Elucidating the cellular response of silver nanoparticles as a potential combinatorial agent for cisplatin chemotherapy

Additional File 2

List of proteins deregulated in HepG2 cells after 24h exposure to AgNP 3.5 ug/mL………………… pages 1 – 25
List of proteins deregulated in HepG2 cells after 24h exposure to CDDP 10 µM………………… pages 26 – 46
List of proteins deregulated in HepG2 cells after 24h exposure to AgNP 3.5 ug/mL + CDDP 10 µM ………………… pages 47 – 110

List of proteins deregulated in HepG2 cells after 24h exposure to AgNP 3.5 ug/mL

ID	Symbol	Expr Log Ratio	Entrez Gene Name
Q9NQ94	A1CF	-0.202	APOBEC1 complementation factor
P01023	A2M	-0.225	alpha-2-macroglobulin
Q86V21-1	AACS	-0.191	acetoacetyl-CoA synthetase
Q2M2I8	AAK1	0.19	AP2 associated kinase 1
Q9NY61	AATF	0.171	apoptosis antagonizing transcription factor
P33527	ABCC1	0.254	ATP binding cassette subfamily C member 1
Q96IU4	ABHD14B	-0.231	abhydrolase domain containing 14B
Q8TB40	ABHD4	0.417	abhydrolase domain containing 4
P09110-1	ACAA1	-0.182	acetyl-CoA acyltransferase 1
Q13085-4	ACACA	-0.19	acetyl-CoA carboxylase alpha
P49748-3	ACADVL	0.251	acyl-CoA dehydrogenase very long chain
Q9BWD1	ACAT2	-0.344	acetyl-CoA acetyltransferase 2
P21399	ACO1	-0.154	aconitase 1
Q9Y305	ACOT9	0.237	acyl-CoA thioesterase 9
P24666	ACP1	-0.145	acid phosphatase 1
O60488-1	ACSL4	-0.4	acyl-CoA synthetase long chain family member 4
Q9ULC5-3	ACSL5	0.416	acyl-CoA synthetase long chain family member 5
Q9NR19-2	ACSS2	-0.298	acyl-CoA synthetase short chain family member 2
P42025	ACTR1B	-0.393	actin related protein 1B
Q03154-1	ACY1	-0.307	aminoacylase 1
P78536	ADAM17	0.137	ADAM metallopeptidase domain 17
P35611-3	ADD1	-0.247	adducin 1
Q9UEY8-2	ADD3	-0.249	adducin 3
P08319-2	ADH4	-0.355	alcohol dehydrogenase 4 (class II), pi polypeptide
P11766	ADH5	-0.271	alcohol dehydrogenase 5 (class III), chi polypeptide
P28332-2	ADH6	-0.333	alcohol dehydrogenase 6 (class V)
Q9BV57	ADI1	-0.289	acireductone dioxygenase 1
P55263	ADK	-0.28	adenosine kinase
Q9H2P0	ADNP	0.193	activity dependent neuroprotector homeobox
Q16186	ADRM1	0.236	adhesion regulating molecule 1
P30566	ADSL	-0.245	adenylosuccinate lyase
Q9UHB7-1	AFF4	0.172	AF4/FMR2 family member 4
P02771	AFP	-0.245	alpha fetoprotein
O95081	AGFG2	-0.119	ArfGAP with FG repeats 2
Q9UKV8	AGO2	0.163	argonaute RISC catalytic component 2
O00468	AGRN	-0.279	agrin
P01019	AGT	-0.564	angiotensinogen
P23526-1	AHCY	-0.231	adenosylhomocysteinase
P00568	AK1	-0.258	adenylate kinase 1

Q02952-1	AKAP12	1.337	A-kinase anchoring protein 12
Q02040-1	AKAP17A	0.224	A-kinase anchoring protein 17A
O43823	AKAP8	0.182	A-kinase anchoring protein 8
Q9ULX6	AKAP8L	0.208	A-kinase anchoring protein 8 like
P14550	AKR1A1	-0.204	aldo-keto reductase family 1 member A1
O60218	AKR1B10	0.146	aldo-keto reductase family 1 member B10
P51857	AKR1D1	-0.229	aldo-keto reductase family 1 member D1
P31749	AKT1	-0.145	AKT serine/threonine kinase 1
P13716-2	ALAD	-0.293	aminolevulinate dehydratase
P13196	ALAS1	0.702	5'-aminolevulinate synthase 1
P02768	ALB	-0.414	albumin
P02769	ALB	0.709	albumin
Q8IZ83	ALDH16A1	-0.165	aldehyde dehydrogenase 16 family member A1
P00352	ALDH1A1	-0.274	aldehyde dehydrogenase 1 family member A1
P09972	ALDOC	-0.179	aldolase, fructose-bisphosphate C
Q9Y673	ALG5	0.142	ALG5 dolichyl-phosphate beta-glucosyltransferase
Q86V81	ALYREF	0.209	Aly/REF export factor
Q9H1A4	ANAPC1	-0.103	anaphase promoting complex subunit 1
Q9P2R3-4	ANKFY1	-0.234	ankyrin repeat and FYVE domain containing 1
Q9NQW6	ANLN	0.174	anillin actin binding protein
Q92688	ANP32B	-0.174	acidic nuclear phosphoprotein 32 family member B
P15144	ANPEP	-0.14	alanyl aminopeptidase, membrane
P07355-2	ANXA2	0.479	annexin A2
P09525	ANXA4	-0.277	annexin A4
P08758	ANXA5	-0.211	annexin A5
P08133	ANXA6	-0.304	annexin A6
Q10567	AP1B1	-0.135	adaptor related protein complex 1 subunit beta 1
O43747	AP1G1	-0.18	adaptor related protein complex 1 subunit gamma 1
P61966	AP1S1	-0.139	adaptor related protein complex 1 subunit sigma 1
P63010-2	AP2B1	-0.165	adaptor related protein complex 2 subunit beta 1
O00203	AP3B1	-0.107	adaptor related protein complex 3 subunit beta 1
O14617-5	AP3D1	-0.167	adaptor related protein complex 3 subunit delta 1
P13798	APEH	-0.264	acylaminoacyl-peptide hydrolase
P02647	APOA1	-0.51	apolipoprotein A1
P04114	APOB	-0.435	apolipoprotein B
P02649	APOE	-0.248	apolipoprotein E
O14791-2	APOL1	-0.318	apolipoprotein L1
Q6UXV4	APOOL	0.191	apolipoprotein O like
P07741	APRT	-0.221	adenine phosphoribosyltransferase
O60306	AQR	0.166	aquarius intron-binding spliceosomal factor
Q96P48-6	ARAP1	-0.109	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 1
P48444	ARCN1	-0.099	archain 1
P84085	ARF5	-0.175	ADP ribosylation factor 5
Q9Y6D5	ARFGEF2	-0.198	ADP ribosylation factor guanine nucleotide exchange factor 2
P78540	ARG2	0.22	arginase 2
Q07960	ARHGAP1	-0.163	Rho GTPase activating protein 1
Q8N392	ARHGAP18	-0.206	Rho GTPase activating protein 18

Q13017-1	ARHGAP5	0.252	Rho GTPase activating protein 5
Q92974	ARHGEF2	0.374	Rho/Rac guanine nucleotide exchange factor 2
Q99856	ARID3A	-0.188	AT-rich interaction domain 3A
Q8IVW6	ARID3B	0.209	AT-rich interaction domain 3B
P40616	ARL1	-0.133	ADP ribosylation factor like GTPase 1
P36405	ARL3	-0.163	ADP ribosylation factor like GTPase 3
Q6NXE6-1	ARMC6	-0.26	armadillo repeat containing 6
Q5T2E6	ARMH3	-0.172	armadillo like helical domain containing 3
Q9H993	ARMT1	-0.207	acidic residue methyltransferase 1
Q92747	ARPC1A	0.133	actin related protein 2/3 complex subunit 1A
O15145	ARPC3	-0.172	actin related protein 2/3 complex subunit 3
P15848	ARSB	-0.237	arylsulfatase B
Q13510-2	ASAH1	-0.174	N-acylsphingosine amidohydrolase 1
P07306	ASGR1	-0.359	asialoglycoprotein receptor 1
P07307	ASGR2	-0.332	asialoglycoprotein receptor 2
P04424	ASL	-0.207	argininosuccinate lyase
P08243	ASNS	0.181	asparagine synthetase (glutamine-hydrolyzing)
Q12797	ASPH	0.289	aspartate beta-hydroxylase
Q7L266	ASRGL1	-0.266	asparaginase and isoaspartyl peptidase 1
P00966	ASS1	-0.398	argininosuccinate synthase 1
Q8NBU5	ATAD1	0.271	ATPase family AAA domain containing 1
P18847	ATF3	0.773	activating transcription factor 3
P31939	ATIC	-0.177	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase
P05023	ATP1A1	0.1	ATPase Na+/K+ transporting subunit alpha 1
P05026	ATP1B1	0.291	ATPase Na+/K+ transporting subunit beta 1
P54709	ATP1B3	0.189	ATPase Na+/K+ transporting subunit beta 3
P25705-1	ATP5F1A	0.143	ATP synthase F1 subunit alpha
P48047	ATP5PO	0.202	ATP synthase peripheral stalk subunit OSCP
P61421	ATP6V0D1	0.187	ATPase H+ transporting V0 subunit d1
Q9UBB4	ATXN10	-0.177	ataxin 10
P54252	ATXN3	0.578	ataxin 3
Q9Y679-1	AUP1	0.139	AUP1 lipid droplet regulating VLDL assembly factor
O14965	AURKA	0.207	aurora kinase A
Q96GD4-5	AURKB	0.283	aurora kinase B
O43505	B4GAT1	-0.466	beta-1,4-glucuronyltransferase 1
O95817	BAG3	0.653	BCL2 associated athanogene 3
O95429	BAG4	-0.246	BCL2 associated athanogene 4
Q9UHR4	BAIAP2L1	0.278	BAR/IMD domain containing adaptor protein 2 like 1
Q07812-2	BAX	-0.208	BCL2 associated X, apoptosis regulator
Q9NRL2	BAZ1A	0.289	bromodomain adjacent to zinc finger domain 1A
Q9UIF9	BAZ2A	0.244	bromodomain adjacent to zinc finger domain 2A
P50895	BCAM	-0.392	basal cell adhesion molecule (Lutheran blood group)
P56945-6	BCAR1	0.328	BCAR1 scaffold protein, Cas family member
Q9BUT1	BDH2	-0.322	3-hydroxybutyrate dehydrogenase 2
Q9NYM9	BET1L	-0.254	Bet1 golgi vesicular membrane trafficking protein like
Q13867	BLMH	-0.178	bleomycin hydrolase
P53004	BLVRA	-0.164	biliverdin reductase A

O95861-2	BPNT1	-0.241	3'(2'), 5'-bisphosphate nucleotidase 1
Q7Z569	BRAP	0.125	BRCA1 associated protein
Q15059	BRD3	-0.243	bromodomain containing 3
Q8TDN6	BRIX1	0.26	biogenesis of ribosomes BRX1
Q5VW32	BROX	-0.191	BRO1 domain and CAAX motif containing
P35613	BSG	-0.167	basigin (Ok blood group)
Q96K17	BTF3L4	-0.247	basic transcription factor 3 like 4
Q7KYR7	BTN2A1	0.28	butyrophilin subfamily 2 member A1
O43683	BUB1	0.182	BUB1 mitotic checkpoint serine/threonine kinase
O60566-3	BUB1B	0.123	BUB1 mitotic checkpoint serine/threonine kinase B
P41223-2	BUD31	0.237	BUD31 homolog
Q13895	BYSL	0.187	bystin like
Q9Y6E2	BZW2	-0.226	basic leucine zipper and W2 domains 2
Q9H0W9	C11orf54	-0.249	chromosome 11 open reading frame 54
O00193	C11orf58	-0.322	chromosome 11 open reading frame 58
Q9H3H3-3	C11orf68	-0.136	chromosome 11 open reading frame 68
A6NCS6	C2orf72	-0.235	chromosome 2 open reading frame 72
P01024	C3	-0.218	complement C3
Q9BRJ6	C7orf50	-0.24	chromosome 7 open reading frame 50
Q8IXQ3	C9orf40	-0.302	chromosome 9 open reading frame 40
Q5T6V5	C9orf64	-0.228	chromosome 9 open reading frame 64
Q9Y376	CAB39	-0.154	calcium binding protein 39
Q13557-10	CAMK2D	-0.158	calcium/calmodulin dependent protein kinase II delta
Q86VP6-1	CAND1	-0.179	cullin associated and neddylation dissociated 1
P07384	CAPN1	-0.138	calpain 1
P47755	CAPZA2	-0.196	capping actin protein of muscle Z-line subunit alpha 2
Q9Y2V2	CARHSP1	-0.129	calcium regulated heat stable protein 1
P35520-2	CBS/CBSL	-0.345	cystathionine beta-synthase
Q5JTY5	CBWD3/CBWD6	-0.133	COBW domain containing 3
Q13185	CBX3	-0.144	chromobox 3
P45973	CBX5	-0.197	chromobox 5
Q96BQ5	CCDC127	0.372	coiled-coil domain containing 127
O60826	CCDC22	-0.163	coiled-coil domain containing 22
Q96A33	CCDC47	0.193	coiled-coil domain containing 47
Q16204	CCDC6	-0.21	coiled-coil domain containing 6
Q9H6F5	CCDC86	0.122	coiled-coil domain containing 86
O60563	CCNT1	0.377	cyclin T1
O14618	CCS	-0.234	copper chaperone for superoxide dismutase
Q12834	CDC20	0.23	cell division cycle 20
Q9H3Q1	CDC42EP4	-0.342	CDC42 effector protein 4
Q6P1J9	CDC73	0.138	cell division cycle 73
P38936	CDKN1A	0.673	cyclin dependent kinase inhibitor 1A
Q9NXV6	CDKN2AIP	0.226	CDKN2A interacting protein
P49715-4	CEBPA	-0.376	CCAAT enhancer binding protein alpha
Q03701	CEBPZ	0.186	CCAAT enhancer binding protein zeta
Q9UHN6	CEMIP2	0.238	cell migration inducing hyaluronidase 2
Q9UPN4	CEP131	-0.131	centrosomal protein 131

Q9HA82	CERS4	-0.176	ceramide synthase 4
O00748	CES2	-0.111	carboxylesterase 2
P41208	CETN2	-0.311	centrin 2
Q9UEE9-1	CFDP1	-0.377	craniofacial development protein 1
P05156	CFI	-0.388	complement factor I
Q9Y281-1	CFL2	-0.306	cofilin 2
Q9P2M7-1	CGN	-0.622	cingulin
Q13111-1	CHAF1A	-0.155	chromatin assembly factor 1 subunit A
Q9NX63	CHCHD3	0.161	coiled-coil-helix-coiled-coil-helix domain containing 3
O14647	CHD2	0.297	chromodomain helicase DNA binding protein 2
Q8IWX8	CHERP	0.132	calcium homeostasis endoplasmic reticulum protein
Q9UQN3-1	CHMP2B	0.128	charged multivesicular body protein 2B
Q9H444	CHMP4B	0.138	charged multivesicular body protein 4B
Q9UHD1	CHORDC1	0.324	cysteine and histidine rich domain containing 1
Q99653	CHP1	0.475	calcineurin like EF-hand protein 1
P12277	CKB	-0.228	creatine kinase B
P56747	CLDN6	0.275	claudin 6
Q16740	CLPP	0.173	caseinolytic mitochondrial matrix peptidase proteolytic subunit
O76031	CLPX	0.166	caseinolytic mitochondrial matrix peptidase chaperone subunit
P09497-2	CLTB	0.338	clathrin light chain B
P10909-2	CLU	0.489	clusterin
I3L2B0	CLUH	-0.265	clustered mitochondria homolog
O75153	CLUH	-0.214	clustered mitochondria homolog
P62633	CNBP	-1.217	CCHC-type zinc finger nucleic acid binding protein
P62633-6	CNBP	-0.857	CCHC-type zinc finger nucleic acid binding protein
Q96KP4	CNDP2	-0.285	carnosine dipeptidase 2
A5YKK6	CNOT1	-0.122	CCR4-NOT transcription complex subunit 1
Q9UIV1-1	CNOT7	-0.194	CCR4-NOT transcription complex subunit 7
Q92600	CNOT9	-0.198	CCR4-NOT transcription complex subunit 9
P09543-1	CNP	-0.133	2',3'-cyclic nucleotide 3' phosphodiesterase
Q96JB2-1	COG3	-0.159	component of oligomeric golgi complex 3
Q9H9E3	COG4	-0.122	component of oligomeric golgi complex 4
Q9NX08	COMMD8	-0.244	COMM domain containing 8
Q9P000-1	COMMD9	-0.36	COMM domain containing 9
P53618	COPB1	-0.108	coatomer protein complex subunit beta 1
P35606	COPB2	-0.117	coatomer protein complex subunit beta 2
Q9Y678	COPG1	-0.121	coatomer protein complex subunit gamma 1
P31146	CORO1A	-0.261	coronin 1A
Q14019	COTL1	-0.28	coactosin like F-actin binding protein 1
O75976	CPD	-0.231	carboxypeptidase D
Q17RY0-1	CPEB4	0.254	cytoplasmic polyadenylation element binding protein 4
O75131	CPNE3	-0.118	copine 3
Q9BRF8-1	CPPED1	-0.283	calcineurin like phosphoesterase domain containing 1
P46108-1	CRK	-0.202	CRK proto-oncogene, adaptor protein
P46109	CRKL	-0.222	CRK like proto-oncogene, adaptor protein
O75718	CRTAP	-0.153	cartilage associated protein
P02511	CRYAB	2.014	crystallin alpha B

Q9Y2S2-1	CRYL1	-0.371	crystallin lambda 1
Q08257	CRYZ	0.127	crystallin zeta
P55060	CSE1L	-0.226	chromosome segregation 1 like
P68400	CSNK2A1	0.164	casein kinase 2 alpha 1
P19784	CSNK2A2	0.145	casein kinase 2 alpha 2
P01034	CST3	-0.426	cystatin C
P04080	CSTB	-0.402	cystatin B
P32929	CTH	0.318	cystathionine gamma-lyase
Q9NSA3	CTNNBIP1	-0.46	catenin beta interacting protein 1
Q9NRF8	CTPS2	-0.224	CTP synthase 2
Q6PD62	CTR9	0.229	CTR9 homolog, Paf1/RNA polymerase II complex component
P53634	CTSC	-0.172	cathepsin C
P09668	CTSH	-0.15	cathepsin H
P07711	CTSL	0.38	cathepsin L
Q13616	CUL1	-0.137	cullin 1
Q13619-1	CUL4A	-0.114	cullin 4A
P00167-1	CYB5A	-0.391	cytochrome b5 type A
P99999	CYCS	-0.346	cytochrome c, somatic
Q7L576-1	CYFIP1	-0.123	cytoplasmic FMR1 interacting protein 1
Q07973-1	CYP24A1	0.886	cytochrome P450 family 24 subfamily A member 1
Q96SQ9-2	CYP2S1	0.314	cytochrome P450 family 2 subfamily S member 1
Q8TAV3	CYP2W1	-0.274	cytochrome P450 family 2 subfamily W member 1
Q9HBI6	CYP4F11	0.355	cytochrome P450 family 4 subfamily F member 11
Q16850-1	CYP51A1	-0.568	cytochrome P450 family 51 subfamily A member 1
Q5VWQ8	DAB2IP	-0.191	DAB2 interacting protein
Q14118	DAG1	-0.169	dystroglycan 1
P51397	DAP	-0.419	death associated protein
O43293-1	DAPK3	0.198	death associated protein kinase 3
P07108-5	DBI	-0.743	diazepam binding inhibitor, acyl-CoA binding protein
P11182	DBT	0.127	dihydrolipoamide branched chain transacylase E2
Q9NV06	DCAF13	0.179	DDB1 and CUL4 associated factor 13
P61962	DCAF7	0.115	DDB1 and CUL4 associated factor 7
Q96C86	DCPS	-0.231	decapping enzyme, scavenger
Q9H773	DCTPP1	-0.244	dCTP pyrophosphatase 1
O94760	DDAH1	-0.336	dimethylarginine dimethylaminohydrolase 1
Q16531	DDB1	-0.183	damage specific DNA binding protein 1
Q5TDH0-3	DDI2	-0.307	DNA damage inducible 1 homolog 2
Q9NVP1	DDX18	0.162	DEAD-box helicase 18
Q9NUU7	DDX19A	-0.146	DEAD-box helicase 19A
Q9NR30	DDX21	0.353	DExD-box helicase 21
Q9GZR7	DDX24	0.3	DEAD-box helicase 24
Q9H0S4	DDX47	0.183	DEAD-box helicase 47
O43583	DENR	-0.303	density regulated re-initiation and release factor
Q9Y315	DERA	-0.171	deoxyribose-phosphate aldolase
Q8WYQ5-1	DGCR8	0.18	DGCR8 microprocessor complex subunit
Q9UPY3	DICER1	-0.154	dicer 1, ribonuclease III
O60832	DKC1	0.161	dyskerin pseudouridine synthase 1

P09622	DLD	0.206	dihydrolipoamide dehydrogenase
P11532-6	DMD	-0.175	dystrophin
Q08495-1	DMTN	-0.206	dematin actin binding protein
Q86Y56	DNAAF5	-0.241	dynein axonemal assembly factor 5
P31689	DNAJA1	0.175	DnaJ heat shock protein family (Hsp40) member A1
P25685	DNAJB1	0.744	DnaJ heat shock protein family (Hsp40) member B1
Q9NXW2-2	DNAJB12	0.278	DnaJ heat shock protein family (Hsp40) member B12
P25686-3	DNAJB2	0.316	DnaJ heat shock protein family (Hsp40) member B2
Q9UDY4	DNAJB4	0.77	DnaJ heat shock protein family (Hsp40) member B4
Q9Y5T4	DNAJC15	0.309	DnaJ heat shock protein family (Hsp40) member C15
Q13217	DNAJC3	0.125	DnaJ heat shock protein family (Hsp40) member C3
Q9H3Z4	DNAJC5	-0.427	DnaJ heat shock protein family (Hsp40) member C5
Q9ULA0	DNPEP	-0.217	aspartyl aminopeptidase
O43598-1	DNPH1	-0.446	2'-deoxynucleoside 5'-phosphate N-hydrolase 1
Q5QJE6	DNTTIP2	0.196	deoxynucleotidyltransferase terminal interacting protein 2
Q9H2P9-5	DPH5	-0.397	diphthamide biosynthesis 5
Q9NY33	DPP3	-0.132	dipeptidyl peptidase 3
Q16555	DPYSL2	-0.258	dihydropyrimidinase like 2
Q8TE96	DQX1	-0.199	DEAQ-box RNA dependent ATPase 1
Q03001-7	DST	0.231	dystonin
P60981-1	DSTN	0.149	destrin, actin depolymerizing factor
P23919	DTYMK	-0.157	deoxythymidylate kinase
Q6P1R4	DUS1L	-0.205	dihydrouridine synthase 1 like
Q99956	DUSP9	-0.277	dual specificity phosphatase 9
P33316-3	DUT	-0.219	deoxyuridine triphosphatase
P63167	DYNLL1	0.384	dynein light chain LC8-type 1
O95905-3	ECD	0.313	ecdysoneless cell cycle regulator
P42892	ECE1	-0.185	endothelin converting enzyme 1
O75521	ECI2	0.096	enoyl-CoA delta isomerase 2
Q9H8V3-3	ECT2	0.196	epithelial cell transforming 2
Q9H223	EHD4	0.113	EH domain containing 4
P41567	EIF1	0.156	eukaryotic translation initiation factor 1
Q9P2K8-1	EIF2AK4	-0.172	eukaryotic translation initiation factor 2 alpha kinase 4
Q14232	EIF2B1	-0.195	eukaryotic translation initiation factor 2B subunit alpha
Q13144	EIF2B5	-0.133	eukaryotic translation initiation factor 2B subunit epsilon
O75822	EIF3J	-0.181	eukaryotic translation initiation factor 3 subunit J
Q9UBQ5	EIF3K	-0.249	eukaryotic translation initiation factor 3 subunit K
P55199	ELL	0.383	elongation factor for RNA polymerase II
O00472	ELL2	0.2	elongation factor for RNA polymerase II 2
Q14241	ELOA	0.338	elongin A
O95163	ELP1	-0.265	elongator complex protein 1
Q9H9T3	ELP3	-0.263	elongator acetyltransferase complex subunit 3
Q15006	EMC2	0.204	ER membrane protein complex subunit 2
Q14249	ENDOG	-0.168	endonuclease G
P13929-1	ENO3	-0.415	enolase 3
Q9UHY7	ENOPH1	-0.27	enolase-phosphatase 1
P22413	ENPP1	-0.179	ectonucleotide pyrophosphatase/phosphodiesterase 1

O43768-4	ENSA	-0.311	endosulfine alpha
P16422	EPCAM	-0.196	epithelial cell adhesion molecule
P29317	EPHA2	0.553	EPH receptor A2
P07099	EPHX1	0.161	epoxide hydrolase 1
P34913	EPHX2	-0.242	epoxide hydrolase 2
P58107	EPPK1	-0.16	epiplakin 1
Q12929	EPS8	0.142	epidermal growth factor receptor pathway substrate 8
Q9H6S3	EPS8L2	-0.148	EPS8 like 2
Q9NZ08-2	ERAP1	-0.126	endoplasmic reticulum aminopeptidase 1
P04626	ERBB2	-0.229	erb-b2 receptor tyrosine kinase 2
P21860	ERBB3	-0.279	erb-b2 receptor tyrosine kinase 3
Q96RT1-8	ERBIN	0.096	erbb2 interacting protein
P19447	ERCC3	0.239	ERCC excision repair 3, TFIIH core complex helicase subunit
Q9Y282-3	ERGIC3	0.157	ERGIC and golgi 3
Q96AP7	ESAM	0.89	endothelial cell adhesion molecule
B1AK53-1	ESPN	-0.556	espin
P62495	ETF1	-0.224	eukaryotic translation termination factor 1
Q01780	EXOSC10	0.178	exosome component 10
Q9NQT5	EXOSC3	0.109	exosome component 3
P07148	FABP1	-0.658	fatty acid binding protein 1
O60427	FADS1	-0.198	fatty acid desaturase 1
O95864	FADS2	-0.5	fatty acid desaturase 2
Q96CS3	FAF2	0.246	Fas associated factor family member 2
P16930	FAH	-0.315	fumarylacetoacetate hydrolase
Q8IWE2	FAM114A1	-0.293	family with sequence similarity 114 member A1
Q9NZB2-6	FAM120A	-0.136	family with sequence similarity 120A
Q96C01	FAM136A	-0.238	family with sequence similarity 136 member A
Q8N128-2	FAM177A1	0.185	family with sequence similarity 177 member A1
Q9GZU8	FAM192A	-0.181	family with sequence similarity 192 member A
Q52LJ0-2	FAM98B	0.108	family with sequence similarity 98 member B
Q9NVI1	FANCI	-0.226	FA complementation group I
Q9Y285	FARSA	-0.131	phenylalanyl-tRNA synthetase subunit alpha
Q9NSD9	FARSB	-0.201	phenylalanyl-tRNA synthetase subunit beta
P25445	FAS	0.158	Fas cell surface death receptor
P49327	FASN	-0.28	fatty acid synthase
Q7L8L6	FASTKD5	0.463	FAST kinase domains 5
Q14517	FAT1	0.32	FAT atypical cadherin 1
P22087	FBL	0.15	fibrillarin
Q8TB52	FBXO30	0.215	F-box protein 30
Q9Y3I1	FBXO7	-0.192	F-box protein 7
P55899	FCGRT	-0.232	Fc fragment of IgG receptor and transporter
P37268	FDFT1	-0.332	farnesyl-diphosphate farnesyltransferase 1
P14324	FDPS	-0.244	farnesyl diphosphate synthase
P02671-2	FGA	-0.626	fibrinogen alpha chain
P02675	FGB	-0.281	fibrinogen beta chain
P22455-1	FGFR4	-0.407	fibroblast growth factor receptor 4
P02679	FGG	-0.54	fibrinogen gamma chain

Q96AY3	FKBP10	-0.137	FKBP prolyl isomerase 10
Q9NWM8	FKBP14	-0.214	FKBP prolyl isomerase 14
P62942	FKBP1A	-0.298	FKBP prolyl isomerase 1A
Q00688	FKBP3	-0.184	FKBP prolyl isomerase 3
Q02790	FKBP4	0.235	FKBP prolyl isomerase 4
Q9Y5Y0	FLVCR1	-0.294	feline leukemia virus subgroup C cellular receptor 1
Q96CP2	FLYWCH2	-0.358	FLYWCH family member 2
P49326-1	FMO5	-0.176	flavin containing dimethylaniline monoxygenase 5
Q9H479	FN3K	-0.254	fructosamine 3 kinase
Q9Y2H6	FNDC3A	0.179	fibronectin type III domain containing 3A
Q5VW36	FOCAD	-0.171	focadhesin
P15407	FOSL1	1.156	FOS like 1, AP-1 transcription factor subunit
Q9H334-8	FOXP1	0.212	forkhead box P1
Q86XX4-2	FRAS1	-0.549	Fraser extracellular matrix complex subunit 1
Q16658	FSCN1	-0.121	fascin actin-bundling protein 1
O95954-1	FTCD	-0.297	formimidoyltransferase cyclodeaminase
P02792	FTL	0.262	ferritin light chain
Q9C0B1-1	FTO	-0.252	FTO alpha-ketoglutarate dependent dioxygenase
P51114	FXR1	0.184	FMR1 autosomal homolog 1
P51116	FXR2	0.123	FMR1 autosomal homolog 2
P11413-2	G6PD	-0.155	glucose-6-phosphate dehydrogenase
Q14376	GALE	-0.345	UDP-galactose-4-epimerase
P51570-2	GALK1	-0.225	galactokinase 1
Q96C23	GALM	-0.359	galactose mutarotase
P07902	GALT	-0.213	galactose-1-phosphate uridylyltransferase
Q14353	GAMT	-0.36	guanidinoacetate N-methyltransferase
P04406	GAPDH	-0.169	glyceraldehyde-3-phosphate dehydrogenase
Q9NY12	GAR1	0.26	GAR1 ribonucleoprotein
P22102	GART	-0.121	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosyl
O43903	GAS2	-0.159	growth arrest specific 2
Q86YP4-3	GATAD2A	0.142	GATA zinc finger domain containing 2A
Q8WXI9	GATAD2B	0.18	GATA zinc finger domain containing 2B
P30047	GCHFR	-0.268	GTP cyclohydrolase I feedback regulator
P48506	GCLC	0.381	glutamate-cysteine ligase catalytic subunit
P48507	GCLM	0.909	glutamate-cysteine ligase modifier subunit
Q92616	GCN1	-0.163	GCN1 activator of EIF2AK4
Q8TB36	GDAP1	0.368	ganglioside induced differentiation associated protein 1
Q9NZC3	GDE1	0.299	glycerophosphodiester phosphodiesterase 1
Q99988	GDF15	0.78	growth differentiation factor 15
P50395-1	GDI2	-0.233	GDP dissociation inhibitor 2
Q7L5D6	GET4	-0.118	guided entry of tail-anchored proteins factor 4
Q06210	GFPT1	-0.11	glutamine--fructose-6-phosphate transaminase 1
Q9H3K2	GHITM	0.335	growth hormone inducible transmembrane protein
Q9BRX5	GINS3	-0.274	GINS complex subunit 3
Q9BRT9	GINS4	-0.187	GINS complex subunit 4
Q8TF65	GIPC2	-0.137	GIPC PDZ domain containing family member 2
P08034	GJB1	-0.663	gap junction protein beta 1

Q92896-2	GLG1	-0.332	golgi glycoprotein 1
Q04760-1	GLO1	-0.184	glyoxalase I
Q9HC38	GLOD4	-0.239	glyoxalase domain containing 4
O94925	GLS	0.315	glutaminase
O94925-3	GLS	0.323	glutaminase
Q68CQ7-1	GLT8D1	-0.213	glycosyltransferase 8 domain containing 1
P15104	GLUL	-0.32	glutamate-ammonia ligase
O60547	GMDS	-0.255	GDP-mannose 4,6-dehydratase
Q9Y5P6-2	GMPPB	-0.293	GDP-mannose pyrophosphorylase B
P49915	GMPS	-0.182	guanine monophosphate synthase
Q14344	GNA13	0.375	G protein subunit alpha 13
P08754	GNAI3	0.145	G protein subunit alpha i3
P62873	GNB1	0.166	G protein subunit beta 1
Q13823	GNL2	0.252	G protein nucleolar 2
Q96EK6	GNPNAT1	-0.192	glucosamine-phosphate N-acetyltransferase 1
Q7Z5G4	GOLGA7	0.215	golgin A7
Q9H4A6	GOLPH3	-0.182	golgi phosphoprotein 3
Q9H4A5	GOLPH3L	-0.178	golgi phosphoprotein 3 like
Q9Y3E0	GOLT1B	0.339	golgi transport 1B
Q9H8Y8	GORASP2	-0.168	golgi reassembly stacking protein 2
P00505	GOT2	0.154	glutamic-oxaloacetic transaminase 2
Q53EU6	GPAT3	0.448	glycerol-3-phosphate acyltransferase 3
P51654-1	GPC3	-0.297	glypican 3
Q9Y625	GPC6	-0.304	glypican 6
P21695	GPD1	-0.376	glycerol-3-phosphate dehydrogenase 1
Q9NQX3-2	GPHN	-0.242	gephyrin
P06744	GPI	-0.188	glucose-6-phosphate isomerase
Q9NQ84-2	GPRC5C	0.451	G protein-coupled receptor class C group 5 member C
P18283	GPX2	-0.395	glutathione peroxidase 2
P36969	GPX4	-0.589	glutathione peroxidase 4
Q9UBQ7	GRHPR	-0.181	glyoxylate and hydroxypyruvate reductase
P25098	GRK2	-0.204	G protein-coupled receptor kinase 2
P48637	GSS	-0.186	glutathione synthetase
P08263	GSTA1	-0.502	glutathione S-transferase alpha 1
P28161	GSTM2	-0.202	glutathione S-transferase mu 2
P21266	GSTM3	-0.165	glutathione S-transferase mu 3
P78417	GSTO1	-0.297	glutathione S-transferase omega 1
P30711	GSTT1	-0.192	glutathione S-transferase theta 1
P78347	GTF2I	-0.141	general transcription factor IIi
Q8N442	GUF1	0.196	GUF1 homolog, GTPase
P0C0S5	H2AZ1	0.367	H2A.Z variant histone 1
O95479	H6PD	-0.135	hexose-6-phosphate dehydrogenase/glucose 1-dehydrogenase
P46952	HAAO	-0.222	3-hydroxyanthranilate 3,4-dioxygenase
O14929	HAT1	-0.113	histone acetyltransferase 1
P51858	HDGF	-0.21	heparin binding growth factor
Q9H0R4	HDHD2	-0.221	haloacid dehalogenase like hydrolase domain containing 2
Q00341	HDLBP	-0.254	high density lipoprotein binding protein

Q7Z4Q2	HEATR3	-0.307	HEAT repeat containing 3
Q86XA9	HEATR5A	-0.249	HEAT repeat containing 5A
Q9P2D3	HEATR5B	-0.128	HEAT repeat containing 5B
Q9NRV9	HEBP1	-0.157	heme binding protein 1
Q9Y5Z4	HEBP2	-0.288	heme binding protein 2
Q93099	HGD	-0.215	homogentisate 1,2-dioxygenase
Q9BTY7	HGH1	-0.108	HGH1 homolog
O14964	HGS	0.203	hepatocyte growth factor-regulated tyrosine kinase substrate
P49773	HINT1	-0.109	histidine triad nucleotide binding protein 1
Q9BX68	HINT2	0.19	histidine triad nucleotide binding protein 2
Q9BW71-1	HIRIP3	-0.18	HIRA interacting protein 3
P08397	HMBS	-0.23	hydroxymethylbilane synthase
Q01581	HMGCS1	-0.385	3-hydroxy-3-methylglutaryl-CoA synthase 1
P05204	HMGN2	0.517	high mobility group nucleosomal binding domain 2
P09601	HMOX1	1.109	heme oxygenase 1
P30519	HMOX2	0.128	heme oxygenase 2
P20823-7	HNF1A	-0.182	HNF1 homeobox A
P41235-4	HNF4A	-0.27	hepatocyte nuclear factor 4 alpha
P50135	HNMT	-0.44	histamine N-methyltransferase
P14866	HNRNPL	0.1	heterogeneous nuclear ribonucleoprotein L
Q00839	HNRNPU	0.164	heterogeneous nuclear ribonucleoprotein U
Q1KMD3	HNRNPUL2	-0.102	heterogeneous nuclear ribonucleoprotein U like 2
Q9NSC5	HOMER3	-0.246	homer scaffold protein 3
P00738	HP	-0.677	haptoglobin
P32754-1	HPD	-0.147	4-hydroxyphenylpyruvate dioxygenase
P07900	HSP90AA1	0.213	heat shock protein 90 alpha family class A member 1
P08238	HSP90AB1	0.141	heat shock protein 90 alpha family class B member 1
P48723	HSPA13	0.195	heat shock protein family A (Hsp70) member 13
P0DMV9	HSPA1A/HSPA1B	1.375	heat shock protein family A (Hsp70) member 1A
P17066	HSPA6	1.615	heat shock protein family A (Hsp70) member 6
P38646	HSPA9	0.149	heat shock protein family A (Hsp70) member 9
P04792	HSPB1	0.759	heat shock protein family B (small) member 1
P10809	HSPD1	0.202	heat shock protein family D (Hsp60) member 1
Q92598	HSPH1	0.662	heat shock protein family H (Hsp110) member 1
P42858	HTT	-0.184	huntingtin
P41252	IARS1	-0.15	isoleucyl-tRNA synthetase 1
Q5T440	IBA57	0.131	iron-sulfur cluster assembly factor IBA57
O75874	IDH1	-0.383	isocitrate dehydrogenase (NADP(+)) 1
P50213	IDH3A	0.116	isocitrate dehydrogenase (NAD(+)) 3 catalytic subunit alpha
O43837	IDH3B	0.169	isocitrate dehydrogenase (NAD(+)) 3 non-catalytic subunit beta
Q13907	IDI1	-0.237	isopentenyl-diphosphate delta isomerase 1
P08833	IGFBP1	0.492	insulin like growth factor binding protein 1
Q8N6C5-4	IGSF1	-0.296	immunoglobulin superfamily member 1
Q70UQ0-4	IKBIP	0.158	IKBKB interacting protein
Q14116	IL18	0.44	interleukin 18
Q96G21	IMP4	0.16	IMP U3 small nucleolar ribonucleoprotein 4
Q27J81	INF2	-0.117	inverted formin, FH2 and WH2 domain containing

Q9UI26-2	IPO11	-0.127	importin 11
Q8TEX9-2	IPO4	-0.351	importin 4
O00410-3	IPO5	-0.317	importin 5
O95373	IPO7	-0.15	importin 7
Q96P70	IPO9	-0.253	importin 9
Q13576-1	IQGAP2	-0.168	IQ motif containing GTPase activating protein 2
Q86U28	ISCA2	-0.212	iron-sulfur cluster assembly 2
P05161	ISG15	-0.144	ISG15 ubiquitin like modifier
Q9H9L3	ISG20L2	0.142	interferon stimulated exonuclease gene 20 like 2
Q96CN7	ISOC1	-0.194	isochorismatase domain containing 1
Q9NPH2	ISYNA1	-0.304	inositol-3-phosphate synthase 1
P56199	ITGA1	-0.199	integrin subunit alpha 1
P17301	ITGA2	0.473	integrin subunit alpha 2
P06756	ITGAV	0.153	integrin subunit alpha V
P05556	ITGB1	0.25	integrin subunit beta 1
P19823	ITIH2	-0.115	inter-alpha-trypsin inhibitor heavy chain 2
Q9BY32	ITPA	-0.195	inosine triphosphatase
P78504	JAG1	0.61	jagged canonical Notch ligand 1
P14923	JUP	0.106	junction plakoglobin
Q9Y2K7	KDM2A	0.24	lysine demethylase 2A
Q9Y4C1	KDM3A	0.302	lysine demethylase 3A
Q7LBC6-1	KDM3B	-0.147	lysine demethylase 3B
Q14145	KEAP1	0.134	kelch like ECH associated protein 1
P50053-2	KHK	-0.342	ketohexokinase
Q9NQT8	KIF13B	-0.161	kinesin family member 13B
Q9NS87	KIF15	-0.149	kinesin family member 15
Q02241-1	KIF23	0.191	kinesin family member 23
Q99661	KIF2C	0.153	kinesin family member 2C
P33176	KIF5B	-0.108	kinesin family member 5B
Q9NSK0-3	KLC4	-0.221	kinesin light chain 4
Q14974	KPNB1	-0.226	karyopherin subunit beta 1
Q13601	KRR1	0.315	KRR1 small subunit processome component homolog
P08727	KRT19	0.325	keratin 19
Q16719	KYNU	0.265	kynureninase
P83111-1	LACTB	0.198	lactamase beta
O15230	LAMA5	-0.384	laminin subunit alpha 5
P55268	LAMB2	-0.274	laminin subunit beta 2
P13473-3	LAMP2	-0.332	lysosomal associated membrane protein 2
O43813	LANCL1	-0.293	LanC like 1
Q71RC2-4	LARP4	0.138	La ribonucleoprotein domain family member 4
P00338-3	LDHA	-0.345	lactate dehydrogenase A
P01130	LDLR	0.296	low density lipoprotein receptor
Q96PV6-2	LENG8	0.295	leukocyte receptor cluster member 8
P09382	LGALS1	0.234	galectin 1
P17931	LGALS3	-0.207	galectin 3
O00214-2	LGALS8	0.291	galectin 8
Q3ZCW2	LGALSL	-0.155	galectin like

P18858	LIG1	-0.287	DNA ligase 1
P20700	LMNB1	-0.133	lamin B1
Q7Z4F1	LRP10	0.493	LDL receptor related protein 10
Q8N1G4	LRRC47	-0.206	leucine rich repeat containing 47
Q96AG4	LRRC59	0.138	leucine rich repeat containing 59
Q8IWT6	LRRC8A	0.17	leucine rich repeat containing 8 VRAC subunit A
Q32MZ4-3	LRRFIP1	0.132	LRR binding FLII interacting protein 1
Q9UFC0	LRWD1	0.101	leucine rich repeats and WD repeat domain containing 1
Q9H089	LSG1	0.27	large 60S subunit nuclear export GTPase 1
P48449	LSS	-0.14	lanosterol synthase
P09960-1	LTA4H	-0.27	leukotriene A4 hydrolase
O94822-3	LTN1	-0.15	listerin E3 ubiquitin protein ligase 1
Q96GA3	LTV1	0.226	LTV1 ribosome biogenesis factor
Q86V48	LUZP1	0.288	leucine zipper protein 1
Q8WZA0-2	LZIC	-0.241	leucine zipper and CTNNBIP1 domain containing
Q9NQ48	LZTFL1	-0.296	leucine zipper transcription factor like 1
Q8WXG6-4	MADD	0.201	MAP kinase activating death domain
Q9ULX9	MAFF	0.467	MAF bZIP transcription factor F
O15525	MAFG	0.715	MAF bZIP transcription factor G
Q9Y5V3-2	MAGED1	-0.289	MAGE family member D1
P33908	MAN1A1	-0.14	mannosidase alpha class 1A member 1
P55145	MANF	-0.172	mesencephalic astrocyte derived neurotrophic factor
P46821	MAP1B	0.551	microtubule associated protein 1B
A6NCE7	MAP1LC3B2	0.826	microtubule associated protein 1 light chain 3 beta 2
P27816-1	MAP4	-0.124	microtubule associated protein 4
Q3KQU3	MAP7D1	0.27	MAP7 domain containing 1
P28482	MAPK1	-0.272	mitogen-activated protein kinase 1
P27361-1	MAPK3	-0.233	mitogen-activated protein kinase 3
Q5VT66-2	MARC1	-0.224	mitochondrial amidoxime reducing component 1
Q00266	MAT1A	-0.316	methionine adenosyltransferase 1A
Q8NI22	MCFD2	-0.479	multiple coagulation factor deficiency 2
P49736	MCM2	-0.248	minichromosome maintenance complex component 2
P25205-2	MCM3	-0.186	minichromosome maintenance complex component 3
P33991	MCM4	-0.201	minichromosome maintenance complex component 4
P33992	MCM5	-0.179	minichromosome maintenance complex component 5
Q14566	MCM6	-0.211	minichromosome maintenance complex component 6
P33993-1	MCM7	-0.12	minichromosome maintenance complex component 7
Q9BTE3-1	MCMBP	-0.128	minichromosome maintenance complex binding protein
Q8NE86	MCU	0.322	mitochondrial calcium uniporter
P40925-3	MDH1	-0.296	malate dehydrogenase 1
Q00987-11	MDM2	0.424	MDM2 proto-oncogene
P51608-2	MECP2	0.201	methyl-CpG binding protein 2
Q14696	MESD	-0.223	mesoderm development LRP chaperone
Q9UBP6	METTL1	-0.145	methyltransferase like 1
Q9H8H3	METTL7A	-0.216	methyltransferase like 7A
Q9H1A3	METTL9	0.312	methyltransferase like 9
Q8IWA4	MFN1	0.215	mitofusin 1

P16455	MGMT	-0.213	O-6-methylguanine-DNA methyltransferase
Q8N108-12	MIER1	-0.122	MIER1 transcriptional regulator
Q9UNW1	MINPP1	-0.126	multiple inositol-polyphosphate phosphatase 1
Q8IVT2	MISP	0.431	mitotic spindle positioning
Q15773	MLF2	0.24	myeloid leukemia factor 2
P51511	MMP15	-0.337	matrix metallopeptidase 15
Q96T76-8	MMS19	-0.211	MMS19 homolog, cytosolic iron-sulfur assembly component
Q7Z3U7	MON2	-0.223	MON2 homolog, regulator of endosome-to-Golgi trafficking
Q15014	MORF4L2	-0.204	mortality factor 4 like 2
Q9HCE1	MOV10	-0.19	Mov10 RISC complex RNA helicase
Q9Y5U8	MPC1	0.194	mitochondrial pyruvate carrier 1
P34949	MPI	-0.26	mannose phosphate isomerase
Q5T2T1	MPP7	-0.14	membrane palmitoylated protein 7
P25325-2	MPST	-0.132	mercaptopyruvate sulfurtransferase
Q9Y605	MRFAP1	-0.313	Morf4 family associated protein 1
Q9P015	MRPL15	0.19	mitochondrial ribosomal protein L15
Q9P0M9	MRPL27	0.264	mitochondrial ribosomal protein L27
P09001	MRPL3	0.209	mitochondrial ribosomal protein L3
Q9NYK5	MRPL39	0.158	mitochondrial ribosomal protein L39
Q9BRJ2	MRPL45	0.211	mitochondrial ribosomal protein L45
Q9BQC6	MRPL57	0.182	mitochondrial ribosomal protein L57
Q9Y399	MRPS2	0.256	mitochondrial ribosomal protein S2
Q96EL2	MRPS24	0.436	mitochondrial ribosomal protein S24
Q9BYN8	MRPS26	0.162	mitochondrial ribosomal protein S26
P82673	MRPS35	0.265	mitochondrial ribosomal protein S35
P82909	MRPS36	0.136	mitochondrial ribosomal protein S36
P82675	MRPS5	0.261	mitochondrial ribosomal protein S5
P82932	MRPS6	0.368	mitochondrial ribosomal protein S6
Q9Y2R9	MRPS7	0.204	mitochondrial ribosomal protein S7
Q9ULH7-5	MRTFB	-0.166	myocardin related transcription factor B
P43246	MSH2	-0.192	mutS homolog 2
P52701	MSH6	-0.132	mutS homolog 6
P07438	MT1B	3.014	metallothionein 1B
O94776	MTA2	0.215	metastasis associated 1 family member 2
Q96E29	MTERF3	0.185	mitochondrial transcription termination factor 3
Q9H019-1	MTFR1L	-0.165	mitochondrial fission regulator 1 like
P11586	MTHFD1	-0.253	methylenetetrahydrofolate dehydrogenase, cyclohydrolase and formyltetrahydrofolate synthetase 1
P13995	MTHFD2	0.186	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2, methenyltetrahydrofolate cyclohyd
Q13496	MTM1	-0.169	myotubularin 1
Q9C0I1	MTMR12	-0.195	myotubularin related protein 12
Q765P7	MTSS2	-0.371	MTSS I-BAR domain containing 2
Q5HYI7	MTX3	0.188	metaxin 3
P53602	MVD	-0.215	mevalonate diphosphate decarboxylase
Q03426	MVK	-0.302	mevalonate kinase
Q14764	MVP	0.168	major vault protein
P35579	MYH9	0.319	myosin heavy chain 9
Q15746	MYLK	-0.216	myosin light chain kinase

Q96H55-1	MYO19	-0.252	myosin XIX
O00159-3	MYO1C	0.122	myosin IC
Q6NSJ0	MYORG	-0.298	myogenesis regulating glycosidase (putative)
Q13564-4	NAE1	-0.166	NEDD8 activating enzyme E1 subunit 1
Q9UJ70-2	NAGK	-0.123	N-acetylglucosamine kinase
Q9NR45	NANS	-0.231	N-acetylneuraminate synthase
O43776	NARS1	-0.145	asparaginyl-tRNA synthetase 1
P49321-3	NASP	-0.28	nuclear autoantigenic sperm protein
A2RRP1	NBAS	-0.129	NBAS subunit of NRZ tethering complex
Q15021	NCAPD2	-0.122	non-SMC condensin I complex subunit D2
Q6PIU2-2	NCEH1	0.261	neutral cholesterol ester hydrolase 1
Q68D85	NCR3LG1	-0.265	natural killer cell cytotoxicity receptor 3 ligand 1
Q9UI09	NDUFA12	0.103	NADH:ubiquinone oxidoreductase subunit A12
Q9P0J0	NDUFA13	0.178	NADH:ubiquinone oxidoreductase subunit A13
O00483	NDUFA4	-0.294	NDUFA4 mitochondrial complex associated
P56556	NDUFA6	0.162	NADH:ubiquinone oxidoreductase subunit A6
O14561	NDUFAB1	0.366	NADH:ubiquinone oxidoreductase subunit AB1
Q8N183	NDUFAF2	0.166	NADH:ubiquinone oxidoreductase complex assembly factor 2
P28331-2	NDUFS1	0.104	NADH:ubiquinone oxidoreductase core subunit S1
P19404	NDUFV2	-0.182	NADH:ubiquinone oxidoreductase core subunit V2
Q15843	NEDD8	-0.268	NEDD8 ubiquitin like modifier
Q6NW34	NEPRO	0.218	nucleolus and neural progenitor protein
P48681	NES	0.297	nestin
Q99519	NEU1	-0.248	neuraminidase 1
Q00653	NFKB2	0.171	nuclear factor kappa B subunit 2
Q9UMS0	NFU1	-0.208	NFU1 iron-sulfur cluster scaffold
Q6ZNB6-1	NFXL1	-0.546	nuclear transcription factor, X-box binding like 1
P14543-1	NID1	-0.31	nidogen 1
Q9GZT8	NIF3L1	-0.168	NGG1 interacting factor 3 like 1
Q9NYR9-1	NKIRAS2	-0.162	NFKB inhibitor interacting Ras like 2
O15226-2	NKRF	0.207	NFKB repressing factor
Q96D46	NMD3	0.185	NMD3 ribosome export adaptor
P22392-2	NME2	-0.293	NME/NM23 nucleoside diphosphate kinase 2
P30419	NMT1	-0.161	N-myristoyltransferase 1
Q9ULX3	NOB1	0.191	NIN1 (RPN12) binding protein 1 homolog
Q9Y3T9	NOC2L	0.218	NOC2 like nucleolar associated transcriptional repressor
Q9BSC4	NOL10	0.135	nucleolar protein 10
Q9UGY1	NOL12	0.28	nucleolar protein 12
Q96MY1	NOL4L	-0.214	nucleolar protein 4 like
Q5C9Z4	NOM1	0.265	nucleolar protein with MIF4G domain 1
Q9NPE3	NOP10	0.202	NOP10 ribonucleoprotein
P46087-4	NOP2	0.303	NOP2 nucleolar protein
Q9Y2X3	NOP58	0.279	NOP58 ribonucleoprotein
P29474	NOS3	0.249	nitric oxide synthase 3
P55786	NPEPPS	-0.157	aminopeptidase puromycin sensitive
O43847-2	NRDC	-0.289	nardilysin convertase
O95478	NSA2	0.274	NSA2 ribosome biogenesis factor

Q8TCD5	NT5C	-0.232	5', 3'-nucleotidase, cytosolic
Q5TFE4	NT5DC1	-0.228	5'-nucleotidase domain containing 1
Q86UY8	NT5DC3	0.304	5'-nucleotidase domain containing 3
Q8TB37	NUBPL	0.177	nucleotide binding protein like
Q9H1E3	NUCKS1	-0.293	nuclear casein kinase and cyclin dependent kinase substrate 1
Q8WVJ2	NUDCD2	-0.178	NudC domain containing 2
Q8IVD9	NUDCD3	-0.278	NudC domain containing 3
Q96DE0	NUDT16	-0.147	nudix hydrolase 16
P50583	NUDT2	-0.163	nudix hydrolase 2
Q9UKK9	NUDT5	-0.263	nudix hydrolase 5
P49790	NUP153	0.349	nucleoporin 153
P61970	NUTF2	-0.232	nuclear transport factor 2
P04181	OAT	0.199	ornithine aminotransferase
O75147	OBSL1	-0.276	obscurin like cytoskeletal adaptor 1
O60502	OGA	0.186	O-GlcNAcase
Q6N063-1	OGFOD2	-0.214	2-oxoglutarate and iron dependent oxygenase domain containing 2
Q9NZT2	OGFR	-0.104	opioid growth factor receptor
Q9NTK5-1	OLA1	-0.195	Obg like ATPase 1
Q9H6K4	OPA3	0.419	outer mitochondrial membrane lipid metabolism regulator OPA3
O14841	OPLAH	-0.162	5-oxoprolinase, ATP-hydrolysing
Q13415	ORC1	0.462	origin recognition complex subunit 1
Q13416	ORC2	-0.109	origin recognition complex subunit 2
P19652	ORM2	-0.421	orosomucoid 2
Q9BZF1-1	OSBPL8	0.175	oxysterol binding protein like 8
Q96G74-1	OTUD5	0.323	OTU deubiquitinase 5
Q8N573-1	OXR1	-0.269	oxidation resistance 1
Q9NWU1-1	OXSM	0.151	3-oxoacyl-ACP synthase, mitochondrial
Q9BRP4	PAAF1	-0.182	proteasomal ATPase associated factor 1
Q9UKS6	PACSIN3	-0.197	protein kinase C and casein kinase substrate in neurons 3
Q15102	PAFAH1B3	-0.209	platelet activating factor acetylhydrolase 1b catalytic subunit 3
P00439	PAH	-0.501	phenylalanine hydroxylase
P22234-2	PAICS	-0.233	phosphoribosylaminoimidazole carboxylase and phosphoribosylaminoimidazolesuccinocarboxamide s
Q9NWT1	PAK1IP1	0.154	PAK1 interacting protein 1
Q9NP74	PALMD	-0.236	palmdelphin
O43252	PAPSS1	-0.179	3'-phosphoadenosine 5'-phosphosulfate synthase 1
Q86W56	PARG	-0.135	poly(ADP-ribose) glycohydrolase
Q9NVD7	PARVA	-0.256	parvin alpha
P61457	PCBD1	-0.205	pterin-4 alpha-carbinolamine dehydratase 1
Q9H4Z3	PCIF1	-0.208	PDX1 C-terminal inhibiting factor 1
Q15154-1	PCM1	-0.159	pericentriolar material 1
Q8WW12	PCNP	-0.181	PEST proteolytic signal containing nuclear protein
Q9UKL6	PCTP	-0.231	phosphatidylcholine transfer protein
Q99447	PCYT2	-0.377	phosphate cytidylyltransferase 2, ethanolamine
Q53EL6	PDCD4	-0.273	programmed cell death 4
O14737	PDCD5	-0.28	programmed cell death 5
Q96HC4	PDLIM5	0.169	PDZ and LIM domain 5
Q9NR12	PDLIM7	0.448	PDZ and LIM domain 7

Q8NCN5	PDPR	0.269	pyruvate dehydrogenase phosphatase regulatory subunit
Q6P996-1	PDXDC1	-0.296	pyridoxal dependent decarboxylase domain containing 1
Q5T2W1	PDZK1	-0.319	PDZ domain containing 1
P30086	PEBP1	-0.338	phosphatidylethanolamine binding protein 1
Q9GZU2	PEG3	-0.154	paternally expressed 3
Q9BRX2	PELO	0.203	pelota mRNA surveillance and ribosome rescue factor
P12955	PEPD	-0.305	peptidase D
O15067	PFAS	-0.211	phosphoribosylformylglycinamidine synthase
O15212	PFDN6	-0.147	prefoldin subunit 6
P17858-1	PFKL	-0.219	phosphofructokinase, liver type
P07737	PFN1	-0.194	profilin 1
P18669	PGAM1	-0.185	phosphoglycerate mutase 1
Q96HS1-1	PGAM5	0.166	PGAM family member 5, mitochondrial serine/threonine protein phosphatase
P00558	PGK1	-0.148	phosphoglycerate kinase 1
O95336	PGLS	-0.252	6-phosphogluconolactonase
P36871-1	PGM1	-0.387	phosphoglucomutase 1
Q96G03	PGM2	-0.176	phosphoglucomutase 2
A6NDG6	PGP	-0.33	phosphoglycolate phosphatase
Q9NXJ5	PGPEP1	-0.384	pyroglutamyl-peptidase I
Q8IZ21-2	PHACTR4	-0.201	phosphatase and actin regulator 4
Q9H814	PHAX	-0.195	phosphorylated adaptor for RNA export
Q99623	PHB2	0.166	prohibitin 2
P46019	PHKA2	-0.122	phosphorylase kinase regulatory subunit alpha 2
Q8WV24	PHLDA1	0.194	pleckstrin homology like domain family A member 1
Q9BTU6	PI4K2A	0.199	phosphatidylinositol 4-kinase type 2 alpha
Q9NWS0-1	PIH1D1	-0.176	PIH1 domain containing 1
Q9Y237-2	PIN4	-0.194	peptidylprolyl cis/trans isomerase, NIMA-interacting 4
Q9P0Z9	PIPOX	-0.141	pipecolic acid and sarcosine oxidase
O00625	PIR	-0.254	pirin
Q5JRX3-2	PITRM1	0.316	pitrilysin metallopeptidase 1
P30613	PKLR	-0.336	pyruvate kinase L/R
Q16512-2	PKN1	-0.23	protein kinase N1
Q01970	PLCB3	-0.225	phospholipase C beta 3
Q99541	PLIN2	0.314	perilipin 2
P53350	PLK1	0.19	polo like kinase 1
Q02809-2	PLOD1	-0.169	procollagen-lysine,2-oxoglutarate 5-dioxygenase 1
O94903	PLPBP	-0.228	pyridoxal phosphate binding protein
O43660	PLRG1	0.11	pleiotropic regulator 1
P13797	PLS3	-0.198	plastin 3
O43157	PLXNB1	-0.147	plexin B1
O15305	PMM2	-0.205	phosphomannomutase 2
O75439	PMPCB	0.168	peptidase, mitochondrial processing beta subunit
Q9NRX1	PNO1	0.325	partner of NOB1 homolog
P41247	PNPLA4	0.246	patatin like phospholipase domain containing 4
Q9NVS9	PNPO	-0.238	pyridoxamine 5'-phosphate oxidase
P09884	POLA1	-0.279	DNA polymerase alpha 1, catalytic subunit
P28340	POLD1	-0.277	DNA polymerase delta 1, catalytic subunit

P49005	POLD2	-0.281	DNA polymerase delta 2, accessory subunit
Q07864	POLE	-0.225	DNA polymerase epsilon, catalytic subunit
Q9NRF9	POLE3	-0.152	DNA polymerase epsilon 3, accessory subunit
P54098	POLG	0.173	DNA polymerase gamma, catalytic subunit
Q06203	PPAT	-0.308	phosphoribosyl pyrophosphate amidotransferase
Q9HAB8	PPCS	-0.184	phosphopantothenoylcysteine synthetase
P62937	PPIA	-0.179	peptidylprolyl isomerase A
P45877	PPIC	-0.171	peptidylprolyl isomerase C
Q9H2H8-1	PPIL3	-0.112	peptidylprolyl isomerase like 3
Q9ULR3	PPM1H	-0.216	protein phosphatase, Mg2+/Mn2+ dependent 1H
Q96C90	PPP1R14B	-0.344	protein phosphatase 1 regulatory inhibitor subunit 14B
Q6NYC8	PPP1R18	0.405	protein phosphatase 1 regulatory subunit 18
Q6ZMI0-1	PPP1R21	-0.18	protein phosphatase 1 regulatory subunit 21
Q15435	PPP1R7	-0.255	protein phosphatase 1 regulatory subunit 7
P60510	PPP4C	-0.153	protein phosphatase 4 catalytic subunit
Q8TF05	PPP4R1	-0.229	protein phosphatase 4 regulatory subunit 1
Q5H9R7-5	PPP6R3	-0.134	protein phosphatase 6 regulatory subunit 3
P32119	PRDX2	-0.195	peroxiredoxin 2
P30041	PRDX6	-0.284	peroxiredoxin 6
P48147	PREP	-0.193	prolyl endopeptidase
P49643	PRIM2	-0.161	DNA primase subunit 2
P17612	PRKACA	-0.163	protein kinase cAMP-activated catalytic subunit alpha
P10644	PRKAR1A	-0.292	protein kinase cAMP-dependent type I regulatory subunit alpha
Q99873	PRMT1	-0.131	protein arginine methyltransferase 1
O14744	PRMT5	-0.116	protein arginine methyltransferase 5
O43395	PRPF3	0.128	pre-mRNA processing factor 3
Q8NAV1-1	PRPF38A	0.142	pre-mRNA processing factor 38A
O43172	PRPF4	0.093	pre-mRNA processing factor 4
Q14558-2	PRPSAP1	-0.128	phosphoribosyl pyrophosphate synthetase associated protein 1
Q8TBF2-8	PRXL2B	-0.219	peroxiredoxin like 2B
P07602-3	PSAP	-0.317	prosaposin
Q9Y617	PSAT1	-0.263	phosphoserine aminotransferase 1
Q16401	PSMD5	-0.203	proteasome 26S subunit, non-ATPase 5
Q06323	PSME1	-0.422	proteasome activator subunit 1
Q9UL46	PSME2	-0.305	proteasome activator subunit 2
Q92530	PSMF1	-0.2	proteasome inhibitor subunit 1
O95456	PSMG1	-0.193	proteasome assembly chaperone 1
P78330	PSPH	-0.372	phosphoserine phosphatase
O95758-4	PTBP3	0.181	polypyrimidine tract binding protein 3
Q14914	PTGR1	0.22	prostaglandin reductase 1
Q13308-6	PTK7	-0.236	protein tyrosine kinase 7 (inactive)
Q86YD1-1	PTOV1	-0.184	PTOV1 extended AT-hook containing adaptor protein
Q15257	PTPA	-0.209	protein phosphatase 2 phosphatase activator
P10586-1	PTPRF	-0.264	protein tyrosine phosphatase receptor type F
Q86Y79	PTRH1	0.277	peptidyl-tRNA hydrolase 1 homolog
Q9Y3E5	PTRH2	0.258	peptidyl-tRNA hydrolase 2
Q15397	PUM3	0.392	pumilio RNA binding family member 3

Q3MIT2	PUS10	-0.311	pseudouridine synthase 10
Q96C36	PYCR2	0.158	pyrroline-5-carboxylate reductase 2
P06737	PYGL	-0.273	glycogen phosphorylase L
Q9BRP8	PYM1	-0.178	PYM homolog 1, exon junction complex associated factor
P09417	QDPR	-0.126	quinoid dihydropteridine reductase
Q15274	QPRT	-0.279	quinolinate phosphoribosyltransferase
Q6ZRP7	QSOX2	-0.117	quiescin sulfhydryl oxidase 2
Q9BXR0	QTRT1	-0.118	queuine tRNA-ribosyltransferase catalytic subunit 1
P61026	RAB10	0.301	RAB10, member RAS oncogene family
Q9NP72	RAB18	0.202	RAB18, member RAS oncogene family
Q9UL26	RAB22A	0.211	RAB22A, member RAS oncogene family
P51159-1	RAB27A	0.167	RAB27A, member RAS oncogene family
P61019	RAB2A	0.147	RAB2A, member RAS oncogene family
P20338	RAB4A	-0.202	RAB4A, member RAS oncogene family
Q9BUV8-5	RAB5IF	0.231	RAB5 interacting factor
P51149	RAB7A	0.31	RAB7A, member RAS oncogene family
P51151	RAB9A	0.143	RAB9A, member RAS oncogene family
Q9UI14	RABAC1	-0.221	Rab acceptor 1
Q9Y3P9	RABGAP1	-0.255	RAB GTPase activating protein 1
Q3YEC7-1	RABL6	-0.187	RAB, member RAS oncogene family like 6
Q9H0H5	RACGAP1	0.267	Rac GTPase activating protein 1
P63244	RACK1	-0.135	receptor for activated C kinase 1
P78406	RAE1	0.199	ribonucleic acid export 1
P11234-2	RALB	0.208	RAS like proto-oncogene B
Q9H6Z4	RANBP3	-0.202	RAN binding protein 3
P52306-5	RAP1GDS1	-0.304	Rap1 GTPase-GDP dissociation stimulator 1
O75884	RBBP9	-0.254	RB binding protein 9, serine hydrolase
Q9H477	RBKS	-0.453	ribokinase
Q8IXT5	RBM12B	0.157	RNA binding motif protein 12B
Q96PK6-1	RBM14	0.169	RNA binding motif protein 14
Q96T37	RBM15	0.162	RNA binding motif protein 15
Q9Y4C8	RBM19	0.155	RNA binding motif protein 19
P52756	RBM5	0.14	RNA binding motif protein 5
P02753	RBP4	-0.5	retinol binding protein 4
Q9P2K3-3	RCOR3	-0.204	REST corepressor 3
Q9HBH5	RDH14	0.166	retinol dehydrogenase 14
Q00765	REEP5	0.187	receptor accessory protein 5
P78509	RELN	-0.155	reelin
Q86VR2	RETREG3	-0.211	reticulophagy regulator family member 3
P35250-1	RFC2	-0.171	replication factor C subunit 2
Q15382	RHEB	0.19	Ras homolog, mTORC1 binding
P84095	RHOG	0.137	ras homolog family member G
P52758	RIDA	-0.24	reactive intermediate imine deaminase A homolog
Q99496	RNF2	0.126	ring finger protein 2
Q63HN8-4	RNF213	-0.157	ring finger protein 213
Q9H4A4	RNPEP	-0.202	arginyl aminopeptidase
Q9H6T3	RPAP3	-0.133	RNA polymerase II associated protein 3

Q07020	RPL18	0.672	ribosomal protein L18
P61254	RPL26	0.268	ribosomal protein L26
P46776	RPL27A	0.28	ribosomal protein L27a
Q96P16-1	RPRD1A	-0.181	regulation of nuclear pre-mRNA domain containing 1A
P63220	RPS21	-0.154	ribosomal protein S21
P62979	RPS27A	0.254	ribosomal protein S27a
P51812	RPS6KA3	-0.3	ribosomal protein S6 kinase A3
P55042	RRAD	1.406	RRAD, Ras related glycolysis inhibitor and calcium channel regulator
Q7L523	RRAGA	0.3	Ras related GTP binding A
Q9HB90	RRAGC	0.163	Ras related GTP binding C
P62070-4	RRAS2	0.343	RAS related 2
P23921	RRM1	-0.104	ribonucleotide reductase catalytic subunit M1
P56182	RRP1	0.16	ribosomal RNA processing 1
Q5JTH9	RRP12	0.265	ribosomal RNA processing 12 homolog
O43159	RRP8	0.167	ribosomal RNA processing 8
Q6NW29	RWDD4	-0.289	RWD domain containing 4
P28702-3	RXRB	-0.153	retinoid X receptor beta
P23297	S100A1	-0.494	S100 calcium binding protein A1
P31949	S100A11	0.64	S100 calcium binding protein A11
Q96FQ6	S100A16	0.236	S100 calcium binding protein A16
P06703	S100A6	0.294	S100 calcium binding protein A6
P25815	S100P	0.238	S100 calcium binding protein P
P35542	SAA4	-0.307	serum amyloid A4, constitutive
Q9Y3Z3	SAMHD1	-0.158	SAM and HD domain containing deoxynucleoside triphosphate triphosphohydrolase 1
O00422	SAP18	0.123	Sin3A associated protein 18
Q9Y6B6	SAR1B	-0.195	secretion associated Ras related GTPase 1B
Q8WTV0-2	SCARB1	-0.167	scavenger receptor class B member 1
O00767	SCD	-0.287	stearoyl-CoA desaturase
P18827	SDC1	-0.343	syndecan 1
P34741	SDC2	-0.751	syndecan 2
O00560	SDCBP	0.304	syndecan binding protein
Q15436	SEC23A	-0.149	Sec23 homolog A, coat complex II component
Q9Y6Y8	SEC23IP	-0.142	SEC23 interacting protein
O95486	SEC24A	-0.314	SEC24 homolog A, COPII coat complex component
O94855-2	SEC24D	-0.183	SEC24 homolog D, COPII coat complex component
O94979-8	SEC31A	-0.219	SEC31 homolog A, COPII coat complex component
Q13228-4	SELENBP1	-0.296	selenium binding protein 1
O60613	SELENOF	-0.361	selenoprotein F
P49903	SEPHS1	-0.158	selenophosphate synthetase 1
Q99611	SEPHS2	-0.24	selenophosphate synthetase 2
Q9P0V9-2	SEPTIN10	0.204	septin 10
Q9UHD8-1	SEPTIN9	-0.134	septin 9
Q8NC51-1	SERBP1	-0.113	SERPINE1 mRNA binding protein 1
P01009-1	SERPINA1	-0.229	serpin family A member 1
P05154	SERPINA5	-0.265	serpin family A member 5
P05543	SERPINA7	-0.328	serpin family A member 7
P35237	SERPINB6	-0.199	serpin family B member 6

P05546	SERPIND1	-0.386	serpin family D member 1
P05121	SERPINE1	0.565	serpin family E member 1
P08697-1	SERPINF2	-0.529	serpin family F member 2
P50454	SERPINH1	0.454	serpin family H member 1
P58004	SESN2	0.593	sestrin 2
Q86TU7	SETD3	-0.239	SET domain containing 3, actin histidine methyltransferase
Q15428	SF3A2	0.196	splicing factor 3a subunit 2
P31947	SFN	0.368	stratifin
P51688	SGSH	-0.261	N-sulfoglucosamine sulfohydrolase
Q9H299	SH3BGRL3	0.157	SH3 domain binding glutamate rich protein like 3
Q9P0V3	SH3BP4	0.429	SH3 domain binding protein 4
Q8NEM2	SHCBP1	0.341	SHC binding and spindle associated 1
Q9NUL5	SHFL	-0.132	shiftless antiviral inhibitor of ribosomal frameshifting
P34896	SHMT1	-0.364	serine hydroxymethyltransferase 1
P34897-1	SHMT2	0.152	serine hydroxymethyltransferase 2
A0A0B4J2A0	SHPK	-0.224	sedoheptulokinase
Q2M3G4-1	SHROOM1	-0.276	shroom family member 1
Q9NXA8-1	SIRT5	-0.135	sirtuin 5
P53985	SLC16A1	0.144	solute carrier family 16 member 1
O15427	SLC16A3	-0.196	solute carrier family 16 member 3
O15403	SLC16A6	0.62	solute carrier family 16 member 6
Q15758	SLC1A5	0.231	solute carrier family 1 member 5
Q8WUM9	SLC20A1	0.266	solute carrier family 20 member 1
Q6NUK1	SLC25A24	0.155	solute carrier family 25 member 24
P12236	SLC25A6	0.379	solute carrier family 25 member 6
O14975	SLC27A2	-0.237	solute carrier family 27 member 2
Q9Y6M5	SLC30A1	0.565	solute carrier family 30 member 1
Q9HBR0	SLC38A10	-0.208	solute carrier family 38 member 10
Q96QD8	SLC38A2	0.477	solute carrier family 38 member 2
Q99624	SLC38A3	-0.26	solute carrier family 38 member 3
Q9ULF5	SLC39A10	0.807	solute carrier family 39 member 10
Q15043	SLC39A14	-0.291	solute carrier family 39 member 14
Q6P5W5-2	SLC39A4	0.174	solute carrier family 39 member 4
P08195-4	SLC3A2	0.2	solute carrier family 3 member 2
Q9Y6M7-7	SLC4A7	0.226	solute carrier family 4 member 7
P30825	SLC7A1	0.296	solute carrier family 7 member 1
Q9UPY5	SLC7A11	0.868	solute carrier family 7 member 11
O14745	SLC9A3R1	-0.348	SLC9A3 regulator 1
Q15599	SLC9A3R2	-0.233	SLC9A3 regulator 2
Q9NWH9-1	SLTM	0.153	SAFB like transcription modulator
Q8IY18	SMC5	0.144	structural maintenance of chromosomes 5
Q9H0W8	SMG9	0.137	SMG9 nonsense mediated mRNA decay factor
P53814-6	SMTN	0.409	smoothelin
Q2TAY7	SMU1	0.128	SMU1 DNA replication regulator and spliceosomal factor
Q6GMV2	SMYD5	-0.269	SMYD family member 5
Q8TAD8	SNIP1	0.201	Smad nuclear interacting protein 1
Q13596	SNX1	-0.131	sorting nexin 1

Q9NRS6	SNX15	-0.144	sorting nexin 15
O60749	SNX2	-0.131	sorting nexin 2
Q9Y5X3	SNX5	-0.195	sorting nexin 5
Q00796	SORD	-0.37	sorbitol dehydrogenase
Q92673	SORL1	-0.693	sortilin related receptor 1
Q99523	SORT1	-0.371	sortilin 1
O75391	SPAG7	-0.377	sperm associated antigen 7
O60271	SPAG9	0.119	sperm associated antigen 9
Q69YQ0-1	SPECC1L	0.128	sperm antigen with calponin homology and coiled-coil domains 1 like
Q9H2V7	SPNS1	0.155	sphingolipid transporter 1 (putative)
P10451	SPP1	0.409	secreted phosphoprotein 1
P35270	SPR	-0.246	sepiapterin reductase
Q01082-3	SPTBN1	0.667	spectrin beta, non-erythrocytic 1
O15270	SPTLC2	0.17	serine palmitoyltransferase long chain base subunit 2
Q68D10	SPTY2D1	0.457	SPT2 chromatin protein domain containing 1
Q14534	SQLE	-0.16	squalene epoxidase
Q9Y6N5	SQOR	0.387	sulfide quinone oxidoreductase
Q13501-1	SQSTM1	0.29	sequestosome 1
P19623	SRM	-0.154	spermidine synthase
P49458	SRP9	-0.18	signal recognition particle 9
Q01130	SRSF2	-0.411	serine and arginine rich splicing factor 2
Q9BYN0	SRXN1	0.908	sulfiredoxin 1
P15907	ST6GAL1	-0.263	ST6 beta-galactoside alpha-2,6-sialyltransferase 1
Q9Y365	STARD10	-0.209	StAR related lipid transfer domain containing 10
Q658P3-2	STEAP3	-0.538	STEAP3 metalloreductase
O94804	STK10	0.351	serine/threonine kinase 10
Q13043-1	STK4	0.238	serine/threonine kinase 4
P16949-1	STMN1	-0.352	stathmin 1
P27105	STOM	0.178	stomatin
Q13277	STX3	0.379	syntaxin 3
O15400	STX7	0.178	syntaxin 7
P50225	SULT1A1	-0.248	sulfotransferase family 1A member 1
P0DMM9	SULT1A3/SULT1A4	-0.285	sulfotransferase family 1A member 3
Q06520	SULT2A1	-0.447	sulfotransferase family 2A member 1
O94901-9	SUN1	0.239	Sad1 and UNC84 domain containing 1
O95425	SVIL	0.327	supervillin
Q9UH65	SWAP70	0.145	switching B cell complex subunit SWAP70
P37802-2	TAGLN2	0.22	transgelin 2
P37837	TALDO1	0.172	transaldolase 1
Q86VP1	TAX1BP1	0.315	Tax1 binding protein 1
O75347	TBCA	-0.226	tubulin folding cofactor A
Q9Y4C2-1	TCAF1	-0.268	TRPM8 channel associated factor 1
O75764	TCEA3	-0.303	transcription elongation factor A3
Q9UGI8	TES	0.244	testin LIM domain protein
Q96BS2	TESC	-0.283	tescalcin
P02787	TF	-0.297	transferrin
Q00059	TFAM	0.489	transcription factor A, mitochondrial

Q9H5Q4	TFB2M	0.368	transcription factor B2, mitochondrial
P01137	TGFB1	0.475	transforming growth factor beta 1
Q03167	TGFBR3	-0.129	transforming growth factor beta receptor 3
Q96EK4	THAP11	-0.217	THAP domain containing 11
P07996	THBS1	0.311	thrombospondin 1
P52888	THOP1	-0.206	thimet oligopeptidase 1
Q9P016	THYN1	-0.112	thymocyte nuclear protein 1
Q9Y5L4	TIMM13	-0.222	translocase of inner mitochondrial membrane 13
Q9UDY2	TJP2	-0.172	tight junction protein 2
Q3LXA3	TKFC	-0.402	triokinase and FMN cyclase
Q9UM00	TMCO1	0.195	transmembrane and coiled-coil domains 1
Q9H061	TMEM126A	0.305	transmembrane protein 126A
P57088	TMEM33	0.239	transmembrane protein 33
Q9BUB7	TMEM70	0.36	transmembrane protein 70
P42167	TMPO	0.222	thymopoietin
P63313	TMSB10/TMSB4X	0.374	thymosin beta 4 X-linked
O00220	TNFRSF10A	0.233	TNF receptor superfamily member 10a
O14787-2	TNPO2	-0.223	transportin 2
Q68CZ2-1	TNS3	-0.172	tensin 3
Q8IZW8	TNS4	0.636	tensin 4
Q15388	TOMM20	-0.2	translocase of outer mitochondrial membrane 20
Q15785	TOMM34	0.342	translocase of outer mitochondrial membrane 34
Q96HA7	TONSL	-0.137	tonsoku like, DNA repair protein
P11387	TOP1	0.488	DNA topoisomerase I
Q5JTV8	TOR1AIP1	0.254	torsin 1A interacting protein 1
P60174	TPI1	-0.194	triosephosphate isomerase 1
Q9ULW0	TPX2	0.518	TPX2 microtubule nucleation factor
Q9Y296	TRAPPC4	0.114	trafficking protein particle complex 4
Q9BQ61	TRIR	-0.279	telomerase RNA component interacting RNase
Q7L0Y3	TRMT10C	0.301	tRNA methyltransferase 10C, mitochondrial RNase P subunit
O95900	TRUB2	0.173	TruB pseudouridine synthase family member 2
Q9H0U9	TSPYL1	0.203	TSPY like 1
Q9H2G4	TSPYL2	0.495	TSPY like 2
Q13630	TSTA3	-0.139	tissue specific transplantation antigen P35B
Q5R3I4	TTC38	-0.409	tetratricopeptide repeat domain 38
Q14166	TTLL12	-0.167	tubulin tyrosine ligase like 12
Q13509	TUBB3	0.209	tubulin beta 3 class III
Q9BUF5	TUBB6	0.177	tubulin beta 6 class V
Q96CW5	TUBGCP3	-0.102	tubulin gamma complex associated protein 3
P49411	TUFM	0.155	Tu translation elongation factor, mitochondrial
Q6IBS0	TWF2	-0.166	twinfilin actin binding protein 2
P40222	TXLNA	-0.111	taxilin alpha
Q9BRA2	TXNDC17	-0.222	thioredoxin domain containing 17
P83876	TXNL4A	-0.296	thioredoxin like 4A
Q16881	TXNRD1	0.246	thioredoxin reductase 1
P19971-2	TYMP	-0.242	thymidine phosphorylase
P26368	U2AF2	-0.136	U2 small nuclear RNA auxiliary factor 2

Q3KQV9	UAP1L1	-0.232	UDP-N-acetylglucosamine pyrophosphorylase 1 like 1
P22314	UBA1	-0.156	ubiquitin like modifier activating enzyme 1
Q8TBC4-1	UBA3	-0.13	ubiquitin like modifier activating enzyme 3
Q9GZZ9-1	UBA5	-0.186	ubiquitin like modifier activating enzyme 5
P63279	UBE2I	-0.155	ubiquitin conjugating enzyme E2 I
P68036	UBE2L3	-0.161	ubiquitin conjugating enzyme E2 L3
P61081	UBE2M	-0.144	ubiquitin conjugating enzyme E2 M
P61088	UBE2N	-0.167	ubiquitin conjugating enzyme E2 N
Q9NPD8	UBE2T	-0.17	ubiquitin conjugating enzyme E2 T
Q13404-1	UBE2V1	-0.234	ubiquitin conjugating enzyme E2 V1
O95155-4	UBE4B	-0.137	ubiquitination factor E4B
Q8WVY7	UBLCP1	-0.153	ubiquitin like domain containing CTD phosphatase 1
Q8N806	UBR7	-0.183	ubiquitin protein ligase E3 component n-recognin 7 (putative)
Q92575	UBXN4	0.109	UBX domain protein 4
Q6UWM9	UGT2A3	-0.122	UDP glucuronosyltransferase family 2 member A3
Q6BDS2	UHRF1BP1	-0.142	UHRF1 binding protein 1
Q9BRT2	UQCC2	-0.174	ubiquinol-cytochrome c reductase complex assembly factor 2
Q8TCY9	URGCP	0.205	upregulator of cell proliferation
P06132	UROD	-0.269	uroporphyrinogen decarboxylase
Q92995	USP13	-0.223	ubiquitin specific peptidase 13
Q8TED0	UTP15	0.192	UTP15 small subunit processome component
Q9Y5J1	UTP18	0.146	UTP18 small subunit processome component
Q9NQZ2	UTP3	0.239	UTP3 small subunit processome component
Q969X6	UTP4	0.259	UTP4 small subunit processome component
Q9P0L0-2	VAPA	0.27	VAMP associated protein A
P26640	VARS	-0.134	valyl-tRNA synthetase 1
Q6EMK4	VASN	-0.294	vasorin
P50552	VASP	0.159	vasodilator stimulated phosphoprotein
Q99536	VAT1	-0.153	vesicle amine transport 1
P52735	VAV2	-0.23	vav guanine nucleotide exchange factor 2
P61758	VBP1	-0.15	VHL binding protein 1
P18206	VCL	-0.176	vinculin
P21796	VDAC1	0.133	voltage dependent anion channel 1
P45880-1	VDAC2	0.273	voltage dependent anion channel 2
P09327	VIL1	-0.111	villin 1
Q9H9C1-1	VIPAS39	-0.277	VPS33B interacting protein, apical-basolateral polarity regulator, spe-39 homolog
Q9BRG1	VPS25	-0.168	vacuolar protein sorting 25 homolog
Q9UBQ0	VPS29	-0.15	VPS29 retromer complex component
Q96QK1	VPS35	-0.191	VPS35 retromer complex component
Q96JG6	VPS50	-0.203	VPS50 subunit of EARP/GARPII complex
P62760	VSNL1	-0.472	visinin like 1
Q9UGM6	WARS2	0.255	tryptophanyl tRNA synthetase 2, mitochondrial
Q2M389	WASHC4	-0.188	WASH complex subunit 4
Q12768	WASHC5	-0.209	WASH complex subunit 5
Q9GZL7	WDR12	-0.16	WD repeat domain 12
Q9UNX4	WDR3	0.172	WD repeat domain 3
Q8NI36	WDR36	0.152	WD repeat domain 36

Q6RFH5	WDR74	0.17	WD repeat domain 74
Q562E7	WDR81	-0.12	WD repeat domain 81
A4D1P6	WDR91	-0.203	WD repeat domain 91
Q9Y3S1	WNK2	-0.646	WNK lysine deficient protein kinase 2
Q9HCS7	XAB2	0.145	XPA binding protein 2
O14980	XPO1	-0.114	exportin 1
Q9C0E2	XPO4	-0.252	exportin 4
O75191	XYLB	-0.235	xylulokinase
P54577	YARS1	-0.137	tyrosyl-tRNA synthetase 1
P67809	YBX1	-0.239	Y-box binding protein 1
Q5BJH7	YIF1B	0.198	Yip1 interacting factor homolog B, membrane trafficking protein
O15498	YKT6	0.243	YKT6 v-SNARE homolog
Q86U90	YRDC	0.242	yrdC N6-threonylcarbamoyltransferase domain containing
Q96MU7-1	YTHDC1	0.142	YTH domain containing 1
P62258	YWHAE	-0.18	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein epsilon
O95625	ZBTB11	0.191	zinc finger and BTB domain containing 11
O75152	ZC3H11A	0.22	zinc finger CCCH-type containing 11A
Q8WU90	ZC3H15	-0.154	zinc finger CCCH-type containing 15
Q7Z2W4	ZC3HAV1	0.147	zinc finger CCCH-type containing, antiviral 1
Q9C0B9	ZCCHC2	-0.231	zinc finger CCHC-type containing 2
Q8N5A5	ZGPAT	0.186	zinc finger CCCH-type and G-patch domain containing
Q14202	ZMYM3	-0.318	zinc finger MYM-type containing 3
Q8NC26	ZNF114	0.394	zinc finger protein 114
O75362	ZNF217	-0.113	zinc finger protein 217
Q9P2Y4	ZNF219	-0.193	zinc finger protein 219
Q5BKZ1	ZNF326	0.112	zinc finger protein 326
Q969S3	ZNF622	0.166	zinc finger protein 622
Q9H900-1	ZWILCH	-0.141	zwilch kinetochore protein
Q9C0D3	ZYG11B	-0.191	zyg-11 family member B, cell cycle regulator
O43149	ZZEF1	-0.307	zinc finger ZZ-type and EF-hand domain containing 1
P00374		-0.26	
P00761		0.251	
P62158		-0.273	
P69905		1.153	

List of proteins deregulated in HepG2 cells after 24h exposure to CDDP 10 mM

ID	Symbol	Expr Log Ratio	Entrez Gene Name
Q9NQ94	A1CF	-0.129	APOBEC1 complementation factor
Q13685	AAMP	-0.192	angio associated migratory cell protein
Q9NRN7	AASDHPPT	0.193	aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase
O95477	ABCA1	-0.274	ATP binding cassette subfamily A member 1
Q8TB40	ABHD4	0.421	abhydrolase domain containing 4
Q9BV23	ABHD6	0.18	abhydrolase domain containing 6
Q9ULW3	ABT1	-0.141	activator of basal transcription 1
Q13085-4	ACACA	-0.274	acetyl-CoA carboxylase alpha
P45954	ACADSB	0.144	acyl-CoA dehydrogenase short/branched chain
Q15057	ACAP2	-0.229	ArfGAP with coiled-coil, ankyrin repeat and PH domains 2
P24752	ACAT1	0.144	acetyl-CoA acetyltransferase 1
Q15067	ACOX1	0.226	acyl-CoA oxidase 1
P11117	ACP2	0.171	acid phosphatase 2, lysosomal
O95573	ACSL3	0.168	acyl-CoA synthetase long chain family member 3
O60488-1	ACSL4	-0.247	acyl-CoA synthetase long chain family member 4
P14621	ACYP2	-0.575	acylphosphatase 2
O14672	ADAM10	-0.165	ADAM metallopeptidase domain 10
P35611-3	ADD1	-0.179	adducin 1
Q9Y653	ADGRG1	1.224	adhesion G protein-coupled receptor G1
Q86SQ4-3	ADGRG6	-0.2	adhesion G protein-coupled receptor G6
P55263	ADK	-0.241	adenosine kinase
Q16186	ADRM1	0.216	adhesion regulating molecule 1
P30566	ADSL	-0.106	adenylosuccinate lyase
Q9UHB7-1	AFF4	0.18	AF4/FMR2 family member 4
Q6ULP2	AFTPH	-0.354	aftiphilin
Q96P47-4	AGAP3	-0.274	ArfGAP with GTPase domain, ankyrin repeat and PH domain 3
Q9BSE5	AGMAT	0.112	agmatinase
O00468	AGRN	-0.246	agrin
P01019	AGT	-0.539	angiotensinogen
O95831-1	AIFM1	0.15	apoptosis inducing factor mitochondria associated 1
Q96IF1	AJUBA	-0.206	ajuba LIM protein
P00568	AK1	0.227	adenylate kinase 1
Q9UIJ7-1	AK3	0.248	adenylate kinase 3
Q12802-2	AKAP13	-0.268	A-kinase anchoring protein 13
Q02040-1	AKAP17A	0.167	A-kinase anchoring protein 17A
O43823	AKAP8	0.218	A-kinase anchoring protein 8
Q9ULX6	AKAP8L	0.204	A-kinase anchoring protein 8 like
O60218	AKR1B10	0.127	aldo-keto reductase family 1 member B10
P30837	ALDH1B1	0.161	aldehyde dehydrogenase 1 family member B1
P05091	ALDH2	0.163	aldehyde dehydrogenase 2 family member
P49419-2	ALDH7A1	0.326	aldehyde dehydrogenase 7 family member A1

P49189	ALDH9A1	0.138	aldehyde dehydrogenase 9 family member A1
P09972	ALDOC	-0.123	aldolase, fructose-bisphosphate C
Q8IWZ3-6	ANKHD1/ANKHD1-EIF4EBP3	-0.18	ankyrin repeat and KH domain containing 1
Q92625	ANKS1A	-0.201	ankyrin repeat and sterile alpha motif domain containing 1A
Q9NQW6	ANLN	0.541	anillin actin binding protein
Q9BZZ5-2	API5	0.118	apoptosis inhibitor 5
P02647	APOA1	-0.233	apolipoprotein A1
P04114	APOB	-0.692	apolipoprotein B
Q9NRW3	APOBEC3C	0.778	apolipoprotein B mRNA editing enzyme catalytic subunit 3C
P02649	APOE	-0.172	apolipoprotein E
O14791-2	APOL1	-0.442	apolipoprotein L1
Q96P48-6	ARAP1	-0.248	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 1
P84085	ARF5	0.172	ADP ribosylation factor 5
P78540	ARG2	0.37	arginase 2
Q8IWW6-1	ARHGAP12	-0.17	Rho GTPase activating protein 12
Q8N392	ARHGAP18	-0.326	Rho GTPase activating protein 18
Q9NRY4	ARHGAP35	-0.224	Rho GTPase activating protein 35
Q92888-3	ARHGEF1	-0.151	Rho guanine nucleotide exchange factor 1
Q8N1W1-6	ARHGEF28	-0.213	Rho guanine nucleotide exchange factor 28
Q8NFD5-3	ARID1B	-0.276	AT-rich interaction domain 1B
Q8IVW6	ARID3B	0.246	AT-rich interaction domain 3B
Q6NXE6-1	ARMC6	-0.141	armadillo repeat containing 6
Q5T2E6	ARMH3	-0.257	armadillo like helical domain containing 3
P15848	ARSB	-0.227	arylsulfatase B
O00192	ARVCF	0.384	ARVCF delta catenin family member
Q8N9N2-2	ASCC1	-0.277	activating signal cointegrator 1 complex subunit 1
Q9H1I8-1	ASCC2	-0.255	activating signal cointegrator 1 complex subunit 2
Q8N3C0	ASCC3	-0.366	activating signal cointegrator 1 complex subunit 3
P07306	ASGR1	-0.156	asialoglycoprotein receptor 1
P07307	ASGR2	-0.146	asialoglycoprotein receptor 2
P08243	ASNS	-0.189	asparagine synthetase (glutamine-hydrolyzing)
Q9NWL6	ASNSD1	-0.23	asparagine synthetase domain containing 1
P00966	ASS1	-0.188	argininosuccinate synthase 1
Q8NBU5	ATAD1	0.171	ATPase family AAA domain containing 1
Q6PL18-1	ATAD2	-0.202	ATPase family AAA domain containing 2
Q5T9A4	ATAD3B	-0.234	ATPase family AAA domain containing 3B
P18847	ATF3	0.857	activating transcription factor 3
Q9NT62	ATG3	-0.156	autophagy related 3
O95352	ATG7	-0.262	autophagy related 7
P98196	ATP11A	-0.267	ATPase phospholipid transporting 11A
P05023	ATP1A1	0.107	ATPase Na+/K+ transporting subunit alpha 1
P05026	ATP1B1	0.211	ATPase Na+/K+ transporting subunit beta 1
P54709	ATP1B3	0.192	ATPase Na+/K+ transporting subunit beta 3
Q9UII2	ATP5IF1	0.346	ATP synthase inhibitory factor subunit 1
O75947-1	ATP5PD	0.156	ATP synthase peripheral stalk subunit d
P18859-2	ATP5PF	0.208	ATP synthase peripheral stalk subunit F6
P48047	ATP5PO	0.263	ATP synthase peripheral stalk subunit OSCP

O75787	ATP6AP2	0.316	ATPase H+ transporting accessory protein 2
P61421	ATP6V0D1	0.218	ATPase H+ transporting V0 subunit d1
P21283	ATP6V1C1	0.137	ATPase H+ transporting V1 subunit C1
Q9Y5K8	ATP6V1D	0.118	ATPase H+ transporting V1 subunit D
Q5TC12	ATPAF1	0.224	ATP synthase mitochondrial F1 complex assembly factor 1
P0C7T5	ATXN1L	-0.679	ataxin 1 like
O14965	AURKA	0.3	aurora kinase A
Q96GD4-5	AURKB	0.329	aurora kinase B
Q9NQS1	AVEN	-0.172	apoptosis and caspase activation inhibitor
Q8NBF6-1	AVL9	-0.289	AVL9 cell migration associated
Q9NY97	B3GNT2	0.223	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 2
Q9NXR7-1	BABAM2	-0.286	BRISC and BRCA1 A complex member 2
P51572-2	BCAP31	0.291	B cell receptor associated protein 31
P56945-6	BCAR1	0.15	BCAR1 scaffold protein, Cas family member
O75934	BCAS2	0.161	BCAS2 pre-mRNA processing factor
Q86UU0	BCL9L	0.333	BCL9 like
Q9NYM9	BET1L	-0.178	Bet1 golgi vesicular membrane trafficking protein like
Q9NR09	BIRC6	-0.219	baculoviral IAP repeat containing 6
Q14692	BMS1	-0.191	BMS1 ribosome biogenesis factor
Q53S33	BOLA3	0.398	bolA family member 3
Q86WA6	BPHL	0.234	biphenyl hydrolase like
Q5VW32	BROX	-0.14	BRO1 domain and CAAX motif containing
Q7KYR7	BTN2A1	0.386	butyrophilin subfamily 2 member A1
O43709	BUD23	-0.218	BUD23 rRNA methyltransferase and ribosome maturation factor
P41223-2	BUD31	0.224	BUD31 homolog
Q9Y6E2	BZW2	-0.18	basic leucine zipper and W2 domains 2
Q8N5I9	C12orf45	0.431	chromosome 12 open reading frame 45
Q8NDD1	C1orf131	-0.465	chromosome 1 open reading frame 131
A6NCS6	C2orf72	-0.223	chromosome 2 open reading frame 72
P01024	C3	-0.205	complement C3
Q9BRJ6	C7orf50	-0.393	chromosome 7 open reading frame 50
P27708	CAD	-0.154	carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase
Q9BY67-3	CADM1	-0.302	cell adhesion molecule 1
Q13557-10	CAMK2D	-0.221	calcium/calmodulin dependent protein kinase II delta
P40123	CAP2	-0.239	cyclase associated actin cytoskeleton regulatory protein 2
P47755	CAPZA2	-0.152	capping actin protein of muscle Z-line subunit alpha 2
P49589-3	CARS1	-0.24	cysteinyl-tRNA synthetase 1
O15234	CASC3	-0.238	CASC3 exon junction complex subunit
O95810	CAVIN2	0.326	caveolae associated protein 2
P45973	CBX5	0.376	chromobox 5
Q8IX12	CCAR1	0.195	cell division cycle and apoptosis regulator 1
Q8IWD4	CCDC117	0.627	coiled-coil domain containing 117
Q96CT7	CCDC124	-0.187	coiled-coil domain containing 124
Q6PK04	CCDC137	-0.473	coiled-coil domain containing 137
O60826	CCDC22	-0.17	coiled-coil domain containing 22
Q8IVM0	CCDC50	-0.226	coiled-coil domain containing 50
Q9P031	CCDC59	-0.365	coiled-coil domain containing 59

Q3V6T2-1	CCDC88A	-0.184	coiled-coil domain containing 88A
P20248	CCNA2	0.542	cyclin A2
P14635	CCNB1	0.245	cyclin B1
O60563	CCNT1	0.377	cyclin T1
P49427	CDC34	0.133	cell division cycle 34
O60508	CDC40	0.125	cell division cycle 40
Q99618	CDCA3	0.242	cell division cycle associated 3
P19022	CDH2	-0.29	cadherin 2
O14735	CDIPT	-0.582	CDP-diacylglycerol--inositol 3-phosphatidyltransferase
P06493	CDK1	0.249	cyclin dependent kinase 1
Q00534	CDK6	-0.269	cyclin dependent kinase 6
P50750-2	CDK9	0.224	cyclin dependent kinase 9
Q5VV42	CDKAL1	-0.482	CDK5 regulatory subunit associated protein 1 like 1
P38936	CDKN1A	1.8	cyclin dependent kinase inhibitor 1A
Q9NXV6	CDKN2AIP	0.328	CDKN2A interacting protein
Q9UHN6	CEMIP2	0.255	cell migration inducing hyaluronidase 2
P49454	CENPF	0.382	centromere protein F
Q8TAP6	CEP76	0.649	centrosomal protein 76
O00748	CES2	0.297	carboxylesterase 2
Q9UEE9-1	CFDP1	-0.22	craniofacial development protein 1
P05156	CFI	-0.343	complement factor I
Q0VF96	CGNL1	-0.996	cingulin like 1
Q13112	CHAF1B	0.239	chromatin assembly factor 1 subunit B
O14757	CHEK1	-0.482	checkpoint kinase 1
Q8IWX8	CHERP	0.125	calcium homeostasis endoplasmic reticulum protein
P35790	CHKA	-0.42	choline kinase alpha
Q9Y3E7	CHMP3	0.294	charged multivesicular body protein 3
Q9H444	CHMP4B	0.223	charged multivesicular body protein 4B
Q8NET6	CHST13	-0.296	carbohydrate sulfotransferase 13
Q99828-2	CIB1	0.283	calcium and integrin binding 1
O14578-4	CIT	-0.25	citron rho-interacting serine/threonine kinase
Q8WWK9	CKAP2	0.652	cytoskeleton associated protein 2
Q07065	CKAP4	0.139	cytoskeleton associated protein 4
P61024	CKS1B	0.459	CDC28 protein kinase regulatory subunit 1B
Q7Z460-1	CLASP1	-0.237	cytoplasmic linker associated protein 1
O00299	CLIC1	0.159	chloride intracellular channel 1
Q9Y696	CLIC4	-0.169	chloride intracellular channel 4
Q9H078-1	CLPB	-0.119	ClpB homolog, mitochondrial AAA ATPase chaperonin
O76031	CLPX	0.191	caseinolytic mitochondrial matrix peptidase chaperone subunit
I3L2B0	CLUH	-0.342	clustered mitochondria homolog
O75153	CLUH	-0.242	clustered mitochondria homolog
Q96DG6	CMBL	0.67	carboxymethylenebutenolidase homolog
Q8IY22	CMIP	-0.706	c-Maf inducing protein
Q9BQ75	CMSS1	-0.388	cms1 ribosomal small subunit homolog
P62633	CNBP	-1.428	CCHC-type zinc finger nucleic acid binding protein
P62633-6	CNBP	-1.085	CCHC-type zinc finger nucleic acid binding protein
Q9H9A5-6	CNOT10	-0.136	CCR4-NOT transcription complex subunit 10

Q9UIV1-1	CNOT7	-0.25	CCR4-NOT transcription complex subunit 7
Q96BR5	COA7	0.284	cytochrome c oxidase assembly factor 7 (putative)
P38432	COIL	0.193	coilin
Q9P000-1	COMMD9	-0.412	COMM domain containing 9
Q9ULV4-3	CORO1C	0.152	coronin 1C
A0A0A6YYL4	CORO7/CORO7-PAM16	-0.118	coronin 7
P13073	COX4I1	0.142	cytochrome c oxidase subunit 4I1
O75976	CPD	-0.23	carboxypeptidase D
Q6PUV4	CPLX2	-0.609	complexin 2
P23786	CPT2	0.254	carnitine palmitoyltransferase 2
P78560	CRADD	-0.421	CASP2 and RIPK1 domain containing adaptor with death domain
P52943	CRIP2	0.307	cysteine rich protein 2
Q8IUI8	CRLF3	-0.161	cytokine receptor like factor 3
O75534-4	CSDE1	-0.179	cold shock domain containing E1
Q12996	CSTF3	0.318	cleavage stimulation factor subunit 3
P35221	CTNNA1	-0.236	catenin alpha 1
Q9UBT7	CTNNAL1	-0.135	catenin alpha like 1
O60716-3	CTNND1	-0.111	catenin delta 1
Q9NRF8	CTPS2	-0.168	CTP synthase 2
Q6PD62	CTR9	0.12	CTR9 homolog, Paf1/RNA polymerase II complex component
P07339	CTSD	0.189	cathepsin D
P07711	CTSL	0.216	cathepsin L
Q2VPK5	CTU2	-0.156	cytosolic thiouridylase subunit 2
P39880-3	CUX1	-0.454	cut like homeobox 1
Q2TBE0	CWF19L2	-0.158	CWF19 like cell cycle control factor 2
P99999	CYCS	0.247	cytochrome c, somatic
Q96SQ9-2	CYP2S1	0.182	cytochrome P450 family 2 subfamily S member 1
Q8TAV3	CYP2W1	-0.27	cytochrome P450 family 2 subfamily W member 1
Q9Y4D1	DAAM1	-0.24	dishevelled associated activator of morphogenesis 1
Q5VWQ8	DAB2IP	-0.218	DAB2 interacting protein
Q14118	DAG1	-0.186	dystroglycan 1
P51397	DAP	-0.185	death associated protein
Q9UK59	DBR1	0.239	debranching RNA lariats 1
P11182	DBT	0.192	dihydrolipoamide branched chain transacylase E2
P61962	DCAF7	0.22	DDB1 and CUL4 associated factor 7
Q9H773	DCTPP1	-0.19	dCTP pyrophosphatase 1
Q96GG9	DCUN1D1	0.209	defective in cullin neddylation 1 domain containing 1
Q92466	DDB2	0.556	damage specific DNA binding protein 2
Q13206	DDX10	-0.249	DEAD-box helicase 10
Q96GQ7	DDX27	-0.238	DEAD-box helicase 27
Q9Y6V7	DDX49	-0.234	DEAD-box helicase 49
Q9NY93	DDX56	-0.524	DEAD-box helicase 56
P26196	DDX6	0.165	DEAD-box helicase 6
Q8WYQ5-1	DGCR8	0.301	DGCR8 microprocessor complex subunit
Q5KSL6	DGKK	-0.346	diacylglycerol kinase kappa
Q86SQ9-2	DHDDS	-0.292	dehydrodolichyl diphosphate synthase subunit
Q8IY37	DHX37	-0.171	DEAH-box helicase 37

Q6P158-1	DHX57	-0.393	DExH-box helicase 57
O60610-1	DIAPH1	-0.14	diaphanous related formin 1
Q9BTC0	DIDO1	0.254	death inducer-obliterator 1
Q9UNQ2	DIMT1	-0.281	DIMT1 rRNA methyltransferase and ribosome maturation factor
Q9P265	DIP2B	-0.22	disco interacting protein 2 homolog B
Q8IYB7	DIS3L2	-0.349	DIS3 like 3'-5' exoribonuclease 2
P09622	DLD	0.228	dihydrolipoamide dehydrogenase
Q15398	DLGAP5	0.383	DLG associated protein 5
P36957	DLST	0.17	dihydrolipoamide S-succinyltransferase
P11532-6	DMD	-0.125	dystrophin
Q86Y56	DNAAF5	-0.288	dynein axonemal assembly factor 5
P31689	DNAJA1	0.161	DnaJ heat shock protein family (Hsp40) member A1
P25686-3	DNAJB2	0.408	DnaJ heat shock protein family (Hsp40) member B2
Q8IXB1	DNAJC10	-0.118	DnaJ heat shock protein family (Hsp40) member C10
Q9Y5T4	DNAJC15	-0.695	DnaJ heat shock protein family (Hsp40) member C15
Q9ULA0	DNPEP	-0.103	aspartyl aminopeptidase
Q9BU89	DOHH	0.275	deoxyhypusine hydroxylase
Q9BQC3	DPH2	-0.113	diphthamide biosynthesis 2
Q9H2P9-5	DPH5	-0.297	diphthamide biosynthesis 5
Q16555	DPYSL2	-0.149	dihydropyrimidinase like 2
Q8TE96	DQX1	0.276	DEAQ-box RNA dependent ATPase 1
Q14919-2	DRAP1	0.205	DR1 associated protein 1
Q9Y295	DRG1	-0.279	developmentally regulated GTP binding protein 1
P60981-1	DSTN	0.196	destrin, actin depolymerizing factor
Q99956	DUSP9	-0.219	dual specificity phosphatase 9
O14641	DVL2	-0.364	dishevelled segment polarity protein 2
Q14204	DYNC1H1	-0.118	dynein cytoplasmic 1 heavy chain 1
P63167	DYNLL1	0.405	dynein light chain LC8-type 1
Q99848	EBNA1BP2	-0.277	EBNA1 binding protein 2
P42892	ECE1	-0.323	endothelin converting enzyme 1
Q13011	ECH1	0.147	enoyl-CoA hydratase 1
Q9NTX5	ECHDC1	0.137	ethylmalonyl-CoA decarboxylase 1
O75521	ECI2	0.201	enoyl-CoA delta isomerase 2
Q9H8V3-3	ECT2	0.333	epithelial cell transforming 2
P13639	EEF2	-0.168	eukaryotic translation elongation factor 2
Q7Z2Z2	EFL1	-0.177	elongation factor like GTPase 1
Q8NDI1	EHBP1	-0.333	EH domain binding protein 1
Q9H223	EHD4	-0.222	EH domain containing 4
P41567	EIF1	0.25	eukaryotic translation initiation factor 1
Q9NZJ5	EIF2AK3	-0.222	eukaryotic translation initiation factor 2 alpha kinase 3
P41214	EIF2D	-0.218	eukaryotic translation initiation factor 2D
Q9UBQ5	EIF3K	-0.191	eukaryotic translation initiation factor 3 subunit K
O60573	EIF4E2	-0.192	eukaryotic translation initiation factor 4E family member 2
O43432-3	EIF4G3	-0.3	eukaryotic translation initiation factor 4 gamma 3
P55199	ELL	0.295	elongation factor for RNA polymerase II
O95163	ELP1	-0.111	elongator complex protein 1
Q9H9T3	ELP3	-0.212	elongator acetyltransferase complex subunit 3

Q14249	ENDOG	0.186	endonuclease G
P13929-1	ENO3	-0.172	enolase 3
Q5NDL2	EOGT	-0.18	EGF domain specific O-linked N-acetylglucosamine transferase
Q96L91	EP400	-0.155	E1A binding protein p400
P29317	EPHA2	0.697	EPH receptor A2
P54760	EPHB4	0.379	EPH receptor B4
P07099	EPHX1	0.244	epoxide hydrolase 1
P34913	EPHX2	-0.194	epoxide hydrolase 2
A0A087X1U6	EPPK1	0.333	epiplakin 1
P58107	EPPK1	0.292	epiplakin 1
P42566	EPS15	-0.14	epidermal growth factor receptor pathway substrate 15
Q9H6S3	EPS8L2	0.279	EPS8 like 2
P04626	ERBB2	-0.204	erb-b2 receptor tyrosine kinase 2
Q96RT1-8	ERBIN	-0.108	erbb2 interacting protein
Q8IUD2-1	ERC1	-0.449	ELKS/RAB6-interacting/CAST family member 1
P18074-1	ERCC2	-0.142	ERCC excision repair 2, TFIIH core complex helicase subunit
P19447	ERCC3	0.21	ERCC excision repair 3, TFIIH core complex helicase subunit
Q9Y282-3	ERGIC3	0.184	ERGIC and golgi 3
P84090	ERH	0.201	ERH mRNA splicing and mitosis factor
B1AK53-1	ESPN	-0.377	espin
A0FGR8-2	ESYT2	0.14	extended synaptotagmin 2
O60645	EXOC3	-0.375	exocyst complex component 3
Q96A65	EXOC4	-0.318	exocyst complex component 4
Q9Y2D4	EXOC6B	-0.557	exocyst complex component 6B
Q9NQT4	EXOSC5	0.13	exosome component 5
Q9Y624	F11R	0.278	F11 receptor
Q9UNN5	FAF1	-0.506	Fas associated factor 1
Q96CS3	FAF2	0.16	Fas associated factor family member 2
Q9Y6X4-1	FAM169A	0.234	family with sequence similarity 169 member A
Q9NSI2	FAM207A	-0.386	family with sequence similarity 207 member A
O75063	FAM20B	-0.127	FAM20B glycosaminoglycan xylosylkinase
Q96KR6	FAM210B	0.547	family with sequence similarity 210 member B
Q9H4H8	FAM83D	0.304	family with sequence similarity 83 member D
Q52LJ0-2	FAM98B	0.156	family with sequence similarity 98 member B
P25445	FAS	0.834	Fas cell surface death receptor
P49327	FASN	-0.246	fatty acid synthase
Q14517	FAT1	0.154	FAT atypical cadherin 1
Q8NEZ5	FBXO22	0.33	F-box protein 22
O94868	FCHSD2	-0.293	FCH and double SH3 domains 2
P22570-7	FDXR	0.614	ferredoxin reductase
Q9BQL6	FERMT1	-0.094	fermitin family member 1
P02671-2	FGA	-0.383	fibrinogen alpha chain
P22455-1	FGFR4	-0.536	fibroblast growth factor receptor 4
P02679	FGG	-0.364	fibrinogen gamma chain
Q9Y613	FHOD1	-0.247	formin homology 2 domain containing 1
O95302-3	FKBP9	0.213	FKBP prolyl isomerase 9
Q14254	FLOT2	0.138	flotillin 2

Q9Y5Y0	FLVCR1	-0.271	feline leukemia virus subgroup C cellular receptor 1
Q96PY5-3	FMNL2	-0.27	formin like 2
P02751-15	FN1	-0.343	fibronectin 1
Q53EP0	FNDC3B	-0.353	fibronectin type III domain containing 3B
Q5VW36	FOCAD	-0.309	focadhesin
P15407	FOSL1	0.937	FOS like 1, AP-1 transcription factor subunit
Q8IWF2	FOXRED2	-0.265	FAD dependent oxidoreductase domain containing 2
Q86XX4-2	FRAS1	-1.025	Fraser extracellular matrix complex subunit 1
Q16658	FSCN1	0.12	fascin actin-bundling protein 1
P02792	FTL	0.311	ferritin light chain
Q9C0B1-1	FTO	-0.31	FTO alpha-ketoglutarate dependent dioxygenase
Q9BTY2	FUCA2	0.188	alpha-L-fucosidase 2
Q06546	GABPA	-0.223	GA binding protein transcription factor subunit alpha
Q14376	GALE	-0.107	UDP-galactose-4-epimerase
O43903	GAS2	-0.2	growth arrest specific 2
P04062	GBA	0.125	glucosylceramidase beta
Q8IWJ2	GCC2	0.147	GRIP and coiled-coil domain containing 2
Q99988	GDF15	0.839	growth differentiation factor 15
P31150	GDI1	0.175	GDP dissociation inhibitor 1
Q06210	GFPT1	-0.161	glutamine--fructose-6-phosphate transaminase 1
Q9BRT9	GINS4	0.149	GINS complex subunit 4
Q9Y2X7-3	GIT1	0.257	GIT ArfGAP 1
P08034	GJB1	-0.637	gap junction protein beta 1
O94925	GLS	0.611	glutaminase
P15104	GLUL	-0.227	glutamate-ammonia ligase
P17900	GM2A	0.723	GM2 ganglioside activator
O60547	GMDS	-0.255	GDP-mannose 4,6-dehydratase
O75496	GMNN	0.403	geminin DNA replication inhibitor
Q9Y5P6-2	GMPPB	-0.188	GDP-mannose pyrophosphorylase B
P29992	GNA11	0.195	G protein subunit alpha 11
Q13823	GNL2	-0.409	G protein nucleolar 2
Q9BVP2	GNL3	-0.452	G protein nucleolar 3
Q9NVN8	GNL3L	-0.283	G protein nucleolar 3 like
Q9Y3E0	GOLT1B	0.141	golgi transport 1B
P17174	GOT1	0.297	glutamic-oxaloacetic transaminase 1
P00505	GOT2	0.207	glutamic-oxaloacetic transaminase 2
P35052	GPC1	0.393	glypican 1
P51654-1	GPC3	-0.235	glypican 3
Q9Y625	GPC6	-0.563	glypican 6
Q9NQX3-2	GPHN	-0.445	gephyrin
Q13889	GTF2H3	0.294	general transcription factor IIH subunit 3
Q9BZE4	GTPBP4	-0.407	GTP binding protein 4
Q9NYZ3	GTSE1	0.454	G2 and S-phase expressed 1
Q4G148	GXYLT1	0.389	glucoside xylosyltransferase 1
O14929	HAT1	0.107	histone acetyltransferase 1
Q00341	HDLBP	-0.231	high density lipoprotein binding protein
Q86XA9	HEATR5A	-0.194	HEAT repeat containing 5A

Q9BYK8	HELZ2	0.292	helicase with zinc finger 2
Q15011-1	HERPUD1	-0.783	homocysteine inducible ER protein with ubiquitin like domain 1
O94992	HEXIM1	0.431	HEXIM P-TEFb complex subunit 1
Q9BTY7	HGH1	-0.187	HGH1 homolog
P01892	HLA-A	0.194	major histocompatibility complex, class I, A
P05534	HLA-A	0.236	major histocompatibility complex, class I, A
Q14527	HLTF	-0.513	helicase like transcription factor
Q8TCT9	HM13	-0.131	histocompatibility minor 13
P09429	HMGB1	0.209	high mobility group box 1
P35914	HMGCL	0.234	3-hydroxy-3-methylglutaryl-CoA lyase
Q01581	HMGCS1	-0.339	3-hydroxy-3-methylglutaryl-CoA synthase 1
P05204	HMGN2	0.307	high mobility group nucleosomal binding domain 2
O75330-3	HMMR	0.462	hyaluronan mediated motility receptor
P20823-7	HNF1A	-0.197	HNF1 homeobox A
P41235-4	HNF4A	-0.396	hepatocyte nuclear factor 4 alpha
Q9UJC3	HOOK1	-0.162	hook microtubule tethering protein 1
P00738	HP	-0.366	haptoglobin
P37235	HPCAL1	-0.158	hippocalcin like 1
P37059	HSD17B2	0.14	hydroxysteroid 17-beta dehydrogenase 2
Q9H2F3	HSD3B7	-0.109	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 7
Q6YN16	HSDL2	0.191	hydroxysteroid dehydrogenase like 2
O95757	HSPA4L	0.327	heat shock protein family A (Hsp70) member 4 like
P04792	HSPB1	0.373	heat shock protein family B (small) member 1
P98160	HSPG2	-0.538	heparan sulfate proteoglycan 2
Q92598	HSPH1	0.204	heat shock protein family H (Hsp110) member 1
P42858	HTT	-0.176	huntingtin
Q7Z6Z7	HUWE1	-0.149	HECT, UBA and WWE domain containing E3 ubiquitin protein ligase 1
Q9P2D0	IBTK	-0.287	inhibitor of Bruton tyrosine kinase
P05362	ICAM1	0.174	intercellular adhesion molecule 1
P48735	IDH2	0.215	isocitrate dehydrogenase (NADP(+)) 2
P15260	IFNGR1	-0.338	interferon gamma receptor 1
Q12894-2	IFRD2	-0.283	interferon related developmental regulator 2
P11717	IGF2R	-0.234	insulin like growth factor 2 receptor
P08833	IGFBP1	1.137	insulin like growth factor binding protein 1
Q8N6C5-4	IGSF1	-0.26	immunoglobulin superfamily member 1
Q70UQ0	IKBIP	0.437	IKBKB interacting protein
Q70UQ0-4	IKBIP	0.375	IKBKB interacting protein
P40189	IL6ST	-0.365	interleukin 6 signal transducer
Q9NQS7	INCENP	0.535	inner centromere protein
Q27J81	INF2	-0.197	inverted formin, FH2 and WH2 domain containing
P49441	INPP1	0.378	inositol polyphosphate-1-phosphatase
Q92835	INPP5D	-0.299	inositol polyphosphate-5-phosphatase D
P06213	INSR	-0.319	insulin receptor
Q5TA45-5	INTS11	-0.181	integrator complex subunit 11
Q96HW7	INTS4	-0.147	integrator complex subunit 4
Q9UI26-2	IPO11	-0.148	importin 11
Q8TEX9-2	IPO4	-0.16	importin 4

O00410-3	IPO5	-0.147	importin 5
O95373	IPO7	-0.21	importin 7
Q13576-1	IQGAP2	-0.268	IQ motif containing GTPase activating protein 2
Q6DN90	IQSEC1	-0.249	IQ motif and Sec7 domain ArfGEF 1
Q9H1K1	ISCU	0.343	iron-sulfur cluster assembly enzyme
P05161	ISG15	0.26	ISG15 ubiquitin like modifier
Q9H9L3	ISG20L2	-0.198	interferon stimulated exonuclease gene 20 like 2
Q96CN7	ISOC1	0.147	isochorismatase domain containing 1
Q9NPH2	ISYNA1	0.472	inositol-3-phosphate synthase 1
P23229-1	ITGA6	-0.279	integrin subunit alpha 6
P06756	ITGAV	0.146	integrin subunit alpha V
Q14571	ITPR2	-0.194	inositol 1,4,5-trisphosphate receptor type 2
P23458	JAK1	-0.428	Janus kinase 1
Q7L273	KCTD9	0.383	potassium channel tetramerization domain containing 9
Q9Y4C1	KDM3A	0.45	lysine demethylase 3A
Q14145	KEAP1	0.132	kelch like ECH associated protein 1
Q5T5P2-1	KIAA1217	-0.24	KIAA1217
Q9P206-2	KIAA1522	-0.126	KIAA1522
Q9BY89-1	KIAA1671	-0.363	KIAA1671
Q9ULH0-1	KIDINS220	-0.213	kinase D interacting substrate 220
P52732	KIF11	0.161	kinesin family member 11
Q9NQT8	KIF13B	-0.219	kinesin family member 13B
Q9NS87	KIF15	-0.193	kinesin family member 15
Q96L93-2	KIF16B	-0.494	kinesin family member 16B
Q86Y91-4	KIF18B	0.353	kinesin family member 18B
O60333-4	KIF1B	-0.126	kinesin family member 1B
O95235	KIF20A	0.455	kinesin family member 20A
Q96Q89-2	KIF20B	0.311	kinesin family member 20B
Q14807	KIF22	0.179	kinesin family member 22
Q99661	KIF2C	0.263	kinesin family member 2C
Q9BW19	KIFC1	0.323	kinesin family member C1
Q9NSK0-3	KLC4	-0.138	kinesin light chain 4
Q9BXK1	KLF16	-0.432	Kruppel like factor 16
P52292	KPNA2	0.162	karyopherin subunit alpha 2
P83111-1	LACTB	0.308	lactamase beta
O15230	LAMA5	-0.401	laminin subunit alpha 5
P11279	LAMP1	0.267	lysosomal associated membrane protein 1
O43813	LANCL1	-0.206	LanC like 1
Q659C4	LARP1B	-0.377	La ribonucleoprotein domain family member 1B
P01130	LDLR	-0.245	low density lipoprotein receptor
O95202	LETM1	0.204	leucine zipper and EF-hand containing transmembrane protein 1
Q99538	LGMN	0.288	legumain
P18858	LIG1	0.127	DNA ligase 1
Q6P1M3-1	LLGL2	-0.207	LLGL scribble cell polarity complex component 2
Q9BRT6	LLPH	-0.363	LLP homolog, long-term synaptic facilitation factor
Q9BU23-1	LMF2	0.134	lipase maturation factor 2
Q8NF37	LPCAT1	-0.189	lysophosphatidylcholine acyltransferase 1

Q93052	LPP	-0.436	LIM domain containing preferred translocation partner in lipoma
P50851-2	LRBA	-0.279	LPS responsive beige-like anchor protein
Q7Z4F1	LRP10	0.97	LDL receptor related protein 10
P30533	LRPAP1	0.198	LDL receptor related protein associated protein 1
Q9H9A6	LRRC40	-0.104	leucine rich repeat containing 40
Q8IWT6	LRRC8A	0.158	leucine rich repeat containing 8 VRAC subunit A
Q9UFC0	LRWD1	0.128	leucine rich repeats and WD repeat domain containing 1
O15116	LSM1	0.187	LSM1 homolog, mRNA degradation associated
P48449	LSS	-0.138	lanosterol synthase
Q96GA3	LTV1	-0.368	LTV1 ribosome biogenesis factor
Q9Y383	LUC7L2	0.211	LUC7 like 2, pre-mRNA splicing factor
P61626	LYZ	0.303	lysozyme
Q9UPN3	MACF1	-0.27	microtubule actin crosslinking factor 1
Q9Y6D9	MAD1L1	-0.286	mitotic arrest deficient 1 like 1
Q8WXG6-4	MADD	0.231	MAP kinase activating death domain
Q9Y5V3-2	MAGED1	-0.401	MAGE family member D1
Q96QZ7	MAGI1	-0.474	membrane associated guanylate kinase, WW and PDZ domain containing 1
Q9UDY8	MALT1	-0.141	MALT1 paracaspase
P33908	MAN1A1	-0.209	mannosidase alpha class 1A member 1
Q9NYL2	MAP3K20	-0.325	mitogen-activated protein kinase kinase kinase 20
P27816-1	MAP4	-0.322	microtubule associated protein 4
Q15691	MAPRE1	0.187	microtubule associated protein RP/EB family member 1
P49006	MARCKSL1	0.203	MARCKS like 1
P43121	MCAM	0.496	melanoma cell adhesion molecule
Q8NI22	MCFD2	-0.212	multiple coagulation factor deficiency 2
P25205-2	MCM3	-0.167	minichromosome maintenance complex component 3
P33992	MCM5	-0.196	minichromosome maintenance complex component 5
Q14676	MDC1	-0.228	mediator of DNA damage checkpoint 1
P40926	MDH2	0.179	malate dehydrogenase 2
Q00987-11	MDM2	0.624	MDM2 proto-oncogene
Q9NU22	MDN1	-0.137	midasin AAA ATPase 1
Q9NPJ6	MED4	0.143	mediator complex subunit 4
Q9H8H3	METTL7A	0.226	methyltransferase like 7A
P26572	MGAT1	0.137	mannosyl (alpha-1,3-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase
Q09328	MGAT5	-0.437	alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase
Q9BQP7	MGME1	0.376	mitochondrial genome maintenance exonuclease 1
P16455	MGMT	-0.263	O-6-methylguanine-DNA methyltransferase
Q8N3F8	MICALL1	0.45	MICAL like 1
Q8IYU8	MICU2	-0.202	mitochondrial calcium uptake 2
Q9NPA3	MID1IP1	-0.383	MID1 interacting protein 1
Q9H000	MKRN2	-0.191	makorin ring finger protein 2
Q14165	MLEC	0.11	malectin
Q15773	MLF2	0.342	myeloid leukemia factor 2
P51511	MMP15	-0.43	matrix metallopeptidase 15
Q96EN8	MOCOS	-0.145	molybdenum cofactor sulfurase
Q15014	MORF4L2	-0.386	mortality factor 4 like 2
Q9Y5U8	MPC1	0.277	mitochondrial pyruvate carrier 1

P29372	MPG	-0.182	N-methylpurine DNA glycosylase
Q8N3R9-1	MPP5	-0.207	membrane palmitoylated protein 5
Q5T2T1	MPP7	-0.233	membrane palmitoylated protein 7
Q9Y605	MRFAP1	-0.303	Morf4 family associated protein 1
Q9NV56	MRGBP	0.125	MRG domain binding protein
Q9NYK5	MRPL39	0.169	mitochondrial ribosomal protein L39
Q86TS9	MRPL52	0.211	mitochondrial ribosomal protein L52
P82663	MRPS25	0.164	mitochondrial ribosomal protein S25
Q9ULH7-5	MRTFB	-0.225	myocardin related transcription factor B
O94776	MTA2	0.189	metastasis associated 1 family member 2
Q13496	MTM1	-0.227	myotubularin 1
P42345	MTOR	-0.162	mechanistic target of rapamycin kinase
Q99707	MTR	-0.196	5-methyltetrahydrofolate-homocysteine methyltransferase
Q9UBK8-1	MTRR	-0.222	5-methyltetrahydrofolate-homocysteine methyltransferase reductase
Q765P7	MTSS2	-0.132	MTSS I-BAR domain containing 2
P84157-2	MXRA7	0.335	matrix remodeling associated 7
Q969H8	MYDGF	0.192	myeloid derived growth factor
Q7Z406-2	MYH14	-0.165	myosin heavy chain 14
O14950	MYL12B	-0.185	myosin light chain 12B
Q15746	MYLK	-0.24	myosin light chain kinase
Q92614-1	MYO18A	-0.212	myosin XVIIIA
O94832	MYO1D	-0.229	myosin ID
Q12965	MYO1E	-0.173	myosin IE
Q9NQX4	MYO5C	-0.175	myosin VC
Q6NSJ0	MYORG	-0.355	myogenesis regulating glycosidase (putative)
Q14CX7	NAA25	-0.165	N(alpha)-acetyltransferase 25, NatB auxiliary subunit
A2RRP1	NBAS	-0.295	NBAS subunit of NRZ tethering complex
Q15021	NCAPD2	-0.13	non-SMC condensin I complex subunit D2
Q6PIU2-2	NCEH1	0.182	neutral cholesterol ester hydrolase 1
Q9NZQ3	NCKIPSD	0.16	NCK interacting protein with SH3 domain
Q68D85	NCR3LG1	-0.347	natural killer cell cytotoxicity receptor 3 ligand 1
Q92542-1	NCSTN	0.156	nicastrin
Q9UGV2	NDRG3	-0.295	NDRG family member 3
Q9UI09	NDUFA12	0.14	NADH:ubiquinone oxidoreductase subunit A12
P56556	NDUFA6	0.216	NADH:ubiquinone oxidoreductase subunit A6
P51970	NDUFA8	0.394	NADH:ubiquinone oxidoreductase subunit A8
O14561	NDUFAB1	0.213	NADH:ubiquinone oxidoreductase subunit AB1
P28331-2	NDUFS1	0.104	NADH:ubiquinone oxidoreductase core subunit S1
O43181	NDUFS4	0.205	NADH:ubiquinone oxidoreductase subunit S4
O43920	NDUFS5	0.237	NADH:ubiquinone oxidoreductase subunit S5
P46934-4	NEDD4	-0.23	NEDD4 E3 ubiquitin protein ligase
P48681	NES	-0.222	nestin
Q99519	NEU1	0.207	neuraminidase 1
Q8N5V2	NGEF	-0.551	neuronal guanine nucleotide exchange factor
Q9H9Q4-2	NHEJ1	-0.248	non-homologous end joining factor 1
P14543-1	NID1	-0.374	nidogen 1
Q9BYG3	NIFK	-0.248	nucleolar protein interacting with the FHA domain of MKI67

Q92982	NINJ1	0.361	ninjurin 1
Q969G9	NKD1	-0.597	NKD inhibitor of WNT signaling pathway 1
Q9ULX3	NOB1	-0.175	NIN1 (RPN12) binding protein 1 homolog
Q9BSC4	NOL10	-0.132	nucleolar protein 10
Q9UGY1	NOL12	-0.182	nucleolar protein 12
Q9H6R4-1	NOL6	-0.177	nucleolar protein 6
Q9UMY1	NOL7	-0.248	nucleolar protein 7
Q9Y3C1	NOP16	-0.366	NOP16 nucleolar protein
Q9NZM5	NOP53	-0.407	NOP53 ribosome biogenesis factor
P29474	NOS3	-0.31	nitric oxide synthase 3
P61916	NPC2	0.264	NPC intracellular cholesterol transporter 2
O95478	NSA2	-0.676	NSA2 ribosome biogenesis factor
P49902	NT5C2	-0.177	5'-nucleotidase, cytosolic II
Q9BSD7	NTPCR	0.259	nucleoside-triphosphatase, cancer-related
Q8IVD9	NUDCD3	-0.221	NudC domain containing 3
P50583	NUDT2	-0.181	nudix hydrolase 2
O43809	NUDT21	0.173	nudix hydrolase 21
Q7Z417	NUFIP2	0.111	nuclear FMR1 interacting protein 2
P49757	NUMB	-0.133	NUMB endocytic adaptor protein
P49790	NUP153	0.126	nucleoporin 153
Q8NFH4	NUP37	0.182	nucleoporin 37
Q7Z3B4	NUP54	0.156	nucleoporin 54
Q9UBU9-1	NXF1	0.125	nuclear RNA export factor 1
P04181	OAT	0.323	ornithine aminotransferase
Q9NX40	OCIAD1	0.137	OCIA domain containing 1
Q16625	OCLN	-0.136	occludin
O60502	OGA	0.172	O-GlcNAcase
Q8N543	OGFOD1	0.199	2-oxoglutarate and iron dependent oxygenase domain containing 1
O15294	OGT	-0.144	O-linked N-acetylglucosamine (GlcNAc) transferase
Q9H6K4	OPA3	0.24	outer mitochondrial membrane lipid metabolism regulator OPA3
O14841	OPLAH	-0.146	5-oxoprolinase, ATP-hydrolysing
Q6GQQ9-1	OTUD7B	0.248	OTU deubiquitinase 7B
O15460	P4HA2	0.405	prolyl 4-hydroxylase subunit alpha 2
Q6VY07-2	PACS1	-0.334	phosphofurin acidic cluster sorting protein 1
P00439	PAH	-0.252	phenylalanine hydroxylase
P22234-2	PAICS	-0.124	phosphoribosylaminoimidazole carboxylase and phosphoribosylaminoimidazolesuccinocar
O96013	PAK4	-0.339	p21 (RAC1) activated kinase 4
O95453	PARN	-0.128	poly(A)-specific ribonuclease
Q9UKK3	PARP4	-0.172	poly(ADP-ribose) polymerase family member 4
Q9NVD7	PARVA	-0.248	parvin alpha
P05166-2	PCCB	-0.208	propionyl-CoA carboxylase subunit beta
P12004	PCNA	0.42	proliferating cell nuclear antigen
Q99447	PCYT2	-0.163	phosphate cytidylyltransferase 2, ethanolamine
Q9GZU2	PEG3	-0.15	paternally expressed 3
O15067	PFAS	-0.209	phosphoribosylformylglycinamidine synthase
Q01813	PFKP	-0.299	phosphofructokinase, platelet
Q7RTV0	PHF5A	0.22	PHD finger protein 5A

Q6NSJ2-1	PHLDB3	0.319	pleckstrin homology like domain family B member 3
Q9P1Y6	PHRF1	-0.19	PHD and ring finger domains 1
Q13492	PICALM	0.159	phosphatidylinositol binding clathrin assembly protein
Q92643	PIGK	0.143	phosphatidylinositol glycan anchor biosynthesis class K
Q8TEQ8-1	PIGO	-0.229	phosphatidylinositol glycan anchor biosynthesis class O
Q9H490	PIGU	-0.275	phosphatidylinositol glycan anchor biosynthesis class U
Q9Y237-2	PIN4	-0.135	peptidylprolyl cis/trans isomerase, NIMA-interacting 4
Q96BK5	PINX1	-0.236	PIN2 (TERF1) interacting telomerase inhibitor 1
Q9UG56-3	PISD	-0.114	phosphatidylserine decarboxylase
P30613	PKLR	-0.268	pyruvate kinase L/R
Q16513	PKN2	-0.215	protein kinase N2
Q6IQ23-2	PLEKHA7	-0.506	pleckstrin homology domain containing A7
Q99541	PLIN2	0.384	perilipin 2
O43660	PLRG1	0.109	pleiotropic regulator 1
Q14651	PLS1	-0.175	plastin 1
O43157	PLXNB1	-0.14	plexin B1
O15031	PLXNB2	0.24	plexin B2
P29590	PML	0.226	promyelocytic leukemia
O15305	PMM2	-0.162	phosphomannomutase 2
Q8N490	PNKD	-0.602	PNKD metallo-beta-lactamase domain containing
Q9NRX1	PNO1	-0.359	partner of NOB1 homolog
P09884	POLA1	-0.286	DNA polymerase alpha 1, catalytic subunit
P06746	POLB	0.307	DNA polymerase beta
P28340	POLD1	-0.163	DNA polymerase delta 1, catalytic subunit
P49005	POLD2	-0.184	DNA polymerase delta 2, accessory subunit
P52435	POLR2J	0.314	RNA polymerase II subunit J
Q9BUI4	POLR3C	0.118	RNA polymerase III subunit C
O95707	POP4	-0.112	POP4 homolog, ribonuclease P/MRP subunit
Q9HAB8	PPCS	0.151	phosphopantothenoylcysteine synthetase
P45877	PPIC	0.184	peptidylprolyl isomerase C
P30405	PPIF	0.177	peptidylprolyl isomerase F
Q9H2H8-1	PPIL3	-0.132	peptidylprolyl isomerase like 3
P35813-3	PPM1A	0.319	protein phosphatase, Mg2+/Mn2+ dependent 1A
O15297	PPM1D	0.487	protein phosphatase, Mg2+/Mn2+ dependent 1D
Q9ULR3	PPM1H	-0.333	protein phosphatase, Mg2+/Mn2+ dependent 1H
Q96QC0	PPP1R10	0.262	protein phosphatase 1 regulatory subunit 10
Q6ZMI0-1	PPP1R21	-0.191	protein phosphatase 1 regulatory subunit 21
Q12972	PPP1R8	0.148	protein phosphatase 1 regulatory subunit 8
Q9ULJ8-3	PPP1R9A	-0.335	protein phosphatase 1 regulatory subunit 9A
Q6IN85	PPP4R3A	0.152	protein phosphatase 4 regulatory subunit 3A
O43663	PRC1	0.347	protein regulator of cytokinesis 1
P48147	PREP	-0.157	prolyl endopeptidase
Q4J6C6	PREPL	0.266	prolyl endopeptidase like
P49643	PRIM2	-0.417	DNA primase subunit 2
P31321	PRKAR1B	-0.584	protein kinase cAMP-dependent type I regulatory subunit beta
P17252	PRKCA	-0.378	protein kinase C alpha
O75569	PRKRA	0.228	protein activator of interferon induced protein kinase EIF2AK2

Q9H875	PRKRIP1	0.266	PRKR interacting protein 1
Q9UNN8	PROCR	0.845	protein C receptor
Q9UMS4	PRPF19	0.126	pre-mRNA processing factor 19
Q8NAV1-1	PRPF38A	0.122	pre-mRNA processing factor 38A
Q13523	PRPF4B	0.165	pre-mRNA processing factor 4B
P61289-2	PSME3	0.131	proteasome activator subunit 3
Q92530	PSMF1	-0.217	proteasome inhibitor subunit 1
O95456	PSMG1	-0.151	proteasome assembly chaperone 1
O95758-4	PTBP3	0.176	polypyrimidine tract binding protein 3
Q9BVG9	PTDSS2	-0.415	phosphatidylserine synthase 2
Q86YD1-1	PTOV1	-0.222	PTOV1 extended AT-hook containing adaptor protein
Q05209	PTPN12	-0.223	protein tyrosine phosphatase non-receptor type 12
P17706-1	PTPN2	-0.24	protein tyrosine phosphatase non-receptor type 2
P10586-1	PTPRF	-0.397	protein tyrosine phosphatase receptor type F
Q15262-3	PTPRK	-0.531	protein tyrosine phosphatase receptor type K
Q15397	PUM3	-0.48	pumilio RNA binding family member 3
Q96C36	PYCR2	0.248	pyrroline-5-carboxylate reductase 2
Q6WKZ4	RAB11FIP1	-0.174	RAB11 family interacting protein 1
P61106	RAB14	0.131	RAB14, member RAS oncogene family
Q9UL25	RAB21	0.167	RAB21, member RAS oncogene family
Q15286	RAB35	0.144	RAB35, member RAS oncogene family
O95716	RAB3D	-0.181	RAB3D, member RAS oncogene family
Q9Y3P9	RABGAP1	-0.272	RAB GTPase activating protein 1
P63000-2	RAC1	0.18	Rac family small GTPase 1
Q9H0H5	RACGAP1	0.302	Rac GTPase activating protein 1
P63244	RACK1	-0.181	receptor for activated C kinase 1
P78406	RAE1	0.15	ribonucleic acid export 1
P11234-2	RALB	0.246	RAS like proto-oncogene B
P62826	RAN	0.104	RAN, member RAS oncogene family
Q96S59-1	RANBP9	0.133	RAN binding protein 9
P52306-5	RAP1GDS1	-0.203	Rap1 GTPase-GDP dissociation stimulator 1
P61225	RAP2B	0.437	RAP2B, member of RAS oncogene family
Q7Z6E9	RBBP6	0.438	RB binding protein 6, ubiquitin ligase
O43251-8	RBFOX2	-0.573	RNA binding fox-1 homolog 2
Q8N0T1	RBIS	-0.77	ribosomal biogenesis factor
Q96T37	RBM15	0.156	RNA binding motif protein 15
Q9Y4C8	RBM19	-0.221	RNA binding motif protein 19
Q9NW64	RBM22	0.214	RNA binding motif protein 22
P49756-1	RBM25	0.106	RNA binding motif protein 25
Q9P2N5	RBM27	0.142	RNA binding motif protein 27
P42696	RBM34	-0.24	RNA binding motif protein 34
P52756	RBM5	0.193	RNA binding motif protein 5
P09455-1	RBP1	-0.168	retinol binding protein 1
Q8IZV5	RDH10	0.347	retinol dehydrogenase 10
P35241-5	RDX	0.212	radixin
Q9H6H4	REEP4	0.283	receptor accessory protein 4
Q00765	REEP5	0.236	receptor accessory protein 5

P78509	RELN	-0.47	reelin
Q6NUM9-1	RETSAT	0.631	retinol saturase
P35250-1	RFC2	-0.119	replication factor C subunit 2
Q969G6	RFK	0.371	riboflavin kinase
Q13671	RIN1	0.885	Ras and Rab interactor 1
Q9BRS2	RIOK1	-0.287	RIO kinase 1
Q96DB5	RMDN1	0.163	regulator of microtubule dynamics 1
Q9Y508	RNF114	0.367	ring finger protein 114
O75150	RNF40	0.116	ring finger protein 40
Q9Y6N7-2	ROBO1	-0.477	roundabout guidance receptor 1
Q9H9Y2	RPF1	-0.524	ribosome production factor 1 homolog
P30050	RPL12	-0.179	ribosomal protein L12
P18621-3	RPL17	-0.304	ribosomal protein L17
P84098	RPL19	-0.351	ribosomal protein L19
P35268	RPL22	-0.152	ribosomal protein L22
P62829	RPL23	-0.364	ribosomal protein L23
P62750	RPL23A	-0.206	ribosomal protein L23a
P62888	RPL30	-0.246	ribosomal protein L30
P62899	RPL31	-0.168	ribosomal protein L31
Q9Y3U8	RPL36	-0.249	ribosomal protein L36
P46777	RPL5	-0.14	ribosomal protein L5
Q6DKI1	RPL7L1	-0.376	ribosomal protein L7 like 1
P05388	RPLP0	-0.169	ribosomal protein lateral stalk subunit P0
P46783	RPS10	-0.166	ribosomal protein S10
P62263	RPS14	-0.222	ribosomal protein S14
P08708	RPS17	-0.124	ribosomal protein S17
P39019	RPS19	-0.105	ribosomal protein S19
P15880	RPS2	-0.285	ribosomal protein S2
P60866	RPS20	-0.17	ribosomal protein S20
P63220	RPS21	-0.252	ribosomal protein S21
P62854	RPS26	-0.189	ribosomal protein S26
P42677	RPS27	-0.285	ribosomal protein S27
P23396	RPS3	-0.183	ribosomal protein S3
P46782	RPS5	-0.185	ribosomal protein S5
Q15418-2	RPS6KA1	0.201	ribosomal protein S6 kinase A1
P51812	RPS6KA3	-0.211	ribosomal protein S6 kinase A3
O75676	RPS6KA4	-0.239	ribosomal protein S6 kinase A4
Q8N122	RPTOR	-0.426	regulatory associated protein of MTOR complex 1
P55042	RRAD	1.701	RRAD, Ras related glycolysis inhibitor and calcium channel regulator
Q7L523	RRAGA	0.31	Ras related GTP binding A
Q92766-2	RREB1	-0.275	ras responsive element binding protein 1
P23921	RRM1	0.164	ribonucleotide reductase catalytic subunit M1
P31350-2	RRM2	0.44	ribonucleotide reductase regulatory subunit M2
Q7LG56	RRM2B	0.666	ribonucleotide reductase regulatory TP53 inducible subunit M2B
Q7LG56-6	RRM2B	0.922	ribonucleotide reductase regulatory TP53 inducible subunit M2B
Q96EU6	RRP36	-0.376	ribosomal RNA processing 36
Q15050	RRS1	-0.313	ribosome biogenesis regulator 1 homolog

Q9UHA3	RSL24D1	-0.317	ribosomal L24 domain containing 1
Q15404	RSU1	-0.146	Ras suppressor protein 1
P19793	RXRA	-0.57	retinoid X receptor alpha
P28702-3	RXRB	-0.224	retinoid X receptor beta
P31949	S100A11	0.346	S100 calcium binding protein A11
Q99584	S100A13	0.216	S100 calcium binding protein A13
Q96FQ6	S100A16	0.195	S100 calcium binding protein A16
P06703	S100A6	0.308	S100 calcium binding protein A6
P25815	S100P	0.156	S100 calcium binding protein P
P35542	SAA4	0.741	serum amyloid A4, constitutive
O00422	SAP18	0.14	Sin3A associated protein 18
Q9Y6B6	SAR1B	-0.14	secretion associated Ras related GTPase 1B
P82979	SARNP	0.212	SAP domain containing ribonucleoprotein
O00767	SCD	-0.357	stearoyl-CoA desaturase
Q8WU76-1	SCFD2	-0.402	sec1 family domain containing 2
P18827	SDC1	0.356	syndecan 1
P34741	SDC2	-0.521	syndecan 2
P31431-1	SDC4	0.501	syndecan 4
O00560	SDCBP	0.262	syndecan binding protein
Q99470	SDF2	0.238	stromal cell derived factor 2
P31040	SDHA	0.228	succinate dehydrogenase complex flavoprotein subunit A
Q15437	SEC23B	-0.186	SEC23 homolog B, coat complex II component
O95486	SEC24A	-0.176	SEC24 homolog A, COPII coat complex component
O94855-2	SEC24D	-0.188	SEC24 homolog D, COPII coat complex component
Q16181	SEPTIN7	0.123	septin 7
Q9UHD8-1	SEPTIN9	-0.179	septin 9
Q8NC51-1	SERBP1	-0.154	SERPINE1 mRNA binding protein 1
P05543	SERPINA7	0.511	serpin family A member 7
P30740	SERPINB1	0.155	serpin family B member 1
P05121	SERPINE1	1.153	serpin family E member 1
P58004	SESN2	0.594	sestrin 2
Q15428	SF3A2	0.218	splicing factor 3a subunit 2
Q12874	SF3A3	0.184	splicing factor 3a subunit 3
Q9BWJ5	SF3B5	0.125	splicing factor 3b subunit 5
P31947	SFN	0.415	stratifin
P51688	SGSH	0.176	N-sulfoglucosamine sulfohydrolase
Q9H299	SH3BGRL3	0.238	SH3 domain binding glutamate rich protein like 3
Q8NEM2	SHCBP1	0.63	SHC binding and spindle associated 1
A0A0B4J2A0	SHPK	-0.117	sedoheptulokinase
Q9UP95	SLC12A4	0.359	solute carrier family 12 member 4
P53985	SLC16A1	0.153	solute carrier family 16 member 1
P43007	SLC1A4	-0.248	solute carrier family 1 member 4
Q8WUM9	SLC20A1	-0.253	solute carrier family 20 member 1
Q9Y619	SLC25A15	0.308	solute carrier family 25 member 15
O14975	SLC27A2	-0.123	solute carrier family 27 member 2
P11166	SLC2A1	-0.303	solute carrier family 2 member 1
P14672	SLC2A4	-0.34	solute carrier family 2 member 4

Q8NEW0	SLC30A7	-0.204	solute carrier family 30 member 7
Q9HBR0	SLC38A10	-0.158	solute carrier family 38 member 10
Q99624	SLC38A3	-0.172	solute carrier family 38 member 3
Q15043	SLC39A14	-0.393	solute carrier family 39 member 14
Q8WWI5	SLC44A1	-0.266	solute carrier family 44 member 1
Q9BWU0	SLC4A1AP	0.232	solute carrier family 4 member 1 adaptor protein
P04920	SLC4A2	-0.133	solute carrier family 4 member 2
Q9UPY5	SLC7A11	-0.312	solute carrier family 7 member 11
Q15599	SLC9A3R2	-0.276	SLC9A3 regulator 2
Q14BN4	SLMAP	-0.17	sarcolemma associated protein
Q92925	SMARCD2	-0.257	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d,
Q86US8-1	SMG6	-0.47	SMG6 nonsense mediated mRNA decay factor
P53814-6	SMTN	0.953	smoothelin
Q2TAY7	SMU1	0.106	SMU1 DNA replication regulator and spliceosomal factor
Q7KZF4	SND1	-0.248	staphylococcal nuclease and tudor domain containing 1
Q8WVK2	SNRNP27	0.364	small nuclear ribonucleoprotein U4/U6.U5 subunit 27
Q13884	SNTB1	-0.138	syntrophin beta 1
P55769	SNU13	-0.193	small nuclear ribonucleoprotein 13
Q9NRS6	SNX15	-0.286	sorting nexin 15
Q15036-1	SNX17	-0.28	sorting nexin 17
Q5VWJ9	SNX30	-0.235	sorting nexin family member 30
Q9Y5X2	SNX8	-0.261	sorting nexin 8
P04179	SOD2	0.346	superoxide dismutase 2
Q92673	SORL1	-0.495	sortilin related receptor 1
Q99523	SORT1	-0.164	sortilin 1
Q96R06	SPAG5	0.303	sperm associated antigen 5
O75391	SPAG7	-0.303	sperm associated antigen 7
Q96EA4	SPDL1	0.48	spindle apparatus coiled-coil protein 1
P10451	SPP1	-0.514	secreted phosphoprotein 1
P35270	SPR	0.163	sepiapterin reductase
Q5W111	SPRYD7	0.213	SPRY domain containing 7
Q9NUV7	SPTLC3	-0.622	serine palmitoyltransferase long chain base subunit 3
Q14534	SQLE	-0.31	squalene epoxidase
Q8NEF9	SRFBP1	-0.212	serum response factor binding protein 1
O75044	SRGAP2	-0.217	SLIT-ROBO Rho GTPase activating protein 2
Q96SB4	SRPK1	-0.147	SRSF protein kinase 1
Q9BXP5	SRRT	0.23	serrate, RNA effector molecule
Q16629	SRSF7	0.199	serine and arginine rich splicing factor 7
Q08945	SSRP1	0.148	structure specific recognition protein 1
Q9NP77	SSU72	-0.143	SSU72 homolog, RNA polymerase II CTD phosphatase
P15907	ST6GAL1	-0.345	ST6 beta-galactoside alpha-2,6-sialyltransferase 1
P42224-1	STAT1	0.108	signal transducer and activator of transcription 1
P40763	STAT3	0.433	signal transducer and activator of transcription 3
Q9NUL3	STAU2	-0.322	staufen double-stranded RNA binding protein 2
Q658P3-2	STEAP3	-0.519	STEAP3 metalloreductase
Q13586	STIM1	-0.22	stromal interaction molecule 1
O94804	STK10	-0.33	serine/threonine kinase 10

Q13188-2	STK3	-0.812	serine/threonine kinase 3
P27105	STOM	0.706	stomatin
Q86Y82	STX12	0.21	syntaxin 12
Q13277	STX3	0.161	syntaxin 3
Q12846	STX4	0.109	syntaxin 4
O43752	STX6	0.437	syntaxin 6
O00186	STXBP3	0.214	syntaxin binding protein 3
P53999	SUB1	0.374	SUB1 regulator of transcription
O75683	SURF6	-0.542	surfeit 6
Q9UH65	SWAP70	0.146	switching B cell complex subunit SWAP70
O95359	TACC2	-0.203	transforming acidic coiled-coil containing protein 2
Q9Y6A5	TACC3	0.235	transforming acidic coiled-coil containing protein 3
P37837	TALDO1	0.245	transaldolase 1
Q03518	TAP1	0.462	transporter 1, ATP binding cassette subfamily B member
Q86VP1	TAX1BP1	-0.25	Tax1 binding protein 1
O14907	TAX1BP3	0.339	Tax1 binding protein 3
O60343-1	TBC1D4	-0.174	TBC1 domain family member 4
Q92609-2	TBC1D5	-0.347	TBC1 domain family member 5
Q9Y4C2-1	TCAF1	-0.182	TRPM8 channel associated factor 1
Q9BQ70	TCF25	-0.24	transcription factor 25
Q9NYB0	TERF2IP	0.371	TERF2 interacting protein
Q96BS2	TESC	-0.326	tescalcin
Q8IWB9-2	TEX2	-0.229	testis expressed 2
P02787	TF	-0.328	transferrin
P01137	TGFB1	0.312	transforming growth factor beta 1
P37173-2	TGFBR2	-0.361	transforming growth factor beta receptor 2
Q03167	TGFBR3	-0.276	transforming growth factor beta receptor 3
P21980	TGM2	-0.16	transglutaminase 2
Q96EK4	THAP11	-0.181	THAP domain containing 11
P07996	THBS1	-0.351	thrombospondin 1
Q9NXG2	THUMPD1	0.267	THUMP domain containing 1
Q9BV44	THUMPD3	-0.141	THUMP domain containing 3
Q9NQ88	TIGAR	0.756	TP53 induced glycolysis regulatory phosphatase
Q9Y5J6	TIMM10B	0.116	translocase of inner mitochondrial membrane 10B
Q9UDY2	TJP2	-0.176	tight junction protein 2
P04183	TK1	0.494	thymidine kinase 1
Q9Y3A6	TMED5	0.257	transmembrane p24 trafficking protein 5
Q9P0S9	TMEM14C	0.187	transmembrane protein 14C
Q9HC07	TMEM165	0.118	transmembrane protein 165
Q8N511	TMEM199	0.23	transmembrane protein 199
Q9H1E5	TMX4	0.304	thioredoxin related transmembrane protein 4
O00220	TNFRSF10A	0.294	TNF receptor superfamily member 10a
Q68CZ2-1	TNS3	-0.335	tensin 3
Q96GM8	TOE1	0.122	target of EGR1, exonuclease
O60784	TOM1	-0.213	target of myb1 membrane trafficking protein
Q15785	TOMM34	0.11	translocase of outer mitochondrial membrane 34
Q8N4H5	TOMM5	0.21	translocase of outer mitochondrial membrane 5

O14656	TOR1A	0.212	torsin family 1 member A
O94842	TOX4	0.232	TOX high mobility group box family member 4
P04637	TP53	1.13	tumor protein p53
Q53FA7	TP53I3	1.179	tumor protein p53 inducible protein 3
Q9ULW0	TPX2	0.647	TPX2 microtubule nucleation factor
Q9Y296	TRAPPC4	0.16	trafficking protein particle complex 4
O15164	TRIM24	-0.198	tripartite motif containing 24
Q14258	TRIM25	-0.195	tripartite motif containing 25
Q13263	TRIM28	0.202	tripartite motif containing 28
Q15643	TRIP11	0.153	thyroid hormone receptor interactor 11
Q15650	TRIP4	-0.405	thyroid hormone receptor interactor 4
Q8TEL6	TRPC4AP	-0.233	transient receptor potential cation channel subfamily C member 4 associated protein
Q9BSV6	TSEN34	-0.219	tRNA splicing endonuclease subunit 34
Q9H2G4	TSPYL2	0.331	TSPY like 2
Q2NL82	TSR1	-0.117	TSR1 ribosome maturation factor
Q16762	TST	0.266	thiosulfate sulfurtransferase
Q6P3X3	TTC27	-0.298	tetratricopeptide repeat domain 27
Q13509	TUBB3	0.166	tubulin beta 3 class III
Q9BUF5	TUBB6	0.398	tubulin beta 6 class V
Q96CW5	TUBGCP3	-0.157	tubulin gamma complex associated protein 3
Q5TAX3	TUT4	-0.246	terminal uridylyl transferase 4
Q6IBS0	TWF2	0.526	twinfilin actin binding protein 2
P26368	U2AF2	0.136	U2 small nuclear RNA auxiliary factor 2
Q9BSL1	UBAC1	-0.335	UBA domain containing 1
P62256	UBE2H	0.144	ubiquitin conjugating enzyme E2 H
O95155-4	UBE4B	-0.209	ubiquitination factor E4B
O95071	UBR5	0.114	ubiquitin protein ligase E3 component n-recognin 5
Q04323-1	UBXN1	-0.164	UBX domain protein 1
Q9BZX2-1	UCK2	-0.208	uridine-cytidine kinase 2
P16662	UGT2B7	0.494	UDP glucuronosyltransferase family 2 member B7
Q96T88-2	UHRF1	-0.634	ubiquitin like with PHD and ring finger domains 1
Q70J99-3	UNC13D	-0.203	unc-13 homolog D
P13051	UNG	-0.259	uracil DNA glycosylase
Q9BZI7-1	UPF3B	0.196	UPF3B regulator of nonsense mediated mRNA decay
P51784	USP11	0.227	ubiquitin specific peptidase 11
Q92995	USP13	-0.23	ubiquitin specific peptidase 13
Q8NFA0	USP32	-0.323	ubiquitin specific peptidase 32
Q9P275-2	USP36	-0.11	ubiquitin specific peptidase 36
Q93008	USP9X	-0.144	ubiquitin specific peptidase 9 X-linked
Q9BVJ6-1	UTP14A	-0.25	UTP14A small subunit processome component
Q9Y5J1	UTP18	-0.105	UTP18 small subunit processome component
P46939	UTRN	-0.259	utrophin
Q9BV40	VAMP8	0.32	vesicle associated membrane protein 8
Q6EMK4	VASN	-0.329	vasorin
P50552	VASP	0.126	vasodilator stimulated phosphoprotein
P52735	VAV2	-0.331	vav guanine nucleotide exchange factor 2
P18206	VCL	-0.121	vinculin

P21796	VDAC1	0.163	voltage dependent anion channel 1
P45880-1	VDAC2	0.298	voltage dependent anion channel 2
Q9Y277-2	VDAC3	0.256	voltage dependent anion channel 3
Q9H9C1-1	VIPAS39	-0.218	VPS33B interacting protein, apical-basolateral polarity regulator, spe-39 homolog
Q69YN4	VIRMA	0.168	vir like m6A methyltransferase associated
Q96GC9	VMP1	-0.139	vacuole membrane protein 1
Q96JG6	VPS50	-0.222	VPS50 subunit of EARP/GARPII complex
Q9UID3-1	VPS51	-0.191	VPS51 subunit of GARP complex
Q5VIR6-4	VPS53	-0.355	VPS53 subunit of GARP complex
P62760	VSNL1	-0.24	visinin like 1
Q96AJ9	VTI1A	-0.273	vesicle transport through interaction with t-SNAREs 1A
Q9Y6W5	WASF2	0.115	WASP family member 2
Q12768	WASHC5	-0.172	WASH complex subunit 5
O00401	WASL	-0.132	WASP like actin nucleation promoting factor
Q9H6R7	WDCP	-0.21	WD repeat and coiled coil containing
P61964	WDR5	0.167	WD repeat domain 5
Q6RFH5	WDR74	-0.232	WD repeat domain 74
O00308	WWP2	-0.697	WW domain containing E3 ubiquitin protein ligase 2
Q9C0E2	XPO4	-0.281	exportin 4
O75191	XYLB	-0.18	xylulokinase
P54577	YARS1	-0.147	tyrosyl-tRNA synthetase 1
P07947	YES1	0.108	YES proto-oncogene 1, Src family tyrosine kinase
O15498	YKT6	0.289	YKT6 v-SNARE homolog
Q9H6S0	YTHDC2	-0.233	YTH domain containing 2
Q04917	YWHAH	0.124	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein eta
Q8N4Q0	ZADH2	0.24	zinc binding alcohol dehydrogenase domain containing 2
Q8WU90	ZC3H15	-0.307	zinc finger CCCH-type containing 15
Q7Z2W4	ZC3HAV1	0.148	zinc finger CCCH-type containing, antiviral 1
Q9C0B9	ZCCHC2	-0.371	zinc finger CCHC-type containing 2
Q8N5A5	ZGPAT	0.193	zinc finger CCCH-type and G-patch domain containing
Q9Y6X8	ZHX2	-0.367	zinc fingers and homeoboxes 2
Q14202	ZMYM3	-0.213	zinc finger MYM-type containing 3
Q5BKZ1	ZNF326	0.272	zinc finger protein 326
Q86UK7	ZNF598	-0.197	zinc finger protein 598
Q9H582	ZNF644	-0.313	zinc finger protein 644
Q9P2E3	ZNFX1	0.267	zinc finger NFX1-type containing 1
O43149	ZZEF1	-0.265	zinc finger ZZ-type and EF-hand domain containing 1
Q16637		0.342	
Q96JG8-4		-0.216	

List of proteins deregulated in HepG2 cells after 24h exposure to AgNP 3.5 ug/mL + CDDP 10 mM

ID	Symbol	Expr Log Ratio	Entrez Gene Name
Q9NQ94	A1CF	-0.214	APOBEC1 complementation factor
P01023	A2M	-0.4	alpha-2-macroglobulin
Q86V21-1	AACS	-0.181	acetoacetyl-CoA synthetase
Q9H7C9-1	AAMDC	-0.387	adipogenesis associated Mth938 domain containing
Q9Y312	AAR2	0.301	AAR2 splicing factor
P49588	AARS1	-0.2	alanyl-tRNA synthetase 1
Q5JTZ9	AARS2	0.233	alanyl-tRNA synthetase 2, mitochondrial
Q9NRN7	AASDHPPT	0.161	aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase
Q9UDR5	AASS	0.301	aminoadipate-semialdehyde synthase
Q9NY61	AATF	0.184	apoptosis antagonizing transcription factor
P80404	ABAT	0.207	4-aminobutyrate aminotransferase
O95477	ABCA1	-0.363	ATP binding cassette subfamily A member 1
Q9NRK6	ABCB10	0.317	ATP binding cassette subfamily B member 10
O75027-2	ABCB7	0.275	ATP binding cassette subfamily B member 7
Q9NUT2-1	ABCB8	0.19	ATP binding cassette subfamily B member 8
P33897	ABCD1	0.239	ATP binding cassette subfamily D member 1
P28288	ABCD3	0.309	ATP binding cassette subfamily D member 3
P61221	ABCE1	-0.079	ATP binding cassette subfamily E member 1
Q9NUQ8	ABCF3	0.134	ATP binding cassette subfamily F member 3
Q8NFV4	ABHD11	0.172	abhydrolase domain containing 11
Q8N2K0-2	ABHD12	0.119	abhydrolase domain containing 12
Q96IU4	ABHD14B	-0.259	abhydrolase domain containing 14B
Q8TB40	ABHD4	1.016	abhydrolase domain containing 4
Q8IZP0	ABI1	-0.254	abl interactor 1
Q9ULW3	ABT1	-0.113	activator of basal transcription 1
P09110-1	ACAA1	-0.118	acetyl-CoA acyltransferase 1
P42765	ACAA2	0.309	acetyl-CoA acyltransferase 2
Q13085-4	ACACA	-0.233	acetyl-CoA carboxylase alpha
Q9UKU7	ACAD8	0.549	acyl-CoA dehydrogenase family member 8
P11310-2	ACADM	0.231	acyl-CoA dehydrogenase medium chain
P16219	ACADS	0.345	acyl-CoA dehydrogenase short chain
P45954	ACADSB	0.151	acyl-CoA dehydrogenase short/branched chain
P49748-3	ACADVL	0.363	acyl-CoA dehydrogenase very long chain
Q15057	ACAP2	-0.186	ArfGAP with coiled-coil, ankyrin repeat and PH domains 2
P24752	ACAT1	0.338	acetyl-CoA acetyltransferase 1
Q9BWD1	ACAT2	-0.355	acetyl-CoA acetyltransferase 2
Q5T8D3-3	ACBD5	0.268	acyl-CoA binding domain containing 5
Q9UKV3-5	ACIN1	0.384	apoptotic chromatin condensation inducer 1
P21399	ACO1	-0.17	aconitase 1
Q99798	ACO2	0.282	aconitase 2
Q86TX2	ACOT1	0.243	acyl-CoA thioesterase 1

Q9NPJ3	ACOT13	0.195	acyl-CoA thioesterase 13
O00154	ACOT7	-0.185	acyl-CoA thioesterase 7
O14734	ACOT8	0.378	acyl-CoA thioesterase 8
Q9Y305	ACOT9	0.259	acyl-CoA thioesterase 9
Q15067	ACOX1	0.212	acyl-CoA oxidase 1
Q99424	ACOX2	0.187	acyl-CoA oxidase 2
O15254	ACOX3	0.175	acyl-CoA oxidase 3, pristanoyl
P24666	ACP1	-0.218	acid phosphatase 1
P11117	ACP2	0.096	acid phosphatase 2, lysosomal
Q96CM8-2	ACSF2	0.268	acyl-CoA synthetase family member 2
Q4G176	ACSF3	0.234	acyl-CoA synthetase family member 3
O60488-1	ACSL4	-0.573	acyl-CoA synthetase long chain family member 4
Q9ULC5-3	ACSL5	0.241	acyl-CoA synthetase long chain family member 5
Q68CK6	ACSM2B	0.334	acyl-CoA synthetase medium chain family member 2B
Q9NUB1	ACSS1	0.28	acyl-CoA synthetase short chain family member 1
Q9NR19-2	ACSS2	-0.257	acyl-CoA synthetase short chain family member 2
Q9H6R3	ACSS3	0.346	acyl-CoA synthetase short chain family member 3
P12814-3	ACTN1	-0.216	actinin alpha 1
O43707	ACTN4	-0.267	actinin alpha 4
P61163	ACTR1A	-0.134	actin related protein 1A
P42025	ACTR1B	-0.456	actin related protein 1B
P61160-1	ACTR2	-0.106	actin related protein 2
Q03154-1	ACY1	-0.322	aminoacylase 1
P14621	ACYP2	-0.486	acylphosphatase 2
O14672	ADAM10	-0.26	ADAM metallopeptidase domain 10
Q13443	ADAM9	-0.313	ADAM metallopeptidase domain 9
P55265-4	ADAR	0.121	adenosine deaminase RNA specific
O60503	ADCY9	-0.79	adenylate cyclase 9
P35611-3	ADD1	-0.331	adducin 1
Q9UEY8-2	ADD3	-0.318	adducin 3
Q9Y653	ADGRG1	0.597	adhesion G protein-coupled receptor G1
Q86SQ4-3	ADGRG6	-0.405	adhesion G protein-coupled receptor G6
P08319-2	ADH4	-0.285	alcohol dehydrogenase 4 (class II), pi polypeptide
P11766	ADH5	-0.251	alcohol dehydrogenase 5 (class III), chi polypeptide
P28332-2	ADH6	-0.312	alcohol dehydrogenase 6 (class V)
Q9BV57	ADI1	-0.268	acireductone dioxygenase 1
P55263	ADK	-0.396	adenosine kinase
Q9H2P0	ADNP	0.29	activity dependent neuroprotector homeobox
Q9BRR6-1	ADPGK	0.158	ADP dependent glucokinase
Q16186	ADRM1	0.27	adhesion regulating molecule 1
P30566	ADSL	-0.348	adenylosuccinate lyase
P30520	ADSS2	-0.185	adenylosuccinate synthase 2
P55196-5	AFDN	-0.121	afadin, adherens junction formation factor
Q9UHB7-1	AFF4	0.467	AF4/FMR2 family member 4
Q9Y4W6	AFG3L2	0.323	AFG3 like matrix AAA peptidase subunit 2
P02771	AFP	-0.343	alpha fetoprotein
Q6ULP2	AFTPH	-0.29	aftiphilin

P52594-4	AGFG1	-0.167	ArfGAP with FG repeats 1
O95081	AGFG2	-0.275	ArfGAP with FG repeats 2
Q9BSE5	AGMAT	0.286	agmatinase
Q9NUQ2	AGPAT5	0.146	1-acylglycerol-3-phosphate O-acyltransferase 5
O95994	AGR2	0.397	anterior gradient 2, protein disulphide isomerase family member
O00468	AGRN	-0.298	agrin
P01019	AGT	-0.657	angiotensinogen
Q8WYP5-2	AHCTF1	0.382	AT-hook containing transcription factor 1
P23526-1	AHCY	-0.321	adenosylhomocysteinase
O43865	AHCYL1	-0.12	adenosylhomocysteinase like 1
Q09666-1	AHNAK	-0.23	AHNAK nucleoprotein
P02765	AHSG	-0.474	alpha 2-HS glycoprotein
O95831-1	AIFM1	0.17	apoptosis inducing factor mitochondria associated 1
Q9BRQ8	AIFM2	0.132	apoptosis inducing factor mitochondria associated 2
Q96IF1	AJUBA	-0.117	ajuba LIM protein
P00568	AK1	-0.186	adenylate kinase 1
Q9UIJ7-1	AK3	0.28	adenylate kinase 3
P27144	AK4	0.198	adenylate kinase 4
Q92667	AKAP1	0.146	A-kinase anchoring protein 1
Q12802-2	AKAP13	-0.365	A-kinase anchoring protein 13
Q02040-1	AKAP17A	0.328	A-kinase anchoring protein 17A
O43823	AKAP8	0.296	A-kinase anchoring protein 8
Q9ULX6	AKAP8L	0.301	A-kinase anchoring protein 8 like
P14550	AKR1A1	-0.203	aldo-keto reductase family 1 member A1
O60218	AKR1B10	0.192	aldo-keto reductase family 1 member B10
P52895	AKR1C1/AKR1C2	0.172	aldo-keto reductase family 1 member C2
Q04828	AKR1C1/AKR1C2	0.156	aldo-keto reductase family 1 member C2
P51857	AKR1D1	-0.171	aldo-keto reductase family 1 member D1
O43488	AKR7A2	-0.204	aldo-keto reductase family 7 member A2
P31749	AKT1	-0.15	AKT serine/threonine kinase 1
P13716-2	ALAD	-0.384	aminolevulinate dehydratase
P13196	ALAS1	0.65	5'-aminolevulinate synthase 1
P02768	ALB	-0.497	albumin
P02769	ALB	1.177	albumin
Q8IZ83	ALDH16A1	-0.229	aldehyde dehydrogenase 16 family member A1
P00352	ALDH1A1	-0.388	aldehyde dehydrogenase 1 family member A1
P30837	ALDH1B1	0.318	aldehyde dehydrogenase 1 family member B1
P05091	ALDH2	0.318	aldehyde dehydrogenase 2 family member
P51648-2	ALDH3A2	0.118	aldehyde dehydrogenase 3 family member A2
P30038	ALDH4A1	0.266	aldehyde dehydrogenase 4 family member A1
P51649-2	ALDH5A1	0.352	aldehyde dehydrogenase 5 family member A1
Q02252	ALDH6A1	0.144	aldehyde dehydrogenase 6 family member A1
P49419-2	ALDH7A1	0.131	aldehyde dehydrogenase 7 family member A1
P09972	ALDOC	-0.238	aldolase, fructose-bisphosphate C
Q9H553	ALG2	0.229	ALG2 alpha-1,3/1,6-mannosyltransferase
Q9Y673	ALG5	0.334	ALG5 dolichyl-phosphate beta-glucosyltransferase
Q9H6U8-3	ALG9	0.243	ALG9 alpha-1,2-mannosyltransferase

Q9BT30	ALKBH7	-0.354	alkB homolog 7
Q86V81	ALYREF	0.178	Aly/REF export factor
Q9UHK6-5	AMACR	0.283	alpha-methylacyl-CoA racemase
Q9Y2J4-4	AMOTL2	0.682	angiomotin like 2
Q01433-1	AMPD2	-0.268	adenosine monophosphate deaminase 2
P48728	AMT	0.298	aminomethyltransferase
Q9H1A4	ANAPC1	-0.161	anaphase promoting complex subunit 1
Q9UJX6	ANAPC2	-0.201	anaphase promoting complex subunit 2
Q9P2R3-4	ANKFY1	-0.254	ankyrin repeat and FYVE domain containing 1
Q8IWZ3-6	ANKHD1/ANKHD1-EIF4EBP3	-0.205	ankyrin repeat and KH domain containing 1
Q15327	ANKRD1	0.826	ankyrin repeat domain 1
O75179	ANKRD17	-0.114	ankyrin repeat domain 17
Q8NB46	ANKRD52	-0.493	ankyrin repeat domain 52
Q92625	ANKS1A	-0.239	ankyrin repeat and sterile alpha motif domain containing 1A
Q9NQW6	ANLN	0.411	anillin actin binding protein
P39687	ANP32A	-0.178	acidic nuclear phosphoprotein 32 family member A
Q92688	ANP32B	-0.307	acidic nuclear phosphoprotein 32 family member B
Q9BTT0	ANP32E	-0.162	acidic nuclear phosphoprotein 32 family member E
P15144	ANPEP	-0.124	alanyl aminopeptidase, membrane
P50995	ANXA11	-0.17	annexin A11
P09525	ANXA4	-0.216	annexin A4
P08758	ANXA5	-0.194	annexin A5
P08133	ANXA6	-0.344	annexin A6
P20073	ANXA7	-0.167	annexin A7
Q10567	AP1B1	-0.129	adaptor related protein complex 1 subunit beta 1
O43747	AP1G1	-0.317	adaptor related protein complex 1 subunit gamma 1
Q9BXS5-1	AP1M1	-0.079	adaptor related protein complex 1 subunit mu 1
P61966	AP1S1	-0.167	adaptor related protein complex 1 subunit sigma 1
O94973-2	AP2A2	-0.135	adaptor related protein complex 2 subunit alpha 2
P63010-2	AP2B1	-0.256	adaptor related protein complex 2 subunit beta 1
Q96CW1	AP2M1	0.111	adaptor related protein complex 2 subunit mu 1
O00203	AP3B1	-0.161	adaptor related protein complex 3 subunit beta 1
O14617-5	AP3D1	-0.282	adaptor related protein complex 3 subunit delta 1
P13798	APEH	-0.329	acylaminoacyl-peptide hydrolase
P27695	APEX1	-0.231	apurinic/apyrimidinic endodeoxyribonuclease 1
Q96GX9-1	APIP	-0.23	APAF1 interacting protein
Q06481	APLP2	-0.208	amyloid beta precursor like protein 2
Q9HDC9	APMAP	0.229	adipocyte plasma membrane associated protein
P02647	APOA1	-0.697	apolipoprotein A1
P02652	APOA2	-0.337	apolipoprotein A2
P04114	APOB	-0.946	apolipoprotein B
Q9UH17	APOBEC3B	0.479	apolipoprotein B mRNA editing enzyme catalytic subunit 3B
Q9NRW3	APOBEC3C	0.535	apolipoprotein B mRNA editing enzyme catalytic subunit 3C
P02655	APOC2	-0.619	apolipoprotein C2
P02649	APOE	-0.35	apolipoprotein E
O14791-2	APOL1	-0.572	apolipoprotein L1
Q9BUR5-1	APOO	0.193	apolipoprotein O

Q6UXV4	APOOL	0.296	apolipoprotein O like
P05067	APP	-0.7	amyloid beta precursor protein
P07741	APRT	-0.276	adenine phosphoribosyltransferase
Q7Z2E3-1	APTX	0.171	aprataxin
O60306	AQR	0.215	aquarius intron-binding spliceosomal factor
Q96P48-6	ARAP1	-0.228	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 1
P48444	ARCN1	-0.116	archain 1
P18085	ARF4	-0.134	ADP ribosylation factor 4
Q8N6T3-1	ARFGAP1	-0.151	ADP ribosylation factor GTPase activating protein 1
Q8N6H7	ARFGAP2	-0.117	ADP ribosylation factor GTPase activating protein 2
Q9NP61	ARFGAP3	-0.216	ADP ribosylation factor GTPase activating protein 3
Q9Y6D6	ARFGEF1	-0.107	ADP ribosylation factor guanine nucleotide exchange factor 1
Q9Y6D5	ARFGEF2	-0.245	ADP ribosylation factor guanine nucleotide exchange factor 2
P53365	ARFIP2	-0.216	ADP ribosylation factor interacting protein 2
P78540	ARG2	0.3	arginase 2
Q07960	ARHGAP1	-0.172	Rho GTPase activating protein 1
Q8IWW6-1	ARHGAP12	-0.174	Rho GTPase activating protein 12
Q68EM7	ARHGAP17	-0.186	Rho GTPase activating protein 17
Q8N392	ARHGAP18	-0.486	Rho GTPase activating protein 18
Q9NRY4	ARHGAP35	-0.284	Rho GTPase activating protein 35
P52565	ARHGDIA	-0.209	Rho GDP dissociation inhibitor alpha
Q92888-3	ARHGEF1	-0.156	Rho guanine nucleotide exchange factor 1
Q9HCE6	ARHGEF10L	-0.296	Rho guanine nucleotide exchange factor 10 like
Q9NZN5	ARHGEF12	-0.401	Rho guanine nucleotide exchange factor 12
Q5VV41	ARHGEF16	-0.126	Rho guanine nucleotide exchange factor 16
Q92974	ARHGEF2	0.378	Rho/Rac guanine nucleotide exchange factor 2
Q8N1W1-6	ARHGEF28	-0.179	Rho guanine nucleotide exchange factor 28
Q14155-5	ARHGEF7	-0.277	Rho guanine nucleotide exchange factor 7
Q8NFD5-3	ARID1B	-0.18	AT-rich interaction domain 1B
Q99856	ARID3A	-0.21	AT-rich interaction domain 3A
Q8IVW6	ARID3B	0.186	AT-rich interaction domain 3B
Q9Y4X5	ARIH1	0.141	ariadne RBR E3 ubiquitin protein ligase 1
P40616	ARL1	-0.09	ADP ribosylation factor like GTPase 1
P36405	ARL3	-0.177	ADP ribosylation factor like GTPase 3
Q15041	ARL6IP1	0.391	ADP ribosylation factor like GTPase 6 interacting protein 1
Q96C12	ARMC5	0.61	armadillo repeat containing 5
Q6NXE6-1	ARMC6	-0.433	armadillo repeat containing 6
Q9UH62	ARMCX3	0.115	armadillo repeat containing X-linked 3
Q5T2E6	ARMH3	-0.343	armadillo like helical domain containing 3
Q9H993	ARMT1	-0.343	acidic residue methyltransferase 1
O15143	ARPC1B	-0.178	actin related protein 2/3 complex subunit 1B
O15144	ARPC2	-0.15	actin related protein 2/3 complex subunit 2
O15145	ARPC3	-0.339	actin related protein 2/3 complex subunit 3
P59998-3	ARPC4	-0.093	actin related protein 2/3 complex subunit 4
O15511	ARPC5	-0.179	actin related protein 2/3 complex subunit 5
Q7Z6K5	ARPIN/ARPIN-AP3S2	-0.394	ARPIN-AP3S2 readthrough
P56211	ARPP19	-0.228	cAMP regulated phosphoprotein 19

P49407	ARRB1	-0.312	arrestin beta 1
P49407-2	ARRB1	-0.179	arrestin beta 1
P15848	ARSB	-0.322	arylsulfatase B
P51690	ARSL	-0.721	arylsulfatase L
O00192	ARVCF	0.256	ARVCF delta catenin family member
Q8TDY4-1	ASAP3	-0.419	ArfGAP with SH3 domain, ankyrin repeat and PH domain 3
Q8N9N2-2	ASCC1	-0.452	activating signal cointegrator 1 complex subunit 1
Q9H1I8-1	ASCC2	-0.155	activating signal cointegrator 1 complex subunit 2
Q8N3C0	ASCC3	-0.355	activating signal cointegrator 1 complex subunit 3
Q9NVP2	ASF1B	0.443	anti-silencing function 1B histone chaperone
P07306	ASGR1	-0.279	asialoglycoprotein receptor 1
P07307	ASGR2	-0.329	asialoglycoprotein receptor 2
P04424	ASL	-0.173	argininosuccinate lyase
O95671	ASMTL	-0.158	acetylserotonin O-methyltransferase like
P08243	ASNS	0.183	asparagine synthetase (glutamine-hydrolyzing)
Q9NWL6	ASNSD1	-0.121	asparagine synthetase domain containing 1
Q12797	ASPH	0.322	aspartate beta-hydroxylase
Q9BZE9-2	ASPSCR1	-0.208	ASPSCR1 tether for SLC2A4, UBX domain containing
Q7L266	ASRGL1	-0.225	asparaginase and isoaspartyl peptidase 1
P00966	ASS1	-0.428	argininosuccinate synthase 1
Q8NBU5	ATAD1	0.441	ATPase family AAA domain containing 1
Q6PL18-1	ATAD2	0.117	ATPase family AAA domain containing 2
Q9NVI7-2	ATAD3A	0.257	ATPase family AAA domain containing 3A
Q5T9A4	ATAD3B	0.237	ATPase family AAA domain containing 3B
Q5SQI0-1	ATAT1	0.427	alpha tubulin acetyltransferase 1
P15336-1	ATF2	-0.406	activating transcription factor 2
P18847	ATF3	2.039	activating transcription factor 3
Q9BSB4	ATG101	0.638	autophagy related 101
Q676U5	ATG16L1	-0.12	autophagy related 16 like 1
Q9Y4P1-2	ATG4B	-0.115	autophagy related 4B cysteine peptidase
O95352	ATG7	-0.295	autophagy related 7
P31939	ATIC	-0.276	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase
O00244	ATOX1	-0.469	antioxidant 1 copper chaperone
P98196	ATP11A	-0.2	ATPase phospholipid transporting 11A
P05023	ATP1A1	0.123	ATPase Na+/K+ transporting subunit alpha 1
P05026	ATP1B1	0.331	ATPase Na+/K+ transporting subunit beta 1
P54709	ATP1B3	0.472	ATPase Na+/K+ transporting subunit beta 3
P16615	ATP2A2	0.156	ATPase sarcoplasmic/endoplasmic reticulum Ca2+ transporting 2
P20020	ATP2B1	0.122	ATPase plasma membrane Ca2+ transporting 1
P25705-1	ATP5F1A	0.348	ATP synthase F1 subunit alpha
P06576	ATP5F1B	0.231	ATP synthase F1 subunit beta
P56381	ATP5F1E	0.455	ATP synthase F1 subunit epsilon
Q9UII2	ATP5IF1	0.207	ATP synthase inhibitory factor subunit 1
P56385	ATP5ME	0.162	ATP synthase membrane subunit e
O75964	ATP5MG	0.3	ATP synthase membrane subunit g
P24539	ATP5PB	0.538	ATP synthase peripheral stalk-membrane subunit b
O75947-1	ATP5PD	0.183	ATP synthase peripheral stalk subunit d

P18859-2	ATP5PF	0.232	ATP synthase peripheral stalk subunit F6
P48047	ATP5PO	0.48	ATP synthase peripheral stalk subunit OSCP
O75787	ATP6AP2	0.26	ATPase H+ transporting accessory protein 2
P61421	ATP6V0D1	0.391	ATPase H+ transporting V0 subunit d1
P38606	ATP6V1A	-0.106	ATPase H+ transporting V1 subunit A
P21283	ATP6V1C1	0.115	ATPase H+ transporting V1 subunit C1
Q9Y5K8	ATP6V1D	0.23	ATPase H+ transporting V1 subunit D
Q5TC12	ATPAF1	0.358	ATP synthase mitochondrial F1 complex assembly factor 1
Q8N5M1	ATPAF2	0.262	ATP synthase mitochondrial F1 complex assembly factor 2
O75882	ATRN	-0.447	attractin
Q9UBB4	ATXN10	-0.188	ataxin 10
Q8WWM7-1	ATXN2L	-0.114	ataxin 2 like
P54252	ATXN3	0.48	ataxin 3
Q9Y679-1	AUP1	0.236	AUP1 lipid droplet regulating VLDL assembly factor
O14965	AURKA	0.269	aurora kinase A
Q96GD4-5	AURKB	0.58	aurora kinase B
Q9NQS1	AVEN	-0.193	apoptosis and caspase activation inhibitor
Q8NBF6-1	AVL9	-0.237	AVL9 cell migration associated
O15169	AXIN1	-0.326	axin 1
O94766	B3GAT3	0.201	beta-1,3-glucuronyltransferase 3
Q9NY97	B3GNT2	0.249	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 2
O60513	B4GALT4	-0.251	beta-1,4-galactosyltransferase 4
O43505	B4GAT1	-0.346	beta-1,4-glucuronyltransferase 1
Q9NWV8	BABAM1	-0.22	BRISC and BRCA1 A complex member 1
Q9NXR7-1	BABAM2	-0.326	BRISC and BRCA1 A complex member 2
O95816	BAG2	0.329	BCL2 associated athanogene 2
O95817	BAG3	0.791	BCL2 associated athanogene 3
O95429	BAG4	-0.346	BCL2 associated athanogene 4
P46379-3	BAG6	-0.096	BCL2 associated athanogene 6
O75531	BANF1	0.142	barrier to autointegration factor 1
Q07812-2	BAX	-0.088	BCL2 associated X, apoptosis regulator
Q9NRL2	BAZ1A	0.459	bromodomain adjacent to zinc finger domain 1A
Q9UIG0	BAZ1B	0.426	bromodomain adjacent to zinc finger domain 1B
Q9UIF9	BAZ2A	0.232	bromodomain adjacent to zinc finger domain 2A
Q9BXH1	BBC3	0.308	BCL2 binding component 3
P50895	BCAM	-0.35	basal cell adhesion molecule (Lutheran blood group)
P51572-2	BCAP31	0.417	B cell receptor associated protein 31
P56945-6	BCAR1	0.233	BCAR1 scaffold protein, Cas family member
O75934	BCAS2	0.167	BCAS2 pre-mRNA processing factor
P54687-5	BCAT1	-0.345	branched chain amino acid transaminase 1
Q9P287-2	BCCIP	0.285	BRCA2 and CDKN1A interacting protein
P12694	BCKDHA	0.371	branched chain keto acid dehydrogenase E1 subunit alpha
O14874	BCKDK	0.306	branched chain keto acid dehydrogenase kinase
O95999	BCL10	-0.199	BCL10 immune signaling adaptor
Q86UU0	BCL9L	0.191	BCL9 like
Q9Y276	BCS1L	0.337	BCS1 homolog, ubiquinol-cytochrome c reductase complex chaperone
Q9BUT1	BDH2	-0.237	3-hydroxybutyrate dehydrogenase 2

Q5T5X7	BEND3	0.129	BEN domain containing 3
O15155	BET1	0.331	Bet1 golgi vesicular membrane trafficking protein
Q9NYM9	BET1L	-0.395	Bet1 golgi vesicular membrane trafficking protein like
O15392-2	BIRC5	0.112	baculoviral IAP repeat containing 5
Q9NR09	BIRC6	-0.354	baculoviral IAP repeat containing 6
Q13867	BLMH	-0.193	bleomycin hydrolase
P78537	BLOC1S1	-0.227	biogenesis of lysosomal organelles complex 1 subunit 1
P53004	BLVRA	-0.174	biliverdin reductase A
Q14692	BMS1	-0.26	BMS1 ribosome biogenesis factor
Q12983	BNIP3	0.6	BCL2 interacting protein 3
Q53S33	BOLA3	0.283	bolA family member 3
Q96GS4	BORCS6	-0.413	BLOC-1 related complex subunit 6
Q86WA6	BPHL	0.385	biphenyl hydrolase like
O95861-1	BPNT1	-0.549	3'(2'), 5'-bisphosphate nucleotidase 1
O95861-2	BPNT1	-0.333	3'(2'), 5'-bisphosphate nucleotidase 1
Q7Z569	BRAP	0.117	BRCA1 associated protein
P46736	BRCC3	-0.213	BRCA1/BRCA2-containing complex subunit 3
O95696-2	BRD1	0.201	bromodomain containing 1
P25440-2	BRD2	0.356	bromodomain containing 2
Q15059	BRD3	-0.315	bromodomain containing 3
Q5VW32	BROX	-0.307	BRO1 domain and CAAX motif containing
P55201-2	BRPF1	0.304	bromodomain and PHD finger containing 1
Q96K17	BTF3L4	-0.249	basic transcription factor 3 like 4
Q7KYR7	BTN2A1	0.693	butyrophilin subfamily 2 member A1
O43683	BUB1	0.247	BUB1 mitotic checkpoint serine/threonine kinase
O43684	BUB3	0.178	BUB3 mitotic checkpoint protein
P41223-2	BUD31	0.403	BUD31 homolog
Q9Y6E2	BZW2	-0.361	basic leucine zipper and W2 domains 2
Q9H0W9	C11orf54	-0.221	chromosome 11 open reading frame 54
O00193	C11orf58	-0.373	chromosome 11 open reading frame 58
E9PRG8	C11orf98	-0.564	chromosome 11 open reading frame 98
Q9HB07	C12orf10	-0.152	chromosome 12 open reading frame 10
Q8N5I9	C12orf45	0.333	chromosome 12 open reading frame 45
Q4G0I0	C16orf91	0.31	chromosome 16 open reading frame 91
Q9HAS0	C17orf75	-0.261	chromosome 17 open reading frame 75
Q9UNZ5	C19orf53	0.566	chromosome 19 open reading frame 53
Q6ZSJ8	C1orf122	0.091	chromosome 1 open reading frame 122
Q8NDD1	C1orf131	-0.334	chromosome 1 open reading frame 131
Q8N6N3	C1orf52	-0.367	chromosome 1 open reading frame 52
Q9GZN8-2	C20orf27	-0.149	chromosome 20 open reading frame 27
A6NCS6	C2orf72	-0.175	chromosome 2 open reading frame 72
P01024	C3	-0.468	complement C3
P01031	C5	-0.298	complement C5
Q8NC54	C5orf15	-0.235	chromosome 5 open reading frame 15
A6NDU8	C5orf51	-0.419	chromosome 5 open reading frame 51
Q9BRJ6	C7orf50	-0.545	chromosome 7 open reading frame 50
Q8IXQ3	C9orf40	-0.347	chromosome 9 open reading frame 40

Q5T6V5	C9orf64	-0.315	chromosome 9 open reading frame 64
Q9H8G2-1	CAAP1	-0.359	caspase activity and apoptosis inhibitor 1
Q9Y376	CAB39	-0.432	calcium binding protein 39
Q8WUQ7-2	CACTIN	-0.111	cactin, spliceosome C complex subunit
Q9HB71	CACYBP	0.112	calcyclin binding protein
P27708	CAD	-0.158	carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase
Q9BY67-3	CADM1	-0.243	cell adhesion molecule 1
Q13137-4	CALCOCO2	-0.22	calcium binding and coiled-coil domain 2
O43852-3	CALU	-0.148	calumenin
O43852-4	CALU	-0.315	calumenin
Q14012	CAMK1	-0.388	calcium/calmodulin dependent protein kinase I
Q13557-10	CAMK2D	-0.205	calcium/calmodulin dependent protein kinase II delta
Q86VP6-1	CAND1	-0.256	cullin associated and neddylation dissociated 1
P27824-2	CANX	0.094	calnexin
P40123	CAP2	-0.192	cyclase associated actin cytoskeleton regulatory protein 2
P40121	CAPG	-0.228	capping actin protein, gelsolin like
P07384	CAPN1	-0.172	calpain 1
P04632	CAPNS1	-0.21	calpain small subunit 1
Q14444	CAPRIN1	-0.215	cell cycle associated protein 1
P52907	CAPZA1	-0.292	capping actin protein of muscle Z-line subunit alpha 1
P47755	CAPZA2	-0.288	capping actin protein of muscle Z-line subunit alpha 2
P47756-2	CAPZB	-0.202	capping actin protein of muscle Z-line subunit beta
Q96LW7-2	CARD19	0.436	caspase recruitment domain family member 19
Q9Y2V2	CARHSP1	-0.092	calcium regulated heat stable protein 1
Q86X55	CARM1	-0.091	coactivator associated arginine methyltransferase 1
P49589-3	CARS1	-0.282	cysteinyl-tRNA synthetase 1
Q9HA77	CARS2	0.235	cysteinyl-tRNA synthetase 2, mitochondrial
O15234	CASC3	-0.231	CASC3 exon junction complex subunit
O14936	CASK	0.135	calcium/calmodulin dependent serine protein kinase
P49662	CASP4	0.301	caspase 4
P55212	CASP6	-0.094	caspase 6
Q14790-9	CASP8	-0.106	caspase 8
P20810-6	CAST	-0.269	calpastatin
A6NHX0	CASTOR2	-0.501	cytosolic arginine sensor for mTORC1 subunit 2
O95810	CAVIN2	0.145	caveolae associated protein 2
P22681	CBL	-0.214	Cbl proto-oncogene
P16152	CBR1	-0.155	carbonyl reductase 1
Q8N4T8	CBR4	0.22	carbonyl reductase 4
P35520-2	CBS/CBSL	-0.386	cystathionine beta-synthase
Q5JTY5	CBWD3/CBWD6	-0.157	COBW domain containing 3
O00257	CBX4	0.2	chromobox 4
P45973	CBX5	0.197	chromobox 5
Q9HC52	CBX8	0.433	chromobox 8
Q8IWD4	CCDC117	0.52	coiled-coil domain containing 117
Q8WUD4	CCDC12	-0.293	coiled-coil domain containing 12
Q96CT7	CCDC124	-0.12	coiled-coil domain containing 124
Q96BQ5	CCDC127	0.627	coiled-coil domain containing 127

Q9H6E4	CCDC134	0.206	coiled-coil domain containing 134
Q6PK04	CCDC137	-0.36	coiled-coil domain containing 137
O60826	CCDC22	-0.262	coiled-coil domain containing 22
Q96MW1	CCDC43	-0.4	coiled-coil domain containing 43
Q96A33	CCDC47	0.279	coiled-coil domain containing 47
Q8IVM0	CCDC50	-0.328	coiled-coil domain containing 50
Q8IVM0-2	CCDC50	-0.305	coiled-coil domain containing 50
Q96ER9	CCDC51	0.162	coiled-coil domain containing 51
Q16204	CCDC6	-0.332	coiled-coil domain containing 6
A6NKD9	CCDC85C	-0.398	coiled-coil domain containing 85C
Q3V6T2-1	CCDC88A	-0.189	coiled-coil domain containing 88A
Q9P219	CCDC88C	-0.632	coiled-coil domain containing 88C
P20248	CCNA2	0.218	cyclin A2
O95067	CCNB2	0.359	cyclin B2
P51946	CCNH	0.34	cyclin H
O60563	CCNT1	0.668	cyclin T1
O14618	CCS	-0.267	copper chaperone for superoxide dismutase
P49368-1	CCT3	-0.104	chaperonin containing TCP1 subunit 3
P50991	CCT4	-0.193	chaperonin containing TCP1 subunit 4
P48643	CCT5	-0.142	chaperonin containing TCP1 subunit 5
Q99832	CCT7	-0.132	chaperonin containing TCP1 subunit 7
P50990	CCT8	-0.188	chaperonin containing TCP1 subunit 8
Q6YHK3	CD109	0.316	CD109 molecule
Q9Y5K6	CD2AP	-0.31	CD2 associated protein
Q13042	CDC16	-0.254	cell division cycle 16
Q12834	CDC20	0.211	cell division cycle 20
P49427	CDC34	0.29	cell division cycle 34
Q99459	CDC5L	0.168	cell division cycle 5 like
Q6P1J9	CDC73	0.105	cell division cycle 73
Q69YH5-1	CDCA2	0.409	cell division cycle associated 2
Q96FF9	CDCA5	0.532	cell division cycle associated 5
Q53HL2	CDCA8	0.215	cell division cycle associated 8
P19022	CDH2	-0.233	cadherin 2
O14735	CDIPT	-0.975	CDP-diacylglycerol--inositol 3-phosphatidyltransferase
P50750-2	CDK9	0.408	cyclin dependent kinase 9
Q5VV42	CDKAL1	-0.205	CDK5 regulatory subunit associated protein 1 like 1
P38936	CDKN1A	1.182	cyclin dependent kinase inhibitor 1A
Q9NXV6	CDKN2AIP	0.338	CDKN2A interacting protein
Q96HQ2-1	CDKN2AIPNL	-0.501	CDKN2A interacting protein N-terminal like
O95674-1	CDS2	-0.115	CDP-diacylglycerol synthase 2
Q9UKY7	CDV3	-0.218	CDV3 homolog
P13688	CEACAM1	0.32	CEA cell adhesion molecule 1
P49715-4	CEBPA	-0.396	CCAAT enhancer binding protein alpha
Q03701	CEBPZ	0.315	CCAAT enhancer binding protein zeta
Q9UHN6	CEMIP2	0.249	cell migration inducing hyaluronidase 2
P49454	CENPF	0.229	centromere protein F
Q7Z7K6-1	CENPV	0.497	centromere protein V

Q9UPN4	CEP131	-0.134	centrosomal protein 131
O15078	CEP290	-0.159	centrosomal protein 290
Q8TAP6	CEP76	0.545	centrosomal protein 76
Q96G23	CERS2	0.205	ceramide synthase 2
Q9HA82	CERS4	-0.129	ceramide synthase 4
Q9Y5P4-3	CERT1	-0.382	ceramide transporter 1
O00748	CES2	0.129	carboxylesterase 2
P41208	CETN2	-0.169	centrin 2
Q9Y6A4	CFAP20	0.177	cilia and flagella associated protein 20
Q9UEE9-1	CFDP1	-0.631	craniofacial development protein 1
P05156	CFI	-0.36	complement factor I
P23528	CFL1	-0.121	cofilin 1
Q9Y281-1	CFL2	-0.338	cofilin 2
Q9P2M7-1	CGN	-0.788	cingulin
Q0VF96	CGNL1	-0.861	cingulin like 1
Q13111-1	CHAF1A	-0.221	chromatin assembly factor 1 subunit A
Q13112	CHAF1B	0.125	chromatin assembly factor 1 subunit B
Q9NX63	CHCHD3	0.17	coiled-coil-helix-coiled-coil-helix domain containing 3
O14646	CHD1	0.283	chromodomain helicase DNA binding protein 1
O14647	CHD2	0.3	chromodomain helicase DNA binding protein 2
Q14839-2	CHD4	0.266	chromodomain helicase DNA binding protein 4
Q9HCK8-1	CHD8	0.192	chromodomain helicase DNA binding protein 8
Q8NE62	CHDH	0.131	choline dehydrogenase
O14757	CHEK1	-0.53	checkpoint kinase 1
O96017-9	CHEK2	-0.199	checkpoint kinase 2
Q8IWX8	CHERP	0.243	calcium homeostasis endoplasmic reticulum protein
Q9BWS9-1	CHID1	-0.18	chitinase domain containing 1
P35790	CHKA	-0.227	choline kinase alpha
P24386-1	CHM	-0.181	CHM Rab escort protein
Q9HD42	CHMP1A	-0.231	charged multivesicular body protein 1A
Q9UQN3-1	CHMP2B	0.098	charged multivesicular body protein 2B
Q9BY43-2	CHMP4A	-0.29	charged multivesicular body protein 4A
Q9H444	CHMP4B	0.14	charged multivesicular body protein 4B
Q9NZZ3	CHMP5	0.162	charged multivesicular body protein 5
Q96FZ7	CHMP6	0.095	charged multivesicular body protein 6
Q9UHD1	CHORDC1	0.47	cysteine and histidine rich domain containing 1
Q99653	CHP1	0.501	calcineurin like EF-hand protein 1
Q8NET6	CHST13	-0.418	carbohydrate sulfotransferase 13
Q8WVB6-2	CHTF18	-0.346	chromosome transmission fidelity factor 18
O76071	CIAO1	-0.199	cytosolic iron-sulfur assembly component 1
Q9Y3D0	CIAO2B	-0.273	cytosolic iron-sulfur assembly component 2B
Q6FI81	CIAPIN1	-0.125	cytokine induced apoptosis inhibitor 1
Q99828-2	CIB1	0.283	calcium and integrin binding 1
Q8TCG1	CIP2A	-0.134	cell proliferation regulating inhibitor of protein phosphatase 2A
Q86X95	CIR1	0.155	corepressor interacting with RBPJ, 1
Q14011	CIRBP	-0.27	cold inducible RNA binding protein
Q9NZ45	CISD1	0.112	CDGSH iron sulfur domain 1

O14578-4	CIT	-0.328	citron rho-interacting serine/threonine kinase
Q8WWK9	CKAP2	0.914	cytoskeleton associated protein 2
Q07065	CKAP4	0.316	cytoskeleton associated protein 4
P12277	CKB	-0.167	creatine kinase B
Q7Z460-1	CLASP1	-0.19	cytoplasmic linker associated protein 1
O75122-3	CLASP2	-0.222	cytoplasmic linker associated protein 2
P56747	CLDN6	0.299	claudin 6
Q9Y696	CLIC4	-0.25	chloride intracellular channel 4
Q14677	CLINT1	-0.375	clathrin interactor 1
Q14677-3	CLINT1	-0.361	clathrin interactor 1
P49761	CLK3	0.686	CDC like kinase 3
Q9NWW5	CLN6	0.103	CLN6 transmembrane ER protein
Q16740	CLPP	0.28	caseinolytic mitochondrial matrix peptidase proteolytic subunit
O76031	CLPX	0.223	caseinolytic mitochondrial matrix peptidase chaperone subunit
Q9HAW4	CLSPN	0.312	claspin
P09496-2	CLTA	-0.152	clathrin light chain A
P09497-2	CLTB	0.462	clathrin light chain B
P10909-2	CLU	0.877	clusterin
I3L2B0	CLUH	-0.367	clustered mitochondria homolog
O75153	CLUH	-0.354	clustered mitochondria homolog
Q8N0X4	CLYBL	0.126	citrate lyase beta like
Q96DG6	CMBL	0.267	carboxymethylenebutenolidase homolog
Q8IY22	CMIP	-0.694	c-Maf inducing protein
Q9BQ75	CMSS1	-0.185	cms1 ribosomal small subunit homolog
P62633	CNBP	-1.238	CCHC-type zinc finger nucleic acid binding protein
P62633-6	CNBP	-0.982	CCHC-type zinc finger nucleic acid binding protein
Q96KP4	CNDP2	-0.335	carnosine dipeptidase 2
Q99439	CNN2	-0.118	calponin 2
Q15417	CNN3	0.103	calponin 3
A5YKK6	CNOT1	-0.207	CCR4-NOT transcription complex subunit 1
Q9H9A5-6	CNOT10	-0.27	CCR4-NOT transcription complex subunit 10
Q9NZN8	CNOT2	-0.18	CCR4-NOT transcription complex subunit 2
Q96LI5	CNOT6L	-0.452	CCR4-NOT transcription complex subunit 6 like
Q9UIV1-1	CNOT7	-0.521	CCR4-NOT transcription complex subunit 7
Q92600	CNOT9	-0.331	CCR4-NOT transcription complex subunit 9
Q9Y2R0	COA3	0.127	cytochrome c oxidase assembly factor 3
Q9NYJ1-2	COA4	-0.45	cytochrome c oxidase assembly factor 4 homolog
Q96JB2-1	COG3	-0.194	component of oligomeric golgi complex 3
Q9H9E3	COG4	-0.161	component of oligomeric golgi complex 4
Q9Y2V7-1	COG6	-0.129	component of oligomeric golgi complex 6
Q96MW5	COG8	-0.12	component of oligomeric golgi complex 8
P38432	COIL	0.272	coilin
P39060-3	COL18A1	-0.296	collagen type XVIII alpha 1 chain
Q86X83	COMMD2	-0.126	COMM domain containing 2
Q7Z4G1-2	COMMD6	-0.704	COMM domain containing 6
Q9NX08	COMMD8	-0.489	COMM domain containing 8
Q9P000-1	COMMD9	-0.535	COMM domain containing 9

P53621-2	COPA	-0.145	coatomer protein complex subunit alpha
P53618	COPB1	-0.135	coatomer protein complex subunit beta 1
P35606	COPB2	-0.17	coatomer protein complex subunit beta 2
O14579-1	COPE	-0.194	coatomer protein complex subunit epsilon
Q9Y678	COPG1	-0.103	coatomer protein complex subunit gamma 1
Q9UBF2	COPG2	-0.23	coatomer protein complex subunit gamma 2
P61201-1	COPS2	-0.173	COP9 signalosome subunit 2
Q9UNS2	COPS3	-0.182	COP9 signalosome subunit 3
Q9BT78	COPS4	-0.21	COP9 signalosome subunit 4
Q92905	COPS5	-0.176	COP9 signalosome subunit 5
Q9UBW8	COPS7A	-0.151	COP9 signalosome subunit 7A
Q99627	COPS8	-0.126	COP9 signalosome subunit 8
P61923-4	COPZ1	-0.138	coatomer protein complex subunit zeta 1
Q5HYK3-1	COQ5	-0.394	coenzyme Q5, methyltransferase
P31146	CORO1A	-0.187	coronin 1A
Q9ULV4-3	CORO1C	0.154	coronin 1C
Q14019	COTL1	-0.414	coactosin like F-actin binding protein 1
Q7KZN9	COX15	-0.092	cytochrome c oxidase assembly homolog COX15
P13073	COX4I1	0.289	cytochrome c oxidase subunit 4I1
P20674	COX5A	0.142	cytochrome c oxidase subunit 5A
P09669	COX6C	0.198	cytochrome c oxidase subunit 6C
P14406	COX7A2	0.16	cytochrome c oxidase subunit 7A2
O75976	CPD	-0.405	carboxypeptidase D
Q17RY0-1	CPEB4	0.255	cytoplasmic polyadenylation element binding protein 4
Q6PUV4	CPLX2	-0.569	complexin 2
Q9BRF8-1	CPPED1	-0.392	calcineurin like phosphoesterase domain containing 1
P31327-3	CPS1	0.149	carbamoyl-phosphate synthase 1
Q16630-2	CPSF6	0.141	cleavage and polyadenylation specific factor 6
P50416	CPT1A	0.116	carnitine palmitoyltransferase 1A
P23786	CPT2	0.403	carnitine palmitoyltransferase 2
P78560	CRADD	-0.389	CASP2 and RIPK1 domain containing adaptor with death domain
P43155	CRAT	0.441	carnitine O-acetyltransferase
Q92793-1	CREBBP	-0.26	CREB binding protein
P52943	CRIP2	0.219	cysteine rich protein 2
P46108-1	CRK	-0.275	CRK proto-oncogene, adaptor protein
P46109	CRKL	-0.245	CRK like proto-oncogene, adaptor protein
Q8IUI8	CRLF3	-0.163	cytokine receptor like factor 3
Q9BZJ0	CRNKL1	0.219	crooked neck pre-mRNA splicing factor 1
P02511	CRYAB	1.788	crystallin alpha B
Q9Y2S2-1	CRYL1	-0.381	crystallin lambda 1
Q08257	CRYZ	0.16	crystallin zeta
O75390	CS	0.31	citrate synthase
P55060	CSE1L	-0.361	chromosome segregation 1 like
P41240	CSK	-0.189	C-terminal Src kinase
P48729	CSNK1A1	0.136	casein kinase 1 alpha 1
P68400	CSNK2A1	0.226	casein kinase 2 alpha 1
P19784	CSNK2A2	0.301	casein kinase 2 alpha 2

P67870	CSNK2B	0.361	casein kinase 2 beta
P01034	CST3	-0.296	cystatin C
Q12996	CSTF3	0.275	cleavage stimulation factor subunit 3
Q13363	CTBP1	-0.158	C-terminal binding protein 1
P49711-1	CTCF	0.251	CCCTC-binding factor
Q9Y5B0	CTDP1	-0.208	CTD phosphatase subunit 1
P32929	CTH	0.252	cystathionine gamma-lyase
P35221	CTNNA1	-0.273	catenin alpha 1
Q9NSA3	CTNNBIP1	-0.505	catenin beta interacting protein 1
Q8WYA6	CTNNBL1	-0.118	catenin beta like 1
O60716-3	CTNND1	-0.146	catenin delta 1
P17812	CTPS1	-0.158	CTP synthase 1
Q9NRF8	CTPS2	-0.31	CTP synthase 2
Q6PD62	CTR9	0.328	CTR9 homolog, Paf1/RNA polymerase II complex component
P07858	CTSB	0.186	cathepsin B
P07711	CTSL	0.529	cathepsin L
Q14247-1	CTTN	-0.33	cortactin
Q2VPK5	CTU2	-0.183	cytosolic thiouridylase subunit 2
Q13616	CUL1	-0.176	cullin 1
Q13617-2	CUL2	-0.1	cullin 2
Q13619-1	CUL4A	-0.096	cullin 4A
Q93034	CUL5	-0.174	cullin 5
O60888-2	CUTA	-0.168	cutA divalent cation tolerance homolog
P39880-3	CUX1	-0.354	cut like homeobox 1
Q6UX04	CWC27	-0.216	CWC27 spliceosome associated cyclophilin
Q2TBE0	CWF19L2	-0.111	CWF19 like cell cycle control factor 2
P78310-1	CXADR	-0.108	CXADR Ig-like cell adhesion molecule
Q9P0U4-2	CXXC1	0.199	CXXC finger protein 1
P00167-1	CYB5A	-0.414	cytochrome b5 type A
Q9UHQ9	CYB5R1	0.362	cytochrome b5 reductase 1
P00387-3	CYB5R3	0.205	cytochrome b5 reductase 3
Q7L1T6	CYB5R4	-0.142	cytochrome b5 reductase 4
P08574	CYC1	0.302	cytochrome c1
Q7L576-1	CYFIP1	-0.241	cytoplasmic FMR1 interacting protein 1
Q07973-1	CYP24A1	0.262	cytochrome P450 family 24 subfamily A member 1
Q96SQ9-2	CYP2S1	0.436	cytochrome P450 family 2 subfamily S member 1
Q8TAV3	CYP2W1	-0.229	cytochrome P450 family 2 subfamily W member 1
Q9HBI6	CYP4F11	0.333	cytochrome P450 family 4 subfamily F member 11
Q16850-1	CYP51A1	-0.564	cytochrome P450 family 51 subfamily A member 1
Q9Y4D1	DAAM1	-0.182	dishevelled associated activator of morphogenesis 1
Q5VWQ8	DAB2IP	-0.418	DAB2 interacting protein
Q14118	DAG1	-0.287	dystroglycan 1
P51397	DAP	-0.539	death associated protein
O43293-1	DAPK3	0.274	death associated protein kinase 3
Q6PI48	DARS2	0.256	aspartyl-tRNA synthetase 2, mitochondrial
P07108-5	DBI	-0.948	diazepam binding inhibitor, acyl-CoA binding protein
Q9UK59	DBR1	0.207	debranching RNA lariats 1

P11182	DBT	0.328	dihydrolipoamide branched chain transacylase E2
Q9Y4B6	DCAF1	-0.321	DDB1 and CUL4 associated factor 1
Q8TEB1	DCAF11	-0.11	DDB1 and CUL4 associated factor 11
Q96JK2	DCAF5	0.154	DDB1 and CUL4 associated factor 5
P61962	DCAF7	0.379	DDB1 and CUL4 associated factor 7
Q8WVC6-1	DCAKD	0.152	dephospho-CoA kinase domain containing
Q9NPI6	DCP1A	0.197	decapping mRNA 1A
Q8IZD4	DCP1B	0.205	decapping mRNA 1B
Q96C86	DCPS	-0.404	decapping enzyme, scavenger
Q14203-4	DCTN1	-0.215	dynactin subunit 1
Q13561-2	DCTN2	-0.245	dynactin subunit 2
O75935	DCTN3	-0.219	dynactin subunit 3
Q9UJW0-3	DCTN4	0.312	dynactin subunit 4
O00399	DCTN6	0.362	dynactin subunit 6
Q9H773	DCTPP1	-0.434	dCTP pyrophosphatase 1
Q8IWE4	DCUN1D3	0.353	defective in cullin neddylation 1 domain containing 3
Q7Z4W1	DCXR	0.173	dicarbonyl and L-xylulose reductase
Q9BW61	DDA1	-0.175	DET1 and DDB1 associated 1
O94760	DDAH1	-0.401	dimethylarginine dimethylaminohydrolase 1
Q16531	DDB1	-0.172	damage specific DNA binding protein 1
Q92466	DDB2	0.393	damage specific DNA binding protein 2
Q5TDH0-3	DDI2	-0.302	DNA damage inducible 1 homolog 2
P39656	DDOST	0.198	dolichyl-diphosphooligosaccharide--protein glycosyltransferase non-catalytic subunit
P30046	DDT	-0.396	D-dopachrome tautomerase
Q92841	DDX17	-0.128	DEAD-box helicase 17
Q9NUU7	DDX19A	-0.164	DEAD-box helicase 19A
Q9NR30	DDX21	0.507	DExD-box helicase 21
Q9BUQ8	DDX23	0.125	DEAD-box helicase 23
Q9GZR7	DDX24	0.292	DEAD-box helicase 24
Q96GQ7	DDX27	-0.214	DEAD-box helicase 27
O00148	DDX39A	-0.221	DExD-box helicase 39A
Q13838-2	DDX39B	-0.176	DExD-box helicase 39B
O15523	DDX3Y	0.182	DEAD-box helicase 3 Y-linked
Q86XP3	DDX42	-0.166	DEAD-box helicase 42
Q9H0S4	DDX47	0.224	DEAD-box helicase 47
P17844	DDX5	-0.121	DEAD-box helicase 5
Q9Y2R4	DDX52	0.266	DExD-box helicase 52
Q9NY93	DDX56	-0.566	DEAD-box helicase 56
P26196	DDX6	0.115	DEAD-box helicase 6
Q16698	DECR1	0.368	2,4-dienoyl-CoA reductase 1
Q9NUI1	DECR2	0.275	2,4-dienoyl-CoA reductase 2
Q9H4E7	DEF6	-0.145	DEF6 guanine nucleotide exchange factor
Q8TCE6-1	DENND10	-0.275	DENN domain containing 10
O43583	DENR	-0.418	density regulated re-initiation and release factor
Q9Y315	DERA	-0.194	deoxyribose-phosphate aldolase
Q8WYQ5-1	DGCR8	0.416	DGCR8 microprocessor complex subunit
Q5KSL6	DGKK	-0.44	diacylglycerol kinase kappa

Q16854	DGUOK	0.216	deoxyguanosine kinase
Q02127	DHODH	0.146	dihydroorotate dehydrogenase (quinone)
Q13268	DHRS2	0.124	dehydrogenase/reductase 2
Q9BTZ2	DHRS4	0.256	dehydrogenase/reductase 4
Q9Y394	DHRS7	0.293	dehydrogenase/reductase 7
O43143	DHX15	0.161	DEAH-box helicase 15
Q7L2E3-2	DHX30	0.374	DExH-box helicase 30
Q9H5Z1	DHX35	0.317	DEAH-box helicase 35
Q92620	DHX38	0.156	DEAH-box helicase 38
Q6P158-1	DHX57	-0.44	DExH-box helicase 57
Q08211	DHX9	0.191	DExH-box helicase 9
O60610-1	DIAPH1	-0.268	diaphanous related formin 1
Q9UPY3	DICER1	-0.198	dicer 1, ribonuclease III
Q9BTC0	DIDO1	0.277	death inducer-obliterator 1
Q9UNQ2	DIMT1	-0.207	DIMT1 rRNA methyltransferase and ribosome maturation factor
Q9P265	DIP2B	-0.259	disco interacting protein 2 homolog B
Q9Y2L1	DIS3	0.151	DIS3 homolog, exosome endoribonuclease and 3'-5' exoribonuclease
Q8IYB7	DIS3L2	-0.305	DIS3 like 3'-5' exoribonuclease 2
O60832	DKC1	0.29	dyskerin pseudouridine synthase 1
P10515	DLAT	0.109	dihydrolipoamide S-acetyltransferase
P09622	DLD	0.363	dihydrolipoamide dehydrogenase
Q9Y2H0	DLGAP4	-0.173	DLG associated protein 4
P36957	DLST	0.289	dihydrolipoamide S-succinyltransferase
Q9NPF5	DMAP1	0.126	DNA methyltransferase 1 associated protein 1
P11532-6	DMD	-0.155	dystrophin
Q08495-1	DMTN	-0.268	dematin actin binding protein
Q86Y56	DNAAF5	-0.421	dynein axonemal assembly factor 5
P31689	DNAJA1	0.543	DnaJ heat shock protein family (Hsp40) member A1
P25685	DNAJB1	0.934	DnaJ heat shock protein family (Hsp40) member B1
Q9UBS4	DNAJB11	0.122	DnaJ heat shock protein family (Hsp40) member B11
P25686-3	DNAJB2	0.478	DnaJ heat shock protein family (Hsp40) member B2
Q9UDY4	DNAJB4	1.193	DnaJ heat shock protein family (Hsp40) member B4
Q9NVH1-1	DNAJC11	0.162	DnaJ heat shock protein family (Hsp40) member C11
O75165	DNAJC13	-0.112	DnaJ heat shock protein family (Hsp40) member C13
Q9Y5T4	DNAJC15	-0.583	DnaJ heat shock protein family (Hsp40) member C15
Q9NVM6	DNAJC17	-0.142	DnaJ heat shock protein family (Hsp40) member C17
Q96DA6	DNAJC19	0.398	DnaJ heat shock protein family (Hsp40) member C19
Q99543-1	DNAJC2	-0.288	DnaJ heat shock protein family (Hsp40) member C2
Q9H3Z4	DNAJC5	-0.693	DnaJ heat shock protein family (Hsp40) member C5
Q99615-1	DNAJC7	0.117	DnaJ heat shock protein family (Hsp40) member C7
P50570	DNM2	-0.364	dynamin 2
Q9Y6K1	DNMT3A	0.131	DNA methyltransferase 3 alpha
Q9ULA0	DNPEP	-0.282	aspartyl aminopeptidase
O43598-1	DNPH1	-0.462	2'-deoxynucleoside 5'-phosphate N-hydrolase 1
Q5QJE6	DNTTIP2	0.385	deoxynucleotidyltransferase terminal interacting protein 2
Q8N1I0-3	DOCK4	-0.25	dedicator of cytokinesis 4
Q9H3H5	DPAGT1	0.926	dolichyl-phosphate N-acetylglucosaminephosphotransferase 1

Q9BZG8	DPH1	-0.495	diphthamide biosynthesis 1
Q9BQC3	DPH2	-0.179	diphthamide biosynthesis 2
Q9H2P9-5	DPH5	-0.64	diphthamide biosynthesis 5
O60762	DPM1	0.106	dolichyl-phosphate mannosyltransferase subunit 1, catalytic
Q9NY33	DPP3	-0.2	dipeptidyl peptidase 3
P27487	DPP4	0.154	dipeptidyl peptidase 4
Q86TI2-2	DPP9	-0.188	dipeptidyl peptidase 9
Q16555	DPYSL2	-0.331	dihydropyrimidinase like 2
Q9Y295	DRG1	-0.187	developmentally regulated GTP binding protein 1
Q9H410	DSN1	-0.281	DSN1 component of MIS12 kinetochore complex
P60981-1	DSTN	0.165	destrin, actin depolymerizing factor
Q8TEA8	DTD1	-0.139	D-aminoacyl-tRNA deacylase 1
P23919	DTYMK	-0.136	deoxythymidylate kinase
Q6P1R4	DUS1L	-0.14	dihydrouridine synthase 1 like
P28562	DUSP1	1.431	dual specificity phosphatase 1
O75319-1	DUSP11	0.221	dual specificity phosphatase 11
P33316-3	DUT	-0.261	deoxyuridine triphosphatase
O14641	DVL2	-0.283	dishevelled segment polarity protein 2
Q14204	DYNC1H1	-0.261	dynein cytoplasmic 1 heavy chain 1
Q9Y6G9	DYNC1LI1	-0.17	dynein cytoplasmic 1 light intermediate chain 1
O43237	DYNC1LI2	-0.11	dynein cytoplasmic 1 light intermediate chain 2
P63167	DYNLL1	0.865	dynein light chain LC8-type 1
Q96FJ2	DYNLL2	0.539	dynein light chain LC8-type 2
Q9NP97	DYNLRB1	-0.13	dynein light chain roadblock-type 1
Q16254	E2F4	-0.272	E2F transcription factor 4
Q99848	EBNA1BP2	-0.218	EBNA1 binding protein 2
O95905-3	ECD	0.288	ecdysoneless cell cycle regulator
P42892	ECE1	-0.394	endothelin converting enzyme 1
Q13011	ECH1	0.287	enoyl-CoA hydratase 1
Q9NTX5	ECHDC1	0.219	ethylmalonyl-CoA decarboxylase 1
P30084	ECHS1	0.187	enoyl-CoA hydratase, short chain 1
P42126	ECI1	0.204	enoyl-CoA delta isomerase 1
O75521	ECI2	0.342	enoyl-CoA delta isomerase 2
Q5VYK3	ECPAS	-0.135	Ecm29 proteasome adaptor and scaffold
Q9BQ95	ECSIT	0.261	ECSIT signalling integrator
Q9H8V3-3	ECT2	0.27	epithelial cell transforming 2
O60869	EDF1	0.254	endothelial differentiation related factor 1
P68104	EEF1A1	0.127	eukaryotic translation elongation factor 1 alpha 1
P26641-2	EEF1G	-0.109	eukaryotic translation elongation factor 1 gamma
P13639	EEF2	-0.168	eukaryotic translation elongation factor 2
O00418	EEF2K	-0.476	eukaryotic elongation factor 2 kinase
Q7Z2Z2	EFL1	-0.355	elongation factor like GTPase 1
Q8NDI1	EHBP1	-0.436	EH domain binding protein 1
Q9H4M9	EHD1	-0.092	EH domain containing 1
Q08426	EHHADH	0.257	enoyl-CoA hydratase and 3-hydroxyacyl CoA dehydrogenase
P41567	EIF1	0.653	eukaryotic translation initiation factor 1
P19525	EIF2AK2	0.154	eukaryotic translation initiation factor 2 alpha kinase 2

Q9NZJ5	EIF2AK3	-0.305	eukaryotic translation initiation factor 2 alpha kinase 3
Q9P2K8-1	EIF2AK4	-0.218	eukaryotic translation initiation factor 2 alpha kinase 4
Q14232	EIF2B1	-0.347	eukaryotic translation initiation factor 2B subunit alpha
Q9NR50-1	EIF2B3	-0.138	eukaryotic translation initiation factor 2B subunit gamma
Q13144	EIF2B5	-0.219	eukaryotic translation initiation factor 2B subunit epsilon
P41214	EIF2D	-0.326	eukaryotic translation initiation factor 2D
P05198	EIF2S1	0.098	eukaryotic translation initiation factor 2 subunit alpha
Q14152	EIF3A	-0.196	eukaryotic translation initiation factor 3 subunit A
P55884-2	EIF3B	-0.115	eukaryotic translation initiation factor 3 subunit B
Q99613	EIF3C	-0.105	eukaryotic translation initiation factor 3 subunit C
O75821	EIF3G	-0.307	eukaryotic translation initiation factor 3 subunit G
O15372	EIF3H	-0.088	eukaryotic translation initiation factor 3 subunit H
O75822	EIF3J	-0.29	eukaryotic translation initiation factor 3 subunit J
Q9UBQ5	EIF3K	-0.48	eukaryotic translation initiation factor 3 subunit K
Q7L2H7	EIF3M	-0.261	eukaryotic translation initiation factor 3 subunit M
Q14240-2	EIF4A2	-0.214	eukaryotic translation initiation factor 4A2
P38919	EIF4A3	0.191	eukaryotic translation initiation factor 4A3
P23588	EIF4B	-0.299	eukaryotic translation initiation factor 4B
P06730-2	EIF4E	-0.178	eukaryotic translation initiation factor 4E
O60573	EIF4E2	-0.235	eukaryotic translation initiation factor 4E family member 2
Q13541	EIF4EBP1	-0.288	eukaryotic translation initiation factor 4E binding protein 1
Q04637-9	EIF4G1	-0.308	eukaryotic translation initiation factor 4 gamma 1
O43432-3	EIF4G3	-0.403	eukaryotic translation initiation factor 4 gamma 3
Q15056-1	EIF4H	-0.296	eukaryotic translation initiation factor 4H
P55010	EIF5	0.152	eukaryotic translation initiation factor 5
P63241-2	EIF5A	-0.198	eukaryotic translation initiation factor 5A
Q9BQ52	ELAC2	-0.108	elaC ribonuclease Z 2
P32519	ELF1	-0.173	E74 like ETS transcription factor 1
P55199	ELL	0.507	elongation factor for RNA polymerase II
O00472	ELL2	0.224	elongation factor for RNA polymerase II 2
Q14241	ELOA	0.496	elongin A
Q15370-2	ELOB	-0.249	elongin B
O95163	ELP1	-0.274	elongator complex protein 1
Q6IA86-6	ELP2	-0.197	elongator acetyltransferase complex subunit 2
Q9H9T3	ELP3	-0.366	elongator acetyltransferase complex subunit 3
Q15006	EMC2	0.214	ER membrane protein complex subunit 2
Q9P0I2	EMC3	0.212	ER membrane protein complex subunit 3
Q9NPA0	EMC7	0.134	ER membrane protein complex subunit 7
O43402	EMC8	0.187	ER membrane protein complex subunit 8
P50402	EMD	0.167	emerin
Q92979	EMG1	-0.136	EMG1 N1-specific pseudouridine methyltransferase
Q9HC35	EML4	-0.165	EMAP like 4
Q8N8S7	ENAH	-0.224	ENAH actin regulator
O14682	ENC1	0.674	ectodermal-neural cortex 1
O94919	ENDOD1	0.191	endonuclease domain containing 1
Q14249	ENDOG	-0.093	endonuclease G
P06733-1	ENO1	-0.259	enolase 1

P09104	ENO2	-0.153	enolase 2
P13929-1	ENO3	-0.486	enolase 3
Q9UHY7	ENOPH1	-0.362	enolase-phosphatase 1
Q7L5Y1-5	ENOSF1	-0.202	enolase superfamily member 1
P22413	ENPP1	-0.23	ectonucleotide pyrophosphatase/phosphodiesterase 1
O43768-4	ENSA	-0.527	endosulfine alpha
Q5NDL2	EOGT	-0.132	EGF domain specific O-linked N-acetylglucosamine transferase
O43491-4	EPB41L2	-0.244	erythrocyte membrane protein band 4.1 like 2
P16422	EPCAM	-0.177	epithelial cell adhesion molecule
P29317	EPHA2	0.832	EPH receptor A2
P54760	EPHB4	0.155	EPH receptor B4
P07099	EPHX1	0.445	epoxide hydrolase 1
Q7L775	EPM2AIP1	0.198	EPM2A interacting protein 1
O95208	EPN2	-0.569	epsin 2
P42566	EPS15	-0.236	epidermal growth factor receptor pathway substrate 15
O75616	ERAL1	0.303	Era like 12S mitochondrial rRNA chaperone 1
Q9NZ08-2	ERAP1	-0.116	endoplasmic reticulum aminopeptidase 1
P04626	ERBB2	-0.268	erb-b2 receptor tyrosine kinase 2
P21860	ERBB3	-0.316	erb-b2 receptor tyrosine kinase 3
Q8IUD2-1	ERC1	-0.353	ELKS/RAB6-interacting/CAST family member 1
P18074-1	ERCC2	-0.084	ERCC excision repair 2, TFIIH core complex helicase subunit
P19447	ERCC3	0.516	ERCC excision repair 3, TFIIH core complex helicase subunit
Q969X5	ERGIC1	0.102	endoplasmic reticulum-golgi intermediate compartment 1
Q96RQ1	ERGIC2	0.124	ERGIC and golgi 2
Q9Y282-3	ERGIC3	0.325	ERGIC and golgi 3
P84090	ERH	0.25	ERH mRNA splicing and mitosis factor
O94905	ERLIN2	0.185	ER lipid raft associated 2
Q7Z2K6	ERMP1	0.14	endoplasmic reticulum metallopeptidase 1
P30040	ERP29	0.186	endoplasmic reticulum protein 29
Q96AP7	ESAM	0.313	endothelial cell adhesion molecule
P10768	ESD	-0.117	esterase D
B1AK53-1	ESPN	-0.733	espin
Q9H6T0	ESRP2	-0.14	epithelial splicing regulatory protein 2
Q96DF8	ESS2	-0.326	ess-2 splicing factor homolog
A0FGR8-2	ESYT2	0.176	extended synaptotagmin 2
P62495	ETF1	-0.381	eukaryotic translation termination factor 1
P13804-1	ETFA	0.205	electron transfer flavoprotein subunit alpha
P38117	ETFB	0.328	electron transfer flavoprotein subunit beta
Q01844-5	EWSR1	-0.244	EWS RNA binding protein 1
O60645	EXOC3	-0.339	exocyst complex component 3
Q9Y2D4	EXOC6B	-0.355	exocyst complex component 6B
Q9UPT5	EXOC7	-0.094	exocyst complex component 7
Q9Y2C4	EXOG	0.165	exo/endonuclease G
Q01780	EXOSC10	0.253	exosome component 10
Q9NQT5	EXOSC3	0.197	exosome component 3
Q96B26	EXOSC8	-0.301	exosome component 8
P00734	F2	-0.322	coagulation factor II, thrombin

P07148	FABP1	-0.848	fatty acid binding protein 1
O60427	FADS1	-0.096	fatty acid desaturase 1
O95864	FADS2	-0.378	fatty acid desaturase 2
Q9UNN5	FAF1	-0.539	Fas associated factor 1
Q96CS3	FAF2	0.262	Fas associated factor family member 2
P16930	FAH	-0.37	fumarylacetoacetate hydrolase
Q6P587-3	FAHD1	0.105	fumarylacetoacetate hydrolase domain containing 1
Q9H098-2	FAM107B	-0.114	family with sequence similarity 107 member B
Q8IWE2	FAM114A1	-0.284	family with sequence similarity 114 member A1
Q9NRY5	FAM114A2	-0.319	family with sequence similarity 114 member A2
Q9NZB2-6	FAM120A	-0.172	family with sequence similarity 120A
Q96E09	FAM122A	-0.325	family with sequence similarity 122A
Q96C01	FAM136A	-0.237	family with sequence similarity 136 member A
Q8N128-2	FAM177A1	0.214	family with sequence similarity 177 member A1
Q9GZU8	FAM192A	-0.139	family with sequence similarity 192 member A
Q9NSI2	FAM207A	-0.423	family with sequence similarity 207 member A
Q96ND0	FAM210A	0.593	family with sequence similarity 210 member A
Q96KR6	FAM210B	0.433	family with sequence similarity 210 member B
Q92520	FAM3C	0.15	family with sequence similarity 3 member C
Q9NUQ9	FAM49B	-0.128	family with sequence similarity 49 member B
Q9H4H8	FAM83D	0.297	family with sequence similarity 83 member D
Q52LJ0-2	FAM98B	0.212	family with sequence similarity 98 member B
Q9BXW9-1	FANCD2	-0.197	FA complementation group D2
Q9NVI1	FANCI	-0.261	FA complementation group I
Q9Y285	FARSA	-0.185	phenylalanyl-tRNA synthetase subunit alpha
Q9NSD9	FARSB	-0.246	phenylalanyl-tRNA synthetase subunit beta
P25445	FAS	0.699	Fas cell surface death receptor
P49327	FASN	-0.353	fatty acid synthase
Q9NYY8	FASTKD2	0.185	FAST kinase domains 2
Q7L8L6	FASTKD5	0.862	FAST kinase domains 5
P22087	FBL	0.238	fibrillarin
Q8WUP2-2	FBLIM1	0.332	filamin binding LIM protein 1
Q8N531-1	FBXL6	0.358	F-box and leucine rich repeat protein 6
Q8TB52	FBXO30	0.368	F-box protein 30
Q6PIJ6-1	FBXO38	0.233	F-box protein 38
O94868	FCHSD2	-0.431	FCH and double SH3 domains 2
P37268	FDFT1	-0.246	farnesyl-diphosphate farnesyltransferase 1
P14324	FDPS	-0.216	farnesyl diphosphate synthase
P22570-7	FDXR	0.472	ferredoxin reductase
P22830-2	FECH	0.415	ferrochelatase
P39748	FEN1	0.086	flap structure-specific endonuclease 1
P02671-1	FGA	-0.65	fibrinogen alpha chain
P02671-2	FGA	-0.695	fibrinogen alpha chain
P02675	FGB	-0.242	fibrinogen beta chain
O95684	FGFR1OP	-0.248	FGFR1 oncogene partner
P22455-1	FGFR4	-0.606	fibroblast growth factor receptor 4
P02679	FGG	-0.429	fibrinogen gamma chain

Q13643	FHL3	0.709	four and a half LIM domains 3
Q9Y613	FHOD1	-0.236	formin homology 2 domain containing 1
O43427	FIBP	-0.404	FGF1 intracellular binding protein
Q9NWM8	FKBP14	-0.432	FKBP prolyl isomerase 14
P62942	FKBP1A	-0.33	FKBP prolyl isomerase 1A
Q00688	FKBP3	-0.161	FKBP prolyl isomerase 3
Q02790	FKBP4	0.201	FKBP prolyl isomerase 4
Q14318-2	FKBP8	0.118	FKBP prolyl isomerase 8
O95302-3	FKBP9	0.147	FKBP prolyl isomerase 9
P21333	FLNA	-0.164	filamin A
O75369-8	FLNB	-0.313	filamin B
Q9Y5Y0	FLVCR1	-0.403	feline leukemia virus subgroup C cellular receptor 1
Q96CP2	FLYWCH2	-0.36	FLYWCH family member 2
Q96PY5-3	FMNL2	-0.136	formin like 2
P02751-15	FN1	-0.635	fibronectin 1
Q9H479	FN3K	-0.129	fructosamine 3 kinase
Q96RU3-1	FNBP1	-0.564	formin binding protein 1
Q5T0N5-1	FNBP1L	-0.188	formin binding protein 1 like
Q8N3X1-2	FNBP4	-0.221	formin binding protein 4
Q9Y2H6	FNDC3A	0.242	fibronectin type III domain containing 3A
Q53EP0	FNDC3B	-0.504	fibronectin type III domain containing 3B
P49354	FNTA	-0.235	farnesyltransferase, CAAX box, alpha
Q5VW36	FOCAD	-0.32	focadhesin
P15407	FOSL1	1.38	FOS like 1, AP-1 transcription factor subunit
P85037	FOXK1	0.226	forkhead box K1
Q8IWF2	FOXRED2	-0.27	FAD dependent oxidoreductase domain containing 2
Q86XX4-2	FRAS1	-1.124	Fraser extracellular matrix complex subunit 1
Q14331	FRG1	0.187	FSHD region gene 1
Q9BZ67	FRMD8	0.215	FERM domain containing 8
O95954-1	FTCD	-0.285	formimidoyltransferase cyclodeaminase
P02794	FTH1	0.377	ferritin heavy chain 1
P02792	FTL	0.761	ferritin light chain
Q9C0B1-1	FTO	-0.463	FTO alpha-ketoglutarate dependent dioxygenase
Q96AE4	FUBP1	-0.217	far upstream element binding protein 1
Q9BTY2	FUCA2	0.092	alpha-L-fucosidase 2
P09958	FURIN	-0.4	furin, paired basic amino acid cleaving enzyme
P51114	FXR1	0.136	FMR1 autosomal homolog 1
P51116	FXR2	0.22	FMR1 autosomal homolog 2
Q9BQS8-4	FYCO1	-0.297	FYVE and coiled-coil domain containing 1
Q13283	G3BP1	-0.189	G3BP stress granule assembly factor 1
P11413-2	G6PD	-0.114	glucose-6-phosphate dehydrogenase
O95166	GABARAP	-0.254	GABA type A receptor-associated protein
P60520	GABARAPL2	0.181	GABA type A receptor associated protein like 2
Q06546	GABPA	-0.198	GA binding protein transcription factor subunit alpha
Q06547	GABPB1	0.247	GA binding protein transcription factor subunit beta 1
O14976	GAK	-0.177	cyclin G associated kinase
Q14376	GALE	-0.45	UDP-galactose-4-epimerase

P51570-2	GALK1	-0.147	galactokinase 1
Q96C23	GALM	-0.479	galactose mutarotase
P34059	GALNS	-0.134	galactosamine (N-acetyl)-6-sulfatase
Q10472	GALNT1	0.167	polypeptide N-acetylgalactosaminyltransferase 1
P07902	GALT	-0.206	galactose-1-phosphate uridylyltransferase
Q14353	GAMT	-0.258	guanidinoacetate N-methyltransferase
P04406	GAPDH	-0.187	glyceraldehyde-3-phosphate dehydrogenase
Q9NY12	GAR1	0.274	GAR1 ribonucleoprotein
P22102	GART	-0.167	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, ph
O43903	GAS2	-0.215	growth arrest specific 2
Q86YP4-3	GATAD2A	0.102	GATA zinc finger domain containing 2A
P04062	GBA	0.145	glucosylceramidase beta
Q04446	GBE1	-0.171	1,4-alpha-glucan branching enzyme 1
Q92538	GBF1	-0.189	golgi brefeldin A resistant guanine nucleotide exchange factor 1
P28676	GCA	-0.352	grancalcin
Q96CN9	GCC1	0.324	GRIP and coiled-coil domain containing 1
Q8IWJ2	GCC2	0.131	GRIP and coiled-coil domain containing 2
Q92947-1	GCDH	0.183	glutaryl-CoA dehydrogenase
P16383	GCFC2	-0.104	GC-rich sequence DNA-binding factor 2
P30793-1	GCH1	0.365	GTP cyclohydrolase 1
P48506	GCLC	0.189	glutamate-cysteine ligase catalytic subunit
P48507	GCLM	1.098	glutamate-cysteine ligase modifier subunit
Q92616	GCN1	-0.167	GCN1 activator of EIF2AK4
Q8TB36	GDAP1	0.582	ganglioside induced differentiation associated protein 1
Q9NZC3	GDE1	0.326	glycerophosphodiester phosphodiesterase 1
Q99988	GDF15	1.155	growth differentiation factor 15
P31150	GDI1	0.167	GDP dissociation inhibitor 1
P50395-1	GDI2	-0.26	GDP dissociation inhibitor 2
Q8TEQ6	GEMIN5	-0.082	gem nuclear organelle associated protein 5
Q7L5D6	GET4	-0.294	guided entry of tail-anchored proteins factor 4
Q969S9	GFM2	0.185	G elongation factor mitochondrial 2
Q06210	GFPT1	-0.173	glutamine--fructose-6-phosphate transaminase 1
Q9UJY5-6	GGA1	-0.353	golgi associated, gamma adaptin ear containing, ARF binding protein 1
Q9NZ52	GGA3	-0.107	golgi associated, gamma adaptin ear containing, ARF binding protein 3
O75223	GGCT	-0.333	gamma-glutamylcyclotransferase
P19440	GGT1	-0.133	gamma-glutamyltransferase 1
Q9UJ14	GGT7	-0.257	gamma-glutamyltransferase 7
Q9H3K2	GHITM	0.369	growth hormone inducible transmembrane protein
Q6Y7W6-1	GIGYF2	-0.238	GRB10 interacting GYF protein 2
Q9BRX5	GINS3	-0.414	GINS complex subunit 3
O14908-1	GIPC1	-0.106	GIPC PDZ domain containing family member 1
Q8TF65	GIPC2	-0.109	GIPC PDZ domain containing family member 2
Q9Y2X7-3	GIT1	0.167	GIT ArfGAP 1
Q14161-1	GIT2	-0.166	GIT ArfGAP 2
P08034	GJB1	-0.803	gap junction protein beta 1
P06280	GLA	0.604	galactosidase alpha
P23378	GLDC	0.133	glycine decarboxylase

Q53GS7-1	GLE1	0.135	GLE1 RNA export mediator
Q92896-2	GLG1	-0.476	golgi glycoprotein 1
Q92990	GLMN	-0.189	glomulin, FKBP associated protein
Q9HC38	GLOD4	-0.219	glyoxalase domain containing 4
O76003	GLRX3	-0.2	glutaredoxin 3
O94925	GLS	1.065	glutaminase
O94925-3	GLS	0.451	glutaminase
Q68CQ7-1	GLT8D1	-0.139	glycosyltransferase 8 domain containing 1
P00367	GLUD1	0.267	glutamate dehydrogenase 1
Q49A26	GLYR1	0.264	glyoxylate reductase 1 homolog
O60547	GMDS	-0.309	GDP-mannose 4,6-dehydratase
Q9UKD1	GMEB2	0.239	glucocorticoid modulatory element binding protein 2
P60983	GMFB	-0.183	glia maturation factor beta
O75496	GMNN	0.18	geminin DNA replication inhibitor
Q96IJ6	GMPPA	-0.209	GDP-mannose pyrophosphorylase A
Q9Y5P6-2	GMPPB	-0.52	GDP-mannose pyrophosphorylase B
Q9P2T1	GMPR2	-0.19	guanosine monophosphate reductase 2
P49915	GMPS	-0.201	guanine monophosphate synthase
P29992	GNA11	0.14	G protein subunit alpha 11
Q14344	GNA13	0.464	G protein subunit alpha 13
P04899	GNAI2	0.275	G protein subunit alpha i2
P08754	GNAI3	0.187	G protein subunit alpha i3
P50148	GNAQ	-0.336	G protein subunit alpha q
P62873	GNB1	0.134	G protein subunit beta 1
P36915	GNL1	0.156	G protein nucleolar 1 (putative)
Q9BVP2	GNL3	-0.552	G protein nucleolar 3
P46926	GNPDA1	-0.093	glucosamine-6-phosphate deaminase 1
Q96EK6	GNPNAT1	-0.186	glucosamine-phosphate N-acetyltransferase 1
Q08379	GOLGA2	0.136	golgin A2
Q08378	GOLGA3	-0.21	golgin A3
Q13439-5	GOLGA4	-0.148	golgin A4
Q7Z5G4	GOLGA7	0.236	golgin A7
Q9H4A6	GOLPH3	-0.203	golgi phosphoprotein 3
Q9H4A5	GOLPH3L	-0.125	golgi phosphoprotein 3 like
Q9Y3E0	GOLT1B	0.481	golgi transport 1B
Q9H8Y8	GORASP2	-0.266	golgi reassembly stacking protein 2
O14653-2	GOSR2	0.254	golgi SNAP receptor complex member 2
P00505	GOT2	0.402	glutamic-oxaloacetic transaminase 2
Q8IXQ4	GPALPP1	-0.131	GPALPP motifs containing 1
Q53EU6	GPAT3	0.424	glycerol-3-phosphate acyltransferase 3
Q5T3I0-3	GPATCH4	-0.334	G-patch domain containing 4
Q9UKJ3-1	GPATCH8	-0.161	G-patch domain containing 8
P35052	GPC1	0.254	glypican 1
P51654-1	GPC3	-0.386	glypican 3
Q9Y625	GPC6	-0.582	glypican 6
P21695	GPD1	-0.384	glycerol-3-phosphate dehydrogenase 1
Q9NQX3-2	GPHN	-0.531	gephyrin

P06744	GPI	-0.22	glucose-6-phosphate isomerase
Q9NQ84-2	GPRC5C	0.15	G protein-coupled receptor class C group 5 member C
P18283	GPX2	-0.354	glutathione peroxidase 2
P36969	GPX4	-0.62	glutathione peroxidase 4
Q14451-3	GRB7	-0.106	growth factor receptor bound protein 7
Q9UBQ7	GRHPR	-0.14	glyoxylate and hydroxypyruvate reductase
P25098	GRK2	-0.121	G protein-coupled receptor kinase 2
Q9HAV7	GRPEL1	0.227	GrpE like 1, mitochondrial
Q12849	GRSF1	0.111	G-rich RNA sequence binding factor 1
Q14687	GSE1	-0.181	Gse1 coiled-coil protein
P00390	GSR	-0.092	glutathione-disulfide reductase
P48637	GSS	-0.216	glutathione synthetase
P08263	GSTA1	-0.468	glutathione S-transferase alpha 1
Q9Y2Q3-1	GSTK1	0.246	glutathione S-transferase kappa 1
P21266	GSTM3	-0.208	glutathione S-transferase mu 3
P78417	GSTO1	-0.414	glutathione S-transferase omega 1
P30711	GSTT1	-0.215	glutathione S-transferase theta 1
Q00403	GTF2B	0.415	general transcription factor IIB
P35269	GTF2F1	-0.259	general transcription factor IIF subunit 1
P13984	GTF2F2	-0.173	general transcription factor IIF subunit 2
Q13889	GTF2H3	0.487	general transcription factor IIH subunit 3
Q92759	GTF2H4	0.15	general transcription factor IIH subunit 4
P78347	GTF2I	-0.186	general transcription factor IIi
Q12789	GTF3C1	0.093	general transcription factor IIIC subunit 1
Q9UKN8	GTF3C4	0.091	general transcription factor IIIC subunit 4
Q9Y5Q8-1	GTF3C5	0.26	general transcription factor IIIC subunit 5
A4D1E9	GTPBP10	0.306	GTP binding protein 10
Q969Y2-2	GTPBP3	0.134	GTP binding protein 3, mitochondrial
Q9NYZ3	GTSE1	0.388	G2 and S-phase expressed 1
Q8N442	GUF1	0.281	GUF1 homolog, GTPase
Q4G148	GXYLT1	0.249	glucoside xylosyltransferase 1
Q9H116	GZF1	0.227	GDNF inducible zinc finger protein 1
P07305	H1-0	1.066	H1.0 linker histone
P16401	H1-5	0.876	H1.5 linker histone, cluster member
P16104	H2AX	0.377	H2A.X variant histone
P0C0S5	H2AZ1	0.771	H2A.Z variant histone 1
O95479	H6PD	-0.141	hexose-6-phosphate dehydrogenase/glucose 1-dehydrogenase
P46952	HAAO	-0.208	3-hydroxyanthranilate 3,4-dioxygenase
Q5JVS0	HABP4	-0.292	hyaluronan binding protein 4
Q6Y1H2	HACD2	0.395	3-hydroxyacyl-CoA dehydratase 2
Q9P035	HACD3	0.159	3-hydroxyacyl-CoA dehydratase 3
Q9UJ83	HACL1	0.135	2-hydroxyacyl-CoA lyase 1
P40939	HADHA	0.333	hydroxyacyl-CoA dehydrogenase trifunctional multienzyme complex subunit alpha
P55084	HADHB	0.319	hydroxyacyl-CoA dehydrogenase trifunctional multienzyme complex subunit beta
P12081	HARS1	-0.237	histidyl-tRNA synthetase 1
O14929	HAT1	-0.08	histone acetyltransferase 1
O94927	HAUS5	-0.202	HAUS augmin like complex subunit 5

Q9Y450	HBS1L	-0.162	HBS1 like translational GTPase
P53701	HCCS	0.261	holocytochrome c synthase
Q92769	HDAC2	0.122	histone deacetylase 2
Q7Z4H3	HDDC2	-0.206	HD domain containing 2
Q8N4P3	HDDC3	-0.249	HD domain containing 3
P51858	HDGF	-0.32	heparin binding growth factor
Q9H0R4	HDHD2	-0.163	haloacid dehalogenase like hydrolase domain containing 2
Q00341	HDLBP	-0.555	high density lipoprotein binding protein
Q9H583	HEATR1	0.202	HEAT repeat containing 1
Q7Z4Q2	HEATR3	-0.376	HEAT repeat containing 3
Q86XA9	HEATR5A	-0.35	HEAT repeat containing 5A
Q9P2D3	HEATR5B	-0.306	HEAT repeat containing 5B
Q9Y5Z4	HEBP2	-0.387	heme binding protein 2
Q9BYK8	HELZ2	0.264	helicase with zinc finger 2
Q15011-1	HERPUD1	-0.686	homocysteine inducible ER protein with ubiquitin like domain 1
P07686	HEXB	0.16	hexosaminidase subunit beta
Q96MH2	HEXIM2	-0.25	HEXIM P-TEFb complex subunit 2
Q93099	HGD	-0.177	homogentisate 1,2-dioxygenase
Q9BTY7	HGH1	-0.146	HGH1 homolog
P31937	HIBADH	0.275	3-hydroxyisobutyrate dehydrogenase
Q6NVY1	HIBCH	0.155	3-hydroxyisobutyryl-CoA hydrolase
Q9NWT6	HIF1AN	-0.281	hypoxia inducible factor 1 subunit alpha inhibitor
P49773	HINT1	-0.096	histidine triad nucleotide binding protein 1
Q9BX68	HINT2	0.42	histidine triad nucleotide binding protein 2
Q9NQE9	HINT3	-0.154	histidine triad nucleotide binding protein 3
Q9BW71-1	HIRIP3	-0.192	HIRA interacting protein 3
P52789	HK2	-0.147	hexokinase 2
Q2TB90-1	HKDC1	0.24	hexokinase domain containing 1
P01892	HLA-A	0.356	major histocompatibility complex, class I, A
P05534	HLA-A	0.389	major histocompatibility complex, class I, A
Q14527	HLTF	-0.356	helicase like transcription factor
P08397	HMBS	-0.298	hydroxymethylbilane synthase
Q96FZ2	HMCES	-0.221	5-hydroxymethylcytosine binding, ES cell specific
P17096-1	HMGA1	0.419	high mobility group AT-hook 1
P52926-1	HMGA2	0.401	high mobility group AT-hook 2
P09429	HMGB1	0.199	high mobility group box 1
P35914	HMGCL	0.218	3-hydroxy-3-methylglutaryl-CoA lyase
Q01581	HMGCS1	-0.494	3-hydroxy-3-methylglutaryl-CoA synthase 1
P05114	HMGN1	0.317	high mobility group nucleosome binding domain 1
P05204	HMGN2	0.991	high mobility group nucleosomal binding domain 2
Q9UGU5	HMGXB4	0.234	HMG-box containing 4
O75330-3	HMMR	0.437	hyaluronan mediated motility receptor
P09601	HMOX1	1.422	heme oxygenase 1
P30519	HMOX2	0.159	heme oxygenase 2
P20823-7	HNF1A	-0.236	HNF1 homeobox A
P41235-4	HNF4A	-0.58	hepatocyte nuclear factor 4 alpha
P50135	HNMT	-0.327	histamine N-methyltransferase

Q13151	HNRNPA0	0.226	heterogeneous nuclear ribonucleoprotein A0
Q14103-3	HNRNPD	-0.184	heterogeneous nuclear ribonucleoprotein D
O14979-1	HNRNPDL	-0.227	heterogeneous nuclear ribonucleoprotein D like
P55795	HNRNPH2	0.181	heterogeneous nuclear ribonucleoprotein H2
P14866	HNRNPL	0.16	heterogeneous nuclear ribonucleoprotein L
Q00839	HNRNPU	0.235	heterogeneous nuclear ribonucleoprotein U
Q9NSC5	HOMER3	-0.191	homer scaffold protein 3
Q9UJC3	HOOK1	-0.228	hook microtubule tethering protein 1
P00738	HP	-0.722	haptoglobin
Q5SSJ5	HP1BP3	0.474	heterochromatin protein 1 binding protein 3
P37235	HPCAL1	-0.325	hippocalcin like 1
P32754-1	HPD	-0.314	4-hydroxyphenylpyruvate dioxygenase
Q9NWY4	HPF1	-0.223	histone PARylation factor 1
P00492	HPRT1	-0.144	hypoxanthine phosphoribosyltransferase 1
O75506	HSBP1	-0.346	heat shock factor binding protein 1
Q8IWL3	HSCB	0.202	HscB mitochondrial iron-sulfur cluster cochaperone
Q99714-1	HSD17B10	0.18	hydroxysteroid 17-beta dehydrogenase 10
Q53GQ0	HSD17B12	0.158	hydroxysteroid 17-beta dehydrogenase 12
P51659-1	HSD17B4	0.232	hydroxysteroid 17-beta dehydrogenase 4
Q3SXM5	HSDL1	0.268	hydroxysteroid dehydrogenase like 1
Q6YN16	HSDL2	0.177	hydroxysteroid dehydrogenase like 2
P07900	HSP90AA1	0.197	heat shock protein 90 alpha family class A member 1
P08238	HSP90AB1	0.133	heat shock protein 90 alpha family class B member 1
P14625	HSP90B1	0.27	heat shock protein 90 beta family member 1
P48723	HSPA13	0.184	heat shock protein family A (Hsp70) member 13
Q0VDF9	HSPA14	-0.197	heat shock protein family A (Hsp70) member 14
P0DMV9	HSPA1A/HSPA1B	1.605	heat shock protein family A (Hsp70) member 1A
O95757	HSPA4L	0.137	heat shock protein family A (Hsp70) member 4 like
P17066	HSPA6	2.196	heat shock protein family A (Hsp70) member 6
P38646	HSPA9	0.294	heat shock protein family A (Hsp70) member 9
P04792	HSPB1	0.996	heat shock protein family B (small) member 1
Q9NZL4-3	HSPBP1	-0.252	HSPA (Hsp70) binding protein 1
P10809	HSPD1	0.364	heat shock protein family D (Hsp60) member 1
P61604	HSPE1	0.572	heat shock protein family E (Hsp10) member 1
Q92598	HSPH1	0.838	heat shock protein family H (Hsp110) member 1
P42858	HTT	-0.355	huntingtin
Q7Z6Z7	HUWE1	-0.246	HECT, UBA and WWE domain containing E3 ubiquitin protein ligase 1
Q9NX55-2	HYPK	-0.168	huntingtin interacting protein K
Q2TAA2	IAH1	-0.136	isoamyl acetate hydrolyzing esterase 1 (putative)
P41252	IARS1	-0.125	isoleucyl-tRNA synthetase 1
Q9NSE4	IARS2	0.349	isoleucyl-tRNA synthetase 2, mitochondrial
Q5T440	IBA57	0.341	iron-sulfur cluster assembly factor IBA57
Q9P2D0	IBTK	-0.227	inhibitor of Bruton tyrosine kinase
P14735	IDE	-0.192	insulin degrading enzyme
O75874	IDH1	-0.332	isocitrate dehydrogenase (NADP(+)) 1
P48735	IDH2	0.275	isocitrate dehydrogenase (NADP(+)) 2
P50213	IDH3A	0.202	isocitrate dehydrogenase (NAD(+)) 3 catalytic subunit alpha

O43837	IDH3B	0.232	isocitrate dehydrogenase (NAD(+)) 3 non-catalytic subunit beta
P51553-1	IDH3G	0.282	isocitrate dehydrogenase (NAD(+)) 3 non-catalytic subunit gamma
Q13907	IDI1	-0.17	isopentenyl-diphosphate delta isomerase 1
Q9BYX4-1	IFIH1	-0.344	interferon induced with helicase C domain 1
O00425	IGF2BP3	-0.098	insulin like growth factor 2 mRNA binding protein 3
P11717	IGF2R	-0.342	insulin like growth factor 2 receptor
P08833	IGFBP1	0.545	insulin like growth factor binding protein 1
Q8N6C5-4	IGSF1	-0.326	immunoglobulin superfamily member 1
Q13123	IK	0.171	IK cytokine
Q70UQ0	IKBIP	0.27	IKBKB interacting protein
Q70UQ0-4	IKBIP	0.365	IKBKB interacting protein
Q9Y6K9-2	IKBKG	0.139	inhibitor of nuclear factor kappa B kinase regulatory subunit gamma
Q14116	IL18	0.218	interleukin 18
Q9NPH3	IL1RAP	-0.207	interleukin 1 receptor accessory protein
P40189	IL6ST	-0.307	interleukin 6 signal transducer
Q13418	ILK	0.122	integrin linked kinase
Q9H0C8	ILKAP	-0.19	ILK associated serine/threonine phosphatase
Q9NV31	IMP3	0.182	IMP U3 small nucleolar ribonucleoprotein 3
Q96G21	IMP4	0.282	IMP U3 small nucleolar ribonucleoprotein 4
Q9NX62	IMPAD1	0.143	inositol monophosphatase domain containing 1
Q9NQS7	INCENP	0.477	inner centromere protein
Q27J81	INF2	-0.204	inverted formin, FH2 and WH2 domain containing
Q9UK53-1	ING1	0.307	inhibitor of growth family member 1
Q92835	INPP5D	-0.343	inositol polyphosphate-5-phosphatase D
P06213	INSR	-0.346	insulin receptor
Q9NVM9	INTS13	-0.189	integrator complex subunit 13
Q96SY0	INTS14	-0.195	integrator complex subunit 14
Q96HW7	INTS4	-0.092	integrator complex subunit 4
Q9NV88-1	INTS9	-0.121	integrator complex subunit 9
Q9UI26-2	IPO11	-0.272	importin 11
Q8TEX9-2	IPO4	-0.445	importin 4
O00410-3	IPO5	-0.466	importin 5
O95373	IPO7	-0.356	importin 7
Q96P70	IPO9	-0.299	importin 9
P46940	IQGAP1	-0.095	IQ motif containing GTPase activating protein 1
Q13576-1	IQGAP2	-0.253	IQ motif containing GTPase activating protein 2
Q6DN90	IQSEC1	-0.291	IQ motif and Sec7 domain ArfGEF 1
P48200	IREB2	-0.149	iron responsive element binding protein 2
Q9H1B7	IRF2BPL	0.164	interferon regulatory factor 2 binding protein like
Q14653	IRF3	-0.184	interferon regulatory factor 3
Q8WZA9	IRGQ	-0.151	immunity related GTPase Q
Q86U28	ISCA2	-0.228	iron-sulfur cluster assembly 2
Q9H1K1	ISCU	0.337	iron-sulfur cluster assembly enzyme
P05161	ISG15	-0.108	ISG15 ubiquitin like modifier
Q9H9L3	ISG20L2	-0.105	interferon stimulated exonuclease gene 20 like 2
Q96CN7	ISOC1	-0.127	isochorismatase domain containing 1
Q96AB3-2	ISOC2	0.198	isochorismatase domain containing 2

P53990-1	IST1	0.104	IST1 factor associated with ESCRT-III
Q9ULR0-1	ISY1	0.205	ISY1 splicing factor homolog
P56199	ITGA1	-0.131	integrin subunit alpha 1
P23229-1	ITGA6	-0.336	integrin subunit alpha 6
P23229-6	ITGA6	-0.426	integrin subunit alpha 6
P19823	ITIH2	-0.103	inter-alpha-trypsin inhibitor heavy chain 2
Q9NQX7	ITM2C	-0.166	integral membrane protein 2C
Q9BY32	ITPA	-0.283	inosine triphosphatase
P28290	ITPRID2	0.159	ITPR interacting domain containing 2
P26440	IVD	0.202	isovaleryl-CoA dehydrogenase
Q96ST2	IWS1	-0.209	interacts with SUPT6H, CTD assembly factor 1
Q6IE81-1	JADE1	-0.184	jade family PHD finger 1
P78504	JAG1	0.114	jagged canonical Notch ligand 1
P23458	JAK1	-0.342	Janus kinase 1
Q9UK76	JPT1	-0.184	Jupiter microtubule associated homolog 1
Q9UK76-2	JPT1	-0.353	Jupiter microtubule associated homolog 1
P17275	JUNB	0.907	JunB proto-oncogene, AP-1 transcription factor subunit
P14923	JUP	0.081	junction plakoglobin
Q63ZY3-2	KANK2	-0.353	KN motif and ankyrin repeat domains 2
Q15046-2	KARS1	-0.106	lysyl-tRNA synthetase 1
Q9H7Z6-2	KAT8	-0.175	lysine acetyltransferase 8
Q86V97	KBTBD6	0.195	kelch repeat and BTB domain containing 6
Q9P0J7	KCMF1	0.195	potassium channel modulatory factor 1
Q9Y597	KCTD3	-0.421	potassium channel tetramerization domain containing 3
Q9NXV2	KCTD5	0.349	potassium channel tetramerization domain containing 5
Q7L273	KCTD9	0.351	potassium channel tetramerization domain containing 9
Q9Y2K7	KDM2A	0.379	lysine demethylase 2A
Q9Y4C1	KDM3A	0.703	lysine demethylase 3A
Q7LBC6-1	KDM3B	-0.138	lysine demethylase 3B
O75164	KDM4A	-0.309	lysine demethylase 4A
Q14145	KEAP1	0.174	kelch like ECH associated protein 1
Q7Z7F0-1	KHDC4	-0.214	KH domain containing 4, pre-mRNA splicing factor
P50053-2	KHK	-0.445	ketohexokinase
Q5T5P2-1	KIAA1217	-0.183	KIAA1217
Q9BY89-1	KIAA1671	-0.313	KIAA1671
Q9ULH0-1	KIDINS220	-0.249	kinase D interacting substrate 220
Q9NQT8	KIF13B	-0.307	kinesin family member 13B
Q9NS87	KIF15	-0.205	kinesin family member 15
Q96L93-2	KIF16B	-0.296	kinesin family member 16B
O60333-4	KIF1B	-0.289	kinesin family member 1B
O43896	KIF1C	-0.168	kinesin family member 1C
O95235	KIF20A	0.264	kinesin family member 20A
Q96Q89-2	KIF20B	0.297	kinesin family member 20B
Q14807	KIF22	0.258	kinesin family member 22
Q02241-1	KIF23	0.175	kinesin family member 23
O00139-2	KIF2A	0.279	kinesin family member 2A
Q99661	KIF2C	0.306	kinesin family member 2C

O95239-1	KIF4A	-0.11	kinesin family member 4A
P33176	KIF5B	-0.144	kinesin family member 5B
Q92845	KIFAP3	-0.31	kinesin associated protein 3
Q9BW19	KIFC1	0.201	kinesin family member C1
Q86Z14	KLB	-0.392	klotho beta
Q9NSK0-3	KLC4	-0.248	kinesin light chain 4
Q9BXK1	KLF16	-0.213	Kruppel like factor 16
Q9NVR0	KLHL11	0.359	kelch like family member 11
Q1ED39	KNOP1	0.192	lysine rich nucleolar protein 1
P50748	KNTC1	-0.216	kinetochore associated 1
P52292	KPNA2	0.223	karyopherin subunit alpha 2
O00505	KPNA3	-0.174	karyopherin subunit alpha 3
Q14974	KPNB1	-0.336	karyopherin subunit beta 1
Q8N9T8	KRI1	0.144	KRI1 homolog
Q13601	KRR1	0.248	KRR1 small subunit processome component homolog
P05783	KRT18	0.181	keratin 18
P08727	KRT19	0.406	keratin 19
P05787-2	KRT8	0.202	keratin 8
Q86UP2	KTN1	0.129	kinectin 1
Q16719	KYNU	-0.088	kynureninase
Q9H9P8-1	L2HGDH	0.27	L-2-hydroxyglutarate dehydrogenase
P83111-1	LACTB	0.408	lactamase beta
O15230	LAMA5	-0.52	laminin subunit alpha 5
P55268	LAMB2	-0.381	laminin subunit beta 2
P11047	LAMC1	-0.139	laminin subunit gamma 1
P13473-3	LAMP2	-0.313	lysosomal associated membrane protein 2
O43813	LANCL1	-0.453	LanC like 1
Q6PKG0-1	LARP1	-0.146	La ribonucleoprotein domain family member 1
Q659C4	LARP1B	-0.324	La ribonucleoprotein domain family member 1B
Q71RC2-4	LARP4	0.108	La ribonucleoprotein domain family member 4
Q92615	LARP4B	0.134	La ribonucleoprotein domain family member 4B
Q4G0J3-3	LARP7	-0.148	La ribonucleoprotein domain family member 7
Q15031	LARS2	0.326	leucyl-tRNA synthetase 2, mitochondrial
Q14847	LASP1	-0.094	LIM and SH3 protein 1
Q14739	LBR	0.403	lamin B receptor
Q96JN0-3	LCOR	0.553	ligand dependent nuclear receptor corepressor
Q9H6V9-2	LDAH	-0.267	lipid droplet associated hydrolase
P00338-3	LDHA	-0.466	lactate dehydrogenase A
P01130	LDLR	-0.232	low density lipoprotein receptor
Q9Y2U8	LEMD3	0.32	LEM domain containing 3
Q96PV6-2	LENG8	0.203	leukocyte receptor cluster member 8
O95202	LETM1	0.297	leucine zipper and EF-hand containing transmembrane protein 1
P09382	LGALS1	0.147	galectin 1
P17931	LGALS3	-0.182	galectin 3
O00214-2	LGALS8	0.129	galectin 8
Q99538	LGMN	0.287	legumain
P18858	LIG1	-0.268	DNA ligase 1

Q9NUP9	LIN7C	-0.134	lin-7 homolog C, crumbs cell polarity complex component
P38571	LIPA	-0.315	lipase A, lysosomal acid type
Q9BRT6	LLPH	-0.514	LLP homolog, long-term synaptic facilitation factor
Q9BU23-1	LMF2	0.176	lipase maturation factor 2
Q03252	LMNB2	0.163	lamin B2
Q9UIQ6	LNPEP	-0.208	leucyl and cystinyl aminopeptidase
P36776	LONP1	0.282	lon peptidase 1, mitochondrial
Q92604	LPGAT1	0.155	lysophosphatidylglycerol acyltransferase 1
Q93052	LPP	-0.281	LIM domain containing preferred translocation partner in lipoma
P50851-2	LRBA	-0.276	LPS responsive beige-like anchor protein
Q96II8-2	LRCH3	-0.315	leucine rich repeats and calponin homology domain containing 3
Q5T3J3	LRIF1	0.487	ligand dependent nuclear receptor interacting factor 1
Q7Z4F1	LRP10	0.859	LDL receptor related protein 10
P42704	LRPPRC	0.329	leucine rich pentatricopeptide repeat containing
Q9H9A6	LRRC40	-0.181	leucine rich repeat containing 40
Q15345-2	LRRC41	0.275	leucine rich repeat containing 41
Q8N1G4	LRRC47	-0.336	leucine rich repeat containing 47
Q96AG4	LRRC59	0.275	leucine rich repeat containing 59
Q8IWT6	LRRC8A	0.404	leucine rich repeat containing 8 VRAC subunit A
Q32MZ4-3	LRRFIP1	-0.101	LRR binding FLII interacting protein 1
Q9UFC0	LRWD1	0.133	leucine rich repeats and WD repeat domain containing 1
Q9H089	LSG1	0.284	large 60S subunit nuclear export GTPase 1
O15116	LSM1	-0.103	LSM1 homolog, mRNA degradation associated
Q9Y333	LSM2	-0.159	LSM2 homolog, U6 small nuclear RNA and mRNA degradation associated
Q9Y4Z0	LSM4	0.231	LSM4 homolog, U6 small nuclear RNA and mRNA degradation associated
Q9Y4Y9	LSM5	-0.18	LSM5 homolog, U6 small nuclear RNA and mRNA degradation associated
P48449	LSS	-0.152	lanosterol synthase
P09960-1	LTA4H	-0.34	leukotriene A4 hydrolase
O94822-3	LTN1	-0.166	listerin E3 ubiquitin protein ligase 1
Q96GA3	LTV1	-0.245	LTV1 ribosome biogenesis factor
Q9NQ29	LUC7L	0.231	LUC7 like
Q9Y383	LUC7L2	0.144	LUC7 like 2, pre-mRNA splicing factor
Q86V48	LUZP1	0.295	leucine zipper protein 1
O75608	LYPLA1	-0.124	lysophospholipase 1
O95372	LYPLA2	-0.109	lysophospholipase 2
Q9HD34	LYRM4	0.259	LYR motif containing 4
Q8WZA0-2	LZIC	-0.371	leucine zipper and CTNNBIP1 domain containing
Q9NQ48	LZTFL1	-0.472	leucine zipper transcription factor like 1
Q9UPN3	MACF1	-0.287	microtubule actin crosslinking factor 1
O75367	MACROH2A1	0.552	macroH2A.1 histone
Q9P0M6	MACROH2A2	0.292	macroH2A.2 histone
Q9Y6D9	MAD1L1	-0.233	mitotic arrest deficient 1 like 1
Q15013-3	MAD2L1BP	0.509	MAD2L1 binding protein
Q8WXG6-4	MADD	0.288	MAP kinase activating death domain
Q7L5Y9-1	MAEA	0.132	macrophage erythroblast attacher
Q9ULX9	MAFF	1.243	MAF bZIP transcription factor F
O15525	MAFG	1.206	MAF bZIP transcription factor G

Q9Y5V3-2	MAGED1	-0.277	MAGE family member D1
Q96QZ7	MAGI1	-0.37	membrane associated guanylate kinase, WW and PDZ domain containing 1
Q9H0U3	MAGT1	0.329	magnesium transporter 1
Q8WWC4	MAIP1	0.344	matrix AAA peptidase interacting protein 1
Q9BXY0	MAK16	0.254	MAK16 homolog
Q96EH3	MALSU1	-0.124	mitochondrial assembly of ribosomal large subunit 1
Q9UDY8	MALT1	-0.25	MALT1 paracaspase
P33908	MAN1A1	-0.284	mannosidase alpha class 1A member 1
O00754	MAN2B1	0.133	mannosidase alpha class 2B member 1
O00462	MANBA	-0.363	mannosidase beta
P55145	MANF	-0.208	mesencephalic astrocyte derived neurotrophic factor
P27338	MAOB	0.229	monoamine oxidase B
A6NCE7	MAP1LC3B2	1.462	microtubule associated protein 1 light chain 3 beta 2
Q66K74	MAP1S	0.25	microtubule associated protein 1S
Q02750	MAP2K1	-0.321	mitogen-activated protein kinase kinase 1
P36507	MAP2K2	-0.128	mitogen-activated protein kinase kinase 2
Q9NYL2	MAP3K20	-0.383	mitogen-activated protein kinase kinase kinase 20
Q9Y6R4-1	MAP3K4	-0.399	mitogen-activated protein kinase kinase kinase 4
P27816-1	MAP4	-0.417	microtubule associated protein 4
Q8IVH8	MAP4K3	-0.15	mitogen-activated protein kinase kinase kinase kinase 3
Q3KQU3	MAP7D1	0.31	MAP7 domain containing 1
P28482	MAPK1	-0.349	mitogen-activated protein kinase 1
P27361-1	MAPK3	-0.156	mitogen-activated protein kinase 3
Q16644	MAPKAPK3	-0.18	MAPK activated protein kinase 3
Q15691	MAPRE1	0.147	microtubule associated protein RP/EB family member 1
Q5VT66-2	MARC1	-0.109	mitochondrial amidoxime reducing component 1
P29966	MARCKS	-0.271	myristoylated alanine rich protein kinase C substrate
P49006	MARCKSL1	0.178	MARCKS like 1
Q96GW9	MARS2	0.352	methionyl-tRNA synthetase 2, mitochondrial
Q00266	MAT1A	-0.323	methionine adenosyltransferase 1A
Q9NZL9	MAT2B	-0.201	methionine adenosyltransferase 2B
Q7Z434	MAVS	-0.112	mitochondrial antiviral signaling protein
P61244	MAX	-0.15	MYC associated factor X
P56270-2	MAZ	0.213	MYC associated zinc finger protein
O95983-1	MBD3	0.093	methyl-CpG binding domain protein 3
Q96N66-1	MBOAT7	0.318	membrane bound O-acyltransferase domain containing 7
P43121	MCAM	0.361	melanoma cell adhesion molecule
Q8IVS2	MCAT	0.223	malonyl-CoA-acyl carrier protein transacylase
Q96RQ3	MCCC1	0.159	methylcrotonoyl-CoA carboxylase 1
Q9HCC0-1	MCCC2	0.182	methylcrotonoyl-CoA carboxylase 2
Q8NI22	MCFD2	-0.742	multiple coagulation factor deficiency 2
P49736	MCM2	-0.266	minichromosome maintenance complex component 2
P25205-2	MCM3	-0.179	minichromosome maintenance complex component 3
P33991	MCM4	-0.19	minichromosome maintenance complex component 4
P33992	MCM5	-0.203	minichromosome maintenance complex component 5
Q14566	MCM6	-0.234	minichromosome maintenance complex component 6
P33993-1	MCM7	-0.075	minichromosome maintenance complex component 7

Q9BTE3-1	MCMBP	-0.198	minichromosome maintenance complex binding protein
C9JLW8	MCRIP1	-0.285	MAPK regulated corepressor interacting protein 1
Q8NE86	MCU	0.352	mitochondrial calcium uniporter
P40925-3	MDH1	-0.256	malate dehydrogenase 1
P40926	MDH2	0.306	malate dehydrogenase 2
Q00987-11	MDM2	0.55	MDM2 proto-oncogene
P23368	ME2	0.342	malic enzyme 2
Q9HAF1-3	MEAF6	0.442	MYST/Esa1 associated factor 6
P51608-2	MECP2	0.3	methyl-CpG binding protein 2
Q93074-2	MED12	0.15	mediator complex subunit 12
O60244	MED14	0.239	mediator complex subunit 14
Q9NVC6	MED17	0.125	mediator complex subunit 17
Q71SY5-3	MED25	0.183	mediator complex subunit 25
Q96G25-2	MED8	-0.232	mediator complex subunit 8
Q9Y316-3	MEMO1	-0.26	mediator of cell motility 1
Q7L2J0-1	MEPCE	0.219	methylphosphate capping enzyme
Q14696	MESD	-0.249	mesoderm development LRP chaperone
P08581-1	MET	-0.417	MET proto-oncogene, receptor tyrosine kinase
P08581-2	MET	-0.472	MET proto-oncogene, receptor tyrosine kinase
P53582	METAP1	-0.136	methionyl aminopeptidase 1
Q9UBP6	METTL1	-0.231	methyltransferase like 1
Q86W50-1	METTL16	-0.192	methyltransferase like 16
Q9H7H0-3	METTL17	0.169	methyltransferase like 17
Q6P1Q9-1	METTL2B	-0.142	methyltransferase like 2B
Q86U44	METTL3	-0.179	methyltransferase like 3
Q9NRN9	METTL5	0.193	methyltransferase like 5
B3KW44	METTL8	0.307	methyltransferase like 8
Q8IWA4	MFN1	0.138	mitofusin 1
O95140	MFN2	0.247	mitofusin 2
Q8IWI9-4	MGA	-0.221	MAX dimerization protein MGA
P26572	MGAT1	0.307	mannosyl (alpha-1,3-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase
Q10469	MGAT2	0.16	mannosyl (alpha-1,6-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase
Q9UQ53-3	MGAT4B	0.425	alpha-1,3-mannosyl-glycoprotein 4-beta-N-acetylglucosaminyltransferase B
Q09328	MGAT5	-0.405	alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase
Q9BQP7	MGME1	0.363	mitochondrial genome maintenance exonuclease 1
P16455	MGMT	-0.241	O-6-methylguanine-DNA methyltransferase
O60291-2	MGRN1	-0.329	mahogunin ring finger 1
P10620	MGST1	0.286	microsomal glutathione S-transferase 1
Q99735	MGST2	0.09	microsomal glutathione S-transferase 2
Q7RTP6	MICAL3	-0.399	microtubule associated monooxygenase, calponin and LIM domain containing 3
Q8N3F8	MICALL1	0.216	MICAL like 1
Q9NPA3	MID1IP1	-0.397	MID1 interacting protein 1
L0R8F8	MIEF1	-0.148	mitochondrial elongation factor 1
Q9BRT3	MIEN1	-0.612	migration and invasion enhancer 1
Q8N108-12	MIER1	-0.302	MIER1 transcriptional regulator
Q9UNW1	MINPP1	-0.129	multiple inositol-polyphosphate phosphatase 1
Q9NXC5-1	MIOS	-0.242	meiosis regulator for oocyte development

Q99797	MIPEP	0.226	mitochondrial intermediate peptidase
Q8IVT2	MISP	0.205	mitotic spindle positioning
P46013	MKI67	0.401	marker of proliferation Ki-67
Q14165	MLEC	0.262	malectin
Q15773	MLF2	0.418	myeloid leukemia factor 2
P40692-1	MLH1	-0.154	mutL homolog 1
P51511	MMP15	-0.544	matrix metallopeptidase 15
Q96T76-8	MMS19	-0.266	MMS19 homolog, cytosolic iron-sulfur assembly component
P22033	MMUT	0.197	methylmalonyl-CoA mutase
P51948-1	MNAT1	0.172	MNAT1 component of CDK activating kinase
Q7L9L4-2	MOB1B	0.094	MOB kinase activator 1B
Q96EN8	MOCOS	-0.152	molybdenum cofactor sulfurase
O96007	MOCS2	-0.221	molybdenum cofactor synthesis 2
Q7Z3U7	MON2	-0.311	MON2 homolog, regulator of endosome-to-Golgi trafficking
Q9Y6X9	MORC2	0.135	MORC family CW-type zinc finger 2
Q15014	MORF4L2	-0.243	mortality factor 4 like 2
Q8NHP6	MOSPD2	0.101	motile sperm domain containing 2
Q9HCE1	MOV10	-0.133	Mov10 RISC complex RNA helicase
Q9Y5U8	MPC1	0.555	mitochondrial pyruvate carrier 1
O95563	MPC2	0.213	mitochondrial pyruvate carrier 2
Q99549-2	MPHOSPH8	0.302	M-phase phosphoprotein 8
P34949	MPI	-0.206	mannose phosphate isomerase
Q8N3R9-1	MPP5	-0.183	membrane palmitoylated protein 5
Q6WCQ1-2	MPRIP	0.203	myosin phosphatase Rho interacting protein
P25325-2	MPST	-0.134	mercaptopyruvate sulfurtransferase
Q9Y605	MRFAP1	-0.345	Morf4 family associated protein 1
Q9NV56	MRGBP	0.181	MRG domain binding protein
Q9HC36	MRM3	0.451	mitochondrial rRNA methyltransferase 3
Q9BYD6	MRPL1	0.16	mitochondrial ribosomal protein L1
Q9Y3B7-1	MRPL11	0.159	mitochondrial ribosomal protein L11
P52815	MRPL12	0.214	mitochondrial ribosomal protein L12
Q9BYD1	MRPL13	0.293	mitochondrial ribosomal protein L13
Q6P1L8	MRPL14	0.363	mitochondrial ribosomal protein L14
Q9P015	MRPL15	0.362	mitochondrial ribosomal protein L15
Q9NX20	MRPL16	0.533	mitochondrial ribosomal protein L16
Q9NRX2	MRPL17	0.25	mitochondrial ribosomal protein L17
Q9H0U6	MRPL18	0.235	mitochondrial ribosomal protein L18
P49406	MRPL19	0.171	mitochondrial ribosomal protein L19
Q5T653	MRPL2	0.266	mitochondrial ribosomal protein L2
Q9BYC9	MRPL20	0.279	mitochondrial ribosomal protein L20
Q7Z2W9	MRPL21	0.434	mitochondrial ribosomal protein L21
Q9NWU5	MRPL22	0.22	mitochondrial ribosomal protein L22
Q16540	MRPL23	0.228	mitochondrial ribosomal protein L23
Q96A35	MRPL24	0.188	mitochondrial ribosomal protein L24
Q9P0M9	MRPL27	0.472	mitochondrial ribosomal protein L27
Q13084	MRPL28	0.289	mitochondrial ribosomal protein L28
P09001	MRPL3	0.244	mitochondrial ribosomal protein L3

Q8TCC3-2	MRPL30	0.41	mitochondrial ribosomal protein L30
Q9BYC8	MRPL32	-0.465	mitochondrial ribosomal protein L32
Q9BZE1	MRPL37	0.383	mitochondrial ribosomal protein L37
Q96DV4	MRPL38	0.363	mitochondrial ribosomal protein L38
Q9NYK5	MRPL39	0.269	mitochondrial ribosomal protein L39
Q9BYD3	MRPL4	0.258	mitochondrial ribosomal protein L4
Q9H9J2	MRPL44	0.423	mitochondrial ribosomal protein L44
Q9BRJ2	MRPL45	0.34	mitochondrial ribosomal protein L45
Q13405	MRPL49	0.23	mitochondrial ribosomal protein L49
Q4U2R6	MRPL51	0.433	mitochondrial ribosomal protein L51
Q86TS9	MRPL52	0.291	mitochondrial ribosomal protein L52
Q7Z7F7-2	MRPL55	0.238	mitochondrial ribosomal protein L55
Q9BQC6	MRPL57	0.386	mitochondrial ribosomal protein L57
Q14197	MRPL58	0.095	mitochondrial ribosomal protein L58
Q9BYD2	MRPL9	0.104	mitochondrial ribosomal protein L9
P82912	MRPS11	0.213	mitochondrial ribosomal protein S11
O15235	MRPS12	1.143	mitochondrial ribosomal protein S12
O60783	MRPS14	0.187	mitochondrial ribosomal protein S14
P82914	MRPS15	0.394	mitochondrial ribosomal protein S15
Q9Y3D3	MRPS16	0.162	mitochondrial ribosomal protein S16
Q9NVS2	MRPS18A	0.422	mitochondrial ribosomal protein S18A
Q9Y399	MRPS2	0.381	mitochondrial ribosomal protein S2
P82921	MRPS21	0.353	mitochondrial ribosomal protein S21
P82650	MRPS22	0.114	mitochondrial ribosomal protein S22
Q96EL2	MRPS24	0.622	mitochondrial ribosomal protein S24
P82663	MRPS25	0.213	mitochondrial ribosomal protein S25
Q9BYN8	MRPS26	0.255	mitochondrial ribosomal protein S26
Q9NP92	MRPS30	0.304	mitochondrial ribosomal protein S30
Q92665	MRPS31	0.171	mitochondrial ribosomal protein S31
Q9Y291	MRPS33	0.616	mitochondrial ribosomal protein S33
P82930	MRPS34	0.144	mitochondrial ribosomal protein S34
P82673	MRPS35	0.368	mitochondrial ribosomal protein S35
P82909	MRPS36	0.177	mitochondrial ribosomal protein S36
P82675	MRPS5	0.432	mitochondrial ribosomal protein S5
P82932	MRPS6	0.493	mitochondrial ribosomal protein S6
Q9Y2R9	MRPS7	0.312	mitochondrial ribosomal protein S7
P82933	MRPS9	0.437	mitochondrial ribosomal protein S9
Q96E11	MRRF	0.129	mitochondrial ribosome recycling factor
Q9ULH7-5	MRTFB	-0.339	myocardin related transcription factor B
P43246	MSH2	-0.274	mutS homolog 2
P52701	MSH6	-0.123	mutS homolog 6
Q96DH6-1	MSI2	-0.361	musashi RNA binding protein 2
P03928	MT-ATP8	0.35	ATP synthase F0 subunit 8
P03915	MT-ND5	0.527	NADH dehydrogenase, subunit 5 (complex I)
P07438	MT1B	2.98	metallothionein 1B
O94776	MTA2	0.396	metastasis associated 1 family member 2
Q13126-1	MTAP	-0.248	methylthioadenosine phosphorylase

Q9NZJ7	MTCH1	0.339	mitochondrial carrier 1
Q96E29	MTERF3	0.249	mitochondrial transcription termination factor 3
Q9Y483	MTF2	0.398	metal response element binding transcription factor 2
Q9H019-1	MTFR1L	-0.155	mitochondrial fission regulator 1 like
P11586	MTHFD1	-0.297	methylenetetrahydrofolate dehydrogenase, cyclohydrolase and formyltetrahydrofolate s
P13995	MTHFD2	0.344	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2, methenyltetrahydrofo
Q13496	MTM1	-0.338	myotubularin 1
Q13613	MTMR1	-0.239	myotubularin related protein 1
Q9C0I1	MTMR12	-0.309	myotubularin related protein 12
P42345	MTOR	-0.098	mechanistic target of rapamycin kinase
P58546	MTPN	-0.246	myotrophin
Q99707	MTR	-0.405	5-methyltetrahydrofolate-homocysteine methyltransferase
Q9UBK8-1	MTRR	-0.28	5-methyltetrahydrofolate-homocysteine methyltransferase reductase
Q765P7	MTSS2	-0.53	MTSS I-BAR domain containing 2
Q13505	MTX1	0.228	metaxin 1
Q5HYI7	MTX3	0.359	metaxin 3
Q969V5	MUL1	0.262	mitochondrial E3 ubiquitin protein ligase 1
P53602	MVD	-0.215	mevalonate diphosphate decarboxylase
Q03426	MVK	-0.257	mevalonate kinase
P84157-2	MXRA7	0.177	matrix remodeling associated 7
Q9BQG0-2	MYBBP1A	-0.213	MYB binding protein 1a
Q969H8	MYDGF	0.265	myeloid derived growth factor
Q7Z406-2	MYH14	-0.178	myosin heavy chain 14
P35579	MYH9	0.089	myosin heavy chain 9
O14950	MYL12B	-0.155	myosin light chain 12B
Q15746	MYLK	-0.19	myosin light chain kinase
Q96JP2	MYO15B	-0.427	myosin XVB
Q92614-1	MYO18A	-0.211	myosin XVIIIA
Q96H55-1	MYO19	-0.216	myosin XIX
O00159-3	MYO1C	0.182	myosin IC
Q12965	MYO1E	-0.17	myosin IE
Q6NSJ0	MYORG	-0.445	myogenesis regulating glycosidase (putative)
P41227	NAA10	-0.355	N(alpha)-acetyltransferase 10, NatA catalytic subunit
Q9BXJ9	NAA15	-0.105	N(alpha)-acetyltransferase 15, NatA auxiliary subunit
P61599	NAA20	-0.321	N(alpha)-acetyltransferase 20, NatB catalytic subunit
Q14CX7	NAA25	-0.271	N(alpha)-acetyltransferase 25, NatB auxiliary subunit
Q15742	NAB2	0.25	NGFI-A binding protein 2
Q4G0N4	NADK2	0.173	NAD kinase 2, mitochondrial
Q6IA69	NADSYN1	-0.26	NAD synthetase 1
Q13564-4	NAE1	-0.324	NEDD8 activating enzyme E1 subunit 1
Q9UJ70-2	NAGK	-0.213	N-acetylglucosamine kinase
P43490	NAMPT	-0.079	nicotinamide phosphoribosyltransferase
Q9NR45	NANS	-0.221	N-acetylneuraminate synthase
P55209	NAP1L1	-0.124	nucleosome assembly protein 1 like 1
Q99733-2	NAP1L4	-0.126	nucleosome assembly protein 1 like 4
O43776	NARS1	-0.21	asparaginyl-tRNA synthetase 1
Q96I59	NARS2	0.363	asparaginyl-tRNA synthetase 2, mitochondrial

P49321-3	NASP	-0.435	nuclear autoantigenic sperm protein
Q9H0A0	NAT10	0.196	N-acetyltransferase 10
Q8IVL1	NAV2	-0.554	neuron navigator 2
A2RRP1	NBAS	-0.319	NBAS subunit of NRZ tethering complex
Q15021	NCAPD2	-0.263	non-SMC condensin I complex subunit D2
Q9BPX3	NCAPG	-0.22	non-SMC condensin I complex subunit G
Q15003	NCAPH	-0.237	non-SMC condensin I complex subunit H
Q09161	NCBP1	-0.237	nuclear cap binding protein subunit 1
Q6PIU2-2	NCEH1	0.451	neutral cholesterol ester hydrolase 1
Q9NZQ3	NCKIPSD	0.146	NCK interacting protein with SH3 domain
Q9Y6Q9	NCOA3	-0.277	nuclear receptor coactivator 3
Q13772-4	NCOA4	0.179	nuclear receptor coactivator 4
Q9HCD5	NCOA5	0.098	nuclear receptor coactivator 5
O75376	NCOR1	-0.216	nuclear receptor corepressor 1
Q68D85	NCR3LG1	-0.655	natural killer cell cytotoxicity receptor 3 ligand 1
Q92542-1	NCSTN	0.109	nicastrin
O14777	NDC80	-0.223	NDC80 kinetochore complex component
Q9NXR1-1	NDE1	-0.303	nudE neurodevelopment protein 1
Q9UGV2	NDRG3	-0.463	NDRG family member 3
O95299	NDUFA10	0.465	NADH:ubiquinone oxidoreductase subunit A10
Q9UI09	NDUFA12	0.292	NADH:ubiquinone oxidoreductase subunit A12
Q9P0J0	NDUFA13	0.437	NADH:ubiquinone oxidoreductase subunit A13
O00483	NDUFA4	-0.159	NDUFA4 mitochondrial complex associated
P56556	NDUFA6	0.456	NADH:ubiquinone oxidoreductase subunit A6
O95182	NDUFA7	0.29	NADH:ubiquinone oxidoreductase subunit A7
P51970	NDUFA8	0.29	NADH:ubiquinone oxidoreductase subunit A8
Q16795	NDUFA9	0.47	NADH:ubiquinone oxidoreductase subunit A9
O14561	NDUFAB1	0.385	NADH:ubiquinone oxidoreductase subunit AB1
Q8N183	NDUFAF2	0.188	NADH:ubiquinone oxidoreductase complex assembly factor 2
Q9BU61-1	NDUFAF3	-0.142	NADH:ubiquinone oxidoreductase complex assembly factor 3
Q9P032	NDUFAF4	0.172	NADH:ubiquinone oxidoreductase complex assembly factor 4
Q7L592	NDUFAF7	0.312	NADH:ubiquinone oxidoreductase complex assembly factor 7
O96000	NDUFB10	0.161	NADH:ubiquinone oxidoreductase subunit B10
O43676	NDUFB3	0.428	NADH:ubiquinone oxidoreductase subunit B3
O95168	NDUFB4	0.374	NADH:ubiquinone oxidoreductase subunit B4
O43674-1	NDUFB5	0.353	NADH:ubiquinone oxidoreductase subunit B5
O95139	NDUFB6	0.123	NADH:ubiquinone oxidoreductase subunit B6
P17568	NDUFB7	0.287	NADH:ubiquinone oxidoreductase subunit B7
O95169	NDUFB8	0.38	NADH:ubiquinone oxidoreductase subunit B8
Q9Y6M9	NDUFB9	0.44	NADH:ubiquinone oxidoreductase subunit B9
O95298	NDUFC2	0.4	NADH:ubiquinone oxidoreductase subunit C2
P28331-2	NDUFS1	0.194	NADH:ubiquinone oxidoreductase core subunit S1
O75306	NDUFS2	0.285	NADH:ubiquinone oxidoreductase core subunit S2
O75489	NDUFS3	0.338	NADH:ubiquinone oxidoreductase core subunit S3
O43181	NDUFS4	0.27	NADH:ubiquinone oxidoreductase subunit S4
O43920	NDUFS5	0.372	NADH:ubiquinone oxidoreductase subunit S5
O75380	NDUFS6	0.201	NADH:ubiquinone oxidoreductase subunit S6

O75251	NDUFS7	0.514	NADH:ubiquinone oxidoreductase core subunit S7
O00217	NDUFS8	0.188	NADH:ubiquinone oxidoreductase core subunit S8
P49821	NDUFV1	0.319	NADH:ubiquinone oxidoreductase core subunit V1
P19404	NDUFV2	-0.113	NADH:ubiquinone oxidoreductase core subunit V2
Q92692-2	NECTIN2	-0.167	nectin cell adhesion molecule 2
Q8NHV4-3	NEDD1	0.445	NEDD1 gamma-tubulin ring complex targeting factor
P46934-4	NEDD4	-0.269	NEDD4 E3 ubiquitin protein ligase
Q15843	NEDD8	-0.262	NEDD8 ubiquitin like modifier
Q9H3P2	NELFA	-0.16	negative elongation factor complex member A
Q6NW34	NEPRO	0.148	nucleolus and neural progenitor protein
P48681	NES	-0.226	nestin
Q0ZGT2	NEXN	0.434	nexilin F-actin binding protein
O94916-4	NFAT5	0.329	nuclear factor of activated T cells 5
P19838-2	NFKB1	-0.093	nuclear factor kappa B subunit 1
Q9Y697	NFS1	0.15	NFS1 cysteine desulfurase
Q9UMS0	NFU1	-0.271	NFU1 iron-sulfur cluster scaffold
Q6ZNB6-1	NFXL1	-0.59	nuclear transcription factor, X-box binding like 1
Q8N5V2	NGEF	-0.368	neuronal guanine nucleotide exchange factor
Q96IV0	NGLY1	-0.6	N-glycanase 1
Q9NPE2-2	NGRN	0.311	neugrin, neurite outgrowth associated
Q9H9Q4-1	NHEJ1	-0.502	non-homologous end joining factor 1
Q9H9Q4-2	NHEJ1	-0.382	non-homologous end joining factor 1
Q5SYE7	NHSL1	-0.362	NHS like 1
P14543-1	NID1	-0.436	nidogen 1
Q9GZT8	NIF3L1	-0.332	NGG1 interacting factor 3 like 1
Q9BYG3	NIFK	-0.155	nucleolar protein interacting with the FHA domain of MKI67
Q92982	NINJ1	0.21	ninjurin 1
Q9Y221	NIP7	0.192	nucleolar pre-rRNA processing protein NIP7
Q9BPW8	NIPSNAP1	0.383	nipsnap homolog 1
O75323-1	NIPSNAP2	0.372	nipsnap homolog 2
Q9UFN0	NIPSNAP3A	0.205	nipsnap homolog 3A
Q9NQR4	NIT2	-0.19	nitrilase family member 2
Q8N5F7	NKAP	0.125	NFKB activating protein
Q969G9	NKD1	-0.461	NKD inhibitor of WNT signaling pathway 1
O15226-2	NKRF	0.381	NFKB repressing factor
P30414	NKTR	0.292	natural killer cell triggering receptor
Q9NVX2	NLE1	-0.207	notchless homolog 1
Q96D46	NMD3	0.335	NMD3 ribosome export adaptor
P22392-2	NME2	-0.41	NME/NM23 nucleoside diphosphate kinase 2
P30419	NMT1	-0.346	N-myristoyltransferase 1
Q13423	NNT	0.393	nicotinamide nucleotide transhydrogenase
Q8NC60	NOA1	0.202	nitric oxide associated 1
Q9ULX3	NOB1	0.162	NIN1 (RPN12) binding protein 1 homolog
Q9Y3T9	NOC2L	0.335	NOC2 like nucleolar associated transcriptional repressor
Q8WTT2	NOC3L	0.498	NOC3 like DNA replication regulator
Q9H8H0	NOL11	0.116	nucleolar protein 11
Q96MY1	NOL4L	-0.317	nucleolar protein 4 like

Q9UMY1	NOL7	-0.375	nucleolar protein 7
Q76FK4	NOL8	0.145	nucleolar protein 8
Q5C9Z4	NOM1	0.336	nucleolar protein with MIF4G domain 1
Q15233	NONO	0.142	non-POU domain containing octamer binding
Q9NPE3	NOP10	0.258	NOP10 ribonucleoprotein
Q9Y3C1	NOP16	-0.471	NOP16 nucleolar protein
P46087-4	NOP2	0.495	NOP2 nucleolar protein
Q9NZM5	NOP53	-0.567	NOP53 ribosome biogenesis factor
O00567	NOP56	0.498	NOP56 ribonucleoprotein
Q9Y2X3	NOP58	0.414	NOP58 ribonucleoprotein
O75052	NOS1AP	-0.343	nitric oxide synthase 1 adaptor protein
O15118	NPC1	0.263	NPC intracellular cholesterol transporter 1
P55786	NPEPPS	-0.259	aminopeptidase puromycin sensitive
P10588	NR2F6	0.335	nuclear receptor subfamily 2 group F member 6
O43847-2	NRDC	-0.401	nardilysin convertase
O95478	NSA2	-0.65	NSA2 ribosome biogenesis factor
O96028-1	NSD2	-0.273	nuclear receptor binding SET domain protein 2
Q15738	NSDHL	0.088	NAD(P) dependent steroid dehydrogenase-like
Q9UNZ2-5	NSFL1C	-0.14	NSFL1 cofactor
Q9H0G5	NSRP1	-0.19	nuclear speckle splicing regulatory protein 1
Q8TCD5	NT5C	-0.221	5', 3'-nucleotidase, cytosolic
P49902	NT5C2	-0.148	5'-nucleotidase, cytosolic II
Q5TFE4	NT5DC1	-0.24	5'-nucleotidase domain containing 1
Q9H857-2	NT5DC2	0.446	5'-nucleotidase domain containing 2
Q86UY8	NT5DC3	0.377	5'-nucleotidase domain containing 3
P21589-1	NT5E	0.258	5'-nucleotidase ecto
P78549	NTHL1	-0.177	nth like DNA glycosylase 1
Q9BSD7	NTPCR	0.235	nucleoside-triphosphatase, cancer-related
Q8TB37	NUBPL	0.283	nucleotide binding protein like
Q9H1E3	NUCKS1	-0.479	nuclear casein kinase and cyclin dependent kinase substrate 1
Q9Y266	NUDC	-0.23	nuclear distribution C, dynein complex regulator
Q96RS6	NUDCD1	-0.123	NudC domain containing 1
Q8WVJ2	NUDCD2	-0.268	NudC domain containing 2
Q8IVD9	NUDCD3	-0.423	NudC domain containing 3
Q9NV35	NUDT15	-0.129	nudix hydrolase 15
Q96DE0	NUDT16	-0.115	nudix hydrolase 16
Q9BRJ7-1	NUDT16L1	0.33	nudix hydrolase 16 like 1
A8MXV4	NUDT19	0.494	nudix hydrolase 19
P50583	NUDT2	-0.411	nudix hydrolase 2
Q9UKK9	NUDT5	-0.327	nudix hydrolase 5
Q7Z417	NUFIP2	0.13	nuclear FMR1 interacting protein 2
P49757	NUMB	-0.209	NUMB endocytic adaptor protein
Q8WUM0	NUP133	0.095	nucleoporin 133
P49790	NUP153	0.311	nucleoporin 153
Q5SRE5	NUP188	0.094	nucleoporin 188
Q8TEM1-1	NUP210	0.272	nucleoporin 210
Q8NFH4	NUP37	0.192	nucleoporin 37

Q9UKX7	NUP50	0.13	nucleoporin 50
P37198	NUP62	-0.175	nucleoporin 62
P61970	NUTF2	-0.228	nuclear transport factor 2
Q9UBU9-1	NXF1	0.315	nuclear RNA export factor 1
Q6DKJ4	NXN	-0.226	nucleoredoxin
Q9Y530	OARD1	0.097	O-acyl-ADP-ribose deacylase 1
P04181	OAT	0.549	ornithine aminotransferase
O75147	OBSL1	-0.184	obscurin like cytoskeletal adaptor 1
Q9NX40	OCIAD1	0.155	OCIA domain containing 1
Q16625	OCLN	-0.215	occludin
O60502	OGA	0.096	O-GlcNAcase
Q02218	OGDH	0.365	oxoglutarate dehydrogenase
Q6N063-1	OGFOD2	-0.2	2-oxoglutarate and iron dependent oxygenase domain containing 2
Q9NZT2	OGFR	-0.186	opioid growth factor receptor
O15294	OGT	-0.166	O-linked N-acetylglucosamine (GlcNAc) transferase
Q9NTK5-1	OLA1	-0.3	Obg like ATPase 1
Q9H6K4	OPA3	0.499	outer mitochondrial membrane lipid metabolism regulator OPA3
O14841	OPLAH	-0.198	5-oxoprolinase, ATP-hydrolysing
Q96CV9-1	OPTN	-0.82	optineurin
Q13415	ORC1	0.744	origin recognition complex subunit 1
Q13416	ORC2	-0.126	origin recognition complex subunit 2
Q9UBD5-2	ORC3	0.179	origin recognition complex subunit 3
O43929	ORC4	0.098	origin recognition complex subunit 4
Q9Y5N6	ORC6	0.7	origin recognition complex subunit 6
P19652	ORM2	-0.376	orosomucoid 2
Q9BZF1-1	OSBPL8	0.122	oxysterol binding protein like 8
Q92882	OSTF1	-0.138	osteoclast stimulating factor 1
Q96G74-1	OTUD5	0.406	OTU deubiquitinase 5
Q6GQQ9-1	OTUD7B	0.188	OTU deubiquitinase 7B
Q8N573-1	OXR1	-0.48	oxidation resistance 1
Q9NWU1-1	OXSM	0.24	3-oxoacyl-ACP synthase, mitochondrial
O95747	OXSR1	-0.236	oxidative stress responsive kinase 1
P07237	P4HB	0.133	prolyl 4-hydroxylase subunit beta
Q9BRP4	PAAF1	-0.213	proteasomal ATPase associated factor 1
Q6VY07-2	PACS1	-0.388	phosphofurin acidic cluster sorting protein 1
Q9UNF0	PACSIN2	-0.204	protein kinase C and casein kinase substrate in neurons 2
Q9UKS6	PACSIN3	-0.189	protein kinase C and casein kinase substrate in neurons 3
Q8N7H5	PAF1	0.251	PAF1 homolog, Paf1/RNA polymerase II complex component
P43034	PAFAH1B1	-0.188	platelet activating factor acetylhydrolase 1b regulatory subunit 1
Q15102	PAFAH1B3	-0.268	platelet activating factor acetylhydrolase 1b catalytic subunit 3
P00439	PAH	-0.464	phenylalanine hydroxylase
P22234-2	PAICS	-0.269	phosphoribosylaminoimidazole carboxylase and phosphoribosylaminoimidazolesuccinoca
Q9H074	PAIP1	-0.258	poly(A) binding protein interacting protein 1
Q9BPZ3	PAIP2	0.346	poly(A) binding protein interacting protein 2
Q9NWT1	PAK1IP1	0.132	PAK1 interacting protein 1
Q13177	PAK2	-0.073	p21 (RAC1) activated kinase 2
O96013	PAK4	-0.153	p21 (RAC1) activated kinase 4

A6NDB9	PALM3	-0.433	paralemmin 3
Q9NP74	PALMD	-0.419	palmdelphin
Q9BZ23	PANK2	-0.113	pantothenate kinase 2
Q9NVE7	PANK4	-0.101	pantothenate kinase 4
P51003	PAPOLA	-0.123	poly(A) polymerase alpha
O43252	PAPSS1	-0.18	3'-phosphoadenosine 5'-phosphosulfate synthase 1
Q9BYG5	PARD6B	0.197	par-6 family cell polarity regulator beta
Q86W56	PARG	-0.135	poly(ADP-ribose) glycohydrolase
O95453	PARN	-0.195	poly(A)-specific ribonuclease
P09874	PARP1	0.339	poly(ADP-ribose) polymerase 1
Q9UGN5-2	PARP2	0.145	poly(ADP-ribose) polymerase 2
Q7L3T8	PARS2	0.188	prolyl-tRNA synthetase 2, mitochondrial
Q9NVD7	PARVA	-0.471	parvin alpha
Q86TB9	PATL1	0.161	PAT1 homolog 1, processing body mRNA decay factor
Q9BVG4	PBDC1	-0.144	polysaccharide biosynthesis domain containing 1
P11498	PC	0.197	pyruvate carboxylase
P05165-1	PCCA	0.19	propionyl-CoA carboxylase subunit alpha
O94913	PCF11	0.133	PCF11 cleavage and polyadenylation factor subunit
P35227	PCGF2	0.306	polycomb group ring finger 2
Q9H4Z3	PCIF1	-0.267	PDX1 C-terminal inhibiting factor 1
Q16822	PCK2	0.282	phosphoenolpyruvate carboxykinase 2, mitochondrial
Q15004	PCLAF	0.25	PCNA clamp associated factor
Q15154-1	PCM1	-0.208	pericentriolar material 1
P12004	PCNA	0.126	proliferating cell nuclear antigen
Q8WW12	PCNP	-0.274	PEST proteolytic signal containing nuclear protein
Q9UKL6	PCTP	-0.261	phosphatidylcholine transfer protein
P49585	PCYT1A	-0.198	phosphate cytidylyltransferase 1, choline, alpha
Q99447	PCYT2	-0.495	phosphate cytidylyltransferase 2, ethanolamine
Q13442	PDAP1	-0.127	PDGFA associated protein 1
Q53EL6	PDCD4	-0.23	programmed cell death 4
O14737	PDCD5	-0.276	programmed cell death 5
Q8WUM4	PDCD6IP	-0.184	programmed cell death 6 interacting protein
Q13371	PDCL	0.378	phosducin like
Q9H2J4	PDCL3	-0.26	phosducin like 3
Q6L8Q7-1	PDE12	0.137	phosphodiesterase 12
Q13370	PDE3B	-0.339	phosphodiesterase 3B
Q9HBH1	PDF	0.334	peptide deformylase, mitochondrial
P08559-4	PDHA1	0.097	pyruvate dehydrogenase E1 alpha 1 subunit
P11177	PDHB	0.185	pyruvate dehydrogenase E1 beta subunit
O00330-1	PDHX	0.227	pyruvate dehydrogenase complex component X
P30101	PDIA3	0.157	protein disulfide isomerase family A member 3
Q15084-2	PDIA6	0.117	protein disulfide isomerase family A member 6
Q96JY6-5	PDLIM2	-0.384	PDZ and LIM domain 2
Q9NR12	PDLIM7	0.43	PDZ and LIM domain 7
Q9P0J1-2	PDP1	0.424	pyruvate dehyrogenase phosphatase catalytic subunit 1
Q8NCN5	PDPR	0.367	pyruvate dehydrogenase phosphatase regulatory subunit
Q6P996-1	PDXDC1	-0.345	pyridoxal dependent decarboxylase domain containing 1

Q5EBL8-2	PDZD11	-0.121	PDZ domain containing 11
Q5T2W1	PDZK1	-0.181	PDZ domain containing 1
Q15121-2	PEA15	0.337	proliferation and apoptosis adaptor protein 15
P30086	PEBP1	-0.338	phosphatidylethanolamine binding protein 1
Q9BY49-1	PECR	0.298	peroxisomal trans-2-enoyl-CoA reductase
Q9UBV8	PEF1	-0.204	penta-EF-hand domain containing 1
Q9GZU2	PEG3	-0.226	paternally expressed 3
Q9BRX2	PELO	0.306	pelota mRNA surveillance and ribosome rescue factor
P12955	PEPD	-0.375	peptidase D
O15067	PFAS	-0.38	phosphoribosylformylglycinamidine synthase
Q9UHV9	PFDN2	-0.297	prefoldin subunit 2
Q99471	PFDN5	-0.264	prefoldin subunit 5
O15212	PFDN6	-0.259	prefoldin subunit 6
O60825	PFKFB2	0.141	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2
P17858-1	PFKL	-0.18	phosphofructokinase, liver type
Q01813	PFKP	-0.376	phosphofructokinase, platelet
P07737	PFN1	-0.278	profilin 1
P35080-2	PFN2	-0.263	profilin 2
P18669	PGAM1	-0.154	phosphoglycerate mutase 1
Q96HS1-1	PGAM5	0.347	PGAM family member 5, mitochondrial serine/threonine protein phosphatase
P00558	PGK1	-0.125	phosphoglycerate kinase 1
O95336	PGLS	-0.29	6-phosphogluconolactonase
P36871-1	PGM1	-0.398	phosphoglucomutase 1
Q96G03	PGM2	-0.252	phosphoglucomutase 2
O95394-4	PGM3	-0.318	phosphoglucomutase 3
A6NDG6	PGP	-0.409	phosphoglycolate phosphatase
Q9NXJ5	PGPEP1	-0.3	pyroglutamyl-peptidase I
O00264	PGRMC1	0.446	progesterone receptor membrane component 1
O75167-4	PHACTR2	-0.401	phosphatase and actin regulator 2
Q8IZ21-2	PHACTR4	-0.29	phosphatase and actin regulator 4
Q9H814	PHAX	-0.284	phosphorylated adaptor for RNA export
P35232	PHB	0.251	prohibitin
Q99623	PHB2	0.374	prohibitin 2
O94880	PHF14	-0.146	PHD finger protein 14
O75151	PHF2	0.334	PHD finger protein 2
A8MW92	PHF20L1	-0.408	PHD finger protein 20 like 1
Q9BUL5	PHF23	0.235	PHD finger protein 23
Q7RTV0	PHF5A	0.243	PHD finger protein 5A
Q8IWS0-1	PHF6	0.113	PHD finger protein 6
O43175	PHGDH	-0.1	phosphoglycerate dehydrogenase
Q8WWQ0	PHIP	0.356	pleckstrin homology domain interacting protein
P46019	PHKA2	-0.136	phosphorylase kinase regulatory subunit alpha 2
Q6NSJ2-1	PHLDB3	0.302	pleckstrin homology like domain family B member 3
Q96FC7	PHYHIPL	-0.348	phytanoyl-CoA 2-hydroxylase interacting protein like
Q9BTU6	PI4K2A	0.167	phosphatidylinositol 4-kinase type 2 alpha
O75925-2	PIAS1	-0.528	protein inhibitor of activated STAT 1
Q5H8A4-1	PIGG	0.308	phosphatidylinositol glycan anchor biosynthesis class G

Q92643	PIGK	0.267	phosphatidylinositol glycan anchor biosynthesis class K
Q96S52	PIGS	0.13	phosphatidylinositol glycan anchor biosynthesis class S
Q969N2	PIGT	0.188	phosphatidylinositol glycan anchor biosynthesis class T
Q9NWS0-1	PIH1D1	-0.267	PIH1 domain containing 1
Q9Y237-2	PIN4	-0.203	peptidylprolyl cis/trans isomerase, NIMA-interacting 4
Q96BK5	PINX1	-0.263	PIN2 (TERF1) interacting telomerase inhibitor 1
P48426	PIP4K2A	-0.25	phosphatidylinositol-5-phosphate 4-kinase type 2 alpha
P78356	PIP4K2B	-0.144	phosphatidylinositol-5-phosphate 4-kinase type 2 beta
Q99755	PIP5K1A	0.171	phosphatidylinositol-4-phosphate 5-kinase type 1 alpha
O00625	PIR	-0.285	pirin
Q9UG56-3	PISD	-0.123	phosphatidylserine decarboxylase
Q00169	PITPNA	-0.18	phosphatidylinositol transfer protein alpha
P48739-3	PITPNB	-0.115	phosphatidylinositol transfer protein beta
Q5JRX3-2	PITRM1	0.371	pitrilysin metallopeptidase 1
P30613	PKLR	-0.451	pyruvate kinase L/R
P14618	PKM	-0.136	pyruvate kinase M1/2
Q99640	PKMYT1	0.198	protein kinase, membrane associated tyrosine/threonine 1
Q16512-2	PKN1	-0.162	protein kinase N1
Q16513	PKN2	-0.118	protein kinase N2
Q99959-2	PKP2	-0.094	plakophilin 2
Q9Y263	PLAA	-0.156	phospholipase A2 activating protein
Q9NQ66-1	PLCB1	-0.54	phospholipase C beta 1
Q01970	PLCB3	-0.351	phospholipase C beta 3
Q13393-1	PLD1	-0.201	phospholipase D1
Q9Y2H5	PLEKHA6	-0.248	pleckstrin homology domain containing A6
Q6IQ23-2	PLEKHA7	-0.437	pleckstrin homology domain containing A7
Q9H8W4	PLEKHF2	0.445	pleckstrin homology and FYVE domain containing 2
Q8TD55	PLEKHO2	0.317	pleckstrin homology domain containing O2
Q99541	PLIN2	0.59	perilipin 2
O60664	PLIN3	-0.126	perilipin 3
Q02809-2	PLOD1	-0.154	procollagen-lysine,2-oxoglutarate 5-dioxygenase 1
O60568	PLOD3	0.133	procollagen-lysine,2-oxoglutarate 5-dioxygenase 3
O94903	PLPBP	-0.164	pyridoxal phosphate binding protein
O43660	PLRG1	0.196	pleiotropic regulator 1
Q14651	PLS1	-0.302	plastin 1
P13797	PLS3	-0.285	plastin 3
O43157	PLXNB1	-0.227	plexin B1
Q9Y4D7-1	PLXND1	-0.397	plexin D1
Q8IYS1	PM20D2	-0.166	peptidase M20 domain containing 2
Q6P1K2-2	PMF1/PMF1-BGLAP	-0.4	polyamine modulated factor 1
O15305	PMM2	-0.443	phosphomannomutase 2
Q10713	PMPCA	0.247	peptidase, mitochondrial processing alpha subunit
O75439	PMPCB	0.26	peptidase, mitochondrial processing beta subunit
Q8TF01	PNISR	-0.246	PNN interacting serine and arginine rich protein
Q8N490	PNKD	-0.835	PNKD metallo-beta-lactamase domain containing
Q96T60	PNKP	0.142	polynucleotide kinase 3'-phosphatase
Q9H307	PNN	0.16	pinin, desmosome associated protein

P41247	PNPLA4	0.433	patatin like phospholipase domain containing 4
Q9NVS9	PNPO	-0.318	pyridoxamine 5'-phosphate oxidase
Q8TCS8	PNPT1	0.14	polyribonucleotide nucleotidyltransferase 1
Q8NBL1	POGLUT1	0.148	protein O-glucosyltransferase 1
Q7Z3K3-1	POGZ	0.156	pogo transposable element derived with ZNF domain
P09884	POLA1	-0.426	DNA polymerase alpha 1, catalytic subunit
Q14181	POLA2	-0.173	DNA polymerase alpha 2, accessory subunit
P06746	POLB	0.236	DNA polymerase beta
P28340	POLD1	-0.364	DNA polymerase delta 1, catalytic subunit
P49005	POLD2	-0.341	DNA polymerase delta 2, accessory subunit
Q9Y2S7	POLDIP2	0.141	DNA polymerase delta interacting protein 2
Q07864	POLE	-0.277	DNA polymerase epsilon, catalytic subunit
Q9NRF9	POLE3	-0.155	DNA polymerase epsilon 3, accessory subunit
P54098	POLG	0.348	DNA polymerase gamma, catalytic subunit
O15160	POLR1C	0.117	RNA polymerase I and III subunit C
Q9GZS1-2	POLR1E	0.322	RNA polymerase I subunit E
P24928	POLR2A	-0.174	RNA polymerase II subunit A
P19388	POLR2E	-0.158	RNA polymerase II subunit E
P52434	POLR2H	-0.403	RNA polymerase II subunit H
P52435	POLR2J	0.332	RNA polymerase II subunit J
Q9BUI4	POLR3C	0.209	RNA polymerase III subunit C
Q9NVU0	POLR3E	-0.182	RNA polymerase III subunit E
A8CG34	POM121/POM121C	0.606	POM121 transmembrane nucleoporin
Q8WZA1-2	POMGNT1	0.401	protein O-linked mannose N-acetylglucosaminyltransferase 1 (beta 1,2-)
Q8NAT1	POMGNT2	0.301	protein O-linked mannose N-acetylglucosaminyltransferase 2 (beta 1,4-)
Q9H5K3	POMK	0.335	protein O-mannose kinase
Q9Y244	POMP	-0.331	proteasome maturation protein
O95707	POP4	-0.144	POP4 homolog, ribonuclease P/MRP subunit
P16435	POR	0.238	cytochrome p450 oxidoreductase
P14859-6	POU2F1	-0.225	POU class 2 homeobox 1
Q06203	PPAT	-0.284	phosphoribosyl pyrophosphate amidotransferase
Q9HAB8	PPCS	-0.143	phosphopantothenoylcysteine synthetase
P62937	PPIA	-0.119	peptidylprolyl isomerase A
P23284	PPIB	0.136	peptidylprolyl isomerase B
P45877	PPIC	-0.143	peptidylprolyl isomerase C
Q08752	PPID	-0.188	peptidylprolyl isomerase D
P30405	PPIF	0.432	peptidylprolyl isomerase F
Q9H2H8-1	PPIL3	-0.185	peptidylprolyl isomerase like 3
O15297	PPM1D	0.543	protein phosphatase, Mg2+/Mn2+ dependent 1D
P49593	PPM1F	-0.23	protein phosphatase, Mg2+/Mn2+ dependent 1F
O15355	PPM1G	-0.125	protein phosphatase, Mg2+/Mn2+ dependent 1G
Q9ULR3	PPM1H	-0.359	protein phosphatase, Mg2+/Mn2+ dependent 1H
Q96QC0	PPP1R10	0.357	protein phosphatase 1 regulatory subunit 10
Q96C90	PPP1R14B	-0.594	protein phosphatase 1 regulatory inhibitor subunit 14B
Q6NYC8	PPP1R18	0.566	protein phosphatase 1 regulatory subunit 18
Q6ZMI0-1	PPP1R21	-0.3	protein phosphatase 1 regulatory subunit 21
Q15435	PPP1R7	-0.284	protein phosphatase 1 regulatory subunit 7

Q9ULJ8-3	PPP1R9A	-0.223	protein phosphatase 1 regulatory subunit 9A
P30153	PPP2R1A	-0.163	protein phosphatase 2 scaffold subunit Aalpha
P30154	PPP2R1B	-0.221	protein phosphatase 2 scaffold subunit Abeta
Q15172-1	PPP2R5A	-0.334	protein phosphatase 2 regulatory subunit B'alpha
Q13362	PPP2R5C	-0.193	protein phosphatase 2 regulatory subunit B'gamma
Q16537	PPP2R5E	-0.184	protein phosphatase 2 regulatory subunit B'epsilon
Q08209	PPP3CA	-0.321	protein phosphatase 3 catalytic subunit alpha
P63098	PPP3R1	-0.269	protein phosphatase 3 regulatory subunit B, alpha
P60510	PPP4C	-0.148	protein phosphatase 4 catalytic subunit
Q8TF05	PPP4R1	-0.301	protein phosphatase 4 regulatory subunit 1
Q9NY27	PPP4R2	-0.214	protein phosphatase 4 regulatory subunit 2
P53041	PPP5C	-0.206	protein phosphatase 5 catalytic subunit
O00743-3	PPP6C	-0.197	protein phosphatase 6 catalytic subunit
O75170	PPP6R2	-0.189	protein phosphatase 6 regulatory subunit 2
Q5H9R7-5	PPP6R3	-0.331	protein phosphatase 6 regulatory subunit 3
O43663	PRC1	0.438	protein regulator of cytokinesis 1
Q92733	PRCC	-0.123	proline rich mitotic checkpoint control factor
P30048	PRDX3	0.279	peroxiredoxin 3
P30041	PRDX6	-0.337	peroxiredoxin 6
Q9HCU5	PREB	0.207	prolactin regulatory element binding
P48147	PREP	-0.318	prolyl endopeptidase
Q4J6C6	PREPL	0.222	prolyl endopeptidase like
P49642	PRIM1	-0.196	DNA primase subunit 1
P49643	PRIM2	-0.403	DNA primase subunit 2
P17612	PRKACA	-0.197	protein kinase cAMP-activated catalytic subunit alpha
P10644	PRKAR1A	-0.285	protein kinase cAMP-dependent type I regulatory subunit alpha
P31321	PRKAR1B	-0.661	protein kinase cAMP-dependent type I regulatory subunit beta
P17252	PRKCA	-0.131	protein kinase C alpha
Q05655	PRKCD	0.1	protein kinase C delta
O75569	PRKRA	0.145	protein activator of interferon induced protein kinase EIF2AK2
Q9H875	PRKRIP1	-0.153	PRKR interacting protein 1
Q99873	PRMT1	-0.164	protein arginine methyltransferase 1
O14744	PRMT5	-0.159	protein arginine methyltransferase 5
Q6P2P2	PRMT9	-0.168	protein arginine methyltransferase 9
P04070-2	PROC	-0.428	protein C, inactivator of coagulation factors Va and VIIIa
Q9UNN8	PROCR	0.64	protein C receptor
Q92786	PROX1	0.153	prospero homeobox 1
Q9UMS4	PRPF19	0.094	pre-mRNA processing factor 19
O43395	PRPF3	0.122	pre-mRNA processing factor 3
Q8NAV1-1	PRPF38A	0.266	pre-mRNA processing factor 38A
Q5VTL8	PRPF38B	0.114	pre-mRNA processing factor 38B
O43172	PRPF4	0.08	pre-mRNA processing factor 4
Q13523	PRPF4B	0.245	pre-mRNA processing factor 4B
P11908-2	PRPS2	-0.157	phosphoribosyl pyrophosphate synthetase 2
Q14558-2	PRPSAP1	-0.191	phosphoribosyl pyrophosphate synthetase associated protein 1
O60256-1	PRPSAP2	-0.218	phosphoribosyl pyrophosphate synthetase associated protein 2
Q5JSZ5-1	PRRC2B	-0.165	proline rich coiled-coil 2B

P07602-3	PSAP	-0.404	prosaposin
Q9Y617	PSAT1	-0.255	phosphoserine aminotransferase 1
P25786-2	PSMA1	-0.152	proteasome subunit alpha 1
P28066	PSMA5	-0.151	proteasome subunit alpha 5
P60900	PSMA6	0.114	proteasome subunit alpha 6
P28070	PSMB4	0.126	proteasome subunit beta 4
P28072	PSMB6	-0.142	proteasome subunit beta 6
Q99436	PSMB7	-0.11	proteasome subunit beta 7
Q99460	PSMD1	-0.133	proteasome 26S subunit, non-ATPase 1
Q9UNM6	PSMD13	-0.141	proteasome 26S subunit, non-ATPase 13
O00487	PSMD14	0.115	proteasome 26S subunit, non-ATPase 14
Q16401	PSMD5	-0.297	proteasome 26S subunit, non-ATPase 5
P48556	PSMD8	-0.153	proteasome 26S subunit, non-ATPase 8
O00233	PSMD9	-0.121	proteasome 26S subunit, non-ATPase 9
Q06323	PSME1	-0.597	proteasome activator subunit 1
Q9UL46	PSME2	-0.322	proteasome activator subunit 2
P61289-2	PSME3	-0.161	proteasome activator subunit 3
Q92530	PSMF1	-0.314	proteasome inhibitor subunit 1
O95456	PSMG1	-0.358	proteasome assembly chaperone 1
P78330	PSPH	-0.421	phosphoserine phosphatase
P26599-3	PTBP1	-0.086	polypyrimidine tract binding protein 1
O95758-4	PTBP3	0.223	polypyrimidine tract binding protein 3
O75127	PTCD1	0.304	pentatricopeptide repeat domain 1
Q96EY7-1	PTCD3	0.3	pentatricopeptide repeat domain 3
P48651	PTDSS1	0.113	phosphatidylserine synthase 1
Q9BVG9	PTDSS2	-0.348	phosphatidylserine synthase 2
Q14914	PTGR1	0.326	prostaglandin reductase 1
Q13308-6	PTK7	-0.227	protein tyrosine kinase 7 (inactive)
P06454	PTMA	-0.314	prothymosin alpha
P20962	PTMS	-0.212	parathymosin
Q15257	PTPA	-0.364	protein phosphatase 2 phosphatase activator
Q15257-2	PTPA	-0.416	protein phosphatase 2 phosphatase activator
Q06124	PTPN11	-0.098	protein tyrosine phosphatase non-receptor type 11
Q05209	PTPN12	-0.217	protein tyrosine phosphatase non-receptor type 12
P17706-1	PTPN2	-0.253	protein tyrosine phosphatase non-receptor type 2
Q9H3S7	PTPN23	-0.181	protein tyrosine phosphatase non-receptor type 23
P18433	PTPRA	-0.251	protein tyrosine phosphatase receptor type A
P10586-1	PTPRF	-0.522	protein tyrosine phosphatase receptor type F
Q15262-3	PTPRK	-0.547	protein tyrosine phosphatase receptor type K
Q15262-4	PTPRK	-0.45	protein tyrosine phosphatase receptor type K
Q86Y79	PTRH1	0.27	peptidyl-tRNA hydrolase 1 homolog
Q9Y3E5	PTRH2	0.462	peptidyl-tRNA hydrolase 2
Q00577	PURA	-0.188	purine rich element binding protein A
Q9Y606	PUS1	0.147	pseudouridine synthase 1
Q3MIT2	PUS10	-0.402	pseudouridine synthase 10
Q96PZ0	PUS7	-0.251	pseudouridine synthase 7
P15151-1	PVR	0.339	PVR cell adhesion molecule

P32322-3	PYCR1	0.177	pyrroline-5-carboxylate reductase 1
Q96C36	PYCR2	0.41	pyrroline-5-carboxylate reductase 2
P11216	PYGB	-0.175	glycogen phosphorylase B
P06737	PYGL	-0.25	glycogen phosphorylase L
Q9BRP8	PYM1	-0.26	PYM homolog 1, exon junction complex associated factor
Q96PU8	QKI	-0.319	QKI, KH domain containing RNA binding
Q15274	QPRT	-0.223	quinolinate phosphoribosyltransferase
Q6ZRP7	QSOX2	-0.219	quiescin sulfhydryl oxidase 2
Q9BXR0	QTRT1	-0.129	queuine tRNA-ribosyltransferase catalytic subunit 1
P61026	RAB10	0.245	RAB10, member RAS oncogene family
Q6IQ22	RAB12	0.105	RAB12, member RAS oncogene family
P61106	RAB14	0.128	RAB14, member RAS oncogene family
Q9NP72	RAB18	0.194	RAB18, member RAS oncogene family
P62820	RAB1A	0.1	RAB1A, member RAS oncogene family
Q9UL25	RAB21	0.199	RAB21, member RAS oncogene family
Q9UL26	RAB22A	0.276	RAB22A, member RAS oncogene family
P51159-1	RAB27A	0.184	RAB27A, member RAS oncogene family
P61019	RAB2A	0.098	RAB2A, member RAS oncogene family
Q8WUD1	RAB2B	0.348	RAB2B, member RAS oncogene family
Q13637	RAB32	0.134	RAB32, member RAS oncogene family
Q15286	RAB35	0.15	RAB35, member RAS oncogene family
O95716	RAB3D	-0.209	RAB3D, member RAS oncogene family
Q15042-1	RAB3GAP1	-0.165	RAB3 GTPase activating protein catalytic subunit 1
Q9H2M9	RAB3GAP2	-0.186	RAB3 GTPase activating non-catalytic protein subunit 2
Q86YS6	RAB43	-0.104	RAB43, member RAS oncogene family
P20338	RAB4A	-0.182	RAB4A, member RAS oncogene family
P51148-2	RAB5C	0.092	RAB5C, member RAS oncogene family
Q9BUV8-5	RAB5IF	0.309	RAB5 interacting factor
P61006	RAB8A	0.177	RAB8A, member RAS oncogene family
P51151	RAB9A	0.141	RAB9A, member RAS oncogene family
Q9UI14	RABAC1	-0.223	Rab acceptor 1
Q7Z6M1-1	RABEPK	-0.341	Rab9 effector protein with kelch motifs
Q9Y3P9	RABGAP1	-0.47	RAB GTPase activating protein 1
P53611	RABGGTB	-0.2	Rab geranylgeranyltransferase subunit beta
Q3YEC7-1	RABL6	-0.174	RAB, member RAS oncogene family like 6
P63000-2	RAC1	0.267	Rac family small GTPase 1
Q9H0H5	RACGAP1	0.28	Rac GTPase activating protein 1
P63244	RACK1	-0.265	receptor for activated C kinase 1
P54725-1	RAD23A	-0.29	RAD23 homolog A, nucleotide excision repair protein
P54725-3	RAD23A	-0.437	RAD23 homolog A, nucleotide excision repair protein
P54727	RAD23B	-0.26	RAD23 homolog B, nucleotide excision repair protein
Q96B01	RAD51AP1	0.348	RAD51 associated protein 1
P78406	RAE1	0.331	ribonucleic acid export 1
P11233	RALA	0.13	RAS like proto-oncogene A
P11234-2	RALB	0.355	RAS like proto-oncogene B
Q9UKM9	RALY	0.24	RALY heterogeneous nuclear ribonucleoprotein
P62826	RAN	0.119	RAN, member RAS oncogene family

P43487-2	RANBP1	-0.779	RAN binding protein 1
Q9H6Z4	RANBP3	-0.331	RAN binding protein 3
Q96S59-1	RANBP9	0.128	RAN binding protein 9
P46060	RANGAP1	-0.149	Ran GTPase activating protein 1
P52306-5	RAP1GDS1	-0.494	Rap1 GTPase-GDP dissociation stimulator 1
P61225	RAP2B	0.213	RAP2B, member of RAS oncogene family
Q8IY67-2	RAVER1	-0.225	ribonucleoprotein, PTB binding 1
P06400	RB1	-0.183	RB transcriptional corepressor 1
Q09028	RBBP4	-0.149	RB binding protein 4, chromatin remodeling factor
Q7Z6E9	RBBP6	0.672	RB binding protein 6, ubiquitin ligase
O75884	RBBP9	-0.273	RB binding protein 9, serine hydrolase
Q9BYM8	RBCK1	-0.212	RANBP2-type and C3HC4-type zinc finger containing 1
O43251-8	RBFOX2	-0.623	RNA binding fox-1 homolog 2
Q8N0T1	RBIS	-0.955	ribosomal biogenesis factor
Q9H477	RBKS	-0.451	ribokinase
Q8IXT5	RBM12B	0.203	RNA binding motif protein 12B
Q96PK6-1	RBM14	0.147	RNA binding motif protein 14
Q96T37	RBM15	0.313	RNA binding motif protein 15
Q96I25	RBM17	0.166	RNA binding motif protein 17
Q9Y4C8	RBM19	-0.154	RNA binding motif protein 19
Q9NW64	RBM22	0.261	RNA binding motif protein 22
P49756-1	RBM25	0.169	RNA binding motif protein 25
P98179	RBM3	-0.211	RNA binding motif protein 3
Q96EV2	RBM33	0.176	RNA binding motif protein 33
P42696	RBM34	-0.288	RNA binding motif protein 34
Q9BTD8	RBM42	-0.145	RNA binding motif protein 42
Q9BQ04	RBM4B	0.376	RNA binding motif protein 4B
P52756	RBM5	0.345	RNA binding motif protein 5
P38159-1	RBMX	0.191	RNA binding motif protein X-linked
Q9Y388	RBMX2	0.207	RNA binding motif protein X-linked 2
P02753	RBP4	-0.302	retinol binding protein 4
Q93062-3	RBPMS	-0.253	RNA binding protein, mRNA processing factor
Q5TC82-1	RC3H1	-0.136	ring finger and CCCH-type domains 1
P18754-2	RCC1	0.086	regulator of chromosome condensation 1
Q96I51	RCC1L	0.195	RCC1 like
Q9UKL0	RCOR1	-0.175	REST corepressor 1
Q8IZV5	RDH10	0.163	retinol dehydrogenase 10
Q8TC12	RDH11	0.187	retinol dehydrogenase 11
Q9HBH5	RDH14	0.355	retinol dehydrogenase 14
P35241-5	RDX	0.132	radixin
Q9H6H4	REEP4	0.336	receptor accessory protein 4
Q00765	REEP5	0.339	receptor accessory protein 5
Q04206	RELA	-0.34	RELA proto-oncogene, NF-kB subunit
Q9P260-2	RELCH	-0.128	RAB11 binding and LisH domain, coiled-coil and HEAT repeat containing
P78509	RELN	-0.468	reelin
Q9BWE0-4	REPIN1	0.251	replication initiator 1
Q8NC44	RETREG2	-0.127	reticulophagy regulator family member 2

Q86VR2	RETREG3	-0.156	reticulophagy regulator family member 3
Q6NUM9-1	RETSAT	0.39	retinol saturase
P35250-1	RFC2	-0.233	replication factor C subunit 2
P40937-1	RFC5	-0.075	replication factor C subunit 5
Q969G6	RFK	0.422	riboflavin kinase
Q6NTF9-2	RHBDD2	0.347	rhomboid domain containing 2
Q15382	RHEB	0.149	Ras homolog, mTORC1 binding
P84095	RHOG	0.18	ras homolog family member G
Q8IXI1	RHOT2	0.176	ras homolog family member T2
Q6R327-3	RICTOR	-0.148	RPTOR independent companion of MTOR complex 2
Q5UIP0	RIF1	0.238	replication timing regulatory factor 1
Q13671	RIN1	0.667	Ras and Rab interactor 1
Q6NUQ1	RINT1	-0.09	RAD50 interactor 1
Q9BRS2	RIOK1	-0.238	RIO kinase 1
Q9BVS4	RIOK2	-0.204	RIO kinase 2
O14730	RIOK3	0.2	RIO kinase 3
Q8IUF8	RIOX2	-0.161	ribosomal oxygenase 2
Q13546	RIPK1	0.098	receptor interacting serine/threonine kinase 1
Q96TC7	RMDN3	0.296	regulator of microtubule dynamics 3
Q9NWS8	RMND1	0.398	required for meiotic nuclear division 1 homolog
Q8TDP1	RNASEH2C	-0.379	ribonuclease H2 subunit C
Q9Y508	RNF114	0.538	ring finger protein 114
Q8NC42	RNF149	-0.234	ring finger protein 149
Q99496	RNF2	0.091	ring finger protein 2
Q63HN8-4	RNF213	-0.194	ring finger protein 213
Q8ND24	RNF214	-0.088	ring finger protein 214
O75150	RNF40	0.118	ring finger protein 40
O60942-1	RNGTT	-0.239	RNA guanylyltransferase and 5'-phosphatase
P13489	RNH1	-0.247	ribonuclease/angiogenin inhibitor 1
Q9H4A4	RNPEP	-0.174	arginyl aminopeptidase
Q15287-1	RNPS1	0.224	RNA binding protein with serine rich domain 1
Q9Y6N7-2	ROBO1	-0.534	roundabout guidance receptor 1
O75116	ROCK2	-0.211	Rho associated coiled-coil containing protein kinase 2
Q8TA86	RP9	-0.353	RP9 pre-mRNA splicing factor
Q9BWH6	RPAP1	-0.164	RNA polymerase II associated protein 1
Q9H6T3	RPAP3	-0.234	RNA polymerase II associated protein 3
Q96AT9	RPE	-0.187	ribulose-5-phosphate-3-epimerase
P49247	RPIA	-0.126	ribose 5-phosphate isomerase A
P30050	RPL12	-0.24	ribosomal protein L12
P50914	RPL14	0.831	ribosomal protein L14
Q07020	RPL18	0.601	ribosomal protein L18
P62829	RPL23	-0.301	ribosomal protein L23
P61254	RPL26	0.273	ribosomal protein L26
Q9UNX3	RPL26L1	-0.532	ribosomal protein L26 like 1
P46776	RPL27A	0.197	ribosomal protein L27a
P46779	RPL28	0.442	ribosomal protein L28
P62899	RPL31	-0.343	ribosomal protein L31

P18077	RPL35A	0.318	ribosomal protein L35a
Q9Y3U8	RPL36	-0.163	ribosomal protein L36
Q969Q0	RPL36AL	0.848	ribosomal protein L36a like
P05388	RPLP0	-0.215	ribosomal protein lateral stalk subunit P0
P04843	RPN1	0.169	ribophorin I
P04844-1	RPN2	0.198	ribophorin II
O75818	RPP40	-0.076	ribonuclease P/MRP subunit p40
Q96P16-1	RPRD1A	-0.113	regulation of nuclear pre-mRNA domain containing 1A
P62280	RPS11	0.648	ribosomal protein S11
P62841	RPS15	-0.199	ribosomal protein S15
P08708	RPS17	-0.233	ribosomal protein S17
P39019	RPS19	-0.19	ribosomal protein S19
Q86WX3	RPS19BP1	-0.435	ribosomal protein S19 binding protein 1
P15880	RPS2	-0.167	ribosomal protein S2
P60866	RPS20	-0.137	ribosomal protein S20
P63220	RPS21	-0.385	ribosomal protein S21
P42677	RPS27	-0.214	ribosomal protein S27
P62979	RPS27A	0.682	ribosomal protein S27a
Q71UM5	RPS27L	0.225	ribosomal protein S27 like
P62857	RPS28	-0.172	ribosomal protein S28
P62701	RPS4X	0.16	ribosomal protein S4 X-linked
P51812	RPS6KA3	-0.323	ribosomal protein S6 kinase A3
P46781	RPS9	0.309	ribosomal protein S9
P08865	RPSA	-0.211	ribosomal protein SA
Q8N122	RPTOR	-0.332	regulatory associated protein of MTOR complex 1
Q8IZ73	RPUSD2	-0.169	RNA pseudouridine synthase domain containing 2
P55042	RRAD	2.84	RRAD, Ras related glycolysis inhibitor and calcium channel regulator
Q7L523	RRAGA	0.46	Ras related GTP binding A
Q9HB90	RRAGC	0.157	Ras related GTP binding C
P62070-4	RRAS2	0.363	RAS related 2
Q9P2E9-1	RRBP1	0.09	ribosome binding protein 1
Q92766-2	RREB1	-0.263	ras responsive element binding protein 1
Q7LG56	RRM2B	0.216	ribonucleotide reductase regulatory TP53 inducible subunit M2B
Q7LG56-6	RRM2B	0.497	ribonucleotide reductase regulatory TP53 inducible subunit M2B
Q9NYV6	RRN3	0.325	RRN3 homolog, RNA polymerase I transcription factor
P56182	RRP1	0.184	ribosomal RNA processing 1
Q14684	RRP1B	0.148	ribosomal RNA processing 1B
Q96EU6	RRP36	-0.412	ribosomal RNA processing 36
O43159	RRP8	0.154	ribosomal RNA processing 8
Q15050	RRS1	-0.405	ribosome biogenesis regulator 1 homolog
Q9UHA3	RSL24D1	-0.215	ribosomal L24 domain containing 1
Q15404	RSU1	-0.121	Ras suppressor protein 1
Q9BY42	RTF2	-0.122	replication termination factor 2
Q9Y230	RUVBL2	-0.143	RuvB like AAA ATPase 2
Q6NW29	RWDD4	-0.543	RWD domain containing 4
P19793	RXRA	-0.637	retinoid X receptor alpha
P28702-3	RXRB	-0.274	retinoid X receptor beta

P23297	S100A1	-0.67	S100 calcium binding protein A1
P31949	S100A11	0.833	S100 calcium binding protein A11
Q99584	S100A13	-0.097	S100 calcium binding protein A13
Q96FQ6	S100A16	0.221	S100 calcium binding protein A16
P06703	S100A6	0.154	S100 calcium binding protein A6
P25815	S100P	0.219	S100 calcium binding protein P
Q96ER3	SAAL1	-0.18	serum amyloid A like 1
Q9UBE0	SAE1	-0.24	SUMO1 activating enzyme subunit 1
Q9Y3Z3	SAMHD1	-0.154	SAM and HD domain containing deoxynucleoside triphosphate triphosphohydrolase 1
O00422	SAP18	0.305	Sin3A associated protein 18
Q9Y6B6	SAR1B	-0.226	secretion associated Ras related GTPase 1B
P82979	SARNP	0.253	SAP domain containing ribonucleoprotein
Q9NP81	SARS2	0.241	seryl-tRNA synthetase 2, mitochondrial
O43290	SART1	-0.1	spliceosome associated factor 1, recruiter of U4/U6.U5 tri-snRNP
A3KN83	SBNO1	0.221	strawberry notch homolog 1
O15127	SCAMP2	0.091	secretory carrier membrane protein 2
Q8WTV0-2	SCARB1	-0.126	scavenger receptor class B member 1
Q8NBX0	SCCPDH	0.204	saccharopine dehydrogenase (putative)
Q8WU76-1	SCFD2	-0.361	sec1 family domain containing 2
O75880	SCO1	0.333	SCO cytochrome c oxidase assembly protein 1
O43819	SCO2	0.14	SCO cytochrome c oxidase assembly protein 2
P22307	SCP2	0.235	sterol carrier protein 2
Q9HB40	SCPEP1	-0.226	serine carboxypeptidase 1
Q12765-2	SCRN1	-0.172	secernin 1
P18827	SDC1	-0.476	syndecan 1
P34741	SDC2	-1.046	syndecan 2
O00560	SDCBP	0.522	syndecan binding protein
Q6IQ49-1	SDE2	0.175	SDE2 telomere maintenance homolog
Q99470	SDF2	0.412	stromal cell derived factor 2
P31040	SDHA	0.33	succinate dehydrogenase complex flavoprotein subunit A
P21912	SDHB	0.164	succinate dehydrogenase complex iron sulfur subunit B
Q9NRG7-2	SDR39U1	0.246	short chain dehydrogenase/reductase family 39U member 1
P67812-3	SEC11A	0.29	SEC11 homolog A, signal peptidase complex subunit
O75396	SEC22B	0.204	SEC22 homolog B, vesicle trafficking protein (gene/pseudogene)
Q15436	SEC23A	-0.232	Sec23 homolog A, coat complex II component
Q15437	SEC23B	-0.246	SEC23 homolog B, coat complex II component
Q9Y6Y8	SEC23IP	-0.228	SEC23 interacting protein
O95486	SEC24A	-0.449	SEC24 homolog A, COPII coat complex component
O95487-3	SEC24B	-0.139	SEC24 homolog B, COPII coat complex component
P53992	SEC24C	-0.194	SEC24 homolog C, COPII coat complex component
O94855-2	SEC24D	-0.36	SEC24 homolog D, COPII coat complex component
O94979-8	SEC31A	-0.25	SEC31 homolog A, COPII coat complex component
P61619	SEC61A1	-0.132	SEC61 translocon alpha 1 subunit
Q99442	SEC62	0.154	SEC62 homolog, preprotein translocation factor
Q13228-4	SELENBP1	-0.334	selenium binding protein 1
O60613	SELENOF	-0.305	selenoprotein F
Q9C0D9	SELENOI	0.533	selenoprotein I

P49903	SEPHS1	-0.201	selenophosphate synthetase 1
Q99611	SEPHS2	-0.133	selenophosphate synthetase 2
Q9NVA2-2	SEPTIN11	-0.293	septin 11
Q92599-1	SEPTIN8	-0.23	septin 8
Q9UHD8-1	SEPTIN9	-0.346	septin 9
Q8NC51-1	SERBP1	-0.306	SERPINE1 mRNA binding protein 1
P84101-1	SERF2	-0.308	small EDRK-rich factor 2
P05154	SERPINA5	-0.349	serpin family A member 5
P08185	SERPINA6	-0.389	serpin family A member 6
P05543	SERPINA7	-0.253	serpin family A member 7
P35237	SERPINB6	-0.186	serpin family B member 6
P50453	SERPINB9	0.211	serpin family B member 9
P01008	SERPINC1	-0.637	serpin family C member 1
P05546	SERPIND1	-0.437	serpin family D member 1
P05121	SERPINE1	0.899	serpin family E member 1
P08697-1	SERPINF2	-0.493	serpin family F member 2
P50454	SERPINH1	0.611	serpin family H member 1
P58004	SESN2	1.277	sestrin 2
Q01105	SET	-0.172	SET nuclear proto-oncogene
Q9BYW2	SETD2	-0.275	SET domain containing 2, histone lysine methyltransferase
Q86TU7	SETD3	-0.305	SET domain containing 3, actin histidine methyltransferase
Q15637-5	SF1	-0.27	splicing factor 1
Q15428	SF3A2	0.239	splicing factor 3a subunit 2
Q9Y3B4	SF3B6	0.187	splicing factor 3b subunit 6
P31947	SFN	0.41	stratifin
Q587I9	SFT2D3	0.262	SFT2 domain containing 3
Q9H9B4	SFXN1	0.268	sideroflexin 1
A0A0A0MS41	SFXN3	0.338	sideroflexin 3
Q8TD22	SFXN5	0.295	sideroflexin 5
Q562F6	SGO2	0.415	shugoshin 2
O95470	SGPL1	0.148	sphingosine-1-phosphate lyase 1
Q96EQ0	SGTB	-0.326	small glutamine rich tetratricopeptide repeat containing beta
Q9Y3L3-1	SH3BP1	-0.222	SH3 domain binding protein 1
Q9P0V3	SH3BP4	0.436	SH3 domain binding protein 4
Q9NR46-2	SH3GLB2	-0.364	SH3 domain containing GRB2 like, endophilin B2
Q8NEM2	SHCBP1	0.617	SHC binding and spindle associated 1
P34896	SHMT1	-0.442	serine hydroxymethyltransferase 1
P34897-1	SHMT2	0.304	serine hydroxymethyltransferase 2
Q9UQ13	SHOC2	0.491	SHOC2 leucine rich repeat scaffold protein
A0A0B4J2A0	SHPK	-0.305	sedoheptulokinase
Q2M3G4-1	SHROOM1	-0.383	shroom family member 1
A0MZ66-3	SHTN1	-0.125	shootin 1
Q99720	SIGMAR1	0.371	sigma non-opioid intracellular receptor 1
Q96EB6	SIRT1	0.37	sirtuin 1
Q9NTG7	SIRT3	0.241	sirtuin 3
Q9NXA8-1	SIRT5	-0.115	sirtuin 5
Q9NRC8	SIRT7	0.272	sirtuin 7

Q15477	SKIV2L	-0.13	Ski2 like RNA helicase
Q9UP95	SLC12A4	0.148	solute carrier family 12 member 4
Q9UHW9-2	SLC12A6	-0.279	solute carrier family 12 member 6
Q9Y666	SLC12A7	-0.232	solute carrier family 12 member 7
P53985	SLC16A1	0.272	solute carrier family 16 member 1
O15427	SLC16A3	-0.205	solute carrier family 16 member 3
P43007	SLC1A4	-0.291	solute carrier family 1 member 4
Q15758	SLC1A5	0.101	solute carrier family 1 member 5
Q8WUM9	SLC20A1	-0.424	solute carrier family 20 member 1
Q08357	SLC20A2	0.719	solute carrier family 20 member 2
Q9UGH3	SLC23A2	-0.318	solute carrier family 23 member 2
P53007	SLC25A1	0.17	solute carrier family 25 member 1
Q9UBX3-2	SLC25A10	0.308	solute carrier family 25 member 10
O75746	SLC25A12	0.192	solute carrier family 25 member 12
Q9UJS0-2	SLC25A13	0.346	solute carrier family 25 member 13
Q9Y619	SLC25A15	0.284	solute carrier family 25 member 15
Q6NUK1	SLC25A24	0.22	solute carrier family 25 member 24
Q00325-1	SLC25A3	0.608	solute carrier family 25 member 3
P05141	SLC25A5	0.549	solute carrier family 25 member 5
P12236	SLC25A6	0.675	solute carrier family 25 member 6
O14975	SLC27A2	-0.184	solute carrier family 27 member 2
Q6P1M0	SLC27A4	-0.162	solute carrier family 27 member 4
P11166	SLC2A1	-0.16	solute carrier family 2 member 1
Q9Y6M5	SLC30A1	0.977	solute carrier family 30 member 1
Q9HBR0	SLC38A10	-0.224	solute carrier family 38 member 10
Q99624	SLC38A3	-0.234	solute carrier family 38 member 3
Q15043	SLC39A14	-0.379	solute carrier family 39 member 14
P08195-4	SLC3A2	0.359	solute carrier family 3 member 2
Q8WWI5	SLC44A1	-0.334	solute carrier family 44 member 1
Q9UPY5	SLC7A11	0.696	solute carrier family 7 member 11
Q01650	SLC7A5	0.255	solute carrier family 7 member 5
O14745	SLC9A3R1	-0.376	SLC9A3 regulator 1
Q15599	SLC9A3R2	-0.297	SLC9A3 regulator 2
O95391	SLU7	0.398	SLU7 homolog, splicing factor
Q99717	SMAD5	0.532	SMAD family member 5
P51532-1	SMARCA4	0.13	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a
O60264	SMARCA5	0.298	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a,
Q92925	SMARCD2	-0.231	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d
Q9NTJ3-1	SMC4	0.074	structural maintenance of chromosomes 4
Q8IY18	SMC5	0.147	structural maintenance of chromosomes 5
A6NHR9-1	SMCHD1	0.139	structural maintenance of chromosomes flexible hinge domain containing 1
Q96Q15-1	SMG1	-0.272	SMG1 nonsense mediated mRNA decay associated PI3K related kinase
Q86US8-1	SMG6	-0.547	SMG6 nonsense mediated mRNA decay factor
Q8ND04-2	SMG8	0.231	SMG8 nonsense mediated mRNA decay factor
Q8N5G0-2	SMIM20	0.555	small integral membrane protein 20
O75940	SMNDC1	-0.216	survival motor neuron domain containing 1
Q9NWM0	SMOX	0.462	spermine oxidase

P52788	SMS	-0.228	spermine synthase
P53814-6	SMTN	0.989	smoothelin
Q2TAY7	SMU1	0.248	SMU1 DNA replication regulator and spliceosomal factor
Q9NRG4	SMYD2	-0.364	SET and MYND domain containing 2
Q6GMV2	SMYD5	-0.355	SMYD family member 5
O00161	SNAP23	-0.148	synaptosome associated protein 23
Q7KZF4	SND1	-0.232	staphylococcal nuclease and tudor domain containing 1
Q96H20	SNF8	-0.213	SNF8 subunit of ESCRT-II
Q8TAD8	SNIP1	0.341	Smad nuclear interacting protein 1
O75643-1	SNRNP200	0.187	small nuclear ribonucleoprotein U5 subunit 200
P62314	SNRPD1	0.284	small nuclear ribonucleoprotein D1 polypeptide
P62316	SNRPD2	-0.147	small nuclear ribonucleoprotein D2 polypeptide
P62304	SNRPE	0.115	small nuclear ribonucleoprotein polypeptide E
Q13425-1	SNTB2	0.217	syntrophin beta 2
P55769	SNU13	-0.152	small nuclear ribonucleoprotein 13
Q13596	SNX1	-0.173	sorting nexin 1
Q9UMY4	SNX12	-0.31	sorting nexin 12
Q9NRS6	SNX15	-0.363	sorting nexin 15
Q15036-1	SNX17	-0.228	sorting nexin 17
O60749	SNX2	-0.173	sorting nexin 2
Q96L92	SNX27	-0.168	sorting nexin 27
Q5VWJ9	SNX30	-0.265	sorting nexin family member 30
O95219	SNX4	-0.244	sorting nexin 4
Q9Y5X3	SNX5	-0.178	sorting nexin 5
Q9UNH6-3	SNX7	-0.363	sorting nexin 7
Q9Y5X2	SNX8	-0.389	sorting nexin 8
P04179	SOD2	0.419	superoxide dismutase 2
O94964-2	SOGA1	-0.124	suppressor of glucose, autophagy associated 1
O94875-11	SORBS2	-0.371	sorbin and SH3 domain containing 2
Q00796	SORD	-0.414	sorbitol dehydrogenase
Q92673	SORL1	-0.946	sortilin related receptor 1
Q99523	SORT1	-0.378	sortilin 1
P48436	SOX9	-0.291	SRY-box transcription factor 9
Q07617	SPAG1	0.343	sperm associated antigen 1
Q96R06	SPAG5	0.148	sperm associated antigen 5
O75391	SPAG7	-0.69	sperm associated antigen 7
O60271	SPAG9	-0.211	sperm associated antigen 9
Q8TB22-2	SPATA20	0.238	spermatogenesis associated 20
Q8NB90-1	SPATA5	-0.443	spermatogenesis associated 5
Q9HBM1	SPC25	-0.197	SPC25 component of NDC80 kinetochore complex
Q15005	SPCS2	0.232	signal peptidase complex subunit 2
P61009	SPCS3	0.729	signal peptidase complex subunit 3
Q96EA4	SPDL1	0.479	spindle apparatus coiled-coil protein 1
Q9H2V7	SPNS1	0.11	sphingolipid transporter 1 (putative)
P10451	SPP1	-0.308	secreted phosphoprotein 1
P35270	SPR	-0.104	sepiapterin reductase
Q5W111	SPRYD7	0.115	SPRY domain containing 7

Q01082-3	SPTBN1	0.677	spectrin beta, non-erythrocytic 1
Q9NUV7	SPTLC3	-0.412	serine palmitoyltransferase long chain base subunit 3
Q68D10	SPTY2D1	0.805	SPT2 chromatin protein domain containing 1
Q14534	SQLE	-0.153	squalene epoxidase
Q9Y6N5	SQOR	0.5	sulfide quinone oxidoreductase
Q13501-1	SQSTM1	0.323	sequestosome 1
Q9HD15	SRA1	-0.222	steroid receptor RNA activator 1
P12931-2	SRC	0.16	SRC proto-oncogene, non-receptor tyrosine kinase
Q6ZRS2	SRCAP	0.298	Snf2 related CREBBP activator protein
O75044	SRGAP2	-0.265	SLIT-ROBO Rho GTPase activating protein 2
P19623	SRM	-0.114	spermidine synthase
Q9UHB9	SRP68	-0.108	signal recognition particle 68
O76094	SRP72	-0.12	signal recognition particle 72
P49458	SRP9	-0.188	signal recognition particle 9
Q96SB4	SRPK1	-0.249	SRSF protein kinase 1
Q9BXP5	SRRT	0.157	serrate, RNA effector molecule
Q01130	SRSF2	-0.296	serine and arginine rich splicing factor 2
Q13247	SRSF6	0.239	serine and arginine rich splicing factor 6
Q16629	SRSF7	0.448	serine and arginine rich splicing factor 7
Q9BYN0	SRXN1	1.178	sulfiredoxin 1
Q04837	SSBP1	0.3	single stranded DNA binding protein 1
P43307	SSR1	0.14	signal sequence receptor subunit 1
Q9UNL2-2	SSR3	0.169	signal sequence receptor subunit 3
P51571	SSR4	0.19	signal sequence receptor subunit 4
Q9NP77	SSU72	-0.197	SSU72 homolog, RNA polymerase II CTD phosphatase
P50502	ST13	-0.196	ST13 Hsp70 interacting protein
P15907	ST6GAL1	-0.426	ST6 beta-galactoside alpha-2,6-sialyltransferase 1
O95630	STAMBP	-0.232	STAM binding protein
Q9Y365	STARD10	-0.184	StAR related lipid transfer domain containing 10
Q9NUL3	STAU2	-0.289	staufen double-stranded RNA binding protein 2
Q658P3-2	STEAP3	-0.877	STEAP3 metalloreductase
Q9Y6E0	STK24	-0.303	serine/threonine kinase 24
Q13188-2	STK3	-0.721	serine/threonine kinase 3
Q8TDR2	STK35	0.214	serine/threonine kinase 35
Q9UEW8	STK39	-0.46	serine/threonine kinase 39
Q13043-1	STK4	-0.095	serine/threonine kinase 4
P16949-1	STMN1	-0.308	stathmin 1
P27105	STOM	0.609	stomatin
Q9UJZ1	STOML2	0.256	stomatin like 2
O43815	STRN	-0.161	striatin
P46977	STT3A	0.144	STT3 oligosaccharyltransferase complex catalytic subunit A
Q8TCJ2	STT3B	0.137	STT3 oligosaccharyltransferase complex catalytic subunit B
Q9UNE7-1	STUB1	-0.19	STIP1 homology and U-box containing protein 1
Q86Y82	STX12	0.137	syntaxin 12
Q9P2W9	STX18	-0.165	syntaxin 18
Q13277	STX3	0.455	syntaxin 3
Q12846	STX4	0.153	syntaxin 4

O43752	STX6	0.307	syntaxin 6
Q9UNK0	STX8	-0.416	syntaxin 8
O00186	STXBP3	0.189	syntaxin binding protein 3
P53999	SUB1	0.211	SUB1 regulator of transcription
Q9P2R7	SUCLA2	0.314	succinate-CoA ligase ADP-forming beta subunit
P53597	SUCLG1	0.396	succinate-CoA ligase alpha subunit
Q96I99	SUCLG2	0.195	succinate-CoA ligase GDP-forming beta subunit
P50225	SULT1A1	-0.21	sulfotransferase family 1A member 1
P0DMM9	SULT1A3/SULT1A4	-0.241	sulfotransferase family 1A member 3
Q06520	SULT2A1	-0.357	sulfotransferase family 2A member 1
O94901-9	SUN1	0.323	Sad1 and UNC84 domain containing 1
Q9Y5B9	SUPT16H	0.143	SPT16 homolog, facilitates chromatin remodeling subunit
Q8IYB8	SUPV3L1	0.35	Suv3 like RNA helicase
O15260	SURF4	0.101	surfeit 4
O75683	SURF6	-0.855	surfeit 6
Q9UH65	SWAP70	0.099	switching B cell complex subunit SWAP70
Q96A49	SYAP1	-0.283	synapse associated protein 1
O95926	SYF2	-0.279	SYF2 pre-mRNA splicing factor
Q9UMZ2	SYNRG	-0.393	synergin gamma
Q86TM6	SYVN1	0.625	synoviolin 1
Q15750-1	TAB1	-0.217	TGF-beta activated kinase 1 (MAP3K7) binding protein 1
O75410-2	TACC1	-0.176	transforming acidic coiled-coil containing protein 1
O95359	TACC2	-0.187	transforming acidic coiled-coil containing protein 2
Q9BSH4	TACO1	0.161	translational activator of cytochrome c oxidase I
O75528	TADA3	0.172	transcriptional adaptor 3
P49848-3	TAF6	-0.152	TATA-box binding protein associated factor 6
Q15545	TAF7	0.138	TATA-box binding protein associated factor 7
Q7Z7C8-4	TAF8	0.117	TATA-box binding protein associated factor 8
Q01995	TAGLN	-0.316	transgelin
P37802-2	TAGLN2	0.225	transgelin 2
Q96BW9-3	TAMM41	0.483	TAM41 mitochondrial translocator assembly and maintenance homolog
Q9C0B7	TANGO6	-0.331	transport and golgi organization 6 homolog
Q03518	TAP1	0.416	transporter 1, ATP binding cassette subfamily B member
O15533-3	TAPBP	0.265	TAP binding protein
P26639-2	TARS1	-0.164	threonyl-tRNA synthetase 1
Q9BW92	TARS2	0.232	threonyl-tRNA synthetase 2, mitochondrial
O14907	TAX1BP3	0.156	Tax1 binding protein 3
Q9BXI6-2	TBC1D10A	0.304	TBC1 domain family member 10A
Q9NVG8	TBC1D13	-0.308	TBC1 domain family member 13
Q96BZ9-3	TBC1D20	0.423	TBC1 domain family member 20
Q8WUA7	TBC1D22A	-0.335	TBC1 domain family member 22A
O60343-1	TBC1D4	-0.235	TBC1 domain family member 4
Q92609-2	TBC1D5	-0.231	TBC1 domain family member 5
O75347	TBCA	-0.28	tubulin folding cofactor A
Q99426	TBCB	-0.203	tubulin folding cofactor B
Q9BTW9-4	TBCD	-0.214	tubulin folding cofactor D
Q15813-2	TBCE	-0.131	tubulin folding cofactor E

Q9BZK7	TBL1XR1	-0.209	transducin beta like 1 X-linked receptor 1
Q9Y4P3	TBL2	0.143	transducin beta like 2
Q969Z0	TBRG4	0.418	transforming growth factor beta regulator 4
O75764	TCEA3	-0.161	transcription elongation factor A3
Q15170-2	TCEAL1	-0.269	transcription elongation factor A like 1
Q9NUW8	TDP1	-0.217	tyrosyl-DNA phosphodiesterase 1
Q9NZ01-1	TECR	0.237	trans-2,3-enoyl-CoA reductase
Q96QE5	TEFM	0.477	transcription elongation factor, mitochondrial
Q9Y4R8	TELO2	-0.144	telomere maintenance 2
Q15554	TERF2	0.157	telomeric repeat binding factor 2
Q9NYB0	TERF2IP	0.443	TERF2 interacting protein
Q9UGI8	TES	0.253	testin LIM domain protein
Q96BS2	TESC	-0.371	tescalcin
Q9NXF1	TEX10	0.188	testis expressed 10
Q8IWB9-2	TEX2	-0.196	testis expressed 2
P02787	TF	-0.282	transferrin
Q00059	TFAM	0.939	transcription factor A, mitochondrial
Q9H5Q4	TFB2M	0.51	transcription factor B2, mitochondrial
Q14186	TFDP1	-0.17	transcription factor Dp-1
Q92734	TFG	-0.131	trafficking from ER to golgi regulator
P10646	TFPI	-0.24	tissue factor pathway inhibitor
P01137	TGFB1	0.56	transforming growth factor beta 1
P37173-2	TGFBR2	-0.47	transforming growth factor beta receptor 2
Q03167	TGFBR3	-0.652	transforming growth factor beta receptor 3
P21980	TGM2	-0.121	transglutaminase 2
O43493-1	TGOLN2	-0.229	trans-golgi network protein 2
P07996	THBS1	0.377	thrombospondin 1
Q96FV9	THOC1	0.139	THO complex 1
Q13769	THOC5	0.108	THO complex 5
Q6I9Y2	THOC7	-0.193	THO complex 7
P52888	THOP1	-0.279	thimet oligopeptidase 1
Q9NXG2	THUMPD1	0.132	THUMP domain containing 1
Q9BV44	THUMPD3	-0.128	THUMP domain containing 3
Q9P016	THYN1	-0.168	thymocyte nuclear protein 1
Q01085-2	TIAL1	-0.215	TIA1 cytotoxic granule associated RNA binding protein like 1
Q9NQ88	TIGAR	0.3	TP53 induced glycolysis regulatory phosphatase
P62072	TIMM10	0.097	translocase of inner mitochondrial membrane 10
Q9Y5J6	TIMM10B	-0.123	translocase of inner mitochondrial membrane 10B
Q9Y5L4	TIMM13	-0.253	translocase of inner mitochondrial membrane 13
Q99595	TIMM17A	-0.465	translocase of inner mitochondrial membrane 17A
Q9BVV7	TIMM21	0.302	translocase of inner mitochondrial membrane 21
O14925	TIMM23	-0.138	translocase of inner mitochondrial membrane 23
Q9BSF4	TIMM29	-0.571	translocase of inner mitochondrial membrane 29
O43615	TIMM44	0.505	translocase of inner mitochondrial membrane 44
Q3ZCQ8-2	TIMM50	0.21	translocase of inner mitochondrial membrane 50
Q9BVW5	TIPIN	-0.268	TIMELESS interacting protein
Q5JTD0	TJAP1	-0.125	tight junction associated protein 1

Q9UDY2	TJP2	-0.326	tight junction protein 2
P04183	TK1	0.44	thymidine kinase 1
Q3LXA3	TKFC	-0.415	triokinase and FMN cyclase
P29401-2	TKT	-0.086	transketolase
Q99805	TM9SF2	-0.196	transmembrane 9 superfamily member 2
Q9HD45	TM9SF3	0.298	transmembrane 9 superfamily member 3
Q96EY4	TMA16	0.17	translation machinery associated 16 homolog
Q9Y2S6	TMA7	0.177	translation machinery associated 7 homolog
Q9UM00	TMCO1	0.393	transmembrane and coiled-coil domains 1
P49755	TMED10	0.158	transmembrane p24 trafficking protein 10
Q9Y3A6	TMED5	0.378	transmembrane p24 trafficking protein 5
Q9NUM4	TMEM106B	-0.143	transmembrane protein 106B
P17152	TMEM11	0.332	transmembrane protein 11
Q9H061	TMEM126A	0.401	transmembrane protein 126A
Q9P0S9	TMEM14C	0.32	transmembrane protein 14C
Q9HC07	TMEM165	0.082	transmembrane protein 165
Q8TBQ9	TMEM167A	0.354	transmembrane protein 167A
Q53S58	TMEM177	0.359	transmembrane protein 177
Q8N511	TMEM199	0.298	transmembrane protein 199
Q5SNT2-1	TMEM201	0.573	transmembrane protein 201
Q96SK2	TMEM209	0.298	transmembrane protein 209
Q96A57-2	TMEM230	0.354	transmembrane protein 230
Q8WUH6	TMEM263	0.188	transmembrane protein 263
P57088	TMEM33	0.397	transmembrane protein 33
Q9BTV4	TMEM43	0.164	transmembrane protein 43
Q9BXS4	TMEM59	-0.213	transmembrane protein 59
Q9BUB7	TMEM70	0.551	transmembrane protein 70
P42166	TMPO	0.218	thymopoietin
P42167	TMPO	0.341	thymopoietin
P63313	TMSB10/TMSB4X	0.433	thymosin beta 4 X-linked
Q9H3N1	TMX1	0.177	thioredoxin related transmembrane protein 1
Q9Y320	TMX2	0.246	thioredoxin related transmembrane protein 2
Q9H1E5	TMX4	0.277	thioredoxin related transmembrane protein 4
O00220	TNFRSF10A	0.421	TNF receptor superfamily member 10a
O14763	TNFRSF10B	0.168	TNF receptor superfamily member 10b
Q9C0C2	TNKS1BP1	-0.123	tankyrase 1 binding protein 1
O14787-2	TNPO2	-0.231	transportin 2
Q8NDV7	TNRC6A	-0.137	trinucleotide repeat containing adaptor 6A
Q68CZ2-1	TNS3	-0.333	tensin 3
O60784	TOM1	-0.327	target of myb1 membrane trafficking protein
Q9NS69	TOMM22	0.156	translocase of outer mitochondrial membrane 22
Q15785	TOMM34	0.269	translocase of outer mitochondrial membrane 34
O96008	TOMM40	0.134	translocase of outer mitochondrial membrane 40
Q8N4H5	TOMM5	0.233	translocase of outer mitochondrial membrane 5
O94826	TOMM70	0.196	translocase of outer mitochondrial membrane 70
P11387	TOP1	0.629	DNA topoisomerase I
P11388-4	TOP2A	0.69	DNA topoisomerase II alpha

Q02880	TOP2B	0.436	DNA topoisomerase II beta
O14656	TOR1A	0.175	torsin family 1 member A
Q5JTV8	TOR1AIP1	0.402	torsin 1A interacting protein 1
Q8NFQ8	TOR1AIP2	0.293	torsin 1A interacting protein 2
O14657	TOR1B	0.131	torsin family 1 member B
O94842	TOX4	0.229	TOX high mobility group box family member 4
P04637	TP53	1.04	tumor protein p53
Q53FA7	TP53I3	0.428	tumor protein p53 inducible protein 3
P55327-3	TPD52	-0.403	tumor protein D52
P60174	TPI1	-0.186	triosephosphate isomerase 1
P09493-2	TPM1	-0.375	tropomyosin 1
P67936	TPM4	-0.179	tropomyosin 4
Q9ULW0	TPX2	0.802	TPX2 microtubule nucleation factor
Q13595	TRA2A	0.183	transformer 2 alpha homolog
P62995	TRA2B	0.267	transformer 2 beta homolog
Q9H4I3-1	TRABD	0.215	TraB domain containing
Q12931	TRAP1	0.295	TNF receptor associated protein 1
O43617-1	TRAPPC3	-0.167	trafficking protein particle complex 3
Q9Y296	TRAPPC4	0.182	trafficking protein particle complex 4
Q8IUR0	TRAPPC5	0.105	trafficking protein particle complex 5
Q86SZ2	TRAPPC6B	-0.207	trafficking protein particle complex 6B
O15164	TRIM24	-0.26	tripartite motif containing 24
Q14258	TRIM25	-0.121	tripartite motif containing 25
Q12899	TRIM26	0.191	tripartite motif containing 26
P14373	TRIM27	-0.166	tripartite motif containing 27
Q13263	TRIM28	0.274	tripartite motif containing 28
Q9UPN9-1	TRIM33	-0.319	tripartite motif containing 33
O75962-1	TRIO	-0.798	trio Rho guanine nucleotide exchange factor
Q9H2D6	TRIOBP	0.195	TRIO and F-actin binding protein
Q15642	TRIP10	-0.181	thyroid hormone receptor interactor 10
Q15643	TRIP11	0.188	thyroid hormone receptor interactor 11
Q15645	TRIP13	-0.176	thyroid hormone receptor interactor 13
Q15650	TRIP4	-0.424	thyroid hormone receptor interactor 4
Q9BQ61	TRIR	-0.399	telomerase RNA component interacting RNase
Q7L0Y3	TRMT10C	0.559	tRNA methyltransferase 10C, mitochondrial RNase P subunit
Q8IZ69	TRMT2A	-0.296	tRNA methyltransferase 2 homolog A
O75648	TRMU	0.242	tRNA 5-methylaminomethyl-2-thiouridylate methyltransferase
Q8TEL6	TRPC4AP	-0.364	transient receptor potential cation channel subfamily C member 4 associated protein
O95900	TRUB2	0.173	TruB pseudouridine synthase family member 2
Q15631-1	TSN	-0.205	translin
Q99598	TSNAX	-0.087	translin associated factor X
Q9H0U9	TSPYL1	0.46	TSPY like 1
Q9H2G4	TSPYL2	0.961	TSPY like 2
Q16762	TST	0.394	thiosulfate sulfurtransferase
Q13630	TSTA3	-0.208	tissue specific transplantation antigen P35B
Q99614	TTC1	-0.23	tetratricopeptide repeat domain 1
Q96AE7-2	TTC17	-0.18	tetratricopeptide repeat domain 17

Q6P3X3	TTC27	-0.474	tetratricopeptide repeat domain 27
Q5R3I4	TTC38	-0.486	tetratricopeptide repeat domain 38
Q14166	TTLL12	-0.235	tubulin tyrosine ligase like 12
Q9BTX7	TTPAL	-0.371	alpha tocopherol transfer protein like
P68366	TUBA4A	0.394	tubulin alpha 4a
P07437	TUBB	-0.074	tubulin beta class I
Q13885	TUBB2A	0.38	tubulin beta 2A class IIa
Q13509	TUBB3	0.24	tubulin beta 3 class III
Q9BUF5	TUBB6	0.498	tubulin beta 6 class V
Q9BSJ2-4	TUBGCP2	-0.09	tubulin gamma complex associated protein 2
Q96CW5	TUBGCP3	-0.123	tubulin gamma complex associated protein 3
P49411	TUFM	0.308	Tu translation elongation factor, mitochondrial
O75896	TUSC2	0.175	tumor suppressor 2, mitochondrial calcium regulator
Q5TAX3	TUT4	-0.251	terminal uridylyl transferase 4
Q96RR1	TWNK	0.314	twinkle mtDNA helicase
P10599-1	TXN	-0.227	thioredoxin
Q99757	TXN2	0.878	thioredoxin 2
Q96J42-1	TXNDC15	-0.205	thioredoxin domain containing 15
Q9BRA2	TXNDC17	-0.183	thioredoxin domain containing 17
O14530	TXNDC9	0.232	thioredoxin domain containing 9
O43396	TXNL1	-0.114	thioredoxin like 1
P83876	TXNL4A	-0.376	thioredoxin like 4A
Q9NX01	TXNL4B	0.38	thioredoxin like 4B
P19971-2	TYMP	-0.478	thymidine phosphorylase
P04818	TYMS	0.172	thymidylate synthetase
Q2T9J0	TYSND1	-0.401	trypsin domain containing 1
Q01081	U2AF1/U2AF1L5	0.155	U2 small nuclear RNA auxiliary factor 1
P26368	U2AF2	-0.099	U2 small nuclear RNA auxiliary factor 2
Q9BZF9	UACA	-0.226	uveal autoantigen with coiled-coil domains and ankyrin repeats
Q3KQV9	UAP1L1	-0.255	UDP-N-acetylglucosamine pyrophosphorylase 1 like 1
P22314	UBA1	-0.169	ubiquitin like modifier activating enzyme 1
Q9UBT2	UBA2	-0.174	ubiquitin like modifier activating enzyme 2
Q8TBC4-1	UBA3	-0.12	ubiquitin like modifier activating enzyme 3
Q9GZZ9-1	UBA5	-0.212	ubiquitin like modifier activating enzyme 5
A0AVT1-1	UBA6	-0.125	ubiquitin like modifier activating enzyme 6
Q9BSL1	UBAC1	-0.364	UBA domain containing 1
Q5T6F2	UBAP2	-0.159	ubiquitin associated protein 2
O00762	UBE2C	0.083	ubiquitin conjugating enzyme E2 C
P51965-1	UBE2E1	-0.395	ubiquitin conjugating enzyme E2 E1
Q969T4	UBE2E3	-0.449	ubiquitin conjugating enzyme E2 E3
P62253	UBE2G1	-0.199	ubiquitin conjugating enzyme E2 G1
P63279	UBE2I	-0.189	ubiquitin conjugating enzyme E2 I
P61086	UBE2K	-0.348	ubiquitin conjugating enzyme E2 K
P68036	UBE2L3	-0.295	ubiquitin conjugating enzyme E2 L3
P61081	UBE2M	-0.205	ubiquitin conjugating enzyme E2 M
P61088	UBE2N	-0.321	ubiquitin conjugating enzyme E2 N
Q9C0C9	UBE2O	-0.194	ubiquitin conjugating enzyme E2 O

Q712K3	UBE2R2	-0.359	ubiquitin conjugating enzyme E2 R2
Q16763	UBE2S	0.859	ubiquitin conjugating enzyme E2 S
Q9NPD8	UBE2T	-0.152	ubiquitin conjugating enzyme E2 T
Q13404-1	UBE2V1	-0.299	ubiquitin conjugating enzyme E2 V1
Q15386-1	UBE3C	-0.23	ubiquitin protein ligase E3C
Q14139-2	UBE4A	-0.212	ubiquitination factor E4A
O95155-4	UBE4B	-0.309	ubiquitination factor E4B
P11441	UBL4A	-0.147	ubiquitin like 4A
Q96S82	UBL7	-0.316	ubiquitin like 7
Q8WVY7	UBLCP1	-0.315	ubiquitin like domain containing CTD phosphatase 1
Q9UMX0-1	UBQLN1	-0.139	ubiquilin 1
Q9NRR5	UBQLN4	-0.276	ubiquilin 4
Q8IWV7	UBR1	-0.304	ubiquitin protein ligase E3 component n-recognin 1
Q8IWV8	UBR2	-0.2	ubiquitin protein ligase E3 component n-recognin 2
Q5T4S7-2	UBR4	-0.264	ubiquitin protein ligase E3 component n-recognin 4
Q8N806	UBR7	-0.203	ubiquitin protein ligase E3 component n-recognin 7 (putative)
Q04323-1	UBXN1	-0.261	UBX domain protein 1
Q92575	UBXN4	0.183	UBX domain protein 4
Q9BZX2-1	UCK2	-0.13	uridine-cytidine kinase 2
Q9Y3C8	UFC1	-0.191	ubiquitin-fold modifier conjugating enzyme 1
Q9NUQ7	UFSP2	0.187	UFM1 specific peptidase 2
O60701	UGDH	-0.092	UDP-glucose 6-dehydrogenase
Q16851	UGP2	-0.128	UDP-glucose pyrophosphorylase 2
P16662	UGT2B7	0.581	UDP glucuronosyltransferase family 2 member B7
Q96T88-2	UHRF1	-0.445	ubiquitin like with PHD and ring finger domains 1
Q6BDS2	UHRF1BP1	-0.181	UHRF1 binding protein 1
A0JNW5	UHRF1BP1L	-0.263	UHRF1 binding protein 1 like
Q96RL1	UIMC1	-0.151	ubiquitin interaction motif containing 1
Q70J99-3	UNC13D	-0.262	unc-13 homolog D
Q92900	UPF1	-0.119	UPF1 RNA helicase and ATPase
Q9HAU5	UPF2	-0.178	UPF2 regulator of nonsense mediated mRNA decay
Q9BZI7-1	UPF3B	0.227	UPF3B regulator of nonsense mediated mRNA decay
Q9BRT2	UQCC2	-0.132	ubiquinol-cytochrome c reductase complex assembly factor 2
P31930	UQCRC1	0.276	ubiquinol-cytochrome c reductase core protein 1
P47985	UQCRFS1	0.18	ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1
O14949	UQCRQ	0.301	ubiquinol-cytochrome c reductase complex III subunit VII
Q8TCY9	URGCP	0.151	upregulator of cell proliferation
P06132	UROD	-0.322	uroporphyrinogen decarboxylase
O60763-1	USO1	-0.175	USO1 vesicle transport factor
O60763-2	USO1	-0.3	USO1 vesicle transport factor
Q14694-2	USP10	-0.178	ubiquitin specific peptidase 10
Q92995	USP13	-0.364	ubiquitin specific peptidase 13
P54578	USP14	-0.134	ubiquitin specific peptidase 14
O94966-5	USP19	0.144	ubiquitin specific peptidase 19
Q9UPU5	USP24	-0.155	ubiquitin specific peptidase 24
Q96RU2-2	USP28	-0.191	ubiquitin specific peptidase 28
Q9Y6I4	USP3	0.121	ubiquitin specific peptidase 3

Q8NFA0	USP32	-0.421	ubiquitin specific peptidase 32
Q8TEY7	USP33	-0.413	ubiquitin specific peptidase 33
Q70CQ2	USP34	-0.298	ubiquitin specific peptidase 34
Q96K76	USP47	-0.166	ubiquitin specific peptidase 47
Q86UV5-8	USP48	-0.358	ubiquitin specific peptidase 48
P45974-1	USP5	-0.159	ubiquitin specific peptidase 5
Q93009	USP7	-0.123	ubiquitin specific peptidase 7
P40818	USP8	-0.088	ubiquitin specific peptidase 8
Q93008	USP9X	-0.247	ubiquitin specific peptidase 9 X-linked
Q9BVJ6-1	UTP14A	-0.347	UTP14A small subunit processome component
Q8TED0	UTP15	0.206	UTP15 small subunit processome component
Q68CQ4	UTP25	0.157	UTP25 small subunit processor component
Q9NQZ2	UTP3	0.501	UTP3 small subunit processome component
Q969X6	UTP4	0.314	UTP4 small subunit processome component
P46939	UTRN	-0.103	utrophin
Q08AM6	VAC14	-0.337	VAC14 component of PIKFYVE complex
P51809	VAMP7	0.172	vesicle associated membrane protein 7
Q9BV40	VAMP8	0.185	vesicle associated membrane protein 8
Q9P0L0-2	VAPA	0.401	VAMP associated protein A
O95292	VAPB	0.191	VAMP associated protein B and C
P26640	VARS	-0.179	valyl-tRNA synthetase 1
Q6EMK4	VASN	-0.405	vasorin
Q99536	VAT1	-0.17	vesicle amine transport 1
P52735	VAV2	-0.362	vav guanine nucleotide exchange factor 2
P52735-2	VAV2	-0.421	vav guanine nucleotide exchange factor 2
P61758	VBP1	-0.212	VHL binding protein 1
P18206	VCL	-0.386	vinculin
P21796	VDAC1	0.319	voltage dependent anion channel 1
P45880-1	VDAC2	0.532	voltage dependent anion channel 2
Q9Y277-2	VDAC3	0.289	voltage dependent anion channel 3
Q9H9C1-1	VIPAS39	-0.427	VPS33B interacting protein, apical-basolateral polarity regulator, spe-39 homolog
Q69YN4	VIRMA	0.199	vir like m6A methyltransferase associated
Q9BRG1	VPS25	-0.217	vacuolar protein sorting 25 homolog
O75436	VPS26A	-0.075	VPS26, retromer complex component A
Q4G0F5	VPS26B	-0.181	VPS26, retromer complex component B
Q9UK41-1	VPS28	-0.228	VPS28 subunit of ESCRT-I
Q9UBQ0	VPS29	-0.285	VPS29 retromer complex component
Q96QK1	VPS35	-0.303	VPS35 retromer complex component
Q86VN1	VPS36	-0.14	vacuolar protein sorting 36 homolog
Q96JG6	VPS50	-0.364	VPS50 subunit of EARP/GARPII complex
Q9UID3-1	VPS51	-0.102	VPS51 subunit of GARP complex
Q5VIR6-4	VPS53	-0.36	VPS53 subunit of GARP complex
P62760	VSNL1	-0.467	visinin like 1
P23381	WARS1	-0.375	tryptophanyl-tRNA synthetase 1
Q9UGM6	WARS2	0.285	tryptophanyl tRNA synthetase 2, mitochondrial
Q9Y6W5	WASF2	-0.097	WASP family member 2
Q2M389	WASHC4	-0.25	WASH complex subunit 4

Q12768	WASHC5	-0.357	WASH complex subunit 5
Q9H6R7	WDCP	-0.17	WD repeat and coiled coil containing
O75717	WDHD1	-0.174	WD repeat and HMG-box DNA binding protein 1
Q9BZH6	WDR11	-0.192	WD repeat domain 11
Q9GZL7	WDR12	-0.252	WD repeat domain 12
Q9H7D7	WDR26	0.102	WD repeat domain 26
Q9UNX4	WDR3	0.263	WD repeat domain 3
Q9C0J8	WDR33	-0.078	WD repeat domain 33
Q8NI36	WDR36	0.185	WD repeat domain 36
Q9Y2I8-2	WDR37	-0.232	WD repeat domain 37
Q15061	WDR43	0.171	WD repeat domain 43
Q8TAF3-1	WDR48	-0.105	WD repeat domain 48
P61964	WDR5	0.177	WD repeat domain 5
Q9NW82	WDR70	-0.257	WD repeat domain 70
Q8IWA0	WDR75	0.138	WD repeat domain 75
Q9BQA1	WDR77	-0.148	WD repeat domain 77
Q562E7	WDR81	-0.099	WD repeat domain 81
A4D1P6	WDR91	-0.205	WD repeat domain 91
Q8N9V3	WDSUB1	-0.355	WD repeat, sterile alpha motif and U-box domain containing 1
O76024	WFS1	-0.14	wolframin ER transmembrane glycoprotein
Q9Y3S1	WNK2	-1.031	WNK lysine deficient protein kinase 2
Q9BUR4	WRAP53	-0.155	WD repeat containing antisense to TP53
Q15007	WTAP	0.275	WT1 associated protein
O00308	WWP2	-0.601	WW domain containing E3 ubiquitin protein ligase 2
Q9HCS7	XAB2	0.195	XPA binding protein 2
P98170	XIAP	-0.504	X-linked inhibitor of apoptosis
Q01831	XPC	0.374	XPC complex subunit, DNA damage recognition and repair factor
Q9NQW7-3	XPNPEP1	-0.13	X-prolyl aminopeptidase 1
O14980	XPO1	-0.17	exportin 1
Q9C0E2	XPO4	-0.439	exportin 4
Q9HAV4	XPO5	-0.192	exportin 5
Q9UIA9	XPO7	-0.175	exportin 7
O43592	XPOT	-0.234	exportin for tRNA
Q13426	XRCC4	-0.371	X-ray repair cross complementing 4
P13010	XRCC5	-0.089	X-ray repair cross complementing 5
O75191	XYLB	-0.322	xylulokinase
P46937-9	YAP1	-0.142	Yes associated protein 1
P54577	YARS1	-0.275	tyrosyl-tRNA synthetase 1
Q9Y2Z4	YARS2	0.392	tyrosyl-tRNA synthetase 2
P67809	YBX1	-0.557	Y-box binding protein 1
P16989	YBX3	-0.325	Y-box binding protein 3
O95619	YEATS4	-0.182	YEATS domain containing 4
P07947	YES1	0.139	YES proto-oncogene 1, Src family tyrosine kinase
Q5BJH7	YIF1B	0.254	Yip1 interacting factor homolog B, membrane trafficking protein
Q9BW85	YJU2	-0.142	YJU2 splicing factor homolog
O15498	YKT6	0.343	YKT6 v-SNARE homolog
Q96TA2-1	YME1L1	0.275	YME1 like 1 ATPase

Q86U90	YRDC	0.34	yrdC N6-threonylcarbamoyltransferase domain containing
Q96MU7-1	YTHDC1	0.237	YTH domain containing 1
Q9H6S0	YTHDC2	-0.199	YTH domain containing 2
Q9Y5A9	YTHDF2	-0.343	YTH N6-methyladenosine RNA binding protein 2
P62258	YWHAE	-0.284	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein epsilon
P25490	YY1	0.272	YY1 transcription factor
Q8N4Q0	ZADH2	0.298	zinc binding alcohol dehydrogenase domain containing 2
O96006	ZBED1	-0.527	zinc finger BED-type containing 1
O95625	ZBTB11	0.427	zinc finger and BTB domain containing 11
O43829	ZBTB14	-0.397	zinc finger and BTB domain containing 14
Q96GY0	ZC2HC1A	0.335	zinc finger C2HC-type containing 1A
O75152	ZC3H11A	0.428	zinc finger CCCH-type containing 11A
Q8WU90	ZC3H15	-0.339	zinc finger CCCH-type containing 15
Q86VM9	ZC3H18	0.095	zinc finger CCCH-type containing 18
Q7Z2W4	ZC3HAV1	0.318	zinc finger CCCH-type containing, antiviral 1
Q86WB0	ZC3HC1	-0.309	zinc finger C3HC-type containing 1
Q9C0B9	ZCCHC2	-0.253	zinc finger CCHC-type containing 2
Q9C0B5	ZDHHC5	0.159	zinc finger DHHC-type containing 5
Q15911-1	ZFHX3	-0.343	zinc finger homeobox 3
Q07352	ZFP36L1	0.778	ZFP36 ring finger protein like 1
Q96KR1	ZFR	-0.097	zinc finger RNA binding protein
Q8N5A5	ZGPAT	0.278	zinc finger CCCH-type and G-patch domain containing
Q9Y6X8	ZHX2	-0.238	zinc fingers and homeoboxes 2
P17029	ZKSCAN1	0.322	zinc finger with KRAB and SCAN domains 1
O75844	ZMPSTE24	0.205	zinc metallopeptidase STE24
Q14202	ZMYM3	-0.416	zinc finger MYM-type containing 3
O75362	ZNF217	0.086	zinc finger protein 217
P17028-1	ZNF24	0.241	zinc finger protein 24
Q8ND82	ZNF280C	0.335	zinc finger protein 280C
Q9Y2X9	ZNF281	0.244	zinc finger protein 281
Q5BKZ1	ZNF326	0.255	zinc finger protein 326
Q9Y3S2	ZNF330	0.398	zinc finger protein 330
Q8TF68-2	ZNF384	0.308	zinc finger protein 384
Q92610	ZNF592	0.133	zinc finger protein 592
Q86UK7	ZNF598	-0.178	zinc finger protein 598
Q969S3	ZNF622	0.48	zinc finger protein 622
Q14966	ZNF638	0.24	zinc finger protein 638
Q9H582	ZNF644	-0.223	zinc finger protein 644
Q8N1G0	ZNF687	0.346	zinc finger protein 687
Q2TB10	ZNF800	0.972	zinc finger protein 800
Q9P2E3	ZNFX1	0.337	zinc finger NFX1-type containing 1
O75312	ZPR1	-0.172	ZPR1 zinc finger
O95218-1	ZRANB2	-0.364	zinc finger RANBP2-type containing 2
Q9H900-1	ZWILCH	-0.19	zwilch kinetochore protein
Q9C0D3	ZYG11B	-0.153	zyg-11 family member B, cell cycle regulator
O43149	ZZEF1	-0.338	zinc finger ZZ-type and EF-hand domain containing 1
F8W031		0.189	

H0YIV9		-0.188	
P00761		0.493	
P04908		1.037	
P30042		0.233	
P62158		-0.362	
P62805		0.789	
P69905		1.653	
P84243		0.835	
Q15269		0.233	
Q16637		0.289	
Q6FI13		0.768	
Q6NSW5		-0.474	
Q96JG8-4		0.189	
Q9BV94-1		-0.396	