68	3.24	3.05	NaN	0.83	1.28	0.72
H0YBF7	Arf-GAP with SH3 domain, ANK repeat and PH domain-containing protein 1	ASAP1	664	S	1	78.67	3.41	1.70	2.30	1.85	3.05	NaN	1.55	1.68	NaN
A0A0A0MRI1	GPALPP motifs-containing protein 1	GPALPP1	138	S	1	110.3	NaN	NaN	NaN	NaN	0.83	0.58	0.50	0.54	NaN
A0A0A0MRI1	GPALPP motifs-containing protein 1	GPALPP1	139	S	1	110.3	NaN	NaN	NaN	NaN	0.83	0.58	0.50	0.54	NaN
A0A0A0MRI1	GPALPP motifs-containing protein 1	GPALPP1	103	S	1	172.8	0.92	0.82	NaN	0.86	0.86	NaN	0.99	0.99	1.00
A0A0A0MRJ3	Neuron navigator 1	NAV1	773	S	1	100.9	NaN	1.45	1.88	1.09	1.18	1.15	NaN	2.50	2.15
J3QSX6	Actin-binding LIM protein 1	ABLIM1	329	S	1	119.6	1.18	1.01	NaN	1.71	1.49	1.87	0.44	NaN	0.43
J3QSX6	Actin-binding LIM protein 1	ABLIM1	89	S	1	211.7	1.85	1.74	1.75	1.51	1.53	1.40	1.83	1.60	1.76
A0A0A0MRM9	Nucleolar and coiled-body phosphoprotein 1	NOLC1	572	S	1	156.1	1.01	1.02	0.87	1.01	0.86	0.91	0.95	0.91	0.98
A0A0A0MRM9	Nucleolar and coiled-body phosphoprotein 1	NOLC1	547	S	1	95.85	0.66	0.65	0.59	0.81	NaN	0.82	0.73	0.72	0.77
A0A0A0MRN0	Pre-mRNA-splicing factor 38B	PRPF38B	416	S	1	76.05	1.57	1.66	1.25	1.48	1.66	1.39	1.32	1.18	1.21
A0A0A0MRN0	Pre-mRNA-splicing factor 38B	PRPF38B	418	S	1	110.1	1.15	1.00	0.95	0.91	0.77	1.18	1.07	0.82	1.40
A0A0A0MRN5	Opioid growth factor receptor	OGFR	485	S	0.988	107.4	0.95	NaN	0.88	0.96	1.03	1.42	0.78	0.66	NaN
A0A0A0MRN5	Opioid growth factor receptor	OGFR	465	S	0.794	142.6	NaN	NaN	1.20	NaN	NaN	NaN	1.08	NaN	1.30
A0A0A0MRN5	Opioid growth factor receptor	OGFR	263	S	1	76.11	NaN	NaN	NaN	1.01	NaN	1.16	1.05	1.17	0.96
A0A0A0MRN5	Opioid growth factor receptor	OGFR	326	S	1	185	1.01	1.01	1.04	1.04	1.02	1.01	1.05	1.08	1.10
A0A0A0MRP0	MAP7 domain-containing protein 3	MAP7D3	183	S	0.604	79.31	NaN	NaN	NaN	0.98	1.07	NaN	NaN	NaN	NaN
A0A0A0MRP0	MAP7 domain-containing protein 3	MAP7D3	185	S	0.806	84.57	0.64	0.88	1.04	NaN	NaN	1.02	0.54	NaN	NaN
A0A0A0MRP6	Probable global transcription activator SNF2L1	SMARCA 1	119	S	0.96	51.77	0.49	0.51	0.63	NaN	0.97	0.87	NaN	0.54	NaN

A0A0A0MRT2	WW domain-containing adapter protein with coiled-coil	WAC	8	S	1	78.1	0.71	0.73	1.00	1.15	0.99	1.31	NaN	NaN	1.62
A0A0A0MRT2	WW domain-containing adapter protein with coiled-coil	WAC	359	S	1	155.6	1.21	1.01	0.86	1.14	0.95	1.02	0.72	1.03	1.00
B6VEX4	Abl interactor 1	ABI1	225	S	1	81.38	1.45	1.44	1.29	1.26	1.24	1.12	NaN	1.45	NaN
B6VEX4	Abl interactor 1	ABI1	183	S	1	132.7	0.73	0.79	0.79	1.01	1.00	0.93	0.77	0.78	0.79
A0A0A0MRW1	Protein FAM219A	FAM219A	86	S	1	189.9	1.06	1.46	NaN	1.84	NaN	1.26	NaN	0.82	1.11
A0A0A0MSA7	Eukaryotic translation initiation factor 4 gamma 3	EIF4G3	303	S	0.5	58.23	0.87	1.14	0.95	NaN	NaN	0.96	NaN	NaN	NaN
A0A0A0MSA7	Eukaryotic translation initiation factor 4 gamma 3	EIF4G3	304	S	0.5	58.23	0.87	1.14	0.95	NaN	NaN	0.96	NaN	NaN	NaN
A0A0A0MSA7	Eukaryotic translation initiation factor 4 gamma 3	EIF4G3	494	S	1	105	1.13	1.20	1.24	1.22	1.21	1.25	1.29	1.32	1.27
B3KPJ4	Polyhomeotic-like protein 2	PHC2	357	S	0.768	61.35	NaN	NaN	NaN	1.21	0.92	NaN	NaN	NaN	NaN
A0A0A0MSK5	Torsin-1A-interacting protein 1	TOR1AIP1	33	S	1	148.9	1.42	1.24	1.81	3.30	2.60	2.74	2.35	3.16	1.75
A0A0A0MSK5	Torsin-1A-interacting protein 1	TOR1AIP1	35	S	1	187.8	1.30	1.24	1.81	3.30	2.60	2.74	2.35	3.16	1.47
A0A0A0MSK5	Torsin-1A-interacting protein 1	TOR1AIP1	36	S	1	187.8	1.30	1.24	1.81	3.30	2.60	2.74	2.35	3.16	1.47
A0A0A0MSK5	Torsin-1A-interacting protein 1	TOR1AIP1	22	S	0.908	65.2	NaN	4.14	3.93	3.28	NaN	NaN	NaN	NaN	NaN
A0A0A0MSL3	Ubiquitin-conjugating enzyme E2 variant 1	UBE2V1	102	S	1	99.83	0.77	0.83	0.63	0.96	0.93	0.70	0.84	0.88	1.17
Q5TBM3	Heat shock protein 105 kDa	HSPH1	73	S	1	95.62	NaN	1.42	1.33	1.11	1.12	1.12	0.95	0.89	0.97
A0A0G2JI50	Negative elongation factor E	NELFE	174	S	0.747	117.2	NaN	0.83	0.73	NaN	NaN	0.91	0.88	NaN	0.52
A0A0G2JI50	Negative elongation factor E	NELFE	176	S	0.861	122.2	0.97	0.66	NaN	0.84	NaN	0.54	0.80	0.81	0.92
A0A0G2JI50	Negative elongation factor E	NELFE	115	S	1	154.2	1.65	1.66	NaN	NaN	NaN	NaN	NaN	NaN	NaN
A0A0A0MSU2	ELM2 and SANT domain-containing protein 1	ELMSAN1	461	S	1	88.22	0.56	0.40	NaN	0.64	0.86	NaN	0.68	NaN	NaN
Q5TCC6	Isoleucine--tRNA ligase, cytoplasmic	IARS	100	S	0.964	77.22	NaN	1.11	1.25	NaN	NaN	1.73	NaN	0.94	NaN
A0A0A0MSY4		DOCK9	37	S	1	131.4	1.72	1.84	NaN	NaN	NaN	NaN	NaN	NaN	NaN
A0A0A0MT33	Protein SCAF8	SCAF8	695	S	0.999	203.2	0.93	0.91	0.99	1.00	1.33	1.08	1.01	1.19	1.05
A0A2R8YF38	Transcription activator BRG1	SMARCA4	18	S	1	62.65	NaN	NaN	NaN	1.00	1.26	NaN	NaN	0.87	NaN
A0A0A0MT60	Peptidyl-prolyl cis-trans isomerase;FK506-binding protein 15	FKBP15	1139	S	1	91.59	0.95	1.02	0.80	0.74	0.73	NaN	0.95	1.00	0.89
A0A0A0MTR7	E3 ubiquitin-protein ligase RNF213	RNF213	1258	S	1	158.5	0.92	0.81	0.92	0.97	NaN	0.58	1.08	1.03	1.07
H3BMG9	Protein FAM65A	FAM65A	310	S	1	246.3	1.09	0.99	1.04	0.77	0.83	0.77	1.53	1.47	1.52
A0A0A0MTP7	Protein SCAF11	SCAF11	278	S	0.605	148.3	NaN	0.74	NaN	NaN	NaN	NaN	0.87	0.94	NaN
A0A0A0MTP7	Protein SCAF11	SCAF11	548	S	1	175.8	0.86	0.84	NaN	0.94	1.03	0.82	0.99	0.83	0.99
A0A0A0MTP7	Protein SCAF11	SCAF11	841	S	0.5	65.59	0.73	NaN	NaN	0.86	NaN	0.67	0.69	NaN	NaN
A0A0A0MTP7	Protein SCAF11	SCAF11	842	S	0.5	65.59	0.73	NaN	NaN	0.86	NaN	0.67	0.69	NaN	NaN

A0A0A0MTQ8	Coiled-coil domain-containing protein 175	CCDC175	583	S	1	48.95	0.42	0.44	NaN	0.25	NaN	NaN	0.35	0.33	NaN
A0A0A6YYC0	Ribosomal protein S6 kinase;Ribosomal protein S6 kinase alpha-4	RPS6KA4	331	S	0.999	108.7	0.55	0.43	NaN	NaN	NaN	NaN	NaN	0.99	0.79
A0A0A6YYC7	E3 ubiquitin-protein ligase ZFP91	ZFP91-CNTF	83	S	0.823	93.45	0.76	NaN	NaN	0.66	0.69	NaN	NaN	0.89	NaN
A8MV53	Suppressor of SWI4 1	PPAN	306	S	1	148.9	1.21	1.30	1.34	1.29	1.28	1.31	1.08	1.05	1.06
A0A0A6YYJ8	Putative RNA-binding protein Luc7-like 2	LUC7L2	449	S	1	106.9	0.95	0.99	1.01	0.89	0.90	0.91	0.93	0.95	0.99
A0A0A6YYJ8	Putative RNA-binding protein Luc7-like 2	LUC7L2	450	S	1	106.9	0.95	0.99	1.01	0.89	0.90	0.91	0.93	0.95	0.99
A0A0B4J1S8	Phosphatidylinositol 4-kinase beta	PI4KB	440	S	1	118.5	1.77	1.91	NaN	1.16	1.43	NaN	1.82	1.84	2.33
H0YEG1	Mediator of RNA polymerase II transcription subunit 24	MED24	49	S	0.83	156.1	1.46	0.95	0.91	1.29	NaN	NaN	NaN	0.81	0.68
A0A0C4DFS6	Protein sprouty homolog 4	SPRY4	148	S	1	82.48	2.62	2.24	2.75	2.47	2.27	2.41	1.49	1.25	1.98
E7EQD7	Disks large homolog 1	DLG1	102	S	0.666	137	1.72	1.95	2.06	1.79	1.86	NaN	NaN	NaN	NaN
H0Y3X6	Negative elongation factor A	NELFA	367	S	0.962	49.09	0.97	0.92	NaN	NaN	1.46	NaN	NaN	1.27	1.28
A0A0C4DG07	Nibrin	NBN	350	S	0.968	49.09	0.74	0.78	NaN	NaN	1.10	1.01	0.69	0.59	NaN
H7C3Q7	Abl interactor 2	ABI2	93	S	0.87	69.35	1.13	1.43	NaN	1.59	NaN	NaN	NaN	NaN	NaN
H7C3Q7	Abl interactor 2	ABI2	49	S	0.965	82.19	0.70	NaN	0.68	0.84	0.83	0.81	0.69	0.67	0.63
H7BZV4	ADP-ribosylation factor-like protein 6-interacting protein 4	ARL6IP4	130	S	1	276.8	1.66	1.54	1.74	1.45	1.52	1.44	1.70	1.68	1.69
A0A0C4DG89	Probable ATP-dependent RNA helicase DDX46	DDX46	804	S	1	225.1	0.59	0.61	0.61	0.63	0.69	0.72	0.48	0.48	0.53
H7C477	THO complex subunit 2	THOC2	153	S	0.967	67.17	0.73	0.63	NaN	NaN	NaN	NaN	NaN	NaN	NaN
A0A0C4DGA7	Actin-binding LIM protein 3	ABLIM3	470	S	1	40.32	NaN	1.99	NaN	NaN	1.37	NaN	2.24	2.38	2.75
A0A0C4DGA7	Actin-binding LIM protein 3	ABLIM3	471	S	1	40.32	NaN	1.99	NaN	NaN	1.37	NaN	2.24	2.38	2.75
A0A0C4DGB5	Calpastatin	CAST	289	S	0.987	309	1.15	0.90	0.96	0.76	1.76	1.32	0.81	0.46	1.03
A0A0C4DGB5	Calpastatin	CAST	412	S	0.62	99.11	1.11	1.27	NaN	1.21	NaN	NaN	NaN	1.32	NaN
A0A0C4DGG1	Protein kinase C and casein kinase substrate in neurons protein 3	PACSIN3	354	S	0.998	150.3	0.37	0.59	0.38	NaN	NaN	NaN	1.42	NaN	1.58
A0A0C4DGG1	Protein kinase C and casein kinase substrate in neurons protein 3	PACSIN3	319	S	0.995	68.82	1.07	1.21	NaN	0.94	NaN	NaN	1.10	1.40	NaN
A0A2R8YE38	Chromodomain-helicase-DNA-binding protein 4	CHD4	286	S	0.997	152.4	0.45	0.50	0.53	0.63	0.62	0.63	0.44	0.44	0.44
A0A0C4DGH6	UHRF1-binding protein 1-like	UHRF1BP1L	639	S	0.947	97.9	NaN	NaN	NaN	0.54	0.59	NaN	0.77	NaN	NaN
H0YHL2	Bromodomain adjacent to zinc finger domain protein 2A	BAZ2A	66	S	0.894	47.06	NaN	NaN	NaN	NaN	NaN	0.94	NaN	0.51	0.87
J3QRU8	ARF GTPase-activating protein GIT1	GIT1	592	S	0.676	64.55	NaN	NaN	NaN	NaN	NaN	NaN	0.87	0.97	NaN
J3QRU8	ARF GTPase-activating protein GIT1	GIT1	362	S	0.953	101.8	0.92	NaN	NaN	NaN	1.20	1.28	0.73	0.66	0.79

J3QRU8	ARF GTPase-activating protein GIT1	GIT1	388	S	1	317.9	NaN	NaN	NaN	NaN	NaN	NaN	0.70	NaN	0.63
H7BXT7	BET1-like protein	BET1L	9	S	1	130.6	2.21	2.46	2.82	NaN	NaN	NaN	2.38	NaN	NaN
A0A0C4DH22	Band 4.1-like protein 1	EPB41L1	783	S	1	108	1.90	2.12	NaN	1.29	1.25	1.40	1.54	1.66	1.56
Q5QPR4	Cyclin-dependent kinase 11A;Cyclin-dependent kinase 11B	CDK11A	234	S	0.982	190.8	0.61	0.66	NaN	0.84	0.81	0.80	0.86	NaN	NaN
Q5QPR4	Cyclin-dependent kinase 11A;Cyclin-dependent kinase 11B	CDK11A	540	S	1	81.26	0.87	NaN	0.90	0.81	0.77	0.83	0.96	1.02	1.07
Q5QPR4	Cyclin-dependent kinase 11A;Cyclin-dependent kinase 11B	CDK11A	13	S	1	88.77	0.97	0.97	NaN	0.82	1.04	0.89	NaN	0.94	0.86
H7C3Z6	Mitogen-activated protein kinase kinase kinase kinase 4	MAP4K4	243	S	0.946	50.9	1.36	1.42	NaN	NaN	NaN	1.02	NaN	NaN	NaN
E7EXA6	Chromosome transmission fidelity protein 18 homolog	CHTF18	871	S	1	108.4	0.53	0.43	0.64	0.62	0.65	0.53	0.83	NaN	0.76
A0A0D9SFE4		DNM1	847	S	0.99	63.8	0.85	0.70	0.90	0.84	NaN	0.83	0.92	1.11	0.85
A0A0G2JHC2	Phostensin	PPP1R18	125	S	1	47.56	1.01	NaN	NaN	1.20	0.91	1.15	NaN	NaN	0.84
A0A0G2JHC2	Phostensin	PPP1R18	224	S	1	103.9	1.02	NaN	1.26	1.51	NaN	NaN	NaN	NaN	1.27
A0A0G2JHN8	Bromodomain-containing protein 2	BRD2	160	S	0.995	123.8	NaN	0.81	NaN	0.97	0.74	0.90	NaN	NaN	NaN
A0A0G2JMS7	Protein scribble homolog	SCRIB	1405	S	1	120.3	1.80	2.40	NaN	NaN	2.31	2.36	NaN	0.97	1.46
A0A0G2JMS7	Protein scribble homolog	SCRIB	1485	S	0.971	101.5	1.19	NaN	NaN	1.34	1.05	NaN	1.08	NaN	0.60
A0A0G2JMS7	Protein scribble homolog	SCRIB	1394	S	1	62.34	2.88	NaN	NaN	1.90	1.94	NaN	1.07	1.20	NaN
A0A0G2JMS7	Protein scribble homolog	SCRIB	1225	S	0.997	88.54	0.60	0.57	0.62	0.86	NaN	0.67	0.90	0.76	0.74
A0A0G2JMS7	Protein scribble homolog	SCRIB	1228	S	1	88.54	0.60	0.57	0.62	0.86	NaN	0.67	0.90	0.76	0.74
A0A0G2JMS7	Protein scribble homolog	SCRIB	754	S	0.998	117.5	0.93	NaN	NaN	0.94	0.99	NaN	0.99	NaN	1.12
A0A0G2JMS7	Protein scribble homolog	SCRIB	1367	S	1	119.5	NaN	1.39	1.43	1.31	1.16	1.21	1.19	1.21	1.14
A0A0G2JNJ7	CCR4-NOT transcription complex subunit 3	CNOT3	221	S	0.757	71.73	0.85	NaN	NaN	NaN	1.31	1.48	0.76	0.79	NaN
F6RP06	BCL2/adenovirus E1B 19 kDa protein-interacting protein 3	BNIP3	105	S	1	59.27	NaN	1.14	NaN	0.85	NaN	0.93	0.96	NaN	1.12
A0A0J9YX88	PHD and RING finger domain-containing protein 1	PHRF1	1360	S	1	153	0.58	NaN	0.90	0.77	0.73	0.74	1.02	1.39	0.91
A0A0J9YX88	PHD and RING finger domain-containing protein 1	PHRF1	1371	S	0.974	92.96	0.58	NaN	0.79	0.64	NaN	0.74	NaN	0.99	0.99
A0A0J9YX88	PHD and RING finger domain-containing protein 1	PHRF1	1202	S	1	98.3	1.65	1.68	1.68	NaN	NaN	1.12	NaN	NaN	1.60
A0A0J9YX88	PHD and RING finger domain-containing protein 1	PHRF1	915	S	0.989	169.9	NaN	1.52	1.51	NaN	NaN	0.95	NaN	NaN	0.91
A0A0J9YX88	PHD and RING finger domain-containing protein 1	PHRF1	1229	S	0.969	44.18	NaN	NaN	0.53	NaN	0.69	NaN	0.95	1.04	NaN
A0A0J9YX88	PHD and RING finger domain-containing protein 1	PHRF1	973	S	1	108	1.36	1.20	NaN	1.86	1.30	1.18	1.31	1.15	1.19
A0A0J9YWL0	Absent in melanoma 1 protein	AIM1	941	S	0.692	96.55	0.58	NaN	0.69	NaN	NaN	NaN	0.75	NaN	1.01

E9PH18	DnaJ homolog subfamily B member 6	DNAJB6	162	S	1	179.6	1.97	NaN	NaN	2.11	2.04	NaN	NaN	NaN	NaN
A0A0J9YXZ5	Ras GTPase-activating-like protein IQGAP1	IQGAP1	330	S	1	120.9	1.95	2.08	2.09	3.11	2.99	2.91	1.10	1.02	1.18
A0A0J9YYJ3	Transmembrane protein 184B	TMEM184B	343	S	0.997	82.75	1.27	1.29	0.67	1.22	1.24	1.10	1.14	1.16	1.14
A0A0J9YYJ3	Transmembrane protein 184B	TMEM184B	344	S	0.999	92.05	0.56	1.29	NaN	1.22	1.24	0.82	1.14	1.16	1.04
D6REM6	Matrin-3	MATR3	188	S	1	80.46	2.23	NaN	NaN	1.27	1.35	NaN	NaN	NaN	NaN
D6REM6	Matrin-3	MATR3	596	S	0.949	55.71	0.59	0.65	0.75	0.74	NaN	NaN	NaN	1.03	1.00
D6REM6	Matrin-3	MATR3	598	S	1	216.4	0.83	0.99	0.78	0.80	0.79	0.81	0.79	0.79	0.82
D6REM6	Matrin-3	MATR3	604	S	0.984	127	0.46	0.45	3.55	0.55	0.51	0.52	0.82	0.86	0.91
A0A0U1RQF0	Fatty acid synthase;[Acyl-carrier-protein] S-acetyltransferase;[Acyl-carrier-protein] S-malonyltransferase;3-oxoacyl-[acyl-carrier-protein] synthase;3-oxoacyl-[acyl-carrier-protein] reductase;3-hydroxyacyl-[acyl-carrier-protein] dehydratase;Enoyl-[acyl-carrier-protein]	FASN	207	S	0.994	84.17	NaN	NaN	0.63	0.95	0.74	0.87	0.45	0.44	0.55
A0A0U1RRM7	ATR-interacting protein	ATRIP	131	S	0.997	80.05	NaN	NaN	0.96	0.92	NaN	0.99	1.16	0.94	0.83
A0A0U1RQU3	Calcium-transporting ATPase;Plasma membrane calcium-transporting ATPase	ATP2B1	258	S	0.986	84.19	0.43	0.35	0.37	0.47	0.52	0.51	0.49	0.44	0.58
A0A0U1RRD7	InaD-like protein	INADL	28	S	0.986	102.2	NaN	NaN	NaN	0.62	0.78	NaN	NaN	0.46	NaN
A0A1B0GW38	E3 ubiquitin-protein ligase	CBL	481	S	1	89.77	1.11	1.05	1.19	1.18	1.34	1.10	0.88	0.75	NaN
A0A140T9I0	HLA class I histocompatibility antigen, A-80 alpha chain;HLA class I histocompatibility antigen, A-23 alpha chain;HLA class I histocompatibility antigen, A-69 alpha chain;HLA class I histocompatibility antigen, A-24 alpha chain;HLA class I histocompatibility antigen, A-2 alpha chain;HLA class I histocompatibility	HLA-A	356	S	0.997	134.1	3.07	3.16	NaN	3.39	1.93	NaN	NaN	NaN	NaN
A2AB15	Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16	DHX16	43	S	1	219.5	0.42	0.49	1.19	1.16	0.82	0.80	1.41	0.62	1.35

A2AB15	Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16	DHX16	46	S	1	219.5	1.23	1.15	1.19	1.16	1.19	1.14	1.41	1.37	1.35
A2AB15	Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16	DHX16	100	S	1	207.6	0.71	0.80	0.80	0.91	0.75	0.65	0.83	0.89	NaN
A0A1B0GTJ6			248	S	0.955	71.15	1.10	1.08	1.23	1.08	NaN	1.01	1.19	NaN	1.36
A0A1B0GTL5			634	S	0.998	66.92	1.34	1.29	NaN	NaN	NaN	NaN	NaN	1.50	1.59
A0A1B0GTL5			640	S	0.997	77.81	1.05	1.16	1.25	1.05	1.13	1.11	1.27	1.27	1.25
A0A1B0GTL5			866	S	0.999	150.7	0.76	0.72	1.20	0.94	1.04	0.93	1.20	1.28	1.30
A0A1B0GTL5			871	S	0.951	69.58	NaN	NaN	NaN	0.34	NaN	1.52	NaN	NaN	NaN
A0A1B0GTL5			938	S	0.988	102.7	NaN	NaN	NaN	1.05	0.96	0.91	1.01	1.08	NaN
A0A1B0GTL5			911	S	0.802	91.65	NaN	NaN	NaN	1.27	NaN	1.26	NaN	NaN	NaN
A0A1B0GTL5			913	S	0.987	166.4	1.47	1.97	1.76	NaN	1.26	1.22	NaN	1.93	1.55
A0A1B0GTL5	Rab11 family-interacting protein 5	RAB11FIP5	482;482	S	0.977	64.91	3.33	NaN	2.33	1.77	NaN	NaN	2.84	NaN	NaN
A0A1B0GTL5	Rab11 family-interacting protein 5	RAB11FIP5	307;307	S	1	120	1.08	1.15	1.16	1.12	1.19	1.11	0.78	0.82	NaN
F5GZ78	Paxillin	PXN	300	S	0.639	136.4	1.37	1.47	NaN	1.19	1.23	NaN	1.09	0.85	NaN
F5GZ78	Paxillin	PXN	301	S	0.978	115.7	1.62	1.38	1.32	1.19	1.08	1.40	NaN	1.01	1.25
F5GZ78	Paxillin	PXN	83	S	0.911	250.3	1.70	1.81	1.80	1.74	2.15	1.73	1.20	1.11	1.28
F5GZ78	Paxillin	PXN	256	S	0.971	42.21	NaN	2.20	2.53	2.54	2.15	2.52	2.77	2.01	NaN
F5GZ78	Paxillin	PXN	320	S	0.999	396.1	0.81	0.80	0.77	0.90	NaN	1.00	0.83	0.79	0.83
F5GZ78	Paxillin	PXN	104	S	1	378.2	4.54	5.48	4.12	3.79	3.86	3.12	1.57	1.41	1.63
F5GZ78	Paxillin	PXN	117	S	0.676	60.36	NaN	NaN	2.14	NaN	NaN	NaN	NaN	1.03	2.47
A0A3B3ITE1	Tight junction protein ZO-2	TJP2	979	S	0.994	91.47	1.24	1.12	1.13	0.96	1.04	1.17	1.68	1.57	1.67
A0A3B3ITE1	Tight junction protein ZO-2	TJP2	267	S	1	115.7	1.19	1.21	1.21	1.16	1.14	1.08	1.29	1.26	1.34
A0A3B3ITE1	Tight junction protein ZO-2	TJP2	987	S	1	128.9	0.85	0.84	0.79	0.83	0.85	0.82	0.91	0.93	0.94
A0A3B3ITE1	Tight junction protein ZO-2	TJP2	395	S	0.963	79.9	2.12	0.94	NaN	NaN	NaN	NaN	NaN	NaN	NaN
A0A3B3ITE1	Tight junction protein ZO-2	TJP2	399	S	0.973	172.3	2.12	0.94	NaN	NaN	NaN	NaN	1.26	NaN	NaN
A0A3B3ITE1	Tight junction protein ZO-2	TJP2	401	S	0.718	94.5	2.12	0.94	NaN	NaN	NaN	NaN	NaN	NaN	NaN
A0A3B3ITE1	Tight junction protein ZO-2	TJP2	416	S	1	112.4	1.16	0.60	0.63	0.59	0.60	0.60	0.76	0.75	0.77
A0A3B3ITE1	Tight junction protein ZO-2	TJP2	1160	S	1	255.9	1.69	1.78	1.53	1.42	NaN	1.33	1.78	1.93	1.93
A0A3B3ITE1	Tight junction protein ZO-2	TJP2	967	S	1	87	1.13	1.34	NaN	NaN	1.05	NaN	NaN	1.18	NaN
A0A3B3ITE1	Tight junction protein ZO-2	TJP2	131	S	1	145.8	0.92	1.08	1.02	1.08	1.26	1.13	0.93	0.84	0.89
A0A3B3ITE1	Tight junction protein ZO-2	TJP2	1068	S	0.832	90.3	1.58	1.32	1.39	1.68	NaN	1.36	1.66	1.18	1.56
A0A3B3ITE1	Tight junction protein ZO-2	TJP2	1069	S	0.545	75.05	0.82	NaN	NaN	1.44	1.41	1.36	NaN	1.18	NaN
A0A3B3ITE1	Tight junction protein ZO-2	TJP2	171	S	1	102.9	0.46	0.47	1.38	1.27	1.25	1.25	1.66	1.61	1.62
A0A3B3ITE1	Tight junction protein ZO-2	TJP2	175	S	1	104.8	1.17	1.23	1.02	0.92	1.07	1.01	1.06	1.08	1.02
A0A1B0GUM1	Pleckstrin homology domain-containing family A member 7	PLEKHA7	88	S	0.983	92.73	0.51	1.04	0.69	NaN	NaN	NaN	NaN	NaN	NaN
Q5VTI5	Pleckstrin homology domain-containing family A member 6	PLEKHA6	797	S	0.947	155.2	0.70	NaN	NaN	0.88	NaN	NaN	0.72	0.79	NaN
A0A1B0GV68	FERM, RhoGEF and pleckstrin domain-containing	FARP1	427	S	0.978	47.08	NaN	NaN	3.04	NaN	NaN	NaN	3.90	3.44	NaN
E7EUR8	Protein FAM193A	FAM193A	147	S	0.919	82.48	NaN	0.95	NaN	1.31	1.20	NaN	0.86	NaN	NaN

A0A1B0GVY1	E3 ubiquitin-protein ligase NEDD4-like	NEDD4L	582	S	0.976	79.61	0.75	0.70	NaN	0.66	0.67	NaN	NaN	NaN	NaN
R4GMM6	Ubiquitin-conjugating enzyme E2 E3	UBE2E3	8	S	1	169.1	0.87	0.86	NaN	NaN	NaN	NaN	NaN	NaN	NaN
A0A1C7CYX9			27	S	0.997	92.79	1.72	1.98	1.71	1.33	NaN	1.34	1.69	1.80	1.87
A0A1W2PNZ9	Probable JmjC domain-containing histone demethylation protein 2C	JMJD1C	1825	S	0.815	75.33	NaN	0.45	NaN	0.70	0.50	NaN	NaN	NaN	NaN
A0A1W2PP04	RNA-binding motif protein, X-linked 2	RBMX2	187	S	0.674	209.2	NaN	NaN	NaN	NaN	0.82	NaN	0.95	0.97	NaN
A0A1W2PRI6	Heterogeneous nuclear ribonucleoprotein U	HNRNPU	53	S	1	184.4	0.63	0.60	0.74	0.51	0.64	0.81	NaN	NaN	NaN
E5RIS7	Transcription elongation factor A protein 1	TCEA1	97	S	0.829	91.93	NaN	0.94	NaN	0.83	NaN	0.79	NaN	NaN	1.00
E5RIS7	Transcription elongation factor A protein 1	TCEA1	100	S	1	183.1	0.76	0.79	0.83	0.85	0.89	0.85	0.87	1.02	0.91
B4DP61	Survival motor neuron protein	SMN2	28	S	1	291.7	1.03	0.98	0.92	1.10	1.05	1.03	0.92	0.86	0.95
B4DP61	Survival motor neuron protein	SMN2	31	S	1	133.7	3.19	2.68	3.72	2.50	2.87	2.39	2.28	0.96	1.90
A0A286YEX4	Nuclear factor 1 C-type	NFIC	345	S	0.944	219.3	NaN	0.55	0.80	0.92	0.84	0.92	0.64	NaN	NaN
A0A286YEX4	Nuclear factor 1 C-type	NFIC	361	S	0.96	86.51	0.50	0.57	0.55	0.82	0.67	0.79	NaN	0.57	0.55
H0Y9X0	Protein furry homolog-like	FRYL	1142	S	0.86	89.23	NaN	NaN	NaN	1.51	NaN	1.33	NaN	NaN	NaN
A0A286YFD6	Ribonucleoside-diphosphate reductase subunit M2	RRM2	20	S	1	122.2	1.13	1.09	1.01	0.98	1.13	1.18	1.03	1.07	1.00
A0A286YFG8			128	S	1	41.09	NaN	NaN	NaN	0.91	NaN	0.92	1.36	1.37	NaN
A0A2R8Y5E8	Probable histidine--tRNA ligase, mitochondrial	HARS2	56	S	1	42.29	0.59	0.95	NaN	NaN	NaN	NaN	NaN	NaN	NaN
A0A2R8Y5T7	Glutathione synthetase	GSS	301	S	1	52.06	NaN	0.64	NaN	1.27	1.07	NaN	1.27	1.11	NaN
A0A2R8Y443	Dual specificity tyrosine-phosphorylation-regulated kinase 1B;Dual specificity tyrosine-phosphorylation-regulated kinase 1A	DYRK1B	286	S	0.788	45.72	0.71	NaN	0.91	NaN	0.84	NaN	0.90	0.93	0.91
A0A2R8Y679	Serine/threonine-protein kinase B-raf	BRAF	128	S	0.6	50.95	1.09	0.77	NaN	NaN	NaN	NaN	NaN	NaN	NaN
F5H777	Coiled-coil domain-containing protein 82	CCDC82	154	S	1	157.3	0.88	0.60	NaN	NaN	NaN	NaN	NaN	NaN	NaN
A0A2R8Y4N5	DnaJ homolog subfamily C member 21	DNAJC21	254	S	1	339.3	0.58	0.53	0.70	0.95	0.87	0.91	0.73	0.67	0.71
A0A2R8YF61	Cyclin-dependent kinase 13	CDK13	102	S	0.843	103.4	NaN	0.50	1.89	NaN	NaN	NaN	NaN	NaN	NaN
A0A2R8Y4Z8	Coiled-coil domain-containing protein 9	CCDC9	386	S	0.882	165.7	1.05	1.17	1.01	0.86	0.85	0.86	0.91	1.00	1.18
A0A2R8Y4Z8			521	S	1	123.7	1.89	NaN	2.12	1.74	1.90	1.77	1.12	1.24	1.22
A0A2R8Y6I5	Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	209	S	0.667	50.66	0.76	NaN	NaN	1.17	0.96	NaN	1.15	NaN	NaN
A0A2R8Y7R5	Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	33	S	1	211.2	0.53	0.53	0.46	0.48	0.50	0.47	0.57	NaN	0.65
H0YH87	Ataxin-2	ATXN2	701	S	0.934	166.1	1.13	NaN	1.09	1.33	1.35	NaN	1.25	NaN	1.45

H0YH87	Ataxin-2	ATXN2	705	S	0.979	166.1	1.13	NaN	1.09	1.33	1.35	1.37	1.25	NaN	1.45
H0YH87	Ataxin-2	ATXN2	612	S	0.953	89.51	1.14	0.50	0.53	NaN	NaN	0.76	NaN	0.88	0.95
H0YH87	Ataxin-2	ATXN2	598	S	0.86	63.1	NaN	NaN	0.65	1.11	1.06	0.75	0.62	0.67	0.94
H3BQK4	Tuberin	TSC2	157	S	1	138.1	0.33	NaN	NaN	0.48	0.62	NaN	0.44	1.09	1.42
A0A494C1R1	Putative Polycomb group protein ASXL1	ASXH1	503	S	0.535	74.91	NaN	NaN	NaN	NaN	NaN	NaN	0.91	0.78	NaN
A0A2R8Y611	AP-3 complex subunit delta-1	AP3D1	374	S	1	107.7	0.44	0.43	NaN	NaN	NaN	NaN	NaN	NaN	NaN
A0A2R8Y611	AP-3 complex subunit delta-1	AP3D1	376	S	1	107.7	0.59	0.43	NaN	NaN	NaN	NaN	NaN	NaN	NaN
A0A2R8Y611	AP-3 complex subunit delta-1	AP3D1	378	S	1	103.8	0.33	0.43	NaN	NaN	NaN	NaN	NaN	NaN	NaN
A0A2R8Y611	AP-3 complex subunit delta-1	AP3D1	569	S	0.806	135.7	0.71	NaN	NaN	1.16	1.08	NaN	NaN	0.64	NaN
A0A2R8Y611	AP-3 complex subunit delta-1	AP3D1	571	S	0.79	89.63	NaN	NaN	0.73	NaN	NaN	NaN	0.65	NaN	0.55
H0Y8T6	Rap guanine nucleotide exchange factor 2	RAPGEF2	128	S	0.958	119.5	0.85	NaN	0.86	0.67	0.60	0.84	1.12	1.14	NaN
Q5JS72		CASK	192	S	0.991	284.3	1.13	1.09	1.33	1.01	0.88	1.03	1.14	1.21	1.39
A0A2R8Y6G6	Alpha-enolase	ENO1	419	S	1	48.66	NaN	NaN	NaN	NaN	NaN	NaN	0.49	NaN	0.72
H0Y470	Girdin	CCDC88A	65	S	0.834	88.04	NaN	NaN	NaN	2.75	1.79	NaN	NaN	NaN	2.37
H0Y470	Girdin	CCDC88A	670	S	0.994	66.32	NaN	NaN	1.02	0.85	0.86	0.77	1.14	1.16	NaN
H0Y470	Girdin	CCDC88A	719	S	1	213.8	0.64	NaN	0.65	NaN	NaN	0.83	0.95	1.10	1.09
F8WF45	TATA element modulatory factor	TMF1	399	S	0.556	139.8	1.37	1.39	1.72	1.19	1.08	1.29	0.99	1.29	NaN
F8WF45	TATA element modulatory factor	TMF1	344	S	1	231.4	1.16	0.97	1.01	1.03	0.93	1.02	0.83	0.86	0.91
A0A2R8Y7R9	Liprin-alpha-1;Liprin-alpha-4	PPFIA1	733	S	0.925	62.09	1.66	0.47	1.40	1.22	1.21	0.51	1.47	NaN	NaN
A0A2R8Y7R9	Liprin-alpha-1;Liprin-alpha-4	PPFIA1	736	S	0.575	54.02	1.66	1.35	1.40	1.22	1.21	NaN	1.47	NaN	NaN
A0A2R8Y7R9	Liprin-alpha-1	PPFIA1	224	S	0.995	73.14	2.05	1.55	NaN	NaN	NaN	NaN	NaN	NaN	NaN
A0A2R8Y880	E3 ubiquitin-protein ligase RBBP6	RBBP6	282	S	1	57.3	0.84	0.70	NaN	NaN	NaN	NaN	NaN	NaN	NaN
A0A2R8Y880	E3 ubiquitin-protein ligase RBBP6	RBBP6	283	S	1	57.3	0.84	0.70	NaN	NaN	NaN	NaN	NaN	NaN	NaN
A0A2R8Y880	E3 ubiquitin-protein ligase RBBP6	RBBP6	284	S	1	57.3	0.84	0.70	NaN	NaN	NaN	NaN	NaN	NaN	NaN
A0A2R8Y880	E3 ubiquitin-protein ligase RBBP6	RBBP6	285	S	1	57.3	0.84	0.70	NaN	NaN	NaN	NaN	NaN	NaN	NaN
A0A2R8YCL1	Growth factor receptor-bound protein 10	GRB10	188	S	0.974	54.63	NaN	1.38	NaN	NaN	0.93	NaN	1.99	NaN	1.60
C9JEF4	Histone deacetylase 6	HDAC6	22	S	1	127.7	0.45	0.35	NaN	NaN	NaN	0.65	1.14	1.12	1.00
A0A2R8YDS4	Nitric oxide synthase,	NOS2	887	S	0.958	42.52	NaN	NaN	0.59	1.19	1.15	NaN	NaN	0.49	NaN
E9PDQ5	Rho guanine nucleotide exchange factor 7	ARHGEF 7	420	S	0.907	63.09	NaN	1.05	1.10	1.10	0.97	1.08	NaN	1.27	NaN
E9PDQ5	Rho guanine nucleotide exchange factor 7;Rho guanine nucleotide exchange	ARHGEF 7	262	S	1	92.44	1.76	1.53	1.79	2.27	2.05	1.97	NaN	0.60	0.67
A0A2U3TZL8	Kinesin-like protein;Kinesin-like protein KIF23	KIF23	717	S	1	123.3	0.23	0.20	NaN	0.36	NaN	0.34	0.38	0.40	0.50
C9J7T7	Nuclear receptor corepressor	NCOR2	496	S	1	56.6	NaN	NaN	2.30	NaN	NaN	NaN	1.86	2.60	2.31
Q5JU47	TBC1 domain family member	TBC1D4	103	S	0.998	62.34	0.73	NaN	1.23	NaN	0.89	NaN	2.33	2.47	NaN
Q5JU47	TBC1 domain family member	TBC1D4	200	S	0.838	177.1	NaN	2.15	NaN	NaN	NaN	NaN	1.92	NaN	2.26

Q5JU47	TBC1 domain family member	TBC1D4	203	S	1	249.3	1.57	0.69	0.72	2.17	0.89	NaN	0.97	0.70	2.26
C9JBX5	Translocon-associated protein subunit alpha	SSR1	200	S	1	163.9	1.91	1.66	NaN	1.91	NaN	1.93	NaN	0.98	0.61
A0A3B3IS71	Retinoblastoma-associated protein	RB1	807	S	1	86.54	1.41	NaN	0.83	0.77	0.91	0.81	0.54	0.54	0.54
A0A3B3IS71	Retinoblastoma-associated protein	RB1	37	S	1	123.6	0.78	0.77	0.84	0.90	1.01	0.89	0.77	0.67	0.70
A0A3B3IS71	Retinoblastoma-associated protein	RB1	249	S	1	71.51	1.10	1.51	NaN	NaN	NaN	NaN	NaN	NaN	NaN
A0A3B3IU78	Coatomer subunit alpha;Xenin;Proxenin	COPA	43	S	1	66.57	1.75	1.88	1.51	NaN	NaN	NaN	0.67	NaN	NaN
A0A3B3ISN0			190	S	0.99	81.77	2.13	2.28	2.43	NaN	1.10	1.03	3.04	3.11	3.13
A0A3B3ISQ4	Epidermal growth factor receptor kinase substrate 8-like protein 2	EPS8L2	479	S	0.785	114.7	1.01	NaN	NaN	NaN	NaN	1.00	1.06	1.04	NaN
A0A3B3ISQ4	Epidermal growth factor receptor kinase substrate 8-like protein 2	EPS8L2	459	S	0.794	114.7	NaN	NaN	NaN	NaN	NaN	NaN	0.74	1.04	NaN
A0A3B3ISQ4	Epidermal growth factor receptor kinase substrate 8-like protein 2	EPS8L2	570	S	0.993	121.9	0.91	0.89	0.95	1.06	0.95	1.00	1.10	1.05	1.16
A0A3B3ISZ4	Polycomb group RING finger protein 6	PCGF6	115	S	1	103.7	NaN	NaN	NaN	0.75	NaN	NaN	0.89	0.79	0.77
A0A3B3ITD8	Nuclear pore complex protein Nup98-Nup96;Nuclear pore complex protein Nup98;Nuclear pore complex	NUP98	606	S	1	312.6	1.80	1.60	2.08	1.55	1.52	1.43	1.80	1.89	1.49
A0A3B3ITD8	Nuclear pore complex protein Nup98-Nup96;Nuclear pore complex protein Nup98;Nuclear pore complex	NUP98	871	S	1	235.5	0.88	0.81	0.86	0.91	0.86	0.76	1.01	0.99	1.05
A0A3B3ITE3	Gamma-tubulin complex component 3	TUBGCP3	515	S	0.851	211.6	0.59	1.62	NaN	NaN	0.61	NaN	NaN	0.68	NaN
H0Y3A3	Disabled homolog 2-interacting protein	DAB2IP	887	S	1	118.8	NaN	NaN	NaN	0.21	0.34	NaN	0.38	0.48	0.66
A0A3B3ITG6	Translation initiation factor eIF-2B subunit epsilon	EIF2B5	500	S	1	128.2	0.53	0.56	NaN	0.80	0.79	NaN	NaN	0.65	0.65
A0A3B3ITK7	Phosphoglucomutase-1	PGM1	117	S	1	156.1	1.09	1.07	NaN	NaN	NaN	NaN	NaN	1.23	NaN
A0A3B3IU46	RNMT-activating mini protein	FAM103A1	36	S	1	90.02	1.23	1.16	NaN	1.42	1.35	NaN	0.82	0.89	NaN
A0A3B3IUA7	E3 ubiquitin/ISG15 ligase TRIM25	TRIM25	100	S	1	171.5	1.11	1.09	1.27	1.75	1.72	1.32	0.96	0.88	0.43
A0A3F2YNX0	Protein transport protein Sec16A	SEC16A	1905	S	0.967	55.34	NaN	1.84	1.85	1.76	1.53	NaN	1.27	1.33	NaN
A0A3F2YNX0	Protein transport protein Sec16A	SEC16A	891	S	1	86.08	0.72	0.72	0.72	0.83	0.83	0.88	0.92	0.94	0.87

A0A3F2YNX0	Protein transport protein Sec16A	SEC16A	417	S	1	130.9	0.73	0.54	0.66	0.63	1.04	NaN	1.10	NaN	NaN
A0A3F2YNX0	Protein transport protein Sec16A	SEC16A	1786	S	1	88.32	NaN	3.42	3.56	2.48	3.00	2.77	1.89	NaN	2.68
A0A3F2YNX0	Protein transport protein Sec16A	SEC16A	390	S	0.635	118.8	NaN	1.09	NaN	NaN	NaN	NaN	1.03	1.14	NaN
A0A3F2YNX0	Protein transport protein Sec16A	SEC16A	391	S	0.971	225.1	NaN	NaN	0.78	0.98	1.10	0.92	NaN	0.87	NaN
A0A3F2YNY6	Pre-mRNA-processing factor 40 homolog A	PRPF40A	975	S	0.999	169.4	NaN	NaN	NaN	0.48	NaN	0.51	1.41	NaN	0.36
A0A3F2YNY6	Pre-mRNA-processing factor 40 homolog A	PRPF40A	920	S	1	93.92	0.94	0.89	0.88	0.93	0.89	0.87	0.91	0.88	0.93
A0A3F2YNY6	Pre-mRNA-processing factor 40 homolog A	PRPF40A	922	S	1	93.92	0.94	0.89	0.88	0.93	0.89	0.87	0.91	0.88	0.93
A0A3F2YNY6	Pre-mRNA-processing factor 40 homolog A	PRPF40A	925	S	1	93.92	0.94	1.78	2.13	0.93	0.89	0.87	0.91	0.88	0.93
A0A494BZT8	Transforming acidic coiled-coil-containing protein 3	TACC3	250	S	0.745	81.14	2.07	NaN	NaN	3.66	3.19	3.22	NaN	NaN	NaN
A0A494BZT8	Transforming acidic coiled-coil-containing protein 3	TACC3	434	S	0.991	149.9	3.12	2.83	NaN	NaN	3.24	NaN	NaN	NaN	NaN
A0A494BZV2	Myosin phosphatase Rho-interacting protein	MPRIP	2364	S	1	194.1	0.77	0.77	0.98	1.28	1.59	1.19	0.44	0.53	0.71
A0A494BZV2	Myosin phosphatase Rho-interacting protein	MPRIP	289	S	0.999	81.53	1.37	1.42	1.40	1.30	NaN	1.15	1.45	1.44	1.12
A0A494BZV2	Myosin phosphatase Rho-interacting protein	MPRIP	292	S	0.819	81.53	1.37	1.42	1.40	1.30	NaN	NaN	1.45	NaN	NaN
A0A494BZV2	Myosin phosphatase Rho-interacting protein	MPRIP	483	S	0.672	197.4	2.00	1.97	NaN	NaN	2.09	1.14	NaN	NaN	NaN
A0A494BZV2	Myosin phosphatase Rho-interacting protein	MPRIP	220	S	0.969	166.1	1.45	1.15	1.57	1.69	1.19	1.65	1.11	1.76	1.06
A0A494BZV2	Myosin phosphatase Rho-interacting protein	MPRIP	224	S	0.998	166.1	1.45	1.15	1.54	1.57	1.22	1.65	1.00	1.46	1.04
A0A494BZV2	Myosin phosphatase Rho-interacting protein	MPRIP	737	S	1	121.6	1.37	1.29	1.24	NaN	1.80	1.69	0.84	0.81	0.74
A0A494BZV2	Myosin phosphatase Rho-interacting protein	MPRIP	2380	S	0.998	84.76	NaN	1.29	1.33	1.43	1.41	1.34	2.00	1.76	1.74
A0A494C050	NF-kappa-B-activating protein	NKAP	149	S	1	111.7	0.99	1.05	1.07	0.86	1.01	1.13	0.96	1.00	0.95
H0Y6K5	Transcription factor Sp3	SP3	5	S	1	128.3	0.94	NaN	NaN	0.76	NaN	0.89	NaN	NaN	1.47
D6RC77	Phosphoacetylglucosamine mutase	PGM3	92	S	0.751	203.3	0.47	0.48	NaN	0.72	NaN	NaN	NaN	0.47	NaN
A0A494C0B4	UV excision repair protein RAD23 homolog A	RAD23A	128	S	0.761	117.4	NaN	NaN	NaN	0.76	NaN	0.76	NaN	NaN	NaN
A0A494C0B4	UV excision repair protein RAD23 homolog A	RAD23A	133	S	0.86	82.51	0.50	NaN	0.57	NaN	NaN	NaN	NaN	NaN	NaN
A0A494C0Q6	Poly(A)-specific ribonuclease PARN	PARN	561	S	1	73.35	1.05	NaN	1.60	NaN	1.12	1.66	1.30	NaN	1.61

H7BZ50	Mitotic-spindle organizing protein 2B	MZT2B	115	S	0.949	86.26	0.87	NaN	0.96	NaN	NaN	NaN	1.01	0.91	NaN
A0A494C108	Protein KRI1 homolog	KRI1	177	S	1	327.6	1.14	1.13	1.14	1.10	1.23	1.22	1.13	1.27	1.20
A0A494C108	Protein KRI1 homolog	KRI1	634	S	1	173.6	0.51	0.43	0.65	0.44	0.52	1.06	0.61	0.75	0.88
A0A494C108	Protein KRI1 homolog	KRI1	645	S	1	148.4	NaN	0.77	1.11	1.22	NaN	1.06	0.66	0.61	NaN
A0A494C108	Protein KRI1 homolog	KRI1	142	S	1	78.09	1.29	NaN	1.40	1.04	1.17	NaN	NaN	1.01	NaN
A0A494C198	Protein DEK	DEK	229	S	1	124.1	0.75	0.83	0.80	0.89	0.90	0.86	0.84	0.89	0.84
A0A494C198	Protein DEK	DEK	231	S	1	124.1	0.75	0.83	0.80	0.89	0.90	0.86	0.84	0.82	0.81
A0A494C198	Protein DEK	DEK	234	S	1	124.1	0.75	0.83	0.80	0.89	0.91	0.85	0.82	0.82	0.81
A0A494C198	Protein DEK	DEK	235	S	1	124.1	0.75	0.83	0.80	0.89	0.91	0.85	0.82	0.82	0.81
A0A494C1A5	U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	225	S	1	440.6	0.62	0.64	0.62	0.83	0.70	0.77	0.67	0.66	0.67
A0A494C1F2	Nuclear pore complex protein Nup214	NUP214	666	S	1	85.62	0.89	0.80	0.82	0.94	0.96	0.95	0.84	0.85	0.87
A0A494C1F2	Nuclear pore complex protein Nup214	NUP214	430	S	0.983	132.4	0.46	0.42	1.58	0.60	1.38	1.27	NaN	0.63	NaN
A0A494C1F2	Nuclear pore complex protein Nup214	NUP214	433	S	0.829	71.4	NaN	NaN	NaN	NaN	NaN	NaN	0.66	NaN	0.64
C9J8U1	Cytospin-A	SPECC1L	384	S	1	110.6	0.71	NaN	NaN	NaN	0.91	0.46	1.00	1.14	1.36
C9J8U1	Cytospin-A	SPECC1L	385	S	1	110.6	0.71	NaN	NaN	NaN	0.91	0.46	1.00	1.14	1.36
A0A494C1K3	General transcription factor II-I	GTF2I	984	S	0.999	154.9	0.59	0.63	0.61	0.74	0.73	0.69	0.88	0.83	0.85
C9JXK0	Lamin-B receptor	LBR	84	S	1	94.69	NaN	0.95	1.05	NaN	0.99	0.99	NaN	NaN	NaN
C9JXK0	Lamin-B receptor	LBR	86	S	1	87.22	0.35	0.95	1.05	NaN	0.99	0.99	NaN	NaN	NaN
Q7Z6P5	DNA replication licensing factor MCM3	MCM3	206	S	0.991	246.4	0.59	0.60	0.62	0.85	0.88	0.78	0.46	0.46	0.48
Q7Z6P5	DNA replication licensing factor MCM3	MCM3	167	S	1	196.8	0.82	0.83	NaN	NaN	NaN	NaN	3.06	2.94	1.06
H0Y917	WD repeat-containing protein 26	WDR26	113	S	0.999	82.65	0.76	1.08	NaN	NaN	1.26	NaN	NaN	NaN	NaN
A0A499FJI4	E3 ubiquitin-protein ligase MYCBP2	MYCBP2	2751	S	0.972	64.24	0.57	0.78	NaN	0.68	0.63	NaN	NaN	NaN	NaN
A0A499FJI4	E3 ubiquitin-protein ligase MYCBP2	MYCBP2	3467	S	0.965	47.64	NaN	NaN	NaN	NaN	1.49	NaN	1.65	1.41	NaN
A0A499FJS7	Inhibitor of nuclear factor kappa-B kinase subunit beta	IKBKB	608	S	0.932	66.51	NaN	NaN	0.78	1.09	0.95	1.04	NaN	0.65	0.66
A0A4W8VX11	Pericentriolar material 1	PCM1	1676	S	1	167.6	0.50	0.60	NaN	0.43	NaN	0.84	NaN	0.72	NaN
A0A4W8VX11	Pericentriolar material 1	PCM1	1711	S	1	156.6	0.62	1.46	1.15	0.73	1.34	0.69	1.41	1.35	1.73
A0A4W8VX11	Pericentriolar material 1	PCM1	1714	S	1	123.2	1.52	1.46	0.62	1.38	1.34	1.04	0.67	1.35	0.62
A0A4W8VX11	Pericentriolar material 1	PCM1	862	S	0.999	150	NaN	NaN	0.41	0.46	NaN	NaN	0.55	NaN	0.79
A0A4W8VX11	Pericentriolar material 1	PCM1	65	S	0.998	172.6	0.76	0.80	0.79	0.76	0.73	0.75	0.89	0.95	0.97
H0Y8W5	Rho GTPase-activating protein 10	ARHGAP10	269	S	0.981	67.08	NaN	NaN	1.29	NaN	NaN	1.14	1.09	NaN	1.15
A1L170	Uncharacterized protein C1orf226	C1orf226	223	S	0.989	78.34	1.15	1.21	NaN	1.23	1.37	1.27	NaN	1.34	1.30
A1L170	Uncharacterized protein C1orf226	C1orf226	249	S	1	150	1.18	1.22	1.34	1.20	1.07	1.03	1.05	1.14	0.89

A2A2D0	Stathmin	STMN1	16	S	1	222.4	2.01	2.10	2.12	2.50	2.50	NaN	1.50	1.40	1.59
A2A2D0	Stathmin	STMN1	25	S	1	455.1	5.68	5.70	5.91	6.11	6.27	6.48	1.66	1.64	1.63
A2A2D0	Stathmin;Stathmin-2	STMN1	46	S	1	96.24	1.77	NaN	NaN	2.56	2.68	NaN	0.76	0.79	NaN
A2A2D0	Stathmin	STMN1	38	S	1	200.8	1.38	1.36	1.37	2.14	2.18	2.01	0.73	0.68	0.75
A2A2D0	Stathmin	STMN1	63	S	1	130.7	2.48	2.29	2.66	4.42	3.31	3.89	0.66	0.59	0.71
H7C5M1	RNA-binding protein 34	RBM34	31	S	1	110	NaN	NaN	NaN	0.79	0.55	NaN	NaN	NaN	NaN
A2AAT0	Zinc transporter SLC39A7	SLC39A7	185	S	1	132.7	0.93	0.99	0.92	0.97	0.97	0.97	0.95	0.99	0.99
A2AAT0	Zinc transporter SLC39A7	SLC39A7	186	S	1	132.7	0.93	0.96	0.92	0.97	0.97	0.97	0.95	0.99	0.99
A2RU67	Uncharacterized protein KIAA1467	KIAA1467	30	S	1	104.3	1.90	1.44	NaN	1.59	NaN	NaN	NaN	NaN	NaN
A2RU67	Uncharacterized protein KIAA1467	KIAA1467	33	S	0.999	104.3	1.90	1.44	NaN	1.59	NaN	NaN	NaN	NaN	NaN
A6NL93	Non-histone chromosomal protein HMG-14	HMGN1	76	S	0.999	170.9	0.67	0.66	0.72	0.69	0.52	0.79	0.84	1.01	0.63
A6NL93	Non-histone chromosomal protein HMG-14	HMGN1	79	S	1	152.6	0.59	0.64	0.69	0.60	0.55	0.58	0.72	0.83	0.77
A6NL93	Non-histone chromosomal protein HMG-14	HMGN1	89	S	1	129.8	0.80	0.72	NaN	0.81	0.71	0.68	0.64	0.72	0.71
A6NGP5	Hematological and neurological expressed 1-like	HN1L	18	S	0.998	156.3	2.37	NaN	2.34	5.13	4.25	6.13	0.81	0.61	NaN
P07355	Annexin A2;Putative annexin A2-like protein;Annexin	ANXA2	26	S	0.774	154.1	NaN	NaN	0.74	NaN	0.90	NaN	NaN	0.80	0.85
A6NNK5	Tumor suppressor p53-binding protein 1	TP53BP1	1381	S	1	92.9	0.73	0.61	NaN	0.95	1.22	0.99	0.99	1.21	NaN
A6NNK5	Tumor suppressor p53-binding protein 1	TP53BP1	1385	S	1	92.9	0.53	0.61	NaN	0.71	1.22	0.99	0.64	0.96	1.02
A6NNK5	Tumor suppressor p53-binding protein 1	TP53BP1	585	S	0.979	135.9	0.61	0.52	NaN	0.96	NaN	0.91	1.03	NaN	0.97
A6NNK5	Tumor suppressor p53-binding protein 1	TP53BP1	557	S	0.998	121.7	0.48	0.46	0.50	0.62	0.63	0.76	0.62	0.59	0.63
A6NNK5	Tumor suppressor p53-binding protein 1	TP53BP1	1118	S	0.572	106.2	0.38	0.37	NaN	0.61	0.61	0.43	NaN	0.47	NaN
A6NNK5	Tumor suppressor p53-binding protein 1	TP53BP1	1119	S	0.994	212.4	0.38	0.32	0.36	0.54	0.61	0.59	0.42	0.43	0.42
A6NNK5	Tumor suppressor p53-binding protein 1	TP53BP1	505	S	1	160.8	0.54	0.49	0.66	0.95	0.86	0.69	0.98	1.04	0.98
A6NNK5	Tumor suppressor p53-binding protein 1	TP53BP1	1099	S	1	150.6	0.44	0.47	NaN	0.54	0.57	0.49	0.50	0.50	0.49
A6NNK5	Tumor suppressor p53-binding protein 1	TP53BP1	1106	S	0.975	125	0.44	0.46	NaN	0.84	0.72	0.49	NaN	NaN	0.49
A6NNK5	Tumor suppressor p53-binding protein 1	TP53BP1	1109	S	0.836	150.6	NaN	NaN	NaN	NaN	NaN	NaN	0.52	0.55	NaN
A6NNK5	Tumor suppressor p53-binding protein 1	TP53BP1	270	S	1	97.91	0.64	0.62	NaN	0.99	0.89	0.93	0.89	0.94	0.86
A6NNK5	Tumor suppressor p53-binding protein 1	TP53BP1	1713	S	0.963	141.1	NaN	0.59	0.90	0.87	NaN	0.84	1.11	1.04	1.07

A6NNK5	Tumor suppressor p53-binding protein 1	TP53BP1	1714	S	0.988	141.1	NaN	0.59	0.90	0.87	NaN	0.84	1.11	1.04	1.07
A6NNK5	Tumor suppressor p53-binding protein 1	TP53BP1	385	S	0.938	166.5	0.68	NaN	0.75	0.67	0.85	NaN	1.01	0.82	1.37
G3V174	Rho GTPase-activating protein 32	ARHGAP 32	782	S	1	169.9	NaN	NaN	NaN	NaN	NaN	NaN	1.87	1.82	2.67
G3V174	Rho GTPase-activating protein 32	ARHGAP 32	797	S	0.999	204	1.08	0.92	0.90	0.91	0.93	0.59	1.16	1.39	1.18
A8MQ02	Afadin	MLLT4	1736	S	1	208.5	0.61	0.62	0.68	0.80	NaN	0.79	1.03	1.04	0.88
A8MQ02	Afadin	MLLT4	1141	S	1	100.4	NaN	0.66	NaN	NaN	NaN	0.93	NaN	0.99	1.27
A8MQ02	Afadin	MLLT4	1042	S	0.991	107.2	3.79	NaN	NaN	2.99	NaN	3.33	0.86	NaN	NaN
H7BY10	60S ribosomal protein L23a	RPL23A	45	S	0.715	60.75	1.26	1.25	NaN	NaN	NaN	NaN	NaN	NaN	NaN
A8MZ87	Kinesin light chain 2	KLC2	306	S	0.991	63.91	NaN	0.95	1.13	1.24	NaN	1.38	1.20	0.96	2.00
A9Z1X7	Serine/arginine repetitive matrix protein 1	SRRM1	747	S	1	120.2	1.04	1.18	1.02	0.80	1.04	0.75	1.01	1.13	0.85
A9Z1X7	Serine/arginine repetitive matrix protein 1	SRRM1	749	S	1	98.44	1.09	1.11	1.16	1.07	1.04	1.03	1.26	1.13	1.19
A9Z1X7	Serine/arginine repetitive matrix protein 1	SRRM1	800	S	1	61.1	0.67	0.70	NaN	NaN	0.82	0.85	NaN	1.06	NaN
A9Z1X7	Serine/arginine repetitive matrix protein 1	SRRM1	804	S	1	61.1	0.67	0.70	NaN	NaN	0.82	0.85	NaN	1.06	NaN
A9Z1X7	Serine/arginine repetitive matrix protein 1	SRRM1	806	S	1	61.1	0.67	0.70	NaN	NaN	0.82	0.85	NaN	1.06	NaN
A9Z1X7	Serine/arginine repetitive matrix protein 1	SRRM1	703	S	0.733	53.4	NaN	NaN	NaN	1.08	0.98	0.96	NaN	1.23	1.18
A9Z1X7	Serine/arginine repetitive matrix protein 1	SRRM1	704	S	0.965	121.6	NaN	NaN	1.11	1.08	1.01	0.96	0.96	0.93	0.85
A9Z1X7	Serine/arginine repetitive matrix protein 1	SRRM1	705	S	0.948	191	1.15	1.10	NaN	1.04	NaN	NaN	1.15	1.12	NaN
A9Z1X7	Serine/arginine repetitive matrix protein 1	SRRM1	684	S	1	95.48	1.20	1.24	1.27	1.04	1.17	1.05	NaN	1.02	NaN
A9Z1X7	Serine/arginine repetitive matrix protein 1	SRRM1	397	S	1	152	0.41	0.39	0.43	0.59	0.56	0.57	0.50	0.50	0.51
A9Z1X7	Serine/arginine repetitive matrix protein 1	SRRM1	883	S	1	180	1.38	1.48	1.59	1.42	1.67	1.53	1.29	1.77	1.50
A9Z1X7	Serine/arginine repetitive matrix protein 1	SRRM1	778	S	1	203.3	0.67	0.76	0.74	0.88	0.79	0.93	0.52	0.59	0.60
A9Z1X7	Serine/arginine repetitive matrix protein 1	SRRM1	784	S	1	203.3	0.89	0.84	0.86	0.96	1.03	0.94	0.86	0.85	0.87
A9Z1X7	Serine/arginine repetitive matrix protein 1	SRRM1	790	S	0.849	88.84	NaN	NaN	1.23	1.24	0.83	1.32	1.03	1.07	1.56
A9Z1X7	Serine/arginine repetitive matrix protein 1	SRRM1	458	S	1	104.3	1.43	1.48	0.65	1.25	1.32	1.27	1.07	1.24	0.77
A9Z1X7	Serine/arginine repetitive matrix protein 1	SRRM1	460	S	1	104.3	1.43	1.48	1.13	1.25	1.32	1.27	1.07	1.24	1.31
A9Z1X7	Serine/arginine repetitive matrix protein 1	SRRM1	654	S	0.755	59.37	NaN	1.01	NaN	1.01	1.09	NaN	1.09	NaN	1.15

A9Z1X7	Serine/arginine repetitive matrix protein 1	SRRM1	635	S	1	65.3	0.90	0.96	0.97	0.92	0.79	0.89	0.99	0.91	0.85
A9Z1X7	Serine/arginine repetitive matrix protein 1	SRRM1	637	S	1	65.3	0.90	0.96	0.97	0.92	0.79	0.89	0.99	0.91	0.85
A9Z1X7	Serine/arginine repetitive matrix protein 1	SRRM1	445	S	0.999	131.9	1.21	1.11	1.18	1.08	1.08	1.07	1.11	1.10	1.13
A9Z1X7	Serine/arginine repetitive matrix protein 1	SRRM1	384	S	1	128.1	0.70	0.70	0.72	1.38	0.74	0.71	0.76	0.78	0.80
A9Z1X7	Serine/arginine repetitive matrix protein 1	SRRM1	386	S	1	117.2	0.70	0.70	0.72	0.72	0.76	0.71	NaN	0.78	NaN
A9Z1X7	Serine/arginine repetitive matrix protein 1	SRRM1	388	S	1	128.1	1.65	1.91	1.76	0.72	0.76	NaN	0.76	0.78	0.80
A9Z1X7	Serine/arginine repetitive matrix protein 1	SRRM1	722	S	1	78.69	0.97	1.23	1.11	1.00	NaN	0.98	0.97	0.99	0.93
A9Z1X7	Serine/arginine repetitive matrix protein 1	SRRM1	724	S	0.996	68.28	0.87	NaN	1.15	1.06	1.09	1.01	NaN	0.98	NaN
A9Z1X7	Serine/arginine repetitive matrix protein 1	SRRM1	726	S	0.75	65.04	NaN	NaN	1.02	1.08	NaN	NaN	1.21	0.93	0.96
A9Z1X7	Serine/arginine repetitive matrix protein 1	SRRM1	662	S	1	115.3	1.00	0.99	1.02	0.96	0.99	0.97	0.95	NaN	0.96
A9Z1X7	Serine/arginine repetitive matrix protein 1	SRRM1	569	S	1	100.8	0.52	0.57	0.54	0.78	0.78	0.68	0.61	0.61	0.55
A9Z1X7	Serine/arginine repetitive matrix protein 1	SRRM1	571	S	1	100.8	1.41	1.48	1.45	1.25	1.22	1.17	1.37	1.46	1.38
A9Z1X7	Serine/arginine repetitive matrix protein 1	SRRM1	558	S	1	62.68	1.05	1.08	NaN	NaN	0.99	0.96	NaN	NaN	NaN
A9Z1X7	Serine/arginine repetitive matrix protein 1	SRRM1	560	S	1	62.68	1.05	1.08	NaN	NaN	0.99	0.96	NaN	NaN	NaN
A9Z1X7	Serine/arginine repetitive matrix protein 1	SRRM1	592	S	1	65.88	1.15	1.15	1.31	1.14	1.19	1.24	1.24	1.27	1.32
A9Z1X7	Serine/arginine repetitive matrix protein 1	SRRM1	645	S	1	64.5	1.05	1.08	0.79	1.04	NaN	NaN	1.04	1.00	1.01
A9Z1X7	Serine/arginine repetitive matrix protein 1	SRRM1	647	S	1	77.38	0.92	1.08	0.79	0.78	NaN	0.69	1.04	0.79	0.74
A9Z1X7	Serine/arginine repetitive matrix protein 1	SRRM1	763	S	1	190.2	0.54	0.88	0.56	0.63	0.64	0.62	0.56	0.74	0.69
A9Z1X7	Serine/arginine repetitive matrix protein 1	SRRM1	765	S	1	190.2	0.57	0.61	0.56	0.60	0.59	0.55	0.51	0.49	0.45
A9Z1X7		SRRM1	547	S	0.997	50.83	2.00	2.08	2.29	NaN	NaN	1.60	1.61	1.54	1.76
A9Z1X7	Serine/arginine repetitive matrix protein 1	SRRM1	606	S	1	101.5	1.49	1.56	1.81	1.46	0.98	1.45	1.63	1.02	1.71
A9Z1X7	Serine/arginine repetitive matrix protein 1	SRRM1	614	S	0.919	79.89	NaN	1.07	1.05	0.99	0.97	0.97	1.05	1.02	1.02
A9Z1X7	Serine/arginine repetitive matrix protein 1	SRRM1	616	S	1	79.89	NaN	1.07	1.05	0.99	0.97	0.97	1.05	1.02	1.02
A9Z1X7	Serine/arginine repetitive matrix protein 1	SRRM1	424	S	0.998	79.8	1.52	1.58	1.59	1.37	1.35	1.37	1.47	1.48	NaN

A9Z1X7	Serine/arginine repetitive matrix protein 1	SRRM1	426	S	1	79.8	0.69	0.71	0.74	0.66	0.69	0.68	0.71	0.74	NaN
A9Z1X7	Serine/arginine repetitive matrix protein 1	SRRM1	625	S	1	129	0.90	0.95	0.96	1.36	1.00	0.91	1.24	0.91	0.94
A9Z1X7	Serine/arginine repetitive matrix protein 1	SRRM1	409	S	0.996	81.43	NaN	1.28	1.08	0.95	NaN	0.97	NaN	1.14	1.12
A9Z1X7	Serine/arginine repetitive matrix protein 1	SRRM1	375	S	0.993	78.15	1.08	1.06	1.07	1.00	NaN	NaN	1.02	NaN	NaN
A9Z1X7	Serine/arginine repetitive matrix protein 1	SRRM1	260	S	1	108.3	0.90	0.90	0.95	0.93	0.95	0.96	0.96	0.99	0.98
B7Z2E6	14-3-3 protein zeta/delta	YWHAZ	87	S	0.994	134.5	0.84	0.72	0.74	0.73	NaN	0.73	1.23	NaN	0.97
B0YIW6	Coatomer subunit delta	ARCN1	534	S	1	84.89	2.00	2.12	1.72	2.37	2.39	2.34	0.80	0.90	1.06
F5H7V1	Nardilysin	NRD1	94	S	0.998	115.6	1.18	1.17	1.20	1.22	1.30	NaN	1.11	0.93	1.18
F5H7V1	Nardilysin	NRD1	96	S	0.565	82.93	NaN	NaN	NaN	NaN	1.25	NaN	0.99	1.09	NaN
B1AKL4	Eukaryotic translation initiation factor 4E transporter	EIF4ENIF1	563	S	0.996	84.69	2.23	2.32	NaN	NaN	NaN	NaN	1.03	1.88	1.05
B1AKL4	Eukaryotic translation initiation factor 4E transporter	EIF4ENIF1	927	S	0.921	44.57	NaN	1.97	NaN	NaN	1.61	NaN	1.16	NaN	1.31
B1AKN3	Arginine-glutamic acid dipeptide repeats protein	RERE	838	S	1	126.6	1.36	1.00	NaN	NaN	NaN	NaN	0.88	NaN	NaN
B1AKN3	Arginine-glutamic acid dipeptide repeats protein	RERE	845	S	0.992	126.6	1.36	1.00	NaN	NaN	NaN	NaN	0.88	NaN	NaN
B1AKN3	Arginine-glutamic acid dipeptide repeats protein	RERE	847	S	0.992	126.6	1.36	1.00	NaN	NaN	NaN	NaN	0.88	NaN	NaN
B1AKZ5	Astrocytic phosphoprotein PEA-15	PEA15	94	S	1	172.7	1.42	1.41	1.39	1.23	1.27	1.30	1.37	1.41	1.42
E5RHT1	Presenilin;Presenilin-2;Presenilin-2 NTF subunit;Presenilin-2 CTF subunit	PSEN2	25	S	0.998	181.9	0.51	0.50	NaN	NaN	NaN	NaN	0.49	NaN	NaN
B1AUU8	Epidermal growth factor receptor substrate 15	EPS15	662	S	1	78.66	1.45	1.59	1.73	1.43	1.32	NaN	1.34	1.53	1.81
B1AUU8	Epidermal growth factor receptor substrate 15	EPS15	680	S	0.998	45.55	0.73	1.80	NaN	NaN	NaN	NaN	NaN	NaN	NaN
B1AUU8	Epidermal growth factor receptor substrate 15	EPS15	428	S	0.5	111.2	NaN	0.97	NaN	NaN	NaN	NaN	0.93	NaN	0.86
B1AUU8	Epidermal growth factor receptor substrate 15	EPS15	429	S	0.5	111.2	NaN	0.97	NaN	NaN	NaN	NaN	0.93	NaN	0.86
H0YCM0	Non-specific serine/threonine protein kinase;Serine/threonine-protein	PAK1	65	S	1	166.5	0.96	1.09	NaN	0.94	1.00	0.86	NaN	1.07	0.97
B3KR00	AMSH-like protease	STAMBPL1	76	S	0.983	71.39	NaN	NaN	1.05	0.99	0.66	0.93	NaN	NaN	NaN
H3BN34	Pyruvate kinase;Pyruvate kinase PKM	PKM	37	S	1	151.5	NaN	1.36	1.35	1.35	NaN	1.24	1.14	1.20	1.13
C9JUN4	Phosphoribosyl pyrophosphate synthase-	PRPSAP1	141	S	1	226.1	0.57	0.58	0.66	0.65	0.75	0.72	NaN	0.50	NaN

C9JEN3	Protein lifeguard 3	TMBIM1	81	S	0.999	85.52	NaN	1.56	1.01	NaN	NaN	NaN	NaN	1.90	NaN
I3L0Y9	Brain-specific angiogenesis inhibitor 1-associated protein 2	BAIAP2	82	S	1	89.3	NaN	NaN	1.36	1.23	1.26	1.28	0.84	0.90	0.89
B4DWJ1	Focal adhesion kinase 1	PTK2	220	S	0.999	79.51	2.73	2.23	2.53	1.97	2.06	2.23	1.02	1.23	1.32
G3V2D6	Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	220;141	S	1	144.3	0.80	0.80	0.86	0.84	0.83	0.82	0.79	0.81	0.83
B4DYP1	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1	DDAH1	105	S	1	44.3	NaN	NaN	1.77	1.01	NaN	1.11	NaN	0.70	NaN
B4E1E0	CTP synthase;CTP synthase	CTPS1	415	S	0.571	46.5	NaN	NaN	1.62	NaN	NaN	0.99	2.21	1.88	NaN
B4E1E0	CTP synthase;CTP synthase	CTPS1	418	S	0.983	169.8	0.71	0.62	NaN	0.53	0.51	0.46	1.23	1.47	0.88
B4E1E0	CTP synthase;CTP synthase	CTPS1	419	S	1	169.8	1.19	1.06	1.10	0.66	0.72	0.58	0.96	1.22	0.94
H7C118	Protein phosphatase 1 regulatory subunit 7	PPP1R7	33	S	1	95.62	0.51	0.55	0.59	0.71	0.58	1.08	0.86	0.76	0.79
H7C118	Protein phosphatase 1 regulatory subunit 7	PPP1R7	36	S	1	95.62	0.59	1.05	0.61	1.12	0.62	1.08	1.24	0.86	0.97
H7C2Y0	Septin-2	2-Sep	73	S	1	288.9	0.95	0.93	0.94	0.88	0.87	0.94	0.97	0.99	1.07
B5MDQ0	DNA excision repair protein ERCC-6-like	ERCC6L	823	S	0.833	117.5	1.11	NaN	1.12	NaN	NaN	NaN	NaN	1.42	NaN
B5MDQ0	DNA excision repair protein ERCC-6-like	ERCC6L	946	S	1	73.5	0.76	0.77	NaN	0.97	0.90	0.95	1.03	1.04	NaN
H3BPE4	Eukaryotic translation initiation factor 3 subunit C;Eukaryotic translation initiation factor 3 subunit C-like protein	EIF3C	13	S	0.705	85.24	NaN	NaN	NaN	NaN	NaN	NaN	0.42	NaN	0.49
H3BPE4	Eukaryotic translation initiation factor 3 subunit C;Eukaryotic translation initiation factor 3 subunit C-like protein	EIF3C	15	S	0.722	85.24	NaN	NaN	NaN	NaN	NaN	NaN	0.42	NaN	0.49
H3BPE4	Eukaryotic translation initiation factor 3 subunit C;Eukaryotic translation initiation factor 3 subunit C-like protein	EIF3C	16	S	0.495	83.19	NaN	NaN	NaN	NaN	NaN	NaN	0.42	NaN	0.49
H3BPE4	Eukaryotic translation initiation factor 3 subunit C;Eukaryotic translation initiation factor 3 subunit C-like protein	EIF3C	18	S	0.894	85.24	NaN	NaN	NaN	NaN	NaN	NaN	0.42	NaN	0.49
H3BPE4	Eukaryotic translation initiation factor 3 subunit C;Eukaryotic translation initiation factor 3 subunit C-like protein	EIF3C	39	S	1	168	1.62	1.68	1.61	1.33	1.37	1.47	1.36	1.33	1.43
B7Z4K4	Putative tRNA (cytidine(32)/guanosine(34)-2'-O)-methyltransferase	FTSJ1	134	S	0.983	62.61	1.16	1.38	NaN	NaN	NaN	NaN	NaN	NaN	NaN
B7Z7F3	Ran-binding protein 3	RANBP3	32	S	1	171.2	0.77	0.80	0.73	0.77	NaN	0.81	0.64	0.68	0.63
B7Z7F3	Ran-binding protein 3	RANBP3	33	S	1	171.9	0.66	0.60	1.34	0.77	0.68	0.83	0.61	0.68	0.61
B7Z7F3	Ran-binding protein 3	RANBP3	40	S	1	134.6	NaN	0.27	1.00	NaN	0.66	0.85	NaN	1.38	1.19
B7Z7F3	Ran-binding protein 3	RANBP3	260	S	1	160.3	1.02	1.09	1.06	1.13	1.20	1.10	1.02	1.01	1.04

F8WF16	Periphilin-1	PPHLN1	138	S	0.996	110.6	0.75	0.76	0.75	0.72	0.79	0.74	0.82	0.82	0.83
B7ZBM3	Forkhead box protein P4	FOXP4	542	S	0.873	46.84	NaN	NaN	NaN	NaN	NaN	1.20	0.67	NaN	0.65
B7ZKW8	CapZ-interacting protein	RCSD1	90;120	S	1	153.1	0.36	0.37	NaN	NaN	0.34	NaN	NaN	NaN	0.34
B7ZKW8	CapZ-interacting protein	RCSD1	186;216	S	0.999	128.4	0.56	0.58	0.55	0.71	0.61	0.57	0.57	0.63	0.60
B7ZKW8	CapZ-interacting protein	RCSD1	321;351	S	1	97.78	0.49	0.52	0.58	0.68	0.72	0.70	0.73	0.68	0.69
B7ZKW8	CapZ-interacting protein	RCSD1	237;267	S	0.619	223.3	0.47	NaN	NaN	0.79	1.48	NaN	NaN	NaN	NaN
B7ZKW8	CapZ-interacting protein	RCSD1	238;268	S	0.834	190	0.47	NaN	NaN	0.72	1.48	NaN	NaN	NaN	NaN
B7ZKW8	CapZ-interacting protein	RCSD1	53;83	S	0.796	75.74	0.58	0.55	NaN	NaN	NaN	NaN	NaN	NaN	NaN
E5RJM0	Cytoplasmic polyadenylation element-binding protein 4	CPEB4	97	S	0.701	44.75	2.11	NaN	0.82	NaN	NaN	1.77	NaN	NaN	NaN
B8ZZ08	Putative RNA-binding protein Luc7-like 1	LUC7L	162	S	1	72.32	NaN	NaN	1.23	1.04	NaN	NaN	1.16	1.10	NaN
B8ZZF5	Protein eva-1 homolog A	EVA1A	102	S	0.939	90.86	NaN	NaN	1.06	NaN	NaN	NaN	1.73	NaN	1.97
B8ZZI9	Aftiphilin	AFTPH	37	S	0.997	70.96	1.16	NaN	1.43	NaN	NaN	NaN	1.22	1.23	1.13
C9J2I0	Arf-GAP domain and FG repeat-containing protein 1	AGFG1	103	S	0.995	65.63	2.93	1.78	NaN	1.64	1.71	1.30	1.87	1.75	NaN
B9ZVT1	RNA-binding protein 12B	RBM12B	575	S	1	53.45	0.69	0.59	NaN	0.72	0.73	NaN	NaN	0.87	NaN
B9ZVT1	RNA-binding protein 12B	RBM12B	719	S	0.998	42.94	NaN	NaN	NaN	NaN	NaN	NaN	0.99	1.00	0.98
C9JWF0	Structural maintenance of chromosomes protein 4;Structural maintenance of chromosomes protein	SMC4	22	S	1	190.4	1.20	1.10	0.84	0.96	0.83	0.84	1.17	1.18	0.90
C9JWF0	Structural maintenance of chromosomes protein 4;Structural maintenance of chromosomes protein	SMC4	27	S	0.914	190.4	0.86	NaN	NaN	1.11	1.20	0.96	0.68	NaN	0.82
C9JWF0	Structural maintenance of chromosomes protein 4;Structural maintenance of chromosomes protein	SMC4	28	S	0.841	159.5	NaN	1.10	1.03	NaN	NaN	0.97	NaN	NaN	NaN
C9JWF0	Structural maintenance of chromosomes protein 4	SMC4	41	S	0.982	220.5	NaN	1.10	NaN	0.97	NaN	0.97	NaN	1.27	NaN
C9JIY9	Nucleoporin NUP53	NUP35	49	S	0.727	55.01	0.88	0.89	NaN	1.61	1.49	NaN	NaN	NaN	NaN
H7C559	Serine/threonine-protein phosphatase 4 regulatory subunit 2	PPP4R2	58	S	0.98	75.53	0.65	0.70	1.00	1.23	1.67	0.99	0.59	0.66	NaN
C9J3R1	Zinc finger protein 639	ZNF639	60	S	0.995	96.53	NaN	NaN	0.98	1.39	1.25	0.95	NaN	1.01	NaN
C9J0A7	Charged multivesicular body protein 2b	CHMP2B	169	S	1	135	1.05	1.13	1.12	1.00	1.11	1.04	1.17	1.01	1.12
C9J0I9	Nuclear-interacting partner of ALK	ZC3HC1	24	S	0.999	127.4	0.62	0.75	NaN	1.28	NaN	NaN	0.91	0.74	NaN
C9J0I9	Nuclear-interacting partner of ALK	ZC3HC1	351	S	0.5	162.4	NaN	0.98	NaN	1.62	1.64	NaN	NaN	0.84	NaN
C9J0I9	Nuclear-interacting partner of ALK	ZC3HC1	352	S	0.932	162.8	1.01	1.03	0.87	1.32	1.34	1.12	0.76	0.84	0.78
C9J0I9	Nuclear-interacting partner of ALK	ZC3HC1	292	S	0.98	77.73	1.26	0.94	NaN	NaN	1.17	NaN	NaN	NaN	NaN

C9J0I9	Nuclear-interacting partner of ALK	ZC3HC1	295	S	0.591	97.35	1.26	1.28	NaN	NaN	1.17	NaN	NaN	NaN	NaN
C9J0I9	Nuclear-interacting partner of ALK	ZC3HC1	301	S	0.98	153.9	1.56	NaN	NaN	1.41	1.32	NaN	1.25	1.18	NaN
C9J0I9	Nuclear-interacting partner of ALK	ZC3HC1	316	S	0.771	89.98	1.04	1.31	NaN	0.94	NaN	1.08	NaN	NaN	NaN
C9J1H7	Nucleolin	NCL	51	S	0.998	114.9	0.87	0.89	0.85	1.26	1.29	1.28	0.57	0.55	0.54
F5H5B7	Cleavage and polyadenylation specificity factor subunit 7	CPSF7	60	S	1	56.95	1.13	1.19	NaN	NaN	1.26	NaN	0.87	NaN	NaN
C9J3F6	TBC1 domain family member	TBC1D5	528	S	0.981	77.66	0.96	1.01	1.12	NaN	1.12	1.02	0.87	1.02	0.81
M0R1Q8	Regulator of chromosome condensation	RCC1	113	S	1	122.7	0.79	0.84	0.82	0.87	0.87	0.89	0.89	0.92	0.95
C9J4C4	Folliculin	FLCN	9	S	0.998	90.26	0.85	0.76	0.80	0.73	0.61	0.70	0.84	0.88	0.68
C9J4K0	Ashwin	C2orf49	151	S	0.95	51.52	NaN	NaN	2.49	NaN	2.66	2.43	0.89	1.00	1.24
C9J542	PDZ and LIM domain protein 4	PDLIM4	53	S	0.98	183.8	2.29	2.41	2.24	0.97	1.06	0.93	2.76	2.83	2.87
E9PNJ7	Nucleosome assembly protein 1-like 4	NAP1L4	125	S	1	457.2	0.87	0.88	0.89	0.94	0.96	0.98	0.75	0.77	0.81
C9JM54	Chromobox protein homolog 8	CBX8	165	S	0.702	72.8	0.46	0.45	0.56	0.59	0.88	0.78	NaN	0.56	0.57
C9JM54	Chromobox protein homolog 8	CBX8	166	S	0.565	49.17	NaN	NaN	NaN	NaN	NaN	NaN	0.54	NaN	0.31
C9J6P4	Zinc finger CCCH-type antiviral protein 1	ZC3HAV1	284	S	1	113.3	1.44	1.23	NaN	1.39	NaN	NaN	0.97	NaN	1.16
C9J6P4	Zinc finger CCCH-type antiviral protein 1	ZC3HAV1	275	S	1	94.02	NaN	1.15	NaN	1.16	NaN	0.80	NaN	NaN	NaN
C9J813		CALD1	202	S	1	104.3	0.99	1.01	1.02	1.12	NaN	1.09	1.34	1.20	1.42
C9J9H5	Mitotic spindle assembly checkpoint protein MAD1	MAD1L1	18	S	0.668	53.21	0.75	0.65	NaN	NaN	NaN	NaN	NaN	NaN	NaN
C9J9W2	LIM and SH3 domain protein 1	LASP1	110	S	1	190.2	1.48	1.18	1.17	2.29	2.25	2.30	NaN	0.65	1.68
C9JA69	HMG box transcription factor BBX	BBX	794	S	0.996	84.94	0.57	0.46	0.55	0.54	0.69	0.58	1.14	1.18	NaN
C9JA93		TBC1D15	106	S	0.973	168.6	0.97	1.00	0.86	0.81	0.87	0.66	1.02	NaN	1.02
C9JAE6	Multidrug and toxin extrusion protein 2	SLC47A2	338	S	0.885	45.86	NaN	NaN	NaN	0.80	0.74	NaN	NaN	0.53	NaN
C9JAE6	Multidrug and toxin extrusion protein 2	SLC47A2	343	S	0.824	45.86	NaN	NaN	NaN	0.80	0.74	NaN	NaN	0.53	NaN
C9JL19	60 kDa heat shock protein, mitochondrial	HSPD1	70	S	0.985	150.1	2.79	2.85	2.26	1.77	NaN	NaN	NaN	1.73	NaN
C9JED2	SH3 domain-binding protein 4	SH3BP4	131	S	1	102.6	1.15	1.15	1.16	1.72	1.57	1.49	0.55	0.58	0.78
C9JEZ4	Cdc42 effector protein 3	CDC42EP 3	100	S	0.999	298.8	5.12	5.23	6.80	5.84	NaN	5.74	1.91	1.45	1.99
E7EV54	Proline-, glutamic acid- and leucine-rich protein 1	PELP1	819	S	1	86.51	0.81	NaN	NaN	NaN	NaN	NaN	0.92	NaN	1.11
E7EV54	Proline-, glutamic acid- and leucine-rich protein 1	PELP1	334	S	1	156.1	0.82	0.82	0.70	0.88	0.94	0.87	0.85	0.95	0.86
C9JHG2	Raftlin	RFTN1	220	S	0.999	60.47	2.93	2.79	3.55	NaN	NaN	1.74	NaN	1.34	NaN
C9JI87	Voltage-dependent anion-selective channel protein 1	VDAC1	104	S	0.997	138.7	0.85	0.81	0.95	1.08	1.08	1.04	1.07	NaN	1.07

C9JIG9	Serine/threonine-protein kinase OSR1	OXSR1	339	S	1	308.4	1.13	NaN	1.06	NaN	2.39	1.00	0.79	NaN	0.94
C9JIG9	Serine/threonine-protein kinase OSR1	OXSR1	427	S	0.853	154.3	NaN	NaN	NaN	1.62	1.78	1.53	NaN	NaN	NaN
C9JKH7	Fibronectin type III domain-containing protein 3B	FNDC3B	181	S	0.995	84.82	2.04	1.84	1.97	1.14	1.06	1.00	1.87	1.96	1.98
C9JKL2	MLN64 N-terminal domain homolog	STARD3NL	192	S	0.973	180.2	0.72	0.60	0.64	0.66	NaN	0.63	0.81	NaN	0.96
C9JKL2	MLN64 N-terminal domain homolog	STARD3NL	200	S	1	180.2	0.64	0.60	0.64	0.75	NaN	0.56	0.81	NaN	0.72
I3L3A7	Protein FAM195B	FAM195B	21	S	0.993	98.93	0.99	0.98	1.16	1.03	1.01	NaN	1.25	NaN	1.14
C9JN71	Zinc finger protein 878	ZNF878	209	S	0.92	62.24	NaN	NaN	0.55	1.02	0.67	0.53	0.62	0.90	0.67
C9JNP9	Ubiquitin fusion degradation protein 1 homolog	UFD1L	151	S	0.804	67.58	1.70	1.51	1.47	2.53	2.73	2.65	0.93	NaN	1.37
F8WBS8	26S proteasome non-ATPase regulatory subunit 2	PSMD2	16	S	1	174.9	1.21	1.28	1.18	1.65	1.73	1.81	0.96	0.96	0.99
C9JRJ5	LIM domain-containing protein	LIMD1	384	S	0.982	90.69	NaN	0.85	NaN	0.91	1.03	NaN	NaN	0.67	NaN
C9JRM9	Zinc finger protein with KRAB and SCAN domains 1	ZKSCAN1	13	S	1	82.53	NaN	NaN	NaN	NaN	NaN	0.43	NaN	0.61	1.03
C9JWC4	Holliday junction recognition protein	HJURP	388	S	1	81.59	1.39	1.16	NaN	NaN	NaN	NaN	NaN	NaN	NaN
C9JZG1	Eukaryotic translation initiation factor 3 subunit B	EIF3B	115	S	1	287.9	1.07	1.09	1.09	1.06	1.00	0.97	1.06	1.05	1.08
C9JZG1	Eukaryotic translation initiation factor 3 subunit B	EIF3B	125	S	1	287.9	1.09	1.09	1.09	1.01	0.91	0.97	1.15	1.16	1.15
C9JZW3	Elongation factor 1-beta	EEF1B2	106	S	1	478.2	1.13	1.07	1.09	1.05	0.92	1.08	NaN	1.06	1.29
C9K0J5	Ras-associated and pleckstrin homology domains-containing protein 1	RAPH1	1206	S	0.736	98.99	1.61	NaN	1.67	2.12	1.83	1.85	NaN	0.98	NaN
C9K0J5	Ras-associated and pleckstrin homology domains-containing protein 1	RAPH1	662	S	1	56.95	2.73	2.01	NaN	2.71	NaN	NaN	NaN	NaN	NaN
C9K0K7	Phosphoribosyl pyrophosphate synthase-	PRPSAP2	227	S	0.999	183.9	NaN	0.67	0.89	0.74	0.79	NaN	0.70	0.78	NaN
D6R9B6	40S ribosomal protein S3a	RPS3A	144	S	1	66.49	NaN	1.47	1.49	1.45	1.75	1.60	1.02	0.99	0.93
D6REC6	Cyclin-dependent kinase 7	CDK7	71	S	1	86.87	0.54	NaN	0.49	0.56	0.56	0.55	NaN	0.90	0.83
D6R9K7	RNA-binding protein 4	RBM4	86	S	0.963	100.2	NaN	NaN	1.66	1.58	1.69	NaN	NaN	NaN	NaN
D6RAF8	Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	80	S	1	100.8	0.71	0.79	0.72	0.76	NaN	NaN	NaN	NaN	NaN
D6RAF8	Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	82	S	0.792	319.9	NaN	0.82	0.81	0.76	0.90	NaN	NaN	NaN	NaN
D6RAF8	Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	83	S	0.996	362.1	0.76	0.79	0.76	0.88	0.91	0.87	0.91	0.91	0.93
D6RAY8	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A containing	SMARCAD1	211	S	0.989	87.74	1.09	1.19	NaN	1.92	1.24	NaN	NaN	3.22	NaN

D6RAY8	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A containing	SMARCAD1	212	S	0.989	87.74	1.09	1.19	NaN	1.92	1.24	NaN	NaN	3.22	NaN
D6RAY8	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A containing	SMARCAD1	214	S	0.826	87.74	1.09	1.19	NaN	1.92	1.24	NaN	NaN	3.22	NaN
D6RB55	Amyloid beta A4 precursor protein-binding family B member 2	APBB2	106	S	0.985	43.52	NaN	0.90	NaN	1.03	1.18	NaN	NaN	NaN	NaN
H7BXG7	Protein transport protein Sec31A	SEC31A	532	S	1	153.9	1.95	1.84	2.06	1.59	1.48	1.60	1.98	2.09	1.76
H7BXG7	Protein transport protein Sec31A	SEC31A	912	S	0.998	161	1.47	1.38	1.24	1.50	1.29	1.51	1.11	1.01	NaN
E3W994	CLIP-associating protein 2	CLASP2	575	S	0.984	146.7	2.35	1.68	NaN	NaN	NaN	NaN	2.41	1.45	NaN
E5RHJ2	Aspartyl/asparaginyl beta-hydroxylase	ASPH	29	S	0.827	104.8	0.87	NaN	1.04	NaN	NaN	1.21	0.70	NaN	0.68
E5RGC1	F-box/WD repeat-containing protein 11	FBXW11	5	S	0.995	46.62	NaN	NaN	0.69	0.78	0.74	NaN	1.00	0.87	NaN
E5RGC1	F-box/WD repeat-containing protein 11	FBXW11	17	S	0.991	46.62	NaN	NaN	0.69	0.78	0.74	NaN	1.00	0.87	NaN
E5RHA3	Glutamate-rich protein 1	ERICH1	144	S	1	137.2	0.71	0.84	0.75	0.82	1.15	NaN	NaN	NaN	1.21
E5RJU9	Protein LYRIC	MTDH	370	S	1	234.8	0.70	0.88	7.83	0.81	0.78	0.85	0.99	1.00	1.01
E7EMD6	A-kinase anchor protein 10, mitochondrial	AKAP10	187	S	0.981	134	0.97	0.89	1.12	1.11	0.97	1.14	1.02	NaN	NaN
E7EMN6	Protein phosphatase inhibitor 2-like protein 3;Protein phosphatase inhibitor 2	PPP1R2	95	S	1	235.1	0.85	0.89	0.54	0.60	0.52	NaN	1.03	0.77	1.08
E7EMN6	Protein phosphatase inhibitor 2-like protein 3;Protein phosphatase inhibitor 2	PPP1R2	96	S	1	235.1	0.85	0.62	0.54	NaN	NaN	NaN	1.10	1.06	1.08
E7EMW7	E3 ubiquitin-protein ligase UBR5	UBR5	446	S	0.992	51.82	0.59	NaN	NaN	1.00	1.06	NaN	NaN	NaN	NaN
E7EMW7	E3 ubiquitin-protein ligase UBR5	UBR5	447	S	0.999	51.82	0.59	NaN	NaN	1.00	1.06	NaN	NaN	NaN	NaN
E7EMW7	E3 ubiquitin-protein ligase UBR5	UBR5	450	S	1	51.82	0.59	NaN	NaN	1.00	1.06	NaN	NaN	NaN	NaN
E7EMZ9	Transforming acidic coiled-coil-containing protein 2	TACC2	2467	S	0.967	128.1	0.86	NaN	1.14	0.94	NaN	1.07	1.33	NaN	1.50
E7EMZ9	Transforming acidic coiled-coil-containing protein 2	TACC2	2272	S	0.994	76.51	1.45	1.48	1.13	1.35	1.44	1.37	1.25	0.40	1.26
E7EMZ9	Transforming acidic coiled-coil-containing protein 2	TACC2	2276	S	1	77.07	1.45	1.48	1.20	1.35	1.44	1.30	1.25	1.33	1.26
E7EMZ9	Transforming acidic coiled-coil-containing protein 2	TACC2	2524	S	0.748	190.7	0.98	0.96	NaN	NaN	NaN	1.18	0.86	NaN	NaN
E7EN95	Filamin-B	FLNB	1914	S	1	113.5	3.26	2.66	2.77	3.36	NaN	3.83	1.03	0.86	0.83

E7EN95	Filamin-B	FLNB	814	S	0.999	163.5	9.87	8.62	10.61	16.86	16.68	15.30	1.01	0.80	0.98
E7EN95	Filamin-B	FLNB	2285	S	1	204.5	0.70	0.73	0.75	0.98	1.01	1.00	0.74	0.76	0.76
E7EN95	Filamin-B	FLNB	2288	S	0.571	63.18	0.70	0.76	0.88	1.09	NaN	1.08	NaN	NaN	NaN
E7EN95	Filamin-B	FLNB	1336	S	1	130.3	3.02	3.10	2.59	3.60	3.92	3.46	1.20	1.36	1.13
F5H3K2	Uncharacterized protein C12orf43	C12orf43	134	S	0.926	98.19	1.23	1.27	NaN	1.29	NaN	0.85	1.19	1.44	NaN
F5H3K2	Uncharacterized protein C12orf43	C12orf43	92	S	1	41.6	NaN	NaN	NaN	0.59	NaN	NaN	0.89	0.72	NaN
E7EV99	Alpha-adducin	ADD1	12	S	0.98	90.85	NaN	2.66	NaN	3.03	2.74	NaN	NaN	0.76	NaN
E7EV99	Alpha-adducin	ADD1	358	S	1	244	0.87	1.00	0.84	0.77	0.83	0.86	0.97	0.97	0.91
E7EPJ7	Triple functional domain	TRIO	2188	S	0.999	59.47	0.79	0.88	NaN	NaN	0.78	1.78	1.15	0.99	1.40
E7EPJ7	Triple functional domain	TRIO	2192	S	0.987	42.92	1.87	1.51	NaN	NaN	2.11	1.64	2.58	2.31	1.29
E7EPJ7	Triple functional domain	TRIO	2162	S	0.774	48.9	NaN	0.69	0.84	NaN	NaN	NaN	1.07	1.18	0.91
E7EPK0	LIM and calponin homology domains-containing protein 1	LIMCH1	511	S	0.999	164	NaN	0.64	NaN	1.03	NaN	0.81	0.71	0.82	0.88
E7EPK0	LIM and calponin homology domains-containing protein 1	LIMCH1	522	S	0.728	64.38	NaN	NaN	NaN	NaN	NaN	NaN	1.08	1.16	NaN
E7EPK0	LIM and calponin homology domains-containing protein 1	LIMCH1	84	S	0.956	85.81	0.80	0.70	0.72	0.85	0.84	0.82	NaN	NaN	NaN
E7EPK0	LIM and calponin homology domains-containing protein 1	LIMCH1	70	S	1	80.51	0.70	0.86	1.03	NaN	1.00	0.87	NaN	1.03	1.01
E7EPK0	LIM and calponin homology domains-containing protein 1	LIMCH1	813	S	1	162	1.48	1.44	1.45	1.35	1.36	1.31	2.24	2.16	NaN
E7EPK0	LIM and calponin homology domains-containing protein 1	LIMCH1	559	S	1	189.1	1.08	1.09	1.04	1.06	1.10	1.15	1.10	1.17	0.97
E7EPK0	LIM and calponin homology domains-containing protein 1	LIMCH1	156	S	0.781	70.91	2.13	2.27	NaN	NaN	NaN	NaN	NaN	NaN	NaN
E7EPN9	Protein PRRC2C	PRRC2C	189	S	0.983	150.2	NaN	1.44	1.03	2.07	NaN	NaN	NaN	NaN	0.75
E7EPN9	Protein PRRC2C	PRRC2C	2107	S	1	121.8	1.13	0.99	1.00	1.43	1.57	1.27	0.71	0.72	NaN
E7EPN9	Protein PRRC2C	PRRC2C	880	S	0.834	63.72	NaN	NaN	1.83	1.59	2.15	NaN	1.82	1.65	NaN
E9PGG1		DYNC1I2	81	S	0.768	146.5	0.82	0.89	0.83	1.37	1.35	1.33	0.54	0.58	0.52
S4R3H4	Apoptotic chromatin condensation inducer in the nucleus	ACIN1	432	S	1	221.6	0.67	0.68	0.66	0.67	0.74	0.72	1.18	1.17	1.18
S4R3H4	Apoptotic chromatin condensation inducer in the nucleus	ACIN1	352	S	0.952	112.6	NaN	0.97	1.00	1.07	1.19	1.14	NaN	1.11	0.97
S4R3H4	Apoptotic chromatin condensation inducer in the nucleus	ACIN1	671	S	1	84.9	0.79	NaN	0.93	0.94	NaN	0.92	0.95	NaN	1.04
S4R3H4	Apoptotic chromatin condensation inducer in the nucleus	ACIN1	652	S	1	78.53	1.70	1.79	1.62	1.45	1.38	0.83	1.56	1.42	2.03
S4R3H4	Apoptotic chromatin condensation inducer in the nucleus	ACIN1	326	S	0.968	45.09	NaN	NaN	NaN	0.73	0.79	NaN	NaN	NaN	0.80

S4R3H4	Apoptotic chromatin condensation inducer in the nucleus	ACIN1	328	S	0.97	69.03	NaN	NaN	NaN	NaN	NaN	NaN	0.85	0.82	NaN
S4R3H4	Apoptotic chromatin condensation inducer in the nucleus	ACIN1	330	S	0.982	69.03	NaN	NaN	NaN	0.73	0.79	NaN	0.85	0.82	0.80
S4R3H4	Apoptotic chromatin condensation inducer in the nucleus	ACIN1	597	S	1	92.43	0.78	NaN	NaN	0.79	0.85	NaN	0.84	0.80	NaN
S4R3H4	Apoptotic chromatin condensation inducer in the nucleus	ACIN1	599	S	1	92.43	0.78	NaN	NaN	0.34	0.37	NaN	0.54	0.53	NaN
S4R3H4	Apoptotic chromatin condensation inducer in the nucleus	ACIN1	158	S	1	284.4	0.79	0.72	0.76	0.83	0.81	0.76	0.94	0.95	0.96
S4R3H4	Apoptotic chromatin condensation inducer in the nucleus	ACIN1	946	S	1	140.2	0.96	1.02	0.94	0.85	0.89	0.89	0.77	0.77	1.05
S4R3H4	Apoptotic chromatin condensation inducer in the nucleus	ACIN1	307	S	0.999	106.5	NaN	0.98	NaN	1.20	1.30	NaN	NaN	NaN	NaN
E7ERS3	Zinc finger CCCH domain-containing protein 18	ZC3H18	46	S	1	86.8	1.61	2.04	NaN	1.72	2.03	NaN	NaN	NaN	NaN
E7ERS3	Zinc finger CCCH domain-containing protein 18	ZC3H18	67	S	1	148.3	0.74	0.68	NaN	0.86	NaN	0.88	NaN	NaN	NaN
E7ERS3	Zinc finger CCCH domain-containing protein 18	ZC3H18	95	S	0.891	83.32	0.89	0.72	NaN	NaN	1.35	1.12	NaN	NaN	NaN
E7ERS3	Zinc finger CCCH domain-containing protein 18	ZC3H18	558	S	0.959	77.74	0.95	1.00	1.10	0.99	1.06	1.06	1.11	1.12	1.13
E7ERS3	Zinc finger CCCH domain-containing protein 18	ZC3H18	917	S	1	115.8	1.06	1.05	1.08	1.00	1.01	1.05	1.05	1.06	0.99
E7ERS3	Zinc finger CCCH domain-containing protein 18	ZC3H18	866	S	1	79.57	0.98	0.75	0.98	0.63	0.91	NaN	0.74	0.97	NaN
F8W7U3	WASH complex subunit FAM21A	FAM21A	451	S	1	303.5	1.32	1.19	1.21	1.51	0.49	1.25	1.21	1.04	1.08
E7ETM8	Nexilin	NEXN	16	S	1	306.3	0.95	1.00	0.91	1.03	1.12	1.09	0.77	0.81	0.85
E7ETM8	Nexilin	NEXN	179	S	0.995	65.56	0.71	0.84	0.80	1.02	0.96	1.00	0.88	0.91	0.92
Q13428	Treacle protein	TCOF1	906;906	S	1	73.44	3.68	4.07	3.96	3.29	2.88	2.78	2.25	2.43	2.17
Q13428	Treacle protein	TCOF1	375;375	S	0.774	99.6	1.24	1.27	NaN	NaN	NaN	NaN	1.68	NaN	NaN
Q13428	Treacle protein	TCOF1	381;381	S	1	200	2.13	1.63	1.59	1.44	1.74	1.62	1.23	1.23	1.13
Q13428	Treacle protein	TCOF1	233;233	S	0.944	64.21	NaN	3.91	0.53	0.88	0.92	0.86	0.79	0.82	NaN
Q13428	Treacle protein	TCOF1	1219;125	S	1	95.43	0.86	1.00	0.81	1.52	1.37	1.46	0.63	0.71	0.57
Q13428	Treacle protein	TCOF1	1312;135	S	1	94.02	1.18	1.22	1.02	1.07	1.13	1.00	1.05	0.91	0.90
J3KQ96		TCOF1	1073	S	0.845	103.8	NaN	0.69	NaN	1.04	NaN	NaN	0.80	NaN	1.49
Q13428	Treacle protein	TCOF1	171;171	S	0.962	140.2	0.97	1.51	NaN	1.60	NaN	1.50	2.32	NaN	2.36
Q13428	Treacle protein	TCOF1	1190;122	S	0.918	109.1	0.78	0.97	NaN	NaN	0.76	NaN	NaN	NaN	NaN
Q13428	Treacle protein	TCOF1	1340;137	S	0.857	73.75	0.79	0.81	NaN	NaN	NaN	NaN	NaN	NaN	NaN

Q13428	Treacle protein	TCOF1	156;156	S	1	138.3	1.05	1.03	1.13	1.53	1.47	1.42	0.91	0.96	1.02
E7ETY4	Serine/threonine-protein kinase MARK2	MARK2	452	S	0.952	65.33	1.34	1.73	NaN	NaN	NaN	NaN	NaN	NaN	NaN
E7EUU4	Eukaryotic translation initiation factor 4 gamma 1	EIF4G1	1192	S	1	148.7	2.00	2.09	2.12	2.52	2.39	2.38	1.18	1.16	1.10
E7EUU4	Eukaryotic translation initiation factor 4 gamma 1	EIF4G1	1053	S	1	96.46	1.59	1.91	2.06	NaN	NaN	1.82	1.58	NaN	1.28
E7EUU4	Eukaryotic translation initiation factor 4 gamma 1	EIF4G1	1148	S	1	78.16	1.97	1.84	1.99	1.52	1.44	NaN	NaN	1.94	NaN
E7EUV9	Histone RNA hairpin-binding protein	SLBP	20	S	1	61.27	NaN	0.69	0.79	0.97	1.04	NaN	0.88	0.64	0.67
E7EUV9	Histone RNA hairpin-binding protein	SLBP	23	S	1	61.27	NaN	0.69	0.79	0.97	1.12	NaN	0.53	0.64	0.67
E7EVX2	Golgin subfamily A member 4	GOLGA4	271	S	1	50.87	NaN	NaN	0.97	NaN	NaN	NaN	NaN	0.90	1.26
E7EX17	Eukaryotic translation initiation factor 4B	EIF4B	464	S	0.935	78.1	1.01	0.90	NaN	NaN	NaN	NaN	NaN	NaN	NaN
E7EX17	Eukaryotic translation initiation factor 4B	EIF4B	93	S	0.878	77.24	1.60	NaN	NaN	1.63	NaN	NaN	1.08	NaN	0.97
E7EX17	Eukaryotic translation initiation factor 4B	EIF4B	500	S	0.663	112	NaN	NaN	NaN	2.23	NaN	1.69	NaN	1.26	NaN
E7EX17	Eukaryotic translation initiation factor 4B	EIF4B	502	S	0.99	313.6	2.83	1.85	2.01	2.23	1.60	1.69	NaN	NaN	1.30
E7EX17	Eukaryotic translation initiation factor 4B	EIF4B	503	S	0.997	287.5	1.93	NaN	NaN	1.55	1.64	1.75	1.30	NaN	NaN
E7EX17	Eukaryotic translation initiation factor 4B	EIF4B	509	S	1	302.9	0.63	0.60	0.67	0.80	0.77	0.76	0.75	0.76	0.75
E7EX40	Rab11 family-interacting protein 1	RAB11FIP1	51	S	0.568	98.75	NaN	NaN	NaN	NaN	0.74	NaN	0.71	0.91	NaN
E7EX40	Rab11 family-interacting protein 1	RAB11FIP1	54	S	0.985	141.2	0.79	NaN	0.73	0.76	0.81	NaN	0.84	NaN	0.72
E7EX40	Rab11 family-interacting protein 1	RAB11FIP1	190	S	0.559	70.33	0.95	0.86	NaN	NaN	NaN	0.92	0.85	NaN	NaN
E7EX40	Rab11 family-interacting protein 1	RAB11FIP1	191	S	0.998	116.5	NaN	NaN	NaN	0.45	0.57	NaN	0.98	NaN	0.39
E7EX40	Rab11 family-interacting protein 1	RAB11FIP1	193	S	0.787	110.2	0.95	NaN	NaN	NaN	0.75	0.92	NaN	0.85	0.78
E7EX40	Rab11 family-interacting protein 1	RAB11FIP1	195	S	0.669	110.2	NaN	NaN	NaN	NaN	0.75	NaN	NaN	0.85	0.78
E7EX40	Rab11 family-interacting protein 1	RAB11FIP1	197	S	1	110.2	0.95	0.86	NaN	1.01	0.75	0.92	0.85	0.85	0.78
E7EX40	Rab11 family-interacting protein 1	RAB11FIP1	380	S	0.617	64.22	NaN	2.58	2.47	2.39	1.80	NaN	NaN	1.78	1.78
E7EX40	Rab11 family-interacting protein 1	RAB11FIP1	381	S	0.5	63.73	NaN	2.58	2.47	2.39	1.80	NaN	NaN	1.78	1.78
E7EX44	Caldesmon	CALD1	553	S	0.918	105.8	1.05	1.13	NaN	1.30	1.40	NaN	1.00	0.97	1.00
E7EX44		CALD1	196	S	1	60.6	0.82	NaN	1.00	NaN	NaN	NaN	NaN	NaN	0.90

F8VZJ2	Nascent polypeptide-associated complex subunit alpha;Nascent polypeptide-associated complex subunit alpha, muscle-specific form	NACA	87	S	1	301.7	1.15	1.04	1.03	1.05	1.04	1.01	1.08	1.06	1.00
E9PCY7	Heterogeneous nuclear ribonucleoprotein H;Heterogeneous nuclear ribonucleoprotein H, N-terminally processed;Heterogeneous nuclear ribonucleoprotein F;Heterogeneous nuclear ribonucleoprotein F, N-	HNRNPH1	310	S	1	81.88	NaN	1.60	NaN	1.99	1.67	NaN	NaN	NaN	NaN
E9PCY7	Heterogeneous nuclear ribonucleoprotein H;Heterogeneous nuclear ribonucleoprotein H, N-terminally processed;Heterogeneous nuclear ribonucleoprotein H2	HNRNPH1	104;104	S	1	235.3	1.69	1.76	1.68	2.03	2.08	2.03	1.05	1.03	0.98
H0YF64	Calcipressin-3;Calcipressin-1	RCAN3	15	S	1	81.35	0.52	0.62	0.59	NaN	0.54	0.63	0.78	0.70	0.76
H0YF64	Calcipressin-3;Calcipressin-1	RCAN3	19	S	1	81.35	0.72	0.99	0.59	NaN	0.54	0.63	0.78	0.70	0.77
E9PER6	Putative 3-phosphoinositide-dependent protein kinase 2;3-phosphoinositide-dependent protein kinase 1	PDPK1	214	S	0.822	49.19	0.88	1.06	NaN	1.05	2.65	NaN	2.30	1.45	NaN
E9PF10	Nuclear pore complex protein Nup155	NUP155	928	S	0.989	125.4	1.49	1.61	1.57	1.54	1.59	1.51	1.23	1.28	1.27
E9PFP1	Phosphatidylinositol 3-kinase regulatory subunit beta	PIK3R2	262	S	0.537	85.2	NaN	0.94	0.93	1.05	1.00	1.00	1.09	NaN	1.01
E9PFP1	Phosphatidylinositol 3-kinase regulatory subunit beta	PIK3R2	263	S	0.5	85.2	NaN	NaN	0.93	1.05	1.00	NaN	NaN	NaN	NaN
G5E9V3	Pleckstrin homology-like domain family B member 2	PHLDB2	489	S	1	152.2	0.69	0.81	0.78	0.78	0.64	0.88	0.80	NaN	0.86
G5E9V3	Pleckstrin homology-like domain family B member 2	PHLDB2	204	S	0.96	184.3	1.53	1.48	1.33	1.62	1.51	1.29	1.62	NaN	1.84
E9PFQ8	Serine/threonine-protein kinase RIO1	RIOK1	21	S	0.708	134.2	1.07	NaN	1.13	0.97	NaN	0.89	1.34	NaN	NaN
E9PFQ8	Serine/threonine-protein kinase RIO1	RIOK1	22	S	0.742	167.1	NaN	0.87	0.75	NaN	1.19	0.88	NaN	1.43	1.26
E9PG73	Peptidyl-prolyl cis-trans isomerase G	PPIG	672	S	0.999	106.2	1.25	NaN	NaN	0.91	0.98	NaN	1.07	1.08	1.12
E9PG73	Peptidyl-prolyl cis-trans isomerase G	PPIG	702	S	0.909	84.84	NaN	0.90	NaN	1.04	1.01	1.01	1.07	0.91	NaN

E9PG73	Peptidyl-prolyl cis-trans isomerase G	PPIG	275	S	1	55.26	NaN	NaN	0.76	0.96	0.88	NaN	0.72	NaN	NaN
E9PG73	Peptidyl-prolyl cis-trans isomerase G	PPIG	239	S	0.917	128.6	1.15	1.15	1.11	1.08	NaN	1.03	NaN	1.16	1.36
E9PG73	Peptidyl-prolyl cis-trans isomerase G	PPIG	241	S	0.997	128.6	1.15	1.15	1.11	1.08	NaN	1.03	NaN	1.16	1.36
E9PG73	Peptidyl-prolyl cis-trans isomerase G	PPIG	242	S	0.999	128.6	1.15	1.15	1.11	1.08	NaN	1.03	NaN	1.16	1.36
E9PG73	Peptidyl-prolyl cis-trans isomerase G	PPIG	244	S	1	128.6	1.15	1.15	1.11	1.08	NaN	1.03	NaN	1.16	1.36
E9PGC0	Ras GTPase-activating protein 1	RASA1	665	S	0.944	56.34	NaN	NaN	NaN	NaN	1.44	1.56	NaN	0.96	NaN
E9PHI6	Cytoplasmic dynein 1 light intermediate chain 1	DYNC1LI1	91	S	1	265.6	1.14	1.15	1.23	1.23	1.25	1.18	0.95	1.00	1.01
E9PHI6	Cytoplasmic dynein 1 light intermediate chain 1	DYNC1LI1	394	S	0.981	160.6	1.18	1.03	1.57	1.70	0.68	2.29	NaN	0.93	0.82
E9PHI6	Cytoplasmic dynein 1 light intermediate chain 1	DYNC1LI1	400	S	0.999	176.1	0.98	0.98	1.03	0.81	1.03	0.80	0.89	0.93	0.94
E9PHI6	Cytoplasmic dynein 1 light intermediate chain 1	DYNC1LI1	305	S	1	231.6	1.55	NaN	NaN	5.06	5.31	NaN	NaN	NaN	NaN
E9PHV6	Nuclear autoantigen Sp-100	SP100	132	S	1	133.2	1.13	1.14	NaN	NaN	1.23	1.22	1.05	1.28	1.06
E9PHV6	Nuclear autoantigen Sp-100	SP100	426	S	0.647	77.69	0.90	1.33	NaN	1.57	1.25	NaN	NaN	NaN	NaN
E9PHV6	Nuclear autoantigen Sp-100	SP100	427	S	0.648	77.69	0.90	1.33	NaN	1.57	1.25	NaN	NaN	NaN	NaN
E9PHV6	Nuclear autoantigen Sp-100	SP100	428	S	0.65	77.69	0.90	1.33	NaN	1.57	1.25	NaN	NaN	NaN	NaN
E9PHV6	Nuclear autoantigen Sp-100	SP100	382	S	1	130.5	0.27	NaN	NaN	NaN	0.38	NaN	1.07	0.86	0.82
E9PHV6	Nuclear autoantigen Sp-100	SP100	384	S	1	130.5	0.27	NaN	NaN	NaN	0.38	NaN	0.84	0.86	0.82
E9PHV6	Nuclear autoantigen Sp-100	SP100	385	S	1	130.5	0.27	NaN	NaN	NaN	0.38	NaN	0.84	0.86	0.82
E9PHV6	Nuclear autoantigen Sp-100	SP100	337	S	1	167.6	1.09	1.20	1.55	1.40	NaN	1.62	1.02	NaN	1.18
E9PK52	Band 4.1-like protein 2	EPB41L2	645	S	1	110.4	NaN	NaN	1.13	1.57	1.54	1.41	0.97	0.95	NaN
E9PK52	Band 4.1-like protein 2	EPB41L2	38	S	0.762	190.1	1.07	NaN	1.15	1.00	1.25	1.23	NaN	1.43	NaN
E9PK52	Band 4.1-like protein 2	EPB41L2	39	S	0.938	213.4	NaN	1.18	1.05	0.99	1.27	1.23	0.87	1.10	1.20
E9PK52	Band 4.1-like protein 2	EPB41L2	598	S	0.868	80.98	1.72	1.77	NaN	2.07	2.09	1.84	NaN	NaN	0.83
E9PI52	Arginine/serine-rich coiled-coil protein 2	RSRC2	17	S	0.751	92.45	0.83	0.95	1.04	0.97	1.10	0.81	NaN	0.88	1.41
E9PI52	Arginine/serine-rich coiled-coil protein 2	RSRC2	32	S	0.999	159.6	1.18	1.19	1.23	1.23	1.32	1.07	0.99	0.96	0.82
E9PIE3	Protein kinase C delta-binding protein	PRKCDBP	197	S	0.998	67.2	1.63	1.49	1.45	1.34	NaN	1.33	1.66	1.61	1.72
E9PIE3	Protein kinase C delta-binding protein	PRKCDBP	198	S	0.998	67.2	1.63	1.49	1.45	1.34	NaN	1.33	1.66	1.61	1.72
E9PJ04	Splicing factor 3B subunit 2	SF3B2	300	S	0.761	67.19	1.20	1.21	1.26	NaN	1.16	NaN	1.04	1.43	1.38
E9PJ04	Splicing factor 3B subunit 2	SF3B2	301	S	0.775	67.19	1.20	1.21	1.26	NaN	1.16	NaN	NaN	1.43	1.38
E9PJ04	Splicing factor 3B subunit 2	SF3B2	305	S	1	115.1	1.10	1.09	1.11	1.20	1.12	1.13	0.90	0.93	0.86
E9PJ04	Splicing factor 3B subunit 2	SF3B2	307	S	0.995	115.1	1.16	1.10	1.11	1.20	1.12	1.13	0.90	0.93	0.86
E9PJ38	Receptor-binding cancer antigen expressed on SiSo	EBAG9	36	S	1	107.7	0.84	0.88	0.82	0.86	NaN	0.91	0.80	0.86	0.85

E9PJ60	Probable ATP-dependent RNA helicase DDX20	DDX20	285	S	1	116.3	0.96	0.91	0.93	0.83	0.95	0.93	1.06	1.02	0.99
E9PJ60	Probable ATP-dependent RNA helicase DDX20	DDX20	286	S	1	116.3	0.96	0.91	0.93	0.83	0.95	0.93	1.06	1.02	0.99
E9PJF4	Methylosome subunit pICln	CLNS1A	102	S	1	330	1.06	1.11	1.09	1.06	1.10	1.07	0.98	1.00	1.10
E9PK91	Bcl-2-associated transcription factor 1	BCLAF1	177	S	1	193.6	0.99	0.93	0.84	0.97	1.01	0.96	0.91	0.81	1.01
E9PK91	Bcl-2-associated transcription factor 1	BCLAF1	385	S	0.988	169.7	2.28	2.78	NaN	1.71	1.29	NaN	2.13	2.47	2.58
E9PK91	Bcl-2-associated transcription factor 1	BCLAF1	512	S	1	158.6	0.89	0.88	0.90	0.94	0.92	0.96	0.93	0.93	1.00
E9PK91	Bcl-2-associated transcription factor 1	BCLAF1	496	S	1	196.2	0.85	0.92	0.87	0.96	0.96	0.90	1.02	0.87	0.94
E9PK91	Bcl-2-associated transcription factor 1	BCLAF1	397	S	1	338.7	1.06	1.07	1.09	1.02	1.03	0.97	1.14	1.21	1.04
E9PK91	Bcl-2-associated transcription factor 1	BCLAF1	658	S	1	149.2	1.01	1.01	1.16	1.01	0.99	0.96	1.08	0.93	1.07
E9PK91	Bcl-2-associated transcription factor 1	BCLAF1	268	S	0.999	181.6	1.06	1.07	1.00	1.03	0.99	0.93	0.88	0.97	0.92
E9PK91	Bcl-2-associated transcription factor 1	BCLAF1	648	S	1	96.95	1.04	1.15	1.20	1.03	1.12	1.04	0.93	1.02	1.19
E9PK91	Bcl-2-associated transcription factor 1	BCLAF1	183	S	0.997	101.3	1.20	1.36	NaN	2.09	NaN	NaN	4.56	NaN	NaN
E9PK91	Bcl-2-associated transcription factor 1	BCLAF1	222	S	1	193.7	0.56	0.64	0.80	0.71	0.82	0.68	1.00	0.94	0.94
E9PK91	Bcl-2-associated transcription factor 1	BCLAF1	531	S	1	113.9	2.19	2.19	2.21	1.87	1.48	1.61	2.12	2.13	2.21
E9PK91	Bcl-2-associated transcription factor 1	BCLAF1	285	S	0.978	105.5	0.59	0.72	NaN	0.86	0.83	1.30	NaN	1.61	1.77
E9PK91	Bcl-2-associated transcription factor 1	BCLAF1	287	S	0.931	89.44	NaN	1.45	NaN	1.44	1.55	1.30	NaN	1.27	NaN
F5H0D8		CELF1	18	S	0.726	134	0.93	0.74	NaN	NaN	NaN	NaN	NaN	NaN	NaN
E9PS47	Phosphatidylserine synthase 2	PTDSS2	16	S	1	57.29	1.65	1.66	NaN	NaN	NaN	NaN	NaN	NaN	NaN
H0YE74	Cleavage stimulation factor subunit 3	CSTF3	65	S	1	197.8	1.10	1.07	0.98	1.08	1.02	1.09	0.87	0.80	0.97
E9PQA1	Small acidic protein	C11orf58	15	S	0.992	281.5	NaN	1.29	1.36	1.21	1.14	1.20	1.33	1.25	NaN
E9PQA1	Small acidic protein	C11orf58	17	S	1	663	1.27	1.25	1.16	1.13	0.91	1.08	1.05	1.07	1.35
E9PMG1	RalBP1-associated Eps domain-containing protein 1	REPS1	650	S	1	171.8	1.26	1.25	1.24	1.03	0.98	1.51	1.32	1.31	1.29
E9PMG1	RalBP1-associated Eps domain-containing protein 1	REPS1	535	S	0.965	64.1	NaN	1.59	1.82	1.80	1.72	1.76	1.17	1.21	NaN
E9PMG1	RalBP1-associated Eps domain-containing protein 1	REPS1	455	S	0.746	49.09	1.32	NaN	NaN	NaN	NaN	NaN	1.12	1.38	NaN
E9PMG1	RalBP1-associated Eps domain-containing protein 1	REPS1	162	S	1	93.79	NaN	1.62	NaN	1.51	1.70	NaN	NaN	NaN	NaN
E9PMG1	RalBP1-associated Eps domain-containing protein 1	REPS1	166	S	1	93.79	NaN	1.62	NaN	1.51	1.70	NaN	NaN	NaN	NaN

E9PMG1	RalBP1-associated Eps domain-containing protein 1	REPS1	170	S	0.995	177.1	NaN	1.62	0.75	0.82	1.70	0.77	NaN	NaN	0.84
E9PMG4	Telomerase Cajal body protein 1	WRAP53	85	S	0.951	82.49	NaN	NaN	0.67	0.43	0.55	NaN	1.19	1.18	1.17
E9PMG4	Telomerase Cajal body protein 1	WRAP53	90	S	0.974	82.49	NaN	NaN	0.67	0.43	0.55	NaN	1.19	1.18	1.17
E9PMG4	Telomerase Cajal body protein 1	WRAP53	54	S	1	85.19	0.71	0.68	NaN	0.76	0.78	NaN	0.97	1.20	NaN
E9PMG4	Telomerase Cajal body protein 1	WRAP53	458	S	0.985	182.3	0.51	0.61	0.60	0.53	NaN	0.67	1.39	NaN	1.43
E9PMW5	Tripartite motif-containing protein 3	TRIM3	7	S	1	100.6	0.54	0.53	0.70	0.71	NaN	0.81	0.57	0.66	0.62
E9PMQ6	Heat shock factor protein 1	HSF1	363	S	0.999	127.3	0.75	0.65	0.69	0.57	NaN	0.58	1.13	1.08	1.05
E9PMQ6	Heat shock factor protein 1	HSF1	314	S	0.714	81.13	NaN	NaN	NaN	0.69	0.78	NaN	NaN	NaN	NaN
E9PMR6	Rho guanine nucleotide exchange factor 12	ARHGEF 12	1286	S	1	75.1	0.57	1.45	NaN	NaN	NaN	NaN	NaN	NaN	NaN
E9PMR6	Rho guanine nucleotide exchange factor 12	ARHGEF 12	206	S	0.995	71.3	0.92	0.77	NaN	1.16	0.87	1.16	NaN	1.06	1.23
E9PMS6	LIM domain only protein 7	LMO7	591	S	1	130.8	0.69	0.83	0.66	0.87	0.99	0.98	0.78	0.75	0.78
E9PMS6	LIM domain only protein 7	LMO7	155	S	1	89.99	1.95	2.02	NaN	NaN	0.80	NaN	1.86	NaN	1.37
E9PMS6	LIM domain only protein 7	LMO7	553	S	0.999	243.8	0.72	0.67	0.69	0.56	0.71	0.65	0.64	0.65	0.65
E9PMS6	LIM domain only protein 7	LMO7	556	S	0.95	218.7	2.14	1.62	1.78	2.06	NaN	1.85	1.29	NaN	1.31
E9PMS6	LIM domain only protein 7	LMO7	1102	S	1	96.33	5.41	3.75	NaN	NaN	NaN	NaN	NaN	NaN	NaN
E9PMS6	LIM domain only protein 7	LMO7	1085	S	0.983	60.03	1.41	2.46	NaN	NaN	NaN	NaN	NaN	NaN	NaN
E9PMS6	LIM domain only protein 7	LMO7	1185	S	0.999	80.47	NaN	2.87	2.39	1.93	1.64	1.72	1.19	1.36	1.15
E9PMS6	LIM domain only protein 7	LMO7	1015	S	0.859	103.4	NaN	NaN	NaN	NaN	NaN	NaN	0.86	0.89	NaN
E9PMS6	LIM domain only protein 7	LMO7	432	S	0.998	169.7	NaN	1.31	1.40	1.23	1.24	1.20	1.09	NaN	1.01
E9PNJ4	Stromal interaction molecule 1	STIM1	348	S	0.533	66.64	NaN	NaN	NaN	NaN	2.21	NaN	2.28	NaN	1.77
E9PNJ4	Stromal interaction molecule 1	STIM1	445	S	0.956	242.1	1.11	NaN	NaN	0.98	0.99	NaN	1.11	1.45	NaN
H0YDN6	Diacylglycerol kinase;Diacylglycerol kinase zeta	DGKZ	19	S	0.5	54.07	0.96	1.01	NaN	1.07	1.09	NaN	1.01	0.96	NaN
H0YDN6	Diacylglycerol kinase;Diacylglycerol kinase zeta	DGKZ	20	S	0.5	54.07	0.96	1.01	NaN	1.07	1.09	NaN	1.01	0.96	NaN
E9PP21	Cysteine and glycine-rich protein 1	CSRP1	159	S	1	202.8	NaN	1.03	1.18	NaN	NaN	1.23	NaN	0.81	NaN
E9PPY3	Ribosomal RNA-processing protein 8	RRP8	62	S	0.99	109.6	NaN	NaN	1.28	1.03	1.10	0.78	NaN	NaN	1.19
E9PPY3	Ribosomal RNA-processing protein 8	RRP8	64	S	0.999	109.6	NaN	NaN	1.28	1.03	1.10	0.78	NaN	NaN	1.19
E9PPY3	Ribosomal RNA-processing protein 8	RRP8	104	S	1	80.41	NaN	NaN	NaN	0.90	0.87	1.00	NaN	1.16	1.29
E9PPY3	Ribosomal RNA-processing protein 8	RRP8	106	S	1	80.41	NaN	NaN	NaN	0.90	0.87	1.00	NaN	1.16	1.29
E9PQC4	Kinetochore protein Nuf2	NUF2	247	S	1	67.39	0.52	0.59	0.68	0.99	0.96	0.88	0.72	0.71	0.69

E9PQP7	Serine/threonine-protein phosphatase 6 regulatory subunit 3	PPP6R3	619	S	0.663	84.75	0.97	0.96	NaN	NaN	NaN	NaN	NaN	NaN	NaN
E9PQP7	Serine/threonine-protein phosphatase 6 regulatory subunit 3	PPP6R3	385	S	1	299	0.86	0.87	0.86	0.89	0.91	0.83	0.98	0.93	0.93
E9PRB3	Deoxynucleotidyltransferase terminal-interacting protein 2	DNTTIP2	124	S	0.972	132.4	1.24	1.27	NaN	1.61	1.65	1.53	0.89	0.75	NaN
F2Z2E2	Ras GTPase-activating-like protein IQGAP3	IQGAP3	496	S	1	116.5	1.01	NaN	NaN	2.11	2.26	1.96	NaN	0.75	NaN
F2Z2T1	Nuclear cap-binding protein subunit 1	NCBP1	22	S	0.729	90.4	NaN	NaN	NaN	0.95	NaN	0.85	NaN	NaN	NaN
F2Z3H6	B-cell CLL/lymphoma 7 protein family member B	BCL7B	133	S	0.969	144.3	NaN	NaN	NaN	0.99	0.80	NaN	1.03	NaN	NaN
F5GWT4	Serine/threonine-protein kinase WNK1	WNK1	1781	S	0.932	90.08	0.92	NaN	0.92	1.00	1.05	1.04	0.77	0.85	0.98
F5GWT4	Serine/threonine-protein kinase WNK1	WNK1	1784	S	0.997	90.08	0.92	1.05	0.92	1.00	1.06	1.13	0.77	0.85	0.88
F5GWT4	Serine/threonine-protein kinase WNK1	WNK1	1730	S	1	131.9	1.13	1.05	1.08	1.21	1.37	1.32	0.72	0.70	0.85
F5GWT4	Serine/threonine-protein kinase WNK1	WNK1	185	S	0.746	67.65	0.71	NaN	NaN	0.91	0.69	0.84	0.82	NaN	0.75
F5GX09	Protein FAM76B	FAM76B	193	S	1	118.5	1.41	NaN	NaN	0.59	0.48	NaN	NaN	NaN	0.54
F5GX58	Cell division cycle-associated protein 3	CDCA3	87	S	0.998	47.53	1.61	1.23	1.76	2.84	NaN	2.58	NaN	0.88	NaN
F5GYF8	Signal-induced proliferation-associated 1-like protein 1	SIPA1L1	1003	S	0.997	156.6	NaN	1.67	NaN	1.84	1.68	NaN	2.62	2.41	NaN
F5GYF8	Signal-induced proliferation-associated 1-like protein 1	SIPA1L1	1039	S	0.998	133	1.31	NaN	1.63	1.21	1.29	1.53	1.84	2.08	1.84
F5H3F0	Ubiquitin thioesterase OTUB1	OTUB1	16	S	0.847	89.68	0.67	NaN	NaN	0.92	NaN	1.10	NaN	NaN	0.80
R4GN16	Striatin-4	STRN4	126	S	1	215.7	0.95	1.11	1.16	NaN	1.31	0.93	0.99	1.18	1.34
F5H1K3	tRNA 2'-phosphotransferase 1	TRPT1	98	S	0.938	95.21	NaN	NaN	0.98	0.82	NaN	NaN	0.83	1.10	1.18
F5H1U9	Multiple PDZ domain protein	MPDZ	483	S	0.998	77.37	NaN	NaN	NaN	NaN	NaN	NaN	0.95	0.73	NaN
F5H1U9	Multiple PDZ domain protein	MPDZ	354	S	0.783	107.2	1.06	1.07	NaN	0.99	NaN	NaN	1.20	0.92	0.86
F5H452	Transcription factor Dp-1	TFDP1	23	S	1	60.3	0.49	0.57	NaN	0.88	1.15	NaN	0.69	0.72	NaN
F5H658	ATP-dependent RNA helicase DHX8	DHX8	460	S	1	60.3	0.43	0.45	0.49	NaN	0.69	0.78	0.38	0.41	0.38
F5H6E2	Unconventional myosin-Ic	MYO1C	384	S	0.989	109.8	1.17	1.14	1.34	1.74	1.84	1.63	0.92	0.98	1.04
F5H7D6	Transducin-like enhancer protein 3	TLE3	230	S	0.997	136.7	NaN	NaN	NaN	0.55	NaN	NaN	1.62	1.17	1.47
F5H7D6	Transducin-like enhancer protein 3	TLE3	184	S	0.899	96.69	NaN	0.27	0.38	0.30	0.39	NaN	0.92	NaN	0.86
F5H7D6	Transducin-like enhancer protein 3	TLE3	189	S	0.994	120.3	NaN	NaN	0.48	0.44	0.37	0.38	1.09	NaN	1.14
F5H8D7	DNA repair protein XRCC1	XRCC1	415	S	0.626	115.3	0.50	NaN	NaN	0.75	NaN	0.69	NaN	NaN	NaN
F5H8D7	DNA repair protein XRCC1	XRCC1	416	S	0.845	85.73	0.52	NaN	NaN	0.65	0.71	0.72	0.68	0.76	NaN

H0YAQ0	Set1/Ash2 histone methyltransferase complex subunit ASH2	ASH2L	85	S	1	53.76	0.79	0.80	0.97	0.77	0.76	0.71	NaN	1.02	0.97
F6PQP6		EPN2	192	S	1	61.73	0.51	0.68	NaN	NaN	NaN	NaN	0.78	NaN	NaN
F6RY50	Signal-induced proliferation-associated protein 1	SIPA1	737	S	0.843	78.7	NaN	NaN	NaN	0.96	0.98	NaN	NaN	1.21	NaN
F6VDH7	Hsc70-interacting protein	ST13	38	S	1	50.24	0.56	NaN	NaN	NaN	0.77	NaN	0.83	0.74	NaN
F6VDH7	Hsc70-interacting protein	ST13	39	S	1	50.24	0.56	NaN	NaN	NaN	0.77	NaN	0.83	0.74	NaN
F6VDH7	Hsc70-interacting protein	ST13	42	S	1	50.24	0.56	NaN	NaN	NaN	0.77	NaN	0.83	0.74	NaN
F8VPD4	CAD protein;Glutamine-dependent carbamoyl-phosphate synthase;Aspartate carbamoyltransferase;Dihydro orotase	CAD	1796	S	1	59.92	0.86	1.17	0.86	0.97	1.03	NaN	1.59	1.55	1.65
H3BV98	RISC-loading complex subunit TARBP2	TARBP2	53	S	1	156.5	0.91	1.12	0.79	NaN	NaN	0.75	0.78	0.49	NaN
F8VTQ5	Heterogeneous nuclear ribonucleoprotein A1;Heterogeneous nuclear ribonucleoprotein A1, N-terminally processed	HNRNPA1	6	S	1	257.2	1.48	1.42	1.32	1.46	1.42	1.43	1.11	1.14	1.16
F8VVL1	Density-regulated protein	DENR	73	S	1	250.5	0.63	0.61	0.62	0.91	0.90	0.97	0.91	1.02	1.04
F8VXC8	SWI/SNF complex subunit SMARCC2	SMARCC2	347	S	1	127.3	0.79	0.76	0.70	1.17	1.12	1.02	0.77	0.67	0.79
F8VXC8	SWI/SNF complex subunit SMARCC2	SMARCC2	302	S	1	118.7	0.87	0.87	0.88	0.89	0.93	0.92	0.95	0.97	0.98
F8VXC8	SWI/SNF complex subunit SMARCC2	SMARCC2	304	S	1	118.7	0.85	0.86	0.88	0.93	0.93	0.92	0.94	0.97	0.97
F8VXC8	SWI/SNF complex subunit SMARCC2	SMARCC2	306	S	0.978	72.52	1.67	1.61	NaN	NaN	0.87	NaN	0.95	1.17	0.99
F8VXC8	SWI/SNF complex subunit SMARCC2	SMARCC2	283	S	0.999	153	0.80	0.74	0.90	1.09	1.09	1.12	1.11	1.22	1.04
F8VY01	FYVE, RhoGEF and PH domain-containing protein 6	FGD6	721	S	1	71.81	NaN	NaN	NaN	NaN	0.76	NaN	0.88	0.67	NaN
F8W038	Chromatin complexes subunit BAP18	C17orf49	96	S	1	154.5	1.31	1.29	1.48	1.43	1.50	1.49	0.93	0.92	0.95
F8W038	Chromatin complexes subunit BAP18	C17orf49	35	S	0.5	97.12	2.62	2.36	NaN	NaN	NaN	NaN	NaN	NaN	NaN
F8W038	Chromatin complexes subunit BAP18	C17orf49	36	S	0.5	97.12	2.62	2.36	NaN	NaN	NaN	NaN	NaN	NaN	NaN
F8W726	Ubiquitin-associated protein 2-like	UBAP2L	620	S	0.885	155.9	1.07	1.17	1.25	1.35	1.30	1.23	0.85	0.88	0.92
F8W726	Ubiquitin-associated protein 2-like	UBAP2L	464	S	0.622	168.9	3.68	3.56	4.11	NaN	NaN	NaN	NaN	NaN	NaN
F8W726	Ubiquitin-associated protein 2-like	UBAP2L	465	S	0.906	129.3	NaN	4.41	3.84	3.19	NaN	2.97	2.56	3.39	2.39

F8W726	Ubiquitin-associated protein 2-like	UBAP2L	478	S	1	243.2	1.04	1.43	0.64	0.79	NaN	0.78	0.57	NaN	0.63
F8W726	Ubiquitin-associated protein 2-like	UBAP2L	488	S	0.906	155.6	1.04	1.43	1.18	1.79	1.90	1.94	0.57	0.53	0.68
F8W914	Reticulon	RTN4	153	S	0.994	244.7	0.96	1.14	NaN	NaN	1.28	NaN	1.02	1.08	NaN
F8W930	Insulin-like growth factor 2 mRNA-binding protein 2	IGF2BP2	168	S	0.984	142.4	1.36	1.39	1.30	1.39	1.47	1.23	NaN	1.10	1.21
F8W930	Insulin-like growth factor 2 mRNA-binding protein 2	IGF2BP2	170	S	0.999	149.2	0.82	0.89	1.67	0.69	0.75	2.00	1.06	1.02	0.95
F8W9J4	Dystonin	DST	1378	S	0.77	64.1	NaN	0.91	0.78	1.54	1.58	1.39	0.45	NaN	0.52
F8W9J4	Dystonin	DST	1382	S	0.999	81.33	0.73	0.74	NaN	1.53	1.58	1.46	0.49	0.55	0.50
F8W9J4	Dystonin	DST	2919	S	1	78.43	0.92	0.85	NaN	0.91	1.34	1.55	1.06	1.34	1.32
F8W9J4	Dystonin	DST	2671	S	0.997	85.88	NaN	NaN	NaN	NaN	2.49	1.25	NaN	NaN	NaN
F8WA39	Myotubularin-related protein 1	MTMR1	43	S	0.993	87.49	NaN	0.81	1.30	NaN	0.93	NaN	1.08	1.03	1.63
F8WAE5	Eukaryotic translation initiation factor 2A;Eukaryotic translation initiation factor 2A, N-terminally processed	EIF2A	498	S	0.591	88.95	0.73	NaN	0.68	0.69	0.72	0.73	0.89	0.81	0.93
F8WAE5	Eukaryotic translation initiation factor 2A;Eukaryotic translation initiation factor 2A, N-terminally processed	EIF2A	501	S	1	233.5	0.77	0.66	0.76	0.72	0.66	0.73	0.96	0.96	0.88
F8WAZ4	GTP-binding protein 1	GTPBP1	44	S	1	79.88	NaN	1.10	1.30	1.43	1.25	1.42	1.35	1.71	1.88
F8WAZ4	GTP-binding protein 1	GTPBP1	47	S	1	79.88	NaN	1.10	1.30	1.43	1.25	1.42	1.35	1.71	1.88
F8WAZ4	GTP-binding protein 1	GTPBP1	25	S	0.677	78.94	0.90	0.84	NaN	NaN	NaN	NaN	NaN	NaN	NaN
F8WBF9	Protein NDRG3	NDRG3	266	S	1	104.2	NaN	NaN	1.44	NaN	NaN	0.99	2.07	1.29	1.24
F8WBL2	Bystin	BYSL	98	S	1	184.2	0.74	0.89	0.75	0.95	0.90	1.02	0.59	0.59	0.58
F8WCX2	Zinc finger protein 687	ZNF687	253	S	0.96	113.7	0.65	NaN	NaN	NaN	0.55	0.73	0.80	0.79	NaN
F8WCX2	Zinc finger protein 687	ZNF687	183	S	0.685	49.91	0.67	0.94	NaN	0.62	0.87	NaN	NaN	NaN	NaN
F8WD88	Histone H3-like centromeric protein A	CENPA	17	S	0.996	61.86	0.96	1.08	0.96	1.04	1.00	NaN	0.89	1.01	0.91
F8WD88	Histone H3-like centromeric protein A	CENPA	19	S	0.958	61.86	0.96	1.08	0.96	1.04	1.00	NaN	0.89	1.01	0.91
F8WDB4	Leucine-rich repeat and WD repeat-containing protein 1	LRWD1	99	S	0.952	125.6	NaN	0.92	0.89	NaN	NaN	NaN	1.30	NaN	NaN
F8WDB4	Leucine-rich repeat and WD repeat-containing protein 1	LRWD1	60	S	1	93.8	0.60	0.66	0.69	NaN	0.74	0.84	0.79	NaN	NaN
F8WF93	Dol-P-Man:Man(5)GlcNAc(2)-PP-Dol alpha-1,3-mannosyltransferase	ALG3	13	S	0.996	86.09	2.10	2.02	2.15	1.92	2.45	2.03	1.74	1.24	1.41
G3V1D1	Ferritin;Ferritin heavy chain;Ferritin heavy chain, N-terminally processed	FTH1	109	S	0.997	175.1	0.69	0.67	0.61	0.79	0.98	0.88	0.40	0.58	NaN
G3V198	Nuclear pore complex protein Nup160	NUP160	1122	S	0.999	102.4	0.57	0.66	0.60	0.65	0.70	0.67	0.85	0.90	0.90
H0YER7	Apoptosis inhibitor 5	API5	277	S	0.797	166	NaN	NaN	0.87	NaN	1.04	1.03	1.09	NaN	NaN
H0YER7	Apoptosis inhibitor 5	API5	279	S	0.97	225.1	0.81	0.81	0.81	1.01	0.95	0.99	0.79	0.76	0.86

G3V2D6	Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	207	S	1	243	0.57	NaN	NaN	NaN	0.71	NaN	0.90	0.88	NaN
G3V2R1	Protein Smaug homolog 1	SAMD4A	11	S	0.995	117.3	1.01	1.01	1.12	NaN	NaN	NaN	NaN	NaN	NaN
G3V340	Striatin-3	STRN3	257	S	1	170.3	0.70	0.81	0.57	0.98	1.07	0.84	0.67	0.78	0.61
G3V4X8	SNW domain-containing protein 1	SNW1	62	S	1	129.9	0.58	0.49	0.41	0.62	0.61	0.62	0.30	0.32	0.32
G3V4X8	SNW domain-containing protein 1	SNW1	70	S	0.993	129.9	0.83	0.79	0.84	1.03	0.83	0.97	0.71	0.74	0.74
G3V4X8	SNW domain-containing protein 1	SNW1	72	S	0.5	91.97	NaN	NaN	NaN	NaN	0.96	NaN	0.67	0.60	NaN
Q5TAQ8	DDB1- and CUL4-associated factor 8	DCAF8	99	S	1	131	NaN	NaN	NaN	NaN	NaN	NaN	1.03	1.09	1.12
G3V411	Zinc finger CCCH domain-containing protein 14	ZC3H14	217	S	1	113.6	1.70	1.75	1.37	1.58	1.63	1.46	1.78	1.56	1.43
H0YJ03	Proteasome subunit alpha type-3	PSMA3	78	S	1	227.4	0.63	0.60	0.63	0.88	1.01	0.91	0.48	0.47	0.57
G3V529	ATP-dependent RNA helicase DDX24	DDX24	39	S	1	162.8	1.00	1.28	1.29	0.79	0.86	0.84	0.77	0.80	0.67
G3V529	ATP-dependent RNA helicase DDX24	DDX24	252	S	0.677	79.02	1.05	NaN	1.21	NaN	NaN	1.14	NaN	NaN	NaN
G3V599	Melanoma inhibitory activity protein 2	MIA2	1071	S	1	124.6	3.24	2.89	2.93	NaN	NaN	2.47	NaN	NaN	NaN
G3V5E1	Cyclin-K	CCNK	340	S	1	101.5	0.99	0.79	0.81	0.88	0.83	0.82	0.88	0.95	0.88
G3V5E1	Cyclin-K	CCNK	324	S	1	79.47	0.92	0.81	0.82	0.88	0.78	0.92	0.92	1.01	1.09
G3V5E1	Cyclin-K	CCNK	328	S	0.639	79.47	0.92	0.81	0.82	0.88	0.93	0.92	1.04	1.01	1.09
H0YG16	Kinesin light chain 1	KLC1	152	S	0.967	77.75	1.19	1.16	NaN	0.89	1.17	NaN	NaN	NaN	1.04
H0YG16	Kinesin light chain 1	KLC1	155	S	0.883	72.89	NaN	NaN	1.27	NaN	1.17	1.11	0.93	0.93	NaN
H0YG16	Kinesin light chain 1	KLC1	66	S	0.985	43.72	2.74	NaN	2.71	5.54	4.79	NaN	1.59	1.05	NaN
G3V5V3	Nuclear export mediator factor NEMF	NEMF	705	S	1	102.7	0.46	0.57	NaN	0.60	0.60	0.66	NaN	NaN	0.78
G3V5V3	Nuclear export mediator factor NEMF	NEMF	706	S	1	102.7	0.46	0.57	NaN	0.60	0.60	0.66	NaN	NaN	0.78
Q5QP22	RNA-binding protein 39	RBM39	136	S	1	142.4	1.07	1.10	1.09	1.15	1.13	1.10	0.89	0.92	0.85
Q5QP22	RNA-binding protein 39	RBM39	97	S	0.996	70.4	1.30	NaN	1.99	NaN	1.32	1.34	1.37	1.28	1.38
G3XAM7	Catenin alpha-1	CTNNA1	641	S	1	299.9	1.36	1.46	1.42	1.28	1.28	1.27	1.16	1.08	1.18
P42166	Lamina-associated polypeptide 2, isoforms beta/gamma;Thymopoietin;Thymopentin;Lamina-associated polypeptide 2, isoform alpha;Thymopoietin;Thymopentin	TMPO	66;66	S	1	311.2	1.28	1.29	0.62	1.27	0.67	1.38	0.94	0.72	0.94

P42166	Lamina-associated polypeptide 2, isoforms beta/gamma;Thymopoietin;Thymopentin;Lamina-associated polypeptide 2, isoform alpha;Thymopoietin;Thymopentin	TMPO	67;67	S	1	312.7	0.62	0.71	1.28	0.69	0.67	0.70	0.69	0.72	0.83
G5E9A6	Ubiquitin carboxyl-terminal hydrolase;Ubiquitin carboxyl-terminal hydrolase 11	USP11	905	S	0.98	67.83	NaN	NaN	0.33	NaN	NaN	NaN	0.75	0.96	NaN
G5E9A6	Ubiquitin carboxyl-terminal hydrolase;Ubiquitin carboxyl-terminal hydrolase 11	USP11	605	S	0.997	115.3	0.49	NaN	NaN	NaN	NaN	NaN	1.25	1.92	0.91
G5E9C0	Sp110 nuclear body protein	SP110	256	S	1	86.54	0.34	0.48	NaN	0.78	NaN	NaN	NaN	NaN	NaN
G5E9C8	Son of sevenless homolog 1	SOS1	1195	S	0.998	56.91	1.10	NaN	NaN	0.95	0.95	NaN	0.92	0.83	NaN
G8JLD5	Dynamin-1-like protein	DNM1L	592	S	1	73.98	0.97	0.99	1.09	NaN	1.65	1.50	0.75	0.77	0.66
G8JLH9	Signal transducer and activator of transcription;Signal transducer and activator of transcription 3	STAT3	629	S	1	131.9	1.73	1.73	1.63	1.83	1.90	2.01	0.88	0.81	NaN
H0Y2P0	CD44 antigen	CD44	254	S	1	108.8	1.01	1.03	0.99	0.84	0.88	0.82	1.09	1.20	1.19
H0Y2V6	Centrosomal protein of 170	CEP170	935	S	0.97	97.22	3.01	3.48	3.89	1.63	1.46	3.63	2.51	1.89	2.10
H0Y2V6	Centrosomal protein of 170	CEP170	410	S	0.949	78.79	3.25	1.83	NaN	NaN	NaN	NaN	NaN	NaN	NaN
H0Y2V6	Centrosomal protein of 170	CEP170	1043	S	0.693	43.37	NaN	NaN	NaN	1.83	2.23	NaN	NaN	NaN	0.81
H0Y2V6	Centrosomal protein of 170 kDa;Cep170-like protein	CEP170	1495	S	0.769	97.61	NaN	NaN	NaN	NaN	1.14	NaN	2.37	1.79	NaN
H0Y2V6	Centrosomal protein of 170 kDa;Cep170-like protein	CEP170	1496	S	0.505	42.33	NaN	NaN	NaN	NaN	1.14	NaN	2.37	1.79	NaN
H0Y2V6	Centrosomal protein of 170 kDa;Cep170-like protein	CEP170	1503	S	1	124	1.11	1.07	0.74	0.88	0.87	0.64	2.37	0.98	0.92
H0Y589	Histone lysine demethylase PHF8	PHF8	585	S	0.968	80.06	NaN	1.09	0.89	NaN	NaN	NaN	NaN	1.95	NaN
H0Y449	Nuclease-sensitive element-binding protein 1	YBX1	364	S	0.886	188.1	1.19	1.31	1.33	1.32	1.17	1.31	1.16	1.24	1.18
H0Y449	Nuclease-sensitive element-binding protein 1	YBX1	215	S	0.997	273.4	3.27	NaN	NaN	1.64	NaN	1.48	2.98	2.09	NaN
H0Y449	Nuclease-sensitive element-binding protein 1	YBX1	224	S	0.991	315	1.58	1.59	NaN	1.40	1.20	1.15	1.85	1.64	1.56
H0Y4R1	Inosine-5'-monophosphate dehydrogenase 2	IMPDH2	372	S	1	74.39	0.92	NaN	NaN	1.04	1.06	NaN	NaN	NaN	NaN
H0Y4V9	La-related protein 4B	LARP4B	165	S	0.827	89.68	NaN	1.18	NaN	1.35	1.42	1.21	NaN	0.99	1.21
H0Y4V9	La-related protein 4B	LARP4B	167	S	0.997	104.5	0.92	0.59	1.60	1.26	1.18	1.34	NaN	1.12	0.52
H0Y4V9	La-related protein 4B	LARP4B	337	S	1	137.9	1.62	1.56	1.77	1.43	1.59	1.62	0.87	0.79	0.91
H0Y4V9	La-related protein 4B	LARP4B	82	S	0.557	59.3	NaN	NaN	NaN	NaN	NaN	0.74	1.09	1.45	NaN
H0Y4V9	La-related protein 4B	LARP4B	90	S	0.899	143.5	0.97	1.07	1.22	1.03	1.26	1.15	1.50	1.11	1.68
H0Y4Z8	Rab-like protein 6	RABL6	426	S	1	93.1	NaN	NaN	NaN	NaN	NaN	NaN	NaN	0.65	0.95
H0Y4Z8	Rab-like protein 6	RABL6	597	S	1	150.5	1.19	1.15	1.46	1.34	1.06	1.09	1.17	1.36	1.28

H0Y4Z8	Rab-like protein 6	RABL6	455	S	1	74.84	1.51	0.54	1.09	0.65	0.89	1.10	1.18	0.80	1.47
H0Y4Z8	Rab-like protein 6	RABL6	465	S	0.981	60.62	1.51	0.54	NaN	0.65	0.89	1.58	NaN	NaN	1.23
H0Y4Z8	Rab-like protein 6	RABL6	471	S	0.926	74.84	1.51	NaN	1.09	NaN	1.35	1.10	1.27	0.49	1.09
H0Y4Z8	Rab-like protein 6	RABL6	472	S	0.943	74.84	1.51	NaN	1.09	NaN	1.35	1.32	1.18	0.49	1.09
H0Y503	Basic leucine zipper and W2 domain-containing protein 1	BZW1	127	S	1	173.1	NaN	0.72	0.77	0.81	NaN	0.71	0.68	0.58	0.63
H0Y507	SH3 and PX domain-containing protein 2A	SH3PXD2A	474	S	1	211.1	0.76	NaN	NaN	0.94	0.83	0.97	NaN	NaN	0.81
H0Y555	Proteasome inhibitor PI31 subunit	PSMF1	13	S	0.757	72.92	NaN	1.12	NaN	1.27	1.18	NaN	NaN	NaN	NaN
H0Y564	Anaphase-promoting complex subunit 1	ANAPC1	221	S	0.5	48.44	NaN	NaN	NaN	NaN	NaN	NaN	0.80	0.95	NaN
H0Y564	Anaphase-promoting complex subunit 1	ANAPC1	223	S	0.994	83.09	0.77	NaN	NaN	NaN	NaN	1.07	0.74	0.83	NaN
H0Y579	UV excision repair protein RAD23 homolog B	RAD23B	30	S	0.954	251.7	1.41	1.46	1.34	1.58	1.61	1.65	0.85	0.91	0.92
H0Y7H7	Dedicator of cytokinesis protein 4	DOCK4	1161	S	1	75.2	1.42	1.59	NaN	0.89	NaN	NaN	1.13	1.29	NaN
H0Y5S9	Casein kinase I isoform	CSNK1E	66	S	0.5	88.16	0.79	NaN	NaN	0.97	0.79	NaN	1.06	1.00	1.01
H0Y626	Tripartite motif-containing protein 16	TRIM16	60	S	1	314.3	0.93	0.89	0.92	1.09	1.01	1.21	0.79	0.78	0.92
H0Y6F5	Zinc fingers and homeoboxes protein 3	ZHX3	655	S	0.968	52.11	1.05	1.06	NaN	NaN	NaN	NaN	0.97	1.15	NaN
H7BZT5	Zinc finger protein 185	ZNF185	205;449	S	0.656	158.5	NaN	NaN	NaN	NaN	0.90	NaN	NaN	1.33	1.24
H7BZT5	Zinc finger protein 185	ZNF185	212;456	S	1	138	1.12	1.21	1.16	1.20	1.05	0.97	1.20	1.18	1.13
H7BZT5	Zinc finger protein 185	ZNF185	278;522	S	0.995	199.6	NaN	0.71	0.89	NaN	0.94	1.26	0.78	NaN	1.51
H7BZT5	Zinc finger protein 185	ZNF185	224;468	S	0.996	113.2	2.53	2.78	3.18	NaN	NaN	2.66	4.37	5.96	3.81
H0Y704		ZNF185	23	S	1	160.5	NaN	0.84	0.93	0.62	0.59	0.62	0.67	NaN	NaN
H0Y7Q2	Coiled-coil domain-containing protein 132	CCDC132	346	S	0.998	150.1	0.82	0.74	NaN	0.91	NaN	NaN	NaN	NaN	0.78
H0Y7W6		FNBP1	311	S	0.997	57.35	1.10	0.93	NaN	1.02	0.87	1.05	1.20	1.17	1.27
Q96RU3	Formin-binding protein 1	FNBP1	258;296	S	0.998	85.4	1.74	1.77	1.70	1.68	1.85	1.87	2.48	2.30	2.32
H0Y7Y8	AT-rich interactive domain-containing protein 4B	ARID4B	75	S	0.976	61.04	NaN	0.30	NaN	0.68	0.68	NaN	NaN	0.43	NaN
H0Y7Z1	Fibronectin;Anastellin;Ugl-Y1;Ugl-Y2;Ugl-Y3	FN1	1101	S	1	188.5	NaN	1.55	1.57	NaN	NaN	1.21	NaN	1.05	NaN
H0Y8X4	2'-deoxynucleoside 5'-phosphate N-hydrolase 1	DNPH1	238	S	0.998	140.7	NaN	1.25	1.25	1.76	1.80	1.35	1.10	1.00	1.05
H0Y9P1	BMP-2-inducible protein	BMP2K	722	S	0.842	40.01	1.53	1.26	NaN	NaN	NaN	NaN	1.00	NaN	NaN
H0Y9P1	BMP-2-inducible protein	BMP2K	724	S	0.856	59.51	1.53	1.26	NaN	NaN	NaN	NaN	1.00	1.06	NaN
H0Y9P1	BMP-2-inducible protein	BMP2K	725	S	0.856	59.51	1.53	1.26	NaN	NaN	NaN	NaN	1.00	1.06	NaN
H0Y9P1	BMP-2-inducible protein	BMP2K	640	S	0.645	99.96	1.55	1.69	1.92	NaN	NaN	NaN	1.80	1.98	2.64
H0Y9T5	m7GpppN-mRNA hydrolase	DCP2	228	S	1	80.85	1.07	0.89	1.24	1.09	0.90	1.07	0.96	0.80	1.15
H0Y9T5	m7GpppN-mRNA hydrolase	DCP2	229	S	1	80.85	1.07	0.89	1.24	1.09	0.90	1.07	0.96	0.80	1.15
H0Y9T5	m7GpppN-mRNA hydrolase	DCP2	231	S	1	80.85	1.07	0.89	1.24	1.09	0.90	1.07	0.96	0.80	1.15
H0YA93	NEDD4-binding protein 2	N4BP2	313	S	0.542	42.35	1.18	0.90	1.96	1.40	1.88	0.83	1.45	NaN	NaN
H0YA93	NEDD4-binding protein 2	N4BP2	333	S	0.826	42.35	1.18	0.90	1.96	1.40	1.88	0.83	1.45	NaN	NaN

H0YA93	NEDD4-binding protein 2	N4BP2	335	S	0.826	42.35	1.18	0.90	1.96	1.40	1.88	0.83	1.45	NaN	NaN
H0YA93	NEDD4-binding protein 2	N4BP2	337	S	0.826	42.35	1.18	0.90	1.96	1.40	1.88	0.83	1.45	NaN	NaN
H0YAC7	Coatomer subunit beta'	COPB2	73	S	1	351.3	0.88	0.86	0.85	0.86	0.97	0.91	0.80	0.88	0.97
H0YAD9	SH3 domain-binding protein 2	SH3BP2	120	S	1	41.54	1.26	NaN	1.12	NaN	0.89	1.10	NaN	NaN	NaN
H0YAZ3	Vinexin	SORBS3	42	S	0.975	184.9	NaN	NaN	1.91	1.70	1.72	1.77	2.10	2.22	2.38
H0YD46	DNA polymerase delta subunit 3	POLD3	31	S	1	164.5	0.51	0.56	NaN	0.68	0.71	NaN	0.51	0.59	NaN
H0YDM2	Protein SOGA1;N-terminal form;C-terminal 80 kDa form	SOGA1	869	S	1	60.34	NaN	0.40	NaN	0.67	0.70	0.57	NaN	0.87	NaN
H0YE29	Rho GTPase-activating protein 1	ARHGAP 1	48	S	0.73	80.91	NaN	NaN	NaN	1.38	1.42	1.32	1.25	NaN	NaN
H0YE29	Rho GTPase-activating protein 1	ARHGAP 1	49	S	0.981	169.2	1.63	1.64	1.80	1.44	NaN	1.38	1.20	1.20	1.24
H0YE35	Synembryn-A	RIC8A	44	S	1	290.8	0.63	0.64	0.60	0.76	0.76	0.76	0.43	0.51	0.53
H0YE35	Synembryn-A	RIC8A	118	S	1	51.57	NaN	1.75	1.78	2.89	NaN	NaN	1.02	1.01	NaN
H0YGG4		EIF2B1	7	S	1	47.81	NaN	NaN	NaN	NaN	NaN	NaN	0.55	0.38	NaN
H0YGI8	Stress-induced-phosphoprotein 1	STIP1	80	S	1	131.1	1.60	1.59	1.45	2.64	2.61	2.43	1.02	0.99	1.02
H0YK04	Rho GTPase-activating protein 5	ARHGAP 5	96	S	0.965	186.1	1.73	1.15	NaN	1.84	NaN	NaN	1.68	1.82	1.88
J3KPH4	Sorting nexin-1	SNX1	32	S	1	161.4	1.04	1.13	1.02	1.09	1.09	1.04	1.13	1.80	1.17
J3KPH4	Sorting nexin-1	SNX1	39	S	1	198.4	1.04	1.12	1.02	1.05	1.09	1.04	0.82	0.69	1.10
H0YLQ7	DnaJ homolog subfamily C member 17	DNAJC17	112	S	1	218.4	0.96	0.89	0.94	0.86	0.87	NaN	0.81	1.00	1.04
H0YM23	Ankyrin repeat domain-containing protein 17	ANKRD17	1931	S	0.982	59.98	NaN	0.72	NaN	0.70	0.79	0.87	NaN	0.98	NaN
H0YNU8	Tropomodulin-3	TMOD3	25	S	0.972	91.11	NaN	2.15	NaN	2.26	2.15	NaN	1.87	1.40	NaN
H3BLV9	SRSF protein kinase 1	SRPK1	327	S	0.96	85.93	0.99	0.84	NaN	NaN	NaN	NaN	0.94	0.97	0.95
H3BLZ2		DBNDD1	7	S	0.939	81.01	1.20	1.14	1.11	1.04	1.07	1.08	1.03	1.03	1.09
H3BM18	Gamma-interferon-inducible protein 16	IFI16	106	S	1	238.8	NaN	1.47	1.16	2.15	2.07	2.16	1.20	1.16	1.33
H3BM18	Gamma-interferon-inducible protein 16	IFI16	153	S	1	183.7	0.60	0.58	0.64	0.88	0.80	0.91	NaN	NaN	0.55
H3BM38	Synaptosomal-associated protein;Synaptosomal-associated protein 23	SNAP23	110	S	1	257.8	2.61	3.01	2.90	2.66	NaN	1.78	2.20	2.07	1.78
H3BM89	60S ribosomal protein L4	RPL4	201	S	1	71.22	1.25	1.42	NaN	NaN	1.42	1.22	0.87	0.84	1.09
H3BTD3	cAMP-regulated phosphoprotein 19	ARPP19	7	S	0.765	43.3	0.73	0.67	NaN	NaN	NaN	NaN	NaN	NaN	NaN
H3BMF6	Ubiquitin carboxyl-terminal hydrolase 7	USP7	18	S	1	118.7	0.90	NaN	0.77	NaN	1.02	1.04	NaN	NaN	NaN
H3BMI8	Telomeric repeat-binding factor 2-interacting protein 1	TERF2IP	32	S	0.966	183.3	NaN	NaN	NaN	2.02	NaN	NaN	1.15	1.08	NaN
H3BUL0	RNA-binding protein with serine-rich domain 1	RNPS1	155	S	1	61.17	0.80	0.84	NaN	0.90	0.89	0.91	0.77	0.86	0.89
H3BUL0	RNA-binding protein with serine-rich domain 1	RNPS1	157	S	0.996	61.17	0.80	0.84	NaN	0.90	0.89	0.91	0.77	0.86	0.89

H3BN50		SLC9A3R2	20	S	1	67.87	1.61	1.65	1.64	1.34	1.39	1.39	1.40	1.34	1.46
H3BTK3	Calcium-regulated heat stable protein 1	CARHSP1	30	S	1	154.1	0.77	0.81	0.60	0.85	0.67	0.63	0.99	0.81	0.77
H3BTK3	Calcium-regulated heat stable protein 1	CARHSP1	32	S	1	154.1	0.91	0.95	0.71	0.88	0.67	0.92	1.09	0.81	1.19
H3BTK3	Calcium-regulated heat stable protein 1	CARHSP1	41	S	0.999	119.4	2.33	2.19	2.12	2.08	2.12	2.05	2.47	2.69	2.21
H3BNW0	THUMP domain-containing protein 1	THUMPD1	86	S	1	147.7	0.56	0.89	0.87	0.90	0.95	0.92	0.98	0.99	0.90
H3BNW0	THUMP domain-containing protein 1	THUMPD1	88	S	1	147.7	0.81	0.89	0.49	0.90	0.95	0.92	0.65	0.96	0.90
H3BPG4	Cytoplasmic tRNA 2-thiolation protein 2	CTU2	101	S	1	84.82	1.15	1.08	1.15	0.85	1.12	0.89	1.10	1.18	1.22
H3BUH7	Fructose-bisphosphate aldolase;Fructose-bisphosphate aldolase A	ALDOA	36	S	0.921	127.7	1.12	1.46	NaN	NaN	NaN	NaN	1.94	NaN	NaN
H3BTD6	Enhancer of mRNA-decapping protein 3	EDC3	18	S	1	173	1.14	1.23	1.06	1.39	1.16	1.24	1.26	1.06	1.33
H3BPZ1	Very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase	HACD3	89	S	1	123	1.35	1.59	1.43	1.36	1.19	1.35	0.79	0.79	0.62
H3BRT8	Dual specificity protein kinase CLK3	CLK3	76	S	0.958	57.07	0.69	0.64	NaN	0.65	0.98	NaN	NaN	0.93	NaN
H3BRT8	Dual specificity protein kinase CLK3	CLK3	9	S	0.975	55.84	1.13	1.13	NaN	NaN	NaN	NaN	1.14	NaN	NaN
H3BQK9	Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5	MACF1	4553	S	1	157.4	0.63	0.68	0.69	1.24	0.98	1.03	0.98	0.92	0.91
H3BQK9	Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5	MACF1	4527	S	0.564	108.5	NaN	NaN	NaN	NaN	NaN	NaN	0.49	NaN	0.42
H3BQK9	Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5	MACF1	4528	S	0.995	195.4	0.38	NaN	NaN	0.83	0.86	0.68	0.36	0.35	NaN
H3BQZ7	Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2-BSCL2	161	S	1	304.8	0.98	0.92	0.92	0.99	0.93	0.97	1.09	0.98	1.10
H3BQZ7	Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2-BSCL2	226	S	0.696	220.2	0.45	0.45	NaN	0.56	0.63	NaN	NaN	0.71	0.55
H3BQZ7	Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2-BSCL2	228	S	0.832	200.5	0.45	0.45	NaN	NaN	NaN	NaN	0.67	NaN	NaN
H3BRM1	Abscission/NoCut checkpoint regulator	ZFYVE19	262	S	1	213	0.93	1.05	0.84	0.97	0.88	0.80	1.09	1.22	0.99
H3BRM1	Abscission/NoCut checkpoint regulator	ZFYVE19	115	S	1	74.46	0.83	0.69	0.82	NaN	0.79	0.76	0.87	0.97	1.11
H3BRG5	StAR-related lipid transfer protein 13	STARD13	299	S	1	43.52	NaN	0.84	1.17	NaN	NaN	NaN	NaN	NaN	NaN

H3BRG5	StAR-related lipid transfer protein 13	STARD13	118	S	1	109.1	1.25	1.07	1.04	0.93	0.89	0.93	1.00	1.17	NaN
H3BS42	Zinc finger protein 768	ZNF768	52	S	0.782	42	NaN	NaN	NaN	NaN	0.84	NaN	1.05	0.90	1.04
H3BS86	E3 ubiquitin-protein ligase	STUB1	19	S	1	183	0.68	0.72	0.68	0.71	0.81	0.78	0.77	0.79	0.83
H3BS86	E3 ubiquitin-protein ligase	STUB1	23	S	0.981	81.32	0.90	1.29	1.52	1.24	NaN	1.59	1.03	NaN	NaN
H3BTX0	PAXIP1-associated glutamate-rich protein 1	PAGR1	67	S	1	194.9	0.96	1.16	1.29	1.09	1.20	NaN	1.24	1.20	1.48
J3QLT7	Nucleolar protein 3	NOL3	70	S	0.572	99.89	NaN	0.80	0.85	NaN	NaN	NaN	0.83	NaN	NaN
H3BUV9	Ubiquitin-like protein 7	UBL7	174	S	1	260.8	0.80	0.97	NaN	0.83	NaN	0.10	0.95	0.88	NaN
P29590	Protein PML	PML	162;518	S	1	154.8	0.50	0.46	0.57	0.61	0.51	0.51	0.74	0.82	0.92
P29590	Protein PML	PML	171;527	S	1	154.8	0.63	0.54	0.82	0.69	0.79	0.82	1.07	1.25	1.44
P29590	Protein PML	PML	174;530	S	1	169.7	1.47	NaN	1.41	NaN	1.16	1.23	1.63	NaN	1.64
P29590	Protein PML	PML	47;403	S	0.999	88.67	0.94	1.04	1.03	1.60	NaN	1.28	1.25	1.15	1.05
P29590	Protein PML	PML	149;505	S	0.987	116.9	0.82	0.85	0.88	0.87	0.90	0.89	1.22	1.16	1.20
H7BZX1	Sorbin and SH3 domain-containing protein 2	SORBS2	224	S	0.989	71.14	0.37	0.36	0.52	0.61	NaN	NaN	NaN	NaN	NaN
H7BZ88	Signal transducer and activator of transcription 1-	STAT1	17	S	1	96.05	1.34	1.34	1.48	1.96	1.96	1.63	0.67	0.69	NaN
H7BZT5	Zinc finger protein 185	ZNF185	153	S	0.77	138.1	1.69	NaN	NaN	NaN	NaN	NaN	1.79	1.85	NaN
H7BZZ1	HCLS1-binding protein 3	HS1BP3	13	S	1	190.7	0.80	0.87	1.20	1.25	1.38	0.81	1.03	0.99	1.04
H7BZZ1	HCLS1-binding protein 3	HS1BP3	68	S	1	115	0.72	0.85	0.76	0.85	0.91	0.71	0.81	0.75	0.81
H7BZZ6	Serine/arginine-rich splicing factor 7	SRSF7	103	S	1	81.88	0.95	0.98	0.99	1.04	1.05	1.10	NaN	0.84	0.87
H7BZZ6	Serine/arginine-rich splicing factor 7	SRSF7	105	S	1	81.88	0.26	0.25	0.27	0.39	0.40	0.38	NaN	0.17	0.87
H7BZZ6	Serine/arginine-rich splicing factor 7	SRSF7	76	S	0.994	97.74	1.03	1.17	0.31	0.28	1.00	1.12	0.29	1.03	0.30
H7BZZ6	Serine/arginine-rich splicing factor 7	SRSF7	78	S	0.993	66.96	1.03	1.17	1.07	1.06	1.00	1.12	1.11	0.30	1.14
H7C072	THO complex subunit 5 homolog	THOC5	183	S	1	187.3	0.86	0.77	0.76	0.91	0.76	0.81	1.23	0.82	1.03
H7C072	THO complex subunit 5 homolog	THOC5	185	S	1	187.3	0.86	0.77	0.76	0.91	0.76	0.81	1.23	0.82	1.03
H7C0X8	Macrophage-capping protein	CAPG	92	S	0.999	55.16	0.93	1.26	NaN	2.28	NaN	NaN	0.68	NaN	NaN
H7C113	Phospholipid-transporting ATPase IG	ATP11C	159	S	0.845	56.21	1.20	1.63	NaN	NaN	NaN	NaN	0.92	0.87	NaN
H7C1Q8	DIS3-like exonuclease 2	DIS3L2	156	S	1	116.8	0.86	NaN	0.75	0.78	NaN	0.66	NaN	NaN	0.89
H7C2H2	Ras-specific guanine nucleotide-releasing factor RalGPS2	RALGPS2	67	S	1	115	0.69	0.58	0.68	0.95	1.13	NaN	0.95	0.86	NaN
J3KQW3	Transmembrane protein 44	TMEM44	194	S	0.994	60.02	0.85	0.83	NaN	1.03	0.99	0.98	0.93	0.96	1.17
H7C409	Bromodomain and WD repeat-containing protein 1	BRWD1	413	S	0.813	47.6	NaN	NaN	NaN	0.89	NaN	0.68	1.14	NaN	NaN
H7C4B6	Transcription regulator protein BACH1	BACH1	11	S	0.981	47.56	NaN	NaN	1.53	NaN	1.65	1.56	NaN	NaN	NaN

I1E4Y6	PERQ amino acid-rich with GYF domain-containing protein 2	GIGYF2	26	S	0.966	146.9	1.85	1.69	1.62	1.69	2.08	1.87	1.40	1.44	1.67
I1E4Y6	PERQ amino acid-rich with GYF domain-containing protein 2	GIGYF2	258	S	1	55.98	1.27	1.21	NaN	1.08	1.26	NaN	NaN	NaN	NaN
I3L0L0		RUNX2	419	S	0.682	141.5	NaN	NaN	NaN	1.00	NaN	NaN	0.82	0.83	NaN
I3L4F6	Coiled-coil domain-containing protein 137	CCDC137	18	S	1	69.28	NaN	1.44	1.51	NaN	NaN	NaN	0.99	NaN	NaN
I3L467	Unconventional prefoldin RPB5 interactor 1	URI1	16	S	0.842	46.98	NaN	NaN	NaN	0.89	NaN	NaN	0.60	0.82	NaN
I3L1Q2	B-cell CLL/lymphoma 7 protein family member C	BCL7C	114	S	0.985	84.66	0.82	1.07	1.18	0.71	0.81	NaN	NaN	NaN	NaN
I3L1Q2	B-cell CLL/lymphoma 7 protein family member C	BCL7C	122	S	0.561	98.74	0.94	NaN	1.30	NaN	NaN	NaN	NaN	NaN	NaN
I3L1Q2	B-cell CLL/lymphoma 7 protein family member C	BCL7C	126	S	0.993	172.2	0.82	1.18	1.18	1.63	0.81	NaN	1.10	1.05	0.80
I3L4I0	FLYWCH family member 2	FLYWCH 2	21	S	0.985	56.3	1.18	NaN	0.72	NaN	1.58	1.32	NaN	NaN	0.98
I3L436	Regulatory-associated protein of mTOR	RPTOR	37	S	0.984	106.8	0.57	0.52	0.61	NaN	NaN	0.62	NaN	NaN	0.83
I3L436	Regulatory-associated protein of mTOR	RPTOR	23	S	0.998	254.8	0.69	0.62	0.70	0.69	0.70	0.71	0.88	1.05	1.21
I3L4J1	Vacuolar protein sorting-associated protein 4A	VPS4A	119	S	0.839	53.2	NaN	NaN	0.96	0.97	0.85	0.84	0.94	1.11	1.09
I3L4J1	Vacuolar protein sorting-associated protein 4A	VPS4A	121	S	0.97	53.2	NaN	NaN	0.96	0.97	0.85	0.84	0.94	1.11	1.09
J3KNG6	Protein spire homolog 1	SPIRE1	467	S	0.936	63.71	NaN	NaN	0.87	NaN	NaN	1.07	1.03	0.97	NaN
J3KNN7	BRCA1-associated protein	BRAP	87	S	0.994	151.4	0.88	NaN	1.04	1.12	1.03	0.95	0.96	1.01	0.93
J3KR72	Transcription initiation factor TFIID subunit 6	TAF6	710	S	1	99.71	NaN	NaN	NaN	NaN	0.93	NaN	0.94	0.77	NaN
J3KRY8	Tether containing UBX domain for GLUT4	ASPSCR1	331	S	0.727	71.55	NaN	NaN	NaN	3.30	2.26	NaN	NaN	NaN	NaN
J3KRY8	Tether containing UBX domain for GLUT4	ASPSCR1	104	S	0.933	65.41	1.50	1.50	1.69	2.66	1.97	2.65	0.92	0.92	NaN
J3QLL0	Importin subunit alpha-1	KPNA2	62	S	0.966	214.5	2.32	2.27	2.46	3.99	3.97	4.44	0.84	0.93	NaN
J3KSG3	ADP-ribosylation factor-binding protein GGA3	GGA3	37	S	1	77.19	1.29	1.05	1.29	0.91	1.08	1.29	0.90	1.09	1.04
J3KSI3	E3 ubiquitin-protein ligase rififylin	RFFL	89	S	0.967	83.22	1.23	NaN	NaN	NaN	0.89	NaN	1.23	NaN	1.24
J3KSI3	E3 ubiquitin-protein ligase rififylin	RFFL	92	S	0.942	83.22	1.23	NaN	NaN	NaN	NaN	NaN	1.23	NaN	1.24
J3KSR8	Serine/arginine-rich splicing factor 1	SRSF1	94	S	1	158.5	0.75	0.76	0.78	0.75	0.75	0.75	0.70	0.67	0.75
J3KSR8	Serine/arginine-rich splicing factor 1	SRSF1	96	S	0.983	65.63	1.26	1.38	1.27	1.48	1.34	1.27	1.45	1.29	1.54

J3KSR8	Serine/arginine-rich splicing factor 1	SRSF1	100	S	0.993	65.63	NaN	NaN	1.36	NaN	1.22	1.23	1.74	1.39	1.54
J3KSY7	Protein CASC3	CASC3	35	S	1	270.2	0.82	0.81	0.80	0.71	0.73	0.72	1.00	0.95	1.04
J3KTD8		CBFB	46	S	0.992	78.76	NaN	1.34	1.19	NaN	NaN	1.08	1.42	1.31	1.42
J3QK89	Calcium homeostasis endoplasmic reticulum protein	CHERP	826	S	0.995	107	0.85	1.03	1.03	NaN	0.99	NaN	1.13	1.07	1.13
J3QK89	Calcium homeostasis endoplasmic reticulum protein	CHERP	828	S	0.996	107	0.85	1.03	1.03	NaN	0.99	NaN	1.13	1.07	1.13
J3QK89	Calcium homeostasis endoplasmic reticulum protein	CHERP	824	S	0.998	82.77	NaN	1.00	1.06	NaN	0.87	NaN	NaN	NaN	1.08
J3QQN1	Proteasome subunit beta type-10	PSMB10	110	S	0.917	61.42	1.23	NaN	NaN	NaN	1.08	0.78	NaN	NaN	0.91
J3QQQ3	Zinc finger protein 830	ZNF830	85	S	1	161.7	1.07	1.03	NaN	1.33	1.22	NaN	1.19	1.41	1.70
J3QR07	YTH domain-containing protein 1	YTHDC1	308	S	1	165.6	NaN	NaN	1.15	0.67	0.68	NaN	0.77	0.84	NaN
J3QRP6	Na(+)/H(+) exchange regulatory cofactor NHE-RF1	SLC9A3R1	161	S	1	163.8	4.92	4.60	4.90	4.45	4.74	4.85	2.65	NaN	2.93
J3QRP6	Na(+)/H(+) exchange regulatory cofactor NHE-RF1	SLC9A3R1	169	S	0.609	114.9	0.83	NaN	NaN	NaN	NaN	NaN	0.94	0.89	NaN
J3QRP6	Na(+)/H(+) exchange regulatory cofactor NHE-RF1	SLC9A3R1	171	S	0.999	350.6	0.79	0.90	0.70	0.89	0.80	0.93	0.88	1.29	0.77
J3QSD7	Cyclin-dependent kinase 12	CDK12	680	S	1	78.41	0.92	0.54	0.80	1.08	1.13	NaN	0.80	0.90	0.87
J3QSD7	Cyclin-dependent kinase 12	CDK12	684	S	1	78.41	0.92	0.87	0.80	1.08	1.13	NaN	1.12	0.90	0.87
K7EMU2	cAMP-dependent protein kinase type I-alpha regulatory subunit;cAMP-dependent protein kinase type I-alpha regulatory subunit, N-terminally processed	PRKAR1A	83	S	1	150.1	0.85	0.86	0.72	0.87	0.87	0.85	0.94	0.96	1.02
K7ERL1	Formin-like protein 1	FMNL1	64	S	1	180.9	0.87	0.85	0.87	0.87	0.94	0.88	1.00	1.00	0.90
K7EQ06		HDGFRP2	12	S	0.936	109.6	1.36	1.28	0.85	NaN	NaN	0.88	NaN	NaN	1.16
K7EKZ3	Vacuolar protein sorting-associated protein 4B	VPS4B	102	S	1	195.1	0.94	0.89	0.85	0.90	0.81	0.88	0.99	0.94	0.85
K7EL01	F-box/WD repeat-containing protein 9	FBXW9	18	S	1	188.9	NaN	0.50	0.64	0.40	NaN	0.68	0.82	NaN	1.26
K7EL60	Eukaryotic translation initiation factor 3 subunit G	EIF3G	42	S	0.897	174.4	1.32	1.37	1.42	1.24	2.15	1.23	1.04	1.33	1.04
K7ENR9	DNA ligase 3	LIG3	123	S	0.763	130.2	0.66	0.62	0.57	1.03	1.08	NaN	0.59	0.69	0.68
K7EQA1	Programmed cell death protein 5	PDCD5	81	S	1	179.6	1.05	1.27	1.06	1.26	1.32	1.24	0.74	0.70	0.73
K7EQI9	Protein FAM134C	FAM134C	216	S	0.995	54.33	NaN	NaN	1.24	1.14	1.20	NaN	1.12	1.17	NaN
K7EQI9	Protein FAM134C	FAM134C	223	S	1	267	1.03	0.97	0.92	0.86	1.20	0.82	0.98	1.02	1.00
K7EQI9	Protein FAM134C	FAM134C	336	S	0.942	126.2	2.25	2.32	NaN	NaN	1.89	NaN	NaN	1.64	NaN
K7EQI9	Protein FAM134C	FAM134C	338	S	0.942	177.1	2.25	2.32	NaN	NaN	1.89	NaN	NaN	1.64	NaN
K7EQI9	Protein FAM134C	FAM134C	339	S	0.672	177.1	2.25	2.32	NaN	NaN	NaN	NaN	NaN	1.64	NaN

K7ER94	FH1/FH2 domain-containing protein 3	FHOD3	541	S	1	166.6	0.61	0.37	0.47	0.62	NaN	0.53	1.66	0.71	0.76
K7ERB6	Homologous-pairing protein 2 homolog	PSMC3IP	131	S	0.908	61.99	NaN	NaN	NaN	NaN	NaN	NaN	1.56	1.08	NaN
K7ERU2	KN motif and ankyrin repeat domain-containing protein 2	KANK2	98	S	1	88.55	1.72	1.45	1.70	1.47	1.64	1.50	1.11	1.09	1.07
K7ERU2	KN motif and ankyrin repeat domain-containing protein 2	KANK2	46	S	0.999	119.8	1.57	2.02	NaN	1.83	1.68	1.61	NaN	0.97	NaN
M0QXN5	Nuclear pore glycoprotein p62	NUP62	332	S	1	179.2	1.35	NaN	NaN	1.59	1.72	NaN	1.07	0.83	NaN
M0QYF9	Homer protein homolog 3	HOMER3	47	S	1	69.15	NaN	NaN	NaN	NaN	NaN	NaN	1.39	1.48	2.12
M0QZ09	NAD-dependent protein deacetylase sirtuin-6	SIRT6	264	S	0.823	53.98	1.24	1.11	1.39	1.05	NaN	NaN	NaN	NaN	NaN
M0QZR4	Rho guanine nucleotide exchange factor 1	ARHGEF 1	919	S	1	100.8	NaN	NaN	NaN	2.71	2.86	NaN	0.98	0.90	NaN
M0R2H7	Cdc42-interacting protein 4	TRIP10	296	S	0.999	164.8	0.97	0.98	0.95	0.94	0.94	0.80	1.70	1.70	1.49
M0R0P8	Unconventional myosin-IXb	MYO9B	717	S	0.898	115.5	0.84	0.89	0.87	1.28	1.36	1.08	0.71	0.60	0.73
M0R0P8	Unconventional myosin-IXb	MYO9B	1122	S	1	76.21	0.68	NaN	0.54	0.82	0.60	0.55	0.78	0.85	0.74
M0R0P8	Unconventional myosin-IXb	MYO9B	1405	S	0.993	89.4	NaN	0.45	NaN	0.62	0.58	0.54	NaN	NaN	NaN
M0R0P8	Unconventional myosin-IXb	MYO9B	1935	S	1	124.1	0.83	0.82	1.25	1.25	1.25	1.31	0.72	0.86	0.83
M0R0P8	Unconventional myosin-IXb	MYO9B	1115	S	0.538	76.21	NaN	NaN	0.54	0.71	0.60	0.55	NaN	0.85	0.74
M0R0P8	Unconventional myosin-IXb	MYO9B	1290	S	1	214.3	0.47	0.48	0.51	0.59	0.47	0.62	0.85	0.80	0.77
M0R0W6	Receptor protein-tyrosine kinase;Tyrosine-protein kinase receptor UFO	AXL	616	S	0.983	72.88	NaN	0.61	NaN	NaN	NaN	NaN	1.30	NaN	1.03
M0R2S2	Epidermal growth factor receptor substrate 15-like 1	EPS15L1	101	S	0.999	317.3	0.99	1.08	1.27	1.13	0.98	1.06	1.10	1.11	1.02
M0R2S2	Epidermal growth factor receptor substrate 15-like 1	EPS15L1	75	S	1	129.3	1.64	1.68	1.72	1.65	1.72	1.69	1.00	0.98	1.11
O00203	AP-3 complex subunit beta-1	AP3B1	276	S	1	229.7	1.00	1.01	1.05	1.15	1.18	1.00	1.08	1.15	1.08
O00264	Membrane-associated progesterone receptor component 1	PGRMC1	181	S	1	414.9	0.95	0.98	1.00	0.93	0.95	1.05	1.04	1.07	1.16
O00264	Membrane-associated progesterone receptor component 1	PGRMC1	54	S	0.949	118.2	NaN	NaN	NaN	1.00	0.96	NaN	NaN	1.10	1.14
O00264	Membrane-associated progesterone receptor component 1	PGRMC1	57	S	1	322.5	1.00	1.26	0.99	1.13	1.12	0.98	1.14	1.06	1.12
O00273	DNA fragmentation factor subunit alpha	DFFA	315	S	0.998	134.8	0.76	0.81	NaN	1.49	1.33	1.05	1.38	1.42	0.98
O00303	Eukaryotic translation initiation factor 3 subunit F	EIF3F	258	S	1	106.9	1.03	1.03	0.99	1.28	1.37	1.20	1.14	0.97	0.98
O00308	NEDD4-like E3 ubiquitin-protein ligase WWP2	WWP2	211	S	0.991	84.95	1.00	0.86	1.06	0.84	NaN	3.13	4.01	4.20	1.44
O00425	Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	184	S	0.999	49.03	0.95	NaN	0.98	0.89	NaN	NaN	1.05	NaN	NaN

O00499	Myc box-dependent-interacting protein 1	BIN1	296	S	1	102.6	1.23	2.38	1.01	0.80	0.85	0.84	1.53	0.87	0.87
O00499	Myc box-dependent-interacting protein 1	BIN1	298	S	1	182.2	1.05	0.97	0.93	1.04	0.92	0.94	1.12	1.20	1.13
O00499	Myc box-dependent-interacting protein 1	BIN1	303	S	1	136.4	1.23	2.38	1.58	1.32	0.85	NaN	1.46	1.08	0.78
O00505	Importin subunit alpha-4	KPNA3	60	S	1	226.2	1.73	1.81	1.81	1.36	1.36	1.40	1.91	2.09	2.03
U3KQ48	U3 small nucleolar ribonucleoprotein protein MPP10	MPHOSPH10	163	S	1	160.1	0.76	0.68	0.83	0.76	0.90	0.97	0.65	0.48	1.17
U3KQ48	U3 small nucleolar ribonucleoprotein protein MPP10	MPHOSPH10	167	S	1	160.1	0.76	0.68	0.83	0.76	0.90	0.97	0.65	0.48	1.17
U3KQ48	U3 small nucleolar ribonucleoprotein protein MPP10	MPHOSPH10	171	S	1	122.5	1.05	1.03	0.83	1.02	1.01	0.97	1.19	1.14	1.17
O00567	Nucleolar protein 56	NOP56	519	S	1	142.3	0.93	0.99	0.93	1.22	NaN	0.92	0.70	1.05	1.14
O00567	Nucleolar protein 56	NOP56	520	S	1	178.5	0.74	0.96	0.82	0.97	1.23	0.96	0.85	0.92	0.87
O00567	Nucleolar protein 56	NOP56	569	S	1	63.73	0.76	1.22	NaN	NaN	NaN	NaN	NaN	NaN	NaN
O00567	Nucleolar protein 56	NOP56	570	S	1	106.4	1.57	NaN	NaN	1.44	NaN	NaN	0.98	NaN	1.24
O14497	AT-rich interactive domain-containing protein 1A	ARID1A	696	S	0.998	104.2	1.21	1.09	NaN	1.92	1.44	1.14	NaN	1.29	NaN
O14497	AT-rich interactive domain-containing protein 1A	ARID1A	1600	S	0.896	78.79	NaN	NaN	NaN	NaN	NaN	NaN	0.33	0.51	0.44
O14523	C2 domain-containing protein 2-like	C2CD2L	662	S	0.799	106.3	1.63	NaN	NaN	1.22	NaN	1.34	1.17	1.23	1.26
O14545	TRAF-type zinc finger domain-containing protein 1	TRAFD1	415	S	0.966	159.4	0.99	0.92	0.82	0.92	0.78	0.96	0.94	1.01	NaN
O14613	Cdc42 effector protein 2	CDC42EP2	141	S	0.991	61.52	4.09	2.62	NaN	NaN	NaN	NaN	NaN	NaN	NaN
O14686	Histone-lysine N-methyltransferase 2D	KMT2D	4738	S	1	51.01	1.05	1.05	NaN	NaN	NaN	NaN	1.23	NaN	1.20
O14686	Histone-lysine N-methyltransferase 2D	KMT2D	1671	S	1	66.02	NaN	0.62	NaN	1.12	1.35	NaN	NaN	NaN	NaN
O14828	Secretory carrier-associated membrane protein 3	SCAMP3	76	S	0.997	96.67	0.91	0.95	0.98	1.15	1.13	1.10	0.70	0.69	0.71
O14879	Interferon-induced protein with tetratricopeptide repeats 3	IFIT3	478	S	0.888	69.02	NaN	NaN	NaN	NaN	1.14	1.49	NaN	NaN	NaN
O14974	Protein phosphatase 1 regulatory subunit 12A	PPP1R12A	299	S	1	107	0.52	0.33	NaN	0.83	NaN	NaN	NaN	0.49	NaN
O14974	Protein phosphatase 1 regulatory subunit 12A	PPP1R12A	862	S	1	227.4	NaN	0.87	NaN	NaN	NaN	NaN	1.49	NaN	0.83
O14974	Protein phosphatase 1 regulatory subunit 12A	PPP1R12A	871	S	0.986	326.5	1.02	NaN	1.02	0.88	NaN	1.24	1.26	1.04	1.04
O15173	Membrane-associated progesterone receptor component 2	PGRMC2	90	S	0.997	218.1	NaN	NaN	NaN	3.14	3.40	NaN	1.19	NaN	1.08

O15173	Membrane-associated progesterone receptor component 2	PGRMC2	208	S	0.998	125.7	1.70	1.85	1.91	2.20	1.99	2.08	1.98	1.23	1.67
O15446	DNA-directed RNA polymerase I subunit RPA34	CD3EAP	136	S	1	85.02	NaN	2.21	2.23	NaN	2.63	NaN	1.26	1.40	1.75
O15446	DNA-directed RNA polymerase I subunit RPA34	CD3EAP	285	S	0.94	153.4	1.42	1.54	1.34	1.41	1.51	1.58	0.64	0.60	0.75
O15541	RING finger protein 113A	RNF113A	84	S	0.997	121.3	1.14	1.25	1.02	0.85	0.93	0.78	0.85	0.83	0.77
O15541	RING finger protein 113A	RNF113A	85	S	0.995	121.3	1.14	1.25	1.02	0.85	0.93	0.78	0.85	0.83	0.77
O15541	RING finger protein 113A	RNF113A	253	S	1	201.7	1.47	1.56	1.58	1.34	1.39	1.25	1.14	1.36	1.34
O43150	Arf-GAP with SH3 domain, ANK repeat and PH domain-containing protein 2	ASAP2	701	S	1	316.6	0.90	0.87	0.77	1.08	1.13	0.98	0.62	0.66	0.58
O43237	Cytoplasmic dynein 1 light intermediate chain 2	DYNC1LI2	194	S	1	201.2	0.66	0.63	0.74	0.85	0.83	0.86	0.71	0.67	0.68
O43237	Cytoplasmic dynein 1 light intermediate chain 2	DYNC1LI2	407	S	0.719	111	1.96	2.92	NaN	NaN	NaN	NaN	NaN	NaN	NaN
O43290	U4/U6.U5 tri-snRNP-associated protein 1	SART1	448	S	1	114.1	1.74	1.85	1.39	1.66	1.49	1.47	2.20	2.17	1.84
O43290	U4/U6.U5 tri-snRNP-associated protein 1	SART1	598	S	0.894	83.56	0.70	0.59	NaN	0.71	NaN	NaN	NaN	0.82	NaN
O43290	U4/U6.U5 tri-snRNP-associated protein 1	SART1	474	S	1	137.7	0.60	0.51	0.58	0.91	1.10	0.70	0.77	0.77	0.67
O43290	U4/U6.U5 tri-snRNP-associated protein 1	SART1	486	S	1	137.7	0.60	0.51	0.58	0.91	1.10	0.70	0.77	0.77	0.67
O43294	Transforming growth factor beta-1-induced transcript 1 protein	TGFB1I1	137	S	1	87.33	2.47	2.36	2.61	0.74	1.30	2.91	1.40	1.53	NaN
O43294	Transforming growth factor beta-1-induced transcript 1 protein	TGFB1I1	140	S	0.612	87.33	2.47	2.36	2.61	NaN	NaN	2.91	2.13	NaN	NaN
O43294	Transforming growth factor beta-1-induced transcript 1 protein	TGFB1I1	141	S	0.934	79.88	NaN	NaN	NaN	2.49	2.71	NaN	NaN	2.22	NaN
O43294	Transforming growth factor beta-1-induced transcript 1 protein	TGFB1I1	68	S	1	145.1	1.47	1.21	1.39	1.39	1.37	1.50	1.39	1.45	1.40
O43294	Transforming growth factor beta-1-induced transcript 1 protein	TGFB1I1	194	S	0.945	97.08	0.96	0.64	1.07	1.34	1.15	NaN	1.39	1.17	1.30
Q9UG54	Mitogen-activated protein kinase kinase kinase 7	DKFZp586F0420	93	S	1	177.6	1.91	1.78	1.48	1.46	1.44	NaN	1.86	1.92	1.86
O43379	WD repeat-containing protein 62	WDR62	1144	S	0.881	83.6	0.35	0.41	NaN	NaN	NaN	NaN	0.62	NaN	NaN
O43379	WD repeat-containing protein 62	WDR62	32	S	0.64	80.91	0.70	NaN	0.78	NaN	0.57	0.94	1.17	NaN	1.02

O43379	WD repeat-containing protein 62	WDR62	33	S	0.941	78.89	NaN	0.97	0.78	NaN	0.57	NaN	1.17	0.79	1.02
O43379	WD repeat-containing protein 62	WDR62	1228	S	0.99	139.8	1.04	1.14	0.77	NaN	NaN	NaN	NaN	NaN	NaN
O43395	U4/U6 small nuclear ribonucleoprotein Prp3	PRPF3	619	S	1	47.73	NaN	NaN	0.44	NaN	0.70	0.88	NaN	0.74	0.85
O43399	Tumor protein D54	TPD52L2	166	S	1	190.8	1.46	1.65	1.58	1.28	1.27	1.31	3.55	3.45	3.46
O43463	Histone-lysine N-methyltransferase SUV39H1	SUV39H1	391	S	1	79.49	NaN	NaN	NaN	0.54	0.75	NaN	NaN	NaN	NaN
O43493	Trans-Golgi network integral membrane protein 2	TGOLN2	71	S	0.991	210.7	0.71	0.94	0.91	0.92	NaN	0.97	0.74	0.94	0.82
O43493	Trans-Golgi network integral membrane protein 2	TGOLN2	298	S	1	257	NaN	1.13	NaN	1.31	NaN	NaN	1.17	NaN	1.98
O43719	HIV Tat-specific factor 1	HTATSF1	579	S	1	104.8	NaN	1.11	0.97	1.02	1.06	NaN	1.17	NaN	1.26
O43719	HIV Tat-specific factor 1	HTATSF1	624	S	1	251.7	0.73	0.70	0.71	0.82	0.80	0.78	0.82	0.90	0.73
O43719	HIV Tat-specific factor 1	HTATSF1	498	S	1	145.4	0.76	0.82	1.18	NaN	NaN	1.39	0.87	NaN	0.99
O43719	HIV Tat-specific factor 1	HTATSF1	453	S	0.985	157.3	0.93	0.92	0.93	1.04	1.04	1.13	0.95	1.02	1.29
O43719	HIV Tat-specific factor 1	HTATSF1	676	S	1	311.8	0.80	0.83	0.82	0.91	0.96	0.87	0.89	0.87	0.91
O43719	HIV Tat-specific factor 1	HTATSF1	642	S	1	252.1	0.90	0.84	0.88	0.98	1.24	0.88	1.14	1.15	1.05
O43719	HIV Tat-specific factor 1	HTATSF1	616	S	1	155.9	0.75	0.75	0.77	0.99	1.01	1.01	0.97	1.01	1.05
O43765	Small glutamine-rich tetratricopeptide repeat-containing protein alpha	SGTA	77	S	1	121.9	1.35	1.57	1.43	2.40	2.39	2.43	0.83	0.80	0.85
O43765	Small glutamine-rich tetratricopeptide repeat-containing protein alpha	SGTA	305	S	0.977	237.1	NaN	NaN	1.24	1.60	NaN	1.51	NaN	1.36	NaN
O43815	Striatin	STRN	245	S	1	176.4	0.96	NaN	NaN	NaN	NaN	NaN	1.11	NaN	1.29
O43815	Striatin	STRN	137	S	0.998	204.2	0.36	0.44	0.34	0.76	0.70	0.75	0.36	0.34	0.49
O60244	Mediator of RNA polymerase II transcription subunit 14	MED14	986	S	1	140.5	0.37	0.36	0.42	0.63	NaN	0.55	0.34	0.42	0.50
O60264	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	66	S	1	231.5	NaN	0.50	NaN	0.75	0.86	0.88	0.67	NaN	0.46
O60271	C-Jun-amino-terminal kinase-interacting protein 4	SPAG9	329	S	0.936	66.57	NaN	0.54	NaN	1.00	0.92	0.72	0.95	1.09	NaN
O60271	C-Jun-amino-terminal kinase-interacting protein 4	SPAG9	332	S	0.997	79.61	0.46	0.47	0.68	0.57	0.67	0.59	1.08	1.15	1.17
O60271	C-Jun-amino-terminal kinase-interacting protein 4	SPAG9	730	S	0.999	125.2	0.93	1.06	1.41	1.31	1.37	NaN	0.96	1.00	1.21
O60271	C-Jun-amino-terminal kinase-interacting protein 4	SPAG9	732	S	0.688	66.78	NaN	NaN	1.41	NaN	1.34	NaN	1.38	NaN	0.90
O60271	C-Jun-amino-terminal kinase-interacting protein 4	SPAG9	733	S	0.985	192.9	0.86	0.68	0.66	0.82	0.81	0.64	0.79	0.82	0.66
O60271	C-Jun-amino-terminal kinase-interacting protein 4	SPAG9	251	S	1	105.9	0.72	0.73	0.79	0.98	0.90	0.90	1.03	0.92	0.96

O60292	Signal-induced proliferation-associated 1-like protein 3	SIPA1L3	1364	S	1	65.57	NaN	NaN	NaN	NaN	NaN	NaN	2.21	3.49	NaN
O60292	Signal-induced proliferation-associated 1-like protein 3	SIPA1L3	1534	S	0.5	48.33	NaN	0.97	0.81	1.09	NaN	NaN	NaN	NaN	NaN
O60292	Signal-induced proliferation-associated 1-like protein 3	SIPA1L3	1544	S	0.996	88.1	NaN	1.28	1.24	NaN	0.89	NaN	1.81	1.81	1.70
O60502	Protein O-GlcNAcase	MGEA5	364	S	1	101	0.67	0.61	0.64	0.93	0.95	0.82	0.65	0.61	NaN
O60551	Glycylpeptide N-tetradecanoyltransferase 2	NMT2	66	S	0.959	78.78	0.51	0.50	0.52	0.72	0.62	0.55	0.59	0.55	1.00
O60551	Glycylpeptide N-tetradecanoyltransferase 2	NMT2	68	S	0.997	78.78	0.51	0.50	1.54	1.03	1.16	1.00	0.94	1.33	1.05
O60551	Glycylpeptide N-tetradecanoyltransferase 2	NMT2	70	S	0.98	78.78	NaN	NaN	0.84	NaN	0.90	NaN	NaN	0.96	1.00
O60551	Glycylpeptide N-tetradecanoyltransferase 2	NMT2	38	S	1	91.75	NaN	0.78	0.76	0.98	NaN	0.93	1.01	0.98	0.96
O60566	Mitotic checkpoint serine/threonine-protein kinase BUB1 beta	BUB1B	670	S	1	43.54	NaN	NaN	NaN	1.15	1.25	NaN	NaN	NaN	NaN
O60763	General vesicular transport factor p115	USO1	942	S	1	269.8	1.24	1.32	1.32	1.30	1.09	NaN	0.89	NaN	1.07
O60784	Target of Myb protein 1	TOM1	462	S	0.8	86.48	1.97	NaN	NaN	1.62	1.85	NaN	1.22	NaN	1.39
O60832	H/ACA ribonucleoprotein complex subunit 4	DKC1	485	S	1	129.5	NaN	NaN	1.43	1.54	0.60	1.55	1.40	1.17	NaN
O60832	H/ACA ribonucleoprotein complex subunit 4	DKC1	494	S	0.998	310.1	0.89	0.86	0.97	0.92	0.96	0.96	0.96	0.78	0.90
O60832	H/ACA ribonucleoprotein complex subunit 4	DKC1	513	S	1	118.9	1.21	1.17	1.30	1.11	NaN	1.11	1.04	0.96	1.10
O60832	H/ACA ribonucleoprotein complex subunit 4	DKC1	451	S	1	99.37	1.00	1.06	1.30	1.00	1.03	0.87	0.98	0.96	0.56
O60832	H/ACA ribonucleoprotein complex subunit 4	DKC1	453	S	1	99.37	1.00	1.06	1.30	1.00	1.03	1.00	0.98	0.96	0.97
O60832	H/ACA ribonucleoprotein complex subunit 4	DKC1	455	S	1	98.63	1.17	1.26	1.30	0.93	1.78	1.49	1.26	0.95	1.09
O75379	Vesicle-associated membrane protein 4	VAMP4	30	S	1	221.9	1.01	1.11	1.08	1.12	0.95	0.95	1.03	1.14	1.01
O75436	Vacuolar protein sorting-associated protein 26A	VPS26A	315	S	1	229.5	NaN	NaN	2.03	2.43	2.60	2.76	NaN	0.40	0.41
O75475	PC4 and SFRS1-interacting protein	PSIP1	106	S	0.985	179	0.69	NaN	NaN	0.76	0.73	0.77	0.82	0.81	0.89
O75475	PC4 and SFRS1-interacting protein	PSIP1	273	S	0.977	287	0.53	0.56	0.50	0.56	NaN	0.52	0.62	NaN	0.63
O75475	PC4 and SFRS1-interacting protein	PSIP1	275	S	1	287	0.53	0.56	0.50	0.56	0.57	0.52	0.62	0.73	0.63
Q5JRI1	Serine/arginine-rich splicing factor 10	SRSF10	133	S	1	84.06	1.00	1.08	1.08	1.01	1.07	0.97	1.38	1.14	1.34
Q5JRI1	Serine/arginine-rich splicing factor 10	SRSF10	131	S	1	61.11	1.02	1.06	1.01	0.95	0.97	0.93	1.24	1.25	1.24

Q5JRI1	Serine/arginine-rich splicing factor 10	SRSF10	129	S	1	61.11	NaN	1.09	1.08	0.96	0.96	NaN	1.25	1.28	NaN
O75533	Splicing factor 3B subunit 1	SF3B1	488	S	0.993	128.9	2.04	2.18	2.43	3.80	3.69	3.07	NaN	0.66	NaN
O75533	Splicing factor 3B subunit 1	SF3B1	129	S	1	129	0.90	0.85	0.82	1.12	0.93	0.98	0.63	0.71	0.74
O75683	Surfeit locus protein 6	SURF6	138	S	1	97.16	0.95	NaN	0.90	0.93	0.99	0.93	0.92	0.97	0.92
S4R419	Transcription elongation factor A protein 3	TCEA3	78	S	1	107.6	0.41	0.40	0.67	0.52	0.55	0.63	0.42	0.57	0.62
O76021	Ribosomal L1 domain-containing protein 1	RSL1D1	427	S	0.952	67.93	NaN	NaN	0.83	1.65	NaN	1.31	0.62	NaN	0.75
O76021	Ribosomal L1 domain-containing protein 1	RSL1D1	361	S	1	220.1	1.65	1.64	1.63	1.73	1.68	1.73	1.03	0.86	1.09
O76021	Ribosomal L1 domain-containing protein 1	RSL1D1	443	S	0.997	48.57	1.46	1.58	NaN	2.14	2.37	NaN	NaN	0.60	0.80
Q5QPB1	AN1-type zinc finger protein 5	ZFAND5	100	S	0.958	105.1	NaN	1.43	NaN	1.20	1.80	NaN	NaN	NaN	NaN
O76094	Signal recognition particle subunit SRP72	SRP72	620	S	0.772	146.6	0.54	1.07	NaN	1.20	NaN	NaN	NaN	NaN	NaN
O76094	Signal recognition particle subunit SRP72	SRP72	621	S	0.976	264.8	0.64	0.81	0.52	0.53	NaN	0.57	0.81	NaN	1.00
O76094	Signal recognition particle subunit SRP72	SRP72	625	S	0.994	264.8	1.09	1.08	1.13	1.10	NaN	1.09	0.87	0.88	0.94
O94804	Serine/threonine-protein kinase 10	STK10	438	S	1	304.7	1.13	1.16	1.13	1.03	1.05	1.01	1.18	1.16	1.10
O94806	Serine/threonine-protein kinase D3	PRKD3	27	S	0.705	80.24	0.94	1.21	1.76	1.07	NaN	NaN	NaN	NaN	NaN
O94806	Serine/threonine-protein kinase D3	PRKD3	30	S	0.844	80.24	0.94	1.21	1.76	1.07	NaN	NaN	1.55	2.10	NaN
O94806	Serine/threonine-protein kinase D3	PRKD3	31	S	0.844	73.06	0.94	1.21	1.76	1.07	NaN	NaN	1.55	2.10	NaN
O94826	Mitochondrial import receptor subunit TOM70	TOMM70A	91	S	1	184.3	1.01	1.07	1.09	1.07	1.23	1.06	0.88	0.89	0.90
O94874	E3 UFM1-protein ligase 1	UFL1	458	S	1	171.4	0.71	0.81	0.84	0.83	0.82	0.80	0.89	0.94	0.89
O95104	Splicing factor, arginine/serine-rich 15	SCAF4	154	S	1	191.8	0.80	0.81	0.80	1.05	NaN	0.93	0.72	NaN	0.72
O95155	Ubiquitin conjugation factor E4 B	UBE4B	88	S	0.949	175.2	0.55	NaN	NaN	0.63	NaN	0.75	0.98	NaN	NaN
O95218	Zinc finger Ran-binding domain-containing protein 2	ZRANB2	120	S	1	209.7	NaN	NaN	NaN	1.01	NaN	NaN	1.44	1.51	NaN
O95218	Zinc finger Ran-binding domain-containing protein 2	ZRANB2	153	S	1	178.9	1.17	NaN	1.09	NaN	NaN	NaN	NaN	NaN	1.56
O95218	Zinc finger Ran-binding domain-containing protein 2	ZRANB2	188	S	1	103.4	1.10	NaN	0.98	0.81	NaN	NaN	1.01	1.06	2.19
O95297	Myelin protein zero-like protein 1	MPZL1	210	S	0.996	192.2	2.11	2.13	NaN	2.14	1.75	1.65	0.75	0.84	0.87
O95297	Myelin protein zero-like protein 1	MPZL1	219	S	0.992	57.28	NaN	1.59	NaN	2.28	2.02	NaN	1.01	0.99	NaN
O95365	Zinc finger and BTB domain-containing protein 7A	ZBTB7A	337	S	1	172.6	1.01	1.02	0.87	0.91	0.91	0.82	1.00	0.93	1.09

O95365	Zinc finger and BTB domain-containing protein 7A	ZBTB7A	525	S	0.652	148.4	0.80	0.89	0.92	NaN	NaN	1.02	0.96	0.93	NaN
O95365	Zinc finger and BTB domain-containing protein 7A	ZBTB7A	526	S	0.573	148.4	NaN	NaN	NaN	NaN	NaN	NaN	NaN	0.93	1.04
O95365	Zinc finger and BTB domain-containing protein 7A	ZBTB7A	549	S	1	55.66	1.07	0.79	NaN	NaN	NaN	NaN	NaN	NaN	NaN
O95391	Pre-mRNA-splicing factor	SLU7	215	S	1	108.2	0.99	1.00	1.04	1.01	0.99	0.94	1.17	1.14	1.11
O95400	CD2 antigen cytoplasmic tail-binding protein 2	CD2BP2	195	S	0.836	54.02	0.74	NaN	NaN	NaN	0.89	NaN	0.91	0.79	NaN
O95425	Supervillin	SVIL	245	S	1	161	0.79	0.88	0.91	1.01	0.93	1.08	1.06	1.05	0.96
O95425	Supervillin	SVIL	1322	S	1	70.45	0.85	0.79	2.57	1.58	NaN	NaN	NaN	NaN	NaN
O95425	Supervillin	SVIL	968	S	1	215.5	1.10	0.98	1.10	1.33	1.49	1.39	1.27	1.45	1.39
O95613	Pericentrin	PCNT	2177	S	1	88.49	NaN	NaN	NaN	1.43	1.52	NaN	0.65	0.70	NaN
O95628	CCR4-NOT transcription complex subunit 4	CNOT4	430	S	0.674	136	1.83	1.58	NaN	NaN	NaN	NaN	NaN	NaN	NaN
O95628	CCR4-NOT transcription complex subunit 4	CNOT4	432	S	0.938	195.9	NaN	NaN	1.77	1.96	2.11	1.77	1.48	NaN	NaN
O95674	Phosphatidate cytidylyltransferase 2	CDS2	23	S	0.902	74.81	1.52	1.29	NaN	NaN	NaN	NaN	NaN	NaN	NaN
O95674	Phosphatidate cytidylyltransferase 2	CDS2	33	S	0.672	135.9	0.95	1.29	1.00	0.97	1.00	1.04	NaN	1.01	0.94
O95684	FGFR1 oncogene partner	FGFR1OP	156	S	1	124.4	0.80	0.99	0.84	0.84	0.95	0.89	0.83	0.72	0.69
O95684	FGFR1 oncogene partner	FGFR1OP	160	S	1	124.4	0.80	0.77	0.84	0.84	0.95	0.89	0.83	0.72	0.77
O95810	Serum deprivation-response protein	SDPR	25	S	0.974	157.3	0.73	0.71	0.67	1.05	1.10	1.04	0.33	0.34	0.39
O95810	Serum deprivation-response protein	SDPR	27	S	0.952	104.1	1.00	0.87	NaN	1.16	NaN	0.69	NaN	1.33	NaN
O95810	Serum deprivation-response protein	SDPR	293	S	0.995	78.07	0.56	0.60	0.88	0.53	0.50	1.45	0.84	NaN	NaN
O95817	BAG family molecular chaperone regulator 3	BAG3	171	S	0.614	145.8	2.08	2.10	2.39	1.73	1.91	1.70	1.17	1.08	1.19
O95817	BAG family molecular chaperone regulator 3	BAG3	173	S	1	359.9	2.40	2.31	1.98	2.00	1.79	1.94	1.11	1.19	1.21
O95817	BAG family molecular chaperone regulator 3	BAG3	275	S	0.874	86.25	5.71	6.01	5.48	3.44	3.60	2.93	3.32	3.33	3.29
O95817	BAG family molecular chaperone regulator 3	BAG3	279	S	1	86.25	6.19	6.20	5.48	3.44	3.60	2.93	3.32	3.33	3.29
O95817	BAG family molecular chaperone regulator 3	BAG3	377	S	1	151.3	1.49	1.63	1.69	1.42	2.82	1.45	1.27	1.33	1.30
O95817	BAG family molecular chaperone regulator 3	BAG3	385	S	0.656	133.5	1.41	1.57	2.61	1.49	2.82	1.83	0.68	0.79	0.71
O95817	BAG family molecular chaperone regulator 3	BAG3	386	S	0.836	151.3	1.69	1.64	1.63	1.53	1.18	1.57	0.69	1.24	1.29
O95835	Serine/threonine-protein kinase LATS1	LATS1	613	S	0.971	114.9	NaN	NaN	1.37	NaN	1.31	1.30	0.82	0.88	NaN

Q9NZH5	Securin-2;Securin	PTTG2	165	S	1	122.5	0.83	NaN	NaN	1.57	1.50	NaN	0.99	NaN	1.07
O96007	Molybdopterin synthase catalytic subunit	MOCS2	20	S	0.984	45.01	NaN	2.69	NaN	2.52	3.01	NaN	0.91	NaN	NaN
O96013	Serine/threonine-protein kinase PAK 4	PAK4	181	S	0.99	53.1	0.76	0.73	NaN	0.73	0.78	NaN	NaN	1.12	NaN
O96013	Serine/threonine-protein kinase PAK 4	PAK4	104	S	1	81.57	0.75	0.73	0.73	NaN	0.70	0.66	NaN	NaN	0.85
P00558	Phosphoglycerate kinase 1	PGK1	203	S	1	228.6	1.05	1.09	1.05	1.14	1.13	1.08	1.17	1.19	1.22
P02545	Prelamin-A/C;Lamin-A/C	LMNA	390	S	1	209.8	1.36	1.42	1.38	1.40	1.32	1.41	1.34	1.34	1.40
P02545	Prelamin-A/C;Lamin-A/C	LMNA	392	S	1	201.8	1.02	1.02	0.93	1.25	1.24	1.27	1.23	1.17	1.20
P02545	Prelamin-A/C;Lamin-A/C	LMNA	458	S	1	148.5	0.63	0.58	0.61	1.00	0.85	0.88	0.56	0.60	0.62
P02545	Prelamin-A/C;Lamin-A/C	LMNA	22	S	0.998	295.7	2.65	2.74	2.49	4.48	4.30	4.11	0.87	0.89	0.92
P04406	Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	83	S	1	76.21	1.20	1.39	NaN	NaN	NaN	NaN	NaN	NaN	NaN
P05387	60S acidic ribosomal protein P2;60S acidic ribosomal protein P1	RPLP2	102	S	1	315.9	0.30	0.27	0.99	0.98	0.37	0.98	0.92	0.67	0.84
P05387	60S acidic ribosomal protein P2;60S acidic ribosomal protein P1	RPLP2	105	S	1	315.9	0.52	0.43	0.28	0.35	0.35	0.35	0.68	0.83	0.70
P05387	60S acidic ribosomal protein	RPLP2	17	S	0.853	116.3	1.06	NaN	1.33	1.46	1.55	1.67	0.28	NaN	NaN
P17535	Transcription factor AP-1;Transcription factor jun-D	JUN	73;100	S	1	98.63	1.09	1.01	1.04	1.21	1.22	1.17	1.18	1.20	1.24
P05455	Lupus La protein	SSB	366	S	1	325.3	0.84	0.84	0.87	0.90	0.88	0.89	1.00	0.95	0.98
P06748	Nucleophosmin	NPM1	125	S	1	359.6	0.97	1.00	0.96	0.85	0.90	0.85	0.94	0.93	0.94
P06748	Nucleophosmin	NPM1	70	S	0.994	73.77	NaN	NaN	0.63	0.84	0.78	NaN	0.63	0.91	1.14
P06748	Nucleophosmin	NPM1	243	S	0.903	60.26	3.72	3.21	3.37	5.67	6.53	NaN	NaN	NaN	0.76
V9GYZ6	Bifunctional glutamate/proline--tRNA ligase;Glutamate--tRNA ligase;Proline--tRNA ligase	EPRS	889	S	0.739	110.6	0.96	1.01	NaN	NaN	NaN	NaN	1.38	NaN	NaN
V9GYZ6	Bifunctional glutamate/proline--tRNA ligase;Glutamate--tRNA ligase;Proline--tRNA ligase	EPRS	892	S	0.808	250.9	0.76	1.01	0.78	NaN	0.82	NaN	1.38	NaN	NaN
V9GYZ6	Bifunctional glutamate/proline--tRNA ligase;Glutamate--tRNA ligase;Proline--tRNA ligase	EPRS	893	S	0.89	312.5	0.71	0.74	0.73	0.81	0.79	0.80	0.93	0.91	0.96
P07900	Heat shock protein HSP 90-alpha	HSP90AA1	231	S	1	173.2	0.95	0.94	NaN	0.86	0.94	0.96	0.87	0.92	0.73
P07900	Heat shock protein HSP 90-alpha	HSP90AA1	263	S	1	340	0.91	0.94	0.91	1.02	1.00	1.05	0.98	0.94	0.99
P08238	Heat shock protein HSP 90-beta;Putative heat shock protein HSP 90-beta-3	HSP90AB1	226	S	1	157.4	0.89	0.84	0.99	0.76	0.83	0.87	1.10	1.07	1.36
P08238	Heat shock protein HSP 90-beta;Putative heat shock protein HSP 90-beta 2	HSP90AB1	255	S	1	332.4	0.91	0.95	0.86	0.89	0.90	0.89	0.95	0.93	0.99

P08238	Heat shock protein HSP 90-beta;Putative heat shock protein HSP 90-beta 2	HSP90AB1	261	S	1	306.1	0.87	1.16	NaN	0.87	1.04	0.88	0.86	1.01	NaN
P08240	Signal recognition particle receptor subunit alpha	SRPR	296	S	0.987	118.5	NaN	NaN	0.49	NaN	NaN	NaN	0.90	NaN	1.01
P08240	Signal recognition particle receptor subunit alpha	SRPR	297	S	0.842	118.5	NaN	NaN	0.49	NaN	NaN	NaN	0.90	NaN	1.01
P08240	Signal recognition particle receptor subunit alpha	SRPR	298	S	0.667	115.7	NaN	NaN	0.49	NaN	NaN	NaN	0.90	NaN	1.01
P08621	U1 small nuclear ribonucleoprotein 70 kDa	SNRNP70	226	S	0.973	45.68	NaN	NaN	NaN	NaN	0.97	NaN	1.43	1.50	1.84
P08670	Vimentin	VIM	26	S	0.809	109	NaN	NaN	NaN	NaN	NaN	NaN	NaN	0.87	0.84
P08670	Vimentin	VIM	214	S	1	59.98	NaN	NaN	NaN	1.39	1.47	NaN	NaN	NaN	NaN
P08670	Vimentin	VIM	325	S	1	134.9	1.32	1.48	NaN	1.91	1.19	NaN	2.12	1.51	1.30
P08670	Vimentin	VIM	339	S	0.901	170	1.08	1.09	NaN	NaN	NaN	0.88	NaN	NaN	NaN
P08670	Vimentin	VIM	55	S	0.792	147.1	NaN	1.20	1.20	NaN	NaN	NaN	NaN	NaN	NaN
P08670	Vimentin	VIM	56	S	0.991	157.4	1.08	NaN	NaN	0.99	0.97	1.12	0.54	0.46	0.54
P0C1Z6	TCF3 fusion partner	TFPT	249	S	1	104.6	0.82	0.76	NaN	1.18	0.92	0.72	1.14	1.05	1.01
P0C1Z6	TCF3 fusion partner	TFPT	252	S	1	104.6	0.82	0.79	NaN	1.18	0.92	0.72	1.14	1.05	1.01
Q96II5	Serine/threonine-protein kinase A-Raf	ARAF	260	S	1	77.64	NaN	NaN	1.03	NaN	NaN	1.03	1.10	1.23	1.58
Q96II5	Serine/threonine-protein kinase A-Raf;RAF proto-oncogene serine/threonine-	ARAF	585	S	1	85.82	0.91	0.93	NaN	NaN	1.19	1.16	NaN	2.19	2.07
P11166	Solute carrier family 2, facilitated glucose transporter member 1	SLC2A1	473	S	0.688	64.25	NaN	NaN	NaN	NaN	NaN	NaN	3.04	2.97	NaN
P11274	Breakpoint cluster region protein	BCR	122	S	1	107.7	0.75	0.79	0.72	0.86	0.88	NaN	0.73	NaN	0.74
P11388	DNA topoisomerase 2-alpha	TOP2A	1106	S	1	220.9	0.83	0.84	0.84	1.35	1.78	1.59	1.01	1.02	1.04
P11388	DNA topoisomerase 2-alpha	TOP2A	1393	S	0.968	222.6	1.07	1.08	1.12	2.04	2.17	2.05	1.01	NaN	0.96
P11388	DNA topoisomerase 2-alpha	TOP2A	1247	S	1	178.2	1.77	2.47	2.43	5.01	4.62	3.56	1.08	0.88	NaN
P11388	DNA topoisomerase 2-alpha	TOP2A	1377	S	1	173.4	1.69	NaN	1.68	2.54	2.23	2.56	1.33	1.29	1.34
P11388	DNA topoisomerase 2-alpha	TOP2A	1525	S	1	173.3	1.21	1.22	1.27	1.95	NaN	1.99	1.00	1.06	1.00
P11717	Cation-independent mannose-6-phosphate receptor	IGF2R	2409	S	1	224.4	1.22	1.28	1.32	1.31	1.39	1.20	1.10	1.09	1.11
P11717	Cation-independent mannose-6-phosphate receptor	IGF2R	2484	S	1	331.7	1.05	1.06	1.10	1.07	1.09	1.03	1.00	0.98	1.02
P11831	Serum response factor	SRF	224	S	0.998	275.9	1.23	1.42	0.80	1.03	1.09	1.07	1.22	1.30	1.27
P12931	Proto-oncogene tyrosine-protein kinase Src	SRC	17	S	1	185.2	NaN	1.08	0.81	1.04	1.05	0.53	1.11	1.17	1.00
P13051	Uracil-DNA glycosylase	UNG	23	S	1	107.2	0.42	NaN	NaN	NaN	NaN	NaN	0.65	0.61	NaN
P13861	cAMP-dependent protein kinase type II-alpha regulatory	PRKAR2A	78	S	1	254.9	1.00	0.34	0.35	0.33	0.30	0.51	0.67	1.20	1.22
P13861	cAMP-dependent protein kinase type II-alpha regulatory	PRKAR2A	80	S	1	254.9	1.00	1.02	1.01	0.86	0.86	0.92	1.12	0.61	0.78

P13861	cAMP-dependent protein kinase type II-alpha regulatory	PRKAR2A	99	S	1	123.6	1.60	1.37	NaN	2.34	NaN	2.06	1.64	1.48	1.31
P13994	Coiled-coil domain-containing protein 130	CCDC130	362	S	0.995	88.87	0.56	0.54	0.45	0.65	0.66	NaN	0.67	0.89	0.81
P14625	Endoplasmin	HSP90B1	306	S	1	235.2	1.07	0.52	0.80	0.82	0.84	0.80	NaN	NaN	0.52
Q86XA6	Beta-1,4-galactosyltransferase 1;Lactose synthase A protein;N-acetyllactosamine synthase;Beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase;Beta-N-acetylglucosaminyl-glycolipid beta-1,4-galactosyltransferase;Processed beta-1,4-	B4GALT1	74	S	0.882	149	NaN	NaN	NaN	NaN	NaN	NaN	NaN	0.81	0.94
P15407	Fos-related antigen 1	FOSL1	101	S	1	76	NaN	NaN	NaN	4.13	4.30	NaN	NaN	NaN	NaN
P16383	GC-rich sequence DNA-binding factor 2	GCFC2	429	S	0.898	106.2	0.81	0.79	0.81	NaN	0.89	0.85	0.53	0.56	0.58
P16383	GC-rich sequence DNA-binding factor 2	GCFC2	430	S	0.944	106.2	0.81	0.79	0.81	NaN	0.78	0.76	0.53	0.56	0.58
P16989	Y-box-binding protein 3	YBX3	38	S	0.603	178.8	1.07	1.71	1.25	NaN	NaN	1.45	NaN	NaN	1.24
P17096	High mobility group protein HMG-I/HMG-Y	HMGA1	99	S	1	255.6	1.18	1.15	1.06	1.01	0.62	1.01	0.94	0.63	0.97
P17096	High mobility group protein HMG-I/HMG-Y	HMGA1	102	S	1	255.6	0.59	0.56	0.57	0.68	0.62	0.37	0.92	0.91	0.99
P17096	High mobility group protein HMG-I/HMG-Y	HMGA1	103	S	1	255.6	0.59	0.56	0.57	0.68	0.63	0.59	0.92	0.90	0.58
P17096	High mobility group protein HMG-I/HMG-Y	HMGA1	36	S	0.999	129.1	3.37	3.42	3.15	6.22	6.04	5.84	0.95	0.96	0.91
P17252	Protein kinase C alpha type	PRKCA	226	S	0.908	170	1.78	2.11	NaN	1.62	1.60	NaN	0.76	0.68	0.60
P17252	Protein kinase C alpha type	PRKCA	319	S	0.985	81.53	NaN	NaN	1.82	2.29	2.28	NaN	1.28	1.40	1.44
P17275	Transcription factor jun-B	JUNB	259	S	1	140.3	4.31	NaN	NaN	0.99	NaN	1.22	NaN	5.63	5.63
P17535	Transcription factor jun-D	JUND	255	S	0.997	111.6	0.13	0.40	0.32	0.50	0.52	0.39	0.36	0.45	0.19
P17535	Transcription factor jun-D	JUND	259	S	1	107	0.39	0.40	0.32	0.95	0.94	0.82	0.36	0.35	0.36
P18031	Tyrosine-protein phosphatase non-receptor type 1	PTPN1	50	S	1	68.11	1.74	1.32	1.69	NaN	1.30	1.10	1.11	1.42	1.37
P18206	Vinculin	VCL	290	S	1	126.2	0.95	1.01	0.89	1.07	1.04	0.99	0.96	1.05	1.00
P18206	Vinculin	VCL	346	S	0.999	177.4	0.80	2.57	1.13	2.13	2.10	NaN	NaN	1.09	NaN
P18206	Vinculin	VCL	721	S	1	99.07	2.83	3.23	3.29	3.08	3.19	2.98	1.91	1.63	1.92
P18206	Vinculin	VCL	820	S	0.92	81.55	1.18	NaN	1.28	1.31	1.34	1.21	1.06	NaN	1.08
P18583	Protein SON	SON	1697	S	1	152.3	1.75	1.62	1.64	1.27	1.45	1.31	1.18	1.26	1.22
P18583	Protein SON	SON	1556	S	0.998	219.8	1.02	1.00	0.92	1.00	0.92	1.17	0.78	0.76	0.80
P18583	Protein SON	SON	2129	S	0.905	43.35	1.08	1.30	NaN	NaN	NaN	NaN	NaN	NaN	NaN
P18583	Protein SON	SON	2011	S	1	59.29	0.57	1.50	NaN	NaN	1.14	NaN	NaN	NaN	NaN
P18583	Protein SON	SON	2013	S	1	74.53	NaN	0.46	NaN	0.60	0.66	0.82	NaN	0.41	NaN

P18583	Protein SON	SON	283	S	0.998	187.1	1.27	NaN	1.18	NaN	1.26	1.24	1.01	1.05	NaN
P18669	Phosphoglycerate mutase 1	PGAM1	31	S	1	89.51	1.06	0.90	NaN	1.15	1.27	NaN	0.93	NaN	NaN
P18669	Phosphoglycerate mutase 1;Probable phosphoglycerate mutase 4	PGAM1	118	S	1	124.3	0.81	0.79	0.82	0.95	1.00	0.98	0.69	0.67	0.71
P18858	DNA ligase 1;DNA ligase	LIG1	91	S	0.975	87.9	0.71	NaN	NaN	NaN	0.71	0.69	NaN	NaN	NaN
P18858	DNA ligase 1;DNA ligase	LIG1	98	S	0.816	78.65	0.71	NaN	NaN	NaN	0.71	0.69	NaN	NaN	NaN
P18858	DNA ligase 1;DNA ligase	LIG1	911	S	0.994	94.06	NaN	NaN	NaN	1.28	1.04	NaN	NaN	NaN	NaN
P18858	DNA ligase 1;DNA ligase	LIG1	913	S	0.994	94.06	NaN	NaN	NaN	1.28	1.04	NaN	NaN	NaN	NaN
P18858	DNA ligase 1;DNA ligase	LIG1	141	S	1	165.5	0.94	NaN	6.77	NaN	NaN	NaN	NaN	NaN	NaN
P18858	DNA ligase 1;DNA ligase	LIG1	66	S	1	244.7	0.77	0.69	0.72	0.48	0.47	0.45	0.77	0.82	0.76
P18858	DNA ligase 1;DNA ligase	LIG1	76	S	1	244.7	0.35	0.45	0.41	0.76	0.60	0.59	0.48	0.52	0.58
P19634	Sodium/hydrogen exchanger 1	SLC9A1	703	S	1	102.7	NaN	NaN	NaN	NaN	NaN	NaN	NaN	1.42	1.51
P19634	Sodium/hydrogen exchanger 1	SLC9A1	693	S	0.996	54.54	0.98	1.07	NaN	0.88	NaN	1.09	1.19	1.10	1.14
P19634	Sodium/hydrogen exchanger 1	SLC9A1	785	S	0.864	111.8	0.82	0.83	0.79	NaN	NaN	0.71	1.05	1.16	0.83
P19838	Nuclear factor NF-kappa-B p105 subunit;Nuclear factor NF-kappa-B p50 subunit	NFKB1	893	S	0.974	77.89	0.97	0.85	NaN	NaN	1.30	NaN	NaN	0.57	NaN
P20700	Lamin-B1	LMNB1	23	S	0.937	107.5	NaN	1.96	1.69	NaN	NaN	NaN	NaN	NaN	0.75
Q03252	Lamin-B1;Lamin-B2	LMNB1	391;405	S	0.998	84.37	0.53	0.59	0.62	0.90	0.96	0.89	0.92	0.86	1.16
Q03252	Lamin-B1;Lamin-B2	LMNB1	393;407	S	0.993	84.37	0.42	0.45	NaN	0.66	0.64	0.64	1.11	0.83	1.12
Q03252	Lamin-B1;Lamin-B2	LMNB1	396;410	S	0.999	77.63	1.79	1.30	1.49	2.43	2.64	NaN	NaN	0.69	1.09
Q60FE5	Filamin-A	FLNA	2125	S	1	146.3	1.30	1.33	1.31	1.29	1.31	NaN	1.19	1.12	1.08
Q60FE5	Filamin-A	FLNA	1432	S	1	159	0.75	0.79	0.71	1.32	1.32	1.26	0.84	0.83	0.83
Q60FE5	Filamin-A	FLNA	2300	S	0.961	78.31	1.64	1.78	NaN	NaN	2.11	NaN	NaN	0.90	NaN
Q60FE5	Filamin-A	FLNA	2153	S	0.938	141.9	1.16	1.17	1.22	1.51	1.30	1.39	0.78	0.84	0.81
P22059	Oxysterol-binding protein 1	OSBP	351	S	1	270.8	0.48	0.48	0.51	0.85	0.92	0.89	0.45	0.36	0.47
P22059	Oxysterol-binding protein 1	OSBP	190	S	1	211	0.85	0.80	0.80	0.90	1.12	0.90	0.75	0.84	0.77
P22059	Oxysterol-binding protein 1	OSBP	193	S	1	211	0.85	0.80	0.80	0.90	1.12	0.90	0.75	0.84	0.77
P22059	Oxysterol-binding protein 1	OSBP	240	S	0.998	76.42	3.25	3.21	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Q5JRR6	Ubiquitin-like modifier-activating enzyme 1	UBA1	283	S	1	96.67	0.94	0.94	0.84	1.19	1.08	1.20	0.75	1.08	1.02
P22626	Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	259	S	1	131.4	1.60	NaN	1.75	2.04	2.34	2.21	NaN	1.17	1.10
P22626	Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	344	S	0.872	78.32	NaN	NaN	1.62	2.08	2.73	NaN	NaN	NaN	NaN
P23381	Tryptophan--tRNA ligase, cytoplasmic;T1-TrpRS;T2-TrpRS	WARS	467	S	1	76.83	0.89	0.79	1.23	0.82	0.80	NaN	1.04	0.70	NaN
P24928	DNA-directed RNA polymerase II subunit RPB1	POLR2A	1913	S	0.922	83.69	0.52	0.54	0.63	NaN	NaN	NaN	NaN	NaN	0.70
P24928	DNA-directed RNA polymerase II subunit RPB1	POLR2A	1920	S	0.767	101.5	NaN	0.84	0.63	NaN	NaN	NaN	NaN	NaN	NaN
P24928	DNA-directed RNA polymerase II subunit RPB1	POLR2A	1878	S	0.994	110.5	0.94	0.80	NaN	NaN	0.92	NaN	NaN	0.98	0.90
P26038	Moesin	MSN	576	S	1	105	0.77	0.63	NaN	1.34	1.17	1.00	NaN	NaN	NaN

P26358	DNA (cytosine-5)-methyltransferase 1	DNMT1	714	S	1	259.6	0.26	0.25	0.27	0.52	0.55	0.49	0.34	0.33	0.34
P26358	DNA (cytosine-5)-methyltransferase 1	DNMT1	127	S	1	72.17	NaN	NaN	NaN	0.87	0.68	0.96	NaN	NaN	NaN
P26368	Splicing factor U2AF 65 kDa subunit	U2AF2	79	S	1	111.4	0.95	1.00	1.04	1.08	1.08	1.01	0.88	0.91	0.90
P27816	Microtubule-associated protein 4;Microtubule-associated protein	MAP4	358	S	1	127.2	0.58	0.56	0.60	1.04	1.06	1.05	0.62	0.64	0.67
P27816	Microtubule-associated protein 4;Microtubule-associated protein	MAP4	787	S	1	95.03	1.07	1.09	1.06	1.84	1.79	1.88	0.84	0.82	0.83
P27816	Microtubule-associated protein 4;Microtubule-associated protein	MAP4	789	S	0.842	74.85	NaN	NaN	NaN	2.07	1.81	1.99	0.82	0.74	0.71
P27816	Microtubule-associated protein 4;Microtubule-associated protein	MAP4	280	S	1	223.3	0.54	0.53	0.49	0.73	0.75	0.76	0.58	0.53	0.56
P27816	Microtubule-associated protein 4;Microtubule-associated protein	MAP4	507	S	1	279.1	0.30	0.32	0.36	0.64	0.70	0.69	0.27	0.31	0.26
P27816	Microtubule-associated protein 4;Microtubule-associated protein	MAP4	510	S	0.998	150.1	0.74	0.74	0.94	1.70	1.86	1.50	0.67	0.33	0.62
P27816	Microtubule-associated protein 4;Microtubule-associated protein	MAP4	696	S	1	87.48	1.01	1.07	1.08	1.58	1.58	1.73	0.64	0.62	0.61
P27816	Microtubule-associated protein 4;Microtubule-associated protein	MAP4	624	S	0.919	106.8	NaN	NaN	NaN	0.91	1.13	1.52	0.66	NaN	0.77
P27816	Microtubule-associated protein 4;Microtubule-associated protein	MAP4	636	S	1	128.4	0.70	0.79	0.80	2.03	1.75	1.76	1.05	0.91	0.87
P27816	Microtubule-associated protein 4;Microtubule-associated protein	MAP4	1073	S	1	133.9	0.65	0.63	0.64	0.64	0.58	0.58	2.06	2.09	1.92
P27824	Calnexin	CANX	583	S	1	367.3	1.21	1.19	1.01	1.08	1.10	1.08	1.01	0.97	1.06
P27824	Calnexin	CANX	554	S	1	430.6	0.82	0.84	0.79	0.86	0.82	0.81	0.91	0.87	0.95
P27824	Calnexin	CANX	564	S	1	298.7	0.91	0.98	0.95	0.80	0.81	0.75	0.97	1.04	1.52
P28066	Proteasome subunit alpha type-5	PSMA5	16	S	0.998	111	4.12	4.16	3.85	6.45	4.84	4.89	1.17	0.90	1.05
P28066	Proteasome subunit alpha type-5	PSMA5	56	S	0.974	70.63	NaN	NaN	NaN	NaN	NaN	NaN	NaN	0.54	1.06
P28290	Sperm-specific antigen 2	SSFA2	641	S	1	122.9	0.74	0.81	0.85	0.89	0.88	0.83	1.14	1.25	1.17
P28290	Sperm-specific antigen 2	SSFA2	591	S	0.543	119.3	1.04	0.78	0.93	NaN	0.90	0.79	1.23	NaN	1.33
P28290	Sperm-specific antigen 2	SSFA2	593	S	0.764	119.3	1.15	0.92	0.93	1.10	1.12	1.16	1.23	1.14	1.33
P28290	Sperm-specific antigen 2	SSFA2	668	S	0.998	97.73	1.37	1.56	1.50	1.19	NaN	1.22	2.69	2.03	2.42

P28290	Sperm-specific antigen 2	SSFA2	739	S	1	142.5	2.39	NaN	0.90	0.79	0.55	NaN	2.01	NaN	1.86
P29317	Ephrin type-A receptor 2	EPHA2	901	S	0.913	48.28	NaN	NaN	1.49	NaN	NaN	1.31	1.23	1.14	NaN
P29590	Protein PML	PML	36	S	0.998	112.3	0.70	0.68	0.95	NaN	0.68	NaN	NaN	1.36	1.34
P29966	Myristoylated alanine-rich C-kinase substrate	MARCKS	145	S	1	289.1	0.63	0.63	0.67	0.68	0.67	0.68	1.12	1.15	1.09
P29966	Myristoylated alanine-rich C-kinase substrate	MARCKS	147	S	0.879	204.5	NaN	3.23	2.16	1.74	1.70	3.55	2.15	1.83	3.63
P29966	Myristoylated alanine-rich C-kinase substrate	MARCKS	118	S	0.997	206.1	2.30	2.36	2.21	2.23	2.44	2.22	1.06	1.05	1.04
P29966	Myristoylated alanine-rich C-kinase substrate	MARCKS	128	S	0.993	94.15	0.68	1.14	0.78	0.68	NaN	NaN	NaN	NaN	NaN
P29966	Myristoylated alanine-rich C-kinase substrate	MARCKS	131	S	0.909	94.15	0.68	1.14	0.78	0.68	NaN	NaN	NaN	2.05	NaN
P29966	Myristoylated alanine-rich C-kinase substrate	MARCKS	132	S	0.751	94.15	NaN	1.14	1.39	0.68	NaN	NaN	NaN	0.94	NaN
P29966	Myristoylated alanine-rich C-kinase substrate	MARCKS	135	S	0.953	206.1	0.88	0.75	0.76	0.87	0.74	0.82	0.84	1.06	1.05
P29966	Myristoylated alanine-rich C-kinase substrate	MARCKS	81	S	0.876	248.8	2.33	2.06	NaN	3.13	NaN	4.03	NaN	NaN	1.05
P29966	Myristoylated alanine-rich C-kinase substrate	MARCKS	26	S	0.748	138.2	NaN	NaN	1.12	NaN	1.46	1.28	1.12	1.09	NaN
P29966	Myristoylated alanine-rich C-kinase substrate	MARCKS	27	S	0.988	226.7	1.54	1.45	1.28	1.30	NaN	1.32	1.04	NaN	1.20
P29966	Myristoylated alanine-rich C-kinase substrate	MARCKS	101	S	1	208.4	2.53	2.73	3.00	3.94	4.04	3.81	1.12	1.02	1.01
P29966	Myristoylated alanine-rich C-kinase substrate	MARCKS	46	S	1	158.9	1.39	1.44	1.50	2.08	2.02	1.96	1.26	1.23	1.22
P30050	60S ribosomal protein L12	RPL12	38	S	1	72.29	1.37	1.43	1.57	2.30	2.08	2.02	0.50	0.45	0.46
P30419	Glycylpeptide N-tetradecanoyltransferase 1	NMT1	47	S	1	160.9	NaN	NaN	NaN	1.15	1.09	1.06	NaN	NaN	NaN
P31629	Transcription factor HIVEP2	HIVEP2	1443	S	0.998	83.69	0.40	0.49	NaN	NaN	NaN	NaN	NaN	0.41	NaN
P31689	DnaJ homolog subfamily A member 1	DNAJA1	335	S	1	149.7	3.65	4.35	5.08	5.72	5.64	5.50	0.68	0.73	0.88
P31749	RAC-alpha serine/threonine-protein kinase	AKT1	122	S	0.544	74.4	NaN	NaN	0.99	0.86	NaN	0.95	NaN	0.85	NaN
P31749	RAC-alpha serine/threonine-protein kinase	AKT1	124	S	0.997	149.9	0.53	0.46	0.47	0.60	1.04	0.60	0.53	0.53	0.59
P31749	RAC-alpha serine/threonine-protein kinase	AKT1	126	S	0.989	74.4	NaN	NaN	0.99	0.86	1.04	0.95	0.83	0.85	0.84
P31749	RAC-alpha serine/threonine-protein kinase	AKT1	129	S	0.999	74.4	NaN	NaN	0.99	0.86	1.04	0.95	0.83	0.85	0.84
P31942	Heterogeneous nuclear ribonucleoprotein H3	HNRNPH3	216	S	1	61.54	2.35	2.26	NaN	NaN	2.49	NaN	NaN	NaN	NaN
P33981	Dual specificity protein kinase TTK	TTK	821	S	0.999	118.2	2.61	1.38	NaN	4.46	3.17	3.84	NaN	NaN	NaN
P35251	Replication factor C subunit 1	RFC1	69	S	0.999	92.1	0.72	NaN	NaN	NaN	0.94	0.72	1.08	NaN	1.12
P35251	Replication factor C subunit 1	RFC1	71	S	0.951	92.1	0.72	NaN	NaN	NaN	0.94	0.72	1.08	NaN	1.12

P35367	Histamine H1 receptor	HRH1	275	S	0.825	78.38	0.66	4.14	4.02	NaN	NaN	2.47	NaN	NaN	NaN
P35568	Insulin receptor substrate 1	IRS1	1078	S	1	83.78	0.77	0.78	0.64	0.97	NaN	1.04	0.86	NaN	0.83
P35579	Myosin-9	MYH9	1943	S	1	362.9	0.81	0.83	0.76	0.82	0.81	0.80	1.02	1.04	1.03
P35579	Myosin-9	MYH9	1713	S	0.5	75.54	1.10	1.14	NaN	NaN	NaN	NaN	NaN	NaN	2.16
P35579	Myosin-9	MYH9	1714	S	0.5	75.54	1.10	1.14	NaN	NaN	NaN	NaN	NaN	NaN	2.16
P35580	Myosin-10	MYH10	1952	S	1	98.8	0.73	0.74	NaN	0.77	0.82	NaN	1.30	NaN	NaN
P35580	Myosin-10	MYH10	1956	S	1	282.6	0.80	0.85	0.81	0.81	0.84	0.77	0.93	0.92	0.87
P36507	Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	293	S	0.746	134.6	NaN	NaN	1.68	1.78	1.87	1.81	0.93	0.99	NaN
P36507	Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	295	S	0.994	207.4	1.74	1.90	NaN	1.89	NaN	1.81	0.99	1.08	NaN
P38159	RNA-binding motif protein, X chromosome;RNA-binding motif protein, X chromosome, N-terminally processed;RNA binding motif protein, X-linked-like-1	RBMX	208	S	1	112.1	0.81	0.80	0.80	0.93	0.96	0.95	0.85	0.85	0.87
P38159	RNA-binding motif protein, X chromosome;RNA-binding motif protein, X chromosome, N-terminally processed	RBMX	352	S	1	66.6	NaN	0.78	NaN	0.93	NaN	0.81	NaN	1.05	0.87
P38432	Coilin	COIL	566	S	0.934	82.2	NaN	NaN	NaN	1.54	NaN	1.05	0.98	0.83	0.97
P40222	Alpha-taxilin	TXLNA	515	S	0.993	124.5	1.53	1.65	1.63	1.48	1.46	1.53	1.06	1.05	1.11
P40222	Alpha-taxilin	TXLNA	19	S	0.788	119.8	1.44	1.10	NaN	NaN	2.06	NaN	NaN	NaN	NaN
P40818	Ubiquitin carboxyl-terminal hydrolase 8	USP8	718	S	0.99	115.4	NaN	2.28	1.92	2.07	2.10	1.86	1.77	2.10	2.29
P41208	Centrin-2	CETN2	20	S	1	62.53	1.04	0.78	NaN	1.11	1.18	NaN	NaN	NaN	NaN
P41227	N-alpha-acetyltransferase 10	NAA10	205	S	0.999	197.6	0.80	0.95	0.95	2.05	1.30	0.96	NaN	NaN	0.83
P41227	N-alpha-acetyltransferase 10	NAA10	209	S	0.585	169.2	NaN	NaN	NaN	NaN	NaN	NaN	0.95	1.00	NaN
P41227	N-alpha-acetyltransferase 10	NAA10	186	S	1	85.36	0.97	0.90	1.02	1.16	1.29	1.21	0.88	0.77	0.91
P42684	Abelson tyrosine-protein kinase 2	ABL2	631	S	0.972	51.01	0.80	0.85	0.94	1.09	1.00	NaN	0.89	0.89	NaN
P42684	Abelson tyrosine-protein kinase 2	ABL2	936	S	0.987	70.49	1.60	1.58	NaN	NaN	NaN	NaN	NaN	NaN	NaN
P42858	Huntingtin	HTT	1199	S	0.996	44.42	1.00	NaN	NaN	NaN	1.04	NaN	0.82	0.75	0.77
P42858	Huntingtin	HTT	432	S	0.977	123.5	0.92	0.81	0.96	0.83	0.82	0.93	1.13	1.20	1.39
P43490	Nicotinamide phosphoribosyltransferase	NAMPT	472	S	1	90.15	1.77	1.35	1.39	2.45	2.00	2.05	1.09	1.09	1.03
P46013	Antigen KI-67	MKI67	827	S	0.998	70.94	NaN	NaN	0.58	1.27	1.48	1.66	NaN	NaN	NaN
P46013	Antigen KI-67	MKI67	2105	S	1	62.66	NaN	NaN	NaN	NaN	1.68	2.16	NaN	NaN	NaN
P46013	Antigen KI-67	MKI67	1131	S	1	84.13	0.54	0.54	0.75	1.95	1.92	NaN	0.62	0.55	0.58
P46013	Antigen KI-67	MKI67	1861	S	0.998	71.69	NaN	NaN	NaN	1.75	2.04	1.59	NaN	NaN	NaN
P46013	Antigen KI-67	MKI67	1376	S	0.826	133.9	NaN	NaN	NaN	NaN	1.52	2.07	NaN	NaN	NaN
P46013	Antigen KI-67	MKI67	308	S	1	117.1	0.49	0.45	0.47	1.02	1.04	1.13	0.68	0.72	0.66
P46013	Antigen KI-67	MKI67	357	S	1	80.6	NaN	NaN	NaN	NaN	1.25	1.60	NaN	0.59	NaN

P46060	Ran GTPase-activating protein 1	RANGAP 1	428	S	0.851	73.03	1.58	NaN	1.40	NaN	3.07	2.97	0.77	0.82	0.68
P46060	Ran GTPase-activating protein 1	RANGAP 1	442	S	1	92.82	0.55	NaN	0.44	0.86	0.80	0.86	0.73	0.82	0.88
P46087	Probable 28S rRNA (cytosine(4447)-C(5))-methyltransferase	NOP2	786	S	0.849	85.4	NaN	1.42	1.33	NaN	NaN	1.97	NaN	NaN	NaN
P46087	Probable 28S rRNA (cytosine(4447)-C(5))-methyltransferase	NOP2	732	S	0.975	106.5	1.23	0.85	1.37	1.39	1.55	1.57	NaN	NaN	NaN
P46100	Transcriptional regulator	ATRX	849	S	1	77.53	0.51	0.49	0.57	0.65	0.64	0.65	0.82	0.91	0.90
P46100	Transcriptional regulator	ATRX	850	S	1	77.53	0.51	0.49	0.57	0.65	0.64	0.65	0.82	0.91	0.90
P46100	Transcriptional regulator	ATRX	1527	S	0.984	109.9	0.25	NaN	NaN	0.83	0.79	0.74	0.53	0.51	0.57
P46100	Transcriptional regulator	ATRX	594	S	0.631	59.16	NaN	NaN	NaN	0.91	1.10	NaN	0.67	0.72	NaN
P46100	Transcriptional regulator	ATRX	598	S	0.741	72.79	0.54	0.59	NaN	NaN	NaN	NaN	0.86	NaN	NaN
P46100	Transcriptional regulator	ATRX	729	S	1	179.1	0.45	0.76	0.47	0.62	0.67	0.63	0.58	0.60	0.69
P46100	Transcriptional regulator	ATRX	731	S	1	179.1	0.45	0.38	0.47	0.62	0.67	0.63	0.58	0.60	0.69
P46100	Transcriptional regulator	ATRX	675	S	0.869	108.5	NaN	NaN	NaN	NaN	NaN	NaN	NaN	0.66	0.63
P46100	Transcriptional regulator	ATRX	677	S	0.999	108.5	0.61	0.55	NaN	NaN	0.71	NaN	0.81	NaN	0.63
P46100	Transcriptional regulator	ATRX	92	S	1	250.1	0.53	0.29	0.64	0.51	0.71	0.63	0.53	0.61	0.48
P46821	Microtubule-associated protein 1B;MAP1B heavy chain;MAP1 light chain LC1	MAP1B	541	S	0.971	78.72	NaN	0.48	0.55	0.45	0.37	0.44	1.27	1.23	1.28
P46821	Microtubule-associated protein 1B;MAP1B heavy chain;MAP1 light chain LC1	MAP1B	1016	S	1	157.4	NaN	0.45	0.55	0.82	0.64	0.64	1.04	0.93	0.93
P46821	Microtubule-associated protein 1B;MAP1B heavy chain;MAP1 light chain LC1	MAP1B	1376	S	0.561	116.4	0.49	0.47	0.56	0.54	0.60	0.67	0.37	0.34	0.49
P46821	Microtubule-associated protein 1B;MAP1B heavy chain;MAP1 light chain LC1	MAP1B	1378	S	1	272.3	0.54	0.50	0.42	0.53	0.55	0.56	0.48	0.43	0.60
P46821	Microtubule-associated protein 1B;MAP1B heavy chain;MAP1 light chain LC1	MAP1B	1387	S	0.95	253.7	0.96	0.72	NaN	NaN	1.77	1.10	NaN	NaN	NaN
P46821	Microtubule-associated protein 1B;MAP1B heavy chain;MAP1 light chain LC1	MAP1B	1389	S	1	265.4	0.78	0.87	0.93	0.94	0.98	1.72	0.67	0.62	0.68
P46821	Microtubule-associated protein 1B;MAP1B heavy chain;MAP1 light chain LC1	MAP1B	1252	S	0.9	114.8	0.28	0.45	0.46	0.13	0.64	0.31	0.89	0.69	0.53
P46821	Microtubule-associated protein 1B;MAP1B heavy chain;MAP1 light chain LC1	MAP1B	1254	S	0.677	114.8	0.44	0.47	0.77	NaN	1.08	0.66	0.97	0.69	0.83
P46821	Microtubule-associated protein 1B;MAP1B heavy chain;MAP1 light chain LC1	MAP1B	1256	S	0.963	114.8	0.28	1.05	1.09	1.11	1.08	0.95	0.96	1.02	0.87

P46821	Microtubule-associated protein 1B;MAP1B heavy chain;MAP1 light chain LC1	MAP1B	1258	S	0.826	114.6	0.28	0.74	1.09	1.08	NaN	0.75	0.96	NaN	0.91
P46821	Microtubule-associated protein 1B;MAP1B heavy chain;MAP1 light chain LC1	MAP1B	1260	S	0.98	114.7	1.14	NaN	0.50	0.44	1.08	0.92	1.09	1.12	0.75
P46821	Microtubule-associated protein 1B;MAP1B heavy chain;MAP1 light chain LC1	MAP1B	1265	S	1	217.8	1.03	1.03	1.05	0.83	0.85	0.88	1.05	1.02	0.27
P46821	Microtubule-associated protein 1B;MAP1B heavy chain;MAP1 light chain LC1	MAP1B	1154	S	0.993	204.9	0.62	0.62	0.58	0.66	0.86	0.85	0.43	0.48	0.54
P46821	Microtubule-associated protein 1B;MAP1B heavy chain;MAP1 light chain LC1	MAP1B	1208	S	0.981	243.8	0.44	0.46	NaN	0.74	0.86	0.75	NaN	0.56	0.50
P46821	Microtubule-associated protein 1B;MAP1B heavy chain;MAP1 light chain LC1	MAP1B	614	S	1	110	0.38	0.37	0.41	0.63	0.55	0.66	0.76	0.80	0.77
P46821	Microtubule-associated protein 1B;MAP1B heavy chain;MAP1 light chain LC1	MAP1B	1792	S	0.872	246.1	0.60	0.59	0.70	NaN	0.52	0.54	1.02	1.02	0.94
P46821	Microtubule-associated protein 1B;MAP1B heavy chain;MAP1 light chain LC1	MAP1B	1793	S	0.989	239.2	0.60	0.58	0.64	0.50	0.50	0.49	0.93	1.01	1.02
P46821	Microtubule-associated protein 1B;MAP1B heavy chain;MAP1 light chain LC1	MAP1B	1797	S	1	246.1	1.24	1.23	1.57	1.34	1.26	1.43	1.11	0.84	1.05
P46821	Microtubule-associated protein 1B;MAP1B heavy chain;MAP1 light chain LC1	MAP1B	995	S	1	101.6	0.43	0.43	NaN	NaN	NaN	NaN	1.57	NaN	NaN
P46821	Microtubule-associated protein 1B;MAP1B heavy chain;MAP1 light chain LC1	MAP1B	1427	S	1	204.2	1.18	1.21	1.21	1.19	1.22	1.20	1.31	1.25	1.35
P46821	Microtubule-associated protein 1B;MAP1B heavy chain;MAP1 light chain LC1	MAP1B	891	S	0.995	90.34	1.04	0.61	NaN	NaN	NaN	NaN	NaN	NaN	NaN
P46821	Microtubule-associated protein 1B;MAP1B heavy chain;MAP1 light chain LC1	MAP1B	2209	S	1	108.6	0.77	0.80	0.85	0.95	0.90	0.90	0.78	0.79	NaN
P46821	Microtubule-associated protein 1B;MAP1B heavy chain;MAP1 light chain LC1	MAP1B	2211	S	1	108.6	0.77	0.80	0.85	0.95	0.90	0.90	0.78	0.79	NaN
P46821	Microtubule-associated protein 1B;MAP1B heavy chain;MAP1 light chain LC1	MAP1B	561	S	0.985	63.68	0.32	NaN	NaN	0.24	NaN	NaN	0.26	0.25	0.65

P46821	Microtubule-associated protein 1B;MAP1B heavy chain;MAP1 light chain LC1	MAP1B	1501	S	1	199.4	0.89	0.88	0.64	0.85	0.85	0.81	0.90	0.56	0.92
P46821	Microtubule-associated protein 1B;MAP1B heavy chain;MAP1 light chain LC1	MAP1B	1438	S	1	241.1	0.31	0.32	0.34	0.41	0.59	0.46	0.47	0.62	0.86
P46821	Microtubule-associated protein 1B;MAP1B heavy chain;MAP1 light chain LC1	MAP1B	1443	S	1	241.1	0.63	0.68	0.67	0.83	0.77	0.73	0.66	0.51	0.58
P46821	Microtubule-associated protein 1B;MAP1B heavy chain;MAP1 light chain LC1	MAP1B	937	S	0.784	221.1	0.71	0.55	NaN	0.52	NaN	0.66	0.89	0.82	NaN
P46821	Microtubule-associated protein 1B;MAP1B heavy chain;MAP1 light chain LC1	MAP1B	1666	S	0.999	179.2	NaN	0.27	0.54	0.69	0.62	NaN	0.83	NaN	0.74
P46821	Microtubule-associated protein 1B;MAP1B heavy chain;MAP1 light chain LC1	MAP1B	1782	S	1	120.4	1.42	1.65	1.17	0.81	1.14	1.15	1.55	1.49	1.69
P46821	Microtubule-associated protein 1B;MAP1B heavy chain;MAP1 light chain LC1	MAP1B	1785	S	1	146.8	0.37	0.34	0.36	0.36	0.36	0.38	0.41	0.37	0.36
P46821	Microtubule-associated protein 1B;MAP1B heavy chain;MAP1 light chain LC1	MAP1B	831	S	1	209.4	0.58	0.59	0.63	0.30	0.77	0.76	0.31	0.19	0.69
P46821	Microtubule-associated protein 1B;MAP1B heavy chain;MAP1 light chain LC1	MAP1B	832	S	1	209.4	0.21	0.28	0.63	0.32	0.32	0.76	0.24	0.66	0.69
P46821	Microtubule-associated protein 1B;MAP1B heavy chain;MAP1 light chain LC1	MAP1B	1915	S	0.999	205	0.82	0.67	0.70	0.91	0.90	0.80	0.97	0.93	0.91
P46821	Microtubule-associated protein 1B;MAP1B heavy chain;MAP1 light chain LC1	MAP1B	2256	S	0.989	84.62	0.76	NaN	1.06	NaN	NaN	NaN	0.83	NaN	0.65
P46821	Microtubule-associated protein 1B;MAP1B heavy chain;MAP1 light chain LC1	MAP1B	1322	S	1	215.4	0.27	0.30	0.33	0.47	0.44	0.48	0.61	0.65	0.57
P46821	Microtubule-associated protein 1B;MAP1B heavy chain;MAP1 light chain LC1	MAP1B	1326	S	0.613	106.3	0.37	0.42	NaN	NaN	NaN	NaN	1.28	NaN	NaN
P46821	Microtubule-associated protein 1B;MAP1B heavy chain;MAP1 light chain LC1	MAP1B	1339	S	0.938	224	0.51	0.30	0.49	0.47	0.44	0.59	0.47	1.78	0.52
P46821	Microtubule-associated protein 1B;MAP1B heavy chain;MAP1 light chain LC1	MAP1B	1881	S	0.989	237.6	0.44	NaN	NaN	NaN	0.64	0.62	0.58	0.55	0.53

P46821	Microtubule-associated protein 1B;MAP1B heavy chain;MAP1 light chain LC1	MAP1B	1396	S	1	375.4	1.07	0.81	1.03	0.99	0.96	0.91	0.80	1.10	0.89
P46821	Microtubule-associated protein 1B;MAP1B heavy chain;MAP1 light chain LC1	MAP1B	1400	S	1	375.4	0.52	0.63	1.19	0.62	0.57	0.58	1.00	1.11	1.16
P46821	Microtubule-associated protein 1B;MAP1B heavy chain;MAP1 light chain LC1	MAP1B	1779	S	1	154.5	0.44	0.46	0.43	0.45	0.46	0.44	0.64	0.64	0.62
P46821	Microtubule-associated protein 1B;MAP1B heavy chain;MAP1 light chain LC1	MAP1B	1298	S	1	183.6	1.29	1.33	1.36	0.73	1.02	1.26	1.04	0.89	0.98
P46821	Microtubule-associated protein 1B;MAP1B heavy chain;MAP1 light chain LC1	MAP1B	1312	S	1	205.6	0.67	0.65	0.55	0.70	0.62	0.69	0.78	0.93	1.57
P46937	Transcriptional coactivator YAP1	YAP1	61	S	1	222.8	0.71	0.75	0.87	0.84	0.75	0.86	2.26	1.67	0.66
P46937	Transcriptional coactivator YAP1	YAP1	289	S	1	116.5	NaN	NaN	NaN	NaN	2.01	2.28	NaN	NaN	NaN
P46937	Transcriptional coactivator YAP1	YAP1	163	S	0.969	93.88	NaN	1.03	NaN	NaN	1.11	NaN	NaN	1.05	1.04
P46937	Transcriptional coactivator YAP1	YAP1	164	S	0.966	114.1	0.99	0.97	1.07	0.97	0.96	1.10	1.08	0.88	1.17
P46937	Transcriptional coactivator YAP1	YAP1	367	S	0.982	140.9	1.05	NaN	NaN	1.61	1.62	NaN	NaN	NaN	1.04
P48634	Protein PRRC2A	PRRC2A	380	S	0.99	52.07	0.70	0.68	NaN	NaN	0.97	NaN	NaN	NaN	NaN
P48634	Protein PRRC2A	PRRC2A	1219	S	1	86.29	2.23	2.23	2.13	2.15	2.24	2.09	1.31	1.28	NaN
P48634	Protein PRRC2A	PRRC2A	342	S	1	106.1	1.77	NaN	1.16	NaN	NaN	NaN	1.04	0.98	1.11
P48634	Protein PRRC2A	PRRC2A	350	S	1	106.1	1.77	NaN	1.16	NaN	NaN	NaN	1.04	0.98	1.11
P48651	Phosphatidylserine synthase 1	PTDSS1	442	S	1	77.19	0.74	0.63	NaN	0.94	0.78	0.88	0.96	NaN	0.76
P48681	Nestin	NES	680	S	1	85.75	1.18	1.05	NaN	NaN	NaN	NaN	1.03	0.93	1.04
P48681	Nestin	NES	471	S	0.995	176.5	0.84	0.75	1.16	0.77	NaN	1.16	1.53	NaN	NaN
P48681	Nestin	NES	768	S	1	50.87	NaN	NaN	NaN	NaN	NaN	NaN	1.35	1.27	NaN
P48960	CD97 antigen;CD97 antigen subunit alpha;CD97 antigen subunit beta	CD97	831	S	0.86	63.69	NaN	NaN	1.65	1.88	NaN	1.81	3.86	3.63	NaN
P49321	Nuclear autoantigenic sperm protein	NASP	480	S	1	248.2	NaN	0.33	0.31	0.56	0.62	0.57	0.36	0.38	NaN
P49321	Nuclear autoantigenic sperm protein	NASP	726	S	1	85.36	0.78	0.83	0.80	1.02	NaN	0.95	0.74	NaN	0.73
P49321	Nuclear autoantigenic sperm protein	NASP	421	S	0.999	67.93	2.19	2.34	2.98	1.61	1.23	3.42	1.13	1.23	3.20
P49321	Nuclear autoantigenic sperm protein	NASP	451	S	0.528	41.32	NaN	NaN	NaN	1.33	1.47	NaN	NaN	1.03	0.96
P49454	Centromere protein F	CENPF	3079	S	0.832	70.99	0.54	0.63	NaN	NaN	NaN	1.51	NaN	NaN	0.52
P49585	Choline-phosphate cytidylyltransferase A	PCYT1A	362	S	1	116.8	2.16	2.24	2.32	2.34	2.04	2.06	1.30	1.26	1.29

P49585	Choline-phosphate cytidylyltransferase A	PCYT1A	329	S	1	71.15	NaN	NaN	0.82	0.93	NaN	0.87	0.90	0.80	0.87
P49585	Choline-phosphate cytidylyltransferase A	PCYT1A	331	S	0.996	71.15	NaN	NaN	0.82	0.93	1.09	0.87	0.90	0.80	0.87
P49585	Choline-phosphate cytidylyltransferase A	PCYT1A	315	S	1	120.8	0.72	0.59	0.70	0.89	1.00	0.75	0.57	0.54	NaN
P49585	Choline-phosphate cytidylyltransferase A	PCYT1A	319	S	0.999	120.8	0.72	0.59	0.70	0.89	1.00	0.75	0.57	0.52	NaN
P49585	Choline-phosphate cytidylyltransferase A	PCYT1A	321	S	0.569	63.46	NaN	0.47	NaN	0.93	1.04	NaN	0.55	0.54	NaN
P49585	Choline-phosphate cytidylyltransferase A	PCYT1A	322	S	0.884	118	0.72	0.47	NaN	0.93	1.04	NaN	0.55	0.52	NaN
P49585	Choline-phosphate cytidylyltransferase A	PCYT1A	323	S	0.872	120.8	NaN	0.53	0.70	0.88	1.00	0.75	0.57	0.52	NaN
P49736	DNA replication licensing factor MCM2	MCM2	139	S	1	343.7	0.80	0.81	0.76	0.85	0.88	0.84	0.85	0.82	0.84
P49736	DNA replication licensing factor MCM2	MCM2	26	S	0.588	229.8	NaN	0.86	NaN	0.96	1.00	NaN	0.80	NaN	0.69
P49736	DNA replication licensing factor MCM2	MCM2	27	S	0.977	229.8	0.85	NaN	0.90	0.96	0.95	0.99	NaN	NaN	NaN
P49736	DNA replication licensing factor MCM2	MCM2	41	S	0.957	150.4	0.70	0.69	NaN	NaN	NaN	NaN	0.66	NaN	NaN
P49756	RNA-binding protein 25	RBM25	583	S	1	181.8	1.07	0.96	1.53	1.48	1.43	1.45	1.66	1.52	0.93
P49790	Nuclear pore complex protein Nup153	NUP153	687	S	1	112.2	NaN	NaN	1.16	1.55	1.59	1.32	0.57	NaN	0.56
P49792	E3 SUMO-protein ligase RanBP2;RanBP2-like and GRIP domain-containing protein 4;RanBP2-like and GRIP domain-containing protein 3;RANBP2-like and GRIP domain-containing protein 1;RANBP2-like and GRIP domain-containing protein 2;RANBP2-like and GRIP domain-containing protein 5/6;RANBP2-like and	RANBP2	2510	S	1	61.18	NaN	0.46	0.54	0.84	0.88	1.10	0.84	0.82	1.19
P49792	E3 SUMO-protein ligase RanBP2;RanBP2-like and GRIP domain-containing protein 4;RanBP2-like and GRIP domain-containing protein 3;RANBP2-like and GRIP domain-containing protein 5/6;RANBP2-like and GRIP domain-containing	RANBP2	2246	S	0.989	152.2	0.98	1.32	1.62	1.27	NaN	1.25	1.31	1.27	1.04

P49792	E3 SUMO-protein ligase RanBP2;RanBP2-like and GRIP domain-containing protein 4;RanBP2-like and GRIP domain-containing protein 3;RANBP2-like and GRIP domain-containing protein 5/6;RANBP2-like and GRIP domain-containing	RANBP2	2250	S	0.902	217.6	0.98	2.06	1.09	1.27	NaN	1.25	1.31	1.27	NaN
P49792	E3 SUMO-protein ligase RanBP2;RanBP2-like and GRIP domain-containing protein 4;RanBP2-like and GRIP domain-containing protein 3;RANBP2-like and GRIP domain-containing protein 5/6;RANBP2-like and GRIP domain-containing	RANBP2	2251	S	0.835	160.5	NaN	NaN	NaN	NaN	NaN	NaN	NaN	1.27	1.04
P49792	E3 SUMO-protein ligase RanBP2	RANBP2	1400	S	0.953	62.56	0.64	0.91	0.82	1.07	1.00	NaN	1.04	1.02	NaN
P49792	E3 SUMO-protein ligase RanBP2	RANBP2	781	S	0.697	45.16	NaN	NaN	0.87	0.83	0.79	NaN	NaN	0.78	NaN
P49792	E3 SUMO-protein ligase RanBP2;RanBP2-like and GRIP domain-containing	RANBP2	2276	S	0.988	56.08	0.75	0.86	0.78	NaN	1.41	1.64	0.76	0.81	NaN
P49792	E3 SUMO-protein ligase RanBP2;RanBP2-like and GRIP domain-containing	RANBP2	2280	S	0.934	82.77	0.75	0.84	0.78	NaN	1.00	1.64	NaN	0.87	NaN
P49792	E3 SUMO-protein ligase RanBP2	RANBP2	2900	S	1	164.5	0.91	0.79	0.94	NaN	NaN	0.86	0.90	0.96	1.21
P49915	GMP synthase [glutamine-hydrolyzing]	GMPS	332	S	0.722	87.73	NaN	1.00	0.60	NaN	NaN	NaN	NaN	NaN	NaN
P50914	60S ribosomal protein L14	RPL14	139	S	1	80.56	1.47	1.57	NaN	2.00	2.04	1.99	0.54	0.56	0.54
P51116	Fragile X mental retardation syndrome-related protein 2	FXR2	601	S	0.998	142.3	1.61	1.69	0.87	1.15	1.29	NaN	1.03	1.05	1.91
P51116	Fragile X mental retardation syndrome-related protein 2	FXR2	603	S	1	142.3	1.59	1.59	1.65	1.05	1.29	NaN	1.75	1.81	1.91
P51608	Methyl-CpG-binding protein 2	MECP2	80	S	0.765	64.78	0.42	0.40	NaN	NaN	NaN	NaN	NaN	NaN	NaN

P51610	Host cell factor 1;HCF N-terminal chain 1;HCF N-terminal chain 2;HCF N-terminal chain 3;HCF N-terminal chain 4;HCF N-terminal chain 5;HCF N-terminal chain 6;HCF C-terminal chain 1;HCF C-terminal chain 2;HCF C-terminal chain 3;HCF C-	HCFC1	1507	S	1	89.68	1.73	2.03	2.15	NaN	NaN	2.07	1.60	1.35	NaN
P51812	Ribosomal protein S6 kinase alpha-3	RPS6KA3	715	S	1	57.43	NaN	NaN	NaN	1.78	NaN	NaN	1.24	1.08	1.18
P51812	Ribosomal protein S6 kinase alpha-3	RPS6KA3	369	S	0.987	51	NaN	NaN	NaN	NaN	NaN	1.24	0.80	0.83	0.87
P51858	Hepatoma-derived growth factor	HDGF	165	S	1	191.9	0.98	0.94	0.98	0.99	0.99	1.00	1.09	1.10	1.11
P51858	Hepatoma-derived growth factor	HDGF	132	S	1	219	1.03	1.00	0.66	0.94	0.92	0.75	1.16	1.14	0.98
P51858	Hepatoma-derived growth factor	HDGF	133	S	1	219	0.84	0.66	0.72	0.62	0.73	0.80	0.73	0.65	0.83
P51991	Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	358	S	1	277.5	1.01	1.03	0.94	0.91	0.99	0.96	1.19	1.10	0.97
P52756	RNA-binding protein 5	RBM5	59	S	0.852	40.62	1.02	0.86	NaN	NaN	NaN	NaN	NaN	NaN	NaN
P52756	RNA-binding protein 5	RBM5	624	S	1	176.9	1.33	1.12	NaN	NaN	1.11	0.90	1.31	1.42	NaN
P52926	High mobility group protein HMGI-C	HMGA2	44	S	1	108.4	0.37	NaN	0.61	1.11	1.03	0.48	NaN	0.78	0.79
P53396	ATP-citrate synthase	ACLY	481	S	1	92.77	1.65	1.59	1.68	2.08	2.24	2.07	0.99	1.02	0.91
P54198	Protein HIRA	HIRA	610	S	1	57.41	0.66	NaN	NaN	NaN	0.60	NaN	NaN	0.96	0.86
P54198	Protein HIRA	HIRA	611	S	1	57.41	0.66	NaN	NaN	NaN	0.60	NaN	NaN	0.96	0.86
P54198	Protein HIRA	HIRA	612	S	1	57.41	0.66	NaN	NaN	NaN	0.60	NaN	NaN	0.96	0.86
P54198	Protein HIRA	HIRA	614	S	1	57.41	0.66	NaN	NaN	NaN	0.60	NaN	NaN	0.96	0.86
P54259	Atrophin-1	ATN1	661	S	0.926	77.63	NaN	1.05	1.07	1.02	NaN	0.96	0.95	0.81	0.94
P54259	Atrophin-1	ATN1	101	S	0.958	62.65	NaN	0.58	0.80	0.60	0.57	NaN	NaN	NaN	NaN
P55081	Microfibrillar-associated protein 1	MFAP1	116	S	1	155.9	1.10	1.00	1.11	1.08	1.04	1.11	1.05	0.96	1.16
P55081	Microfibrillar-associated protein 1	MFAP1	118	S	1	155.9	1.27	1.29	1.27	1.15	1.02	1.05	1.29	0.99	1.24
P55081	Microfibrillar-associated protein 1	MFAP1	52	S	1	134.1	0.62	0.66	0.66	0.84	0.80	0.72	0.52	0.50	0.59
P55081	Microfibrillar-associated protein 1	MFAP1	53	S	1	134.1	0.62	0.66	0.66	0.84	0.80	0.72	0.52	0.50	0.59
P55327	Tumor protein D52	TPD52	171	S	0.955	66.39	1.64	NaN	NaN	2.65	2.90	3.05	0.78	0.87	1.20
P55327	Tumor protein D52	TPD52	176	S	1	76.07	0.66	0.59	0.83	0.49	0.56	0.63	3.08	2.88	3.51
P56524	Histone deacetylase 4	HDAC4	565	S	1	140	0.90	1.02	0.89	0.73	0.66	0.93	0.98	1.17	1.06
P60174	Triosephosphate isomerase	TPI1	58	S	1	257.5	1.00	1.09	1.00	1.18	1.16	1.11	1.06	0.96	1.13
P61006	Ras-related protein Rab-8A	RAB8A	181	S	1	158.7	NaN	NaN	8.22	20.18	NaN	11.42	1.97	NaN	NaN

P61978	Heterogeneous nuclear ribonucleoprotein K	HNRNPK	284	S	1	113.6	1.22	1.32	1.26	1.24	NaN	1.18	1.19	1.18	1.31
P61978	Heterogeneous nuclear ribonucleoprotein K	HNRNPK	379	S	0.952	92.43	1.93	NaN	NaN	NaN	2.54	2.87	1.62	NaN	NaN
P61978	Heterogeneous nuclear ribonucleoprotein K	HNRNPK	214	S	0.979	106.3	1.98	2.14	2.66	NaN	NaN	NaN	0.90	0.86	0.85
P61978	Heterogeneous nuclear ribonucleoprotein K	HNRNPK	216	S	0.985	139	1.90	2.20	2.32	3.68	3.59	NaN	NaN	NaN	0.95
P61978	Heterogeneous nuclear ribonucleoprotein K	HNRNPK	116	S	1	252.8	1.05	1.02	0.95	0.98	1.09	1.02	0.49	0.48	0.45
P62070	Ras-related protein R-Ras2	RRAS2	186	S	1	181.7	1.39	1.42	1.34	1.48	1.49	1.49	1.01	0.94	1.03
P62258	14-3-3 protein epsilon	YWHAE	210	S	0.989	125.5	1.01	1.06	1.18	0.99	1.01	1.02	1.03	0.98	0.99
P62328	Thymosin beta-4;Hematopoietic system	TMSB4X	44	S	1	145.5	1.03	1.27	1.40	1.62	1.66	1.80	1.02	1.01	NaN
P62995	Transformer-2 protein homolog beta	TRA2B	95	S	0.999	53.74	0.77	0.80	NaN	NaN	NaN	NaN	NaN	NaN	NaN
P62995	Transformer-2 protein homolog beta	TRA2B	97	S	0.994	53.74	0.77	0.80	NaN	NaN	NaN	NaN	NaN	NaN	NaN
P62995	Transformer-2 protein homolog beta	TRA2B	99	S	0.757	53.74	0.77	0.80	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Q13595	Transformer-2 protein homolog beta;Transformer-2 protein homolog alpha	TRA2B	264;260	S	1	105.8	0.63	0.66	0.56	0.64	0.60	0.90	1.14	1.14	0.61
Q13595	Transformer-2 protein homolog beta;Transformer-2 protein homolog alpha	TRA2B	266;262	S	0.999	103.1	0.92	0.75	1.00	0.91	0.95	0.90	1.14	1.10	1.19
Q13595	Transformer-2 protein homolog beta;Transformer-2 protein homolog alpha	TRA2B	270;266	S	0.894	105.8	0.93	NaN	NaN	NaN	NaN	NaN	1.09	NaN	1.14
Q5VU10	Ribonuclease P protein subunit p30	RPP30	195	S	1	59.56	0.83	0.78	NaN	1.17	1.06	NaN	NaN	NaN	NaN
P78527	DNA-dependent protein kinase catalytic subunit	PRKDC	2612	S	0.992	159.8	0.91	0.98	0.93	1.27	1.22	1.13	0.65	0.73	NaN
P78536	Disintegrin and metalloproteinase domain-containing protein 17	ADAM17	791	S	1	137	2.04	2.33	2.60	2.44	2.30	1.96	1.66	1.77	1.86
P80723	Brain acid soluble protein 1	BASP1	164	S	0.99	60.62	NaN	0.91	NaN	0.80	0.85	NaN	NaN	1.38	NaN
P80723	Brain acid soluble protein 1	BASP1	170	S	0.888	51.62	1.04	NaN	1.11	NaN	NaN	0.92	NaN	NaN	NaN
P84103	Serine/arginine-rich splicing factor 3	SRSF3	138	S	1	67.19	1.31	1.36	1.27	1.17	1.16	1.10	1.51	1.48	1.43
P84103	Serine/arginine-rich splicing factor 3	SRSF3	140	S	1	67.19	1.31	1.36	1.27	1.17	1.16	1.10	1.51	1.48	1.43
P85037	Forkhead box protein K1	FOXK1	299	S	0.695	197	NaN	NaN	NaN	NaN	NaN	NaN	0.78	0.61	NaN
P85037	Forkhead box protein K1	FOXK1	213	S	0.999	75.18	NaN	0.93	NaN	0.74	NaN	0.88	0.73	0.88	NaN
P85037	Forkhead box protein K1	FOXK1	445	S	1	158.9	0.96	0.99	1.00	0.92	0.91	0.89	0.97	0.98	0.95
P85037	Forkhead box protein K1	FOXK1	420	S	0.987	142.3	0.79	0.74	0.74	0.76	0.81	0.72	0.68	0.63	0.73
P85037	Forkhead box protein K1	FOXK1	243	S	0.976	103.9	0.83	0.77	0.67	1.33	0.97	0.92	NaN	1.19	NaN

P85037	Forkhead box protein K1	FOXK1	253	S	0.684	62.61	NaN	NaN	NaN	NaN	0.97	0.79	NaN	1.19	NaN
P85037	Forkhead box protein K1	FOXK1	257	S	0.972	90.32	0.83	0.77	0.67	NaN	NaN	NaN	0.97	0.67	NaN
P98082	Disabled homolog 2	DAB2	401	S	1	62.69	0.87	1.00	NaN	0.86	1.15	NaN	NaN	NaN	NaN
P98175	RNA-binding protein 10	RBM10	736	S	1	120.9	0.99	0.95	1.04	0.88	0.94	0.86	1.09	1.17	1.04
P98175	RNA-binding protein 10	RBM10	738	S	1	136.6	0.99	0.95	1.04	0.88	0.94	0.86	1.09	1.17	1.04
P98175	RNA-binding protein 10	RBM10	723	S	1	121.5	1.21	1.30	1.22	1.14	1.13	1.11	1.15	1.15	1.18
Q00587	Cdc42 effector protein 1	CDC42EP1	350	S	1	92.3	NaN	0.93	0.96	NaN	0.78	0.84	1.36	1.28	NaN
Q00587	Cdc42 effector protein 1	CDC42EP1	101	S	0.985	41.67	NaN	1.21	NaN	1.51	1.64	NaN	NaN	0.61	NaN
Q00587	Cdc42 effector protein 1	CDC42EP1	303	S	0.998	81.19	1.32	1.25	1.26	NaN	NaN	0.94	NaN	1.73	1.83
Q01130	Serine/arginine-rich splicing factor 2	SRSF2	206	S	1	60.74	NaN	0.54	1.08	0.76	0.57	NaN	1.14	0.97	NaN
Q01130	Serine/arginine-rich splicing factor 2	SRSF2	208	S	1	60.74	NaN	0.54	1.08	0.76	0.57	NaN	1.14	0.97	NaN
Q01130	Serine/arginine-rich splicing factor 2	SRSF2	212	S	1	58.69	NaN	0.54	1.08	1.06	NaN	NaN	1.14	1.27	NaN
Q01130	Serine/arginine-rich splicing factor 2	SRSF2	220	S	0.545	60.74	NaN	NaN	1.08	0.76	0.57	NaN	1.14	0.97	NaN
Q01130	Serine/arginine-rich splicing factor 2	SRSF2	189	S	1	73.44	1.07	1.06	1.01	0.95	0.97	0.97	1.15	1.12	1.16
Q01130	Serine/arginine-rich splicing factor 2	SRSF2	191	S	1	73.44	1.07	1.06	1.01	0.30	0.97	0.97	0.29	0.28	1.16
Q01130	Serine/arginine-rich splicing factor 2	SRSF2	187	S	1	60.55	0.97	0.98	NaN	NaN	0.88	0.90	1.07	1.13	1.04
Q01130	Serine/arginine-rich splicing factor 2	SRSF2	26	S	0.999	157	1.00	0.97	0.98	1.22	1.15	1.21	1.05	0.85	1.13
Q01167	Forkhead box protein K2	FOXK2	398	S	1	182.1	0.59	0.42	NaN	NaN	NaN	NaN	0.87	0.73	NaN
Q01167	Forkhead box protein K2	FOXK2	170	S	0.732	47.31	NaN	NaN	0.57	NaN	1.01	0.98	0.68	0.68	NaN
Q01518	Adenylyl cyclase-associated protein 1;Adenylyl cyclase-associated protein	CAP1	34	S	0.999	157.8	3.02	2.54	2.96	4.15	4.26	4.46	0.96	0.87	1.00
Q01518	Adenylyl cyclase-associated protein 1	CAP1	308	S	0.882	78.35	NaN	NaN	0.35	0.36	0.36	0.32	0.20	0.24	0.21
Q01804	OTU domain-containing protein 4	OTUD4	1006	S	0.999	88.49	1.65	1.61	NaN	NaN	NaN	NaN	0.82	NaN	NaN
Q01804	OTU domain-containing protein 4	OTUD4	1023	S	0.999	117.2	1.08	1.06	NaN	0.75	NaN	NaN	NaN	1.01	NaN
Q01804	OTU domain-containing protein 4	OTUD4	1024	S	0.999	117.2	1.08	1.06	NaN	0.75	NaN	NaN	NaN	1.01	NaN
Q02040	A-kinase anchor protein 17A	AKAP17A	537	S	1	77.59	NaN	1.81	0.80	0.85	0.88	0.96	0.93	0.92	0.95
Q02880	DNA topoisomerase 2-beta	TOP2B	1336	S	0.998	52.35	0.63	0.81	0.78	0.67	NaN	NaN	NaN	1.50	0.89
Q02880	DNA topoisomerase 2-beta	TOP2B	1340	S	0.999	52.35	0.63	0.81	0.78	0.67	NaN	NaN	NaN	1.50	0.89
Q02880	DNA topoisomerase 2-beta	TOP2B	1342	S	0.996	52.35	0.63	0.81	0.78	0.67	NaN	NaN	NaN	1.50	0.89
Q02880	DNA topoisomerase 2-beta	TOP2B	1344	S	0.995	52.35	0.63	0.81	0.78	0.67	NaN	NaN	NaN	1.50	0.89
Q02880	DNA topoisomerase 2-beta	TOP2B	1581	S	0.995	110.3	0.77	0.78	0.76	0.80	0.80	0.71	1.00	1.04	1.03

Q02880	DNA topoisomerase 2-beta	TOP2B	1522	S	1	173	0.72	0.37	0.81	0.93	0.69	0.88	0.99	1.05	0.87
Q02880	DNA topoisomerase 2-beta	TOP2B	1524	S	0.998	173	0.72	0.69	0.81	0.93	0.58	0.88	0.99	1.05	0.87
Q02880	DNA topoisomerase 2-beta	TOP2B	1526	S	0.958	89.14	NaN	NaN	NaN	NaN	0.84	0.94	NaN	0.88	NaN
Q02880	DNA topoisomerase 2-beta	TOP2B	1400	S	0.952	93.86	NaN	0.57	NaN	NaN	0.88	0.67	NaN	0.37	NaN
Q02880	DNA topoisomerase 2-beta	TOP2B	1413	S	0.995	93.86	NaN	0.50	NaN	NaN	0.88	0.67	NaN	0.37	NaN
Q02952	A-kinase anchor protein 12	AKAP12	1331	S	0.999	55.31	1.66	1.87	NaN	NaN	0.79	0.92	2.46	NaN	NaN
Q03111	Protein ENL	MLLT1	475	S	0.993	47.54	NaN	NaN	NaN	1.03	1.16	0.68	NaN	NaN	0.74
Q03111	Protein ENL	MLLT1	315	S	0.5	84.82	NaN	NaN	NaN	0.93	NaN	NaN	0.97	NaN	0.85
Q03164	Histone-lysine N-methyltransferase 2A;MLL cleavage product N320;MLL cleavage product C180	KMT2A	1837	S	0.973	93.15	0.59	0.58	0.80	0.64	NaN	NaN	NaN	NaN	0.74
Q03164	Histone-lysine N-methyltransferase 2A;MLL cleavage product N320;MLL cleavage product C180	KMT2A	3527	S	0.949	50.4	0.69	0.83	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Q03164	Histone-lysine N-methyltransferase 2A;MLL cleavage product N320;MLL cleavage product C180	KMT2A	2098	S	0.98	83.72	NaN	0.54	0.51	NaN	0.72	NaN	0.51	NaN	NaN
Q03252	Lamin-B2	LMNB2	37	S	0.999	165	3.48	3.56	3.37	NaN	NaN	5.36	0.88	NaN	0.98
Q04721	Neurogenic locus notch homolog protein 2;Notch 2 extracellular truncation;Notch 2 intracellular domain	NOTCH2	1845	S	0.992	206.4	1.01	1.40	NaN	NaN	NaN	1.14	1.05	NaN	0.87
Q05209	Tyrosine-protein phosphatase non-receptor type 12	PTPN12	603	S	1	121.6	1.13	1.07	1.25	0.81	0.90	0.86	1.09	0.89	1.10
Q05209	Tyrosine-protein phosphatase non-receptor type 12	PTPN12	606	S	0.999	121.6	1.13	1.07	1.11	0.49	0.90	0.86	0.76	1.31	1.00
Q5T757	Serine/arginine-rich splicing factor 11	SRSF11	374	S	1	237.9	1.09	1.15	1.08	1.05	1.15	8.01	1.56	1.31	1.36
Q5T757	Serine/arginine-rich splicing factor 11	SRSF11	389	S	1	115.9	NaN	0.90	0.87	0.98	1.01	0.96	0.92	NaN	0.90
Q5T757	Serine/arginine-rich splicing factor 11	SRSF11	147	S	0.994	113.5	2.82	2.73	3.13	3.72	NaN	3.27	1.18	1.24	1.65
Q96PN7	Transcriptional-regulating factor 1	BCAR2	491;491	S	0.991	78.4	0.43	0.44	0.35	0.62	0.61	0.54	0.67	0.60	0.62
Q06210	Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1	GFPT1	261	S	0.905	100.2	22.02	20.07	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Q07065	Cytoskeleton-associated protein 4	CKAP4	17	S	0.987	129.8	2.84	NaN	NaN	4.15	5.10	NaN	NaN	NaN	NaN
Q08211	ATP-dependent RNA helicase	DHX9	87	S	1	247.7	0.95	0.97	0.98	1.42	1.16	1.34	0.74	0.83	0.87
Q08AD1	Calmodulin-regulated spectrin-associated protein 2	CAMSAP2	599	S	0.733	56.47	NaN	NaN	NaN	0.75	0.65	1.04	0.86	0.88	NaN
Q08AD1	Calmodulin-regulated spectrin-associated protein 2	CAMSAP2	464	S	0.999	103.6	NaN	2.38	2.50	1.91	NaN	NaN	1.80	2.10	2.17

Q08J23	tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	456	S	0.982	61.49	0.39	NaN	0.58	0.52	NaN	NaN	0.94	1.21	0.97
Q09472	Histone acetyltransferase	EP300	1038	S	0.953	146.8	NaN	NaN	NaN	0.98	NaN	0.93	NaN	0.94	NaN
Q09666	Neuroblast differentiation-associated protein AHNAK	AHNAK	5110	S	1	128.9	1.84	2.00	1.92	2.17	2.14	2.18	1.34	1.36	1.41
Q09666	Neuroblast differentiation-associated protein AHNAK	AHNAK	5749	S	1	181.3	0.79	0.65	0.59	0.70	0.84	0.66	0.88	0.83	0.81
Q09666	Neuroblast differentiation-associated protein AHNAK	AHNAK	5752	S	1	318	0.60	0.62	0.66	0.49	0.55	0.53	0.86	0.83	0.87
Q09666	Neuroblast differentiation-associated protein AHNAK	AHNAK	5762	S	0.889	283.8	1.19	1.24	0.90	0.95	NaN	0.66	1.03	NaN	0.94
Q09666	Neuroblast differentiation-associated protein AHNAK	AHNAK	5763	S	0.99	387.5	0.87	0.87	1.17	1.48	1.40	1.34	1.01	1.00	0.99
Q09666	Neuroblast differentiation-associated protein AHNAK	AHNAK	41	S	1	202.8	2.71	NaN	2.93	4.37	3.90	4.23	1.09	0.94	NaN
Q09666	Neuroblast differentiation-associated protein AHNAK	AHNAK	177	S	0.996	196.3	1.07	1.12	NaN	1.27	1.28	1.22	0.99	1.00	1.03
Q09666	Neuroblast differentiation-associated protein AHNAK	AHNAK	4986	S	1	58.74	1.73	1.76	1.77	1.96	1.83	1.70	1.61	1.68	1.40
Q09666	Neuroblast differentiation-associated protein AHNAK	AHNAK	5731	S	1	207.9	0.79	0.86	0.81	1.01	0.99	1.01	0.91	0.89	0.89
Q09666	Neuroblast differentiation-associated protein AHNAK	AHNAK	5841	S	1	239.5	0.86	0.85	0.83	0.82	0.85	0.87	1.10	1.04	0.89
Q09666	Neuroblast differentiation-associated protein AHNAK	AHNAK	5857	S	0.725	41.76	NaN	NaN	NaN	NaN	0.82	1.23	NaN	NaN	NaN
Q09666	Neuroblast differentiation-associated protein AHNAK	AHNAK	5552	S	1	237.3	2.19	1.96	1.93	4.22	5.55	5.11	0.43	NaN	0.49
Q09666	Neuroblast differentiation-associated protein AHNAK	AHNAK	5448	S	1	105.6	0.87	0.90	0.58	0.64	0.74	0.65	1.64	1.87	1.83
Q09666	Neuroblast differentiation-associated protein AHNAK	AHNAK	2397	S	1	168.3	2.06	2.25	2.16	3.25	3.34	3.05	0.84	0.93	0.95
Q09666	Neuroblast differentiation-associated protein AHNAK	AHNAK	511	S	1	178.1	2.40	2.40	2.35	3.63	4.11	3.34	1.23	1.28	1.08
Q09666	Neuroblast differentiation-associated protein AHNAK	AHNAK	93	S	1	118.7	0.31	0.34	NaN	NaN	0.35	0.37	NaN	NaN	0.23
Q09666	Neuroblast differentiation-associated protein AHNAK	AHNAK	559	S	1	106.6	0.84	0.44	0.58	1.03	0.87	1.01	0.77	NaN	0.76
Q09666	Neuroblast differentiation-associated protein AHNAK	AHNAK	135	S	1	260	0.80	0.80	0.84	1.29	1.30	1.32	1.36	1.34	1.43
Q09666	Neuroblast differentiation-associated protein AHNAK	AHNAK	210	S	0.946	119.6	1.99	1.92	1.24	1.41	2.13	NaN	1.28	NaN	NaN
Q09666	Neuroblast differentiation-associated protein AHNAK	AHNAK	212	S	0.758	111.1	4.51	3.33	NaN	2.66	NaN	1.77	NaN	0.99	1.87
Q09666	Neuroblast differentiation-associated protein AHNAK	AHNAK	216	S	0.999	293.1	0.81	1.05	0.79	0.95	0.92	0.96	0.95	0.96	0.99
Q09666	Neuroblast differentiation-associated protein AHNAK	AHNAK	5099	S	1	104.8	5.17	4.84	NaN	NaN	NaN	NaN	NaN	NaN	NaN

Q09666	Neuroblast differentiation-associated protein AHNAK	AHNAK	5782	S	0.999	147.3	1.09	1.14	1.17	0.93	0.93	0.94	1.43	1.43	1.45
Q09666	Neuroblast differentiation-associated protein AHNAK	AHNAK	5745	S	0.62	118.4	0.42	NaN	0.90	NaN	NaN	0.33	NaN	NaN	NaN
Q09666	Neuroblast differentiation-associated protein AHNAK	AHNAK	5746	S	0.659	118.4	0.42	0.44	0.90	NaN	NaN	0.33	NaN	NaN	NaN
Q09666	Neuroblast differentiation-associated protein AHNAK	AHNAK	3426	S	1	107.8	3.73	3.94	4.23	3.51	3.86	3.23	1.51	1.68	1.40
Q0JRZ9	F-BAR domain only protein 2	FCHO2	403	S	1	80.78	1.15	1.22	1.23	0.91	0.98	0.98	1.24	1.29	1.29
Q12802	A-kinase anchor protein 13	AKAP13	2398	S	0.728	61.11	NaN	0.76	1.23	1.17	NaN	NaN	NaN	NaN	NaN
Q12872	Splicing factor, suppressor of white-apricot homolog	SFSWAP	604	S	0.992	174.9	0.93	0.93	0.87	0.91	0.96	0.92	0.86	NaN	0.85
Q12906	Interleukin enhancer-binding factor 3	ILF3	482	S	1	156.2	0.73	0.69	NaN	0.85	0.88	NaN	0.85	NaN	0.84
Q12906	Interleukin enhancer-binding factor 3	ILF3	382	S	1	226.1	0.55	0.55	0.55	1.06	1.07	0.95	0.36	0.37	0.35
Q12906	Interleukin enhancer-binding factor 3	ILF3	384	S	0.888	96.39	0.55	NaN	0.55	1.01	1.06	NaN	0.56	0.44	0.43
Q5T8C6	Cell division cycle protein 16 homolog	CDC16	415	S	1	48.57	1.41	1.65	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Q13045	Protein flightless-1 homolog	FLII	856	S	1	154.5	NaN	1.02	1.05	NaN	1.21	1.25	1.36	1.33	1.43
Q13085	Acetyl-CoA carboxylase 1;Biotin carboxylase	ACACA	23	S	0.641	109.7	0.75	0.68	NaN	NaN	1.31	NaN	NaN	NaN	NaN
Q13085	Acetyl-CoA carboxylase 1;Biotin carboxylase	ACACA	25	S	0.88	110.6	NaN	NaN	NaN	0.92	1.31	0.96	1.93	NaN	1.62
Q13085	Acetyl-CoA carboxylase 1;Biotin carboxylase	ACACA	29	S	1	263.7	0.68	0.64	0.70	0.79	0.68	0.78	0.78	0.73	0.83
Q13085	Acetyl-CoA carboxylase 1;Biotin carboxylase	ACACA	1259	S	0.999	210.1	0.71	0.69	0.73	0.98	NaN	0.85	0.75	NaN	0.71
Q13085	Acetyl-CoA carboxylase 1;Biotin carboxylase	ACACA	1263	S	0.976	210.1	0.71	0.69	0.73	0.98	NaN	0.85	0.75	0.78	0.71
Q13111	Chromatin assembly factor 1 subunit A	CHAF1A	951	S	0.951	69.67	0.53	0.58	NaN	0.90	0.79	NaN	0.70	0.65	0.87
Q13112	Chromatin assembly factor 1 subunit B	CHAF1B	409	S	0.564	61.28	NaN	0.68	0.86	1.04	1.13	0.93	NaN	NaN	NaN
Q13112	Chromatin assembly factor 1 subunit B	CHAF1B	410	S	0.956	98.42	0.78	0.76	0.89	1.04	0.89	1.00	0.85	0.77	1.05
Q13112	Chromatin assembly factor 1 subunit B	CHAF1B	538	S	0.992	77.45	0.59	0.69	NaN	NaN	NaN	0.96	0.54	NaN	0.85
Q13112	Chromatin assembly factor 1 subunit B	CHAF1B	429	S	0.97	160.8	0.64	0.52	NaN	0.65	NaN	1.23	0.64	NaN	0.61
Q13177	Serine/threonine-protein kinase PAK 2;PAK-2p27;PAK-	PAK2	141	S	1	197.7	2.05	1.98	2.23	2.83	2.94	2.96	1.04	1.01	1.06
Q13185	Chromobox protein homolog 3	CBX3	93	S	1	104.4	0.63	0.93	0.66	1.04	1.44	1.32	0.74	0.79	0.93
Q13185	Chromobox protein homolog 3	CBX3	95	S	1	309	1.03	1.06	1.08	1.10	1.05	1.01	0.86	0.85	0.64
Q13185	Chromobox protein homolog 3	CBX3	97	S	1	107.2	1.18	1.03	0.71	1.03	0.91	1.04	0.83	0.87	0.75
Q13185	Chromobox protein homolog 3	CBX3	99	S	1	103.3	1.27	1.04	1.47	0.95	0.94	0.85	0.72	0.87	0.75

Q13185	Chromobox protein homolog 3	CBX3	176	S	0.966	124.2	1.06	1.25	1.35	1.06	1.17	0.93	1.07	0.99	1.15
Q13242	Serine/arginine-rich splicing factor 9	SRSF9	204	S	1	108.7	1.45	1.33	1.29	1.14	NaN	1.00	1.37	1.35	NaN
Q13242	Serine/arginine-rich splicing factor 9	SRSF9	211	S	1	150.5	1.02	1.06	1.03	0.93	0.90	0.96	0.97	0.97	0.99
Q13242	Serine/arginine-rich splicing factor 9	SRSF9	216	S	1	119.5	0.90	1.03	1.00	1.10	0.92	0.82	1.13	1.13	1.07
Q13242	Serine/arginine-rich splicing factor 9	SRSF9	189	S	0.928	42.16	1.15	1.03	NaN	NaN	0.90	NaN	NaN	NaN	NaN
Q13247	Serine/arginine-rich splicing factor 6	SRSF6	314	S	1	78.49	1.16	1.14	1.12	1.03	1.05	1.08	1.11	1.00	1.12
Q13247	Serine/arginine-rich splicing factor 6	SRSF6	316	S	1	86.9	1.16	1.14	0.27	0.30	0.28	0.31	0.40	0.29	0.29
Q13247	Serine/arginine-rich splicing factor 6	SRSF6	303	S	1	172.3	1.05	1.02	1.15	0.98	1.00	1.01	0.91	0.91	0.95
Q13263	Transcription intermediary factor 1-beta	TRIM28	50	S	0.995	169.4	1.02	0.97	0.82	1.08	NaN	NaN	1.08	NaN	NaN
Q13283	Ras GTPase-activating protein-binding protein 1	G3BP1	232	S	1	494	1.26	1.29	1.43	1.09	NaN	1.11	1.17	1.04	1.21
Q13283	Ras GTPase-activating protein-binding protein 1	G3BP1	149	S	1	148.2	1.20	1.32	2.34	1.64	NaN	1.16	1.15	1.25	NaN
Q13425	Beta-2-syntrophin	SNTB2	95	S	1	160.4	NaN	1.01	0.92	NaN	NaN	0.95	NaN	NaN	0.99
Q13425	Beta-2-syntrophin	SNTB2	110	S	1	112.7	0.68	0.58	NaN	0.63	0.70	0.75	0.82	0.66	0.83
Q13425	Beta-2-syntrophin	SNTB2	233	S	0.879	125.4	0.70	0.61	0.60	0.64	0.61	0.55	0.89	0.90	0.83
Q13428	Treacle protein	TCOF1	1111	S	0.965	119.4	NaN	NaN	NaN	0.90	0.87	NaN	NaN	0.76	0.99
Q13442	28 kDa heat- and acid-stable phosphoprotein	PDAP1	60	S	1	571.9	0.19	0.20	0.22	0.27	0.27	0.25	0.58	0.49	0.53
Q13442	28 kDa heat- and acid-stable phosphoprotein	PDAP1	63	S	1	398.3	NaN	NaN	0.19	0.21	NaN	0.23	0.50	0.55	0.45
Q13443	Disintegrin and metalloproteinase domain-containing protein 9	ADAM9	758	S	1	99.86	1.10	1.20	1.31	0.93	1.02	1.11	1.04	0.90	1.19
Q13469	Nuclear factor of activated T-cells, cytoplasmic 2	NFATC2	326	S	0.983	105.1	NaN	NaN	1.28	0.76	0.68	0.75	NaN	1.71	NaN
Q13501	Sequestosome-1	SQSTM1	366	S	0.951	215.3	1.56	1.48	1.60	1.95	NaN	2.01	0.83	NaN	0.90
Q13501	Sequestosome-1	SQSTM1	332	S	0.998	117	0.82	0.99	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Q13501	Sequestosome-1	SQSTM1	272	S	1	205.3	1.14	1.70	1.12	2.61	2.65	1.45	0.64	0.61	0.61
Q13501	Sequestosome-1	SQSTM1	24	S	0.961	145.8	3.27	2.86	NaN	3.83	4.80	4.30	NaN	NaN	NaN
Q13501	Sequestosome-1	SQSTM1	28	S	0.688	100.9	NaN	NaN	3.13	NaN	4.80	NaN	0.86	0.77	NaN
Q13501	Sequestosome-1	SQSTM1	284	S	0.95	161.7	1.09	1.26	NaN	1.75	NaN	NaN	NaN	NaN	NaN
Q13523	Serine/threonine-protein kinase PRP4 homolog	PRPF4B	257	S	0.998	100.4	0.88	0.88	0.91	0.89	0.87	0.92	0.90	0.89	0.90
Q13523	Serine/threonine-protein kinase PRP4 homolog	PRPF4B	431	S	1	83.82	NaN	1.19	1.40	0.85	1.17	0.94	0.68	0.59	0.96
Q13523	Serine/threonine-protein kinase PRP4 homolog	PRPF4B	437	S	0.943	72.32	NaN	1.19	1.40	0.95	1.17	1.23	0.68	0.59	1.55

Q13523	Serine/threonine-protein kinase PRP4 homolog	PRPF4B	20	S	1	123.6	0.52	0.45	0.40	NaN	0.62	0.66	0.39	0.42	0.42
Q13523	Serine/threonine-protein kinase PRP4 homolog	PRPF4B	277	S	1	85.99	0.88	0.91	0.84	NaN	NaN	0.94	0.84	0.89	0.92
Q13523	Serine/threonine-protein kinase PRP4 homolog	PRPF4B	427	S	1	45.83	NaN	1.19	NaN	NaN	NaN	NaN	NaN	1.36	1.61
Q13523	Serine/threonine-protein kinase PRP4 homolog	PRPF4B	368	S	1	75.48	1.05	0.48	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Q13523	Serine/threonine-protein kinase PRP4 homolog	PRPF4B	578	S	0.975	98.42	0.36	0.36	NaN	NaN	0.49	0.49	NaN	NaN	NaN
Q13523	Serine/threonine-protein kinase PRP4 homolog	PRPF4B	580	S	1	98.42	0.36	0.36	NaN	NaN	0.49	0.49	NaN	NaN	NaN
Q13541	Eukaryotic translation initiation factor 4E-binding protein 1	EIF4EBP1	96	S	0.515	176.9	NaN	NaN	NaN	NaN	NaN	NaN	0.81	NaN	0.55
Q13541	Eukaryotic translation initiation factor 4E-binding protein 1	EIF4EBP1	65	S	0.991	152.9	2.90	2.76	2.72	2.12	0.86	2.39	2.18	2.00	2.30
Q13547	Histone deacetylase 1	HDAC1	393	S	1	144.3	0.63	0.57	NaN	0.92	0.77	0.67	0.54	0.56	0.55
Q13595	Transformer-2 protein homolog alpha	TRA2A	96	S	1	70.56	0.70	0.64	NaN	NaN	NaN	0.83	NaN	0.68	0.67
Q13595	Transformer-2 protein homolog alpha	TRA2A	98	S	1	70.56	0.70	0.64	NaN	NaN	NaN	0.83	NaN	0.68	0.67
Q13595	Transformer-2 protein homolog alpha	TRA2A	100	S	0.996	70.56	0.70	0.64	NaN	NaN	NaN	0.83	NaN	0.68	0.67
Q13595	Transformer-2 protein homolog alpha	TRA2A	84	S	0.962	61.44	1.08	NaN	0.97	0.90	0.83	0.94	1.32	1.24	1.25
Q13610	Periodic tryptophan protein 1 homolog	PWP1	50	S	1	151.5	0.55	0.49	0.50	0.61	0.66	0.64	0.69	0.62	0.72
Q13614	Myotubularin-related protein 2	MTMR2	630	S	0.562	54.65	1.27	1.03	NaN	0.70	0.60	NaN	NaN	NaN	NaN
Q13625	Apoptosis-stimulating of p53 protein 2	TP53BP2	698	S	0.969	65.84	0.88	0.90	NaN	0.96	NaN	0.94	NaN	0.93	NaN
Q13905	Rap guanine nucleotide exchange factor 1	RAPGEF1	296	S	0.94	87.57	0.86	0.81	0.92	0.73	0.78	0.84	NaN	NaN	1.08
Q14166	Tubulin--tyrosine ligase-like protein 12	TTLL12	16	S	0.994	305.8	0.70	0.47	NaN	0.88	0.79	0.85	0.79	0.85	NaN
Q14247	Src substrate cortactin	CTTN	405	S	1	252.6	1.08	1.02	0.68	1.04	2.76	1.90	0.83	0.89	1.44
Q14247	Src substrate cortactin	CTTN	417	S	0.726	196.4	0.79	0.79	3.10	1.32	1.48	0.68	1.08	0.86	0.83
Q14247	Src substrate cortactin	CTTN	418	S	0.999	246.6	1.31	1.33	0.99	1.35	1.44	1.34	0.95	0.96	0.92
Q14315	Filamin-C	FLNC	2233	S	0.999	70.41	2.61	2.32	NaN	NaN	NaN	NaN	3.56	4.24	NaN
Q14566	DNA replication licensing factor MCM6	MCM6	762	S	1	194.6	NaN	1.31	NaN	NaN	NaN	NaN	0.74	0.66	0.95
Q14573	Inositol 1,4,5-trisphosphate receptor type 3	ITPR3	2670	S	1	88.51	0.93	1.05	0.88	NaN	NaN	NaN	2.32	2.23	2.45
Q14669	E3 ubiquitin-protein ligase TRIP12	TRIP12	77	S	0.935	46.02	NaN	NaN	NaN	1.27	1.00	1.23	0.81	0.86	NaN
Q14669	E3 ubiquitin-protein ligase TRIP12	TRIP12	312	S	1	84.73	1.15	1.08	1.29	1.03	1.20	NaN	1.13	1.01	NaN

Q14669	E3 ubiquitin-protein ligase TRIP12	TRIP12	1016	S	0.934	47.02	NaN	NaN	0.55	NaN	0.60	NaN	0.72	0.71	0.67
Q14676	Mediator of DNA damage checkpoint protein 1	MDC1	329	S	0.995	233.6	0.75	0.84	0.83	1.25	NaN	0.99	0.68	0.56	0.55
Q14676	Mediator of DNA damage checkpoint protein 1	MDC1	376	S	0.998	296.4	1.04	1.01	1.03	0.95	1.43	0.99	0.88	0.79	0.93
Q14676	Mediator of DNA damage checkpoint protein 1	MDC1	168	S	1	114.6	1.01	1.04	0.95	NaN	0.99	1.01	0.92	0.98	0.99
Q14676	Mediator of DNA damage checkpoint protein 1	MDC1	453	S	0.953	337.1	0.98	0.95	0.91	0.97	NaN	NaN	NaN	NaN	NaN
Q14677	Clathrin interactor 1	CLINT1	299	S	0.797	106.2	0.78	NaN	NaN	1.18	NaN	NaN	0.83	0.77	0.54
Q14684	Ribosomal RNA processing protein 1 homolog B	RRP1B	732	S	0.922	91.71	NaN	NaN	0.81	0.63	NaN	NaN	NaN	0.57	0.70
Q14684	Ribosomal RNA processing protein 1 homolog B	RRP1B	245	S	1	188.6	1.70	1.42	1.71	1.79	1.74	1.72	1.41	1.41	1.42
Q14764	Major vault protein	MVP	873	S	1	149.7	0.86	NaN	0.85	NaN	1.15	1.93	1.36	NaN	0.97
Q14814	Myocyte-specific enhancer factor 2D	MEF2D	251	S	0.999	75.72	1.73	1.48	1.78	1.67	1.77	1.97	1.28	1.51	NaN
Q14966	Zinc finger protein 638	ZNF638	1400	S	0.716	91.87	NaN	2.37	1.84	2.42	2.05	2.30	1.50	1.11	1.49
Q14966	Zinc finger protein 638	ZNF638	1401	S	0.5	85.73	NaN	NaN	1.84	NaN	2.05	NaN	NaN	1.11	1.49
Q14993	Collagen alpha-1(XIX) chain	COL19A1	81	S	1	50.37	NaN	0.68	0.77	NaN	NaN	NaN	NaN	0.72	NaN
Q14C86	GTPase-activating protein and VPS9 domain-containing protein 1	GAPVD1	946	S	0.649	259	NaN	NaN	NaN	1.29	1.27	NaN	NaN	NaN	NaN
Q15007	Pre-mRNA-splicing regulator WTAP	WTAP	306	S	0.99	288	1.06	0.99	NaN	NaN	NaN	NaN	1.36	NaN	NaN
Q15036	Sorting nexin-17	SNX17	333	S	0.551	121.3	NaN	NaN	NaN	NaN	NaN	NaN	NaN	0.78	0.90
Q15059	Bromodomain-containing protein 3	BRD3	263	S	0.994	100.9	0.79	0.99	0.67	0.75	NaN	0.78	0.84	0.80	0.79
Q15061	WD repeat-containing protein 43	WDR43	77	S	1	117.2	0.90	0.99	0.92	0.98	0.96	0.98	0.85	0.85	0.82
Q15084	Protein disulfide-isomerase A6	PDIA6	428	S	1	344.7	1.11	1.19	1.28	0.98	0.96	0.98	1.41	1.11	1.00
Q15149	Plectin	PLEC	1435	S	1	108.4	1.31	1.25	1.22	1.89	2.07	1.77	0.86	1.08	0.85
Q15149	Plectin	PLEC	720	S	1	160.5	1.40	1.39	1.42	1.73	1.75	1.61	NaN	1.33	1.16
Q15149	Plectin	PLEC	4613	S	1	247.4	1.26	1.35	1.16	1.26	1.36	1.34	1.96	1.86	1.94
Q15149	Plectin	PLEC	4386	S	1	366.2	1.69	1.72	1.76	1.15	1.15	1.26	2.20	2.25	2.41
Q15149	Plectin	PLEC	4396	S	0.999	267.6	2.80	2.67	2.36	1.87	2.23	2.18	2.31	2.08	2.26
Q15149	Plectin	PLEC	125	S	1	78.78	0.99	0.81	0.96	NaN	1.21	NaN	NaN	1.28	NaN
Q15149	Plectin	PLEC	4406	S	0.896	199.2	1.10	1.30	0.97	1.30	NaN	1.99	1.13	NaN	1.20
Q15311	RalA-binding protein 1	RALBP1	645	S	0.964	59.71	0.63	0.76	0.81	NaN	0.80	0.79	1.04	1.00	1.00
Q15311	RalA-binding protein 1	RALBP1	92	S	0.999	115.4	0.72	0.67	0.86	0.65	0.67	0.67	0.97	0.93	1.00
Q15311	RalA-binding protein 1	RALBP1	93	S	0.999	115.4	0.72	0.67	0.86	0.65	0.67	0.67	0.97	0.93	1.00
Q15311	RalA-binding protein 1	RALBP1	48	S	0.988	91.44	1.44	1.55	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Q15311	RalA-binding protein 1	RALBP1	62	S	1	91.44	1.44	1.55	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Q15311	RalA-binding protein 1	RALBP1	29	S	0.716	41.52	NaN	1.96	NaN	NaN	NaN	NaN	1.61	1.39	NaN
Q15365	Poly(rC)-binding protein 1	PCBP1	171	S	0.937	284.2	0.68	0.79	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Q15365	Poly(rC)-binding protein 1	PCBP1	173	S	1	340.6	1.01	1.12	1.04	1.37	1.38	1.39	0.75	0.79	1.31

Q15365	Poly(rC)-binding protein 1	PCBP1	190	S	0.961	122.5	1.59	1.75	1.67	2.95	NaN	2.91	1.03	0.97	1.09
Q15366	Poly(rC)-binding protein 2	PCBP2	189	S	0.652	127.2	NaN	2.06	1.67	NaN	NaN	NaN	NaN	1.06	NaN
Q15366	Poly(rC)-binding protein 2	PCBP2	173	S	0.996	93.5	0.60	0.43	NaN	0.72	0.88	NaN	0.61	0.53	NaN
Q15398	Disks large-associated protein 5	DLGAP5	662	S	0.987	79.46	NaN	0.77	NaN	NaN	1.76	NaN	0.47	0.38	0.52
Q15398	Disks large-associated protein 5	DLGAP5	690	S	0.775	108.7	4.96	3.27	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Q15424	Scaffold attachment factor B1	SAFB	383	S	1	222	0.65	0.66	0.65	0.99	0.94	0.98	0.52	0.55	0.57
Q15424	Scaffold attachment factor B1	SAFB	384	S	0.998	222	0.65	0.66	0.65	0.99	0.99	0.98	0.52	0.55	0.57
Q15424	Scaffold attachment factor B1	SAFB	604	S	1	113.8	1.07	1.12	0.99	1.14	1.05	1.03	1.17	1.43	NaN
Q15424	Scaffold attachment factor B1;Scaffold attachment factor B2	SAFB	344	S	0.969	101.2	NaN	1.53	NaN	NaN	1.74	NaN	1.55	1.75	NaN
Q15459	Splicing factor 3A subunit 1	SF3A1	451	S	0.994	55.03	1.58	0.94	NaN	1.51	NaN	NaN	NaN	NaN	NaN
Q15459	Splicing factor 3A subunit 1	SF3A1	329	S	1	211.1	0.98	0.78	0.93	0.91	1.05	0.95	1.04	0.59	0.61
Q15477	Helicase SKI2W	SKIV2L	256	S	0.999	145.1	0.17	0.14	NaN	0.22	0.19	0.19	1.01	1.00	0.91
Q15545	Transcription initiation factor TFIID subunit 7	TAF7	201	S	0.8	65.75	1.45	NaN	NaN	1.33	1.03	1.46	1.05	0.88	1.03
Q15637	Splicing factor 1	SF1	80	S	1	188.3	1.02	1.06	0.95	1.00	0.98	0.96	0.84	0.87	0.91
Q15637	Splicing factor 1	SF1	82	S	1	188.3	1.02	1.06	0.95	1.00	1.01	0.96	0.84	0.87	0.91
Q15648	Mediator of RNA polymerase II transcription subunit 1	MED1	1049	S	0.544	44.2	0.64	0.79	NaN	NaN	NaN	0.81	NaN	NaN	NaN
Q15648	Mediator of RNA polymerase II transcription subunit 1	MED1	1479	S	0.998	85	0.80	0.65	0.74	0.87	0.89	0.91	NaN	0.78	0.69
Q15648	Mediator of RNA polymerase II transcription subunit 1	MED1	1481	S	0.566	59.66	NaN	NaN	0.74	NaN	0.89	0.91	NaN	NaN	NaN
Q15648	Mediator of RNA polymerase II transcription subunit 1	MED1	1482	S	0.805	85	0.80	0.65	NaN	0.87	NaN	NaN	NaN	0.78	0.69
Q15678	Tyrosine-protein phosphatase non-receptor type 14	PTPN14	314	S	0.995	85.74	0.98	NaN	1.01	NaN	NaN	0.77	1.25	1.06	1.26
Q15678	Tyrosine-protein phosphatase non-receptor type 14	PTPN14	593	S	0.998	97.2	NaN	1.41	1.26	0.90	NaN	0.89	1.30	1.72	1.67
Q15678	Tyrosine-protein phosphatase non-receptor type 14	PTPN14	594	S	0.999	175.9	0.95	0.93	1.26	0.87	0.91	0.89	1.65	1.72	1.67
Q15942	Zyxin	ZYX	281	S	1	105.6	NaN	NaN	1.73	1.81	2.30	2.75	NaN	1.23	NaN
Q15942	Zyxin	ZYX	267	S	1	93.7	1.57	1.47	1.77	1.99	2.03	1.92	1.33	1.28	1.28
Q15942	Zyxin	ZYX	259	S	0.994	87.21	7.05	9.04	NaN	5.03	NaN	NaN	4.90	3.94	4.06
Q15942	Zyxin	ZYX	344	S	1	57.57	1.94	2.04	NaN	2.13	2.12	NaN	1.01	1.04	1.04
Q16204	Coiled-coil domain-containing protein 6	CCDC6	244	S	1	176.3	1.74	1.69	1.62	1.87	1.89	1.76	1.10	1.09	1.05
Q16204	Coiled-coil domain-containing protein 6	CCDC6	419	S	0.999	85.54	0.89	0.93	0.85	0.82	0.80	0.88	0.99	0.88	0.91
Q16512	Serine/threonine-protein kinase N1	PKN1	562	S	0.74	118	NaN	NaN	NaN	0.75	0.99	NaN	NaN	NaN	NaN
Q16512	Serine/threonine-protein kinase N1	PKN1	916	S	0.999	273.3	NaN	1.02	0.98	0.74	0.89	NaN	0.98	1.17	1.04

Q16513	Serine/threonine-protein kinase N2	PKN2	583	S	1	208.5	0.84	1.00	0.98	0.93	0.99	1.14	0.95	0.93	1.03
Q16514	Transcription initiation factor TFIID subunit 12	TAF12	51	S	0.838	59.28	NaN	0.99	NaN	NaN	NaN	NaN	0.91	0.93	NaN
Q16643	Drebrin	DBN1	142	S	0.998	99.26	0.91	1.00	0.97	0.78	0.79	0.79	1.31	1.39	1.44
Q1RLN5	Rho GTPase-activating protein 12	ARHGAP 12	240	S	1	117.9	0.59	0.60	0.65	0.84	0.87	0.70	0.86	0.78	0.80
Q27J81	Inverted formin-2	INF2	1149	S	0.876	88.74	1.27	1.13	NaN	0.66	NaN	NaN	NaN	1.19	NaN
Q2M2I8	AP2-associated protein kinase 1	AAK1	623	S	0.866	131.1	1.29	NaN	1.41	1.26	1.28	1.34	1.53	1.48	1.49
Q32MZ4	Leucine-rich repeat flightless-interacting protein 1	LRRFIP1	733	S	0.999	327.2	NaN	NaN	0.72	0.87	0.85	0.90	NaN	1.23	1.24
Q32MZ4	Leucine-rich repeat flightless-interacting protein 1	LRRFIP1	714	S	0.988	205.5	0.50	0.51	NaN	0.80	0.84	0.80	NaN	0.93	0.93
Q32MZ4	Leucine-rich repeat flightless-interacting protein 1	LRRFIP1	120	S	0.928	114.5	1.30	NaN	NaN	NaN	NaN	1.14	1.25	NaN	1.28
Q32MZ4	Leucine-rich repeat flightless-interacting protein 1	LRRFIP1	521	S	0.984	155.3	NaN	NaN	NaN	1.58	NaN	0.87	0.85	NaN	NaN
Q3KQU3	MAP7 domain-containing protein 1	MAP7D1	741	S	0.791	127.9	NaN	0.56	0.54	NaN	NaN	NaN	NaN	0.68	NaN
Q3KQU3	MAP7 domain-containing protein 1	MAP7D1	544	S	0.998	96.56	1.32	1.02	2.08	1.16	NaN	1.68	1.12	1.63	0.88
Q3KQU3	MAP7 domain-containing protein 1	MAP7D1	552	S	0.981	96.56	1.32	2.32	2.08	NaN	NaN	1.68	1.55	1.63	1.36
Q3KQU3	MAP7 domain-containing protein 1	MAP7D1	460	S	0.965	79.27	NaN	2.01	2.21	1.93	2.05	1.95	1.30	1.15	1.17
Q3KQU3	MAP7 domain-containing protein 1	MAP7D1	86	S	0.862	147.4	NaN	1.27	1.11	0.54	NaN	1.47	0.90	NaN	1.22
Q3KQU3	MAP7 domain-containing protein 1	MAP7D1	113	S	0.774	59.05	1.44	1.42	1.28	1.17	1.17	1.03	0.90	0.82	0.89
Q3KQU3	MAP7 domain-containing protein 1	MAP7D1	116	S	0.837	59.05	1.44	1.42	1.28	1.17	1.17	1.31	0.90	0.82	0.89
Q4G0J3	La-related protein 7	LARP7	337	S	1	115.3	1.07	1.03	1.12	NaN	1.20	0.91	1.31	1.14	0.97
Q4G0J3	La-related protein 7	LARP7	261	S	1	144.3	0.88	0.89	NaN	1.31	NaN	NaN	NaN	0.94	NaN
Q4KMP7	TBC1 domain family member 10B	TBC1D10 B	678	S	1	59.25	1.24	1.19	1.37	1.07	NaN	1.14	NaN	1.20	1.22
Q4KMP7	TBC1 domain family member 10B	TBC1D10 B	132	S	1	120	NaN	0.38	0.96	0.64	0.87	0.65	NaN	1.19	1.21
Q4L180	Filamin A-interacting protein 1-like	FILIP1L	791	S	1	68.17	0.84	0.87	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Q4VCS5	Angiomotin	AMOT	4	S	1	61.17	0.83	NaN	0.87	0.70	0.78	0.74	0.90	0.94	NaN
Q4VCS5	Angiomotin	AMOT	9	S	0.691	61.17	0.83	NaN	0.87	0.70	0.78	0.74	0.90	0.94	NaN
Q52LW3	Rho GTPase-activating protein 29	ARHGAP 29	949	S	1	151.1	1.20	1.23	1.22	1.33	1.42	1.34	1.30	1.41	1.31
Q52LW3	Rho GTPase-activating protein 29	ARHGAP 29	589	S	0.999	132.1	NaN	NaN	NaN	NaN	0.49	0.88	0.46	0.79	0.79

Q52LW3	Rho GTPase-activating protein 29	ARHGAP29	1185	S	0.985	106.9	NaN	1.52	1.67	2.09	2.18	1.70	1.08	1.00	1.05
Q52LW3	Rho GTPase-activating protein 29	ARHGAP29	190	S	1	259.2	1.09	0.98	1.60	1.73	1.83	1.94	0.48	0.30	0.72
Q52LW3	Rho GTPase-activating protein 29	ARHGAP29	499	S	1	106.4	0.87	NaN	1.13	NaN	0.88	NaN	1.46	1.54	NaN
Q52LW3	Rho GTPase-activating protein 29	ARHGAP29	913	S	1	210.1	0.95	1.02	0.84	1.61	1.54	1.37	0.55	NaN	0.48
Q52LW3	Rho GTPase-activating protein 29	ARHGAP29	1029	S	1	142.1	NaN	1.05	1.01	1.31	1.33	1.34	0.92	0.93	0.94
Q52LW3	Rho GTPase-activating protein 29	ARHGAP29	171	S	1	161.9	NaN	NaN	0.72	0.70	0.63	NaN	1.10	1.28	1.34
Q52LW3	Rho GTPase-activating protein 29	ARHGAP29	559	S	0.976	173	0.60	NaN	0.67	0.96	0.87	0.88	0.68	0.74	NaN
Q5VZS7	Programmed cell death protein 4	PDCD4	80	S	0.752	155.2	0.76	0.75	NaN	NaN	NaN	0.87	NaN	NaN	1.08
Q53EZ4	Centrosomal protein of 55 kDa	CEP55	428	S	0.978	171	1.58	1.61	1.59	2.32	1.03	1.81	0.66	0.75	0.66
Q53EZ4	Centrosomal protein of 55 kDa	CEP55	425	S	1	171	1.68	1.65	2.04	2.32	2.70	2.77	0.76	NaN	0.86
Q53F19	Uncharacterized protein C17orf85	C17orf85	415	S	0.993	77.74	NaN	NaN	NaN	1.09	1.19	0.99	0.44	NaN	NaN
Q58WW2	DDB1- and CUL4-associated factor 6	DCAF6	657	S	0.999	76.2	0.61	0.62	0.62	NaN	NaN	NaN	NaN	NaN	NaN
Q5C9Z4	Nucleolar MIF4G domain-containing protein 1	NOM1	139	S	0.978	47.92	NaN	0.86	1.03	NaN	0.88	0.98	NaN	0.96	NaN
Q5H909	Melanoma-associated antigen D2	MAGED2	173	S	0.999	233.3	0.63	0.70	0.66	0.64	NaN	0.65	1.02	1.10	1.02
Q5JPT2	SH3 domain-containing kinase-binding protein 1	SH3KBP1	567	S	0.999	133.2	3.33	4.27	3.89	2.43	2.83	2.41	2.93	2.95	2.80
Q5JSH3	WD repeat-containing protein 44	WDR44	96	S	0.985	172.1	NaN	2.11	2.20	NaN	NaN	1.83	2.90	2.44	1.71
Q5JSH3	WD repeat-containing protein 44	WDR44	403	S	1	367	0.71	0.77	0.84	0.87	0.83	0.90	1.04	1.10	1.10
Q5JSH3	WD repeat-containing protein 44	WDR44	162	S	0.702	184	0.82	NaN	0.99	NaN	0.94	NaN	1.25	NaN	NaN
Q5JSH3	WD repeat-containing protein 44	WDR44	50	S	1	111.7	0.96	NaN	NaN	0.96	0.96	0.99	1.14	1.19	NaN
Q5JSZ5	Protein PRRC2B	PRRC2B	613	S	1	59.12	1.30	1.37	1.70	1.27	1.48	1.25	0.96	1.02	0.81
Q5JSZ5	Protein PRRC2B	PRRC2B	556	S	0.977	82.36	NaN	2.54	1.97	2.44	2.07	2.61	1.39	1.23	1.74
Q5JTD0	Tight junction-associated protein 1	TJAP1	300	S	1	281.5	0.86	0.89	0.85	0.94	0.97	0.92	0.80	0.96	0.92
Q5JTH9	RRP12-like protein	RRP12	1080	S	1	223.4	0.89	0.69	0.88	0.95	0.94	0.81	1.06	1.03	0.96
Q5M775	Cytospin-B	SPECC1	134	S	0.991	134.9	2.50	2.50	2.06	NaN	1.25	1.46	NaN	NaN	1.49
Q5M775	Cytospin-B	SPECC1	810	S	0.955	66.92	NaN	1.54	1.55	NaN	1.22	1.15	NaN	1.54	1.43
Q5S007	Leucine-rich repeat serine/threonine-protein kinase 2	LRRK2	954	S	0.998	72.73	NaN	NaN	NaN	1.05	1.10	NaN	NaN	1.13	NaN

Q5S007	Leucine-rich repeat serine/threonine-protein kinase 2	LRRK2	955	S	0.992	72.73	NaN	NaN	NaN	1.05	1.10	NaN	NaN	1.13	NaN
Q5SQI0	Alpha-tubulin N-acetyltransferase 1	ATAT1	276	S	1	71.22	NaN	NaN	NaN	0.61	0.68	0.41	0.98	0.72	NaN
Q5SRE5	Nucleoporin NUP188 homolog	NUP188	1709	S	0.966	68.49	1.39	1.37	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Q5STZ8	ATP-binding cassette sub-family F member 1	ABCF1	229	S	1	225.4	0.64	0.63	0.79	0.84	0.76	0.88	0.77	0.79	0.84
Q5STZ8	ATP-binding cassette sub-family F member 1	ABCF1	106	S	1	108	0.53	0.45	0.48	0.65	0.75	0.70	1.09	1.08	1.03
Q5STZ8	ATP-binding cassette sub-family F member 1	ABCF1	110	S	1	230.7	0.77	0.91	0.76	0.88	0.94	0.89	0.57	0.50	0.59
Q5STZ8	ATP-binding cassette sub-family F member 1	ABCF1	22	S	0.961	146.1	0.83	0.88	0.73	1.19	1.20	1.13	0.85	0.86	0.69
Q5T200	Zinc finger CCCH domain-containing protein 13	ZC3H13	198	S	1	93.62	0.81	0.89	NaN	1.05	0.95	NaN	NaN	0.87	0.97
Q5T200	Zinc finger CCCH domain-containing protein 13	ZC3H13	993	S	1	129.9	1.73	1.11	NaN	1.33	1.38	NaN	NaN	NaN	NaN
Q5T200	Zinc finger CCCH domain-containing protein 13	ZC3H13	265	S	1	78.99	0.82	0.84	0.91	0.82	0.88	1.04	0.81	0.98	0.75
Q5T200	Zinc finger CCCH domain-containing protein 13	ZC3H13	110	S	0.732	49.15	1.03	NaN	0.91	NaN	1.03	0.92	1.02	0.83	NaN
Q5T200	Zinc finger CCCH domain-containing protein 13	ZC3H13	77	S	1	56.87	0.73	NaN	NaN	0.74	0.85	NaN	NaN	NaN	NaN
Q5T2Z0	Proline/serine-rich coiled-coil protein 1	PSRC1	189	S	0.635	56.71	NaN	NaN	0.71	0.67	NaN	0.74	0.90	1.05	0.96
Q5T4S7	E3 ubiquitin-protein ligase UBR4	UBR4	619	S	0.911	124.4	NaN	NaN	NaN	1.14	1.08	1.30	1.06	1.12	0.96
Q5T4S7	E3 ubiquitin-protein ligase UBR4	UBR4	620	S	0.621	124.4	NaN	0.77	0.80	1.14	NaN	1.66	1.20	1.12	0.96
Q5T4S7	E3 ubiquitin-protein ligase UBR4	UBR4	178	S	0.978	77.24	1.25	1.35	1.67	0.48	NaN	NaN	0.77	NaN	NaN
Q5T4S7	E3 ubiquitin-protein ligase UBR4	UBR4	2719	S	0.983	131.5	1.02	NaN	0.98	NaN	0.96	0.95	0.95	0.94	0.99
Q5T4S7	E3 ubiquitin-protein ligase UBR4	UBR4	362	S	0.97	215.5	0.92	0.89	0.91	1.19	NaN	1.27	1.08	NaN	1.49
Q5T5P2	Sickle tail protein homolog	KIAA1217	1044	S	1	76.53	0.90	1.03	NaN	1.43	1.44	NaN	NaN	NaN	NaN
Q5T5U3	Rho GTPase-activating protein 21	ARHGAP 21	1504	S	0.94	56.71	NaN	1.00	0.77	1.07	NaN	0.86	NaN	0.75	NaN
Q5T5Y3	Calmodulin-regulated spectrin-associated protein 1	CAMSAP 1	563	S	1	81.43	NaN	1.33	1.63	1.00	1.14	1.13	1.37	1.24	NaN
Q5TBR0	Sialic acid synthase	NANS	83	S	0.994	91.32	1.04	0.77	0.81	0.91	0.77	1.17	1.14	0.95	0.98
Q5UIP0	Telomere-associated protein RIF1	RIF1	2393	S	0.998	75.65	0.75	0.65	0.68	0.93	0.94	0.77	0.55	0.77	NaN
Q5VSL9	Striatin-interacting protein 1	STRIP1	335	S	1	170.1	0.80	0.70	0.85	0.78	1.00	0.83	1.05	NaN	0.98

Q5VT52	Regulation of nuclear pre-mRNA domain-containing protein 2	RPRD2	374	S	1	193	0.87	1.00	1.23	1.23	1.07	1.34	0.88	0.91	NaN
Q5VT52	Regulation of nuclear pre-mRNA domain-containing protein 2	RPRD2	485	S	0.632	103.1	1.03	0.94	NaN	1.11	NaN	NaN	0.99	NaN	NaN
Q5VTR2	E3 ubiquitin-protein ligase BRE1A	RNF20	138	S	0.969	97.9	NaN	NaN	NaN	NaN	NaN	NaN	1.42	1.64	1.10
Q5VUA4	Zinc finger protein 318	ZNF318	173	S	1	73.77	0.61	0.59	NaN	0.71	0.72	NaN	NaN	0.57	NaN
Q5VUB5	Protein FAM171A1	FAM171A1	849	S	0.999	51.69	NaN	NaN	NaN	1.25	0.99	2.28	NaN	0.90	1.57
Q5VWV2	Partitioning defective 3	PARD3	792	S	1	47.62	0.69	NaN	NaN	NaN	NaN	NaN	0.72	0.68	0.64
Q5VWV2	Partitioning defective 3	PARD3	635	S	0.557	67.25	0.89	1.25	NaN	NaN	1.38	NaN	NaN	1.09	1.13
Q5VWV2	Partitioning defective 3	PARD3	638	S	0.526	58.95	0.89	1.25	NaN	NaN	NaN	NaN	1.03	NaN	1.13
Q5VY60	HAUS augmin-like complex subunit 6	HAUS6	416	S	0.997	106.4	NaN	NaN	1.28	NaN	1.56	2.65	1.08	1.51	0.96
Q5VZ89	DENN domain-containing protein 4C	DENND4C	1125	S	0.5	135.9	0.59	0.68	0.90	0.69	NaN	NaN	NaN	NaN	NaN
Q5VZ89	DENN domain-containing protein 4C	DENND4C	1126	S	0.5	135.9	0.59	0.68	0.90	0.69	NaN	NaN	NaN	NaN	NaN
Q5VZL5	Zinc finger MYM-type protein 4	ZMYM4	122	S	0.993	135.3	0.18	NaN	NaN	NaN	0.54	0.66	0.89	NaN	1.49
Q63ZY6	Putative methyltransferase NSUN5C	NSUN5P2	260	S	0.999	42.63	NaN	NaN	0.59	NaN	1.12	0.72	NaN	NaN	0.60
Q66K14	TBC1 domain family member 9B	TBC1D9B	435	S	0.956	128.2	1.04	0.92	0.92	1.06	0.65	1.14	1.26	1.17	1.43
Q66K14	TBC1 domain family member 9B	TBC1D9B	994	S	0.693	66.96	NaN	NaN	1.06	NaN	1.21	NaN	0.86	0.88	NaN
Q66K74	Microtubule-associated protein 1S;MAP1S heavy chain;MAP1S light chain	MAP1S	631	S	0.567	97.06	NaN	NaN	NaN	0.82	0.62	NaN	NaN	NaN	NaN
Q66K74	Microtubule-associated protein 1S;MAP1S heavy chain;MAP1S light chain	MAP1S	632	S	0.7	162	NaN	NaN	NaN	0.84	0.62	NaN	1.15	NaN	NaN
Q66K74	Microtubule-associated protein 1S;MAP1S heavy chain;MAP1S light chain	MAP1S	640	S	0.997	176	0.94	0.94	0.91	0.86	0.93	0.87	1.08	1.04	1.08
Q66K74	Microtubule-associated protein 1S;MAP1S heavy chain;MAP1S light chain	MAP1S	643	S	0.511	54.98	NaN	NaN	NaN	0.99	0.56	NaN	NaN	NaN	NaN
Q66K74	Microtubule-associated protein 1S;MAP1S heavy chain;MAP1S light chain	MAP1S	759	S	1	237.3	0.56	0.59	0.62	0.87	0.83	0.84	0.66	0.68	0.69
Q66K74	Microtubule-associated protein 1S;MAP1S heavy chain;MAP1S light chain	MAP1S	592	S	0.899	64.38	0.60	NaN	0.41	0.98	NaN	0.71	1.06	NaN	0.93

Q66K74	Microtubule-associated protein 1S;MAP1S heavy chain;MAP1S light chain	MAP1S	582	S	0.986	66.08	NaN	NaN	0.55	0.77	NaN	0.85	0.89	0.86	NaN
Q66K74	Microtubule-associated protein 1S;MAP1S heavy chain;MAP1S light chain	MAP1S	731	S	0.845	111.7	1.33	1.15	NaN	NaN	NaN	NaN	1.19	1.35	NaN
Q68CZ2	Tensin-3	TNS3	1154	S	1	65.74	0.65	0.90	NaN	NaN	1.25	1.21	0.55	0.80	0.71
Q68CZ2	Tensin-3	TNS3	690	S	0.937	169.8	0.85	NaN	NaN	0.92	0.97	0.87	NaN	NaN	NaN
Q68CZ2	Tensin-3	TNS3	660	S	0.995	148.3	0.74	0.84	0.81	1.20	1.32	1.44	0.62	0.57	0.58
Q68CZ2	Tensin-3	TNS3	776	S	0.972	60.1	1.11	0.87	NaN	NaN	1.60	NaN	NaN	NaN	NaN
Q68CZ2	Tensin-3	TNS3	1441	S	1	64.71	0.46	0.41	0.47	0.90	NaN	0.70	0.61	0.52	NaN
Q68DQ2	Very large A-kinase anchor protein	CRYBG3	1280	S	0.97	65.11	1.03	0.89	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Q68E01	Integrator complex subunit 3	INTS3	502	S	0.999	65.65	NaN	NaN	NaN	0.72	NaN	NaN	0.95	0.93	NaN
Q68EM7	Rho GTPase-activating protein 17	ARHGAP 17	575	S	1	208.1	0.57	0.62	NaN	0.71	0.75	0.90	NaN	NaN	0.79
Q68EM7	Rho GTPase-activating protein 17	ARHGAP 17	676	S	0.997	188.3	0.85	0.90	0.96	0.89	0.96	0.87	1.00	1.05	1.09
Q69YN4	Protein virilizer homolog	KIAA1429	133	S	0.544	67.31	1.03	0.95	1.01	0.95	NaN	NaN	NaN	NaN	NaN
Q69YN4	Protein virilizer homolog	KIAA1429	138	S	0.883	105.4	1.03	0.95	NaN	0.95	1.06	NaN	0.96	0.89	1.04
Q6GQQ9	OTU domain-containing protein 7B	OTUD7B	464	S	0.998	84.74	1.23	1.35	NaN	1.32	1.77	NaN	NaN	1.55	NaN
Q6GQQ9	OTU domain-containing protein 7B	OTUD7B	467	S	0.999	84.74	2.15	1.35	NaN	1.32	1.77	NaN	NaN	1.55	NaN
Q6IQ49	Protein SDE2 homolog	SDE2	278	S	0.651	90.13	1.27	1.08	NaN	1.15	NaN	0.92	0.97	0.99	NaN
Q6KC79	Nipped-B-like protein	NIPBL	350	S	0.627	124.7	1.07	0.83	1.24	1.99	2.13	NaN	0.84	NaN	NaN
Q6KC79	Nipped-B-like protein	NIPBL	2658	S	1	165.6	0.74	0.72	0.75	0.74	0.86	0.81	0.85	0.94	0.84
Q6KC79	Nipped-B-like protein	NIPBL	318	S	1	59.59	0.85	0.96	NaN	0.86	0.80	NaN	0.82	0.73	NaN
Q6NZI2	Polymerase I and transcript release factor	PTRF	202	S	1	183.7	1.10	1.07	1.08	NaN	0.98	1.04	1.19	NaN	NaN
Q6NZI2	Polymerase I and transcript release factor	PTRF	203	S	1	183.7	1.10	1.07	1.08	NaN	0.98	1.04	1.19	NaN	NaN
Q6NZI2	Polymerase I and transcript release factor	PTRF	365	S	1	200	1.38	1.31	1.18	0.95	0.83	1.04	1.00	0.86	0.96
Q6NZI2	Polymerase I and transcript release factor	PTRF	366	S	1	200	1.38	1.35	1.18	0.95	1.00	1.04	1.00	1.03	0.96
Q6NZI2	Polymerase I and transcript release factor	PTRF	379	S	0.991	173	0.76	0.69	NaN	0.58	NaN	NaN	0.74	0.72	NaN
Q6NZI2	Polymerase I and transcript release factor	PTRF	387	S	1	200	0.63	0.55	0.60	0.61	0.57	0.68	0.67	0.87	1.05
Q6NZI2	Polymerase I and transcript release factor	PTRF	389	S	1	200	0.63	0.55	0.60	0.61	0.57	0.68	0.67	0.87	1.05
Q6P2E9	Enhancer of mRNA-decapping protein 4	EDC4	879	S	0.998	161	1.47	1.67	1.01	1.02	NaN	0.86	1.45	NaN	NaN
Q6P2E9	Enhancer of mRNA-decapping protein 4	EDC4	723	S	0.981	139	1.49	NaN	0.85	NaN	1.93	1.55	1.19	1.40	1.51
Q6P597	Kinesin light chain 3	KLC3	502	S	0.994	94.51	1.04	0.91	NaN	NaN	NaN	1.04	NaN	1.07	NaN

Q6PD62	RNA polymerase-associated protein CTR9 homolog	CTR9	970	S	1	313.9	0.62	0.57	0.63	0.58	0.62	NaN	0.69	0.91	0.74
Q6PKG0	La-related protein 1	LARP1	90	S	1	99.79	NaN	NaN	1.09	NaN	0.92	NaN	NaN	1.05	0.52
Q6PKG0	La-related protein 1	LARP1	521	S	1	157	1.18	1.14	1.12	1.08	1.11	1.09	1.04	1.03	1.09
Q6PKG0	La-related protein 1	LARP1	546	S	0.5	209.6	3.14	3.44	NaN	NaN	NaN	2.28	2.55	NaN	NaN
Q6PKG0	La-related protein 1	LARP1	548	S	1	276	3.36	3.44	NaN	3.76	3.04	2.28	2.55	NaN	NaN
Q6PKG0	La-related protein 1	LARP1	627	S	0.983	78.92	NaN	NaN	NaN	NaN	NaN	NaN	2.14	2.38	NaN
Q6PKG0	La-related protein 1	LARP1	143	S	0.99	90.3	0.87	NaN	1.01	0.93	NaN	0.93	0.81	0.79	0.86
Q6PKG0	La-related protein 1	LARP1	774	S	1	109.1	NaN	NaN	2.66	2.32	2.39	2.48	2.23	2.17	2.48
Q6PKG0	La-related protein 1	LARP1	851	S	0.744	162.8	NaN	NaN	NaN	0.93	0.79	NaN	NaN	NaN	NaN
Q6QNY0	Biogenesis of lysosome-related organelles complex 1	BLOC1S3	65	S	1	128.9	1.15	1.16	1.25	1.09	1.11	NaN	1.09	1.11	1.16
Q6SPF0	Atherin	SAMD1	161	S	0.993	67.36	NaN	0.75	1.66	1.55	1.17	NaN	2.09	2.13	NaN
Q6UN15	Pre-mRNA 3'-end-processing factor FIP1	FIP1L1	259	S	0.976	108.7	1.29	1.31	1.21	1.96	2.09	1.88	NaN	NaN	0.91
Q6UN15	Pre-mRNA 3'-end-processing factor FIP1	FIP1L1	304	S	1	75.04	NaN	NaN	NaN	NaN	NaN	NaN	3.28	NaN	3.83
Q6UN15	Pre-mRNA 3'-end-processing factor FIP1	FIP1L1	492	S	1	128	0.89	0.94	0.93	0.92	0.86	0.90	1.03	1.01	0.96
Q6UN15	Pre-mRNA 3'-end-processing factor FIP1	FIP1L1	500	S	0.999	128	1.21	1.10	1.49	0.85	1.00	1.24	1.12	1.06	1.03
Q6VMQ6	Activating transcription factor 7-interacting protein 1	ATF7IP	557	S	0.5	41.3	NaN	NaN	NaN	NaN	0.96	1.12	0.91	0.88	NaN
Q6VMQ6	Activating transcription factor 7-interacting protein 1	ATF7IP	559	S	0.976	67.1	0.43	NaN	NaN	0.81	0.85	1.12	0.91	0.75	0.79
Q6VY07	Phosphofurin acidic cluster sorting protein 1	PACS1	495	S	0.917	112.6	2.53	2.16	1.71	NaN	NaN	NaN	1.38	NaN	1.50
Q6VY07	Phosphofurin acidic cluster sorting protein 1	PACS1	529	S	0.778	106.4	NaN	NaN	1.21	1.07	1.27	0.95	2.12	NaN	NaN
Q6VY07	Phosphofurin acidic cluster sorting protein 1	PACS1	534	S	0.95	106.4	1.01	0.43	0.74	1.07	1.27	0.95	1.13	NaN	1.73
Q6ZRP7	Sulfhydryl oxidase 2	QSOX2	578	S	0.854	342.2	1.01	0.95	0.78	0.88	0.78	0.87	0.99	0.80	1.06
Q6ZTN6	Ankyrin repeat domain-containing protein 13D	ANKRD13D	465	S	1	66.08	0.81	0.71	NaN	1.00	1.13	0.81	0.94	1.20	0.91
Q6ZUT6	Uncharacterized protein C15orf52	C15orf52	201	S	0.943	99.81	NaN	NaN	0.81	0.97	0.78	0.91	0.94	1.01	1.08
Q71RC2	La-related protein 4	LARP4	597	S	0.718	134.5	1.72	1.93	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Q71RC2	La-related protein 4	LARP4	583	S	0.979	158.7	1.23	1.28	1.28	1.44	1.44	1.50	0.82	0.75	0.82
Q71RC2	La-related protein 4	LARP4	722	S	1	81.24	2.13	1.94	NaN	NaN	1.70	1.43	0.93	1.25	1.06
Q7KZ85	Transcription elongation factor SPT6	SUPT6H	125	S	1	106	0.59	NaN	0.53	0.87	0.88	0.91	0.47	NaN	0.72
Q7L7X3	Serine/threonine-protein kinase TAO1	TAOK1	421	S	0.995	84.09	NaN	0.97	NaN	NaN	NaN	NaN	1.25	1.38	NaN
Q7L8J4	SH3 domain-binding protein 5-like	SH3BP5L	30	S	1	173	1.03	1.16	1.49	1.11	NaN	1.21	1.26	1.52	NaN
Q7LBC6	Lysine-specific demethylase	KDM3B	744	S	0.964	230.4	NaN	0.81	0.65	0.87	0.99	0.79	0.78	NaN	0.80

Q7RTP6	Protein-methionine sulfoxide oxidase MICAL3	MICAL3	1649	S	0.867	43.86	NaN	NaN	NaN	NaN	NaN	NaN	1.31	1.23	NaN
Q7Z333	Probable helicase senataxin	SETX	1017	S	1	127.3	NaN	NaN	NaN	NaN	NaN	NaN	1.12	0.95	NaN
Q7Z333	Probable helicase senataxin	SETX	1019	S	1	127.3	NaN	NaN	NaN	NaN	NaN	NaN	1.12	0.95	NaN
Q7Z3C6	Autophagy-related protein 9A	ATG9A	18	S	0.973	117.3	0.82	1.01	NaN	0.83	NaN	NaN	0.97	0.69	1.04
Q7Z3K3	Pogo transposable element with ZNF domain	POGZ	1338	S	0.838	63.3	NaN	0.73	1.37	NaN	NaN	1.07	NaN	NaN	NaN
Q7Z3K3	Pogo transposable element with ZNF domain	POGZ	425	S	0.969	112.3	0.62	0.48	0.50	0.72	0.67	0.65	0.83	0.76	0.79
Q7Z417	Nuclear fragile X mental retardation-interacting protein	NUFIP2	629	S	1	276.3	2.91	2.88	3.05	2.52	NaN	2.66	1.10	1.18	1.12
Q7Z417	Nuclear fragile X mental retardation-interacting protein	NUFIP2	212	S	1	253.3	2.51	3.41	3.11	2.38	2.14	2.14	1.69	1.74	1.64
Q7Z417	Nuclear fragile X mental retardation-interacting protein	NUFIP2	652	S	1	73.88	2.39	2.73	2.83	2.18	2.13	NaN	0.95	0.99	NaN
Q7Z417	Nuclear fragile X mental retardation-interacting protein	NUFIP2	572	S	0.98	90.86	1.73	1.84	1.90	2.05	1.94	1.82	0.90	1.17	NaN
Q7Z422	SUZ domain-containing protein 1	SZRD1	107	S	0.997	95.52	0.66	0.63	0.67	0.70	0.70	0.72	0.89	0.81	0.82
Q7Z422	SUZ domain-containing protein 1	SZRD1	39	S	0.997	175	NaN	0.67	NaN	0.80	0.72	NaN	0.83	0.74	NaN
Q7Z434	Mitochondrial antiviral-signaling protein	MAVS	152	S	0.988	124.5	1.37	0.94	1.88	2.10	1.91	1.98	0.51	NaN	0.79
Q7Z434	Mitochondrial antiviral-signaling protein	MAVS	165	S	0.989	156.9	1.47	1.08	1.33	1.51	1.44	1.43	0.66	0.69	0.77
Q7Z434	Mitochondrial antiviral-signaling protein	MAVS	222	S	0.981	106.7	2.71	2.55	2.26	NaN	3.00	NaN	1.63	NaN	1.50
Q7Z460	CLIP-associating protein 1	CLASP1	1091	S	0.99	120.5	NaN	1.41	1.51	1.31	1.77	1.63	1.19	1.26	1.65
Q7Z4V5	Hepatoma-derived growth factor-related protein 2	HDGFRP2	366	S	1	99.45	0.89	1.01	1.00	0.96	0.98	0.95	1.06	0.98	1.01
Q7Z4V5	Hepatoma-derived growth factor-related protein 2	HDGFRP2	369	S	1	99.45	0.89	1.01	1.00	0.96	0.98	0.95	1.06	0.98	1.01
Q7Z4V5	Hepatoma-derived growth factor-related protein 2	HDGFRP2	370	S	1	99.45	0.89	1.01	1.00	0.96	0.98	0.95	1.06	0.98	1.01
Q7Z4V5	Hepatoma-derived growth factor-related protein 2	HDGFRP2	664	S	1	113.8	1.57	1.54	1.53	1.43	1.45	1.66	1.57	1.85	1.53
Q7Z4V5	Hepatoma-derived growth factor-related protein 2	HDGFRP2	652	S	1	67.4	1.17	NaN	NaN	1.33	1.15	NaN	NaN	NaN	NaN
Q7Z4V5	Hepatoma-derived growth factor-related protein 2	HDGFRP2	230	S	0.999	54.31	NaN	NaN	0.45	0.66	0.67	0.64	NaN	0.44	0.58
Q7Z4V5	Hepatoma-derived growth factor-related protein 2	HDGFRP2	232	S	0.996	72.14	NaN	0.46	0.47	0.66	0.67	0.59	NaN	0.44	0.58
Q7Z4V5	Hepatoma-derived growth factor-related protein 2	HDGFRP2	234	S	0.982	72.14	NaN	0.46	0.47	0.66	0.64	0.59	NaN	0.43	0.58
Q7Z4V5	Hepatoma-derived growth factor-related protein 2	HDGFRP2	240	S	0.989	72.14	NaN	0.46	0.47	0.66	0.67	0.59	NaN	0.43	0.58

Q7Z5K2	Wings apart-like protein homolog	WAPAL	221	S	0.996	91.66	0.80	1.02	0.77	0.66	NaN	1.37	1.14	0.90	1.13
Q7Z5K2	Wings apart-like protein homolog	WAPAL	223	S	0.957	77.29	NaN	NaN	NaN	NaN	0.69	0.72	NaN	NaN	NaN
Q7Z5K2	Wings apart-like protein homolog	WAPAL	77	S	0.999	164.4	1.02	1.07	1.04	0.86	0.93	1.05	0.93	1.35	0.98
Q7Z5L9	Interferon regulatory factor 2-binding protein 2	IRF2BP2	360	S	1	143.6	0.52	0.49	0.58	0.50	0.42	0.50	0.83	0.94	0.96
Q7Z5L9	Interferon regulatory factor 2-binding protein 2	IRF2BP2	175	S	1	129.8	NaN	1.38	NaN	NaN	0.83	NaN	2.33	2.26	2.69
Q7Z5L9	Interferon regulatory factor 2-binding protein 2	IRF2BP2	457	S	0.969	77.36	0.49	0.47	NaN	NaN	NaN	0.40	0.56	0.64	0.80
Q7Z5L9	Interferon regulatory factor 2-binding protein 2	IRF2BP2	460	S	0.959	109.1	0.49	0.47	NaN	0.40	NaN	0.40	0.59	0.59	NaN
Q7Z6Z7	E3 ubiquitin-protein ligase HUWE1	HUWE1	3373	S	0.983	163.6	1.00	0.97	0.89	1.43	NaN	1.41	1.34	NaN	1.34
Q7Z6Z7	E3 ubiquitin-protein ligase HUWE1	HUWE1	1395	S	1	106.4	NaN	NaN	1.63	1.47	1.40	1.46	1.37	1.36	1.39
Q7Z6Z7	E3 ubiquitin-protein ligase HUWE1	HUWE1	2887	S	0.872	138.3	NaN	NaN	NaN	1.25	1.60	NaN	NaN	0.71	NaN
Q7Z6Z7	E3 ubiquitin-protein ligase HUWE1	HUWE1	3662	S	0.991	93.23	2.36	NaN	2.00	2.60	2.76	2.21	0.98	1.00	0.89
Q7Z6Z7	E3 ubiquitin-protein ligase HUWE1	HUWE1	3919	S	0.999	90.66	4.90	5.39	3.39	3.85	NaN	3.60	1.76	NaN	NaN
Q7Z6Z7	E3 ubiquitin-protein ligase HUWE1	HUWE1	2362	S	1	80.47	0.38	0.44	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Q7Z6Z7	E3 ubiquitin-protein ligase HUWE1	HUWE1	1907	S	1	216.5	1.12	1.11	1.17	1.05	1.03	1.07	1.14	1.08	1.11
Q7Z6Z7	E3 ubiquitin-protein ligase HUWE1	HUWE1	3816	S	0.997	153.9	0.81	0.76	0.73	1.16	1.04	1.04	0.56	NaN	0.54
Q7Z6Z7	E3 ubiquitin-protein ligase HUWE1	HUWE1	2918	S	0.915	120.3	NaN	1.03	1.03	NaN	1.35	1.40	1.02	1.08	1.23
Q86TB9	Protein PAT1 homolog 1	PATL1	179	S	0.995	97.46	1.01	1.37	NaN	NaN	NaN	0.90	NaN	0.98	1.12
Q86TB9	Protein PAT1 homolog 1	PATL1	184	S	1	88.28	1.29	1.37	NaN	NaN	NaN	NaN	NaN	1.37	NaN
Q86U06	Probable RNA-binding protein 23	RBM23	149	S	1	73.57	0.84	NaN	0.93	1.03	1.02	0.89	0.83	0.66	NaN
Q86U42	Polyadenylate-binding protein	PABPN1	95	S	0.955	73.24	1.52	1.26	1.38	1.20	1.05	1.43	1.57	NaN	1.10
Q86U42	Polyadenylate-binding protein	PABPN1	150	S	1	91.66	0.70	0.81	0.76	1.31	1.75	1.17	NaN	0.36	NaN
Q86U86	Protein polybromo-1	PBRM1	10	S	0.976	129.9	NaN	0.74	0.66	0.84	0.95	NaN	1.01	0.92	NaN
Q86U90	YrdC domain-containing protein, mitochondrial	YRDC	37	S	1	60.62	NaN	1.13	NaN	1.04	1.00	NaN	NaN	1.11	0.96
Q86UP2	Kinectin	KTN1	75	S	0.994	97.93	2.66	1.94	NaN	NaN	1.92	NaN	NaN	2.16	NaN
Q86UU0	B-cell CLL/lymphoma 9-like protein	BCL9L	21	S	1	100.2	2.49	NaN	2.64	NaN	NaN	0.65	NaN	0.97	1.11
Q86UU0	B-cell CLL/lymphoma 9-like protein	BCL9L	25	S	1	64.22	2.49	NaN	2.64	NaN	NaN	NaN	NaN	NaN	NaN

Q86UU1	Pleckstrin homology-like domain family B member 1	PHLDB1	518	S	0.838	97.35	3.37	2.96	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Q86UX6	Serine/threonine-protein kinase 32C	STK32C	18	S	0.979	112.3	0.59	0.72	NaN	0.69	0.70	NaN	0.78	0.94	NaN
Q86V15	Zinc finger protein castor homolog 1	CASZ1	1758	S	0.959	60.1	0.28	NaN	NaN	NaN	NaN	NaN	NaN	0.43	0.84
Q86V48	Leucine zipper protein 1	LUZP1	659	S	1	179.2	1.84	1.60	2.05	1.17	1.27	1.25	1.18	1.42	1.56
Q86V48	Leucine zipper protein 1	LUZP1	394	S	1	63.18	1.61	1.34	1.52	1.08	1.16	1.07	1.39	1.66	1.37
Q86VQ1	Glucocorticoid-induced transcript 1 protein	GLCCI1	105	S	0.983	147.5	NaN	NaN	0.45	0.57	0.55	NaN	0.82	0.87	NaN
Q86VQ1	Glucocorticoid-induced transcript 1 protein	GLCCI1	107	S	0.693	71.42	NaN	NaN	NaN	NaN	0.55	NaN	0.82	0.87	NaN
Q86VQ1	Glucocorticoid-induced transcript 1 protein	GLCCI1	223	S	1	86.29	0.66	0.46	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Q86VQ1	Glucocorticoid-induced transcript 1 protein	GLCCI1	303	S	1	56.77	NaN	NaN	NaN	0.62	NaN	NaN	0.70	0.74	0.70
Q86W56	Poly(ADP-ribose) glycohydrolase	PARG	130	S	0.776	66.64	NaN	NaN	1.14	NaN	1.21	1.03	NaN	1.03	NaN
Q86W56	Poly(ADP-ribose) glycohydrolase	PARG	137	S	0.704	57.77	0.94	1.01	NaN	NaN	NaN	NaN	1.05	NaN	1.17
Q86W56	Poly(ADP-ribose) glycohydrolase	PARG	448	S	1	74.79	NaN	0.75	NaN	0.99	0.89	NaN	NaN	NaN	NaN
Q86W92	Liprin-beta-1	PPFIBP1	466	S	0.938	51.77	1.81	1.87	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Q86WR7	Proline and serine-rich protein 2	PROSER2	179	S	1	99.5	1.89	2.10	2.01	0.92	0.94	0.91	1.97	2.03	1.97
Q86WR7	Proline and serine-rich protein 2	PROSER2	212	S	0.907	94.13	NaN	4.02	4.54	NaN	2.82	NaN	NaN	NaN	NaN
Q86WR7	Proline and serine-rich protein 2	PROSER2	43	S	0.959	86.11	NaN	5.29	3.40	NaN	NaN	NaN	3.73	NaN	NaN
Q86X95	Corepressor interacting with RBPJ 1	CIR1	202	S	1	204.9	1.33	1.50	0.83	0.99	0.92	0.80	1.13	0.95	0.98
Q86XP3	ATP-dependent RNA helicase DDX42	DDX42	109	S	1	272.3	0.77	0.87	0.86	0.99	1.10	NaN	NaN	NaN	NaN
Q86XP3	ATP-dependent RNA helicase DDX42	DDX42	111	S	1	272.3	0.77	0.87	0.86	0.99	1.10	NaN	NaN	NaN	NaN
Q86XP3	ATP-dependent RNA helicase DDX42	DDX42	185	S	1	341.6	0.64	0.68	0.71	0.80	0.88	0.76	0.60	0.59	0.65
Q86YD1	Prostate tumor-overexpressed gene 1 protein	PTOV1	34	S	0.96	78.15	0.98	1.29	NaN	NaN	NaN	1.03	NaN	NaN	NaN
Q86YP4	Transcriptional repressor p66-alpha	GATAD2A	100	S	1	123.4	0.70	0.64	1.30	0.74	1.13	NaN	0.77	0.76	1.26
Q86YP4	Transcriptional repressor p66-alpha	GATAD2A	107	S	1	113.8	NaN	1.17	1.17	1.12	1.13	NaN	1.19	1.21	1.26
Q86YP4	Transcriptional repressor p66-alpha	GATAD2A	113	S	0.668	78.66	NaN	0.55	1.17	NaN	NaN	NaN	NaN	NaN	NaN
Q86YP4	Transcriptional repressor p66-alpha	GATAD2A	114	S	0.952	123.4	NaN	1.17	NaN	0.74	1.13	NaN	1.19	0.74	1.26

Q86YS7	C2 domain-containing protein	C2CD5	295	S	0.851	49.36	NaN	NaN	NaN	0.94	0.65	NaN	NaN	NaN	NaN
Q86YV5	Tyrosine-protein kinase SgK223	SGK223	263	S	1	95.11	NaN	NaN	NaN	0.88	NaN	0.64	0.62	NaN	NaN
Q86YV5	Tyrosine-protein kinase SgK223	SGK223	148	S	0.874	112.9	0.54	0.81	NaN	1.21	1.05	1.11	NaN	NaN	0.45
Q8IU81	Interferon regulatory factor 2-binding protein 1	IRF2BP1	384	S	1	105.2	0.84	0.59	0.84	0.86	0.84	0.83	0.91	0.94	0.91
Q8IVF2	Protein AHNAK2	AHNAK2	294	S	0.883	125.1	NaN	1.40	1.30	2.21	NaN	NaN	1.51	1.71	3.12
Q8IVF2	Protein AHNAK2	AHNAK2	5175	S	1	96.02	NaN	0.53	NaN	0.43	0.63	NaN	0.80	0.83	NaN
Q8IWE2	Protein NOXP20	FAM114A1	196	S	0.972	76.2	1.09	NaN	1.25	NaN	NaN	NaN	1.98	NaN	NaN
Q8IWE2	Protein NOXP20	FAM114A1	120	S	0.991	94.8	0.80	NaN	NaN	1.16	1.18	NaN	NaN	NaN	NaN
Q8IWZ3	Ankyrin repeat and KH domain-containing protein 1	ANKHD1	93	S	0.925	154.4	0.83	0.70	NaN	0.68	0.86	1.13	0.87	0.71	0.59
Q8IWZ3	Ankyrin repeat and KH domain-containing protein 1	ANKHD1	95	S	0.994	154.4	0.83	0.70	NaN	0.68	0.81	1.13	0.87	0.71	0.59
Q8IY81	pre-rRNA processing protein FTSJ3	FTSJ3	335	S	1	219.2	1.15	1.12	1.14	NaN	0.66	0.92	1.30	1.04	1.15
Q8IY81	pre-rRNA processing protein FTSJ3	FTSJ3	336	S	1	219.2	1.15	1.12	1.14	NaN	0.66	0.92	1.30	1.04	1.15
Q8N1G2	Cap-specific mRNA (nucleoside-2'-O-)-methyltransferase 1	CMTR1	49	S	0.895	100.6	NaN	NaN	0.55	0.61	NaN	0.52	0.43	0.50	0.68
Q8N1G2	Cap-specific mRNA (nucleoside-2'-O-)-methyltransferase 1	CMTR1	51	S	0.988	133.3	NaN	0.98	0.59	0.38	NaN	0.69	0.75	0.50	0.88
Q8N1G2	Cap-specific mRNA (nucleoside-2'-O-)-methyltransferase 1	CMTR1	53	S	0.981	192.4	0.32	0.98	0.45	0.34	NaN	0.39	0.75	0.56	0.55
Q8N1G4	Leucine-rich repeat-containing protein 47	LRRC47	520	S	0.942	151.7	0.83	0.86	0.68	0.89	NaN	0.89	1.06	NaN	1.13
Q8N392	Rho GTPase-activating protein 18	ARHGAP18	64	S	0.692	145.2	NaN	NaN	NaN	NaN	NaN	NaN	NaN	1.08	1.57
Q8N392	Rho GTPase-activating protein 18	ARHGAP18	66	S	0.761	145.2	1.87	2.14	NaN	2.36	NaN	NaN	1.38	1.08	1.57
Q8N392	Rho GTPase-activating protein 18	ARHGAP18	69	S	0.986	133.4	1.87	2.14	NaN	2.36	NaN	NaN	1.38	1.08	1.57
Q8N3D4	EH domain-binding protein 1-like protein 1	EHBP1L1	285	S	0.5	152.3	NaN	NaN	0.98	1.15	1.13	1.03	0.96	0.83	0.82
Q8N3D4	EH domain-binding protein 1-like protein 1	EHBP1L1	964	S	1	65.8	NaN	0.75	NaN	1.14	1.04	0.99	1.00	0.89	0.96
Q8N3F8	MICAL-like protein 1	MICALL1	621	S	0.908	77.63	NaN	1.23	NaN	0.86	1.16	NaN	1.27	1.06	1.28
Q8N3V7	Synaptopodin	SYNPO	833	S	0.998	106.4	0.98	0.96	NaN	0.78	1.08	NaN	1.45	1.32	NaN
Q8N3V7	Synaptopodin	SYNPO	685	S	1	65.18	0.95	0.86	NaN	0.70	NaN	NaN	1.30	1.53	NaN
Q8N3X1	Formin-binding protein 4	FNBP4	116	S	0.927	51.46	NaN	NaN	NaN	0.98	0.98	NaN	1.35	1.28	NaN
Q8N3X1	Formin-binding protein 4	FNBP4	18	S	1	54.86	0.99	NaN	1.02	NaN	1.11	1.12	1.13	1.15	0.98

Q8N4X5	Actin filament-associated protein 1-like 2	AFAP1L2	640	S	0.999	66.91	NaN	NaN	NaN	0.59	NaN	NaN	1.30	1.31	1.79
Q8N4X5	Actin filament-associated protein 1-like 2	AFAP1L2	414	S	0.62	107.2	0.43	NaN	NaN	NaN	0.64	NaN	1.87	1.26	NaN
Q8N556	Actin filament-associated protein 1	AFAP1	264	S	0.594	167.1	NaN	NaN	1.42	NaN	1.36	1.59	0.87	NaN	0.96
Q8N556	Actin filament-associated protein 1	AFAP1	265	S	0.876	167.1	1.35	1.43	NaN	1.34	1.36	NaN	NaN	0.96	NaN
Q8N556	Actin filament-associated protein 1	AFAP1	665	S	0.978	101.4	0.20	1.50	1.12	1.38	NaN	NaN	1.11	NaN	NaN
Q8N556	Actin filament-associated protein 1	AFAP1	668	S	1	133	1.47	1.93	2.05	1.38	1.48	1.47	1.79	NaN	1.65
Q8N556	Actin filament-associated protein 1	AFAP1	679	S	0.919	111.4	NaN	NaN	NaN	0.47	0.43	NaN	NaN	NaN	NaN
Q8N6N3	UPF0690 protein C1orf52	C1orf52	158	S	1	261.5	1.22	1.26	1.18	1.14	1.16	1.14	1.00	0.89	0.97
Q8N8A6	ATP-dependent RNA helicase DDX51	DDX51	83	S	1	125.4	0.60	0.63	0.71	0.74	0.64	0.61	0.85	0.84	0.93
Q8N9M5	Transmembrane protein 102	TMEM102	246	S	1	52.73	NaN	NaN	2.37	1.92	2.04	NaN	1.12	1.25	1.74
Q8NAV1	Pre-mRNA-splicing factor 38A	PRPF38A	209	S	1	78.15	1.00	1.00	NaN	NaN	0.96	NaN	NaN	1.12	NaN
Q8NBN3	Transmembrane protein 87A	TMEM87A	540	S	1	145.1	1.37	1.62	1.11	1.17	1.38	0.87	1.11	0.84	1.28
Q8NC44	Protein FAM134A	FAM134A	281	S	0.966	118.3	NaN	0.99	0.95	NaN	2.01	1.01	1.32	NaN	1.65
Q8NC44	Protein FAM134A	FAM134A	283	S	0.769	118.3	NaN	NaN	0.95	NaN	NaN	NaN	NaN	1.34	1.65
Q8NC44	Protein FAM134A	FAM134A	385	S	1	266.4	1.20	1.15	1.15	1.28	2.06	1.23	1.18	1.18	1.17
Q8NC56	LEM domain-containing protein 2	LEMD2	134	S	1	81.64	NaN	2.20	NaN	NaN	1.86	10.75	NaN	2.41	NaN
Q8NC56	LEM domain-containing protein 2	LEMD2	138	S	1	131.1	0.81	0.83	0.87	0.81	0.90	0.84	0.64	0.68	0.71
Q8NC56	LEM domain-containing protein 2	LEMD2	139	S	1	81.64	0.86	0.88	0.82	0.81	0.90	0.82	0.64	0.68	0.71
Q8ND56	Protein LSM14 homolog A	LSM14A	216	S	1	56.6	1.17	1.12	1.23	1.09	1.13	1.06	NaN	1.02	1.08
Q8ND56	Protein LSM14 homolog A	LSM14A	192	S	0.986	116.1	1.24	NaN	1.25	1.28	1.24	1.21	0.91	0.94	0.85
Q8ND56	Protein LSM14 homolog A	LSM14A	182	S	0.896	110	1.38	1.30	NaN	1.09	NaN	1.25	1.26	NaN	1.37
Q8ND56	Protein LSM14 homolog A	LSM14A	183	S	0.942	116.8	1.16	1.23	1.33	1.25	1.10	1.12	1.47	1.18	1.45
Q8ND76	Cyclin-Y	CCNY	326	S	1	149.7	1.59	1.20	1.43	1.18	0.96	1.13	1.70	1.92	1.68
Q8NDI1	EH domain-binding protein 1	EHBP1	428	S	0.874	130.1	0.58	0.63	0.59	1.59	0.87	0.52	0.43	2.00	0.56
Q8NDI1	EH domain-binding protein 1	EHBP1	432	S	1	101.5	1.84	1.85	2.00	1.59	1.62	1.64	2.14	2.00	2.11
Q8NDI1	EH domain-binding protein 1	EHBP1	436	S	1	130.1	0.91	0.82	0.92	0.84	0.87	0.92	0.91	0.80	0.87
Q8NDI1	EH domain-binding protein 1	EHBP1	335	S	0.953	244.9	0.70	0.92	0.91	0.98	0.86	0.96	1.13	NaN	0.93
Q8NDI1	EH domain-binding protein 1	EHBP1	1058	S	1	98.9	NaN	0.80	1.06	1.67	1.36	1.19	1.81	1.65	1.06
Q8NDI1	EH domain-binding protein 1	EHBP1	751	S	1	67.93	1.21	1.17	1.28	1.28	1.26	1.28	1.05	1.02	1.05
Q8NDI1	EH domain-binding protein 1	EHBP1	759	S	0.962	58.7	NaN	NaN	2.16	2.11	2.35	2.04	0.93	1.00	NaN
Q8NDX6	Zinc finger protein 740	ZNF740	44	S	1	57.53	NaN	NaN	NaN	NaN	NaN	NaN	0.91	1.00	0.89
Q8NE01	Metal transporter CNNM3	CNNM3	700	S	0.983	77.49	1.39	1.20	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Q8NEF9	Serum response factor-binding protein 1	SRFBP1	203	S	0.956	85.36	1.68	NaN	1.62	NaN	1.56	NaN	1.21	0.82	NaN

Q8NFC6	Biorientation of chromosomes in cell division protein 1-like 1	BOD1L1	3029	S	1	64.19	NaN	0.79	0.93	0.83	0.89	0.91	1.13	NaN	NaN
Q8NFC6	Biorientation of chromosomes in cell division protein 1-like 1	BOD1L1	2986	S	1	274.6	0.68	0.79	0.86	NaN	NaN	0.72	0.52	0.92	0.77
Q8NFJ5	Retinoic acid-induced protein	GPRC5A	345	S	1	79.39	0.78	NaN	NaN	0.61	0.68	NaN	NaN	NaN	NaN
Q8NHG8	E3 ubiquitin-protein ligase ZNRF2	ZNRF2	135	S	1	50.11	1.27	1.17	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Q8NHV4	Protein NEDD1	NEDD1	516	S	0.99	93.22	0.67	0.53	NaN	NaN	0.70	NaN	NaN	1.01	1.39
Q8NI08	Nuclear receptor coactivator 7	NCOA7	211	S	0.82	130.5	NaN	0.94	0.67	NaN	NaN	NaN	NaN	1.10	0.90
Q8TAD8	Smad nuclear-interacting protein 1	SNIP1	35	S	1	103	0.90	NaN	1.15	0.93	0.95	0.88	1.02	0.99	1.01
Q8TAP8	Protein phosphatase 1 regulatory subunit 35	PPP1R35	52	S	0.98	82.34	NaN	2.04	1.85	1.40	1.27	NaN	1.56	1.51	NaN
Q8TB61	Adenosine 3'-phospho 5'-phosphosulfate transporter 1	SLC35B2	427	S	1	103	1.64	1.30	1.36	3.49	2.27	2.02	0.83	0.99	0.80
Q8TCJ2	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B	STT3B	498	S	1	199	1.06	1.01	0.94	0.79	0.76	0.96	0.81	0.67	1.12
Q8TCJ2	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B	STT3B	499	S	1	133.8	0.93	1.01	0.99	1.02	0.73	0.99	1.09	0.82	1.02
Q8TD16	Protein bicaudal D homolog 2	BICD2	582	S	1	43	1.06	1.04	1.08	0.97	0.98	1.12	1.08	1.10	1.08
Q8TD19	Serine/threonine-protein kinase Nek9	NEK9	868	S	0.5	127.2	1.54	1.56	1.45	1.81	NaN	1.89	0.95	1.04	0.94
Q8TD19	Serine/threonine-protein kinase Nek9	NEK9	869	S	0.619	127.2	1.43	1.56	1.45	1.81	NaN	1.89	0.95	1.04	0.94
Q8TDB6	E3 ubiquitin-protein ligase DTX3L	DTX3L	202	S	0.994	77.26	NaN	NaN	NaN	1.10	1.14	0.90	NaN	NaN	NaN
Q8TDD1	ATP-dependent RNA helicase DDX54	DDX54	782	S	1	180.7	NaN	NaN	1.87	1.44	1.62	1.34	NaN	1.21	1.11
Q8TDY2	RB1-inducible coiled-coil protein 1	RB1CC1	647	S	0.896	101.3	NaN	NaN	1.20	NaN	0.60	0.52	NaN	NaN	NaN
Q8TDY2	RB1-inducible coiled-coil protein 1	RB1CC1	237	S	0.862	75.89	0.43	0.59	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Q8TEA8	D-tyrosyl-tRNA(Tyr) deacylase 1	DTD1	194	S	0.751	182.2	1.49	NaN	NaN	1.38	NaN	1.13	NaN	1.91	1.38
Q8TEA8	D-tyrosyl-tRNA(Tyr) deacylase 1	DTD1	196	S	0.993	261.9	1.49	2.03	1.63	1.38	1.23	NaN	1.82	1.44	NaN
Q8TEA8	D-tyrosyl-tRNA(Tyr) deacylase 1	DTD1	197	S	1	372.7	1.49	1.82	1.79	1.38	1.40	1.48	1.39	1.89	1.93
Q8TF01	Arginine/serine-rich protein PNISR	PNISR	290	S	0.941	196.8	0.86	NaN	0.85	NaN	NaN	0.70	0.77	NaN	0.59
Q8WUA2	Peptidyl-prolyl cis-trans isomerase-like 4	PPIL4	178	S	0.97	235.1	NaN	1.63	1.26	1.25	1.02	1.02	1.09	NaN	NaN

Q8WUF5	RelA-associated inhibitor	PPP1R13L	567	S	0.973	49.89	NaN	NaN	NaN	NaN	NaN	NaN	0.85	1.03	NaN
Q8WUX9	Charged multivesicular body protein 7	CHMP7	417	S	1	163.2	1.41	1.28	1.40	NaN	0.81	1.46	NaN	NaN	NaN
Q8WVC0	RNA polymerase-associated protein LEO1	LEO1	171	S	1	97.3	0.64	0.66	NaN	0.99	NaN	NaN	NaN	0.80	NaN
Q8WVC0	RNA polymerase-associated protein LEO1	LEO1	179	S	1	97.3	0.64	0.66	NaN	0.99	NaN	NaN	NaN	0.80	NaN
Q8WVC0	RNA polymerase-associated protein LEO1	LEO1	630	S	0.93	106.9	0.85	0.89	0.83	1.07	0.83	0.68	0.98	1.01	0.94
Q8WVC0	RNA polymerase-associated protein LEO1	LEO1	294	S	1	121.8	0.67	1.18	NaN	1.13	0.49	1.00	0.79	1.53	1.04
Q8WVC0	RNA polymerase-associated protein LEO1	LEO1	296	S	1	121.8	1.10	1.18	NaN	1.13	1.03	1.00	1.42	1.53	1.12
Q8WVC0	RNA polymerase-associated protein LEO1	LEO1	300	S	0.99	121.8	0.67	1.18	NaN	1.13	0.49	1.00	0.79	1.53	1.04
Q8WVC0	RNA polymerase-associated protein LEO1	LEO1	658	S	1	212.3	0.94	0.98	0.82	0.98	0.88	0.87	1.08	1.03	1.00
Q8WVC0	RNA polymerase-associated protein LEO1	LEO1	197	S	1	56.47	0.68	0.46	NaN	NaN	NaN	NaN	0.66	NaN	NaN
Q8WW12	PEST proteolytic signal-containing nuclear protein	PCNP	119	S	1	178.9	1.15	1.16	1.05	0.99	1.12	1.06	0.73	0.72	0.93
Q8WWM7	Ataxin-2-like protein	ATXN2L	594	S	0.992	278.3	1.14	0.97	0.98	1.23	1.37	1.19	0.55	0.50	0.50
Q8WWM7	Ataxin-2-like protein	ATXN2L	111	S	1	138.7	2.34	2.58	2.31	2.09	2.01	1.99	0.95	0.93	0.92
Q8WWM7	Ataxin-2-like protein	ATXN2L	449	S	1	68.89	2.18	2.09	2.17	2.25	2.02	2.18	1.17	1.19	1.23
Q8WWM7	Ataxin-2-like protein	ATXN2L	339	S	0.987	85.47	3.00	3.50	3.73	NaN	NaN	NaN	NaN	2.80	4.07
Q8WWM7	Ataxin-2-like protein	ATXN2L	634	S	0.977	124	0.92	0.99	0.79	0.96	0.95	1.04	0.93	0.90	0.92
Q8WWQ0	PH-interacting protein	PHIP	1281	S	1	96.53	1.45	NaN	0.85	0.78	0.46	0.83	0.85	0.88	0.88
Q8WWQ0	PH-interacting protein	PHIP	1283	S	1	96.53	1.45	NaN	0.85	0.78	0.46	0.83	0.85	0.88	0.88
Q8WWQ0	PH-interacting protein	PHIP	1783	S	1	253.1	1.16	1.04	1.22	1.30	1.03	1.25	0.98	0.95	1.02
Q8WX92	Negative elongation factor B	NELFB	557	S	0.999	125.6	0.81	0.89	0.84	NaN	0.99	0.75	1.17	NaN	0.94
Q8WX93	Palladin	PALLD	893	S	1	176.3	1.00	NaN	0.98	1.59	1.52	1.63	1.34	1.35	1.46
Q8WX93	Palladin	PALLD	1118	S	1	117.3	0.56	0.43	NaN	0.53	1.51	0.61	0.54	1.96	0.49
Q8WX93	Palladin	PALLD	1121	S	1	214.3	0.55	0.53	0.51	0.58	0.64	0.55	0.62	0.55	0.49
Q8WX93	Palladin	PALLD	1116	S	1	117.3	1.57	1.49	NaN	1.52	1.51	1.55	1.90	1.96	1.94
Q8WXH0	Nesprin-2	SYNE2	6361	S	0.99	108.7	0.65	0.63	0.85	1.14	1.12	1.12	NaN	0.78	0.78
Q8WYL5	Protein phosphatase Slingshot homolog 1	SSH1	897	S	0.962	92.41	NaN	NaN	1.24	NaN	NaN	NaN	NaN	0.98	1.18
Q8WYP5	Protein ELYS	AHCTF1	528	S	1	78.69	1.16	0.87	NaN	1.65	1.99	NaN	NaN	NaN	NaN
Q8WYP5	Protein ELYS	AHCTF1	1944	S	0.986	54.54	0.48	NaN	0.52	0.53	NaN	NaN	0.56	NaN	0.76
Q8WYP5	Protein ELYS	AHCTF1	1222	S	0.924	94.38	NaN	NaN	NaN	NaN	1.66	1.99	1.75	1.38	NaN
Q8WYQ5	Microprocessor complex subunit DGCR8	DGCR8	377	S	0.982	98.84	2.76	2.19	2.45	NaN	2.50	2.38	0.67	1.01	0.96
Q8WYQ5	Microprocessor complex subunit DGCR8	DGCR8	275	S	0.995	74.28	NaN	NaN	NaN	1.63	1.81	NaN	NaN	NaN	NaN
Q92508	Piezo-type mechanosensitive ion channel component 1	PIEZO1	1621	S	0.999	177.4	NaN	0.74	0.90	0.68	NaN	NaN	0.99	0.99	1.25

Q92522	Histone H1x	H1FX	31	S	0.98	83.53	0.65	NaN	0.59	1.22	1.24	1.03	NaN	0.61	NaN
Q92538	Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	GBF1	1780	S	0.83	44.83	NaN	NaN	NaN	NaN	NaN	NaN	10.22	4.30	NaN
Q92538	Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	GBF1	1784	S	0.918	44.83	NaN	NaN	NaN	NaN	NaN	NaN	10.22	4.30	NaN
Q92538	Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	GBF1	1298	S	1	350.1	1.12	1.28	1.28	1.13	1.12	1.51	1.91	1.87	1.67
Q92538	Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	GBF1	1318	S	0.994	130.3	1.60	1.70	1.52	1.55	1.52	1.53	2.48	2.44	2.36
Q92538	Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	GBF1	1773	S	1	144.2	1.22	1.37	2.85	2.90	NaN	2.49	NaN	NaN	1.04
Q92576	PHD finger protein 3	PHF3	1133	S	1	84.3	NaN	0.55	0.62	0.95	1.06	1.13	0.57	NaN	0.62
Q92576	PHD finger protein 3	PHF3	1642	S	1	44.72	0.90	0.76	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Q92614	Unconventional myosin-XVIIIa	MYO18A	1998	S	1	72.82	0.61	0.59	NaN	0.75	NaN	0.71	NaN	NaN	0.60
Q92614	Unconventional myosin-XVIIIa	MYO18A	102	S	0.905	77.44	1.01	0.69	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Q92614	Unconventional myosin-XVIIIa	MYO18A	1942	S	1	123.4	NaN	NaN	NaN	0.69	0.78	1.05	NaN	NaN	NaN
Q92614	Unconventional myosin-XVIIIa	MYO18A	1970	S	1	91.1	0.75	0.74	NaN	0.97	1.51	NaN	NaN	NaN	NaN
Q92614	Unconventional myosin-XVIIIa	MYO18A	2020	S	1	184.4	0.97	0.97	0.95	1.03	1.07	0.88	1.01	1.03	0.92
Q92614	Unconventional myosin-XVIIIa	MYO18A	2007	S	0.999	115.8	NaN	0.78	0.62	0.75	0.73	0.76	0.61	0.60	0.54
Q92614	Unconventional myosin-XVIIIa	MYO18A	2041	S	1	185	0.94	0.71	0.93	0.86	0.92	0.90	1.02	0.93	0.84
Q92614	Unconventional myosin-XVIIIa	MYO18A	2043	S	0.993	145.7	1.03	0.96	0.88	0.89	0.85	0.90	0.99	0.80	0.92
Q92619	Minor histocompatibility protein HA-1;Minor histocompatibility antigen HA-	HMHA1	23	S	0.996	103.7	NaN	4.72	1.35	1.04	1.09	0.88	1.68	1.75	1.44
Q92667	A-kinase anchor protein 1, mitochondrial	AKAP1	150	S	0.699	139.5	1.36	1.37	NaN	2.07	2.04	NaN	NaN	NaN	NaN
Q92667	A-kinase anchor protein 1, mitochondrial	AKAP1	151	S	0.5	122.5	1.36	NaN	NaN	2.07	2.04	NaN	NaN	NaN	NaN
Q92733	Proline-rich protein PRCC	PRCC	157	S	1	104.8	1.01	1.04	NaN	0.98	1.02	1.00	1.05	0.92	1.03
Q92733	Proline-rich protein PRCC	PRCC	159	S	1	104.8	1.01	1.04	NaN	0.98	1.02	1.00	1.05	0.92	1.03
Q92733	Proline-rich protein PRCC	PRCC	267	S	1	128.7	0.76	0.73	0.66	0.63	0.68	0.72	0.59	0.66	0.62
X6RAB3	USP6 N-terminal-like protein	USP6NL	739	S	0.948	83.88	1.62	1.41	1.28	1.42	1.40	NaN	1.53	NaN	1.17
Q92769	Histone deacetylase 2	HDAC2	422	S	1	171.3	0.47	NaN	0.46	NaN	0.53	0.48	NaN	0.45	NaN
Q92769	Histone deacetylase 2	HDAC2	394	S	1	243.5	0.53	0.53	NaN	0.71	1.39	NaN	0.47	0.37	0.31
Q92797	Symplekin	SYMPK	1171	S	0.895	76.97	NaN	0.91	NaN	NaN	1.05	NaN	1.27	NaN	1.76
Q92797	Symplekin	SYMPK	1259	S	1	120.7	0.67	0.85	0.62	1.11	NaN	1.07	0.78	0.67	0.84
Q92882	Osteoclast-stimulating factor 1	OSTF1	213	S	1	281.5	0.92	0.94	0.92	0.82	0.86	0.86	1.03	1.01	0.98
Q92917	G patch domain and KOW motifs-containing protein	GPKOW	42	S	0.999	62.1	1.49	1.65	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Q92922	SWI/SNF complex subunit SMARCC1	SMARCC1	328	S	1	101.2	0.90	0.97	0.93	NaN	1.16	NaN	1.01	1.02	1.23

Q92922	SWI/SNF complex subunit SMARCC1	SMARCC1	330	S	1	101.2	0.90	0.97	0.93	NaN	1.16	NaN	1.01	1.02	1.23
V9GYM8	Rho guanine nucleotide exchange factor 2	ARHGEF2	741	S	1	111.2	NaN	NaN	NaN	1.21	1.42	1.30	0.84	0.90	1.05
V9GYM8	Rho guanine nucleotide exchange factor 2	ARHGEF2	977	S	1	139.9	0.78	0.72	0.61	0.85	0.76	0.81	0.92	0.89	NaN
V9GYM8	Rho guanine nucleotide exchange factor 2	ARHGEF2	1005	S	0.988	70.18	NaN	1.05	0.90	NaN	0.87	1.12	NaN	0.91	1.00
V9GYM8	Rho guanine nucleotide exchange factor 2	ARHGEF2	690	S	0.99	76.28	5.38	5.97	5.34	4.20	4.83	NaN	NaN	NaN	NaN
Q93008	Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	2563	S	0.997	70.7	NaN	NaN	0.81	1.54	1.66	NaN	0.88	0.96	NaN
Q969E4	Transcription elongation factor A protein-like 3	TCEAL3	65	S	1	242.2	1.32	1.25	1.21	1.04	1.17	1.09	1.26	1.32	1.11
Q969E4	Transcription elongation factor A protein-like 3;Transcription elongation factor A protein-like 6;Transcription elongation factor A protein-like 5	TCEAL3	121	S	1	276	0.80	0.80	0.89	1.11	1.06	1.15	1.16	1.26	1.14
Q969E4	Transcription elongation factor A protein-like 3;Transcription elongation factor A protein-like 6;Transcription elongation factor A protein-like 5	TCEAL3	125	S	1	130.7	2.49	2.01	NaN	NaN	NaN	NaN	2.80	2.25	NaN
Q969S3	Zinc finger protein 622	ZNF622	141	S	0.794	80.69	NaN	1.11	1.05	1.61	1.65	1.66	NaN	0.49	0.43
Q969S3	Zinc finger protein 622	ZNF622	143	S	0.76	71.35	1.12	NaN	1.05	NaN	NaN	NaN	0.51	NaN	NaN
Q96AE4	Far upstream element-binding protein 1	FUBP1	630	S	0.906	109.9	1.03	NaN	NaN	1.44	1.49	NaN	NaN	NaN	NaN
Q96AT1	Uncharacterized protein KIAA1143	KIAA1143	50	S	1	178.9	0.67	0.77	0.63	0.74	0.68	0.76	0.76	0.81	0.80
Q96B36	Proline-rich AKT1 substrate 1	AKT1S1	88	S	0.994	119.7	1.17	NaN	1.10	1.30	1.14	1.11	NaN	NaN	1.00
Q96B36	Proline-rich AKT1 substrate 1	AKT1S1	92	S	0.879	119.7	1.36	NaN	1.07	1.30	1.14	1.11	NaN	NaN	NaN
Q96B36	Proline-rich AKT1 substrate 1	AKT1S1	203	S	0.999	221.9	1.03	0.90	1.12	0.98	0.93	0.93	1.21	1.33	1.14
Q96B36	Proline-rich AKT1 substrate 1	AKT1S1	211	S	0.839	211.1	1.05	0.99	1.03	NaN	0.96	0.96	1.21	1.33	NaN
Q96B36	Proline-rich AKT1 substrate 1	AKT1S1	212	S	0.9	229.8	0.93	0.90	1.22	0.98	0.99	0.90	NaN	1.22	1.14
Q96C19	EF-hand domain-containing protein D2	EFHD2	74	S	0.959	126	3.70	3.35	3.21	2.32	2.48	3.22	NaN	1.92	NaN
Q96C19	EF-hand domain-containing protein D2	EFHD2	76	S	0.5	65.44	NaN	NaN	NaN	2.64	3.39	NaN	NaN	NaN	NaN
Q96C90	Protein phosphatase 1 regulatory subunit 14B	PPP1R14B	32	S	1	76.82	5.00	3.75	NaN	4.39	3.29	NaN	NaN	NaN	NaN
Q96CW6	Probable RNA polymerase II nuclear localization protein SLC7A6OS	SLC7A6OS	308	S	1	178.4	0.70	0.56	0.66	0.96	0.98	0.87	0.71	0.70	0.75
Q96CX2	BTB/POZ domain-containing protein KCTD12	KCTD12	176	S	0.807	137.5	0.91	0.98	0.88	NaN	1.40	1.19	NaN	NaN	NaN

Q96CX2	BTB/POZ domain-containing protein KCTD12	KCTD12	185	S	0.887	105.7	NaN	0.91	0.76	0.96	0.90	1.12	0.78	0.72	1.07
Q96CX2	BTB/POZ domain-containing protein KCTD12	KCTD12	187	S	0.54	97.49	0.94	0.91	NaN	NaN	0.90	1.12	NaN	NaN	NaN
Q96E09	Protein FAM122A	FAM122A	270	S	0.942	87.2	0.81	0.96	NaN	0.91	0.81	1.00	1.21	1.20	1.30
Q96EB6	NAD-dependent protein deacetylase sirtuin-1;SirtT1 75 kDa fragment	SIRT1	27	S	0.936	97.96	NaN	NaN	0.84	0.89	NaN	1.25	1.22	1.13	1.17
Q96EU6	Ribosomal RNA processing protein 36 homolog	RRP36	73	S	1	88.19	1.19	0.98	0.78	1.14	1.12	1.15	0.58	0.55	NaN
Q96EV2	RNA-binding protein 33	RBM33	41	S	1	139.7	2.02	2.02	NaN	NaN	NaN	NaN	2.35	2.07	0.76
Q96EV2	RNA-binding protein 33	RBM33	205	S	1	248.7	0.85	1.13	1.03	0.99	1.02	1.00	0.94	0.95	1.02
Q96EV2	RNA-binding protein 33	RBM33	765	S	1	79.99	NaN	0.81	0.83	1.00	0.91	0.95	0.76	0.86	0.82
Q96G46	tRNA-dihydrouridine(47) synthase [NAD(P)(+)]-like	DUS3L	276	S	0.629	101	NaN	NaN	NaN	0.94	0.65	NaN	NaN	1.32	1.16
Q96GM8	Target of EGR1 protein 1	TOE1	5	S	1	241.9	0.69	0.62	NaN	NaN	NaN	0.69	0.69	NaN	0.89
S4R3D6	Methylthioribulose-1-phosphate dehydratase	APIP	40	S	0.974	114.7	1.02	1.11	1.18	0.97	1.01	1.06	1.17	0.86	1.08
Q96HR8	H/ACA ribonucleoprotein complex non-core subunit	NAF1	315	S	1	94	0.96	1.14	1.14	1.25	1.18	1.45	1.00	1.11	1.07
Q96I25	Splicing factor 45	RBM17	222	S	0.859	179.7	0.70	0.57	0.69	NaN	NaN	0.88	0.61	NaN	NaN
Q96I25	Splicing factor 45	RBM17	155	S	1	188.3	0.99	1.01	0.90	0.92	0.93	1.04	1.06	1.03	0.82
Q96IF1	LIM domain-containing protein ajuba	AJUBA	119	S	1	144.6	NaN	1.68	1.49	1.49	1.54	NaN	1.12	1.08	NaN
Q96IF1	LIM domain-containing protein ajuba	AJUBA	137	S	0.999	401.3	1.47	1.15	NaN	1.13	1.07	0.83	0.84	0.73	0.70
Q96JM3	Chromosome alignment-maintaining phosphoprotein 1	CHAMP1	416	S	1	85.81	1.03	0.87	1.13	NaN	NaN	1.58	1.04	0.97	NaN
Q96JM3	Chromosome alignment-maintaining phosphoprotein 1	CHAMP1	476	S	1	135.6	0.84	0.88	0.86	0.95	1.04	1.08	1.09	1.03	1.17
Q96JM3	Chromosome alignment-maintaining phosphoprotein 1	CHAMP1	651	S	0.911	106.9	NaN	0.70	0.80	0.82	0.68	0.82	0.91	1.06	0.72
Q96JM3	Chromosome alignment-maintaining phosphoprotein 1	CHAMP1	652	S	0.787	73.68	NaN	NaN	NaN	NaN	0.68	0.82	0.91	1.06	0.72
Q96JM3	Chromosome alignment-maintaining phosphoprotein 1	CHAMP1	653	S	0.818	106.9	NaN	0.70	0.80	0.82	0.68	NaN	NaN	NaN	0.72
Q96JM3	Chromosome alignment-maintaining phosphoprotein 1	CHAMP1	427	S	1	58.78	1.53	NaN	1.54	1.99	2.21	1.76	0.82	1.78	1.30
Q96JM3	Chromosome alignment-maintaining phosphoprotein 1	CHAMP1	432	S	1	58.78	1.53	NaN	1.54	1.99	2.21	1.76	NaN	1.78	1.78
Q96JM3	Chromosome alignment-maintaining phosphoprotein 1	CHAMP1	436	S	1	58.78	1.53	NaN	1.54	1.99	2.21	1.76	NaN	1.78	1.78
Q96JM3	Chromosome alignment-maintaining phosphoprotein 1	CHAMP1	443	S	0.737	56.47	NaN	NaN	NaN	0.98	0.96	0.88	1.04	0.91	NaN
Q96JM3	Chromosome alignment-maintaining phosphoprotein 1	CHAMP1	445	S	0.598	83.25	0.46	0.58	NaN	0.98	0.96	0.88	0.59	NaN	0.40

Q96JM3	Chromosome alignment-maintaining phosphoprotein 1	CHAMP1	452	S	1	83.25	0.46	0.58	NaN	1.10	0.94	0.88	0.59	NaN	0.40
Q96JM3	Chromosome alignment-maintaining phosphoprotein 1	CHAMP1	282	S	0.983	86.3	0.44	0.92	0.53	0.48	NaN	0.46	0.86	0.87	1.24
Q96JM3	Chromosome alignment-maintaining phosphoprotein 1	CHAMP1	405	S	0.993	79.35	1.19	0.71	NaN	0.96	1.13	0.92	0.49	0.58	0.81
Q96JM3	Chromosome alignment-maintaining phosphoprotein 1	CHAMP1	204	S	1	115.1	0.59	0.64	0.63	0.75	0.75	0.64	0.81	0.90	0.84
Q96JM3	Chromosome alignment-maintaining phosphoprotein 1	CHAMP1	214	S	0.996	115.1	0.77	0.60	0.68	0.98	0.99	0.91	0.85	0.82	0.83
Q96JM3	Chromosome alignment-maintaining phosphoprotein 1	CHAMP1	382	S	0.715	69.47	NaN	NaN	1.29	2.05	1.73	NaN	1.17	1.22	NaN
Q96JM3	Chromosome alignment-maintaining phosphoprotein 1	CHAMP1	386	S	0.964	69.47	NaN	NaN	1.29	2.05	1.73	NaN	1.17	1.22	NaN
Q96JM3	Chromosome alignment-maintaining phosphoprotein 1	CHAMP1	275	S	0.993	114.2	0.70	NaN	NaN	NaN	NaN	NaN	1.06	NaN	0.79
Q96K76	Ubiquitin carboxyl-terminal hydrolase 47	USP47	910	S	1	220.1	1.09	NaN	NaN	NaN	NaN	NaN	0.72	1.07	NaN
Q96KR1	Zinc finger RNA-binding	ZFR	1054	S	1	115.6	1.07	0.99	1.05	0.91	0.98	0.95	1.14	1.17	1.51
Q96N66	Lysophospholipid acyltransferase 7	MBOAT7	284	S	0.933	157.4	1.00	0.99	1.21	1.74	1.69	1.67	1.00	0.92	NaN
Q96N66	Lysophospholipid acyltransferase 7	MBOAT7	285	S	0.529	76.03	1.09	NaN	1.21	1.59	NaN	1.55	1.00	0.92	NaN
Q96N67	Dedicator of cytokinesis protein 7	DOCK7	900	S	0.998	268.4	0.89	NaN	1.04	1.18	1.44	NaN	3.18	NaN	NaN
Q96N67	Dedicator of cytokinesis protein 7	DOCK7	910	S	0.873	207	NaN	NaN	1.04	1.18	0.98	NaN	3.18	0.88	NaN
Q96NE9	FERM domain-containing protein 6	FRMD6	522	S	0.997	151.6	NaN	NaN	1.82	1.13	1.10	NaN	NaN	2.94	2.65
Q96NE9	FERM domain-containing protein 6	FRMD6	544	S	1	127.2	2.31	1.98	NaN	1.17	1.12	1.30	2.06	2.40	1.91
Q96NY7	Chloride intracellular channel protein 6	CLIC6	293	S	1	156.2	2.04	2.11	1.92	0.99	1.68	NaN	NaN	1.20	NaN
Q96NY7	Chloride intracellular channel protein 6	CLIC6	305	S	0.999	156.2	2.04	2.11	1.92	1.96	1.68	NaN	NaN	1.20	NaN
Q96P48	Arf-GAP with Rho-GAP domain, ANK repeat and PH domain-containing protein 1	ARAP1	229	S	1	102.6	0.76	0.63	0.59	0.77	0.71	NaN	1.36	1.33	1.30
Q96PK6	RNA-binding protein 14	RBM14	215	S	1	68.17	1.41	NaN	1.24	1.09	1.19	1.19	1.30	1.27	1.25
Q96PK6	RNA-binding protein 14	RBM14	220	S	1	68.17	1.41	NaN	1.24	1.09	1.19	1.19	1.30	1.27	1.25
Q96PX8	SLIT and NTRK-like protein 1	SLITRK1	586	S	0.986	79.04	NaN	NaN	1.05	0.91	0.70	NaN	1.17	1.14	NaN
Q96QB1	Rho GTPase-activating protein 7	DLC1	523	S	1	91.73	1.42	NaN	2.02	1.04	1.10	NaN	1.88	1.76	2.03
Q96QB1	Rho GTPase-activating protein 7	DLC1	526	S	1	180.7	1.42	NaN	2.02	1.04	1.10	NaN	1.88	1.76	2.03

Q96QC0	Serine/threonine-protein phosphatase 1 regulatory subunit 10	PPP1R10	545	S	0.93	88.72	0.40	0.59	NaN	NaN	0.96	0.95	0.49	NaN	NaN
Q96QC0	Serine/threonine-protein phosphatase 1 regulatory subunit 10	PPP1R10	313	S	0.997	78.92	1.74	2.44	2.34	1.99	1.93	2.23	1.46	1.55	NaN
Q96QR8	Transcriptional activator protein Pur-beta	PURB	304	S	1	165.2	1.36	1.43	1.59	1.22	1.17	1.33	1.38	1.51	1.61
Q96RL1	BRCA1-A complex subunit RAP80	UIMC1	677	S	1	57.2	NaN	NaN	NaN	NaN	1.27	1.14	1.21	NaN	1.42
Q96RT1	Protein LAP2	ERBB2IP	852	S	0.877	68.36	1.07	NaN	NaN	NaN	0.60	NaN	1.35	0.97	NaN
Q96RT1	Protein LAP2	ERBB2IP	857	S	1	97.45	1.18	0.27	NaN	1.44	1.56	0.95	1.02	NaN	1.07
Q96RU3	Formin-binding protein 1	FNBP1	359	S	0.999	94.73	0.74	0.73	0.66	0.79	0.80	0.74	0.74	0.75	0.71
Q96S55	ATPase WRNIP1	WRNIP1	65	S	1	78.52	NaN	NaN	0.73	0.80	0.85	0.87	0.88	0.85	0.82
Q96S94	Cyclin-L2	CCNL2	369	S	1	70.52	NaN	NaN	1.08	NaN	NaN	NaN	1.08	0.99	NaN
Q96S94	Cyclin-L2	CCNL2	348	S	0.933	40.73	NaN	NaN	0.92	NaN	0.78	NaN	1.02	1.15	NaN
Q96ST2	Protein IWS1 homolog	IWS1	398	S	1	105.5	0.96	1.01	0.97	0.94	0.93	0.99	1.09	1.11	1.15
Q96ST2	Protein IWS1 homolog	IWS1	400	S	1	105.5	0.96	1.01	0.97	0.94	0.93	0.99	1.09	1.11	1.15
Q96ST2	Protein IWS1 homolog	IWS1	511	S	1	127.1	0.74	0.87	0.89	0.93	0.89	1.14	0.97	1.00	1.45
Q96ST2	Protein IWS1 homolog	IWS1	513	S	1	127.1	0.74	0.87	0.89	0.93	0.89	1.14	0.97	1.00	1.45
Q96ST2	Protein IWS1 homolog	IWS1	235	S	1	52.27	NaN	NaN	NaN	NaN	0.89	0.88	1.21	1.00	1.17
Q96ST2	Protein IWS1 homolog	IWS1	237	S	1	52.27	NaN	NaN	NaN	NaN	0.89	0.88	1.21	1.00	1.17
Q96ST2	Protein IWS1 homolog	IWS1	196	S	1	46.57	NaN	NaN	1.71	1.44	1.34	0.81	NaN	1.50	1.66
Q96ST2	Protein IWS1 homolog	IWS1	198	S	1	46.57	NaN	NaN	1.71	1.44	1.34	NaN	NaN	1.50	1.66
Q96ST2	Protein IWS1 homolog	IWS1	248	S	1	74.78	1.32	1.47	1.46	1.68	1.60	0.76	1.87	1.50	0.98
Q96ST2	Protein IWS1 homolog	IWS1	250	S	0.996	74.78	1.32	1.47	1.46	1.68	1.60	NaN	1.87	1.50	NaN
Q96ST2	Protein IWS1 homolog	IWS1	261	S	0.894	49	0.85	0.94	0.93	NaN	0.62	0.76	NaN	0.98	0.98
Q96ST2	Protein IWS1 homolog	IWS1	263	S	0.925	49	0.85	0.94	0.93	NaN	0.62	0.76	NaN	0.98	0.98
Q96ST2	Protein IWS1 homolog	IWS1	274	S	0.977	59.36	NaN	0.91	0.97	NaN	0.85	NaN	NaN	0.94	0.70
Q96ST2	Protein IWS1 homolog	IWS1	287	S	1	92.68	NaN	0.91	0.97	NaN	0.85	NaN	NaN	0.94	NaN
Q96ST2	Protein IWS1 homolog	IWS1	289	S	1	92.68	NaN	0.91	0.97	NaN	0.85	NaN	NaN	0.94	0.70
Q96ST2	Protein IWS1 homolog	IWS1	377	S	1	131.7	0.74	0.70	0.70	0.70	0.87	0.80	0.72	0.63	0.80
Q96ST2	Protein IWS1 homolog	IWS1	438	S	1	199.8	0.99	0.89	1.05	0.94	0.92	0.90	0.96	1.22	1.02
Q96ST2	Protein IWS1 homolog	IWS1	440	S	1	199.8	0.99	0.89	1.05	0.94	0.92	0.90	0.96	1.22	1.02
Q96ST2	Protein IWS1 homolog	IWS1	300	S	0.999	101.2	NaN	NaN	0.45	0.42	NaN	0.67	0.43	1.11	0.60
Q96ST2	Protein IWS1 homolog	IWS1	313	S	0.996	101.2	NaN	NaN	0.45	0.42	NaN	0.50	0.43	0.37	0.60
Q96ST2	Protein IWS1 homolog	IWS1	415	S	1	166.7	0.36	NaN	NaN	NaN	0.34	0.40	NaN	NaN	0.41
Q96ST2	Protein IWS1 homolog	IWS1	420	S	1	196.7	0.36	NaN	0.36	0.28	NaN	0.40	0.34	0.38	0.41
Q96ST2	Protein IWS1 homolog	IWS1	422	S	1	196.7	NaN	NaN	0.36	0.28	0.34	NaN	0.34	0.38	NaN
Q96ST3	Paired amphipathic helix protein Sin3a	SIN3A	832	S	1	196.5	NaN	0.49	0.47	NaN	0.87	0.73	NaN	0.72	0.75
Q96T23	Remodeling and spacing factor 1	RSF1	604	S	1	92.83	0.77	0.77	0.75	1.00	0.72	0.81	0.93	1.07	0.97
Q96T23	Remodeling and spacing factor 1	RSF1	1345	S	1	138.3	0.91	NaN	NaN	NaN	0.57	0.76	NaN	NaN	1.02
Q96T23	Remodeling and spacing factor 1	RSF1	397	S	1	55.45	0.63	NaN	0.77	NaN	1.12	1.01	0.68	0.78	0.59

Q96T23	Remodeling and spacing factor 1	RSF1	622	S	0.999	116.9	0.76	0.72	0.69	0.96	0.73	0.78	0.94	1.01	1.07
Q96T23	Remodeling and spacing factor 1	RSF1	629	S	0.773	100.8	0.73	0.84	NaN	0.96	0.99	0.65	0.89	NaN	1.07
Q96T23	Remodeling and spacing factor 1	RSF1	1359	S	0.984	65.89	0.64	0.69	0.54	0.59	0.69	0.58	0.70	0.51	0.76
Q96T23	Remodeling and spacing factor 1	RSF1	1375	S	0.904	65.89	0.64	0.69	0.54	0.59	0.69	0.58	0.70	0.51	0.76
Q96T58	Msx2-interacting protein	SPEN	727	S	1	64.06	0.95	0.76	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Q96TA1	Niban-like protein 1	FAM129B	691	S	0.89	232.1	NaN	1.05	2.74	2.98	0.81	0.83	0.95	1.00	1.32
Q96TA1	Niban-like protein 1	FAM129B	692	S	0.995	261.7	1.10	1.15	1.07	0.80	NaN	0.65	1.07	0.83	1.01
Q96TA1	Niban-like protein 1	FAM129B	696	S	1	211.3	2.65	2.71	2.92	2.59	2.49	2.64	1.31	1.28	1.32
Q96TA1	Niban-like protein 1	FAM129B	665	S	1	116.4	2.00	1.93	1.68	2.25	3.02	2.09	1.51	1.25	0.98
Q96TA1	Niban-like protein 1	FAM129B	681	S	1	112.7	2.00	1.93	1.68	2.25	3.02	2.09	0.95	NaN	0.98
Q96TA1	Niban-like protein 1	FAM129B	638	S	1	107	2.91	3.29	3.57	3.45	4.21	4.98	NaN	NaN	NaN
Q96TA1	Niban-like protein 1	FAM129B	641	S	1	147.2	3.43	3.54	3.10	2.70	4.21	2.82	NaN	NaN	NaN
Q96TA1	Niban-like protein 1	FAM129B	646	S	0.998	147.2	3.43	3.54	3.10	2.70	4.21	2.82	NaN	NaN	NaN
Q99459	Cell division cycle 5-like	CDC5L	303	S	1	157.3	1.32	2.11	2.07	1.62	1.84	1.75	2.65	2.42	2.85
Q99523	Sortilin	SORT1	825	S	1	156	0.94	0.93	NaN	0.72	0.80	0.68	0.82	0.73	0.76
Q99549	M-phase phosphoprotein 8	MPHOSPH8	164	S	1	51.61	NaN	0.46	NaN	0.47	NaN	0.59	0.59	0.64	0.73
Q99549	M-phase phosphoprotein 8	MPHOSPH8	51	S	1	250	0.52	0.47	NaN	0.71	0.58	0.46	0.63	0.58	0.79
Q99549	M-phase phosphoprotein 8	MPHOSPH8	403	S	0.929	120.3	0.56	NaN	NaN	0.57	NaN	0.99	1.09	0.86	NaN
Q99549	M-phase phosphoprotein 8	MPHOSPH8	85	S	0.964	166.2	0.44	0.37	0.38	0.54	0.45	0.50	0.61	0.58	0.65
Q99567	Nuclear pore complex protein Nup88	NUP88	517	S	1	71.51	1.42	1.28	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Q99567	Nuclear pore complex protein Nup88	NUP88	35	S	0.995	107	NaN	NaN	NaN	2.01	1.65	1.42	1.58	1.64	NaN
Q99638	Cell cycle checkpoint control protein RAD9A	RAD9A	375	S	0.675	40.76	NaN	NaN	NaN	NaN	NaN	1.65	1.98	1.60	1.61
Q99638	Cell cycle checkpoint control protein RAD9A	RAD9A	380	S	0.674	40.76	NaN	NaN	NaN	NaN	NaN	1.65	1.98	1.60	1.61
Q99638	Cell cycle checkpoint control protein RAD9A	RAD9A	387	S	1	112.7	NaN	NaN	NaN	NaN	NaN	1.65	1.98	1.60	1.61
Q99959	Plakophilin-2	PKP2	151	S	1	97.42	NaN	NaN	1.10	NaN	0.83	1.11	1.13	0.80	0.92
Q99959	Plakophilin-2	PKP2	154	S	0.823	97.42	NaN	NaN	1.10	NaN	NaN	1.11	1.13	0.80	0.92
Q9BPX3	Condensin complex subunit 3	NCAPG	975	S	1	167.3	NaN	NaN	NaN	0.81	0.88	0.66	NaN	0.72	NaN
Q9BPX3	Condensin complex subunit 3	NCAPG	1015	S	1	151.7	1.41	1.33	1.23	1.31	1.43	1.14	1.06	1.09	1.15
Q9BPX3	Condensin complex subunit 3	NCAPG	674	S	1	376.2	0.82	0.71	0.93	0.85	0.86	0.97	0.94	0.93	0.93
Q9BQG0	Myb-binding protein 1A	MYBBP1	11	S	0.996	79.46	0.88	NaN	NaN	NaN	1.18	1.33	NaN	NaN	NaN
Q9BQG0	Myb-binding protein 1A	MYBBP1	1163	S	0.961	112.6	0.87	0.86	0.88	1.41	1.50	NaN	0.66	0.66	0.63
Q9BRD0	BUD13 homolog	BUD13	357	S	0.731	147.2	0.71	0.79	NaN	0.81	0.80	NaN	0.94	0.98	0.84
Q9BRD0	BUD13 homolog	BUD13	197	S	1	70.09	NaN	0.82	0.90	0.88	0.87	0.95	0.99	0.98	1.04
Q9BRD0	BUD13 homolog	BUD13	201	S	1	70.09	NaN	0.82	0.90	0.88	0.87	0.95	0.99	0.98	1.04

Q9BRD0	BUD13 homolog	BUD13	163	S	1	58.78	1.42	1.92	NaN	NaN	NaN	NaN	2.23	2.11	NaN
Q9BRD0	BUD13 homolog	BUD13	139	S	1	71.56	1.47	NaN	1.90	NaN	NaN	NaN	1.76	NaN	NaN
Q9BRD0	BUD13 homolog	BUD13	325	S	1	115.6	0.89	0.79	NaN	0.86	0.78	0.89	1.17	0.99	NaN
Q9BRG2	SH2 domain-containing protein 3A	SH2D3A	180	S	0.992	92.61	NaN	NaN	0.39	0.60	NaN	NaN	0.99	0.98	NaN
Q9BRL6	Serine/arginine-rich splicing factor 8	SRSF8	273	S	1	71.47	NaN	1.18	1.95	2.55	2.17	NaN	1.75	1.98	1.59
Q9BRL6	Serine/arginine-rich splicing factor 8	SRSF8	282	S	0.756	71.47	NaN	1.18	1.95	2.55	2.17	NaN	1.75	1.98	1.59
Q9BRQ0	Pygopus homolog 2	PYGO2	40	S	1	55.11	0.97	1.25	0.85	NaN	1.21	1.54	0.48	0.46	NaN
Q9BRS8	La-related protein 6	LARP6	447	S	0.829	57.15	NaN	NaN	NaN	NaN	NaN	NaN	1.48	1.76	1.74
Q9BSJ8	Extended synaptotagmin-1	ESYT1	1034	S	1	107.1	NaN	NaN	NaN	0.95	0.92	NaN	1.07	1.16	1.41
Q9BTC0	Death-inducer obliterator 1	DIDO1	1260	S	0.984	60.66	NaN	0.85	1.25	1.11	1.40	1.24	0.75	NaN	NaN
Q9BTC0	Death-inducer obliterator 1	DIDO1	1456	S	1	76.35	NaN	1.94	NaN	1.70	1.80	1.76	NaN	1.85	NaN
Q9BTC0	Death-inducer obliterator 1	DIDO1	1713	S	0.519	61.94	NaN	NaN	NaN	0.72	1.12	NaN	NaN	1.04	NaN
Q9BTC0	Death-inducer obliterator 1	DIDO1	1714	S	0.831	82.54	1.11	1.03	0.86	NaN	NaN	0.94	1.24	NaN	1.03
Q9BTU6	Phosphatidylinositol 4-kinase type 2-alpha	PI4K2A	44	S	0.536	66.36	NaN	0.53	NaN	NaN	0.96	1.49	NaN	NaN	NaN
Q9BTU6	Phosphatidylinositol 4-kinase type 2-alpha	PI4K2A	47	S	1	178.1	1.39	1.34	1.71	1.79	0.60	0.60	0.99	0.97	1.06
Q9BTU6	Phosphatidylinositol 4-kinase type 2-alpha	PI4K2A	51	S	1	178.1	1.39	1.34	1.35	1.79	1.01	1.32	1.30	1.61	1.28
Q9BU76	Multiple myeloma tumor-associated protein 2	MMTAG2	220	S	0.937	88.78	NaN	NaN	NaN	0.68	0.60	NaN	0.65	0.71	NaN
Q9BUA3	Uncharacterized protein C11orf84	C11orf84	308	S	1	134.6	1.27	1.19	NaN	1.11	1.15	NaN	1.30	1.32	1.25
Q9BUA3	Uncharacterized protein C11orf84	C11orf84	248	S	1	106.1	1.20	0.85	1.07	0.76	NaN	0.95	NaN	NaN	1.18
Q9BUA3	Uncharacterized protein C11orf84	C11orf84	251	S	0.97	106.1	1.20	2.58	1.07	0.76	NaN	0.95	NaN	NaN	1.18
Q9BUH6	Protein PAXX	C9orf142	148	S	1	222.6	1.39	1.29	1.51	1.42	1.46	1.55	1.07	1.10	0.95
Q9BV36	Melanophilin	MLPH	266	S	0.872	200.4	2.63	1.42	NaN	3.10	2.02	NaN	NaN	NaN	NaN
Q9BVG4	Protein PBDC1	PBDC1	197	S	1	132	0.91	1.06	0.82	0.94	0.96	0.90	0.92	0.95	0.97
Q9BVV8	Uncharacterized membrane protein C19orf24	C19orf24	117	S	0.998	128.9	1.19	1.13	0.57	NaN	1.65	1.62	NaN	NaN	NaN
Q9BVV8	Uncharacterized membrane protein C19orf24	C19orf24	120	S	0.999	128.9	1.19	1.13	NaN	NaN	1.65	1.62	NaN	NaN	NaN
Q9BW61	DET1- and DDB1-associated protein 1	DDA1	95	S	1	101.1	0.43	0.38	0.41	0.55	0.44	0.44	0.65	0.77	0.69
Q9BW71	HIRA-interacting protein 3	HIRIP3	159	S	1	46.07	NaN	NaN	NaN	NaN	0.90	NaN	NaN	0.96	0.93
Q9BW71	HIRA-interacting protein 3	HIRIP3	160	S	1	46.07	NaN	NaN	NaN	NaN	0.90	NaN	NaN	0.96	0.93
Q9BW71	HIRA-interacting protein 3	HIRIP3	196	S	1	289.4	0.59	0.58	NaN	NaN	NaN	0.62	NaN	NaN	0.88
Q9BW85	Coiled-coil domain-containing protein 94	CCDC94	211	S	1	144.9	0.86	0.81	0.68	0.83	0.80	0.74	0.88	0.86	0.85
Q9BW85	Coiled-coil domain-containing protein 94	CCDC94	213	S	1	144.9	0.86	0.81	0.68	0.83	0.80	0.74	0.88	0.86	0.85

Q9BX95	Sphingosine-1-phosphate phosphatase 1	SGPP1	112	S	0.994	77.05	1.04	0.72	NaN	NaN	NaN	NaN	1.05	0.89	NaN
Q9BXP5	Serrate RNA effector molecule homolog	SRRT	67	S	1	107	1.04	1.16	1.01	0.97	0.97	0.90	1.22	1.20	1.11
Q9BXP5	Serrate RNA effector molecule homolog	SRRT	74	S	1	118.3	1.19	1.14	1.22	1.15	1.20	1.10	1.25	1.34	1.22
Q9BXW6	Oxysterol-binding protein-related protein 1	OSBPL1A	499	S	1	42.32	1.18	0.80	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Q9BY89	Uncharacterized protein KIAA1671	KIAA1671	1701	S	1	99.71	0.66	0.65	NaN	0.74	0.68	NaN	0.88	0.95	NaN
Q9BY89	Uncharacterized protein KIAA1671	KIAA1671	1019	S	1	84.9	0.98	0.91	0.99	1.10	1.16	1.14	0.98	0.96	0.80
Q9BY89	Uncharacterized protein KIAA1671	KIAA1671	1363	S	0.557	58.37	NaN	NaN	NaN	1.20	NaN	0.88	1.15	0.94	0.76
Q9BY89	Uncharacterized protein KIAA1671	KIAA1671	1366	S	0.832	54.2	0.74	0.84	NaN	NaN	1.04	NaN	0.96	0.85	1.01
Q9BYW2	Histone-lysine N-methyltransferase SETD2	SETD2	624	S	0.951	57.79	NaN	0.86	NaN	1.60	NaN	1.30	1.40	NaN	1.38
Q9BYX2	TBC1 domain family member 2A	TBC1D2	920	S	1	145.6	0.75	0.87	0.88	0.75	0.75	0.78	1.18	1.06	1.09
Q9BZF1	Oxysterol-binding protein-related protein 8	OSBPL8	807	S	0.998	160.8	0.84	0.75	0.76	0.72	0.73	0.65	0.92	1.10	0.92
Q9BZF1	Oxysterol-binding protein-related protein 8	OSBPL8	808	S	0.999	160.8	0.84	0.75	0.76	0.72	NaN	0.65	0.92	1.10	0.92
Q9BZF1	Oxysterol-binding protein-related protein 8	OSBPL8	810	S	0.997	81.97	1.49	1.17	1.06	NaN	0.73	NaN	1.91	NaN	NaN
Q9BZH6	WD repeat-containing protein 11	WDR11	208	S	0.857	143.8	NaN	NaN	NaN	NaN	NaN	NaN	1.04	0.91	NaN
Q9BZQ8	Protein Niban	FAM129A	622	S	1	178.3	0.59	0.92	0.90	0.68	NaN	NaN	0.91	0.84	NaN
Q9BZQ8	Protein Niban	FAM129A	926	S	1	102.6	1.75	1.65	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Q9BZQ8	Protein Niban	FAM129A	646	S	1	98.15	1.48	1.72	NaN	NaN	2.24	NaN	1.12	NaN	NaN
Q9C0B5	Palmitoyltransferase ZDHHC5	ZDHHC5	529	S	0.831	66.87	1.61	NaN	NaN	1.24	1.30	NaN	NaN	NaN	1.18
Q9C0C2	182 kDa tankyrase-1-binding protein	TNKS1BP1	672	S	1	195.4	1.26	1.28	1.22	1.17	1.06	1.13	1.48	1.41	1.37
Q9C0C2	182 kDa tankyrase-1-binding protein	TNKS1BP1	1620	S	1	171.8	1.02	1.11	1.10	0.99	1.03	1.01	1.25	1.24	1.20
Q9C0C2	182 kDa tankyrase-1-binding protein	TNKS1BP1	1621	S	1	171.8	1.02	1.11	1.10	0.99	1.03	1.01	1.25	1.24	1.20
Q9C0C2	182 kDa tankyrase-1-binding protein	TNKS1BP1	1024	S	0.999	77.4	NaN	1.16	1.49	NaN	NaN	NaN	1.35	1.66	NaN
Q9C0C2	182 kDa tankyrase-1-binding protein	TNKS1BP1	494	S	1	224.6	0.69	0.77	0.85	0.77	1.39	2.00	1.85	NaN	1.06
Q9C0C2	182 kDa tankyrase-1-binding protein	TNKS1BP1	498	S	0.999	224.6	1.81	1.56	1.97	1.57	NaN	2.00	1.85	0.93	2.40
Q9C0C2	182 kDa tankyrase-1-binding protein	TNKS1BP1	1666	S	1	85.29	0.68	0.69	NaN	0.68	0.92	1.27	NaN	1.22	1.24

Q9C0C2	182 kDa tankyrase-1-binding protein	TNKS1BP1	987	S	0.962	202	2.98	2.94	NaN	3.39	NaN	NaN	NaN	NaN	NaN
Q9C0C2	182 kDa tankyrase-1-binding protein	TNKS1BP1	1554	S	0.719	145.9	NaN	1.16	2.47	NaN	NaN	NaN	NaN	NaN	NaN
Q9C0C2	182 kDa tankyrase-1-binding protein	TNKS1BP1	836	S	1	148.7	3.52	3.78	3.96	2.50	2.46	2.44	2.32	2.60	2.67
Q9C0C2	182 kDa tankyrase-1-binding protein	TNKS1BP1	1138	S	0.921	79.28	1.39	1.40	NaN	NaN	2.11	NaN	1.06	1.24	NaN
Q9C0C2	182 kDa tankyrase-1-binding protein	TNKS1BP1	601	S	1	185	1.60	1.85	NaN	1.40	1.62	1.56	1.27	1.37	1.50
Q9C0C9	E2/E3 hybrid ubiquitin-protein ligase UBE2O	UBE2O	87	S	1	180.1	0.58	0.62	0.63	0.87	0.85	0.71	0.79	0.75	0.81
Q9C0C9	E2/E3 hybrid ubiquitin-protein ligase UBE2O	UBE2O	89	S	1	180.1	0.58	0.62	0.63	0.87	0.85	0.71	0.79	0.75	0.81
Q9C0C9	E2/E3 hybrid ubiquitin-protein ligase UBE2O	UBE2O	836	S	0.919	103.9	1.34	0.88	0.72	1.53	1.52	1.15	NaN	NaN	NaN
Q9C0C9	E2/E3 hybrid ubiquitin-protein ligase UBE2O	UBE2O	839	S	0.786	224.5	0.87	0.74	1.06	1.17	NaN	1.37	0.54	0.81	0.75
Q9GZP8	Immortalization up-regulated protein	IMUP	29	S	1	91.47	0.99	1.07	1.08	1.09	1.13	1.04	1.06	1.06	1.13
Q9H0D6	5'-3' exoribonuclease 2	XRN2	499	S	1	186.6	0.72	0.40	0.72	0.60	0.55	0.72	0.80	0.76	0.92
Q9H0D6	5'-3' exoribonuclease 2	XRN2	501	S	1	217.7	0.72	0.76	0.79	0.75	0.78	0.72	0.90	0.99	0.92
Q9H0D6	5'-3' exoribonuclease 2	XRN2	448	S	1	87.88	1.00	1.52	NaN	1.75	1.78	1.78	0.94	1.11	1.07
Q9H0G5	Nuclear speckle splicing regulatory protein 1	NSRP1	33	S	1	167	1.09	1.00	NaN	NaN	NaN	NaN	1.20	NaN	1.80
Q9H1B7	Interferon regulatory factor 2-binding protein-like	IRF2BPL	547	S	1	90.82	0.78	0.87	0.78	0.73	0.66	0.78	1.37	1.33	1.43
Q9H1E3	Nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	NUCKS1	181	S	1	198.5	2.75	2.68	2.59	2.88	3.22	2.72	1.16	1.14	1.16
Q9H1E3	Nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	NUCKS1	73	S	1	89.68	1.17	1.07	NaN	NaN	NaN	1.01	NaN	NaN	NaN
Q9H1E3	Nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	NUCKS1	75	S	1	163.1	0.29	0.34	1.03	1.01	1.02	1.11	0.59	0.53	1.06
Q9H1E3	Nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	NUCKS1	79	S	1	170.3	0.32	0.30	0.31	1.01	1.02	1.05	0.49	0.46	1.06
Q9H1E3	Nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	NUCKS1	214	S	1	271.5	0.74	0.75	0.69	0.75	0.76	0.72	0.90	0.91	0.89
Q9H1E3	Nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	NUCKS1	204	S	1	144.7	0.92	1.23	1.27	1.07	0.89	1.17	0.96	1.03	1.37

Q9H1E3	Nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	NUCKS1	113	S	1	162.2	NaN	NaN	0.29	0.36	0.31	0.27	0.22	0.26	0.25
Q9H1E3	Nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	NUCKS1	19	S	1	349	1.19	1.18	1.15	1.10	1.08	1.08	1.16	1.18	1.19
Q9H1E3	Nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	NUCKS1	54	S	0.998	159	0.92	0.65	0.99	0.69	0.81	1.02	0.57	0.98	0.85
Q9H1E3	Nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	NUCKS1	58	S	1	187	0.68	0.85	0.74	0.88	0.70	0.70	0.98	0.62	0.84
Q9H1E3	Nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	NUCKS1	61	S	1	228.6	0.63	0.67	0.62	0.70	0.71	0.87	0.83	0.94	0.99
Q9H1E3	Nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	NUCKS1	50	S	0.547	63.48	0.76	0.85	NaN	NaN	0.97	NaN	NaN	NaN	NaN
Q9H1E3	Nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	NUCKS1	223	S	1	150.2	0.32	0.35	0.36	0.39	0.38	0.39	0.47	0.47	0.49
Q9H246	Uncharacterized protein C1orf21	C1orf21	115	S	0.999	65.09	NaN	NaN	NaN	1.19	1.01	0.93	1.13	1.05	NaN
Q9H307	Pinin	PNN	375	S	0.954	104.3	NaN	NaN	0.87	1.32	1.10	1.18	0.54	0.55	0.48
Q9H307	Pinin	PNN	381	S	1	224.6	0.88	0.89	0.75	1.19	1.18	0.99	0.57	0.56	0.55
Q9H307	Pinin	PNN	100	S	1	209.1	0.87	0.89	0.96	0.93	0.95	0.92	0.95	0.91	0.96
Q9H330	Transmembrane protein 245	TMEM245	332	S	0.638	121.1	NaN	NaN	NaN	NaN	0.99	NaN	1.25	1.26	NaN
Q9H3N1	Thioredoxin-related transmembrane protein 1	TMX1	247	S	1	302	1.15	1.07	1.10	0.95	0.91	1.05	1.05	0.99	1.15
Q9H3Q1	Cdc42 effector protein 4	CDC42EP4	141	S	0.733	84.31	0.75	NaN	NaN	0.89	NaN	0.86	NaN	NaN	NaN
Q9H3Q1	Cdc42 effector protein 4	CDC42EP4	142	S	0.788	91.96	NaN	0.78	0.81	NaN	0.89	NaN	0.51	0.53	0.52
Q9H3Z4	DnaJ homolog subfamily C member 5	DNAJC5	10	S	0.999	429.1	1.18	1.24	1.20	0.99	0.98	0.99	1.01	0.89	1.01
Q9H4L5	Oxysterol-binding protein-related protein 3	OSBPL3	437	S	1	159.5	1.52	1.14	NaN	NaN	NaN	6.56	NaN	1.20	NaN
Q9H4L5	Oxysterol-binding protein-related protein 3	OSBPL3	410	S	1	117	0.93	1.01	0.96	1.55	1.37	1.39	0.85	0.87	1.06
Q9H4L5	Oxysterol-binding protein-related protein 3	OSBPL3	304	S	0.959	127.6	1.13	1.05	NaN	NaN	1.02	NaN	NaN	NaN	NaN
Q9H4L5	Oxysterol-binding protein-related protein 3	OSBPL3	34	S	1	94.72	1.57	1.90	1.67	1.41	1.28	NaN	1.37	1.56	1.56
Q9H4L5	Oxysterol-binding protein-related protein 3	OSBPL3	372	S	0.963	322.4	0.70	0.69	0.67	1.31	1.33	1.37	0.57	0.68	0.69
Q9H4L5	Oxysterol-binding protein-related protein 3	OSBPL3	262	S	0.706	122.4	NaN	1.17	0.98	1.79	NaN	1.60	0.62	NaN	1.23

Q9H4L5	Oxysterol-binding protein-related protein 3	OSBPL3	265	S	0.995	142.5	1.16	1.13	NaN	1.27	1.85	NaN	NaN	0.65	0.69
Q9H501	ESF1 homolog	ESF1	657	S	1	140.6	0.86	0.94	0.99	0.98	0.97	1.13	0.80	0.82	0.78
Q9H501	ESF1 homolog	ESF1	663	S	1	134.6	1.24	0.80	NaN	1.11	1.26	1.18	1.41	1.65	1.31
Q9H501	ESF1 homolog	ESF1	153	S	1	110.4	1.02	0.96	0.90	1.15	1.26	1.17	0.48	0.70	0.53
Q9H501	ESF1 homolog	ESF1	198	S	0.989	68.42	0.77	1.23	NaN	1.88	NaN	NaN	NaN	NaN	NaN
Q9H6F5	Coiled-coil domain-containing protein 86	CCDC86	58	S	1	93.65	1.21	1.46	1.36	1.58	1.58	1.61	0.68	0.70	0.70
Q9H6F5	Coiled-coil domain-containing protein 86	CCDC86	66	S	0.668	64.04	0.74	0.65	0.62	0.77	0.74	NaN	NaN	NaN	0.80
Q9H6F5	Coiled-coil domain-containing protein 86	CCDC86	69	S	1	111.6	1.19	0.65	0.62	0.77	0.74	0.83	0.98	NaN	0.71
Q9H6F5	Coiled-coil domain-containing protein 86	CCDC86	47	S	1	319.2	1.12	1.12	1.11	1.14	1.15	1.11	0.95	0.99	0.95
Q9H6F5	Coiled-coil domain-containing protein 86	CCDC86	18	S	0.999	88.68	1.55	1.43	1.78	NaN	1.21	1.46	1.62	1.39	1.35
Q9H6F5	Coiled-coil domain-containing protein 86	CCDC86	91	S	1	331.6	1.04	1.07	1.14	1.15	1.08	1.07	1.07	0.94	1.13
Q9H6F5	Coiled-coil domain-containing protein 86	CCDC86	102	S	1	110.2	0.86	NaN	0.86	NaN	1.59	NaN	1.08	1.03	NaN
Q9H6F5	Coiled-coil domain-containing protein 86	CCDC86	110	S	0.97	94.15	0.80	NaN	0.86	NaN	1.59	0.92	1.08	1.03	NaN
Q9H6F5	Coiled-coil domain-containing protein 86	CCDC86	113	S	0.998	70.63	NaN	1.00	0.86	NaN	0.92	NaN	1.08	1.08	1.08
Q9H6X2	Anthrax toxin receptor 1	ANTXR1	362	S	1	173.6	0.85	NaN	0.86	0.89	0.89	0.87	1.03	0.91	1.13
Q9H7D0	Dedicator of cytokinesis protein 5	DOCK5	1789	S	0.985	47.43	1.53	NaN	1.12	NaN	1.02	NaN	NaN	1.08	NaN
Q9H7D0	Dedicator of cytokinesis protein 5	DOCK5	1756	S	0.93	103.4	NaN	NaN	1.23	1.86	NaN	1.26	NaN	NaN	NaN
Q9H7L9	Sin3 histone deacetylase corepressor complex component SDS3	SUDS3	234	S	0.985	125.4	0.83	0.90	NaN	0.65	0.79	NaN	NaN	0.89	1.04
Q9H7N4	Splicing factor, arginine/serine-rich 19	SCAF1	734	S	1	116.8	1.41	1.63	1.20	1.13	1.03	1.44	1.15	1.14	1.71
Q9H7N4	Splicing factor, arginine/serine-rich 19	SCAF1	738	S	1	116.8	1.41	1.63	1.20	1.13	1.03	1.44	1.15	1.14	1.71
Q9H7N4	Splicing factor, arginine/serine-rich 19	SCAF1	239	S	1	156	0.82	0.84	0.85	0.82	0.87	0.93	1.02	0.86	0.78
Q9H7N4	Splicing factor, arginine/serine-rich 19	SCAF1	963	S	0.982	175.2	1.09	0.88	NaN	NaN	1.13	1.13	NaN	0.87	NaN
Q9H7N4	Splicing factor, arginine/serine-rich 19	SCAF1	724	S	0.937	97.75	NaN	0.57	0.61	0.53	0.85	NaN	0.70	0.61	0.64
Q9H7N4	Splicing factor, arginine/serine-rich 19	SCAF1	725	S	0.894	97.75	NaN	0.51	0.61	0.30	NaN	NaN	0.70	0.52	0.64
Q9H7N4	Splicing factor, arginine/serine-rich 19	SCAF1	498	S	1	136.3	1.09	1.20	1.21	1.16	1.20	1.07	1.36	1.30	1.18

Q9H7N4	Splicing factor, arginine/serine-rich 19	SCAF1	500	S	1	136.3	1.09	1.20	1.21	1.16	1.20	1.07	1.36	1.30	1.18
Q9H7N4	Splicing factor, arginine/serine-rich 19	SCAF1	612	S	1	51.76	NaN	NaN	NaN	0.91	0.90	NaN	0.92	NaN	0.88
Q9H7N4	Splicing factor, arginine/serine-rich 19	SCAF1	614	S	1	51.76	NaN	NaN	NaN	0.91	0.90	NaN	0.92	NaN	0.88
Q9H8G2	Caspase activity and apoptosis inhibitor 1	CAAP1	203	S	1	97.77	0.59	0.64	0.63	0.98	0.94	0.91	0.93	1.13	0.38
Q9H8G2	Caspase activity and apoptosis inhibitor 1	CAAP1	312	S	0.909	88.18	1.05	1.26	NaN	NaN	1.61	1.69	NaN	1.39	1.12
Q9H8M2	Bromodomain-containing protein 9	BRD9	588	S	1	143.6	0.88	0.66	NaN	0.99	0.78	0.66	1.04	0.83	0.79
Q9H8Y8	Golgi reassembly-stacking protein 2	GORASP 2	451	S	1	122.7	0.72	0.88	0.86	1.24	1.18	1.39	1.00	0.99	0.99
Q9HA65	TBC1 domain family member	TBC1D17	602	S	0.997	161.7	1.31	0.85	2.02	NaN	NaN	NaN	1.03	1.57	1.32
Q9HA65	TBC1 domain family member	TBC1D17	604	S	0.928	161.7	1.31	0.85	2.02	NaN	NaN	NaN	1.03	1.57	1.32
Q9HA65	TBC1 domain family member	TBC1D17	613	S	0.88	127.3	NaN	0.85	2.02	NaN	NaN	NaN	0.65	1.42	NaN
Q9HCD6	Protein TANC2	TANC2	169	S	0.986	228.5	0.87	1.19	NaN	1.34	1.41	1.25	1.29	1.13	NaN
Q9HCD6	Protein TANC2	TANC2	1579	S	0.93	75.33	1.27	1.51	NaN	1.47	1.20	NaN	NaN	1.51	1.37
Q9HCE5	N6-adenosine-methyltransferase subunit METTL14	METTL14	399	S	1	77.59	0.56	NaN	0.57	0.70	NaN	0.69	0.88	NaN	0.84
Q9HCN4	GPN-loop GTPase 1	GPN1	314	S	0.996	90.56	1.31	1.56	1.13	1.40	1.29	1.37	0.89	0.90	NaN
Q9NQC3	Reticulon-4	RTN4	181	S	0.807	114.5	0.48	1.07	0.94	1.01	0.89	0.98	1.19	0.80	NaN
Q9NQC3	Reticulon-4	RTN4	182	S	0.808	115.1	1.00	1.07	0.94	1.01	0.89	0.98	1.14	0.80	NaN
Q9NQC3	Reticulon-4	RTN4	184	S	0.837	115.1	1.16	1.28	0.94	1.01	0.89	0.98	1.00	0.99	NaN
Q9NQG5	Regulation of nuclear pre-mRNA domain-containing protein 1B	RPRD1B	134	S	0.906	73.98	0.78	0.53	0.74	0.53	NaN	NaN	NaN	NaN	0.55
Q9NQG5	Regulation of nuclear pre-mRNA domain-containing protein 1B	RPRD1B	166	S	1	225.5	1.00	1.02	1.00	1.01	1.18	0.94	1.46	1.13	0.94
Q9NQP4	Prefoldin subunit 4	PFDN4	125	S	1	53.14	1.94	2.04	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Q9NQS7	Inner centromere protein	INCENP	197	S	0.973	150.5	1.18	NaN	NaN	2.16	2.15	1.83	NaN	NaN	NaN
Q9NQS7	Inner centromere protein	INCENP	214	S	0.783	150.5	1.18	NaN	NaN	2.16	2.15	1.83	NaN	NaN	NaN
Q9NQW6	Actin-binding protein anillin	ANLN	182	S	1	209.2	0.91	1.01	0.98	1.84	1.97	2.00	0.63	0.65	0.70
Q9NQW6	Actin-binding protein anillin	ANLN	54	S	1	83.31	1.27	1.57	1.26	2.75	2.78	NaN	0.82	1.01	NaN
Q9NQW6	Actin-binding protein anillin	ANLN	517	S	0.815	149.5	0.81	NaN	1.05	2.25	2.39	NaN	NaN	0.92	0.80
Q9NQW6	Actin-binding protein anillin	ANLN	518	S	0.992	260.1	0.70	0.65	0.86	2.04	2.18	2.26	1.04	0.86	NaN
Q9NQW6	Actin-binding protein anillin	ANLN	792	S	0.999	98.16	0.93	0.84	NaN	2.01	1.94	2.16	0.27	0.30	NaN
Q9NQW6	Actin-binding protein anillin	ANLN	323	S	1	77.64	NaN	NaN	0.79	NaN	NaN	1.80	NaN	0.65	0.64
Q9NQW6	Actin-binding protein anillin	ANLN	65	S	0.994	102.6	0.73	0.67	0.68	1.64	1.67	1.58	0.58	0.58	0.56
Q9NQZ2	Something about silencing protein 10	UTP3	365	S	1	162	1.50	1.23	2.13	NaN	1.33	NaN	1.69	2.14	NaN
Q9NQZ2	Something about silencing protein 10	UTP3	368	S	1	162	1.50	1.23	2.13	NaN	1.33	NaN	1.69	2.14	NaN

Q9NR19	Acetyl-coenzyme A synthetase, cytoplasmic	ACSS2	267	S	0.995	167.9	NaN	0.49	NaN	0.77	NaN	0.81	NaN	0.51	0.60
Q9NR19	Acetyl-coenzyme A synthetase, cytoplasmic	ACSS2	30	S	1	135.2	0.55	0.57	0.59	0.66	0.68	0.68	0.91	0.92	0.93
Q9NR30	Nucleolar RNA helicase 2	DDX21	71	S	1	64.41	1.27	1.24	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Q9NR30	Nucleolar RNA helicase 2	DDX21	89	S	1	103.2	0.61	0.67	0.77	0.73	1.05	1.02	0.67	0.61	0.65
Q9NR30	Nucleolar RNA helicase 2	DDX21	121	S	1	151.4	1.06	0.99	0.78	1.12	0.91	1.12	0.74	0.67	0.75
Q9NRF2	SH2B adapter protein 1	SH2B1	125	S	0.859	100.7	0.95	0.97	0.68	NaN	NaN	NaN	NaN	NaN	NaN
Q9NRX5	Serine incorporator 1	SERINC1	364	S	1	83.77	1.64	2.17	1.40	1.35	1.34	NaN	1.15	0.85	NaN
Q9NRY4	Rho GTPase-activating protein 35	ARHGAP 35	975	S	1	144.4	0.97	NaN	0.87	0.79	1.33	0.84	NaN	NaN	NaN
Q9NRY4	Rho GTPase-activating protein 35	ARHGAP 35	1179	S	1	254.6	0.93	0.92	0.84	0.94	0.99	0.85	1.00	0.98	1.02
Q9NSV4	Protein diaphanous homolog 3	DIAPH3	1093	S	0.984	54.97	0.87	NaN	0.75	1.18	1.26	NaN	0.91	0.90	0.96
Q9NTI5	Sister chromatid cohesion protein PDS5 homolog B	PDS5B	1358	S	1	250.4	NaN	NaN	NaN	1.78	NaN	NaN	2.07	NaN	2.75
Q9NTI5	Sister chromatid cohesion protein PDS5 homolog B	PDS5B	1283	S	1	124.8	0.94	0.86	0.81	1.29	1.21	1.15	0.74	0.84	0.76
Q9NTI5	Sister chromatid cohesion protein PDS5 homolog B	PDS5B	1166	S	0.975	401.3	0.71	0.56	0.84	0.94	1.10	0.94	0.50	0.50	NaN
Q9NTZ6	RNA-binding protein 12	RBM12	411	S	0.968	61.42	NaN	NaN	NaN	NaN	NaN	NaN	0.90	NaN	0.99
Q9NTZ6	RNA-binding protein 12	RBM12	413	S	0.93	54.65	1.10	NaN	NaN	0.98	NaN	0.99	NaN	NaN	NaN
Q9NVD7	Alpha-parvin	PARVA	8	S	0.711	68.88	NaN	NaN	NaN	NaN	1.08	1.44	NaN	0.98	NaN
Q9NVD7	Alpha-parvin	PARVA	14	S	0.997	129.5	1.71	1.32	1.29	1.34	1.30	1.35	1.48	1.60	1.61
Q9NVD7	Alpha-parvin	PARVA	19	S	0.983	113.7	0.60	0.61	0.61	0.48	0.45	1.28	0.90	0.97	0.90
Q9NW82	WD repeat-containing protein 70	WDR70	638	S	1	161.3	0.65	0.52	NaN	1.38	1.17	NaN	NaN	2.72	1.90
Q9NWB6	Arginine and glutamate-rich protein 1	ARGLU1	76	S	0.709	95.07	NaN	NaN	NaN	NaN	0.84	NaN	1.10	0.91	NaN
Q9NWB6	Arginine and glutamate-rich protein 1	ARGLU1	77	S	0.999	155.3	0.93	0.88	0.85	0.78	0.77	0.76	0.86	0.90	0.91
Q9NWH9	SAFB-like transcription modulator	SLTM	289	S	1	218.4	0.64	0.64	0.65	0.71	0.70	0.70	0.68	0.71	0.71
Q9NWZ5	Uridine-cytidine kinase-like 1	UCKL1	56	S	0.982	91.59	1.31	1.28	1.30	1.81	1.97	NaN	NaN	0.93	NaN
Q9NWZ5	Uridine-cytidine kinase-like 1	UCKL1	539	S	1	126.2	0.52	0.74	NaN	NaN	NaN	NaN	0.90	NaN	1.13
Q9NXC5	WD repeat-containing protein mio	MIOS	766	S	0.888	125.3	NaN	NaN	NaN	0.69	NaN	NaN	0.63	0.69	0.80
Q9NXE8	Pre-mRNA-splicing factor CWC25 homolog	CWC25	218	S	0.62	68.46	NaN	NaN	NaN	0.99	0.96	NaN	0.68	0.57	NaN
Q9NY61	Protein AATF	AATF	316	S	1	131.1	0.70	0.74	0.72	0.80	0.80	0.74	0.72	0.87	0.79
Q9NY61	Protein AATF	AATF	320	S	1	141.7	0.58	0.63	0.86	0.85	0.59	0.55	1.12	1.08	0.79
Q9NY61	Protein AATF	AATF	321	S	1	141.7	0.58	0.63	0.86	0.85	0.59	0.55	1.12	1.08	0.79
Q9NYQ8	Protocadherin Fat 2	FAT2	1873	S	0.971	43.8	NaN	NaN	NaN	0.89	0.93	0.95	0.40	0.46	NaN
Q9NZ63	Uncharacterized protein C9orf78	C9orf78	261	S	1	102.5	1.19	1.07	1.08	NaN	NaN	1.08	NaN	1.10	1.19
Q9NZL4	Hsp70-binding protein 1	HSPBP1	351	S	0.803	154.5	NaN	1.53	1.40	NaN	NaN	NaN	NaN	NaN	NaN
Q9NZM1	Myoferlin	MYOF	1915	S	0.998	48.39	0.65	0.65	NaN	NaN	NaN	0.85	NaN	1.15	0.87

Q9NZN4	EH domain-containing protein	EHD2	438	S	1	288.3	0.44	0.46	0.49	0.64	0.63	0.62	0.58	0.57	0.58
Q9NZN4	EH domain-containing protein	EHD2	468	S	0.85	52.47	NaN	NaN	NaN	NaN	0.87	0.74	0.62	NaN	NaN
Q9NZN4	EH domain-containing protein	EHD2	470	S	0.575	78.76	1.31	NaN	NaN	0.79	NaN	0.74	0.62	0.65	0.71
Q9NZQ7	Programmed cell death 1 ligand 1	CD274	283	S	0.976	58.57	NaN	NaN	2.48	NaN	NaN	NaN	1.86	NaN	1.82
Q9P0K7	Ankycorbin	RAI14	327	S	0.971	112.4	1.36	1.34	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Q9P0K7	Ankycorbin	RAI14	281	S	0.996	105.3	1.32	NaN	1.75	1.57	1.33	1.30	1.10	1.09	NaN
Q9P0K7	Ankycorbin	RAI14	412	S	0.742	60.36	NaN	1.43	NaN	NaN	1.34	1.38	1.47	1.44	1.32
Q9P206	Uncharacterized protein KIAA1522	KIAA1522	669	S	1	88	1.22	0.98	0.68	0.65	0.70	0.62	1.02	1.02	1.01
Q9P206	Uncharacterized protein KIAA1522	KIAA1522	673	S	0.997	88	1.22	0.98	0.68	0.65	0.70	0.62	1.02	1.02	1.01
Q9P206	Uncharacterized protein KIAA1522	KIAA1522	545	S	1	104.2	NaN	2.23	2.23	NaN	NaN	NaN	1.37	2.11	2.33
Q9P2B4	CTTNBP2 N-terminal-like protein	CTTNBP2 NL	488	S	1	113.4	0.76	0.73	0.64	0.63	0.71	0.57	0.61	0.69	0.69
Q9P2B4	CTTNBP2 N-terminal-like protein	CTTNBP2 NL	481	S	0.889	85.85	1.01	NaN	0.78	NaN	0.49	NaN	1.07	0.88	0.89
Q9P2B4	CTTNBP2 N-terminal-like protein	CTTNBP2 NL	568	S	0.939	129.3	0.93	0.94	NaN	0.85	NaN	0.71	1.51	1.63	1.46
Q9P2C4	Transmembrane protein 181	TMEM181	580	S	0.992	98.99	NaN	NaN	NaN	0.96	NaN	1.42	NaN	NaN	NaN
Q9P2E9	Ribosome-binding protein 1	RRBP1	615	S	1	168.7	0.59	0.66	0.74	1.08	1.13	1.19	0.76	0.66	0.64
Q9P2E9	Ribosome-binding protein 1	RRBP1	1276	S	0.726	111.2	0.99	0.95	0.80	0.93	0.99	NaN	0.70	0.60	0.47
Q9P2E9	Ribosome-binding protein 1	RRBP1	1277	S	0.779	111.2	NaN	NaN	NaN	0.93	0.95	NaN	NaN	0.68	0.47
Q9P2G1	Ankyrin repeat and IBR domain-containing protein 1	ANKIB1	737	S	1	92.04	0.62	0.87	NaN	0.36	NaN	NaN	NaN	0.79	NaN
Q9P2I0	Cleavage and polyadenylation specificity factor subunit 2	CPSF2	419	S	0.912	110.8	0.42	0.19	3.75	0.63	NaN	NaN	2.02	NaN	NaN
Q9P2I0	Cleavage and polyadenylation specificity factor subunit 2	CPSF2	420	S	0.912	110.8	0.42	0.19	3.75	0.63	NaN	NaN	2.02	NaN	NaN
Q9P2I0	Cleavage and polyadenylation specificity factor subunit 2	CPSF2	423	S	0.734	93.73	0.42	NaN	3.75	NaN	NaN	NaN	2.02	NaN	NaN
Q9P2Q2	FERM domain-containing protein 4A	FRMD4A	694	S	0.798	79.07	NaN	NaN	NaN	NaN	0.74	1.52	NaN	0.86	NaN
Q9UBB9	Tuftelin-interacting protein 11	TFIP11	98	S	1	165.5	0.79	0.92	0.95	1.02	0.87	0.84	1.14	1.29	1.17
Q9UBB9	Tuftelin-interacting protein 11	TFIP11	210	S	1	144.7	0.80	0.82	1.02	1.01	0.92	1.39	0.69	0.83	0.71
Q9UDT6	CAP-Gly domain-containing linker protein 2	CLIP2	53	S	0.538	83.32	NaN	NaN	1.25	NaN	NaN	2.10	0.61	NaN	0.78
Q9UER7	Death domain-associated protein 6	DAXX	495	S	1	168.4	NaN	0.51	0.71	0.73	0.72	0.98	0.63	0.83	0.62
Q9UEY8	Gamma-adducin	ADD3	677	S	0.957	132.8	0.58	0.58	NaN	0.57	0.66	NaN	0.46	0.87	NaN
Q9UEY8	Gamma-adducin	ADD3	679	S	0.926	99.93	0.58	0.58	0.48	0.57	0.66	NaN	0.46	0.91	NaN
Q9UEY8	Gamma-adducin	ADD3	681	S	0.689	87.67	0.50	0.52	NaN	NaN	0.66	NaN	NaN	NaN	NaN
Q9UGU5	HMG domain-containing protein 4	HMGXB4	497	S	0.997	52.25	NaN	NaN	0.95	1.07	1.38	NaN	1.09	NaN	NaN
Q9UHB6	LIM domain and actin-binding protein 1	LIMA1	373	S	0.912	172.1	0.67	NaN	NaN	0.99	NaN	1.08	0.81	NaN	0.89

Q9UHB6	LIM domain and actin-binding protein 1	LIMA1	374	S	0.983	168.8	NaN	0.67	0.73	NaN	0.99	NaN	NaN	0.80	NaN
Q9UHB6	LIM domain and actin-binding protein 1	LIMA1	686	S	0.987	75.77	NaN	NaN	NaN	0.11	0.14	0.14	0.09	0.18	0.18
Q9UHB6	LIM domain and actin-binding protein 1	LIMA1	490	S	1	199.4	1.03	1.04	0.98	1.10	1.13	1.06	0.93	0.89	0.91
Q9UHB6	LIM domain and actin-binding protein 1	LIMA1	132	S	1	78.71	0.82	0.91	1.10	0.98	0.97	1.28	NaN	0.71	0.98
Q9UHB6	LIM domain and actin-binding protein 1	LIMA1	698	S	1	168.5	0.76	0.71	0.90	0.89	0.88	0.86	0.83	NaN	0.99
Q9UHB6	LIM domain and actin-binding protein 1	LIMA1	362	S	1	203.3	0.65	0.70	0.68	0.95	0.97	0.89	0.74	0.76	0.82
Q9UHB6	LIM domain and actin-binding protein 1	LIMA1	609	S	1	117.8	0.70	0.65	0.62	0.75	NaN	0.77	NaN	1.08	0.92
Q9UHB7	AF4/FMR2 family member 4	AFF4	1055	S	1	94.19	NaN	NaN	NaN	1.85	NaN	NaN	1.08	0.74	NaN
Q9UHB7	AF4/FMR2 family member 4	AFF4	1058	S	1	99.53	NaN	1.13	1.01	1.39	1.29	1.16	0.55	NaN	0.73
Q9UHB7	AF4/FMR2 family member 4	AFF4	703	S	1	113.2	1.16	1.14	1.25	1.63	1.71	1.13	1.13	0.97	0.99
Q9UHB7	AF4/FMR2 family member 4	AFF4	706	S	1	69.7	2.54	2.10	2.19	2.55	2.62	2.25	1.38	1.22	NaN
Q9UHB7	AF4/FMR2 family member 4	AFF4	180	S	0.957	88.28	1.70	0.93	1.60	1.60	NaN	1.51	NaN	NaN	0.92
Q9UHD8	Septin-9	9-Sep	85	S	1	150.4	1.38	1.36	1.28	1.10	1.02	1.17	1.20	1.16	1.23
Q9UHD8	Septin-9	9-Sep	30	S	1	262.4	1.77	1.72	1.86	1.62	1.65	1.47	1.86	1.38	1.75
Q9UHK0	Nuclear fragile X mental retardation-interacting protein	NUFIP1	338	S	1	70.42	1.08	1.30	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Q9UHK0	Nuclear fragile X mental retardation-interacting protein	NUFIP1	340	S	0.997	70.42	1.08	1.30	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Q9UHK0	Nuclear fragile X mental retardation-interacting protein	NUFIP1	342	S	0.994	70.42	1.08	1.30	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Q9UHR4	Brain-specific angiogenesis inhibitor 1-associated protein 2-like protein 1	BAIAP2L1	414	S	0.779	79.46	2.09	1.48	1.57	1.90	NaN	NaN	2.53	NaN	2.53
Q9UHV7	Mediator of RNA polymerase II transcription subunit 13	MED13	890	S	0.97	53.36	1.08	NaN	NaN	NaN	1.02	NaN	0.93	1.18	NaN
Q9UIG0	Tyrosine-protein kinase	BAZ1B	1468	S	1	173.9	0.88	1.14	NaN	0.80	NaN	NaN	1.56	1.11	1.03
Q9UIQ6	Leucyl-cystinyl aminopeptidase;Leucyl-cystinyl aminopeptidase, pregnancy serum form	LNPEP	329	S	0.644	45.92	0.64	NaN	0.65	0.66	0.80	0.68	NaN	0.60	0.91
Q9UJM3	ERBB receptor feedback inhibitor 1	ERRFI1	273	S	0.995	50.36	NaN	NaN	1.84	NaN	NaN	NaN	1.43	2.42	NaN
Q9UJM3	ERBB receptor feedback inhibitor 1	ERRFI1	251	S	0.997	93.92	2.71	2.64	2.71	2.14	2.26	NaN	2.15	2.13	2.13
Q9UJX2	Cell division cycle protein 23 homolog	CDC23	588	S	0.996	79.88	NaN	0.59	1.33	NaN	NaN	NaN	1.18	NaN	0.86
Q9UK58	Cyclin-L1	CCNL1	352	S	1	104.1	1.13	1.10	1.10	1.12	1.14	0.99	0.98	0.97	1.04
Q9UK58	Cyclin-L1	CCNL1	335	S	0.982	149.2	2.35	NaN	1.95	NaN	NaN	1.75	2.24	NaN	1.78
Q9UK58	Cyclin-L1	CCNL1	341	S	0.778	140.3	NaN	0.77	1.95	NaN	NaN	1.75	NaN	0.62	1.78
Q9UK61	Protein FAM208A	FAM208A	927	S	0.763	47.73	NaN	NaN	NaN	0.60	0.54	0.56	1.01	0.96	NaN

Q9UK76	Hematological and neurological expressed 1 protein;Hematological and neurological expressed 1 protein, N-terminally	HN1	131	S	1	101.9	3.53	2.89	NaN	2.96	NaN	3.45	NaN	2.55	2.58
Q9UK76	Hematological and neurological expressed 1 protein;Hematological and neurological expressed 1 protein, N-terminally	HN1	87	S	0.997	319.4	1.03	1.04	0.99	0.83	0.83	0.82	1.75	1.74	1.82
Q9UK76	Hematological and neurological expressed 1 protein;Hematological and neurological expressed 1 protein, N-terminally	HN1	88	S	0.627	172.1	NaN	1.16	NaN	0.81	0.81	0.88	1.69	1.61	NaN
Q9UKA4	A-kinase anchor protein 11	AKAP11	448	S	1	115.6	3.19	2.94	2.89	NaN	NaN	NaN	NaN	NaN	NaN
Q9UKA4	A-kinase anchor protein 11	AKAP11	1240	S	0.501	66.33	NaN	0.78	0.77	NaN	NaN	NaN	NaN	NaN	NaN
Q9UKA4	A-kinase anchor protein 11	AKAP11	1242	S	1	152.9	0.89	0.82	0.81	0.95	0.85	0.88	0.77	0.68	0.76
Q9UKE5	TRAF2 and NCK-interacting protein kinase	TNIK	769	S	1	93.77	0.55	0.47	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Q9UKG1	DCC-interacting protein 13-alpha	APPL1	401	S	0.829	91.59	NaN	NaN	4.72	5.07	NaN	3.88	4.80	NaN	3.93
Q9UKJ3	G patch domain-containing protein 8	GPATCH8	1081	S	0.982	71.4	NaN	NaN	NaN	NaN	1.05	1.12	NaN	0.82	NaN
Q9UKJ3	G patch domain-containing protein 8	GPATCH8	740	S	0.979	98	1.71	1.52	1.58	1.63	NaN	1.53	1.35	NaN	1.18
Q9UKJ3	G patch domain-containing protein 8	GPATCH8	653	S	0.822	57.62	1.58	1.33	1.55	NaN	NaN	NaN	NaN	NaN	NaN
Q9UKL0	REST corepressor 1	RCOR1	260	S	1	170.2	0.74	0.65	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Q9UKM9	RNA-binding protein Raly	RALY	135	S	1	110.8	1.13	1.14	1.13	1.10	1.08	1.11	1.05	1.06	1.09
Q9ULE0	Protein WWC3	WWC3	927	S	0.995	79.23	NaN	NaN	NaN	NaN	0.64	NaN	1.24	1.19	0.96
Q9ULL5	Proline-rich protein 12	PRR12	651	S	1	98.63	0.51	0.58	NaN	0.49	NaN	NaN	NaN	NaN	NaN
Q9ULW0	Targeting protein for Xklp2	TPX2	186	S	0.927	52.74	0.41	0.38	NaN	1.03	NaN	NaN	0.43	NaN	NaN
Q9ULW0	Targeting protein for Xklp2	TPX2	738	S	1	144	2.34	3.77	2.45	4.98	6.39	NaN	1.34	1.30	1.49
Q9ULX3	RNA-binding protein NOB1	NOB1	201	S	1	142.2	NaN	NaN	NaN	NaN	0.85	0.92	NaN	NaN	NaN
Q9UNZ2	NSFL1 cofactor p47	NSFL1C	114	S	1	136.4	1.00	NaN	1.02	1.11	1.01	0.88	0.83	0.86	0.80
Q9UPT8	Zinc finger CCCH domain-containing protein 4	ZC3H4	1104	S	0.947	89.15	1.05	NaN	1.13	0.90	0.96	0.88	0.82	0.90	0.96
Q9UPT8	Zinc finger CCCH domain-containing protein 4	ZC3H4	1110	S	0.754	88.57	1.08	NaN	0.93	0.98	NaN	NaN	1.05	NaN	0.87
Q9UPT8	Zinc finger CCCH domain-containing protein 4	ZC3H4	1114	S	0.917	94.62	1.05	0.98	0.95	0.94	0.86	0.78	NaN	0.95	0.78
Q9UPT8	Zinc finger CCCH domain-containing protein 4	ZC3H4	908	S	0.83	80.36	NaN	NaN	1.09	1.23	1.92	2.02	1.02	NaN	NaN
Q9UPT8	Zinc finger CCCH domain-containing protein 4	ZC3H4	159	S	1	87.16	1.10	1.16	1.12	1.06	1.25	1.07	0.93	0.83	NaN

Q9UPT8	Zinc finger CCCH domain-containing protein 4	ZC3H4	1269	S	0.695	45.13	1.54	1.80	NaN	NaN	NaN	NaN	1.96	NaN	NaN
Q9UPT8	Zinc finger CCCH domain-containing protein 4	ZC3H4	1275	S	1	94.92	0.89	1.80	1.04	1.11	1.06	0.59	1.96	1.04	0.97
Q9UPU5	Ubiquitin carboxyl-terminal hydrolase 24	USP24	1943	S	1	111.7	NaN	NaN	NaN	1.01	NaN	NaN	0.77	NaN	0.67
Q9UPU5	Ubiquitin carboxyl-terminal hydrolase 24	USP24	2047	S	1	103.3	0.72	0.83	0.83	0.74	0.94	0.79	0.90	1.11	0.89
Q9UPU7	TBC1 domain family member 2B	TBC1D2B	957	S	1	172.1	1.81	0.85	0.94	0.76	0.74	0.58	1.10	1.49	1.35
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	1404	S	0.997	270.5	0.73	0.82	0.65	0.86	NaN	0.71	0.62	0.70	0.59
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	1415	S	0.905	52.1	0.72	0.61	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	1012	S	0.625	79.37	1.58	1.33	NaN	NaN	NaN	NaN	1.40	NaN	NaN
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	1014	S	0.998	150.9	1.33	1.38	NaN	1.37	1.37	1.28	NaN	1.44	1.57
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	2132	S	1	85.86	1.34	1.28	1.62	NaN	NaN	1.39	1.41	1.55	1.42
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	1188	S	0.999	60.46	2.33	2.11	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	454	S	1	110.4	0.97	NaN	NaN	NaN	NaN	NaN	1.25	0.72	NaN
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	455	S	0.989	114.9	0.88	0.74	NaN	0.68	NaN	NaN	0.70	NaN	0.63
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	456	S	0.995	114.9	0.88	NaN	NaN	0.80	0.72	0.63	1.20	NaN	0.62
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	1318	S	1	122.8	0.48	0.55	0.71	0.82	0.79	0.66	1.81	1.21	1.41
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	1320	S	1	246.3	1.24	1.27	1.41	1.04	1.06	1.05	1.06	1.25	1.12
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	1329	S	1	160.8	1.11	1.08	1.12	1.08	1.01	1.04	1.39	1.39	1.38
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	2740	S	1	60.12	1.11	1.09	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	1124	S	0.999	134	1.04	0.95	1.08	1.28	1.18	1.32	0.98	0.96	0.89
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	322	S	0.999	263.5	0.84	0.82	1.18	0.91	1.15	1.05	1.40	1.25	0.94
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	323	S	0.999	245	0.90	0.96	0.93	0.88	0.88	0.83	0.95	0.99	1.12
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	1072	S	0.787	97.47	NaN	0.49	NaN	NaN	NaN	NaN	0.58	0.46	NaN
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	1073	S	0.905	97.16	0.54	NaN	0.53	0.51	NaN	0.53	NaN	NaN	0.51

Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	1482	S	1	120.8	0.51	0.48	0.61	0.71	0.62	0.74	0.98	0.60	0.58
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	1483	S	1	172.2	0.64	0.58	0.49	0.78	0.62	0.63	0.73	0.60	0.70
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	1762	S	1	53	1.13	NaN	NaN	NaN	1.15	NaN	1.16	1.16	NaN
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	1764	S	1	53	1.13	NaN	NaN	NaN	1.15	NaN	1.16	1.16	NaN
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	435	S	1	121	0.95	0.95	1.02	0.97	0.83	0.99	0.99	0.97	0.98
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	436	S	1	121	0.95	0.95	1.02	0.97	0.83	0.99	0.99	0.97	0.98
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	437	S	1	121	0.95	0.95	1.02	0.97	0.84	0.99	0.99	0.91	0.89
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	440	S	1	121	0.95	0.95	1.02	0.97	0.84	0.99	0.99	0.91	0.89
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	377	S	0.999	170.5	1.00	1.91	0.97	1.33	0.88	1.53	1.08	1.10	NaN
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	387	S	0.986	92.7	NaN	2.09	1.20	NaN	NaN	NaN	NaN	NaN	NaN
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	398	S	0.873	170.5	0.97	1.07	0.97	1.33	0.92	1.53	0.82	1.10	NaN
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	892	S	0.792	92.94	NaN	NaN	NaN	NaN	0.98	0.86	NaN	1.03	NaN
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	895	S	0.724	79.29	NaN	NaN	1.00	NaN	NaN	NaN	1.12	NaN	1.01
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	1462	S	0.659	137.4	NaN	NaN	NaN	NaN	0.87	0.55	0.48	NaN	NaN
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	1463	S	0.922	129.2	0.59	NaN	0.62	0.83	NaN	0.81	0.48	NaN	NaN
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	2690	S	0.942	105.2	0.74	NaN	1.51	NaN	NaN	NaN	NaN	NaN	1.47
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	2692	S	0.999	94.19	1.40	1.59	NaN	1.30	1.18	1.27	1.39	1.41	NaN
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	2694	S	1	105.2	1.40	1.59	1.51	1.30	1.18	1.27	1.39	1.41	1.47
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	1179	S	1	160	0.86	0.83	0.87	0.99	1.04	0.97	0.56	0.78	0.80
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	2449	S	0.948	211.3	2.16	2.23	2.42	NaN	2.09	1.75	NaN	2.06	1.89
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	2121	S	0.927	55.84	0.98	1.41	1.44	NaN	2.10	NaN	NaN	0.84	NaN
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	2123	S	0.934	55.84	0.98	1.41	1.44	NaN	2.10	NaN	NaN	0.84	NaN
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	2100	S	1	98	1.00	1.00	1.21	1.01	0.93	1.07	1.12	1.18	NaN

Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	2102	S	1	98	1.00	1.00	1.21	1.01	0.93	1.07	1.12	1.18	NaN
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	854	S	0.917	78.16	0.95	0.78	1.60	0.91	NaN	1.55	0.83	2.17	2.32
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	857	S	1	203.2	0.76	0.75	0.74	0.87	0.77	1.55	0.92	0.88	0.92
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	1083	S	1	173.6	0.98	0.99	0.99	0.95	1.07	0.97	1.07	1.07	1.11
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	994	S	0.98	86.55	1.96	1.70	1.96	1.71	1.45	1.68	1.83	2.13	1.86
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	839	S	0.746	70.65	1.23	1.26	1.32	1.23	1.14	1.31	1.24	NaN	1.38
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	2702	S	1	89.56	1.04	1.10	0.99	0.92	0.94	0.97	1.05	1.07	1.14
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	1729	S	1	59.15	NaN	1.31	0.43	NaN	0.51	NaN	NaN	0.77	NaN
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	1732	S	1	59.15	NaN	1.31	0.43	NaN	0.51	NaN	NaN	0.77	NaN
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	950	S	1	76.05	1.22	1.36	1.18	1.27	1.18	1.15	NaN	1.59	1.56
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	952	S	1	102.7	0.80	0.91	1.02	1.28	1.02	0.95	0.95	0.95	0.75
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	954	S	0.999	127.3	0.39	0.40	0.42	0.45	0.45	0.42	0.40	0.41	0.38
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	957	S	0.917	69.11	NaN	NaN	NaN	NaN	1.18	1.21	NaN	1.59	1.56
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	1691	S	0.896	47.61	1.12	1.37	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	1694	S	0.964	80.68	0.58	0.55	0.54	0.65	0.59	0.63	NaN	NaN	NaN
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	2581	S	0.984	127.8	0.97	1.01	0.97	0.97	0.98	0.94	1.06	1.07	1.09
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	346	S	0.975	51.7	1.06	1.09	NaN	NaN	1.01	0.92	1.15	NaN	NaN
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	351	S	0.996	102.1	1.00	1.04	1.05	0.95	0.94	0.92	1.09	1.08	1.10
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	353	S	1	102.1	1.00	1.04	1.05	0.95	0.94	0.92	1.09	1.08	1.09
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	875	S	1	156.7	1.04	1.10	NaN	NaN	1.06	1.37	1.27	1.23	1.92
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	876	S	1	236.9	1.02	1.08	0.98	1.02	1.06	1.09	1.25	NaN	1.25
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	1132	S	1	131	NaN	0.82	0.84	0.95	0.95	0.94	0.71	0.74	0.76
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	1444	S	1	148.5	NaN	0.65	0.69	0.74	0.71	NaN	NaN	0.60	NaN

Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	1541	S	0.97	51	NaN	NaN	0.54	NaN	0.89	0.38	0.75	0.66	NaN
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	1550	S	0.604	50.51	NaN	NaN	0.54	NaN	0.89	NaN	0.59	0.66	NaN
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	846	S	0.538	75.18	0.95	NaN	1.02	1.58	NaN	1.09	2.11	0.81	2.32
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	778	S	1	85.86	2.64	2.39	2.47	1.99	4.32	1.49	2.07	3.97	2.58
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	780	S	1	85.86	2.64	2.56	2.47	1.99	1.85	1.49	1.68	3.16	2.25
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	782	S	0.671	96.64	1.04	2.39	0.92	NaN	1.85	1.07	2.56	NaN	NaN
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	783	S	0.988	89.9	2.64	2.56	2.47	0.97	4.32	1.84	2.47	2.51	0.96
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	2067	S	1	73.93	2.36	1.20	0.24	1.22	1.23	1.28	1.19	1.21	1.28
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	2071	S	1	73.93	2.36	1.20	1.32	1.22	1.23	1.28	1.19	1.21	1.28
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	1916	S	1	112.6	0.92	0.94	0.96	0.95	0.97	0.98	1.11	1.01	NaN
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	2046	S	1	80.98	0.24	0.19	1.58	1.29	1.35	1.35	1.58	1.59	1.67
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	1497	S	1	122.6	0.80	0.52	1.09	1.03	1.08	1.00	1.25	1.19	1.19
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	1499	S	1	122.6	0.80	1.10	1.09	1.03	1.08	1.00	1.25	1.19	1.19
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	1501	S	1	103.3	1.17	0.52	1.09	1.07	1.10	1.02	1.28	1.27	1.22
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	1502	S	1	122.6	1.11	1.10	1.09	1.03	1.08	1.00	1.25	1.19	1.19
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	1099	S	0.99	52.93	NaN	NaN	NaN	1.11	1.16	1.07	1.37	1.27	1.54
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	1101	S	0.986	52.93	1.31	1.19	NaN	1.11	1.16	1.07	1.37	1.27	1.54
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	1102	S	0.887	88.77	1.31	1.19	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	1103	S	0.999	166.5	0.89	0.86	0.81	0.63	0.56	0.57	0.70	0.75	0.85
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	1112	S	0.955	93.88	0.68	0.63	0.69	0.72	0.59	0.65	0.56	0.80	0.77
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	2020	S	1	76.85	1.36	1.42	1.34	1.17	1.22	1.20	1.42	1.43	1.48
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	2407	S	0.992	57.53	1.67	1.67	1.60	1.38	NaN	1.38	1.48	1.58	1.49
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	1925	S	1	72.58	1.37	1.38	1.27	1.19	NaN	1.20	1.45	1.42	1.52

Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	1975	S	0.948	86.11	1.14	0.75	0.76	0.81	0.83	0.84	0.90	0.85	NaN
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	1893	S	0.91	77.87	0.70	0.73	NaN	0.84	0.80	0.79	0.94	0.94	0.88
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	1987	S	0.997	128.9	0.75	0.72	0.70	0.76	0.78	0.79	0.91	0.92	0.93
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	1382	S	0.905	170	1.60	1.33	NaN	NaN	NaN	NaN	0.92	NaN	NaN
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	1387	S	1	232.7	0.92	0.89	0.88	0.83	0.76	0.80	0.86	0.89	0.83
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	901	S	0.766	66.39	NaN	NaN	0.91	NaN	0.89	0.83	NaN	NaN	0.97
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	902	S	0.717	76.16	NaN	NaN	NaN	NaN	NaN	NaN	NaN	1.08	1.09
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	908	S	0.996	93.39	0.97	0.91	0.91	0.84	0.87	0.84	1.06	1.08	0.97
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	910	S	0.652	52.25	NaN	1.80	1.06	NaN	NaN	NaN	NaN	1.11	1.14
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	912	S	0.968	93.39	NaN	1.02	1.07	1.00	NaN	NaN	1.07	1.11	1.14
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	913	S	0.584	48.33	NaN	1.80	1.06	NaN	NaN	NaN	1.07	NaN	1.18
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	914	S	0.818	93.39	NaN	1.02	1.07	1.00	NaN	NaN	1.07	1.11	1.10
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	295	S	1	199	1.15	1.14	1.08	0.93	1.01	0.92	1.11	1.09	1.22
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	297	S	0.999	199	1.15	1.14	1.08	0.93	0.99	0.92	1.11	1.12	1.22
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	2398	S	0.993	158.9	1.02	1.06	1.10	1.01	0.99	0.95	1.04	1.21	1.20
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	972	S	0.812	91.28	NaN	NaN	NaN	0.66	NaN	0.80	0.76	NaN	NaN
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	973	S	0.773	91.28	NaN	NaN	NaN	0.66	NaN	0.80	0.76	NaN	NaN
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	974	S	0.8	86.94	NaN	NaN	NaN	0.66	0.75	0.80	NaN	NaN	NaN
Q9UQR0	Sex comb on midleg-like protein 2	SCML2	267	S	0.548	81.73	NaN	NaN	NaN	NaN	0.96	0.91	NaN	0.49	NaN
Q9Y232	Chromodomain Y-like protein	CDYL	201	S	1	80.98	0.98	0.94	1.17	1.10	1.26	1.32	0.71	0.81	0.85
Q9Y2D5	A-kinase anchor protein 2	AKAP2	152	S	0.955	218.9	2.21	2.48	2.48	1.67	1.61	1.72	1.57	1.61	1.62
Q9Y2D5	A-kinase anchor protein 2	AKAP2	393	S	1	195.5	1.04	0.87	1.25	1.01	1.07	0.99	0.79	1.29	1.04
Q9Y2D5	A-kinase anchor protein 2	AKAP2	778	S	0.985	229.3	1.24	1.36	1.51	1.05	0.96	1.17	1.25	1.34	1.30
Q9Y2U5	Mitogen-activated protein kinase kinase kinase 2	MAP3K2	163	S	0.63	98.53	1.14	0.96	NaN	NaN	NaN	NaN	1.11	NaN	NaN
Q9Y2U8	Inner nuclear membrane protein Man1	LEMD3	140	S	0.998	85.56	1.37	1.19	1.72	1.49	1.79	1.28	0.91	1.11	1.20

Q9Y2U8	Inner nuclear membrane protein Man1	LEMD3	141	S	0.994	85.56	1.37	1.19	1.72	1.49	1.79	1.28	0.91	1.11	1.20
Q9Y2W1	Thyroid hormone receptor-associated protein 3	THRAP3	243	S	1	228.6	1.19	1.16	1.15	1.09	1.17	1.15	1.28	1.25	1.32
Q9Y2W1	Thyroid hormone receptor-associated protein 3	THRAP3	248	S	1	110.9	1.27	1.31	1.24	1.13	1.14	1.13	1.46	1.44	1.48
Q9Y2W1	Thyroid hormone receptor-associated protein 3	THRAP3	253	S	1	110.9	3.18	3.17	3.22	4.02	4.42	1.36	1.00	0.77	NaN
Q9Y2W1	Thyroid hormone receptor-associated protein 3	THRAP3	379	S	1	205.9	2.03	2.78	2.77	1.99	2.36	NaN	2.66	2.44	2.60
Q9Y2W1	Thyroid hormone receptor-associated protein 3	THRAP3	682	S	0.999	155.5	1.05	1.10	1.10	1.02	1.08	1.08	1.28	1.13	1.34
Q9Y2W1	Thyroid hormone receptor-associated protein 3	THRAP3	575	S	1	65.81	0.98	1.09	1.32	1.94	1.81	1.55	1.67	1.56	NaN
Q9Y2W1	Thyroid hormone receptor-associated protein 3	THRAP3	672	S	1	66.71	0.90	0.97	0.93	0.87	NaN	0.90	0.97	0.97	1.01
Q9Y2W1	Thyroid hormone receptor-associated protein 3	THRAP3	535	S	0.995	91.32	0.99	NaN	NaN	0.94	NaN	NaN	1.21	NaN	1.09
Q9Y2W1	Thyroid hormone receptor-associated protein 3	THRAP3	55	S	0.994	76.28	0.42	NaN	NaN	NaN	0.50	NaN	0.42	0.45	0.48
Q9Y2X3	Nucleolar protein 58	NOP58	502	S	1	168.5	0.89	0.88	0.89	0.74	0.66	0.67	1.15	0.90	1.03
Q9Y2X3	Nucleolar protein 58	NOP58	514	S	1	168.5	1.13	1.09	1.01	1.58	2.58	1.32	0.73	0.78	0.97
Q9Y3E7	Charged multivesicular body protein 3	CHMP3	200	S	1	153	1.02	1.02	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Q9Y3F4	Serine-threonine kinase receptor-associated protein	STRAP	335	S	0.998	110	NaN	3.32	NaN	2.27	NaN	2.22	1.34	1.65	NaN
Q9Y3F4	Serine-threonine kinase receptor-associated protein	STRAP	338	S	0.998	110	NaN	3.32	NaN	2.27	NaN	2.22	1.34	1.65	NaN
Q9Y3T9	Nucleolar complex protein 2 homolog	NOC2L	672	S	1	218.4	1.20	NaN	NaN	1.13	1.13	NaN	NaN	1.05	NaN
Q9Y3T9	Nucleolar complex protein 2 homolog	NOC2L	673	S	1	218.4	1.20	NaN	NaN	1.13	1.13	NaN	NaN	1.05	NaN
Q9Y3T9	Nucleolar complex protein 2 homolog	NOC2L	49	S	1	78.65	0.67	0.73	0.71	0.97	1.04	0.57	0.90	0.83	0.96
Q9Y3T9	Nucleolar complex protein 2 homolog	NOC2L	56	S	0.885	78.65	1.49	NaN	NaN	NaN	1.30	1.38	0.59	NaN	NaN
Q9Y426	C2 domain-containing protein	C2CD2	438	S	0.608	52.73	0.88	1.11	NaN	NaN	NaN	NaN	0.84	NaN	NaN
Q9Y490	Talin-1	TLN1	425	S	0.996	161	0.74	NaN	NaN	1.63	1.74	NaN	NaN	NaN	NaN
Q9Y4B5	Microtubule cross-linking factor 1	MTCL1	756	S	0.947	81.2	0.32	NaN	0.37	0.56	0.51	NaN	NaN	0.46	0.42
Q9Y4B5	Microtubule cross-linking factor 1	MTCL1	1421	S	1	80.53	0.84	0.90	0.77	0.99	0.97	0.94	0.86	0.89	0.79
Q9Y4B5	Microtubule cross-linking factor 1	MTCL1	263	S	1	90.53	1.04	1.01	1.17	1.40	1.34	1.31	1.22	1.26	1.47
Q9Y4B5	Microtubule cross-linking factor 1	MTCL1	306	S	1	65.09	NaN	0.71	0.59	NaN	NaN	0.72	0.78	0.82	0.78

Q9Y4B5	Microtubule cross-linking factor 1	MTCL1	1812	S	1	80.54	0.76	NaN	0.80	1.11	0.95	NaN	0.83	0.92	0.80
Q9Y4B5	Microtubule cross-linking factor 1	MTCL1	1814	S	1	80.54	0.76	NaN	0.80	1.11	0.95	NaN	0.83	0.92	0.80
Q9Y4B5	Microtubule cross-linking factor 1	MTCL1	776	S	1	215.1	0.76	0.81	NaN	NaN	NaN	0.85	NaN	NaN	0.67
Q9Y4B5	Microtubule cross-linking factor 1	MTCL1	549	S	0.994	67.5	NaN	NaN	0.94	1.44	NaN	1.46	NaN	NaN	0.82
Q9Y4G2	Pleckstrin homology domain-containing family M member 1	PLEKHM1	435	S	0.778	80.78	NaN	NaN	NaN	0.78	NaN	1.24	NaN	NaN	NaN
Q9Y4H2	Insulin receptor substrate 2	IRS2	730	S	0.592	111.8	1.41	1.88	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Q9Y4H2	Insulin receptor substrate 2	IRS2	731	S	0.948	183.8	NaN	1.24	NaN	1.30	0.94	0.86	NaN	NaN	NaN
Q9Y4H2	Insulin receptor substrate 2	IRS2	735	S	0.864	183.8	1.20	1.88	1.08	0.91	2.53	NaN	0.94	0.97	0.86
Q9Y4H2	Insulin receptor substrate 2	IRS2	1203	S	0.866	217.7	2.25	1.93	2.40	NaN	1.62	NaN	NaN	NaN	NaN
Q9Y4H2	Insulin receptor substrate 2	IRS2	973	S	0.852	102.6	0.79	0.87	NaN	NaN	NaN	NaN	NaN	0.81	NaN
Q9Y4H2	Insulin receptor substrate 2	IRS2	976	S	0.867	69.98	NaN	NaN	NaN	0.74	0.72	NaN	0.92	NaN	NaN
Q9Y4P1	Cysteine protease ATG4B	ATG4B	383	S	1	158.4	1.27	1.33	NaN	1.52	1.21	1.27	1.36	1.36	NaN
Q9Y4P8	WD repeat domain phosphoinositide-interacting protein 2	WIPI2	412	S	0.7	139	0.83	NaN	0.73	0.83	NaN	0.82	1.07	NaN	1.05
Q9Y5B6	PAX3- and PAX7-binding protein 1	PAXBP1	262	S	1	84.67	1.11	1.16	NaN	1.02	1.18	1.09	NaN	NaN	0.96
Q9Y5J1	U3 small nucleolar RNA-associated protein 18 homolog	UTP18	206	S	0.999	245.6	0.68	NaN	NaN	0.89	0.82	NaN	NaN	0.87	NaN
Q9Y5J1	U3 small nucleolar RNA-associated protein 18 homolog	UTP18	210	S	1	245.6	0.71	0.79	0.94	0.84	0.82	0.83	0.79	0.95	0.90
Q9Y5J1	U3 small nucleolar RNA-associated protein 18 homolog	UTP18	121	S	1	271.7	0.69	0.71	0.77	0.79	0.77	0.72	0.66	0.63	0.67
Q9Y5J1	U3 small nucleolar RNA-associated protein 18 homolog	UTP18	124	S	1	183.6	0.83	0.57	0.49	0.49	0.52	0.54	0.68	0.76	0.78
Q9Y5T5	Ubiquitin carboxyl-terminal hydrolase 16	USP16	415	S	1	197.3	0.59	0.64	0.56	0.69	0.58	0.58	0.77	0.80	0.66
Q9Y5T5	Ubiquitin carboxyl-terminal hydrolase 16	USP16	552	S	0.748	190	0.55	0.64	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Q9Y608	Leucine-rich repeat flightless-interacting protein 2	LRRFIP2	260	S	0.999	70.06	NaN	NaN	2.03	1.61	1.28	1.54	3.46	3.85	4.08
Q9Y608	Leucine-rich repeat flightless-interacting protein 2	LRRFIP2	328	S	1	254.2	1.07	1.10	1.03	0.90	0.93	0.88	1.09	1.07	NaN
Q9Y608	Leucine-rich repeat flightless-interacting protein 2	LRRFIP2	320	S	0.817	109	NaN	NaN	NaN	NaN	NaN	NaN	2.43	1.76	NaN
Q9Y613	FH1/FH2 domain-containing protein 1	FHOD1	523	S	1	51.98	3.30	2.88	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Q9Y6D5	Brefeldin A-inhibited guanine nucleotide-exchange protein 2	ARFGEF2	218	S	0.999	133.7	1.76	1.76	1.65	1.50	1.47	1.60	1.28	1.38	1.34
Q9Y6D5	Brefeldin A-inhibited guanine nucleotide-exchange protein 2	ARFGEF2	227	S	1	133.7	1.76	1.76	1.65	1.50	1.47	1.60	1.28	1.38	1.34

Q9Y6D5	Brefeldin A-inhibited guanine nucleotide-exchange protein 2	ARFGEF2	1528	S	1	133.9	NaN	NaN	NaN	NaN	0.81	1.21	1.34	NaN	1.46
Q9Y6D5	Brefeldin A-inhibited guanine nucleotide-exchange protein 2	ARFGEF2	349	S	0.704	77.36	NaN	0.82	NaN	NaN	NaN	NaN	1.13	1.22	NaN
Q9Y6I3	Epsin-1	EPN1	435	S	1	103.9	NaN	NaN	NaN	3.19	2.66	NaN	NaN	NaN	NaN
Q9Y6Q9	Nuclear receptor coactivator 3	NCOA3	728	S	1	66.57	NaN	2.08	1.70	2.47	2.96	1.64	0.80	1.19	0.86
Q9Y6X9	MORC family CW-type zinc finger protein 2	MORC2	615	S	1	43.12	0.71	0.54	NaN	NaN	NaN	NaN	NaN	NaN	NaN
S5FZ81		PHF10	376	S	0.999	45.14	0.86	NaN	NaN	NaN	1.23	0.87	0.93	1.57	NaN
S5FZ81	PHD finger protein 10	PHF10	297	S	1	119.9	0.81	0.58	0.81	NaN	0.89	0.53	0.71	0.93	0.77
S5FZ81	PHD finger protein 10	PHF10	301	S	1	119.9	0.81	0.58	0.81	NaN	0.89	0.53	0.71	0.93	0.77
E7ER32	MKL/myocardin-like protein 1	MKL1	450	T	0.98	172.9	1.26	1.45	NaN	NaN	NaN	NaN	NaN	NaN	NaN
A0A087WUZ3	Spectrin beta chain, non-erythrocytic 1	SPTBN1	2161	T	0.806	107.4	NaN	0.65	NaN	0.74	0.87	0.76	1.12	1.06	0.96
A0A087WVA8	Testis-expressed sequence 2 protein	TEX2	269	T	0.836	116.8	NaN	NaN	NaN	NaN	1.25	1.35	NaN	0.90	NaN
Q15136	cAMP-dependent protein kinase catalytic subunit beta;cAMP-dependent protein kinase catalytic subunit gamma;cAMP-dependent protein kinase catalytic subunit	KIN27	181	T	1	216.2	1.24	1.00	1.10	1.29	NaN	NaN	0.80	0.87	1.01
A0A087WW66	26S proteasome non-ATPase regulatory subunit 1	PSMD1	311	T	0.998	84.95	NaN	0.95	0.95	1.04	1.08	1.22	1.01	0.98	1.26
A0A087WW66	26S proteasome non-ATPase regulatory subunit 1	PSMD1	273	T	1	218	1.72	1.62	NaN	2.09	2.25	NaN	NaN	NaN	NaN
A0A087WWA3	Kinesin-like protein;Kinesin-like protein KIF1B	KIF1B	1049	T	0.972	46.76	0.70	0.64	NaN	NaN	NaN	NaN	NaN	NaN	NaN
A0A087WWA3	Kinesin-like protein;Kinesin-like protein KIF1B	KIF1B	1426	T	0.804	69.82	NaN	0.48	0.62	NaN	NaN	NaN	NaN	NaN	NaN
A0A087WWJ1	DNA mismatch repair protein Msh6	MSH6	923	T	0.987	64.04	NaN	NaN	NaN	1.29	1.28	NaN	0.53	NaN	NaN
A0A499FJY3	Putative RNA-binding protein 15	RBM15	524	T	1	76.68	0.88	0.87	0.76	0.82	0.88	0.83	0.89	0.89	0.92
A0A087WWY2		FOLR2	157	T	0.964	48.11	0.80	0.67	NaN	NaN	0.73	NaN	0.81	0.98	NaN
A0A087WWY2		FOLR2	160	T	0.963	48.11	0.80	0.67	NaN	NaN	0.73	NaN	0.81	0.98	NaN
A0A087WZ13	Ribonucleoprotein PTB-binding 1	RAVER1	463	T	1	81.79	1.77	1.88	NaN	1.79	1.84	NaN	NaN	1.39	NaN
B7Z385	Adenylyl cyclase-associated protein;Adenylyl cyclase-associated protein 2	CAP2	199	T	0.711	121.6	NaN	0.48	NaN	0.86	0.66	NaN	0.56	0.54	NaN
A0A087X1A5	Double-stranded RNA-binding protein Staufen homolog 1	STAU1	196	T	0.615	56.37	1.44	1.23	1.63	NaN	NaN	2.32	NaN	NaN	NaN
E9PL71	Elongation factor 1-delta	EEF1D	123	T	1	359	1.18	1.20	1.12	1.45	1.45	1.50	1.91	1.31	1.35
F8W7U3	WASH complex subunit FAM21C;WASH complex subunit FAM21A	FAM21C	331;243	T	1	98.76	1.10	1.12	1.31	1.19	1.00	1.14	1.01	1.21	1.10

Q5JSD2	Voltage-dependent anion-selective channel protein 2	VDAC2	113	T	0.691	73.31	NaN	NaN	NaN	0.70	0.70	NaN	NaN	NaN	NaN
A0A0A0MRW1	Protein FAM219A	FAM219A	84	T	1	172.4	1.06	1.19	NaN	1.84	NaN	1.26	NaN	0.82	1.11
A0A0A0MSK5	Torsin-1A-interacting protein 1	TOR1AIP 1	99	T	1	185	2.19	2.16	NaN	NaN	NaN	NaN	2.16	1.49	NaN
K7EP41	Glucose-6-phosphate isomerase	GPI	109	T	0.98	49.24	1.17	NaN	1.12	NaN	NaN	0.93	NaN	1.13	1.37
F8WF49	Disks large-associated protein 4	DLGAP4	221	T	1	105.8	1.00	1.36	NaN	1.28	1.67	NaN	1.46	1.25	NaN
A0A2R8YCY2	Protein furry homolog	FRY	1920	T	0.522	47.65	NaN	NaN	NaN	0.79	0.82	NaN	NaN	0.86	NaN
A0A0C4DH22	Band 4.1-like protein 1	EPB41L1	475	T	0.995	119.9	NaN	NaN	1.58	1.33	1.38	1.16	0.95	0.96	0.95
Q5QPR4	Cyclin-dependent kinase 11A;Cyclin-dependent kinase 11B	CDK11A	702	T	0.542	98.7	1.25	1.29	1.60	1.12	NaN	NaN	1.13	NaN	NaN
A0A0D9SEV0	Bifunctional polynucleotide phosphatase/kinase;Polynucleotide 3'-phosphatase;Polynucleotide 5'-hydroxyl-kinase	PNKP	118	T	1	174.5	0.57	0.63	0.52	0.64	0.50	0.62	0.78	0.61	0.75
H7C3Z6	Mitogen-activated protein kinase kinase kinase kinase 4	MAP4K4	240	T	0.705	54.2	NaN	NaN	NaN	NaN	NaN	NaN	NaN	1.03	1.16
A0A0G2JMS7	Protein scribble homolog	SCRIB	1468	T	0.937	101.5	NaN	NaN	NaN	NaN	NaN	NaN	1.44	NaN	1.33
A0A0J9YWL0	Absent in melanoma 1 protein	AIM1	933	T	0.813	72.91	0.58	NaN	0.69	NaN	NaN	NaN	0.75	NaN	1.01
A0A1B0GTL5			899	T	0.887	95.07	1.04	1.05	1.21	1.13	NaN	1.10	1.28	1.26	1.23
A0A1B0GUM1	Pleckstrin homology domain-containing family A member 7	PLEKHA7	91	T	0.541	92.73	0.51	1.04	0.69	NaN	NaN	NaN	NaN	NaN	NaN
H0YN01	Talin-2	TLN2	236	T	1	94.36	1.42	0.78	0.73	0.75	0.74	0.71	1.13	1.09	1.05
B4DP61	Survival motor neuron protein	SMN2	25	T	0.809	132.5	NaN	2.60	NaN	2.50	1.05	1.04	0.96	0.99	0.99
A0A2R8YF61	Cyclin-dependent kinase 13	CDK13	649	T	1	82.55	0.95	1.10	1.28	1.24	1.24	1.18	1.30	1.40	1.10
A0A2R8Y4Z8	Coiled-coil domain-containing protein 9	CCDC9	389	T	0.714	98.77	0.82	0.80	NaN	0.80	NaN	0.98	NaN	NaN	0.78
H0YH87	Ataxin-2	ATXN2	581	T	0.997	64.73	2.07	NaN	0.61	1.90	1.81	2.31	1.91	1.61	1.67
H0Y470	Girdin	CCDC88A	690	T	0.592	230.1	NaN	0.66	NaN	0.82	NaN	0.77	NaN	NaN	0.77
F8WF45	TATA element modulatory factor	TMF1	401	T	0.789	139.8	NaN	NaN	NaN	NaN	1.08	NaN	NaN	1.29	1.08
C9JBX5	Translocon-associated protein subunit alpha	SSR1	192	T	0.644	62.41	1.90	NaN	NaN	NaN	NaN	2.08	0.95	NaN	0.91
A0A3B3ISN0			192	T	0.985	81.77	2.13	2.28	2.43	NaN	1.10	1.03	3.04	3.11	3.13
A0A3F2YNX0	Protein transport protein Sec16A	SEC16A	415	T	0.917	130.9	0.73	NaN	NaN	0.63	1.04	NaN	1.10	NaN	NaN
A0A494BZT8	Transforming acidic coiled-coil-containing protein 3	TACC3	249	T	0.573	73.46	NaN	2.32	NaN	NaN	3.19	3.22	NaN	NaN	NaN
D6RC77	Phosphoacetylglucosamine mutase	PGM3	90	T	0.87	124.1	NaN	NaN	0.46	NaN	0.69	0.84	0.38	NaN	NaN
A0A494C1F2	Nuclear pore complex protein Nup214	NUP214	437	T	0.947	91.66	1.39	NaN	1.62	1.59	NaN	1.50	1.70	NaN	1.33

Q7Z6P5	DNA replication licensing factor MCM3	MCM3	217	T	1	153.3	0.37	0.40	0.42	0.62	0.65	0.67	0.36	0.41	NaN
P07355	Annexin A2;Putative annexin A2-like protein;Annexin	ANXA2	19	T	0.992	220.9	7.38	6.29	6.83	NaN	11.44	11.86	0.65	0.65	0.65
A9Z1X7	Serine/arginine repetitive matrix protein 1	SRRM1	802	T	1	61.1	0.67	0.70	NaN	NaN	0.82	0.85	NaN	1.06	NaN
A9Z1X7	Serine/arginine repetitive matrix protein 1	SRRM1	220	T	1	146.3	0.99	1.01	0.97	0.95	0.96	0.96	1.01	1.00	1.05
A9Z1X7	Serine/arginine repetitive matrix protein 1	SRRM1	401	T	1	109.5	1.68	1.63	1.46	1.30	1.17	1.36	1.34	1.37	1.48
A9Z1X7	Serine/arginine repetitive matrix protein 1	SRRM1	881	T	1	180	1.88	1.64	2.18	1.86	1.43	1.43	2.55	1.30	1.94
A9Z1X7	Serine/arginine repetitive matrix protein 1	SRRM1	590	T	1	65.88	1.15	1.15	1.31	1.14	1.19	1.24	1.24	1.27	1.32
A9Z1X7	Serine/arginine repetitive matrix protein 1	SRRM1	581	T	1	68	1.15	1.25	1.22	1.10	1.11	1.10	1.15	1.17	1.20
A9Z1X7	Serine/arginine repetitive matrix protein 1	SRRM1	583	T	1	68	1.15	1.25	1.22	1.10	1.11	1.10	1.15	1.17	1.20
A9Z1X7	Serine/arginine repetitive matrix protein 1	SRRM1	623	T	1	106.3	1.24	1.32	1.34	0.93	1.18	1.14	0.90	1.26	1.27
H0YCM0	Non-specific serine/threonine protein kinase;Serine/threonine-	PAK1	121	T	0.769	79.36	NaN	NaN	NaN	NaN	NaN	NaN	0.92	0.87	NaN
E7EX54	Mitogen-activated protein kinase 14	MAPK14	103	T	0.905	109.2	NaN	NaN	NaN	0.91	1.15	NaN	NaN	NaN	NaN
B5MBZ0	Echinoderm microtubule-associated protein-like 4	EML4	910	T	0.995	130.4	NaN	NaN	0.85	0.92	NaN	NaN	1.21	NaN	1.20
F8VRJ2	Nucleosome assembly protein 1-like 1	NAP1L1	21	T	1	185	3.75	3.40	NaN	NaN	3.56	2.34	1.11	NaN	NaN
C9J1H7	Nucleolin	NCL	53	T	0.92	87.9	NaN	NaN	NaN	1.29	1.29	NaN	0.53	0.53	NaN
C9J6P4	Zinc finger CCCH-type antiviral protein 1	ZC3HAV1	273	T	0.998	94.02	NaN	1.15	NaN	1.16	NaN	0.80	NaN	NaN	NaN
C9JC20	NCK-interacting protein with SH3 domain	NCKIPSD	65	T	0.918	50.48	NaN	NaN	NaN	NaN	NaN	NaN	1.17	1.15	NaN
E7EV54	Proline-, glutamic acid- and leucine-rich protein 1	PELP1	598	T	0.941	98.8	NaN	1.14	0.88	NaN	0.97	NaN	1.36	NaN	1.18
C9JN71	Zinc finger protein 878	ZNF878	216	T	0.851	62.24	NaN	NaN	0.55	1.02	0.67	0.53	0.62	0.90	0.67
C9JN71	Zinc finger protein 878	ZNF878	222	T	0.997	62.24	NaN	NaN	0.55	1.02	0.67	0.53	0.62	0.90	0.67
C9K0J5	Ras-associated and pleckstrin homology domains-containing protein 1	RAPH1	1205	T	0.623	77.52	NaN	1.77	NaN	1.84	1.49	NaN	0.86	0.98	0.84
H0Y3P2	Eukaryotic translation initiation factor 4 gamma 2	EIF4G2	468	T	0.713	89.91	NaN	NaN	NaN	1.01	NaN	1.26	1.32	1.37	NaN
H0Y3P2	Eukaryotic translation initiation factor 4 gamma 2	EIF4G2	470	T	1	117.4	NaN	NaN	1.17	1.13	1.12	1.25	1.38	1.23	1.27

H0Y9J2	Calcium/calmodulin-dependent protein kinase type II subunit delta	CAMK2D	41	T	0.988	337.4	0.66	0.57	NaN	NaN	NaN	0.88	0.71	NaN	0.62
D6REC6	Cyclin-dependent kinase 7	CDK7	77	T	0.999	65.84	0.66	NaN	0.53	0.89	0.89	0.83	0.58	0.70	0.80
D6RCF2	Histone H2A;Core histone macro-H2A.1	H2AFY	129	T	1	58.67	NaN	1.71	NaN	3.88	3.61	NaN	NaN	NaN	NaN
E3W994	CLIP-associating protein 2	CLASP2	573	T	0.677	96.81	1.76	2.06	1.62	1.92	NaN	NaN	1.26	1.83	1.63
E5RHT6	ADP-ribosylation factor GTPase-activating protein 1	ARFGAP1	61	T	1	67.99	NaN	1.71	1.78	1.36	1.86	NaN	NaN	2.80	NaN
E7ERH2	S-phase kinase-associated protein 1	SKP1	131	T	1	58.34	0.71	NaN	0.96	NaN	NaN	NaN	1.24	1.13	1.19
E7EV99	Alpha-adducin	ADD1	11	T	0.586	67.9	1.33	2.66	NaN	3.03	2.74	NaN	NaN	0.76	NaN
E7EPK0	LIM and calponin homology domains-containing protein 1	LIMCH1	513	T	0.587	70.41	0.52	0.62	NaN	NaN	NaN	0.82	0.91	1.16	0.64
G3V1Q4	Septin-7	7-Sep	192	T	1	76.49	1.01	1.03	1.10	1.13	1.33	0.94	0.94	0.75	1.15
E7EPN9	Protein PRRC2C	PRRC2C	2675	T	1	126.3	3.68	3.80	4.05	2.84	NaN	2.67	NaN	2.41	2.35
E7EPN9	Protein PRRC2C	PRRC2C	2684	T	0.996	67.06	NaN	3.56	3.34	NaN	NaN	2.20	2.38	2.06	2.34
S4R3H4	Apoptotic chromatin condensation inducer in the nucleus	ACIN1	356	T	0.995	94.38	NaN	0.83	1.32	1.25	1.14	1.27	1.06	0.91	1.08
E7ESS4	Intercellular adhesion molecule 1	ICAM1	308	T	0.999	73.93	0.67	0.59	0.70	1.58	NaN	1.06	NaN	0.53	NaN
E7EX17	Eukaryotic translation initiation factor 4B	EIF4B	97	T	0.739	69.15	NaN	1.41	1.41	NaN	NaN	1.34	NaN	1.26	NaN
E7EX44	Caldesmon	CALD1	552	T	0.794	56.75	0.99	1.11	1.06	NaN	1.12	1.26	1.05	1.03	NaN
F8VZJ2	Nascent polypeptide-associated complex subunit alpha;Nascent polypeptide-associated complex subunit alpha, muscle-specific form	NACA	82	T	1	217.1	1.20	1.09	1.16	1.03	1.02	1.05	1.08	NaN	1.11
E9PFD7	Receptor protein-tyrosine kinase;Epidermal growth factor receptor	EGFR	648	T	0.996	121.4	NaN	NaN	NaN	NaN	NaN	NaN	2.75	NaN	2.86
E9PHI6	Cytoplasmic dynein 1 light intermediate chain 1	DYNC1LI1	396	T	0.822	154.3	NaN	NaN	1.27	0.64	NaN	1.18	0.95	NaN	0.93
E9PHI6	Cytoplasmic dynein 1 light intermediate chain 1	DYNC1LI1	397	T	0.985	147.5	0.94	0.91	1.57	1.70	NaN	2.29	NaN	0.76	0.82
E9PHI6	Cytoplasmic dynein 1 light intermediate chain 1	DYNC1LI1	399	T	0.968	176.1	NaN	0.91	NaN	1.70	0.80	NaN	NaN	NaN	NaN
E9PK52	Band 4.1-like protein 2	EPB41L2	600	T	0.531	58.07	NaN	NaN	NaN	2.04	2.11	NaN	0.86	0.96	NaN
E9PI52	Arginine/serine-rich coiled-coil protein 2	RSRC2	16	T	0.772	79.01	0.83	0.95	1.04	0.97	1.10	0.81	1.29	0.88	1.41
E9PSF4	40S ribosomal protein S3	RPS3	95	T	0.996	167.9	1.74	1.96	2.35	2.12	1.77	2.17	2.05	1.77	2.01
E9PMG1	RalBP1-associated Eps domain-containing protein 1	REPS1	173	T	0.722	132.6	NaN	NaN	0.75	NaN	1.70	0.77	NaN	NaN	0.84
E9PMS6	LIM domain only protein 7	LMO7	555	T	0.839	187.1	2.08	2.09	2.13	2.13	2.18	NaN	1.43	1.18	1.55
E9PMS6	LIM domain only protein 7	LMO7	613	T	1	68.84	NaN	1.07	0.85	NaN	1.14	1.47	0.64	0.73	0.71

E9PS23	Cofilin-1	CFL1	25	T	0.997	128.9	2.66	2.75	2.32	4.77	NaN	4.42	0.93	NaN	0.92
F5H8D7	DNA repair protein XRCC1	XRCC1	422	T	0.999	115.3	0.51	0.54	0.61	0.75	0.69	0.70	0.90	0.87	0.93
F8W6N3	Ubiquitin carboxyl-terminal hydrolase;Ubiquitin carboxyl-terminal hydrolase BAP1	BAP1	499	T	0.876	63.23	1.01	0.69	NaN	NaN	NaN	0.79	0.76	0.78	NaN
P42166	Lamina-associated polypeptide 2, isoforms beta/gamma;Thymopoietin;Thymopentin;Lamina-associated polypeptide 2, isoform alpha;Thymopoietin;Thymopentin	TMPO	74;74	T	1	159.8	1.56	2.60	2.75	2.45	2.58	1.02	2.88	0.70	2.86
H0Y4V9	La-related protein 4B	LARP4B	84	T	0.953	107.2	1.63	1.35	1.22	1.06	NaN	1.18	1.50	0.98	1.68
H0Y4Z8	Rab-like protein 6	RABL6	600	T	1	150.5	1.19	1.15	1.46	1.34	1.06	1.09	1.17	1.36	1.28
H0Y4Z8	Rab-like protein 6	RABL6	469	T	0.967	60.62	1.51	0.54	NaN	0.65	1.35	1.58	1.10	0.49	1.23
H0Y5S9	Casein kinase I isoform	CSNK1E	65	T	0.5	88.16	0.79	NaN	NaN	0.97	0.79	NaN	1.06	1.00	1.01
H0Y6J7		PLXNB2	185	T	0.993	56.92	0.97	0.91	0.91	0.87	0.91	NaN	1.04	1.06	1.08
H7BZT5	Zinc finger protein 185	ZNF185	206;450	T	0.935	187.5	0.92	0.88	0.87	0.92	0.91	0.80	1.38	1.39	1.24
H7BZT5	Zinc finger protein 185	ZNF185	272;516	T	0.963	199.6	NaN	1.08	0.89	NaN	NaN	0.87	NaN	NaN	1.45
H0YE35	Synembryn-A	RIC8A	49	T	0.989	243.2	0.93	1.03	0.95	1.15	0.74	1.11	1.02	1.06	1.00
J3KPH4	Sorting nexin-1	SNX1	41	T	1	198.4	0.69	0.64	1.02	0.75	1.09	0.79	0.82	1.12	0.83
H3BN50		SLC9A3R2	8	T	1	152.7	2.12	1.93	2.11	1.43	1.46	1.41	2.07	NaN	2.14
H3BRW3	Sulfhydryl oxidase;FAD-linked sulfhydryl oxidase ALR	GFER	79	T	1	56.12	NaN	0.75	0.77	0.90	NaN	NaN	1.23	0.86	1.15
J3QLT7	Nucleolar protein 3	NOL3	72	T	0.995	186.2	1.24	0.70	0.85	NaN	0.98	1.03	1.35	1.15	1.11
H7BZT5	Zinc finger protein 185	ZNF185	158	T	0.998	184.4	1.69	1.40	1.89	1.41	1.44	1.27	2.41	2.96	2.38
H7C128		BRD8	255	T	1	85.53	0.73	0.61	NaN	1.06	0.86	NaN	1.06	0.82	0.88
I3L467	Unconventional prefoldin RPB5 interactor 1	URI1	5	T	0.838	46.98	NaN	NaN	NaN	0.89	NaN	NaN	0.60	0.82	NaN
J3QLL0	Importin subunit alpha-1	KPNA2	61	T	0.517	135.4	NaN	NaN	NaN	NaN	NaN	4.44	0.76	0.67	0.84
J3QK89	Calcium homeostasis endoplasmic reticulum protein	CHERP	830	T	0.972	107	0.85	1.03	1.06	NaN	0.87	NaN	1.13	1.07	1.13
J3QSD7	Cyclin-dependent kinase 12	CDK12	691	T	1	58.68	0.68	NaN	0.78	0.62	0.96	0.76	0.84	0.73	0.82
K4DI93	Cullin-4B	CUL4B	36	T	0.73	76.05	NaN	0.70	NaN	1.22	1.11	1.29	0.71	0.61	NaN
K7ELG9	Protein LSM12 homolog	LSM12	75	T	1	72.89	1.19	1.30	NaN	1.30	0.97	NaN	NaN	2.35	NaN
K7EMR2	Choline transporter-like protein 2	SLC44A2	14	T	1	74.79	0.63	0.70	0.58	0.81	NaN	0.69	0.70	0.91	NaN
M0QXD6	General transcription factor IIF subunit 1	GTF2F1	305	T	0.929	90.96	NaN	2.18	6.35	NaN	NaN	NaN	NaN	NaN	NaN
M0QXD6	General transcription factor IIF subunit 1	GTF2F1	247	T	1	68.13	NaN	0.82	0.73	0.98	1.00	1.03	0.94	0.91	0.97
M0QZ09	NAD-dependent protein deacetylase sirtuin-6	SIRT6	220	T	1	66.6	1.30	1.10	1.15	1.17	0.96	1.10	1.03	0.86	1.09
O00267	Transcription elongation factor SPT5	SUPT5H	1034	T	0.981	69.76	NaN	NaN	1.81	3.84	NaN	NaN	0.64	0.95	NaN

O15173	Membrane-associated progesterone receptor component 2	PGRMC2	211	T	1	311.2	0.93	0.84	0.89	0.98	0.93	1.00	1.20	1.20	1.19
O43379	WD repeat-containing protein 62	WDR62	1148	T	0.827	60.01	NaN	NaN	0.37	NaN	0.64	NaN	NaN	0.67	0.67
O43379	WD repeat-containing protein 62	WDR62	1053	T	0.693	52.96	NaN	NaN	0.59	NaN	NaN	NaN	NaN	0.65	0.80
O43493	Trans-Golgi network integral membrane protein 2	TGOLN2	296	T	0.788	152.6	NaN	1.40	NaN	NaN	2.11	1.33	NaN	1.28	NaN
O43765	Small glutamine-rich tetratricopeptide repeat-containing protein alpha	SGTA	81	T	0.989	121.9	0.64	0.87	0.77	1.25	1.16	1.08	0.91	1.22	0.95
O43765	Small glutamine-rich tetratricopeptide repeat-containing protein alpha	SGTA	303	T	0.525	239.4	1.45	1.29	NaN	NaN	NaN	NaN	NaN	NaN	NaN
O60271	C-Jun-amino-terminal kinase-interacting protein 4	SPAG9	217	T	1	130.1	3.06	3.42	NaN	2.45	3.05	NaN	3.31	3.75	NaN
O60292	Signal-induced proliferation-associated 1-like protein 3	SIPA1L3	1531	T	0.5	48.33	NaN	0.97	0.81	1.09	NaN	NaN	NaN	NaN	NaN
O60832	H/ACA ribonucleoprotein complex subunit 4	DKC1	458	T	1	45.94	NaN	0.92	1.00	NaN	0.97	0.97	NaN	0.99	NaN
O75475	PC4 and SFRS1-interacting protein	PSIP1	272	T	0.845	271.3	NaN	NaN	0.50	NaN	NaN	NaN	NaN	0.73	0.63
O95674	Phosphatidate cytidylyltransferase 2	CDS2	31	T	0.58	138.9	NaN	1.11	NaN	1.01	0.91	1.02	0.84	0.75	NaN
O95684	FGFR1 oncogene partner	FGFR1OP	170	T	0.895	64.52	NaN	NaN	NaN	3.03	3.10	NaN	NaN	NaN	NaN
O95817	BAG family molecular chaperone regulator 3	BAG3	406	T	1	87.28	1.35	1.01	1.36	2.10	2.30	2.27	0.75	0.82	0.83
P07948	Tyrosine-protein kinase Lyn;Non-specific protein-tyrosine kinase;Tyrosine-protein kinase HCK	LYN	398	T	0.605	76.22	0.55	NaN	0.47	0.30	0.36	0.33	0.95	0.64	NaN
P08670	Vimentin	VIM	336	T	0.897	94.03	NaN	NaN	1.16	1.03	1.09	NaN	1.27	1.18	1.02
P12931	Proto-oncogene tyrosine-protein kinase Src;Non-specific protein-tyrosine kinase;Tyrosine-protein kinase Lck;Tyrosine-protein kinase Fyn;Tyrosine-protein kinase Yes	SRC	420	T	0.759	119.8	NaN	0.81	0.77	0.76	0.80	0.71	1.21	1.05	NaN
P13639	Elongation factor 2	EEF2	435	T	1	82.58	0.93	0.89	0.87	1.50	1.70	1.65	0.67	0.64	0.63
P16144	Integrin beta-4	ITGB4	1530	T	0.993	124.5	1.00	0.99	1.11	1.47	1.40	1.27	1.31	1.40	1.39
P17252	Protein kinase C alpha type;Protein kinase C beta type;Protein kinase C gamma type	PRKCA	501	T	0.587	88.79	0.62	0.60	NaN	NaN	NaN	0.58	1.09	1.11	NaN

P17275	Transcription factor jun-B	JUNB	255	T	1	140.3	4.31	NaN	NaN	0.99	NaN	1.22	NaN	5.63	5.63
P18858	DNA ligase 1;DNA ligase	LIG1	195	T	0.967	128.7	0.49	0.54	NaN	NaN	0.81	NaN	NaN	NaN	NaN
P26641	Elongation factor 1-gamma	EEF1G	43	T	0.837	61.37	0.93	0.98	NaN	NaN	NaN	NaN	NaN	NaN	NaN
P27816	Microtubule-associated protein 4;Microtubule-associated protein	MAP4	512	T	0.59	117.2	0.55	0.76	NaN	NaN	1.65	1.81	NaN	NaN	0.68
P27816	Microtubule-associated protein 4;Microtubule-associated protein	MAP4	521	T	1	279.1	0.65	0.65	0.66	0.85	0.85	0.90	0.78	1.10	0.80
P27816	Microtubule-associated protein 4	MAP4	687	T	0.956	72.37	NaN	NaN	NaN	NaN	NaN	0.53	0.83	0.81	1.08
P27824	Calnexin	CANX	562	T	1	187.3	1.11	1.11	0.81	0.81	1.44	1.08	1.06	0.96	0.82
P29966	Myristoylated alanine-rich C-kinase substrate	MARCKS	143	T	1	213	1.04	1.42	1.15	2.23	2.69	1.67	1.05	1.07	0.75
P29966	Myristoylated alanine-rich C-kinase substrate	MARCKS	150	T	1	301.2	1.97	2.17	2.35	1.82	1.93	1.93	2.38	3.47	2.51
P29966	Myristoylated alanine-rich C-kinase substrate	MARCKS	120	T	0.731	170.9	2.78	2.75	NaN	NaN	0.76	NaN	NaN	NaN	NaN
P29966	Myristoylated alanine-rich C-kinase substrate	MARCKS	133	T	0.671	91.1	NaN	1.14	1.39	0.68	NaN	NaN	NaN	NaN	NaN
P36507	Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	394	T	1	144.6	1.24	1.31	1.24	NaN	NaN	1.17	1.50	1.43	1.54
P41743	Protein kinase C iota type	PRKCI	564	T	1	186.1	0.56	0.94	0.88	0.75	0.77	0.76	0.82	0.89	0.77
P46087	Probable 28S rRNA (cytosine(4447)-C(5))-methyltransferase	NOP2	784	T	0.637	68.52	1.44	NaN	1.33	NaN	NaN	1.97	NaN	NaN	NaN
P46821	Microtubule-associated protein 1B;MAP1B heavy chain;MAP1 light chain LC1	MAP1B	1067	T	0.97	102.2	1.10	1.31	1.42	2.20	2.41	2.38	1.37	NaN	1.25
P46821	Microtubule-associated protein 1B;MAP1B heavy chain;MAP1 light chain LC1	MAP1B	2305	T	0.73	43.81	NaN	NaN	NaN	NaN	NaN	4.40	0.69	NaN	1.00
P46821	Microtubule-associated protein 1B;MAP1B heavy chain;MAP1 light chain LC1	MAP1B	704	T	1	51.01	NaN	0.48	NaN	NaN	0.67	NaN	0.80	0.79	0.80
P46821	Microtubule-associated protein 1B;MAP1B heavy chain;MAP1 light chain LC1	MAP1B	1503	T	0.567	104.8	NaN	0.71	NaN	0.85	0.91	NaN	NaN	0.99	NaN
P46821	Microtubule-associated protein 1B;MAP1B heavy chain;MAP1 light chain LC1	MAP1B	1788	T	1	134.8	1.41	1.38	1.51	1.42	1.32	1.32	1.98	1.74	2.13
P46821	Microtubule-associated protein 1B;MAP1B heavy chain;MAP1 light chain LC1	MAP1B	1282	T	1	122.1	2.11	1.79	2.11	3.51	3.23	3.00	0.81	1.06	0.76

P46821	Microtubule-associated protein 1B;MAP1B heavy chain;MAP1 light chain LC1	MAP1B	1913	T	0.748	169.1	0.73	0.74	0.77	0.91	NaN	0.85	0.89	NaN	0.91
P46821	Microtubule-associated protein 1B;MAP1B heavy chain;MAP1 light chain LC1	MAP1B	1930	T	0.541	139.8	1.08	0.94	NaN	NaN	NaN	1.03	0.74	NaN	NaN
P46821	Microtubule-associated protein 1B;MAP1B heavy chain;MAP1 light chain LC1	MAP1B	1932	T	0.985	125.4	1.19	NaN	NaN	NaN	NaN	NaN	0.82	NaN	0.83
P46821	Microtubule-associated protein 1B;MAP1B heavy chain;MAP1 light chain LC1	MAP1B	1947	T	0.67	143.5	0.78	NaN	NaN	NaN	NaN	NaN	1.19	NaN	1.05
P46937	Transcriptional coactivator YAP1	YAP1	63	T	0.552	222.8	NaN	NaN	0.83	NaN	1.06	0.91	NaN	NaN	0.66
P48634	Protein PRRC2A	PRRC2A	610	T	0.828	71.65	1.65	NaN	1.60	1.78	1.89	1.69	1.29	1.44	1.25
P49006	MARCKS-related protein	MARCKS L1	148	T	0.999	101.4	0.98	0.83	0.83	0.82	1.01	0.73	0.80	0.69	0.63
P49585	Choline-phosphate cytidylyltransferase A	PCYT1A	342	T	0.847	57.2	NaN	NaN	NaN	NaN	NaN	NaN	0.83	NaN	0.58
P51116	Fragile X mental retardation syndrome-related protein 2	FXR2	598	T	0.992	109.7	1.57	1.50	NaN	0.95	NaN	NaN	1.55	NaN	NaN
P52732	Kinesin-like protein KIF11	KIF11	926	T	0.767	78.9	1.38	1.44	1.31	NaN	NaN	2.54	0.53	NaN	0.62
P55081	Microfibrillar-associated protein 1	MFAP1	267	T	1	281.1	0.95	1.20	1.18	0.94	1.14	0.99	1.20	1.13	1.16
P80723	Brain acid soluble protein 1	BASP1	36	T	1	241.5	NaN	1.17	NaN	0.50	0.55	NaN	0.54	0.43	NaN
P80723	Brain acid soluble protein 1	BASP1	196	T	0.929	192.4	2.53	NaN	NaN	3.54	3.07	NaN	2.48	NaN	NaN
P85037	Forkhead box protein K1	FOXK1	436	T	0.999	69.46	1.75	1.84	NaN	1.56	NaN	NaN	NaN	NaN	NaN
P85037	Forkhead box protein K1	FOXK1	245	T	0.687	83.25	NaN	NaN	NaN	1.33	0.84	NaN	NaN	NaN	NaN
Q01130	Serine/arginine-rich splicing factor 2	SRSF2	22	T	0.774	89.98	0.94	NaN	NaN	NaN	NaN	1.15	0.64	NaN	0.88
Q03111	Protein ENL	MLLT1	314	T	0.836	85.62	NaN	NaN	NaN	0.93	NaN	NaN	0.97	NaN	0.87
Q05209	Tyrosine-protein phosphatase non-receptor type 12	PTPN12	509	T	0.915	92.55	NaN	0.79	NaN	NaN	NaN	NaN	1.05	NaN	1.09
Q09666	Neuroblast differentiation-associated protein AHNAK	AHNAK	5729	T	0.67	84.38	NaN	NaN	NaN	1.00	1.11	NaN	0.82	0.84	NaN
Q09666	Neuroblast differentiation-associated protein AHNAK	AHNAK	5839	T	0.738	108.7	NaN	0.89	0.83	0.72	0.87	NaN	0.81	1.13	1.01
Q09666	Neuroblast differentiation-associated protein AHNAK	AHNAK	490	T	1	120.9	0.61	0.75	0.68	1.15	1.27	1.17	0.64	0.60	0.68
Q12906	Interleukin enhancer-binding factor 3	ILF3	486	T	0.545	73.39	0.52	NaN	0.81	NaN	NaN	0.76	1.05	0.96	0.97
Q12906	Interleukin enhancer-binding factor 3	ILF3	592	T	1	133.2	2.88	2.63	2.52	4.67	5.09	4.21	0.76	0.75	0.76
Q13177	Serine/threonine-protein kinase PAK 2;PAK-2p27;PAK-	PAK2	169	T	1	166.9	2.25	1.71	2.19	1.91	1.86	1.46	1.77	1.70	NaN

Q13443	Disintegrin and metalloproteinase domain-containing protein 9	ADAM9	761	T	1	73.41	2.24	NaN	NaN	NaN	2.76	2.66	NaN	NaN	NaN
Q13469	Nuclear factor of activated T-cells, cytoplasmic 2	NFATC2	325	T	0.678	113.2	1.44	0.98	NaN	NaN	NaN	NaN	1.67	NaN	1.55
Q13501	Sequestosome-1	SQSTM1	269	T	1	189.4	1.17	1.42	1.39	1.75	1.49	1.40	0.67	0.58	0.80
Q13541	Eukaryotic translation initiation factor 4E-binding protein 1	EIF4EBP1	68	T	0.882	152.9	0.84	0.71	NaN	2.03	2.61	2.44	1.84	1.44	1.88
Q13541	Eukaryotic translation initiation factor 4E-binding protein 1	EIF4EBP1	70	T	0.757	98.69	2.91	2.68	2.72	2.12	2.38	2.33	0.72	0.83	2.30
Q13541	Eukaryotic translation initiation factor 4E-binding protein 1	EIF4EBP1	37	T	0.883	106.9	2.50	2.34	2.68	2.04	NaN	2.08	2.60	NaN	2.26
Q13541	Eukaryotic translation initiation factor 4E-binding protein 1	EIF4EBP1	46	T	0.951	106.9	2.40	1.93	2.68	2.01	1.91	2.10	NaN	NaN	2.26
Q13542	Eukaryotic translation initiation factor 4E-binding protein 2	EIF4EBP2	36	T	0.736	79.87	NaN	3.40	NaN	NaN	NaN	2.17	3.25	2.70	NaN
Q13595	Transformer-2 protein homolog alpha	TRA2A	88	T	0.997	68.37	1.08	0.50	0.39	0.53	0.83	0.94	1.32	1.24	1.25
Q14247	Src substrate cortactin	CTTN	399	T	0.633	101.8	1.15	1.11	1.22	2.74	2.95	1.02	1.36	1.08	1.43
Q14247	Src substrate cortactin	CTTN	401	T	1	252.6	1.11	0.97	0.95	1.14	1.22	0.99	1.31	1.41	1.32
Q15648	Mediator of RNA polymerase II transcription subunit 1	MED1	1051	T	0.993	64.41	0.81	0.69	0.79	0.84	1.01	0.62	1.27	1.46	0.95
Q15678	Tyrosine-protein phosphatase non-receptor type 14	PTPN14	309	T	0.509	48.22	NaN	NaN	NaN	NaN	0.86	NaN	NaN	1.47	1.30
Q15910	Histone-lysine N-methyltransferase EZH2	EZH2	487	T	1	175.8	0.54	0.54	0.67	1.02	0.70	0.69	0.96	0.82	0.87
Q16513	Serine/threonine-protein kinase N2	PKN2	958	T	1	106.5	NaN	NaN	0.88	0.89	1.24	1.26	0.91	1.00	NaN
Q1RLN5	Rho GTPase-activating protein 12	ARHGAP12	230	T	0.603	117.9	NaN	NaN	NaN	0.88	0.93	1.14	NaN	0.83	0.87
Q1RLN5	Rho GTPase-activating protein 12	ARHGAP12	231	T	0.965	79.29	0.84	0.85	0.80	NaN	0.93	1.46	0.86	0.83	NaN
Q27J81	Inverted formin-2	INF2	1148	T	0.663	88.74	1.27	1.13	NaN	0.66	NaN	NaN	NaN	1.19	NaN
Q2M2I8	AP2-associated protein kinase 1	AAK1	620	T	1	131.1	0.51	0.42	1.41	0.60	0.56	1.34	0.56	0.57	0.55
Q2M2I8	AP2-associated protein kinase 1	AAK1	606	T	0.966	98.37	0.61	0.60	NaN	0.94	NaN	0.94	NaN	NaN	0.88
Q32MZ4	Leucine-rich repeat flightless-interacting protein 1	LRRFIP1	123	T	0.869	114.5	NaN	1.14	1.26	NaN	NaN	NaN	NaN	NaN	NaN
Q3KQU3	MAP7 domain-containing protein 1	MAP7D1	97	T	0.6	46.96	1.03	0.98	0.87	0.95	1.03	1.23	0.90	NaN	NaN
Q4G0J3	La-related protein 7	LARP7	338	T	1	115.3	1.07	1.03	0.93	NaN	1.20	0.91	1.31	1.14	0.97
Q4KMP7	TBC1 domain family member 10B	TBC1D10B	148	T	0.995	99.87	1.50	1.87	NaN	NaN	NaN	NaN	4.15	NaN	NaN
Q4VCS5	Angiomotin	AMOT	12	T	0.691	61.17	0.83	NaN	0.87	0.70	0.78	0.74	0.90	0.94	NaN
Q5VZS7	Programmed cell death protein 4	PDCD4	79	T	0.873	155.2	0.76	0.75	NaN	0.84	NaN	NaN	1.04	NaN	NaN

Q53TN4	Cytochrome b reductase 1	CYBRD1	285	T	0.737	172.6	NaN	0.40	NaN	0.70	NaN	0.76	NaN	NaN	NaN
Q58WW2	DDB1- and CUL4-associated factor 6	DCAF6	654	T	0.999	76.2	0.61	0.62	0.62	NaN	NaN	NaN	NaN	0.98	NaN
Q5JTD0	Tight junction-associated protein 1	TJAP1	422	T	1	82.59	2.30	2.05	NaN	2.30	2.66	2.68	1.12	1.25	NaN
Q5STZ8	ATP-binding cassette sub-family F member 1	ABCF1	109	T	1	123.2	1.17	0.45	2.28	1.61	1.56	1.51	1.76	0.55	0.54
Q5T200	Zinc finger CCCH domain-containing protein 13	ZC3H13	263	T	1	78.99	0.82	0.84	0.91	0.82	0.88	1.04	0.81	0.98	0.75
Q5T2Z0	Proline/serine-rich coiled-coil protein 1	PSRC1	177	T	0.812	56.71	NaN	NaN	0.71	0.67	NaN	0.74	0.90	1.05	0.96
Q5VT52	Regulation of nuclear pre-mRNA domain-containing protein 2	RPRD2	723	T	0.997	57.21	1.19	1.27	NaN	NaN	NaN	NaN	NaN	NaN	2.13
Q5VT52	Regulation of nuclear pre-mRNA domain-containing protein 2	RPRD2	732	T	0.993	117.3	0.43	0.51	0.62	0.80	NaN	0.82	NaN	0.33	NaN
Q63ZY6	Putative methyltransferase NSUN5C	NSUN5P2	258	T	0.986	42.63	NaN	NaN	0.59	NaN	1.12	0.72	NaN	NaN	0.60
Q66K74	Microtubule-associated protein 1S;MAP1S heavy chain;MAP1S light chain	MAP1S	638	T	1	176	0.94	0.99	0.91	0.99	0.93	0.87	1.01	1.04	1.08
Q6IQ49	Protein SDE2 homolog	SDE2	274	T	0.545	78.98	NaN	1.08	NaN	1.15	NaN	NaN	0.97	NaN	1.41
Q6NZI2	Polymerase I and transcript release factor	PTRF	376	T	0.85	131.5	0.57	0.48	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Q6PD62	RNA polymerase-associated protein CTR9 homolog	CTR9	925	T	1	135.8	0.80	0.90	0.79	0.86	0.69	0.89	0.96	0.88	0.98
Q6PKG0	La-related protein 1	LARP1	526	T	1	59.43	2.69	2.45	1.97	NaN	1.97	1.54	2.06	2.20	NaN
Q6QNY0	Biogenesis of lysosome-related organelles complex 1	BLOC1S3	63	T	1	128.9	1.15	1.16	1.25	1.09	1.11	0.39	1.09	0.45	1.16
Q6UN15	Pre-mRNA 3'-end-processing factor FIP1	FIP1L1	494	T	0.565	79.34	NaN	NaN	NaN	NaN	NaN	NaN	1.20	1.02	NaN
Q6ZTN6	Ankyrin repeat domain-containing protein 13D	ANKRD13D	469	T	1	66.08	0.81	0.71	NaN	1.00	1.13	0.81	0.94	1.20	0.91
Q7L4S7	Protein ARMCX6	ARMCX6	166	T	0.587	53.33	1.32	1.22	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Q7Z417	Nuclear fragile X mental retardation-interacting protein	NUFIP2	571	T	0.889	93.84	1.86	1.55	NaN	1.80	1.64	NaN	1.43	0.86	NaN
Q86TB9	Protein PAT1 homolog 1	PATL1	194	T	1	99.34	1.15	1.43	1.64	1.41	1.59	1.65	1.60	1.36	1.58
Q86UP2	Kinectin	KTN1	153	T	1	62.04	0.91	NaN	NaN	1.20	NaN	1.07	1.07	1.08	NaN
Q86UU1	Pleckstrin homology-like domain family B member 1	PHLDB1	417	T	0.732	59.15	5.48	5.63	6.05	NaN	1.96	2.08	6.17	NaN	4.83
Q8N3D4	EH domain-binding protein 1-like protein 1	EHBP1L1	284	T	0.616	180	1.00	NaN	0.98	1.15	1.13	1.03	0.96	0.83	0.82
Q8NC44	Protein FAM134A	FAM134A	279	T	0.997	118.3	NaN	0.99	0.95	NaN	2.01	1.01	1.32	1.34	1.65
Q8NC56	LEM domain-containing protein 2	LEMD2	147	T	1	131.1	0.77	0.78	0.94	0.88	1.04	0.98	NaN	NaN	NaN
Q8ND56	Protein LSM14 homolog A	LSM14A	194	T	0.805	116.8	NaN	1.35	NaN	NaN	NaN	NaN	0.89	NaN	1.25

Q8NI08	Nuclear receptor coactivator 7	NCOA7	210	T	0.673	116.6	0.88	NaN	NaN	1.06	NaN	0.87	0.94	NaN	NaN
Q8WVC0	RNA polymerase-associated protein LEO1	LEO1	629	T	0.681	77.07	0.83	0.86	0.90	NaN	0.62	0.58	NaN	NaN	0.66
Q8WVC0	RNA polymerase-associated protein LEO1	LEO1	188	T	1	56.47	0.68	0.46	NaN	NaN	NaN	NaN	0.66	NaN	NaN
Q8WXX0	Dynein heavy chain 7, axonemal	DNAH7	2197	T	0.989	72.88	NaN	NaN	NaN	0.94	0.76	NaN	NaN	NaN	NaN
Q8WXX0	Dynein heavy chain 7, axonemal	DNAH7	2198	T	0.989	72.88	NaN	NaN	NaN	0.94	0.76	NaN	NaN	NaN	NaN
Q92688	Acidic leucine-rich nuclear phosphoprotein 32 family member B	ANP32B	244	T	1	251.9	0.93	0.96	0.96	0.96	0.97	0.80	0.94	0.95	0.96
Q92692	Nectin-2	PVRL2	410	T	0.997	137.5	0.93	1.14	1.31	1.32	1.28	0.89	1.15	1.43	1.83
Q92797	Symplekin	SYMPK	1257	T	1	120.7	0.67	0.85	0.62	1.11	NaN	1.07	0.78	0.67	0.84
Q92995	Ubiquitin carboxyl-terminal hydrolase 13	USP13	122	T	1	105.5	0.66	0.68	NaN	NaN	NaN	NaN	0.42	NaN	NaN
Q96A49	Synapse-associated protein 1	SYAP1	248	T	1	190.8	NaN	NaN	1.03	0.91	0.88	0.94	1.32	1.32	1.16
Q96N67	Dedicator of cytokinesis protein 7	DOCK7	909	T	0.964	325.4	NaN	0.84	1.09	0.91	NaN	0.78	0.86	NaN	NaN
Q96PK6	RNA-binding protein 14	RBM14	206	T	1	117.5	1.31	1.23	1.28	1.09	1.13	1.09	1.32	1.24	1.27
Q96PX8	SLIT and NTRK-like protein 1	SLITRK1	590	T	0.918	79.04	NaN	NaN	1.05	0.91	0.70	NaN	1.17	1.14	NaN
Q96T23	Remodeling and spacing factor 1	RSF1	628	T	0.599	116.9	NaN	0.62	0.69	NaN	0.95	0.93	0.98	1.11	NaN
Q99442	Translocation protein SEC62	SEC62	158	T	0.972	74.53	1.39	1.37	NaN	NaN	NaN	0.86	1.25	NaN	NaN
Q9BQA1	Methylosome protein 50	WDR77	5	T	1	48.11	1.17	1.28	1.19	1.30	1.18	1.37	1.10	1.00	1.13
Q9BRD0	BUD13 homolog	BUD13	159	T	1	58.78	1.42	1.92	NaN	NaN	NaN	NaN	2.23	2.11	NaN
Q9BRD0	BUD13 homolog	BUD13	135	T	1	71.56	1.47	NaN	1.90	NaN	NaN	NaN	1.76	NaN	NaN
Q9BRQ0	Pygopus homolog 2	PYGO2	302	T	1	167.3	1.06	0.91	1.00	NaN	NaN	0.94	1.01	1.05	0.97
Q9BRS8	La-related protein 6	LARP6	450	T	0.533	57.15	NaN	NaN	NaN	NaN	NaN	NaN	1.48	1.76	1.74
Q9BTC0	Death-inducer obliterator 1	DIDO1	1255	T	0.841	41.59	NaN	NaN	NaN	1.10	1.24	NaN	0.95	NaN	NaN
Q9BTC0	Death-inducer obliterator 1	DIDO1	1256	T	0.841	60.66	NaN	NaN	NaN	1.10	1.24	NaN	0.95	NaN	NaN
Q9BU76	Multiple myeloma tumor-associated protein 2	MMTAG2	215	T	0.956	90.87	0.59	0.73	NaN	NaN	1.35	NaN	1.61	NaN	NaN
Q9BU76	Multiple myeloma tumor-associated protein 2	MMTAG2	219	T	0.95	90.87	0.59	0.73	NaN	0.74	0.60	NaN	NaN	0.76	NaN
Q9BXP5	Serrate RNA effector molecule homolog	SRRT	544	T	1	144.4	0.91	0.97	1.02	1.12	1.12	1.08	1.15	1.24	1.06
Q9C0B5	Palmitoyltransferase ZDHHC5	ZDHHC5	524	T	0.568	60.76	NaN	1.56	1.68	NaN	NaN	1.25	NaN	NaN	NaN
Q9H1E3	Nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	NUCKS1	179	T	1	155.5	1.79	1.89	2.00	3.16	2.83	3.27	1.05	1.04	1.08
Q9H1E3	Nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	NUCKS1	202	T	1	144.7	0.78	1.23	1.27	1.07	0.89	1.17	0.96	1.03	1.37
Q9H6F5	Coiled-coil domain-containing protein 86	CCDC86	65	T	0.874	64.04	0.74	0.65	0.62	0.77	0.74	0.83	NaN	NaN	0.55

Q9H6F5	Coiled-coil domain-containing protein 86	CCDC86	42	T	0.998	122	1.12	NaN	NaN	1.21	NaN	NaN	1.00	1.01	NaN
Q9H7N4	Splicing factor, arginine/serine-rich 19	SCAF1	989	T	1	177	0.77	0.86	0.78	1.30	1.03	0.83	0.64	0.66	1.26
Q9H7N4	Splicing factor, arginine/serine-rich 19	SCAF1	1001	T	0.865	116.5	NaN	NaN	NaN	1.03	NaN	0.99	NaN	NaN	NaN
Q9H7N4	Splicing factor, arginine/serine-rich 19	SCAF1	976	T	0.981	72.37	1.02	0.94	0.89	NaN	0.97	1.00	1.01	0.98	NaN
Q9HA65	TBC1 domain family member	TBC1D17	606	T	0.802	97.04	NaN	NaN	2.02	NaN	NaN	NaN	0.65	1.74	NaN
Q9NQS7	Inner centromere protein	INCENP	219	T	0.787	150.5	1.18	NaN	NaN	2.16	NaN	1.83	NaN	NaN	NaN
Q9NVD7	Alpha-parvin	PARVA	16	T	0.941	129.5	NaN	1.32	0.61	NaN	1.13	0.46	0.90	0.89	1.08
Q9NWZ5	Uridine-cytidine kinase-like 1	UCKL1	53	T	0.86	125.4	1.26	1.23	NaN	NaN	NaN	1.88	0.91	NaN	0.83
Q9P2Q2	FERM domain-containing protein 4A	FRMD4A	696	T	0.5	79.07	NaN	NaN	NaN	NaN	0.74	1.52	NaN	0.86	NaN
Q9UIQ6	Leucyl-cystinyl aminopeptidase;Leucyl-cystinyl aminopeptidase, pregnancy serum form	LNPEP	326	T	0.644	45.92	0.64	NaN	0.65	0.66	0.80	0.68	NaN	0.60	0.91
Q9UK61	Protein FAM208A	FAM208A	921	T	0.598	53.78	0.50	0.50	NaN	NaN	NaN	NaN	NaN	NaN	0.95
Q9UK76	Hematological and neurological expressed 1 protein;Hematological and neurological expressed 1 protein, N-terminally	HN1	54	T	1	183.8	5.27	5.14	4.83	9.89	8.91	10.25	NaN	2.08	NaN
Q9UKJ3	G patch domain-containing protein 8	GPATCH 8	655	T	0.626	69.74	NaN	NaN	NaN	1.50	NaN	1.27	NaN	NaN	0.94
Q9UKK3	Poly [ADP-ribose] polymerase	PARP4	1493	T	0.5	129	0.83	0.65	0.75	0.74	0.70	0.86	1.01	1.03	0.99
Q9UKK3	Poly [ADP-ribose] polymerase	PARP4	1494	T	0.5	129	0.83	0.65	0.75	0.74	0.70	0.86	1.01	1.03	0.99
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	1492	T	1	73.63	NaN	1.25	NaN	NaN	NaN	NaN	1.81	NaN	2.06
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	1003	T	1	181	0.55	0.60	0.50	1.37	0.71	0.74	0.83	0.67	0.85
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	1434	T	1	72.53	1.75	1.78	1.78	1.46	1.59	1.57	1.77	1.65	1.61
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	1208	T	1	110.4	1.05	1.14	1.14	1.06	1.18	1.10	1.13	1.10	1.14
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	1231	T	0.708	77.85	NaN	1.05	0.97	NaN	NaN	NaN	NaN	NaN	NaN
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	2738	T	1	51.03	1.11	1.09	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	383	T	0.778	96.79	NaN	1.75	1.53	1.33	NaN	NaN	NaN	NaN	NaN
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	1177	T	0.726	79.02	0.59	0.62	0.72	0.80	NaN	NaN	NaN	NaN	0.83
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	2104	T	1	98	1.00	1.00	1.21	1.01	0.93	1.07	1.12	1.18	NaN

Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	856	T	0.812	115.8	1.35	1.81	0.68	NaN	NaN	NaN	2.11	0.74	2.32
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	866	T	0.989	119.2	2.66	1.81	1.85	2.15	1.58	1.60	2.45	2.85	2.34
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	2583	T	0.978	66.5	0.94	NaN	1.06	0.98	NaN	0.97	1.06	NaN	1.11
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	2092	T	0.985	56.01	NaN	NaN	0.44	0.58	NaN	0.63	NaN	NaN	0.44
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	848	T	0.917	115.8	0.89	0.83	0.83	0.84	0.82	1.60	0.73	0.74	0.72
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	2069	T	1	68.46	2.36	2.46	2.63	2.00	1.96	NaN	0.28	2.61	NaN
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	2022	T	1	76.85	1.36	1.42	1.34	1.17	1.22	1.20	1.42	1.43	1.48
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	2409	T	1	106.3	0.91	1.07	0.88	0.91	0.98	0.81	1.08	0.97	0.89
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	1927	T	1	72.58	1.37	1.38	1.27	1.19	NaN	1.20	1.45	1.42	1.52
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	1043	T	0.987	157.4	0.88	0.80	0.76	0.97	0.81	0.75	0.99	0.93	0.93
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	903	T	0.903	93.39	0.97	0.91	1.07	NaN	0.85	0.84	1.06	NaN	NaN
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	1527	T	0.862	62.34	2.57	NaN	1.78	1.47	1.57	NaN	2.41	NaN	NaN
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	983	T	1	173.4	0.82	0.80	0.86	0.81	0.85	0.88	0.87	1.05	0.81
Q9Y3P9	Rab GTPase-activating protein 1	RABGAP 1	996	T	1	163.9	1.03	0.84	0.66	0.77	0.81	0.54	0.66	0.89	0.67
Q9Y4B5	Microtubule cross-linking factor 1	MTCL1	1417	T	1	80.53	0.84	0.90	NaN	0.99	0.97	NaN	NaN	0.89	NaN
Q9Y4D8	Probable E3 ubiquitin-protein ligase HECTD4	HECTD4	2080	T	0.999	69.03	0.69	0.76	0.70	0.86	NaN	0.88	1.02	0.80	0.93
Q9Y4H2	Insulin receptor substrate 2	IRS2	1202	T	0.832	183.2	2.45	NaN	2.40	1.37	NaN	1.41	2.38	1.73	1.79
Q9Y4H2	Insulin receptor substrate 2	IRS2	779	T	0.946	56.9	NaN	NaN	NaN	1.45	NaN	1.29	NaN	NaN	NaN
G3V317	Cyclin-dependent kinase 1;Cyclin-dependent kinase 2;Cyclin-dependent kinase 3	CDK2	15	Y	1	100.8	NaN	0.91	NaN	NaN	1.47	1.50	NaN	0.69	0.71
A0A087WY22	Protein-tyrosine-phosphatase;Receptor-type tyrosine-protein phosphatase	PTPRT	1045	Y	1	63.73	NaN	0.80	NaN	0.78	0.74	NaN	NaN	NaN	0.91
A0A087WTN1	Uncharacterized protein C9orf173	C9orf173	76	Y	0.864	46.92	NaN	NaN	NaN	NaN	0.78	0.77	NaN	NaN	0.82
A0A087WWY2		FOLR2	144	Y	0.991	48.11	0.80	0.67	NaN	NaN	0.73	NaN	0.81	0.98	NaN
A0A087X0K9	Tight junction protein ZO-1	TJP1	120;132	Y	0.703	77.04	NaN	NaN	NaN	1.80	1.42	NaN	1.52	NaN	NaN
A0A087X0K9	Tight junction protein ZO-1	TJP1	1440;153	Y	0.527	42.81	0.32	0.57	NaN	NaN	NaN	NaN	NaN	NaN	NaN
A0A096LP07		GPS1	207	Y	0.722	47.13	NaN	NaN	1.60	1.42	1.41	1.36	1.54	1.52	NaN
A0A096LP07		GPS1	217	Y	0.743	47.13	NaN	NaN	1.60	1.42	1.41	1.36	1.54	1.52	NaN

A0A0A0MRA3	Titin	TTN	25698	Y	1	59.26	NaN	NaN	0.78	0.69	0.61	0.71	1.11	1.02	0.95
A0A0A0MRZ4	TNFAIP3-interacting protein 1	TNIP1	7	Y	0.506	50.23	2.02	1.69	NaN	2.72	3.58	NaN	NaN	0.76	NaN
A0A0A0MRZ4	TNFAIP3-interacting protein 1	TNIP1	10	Y	0.506	50.23	2.02	1.69	NaN	2.72	3.58	NaN	NaN	0.76	NaN
A0A0D9SEV1		KCNQ2	566	Y	1	43.99	NaN	NaN	1.49	1.34	1.29	1.02	1.07	1.20	1.14
F5GZ78	Paxillin	PXN	116	Y	0.923	81.8	2.09	2.28	NaN	1.61	1.67	1.38	0.91	NaN	NaN
A0A2R8Y6M1	ATP-binding cassette sub-family G member 8	ABCG8	325	Y	0.998	45.72	NaN	NaN	1.05	NaN	0.83	0.83	NaN	1.24	1.04
A0A2R8YEM9	TPR and ankyrin repeat-containing protein 1	TRANK1	1677	Y	0.999	40.29	NaN	NaN	NaN	1.12	0.95	NaN	NaN	NaN	NaN
A8MT37	Glycogen synthase kinase-3 beta;Glycogen synthase kinase-3 alpha	GSK3A	197	Y	0.987	163.5	NaN	NaN	0.76	NaN	0.71	0.78	1.16	1.16	1.26
A0A3B3IUF8	Rho guanine nucleotide exchange factor 15	ARHGEF 15	253	Y	0.657	47.22	1.43	1.63	NaN	NaN	1.41	NaN	0.89	1.57	NaN
A6NCQ9	RING finger protein 222	RNF222	66	Y	0.784	47.54	NaN	NaN	1.44	1.27	0.73	NaN	0.72	0.91	NaN
P07355	Annexin A2;Putative annexin A2-like protein;Annexin	ANXA2	24	Y	0.896	242.1	0.60	0.68	0.77	0.82	NaN	0.94	0.75	0.76	NaN
E7EX54	Mitogen-activated protein kinase 14	MAPK14	105	Y	0.71	101.6	NaN	NaN	NaN	NaN	NaN	NaN	1.00	NaN	0.88
D6R9P1	Ectonucleotide pyrophosphatase/phosphodiesterase family member 6	ENPP6	131	Y	0.976	46.88	NaN	NaN	NaN	0.75	0.89	NaN	NaN	NaN	NaN
H0YDD4	Acetyltransferase component of pyruvate dehydrogenase complex;Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	DLAT	278	Y	0.599	40.09	NaN	NaN	NaN	0.95	1.17	NaN	NaN	NaN	NaN
H0YE41	Tyrosine-protein kinase;Non-receptor tyrosine-protein kinase TYK2	TYK2	71	Y	1	93.26	NaN	NaN	NaN	NaN	NaN	NaN	1.41	1.27	1.59
F5GZJ9		PPP1R32	26	Y	1	41.62	0.46	0.56	NaN	NaN	NaN	NaN	0.86	0.74	NaN
F5H7D6	Transducin-like enhancer protein 3	TLE3	182	Y	0.949	95.34	NaN	NaN	NaN	0.44	0.39	NaN	NaN	NaN	1.14
F5H7P5	Palmitoyltransferase;Probable palmitoyltransferase ZDHHC11B	ZDHHC11 B	282	Y	0.911	54.74	NaN	NaN	NaN	1.37	NaN	NaN	1.50	1.48	1.45
F6VUX8	Centromere protein J	CENPJ	980	Y	1	44.83	0.70	0.95	1.14	1.00	0.55	NaN	1.28	0.81	NaN
F8VXW2		ARPC1B	124	Y	0.998	41.05	1.25	1.39	NaN	1.11	NaN	0.84	1.29	1.68	NaN
F8W6Z3		ODF3	51	Y	0.991	41.08	NaN	NaN	NaN	NaN	NaN	NaN	2.31	1.26	NaN
H0YGI1	Uncharacterized protein C12orf56	C12orf56	39	Y	0.999	40.29	NaN	NaN	NaN	NaN	NaN	NaN	0.50	0.81	NaN
H7C1A6		ADCY3	10	Y	0.951	40.55	1.07	NaN	NaN	1.02	1.10	NaN	1.29	NaN	NaN
H7C1A6		ADCY3	11	Y	0.999	40.55	1.07	NaN	NaN	1.02	1.10	NaN	1.29	NaN	NaN
J3KSR8	Serine/arginine-rich splicing factor 1	SRSF1	97	Y	0.924	54.95	NaN	NaN	1.27	1.48	1.34	1.27	1.45	1.29	NaN

P49448	Glutamate dehydrogenase 2, mitochondrial;Glutamate dehydrogenase 1,	GLUD2	170	Y	0.937	43.79	NaN	NaN	NaN	NaN	1.23	1.10	1.17	1.08	0.97
P28482	Mitogen-activated protein kinase 1	MAPK1	187	Y	1	250.5	1.99	2.07	1.93	1.93	1.84	1.75	1.11	1.16	1.08
Q13523	Serine/threonine-protein kinase PRP4 homolog	PRPF4B	849	Y	0.986	261.3	1.10	1.07	1.09	1.17	1.12	1.17	1.15	1.14	1.10
Q13541	Eukaryotic translation initiation factor 4E-binding protein 1	EIF4EBP1	34	Y	0.72	81.21	NaN	2.29	2.19	2.01	NaN	2.06	2.05	NaN	2.05
Q13595	Transformer-2 protein homolog alpha	TRA2A	87	Y	0.671	61.44	1.08	NaN	0.97	0.90	0.83	0.94	1.32	1.24	1.25
Q8N2E6	Prosalusin;Salusin-alpha;Salusin-beta;Torsin-2A	TOR2A	185	Y	0.605	42.68	0.96	0.78	1.08	0.90	0.70	0.97	NaN	0.73	NaN
Q8N2E6	Prosalusin;Salusin-alpha;Salusin-beta;Torsin-2A	TOR2A	189	Y	0.992	42.68	0.96	0.78	1.08	0.90	0.70	0.97	NaN	0.73	NaN
Q68DU9	Kelch-like protein 8	DKFZp781C1855	353	Y	0.999	43.18	NaN	NaN	NaN	0.96	1.13	1.21	NaN	NaN	1.04
Q6PI26	Protein SHQ1 homolog	SHQ1	344	Y	1	43.59	NaN	NaN	NaN	NaN	NaN	NaN	1.05	0.85	NaN
Q86YV5	Tyrosine-protein kinase SgK223	SGK223	413	Y	0.926	57.29	1.23	0.86	NaN	NaN	0.66	NaN	NaN	NaN	NaN
Q96M20	Cyclic nucleotide-binding domain-containing protein 2	CNBD2	302	Y	0.971	45.88	NaN	NaN	NaN	1.56	2.72	NaN	NaN	NaN	NaN
Q9NWQ8	Phosphoprotein associated with glycosphingolipid-enriched microdomains 1	PAG1	417	Y	1	124.5	NaN	NaN	NaN	0.75	0.52	NaN	NaN	1.13	NaN
Q9NYQ8	Protocadherin Fat 2	FAT2	1877	Y	0.994	43.8	NaN	NaN	NaN	0.89	0.93	0.95	0.40	0.46	NaN
Q9UIQ6	Leucyl-cystinyl aminopeptidase;Leucyl-cystinyl aminopeptidase, pregnancy serum form	LNPEP	325	Y	0.73	45.92	0.64	NaN	0.65	0.66	0.80	0.68	NaN	0.60	0.91

Supplementary Table S3 The Bonding Energy of SFN docking to RAFs

Software			Autodock4 [1]	Autodock Vina [2]	DockThor [3]
Protein	PDB id	ligand	Bonding energy (Kcal/mol)	Bonding energy (Kcal/mol)	Affinity (Kcal/mol)
A-RAF	1wxm	R,S-SFN	-2.8	-3.78	-6.909
		R-SFN	-3.0	-3.69	-6.988
		S-SFN	-2.8	-4.37	-6.909
B-RAF	6p3d	R,S-SFN	-3.7	-5.19	-7.139
		R-SFN	-4.0	-5.12	-7.139
		S-SFN	-4.0	-5.47	-7.144
C-RAF	3omv	R,S-SFN	-3.8	-5.0	-7.522
		R-SFN	-3.0	-5.34	-7.421
		S-SFN	-3.4	-5.27	-6.849

References

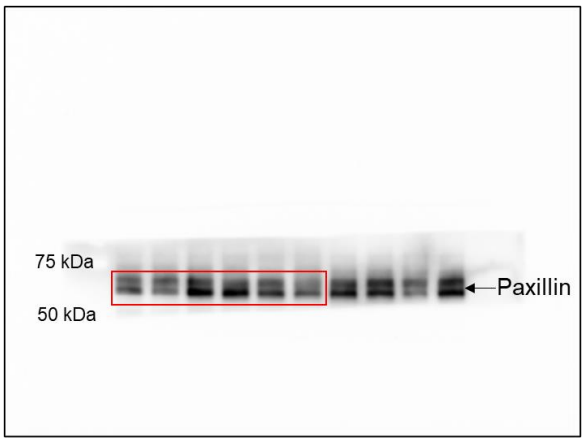
[1] Morris, G.M. et al. AutoDock4 and AutoDockTools4: Automated docking with selective receptor flexibility. *J Comput Chem* **30,** 2785-2791 (2009).

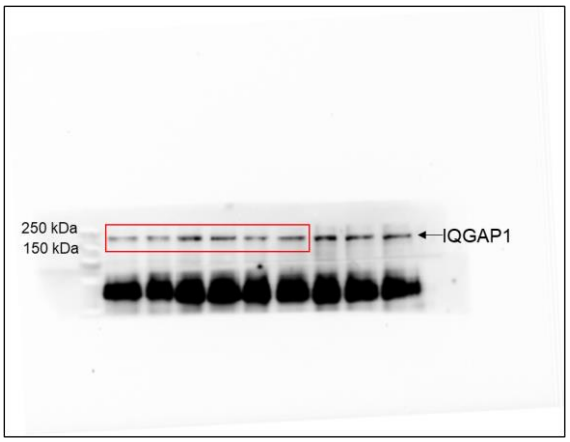
[2] Trott, O., & Olson, A.J. AutoDock Vina: improving the speed and accuracy of docking with a new scoring function, efficient optimization, and multithreading. *J Comput Chem* **31,** 455-461 (2010).

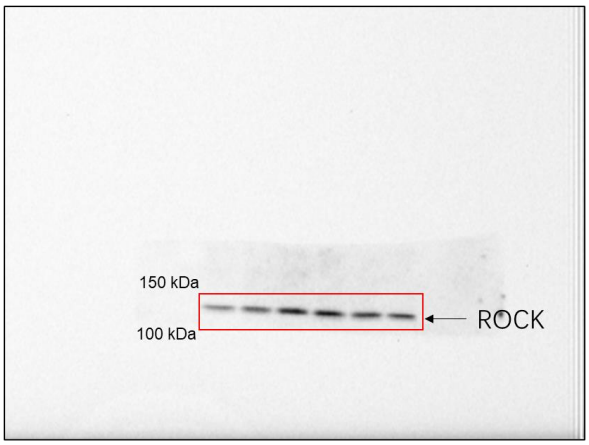
[3] Santos, K.B., Guedes, I.A., Karl, A.L.M., & Dardenne, L.E. Highly Flexible Ligand Docking: Benchmarking of the DockThor Program on the LEADS-PEP Protein-Peptide Data Set. *J Chem Inf Model* **60,** 667-683 (2020).

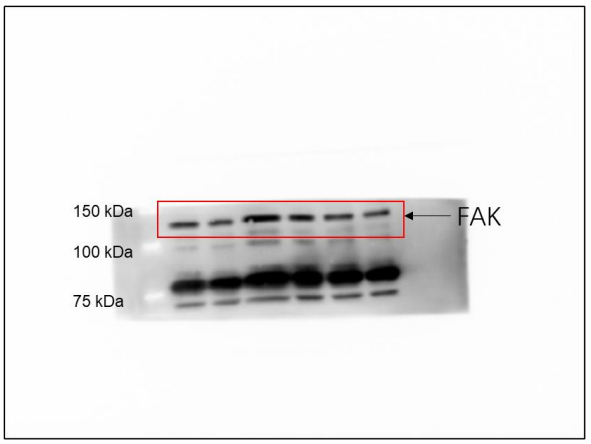
Supplementary Figure S1

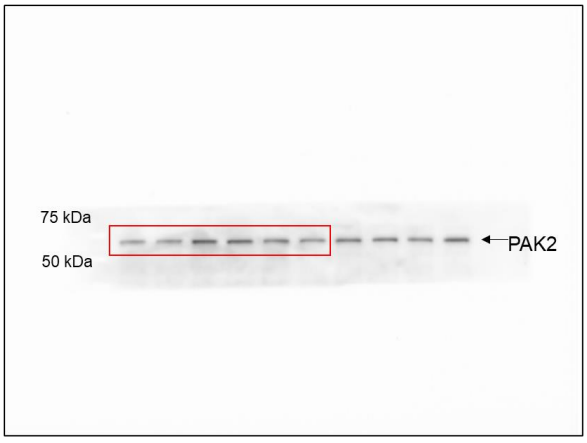
Uncropped western blots presented in Figure 7A are shown.

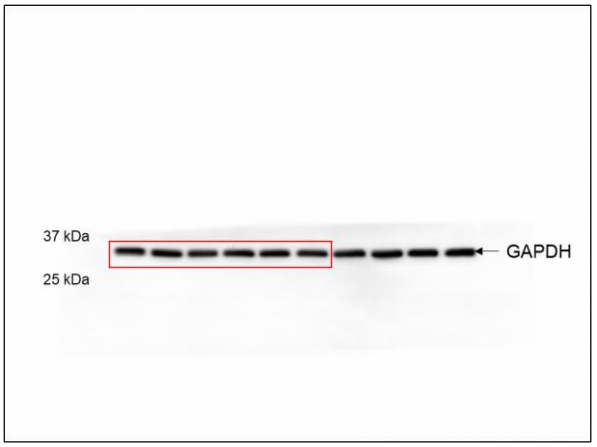






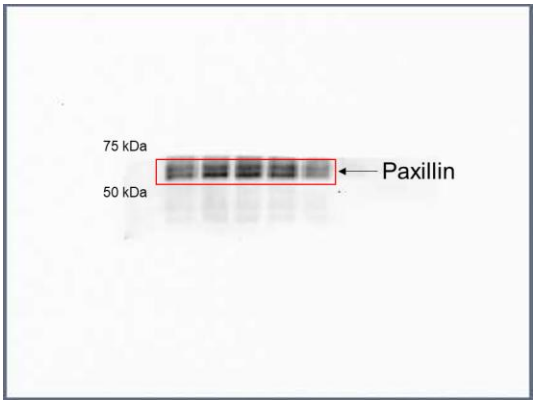


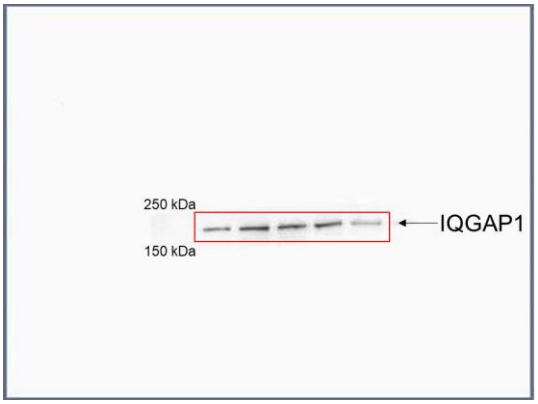


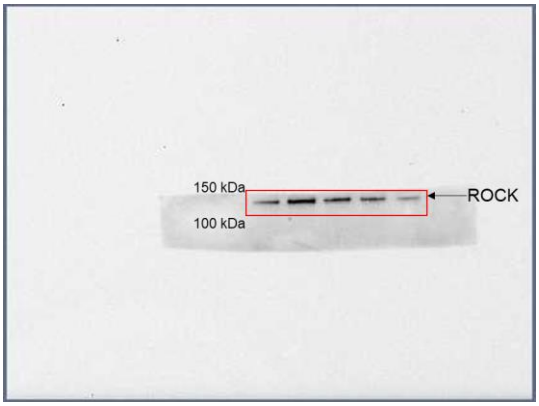


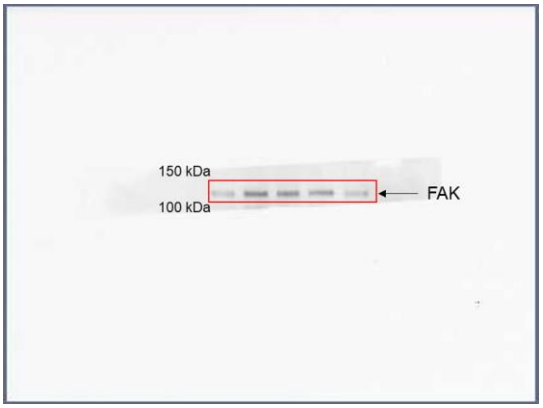
Supplementary Figure S1

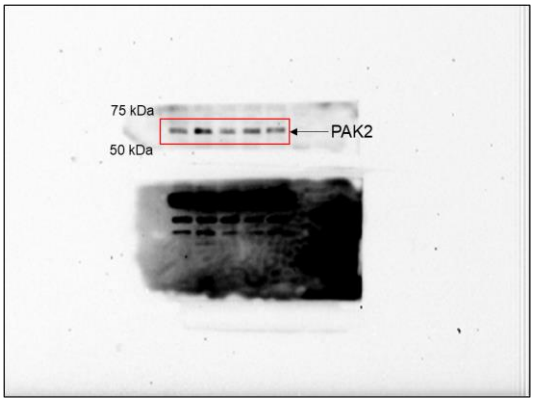
Uncropped western blots presented in Figure 7B are shown.

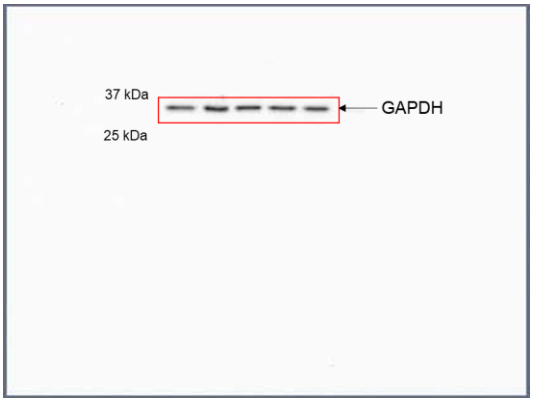












Supplementary Figure S1

Uncropped western blots presented in Figure 8A are shown.