Table S2 List of identified proteins with replicate data of all samples in RAW 264.7 macrophages during the treatment of bio-LPS, statin-bio-LPS, and statin along with cross-linkers. The PSMs were normalized by percentage.

Accession	Description	Control	Bio-LPS	Statin-Bio-LP	Statin	DUCCT	Bio-LPS-DUCCT	Bio-LPS-Statin-DUCCT	Statin-DUCCT	BS3	Bio-LPS-BS3	Bio-LPS-Statin-BS3	Statin-BS3
A0A023T778	Mago nashi protein												0.02
A0A068BEQ2	H2-K region expressed gene 6, isoform CRA_a		0.03	0.03	0.02	0.03		0.02		0.05		0.03	
A0A068BFR3	RAS oncogene family protein	0.09	0.06	0.13	0.13	0.23	0.11	0.15	0.09	0.21	0.09	0.19	0.18
A0A068BFS0	WD repeat domain 46		0.03		0.01								
A0A075DC90	Cytochrome c oxidase subunit 2	0.12	0.10	0.11	0.11	0.16	0.08	0.04	0.07	0.12	0.10	0.08	0.13
A0A077S2U6	Lysozyme C-2								0.03				0.02
A0A077S9N1	Lysozyme C-1			0.02	0.04		0.03	0.02	0.07	0.02		0.03	0.06
A0A087WQ39	IQ motif and SEC7 domain-containing protein 1						0.01						0.01
A0A087WQS2	Basic leucine zipper and W2 domain-containing protein 1			0.05	0.02	0.02	0.02	0.02		0.04		0.03	
A0A087WSP5	Signal transducer and activator of transcription						0.02						
A0A0A0MQA5	Tubulin alpha-4A chain	0.75	0.57	0.40	0.45	0.28	0.30	0.14	0.13	0.42	0.56	0.27	0.59
A0A0A0MQF6	Glyceraldehyde-3-phosphate dehydrogenase	0.93	1.01	0.52	1.14	0.92	0.59	0.36	0.79	0.91	0.82	0.67	1.22
A0A0A0MQN4	Ubiquitin-like modifier-activating enzyme ATG7			0.06	0.04	0.02	0.02	0.03		0.04		0.04	0.02
A0A0A6YVS2	Transmembrane and coiled-coil domain-containing protein 1			0.04	0.06	0.04	0.02	0.02	0.05			0.03	0.06
A0A0A6YVU8	MCG119397	0.05	0.03	0.01	0.01		0.01						
A0A0N4SVL0	Eukaryotic translation initiation factor 4 gamma 3		0.04	0.02			0.01				0.07		
A0JNY7	Eukaryotic translation initiation factor 4, gamma 2		0.07	0.04	0.02	0.02	0.03			0.03	0.10	0.02	
A1A4A7	Pgam5 protein						0.01						
A1A4T2	Alpha glucosidase 2 alpha neutral subunit					0.02		0.04	0.07			0.03	0.11
A1L2Z3	C230096C10Rik protein		0.07	0.09	0.09	0.05	0.03	0.04	0.04	0.07	0.08	0.07	0.04
A1L3C2	Polr1c protein			0.02						0.01		0.02	
A2A432	Cullin-4B		0.03							0.01	0.08		
A2A4J8	Vacuolar protein-sorting-associated protein 25				0.01								0.02
A2A4P4	Protein Gm27029		0.04				0.02			0.02			
A2A7S7	Tyrosine--tRNA ligase	0.16	0.19	0.15	0.08	0.06	0.12	0.08	0.03	0.15	0.22	0.11	0.02
A2ADH1	Magnesium transporter protein 1			0.02	0.01		0.01		0.01			0.02	0.01
A2AE27	AMP deaminase 2							0.01				0.02	
A2AFP5	Ras-related protein Rab-9A												0.02
A2AFQ0	E3 ubiquitin-protein ligase HUWE1		0.06	0.02	0.03		0.02			0.05	0.05	0.04	0.01
A2AGT5	Cytoskeleton-associated protein 5			0.02	0.01		0.01	0.02		0.03	0.09	0.03	0.01
A2AL50	Alkyldihydroxyacetonephosphate synthase, peroxisomal	0.07	0.07	0.10	0.10	0.04	0.06	0.03	0.03	0.05		0.08	0.01
A2AMU9	Mrto4 protein		0.04	0.02	0.01	0.04		0.01	0.02	0.03			0.02
A2AP31	MCG9810												0.01
A2APM2	CD44 antigen			0.04	0.04			0.03	0.06			0.06	
A2ASS6	Titin								0.01				0.01
A2AWP8	Rho guanine nucleotide exchange factor 10-like protein			0.02						0.01			0.01
A2BE28	Ribosomal biogenesis protein LAS1L		0.03										
A2CG35	Ras-related protein Rab-12	0.04		0.03		0.04	0.01	0.03	0.03	0.03		0.03	0.02
A2RRJ4	Exportin 5		0.07				0.01			0.02	0.08		
A2RS96	Transmembrane emp24 domain-containing protein 5			0.04	0.05	0.02	0.02	0.04	0.01	0.01		0.04	0.01
A2RSV8	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial				0.07		0.04	0.04	0.05			0.07	0.05
A3KG93	Lysine-specific histone demethylase 1A									0.01			

A4FVC9	Ahr protein								0.01				0.03
A6ZI44	Fructose-bisphosphate aldolase	0.18	0.15	0.06	0.08	0.06	0.05	0.04	0.04	0.06	0.11	0.05	0.04
A8C1T7	Cysteine-rich with EGF-like domain protein 1			0.02	0.02			0.02				0.03	
A8C756	Thyroid adenoma-associated protein homolog									0.01			0.02
A8DUK2	Beta-globin					0.35			0.01	0.03			
A8IP69	14-3-3 protein gamma			0.07	0.05	0.14	0.03	0.13	0.16	0.10		0.12	0.19
B0QZN5	Vesicle-associated membrane protein 2								0.02				0.01
B1AQF4	Dual-specificity protein phosphatase 3		0.03		0.02								0.03
B1AT82	MCG6846, isoform CRA_c			0.03	0.04		0.02	0.01		0.04		0.03	0.02
B1ATD2	Lymphocyte cytosolic protein 2												0.02
B1AUN2	MCG14442			0.02			0.01						
B1AWD9	Clathrin light chain A					0.06			0.01				0.06
B1AX58	Plastin-3												0.01
B1AZI6	THO complex subunit 2									0.02			
B2CY77	Laminin receptor	0.64	0.52	0.48	0.73	0.57	0.47	0.44	0.44	0.57	0.49	0.65	0.38
B2M0S2	Clk2-Scamp3 protein	0.11	0.12	0.04	0.05	0.05	0.05	0.02	0.02	0.04	0.11	0.06	0.01
B2RQC6	CAD protein	0.38	0.35	0.15	0.15	0.12	0.12	0.05	0.02	0.25	0.42	0.07	0.18
B2RRZ7	TNFRSF1A-associated via death domain												0.01
B2RSR7	Glycerol-3-phosphate dehydrogenase [NAD(+)]	0.11	0.09	0.04	0.04		0.06	0.02		0.06	0.06	0.03	0.01
B2RSV4	Splicing factor 3b, subunit 3	0.35	0.23	0.14	0.16	0.20	0.12	0.10	0.07	0.25	0.45	0.16	0.05
B2RTK3	Histone H2B		0.11	0.16	0.42	0.22	0.15	0.20	0.40	0.08	0.16	0.26	0.46
B2RTM0	Histone H4					0.03		0.02	0.46	0.02		0.03	0.57
B2RTP7	Krt2 protein	0.42	0.24	0.67	0.49	0.39	0.35	0.29	0.35	0.34	0.37	0.48	0.27
B2RUC7	Serine-threonine kinase receptor-associated protein		0.03										
B2RUR3	ATP-binding cassette, sub-family B (MDR/TAP), member 1B	0.06	0.04	0.03	0.02	0.02	0.01			0.02	0.06	0.02	
B2RVP5	Histone H2A			0.05	0.16	0.11	0.07	0.16	0.23	0.01		0.15	0.18
B2RWW1	Microtubule-associated protein 1S			0.02									
B2RXQ5	Phosphatidylinositol-3,4, 5-trisphosphate-dependent Rac exchange factor 1										0.05		
B2RXR1	Coiled-coil domain containing 88B		0.05	0.05				0.03			0.11	0.05	
B2RXS4	Plexin-B2	0.05	0.04	0.06	0.06		0.01	0.04	0.03	0.01	0.06	0.06	0.03
B2RXY7	Carbonyl reductase 1		0.05	0.02	0.02	0.06	0.05			0.05		0.02	0.01
B2RY56	RNA-binding protein 25												0.01
B2RY90	Isoc2a protein			0.02	0.03								0.02
B3VQI8	Cytochrome b-245 light chain			0.02	0.03	0.03	0.02		0.02			0.02	0.02
B6DT57	p40phox	0.14	0.14	0.08	0.05	0.05	0.08	0.05		0.14		0.09	0.01
B7STB7	Annexin		0.06	0.14	0.07	0.09	0.03	0.11	0.05	0.15		0.16	0.11
B7ZNK9	Spata5 protein					0.02		0.01	0.01	0.01		0.02	
B7ZWC0	N-myc downstream regulated gene 1		0.05	0.07	0.04			0.05	0.10			0.06	0.08
B7ZWC4	Insulin-like growth factor 2 receptor			0.06	0.03		0.01	0.05	0.01	0.04		0.06	
B9EHN0	Ubiquitin-activating enzyme E1, Chr X		0.04	0.06	0.03	0.08	0.01	0.08	0.05	0.11	0.14	0.10	0.06
B9EIU1	Glutamyl-prolyl-tRNA synthetase	0.24	0.33	0.24	0.19	0.19	0.17	0.13	0.04	0.30	0.48	0.22	0.19
B9EJ86	Oxysterol-binding protein-related protein 8	0.04	0.05	0.05	0.03	0.04	0.03	0.02	0.01	0.05	0.10	0.04	0.02
B9EK95	Myof protein			0.34	0.11	0.10	0.06	0.26	0.10	0.16	0.27	0.34	0.03
B9EKP5	Filamin, alpha	0.23	0.30	0.45	0.33	0.16	0.14	0.30	0.16	0.29	0.41	0.46	0.30
C7G3P2	MKIAA0536 protein												0.01
D0ESZ4	Elastin microfibril interfacer 2			0.02	0.02								
D1FNM9	Calcium-transporting ATPase		0.05		0.02		0.01		0.01			0.02	0.01
D3YTQ3	Heterogeneous nuclear ribonucleoprotein D-like			0.04	0.03	0.04	0.02	0.01	0.04	0.05		0.03	0.03
D3YTS1	Signal peptidase complex catalytic subunit SEC11			0.04	0.04	0.02	0.01	0.02	0.05			0.04	0.09
D3YTT4	Isobutyryl-CoA dehydrogenase, mitochondrial		0.06	0.04	0.04		0.01			0.03		0.04	

D3YX87	Protein misato homolog 1												0.01
D3YYI8	Histone deacetylase		0.04		0.02		0.02			0.01			0.02
D3YYT1	Putative oxidoreductase GLYR1		0.03	0.02	0.02		0.02			0.02			
D3YZZ5	Protein Tmed7			0.02				0.02				0.02	
D3Z041	Long-chain-fatty-acid--CoA ligase 1			0.03	0.01	0.02		0.01				0.02	
D3Z0M9	MCG18410, isoform CRA_a					0.02				0.01			
D3Z1N9	MCG9889			0.05	0.03	0.05	0.04	0.02	0.02	0.04		0.04	0.02
D3Z3G6	Mitogen-activated protein kinase			0.02				0.01		0.01		0.02	
D3Z3N4	MCG11326, isoform CRA_a						0.01						
D3Z4L9	Tumor necrosis factor alpha-induced protein 2			0.01									
D3Z5I1	Zinc finger CCCH-type antiviral protein 1			0.02	0.01							0.02	0.02
D3Z780	Translation initiation factor eIF-2B subunit delta						0.01						
D3Z7P0	BRCA1-A complex subunit BRE			0.02	0.01		0.01			0.02		0.02	0.01
D3Z7P3	Glutaminase kidney isoform, mitochondrial		0.08	0.06	0.04		0.02			0.02		0.02	
D4AFX6	Centaurin beta 2										0.05		
D4AFX7	Protein Dnajc13		0.03		0.02					0.02			0.01
D6Q0F5	Cytoplasmic dynein intermediate chain 2 isoform 2.1			0.01				0.02	0.02	0.01		0.02	0.02
E0CXZ9	Voltage-gated potassium channel subunit beta-2								0.01				0.01
E0CYV0	Protein-L-isoaspartate O-methyltransferase			0.02	0.02		0.01						
E5Q371	Integrin-associated protein			0.01									
E9PUF7	Rho guanine nucleotide exchange factor 1		0.05										
E9PUW7	Exportin-7												0.01
E9PVX6	Protein Mki67		0.03										
E9PVY8	Microtubule-actin cross-linking factor 1		0.06	0.03	0.03			0.01	0.01	0.01		0.04	0.03
E9PW43	Protein Gm10320								0.03				0.02
E9PW66	Nucleosome assembly protein 1-like 1	0.05	0.04	0.02		0.03	0.04	0.02	0.02	0.03		0.02	
E9PWG6	Protein Ncapg	0.06	0.05	0.02	0.04	0.03	0.04			0.06	0.10		0.02
E9PY39	Protein Gm20431	0.08	0.04	0.04	0.05	0.04	0.04	0.02	0.02		0.04	0.03	0.06
E9PYH2	Cytosolic acyl coenzyme A thioester hydrolase			0.03				0.02	0.01	0.03		0.04	0.02
E9PYK0	Protein unc-93 homolog B1				0.01	0.02	0.01		0.01	0.02		0.02	0.01
E9PYL9	Protein Gm10036	0.24	0.11	0.13	0.17	0.24	0.11	0.10	0.13		0.15	0.15	0.18
E9Q035	Protein Gm20425	0.12	0.12	0.07	0.09	0.05	0.05	0.05	0.04	0.04	0.12	0.10	0.03
E9Q0F0	Protein Krt78	0.65	0.36	0.57	0.37	0.39	0.39	0.22	0.28	0.29	0.55	0.41	0.24
E9Q1G8	Septin-7												0.01
E9Q2M9	Protein Wdfy4			0.01									0.01
E9Q317	Histone deacetylase complex subunit SAP18				0.02								0.01
E9Q3G8	Protein Nup153		0.05								0.08		
E9Q3X0	Major vault protein	0.10	0.09	0.09	0.06	0.06	0.04	0.04	0.02	0.08	0.30	0.06	0.03
E9Q455	Tropomyosin alpha-1 chain					0.06				0.03			0.01
E9Q481	Serine/threonine-protein phosphatase 4 regulatory subunit 3A									0.01			0.01
E9Q557	Desmoplakin	0.10	0.07	0.19	0.17		0.06	0.04	0.02		0.08	0.09	0.08
E9Q586	Dynactin subunit 1		0.04	0.03	0.05	0.02	0.03	0.02		0.06		0.04	0.03
E9Q5A0	60S ribosomal protein L13a	0.14	0.10	0.08	0.13	0.11	0.05	0.07	0.06	0.08	0.09	0.09	0.21
E9Q616	Protein Ahnak	0.13	0.21	0.18	0.20	0.10	0.10	0.09	0.13	0.09	0.16	0.19	0.06
E9Q634	Unconventional myosin-Ie	0.07		0.03	0.05		0.02		0.02	0.04		0.02	0.06
E9Q7G0	Protein Numa1		0.13							0.01			0.01
E9Q852	Afadin			0.04	0.02		0.03				0.08	0.03	
E9Q912	Protein Rap1gds1											0.02	
E9QAZ2	Ribosomal protein L15	0.04	0.05	0.04	0.04	0.06	0.02	0.02	0.07	0.03		0.03	0.18
E9QB02	Methionine--tRNA ligase, cytoplasmic	0.16	0.14	0.06	0.10	0.05	0.06	0.02		0.08	0.14	0.03	0.06
E9QJS7	Protein Adgre5			0.04	0.04			0.02	0.01			0.03	0.02

E9QK83	Small subunit processome component 20 homolog		0.06										
E9QKR0	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	0.07	0.06	0.07	0.05	0.08	0.04	0.05	0.06	0.07	0.07	0.09	0.09
E9QLA5	Inverted formin-2		0.04										
E9QM99	Dedicator of cytokinesis protein 10		0.04										
E9QMK9	Protein 9030617O03Rik			0.02									
E9QN31	Probable 28S rRNA (cytosine-C(5))-methyltransferase		0.06	0.04	0.05	0.06	0.04	0.02	0.03	0.04	0.10	0.05	0.03
E9QNN1	ATP-dependent RNA helicase A	0.28	0.22	0.22	0.23	0.22	0.12	0.07	0.07	0.33	0.30	0.15	0.12
E9QP00	Transformer-2 protein homolog alpha												0.01
E9QP62	LIM and senescent cell antigen-like-containing domain protein 1												0.01
E9QPD7	Pyruvate carboxylase	0.46	0.26	0.16	0.19	0.12	0.16	0.02	0.01	0.10	0.52	0.08	
E9QPI5	Sister chromatid cohesion protein PDS5 homolog A		0.04	0.02	0.03	0.03	0.01			0.03	0.05		0.01
F2Z456	NADH-cytochrome b5 reductase	0.10		0.09	0.05	0.06	0.05	0.05	0.06	0.03		0.13	0.02
F6UND7	Tyrosine-protein kinase	0.04		0.05	0.01		0.02		0.01		0.04	0.02	0.02
F6VW30	14-3-3 protein theta		0.05	0.06	0.04	0.09	0.04	0.10	0.10	0.08		0.09	0.11
F6YVP7	Protein Gm10260	0.43	0.19	0.26	0.27	0.39	0.21	0.18	0.23		0.29	0.27	0.36
F7A6H4	E3 ubiquitin-protein ligase RNF213		0.08										0.01
F7C846	Metaxin-1		0.06	0.02	0.03	0.03	0.02		0.02	0.02			0.01
F7DEU6	Inosine-5'-monophosphate dehydrogenase			0.04	0.02		0.02	0.01		0.01		0.02	
F8VPK0	Protein Ttc37			0.02	0.01		0.01						0.01
F8VQC1	Signal recognition particle subunit SRP72		0.05	0.03	0.01		0.02			0.02	0.06		
F8WGM5	Syntaxin-binding protein 2		0.05	0.03	0.02		0.03	0.02	0.01	0.03		0.02	0.01
F8WH69	Neutrophil cytosol factor 1	0.10	0.10	0.04	0.04	0.02	0.04	0.02		0.02	0.09	0.03	0.04
F8WHQ1	Tumor protein D52											0.02	
F8WIJ0	Solute carrier family 12 member 4			0.02									
F8WIV2	Serpin B6	0.11	0.07	0.09	0.06	0.06	0.03	0.07	0.03	0.11		0.13	0.07
F8WIV5	Dynamin-2	0.08	0.07	0.05	0.03	0.04	0.02	0.02		0.06		0.03	0.03
F8WJA0	ATP-dependent RNA helicase DDX24		0.04								0.07		
F8WJA1	FXYD domain-containing ion transport regulator 5								0.01				
F8WJD4	Symplekin	0.03	0.06	0.02	0.01		0.03			0.03	0.06		0.01
F8WJE0	Deoxynucleoside triphosphate triphosphohydrolase SAMHD1		0.03				0.01			0.01			0.01
G3UWS4	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform			0.02	0.02	0.02				0.03		0.02	0.04
G3UXA6	Polypyrimidine tract-binding protein 3		0.07	0.07	0.07	0.06	0.07	0.03	0.03	0.07	0.05	0.05	0.05
G3UXL2	Protein Prps1l3		0.07	0.07	0.10	0.14	0.05	0.05	0.04	0.13	0.05	0.09	0.07
G3UXW9	COP9 signalosome complex subunit 1		0.04	0.03	0.01	0.02	0.01	0.02		0.02		0.03	0.01
G3X8R0	Receptor expression-enhancing protein								0.03				0.02
G3X8T3	Carboxypeptidase						0.01	0.02	0.02				0.01
G3X8Y3	N-alpha-acetyltransferase 15, NatA auxiliary subunit		0.05	0.02	0.03	0.02	0.01		0.01	0.04			0.02
G3X8Y8	Toll-like receptor		0.03	0.01	0.01	0.02				0.02	0.05	0.02	
G3X914	Cullin 5												0.01
G3X956	FACT complex subunit SPT16		0.12	0.03	0.02	0.03	0.04	0.02		0.05	0.19	0.02	
G3X972	Protein Sec24c		0.05					0.01		0.01	0.05		
G3X9B1	HEAT repeat containing 1			0.02	0.01								
G3X9M0	28S ribosomal protein S29, mitochondrial	0.10	0.05	0.03	0.04		0.03	0.01	0.01	0.03		0.02	0.01
G3X9Q3	Histocompatibility (Minor) HA-1, isoform CRA_a		0.04	0.02	0.03		0.01						0.01
G3XA48	Isopentenyl-diphosphate Delta-isomerase 1				0.01	0.02	0.02			0.02			0.02
G4V4Z1	Gag-pro-pol polyprotein			0.02	0.02				0.01			0.02	
G5E829	Plasma membrane calcium-transporting ATPase 1	0.08	0.10	0.05	0.05	0.03	0.03	0.03	0.03	0.04	0.12	0.06	0.02
G5E866	Splicing factor 3B subunit 1	0.07	0.07	0.06	0.05	0.05	0.02	0.01	0.02	0.05	0.07	0.04	0.04

G5E896	Enhancer of mRNA decapping 4, isoform CRA_b		0.05								0.08		
G5E8U5	28S ribosomal protein S10, mitochondrial												0.03
H3BJW3	Cleavage and polyadenylation-specificity factor subunit 6		0.04	0.02	0.02	0.02	0.02				0.04		
I1E4X5	Protein 9030624J02Rik		0.03										
I7DM66	PexRAP	0.06	0.04	0.09	0.04	0.04	0.03	0.04	0.02	0.03		0.07	0.01
J3QMG3	Voltage-dependent anion-selective channel protein 3	0.14	0.15	0.13	0.08	0.17	0.08	0.09	0.06	0.19	0.16	0.15	0.09
J3QN31	Adenylosuccinate synthetase isozyme 1			0.01		0.07	0.02	0.03	0.02	0.07		0.04	0.06
J9RV59	Anion exchange protein			0.02									
M1VMF6	Metastasis-associated protein MTA1 isoform 9									0.01			
O08528	Hexokinase-2	0.16	0.17	0.15	0.15	0.08	0.07	0.10	0.08	0.16	0.25	0.14	0.16
O08529	Calpain-2 catalytic subunit												0.01
O08547	Vesicle-trafficking protein SEC22b	0.16	0.15	0.10	0.15	0.09	0.10	0.03	0.06	0.08	0.16	0.07	0.12
O08553	Dihydropyrimidinase-related protein 2								0.01	0.01			0.01
O08582	GTP-binding protein 1	0.04	0.04		0.01		0.01			0.02	0.08		
O08599	Syntaxin-binding protein 1			0.03								0.02	
O08734	Bcl-2 homologous antagonist/killer			0.02	0.02	0.03	0.01	0.01	0.01	0.02		0.03	
O08749	Dihydrolipoyl dehydrogenase, mitochondrial	0.08	0.09	0.07	0.07	0.07	0.02	0.05	0.07	0.06	0.06	0.07	0.07
O08756	3-hydroxyacyl-CoA dehydrogenase type-2	0.11	0.12	0.09	0.17	0.09	0.10	0.03	0.05	0.10	0.15	0.09	0.07
O09061	Proteasome subunit beta type-1												0.01
O09131	Glutathione S-transferase omega-1			0.02						0.02			
O09167	60S ribosomal protein L21		0.08	0.04	0.05	0.03	0.02	0.02	0.05		0.08	0.05	0.12
O09172	Glutamate--cysteine ligase regulatory subunit			0.02			0.02						0.01
O35075	Down syndrome critical region protein 3 homolog		0.05	0.02						0.02			
O35134	DNA-directed RNA polymerase I subunit RPA1										0.06		
O35218	Cleavage and polyadenylation specificity factor subunit 2					0.02				0.02			
O35295	Transcriptional activator protein Pur-beta		0.04		0.02		0.02			0.02			
O35379	Multidrug resistance-associated protein 1			0.02	0.02				0.02			0.02	
O35593	26S proteasome non-ATPase regulatory subunit 14	0.10	0.10	0.09	0.07	0.07	0.06	0.05	0.05	0.07	0.08	0.07	0.06
O35604	Niemann-Pick C1 protein			0.02			0.01	0.01		0.01		0.02	
O35685	Nuclear migration protein nudC			0.02								0.02	
O35704	Serine palmitoyltransferase 1			0.02									
O35841	Apoptosis inhibitor 5		0.08	0.02	0.03		0.02	0.02		0.01	0.11	0.02	0.01
O35857	Mitochondrial import inner membrane translocase subunit TIM44			0.04	0.02		0.01	0.04	0.02	0.04		0.04	0.02
O35864	COP9 signalosome complex subunit 5	0.04		0.02		0.02	0.01	0.01	0.01	0.02			0.01
O35972	39S ribosomal protein L23, mitochondrial			0.01	0.04		0.01		0.00				0.08
O54734	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	0.14	0.10	0.18	0.16	0.16	0.08	0.13	0.12	0.14	0.10	0.21	0.09
O54752	Naglu			0.03		0.02	0.01	0.04		0.02		0.05	
O54774	AP-3 complex subunit delta-1									0.01			
O54946	DnaJ homolog subfamily B member 6			0.01									
O54984	ATPase Asna1			0.05	0.05	0.03	0.07	0.04	0.01	0.06		0.07	
O54988	STE20-like serine/threonine-protein kinase	0.06	0.04							0.02	0.07	0.02	0.01
O55013	Trafficking protein particle complex subunit 3			0.02	0.01			0.01					0.02
O55022	Membrane-associated progesterone receptor component 1			0.02	0.03			0.02	0.01			0.03	
O55029	Coatomer subunit beta'		0.04	0.03	0.02	0.02		0.02			0.05	0.03	
O55100	Synaptogyrin-1			0.04	0.03	0.04	0.01	0.03	0.02			0.04	0.02
O55142	60S ribosomal protein L35a						0.01		0.09				0.13
O55201	Transcription elongation factor SPT5		0.04				0.01						

O55234	Proteasome subunit beta type-5					0.02							0.02
O70145	Neutrophil cytosol factor 2		0.05	0.05	0.04	0.02	0.02	0.03		0.07	0.04	0.06	0.02
O70152	Dolichol-phosphate mannosyltransferase subunit 1	0.04	0.04	0.03	0.06		0.02		0.01	0.02		0.02	0.02
O70194	Eukaryotic translation initiation factor 3 subunit D		0.03	0.02	0.03		0.02		0.01	0.03		0.02	0.02
O70251	Elongation factor 1-beta	0.04	0.07	0.03	0.02	0.03	0.02	0.02	0.02	0.03		0.04	0.04
O70252	Heme oxygenase 2			0.02			0.01	0.01		0.02			
O70404	Vesicle-associated membrane protein 8								0.02				0.02
O70439	Syntaxin-7		0.04	0.02		0.02	0.03	0.02		0.01		0.03	
O70469	Docking protein 2			0.05	0.04			0.02	0.02			0.05	0.03
O70480	Vesicle-associated membrane protein 4								0.01				
O70492	Sorting nexin-3						0.01						0.02
O70499	Small nuclear ribonucleoprotein-associated protein		0.06	0.01	0.03		0.02			0.01	0.04	0.02	0.01
O70503	Very-long-chain 3-oxoacyl-CoA reductase	0.07	0.10	0.08	0.12	0.06	0.04	0.02	0.06	0.06	0.05	0.07	0.10
O70569	Ribosomal protein S14		0.09	0.15	0.13	0.09	0.10	0.10	0.08		0.13	0.12	0.16
O88384	Vesicle transport through interaction with t-SNAREs homolog 1B			0.02				0.02				0.03	
O88441	Metaxin-2			0.03	0.05	0.04	0.02	0.01	0.01	0.03		0.03	0.01
O88456	Calpain small subunit 1			0.04	0.04		0.02	0.04	0.01			0.05	0.01
O88543	COP9 signalosome complex subunit 3		0.03	0.02				0.01				0.02	0.01
O88569	Heterogeneous nuclear ribonucleoproteins A2/B1	0.18	0.17	0.12	0.16	0.20	0.15	0.07	0.06	0.19	0.13	0.12	0.16
O88587	Catechol O-methyltransferase				0.03	0.02		0.02	0.02	0.02		0.04	0.02
O88696	ATP-dependent Clp protease proteolytic subunit, mitochondrial		0.05	0.01	0.06		0.03		0.01			0.02	0.01
O88738	Baculoviral IAP repeat-containing protein 6		0.04							0.02			
O88783	Coagulation factor V			0.03				0.02	0.01			0.04	
O88796	Ribonuclease P protein subunit p30											0.02	0.01
O88952	Protein lin-7 homolog C						0.01	0.02					
O88967	ATP-dependent zinc metalloprotease YME1L1		0.05		0.02		0.01						0.01
O88986	2-amino-3-ketobutyrate coenzyme A ligase, mitochondrial		0.04		0.04		0.01			0.02			
O89017	Legumain		0.03	0.05	0.04	0.06	0.05	0.02	0.02	0.05		0.03	0.02
O89023	Tripeptidyl-peptidase 1							0.02					
O89079	Coatomer subunit epsilon	0.07	0.04	0.03		0.02	0.02			0.02		0.02	0.02
P00375	Dihydrofolate reductase				0.01	0.03			0.01				0.03
P00493	Hypoxanthine-guanine phosphoribosyltransferase								0.01				0.01
P00920	Carbonic anhydrase 2					0.04			0.01	0.03		0.02	0.05
P01887	Beta-2-microglobulin								0.01				0.01
P01897	H-2 class I histocompatibility antigen, L-D alpha chain		0.04	0.06	0.02	0.03	0.02	0.05	0.03	0.03		0.07	0.03
P01900	H-2 class I histocompatibility antigen, D-D alpha chain		0.04	0.07	0.04	0.04	0.03	0.06	0.04	0.03		0.08	0.03
P05132	cAMP-dependent protein kinase catalytic subunit alpha		0.03	0.03	0.01		0.01	0.02		0.03		0.03	0.01
P05202	Aspartate aminotransferase, mitochondrial			0.02	0.03	0.19	0.03	0.03	0.24	0.17		0.08	0.30
P06745	Glucose-6-phosphate isomerase		0.09	0.02	0.03	0.28	0.02	0.18	0.20	0.27	0.05	0.25	0.35
P06804	Tumor necrosis factor			0.06	0.01			0.05				0.08	
P08003	Protein disulfide-isomerase A4			0.06	0.03	0.09	0.02	0.13	0.13	0.05		0.13	0.08
P08030	Adenine phosphoribosyltransferase				0.03	0.08		0.03	0.04			0.02	0.11
P08249	Malate dehydrogenase, mitochondrial		0.04	0.05	0.07	0.38	0.10	0.17	0.18	0.17		0.31	0.24
P08752	Guanine nucleotide-binding protein G(i) subunit alpha-2	0.32	0.23	0.21	0.28	0.20	0.16	0.16	0.17	0.27	0.26	0.25	0.19
P08775	DNA-directed RNA polymerase II subunit RPB1		0.03										
P09055	Integrin beta-1			0.02				0.02				0.02	
P09103	Protein disulfide-isomerase			0.02		0.04		0.10	0.16	0.01		0.10	0.08
P09405	Nucleolin	0.25	0.24	0.15	0.17	0.23	0.12	0.04	0.03	0.22	0.29	0.12	0.04

P09411	Phosphoglycerate kinase 1			0.08		0.38	0.01	0.32	0.57	0.31		0.39	0.60
P09450	Transcription factor jun-B			0.01									
P10605	Cathepsin B		0.05	0.03	0.04		0.03			0.03			
P10639	Thioredoxin								0.04				0.05
P10833	Ras-related protein R-Ras						0.02	0.01		0.02			0.01
P10852	4F2 cell-surface antigen heavy chain	0.06	0.06	0.12	0.10	0.13	0.07	0.10	0.13	0.11	0.11	0.14	0.06
P11152	Lipoprotein lipase				0.03				0.02				0.02
P11440	Cyclin-dependent kinase 1	0.10	0.08	0.04	0.02	0.04	0.04	0.01	0.02	0.03	0.10	0.02	0.03
P11499	Heat shock protein HSP 90-beta	1.31	0.96	1.06	1.09	1.42	0.83	1.05	0.85	1.80	1.57	1.37	1.12
P11688	Integrin alpha-5											0.02	
P11835	Integrin beta-2		0.05	0.36	0.20	0.06	0.04	0.31	0.16	0.04	0.07	0.38	0.04
P11983	T-complex protein 1 subunit alpha	0.38	0.33	0.19	0.19	0.38	0.14	0.24	0.16	0.34	0.34	0.28	0.29
P12382	ATP-dependent 6-phosphofructokinase, liver type	0.19	0.11	0.12	0.08	0.02	0.06	0.04	0.04	0.08	0.16	0.11	0.09
P12787	Cytochrome c oxidase subunit 5A, mitochondrial								0.01				0.02
P12815	Programmed cell death protein 6												0.03
P13020	Gelsolin					0.02		0.03		0.04		0.02	0.01
P14115	60S ribosomal protein L27a	0.15	0.04	0.10	0.09	0.08	0.07	0.08	0.05		0.08	0.09	0.13
P14148	60S ribosomal protein L7	0.25	0.22	0.23	0.25	0.27	0.12	0.15	0.20	0.23	0.15	0.24	0.40
P14152	Malate dehydrogenase, cytoplasmic					0.02			0.01				0.04
P14211	Calreticulin							0.02	0.02	0.01		0.02	0.01
P14234	Tyrosine-protein kinase Fgr		0.03	0.05	0.04		0.02	0.01	0.02			0.04	0.03
P14576	Signal recognition particle 54 kDa protein			0.02				0.02				0.02	
P14685	26S proteasome non-ATPase regulatory subunit 3	0.09	0.12	0.09	0.11	0.06	0.06	0.04	0.03	0.08	0.10	0.08	0.08
P14733	Lamin-B1	0.18	0.16	0.06	0.03	0.04	0.06			0.02	0.14		
P14824	Annexin A6			0.03				0.02		0.02		0.03	
P15532	Nucleoside diphosphate kinase A					0.03			0.02				0.04
P16045	Galectin-1								0.03				0.03
P16110	Galectin-3			0.10	0.02	0.09	0.06	0.05	0.03	0.08		0.09	0.01
P17426	AP-2 complex subunit alpha-1		0.07	0.03	0.04	0.04	0.02	0.02	0.01	0.07	0.11	0.06	0.04
P17439	Glucosylceramidase			0.04					0.01			0.05	
P17710	Hexokinase-1	0.04	0.03	0.05	0.04	0.03	0.02	0.05	0.10	0.04	0.05	0.07	0.10
P17742	Peptidyl-prolyl cis-trans isomerase A					0.09		0.03	0.09	0.03			0.19
P17751	Triosephosphate isomerase	0.07	0.06	0.08	0.09	0.15	0.08	0.11	0.23	0.06		0.12	0.23
P17809	Solute carrier family 2, facilitated glucose transporter member 1			0.18	0.13		0.01	0.14	0.16			0.17	0.09
P17879	Heat shock 70 kDa protein 1B	0.15	0.08	0.07	0.09	0.10	0.06	0.11	0.10	0.06	0.11	0.14	0.09
P17918	Proliferating cell nuclear antigen	0.45	0.38	0.23	0.28	0.39	0.27	0.18	0.18	0.44	0.40	0.27	0.18
P18155	Bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase, mitochondrial	0.04	0.04	0.03	0.06	0.03	0.03	0.01		0.03	0.05	0.03	
P18572	Basigin			0.14	0.08	0.04	0.02	0.12	0.11	0.04		0.13	0.03
P18760	Cofilin-1	0.34	0.19	0.29	0.25	0.57	0.31	0.33	0.93	0.21	0.25	0.39	0.83
P19096	Fatty acid synthase	0.45	0.37	0.38	0.26	0.29	0.16	0.29	0.09	0.73	0.70	0.46	0.42
P20029	78 kDa glucose-regulated protein	0.57	0.48	0.34	0.41	0.44	0.28	0.42	0.66	0.26	0.80	0.59	0.47
P20108	Thioredoxin-dependent peroxide reductase, mitochondrial			0.03	0.05	0.12	0.05	0.07	0.08	0.07	0.05	0.07	0.10
P21279	Guanine nucleotide-binding protein G(q) subunit alpha			0.03			0.01	0.02	0.01	0.02		0.04	
P21619	Lamin-B2		0.03	0.02			0.01						
P22437	Prostaglandin G/H synthase 1			0.03				0.02				0.02	0.01
P23116	Eukaryotic translation initiation factor 3 subunit A	0.21	0.20	0.20	0.21	0.17	0.15	0.10	0.08	0.31	0.29	0.17	0.20
P24527	Leukotriene A-4 hydrolase									0.01			0.02
P24547	Inosine-5'-monophosphate dehydrogenase 2			0.01	0.02			0.01		0.01		0.02	0.01
P24668	Cation-dependent mannose-6-phosphate receptor	0.05	0.07	0.10	0.07		0.04	0.05	0.01	0.03		0.09	

P25206	DNA replication licensing factor MCM3	0.08	0.12	0.02	0.02	0.07	0.05			0.09	0.13		0.01
P25444	40S ribosomal protein S2	0.32	0.27	0.27	0.28	0.27	0.16	0.21	0.17	0.27	0.25	0.28	0.28
P26041	Moesin			0.05	0.01	0.13		0.10	0.07	0.08		0.12	0.12
P26443	Glutamate dehydrogenase 1, mitochondrial	0.05	0.07	0.12		0.02		0.09	0.01	0.03	0.06	0.12	0.04
P26516	26S proteasome non-ATPase regulatory subunit 7		0.05	0.07	0.07	0.05	0.04	0.04	0.01	0.06	0.04	0.07	0.02
P27046	Alpha-mannosidase 2			0.02	0.02							0.02	0.01
P27601	Guanine nucleotide-binding protein subunit alpha-13		0.04	0.05	0.06	0.07	0.04	0.04	0.05	0.10		0.08	0.04
P27612	Phospholipase A-2-activating protein		0.05				0.02				0.10		
P27659	60S ribosomal protein L3	0.13	0.18	0.22	0.16	0.14	0.11	0.14	0.11	0.12	0.17	0.19	0.26
P27773	Protein disulfide-isomerase A3		0.08	0.23	0.08	0.27	0.07	0.45	0.55	0.16	0.12	0.56	0.39
P28658	Ataxin-10	0.05	0.04	0.02	0.02		0.03			0.02	0.07	0.02	0.01
P29341	Polyadenylate-binding protein 1	0.07	0.06	0.03	0.04	0.02	0.02		0.01	0.02	0.07	0.02	0.03
P29391	Ferritin light chain 1					0.02							
P29452	Caspase-1	0.04	0.03	0.03			0.01			0.02			
P30355	Arachidonate 5-lipoxygenase-activating protein			0.03	0.05	0.04		0.04	0.05			0.04	0.07
P30416	Peptidyl-prolyl cis-trans isomerase FKBP4		0.03	0.02	0.02	0.04	0.02	0.03	0.02	0.05		0.04	0.03
P30993	C5a anaphylatoxin chemotactic receptor 1			0.02	0.02				0.01				0.01
P31938	Dual specificity mitogen-activated protein kinase kinase 1		0.05	0.03	0.05		0.01	0.02		0.02		0.03	0.02
P31996	Macrosialin			0.03		0.04	0.03	0.02	0.01	0.03		0.04	
P32067	Lupus La protein homolog		0.02	0.03	0.02	0.04	0.02	0.03	0.01	0.03		0.04	0.01
P32921	Tryptophan--tRNA ligase, cytoplasmic		0.08	0.01	0.02	0.04	0.02	0.04	0.01	0.02	0.10	0.02	0.05
P33175	Kinesin heavy chain isoform 5A		0.03	0.07	0.07	0.03	0.04	0.04	0.01	0.07	0.10	0.05	0.01
P34022	Ran-specific GTPase-activating protein		0.05	0.02	0.03	0.05	0.03	0.03	0.04	0.05		0.03	0.06
P34884	Macrophage migration inhibitory factor								0.01				0.02
P35123	Ubiquitin carboxyl-terminal hydrolase 4		0.03										
P35276	Ras-related protein Rab-3D	0.05		0.02	0.02	0.07	0.02	0.04	0.04	0.03		0.04	0.03
P35279	Ras-related protein Rab-6A	0.13	0.07	0.07	0.10	0.16	0.07	0.09	0.06	0.11	0.07	0.09	0.09
P35293	Ras-related protein Rab-18	0.06	0.04	0.04	0.06	0.05	0.04	0.03	0.02	0.05		0.05	0.04
P35456	Urokinase plasminogen activator surface receptor											0.02	
P35486	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial			0.05	0.04	0.06		0.06	0.07	0.05	0.04	0.10	0.03
P35550	rRNA 2'-O-methyltransferase fibrillarin	0.08	0.07	0.07	0.06	0.07	0.05	0.02	0.02	0.05	0.08	0.03	0.04
P35585	AP-1 complex subunit mu-1			0.04	0.02	0.02	0.01			0.02		0.02	0.01
P35700	Peroxiredoxin-1	0.41	0.27	0.22	0.37	0.73	0.26	0.31	0.34	0.29	0.38	0.40	0.29
P35979	60S ribosomal protein L12	0.15	0.10	0.05	0.11	0.15	0.06	0.04	0.22		0.12	0.06	0.26
P37040	NADPH--cytochrome P450 reductase			0.06	0.03		0.01	0.04	0.03			0.06	0.05
P38060	Hydroxymethylglutaryl-CoA lyase, mitochondrial	0.09	0.11	0.04	0.08	0.06	0.04	0.02	0.03	0.06	0.08	0.06	0.02
P38647	Stress-70 protein, mitochondrial	0.33	0.33	0.35	0.38	0.59	0.20	0.39	0.37	0.34	0.40	0.54	0.25
P40124	Adenylyl cyclase-associated protein 1		0.05	0.03				0.05	0.01			0.06	0.01
P40142	Transketolase			0.02	0.01	0.35		0.11	0.17	0.22		0.14	0.42
P40240	CD9 antigen			0.02				0.02				0.03	
P40336	Vacuolar protein sorting-associated protein 26A	0.05	0.08	0.01	0.04	0.02	0.04	0.02	0.01	0.04	0.07	0.04	0.02
P40630	Transcription factor A, mitochondrial					0.02		0.01					0.01
P41105	60S ribosomal protein L28	0.10	0.05	0.10	0.09	0.10	0.06	0.06	0.07		0.08	0.08	0.17
P41241	Tyrosine-protein kinase CSK		0.04		0.02								
P42125	Enoyl-CoA delta isomerase 1, mitochondrial	0.06	0.08	0.06	0.11	0.09	0.06	0.04	0.06	0.08		0.08	0.05
P42208	Septin-2												0.01
P42669	Transcriptional activator protein Pur-alpha			0.03		0.03	0.01			0.03			
P43247	DNA mismatch repair protein Msh2		0.04				0.02			0.01	0.09		
P43274	Histone H1.4	0.13	0.11	0.13	0.27	0.23	0.10	0.10	0.32	0.12	0.12	0.15	0.13
P43275	Histone H1.1		0.04	0.02	0.08	0.06	0.02	0.01	0.11	0.03		0.03	0.01

P45376	Aldose reductase				0.02	0.05		0.02	0.05			0.02	0.08
P45952	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial		0.06	0.09	0.04	0.03	0.02	0.04	0.04	0.09	0.04	0.06	0.02
P46460	Vesicle-fusing ATPase	0.10	0.12	0.13	0.08	0.05	0.07	0.04	0.02	0.06	0.11	0.06	0.06
P46664	Adenylosuccinate synthetase isozyme 2					0.02		0.03	0.01	0.01		0.04	0.03
P46737	Lys-63-specific deubiquitinase BRCC36		0.04	0.02	0.01							0.02	
P47226	Testin			0.02	0.02		0.01					0.02	
P47713	Cytosolic phospholipase A2	0.14	0.12	0.16	0.12	0.08	0.08	0.09	0.08	0.11	0.35	0.16	0.07
P47738	Aldehyde dehydrogenase, mitochondrial		0.04	0.10	0.07	0.13	0.02	0.11	0.23	0.04		0.13	0.09
P47811	Mitogen-activated protein kinase 14			0.02						0.01			
P47856	Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1	0.11	0.13	0.13	0.10		0.03				0.15	0.04	0.04
P47911	60S ribosomal protein L6	0.36	0.30	0.29	0.41	0.41	0.18	0.24	0.35	0.41	0.30	0.34	0.76
P47962	60S ribosomal protein L5	0.47	0.35	0.24	0.20	0.24	0.12	0.13	0.23	0.20	0.34	0.25	0.37
P47963	60S ribosomal protein L13	0.26	0.19	0.30	0.46	0.39	0.27	0.20	0.30	0.29	0.26	0.30	0.35
P48036	Annexin A5	0.12	0.16	0.42	0.34	0.37	0.16	0.34	0.15	0.44	0.08	0.67	0.33
P48678	Prelamin-A/C	0.32	0.42	0.17	0.14	0.08	0.10		0.01	0.05	0.41	0.04	0.01
P48722	Heat shock 70 kDa protein 4L			0.03	0.02		0.01	0.01	0.03	0.01		0.03	0.03
P48962	ADP/ATP translocase 1	0.25	0.23	0.29	0.51	0.38	0.29	0.20	0.33	0.29	0.23	0.31	0.61
P48999	Arachidonate 5-lipoxygenase			0.07	0.03			0.03	0.02			0.07	0.02
P50247	Adenosylhomocysteinase		0.05			0.12	0.01	0.08	0.06	0.13	0.07	0.03	0.08
P50431	Serine hydroxymethyltransferase, cytosolic	0.07	0.03	0.06	0.11	0.07	0.06	0.04	0.04	0.08		0.07	0.06
P50516	V-type proton ATPase catalytic subunit A	0.17	0.18	0.16	0.11	0.08	0.08	0.09	0.07	0.11	0.17	0.15	0.05
P50518	V-type proton ATPase subunit E 1	0.05	0.06	0.11	0.06	0.03	0.05	0.10	0.05	0.06		0.11	0.03
P50544	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial	0.04	0.07	0.07	0.08	0.02	0.02	0.01		0.03		0.05	0.01
P51150	Ras-related protein Rab-7a	0.28	0.14	0.11	0.11	0.33	0.14	0.12	0.11	0.28	0.17	0.19	0.11
P51174	Long-chain specific acyl-CoA dehydrogenase, mitochondrial	0.07	0.07	0.09	0.06	0.03	0.02	0.04	0.02	0.06		0.08	0.03
P51660	Peroxisomal multifunctional enzyme type 2	0.80	0.42	1.03	0.67	0.71	0.47	0.65	0.35	0.77	0.47	1.06	0.17
P51863	V-type proton ATPase subunit d 1	0.10	0.11	0.13	0.20	0.13	0.14	0.11	0.11	0.15	0.06	0.16	0.11
P51881	ADP/ATP translocase 2	0.44	0.31	0.50	0.62	0.56	0.45	0.32	0.57	0.46	0.37	0.48	0.95
P52431	DNA polymerase delta catalytic subunit		0.04				0.01						0.01
P52480	Pyruvate kinase PKM	0.94	1.04	0.88	1.16	2.17	0.82	1.35	1.84	1.51	1.05	1.33	2.36
P52875	Transmembrane protein 165												0.01
P53395	Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial									0.01			0.01
P53986	Monocarboxylate transporter 1	0.09	0.10	0.05	0.07	0.03	0.05	0.05	0.08	0.03	0.08	0.07	0.04
P54071	Isocitrate dehydrogenase [NADP], mitochondrial	0.15	0.11	0.11	0.07	0.13	0.04	0.09	0.08	0.12	0.13	0.13	0.12
P54103	DnaJ homolog subfamily C member 2			0.02						0.03			
P54116	Erythrocyte band 7 integral membrane protein	0.26	0.29	0.38	0.47	0.37	0.23	0.25	0.32	0.28	0.24	0.45	0.24
P54276	DNA mismatch repair protein Msh6		0.06	0.02	0.01	0.03	0.02			0.04	0.11		
P54775	26S protease regulatory subunit 6B	0.07	0.07	0.06	0.04	0.03	0.02	0.03	0.02	0.05		0.04	0.03
P54823	Probable ATP-dependent RNA helicase DDX6		0.05	0.04	0.05		0.03	0.02	0.01	0.03		0.04	0.01
P54923	[Protein ADP-ribosylarginine] hydrolase	0.08	0.08		0.02		0.03			0.02			
P56399	Ubiquitin carboxyl-terminal hydrolase 5				0.01	0.03	0.03	0.04		0.05		0.05	0.02
P56477	Interferon regulatory factor 5			0.02				0.01				0.03	
P56480	ATP synthase subunit beta, mitochondrial	1.50	1.19	1.41	1.49	1.18	1.03	0.83	0.96	1.05	1.26	1.21	1.07
P57746	V-type proton ATPase subunit D			0.02	0.01			0.02		0.03		0.02	0.01
P57759	Endoplasmic reticulum resident protein 29			0.01		0.05	0.01	0.03	0.01	0.02		0.02	
P57784	U2 small nuclear ribonucleoprotein A'	0.06	0.07	0.06	0.06	0.09	0.07	0.04	0.04	0.08	0.05	0.07	0.03

P58252	Elongation factor 2	0.05	0.11	0.16	0.13	0.53	0.10	0.44	0.39	0.46	0.17	0.36	0.41
P58389	Serine/threonine-protein phosphatase 2A activator									0.02		0.02	0.01
P58742	Aladin		0.03	0.02	0.02								
P59325	Eukaryotic translation initiation factor 5			0.02									0.01
P59708	Splicing factor 3B subunit 6												0.04
P59999	Actin-related protein 2/3 complex subunit 4			0.03	0.02	0.08	0.01	0.04	0.06			0.04	0.12
P60122	RuvB-like 1	0.15	0.14	0.14	0.12	0.16	0.05	0.09	0.10	0.13	0.10	0.12	0.11
P60335	Poly(rC)-binding protein 1	0.58	0.46	0.19	0.27	0.20	0.28	0.14	0.12	0.30	0.42	0.21	0.18
P60766	Cell division control protein 42 homolog	0.05	0.03	0.08	0.09	0.18	0.07	0.08	0.07		0.05	0.08	0.08
P60843	Eukaryotic initiation factor 4A-I	1.06	0.72	0.47	0.40	0.46	0.39	0.34	0.23	0.56	0.87	0.51	0.39
P61022	Calcineurin B homologous protein 1				0.04								
P61082	NEDD8-conjugating enzyme Ubc12								0.01				0.02
P61089	Ubiquitin-conjugating enzyme E2 N			0.02	0.03		0.03	0.02	0.03			0.04	0.07
P61161	Actin-related protein 2	0.06	0.05	0.03	0.01	0.03	0.03	0.04	0.05	0.04		0.06	0.06
P61164	Alpha-centractin	0.03		0.03	0.05	0.07	0.03	0.06	0.06	0.08		0.05	0.06
P61211	ADP-ribosylation factor-like protein 1												0.03
P61222	ATP-binding cassette sub-family E member 1		0.06		0.03	0.06	0.02	0.05	0.03	0.07		0.07	0.07
P61226	Ras-related protein Rap-2b			0.02		0.07	0.02		0.02			0.03	0.04
P61255	60S ribosomal protein L26	0.17	0.07	0.16	0.17	0.19	0.09	0.09	0.12		0.11	0.16	0.23
P61290	Proteasome activator complex subunit 3		0.03	0.02	0.02	0.02	0.01	0.01	0.01	0.03		0.03	0.02
P61620	Protein transport protein Sec61 subunit alpha isoform 1	0.06	0.05	0.05	0.05	0.03	0.04	0.03	0.02	0.02		0.03	0.04
P61750	ADP-ribosylation factor 4	0.15	0.08	0.09	0.15	0.15	0.10	0.05	0.05		0.11	0.10	0.17
P61967	AP-1 complex subunit sigma-1A						0.01						0.01
P62137	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit		0.07	0.05	0.06	0.06	0.03	0.03	0.02	0.07	0.05	0.06	0.09
P62196	26S protease regulatory subunit 8	0.27	0.21	0.14	0.13	0.07	0.10	0.07	0.03	0.08	0.18	0.13	0.06
P62301	40S ribosomal protein S13	0.19	0.08	0.17	0.19	0.22	0.10	0.09	0.07		0.11	0.15	0.12
P62320	Small nuclear ribonucleoprotein Sm D3				0.02		0.01	0.02	0.03			0.02	0.03
P62334	26S protease regulatory subunit 10B	0.16	0.15	0.14	0.10	0.06	0.07	0.08	0.03	0.13		0.12	0.06
P62340	TATA box-binding protein-like protein 1												0.01
P62342	Selenoprotein T												0.01
P62717	60S ribosomal protein L18a	0.11	0.03	0.04	0.09	0.07	0.03	0.02	0.06		0.06	0.04	0.18
P62743	AP-2 complex subunit sigma												0.02
P62814	V-type proton ATPase subunit B, brain isoform	0.14	0.11	0.12	0.10	0.10	0.09	0.09	0.07	0.12	0.11	0.14	0.10
P62827	GTP-binding nuclear protein Ran	0.32	0.18	0.16	0.22	0.29	0.15	0.16	0.14	0.22	0.23	0.18	0.20
P62830	60S ribosomal protein L23				0.16		0.11	0.07	0.07			0.09	0.17
P62843	40S ribosomal protein S15			0.04	0.06	0.03		0.02	0.04			0.04	0.05
P62852	40S ribosomal protein S25			0.09	0.10	0.14	0.06	0.08	0.07		0.05	0.11	0.05
P62855	40S ribosomal protein S26		0.04	0.02	0.09		0.05	0.05	0.04			0.08	0.11
P62889	60S ribosomal protein L30				0.17		0.12	0.09	0.20			0.09	0.29
P62911	60S ribosomal protein L32	0.13	0.07	0.12	0.13	0.08	0.06	0.09	0.05	0.06	0.09	0.12	0.18
P62918	60S ribosomal protein L8	0.17	0.14	0.14	0.14	0.20	0.10	0.08	0.14	0.13	0.17	0.15	0.26
P62960	Nuclease-sensitive element-binding protein 1		0.09				0.01						
P62962	Profilin-1								0.10				0.18
P63005	Platelet-activating factor acetylhydrolase IB subunit alpha												0.01
P63017	Heat shock cognate 71 kDa protein	0.79	0.47	0.34	0.35	0.47	0.26	0.38	0.40	0.25	0.50	0.47	0.33
P63037	DnaJ homolog subfamily A member 1	0.04	0.05	0.04	0.01		0.03			0.02		0.02	0.01
P63038	60 kDa heat shock protein, mitochondrial	0.48	0.59	0.73	0.61	0.55	0.48	0.57	0.41	0.59	0.56	0.75	0.44
P63101	14-3-3 protein zeta/delta	0.05	0.04	0.04	0.05	0.09	0.03	0.10	0.12	0.08		0.09	0.17
P63242	Eukaryotic translation initiation factor 5A-1								0.02				0.01

P63330	Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform	0.07	0.07	0.03	0.03	0.04	0.01	0.02	0.06	0.04	0.07	0.04	0.12
P67778	Prohibitin	0.35	0.28	0.34	0.37	0.50	0.31	0.25	0.26	0.43	0.27	0.42	0.44
P68040	Guanine nucleotide-binding protein subunit beta-2-like 1	0.45	0.40	0.42	0.21	0.25	0.14	0.15	0.13	0.25	0.38	0.35	0.34
P68181	cAMP-dependent protein kinase catalytic subunit beta			0.03				0.02		0.02		0.04	0.01
P68510	14-3-3 protein eta			0.05	0.04	0.08	0.03	0.09	0.10	0.06		0.08	0.12
P70122	Ribosome maturation protein SBDS									0.02		0.02	0.01
P70168	Importin subunit beta-1	0.16	0.13	0.20	0.14	0.15	0.07	0.14	0.18	0.21	0.22	0.19	0.17
P70245	3-beta-hydroxysteroid-Delta(8),Delta(7)-isomerase												0.01
P70288	Histone deacetylase 2		0.04			0.02	0.01			0.02			0.02
P70290	55 kDa erythrocyte membrane protein									0.01			
P70318	Nucleolysin TIAR			0.04	0.02		0.01			0.02		0.02	
P70333	Heterogeneous nuclear ribonucleoprotein H2	0.20	0.15	0.08	0.09	0.08	0.08	0.02	0.04	0.09	0.14	0.08	0.03
P70349	Histidine triad nucleotide-binding protein 1								0.04				0.04
P70362	Ubiquitin fusion degradation protein 1 homolog		0.04		0.02		0.02			0.01			
P70372	ELAV-like protein 1	0.30	0.28	0.11	0.11	0.14	0.13	0.06	0.06	0.15	0.21	0.10	0.07
P70398	Probable ubiquitin carboxyl-terminal hydrolase FAF-X		0.03		0.01								
P70404	Isocitrate dehydrogenase [NAD] subunit gamma 1, mitochondrial		0.05	0.02	0.03		0.02			0.01			
P70452	Syntaxin-4			0.02									
P70460	Vasodilator-stimulated phosphoprotein		0.04	0.03	0.01								0.02
P70670	Nascent polypeptide-associated complex subunit alpha, muscle-specific form		0.04	0.04	0.10	0.08	0.04	0.03	0.06	0.04		0.07	0.05
P70696	Histone H2B type 1-A			0.06	0.15	0.08	0.06	0.09	0.13	0.03		0.11	0.15
P70698	CTP synthase 1		0.03	0.05	0.04		0.02			0.03	0.05	0.02	0.02
P80315	T-complex protein 1 subunit delta	0.26	0.34	0.31	0.24	0.37	0.19	0.33	0.23	0.38	0.40	0.41	0.35
P80316	T-complex protein 1 subunit epsilon	0.23	0.29	0.24	0.14	0.32	0.15	0.29	0.20	0.34	0.30	0.36	0.29
P84084	ADP-ribosylation factor 5	0.20	0.08	0.12	0.16	0.20	0.13	0.08	0.07		0.14	0.10	0.19
P84091	AP-2 complex subunit mu												0.01
P97287	Induced myeloid leukemia cell differentiation protein Mcl-1 homolog		0.03				0.01						
P97351	40S ribosomal protein S3a	0.41	0.33	0.37	0.42	0.41	0.32	0.32	0.26	0.43	0.32	0.39	0.40
P97363	Serine palmitoyltransferase 2		0.03	0.03	0.02								
P97370	Sodium/potassium-transporting ATPase subunit beta-3	0.20	0.19	0.16	0.14	0.10	0.09	0.11	0.08	0.13	0.18	0.16	0.07
P97371	Proteasome activator complex subunit 1											0.02	
P97376	Protein FRG1		0.04				0.02						
P97377	Cyclin-dependent kinase 2			0.04	0.02	0.02	0.03		0.02	0.02		0.02	0.03
P97384	Annexin A11		0.04	0.04			0.01	0.02	0.01	0.02		0.02	
P97429	Annexin A4		0.05	0.12	0.06	0.11	0.07	0.04	0.03	0.17		0.12	0.04
P97449	Aminopeptidase N			0.08	0.02	0.03		0.06	0.01	0.08		0.10	
P97807	Fumarate hydratase, mitochondrial	0.19	0.18	0.22	0.29	0.14	0.21	0.10	0.07	0.21	0.19	0.19	0.12
P97930	Thymidylate kinase				0.02	0.02							0.01
P98078	Disabled homolog 2			0.06	0.06			0.03	0.01			0.04	0.04
P99024	Tubulin beta-5 chain	1.44	1.04	0.96	1.09	0.78	0.92	0.41	0.33	1.02	0.99	0.68	1.09
P99026	Proteasome subunit beta type-4								0.01				0.02
P99027	60S acidic ribosomal protein P2				0.12		0.04	0.03	0.06			0.07	0.08
P99029	Peroxiredoxin-5, mitochondrial							0.02	0.03			0.02	0.09
Q00612	Glucose-6-phosphate 1-dehydrogenase X								0.02				0.03
Q00651	Integrin alpha-4	0.11	0.09	0.06	0.06	0.06	0.04	0.04	0.04	0.08	0.07	0.05	
Q00PI9	Heterogeneous nuclear ribonucleoprotein U-like protein 2	0.06	0.05	0.02	0.02		0.02			0.02		0.02	

Q01320	DNA topoisomerase 2-alpha		0.03		0.01		0.01			0.02			
Q01405	Protein transport protein Sec23A			0.01								0.02	0.01
Q01730	Ras suppressor protein 1			0.05	0.05	0.03	0.07			0.06		0.03	0.03
Q01853	Transitional endoplasmic reticulum ATPase		0.03	0.04	0.02	0.17	0.02	0.08	0.12	0.15		0.10	0.08
Q02257	Junction plakoglobin		0.03	0.12	0.09		0.06	0.03	0.02			0.08	0.03
Q03145	Ephrin type-A receptor 2			0.05				0.01				0.02	
Q03265	ATP synthase subunit alpha, mitochondrial	0.91	0.82	1.13	1.18	0.87	0.78	0.51	0.67	0.84	0.85	0.87	0.98
Q04447	Creatine kinase B-type					0.14		0.09	0.09	0.06		0.11	0.25
Q04750	DNA topoisomerase 1		0.05		0.02	0.02	0.01	0.01	0.02	0.02	0.08		0.01
Q05144	Ras-related C3 botulinum toxin substrate 2	0.23	0.12	0.12	0.17	0.24	0.14	0.14	0.08		0.16	0.12	0.13
Q05769	Prostaglandin G/H synthase 2			0.02				0.02				0.02	
Q059G7	28S ribosomal protein S21, mitochondrial												0.02
Q059T9	PRP4 pre-mRNA processing factor 4 homolog (Yeast)		0.04		0.02		0.01			0.01			0.01
Q059U9	A kinase (PRKA) anchor protein 8						0.01						
Q05D44	Eukaryotic translation initiation factor 5B		0.04	0.02				0.02		0.02		0.02	
Q06185	ATP synthase subunit e, mitochondrial								0.04				0.05
Q06EZ3	O-acyltransferase			0.02	0.02								0.01
Q07076	Annexin A7	0.08	0.08	0.17	0.15	0.03	0.06	0.11	0.07	0.07		0.20	0.10
Q07417	Short-chain specific acyl-CoA dehydrogenase, mitochondrial	0.19	0.12	0.10	0.07	0.07	0.08	0.03	0.03	0.10	0.13	0.08	0.04
Q08943	FACT complex subunit SSRP1	0.06	0.08	0.03		0.02	0.03			0.04	0.12		
Q0P635	Colony stimulating factor 1 receptor									0.02			
Q0PD23	RAB32, member RAS oncogene family				0.01	0.02	0.01	0.01		0.03		0.02	
Q0PD49	RAB8B, member RAS oncogene family	0.12	0.07	0.07	0.08	0.15	0.09	0.07	0.07	0.12		0.10	0.12
Q0PD56	Rab5B			0.06	0.06	0.14	0.06	0.07	0.05	0.10	0.06	0.09	0.05
Q0PD65	RAB2, member RAS oncogene family	0.13	0.07	0.05	0.11	0.20	0.09	0.07	0.09	0.09	0.12	0.08	0.06
Q0VE46	Myadm protein			0.02	0.11	0.05	0.01	0.02	0.19	0.03		0.02	0.08
Q0VGU0	GTP-binding protein SAR1b			0.05	0.06	0.10	0.04	0.04	0.03	0.06	0.05	0.06	0.06
Q11011	Puromycin-sensitive aminopeptidase	0.12	0.08	0.10	0.05	0.07	0.05	0.09	0.02	0.13	0.15	0.14	0.05
Q149C8	Hexokinase			0.02	0.03	0.03	0.02	0.02	0.04	0.04		0.03	0.04
Q14AF6	MCG4862						0.01		0.03				0.02
Q14AI7	COP9 (Constitutive photomorphogenic) homolog, subunit 4 (Arabidopsis thaliana)	0.07	0.07	0.03		0.02	0.02	0.02		0.05		0.04	0.01
Q14B21	39S ribosomal protein L9, mitochondrial				0.02								0.01
Q14C24	MCG14259, isoform CRA_a			0.03	0.04	0.02	0.04	0.01	0.01	0.02		0.02	0.02
Q14C26	ER membrane protein complex subunit 7								0.01				0.01
Q14C51	Pentatricopeptide repeat domain-containing protein 3, mitochondrial	0.07	0.10	0.05	0.09	0.08	0.04	0.03	0.03	0.06	0.16	0.06	0.05
Q14DR9	ERO1-like beta (S. cerevisiae)			0.02	0.01							0.02	
Q1HFZ0	tRNA (cytosine(34)-C(5))-methyltransferase	0.17	0.12	0.07	0.09	0.04	0.08	0.03	0.02	0.07	0.24	0.06	0.04
Q1HL32	Structural maintenance of chromosomes protein		0.09	0.04	0.04	0.04	0.03			0.05	0.08	0.03	0.02
Q1MWP9	EH-domain containing 4	0.16	0.11	0.11	0.11	0.11	0.13	0.04	0.04	0.13	0.09	0.09	0.09
Q1W5W7	Putative gag-pol protein			0.02									
Q1WWK3	Hist1h1b protein		0.03	0.04	0.10	0.05	0.03	0.03	0.17	0.02		0.05	0.03
Q20BD0	Heterogeneous nuclear ribonucleoprotein A/B	0.12	0.11	0.09	0.12	0.14	0.09	0.06	0.12	0.12	0.09	0.09	0.12
Q3KNM2	E3 ubiquitin-protein ligase MARCH5				0.02								
Q3T9S3	SET translocation					0.07	0.01			0.03			
Q3TAQ9	Protein Wdr36		0.03		0.02		0.01			0.01	0.06		
Q3TAV1	Putative uncharacterized protein		0.04	0.05		0.03	0.02	0.02	0.01	0.03	0.04	0.04	0.01
Q3TBT3	Stimulator of interferon genes protein				0.02								
Q3TC14	Putative uncharacterized protein					0.02				0.02			
Q3TC56	Putative uncharacterized protein						0.01						

Q3TCI7	L-lactate dehydrogenase	0.58	0.42	0.73	0.71	0.82	0.53	0.59	0.53	0.72	0.43	0.88	1.36
Q3TCP5	Putative uncharacterized protein			0.02		0.03		0.03	0.02	0.02		0.03	0.02
Q3TCS0	Putative uncharacterized protein					0.02			0.01	0.02			0.08
Q3TCS3	Tyrosine-protein kinase		0.11	0.09	0.04		0.03	0.01	0.01	0.02	0.07	0.05	0.03
Q3TDE6	Putative uncharacterized protein	0.05	0.07	0.06	0.05	0.03	0.05		0.01	0.04		0.03	0.02
Q3TDF8	Putative uncharacterized protein	0.12	0.17	0.12	0.13	0.08	0.07	0.07	0.04	0.09	0.17	0.11	0.07
Q3TDG9	Putative uncharacterized protein			0.02				0.02				0.03	
Q3TDN2	FAS-associated factor 2			0.01									
Q3TDQ1	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B			0.02					0.01			0.02	
Q3TDU5	Milk fat globule-EGF factor 8 protein, isoform CRA_a			0.02				0.01	0.01			0.03	
Q3TE45	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial			0.07	0.07	0.09	0.04	0.07	0.09	0.03		0.09	0.06
Q3TEA8	Heterochromatin protein 1-binding protein 3			0.02						0.02		0.02	
Q3TED1	S-adenosylmethionine synthase	0.08	0.08	0.04	0.03	0.02	0.02	0.02		0.02		0.03	0.03
Q3TEU8	Coronin				0.01	0.02			0.03	0.01			0.04
Q3TFA9	Putative uncharacterized protein					0.03		0.01		0.05			
Q3TFD9	Putative uncharacterized protein	0.49	0.69	0.50	0.55	0.33	0.29	0.02	0.07	0.11	0.49	0.04	0.06
Q3TFE5	Putative uncharacterized protein			0.03	0.02	0.10	0.01	0.03	0.04	0.09	0.05	0.05	0.12
Q3TFF0	Putative uncharacterized protein		0.04	0.03	0.04	0.02	0.01			0.02		0.02	
Q3TFQ8	Alpha-1,4 glucan phosphorylase		0.03	0.03	0.02		0.01			0.03		0.03	0.01
Q3TFU8	Putative uncharacterized protein			0.07	0.06	0.05	0.03	0.04	0.05	0.02		0.06	0.02
Q3TG21	Putative uncharacterized protein	0.05	0.06	0.08	0.05	0.05	0.07	0.04	0.03	0.10	0.05	0.08	0.03
Q3TG52	Putative uncharacterized protein		0.04			0.02		0.02	0.03			0.02	0.02
Q3TGC5	Putative uncharacterized protein					0.02							0.02
Q3TGE4	Protein kinase C delta type			0.02						0.02		0.02	0.01
Q3TGU7	Proliferation-associated 2G4			0.04	0.02	0.03	0.03	0.03	0.03	0.03		0.04	0.01
Q3TGW0	Putative uncharacterized protein			0.02				0.04	0.05			0.04	0.09
Q3TH64	Putative uncharacterized protein								0.01				
Q3THA0	Eukaryotic translation initiation factor 3 subunit G	0.09	0.07	0.06	0.02		0.03	0.02		0.02		0.04	0.02
Q3THB4	L-lactate dehydrogenase	0.53	0.38	0.70	0.67	0.75	0.50	0.57	0.49	0.67	0.39	0.85	1.28
Q3THC1	Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 9						0.02						
Q3THH1	Putative uncharacterized protein	0.09	0.10	0.19	0.13	0.28	0.11	0.25	0.29	0.16	0.11	0.31	0.28
Q3THK7	GMP synthase [glutamine-hydrolyzing]		0.05	0.03	0.02	0.04	0.05	0.02	0.01	0.04	0.12	0.03	0.02
Q3THN2	Putative uncharacterized protein		0.07	0.05	0.06		0.01			0.03		0.02	0.01
Q3THS8	Putative uncharacterized protein		0.03	0.02	0.02								
Q3THU8	Putative uncharacterized protein	0.24	0.24	0.22	0.19	0.25	0.14	0.20	0.21	0.20	0.20	0.25	0.30
Q3THW7	Eukaryotic translation initiation factor 3 subunit H	0.11	0.07	0.08	0.05		0.07	0.07	0.02	0.07		0.11	0.01
Q3TI05	Chaperonin containing Tcp1, subunit 6a (Zeta)	0.22	0.20	0.21	0.17	0.40	0.11	0.25	0.12	0.42	0.22	0.31	0.28
Q3TI63	Putative uncharacterized protein	0.04	0.03	0.04	0.01		0.02	0.01		0.02	0.06	0.03	0.01
Q3TIC8	Putative uncharacterized protein		0.03	0.06	0.01	0.03	0.02	0.03	0.05	0.02		0.04	0.06
Q3TIN2	Putative uncharacterized protein	0.07	0.08	0.07	0.04	0.03	0.02	0.02		0.06	0.11	0.05	0.04
Q3TIS3	Putative uncharacterized protein			0.02	0.01			0.01		0.02		0.02	0.01
Q3TIV3	Poly [ADP-ribose] polymerase	0.18	0.18	0.04	0.05	0.02	0.03			0.02	0.25	0.02	0.02
Q3TIX6	Protein Fubp3				0.02		0.02			0.02			
Q3TIX9	U4/U6.U5 tri-snRNP-associated protein 2	0.03	0.05	0.03	0.03	0.02	0.02			0.02			
Q3TJ01	tRNA-splicing ligase RtcB homolog		0.06	0.07	0.01	0.02	0.04	0.02	0.02	0.05	0.09	0.05	0.01
Q3TJ39	RAB5C, member RAS oncogene family, isoform CRA_a	0.18	0.14	0.15	0.18	0.32	0.15	0.15	0.15	0.25	0.19	0.18	0.16
Q3TJ43	Putative uncharacterized protein	0.09	0.10	0.04	0.03	0.07	0.05	0.03	0.03	0.15	0.09	0.08	0.08
Q3TJ51	Isocitrate dehydrogenase [NADP]			0.04		0.06		0.05	0.06	0.06		0.04	0.12
Q3TJ75	60 kDa SS-A/Ro ribonucleoprotein			0.02									

Q3TJ95	Putative uncharacterized protein												0.01
Q3TJC2	Platelet-activating factor acetylhydrolase IB subunit gamma		0.03	0.03	0.03	0.05	0.03	0.03	0.01	0.04		0.02	
Q3TJF2	Obg-like ATPase 1			0.01		0.02		0.01		0.02		0.02	
Q3TJG6	Putative uncharacterized protein								0.01				0.02
Q3TJH1	Putative uncharacterized protein	0.16	0.11	0.10	0.13	0.13	0.08	0.08	0.09	0.17	0.10	0.14	0.10
Q3TJN6	Putative uncharacterized protein							0.02					
Q3TJX0	Putative uncharacterized protein					0.15	0.01	0.03	0.03	0.05			0.03
Q3TK27	Putative uncharacterized protein		0.04	0.02						0.01			
Q3TK29	Putative uncharacterized protein	0.44	0.28	0.32	0.37	0.25	0.24	0.15	0.15	0.33	0.34	0.25	0.20
Q3TKB7	Putative uncharacterized protein												0.01
Q3TKG4	Putative uncharacterized protein	0.16	0.14	0.17	0.08	0.07	0.06	0.07	0.02	0.08		0.17	0.05
Q3TKM9	Actin-related protein 2/3 complex subunit 5						0.01	0.02	0.01	0.02		0.02	0.04
Q3TKT4	Transcription activator BRG1		0.06		0.03		0.01			0.03	0.08		
Q3TL71	Putative uncharacterized protein	0.07	0.08	0.07	0.07	0.11	0.04	0.09	0.07	0.11	0.10	0.13	0.09
Q3TL79	Putative uncharacterized protein	0.11	0.12	0.06	0.01	0.02	0.03	0.02		0.08		0.04	0.02
Q3TLP8	RAS-related C3 botulinum substrate 1, isoform CRA_a	0.15	0.07	0.08	0.12	0.22	0.09	0.12	0.09		0.11	0.10	0.09
Q3TLX1	Putative uncharacterized protein	0.09	0.07	0.06	0.06	0.03	0.06	0.01		0.04	0.07	0.03	0.03
Q3TMA0	Putative uncharacterized protein			0.03				0.02	0.01			0.04	
Q3TMZ1	Pyrroline-5-carboxylate reductase	0.09	0.09	0.11	0.11	0.06	0.08	0.02	0.04	0.04		0.05	0.07
Q3TN31	Proteasome subunit alpha type		0.04	0.03	0.04	0.06	0.03	0.02	0.03	0.05		0.04	0.05
Q3TND1	Peptidyl-prolyl cis-trans isomerase												0.01
Q3TPL7	Putative uncharacterized protein	0.18	0.16	0.15	0.10	0.14	0.07	0.09	0.06	0.14	0.15	0.12	0.08
Q3TPU5	ER membrane protein complex subunit 8			0.04	0.07	0.04	0.03		0.04	0.03		0.04	0.02
Q3TQ70	Beta1 subunit of GTP-binding protein			0.06	0.04	0.07	0.04	0.05	0.05	0.05		0.08	0.07
Q3TQK8	Squalene epoxidase												0.01
Q3TQP7	Putative uncharacterized protein	0.05	0.10	0.05	0.06	0.09	0.03	0.05	0.04	0.14	0.08	0.07	0.09
Q3TQX5	ATP-dependent RNA helicase DDX3X	0.26	0.23	0.17	0.15	0.10	0.14	0.03	0.04	0.14	0.33	0.09	0.13
Q3TTM6	Putative uncharacterized protein			0.02				0.01	0.01			0.02	
Q3TUI9	Proteasome subunit alpha type	0.07	0.04	0.03	0.05	0.04	0.06	0.03	0.01	0.04		0.04	0.02
Q3TV20	Putative uncharacterized protein	0.07	0.08	0.02	0.02	0.02	0.01	0.03	0.01	0.07	0.06	0.05	0.06
Q3TV93	Putative uncharacterized protein	0.04			0.02		0.01			0.02			0.02
Q3TVK3	Aspartyl aminopeptidase												0.01
Q3TVK4	Putative uncharacterized protein					0.05		0.02	0.02	0.04		0.02	0.01
Q3TVV6	Putative uncharacterized protein	0.64	0.49	0.40	0.34	0.31	0.32	0.14	0.13	0.47	0.73	0.32	0.16
Q3TVV7	Putative uncharacterized protein			0.03			0.02	0.01		0.03		0.03	
Q3TW51	Putative uncharacterized protein	0.26	0.25	0.27	0.17	0.17	0.15	0.16	0.07	0.30	0.60	0.25	0.10
Q3TW71	Putative uncharacterized protein	0.22	0.17	0.14	0.12	0.07	0.06	0.08	0.06	0.15	0.34	0.16	0.08
Q3TW74	Putative uncharacterized protein	0.47	0.31	0.22	0.21	0.12	0.24	0.06	0.03	0.25	0.60	0.13	0.13
Q3TW77	Putative uncharacterized protein			0.02									
Q3TWB8	Putative uncharacterized protein		0.04										
Q3TWG2	Putative uncharacterized protein							0.01				0.03	
Q3TWN5	Putative uncharacterized protein	0.62	0.48	0.38	0.33	0.31	0.30	0.13	0.12	0.46	0.72	0.31	0.15
Q3TWN8	Putative uncharacterized protein	0.25	0.19	0.17	0.18	0.12	0.11	0.03	0.03	0.14	0.30	0.07	0.07
Q3TWT5	Putative uncharacterized protein			0.04	0.01	0.03	0.01	0.03	0.01	0.02		0.05	0.01
Q3TWV0	Putative uncharacterized protein	0.46	0.64	0.49	0.54	0.32	0.29	0.02	0.07	0.11	0.46	0.04	0.06
Q3TWW8	Serine/arginine-rich splicing factor 6			0.02	0.02	0.09	0.02	0.02	0.02	0.06	0.04	0.03	0.05
Q3TXC4	Putative uncharacterized protein			0.02	0.02		0.01			0.03			0.01
Q3TXD3	Putative uncharacterized protein	0.06	0.05	0.08	0.04	0.05	0.04	0.07	0.04	0.04		0.11	0.02
Q3TXS7	26S proteasome non-ATPase regulatory subunit 1	0.08	0.06	0.06	0.05	0.03	0.02	0.04		0.06	0.11	0.07	0.01
Q3TXV4	Rab22B			0.03	0.04	0.03	0.03	0.02				0.03	0.05
Q3TYK5	Putative uncharacterized protein		0.04										

Q3TZ32	Putative uncharacterized protein		0.03	0.03	0.01		0.02	0.02	0.02	0.03		0.03	0.03
Q3TZP3	Putative uncharacterized protein	0.05	0.05	0.02	0.02	0.03	0.03			0.03	0.05	0.02	0.02
Q3TZU7	Sorting nexin			0.03	0.03	0.02	0.01	0.02	0.03	0.03		0.05	0.06
Q3TZW9	Tyrosine-protein phosphatase non-receptor type			0.02									
Q3TZZ7	Extended synaptotagmin-2											0.02	
Q3U026	Putative uncharacterized protein	0.10	0.05	0.15	0.12	0.04	0.05	0.03	0.06	0.08	0.14	0.11	0.05
Q3U0D7	ADP-ribosylation factor 6			0.06	0.08	0.04	0.02	0.03	0.02			0.04	0.08
Q3U0M8	Putative uncharacterized protein												0.01
Q3U0U7	Putative uncharacterized protein			0.01				0.02					
Q3U0V1	Far upstream element-binding protein 2	0.08	0.04	0.05	0.02	0.05	0.04	0.02	0.02	0.06	0.13	0.05	0.01
Q3U125	Redox-regulatory protein FAM213A			0.02	0.02		0.01					0.02	0.01
Q3U1N0	Coronin		0.03	0.04	0.03	0.07		0.06	0.16	0.03		0.07	0.31
Q3U1U4	Integrin alpha-M			0.17	0.08	0.06	0.01	0.14	0.11	0.05		0.19	0.02
Q3U2C3	Putative uncharacterized protein							0.02				0.02	
Q3U2U4	Putative uncharacterized protein			0.02			0.01					0.02	0.01
Q3U2W2	MYB binding protein (P160) 1a, isoform CRA_b	0.48	0.44	0.29	0.27	0.22	0.23	0.06	0.10	0.27	0.49	0.14	0.10
Q3U2W7	Putative uncharacterized protein			0.02		0.03		0.02	0.05			0.02	0.05
Q3U2X5	Amine oxidase [flavin-containing]			0.02				0.02				0.02	
Q3U3J1	2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial			0.03		0.03				0.02		0.02	
Q3U3T6	Putative uncharacterized protein		0.04										
Q3U3X7	Putative uncharacterized protein			0.01									
Q3U4G3	Xyloside xylosyltransferase 1	0.05		0.09	0.04	0.02	0.02	0.09		0.04		0.10	
Q3U4J9	Putative uncharacterized protein		0.02	0.03			0.02		0.01			0.02	0.02
Q3U4P0	Putative uncharacterized protein	0.05	0.04	0.14	0.11	0.12	0.05	0.10	0.10	0.13		0.15	0.06
Q3U4U6	T-complex protein 1 subunit gamma	0.30	0.32	0.26	0.19	0.31	0.14	0.26	0.23	0.32	0.35	0.33	0.31
Q3U4X8	DNA ligase		0.05				0.02			0.02	0.06		
Q3U505	Putative uncharacterized protein	0.17	0.16	0.17	0.34	0.16	0.11	0.09	0.11	0.18		0.13	0.14
Q3U547	Putative uncharacterized protein		0.04	0.06	0.08	0.03	0.03	0.03	0.07	0.04	0.05	0.06	0.06
Q3U5L3	Putative uncharacterized protein	0.11	0.08	0.04	0.04	0.02	0.04	0.02		0.03		0.04	0.01
Q3U643	Putative uncharacterized protein		0.03	0.03	0.06								0.02
Q3U6A3	Monocyte differentiation antigen CD14	0.07	0.06	0.13	0.07	0.08	0.03	0.07	0.06	0.04	0.12	0.11	
Q3U6C7	Succinyl-CoA ligase subunit beta	0.12	0.11	0.09	0.07	0.04	0.03	0.03	0.03	0.09		0.05	0.03
Q3U6P5	Putative uncharacterized protein	0.07	0.10	0.05	0.08	0.07	0.08	0.04	0.04	0.07	0.09	0.05	0.20
Q3U741	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17, isoform CRA_a	0.13	0.18	0.12	0.10	0.10	0.10	0.04	0.06	0.12	0.19	0.09	0.08
Q3U7R1	Extended synaptotagmin-1	0.05	0.03	0.17	0.11	0.10	0.02	0.06	0.06	0.13		0.10	0.06
Q3U890	Putative uncharacterized protein			0.01		0.07	0.02	0.05	0.02	0.07		0.07	0.03
Q3U893	Putative uncharacterized protein							0.01	0.01			0.02	
Q3U8F5	Putative uncharacterized protein	0.12	0.14	0.09	0.10	0.07	0.06	0.06	0.04	0.11	0.13	0.10	0.07
Q3U8X1	Eukaryotic translation initiation factor 3 subunit F	0.15	0.13	0.13	0.13	0.09	0.09	0.07	0.05	0.12	0.14	0.10	0.07
Q3U944	Putative uncharacterized protein			0.06	0.04	0.04	0.04	0.02	0.03	0.03		0.03	0.02
Q3U9A8	SH3 domain-binding glutamic acid-rich-like protein												0.01
Q3U9G9	Lamin-B receptor		0.09	0.03	0.06		0.03		0.02				0.03
Q3U9P0	Putative uncharacterized protein	0.17	0.10	0.15	0.14	0.19	0.11	0.11	0.08		0.13	0.13	0.17
Q3U9U5	Putative uncharacterized protein			0.06	0.03	0.03	0.01	0.05	0.03	0.02		0.07	0.01
Q3UA17	Putative uncharacterized protein			0.05	0.03	0.04	0.02	0.02	0.02	0.04		0.07	0.01
Q3UA65	Putative uncharacterized protein	0.10	0.10	0.02	0.03	0.03	0.04			0.06	0.10		0.01
Q3UA81	Elongation factor 1-alpha	1.47	1.05	1.41	1.08	1.14	0.89	0.85	0.81	1.16	1.12	1.29	1.02
Q3UAD6	Endoplasmin	0.80	0.73	0.97	0.98	1.11	0.59	0.85	0.86	1.17	1.23	1.08	0.93
Q3UAG2	6-phosphogluconate dehydrogenase, decarboxylating		0.08	0.11	0.05	0.33	0.03	0.16	0.29	0.18	0.11	0.16	0.48
Q3UAI4	Putative uncharacterized protein			0.02									

Q3UAT2	Translocating chain-associated membrane protein				0.02								0.01
Q3UB60	Putative uncharacterized protein												0.01
Q3UB66	Putative uncharacterized protein	0.25	0.14	0.14	0.22	0.29	0.21	0.15	0.17	0.30	0.19	0.20	0.30
Q3UBW8	Putative uncharacterized protein							0.03	0.01			0.02	0.01
Q3UBX0	Transmembrane protein 109			0.02	0.03	0.04	0.01	0.02	0.03			0.03	0.02
Q3UBZ3	Putative uncharacterized protein					0.04				0.02			
Q3UC10	DNA helicase	0.13	0.10	0.03	0.03	0.03	0.06			0.07	0.16	0.02	0.01
Q3UC76	Putative uncharacterized protein								0.02				0.02
Q3UCJ0	Tyrosine-protein phosphatase non-receptor type	0.42	0.37	0.28	0.36	0.18	0.22	0.10	0.11	0.27	0.36	0.17	0.25
Q3UCL7	Putative uncharacterized protein	0.76	0.56	0.65	0.54	0.65	0.37	0.47	0.32	0.64	0.59	0.70	0.54
Q3UD06	ATP synthase subunit gamma	0.14	0.16	0.19	0.18	0.16	0.12	0.08	0.12	0.17	0.15	0.18	0.19
Q3UDI8	DNA helicase		0.14	0.03	0.03	0.03	0.06			0.09	0.21		0.02
Q3UDJ7	Putative uncharacterized protein												0.02
Q3UDK3	Putative uncharacterized protein		0.03		0.02	0.02	0.02			0.01			
Q3UDM0	MOB kinase activator 1B				0.02		0.02	0.01		0.02		0.02	0.01
Q3UDS4	Putative uncharacterized protein			0.03				0.01		0.01		0.02	
Q3UDW8	Heparan-alpha-glucosaminide N-acetyltransferase								0.01				0.01
Q3UDZ1	Ras homolog gene family, member G	0.09		0.03	0.05	0.06	0.03	0.03	0.02		0.10	0.04	0.05
Q3UE92	X-prolyl aminopeptidase (Aminopeptidase P) 1, soluble, isoform CRA_b								0.03				0.04
Q3UF16	Putative uncharacterized protein		0.03	0.02	0.03				0.01				0.02
Q3UFR4	Amino acid transporter	0.12	0.10	0.20	0.15	0.13	0.04	0.23	0.20	0.12	0.17	0.24	0.07
Q3UG80	Putative uncharacterized protein												0.01
Q3UGB5	DAZ associated protein 1, isoform CRA_b				0.02		0.02						
Q3UGB8	Putative uncharacterized protein			0.01	0.02		0.01		0.01				0.03
Q3UGC8	Propionyl-CoA carboxylase alpha chain, mitochondrial	0.37	0.22	0.24	0.31	0.22	0.20	0.16	0.25	0.11	0.45	0.19	0.02
Q3UGR5	Haloacid dehalogenase-like hydrolase domain-containing protein 2									0.01			
Q3UH59	Myosin-10					0.35		0.10		0.42			0.14
Q3UHQ5	Putative uncharacterized protein	0.12	0.11	0.05	0.04	0.03	0.02			0.05	0.12		0.05
Q3UHW5	Putative uncharacterized protein	0.13	0.07	0.06	0.08	0.16	0.08	0.07	0.07	0.12		0.09	0.12
Q3UI84	Replication factor C subunit 4	0.03	0.05				0.02			0.02			
Q3UIA5	Putative uncharacterized protein									0.02			
Q3UIG0	Eukaryotic translation initiation factor 3 subunit E	0.09	0.11	0.11	0.07	0.07	0.05	0.03	0.05	0.07	0.09	0.06	0.07
Q3UIH7	Putative uncharacterized protein			0.01									
Q3UIJ2	Putative uncharacterized protein	0.12	0.11	0.06	0.06	0.02	0.05	0.04	0.03	0.06		0.04	0.02
Q3UIT2	COP9 (Constitutive photomorphogenic) homolog, subunit 6 (Arabidopsis thaliana), isoform CRA_b		0.02	0.01			0.02			0.01		0.02	
Q3UJ44	Putative uncharacterized protein	0.12	0.12	0.07	0.04	0.10	0.05	0.10	0.12	0.11	0.07	0.13	0.09
Q3UJL7	Putative uncharacterized protein					0.05			0.03	0.02		0.02	0.01
Q3UJM1	Putative uncharacterized protein		0.02										
Q3UJN1	DNA helicase	0.15	0.14	0.04	0.02	0.06	0.05			0.09	0.19	0.02	0.02
Q3UJR3	Putative uncharacterized protein		0.05										
Q3UJV2	Putative uncharacterized protein					0.03				0.02			
Q3UJZ7	Putative uncharacterized protein	0.12	0.09	0.15	0.10	0.06	0.05	0.03		0.07	0.08	0.07	0.05
Q3UK56	Putative uncharacterized protein	0.72	0.56	0.58	0.45	0.54	0.31	0.41	0.27	0.55	0.55	0.63	0.46
Q3UK60	Putative uncharacterized protein				0.02		0.07	0.02	0.03			0.02	0.03
Q3UK83	Putative uncharacterized protein	0.06	0.06	0.02	0.04	0.05	0.04	0.02	0.02	0.04		0.03	0.11
Q3UKJ7	WD40 repeat-containing protein SMU1												0.01
Q3UKS0	Putative uncharacterized protein		0.04	0.05	0.06	0.03	0.02	0.02	0.01			0.03	0.02
Q3UKX8	Putative uncharacterized protein			0.02	0.02		0.01			0.04			0.02
Q3UL32	Putative uncharacterized protein		0.06	0.03	0.02		0.03			0.02		0.02	0.01

Q3UL54	Putative uncharacterized protein		0.06		0.02		0.01						
Q3ULD5	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial			0.02									
Q3ULG4	Putative uncharacterized protein			0.02			0.01	0.01	0.01			0.02	
Q3ULL5	Eif2s2 protein	0.09	0.09	0.05	0.07	0.06	0.04	0.04	0.03	0.06		0.05	0.07
Q3ULN8	Putative uncharacterized protein			0.02								0.02	
Q3ULS2	Structural maintenance of chromosomes protein		0.07	0.02	0.02		0.02			0.02	0.09		0.01
Q3ULU3	Branched-chain-amino-acid aminotransferase						0.01						
Q3ULZ3	Phosphoserine aminotransferase	0.11	0.12	0.06	0.10	0.19	0.13	0.11	0.10	0.34	0.13	0.15	0.11
Q3UM23	Putative uncharacterized protein		0.11	0.09	0.05	0.13	0.04	0.13	0.07	0.09	0.10	0.12	0.11
Q3UMR5	Calcium uniporter protein, mitochondrial												0.01
Q3UN35	Beta-1,4 N-acetylgalactosaminyltransferase 1			0.02		0.02		0.02				0.02	
Q3UNF2	Serine/threonine-protein phosphatase		0.02						0.01				0.01
Q3UNH3	Putative uncharacterized protein		0.02							0.01			
Q3UPA3	Putative uncharacterized protein		0.03	0.02		0.08	0.02	0.02	0.05	0.07		0.03	0.11
Q3UPI8	Transporter					0.02	0.01	0.01	0.02	0.04		0.02	
Q3UPL0	Protein transport protein Sec31A	0.09	0.10	0.06	0.04	0.03	0.04	0.01	0.01	0.08	0.10	0.04	0.02
Q3UQM7	Putative uncharacterized protein		0.03	0.02	0.02		0.03	0.02	0.02	0.02		0.03	
Q3UR33	Putative uncharacterized protein		0.10	0.05			0.03	0.02	0.02		0.12	0.03	
Q3URF5	Putative uncharacterized protein		0.05	0.04	0.03	0.07	0.04	0.03	0.02	0.07		0.04	0.01
Q3URM4	Putative uncharacterized protein								0.01				0.01
Q3US15	NAD(P) dependent steroid dehydrogenase-like	0.04	0.04	0.03	0.03	0.03	0.01	0.02		0.02		0.02	0.02
Q3UTB8	GrpE protein homolog			0.02	0.04	0.04	0.01	0.01	0.01	0.02		0.02	0.04
Q3UUU2	Far upstream element-binding protein 1			0.02	0.01			0.01		0.02		0.02	
Q3UUX3	Putative uncharacterized protein			0.02	0.02	0.02	0.01		0.01				0.01
Q3UVI9	Putative uncharacterized protein		0.10		0.02		0.01			0.01	0.11		0.01
Q3UVK0	Endoplasmic reticulum metallopeptidase 1							0.01	0.02			0.02	
Q3UW40	Putative uncharacterized protein	0.16	0.08	0.11	0.14	0.18	0.09	0.06	0.08	0.09	0.12	0.09	0.17
Q3UWW9	Putative uncharacterized protein	0.18	0.18	0.20	0.17	0.12	0.11	0.09	0.07	0.13	0.20	0.14	0.09
Q3UXQ6	40S ribosomal protein S4	0.27	0.28	0.31	0.40	0.34	0.26	0.19	0.16	0.37	0.24	0.37	0.39
Q3UY05	Putative uncharacterized protein			0.04	0.06	0.03	0.03	0.03	0.01	0.02		0.03	0.03
Q3UYK2	Presenilin				0.02	0.03	0.02	0.02	0.03	0.02		0.03	0.03
Q3UYV9	Nuclear cap-binding protein subunit 1			0.03	0.02					0.02		0.02	0.01
Q3UZG3	Putative uncharacterized protein	0.13	0.13	0.04	0.04	0.06	0.06	0.03	0.03	0.07	0.14	0.04	0.05
Q3UZG4	Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	0.07	0.09	0.02	0.03		0.03			0.03	0.06	0.02	0.03
Q3UZR5	Calcium-transporting ATPase				0.02								
Q3UZR8	Eukaryotic translation initiation factor 2B, subunit 1 (Alpha)				0.02		0.02			0.02			0.01
Q3V0Z8	Putative uncharacterized protein	0.26	0.25	0.23	0.20	0.16	0.20	0.06	0.08	0.18	0.32	0.14	0.12
Q3V117	ATP-citrate synthase					0.02		0.03	0.03	0.01		0.03	0.03
Q3V1M8	Putative uncharacterized protein	0.15	0.14	0.10	0.08		0.04	0.02	0.02	0.02	0.23	0.06	0.05
Q3V214	DNA-directed RNA polymerases I, II, and III subunit RPABC1	0.05	0.04	0.01	0.04	0.03	0.03			0.02			0.02
Q3V235	Prohibitin 2	0.38	0.30	0.50	0.40	0.49	0.24	0.33	0.33	0.33	0.33	0.50	0.46
Q3V3R1	Monofunctional C1-tetrahydrofolate synthase, mitochondrial	0.37	0.26	0.30	0.37	0.17	0.14	0.08	0.08	0.28	0.46	0.17	0.17
Q497E9	40S ribosomal protein S8	0.36	0.30	0.28	0.34	0.30	0.20	0.19	0.19	0.29	0.32	0.28	0.54
Q4FJL0	RAB10, member RAS oncogene family	0.13	0.04	0.08	0.08	0.17	0.07	0.09	0.08	0.15	0.08	0.10	0.13
Q4FJM5	Ras homolog gene family, member B							0.02					0.01
Q4FJP3	Nras protein					0.04	0.01	0.02	0.04			0.02	0.04
Q4FJR4	Pdk3 protein			0.02	0.02								

Q4FK49	Inorganic pyrophosphatase												0.01
Q4FK57	ERO1-like protein alpha		0.05	0.06	0.05	0.04	0.03	0.05	0.05	0.03		0.09	0.04
Q4FK74	ATP synthase subunit delta, mitochondrial				0.03		0.02	0.02	0.03			0.03	0.03
Q4FZC9	Nesprin-3			0.01								0.02	
Q4FZE6	40S ribosomal protein S7	0.14	0.10	0.12	0.23	0.08	0.11	0.06	0.04	0.11	0.07	0.15	0.20
Q4KL41	MCG10089								0.01				
Q4TVN0	TBC1 domain family member 15			0.04	0.02		0.02					0.02	
Q4VA32	Acyl-coenzyme A thioesterase 13								0.02				0.02
Q4VAE6	Ras family member A			0.06	0.07	0.20	0.06	0.11	0.09	0.08	0.05	0.09	0.07
Q4VAE8	Ndufb4 protein								0.01				0.02
Q4VAG4	60S ribosomal protein L22		0.06	0.09	0.13	0.03	0.10	0.07	0.10		0.09	0.08	0.15
Q4VBE8	WD repeat-containing protein 18			0.02									
Q4VBG1	DEAD (Asp-Glu-Ala-Asp) box polypeptide 47						0.01						
Q50HX4	RAB14 protein	0.20	0.11	0.11	0.11	0.30	0.09	0.13	0.12	0.20	0.12	0.19	0.14
Q52KC1	Eukaryotic translation initiation factor 4A2	0.73	0.43	0.27	0.24	0.31	0.26	0.21	0.14	0.37	0.53	0.33	0.25
Q52KC3	DNA helicase	0.08	0.08	0.03	0.03	0.04	0.04			0.10	0.11	0.03	0.02
Q52L67	Gpsn2 protein		0.04		0.01		0.02			0.02			0.02
Q52L97	Importin subunit alpha	0.08	0.11			0.02	0.02			0.02			
Q52PE3	Translocon-associated protein alpha, muscle specific isoform	0.06	0.05	0.10	0.17	0.13	0.10	0.11	0.10	0.12		0.17	0.13
Q53ZU7	Peroxiredoxin 6				0.02	0.06		0.01	0.08	0.10		0.02	0.06
Q542A1	B-cell receptor-associated protein 29			0.03	0.01			0.01				0.02	
Q542I9	26S protease regulatory subunit 4	0.22	0.16	0.10	0.11	0.08	0.08	0.05	0.04	0.08		0.10	0.08
Q542M2	Coatomer protein complex, subunit zeta 1, isoform CRA_c												0.05
Q542P8	EMG1 nucleolar protein homolog (S. cerevisiae), isoform CRA_a		0.05		0.08	0.02	0.03	0.01		0.03		0.02	0.01
Q542X7	Chaperonin subunit 2 (Beta), isoform CRA_a	0.31	0.40	0.25	0.25	0.38	0.20	0.29	0.22	0.48	0.43	0.35	0.31
Q543C2	Uridine-cytidine kinase						0.02			0.01			
Q543F6	Cyclin-dependent kinase 5, isoform CRA_c			0.03			0.02		0.01			0.02	0.02
Q543N3	LIM and SH3 domain protein 1	0.09	0.09	0.04	0.03	0.02	0.06	0.03		0.01		0.04	0.04
Q544Z6	Bcl2-associated X protein, isoform CRA_b	0.25	0.13	0.16	0.17	0.21	0.14	0.13	0.11		0.15	0.18	0.07
Q544Z7	DNA-(apurinic or apyrimidinic site) lyase					0.02				0.02			
Q544Z9	Cytochrome b-5, isoform CRA_d	0.04		0.05	0.03	0.03		0.04	0.03			0.05	0.01
Q545C3	Cyclin-dependent kinase 4	0.06	0.05	0.03			0.03		0.01	0.02	0.05	0.02	0.02
Q545N8	Phosphomannomutase				0.02	0.04	0.02	0.02		0.04		0.02	0.01
Q545Y5	CD74 antigen (Invariant polypeptide of major histocompatibility complex, class II antigen-associated)			0.03	0.03		0.01	0.02	0.01			0.03	
Q548J0	Tlr7 protein			0.02		0.02						0.02	
Q54AJ5	CD166 antigen							0.03				0.03	
Q564E8	60S ribosomal protein L4	0.22	0.20	0.28	0.23	0.12	0.11	0.20	0.16	0.13	0.20	0.26	0.37
Q569X8	Nucleoporin 107			0.03	0.02	0.02				0.02	0.05		0.01
Q569Z5	Probable ATP-dependent RNA helicase DDX46	0.07	0.08	0.03	0.03	0.02	0.04	0.01	0.01	0.03	0.15	0.03	0.02
Q569Z6	Thyroid hormone receptor-associated protein 3		0.03	0.03			0.02			0.01		0.02	
Q570Z8	MKIAA4114 protein	0.05	0.07	0.08	0.06	0.04	0.03	0.04	0.02	0.06		0.08	0.04
Q571B0	MKIAA4036 protein		0.04	0.03	0.04	0.02	0.02	0.03	0.04	0.02		0.04	0.02
Q571D6	MKIAA0281 protein	0.06	0.05	0.02	0.03		0.03		0.02	0.02	0.08	0.02	0.01
Q571E2	MFLJ00383 protein			0.03	0.03			0.02				0.02	
Q571F9	MKIAA4115 protein				0.02	0.02	0.02					0.02	0.01
Q571G2	MKIAA4013 protein					0.02			0.01				
Q571I9	Aldehyde dehydrogenase family 16 member A1	0.13	0.07	0.14	0.11		0.05	0.01		0.02	0.11	0.06	0.03
Q571J1	MFLJ00017 protein			0.03								0.02	

Q58E29	Proteolipid protein 2			0.05	0.03	0.02		0.03	0.03			0.04	0.02
Q58E35	60S acidic ribosomal protein P1			0.05	0.05		0.02	0.04	0.05			0.03	0.07
Q58EV4	Proteasome subunit alpha type					0.03	0.01	0.01		0.02		0.02	0.02
Q58EW0	60S ribosomal protein L18	0.47	0.31	0.34	0.45	0.43	0.25	0.30	0.27	0.34	0.34	0.35	0.73
Q58NB6	Dehydrogenase/reductase SDR family member 9			0.02				0.01	0.01			0.02	
Q5BLJ9	60S ribosomal protein L27	0.10	0.03	0.08	0.09	0.11	0.05	0.04	0.08	0.07	0.08	0.07	0.11
Q5BLK1	40S ribosomal protein S6	0.25	0.21	0.16	0.16	0.12	0.09	0.14	0.11	0.13	0.21	0.18	0.23
Q5BLK2	40S ribosomal protein S20				0.05		0.02	0.05	0.06			0.06	0.07
Q5CZY9	Rps16 protein		0.13	0.23	0.30	0.05	0.20	0.18	0.18	0.04	0.21	0.26	0.34
Q5DTH1	MKIAA4216 protein	0.06	0.04		0.03		0.01				0.10		0.01
Q5DTI2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2, isoform CRA_b	0.44	0.37	0.38	0.46	0.27	0.23	0.19	0.24	0.28	0.55	0.30	0.29
Q5DTL8	MKIAA4137 protein				0.03								
Q5DTP7	MKIAA4075 protein		0.06	0.04	0.04	0.02	0.04	0.02		0.06	0.11	0.03	0.01
Q5DTQ4	MKIAA4062 protein			0.02	0.04							0.02	0.02
Q5DTS2	MKIAA4026 protein			0.05	0.02			0.01				0.05	0.02
Q5EBQ6	60S ribosomal protein L9	0.13	0.12	0.09	0.13	0.17	0.08	0.06	0.07	0.11	0.08	0.11	0.21
Q5FW97	Alpha-enolase	0.67	0.75	0.45	0.44	1.46	0.36	0.69	1.14	0.88	0.62	0.81	1.51
Q5FWB6	60S acidic ribosomal protein P0	0.38	0.32	0.29	0.36	0.44	0.25	0.26	0.33	0.32	0.30	0.32	0.60
Q5H8C4	Vacuolar protein sorting-associated protein 13A				0.01								
Q5HZI6	GDP-L-fucose synthase						0.01			0.02			
Q5I0T8	Ribosomal protein L19	0.08	0.04	0.07	0.07	0.09	0.04	0.06	0.07	0.05	0.07	0.09	0.04
Q5I0W0	ATP synthase F(0) complex subunit B1, mitochondrial	0.12	0.12	0.15	0.24	0.19	0.12	0.10	0.17	0.13	0.10	0.17	0.24
Q5KTQ1	MHC class I heavy chain H2-K		0.04	0.02		0.02	0.02	0.02	0.01	0.02		0.03	
Q5M9K5	NADH dehydrogenase (Ubiquinone) 1 alpha subcomplex, 12			0.01									0.01
Q5M9K9	60S ribosomal protein L31		0.07	0.12	0.16	0.04	0.10	0.08	0.09		0.10	0.12	0.15
Q5M9L1	60S ribosomal protein L36				0.05		0.03	0.04	0.02			0.03	0.02
Q5M9M4	40S ribosomal protein S15a				0.09		0.07	0.07	0.07			0.10	0.16
Q5M9M5	60S ribosomal protein L23a	0.17	0.08	0.08	0.13	0.12	0.06	0.05	0.10		0.11	0.07	0.14
Q5M9P1	60S ribosomal protein L36a			0.04	0.03			0.01	0.03			0.03	0.05
Q5M9P3	Rps19 protein			0.06	0.11		0.08	0.10	0.07			0.13	0.08
Q5NBZ3	Developmentally-regulated GTP-binding protein 1	0.11	0.07	0.06	0.05	0.06	0.06	0.04	0.02	0.08	0.09	0.06	0.04
Q5RJV5	Polypyrimidine tract binding protein 1	0.19	0.22	0.13	0.19	0.10	0.14	0.04	0.06	0.13	0.21	0.08	0.10
Q5RL20	39S ribosomal protein L43, mitochondrial				0.01				0.01				0.02
Q5RL55	ATP-binding cassette, sub-family F (GCN20), member 1										0.06		
Q5SQ20	Pescadillo homolog			0.01			0.01			0.01			0.01
Q5SQB7	MCG68069	0.04	0.05	0.03	0.05	0.08	0.04		0.02	0.02		0.02	0.04
Q5SS40	14-3-3 protein epsilon			0.04	0.03	0.08	0.02	0.09	0.10	0.06		0.05	0.12
Q5SSL4	Active breakpoint cluster region-related protein	0.05	0.04				0.02			0.01	0.08		
Q5SUC3	Calnexin	0.37	0.26	0.46	0.33	0.29	0.21	0.29	0.26	0.34	0.36	0.36	0.21
Q5SUF2	Luc7-like protein 3		0.04										
Q5SUH6	Clathrin interactor 1		0.18	0.27			0.06	0.18			0.21	0.24	
Q5SUS9	RNA-binding protein EWS		0.03										
Q5SW19	Clustered mitochondria protein homolog												0.01
Q5SWD9	Pre-rRNA-processing protein TSR1 homolog				0.02								0.01
Q5SWR1	AP complex subunit beta	0.10	0.14	0.12	0.09	0.10	0.07	0.07	0.06	0.20	0.27	0.13	0.07
Q5SWU9	Acetyl-CoA carboxylase 1	0.15	0.09	0.06	0.10	0.03	0.07	0.01		0.06	0.12	0.05	0.02
Q5SX53	Mitochondrial 2-oxoglutarate/malate carrier protein	0.11	0.12	0.08	0.13	0.12	0.08	0.08	0.08	0.10	0.13	0.10	0.07
Q5SZA3	Histone H1.2	0.17	0.14	0.14	0.26	0.24	0.11	0.11	0.33	0.12	0.15	0.16	0.13
Q5XJF6	Ribosomal protein		0.10	0.05	0.13	0.17	0.06	0.05	0.12	0.10	0.10	0.07	0.12
Q5XJY5	Coatomer subunit delta			0.04	0.06	0.02	0.04	0.01	0.01	0.04		0.03	0.05

Q5XKN4	Protein jagunal homolog 1												0.01
Q5XW49	Tapasin			0.05	0.04	0.03	0.03	0.02	0.02	0.03		0.04	
Q60597	2-oxoglutarate dehydrogenase, mitochondrial			0.02	0.02	0.05		0.02	0.01	0.07		0.03	0.04
Q60668	Heterogeneous nuclear ribonucleoprotein D0	0.09	0.06	0.06	0.06	0.07	0.06	0.03	0.06	0.08	0.05	0.06	0.05
Q60692	Proteasome subunit beta type-6					0.03		0.01	0.01	0.02		0.02	0.02
Q60749	KH domain-containing, RNA-binding, signal transduction-associated protein 1	0.05	0.04	0.10	0.06	0.03	0.06	0.02	0.02	0.06		0.08	
Q60766	Immunity-related GTPase family M protein 1						0.01						
Q60865	Caprin-1							0.01	0.01				0.02
Q60875	Rho guanine nucleotide exchange factor 2	0.05	0.05	0.03	0.03	0.03	0.02	0.02	0.01	0.03	0.06	0.02	0.03
Q60930	Voltage-dependent anion-selective channel protein 2	0.36	0.34	0.22	0.27	0.47	0.21	0.22	0.19	0.46	0.36	0.30	0.20
Q60932	Voltage-dependent anion-selective channel protein 1	0.30	0.33	0.21	0.16	0.28	0.13	0.14	0.15	0.27	0.25	0.27	0.11
Q61033	Lamina-associated polypeptide 2, isoforms alpha/zeta		0.06								0.10		
Q61074	Protein phosphatase 1G						0.02					0.02	0.02
Q61081	Hsp90 co-chaperone Cdc37	0.06	0.05	0.05	0.02	0.02	0.02	0.03	0.02	0.02		0.05	0.03
Q61102	ATP-binding cassette sub-family B member 7, mitochondrial				0.02					0.01			0.01
Q61171	Peroxiredoxin-2			0.02	0.05	0.11	0.02	0.04	0.06			0.04	0.07
Q61213	Gag			0.06								0.02	0.01
Q61316	Heat shock 70 kDa protein 4	0.12	0.08	0.09	0.10	0.09	0.08	0.06	0.17	0.16	0.07	0.12	0.19
Q61425	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial					0.03			0.02				0.01
Q61543	Golgi apparatus protein 1			0.03			0.01	0.02	0.01	0.01		0.04	
Q61655	ATP-dependent RNA helicase DDX19A		0.04				0.01						0.02
Q61699	Heat shock protein 105 kDa	0.21	0.16	0.17	0.16	0.06	0.12	0.04	0.04	0.14	0.33	0.14	0.08
Q61733	28S ribosomal protein S31, mitochondrial		0.02		0.01								
Q61753	D-3-phosphoglycerate dehydrogenase	0.61	0.51	0.45	0.40	0.38	0.37	0.28	0.16	0.56	0.58	0.46	0.28
Q61768	Kinesin-1 heavy chain	0.11	0.12	0.16	0.16	0.07	0.09	0.08	0.01	0.15	0.38	0.13	0.02
Q61941	NAD(P) transhydrogenase, mitochondrial		0.04	0.04	0.04	0.02	0.03	0.02		0.03	0.06	0.03	
Q61990	Poly(rC)-binding protein 2	0.39	0.32	0.16	0.22	0.17	0.20	0.10	0.07	0.22	0.28	0.14	0.10
Q62087	Serum paraoxonase/lactonase 3			0.03	0.02		0.01	0.03	0.01	0.01		0.05	
Q62159	Rho-related GTP-binding protein RhoC			0.05	0.05	0.15	0.05	0.09	0.06	0.07	0.05	0.07	0.06
Q62189	U1 small nuclear ribonucleoprotein A			0.02								0.03	
Q62318	Transcription intermediary factor 1-beta	0.24	0.21	0.12	0.09	0.03	0.12	0.02	0.01	0.08	0.34	0.06	0.03
Q62348	Translin								0.01				0.01
Q62351	Transferrin receptor protein 1	0.29	0.27	0.21	0.23	0.15	0.14	0.19	0.17	0.13	0.33	0.23	0.15
Q62383	Transcription elongation factor SPT6									0.01			
Q63829	COMM domain-containing protein 3					0.03	0.02						0.02
Q64012	RNA-binding protein Raly		0.03	0.03	0.03	0.09	0.03	0.03	0.03	0.05		0.03	0.02
Q642K0	MCG140959, isoform CRA_a				0.04	0.02	0.03	0.11	0.08			0.04	0.26
Q642L7	MCG13441	0.20	0.23	0.16	0.24	0.32	0.10	0.22	0.18	0.16	0.26	0.22	0.15
Q64310	Surfeit locus protein 4			0.03	0.08	0.03	0.02	0.03	0.02	0.02		0.03	0.10
Q64511	DNA topoisomerase 2-beta			0.03	0.03	0.02	0.01			0.03			
Q64514	Tripeptidyl-peptidase 2		0.06	0.02	0.01	0.03	0.02	0.04	0.02	0.07	0.11	0.05	0.05
Q64516	Glycerol kinase			0.02								0.03	
Q64518	Sarcoplasmic/endoplasmic reticulum calcium ATPase 3	0.11	0.08	0.08	0.09	0.03	0.04	0.03	0.04	0.04	0.15	0.06	0.05
Q64521	Glycerol-3-phosphate dehydrogenase, mitochondrial			0.03	0.02			0.01	0.02			0.03	0.02
Q64522	Histone H2A type 2-B			0.03	0.14	0.06	0.05	0.09	0.12	0.01		0.09	0.10
Q64737	Trifunctional purine biosynthetic protein adenosine-3	0.24	0.22	0.05	0.08	0.03	0.10	0.02		0.09	0.35	0.05	0.04
Q68FH4	N-acetylgalactosamine kinase									0.01			
Q69Z43	MKIAA1995 protein				0.02					0.02			
Q69ZN1	MKIAA1252 protein	0.09	0.09	0.07	0.04	0.02	0.03	0.02	0.02	0.04		0.05	0.04

Q69ZV4	MKIAA0923 protein	0.15	0.05	0.10	0.10	0.03	0.07	0.04	0.06	0.03	0.07	0.03	0.05
Q69ZW4	MKIAA0899 protein		0.05	0.04	0.05	0.06	0.03	0.03	0.02	0.08	0.08	0.07	0.05
Q69ZX3	MKIAA0866 protein		0.16	0.03	0.02	0.53	0.01	0.17	0.03	0.57		0.03	0.20
Q6A028	Switch-associated protein 70			0.03						0.02		0.02	
Q6A0A2	La-related protein 4B		0.03								0.06		
Q6A0A9	Constitutive coactivator of PPAR-gamma-like protein 1		0.04										
Q6A0C7	MKIAA0118 protein			0.05	0.04	0.02	0.03	0.04		0.02		0.04	0.03
Q6A0D1	ER membrane protein complex subunit 2	0.14	0.12	0.14	0.12	0.10	0.07	0.06	0.10	0.07	0.09	0.14	0.03
Q6A0E3	MKIAA0031 protein		0.04	0.02		0.05	0.02	0.04	0.02	0.05	0.07	0.04	0.02
Q6DFW4	Nucleolar protein 58		0.05	0.08	0.09	0.02	0.03		0.02	0.02		0.02	0.01
Q6DI95	Transportin 3												0.01
Q6GQT9	Nodal modulator 1	0.07	0.08	0.13	0.14	0.07	0.07	0.09	0.08	0.08	0.13	0.13	0.05
Q6GV12	3-ketodihydrosphingosine reductase									0.02		0.02	
Q6IFZ8	MCG1050941	0.16		0.28	0.18	0.14	0.14	0.09	0.07	0.17	0.17	0.18	0.07
Q6KCD5	Nipped-B-like protein		0.04	0.05	0.08	0.05	0.04	0.05	0.05	0.04		0.07	0.02
Q6NS46	Protein RRP5 homolog		0.05	0.02	0.02		0.02						
Q6NSU0	Fam3c protein			0.02	0.02	0.02	0.01	0.02	0.01			0.02	
Q6NWW9	Fibronectin type III domain-containing protein 3B			0.02	0.01								
Q6P069	Sorcin								0.01				0.01
Q6P3A8	2-oxoisovalerate dehydrogenase subunit beta, mitochondrial				0.01								0.01
Q6P4T2	U5 small nuclear ribonucleoprotein 200 kDa helicase		0.14	0.08	0.10	0.14	0.09	0.05	0.05	0.17	0.11	0.07	0.07
Q6P5B0	RRP12-like protein		0.04	0.02						0.02	0.09		
Q6P5D8	Structural maintenance of chromosomes flexible hinge domain-containing protein 1									0.01	0.05		
Q6P5E4	UDP-glucose:glycoprotein glucosyltransferase 1	0.06	0.06	0.07	0.08	0.02	0.02	0.03	0.03	0.05	0.10	0.05	0.02
Q6P5F9	Exportin-1	0.16	0.21	0.08	0.09	0.07	0.07	0.01	0.04	0.11	0.17	0.05	0.09
Q6P9Q6	FK506-binding protein 15		0.03								0.05		
Q6P9R2	Serine/threonine-protein kinaseR1			0.06	0.04		0.02			0.02		0.03	0.02
Q6PB66	Leucine-rich PPR motif-containing protein, mitochondrial	0.39	0.38	0.33	0.42	0.29	0.22	0.06	0.08	0.40	0.56	0.17	0.13
Q6PCP0	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21	0.39	0.34	0.18	0.17	0.11	0.16	0.03	0.04	0.16	0.43	0.09	0.08
Q6PDG5	SWI/SNF complex subunit SMARCC2									0.01			
Q6PDI5	Proteasome-associated protein ECM29 homolog	0.09	0.10	0.07	0.06	0.02	0.03	0.01	0.01	0.07	0.09	0.05	0.03
Q6PFD9	Nuclear pore complex protein Nup98-Nup96		0.04	0.02						0.01			0.01
Q6PGB6	N-alpha-acetyltransferase 50				0.02		0.01						0.03
Q6PGG2	GEM-interacting protein									0.02	0.05		
Q6PHN9	Ras-related protein Rab-35	0.10	0.05	0.06	0.07	0.14	0.06	0.07	0.07	0.09	0.09	0.08	0.12
Q6PHQ9	Polyadenylate-binding protein		0.06	0.03	0.03		0.01		0.01		0.09		0.03
Q6R0H7	Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas	0.06	0.03	0.04	0.05	0.06	0.03	0.04	0.04	0.08	0.07	0.06	0.03
Q6ZPH4	MKIAA1835 protein	0.04	0.06	0.01							0.08		
Q6ZQ08	CCR4-NOT transcription complex subunit 1			0.02						0.02	0.08	0.02	0.01
Q6ZQ38	Cullin-associated NEDD8-dissociated protein 1	0.25	0.21	0.17	0.18	0.21	0.08	0.09	0.05	0.37	0.27	0.16	0.15
Q6ZQ45	MKIAA0791 protein	0.10	0.07	0.02	0.02					0.01	0.09		
Q6ZQ49	Sodium/potassium-transporting ATPase subunit alpha	0.40	0.35	0.30	0.35	0.23	0.24	0.22	0.27	0.30	0.49	0.32	0.23
Q6ZQ58	La-related protein 1						0.02				0.05	0.02	
Q6ZQ61	MCG121979, isoform CRA_c	0.11	0.12	0.06	0.04	0.02	0.05	0.02	0.01	0.04	0.18	0.05	0.01
Q6ZQ84	MKIAA0617 protein			0.02						0.01		0.02	
Q6ZQF2	MKIAA0253 protein			0.06	0.03	0.02	0.01	0.04	0.03	0.02		0.05	
Q6ZQG1	MCG21756, isoform CRA_a		0.03										0.01
Q6ZQI3	Malectin		0.08	0.07	0.06	0.03	0.02	0.04	0.03			0.07	0.03

Q6ZQM8	UDP-glucuronosyltransferase 1-7C	0.05	0.04	0.06	0.08	0.05	0.03	0.02	0.04	0.04		0.06	0.03
Q6ZWN5	40S ribosomal protein S9	0.37	0.26	0.29	0.38	0.43	0.25	0.21	0.14	0.27	0.34	0.33	0.46
Q6ZWQ6	Huntingtin interacting protein 2, isoform CRA_e												0.02
Q6ZWQ7	Signal peptidase complex subunit 3			0.04	0.07	0.05	0.03	0.02	0.05			0.03	0.06
Q6ZWU9	40S ribosomal protein S27												0.03
Q6ZWV7	60S ribosomal protein L35			0.04	0.05	0.05	0.03	0.04	0.02			0.06	0.02
Q6ZWX6	Eukaryotic translation initiation factor 2 subunit 1	0.29	0.27	0.13	0.15	0.12	0.13	0.09	0.07	0.14	0.26	0.12	0.07
Q6ZWZ6	40S ribosomal protein S12						0.02		0.08			0.02	0.11
Q71FD5	E3 ubiquitin-protein ligase ZNRF2			0.02			0.02	0.01		0.01			
Q76MZ3	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	0.08	0.10	0.11	0.06	0.09	0.04	0.08	0.04	0.09		0.12	0.13
Q78JE5	F-box only protein 22									0.01			
Q790I0	Valine--tRNA ligase	0.38	0.31	0.22	0.22	0.24	0.16	0.13	0.18	0.33	0.58	0.21	0.18
Q791T5	Mitochondrial carrier homolog 1				0.01		0.01		0.01				
Q7JCY6	NADH-ubiquinone oxidoreductase chain 4			0.01									
Q7TMB8	Cytoplasmic FMR1-interacting protein 1		0.10	0.09	0.07	0.03	0.03	0.03	0.02	0.08		0.05	0.11
Q7TMF4	Propionyl Coenzyme A carboxylase, beta polypeptide	0.22	0.15	0.25	0.32	0.17	0.17	0.14	0.29	0.12	0.14	0.18	0.04
Q7TMK9	Heterogeneous nuclear ribonucleoprotein Q			0.02	0.02	0.04	0.02	0.01	0.01	0.02		0.02	0.01
Q7TMM9	Tubulin beta-2A chain	1.03	0.80	0.67	0.67	0.53	0.58	0.28	0.24	0.68	0.69	0.45	0.75
Q7TMY2	Acyl-Coenzyme A dehydrogenase, short/branched chain			0.02									
Q7TMY7	Importin-8									0.02			
Q7TNC4	Putative RNA-binding protein Luc7-like 2	0.05	0.08	0.06	0.03	0.03	0.03	0.03	0.01	0.02		0.04	0.02
Q7TPW6	Solute carrier family 25 (Mitochondrial carnitine/acylcarnitine translocase), member 20								0.01			0.02	0.01
Q7TQ39	Gag protein			0.06								0.03	0.01
Q7TQH0	Ataxin-2-like protein			0.02							0.10		
Q7TQI3	Ubiquitin thioesterase OTUB1	0.06	0.11			0.02	0.02		0.01	0.04			0.03
Q7TSJ0	DNA (cytosine-5)-methyltransferase	0.05	0.05				0.02			0.02	0.11		
Q7TSZ3	Leucyl-tRNA synthetase	0.16	0.19	0.13	0.09	0.09	0.08	0.05	0.02	0.21	0.27	0.08	0.12
Q7TT37	Elongator complex protein 1						0.01						
Q80TM2	MKIAA1027 protein	0.82	0.75	1.04	0.68	0.42	0.35	0.54	0.46	0.75	1.35	0.94	0.67
Q80TP8	MKIAA0885 protein		0.03				0.01						
Q80TT4	MKIAA0719 protein			0.03				0.02		0.02		0.02	
Q80U89	MKIAA0034 protein	0.19	0.32	0.12	0.12	0.67	0.07	0.06	0.31	0.49	0.14	0.11	0.99
Q80U93	Nuclear pore complex protein Nup214				0.02								
Q80UL3	Galactokinase 1	0.19	0.10	0.11	0.09	0.06	0.11	0.06	0.02	0.12	0.09	0.10	0.05
Q80UT7	Rpl7a protein	0.33	0.33	0.15	0.26	0.32	0.13	0.11	0.23	0.22	0.35	0.17	0.32
Q80UU9	Membrane-associated progesterone receptor component 2			0.04	0.02		0.01	0.01	0.02	0.02		0.04	
Q80V08	Rpl17 protein	0.09	0.04	0.10	0.13	0.10	0.08	0.05	0.03		0.08	0.09	0.13
Q80VA0	N-acetylgalactosaminyltransferase 7			0.04	0.02			0.02				0.04	
Q80VD1	Protein FAM98B	0.04	0.06	0.03			0.02			0.02		0.02	
Q80W54	CAAX prenyl protease 1 homolog								0.01				
Q80WJ7	Protein LYRIC			0.02	0.01			0.02				0.02	
Q80X41	Serine/threonine-protein kinase VRK1		0.04										
Q80X50	Ubiquitin-associated protein 2-like	0.11	0.09	0.04	0.03		0.02				0.17		
Q80X85	28S ribosomal protein S7, mitochondrial		0.03	0.02	0.03		0.02			0.01		0.02	0.01
Q80X90	Filamin-B	0.06	0.07	0.10	0.08	0.04	0.02	0.07	0.03	0.09	0.13	0.11	0.10
Q80Y09	Pdcd6ip protein	0.23	0.18	0.16	0.15	0.11	0.09	0.08	0.03	0.18	0.27	0.14	0.07
Q80Y14	Glutaredoxin-related protein 5, mitochondrial												0.01

Q80Y52	Heat shock protein 90, alpha (Cytosolic), class A member 1	0.83	0.63	0.67	0.64	0.97	0.50	0.79	0.57	1.22	1.06	0.97	0.81
Q80YG4	SEC63		0.04	0.03	0.04		0.01	0.01	0.02		0.07	0.02	0.02
Q80ZI9	WD repeat domain 1			0.09	0.04	0.03	0.05	0.04		0.05		0.09	0.02
Q80ZS3	28S ribosomal protein S26, mitochondrial		0.03	0.02	0.05	0.03	0.02			0.02		0.03	0.03
Q810B6	Rabankyrin-5		0.04	0.03	0.02		0.01			0.02	0.06		0.02
Q810D6	Glutamate-rich WD repeat-containing protein 1												0.01
Q811E7	Myosin IF	0.05		0.02	0.04	0.02	0.01			0.03			0.03
Q861Q5	H13 protein			0.05	0.05		0.02	0.04	0.01	0.02		0.05	0.01
Q8BFP9	[Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 1, mitochondrial				0.01								
Q8BFQ8	Parkinson disease 7 domain-containing protein 1									0.01			
Q8BFR5	Elongation factor Tu, mitochondrial	0.23	0.22	0.18	0.16	0.12	0.10	0.05	0.04	0.12	0.20	0.11	0.07
Q8BFY6	Peflin			0.01	0.02					0.01		0.02	0.02
Q8BFY9	Transportin-1	0.11	0.09	0.09	0.06	0.06	0.06	0.04	0.03	0.11	0.18	0.08	0.05
Q8BFZ3	Beta-actin-like protein 2	0.43	0.28	0.23	0.28	0.70	0.17	0.38	0.36	0.69	0.24	0.54	0.46
Q8BFZ9	Erlin-2			0.02	0.02		0.01		0.01				0.02
Q8BG51	Mitochondrial Rho GTPase 1			0.03		0.02				0.02		0.02	
Q8BGH2	Sorting and assembly machinery component 50 homolog		0.03										
Q8BGS0	Protein MAK16 homolog			0.02									
Q8BH24	Transmembrane 9 superfamily member 4			0.02				0.02				0.03	
Q8BH59	Calcium-binding mitochondrial carrier protein Aralar1	0.11	0.11	0.10	0.24	0.15	0.07	0.07	0.15	0.14		0.10	0.09
Q8BH80	Vesicle-associated membrane protein, associated protein B and C	0.07		0.03	0.02	0.03	0.03	0.04		0.04		0.05	
Q8BH95	Enoyl-CoA hydratase, mitochondrial		0.05	0.02	0.04	0.04	0.03	0.02	0.02	0.02		0.03	0.01
Q8BHC4	Dephospho-CoA kinase domain-containing protein				0.01								
Q8BIG7	Catechol O-methyltransferase domain-containing protein 1		0.03	0.03	0.04	0.02	0.03	0.02	0.01	0.02		0.03	0.03
Q8BIV3	Ran-binding protein 6				0.01		0.02			0.02	0.05		0.01
Q8BJ71	Nuclear pore complex protein Nup93	0.11	0.11	0.08	0.08	0.05	0.04	0.02	0.02	0.05	0.16	0.05	0.02
Q8BJW6	Eukaryotic translation initiation factor 2A												0.02
Q8BJX0	Proteasome subunit beta type					0.02							0.03
Q8BJY1	26S proteasome non-ATPase regulatory subunit 5				0.01		0.01			0.01			0.02
Q8BJZ4	28S ribosomal protein S35, mitochondrial		0.04	0.02	0.02		0.01						
Q8BK37	Putative uncharacterized protein			0.04	0.04		0.03	0.03	0.01	0.04		0.05	0.06
Q8BK67	Protein RCC2									0.02			
Q8BK72	28S ribosomal protein S27, mitochondrial			0.03	0.02	0.02		0.01		0.04		0.02	0.02
Q8BKC5	Importin-5	0.62	0.47	0.26	0.24	0.20	0.21	0.13	0.08	0.35	0.69	0.23	0.15
Q8BL97	Serine/arginine-rich splicing factor 7	0.05	0.05	0.03	0.03	0.03	0.02	0.03	0.03	0.02		0.03	0.05
Q8BLF1	Neutral cholesterol ester hydrolase 1			0.04	0.02		0.01	0.02		0.01		0.02	0.01
Q8BM55	Transmembrane protein 214			0.01									
Q8BMA6	Signal recognition particle subunit SRP68		0.04	0.04	0.02	0.02	0.01	0.01		0.02		0.04	0.01
Q8BMD8	Calcium-binding mitochondrial carrier protein SCaMC-1								0.01				0.01
Q8BMF4	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial		0.03	0.02	0.03	0.02		0.02		0.03		0.03	0.01
Q8BMK4	Cytoskeleton-associated protein 4			0.07	0.05	0.02		0.08	0.03			0.06	0.01
Q8BMR3	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	0.20	0.18	0.23	0.21	0.15	0.09	0.15	0.19	0.12		0.22	0.13
Q8BMS1	Trifunctional enzyme subunit alpha, mitochondrial	0.35	0.30	0.30	0.25	0.36	0.18	0.15	0.07	0.39	0.49	0.22	0.17

Q8BMS4	Ubiquinone biosynthesis O-methyltransferase, mitochondrial						0.01						
Q8BNI4	Derlin-2				0.02	0.03			0.02				0.03
Q8BNW9	Kelch repeat and BTB domain-containing protein 11	0.13	0.06	0.04	0.03	0.03	0.03	0.02	0.01	0.06		0.02	0.02
Q8BP40	Lysophosphatidic acid phosphatase type 6			0.03				0.01				0.02	
Q8BP47	Asparagine--tRNA ligase, cytoplasmic	0.12	0.09	0.10	0.09	0.09	0.08	0.07	0.03	0.08	0.10	0.08	0.06
Q8BP48	Methionine aminopeptidase 1									0.02		0.02	
Q8BQS7	Putative uncharacterized protein				0.02			0.02					
Q8BRF7	Sec1 family domain-containing protein 1		0.04	0.03									0.01
Q8BSL7	ADP-ribosylation factor 2	0.23	0.15	0.16	0.23	0.26	0.17	0.12	0.11		0.21	0.18	0.23
Q8BSY0	Aspartyl/asparaginyl beta-hydroxylase	0.12	0.09	0.13	0.12		0.05	0.05	0.07	0.04	0.11	0.08	0.06
Q8BT90	Putative uncharacterized protein	0.07		0.13	0.12	0.10	0.07	0.09	0.09			0.11	0.09
Q8BTF0	Coatomer subunit alpha	0.17	0.16	0.14	0.11	0.08	0.06	0.05	0.04	0.18	0.25	0.13	0.07
Q8BTZ7	Mannose-1-phosphate guanyltransferase beta						0.01			0.02		0.02	
Q8BU20	Putative uncharacterized protein			0.02		0.02		0.01				0.02	0.01
Q8BU30	Isoleucine--tRNA ligase, cytoplasmic	0.08	0.11	0.14	0.08	0.07	0.06	0.03		0.17		0.08	0.09
Q8BU31	Ras-related protein Rap-2c			0.03	0.01	0.03	0.02		0.01			0.03	0.05
Q8BU88	39S ribosomal protein L22, mitochondrial			0.01	0.04	0.02	0.02		0.01			0.02	0.03
Q8BUE4	Apoptosis-inducing factor 2			0.01									
Q8BV66	Interferon-induced protein 44						0.02						
Q8BVE3	V-type proton ATPase subunit H		0.04	0.03	0.02			0.01		0.02		0.02	0.01
Q8BVK3	Putative uncharacterized protein					0.02		0.01	0.01			0.02	
Q8BVQ5	Protein phosphatase methylesterase 1											0.02	
Q8BVQ9	26S protease regulatory subunit 7	0.19	0.15	0.16	0.13	0.09	0.07	0.07	0.04	0.13	0.15	0.13	0.08
Q8BWT1	3-ketoacyl-CoA thiolase, mitochondrial	0.10	0.08	0.06	0.06	0.04	0.03			0.06		0.02	0.02
Q8BWU5	Probable tRNA N6-adenosine threonylcarbamoyltransferase	0.05	0.05										
Q8BWZ3	N-alpha-acetyltransferase 25, NatB auxiliary subunit								0.01	0.03			0.02
Q8BX70	Vacuolar protein sorting-associated protein 13C	0.23	0.30	0.28	0.17	0.22	0.11	0.12	0.03	0.40	0.44	0.23	0.09
Q8BXC6	COMM domain-containing protein 2				0.02	0.03	0.02		0.01				0.01
Q8BXK9	Chloride intracellular channel protein 5			0.01	0.02		0.02						0.02
Q8BXL7	ADP-ribosylation factor-related protein 1				0.01		0.01						0.01
Q8BXV2	BRI3-binding protein			0.02	0.04	0.02	0.02	0.02				0.02	0.01
Q8BXZ1	Protein disulfide-isomerase TMX3			0.04	0.03	0.03	0.01	0.01	0.03	0.02		0.03	0.02
Q8BYA0	Tubulin-specific chaperone D	0.05	0.06	0.03	0.03		0.03	0.02		0.04		0.02	0.02
Q8BYB9	Protein O-glucosyltransferase 1			0.02									
Q8BYI6	Lysophosphatidylcholine acyltransferase 2						0.01						
Q8BYK6	YTH domain-containing family protein 3									0.01			
Q8BYL4	Tyrosine--tRNA ligase, mitochondrial			0.01									
Q8BZA9	Fructose-2,6-bisphosphatase TIGAR		0.04		0.02		0.01			0.01			
Q8C0C7	Phenylalanine--tRNA ligase alpha subunit		0.04	0.06	0.04	0.02	0.01			0.04		0.02	0.02
Q8C0E2	Vacuolar protein sorting-associated protein 26B											0.02	0.01
Q8C129	Leucyl-cystinyl aminopeptidase			0.06	0.06		0.01	0.04	0.03	0.01		0.05	0.01
Q8C142	Low density lipoprotein receptor adapter protein 1												0.01
Q8C1A5	Thimet oligopeptidase												0.01
Q8C1W9	Putative uncharacterized protein			0.02		0.02	0.02					0.02	
Q8C243	Putative uncharacterized protein											0.02	
Q8C2E7	WASH complex subunit strumpellin												0.01
Q8C2Q3	RNA-binding protein 14		0.04										
Q8C2Q7	Heterogeneous nuclear ribonucleoprotein H	0.25	0.18	0.13	0.14	0.14	0.11	0.03	0.07	0.14	0.18	0.11	0.08
Q8C338	Isocitrate dehydrogenase [NADP]			0.04		0.06		0.06	0.06	0.06		0.04	0.12
Q8C3J5	Dedicator of cytokinesis protein 2		0.12	0.08	0.05	0.03	0.03	0.01		0.08	0.11	0.03	0.06

Q8C483	Serine--tRNA ligase, cytoplasmic					0.02		0.03	0.01	0.03		0.03	
Q8C4C9	DnaJ (Hsp40) homolog, subfamily B, member 12, isoform CRA_d			0.02									
Q8C4J7	Transducin beta-like protein 3				0.02								
Q8C5K0	Lysosomal membrane glycoprotein 2, isoform CRA_a			0.02				0.01		0.02		0.04	
Q8C5X6	Putative uncharacterized protein		0.03	0.02	0.02	0.02	0.01			0.02		0.02	
Q8C605	ATP-dependent 6-phosphofructokinase	0.22	0.16	0.13	0.17	0.03	0.08	0.07	0.04	0.08	0.31	0.12	0.13
Q8C622	Putative uncharacterized protein				0.10	0.02		0.03	0.10			0.05	0.09
Q8C671	Putative uncharacterized protein												0.01
Q8C6F4	Putative uncharacterized protein			0.03				0.01				0.02	0.01
Q8C7R4	Ubiquitin-like modifier-activating enzyme 6	0.05	0.06	0.09	0.05	0.02	0.04	0.04		0.08	0.13	0.09	0.02
Q8C845	EF-hand domain-containing protein D2	0.06	0.14			0.06	0.02	0.01	0.01	0.07		0.02	0.02
Q8C854	Myelin expression factor 2		0.02		0.01					0.01			
Q8CAQ8	MICOS complex subunit Mic60	0.18	0.14	0.08	0.06	0.09	0.08	0.02	0.03	0.11	0.20	0.06	0.05
Q8CB96	Ras association domain-containing protein 4		0.03										
Q8CC13	AP complex subunit beta	0.12	0.16	0.12	0.09	0.11	0.08	0.06	0.06	0.21	0.25	0.14	0.07
Q8CC88	von Willebrand factor A domain-containing protein 8			0.01						0.01			
Q8CCF0	U4/U6 small nuclear ribonucleoprotein Prp31		0.06				0.01						
Q8CCJ3	E3 UFM1-protein ligase 1		0.03										
Q8CCP0	Nuclear export mediator factor Nemf										0.05		
Q8CDZ5	Putative uncharacterized protein			0.02									
Q8CFE6	Sodium-coupled neutral amino acid transporter 2			0.03				0.02				0.02	
Q8CFJ7	Solute carrier family 25 member 45												0.01
Q8CG47	Structural maintenance of chromosomes protein 4									0.02			0.01
Q8CGB9	Insulin degrading enzyme												0.01
Q8CGC6	RNA-binding protein 28		0.03										
Q8CGK3	Lon protease homolog, mitochondrial	0.21	0.19	0.19	0.13	0.13	0.09	0.06	0.04	0.18	0.32	0.11	0.07
Q8CGY8	UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit			0.02			0.01			0.01			
Q8CHW4	Translation initiation factor eIF-2B subunit epsilon			0.02						0.01			
Q8CIG8	Protein arginine N-methyltransferase 5							0.02					0.02
Q8CIH5	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-2		0.03	0.06	0.03	0.02	0.02	0.03	0.01	0.05		0.05	0.03
Q8CIJ3	Eukaryotic translation initiation factor 3 subunit B		0.07	0.09	0.09	0.07	0.07	0.04	0.04	0.12	0.11	0.09	0.07
Q8CIN4	Serine/threonine-protein kinase PAK 2	0.04	0.07	0.02	0.02	0.03	0.03	0.02		0.03		0.03	0.01
Q8JZN5	Acyl-CoA dehydrogenase family member 9, mitochondrial		0.06	0.09	0.07	0.03	0.03	0.03	0.02	0.03		0.06	0.02
Q8JZN7	Mitochondrial Rho GTPase 2			0.03						0.01			
Q8JZU2	Tricarboxylate transport protein, mitochondrial			0.05	0.04	0.05	0.01	0.04	0.04	0.03		0.03	0.04
Q8K009	Mitochondrial 10-formyltetrahydrofolate dehydrogenase			0.05	0.04	0.03	0.04	0.02		0.04		0.05	0.01
Q8K078	Solute carrier organic anion transporter family member 4A1			0.05	0.02		0.01	0.04	0.02	0.02	0.06	0.06	0.01
Q8K0C9	GDP-mannose 4,6 dehydratase							0.01					
Q8K0D5	Elongation factor G, mitochondrial								0.01				
Q8K183	Pyridoxal kinase												0.01
Q8K1B8	Fermitin family homolog 3	0.18	0.15	0.14	0.12	0.07	0.09	0.05	0.04	0.15		0.13	0.10
Q8K1J6	CCA tRNA nucleotidyltransferase 1, mitochondrial			0.03									
Q8K1M6	Dynamin-1-like protein	0.06	0.08	0.02	0.04	0.02	0.02			0.02	0.11	0.02	0.01
Q8K1X4	NCK associated protein 1 like		0.03		0.03	0.02	0.02			0.02	0.05		0.02
Q8K1X5	EH-domain containing 1		0.09	0.12	0.09		0.03	0.04	0.04	0.02		0.08	0.04
Q8K205	Blood vessel epicardial substance												0.01

Q8K224	N-acetyltransferase 10		0.04	0.02	0.02					0.01	0.06		
Q8K297	Procollagen galactosyltransferase 1	0.07	0.09	0.06	0.08	0.05	0.03	0.01	0.02	0.04	0.11	0.03	0.03
Q8K2B3	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial		0.03	0.10	0.04	0.08	0.02	0.11	0.19	0.05		0.11	0.11
Q8K2C7	Protein-9				0.02								
Q8K2M0	39S ribosomal protein L38, mitochondrial			0.02								0.02	
Q8K2T1	NmrA-like family domain-containing protein 1		0.04	0.02	0.02	0.02	0.02			0.01			0.02
Q8K2Y7	39S ribosomal protein L47, mitochondrial				0.03		0.02		0.01				0.05
Q8K2Z4	Condensin complex subunit 1					0.02				0.02			
Q8K363	ATP-dependent RNA helicase DDX18		0.04	0.03	0.02		0.02			0.01		0.02	
Q8K469	2'-5'olygoadenylate synthetase 1G		0.03				0.01						
Q8K4Z5	Splicing factor 3A subunit 1	0.06	0.05	0.02	0.02		0.01	0.02		0.02	0.05	0.03	
Q8QZY1	Eukaryotic translation initiation factor 3 subunit L	0.08	0.11	0.10	0.08	0.07	0.04	0.06	0.07	0.10	0.09	0.08	0.11
Q8R010	Aminoacyl tRNA synthase complex-interacting multifunctional protein 2		0.04	0.02	0.02		0.02			0.02			0.02
Q8R050	Eukaryotic peptide chain release factor GTP-binding subunit ERF3A		0.05	0.03	0.02		0.02	0.03		0.03		0.04	0.01
Q8R0J2	Mannose-P-dolichol utilization defect 1								0.01				0.03
Q8R1B4	Eukaryotic translation initiation factor 3 subunit C	0.15	0.11	0.09	0.08	0.04	0.05	0.04	0.04	0.10	0.18	0.07	0.05
Q8R1F1	Niban-like protein 1			0.07	0.07		0.02	0.03	0.04	0.03		0.07	0.06
Q8R1Q8	Cytoplasmic dynein 1 light intermediate chain 1		0.07	0.06	0.05	0.03	0.03	0.01		0.05	0.06	0.04	0.02
Q8R1V4	Transmembrane emp24 domain-containing protein 4			0.02	0.02	0.02	0.02	0.01	0.01			0.02	
Q8R2P8	Lysine--tRNA ligase		0.05	0.02	0.02	0.03	0.02	0.04	0.01	0.06	0.12	0.05	0.02
Q8R2Q8	Bone marrow stromal antigen 2				0.02	0.07	0.04		0.06	0.01			0.01
Q8R2Y0	Monoacylglycerol lipase ABHD6				0.01								
Q8R2Y8	Peptidyl-tRNA hydrolase 2, mitochondrial			0.01	0.02							0.02	0.01
Q8R323	Replication factor C subunit 3	0.07	0.05				0.01						
Q8R395	COMM domain-containing protein 5				0.02		0.01			0.01			
Q8R480	Nuclear pore complex protein Nup85		0.02		0.02					0.02			
Q8R4R6	Nucleoporin NUP53	0.05	0.09	0.03	0.04		0.03		0.01		0.08		0.03
Q8R5C5	Beta-centractin			0.03	0.04	0.07	0.03	0.05	0.05	0.08		0.05	0.06
Q8VBT0	Thioredoxin-related transmembrane protein 1			0.03	0.02		0.02	0.03	0.02			0.03	0.01
Q8VBX5	Palmitoyl-protein thioesterase				0.02		0.02	0.02				0.02	
Q8VBZ3	Cleft lip and palate transmembrane protein 1 homolog		0.04								0.05		
Q8VCE0	Sodium/potassium-transporting ATPase subunit alpha	0.42	0.38	0.34	0.37	0.26	0.26	0.24	0.27	0.34	0.55	0.36	0.23
Q8VCG1	Deoxyuridine triphosphatase, isoform CRA_b												0.01
Q8VCM8	Nicalin		0.04	0.04	0.03		0.02	0.01	0.01	0.01	0.04	0.02	0.03
Q8VCS9	Transporter			0.02	0.01		0.01		0.01	0.02			0.01
Q8VCT3	Aminopeptidase B					0.02	0.02		0.01	0.02			0.04
Q8VDC3	Aconitate hydratase			0.03	0.04	0.06	0.03	0.02	0.01	0.06		0.04	0.04
Q8VDD5	Myosin-9	0.61	1.07	0.26	0.08	3.89	0.07	1.15	0.17	4.03	0.15	0.19	1.45
Q8VDL4	ADP-dependent glucokinase			0.04				0.02	0.01			0.03	
Q8VDN2	Sodium/potassium-transporting ATPase subunit alpha-1	0.91	0.76	0.78	0.85	0.63	0.55	0.59	0.62	0.79	1.21	0.86	0.55
Q8VDP4	Cell cycle and apoptosis regulator protein 2			0.02	0.02		0.02				0.06		
Q8VDP6	CDP-diacylglycerol--inositol 3-phosphatidyltransferase			0.02	0.02				0.03				0.04
Q8VE70	Programmed cell death protein 10						0.01						
Q8VE96	Solute carrier family 35 member F6												0.01
Q8VE99	Coiled-coil domain-containing protein 115			0.02	0.02							0.02	
Q8VEH3	ADP-ribosylation factor-like protein 8A	0.04	0.03	0.05	0.06	0.05	0.03	0.05	0.06			0.05	0.05
Q8VH51	RNA-binding protein 39	0.13	0.06	0.03	0.03		0.02					0.02	0.01
Q8VHK9	ATP-dependent RNA helicase DHX36		0.03							0.02			

Q8VI75	Importin-4		0.06	0.02	0.03		0.01			0.02	0.07		0.02
Q8VI93	2'-5'-oligoadenylate synthase 3		0.03		0.02		0.01						0.01
Q8VIJ6	Splicing factor, proline- and glutamine-rich	0.19	0.15	0.14	0.11	0.11	0.11	0.05	0.05	0.16	0.39	0.08	0.02
Q91V61	Sideroflexin-3												0.01
Q91VA7	Isocitrate dehydrogenase [NAD] subunit, mitochondrial	0.12	0.19	0.09	0.08		0.05	0.03	0.01	0.03		0.05	0.02
Q91VC3	Eukaryotic initiation factor 4A-III	0.19	0.17	0.09	0.07	0.11	0.06	0.05	0.04	0.11	0.15	0.09	0.05
Q91VC9	Growth hormone-inducible transmembrane protein		0.05	0.06	0.05	0.08	0.04	0.06	0.03	0.06		0.07	0.01
Q91VD9	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	0.16	0.21	0.19	0.18	0.13	0.10	0.08	0.09	0.12	0.28	0.17	0.14
Q91VE6	MKI67 FHA domain-interacting nucleolar phosphoprotein		0.07				0.01						
Q91VK1	Basic leucine zipper and W2 domain-containing protein 2	0.07	0.06	0.05	0.01	0.02	0.02			0.05	0.06	0.02	0.01
Q91VM5	RNA binding motif protein, X-linked-like-1			0.06	0.05		0.02			0.04	0.06	0.02	0.01
Q91VN4	MICOS complex subunit Mic25		0.03										
Q91VR5	ATP-dependent RNA helicase DDX1	0.08	0.07	0.10	0.06	0.06	0.04	0.03		0.14	0.15	0.07	0.01
Q91W06	V-type proton ATPase subunit a	0.11	0.10	0.17	0.20	0.17	0.11	0.12	0.15	0.25	0.17	0.17	0.11
Q91W53	Golgin subfamily A member 7												0.01
Q91WD5	NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial	0.08	0.05	0.09	0.05	0.04	0.02	0.05	0.02	0.05	0.06	0.08	0.04
Q91X52	L-xylulose reductase									0.03			
Q91X78	Erlin-1				0.01		0.01		0.01				0.02
Q91XD6	Vacuolar protein-sorting-associated protein 36			0.03	0.02	0.04	0.02	0.02		0.04		0.04	0.01
Q91YE6	Importin-9		0.05	0.02	0.02		0.03	0.01		0.05	0.08		0.02
Q91YH5	Atlastin-3		0.03										
Q91YM4	Protein TBRG4				0.01								
Q91YN9	BAG family molecular chaperone regulator 2				0.01								0.02
Q91YR7	Pre-mRNA-processing factor 6		0.07										
Q91YT0	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial		0.03	0.06	0.06	0.02	0.02	0.04	0.01	0.03		0.05	0.04
Q91YT7	YTH domain-containing family protein 2						0.01			0.02			
Q91YW3	DnaJ homolog subfamily C member 3			0.03	0.03		0.01			0.01			
Q91YY4	ATP synthase mitochondrial F1 complex assembly factor 2				0.02		0.01						0.01
Q91Z25	Actin-related protein 2/3 complex subunit 1B					0.02		0.01	0.01	0.02		0.02	0.03
Q91ZR1	Ras-related protein Rab-4B	0.04		0.03		0.05		0.03	0.03	0.04		0.04	0.02
Q91ZW3	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	0.08	0.06	0.03	0.02	0.02	0.02			0.03	0.06		0.01
Q91ZX7	Prolow-density lipoprotein receptor-related protein 1	0.08	0.05	0.13	0.11	0.07	0.02	0.10	0.06	0.09		0.14	0.05
Q920A5	Retinoid-inducible serine carboxypeptidase			0.02			0.01					0.02	0.01
Q920E5	Farnesyl pyrophosphate synthase	0.15	0.14	0.09	0.20	0.14	0.11	0.07	0.09	0.20	0.09	0.10	0.21
Q920Q6	RNA-binding protein Musashi homolog 2			0.02	0.01								
Q921F2	TAR DNA-binding protein 43	0.12	0.15	0.05	0.04	0.03	0.08	0.02	0.01	0.07	0.13	0.03	0.03
Q921G7	Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial			0.06	0.07	0.02	0.03	0.01		0.01		0.03	
Q921H8	3-ketoacyl-CoA thiolase A, peroxisomal	0.23	0.25	0.18	0.10	0.15	0.12	0.09	0.07	0.19	0.25	0.17	0.15
Q921M7	Protein FAM49B	0.16	0.19	0.11	0.08	0.10	0.08	0.07	0.04	0.10		0.12	0.10
Q921N6	Probable ATP-dependent RNA helicase DDX27									0.02			
Q921S7	39S ribosomal protein L37, mitochondrial												0.01
Q921T2	Torsin-1A-interacting protein 1		0.04	0.04	0.02				0.01				
Q921Y2	U3 small nucleolar ribonucleoprotein protein IMP3	0.05			0.01		0.01						0.01
Q922F4	Tubulin beta-6 chain	0.56	0.46	0.37	0.42	0.28	0.32	0.14	0.13	0.37	0.40	0.22	0.46

Q922J9	Fatty acyl-CoA reductase 1	0.05	0.06	0.06	0.08	0.02	0.03	0.03	0.03	0.02	0.07	0.04	0.05
Q922Q1	Mitochondrial amidoxime reducing component 2			0.02				0.02				0.04	
Q922Q8	Leucine-rich repeat-containing protein 59	0.08	0.05	0.10	0.06	0.06	0.04	0.05	0.07	0.03		0.10	
Q922Y1	UBX domain-containing protein 1									0.01			
Q923G2	DNA-directed RNA polymerases I, II, and III subunit RPABC3	0.06		0.02	0.02	0.04	0.01		0.01			0.02	0.02
Q924T2	28S ribosomal protein S2, mitochondrial		0.03	0.03	0.03	0.02	0.02	0.01	0.01	0.04		0.03	0.02
Q925I1	ATPase family AAA domain-containing protein 3		0.03	0.02	0.03	0.02	0.01			0.03			0.02
Q99J95	Cyclin-dependent kinase 9			0.04	0.03		0.02		0.01	0.02		0.02	0.02
Q99JB2	Stomatin-like protein 2, mitochondrial	0.08	0.10	0.06	0.16	0.05	0.10	0.05	0.05	0.08		0.06	0.04
Q99JI4	26S proteasome non-ATPase regulatory subunit 6	0.09	0.10	0.09	0.04	0.03	0.03	0.04	0.03	0.06		0.09	0.04
Q99JI6	Ras-related protein Rap-1b	0.13		0.06	0.10	0.22	0.05	0.08	0.06			0.08	0.06
Q99JR1	Sideroflexin-1	0.07	0.08	0.04	0.05	0.04	0.04	0.02	0.03	0.03	0.05	0.02	0.06
Q99JX4	Eukaryotic translation initiation factor 3 subunit M	0.12	0.12	0.05	0.04	0.02	0.05	0.03	0.01	0.04		0.05	0.02
Q99JY0	Trifunctional enzyme subunit beta, mitochondrial	0.13	0.11	0.14	0.11	0.14	0.09	0.06	0.03	0.17		0.09	0.05
Q99JZ4	GTP-binding protein SAR1a			0.07	0.09	0.13	0.05	0.04	0.05	0.07	0.06	0.08	0.08
Q99K01	Pyridoxal-dependent decarboxylase domain-containing protein 1		0.05		0.01		0.01				0.07		0.01
Q99K87	Serine hydroxymethyltransferase	0.38	0.32	0.41	0.79	0.46	0.39	0.18	0.20	0.47	0.24	0.32	0.36
Q99KC8	von Willebrand factor A domain-containing protein 5A		0.05	0.02	0.04		0.01						
Q99KD5	Protein unc-45 homolog A						0.01						
Q99KI0	Aconitate hydratase, mitochondrial	0.06	0.11	0.15	0.19	0.24	0.13	0.07	0.15	0.35	0.11	0.16	0.17
Q99KI3	ER membrane protein complex subunit 3		0.04	0.02	0.04	0.02	0.02	0.01	0.01	0.02		0.03	0.02
Q99KK9	Probable histidine--tRNA ligase, mitochondrial					0.04		0.02		0.02		0.02	0.01
Q99KV1	DnaJ homolog subfamily B member 11		0.10	0.08	0.06	0.02	0.03	0.02	0.02	0.02		0.07	
Q99L04	Dehydrogenase/reductase SDR family member 1			0.03	0.02	0.02	0.02	0.01	0.02	0.02			0.03
Q99LB6	Methionine adenosyltransferase 2 subunit beta					0.03				0.02			
Q99LC3	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial		0.04	0.03						0.02			0.01
Q99LC5	Electron transfer flavoprotein subunit alpha, mitochondrial	0.26	0.29	0.20	0.23	0.25	0.17	0.10	0.08	0.26	0.25	0.17	0.13
Q99LI7	Cleavage stimulation factor subunit 3									0.02			
Q99LX0	Protein deglycase DJ-1				0.03								
Q99M31	Heat shock 70 kDa protein 14		0.02	0.03			0.01	0.02		0.03		0.03	
Q99M87	DnaJ homolog subfamily A member 3, mitochondrial	0.04	0.04	0.02	0.03		0.02			0.02			
Q99ME9	Nucleolar GTP-binding protein 1			0.02									0.01
Q99MR3	Solute carrier family 12 member 9			0.03						0.02			
Q99MR6	Serrate RNA effector molecule homolog	0.15	0.12	0.10	0.07	0.07	0.06	0.05	0.03	0.10	0.18	0.09	0.02
Q99MR8	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial	0.32	0.15	0.13	0.08	0.02	0.07				0.28		
Q99N96	39S ribosomal protein L1, mitochondrial		0.03		0.01	0.03	0.02			0.03			
Q99P31	Hsp70-binding protein 1		0.05	0.02	0.02	0.02	0.04	0.02		0.05		0.02	0.01
Q99P72	Reticulon-4		0.03	0.04	0.02			0.03	0.01	0.02		0.04	0.01
Q99PL5	Ribosome-binding protein 1		0.05		0.02		0.02		0.01				0.01
Q99PV0	Pre-mRNA-processing-splicing factor 8			0.02	0.03	0.05		0.01	0.02	0.09		0.05	0.03
Q9BDB7	Interferon-induced protein 44-like						0.03						
Q9CPP6	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5												0.02
Q9CPQ3	Mitochondrial import receptor subunit TOM22 homolog	0.08	0.05	0.03	0.06	0.04	0.02	0.01	0.02			0.02	0.06
Q9CPR5	39S ribosomal protein L15, mitochondrial				0.02					0.01			0.02
Q9CPT4	Myeloid-derived growth factor								0.01				
Q9CPT5	Nucleolar protein 16		0.07	0.03			0.03					0.03	

Q9CPU4	Microsomal glutathione S-transferase 3												0.01
Q9CPX7	28S ribosomal protein S16, mitochondrial												0.01
Q9CPY7	Cytosol aminopeptidase				0.01	0.02			0.02			0.02	0.02
Q9CQ02	COMM domain-containing protein 4				0.02								0.01
Q9CQ22	Ragulator complex protein LAMTOR1					0.02							0.02
Q9CQ40	39S ribosomal protein L49, mitochondrial												0.01
Q9CQ60	6-phosphogluconolactonase		0.08	0.04	0.06	0.10	0.05	0.05	0.01	0.08		0.05	0.07
Q9CQ65	S-methyl-5'-thioadenosine phosphorylase												0.01
Q9CQ71	Replication protein A 14 kDa subunit												0.01
Q9CQ92	Mitochondrial fission 1 protein			0.02				0.02				0.02	
Q9CQA1	Trafficking protein particle complex subunit 5				0.02		0.01						0.02
Q9CQB5	CDGSH iron-sulfur domain-containing protein 2				0.02								0.01
Q9CQC8	Maspardin			0.01									
Q9CQD1	Ras-related protein Rab-5A	0.15	0.14	0.09	0.17	0.17	0.10	0.08	0.07	0.13	0.15	0.11	0.09
Q9CQE3	28S ribosomal protein S17, mitochondrial												0.01
Q9CQF0	39S ribosomal protein L11, mitochondrial			0.01	0.03	0.02	0.03	0.02	0.01			0.03	0.01
Q9CQH8	Ribonuclease P protein subunit p14												0.01
Q9CQI6	Coactosin-like protein						0.01						0.02
Q9CQI7	U2 small nuclear ribonucleoprotein B''						0.01						
Q9CQJ8	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9								0.01				
Q9CQK2	40S ribosomal protein S24	0.13	0.08	0.09	0.14	0.15	0.08	0.09	0.06		0.09	0.10	0.21
Q9CQL4	39S ribosomal protein L20, mitochondrial												0.01
Q9CQL5	39S ribosomal protein L18, mitochondrial				0.01	0.02			0.01				0.03
Q9CQM9	Glutaredoxin-3							0.01					
Q9CQN7	39S ribosomal protein L41, mitochondrial								0.01				0.08
Q9CQT1	Methylthioribose-1-phosphate isomerase			0.03	0.02		0.04	0.02		0.04		0.03	
Q9CQV8	14-3-3 protein beta/alpha	0.07	0.07	0.09	0.08	0.12	0.06	0.13	0.13	0.11	0.06	0.13	0.15
Q9CQW0	ER membrane protein complex subunit 6								0.02				0.02
Q9CQW2	ADP-ribosylation factor-like protein 8B	0.06	0.03	0.08	0.06	0.07	0.04	0.07	0.07			0.08	0.06
Q9CQW9	Interferon-induced transmembrane protein 3				0.02				0.02				0.03
Q9CQZ5	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6												0.01
Q9CQZ6	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3												0.01
Q9CR59	Growth arrest and DNA damage-inducible proteins-interacting protein 1				0.01			0.01					
Q9CR61	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7			0.02				0.02	0.01			0.02	0.02
Q9CR67	Transmembrane protein 33	0.05	0.04	0.04	0.07	0.06	0.04	0.02	0.03	0.04		0.03	0.09
Q9CR68	Cytochrome b-c1 complex subunit Rieske, mitochondrial		0.04	0.03	0.08	0.04	0.04	0.01	0.02	0.03		0.03	0.03
Q9CR88	28S ribosomal protein S14, mitochondrial												0.01
Q9CRA5	Golgi phosphoprotein 3												0.01
Q9CRA8	Exosome complex component RRP46									0.02			
Q9CRB2	H/ACA ribonucleoprotein complex subunit 2												0.01
Q9CRB9	MICOS complex subunit Mic19		0.05	0.03	0.04	0.06	0.05	0.02	0.01	0.03	0.06	0.04	0.03
Q9CRT8	Exportin-T	0.03	0.06	0.06	0.05	0.04	0.05	0.02		0.09	0.06	0.05	0.03
Q9CS42	Ribose-phosphate pyrophosphokinase 2	0.04		0.06	0.09	0.13	0.05	0.04	0.04	0.13	0.05	0.08	0.06
Q9CSH3	Exosome complex exonuclease RRP44		0.05				0.01				0.06		
Q9CSU0	Regulation of nuclear pre-mRNA domain-containing protein 1B	0.06	0.09	0.02	0.02	0.03	0.04						

Q9CT10	Ran-binding protein 3	0.05	0.08	0.01	0.03	0.02	0.03		0.01		0.06		0.01
Q9CU62	Structural maintenance of chromosomes protein 1A	0.10	0.08	0.03	0.03	0.03	0.02			0.02	0.09		0.01
Q9CVB6	Actin-related protein 2/3 complex subunit 2			0.02	0.01	0.05	0.01	0.05	0.07	0.04		0.07	0.06
Q9CVF5	Putative uncharacterized protein												0.01
Q9CWJ9	Bifunctional purine biosynthesis protein PURH					0.13		0.04	0.06	0.07		0.05	0.11
Q9CWK0	Putative uncharacterized protein	0.20	0.15	0.21	0.25	0.27	0.13	0.15	0.14	0.22	0.15	0.22	0.34
Q9CWU6	Ubiquinol-cytochrome-c reductase complex assembly factor 1				0.01				0.02				0.02
Q9CX00	IST1 homolog				0.01								
Q9CX30	Protein YIF1B						0.01						0.01
Q9CX34	Protein SGT1 homolog	0.09	0.10				0.02						0.01
Q9CX56	26S proteasome non-ATPase regulatory subunit 8			0.04	0.06	0.05	0.02	0.03	0.03	0.06		0.06	0.04
Q9CX86	Heterogeneous nuclear ribonucleoprotein A0		0.07	0.03	0.06		0.09			0.04		0.03	0.04
Q9CXJ4	ATP-binding cassette sub-family B member 8, mitochondrial			0.09	0.02	0.03	0.02	0.06		0.05		0.08	
Q9CXK8	60S ribosome subunit biogenesis protein NIP7 homolog								0.01				0.02
Q9CXR1	Dehydrogenase/reductase SDR family member 7									0.01			
Q9CXS4	Centromere protein V		0.03	0.02	0.02		0.02			0.02			0.01
Q9CXT8	Mitochondrial-processing peptidase subunit beta			0.02					0.01				0.02
Q9CXW2	28S ribosomal protein S22, mitochondrial	0.06	0.05	0.03	0.02		0.02	0.02				0.02	0.01
Q9CY16	28S ribosomal protein S28, mitochondrial			0.01	0.03	0.03							0.01
Q9CY49	Putative uncharacterized protein			0.02									
Q9CY57	Chromatin target of PRMT1 protein		0.08	0.04	0.02		0.03	0.01	0.01	0.02		0.04	
Q9CY58	Plasminogen activator inhibitor 1 RNA-binding protein			0.02	0.03		0.01						
Q9CY64	Biliverdin reductase A	0.08	0.04	0.08	0.06	0.20	0.03	0.06	0.08	0.10		0.08	0.12
Q9CYI4	Putative RNA-binding protein Luc7-like 1	0.06	0.05	0.04	0.03	0.03	0.03	0.02	0.01	0.02	0.05	0.05	0.02
Q9CYN2	Signal peptidase complex subunit 2	0.06	0.04	0.06	0.07	0.07	0.03	0.06	0.08			0.04	0.08
Q9CYN9	Renin receptor				0.02		0.01		0.02			0.02	0.01
Q9CYT3	Putative uncharacterized protein	0.16	0.18	0.13	0.25	0.15	0.14	0.06	0.08	0.15	0.17	0.13	0.10
Q9CZ04	COP9 signalosome complex subunit 7a	0.03	0.05	0.01	0.02	0.02	0.01	0.02		0.03		0.03	
Q9CZ28	Vacuolar-sorting protein SNF8				0.02		0.01						
Q9CZB4	Putative uncharacterized protein	0.05	0.05	0.06	0.06	0.04	0.03	0.03	0.04	0.04		0.06	0.04
Q9CZD3	Glycine--tRNA ligase	0.10	0.08	0.16	0.12	0.18	0.12	0.14	0.09	0.17	0.16	0.17	0.12
Q9CZH3	Proteasome assembly chaperone 3												0.02
Q9CZI5	Putative uncharacterized protein		0.02	0.08	0.09	0.10	0.04	0.05	0.03		0.05	0.07	0.10
Q9CZR8	Elongation factor Ts, mitochondrial	0.04	0.05	0.03	0.05	0.05	0.03		0.02	0.03		0.02	0.02
Q9CZU3	Superkiller viralicidic activity 2-like 2	0.04		0.02	0.02	0.05	0.02			0.05	0.14		0.01
Q9CZU5	Putative uncharacterized protein			0.15	0.05	0.03	0.04	0.02	0.02	0.08		0.06	0.05
Q9CZU6	Citrate synthase, mitochondrial								0.03				0.02
Q9CZX9	ER membrane protein complex subunit 4				0.01				0.02				0.03
Q9D024	Coiled-coil domain-containing protein 47		0.04	0.03	0.04		0.01		0.01			0.02	0.01
Q9D051	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial		0.12	0.04	0.06	0.11	0.04	0.03	0.06	0.06		0.04	0.11
Q9D071	MMS19 nucleotide excision repair protein homolog					0.02				0.03			
Q9D0D5	General transcription factor IIE subunit 1		0.03				0.01						
Q9D0E1	Heterogeneous nuclear ribonucleoprotein M	0.52	0.45	0.25	0.31	0.18	0.27	0.07	0.11	0.24	0.66	0.13	0.15
Q9D0G0	28S ribosomal protein S30, mitochondrial		0.03				0.01						
Q9D0I9	Arginine--tRNA ligase, cytoplasmic	0.26	0.21	0.21	0.19	0.13	0.14	0.09	0.05	0.18	0.20	0.18	0.20
Q9D0J4	ADP-ribosylation factor-like protein 2				0.02	0.02							0.03
Q9D0K2	Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial		0.07	0.05	0.11	0.12	0.02	0.03	0.06	0.11		0.07	0.11
Q9D0M3	Cytochrome c1, heme protein, mitochondrial	0.11	0.08	0.09	0.11	0.05	0.06	0.04	0.06	0.05	0.06	0.09	0.06

Q9D0R2	Threonine--tRNA ligase, cytoplasmic					0.08		0.04	0.03	0.06			0.10
Q9D0R8	Protein LSM12 homolog				0.04		0.02						
Q9D0T1	NHP2-like protein 1								0.02				0.03
Q9D172	ES1 protein homolog, mitochondrial				0.02								
Q9D1A2	Cytosolic non-specific dipeptidase	0.06	0.08			0.14		0.16	0.06	0.22	0.04	0.20	0.08
Q9D1B9	39S ribosomal protein L28, mitochondrial												0.01
Q9D1C8	Vacuolar protein sorting-associated protein 28 homolog												0.01
Q9D1D4	Transmembrane emp24 domain-containing protein 10	0.05	0.03	0.07	0.09	0.07	0.04	0.06	0.04			0.07	0.04
Q9D1G1	Ras-related protein Rab-1B	0.30	0.24	0.16	0.28	0.27	0.18	0.17	0.14	0.25	0.27	0.22	0.29
Q9D1H7	Golgi to ER traffic protein 4 homolog			0.02						0.02			0.01
Q9D1H8	39S ribosomal protein L53, mitochondrial												0.01
Q9D1K2	V-type proton ATPase subunit F								0.01				0.02
Q9D1M4	Eukaryotic translation elongation factor 1 epsilon-1												0.02
Q9D1M7	Peptidyl-prolyl cis-trans isomerase FKBP11			0.02	0.02	0.03	0.02		0.02			0.02	0.02
Q9D1N9	39S ribosomal protein L21, mitochondrial				0.02				0.02			0.02	0.03
Q9D1P0	39S ribosomal protein L13, mitochondrial			0.02	0.01				0.02				0.04
Q9D1P4	Cysteine and histidine-rich domain-containing protein 1	0.06	0.06	0.03	0.04	0.02	0.05			0.04	0.08	0.03	
Q9D1R9	60S ribosomal protein L34				0.07		0.04	0.03	0.08			0.06	0.14
Q9D289	Trafficking protein particle complex subunit 6B												0.01
Q9D379	Epoxide hydrolase 1			0.02									
Q9D3B1	Very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase 2						0.01						
Q9D3P8	Plasminogen receptor (KT)			0.03	0.02		0.01	0.03	0.02			0.04	0.02
Q9D554	Splicing factor 3A subunit 3			0.02		0.02				0.02			
Q9D6J6	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial			0.02	0.06	0.02	0.02	0.02	0.02	0.02		0.02	0.02
Q9D6R2	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	0.14	0.13	0.10	0.11	0.10	0.08	0.07	0.06	0.16	0.12	0.12	0.09
Q9D6U8	Protein FAM162A								0.01				
Q9D7N3	28S ribosomal protein S9, mitochondrial	0.07	0.06	0.04	0.04	0.02	0.03	0.02	0.01	0.03	0.06	0.02	0.02
Q9D7N9	Adipocyte plasma membrane-associated protein			0.05				0.02				0.03	
Q9D853	Protein-lysine N-methyltransferase Mettl10						0.01						
Q9D868	Peptidyl-prolyl cis-trans isomerase H												0.01
Q9D880	Mitochondrial import inner membrane translocase subunit TIM50	0.10	0.09	0.05	0.07	0.02	0.06	0.02	0.03	0.06	0.10	0.04	0.03
Q9D881	Cytochrome c oxidase subunit 5B, mitochondrial								0.03				0.06
Q9D892	Inosine triphosphate pyrophosphatase	0.08	0.04	0.03	0.06	0.05	0.05	0.03	0.01			0.03	0.05
Q9D8B3	Charged multivesicular body protein 4b				0.03		0.01			0.01			
Q9D8L3	Signal sequence receptor, delta	0.20	0.09	0.12	0.17	0.13	0.07	0.06	0.15		0.13	0.10	0.24
Q9D8N0	Elongation factor 1-gamma	0.16	0.16	0.19	0.14	0.13	0.10	0.13	0.06	0.16	0.21	0.19	0.11
Q9D8S5	MCG7614, isoform CRA_c			0.02	0.02	0.05	0.01	0.02	0.02	0.03		0.02	0.02
Q9D8V0	Minor histocompatibility antigen H13	0.09	0.07	0.10	0.11	0.02	0.06	0.08	0.05	0.05		0.13	0.03
Q9D8V7	Signal peptidase complex catalytic subunit SEC11C				0.02								0.03
Q9D8Y1	Transmembrane protein 126A												0.01
Q9D903	Probable rRNA-processing protein EBP2							0.01					
Q9D964	Glycine amidinotransferase, mitochondrial								0.03				0.05
Q9D9V3	Ethylmalonyl-CoA decarboxylase			0.01	0.01					0.02			0.01
Q9DAV9	Trimeric intracellular cation channel type B	0.09	0.10	0.06	0.12	0.06	0.07	0.04	0.09	0.05	0.11	0.06	0.13
Q9DB05	Alpha-soluble NSF attachment protein		0.03	0.09	0.03	0.08	0.02	0.06	0.09	0.05		0.11	0.07
Q9DB15	39S ribosomal protein L12, mitochondrial			0.02	0.02		0.01						
Q9DB20	ATP synthase subunit O, mitochondrial	0.36	0.25	0.16	0.28	0.21	0.15	0.08	0.14	0.13	0.26	0.16	0.22
Q9DB27	Malignant T-cell-amplified sequence 1												0.01

Q9DB73	NADH-cytochrome b5 reductase 1			0.04		0.02	0.01	0.02		0.01		0.05	
Q9DB77	Cytochrome b-c1 complex subunit 2, mitochondrial	0.38	0.37	0.35	0.42	0.21	0.28	0.19	0.13	0.28		0.32	0.24
Q9DB79	Putative uncharacterized protein	0.12	0.06	0.12	0.14	0.10	0.04	0.08	0.05		0.09	0.11	0.20
Q9DB82	N-acetyltransferase 5 (ARD1 homolog, S. cerevisiae), isoform CRA_a												0.02
Q9DB96	Neuroguidin		0.03				0.01						
Q9DBA6	Peroxisomal leader peptide-processing protease				0.02					0.01		0.02	
Q9DBD5	Proline-, glutamic acid- and leucine-rich protein 1			0.02	0.02					0.02			
Q9DBE9	pre-rRNA processing protein FTSJ3		0.04				0.02			0.01			
Q9DBG7	Signal recognition particle receptor subunit alpha	0.06	0.05	0.07	0.04		0.02	0.03	0.01	0.02	0.08	0.05	0.04
Q9DBH5	Vesicular integral-membrane protein VIP36			0.03	0.02	0.04	0.01	0.04	0.02	0.03		0.04	0.02
Q9DBJ1	Phosphoglycerate mutase 1					0.03		0.02	0.04	0.03		0.02	0.09
Q9DBL7	Bifunctional coenzyme A synthase									0.01			
Q9DBP5	UMP-CMP kinase		0.05	0.04	0.08	0.06	0.06	0.05	0.03	0.07	0.07	0.05	0.06
Q9DBS1	Transmembrane protein 43			0.02				0.02					
Q9DBY8	Nuclear valosin-containing protein-like		0.04								0.08		
Q9DBZ5	Eukaryotic translation initiation factor 3 subunit K	0.04		0.02	0.06	0.04	0.03	0.03	0.02	0.04		0.04	0.05
Q9DC13	Lysosomal membrane glycoprotein 1, isoform CRA_a			0.03	0.02	0.02	0.01	0.03	0.01	0.02		0.05	
Q9DC23	DnaJ homolog subfamily C member 10			0.01	0.01				0.01				0.01
Q9DC37	Major facilitator superfamily domain-containing protein 1			0.03	0.03	0.02	0.02	0.02	0.01	0.02		0.02	0.01
Q9DC53	Copine-8											0.02	
Q9DC69	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial			0.04	0.09	0.04	0.02	0.01		0.05		0.02	0.05
Q9DC70	NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial			0.03	0.05	0.05	0.03	0.02	0.03			0.02	0.06
Q9DC71	28S ribosomal protein S15, mitochondrial				0.03	0.02	0.03	0.01		0.01		0.02	0.01
Q9DCC4	Pyrroline-5-carboxylate reductase 3		0.04				0.02						
Q9DCJ5	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8			0.03	0.01	0.02		0.02	0.02			0.03	0.01
Q9DCJ9	N-acetylneuraminate lyase		0.04	0.02		0.02	0.02			0.03		0.02	
Q9DCL9	Multifunctional protein ADE2		0.03		0.01		0.01	0.03	0.02	0.02		0.03	0.03
Q9DCR2	AP-3 complex subunit sigma-1				0.02	0.02							0.01
Q9DCS3	Trans-2-enoyl-CoA reductase, mitochondrial				0.02								
Q9DCS9	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10		0.03	0.04	0.06	0.03	0.03	0.03	0.03	0.02		0.05	0.04
Q9DCT2	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	0.13	0.10	0.09	0.18	0.13	0.08	0.06	0.09	0.12	0.11	0.10	0.08
Q9DCU6	39S ribosomal protein L4, mitochondrial								0.01				0.01
Q9DCW4	Electron transfer flavoprotein subunit beta	0.11	0.07	0.16	0.21	0.30	0.14	0.10	0.07	0.23	0.09	0.14	0.07
Q9DCX2	ATP synthase subunit d, mitochondrial			0.05	0.06	0.02	0.03	0.05	0.03			0.06	0.06
Q9DCY1	Peptidyl-prolyl cis-trans isomerase			0.02	0.06	0.07	0.02	0.06	0.13		0.05	0.04	0.10
Q9DCZ4	MICOS complex subunit Mic26				0.02		0.01						
Q9EP69	Phosphatidylinositide phosphatase SAC1		0.04	0.05	0.03							0.02	
Q9EPE9	Manganese-transporting ATPase 13A1			0.04	0.02				0.01	0.02		0.02	0.02
Q9EPK6	Nucleotide exchange factor SIL1			0.03	0.03		0.01	0.02	0.01	0.02		0.04	
Q9EPL8	Importin-7	0.18	0.14	0.10	0.11	0.07	0.06	0.05	0.05	0.14	0.20	0.08	0.08
Q9EPL9	Peroxisomal acyl-coenzyme A oxidase 3			0.02		0.02							0.01
Q9EPR4	Solute carrier family 23 member 2				0.02								0.01
Q9EPU0	Regulator of nonsense transcripts 1	0.06	0.05	0.05	0.04	0.04	0.02	0.02	0.02	0.06		0.05	0.03
Q9EPU4	Cleavage and polyadenylation specificity factor subunit 1		0.03										

Q9EQ06	Estradiol 17-beta-dehydrogenase 11			0.02	0.02	0.02				0.02		0.02	0.01
Q9EQH2	Endoplasmic reticulum aminopeptidase 1	0.03		0.02	0.09	0.04	0.05	0.04	0.10	0.03			0.04
Q9EQI8	39S ribosomal protein L46, mitochondrial			0.02	0.01	0.02	0.02	0.02	0.01	0.02		0.02	
Q9ER41	Torsin-1B				0.03								
Q9ERI6	Retinol dehydrogenase 14			0.03	0.03	0.03	0.01	0.02	0.01			0.02	
Q9ERK4	Exportin-2	0.25	0.20	0.08	0.10	0.09	0.10	0.02	0.04	0.15	0.31	0.05	0.08
Q9ERR7	15 kDa selenoprotein								0.01				0.02
Q9ERS2	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13			0.05	0.07		0.04	0.03	0.04			0.05	0.07
Q9ERU9	E3 SUMO-protein ligase RanBP2	0.12	0.14	0.04	0.05	0.02	0.01		0.01	0.04	0.09	0.02	0.02
Q9ES28	Rho guanine nucleotide exchange factor 7			0.02									
Q9ES52	Phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 1		0.06	0.02				0.01		0.04		0.02	0.02
Q9ES94	Cathepsin Z	0.05	0.06	0.03	0.03	0.03	0.02	0.03	0.01	0.03	0.05	0.02	0.01
Q9ES97	Reticulon-3			0.02	0.04	0.03	0.02	0.02	0.01	0.03		0.05	0.01
Q9ESJ0	Exportin-4		0.03										
Q9ESP1	Stromal cell-derived factor 2-like protein 1			0.02	0.02	0.02	0.01	0.02	0.02			0.02	0.02
Q9EST5	Acidic leucine-rich nuclear phosphoprotein 32 family member B			0.02		0.04	0.01	0.02		0.05		0.02	0.02
Q9ESW4	Acylglycerol kinase, mitochondrial			0.02									
Q9JHI5	Isovaleryl-CoA dehydrogenase, mitochondrial												0.01
Q9JHI7	Exosome complex component RRP45					0.02	0.01	0.02	0.01	0.01		0.02	
Q9JHS4	ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial			0.03	0.02		0.02			0.02		0.02	
Q9JHU4	Cytoplasmic dynein 1 heavy chain 1	0.40	0.40	0.32	0.24	0.19	0.14	0.10	0.04	0.47	0.35	0.23	0.34
Q9JI10	Serine/threonine-protein kinase 3		0.05		0.02		0.01						0.01
Q9JI11	Serine/threonine-protein kinase 4		0.04		0.02		0.01						0.01
Q9JIF0	Protein arginine N-methyltransferase 1							0.01	0.03			0.02	0.04
Q9JIF7	Coatomer subunit beta	0.20	0.12	0.06	0.05	0.02	0.07	0.01	0.02	0.04	0.24	0.03	0.06
Q9JIG8	PRA1 family protein 2			0.02	0.03	0.02			0.01			0.02	0.02
Q9JIK9	28S ribosomal protein S34, mitochondrial		0.04	0.02	0.05	0.05	0.02	0.02		0.02		0.02	0.01
Q9JJ28	Protein flightless-1 homolog			0.06	0.05		0.02	0.03	0.01	0.03	0.06	0.05	0.03
Q9JJ80	Ribosome production factor 2 homolog		0.05	0.01	0.05	0.04	0.03		0.03	0.05	0.04	0.03	0.02
Q9JKB1	Ubiquitin carboxyl-terminal hydrolase isozyme L3												0.02
Q9JKR6	Hypoxia up-regulated protein 1	0.52	0.41	0.47	0.46	0.28	0.20	0.18	0.23	0.33	0.76	0.36	0.21
Q9JKX6	ADP-sugar pyrophosphatase		0.03	0.02	0.01	0.03	0.02		0.01	0.03		0.02	0.01
Q9JKY0	Cell differentiation protein RCD1 homolog												0.01
Q9JKZ2	Sodium/myo-inositol cotransporter		0.03		0.01	0.02	0.01		0.02	0.02	0.05	0.02	0.02
Q9JL26	Formin-like protein 1	0.06	0.08	0.08	0.06	0.04	0.03	0.03	0.02	0.08	0.10	0.07	0.05
Q9JLI8	Squamous cell carcinoma antigen recognized by T-cells 3												0.01
Q9JLJ5	Elongation of very long chain fatty acids protein 1				0.02		0.01						0.01
Q9JM62	Receptor expression-enhancing protein 6												0.01
Q9JM76	Actin-related protein 2/3 complex subunit 3			0.02	0.03	0.07	0.01	0.03	0.04			0.04	0.11
Q9JMA1	Ubiquitin carboxyl-terminal hydrolase 14	0.15	0.18	0.11	0.09	0.08	0.09	0.08	0.04	0.13	0.21	0.14	0.06
Q9QUJ7	Long-chain-fatty-acid--CoA ligase 4			0.03								0.02	
Q9QUM9	Proteasome subunit alpha type-6					0.04	0.02	0.02					0.01
Q9QXB9	Developmentally-regulated GTP-binding protein 2	0.06	0.07		0.01		0.03			0.01			0.01
Q9QXK3	Coatomer subunit gamma-2	0.04	0.04	0.01	0.01	0.02				0.03	0.05		0.01
Q9QXS1	Plectin	0.22	0.34	0.69	0.74	0.07	0.02	0.35	0.43	0.15	0.07	0.57	1.13
Q9QXX4	Calcium-binding mitochondrial carrier protein Aralar2	0.11	0.08	0.15	0.36	0.13	0.04	0.09	0.23	0.13		0.16	0.17
Q9QY81	Nuclear pore membrane glycoprotein 210	0.04	0.04	0.02	0.04		0.01						0.01

Q9QYA2	Mitochondrial import receptor subunit TOM40 homolog	0.09	0.07	0.08	0.06	0.04	0.09	0.04	0.05	0.05		0.07	0.07
Q9QYB1	Chloride intracellular channel protein 4	0.13	0.15	0.10	0.11	0.03	0.11	0.04		0.08	0.14	0.10	0.05
Q9QYF1	Retinol dehydrogenase 11	0.05	0.05	0.03	0.04	0.02	0.02		0.01	0.02	0.07	0.02	0.02
Q9QYG0	Protein NDRG2	0.15	0.13	0.07	0.06	0.02	0.04	0.05	0.01	0.06		0.06	0.02
Q9QYS9	Protein quaking		0.04	0.02	0.02		0.02	0.01		0.02		0.02	
Q9QZ88	Vacuolar protein sorting-associated protein 29					0.03			0.01			0.02	0.03
Q9QZD8	Mitochondrial dicarboxylate carrier		0.04		0.05	0.02	0.02		0.01				0.03
Q9QZD9	Eukaryotic translation initiation factor 3 subunit I	0.16	0.13	0.07	0.07	0.05	0.06	0.04	0.02	0.05	0.12	0.07	0.03
Q9QZE5	Coatomer subunit gamma-1	0.11	0.10	0.06	0.08	0.05	0.04	0.02	0.01	0.09	0.18	0.03	0.07
Q9QZQ8	Core histone macro-H2A.1							0.01	0.01				0.01
Q9R059	Four and a half LIM domains protein 3		0.03	0.01						0.01			0.01
Q9R061	Cytosolic Fe-S cluster assembly factor NUBP2	0.03					0.03						
Q9R0E1	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3		0.05	0.08	0.09	0.04	0.04	0.03	0.03	0.06	0.06	0.07	0.03
Q9R0P5	Destrin	0.05		0.04	0.05	0.13	0.04	0.03	0.12		0.05	0.06	0.10
Q9R0Q3	Transmembrane emp24 domain-containing protein 2			0.02	0.06	0.02	0.02	0.02	0.03			0.04	0.02
Q9R0X0	Mediator of RNA polymerase II transcription subunit 20				0.01	0.02		0.01		0.01			
Q9R0X4	Acyl-coenzyme A thioesterase 9, mitochondrial			0.07	0.03							0.02	
Q9R1P0	Proteasome subunit alpha type-4					0.03							0.01
Q9R1P1	Proteasome subunit beta type-3					0.02			0.01				0.04
Q9R1P4	Proteasome subunit alpha type-1					0.03	0.02		0.01	0.03		0.02	0.01
Q9R1T2	SUMO-activating enzyme subunit 1	0.12	0.12	0.03	0.06	0.03	0.08	0.02	0.01	0.06		0.03	0.02
Q9WTI7	Unconventional myosin-Ic	0.05	0.05	0.03	0.05	0.02				0.03		0.02	0.05
Q9WTL7	Acyl-protein thioesterase 2									0.01			
Q9WTM5	RuvB-like 2	0.12	0.14	0.14	0.12	0.16	0.06	0.10	0.12	0.13	0.15	0.13	0.13
Q9WTP7	GTP:AMP phosphotransferase AK3, mitochondrial		0.04	0.02	0.04	0.04	0.04	0.01		0.03		0.02	0.01
Q9WTR1	Transient receptor potential cation channel subfamily V member 2			0.02	0.03				0.02	0.02		0.03	0.01
Q9WU81	Sugar phosphate exchanger 2		0.03	0.02	0.04	0.03	0.02	0.02	0.02	0.02		0.03	0.03
Q9WUK4	Replication factor C subunit 2	0.05	0.06				0.04			0.03	0.04		
Q9WUL7	ADP-ribosylation factor-like protein 3					0.02							0.01
Q9WUM5	Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	0.09	0.09	0.06	0.06	0.04	0.03			0.04	0.04		0.01
Q9WUP7	Ubiquitin carboxyl-terminal hydrolase isozyme L5	0.09	0.06	0.03		0.02	0.02	0.01		0.03		0.03	0.01
Q9WUR2	Enoyl-CoA delta isomerase 2, mitochondrial						0.01						
Q9WUR9	Adenylate kinase 4, mitochondrial			0.03	0.02		0.01	0.02	0.02	0.01		0.03	0.01
Q9WV27	Sodium/potassium-transporting ATPase subunit alpha-4	0.19	0.13	0.17	0.21	0.13	0.11	0.13	0.12	0.15	0.23	0.18	0.12
Q9WV55	Vesicle-associated membrane protein-associated protein A	0.09	0.06	0.08	0.04	0.04	0.03	0.05		0.03		0.07	
Q9WVA3	Mitotic checkpoint protein BUB3		0.04										
Q9WVA4	Transgelin-2								0.01				
Q9WVJ2	26S proteasome non-ATPase regulatory subunit 13	0.24	0.21	0.12	0.15	0.07	0.11	0.07	0.03	0.16		0.12	0.03
Q9WVL0	Maleylacetoacetate isomerase						0.02			0.02			
Q9Z0G0	PDZ domain-containing protein GIPC1		0.06				0.02						
Q9Z0W3	Nuclear pore complex protein Nup160		0.04	0.04	0.03			0.01				0.02	0.01
Q9Z0X1	Apoptosis-inducing factor 1, mitochondrial	0.18	0.15	0.13	0.13	0.10	0.10	0.06	0.06	0.12		0.14	0.06
Q9Z1E4	Glycogen [starch] synthase, muscle												0.01
Q9Z1F9	SUMO-activating enzyme subunit 2	0.06	0.07	0.03	0.04		0.04			0.04	0.10	0.02	0.01
Q9Z1G4	V-type proton ATPase 116 kDa subunit a isoform 1			0.02	0.02			0.02				0.03	
Q9Z1N5	Spliceosome RNA helicase Ddx39b	0.19	0.17	0.18	0.10	0.21	0.09	0.12	0.09	0.21	0.22	0.15	0.08
Q9Z1Q5	Chloride intracellular channel protein 1	0.22	0.20	0.25	0.28	0.20	0.26	0.18	0.13	0.26	0.25	0.27	0.25
Q9Z1R2	Large proline-rich protein BAG6										0.09		

Q9Z1T1	AP-3 complex subunit beta-1			0.01						0.01			
Q9Z1Z0	General vesicular transport factor p115	0.08	0.07	0.05	0.03	0.02	0.02	0.02	0.01	0.05	0.07	0.03	0.03
Q9Z210	Peroxisomal membrane protein 11B			0.03	0.04		0.02	0.02	0.01	0.02		0.03	0.03
Q9Z277	Tyrosine-protein kinase BAZ1B		0.03								0.08		
Q9Z2D8	Methyl-CpG-binding domain protein 3												0.01
Q9Z2I0	LETM1 and EF-hand domain-containing protein 1, mitochondrial			0.03	0.02	0.02	0.02	0.03	0.01	0.01		0.04	
Q9Z2I8	Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	0.26	0.19	0.15	0.11	0.11	0.07	0.04	0.03	0.15	0.18	0.10	0.03
Q9Z2X1	Heterogeneous nuclear ribonucleoprotein F	0.29	0.24	0.14	0.16	0.17	0.13	0.06	0.06	0.17	0.22	0.10	0.13
S4R1S4	Receptor-type tyrosine-protein phosphatase C			0.08	0.03	0.05		0.06	0.05	0.05		0.09	0.06
V9GX06	Protein Gm11214	0.21	0.22	0.14	0.26	0.23	0.15	0.11	0.18	0.21	0.26	0.17	0.25
Z4YJY0	BRISC complex subunit Abro1			0.02			0.01					0.02	0.01