Suppplementary Information for

"6-Thioguanine Induces Mitochondrial Dysfunction and Oxidative DNA Damage in Acute Lymphoblastic Leukemia Cells"

by

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Table S1. A list of all quantified proteins and their expression ratios in ^{S}G-treated cells versus control untreated cells. Displayed are the Maxquant-derived normalized ratios of light/heavy (“L/H”)-labeled proteins (UniProt Protein ID, Protein Name, and Gene Name are shown) obtained from two forward (labeled as “F1” and “F2”) and one reverse (labeled as “R”) SILAC labeling experiments. The “L/H” ratios obtained from forward SILAC experiments represent the protein expression ratios in ^{S}G-treated versus untreated cells. For convenient comparison, the Maxquant-derived normalized ratios of heavy/light (“H/L”)-labeled proteins obtained from reverse SILAC labeling experiment are also listed; these ratios represent the protein expression ratios in ^{S}G-treated versus untreated cells. The mean [“Mean (T/U)”] and standard deviation (“S.D.”) of protein expression ratios in ^{S}G-treated versus untreated cells derived from at least two sets (including one reverse labeling) of SILAC labeling experiments are also listed, where those proteins with a “NA” under the “S.D.” column designate that they were quantified in only one set of SILAC labeling experiment. Shown also are the number of peptides identified for each protein (“Pep. No.”) and percent sequence coverage (“%Seq. Cov.”) for each quantified protein.

UniProt ID	Protein_Name	Gene Name	F1 (L/H)	F2 (L/H)	R1 (H/L)	R1 (L/H)	Mean (T/U)	S.D.	Pep. No.	%Seq. Cov.	PEP
P61626	1,4-beta-N-acetylmuramidase C	LYZ			0.03	33.33	0.03		2	27	1.61E-80
P31025	Lipocalin-1	LCN1			0.04	25.00	0.04		5	27	1.14E-30
Q02383	Semenogelin II	SEMG2			0.05	20.00	0.05		3	7.6	1.07E-13
P05109	Calgranulin-A	CAGA			0.08	12.50	0.08		2	24	5.17E-15
Q6N092	Putative uncharacterized protein DKFZp686K18196	DKFZp686K18196			0.08	12.50	0.08		2	5	1.87E-02
A2NYV2	Light chain Fab	CyAT1			0.08	12.50	0.08		3	15	1.07E-08
P01833	Hepatocellular carcinoma-associated protein TB6	PIGR			0.11	9.09	0.11		3	6.4	3.62E-156
Q9P275	Deubiquitinating enzyme 36	KIAA1453			0.13	7.69	0.13		3	3.8	3.96E-03
P41134-1	Class B basic helix-loop-helix protein 24	BHLHB24	0.14				0.14		2	19	2.74E-13
Q13422	Ikaros family zinc finger protein 3	IKZF3			0.15	6.67	0.15		3	7.5	4.16E-06
P69905	Alpha-globin	HBA1			0.15	6.67	0.15		3	28	9.69E-13
P02788	Lactoferrin	LTF			0.18	5.56	0.18		9	17	2.81E-251
Q96Q83-1	Alkylated DNA repair protein alkB homolog 3	ABH3			0.21	4.76	0.21		2	9.1	4.83E-06
Q8WXE9-1	Stoned B	STN2			0.22	4.55	0.22		2	2.4	2.27E-04
B4DYZ3	Uncharacterized protein C8orf45	C8orf45			0.23	4.35	0.23		2	2.9	1.39E-03

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P11532	Dystrophin	DMD			0.23	4.35	0.23		2	0.6	1.13E-02
Q53172	Putative uncharacterized protein	IGKC			0.24	4.17	0.24		3	23	2.83E-82
P12883	Myosin heavy chain 7	MYH7			0.30	3.33	0.30		5	3.3	2.07E-14
P09382	14 kDa laminin-binding protein	LGALS1	0.32		0.30	3.33	0.31	0.01	3	24	1.00E-25
P02545-1	70 kDa lamin	LMNA		0.32			0.32		5	7.2	8.34E-14
Q6UXB8-1	Cysteine-rich secretory protein 9	CRISP9		0.41	0.30	3.33	0.36	0.08	3	8.4	1.13E-41
Q8WXG9-1	G-protein coupled receptor 98	GPR98	0.24	0.33	0.52	1.92	0.36	0.14	2	0.7	5.22E-02
B4DN86	cDNA FLJ56047, highly similar to A kinase anchor protein 1, mitochondrial	AKAP1			0.40	2.50	0.40		2	5	1.34E-74
Q5H9S7	DDB1- and CUL4-associated factor 8	DCAF8			0.40	2.50	0.40		2	2.5	7.57E-04
Q6ZN13	cDNA FLJ16525 fis, clone OCBBF2005433, weakly similar to N-CHIMAERIN	ARHGAP9		0.41			0.41		2	2.3	1.32E-03
O60443	Inversely correlated with estrogen receptor expression 1	DFNA5			0.43	2.33	0.43		2	4.6	4.17E-05
Q8WVM0	Dimethyladenosine transferase 2, mitochondrial	NS5ATP5			0.43	2.33	0.43		2	6.6	1.47E-05
Q8NB37-2	Parkinson disease 7 domain-containing protein 1	PDDC1	0.32	0.54	0.44	2.27	0.43	0.11	2	14	3.13E-14
Q99707	5-methyltetrahydrofolate--homocysteine methyltransferase	MTR	0.38	0.46	0.48	2.08	0.44	0.05	3	2.9	2.51E-13
Q9Y2C4-1	Endonuclease G-like 1	ENDOGL1			0.44	2.27	0.44		2	7.6	1.45E-08
P11802	Cell division protein kinase 4	CDK4			0.44	2.27	0.44		3	12	4.27E-05
Q9UJY4	ADP-ribosylation factor-binding protein GGA2	GGA2			0.44	2.27	0.44		3	9	5.59E-05
O14776	Nuclear transcription factor, X box-binding protein 1	NFX1			0.45	2.22	0.45		2	2.5	1.66E-03
Q14197	Digestion substraction 1	DS1		0.45			0.45		2	8.9	3.68E-18
P10606	Cytochrome c oxidase polypeptide Vb	COX5B	0.39	0.51	0.46	2.17	0.45	0.06	3	23	1.84E-05
P63313	Thymosin beta-10	PTMB10	0.39	0.52			0.46	0.09	3	32	8.54E-05
Q16342	Programmed cell	PDCD2			0.46	2.17	0.46		3	9.3	1.90E-21

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	death protein 2										
Q8NEY8	Gastric cancer antigen Ga50	HSPC206			0.46	2.17	0.46		3	6.2	3.54E-05
Q9NU22	MIDAS-containing protein	KIAA0301			0.46	2.17	0.46		4	1.5	3.75E-09
A6NMH8	Putative uncharacterized protein CD81	CD81	0.13		0.82	1.22	0.48	0.49	2	16	1.11E-19
Q9H8H0	Nucleolar protein 11	L14			0.48	2.08	0.48		2	4	8.92E-09
P49821-1	Complex I-51kD	NDUFV1		0.48			0.48		2	3.9	2.28E-04
O60488-1	Long-chain acyl-CoA synthetase 4	ACS4		0.48			0.48		2	4.1	1.57E-14
Q9H8V3-2	Epithelial cell-transforming sequence 2 oncogene	ECT2	0.57	0.32	0.56	1.79	0.48	0.14	2	2.2	2.29E-27
B7Z6C0	cDNA FLJ56946, highly similar to Cysteine-rich protein 2	CRIP2	0.31	0.40	0.76	1.32	0.49	0.24	2	17	7.60E-33
Q9Y618-1	CTG repeat protein 26	CTG26			0.49	2.04	0.49		3	2.1	8.00E-08
Q99490-1	Arf-GAP with GTPase, ANK repeat and PH domain-containing protein 2	AGAP2		0.49			0.49		2	1.4	1.37E-03
O75794	Cell division cycle protein 123 homolog	C10orf7	0.64		0.37	2.70	0.51	0.19	3	9.5	6.31E-23
P08590	Cardiac myosin light chain 1	MYL3	0.52	0.50	0.51	1.96	0.51	0.01	2	14	1.52E-77
P00403	Cytochrome c oxidase polypeptide II	MT-CO2	0.56		0.46	2.17	0.51	0.07	3	30	9.46E-27
P49427	Ubiquitin-conjugating enzyme E2 R1	CDC34			0.51	1.96	0.51		2	11	3.82E-04
O95343	Homeobox protein SIX3	SIX3			0.51	1.96	0.51		2	9.3	2.10E-27
Q6PFW2	Rho guanine nucleotide exchange factor (GEF) 11	ARHGEF11		0.51			0.51		2	1.2	7.01E-03
B4DNS2	cDNA FLJ51602, highly similar to Interferon-induced guanylate-binding protein 1	GBP1	0.51				0.51		2	7.6	3.83E-03
P14927	Complex III subunit 7	UQBP	0.51				0.51		4	41	1.05E-32
O75879	Cytochrome oxidase assembly factor PET112 homolog	HSPC199	0.42		0.62	1.61	0.52	0.14	2	4.7	8.02E-09
O43566-5	Regulator of G-protein signaling 14	RGS14		0.52			0.52		2	3.7	7.92E-05
O95865	Dimethylargininase-2	DDAH	0.47	0.45	0.65	1.54	0.52	0.11	9	43	6.37E-120
P42575-1	Caspase-2	CASP2	0.48		0.57	1.75	0.53	0.06	6	21	1.66E-24

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Q9NUV9	GTPase IMAP family member 4	GIMAP4	0.50	0.54	0.54	1.85	0.53	0.02	8	23	6.25E-33
Q01970	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta-3	PLCB3	0.94		0.12	8.33	0.53	0.58	4	4.6	2.60E-22
B4DSL6	cDNA FLJ57190, highly similar to Actin-binding protein anillin	ANLN			0.53	1.89	0.53		2	3.8	8.42E-07
P82094-2	Androgen receptor coactivator 160 kDa protein	ARA160	0.53				0.53		3	4.3	5.49E-18
O75155-1	Cullin-associated and neddylation-dissociated protein 2	CAND2	0.68		0.39	2.56	0.54	0.21	9	11	6.16E-54
P09669	Cytochrome c oxidase polypeptide VIc	COX6C		0.57	0.51	1.96	0.54	0.04	3	21	1.47E-05
Q9UJX4	Anaphase-promoting complex subunit 5	ANAPC5			0.54	1.85	0.54		2	4.8	2.90E-38
Q9ULI4	Kinesin-like protein KIF26A	KIAA1236			0.54	1.85	0.54		2	1.1	3.27E-02
B4DWF2	cDNA FLJ55795, highly similar to Zinc finger protein Helios	hCG_14830		0.54			0.54		3	7.7	3.06E-04
Q86UY6-1	N-acetyltransferase 11	NAA40	0.81		0.28	3.57	0.55	0.37	2	12	1.28E-39
Q15154-1	Pericentriolar material 1 protein	PCM1	0.42	0.66	0.57	1.75	0.55	0.12	12	5.9	6.63E-57
O95229	ZW10 interactor	ZWINT	0.51	0.59			0.55	0.06	3	12	2.37E-47
P12829	Myosin light chain 1, embryonic muscle/atrial isoform	MLC1	0.55				0.55		2	15	8.64E-07
O43683	Mitotic checkpoint serine/threonine-protein kinase BUB1	BUB1		0.68	0.44	2.27	0.56	0.17	3	5.1	3.64E-09
P50748	Kinetochore-associated protein 1	KIAA0166			0.56	1.79	0.56		2	1.1	5.04E-02
Q14699	Cell migration-inducing gene 2 protein	KIAA0084			0.57	1.75	0.57		4	8.1	8.94E-24
Q13190-1	Syntaxin-5	STX5	0.56	0.51	0.66	1.52	0.58	0.08	3	8.2	3.86E-06
O60684	Importin subunit alpha-7	IPOA7			0.58	1.72	0.58		4	11	1.47E-76
O95864	Delta(6) fatty acid desaturase	FADS2			0.58	1.72	0.58		5	13	1.41E-12
Q9UNY4-1	Lodestar homolog	TTF2			0.58	1.72	0.58		9	11	2.60E-52
Q9Y4H4	Activator of G-protein signaling 4	AGS4	0.58				0.58		2	15	7.44E-04
Q9BYD	39S ribosomal protein	MRPL1		0.58			0.58		2	13	1.82E-06

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1	L13, mitochondrial	3									
P61586	Mitochondrial Rho GTPase 1	RHOT1		0.54	0.62	1.61	0.58	0.06	3	4.3	5.32E-17
Q06945	Transcription factor SOX-4	SOX4	0.67	0.49			0.58	0.13	2	12	8.57E-03
P37268	Farnesyl-diphosphate farnesyltransferase	FDFT1	0.53	0.64	0.58	1.72	0.58	0.06	5	15	2.96E-75
Q9NPI6	mRNA-decapping enzyme 1A	DCP1A			0.59	1.69	0.59		2	5.3	9.06E-18
O95486-1	Protein transport protein Sec24A	SEC24A			0.59	1.69	0.59		2	2.6	4.12E-32
Q2M389	WASH complex subunit 7	KIAA1033			0.59	1.69	0.59		4	5.7	1.51E-08
Q15058	Kinesin-like protein KIF14	KIAA0042		0.59			0.59		2	1.3	2.97E-06
O75448	Activator-recruited cofactor 100 kDa component	ARC100	0.59				0.59		2	2.8	6.68E-14
Q9Y2D5-4	AKAP-KL	AKAP2		0.59			0.59		3	2.9	2.31E-17
Q14191	DNA helicase, RecQ-like type 3	RECQ3	0.63		0.55	1.82	0.59	0.06	2	1.5	3.90E-06
A6NED2	RCC1 domain-containing protein 1	RCCD1	0.58	0.68	0.52	1.92	0.59	0.08	3	12	1.81E-24
O95299	NADH dehydrogenase ubiquinone 1 alpha subcomplex	NDUFA10	0.58		0.61	1.64	0.60	0.02	3	13	1.62E-39
P30281	G1/S-specific cyclin-D3	CCND3		0.61	0.58	1.72	0.60	0.02	2	5.5	1.39E-03
Q5TCU8	Tropomyosin 2 (Beta)	RP11-112J3.4-005	0.53	0.66			0.60	0.09	13	27	8.73E-62
Q8ND24	RING finger protein 214	RNF214			0.60	1.67	0.60		2	5.8	4.83E-22
Q15024	Exosome complex exonuclease RRP42	EXOSC7	0.60				0.60		3	13	1.18E-70
P63218	Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-5	GNG5		0.55	0.65	1.54	0.60	0.07	3	27	6.35E-04
Q6RFH5-1	NOP seven-associated protein 1	NSA1		0.71	0.50	2.00	0.61	0.15	3	9.4	1.97E-20
P84101	Gastric cancer-related protein VRG107	FAM2C	0.49	0.72			0.61	0.16	3	32	1.14E-06
C9JG49	Protein tyrosine phosphatase, non-receptor type 6, isoform CRA_b	hCG_25941	0.61	0.59	0.62	1.61	0.61	0.02	31	62	0.00E+00
O60566-3	MAD3/BUB1-related protein kinase	BUB1B	0.55	0.69	0.59	1.69	0.61	0.07	4	5.2	5.97E-46
Q8WVT3	Tetratricopeptide repeat protein 15	CGI-87		0.61			0.61		2	2.9	8.42E-04
Q5T653	39S ribosomal protein	CGI-22		0.61			0.61		2	7.2	1.59E-10

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	L2, mitochondrial										
P50749	Ras association domain-containing protein 2	KIAA0168		0.61			0.61		2	5.5	3.34E-03
Q9UKU7	Activator-recruited cofactor 42 kDa component	ACAD8		0.61			0.61		2	5.8	1.84E-11
P47985	Complex III subunit 5	UQCRFS1	0.61				0.61		9	34	3.15E-90
Q9ULT8	E3 ligase for inhibin receptor	HECTD1	0.51	0.60	0.73	1.37	0.61	0.11	5	2.9	2.20E-47
B4DGI9	cDNA FLJ52589, highly similar to Transcription factor 12	BHLHB20	0.63	0.71	0.51	1.96	0.62	0.10	8	20	2.07E-90
Q9BZL1	Ubiquitin-like protein 5	UBL5	0.64	0.60			0.62	0.03	3	29	4.25E-05
Q96A35	39S ribosomal protein L24, mitochondrial	MRPL24	0.62				0.62		2	9.3	3.32E-08
Q13303-1	K(+) channel subunit beta-2	KCNA2B	0.62				0.62		8	38	2.18E-55
P56962	Syntaxin-17	STX17	0.63	0.65	0.59	1.69	0.62	0.03	2	11	3.45E-42
P51159-1	GTP-binding protein Ram	RAB27	0.67	0.54	0.66	1.52	0.62	0.07	5	24	1.43E-13
Q5T7F6	Novel protein	RP1-153P14.2-002	0.61	0.64			0.63	0.02	2	7.6	1.54E-06
P08670	Vimentin	VIM	0.54	0.54	0.80	1.25	0.63	0.15	51	88	0.00E+00
Q10471	Polypeptide GalNAc transferase 2	GALNT2			0.63	1.59	0.63		5	13	8.60E-64
O43678	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2	NDUFA2	0.63				0.63		2	31	1.74E-04
P22695	Complex III subunit 2	UQCRC2	0.47	0.47	0.96	1.04	0.63	0.28	7	15	4.73E-97
Q96EB1-1	Elongator complex protein 4	C11orf19	0.68	0.55	0.68	1.47	0.64	0.08	4	12	7.59E-12
Q53H12-1	Acylglycerol kinase, mitochondrial	AGK	0.58	0.70			0.64	0.08	3	8.1	5.85E-08
Q14145	Cytosolic inhibitor of Nrf2	INRF2			0.64	1.56	0.64		2	3.4	9.76E-06
Q9H814	Phosphorylated adapter RNA export protein	PHAX			0.64	1.56	0.64		3	10	1.59E-14
Q9NZJ0-1	DDB1- and CUL4-associated factor 2	CDT2		0.64			0.64		2	3	2.18E-04
B4E358	cDNA FLJ54828, highly similar to Src substrate cortactin	CTTN		0.64			0.64		2	2.8	6.53E-03
P0C7P4	Putative cytochrome b-c1 complex subunit Rieske-like protein 1	UQCRFSL1		0.64			0.64		3	8.8	5.35E-04
O00483	Complex I-MLRQ	NDUFA4	0.64				0.64		4	47	3.88E-09

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Q8NDI1-1	EH domain-binding protein 1	EHBP1	0.49	0.72	0.72	1.39	0.64	0.13	3	3.8	5.26E-50
Q96EL3	39S ribosomal protein L53, mitochondrial	MRPL53	0.59	0.70			0.65	0.08	3	41	9.17E-15
Q9UIC8-2	Leucine carboxyl methyltransferase 1	CGI-68	0.57	0.72			0.65	0.11	5	13	9.89E-07
Q9UPP1-1	Histone lysine demethylase PHF8	KIAA1111	0.73	0.56			0.65	0.12	2	2.7	8.84E-16
P31930	Complex III subunit 1	UQCRC1	0.52	0.52	0.90	1.11	0.65	0.22	11	29	7.83E-69
P46108-1	Adapter molecule crk	CRK	0.82	0.87	0.25	4.00	0.65	0.34	5	29	1.47E-136
Q9NP61	ADP-ribosylation factor GTPase-activating protein 3	ARFGAP1	0.77	0.57	0.61	1.64	0.65	0.11	2	4.8	4.11E-07
Q96RT1-1	Densin-180-like protein	ERBB2IP	0.65		0.65	1.54	0.65	0.00	3	3.9	6.35E-16
B7Z6Z4	cDNA FLJ56329, highly similar to Myosin light polypeptide 6	MYL6	0.62	0.65	0.68	1.47	0.65	0.03	7	30	1.78E-142
O94830	DDHD domain-containing protein 2	DDHD2	0.51	0.72	0.72	1.39	0.65	0.12	3	5.2	1.34E-11
Q14CJ1	Amino-terminal enhancer of split	AES	0.75		0.55	1.82	0.65	0.14	3	14	1.39E-22
Q9ULW3	Activator of basal transcription 1	ABT1			0.65	1.54	0.65		2	8.1	1.08E-02
Q86UV5	Deubiquitinating enzyme 48	USP31			0.65	1.54	0.65		2	3.9	3.61E-08
Q5U676	B3GAT3 protein	B3GAT3			0.65	1.54	0.65		2	11	7.71E-08
Q9BTA9	Coiled-coil domain-containing protein 21	CCDC21			0.65	1.54	0.65		2	5.8	9.00E-05
B7Z477	cDNA FLJ55335, highly similar to Tyrosine-protein kinase-like 7	CCK4		0.65			0.65		2	2.1	1.10E-02
Q9H0U6	39S ribosomal protein L18, mitochondrial	HSPC071	0.65				0.65		3	18	4.34E-06
P00167	Cytochrome b5	CYB5	0.65				0.65		2	16	2.01E-04
Q9BQS8-1	FYVE and coiled-coil domain-containing protein 1	FYCO1	0.67		0.65	1.54	0.66	0.01	3	3	1.83E-29
Q9Y448	Putative TRAF4-associated factor 1	C15orf23	0.66	0.64	0.68	1.47	0.66	0.02	3	11	3.84E-32
Q9BXK1	Basic transcription element-binding protein 4	BTEB4	0.69	0.79	0.50	2.00	0.66	0.15	3	31	1.86E-139
A2A305	Ubiquitin associated protein 2	RP11-176F3.6-005	0.79	0.69	0.50	2.00	0.66	0.15	5	12	2.47E-54
Q71RC2-4	La ribonucleoprotein domain family	LARP4	0.78		0.54	1.85	0.66	0.17	4	7.5	7.42E-27

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	member 4										
Q4G148-1	Glucoside xylosyltransferase 1	GLT8D3			0.66	1.52	0.66		2	5.7	1.14E-02
O75330-3	Hyaluronan mediated motility receptor	HMMR			0.66	1.52	0.66		2	4.1	6.20E-05
Q5FBY4	Interferon regulatory factor 3 nirs variant 1	IRF3			0.66	1.52	0.66		2	6.9	1.67E-02
B4DGV1	cDNA FLJ61589	HISPPD1			0.66	1.52	0.66		3	3.8	8.58E-40
Q8IWZ3-4	Ankyrin repeat and KH domain-containing protein 1	ANKHD1			0.66	1.52	0.66		9	4.8	5.07E-77
Q96DF8	DiGeorge syndrome critical region 13	DGCR13		0.66			0.66		2	4.2	9.68E-03
P08648	CD49 antigen-like family member E	FNRA		0.66			0.66		2	3.1	1.00E-19
P08134	Rho cDNA clone 9	ARH9	0.66				0.66		9	68	4.76E-134
P13051-1	Uracil-DNA glycosylase	DGU		0.69	0.65	1.54	0.67	0.03	4	21	5.74E-12
O75146	Huntingtin-interacting protein 12	HIP12	0.71		0.63	1.59	0.67	0.06	3	3.5	3.02E-41
Q9Y3P9-1	GAP and centrosome-associated protein	HSPC094		0.62	0.72	1.39	0.67	0.07	4	4	7.38E-10
P04818	Thymidylate synthase	OK/SW-cl.29	0.63	0.70	0.68	1.47	0.67	0.04	11	51	1.96E-167
Q9UJU2-1	Lymphoid enhancer-binding factor 1	LEF1	0.71	0.62	0.68	1.47	0.67	0.05	6	18	8.34E-20
O15294-1	O-GlcNAc transferase subunit p110	OGT		0.56	0.78	1.28	0.67	0.16	4	5.1	1.72E-42
Q9Y5J7	Mitochondrial import inner membrane translocase subunit Tim9	TIM9			0.67	1.49	0.67		2	26	1.21E-06
O60783	28S ribosomal protein S14, mitochondrial	MRPS14		0.67			0.67		2	22	6.67E-15
Q53GG0	Epithelial protein lost in neoplasm beta variant	LIMA1	0.67	0.68			0.68	0.01	16	28	9.61E-149
Q8WXH0-2	Nesprin-2	KIAA1011	0.69		0.66	1.52	0.68	0.02	13	3	7.39E-92
B5BTZ7	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit epsilon isoform	PPP2R5E	0.7	0.7	0.63	1.59	0.68	0.04	6	16	2.15E-18
Q9Y320-1	Cell proliferation-inducing gene 26 protein	CGI-31	0.98	1.02	0.03	33.33	0.68	0.56	4	21	4.86E-08
Q96R06	Astrin	SPAG5	0.66	0.67	0.71	1.41	0.68	0.03	7	9.1	3.47E-111
P42345	FK506-binding protein 12-rapamycin complex-associated	FRAP			0.68	1.47	0.68		4	2.2	1.89E-20

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	protein 1										
Q658Y4	Protein FAM91A1	FAM91A1	0.68				0.68		2	2.9	1.67E-15
P17026	Zinc finger protein 22	KOX15	0.69	0.68			0.69	0.01	5	29	9.24E-10
A8MXL3	Putative uncharacterized protein ARFGAP2	ARFGAP2		0.66	0.71	1.41	0.69	0.04	4	10	7.22E-136
P51965	UbcH6	UBCH6		0.88	0.49	2.04	0.69	0.28	3	16	3.02E-07
Q00613-1	Heat shock factor protein 1	HSF1	0.92		0.45	2.22	0.69	0.33	2	8.1	4.64E-49
G5IU07	Putative uncharacterized protein DIAPH3	DIAPH3			0.69	1.45	0.69		2	3	3.96E-22
Q8NEM2	SHC SH2 domain-binding protein 1	SHCBP1			0.69	1.45	0.69		3	4.5	1.69E-21
B7Z3U7	cDNA FLJ56007, highly similar to Cip1-interacting zinc finger protein	CIZ1			0.69	1.45	0.69		5	8.2	3.17E-26
Q8NG31-1	ALL1-fused gene from chromosome 15q14 protein	CASC5	0.69				0.69		2	1.1	9.52E-09
Q9HBI0-1	Gamma-parvin	PARVG		0.69			0.69		3	8.8	2.20E-07
Q8WVK2	Nucleic acid-binding protein RY-1	SNRNP27	0.69				0.69		3	18	1.51E-63
Q5EBM0-1	UMP-CMP kinase 2, mitochondrial	CMPK2		0.69			0.69		3	7.1	3.49E-14
Q9P219-1	Coiled-coil domain-containing protein 88C	CCDC88C		0.69			0.69		3	1.5	1.11E-03
Q06787-1	Fragile X mental retardation 1 protein	FMR1	0.64	0.72	0.72	1.39	0.69	0.05	3	5.2	9.44E-06
Q96PK2	Microtubule-actin cross-linking factor 1, isoform 4	ACF7	0.42		0.97	1.03	0.70	0.39	44	11	0.00E+00
P27448-1	Cdc25C-associated protein kinase 1	CTAK1		0.63	0.76	1.32	0.70	0.09	2	4.5	5.50E-36
Q9BW83-1	Putative GTP-binding protein RAY-like	RABL4	0.72	0.69	0.69	1.45	0.70	0.02	7	40	1.89E-110
Q12849	G-rich sequence factor 1	GRSF1	0.71	0.82	0.57	1.75	0.70	0.13	6	22	4.20E-69
Q8TEM1-1	Nuclear envelope pore membrane protein POM 210	KIAA0906	0.70		0.70	1.43	0.70	0.00	15	10	2.71E-64
O94915-1	ALL1-fused gene from chromosome 4p12 protein	AF4P12	0.67		0.73	1.37	0.70	0.04	4	2.3	6.04E-34
B1AKR6	Dynein, light chain, roadblock-type 1	DYNLRB1	0.92		0.48	2.08	0.70	0.31	2	19	1.12E-12
Q8N6R0	Methyltransferase-like protein 13	CGI-01			0.70	1.43	0.70		2	3.4	1.71E-44
Q9UHR	SAP30-binding	HCNGP			0.70	1.43	0.70		2	7.5	2.09E-30

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5-1	protein										
Q7Z442	PC1-like 1 protein	PKD1L1			0.70	1.43	0.70		2	0.5	5.52E-02
A6ND70	Putative uncharacterized protein SSBP2	SSBP2		0.70			0.70		2	6.2	5.96E-04
B4DYY7	cDNA FLJ56809, highly similar to REST corepressor 3	KIAA1343		0.70			0.70		2	3.8	8.19E-06
Q9HAF1-3	Chromatin modification-related protein MEAF6	C1orf149	0.70				0.70		3	18	6.96E-23
B7Z5W8	cDNA FLJ55034, highly similar to Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial (EC 2.3.1.61)	DLST	0.70				0.70		7	22	2.89E-24
Q9UDY4	DnaJ homolog subfamily B member 4	DNAJB4	0.74	0.74	0.63	1.59	0.70	0.06	6	21	1.15E-59
Q9NRZ9-1	Lymphoid-specific helicase	HELLS	0.62	0.59	0.90	1.11	0.70	0.17	9	11	2.52E-22
Q2NKX8	ATP-dependent helicase ERCC6-like	ERCC6L	0.71	1.07	0.33	3.03	0.70	0.37	3	4.1	9.30E-21
Q5MIZ7-1	Serine/threonine-protein phosphatase 4 regulatory subunit 3B	KIAA1387	0.68		0.73	1.37	0.71	0.04	4	6.6	4.40E-12
O60234	Glia maturation factor gamma	GMFG	0.74	0.67			0.71	0.05	4	47	5.95E-67
Q03252	Lamin-B2	LMN2	0.69	0.70	0.73	1.37	0.71	0.02	29	45	2.47E-223
Q9Y5V3-2	MAGE tumor antigen CCF	MAGED1	0.76	0.73	0.63	1.59	0.71	0.07	5	11	1.35E-97
O43736	Integral membrane protein 2A	ITM2A	0.69	0.55	0.88	1.14	0.71	0.17	2	7.6	2.77E-04
Q15022	Chromatin precipitated E2F target 9 protein	CHET9		0.72	0.70	1.43	0.71	0.01	5	9.1	3.40E-26
P61073-2	C-X-C chemokine receptor type 4	CXCR4	0.74	0.74	0.65	1.54	0.71	0.05	3	8.7	9.83E-171
P23610	CpG island protein	F8A			0.71	1.41	0.71		2	11	4.57E-07
Q9NUW8	Tyrosyl-DNA phosphodiesterase 1	TDP1			0.71	1.41	0.71		4	8.6	7.18E-17
Q92731	similar to protein expressed in prostate, ovary, testis, and placenta 2 isoform 2	POTEI			0.71	1.41	0.71		9	9.5	5.32E-34
Q9UIF9-1	Bromodomain adjacent to zinc finger domain protein 2A	BAZ2A	0.71				0.71		3	1.8	1.01E-03

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B4DRS6	cDNA FLJ58980, highly similar to Sideroflexin-3	hCG_24661	0.71				0.71		3	13	5.96E-50
Q96G61	Diadenosine 5,5-P1,P6-hexaphosphate hydrolase 3-beta	APS1	0.71				0.71		4	26	1.54E-08
Q12840	Kinesin heavy chain isoform 5A	KIF5A	0.71				0.71		10	12	5.07E-123
Q9UHB7-1	AF4/FMR2 family member 4	AF5Q31	0.71	0.72			0.72	0.01	3	3.4	6.04E-17
Q9UBU8-1	MORF-related gene 15 protein	FWP006	0.71	0.72			0.72	0.01	5	19	1.45E-44
O60880-1	Duncan disease SH2-protein	DSHP	0.73	0.70			0.72	0.02	4	33	2.03E-18
P57076	Uncharacterized protein C21orf59	C21orf48	0.90		0.53	1.89	0.72	0.26	2	15	1.92E-12
Q14CA3	TRIP12 protein	TRIP12	0.75	0.77	0.63	1.59	0.72	0.08	16	11	9.80E-181
Q9UHB6-1	Epithelial protein lost in neoplasm	EPLIN	0.61	0.54	1.00	1.00	0.72	0.25	16	28	2.34E-159
P07355-2	Annexin A2	ANX2	0.46	0.51	1.18	0.85	0.72	0.40	24	67	0.00E+00
P35453	Homeobox protein Hox-4I	HOX4I			0.72	1.39	0.72		2	12	2.60E-17
Q15691	EB1 protein family member 3	MAPRE3			0.72	1.39	0.72		3	8.5	3.48E-04
A0PJ76	NCAPD2 protein	NCAPD2			0.72	1.39	0.72		6	24	3.17E-171
Q9H008	Phospholysine phosphohistidine inorganic pyrophosphate phosphatase	LHPP	0.72				0.72		2	19	2.99E-36
Q8NDX6	OriLyt TD-element-binding protein 7	TB7	0.72				0.72		2	7.8	3.91E-08
A8MU17	Putative uncharacterized protein TRPT1	TRPT1		0.72			0.72		2	7.5	7.53E-17
Q53H82	Beta-lactamase-like protein 2	CGI-83		0.72			0.72		3	11	2.91E-08
P32780	Basic transcription factor 2 62 kDa subunit	BTF2	0.72	0.72	0.72	1.39	0.72	0.00	2	10	2.68E-07
Q6KC79-1	Delangin	IDN3	0.64	0.60	0.93	1.08	0.72	0.18	8	4.1	9.69E-33
Q9UPN4-1	5-azacytidine-induced protein 1	AZI1		0.82	0.63	1.59	0.73	0.13	10	12	1.17E-64
Q8N543-1	2-oxoglutarate and iron-dependent oxygenase domain-containing protein 1	KIAA1612	0.95		0.50	2.00	0.73	0.32	2	4.4	4.43E-78
Q8TCG1-1	Cancerous inhibitor of PP2A	CIP2A	0.93	0.72	0.53	1.89	0.73	0.20	3	5.7	1.16E-67

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P01116-2	c-Ki-ras	KRAS	0.68	0.68	0.82	1.22	0.73	0.08	6	36	3.54E-75
Q9BZX2-1	Cytidine monophosphokinase 2	UCK2	0.76	0.86	0.56	1.79	0.73	0.15	6	29	3.35E-32
Q9NS87-1	Kinesin-like protein 2	KIF15	0.85	0.79	0.54	1.85	0.73	0.16	8	7.7	2.32E-162
Q5XKP0	Protein P117	C19orf70	0.69	0.75	0.75	1.33	0.73	0.03	2	36	4.52E-06
P42167-1	Lamina-associated polypeptide 2, isoforms beta/gamma	LAP2	0.76	0.79	0.64	1.56	0.73	0.08	24	61	1.38E-274
P51948	CDK7/cyclin-H assembly factor	CAP35	0.84		0.62	1.61	0.73	0.16	3	14	9.76E-33
Q5VT06	Centrosome-associated protein 350	CAP350			0.73	1.37	0.73		2	0.6	2.38E-02
Q6P179-1	Endoplasmic reticulum aminopeptidase 2	ERAP2			0.73	1.37	0.73		2	2.6	1.37E-06
Q5T0F9-2	Coiled-coil and C2 domain-containing protein 1B	CC2D1B			0.73	1.37	0.73		2	4.3	1.10E-02
Q9UJW0	Dynactin subunit 4	DCTN4			0.73	1.37	0.73		2	6.2	6.54E-04
P56270	Myc-associated zinc finger protein	MAZ			0.73	1.37	0.73		3	9.1	3.38E-08
Q8WVM7	Cohesin subunit SA-1	SA1			0.73	1.37	0.73		4	2.4	1.13E-07
Q8NEZ2-1	ESCRT-I complex subunit VPS37A	HCRP1	0.73				0.73		2	9.1	2.13E-46
P07305	Histone H1	H1F0	0.73				0.73		2	12	4.35E-11
Q5TZW1	Src-like-adaptor	SLA	0.73				0.73		2	20	2.80E-03
Q8N1F0	Serine/threonine-protein phosphatase	hCG_18332		0.73			0.73		3	6.1	1.39E-07
Q96K21-1	MLL partner containing FYVE domain	MPFYVE	0.73				0.73		3	8.7	3.94E-04
Q96DV4	39S ribosomal protein L38, mitochondrial	HSPC262	0.73				0.73		3	6.1	2.68E-09
Q12968-1	NFATx	NFAT4	0.73				0.73		4	5.1	3.56E-13
Q92538	Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	GBF1		0.73			0.73		7	4.6	7.00E-67
Q8WWI1-1	F-box only protein 20	FBX20	0.65	0.60	0.95	1.05	0.73	0.19	5	5.8	1.30E-38
Q5T1Z8	Pumilio homolog 1 (Drosophila)	hCG_19946	0.59	0.55	1.06	0.94	0.73	0.28	7	7.5	5.81E-32
Q9HBM1	Kinetochore protein Spc25	AD024	0.88		0.59	1.69	0.74	0.21	4	19	2.75E-06
Q8N0X	Spartin	KIAA0	0.74	0.76	0.71	1.41	0.74	0.03	6	13	8.36E-91

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7		610									
Q9NPD8	Cell proliferation-inducing gene 50 protein	HSPC150	0.80	0.65	0.76	1.32	0.74	0.08	3	17	9.08E-16
Q9UPN9-1	E3 ubiquitin-protein ligase TRIM33	KIAA1113	0.56	0.63	1.02	0.98	0.74	0.25	5	5.3	1.50E-39
Q8IX01-1	Arginine/serine-rich-splicing factor 14	KIAA0365	0.73	0.69	0.8	1.25	0.74	0.06	26	35	2.03E-148
Q9NUQ3	Gamma-taxilin	CXorf15	0.58	0.92	0.72	1.39	0.74	0.17	4	9.1	1.21E-12
B4DT73	cDNA FLJ56409, highly similar to Serine/threonine-protein kinase Chk1 (EC 2.7.11.1)	CHEK1	0.78	0.89	0.55	1.82	0.74	0.17	2	4.9	3.02E-13
O95379-1	Head and neck tumor and metastasis-related protein	TNFAIP8	0.73	0.75			0.74	0.01	3	28	3.56E-120
O95801	Tetratricopeptide repeat protein 4	My044	0.79		0.69	1.45	0.74	0.07	4	10	3.17E-10
B1AJQ6	Syntaxin 12	RP3-426I6.4-002	0.64	0.84			0.74	0.14	3	14	1.17E-15
Q9UQN3	Charged multivesicular body protein 2b	CGI-84	0.91	0.57			0.74	0.24	3	15	7.47E-12
Q9NRG9	Adracalin	AAAS			0.74	1.35	0.74		2	5.7	1.30E-34
Q12802-2	AKAP-Lbc	AKAP13			0.74	1.35	0.74		2	2.1	1.88E-02
Q01167-1	Cellular transcription factor ILF-1	FOXK2			0.74	1.35	0.74		3	8.9	1.14E-31
Q9H6N6	cDNA: FLJ22037 fis, clone HEP08868	MYH16			0.74	1.35	0.74		3	4	9.82E-08
O60879-1	Diaphanous-related formin-2	DIA			0.74	1.35	0.74		4	4.4	4.49E-24
Q969P6	DNA topoisomerase I, mitochondrial	TOP1MT		0.74			0.74		2	2.8	8.12E-08
Q7Z7A4-1	Modulator of Na,K-ATPase	PXK	0.74				0.74		2	4.8	1.57E-08
Q99547	M-phase phosphoprotein 6	MPHOSPH6	0.74				0.74		3	17	2.10E-03
Q9Y5N6	Origin recognition complex subunit 6	ORC6	0.74	0.71	0.78	1.28	0.74	0.04	4	15	1.92E-15
O14976	Cyclin-G-associated kinase	GAK	0.79	0.91	0.53	1.89	0.74	0.19	4	6	1.94E-25
Q659G1	Ankyrin repeat and MYND domain-containing protein 2	ANKMY2	0.66	0.83			0.75	0.12	2	4.8	2.07E-07
Q15057	Arf-GAP with coiled-coil, ANK repeat and PH domain-containing protein 2	ACAP2	0.68	0.61	0.95	1.05	0.75	0.18	4	6.8	4.18E-57

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Q9H9J2	39S ribosomal protein L44, mitochondrial	MRPL44	0.72	0.78			0.75	0.04	2	11	1.51E-20
Q8N6T3-2	ADP-ribosylation factor 1 GTPase-activating protein	ARF1GAP	0.61	0.74	0.90	1.11	0.75	0.15	2	5.6	5.85E-13
Q15738	Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating	H105E3	1.17		0.33	3.03	0.75	0.59	5	17	5.33E-31
Q96AX1	Vacuolar protein sorting-associated protein 33A	VPS33A	1.22		0.28	3.57	0.75	0.66	2	8.6	3.36E-11
Q96I15-1	Selenocysteine lyase	SCLY			0.75	1.33	0.75		2	8.8	1.48E-11
F4WIY2	UPF0399 protein C6orf153	C6orf153			0.75	1.33	0.75		2	3.9	9.15E-03
O75363	Amplified in breast cancer protein 1	ABC1			0.75	1.33	0.75		2	2.5	5.98E-15
Q9UBW7	Fused in myeloproliferative disorders protein	FIM		0.75			0.75		2	1.5	2.19E-05
C9J2A4	Ewings sarcoma EWS-Fli1 (Type 1) oncogene	FLI1		0.75			0.75		2	6.1	5.82E-06
P01112	GTPase HRas	HRAS	0.75				0.75		4	33	6.24E-29
P62834	C21KG	KREV1		0.75			0.75		6	38	6.66E-79
O60313-2	Dynamin-like 120 kDa protein, form S1	KIAA0567	0.86	0.87	0.53	1.89	0.75	0.19	4	4.8	5.50E-12
Q59H50	Integrin beta	ITGB2	0.76		0.75	1.33	0.76	0.01	9	24	9.34E-153
Q96MF7	E3 SUMO-protein ligase NSE2	C8orf36	0.78		0.73	1.37	0.76	0.04	2	14	7.17E-47
Q9UBK9	Androgen receptor trapped clone 27 protein	HSPC024	0.72	0.79			0.76	0.05	2	16	6.86E-24
Q14444-1	Caprin-1	CAPRIN1	0.76	0.73	0.78	1.28	0.76	0.03	18	27	1.54E-256
Q9UK76-2	Androgen-regulated protein 2	ARM2	0.83	0.69	0.75	1.33	0.76	0.07	3	22	4.22E-40
Q53QZ3	ArhGAP15	ARHGAP15	0.59	0.70	0.98	1.02	0.76	0.20	5	13	4.11E-74
O75179-1	Ankyrin repeat domain-containing protein 17	ANKRD17	0.85	0.93	0.49	2.04	0.76	0.23	13	6.6	4.25E-115
Q01826-2	DNA-binding protein SATB1	SATB1	0.58	0.60	1.09	0.92	0.76	0.29	13	26	8.17E-73
Q96CX6	Leucine-rich repeat-containing protein 58	LRRC58	0.82		0.70	1.43	0.76	0.08	4	16	2.98E-38
P25311	Zinc-alpha-2-glycoprotein	AZGP1			0.76	1.32	0.76		2	11	4.44E-04
Q9NVU0-1	DNA-directed RNA polymerase III 80 kDa polypeptide	KIAA1452			0.76	1.32	0.76		2	4.5	5.15E-03

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Q8TEY7	Deubiquitinating enzyme 1	USP1			0.76	1.32	0.76		2	3.6	5.11E-03
Q14CB8-2	Rho GTPase-activating protein 19	ARHGAP19			0.76	1.32	0.76		2	5.2	4.66E-05
P49840	Glycogen synthase kinase-3 alpha	GSK3A			0.76	1.32	0.76		3	10	1.05E-15
O14981	ATP-dependent helicase BTAF1	BTAF1			0.76	1.32	0.76		4	3.3	5.69E-21
P35520-2	Beta-thionase	CBS			0.76	1.32	0.76		4	8.1	1.14E-80
Q96L92-1	Sorting nexin-27	KIAA0488			0.76	1.32	0.76		4	13	3.43E-06
Q9BYC9	39S ribosomal protein L20, mitochondrial	MRPL20		0.76			0.76		2	13	1.41E-11
Q9NVX0-1	Centrosomal protein of 27 kDa	C15orf25	0.76				0.76		2	11	1.48E-04
O75496	Geminin	GMNN		0.76			0.76		2	9.1	3.22E-03
A8MST8	Putative uncharacterized protein NKIRAS2	NKIRAS2	0.76				0.76		2	9.6	1.01E-04
A6NCK0	Putative uncharacterized protein NAE1	NAE1		0.76			0.76		7	14	2.35E-100
Q96RP9-2	Elongation factor G 1, mitochondrial	EFG	0.71	0.78	0.79	1.27	0.76	0.04	2	5.6	1.35E-07
Q15398-2	Discs large homolog 7	DLG7	0.85	0.69	0.74	1.35	0.76	0.08	7	12	9.38E-19
Q9NVN8	Guanine nucleotide-binding protein-like 3-like protein	GNL3L	0.88	0.84	0.56	1.79	0.76	0.17	5	9.8	2.72E-20
P78332	Lung cancer antigen NY-LU-12	DEF3	0.70	0.77	0.82	1.22	0.76	0.06	4	4.5	1.98E-29
P60520	GABA(A) receptor-associated protein-like 2	FLC3A	0.94	0.74	0.61	1.64	0.76	0.17	7	56	2.82E-66
P23921	Ribonucleoside-diphosphate reductase large subunit	RR1	0.87	0.93	0.49	2.04	0.76	0.24	13	23	2.04E-115
Q96A49	Synapse-associated protein 1	PRO3113	0.76		0.77	1.30	0.77	0.01	2	8.2	1.41E-52
Q6ZNE4	cDNA FLJ16180 fis, clone BRHIP3000240, highly similar to Homo sapiens potassium channel beta 2 subunit (HKvbeta2.2) mRNA	KCNAB2		0.62	0.91	1.10	0.77	0.21	5	19	6.16E-11
Q96EH3	Uncharacterized protein C7orf30	C7orf30	0.97		0.56	1.79	0.77	0.29	2	24	4.02E-14
B3KSP9	cDNA FLJ36765 fis, clone 3NB691000191	AARSD1		0.55	0.98	1.02	0.77	0.30	3	7.7	9.53E-72
Q9Y5L4	Mitochondrial import inner membrane	TIM13B	1.04		0.49	2.04	0.77	0.39	3	39	2.49E-29

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	translocase subunit Tim13										
Q9UPN3-2	620 kDa actin-binding protein	ABP620	0.71	0.63	0.97	1.03	0.77	0.18	46	13	0.00E+00
Q9NZD2	Glycolipid transfer protein	GLTP	0.76	0.78			0.77	0.01	2	10	2.48E-34
O95249	28 kDa cis-Golgi SNARE p28	GOSR1	0.80	0.77	0.74	1.35	0.77	0.03	2	10	3.30E-11
Q8TAE8	CKII beta-associating protein	GADD45GIP1	0.80		0.74	1.35	0.77	0.04	5	33	3.74E-23
P07205	Phosphoglycerate kinase 2	PGK2	0.74	0.80			0.77	0.04	9	18	4.52E-88
Q8TDP1	ribonuclease H2 subunit B isoform 2	RNASEH2B	0.85		0.69	1.45	0.77	0.11	10	45	1.50E-41
Q9Y6W5	Protein WAVE-2	WASF2	0.86	0.68			0.77	0.13	5	16	2.70E-34
P05423	DNA-directed RNA polymerase III subunit D	BN51	0.69	0.93	0.69	1.45	0.77	0.14	2	4.8	1.59E-03
B2R8P1	cDNA, FLJ93994, highly similar to Homo sapiens phosphate cytidylyltransferase 1, choline, alpha isoform (PCYT1A), mRNA	PCYT1A	0.87		0.67	1.49	0.77	0.14	4	15	5.70E-55
Q86U44-1	Methyltransferase-like protein 3	METTL3	0.71	1.11	0.49	2.04	0.77	0.31	3	8.4	2.50E-08
P55039	Developmentally-regulated GTP-binding protein 2	DRG2	1.15	0.31	0.85	1.18	0.77	0.43	5	16	1.26E-77
P48651	Phosphatidylserine synthase 1	KIAA0024			0.77	1.30	0.77		2	5.1	6.62E-07
P07996	Thrombospondin-1	THBS1			0.77	1.30	0.77		2	2	4.12E-03
O75962	PTPRF-interacting protein	TRIO			0.77	1.30	0.77		3	1.5	2.62E-11
Q96A08	Histone H2B type 1-A	HIST1H2BA			0.77	1.30	0.77		7	47	2.34E-35
Q13033-1	Cell cycle autoantigen SG2NA	GS2NA		0.77			0.77		2	1.9	3.00E-02
Q96CB9-1	NOL1/NOP2/Sun domain family member 4	NSUN4		0.77			0.77		2	5.7	1.70E-10
Q13588	GRB2-related adapter protein	GRAP		0.77			0.77		3	9.7	6.20E-03
Q9UP83-2	13S Golgi transport complex 90 kDa subunit	COG5		0.77			0.77		3	3.6	2.88E-07
P20671	Histone H2A type 1-D	H2AFG		0.77			0.77		7	32	1.14E-108
Q14318-1	38 kDa FK506-binding protein	FKBP38	0.74	0.74	0.84	1.19	0.77	0.06	9	22	2.97E-77
Q9UEE9-1	Bucentaur	BCNT	0.70	0.72	0.90	1.11	0.77	0.11	4	18	5.14E-26

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Q9BV38	WD repeat-containing protein 18	WDR18	0.70		0.85	1.18	0.78	0.11	2	4.2	3.40E-04
Q14331	FSHD region gene 1 protein	FRG1	1.17		0.38	2.63	0.78	0.56	2	9.7	3.47E-14
Q68EM7-1	Rho GTPase-activating protein 17	ARHGAP17	0.80		0.75	1.33	0.78	0.04	3	5.4	4.78E-05
Q2TAM5	Nuclear factor NF-kappa-B p65 subunit	RELA	0.66		0.89	1.12	0.78	0.16	3	9	1.86E-06
Q9UQR1	Transcription factor ZBP-89	ZBP89		0.64	0.91	1.10	0.78	0.19	2	3.8	4.53E-13
Q96BY6-1	Dedicator of cytokinesis protein 10	DOCK10	0.60	0.85	0.88	1.14	0.78	0.15	7	5	6.07E-50
P11274-1	Breakpoint cluster region protein	BCR	0.49	0.88	0.96	1.04	0.78	0.25	4	5.8	1.40E-33
Q99622	Protein C10	C10	0.57	0.49	1.27	0.79	0.78	0.43	5	58	5.13E-79
P52732	Kinesin-like protein 1	EG5	0.76	0.79	0.79	1.27	0.78	0.02	26	34	5.63E-257
Q9UJU6-1	Cervical mucin-associated protein	CMAP	0.76	0.81	0.77	1.30	0.78	0.03	10	29	2.03E-138
Q53GI2	Testis expressed sequence 264 variant	TEX264	0.79	0.81	0.74	1.35	0.78	0.04	5	17	1.06E-18
Q99590-1	CTD-associated SR protein 11	CASP11	0.67	0.85	0.82	1.22	0.78	0.10	7	5.5	7.35E-65
O00221	I-kappa-B-epsilon	IKBE	0.72	0.70	0.92	1.09	0.78	0.12	2	8	7.43E-07
Q9Y4R8	Protein clk-2 homolog	KIAA0683	0.59	1.12	0.63	1.59	0.78	0.30	5	9.6	3.67E-47
Q92854	A8	CD100	0.43		1.13	0.88	0.78	0.49	2	3.5	1.41E-18
Q9NUQ8-1	ATP-binding cassette sub-family F member 3	ABCF3		0.85	0.71	1.41	0.78	0.10	5	7.3	1.83E-20
Q9H1A4	Anaphase-promoting complex subunit 1	ANAPC1		1.01	0.55	1.82	0.78	0.33	3	2.5	3.61E-21
Q96FZ7	Charged multivesicular body protein 6	CHMP6		1.03	0.53	1.89	0.78	0.35	3	14	5.32E-27
A8MWR0	cDNA FLJ58961, highly similar to APAF1-interacting protein	APIP			0.78	1.28	0.78		2	10	6.10E-06
A8K6A2	cDNA FLJ77317, highly similar to Homo sapiens retinoblastoma binding protein 7 (RBBP7), mRNA	RBBP7			0.78	1.28	0.78		10	27	5.27E-102
Q16594	RNA polymerase II TBP-associated factor subunit G	TAF2G	0.78				0.78		2	11	2.41E-10
Q9UL26	Ras-related protein Rab-22A	RAB22	0.78				0.78		2	16	1.61E-05
O75616-1	Conserved ERA-like GTPase	ERAL1		0.78			0.78		2	4.3	2.45E-04

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P83436	Component of oligomeric Golgi complex 7	COG7		0.78			0.78		2	2.5	1.77E-08
B4DQP1	cDNA FLJ58045, highly similar to NADH dehydrogenase (ubiquinone) 1 alpha subcomplex subunit 13 (EC 1.6.5.3)	NDUFA13		0.78			0.78		2	8.8	2.28E-03
Q9H9B1-3	Euchromatic histone-lysine N-methyltransferase 1	EHMT1	0.78				0.78		2	2.2	4.42E-03
Q9Y3P8	SHP2-interacting transmembrane adapter protein	SIT	0.71	0.88	0.76	1.32	0.78	0.09	3	26	1.52E-65
Q7Z7F5	Excision repair cross-complementing rodent repair deficiency, complementation group 1 (Includes overlapping antisense sequence)	ERCC1	0.70	0.95	0.70	1.43	0.78	0.14	2	9	1.62E-05
Q14008-3	Colonic and hepatic tumor over-expressed gene protein	CKAP5	0.78	0.77	0.80	1.25	0.78	0.02	40	26	3.40E-246
Q9NRS6-1	Sorting nexin-15	SNX15	0.68	0.99	0.68	1.47	0.78	0.18	2	6.4	1.60E-04
Q15628	TNFRSF1A-associated via death domain	TRADD	0.71	1.00	0.64	1.56	0.78	0.19	2	8.3	1.84E-03
Q5T6F2	Ubiquitin-associated protein 2	KIAA1491	0.76	1.00	0.59	1.69	0.78	0.21	6	10	2.06E-54
P15923-1	Class B basic helix-loop-helix protein 21	BHLHB21	0.46	0.45	1.44	0.69	0.78	0.57	7	17	4.21E-64
O14965	Aurora kinase A	AIK		0.88	0.69	1.45	0.79	0.13	2	7.4	1.30E-31
Q8IWI9-1	MAX dimerization protein 5	KIAA0518	0.90		0.67	1.49	0.79	0.16	3	1.5	2.29E-05
Q14157-2	Protein NICE-4	KIAA0144	0.74	0.76	0.86	1.16	0.79	0.06	16	23	1.15E-296
P49815-1	Tuberin	TSC2	0.69	0.81	0.86	1.16	0.79	0.09	3	2.7	2.09E-31
B8ZWD6	Diazepam binding inhibitor, splice form 1G	DBI	0.83	0.87	0.66	1.52	0.79	0.11	2	18	1.10E-15
Q9HB21	Pleckstrin homology domain-containing family A member 1	PLEKHA1	0.68	0.68	1.00	1.00	0.79	0.18	4	14	2.22E-27
Q13084	39S ribosomal protein L28, mitochondrial	MAAT1	0.78		0.80	1.25	0.79	0.01	3	22	3.33E-125
Q8NFU3-1	Thiosulfate sulfurtransferase/rhodanese-like domain-containing protein 1	KAT	0.80	0.78			0.79	0.01	2	12	1.58E-05
O43432	eIF-4-gamma II	EIF4G3	0.77	0.75	0.85	1.18	0.79	0.05	14	9.8	8.81E-50

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-1											
P51398	28S ribosomal protein S29, mitochondrial	DAP3	0.83	0.71	0.83	1.20	0.79	0.07	5	21	4.28E-52
Q9NXX6-1	Non-structural maintenance of chromosomes element 4 homolog A	C10orf86	0.74		0.84	1.19	0.79	0.07	3	12	2.63E-29
P31689	DnaJ homolog subfamily A member 1	DNAJ2	0.82	0.85	0.70	1.43	0.79	0.08	14	46	1.39E-131
P20700	Lamin-B1	LMN1	0.82	0.86	0.69	1.45	0.79	0.09	39	61	0.00E+00
Q9H0H5	Male germ cell RacGap	KIAA1478	0.77	0.89	0.71	1.41	0.79	0.09	6	14	5.08E-64
P02786	p90	TFRC	0.80	0.93	0.64	1.56	0.79	0.15	15	26	3.27E-201
C9JYA1	Putative uncharacterized protein NUPL2	NUPL2	0.68		0.90	1.11	0.79	0.16	2	5.5	2.42E-09
O14920	I-kappa-B kinase 2	IKBKB		0.90	0.68	1.47	0.79	0.16	3	4.1	5.02E-08
P15812-1	R2G1	CD1E	0.69	0.99	0.69	1.45	0.79	0.17	3	12	1.09E-08
Q9H384	Nuclear localized protein 1	FKSG26	0.98		0.60	1.67	0.79	0.27	3	8.6	1.44E-15
Q13094	Lymphocyte cytosolic protein 2	LCP2	0.61	0.63	1.13	0.88	0.79	0.29	8	17	3.79E-73
P56524	Histone deacetylase 4	HDAC4	0.71	1.15	0.51	1.96	0.79	0.33	13	22	1.03E-72
Q5W0V3-1	Protein FAM160B1	FAM160B1	0.52	0.57	1.28	0.78	0.79	0.43	4	7.1	3.24E-31
O95155-1	Homozygously deleted in neuroblastoma 1	HDNB1			0.79	1.27	0.79		2	2.5	9.29E-32
O15381-1	Nuclear valosin-containing protein-like	NVL			0.79	1.27	0.79		2	3.9	6.63E-12
Q9UN36-1	Protein NDRG2	KIAA1248			0.79	1.27	0.79		2	7.8	9.74E-05
Q5VU11	Ribonuclease P (30kD) (RPP30)	RP11-320F15.1			0.79	1.27	0.79		2	11	2.10E-60
Q13439-3	256 kDa golgin	GOLGA4			0.79	1.27	0.79		2	0.7	1.86E-02
Q13107-1	Deubiquitinating enzyme 4	UNP			0.79	1.27	0.79		3	5.9	1.03E-13
P35610	Acyl-coenzyme A:cholesterol acyltransferase 1	ACACT			0.79	1.27	0.79		3	6.9	1.63E-07
O75449-1	Katanin p60 ATPase-containing subunit A1	KATNA1			0.79	1.27	0.79		4	10	5.58E-25
Q96KG9-1	Coated vesicle-associated kinase of 90 kDa	CVAK90			0.79	1.27	0.79		4	9.9	2.44E-14
Q8TBF4	U11/U12 small nuclear ribonucleoprotein 31 kDa protein	ZCRB1			0.79	1.27	0.79		5	36	4.57E-47
B5M45	Solute carrier family 4	SLC4A			0.79	1.27	0.79		5	5.2	2.62E-44

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1	sodium bicarbonate cotransporter member 7	7									
Q8NHG8	E3 ubiquitin-protein ligase ZNRF2	RNF202			0.79	1.27	0.79		6	55	5.47E-123
Q8WUA2	Cyclophilin-like protein PPIL4	PPIL4			0.79	1.27	0.79		6	19	6.76E-92
Q96PE3-1	Inositol polyphosphate 4-phosphatase type I	INPP4A			0.79	1.27	0.79		6	8.8	4.67E-24
Q9UGP4	LIM domain-containing protein 1	LIMD1	0.79				0.79		2	3.8	2.25E-21
Q8IZ21-2	Phosphatase and actin regulator 4	PHACTR4	0.79				0.79		2	3.1	4.09E-03
B4DRT5	Serine/threonine-protein phosphatase	CALNA3	0.79				0.79		2	4.2	6.46E-03
Q96K17	Basic transcription factor 3-like 4	BTF3L4	0.79				0.79		4	40	4.41E-28
Q9NRG7-2	Epimerase family protein SDR39U1	C14orf124	0.79				0.79		6	32	1.36E-46
Q8N1K8	cDNA FLJ40556 fis, clone THYMU2002583, highly similar to DYNAMIN 2	DYNAMIN 2	0.79				0.79		22	32	1.82E-190
Q9Y6A5	Transforming acidic coiled-coil-containing protein 3	ERIC1	0.84	0.80	0.74	1.35	0.79	0.05	12	22	1.11E-137
P07919	Complex III subunit 6	UQCRH	0.74	0.77	0.87	1.15	0.79	0.07	4	39	9.35E-137
Q8WUI4-8	Histone deacetylase 7	HDAC7	0.69	0.88	0.81	1.23	0.79	0.10	2	3	2.08E-03
A8KAH5	cDNA FLJ32696 fis, clone TESTI2000358	IST1	0.76	0.70	0.92	1.09	0.79	0.11	3	8.4	1.82E-06
O00161-1	Synaptosomal-associated protein 23	SNAP23	0.64	0.76	0.98	1.02	0.79	0.17	7	45	1.46E-162
Q9H4I3-1	Protein TTG2	PP2447	0.84	0.98	0.56	1.79	0.79	0.21	3	12	3.38E-28
O15111	Conserved helix-loop-helix ubiquitous kinase	CHUK	0.82	0.77			0.80	0.04	3	4.4	7.83E-05
A8K5U9	cDNA FLJ75056, highly similar to Homo sapiens phosphatidylinositol binding clathrin assembly protein (PICALM), mRNA	PICALM	0.60		0.99	1.01	0.80	0.28	3	7.1	1.19E-92
Q9Y613	FH1/FH2 domain-containing protein 1	FHOD1	1.01		0.58	1.72	0.80	0.30	2	2.6	2.44E-24
B0QZ40	COMM domain containing 6	COMMD6	0.79	0.80			0.80	0.01	2	20	1.09E-03
Q86Y56-1	HEAT repeat-containing protein 2	HEATR2	0.91	1.01	0.47	2.13	0.80	0.29	6	8.3	4.15E-25

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O14777	Highly expressed in cancer protein	HEC	0.77	0.81	0.81	1.23	0.80	0.02	6	9	1.61E-13
Q16531	Damage-specific DNA-binding protein 1	DDB1	0.75	0.81	0.83	1.20	0.80	0.04	26	30	3.97E-156
Q15003	Barren homolog protein 1	BRRN	0.81	0.77	0.82	1.22	0.80	0.03	14	25	1.30E-93
Q99661-1	Kinesin-like protein 6	KIF2C	0.76	0.79	0.85	1.18	0.80	0.05	16	26	7.22E-188
Q9P270	SLAIN motif-containing protein 2	KIAA1458	0.63	0.79	0.98	1.02	0.80	0.18	4	12	3.03E-55
Q9Y296	Hematopoietic stem/progenitor cell protein 172	CGI-104	0.98	1.06	0.36	2.78	0.80	0.38	4	19	1.11E-21
Q9BXY0	NNP78	MAK16	1.13		0.47	2.13	0.80	0.47	3	15	3.91E-23
O43924	Protein p17	PDE6D			0.80	1.25	0.80		2	21	1.51E-11
O75665	Oral-facial-digital syndrome 1 protein	CXorf5			0.80	1.25	0.80		2	1.3	3.31E-02
B4DGS4	cDNA FLJ56073, highly similar to Lipin-1	KIAA0188			0.80	1.25	0.80		2	4.7	3.15E-04
Q6PCB5-1	Round spermatid basic protein 1-like protein	RSBN1L			0.80	1.25	0.80		2	6.3	1.29E-24
Q86US8-1	EST1-like protein A	C17orf31			0.80	1.25	0.80		3	4	7.67E-27
Q5VST6-1	Abhydrolase domain-containing protein FAM108B1	C9orf77			0.80	1.25	0.80		4	17	2.14E-14
Q9H0B6	Kinesin light chain 2	KLC2			0.80	1.25	0.80		16	29	1.14E-154
Q8WXE1-1	ATM and Rad3-related-interacting protein	AGS1		0.80			0.80		2	2.7	1.45E-03
Q6PJ69	Tripartite motif-containing protein 65	TRIM65	0.80				0.80		2	7.2	2.89E-04
Q7Z7F1	Inhibitor of kappaB kinase gamma	IKBKG		0.80			0.80		2	4.7	4.93E-12
Q02252	Aldehyde dehydrogenase family 6 member A1	ALDH6A1		0.80			0.80		3	7.3	8.48E-04
P16402	Histone H1.3	H1F3		0.80			0.80		12	33	4.75E-136
Q9UI08-2	Ena/vasodilator-stimulated phosphoprotein-like	EVL	0.75	0.82	0.84	1.19	0.80	0.05	9	24	8.53E-113
P11388-4	DNA topoisomerase 2-alpha	TOP2	0.77	0.84	0.80	1.25	0.80	0.04	58	38	0.00E+00
P57740	107 kDa nucleoporin	NUP107	0.84	0.76	0.81	1.23	0.80	0.04	14	20	1.65E-114
A7E244	TBC1 domain family, member 10A	TBC1D10A	0.76	0.76	0.89	1.12	0.80	0.08	3	10	8.30E-06
O95239-1	Chromokinesin-A	KIF4	0.75	0.76	0.90	1.11	0.80	0.08	11	10	5.30E-65

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Q92575	Erasin	KIAA0242	0.83	0.67	0.91	1.10	0.80	0.12	4	8.7	1.39E-07
B5MDZ2	Putative uncharacterized protein THOC7	THOC7	0.77	0.65	0.99	1.01	0.80	0.17	7	29	4.17E-30
Q96JY6-1	PDZ and LIM domain protein 2	PDLIM2	0.59	0.89	0.93	1.08	0.80	0.19	4	12	2.50E-13
Q92896-2	CFR-1	CFR1	0.53	0.63	1.25	0.80	0.80	0.39	24	25	3.73E-185
P19404	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial	NDUFV2	0.78		0.83	1.20	0.81	0.04	4	28	6.39E-23
Q7Z6I8-1	UPF0461 protein C5orf24	C5orf24	0.84	0.77			0.81	0.05	2	13	8.44E-39
Q6P996-1	Pyridoxal-dependent decarboxylase domain-containing protein 1	KIAA0251		1.03	0.58	1.72	0.81	0.32	2	4.1	1.12E-04
Q9Y5K8	Vacuolar proton pump subunit D	ATP6M	0.80	0.86	0.76	1.32	0.81	0.05	7	26	3.31E-66
P49006	Macrophage myristoylated alanine-rich C kinase substrate	MARCKSL1	0.76	0.91	0.75	1.33	0.81	0.09	2	14	7.98E-14
P26358-1	CXXC-type zinc finger protein 9	AIM	0.85	0.89	0.68	1.47	0.81	0.11	39	26	2.77E-198
Q969M7-2	NEDD8 carrier protein UBE2F	NCE2	0.94	0.74	0.74	1.35	0.81	0.12	2	5.2	2.98E-05
Q96K76-1	Deubiquitinating enzyme 47	USP47	0.96	0.75	0.71	1.41	0.81	0.13	7	6	4.53E-49
P13612	CD49 antigen-like family member D	CD49D	0.66	1.00	0.76	1.32	0.81	0.17	5	6.1	4.31E-14
A4D218	MAD1 mitotic arrest deficient-like 1 (Yeast)	MAD1L1	0.68	0.71	1.03	0.97	0.81	0.19	9	15	1.53E-19
P49642	DNA primase 49 kDa subunit	PRIM1	0.96	1.07	0.39	2.56	0.81	0.37	3	9	8.52E-22
P25098	Beta-adrenergic receptor kinase 1	ADRBK1	0.74	0.75	0.94	1.06	0.81	0.11	8	10	2.18E-20
A6NJ42	Mitotic checkpoint protein BUB3	BUB3	0.73	0.97	0.73	1.37	0.81	0.14	17	56	1.26E-185
Q8IUR7-6	Armadillo repeat-containing protein 8	ARMC8	0.72	0.72	0.99	1.01	0.81	0.16	2	5.5	2.53E-02
Q9BR61	Acyl-CoA-binding domain-containing protein 6	ACBD6	0.73	1.00	0.70	1.43	0.81	0.17	2	9.2	3.92E-14
Q9BYT8	Angiotensin-binding protein	AGTBP	0.81	0.81			0.81	0.00	2	3.3	5.01E-06
P35612-1	Beta-adducin	ADD2		0.82	0.80	1.25	0.81	0.01	3	4	8.56E-21
Q9P0P0	E3 ubiquitin-protein ligase RNF181	HSPC238	0.85	0.79	0.79	1.27	0.81	0.03	3	22	2.01E-04
Q96AT	Ribulose-5-phosphate-	HUSSY	0.79	0.72	0.92	1.09	0.81	0.10	3	15	1.74E-113

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9-1	3-epimerase	-17									
Q8WTW3	Component of oligomeric Golgi complex 1	COG1	0.93	0.75	0.75	1.33	0.81	0.10	4	7.7	1.74E-24
P52948-5	96 kDa nucleoporin	ADAR2	0.70	0.81	0.92	1.09	0.81	0.11	15	9.9	1.83E-57
O00170	AH receptor-interacting protein	AIP	0.71	1.11	0.61	1.64	0.81	0.26	25	60	0.00E+00
Q9UGJ1	Gamma-ring complex protein 76 kDa	76P			0.81	1.23	0.81		2	2.5	9.94E-03
O43439-1	ETO homologous on chromosome 20	CBFA2T2			0.81	1.23	0.81		2	5.8	1.26E-06
Q96G28-2	Coiled-coil domain-containing protein 104	CCDC104			0.81	1.23	0.81		3	12	3.19E-11
Q15155	Nodal modulator 1	NOMO1			0.81	1.23	0.81		8	8.9	8.55E-57
O95625	Zinc finger and BTB domain-containing protein 11	ZBTB11	0.81				0.81		2	3.3	3.82E-52
P20248	Cyclin-A2	CCN1		0.81			0.81		2	4.4	9.20E-03
Q9NQE9	Histidine triad nucleotide-binding protein 3	HINT3		0.81			0.81		2	11	2.72E-20
A0MZ66-3	Shootin-1	KIAA1598		0.81			0.81		2	3.7	2.17E-06
P46100-4	ATP-dependent helicase ATRX	ATRX	0.81				0.81		2	0.9	5.62E-03
B7Z3B7	ATPase, H+ transporting, lysosomal V0 subunit a1, isoform CRA_a	ATP6V0A1	0.81				0.81		2	2.4	8.94E-03
O75243	U6 snRNA-associated Sm-like protein LSm7	LSM7	0.81				0.81		2	23	1.11E-03
Q9Y608-1	Leucine-rich repeat flightless-interacting protein 2	LRRFIP2		0.81			0.81		3	4.7	3.67E-42
P12532-2	Acidic-type mitochondrial creatine kinase	CKMT		0.81			0.81		3	5.1	1.43E-02
C9JHT3	HZGJ	HZGJ		0.81			0.81		4	4.7	7.15E-08
B3KUB7	cDNA FLJ39535 fis, clone PUAEN2005502, highly similar to Goodpasture antigen-binding protein (EC 2.7.11.9)	COL4A3BP		0.81			0.81		4	5.1	1.16E-04
O95758-4	Regulator of differentiation 1	ROD1		0.81			0.81		4	6.5	2.81E-13
Q567Q0	cDNA FLJ75025, highly similar to Homo sapiens peptidylprolyl	PPIA		0.81			0.81		9	52	9.76E-71

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	isomerase A (cyclophilin A) (PPIA), transcript variant 2, mRNA										
Q13043-1	Mammalian STE20-like protein kinase 1	MST1	0.76	0.81	0.87	1.15	0.81	0.06	3	8.8	2.37E-42
Q9NWY4	UPF0609 protein C4orf27	C4orf27	0.90	0.82	0.72	1.39	0.81	0.09	9	33	1.07E-54
Q14746	Component of oligomeric Golgi complex 2	COG2	0.73	0.75	0.96	1.04	0.81	0.13	2	5.6	4.04E-05
P06400	p105-Rb	RB1	0.69	0.79	0.96	1.04	0.81	0.14	18	24	2.32E-138
Q14761	CD45-associated protein	LPAP	0.67	0.76	1.01	0.99	0.81	0.18	5	25	1.34E-17
O14745	Ezrin-radixin-moesin-binding phosphoprotein 50	NHERF	0.66	0.68	1.10	0.91	0.81	0.25	11	36	1.46E-111
Q8IYS1	Aminoacylase-1-like protein 2	ACY1L2	0.53	0.59	1.32	0.76	0.81	0.44	4	16	5.40E-16
P55011-1	Basolateral Na-K-Cl symporter	NKCC1	0.96		0.67	1.49	0.82	0.21	5	8.6	1.05E-11
Q14161-1	ARF GTPase-activating protein GIT2	GIT2	0.84	0.77	0.84	1.19	0.82	0.04	5	9.9	1.41E-42
Q9H0D6-1	5-3 exoribonuclease 2	XRN2	0.81	0.80	0.84	1.19	0.82	0.02	19	22	1.35E-143
C9JP52	Putative uncharacterized protein TBC1D5	TBC1D5	0.78	0.86	0.81	1.23	0.82	0.04	4	7	8.25E-12
O95721	Soluble 29 kDa NSF attachment protein	SNAP29	0.83	0.88	0.74	1.35	0.82	0.07	7	35	5.02E-51
Q8WUM0	133 kDa nucleoporin	NUP133	0.77	0.93	0.75	1.33	0.82	0.10	10	15	1.47E-128
Q8WUD1	Ras-related protein Rab-2B	RAB2B	0.93	0.99	0.53	1.89	0.82	0.25	9	53	5.63E-163
B4DUT8	cDNA FLJ52765, highly similar to Calponin-2	CNN2	0.49	0.52	1.44	0.69	0.82	0.54	11	44	1.13E-179
Q13432-1	Protein unc-119 homolog A	RG4		0.82	0.82	1.22	0.82	0.00	3	18	2.02E-05
A6NEV4	Putative uncharacterized protein SYNRG	SYNRG	0.82		0.82	1.22	0.82	0.00	3	3.8	5.51E-06
Q14181	DNA polymerase alpha 70 kDa subunit	POLA2	0.80	0.81	0.85	1.18	0.82	0.03	2	6.4	3.23E-17
P36873-2	Protein phosphatase 1C catalytic subunit	PPP1CC	0.78	0.89	0.79	1.27	0.82	0.06	17	60	0.00E+00
O15511-1	Actin-related protein 2/3 complex subunit 5	ARC16	0.75	0.72	0.99	1.01	0.82	0.15	3	40	1.67E-33
Q86VS8	Protein Hook homolog 3	HOOK3	0.65	0.74	1.07	0.93	0.82	0.22	6	12	1.91E-76
A8MVU0	cDNA FLJ58628, highly similar to	LPXN	0.60	0.73	1.13	0.88	0.82	0.28	7	28	8.17E-79

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	Leupaxin										
A8K024	cDNA FLJ78091, highly similar to Homo sapiens ubiquitin-like, containing PHD and RING finger domains, 1 (UHRF1), mRNA	UHRF1	0.64	0.65	1.17	0.85	0.82	0.30	12	17	6.07E-103
Q8NCA5	Protein FAM98A	FAM98A			0.82	1.22	0.82		2	5.4	2.04E-08
Q9HCM7	AUTS2-like protein	AUTS2L			0.82	1.22	0.82		2	1.6	3.02E-02
C9J8D9	12KDa protein	ZC3H15			0.82	1.22	0.82		2	23	7.82E-42
A6NGQ6	Putative uncharacterized protein C10orf32	C10orf32	0.82				0.82		2	22	1.18E-05
Q8NFD5-3	AT-rich interactive domain-containing protein 1B	ARID1B	0.82				0.82		2	2.2	1.45E-09
Q9Y4F3-1	Limkain-b1	KIAA0430	0.82				0.82		2	0.9	1.26E-02
O95630	Associated molecule with the SH3 domain of STAM	AMSH		0.82			0.82		3	5.4	1.42E-02
P18065	Insulin-like growth factor-binding protein 2	BP2		0.82			0.82		3	10	6.19E-17
Q8IVH4	Methylmalonic aciduria type A protein, mitochondrial	MMAA	0.81	0.83			0.82	0.01	2	5	6.13E-05
P09693	T-cell receptor T3 gamma chain	CD3G	0.79		0.85	1.18	0.82	0.04	4	24	9.87E-42
P54278-1	DNA mismatch repair protein PMS2	PMS2		0.85	0.79	1.27	0.82	0.04	6	11	1.19E-48
O95619	Glioma-amplified sequence 41	GAS41		0.75	0.89	1.12	0.82	0.10	2	11	7.35E-07
Q8NBL1	CAP10-like 46 kDa protein	C3orf9		0.75	0.89	1.12	0.82	0.10	3	8.4	9.02E-15
Q14160-3	Protein LAP4	CRIB1		0.93	0.71	1.41	0.82	0.16	5	4	2.07E-18
Q86UK7-1	Zinc finger protein 598	ZNF598	0.78	0.93	0.76	1.32	0.82	0.09	9	12	4.65E-93
P14635	G2/mitotic-specific cyclin-B1	CCNB	0.86	0.90	0.71	1.41	0.82	0.10	6	16	3.32E-87
Q8WX93-1	Palladin	CGI-151	0.73	1.01	0.73	1.37	0.82	0.16	3	3.8	6.56E-11
Q9Y314	eNOS-interacting protein	CGI-25	0.82	0.66	0.99	1.01	0.82	0.17	8	43	1.43E-43
P40763-1	Acute-phase response factor	APRF	0.71	0.72	1.04	0.96	0.82	0.19	3	6.8	1.30E-19
P62851	40S ribosomal protein S25	RPS25	0.94	0.95	0.58	1.72	0.82	0.21	6	36	1.10E-31

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Q86YS6	Ras-related protein Rab-41	RAB41	0.78	0.79	0.90	1.11	0.82	0.07	4	30	9.09E-60
B4DRA4	cDNA FLJ58610	C12orf43	0.82		0.83	1.20	0.83	0.01	2	9.9	4.47E-15
P40306	Low molecular mass protein 10	LMP10	0.83		0.82	1.22	0.83	0.01	3	15	1.15E-28
Q96KP1	Exocyst complex component 2	EXOC2	0.86		0.79	1.27	0.83	0.05	3	4.9	6.34E-21
B4E2C5	Similar to Elongation factor 1-alpha 1	EEF1A1		0.87	0.78	1.28	0.83	0.06	13	24	4.53E-42
P68366	Alpha-tubulin 1	TUBA1	0.77	0.88			0.83	0.08	23	54	0.00E+00
O96005-2	Cleft lip and palate transmembrane protein 1	CLPTM1	0.89		0.76	1.32	0.83	0.09	2	3.6	3.65E-06
Q8WWW0-1	New ras effector 1	NORE1	0.74		0.91	1.10	0.83	0.12	3	12	2.80E-07
Q69YN2-1	CWF19-like protein 1	CWF19L1		0.92	0.73	1.37	0.83	0.13	3	7.6	4.00E-17
Q6PGP7	Tetratricopeptide repeat protein 37	KIAA0372	0.96		0.69	1.45	0.83	0.19	3	3.3	1.96E-26
Q9NY61	Apoptosis-antagonizing transcription factor	AATF	1.02		0.63	1.59	0.83	0.28	4	14	4.58E-38
Q9Y375	Complex I intermediate-associated protein 30, mitochondrial	CGI-65		0.56	1.09	0.92	0.83	0.37	2	5.5	7.09E-04
Q15019-2	Neural precursor cell expressed developmentally down-regulated protein 5	DIFF6	0.81	0.82	0.85	1.18	0.83	0.02	12	46	9.25E-243
Q8NFC6	Biorientation of chromosomes in cell division protein 1-like	BOD1L	0.87	0.82	0.79	1.27	0.83	0.04	7	3.6	3.37E-23
Q7L2H7	Eukaryotic translation initiation factor 3 subunit M	EIF3M	0.91	0.78	0.79	1.27	0.83	0.07	11	39	8.44E-147
Q86WB0-1	Nuclear-interacting partner of ALK	HSPC216	0.77	0.79	0.92	1.09	0.83	0.08	3	10	6.78E-18
P09496-1	Clathrin light chain A	CLTA	0.71	0.81	0.96	1.04	0.83	0.13	8	28	1.54E-77
P20963-3	T-cell receptor T3 zeta chain	CD247	0.69	0.97	0.82	1.22	0.83	0.14	3	29	4.75E-12
A8MTR8	Kinesin-like protein 5	KIF23	0.94	0.87	0.67	1.49	0.83	0.14	5	7.4	3.70E-47
Q9NWZ3	Interleukin-1 receptor-associated kinase 4	IRAK4	0.80	0.70	0.98	1.02	0.83	0.14	2	5.9	3.73E-19
Q14320	Protein FAM50A	DXS9928E	0.71	0.77	1.00	1.00	0.83	0.15	4	17	2.75E-20
Q3V6T2-1	Akt phosphorylation enhancer	CCDC88A	0.62	0.89	0.97	1.03	0.83	0.18	3	1.7	3.09E-21
Q9NRL	ATP-dependent	ACF1	1.17	0.86	0.45	2.22	0.83	0.36	6	5.9	1.28E-34

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2-1	chromatin-remodeling protein										
P49643-1	DNA primase 58 kDa subunit	PRIM2	0.97		0.69	1.45	0.83	0.20	5	13	7.79E-10
Q9NWZ8	Gem-associated protein 8	FAM51A1	1.14		0.52	1.92	0.83	0.44	2	8.7	1.46E-05
Q49A26	3-hydroxyisobutyrate dehydrogenase-like protein	GLYR1			0.83	1.20	0.83		2	3.8	5.13E-03
Q15526-1	Surfeit locus protein 1	SURF1			0.83	1.20	0.83		2	6	2.10E-04
O43822	C21orf2 protein	C21orf2			0.83	1.20	0.83		2	7.2	2.57E-08
O60504-1	SH3-containing adapter molecule 1	SCAM1			0.83	1.20	0.83		5	12	2.05E-14
A2BCW2	MHC class I antigen C	HLA-C			0.83	1.20	0.83		7	23	3.35E-74
Q9BZL4-1	Protein phosphatase 1 myosin-binding subunit of 85 kDa	LENG3	0.83				0.83		2	3.2	3.04E-05
O75191	Xylulose kinase	XYLB	0.83				0.83		2	6.7	8.48E-05
Q9Y3A4	Gastric cancer antigen Zg14	CGI-96	0.83				0.83		2	13	6.77E-19
Q6ZSZ5-1	114 kDa Rho-specific guanine nucleotide exchange factor	ARHGEF18		0.83			0.83		2	1.9	1.76E-02
Q86TI2-2	Dipeptidyl peptidase 9	DPP9		0.83			0.83		2	2.2	2.10E-03
Q02224-1	Centromere protein E	CENPE	0.83				0.83		3	1.6	2.30E-04
Q9BZV1-1	UBX domain-containing protein 1	UBXD1	0.83				0.83		4	18	9.62E-91
Q8N0Z6	Tetratricopeptide repeat protein 5	TTC5	0.83				0.83		8	26	4.14E-25
B7ZC38	SH3-domain GRB2-like endophilin B2	RP11-167N5.3-011	0.83				0.83		11	40	4.38E-59
A6NL76	Putative uncharacterized protein ACTA1	ACTA1	0.83				0.83		27	46	0.00E+00
O94855-2	Protein transport protein Sec24D	KIAA0755	0.80		0.86	1.16	0.83	0.04	3	4.2	1.15E-10
B4DKQ0	cDNA FLJ51236, highly similar to SH3 protein expressed in lymphocytes	CXorf9	0.79		0.87	1.15	0.83	0.06	3	13	1.40E-14
Q68DF1	Putative uncharacterized protein DKFZp779B0247	DKFZp779B0247	0.83	0.90	0.76	1.32	0.83	0.07	19	27	8.48E-120
O75717	Acidic nucleoplasmic DNA-binding protein 1	AND1	0.86	0.91	0.72	1.39	0.83	0.10	16	19	4.06E-209

UniProt ID	**Protein_Name**	**Gene Name**	**F1 (L/H)**	**F2 (L/H)**	**R1 (H/L)**	**R1 (L/H)**	**Mean (T/U)**	**S.D.**	**Pep. No.**	**%Seq. Cov.**	**PEP**
B2R7N7	c-Jun N-terminal kinase kinase 1	JNKK1	0.76		0.90	1.11	0.83	0.10	6	19	1.10E-24
Q12830-1	Bromodomain and PHD finger-containing transcription factor	BPTF	0.90		0.76	1.32	0.83	0.10	3	1.8	1.20E-22
Q9Y5J1	U3 small nucleolar RNA-associated protein 18 homolog	CDABP0061	0.93	0.92	0.64	1.56	0.83	0.16	9	23	3.72E-41
Q9Y4K1	Absent in melanoma 1 protein	AIM1	0.65	0.80	1.04	0.96	0.83	0.20	20	17	1.42E-164
Q6Y7W6-1	GRB10-interacting GYF protein 2	GIGYF2	0.75	0.84	0.91	1.10	0.83	0.08	20	21	2.56E-193
P20674	Cytochrome c oxidase polypeptide Va	COX5A	0.86	0.90	0.74	1.35	0.83	0.08	7	42	6.38E-32
Q5H9R7-5	SAPS domain family member 3	C11orf23	0.77	0.76	0.97	1.03	0.83	0.12	4	7.3	1.22E-11
Q7LBC6-1	JmjC domain-containing histone demethylation protein 2B	C5orf7	0.70	0.94	0.86	1.16	0.83	0.12	5	3.7	6.61E-36
P04921-1	Glycoconnectin	GLPC	0.73	0.80	0.97	1.03	0.83	0.12	2	24	7.38E-30
A6NN80	Annexin A6, isoform CRA_c	ANXA6	0.91	0.90	0.69	1.45	0.83	0.12	37	65	0.00E+00
Q14677-1	Clathrin interactor 1	CLINT1	0.83	0.69	0.98	1.02	0.83	0.15	9	19	2.48E-116
P40692	DNA mismatch repair protein Mlh1	COCA2	0.81	0.99	0.70	1.43	0.83	0.15	8	11	5.46E-15
Q6NYC1-3	Bifunctional arginine demethylase and lysyl-hydroxylase JMJD6	JMJD6	1.02	0.74	0.74	1.35	0.83	0.16	2	8.2	7.72E-52
B4DYX9	cDNA FLJ56180, highly similar to Negative elongation factor E	NELFE	0.97	0.88	0.65	1.54	0.83	0.17	5	15	2.32E-47
O95251	Histone acetyltransferase binding to ORC1	HBO1	0.65	0.82	1.03	0.97	0.83	0.19	4	8.8	2.95E-19
P29966	Myristoylated alanine-rich C-kinase substrate	MACS	0.84	0.83			0.84	0.01	2	7.8	6.28E-06
P08574	Complex III subunit 4	CYC1	0.89		0.78	1.28	0.84	0.08	6	25	7.44E-100
C9J6Z3	cDNA FLJ77867	RBM21	0.96		0.71	1.41	0.84	0.18	6	13	7.45E-71
Q8IY17-1	Neuropathy target esterase	NTE	1.14		0.53	1.89	0.84	0.43	5	7.2	8.06E-15
O15400-1	Syntaxin-7	STX7	0.84	0.85	0.82	1.22	0.84	0.02	3	15	1.14E-43
Q9UID3-1	Another new gene 2 protein	ANG2	0.93	0.86	0.72	1.39	0.84	0.11	5	9.3	8.75E-53
Q6VY07-2	Phosphofurin acidic cluster sorting protein 1	KIAA1175	0.73	0.81	0.97	1.03	0.84	0.12	2	2.9	3.93E-38
P61106	Ras-related protein Rab-14	RAB14	0.90	0.69	0.92	1.09	0.84	0.13	13	69	9.60E-222

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Q96ST2-1	IWS1-like protein	IWS1	0.73	0.78	1.00	1.00	0.84	0.14	6	8.3	1.44E-114
B2RTR1	CLASP2 protein	CLASP2	0.7	0.82	0.99	1.01	0.84	0.15	15	13	1.42E-186
B3KRV2	cDNA FLJ34950 fis, clone NT2RP7017284, highly similar to Casein kinase I isoform epsilon (EC 2.7.11.1)	CSNK1E	0.80	0.70	1.01	0.99	0.84	0.16	3	10	1.49E-13
P01850	T-cell receptor beta-1 chain C region	TRBC1	0.87	1.03	0.61	1.64	0.84	0.21	3	18	5.05E-31
Q9NP72	Ras-related protein Rab-18	RAB18	0.86	0.78	0.87	1.15	0.84	0.05	8	48	3.61E-189
A8MSH7	Putative uncharacterized protein CUL4A	CUL4A	0.80	0.79	0.92	1.09	0.84	0.07	18	24	1.11E-116
Q99700-1	Ataxin-2	ATX2	0.74	0.92	0.85	1.18	0.84	0.09	7	11	2.64E-31
Q92995	Deubiquitinating enzyme 13	ISOT3	0.87	0.98	0.66	1.52	0.84	0.16	3	7.2	5.71E-09
P55212-1	Apoptotic protease Mch-2	CASP6	0.63	0.75	1.14	0.88	0.84	0.27	4	15	8.14E-21
P63220	40S ribosomal protein S21	RPS21	0.86	0.86	0.80	1.25	0.84	0.03	6	59	4.84E-90
Q13177	C-t-PAK2	PAK2	0.85	0.80	0.87	1.15	0.84	0.04	16	48	6.67E-117
O43264	Centromere/kinetochore protein zw10 homolog	ZW10	0.83	0.80	0.89	1.12	0.84	0.05	5	9.6	2.09E-157
Q9NZ43-1	Putative MAPK-activating protein PM26	MDS032	0.76	0.82	0.94	1.06	0.84	0.09	4	16	1.40E-12
B4DZF2	cDNA FLJ59571, highly similar to Eukaryotic translation initiation factor 4gamma 2	DAP5	0.85	0.93	0.74	1.35	0.84	0.10	29	32	1.13E-241
Q01813	6-phosphofructokinase, liver type	PFKL	0.92	0.87	0.73	1.37	0.84	0.10	4	8.3	5.10E-41
Q9H8Y8-2	Golgi phosphoprotein 6	GOLPH6	0.84	0.74	0.94	1.06	0.84	0.10	5	16	6.06E-44
Q7Z5L9-1	Interferon regulatory factor 2-binding protein 2	IRF2BP2	0.76	0.79	0.97	1.03	0.84	0.11	11	29	6.25E-127
Q96F15-2	GTPase IMAP family member 5	GIMAP5	0.76	0.77	0.99	1.01	0.84	0.13	4	16	3.05E-76
Q7Z6I6-1	Rho GTPase-activating protein 30	ARHGAP30	0.64	0.80	1.08	0.93	0.84	0.22	6	9.2	1.01E-68
P40855-1	33 kDa housekeeping protein	HK33	0.94	1.10	0.48	2.08	0.84	0.32	2	10	2.46E-12
O75791	Adapter protein GRID	GADS	0.48	0.47	1.57	0.64	0.84	0.63	15	43	3.56E-66
Q8NEJ9	EIF4E-binding protein	C14orf1			0.84	1.19	0.84		2	7.6	1.03E-41

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-1		20									
Q96T58	Msx2-interacting protein	KIAA0929			0.84	1.19	0.84		2	0.7	2.69E-05
P54707-2	Non-gastric H(+)/K(+) ATPase subunit alpha	ATP12A			0.84	1.19	0.84		3	2.8	2.00E-03
Q9Y2X9	GC-box-binding zinc finger protein 1	GZP1			0.84	1.19	0.84		3	6.1	2.03E-19
Q9UBU8	Mortality factor 4 like 1	MORF4L1			0.84	1.19	0.84		6	21	1.07E-33
P36954	DNA-directed RNA polymerase II subunit I	POLR2I		0.84			0.84		2	19	9.73E-58
Q9UJK0	UPF0293 protein C16orf42	C16orf42		0.84			0.84		2	8.3	3.26E-66
Q9H082	Ras-related protein Rab-33B	RAB33B		0.84			0.84		2	9.6	4.52E-04
Q96HR3	Mediator complex subunit 30	MED30	0.84				0.84		2	12	6.25E-05
P14621	Acylphosphatase, muscle type isozyme	ACYP		0.84			0.84		2	17	4.21E-09
Q9H0E3-2	130 kDa Sin3-associated polypeptide	SAP130		0.84			0.84		3	4	2.50E-06
Q12792-2	Protein A6	PTK9	0.84				0.84		3	5.5	6.01E-06
B4DH95	cDNA FLJ50958, highly similar to Homo sapiens GTPase, IMAP family member 6 (GIMAP6), transcript variant 1, mRNA	FLJ00102		0.84			0.84		3	8.6	1.08E-08
B4DYV5	cDNA FLJ53484, highly similar to Homo sapiens ubiquitin protein ligase E3 component n-recognin 4 (UBR4), mRNA	UBR4		0.84			0.84		3	3.5	8.75E-07
Q09472	E1A-associated protein p300	EP300	0.84				0.84		4	1.7	3.36E-05
Q9UIQ6-1	Insulin-regulated membrane aminopeptidase	LNPEP	0.84				0.84		4	4	1.70E-36
O14618	Copper chaperone for superoxide dismutase	CCS	0.84				0.84		5	23	1.21E-26
P83916	Chromobox protein homolog 1	CBX		0.84			0.84		6	24	3.38E-64
P30464	HLA class I histocompatibility antigen, B-15 alpha chain	HLAB15	0.84				0.84		6	23	5.06E-122
Q9NRW1	Ras-related protein Rab-6B	RAB6B	0.78	0.90			0.84	0.08	7	37	2.47E-77

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B4DN27	cDNA FLJ57057, highly similar to Small subunit processome component 20 homolog	DRIM	1.08		0.60	1.67	0.84	0.34	8	4.2	3.86E-21
Q96S55-1	ATPase WRNIP1	WHIP		1.31	0.37	2.70	0.84	0.66	6	8.9	7.26E-15
Q9GZT3	SRA stem-loop-interacting RNA-binding protein, mitochondrial	C14orf156	0.80	0.91	0.82	1.22	0.84	0.06	6	54	2.50E-57
Q9NXF7	DDB1- and CUL4-associated factor 16	C4orf30	0.95	0.79	0.79	1.27	0.84	0.09	3	27	2.57E-06
Q9HC07	Transmembrane protein 165	TMEM165	0.98	0.77	0.78	1.28	0.84	0.12	2	11	7.70E-08
Q6FIF0-1	AN1-type zinc finger protein 6	AWP1	0.72	0.72	1.09	0.92	0.84	0.21	3	24	8.52E-07
Q9BSJ8-2	Extended synaptotagmin-1	ESYT1	0.75	0.69	1.09	0.92	0.84	0.22	25	33	0.00E+00
B4DX20	cDNA FLJ60932, highly similar to T-complex protein 1 subunit zeta-2	CCT6B	0.86		0.83	1.20	0.85	0.02	6	12	5.34E-24
Q8NC56	LEM domain-containing protein 2	LEMD2	0.83	0.86			0.85	0.02	3	8.5	1.21E-06
Q9NSI2-1	Uncharacterized protein C21orf70	C21orf70	0.90		0.79	1.27	0.85	0.08	4	20	1.01E-39
B4DJL6	cDNA FLJ55475	C15orf44	0.77		0.92	1.09	0.85	0.11	2	3.8	6.55E-04
Q13153-2	Alpha-PAK	PAK1		0.68	1.01	0.99	0.85	0.23	4	9.6	9.67E-67
Q96PZ0	Pseudouridylate synthase 7 homolog	KIAA1897	1.13		0.56	1.79	0.85	0.40	4	13	9.82E-15
P30519	Heme oxygenase 2	HMOX2	0.83	0.80	0.91	1.10	0.85	0.06	8	34	2.15E-102
Q4V328-1	GRIP1-associated protein 1	GRIPAP1	0.79	0.93	0.82	1.22	0.85	0.07	9	15	1.55E-55
B5MBX9	Putative uncharacterized protein ZC3H14	ZC3H14	0.92	0.90	0.72	1.39	0.85	0.11	10	19	7.11E-87
O75976	Carboxypeptidase D	CPD	0.98	0.87	0.69	1.45	0.85	0.15	4	3.6	1.24E-82
P53384-1	Cytosolic Fe-S cluster assembly factor NUBP1	NBP	0.69	0.71	1.14	0.88	0.85	0.25	2	6.2	1.77E-10
P35611-3	Alpha-adducin	ADD1	0.63	0.62	1.29	0.78	0.85	0.38	15	28	4.51E-131
Q9BZD4	Cell division cycle-associated protein 1	CDCA1	0.89	0.80	0.86	1.16	0.85	0.05	2	4.5	4.13E-23
Q9NP81	Serine--tRNA ligase	SARS2	0.82	0.92	0.81	1.23	0.85	0.06	7	18	1.36E-91
Q9NVM6	DnaJ homolog subfamily C member 17	DNAJC17	0.89	0.88	0.78	1.28	0.85	0.06	5	18	8.96E-41

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O76003	Glutaredoxin-3	GLRX3	0.80	0.80	0.95	1.05	0.85	0.09	13	40	1.02E-68
Q07866-4	Kinesin light chain 1	KLC	0.77	0.82	0.96	1.04	0.85	0.10	24	39	8.53E-185
Q27J81-1	HBEBP2-binding protein C	C14orf151	0.84	0.96	0.75	1.33	0.85	0.11	8	11	1.06E-96
Q7Z4H3-1	HD domain-containing protein 2	C6orf74	0.80	0.75	1.00	1.00	0.85	0.13	6	38	1.39E-28
O95071	E3 ubiquitin-protein ligase UBR5	EDD	0.89	0.96	0.70	1.43	0.85	0.13	8	5	8.47E-33
Q6PID6	Osmosis-responsive factor	TTC33	1.01	0.76	0.78	1.28	0.85	0.14	5	31	2.79E-28
P62070	Ras-like protein TC21	RRAS2	0.75	0.95			0.85	0.14	5	29	1.51E-25
Q9Y3B7	39S ribosomal protein L11, mitochondrial	CGI-113	0.96	0.74			0.85	0.16	5	37	1.32E-52
Q9UK61-1	CTCL tumor antigen se89-1	C3orf63	0.74	0.96			0.85	0.16	5	3.2	6.61E-07
Q13610	Keratinocyte protein IEF SSP 9502	PWP1	0.76	0.76	1.03	0.97	0.85	0.16	5	14	5.03E-10
P31153	Methionine adenosyltransferase 2	AMS2	0.94	0.95	0.66	1.52	0.85	0.16	10	24	7.17E-91
Q8WUX9	Charged multivesicular body protein 7	CHMP7	0.74	0.76	1.05	0.95	0.85	0.17	4	12	2.90E-42
P08754	G(i) alpha-3	GNAI3	0.98		0.72	1.39	0.85	0.18	11	44	5.71E-62
Q9Y2P8	RNA 3-terminal phosphate cyclase-like protein	HSPC338	0.85	1.05	0.65	1.54	0.85	0.20	3	8.3	4.10E-31
Q16222-1	AGX-1	SPAG2	0.65	0.84	1.06	0.94	0.85	0.21	8	21	6.97E-58
Q92974-2	Guanine nucleotide exchange factor H1	ARHGEF2	0.63	0.62	1.30	0.77	0.85	0.39	30	31	2.76E-272
B4DTS2	cDNA FLJ60070, highly similar to Serine/threonine-protein kinase D2 (EC 2.7.11.13)	HSPC187			0.85	1.18	0.85		2	3.5	5.18E-08
O95159	Zinc finger protein MCG4	ZFPL1			0.85	1.18	0.85		2	5.5	1.94E-02
Q9UFV9	Putative uncharacterized protein DKFZp434J046	DKFZp434J046			0.85	1.18	0.85		2	2.6	2.09E-09
Q86VV8	Rotatin	RTTN			0.85	1.18	0.85		3	1.7	8.90E-05
Q16773-1	Cysteine-S-conjugate beta-lyase	CCBL1	0.85				0.85		2	7.8	6.77E-04
Q9H9P8-1	L-2-hydroxyglutarate dehydrogenase, mitochondrial	C14orf160		0.85			0.85		2	4.3	1.37E-03
Q4KWH8-1	1-phosphatidylinositol-4,5-bisphosphate	KIAA1069	0.85				0.85		2	0.8	1.67E-02

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	phosphodiesterase eta-1										
P61018-2	Ras-related protein Rab-4B	PP1596	0.85				0.85		2	16	1.65E-52
Q14527-1	DNA-binding protein/plasminogen activator inhibitor 1 regulator	HIP116A	0.85				0.85		2	3.6	1.39E-12
P61129	Zinc finger CCCH domain-containing protein 6	KIAA2035	0.85				0.85		2	3.8	5.06E-05
Q5Y190	Anchor protein	RESDA1	0.85				0.85		2	0.5	1.13E-03
Q96EY5-1	CIN85/CD2AP family-binding protein	CFBP	0.85				0.85		2	13	1.18E-30
P10746	Hydroxymethylbilane hydrolyase [cyclizing]	UROS	0.85				0.85		2	13	3.98E-09
Q14257	Calcium-binding protein ERC-55	ERC55	0.85				0.85		2	11	4.48E-42
Q5UCC4-3	Hematopoietic signal peptide-containing membrane domain-containing protein 1	C19orf63	0.85				0.85		2	8.9	1.44E-77
Q99828	Calcium- and integrin-binding protein	CIB	0.85				0.85		3	20	4.03E-21
Q9BVL4	Selenoprotein O	SELO	0.85				0.85		3	8.7	3.67E-41
Q9Y3L3-1	SH3 domain-binding protein 1	SH3BP1		0.85			0.85		3	3.9	1.69E-03
Q6YP21-1	Cysteine-S-conjugate beta-lyase 2	CCBL2		0.85			0.85		3	8.6	9.94E-24
Q96Q89-2	Cancer/testis antigen 90	KIF20B		0.85			0.85		3	1.8	3.25E-02
O00459	Phosphatidylinositol 3-kinase 85 kDa regulatory subunit beta	PIK3R2	0.85				0.85		4	8.2	1.44E-11
Q9UNP9-1	Cyclophilin E	CYP33	0.85				0.85		9	34	2.23E-51
Q96B97-1	Cbl-interacting protein of 85 kDa	CIN85	0.85				0.85		11	27	5.01E-57
Q4LE64	NUMA1 variant protein	NUMA1 variant protein	0.85				0.85		83	46	0.00E+00
O60828-1	38 kDa nuclear protein containing a WW domain	JM26	1.06	0.83	0.66	1.52	0.85	0.20	4	36	3.07E-28
Q9BZF1-1	Oxysterol-binding protein-related protein 8	KIAA1451	0.72	0.89	0.95	1.05	0.85	0.12	9	16	2.60E-62
Q8ND56-2	Protein FAM61A	C19orf13	0.64	0.78	1.14	0.88	0.85	0.26	3	7.8	1.55E-08
O00571	ATP-dependent RNA	DBX	0.85	0.83	0.88	1.14	0.85	0.03	27	44	0.00E+00

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	helicase DDX3X										
B4DXJ1	cDNA FLJ56334, highly similar to SEC13-related protein	D3S1231E	0.91	0.87	0.78	1.28	0.85	0.07	6	23	1.98E-55
Q9Y4C8	Probable RNA-binding protein 19	KIAA0682	0.80	0.94	0.82	1.22	0.85	0.08	6	7.6	1.19E-85
Q9NPI1-2	75 kDa bromodomain protein	BP75	0.73	0.91	0.92	1.09	0.85	0.11	4	9.4	1.22E-73
Q8TB72-1	Pumilio homolog 2	KIAA0235	0.72	0.92	0.92	1.09	0.85	0.12	6	6.3	1.23E-32
P19387	DNA-directed RNA polymerase II 33 kDa polypeptide	A-152E5.7	1.07	0.78	0.71	1.41	0.85	0.19	8	42	6.07E-79
Q2I5I4	Four and a half LIM-domain protein 2	FHL2	0.56	0.70	1.30	0.77	0.85	0.39	5	15	9.62E-21
Q6IQ49-1	UPF0667 protein C1orf55	C1orf55		0.86	0.85	1.18	0.86	0.01	3	6.7	5.65E-13
P40818	Deubiquitinating enzyme 8	KIAA0055		0.86	0.85	1.18	0.86	0.01	7	9.2	1.74E-39
O95671-1	N-acetylserotonin O-methyltransferase-like protein	ASMTL	0.85	0.86			0.86	0.01	2	5.6	2.42E-23
Q6UWE0-1	E3 ubiquitin-protein ligase LRSAM1	LRSAM1		0.84	0.87	1.15	0.86	0.02	3	5.4	1.11E-03
Q9P1Y6-1	PHD and RING finger domain-containing protein 1	KIAA1542		0.81	0.90	1.11	0.86	0.06	4	5	3.78E-11
P57679	Ellis-van Creveld syndrome protein	EVC	0.91	0.80			0.86	0.08	2	2.6	7.37E-03
B4DZ73	cDNA FLJ59791, highly similar to Importin-11	IPO11	0.92		0.79	1.27	0.86	0.09	5	9.3	2.78E-45
O15234	Cancer susceptibility candidate gene 3 protein	CASC3	0.97		0.74	1.35	0.86	0.16	3	5.4	2.94E-10
Q9Y6Y8-1	SEC23-interacting protein	MSTP053	0.76	0.91	0.90	1.11	0.86	0.08	5	6.1	1.18E-17
Q92556-1	Engulfment and cell motility protein 1	ELMO1	0.96	0.94	0.67	1.49	0.86	0.16	10	19	3.35E-59
A4D212	DKFZP586J0619 protein	DKFZP586J0619	1.04	0.94	0.59	1.69	0.86	0.24	6	3.4	2.12E-38
Q8IXQ3	Uncharacterized protein C9orf40	C9orf40	0.99	1.02	0.56	1.79	0.86	0.26	4	42	4.12E-17
Q96T51-1	FYVE-finger protein EIP1	RABIP4	0.93	0.81	0.83	1.20	0.86	0.06	5	11	7.81E-27
Q96NB3	Coiled-coil domain-containing protein 16	CCDC16	0.91	0.94	0.72	1.39	0.86	0.12	5	18	6.69E-75
Q96MX4	cDNA FLJ31747 fis, clone NT2RI2007377, highly similar to RNA-BINDING PROTEIN EWS	EWSR1	0.79	0.78	1.00	1.00	0.86	0.12	6	15	9.64E-93

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Q7Z2W4-1	Zinc finger antiviral protein	PRO1677	0.78	0.77	1.02	0.98	0.86	0.14	14	22	3.70E-265
B3KNU0	cDNA FLJ30470 fis, clone BRAWH1000040, highly similar to Rap1 GTPase-GDP dissociation stimulator 1	RAP1GDS1	0.75	0.71	1.11	0.90	0.86	0.22	22	53	0.00E+00
Q9BRD0-1	BUD13 homolog	BUD13	0.67	0.79	1.11	0.90	0.86	0.23	2	3.2	1.29E-05
Q9Y4W2-1	Protein LAS1 homolog	LAS1L	0.92	1.09	0.56	1.79	0.86	0.27	4	9.5	1.09E-14
Q86Z22	Putative uncharacterized protein	P1725	0.61	0.62	1.34	0.75	0.86	0.42	5	26	2.00E-103
P05107	Cell surface adhesion glycoproteins LFA-1/CR3/p150,95 subunit beta	CD18	0.86	0.87	0.85	1.18	0.86	0.01	16	24	1.39E-171
Q13885	Tubulin beta-2A chain	TUBB2	0.83	0.89	0.86	1.16	0.86	0.03	21	54	0.00E+00
Q9NSY1-1	BMP-2-inducible protein kinase	BIKE	0.83		0.89	1.12	0.86	0.04	4	6.3	4.66E-34
P52294	Importin subunit alpha-1	KPNA1	0.88	0.90	0.80	1.25	0.86	0.05	5	11	1.58E-31
Q8NF64-1	PIAS-like protein Zimp7	HRIHFB2007	0.82		0.90	1.11	0.86	0.06	2	4.5	2.55E-26
Q86SZ2-1	Trafficking protein particle complex subunit 6B	TRAPPC6B		0.82	0.90	1.11	0.86	0.06	2	11	1.50E-04
P09972	Brain-type aldolase	ALDC	0.83	0.82	0.93	1.08	0.86	0.06	12	27	1.76E-236
Q96SI9-1	Spermatid perinuclear RNA-binding protein	SPNR	0.81	0.84	0.93	1.08	0.86	0.06	14	23	2.60E-100
O95819-3	HPK/GCK-like kinase HGK	HGK	0.85	0.78	0.95	1.05	0.86	0.09	16	13	1.12E-178
Q86W50-1	Methyltransferase 10 domain-containing protein	METT10D	0.81	1.00	0.77	1.30	0.86	0.12	4	7.5	1.44E-15
Q96G25-2	Activator-recruited cofactor 32 kDa component	MED8	0.95		0.77	1.30	0.86	0.13	5	24	1.06E-24
Q5VIR6-1	Vacuolar protein sorting-associated protein 53 homolog	PP13624	0.75		0.97	1.03	0.86	0.16	3	7.5	2.79E-23
P07766	T-cell surface antigen T3/Leu-4 epsilon chain	CD3E	1.02	0.87	0.69	1.45	0.86	0.17	5	36	1.66E-82
Q15542-1	Transcription initiation factor TFIID 100 kDa subunit	TAF2D			0.86	1.16	0.86		2	2.8	6.19E-07
Q8N3P4	Vacuolar protein sorting-associated protein 8 homolog	KIAA0804			0.86	1.16	0.86		2	1.5	1.32E-04

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O43716	GatC-like protein	15E1.2	0.86				0.86		2	21	5.92E-03
Q9H967	WD repeat-containing protein 76	WDR76		0.86			0.86		2	4.2	2.10E-02
O76054	Alpha-tocopherol-associated protein	C22orf6	0.86				0.86		2	9.9	1.70E-04
Q9H081	Protein MIS12 homolog	MIS12	0.86				0.86		2	9.3	8.26E-08
Q9BVS5	Potential tRNA (adenine-N(1)-)-methyltransferase catalytic subunit TRMT61B	TRMT61B	0.86				0.86		2	5	1.62E-02
B4DH58	cDNA FLJ56344, highly similar to Implantation-associated protein	IAG2	0.86				0.86		2	5.2	1.69E-03
Q86U28	HESB-like domain-containing protein 1	HBLD1	0.86				0.86		2	13	2.96E-15
Q76I76-1	Protein phosphatase Slingshot homolog 2	KIAA1725	0.86				0.86		2	3.9	2.05E-10
B4DEF8	cDNA FLJ61100, highly similar to 39S ribosomal protein L45, mitochondrial	MRPL45	0.86				0.86		2	13	1.85E-07
A8MWD6	Putative uncharacterized protein MRPS36	MRPS36	0.86				0.86		2	27	5.25E-05
B4DFT0	cDNA FLJ50476, weakly similar to Serine/threonine-protein kinase ULK1 (EC2.7.11.1)	ULK3	0.86				0.86		2	5.8	1.08E-02
Q15773	Myelodysplasia-myeloid leukemia factor 2	MLF2		0.86			0.86		3	13	1.76E-06
Q86VR2	Protein FAM134C	FAM134C	0.86				0.86		3	10	7.89E-31
Q9HBL8	NmrA-like family domain-containing protein 1	HSCARG	0.86				0.86		3	12	2.25E-64
Q4LE39-1	180 kDa Sin3-associated polypeptide	ARID4B		0.86			0.86		4	3	1.23E-30
Q13085-4	ACC-alpha	ACAC	0.86				0.86		5	3	4.67E-20
P31321	cAMP-dependent protein kinase type I-beta regulatory subunit	PRKAR1B	0.86				0.86		6	15	7.56E-05
Q16644	Chromosome 3p kinase	MAPKAPK3	1.04		0.68	1.47	0.86	0.25	4	13	1.20E-10
Q0P5N8	TMSB4X protein	TMSB4X	0.77	0.86	0.96	1.04	0.86	0.10	6	36	5.14E-39
Q9Y5X3	Sorting nexin-5	SNX5	0.76	0.96	0.87	1.15	0.86	0.10	10	32	9.48E-120
Q9P000	COMM domain-	COMM	0.74	0.86	0.99	1.01	0.86	0.13	8	57	7.04E-65

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	containing protein 9	D9									
Q15067-1	Palmitoyl-CoA oxidase	ACOX	0.81	0.76	1.02	0.98	0.86	0.14	8	18	2.36E-93
Q5SRE5-1	Nucleoporin NUP188 homolog	KIAA0169	0.78	1.14	0.67	1.49	0.86	0.25	5	4.2	5.77E-135
P35221-2	Alpha E-catenin	CTNNA1	0.73	0.69	1.17	0.85	0.86	0.27	5	6.7	2.18E-105
O00499-1	Amphiphysin II	AMPHL	0.61	0.43	1.55	0.65	0.86	0.60	3	8.3	2.89E-24
O00182-1	Ecalectin	LGALS9	0.93	0.77	0.89	1.12	0.86	0.08	5	16	1.58E-63
O43164-1	E3 ubiquitin-protein ligase Praja-2	KIAA0438	0.68	0.98	0.93	1.08	0.86	0.16	4	8.6	8.58E-100
Q99471	C-Myc-binding protein Mm-1	MM1	0.85	0.88			0.87	0.02	4	25	1.75E-171
Q14807	Kinesin-like DNA-binding protein	KID		0.91	0.82	1.22	0.87	0.06	4	9.6	3.97E-74
Q8WYP5-2	Embryonic large molecule derived from yolk sac	AHCTF1	0.92		0.81	1.23	0.87	0.08	15	9.5	7.59E-65
B3KSH1	cDNA FLJ36192 fis, clone TESTI2027450, highly similar to Eukaryotic translation initiation factor 3 subunit 5	hCG_1784554	0.88	0.94	0.78	1.28	0.87	0.08	8	29	6.51E-169
Q86TU7-1	SET domain-containing protein 3	C14orf154	0.87	0.95	0.78	1.28	0.87	0.09	9	18	3.34E-110
Q96KR1	M-phase phosphoprotein homolog	ZFR	1.01	0.83	0.76	1.32	0.87	0.13	13	20	1.25E-206
O00151	C-terminal LIM domain protein 1	CLIM1	0.70	0.68	1.22	0.82	0.87	0.31	16	66	8.90E-136
Q9H6Z4-1	Ran-binding protein 3	RANBP3	0.59	0.69	1.32	0.76	0.87	0.40	7	15	1.56E-39
Q8N1F7	93 kDa nucleoporin	KIAA0095	0.83	0.88	0.89	1.12	0.87	0.03	25	38	1.17E-254
Q6DD88-1	Atlastin-3	ATL3	0.91	0.82	0.87	1.15	0.87	0.05	18	51	4.57E-281
Q13765	Alpha-NAC	HSD48	0.81	0.94	0.85	1.18	0.87	0.07	5	7.6	8.17E-279
Q9NRA8-1	Eukaryotic translation initiation factor 4E nuclear import factor 1	EIF4ENIF1	1.01	0.77	0.82	1.22	0.87	0.13	6	11	4.46E-25
P60468	Protein transport protein Sec61 subunit beta	SEC61B	1.05	0.88	0.67	1.49	0.87	0.19	3	38	3.85E-08
Q14011	A18 hnRNP	A18HNRNP	1.05	0.94	0.61	1.64	0.87	0.23	4	33	3.03E-131
P27701	C33 antigen	CD82	0.69	0.62	1.29	0.78	0.87	0.37	2	7.1	1.44E-30
B7Z2T0	cDNA FLJ59513, highly similar to Sodium/potassium-	ATP1A3	1.16		0.58	1.72	0.87	0.41	17	18	6.37E-252

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	transporting ATPase alpha-3 chain (EC 3.6.3.9)										
O60870	Binding to curved DNA	BTCD		0.86	0.88	1.14	0.87	0.01	3	8.1	2.68E-11
Q8NDX1-1	Exchange factor for ADP-ribosylation factor guanine nucleotide factor 6B	EFA6B	0.89	0.85			0.87	0.03	3	5.4	3.52E-25
P60228	Eukaryotic translation initiation factor 3 subunit 6	EIF3E	0.90	0.87	0.84	1.19	0.87	0.03	14	38	4.16E-65
P82932	28S ribosomal protein S6, mitochondrial	C21orf101	0.82	0.92			0.87	0.07	2	16	2.67E-03
Q15397	HBV XAg-transactivated protein 5	KIAA0020	0.94	0.92	0.75	1.33	0.87	0.10	5	10	6.67E-33
Q14C86-6	GTPase-activating protein and VPS9 domain-containing protein 1	GAPEX5	0.83	0.99	0.79	1.27	0.87	0.11	6	6.1	2.07E-32
O95453	Deadenylating nuclease	DAN		0.95	0.79	1.27	0.87	0.11	4	6.7	1.35E-05
Q14651	Intestine-specific plastin	PLS1	0.91	0.99	0.71	1.41	0.87	0.14	8	19	6.29E-84
O00399	Dynactin subunit 6	DCTN6	0.76	0.98			0.87	0.16	2	9.5	1.04E-04
P07858	APP secretase	CPSB	1.05	0.85	0.71	1.41	0.87	0.17	4	17	1.03E-07
A2A2L5	Chromosome 20 open reading frame 43	C20orf43	0.99	0.95	0.67	1.49	0.87	0.17	5	19	6.29E-43
Q9H6D7-1	HAUS augmin-like complex subunit 4	C14orf94		1.03	0.71	1.41	0.87	0.23	2	6.1	2.99E-05
Q96EP5-1	DAZ-associated protein 1	DAZAP1	0.71	0.76	1.14	0.88	0.87	0.24	5	19	8.53E-96
Q9BYD3-1	39S ribosomal protein L4, mitochondrial	CDABP0091	0.68	0.74	1.19	0.84	0.87	0.28	2	11	4.85E-102
Q2M2I8	Adaptor-associated kinase 1	AAK1	0.14	0.76	1.71	0.58	0.87	0.79	4	9.1	5.79E-67
Q9H981	Actin-related protein 8	ACTR8			0.87	1.15	0.87		2	3.5	6.74E-04
P53367-2	ADP-ribosylation factor-interacting protein 1	ARFIP1			0.87	1.15	0.87		2	8.5	3.45E-35
O43149	Zinc finger ZZ-type and EF-hand domain-containing protein 1	KIAA0399			0.87	1.15	0.87		2	1.3	5.16E-23
Q9P2R3-1	Ankyrin repeat and FYVE domain-containing protein 1	ANKFY1			0.87	1.15	0.87		4	3.8	1.56E-12
Q12770-1	Sterol regulatory element-binding protein cleavage-activating protein	KIAA0199	0.87				0.87		2	1.7	3.14E-04
Q9Y3D5	28S ribosomal protein S18-1, mitochondrial	CGI-134	0.87				0.87		2	22	3.20E-65

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Q7L2Z9	Centromere protein Q	C6orf139	0.87				0.87		2	10	7.24E-04
Q9NRP2	Uncharacterized protein C16orf61	C16orf61	0.87				0.87		2	25	3.81E-11
O60645-1	Exocyst complex component 3	EXOC3		0.87			0.87		2	2.6	4.19E-03
Q8NHH9-1	ADP-ribosylation factor-like protein 6-interacting protein 2	ARL6IP2	0.87				0.87		2	4.3	4.43E-03
B5MDA0	Putative uncharacterized protein WDR73	WDR73	0.87				0.87		2	9.1	1.19E-04
Q8IZD4	mRNA-decapping enzyme 1B	DCP1B	0.87				0.87		2	4.9	3.77E-05
Q9H2P9-5	Diphthamide biosynthesis methyltransferase	AD-018	0.87				0.87		2	8.4	1.15E-152
A8MTZ7	Uncharacterized protein C12orf71	C12orf71	0.87				0.87		2	13	8.19E-03
B4DKM0	cDNA FLJ51883, highly similar to Mitochondrial 39S ribosomal protein L3	MRL3	0.87				0.87		2	12	1.62E-02
B3KUL1	cDNA FLJ40132 fis, clone TESTI2012155, highly similar to NUCLEOPORIN-LIKE PROTEIN RIP	AGFG1		0.87			0.87		2	5.8	7.66E-20
Q96MW5	Component of oligomeric Golgi complex 8	COG8	0.87				0.87		3	8.5	9.27E-08
P56385	ATP synthase subunit e, mitochondrial	ATP5I		0.87			0.87		3	33	3.87E-05
Q9Y5B8	Nucleoside diphosphate kinase 7	NME7		0.87			0.87		3	10	8.02E-16
Q13905-2	CRK SH3-binding GNRP	GRF2	0.87				0.87		3	6.1	1.10E-32
Q66PJ3-2	ADP-ribosylation factor-like protein 6-interacting protein 4	ARL6IP4	0.87				0.87		3	13	4.72E-16
Q8TEW0-1	Atypical PKC isotype-specific-interacting protein	PAR3	0.87				0.87		4	4.5	5.35E-08
B4DHL6	cDNA FLJ60542, highly similar to Protein vav-3	VAV3		0.87			0.87		4	5.8	1.58E-05
Q9NQT8	Kinesin-like protein GAKIN	GAKIN	0.87				0.87		5	4.2	6.36E-18
Q9Y5U2-1	Protein TSSC4	TSSC4	0.87				0.87		5	17	2.85E-09
Q9P260-1	LisH domain and HEAT repeat-containing protein KIAA1468	KIAA1468	0.87				0.87		5	5.3	6.43E-73

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Q9P287-2	BRCA2 and CDKN1A-interacting protein	BCCIP	0.93	0.75	0.93	1.08	0.87	0.10	4	19	6.18E-44
O00139-2	Kinesin-2	KIF2	0.81	0.80	1.00	1.00	0.87	0.11	13	21	2.49E-79
P12955	Imidodipeptidase	PEPD	0.77	0.76	1.08	0.93	0.87	0.18	5	15	6.20E-39
Q8N5A5-1	G patch domain-containing protein 6	GPATC6	0.75	0.78	1.08	0.93	0.87	0.18	5	12	3.36E-37
C9JS35	Putative uncharacterized protein UFD1L	UFD1L	0.86	0.87	0.89	1.12	0.87	0.02	7	29	4.92E-41
P62857	40S ribosomal protein S28	RPS28	0.88	0.89	0.85	1.18	0.87	0.02	5	57	1.85E-88
P13984	ATP-dependent helicase GTF2F2	GTF2F2	0.85	0.84	0.93	1.08	0.87	0.05	8	33	1.30E-30
Q5W0H4	Tumor protein, translationally-controlled 1	RP11-290D2.1-004	0.83	0.86	0.93	1.08	0.87	0.05	10	79	1.36E-94
Q9P2I0	Cleavage and polyadenylation specificity factor 100 kDa subunit	CPSF100	0.77	0.98	0.87	1.15	0.87	0.11	8	13	2.92E-69
O14737	Programmed cell death protein 5	PDCD5	0.96	0.93	0.73	1.37	0.87	0.13	5	47	5.39E-161
Q8TBC4	NEDD8-activating enzyme E1 catalytic subunit	UBA3	0.85	0.76	1.01	0.99	0.87	0.13	7	24	1.04E-30
O43663-1	Protein regulator of cytokinesis 1	PRC1	0.92	1.00	0.70	1.43	0.87	0.16	6	12	2.54E-10
Q9Y679-1	Ancient ubiquitous protein 1	AUP1	0.98	0.96	0.68	1.47	0.87	0.17	3	10	1.04E-20
Q9Y4B6-1	DDB1- and CUL4-associated factor 1	DCAF1		0.87	0.88	1.14	0.88	0.01	2	1.4	3.86E-07
Q9NQP4	Prefoldin subunit 4	PFD4	0.90	0.85			0.88	0.04	2	20	7.42E-73
Q96RN5-1	Activator-recruited cofactor 105 kDa component	ARC105	0.92		0.83	1.20	0.88	0.06	2	6.1	1.80E-78
P61764-2	N-Sec1	STXBP1	0.92	0.83			0.88	0.06	3	4.8	6.83E-05
Q5T447-1	HECT domain-containing protein 3	HECTD3	0.82		0.93	1.08	0.88	0.08	3	5.3	3.42E-21
Q9P107	GEM-interacting protein	GMIP	0.93		0.82	1.22	0.88	0.08	6	11	3.35E-81
Q92733	Papillary renal cell carcinoma translocation-associated gene protein	PRCC		0.94	0.81	1.23	0.88	0.09	3	9	8.92E-58
P16333	Cytoplasmic protein NCK1	NCK		0.73	1.02	0.98	0.88	0.21	3	8.5	9.39E-06
Q5VYK3	Proteasome-associated protein ECM29	ECM29	1.10		0.65	1.54	0.88	0.32	7	5.2	5.27E-35

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	homolog										
Q9H4L5-1	Oxysterol-binding protein-related protein 3	KIAA0704		0.63	1.12	0.89	0.88	0.35	3	3.8	1.65E-06
Q13573	Nuclear protein SkiP	SKIIP	0.89	0.85	0.89	1.12	0.88	0.02	10	22	3.60E-59
Q9C0C9	Ubiquitin carrier protein O	KIAA1734	0.89	0.89	0.85	1.18	0.88	0.02	12	15	1.72E-53
P06239-3	Lymphocyte cell-specific protein-tyrosine kinase	LCK	0.90	0.89	0.84	1.19	0.88	0.03	16	40	9.27E-210
O95373	Importin-7	IPO7	0.90	0.82	0.91	1.10	0.88	0.05	9	12	9.55E-78
Q6NW29	Protein FAM28A	FAM28A	0.88	0.93	0.82	1.22	0.88	0.06	3	15	1.32E-10
P62081	40S ribosomal protein S7	RPS7	0.89	0.93	0.81	1.23	0.88	0.06	13	71	4.22E-129
Q53G62	Mitochondrial ribosomal protein S28 variant	HSPC007	0.81	0.82	1.00	1.00	0.88	0.11	5	31	2.24E-61
P49366-1	Deoxyhypusine synthase	DHPS	0.96	0.98	0.69	1.45	0.88	0.16	8	32	7.34E-126
Q9Y371-1	Bax-interacting factor 1	CGI-61	0.72	0.83	1.08	0.93	0.88	0.18	9	30	9.32E-99
Q15054	DNA polymerase delta subunit 3	KIAA0039	0.77	0.76	1.10	0.91	0.88	0.19	5	12	7.08E-32
Q9UBV2-1	Protein sel-1 homolog 1	SEL1L	0.70	1.09	0.84	1.19	0.88	0.20	3	7.2	1.68E-20
P11182	Branched-chain alpha-keto acid dehydrogenase complex component E2	BCATE2		0.82	0.94	1.06	0.88	0.08	2	4.8	9.16E-80
P50851-1	Beige-like protein	BGL		0.82	0.94	1.06	0.88	0.08	3	1.6	8.44E-13
A3KN83-1	Monocyte protein 3	MOP3	0.94		0.82	1.22	0.88	0.08	8	10	4.28E-55
Q15361	RNA polymerase I termination factor	TTF1	0.83	0.83	0.98	1.02	0.88	0.09	4	6.6	7.98E-24
P09132	Signal recognition particle 19 kDa protein	SRP19	0.98	0.88	0.78	1.28	0.88	0.10	4	29	7.83E-133
Q13618-1	Cullin-3	CUL3	0.91	0.97	0.76	1.32	0.88	0.11	7	12	5.88E-53
P54709	Sodium/potassium-dependent ATPase subunit beta-3	ATP1B3	0.90	0.98	0.76	1.32	0.88	0.11	2	6.8	1.64E-07
Q9NZ63	Hepatocellular carcinoma-associated antigen 59	C9orf78	0.82	0.75	1.07	0.93	0.88	0.17	6	18	1.12E-26
P78347-1	Bruton tyrosine kinase-associated protein 135	BAP135	0.78	0.73	1.13	0.88	0.88	0.22	17	23	2.31E-106
Q9BUR4	Telomerase Cajal body protein 1	TCAB1	1.16	0.74	0.74	1.35	0.88	0.24	3	11	1.54E-45

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Q13464	Renal carcinoma antigen NY-REN-35	ROCK1	0.72	0.76	1.16	0.86	0.88	0.24	14	12	1.21E-48
Q14258	E3 ubiquitin/ISG15 ligase TRIM25	EFP	1.15		0.61	1.64	0.88	0.38	5	13	5.02E-167
Q4VBZ6	EEF1D protein	EEF1D	0.88	0.88			0.88	0.00	11	55	8.15E-259
Q96QE3-1	ATPase family AAA domain-containing protein 5	ATAD5		0.87	0.89	1.12	0.88	0.01	2	1.3	6.13E-41
Q01518-1	Adenylyl cyclase-associated protein 1	CAP	0.86	0.87	0.91	1.10	0.88	0.03	28	64	0.00E+00
P49459	RAD6 homolog A	RAD6A	0.86		0.90	1.11	0.88	0.03	2	7.2	5.65E-18
B7Z596	cDNA FLJ55130, highly similar to Rattus norvegicus tropomyosin 1, alpha (Tpm1), transcript variant 8, mRNA	hCG_33495	0.92		0.84	1.19	0.88	0.06	9	24	8.71E-75
O95989	Diadenosine 5,5-P1,P6-hexaphosphate hydrolase 1	DIPP	0.83	0.93			0.88	0.07	4	25	1.74E-07
O43491	Band 4.1-like protein 2	EPB41L2	0.79	0.85	1.00	1.00	0.88	0.11	26	32	2.07E-175
A8K0H3	cDNA FLJ78093, highly similar to Homo sapiens ribosomal protein L29 (RPL29), mRNA	RPL29	1.02	0.74	0.88	1.14	0.88	0.14	3	20	4.23E-25
Q9NVM9	Cell cycle regulator Mat89Bb homolog	C12orf11		0.98	0.78	1.28	0.88	0.14	3	4.4	2.15E-18
P36507	Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	0.77	0.81	1.06	0.94	0.88	0.16	15	52	3.16E-92
Q15645-1	Human papillomavirus type 16 E1 protein-binding protein	TRIP13	0.91	1.04	0.69	1.45	0.88	0.18	12	38	1.26E-123
Q969G3-1	BRG1-associated factor 57	BAF57	0.74	0.82	1.08	0.93	0.88	0.18	10	26	7.91E-54
Q86U90	Dopamine receptor-interacting protein 3	DRIP3	1.08	0.98	0.58	1.72	0.88	0.26	9	46	4.25E-84
Q9GZS1-1	DNA-directed RNA polymerase I subunit E	PAF53		1.07	0.69	1.45	0.88	0.27	5	11	1.19E-17
Q02952-1	A-kinase anchor protein 12	AKAP12			0.88	1.14	0.88		5	5.5	9.66E-57
P51610-1	C1 factor	HCF1			0.88	1.14	0.88		27	21	4.30E-174
P22415	Class B basic helix-loop-helix protein 11	BHLHB11		0.88			0.88		2	5.5	1.24E-03
Q9Y467	Sal-like protein 2	KIAA0360	0.88				0.88		2	2.9	1.89E-64
Q9P0J7	E3 ubiquitin-protein ligase KCMF1	FIGC	0.88				0.88		2	8.1	4.53E-04
B4DW	cDNA FLJ55258,	APPD		0.88			0.88		2	6	5.48E-04

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N9	highly similar to Homo sapiens pleckstrin homology domain containing, family F member 1, mRNA										
P30260	Anaphase-promoting complex subunit 3	ANAPC3		0.88			0.88		2	3.5	4.98E-04
Q8N8N7-1	15-oxoprostaglandin 13-reductase	PTGR2	0.88				0.88		3	11	1.85E-30
Q8WUW1-2	Probable protein BRICK1	C3orf10	0.88				0.88		3	31	4.07E-22
Q7Z3U7-1	Protein MON2 homolog	KIAA1040		0.88			0.88		3	2.1	2.08E-47
O75600	2-amino-3-ketobutyrate coenzyme A ligase, mitochondrial	GCAT	0.88				0.88		3	13	1.47E-106
A6NCE7	Microtubule-associated proteins 1A/1B light chain 3 beta 2	MAP1LC3B2	0.88				0.88		4	21	2.07E-07
Q04206-1	Nuclear factor NF-kappa-B p65 subunit	NFKB3		0.88			0.88		4	7.6	2.09E-15
Q9Y2I7	1-phosphatidylinositol-3-phosphate 5-kinase	KIAA0981	0.88				0.88		4	2	1.56E-05
Q92769-2	Histone deacetylase 2	HDAC2	0.88				0.88		5	11	2.53E-84
P49590	Histidine--tRNA ligase	HARS2	0.88				0.88		6	16	3.34E-09
A6NKH4	Putative uncharacterized protein SNX1	hCG_33348	0.88				0.88		8	21	1.10E-40
P46934-1	Cell proliferation-inducing gene 53 protein	KIAA0093	0.88				0.88		10	12	1.93E-54
Q6XZF7-1	Dynamin-binding protein	DNMBP	0.88				0.88		12	9.8	7.65E-22
Q9NSK0-3	Kinesin light chain 4	KLC4	0.88				0.88		17	35	1.01E-267
Q96J01	hTREX45	THOC3	1.11		0.65	1.54	0.88	0.33	3	12	1.10E-05
Q99613	Eukaryotic translation initiation factor 3 subunit 8	EIF3C	0.84	0.92	0.89	1.12	0.88	0.04	31	33	5.26E-298
P63208-1	Cyclin-A/CDK2-associated protein p19	EMC19	0.96	0.81	0.88	1.14	0.88	0.08	7	52	3.16E-77
P15428	15-hydroxyprostaglandin dehydrogenase [NAD+]	HPGD	0.82	0.82	1.01	0.99	0.88	0.11	5	26	1.58E-31
Q15021	Chromosome condensation-related	CAPD2	1.00	0.92	0.73	1.37	0.88	0.14	28	29	0.00E+00

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	SMC-associated protein 1										
Q9BRT8-1	Cobalamin synthase W domain-containing protein 1	CBWD1	0.68	0.97	1.00	1.00	0.88	0.18	3	11	6.74E-90
Q86V81	Ally of AML-1 and LEF-1	ALY	0.89	0.63	1.13	0.88	0.88	0.25	8	45	1.45E-78
Q9UBQ5	eIF-3 p25	ARG134	0.92	0.97	0.76	1.32	0.88	0.11	6	33	4.68E-100
Q8NI08-1	140 kDa estrogen receptor-associated protein	ERAP140	1.07	0.79	0.79	1.27	0.88	0.16	2	3.1	2.61E-05
O60869-1	Endothelial differentiation-related factor 1	EDF1	0.85	1.06	0.74	1.35	0.88	0.16	3	24	5.30E-25
Q6JBY9-1	CapZ-interacting protein	CAPZIP	0.77	0.77	1.11	0.90	0.88	0.20	10	31	5.86E-115
P82675-1	28S ribosomal protein S5, mitochondrial	MRPS5	0.80	0.97			0.89	0.12	3	8.6	7.13E-20
O60888-2	Acetylcholinesterase-associated protein	ACHAP	1.03		0.74	1.35	0.89	0.21	3	30	1.31E-39
O75592-1	Myc-binding protein 2	KIAA0916	0.69		1.08	0.93	0.89	0.28	2	0.6	3.47E-17
P17706-1	T-cell protein-tyrosine phosphatase	PTPN2		1.09	0.68	1.47	0.89	0.29	2	7.5	2.37E-04
Q9NRX2	39S ribosomal protein L17, mitochondrial	LIP2	0.58		1.19	0.84	0.89	0.43	4	30	3.65E-27
Q9BPX3	Chromosome-associated protein G	CAPG	0.95	0.87	0.84	1.19	0.89	0.06	16	21	8.15E-198
Q7Z4Q2-1	HEAT repeat-containing protein 3	HEATR3	0.90	0.89	0.87	1.15	0.89	0.02	3	4	5.37E-05
B7Z4C8	cDNA FLJ57527, highly similar to 60S ribosomal protein L31	RPL31	0.88	0.91	0.87	1.15	0.89	0.02	5	33	1.97E-48
Q96H20-1	ELL-associated protein of 30 kDa	EAP30	0.86	0.90	0.90	1.11	0.89	0.02	5	26	9.27E-52
Q13148	TAR DNA-binding protein 43	TARDBP	0.89	0.91	0.86	1.16	0.89	0.03	13	45	0.00E+00
Q3KQU3-1	Arginine/proline-rich coiled-coil domain-containing protein 1	KIAA1187	0.88	0.85	0.93	1.08	0.89	0.04	19	24	6.16E-113
Q9HC36	RNA methyltransferase-like protein 1	HC90	0.90	0.84	0.92	1.09	0.89	0.04	5	17	3.01E-13
P49005	DNA polymerase delta subunit 2	POLD2	0.91	0.81	0.94	1.06	0.89	0.07	6	14	1.41E-70
P49916-1	DNA ligase 3	LIG3	0.83	0.86	0.97	1.03	0.89	0.07	13	19	4.07E-126
Q9UKX7	50 kDa nucleoporin	NPAP60L	0.80	0.93	0.93	1.08	0.89	0.08	14	39	1.53E-186
P53582	Methionine aminopeptidase 1	KIAA0094	0.82	0.86	0.98	1.02	0.89	0.08	9	38	2.38E-96

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B4DEE8	cDNA FLJ56323, highly similar to Methylated-DNA--protein-cysteinemethyltransferase (EC 2.1.1.63)	MGMT	0.80	0.89	0.97	1.03	0.89	0.09	6	35	3.70E-129
Q96QF2	Ovarian/Breast septin epsilon	Ov/Br septin	0.82	0.85	0.99	1.01	0.89	0.09	24	43	5.29E-153
Q8TDX7	Never in mitosis A-related kinase 7	NEK7	0.86	0.81	0.99	1.01	0.89	0.09	8	33	4.42E-37
P20290-1	RNA polymerase B transcription factor 3	BTF3	0.95	0.97	0.74	1.35	0.89	0.13	14	75	5.78E-162
A7YIJ8	Radixin isoform b	hCG_39182	0.82	0.80	1.04	0.96	0.89	0.13	20	29	3.56E-111
Q8IXH7-1	Negative elongation factor C/D	HSPC130	1.02	0.89	0.75	1.33	0.89	0.14	4	8.3	1.19E-17
A0PJ72	ABCF1 protein	ABCF1	0.74	0.89	1.03	0.97	0.89	0.15	5	11	3.27E-244
O95551-2	5-tyrosyl-DNA phosphodiesterase	AD-022	0.94	1.00	0.72	1.39	0.89	0.15	5	15	8.67E-15
Q13451	51 kDa FK506-binding protein	AIG6	0.80	0.79	1.07	0.93	0.89	0.16	5	13	2.36E-29
P63172	Dynein light chain Tctex-type 1	DYNLT1	1.08	0.79	0.79	1.27	0.89	0.17	2	25	1.37E-69
P22681	Casitas B-lineage lymphoma proto-oncogene	CBL	0.79	0.78	1.09	0.92	0.89	0.18	10	14	4.13E-32
P48449	2,3-epoxysqualene--lanosterol cyclase	LSS	1.03	0.95	0.68	1.47	0.89	0.18	6	9.4	3.94E-37
O60496	Docking protein 2	DOK2	0.71	0.81	1.14	0.88	0.89	0.23	5	14	1.17E-43
Q9Y4Z0	Glycine-rich protein	LSM4	1.04	1.08	0.54	1.85	0.89	0.30	4	19	9.62E-12
O75380	Complex I-13kD-A	NDUFS6	0.68	0.68	1.30	0.77	0.89	0.36	3	35	5.37E-06
P16989-1	Cold shock domain-containing protein A	CSDA	1.10	1.13	0.43	2.33	0.89	0.40	13	50	5.55E-223
P16150	Galactoglycoprotein	CD43	0.55	0.78	1.33	0.75	0.89	0.40	2	4.5	5.28E-04
Q9Y294	Anti-silencing function protein 1 homolog A	ASF1A	1.24	1.24	0.18	5.56	0.89	0.61	6	48	2.49E-44
B2REA7	Ribosomal protein L36a	RP1-164F3.1-004		0.96	0.82	1.22	0.89	0.10	6	37	1.57E-16
P25398	40S ribosomal protein S12	RPS12	0.91	0.90	0.86	1.16	0.89	0.03	9	61	5.12E-83
B7Z3A4	cDNA FLJ56906, highly similar to RNA-binding protein 16	CCAP7	0.87		0.91	1.10	0.89	0.03	6	7.2	1.28E-32
P11940-1	Polyadenylate-binding protein 1	PAB1	0.90	0.92	0.85	1.18	0.89	0.04	31	46	0.00E+00
Q8NFH3	Nucleoporin Nup43	NUP43	0.86		0.92	1.09	0.89	0.04	3	14	1.81E-23

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Q9NUQ9	Protein FAM49B	BM-009	0.88	0.85	0.94	1.06	0.89	0.05	12	50	2.41E-210
Q6IBW4-4	Chromosome-associated protein H2	CAPH2	0.93		0.85	1.18	0.89	0.06	3	9.1	2.61E-22
O75348	Vacuolar proton pump subunit G 1	ATP6G	0.93	0.85			0.89	0.06	3	36	3.97E-106
P35219	Carbonic anhydrase VIII	CA8	0.93	0.85			0.89	0.06	3	19	5.61E-17
B7Z1E5	cDNA FLJ58752, highly similar to Homo sapiens RCD1 required for cell differentiation 1 homolog (RQCD1), mRNA	RCD1	0.89	0.82	0.96	1.04	0.89	0.07	2	8.8	6.21E-25
Q9H6T3-1	RNA polymerase II-associated protein 3	RPAP3	0.97	0.87	0.83	1.20	0.89	0.07	7	13	5.96E-116
P48729-2	Casein kinase I isoform alpha	CSNK1A1	0.94	0.95	0.78	1.28	0.89	0.10	3	11	1.49E-126
P23258	Gamma-1-tubulin	TUBG	0.93	0.78	0.96	1.04	0.89	0.10	10	35	3.50E-101
Q15276-1	Rab GTPase-binding effector protein 1	RAB5EP		0.97	0.81	1.23	0.89	0.11	5	6.7	5.56E-55
O75821	eIF3 p42	EIF3G	0.95	0.97	0.75	1.33	0.89	0.12	11	33	7.22E-96
Q8WTT2	Factor for adipocyte differentiation 24	AD24	0.99	0.94	0.74	1.35	0.89	0.13	9	14	3.03E-119
C9JXC1	Putative uncharacterized protein RRM2	RRM2	0.97	0.98	0.72	1.39	0.89	0.15	11	35	1.10E-188
Q14738-1	PP2A B subunit isoform B56-delta	PPP2R5D	0.84	0.77	1.06	0.94	0.89	0.15	8	18	1.51E-187
Q496C9	D-tyrosyl-tRNA(Tyr) deacylase	DTD1	1.00		0.78	1.28	0.89	0.16	2	7.7	6.40E-76
Q13620-2	Cullin-4B	CUL4B	0.71	0.93	1.03	0.97	0.89	0.16	11	13	3.58E-84
A8K1V0	cDNA FLJ77529, highly similar to Homo sapiens R3H domain containing 1 (R3HDM1), mRNA	KIAA0029	0.67	1.01	0.99	1.01	0.89	0.19	2	2.4	9.74E-20
P51114-1	Fragile X mental retardation syndrome-related protein 1	FXR1	1.05	0.96	0.66	1.52	0.89	0.20	9	25	2.36E-94
Q9BVI4	NOC4-like protein	NOC4L	1.04		0.74	1.35	0.89	0.21	7	23	3.14E-83
P08397-1	Hydroxymethylbilane synthase	HMBS	1.05		0.73	1.37	0.89	0.23	5	22	6.63E-193
B4DGM9	cDNA FLJ56343, highly similar to Torsin A	hCG_30595	0.72		1.06	0.94	0.89	0.24	3	10	3.40E-09
A8MW61	Putative uncharacterized protein PLRG1	PLRG1	1.06		0.72	1.39	0.89	0.24	4	15	2.06E-10
O60271	Cancer/testis antigen 89	HLC6	0.56	0.94	1.17	0.85	0.89	0.31	9	9.9	1.71E-72

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-1											
P67936-1	TM30p1	TPM4	0.49	0.54	1.64	0.61	0.89	0.65	25	67	2.43E-245
P06280	Alpha-D-galactosidase A	GLA			0.89	1.12	0.89		2	4.4	1.35E-22
Q13371	Phosducin-like protein	PDCL			0.89	1.12	0.89		2	8.3	3.64E-15
Q8BMH2	Putative uncharacterized protein RNPEP	RNPEP			0.89	1.12	0.89		3	8.2	5.12E-31
Q9BSC4	Nucleolar protein 10	NOL10			0.89	1.12	0.89		5	10	4.08E-08
P56282	DNA polymerase epsilon subunit 2	DPE2	0.89				0.89		2	7	6.88E-08
Q9BXK5-1	Bcl-2-like protein 13	BCL2L13	0.89				0.89		2	5.2	1.83E-16
Q96CN9	Golgi coiled-coil protein 1	GCC1		0.89			0.89		2	2.5	1.48E-03
Q5TBT2	230 kDa bullous pemphigoid antigen	BPAG1	0.89				0.89		2	0.3	1.81E-02
Q5JU85-2	IQ motif and SEC7 domain-containing protein 2	IQSEC2		0.89			0.89		2	1.1	1.63E-02
Q8N2M8-1	Splicing factor, arginine/serine-rich 16	SFRS16	0.89				0.89		3	10	1.18E-23
Q8TDH9-1	Protein Muted homolog	MUTED	0.89				0.89		3	16	7.94E-07
P0CB38	Polyadenylate-binding protein 4-like	PABPC4L		0.89			0.89		3	4.9	2.29E-16
Q02338	3-hydroxybutyrate dehydrogenase	BDH	0.89				0.89		4	14	2.47E-32
Q96FV2	Secernin-2	SCRN2	0.89				0.89		5	22	6.59E-26
P50238	Cysteine-rich heart protein	CRIP	0.89				0.89		5	52	1.50E-19
Q9BWU0	Human lung cancer oncogene 3 protein	HLC3	0.87	0.87	0.94	1.06	0.89	0.04	9	17	3.51E-52
Q92615	La ribonucleoprotein domain family member 4B	KIAA0217	0.96	0.82	0.90	1.11	0.89	0.07	5	9.3	3.43E-82
Q8WW12-1	PEST proteolytic signal-containing nuclear protein	PCNP	0.78	0.94	0.96	1.04	0.89	0.10	9	55	1.50E-67
Q15052-1	Alpha-Pix	ARHGEF6	0.88	0.79	1.01	0.99	0.89	0.11	7	13	2.19E-25
Q6FI81-1	Anamorsin	CIAPIN1	0.94	0.98	0.76	1.32	0.89	0.12	9	29	1.86E-44
P53597	Succinyl-CoA ligase [GDP-forming] subunit alpha, mitochondrial	SUCLG1	0.84	0.81	1.03	0.97	0.89	0.12	3	12	2.25E-28
Q9NYZ3	G2 and S phase-expressed protein 1	GTSE1	0.70	1.02	0.96	1.04	0.89	0.17	3	5.8	4.11E-15
Q96LR5	UbcH8	UBCH8	0.99	1.02	0.67	1.49	0.89	0.19	3	22	4.46E-82

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Q8N335	Glycerol-3-phosphate dehydrogenase 1-like protein	GPD1L	0.74	0.78	1.16	0.86	0.89	0.23	3	8.8	3.56E-20
P33176	Conventional kinesin heavy chain	KIF5B	0.72	0.80	1.16	0.86	0.89	0.23	40	50	0.00E+00
Q05D32-1	CTD small phosphatase-like protein 2	CTDSPL2	0.64	0.89	1.15	0.87	0.89	0.26	4	6.9	3.13E-61
Q92734	Protein TFG	TFG	0.84	0.91	0.93	1.08	0.89	0.05	3	11	5.89E-33
Q9GZS3	Meiotic recombination REC14 protein homolog	WDR61	0.98	0.87	0.83	1.20	0.89	0.08	8	40	1.98E-98
P63173	60S ribosomal protein L38	RPL38	0.89	0.98	0.81	1.23	0.89	0.09	6	50	2.62E-50
Q9GZT8-1	Amyotrophic lateral sclerosis 2 chromosomal region candidate gene 1 protein	ALS2CR1	0.81	0.83	1.04	0.96	0.89	0.13	6	22	2.83E-49
Q9Y2R9	28S ribosomal protein S7, mitochondrial	MRPS7	0.71	0.85	1.12	0.89	0.89	0.21	6	30	1.31E-17
P30626	22 kDa protein	SRI	1.11	0.90	0.67	1.49	0.89	0.22	7	43	1.27E-36
Q9BXW9-1	Fanconi anemia group D2 protein	FACD	1.03	1.12	0.53	1.89	0.89	0.32	6	4.9	1.87E-60
Q15417	Calponin, acidic isoform	CNN3		0.87	0.92	1.09	0.90	0.04	3	12	6.83E-24
Q14241	Elongin 110 kDa subunit	MSTP059	0.93		0.86	1.16	0.90	0.05	5	6.9	3.57E-23
Q9H2M9-1	Rab3 GTPase-activating protein 150 kDa subunit	KIAA0839	0.83	0.96			0.90	0.09	3	2.5	1.90E-10
P22670	Enhancer factor C	RFX1	1.15	0.64			0.90	0.36	2	2.9	7.69E-04
Q8N8S7-1	Protein enabled homolog	ENAH	0.60		1.19	0.84	0.90	0.42	2	4	7.67E-08
Q96C90	Phospholipase C-beta-3 neighbouring gene protein	PLCB3N	1.20		0.59	1.69	0.90	0.43	2	19	5.34E-114
Q86WR0	Coiled-coil domain-containing protein 25	CCDC25	0.89	0.91	0.89	1.12	0.90	0.01	4	20	1.96E-15
Q9HC52	Chromobox protein homolog 8	CBX8	0.91	0.85	0.93	1.08	0.90	0.04	2	5.9	7.21E-05
Q05639	Elongation factor 1-alpha 2	EEF1A2	0.84	0.92	0.93	1.08	0.90	0.05	14	32	1.68E-134
Q15648-1	Activator-recruited cofactor 205 kDa component	ARC205	0.84	0.93	0.92	1.09	0.90	0.05	4	3.2	1.04E-22
P42766	60S ribosomal protein L35	RPL35	0.92	0.95	0.82	1.22	0.90	0.07	6	30	1.26E-81
Q8WU90	DRG family-regulatory protein 1	DFRP1	0.96	0.91	0.82	1.22	0.90	0.07	7	17	3.73E-43
Q13951-2	Core-binding factor subunit beta,isoform 2	PEBP2b	0.87	0.84	0.98	1.02	0.90	0.07	7	41	4.33E-151
Q14694	Deubiquitinating	KIAA0	0.88	0.98	0.83	1.20	0.90	0.08	8	17	4.33E-52

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	enzyme 10	190									
P42704	130 kDa leucine-rich protein	LRP130	0.84	0.86	0.99	1.01	0.90	0.08	67	56	0.00E+00
Q6UX04-1	Antigen NY-CO-10	CWC27	0.99	0.86	0.84	1.19	0.90	0.08	4	14	6.62E-60
Q9UN37	Protein SKD2	VPS4	1.00	0.92	0.77	1.30	0.90	0.12	6	16	1.27E-11
P08708	40S ribosomal protein S17	RPS17	1.06	0.99	0.64	1.56	0.90	0.23	8	56	1.26E-171
Q6NYC8-1	Phostensin	HKMT1098	0.85	0.67	1.17	0.85	0.90	0.25	12	24	3.87E-45
Q6P1J9	Cell division cycle protein 73 homolog	C1orf28	0.92	0.97	0.80	1.25	0.90	0.09	14	28	1.81E-57
Q15061	WD repeat-containing protein 43	KIAA0007	0.98	0.93	0.78	1.28	0.90	0.10	6	8	4.68E-12
Q86U38	Pumilio domain-containing protein C14orf21	C14orf21	0.89	0.77	1.03	0.97	0.90	0.13	5	12	6.76E-131
P15498	Proto-oncogene vav	VAV	0.80	0.78	1.11	0.90	0.90	0.19	25	35	1.34E-246
Q9Y3D9	28S ribosomal protein S23, mitochondrial	CGI-138	0.82	0.76	1.11	0.90	0.90	0.19	8	50	6.52E-40
Q9NQY0-1	Bridging integrator 3	BIN3		0.95	0.85	1.18	0.90	0.07	2	8.7	2.65E-05
P19525	Eukaryotic translation initiation factor 2-alpha kinase 2	EIF2AK2	0.85	0.95			0.90	0.07	2	3.8	1.80E-27
Q96Q11-1	Mitochondrial tRNA nucleotidyl transferase, CCA-adding	CGI-47	0.82	0.96	0.92	1.09	0.90	0.07	3	5.8	4.99E-53
Q13185	Chromobox protein homolog 3	CBX3	0.92	0.96	0.82	1.22	0.90	0.07	14	65	0.00E+00
Q53ET0	CREB-regulated transcription coactivator 2	CRTC2		0.82	0.98	1.02	0.90	0.11	4	9.7	1.07E-04
O95817	BAG family molecular chaperone regulator 3	BAG3		0.82	0.98	1.02	0.90	0.11	6	16	1.25E-19
B3KNP2	cDNA FLJ30079 fis, clone BGGI12000544, highly similar to Snurportin-1 (RNA U transporter 1)	SNUPN		0.90	0.90	1.11	0.90	0.00	3	7.7	1.33E-06
Q92520	Protein FAM3C	FAM3C	0.90	0.90			0.90	0.00	3	18	1.66E-29
B3KS98	cDNA FLJ35809 fis, clone TESTI2006016, highly similar to Eukaryotic translation initiation factor 3 subunit 3	EIF3S3	0.88	0.89	0.93	1.08	0.90	0.03	14	48	3.00E-161
P78318	B-cell signal transduction molecule alpha 4	IBP1	0.87	0.92	0.91	1.10	0.90	0.03	6	18	1.05E-47
O00429	Dnm1p/Vps1p-like	DLP1	0.88	0.92			0.90	0.03	25	46	0.00E+00

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-3	protein										
C9JKP3	Putative uncharacterized protein YAF2	YAF2	0.83	0.92	0.95	1.05	0.90	0.06	3	23	2.00E-35
Q9BWF3-1	Lark homolog	RBM4	0.86	0.85	0.99	1.01	0.90	0.08	18	60	1.19E-163
Q9BQ39	ATP-dependent RNA helicase DDX50	DDX50	0.86	0.84	1.00	1.00	0.90	0.09	14	22	2.11E-81
P48147	Post-proline cleaving enzyme	PEP	0.83	0.87	1.00	1.00	0.90	0.09	11	22	1.34E-175
P18887	DNA repair protein XRCC1	XRCC1	0.82	0.87	1.01	0.99	0.90	0.10	11	22	8.53E-49
Q9BWD1	Acetyl-CoA acetyltransferase, cytosolic	ACAT2	0.92	0.79	0.99	1.01	0.90	0.10	13	47	1.75E-139
P41240	C-Src kinase	CSK	0.83	0.85	1.02	0.98	0.90	0.10	12	32	6.94E-42
Q6PJG6-1	HEAT repeat-containing protein C7orf27	C7orf27	0.98	0.95	0.77	1.30	0.90	0.11	17	26	3.36E-216
Q92888-3	115 kDa guanine nucleotide exchange factor	ARHGEF1	0.91	0.77	1.02	0.98	0.90	0.13	19	26	2.93E-104
Q92576-1	PHD finger protein 3	KIAA0244	0.99		0.81	1.23	0.90	0.13	3	2.2	3.00E-27
Q14919-2	Dr1-associated corepressor	DRAP1	0.99	0.81			0.90	0.13	3	15	1.98E-25
O75694-1	155 kDa nucleoporin	KIAA0791	1.05	0.86	0.79	1.27	0.90	0.13	11	11	2.77E-133
Q5VT52-1	Regulation of nuclear pre-mRNA domain-containing protein 2	HSPC099	0.93	1.02	0.75	1.33	0.90	0.14	13	15	4.08E-101
Q96EV2-1	Proline-rich protein 8	PRR8	0.80	0.80	1.10	0.91	0.90	0.17	4	5.5	3.80E-19
P38117-1	Electron transfer flavoprotein subunit beta	ETFB	0.79	0.80	1.11	0.90	0.90	0.18	12	48	8.69E-130
Q96A65	Exocyst complex component 4	EXOC4	0.67	0.95	1.08	0.93	0.90	0.21	7	9.8	9.43E-123
Q6PK04	Coiled-coil domain-containing protein 137	CCDC137	0.70	0.86	1.14	0.88	0.90	0.22	3	12	1.91E-04
Q01082-1	Beta-II spectrin	SPTB2	0.76	0.77	1.17	0.85	0.90	0.23	##	64	0.00E+00
Q96BN8	Protein FAM105B	FAM105B	0.67	0.89	1.14	0.88	0.90	0.24	4	11	6.84E-11
Q9BVW5	TIMELESS-interacting protein	TIPIN	0.76	1.18	0.76	1.32	0.90	0.24	2	6.6	3.18E-22
Q8TC07-1	GTPase-activating protein RAB7	TBC1D15	0.74	0.75	1.21	0.83	0.90	0.27	5	7.9	1.54E-51
O43156	Uncharacterized protein KIAA0406	KIAA0406	1.09		0.71	1.41	0.90	0.27	4	6.5	3.25E-77
C9JJ71	Putative uncharacterized	QTRTD1	1.10		0.70	1.43	0.90	0.28	3	13	3.12E-87

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	protein QTRTD1										
P09622	Dihydrolipoamide dehydrogenase	DLD	0.74	0.68	1.28	0.78	0.90	0.33	11	26	2.09E-96
O14964-1	Hepatocyte growth factor-regulated tyrosine kinase substrate	HGS	0.63	0.78	1.29	0.78	0.90	0.35	9	11	1.13E-39
P04350	Tubulin 5 beta	TUBB4	0.72	0.63	1.35	0.74	0.90	0.39	24	74	0.00E+00
Q13576-1	Ras GTPase-activating-like protein IQGAP2	IQGAP2	0.68	0.65	1.37	0.73	0.90	0.41	37	34	8.87E-230
B3KST9	cDNA FLJ36938 fis, clone BRACE2005434, highly similar to Histone RNA hairpin-binding protein	SLBP			0.90	1.11	0.90		3	12	2.93E-09
P51151	Ras-related protein Rab-9A	RAB9	0.90				0.90		2	10	3.17E-26
Q7Z3D6-2	UPF0317 protein C14orf159, mitochondrial	C14orf159	0.90				0.90		2	3.7	7.91E-04
Q86SQ4-3	Developmentally regulated G-protein-coupled receptor	DREG	0.90				0.90		2	2.6	2.22E-02
B4DGT3	Ubiquitin carboxyl-terminal hydrolase	KIAA0891	0.90				0.90		2	3.3	6.79E-38
Q9BQP7	Uncharacterized protein C20orf72	C20orf72	0.90				0.90		3	15	1.34E-09
O43427-1	Acidic fibroblast growth factor intracellular-binding protein	FIBP	0.90				0.90		3	10	2.64E-13
Q9BZE1	39S ribosomal protein L2, mitochondrial	HSPC235		0.90			0.90		3	7.6	1.09E-19
Q93008-2	Deubiquitinating enzyme FAF-X	DFFRX	0.90				0.90		3	1.6	1.29E-17
P54252-1	Ataxin-3	ATX3	0.90				0.90		4	12	5.71E-17
Q04446	1,4-alpha-glucan-branching enzyme	GBE1	0.90				0.90		5	9	4.49E-31
Q9UBW5-1	Breast cancer-associated protein 1	BIN2	0.90				0.90		6	17	8.21E-56
Q9BY43	Charged multivesicular body protein 4a	C14orf123	0.90				0.90		6	31	2.83E-54
Q8IWZ8-1	RNA-binding protein RBP	SF4	0.89	0.95	0.87	1.15	0.90	0.04	2	6.2	9.08E-33
O00273-1	DNA fragmentation factor 45 kDa subunit	DFF1	0.96	0.86	0.89	1.12	0.90	0.05	7	26	9.36E-51
B3KNW1	cDNA FLJ30560 fis, clone BRAWH2004217,	AP1G1	0.89	0.85	0.97	1.03	0.90	0.06	7	10	4.07E-50

UniProt ID	**Protein_Name**	**Gene Name**	**F1 (L/H)**	**F2 (L/H)**	**R1 (H/L)**	**R1 (L/H)**	**Mean (T/U)**	**S.D.**	**Pep. No.**	**%Seq. Cov.**	**PEP**
	highly similar to AP-1 complex subunit gamma-1										
Q5TH30	NDRG family member 3	hCG_1785125	0.83	0.93	0.95	1.05	0.90	0.06	3	11	9.66E-15
Q9BVP2-1	E2-induced gene 3 protein	E2IG3	0.83	0.99	0.89	1.12	0.90	0.08	8	19	1.19E-103
Q15027	Arf-GAP with coiled-coil, ANK repeat and PH domain-containing protein 1	ACAP1	0.97	0.95	0.79	1.27	0.90	0.10	7	16	2.85E-58
Q16181-1	CDC10 protein homolog	CDC10	0.84	0.83	1.04	0.96	0.90	0.12	17	42	2.36E-211
B4DZW0	cDNA FLJ58821, highly similar to Septin-6	KIAA0128	0.85	0.82	1.04	0.96	0.90	0.12	15	43	0.00E+00
P32969	60S ribosomal protein L9	OK/SW-cl.103	1.01	0.93	0.77	1.30	0.90	0.12	9	62	3.88E-224
P62491	Ras-related protein Rab-11A	RAB11	0.92	0.77	1.02	0.98	0.90	0.13	20	68	3.37E-128
A6NHR9-1	Structural maintenance of chromosomes flexible hinge domain-containing protein 1	KIAA0650	0.91	1.03	0.77	1.30	0.90	0.13	10	6.8	2.81E-89
A8KAG1	G patch domain-containing protein 4	GPATC4	0.87	0.77	1.07	0.93	0.90	0.15	2	6.1	9.21E-04
Q16643-2	Developmentally-regulated brain protein	D0S117E	0.97	1.02	0.72	1.39	0.90	0.16	42	59	0.00E+00
Q9C0K0-1	B-cell CLL/lymphoma 11B	BCL11B	0.81	0.80	1.10	0.91	0.90	0.17	12	19	1.01E-34
Q9GZU8	NEFA-interacting nuclear protein NIP30	C16orf94	0.97	1.10	0.64	1.56	0.90	0.24	4	20	3.98E-52
P61956	HSMT3	SMT3B	0.91	0.90			0.91	0.01	3	27	7.96E-56
O14967	Calmegin	CLGN		0.81	1.00	1.00	0.91	0.13	4	5.1	1.80E-05
O43795-1	MYH-1c	MYO1B	1.34		0.47	2.13	0.91	0.62	3	4.2	1.38E-12
Q9NV88	Integrator complex subunit 9	INTS9	1.46		0.35	2.86	0.91	0.78	3	5.5	2.94E-21
P39019	40S ribosomal protein S19	RPS19	0.94	0.94	0.84	1.19	0.91	0.06	13	64	1.10E-134
Q8NI27-1	hTREX120	CXorf3	0.84	0.96	0.92	1.09	0.91	0.06	16	14	7.05E-71
P48426	1-phosphatidylinositol-5-phosphate 4-kinase 2-alpha	PIP4K2A	0.83	0.93	0.96	1.04	0.91	0.07	3	10	1.43E-41
Q86UP2-1	CG-1 antigen	CG1	0.83	0.97	0.92	1.09	0.91	0.07	37	32	0.00E+00
P17844	DEAD box protein 5	DDX5	0.85	0.87	1.00	1.00	0.91	0.08	38	58	0.00E+00
Q0VDC6	FKBP1A protein	FKBP1A	0.83	0.88	1.01	0.99	0.91	0.09	6	31	2.77E-121
Q03164	ALL-1	ALL1	0.83	1.01	0.88	1.14	0.91	0.09	4	1.4	6.02E-11

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-1											
A8K3B4	cDNA FLJ77653	DKFZp686G04235	0.91	1.01	0.80	1.25	0.91	0.11	3	7.5	2.89E-63
B4DRT2	cDNA FLJ54536, highly similar to Mitochondrial 28S ribosomal protein S27	KIAA0264	0.85	1.03	0.84	1.19	0.91	0.11	5	15	2.08E-56
O00299	Chloride channel ABP	CLIC1	0.81	0.86	1.05	0.95	0.91	0.13	13	66	1.38E-289
Q9H1B7	Enhanced at puberty protein 1	C14orf4	0.94	0.75	1.03	0.97	0.91	0.14	7	12	3.06E-47
Q8N684-1	Cleavage and polyadenylation specificity factor 59 kDa subunit	CPSF7	0.78	0.87	1.07	0.93	0.91	0.15	7	18	1.13E-73
Q8IW35-1	Centrosomal protein of 97 kDa	CEP97	0.74	0.74	1.24	0.81	0.91	0.29	8	9.9	3.53E-67
Q16775-1	Glyoxalase II	GLO2	0.65	0.65	1.42	0.70	0.91	0.44	9	34	4.43E-44
P40937	Activator 1 36 kDa subunit	RFC5	0.89	0.93	0.90	1.11	0.91	0.02	11	40	6.18E-127
Q9UQR0-1	Sex comb on midleg-like protein 2	SCML2	0.88	0.92	0.92	1.09	0.91	0.02	4	8	3.23E-17
Q9HD26-1	CFTR-associated ligand	CAL	0.87	0.93	0.92	1.09	0.91	0.03	3	6.5	2.27E-07
O14980	Chromosome region maintenance 1 protein homolog	CRM1	0.96	0.87	0.89	1.12	0.91	0.05	21	27	3.81E-247
Q8WWY3-1	Pre-mRNA-processing factor 31	PRP31	0.96	0.91	0.85	1.18	0.91	0.06	10	23	2.90E-111
Q9NW64-1	Pre-mRNA-splicing factor RBM22	199G4	0.85	1.02	0.85	1.18	0.91	0.10	3	4.3	1.74E-08
Q68D10-1	Protein KU002155	SPTY2D1	0.84	1.03	0.85	1.18	0.91	0.11	4	6.3	6.89E-06
Q7Z460-1	CLIP-associating protein 1	CLASP1	0.80	0.84	1.08	0.93	0.91	0.15	11	12	2.16E-139
Q92665	28S ribosomal protein S31, mitochondrial	IMOGN38	0.89	0.75	1.08	0.93	0.91	0.17	10	33	2.68E-86
P30622-3	CAP-Gly domain-containing linker protein 1	CLIP1	0.71	0.86	1.16	0.86	0.91	0.23	8	6.3	1.38E-117
P21283	Vacuolar proton pump subunit C 1	ATP6C		0.98	0.84	1.19	0.91	0.10	5	12	6.60E-08
Q9UPS6	Histone-lysine N-methyltransferase SETD1B	KIAA1076		0.82	1.00	1.00	0.91	0.13	2	2.7	1.47E-05
P14854	Cytochrome c oxidase subunit 6B1	COX6B	0.67		1.15	0.87	0.91	0.34	4	48	3.33E-45
Q9UKZ1	UPF0760 protein C2orf29	C2orf29		0.91	0.91	1.10	0.91	0.00	3	11	1.35E-14
Q6PJG2	Uncharacterized protein C14orf43	C14orf117	0.90	0.92			0.91	0.01	2	2.6	6.12E-15

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Q9Y4W6	AFG3-like protein 2	AFG3L2	0.94	0.89	0.90	1.11	0.91	0.03	9	12	6.87E-21
P62753	40S ribosomal protein S6	OK/SW-cl.2	0.89	0.94	0.90	1.11	0.91	0.03	15	42	1.00E-206
Q15056-1	Eukaryotic translation initiation factor 4H	EIF4H	0.94	0.89	0.90	1.11	0.91	0.03	20	66	9.89E-248
Q32Q10	RSU1 protein	RSU1		0.89	0.93	1.08	0.91	0.03	10	49	7.31E-157
A2ICT2	Heat shock 70 kDa protein 4-like protein	hCG_37382	0.95	0.92	0.86	1.16	0.91	0.05	17	26	2.10E-173
Q9UNN5-1	FAS-associated factor 1	CGI-03	0.86	0.95	0.92	1.09	0.91	0.05	8	13	2.97E-16
P37198	62 kDa nucleoporin	NUP62	0.96	0.87	0.90	1.11	0.91	0.05	5	15	8.72E-22
P05556-1	Fibronectin receptor subunit beta	FNRB	0.88	0.97	0.88	1.14	0.91	0.05	7	11	5.35E-38
P46781	40S ribosomal protein S9	RPS9	0.89	0.97	0.87	1.15	0.91	0.05	16	52	6.30E-102
P04075	Fructose-bisphosphate aldolase A	ALDA	0.89	0.86	0.98	1.02	0.91	0.06	33	79	0.00E+00
B1ALS2	Protein tyrosine phosphatase, receptor type, C	hCG_1811178	0.87	0.86	1.00	1.00	0.91	0.08	40	39	8.95E-193
O75947-1	ATP synthase subunit d, mitochondrial	ATP5H	0.98	0.81	0.94	1.06	0.91	0.09	12	74	6.22E-127
B4E0Y9	cDNA FLJ54528, highly similar to Serine/threonine-protein kinase MST4 (EC 2.7.11.1)	MASK	0.82	0.90	1.01	0.99	0.91	0.10	9	29	7.78E-123
B4DQJ1	cDNA FLJ56825, highly similar to WD repeat protein 57	SNRNP40	1.03	0.84	0.86	1.16	0.91	0.10	11	27	9.53E-35
Q00341	High density lipoprotein-binding protein	HDLBP	0.95	1.02	0.76	1.32	0.91	0.13	20	20	8.32E-175
A0AVT1-1	Monocyte protein 4	MOP4	0.81	0.84	1.08	0.93	0.91	0.15	13	17	2.08E-33
O14672	CDw156	ADAM10		0.77	1.05	0.95	0.91	0.20	3	4.1	2.56E-11
Q01804-1	HIV-1-induced protein HIN-1	HIN1		1.05	0.77	1.30	0.91	0.20	3	3.2	4.71E-14
P51970	Complex I-19kD	NDUFA8	0.91	1.13	0.69	1.45	0.91	0.22	6	48	2.70E-62
Q13907-2	Isopentenyl pyrophosphate isomerase 1	IDI1	1.11	0.95	0.67	1.49	0.91	0.22	5	26	2.17E-57
Q9NX24	H/ACA ribonucleoprotein complex subunit 2	HSPC286	1.09		0.73	1.37	0.91	0.25	3	25	2.99E-102
P14324	Dimethylallyltranstransferase	FDPS	0.78	0.74	1.21	0.83	0.91	0.26	7	20	4.06E-28
Q8TDZ2-1	Molecule interacting with CasL protein 1	MICAL	0.75	0.76	1.22	0.82	0.91	0.27	11	13	5.47E-92
Q9H2U	DEAH box protein 36	DDX36	1.22	0.75	0.76	1.32	0.91	0.27	7	11	2.97E-59

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1-1											
O43237	Cytoplasmic dynein 1 light intermediate chain 2	DNCLI2	0.97	1.15	0.61	1.64	0.91	0.27	3	6.9	1.67E-13
C4AMC7	Protein FAM39DP	FAM39DP			0.91	1.10	0.91		2	6.7	1.86E-04
Q9GZT9-1	Egl nine homolog 1	C1orf12	0.91				0.91		2	9.6	3.09E-07
Q14997-1	Proteasome activator complex subunit 4	KIAA0077		0.91			0.91		2	1.4	2.96E-02
Q9NX76	Chemokine-like factor superfamily member 6	CKLFSF6	0.91				0.91		2	9.3	2.06E-03
Q96FS4	GTPase-activating protein Spa-1	SIPA1	0.91				0.91		2	1.2	7.48E-07
Q96JB2-1	Component of oligomeric Golgi complex 3	COG3	0.91				0.91		2	4	6.24E-11
Q8IW45-2	Carbohydrate kinase domain-containing protein	CARKD	0.91				0.91		2	9.2	7.32E-27
C9K0J5	Putative uncharacterized protein RAPH1	hCG_2043066		0.91			0.91		2	1.2	2.67E-02
Q5VWQ0-1	Round spermatid basic protein 1	RSBN1		0.91			0.91		3	5.2	7.10E-14
Q96BJ3-1	Axin interaction partner and dorsalization antagonist	AIDA	0.91				0.91		3	10	2.88E-07
P30414	Natural-killer cells cyclophilin-related protein	NKTR	0.91				0.91		5	5.3	2.13E-12
Q9BSL1	E3 ubiquitin-protein ligase subunit KPC2	GBDR1	0.91				0.91		5	14	8.49E-11
Q93052	LIM domain-containing preferred translocation partner in lipoma	LPP	0.91				0.91		6	18	5.53E-13
Q12996	CF-1 77 kDa subunit	CSTF3	0.81	0.91	1.01	0.99	0.91	0.10	4	7.7	4.60E-82
Q3YEC7-1	Partner of ARF	C9orf86	0.78	0.88	1.07	0.93	0.91	0.15	6	10	8.29E-58
Q15050	Ribosome biogenesis regulatory protein homolog	KIAA0112	1.07	0.96	0.70	1.43	0.91	0.19	7	24	1.67E-125
P84098	60S ribosomal protein L19	RPL19	0.88	0.93	0.93	1.08	0.91	0.03	14	41	2.57E-109
Q86U86-1	BRG1-associated factor 180	BAF180	0.87	0.92	0.95	1.05	0.91	0.04	15	10	2.16E-112
Q14152	eIF3 p167	EIF3A	0.9	0.97	0.87	1.15	0.91	0.05	70	47	0.00E+00
Q9NRY5-1	Protein FAM114A2	C5orf3	0.91	0.98	0.85	1.18	0.91	0.07	3	12	4.61E-25
Q86TB9	PAT1-like protein 1	OK/KN	0.88	0.87	0.99	1.01	0.91	0.07	4	7.8	3.03E-21

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-1		S-cl.5									
Q9UEW8	Serine/threonine-protein kinase 39	SPAK	0.85	0.90	0.99	1.01	0.91	0.07	5	12	1.39E-45
P42285	ATP-dependent helicase SKIV2L2	KIAA0052	0.99	0.90	0.85	1.18	0.91	0.07	17	19	2.42E-78
O75351	Cell migration-inducing gene 1 protein	MIG1	0.93	0.82	0.99	1.01	0.91	0.09	11	34	4.99E-27
O14579	Coatomer subunit epsilon	COPE	0.82	0.91	1.01	0.99	0.91	0.10	11	49	6.56E-160
Q9H4E7	Differentially expressed in FDCP 6 homolog	DEF6	0.82	0.89	1.03	0.97	0.91	0.11	14	27	4.76E-237
O14908	GAIP C-terminus-interacting protein	C19orf3	0.90	1.03	0.81	1.23	0.91	0.11	6	22	9.41E-37
Q8TF05-1	Serine/threonine-protein phosphatase 4 regulatory subunit 1	MEG1	0.84	0.85	1.05	0.95	0.91	0.12	5	7.3	6.10E-16
P61586	Rho cDNA clone 12	ARH12	0.84	0.84	1.06	0.94	0.91	0.13	10	75	1.65E-151
Q9NP79	Dopamine-responsive gene 1 protein	C6orf55	0.95	1.04	0.75	1.33	0.91	0.15	6	26	3.78E-58
Q9NQ48	Leucine zipper transcription factor-like protein 1	LZTFL1	0.82	0.83	1.09	0.92	0.91	0.15	6	25	7.65E-66
B4DHD2	cDNA FLJ55458, highly similar to Programmed cell death 6-interacting protein	DRIP4	0.80	0.85	1.09	0.92	0.91	0.16	34	47	0.00E+00
Q9NVI1-3	Fanconi anemia group I protein	FANCI	1.08	0.93	0.73	1.37	0.91	0.18	13	13	3.51E-102
A0FGR8-2	Chr2Syt	ESYT2	0.76	0.86	1.12	0.89	0.91	0.19	12	18	2.35E-80
Q9ULX3	Phosphorylation regulatory protein HP-10	ART4	0.87	1.12	0.75	1.33	0.91	0.19	4	9.5	4.92E-29
Q9UDY2-1	Tight junction protein 2	TJP2	0.69	0.99	1.06	0.94	0.91	0.20	6	8.7	3.04E-44
P04632	Calcium-activated neutral proteinase small subunit	CAPN4	0.85	0.73	1.16	0.86	0.91	0.22	8	59	2.77E-250
C9JI70	Putative uncharacterized protein RIF1	RIF1	1.04	1.08	0.62	1.61	0.91	0.25	18	11	6.17E-159
Q32MZ4-2	GC-binding factor 2	GCF2	0.7	0.76	1.28	0.78	0.91	0.32	21	34	0.00E+00
Q9HA77	Cysteine--tRNA ligase	CARS2	1.15	1.05	0.54	1.85	0.91	0.33	3	7.1	4.36E-20
Q9BYD2	39S ribosomal protein L9, mitochondrial	MRPL9	0.77	0.68	1.29	0.78	0.91	0.33	5	22	1.41E-68
P16219	Butyryl-CoA dehydrogenase	ACADS	0.60	0.79	1.35	0.74	0.91	0.39	3	8	1.31E-71
Q96RU	Formin-binding	FBP17	0.65	0.68	1.41	0.71	0.91	0.43	10	17	4.19E-64

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3-1	protein 1										
Q9Y3C1	HBV pre-S2 trans-regulated protein 3	CGI-117	1.14		0.69	1.45	0.92	0.32	7	39	3.02E-79
A8MVT9	3-ketoacyl-CoA thiolase, mitochondrial	ACAA2	0.98	0.85			0.92	0.09	2	9.8	6.38E-36
Q9NUI1-1	2,4-dienoyl-CoA reductase 2	DECR2	1.01	0.82			0.92	0.13	3	12	2.99E-18
Q9UFW8	20 kDa CGG-binding protein	CGGBP	0.76	1.07			0.92	0.22	6	42	7.24E-18
Q14CX7-1	Mitochondrial distribution and morphology protein 20	C12orf30	1.17		0.66	1.52	0.92	0.36	5	8.1	1.83E-22
A6NGG4	Putative uncharacterized protein RPS6KA1	RPS6KA1		0.63	1.20	0.83	0.92	0.40	3	7	1.28E-21
P61247	40S ribosomal protein S3a	FTE1	0.93	0.93	0.89	1.12	0.92	0.02	19	62	0.00E+00
Q9H4A3-1	Erythrocyte 65 kDa protein	KDP	0.89	0.92	0.94	1.06	0.92	0.03	8	4	1.47E-50
Q9Y224	UPF0568 protein C14orf166	C14orf166	0.90	0.96	0.89	1.12	0.92	0.04	15	65	0.00E+00
Q96RR5	Hepatocellular carcinoma-associated antigen 90	HCA90	0.93	0.97	0.85	1.18	0.92	0.06	16	25	5.37E-114
Q8IUR0	Trafficking protein particle complex subunit 5	TRAPPC5	0.95	0.98	0.82	1.22	0.92	0.09	5	36	4.54E-92
Q9NPD3	Exosome complex exonuclease RRP41	EXOSC4	0.91	0.83	1.01	0.99	0.92	0.09	5	21	8.17E-38
P55210-3	Apoptotic protease Mch-3	CASP7	0.82	0.92	1.01	0.99	0.92	0.10	4	16	8.15E-54
P49792	358 kDa nucleoporin	NUP358	0.94	1.00	0.81	1.23	0.92	0.10	46	21	0.00E+00
O75368	SH3 domain-binding glutamic acid-rich-like protein	SH3BGRL	0.88	0.84	1.03	0.97	0.92	0.10	7	77	4.30E-93
O75116	p164 ROCK-2	KIAA0619	0.81	0.89	1.05	0.95	0.92	0.12	12	9.1	2.08E-57
P20073-1	Annexin A7	ANX7	0.84	0.84	1.07	0.93	0.92	0.13	13	28	1.39E-145
Q9UNS2	COP9 signalosome complex subunit 3	COPS3	0.90	1.06	0.79	1.27	0.92	0.14	5	12	3.77E-26
Q96GK7	Fumarylacetoacetate hydrolase domain-containing protein 2A	CGI-105	0.84	0.81	1.10	0.91	0.92	0.16	4	16	4.01E-39
Q9Y3C8	Ubiquitin-fold modifier-conjugating enzyme 1	CGI-126	0.83	0.81	1.11	0.90	0.92	0.17	5	29	4.78E-10
P54886-1	Aldehyde dehydrogenase family 18 member A1	ALDH18A1	1.04	1.00	0.71	1.41	0.92	0.18	21	29	6.86E-146
Q96SB4-2	Serine/arginine-rich protein-specific kinase	SRPK1	1.08	0.95	0.72	1.39	0.92	0.18	6	13	1.80E-48

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	1										
B7Z6Q4	cDNA FLJ54837, highly similar to Inositol monophosphatase (EC 3.1.3.25)	IMPA	0.82	0.79	1.14	0.88	0.92	0.19	7	27	1.03E-59
Q9Y285	CML33	FARS	1.11	0.93	0.71	1.41	0.92	0.20	8	22	2.76E-154
P62861	40S ribosomal protein S30	FAU	1.01	1.07	0.67	1.49	0.92	0.22	2	8.3	5.72E-03
Q96BK5-1	Liver-related putative tumor suppressor	LPTL	1.04	1.24	0.47	2.13	0.92	0.40	3	19	5.31E-48
Q53HL1	Myosin regulatory light chain MRCL3 variant	MRLC2	0.63	0.64	1.48	0.68	0.92	0.49	7	55	1.84E-189
P20701-2	CD11 antigen-like family member A	CD11A	0.63	0.62	1.50	0.67	0.92	0.51	4	4.1	5.50E-45
P04183	Thymidine kinase, cytosolic	TK1	1.11	1.08	0.56	1.79	0.92	0.31	6	26	1.38E-75
Q7Z417	82 kDa FMRP-interacting protein	KIAA1321	0.91	0.95	0.90	1.11	0.92	0.03	10	15	4.76E-57
B4DSU8	Dnm1p/Vps1p-like protein	DNM1L	0.88		0.96	1.04	0.92	0.06	14	29	0.00E+00
B7Z2W9	Serine/threonine-protein phosphatase	PPP6	0.87		0.97	1.03	0.92	0.07	9	37	6.74E-188
O75131	Copine III	CPN3	0.97		0.87	1.15	0.92	0.07	3	7.6	6.74E-08
Q99986	Serine/threonine-protein kinase VRK1	VRK1	0.93	0.99	0.84	1.19	0.92	0.08	8	26	8.61E-112
Q96ER3	Protein SAAL1	SAAL1	0.90	1.02	0.84	1.19	0.92	0.09	7	19	3.91E-116
Q9Y5A9-1	CLL-associated antigen KW-14	HGRG8	0.85	0.84	1.07	0.93	0.92	0.13	10	16	1.10E-72
Q15274	Nicotinate-nucleotide pyrophosphorylase [carboxylating]	QPRT	0.97	1.02	0.77	1.30	0.92	0.13	3	11	7.44E-12
Q8N108-9	Mesoderm induction early response protein 1	KIAA1610	0.93	0.78	1.05	0.95	0.92	0.14	3	5.6	1.23E-13
Q13769	Functional spliceosome-associated protein 79	C22orf19	0.78	0.87	1.11	0.90	0.92	0.17	6	11	1.57E-07
O00116	Aging-associated gene 5 protein	AAG5	0.77	0.81	1.18	0.85	0.92	0.23	13	27	1.09E-168
Q13422-1	DNA-binding protein Ikaros	IK1	0.79	0.76	1.21	0.83	0.92	0.25	9	22	4.36E-40
Q9UBE0	SUMO-activating enzyme subunit 1	AOS1	0.79	0.76	1.21	0.83	0.92	0.25	18	62	2.28E-206
Q14847-1	LIM and SH3 domain protein 1	LASP1	0.69	0.69	1.38	0.72	0.92	0.40	10	47	1.34E-79
P18564	Integrin beta-6	ITGB6		0.93	0.91	1.10	0.92	0.01	2	2.2	8.93E-03
P62269	40S ribosomal protein S18	D6S218E	0.94	0.91	0.91	1.10	0.92	0.02	10	45	1.23E-55
Q08J23	NOL1/NOP2/Sun domain family	NSUN2	0.95	0.92	0.89	1.12	0.92	0.03	31	49	5.41E-214

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	member 2										
Q9BYN8	28S ribosomal protein S13, mitochondrial	C20orf193	0.98	0.91	0.87	1.15	0.92	0.06	6	32	4.70E-73
Q9H6F5	Coiled-coil domain-containing protein 86	CCDC86	0.79	1.06	0.91	1.10	0.92	0.14	5	18	1.30E-11
P53041	Serine/threonine-protein phosphatase 5	PPP5	0.88	0.80	1.08	0.93	0.92	0.14	6	15	5.79E-99
Q9UPU5	Deubiquitinating enzyme 24	KIAA1057	0.84	0.80	1.12	0.89	0.92	0.17	7	3.6	2.41E-29
Q6FHU2	Similar to Phosphoglycerate mutase 1	PGAM1	1.05		0.79	1.27	0.92	0.18	5	24	9.37E-74
B0I1S2	MYH14 variant protein	FP17425	0.76		1.08	0.93	0.92	0.23	10	4.1	4.36E-66
Q9H2K0	Translation initiation factor IF-3, mitochondrial	DC38	0.73		1.11	0.90	0.92	0.27	2	6.5	3.74E-04
P43146	Immunoglobulin superfamily DCC subclass member 2	IGDCC2			0.92	1.09	0.92		2	2.3	4.33E-14
Q9H6W3	Lysine-specific demethylase NO66	C14orf169	0.92				0.92		2	4.8	1.18E-14
O00308	Atrophin-1-interacting protein 2	WWP2		0.92			0.92		2	2.9	2.43E-05
Q15031	Leucine--tRNA ligase	KIAA0028		0.92			0.92		2	2.1	6.00E-03
Q9BUT9-1	Protein FAM195A	C16orf14	0.92				0.92		2	19	1.30E-26
Q8TBM8-1	DnaJ homolog subfamily B member 14	DNAJB14		0.92			0.92		2	6.3	2.25E-04
Q5U5X0	LYR motif-containing protein 7	C5orf31	0.92				0.92		2	32	3.74E-06
Q7Z6B0-1	Coiled-coil domain-containing protein 91	CCDC91	0.92				0.92		2	3.4	1.62E-02
Q8N0X4-1	Citrate lyase subunit beta-like protein, mitochondrial	CLB	0.92				0.92		2	9.1	5.12E-05
Q1ED39	Protein C16orf88	C16orf88		0.92			0.92		2	5	7.97E-06
C9JB44	60S ribosomal protein L39	RPL39	0.92				0.92		2	12	1.17E-03
C9JLW8	Protein FAM195B	FAM195B	0.92				0.92		2	30	2.74E-05
Q9P0J0	Cell death regulatory protein GRIM-19	CDA016	0.92				0.92		2	12	3.96E-07
Q8N5L8	Alba-like protein C9orf23	C9orf23	0.92				0.92		3	25	8.64E-20
O00159-1	Myosin I beta	MYO1C	0.92				0.92		3	4.5	3.91E-32
P51648-2	Aldehyde dehydrogenase 10	ALDH10		0.92			0.92		4	8.9	3.26E-14

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Q9HBH5	Alcohol dehydrogenase PAN2	PAN2	0.92				0.92		5	19	4.18E-41
Q9NZ32	Actin-related protein 10	ACTR10	0.92				0.92		6	17	2.74E-24
O75391	Sperm-associated antigen 7	SPAG7	0.86	0.96	0.95	1.05	0.92	0.06	5	23	2.81E-49
P56182	Novel nuclear protein 1	D21S2056E	0.98	1.07	0.72	1.39	0.92	0.18	6	14	3.29E-68
Q8WYJ6-1	LARP	LARP	0.93	0.92	0.92	1.09	0.92	0.01	14	44	1.80E-145
Q05086-1	E6AP ubiquitin-protein ligase	E6AP	0.89	0.96	0.92	1.09	0.92	0.04	7	12	4.21E-76
A8MV58	Putative uncharacterized protein DBN1	DBN1	0.94	0.96	0.87	1.15	0.92	0.05	18	31	1.39E-146
Q16512-2	Protease-activated kinase 1	PKN1	0.95	0.86	0.96	1.04	0.92	0.06	14	22	2.39E-89
P11717	300 kDa mannose 6-phosphate receptor	IGF2R	0.97	0.95	0.85	1.18	0.92	0.06	33	17	2.31E-116
Q9BZZ5-2	Antiapoptosis clone 11 protein	API5	0.85	0.9	1.02	0.98	0.92	0.09	13	23	6.71E-93
Q5HYG7	Putative uncharacterized protein DKFZp686M24262	DKFZp686M24262	0.91	0.83	1.03	0.97	0.92	0.10	11	27	5.71E-150
Q9BW27	85 kDa nucleoporin	NUP75	1.04	0.92	0.81	1.23	0.92	0.12	3	7.5	8.89E-67
Q96H79-1	Zinc finger CCCH-type antiviral protein 1-like	C7orf39	1.04	0.92	0.81	1.23	0.92	0.12	9	55	1.84E-26
P18031	Protein-tyrosine phosphatase 1B	PTP1B	0.86	0.85	1.06	0.94	0.92	0.12	7	19	9.33E-58
Q9HD42-1	Charged multivesicular body protein 1a	CHMP1	0.83	0.88	1.06	0.94	0.92	0.12	5	22	1.10E-06
Q9NTI5-1	Androgen-induced proliferation inhibitor	APRIN	0.84	0.86	1.07	0.93	0.92	0.13	23	18	4.29E-130
Q9NZN5-1	Leukemia-associated RhoGEF	ARHGEF12	1.00	1.00	0.77	1.30	0.92	0.13	3	3	1.59E-07
P62750	60S ribosomal protein L23a	RPL23A	0.94	1.05	0.78	1.28	0.92	0.14	11	52	1.30E-51
P35080-1	Profilin II	PFN2	0.83	0.86	1.08	0.93	0.92	0.14	3	26	3.02E-28
Q9BUQ8	100 kDa U5 snRNP-specific protein	DDX23	0.81	0.88	1.08	0.93	0.92	0.14	17	23	3.81E-60
O75083-1	Actin-interacting protein 1	WDR1	0.86	0.81	1.10	0.91	0.92	0.16	25	56	7.82E-147
Q9HDC9-1	Adipocyte plasma membrane-associated protein	APMAP	0.82	0.83	1.12	0.89	0.92	0.17	10	33	4.59E-50
P82933	28S ribosomal protein S9, mitochondrial	MRPS9	0.80	0.80	1.17	0.85	0.92	0.21	5	14	2.82E-16

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Q59F66	DEAD box polypeptide 17 isoform p82 variant	DDX17	0.79	0.79	1.19	0.84	0.92	0.23	32	49	1.95E-272
Q92625	Ankyrin repeat and SAM domain-containing protein 1A	ANKS1	1.19	0.79	0.79	1.27	0.92	0.23	3	4.4	3.90E-10
Q9UL15-2	BAG family molecular chaperone regulator 5	BAG5	1.15	1.14	0.48	2.08	0.92	0.38	4	13	8.83E-102
O75475-1	CLL-associated antigen KW-7	DFS70	0.66	0.71	1.40	0.71	0.92	0.41	19	38	9.63E-208
Q92619	Minor histocompatibility antigen HA-1	HMHA1	0.67	0.63	1.47	0.68	0.92	0.47	21	25	2.47E-191
Q53F19-1	Protein ELG	C17orf85	0.89	0.81	1.07	0.93	0.92	0.13	6	9.7	1.39E-13
Q9Y376	Calcium-binding protein 39	CAB39	0.81	0.89	1.07	0.93	0.92	0.13	7	16	3.05E-52
O75531	Barrier-to-autointegration factor	BAF	1.07	0.90	0.80	1.25	0.92	0.14	5	57	9.10E-30
P42224-1	Signal transducer and activator of transcription 1-alpha/beta	STAT1	0.86	1.11	0.80	1.25	0.92	0.16	4	7.1	6.58E-56
P20645	46 kDa mannose 6-phosphate receptor	M6PR	0.91		0.94	1.06	0.93	0.02	4	18	6.16E-30
Q9NQ50	39S ribosomal protein L40, mitochondrial	MRPL40	0.90		0.95	1.05	0.93	0.04	2	17	9.83E-29
Q8N9B5-1	Junction-mediating and -regulatory protein	JMY		0.95	0.90	1.11	0.93	0.04	2	3.4	1.82E-19
Q9Y5Y2	Cytosolic Fe-S cluster assembly factor NUBP2	NUBP2	1.03		0.82	1.22	0.93	0.15	6	38	4.59E-75
Q5HYI8	Rab-like protein 3	RABL3	1.03	0.82			0.93	0.15	3	14	1.22E-14
B4E1N4	cDNA FLJ61695, highly similar to Glioma tumor suppressor candidate region gene 2 protein	GLTSCR2	1.09		0.76	1.32	0.93	0.23	4	9.6	3.93E-58
Q96I59	Asparagine--tRNA ligase	NARS2	0.75		1.10	0.91	0.93	0.25	3	6.3	2.61E-07
Q9NT62-1	Autophagy-related protein 3	APG3	0.94	0.96	0.88	1.14	0.93	0.04	6	22	2.58E-43
B3KPG9	Calumenin, isoform CRA_c	CALU	0.87	0.99	0.92	1.09	0.93	0.06	5	26	1.25E-20
Q7Z434-1	CARD adapter inducing interferon beta	IPS1	0.73	0.82	1.23	0.81	0.93	0.27	2	8.1	3.31E-45
Q9P031	Coiled-coil domain-containing protein 59	BR22	0.73	1.32	0.73	1.37	0.93	0.34	2	7.1	1.87E-10
A6NDZ0	33 kDa VAMP-associated protein	VAP33	0.90	0.92	0.96	1.04	0.93	0.03	11	37	1.48E-66
O95347-1	Chromosome-associated protein E	CAPE	0.90	0.90	0.98	1.02	0.93	0.05	40	36	4.94E-265

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A8CGI3	Nucleosome assembly protein 1-like 4	NAP1L4	0.89	0.90	0.99	1.01	0.93	0.06	12	36	7.07E-122
Q02880-1	DNA topoisomerase 2-beta	TOP2B	0.90	0.89	0.99	1.01	0.93	0.06	35	25	1.33E-292
O43290	SNU66 homolog	SART1	0.88	0.91	0.99	1.01	0.93	0.06	27	41	3.19E-279
Q9BVJ6-1	Antigen NY-CO-16	SDCCAG16	0.89	1.00	0.89	1.12	0.93	0.06	14	24	7.06E-122
P61964	BMP2-induced 3-kb gene protein	BIG3	1.02	0.95	0.81	1.23	0.93	0.11	5	17	8.03E-36
Q8NFH5	35 kDa nucleoporin	MP44	0.87	1.06	0.85	1.18	0.93	0.12	6	26	2.99E-43
P08865	37 kDa laminin receptor precursor	LAMBR	1.01	0.99	0.78	1.28	0.93	0.13	14	57	2.06E-192
Q15942	Zyxin	ZYX	0.76	0.96	1.06	0.94	0.93	0.15	6	18	2.47E-33
Q9UNS1-1	Protein timeless homolog	TIM	1.00	1.03	0.75	1.33	0.93	0.15	8	8.8	2.13E-75
Q96ME7	Zinc finger protein 512	KIAA1805	0.87	0.77	1.14	0.88	0.93	0.19	3	6.7	3.13E-18
Q9P2R7-1	ATP-specific succinyl-CoA synthetase subunit beta	SUCLA2	0.70	0.80	1.28	0.78	0.93	0.31	10	21	5.33E-98
P55084	3-ketoacyl-CoA thiolase	HADHB	0.71	0.74	1.33	0.75	0.93	0.35	11	35	3.76E-36
Q9NXE4-4	Neutral sphingomyelinase 3	KIAA1418	1.40	0.80	0.58	1.72	0.93	0.42	2	3.2	2.70E-07
B0I1T2-1	Minor histocompatibility antigen HA-2	MYO1G	0.62	0.64	1.52	0.66	0.93	0.51	25	31	0.00E+00
Q9UGV2-1	Protein NDRG3	NDRG3		0.96	0.90	1.11	0.93	0.04	7	28	3.92E-171
Q6NUQ4	Transmembrane protein 214	PP446		0.86	1.00	1.00	0.93	0.10	4	6	3.56E-06
P10301	Ras-related protein R-Ras	RRAS	0.84		1.02	0.98	0.93	0.13	4	25	1.91E-12
Q04837	PWP1-interacting protein 17	SSBP	1.02		0.84	1.19	0.93	0.13	5	39	0.00E+00
Q9NVK5-1	FGFR1 oncogene partner 2	FGFR1OP2	1.04	0.82			0.93	0.16	2	11	4.42E-21
Q5HY50	Ribosomal protein L10	RPL10	0.95	0.92	0.92	1.09	0.93	0.02	12	51	3.94E-163
O95232-1	cAMP regulatory element-associated protein 1	CREAP1	0.91	0.95	0.93	1.08	0.93	0.02	10	30	5.72E-165
Q9UHY1	Nuclear receptor-binding protein	BCON3	0.91	0.92	0.96	1.04	0.93	0.03	3	7.9	8.94E-18
P46783	40S ribosomal protein S10	RPS10	0.96	0.90	0.93	1.08	0.93	0.03	8	53	4.86E-178
O14562	Ubiquitin domain-containing protein UBFD1	UBFD1	0.91	0.98	0.90	1.11	0.93	0.04	4	8.4	8.19E-20
B4DKA3	cDNA FLJ60624, highly similar to	EPS15L1	0.93	0.98	0.88	1.14	0.93	0.05	10	18	3.44E-41

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	Epidermal growth factor receptor substrate 15-like 1										
Q8NB90-1	ATPase family protein 2 homolog	AFG2	0.87	0.95	0.97	1.03	0.93	0.05	9	13	1.46E-85
Q9NWV4	Chromosome 1 open reading frame 123	C1orf123	1.00	0.90	0.89	1.12	0.93	0.06	3	35	4.52E-15
Q6NXE6	Armadillo repeat-containing protein 6	ARMC6	0.88	0.91	1.00	1.00	0.93	0.06	7	23	1.47E-81
P23528	18 kDa phosphoprotein	CFL	0.91	0.88	1.00	1.00	0.93	0.06	15	68	0.00E+00
P46782	40S ribosomal protein S5	RPS5	0.86	0.94	0.99	1.01	0.93	0.07	11	47	1.08E-238
Q9NZZ3	Charged multivesicular body protein 5	C9orf83	0.97	0.85	0.97	1.03	0.93	0.07	6	42	3.08E-16
P23588	Eukaryotic translation initiation factor 4B	EIF4B	0.97	0.97	0.85	1.18	0.93	0.07	27	40	0.00E+00
O00255-1	Menin	MEN1	1.01	0.89	0.89	1.12	0.93	0.07	3	5.9	8.45E-14
P62701	40S ribosomal protein S4, X isoform	CCG2	0.96	0.98	0.85	1.18	0.93	0.07	25	67	2.23E-289
P63244	Cell proliferation-inducing gene 21 protein	GNB2L1	0.95	1.00	0.84	1.19	0.93	0.08	21	79	0.00E+00
P31483-1	Nucleolysin TIA-1 isoform p15	TIA1	0.88	0.88	1.03	0.97	0.93	0.09	7	24	1.76E-68
Q9Y2Z4	Tyrosine--tRNA ligase	CGI-04	0.99	0.83	0.97	1.03	0.93	0.09	4	8.8	1.96E-35
Q9NPQ8-1	Protein Ric-8A	RIC8A	1	0.99	0.8	1.25	0.93	0.11	11	29	5.19E-228
Q8IU60-1	mRNA-decapping enzyme 2	DCP2	0.97	1.02	0.80	1.25	0.93	0.12	2	6	2.98E-10
O95218-1	Zinc finger protein 265	ZIS	0.84	0.88	1.07	0.93	0.93	0.12	5	15	5.02E-18
Q9H0A8-1	COMM domain-containing protein 4	COMMD4	1.03	0.98	0.78	1.28	0.93	0.13	5	37	9.47E-145
Q96DI7	38 kDa-splicing factor	PRP8BP	0.96	0.78	1.05	0.95	0.93	0.14	17	54	2.77E-117
Q9UPN7	SAPS domain family member 1	KIAA1115	1.09	0.89	0.81	1.23	0.93	0.14	12	26	1.13E-93
Q6YN16-1	Hydroxysteroid dehydrogenase-like protein 2	C9orf99	0.90	0.79	1.10	0.91	0.93	0.16	3	9.3	2.85E-16
O76094	Signal recognition particle 72 kDa protein	SRP72	0.81	0.87	1.11	0.90	0.93	0.16	22	42	0.00E+00
O43665-3	Regulator of G-protein signaling 10	RGS10	1.05		0.81	1.23	0.93	0.17	4	28	1.25E-26
Q14344	Guanine nucleotide-binding protein subunit alpha-13	GNA13	0.95	1.09	0.75	1.33	0.93	0.17	4	14	3.76E-32
Q8NEL	DDHD domain-containing protein 1	DDHD1	0.90	0.77	1.12	0.89	0.93	0.18	2	4	2.53E-02

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9-1											
A5YVE9	cDNA FLJ59461, highly similar to Pyruvate dehydrogenase E1 component alpha subunit, somatic form, mitochondrial (EC 1.2.4.1)	PDHA1	0.76	0.90	1.13	0.88	0.93	0.19	12	32	7.51E-42
P61024	Cyclin-dependent kinases regulatory subunit 1	CKS1	0.7	1.14	0.95	1.05	0.93	0.22	3	66	1.64E-05
Q9BXR0	Guanine insertion enzyme	QTRT1	1.14	0.98	0.67	1.49	0.93	0.24	3	12	8.73E-11
Q99536	Synaptic vesicle membrane protein VAT-1 homolog	VAT1	0.71	0.77	1.31	0.76	0.93	0.33	7	24	1.77E-62
O95571	Ethylmalonic encephalopathy protein 1	ETHE1	0.74	0.67	1.38	0.72	0.93	0.39	7	43	9.57E-52
P14317	Hematopoietic cell-specific LYN substrate 1	HCLS1	0.61	0.56	1.62	0.62	0.93	0.60	8	21	1.68E-54
Q9Y3S2	Nucleolar autoantigen 36	NOA36		0.93			0.93		2	7.2	2.36E-20
Q9Y221-1	60S ribosome subunit biogenesis protein NIP7 homolog	CGI-37	0.93				0.93		2	22	6.43E-10
Q6UWP2-1	Dehydrogenase/reductase SDR family member 11	DHRS11	0.93				0.93		2	8.1	6.21E-16
Q7Z6V5-1	Deaminase domain-containing protein 1	ADAT2	0.93				0.93		2	22	1.18E-07
Q9H8Y5	Ankyrin repeat and zinc finger domain-containing protein 1	ANKZF1		0.93			0.93		2	3	1.47E-02
Q5JSP0-1	FYVE, RhoGEF and PH domain-containing protein 3	FGD3		0.93			0.93		2	3.2	1.56E-04
A8K1Z3	cDNA FLJ75002, highly similar to Homo sapiens, neural cell expressed,developmentally down-regulated gene 1	NEDD1	0.93				0.93		2	5.8	7.38E-172
Q9H0P0-4	Cytosolic 5-nucleotidase 3	HSPC233		0.93			0.93		2	7.4	9.74E-23
B7Z2Z4	cDNA FLJ54352, highly similar to Propionyl-CoA carboxylase beta chain, mitochondrial (EC 6.4.1.3)	hCG_15235	0.93				0.93		2	5.6	5.31E-73

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P52657	General transcription factor IIA subunit 2	GTF2A2	0.93				0.93		3	22	4.48E-23
O75157-1	TSC22 domain family protein 2	KIAA0669	0.93				0.93		3	6.8	2.64E-05
Q5R2V8	C2orf4 protein	C2orf4	0.93				0.93		3	17	1.63E-08
Q6ULP2-1	Aftiphilin	AFTH	0.93				0.93		3	3.3	3.77E-08
Q96JM4-2	Leucine-rich repeat and IQ domain-containing protein 1	KIAA1801	0.93				0.93		3	2.2	5.60E-03
B4E040	cDNA FLJ55177, highly similar to Ras-related protein Ral-B	RALB	0.93				0.93		4	15	7.05E-15
P22090	40S ribosomal protein S4, Y isoform 1	PRO2646	0.93				0.93		9	29	1.53E-27
Q8IUI8	Cytokine receptor-like factor 3	CREME9	0.95	0.93	0.92	1.09	0.93	0.02	5	17	2.28E-24
P50213-1	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A	0.92	0.96	0.92	1.09	0.93	0.02	9	26	8.62E-53
P38606	Vacuolar ATPase isoform VA68	ATP6A1	0.92	0.90	0.98	1.02	0.93	0.04	18	35	0.00E+00
Q7L2E3-2	DEAH box protein 30	DDX30	0.97	0.95	0.88	1.14	0.93	0.05	22	21	8.23E-158
Q9BYD6	39S ribosomal protein L1, mitochondrial	BM-022	0.95	0.99	0.86	1.16	0.93	0.07	8	30	1.05E-81
Q09028	Chromatin assembly factor 1 subunit C	RBAP48	0.89	0.90	1.01	0.99	0.93	0.07	17	62	5.83E-103
C9JW58	Putative uncharacterized protein DENR	DENR	0.89	1.01	0.90	1.11	0.93	0.07	5	25	3.87E-85
B0UX85	HLA-B associated transcript 3	BAT3	0.94	1.01	0.85	1.18	0.93	0.08	13	17	4.13E-84
Q29RF7-1	Cell proliferation-inducing gene 54 protein	KIAA0648	0.95	1.02	0.83	1.20	0.93	0.10	25	27	0.00E+00
B1AKJ5	Nardilysin (N-arginine dibasic convertase)	hCG_40292	0.97	1.01	0.82	1.22	0.93	0.10	10	9.5	8.95E-58
P63010-2	Adapter-related protein complex 2 beta subunit	ADTB2	0.85	0.90	1.05	0.95	0.93	0.10	27	36	0.00E+00
Q15691	APC-binding protein EB1	MAPRE1	0.87	0.87	1.06	0.94	0.93	0.11	17	63	1.11E-295
Q99447	CTP:phosphoethanolamine cytidylyltransferase	PCYT2	1.02	0.99	0.79	1.27	0.93	0.13	2	6.7	1.03E-49
P17980	26S protease regulatory subunit 6A	PSMC3	1.01	1.01	0.78	1.28	0.93	0.13	15	47	6.98E-286
Q9UBI1	COMM domain-containing protein 3	BUP	0.90	0.81	1.09	0.92	0.93	0.14	5	30	1.53E-164
P30566-1	Adenylosuccinase	ADSL	1.09	0.97	0.74	1.35	0.93	0.18	11	28	2.09E-73

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P07311	Acylphosphatase, erythrocyte isozyme	ACYP1	0.85	0.81	1.14	0.88	0.93	0.18	5	54	4.27E-49
P30520	Adenylosuccinate synthetase isozyme 2	ADSS	1.05	1.04	0.71	1.41	0.93	0.19	11	28	5.83E-138
O60749	Sorting nexin-2	SNX2	0.79	0.85	1.16	0.86	0.93	0.20	13	32	2.31E-62
P52815	39S ribosomal protein L12, mitochondrial	MRPL12	1.12	0.70	0.98	1.02	0.93	0.21	4	11	3.50E-34
Q8WUJ0	Protein tyrosine phosphatase-like protein	STYX	1.18	0.78	0.84	1.19	0.93	0.22	2	14	7.81E-28
P23634-1	Matrix-remodeling-associated protein 1	ATP2B2	0.75	0.86	1.19	0.84	0.93	0.23	15	17	2.10E-145
Q96BW5-1	Parathion hydrolase-related protein	PTER	0.80	0.79	1.21	0.83	0.93	0.24	5	14	1.21E-13
Q96EY7-1	Pentatricopeptide repeat-containing protein 3, mitochondrial	PTCD3	0.77	0.82	1.21	0.83	0.93	0.24	2	6.1	2.74E-32
O94888	UBX domain-containing protein 7	KIAA0794	0.73	0.87	1.20	0.83	0.93	0.24	6	16	9.76E-27
Q5BKZ1-1	Zinc finger protein 326	ZNF326	0.74	0.83	1.23	0.81	0.93	0.26	9	16	1.70E-78
Q9P2W9	Cell growth-inhibiting gene 9 protein	GIG9	1.10	1.07	0.63	1.59	0.93	0.26	3	13	7.11E-43
A8MWQ4	Putative uncharacterized protein GLIPR2	GLIPR2	0.78	0.77	1.25	0.80	0.93	0.27	3	28	2.95E-68
O14617-5	Adapter-related protein complex 3 subunit delta-1	AP3D1	0.64	1.21	0.95	1.05	0.93	0.29	5	7.2	4.21E-55
Q9Y3T9	NOC2-like protein	NOC2L	0.91	1.24	0.65	1.54	0.93	0.30	5	6.5	1.62E-09
A9CQZ4	Dihydropyrimidinase-like 2 long form	DPYSL2	0.76	0.75	1.29	0.78	0.93	0.31	7	45	6.91E-34
O00425-1	IGF-II mRNA-binding protein 3	IGF2BP3	0.75	0.70	1.35	0.74	0.93	0.36	18	39	3.46E-294
P43246	DNA mismatch repair protein Msh2	MSH2	0.91	0.96	0.93	1.08	0.93	0.03	16	23	5.71E-116
O43617	BET3 homolog	BET3	1.06	1.01	0.73	1.37	0.93	0.18	4	23	4.90E-10
Q6PIZ9	pp29/30	HSPC062	0.68	1.19	0.93	1.08	0.93	0.26	2	29	1.71E-07
Q96L91-1	CAG repeat protein 32	CAGH32	1.13		0.74	1.35	0.94	0.28	8	4.2	5.40E-33
B4DQX2	cDNA FLJ55586, highly similar to MMS19-like protein	MMS19	1.16		0.71	1.41	0.94	0.32	8	14	6.05E-89
Q96FK6	WD repeat-containing protein 89	C14orf150		1.17	0.70	1.43	0.94	0.33	2	6.5	1.24E-05
Q7L5D6-1	Conserved edge-expressed protein	C7orf20		0.93	0.94	1.06	0.94	0.01	2	6.1	4.12E-09
Q8IZQ5	Selenoprotein H	C11orf31	0.92	0.95			0.94	0.02	3	25	7.38E-31

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Q9NV35	8-oxo-dGTPase NUDT15	MTH2		0.97	0.90	1.11	0.94	0.05	2	16	1.06E-08
P62273	40S ribosomal protein S29	RPS29	0.88	0.99			0.94	0.08	4	59	8.41E-05
B4DNB9	cDNA FLJ53069, highly similar to AP-2 complex subunit mu-1	AP2M1		0.85	1.02	0.98	0.94	0.12	3	5.7	2.00E-04
Q2TAA2	Isoamyl acetate-hydrolyzing esterase 1 homolog	IAH1	0.83		1.04	0.96	0.94	0.15	4	27	5.41E-27
Q14004-2	CDC2-related protein kinase 5	CDC2L		0.82	1.05	0.95	0.94	0.16	4	5	2.24E-40
Q9NV70-1	Exocyst complex component 1	BM-012		0.81	1.06	0.94	0.94	0.18	3	4.1	5.89E-08
Q9NUL3-1	Double-stranded RNA-binding protein Staufen homolog 2	STAU2		1.12	0.75	1.33	0.94	0.26	6	11	1.65E-25
Q9NRW7	Vacuolar protein sorting-associated protein 45	VPS45	0.66		1.21	0.83	0.94	0.39	2	4.2	5.46E-09
P45974-1	Deubiquitinating enzyme 5	ISOT	0.95	0.91	0.95	1.05	0.94	0.02	20	35	6.62E-169
Q5T1M5-1	133 kDa FK506-binding protein	FKBP15	0.85	0.99	0.97	1.03	0.94	0.08	7	10	1.40E-93
B4DX78	ATP-dependent RNA helicase DDX39	DDX39	0.99	1.02	0.8	1.25	0.94	0.12	15	33	5.42E-63
P50570-1	Dynamin-2	DNM2	0.76	0.85	1.20	0.83	0.94	0.23	22	32	5.32E-192
Q9H7B4-1	SET and MYND domain-containing protein 3	SMYD3	1.21	1.05	0.55	1.82	0.94	0.34	4	11	1.29E-18
P30050-1	60S ribosomal protein L12	RPL12	0.96	0.95	0.90	1.11	0.94	0.03	7	59	3.23E-160
A8K3A8	cDNA FLJ75085, highly similar to Homo sapiens glutaminyl-tRNA synthetase (QARS), mRNA	QARS	0.93	0.98	0.90	1.11	0.94	0.04	24	35	2.78E-223
Q9UNZ2-5	NSFL1 cofactor p47	NSFL1C	0.9	0.92	0.99	1.01	0.94	0.05	13	43	2.64E-273
Q9NRX1	RNA-binding protein PNO1	PNO1	0.90	1.00	0.91	1.10	0.94	0.06	5	23	4.42E-76
O95793-1	Double-stranded RNA-binding protein Staufen homolog 1	STAU	0.89	0.92	1.00	1.00	0.94	0.06	6	15	2.33E-48
Q96QK1	Maternal-embryonic 3	MEM3	0.89	0.90	1.02	0.98	0.94	0.07	20	32	0.00E+00
O15355	Protein phosphatase 1C	PPM1C	0.90	1.02	0.89	1.12	0.94	0.07	13	37	1.89E-190
P82650	28S ribosomal protein S22, mitochondrial	C3orf5	0.87	1.02	0.92	1.09	0.94	0.08	7	24	5.85E-63
Q9NTJ5	Phosphatidylinositide	KIAA0	0.90	0.88	1.03	0.97	0.94	0.08	5	9.4	5.12E-17

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	phosphatase SAC1	851									
Q8WWC4	Uncharacterized protein C2orf47, mitochondrial	C2orf47	0.85	1.02	0.94	1.06	0.94	0.09	3	11	1.32E-06
P52788-1	Spermidine aminopropyltransferase	SMS	0.86	0.92	1.03	0.97	0.94	0.09	7	33	5.14E-47
P06493-1	Cell division control protein 2 homolog	CDC2	0.98	1.01	0.82	1.22	0.94	0.10	17	66	8.49E-165
Q96PU5-8	E3 ubiquitin-protein ligase NEDD4-like	KIAA0439	0.97	1.02	0.82	1.22	0.94	0.10	4	6.2	3.73E-10
Q9NQW7-1	Aminoacylproline aminopeptidase	XPNPEP1	0.85	0.90	1.06	0.94	0.94	0.11	11	23	1.18E-111
Q9H993	UPF0364 protein C6orf211	C6orf211	0.97	0.79	1.05	0.95	0.94	0.13	4	8.2	2.91E-33
Q86WV7	CCDC43 protein	CCDC43	0.81	1.09	0.91	1.10	0.94	0.14	3	13	4.56E-17
Q13347	eIF3 p36	EIF3I	1.03	1.03	0.75	1.33	0.94	0.16	16	69	1.26E-94
A5JGZ4	Non-functional aryl hydrocarbon receptor interacting protein	AIP	0.88	0.81	1.12	0.89	0.94	0.16	15	53	2.04E-169
Q9NY94	Class A basic helix-loop-helix protein 17	SCL	0.96	1.12	0.73	1.37	0.94	0.20	4	15	6.65E-12
Q96GG9	DCN1-like protein 1	DCUN1D1	0.80	0.84	1.17	0.85	0.94	0.20	5	18	5.99E-59
Q9Y478	5-AMP-activated protein kinase subunit beta-1	AMPK	1.23	0.79	0.79	1.27	0.94	0.25	3	23	1.55E-20
P15311	Cytovillin	EZR	0.72	0.76	1.33	0.75	0.94	0.34	37	55	0.00E+00
P99999	Cytochrome c	CYC	0.93	0.95			0.94	0.01	4	32	1.30E-15
Q9Y5L0-2	Importin-12	IPO12	0.93	0.97	0.92	1.09	0.94	0.03	9	14	4.66E-100
Q9UFC0	Leucine-rich repeat and WD repeat-containing protein 1	LRWD1	0.96		0.92	1.09	0.94	0.03	4	6.4	1.68E-24
Q13131-2	5-AMP-activated protein kinase catalytic subunit alpha-1	AMPK1	0.94	0.90	0.98	1.02	0.94	0.04	4	7.7	1.93E-10
O75439	Beta-MPP	MPPB	0.90	0.94	0.98	1.02	0.94	0.04	10	24	2.71E-113
Q9H0R4-1	Haloacid dehalogenase-like hydrolase domain-containing protein 2	HDHD2	0.91		0.97	1.03	0.94	0.04	4	17	9.69E-61
Q9Y508-1	RING finger protein 114	RNF114	0.95	0.98	0.89	1.12	0.94	0.05	9	47	1.15E-55
B4DIM0	cDNA FLJ56442, highly similar to ATP-citrate synthase (EC 2.3.3.8)	ACLY	0.92	1.00	0.90	1.11	0.94	0.05	24	27	1.27E-182
P62424	60S ribosomal protein L7a	RPL7A	0.97	0.99	0.86	1.16	0.94	0.07	18	53	4.08E-218

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Q16204	Coiled-coil domain-containing protein 6	CCDC6	0.89		0.99	1.01	0.94	0.07	4	7.2	5.94E-32
P20585	Divergent upstream protein	DUC1		0.99	0.89	1.12	0.94	0.07	3	3.3	2.86E-05
P18621	60S ribosomal protein L17	RPL17	0.95	1.02	0.85	1.18	0.94	0.09	9	42	4.80E-102
Q9H2K8	Cutaneous T-cell lymphoma-associated antigen HD-CL-09	DPK	0.99	0.99	0.84	1.19	0.94	0.09	6	7.5	3.35E-14
Q9H2J4	HTPHLP	PDCL3	1.04	0.94	0.84	1.19	0.94	0.10	7	35	4.03E-66
B9EGG0	ANO6 protein	ANO6	1.00	1.00	0.82	1.22	0.94	0.10	3	4.4	1.37E-09
O15541	RING finger protein 113A	RNF113		1.02	0.86	1.16	0.94	0.11	4	15	1.30E-12
Q8NC51-1	PAI1 RNA-binding protein 1	CGI-55	0.98	1.07	0.77	1.30	0.94	0.15	25	57	0.00E+00
P53004	Biliverdin reductase A	BLVR	0.86	0.83	1.13	0.88	0.94	0.17	9	35	6.60E-93
Q969X5-1	Endoplasmic reticulum-Golgi intermediate compartment protein 1	ERGIC1		0.82	1.06	0.94	0.94	0.17	5	23	2.35E-18
Q13586	Stromal interaction molecule 1	GOK	0.73	0.96	1.13	0.88	0.94	0.20	4	7.9	7.21E-14
O94973-2	100 kDa coated vesicle protein C	ADTAB	0.96	0.73	1.13	0.88	0.94	0.20	13	22	6.58E-139
O75323	Glioblastoma-amplified sequence	GBAS	0.79	0.86	1.17	0.85	0.94	0.20	6	23	3.43E-31
Q9BWH6-1	RNA polymerase II-associated protein 1	KIAA1403	1.19		0.69	1.45	0.94	0.35	4	6.2	3.20E-33
B3KN28	cDNA FLJ13370 fis, clone PLACE1000653, highly similar to Phosphoacetylglucosamine mutase (EC 5.4.2.3)	AGM1			0.94	1.06	0.94		2	4	9.45E-05
Q9BYW2-1	HIF-1	HIF1			0.94	1.06	0.94		2	1	1.68E-04
B3KNH5	cDNA FLJ14622 fis, clone NT2RP2000147, highly similar to Adaptor-related protein complex 1 mu-1 subunit	AP1M1			0.94	1.06	0.94		2	7.1	6.74E-10
Q9P2R6-1	Arginine-glutamic acid dipeptide repeats protein	ARG	0.94				0.94		2	1.6	2.64E-02
P37235	Calcium-binding protein BDR-1	BDR1	0.94				0.94		2	11	1.89E-13
P55263-1	Adenosine 5-phosphotransferase	ADK		0.94			0.94		2	6.4	3.39E-03
Q59EV6	Carrier family 6, member 8 variant	hCG_38374		0.94			0.94		2	4.2	4.15E-28

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B4DG66	cDNA FLJ61231, highly similar to Apoptosis-stimulating of p53 protein 2	ASPP2	0.94				0.94		2	3.3	4.41E-09
Q9Y536	Chromosome 1-amplified sequence 2	COAS2	0.94				0.94		3	21	3.19E-15
Q9NZJ7-1	Mitochondrial carrier homolog 1	CGI-64		0.94			0.94		3	7.5	2.72E-03
Q9BS14	GANAB protein	GANAB		0.94			0.94		3	8.3	2.26E-07
Q9NPA8	Enhancer of yellow 2 transcription factor homolog	DC6	0.94				0.94		4	44	1.13E-33
Q7Z422-1	Putative MAPK-activating protein PM18/PM20/PM22	C1orf144	0.94				0.94		4	42	7.91E-09
O00512	B-cell CLL/lymphoma 9 protein	BCL9	0.94				0.94		5	6.1	2.50E-24
C9J2K4	Putative uncharacterized protein ATP6V1F	ATP6V1F	0.94				0.94		5	52	3.00E-40
Q15404	Ras suppressor protein 1	RSP1	0.94				0.94		7	41	3.60E-62
Q9UFY1	Putative uncharacterized protein DKFZp434N101	DKFZp434N101		0.94			0.94		8	17	3.81E-75
Q92541	RNA polymerase-associated protein RTF1 homolog	KIAA0252	0.93	0.94	0.95	1.05	0.94	0.01	9	13	9.41E-57
P62136	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit	PPP1A	0.95	0.92	0.95	1.05	0.94	0.02	19	59	0.00E+00
P55209	NAP-1-related protein	NAP1L1	0.91	0.92	0.99	1.01	0.94	0.04	9	29	7.15E-117
Q96P70	Importin-9	HSPC273	0.91	0.90	1.01	0.99	0.94	0.06	6	10	2.13E-186
Q5JVF3-4	CSN12-like protein	HT004	0.94	0.87	1.01	0.99	0.94	0.07	4	11	1.45E-67
Q12769-1	160 kDa nucleoporin	KIAA0197	0.89	1.04	0.89	1.12	0.94	0.09	6	7	2.76E-49
Q92499	ATP-dependent RNA helicase DDX1	DDX1	0.91	0.87	1.04	0.96	0.94	0.09	26	43	0.00E+00
Q9Y4X5	H7-AP2	ARI	0.84	1.05	0.93	1.08	0.94	0.11	2	5.7	1.33E-62
Q53H29	Nucleoporin 54kDa variant	NUP54	1.07	0.86	0.89	1.12	0.94	0.11	7	17	5.59E-93
Q9Y3U8	60S ribosomal protein L36	RPL36	0.97	1.05	0.80	1.25	0.94	0.13	6	36	3.14E-94
P37802	SM22-alpha homolog	CDABP0035	0.86	0.87	1.09	0.92	0.94	0.13	19	82	0.00E+00
Q8WWK9-1	CTCL tumor antigen se20-10	CKAP2	0.83	0.90	1.09	0.92	0.94	0.13	5	10	1.33E-41

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P55036-2	26S proteasome non-ATPase regulatory subunit 4	MCB1	1.08	0.95	0.79	1.27	0.94	0.15	7	20	1.26E-57
P14735	Abeta-degrading protease	IDE	1.02	1.05	0.75	1.33	0.94	0.17	11	14	1.03E-28
Q9Y6G9	Cytoplasmic dynein 1 light intermediate chain 1	DNCLI1	1.03	1.05	0.74	1.35	0.94	0.17	9	30	6.98E-187
Q10570	Cleavage and polyadenylation specificity factor 160 kDa subunit	CPSF1	0.98	1.12	0.72	1.39	0.94	0.20	10	7.1	7.74E-61
P82673-1	28S ribosomal protein S28, mitochondrial	HDCMD11P	0.86	0.74	1.22	0.82	0.94	0.25	5	21	7.76E-57
Q7Z4H7-1	HAUS augmin-like complex subunit 6	DGT6	0.79	0.80	1.23	0.81	0.94	0.25	3	4	4.05E-14
Q96KA5-1	Cisplatin resistance-related protein 9	CLPTM1L	1.12		0.76	1.32	0.94	0.25	3	5.2	5.81E-29
Q8N488	Apoptin-associating protein 1	DEDAF	0.84	0.72	1.26	0.79	0.94	0.28	2	18	2.74E-66
Q08170	Pre-mRNA-splicing factor SRP75	SFRS4	0.74	0.78	1.30	0.77	0.94	0.31	12	23	3.23E-153
Q14781-1	Chromobox protein homolog 2	CBX2	0.91	0.63	1.28	0.78	0.94	0.33	2	4.9	2.00E-10
O14974-1	Myosin phosphatase-targeting subunit 1	MBS	0.70	0.76	1.36	0.74	0.94	0.36	23	23	1.52E-264
Q9H7P9-1	Pleckstrin homology domain-containing family G member 2	PLEKHG2	0.99	1.02	0.82	1.22	0.94	0.11	3	3.2	6.84E-05
Q641Q2-1	WASH complex subunit FAM21A	FAM21A	0.88	1.13	0.82	1.22	0.94	0.16	9	11	5.94E-101
Q92917	G patch domain and KOW motifs-containing protein	GPATC5	0.93	0.95	0.95	1.05	0.94	0.01	6	22	1.24E-53
P28340	DNA polymerase delta catalytic subunit	POLD	0.93	0.93	0.97	1.03	0.94	0.02	19	26	4.30E-102
Q13547	Histone deacetylase 1	HDAC1	0.92	0.94	0.97	1.03	0.94	0.03	15	43	1.09E-115
O75489	Complex I-30kD	NDUFS3	0.98	0.97	0.88	1.14	0.94	0.06	12	52	4.33E-216
B4DJV9	cDNA FLJ60607, highly similar to Acyl-protein thioesterase 1 (EC 3.1.2.-)	APT1	0.93	1.01	0.89	1.12	0.94	0.06	6	36	2.13E-83
Q9NRX4	14 kDa phosphohistidine phosphatase	CGI-202	0.95	0.87	1.01	0.99	0.94	0.07	2	22	4.78E-15
Q92878-2	DNA repair protein RAD50	RAD50	0.86	0.98	0.99	1.01	0.94	0.07	16	13	4.92E-223
Q9Y230	48 kDa TATA box-binding protein-interacting protein	CGI-46	0.99	0.98	0.86	1.16	0.94	0.07	18	43	4.50E-171
Q9BXW7-1	Cat eye syndrome critical region protein	CECR5	1.01	0.96	0.86	1.16	0.94	0.08	10	32	2.25E-71

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	5										
Q9ULR0-1	Pre-mRNA-splicing factor ISY1 homolog	ISY1	0.86	0.94	1.03	0.97	0.94	0.09	4	17	1.06E-170
Q9P0I2-1	Transmembrane protein 111	TMEM111	0.91	1.04	0.88	1.14	0.94	0.09	2	12	2.83E-21
Q9H0C8	Integrin-linked kinase-associated serine/threonine phosphatase 2C	ILKAP	0.85	0.96	1.02	0.98	0.94	0.09	9	27	1.96E-69
Q13505-1	Metaxin-1	MTX	0.97	1.02	0.84	1.19	0.94	0.09	6	18	7.00E-44
O75431	Metaxin-2	MTX2	0.83	1.01	0.99	1.01	0.94	0.10	7	33	1.18E-102
P62879	G protein subunit beta-2	GNB2	0.91	0.86	1.06	0.94	0.94	0.10	10	41	1.29E-45
Q9Y333	Small nuclear ribonuclear protein D homolog	C6orf28	1.05	0.94	0.84	1.19	0.94	0.11	5	60	5.97E-78
P52565	Rho GDP-dissociation inhibitor 1	ARHGDIA	0.84	0.86	1.13	0.88	0.94	0.16	8	27	3.84E-120
Q9UEU0-1	Vesicle transport through interaction with t-SNAREs homolog 1B	VTI1	1.06	1.03	0.74	1.35	0.94	0.18	3	18	1.09E-49
O43148-2	mRNA (guanine-N(7)-)-methyltransferase	KIAA0398	1.10	0.75	0.98	1.02	0.94	0.18	3	7.5	5.24E-45
Q9Y6C9	Met-induced mitochondrial protein	HSPC032	1.06	1.06	0.71	1.41	0.94	0.20	5	19	1.93E-40
P40939	78 kDa gastrin-binding protein	HADH	0.77	0.75	1.31	0.76	0.94	0.32	21	36	0.00E+00
Q8N4V1-2	Membrane magnesium transporter 1	MMGT1	1.07	1.22	0.54	1.85	0.94	0.36	2	18	3.66E-26
Q96I99	GTP-specific succinyl-CoA synthetase subunit beta	SUCLG2	0.74	0.72	1.37	0.73	0.94	0.37	7	19	1.17E-79
O43719	HIV Tat-specific factor 1	HTATSF1	0.72	0.69	1.42	0.70	0.94	0.41	17	26	1.37E-124
O15498	Synaptobrevin homolog YKT6	YKT6	1.11	1.28	0.44	2.27	0.94	0.44	3	13	2.78E-11
O95466-2	CLL-associated antigen KW-13	C17orf1	0.62	0.68	1.53	0.65	0.94	0.51	21	20	1.27E-209
Q9H9A6	Leucine-rich repeat-containing protein 40	LRRC40	1.14	0.75			0.95	0.28	3	7.3	1.01E-08
Q9H0L4	CF-1 64 kDa subunit tau variant	CSTF2T		1.17	0.72	1.39	0.95	0.32	5	13	3.07E-15
P35754	Glutaredoxin-1	GLRX	0.70		1.19	0.84	0.95	0.35	3	43	5.79E-31
Q9Y3A3-1	2C4D	CGI-95	0.96	0.93			0.95	0.02	5	37	1.14E-09
Q96PM5-1	Androgen receptor N-terminal-interacting protein	ARNIP	0.91		0.98	1.02	0.95	0.05	2	8.4	3.13E-20
Q9NQT4	Chronic myelogenous leukemia tumor	CML28	0.98		0.91	1.10	0.95	0.05	5	25	3.34E-39

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	antigen 28										
P02686-1	Myelin A1 protein	MBP		0.81	1.08	0.93	0.95	0.19	2	15	8.44E-19
B4E175	cDNA FLJ54775, highly similar to Syntaxin-binding protein 2	STXBP2		1.08	0.81	1.23	0.95	0.19	5	11	7.21E-67
C9IZQ1	Putative uncharacterized protein SSR1	SSR1	0.96	0.94	0.94	1.06	0.95	0.01	3	11	2.23E-78
P12081	Histidine--tRNA ligase	HARS	0.93	0.94	0.97	1.03	0.95	0.02	17	38	2.40E-186
Q99653	Calcineurin B homolog	CHP	0.97	0.93	0.94	1.06	0.95	0.02	6	38	1.87E-45
P61163	Actin-RPV	ACTR1A	0.93	0.93	0.98	1.02	0.95	0.03	11	41	6.20E-208
P62917	60S ribosomal protein L8	RPL8	0.97	0.96	0.91	1.10	0.95	0.03	12	42	8.06E-91
Q9Y3B4	Pre-mRNA branch site protein p14	CGI-110	0.94	0.99	0.91	1.10	0.95	0.04	5	46	6.83E-123
Q5JWF2-1	Adenylate cyclase-stimulating G alpha protein	GNAS	0.97	0.89	0.98	1.02	0.95	0.05	9	12	7.88E-130
P47755	F-actin-capping protein subunit alpha-2	CAPZA2	0.92	0.91	1.01	0.99	0.95	0.06	8	42	4.29E-38
Q9BRX2	Protein pelota homolog	CGI-17	0.87	1.00	0.97	1.03	0.95	0.07	5	11	4.75E-56
P82930	28S ribosomal protein S34, mitochondrial	MRPS34	0.87	0.95	1.02	0.98	0.95	0.08	5	33	8.52E-20
Q13242	Pre-mRNA-splicing factor SRp30C	SFRS9	0.88	0.91	1.05	0.95	0.95	0.09	14	55	1.24E-87
P18077	60S ribosomal protein L35a	GIG33	0.99	1.01	0.84	1.19	0.95	0.09	5	34	1.27E-11
Q9H1E3-1	Nuclear ubiquitous casein and cyclin-dependent kinases substrate	JC7	0.99	1.02	0.83	1.20	0.95	0.10	10	42	1.43E-66
P62333	26S protease regulatory subunit 10B	PSMC6	1.05	0.95	0.84	1.19	0.95	0.11	16	45	2.20E-113
O60763	General vesicular transport factor p115	USO1	0.89	0.88	1.07	0.93	0.95	0.11	20	28	6.70E-251
O60502-1	Beta-hexosaminidase	HEXC	0.83	1.04	0.97	1.03	0.95	0.11	4	4.1	2.07E-05
P00387-1	Diaphorase-1	CYB5R3	0.86	0.91	1.07	0.93	0.95	0.11	6	27	9.54E-152
Q13561	50 kDa dynein-associated polypeptide	DCTN2	0.88	0.88	1.08	0.93	0.95	0.12	10	28	4.99E-153
Q7L014	DEAD box protein 46	DDX46	0.84	0.92	1.08	0.93	0.95	0.12	25	25	1.60E-152
Q96S59-1	BPM90	RANBP9	0.85	1.09	0.90	1.11	0.95	0.13	4	7.3	5.51E-25
O15126-1	Secretory carrier-associated membrane	SCAMP	0.80	1.04	1.00	1.00	0.95	0.13	2	11	9.77E-22

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	protein 1										
Q96CW5-1	Gamma-ring complex protein 104 kDa	GCP3	0.80	0.98	1.06	0.94	0.95	0.13	6	8.7	1.86E-82
P23743-1	80 kDa diacylglycerol kinase	DAGK	1.04	1.01	0.79	1.27	0.95	0.14	6	13	1.59E-71
O60256	41 kDa phosphoribosypyrophosphate synthetase-associated protein	PRPSAP2	0.95	0.80	1.09	0.92	0.95	0.15	10	38	2.32E-227
B3KTC7	cDNA FLJ38069 fis, clone CTONG2015434, highly similar to DOUBLE-STRAND BREAK REPAIR PROTEIN MRE11A	HNGS1	0.86	0.86	1.12	0.89	0.95	0.15	5	9.1	2.44E-74
Q96FV9-1	Nuclear matrix protein p84	HPR1	0.84	0.88	1.12	0.89	0.95	0.15	8	13	5.70E-69
P52888	Endopeptidase 24.15	THOP1	0.80	0.93	1.11	0.90	0.95	0.16	15	29	3.43E-140
Q8IZL8-2	Modulator of non-genomic activity of estrogen receptor	HMX3	0.98	1.11	0.75	1.33	0.95	0.18	5	5.9	1.10E-85
O00629	Importin alpha Q1	KPNA4	0.78	0.90	1.16	0.86	0.95	0.19	5	15	1.66E-83
B4DLZ8	cDNA FLJ55789, highly similar to Rattus norvegicus basic leucine zipper and W2 domains 1 (Bzw1), mRNA	BZAP45	1.05	1.07	0.72	1.39	0.95	0.20	8	17	1.81E-91
Q5SSJ5-1	Heterochromatin protein 1-binding protein 3	HP1BP3	0.78	0.87	1.19	0.84	0.95	0.22	19	39	9.05E-129
Q9BVA1	Tubulin beta-2B chain	TUBB2B	1.16	0.71	0.97	1.03	0.95	0.23	22	63	0.00E+00
P62979	40S ribosomal protein S27a	RPS27A	0.99	1.16	0.69	1.45	0.95	0.24	12	64	1.83E-206
P10155-1	60 kDa SS-A/Ro ribonucleoprotein	RO60	0.81	0.78	1.25	0.80	0.95	0.26	2	4.5	3.47E-16
P11387	DNA topoisomerase 1	TOP1	0.77	0.82	1.25	0.80	0.95	0.26	29	35	4.20E-127
P28715-1	DNA excision repair protein ERCC-5	ERCC5	0.71	1.26	0.87	1.15	0.95	0.28	7	9.5	1.15E-36
P11171-1	Band 4.1	E41P	0.62	0.78	1.44	0.69	0.95	0.43	2	3.1	1.31E-22
B3KQ79	B-cell receptor-associated protein 31, isoform CRA_b	BCAP31	0.91	1.00	0.93	1.08	0.95	0.05	11	22	1.10E-27
Q9C0J8	WD repeat-containing protein 33	WDC146	0.95	1.08	0.81	1.23	0.95	0.14	6	7.3	9.81E-11
Q0VDF9	Heat shock 70 kDa protein 14	HSP70	1.05	1.02	0.77	1.30	0.95	0.15	8	22	7.45E-27
P17812	CTP synthase 1	CTPS	0.97	0.93	0.95	1.05	0.95	0.02	20	38	2.88E-166
Q9H5V	UPF0428 protein	CXorf5	0.90	0.96	0.99	1.01	0.95	0.05	4	17	4.50E-41

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9	CXorf56	6									
Q3MHD2-2	Protein LSM12 homolog	LSM12	0.90	1.00	0.95	1.05	0.95	0.05	3	18	3.73E-21
Q8IY81	Protein ftsJ homolog 3	FTSJ3	0.95	1.06	0.84	1.19	0.95	0.11	18	28	7.01E-231
Q9UBF2	Coatomer subunit gamma-2	COPG2	0.97	0.83	1.05	0.95	0.95	0.11	13	20	1.34E-217
Q13813-1	Alpha-II spectrin	SPTA2	0.83	0.89	1.13	0.88	0.95	0.16	##	67	0.00E+00
P68402	PAF acetylhydrolase 30 kDa subunit	PAFAH1B2	0.88	0.79	1.18	0.85	0.95	0.20	6	38	1.07E-54
B4DPJ2	cDNA FLJ51518, highly similar to Annexin A11	ANX11	0.83	0.83	1.19	0.84	0.95	0.21	11	31	5.10E-113
A6ZJA4	Bromodomain containing 1	BRD1	0.62	0.55	1.68	0.60	0.95	0.63	4	3.2	3.08E-06
Q9H3S7	His domain-containing protein tyrosine phosphatase	KIAA1471		0.94	0.96	1.04	0.95	0.01	6	6.2	1.48E-78
Q5T200-1	Zinc finger CCCH domain-containing protein 13	KIAA0853		0.96	0.94	1.06	0.95	0.01	3	2.6	3.12E-07
P42566-1	Epidermal growth factor receptor substrate 15	AF1P		0.92	0.98	1.02	0.95	0.04	5	6	7.50E-37
O75818-1	Ribonuclease P protein subunit p40	RNASEP1	0.91		0.99	1.01	0.95	0.06	2	11	6.86E-05
Q00169	Phosphatidylinositol transfer protein alpha isoform	PITPN	0.86		1.04	0.96	0.95	0.13	6	26	3.69E-43
P04844	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit	RPN2	1.07		0.83	1.20	0.95	0.17	9	29	1.11E-168
Q13564	Amyloid beta precursor protein-binding protein 1, 59 kDa	APPBP1	0.76		1.14	0.88	0.95	0.27	9	28	3.55E-137
O75376-1	Nuclear receptor corepressor 1	KIAA1047	0.69		1.21	0.83	0.95	0.37	6	3.6	2.17E-46
Q6ZNJ1-1	Neurobeachin-like protein 2	KIAA0540	1.22		0.68	1.47	0.95	0.38	8	4.4	2.62E-56
Q9BV68-1	RING finger protein 126	RNF126			0.95	1.05	0.95		2	6.4	7.88E-04
O15269	Long chain base biosynthesis protein 1	LCB1		0.95			0.95		2	4	9.82E-04
Q14554	Protein disulfide isomerase-related protein	PDIA5	0.95				0.95		2	4.4	3.41E-03
Q9HAB8	Phosphopantothenate--cysteine ligase	COAB		0.95			0.95		3	9	7.09E-07
P18859	ATP synthase-coupling factor 6,	ATP6	0.95				0.95		3	25	4.47E-39

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	mitochondrial										
A8MSZ6	Putative uncharacterized protein TAF9	hCG_37060	0.95				0.95		4	29	5.14E-07
P35249	Activator 1 37 kDa subunit	RFC4	0.94	0.93	0.98	1.02	0.95	0.03	17	49	2.64E-269
P68104	Elongation factor 1-alpha 1	EEF1A	0.98	0.97	0.90	1.11	0.95	0.04	26	59	0.00E+00
B4E1G6	cDNA FLJ56840, highly similar to Galactokinase (EC 2.7.1.6)	GALK1	0.94	1.00	0.91	1.10	0.95	0.05	12	38	7.88E-69
Q9BW71-1	HIRA-interacting protein 3	HIRIP3	0.95	0.90	1.00	1.00	0.95	0.05	6	14	4.19E-65
P55786	Puromycin-sensitive aminopeptidase	NPEPPS	0.89	1.00	0.96	1.04	0.95	0.06	13	20	2.80E-133
A6NDG6	Phosphoglycolate phosphatase	PGP	0.94	1.03	0.88	1.14	0.95	0.08	7	29	1.53E-77
Q9NRN7	4-phosphopantetheinyl transferase	AASDHPPT	0.99	1.03	0.83	1.20	0.95	0.11	9	36	6.50E-109
P38432	Coilin	CLN80	0.80	1.02	1.03	0.97	0.95	0.13	6	14	5.99E-47
Q8TCJ2	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B	SIMP	0.80	1.07	0.98	1.02	0.95	0.14	11	14	5.74E-44
P50750-2	Cell division cycle 2-like protein kinase 4	CDC2L4	0.80	0.95	1.10	0.91	0.95	0.15	12	22	2.42E-148
Q9NYB0	Telomeric repeat-binding factor 2-interacting protein 1	PP8000	0.92	1.12	0.81	1.23	0.95	0.16	6	23	2.76E-90
Q96EY4	UPF0534 protein C4orf43	C4orf43	1.00	1.08	0.77	1.30	0.95	0.16	6	31	2.30E-30
P06753-2	Gamma-tropomyosin	TPM3	0.77	0.91	1.17	0.85	0.95	0.20	28	73	0.00E+00
O75175-1	CCR4-associated factor 3	CNOT3	1.20	0.86	0.79	1.27	0.95	0.22	3	6.1	1.95E-72
Q13283	ATP-dependent DNA helicase VIII	G3BP	1.11	1.10	0.64	1.56	0.95	0.27	14	41	1.68E-169
Q92882	Osteoclast-stimulating factor 1	OSTF1	0.78	0.77	1.30	0.77	0.95	0.30	8	47	1.91E-122
Q13951-1	Core-binding factor subunit beta,isoform 1	CBFB	0.76	0.75	1.34	0.75	0.95	0.34	7	43	3.29E-110
Q9HD33-1	39S ribosomal protein L47, mitochondrial	CGI-204	0.65	0.65	1.55	0.65	0.95	0.52	5	21	8.54E-16
P41227	N-alpha-acetyltransferase 10, NatA catalytic subunit	NAA10	1	1.07	0.78	1.28	0.95	0.15	9	48	6.72E-40
Q9Y520-7	BAT2 domain-containing protein 1	BAT2D1	1.03	1.12	0.70	1.43	0.95	0.22	21	9.8	2.70E-100
Q99543-1	DnaJ homolog subfamily C member 2	DNAJC2	1.07	1.12	0.66	1.52	0.95	0.25	15	30	1.38E-81

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Q12834	Cell division cycle protein 20 homolog	CDC20	0.99	1.15	0.72	1.39	0.95	0.22	4	8	1.87E-24
Q10713	Alpha-MPP	INPP5E	0.94	0.97	0.95	1.05	0.95	0.02	9	22	8.15E-53
O14979-1	AU-rich element RNA-binding factor	HNRPDL	0.94	0.94	0.98	1.02	0.95	0.02	14	32	1.98E-235
Q08379-2	130 kDa cis-Golgi matrix protein	GOLGA2	0.93	0.95	0.98	1.02	0.95	0.03	7	7.8	3.63E-58
Q01469	Epidermal-type fatty acid-binding protein	FABP5	0.99	0.95	0.92	1.09	0.95	0.04	11	69	1.80E-222
P62906	60S ribosomal protein L10a	NEDD6	0.94	1.00	0.92	1.09	0.95	0.04	12	43	3.21E-111
Q9Y3B9	Ribosomal RNA-processing protein 15	CGI-115	0.99	0.98	0.89	1.12	0.95	0.06	5	18	1.12E-83
P62195	26S protease regulatory subunit 8	PSMC5	0.95	1.01	0.90	1.11	0.95	0.06	16	53	0.00E+00
Q9BXJ9-1	Gastric cancer antigen Ga19	GA19	1.00	0.97	0.89	1.12	0.95	0.06	25	28	6.81E-125
O95235	Kinesin-like protein KIF20A	KIF20A	1.01	0.98	0.87	1.15	0.95	0.07	7	9.7	2.27E-67
A8MWD3	Putative uncharacterized protein EIF3D	EIF3D	1.04	0.92	0.90	1.11	0.95	0.08	14	37	9.85E-146
P61011	Signal recognition particle 54 kDa protein	SRP54	0.98	0.86	1.02	0.98	0.95	0.08	9	24	1.52E-61
Q8IXB1-1	DnaJ homolog subfamily C member 10	DNAJC10	0.91	1.05	0.90	1.11	0.95	0.08	3	3.8	2.38E-07
O76071	Probable cytosolic iron-sulfur protein assembly protein CIAO1	CIAO1	0.85	1.03	0.98	1.02	0.95	0.09	4	15	8.34E-24
Q96C19	EF-hand domain-containing protein D2	EFHD2	0.97	1.04	0.85	1.18	0.95	0.10	11	40	8.20E-96
O00410-3	Importin subunit beta-3	IPO5	1.00	1.02	0.84	1.19	0.95	0.10	39	50	0.00E+00
P36578	60S ribosomal protein L1	RPL1	1.01	1.03	0.82	1.22	0.95	0.12	26	52	1.48E-224
P62847-1	40S ribosomal protein S24	RPS24	1.11	0.93	0.82	1.22	0.95	0.15	4	16	3.47E-73
P62873	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1	GNB1	0.82	0.89	1.15	0.87	0.95	0.17	12	44	0.00E+00
P36871-1	Glucose phosphomutase 1	PGM1	0.89	0.82	1.15	0.87	0.95	0.17	12	32	5.40E-90
P45973	Antigen p25	CBX5	0.83	0.87	1.16	0.86	0.95	0.18	15	64	6.58E-214
B4DI36	cDNA FLJ55061, highly similar to RPA-interacting protein	RIP	1.15	0.78	0.93	1.08	0.95	0.19	2	16	2.29E-06
Q63HN8-1	RING finger protein 213	C17orf27	1.08	1.05	0.73	1.37	0.95	0.19	27	7.8	1.18E-145
P27348	14-3-3 protein tau	YWHAQ	0.78	0.91	1.17	0.85	0.95	0.20	22	69	0.00E+00

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O75381-1	Peroxin-14	PEX14	0.82	0.81	1.23	0.81	0.95	0.24	3	6.6	6.11E-33
Q9HC38-2	Glyoxalase domain-containing protein 4	C17orf25	0.71	0.76	1.39	0.72	0.95	0.38	19	65	2.25E-123
Q9NW82	WD repeat-containing protein 70	WDR70	0.92	0.99	0.95	1.05	0.95	0.04	3	5.4	2.81E-12
Q06210-1	D-fructose-6-phosphate amidotransferase 1	GFAT	0.93	0.92	1.01	0.99	0.95	0.05	15	28	3.83E-112
B2RB47	cDNA, FLJ95309, highly similar to Homo sapiens adenosine monophosphate deaminase 2 (isoform L)(AMPD2), mRNA	AMPD2	0.97	0.88	1.01	0.99	0.95	0.07	9	9.9	4.90E-34
Q12874	Spliceosome-associated protein 61	SAP61	0.97	0.88	1.01	0.99	0.95	0.07	19	40	8.94E-213
O00505	Importin alpha Q2	KPNA3	1.03	0.92	0.91	1.10	0.95	0.07	8	26	8.99E-23
P30533	Alpha-2-macroglobulin receptor-associated protein	A2MRAP	0.87	0.96	1.03	0.97	0.95	0.08	2	9	2.09E-17
B3KXE1	cDNA FLJ45281 fis, clone BRHIP3001481, highly similar to Tyrosine-protein phosphatase non-receptor type 7 (EC 3.1.3.48)	PTPN7	1.05	0.90	0.91	1.10	0.95	0.08	6	19	1.22E-148
Q96A33-1	Coiled-coil domain-containing protein 47	CCDC47	0.87	1.08	0.91	1.10	0.95	0.11	5	12	1.89E-13
Q9NSD9	Phenylalanine--tRNA ligase beta chain	FARSB	1.05	1.01	0.80	1.25	0.95	0.13	19	33	1.90E-175
Q96PK6-1	Paraspeckle protein 2	RBM14	0.87	0.88	1.11	0.90	0.95	0.14	21	31	2.20E-127
O75390	Citrate synthase, mitochondrial	CS	0.86	0.88	1.12	0.89	0.95	0.14	13	37	2.12E-68
Q8TCS8	3-5 RNA exonuclease OLD35	PNPASE	0.98	1.09	0.79	1.27	0.95	0.15	7	13	2.90E-58
Q9H845	Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	0.76	1.03	1.07	0.93	0.95	0.17	6	16	2.56E-38
Q9Y315	Phosphodeoxyriboaldolase	CGI-26	1.00	0.76	1.10	0.91	0.95	0.17	4	18	8.94E-18
Q8WYA6-1	Beta-catenin-like protein 1	C20orf33	0.79	0.89	1.18	0.85	0.95	0.20	7	16	7.08E-56
P52789	Hexokinase type II	HK2	1.02	1.12	0.72	1.39	0.95	0.21	12	16	1.09E-87
B7ZKL8	TUBGCP2 protein	TUBGCP2	0.76	0.92	1.18	0.85	0.95	0.21	5	5.9	2.85E-24
P67809	CCAAT-binding transcription factor I	NSEP1	1.02	1.14	0.70	1.43	0.95	0.23	18	65	0.00E+00

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	subunit A										
P04083	Annexin A1	ANX1	0.69	0.68	1.49	0.67	0.95	0.46	21	65	0.00E+00
O60826	Coiled-coil domain-containing protein 22	CCDC22	0.69		1.22	0.82	0.96	0.37	6	17	2.78E-31
P36405	ADP-ribosylation factor-like protein 3	ARFL3	0.98		0.93	1.08	0.96	0.04	8	60	1.23E-42
A8MWD9	Small nuclear ribonucleoprotein G-like protein	PBSCG		1.01	0.90	1.11	0.96	0.08	3	37	2.40E-23
Q5M8S8	SIX6 protein	SIX6	0.84	1.07			0.96	0.16	3	17	2.74E-26
Q9NS86	LanC-like protein 2	GPR69B	0.79	1.22	0.86	1.16	0.96	0.23	3	6.9	9.89E-35
P61086-1	Huntingtin-interacting protein 2	HIP2	1.02	1.16	0.69	1.45	0.96	0.24	8	58	5.39E-155
P28838-1	Cytosol aminopeptidase	LAP3	0.95	0.96	0.96	1.04	0.96	0.01	23	57	1.54E-304
Q53HL2	Borealin	CDCA8	0.95	0.97	0.95	1.05	0.96	0.01	6	25	7.20E-20
P50914	60S ribosomal protein L14	RPL14	0.98	0.93	0.96	1.04	0.96	0.03	9	38	3.48E-67
Q3S611	Cyclophilin-33B	PPIE	0.98	0.97	0.92	1.09	0.96	0.03	5	23	4.17E-32
P14859-2	Octamer-binding protein 1	41183	0.94	0.92	1.01	0.99	0.96	0.05	3	6.9	2.17E-52
Q9NXV2	BTB/POZ domain-containing protein KCTD5	KCTD5	0.96	1.02	0.89	1.12	0.96	0.07	3	33	1.12E-12
Q5VZU9	Tripeptidyl peptidase II	RP11-29B2.2-002	1.04	0.93	0.90	1.11	0.96	0.07	24	24	1.39E-123
Q9H0U4	Ras-related protein Rab-1B	RAB1B	0.89	0.94	1.04	0.96	0.96	0.08	9	54	8.39E-255
P54132	Bloom syndrome protein	BLM	0.92	1.05	0.90	1.11	0.96	0.08	5	4.7	1.31E-25
Q96D71-1	RalBP1-associated Eps domain-containing protein 1	REPS1	0.92	1.06	0.89	1.12	0.96	0.09	6	12	9.29E-11
P50502	Hsc70-interacting protein	FAM10A1	1.00	1.02	0.85	1.18	0.96	0.09	8	25	2.24E-85
O75165	DnaJ homolog subfamily C member 13	DNAJC13	0.86	1.05	0.96	1.04	0.96	0.10	8	5.9	2.44E-69
O75937	DnaJ homolog subfamily C member 8	DNAJC8	0.85	0.96	1.06	0.94	0.96	0.11	12	42	1.43E-109
P62280	40S ribosomal protein S11	RPS11	1.03	1.01	0.83	1.20	0.96	0.11	12	53	2.81E-55
Q5TBB1	Aicardi-Goutieres syndrome 2 protein	DLEU8	0.85	0.94	1.08	0.93	0.96	0.12	11	34	8.46E-38
Q9NTJ3-1	Chromosome-associated polypeptide C	CAPC	0.95	1.08	0.84	1.19	0.96	0.12	40	33	2.10E-204
P53634	Cathepsin C	CPPI	1.11	0.89	0.87	1.15	0.96	0.13	8	29	5.26E-79

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P35251-1	Activator 1 140 kDa subunit	RFC1	0.85	0.89	1.13	0.88	0.96	0.15	13	14	6.83E-180
P46940	Ras GTPase-activating-like protein IQGAP1	IQGAP1	0.85	0.89	1.13	0.88	0.96	0.15	51	44	0.00E+00
C9JRZ6	Putative uncharacterized protein CHCHD3	CHCHD3	0.81	0.9	1.16	0.86	0.96	0.18	14	46	3.97E-123
P24539	ATP synthase subunit b, mitochondrial	ATP5F1	0.86	0.84	1.17	0.85	0.96	0.19	10	42	1.75E-65
Q12789-2	General transcription factor 3C polypeptide 1	GTF3C1	1.17	0.95	0.75	1.33	0.96	0.21	6	4.8	2.14E-49
Q92930	Ras-related protein Rab-8B	RAB8B	0.81	0.85	1.21	0.83	0.96	0.22	6	36	3.47E-119
Q92922	BRG1-associated factor 155	BAF155	0.83	0.81	1.23	0.81	0.96	0.24	24	23	6.92E-168
Q8IV48	3-5 exonuclease ERI1	3EXO	1.17	1.06	0.64	1.56	0.96	0.28	2	6.6	2.78E-17
P00491	Inosine phosphorylase	NP	0.82	0.76	1.29	0.78	0.96	0.29	17	63	2.07E-288
P62258	14-3-3 protein epsilon	YWHAE	0.76	0.81	1.30	0.77	0.96	0.30	23	77	0.00E+00
Q9H9Q2-1	COP9 signalosome complex subunit 7b	COPS7B	0.71	0.85	1.31	0.76	0.96	0.31	6	28	1.52E-150
P68431	Histone H3.1	H3FA	0.75	0.75	1.37	0.73	0.96	0.36	9	53	4.67E-131
P50579	Initiation factor 2-associated 67 kDa glycoprotein	METAP2	1.05	1.32	0.50	2.00	0.96	0.42	3	8.2	2.77E-80
Q9BT78	COP9 signalosome complex subunit 4	COPS4	0.94	0.94	1.00	1.00	0.96	0.03	9	27	2.41E-87
P11172-1	Orotate phosphoribosyltransferase	OK/SW-cl.21	0.99	0.92	0.97	1.03	0.96	0.04	10	23	9.46E-58
Q9Y606-1	tRNA pseudouridine synthase A	PP8985	0.97	0.92	0.99	1.01	0.96	0.04	7	20	3.12E-51
Q5HYJ3-1	Protein FAM76B	FAM76B	0.94	1.02	0.92	1.09	0.96	0.05	4	12	8.65E-25
Q9Y2L1-1	Exosome complex exonuclease RRP44	DIS3	0.99	1.01	0.88	1.14	0.96	0.07	6	10	9.67E-70
Q14966-1	Cutaneous T-cell lymphoma-associated antigen se33-1	NP220	0.94	1.04	0.90	1.11	0.96	0.07	9	7.6	5.36E-35
Q01196-8	Acute myeloid leukemia 1 protein	AML1	1.01	0.87	1.00	1.00	0.96	0.08	6	18	9.23E-28
O15212	Prefoldin subunit 6	HKE2	0.90	1.02			0.96	0.08	7	40	5.93E-125
Q8NFH4	Nucleoporin Nup37	NUP37	1.03	0.99	0.86	1.16	0.96	0.09	4	17	1.12E-42
Q6B6N3	Galphai2 protein	GNAI2	0.89	0.92	1.07	0.93	0.96	0.10	15	56	8.07E-241
Q9P0S2	Cytochrome c oxidase assembly protein COX16 homolog, mitochondrial	C14orf112	1.03	0.89			0.96	0.10	2	22	2.39E-09

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Q3B867	PABPC4 protein	PABPC4	0.95	1.09	0.84	1.19	0.96	0.13	24	39	0.00E+00
Q14790-9	Apoptotic cysteine protease	CASP8	0.85	0.93	1.10	0.91	0.96	0.13	3	7.2	1.45E-20
P08133	67 kDa calelectrin	ANX6	0.86		1.06	0.94	0.96	0.14	38	66	0.00E+00
P04080	Cystatin-B	CST6	0.85	0.91	1.12	0.89	0.96	0.14	4	52	1.35E-41
Q16401	26S protease subunit S5 basic	KIAA0072	0.91	0.85	1.12	0.89	0.96	0.14	12	32	9.02E-222
Q99460-1	26S proteasome non-ATPase regulatory subunit 1	PSMD1	1.01	1.07	0.80	1.25	0.96	0.14	24	36	1.19E-203
O75170-1	SAPS domain family member 2	KIAA0685	0.85		1.07	0.93	0.96	0.16	2	3.7	1.82E-11
Q9H446	DRG family-regulatory protein 2	CGI-24	1.07	0.85			0.96	0.16	2	11	3.90E-62
Q9NY33-1	Dipeptidyl aminopeptidase III	DPP3	0.89	0.84	1.15	0.87	0.96	0.17	23	45	0.00E+00
B2R9Y2	cDNA, FLJ94609	CCDC55	0.93	1.17	0.78	1.28	0.96	0.20	5	4.4	6.00E-22
Q4G176-1	Acyl-CoA synthetase family member 3, mitochondrial	ACSF3	1.10		0.82	1.22	0.96	0.20	4	13	8.66E-39
Q9Y295	Developmentally-regulated GTP-binding protein 1	DRG1	1.07	1.11	0.70	1.43	0.96	0.23	13	53	1.37E-162
B8ZZD4	Putative uncharacterized protein TAX1BP1	TAX1BP1		0.79	1.13	0.88	0.96	0.24	2	2.1	1.22E-04
Q00013	55 kDa erythrocyte membrane protein	DXS552E	0.69	1.19	1.00	1.00	0.96	0.25	9	31	7.06E-49
B9A001	Putative uncharacterized protein MPP6	MPP6		1.15	0.77	1.30	0.96	0.27	3	5.8	6.33E-09
P50583	Bis(5-nucleosyl)-tetraphosphatase [asymmetrical]	APAH1	1.22		0.70	1.43	0.96	0.37	3	25	1.31E-26
P49406	39S ribosomal protein L15, mitochondrial	KIAA0104		0.50	1.42	0.70	0.96	0.65	2	6.2	9.48E-05
Q8NHQ9	ATP-dependent RNA helicase DDX55	DDX55			0.96	1.04	0.96		2	5.2	1.07E-03
Q9UIV1	BTG1-binding factor 1	CAF1			0.96	1.04	0.96		3	13	3.28E-13
Q14692	Ribosome assembly protein BMS1 homolog	BMS1			0.96	1.04	0.96		4	3.7	1.01E-10
Q9H6L4	Armadillo repeat-containing protein 7	ARMC7	0.96				0.96		2	17	3.26E-64
O60508	Cell division cycle 40 homolog	CDC40	0.96				0.96		2	4.3	4.42E-05
Q12846	Renal carcinoma antigen NY-REN-31	STX4		0.96			0.96		2	9.4	1.73E-24
Q86Y79	Probable peptidyl-tRNA hydrolase	C9orf115	0.96				0.96		2	22	1.94E-17
Q6P1X6	UPF0598 protein	C8orf82	0.96				0.96		2	13	1.89E-03

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-1	C8orf82										
Q8WZA0	Leucine zipper and CTNNBIP1 domain-containing protein	LZIC	0.96				0.96		3	15	2.79E-08
Q969R2	Oxysterol-binding protein 2	KIAA1664	0.96				0.96		4	5.6	2.92E-15
Q6ZN33	cDNA FLJ16473 fis, clone BRHIP3026052, highly similar to Serine/threonine protein phosphatase 2A, 56 kDa regulatory subunit, gamma isoform	KIAA0044	0.96				0.96		4	12	8.91E-163
Q5C9Z4	Nucleolar MIF4G domain-containing protein 1	C7orf3	0.92	1.07	0.89	1.12	0.96	0.10	9	13	4.26E-44
Q9Y5Q8-3	General transcription factor 3C polypeptide 5	CDABP0017	1.00	1.03	0.85	1.18	0.96	0.10	7	14	1.76E-41
Q13895	Bystin	BYSL	1.01	1.06	0.81	1.23	0.96	0.13	10	25	1.04E-52
Q13409-1	Cytoplasmic dynein 1 intermediate chain 2	DNCI2	1.04	1.07	0.77	1.30	0.96	0.17	8	20	1.74E-192
Q13144	eIF-2B GDP-GTP exchange factor subunit epsilon	EIF2B5	1.12	1.07	0.69	1.45	0.96	0.24	8	13	1.89E-46
Q9Y3D0	Protein FAM96B	CGI-128	1.22	1.06	0.60	1.67	0.96	0.32	3	31	1.38E-15
Q16630-2	Cleavage and polyadenylation specificity factor 68 kDa subunit	CFIM68	0.96	0.97	0.96	1.04	0.96	0.01	9	22	1.47E-230
P30085	Cytidine monophosphate kinase	CMK	0.97	0.98	0.94	1.06	0.96	0.02	11	47	4.98E-286
P63167	8 kDa dynein light chain	DLC1	0.96	0.99	0.94	1.06	0.96	0.03	6	64	1.60E-47
P11142-1	Heat shock 70 kDa protein 8	HSC70	0.95	1.00	0.94	1.06	0.96	0.03	47	65	0.00E+00
O96019-1	53 kDa BRG1-associated factor A	ACTL6A	0.98	0.92	0.99	1.01	0.96	0.04	8	25	5.31E-80
Q96I24-1	Far upstream element-binding protein 3	FBP3	0.96	0.92	1.01	0.99	0.96	0.05	16	38	1.23E-50
Q92598-1	Antigen NY-CO-25	HSP105	0.99	1.02	0.88	1.14	0.96	0.07	41	54	0.00E+00
P29692-2	Antigen NY-CO-4	EF1D	0.98	1.03	0.88	1.14	0.96	0.08	12	24	2.50E-296
P61289-2	11S regulator complex subunit gamma	PSME3	1.04	1.01	0.84	1.19	0.96	0.11	9	32	3.23E-211
P50552	Vasodilator-stimulated phosphoprotein	VASP	0.82	0.90	1.17	0.85	0.96	0.18	8	21	5.20E-107
P23368	Malic enzyme 2	ME2	0.86	0.85	1.18	0.85	0.96	0.19	16	49	3.35E-228
P06746	DNA polymerase beta	POLB	0.84	0.85	1.20	0.83	0.96	0.21	2	11	3.30E-08

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A6NIH7	Protein unc-119 homolog B	UNC119B	1.11	1.06	0.72	1.39	0.96	0.21	5	27	8.32E-19
P46459	N-ethylmaleimide-sensitive fusion protein	NSF	0.83	0.84	1.22	0.82	0.96	0.22	16	25	1.42E-108
Q9NP66-1	High mobility group protein 20A	HMG20A	0.68	1.14	1.07	0.93	0.96	0.25	2	9.2	5.05E-05
O95983-1	Methyl-CpG-binding domain protein 3	MBD3	0.75	0.86	1.28	0.78	0.96	0.28	6	24	3.48E-186
Q9H6R4-1	Nucleolar protein 6	NOL6	1.27	1.03	0.59	1.69	0.96	0.34	9	11	1.07E-43
Q15149-4	Hemidesmosomal protein 1	PLEC1	0.74	0.75	1.4	0.71	0.96	0.38	##	30	0.00E+00
Q8WWP7	GTPase IMAP family member 1	GIMAP1	0.58	0.62	1.69	0.59	0.96	0.63	8	29	1.38E-48
P13073	Cytochrome c oxidase polypeptide IV	COX4	0.97	1.00	0.92	1.09	0.96	0.04	7	33	1.88E-20
Q9NQX3-2	Domain E	GPH	0.98	0.89	1.02	0.98	0.96	0.07	5	9.9	3.03E-54
P15880	40S ribosomal protein S2	RPS2	1.00	1.03	0.86	1.16	0.96	0.09	15	49	7.72E-112
P62244	40S ribosomal protein S15a	OK/SW-cl.82	1.02	1.02	0.85	1.18	0.96	0.10	7	58	1.10E-21
Q9UHB9-1	Signal recognition particle 68 kDa protein	SRP68	0.89	0.92	1.08	0.93	0.96	0.10	22	38	7.64E-218
P49321-3	Nuclear autoantigenic sperm protein	NASP	0.85	0.98	1.06	0.94	0.96	0.11	19	28	0.00E+00
Q9Y5P6-2	GDP-mannose pyrophosphorylase B	GMPPB	1.09	0.95	0.85	1.18	0.96	0.12	4	13	3.69E-38
Q5T4S7-2	600 kDa retinoblastoma protein-associated factor	KIAA0462	1.04	1.03	0.82	1.22	0.96	0.12	24	8.4	0.00E+00
P05388	60S acidic ribosomal protein P0	RPLP0	1.02	1.05	0.82	1.22	0.96	0.13	14	53	4.41E-248
Q9NVI7-2	ATPase family AAA domain-containing protein 3A	ATAD3A	0.89	0.89	1.11	0.90	0.96	0.13	16	29	8.55E-90
Q96C86	Hint-related 7meGMP-directed hydrolase	DCPS	0.89	0.88	1.12	0.89	0.96	0.14	9	38	2.77E-218
A8MSQ1	Putative uncharacterized protein PHF14	PHF14	0.80	0.99	1.10	0.91	0.96	0.15	4	5.4	3.39E-41
Q9BQ52-1	ElaC homolog protein 2	ELAC2	1.07	1.05	0.77	1.30	0.96	0.17	20	31	5.24E-110
Q15555-1	APC-binding protein EB2	MAPRE2	1.02	1.12	0.75	1.33	0.96	0.19	15	39	3.87E-96
O14646-1	ATP-dependent helicase CHD1	CHD1	1.12	1.10	0.67	1.49	0.96	0.25	14	13	2.70E-57
O94925-1	Glutaminase kidney isoform, mitochondrial	GLS	0.68	1.28	0.93	1.08	0.96	0.30	10	19	2.45E-103

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P63104	14-3-3 protein zeta/delta	YWHAZ	0.77	0.80	1.32	0.76	0.96	0.31	25	78	0.00E+00
P04234	T-cell receptor T3 delta chain	CD3D	0.65	0.76	1.48	0.68	0.96	0.45	6	52	1.24E-78
P61923	Coatomer subunit zeta-1	CGI-120	1.05	1.10	0.74	1.35	0.96	0.20	4	25	8.15E-43
O60341-2	BRAF35-HDAC complex protein BHC110	AOF2	1.23		0.70	1.43	0.97	0.37	8	13	3.45E-68
Q06323	11S regulator complex subunit alpha	IFI5111	0.93		1.00	1.00	0.97	0.05	15	61	0.00E+00
P29084	General transcription factor IIE subunit 2	GTF2E2	0.92	1.01			0.97	0.06	2	9.3	4.00E-41
P49593	Ca(2+)/calmodulin-dependent protein kinase phosphatase	KIAA0015	1.02		0.91	1.10	0.97	0.08	8	32	9.79E-32
P298288	70 kDa peroxisomal membrane protein	ABCD3	1.06		0.87	1.15	0.97	0.13	8	17	1.97E-34
Q9BTV4	Protein LUMA	TMEM43	0.84		1.09	0.92	0.97	0.18	3	17	3.20E-17
Q53FI6	Transporter 2, ATP-binding cassette, sub-family B isoform 1 variant	DAAP-57C1.2-001		0.81	1.12	0.89	0.97	0.22	2	4.4	3.17E-20
Q7Z3K3-1	Pogo transposable element with ZNF domain	KIAA0461	0.97	0.96	0.97	1.03	0.97	0.01	8	8.9	3.93E-52
P24534	Elongation factor 1-beta	EEF1B	0.97	0.99	0.94	1.06	0.97	0.03	8	48	3.88E-121
B4DTG2	cDNA FLJ56389, highly similar to Elongation factor 1-gamma	EEF1G	0.98	1.00	0.92	1.09	0.97	0.04	25	59	0.00E+00
Q8NF37	1-acylglycerophosphocholine O-acyltransferase	AYTL2	1.02	0.96	0.92	1.09	0.97	0.05	4	9.9	3.77E-77
A8MVV7	60S ribosomal protein L7	RPL7	0.98	1.01	0.91	1.10	0.97	0.05	21	49	4.62E-175
A6NFN2	Putative uncharacterized protein ABI1	ABI1	1.00	1.00	0.90	1.11	0.97	0.06	4	12	6.50E-33
O00178	GTP-binding protein 1	GTPBP1	0.89	0.95	1.06	0.94	0.97	0.09	2	4	1.23E-19
P31939	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase	ATIC	1.02	1.02	0.86	1.16	0.97	0.09	36	76	0.00E+00
Q5LJA9	Ubiquitin carboxyl-terminal hydrolase L5	RP11-101E13.2-006	1.01	1.04	0.85	1.18	0.97	0.10	9	33	1.53E-86
Q5SRQ6	Casein kinase 2 beta polypeptide	CSNK2B	0.97	0.85	1.08	0.93	0.97	0.12	7	35	2.01E-99
A2A284	Phospholipase C,	hCG_20	0.85	1.09	0.96	1.04	0.97	0.12	11	13	1.67E-98

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	gamma 1	18597									
Q6P2E9-1	Autoantigen Ge-1	EDC4	0.86	0.94	1.10	0.91	0.97	0.12	21	23	5.52E-179
P22307-1	Non-specific lipid-transfer protein	SCP2	0.85	0.95	1.10	0.91	0.97	0.13	13	16	1.33E-78
Q9UBB4	Ataxin-10	ATXN10	1.01	1.07	0.82	1.22	0.97	0.13	10	26	2.81E-227
B4DLZ5	cDNA FLJ56394, highly similar to N-acetylglucosamine kinase (EC 2.7.1.59)	hCG_41008	0.89	0.86	1.15	0.87	0.97	0.16	9	27	6.19E-37
Q8WXX5	DnaJ homolog subfamily C member 9	DNAJC9	0.90	0.85	1.15	0.87	0.97	0.16	16	57	1.09E-122
Q96GM5-1	60 kDa BRG-1/Brm-associated factor subunit A	BAF60A	0.74	1.00	1.16	0.86	0.97	0.21	6	15	4.37E-100
Q9UNH7	Sorting nexin-6	SNX6	0.88	0.81	1.21	0.83	0.97	0.21	6	17	3.87E-81
P31937	3-hydroxyisobutyrate dehydrogenase, mitochondrial	HIBADH	0.73	0.90	1.27	0.79	0.97	0.28	7	27	1.23E-155
Q9NQI0-1	DEAD box protein 4	DDX4	0.96	0.93	1.01	0.99	0.97	0.04	3	4.1	1.05E-04
Q53GS9	Inactive ubiquitin-specific peptidase 39	CGI-21	0.96	0.93	1.01	0.99	0.97	0.04	10	25	3.56E-95
Q92804-1	68 kDa TATA-binding protein-associated factor	RBP56	0.90	0.99	1.01	0.99	0.97	0.06	11	23	1.17E-166
Q16186	110 kDa cell membrane glycoprotein	ADRM1	0.90	1.01	0.99	1.01	0.97	0.06	9	20	1.05E-90
Q7Z5K2-3	Friend of EBNA2 protein	FOE	1.03	0.90	0.97	1.03	0.97	0.07	7	9.1	6.01E-59
P35269	General transcription factor IIF 74 kDa subunit	GTF2F1	0.91	0.94	1.05	0.95	0.97	0.07	10	23	7.63E-201
C9JE52	Putative uncharacterized protein PSME2	PSME2	0.88	1.01	1.01	0.99	0.97	0.08	9	40	1.89E-152
P62158	Calmodulin	CALM	0.89	0.93	1.08	0.93	0.97	0.10	7	53	8.59E-249
P60891	Phosphoribosyl pyrophosphate synthase I	PRPS1	0.90	0.91	1.09	0.92	0.97	0.11	13	44	1.80E-159
P21333-1	Actin-binding protein 280	FLN	0.89	0.91	1.10	0.91	0.97	0.12	##	57	0.00E+00
Q9UBQ0-2	PEP11 homolog	DC15	1.03	1.11	0.76	1.32	0.97	0.18	6	35	5.49E-37
P49915	Glutamine amidotransferase	GMPS	1.12	1.03	0.75	1.33	0.97	0.19	28	55	0.00E+00
Q14155-5	Beta-Pix	ARHGEF7	0.79	0.91	1.20	0.83	0.97	0.21	8	14	2.95E-42
B7Z7I3	DnaJ homolog subfamily B member	DNAJB12	1.00	1.20	0.70	1.43	0.97	0.25	4	14	3.04E-12

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	12										
O75113	NEDD4-binding protein 1	KIAA0615	0.99	1.02	0.90	1.11	0.97	0.06	3	5.1	1.16E-05
P78527-1	DNA-dependent protein kinase catalytic subunit	HYRC	1.03	1.06	0.82	1.22	0.97	0.13	80	24	0.00E+00
P12270	Nucleoprotein TPR	TPR	0.99	1.10	0.82	1.22	0.97	0.14	55	30	0.00E+00
Q9NVS9	Pyridoxamine-phosphate oxidase	PNPO	1.23	0.78	0.90	1.11	0.97	0.23	9	49	1.15E-48
Q9BRP4-1	Proteasomal ATPase-associated factor 1	PAAF1	1.17	1.22	0.52	1.92	0.97	0.39	2	6.1	3.55E-10
Q99633-1	Pre-mRNA-splicing factor 18	HPRP18	0.96		0.98	1.02	0.97	0.01	2	7	1.22E-18
Q9NR46-2	Endophilin-B2	KIAA1848	1.01	0.93			0.97	0.06	3	8.9	4.79E-09
Q8WUA4-1	General transcription factor 3C polypeptide 2	GTF3C2		1.02	0.92	1.09	0.97	0.07	5	7.8	2.83E-07
B7ZLH8	EVPL protein	EVPL	0.92	1.02			0.97	0.07	3	1.7	8.13E-03
O95926	CCNDBP1-interactor	CBPIN	1.09		0.85	1.18	0.97	0.17	4	21	2.51E-19
Q9UKF6	Cleavage and polyadenylation specificity factor 73 kDa subunit	CPSF3	1.09		0.85	1.18	0.97	0.17	5	8.2	1.57E-09
Q9UGP8	Translocation protein SEC63 homolog	SEC63		1.11	0.83	1.20	0.97	0.20	5	6.3	1.44E-36
Q06547-1	GA-binding protein subunit beta-1	E4TF1B	0.83	1.11			0.97	0.20	2	4.8	7.47E-05
Q13459-1	Myosin-IXb	MYO9B		0.82	1.12	0.89	0.97	0.21	2	1.3	5.28E-05
Q8NB37-1	Parkinson disease 7 domain-containing protein 1	PDDC1	1.13		0.81	1.23	0.97	0.23	4	33	8.36E-33
Q9HD15	Steroid receptor RNA activator 1	PP7684		1.19	0.75	1.33	0.97	0.31	2	10	1.13E-18
Q6NUK1-1	Calcium-binding mitochondrial carrier protein SCaMC-1	APC1		0.65	1.29	0.78	0.97	0.45	2	6.1	2.90E-26
Q5T5Y3-3	Calmodulin-regulated spectrin-associated protein 1	CAMSAP1			0.97	1.03	0.97		2	2	5.88E-02
Q6XQN6	FHA-HIT-interacting protein	FHIP			0.97	1.03	0.97		4	10	8.05E-38
Q01658	Down-regulator of transcription 1	DR1	0.97				0.97		2	27	6.52E-35
Q9H6S0	Probable ATP-dependent RNA helicase YTHDC2	YTHDC2		0.97			0.97		2	1.6	9.71E-24
P57075-1	Cbl-interacting protein 4	STS2		0.97			0.97		2	3.5	2.02E-15
Q9GZQ	COMM domain-	COMM	0.97				0.97		2	13	2.66E-41

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3	containing protein 5	D5									
P37275	Negative regulator of IL2	AREB6	0.97				0.97		2	2.2	9.10E-05
Q6P4F7	Rho GTPase-activating protein 11A	ARHGAP11A		0.97			0.97		2	2.3	7.78E-05
P55196-5	Afadin	AF6		0.97			0.97		2	1.2	1.36E-14
Q96BZ8	Leukocyte receptor cluster member 1	LENG1	0.97				0.97		4	14	2.09E-39
Q96P92	MBNL protein	hCG_28028	0.97				0.97		6	20	4.20E-17
A6NJG9	Putative uncharacterized protein PSME1	PSME1		0.97			0.97		10	47	2.93E-84
P27797	Calregulin	CALR	0.97	0.98	0.96	1.04	0.97	0.01	24	70	0.00E+00
A8MYA5	Deubiquitinating enzyme 14	TGT	0.96	0.96	0.99	1.01	0.97	0.02	20	44	1.17E-140
Q9UBQ7	Glyoxylate reductase/hydroxypyruvate reductase	GLXR	0.98	0.99	0.94	1.06	0.97	0.03	11	50	2.41E-304
Q08945	Chromatin-specific transcription elongation factor 80 kDa subunit	FACT80	0.96	1.00	0.95	1.05	0.97	0.03	22	32	4.54E-212
B0YIW6	Archain 1, isoform CRA_a	ARCN1	0.97	0.94	1.00	1.00	0.97	0.03	15	34	4.70E-147
P40938	Activator 1 38 kDa subunit	RFC3	0.95	1.01	0.95	1.05	0.97	0.03	13	46	5.68E-233
O60884	Cell cycle progression restoration gene 3 protein	CPR3	0.94	0.96	1.01	0.99	0.97	0.04	10	31	1.01E-75
Q9UBV8	PEF protein with a long N-terminal hydrophobic domain	ABP32	1.00	0.98	0.93	1.08	0.97	0.04	5	27	3.72E-35
P35659	Protein DEK	DEK	0.92	1.00	0.99	1.01	0.97	0.04	11	26	1.48E-38
Q96KB5	Cancer/testis antigen 84	PBK	0.93	0.96	1.02	0.98	0.97	0.05	5	18	1.19E-22
Q8IY71	MRPS17 protein	MRPS17	0.96	1.02	0.93	1.08	0.97	0.05	2	17	1.39E-08
Q86WJ1-1	Amplified in liver cancer protein 1	ALC1	1.03	0.94	0.94	1.06	0.97	0.05	11	14	1.92E-39
O75792	Aicardi-Goutieres syndrome 4 protein	RNASEH2A	1.01	0.99	0.91	1.10	0.97	0.05	15	52	1.39E-163
Q9NQS7-1	Inner centromere protein	INCENP	1.01	1.01	0.89	1.12	0.97	0.07	16	22	1.66E-99
Q14103-3	AU-rich element RNA-binding protein 1	AUF1	0.92	0.94	1.05	0.95	0.97	0.07	23	55	0.00E+00
Q16539-1	Cytokine suppressive anti-inflammatory drug-binding protein	CSBP	1.05	0.94	0.92	1.09	0.97	0.07	13	54	2.43E-89
Q13867	Bleomycin hydrolase	BLMH	0.97	0.90	1.04	0.96	0.97	0.07	5	13	8.67E-24

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Q92785	Apoptosis response zinc finger protein	BAF45D	0.89	0.98	1.04	0.96	0.97	0.08	7	27	4.56E-95
O75400-2	Fas ligand-associated factor 1	FBP11	0.92	0.91	1.08	0.93	0.97	0.10	16	16	5.52E-99
O43395-1	Pre-mRNA-splicing factor 3	HPRP3	0.93	0.89	1.09	0.92	0.97	0.11	11	19	1.67E-84
O94842	Epidermal Langerhans cell protein LCP1	C14orf92	0.97	0.86	1.08	0.93	0.97	0.11	3	5.8	6.90E-23
Q15257-2	Phosphotyrosyl phosphatase activator	PPP2R4	1.01	0.84	1.06	0.94	0.97	0.12	8	34	7.39E-30
P07737	Profilin I	PFN1	0.92	0.88	1.11	0.90	0.97	0.12	15	75	0.00E+00
Q06830	Natural killer cell-enhancing factor A	PAGA	0.92	0.88	1.11	0.90	0.97	0.12	21	90	5.33E-183
Q92614-1	Molecule associated with JAK3 N-terminus	KIAA0216	0.92	0.86	1.13	0.88	0.97	0.14	22	13	6.10E-250
Q96JB5-1	CDK5 activator-binding protein C53	CDK5RAP3	1.12	0.96	0.83	1.20	0.97	0.15	7	14	2.08E-47
Q9UDR5	Alpha-aminoadipic semialdehyde synthase, mitochondrial	AASS	1.06	1.06	0.79	1.27	0.97	0.16	5	8.6	1.44E-11
P46776	60S ribosomal protein L27a	RPL27A	1.06	1.06	0.79	1.27	0.97	0.16	7	38	8.81E-132
Q9NTK5-1	GTP-binding protein 9	GTPBP9	1.03	1.09	0.79	1.27	0.97	0.16	9	30	2.44E-64
Q75MJ1	ATP-binding cassette, sub-family F (GCN20), member 2, isoform CRA_d	ABCF2	1.10	1.03	0.78	1.28	0.97	0.17	6	12	2.38E-30
P82914	28S ribosomal protein S15, mitochondrial	DC37	0.84	0.89	1.18	0.85	0.97	0.18	5	18	1.74E-08
Q04917	14-3-3 protein eta	YWHA1	0.84	0.87	1.20	0.83	0.97	0.20	19	76	3.41E-302
Q8N2K0-2	2-arachidonoylglycerol hydrolase	ABHD12	0.68	1.16	1.07	0.93	0.97	0.26	2	7.7	2.60E-05
P31146	Coronin-1A	CORO1	0.81	0.83	1.27	0.79	0.97	0.26	30	60	1.09E-295
Q2TAL8	Glutamine-rich protein 1	QRICH1	0.87	0.77	1.27	0.79	0.97	0.26	8	14	8.24E-62
Q9UI30	TRM112-like protein	AD-001	1.19	1.21	0.51	1.96	0.97	0.40	6	59	2.98E-82
Q9UBT2	Anthracycline-associated resistance ARX	HRIHFB2115	0.78	0.70	1.43	0.70	0.97	0.40	17	43	1.48E-118
Q13243-1	Delayed-early protein HRS	HRS	0.98	0.99	0.95	1.05	0.97	0.02	7	25	3.38E-59
Q15459	Spliceosome-associated protein 114	SAP114	0.95	0.97	1.00	1.00	0.97	0.03	28	40	3.40E-241
Q5JWU6	Tumor protein D52-like 2	hCG_22755	0.97	1.00	0.95	1.05	0.97	0.03	10	51	1.52E-206
Q13111-1	Chromatin assembly factor 1 subunit A	CAF	0.97	1.00	0.95	1.05	0.97	0.03	12	21	1.39E-169
Q13435	Pre-mRNA-splicing	SAP145	0.97	1.00	0.95	1.05	0.97	0.03	32	42	1.69E-240

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	factor SF3b 145 kDa subunit										
B2R5Y4	cDNA, FLJ92684, highly similar to Homo sapiens IK cytokine, down-regulator of HLA II (IK), mRNA	IK	1.01	0.93	0.98	1.02	0.97	0.04	8	17	7.37E-41
Q9NZ52-1	ADP-ribosylation factor-binding protein GGA3	GGA3	0.96	1.02	0.94	1.06	0.97	0.04	7	14	8.30E-20
P26373	60S ribosomal protein L13	BBC1	0.98	1.02	0.92	1.09	0.97	0.05	17	49	1.86E-137
B4DRE5	cDNA FLJ55391	FAM54B	0.94	0.94	1.04	0.96	0.97	0.06	2	5.5	3.25E-17
Q99704-1	Docking protein 1	DOK1	0.94	0.94	1.04	0.96	0.97	0.06	3	13	1.70E-19
A6NFX8	Putative uncharacterized protein NUDT5	NUDT5	1.00	1.02	0.90	1.11	0.97	0.06	12	55	1.75E-115
Q3B726	DNA-directed RNA polymerase I subunit RPA43	TWISTNB	1.04	0.91	0.97	1.03	0.97	0.07	2	7.7	4.75E-08
P25789	Macropain subunit C9	HC9	0.91	0.96	1.05	0.95	0.97	0.07	11	56	6.52E-135
Q9HB07	UPF0160 protein MYG1, mitochondrial	C12orf10	1.06	0.94	0.92	1.09	0.97	0.08	8	28	1.27E-49
P42768	Wiskott-Aldrich syndrome protein	IMD2	0.88	1.04	1.00	1.00	0.97	0.08	3	10	1.76E-57
Q5VTR2	E3 ubiquitin-protein ligase BRE1A	BRE1A	0.91	0.94	1.07	0.93	0.97	0.09	16	23	2.43E-194
O95747	Oxidative stress-responsive 1 protein	KIAA1101	0.95	0.90	1.07	0.93	0.97	0.09	9	24	1.34E-94
P21291	Cysteine and glycine-rich protein 1	CSRP	0.87	1.07	0.98	1.02	0.97	0.10	3	28	4.28E-15
Q9NSE4	Isoleucine--tRNA ligase	IARS2	0.93	0.90	1.09	0.92	0.97	0.10	20	23	2.40E-106
Q9Y490	Talin-1	KIAA1027	0.90	0.93	1.09	0.92	0.97	0.10	85	52	0.00E+00
P11586	C-1-tetrahydrofolate synthase, cytoplasmic	MTHFC	1.04	1.04	0.84	1.19	0.97	0.12	47	52	0.00E+00
Q9NZT2-1	Opioid growth factor receptor	OGFR	0.91	1.11	0.90	1.11	0.97	0.12	13	28	4.90E-150
P08621-1	U1 small nuclear ribonucleoprotein 70 kDa	RNPU1Z	0.88	0.93	1.11	0.90	0.97	0.12	17	31	7.44E-100
P62829	60S ribosomal protein L17	RPL23	1.08	1.01	0.83	1.20	0.97	0.13	5	40	2.60E-94
B2RDK6	cDNA, FLJ96656, highly similar to Homo sapiens SPFH domain family, member 1 (SPFH1), mRNA	C10orf69	1.09	1.01	0.82	1.22	0.97	0.14	8	22	1.22E-90

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P49354-1	CAAX farnesyltransferase subunit alpha	FNTA	1.08	0.79	1.05	0.95	0.97	0.16	5	17	6.45E-250
P62263	40S ribosomal protein S14	PRO2640	1.06	1.08	0.78	1.28	0.97	0.17	11	69	1.56E-230
Q9Y3X0	Coiled-coil domain-containing protein 9	CCDC9	0.96	1.15	0.81	1.23	0.97	0.17	3	6	3.46E-15
P40925	Cytosolic malate dehydrogenase	MDH1	0.86	0.89	1.17	0.85	0.97	0.17	13	42	3.68E-160
O75964	ATP synthase subunit g, mitochondrial	ATP5L	1.02	1.12	0.78	1.28	0.97	0.17	4	48	1.60E-40
Q9H2W6	39S ribosomal protein L46, mitochondrial	C15orf4	0.85	0.87	1.20	0.83	0.97	0.20	7	35	1.04E-74
A8MYY8	Actin-related protein 2/3 complex subunit 3	ARC21	0.77	0.96	1.19	0.84	0.97	0.21	4	26	3.15E-29
Q8NDH8	Chromosome transmission fidelity protein 8 homolog	CHTF8	0.90	0.77	1.25	0.80	0.97	0.25	7	22	3.05E-30
O95319-4	Bruno-like protein 3	BRUNOL3	0.86	0.79	1.27	0.79	0.97	0.26	8	17	9.29E-171
Q9NXV6	CDKN2A-interacting protein	CARF	0.84	0.80	1.28	0.78	0.97	0.27	12	29	9.29E-129
P36639-1	7,8-dihydro-8-oxoguanine triphosphatase	MTH1	0.80	0.83	1.29	0.78	0.97	0.27	5	27	1.34E-62
P53701	Cytochrome c-type heme lyase	CCHL	1.07	1.22	0.63	1.59	0.97	0.31	3	13	6.36E-17
Q9NWB6-1	Arginine and glutamate-rich protein 1	ARGLU1	0.62	0.87	1.43	0.70	0.97	0.41	5	15	3.61E-06
O60664-1	47 kDa mannose 6-phosphate receptor-binding protein	M6PRBP1	0.67	0.73	1.52	0.66	0.97	0.47	18	63	4.83E-279
Q5TDF0	Chromosome 1 open reading frame 57	C1orf57		1.13	0.82	1.22	0.98	0.22	4	25	4.86E-34
Q00765	Polyposis locus protein 1	C5orf18	0.99	0.96			0.98	0.02	3	11	1.53E-08
B4E1X0	cDNA FLJ61047, weakly similar to Homo sapiens RAS and EF-hand domain containing (RASEF), mRNA	EFCAB4B		0.81	1.14	0.88	0.98	0.23	2	4.5	1.82E-06
Q96BM9	ADP-ribosylation factor-like protein 10B	ARL10B	1.14	0.81			0.98	0.23	5	37	1.31E-12
Q9Y2U5	MAPK/ERK kinase kinase 2	MAP3K2		1.02	0.93	1.08	0.98	0.06	2	3.4	3.24E-05
Q9UNF0-1	Protein kinase C and casein kinase substrate in neurons protein 2	PACSIN2		0.91	1.04	0.96	0.98	0.09	2	4.1	1.03E-07
P39880-3	CCAAT displacement protein	CUTL1		0.91	1.04	0.96	0.98	0.09	5	4.2	3.03E-20
P80217-	Interferon-induced 35	IFI35		1.05	0.90	1.11	0.98	0.11	7	27	1.72E-53

UniProt ID	**Protein_Name**	**Gene Name**	**F1 (L/H)**	**F2 (L/H)**	**R1 (H/L)**	**R1 (L/H)**	**Mean (T/U)**	**S.D.**	**Pep. No.**	**%Seq. Cov.**	**PEP**
1	kDa protein										
P61513	60S ribosomal protein L37a	RPL37A	0.89	1.06			0.98	0.12	5	51	2.75E-54
Q92540-4	EST1-like protein C	C1orf16		0.84	1.11	0.90	0.98	0.19	2	2.8	6.73E-06
P13639	Elongation factor 2	EEF2	0.97	0.98	0.98	1.02	0.98	0.01	63	73	0.00E+00
Q9Y2W2	Npw38-binding protein	NPWBP	0.97	0.96	1.00	1.00	0.98	0.02	13	26	3.11E-56
B5BU19	SHC-transforming protein 1	SHC1	0.99	0.99	0.95	1.05	0.98	0.02	2	9.8	1.23E-35
Q9NTX5-1	Enoyl-CoA hydratase domain-containing protein 1	ECHDC1	0.95	1.02	0.96	1.04	0.98	0.04	8	35	1.78E-162
P78417	Glutathione S-transferase omega-1	GSTO1	0.93	0.99	1.01	0.99	0.98	0.04	14	51	2.71E-73
O95674-1	CDP-DAG synthase 2	CDS2	0.99	1.02	0.92	1.09	0.98	0.05	2	11	4.17E-15
P62249	40S ribosomal protein S16	RPS16	1.03	0.98	0.92	1.09	0.98	0.06	9	50	3.47E-34
P51991-1	Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	0.91	1.01	1.01	0.99	0.98	0.06	22	44	1.84E-298
Q8WXE0	Caskin-2	CASKIN2	0.95	0.93	1.05	0.95	0.98	0.06	2	3.7	3.10E-04
B4DVA7	cDNA FLJ53927, highly similar to Beta-hexosaminidase alpha chain (EC 3.2.1.52)	HEXA	1.04	0.90	0.99	1.01	0.98	0.07	3	10	8.76E-19
P48643	CCT-epsilon	CCT5	1.03	1.02	0.88	1.14	0.98	0.08	37	73	0.00E+00
Q9HB71-1	Calcyclin-binding protein	CACYBP	1.07	1.02	0.84	1.19	0.98	0.12	17	62	1.01E-202
P10644	cAMP-dependent protein kinase type I-alpha regulatory subunit	PKR1	0.87	0.91	1.15	0.87	0.98	0.15	9	29	5.79E-100
Q6LES2	Annexin A4	ANXA4	0.86	0.91	1.16	0.86	0.98	0.16	6	21	2.59E-153
P52907	F-actin-capping protein subunit alpha-1	CAPZA1	0.85	0.92	1.16	0.86	0.98	0.16	14	70	2.62E-224
Q9MYF2	MHC class I antigen B	HLA-B	0.83	0.92	1.18	0.85	0.98	0.18	7	47	3.79E-66
P62306	Sm protein F	PBSCF	1.04	1.14	0.75	1.33	0.98	0.20	5	50	1.38E-92
Q9Y2U8	Inner nuclear membrane protein Man1	LEMD3	0.74	1.05	1.14	0.88	0.98	0.21	2	2.1	8.14E-03
P32119	Natural killer cell-enhancing factor B	NKEFB	0.86	0.85	1.22	0.82	0.98	0.21	16	68	1.43E-210
P16949	Leukemia-associated phosphoprotein p18	LAP18	0.81	0.90	1.22	0.82	0.98	0.22	15	62	1.80E-139
O14828-1	Secretory carrier-associated membrane protein 3	C1orf3	1.15	1.06	0.72	1.39	0.98	0.23	5	27	7.49E-75
P35573-	4-alpha-	AGL	1.06	1.15	0.72	1.39	0.98	0.23	7	7.1	2.44E-80

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1	glucanotransferase										
Q9BTT0	Acidic leucine-rich nuclear phosphoprotein 32 family member E	ANP32E	0.82	0.87	1.24	0.81	0.98	0.23	7	30	0.00E+00
Q6MZT3	Putative uncharacterized protein DKFZp686C1054	DKFZp686C1054	0.81	0.84	1.28	0.78	0.98	0.26	4	12	8.92E-68
Q9NVA2-2	Septin-11	41163	0.85	0.80	1.28	0.78	0.98	0.26	10	23	2.74E-148
O60573	eIF4E-like protein 4E-LP	EIF4E2	1.31	0.90	0.72	1.39	0.98	0.30	7	40	6.83E-34
Q92783-1	Signal transducing adapter molecule 1	STAM	0.92	0.63	1.38	0.72	0.98	0.38	2	5.2	7.55E-18
O43707	Alpha-actinin-4	ACTN4	0.72	0.75	1.46	0.68	0.98	0.42	54	67	0.00E+00
Q9H7N4	Serine arginine-rich pre-mRNA splicing factor SR-A1	SCAF1	1.47	0.89	0.57	1.75	0.98	0.46	2	3	7.25E-15
P20810-6	Calpain inhibitor	CAST	0.57	0.72	1.64	0.61	0.98	0.58	5	8.3	4.61E-14
Q13330-1	Metastasis-associated protein MTA1	MTA1	0.92	1.05	0.96	1.04	0.98	0.07	11	18	3.34E-73
P62277	40S ribosomal protein S13	RPS13	0.98	1.05	0.90	1.11	0.98	0.08	8	46	3.03E-124
P62241	40S ribosomal protein S8	OK/SW-cl.83	1.04	1.00	0.89	1.12	0.98	0.08	12	59	1.49E-266
Q7RTV0	PHD finger-like domain-containing protein 5A	PHF5A	0.96	0.89	1.08	0.93	0.98	0.10	5	42	1.89E-56
Q9UKY7-1	Protein CDV3 homolog	CDV3	0.95	1.09	0.89	1.12	0.98	0.10	8	63	2.26E-52
P43686-1	26S protease regulatory subunit 6B	MIP224	1.00	1.07	0.86	1.16	0.98	0.11	21	60	0.00E+00
B4E0Q6	cDNA FLJ60209, highly similar to Transcriptional repressor p66 alpha	GATAD2A	0.89	0.94	1.10	0.91	0.98	0.11	12	24	1.61E-50
Q9NUP9	Mammalian lin-seven protein 3	LIN7C	1.01	1.10	0.82	1.22	0.98	0.14	4	22	5.85E-14
Q96I25	45 kDa-splicing factor	RBM17	0.83	1.12	0.98	1.02	0.98	0.15	6	15	3.45E-12
O15533-3	NGS-17	NGS17	1.26	0.77	0.90	1.11	0.98	0.25	5	14	3.91E-21
P82979	Cytokine-induced protein of 29 kDa	HSPC316	0.82	0.94	1.18	0.85	0.98	0.18	6	16	1.22E-158
Q3KQZ2	SYNGR2 protein	SYNGR2	0.97	1.17	0.8	1.25	0.98	0.19	3	10	6.76E-08
P49917	DNA ligase 4	LIG4		0.99	0.97	1.03	0.98	0.01	2	2.4	1.49E-16
P22059-1	Oxysterol-binding protein 1	OSBP	0.98	0.96	1.00	1.00	0.98	0.02	9	18	4.04E-94
Q86YH3	EARS2 protein	EARS2	0.96	1.00			0.98	0.03	2	3.4	8.49E-05

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P10412	Histone H1.4	H1F4	0.96	1.00			0.98	0.03	15	41	2.44E-213
Q9NQG5	Cell cycle-related and expression-elevated protein in tumor	C20orf77	0.95	0.98	1.01	0.99	0.98	0.03	12	50	1.90E-187
Q86XP3-1	ATP-dependent RNA helicase DDX42	DDX42	0.95	0.98	1.01	0.99	0.98	0.03	21	35	6.59E-188
O60264	Sucrose nonfermenting protein 2 homolog	SMARCA5	0.95	0.98	1.01	0.99	0.98	0.03	35	33	1.03E-234
O95429	BAG family molecular chaperone regulator 4	BAG4	0.96	1.02	0.96	1.04	0.98	0.03	2	5.3	2.03E-17
Q16878	Cysteine dioxygenase type 1	CDO1	0.96	1.02	0.96	1.04	0.98	0.03	2	7.5	1.71E-02
Q9BW85	Coiled-coil domain-containing protein 94	CCDC94	0.96	1.02	0.96	1.04	0.98	0.03	5	23	3.57E-21
Q8IXQ4-1	Lipopolysaccharide-specific response protein 7	AD029	0.96	1.02	0.96	1.04	0.98	0.03	5	14	5.33E-11
B1AK88	Capping protein (Actin filament) muscle Z-line, beta	CAPZB	0.96	1.02	0.96	1.04	0.98	0.03	27	54	0.00E+00
P55789	Augmenter of liver regeneration	ALR	1.00	1.00	0.94	1.06	0.98	0.03	3	13	2.34E-32
Q96F07-2	Cytoplasmic FMR1-interacting protein 2	CYFIP2	1.00	1.00	0.94	1.06	0.98	0.03	6	5.5	1.19E-17
Q8IVD9	NudC domain-containing protein 3	KIAA1068	0.98	1.02	0.94	1.06	0.98	0.04	2	6.9	1.83E-11
B7Z5E3	L-lactate dehydrogenase	LDHA	1.00	1.01	0.93	1.08	0.98	0.04	29	81	0.00E+00
P62913-1	60S ribosomal protein L11	RPL11	0.93	1.03	0.98	1.02	0.98	0.05	8	48	7.63E-119
P78371	CCT-beta	99D8.1	1.01	1.01	0.92	1.09	0.98	0.05	38	75	0.00E+00
Q15631	Translin	TSN	0.96	0.94	1.04	0.96	0.98	0.05	9	44	1.30E-149
Q5HY81	Ubiquitin-like 4A	UBL4A	1.00	0.92	1.02	0.98	0.98	0.05	3	19	8.14E-45
Q96SZ5	2-aminoethanethiol dioxygenase	ADO		1.02	0.94	1.06	0.98	0.06	5	22	8.33E-91
Q9BRA2	14 kDa thioredoxin-related protein	TXNDC17	1.03	1.05	0.86	1.16	0.98	0.10	4	38	4.77E-51
P62854	40S ribosomal protein S26	RPS26	1.06	1.02	0.86	1.16	0.98	0.11	2	21	1.80E-29
Q8NB15-2	Zinc finger protein 511	ZNF511	1.05	1.05	0.84	1.19	0.98	0.12	3	21	2.54E-06
P50990	CCT-theta	C21orf112	1.02	1.08	0.84	1.19	0.98	0.12	42	85	0.00E+00
A2VCT3	OGDH protein	OGDH	0.86	0.96	1.12	0.89	0.98	0.13	11	13	2.73E-47
B4DE31	Transketolase	TKT	0.87	0.89	1.18	0.85	0.98	0.17	31	56	0.00E+00
Q9Y6D6	Brefeldin A-inhibited guanine nucleotide-exchange protein 1	ARFGEF1	0.90	0.86	1.18	0.85	0.98	0.17	4	3	5.44E-36
B4DT51	cDNA FLJ54848,	LENG5	1.12		0.84	1.19	0.98	0.20	2	8.7	1.10E-11

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	highly similar to tRNA-splicing endonuclease subunit Sen34 (EC 3.1.27.9)										
Q8IUF8-1	Mineral dust-induced gene protein	MDIG	1.12		0.84	1.19	0.98	0.20	7	22	1.53E-12
P54619	5-AMP-activated protein kinase subunit gamma-1	PRKAG1	0.82	0.91	1.21	0.83	0.98	0.20	3	9.1	1.08E-09
Q9BRF8-1	Calcineurin-like phosphoesterase domain-containing protein 1	CPPED1	0.85	0.87	1.22	0.82	0.98	0.21	4	20	1.62E-64
P13796	LC64P	LCP1	0.84	0.88	1.22	0.82	0.98	0.21	49	84	0.00E+00
P54727	UV excision repair protein RAD23 homolog B	RAD23B	1.07	1.14	0.73	1.37	0.98	0.22	11	40	6.79E-61
P52298-1	20 kDa nuclear cap-binding protein	CBP20	0.76	1.23	0.95	1.05	0.98	0.24	3	22	1.86E-20
C9JIF9	Putative uncharacterized protein APEH	APEH	0.81	0.88	1.25	0.80	0.98	0.24	9	17	1.77E-64
Q9UNX4	WD repeat-containing protein 3	WDR3	1.19	1.12	0.63	1.59	0.98	0.31	4	7.3	6.83E-31
P60981	Actin-depolymerizing factor	ACTDP	0.80	0.73	1.41	0.71	0.98	0.37	3	25	1.04E-31
P22033	Methylmalonyl-CoA isomerase	MUT	0.75	0.76	1.43	0.70	0.98	0.39	4	6.1	1.57E-11
P13804	Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	0.73	0.70	1.51	0.66	0.98	0.46	14	61	2.11E-242
P19793	Nuclear receptor subfamily 2 group B member 1	NR2B1			0.98	1.02	0.98		2	6.7	1.03E-21
P15531	Nucleoside-diphosphate kinase 7 isoform a variant	NME7a			0.98	1.02	0.98		2	8.5	7.85E-04
C9JCT9	Genetic suppressor element 1	GSE1			0.98	1.02	0.98		3	5.5	1.91E-05
Q9H223	EH domain-containing protein 4	EHD4			0.98	1.02	0.98		4	8.7	1.60E-18
Q9Y237-2	Parvulin-14	PIN4	0.98				0.98		2	15	1.73E-27
Q9NZD8	Acid cluster protein 33	ACP33	0.98				0.98		2	11	3.94E-12
A6NDU8	UPF0600 protein C5orf51	C5orf51	0.98				0.98		2	15	2.04E-29
Q9H8D6	cDNA FLJ13729 fis, clone PLACE3000121, weakly similar to VESICULAR TRAFFIC CONTROL PROTEIN SEC15	EXOC6B		0.98			0.98		2	2.2	2.41E-04

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P83881	60S ribosomal protein L36a	GIG15	0.98				0.98		4	38	2.03E-07
Q15435-1	Protein phosphatase 1 regulatory subunit 22	PPP1R7	1.00	1.03	0.91	1.10	0.98	0.06	6	20	5.17E-231
Q9H836	cDNA FLJ13963 fis, clone Y79AA1001299, highly similar to Homo sapiens integrase interactor 1b protein (INI1B)	BAF47	0.88	0.99	1.07	0.93	0.98	0.10	6	19	7.40E-93
Q9NUU7	ATP-dependent RNA helicase DDX19A	DDX19A	0.88	0.99	1.07	0.93	0.98	0.10	7	15	1.87E-62
Q9HAV4-1	Exportin-5	KIAA1291	1.03	1.04	0.87	1.15	0.98	0.10	16	18	4.38E-268
Q86W42-1	Functional spliceosome-associated protein 35	PSEC0006	0.94	0.91	1.09	0.92	0.98	0.10	9	36	1.49E-43
Q9BU89	Deoxyhypusine dioxygenase	DOHH	1.10	0.91	0.93	1.08	0.98	0.10	8	47	6.95E-93
Q13642-2	Four and a half LIM domains protein 1	FHL1	0.84	1.03	1.07	0.93	0.98	0.12	2	6.5	8.91E-06
B4DSZ4	Ubiquitin carrier protein	UBCE7	1.08	1.07	0.79	1.27	0.98	0.16	6	41	2.57E-63
A5YKK6-1	CCR4-associated factor 1	AD-005	1.04	1.12	0.78	1.28	0.98	0.18	10	5	4.51E-41
Q16269	RCC1-I	RCC1	1.01	1.04	0.90	1.11	0.98	0.07	10	34	1.03E-153
Q9Y2Z0-1	Protein 40-6-3	SUGT1	1.11	0.98	0.86	1.16	0.98	0.13	13	41	2.62E-245
Q16698	2,4-dienoyl-CoA reductase [NADPH]	DECR	0.82	0.94	1.19	0.84	0.98	0.19	8	31	1.45E-159
Q96MG7	Hepatocellular carcinoma-associated protein 4	HCA4	1.07	1.31	0.57	1.75	0.98	0.38	3	14	3.90E-42
Q12905	Interleukin enhancer-binding factor 2	ILF2	0.95	1.00	1.00	1.00	0.98	0.03	15	53	2.06E-171
O60499-1	Syntaxin-10	STX10	1.00	1.00	0.95	1.05	0.98	0.03	2	11	1.31E-56
Q13263-1	KRAB-associated protein 1	KAP1	0.96	1.02	0.97	1.03	0.98	0.03	30	45	2.35E-269
P83876	DIM1 protein homolog	DIM1	0.97	1.02	0.96	1.04	0.98	0.03	3	34	1.16E-33
A6NF09	Putative uncharacterized protein SRPK2	hCG_2013856	1.04	0.95	0.96	1.04	0.98	0.05	3	5.1	1.03E-06
O75663-1	Putative MAPK-activating protein PM10	TIPRL	0.99	0.93	1.03	0.97	0.98	0.05	11	54	2.34E-39
Q99832	HIV-1 Nef-interacting protein	CCT7	1.02	1.01	0.92	1.09	0.98	0.06	32	74	0.00E+00
B4DVB8	cDNA FLJ60076, highly similar to ELAV-like protein 1	ELAVL1	0.92	1.00	1.03	0.97	0.98	0.06	17	54	6.96E-158

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Q9NW13	RNA-binding motif protein 28	RBM28	1.00	1.03	0.92	1.09	0.98	0.06	19	29	3.60E-155
Q53FT3	Uncharacterized protein C11orf73	C11orf73	0.95	0.95	1.05	0.95	0.98	0.06	4	16	9.71E-44
Q13427-1	CASP10	PPIG	0.93	0.96	1.06	0.94	0.98	0.07	11	12	8.94E-36
Q6NVY1-1	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial	HIBCH	1.03	1.03	0.89	1.12	0.98	0.08	9	29	1.42E-95
P50991	Stimulator of TAR RNA-binding	CCT4	1.04	1.02	0.89	1.12	0.98	0.08	29	64	0.00E+00
O94979-8	ABP125	HSPC275	0.95	0.92	1.08	0.93	0.98	0.09	7	6.2	8.17E-24
Q9HCS7	Pre-mRNA-splicing factor SYF1	HCNP	0.90	0.97	1.08	0.93	0.98	0.09	15	23	3.81E-122
Q6UN15-1	Factor interacting with PAP	FIP1	0.95	0.91	1.09	0.92	0.98	0.09	10	28	2.88E-161
Q96GD0	Pyridoxal phosphate phosphatase	PDXP	1.01	0.87	1.07	0.93	0.98	0.10	8	37	1.52E-106
Q96NC0	Zinc finger matrin-type protein 2	ZMAT2	0.89	0.96	1.10	0.91	0.98	0.11	5	20	2.63E-07
Q9UI10-2	eIF-2B GDP-GTP exchange factor subunit delta	EIF2B4	1.06	1.04	0.85	1.18	0.98	0.12	6	20	1.29E-43
Q16718	Complex I subunit B13	NDUFA5	0.90	0.92	1.13	0.88	0.98	0.13	6	66	3.65E-107
P25440-2	Bromodomain-containing protein 2	BRD2	0.83	1.12	1	1.00	0.98	0.15	8	10	8.39E-33
P49770	eIF-2B GDP-GTP exchange factor subunit beta	EIF2B2	1.07	1.11	0.77	1.30	0.98	0.19	8	27	1.16E-68
Q06203	Amidophosphoribosyltransferase	GPAT	0.86	0.88	1.21	0.83	0.98	0.20	5	12	1.59E-73
P10515	70 kDa mitochondrial autoantigen of primary biliary cirrhosis	DLAT	0.84	0.89	1.22	0.82	0.98	0.21	10	21	1.20E-137
Q14684-1	Ribosomal RNA processing protein 1 homolog B	KIAA0179	1.16	1.05	0.74	1.35	0.98	0.22	15	24	2.23E-105
Q16543	Hsp90 chaperone protein kinase-targeting subunit	CDC37	1.04	1.17	0.74	1.35	0.98	0.22	16	43	1.68E-130
P61158	Actin-like protein 3	ACTR3	0.84	0.85	1.26	0.79	0.98	0.24	20	64	5.05E-186
P55327-3	Protein N8	TPD52	0.82	0.86	1.27	0.79	0.98	0.25	11	58	0.00E+00
Q9Y657	Ovarian cancer-related protein	OCR	0.83	0.84	1.28	0.78	0.98	0.26	3	18	2.87E-15
Q9UQE7	Basement membrane-associated chondroitin proteoglycan	BAM	0.81	0.82	1.32	0.76	0.98	0.29	39	38	0.00E+00
Q96GD4	Aurora- and IPL1-like midbody-associated protein 1	AIK2	0.97	1.30	0.68	1.47	0.98	0.31	6	22	3.70E-21

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Q9NUJ1	Abhydrolase domain-containing protein 10, mitochondrial	ABHD10	0.77	0.71	1.47	0.68	0.98	0.42	4	20	1.92E-126
Q9UBL3-1	ASH2-like protein	ASH2L		0.99	0.98	1.02	0.99	0.01	2	5.9	3.43E-66
O94992	Cardiac lineage protein 1	CLP1	1.00	0.97			0.99	0.02	2	8.6	8.94E-30
P30043	Biliverdin reductase B	BLVRB	0.97	1.00			0.99	0.02	2	12	8.90E-33
Q8N490-2	Myofibrillogenesis regulator 1	FKSG19	1.00	0.97			0.99	0.02	3	30	5.87E-09
P68133	Actin, alpha skeletal muscle	ACTA	1.00	0.97			0.99	0.02	19	41	9.84E-267
C9J9R3	Cyclophilin J	PPIL3		0.95	1.02	0.98	0.99	0.05	2	21	2.59E-03
A6NMN0	Putative uncharacterized protein PHKA1	PHKA1		0.81	1.16	0.86	0.99	0.25	2	1.9	1.24E-19
Q9UMR2-1	ATP-dependent RNA helicase DDX19B	DBP5	0.74		1.23	0.81	0.99	0.35	6	13	7.99E-50
Q9Y4P3	Transducin beta-like protein 2	TBL2		1.06	0.91	1.10	0.99	0.11	2	5.6	1.69E-78
P22694-1	cAMP-dependent protein kinase catalytic subunit beta	PRKACB	0.89	1.08			0.99	0.13	9	27	2.51E-41
P01111	GTPase NRas	HRAS1	0.85		1.12	0.89	0.99	0.19	6	44	1.82E-31
Q8IWA0	WD repeat-containing protein 75	WDR75	1.34		0.63	1.59	0.99	0.50	3	5.4	1.07E-35
P18669	BPG-dependent PGAM 1	CDABP0006	0.99	0.96	1.01	0.99	0.99	0.03	20	81	0.00E+00
Q14168-3	Discs large homolog 2	DLG2	0.97	1.02	0.97	1.03	0.99	0.03	2	3.7	3.36E-04
P49327	[Acyl-carrier-protein] S-acetyltransferase	FAS	0.97	1.02	0.97	1.03	0.99	0.03	49	29	0.00E+00
Q15369	Elongin 15 kDa subunit	TCEB1	1.01	1.00	0.95	1.05	0.99	0.03	5	41	4.00E-59
Q7KZF4	100 kDa coactivator	SND1	0.97	1.03	0.96	1.04	0.99	0.04	42	52	0.00E+00
O96000	Complex I-PDSW	NDUFB10	1.01	1.01	0.94	1.06	0.99	0.04	4	29	1.50E-35
P49711	11-zinc finger protein	CTCF	0.94	1.04	0.98	1.02	0.99	0.05	8	12	1.05E-33
B4DRY3	cDNA FLJ52228, highly similar to Mps one binder kinase activator-like 1A	C2orf6	0.92	1.00	1.04	0.96	0.99	0.06	5	25	7.90E-48
Q5TDH0-1	Protein DDI1 homolog 2	DDI2	0.95	0.95	1.06	0.94	0.99	0.06	11	47	3.23E-126
Q15084-2	Protein disulfide isomerase P5	PDIA6	1.03	1.02	0.91	1.10	0.99	0.07	15	43	0.00E+00
O00231	26S proteasome non-ATPase regulatory subunit 11	PSMD11	1.00	1.05	0.91	1.10	0.99	0.07	18	46	1.67E-177
Q96F86	Enhancer of mRNA-decapping protein 3	EDC3	1.05	1.01	0.90	1.11	0.99	0.08	5	15	2.19E-54

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Q9NR31	COPII-associated small GTPase	SAR1	0.96	0.92	1.08	0.93	0.99	0.08	11	74	8.17E-158
P52566	Rho GDP-dissociation inhibitor 2	ARHGDIB	0.97	0.91	1.08	0.93	0.99	0.09	17	67	0.00E+00
Q8IY67-2	Protein raver-1	KIAA1978	1.03	1.05	0.88	1.14	0.99	0.09	14	37	5.45E-168
O94874	E3 UFM1-protein ligase 1	KIAA0776	0.92	0.93	1.11	0.90	0.99	0.11	9	13	4.78E-111
Q15233	54 kDa nuclear RNA- and DNA-binding protein	NONO	0.94	0.91	1.11	0.90	0.99	0.11	34	62	3.83E-271
Q08752	40 kDa peptidyl-prolyl cis-trans isomerase	CYP40	1.04	1.06	0.86	1.16	0.99	0.11	13	35	2.90E-86
Q9H4A6	Coat protein GPP34	GOLPH3	0.93	0.91	1.12	0.89	0.99	0.12	6	34	1.88E-140
Q15126	Phosphomevalonate kinase	PMKI	0.95	0.89	1.12	0.89	0.99	0.12	10	58	6.35E-162
Q5JRC6	PHD finger protein 6	AC004383.6-002	0.85	1.02	1.09	0.92	0.99	0.12	8	26	7.55E-117
P62820-1	Ras-related protein Rab-1A	RAB1	0.94	1.13	0.89	1.12	0.99	0.13	11	55	6.81E-230
O75569-1	Interferon-inducible double stranded RNA-dependent protein kinase activator A	HSD14	0.87	0.96	1.13	0.88	0.99	0.13	7	32	9.94E-32
Q6IBS0	A6-related protein	MSTP011	1.08	1.05	0.83	1.20	0.99	0.14	11	50	1.96E-127
Q07666-1	GAP-associated tyrosine phosphoprotein p62	KHDRBS1	0.90	0.91	1.15	0.87	0.99	0.14	12	32	5.33E-178
P11413-2	Glucose-6-phosphate 1-dehydrogenase	G6PD	0.93	0.87	1.16	0.86	0.99	0.15	20	39	1.57E-228
P00558	Cell migration-inducing gene 10 protein	MIG10	0.89	0.90	1.17	0.85	0.99	0.16	32	75	0.00E+00
Q7Z478	ATP-dependent RNA helicase DHX29	DDX29	0.89	1.19	0.88	1.14	0.99	0.18	6	5.4	7.12E-63
Q02750	Dual specificity mitogen-activated protein kinase kinase 1	MAP2K1	0.78	1.08	1.10	0.91	0.99	0.18	9	25	6.56E-32
Q8TAQ2-1	BRG1-associated factor 170	BAF170	0.83	0.94	1.19	0.84	0.99	0.18	27	26	4.46E-184
A8MYX5	60S ribosomal protein L30	RPL30	1.11	1.09	0.76	1.32	0.99	0.20	7	72	5.23E-128
Q15907	GTP-binding protein YPT3	RAB11B	0.84	0.90	1.22	0.82	0.99	0.20	11	56	3.68E-192
Q6P4H0	Glutathione S-transferase kappa 1	GSTK1	1.18	1.02	0.76	1.32	0.99	0.21	5	23	1.04E-78
Q6P1N0-1	Coiled-coil and C2 domain-containing protein 1A	CC2D1A	1.08	1.15	0.73	1.37	0.99	0.23	9	12	4.01E-38
P36543	Vacuolar proton pump subunit E 1	ATP6E	0.85	0.86	1.25	0.80	0.99	0.23	5	24	9.84E-29

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Q9HA64	Fructosamine-3-kinase-related protein	FN3KRP	0.84	0.87	1.25	0.80	0.99	0.23	5	18	3.42E-21
Q96CT7	Coiled-coil domain-containing protein 124	CCDC124	1.07	1.18	0.71	1.41	0.99	0.25	7	37	2.53E-52
C9JEH3	Angio-associated, migratory cell protein, isoform CRA_a	AAMP	1.07	1.23	0.66	1.52	0.99	0.29	3	8.5	1.51E-21
Q7Z4V5-1	Hepatoma-derived growth factor 2	HDGF2	0.66	0.78	1.52	0.66	0.99	0.47	15	24	6.65E-38
Q96BX8	Mob1 homolog 2A	MOB3A	0.55	0.60	1.81	0.55	0.99	0.71	4	31	9.33E-24
P61353	60S ribosomal protein L27	RPL27	1.07	1.04	0.85	1.18	0.99	0.12	5	45	1.82E-19
P48739-2	Phosphatidylinositol transfer protein beta isoform	PITPNB	0.99	0.99	0.99	1.01	0.99	0.00	8	34	1.63E-37
P30154-2	PP2A subunit A isoform PR65-beta	PPP2R1B	0.98	0.99	1	1.00	0.99	0.01	19	36	3.86E-214
Q9NR45	N-acetylneuraminate synthase	NANS	1.00	0.99	0.98	1.02	0.99	0.01	9	37	1.34E-86
Q92973-1	Importin beta-2	KPNB2	0.99	1.01	0.97	1.03	0.99	0.02	22	34	1.30E-257
P52209	6-phosphogluconate dehydrogenase, decarboxylating	PGD	1.00	0.96	1.01	0.99	0.99	0.03	19	50	0.00E+00
O14929	Histone acetyltransferase type B catalytic subunit	HAT1	1.01	0.96	1.00	1.00	0.99	0.03	9	31	4.19E-120
Q13613-1	Myotubularin-related protein 1	MTMR1	0.99	1.02	0.96	1.04	0.99	0.03	3	5.3	7.98E-12
B3KTZ7	cDNA FLJ39003 fis, clone NT2RI2024313, highly similar to Probable fibrosin-1 long transcript protein	FBRS	1.01	1.01	0.95	1.05	0.99	0.03	2	2.7	3.69E-04
P19388	DNA-directed RNA polymerase II 23 kDa polypeptide	POLR2E	0.98	0.96	1.03	0.97	0.99	0.04	5	28	1.29E-42
Q53HE2	Triosephosphate isomerase	TPI	0.96	0.95	1.06	0.94	0.99	0.06	22	77	0.00E+00
A8K7X6	cDNA FLJ77432, highly similar to Homo sapiens poly(rC) binding protein 2 (PCBP2), transcript variant 2, mRNA	hCG_2017557	0.96	1.06	0.95	1.05	0.99	0.06	18	69	0.00E+00
Q9UMX0-1	Protein linking IAP with cytoskeleton 1	DA41	0.90	1.15	0.92	1.09	0.99	0.14	4	11	8.29E-63
Q6UXN9	WD repeat-containing protein 82	UNQ9342/PRO34047	0.93	0.89	1.15	0.87	0.99	0.14	7	25	1.13E-34
P54920	Alpha-soluble NSF	NAPA	0.86	0.95	1.16	0.86	0.99	0.15	14	61	2.43E-176

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	attachment protein										
O95400	CD2 antigen cytoplasmic tail-binding protein 2	CD2BP2	1.00	1.14	0.83	1.20	0.99	0.16	3	11	3.54E-18
P35658-5	214 kDa nucleoporin	CAIN	1.01	1.17	0.79	1.27	0.99	0.19	11	10	4.73E-145
P16220-1	Cyclic AMP-responsive element-binding protein 1	CREB1	0.84	0.89	1.24	0.81	0.99	0.22	3	13	5.30E-11
P29590-1	Probable transcription factor PML	MYL	0.87	0.84	1.26	0.79	0.99	0.23	8	10	2.13E-24
O75521-1	Delta(3),delta(2)-enoyl-CoA isomerase	DRS1	1.13	1.14	0.70	1.43	0.99	0.25	7	22	1.75E-27
Q9NQ29-1	Putative RNA-binding protein Luc7-like 1	LUC7L	1.28	0.89	0.80	1.25	0.99	0.26	10	29	2.66E-115
P85037-1	Forkhead box protein K1	FOXK1	1.00		0.98	1.02	0.99	0.01	4	11	7.14E-08
O60563	Cyclin-T1	CCNT1		0.96	1.02	0.98	0.99	0.04	5	11	3.01E-08
O43639	Cytoplasmic protein NCK2	NCK2	0.94		1.04	0.96	0.99	0.07	2	5.5	1.47E-03
B4DL31	cDNA FLJ52681, highly similar to HLA class I histocompatibility antigen, alpha chain E	HLA-6.2	0.94		1.04	0.96	0.99	0.07	3	9.8	1.11E-12
Q9Y6E0-2	Mammalian STE20-like protein kinase 3	MST3	1.04		0.94	1.06	0.99	0.07	6	18	5.01E-73
O95785-1	Widely-interspaced zinc finger-containing protein	WIZ	1.05		0.93	1.08	0.99	0.08	3	2.2	1.76E-09
Q06546	GA-binding protein alpha chain	E4TF1A		0.87	1.11	0.90	0.99	0.17	6	14	7.83E-30
Q13596-2	Sorting nexin-1	SNX1		0.87	1.11	0.90	0.99	0.17	11	33	4.52E-123
Q96AB6	Protein NH2-terminal asparagine amidohydrolase	NTAN1		0.81	1.17	0.85	0.99	0.25	2	5.5	7.00E-04
Q9NVZ3-1	Adaptin ear-binding coat-associated protein 2	NECAP2		0.80	1.18	0.85	0.99	0.27	4	19	2.42E-122
P61803	Defender against cell death 1	DAD1			0.99	1.01	0.99		2	20	3.18E-18
Q96EE3-1	Nucleoporin SEH1	SEC13L			0.99	1.01	0.99		2	5.2	7.67E-05
Q8WUM4	ALG-2-interacting protein 1	AIP1			0.99	1.01	0.99		34	47	0.00E+00
Q9Y2Y0-1	ADP-ribosylation factor-like protein 2-binding protein	ARL2BP		0.99			0.99		2	8	1.44E-09
P82664	28S ribosomal protein S10, mitochondrial	MRPS10	0.99				0.99		2	14	1.87E-10
A6NDY9	Putative uncharacterized	FLNA	0.99				0.99		96	56	0.00E+00

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	protein FLNA										
Q9Y3I0	UPF0027 protein C22orf28	C22orf28	0.96	0.93	1.08	0.93	0.99	0.08	22	54	3.78E-196
C9JBL2	Putative uncharacterized protein RPL32	RPL32	1.01	1.07	0.89	1.12	0.99	0.09	7	41	6.23E-83
P35613-1	5F7	BSG	0.87	1.06	1.04	0.96	0.99	0.10	5	19	1.72E-31
P48637	Glutathione synthase	GSS	0.98	0.87	1.12	0.89	0.99	0.13	7	14	2.36E-35
O75223-1	Cytochrome c-releasing factor 21	C7orf24	1.12	1.03	0.82	1.22	0.99	0.15	6	34	1.19E-80
P43487	Ran-binding protein 1	RANBP1	1.00	1.16	0.81	1.23	0.99	0.18	10	69	3.19E-171
Q8N806	N-recognin-7	C14orf130	1.19	0.97	0.81	1.23	0.99	0.19	3	8	3.85E-46
O95372	Acyl-protein thioesterase 2	APT2	0.79	0.87	1.31	0.76	0.99	0.28	7	40	2.77E-73
Q8WXF1-1	Paraspeckle component 1	PSP1	0.87	0.77	1.33	0.75	0.99	0.30	17	30	3.91E-139
Q9NX40-1	OCIA domain-containing protein 1	OCIA	1.36	1.17	0.44	2.27	0.99	0.49	6	36	2.73E-20
P09104	2-phospho-D-glycerate hydro-lyase	ENO2	0.69	0.66	1.62	0.62	0.99	0.55	16	53	0.00E+00
Q9Y4Y9	U6 snRNA-associated Sm-like protein LSm5	LSM5	0.99	1.02	0.97	1.03	0.99	0.03	3	30	4.89E-15
Q9H089	Large subunit GTPase 1 homolog	LSG1	1.13	1.05	0.80	1.25	0.99	0.17	2	4.6	4.70E-06
P31947-1	14-3-3 protein sigma	HME1	0.84	0.94	1.20	0.83	0.99	0.19	7	20	4.16E-39
P21912	Iron-sulfur subunit of complex II	SDH	0.82	0.94	1.22	0.82	0.99	0.21	7	28	8.21E-36
Q96IJ6-2	GDP-mannose pyrophosphorylase A	GMPPA	1.39	1.00	0.59	1.69	0.99	0.40	4	11	1.03E-55
Q9Y3D6	FIS1 homolog	CGI-135	0.97	1.02	0.99	1.01	0.99	0.03	3	24	4.10E-21
P0CAP2-1	Glutamate receptor-like protein 1A	GRINL1A	1.01	1.01	0.96	1.04	0.99	0.03	6	30	4.57E-20
Q9Y265-1	49 kDa TATA box-binding protein-interacting protein	INO80H	1.01	1.01	0.96	1.04	0.99	0.03	13	37	2.36E-134
Q07020	60S ribosomal protein L18	RPL18	1.03	1.01	0.94	1.06	0.99	0.05	10	46	0.00E+00
P28066	Macropain zeta chain	PSMA5	1.01	1.03	0.94	1.06	0.99	0.05	11	52	0.00E+00
P35250-1	Activator 1 40 kDa subunit	RFC2	1.04	1.00	0.94	1.06	0.99	0.05	14	50	2.62E-232
Q86XI8	Uncharacterized protein C19orf68	C19orf68	0.95	0.98	1.05	0.95	0.99	0.05	2	1.8	2.10E-02
Q8NE71-1	ATP-binding cassette 50	ABC50	1.05	0.99	0.94	1.06	0.99	0.06	12	16	3.78E-114
P55265-4	136 kDa double-stranded RNA-binding protein	ADAR	0.99	1.05	0.94	1.06	0.99	0.06	26	23	5.89E-228

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P37837	Transaldolase	TAL	0.94	0.96	1.08	0.93	0.99	0.08	18	47	1.27E-165
Q53H96	Pyrroline-5-carboxylate reductase 3	PYCRL	1.01	1.07	0.90	1.11	0.99	0.09	4	18	1.29E-19
P22234	AIR carboxylase	ADE2	1.04	1.05	0.89	1.12	0.99	0.09	23	59	0.00E+00
P46109	Crk-like protein	CRKL	1.09	0.99	0.90	1.11	0.99	0.10	10	48	7.12E-57
P10768	Esterase D	ESD	1.11	0.99	0.88	1.14	0.99	0.12	11	64	1.55E-213
P49720	Proteasome chain 13	PSMB3	1.14	0.88	0.96	1.04	0.99	0.13	6	32	7.10E-98
P19623	Putrescine aminopropyltransferase	SPS1	1.09	1.05	0.84	1.19	0.99	0.13	14	52	3.96E-72
P49247	Phosphoriboisomerase	RPI	1.04	1.10	0.84	1.19	0.99	0.14	10	41	8.03E-68
Q86U42-1	Nuclear poly(A)-binding protein 1	PAB2	0.83	1.02	1.13	0.88	0.99	0.15	6	27	4.24E-33
Q9UQ80	Cell cycle protein p38-2G4 homolog	EBP1	1.07	1.10	0.81	1.23	0.99	0.16	21	59	6.97E-296
P48047	ATP synthase subunit O, mitochondrial	ATP5O	0.89	0.91	1.18	0.85	0.99	0.16	11	63	0.00E+00
P31040	Flavoprotein subunit of complex II	SDH2	0.89	0.89	1.20	0.83	0.99	0.18	8	21	6.48E-110
Q04323-2	SAPK substrate protein 1	SAKS1	1.01	0.8	1.17	0.85	0.99	0.19	6	31	5.57E-11
Q99836	Myeloid differentiation primary response protein MyD88	MYD88	1.22	0.90	0.86	1.16	0.99	0.20	2	14	2.74E-09
Q12888-2	Tumor suppressor p53-binding protein 1	TP53BP1	1.28	0.91	0.79	1.27	0.99	0.26	10	7.2	3.00E-86
Q9UNE7-1	Antigen NY-CO-7	CHIP	1.09	1.32	0.57	1.75	0.99	0.38	5	18	2.24E-11
P98179	Putative RNA-binding protein 3	RBM3	1.23	1.21	0.54	1.85	0.99	0.39	6	49	3.43E-60
P35579-1	Cellular myosin heavy chain, type A	MYH9	0.72	0.76	1.50	0.67	0.99	0.44	##	67	0.00E+00
P49368	CCT-gamma	CCT3	0.99	1.04	0.95	1.05	0.99	0.05	40	71	0.00E+00
P50402	Emerin	EDMD	0.97	1.06	0.95	1.05	0.99	0.06	8	39	3.17E-55
Q8N7H5-1	Pancreatic differentiation protein 2	PAF1	1.01	1.06	0.91	1.10	0.99	0.08	10	22	9.35E-42
Q9UHV9	Prefoldin subunit 2	HSPC231	0.98	1.09	0.91	1.10	0.99	0.09	5	40	7.38E-101
Q09161	80 kDa nuclear cap-binding protein	CBP80	1.11	0.90	0.97	1.03	0.99	0.11	11	19	6.00E-96
P22087	34 kDa nucleolar scleroderma antigen	FBL	1.08	1.10	0.80	1.25	0.99	0.17	9	33	1.28E-32
Q8NBS9	Endoplasmic reticulum resident protein 46	TLP46	1.08	1.11	0.79	1.27	0.99	0.18	11	30	1.24E-60
Q86UE8-1	PKU-alpha	TLK2	0.74	1.12	1.12	0.89	0.99	0.22	3	4.7	1.67E-08
O75312	Zinc finger protein	ZNF259	1.11	1.17	0.70	1.43	0.99	0.26	6	14	2.01E-79

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	259										
P18206-1	Metavinculin	VCL	0.68	0.68	1.62	0.62	0.99	0.54	10	10	1.68E-62
Q9H773	dCTP pyrophosphatase 1	CDA03	0.99		1.00	1.00	1.00	0.01	5	47	8.00E-38
P16383-1	GC-rich sequence DNA-binding factor	C2orf3		1.00	0.99	1.01	1.00	0.01	4	5.9	1.09E-14
Q6UW68	Transmembrane protein 205	TMEM 205	0.94		1.05	0.95	1.00	0.08	2	11	1.53E-03
Q15370	Elongin 18 kDa subunit	TCEB2	0.94		1.05	0.95	1.00	0.08	11	92	4.00E-31
O94804	Lymphocyte-oriented kinase	LOK		0.81	1.18	0.85	1.00	0.26	3	4.4	2.91E-10
Q9UBD5-2	Origin recognition complex subunit 3	LATHEO	1.19		0.80	1.25	1.00	0.28	2	4.6	3.27E-14
Q8N668	COMM domain-containing protein 1	C2orf5		0.91	1.08	0.93	1.00	0.12	2	16	2.83E-49
Q9HCC0-1	3-methylcrotonyl-CoA carboxylase 2	MCCB		0.91	1.08	0.93	1.00	0.12	2	3.9	4.80E-06
Q15269	Periodic tryptophan protein 2 homolog	PWP2	1.31		0.68	1.47	1.00	0.45	6	7.8	2.41E-48
O75367-1	Core histone macro-H2A.1	H2AFY	1.01	1.00	0.98	1.02	1.00	0.02	16	51	7.93E-256
P16083	NRH dehydrogenase [quinone] 2	NMOR 2	0.99	1.02	0.98	1.02	1.00	0.02	8	53	1.75E-47
Q06124-1	Protein-tyrosine phosphatase 1D	PTP2C	1.04	0.97	0.98	1.02	1.00	0.04	9	17	1.33E-52
Q15075	Early endosome antigen 1	EEA1	0.97	1.04	0.98	1.02	1.00	0.04	14	9.6	5.52E-32
O15042-1	140 kDa Ser/Arg-rich domain protein	KIAA0332	1.00	1.05	0.94	1.06	1.00	0.06	25	27	3.09E-190
Q06265-2	Autoantigen PM/Scl 1	EXOSC9	0.94	1.15	0.90	1.11	1.00	0.13	3	7.5	5.92E-07
O00264	Membrane-associated progesterone receptor component 1	HPR6.6	1.17	0.90	0.92	1.09	1.00	0.15	11	59	4.16E-147
Q9Y266	Nuclear distribution protein C homolog	NUDC	1.05	1.13	0.81	1.23	1.00	0.17	21	59	1.76E-164
Q92542-1	Nicastrin	KIAA0253	0.97	1.21	0.81	1.23	1.00	0.20	4	8.5	1.83E-18
P21266	Glutathione S-transferase Mu 3	GST5	0.79	0.82	1.38	0.72	1.00	0.33	13	62	4.20E-117
Q6ZUM4-1	CIN85-associated multi-domain-containing Rho GTPase-activating protein 1	ARHGAP27	1.00	1.00	0.99	1.01	1.00	0.01	3	4.5	1.04E-05
Q8N2Z9-1	Apoptosis-inducing TAF9-like domain-containing protein 1	APITD1	1.01	1.01	0.97	1.03	1.00	0.02	2	15	4.10E-09
B4E171	cDNA FLJ59144, highly similar to Tetraspanin-7	A15	0.97	1.02	1.00	1.00	1.00	0.03	2	8.6	9.05E-227

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Q53GL7	Poly [ADP-ribose] polymerase 10	PARP10	0.97	1.02	1.00	1.00	1.00	0.03	7	13	2.98E-41
Q8N1G4	Leucine-rich repeat-containing protein 47	KIAA1185	1.01	0.96	1.02	0.98	1.00	0.03	18	42	8.02E-205
B5MDU6	Putative uncharacterized protein C2orf43	C2orf43	0.99	0.96	1.04	0.96	1.00	0.04	2	6.5	1.37E-70
P61019	Ras-related protein Rab-2A	RAB2	1.03	1.01	0.95	1.05	1.00	0.04	10	60	1.07E-148
P61758	HIBBJ46	PFDN3	0.94	1.01	1.04	0.96	1.00	0.05	14	40	2.83E-288
O15305	Phosphomannomutase 2	PMM2	0.93	1.03	1.03	0.97	1.00	0.06	4	17	6.53E-13
O14556	Glyceraldehyde-3-phosphate dehydrogenase	GPMDB	0.98	0.94	1.07	0.93	1.00	0.07	5	58	4.63E-101
P40227	Acute morphine dependence-related protein 2	CCT6	1.04	1.03	0.92	1.09	1.00	0.07	27	55	0.00E+00
P63272	DRB sensitivity-inducing factor 14 kDa subunit	SPT4H	0.93	0.99	1.07	0.93	1.00	0.07	3	27	2.23E-08
Q13247-1	Pre-mRNA-splicing factor SRP55	SFRS6	0.94	1.08	0.97	1.03	1.00	0.07	12	31	4.61E-53
Q9HBU6	Ethanolamine kinase 1	EKI1	1.04	1.04	0.91	1.10	1.00	0.08	2	12	2.70E-02
Q9UN86-1	GAP SH3 domain-binding protein 2	G3BP2	1.02	1.06	0.91	1.10	1.00	0.08	11	32	8.63E-80
C9J2F8	HCG22882, isoform CRA_a	hCG_22882	1.05	1.05	0.89	1.12	1.00	0.09	3	33	2.03E-78
Q9NQC3-2	Foocen	KIAA0886	1.05	1.05	0.89	1.12	1.00	0.09	6	26	1.44E-57
Q53G33	U1 small nuclear ribonucleoprotein C	RP3-375P9.1-002	0.89	1.07	1.03	0.97	1.00	0.09	2	17	8.20E-11
Q9Y6E2	Basic leucine zipper and W2 domain-containing protein 2	BZW2	1.03	1.08	0.88	1.14	1.00	0.10	7	20	0.00E+00
P53999	Activated RNA polymerase II transcriptional coactivator p15	PC4	0.93	0.94	1.12	0.89	1.00	0.11	9	47	1.17E-220
Q01130	Protein PR264	SFRS2	0.88	1.02	1.09	0.92	1.00	0.11	8	30	1.98E-84
O60493-1	Protein SDP3	SNX3	0.91	0.96	1.12	0.89	1.00	0.11	6	40	2.21E-19
P23396	40S ribosomal protein S3	OK/SW-cl.26	1.05	1.10	0.84	1.19	1.00	0.14	21	81	4.32E-157
P48507	Gamma-ECS regulatory subunit	GCLM	1.19	0.89	0.91	1.10	1.00	0.17	5	27	1.10E-57
Q6FGM0	cDNA, FLJ96508, Homo sapiens SH3-domain GRB2-like 1 (SH3GL1), mRNA	hCG_21932	0.96	0.85	1.18	0.85	1.00	0.17	4	12	5.39E-34
P31150	Guanosine	GDI1	0.88	0.91	1.20	0.83	1.00	0.18	16	43	9.37E-286

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	diphosphate dissociation inhibitor 1										
Q8TDP1-1	Aicardi-Goutieres syndrome 3 protein	AYP1	1.07	1.13	0.79	1.27	1.00	0.18	6	46	4.75E-93
Q14240-2	ATP-dependent RNA helicase eIF4A-2	DDX2B	0.85	0.92	1.22	0.82	1.00	0.20	15	45	8.91E-230
Q96HY6-1	DDRGK domain-containing protein 1	C20orf116	0.93	1.23	0.83	1.20	1.00	0.21	6	35	1.14E-103
P16403	Histone H1.2	H1F2	0.84	0.91	1.24	0.81	1.00	0.21	17	47	1.35E-217
A8MUM5	Putative uncharacterized protein TOR1AIP1	TOR1AIP1	0.87	0.84	1.28	0.78	1.00	0.25	11	26	1.02E-76
Q8NAV1-1	Pre-mRNA-splicing factor 38A	PRPF38A	1.07	1.20	0.72	1.39	1.00	0.25	5	22	1.73E-13
P15153	GX	RAC2	0.84	0.85	1.30	0.77	1.00	0.26	11	59	1.96E-51
Q14683	Structural maintenance of chromosomes protein 1A	DXS423E	0.82	0.85	1.32	0.76	1.00	0.28	31	29	2.65E-245
Q9H1I8-1	Activating signal cointegrator 1 complex subunit 2	ASC1P100	1.35	0.94	0.70	1.43	1.00	0.33	4	7	1.07E-11
P41214-1	Hepatocellular carcinoma-associated antigen 56	HCA56	1.32	1.04	0.63	1.59	1.00	0.35	5	15	2.42E-82
P26038	Membrane-organizing extension spike protein	MSN	0.69	0.75	1.55	0.65	1.00	0.48	49	68	0.00E+00
P61009	Microsomal signal peptidase 22/23 kDa subunit	SPC22	1.00	1.58	0.41	2.44	1.00	0.59	2	13	2.14E-21
P14174	Glycosylation-inhibiting factor	GLIF	1.13	0.97	0.90	1.11	1.00	0.12	3	36	1.99E-30
Q9BTW9-4	Beta-tubulin cofactor D	KIAA0988	1.02	1.16	0.82	1.22	1.00	0.17	10	8.7	1.20E-107
P51784	Deubiquitinating enzyme 11	UHX1	1.01	1.17	0.82	1.22	1.00	0.18	4	5.8	1.50E-36
Q9Y4I1-3	Dilute myosin heavy chain, non-muscle	MYH12	1.00	1.00	1.00	1.00	1.00	0.00	3	1.1	6.75E-03
B8ZZN6	Putative uncharacterized protein SUMO1	SUMO1		1.00	1.00	1.00	1.00	0.00	3	16	8.09E-05
P14625	94 kDa glucose-regulated protein	GRP94	1.00	1.01	0.99	1.01	1.00	0.01	55	62	0.00E+00
Q9BWT6	Meiotic nuclear division protein 1 homolog	GAJ	1.01		0.99	1.01	1.00	0.01	3	19	1.59E-23
B1PS43	Myosin heavy chain 11 smooth muscle isoform	MYH11	1.01		0.99	1.01	1.00	0.01	17	7.9	1.29E-260
Q5T8P6-2	CTCL tumor antigen se70-2	C13orf10	0.99	1.02	0.99	1.01	1.00	0.02	18	20	4.37E-79
Q8NBT2	Kinetochore protein Spc24	SPBC24	1.01	1.01	0.98	1.02	1.00	0.02	5	43	0.00E+00

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P42025	Actin-related protein 1B	ACTR1B	0.98	1.02	1.00	1.00	1.00	0.02	9	30	2.63E-41
O75347	TCP1-chaperonin cofactor A	TBCA	1.02	0.96	1.02	0.98	1.00	0.03	12	64	1.31E-74
O14818-1	Proteasome subunit alpha type-7	HSPC	1.02	1.02	0.96	1.04	1.00	0.03	19	68	0.00E+00
P60900	27 kDa prosomal protein	PROS27	1.04	0.99	0.97	1.03	1.00	0.04	16	59	5.18E-156
Q8TE02-4	Dermal papilla-derived protein 6	C17orf81		1.03	0.97	1.03	1.00	0.04	2	8.4	1.70E-10
P20618	Macropain subunit C5	PSC5	1.02	0.95	1.03	0.97	1.00	0.04	11	61	4.91E-179
P11766	Alcohol dehydrogenase 5	ADH5	1.03	0.95	1.02	0.98	1.00	0.04	10	38	9.36E-51
O95861-1	3(2),5-bisphosphate nucleotidase 1	BPNT1	1.00	0.95	1.05	0.95	1.00	0.05	10	43	1.32E-53
P28070	26 kDa prosomal protein	PROS26	1.03	0.94	1.03	0.97	1.00	0.05	8	50	5.25E-93
O75832	26S proteasome non-ATPase regulatory subunit 10	PSMD10	1.02	1.04	0.94	1.06	1.00	0.05	6	39	1.54E-27
Q96T60	2(3)-polynucleotidase	PNKP	0.96	1.07	0.97	1.03	1.00	0.06	3	9.2	4.59E-27
Q8IWX8	Calcium homeostasis endoplasmic reticulum protein	CHERP	0.98	1.07	0.95	1.05	1.00	0.06	11	16	1.91E-55
Q8N3X1	Formin-binding protein 30	FBP30	1.05	0.92	1.03	0.97	1.00	0.07	5	7	5.33E-57
Q99720-1	Aging-associated gene 8 protein	AAG8	0.95		1.05	0.95	1.00	0.07	2	14	9.24E-05
A8MX72	cDNA FLJ55157, highly similar to Eukaryotic translation initiation factor 4E	EIF4E	0.91	1.03	1.06	0.94	1.00	0.08	6	27	3.73E-33
P80303-1	DNA-binding protein NEFA	NEFA	1.06		0.94	1.06	1.00	0.08	3	9.8	1.46E-20
P61254	60S ribosomal protein L26	RPL26	1.01	1.08	0.91	1.10	1.00	0.09	10	39	2.61E-22
Q9BT09-1	CTG repeat protein 4a	CNPY3	0.93	1.07			1.00	0.10	2	7.2	1.31E-41
P09651-1	Helix-destabilizing protein	HNRNPA1	0.92	0.94	1.14	0.88	1.00	0.12	26	61	0.00E+00
Q12906-4	Double-stranded RNA-binding protein 76	DRBF	0.90	0.96	1.14	0.88	1.00	0.12	28	42	4.70E-206
P20340-1	Ras-related protein Rab-6A	RAB6	0.92	0.93	1.15	0.87	1.00	0.13	8	33	6.34E-40
Q9UNF1-1	Breast cancer-associated gene 1 protein	BCG1	0.94	0.91	1.15	0.87	1.00	0.13	5	14	2.62E-41
Q00653-1	DNA-binding factor KBF2	LYT10	0.98	0.88	1.14	0.88	1.00	0.13	4	6.3	4.19E-24
Q13526	Peptidyl-prolyl cis-trans isomerase	PIN1	1.12	1.05	0.83	1.20	1.00	0.15	5	43	3.96E-74

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	NIMA-interacting 1										
P30041	1-Cys peroxiredoxin	AOP2	0.91	0.91	1.18	0.85	1.00	0.16	14	63	1.32E-94
P60709	Actin, cytoplasmic 1	ACT1	0.91	0.91	1.18	0.85	1.00	0.16	28	83	0.00E+00
Q96JM3	Zinc finger protein 828	C13orf8	0.93	0.89	1.18	0.85	1.00	0.16	8	13	8.46E-34
Q9BQ67	Glutamate-rich WD repeat-containing protein 1	GRWD	1.07	1.11	0.82	1.22	1.00	0.16	7	18	6.69E-49
Q8WXI9	GATA zinc finger domain-containing protein 2B	GATAD2B	0.88	0.94	1.18	0.85	1.00	0.16	9	20	2.67E-72
P19838-2	DNA-binding factor KBF1	NFKB1	1.12		0.88	1.14	1.00	0.17	6	8.5	2.49E-21
P09960-1	Leukotriene A(4) hydrolase	LTA4	1.10	1.10	0.80	1.25	1.00	0.17	11	25	8.13E-94
A0AV56	SAFB protein	SAFB	0.87	0.93	1.20	0.83	1.00	0.18	27	30	2.52E-298
Q9UL25	Ras-related protein Rab-21	KIAA0118	1.09	1.12	0.79	1.27	1.00	0.18	7	32	1.95E-84
A8K702	cDNA FLJ78285, highly similar to Homo sapiens gasdermin domain containing 1, mRNA	DFNA5L		1.13	0.87	1.15	1.00	0.18	4	9.6	9.48E-46
Q9P2M7-1	Cingulin	CGN	0.87	1.13			1.00	0.18	3	2.7	3.34E-07
Q15428	Spliceosome-associated protein 62	SAP62	0.93	0.86	1.21	0.83	1.00	0.19	11	24	4.61E-73
P49756-1	Arg/Glu/Asp-rich protein of 120 kDa	RBM25	1.06	1.15	0.79	1.27	1.00	0.19	22	28	1.57E-144
Q8N6N3-1	BCL10-associated gene protein	BAG	1.02	1.24	0.74	1.35	1.00	0.25	4	19	2.95E-07
P00390-1	Glutathione reductase, mitochondrial	GLUR	0.85	0.86	1.29	0.78	1.00	0.25	11	35	4.50E-65
Q07960	CDC42 GTPase-activating protein	ARHGAP1		0.80	1.20	0.83	1.00	0.28	6	17	7.56E-74
P09874	NAD(+) ADP-ribosyltransferase 1	ADPRT	0.80	0.84	1.36	0.74	1.00	0.31	48	45	0.00E+00
P13861	cAMP-dependent protein kinase type II-alpha regulatory subunit	PKR2	1.37	0.86	0.77	1.30	1.00	0.32	2	5.7	2.29E-19
A8K8N7	cDNA FLJ77779, highly similar to Homo sapiens phosphoribosylformyl glycinamidine synthase (FGAR amidotransferase) (PFAS), mRNA	hCG_31283	1.23		0.77	1.30	1.00	0.33	18	20	4.20E-170
Q9NR50-1	eIF-2B GDP-GTP exchange factor subunit gamma	EIF2B3	1.38	0.91	0.71	1.41	1.00	0.34	5	14	6.99E-25

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B3KP52	cDNA FLJ31171 fis, clone KIDNE2000046, highly similar to 3-mercaptopyruvate sulfurtransferase	MPST	0.82	0.78	1.40	0.71	1.00	0.35	7	31	4.15E-128
P08758	Anchorin CII	ANX5	0.78	0.75	1.47	0.68	1.00	0.41	15	46	4.77E-153
O75190-1	DnaJ homolog subfamily B member 6	DNAJB6		0.71	1.29	0.78	1.00	0.41	3	13	1.41E-20
Q69YH5-1	Cell division cycle-associated protein 2	CDCA2	1.34		0.66	1.52	1.00	0.48	5	10	1.74E-50
P55957-2	BH3-interacting domain death agonist	BID	0.67	0.74	1.59	0.63	1.00	0.51	9	55	1.17E-279
O14602	Eukaryotic translation initiation factor 1A, Y-chromosomal	EIF1AY		1.39	0.61	1.64	1.00	0.55	3	24	2.27E-05
Q8IV50-1	LysM and putative peptidoglycan-binding domain-containing protein 2	LYSMD2		0.60	1.40	0.71	1.00	0.57	2	8.8	1.04E-13
Q96RE7	BTB/POZ domain-containing protein 14B	BTBD14B			1.00	1.00	1.00		2	4.4	9.42E-10
Q9BWT1-2	Cell division cycle-associated protein 7	CDCA7			1.00	1.00	1.00		2	4.2	1.17E-04
Q53GQ0	17-beta-hydroxysteroid dehydrogenase 12	HSD17B12	1.00				1.00		2	9.6	5.70E-05
Q9H7C9-1	UPF0366 protein C11orf67	C11orf67	1.00				1.00		2	22	4.43E-28
Q6P1N9-1	Hepatocarcinoma high expression protein	CDA11		1.00			1.00		2	6.6	5.59E-11
Q9NVH1-1	DnaJ homolog subfamily C member 11	DNAJC11	1.00				1.00		3	7.3	2.54E-05
Q96NT0	Coiled-coil domain-containing protein 115	CCDC115	1.00				1.00		4	35	4.31E-21
Q99880	Histone H2B type 1-L	H2BFC		1.00			1.00		13	73	7.23E-97
P07437	Tubulin beta chain	OK/SW-cl.56		1.00			1.00		14	31	2.11E-276
Q9H0S4	DEAD box protein 47	DDX47	1.03	1.12	0.85	1.18	1.00	0.14	7	23	2.03E-88
O94903	Proline synthase co-transcribed bacterial homolog protein	PROSC	0.99	1.01	1.01	0.99	1.00	0.01	9	35	2.65E-45
P02795	Metallothionein-2	CES1	1.01	1.01	0.99	1.01	1.00	0.01	3	49	3.53E-18
Q69YJ7	Putative uncharacterized protein DKFZp667H197	DKFZp667H197	1.00	0.99	1.02	0.98	1.00	0.02	9	11	9.32E-60
A8MXP9	Putative uncharacterized protein MATR3	MATR3	1.00	0.99	1.02	0.98	1.00	0.02	39	45	0.00E+00
P21796	Outer mitochondrial membrane protein	VDAC	1.00	1.02	0.99	1.01	1.00	0.02	15	62	5.07E-135

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	porin 1										
P31948	Hsc70/Hsp90-organizing protein	STIP1	0.99	0.99	1.03	0.97	1.00	0.02	46	65	0.00E+00
Q8N0V3-1	Putative ribosome-binding factor A, mitochondrial	C18orf22	0.97	1.02	1.02	0.98	1.00	0.03	2	7.6	6.61E-04
Q01081	Splicing factor U2AF 35 kDa subunit	U2AF1	0.98	1.04	0.99	1.01	1.00	0.03	7	33	4.02E-64
Q99615	DnaJ homolog subfamily C member 7	DNAJC7	1.01	1.04	0.96	1.04	1.00	0.04	18	33	2.40E-95
A1L0V1	ACTN1 protein	ACTN1	0.95	1.01	1.05	0.95	1.00	0.05	46	49	0.00E+00
P55060-1	Cellular apoptosis susceptibility protein	CAS	1.02	1.11	0.88	1.14	1.00	0.12	32	39	0.00E+00
P61224	GTP-binding protein smg p21B	OK/SW-cl.11	0.96	0.91	1.14	0.88	1.00	0.12	9	64	3.35E-94
Q86YV0-1	RAS protein activator like-3	RASAL3	0.96	0.90	1.15	0.87	1.00	0.13	17	25	1.74E-127
P16930	Beta-diketonase	FAH	0.99	1.14	0.88	1.14	1.00	0.13	3	7.2	2.20E-60
Q92879-4	50 kDa nuclear polyadenylated RNA-binding protein	BRUNOL2	0.93	0.91	1.17	0.85	1.00	0.14	4	8.2	3.66E-39
P36542-1	ATP synthase subunit gamma, mitochondrial	ATP5C	0.89	0.92	1.20	0.83	1.00	0.17	10	42	2.10E-70
O75874	Cytosolic NADP-isocitrate dehydrogenase	IDH1	0.90	0.89	1.22	0.82	1.00	0.19	8	22	5.95E-105
A8K4L9	cDNA FLJ75459	TIAL1	1.07	1.15	0.79	1.27	1.00	0.19	7	20	1.25E-63
Q9Y263	Phospholipase A-2-activating protein	PLAA	1.22	0.85	0.94	1.06	1.00	0.19	6	11	1.58E-48
Q99598	Translin-associated factor X	TRAX	1.00	0.81	1.20	0.83	1.00	0.20	10	51	3.11E-93
Q9UKG1	Adapter protein containing PH domain, PTB domain and leucine zipper motif 1	APPL	0.97	0.82	1.22	0.82	1.00	0.20	5	8.3	4.15E-32
P28062-1	Low molecular mass protein 7	LMP7	0.99	0.80	1.22	0.82	1.00	0.21	7	30	8.25E-36
C9JUI0	Putative uncharacterized protein IVD	IVD	0.80	0.96	1.25	0.80	1.00	0.23	5	11	1.02E-16
Q9Y6V0-1	Aczonin	ACZ	0.80	0.93	1.28	0.78	1.00	0.25	2	0.5	1.15E-02
O95433	Activator of 90 kDa heat shock protein ATPase homolog 1	AHSA1	1.18	1.13	0.70	1.43	1.00	0.26	17	55	4.69E-103
P50148	Guanine nucleotide-binding protein alpha-q	GAQ	0.82	0.81	1.38	0.72	1.00	0.33	8	26	1.14E-137
Q9Y3D8	Adenylate kinase isoenzyme 6	AD-004	1.16	1.24	0.61	1.64	1.00	0.34	4	30	8.62E-18
Q8NBX	Probable saccharopine	CGI-49	0.96	1.07	0.98	1.02	1.00	0.06	7	26	4.82E-45

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0	dehydrogenase										
P55809	3-oxoacid-CoA transferase 1	OXCT	1.02	0.93	1.06	0.94	1.00	0.07	9	24	8.31E-196
P62841	40S ribosomal protein S15	RIG	0.99	1.08	0.94	1.06	1.00	0.07	6	64	1.69E-145
Q9NX07-1	SECp43	SECP43	1.00	1.11	0.90	1.11	1.00	0.11	3	16	2.22E-10
Q15436	Protein transport protein Sec23A	SEC23A	0.99	0.9	1.12	0.89	1.00	0.11	7	11	8.12E-27
Q8IW48	SDHA protein	SDHA	0.89	1.00	1.12	0.89	1.00	0.12	11	31	1.08E-143
Q9BQA1	Androgen receptor cofactor p44	HKMT1069	1.10	1.09	0.82	1.22	1.00	0.16	5	18	1.10E-115
Q86VY4	Testis-specific Y-encoded-like protein 5	KIAA1750	0.98	1.30	0.73	1.37	1.00	0.29	4	12	3.76E-61
Q9UMY1-1	Nucleolar protein 7	C6orf90	1.07	1.32	0.62	1.61	1.00	0.35	2	11	7.03E-24
Q9H583	HEAT repeat-containing protein 1	BAP28	1.27	1.14	0.60	1.67	1.00	0.36	10	6	5.93E-53
Q9Y2K7-1	[Histone-H3]-lysine-36 demethylase 1A	CXXC8	1.00		1.01	0.99	1.01	0.01	4	5.1	1.18E-11
Q96EK6	Glucosamine 6-phosphate N-acetyltransferase	GNA1	1.04		0.97	1.03	1.01	0.05	4	33	2.25E-33
O00193	Small acidic protein	C11orf58	1.04	0.97			1.01	0.05	3	25	1.55E-207
Q14353	Guanidinoacetate N-methyltransferase	GAMT	0.96		1.05	0.95	1.01	0.06	5	30	3.69E-38
Q9BUK6-1	Protein misato homolog 1	LST005		0.95	1.06	0.94	1.01	0.08	2	6.8	9.62E-09
Q5Y8C7	Placenta derived apoptotic factor	PDAF		0.95	1.06	0.94	1.01	0.08	2	19	8.06E-04
Q6P1Q9-1	Methyltransferase-like protein 2B	METTL2B	1.06	0.95			1.01	0.08	3	8.5	1.82E-08
O15270	Long chain base biosynthesis protein 2	KIAA0526	1.07	0.94			1.01	0.09	2	3.9	6.39E-11
P41567	Eukaryotic translation initiation factor 1	EIF1	1.15		0.86	1.16	1.01	0.21	7	52	5.49E-61
Q9UMY4-1	Sorting nexin-12	SNX12	1.15	0.86			1.01	0.21	3	22	5.65E-07
P27361	Extracellular signal-regulated kinase 1	ERK1		0.83	1.18	0.85	1.01	0.25	7	15	4.53E-10
Q92544	Transmembrane 9 superfamily member 4	KIAA0255	1.18		0.83	1.20	1.01	0.25	4	9.2	1.38E-15
Q9Y697-1	Cysteine desulfurase, mitochondrial	HUSSY-08		1.24	0.77	1.30	1.01	0.33	3	6.3	2.15E-06
Q9P2N5	RNA-binding motif protein 27	KIAA1311		1.24	0.77	1.30	1.01	0.33	7	9.2	3.64E-35
P52434	DNA-directed RNA polymerase II subunit H	POLR2H	0.93	1.08			1.01	0.11	5	37	2.72E-26
Q9NV31	U3 small nucleolar ribonucleoprotein	C15orf12	1.11		0.90	1.11	1.01	0.15	4	26	5.40E-37

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	protein IMP3										
P07195	LDH heart subunit	LDHB	1.01	1.00	1.01	0.99	1.01	0.01	28	63	0.00E+00
Q9Y4G6	Talin-2	KIAA0320	0.98	1.02	1.02	0.98	1.01	0.02	25	7.6	1.20E-216
Q01105-2	HLA-DR-associated protein II	SET	1.00	1.04	0.98	1.02	1.01	0.03	14	48	0.00E+00
P05455	La autoantigen	SSB	0.97	1.03	1.02	0.98	1.01	0.03	26	57	0.00E+00
P09661	U2 small nuclear ribonucleoprotein A	SNRPA1	1.02	1.03	0.97	1.03	1.01	0.03	13	49	0.00E+00
Q15365	Heterogeneous nuclear ribonucleoprotein E1	PCBP1	0.96	0.99	1.07	0.93	1.01	0.06	19	84	0.00E+00
P12268	IMPDH-II	IMPD2	1.04	1.04	0.94	1.06	1.01	0.06	25	65	1.60E-278
P51149	Ras-related protein Rab-7a	RAB7	1.05	1.03	0.94	1.06	1.01	0.06	16	78	2.56E-281
Q9UHX1-1	60 kDa poly(U)-binding-splicing factor	FIR	1.01	1.08	0.93	1.08	1.01	0.08	14	37	7.30E-128
Q8WWM7-1	Ataxin-2 domain protein	A2D	1.03	1.07	0.92	1.09	1.01	0.08	24	28	4.54E-140
P27986-4	Phosphatidylinositol 3-kinase 85 kDa regulatory subunit alpha	GRB1	1.09	1.00	0.93	1.08	1.01	0.08	7	13	1.33E-38
Q9NX58	Cell growth-regulating nucleolar protein	LYAR	1.06	1.06	0.90	1.11	1.01	0.09	11	30	2.20E-118
P49721	Macropain subunit C7-I	PSMB2	1.02	0.90	1.10	0.91	1.01	0.10	11	43	2.47E-114
P39687	Acidic leucine-rich nuclear phosphoprotein 32 family member A	ANP32A	0.91	0.99	1.12	0.89	1.01	0.11	15	55	3.60E-282
A8MUT5	Putative uncharacterized protein DKC1	DKC1	1.09	1.09	0.84	1.19	1.01	0.14	10	29	3.22E-67
Q99848	EBNA1-binding protein 2	EBNA1BP2	1.08	1.10	0.84	1.19	1.01	0.14	10	29	1.38E-76
A5PLL5	SMARCD2 protein	SMARCD2	1.00	0.86	1.16	0.86	1.01	0.15	6	14	8.38E-43
Q7L5N1	COP9 signalosome complex subunit 6	COPS6	0.88	0.94	1.20	0.83	1.01	0.17	6	19	4.59E-35
Q15181	Inorganic pyrophosphatase	IOPPP	1.09	1.12	0.81	1.23	1.01	0.17	22	86	1.78E-285
Q9C0B1-1	Alpha-ketoglutarate-dependent dioxygenase FTO	FTO	0.91	0.90	1.21	0.83	1.01	0.18	6	13	8.98E-172
Q00535	Cell division protein kinase 5	CDK5	0.88	0.91	1.23	0.81	1.01	0.19	7	30	1.66E-30
Q32Q12	Nucleoside diphosphate kinase	hCG_2001850	1.15	1.13	0.74	1.35	1.01	0.23	14	64	2.99E-281
Q9BYG3	MKI67 FHA domain-interacting nucleolar phosphoprotein	MKI67IP	1.21	1.12	0.69	1.45	1.01	0.28	8	38	1.36E-153
O60287	Nucleolar pre-ribosomal-associated	C21orf108	1.07	1.30	0.65	1.54	1.01	0.33	6	4.3	1.45E-116

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	protein 1										
P04040	Catalase	CAT	0.80	0.82	1.40	0.71	1.01	0.34	10	24	2.80E-101
O15144	Actin-related protein 2/3 complex subunit 2	ARC34	0.80	0.79	1.43	0.70	1.01	0.37	14	54	1.25E-141
Q96FZ2	UPF0361 protein C3orf37	C3orf37	1.29	1.14	0.59	1.69	1.01	0.37	5	16	7.84E-73
Q709C8-1	Vacuolar protein sorting-associated protein 13C	KIAA1421	1.19	1.32	0.51	1.96	1.01	0.44	13	5	2.74E-108
Q14019	Coactosin-like protein	CLP	0.65	0.62	1.75	0.57	1.01	0.64	9	51	4.60E-162
Q14739	Integral nuclear envelope inner membrane protein	LBR	0.92	1.05	1.05	0.95	1.01	0.08	9	14	9.83E-77
Q15637-5	Mammalian branch point-binding protein	SF1	1.00	0.93	1.09	0.92	1.01	0.08	13	22	7.56E-136
P49458	Signal recognition particle 9 kDa protein	SRP9	1.04	1.11	0.87	1.15	1.01	0.12	5	55	1.94E-22
Q96SB8-2	Structural maintenance of chromosomes protein 6	SMC6	0.83	1.08	1.11	0.90	1.01	0.15	3	4.2	6.18E-09
C9J1W7	Putative uncharacterized protein SFRS15	SFRS15	1.11	1.12	0.79	1.27	1.01	0.19	9	12	6.38E-39
Q15527	Surfeit locus protein 2	SURF2		1.01	1.01	0.99	1.01	0.00	3	13	8.89E-04
P31943	Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	1.00	1.02	1.01	0.99	1.01	0.01	17	54	0.00E+00
Q9NRR5	Ataxin-1 ubiquitin-like-interacting protein A1U	C1orf6		1.02	1.00	1.00	1.01	0.01	4	10	3.84E-53
Q9Y678	Coatomer subunit gamma	COPG	1.02	1.02	0.99	1.01	1.01	0.02	28	46	0.00E+00
P17066	Heat shock 70 kDa protein 6	HSP70B	1.00	1.04	0.99	1.01	1.01	0.03	9	15	2.65E-168
Q9NX55-1	Huntingtin yeast partner K	C15orf63	0.99	1.03			1.01	0.03	2	15	3.72E-10
A6NEM2	Putative uncharacterized protein HCFC1	HCFC1	0.99	1.03			1.01	0.03	22	16	6.94E-179
Q9H2G2-1	CTCL tumor antigen se20-9	KIAA0204	0.99	0.99	1.05	0.95	1.01	0.03	13	12	6.98E-64
Q9Y6X4-1	Protein FAM169A	FAM169A	0.97	1.02	1.04	0.96	1.01	0.04	7	17	3.08E-56
Q86VP6-1	Cullin-associated and neddylation-dissociated protein 1	CAND1	0.99	0.98	1.06	0.94	1.01	0.04	39	42	0.00E+00
P55072	15S Mg(2+)-ATPase p97 subunit	VCP	0.99	0.98	1.06	0.94	1.01	0.04	52	69	0.00E+00
O95573	Long-chain acyl-CoA synthetase 3	ACS3	0.95	1.05	1.03	0.97	1.01	0.05	3	6.7	1.15E-55
P06744	Autocrine motility factor	GPI	1.06	1.02	0.95	1.05	1.01	0.06	29	60	0.00E+00
Q9Y2S2-1	Lambda-crystallin homolog	CRY	0.94	1.05	1.04	0.96	1.01	0.06	3	16	4.44E-16

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Q5TDJ6	CD1c molecule	CD1C	0.94	1.05	1.04	0.96	1.01	0.06	3	11	1.93E-42
P06127	Lymphocyte antigen T1/Leu-1	CD5	0.94	1.05	1.04	0.96	1.01	0.06	4	8.9	3.27E-25
Q13217	DnaJ homolog subfamily C member 3	DNAJC3	0.94	1.05	1.04	0.96	1.01	0.06	9	32	6.61E-127
B2R6D7	cDNA, FLJ92904, highly similar to Homo sapiens casein kinase 2, alpha 1 polypeptide (CSNK2A1), mRNA	CSNK2A1	1.02	1.07	0.94	1.06	1.01	0.07	14	50	5.43E-253
O43837-1	Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	0.96	0.98	1.09	0.92	1.01	0.07	13	41	1.33E-144
Q07955-1	Alternative-splicing factor 1	ASF	0.97	0.96	1.10	0.91	1.01	0.08	16	50	3.15E-135
B7WPD3	Putative uncharacterized protein TCEB2	hCG_1778969	1.03	1.08	0.92	1.09	1.01	0.08	4	28	8.63E-31
Q9BZI7-1	Nonsense mRNA reducing factor 3B	RENT3B	1.08	1.03	0.92	1.09	1.01	0.08	5	9.3	3.29E-19
B7Z2T5	cDNA FLJ55427, highly similar to Sodium/potassium-transporting ATPase alpha-1 chain (EC 3.6.3.9)	ATP1A1	1.02	1.10	0.91	1.10	1.01	0.10	15	20	5.39E-234
P07741	Adenine phosphoribosyltransferase	APRT	1.07	1.06	0.90	1.11	1.01	0.10	12	81	2.15E-241
P11233	Ras-related protein Ral-A	RAL	0.94	0.97	1.12	0.89	1.01	0.10	7	30	1.63E-98
Q92572	Adapter-related protein complex 3 sigma-1 subunit	AP3S1	1.08		0.94	1.06	1.01	0.10	3	11	2.87E-33
Q9Y4A5-1	350/400 kDa PCAF-associated factor	PAF400	0.94	1.13	0.96	1.04	1.01	0.10	5	1.5	5.91E-10
Q99627	COP9 homolog	COPS8	0.93		1.09	0.92	1.01	0.11	6	57	1.19E-91
O95292-1	Vesicle-associated membrane protein-associated protein B/C	UNQ484/PRO983	0.92	0.95	1.16	0.86	1.01	0.13	6	24	4.51E-36
B5MBX0	Putative uncharacterized protein CDCA5	CDCA5	1.02	1.14	0.87	1.15	1.01	0.14	3	14	1.00E-36
Q9BZE9-2	Alveolar soft part sarcoma chromosomal region candidate gene 1 protein	ASPL	0.86	1.14	1.03	0.97	1.01	0.14	6	14	2.16E-52
P30046	D-dopachrome decarboxylase	DDT	0.91		1.11	0.90	1.01	0.14	5	45	3.04E-26
Q15363	Membrane protein p24A	RNP24	0.91	1.11			1.01	0.14	3	17	4.96E-22
P49207	60S ribosomal protein	RPL34	1.11	1.08	0.84	1.19	1.01	0.15	6	33	4.02E-22

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	L34										
Q9P013	Protein CWC15 homolog	AD-002	0.89	1.18	0.96	1.04	1.01	0.15	4	24	3.16E-72
Q9H444	Charged multivesicular body protein 4b	C20orf178	0.90	1.20	0.93	1.08	1.01	0.17	4	23	3.97E-88
B4DKQ5	cDNA FLJ54710, highly similar to Target of Myb protein 1	CTA-286B10.5-010	0.89		1.13	0.88	1.01	0.17	3	11	6.60E-41
O15116	Cancer-associated Sm-like	CASM	1.13		0.89	1.12	1.01	0.17	2	17	8.45E-05
P27708	Aspartate carbamoyltransferase	CAD	1.11	1.11	0.81	1.23	1.01	0.17	34	24	3.08E-178
Q92608-1	Dedicator of cytokinesis protein 2	DOCK2	1.13	1.09	0.81	1.23	1.01	0.17	16	11	1.04E-86
P55884-2	eIF3 p110	EIF3B	1.11	1.20	0.72	1.39	1.01	0.26	22	31	2.36E-247
P08107	Heat shock 70 kDa protein 1/2	HSPA1	1.15	1.17	0.71	1.41	1.01	0.26	16	31	5.20E-205
Q9NYL9	Tropomodulin-3	TMOD3	0.82		1.20	0.83	1.01	0.27	8	40	2.94E-52
P07384	Calcium-activated neutral proteinase 1	CANPL1	0.87	0.84	1.32	0.76	1.01	0.27	8	16	2.85E-62
Q9Y4B4	Androgen receptor-interacting protein 4	ARIP4	1.22		0.80	1.25	1.01	0.30	2	3	8.38E-26
O14641	DSH homolog 2	DVL2	0.78	0.86	1.39	0.72	1.01	0.33	2	3.3	1.96E-10
O95163	Elongator complex protein 1	ELP1	1.04	1.36	0.63	1.59	1.01	0.37	3	2.7	5.37E-08
P16401	Histone H1.5	H1F5	0.78	0.81	1.44	0.69	1.01	0.37	16	44	1.40E-191
Q99614	Tetratricopeptide repeat protein 1	TPR1	1.29	1.18	0.56	1.79	1.01	0.39	6	31	1.61E-10
Q9BRQ6	Coiled-coil-helix-coiled-coil-helix domain-containing protein 6	CHCHD6	0.64	0.76	1.63	0.61	1.01	0.54	6	40	3.13E-38
C9JX46	Putative uncharacterized protein ECD	ECD			1.01	0.99	1.01		2	6.6	2.59E-61
Q9BVL2-1	Nucleoporin p58/p45	KIAA0410	1.01				1.01		2	3.3	3.48E-13
Q9NWS8-1	Required for meiotic nuclear division protein 1 homolog	C6orf96		1.01			1.01		2	5.1	1.27E-15
A6NCU1	Putative uncharacterized protein BCAP29	BCAP29	1.01				1.01		2	6.6	5.12E-03
Q9NPJ8-3	NTF2-related export protein 2	BM-025		1.01			1.01		2	7.6	2.87E-02
Q6DKK2	Tetratricopeptide repeat protein 19	TTC19		1.01			1.01		3	6	1.16E-15
A8MQB6	Putative uncharacterized	COMMD8	1.01				1.01		3	28	2.58E-119

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	protein COMMD8										
Q6N069-1	N-alpha-acetyltransferase 16, NatA auxiliary subunit	NAA16	1.01				1.01		4	3.9	4.49E-13
Q96G03	Glucose phosphomutase 2	MSTP006	1.17	1.01	0.86	1.16	1.01	0.16	13	30	2.75E-101
Q9NP92	28S ribosomal protein S30, mitochondrial	BM-047	1.01	1.01	1.02	0.98	1.01	0.01	2	7.3	3.22E-12
Q6PD62	RNA polymerase-associated protein CTR9 homolog	CTR9	1.02	1.00	1.02	0.98	1.01	0.01	8	10	6.07E-34
P21964-1	Catechol O-methyltransferase	COMT	1.03	1.01	1.00	1.00	1.01	0.02	9	52	5.29E-121
Q6ZUY8	cDNA FLJ43203 fis, clone FEBRA2008468, highly similar to LYSOSOMAL ACID LIPASE/CHOLESTERYL ESTER HYDROLASE (EC 3.1.1.13)	LIPA	0.99	1.02	1.03	0.97	1.01	0.02	3	12	1.12E-06
P27707	Deoxycytidine kinase	DCK	1.01	0.99	1.04	0.96	1.01	0.03	7	35	6.28E-34
Q70J99-1	Munc13-4	UNC13D	0.98	1.02	1.04	0.96	1.01	0.03	5	7.1	9.14E-29
Q92905	COP9 signalosome complex subunit 5	COPS5	0.97	1.01	1.06	0.94	1.01	0.05	6	23	1.60E-23
O94906	Pre-mRNA-processing factor 6	C20orf14	0.99	0.98	1.07	0.93	1.01	0.05	26	28	1.25E-175
P46439	Glutathione S-transferase Mu 5	GSTM5	0.94	1.06	1.04	0.96	1.01	0.06	11	37	1.59E-89
Q86UE4	3D3/LYRIC	AEG1	0.99	1.09	0.96	1.04	1.01	0.07	14	36	2.47E-129
B4E1T5	cDNA FLJ55764, highly similar to Apolipoprotein-L2	APOL2	0.99	1.10	0.95	1.05	1.01	0.08	3	8.2	1.45E-12
P54819-1	Adenylate kinase 2, mitochondrial	ADK2	0.93	1.02	1.09	0.92	1.01	0.08	10	56	1.96E-187
Q86V88-1	Magnesium-dependent phosphatase 1	MDP1	0.92	1.09	1.03	0.97	1.01	0.09	3	26	3.73E-165
Q9BV44	THUMP domain-containing protein 3	THUMPD3	0.99	1.12	0.93	1.08	1.01	0.10	7	20	9.48E-73
P14618-1	Cytosolic thyroid hormone-binding protein	OIP3	0.94	0.97	1.13	0.88	1.01	0.10	44	75	0.00E+00
P28482	Extracellular signal-regulated kinase 2	ERK2	0.94	0.96	1.14	0.88	1.01	0.11	14	47	1.54E-60
Q15102	PAF acetylhydrolase 29 kDa subunit	PAFAH1B3	0.94	0.94	1.16	0.86	1.01	0.13	10	59	2.24E-135
O95831-1	Apoptosis-inducing factor 1, mitochondrial	AIF	0.95	0.92	1.17	0.85	1.01	0.14	13	30	1.54E-178
Q14566	DNA replication licensing factor	MCM6	0.91	0.96	1.17	0.85	1.01	0.14	44	53	0.00E+00

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	MCM6										
Q8WVJ2	NudC domain-containing protein 2	NUDCD2	1.11	1.09	0.84	1.19	1.01	0.15	3	30	3.83E-81
Q7KZ85-1	Tat-cotransactivator 2 protein	KIAA0162	1.12	1.09	0.83	1.20	1.01	0.16	24	21	1.74E-210
Q6PKC0	GMP reductase	GMPR2	0.87	0.98	1.19	0.84	1.01	0.16	5	16	1.38E-50
O43447	Peptidyl-prolyl cis-trans isomerase H	CYP20	1.10	1.14	0.80	1.25	1.01	0.19	5	28	1.49E-16
O75396	ER-Golgi SNARE of 24 kDa	SEC22B	0.88	0.90	1.26	0.79	1.01	0.21	13	61	5.92E-219
Q96EY8	Cob(I)alamin adenosyltransferase	MMAB	1.02	1.23	0.79	1.27	1.01	0.22	2	10	9.41E-41
Q5JTZ9	Alanine--tRNA ligase	AARS2	0.84	0.86	1.34	0.75	1.01	0.28	14	21	1.57E-118
B3KXY9	cDNA FLJ46359 fis, clone TESTI4049786, highly similar to Hexokinase-1 (EC 2.7.1.1)	HK1	0.83	0.86	1.35	0.74	1.01	0.29	10	11	4.08E-82
P43897-2	Elongation factor Ts, mitochondrial	TSFM	1.20	1.20	0.64	1.56	1.01	0.32	4	25	4.04E-35
P57088	Protein DB83	DB83	1.17		0.86	1.16	1.02	0.22	3	13	1.19E-25
P00492	Hypoxanthine-guanine phosphoribosyltransferase	HPRT	1.01		1.02	0.98	1.02	0.01	9	45	3.53E-144
Q96S52-1	GPI transamidase component PIG-S	PIGS	0.92		1.11	0.90	1.02	0.13	3	8.3	9.23E-95
Q6DD87	TTF-I-interacting peptide 20	ZNF787		0.81	1.22	0.82	1.02	0.29	2	7	2.57E-02
Q99497	Oncogene DJ1	PARK7	1.04	1.01	1.00	1.00	1.02	0.02	16	83	0.00E+00
P49841-2	Glycogen synthase kinase-3 beta	GSK3B	1.02	0.99	1.04	0.96	1.02	0.03	7	30	2.00E-99
Q8TBA6-1	Cell proliferation-inducing gene 31 protein	GOLGA5	1.00	1.00	1.05	0.95	1.02	0.03	2	2.5	4.97E-03
P19338	Nucleolin	NCL	1.01	1.05	0.99	1.01	1.02	0.03	45	44	0.00E+00
Q8WVM8	Sec1 family domain-containing protein 1	C14orf163	0.98	1.02	1.05	0.95	1.02	0.04	13	32	1.62E-257
P08579	U2 small nuclear ribonucleoprotein B	SNRPB2	0.97	1.02	1.06	0.94	1.02	0.05	9	42	1.07E-69
Q9NQR4	Nitrilase homolog 2	CUA002	1.08	1.00	0.97	1.03	1.02	0.06	14	70	1.27E-164
P36957	2-oxoglutarate dehydrogenase complex component E2	DLTS	0.95	1.04	1.06	0.94	1.02	0.06	7	16	1.01E-49
Q9UBU9	mRNA export factor TAP	NXF1	0.96	1.00	1.09	0.92	1.02	0.07	7	15	1.40E-85
Q9H3U1-1	GCUNC-45	SMAP1	1.07	0.94	1.04	0.96	1.02	0.07	7	9.2	4.74E-46
Q13098	COP9 signalosome	COPS1	1.13	0.96	0.96	1.04	1.02	0.10	5	15	8.08E-49

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-7	complex subunit 1										
P30153	Medium tumor antigen-associated 61 kDa protein	PPP2R1A	0.95	0.96	1.14	0.88	1.02	0.11	29	57	0.00E+00
P68371	Tubulin beta-2 chain	TUBB2C	0.94	0.97	1.14	0.88	1.02	0.11	28	75	0.00E+00
Q9UJZ1	EPB72-like protein 2	HSPC108	1.11	1.06	0.88	1.14	1.02	0.12	15	61	0.00E+00
P30048	Antioxidant protein 1	AOP1	0.93	0.96	1.16	0.86	1.02	0.13	8	43	2.75E-131
P19784	Casein kinase II subunit alpha	CK2A2	0.94	1.17	0.94	1.06	1.02	0.13	12	47	1.22E-97
Q9UPQ9-3	Trinucleotide repeat-containing gene 6B protein	KIAA1093	0.89	1.00	1.16	0.86	1.02	0.14	5	2.9	5.18E-50
Q9NWH9	Modulator of estrogen-induced transcription	MET	0.87	1.02	1.16	0.86	1.02	0.15	18	18	2.33E-46
Q92945-1	Far upstream element-binding protein 2	FUBP2	0.90	0.96	1.19	0.84	1.02	0.15	36	55	0.00E+00
B3V096	BetaCstF-64 variant 2	CSTF2	1.08	1.13	0.84	1.19	1.02	0.16	9	23	2.26E-96
A8MVJ7	Putative uncharacterized protein SCFD1	SCFD1	0.92	1.21	0.92	1.09	1.02	0.17	6	15	2.22E-25
Q16555	Collapsin response mediator protein 2	CRMP2	0.93	0.91	1.21	0.83	1.02	0.17	22	58	8.98E-265
P11177-1	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	0.94	0.90	1.21	0.83	1.02	0.17	11	41	3.48E-205
Q9HCN8	PWP1-interacting protein 8	SDF2L1	1.16	1.10	0.79	1.27	1.02	0.20	21	55	4.65E-195
P25490	Delta transcription factor	INO80S	0.83	0.98	1.24	0.81	1.02	0.21	5	11	3.16E-78
Q9BUT1-1	3-hydroxybutyrate dehydrogenase type 2	BDH2	0.86	0.92	1.27	0.79	1.02	0.22	6	32	1.28E-104
A7E2E7	TBC1 domain family, member 13	TBC1D13	0.95	0.76	1.34	0.75	1.02	0.30	3	12	7.83E-20
B4DJA0	NADH-ubiquinone oxidoreductase 75 kDa subunit	hCG_17250	0.97	0.62	1.46	0.68	1.02	0.42	4	8.8	3.28E-75
Q96SB3	Neurabin-2	PPP1R6	0.80	0.73	1.52	0.66	1.02	0.44	3	5.8	2.31E-62
Q14703	Endopeptidase S1P	KIAA0091	1.06	1.06	0.93	1.08	1.02	0.08	2	1.6	1.27E-01
P17252	Protein kinase C alpha type	PKCA	0.93	1.02	1.10	0.91	1.02	0.09	4	5.2	7.48E-05
P49257	ER-Golgi intermediate compartment 53 kDa protein	ERGIC53	1.09	1.11	0.85	1.18	1.02	0.14	8	19	2.22E-58
P60842	ATP-dependent RNA helicase eIF4A-1	DDX2A	1.09	1.11	0.85	1.18	1.02	0.14	22	57	1.82E-285
P62191	26S protease regulatory subunit 4	PSMC1	1.10	1.12	0.83	1.20	1.02	0.16	17	42	0.00E+00
A8K878	cDNA FLJ77177,	ARME	1.00	1.20	0.85	1.18	1.02	0.18	8	32	4.64E-97

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	highly similar to Homo sapiens arginine-rich, mutated in early stage tumors (ARMET), mRNA	T									
Q13823	Autoantigen NGP-1	GNL2	1.06	1.18	0.81	1.23	1.02	0.19	5	9.8	4.16E-14
Q9NY27-1	Serine/threonine-protein phosphatase 4 regulatory subunit 2	PPP4R2	0.90	1.15	1.01	0.99	1.02	0.13	6	16	5.67E-52
B7Z6L9	cDNA FLJ54755, highly similar to Vacuolar ATP synthase subunit d (EC 3.6.3.14)	ATP6D	0.94	0.94	1.18	0.85	1.02	0.14	3	9.7	9.01E-11
Q9H944	Mediator complex subunit 20	MED20	1.01	1.17	0.88	1.14	1.02	0.15	6	36	7.50E-22
Q9NUB1-1	Acetate--CoA ligase 2	ACAS2L	0.96	0.90	1.20	0.83	1.02	0.16	7	15	4.08E-35
P35998	26S protease regulatory subunit 7	MSS1	1.11	1.15	0.80	1.25	1.02	0.19	18	46	5.31E-192
B4DW28	cDNA FLJ58953, highly similar to 40S ribosomal protein S20	RPS20	1.16	1.10	0.80	1.25	1.02	0.19	6	32	7.85E-60
Q68CP9-1	AT-rich interactive domain-containing protein 2	ARID2	1.28	1.23	0.55	1.82	1.02	0.41	5	5	3.03E-13
O75145-1	Liprin-alpha-3	KIAA0654		1.01	1.03	0.97	1.02	0.01	3	4.1	3.76E-05
P51858	Hepatoma-derived growth factor	HDGF	1.00	1.02	1.04	0.96	1.02	0.02	11	55	4.22E-130
O95197-1	Neuroendocrine-specific protein-like 2	ASYIP		1.04	1.00	1.00	1.02	0.03	2	1.9	1.91E-05
Q99785	Putative uncharacterized protein	PIG11	1.00	1.00	1.06	0.94	1.02	0.03	2	6.4	6.52E-04
P52758	14.5 kDa translational inhibitor protein	HRSP12	1.04	1.04	0.98	1.02	1.02	0.03	3	32	9.90E-14
Q13404-1	CROC-1	CROC1	1.01	0.99	1.06	0.94	1.02	0.04	5	13	4.32E-21
P62304	Sm protein E	SNRPE	0.99		1.05	0.95	1.02	0.04	4	57	2.91E-33
P04406	Glyceraldehyde-3-phosphate dehydrogenase	CDABP0047	1.06		0.98	1.02	1.02	0.06	26	82	0.00E+00
P06132	Uroporphyrinogen decarboxylase	UROD	0.97		1.07	0.93	1.02	0.07	7	28	5.64E-122
Q59GX2	Solute carrier family 2 (Facilitated glucose transporter), member 1 variant	GLUT1	0.96		1.08	0.93	1.02	0.08	2	3.1	8.59E-04
P61981	14-3-3 protein gamma	YWHAG	0.94	1.01	1.11	0.90	1.02	0.09	20	79	0.00E+00
C9J0D0	Putative uncharacterized protein PTMA	PTMA	1.03	1.10	0.93	1.08	1.02	0.09	7	22	2.74E-229

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P36915-1	GTP-binding protein HSR1	GNL1	1.00	1.12	0.94	1.06	1.02	0.09	10	20	6.99E-57
Q96AG4	Leucine-rich repeat-containing protein 59	LRRC59	1.08	1.09	0.89	1.12	1.02	0.11	14	54	5.52E-225
Q969P0-1	CD81 partner 3	CD81P3	0.94	1.10			1.02	0.11	3	6.5	2.29E-19
P09543-1	2,3-cyclic-nucleotide 3-phosphodiesterase	CNP	0.90	1.03	1.13	0.88	1.02	0.12	9	30	2.67E-99
Q9BQ61	Uncharacterized protein C19orf43	C19orf43	1.01	1.14	0.91	1.10	1.02	0.12	8	46	7.26E-20
Q14697-1	Alpha-glucosidase 2	G2AN	0.92	0.95	1.19	0.84	1.02	0.15	49	52	0.00E+00
P49189	4-trimethylaminobutyraldehyde dehydrogenase	ALDH4	0.91	0.96	1.19	0.84	1.02	0.15	8	16	2.32E-105
Q96DH6-1	RNA-binding protein Musashi homolog 2	MSI2	0.91		1.13	0.88	1.02	0.16	4	23	6.40E-93
A6XMH4	Beta-2-microglobulin	B2M	0.92	0.93	1.21	0.83	1.02	0.16	4	39	1.45E-38
Q8WUM5	Gem (Nuclear organelle) associated protein 4	GEMIN4		1.14	0.90	1.11	1.02	0.17	2	4.5	2.43E-04
P05204	High mobility group nucleosome-binding domain-containing protein 2	HMG17		1.14	0.90	1.11	1.02	0.17	4	52	7.38E-28
B4DNJ6	cDNA FLJ51909, highly similar to Serine-threonine kinase receptor-associatedprotein	MAWD	1.11	1.13	0.82	1.22	1.02	0.17	18	64	3.78E-209
O15027-5	Protein transport protein Sec16A	KIAA0310	1.07	1.17	0.82	1.22	1.02	0.18	14	11	1.29E-41
Q969U7	Hepatocellular carcinoma-susceptibility protein 3	HCCA3	1.06	1.18	0.82	1.22	1.02	0.18	5	21	5.98E-11
P33527-1	ATP-binding cassette sub-family C member 1	ABCC1	1.16		0.88	1.14	1.02	0.20	5	5	1.73E-09
Q9BUJ2-1	Adenovirus early region 1B-associated protein 5	E1BAP5	0.90	0.87	1.29	0.78	1.02	0.23	26	37	3.38E-188
B4DGP8	Calnexin	CANX	1.19	1.14	0.73	1.37	1.02	0.25	19	29	4.82E-141
Q07021	Complement component 1 Q subcomponent-binding protein, mitochondrial	C1QBP	1.20		0.84	1.19	1.02	0.25	9	44	1.11E-184
Q9UKM9-1	Autoantigen p542	HNRPCL2	0.85	0.87	1.34	0.75	1.02	0.28	18	66	3.53E-99
Q9HAV0	Guanine nucleotide-binding protein subunit beta-4	GNB4		0.82	1.22	0.82	1.02	0.28	6	19	5.18E-20

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Q8N5M4	Tetratricopeptide repeat protein 9C	TTC9C	0.86	0.85	1.35	0.74	1.02	0.29	7	30	3.70E-22
Q7KZI7-1	ELKL motif kinase 1	EMK1	0.77	1.27			1.02	0.35	2	4.1	2.37E-08
Q13011	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial	ECH1	0.76	0.84	1.46	0.68	1.02	0.38	16	59	1.09E-211
Q16637-1	Gemin-1	SMN	1.42	0.99	0.65	1.54	1.02	0.39	5	17	4.75E-81
B1AMT5	Stromal antigen 2	hCG_15646	0.74		1.30	0.77	1.02	0.40	7	6.9	1.97E-41
Q01831	DNA repair protein complementing XP-C cells	XPC			1.02	0.98	1.02		2	4.4	2.02E-16
Q9UGU0	Nuclear factor SPBP	KIAA0292			1.02	0.98	1.02		2	1.5	1.03E-03
Q8IWY9-2	Codanin-1	CDAN1			1.02	0.98	1.02		2	3.5	9.07E-26
Q8NDT2	One-twenty two protein 3	OTT3			1.02	0.98	1.02		5	7.2	1.40E-11
Q8WZ42-8	Connectin	TTN			1.02	0.98	1.02		7	0.2	5.28E-05
O95999	B-cell CLL/lymphoma 10	BCL10		1.02			1.02		2	9	2.01E-04
P35914	3-hydroxy-3-methylglutarate-CoA lyase	HMGCL		1.02			1.02		2	5.2	1.84E-14
Q5VZE5	Embryonic growth-associated protein homolog	EGAP		1.02			1.02		2	2.8	3.91E-03
Q8TAF3-1	USP1-associated factor 1	KIAA1449		1.02			1.02		2	3.2	1.73E-04
Q6ZRP7	Neuroblastoma-derived sulfhydryl oxidase	QSCN6L1	1.02				1.02		3	4.9	1.95E-14
Q9H074-1	Polyadenylate-binding protein-interacting protein 1	PAIP1		1.02			1.02		3	5.8	6.43E-06
Q15843	NEDD8	NEDD8	1.02				1.02		4	46	1.11E-99
O00764-1	Pyridoxal kinase	C21orf124	1.02				1.02		5	28	6.52E-78
Q16629-1	Splicing factor 9G8	SFRS7	1.06	1.05	0.95	1.05	1.02	0.06	9	34	1.40E-79
Q15046-2	Lysine--tRNA ligase	KARS	1	1.11	0.95	1.05	1.02	0.08	22	37	1.91E-222
Q9NZL4-2	Heat shock protein-binding protein 1	HSPBP	1.17	1.11	0.78	1.28	1.02	0.21	11	60	4.92E-77
Q9UHD1-1	CHORD domain-containing protein 1	CHORDC1	1.21	1.11	0.74	1.35	1.02	0.25	11	43	1.19E-220
P35637-2	75 kDa DNA-pairing protein	FUS	1.03	1.02	1.02	0.98	1.02	0.01	10	25	2.74E-115

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O43172-1	PRP4 homolog	PRP4	1.01	1.00	1.06	0.94	1.02	0.03	11	26	9.02E-91
O95782-1	100 kDa coated vesicle protein A	ADTAA	1.07	0.98	1.02	0.98	1.02	0.05	19	28	5.84E-124
C9JKU1	14KDa protein	PDIA3	0.97	1.04	1.06	0.94	1.02	0.05	7	51	1.74E-164
P13667	Endoplasmic reticulum resident protein 70	ERP70	0.97	1.04	1.06	0.94	1.02	0.05	31	43	8.92E-270
P62993-1	Adapter protein GRB2	ASH	0.98	0.95	1.14	0.88	1.02	0.10	12	61	4.51E-87
P13489	Placental ribonuclease inhibitor	PRI	1.09	1.08	0.90	1.11	1.02	0.11	21	70	0.00E+00
P25705	ATP synthase subunit alpha, mitochondrial	ATP5A	0.96	0.96	1.15	0.87	1.02	0.11	33	60	0.00E+00
Q66K74	BPY2-interacting protein 1	BPY2IP1	1.02	1.15	0.90	1.11	1.02	0.13	9	15	1.87E-44
P15531-2	Granzyme A-activated DNase	NDPKA	1.14	1.08	0.85	1.18	1.02	0.15	11	70	7.76E-109
Q9H3N1	Thioredoxin domain-containing protein 1	PSEC0085	1.13	1.17	0.77	1.30	1.02	0.22	11	40	6.58E-43
P78316-1	Nucleolar complex protein 14	C4orf9	1.21	1.09	0.77	1.30	1.02	0.23	8	8.3	8.27E-20
Q9UHD9	Chap1	HRIHFB2157	0.99	1.27	0.81	1.23	1.02	0.23	6	17	2.65E-88
Q9NR28-1	Diablo homolog, mitochondrial	DIABLO	1.01	1.02	1.04	0.96	1.02	0.02	6	25	4.06E-36
Q5TFE4	5-nucleotidase domain-containing protein 1	LP2642	1.02	1.05	1.00	1.00	1.02	0.03	4	10	7.14E-81
P25788-1	Macropain subunit C8	HC8	0.99	1.03	1.05	0.95	1.02	0.03	13	41	1.76E-45
P21281	Endomembrane proton pump 58 kDa subunit	ATP6B2	1.06	1.04	0.97	1.03	1.02	0.05	12	38	5.80E-139
B4DM45	cDNA FLJ56465, highly similar to Dynactin-1	DCTN1	0.99	1.00	1.08	0.93	1.02	0.05	28	33	2.89E-207
P06576	ATP synthase subunit beta, mitochondrial	ATP5B	0.98	1.01	1.08	0.93	1.02	0.05	28	76	0.00E+00
Q9NPA0	UPF0480 protein C15orf24	C11orf3	0.96	1.04	1.07	0.93	1.02	0.06	6	34	1.35E-11
Q5QJE6	Deoxynucleotidyltransferase terminal-interacting protein 2	DNTTIP2	1.07	1.04	0.96	1.04	1.02	0.06	8	14	1.32E-173
O43516-3	Protein PRPL-2	WASPIP	1.06	1.06	0.95	1.05	1.02	0.06	2	7.3	5.51E-06
Q5SW79-1	Centrosomal protein of 170 kDa	CEP170	1.06	1.06	0.95	1.05	1.02	0.06	13	12	9.52E-84
P30101	58 kDa glucose-regulated protein	ERP57	0.95	1.03	1.09	0.92	1.02	0.07	30	55	0.00E+00
P35244	Replication factor A protein 3	REPA3	1.01	0.95	1.11	0.90	1.02	0.08	3	43	3.73E-52
P52272-	Heterogeneous nuclear	HNRNP	0.94	1.02	1.11	0.90	1.02	0.09	45	64	1.42E-193

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1	ribonucleoprotein M	M									
A8K2W7	cDNA FLJ78119, highly similar to Homo sapiens G1 to S phase transition 1 (GSPT1), mRNA	GSPT1	1.09	1.07	0.91	1.10	1.02	0.10	12	21	1.37E-79
P09110	3-ketoacyl-CoA thiolase, peroxisomal	ACAA	1.13	1.03	0.91	1.10	1.02	0.11	8	33	1.48E-100
O43765	Small glutamine-rich tetratricopeptide repeat-containing protein alpha	SGT	0.92	1.14	1.01	0.99	1.02	0.11	10	36	7.03E-89
B2R7C5	cDNA, FLJ93378, highly similar to Homo sapiens MCM3 minichromosome maintenance deficient 3 (S. cerevisiae) (MCM3), mRNA	hCG_22498	0.92	0.97	1.18	0.85	1.02	0.14	39	52	0.00E+00
Q15018	Abraxas brother protein 1	ABRO1	0.83	1.04	1.20	0.83	1.02	0.19	4	15	2.71E-44
P30038	Aldehyde dehydrogenase family 4 member A1	ALDH4A1	0.84	0.99	1.24	0.81	1.02	0.20	4	9.2	6.46E-39
P30084	Enoyl-CoA hydratase 1	ECHS1	0.87	0.87	1.33	0.75	1.02	0.27	9	34	0.00E+00
P00374	Dihydrofolate reductase	DHFR	1.24	1.17	0.66	1.52	1.02	0.32	7	28	8.15E-75
Q8N9M1-1	Uncharacterized protein C19orf47	C19orf47		1.04	1.01	0.99	1.03	0.02	2	5.9	3.63E-03
P46977	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A	ITM1		1.09	0.96	1.04	1.03	0.09	4	5	9.73E-05
Q9BRJ7-1	NUDT16-like protein 1	NUDT16L1	1.11		0.94	1.06	1.03	0.12	2	13	1.17E-37
Q96DC7-2	Transmembrane and coiled-coil domain-containing protein 6	PRO1580		1.15	0.90	1.11	1.03	0.18	2	7.8	5.12E-08
Q58FF8	Heat shock protein 90-beta b	HSP90AB2P	1.15		0.90	1.11	1.03	0.18	17	26	4.05E-183
O43464-1	High temperature requirement protein A2	HTRA2	1.16		0.89	1.12	1.03	0.19	2	5.2	4.83E-14
P61962	DDB1- and CUL4-associated factor 7	DCAF7	1.02	1.03	1.03	0.97	1.03	0.01	4	16	4.23E-35
P13010	86 kDa subunit of Ku antigen	G22P2	1.00	1.03	1.05	0.95	1.03	0.03	48	70	0.00E+00
Q01780-1	Autoantigen PM/Scl 2	EXOSC10	1.03	1.05	1.00	1.00	1.03	0.03	23	32	6.78E-90
B9EGQ8	SMARCA4 protein	SMARCA4	1.01	1.01	1.06	0.94	1.03	0.03	27	21	8.37E-302
P23246-	100 kDa DNA-pairing	PSF	1.03	0.99	1.06	0.94	1.03	0.04	35	49	0.00E+00

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1	protein										
O75934	Breast carcinoma-amplified sequence 2	BCAS2	0.99	1.06	1.03	0.97	1.03	0.04	10	50	3.19E-89
Q14151	Scaffold attachment factor B2	KIAA0138	1.04	0.98	1.06	0.94	1.03	0.04	22	27	1.77E-104
B2R7M3	cDNA, FLJ93510, highly similar to Homo sapiens JTV1 gene (JTV1), mRNA	AIMP2	1.04	1.06	0.98	1.02	1.03	0.04	8	35	1.91E-100
Q9NQ88	Probable fructose-2,6-bisphosphatase TIGAR	C12orf5	1.00	1.08	1.00	1.00	1.03	0.05	8	44	1.13E-73
P45880-1	Outer mitochondrial membrane protein porin 2	VDAC2	0.97	1.05	1.06	0.94	1.03	0.05	10	44	1.51E-85
P60763	p21-Rac3	RAC3	0.99	0.99	1.10	0.91	1.03	0.06	9	38	1.85E-128
P09012	U1 small nuclear ribonucleoprotein A	SNRPA	0.96	1.01	1.11	0.90	1.03	0.08	8	30	1.84E-19
Q7Z2Z2-1	Elongation factor Tu GTP-binding domain-containing protein 1	EFTUD1	1.12	1.00	0.96	1.04	1.03	0.08	6	8.5	1.02E-68
Q9Y2X3	Nucleolar protein 5	HSPC120	1.08	1.08	0.92	1.09	1.03	0.09	16	38	5.85E-225
Q13442	28 kDa heat- and acid-stable phosphoprotein	HASPP28	1.00	1.13	0.95	1.05	1.03	0.09	8	43	7.73E-34
Q96CS3	FAS-associated factor 2	ETEA	0.93	1.12	1.03	0.97	1.03	0.10	6	16	4.48E-12
P33993-1	CDC47 homolog	CDC47	0.97	0.97	1.14	0.88	1.03	0.10	39	60	0.00E+00
Q8TC12-1	Androgen-regulated short-chain dehydrogenase/reductase 1	ARSDR1	1.03	1.13	0.92	1.09	1.03	0.11	3	13	1.53E-57
Q14498-1	Hepatocellular carcinoma protein 1	HCC1	0.96	0.97	1.15	0.87	1.03	0.11	12	27	1.53E-167
P25685	DnaJ homolog subfamily B member 1	DNAJ1	1.06	1.12	0.90	1.11	1.03	0.11	15	47	1.41E-156
Q08257	NADPH:quinone reductase	CRYZ	0.90	1.06	1.12	0.89	1.03	0.11	8	32	4.23E-65
Q12962	Transcription initiation factor TFIID 30 kDa subunit	TAF10	1.16	1.01	0.91	1.10	1.03	0.13	3	19	1.90E-125
O00442-2	RNA 3-terminal phosphate cyclase	RPC	0.99	0.92	1.17	0.85	1.03	0.13	4	14	1.80E-42
B4DIK2	cDNA FLJ60565, highly similar to Nuclear pore complex protein Nup153	NUP153	1.13	1.07	0.88	1.14	1.03	0.13	10	11	1.33E-117
Q16881-1	Gene associated with retinoic and interferon-induced mortality 12 protein	GRIM12	1.03	0.89	1.16	0.86	1.03	0.14	21	47	1.73E-187
P61221	2-5-oligoadenylate-binding protein	ABCE1	1.09	1.12	0.87	1.15	1.03	0.14	19	41	1.06E-241

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P24941	Cell division protein kinase 2	CDK2	0.88	1.19	1.01	0.99	1.03	0.16	6	30	4.01E-26
Q9UJA5-1	tRNA (adenine-N(1)-)-methyltransferase non-catalytic subunit TRM6	CGI-09	1.18	1.06	0.84	1.19	1.03	0.17	7	14	1.80E-59
Q9NQZ2	Charged amino acid-rich leucine zipper 1	CRLZ1	1.11	1.16	0.81	1.23	1.03	0.19	7	22	2.11E-67
O60231	ATP-dependent RNA helicase #3	DBP2	1.21	1.05	0.82	1.22	1.03	0.20	12	15	3.64E-78
O75554	Formin-binding protein 21	FBP21	1.17	0.78	1.13	0.88	1.03	0.21	4	10	3.66E-15
P00813	Adenosine aminohydrolase	ADA	1.16	1.18	0.74	1.35	1.03	0.25	29	78	0.00E+00
P42574	Caspase-3	CASP3	0.90	0.85	1.33	0.75	1.03	0.26	5	17	4.21E-72
Q16891-1	Cell proliferation-inducing gene 4/52 protein	HMP	0.86	0.84	1.38	0.72	1.03	0.31	31	43	1.77E-200
P61201-2	Alien homolog	COPS2	0.78	0.89	1.41	0.71	1.03	0.34	4	11	2.93E-09
P48735	ICD-M	IDH2	0.66	0.68	1.74	0.57	1.03	0.62	22	51	4.98E-280
Q5JRX3-1	Pitrilysin metalloproteinase 1	KIAA1104	1.08	1.11	0.89	1.12	1.03	0.12	12	18	1.85E-72
O14776-1	TATA box-binding protein-associated factor 2S	CA150	1.08	1.11	0.89	1.12	1.03	0.12	20	20	3.43E-75
Q96AT1	Uncharacterized protein KIAA1143	KIAA1143		1.03	1.03	0.97	1.03	0.00	6	36	4.71E-18
Q8TBE9	Haloacid dehalogenase-like hydrolase domain-containing protein 4	C20orf147		1.04	1.02	0.98	1.03	0.01	4	12	1.83E-86
P10599	ATL-derived factor	TRDX	1.00	1.04	1.05	0.95	1.03	0.03	8	51	1.68E-70
P35268	60S ribosomal protein L22	RPL22	1.03	1.07	0.99	1.01	1.03	0.04	4	51	1.76E-214
P11021	78 kDa glucose-regulated protein	GRP78	1.03	1.07	0.99	1.01	1.03	0.04	36	49	0.00E+00
Q9NP77-1	RNA polymerase II subunit A C-terminal domain phosphatase SSU72	HSPC182	1.00	1.00	1.09	0.92	1.03	0.05	6	35	1.45E-30
Q08378-1	Golgi complex-associated protein of 170 kDa	GOLGA3	1.01	1.09	0.99	1.01	1.03	0.05	12	8.5	9.23E-45
P52292	Importin subunit alpha-2	KPNA2	1.09	1.02	0.98	1.02	1.03	0.06	20	57	0.00E+00
Q5VWZ2-1	Lysophospholipase-like protein 1	LYPLAL1	1.07	0.99			1.03	0.06	2	16	1.21E-12
P24752	Acetoacetyl-CoA thiolase	ACAT	0.97	1.03	1.09	0.92	1.03	0.06	12	44	4.39E-253
O00233-1	26S proteasome non-ATPase regulatory subunit 9	PSMD9	0.96	1.07	1.06	0.94	1.03	0.06	10	51	1.89E-50

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P06733-1	2-phospho-D-glycerate hydro-lyase	ENO1	1.07	1.06	0.96	1.04	1.03	0.06	35	77	0.00E+00
Q99426	Cytoskeleton-associated protein 1	CG22	0.96	1.04	1.09	0.92	1.03	0.07	10	49	1.24E-169
O00567	Nucleolar protein 56	NOL5A	1.07	1.07	0.95	1.05	1.03	0.07	21	43	2.18E-190
O95639-1	Cleavage and polyadenylation specificity factor 30 kDa subunit	CPSF30	0.98		1.08	0.93	1.03	0.07	3	12	2.16E-21
Q15020-1	Squamous cell carcinoma antigen recognized by T-cells 3	KIAA0156	1.01	0.97	1.11	0.90	1.03	0.07	16	22	9.41E-214
P21926	5H9 antigen	CD9	1.09		0.97	1.03	1.03	0.08	2	15	1.75E-58
P46060	Ran GTPase-activating protein 1	KIAA1835	1.00	0.96	1.13	0.88	1.03	0.09	20	43	0.00E+00
P35580-3	Cellular myosin heavy chain, type B	MYH10	0.95	1.01	1.13	0.88	1.03	0.09	83	45	0.00E+00
P17987	CCT-alpha	CCT1	1.09	1.08	0.92	1.09	1.03	0.10	32	69	0.00E+00
Q9Y3B8-1	Oligoribonuclease, mitochondrial	CGI-114	0.94	1.00	1.15	0.87	1.03	0.11	6	19	3.51E-13
Q15029	116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	1.13	1.05	0.91	1.10	1.03	0.11	36	48	0.00E+00
P61077-2	Ubiquitin carrier protein D3	UBCH5C	1.11	0.95			1.03	0.11	2	14	1.97E-04
Q8IZ83-1	Aldehyde dehydrogenase family 16 member A1	ALDH16A1	1.15	1.03	0.91	1.10	1.03	0.12	9	16	7.11E-75
Q9BY77-1	46 kDa DNA polymerase delta interaction protein	KIAA1649	1	0.92	1.17	0.85	1.03	0.13	11	40	1.28E-67
P68363	Alpha-tubulin ubiquitous	TUBA1B	0.96	0.95	1.18	0.85	1.03	0.13	33	76	0.00E+00
P58546	Myotrophin	MTPN	0.90	1.03	1.16	0.86	1.03	0.13	7	74	3.50E-107
B3KWV6	cDNA FLJ43948 fis, clone TESTI4014924, highly similar to Homo sapiens cytoplasmic FMR1 interacting protein 1 (CYFIP1), transcript variant 1, mRNA	CYFIP1	0.91	1.17	1.01	0.99	1.03	0.13	6	5.2	1.50E-14
P00367	Glutamate dehydrogenase 1, mitochondrial	GLUD	0.89	1.01	1.19	0.84	1.03	0.15	16	31	1.47E-78
Q9NY93	ATP-dependent 61 kDa nucleolar RNA helicase	DDX56	1.14	1.10	0.85	1.18	1.03	0.16	6	15	1.36E-57
P36969-1	Glutathione peroxidase 4	GPX4	0.84	1.13	1.12	0.89	1.03	0.16	3	9.8	1.71E-04
B4E1S7	cDNA FLJ61202,	AIMP1	1.10	1.16	0.83	1.20	1.03	0.18	12	50	1.88E-87

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	highly similar to Multisynthetase complex auxiliary component p43										
Q9H9H4	ESCRT-I complex subunit VPS37B	VPS37B	1.17		0.89	1.12	1.03	0.20	5	20	6.63E-38
Q9Y2S7	38 kDa DNA polymerase delta interaction protein	HSPC017	1.19	1.12	0.78	1.28	1.03	0.22	11	40	4.92E-83
O60841	Eukaryotic translation initiation factor 5B	EIF5B	1.10	1.23	0.76	1.32	1.03	0.24	31	32	6.29E-299
Q9NZB2-6	Constitutive coactivator of PPAR-gamma-like protein 1	C9orf10	1.15	1.19	0.75	1.33	1.03	0.24	17	20	2.06E-170
P48506	Gamma-ECS	GCLC		1.22	0.84	1.19	1.03	0.27	6	11	2.68E-40
O75607	Nucleoplasmin-3	NPM3	1.45		0.61	1.64	1.03	0.59	3	32	2.36E-73
Q9UPW0-1	Forkhead box protein J3	FOXJ3			1.03	0.97	1.03		2	4.7	2.09E-20
O60942-1	GTP--RNA guanylyltransferase	CAP1A		1.03			1.03		2	3.4	1.64E-05
B4DX69	cDNA FLJ55158, highly similar to Thioredoxin, mitochondrial	TRX2	1.03				1.03		2	18	1.47E-04
P53602	Diphosphomevalonate decarboxylase	MPD		1.03			1.03		2	5.8	4.72E-19
Q5VW32	BRO1 domain-containing protein BROX	BROFTI		1.03			1.03		2	6.1	1.22E-08
P78356-1	1-phosphatidylinositol-5-phosphate 4-kinase 2-beta	PIP4K2B		1.03			1.03		2	6.7	4.54E-06
B0QY29	Family with sequence similarity 118, member A	CTA-268H5.11-003	1.03				1.03		2	19	3.38E-118
Q9NWU2	Protein C20orf11	C20orf11	1.03				1.03		3	25	1.95E-26
A4UCT1	Glyceraldehyde-3-phosphate dehydrogenase	GAPD		1.03			1.03		11	33	1.45E-144
P84090	Enhancer of rudimentary homolog	ERH	1.04	1.05	1.01	0.99	1.03	0.02	7	46	1.68E-201
Q9BUQ0	Polypyrimidine tract binding protein 1	hCG_20560	1.05	0.96	1.09	0.92	1.03	0.07	20	54	0.00E+00
Q9NXR7-1	Brain and reproductive organ-expressed protein	BRCC45	0.98	1.11	1.01	0.99	1.03	0.07	3	8.2	7.85E-06
Q00688	25 kDa FK506-binding protein	FKBP25	1.01	1.14	0.95	1.05	1.03	0.10	11	53	1.25E-145
Q9Y6B6	GTP-binding protein SAR1b	SAR1B	1.16	0.94	1.00	1.00	1.03	0.11	6	40	7.82E-64
Q9BV8	Methyltransferase-like	AD-003	0.95	0.96	1.19	0.84	1.03	0.14	5	24	1.86E-36

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6	protein 11A										
Q92616	GCN1-like protein 1	GCN1L1	1.15	1.17	0.78	1.28	1.03	0.22	32	18	0.00E+00
Q1KMD3	Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	0.84	0.94	1.32	0.76	1.03	0.25	21	30	1.06E-151
P63241-2	eIF-4D	EIF5A	1.14	1.24	0.72	1.39	1.03	0.28	10	60	0.00E+00
P05387	60S acidic ribosomal protein P2	D11S2243E	1.12	1.26	0.72	1.39	1.03	0.28	9	74	4.95E-235
P16615-1	Calcium pump 2	ATP2A2	1.07	1.04	0.99	1.01	1.03	0.04	13	18	2.08E-182
P14866	Heterogeneous nuclear ribonucleoprotein L	HNRNPL	1.00	1.02	1.08	0.93	1.03	0.04	24	59	0.00E+00
Q96P16-1	Cyclin-dependent kinase inhibitor 2B-related protein	P15RS	1.06	0.97	1.07	0.93	1.03	0.06	8	38	3.01E-48
Q9UJY5-1	ADP-ribosylation factor-binding protein GGA1	GGA1	0.98	1.02	1.1	0.91	1.03	0.06	6	13	3.94E-43
Q9Y676	28S ribosomal protein S18-2, mitochondrial	C6orf14	1.06	0.96	1.08	0.93	1.03	0.06	5	30	2.62E-33
Q15006	Tetratricopeptide repeat protein 35	KIAA0103	1.07	1.08	0.95	1.05	1.03	0.07	7	31	2.28E-131
Q6P6C2-1	Alkylated DNA repair protein alkB homolog 5	ABH5	1.09	1.08	0.93	1.08	1.03	0.09	4	14	4.32E-43
O94913	Pre-mRNA cleavage complex 2 protein Pcf11	KIAA0824	1.07	1.10	0.93	1.08	1.03	0.09	6	4.6	2.32E-36
Q9H3P2-7	Negative elongation factor A	NELFA	1.11	1.07	0.92	1.09	1.03	0.10	6	18	5.48E-82
B3KT15	26S proteasome non-ATPase regulatory subunit 13	PSMD13	1.13	1.07	0.9	1.11	1.03	0.12	17	49	3.40E-255
Q02790	51 kDa FK506-binding protein	FKBP4	1.15	1.10	0.85	1.18	1.03	0.16	26	67	6.82E-281
O43681	Arsenical pump-driving ATPase	ARSA	1.18	1.07	0.85	1.18	1.03	0.17	10	37	1.61E-71
Q9Y5B0-1	RNA polymerase II subunit A C-terminal domain phosphatase	CTDP1	1.15	1.12	0.83	1.20	1.03	0.18	5	8.1	4.09E-45
Q8N6M0	DUBA-5	CGI-77	1.09	1.18	0.83	1.20	1.03	0.18	5	26	1.01E-64
P21399	Citrate hydro-lyase	ACO1	0.92	0.91	1.27	0.79	1.03	0.21	9	16	8.02E-68
Q13200	26S proteasome non-ATPase regulatory subunit 2	PSMD2	1.15	1.18	0.77	1.30	1.03	0.23	28	39	6.67E-300
A8K976	cDNA FLJ76685, highly similar to Homo sapiens WD repeat domain 37 (WDR37), mRNA	KIAA0982		1.17	0.90	1.11	1.04	0.19	2	4.4	6.11E-05

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P14649	Myosin light chain 1 slow-twitch muscle A isoform	MLC1SA	0.86		1.21	0.83	1.04	0.25	9	50	4.02E-63
P13598	Intercellular adhesion molecule 2	ICAM2	0.83		1.24	0.81	1.04	0.29	2	11	8.83E-30
Q7Z2T5-1	TRM1-like protein	C1orf25	1.24		0.83	1.20	1.04	0.29	4	11	1.44E-110
Q9NYB9-1	Abelson interactor 2	ABI2		1.03	1.04	0.96	1.04	0.01	4	11	7.01E-30
B4DQN9	cDNA FLJ50617, highly similar to Tubulin beta-7 chain	DAAP-285E11.4-003	1.03		1.04	0.96	1.04	0.01	25	74	0.00E+00
Q9NVV4-2	PAP-associated domain-containing protein 1	MTPAP	1.09	0.98			1.04	0.08	4	9	2.06E-25
Q9Y3C6	Peptidyl-prolyl cis-trans isomerase-like 1	CGI-124	0.95	1.12			1.04	0.12	4	29	1.98E-46
P62633-1	Zinc finger protein 9	CNBP		1.28	0.79	1.27	1.04	0.35	9	45	4.45E-200
Q8IWJ2-2	CLL-associated antigen KW-11	GCC2	0.76	1.31			1.04	0.39	9	5.3	2.72E-30
P62140	Serine/threonine-protein phosphatase PP1-beta catalytic subunit	PPP1CB	1.14	1.00	0.97	1.03	1.04	0.09	14	49	0.00E+00
Q15427	Pre-mRNA-splicing factor SF3b 49 kDa subunit	SAP49	1.00	1.05	1.06	0.94	1.04	0.03	5	21	6.37E-166
Q04726-1	Enhancer of split groucho-like protein 3	KIAA1547	1.09	1.00	1.02	0.98	1.04	0.05	5	8.2	6.73E-25
P38159	Glycoprotein p43	HNRPG	0.98	1.00	1.13	0.88	1.04	0.08	21	44	1.13E-136
Q9NWV8-1	BRCA1-A complex subunit MERIT40	C19orf62	1.13	1.00	0.98	1.02	1.04	0.08	3	12	2.10E-130
Q99496	E3 ubiquitin-protein ligase RING2	RNF2	1.09	1.08	0.94	1.06	1.04	0.08	4	15	2.63E-14
O94776	Metastasis-associated 1-like 1	MTA1L1	0.97	0.99	1.15	0.87	1.04	0.10	24	37	2.66E-215
P11216	Glycogen phosphorylase, brain form	PYGB	0.94	1.03	1.14	0.88	1.04	0.10	11	18	3.78E-110
P62495	Eukaryotic peptide chain release factor subunit 1	ERF1	1.08	1.13	0.90	1.11	1.04	0.12	10	27	8.49E-71
Q8NF91-1	Enaptin	C6orf98	0.92	1.00	1.19	0.84	1.04	0.14	3	0.5	1.01E-59
Q4G0F5	Vacuolar protein sorting-associated protein 26B	VPS26B	0.94	0.96	1.21	0.83	1.04	0.15	2	6.8	1.41E-09
P07686	Beta-hexosaminidase subunit beta	HCC7	0.91	0.99	1.21	0.83	1.04	0.16	10	23	3.51E-48
Q9HAV7	GrpE protein homolog 1, mitochondrial	GREPEL1	1.14	1.16	0.81	1.23	1.04	0.20	10	54	5.05E-105
P0C0S8	Histone H2A type 1	H2AFC	0.89	0.84	1.38	0.72	1.04	0.30	13	66	0.00E+00

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P40222	Alpha-taxilin	TXLN	1.21	1.23	0.67	1.49	1.04	0.32	6	18	3.35E-55
Q9NV56	MRG-binding protein	C20orf20	1.20	1.24	0.67	1.49	1.04	0.32	2	14	5.15E-119
C9JQC3	Small nuclear ribonucleoprotein Sm D3	SNRPD3	1.03	1.04	1.04	0.96	1.04	0.01	4	24	1.79E-105
Q14974	Importin subunit beta-1	KPNB1	1.03	1.03	1.05	0.95	1.04	0.01	34	47	0.00E+00
P00505	Aspartate aminotransferase, mitochondrial	GOT2	1.02	1.09	1.00	1.00	1.04	0.05	15	41	6.83E-200
Q9UIG0-1	Bromodomain adjacent to zinc finger domain protein 1B	BAZ1B	1.04	1.11	0.96	1.04	1.04	0.08	27	25	6.02E-154
O43823	A-kinase anchor protein 8	AKAP8	1.02	0.91	1.18	0.85	1.04	0.14	6	14	1.29E-43
O76031	ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	CLPX	1.12	1.12	0.87	1.15	1.04	0.14	10	16	6.02E-67
Q14558	39 kDa phosphoribosypyrophosphate synthase-associated protein	PRPSAP1	1.00	0.78	1.33	0.75	1.04	0.28	6	24	1.33E-147
Q9NR30-1	DEAD box protein 21	DDX21	1.25	1.16	0.70	1.43	1.04	0.30	24	41	1.03E-193
Q6NXT1-1	Ankyrin repeat domain-containing protein 54	ANKRD54	0.68	1.37	1.06	0.94	1.04	0.35	5	34	9.57E-23
A2A274	Aconitase 2, mitochondrial	ACO2	0.74	0.78	1.59	0.63	1.04	0.48	20	31	5.19E-229
Q9BTE7	DCN1-like protein 5	DCUN1D5	1.21	0.97	0.94	1.06	1.04	0.15	4	27	9.77E-19
P37108	18 kDa Alu RNA-binding protein	SRP14	1.15	1.13	0.84	1.19	1.04	0.17	8	47	7.07E-111
Q9UKD2	mRNA turnover protein 4 homolog	C1orf33	1.07	1.23	0.82	1.22	1.04	0.21	10	40	4.09E-51
Q7Z6E9-1	p53-associated cellular protein of testis	My038	1.03		1.05	0.95	1.04	0.01	3	3.1	1.14E-07
Q8WVC0-1	Replicative senescence down-regulated leo1-like protein	LEO1	1.03		1.05	0.95	1.04	0.01	5	6.2	3.80E-31
P61970	Nuclear transport factor 2	NTF2	1.05	1.02	1.05	0.95	1.04	0.02	4	50	3.67E-18
B2ZZ91	Golgin B1	GOLGB1	1.02		1.06	0.94	1.04	0.03	11	5.5	1.51E-46
P23919	Thymidylate kinase	CDC8	1.01	1.08	1.03	0.97	1.04	0.04	11	44	2.59E-37
A7MAP0	Coronin-1C_i2 protein	CORO1C	1.03	1.08	1.01	0.99	1.04	0.04	12	27	5.40E-101
Q9NVT9	Armadillo repeat-containing protein 1	ARCP	1.10	1.02	1.00	1.00	1.04	0.05	3	22	2.12E-21
Q96B26	Exosome complex exonuclease RRP43	EXOSC8	1.10	1.07	0.95	1.05	1.04	0.08	4	23	2.17E-29

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O43809	Cleavage and polyadenylation specificity factor 25 kDa subunit	CFIM25	1.02	0.97	1.13	0.88	1.04	0.08	18	82	2.53E-176
C9JC60	Putative uncharacterized protein NAPRT1	NAPRT1	1.10	0.98			1.04	0.08	3	8	8.56E-60
Q9P016-1	Thymocyte nuclear protein 1	HSPC144	1.10	1.08	0.94	1.06	1.04	0.09	17	69	2.55E-63
Q14696	LDLR chaperone MESD	KIAA0081	0.97	1.01	1.14	0.88	1.04	0.09	6	23	3.01E-46
Q9P2X0-2	Dolichol-phosphate mannose synthase subunit 3	DPM3	0.97	1.11			1.04	0.10	2	13	4.55E-116
P62312	U6 snRNA-associated Sm-like protein LSm6	LSM6	1.11	0.97			1.04	0.10	5	56	2.63E-15
P12004	Cyclin	PCNA	0.95	1.02	1.15	0.87	1.04	0.10	17	74	1.82E-282
Q00403	General transcription factor TFIIB	GTF2B	1.07	0.92	1.13	0.88	1.04	0.11	8	37	2.22E-107
P57737-1	70 kDa WD repeat tumor rejection antigen homolog	CORO7	1.04	0.91	1.17	0.85	1.04	0.13	11	18	3.94E-54
O75822	eIF3 p35	EIF3J	1.00	1.19	0.93	1.08	1.04	0.13	10	41	1.00E-49
Q9Y5Z4-1	Heme-binding protein 2	C6orf34		0.94	1.14	0.88	1.04	0.14	4	22	6.14E-60
P61088	Bendless-like ubiquitin-conjugating enzyme	BLU	0.99	0.92	1.21	0.83	1.04	0.15	8	57	3.54E-58
Q15796-1	Mad-related protein 2	MADH2	0.86	1.08	1.18	0.85	1.04	0.16	4	11	7.79E-53
B4E1U9	cDNA FLJ54776, highly similar to Cell division control protein 42 homolog	CDC42	0.95	0.93	1.24	0.81	1.04	0.17	6	30	2.36E-53
Q53EW7	Branched-chain-amino-acid aminotransferase	BCAT2	0.92	0.94	1.26	0.79	1.04	0.19	3	10	5.30E-27
Q7Z7H5-1	Endoplasmic reticulum stress-response protein 25	ERS25	0.90	0.96	1.26	0.79	1.04	0.19	6	22	1.01E-65
C9IZE4	Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 6, isoform CRA_b	hCG_23509	1.18		0.90	1.11	1.04	0.20	11	27	6.36E-79
B2R4K7	60S ribosomal protein L6	RPL6	1.15	1.18	0.79	1.27	1.04	0.22	18	52	1.54E-180
Q06587-1	E3 ubiquitin-protein ligase RING1	RING1	1.20		0.88	1.14	1.04	0.23	3	9.6	1.93E-06
Q99523	100 kDa NT receptor	SORT1		1.21	0.87	1.15	1.04	0.24	2	2.6	1.07E-13
Q9NXH9-1	N(2),N(2)-dimethylguanosine tRNA methyltransferase	TRMT1	1.37	0.98	0.77	1.30	1.04	0.30	3	7.4	2.39E-30

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Q9P2K5-1	Myelin expression factor 2	KIAA1341		0.80	1.28	0.78	1.04	0.34	2	3.5	9.79E-04
C9JWM7	Putative uncharacterized protein ARPC4	ARPC4	0.86	0.81	1.45	0.69	1.04	0.36	6	35	1.76E-45
Q8IZ73	RNA pseudouridylate synthase domain-containing protein 2	C15orf19	1.35		0.73	1.37	1.04	0.44	3	8.4	3.59E-07
Q96HN2	Putative adenosylhomocysteinase 3	AHCYL2			1.04	0.96	1.04		2	3.1	4.72E-03
Q9BXL7	CARD-containing MAGUK protein 1	CARD11			1.04	0.96	1.04		2	2.2	1.94E-12
Q9H254-1	Beta-IV spectrin	KIAA1642		1.04			1.04		2	0.5	2.90E-02
A6NFM4	Putative uncharacterized protein GAA	GAA	1.04				1.04		2	4.5	3.73E-05
Q9Y6N1	Cytochrome c oxidase assembly protein COX11, mitochondrial	COX11	1.04				1.04		4	26	6.53E-27
Q9UK41	ESCRT-I complex subunit VPS28	VPS28	1.04				1.04		6	39	1.16E-50
P29144	Tripeptidyl aminopeptidase	TPP2	1.05	1.05	1.03	0.97	1.04	0.01	21	21	7.66E-144
P67775	Replication protein C	PPP2CA	0.98	1.07	1.08	0.93	1.04	0.06	14	60	1.18E-291
Q8TF01-1	Serine/arginine-rich-splicing regulatory protein 130	C6orf111	1.00	1.13	1.00	1.00	1.04	0.08	3	3.1	6.12E-07
P28072	Macropain delta chain	LMPY	1.10	1.08	0.95	1.05	1.04	0.08	10	59	4.31E-150
B4DLV7	cDNA FLJ60299, highly similar to Rab GDP dissociation inhibitor beta	GDI2	1.05	1.13	0.95	1.05	1.04	0.09	27	69	0.00E+00
O60216	Double-strand-break repair protein rad21 homolog	HR21	0.95	1.03	1.15	0.87	1.04	0.10	6	13	1.18E-50
P27695	APEX nuclease	APE	0.97	0.98	1.18	0.85	1.04	0.12	22	68	0.00E+00
Q9BTE3-1	UPF0557 protein C10orf119	C10orf119	1.17	0.93	1.03	0.97	1.04	0.12	5	10	7.38E-19
Q9BY32	Inosine triphosphate pyrophosphatase	C20orf37	1.19	1.00	0.94	1.06	1.04	0.13	4	31	2.08E-45
P09211	Glutathione S-transferase P	FAEES3	0.92	0.96	1.25	0.80	1.04	0.18	13	70	0.00E+00
P22314	Protein A1S9	A1S9T	0.92	0.94	1.27	0.79	1.04	0.20	49	57	0.00E+00
O75683	Surfeit locus protein 6	SURF6	1.01	0.86	1.26	0.79	1.04	0.20	3	8.6	7.02E-10
A2RRP1-1	Neuroblastoma-amplified gene protein	NAG	0.98	1.28	0.87	1.15	1.04	0.21	7	4	1.55E-65
O15347	High mobility group protein 2a	HMG2A	0.84	0.99	1.30	0.77	1.04	0.23	11	50	3.03E-116
Q9NVP	ATP-dependent RNA helicase DDX18	DDX18	1.23	1.15	0.75	1.33	1.04	0.26	13	24	1.24E-64

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1											
Q96JH7	Deubiquitinating protein VCIP135	KIAA1850	0.76	1.00	1.37	0.73	1.04	0.31	5	5.6	4.64E-74
Q99877	Histone H2B type 1-N	H2BFD	0.80	0.81	1.52	0.66	1.04	0.41	13	55	1.22E-163
O95602	DNA-directed RNA polymerase I largest subunit	POLR1A	1.32	1.28	0.53	1.89	1.04	0.45	9	9.8	1.53E-74
Q96ST3	Histone deacetylase complex subunit Sin3a	SIN3A	1.01	1.10	1.02	0.98	1.04	0.05	16	18	3.97E-77
P30086	Hippocampal cholinergic neurostimulating peptide	PBP	1.10	1.05	0.98	1.02	1.04	0.06	14	82	6.73E-213
Q14232	eIF-2B GDP-GTP exchange factor subunit alpha	EIF2B1	1.10	1.09	0.94	1.06	1.04	0.09	8	33	6.24E-147
Q9BTX1-1	Nucleoporin NDC1	NDC1	1.12	1.33	0.68	1.47	1.04	0.33	3	5.9	4.87E-15
P53801	Pituitary tumor-transforming gene 1 protein-interacting protein	C21orf1		1.04	1.05	0.95	1.05	0.01	3	19	5.15E-19
Q58FF6	Putative heat shock protein HSP 90-beta 4	HSP90AB4P	1.04		1.05	0.95	1.05	0.01	8	12	1.01E-103
P10415-1	Apoptosis regulator Bcl-2	BCL2		1.02	1.07	0.93	1.05	0.04	3	33	6.51E-13
Q6ICC9	Leucine zipper protein down-regulated in cancer cells-like	LDOC1L		1.01	1.08	0.93	1.05	0.05	2	16	5.33E-07
Q9BRX8	Uncharacterized protein C10orf58	C10orf58	1.01	1.08			1.05	0.05	5	20	5.60E-22
Q9H3H3	Basophilic leukemia-expressed protein Bles03	BLES03		0.93	1.16	0.86	1.05	0.16	3	9.2	9.83E-07
Q9UK53-1	Inhibitor of growth protein 1	ING1		0.91	1.18	0.85	1.05	0.19	2	7.3	2.45E-27
Q9HCJ0-2	Trinucleotide repeat-containing gene 6C protein	KIAA1582		0.82	1.27	0.79	1.05	0.32	7	9.4	4.07E-21
Q9BRR8	Evolutionarily conserved G-patch domain-containing protein	ECGP		1.27	0.82	1.22	1.05	0.32	4	6.8	1.01E-14
Q8IZ69-1	HpaII tiny fragments locus 9c protein	HTF9C	1.38		0.71	1.41	1.05	0.47	2	4.5	1.25E-51
Q96ME4	cDNA FLJ32471 fis, clone SKNMC2000322, highly similar to Peptidyl-tRNA hydrolase 2, mitochondrial (EC 3.1.1.29)	BIT1	1.46		0.63	1.59	1.05	0.59	3	32	5.80E-55

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A6PZH2	Glucosamine (UDP-N-acetyl)-2-epimerase/N-acetylmannosamine kinase, isoform CRA_a	GNE	1.06	1.06	1.02	0.98	1.05	0.02	2	3.3	1.55E-25
Q9BQ04	RNA-binding motif protein 30	RBM30	1.06	1.06	1.02	0.98	1.05	0.02	12	32	2.92E-19
A1E282	Beta-actin	ACTB	1.06	1.06	1.02	0.98	1.05	0.02	53	77	0.00E+00
P25787	Macropain subunit C3	HC3	1.08	1.04	1.02	0.98	1.05	0.03	13	55	1.10E-173
Q92688-1	Acidic leucine-rich nuclear phosphoprotein 32 family member B	ANP32B	1.01	1.05	1.08	0.93	1.05	0.04	11	49	2.20E-252
O95166	GABA(A) receptor-associated protein	FLC3B	1.00	1.00	1.14	0.88	1.05	0.08	3	25	9.76E-16
O75940	30 kDa splicing factor SMNrp	SMNDC1	1.14	1.02	0.98	1.02	1.05	0.08	5	33	7.22E-24
Q8WVB6-1	CHL12	C16orf41	0.95	1.14	1.05	0.95	1.05	0.10	14	20	8.35E-133
P62937	Cyclophilin A	CYPA	1.16	1.01	0.97	1.03	1.05	0.10	12	71	2.05E-278
P30508	HLA class I histocompatibility antigen, Cw-12 alpha chain	HLAC	0.96	1.02	1.16	0.86	1.05	0.10	7	24	1.66E-168
P54725	UV excision repair protein RAD23 homolog A	RAD23A	1.16	1.04	0.94	1.06	1.05	0.11	7	29	5.05E-72
O00203-1	Adapter-related protein complex 3 subunit beta-1	ADTB3A	0.92	1.14	1.08	0.93	1.05	0.11	3	3.6	2.36E-06
A1Z1D7	MHC class I antigen	HLA-A	0.99	0.97	1.18	0.85	1.05	0.12	11	38	8.14E-240
B4DTK7	cDNA FLJ61387, highly similar to Homo sapiens conserved nuclear protein NHN1 (NHN1), mRNA	NHN1	0.99	1.18	0.97	1.03	1.05	0.12	8	12	9.88E-32
P34932	Heat shock 70 kDa protein 4	APG2	1.09	1.14	0.91	1.10	1.05	0.12	50	66	0.00E+00
Q9BZE4	Chronic renal failure gene protein	CRFG	1.12	1.12	0.90	1.11	1.05	0.13	12	24	8.36E-64
Q9BRX5-1	DNA replication complex GINS protein PSF3	GINS3	1.19	1.04	0.91	1.10	1.05	0.14	10	62	7.87E-204
O43818	RRP9 homolog	RNU3IP2	1.24	1.11	0.79	1.27	1.05	0.23	11	29	4.20E-121
Q04760	Aldoketomutase	GLO1	0.94	0.86	1.34	0.75	1.05	0.26	9	52	8.37E-126
Q9GZZ1-1	N-acetyltransferase 13	MAK3	1.26	1.14	0.74	1.35	1.05	0.27	6	37	2.53E-38
Q12931	Heat shock protein 75 kDa, mitochondrial	HSP75	1.24	1.18	0.72	1.39	1.05	0.28	17	31	9.44E-201

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Q9UNI6	Dual specificity protein phosphatase 12	DUSP12	0.69	1.15	1.3	0.77	1.05	0.32	2	7.9	4.34E-39
P62805	Histone H4	H4/A	0.85	0.85	1.44	0.69	1.05	0.34	18	69	2.55E-287
B2R960	cDNA, FLJ94230, highly similar to Homo sapiens thioredoxin-like 1 (TXNL1), mRNA	TRP32	1.29	1.20	0.65	1.54	1.05	0.35	11	46	4.01E-119
Q00534	Cell division protein kinase 6	CDK6	1.30	1.30	0.54	1.85	1.05	0.44	11	41	7.45E-211
Q9BXP5-1	Arsenite-resistance protein 2	ARS2	1.01	1.06	1.07	0.93	1.05	0.03	41	46	1.23E-205
Q8N163-1	Deleted in breast cancer gene 1 protein	DBC1	1.08	0.99	1.07	0.93	1.05	0.05	31	46	0.00E+00
O43143	ATP-dependent RNA helicase #46	DBP1	0.99	1.04	1.11	0.90	1.05	0.06	24	30	3.77E-195
B3KUY2	cDNA FLJ40895 fis, clone UTERU2002294, highly similar to Prostaglandin E synthase 3 (EC 5.3.99.3)	hCG_2016483	1.15	1.03	0.97	1.03	1.05	0.09	7	41	2.77E-108
B2R8E4	cDNA, FLJ93859, highly similar to Homo sapiens protein phosphatase 1A (formerly 2C), magnesium-dependent, alpha isoform (PPM1A), mRNA	PPM1A	1.02	1.16	0.97	1.03	1.05	0.10	6	16	5.97E-23
Q9BV73-1	250 kDa centrosomal protein	CEP2		1.13	0.97	1.03	1.05	0.11	4	1.6	6.73E-17
B1AHD1	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)	CTA-216E10.8-008	1.13	1.22	0.80	1.25	1.05	0.22	5	39	1.22E-81
Q9GZL7	Ribosome biogenesis protein WDR12	WDR12	1.16	1.23	0.76	1.32	1.05	0.25	7	20	1.02E-53
Q9NS69	Mitochondrial import receptor subunit TOM22 homolog	TOM22	1.38	1.22	0.55	1.82	1.05	0.44	4	51	9.52E-89
Q13418	59 kDa serine/threonine-protein kinase	ILK	1.05	1.05	1.05	0.95	1.05	0.00	2	5.5	7.12E-03
Q7Z739	YTH domain family protein 3	YTHDF3	1.05	1.05	1.05	0.95	1.05	0.00	7	14	2.06E-56
P23193-1	Transcription elongation factor A protein 1	GTF2S	1.05	1.06	1.04	0.96	1.05	0.01	16	63	1.19E-198
Q99623	B-cell receptor-associated protein BAP37	BAP	1.08	1.06	1.01	0.99	1.05	0.04	18	64	1.56E-227
Q9Y6N	Sulfide:quinone	CGI-44		1.02	1.08	0.93	1.05	0.04	9	29	2.61E-96

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5	oxidoreductase, mitochondrial										
O43169	Cytochrome b5 outer mitochondrial membrane isoform	CYB5B	1.08		1.02	0.98	1.05	0.04	5	55	1.98E-57
Q13595-1	Transformer-2 protein homolog A	TRA2A	1.03	1.02	1.10	0.91	1.05	0.04	7	31	7.17E-75
Q9UBS4	APOBEC1-binding protein 2	DNAJB11	1.06	1.09	1.00	1.00	1.05	0.05	10	30	4.41E-108
Q9UIA9	Exportin-7	KIAA0745	1.07	1.09	0.99	1.01	1.05	0.05	15	20	1.11E-101
Q99459	Cell division cycle 5-like protein	CDC5L	1.05	0.99	1.11	0.90	1.05	0.06	27	44	4.39E-206
P35232	Prohibitin	PHB	1.06	1.11	0.98	1.02	1.05	0.07	19	86	0.00E+00
B4DJQ5	cDNA FLJ59211, highly similar to Glucosidase 2 subunit beta	G19P1	0.97	1.12	1.06	0.94	1.05	0.08	20	40	2.27E-180
P49454	AH antigen	CENPF	0.95	1.09	1.11	0.90	1.05	0.09	14	5.9	3.91E-97
Q9UHY7-1	2,3-diketo-5-methylthio-1-phosphopentane phosphatase	ENOPH1	0.98		1.12	0.89	1.05	0.10	5	24	5.66E-114
Q9UM22-2	Mammalian ependymin-related protein 1	EPDR1	1.04	1.16	0.95	1.05	1.05	0.11	4	12	7.64E-20
P84095	Rho-related GTP-binding protein RhoG	ARHG	0.93	1.08	1.14	0.88	1.05	0.11	9	52	5.91E-149
Q9HD45	EP70-P-iso	SMBP	1.14	1.08	0.93	1.08	1.05	0.11	2	3.7	4.83E-06
O43813	40 kDa erythrocyte membrane protein	GPR69A	1.00	0.97	1.18	0.85	1.05	0.11	6	15	1.65E-28
P46087-1	Nucleolar protein 1	NOL1	1.10	1.13	0.92	1.09	1.05	0.11	28	35	2.37E-210
Q13868	Exosome complex exonuclease RRP4	EXOSC2	0.93	1.06	1.16	0.86	1.05	0.12	4	23	1.44E-37
Q12972-1	Activator of RNA decay	ARD1	1.03	0.94	1.18	0.85	1.05	0.12	6	23	5.01E-25
O15173	Membrane-associated progesterone receptor component 2	DG6	1.12	1.13	0.90	1.11	1.05	0.13	6	22	6.86E-64
Q99567	88 kDa nucleoporin	NUP88	1.19	1.05	0.91	1.10	1.05	0.14	4	9.2	9.36E-20
Q9Y5M8	Protein APMCF1	PSEC0230	1.11	1.15	0.89	1.12	1.05	0.14	7	34	2.26E-161
Q9NX46	[Protein ADP-ribosylarginine] hydrolase-like protein 2	ADPRHL2	0.95	0.99	1.21	0.83	1.05	0.14	3	11	2.15E-29
B4DX18	cDNA FLJ56327, highly similar to 26S proteasome non-ATPase regulatory subunit 8	hCG_42853	1.21	1.04	0.90	1.11	1.05	0.16	6	22	4.50E-27

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O95881	Endoplasmic reticulum resident protein 18	TLP19	1.18	0.92			1.05	0.18	2	13	2.85E-05
P24928	DNA-directed RNA polymerase II subunit A	POLR2	1.06	1.23	0.86	1.16	1.05	0.19	21	16	3.59E-142
Q9BQG0-2	Myb-binding protein 1A	MYBBP1A	1.14	1.18	0.83	1.20	1.05	0.19	32	32	6.16E-239
B0QY89	Eukaryotic translation initiation factor 3, subunit E interacting protein	AL022311.1-001	1.14	1.19	0.82	1.22	1.05	0.20	13	25	1.43E-133
Q6PL18-1	AAA nuclear coregulator cancer-associated protein	ATAD2	0.89		1.21	0.83	1.05	0.23	2	2.9	2.58E-05
Q96TA2-1	ATP-dependent metalloprotease FtsH1	FTSH1	1.28	0.81	1.06	0.94	1.05	0.24	5	9.1	0.00E+00
Q14978-2	140 kDa nucleolar phosphoprotein	KIAA0035	1.2	1.21	0.74	1.35	1.05	0.27	22	26	1.51E-133
Q8TEQ6	Gem-associated protein 5	GEMIN5	1.24		0.86	1.16	1.05	0.27	5	5.3	8.86E-31
Q6ZSA3	cDNA FLJ45695 fis, clone FEBRA2013570, highly similar to 2-oxoisovalerate dehydrogenase alpha subunit, mitochondrial (EC 1.2.4.4)	BCKDHA	0.84	0.93	1.38	0.72	1.05	0.29	3	8.1	1.13E-51
P09417	Dihydropteridine reductase	DHPR	0.86	0.90	1.39	0.72	1.05	0.30	5	33	4.14E-56
P42696-1	RNA-binding motif protein 34	KIAA0117	1.32	1.12	0.71	1.41	1.05	0.31	5	17	1.80E-36
Q9Y388	RNA-binding motif protein, X-linked 2	CGI-79		0.81	1.29	0.78	1.05	0.34	2	7.1	2.98E-12
Q15814	Tubulin-folding cofactor C	TBCC			1.05	0.95	1.05		2	6.1	1.45E-12
Q9NS91	E3 ubiquitin-protein ligase RAD18	RAD18			1.05	0.95	1.05		3	7.5	5.21E-19
Q9Y2S6	Coiled-coil domain-containing protein 72	CCDC72		1.05			1.05		2	30	1.05E-02
P10109	Adrenal ferredoxin	ADX	1.05				1.05		2	9.8	8.94E-04
O60927	Hemochromatosis candidate gene V protein	HCGV	1.05				1.05		2	33	1.09E-11
Q6GMV2	Protein NN8-4AG	RAI15		1.05			1.05		3	7.4	1.62E-07
P61225	Ras-related protein Rap-2b	RAP2B	1.05				1.05		3	27	4.61E-24
O15321	MP70 protein family member	TM9SF1		1.05			1.05		3	3.6	1.72E-33
P54652	Heat shock-related 70 kDa protein 2	HSPA2	1.05				1.05		15	20	2.19E-176

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B7Z8Z6	cDNA FLJ53276, moderately similar to DNA replication licensing factor MCM2	MCM2		1.05			1.05		21	23	3.16E-221
P39748	DNase IV	FEN1	1.01	1.00	1.15	0.87	1.05	0.08	16	47	5.68E-224
Q9BW19	Kinesin-like protein 2	HSET	1.16	1.10	0.90	1.11	1.05	0.14	9	19	2.44E-125
P00441	Superoxide dismutase [Cu-Zn]	SOD1	1.17	1.09	0.90	1.11	1.05	0.14	8	78	3.22E-126
P53621-2	Alpha-coat protein	COPA	1.06	1.20	0.90	1.11	1.05	0.15	27	31	2.15E-190
P46778	60S ribosomal protein L21	RPL21	1.16	1.15	0.85	1.18	1.05	0.18	7	38	7.27E-73
Q9H3K6-1	BolA-like protein 2	BOLA2	1.18	1.17	0.81	1.23	1.05	0.21	4	35	3.37E-56
B4DGU9	cDNA FLJ59232, highly similar to ARF GTPase-activating protein GIT1	GIT1	1.05	1.07	1.04	0.96	1.05	0.02	8	15	1.48E-40
P12956	70 kDa subunit of Ku antigen	G22P1	1.03	1.06	1.07	0.93	1.05	0.02	39	55	0.00E+00
Q9BUL5-1	PDH-containing protein JUNE-1	PHF23	1.04	1.04	1.08	0.93	1.05	0.02	2	6	4.03E-08
O43402	Neighbor of COX4	C16orf2	1.01	1.05	1.10	0.91	1.05	0.05	5	19	3.45E-24
Q96KP4-1	CNDP dipeptidase 2	CN2	1.08	1.08	1.00	1.00	1.05	0.05	14	41	7.05E-51
O95202-1	LETM1 and EF-hand domain-containing protein 1, mitochondrial	LETM1	0.99	1.09	1.08	0.93	1.05	0.06	16	28	1.95E-162
P78406	mRNA export factor	MRNP41	0.99	1.03	1.14	0.88	1.05	0.08	9	24	2.33E-57
O75643-1	Activating signal cointegrator 1 complex subunit 3-like 1	ASCC3L1	1.10	1.11	0.95	1.05	1.05	0.09	65	39	0.00E+00
P49903	Selenide, water dikinase 1	SELD	1.09	0.95	1.12	0.89	1.05	0.09	7	27	2.22E-56
Q9BRG1	Dermal papilla-derived protein 9	DERP9	1.15	1.06	0.95	1.05	1.05	0.10	5	32	4.28E-22
P51665	26S proteasome non-ATPase regulatory subunit 7	MOV34L	1.16	1.05	0.95	1.05	1.05	0.11	10	40	2.44E-74
P26368-1	Splicing factor U2AF 65 kDa subunit	U2AF2	1.16	1.05	0.95	1.05	1.05	0.11	16	50	1.05E-215
Q9NZ09-1	Nasopharyngeal carcinoma-associated gene 20 protein	NAG20	0.96	1.02	1.18	0.85	1.05	0.11	2	5.1	2.10E-41
O43390-1	Heterogeneous nuclear ribonucleoprotein R	HNRNPR	0.96	1.00	1.20	0.83	1.05	0.13	25	40	0.00E+00
P40429	23 kDa highly basic protein	RPL13A	1.10	1.18	0.88	1.14	1.05	0.16	11	33	1.32E-24

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P62266	40S ribosomal protein S23	RPS23	1.04	1.24	0.88	1.14	1.05	0.18	7	50	3.28E-32
Q4G0J3-1	La ribonucleoprotein domain family member 7	HDCMA18P	1.08	1.23	0.85	1.18	1.05	0.19	5	11	1.31E-30
Q12788	Transducin beta-like protein 3	SAZD	1.10	1.28	0.78	1.28	1.05	0.25	8	13	1.64E-49
Q9BRJ6	Uncharacterized protein C7orf50	C7orf50	1.19	1.25	0.72	1.39	1.05	0.29	8	47	1.91E-73
Q2NL82	Pre-rRNA-processing protein TSR1 homolog	KIAA1401	1.19	1.25	0.72	1.39	1.05	0.29	10	16	3.42E-54
O15226	NF-kappa-B-repressing factor	ITBA4		1.14	0.97	1.03	1.06	0.12	4	5.4	2.19E-11
O00560-1	Melanoma differentiation-associated protein 9	MDA9	0.88		1.23	0.81	1.06	0.25	3	26	2.40E-54
Q9NWU5-1	39S ribosomal protein L22, mitochondrial	HSPC158	1.25	0.86			1.06	0.28	2	12	2.02E-22
Q96GN5-1	Cell division cycle-associated 7-like protein	CDCA7L		0.83	1.28	0.78	1.06	0.32	3	5.9	7.87E-07
P42229	Signal transducer and activator of transcription 5A	STAT5		0.73	1.38	0.72	1.06	0.46	4	4.5	8.61E-08
Q9NVU7-1	Nucleolar protein 130	NUC130		1.11	1.00	1.00	1.06	0.08	3	5.5	1.69E-05
Q8NHV1	GTPase IMAP family member 7	GIMAP7	0.74		1.37	0.73	1.06	0.45	5	24	9.44E-260
Q96CN7	Isochorismatase domain-containing protein 1	CGI-111	1.18	1.13	0.86	1.16	1.06	0.17	5	24	3.21E-47
O95816	BAG family molecular chaperone regulator 2	BAG2	1.09	1.07	1.01	0.99	1.06	0.04	14	62	4.40E-222
P30876	DNA-directed RNA polymerase II 140 kDa polypeptide	POLR2B	1.05	1.01	1.11	0.90	1.06	0.05	26	26	1.31E-90
P51148	L1880	RAB5C	0.99	1.05	1.13	0.88	1.06	0.07	10	65	1.55E-254
P07339	Cathepsin D	CPSD	1.07	0.98	1.12	0.89	1.06	0.07	12	32	1.78E-157
Q5TEC6	Histone H3	HIST2H3PS2	1.05	0.97	1.15	0.87	1.06	0.09	7	39	1.01E-21
Q6GSG7	Coiled-coil domain-containing protein 6	CCDC6	0.98	1.02	1.17	0.85	1.06	0.10	8	22	6.05E-32
Q96T37-1	One-twenty two protein 1	OTT	0.94	1.07	1.16	0.86	1.06	0.11	17	23	3.08E-122
Q15007-1	Female-lethal(2)D homolog	KIAA0105	0.94	1.19	1.04	0.96	1.06	0.13	3	12	2.16E-117
P53992	Protein transport protein Sec24C	KIAA0079	1.17	1.09	0.91	1.10	1.06	0.13	8	11	2.78E-50
P49773	Adenosine 5-monophosphoramidase	HINT	1.15	1.12	0.90	1.11	1.06	0.14	8	79	1.52E-63
P15121	Aldehyde reductase	AKR1B1	0.93	1.02	1.22	0.82	1.06	0.15	12	36	2.01E-21

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Q5RKV6	Exosome complex exonuclease MTR3	EXOSC6	1.12	1.17	0.88	1.14	1.06	0.16	10	34	5.73E-63
P14678-3	Sm protein B/B	COD	1.20	1.09	0.88	1.14	1.06	0.16	11	29	4.32E-57
Q9NYU2-1	UDP--Glc:glycoprotein glucosyltransferase	GT	1.17	1.13	0.87	1.15	1.06	0.16	24	24	9.95E-226
Q9BUL8	Cerebral cavernous malformations 3 protein	CCM3	0.98	0.94	1.25	0.80	1.06	0.17	4	29	1.48E-57
Q92797-1	Symplekin	SPK	1.13	1.21	0.83	1.20	1.06	0.20	15	22	1.85E-118
Q00796	L-iditol 2-dehydrogenase	SORD	1.12	1.23	0.82	1.22	1.06	0.21	10	39	2.92E-142
Q9Y5S9-1	Binder of OVCA1-1	HSPC114	1.16	1.22	0.79	1.27	1.06	0.23	7	33	1.70E-98
P15374	Ubiquitin carboxyl-terminal hydrolase isozyme L3	UCHL3	1.23	1.17	0.77	1.30	1.06	0.25	11	73	1.30E-135
Q9BPW8	Protein NipSnap homolog 1	NIPSNAP1	0.74	0.73	1.70	0.59	1.06	0.56	9	30	3.62E-47
P31946-1	14-3-3 protein beta/alpha	YWHAB	1.02	1.09	1.06	0.94	1.06	0.04	19	71	0.00E+00
P07910-2	Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	1.02	1.05	1.10	0.91	1.06	0.04	24	60	0.00E+00
P35606	Beta-coat protein	COPB2	1.04	1.28	0.85	1.18	1.06	0.22	14	18	1.15E-75
P36551	Coproporphyrinogen-III oxidase, mitochondrial	CPO	1.03	1.14	1.01	0.99	1.06	0.07	6	19	4.70E-28
O60925	Prefoldin subunit 1	PFD1	1.04	0.97	1.17	0.85	1.06	0.10	5	36	5.76E-23
P41252	Isoleucine--tRNA ligase	IARS	1.13	1.13	0.92	1.09	1.06	0.12	40	39	0.00E+00
P14550	Alcohol dehydrogenase [NADP+]	AKR1A1	0.98	0.96	1.24	0.81	1.06	0.16	13	51	8.56E-104
P50613	39 kDa protein kinase	CDK7	1.27	0.92	0.99	1.01	1.06	0.19	4	12	1.74E-24
Q99729-3	APOBEC1-binding protein 1	ABBP1	1.15	1.20	0.83	1.20	1.06	0.20	13	42	1.82E-209
O96008-1	Mitochondrial import receptor subunit TOM40 homolog	C19orf1	1.19	1.17	0.82	1.22	1.06	0.21	10	40	2.51E-127
Q8TEX9-2	Importin-4	IMP4B	1.23	1.25	0.70	1.43	1.06	0.31	11	17	2.06E-198
P04843	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 67 kDa subunit	RPN1	1.05	1.05	1.08	0.93	1.06	0.02	26	50	8.59E-183
P04179	Superoxide dismutase [Mn], mitochondrial	SOD2	1.06	1.04	1.08	0.93	1.06	0.02	9	34	6.15E-92
P80294	Metallothionein-0	MT1H	1.08		1.04	0.96	1.06	0.03	2	33	3.96E-06

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A0JLT2-1	Lung cancer metastasis-related protein 1	LCMR1	1.08		1.04	0.96	1.06	0.03	2	20	4.32E-07
Q9Y3A6	Transmembrane emp24 domain-containing protein 5	CGI-100	1.08		1.04	0.96	1.06	0.03	2	7	1.48E-02
Q92622	Uncharacterized protein KIAA0226	KIAA0226	1.08		1.04	0.96	1.06	0.03	2	3	8.45E-05
Q9BQ95-1	Evolutionarily conserved signaling intermediate in Toll pathway, mitochondrial	ECSIT	1.08		1.04	0.96	1.06	0.03	4	19	5.35E-26
P06729	Erythrocyte receptor	CD2	1.08		1.04	0.96	1.06	0.03	10	31	3.28E-79
Q15287-1	RNA-binding protein with serine-rich domain 1	LDC2	1.11		1.01	0.99	1.06	0.07	2	14	4.25E-25
Q59G94	Zinc finger protein 207 variant	ZNF207	1.16	1.04	0.98	1.02	1.06	0.09	4	9.3	3.57E-37
A4FS09	Minichromosome maintenance protein 4	MCM4	0.99		1.13	0.88	1.06	0.10	37	52	0.00E+00
Q92934	Bcl2 antagonist of cell death	BAD	1.13		0.99	1.01	1.06	0.10	2	14	1.82E-05
Q9NR56-1	Muscleblind-like protein 1	EXP		1.13	0.99	1.01	1.06	0.10	5	12	1.70E-08
O00217	Complex I-23kD	NDUFS8	0.95		1.17	0.85	1.06	0.16	3	17	1.72E-43
Q92947-1	Glutaryl-CoA dehydrogenase, mitochondrial	GCDH	1.17	0.95			1.06	0.16	2	5.9	2.84E-33
Q13363	C-terminal-binding protein 1	CTBP	0.90	1.05	1.23	0.81	1.06	0.17	10	29	3.33E-33
P22061-1	L-isoaspartyl protein carboxyl methyltransferase	PCMT1	0.92	0.99	1.27	0.79	1.06	0.19	10	71	2.23E-118
Q9H9B4	Sideroflexin-1	SFXN1	1.11	1.24	0.83	1.20	1.06	0.21	11	46	1.11E-141
P33316-1	Deoxyuridine 5-triphosphate nucleotidohydrolase, mitochondrial	DUT	1.19	1.22	0.77	1.30	1.06	0.25	12	54	1.36E-135
Q9Y5B6-1	GC-rich sequence DNA-binding factor homolog	C21orf66	0.83		1.29	0.78	1.06	0.33	4	7.6	3.26E-07
P57058	Hormonally up-regulated neu tumor-associated kinase	HUNK			1.06	0.94	1.06		2	3.1	1.22E-02
Q5VV67	Peroxisome proliferator-activated receptor gamma coactivator-related protein 1	KIAA0595			1.06	0.94	1.06		2	1	2.00E-02
Q5TEG3	Novel enoyl-CoA hydratase/isomerase family protein	RP3-351K20.2-015			1.06	0.94	1.06		3	21	1.02E-10

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O15118	Niemann-Pick C1 protein	NPC1	1.06				1.06		2	1.7	9.99E-13
Q9H0V9-2	Lectin mannose-binding 2-like	LMAN2L		1.06			1.06		2	6.7	3.48E-02
C9K060	Putative uncharacterized protein WBSCR22	WBSCR22		1.06			1.06		2	10	2.60E-36
P50452	Cytoplasmic antiproteinase 2	PI8		1.06			1.06		3	9.4	7.42E-16
Q5TA95	Tetratricopeptide repeat domain 4	hCG_32473		1.06			1.06		3	8	2.97E-08
P09493-3	Alpha-tropomyosin	C15orf13		1.06			1.06		6	16	1.94E-34
P62987	60S ribosomal protein L40	UBA52		1.06			1.06		7	49	1.67E-66
O75533	Pre-mRNA-splicing factor SF3b 155 kDa subunit	SAP155	1.11	1.12	0.95	1.05	1.06	0.10	55	53	0.00E+00
O94826	Mitochondrial import receptor subunit TOM70	KIAA0719	1.04	1.09	1.06	0.94	1.06	0.03	8	16	2.68E-115
P31942-1	Heterogeneous nuclear ribonucleoprotein 2H9	HNRNPH3	1.02	1.02	1.15	0.87	1.06	0.08	9	38	5.55E-228
P23786	Carnitine O-palmitoyltransferase 2, mitochondrial	CPT2	1.08	0.96	1.15	0.87	1.06	0.10	4	6.5	9.16E-24
Q9BTD8-1	RNA-binding motif protein 42	RBM42	1.00	0.99	1.20	0.83	1.06	0.12	4	11	2.93E-67
P62310	U6 snRNA-associated Sm-like protein LSm3	LSM3	1.16	1.11	0.92	1.09	1.06	0.13	3	22	5.73E-14
P39656	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	DDOST	1.06	1.21	0.92	1.09	1.06	0.15	10	34	1.28E-81
Q13112	Chromatin assembly factor 1 subunit B	CAF1A	1.10	1.19	0.90	1.11	1.06	0.15	5	11	1.35E-29
B7WP27	Putative uncharacterized protein CWC22	CWC22	0.98	0.97	1.24	0.81	1.06	0.15	9	12	1.59E-152
Q8TAT6-2	Nuclear protein localization protein 4 homolog	KIAA1499	0.84	1.15	1.20	0.83	1.06	0.20	5	11	1.50E-113
Q7Z6Z7-1	ARF-binding protein 1	HSPC272	1.14	1.23	0.82	1.22	1.06	0.22	43	16	0.00E+00
Q03701	CCAAT/enhancer-binding protein zeta	CBF2	1.08	1.27	0.84	1.19	1.06	0.22	6	8.7	3.10E-46
Q9GZR7	ATP-dependent RNA helicase DDX24	DDX24	1.20	1.22	0.77	1.30	1.06	0.25	27	43	4.95E-160
Q9H4A4	Aminopeptidase B	APB	1.29	1.13	0.77	1.30	1.06	0.27	3	7.6	1.63E-44
Q8N8A6	ATP-dependent RNA helicase DDX51	DDX51	1.26	1.24	0.69	1.45	1.06	0.32	7	16	2.40E-23

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P48634-1	HLA-B-associated transcript 2	BAT2	1.26	1.26	0.67	1.49	1.06	0.34	22	16	4.70E-125
Q9H4L7-2	ATP-dependent helicase 1	KIAA1122	0.89	1.47	0.83	1.20	1.06	0.35	3	4.1	2.05E-20
A8MUW5	Putative uncharacterized protein FAM98B	FAM98B	1.04	1.04	1.11	0.90	1.06	0.04	8	26	8.20E-110
Q56VL3-1	OCIA domain-containing protein 2	OCIAD2	1.00	1.12	1.07	0.93	1.06	0.06	4	39	2.20E-19
P07237	Cellular thyroid hormone-binding protein	ERBA2L	1.11	1.09	0.99	1.01	1.06	0.06	28	60	1.11E-225
O00232	26S proteasome non-ATPase regulatory subunit 12	PSMD12	1.12	1.08	0.99	1.01	1.06	0.07	12	30	1.23E-122
P27816-1	Microtubule-associated protein 4	MAP4	0.95	1.13	1.11	0.90	1.06	0.10	28	32	2.08E-181
Q8N1K5-1	Protein THEMIS	C6orf190	1.11	1.25	0.83	1.20	1.06	0.21	5	8.2	1.91E-19
Q8ND04-2	Amplified in breast cancer gene 2 protein	ABC2	1.09		1.04	0.96	1.07	0.04	3	5	7.47E-89
P40121	Actin regulatory protein CAP-G	AFCP	1.09		1.04	0.96	1.07	0.04	22	53	0.00E+00
Q9HC35	Echinoderm microtubule-associated protein-like 4	C2orf2	1.02	1.11			1.07	0.06	3	3.6	1.80E-06
Q9UKA9-2	Neural polypyrimidine tract-binding protein	NPTB		1.01	1.12	0.89	1.07	0.08	2	7.1	1.19E-12
Q13616	Cullin-1	CUL1		1.15	0.98	1.02	1.07	0.12	4	5.8	2.36E-38
Q9NTM9	Copper homeostasis protein cutC homolog	CGI-32		0.92	1.21	0.83	1.07	0.21	2	11	1.87E-31
Q04721	Neurogenic locus notch homolog protein 2	NOTCH2	0.91		1.22	0.82	1.07	0.22	2	1.1	3.02E-04
B4DZK0	cDNA FLJ56391, highly similar to Cysteine protease ATG4B (EC 3.4.22.-)	APG4B	1.23		0.90	1.11	1.07	0.23	2	7.1	4.26E-49
Q9BVQ7-1	Spermatogenesis-associated protein 5-like protein 1	SPATA5L1	1.24		0.89	1.12	1.07	0.25	5	13	4.62E-86
Q6DKI1	60S ribosomal protein L7-like 1	RPL7L1	1.31		0.82	1.22	1.07	0.35	3	15	1.37E-20
Q6S8J3-1	ANKRD26-like family C member 1A	A26C1A		1.32	0.81	1.23	1.07	0.36	11	11	9.96E-271
Q9Y570-1	Protein phosphatase methylesterase 1	PME1	1.06	1.05	1.09	0.92	1.07	0.02	6	20	2.68E-33
Q99436	Macropain chain Z	PSMB7	1.05	1.11	1.04	0.96	1.07	0.04	8	38	6.30E-148
Q99714-1	17-beta-hydroxysteroid dehydrogenase 10	ERAB	1.03	1.06	1.11	0.90	1.07	0.04	16	86	0.00E+00

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Q9BVC6	Mitsugumin-23	TMEM109	1.08	1.12	1.00	1.00	1.07	0.06	6	25	2.90E-42
B4DP80	cDNA FLJ56357, highly similar to Homo sapiens apolipoprotein A-I binding protein (APOA1BP), mRNA	AIBP	1.16	1.00	1.04	0.96	1.07	0.08	8	36	1.29E-110
P98175-1	G patch domain-containing protein 9	DXS8237E	1.00	1.02	1.18	0.85	1.07	0.10	13	19	1.06E-55
Q8N9T8-1	Protein KRI1 homolog	KRI1	1.03	1.19	0.98	1.02	1.07	0.11	6	9.6	2.20E-164
P52756-1	Protein G15	H37	1.14	1.12	0.94	1.06	1.07	0.11	4	7.6	1.38E-16
Q9Y5K6	Adapter protein CMS	CD2AP	1.20	1.01	0.99	1.01	1.07	0.12	7	13	8.18E-27
Q14166	Tubulin--tyrosine ligase-like protein 12	KIAA0153	1.10	1.17	0.93	1.08	1.07	0.12	13	35	2.22E-152
Q9Y383-1	Putative RNA-binding protein Luc7-like 2	LUC7L2	0.98	1.01	1.21	0.83	1.07	0.13	15	35	3.67E-113
P61026	Ras-related protein Rab-10	RAB10	1.07	1.23	0.90	1.11	1.07	0.17	7	32	1.10E-80
P23526	Adenosylhomocysteinase	AHCY	1.12	1.21	0.87	1.15	1.07	0.18	15	31	8.55E-83
Q3ZCQ8-2	Mitochondrial import inner membrane translocase subunit TIM50	PRO1512	1.15	1.21	0.84	1.19	1.07	0.20	9	25	1.99E-95
P52701-1	DNA mismatch repair protein Msh6	GTBP	1.17	1.21	0.82	1.22	1.07	0.21	10	9.9	1.53E-48
B7Z3P1	cDNA FLJ59210, highly similar to Tubulin-specific chaperone E	TBCE	1.35	0.9	0.95	1.05	1.07	0.25	8	20	3.13E-41
Q96G46-1	tRNA-dihydrouridine synthase 3-like	DUS3L	1.23	1.21	0.76	1.32	1.07	0.27	10	24	1.40E-102
Q15014	MORF-related gene X protein	KIAA0026	1.16	1.29	0.75	1.33	1.07	0.28	4	19	5.24E-15
Q9ULX6	A-kinase anchor protein 8-like	AKAP8L	1.11	0.75	1.34	0.75	1.07	0.30	3	6.2	3.57E-16
Q96P11-2	NOL1/NOP2/Sun domain family member 5	NSUN5	1.45	0.95	0.80	1.25	1.07	0.34	5	14	4.43E-13
Q9H267	Vacuolar protein sorting-associated protein 33B	VPS33B	0.95	0.78	1.47	0.68	1.07	0.36	2	3.7	3.71E-05
Q9UBP6	Methyltransferase-like protein 1	C12orf1	1.26	1.30	0.64	1.56	1.07	0.37	4	14	7.77E-70
Q8IUE6	Histone H2A type 2-B	HIST2H2AB	0.81	0.74	1.65	0.61	1.07	0.51	9	66	5.93E-244
Q96A26	E2-induced gene 5 protein	C3orf28	0.99	1.15			1.07	0.11	2	12	1.04E-04
Q9UJV	DEAD box protein 41	ABS	0.99	1.15			1.07	0.11	3	6.9	1.39E-32

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9											
Q16540	39S ribosomal protein L23, mitochondrial	L23MRP	0.76		1.38	0.72	1.07	0.44	3	31	5.86E-22
O75865-2	Trafficking protein particle complex subunit 6A	HSPC289	1.07	1.07	1.07	0.93	1.07	0.00	2	24	1.13E-12
Q9Y5Y5-2	Peroxin-16	PEX16	1.07	1.07	1.07	0.93	1.07	0.00	2	5.5	1.36E-02
Q9BUE0	Mediator complex subunit 18	MED18	1.07	1.07	1.07	0.93	1.07	0.00	3	17	4.01E-05
Q9UNX3	60S ribosomal protein L26-like 1	RPL26L1	1.07	1.07	1.07	0.93	1.07	0.00	11	50	1.26E-33
Q9BV20-1	Mediator of RhoA-dependent invasion	MRDI	1.08	1.07	1.06	0.94	1.07	0.01	2	6.2	1.76E-13
Q9Y530	Uncharacterized protein C6orf130	C6orf130	1.09		1.05	0.95	1.07	0.03	2	14	8.33E-05
P20962	Parathymosin	PTMS	1.09		1.05	0.95	1.07	0.03	2	14	7.18E-05
A6NDY0-1	Embryonic poly(A)-binding protein type II	EPABP2	1.09		1.05	0.95	1.07	0.03	2	9.7	5.36E-03
Q99611	Selenide, water dikinase 2	SEPHS2	1.09		1.05	0.95	1.07	0.03	2	7.5	6.34E-06
Q9ULJ3	Zinc finger and BTB domain-containing protein 21	KIAA1227	1.09		1.05	0.95	1.07	0.03	4	7.1	2.50E-19
O95036	Similar to 60S ribosomal protein L7	WUGSC:H_RG054D04.1	1.09		1.05	0.95	1.07	0.03	18	46	1.12E-177
Q16666-1	Gamma-interferon-inducible protein 16	IFI16	1.1	1.09	1.02	0.98	1.07	0.04	21	28	2.01E-185
B4E1T7	cDNA FLJ58665, highly similar to Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform	PPP2R2A	1.05	1.12	1.04	0.96	1.07	0.04	8	21	4.20E-269
Q9NRD1	F-box only protein 6	FBG2	1.02	1.11	1.08	0.93	1.07	0.05	2	12	1.21E-23
P49411	Elongation factor Tu, mitochondrial	TUFM	1.10	1.10	1.01	0.99	1.07	0.05	19	50	9.65E-185
Q8IX12-1	Cell cycle and apoptosis regulatory protein 1	CARP1	1.08	1.15	0.98	1.02	1.07	0.09	11	11	7.32E-95
Q8WXA9-2	Serine/arginine-rich-splicing regulatory protein 86	SFRS12	0.97	1.11	1.13	0.88	1.07	0.09	7	16	4.15E-77
Q8NFW8-1	CMP-N-acetylneuraminic acid synthase	CMAS	1.16	0.98	1.07	0.93	1.07	0.09	4	11	5.10E-25
O75746	Calcium-binding mitochondrial carrier protein Aralar1	ARALAR1	1.13	0.96	1.12	0.89	1.07	0.10	6	9.6	2.12E-30

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P30419-1	Glycylpeptide N-tetradecanoyltransferase 1	NMT1	1.07	1.17	0.97	1.03	1.07	0.10	8	22	7.08E-106
Q9BS26	Endoplasmic reticulum resident protein 44	ERP44	1.10	1.20	0.91	1.10	1.07	0.15	6	19	1.90E-85
P53618	Beta-coat protein	COPB	1.21	1.11	0.89	1.12	1.07	0.16	17	24	2.26E-191
Q6IN85-1	Serine/threonine-protein phosphatase 4 regulatory subunit 3A	KIAA2010	1.24	1.06	0.91	1.10	1.07	0.17	7	14	1.51E-37
O43488	AFB1 aldehyde reductase 1	AFAR	0.93	1.01	1.27	0.79	1.07	0.18	5	18	8.05E-73
B7ZM99	Methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like	MTHFD1L	1.19	1.21	0.81	1.23	1.07	0.23	19	23	1.58E-120
P43490	Nicotinamide phosphoribosyltransferase	NAMPT	1.09	1.31	0.81	1.23	1.07	0.25	9	28	1.62E-132
Q6IAA8	p27Kip1-releasing factor from RhoA	C11orf59	0.89	1.25			1.07	0.25	3	34	1.06E-76
Q12873-1	ATP-dependent helicase CHD3	CHD3	1.11	1.31	0.79	1.27	1.07	0.26	10	9.6	4.90E-88
Q8TDN6	Brix domain-containing protein 2	BRIX	1.19	1.30	0.72	1.39	1.07	0.31	7	30	3.09E-21
O00541-1	Pescadillo homolog	PES1	1.33	1.17	0.71	1.41	1.07	0.32	12	22	1.05E-48
Q9Y2V2	Calcium-regulated heat stable protein 1	CARHSP1	0.84		1.30	0.77	1.07	0.33	3	26	3.27E-32
B4DWA0	cDNA FLJ54188, moderately similar to High mobility group protein HMG-I/HMG-Y	HMGA1	1.31	1.26	0.64	1.56	1.07	0.37	3	10	4.81E-21
Q07065-1	63 kDa membrane protein	CKAP4	0.66	0.79	1.76	0.57	1.07	0.60	6	14	1.17E-84
O60281	Zinc finger protein 292	KIAA0530			1.07	0.93	1.07		2	0.8	5.70E-02
Q96RL1-1	BRCA1-A complex subunit RAP80	RAP80			1.07	0.93	1.07		2	4	1.01E-14
B4DRD7	cDNA FLJ54752, highly similar to Poly(rC)-binding protein 2	PCBP2			1.07	0.93	1.07		13	71	7.48E-269
B2RE77	cDNA, FLJ95224, Homo sapiens proline rich 3 (PRR3), mRNA	CAT56	1.07				1.07		2	15	2.33E-07
P02792	Ferritin light chain	FTL	1.07				1.07		2	17	1.04E-19
Q9BWH2	Cervical cancer proto-oncogene 3 protein	DC44		1.07			1.07		3	16	5.98E-06
P55081	Microfibrillar-associated protein 1	MFAP1	1.13	1.17	0.92	1.09	1.07	0.13	6	15	4.43E-50
B4DKS	cDNA FLJ53381,	MCT1	1.14	1.24	0.84	1.19	1.07	0.21	5	11	6.88E-36

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0	highly similar to Monocarboxylate transporter 1										
Q69YN4-1	Protein virilizer homolog	KIAA1429	1.14	1.26	0.82	1.22	1.07	0.23	2	1.5	1.44E-19
O00267-1	DRB sensitivity-inducing factor 160 kDa subunit	SPT5	1.19	1.24	0.79	1.27	1.07	0.25	12	15	6.25E-49
Q13206	DEAD box protein 10	DDX10	1.07	1.35	0.80	1.25	1.07	0.28	7	13	4.73E-80
Q9NPF4	Probable O-sialoglycoprotein endopeptidase	GCPL1	1.23	1.25	0.74	1.35	1.07	0.29	4	19	2.33E-86
P62316	Small nuclear ribonucleoprotein Sm D2	SNRPD2	1.10	1.06	1.06	0.94	1.07	0.02	9	55	3.58E-181
P22626-1	Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	1.04	1.07	1.11	0.90	1.07	0.04	28	74	0.00E+00
A8MYH0	Lissencephaly-1 protein	LIS1	0.99	1.11	1.12	0.89	1.07	0.07	3	11	5.44E-18
P49755	21 kDa transmembrane-trafficking protein	TMED10	1.15	1.09	0.98	1.02	1.07	0.09	8	41	7.27E-55
O60885-1	Bromodomain-containing protein 4	BRD4	1.09	1.15	0.98	1.02	1.07	0.09	9	8.2	1.65E-27
Q7Z4W1	Carbonyl reductase II	DCXR	1.06	0.97	1.19	0.84	1.07	0.11	11	55	1.38E-42
P56537	B(2)GCN homolog	EIF6	0.95	1.21	1.06	0.94	1.07	0.13	8	56	1.80E-143
P10809	60 kDa chaperonin	HSP60	1.15	1.18	0.89	1.12	1.07	0.16	51	81	0.00E+00
Q13136-1	LAR-interacting protein 1	LIP1	0.85	1.27	1.10	0.91	1.07	0.21	6	6.7	8.23E-24
Q6P1K2-1	Polyamine-modulated factor 1	PMF1	1.16	0.99			1.08	0.12	3	18	4.49E-14
Q96M27-2	Protein PRRC1	PRRC1		0.83	1.32	0.76	1.08	0.35	2	7.1	1.53E-51
Q96HA1-1	Nuclear envelope pore membrane protein POM 121	KIAA0618	1.06		1.09	0.92	1.08	0.02	2	3.1	1.39E-13
Q9BQE3	Alpha-tubulin 6	TUBA1C	1.04		1.11	0.90	1.08	0.05	32	73	0.00E+00
Q9H7P6-1	ESCRT-I complex subunit MVB12B	C9orf28		1.03	1.12	0.89	1.08	0.06	3	16	3.04E-14
Q99549-2	M-phase phosphoprotein 8	MPHOSPH8	1.34		0.81	1.23	1.08	0.37	2	3.6	4.13E-05
B4DRY5	cDNA FLJ54538, highly similar to Transportin-2	TNPO2	0.94	1.07	1.22	0.82	1.08	0.14	9	11	1.51E-31
Q96CP2	FLYWCH family member 2	FLYWCH2	1.17	1.22	0.84	1.19	1.08	0.21	3	30	4.49E-08
O00330	Dihydrolipoamide dehydrogenase-binding protein of	PDHX	0.83	1.01	1.39	0.72	1.08	0.29	4	11	3.53E-07

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	pyruvate dehydrogenase complex										
P38646	75 kDa glucose-regulated protein	GRP75	1.12	1.15	0.96	1.04	1.08	0.10	38	57	0.00E+00
Q14139-2	Ubiquitin conjugation factor E4 A	KIAA0126	1.01	1.20	1.02	0.98	1.08	0.11	7	8.1	5.59E-98
Q13162	Antioxidant enzyme AOE372	PRDX4	1.16	1.18	0.89	1.12	1.08	0.16	10	49	1.43E-44
P84077	ADP-ribosylation factor 1	ARF1	1.22	1.12	0.89	1.12	1.08	0.17	9	58	2.25E-129
Q14690	NF-kappa-B-binding protein	KIAA0185	1.09	1.24	0.90	1.11	1.08	0.17	11	7.5	2.20E-67
P16104	Histone H2A.x	H2AFX	0.98	0.95	1.30	0.77	1.08	0.19	10	62	0.00E+00
Q9UIJ7	Adenylate kinase 3	AK3	0.95	0.96	1.32	0.76	1.08	0.21	9	39	2.16E-111
P62314	Small nuclear ribonucleoprotein Sm D1	SNRPD1	1.21	1.20	0.82	1.22	1.08	0.22	3	28	1.01E-65
Q02543	60S ribosomal protein L18a	RPL18A	1.29	1.23	0.71	1.41	1.08	0.32	13	53	2.57E-86
P22102-1	5-phosphoribosylglycinamide transformylase	GART	1.23	1.29	0.71	1.41	1.08	0.32	31	42	4.46E-257
Q9P258	Protein RCC2	KIAA1470	1.09	1.11	1.03	0.97	1.08	0.04	23	46	4.65E-114
Q9NZI8	Coding region determinant-binding protein	CRDBP	1.06	1.01	1.16	0.86	1.08	0.08	11	24	2.68E-173
Q96HS1-1	Bcl-XL-binding protein v68	PGAM5	1.18	1.27	0.78	1.28	1.08	0.26	13	50	1.80E-75
Q96ER9-1	Coiled-coil domain-containing protein 51	CCDC51	1.17	1.09	0.98	1.02	1.08	0.10	3	10	1.02E-15
Q4KMP7-2	TBC1 domain family member 10B	FP2461	1.22	1.08	0.94	1.06	1.08	0.14	4	10	2.19E-34
Q6F5E8	Leucine-rich repeat-containing protein 16C	LRRC16C	1.26	1.21	0.77	1.30	1.08	0.27	9	9.8	7.47E-111
P46777	60S ribosomal protein L5	MSTP030	1.24	1.27	0.73	1.37	1.08	0.30	17	48	1.75E-146
Q9ULA0	Aspartyl aminopeptidase	ASPEP	1.73	0.94	0.57	1.75	1.08	0.59	5	15	4.84E-27
Q9BVC5	Ashwin	C2orf49	1.08		1.08	0.93	1.08	0.00	3	16	4.62E-08
Q86WA6-1	Biphenyl hydrolase-like protein	BPHL	1.08		1.08	0.93	1.08	0.00	3	14	6.55E-25
Q96BH1	E3 ubiquitin-protein ligase RNF25	RNF25	1.07	1.09			1.08	0.01	4	9.8	3.87E-77
P63279	p18	UBC9	1.10		1.06	0.94	1.08	0.03	6	47	1.41E-65
A8MXB9	C-alpha-formylglycine-generating enzyme 2	PSEC0171	1.10		1.06	0.94	1.08	0.03	13	42	1.36E-149
P09429	High mobility group protein 1	HMG1	1.08	1.12	1.04	0.96	1.08	0.04	19	56	3.12E-265

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Q9UMS4	Nuclear matrix protein 200	NMP200	1.15	1.10	0.99	1.01	1.08	0.08	15	47	2.28E-119
P17612-1	cAMP-dependent protein kinase catalytic subunit alpha	PKACA	1.02		1.14	0.88	1.08	0.08	11	35	2.46E-83
P13674-2	Procollagen-proline,2-oxoglutarate-4-dioxygenase subunit alpha-1	P4HA		1.02	1.14	0.88	1.08	0.08	12	30	4.40E-119
Q9HCD5	Coactivator independent of AF-2	KIAA1637	1.12	0.98	1.14	0.88	1.08	0.09	5	11	5.18E-46
Q59GA1	Splicing factor, arginine/serine-rich 10 (Transformer 2 homolog, Drosophila) variant	SFRS10	1.02	1.02	1.20	0.83	1.08	0.10	9	36	1.44E-66
Q9BTZ2-1	Dehydrogenase/reductase SDR family member 4	DHRS4	1.16		1.00	1.00	1.08	0.11	5	15	1.05E-11
Q16134	Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial	ETFDH	1.17		0.99	1.01	1.08	0.13	6	12	1.57E-115
P05141	Adenine nucleotide translocator 2	ANT2	1.19		0.97	1.03	1.08	0.16	11	33	1.84E-73
B4DLH4	cDNA FLJ53622, highly similar to Hematological and neurological expressed1-like protein	C16orf34	0.92	1.24			1.08	0.23	3	21	3.72E-22
Q6NUL7	SPTLC1 protein	SPTLC1	1.25		0.91	1.10	1.08	0.24	3	10	1.55E-90
P35270	Sepiapterin reductase	SPR	1.36	0.97	0.91	1.10	1.08	0.24	8	41	4.16E-182
Q93045	Stathmin-2	SCG10	0.90	0.98	1.36	0.74	1.08	0.25	5	15	6.52E-37
P13807	Glycogen [starch] synthase, muscle	GYS	1.33		0.83	1.20	1.08	0.35	2	4.7	1.11E-15
B4DHM0	cDNA FLJ59687, highly similar to Secernin-1	KIAA0193	0.82	0.80	1.62	0.62	1.08	0.47	3	9.2	1.47E-18
A8K822	cDNA FLJ77778, highly similar to Homo sapiens death-associated protein 6 (DAXX), mRNA	BING2	1.43		0.73	1.37	1.08	0.49	2	4.9	2.11E-51
B1AKJ7	Oxysterol-binding protein	OSBPL9			1.08	0.93	1.08		2	3.2	3.42E-08
Q9NRG0	Chromatin accessibility complex 15 kDa protein	CHRAC1	1.08				1.08		2	26	6.69E-05
Q8IYQ7	Threonine synthase-like 1	THNSL1		1.08			1.08		2	3.5	5.58E-12
Q7Z7F0	UPF0469 protein	BLOM7		1.08			1.08		2	2.9	1.90E-03

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-1	KIAA0907										
A4D0Z6	Inosine-5-monophosphate dehydrogenase	IMPDH1		1.08			1.08		3	7.2	9.85E-10
A8MSU4	Putative uncharacterized protein HPRT1	HPRT1		1.08			1.08		4	21	1.49E-56
B2RU10	EIF4G1 protein	EIF4G1		1.08			1.08		41	21	0.00E+00
Q00839-1	Heterogeneous nuclear ribonucleoprotein U	HNRNPU	1.07	1.1	1.08	0.93	1.08	0.02	45	47	0.00E+00
P51659	17-beta-hydroxysteroid dehydrogenase 4	EDH17B4	1.12	1.10	1.03	0.97	1.08	0.05	11	23	4.77E-130
P20339	Ras-related protein Rab-5A	RAB5	1.02	1.09	1.14	0.88	1.08	0.06	9	60	2.61E-121
Q9Y2H0-2	Disks large-associated protein 4	DAP4	1.04	1.04	1.17	0.85	1.08	0.08	3	4.9	7.14E-14
P10319	Bw-58	HLA-B	1.15	0.95	1.15	0.87	1.08	0.12	8	28	1.15E-89
Q5QPK0	Dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit	DPM1	0.95	1.09	1.21	0.83	1.08	0.13	3	17	1.62E-32
P39023	60S ribosomal protein L3	OK/SW-cl.32	1.18	1.24	0.83	1.20	1.08	0.22	15	39	1.20E-109
P18085	ADP-ribosylation factor 4	ARF2	1.24	1.20	0.81	1.23	1.08	0.24	7	51	8.17E-67
Q01813	6-phosphofructokinase type C	PFKF	1.19	1.26	0.80	1.25	1.08	0.25	23	36	0.00E+00
Q13151	Heterogeneous nuclear ribonucleoprotein A0	HNRNPA0	0.91	0.96	1.38	0.72	1.08	0.26	15	51	1.92E-218
Q9NYP9	FAPP1-associated protein 1	C21orf45	0.89	0.98	1.38	0.72	1.08	0.26	5	33	2.94E-13
P17480-1	Autoantigen NOR-90	UBF	0.91	0.93	1.41	0.71	1.08	0.28	24	32	2.01E-171
P20042	Eukaryotic translation initiation factor 2 subunit 2	EIF2B	1.20	1.30	0.75	1.33	1.08	0.29	14	38	4.84E-288
Q9NYL4	19 kDa FK506-binding protein	FKBP11	1.30	1.22	0.73	1.37	1.08	0.31	3	18	2.05E-34
Q9BWJ5	Pre-mRNA-splicing factor SF3b 10 kDa subunit	SF3B10	1.00	1.43	0.82	1.22	1.08	0.31	3	40	1.06E-38
Q96PU8-4	Protein quaking	HKQ	1.72	0.74	0.79	1.27	1.08	0.55	2	7.7	1.43E-07
P52597	Heterogeneous nuclear ribonucleoprotein F	HNRNPF	1.11	1.12	1.02	0.98	1.08	0.06	13	55	0.00E+00
P32942	CDw50	ICAM3	1.10		1.07	0.93	1.09	0.02	5	11	6.30E-39
Q12981-4	BCL2/adenovirus E1B 19 kDa protein-interacting protein 1	BNIP1	1.01	1.16			1.09	0.11	3	12	2.64E-05
A8K654	cDNA FLJ75178, highly similar to	CXXC3	1.20		0.97	1.03	1.09	0.16	2	4	2.93E-09

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	Homo sapiens methyl-CpG binding protein splice variant 1 (MBD1) mRNA										
O60613-1	15 kDa selenoprotein	41167	0.96		1.21	0.83	1.09	0.18	2	15	2.29E-27
Q86X76-3	Nitrilase homolog 1	NIT1	1.10	1.01	1.15	0.87	1.09	0.07	6	19	1.58E-29
Q15286	GTP-binding protein RAY	RAB1C	1.01	1.08	1.17	0.85	1.09	0.08	6	40	1.46E-46
Q92621	205 kDa nucleoporin	C7orf14	0.98	1.13	1.15	0.87	1.09	0.09	9	6.5	9.45E-116
Q15437	Protein transport protein Sec23B	SEC23B	1.16	1.12	0.98	1.02	1.09	0.09	9	17	1.07E-64
Q9Y5B9	Chromatin-specific transcription elongation factor 140 kDa subunit	FACT140	1.14	1.15	0.97	1.03	1.09	0.10	31	32	1.19E-287
P07900-2	Heat shock 86 kDa	HSP90A	1.15	1.24	0.87	1.15	1.09	0.19	66	60	0.00E+00
A8K3N2	cDNA FLJ76264, highly similar to Homo sapiens mediator of RNA polymerase II transcription, subunit 6 homolog (yeast) (MED6), mRNA	ARC33	1.29	1.12	0.85	1.18	1.09	0.22	2	7.9	1.04E-06
Q9UI12-1	Nef-binding protein 1	ATP6V1H	0.94	0.96	1.36	0.74	1.09	0.24	5	14	8.26E-17
B9ZVP3	DEAD (Asp-Glu-Ala-Asp) box polypeptide 54, isoform CRA_a	DDX54	1.3	1.14	0.82	1.22	1.09	0.24	7	10	2.93E-42
Q969V3-1	Nicalin	NCLN	1.36	1.06	0.84	1.19	1.09	0.26	3	7.8	1.29E-12
O60232	Autoantigen p27	SSSCA1	1.44	1.20	0.62	1.61	1.09	0.42	7	50	1.66E-96
O00411	DNA-directed RNA polymerase, mitochondrial	POLRMT	1.32	1.39	0.55	1.82	1.09	0.47	8	10	7.88E-100
Q96EK9	Protein KTI12 homolog	KTI12	1.15		1.03	0.97	1.09	0.08	2	10	1.91E-12
P26196	ATP-dependent RNA helicase p54	DDX6	1.17	1.15	0.95	1.05	1.09	0.12	9	30	1.00E-110
P0C0S5	Histone H2A.Z	H2AFZ	0.99	1.23	1.05	0.95	1.09	0.12	6	38	1.11E-114
A8MZI2	Putative uncharacterized protein SAMM50	SAMM50		0.98	1.20	0.83	1.09	0.16	3	8.5	3.23E-26
Q9H9A5-1	CCR4-NOT transcription complex subunit 10	CNOT10	0.83	1.18	1.26	0.79	1.09	0.23	2	3	1.51E-09
P54136-1	Arginine--tRNA ligase	RARS	1.27	1.20	0.80	1.25	1.09	0.25	18	33	1.79E-142
P40926	Malate	MDH2	1.03	1.12	1.12	0.89	1.09	0.05	18	61	0.00E+00

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	dehydrogenase, mitochondrial										
Q8IYI6	Exocyst complex 84 kDa subunit	EXOC8	0.98	1.04	1.25	0.80	1.09	0.14	4	12	1.54E-26
Q96JP5-1	Zinc finger protein 91 homolog	FKSG11	1.04	0.95	1.28	0.78	1.09	0.17	3	8.1	2.46E-33
O00268	RNA polymerase II TBP-associated factor subunit C	TAF2C		0.92	1.26	0.79	1.09	0.24	4	4.4	2.13E-16
Q9BQC3	Diphthamide biosynthesis protein 2	DPH2	1.26		0.92	1.09	1.09	0.24	2	9	8.74E-08
Q92696	Geranylgeranyl transferase type II subunit alpha	RABGGTA		1.26	0.92	1.09	1.09	0.24	3	4.8	7.83E-06
Q9GZR2	Exonuclease XPMC2	PMC2			1.09	0.92	1.09		2	4.7	1.42E-02
Q5JT09	Uridine kinase	RP11-334J6.5-004			1.09	0.92	1.09		3	9.9	2.04E-05
P78560	Caspase and RIP adapter with death domain	CRADD	1.09				1.09		2	16	3.12E-29
O14893-1	Component of gems 2	GEMIN2	1.09				1.09		2	9.6	5.07E-08
Q9UJ83	2-hydroxyacyl-CoA lyase 1	HACL1		1.09			1.09		2	3.6	1.72E-05
B7ZBD6	Putative uncharacterized protein RABL2A	RABL2A	1.09				1.09		2	13	1.53E-07
B7Z268	cDNA FLJ51825, highly similar to Single-stranded DNA-binding protein, mitochondrial	hCG_2014251		1.09			1.09		2	15	7.32E-85
P36404	ADP-ribosylation factor-like protein 2	ARL2	1.09				1.09		4	28	3.10E-108
Q99417	Associate of Myc 1	AMY1	1.09				1.09		4	50	5.03E-11
P32321-2	dCMP deaminase	DCTD	0.96	1.22	1.10	0.91	1.09	0.13	2	15	3.34E-38
P08238	Heat shock 84 kDa	HSP90AB1	1.16	1.19	0.93	1.08	1.09	0.14	60	74	0.00E+00
Q9Y3B2	3-5 exoribonuclease CSL4 homolog	CGI-108	1.22	1.20	0.86	1.16	1.09	0.20	4	28	3.31E-123
Q14691	DNA replication complex GINS protein PSF1	GINS1	1.23	1.19	0.86	1.16	1.09	0.20	3	21	2.42E-112
P29372-1	3-alkyladenine DNA glycosylase	AAG	1.30	1.21	0.77	1.30	1.09	0.28	6	34	7.95E-37
P15927-3	Replication factor A protein 2	REPA2	1.08	1.07	1.13	0.88	1.09	0.03	7	28	1.70E-50
P25786-2	30 kDa prosomal protein	HC2	1.12	1.20	0.96	1.04	1.09	0.12	20	69	2.07E-208
P21127-	Cell division cycle 2-	CDC2L	1.08	1.24	0.96	1.04	1.09	0.14	9	11	2.59E-27

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1	like protein kinase 1	1									
O43252	3-phosphoadenosine-5-phosphosulfate synthase	ATPSK1	1.10	1.29	0.89	1.12	1.09	0.20	10	26	2.61E-153
Q13601	HIV-1 Rev-binding protein 2	HRB2	1.24	1.25	0.79	1.27	1.09	0.26	4	11	5.62E-32
Q04637-3	Eukaryotic translation initiation factor 4 gamma 1	EIF4F	1.12	1.37	0.79	1.27	1.09	0.29	57	37	0.00E+00
O00566	M phase phosphoprotein 10	MPHOSPH10	1.32	1.25	0.71	1.41	1.09	0.33	11	26	7.63E-177
Q6DKJ4-1	Nucleoredoxin	NRX	1.06		1.13	0.88	1.10	0.05	2	10	2.92E-17
Q9NPE3	H/ACA ribonucleoprotein complex subunit 3	NOLA3	1.05	1.14			1.10	0.06	3	58	1.19E-53
Q96G21	Brix domain-containing protein 4	BXDC4	1.14	1.05			1.10	0.06	3	12	2.98E-52
P49736	DNA replication licensing factor MCM2	BM28	1.01		1.18	0.85	1.10	0.12	35	50	0.00E+00
B4DZS0	cDNA FLJ50316, highly similar to DNAation factor subunit beta (EC 3.-.-.-)	DFFB	1.25		0.94	1.06	1.10	0.22	2	8.8	8.80E-08
Q3ZCM7	Tubulin beta-8 chain	TUBB8	0.91		1.28	0.78	1.10	0.26	11	25	8.85E-116
Q9ULI0-1	ATPase family AAA domain-containing protein 2B	ATAD2B		0.87	1.32	0.76	1.10	0.32	2	2.3	4.98E-17
Q6GMV3	Uncharacterized protein C2orf79	C2orf79	1.09	1.10			1.10	0.01	4	25	1.52E-30
O96033	Molybdenum cofactor synthesis protein 2 small subunit	MOCO1	1.12	1.07			1.10	0.04	3	28	9.32E-05
P84103	Pre-mRNA-splicing factor SRP20	SFRS3	1.08	1.08	1.13	0.88	1.10	0.03	12	49	1.30E-83
O75494-1	40 kDa SR-repressor protein	FUSIP1	1.09	1.06	1.14	0.88	1.10	0.04	6	24	1.30E-47
P17174	Aspartate aminotransferase, cytoplasmic	GOT1	1.07	1.06	1.16	0.86	1.10	0.06	14	50	2.21E-240
Q96MU7-1	Putative splicing factor YT521	KIAA1966	1.02	1.16	1.11	0.90	1.10	0.07	9	13	3.29E-36
P83731	60S ribosomal protein L24	RPL24	1.05	1.05	1.19	0.84	1.10	0.08	19	61	2.84E-74
Q13724	Mannosyl-oligosaccharide glucosidase	GCS1	1.08	1.21	1.00	1.00	1.10	0.11	10	21	1.44E-88
Q15393-1	Pre-mRNA-splicing factor SF3b 130 kDa subunit	KIAA0017	1.14	1.23	0.92	1.09	1.10	0.16	25	26	3.73E-248
Q13045	Protein flightless-1	FLII	0.95	1.02	1.32	0.76	1.10	0.20	20	23	8.40E-111

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	homolog										
Q15554-1	Telomeric DNA-binding protein	TERF2	1.20	1.24	0.85	1.18	1.10	0.21	4	12	6.86E-59
Q86SX6	Glutaredoxin-related protein 5, mitochondrial	C14orf87	1.23	1.23	0.83	1.20	1.10	0.23	3	28	2.02E-133
Q9Y3E1	Hepatoma-derived growth factor 2	CGI-142	0.92	1.00	1.37	0.73	1.10	0.24	4	25	2.01E-10
O15160-1	DNA-directed RNA polymerases I and III 40 kDa polypeptide	POLR1C	1.27	1.25	0.77	1.30	1.10	0.28	7	27	3.33E-91
Q9NY12-1	H/ACA ribonucleoprotein complex subunit 1	GAR1	1.18	1.33	0.78	1.28	1.10	0.28	6	28	5.37E-29
Q15785	Mitochondrial import receptor subunit TOM34	TOMM34	1.29	1.23	0.77	1.30	1.10	0.28	11	47	1.23E-193
Q8NAN0	Ferrochelatase	FECH	1.07	1.44	0.78	1.28	1.10	0.33	4	12	1.54E-29
P23527	Histone H2B type 1-O	H2BFH	0.91	0.88	1.50	0.67	1.10	0.35	13	73	1.50E-175
A8K435	cDNA FLJ78564, highly similar to Homo sapiens aldehyde dehydrogenase 5 family, member A1 (succinate-semialdehyde dehydrogenase) (ALDH5A1), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA	ALDH5A1	1.18	1.05	1.07	0.93	1.10	0.07	7	15	3.31E-25
Q9H2U2-1	Inorganic pyrophosphatase 2, mitochondrial	HSPC124	1.05	1.05	1.2	0.83	1.10	0.09	23	63	9.31E-226
Q00610-1	Clathrin heavy chain 1	CLH17	1.09	1.21	1.00	1.00	1.10	0.11	60	43	0.00E+00
Q6JUT2	Toll-like receptor adapter molecule 2 (TICAM-2) (Putative NF-kappa-B-activating protein 502).	hCG_37564	1.00	1.04	1.26	0.79	1.10	0.14	3	10	3.98E-07
Q8TD19	Nercc1 kinase	KIAA1995	1.20	1.26	0.84	1.19	1.10	0.23	4	6.5	1.17E-15
Q6TXQ4	Histone H3	H3	1.07		1.13	0.88	1.10	0.04	6	52	3.54E-95
B0QYN7	Ubiquitin carrier protein	LA16c-358B7.1-006	1.13	1.07			1.10	0.04	4	20	6.91E-37
O60506-1	Glycine- and tyrosine-rich RNA-binding	HNRPQ	1.05	1.15	1.10	0.91	1.10	0.05	25	45	0.00E+00

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	protein										
Q9P1F3	UPF0727 protein C6orf115	C6orf115	1.02		1.18	0.85	1.10	0.11	3	54	1.33E-16
Q08211	ATP-dependent RNA helicase A	DDX9	1.13	1.24	0.93	1.08	1.10	0.16	43	40	0.00E+00
P26885	13 kDa FK506-binding protein	FKBP13	0.98	1.22			1.10	0.17	3	14	4.08E-09
O60306	Intron-binding protein aquarius	AQR	1.07	1.29	0.94	1.06	1.10	0.18	19	15	4.90E-85
Q96GX5-1	Microtubule-associated serine/threonine-protein kinase-like	MASTL			1.10	0.91	1.10		2	4.1	3.70E-05
Q9ULU8-4	Calcium-dependent activator protein for secretion 1	CADPS			1.10	0.91	1.10		2	1	1.66E-03
Q1HDL3	HBeAg-binding protein 2 binding protein A	HBEBP2BPA			1.10	0.91	1.10		2	8	2.44E-12
P10321	MHC class I antigen Cw	HLA-Cw			1.10	0.91	1.10		7	26	9.68E-117
Q9Y2I1-1	Imidazoline receptor 1	IRAS	1.10				1.10		2	1.9	2.37E-04
Q5T6V5	UPF0553 protein C9orf64	C9orf64		1.10			1.10		3	8.8	1.67E-08
Q5U0E9	Cellular nucleic acid binding protein alpha variant 1	CNBP1	1.1				1.10		9	45	2.96E-161
Q86UX7-1	Fermitin family homolog 3	FERMT3	1.06	1.13	1.12	0.89	1.10	0.04	21	46	1.89E-211
Q15005	Microsomal signal peptidase 25 kDa subunit	KIAA0102	1.16	1.07	1.08	0.93	1.10	0.05	6	35	1.32E-137
Q5T0S6	Palmitoyl-protein thioesterase 1	PPT1	1.07	1.16	1.08	0.93	1.10	0.05	7	38	1.63E-75
B0V0T1	Low molecular mass protein 2	LMP2	1.05	1.08	1.18	0.85	1.10	0.07	5	30	2.22E-73
P27694	Replication factor A protein 1	REPA1	1.12	1.02	1.17	0.85	1.10	0.08	17	38	1.21E-267
Q15293	Reticulocalbin-1	RCN	0.90	1.27	1.14	0.88	1.10	0.19	5	18	1.67E-43
P23284	Cyclophilin B	CYPB	1.27	1.22	0.82	1.22	1.10	0.25	12	48	1.64E-98
P61604	10 kDa chaperonin	HSPE1	1.24	1.28	0.79	1.27	1.10	0.27	12	78	2.24E-65
Q13838-2	56 kDa U2AF65-associated protein	BAT1	1.08	1.12	1.11	0.90	1.10	0.02	19	50	6.40E-152
O75150-1	95 kDa retinoblastoma-associated protein	BRE1B	1.05	1.15	1.11	0.90	1.10	0.05	23	25	2.43E-99
Q13445	Interleukin-1 receptor-like 1 ligand	IL1RL1L	1.15		1.06	0.94	1.11	0.06	2	12	2.45E-06
P34913	Cytosolic epoxide hydrolase	EPHX2	1.15		1.06	0.94	1.11	0.06	4	11	4.70E-11
B5MD17	Putative uncharacterized	CBX1	1.04		1.17	0.85	1.11	0.09	7	51	2.98E-140

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	protein CBX1										
Q08623	Haloacid dehalogenase-like hydrolase domain-containing protein 1A	DXF68S1E	1.20		1.01	0.99	1.11	0.13	4	26	4.68E-76
Q96CB8	Integrator complex subunit 12	INTS12		1.00	1.21	0.83	1.11	0.15	2	6.7	7.10E-18
B4DN31	cDNA FLJ55809	CHID1		1.22	0.99	1.01	1.11	0.16	2	5.5	1.74E-06
Q9H5N1-1	Rab GTPase-binding effector protein 2	RABEP2		0.94	1.27	0.79	1.11	0.23	2	3.9	9.12E-07
Q8WUD4	Coiled-coil domain-containing protein 12	CCDC12	0.87		1.34	0.75	1.11	0.33	6	42	3.32E-21
Q9NX70	Intersex-like protein	IXL		0.81	1.40	0.71	1.11	0.42	2	13	4.96E-101
Q9BTC0-4	Death-associated transcription factor 1	C20orf158	0.98	1.32	1.02	0.98	1.11	0.19	7	4.4	1.45E-33
P53007	Citrate transport protein	SLC20A3	1.15	0.85	1.32	0.76	1.11	0.24	4	14	6.53E-14
Q92820	Conjugase	GGH	0.93	0.93	1.46	0.68	1.11	0.31	4	16	9.46E-245
Q9NPL8	Protein M5-14	C3orf1	1.36	1.31	0.65	1.54	1.11	0.40	8	33	3.46E-63
Q99856	AT-rich interactive domain-containing protein 3A	ARID3A	0.78	0.84	1.70	0.59	1.11	0.51	4	12	2.16E-41
Q9H9L3	Interferon-stimulated 20 kDa exonuclease-like 2	HSD38	1.06	1.16			1.11	0.07	2	7.6	1.55E-22
Q13523	PRP4 kinase	KIAA0536	1.04	1.18			1.11	0.10	4	4.5	3.54E-08
P28074	Macropain epsilon chain	LMPX	1.23	1.16	0.94	1.06	1.11	0.15	13	54	8.38E-233
B5MDF5	Putative uncharacterized protein RAN	hCG_1744585	1.23	1.16	0.94	1.06	1.11	0.15	14	44	3.70E-118
Q99575	Ribonucleases P/MRP protein subunit POP1	KIAA0061	0.97	1.54	0.82	1.22	1.11	0.38	7	9.8	2.77E-26
P61960	Ubiquitin-fold modifier 1	BM-002	1.11		1.11	0.90	1.11	0.00	2	59	1.85E-29
A1L0T0-1	Acetolactate synthase-like protein	AHAS	1.10		1.12	0.89	1.11	0.01	2	6.3	1.52E-15
O14497-1	AT-rich interactive domain-containing protein 1A	ARID1A	1.05	1.11	1.17	0.85	1.11	0.06	23	17	1.81E-165
Q2TAY7	Smu-1 suppressor of mec-8 and unc-52 protein homolog	SMU1	1.02	1.27	1.04	0.96	1.11	0.14	7	15	5.96E-43
Q9UHI6	Component of gems 3	DDX20	1.10	1.26	0.97	1.03	1.11	0.15	5	8.3	1.06E-37
Q13423	NAD(P) transhydrogenase, mitochondrial	NNT	0.95	1.13	1.25	0.80	1.11	0.15	8	9.4	5.94E-38
P45954	2-methyl branched chain acyl-CoA	ACADSB	0.91	1.21	1.21	0.83	1.11	0.17	2	5.3	2.91E-05

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	dehydrogenase										
O43615	Mitochondrial import inner membrane translocase subunit TIM44	MIMT44	1.08	1.32	0.93	1.08	1.11	0.20	9	19	1.82E-78
Q9H4M9	EH domain-containing protein 1	CDABP0131	1.01	0.98	1.34	0.75	1.11	0.20	7	19	1.96E-140
Q9H7Z7	Microsomal prostaglandin E synthase 2	C9orf15	1.33		0.89	1.12	1.11	0.31	4	19	8.03E-38
P61313	60S ribosomal protein L15	EC45	1.23	1.43	0.67	1.49	1.11	0.39	10	44	3.99E-55
Q8N766-1	Uncharacterized protein KIAA0090	KIAA0090	1.08	1.53	0.72	1.39	1.11	0.41	4	7	1.55E-13
P50454	47 kDa heat shock protein	CBP1	0.76	0.96	1.61	0.62	1.11	0.44	4	13	1.20E-28
P04181	Ornithine aminotransferase, hepatic form	OAT	1.52	1.34	0.47	2.13	1.11	0.56	7	24	1.99E-68
Q9H8W4	PH and FYVE domain-containing protein 2	PLEKHF2		1.11			1.11		2	7.2	4.56E-04
B7ZKU0	C11orf30 protein	C11orf30		1.11			1.11		2	1.1	1.72E-02
Q9H0E9-1	Bromodomain-containing protein 8	BRD8	1.11				1.11		3	3.8	3.90E-04
Q68CZ6	HAUS augmin-like complex subunit 3	C4orf15		1.11			1.11		3	5.3	9.04E-09
Q9BT73	Proteasome assembly chaperone 3	C7orf48	1.11				1.11		3	43	7.10E-05
A8K0Z3	CXYorf1-like protein on chromosome 9	FAM39E		1.11			1.11		3	7.9	3.18E-20
O15235	28S ribosomal protein S12, mitochondrial	MRPS12	1.11				1.11		4	23	8.83E-07
Q15819	Enterocyte differentiation-associated factor 1	MMS2		1.11			1.11		5	33	1.20E-20
Q8N9N7	Leucine-rich repeat-containing protein 57	LRRC57	1.11				1.11		6	28	8.30E-27
P54577	Tyrosyl--tRNA ligase	YARS	1.07	1.11	1.16	0.86	1.11	0.05	25	53	5.82E-169
P38919	ATP-dependent RNA helicase DDX48	DDX48	1.11	1.16	1.07	0.93	1.11	0.05	18	46	1.18E-202
P43403-1	70 kDa zeta-associated protein	SRK	1.30	1.29	0.75	1.33	1.11	0.31	22	44	4.31E-188
Q86UY3	ARHGAP4 protein	ARHGAP4	1.27	1.26	0.81	1.23	1.11	0.26	9	14	1.43E-80
Q9BUH6-1	Uncharacterized protein C9orf142	C9orf142	1.22	1.52	0.60	1.67	1.11	0.47	2	13	5.57E-34
P09488-1	Glutathione S-transferase Mu 1	GST1	1.19		1.04	0.96	1.12	0.11	7	33	1.26E-71
Q8WVC6-1	Dephospho-CoA kinase domain-	DCAKD	1.24		0.99	1.01	1.12	0.18	3	14	3.59E-08

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	containing protein										
B2RCK3	cDNA, FLJ96127, highly similar to Homo sapiens glutathione transferase zeta 1 (maleylacetoacetate isomerase) (GSTZ1), transcript variant 3, mRNA	GSTZ1	1.31		0.92	1.09	1.12	0.28	3	24	1.22E-34
Q9NX62	Inositol monophosphatase 3	IMPA3	0.91		1.32	0.76	1.12	0.29	2	11	1.81E-09
Q9NYF8-1	Bcl-2-associated transcription factor 1	BCLAF1	1.04	1.18	1.13	0.88	1.12	0.07	24	24	3.14E-105
Q9Y4L1	150 kDa oxygen-regulated protein	GRP170	1.17	1.27	0.91	1.10	1.12	0.19	44	54	0.00E+00
P18858	DNA ligase 1	LIG1	1.23	1.26	0.86	1.16	1.12	0.22	21	30	5.79E-273
P13987	1F5 antigen	CD59	1.31	0.97	1.07	0.93	1.12	0.17	3	25	2.23E-18
Q14204	Cytoplasmic dynein 1 heavy chain 1	DHC1	1.28	1.37	0.70	1.43	1.12	0.36	##	29	0.00E+00
O43242	26S proteasome non-ATPase regulatory subunit 3	PSMD3	1.18	1.20	0.98	1.02	1.12	0.12	16	38	3.56E-158
O76021	Cellular senescence-inhibited gene protein	CATX11	1.19	1.20	0.97	1.03	1.12	0.13	23	46	0.00E+00
O43776	Asparagine--tRNA ligase	NARS	1.26	1.17	0.93	1.08	1.12	0.17	16	36	5.12E-181
Q96S44	Nori-2	C20orf64	1.24	1.20	0.92	1.09	1.12	0.17	4	20	1.88E-82
Q8IUD2-1	ELKS/Rab6-interacting/CAST family member 1	ELKS	1.01	0.91	1.44	0.69	1.12	0.28	4	5.8	1.14E-33
Q13952-1	CAAT box DNA-binding protein subunit C	NFYC	1.18	1.06			1.12	0.08	3	7.6	1.43E-17
Q16836-2	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	HAD	1.07	1.07	1.22	0.82	1.12	0.09	10	35	3.19E-81
O15260-1	Surfeit locus protein 4	SURF4	1.05		1.19	0.84	1.12	0.10	3	15	1.02E-22
P51809-1	Synaptobrevin-like protein 1	SYBL1	1.19	1.05			1.12	0.10	3	11	2.68E-03
O95777	N-alpha-acetyltransferase 38, NatC auxiliary subunit	LSM8	1.08	1.04	1.24	0.81	1.12	0.11	3	47	1.26E-58
Q13158	FAS-associated death domain protein	FADD	1.04		1.20	0.83	1.12	0.11	4	29	2.34E-252
Q9H501	ABT1-associated protein	ABTAP		1.21	1.03	0.97	1.12	0.13	4	5.9	1.64E-23
Q3LXA3	ATP-dependent dihydroxyacetone kinase	DAK	1.09	1.28	0.99	1.01	1.12	0.15	6	18	3.31E-87

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P84243	Histone H3.3	H3.3A	1.01		1.23	0.81	1.12	0.16	8	53	1.24E-86
P33991	CDC21 homolog	CDC21		0.97	1.27	0.79	1.12	0.21	37	49	0.00E+00
B4DMQ9	cDNA FLJ58590, highly similar to YLP motif-containing protein 1	YLPM1	1.23	1.30	0.83	1.20	1.12	0.25	21	14	4.52E-175
Q9UBW8	COP9 signalosome complex subunit 7a	COPS7A	1.62		0.62	1.61	1.12	0.71	2	11	2.03E-45
Q15596	Class E basic helix-loop-helix protein 75	BHLHE75			1.12	0.89	1.12		2	1.4	4.04E-02
Q9BSH4	Coiled-coil domain-containing protein 44	CCDC44			1.12	0.89	1.12		2	11	3.08E-10
Q8TB03-1	Uncharacterized protein CXorf38	CXorf38			1.12	0.89	1.12		3	10	1.06E-05
Q9Y3Q8	TSC22 domain family protein 4	TILZ2	1.12				1.12		2	17	5.52E-17
P30405	Cyclophilin F	CYP3	1.12				1.12		2	7.2	6.55E-03
Q9NSU2-1	3-5 exonuclease TREX1	TREX1	1.12				1.12		2	6.5	8.11E-05
Q7Z5R6	Amyloid beta A4 precursor protein-binding family B member 1-interacting protein	APBB1IP		1.12			1.12		2	2.9	4.44E-05
Q96CS2-1	Coiled-coil domain-containing protein 5	CCDC5	1.12				1.12		2	11	5.91E-05
Q5JRA6-1	C219-reactive peptide	KIAA0268	1.12				1.12		2	1.3	5.30E-18
A4D1Z4	KIAA0415 gene product	KIAA0415		1.12			1.12		2	1.1	4.63E-03
B7WPI0	Linker for activation of T cells, isoform CRA_d	hCG_2039637	1.12				1.12		3	26	1.23E-14
Q9NZM3-1	Intersectin-2	ITSN2	1.12				1.12		5	4.1	3.99E-18
P24666-1	Adipocyte acid phosphatase	ACP1	1.15	1.14	1.08	0.93	1.12	0.04	8	61	3.34E-96
Q9Y3A5	Ribosome maturation protein SBDS	CGI-97	1.18	1.00	1.19	0.84	1.12	0.11	3	12	8.53E-14
Q9Y277-2	Outer mitochondrial membrane protein porin 3	VDAC3	1.26	1.12	0.99	1.01	1.12	0.14	5	22	2.51E-39
P14868	Aspartate--tRNA ligase	DARS	1.17	1.27	0.93	1.08	1.12	0.17	15	33	8.76E-63
Q14839-2	ATP-dependent helicase CHD4	CHD4	1.17	1.33	0.87	1.15	1.12	0.23	32	24	2.68E-189
P51571	Signal sequence receptor subunit delta	SSR4	1.24	1.28	0.85	1.18	1.12	0.24	4	29	4.49E-45
Q96DB5	Protein FAM82B	CGI-90	0.84	1.21	1.32	0.76	1.12	0.25	4	11	4.40E-18
O95456	Chromosome 21 leucine-rich protein	C21LRP	1.28	1.28	0.81	1.23	1.12	0.27	6	28	2.73E-92

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-1											
Q8IXT5	RNA-binding motif protein 12B	RBM12B	1.03	1.44	0.90	1.11	1.12	0.28	4	4.4	1.57E-24
P60510	Protein phosphatase X	PPP4	1.38	1.18	0.81	1.23	1.12	0.29	4	17	3.00E-64
Q9Y2B0-1	MIR-interacting saposin-like protein	CNPY2	1.31	1.27	0.79	1.27	1.12	0.29	8	65	1.90E-120
Q13469-1	NFAT pre-existing subunit	NFAT1	1.21		1.04	0.96	1.13	0.12	2	2.8	2.56E-04
B4DQM4	cDNA FLJ61157, highly similar to XPA-binding protein 1	GPN1	1.01	1.24			1.13	0.16	2	6.4	1.59E-44
Q9HD20-1	Probable cation-transporting ATPase 13A1	ATP13A		1.36	0.89	1.12	1.13	0.33	3	2.8	8.14E-05
Q8N9N8	Eukaryotic translation initiation factor 1A domain-containing protein	EIF1AD	1.16	1.19	1.03	0.97	1.13	0.09	5	39	2.99E-59
O00487	26S proteasome non-ATPase regulatory subunit 14	POH1	1.22	1.13	1.03	0.97	1.13	0.10	6	38	2.85E-96
B1AH57	RAB, member of RAS oncogene family-like 4	LL22NC01-132D12.2-002	1.25	0.98	1.15	0.87	1.13	0.14	3	18	6.72E-80
Q16740	Endopeptidase Clp	CLPP	1.03	1.03	1.32	0.76	1.13	0.17	9	35	4.08E-136
Q562R1	Beta-actin-like protein 2	ACTBL2	1.21	1.24	0.93	1.08	1.13	0.17	8	26	5.96E-120
Q4VC31	Coiled-coil domain-containing protein 58	CCDC58	1.44	1.00	0.94	1.06	1.13	0.27	3	25	4.73E-29
O14744	72 kDa ICln-binding protein	HRMT1L5	1.28	1.34	0.76	1.32	1.13	0.32	12	24	1.72E-34
P15529-2	Membrane cofactor protein	CD46	1.15		1.11	0.90	1.13	0.03	2	5.5	2.64E-18
Q59FB9	Toll interacting protein variant	TOLLIP	1.04		1.22	0.82	1.13	0.13	3	9.9	1.95E-14
O75915	ADP-ribosylation factor-like protein 6-interacting protein 5	ARL6IP5	1.03		1.23	0.81	1.13	0.14	3	17	1.37E-88
P46779	60S ribosomal protein L28	RPL28		1.02	1.24	0.81	1.13	0.16	16	52	1.16E-95
Q8IV63	Serine/threonine-protein kinase VRK3	VRK3			1.13	0.88	1.13		2	4.4	2.32E-17
Q5JRS2	Ubiquitin-like modifier activating enzyme 1	CTD-2522E6.1-008			1.13	0.88	1.13		11	43	3.21E-128
O14925	Mitochondrial import inner membrane translocase subunit Tim23	TIM23	1.13				1.13		2	12	6.57E-29
O15127	Secretory carrier-associated membrane protein 2	SCAMP2	1.13				1.13		3	14	5.62E-94

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Q00746	Nucleoside diphosphate kinase	NME1-NME2	1.13				1.13		5	81	2.30E-92
Q8N257	H2B type 12	HIST3H2BB		1.13			1.13		12	73	2.01E-85
P13929-1	2-phospho-D-glycerate hydro-lyase	ENO3	1.13				1.13		12	26	1.02E-229
Q96HE7	Endoplasmic oxidoreductin-1-like protein	ERO1L	1.22	1.09	1.08	0.93	1.13	0.08	10	26	1.54E-69
O75688-1	Protein phosphatase 1B	PP2CB	0.91	1.11	1.37	0.73	1.13	0.23	3	7.3	6.62E-23
P61160	Actin-like protein 2	ACTR2	0.92		1.34	0.75	1.13	0.30	15	37	3.42E-161
P30044-1	Alu corepressor 1	ACR1	1.16	1.19	1.05	0.95	1.13	0.07	11	56	3.86E-249
Q5JSH3-1	Rabphilin-11	WDR44	1.18	0.83	1.39	0.72	1.13	0.28	2	3.1	1.68E-07
P05114	High mobility group nucleosome-binding domain-containing protein 1	HMG14	1.14	1.24	1.02	0.98	1.13	0.11	7	53	7.14E-67
P49914	5,10-methenyl-tetrahydrofolate synthetase	MTHFS	1.06	1.42	0.92	1.09	1.13	0.26	4	24	6.43E-13
C9JI13	Putative uncharacterized protein CCNK	CCNK	1.54	1.18	0.68	1.47	1.13	0.43	3	9.8	2.83E-42
Q8WX92	Cofactor of BRCA1	COBRA1	1.06	1.30	1.04	0.96	1.13	0.14	6	17	1.10E-25
Q99816-1	ESCRT-I complex subunit TSG101	TSG101		1.14	1.13	0.88	1.14	0.01	3	9.5	3.63E-15
B4DV10	cDNA FLJ59142, highly similar to Epididymal secretory protein E1	HE1	1.15	1.12			1.14	0.02	4	29	4.99E-81
P09234	U1 small nuclear ribonucleoprotein C	SNRPC	1.18		1.09	0.92	1.14	0.06	2	13	1.79E-25
O43933	Peroxin-1	PEX1	1.18		1.09	0.92	1.14	0.06	2	2.5	1.83E-06
Q9NQT5	Exosome complex exonuclease RRP40	CGI-102	1.27	1.00			1.14	0.19	4	30	1.32E-26
O43598	c-Myc-responsive protein Rcl	C6orf108	0.96		1.31	0.76	1.14	0.25	7	58	1.72E-35
Q08722-1	Antigenic surface determinant protein OA3	CD47	1.17	1.20	1.04	0.96	1.14	0.09	4	12	2.54E-04
O75844	CAAX prenyl protease 1 homolog	FACE1	1.02	1.25	1.14	0.88	1.14	0.12	3	6.1	2.05E-65
Q15291-1	Retinoblastoma-binding protein 5	RBBP5	1.00	1.19	1.22	0.82	1.14	0.12	2	4	9.60E-05
P11279	CD107 antigen-like family member A	LAMP1	1.29	1.13	0.99	1.01	1.14	0.15	4	9.8	5.76E-74
O14773-1	Cell growth-inhibiting gene 1 protein	CLN2	1.35	1.12	0.94	1.06	1.14	0.21	5	12	9.83E-64

UniProt ID	Protein_Name	Gene Name	F1 (L/H)	F2 (L/H)	R1 (H/L)	R1 (L/H)	Mean (T/U)	S.D.	Pep. No.	%Seq. Cov.	PEP
B2ZZ83	Filamin B	FLNB	1.33	1.31	0.77	1.30	1.14	0.32	85	47	0.00E+00
Q92530	Proteasome inhibitor PI31 subunit	PSMF1	1.56	1.19	0.66	1.52	1.14	0.45	5	34	2.75E-141
Q9H307-1	140 kDa nuclear and cell adhesion-related phosphoprotein	DRS	1.10	1.19	1.13	0.88	1.14	0.05	20	31	1.29E-126
Q9H2P0	Activity-dependent neuroprotective protein	ADNP	1.15	1.18	1.09	0.92	1.14	0.05	6	10	2.18E-65
Q96AE4-2	DNA helicase V	FUBP1	1.09	1.28	1.05	0.95	1.14	0.12	36	55	0.00E+00
P30049	ATP synthase subunit delta, mitochondrial	ATP5D	1.00	1.30	1.12	0.89	1.14	0.15	3	38	5.97E-81
Q8NBJ5	Glycosyltransferase 25 family member 1	GLT25D1	1.20	1.30	0.92	1.09	1.14	0.20	3	5.1	8.54E-09
Q8WU39-1	Plasma cell-induced resident endoplasmic reticulum protein	HSPC190	1.33	1.33	0.76	1.32	1.14	0.33	6	52	4.07E-126
Q92522	Histone H1x	H1FX	0.85	1.01	1.56	0.64	1.14	0.37	7	30	1.35E-78
Q9Y3C4-3	PRPK-binding protein	CGI-121	1.64		0.64	1.56	1.14	0.71	2	14	4.31E-135
P05771-2	Protein kinase C beta type	PKCB			1.14	0.88	1.14		2	4.8	3.66E-04
O75410-2	Gastric cancer antigen Ga55	KIAA1103			1.14	0.88	1.14		2	2.7	4.72E-04
B3KY41	cDNA FLJ46786 fis, clone TRACH3028837, highly similar to Homo sapiens smoothelin (SMTN), transcript variant 2, mRNA	SMTN			1.14	0.88	1.14		2	2.1	8.27E-09
Q96NL3-1	Zinc finger protein 599	ZNF599	1.14				1.14		2	3.4	2.75E-02
Q8N567	Zinc finger CCHC domain-containing protein 9	ZCCHC9		1.14			1.14		2	8.9	6.62E-05
P15104	Glutamate decarboxylase	GLNS	1.14				1.14		5	15	1.00E-144
O75880	Protein SCO1 homolog, mitochondrial	SCO1	1.18		1.10	0.91	1.14	0.06	4	18	1.17E-10
B1B5P7	N-acylsphingosine amidohydrolase 1	ASAH1	1.19		1.09	0.92	1.14	0.07	3	15	1.97E-11
Q96C01	Protein FAM136A	FAM136A	1.19	1.09			1.14	0.07	3	15	9.46E-17
Q05048	CF-1 50 kDa subunit	CSTF1	1.19	1.09			1.14	0.07	4	10	1.27E-32
O00422	18 kDa Sin3-associated polypeptide	GIG38	1.20	1.08			1.14	0.08	9	52	3.43E-89
Q969Q0	60S ribosomal protein L36a-like	RPL36AL	1.23	1.05			1.14	0.13	6	30	3.19E-24
Q9BX4	Protein FAM61B	C20orf4	1.31		0.97	1.03	1.14	0.24	3	12	1.84E-31

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0-1		0									
Q96EY1-1	DnaJ homolog subfamily A member 3, mitochondrial	DNAJA3	1.34	1.27	0.81	1.23	1.14	0.29	4	14	1.79E-52
O75152	Zinc finger CCCH domain-containing protein 11A	KIAA0663	1.01	1.16	1.26	0.79	1.14	0.13	13	22	1.89E-117
Q14676-1	Mediator of DNA damage checkpoint protein 1	KIAA0170	1.27	1.18	0.98	1.02	1.14	0.15	25	23	4.47E-187
Q9NRV9	Heme-binding protein 1	HBP1	1.07	1.29	1.07	0.93	1.14	0.13	5	33	5.97E-83
Q9H098-2	Protein FAM107B	C10orf45	1.19		1.10	0.91	1.15	0.06	2	7.8	5.23E-15
O43482	Cancer/testis antigen 86	MIS18B	1.02	1.27			1.15	0.18	2	17	2.28E-40
Q16576	Histone acetyltransferase type B subunit 2	RBAP46	1.30	0.99			1.15	0.22	11	28	2.99E-87
Q9Y6D5	Brefeldin A-inhibited guanine nucleotide-exchange protein 2	ARFGEF2	1.34		0.95	1.05	1.15	0.28	3	3.2	9.84E-07
Q13257	Mitotic arrest deficient 2-like protein 1	MAD2		1.40	0.89	1.12	1.15	0.36	4	17	1.25E-04
Q9Y399	28S ribosomal protein S2, mitochondrial	CGI-91		0.87	1.42	0.70	1.15	0.39	3	8.8	6.74E-06
Q9BRP8-1	Partner of Y14 and mago	PYM	1.02	1.23	1.19	0.84	1.15	0.11	6	53	2.76E-89
Q92900-1	ATP-dependent helicase RENT1	KIAA0221	1.12	1.29	1.03	0.97	1.15	0.13	32	31	2.72E-181
A6NHQ2	rRNA/tRNA 2-O-methyltransferase fibrillarin-like protein 1	FBLL1	1.23	1.51	0.70	1.43	1.15	0.41	2	6.6	9.38E-13
Q13057-2	Bifunctional coenzyme A synthase	COASY	1.17		1.13	0.88	1.15	0.03	3	6.4	1.35E-25
B4DU42	cDNA FLJ56153, highly similar to Homo sapiens transforming growth factor beta regulator 4 (TBRG4), transcript variant 1, mRNA	CPR2		1.21	1.09	0.92	1.15	0.08	2	4.8	4.48E-40
P55795	Heterogeneous nuclear ribonucleoprotein H	FTP3	1.22		1.08	0.93	1.15	0.10	11	30	6.46E-265
O75525-1	KH domain-containing, RNA-binding, signal transduction-associated protein 3	KHDRBS3	1.05	1.25			1.15	0.14	4	9.8	7.98E-05
Q96BR5	Hcp beta-lactamase-like protein C1orf163	C1orf163	0.94		1.36	0.74	1.15	0.30	4	19	1.09E-08
P46063	ATP-dependent DNA helicase Q1	RECQ1		0.88	1.42	0.70	1.15	0.38	5	7.6	3.87E-22

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P42695	Condensin-2 complex subunit D3	CAPD3	1.55		0.75	1.33	1.15	0.57	7	7.5	4.43E-126
Q92558	Wiskott-Aldrich syndrome protein family member 4	SCAR2			1.15	0.87	1.15		2	4.2	1.99E-28
Q99728	BRCA1-associated RING domain protein 1	BARD1			1.15	0.87	1.15		2	3.5	4.22E-03
Q9HBM6	Neuronal cell death-related protein 7	TAF9B			1.15	0.87	1.15		2	14	4.26E-04
Q9NPJ3	Acyl-coenzyme A thioesterase 13	ACOT13	1.15				1.15		2	11	3.27E-10
P61457	4-alpha-hydroxy-tetrahydropterin dehydratase	DCOH	1.15				1.15		2	17	9.32E-03
Q8N4P3-1	HD domain-containing protein 3	HDDC3	1.15				1.15		2	16	1.56E-06
Q71UM5	40S ribosomal protein S27-like	RPS27L	1.15				1.15		3	38	1.41E-17
Q9Y2W1	Thyroid hormone receptor-associated protein 3	THRAP3	1.14	1.22	1.09	0.92	1.15	0.07	26	27	9.72E-201
Q13733-1	Sodium pump subunit alpha-4	ATP1A4	0.97	1.02	1.46	0.68	1.15	0.27	7	10	1.42E-20
P84085	ADP-ribosylation factor 5	ARF5	1.14	1	1.32	0.76	1.15	0.16	6	31	2.07E-19
O75340	Apoptosis-linked gene 2 protein	ALG2	0.93	1.48	1.05	0.95	1.15	0.29	7	55	7.75E-129
Q9NZJ9-1	Diadenosine 5,5-P1,P6-hexaphosphate hydrolase 2	DIPP2	0.93	1.53	1	1.00	1.15	0.33	4	22	1.56E-31
Q58FG1	Heat shock 90 kDa protein 1 alpha-like 2	HSP90AA4P	1.22	1.31	0.93	1.08	1.15	0.20	3	7.4	1.40E-10
P26232-1	Alpha N-catenin	CAPR	1.16		1.15	0.87	1.16	0.01	2	3.7	2.11E-65
Q16566	Calcium/calmodulin-dependent protein kinase type IV	CAMK4		1.29	1.02	0.98	1.16	0.19	2	4.9	1.49E-27
O95487-1	Protein transport protein Sec24B	SEC24B	1.29		1.02	0.98	1.16	0.19	3	4.9	7.15E-26
A6NLK4	35-alpha calcimedin	ANX3		1.01	1.30	0.77	1.16	0.21	2	8.4	5.17E-07
Q8WUQ7-2	Cactin	C19orf29	0.93		1.38	0.72	1.16	0.32	2	4.3	2.13E-30
Q14980-2	Nuclear mitotic apparatus protein 1	NUMA		0.89	1.42	0.70	1.16	0.37	80	45	0.00E+00
P26639	Threonine--tRNA ligase	TARS	1.16	1.16	1.15	0.87	1.16	0.01	26	41	2.77E-240
P36776	Lon protease homolog, mitochondrial	LONP1	1.08	1.17	1.22	0.82	1.16	0.07	36	46	0.00E+00
Q9NZL9-1	DTDP-4-keto-6-deoxy-D-glucose 4-reductase	MAT2B	1.26	1.37	0.84	1.19	1.16	0.28	11	40	1.32E-111

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Q9BZJ0-1	Crooked neck homolog	CGI-201	1.12	1.25	1.10	0.91	1.16	0.08	8	11	1.09E-112
Q9H3P7	Acyl-CoA-binding domain-containing protein 3	ACBD3	1.26	1.02	1.19	0.84	1.16	0.12	5	15	1.62E-137
P06748-1	Nucleolar phosphoprotein B23	NPM	1.47	1.36	0.64	1.56	1.16	0.45	15	60	0.00E+00
Q9NPF5	DNA methyltransferase 1-associated protein 1	DMAP1	1.18	1.14			1.16	0.03	2	6.6	2.04E-14
Q8IYB3-2	Ser/Arg-related nuclear matrix protein	SRM160	1.26	1.25	0.97	1.03	1.16	0.16	5	9.3	5.40E-26
P26583	High mobility group protein 2	HMG2	1.01	1.08	1.39	0.72	1.16	0.20	20	67	1.43E-190
Q9BVK6	Glycoprotein 25L2	GP25L2	1.38	1.26	0.84	1.19	1.16	0.28	7	25	1.29E-62
Q9BU76-1	Multiple myeloma tumor-associated protein 2	C1orf35	1.50	0.94	1.04	0.96	1.16	0.30	4	16	5.12E-33
P05198	Eukaryotic translation initiation factor 2 subunit 1	EIF2A	1.42	1.38	0.68	1.47	1.16	0.42	21	65	0.00E+00
P78559	MAP1 light chain LC2	MAP1A	1.48	1.41	0.59	1.69	1.16	0.49	30	15	1.21E-208
Q92793	CREB-binding protein	CBP			1.16	0.86	1.16		3	1.6	4.78E-07
C9J837	Putative uncharacterized protein RAB3GAP1	RAB3GAP1			1.16	0.86	1.16		4	5.8	4.65E-19
P41236	Protein phosphatase inhibitor 2	IPP2	1.16				1.16		2	12	3.25E-06
Q68D91-1	Metallo-beta-lactamase domain-containing protein 2	MBLAC2		1.16			1.16		2	5.4	6.21E-05
Q9H3G5	Carboxypeptidase, vitellogenic-like	CPVL		1.16			1.16		2	4.8	1.48E-03
O95613	Kendrin	KIAA0402		1.16			1.16		2	0.7	1.27E-03
B1AK40	Fumarylacetoacetate hydrolase domain containing 1	AC012180.10-003	1.16				1.16		2	15	1.67E-14
A2A2Q9	Chromosome 20 open reading frame 4	C20orf4		1.16			1.16		2	4	1.74E-08
Q9H061	Transmembrane protein 126A	TMEM126A	1.16				1.16		4	29	2.46E-44
P30042-1	ES1 protein homolog, mitochondrial	C21orf33	1.21	1.11			1.16	0.07	7	53	7.40E-95
Q02447-1	SPR-2	SP3		1.04	1.28	0.78	1.16	0.17	3	2.9	6.63E-11
Q9Y5J9	DDP-like protein	DDP2	1.04	1.28			1.16	0.17	3	27	2.08E-23
Q9BQ75	Uncharacterized protein C3orf26	C3orf26	0.97	1.35			1.16	0.27	2	7.5	5.43E-03
Q9Y3Y2-3	Uncharacterized protein C1orf77	C1orf77	1.12	1.22	1.15	0.87	1.16	0.05	4	21	4.76E-121

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Q96GQ7	DEAD box protein 27	DDX27	1.18	1.21	1.10	0.91	1.16	0.06	14	19	8.83E-158
Q00577	Purine-rich single-stranded DNA-binding protein alpha	PUR1	1.22	1.19	1.08	0.93	1.16	0.07	5	21	2.31E-89
Q9UBB9-1	Septin and tuftelin-interacting protein 1	HSPC006	1.07	1.13	1.29	0.78	1.16	0.11	5	6.7	5.65E-21
Q10567-1	Adapter-related protein complex 1 subunit beta-1	ADTB1	1.35	1.17	0.97	1.03	1.16	0.19	19	21	8.92E-185
Q9UPT8	Zinc finger CCCH domain-containing protein 4	C19orf7	1.11	1.43	0.95	1.05	1.16	0.24	13	18	3.17E-72
Q16763	E2-EPF	E2EPF	1.32	1.45	0.72	1.39	1.16	0.39	6	38	5.82E-67
Q76FK4-2	Nucleolar protein 8	C9orf34	1.17	1.59	0.73	1.37	1.16	0.43	3	3.9	4.16E-22
Q6PKG0-1	La ribonucleoprotein domain family member 1	KIAA0731	1.49	1.44	0.56	1.79	1.16	0.52	18	24	5.34E-96
Q4VY20	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide	RP1-148E22.1-003	1.10		1.23	0.81	1.17	0.09	9	87	2.70E-63
Q9UKL0	Protein CoREST	KIAA0071		1.24	1.09	0.92	1.17	0.11	2	5.8	1.59E-17
Q8IU81	Interferon regulatory factor 2-binding protein 1	IRF2BP1	1.21	1.22	1.07	0.93	1.17	0.08	8	22	7.02E-57
Q7L2J0	7SK snRNA methylphosphate capping enzyme	BCDIN3	1.27	1.16	1.07	0.93	1.17	0.10	3	9.9	1.70E-07
P61006	Oncogene c-mel	MEL	1.07	1.35	1.08	0.93	1.17	0.16	8	40	2.06E-235
P07814	Bifunctional aminoacyl-tRNA synthetase	EPRS	1.18	1.35	0.97	1.03	1.17	0.19	65	56	0.00E+00
Q6L8Q7-1	2,5-phosphodiesterase 12	PDE12	1.40	1.17	0.93	1.08	1.17	0.24	4	13	9.44E-45
Q7Z7K6-1	Centromere protein V	CENPV	1.32	1.30	0.88	1.14	1.17	0.25	5	30	2.51E-96
Q8IXJ6-1	NAD-dependent deacetylase sirtuin-2	SIR2L	1.17		1.17	0.85	1.17	0.00	2	8.5	2.25E-05
Q9GZY8-1	Mitochondrial fission factor	AD030	1.15		1.19	0.84	1.17	0.03	2	11	5.57E-08
P33992	CDC46 homolog	CDC46	1.21	1.22	1.08	0.93	1.17	0.08	28	45	5.92E-96
Q9GZT6-1	Coiled-coil domain-containing protein 90B, mitochondrial	CCDC90B	1.24	1.10			1.17	0.10	2	11	3.09E-05
Q6FI13	Histone H2A type 2-A	H2AFO	1.02		1.32	0.76	1.17	0.21	11	60	0.00E+00
Q8TAD8	FHA domain-containing protein SNIP1	SNIP1	0.95	0.87	1.69	0.59	1.17	0.45	3	7.6	3.89E-67

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P68032	Actin, alpha cardiac muscle 1	ACTC			1.17	0.85	1.17		20	53	9.39E-188
Q9UHA4	MEK-binding partner 1	MAP2K1IP1	1.17				1.17		2	36	8.97E-06
Q9NWS0	Nucleolar protein 17 homolog	NOP17	1.17				1.17		2	14	1.98E-18
P21953	2-oxoisovalerate dehydrogenase subunit beta, mitochondrial	BCKDHB	1.17				1.17		3	14	1.11E-13
A8MYU1	Adenosylhomocysteinase	AHCYL1		1.17			1.17		3	5.1	3.63E-04
Q9BV19	Uncharacterized protein C1orf50	C1orf50	1.17				1.17		4	36	4.22E-43
Q8NF33	FLJ00369 protein	FLJ00369	1.17				1.17		9	14	7.83E-23
Q9P032	Hormone-regulated proliferation-associated protein of 20 kDa	C6orf66	1.09	1.15	1.27	0.79	1.17	0.09	7	43	1.28E-43
Q7L0Y3	HBV pre-S2 trans-regulated protein 2	MRPP1	1.06	1.10	1.35	0.74	1.17	0.16	2	8.7	4.32E-50
B0V043	Valyl-tRNA synthetase	DAAP-21F2.2-001	1.35	1.45	0.72	1.39	1.17	0.40	23	26	1.71E-147
B9VP24	60 kDa chaperonin	HSPD1	1.19	1.23	1.10	0.91	1.17	0.07	3	12	1.99E-13
Q05519	Arginine-rich 54 kDa nuclear protein	SFRS11	1.21	1.33	0.98	1.02	1.17	0.18	5	15	7.72E-45
C9JL30	Putative uncharacterized protein SUMF2	SUMF2	1.29	1.30	0.93	1.08	1.17	0.21	6	25	8.68E-55
Q9HAU5-1	Nonsense mRNA reducing factor 2	KIAA1408	1.30	1.36	0.86	1.16	1.17	0.27	6	6.1	1.16E-22
P49588	Alanine--tRNA ligase	AARS	0.82	0.85	1.85	0.54	1.17	0.59	38	51	0.00E+00
O95478	Hairy cell leukemia protein 1	HUSSY-29	1.56	1.18	0.78	1.28	1.17	0.39	3	13	1.21E-08
P50542-2	Peroxin-5	PEX5		1.08	1.27	0.79	1.18	0.13	2	7.5	1.91E-04
C9J3F9	Putative uncharacterized protein PPAN	PPAN	1.22	1.33	0.98	1.02	1.18	0.18	3	4.2	7.12E-10
Q9BRT9-1	DNA replication complex GINS protein SLD5	GINS4	1.14	1.47	0.92	1.09	1.18	0.28	6	32	4.76E-31
Q96QC0	MHC class I region proline-rich protein CAT53	CAT53	1.18	1.27	1.08	0.93	1.18	0.10	8	13	2.04E-49
O96011	Peroxin-11B	PEX11B	1.16	1.20	1.18	0.85	1.18	0.02	4	16	6.00E-32
O43633	Charged multivesicular body protein 2a	BC2	1.24	1.13	1.17	0.85	1.18	0.06	4	17	1.22E-27
Q9Y6A4	Transcription factor IIB	C16orf80	1.25	1.15	1.14	0.88	1.18	0.06	7	38	1.75E-221

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P30040	Endoplasmic reticulum resident protein 28	C12orf8	1.26	1.29	0.99	1.01	1.18	0.17	12	47	4.03E-114
P07203	Cellular glutathione peroxidase	GPX1	1.25	1.39	0.90	1.11	1.18	0.25	4	37	1.47E-24
Q9Y450-1	ERFS	HBS1	1.59	0.89	1.06	0.94	1.18	0.37	5	9.9	2.23E-19
Q9H0A0	N-acetyltransferase 10	ALP	1.26	1.5	0.78	1.28	1.18	0.37	20	27	3.26E-139
Q9BUP0	EF-hand domain-containing protein 1	EFHD1	0.41		1.95	0.51	1.18	1.09	5	32	6.84E-51
Q8TD16-2	Protein bicaudal D homolog 2	BICD2		1.18			1.18		2	2.6	1.96E-07
P56556	Complex I-B14	LYRM6	1.18				1.18		2	12	4.68E-03
Q86X83	COMM domain-containing protein 2	COMMD2	1.11		1.25	0.80	1.18	0.10	3	17	1.65E-09
B4DJ38	cDNA FLJ56092, highly similar to Pentatricopeptide repeat protein 1	PTCD1	1.05		1.31	0.76	1.18	0.18	2	3.2	6.01E-26
Q96QR8	Purine-rich element-binding protein B	PURB	1.21	1.12	1.22	0.82	1.18	0.06	8	28	2.40E-44
Q9Y580	RNA-binding motif protein 7	RBM7	1.28	0.94	1.33	0.75	1.18	0.21	2	18	2.26E-31
Q8N983-4	39S ribosomal protein L43, mitochondrial	MRPL43	1.16		1.21	0.83	1.19	0.04	3	20	2.37E-15
Q6P3W7	Coated vesicle-associated kinase of 104 kDa	CVAK104		1.44	0.93	1.08	1.19	0.36	2	3.2	1.40E-04
Q9UKV3-1	Apoptotic chromatin condensation inducer in the nucleus	ACIN1	1.19	1.17	1.20	0.83	1.19	0.02	36	31	1.47E-286
Q96EB6	NAD-dependent deacetylase sirtuin-1	SIR2L1	1.28	1.13	1.15	0.87	1.19	0.08	14	31	5.94E-240
Q13426-1	DNA repair protein XRCC4	XRCC4	0.99	1.17	1.40	0.71	1.19	0.21	3	10	3.42E-16
O95336	6-phosphogluconolactonase	PGLS	1.30	1.47	0.79	1.27	1.19	0.35	12	62	1.05E-220
Q9P2J5	Leucine--tRNA ligase	KIAA1352	1.35	1.43	0.78	1.28	1.19	0.35	22	23	0.00E+00
Q71U36	Alpha-tubulin 3	TUBA1A	0.91	0.88	1.77	0.56	1.19	0.51	33	76	0.00E+00
Q8N183	Mimitin, mitochondrial	NDUFA12L	1.15	1.23			1.19	0.06	4	40	8.33E-34
Q9NZ08-2	Adipocyte-derived leucine aminopeptidase	APPILS		1.13	1.25	0.80	1.19	0.08	4	4.4	2.23E-09
Q8WUY1	Mesenchymal stem cell protein DSCD75	C8orf55	1.12	1.26			1.19	0.10	4	18	5.43E-42
Q9HBH1	Peptide deformylase, mitochondrial	PDF	1.17	1.09	1.31	0.76	1.19	0.11	4	33	3.51E-78
Q96AB	Isochorismatase	ISOC2	1.09		1.29	0.78	1.19	0.14	6	48	1.03E-143

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3-2	domain-containing protein 2, mitochondrial										
Q9UHR6	Zinc finger HIT domain-containing protein 2	C11orf5		1.33	1.05	0.95	1.19	0.20	2	5.7	1.08E-05
P56192	Methionine--tRNA ligase	MARS	1.38	1.27	0.92	1.09	1.19	0.24	18	29	4.95E-119
Q9Y5Q9-1	General transcription factor 3C polypeptide 3	GTF3C3		1.49	0.89	1.12	1.19	0.42	2	2.7	7.67E-06
Q15392	24-dehydrocholesterol reductase	DHCR24		1.50	0.88	1.14	1.19	0.44	2	4.1	1.18E-07
Q14562	ATP-dependent RNA helicase DHX8	DDX8		1.54	0.84	1.19	1.19	0.49	4	4.7	1.17E-05
O76024	Wolframin	WFS1			1.19	0.84	1.19		2	3	3.56E-17
O43819	Protein SCO2 homolog, mitochondrial	SCO2		1.19			1.19		2	6.8	1.34E-04
Q9GZP4-1	UPF0424 protein C1orf128	AD039	1.37	1.16	1.04	0.96	1.19	0.17	6	33	4.00E-34
O15397	Importin-8	IPO8	1.37	1.27	0.93	1.08	1.19	0.23	4	4.6	3.64E-22
Q9UK59-1	Lariat debranching enzyme	DBR1	1.27	1.27	1.04	0.96	1.19	0.13	3	7.4	3.52E-13
B4DEA8	cDNA FLJ56425, highly similar to Very-long-chain specific acyl-CoAdehydrogenase, mitochondrial (EC 1.3.99.-)	ACADVL	1.28	1.28	1.02	0.98	1.19	0.15	15	32	8.09E-125
Q9H078-1	Caseinolytic peptidase B protein homolog	CLPB	1.04	1.35			1.20	0.22	7	9.6	1.14E-22
Q00059	Mitochondrial transcription factor 1	TCF6	0.77		1.62	0.62	1.20	0.60	4	15	4.04E-15
Q93009	Deubiquitinating enzyme 7	HAUSP	1.49	1.38	0.72	1.39	1.20	0.42	12	15	7.67E-96
Q12907	Glycoprotein GP36b	C5orf8	1.54	1.35	0.70	1.43	1.20	0.44	5	22	1.90E-17
Q14061	Cytochrome c oxidase copper chaperone	COX17	1.20	1.20			1.20	0.00	2	37	2.60E-22
P11498	Pyruvate carboxylase, mitochondrial	PC	1.19	1.17	1.24	0.81	1.20	0.04	4	6.4	4.28E-15
O14657	Torsin family 1 member B	DQ1	1.17		1.23	0.81	1.20	0.04	2	6.8	1.12E-03
Q6SPF0	Atherin	SAMD1	1.11	1.22	1.27	0.79	1.20	0.08	5	17	2.14E-17
A7BI36	p180/ribosome receptor	RRBP1	1.10	1.27	1.23	0.81	1.20	0.09	19	28	8.51E-216
O00154-1	Acyl-CoA thioesterase 7	ACOT7	1.28	1.47	0.85	1.18	1.20	0.32	11	30	1.08E-101
Q147X3-1	N-acetyltransferase 12	C14orf35		1.44	0.96	1.04	1.20	0.34	2	5.8	1.73E-05
Q5JTH9-1	RRP12-like protein	KIAA0690	1.36	1.48	0.76	1.32	1.20	0.39	8	9.4	8.34E-72

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P63000-2	Cell migration-inducing gene 5 protein	MIG5	1.41	1.45	0.74	1.35	1.20	0.40	10	41	6.29E-53
P07954-1	Fumarate hydratase, mitochondrial	FH	1.42	1.51	0.67	1.49	1.20	0.46	17	54	5.96E-251
O75208-1	Ubiquinone biosynthesis protein COQ9, mitochondrial	C16orf49			1.20	0.83	1.20		4	27	9.51E-77
A8MVZ9	Fructose-bisphosphate aldolase	ALDOC			1.20	0.83	1.20		28	65	0.00E+00
P61244-1	Class D basic helix-loop-helix protein 4	BHLHD4		1.20			1.20		2	13	1.16E-04
Q9UPT5-3	Exocyst complex component 7	EXO70	1.20				1.20		2	3.5	1.93E-02
Q8NFV4-1	Abhydrolase domain-containing protein 11	ABHD11		1.20			1.20		2	6.7	1.68E-09
Q15643	Clonal evolution-related gene on chromosome 14 protein	CEV14		1.20			1.20		3	1.8	1.11E-28
P09497-1	Clathrin light chain B	CLTB		1.20			1.20		3	12	1.22E-05
Q8IYB8	ATP-dependent RNA helicase SUPV3L1, mitochondrial	SUPV3L1		1.20			1.20		3	4.6	4.62E-06
A8MUM1	Putative uncharacterized protein TSSC1	TSSC1	1.20				1.20		3	9.4	1.18E-04
O14561	Acyl carrier protein, mitochondrial	NDUFAB1	1.20				1.20		4	21	1.96E-24
B4DI54	cDNA FLJ56386, highly similar to Heat shock 70 kDa protein 1L	DAAP-21F2.9-001		1.20			1.20		9	15	2.20E-191
Q9BSD7	Nucleoside triphosphate phosphohydrolase	NTPCR	1.2				1.20		11	66	1.21E-48
O96013-1	p21-activated kinase 4	KIAA1142		1.30	1.10	0.91	1.20	0.14	2	2.5	1.74E-03
P61020	Ras-related protein Rab-5B	RAB5B	0.83	0.99	1.79	0.56	1.20	0.51	6	34	3.97E-48
Q93084-6	Calcium pump 3	ATP2A3	1.26		1.15	0.87	1.21	0.08	6	7.4	2.52E-81
Q6PI26	Protein SHQ1 homolog	SHQ1	1.55		0.86	1.16	1.21	0.49	4	13	3.74E-07
P43362	Cancer/testis antigen 1.9	MAGE9	0.80		1.61	0.62	1.21	0.57	6	23	4.55E-130
P34896-1	Serine hydroxymethyltransferase, cytosolic	SHMT1	1.27	1.24	1.11	0.90	1.21	0.09	7	18	7.34E-75
Q6P2Q9	220 kDa U5 snRNP-specific protein	PRPC8	1.22	1.39	1.01	0.99	1.21	0.19	48	25	3.04E-292
Q9UQ3	300 kDa nuclear matrix antigen	HSPC075	1.40	1.43	0.79	1.27	1.21	0.36	23	12	3.46E-160

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5-1											
P34897	Serine hydroxymethyltransferase, mitochondrial	SHMT2	1.16	1.23	1.24	0.81	1.21	0.04	20	50	8.80E-235
Q14165	Malectin	KIAA0152	1.42	1.26	0.95	1.05	1.21	0.24	5	20	3.67E-32
Q96CX2	BTB/POZ domain-containing protein KCTD12	C13orf2	1.38	1.56	0.69	1.45	1.21	0.46	7	31	3.49E-146
Q9H496	cDNA FLJ77012, highly similar to Homo sapiens interferon responsive gene 15 (IFRG15), mRNA	hCG_1759493			1.21	0.83	1.21		2	25	2.32E-18
Q03111	Protein ENL	ENL			1.21	0.83	1.21		2	4.3	1.97E-04
Q9UMS0	HIRA-interacting protein 5	CGI-33			1.21	0.83	1.21		2	9.4	1.69E-03
Q7L5Y9-1	Cell proliferation-inducing gene 5 protein	EMP			1.21	0.83	1.21		2	6.1	5.25E-21
B0S872	HCG1999928, isoform CRA_b	DAAP-218M18.9-001			1.21	0.83	1.21		3	14	7.03E-09
Q9ULH7-1	Megakaryoblastic leukemia 2	KIAA1243			1.21	0.83	1.21		4	5.5	3.96E-20
Q96JJ7-1	Protein disulfide-isomerase TMX3	KIAA1830			1.21	0.83	1.21		6	14	5.02E-31
P42166	Lamina-associated polypeptide 2, isoform alpha	LAP1			1.21	0.83	1.21		12	28	1.71E-56
P30825	Ecotropic retroviral leukemia receptor homolog	ATRC1	1.21				1.21		2	3.3	9.56E-03
O75935-1	Dynactin complex subunit 22 kDa subunit	DCTN22	1.21				1.21		3	23	4.00E-16
Q96RS6-1	Chronic myelogenous leukemia tumor antigen 66	CML66		1.21			1.21		3	5.3	1.79E-14
P21108	Phosphoribosyl pyrophosphate synthase 1-like 1	PRPS1L1		1.21			1.21		4	13	7.51E-19
P60983	Glia maturation factor beta	GMFB	1.21				1.21		4	42	3.50E-37
P54687	Branched-chain-amino-acid aminotransferase, cytosolic	BCAT1	1.22	1.5	0.92	1.09	1.21	0.29	8	25	2.08E-120
Q9P265-1	Disco-interacting protein 2 homolog B	DIP2B	1.32	1.65	0.67	1.49	1.21	0.50	2	1.6	3.25E-19
Q96S19-1	UPF0585 protein C16orf13	C16orf13	1.85	1.06	0.73	1.37	1.21	0.58	3	16	2.17E-19
Q5JPE7	Nodal modulator 2	NOMO2	1.25	1.18			1.22	0.05	9	8.5	1.30E-25

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-1											
B4E137	cDNA FLJ61523, highly similar to Vesicle transport through interaction witht-SNAREs homolog 1A	hCG_1811152	1.04		1.39	0.72	1.22	0.25	4	23	7.69E-90
Q12974-1	HU-PP-1	BM-008	1.32	1.11			1.22	0.15	6	53	7.36E-82
Q96HA7-2	Inhibitor of kappa B-related protein	IKBR	0.93	1.50			1.22	0.40	3	2.3	1.76E-04
P61081	NEDD8 carrier protein	UBC12	1.38	1.15	1.12	0.89	1.22	0.14	7	39	2.11E-150
O75436	Vacuolar protein sorting-associated protein 26A	VPS26	1.27	1.17			1.22	0.07	2	9.2	7.04E-44
O15446-2	Antisense to ERCC-1 protein	ASE1	1.52	1.40	0.74	1.35	1.22	0.42	6	25	3.74E-37
Q6PL24	Protein TMED8	FAM15B			1.22	0.82	1.22		2	11	4.83E-04
Q96RG2-2	PAS domain-containing serine/threonine-protein kinase	KIAA0135			1.22	0.82	1.22		2	2.7	1.30E-07
Q96TC7-1	Cerebral protein 10	FAM82A2			1.22	0.82	1.22		2	8.5	6.55E-06
B4DWW2	cDNA FLJ57641, highly similar to Microcephalin	MCPH1			1.22	0.82	1.22		2	5.2	2.86E-02
Q96B23-1	Uncharacterized protein C18orf25	C18orf25			1.22	0.82	1.22		3	15	1.86E-14
P56545-2	C-terminal-binding protein 2	CTBP2			1.22	0.82	1.22		6	5.4	2.19E-09
B3KTT6	cDNA FLJ38699 fis, clone KIDNE2002168, highly similar to Short chain 3-hydroxyacyl-CoA dehydrogenase, mitochondrial (EC 1.1.1.35)	HADH			1.22	0.82	1.22		24	50	9.39E-155
Q9BYG9	Nucleophosmin (Nucleolar phosphoprotein B23, numatrin)	NPM1			1.22	0.82	1.22		26	88	6.63E-303
P55273	Cyclin-dependent kinase 4 inhibitor D	CDKN2D		1.22			1.22		2	19	5.22E-05
Q99996-6	AKAP 120-like protein	AKAP350		1.22			1.22		2	0.5	2.86E-11
Q6Y1H2	Protein-tyrosine phosphatase-like member B	PTPLB		1.22			1.22		2	7.9	4.97E-05
P62072	Mitochondrial import inner membrane	TIM10		1.22			1.22		3	26	9.24E-15

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	translocase subunit Tim10										
B4E2A6	cDNA FLJ55508, highly similar to Sad1/unc-84-like protein 2	UNC84B	1.21	1.22	1.24	0.81	1.22	0.02	3	7.3	6.46E-64
Q96B54-1	Enzyme-like protein PIT13	C19orf37	1.31	1.60	0.76	1.32	1.22	0.43	3	27	5.03E-66
Q93034	Cullin-5	CUL5		0.95	1.50	0.67	1.23	0.39	3	3.7	1.09E-04
P06396-1	Actin-depolymerizing factor	GSN	1.25	1.46	0.97	1.03	1.23	0.25	4	5.2	2.14E-31
Q8NI36	T-cell activation WD repeat-containing protein	WDR36	1.46	1.60	0.62	1.61	1.23	0.53	8	11	3.28E-51
Q13630	GDP-4-keto-6-deoxy-D-mannose-3,5-epimerase-4-reductase	SDR4E1	1.49	1.40	0.80	1.25	1.23	0.38	5	17	2.63E-42
Q02978	Mitochondrial 2-oxoglutarate/malate carrier protein	SLC20A4	1.43		1.03	0.97	1.23	0.28	4	15	3.73E-50
Q8NFF5-1	FAD pyrophosphorylase	FLAD1	1.66		0.80	1.25	1.23	0.61	3	9.4	1.54E-46
Q96EK7	Constitutive coactivator of peroxisome proliferator-activated receptor gamma	CCPG			1.23	0.81	1.23		2	2.1	1.16E-03
Q13617	Cullin-2	CUL2			1.23	0.81	1.23		4	6.5	1.85E-07
Q9NZ72	SCG10-like protein	SCLIP		1.23			1.23		2	9.4	1.69E-03
Q5J8M3-1	Cell proliferation-inducing gene 17 protein	HSPC184	1.23				1.23		2	14	2.83E-07
Q8IVS2-1	[Acyl-carrier-protein] malonyltransferase	MCAT	1.56	1.25	0.89	1.12	1.23	0.34	3	13	4.35E-57
Q9BU61	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 3	C3orf60	1.31	1.16			1.24	0.11	4	32	3.20E-66
P28907-1	ADP-ribosyl cyclase 1	CD38	1.15		1.32	0.76	1.24	0.12	2	9.3	3.32E-04
O43493-1	TGN38 homolog	TGN46	1.11	1.36			1.24	0.18	2	5.8	5.36E-47
B4DPV7	cDNA FLJ54534, highly similar to Homo sapiens cysteinyl-tRNA synthetase (CARS), transcript variant 3, mRNA	CARS	1.13	1.13	1.45	0.69	1.24	0.18	16	24	7.39E-158
Q9UNQ2	18S rRNA dimethylase	DIMT1	1.22	1.26			1.24	0.03	3	8.9	1.24E-04
Q96IU4	Abhydrolase domain-	ABHD1	1.30	1.22	1.20	0.83	1.24	0.05	6	38	1.66E-55

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-1	containing protein 14B	4B									
A3KMH1-1	Uncharacterized protein KIAA0564	KIAA0564		1.17	1.31	0.76	1.24	0.10	5	2.9	3.62E-14
Q6ZN55-2	Zinc finger protein 574	ZNF574	1.16		1.32	0.76	1.24	0.11	2	3.2	2.24E-02
Q9P015	39S ribosomal protein L15, mitochondrial	HSPC145	1.01		1.47	0.68	1.24	0.33	3	13	4.33E-15
Q9BVG9	Phosphatidylserine synthase 2	PSS2	1.04	1.04	1.64	0.61	1.24	0.35	2	7.8	8.50E-06
Q16795	Complex I-39kD	NDUFA9			1.24	0.81	1.24		2	5.8	5.61E-04
O75695	Protein XRP2	RP2			1.24	0.81	1.24		2	5.1	7.94E-05
Q9H300	Mitochondrial intramembrane cleaving protease PARL	PARL			1.24	0.81	1.24		2	3.4	2.76E-04
P54198	Protein HIRA	DGCR1			1.24	0.81	1.24		2	2.2	2.13E-04
Q8NCC3	1-O-acylceramide synthase	LYPLA3			1.24	0.81	1.24		2	7.5	7.70E-07
Q9Y3D3	28S ribosomal protein S16, mitochondrial	CGI-132			1.24	0.81	1.24		3	45	3.08E-29
Q86Y91-2	Kinesin-like protein KIF18B	KIF18B			1.24	0.81	1.24		3	4.5	1.66E-11
A8K2Y8	cDNA FLJ77052, highly similar to Homo sapiens FYN binding protein (FYB-120/130) (FYB), transcript variant 1, mRNA	FYB			1.24	0.81	1.24		19	34	2.72E-120
Q8WWH5	Probable tRNA pseudouridine synthase 1	PUS4	1.24				1.24		2	6.6	9.80E-04
O15067	Formylglycinamide ribotide amidotransferase	KIAA0361		1.24			1.24		14	11	7.89E-119
Q9HCE1-1	Moloney leukemia virus 10 protein	KIAA1631	1.33	1.51	0.89	1.12	1.24	0.32	9	11	4.14E-129
Q9BXS6-1	Nucleolar and spindle-associated protein 1	ANKT	1.10	1.12	1.53	0.65	1.25	0.24	6	17	2.31E-35
B4DZH6	cDNA FLJ56474, highly similar to Histone deacetylase 6	HDAC6			1.25	0.80	1.25		2	2.5	2.23E-04
P46939	Dystrophin-related protein 1	DMDL			1.25	0.80	1.25		2	0.8	1.42E-07
Q9H410-1	Kinetochore-associated protein DSN1 homolog	C20orf172			1.25	0.80	1.25		2	5.6	2.26E-04
A6QL64-2	UPF0634 protein KIAA1641	KIAA1641			1.25	0.80	1.25		2	1.4	2.26E-02
P13797	Plastin-3	PLS3			1.25	0.80	1.25		8	12	4.29E-139
Q5T5I6	Golgi phosphoprotein	GOLPH		1.25			1.25		2	9.1	1.37E-31

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	3-like	3L									
B4DV13	cDNA FLJ51327, highly similar to Protein CGI-117	hCG_1980223		1.25			1.25		2	7.8	8.14E-06
P51452	Dual specificity protein phosphatase 3	DUSP3	1.25				1.25		2	15	6.44E-56
C9J5N9	Putative uncharacterized protein APOOL	APOOL	1.25				1.25		2	9.7	7.81E-09
Q96E11-1	Ribosome-recycling factor, mitochondrial	MRRF	1.40	1.48	0.88	1.14	1.25	0.33	5	30	5.03E-52
Q9UFN0	Protein NipSnap homolog 3A	HSPC299	1.02		1.49	0.67	1.26	0.33	4	24	1.19E-36
Q9P2W1-1	Homologous-pairing protein 2 homolog	HOP2	1.25	1.44	1.08	0.93	1.26	0.18	3	20	2.43E-37
Q96GM8	Target of EGR1 protein 1	TOE1	1.17	1.61	0.99	1.01	1.26	0.32	3	11	1.90E-26
O60831	PRA1 family protein 2	JM4	1.06	1.17	1.55	0.65	1.26	0.26	3	17	1.30E-52
Q5T4L4	Putative uncharacterized protein RPS27	RP11-422P24.3-002	1.73	1.28	0.77	1.30	1.26	0.48	4	39	2.58E-21
P46926	Glucosamine-6-phosphate deaminase 1	GNPDA1	1.39	1.76	0.63	1.59	1.26	0.58	3	13	2.29E-31
Q9P035	Butyrate-induced protein 1	BIND1			1.26	0.79	1.26		4	13	9.52E-08
Q14242	P-selectin glycoprotein ligand 1	SELPLG			1.26	0.79	1.26		5	9.3	1.43E-08
O75251	Complex I-20kD	NDUFS7	1.26				1.26		2	14	5.26E-13
Q86XL3-1	Ankyrin repeat and LEM domain-containing protein 2	ANKLE2	1.26				1.26		2	5.5	1.63E-12
B4DLW0	cDNA FLJ56622, highly similar to Beta-arrestin-2	ARB2	1.26				1.26		2	7.2	9.67E-07
Q92979	Nucleolar protein EMG1 homolog	C2F	1.38		1.15	0.87	1.27	0.16	3	20	9.34E-13
O60701	UDP-glucose 6-dehydrogenase	UGDH		1.05	1.48	0.68	1.27	0.30	2	4.7	8.96E-07
B0QZ18	Copine I	CPNE1	1.57		0.96	1.04	1.27	0.43	4	12	6.23E-58
P41250	Diadenosine tetraphosphate synthetase	GARS	1.26	1.25	1.29	0.78	1.27	0.02	34	52	0.00E+00
B4DMU0	Pyrroline-5-carboxylate reductase	PYCR1	1.23	1.41	1.16	0.86	1.27	0.13	7	29	3.96E-153
Q14137	Block of proliferation 1 protein	BOP1	1.59	1.62	0.59	1.69	1.27	0.59	13	30	2.06E-109
Q68E01-1	Integrator complex subunit 3	C1orf193	1.99	0.77	1.04	0.96	1.27	0.64	4	8.2	5.30E-15
Q9GZZ9-1	Ubiquitin-activating enzyme E1 domain-containing protein 1	UBA5	1.02	1.87	0.91	1.10	1.27	0.53	3	11	2.84E-17

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P61978-1	Heterogeneous nuclear ribonucleoprotein K	HNRNPK	1.12	1.01	1.68	0.60	1.27	0.36	44	71	0.00E+00
Q9BX68	Histidine triad nucleotide-binding protein 2, mitochondrial	HINT2	1.54	1.31	0.96	1.04	1.27	0.29	5	46	1.04E-90
A6NMJ5	Putative uncharacterized protein YTHDF1	YTHDF1		1.51	1.03	0.97	1.27	0.34	5	9.6	4.55E-46
C9J303	Putative uncharacterized protein SNRPG	SNRPG	0.99		1.55	0.65	1.27	0.40	2	15	1.16E-83
B4E3Q7	3-oxoacyl-ACP synthase, mitochondrial, isoform CRA_a	hCG_28352			1.27	0.79	1.27		2	25	2.15E-03
B4DMB7	cDNA FLJ55986	C14orf133			1.27	0.79	1.27		3	8.7	1.43E-03
Q9H488-1	GDP-fucose protein O-fucosyltransferase 1	FUT12			1.27	0.79	1.27		3	10	3.43E-13
Q9HD47-1	Ran guanine nucleotide release factor	HSPC165	1.27				1.27		3	26	3.44E-20
O95749	Dimethylallyltranstransferase	GGPS1		1.27			1.27		3	8.7	4.72E-05
Q13015	Protein AF1q	AF1Q	1.27				1.27		4	73	1.11E-53
B2RAN1	cDNA, FLJ95012, highly similar to Homo sapiens UDP-glucose pyrophosphorylase 2 (UGP2), mRNA	UGP2	1.45	1.03	1.34	0.75	1.27	0.22	5	13	2.00E-24
Q9BQ69	MACRO domain-containing protein 1	LRP16	0.82		1.73	0.58	1.28	0.64	3	14	2.24E-19
P11908-2	Phosphoribosyl pyrophosphate synthase II	PRPS2	1.40		1.16	0.86	1.28	0.17	10	36	4.08E-146
Q6NZY4-1	Zinc finger CCHC domain-containing protein 8	ZCCHC8	1.18	1.59	1.07	0.93	1.28	0.27	8	15	3.92E-70
O75306	Complex I-49kD	NDUFS2		0.97	1.59	0.63	1.28	0.44	4	7.8	6.21E-60
P49902	Cytosolic 5-nucleotidase II	NT5B	1.63		0.93	1.08	1.28	0.49	3	9.3	6.40E-51
Q6P9B9	Integrator complex subunit 5	INTS5		1.28			1.28		3	3	1.00E-11
Q15008	26S proteasome non-ATPase regulatory subunit 6	KIAA0107		1.28			1.28		11	29	2.13E-46
A6NKT7	RanBP2-like and GRIP domain-containing protein 3	RGP3		1.28			1.28		12	8.4	3.09E-112
Q8WZ82	Ovarian cancer-associated gene 2	OVCA2	1.53	1.60	0.72	1.39	1.28	0.49	5	34	2.16E-50

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	protein										
Q9NVX2	Notchless protein homolog 1	HUSSY-07	1.57	1.21	1.07	0.93	1.28	0.26	2	4.7	1.19E-05
Q99873-1	Interferon receptor 1-bound protein 4	HMT2	1.39	1.82	0.64	1.56	1.28	0.60	5	18	4.08E-49
Q86YV9	Hermansky-Pudlak syndrome 6 protein	HPS6	1.36		1.21	0.83	1.29	0.11	2	5.7	1.76E-19
O75787	ATPase H(+)-transporting lysosomal accessory protein 2	ATP6AP2	1.34	1.61	0.91	1.10	1.29	0.35	3	11	5.35E-67
Q00325-2	Phosphate carrier protein, mitochondrial	OK/SW-cl.48	1.31	1.36	1.20	0.83	1.29	0.08	7	19	3.95E-42
Q9NRF9	Arsenic-transactivated protein	CHRAC17	1.17		1.41	0.71	1.29	0.17	6	34	5.15E-17
Q969H8	Interleukin-25	C19orf10	1.15		1.43	0.70	1.29	0.20	3	21	3.47E-44
Q9BT30	Alkylated DNA repair protein alkB homolog 7	ABH7			1.29	0.78	1.29		2	15	1.50E-05
P05386	60S acidic ribosomal protein P1	RPLP1	1.29				1.29		2	52	5.95E-60
P51812	90 kDa ribosomal protein S6 kinase 3	ISPK1		1.29			1.29		2	3.4	9.00E-03
B4DGY2	cDNA FLJ59683, highly similar to Homo sapiens malignant T cell amplified sequence 1 (MCTS1), mRNA	MCTS1	1.24	1.35			1.30	0.08	5	41	8.21E-87
Q15813	Tubulin-folding cofactor E	TBCE		1.69	0.9	1.11	1.30	0.56	25	54	7.86E-264
P05161	Interferon-induced 15 kDa protein	G1P2	1.99	0.95	0.95	1.05	1.30	0.60	4	37	3.43E-32
Q969S3	Zinc finger protein 622	ZNF622	1.33	1.61	0.96	1.04	1.30	0.33	4	11	2.68E-24
Q96C36	Pyrroline-5-carboxylate reductase 2	PYCR2	1.52	1.52	0.86	1.16	1.30	0.38	7	28	6.37E-77
Q9H5X1	Protein FAM96A	FAM96A			1.30	0.77	1.30		2	13	5.47E-03
Q8NHP8	76 kDa protein	PLBD2			1.30	0.77	1.30		5	11	5.22E-41
B0LM41	Transcriptional coactivator CoAZ	RBM14/RBM4 fusion			1.30	0.77	1.30		11	48	1.69E-243
Q9UKJ3-1	G patch domain-containing protein 8	GPATC8		1.30			1.30		2	1.7	4.91E-09
O14653-2	27 kDa Golgi SNARE protein	GOSR2	1.30				1.30		3	17	7.36E-14
P58107	450 kDa epidermal antigen	EPIPL	1.30				1.30		4	3.6	2.81E-54
P08195-4	4F2 cell-surface antigen heavy chain	MDU1	1.28	1.32	1.31	0.76	1.30	0.02	16	29	4.07E-214

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Q96AQ6-1	Hematopoietic PBX-interacting protein	HPIP	1.32	1.06	1.53	0.65	1.30	0.24	3	5.7	8.27E-12
P55010	Eukaryotic translation initiation factor 5	EIF5	1.53	1.58	0.80	1.25	1.30	0.44	12	29	2.96E-65
Q8WZA9	Immunity-related GTPase family Q protein	FKSG27	1.91	1.03	0.97	1.03	1.30	0.53	5	13	2.12E-14
Q9BZK7	F-box-like/WD repeat-containing protein TBL1XR1	IRA1	2.01	0.83	1.07	0.93	1.30	0.62	4	10	2.54E-57
Q99766	ATP synthase subunit s, mitochondrial	ATP5S	1.18		1.43	0.70	1.31	0.18	2	9.3	2.00E-04
Q8WUF8-1	Protein FAM172A	C5orf21	1.16		1.45	0.69	1.31	0.21	2	8.2	2.54E-06
Q71DI3	Histone H3.2	H3F2	1.01		1.60	0.63	1.31	0.42	8	53	3.03E-113
B4DNA3	Adenylyl cyclase-associated protein	CAP1	0.84	1.81	1.27	0.79	1.31	0.49	26	73	4.75E-269
P46013-1	Antigen KI-67	MKI67	1.38	1.18	1.37	0.73	1.31	0.11	10	5.1	3.16E-38
P07738	2,3-bisphosphoglycerate mutase, erythrocyte	BPGM			1.31	0.76	1.31		2	12	1.34E-13
B7ZM97	SFRS8 protein	SFRS8			1.31	0.76	1.31		3	3.6	7.89E-04
Q9BTU6	Phosphatidylinositol 4-kinase type 2-alpha	PI4K2A	1.31				1.31		2	9.6	1.10E-06
Q9UBB5-1	Demethylase	MBD2	1.31				1.31		2	7.1	4.55E-04
Q96A72	Protein mago nashi homolog 2	MAGOH2	1.37	1.26			1.32	0.08	3	33	2.43E-07
Q9Y248	DNA replication complex GINS protein PSF2	CGI-122	1.17	1.46			1.32	0.21	3	27	1.10E-18
B4DHX5	cDNA FLJ53329, highly similar to NADPH:adrenodoxin oxidoreductase, mitochondrial (EC 1.18.1.2)	ADXR		1.10	1.53	0.65	1.32	0.30	3	5.6	1.38E-03
Q9UL42	40 kDa neuronal protein	KIAA0883	1.36	1.89	0.70	1.43	1.32	0.60	4	19	1.68E-09
Q99442	Translocation protein 1	SEC62		1.05	1.59	0.63	1.32	0.38	2	3	9.20E-04
Q96NY9	Crossover junction endonuclease MUS81	MUS81	1.32				1.32		2	7.1	1.97E-09
Q15070-2	Mitochondrial inner membrane protein OXA1L	OXA1L	1.32				1.32		2	8.8	8.22E-03
P32519	E74-like factor 1	ELF1	1.39	1.49	1.09	0.92	1.32	0.21	4	13	2.67E-23
Q9BTY7	Brain protein 16	BRP16	1.41	1.69	0.87	1.15	1.32	0.42	5	24	2.54E-36
Q96DA	DnaJ homolog subfamily C member	DNAJC19	1.39	1.26			1.33	0.09	3	27	1.38E-15

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6	19										
P41223	Protein BUD31 homolog	BUD31	1.43	1.24	1.31	0.76	1.33	0.10	5	42	6.75E-48
O43175	D-3-phosphoglycerate dehydrogenase	PGDH3	1.19	1.18	1.62	0.62	1.33	0.25	22	55	0.00E+00
Q86TI0	TBC1 domain family member 1	KIAA1108			1.33	0.75	1.33		2	1.8	2.39E-14
O43324	Aminoacyl tRNA synthetase complex-interacting multifunctional protein 3	AIMP3	1.33				1.33		2	9.8	2.04E-10
Q6NUM9-1	All-trans-13,14-dihydroretinol saturase	RETSAT	1.33				1.33		2	4.9	1.85E-09
Q15836	Cellubrevin	SYB3		1.33			1.33		3	40	1.36E-161
Q9BRP1	Programmed cell death protein 2-like	PDCD2L	1.38	1.30			1.34	0.06	3	9.5	3.73E-13
P09471-1	Guanine nucleotide-binding protein G(o) subunit alpha	GNAO1	0.93	1.33	1.76	0.57	1.34	0.42	5	17	7.05E-39
Q9NYV4-1	Cdc2-related kinase, arginine/serine-rich	CDK12	1.87	1.28	0.87	1.15	1.34	0.50	5	5.2	1.14E-117
Q9UDX4	SEC14-like protein 3	SEC14L3			1.34	0.75	1.34		2	8.4	1.57E-02
Q8IY37	DEAH box protein 37	DDX37			1.34	0.75	1.34		2	2.5	4.65E-11
Q8CCF4	Putative uncharacterized protein DOCK11	DOCK11			1.34	0.75	1.34		3	1.4	2.15E-03
P30462	HLA class I histocompatibility antigen, B-14 alpha chain	HLAB14			1.34	0.75	1.34		8	30	2.20E-99
Q9H7E9-2	UPF0488 protein C8orf33	C8orf33	1.34	2.02	0.68	1.47	1.35	0.67	2	12	1.57E-33
B3KM97	cDNA FLJ10554 fis, clone NT2RP2002385, highly similar to Synaptic glycoprotein SC2	GPSN2	1.59		1.11	0.90	1.35	0.34	3	8.7	7.82E-05
Q9Y4E8-1	Deubiquitinating enzyme 15	KIAA0529	1.35				1.35		2	2	1.25E-13
Q15041	ADP-ribosylation factor-like protein 6-interacting protein 1	ARL6IP	1.35				1.35		2	8.9	7.78E-03
C9J4G0	HCG32827, isoform CRA_d	C17orf49	1.35				1.35		3	23	8.38E-24
Q8WY22	BRI3-binding protein	BRI3BP	1.27	1.72	1.07	0.93	1.35	0.33	2	14	1.44E-70
Q8TCA0-1	Leucine-rich repeat-containing protein 20	LRRC20	1.32	1.39			1.36	0.05	3	20	1.78E-07
Q9Y2R4	ATP-dependent RNA helicase ROK1-like	DDX52	1.75		0.96	1.04	1.36	0.56	2	6.7	1.67E-05

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Q9BZQ8	Cell growth-inhibiting gene 39 protein	C1orf24	1.28	1.36	1.43	0.70	1.36	0.08	5	11	6.00E-84
Q15311	76 kDa Ral-interacting protein	RALBP1			1.36	0.74	1.36		3	7.8	1.85E-09
O15320-5	cTAGE family member 5	CTAGE5			1.36	0.74	1.36		3	5.9	1.14E-07
P49137-1	MAP kinase-activated protein kinase 2	MAPKAPK2		1.36			1.36		2	5	8.37E-04
Q9Y3E7	Charged multivesicular body protein 3	CGI-149		1.36			1.36		2	7.7	3.17E-03
Q8IWD4-1	Coiled-coil domain-containing protein 117	CCDC117	1.36				1.36		2	13	1.84E-17
B4E284	cDNA FLJ51188, highly similar to N-acetylglucosamine-6-sulfatase (EC3.1.6.14)	GNS		1.36			1.36		2	3.6	1.35E-06
Q5JYR6	cDNA FLJ38924 fis, clone NT2NE2011896, highly similar to Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit (EC 2.4.1.119)	hCG_37142		1.36			1.36		4	8.5	1.66E-32
O43592	Exportin(tRNA)	XPOT	1.72	1.54	0.83	1.20	1.36	0.47	8	14	3.02E-48
Q6P1L5-1	Amyotrophic lateral sclerosis 2 chromosomal region candidate gene 13 protein	ALS2CR13		1.03	1.70	0.59	1.37	0.47	3	6.1	7.78E-43
A7E2Y1-1	Antigen MLAA-21	KIAA1512			1.37	0.73	1.37		4	2	3.96E-06
A6NFH1	Putative uncharacterized protein GTPBP3	GTPBP3	1.37				1.37		2	8.4	6.23E-25
P47813	Eukaryotic translation initiation factor 1A, X-chromosomal	EIF1A	1.37				1.37		6	35	2.61E-21
Q68Y55	Poly(RC) binding protein 2	PCBP2	1.37				1.37		17	74	0.00E+00
O15143	Actin-related protein 2/3 complex subunit 1B	ARC41	1.23	1.64	1.25	0.80	1.37	0.23	7	20	1.27E-95
Q9Y5X1	SH3 and PX domain-containing protein 1	SH3PX1	1.37	1.39			1.38	0.01	3	6.4	1.40E-14
Q6NS38	Alkylated DNA repair protein alkB homolog 2	ABH2	1.40	1.36			1.38	0.03	3	14	8.69E-67
O75044	Formin-binding protein 2	ARHGAP34		1.03	1.73	0.58	1.38	0.49	4	5	9.40E-08
Q6ZQQ	Testis development	WDR87			1.38	0.72	1.38		2	0.9	1.77E-02

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6-2	protein NYD-SP11										
Q08209-1	Calmodulin-dependent calcineurin A subunit alpha isoform	CALNA			1.38	0.72	1.38		3	6.1	1.16E-06
B7Z6Q5	Beta-galactosidase	ELNR1			1.38	0.72	1.38		3	7.6	1.61E-06
Q93074-3	Activator-recruited cofactor 240 kDa component	ARC240		1.38			1.38		2	0.7	2.99E-02
P48723	Heat shock 70 kDa protein 13	HSPA13		1.38			1.38		2	4	7.35E-03
P51531-1	ATP-dependent helicase SMARCA2	BAF190B		1.38			1.38		6	3.7	1.12E-12
Q01650	4F2 light chain	CD98LC	1.41	1.50	1.25	0.80	1.39	0.13	5	7.9	4.41E-99
P23381-1	Interferon-induced protein 53	IFI53	1.71	1.62	0.84	1.19	1.39	0.48	10	28	8.64E-135
Q9H3Z4-1	Cysteine string protein	CSP			1.39	0.72	1.39		2	25	1.77E-06
P29350-3	Hematopoietic cell protein-tyrosine phosphatase	HCP			1.39	0.72	1.39		28	56	0.00E+00
C9JXA6	Adapter-related protein complex 1 sigma-1A subunit	AP19	1.39				1.39		3	17	1.56E-42
Q96FX7-2	tRNA (adenine-N(1)-)-methyltransferase catalytic subunit TRMT61A	C14orf172	1.55	1.89	0.74	1.35	1.39	0.59	3	15	1.86E-56
P13995	Bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase, mitochondrial	MTHFD2	1.48	1.44	1.27	0.79	1.40	0.11	12	49	8.45E-66
O00115	Acid DNase	DNASE2			1.40	0.71	1.40		2	5.8	3.05E-56
Q9Y3Q3	Membrane protein p24B	C15orf22		1.40			1.40		2	8.8	8.90E-06
Q9BRU9-1	rRNA-processing protein UTP23 homolog	C8orf53		1.40			1.40		3	9.2	8.58E-07
Q9Y696	Chloride intracellular channel protein 4	CLIC4	1.14	1.13	1.95	0.51	1.41	0.47	10	48	6.10E-89
Q9Y6I3-2	EH domain-binding mitotic phosphoprotein	EPN1			1.41	0.71	1.41		2	5	9.27E-27
Q9HCL2	Glycerol-3-phosphate acyltransferase 1, mitochondrial	GPAM			1.41	0.71	1.41		2	5.1	1.72E-01
Q92620	ATP-dependent RNA helicase DHX38	DDX38	1.41				1.41		2	2.3	4.35E-03
O94919	Endonuclease domain-containing 1 protein	ENDOD1	1.75	1.85	0.63	1.59	1.41	0.68	4	16	2.50E-17
P56381	ATP synthase subunit	ATP5E			1.43	0.70	1.43		3	39	3.98E-08

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	epsilon, mitochondrial										
A6NN38	Coactivator-associated arginine methyltransferase 1, isoform CRA_b	CARM1			1.43	0.70	1.43		4	7.7	1.00E-09
O94905-1	Endoplasmic reticulum lipid raft-associated protein 2	C8orf2		1.43			1.43		5	17	6.05E-43
Q9NRK6	ATP-binding cassette sub-family B member 10, mitochondrial	ABCB10			1.44	0.69	1.44		5	9.6	2.18E-56
Q9BVT8	Hepatocyte odd protein shuttling protein	C7orf21	1.44				1.44		2	13	1.28E-04
Q6NXS1	Protein phosphatase 1, regulatory subunit 2 pseudogene 3	PPP1R2P3		1.44			1.44		2	11	3.93E-10
Q14376	Galactowaldenase	GALE	1.44				1.44		2	14	2.91E-70
Q02127	Dihydroorotate dehydrogenase, mitochondrial	DHODH		1.44			1.44		3	10	9.63E-42
Q08380	Basement membrane autoantigen p105	LGALS3BP			1.45	0.69	1.45		2	6.8	1.61E-35
Q68D73	Putative uncharacterized protein DKFZp686H15164	DKFZp686H15164			1.45	0.69	1.45		2	1.1	1.98E-02
Q00266	Methionine adenosyltransferase 1	AMS1			1.45	0.69	1.45		6	16	8.93E-63
B1AVU8	Prosaposin	PSAP	1.45				1.45		5	7.7	6.50E-142
Q9Y6H1	Aging-associated gene 10 protein	AAG10	2.20	1.73	0.43	2.33	1.45	0.92	4	34	1.09E-102
Q969X6-1	Cirhin	CIRH1A	1.46		1.45	0.69	1.46	0.01	4	7.9	3.73E-48
Q92560	BRCA1-associated protein 1	BAP1	1.75		1.17	0.85	1.46	0.41	2	5.6	2.37E-22
P82912-1	28S ribosomal protein S11, mitochondrial	HCC2			1.46	0.68	1.46		3	30	2.47E-12
O94763-1	Protein NNX3	C19orf2			1.46	0.68	1.46		3	13	2.92E-08
Q6DN03	Histone H2B.t	HIST2H2BC			1.46	0.68	1.46		7	30	2.26E-15
B1AZV3	Transporter 1 ATP-binding cassette sub-family B (MDR/TAP)	DASS-67H14.3-001	1.46				1.46		2	3.1	3.45E-09
Q8WV22	Non-structural maintenance of chromosomes element 1 homolog	HSPC333	1.78	1.15			1.47	0.45	2	12	1.15E-16
Q13428-4	Treacher Collins syndrome protein	TCOF1	1.5	1.57	1.33	0.75	1.47	0.12	18	15	3.49E-201
P41091	Eukaryotic translation	EIF2G	1.89	1.84	0.67	1.49	1.47	0.69	12	34	1.36E-82

UniProt ID	Protein_Name	Gene Name	F1 (L/H)	F2 (L/H)	R1 (H/L)	R1 (L/H)	Mean (T/U)	S.D.	Pep. No.	%Seq. Cov.	PEP
	initiation factor 2 subunit 3										
O00754	Lysosomal acid alpha-mannosidase	LAMAN			1.48	0.68	1.48		4	6.2	4.57E-94
P62330	ADP-ribosylation factor 6	ARF6	1.48				1.48		2	26	1.21E-08
Q9BPX5	Actin-related protein 2/3 complex subunit 5-like protein	ARPC5L	0.83	2.29	1.32	0.76	1.48	0.74	2	33	1.44E-19
Q9NZ23	Drug-sensitive protein 1	YA61	1.92	1.36	1.17	0.85	1.48	0.39	8	80	3.71E-54
Q9NWU1	3-oxoacyl-[acyl-carrier-protein] synthase, mitochondrial	OXSM			1.49	0.67	1.49		2	10	1.73E-05
A8MU24	Prolylcarboxypeptidase (Angiotensinase C), isoform CRA_b	hCG_27286			1.49	0.67	1.49		4	11	8.71E-15
P18583-5	Bax antagonist selected in saccharomyces 1	C21orf50	1.37	1.47	1.65	0.61	1.50	0.14	14	11	8.92E-54
Q12906-1	Isoform 1 of Interleukin	ILF3	1.51				1.51		28	42	6.28E-203
O95837	Guanine nucleotide-binding protein subunit alpha-14	GNA14			1.52	0.66	1.52		3	11	1.88E-46
Q9NRF8	CTP synthase 2	CTPS2			1.52	0.66	1.52		3	6.1	1.33E-07
P53801	Putative pituitary tumor-transforming gene 3 protein	PTTG3			1.53	0.65	1.53		2	11	1.51E-03
Q13510-2	Acid ceramidase	ASAH		1.80	1.28	0.78	1.54	0.37	2	4.6	1.89E-03
O75153	Protein KIAA0664	KIAA0664	1.25	1.81	1.57	0.64	1.54	0.28	9	11	7.08E-61
Q8TEM4	ADP-ribosylation factor-like protein 6-interacting protein 4	FLJ00169			1.55	0.65	1.55		2	6.4	1.33E-115
P78330	L-3-phosphoserine phosphatase	PSPH	1.59	1.70	1.38	0.72	1.56	0.16	5	26	2.32E-29
Q9Y324	rRNA-processing protein FCF1 homolog	C14orf111	1.59		1.58	0.63	1.59	0.01	2	10	6.80E-18
Q9UNK0	Syntaxin-8	STX8	1.01		2.18	0.46	1.60	0.83	4	27	3.78E-89
Q96IH1	FSCN1 protein	FSCN1			1.62	0.62	1.62		2	5.2	2.01E-25
Q09666	Desmoyokin	AHNAK			1.62	0.62	1.62		3	1.6	8.38E-05
Q5T440	Putative transferase C1orf69, mitochondrial	C1orf69	1.86	1.39			1.63	0.33	3	12	2.87E-41
B4DHQ3	Phosphoserine aminotransferase	PSA	1.85	1.83	1.20	0.83	1.63	0.37	22	59	9.30E-260
Q7Z2Y	Interferon-induced very large GTPase 1	GVIN1		1.63			1.63		2	0.9	6.26E-04

UniProt ID	Protein_Name	Gene Name	F1 (L/H)	F2 (L/H)	R1 (H/L)	R1 (L/H)	Mean (T/U)	S.D.	Pep. No.	%Seq. Cov.	PEP
8											
B1ANH1	Guanylate kinase 1	GUK1	1.72	1.65	1.53	0.65	1.63	0.10	6	33	1.08E-59
Q5T5C7	Seryl-tRNA synthetase	RP11-352P4.2-004	1.65	1.74	1.53	0.65	1.64	0.11	18	41	1.13E-165
Q15758	Baboon M7 virus receptor	ASCT2	1.75	1.67	1.52	0.66	1.65	0.12	4	10	2.18E-28
Q8TCD5-1	5(3)-deoxyribonucleotidase, cytosolic type	DNT1	1.65				1.65		4	30	1.93E-48
O60547	GDP-D-mannose dehydratase	GMDS	1.66				1.66		2	5.1	8.70E-05
O00165-2	HCLS1-associated protein X-1	HAX1	1.69	1.57	1.73	0.58	1.66	0.08	7	37	1.69E-26
Q9BV57-1	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase	ADI1	1.60		1.74	0.57	1.67	0.10	6	47	7.83E-27
Q8WTS1	1-acylglycerol-3-phosphate O-acyltransferase ABHD5	ABHD5	1.70				1.70		2	10	2.14E-11
Q9UM00-1	Transmembrane and coiled-coil domain-containing protein 1	PNAS-10	2.09	1.84	1.24	0.81	1.72	0.44	2	15	3.24E-08
Q96N66-1	1-acylglycerophosphatidylinositol O-acyltransferase	BB1	2.22	2.10	0.86	1.16	1.73	0.75	3	6.4	1.59E-15
Q7LBR1	Charged multivesicular body protein 1b	C18orf2			1.73	0.58	1.73		2	7.5	1.15E-02
P98155-1	Very low-density lipoprotein receptor	VLDLR			1.74	0.57	1.74		2	4.6	4.89E-07
P02794	Cell proliferation-inducing gene 15 protein	FTH	1.96		1.53	0.65	1.75	0.30	5	42	3.73E-28
Q9UPT6	C-Jun-amino-terminal kinase-interacting protein 3	JIP3			1.78	0.56	1.78		2	3.1	2.28E-02
Q02083-1	Acid ceramidase-like protein	ASAHL	1.78				1.78		2	10	7.34E-07
P25686-3	DnaJ homolog subfamily B member 2	DNAJB2		1.79			1.79		3	9.3	3.83E-03
P82970	High mobility group nucleosome-binding domain-containing protein 5	HMGN5		1.80			1.80		2	8.5	1.03E-04
Q9C005	Dpy-30-like protein	DPY30	1.82				1.82		2	36	5.49E-34
O60610-1	Diaphanous-related formin-1	DIAP1	1.99	2.10	1.39	0.72	1.83	0.38	23	23	1.08E-170
Q9BY50	Microsomal signal peptidase 21 kDa	SEC11C	1.90				1.90		2	16	1.02E-43

UniProt ID	Protein_Name	Gene Name	F1 (L/H)	F2 (L/H)	R1 (H/L)	R1 (L/H)	Mean (T/U)	S.D.	Pep. No.	%Seq. Cov.	PEP
	subunit										
P50416-1	Carnitine O-palmitoyltransferase 1, liver isoform	CPT1	2.01	2.10	1.63	0.61	1.91	0.25	10	15	3.49E-91
Q5JTJ3-2	Uncharacterized protein C1orf31	C1orf31	2.42	1.64	1.69	0.59	1.92	0.44	2	17	1.82E-34
Q14657	L antigen family member 3	DXS9879E	2.06	2.08	1.61	0.62	1.92	0.27	3	38	2.96E-42
B4DW73	cDNA FLJ50710, highly similar to Phosphoenolpyruvate carboxykinase (GTP), mitochondrial (EC 4.1.1.32)	PCK2	1.60	1.66	2.57	0.39	1.94	0.54	6	11	3.49E-54
Q53EL6	Neoplastic transformation inhibitor protein	H731		1.99			1.99		3	7.9	1.86E-09
Q92599-1	Septin-8	SEPT		2.06			2.06		2	3.3	1.46E-03
Q01726	Melanocortin receptor 1	MC1R	1.81		2.35	0.43	2.08	0.38	17	28	0.00E+00
P53350	Polo-like kinase 1	PLK		2.77	1.67	0.60	2.22	0.78	2	5	1.19E-10
Q9UKN8	General transcription factor 3C polypeptide 4	GTF3C4	2.26				2.26		2	4.4	3.96E-03
P08243	Asparagine synthetase [glutamine-hydrolyzing]	ASNS	2.55	2.39	1.88	0.53	2.27	0.35	3	5.3	6.44E-76
P12236	Adenine nucleotide translocator 3	ANT3	3.71	1.31	1.85	0.54	2.29	1.26	9	28	1.20E-35
Q9NVP2	Anti-silencing function protein 1 homolog B	ASF1B	2.86		1.79	0.56	2.33	0.76	4	35	1.28E-21
Q9HB40-1	Retinoid-inducible serine carboxypeptidase	MSTP034			2.34	0.43	2.34		2	5.3	3.37E-11
Q9NQH7-1	Aminopeptidase P3	XPNPEP3	2.95		1.93	0.52	2.44	0.72	2	7.5	9.99E-18
Q05707-1	Collagen alpha-1(XIV) chain	COL14A1		2.48			2.48		2	1.5	2.85E-52
Q8NCD3-1	14-3-3-associated AKT substrate	FAKTS		2.68			2.68		2	3.2	9.86E-07
Q75MQ0	Putative uncharacterized protein EZH2	EZH2	3.87		1.85	0.54	2.86	1.43	3	5.2	3.45E-08
Q3B7T1-1	Erythroid differentiation-related factor 1	C10orf137	3.42				3.42		2	2	1.62E-15
Q9BPZ3	Polyadenylate-binding protein-interacting protein 2	HSPC218	3.75				3.75		2	35	7.30E-09
P15924-1	250/210 kDa paraneoplastic pemphigus antigen	DSP		3.84			3.84		2	0.7	1.76E-03

UniProt ID	Protein_Name	Gene Name	F1 (L/H)	F2 (L/H)	R1 (H/L)	R1 (L/H)	Mean (T/U)	S.D.	Pep. No.	%Seq. Cov.	PEP
Q86YJ6	Threonine synthase-like 2	THNSL2			4.41	0.23	4.41		2	6.2	3.46E-02
P05114	High mobility group nucleosome-binding domain-containing protein 1	HMG14	6.38	3.21	4.66	0.21	4.75	1.59	3	24	3.51E-31
A5JHP3	Dermcidin isoform 2	DCD	7.75	4.37	4.22	0.24	5.45	2.00	2	21	1.93E-35
P06702	Calgranulin-B	CAGB	5.56				5.56		2	26	2.20E-66
Q8TE01	DERP12 (Dermal papilla derived protein 12)	DERP12	6.21	7.55	6.12	0.16	6.63	0.80	11	42	1.60E-164
P17096-1	High mobility group AT-hook protein 1;High mobility group protein HMG-I/HMG-Y	HMGA1		7.67			7.67		3	51	1.42E-55
P05164-3	84 kDa myeloperoxidase	MPO	7.95				7.95		2	2.8	9.94E-06
Q14473	Beta-globin gene from a thalassemia patient	HBB		22.05			22.05		10	51	0.00E+00

Table S2. A list of proteins which could be quantified in both forward and reverse SILAC labeling experiments and whose expressions were changed significantly upon ^{S}G treatment ("S.D." represents standard deviation).

Protein ID	Protein Name	Mean (T/U)	S.D.
P09382	14 kDa laminin-binding protein	0.31	0.01
Q6UXB8-1	Cysteine-rich secretory protein 9	0.36	0.08
Q8WXG9-1	G-protein coupled receptor 98	0.36	0.14
Q8NB37-2	Parkinson disease 7 domain-containing protein 1	0.43	0.11
Q99707	5-methyltetrahydrofolate--homocysteine methyltransferase	0.44	0.05
P10606	Cytochrome c oxidase polypeptide Vb	0.45	0.08
P63313	Thymosin beta-10	0.46	0.09
A6NMH8	Putative uncharacterized protein CD81	0.48	0.49
Q9H8V3-2	Epithelial cell-transforming sequence 2 oncogene	0.48	0.14
B7Z6C0	cDNA FLJ56946, highly similar to Cysteine-rich protein 2	0.49	0.24
O75794	Cell division cycle protein 123 homolog	0.51	0.19
P08590	Cardiac myosin light chain 1	0.51	0.01
P00403	Cytochrome c oxidase polypeptide II	0.51	0.07
O75879	Cytochrome oxidase assembly factor PET112 homolog	0.52	0.14
O95865	Dimethylargininase-2	0.52	0.11
P42575-1	Caspase-2	0.53	0.06
Q9NUV9	GTPase IMAP family member 4	0.53	0.02
Q01970	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta-3	0.53	0.58
O75155-1	Cullin-associated and neddylation-dissociated protein 2	0.54	0.21
P09669	Cytochrome c oxidase polypeptide VIc	0.54	0.04
Q86UY6-1	N-acetyltransferase 11	0.55	0.37
Q15154-1	Pericentriolar material 1 protein	0.55	0.12
O95229	ZW10 interactor	0.55	0.06
O43683	Mitotic checkpoint serine/threonine-protein kinase BUB1	0.56	0.17
Q13190-1	Syntaxin-5	0.58	0.08
Q06945	Transcription factor SOX-4	0.58	0.13
P37268	Farnesyl-diphosphate farnesyltransferase	0.58	0.06
Q14191	DNA helicase, RecQ-like type 3	0.59	0.06
A6NED2	RCC1 domain-containing protein 1	0.59	0.08
P30281	G1/S-specific cyclin-D3	0.60	0.02
O95299	NADH dehydrogenase ubiquinone 1 alpha subcomplex	0.60	0.02
Q5TCU8	Tropomyosin 2 (Beta)	0.60	0.09
P63218	Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-5	0.60	0.07
Q6RFH5-1	NOP seven-associated protein 1	0.61	0.15
P84101	Gastric cancer-related protein VRG107	0.61	0.16
C9JG49	Protein tyrosine phosphatase, non-receptor type 6, isoform CRA_b	0.61	0.02

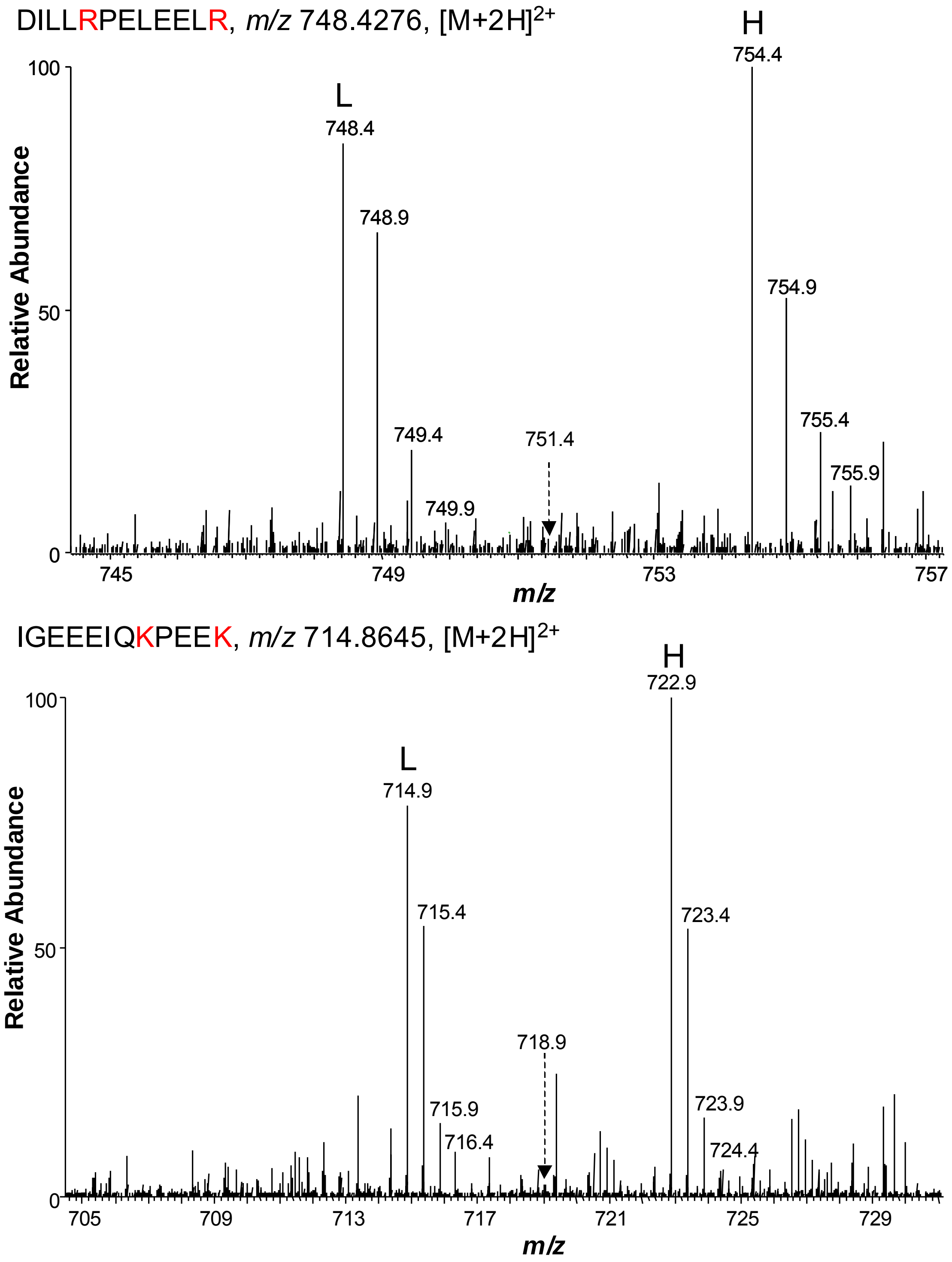
Protein ID	Protein Name	Mean (T/U)	S.D.
O60566-3	MAD3/BUB1-related protein kinase	0.61	0.07
Q9ULT8	E3 ligase for inhibin receptor	0.61	0.11
B4DGI9	cDNA FLJ52589, highly similar to Transcription factor 12	0.62	0.10
Q9BZL1	Ubiquitin-like protein 5	0.62	0.03
P51159-1	GTP-binding protein Ram	0.62	0.07
P56962	Syntaxin-17	0.62	0.03
Q5T7F6	Novel protein	0.63	0.02
P08670	Vimentin	0.63	0.15
P22695	Complex III subunit 2	0.63	0.28
Q96EB1-1	Elongator complex protein 4	0.64	0.08
Q53H12-1	Acylglycerol kinase, mitochondrial	0.64	0.08
Q8NDI1-1	EH domain-binding protein 1	0.64	0.13
Q96EL3	39S ribosomal protein L53, mitochondrial	0.65	0.08
Q9UIC8-2	Leucine carboxyl methyltransferase 1	0.65	0.11
Q9UPP1-1	Histone lysine demethylase PHF8	0.65	0.12
P31930	Complex III subunit 1	0.65	0.22
P46108-1	Adapter molecule crk	0.65	0.34
Q9NP61	ADP-ribosylation factor GTPase-activating protein 3	0.65	0.11
Q96RT1-1	Densin-180-like protein	0.65	0.00
B7Z6Z4	cDNA FLJ56329, highly similar to Myosin light polypeptide 6	0.65	0.03
O94830	DDHD domain-containing protein 2	0.65	0.12
Q14CJ1	Amino-terminal enhancer of split	0.65	0.14
Q9BQS8-1	FYVE and coiled-coil domain-containing protein 1	0.66	0.01
Q9Y448	Putative TRAF4-associated factor 1	0.66	0.02
Q9BXK1	Basic transcription element-binding protein 4	0.66	0.15
A2A305	Ubiquitin associated protein 2	0.66	0.15
Q71RC2-4	La ribonucleoprotein domain family member 4	0.66	0.17
P13051-1	Uracil-DNA glycosylase	0.67	0.03
O75146	Huntingtin-interacting protein 12	0.67	0.06
Q9Y3P9-1	GAP and centrosome-associated protein	0.67	0.07
P04818	Thymidylate synthase	0.67	0.04
Q9UJU2-1	Lymphoid enhancer-binding factor 1	0.67	0.05
O15294-1	O-GlcNAc transferase subunit p110	0.67	0.16
P18583-5	Bax antagonist selected in saccharomyces 1	1.50	0.14
Q13510-2	Acid ceramidase	1.54	0.37
O75153	Protein KIAA0664	1.54	0.28
P78330	L-3-phosphoserine phosphatase	1.56	0.16
Q9Y324	rRNA-processing protein FCF1 homolog	1.59	0.01
Q9UNK0	Syntaxin-8	1.60	0.83
Q5T440	Putative transferase C1orf69, mitochondrial	1.63	0.33
B4DHQ3	Phosphoserine aminotransferase	1.63	0.37

Protein ID	Protein Name	Mean (T/U)	S.D.
B1ANH1	Guanylate kinase 1	1.63	0.10
Q5T5C7	Seryl-tRNA synthetase	1.64	0.11
Q15758	Baboon M7 virus receptor	1.65	0.12
O00165-2	HCLS1-associated protein X-1	1.66	0.08
Q9BV57-1	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase	1.67	0.10
Q9UM00-1	Transmembrane and coiled-coil domain-containing protein 1	1.72	0.44
Q96N66-1	1-acylglycerophosphatidylinositol O-acyltransferase	1.73	0.75
P02794	Cell proliferation-inducing gene 15 protein	1.75	0.30
O60610-1	Diaphanous-related formin-1	1.83	0.38
P50416-1	Carnitine O-palmitoyltransferase 1, liver isoform	1.91	0.25
Q5JTJ3-2	Uncharacterized protein C1orf31	1.92	0.44
Q14657	L antigen family member 3	1.92	0.27
B4DW73	cDNA FLJ50710, highly similar to Phosphoenolpyruvate carboxykinase (GTP), mitochondrial (EC 4.1.1.32)	1.94	0.54
Q01726	Melanocortin receptor 1	2.08	0.38
P53350	Polo-like kinase 1	2.22	0.78
P08243	Asparagine synthetase [glutamine-hydrolyzing]	2.27	0.35
P12236	Adenine nucleotide translocator 3	2.29	1.26
Q9NVP2	Anti-silencing function protein 1 homolog B	2.33	0.76
Q9NQH7-1	Aminopeptidase P3	2.44	0.72
Q75MQ0	Putative uncharacterized protein EZH2	2.86	1.43
P05114	High mobility group nucleosome-binding domain-containing protein 1	4.75	1.59
A5JHP3	Dermcidin isoform 2	5.45	2.00
Q8TE01	DERP12 (Dermal papilla derived protein 12)	6.63	0.80

Table S3. Pathways perturbed by ^{S}G treatment, as identified by IPA. The most statistically significant canonical pathways and molecules identified are listed according to their p-value (-Log). The threshold of p-value is 0.05.

Ingenuity Canonical Pathways	-log(p-value)	# of Molecules	Molecules
Mitochondrial Dysfunction	7.41E00	13	NDUFA4 (0.64), NDUFV1 (0.48), CPT1 (1.91±0.25), MT-CO2 (0.51±0.07), NDUFA2 (0.63), UQCRC2 (0.63±0.28), UQCRFS1 (0.61), NDUFA10 (0.60±0.02), CYB5A (0.65), UQCRC1 (0.65±0.22), COX5B (0.45±0.08), COX6C (0.54±0.04), RHOT1 (0.58±0.06)
RhoGDI Signaling	4.45E00	8	ARHGAP9 (0.41), MYL6 (0.65±0.03), RHOT1 (0.58±0.06), ARH9 (0.66), GNG5 (0.60±0.07), ARHGEF11 (0.51), GNA14 (1.52), MYL3 (0.51±0.01)
CXCR4 Signaling	4.19E00	9	MYL6 (0.65±0.03), RHOT1 (0.58±0.06), ARH9 (0.66), PLCB3 (0.53±0.58), GNG5 (0.60±0.07), CRK (0.65±0.34), ARHGEF11 (0.51), GNA14 (1.52), MYL3 (0.51±0.01)
Signaling by Rho Family GTPases	3.97E00	9	SEPT8 (2.06), MYL6 (0.65±0.03), RHOT1 (0.58±0.06), ARH9 (0.66), VIM (0.63±0.15), GNG5 (0.60±0.07), ARHGEF11 (0.51), GNA14 (1.52), MYL3 (0.51±0.01)
RhoA Signaling	3.59E00	6	SEPT8 (2.06), ARHGAP9 (0.41), MYL6 (0.65±0.03), ANLN (0.53), ARHGEF11 (0.51), MYL3 (0.51±0.01)
ILK Signaling	3.48E00	8	MYL6 (0.65±0.03), RHOT1 (0.58±0.06), ARH9 (0.66), VIM (0.63±0.15), LEF1 (0.67±0.05), MYH7 (0.30), MYL3 (0.51±0.01), DSP (3.84)
Regulation of Actin-based Motility by Rho	2.97E00	4	MYL6 (0.65±0.03), RHOT1 (0.58±0.06), ARH9 (0.66), MYL3 (0.51±0.01)
Epithelial Adherens Junction Signaling	2.95E00	5	MYL6 (0.65±0.03), LEF1 (0.67±0.05), CRK (0.65±0.34), MYH7 (0.30), MYL3 (0.51±0.01)
Thrombin Signaling	2.8E00	8	MYL6 (0.65±0.03), RHOT1 (0.58±0.06), ARH9 (0.66), PLCB3 (0.53±0.58), GNG5 (0.60±0.07), ARHGEF11 (0.51), GNA14 (1.52), MYL3 (0.51±0.01)
Phospholipase C Signaling	2.73E00	9	AHNAK (1.62), MYL6 (0.65±0.03), RHOT1 (0.58±0.06), ARH9 (0.66), CAGA (0.08), PLCB3 (0.53±0.58), GNG5 (0.60±0.07), ARHGEF11 (0.51), MYL3 (0.51±0.01)
Oxidative phosphorylation	2.51E00	11	MYL3 (0.51±0.01), COX5B (0.45±0.08), COX6C (0.54±0.04), NDUFA2 (0.63), NDUFA4 (0.64), NDUFA10 (0.60±0.02), NDUFV1 (0.48), UQCRC1 (0.65±0.22), UQCRC2 (0.63±0.28), ARHGEF11 (0.51), UQCRFS1 (0.61)
Actin Cytoskeleton Signaling	2.46E00	4	MYL6 (0.65±0.03), CRK (0.65±0.34), MYH7 (0.30), MYL3 (0.51±0.01)
Sphingosine-1-phosphate Signaling	2.33E00	4	RHOT1 (0.58±0.06), ARH9 (0.66), CASP2 (0.53±0.06), PLCB3 (0.53±0.58)

Ingenuity Canonical Pathways	-log(p-value)	# of Molecules	Molecules
Actin Nucleation by ARP-WASP Complex	2.1E00	3	RHOT1 (0.58±0.06), ARH9 (0.66), FNRA (0.66)
Cardiac Hypertrophy Signaling	1.84E00	7	MYL6 (0.65±0.03), RHOT1 (0.58±0.06), ARH9 (0.66), PLCB3 (0.53±0.58), GNG5 (0.60±0.07), GNA14 (1.52), MYL3 (0.51±0.01)
Clathrin-mediated Endocytosis Signaling	1.79E00	4	LYZ (0.03), CAGA (0.08), CTTN (0.64), HIP12 (0.67±0.03)
Mitochondrial L-carnitine Shuttle Pathway	1.63E00	2	CPT1 (1.91±0.25), ACS4 (0.48)
LXR/RXR Activation	1.54E00	4	FDFT1 (0.58±0.06), LYZ (0.03), CAGA (0.08), IRF3 (0.66)
GADD45 Signaling	1.50E00	2	CCND3 (0.60±0.02), CDK4 (2.27±0.04)
PAK Signaling	1.44E00	3	MYL6 (0.65±0.03), CAGA (0.08), MYL3 (0.51±0.01)
Cellular effects of sildenafil	1.44E00	4	MYL6 (0.65±0.03), PLCB3 (0.53±0.58), MYH7 (0.30), MYL3 (0.51±0.01)
Production of Nitric Oxide and Reactive Oxygen Species in Macrophages	1.38E00	5	LYZ (0.03), MPO (7.95), RHOT1 (0.58±0.06), ARH9 (0.66), CAGA (0.08)



DILLRPELEELR, *m/z* 748.4276, $[M+2H]^{2+}$

IGEEEIQKPEEK, *m/z* 714.8645, $[M+2H]^{2+}$

Figure S1. Example mass spectra showing the incorporation of heavy labeled K and R. Shown are the ESI-MS of two trypsin-miscleaved peptides which carry two arginines or two lysines; IGEEEIQKPEEK and DILLRPELEELR are derived from splicing factor 3a (SAP114) and NADH-cytochrome b5 reductase (CYB5R3), respectively. The ions of *m/z* 751.4 and *m/z* 718.9 refer to the putative incompletely labeled peptides (i.e., with a single R or K being heavily labeled), which are present at similar abundance levels as the noise peaks.

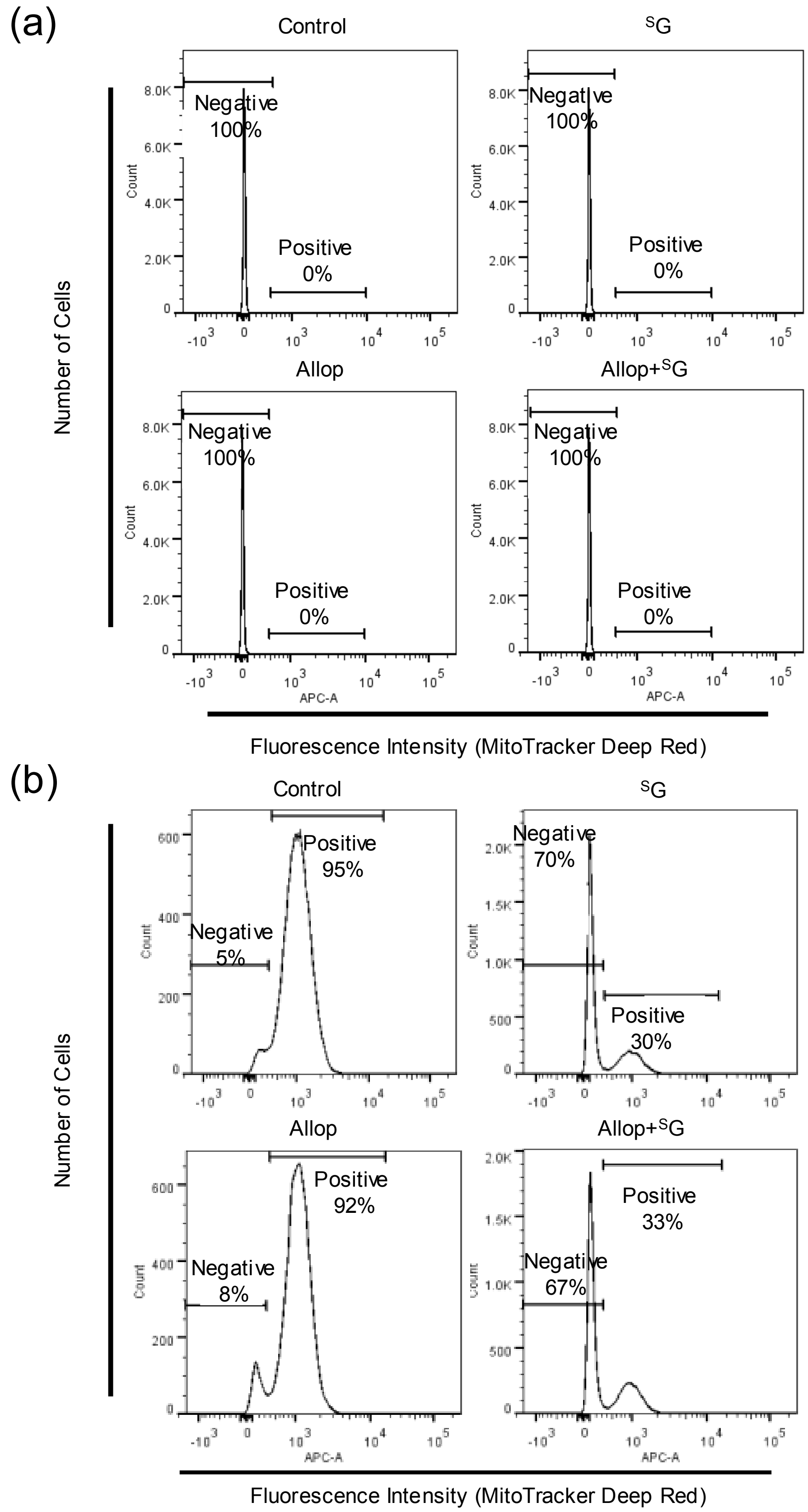


Figure S2. Flow cytometry results for control CEM cells, and CEM cells that were treated for 24 hrs with 3 µM ^{S}G and 500 µM allopurinol, alone or in combination. In (a), no MitoTracker Deep Red was added, whereas MitoTracker Deep Red was added in (b).

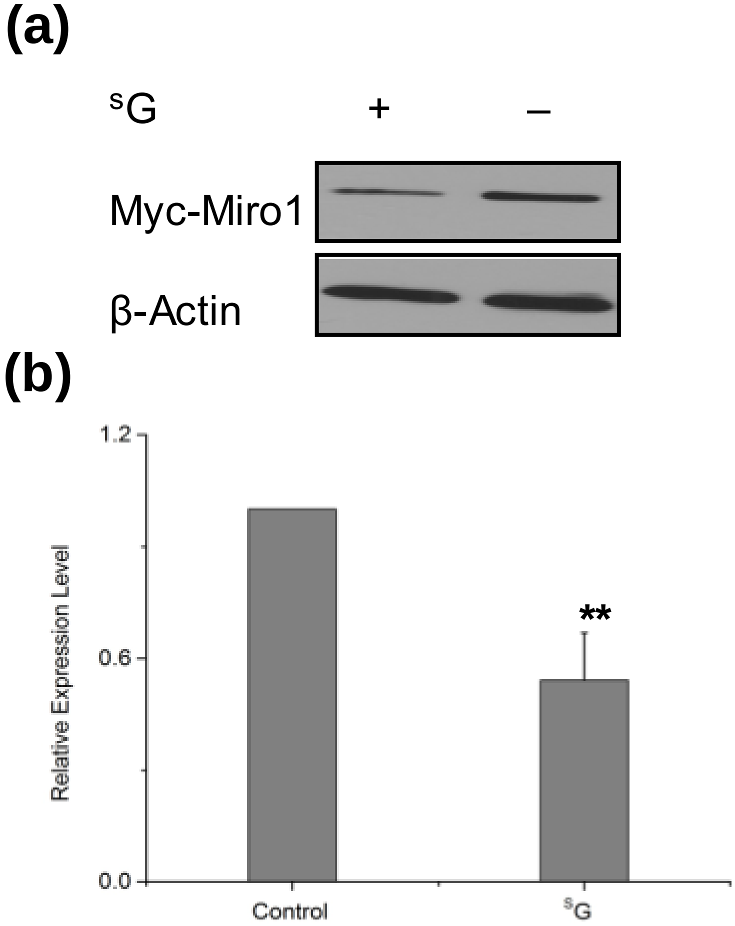


Figure S3. Western blot for monitoring the expression levels of ectopically expressed Myc-Miro1 in HEK293T cells upon treatment with 3 μM ^{S}G (a). β-actin serves as the loading control. Shown in (b) are the quantification data, which represent the mean and S. D. of results from three independent drug treatment and Western blot experiments. "**", $p < 0.01$. The p value was calculated using two-tailed, unpaired student t test.

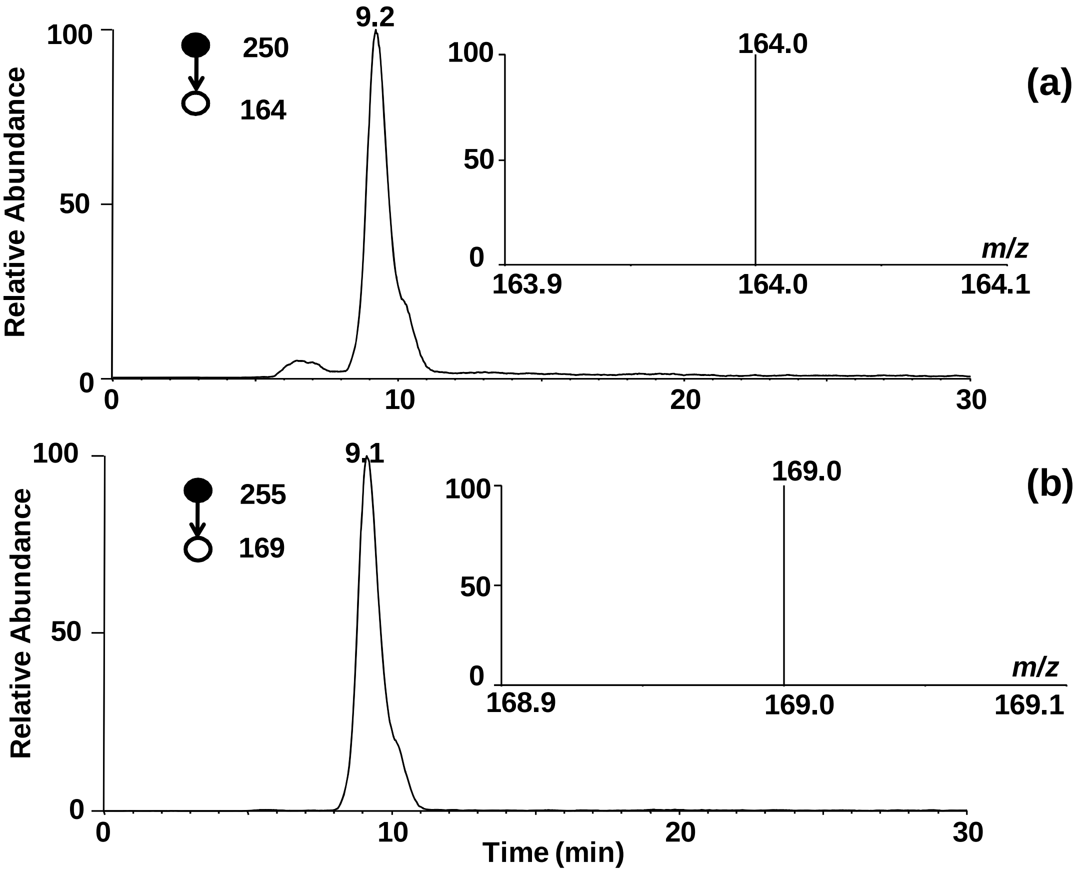


Figure S4. Selected-ion chromatograms for monitoring the transitions of *m/z* 250→164 [(a), for unlabeled *R*-cdA] and *m/z* 255 → 169 [(b), for uniformly ^{15}N-labeled *R*-cdA].

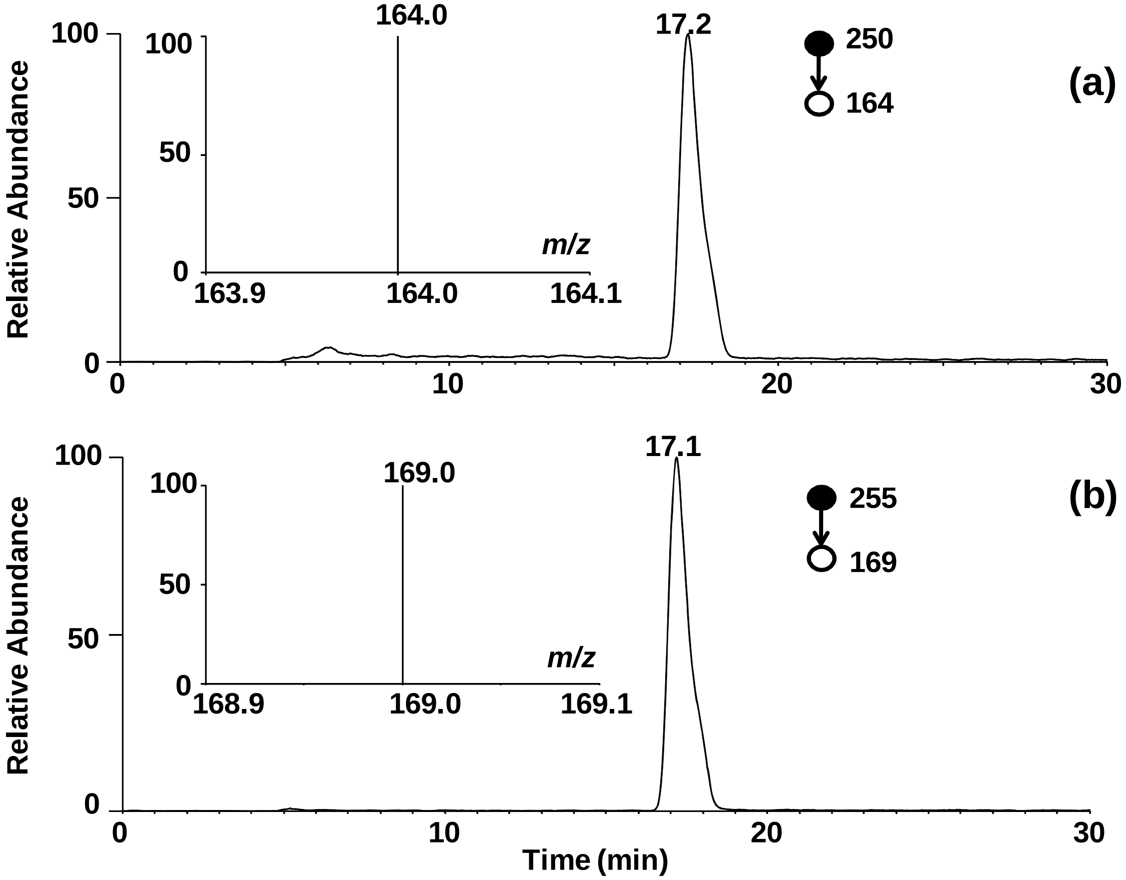


Figure S5. Representative selected-ion chromatograms for monitoring the transitions of *m/z* 250→164 [(a), for unlabeled *S*-cdA] and *m/z* 255 →169 [(b), for uniformly ^{15}N labeled *S*-cdA].

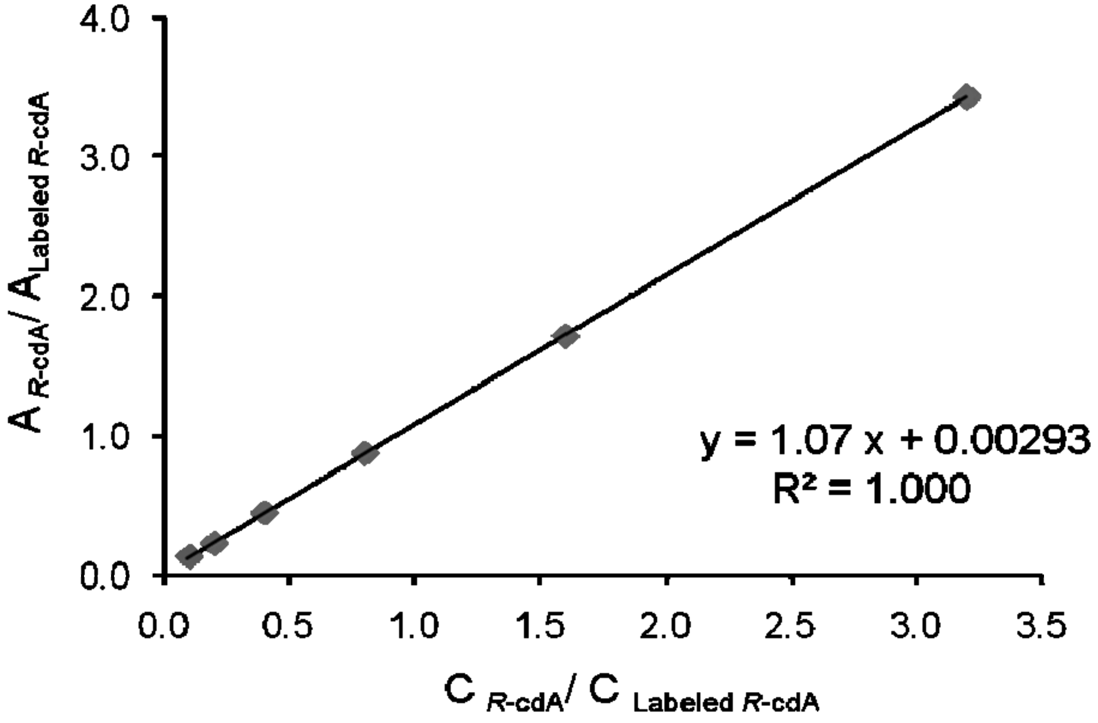


Figure S6. Calibration curve for the quantification of *R*-cdA, where 100 fmol of uniformly ^{15}N-labeled *R*-cdA was added.

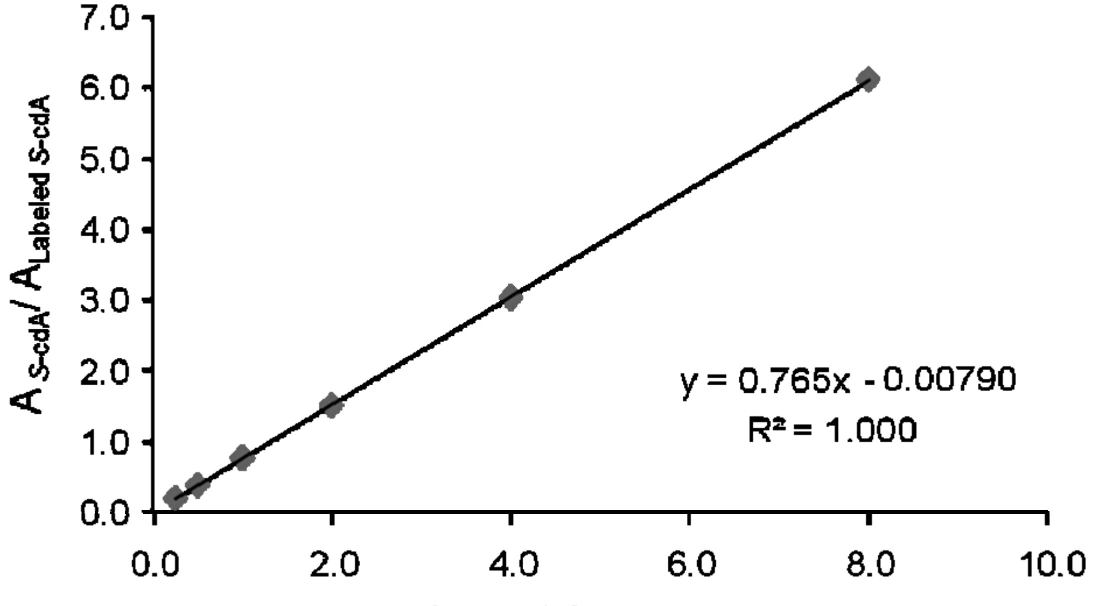


Figure S7. Calibration curve for the quantification of S-cdA, where 40 fmol uniformly ^{15}N-labeled *S*-cdA was added to each sample.

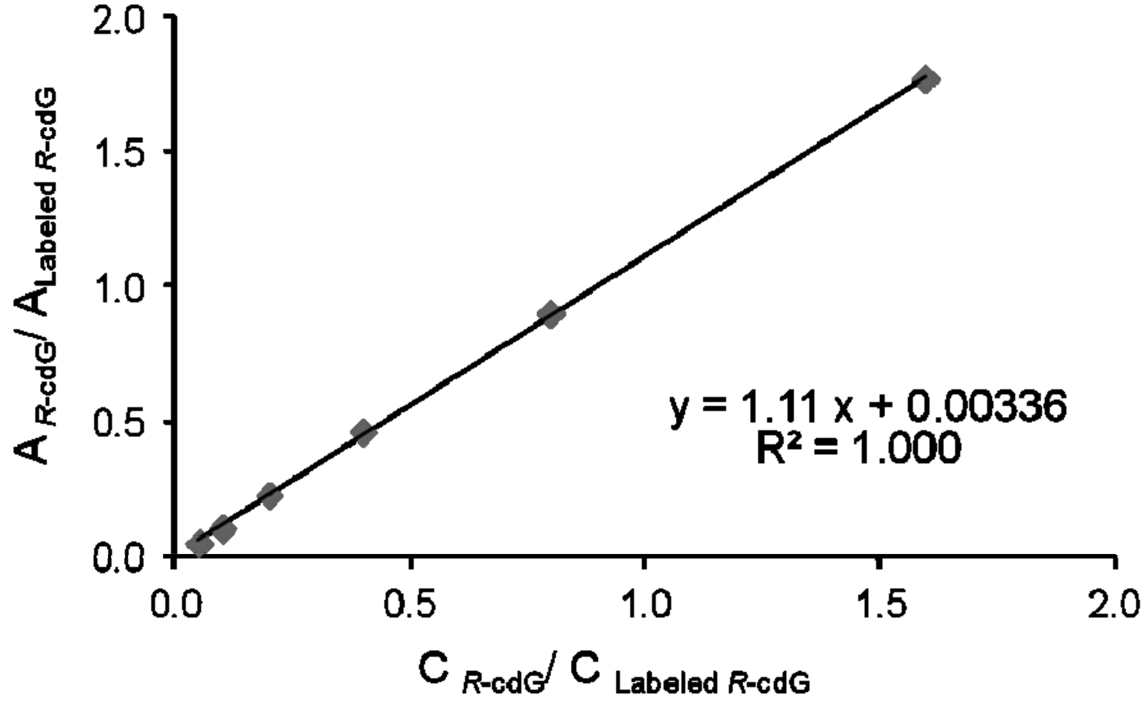


Figure S8. Calibration curve for the quantification of *R*-cdG, where 200 fmol of uniformly ^{15}N-labeled *R*-cdG was added to each sample.

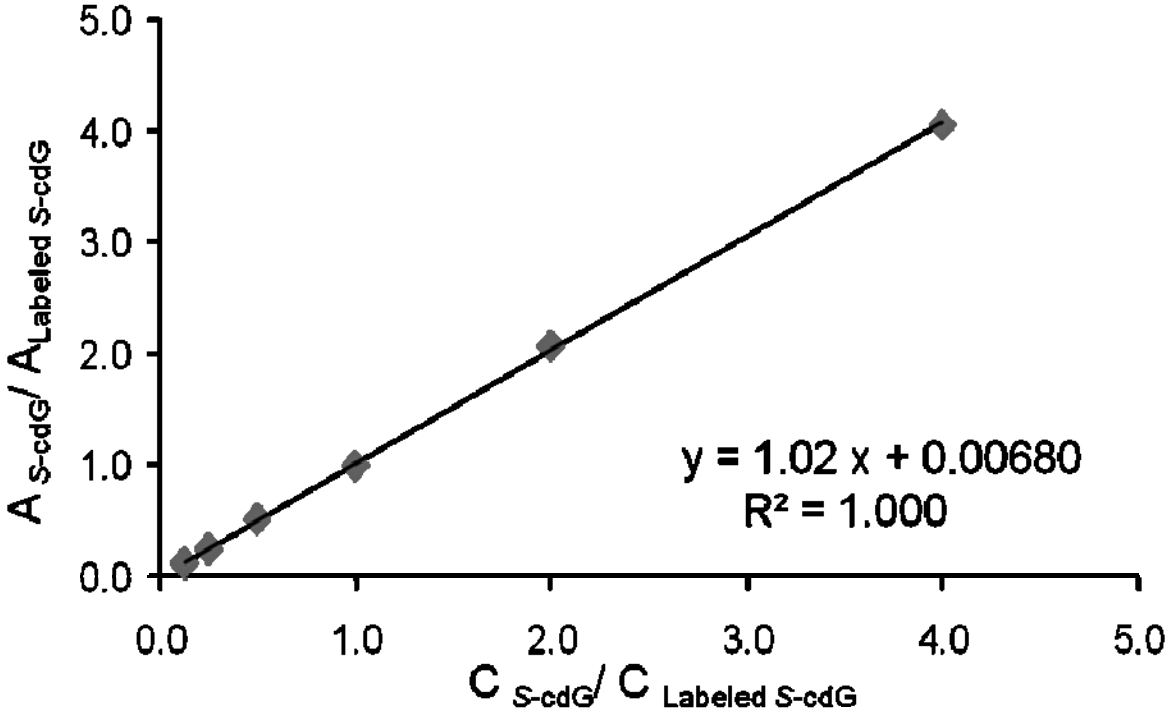


Figure S9. Calibration curve for the quantification of *S*-cdG, where 160 fmol uniformly ^{15}N-labeled *S*-cdG was added to each sample.